Full wwPDB EM Validation Report ⓘ

Dec 9, 2025 – 01:05 AM EST

PDB ID	:	9YA0 / pdb_00009ya0
EMDB ID	:	EMD-72716
Title	:	Cryo-EM structure of pre-conoid ring 2 (PCR P2 ring)from Toxoplasma gondii
Authors	:	Zeng, J.; Zhang, R.
Deposited on	:	2025-09-15
Resolution	:	3.54 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

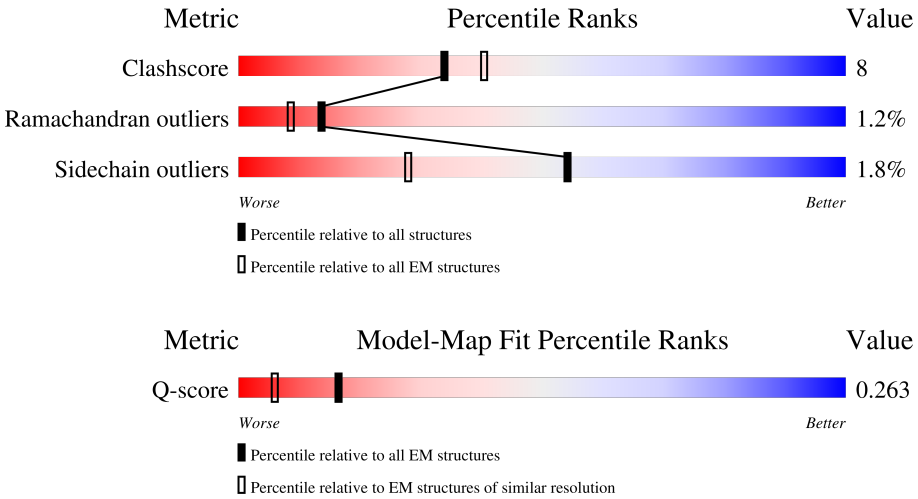
EMDB validation analysis	:	0.0.1.dev129
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.47

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.54 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



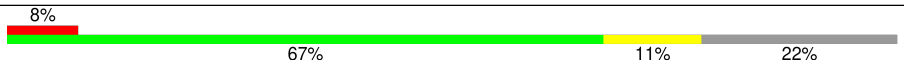
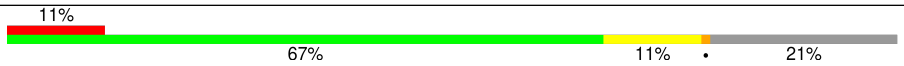
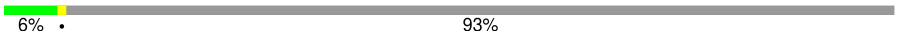
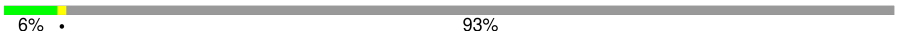
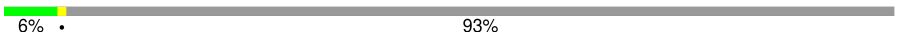
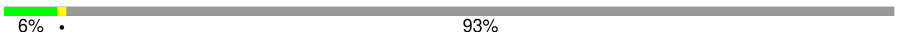
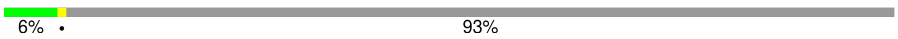
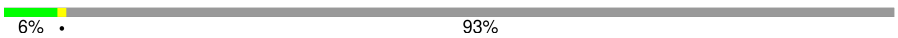
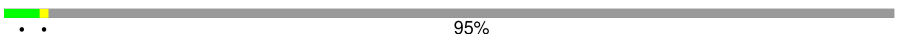
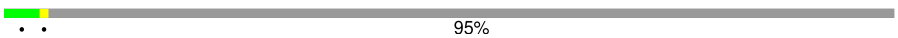
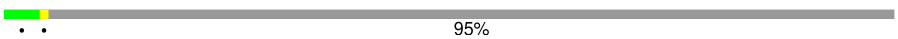
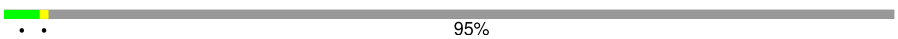
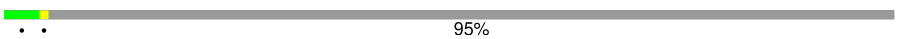
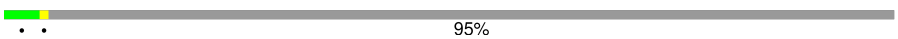
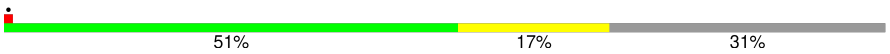
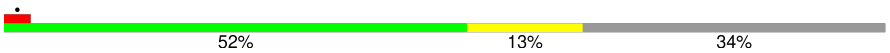
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	12891 (3.04 - 4.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1073	64% 12% 23%
1	AD	1073	70% 10% 19%
1	AE	1073	64% 13% 23%
1	AH	1073	70% 10% 19%

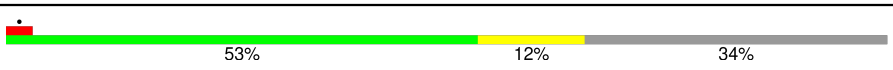
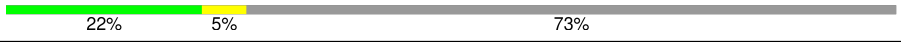
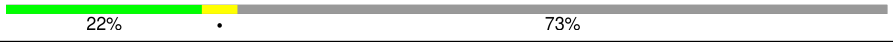
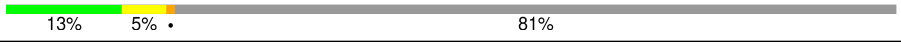
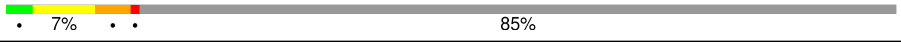
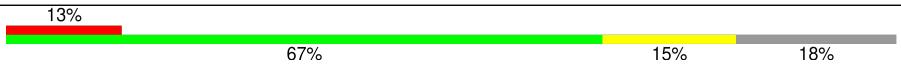
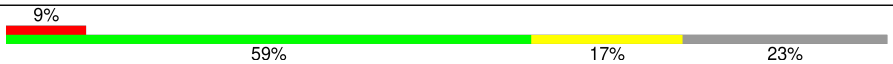
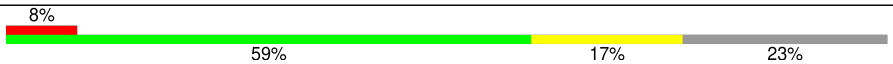
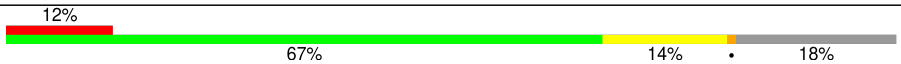
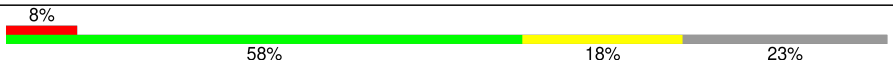
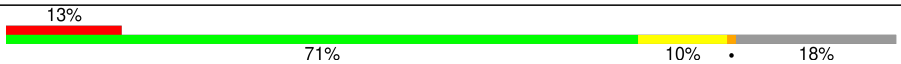
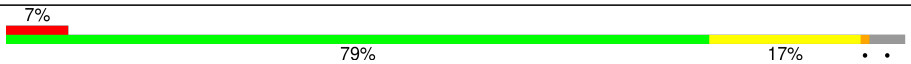
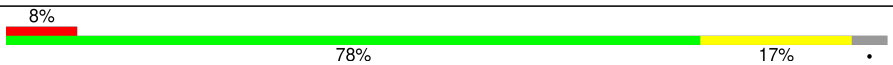
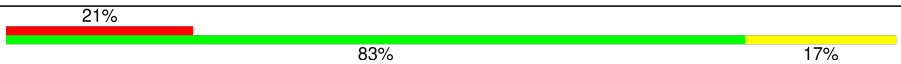
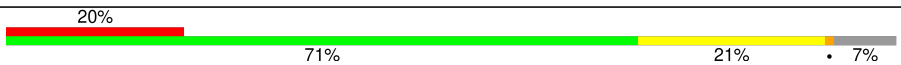
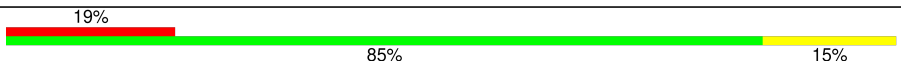
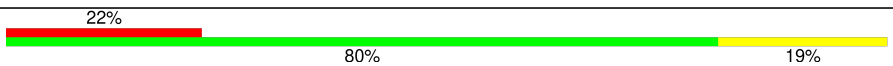
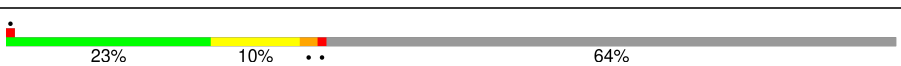
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	AI	1073	
1	AL	1073	
2	AB	603	
2	AC	603	
2	AF	603	
2	AG	603	
2	AJ	603	
2	AK	603	
3	BA	5051	
3	BB	5051	
3	BC	5051	
3	CA	5051	
3	CB	5051	
3	CC	5051	
3	CE	5051	
3	CF	5051	
3	CG	5051	
3	CI	5051	
3	CJ	5051	
3	CL	5051	
4	DA	505	
4	DB	505	
4	DC	505	
4	DD	505	
4	DE	505	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	DF	505	
5	EA	4956	
5	EB	4956	
5	EC	4956	
6	FA	2777	
6	FB	2777	
6	FC	2777	
6	FD	2777	
6	FE	2777	
6	FF	2777	
7	GA	1019	
7	GC	1019	
7	GE	1019	
7	GG	1019	
7	GI	1019	
7	GK	1019	
8	GB	791	
8	GD	791	
8	GF	791	
8	GH	791	
8	GJ	791	
8	GL	791	
9	HA	1192	
9	HB	1192	
9	HC	1192	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	HD	1192	5% 5% 89%
10	IA	1599	61% 11% 28%
10	IB	1599	59% 13% 28%
10	IC	1599	60% 12% 28%
11	JA	2316	55% 14% 31%
11	JB	2316	6% 56% 12% 31%
11	JC	2316	54% 14% 31%
12	KA	728	45% 18% 36%
12	KB	728	49% 14% 36%
12	KC	728	8% 44% 17% 36%
12	KE	728	19% 48% 13% 39%
12	KF	728	15% 49% 13% 39%
12	KG	728	16% 51% 11% 39%
13	LA	1322	12% 86%
13	LB	1322	13% 86%
13	LC	1322	12% 88%
13	LD	1322	11% 88%
13	LE	1322	9% 89%
13	LF	1322	10% 89%
13	LG	1322	96%
13	LH	1322	96%
13	LI	1322	11% 86%
13	LJ	1322	11% 86%
13	LK	1322	11% 88%
13	LL	1322	11% 88%

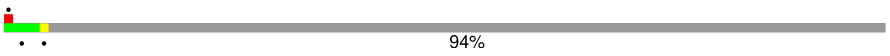
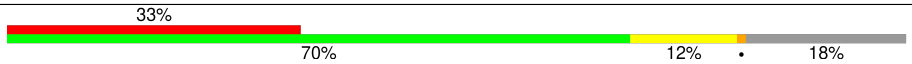
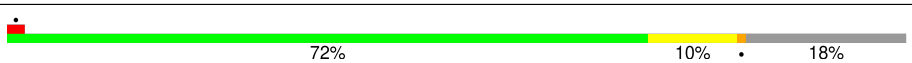
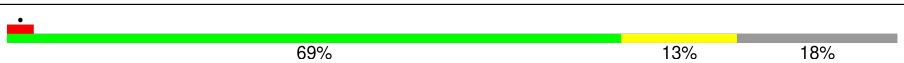
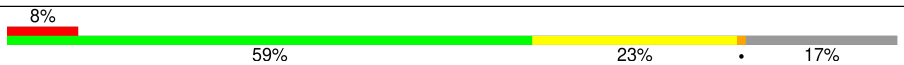
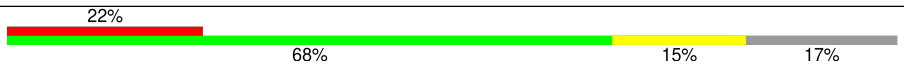
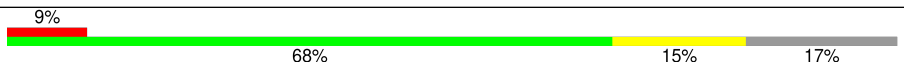
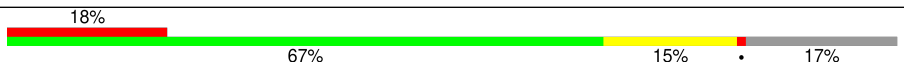
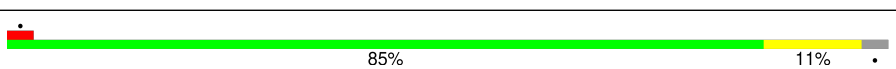
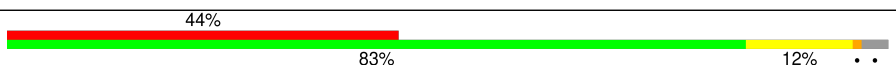
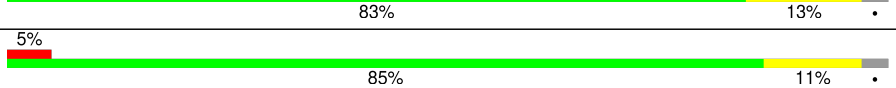
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
13	LM	1322	7% 92%
13	LN	1322	7% 92%
13	LO	1322	7% 92%
13	LP	1322	7% 92%
14	MA	2736	95%
14	MB	2736	96%
14	MC	2736	97%
14	MD	2736	98%
14	ME	2736	95%
14	MF	2736	96%
14	MG	2736	97%
14	MH	2736	98%
14	MI	2736	95%
14	MJ	2736	96%
14	MK	2736	97%
14	ML	2736	98%
15	NA	2484	26% 10% 64%
15	NB	2484	24% 27% 9% 64%
15	NC	2484	25% 10% 64%
15	ND	2484	20% 28% 8% 64%
16	OA	2333	16% 81%
16	OB	2333	16% 81%
16	OC	2333	16% 81%
17	PA	1822	94%
17	PB	1822	94%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
17	PC	1822	
18	QA	172	
18	QB	172	
18	QC	172	
18	QD	172	
19	RA	179	
19	RB	179	
19	RC	179	
19	RD	179	
20	SA	149	
20	SB	149	
20	SC	149	
20	SD	149	

2 Entry composition (i)

There are 20 unique types of molecules in this entry. The entry contains 415078 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PCR5, TGME49_242320.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AD	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		
1	AE	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AH	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		
1	AI	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AL	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		

- Molecule 2 is a protein called PCR4, TGME49_201220.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	473	Total	C	N	O	S	0	0
			3821	2396	699	696	30		
2	AC	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		
2	AF	473	Total	C	N	O	S	0	0
			3821	2396	699	696	30		
2	AG	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		
2	AJ	473	Total	C	N	O	S	0	0
			3815	2393	696	696	30		
2	AK	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		

- Molecule 3 is a protein called Formin 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BB	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		
3	BC	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		
3	CA	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CB	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CC	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CE	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CF	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CG	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CI	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		
3	CJ	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		
3	CL	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		

- Molecule 4 is a protein called PCR11, TGME49_209490.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DA	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DB	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DC	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DD	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		
4	DE	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		
4	DF	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		

- Molecule 5 is a protein called CGP, TGME49_240380.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	EA	1349	Total	C	N	O	S	0	0
			10670	6808	1899	1905	58		
5	EB	1349	Total	C	N	O	S	0	0
			10670	6808	1899	1905	58		
5	EC	1349	Total	C	N	O	S	0	0
			10666	6805	1898	1905	58		

- Molecule 6 is a protein called FLM1, TGME49_271780.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	FA	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FB	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FC	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FD	423	Total	C	N	O	S	0	0
			3255	2086	573	580	16		
6	FE	423	Total	C	N	O	S	0	0
			3261	2089	576	580	16		
6	FF	413	Total	C	N	O	S	0	0
			3182	2038	561	567	16		

- Molecule 7 is a protein called Transport protein Sec24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	GA	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		
7	GC	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GE	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GG	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		
7	GI	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GK	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		

- Molecule 8 is a protein called Protein transport protein SEC23.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GB	758	Total	C	N	O	S	0	0
			5949	3791	1016	1101	41		
8	GD	758	Total	C	N	O	S	0	0
			5949	3791	1016	1101	41		
8	GF	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		
8	GH	738	Total	C	N	O	S	0	0
			5781	3687	984	1070	40		
8	GJ	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		
8	GL	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		

- Molecule 9 is a protein called FLM2, TGME49_285990.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	HA	432	Total	C	N	O	S	0	0
			3361	2105	589	657	10		
9	HB	432	Total	C	N	O	S	0	0
			3361	2105	589	657	10		
9	HC	296	Total	C	N	O	S	0	0
			2288	1435	403	444	6		
9	HD	136	Total	C	N	O	S	0	0
			1073	670	186	213	4		

- Molecule 10 is a protein called PCR12, TGME49_292170.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	IA	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		
10	IB	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		
10	IC	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		

- Molecule 11 is a protein called PCR10, TGME49_298010.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	JA	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		
11	JB	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
11	JC	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	2314	VAL	-	expression tag	UNP S8FEI7
JA	2315	SER	-	expression tag	UNP S8FEI7
JA	2316	SER	-	expression tag	UNP S8FEI7
JB	2314	VAL	-	expression tag	UNP S8FEI7
JB	2315	SER	-	expression tag	UNP S8FEI7
JB	2316	SER	-	expression tag	UNP S8FEI7
JC	2314	VAL	-	expression tag	UNP S8FEI7
JC	2315	SER	-	expression tag	UNP S8FEI7
JC	2316	SER	-	expression tag	UNP S8FEI7

- Molecule 12 is a protein called PCR14, TGME49_311880.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	KA	464	Total	C	N	O	S	0	0
			3674	2356	645	653	20		
12	KB	464	Total	C	N	O	S	0	0
			3674	2356	645	653	20		
12	KC	464	Total	C	N	O	S	0	0
			3668	2353	642	653	20		
12	KE	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		
12	KF	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		
12	KG	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		

- Molecule 13 is a protein called ICAP16, TGME49_202120.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LA	190	Total	C	N	O	S	0	0
			1516	925	286	299	6		
13	LB	191	Total	C	N	O	S	0	0
			1529	934	289	300	6		
13	LC	162	Total	C	N	O	S	0	0
			1312	802	245	259	6		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
13	LD	161	Total C N O S 1304 801 240 257 6	0	0
13	LE	149	Total C N O S 1190 727 227 231 5	0	0
13	LF	150	Total C N O S 1198 732 227 233 6	0	0
13	LG	57	Total C N O S 461 287 83 88 3	0	0
13	LH	55	Total C N O S 448 280 80 85 3	0	0
13	LI	190	Total C N O S 1516 925 286 299 6	0	0
13	LJ	191	Total C N O S 1529 934 289 300 6	0	0
13	LK	163	Total C N O S 1320 808 246 260 6	0	0
13	LL	161	Total C N O S 1304 801 240 257 6	0	0
13	LM	106	Total C N O S 859 521 163 172 3	0	0
13	LN	106	Total C N O S 856 521 160 172 3	0	0
13	LO	105	Total C N O S 841 508 159 171 3	0	0
13	LP	110	Total C N O S 882 535 167 177 3	0	0

- Molecule 14 is a protein called PCR12, TGME49_219070.

Mol	Chain	Residues	Atoms	AltConf	Trace
14	MA	142	Total C N O S 1132 694 210 222 6	0	0
14	MB	120	Total C N O S 976 594 185 192 5	0	0
14	MC	75	Total C N O 594 365 114 115	0	0
14	MD	65	Total C N O 521 319 103 99	0	0
14	ME	142	Total C N O S 1132 694 210 222 6	0	0
14	MF	120	Total C N O S 976 594 185 192 5	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
14	MG	75	Total C N O 594 365 114 115	0	0
14	MH	65	Total C N O 521 319 103 99	0	0
14	MI	142	Total C N O S 1132 694 210 222 6	0	0
14	MJ	120	Total C N O S 976 594 185 192 5	0	0
14	MK	75	Total C N O 594 365 114 115	0	0
14	ML	65	Total C N O 521 319 103 99	0	0

There are 204 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MA	999	GLU	-	insertion	UNP S8EN17
MA	1000	LYS	-	insertion	UNP S8EN17
MA	1001	SER	-	insertion	UNP S8EN17
MA	1002	GLY	-	insertion	UNP S8EN17
MA	1003	THR	-	insertion	UNP S8EN17
MA	1004	ALA	-	insertion	UNP S8EN17
MA	1005	ALA	-	insertion	UNP S8EN17
MA	1006	SER	-	insertion	UNP S8EN17
MA	1007	HIS	-	insertion	UNP S8EN17
MA	1008	ILE	-	insertion	UNP S8EN17
MA	1009	ASP	-	insertion	UNP S8EN17
MA	1010	GLU	-	insertion	UNP S8EN17
MA	1011	GLU	-	insertion	UNP S8EN17
MA	1012	ASP	-	insertion	UNP S8EN17
MA	1013	SER	-	insertion	UNP S8EN17
MA	1014	ARG	-	insertion	UNP S8EN17
MA	1015	SER	ALA	conflict	UNP S8EN17
MB	999	GLU	-	insertion	UNP S8EN17
MB	1000	LYS	-	insertion	UNP S8EN17
MB	1001	SER	-	insertion	UNP S8EN17
MB	1002	GLY	-	insertion	UNP S8EN17
MB	1003	THR	-	insertion	UNP S8EN17
MB	1004	ALA	-	insertion	UNP S8EN17
MB	1005	ALA	-	insertion	UNP S8EN17
MB	1006	SER	-	insertion	UNP S8EN17
MB	1007	HIS	-	insertion	UNP S8EN17
MB	1008	ILE	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
MB	1009	ASP	-	insertion	UNP S8EN17
MB	1010	GLU	-	insertion	UNP S8EN17
MB	1011	GLU	-	insertion	UNP S8EN17
MB	1012	ASP	-	insertion	UNP S8EN17
MB	1013	SER	-	insertion	UNP S8EN17
MB	1014	ARG	-	insertion	UNP S8EN17
MB	1015	SER	ALA	conflict	UNP S8EN17
MC	999	GLU	-	insertion	UNP S8EN17
MC	1000	LYS	-	insertion	UNP S8EN17
MC	1001	SER	-	insertion	UNP S8EN17
MC	1002	GLY	-	insertion	UNP S8EN17
MC	1003	THR	-	insertion	UNP S8EN17
MC	1004	ALA	-	insertion	UNP S8EN17
MC	1005	ALA	-	insertion	UNP S8EN17
MC	1006	SER	-	insertion	UNP S8EN17
MC	1007	HIS	-	insertion	UNP S8EN17
MC	1008	ILE	-	insertion	UNP S8EN17
MC	1009	ASP	-	insertion	UNP S8EN17
MC	1010	GLU	-	insertion	UNP S8EN17
MC	1011	GLU	-	insertion	UNP S8EN17
MC	1012	ASP	-	insertion	UNP S8EN17
MC	1013	SER	-	insertion	UNP S8EN17
MC	1014	ARG	-	insertion	UNP S8EN17
MC	1015	SER	ALA	conflict	UNP S8EN17
MD	999	GLU	-	insertion	UNP S8EN17
MD	1000	LYS	-	insertion	UNP S8EN17
MD	1001	SER	-	insertion	UNP S8EN17
MD	1002	GLY	-	insertion	UNP S8EN17
MD	1003	THR	-	insertion	UNP S8EN17
MD	1004	ALA	-	insertion	UNP S8EN17
MD	1005	ALA	-	insertion	UNP S8EN17
MD	1006	SER	-	insertion	UNP S8EN17
MD	1007	HIS	-	insertion	UNP S8EN17
MD	1008	ILE	-	insertion	UNP S8EN17
MD	1009	ASP	-	insertion	UNP S8EN17
MD	1010	GLU	-	insertion	UNP S8EN17
MD	1011	GLU	-	insertion	UNP S8EN17
MD	1012	ASP	-	insertion	UNP S8EN17
MD	1013	SER	-	insertion	UNP S8EN17
MD	1014	ARG	-	insertion	UNP S8EN17
MD	1015	SER	ALA	conflict	UNP S8EN17
ME	999	GLU	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
ME	1000	LYS	-	insertion	UNP S8EN17
ME	1001	SER	-	insertion	UNP S8EN17
ME	1002	GLY	-	insertion	UNP S8EN17
ME	1003	THR	-	insertion	UNP S8EN17
ME	1004	ALA	-	insertion	UNP S8EN17
ME	1005	ALA	-	insertion	UNP S8EN17
ME	1006	SER	-	insertion	UNP S8EN17
ME	1007	HIS	-	insertion	UNP S8EN17
ME	1008	ILE	-	insertion	UNP S8EN17
ME	1009	ASP	-	insertion	UNP S8EN17
ME	1010	GLU	-	insertion	UNP S8EN17
ME	1011	GLU	-	insertion	UNP S8EN17
ME	1012	ASP	-	insertion	UNP S8EN17
ME	1013	SER	-	insertion	UNP S8EN17
ME	1014	ARG	-	insertion	UNP S8EN17
ME	1015	SER	ALA	conflict	UNP S8EN17
MF	999	GLU	-	insertion	UNP S8EN17
MF	1000	LYS	-	insertion	UNP S8EN17
MF	1001	SER	-	insertion	UNP S8EN17
MF	1002	GLY	-	insertion	UNP S8EN17
MF	1003	THR	-	insertion	UNP S8EN17
MF	1004	ALA	-	insertion	UNP S8EN17
MF	1005	ALA	-	insertion	UNP S8EN17
MF	1006	SER	-	insertion	UNP S8EN17
MF	1007	HIS	-	insertion	UNP S8EN17
MF	1008	ILE	-	insertion	UNP S8EN17
MF	1009	ASP	-	insertion	UNP S8EN17
MF	1010	GLU	-	insertion	UNP S8EN17
MF	1011	GLU	-	insertion	UNP S8EN17
MF	1012	ASP	-	insertion	UNP S8EN17
MF	1013	SER	-	insertion	UNP S8EN17
MF	1014	ARG	-	insertion	UNP S8EN17
MF	1015	SER	ALA	conflict	UNP S8EN17
MG	999	GLU	-	insertion	UNP S8EN17
MG	1000	LYS	-	insertion	UNP S8EN17
MG	1001	SER	-	insertion	UNP S8EN17
MG	1002	GLY	-	insertion	UNP S8EN17
MG	1003	THR	-	insertion	UNP S8EN17
MG	1004	ALA	-	insertion	UNP S8EN17
MG	1005	ALA	-	insertion	UNP S8EN17
MG	1006	SER	-	insertion	UNP S8EN17
MG	1007	HIS	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
MG	1008	ILE	-	insertion	UNP S8EN17
MG	1009	ASP	-	insertion	UNP S8EN17
MG	1010	GLU	-	insertion	UNP S8EN17
MG	1011	GLU	-	insertion	UNP S8EN17
MG	1012	ASP	-	insertion	UNP S8EN17
MG	1013	SER	-	insertion	UNP S8EN17
MG	1014	ARG	-	insertion	UNP S8EN17
MG	1015	SER	ALA	conflict	UNP S8EN17
MH	999	GLU	-	insertion	UNP S8EN17
MH	1000	LYS	-	insertion	UNP S8EN17
MH	1001	SER	-	insertion	UNP S8EN17
MH	1002	GLY	-	insertion	UNP S8EN17
MH	1003	THR	-	insertion	UNP S8EN17
MH	1004	ALA	-	insertion	UNP S8EN17
MH	1005	ALA	-	insertion	UNP S8EN17
MH	1006	SER	-	insertion	UNP S8EN17
MH	1007	HIS	-	insertion	UNP S8EN17
MH	1008	ILE	-	insertion	UNP S8EN17
MH	1009	ASP	-	insertion	UNP S8EN17
MH	1010	GLU	-	insertion	UNP S8EN17
MH	1011	GLU	-	insertion	UNP S8EN17
MH	1012	ASP	-	insertion	UNP S8EN17
MH	1013	SER	-	insertion	UNP S8EN17
MH	1014	ARG	-	insertion	UNP S8EN17
MH	1015	SER	ALA	conflict	UNP S8EN17
MI	999	GLU	-	insertion	UNP S8EN17
MI	1000	LYS	-	insertion	UNP S8EN17
MI	1001	SER	-	insertion	UNP S8EN17
MI	1002	GLY	-	insertion	UNP S8EN17
MI	1003	THR	-	insertion	UNP S8EN17
MI	1004	ALA	-	insertion	UNP S8EN17
MI	1005	ALA	-	insertion	UNP S8EN17
MI	1006	SER	-	insertion	UNP S8EN17
MI	1007	HIS	-	insertion	UNP S8EN17
MI	1008	ILE	-	insertion	UNP S8EN17
MI	1009	ASP	-	insertion	UNP S8EN17
MI	1010	GLU	-	insertion	UNP S8EN17
MI	1011	GLU	-	insertion	UNP S8EN17
MI	1012	ASP	-	insertion	UNP S8EN17
MI	1013	SER	-	insertion	UNP S8EN17
MI	1014	ARG	-	insertion	UNP S8EN17
MI	1015	SER	ALA	conflict	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
MJ	999	GLU	-	insertion	UNP S8EN17
MJ	1000	LYS	-	insertion	UNP S8EN17
MJ	1001	SER	-	insertion	UNP S8EN17
MJ	1002	GLY	-	insertion	UNP S8EN17
MJ	1003	THR	-	insertion	UNP S8EN17
MJ	1004	ALA	-	insertion	UNP S8EN17
MJ	1005	ALA	-	insertion	UNP S8EN17
MJ	1006	SER	-	insertion	UNP S8EN17
MJ	1007	HIS	-	insertion	UNP S8EN17
MJ	1008	ILE	-	insertion	UNP S8EN17
MJ	1009	ASP	-	insertion	UNP S8EN17
MJ	1010	GLU	-	insertion	UNP S8EN17
MJ	1011	GLU	-	insertion	UNP S8EN17
MJ	1012	ASP	-	insertion	UNP S8EN17
MJ	1013	SER	-	insertion	UNP S8EN17
MJ	1014	ARG	-	insertion	UNP S8EN17
MJ	1015	SER	ALA	conflict	UNP S8EN17
MK	999	GLU	-	insertion	UNP S8EN17
MK	1000	LYS	-	insertion	UNP S8EN17
MK	1001	SER	-	insertion	UNP S8EN17
MK	1002	GLY	-	insertion	UNP S8EN17
MK	1003	THR	-	insertion	UNP S8EN17
MK	1004	ALA	-	insertion	UNP S8EN17
MK	1005	ALA	-	insertion	UNP S8EN17
MK	1006	SER	-	insertion	UNP S8EN17
MK	1007	HIS	-	insertion	UNP S8EN17
MK	1008	ILE	-	insertion	UNP S8EN17
MK	1009	ASP	-	insertion	UNP S8EN17
MK	1010	GLU	-	insertion	UNP S8EN17
MK	1011	GLU	-	insertion	UNP S8EN17
MK	1012	ASP	-	insertion	UNP S8EN17
MK	1013	SER	-	insertion	UNP S8EN17
MK	1014	ARG	-	insertion	UNP S8EN17
MK	1015	SER	ALA	conflict	UNP S8EN17
ML	999	GLU	-	insertion	UNP S8EN17
ML	1000	LYS	-	insertion	UNP S8EN17
ML	1001	SER	-	insertion	UNP S8EN17
ML	1002	GLY	-	insertion	UNP S8EN17
ML	1003	THR	-	insertion	UNP S8EN17
ML	1004	ALA	-	insertion	UNP S8EN17
ML	1005	ALA	-	insertion	UNP S8EN17
ML	1006	SER	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
ML	1007	HIS	-	insertion	UNP S8EN17
ML	1008	ILE	-	insertion	UNP S8EN17
ML	1009	ASP	-	insertion	UNP S8EN17
ML	1010	GLU	-	insertion	UNP S8EN17
ML	1011	GLU	-	insertion	UNP S8EN17
ML	1012	ASP	-	insertion	UNP S8EN17
ML	1013	SER	-	insertion	UNP S8EN17
ML	1014	ARG	-	insertion	UNP S8EN17
ML	1015	SER	ALA	conflict	UNP S8EN17

- Molecule 15 is a protein called myosin L, TGME49_291020.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	NA	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	NB	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	NC	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	ND	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		

- Molecule 16 is a protein called PCR13, TGME49_284620.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	OA	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		
16	OB	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		
16	OC	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		

- Molecule 17 is a protein called PCR15, TGME49_232560.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	PA	101	Total	C	N	O	S	0	0
			807	507	142	156	2		
17	PB	101	Total	C	N	O	S	0	0
			807	507	142	156	2		
17	PC	101	Total	C	N	O	S	0	0
			807	507	142	156	2		

- Molecule 18 is a protein called MLC4, TGME49_294390.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	QA	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QB	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QC	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QD	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		

- Molecule 19 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	RA	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RB	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RC	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RD	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		

- Molecule 20 is a protein called Calmodulin.

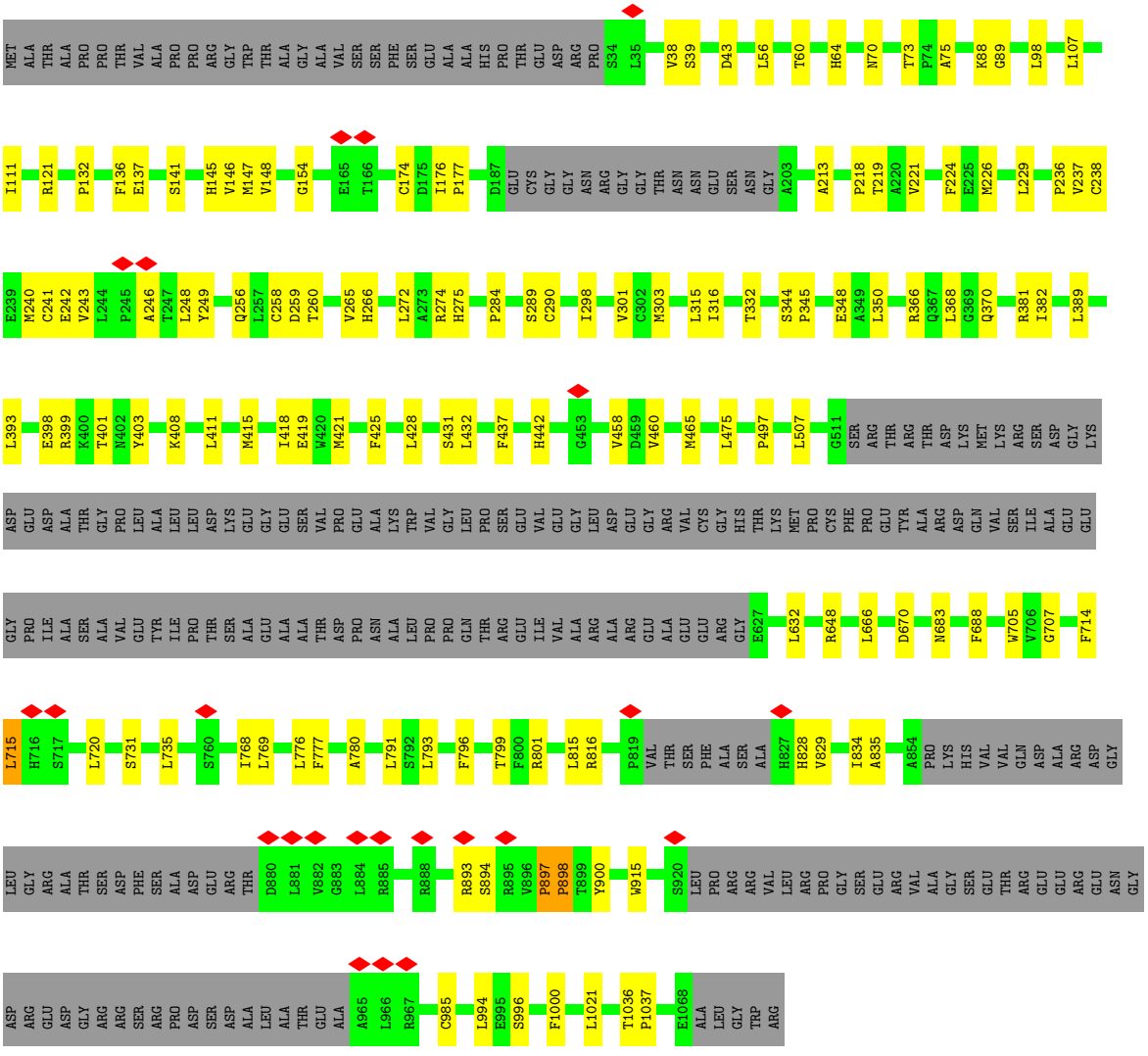
Mol	Chain	Residues	Atoms					AltConf	Trace
20	SA	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SB	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SC	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SD	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

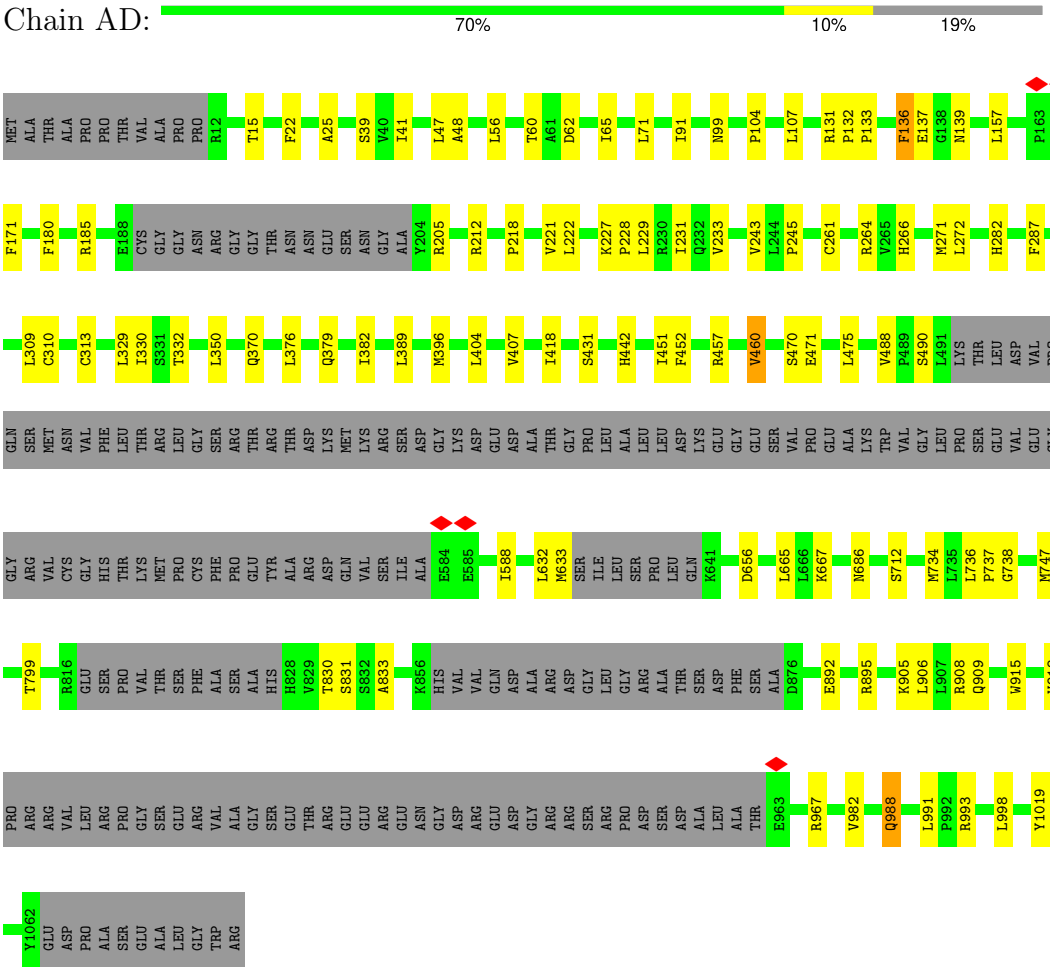
- Molecule 1: PCR5, TGME49_242320

Chain AA:



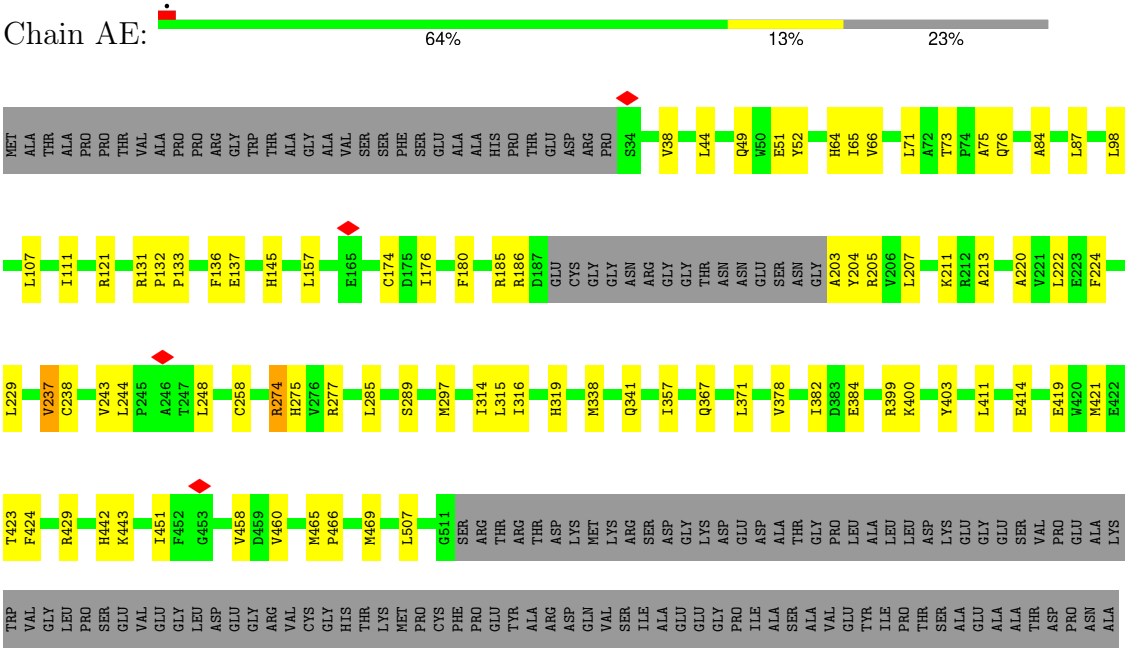
- Molecule 1: PCR5, TGME49_242320

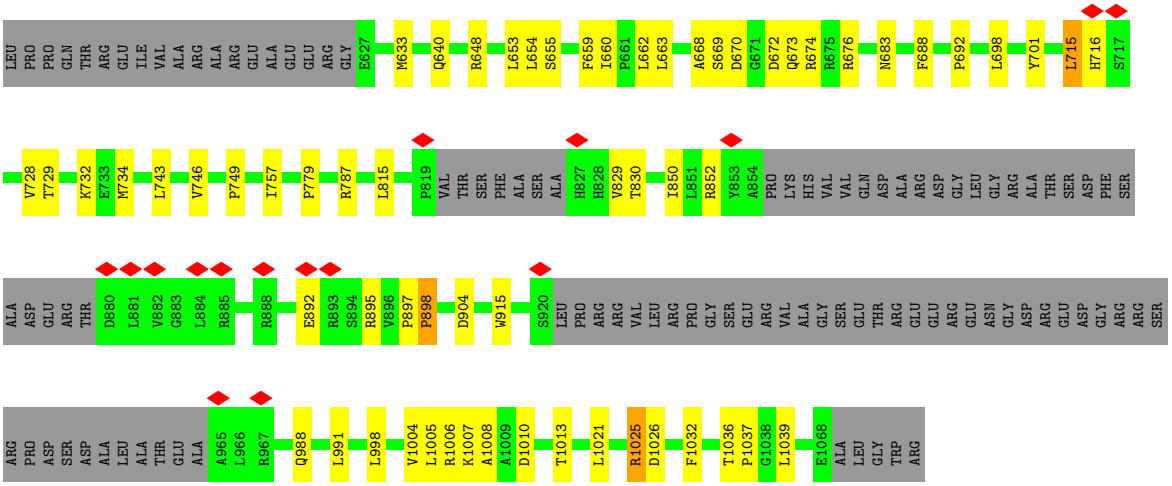
Chain AD:



• Molecule 1: PCR5, TGME49_242320

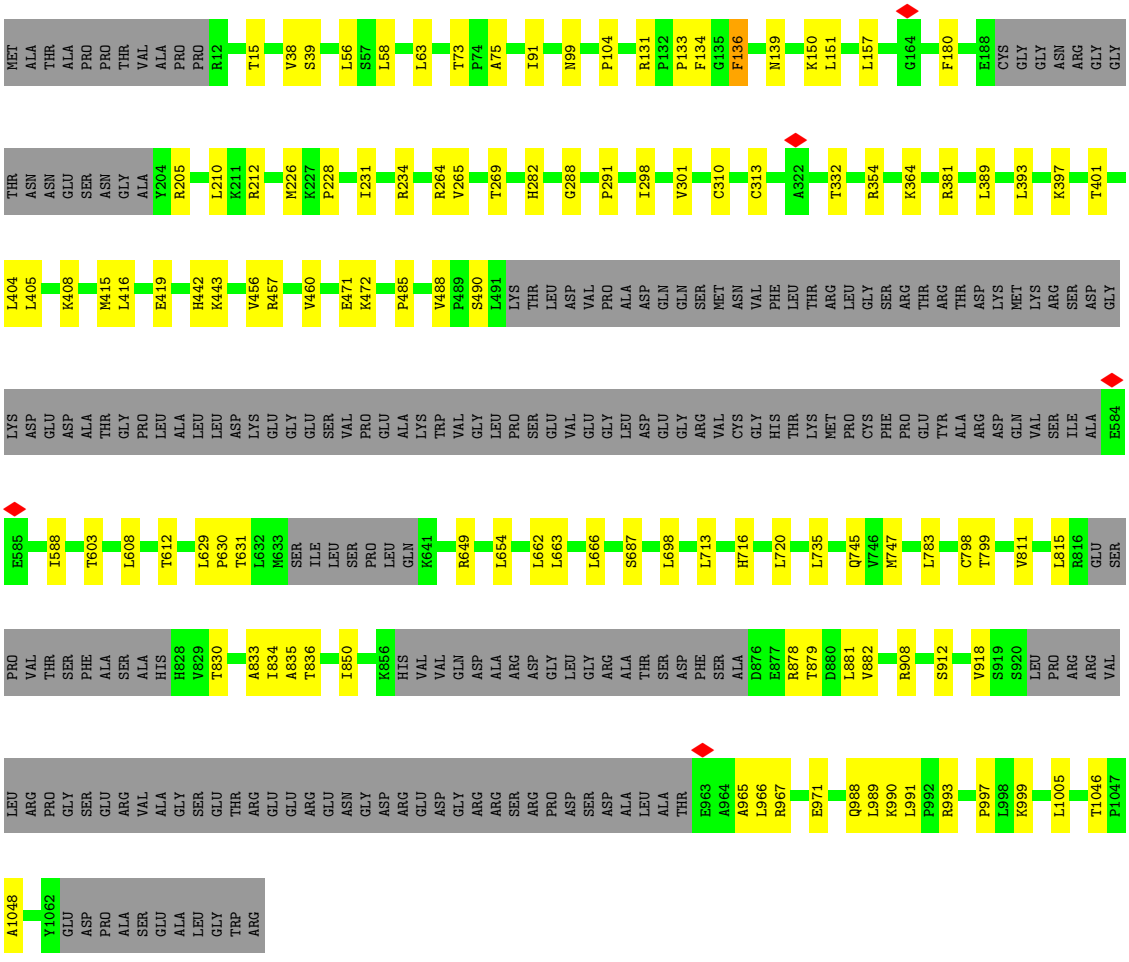
Chain AE:





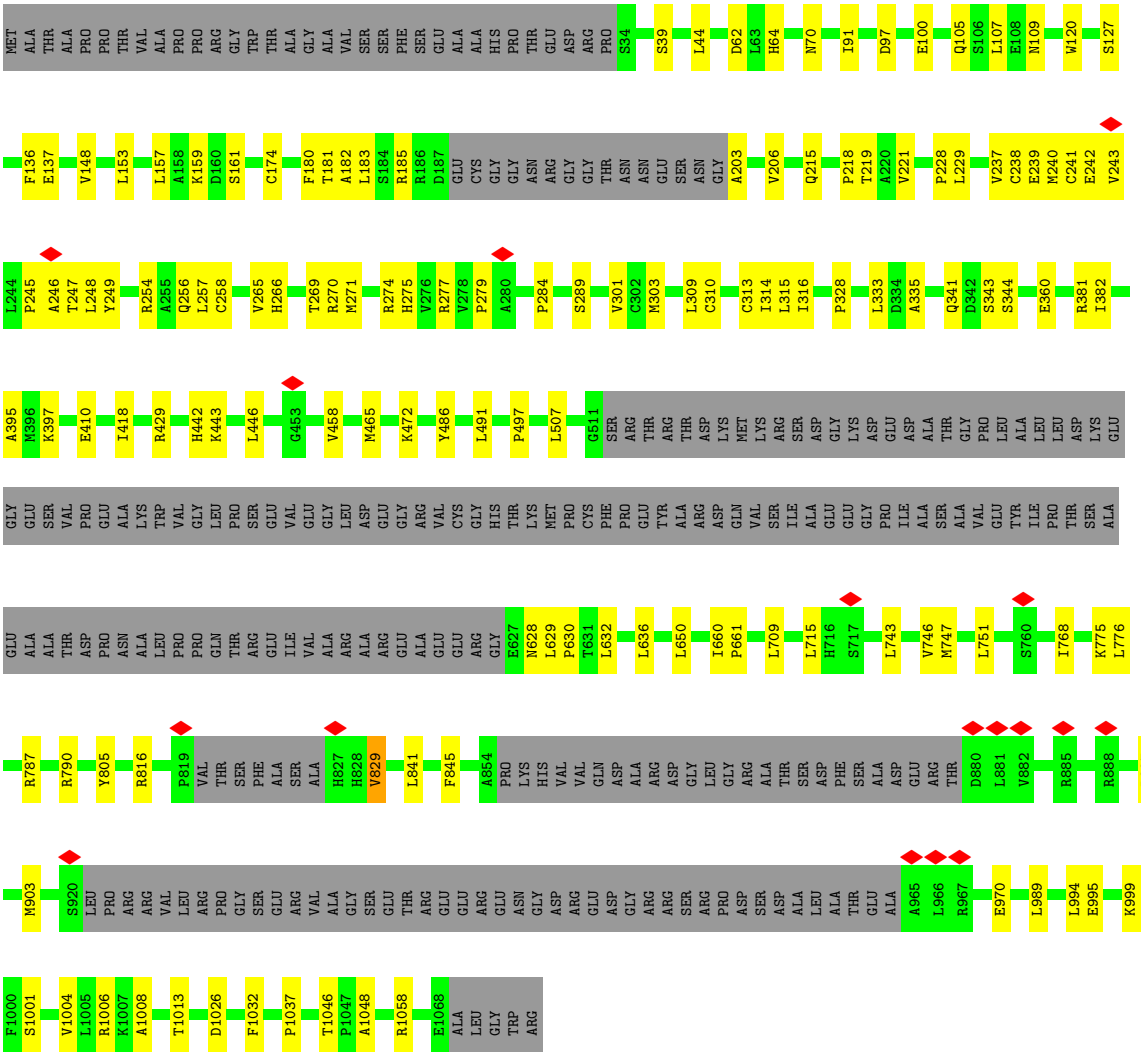
• Molecule 1: PCR5, TGME49_242320

Chain AH:



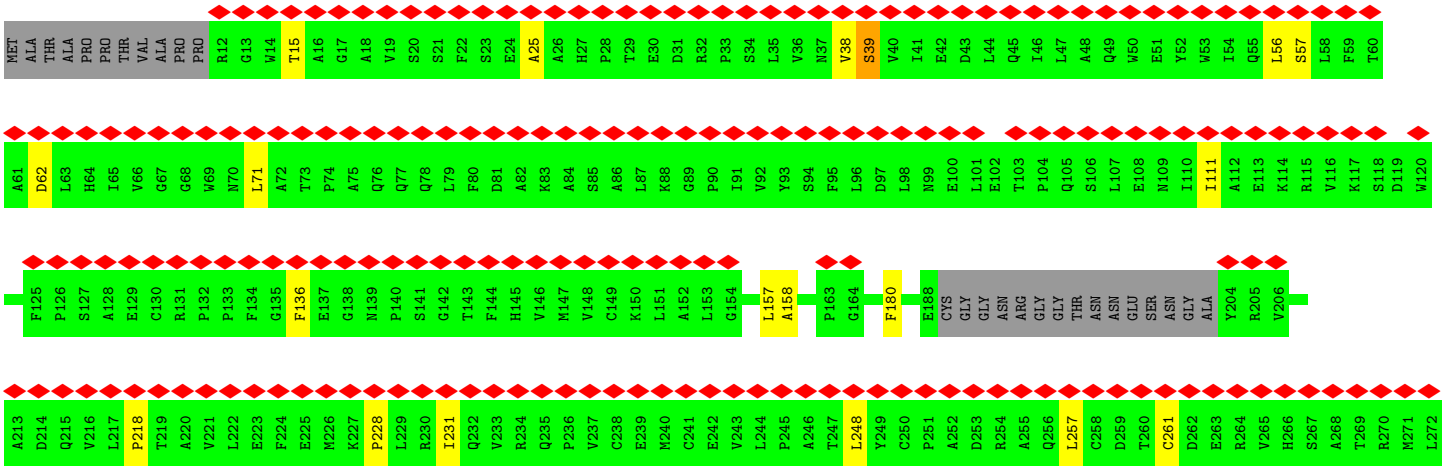
• Molecule 1: PCR5, TGME49_242320

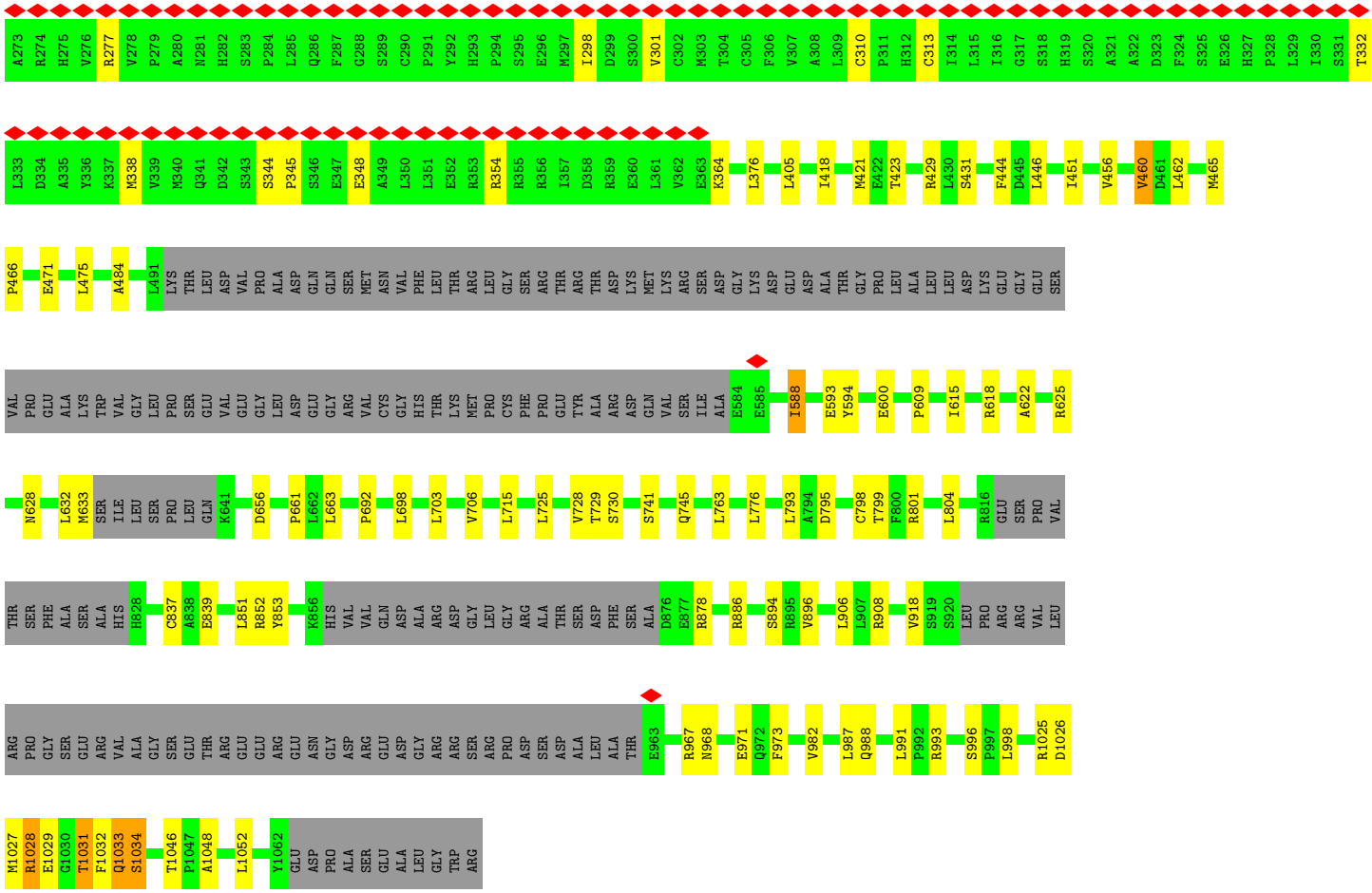
Chain AI:



• Molecule 1: PCR5, TGME49_242320

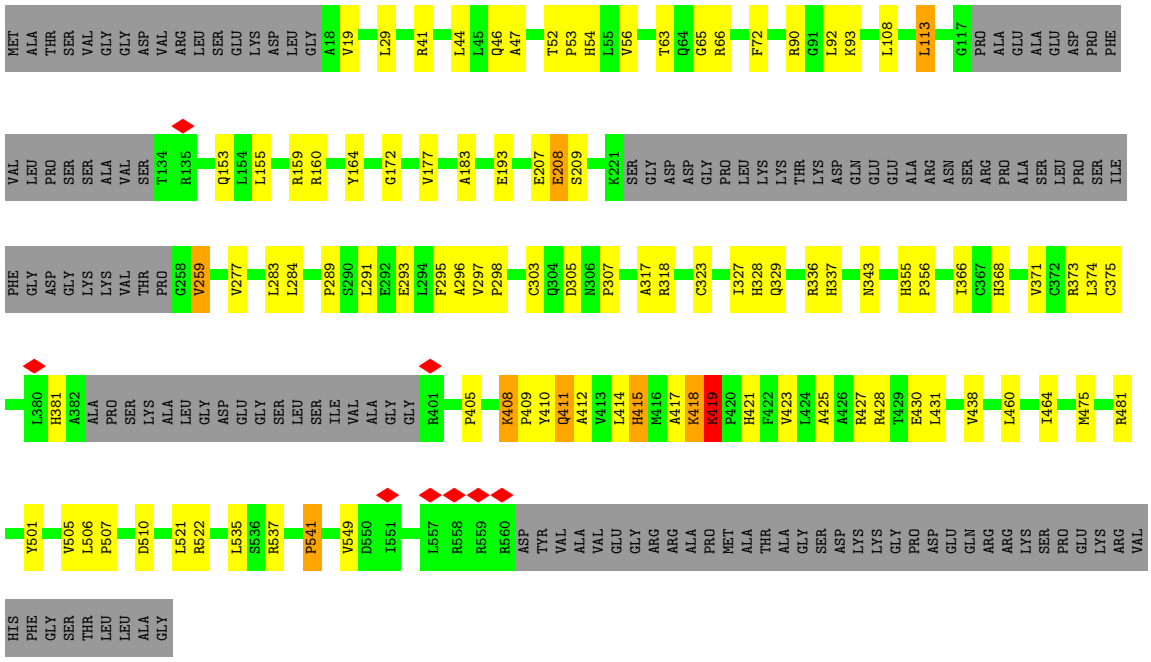
Chain AL:





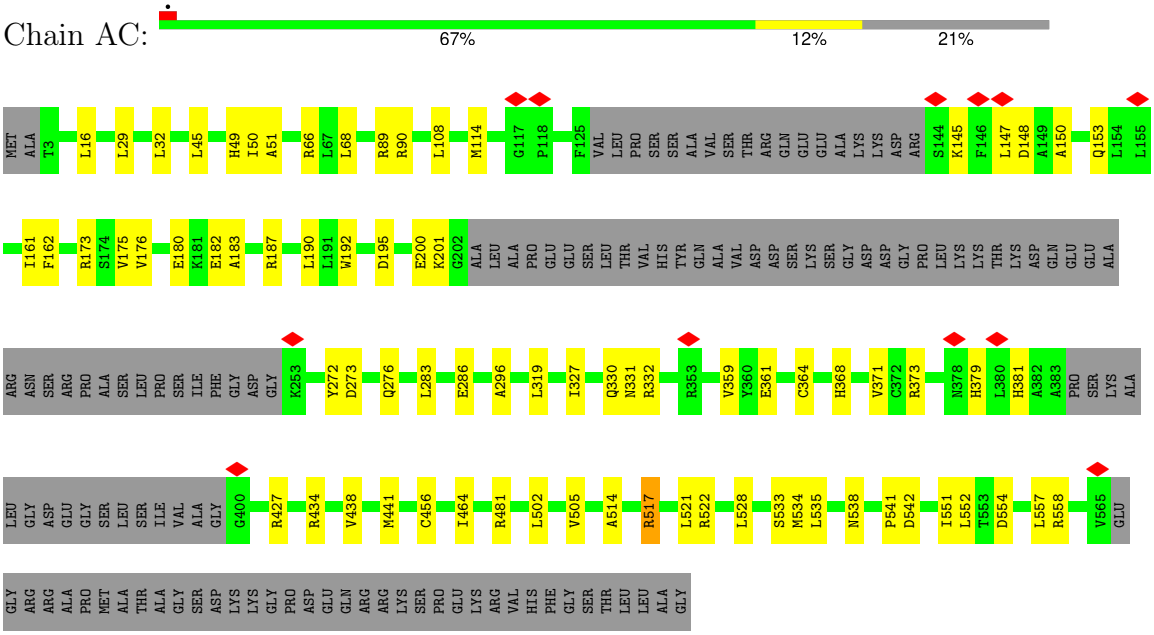
• Molecule 2: PCR4, TGME49_201220

Chain AB:



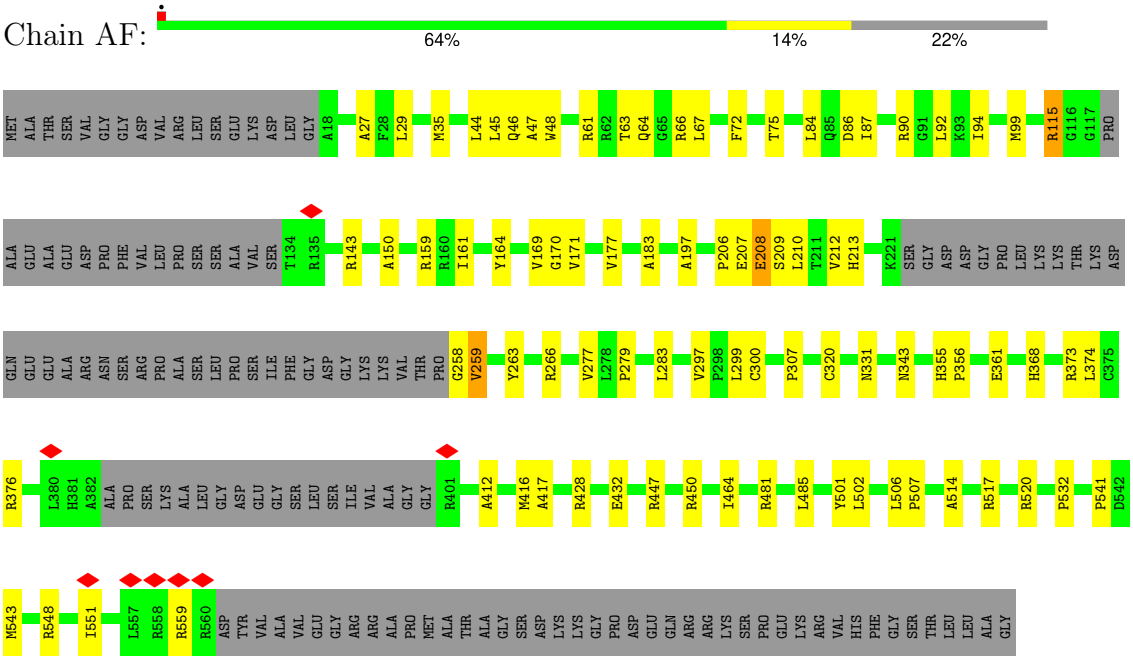
• Molecule 2: PCR4, TGME49_201220

Chain AC:



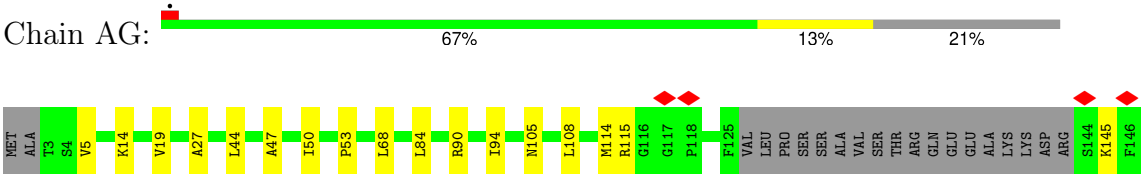
• Molecule 2: PCR4, TGME49_201220

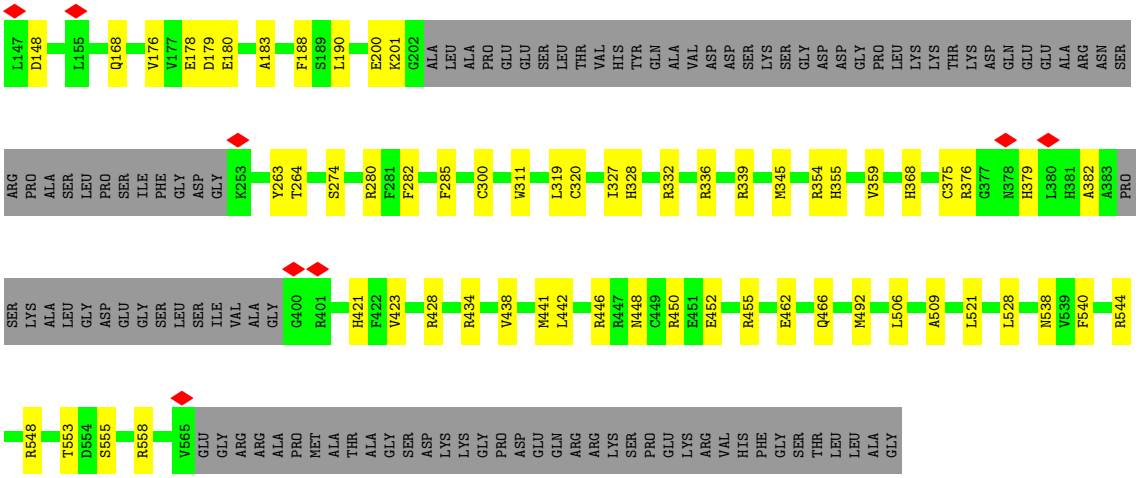
Chain AF:



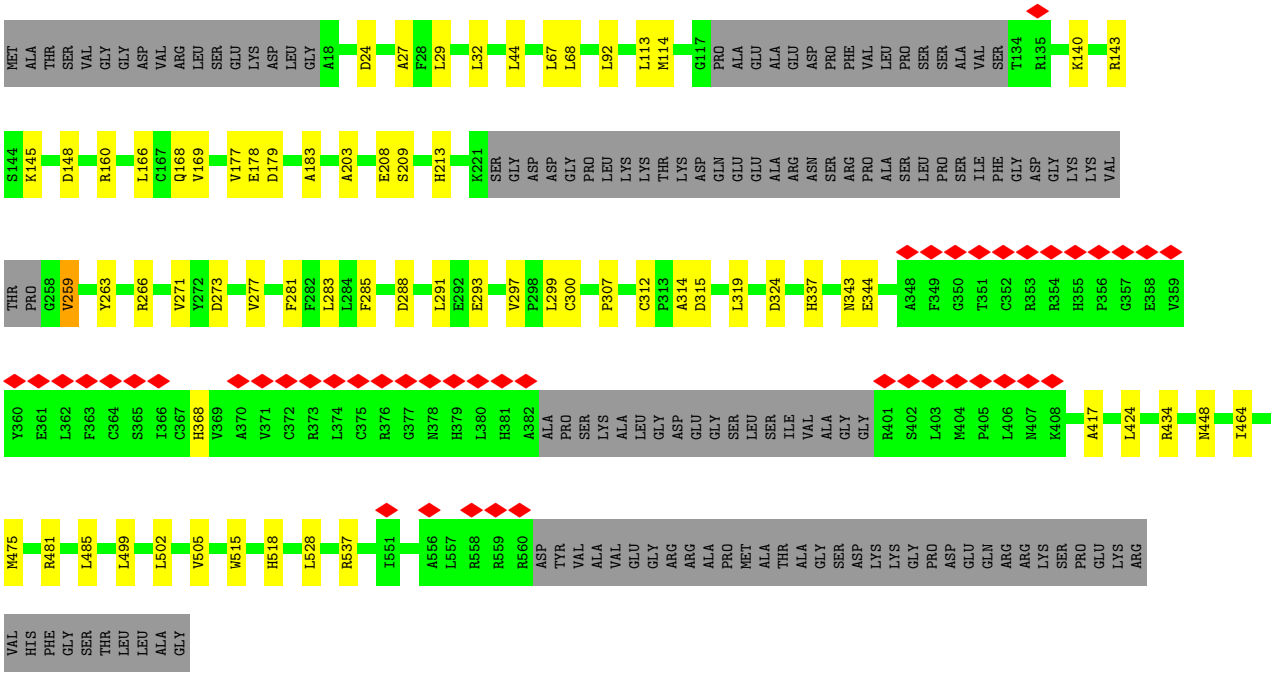
• Molecule 2: PCR4, TGME49_201220

Chain AG:

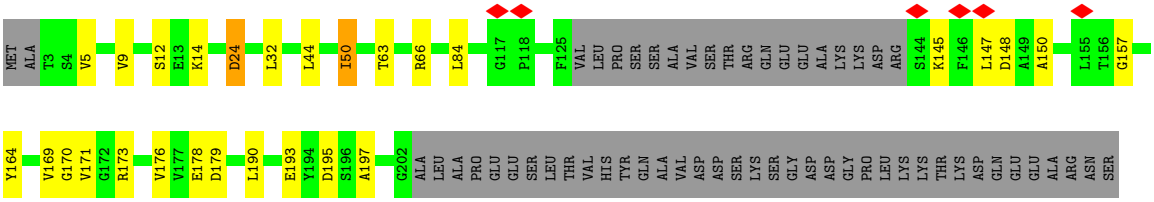


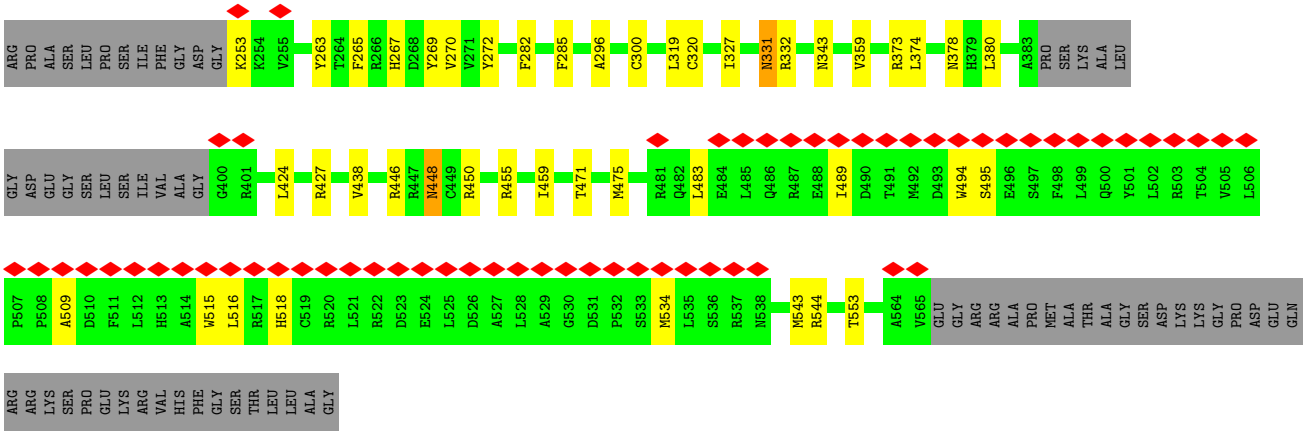


• Molecule 2: PCR4, TGME49_201220



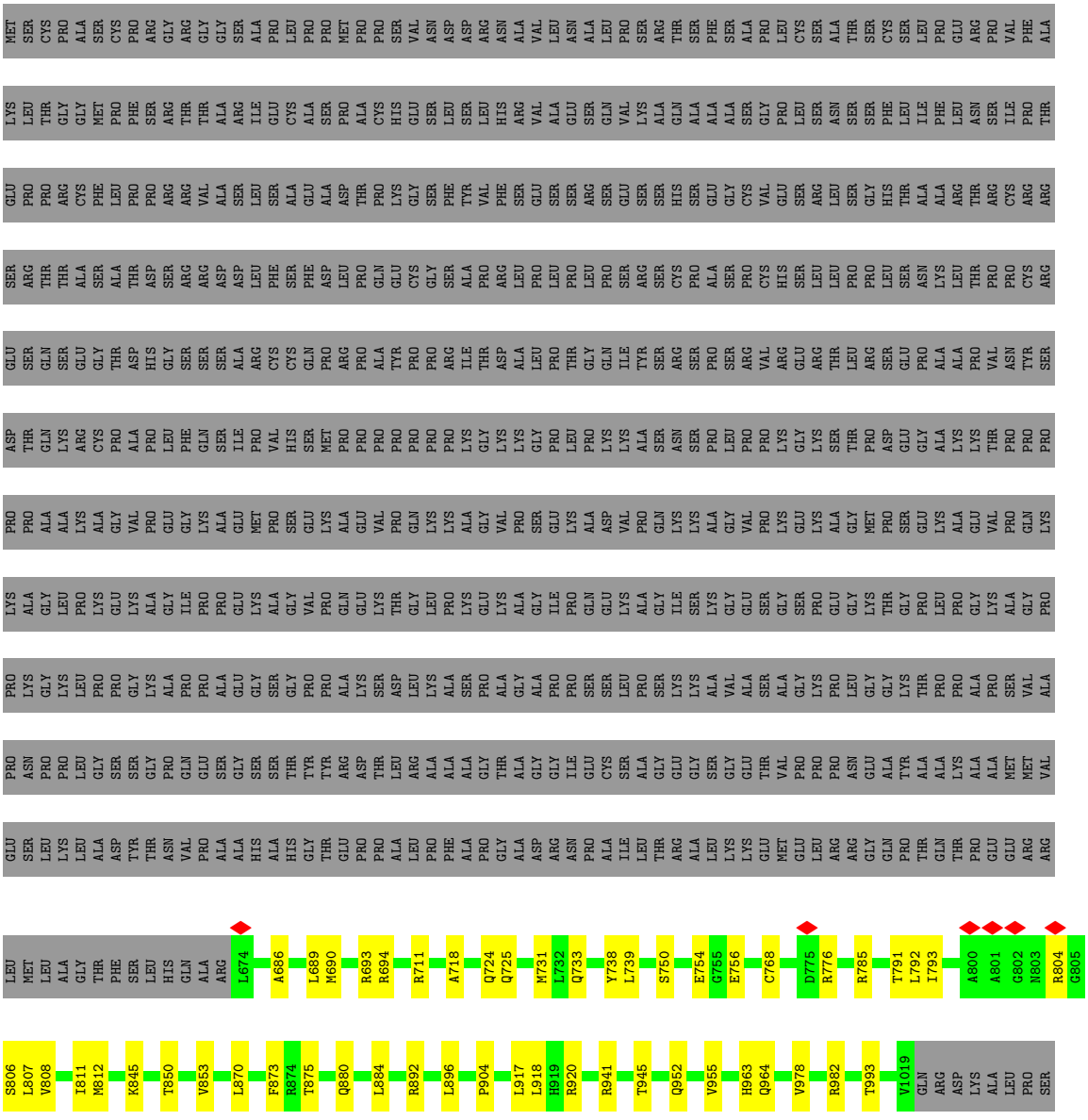
• Molecule 2: PCR4, TGME49_201220

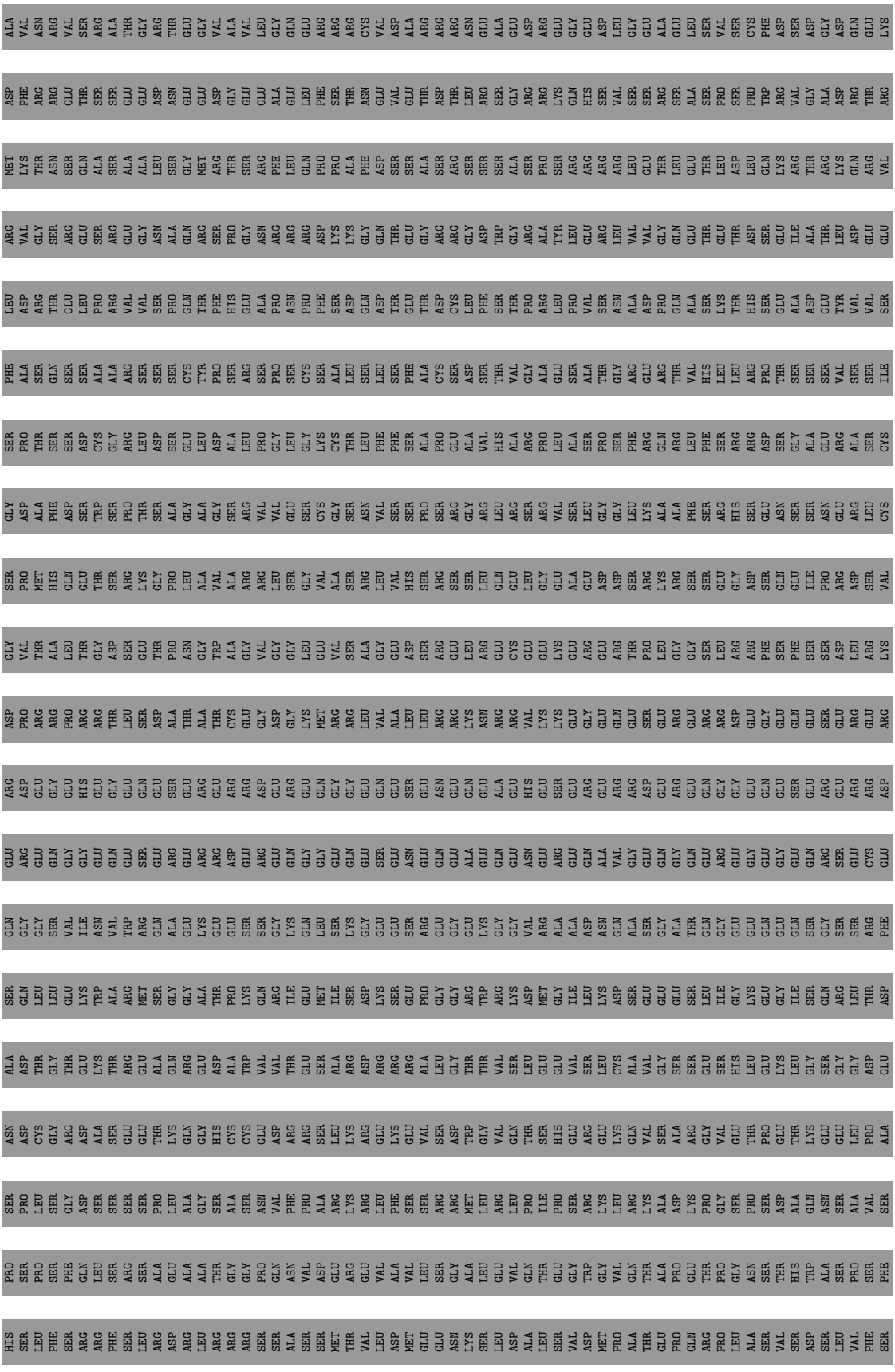




• Molecule 3: Formin 1

Chain BA: 6% 93%





GLY PRO LYS LYS LYS GLY GLU GLY GLY LEU LYS VAL GLY LYS LYS ASP GLU GLY LYS THR LYS ARG PHE PHE TRP ASP PRO ILE PHE GLU ASP GLU ILE PRO GLY THR ILE PHE MET LYS LYS PRO ASN MET VAL LEU LYS LEU GLN ASP VAL GLU GLU THR PHE ALA LYS VAL VAL ALA

LYS LYS LYS THR GLU SER LYS LYS PRO LYS ILE ILE GLN LEU LEU PRO ASP SER LYS ARG ALA TYR ASN MET SER ILE ALA LEU SER LYS PHE ASN ASN TYR SER TYR GLN GLN LEU ARG GLU ALA ILE ILE ASP LEU ASP PRO LYS ILE LEU ILE GLU ALA THR GLU THR LEU LEU

ASN PHE VAL PRO THR GLY GLU GLU ASN GLN VAL VAL LYS GLU TYR ILE ASN SER GLY GLY ASP LEU LYS LEU VAL ASP LYS PRO GLU LEU VAL PRO LEU MET LYS GLN ARG GLY GLY ALA LEU GLU ALA HIS ALA PHE ALA LEU ASN PHE ARG GLU ALA TYR SER ASP

ALA TYR THR PRO LEU GLU ASN MET ALA ASP ALA CYS ASP ALA ILE ASP ASP SER GLN ASN LEU LYS ILE VAL LEU PHE ALA ILE LEU GLU LEU GLY ASN ALA LEU ASN GLU GLY ASP PRO GLN ARG GLY GLY ALA ALA GLY PHE LYS PRO THR THR LEU ALA LYS GLY LEU GLN GLU ILE ARG

THR THR THR LYS PRO VAL ARG THR MET LEU GLN TYR ILE CYS ASP ILE ILE ILE TRP GLU GLN GLN GLN PRO THR ALA LEU ASN ILE TYR GLU GLU ASP LEU LYS ILE CYS ASP LYS ALA GLN ARG VAL ASP MET GLN GLY ILE GLU GLY ARG ILE SER ASN LEU LYS ALA GLY LEU THR LYS VAL LYS

ASN THR LEU GLU ALA ALA LYS LYS GLY ASN GLU SER THR GLY VAL MET GLY ASP ARG ASP PRO LEU ARG ASN ILE MET ASP GLU GLU ALA GLU PRO LYS ILE LYS GLN LEU ASP ASP PHE LEU VAL GLN VAL GLN ASN GLN PHE LEU GLU LYS GLN LEU GLU PRO GLN GLN ILE GLU LEU ILE GLU GLU ALA GLU GLY PHE LEU GLN THR CYS HIS TYR SER GLY TYR

PRO ASP LYS ASP VAL LYS LYS ILE LYS PRO ASP GLU LEU PHE LYS GLN VAL ALA GLY PHE ALA ARG GLN VAL ALA ASP ALA ILE ARG LYS GLN LYS GLN GLU ILE ALA ASP ARG GLU LEU LYS ARG GLU LYS ALA LYS ALA GLU ALA LYS ARG ALA GLY GLY LYS GLY LEU LYS SER THR ALA VAL LYS LYS

VAL GLY MET LYS

- Molecule 3: Formin 1

Chain BB: 6% 93%

MET SER CYS PRO ALA SER CYS PRO ARG GLY ARG GLY GLY SER ALA PRO LEU PRO PRO MET PRO PRO SER VAL ASN ASP ASP ARG ASN ALA VAL LEU ASN ALA LEU PRO SER ARG THR SER PHE SER ALA PRO LEU CYS SER ALA THR SER CYS SER LEU PRO GLU ARG PRO VAL PHE ALA

LYS LEU THR GLY GLY MET PRO PHE SER ARG THR THR ALA ARG ILE GLU CYS ALA SER PRO ALA CYS HIS GLU SER LEU SER LEU HIS ARG VAL ALA GLU SER GLN VAL LYS ALA GLN ALA ALA ALA SER GLY PRO LEU SER SER ASN SER SER PHE LEU ILE PHE LEU ASN SER ILE PRO THR

GLU PRO PRO ARG CYS PHE LEU PRO PRO ARG ARG VAL ALA SER LEU SER ALA GLU ALA ASP THR PRO LYS GLY SER PHE TYR VAL PHE SER GLU SER SER ARG SER GLU SER SER HIS SER GLU GLY CYS VAL GLU SER ARG LEU SER GLY HIS THR ALA ALA ARG THR ARG CYS ARG ARG

SER ARG THR THR ALA SER ALA THR ASP SER ARG ARG ARG ASP ASP LEU PHE SER PHE ASP LEU PRO GLN GLU CYS GLY SER ALA PRO ARG LEU PRO LEU PRO LEU PRO SER ARG SER CYS PRO ALA SER PRO CYS HIS SER LEU LEU PRO PRO LEU SER ASN LYS LEU THR PRO PRO CYS ARG

GLU SER GLN SER GLU GLY THR ASP HIS GLY SER SER SER ALA ARG CYS CYS GLN PRO ARG PRO ILE THR ASP ALA LEU PRO THR GLY GLN ILE TYR SER ARG SER PRO SER ARG VAL ARG GLU ARG THR LEU ARG SER GLU PRO ALA ALA PRO VAL ASN TYR SER

ASP THR GLN LYS ARG CYS PRO ALA HIS SER MET PRO PRO PRO PRO PRO PRO LYS GLY LYS LYS LYS GLY PRO LEU PRO LYS LYS ALA SER ASN SER PRO LEU PRO SER THR PRO GLU GLY GLY ALA LYS LYS THR PRO PRO PRO

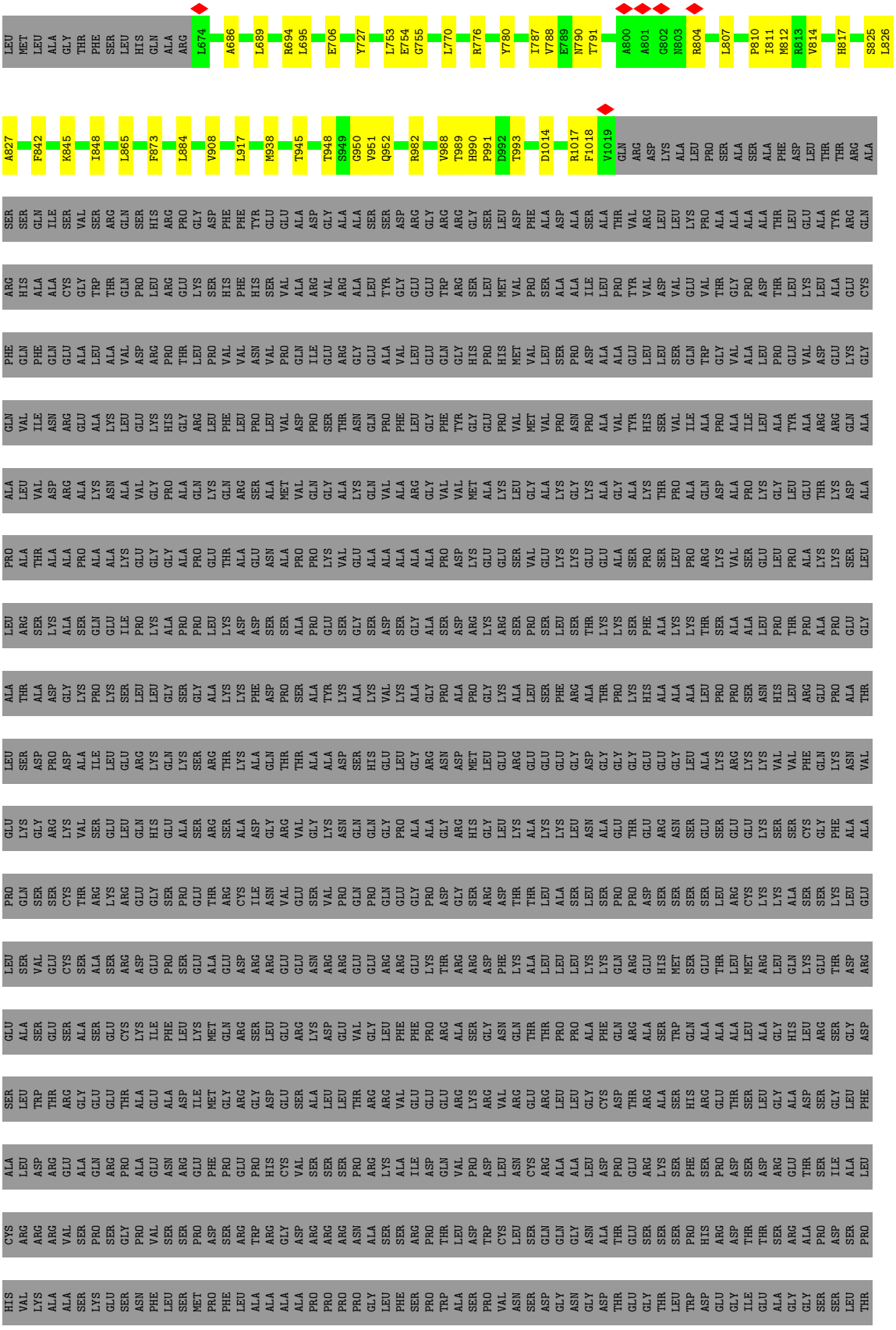
PRO PRO ALA ALA LYS ALA GLY VAL PRO SER GLU LYS ALA GLU GLU VAL PRO GLN LYS LYS ALA GLY VAL PRO PRO LYS GLU LYS ALA GLY MET PRO SER GLU ILE PRO GLN LYS LYS ALA GLY VAL PRO PRO LYS GLY LYS SER GLU LYS ALA LYS LYS ALA GLU VAL PRO LYS GLN

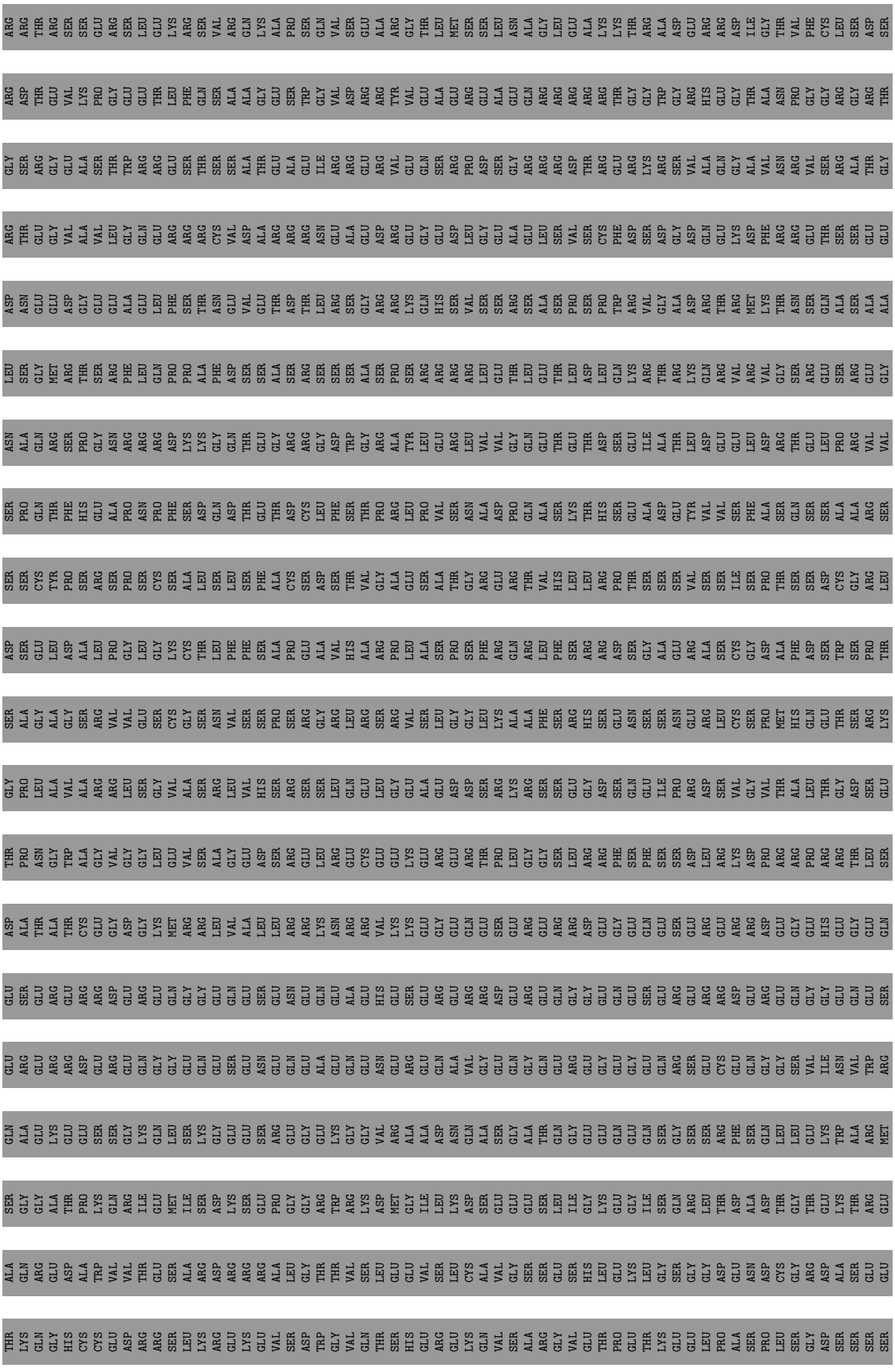
LYS ALA GLY LEU PRO LYS GLU ILE PRO GLN GLU LYS ALA GLY ILE SER LYS GLY GLU SER GLY SER PRO GLU GLY LYS THR LEU GLY PRO LEU PRO LEU PRO LYS GLY

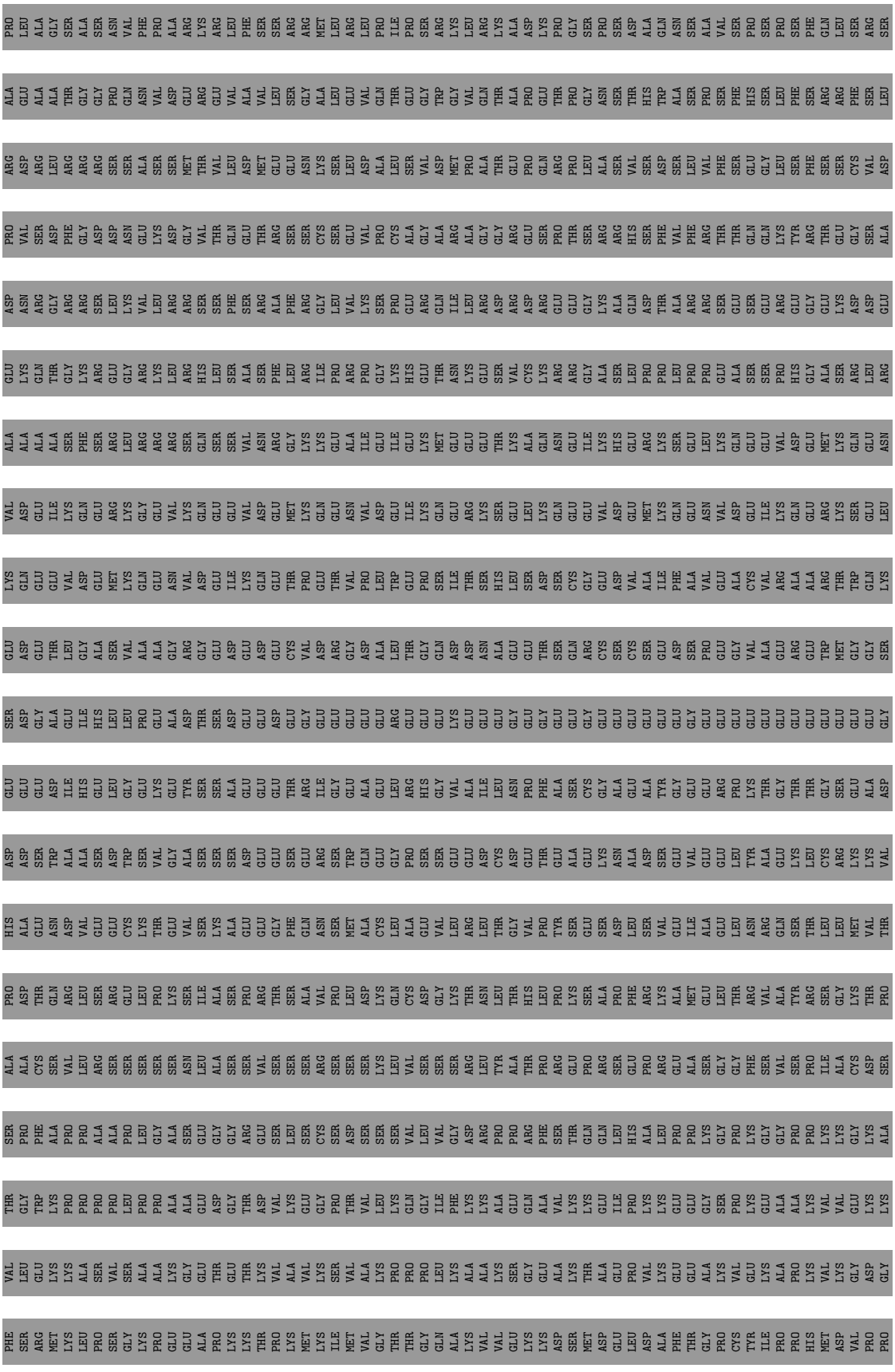
PRO LYS GLY LYS LEU PRO PRO PRO SER GLY ALA GLY ALA ILE PRO PRO SER LEU PRO SER LYS LYS ALA VAL ALA SER ALA GLY LYS PRO LEU GLY GLY LYS THR PRO PRO ALA ALA SER VAL ALA

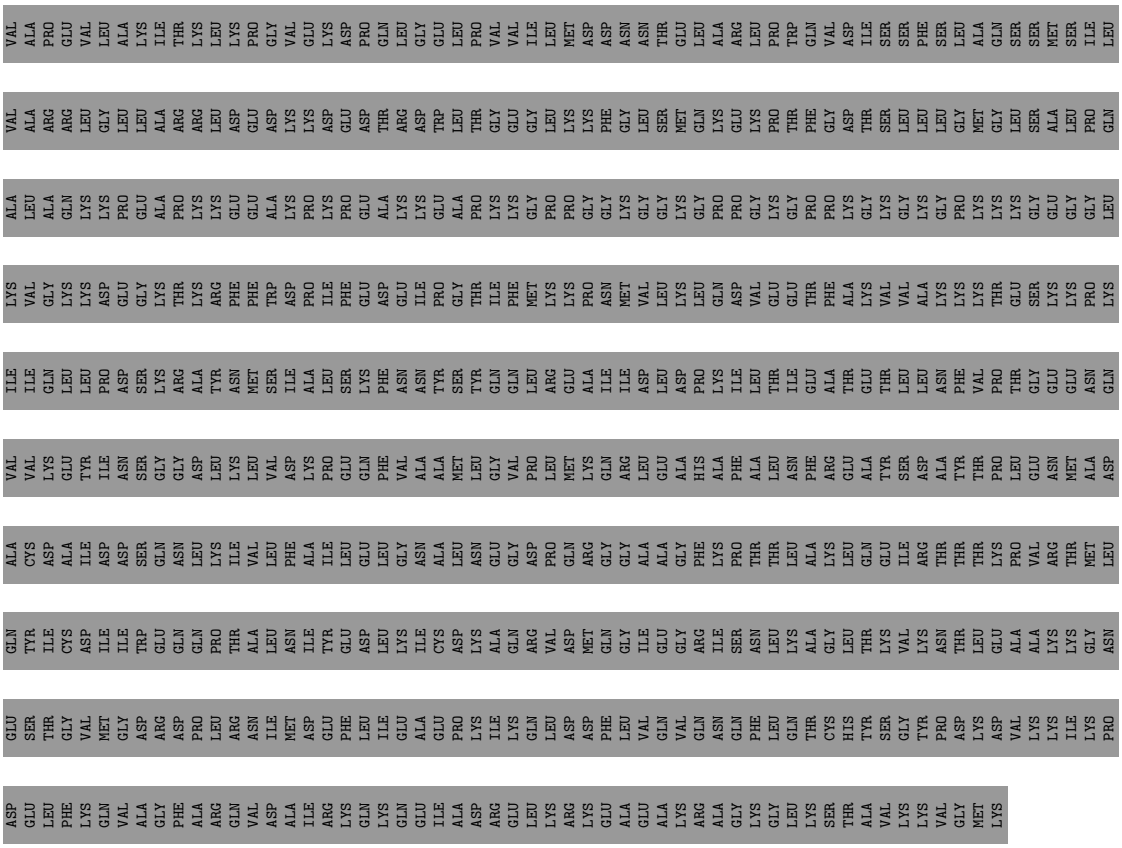
PRO ASN PRO PRO LEU GLY SER SER GLY PRO GLN GLU GLY ALA ARG ASP THR LEU ARG ALA ALA ALA GLY THR ALA GLY GLY ILE GLU CYS SER ALA GLY GLU THR VAL PRO PRO PRO ASN GLU GLY ALA TYR ALA ALA LYS ALA ALA MET MET VAL

GLU SER LEU LYS LEU LEU ALA ASP TYR THR ASN VAL PRO ALA ALA HIS ALA HIS GLY THR GLU PRO PRO ALA LEU PRO PHE ALA PRO GLY ALA ASP ARG ASN PRO ALA ILE LEU THR ARG ALA LEU LYS LYS GLU MET LEU LEU ARG ARG GLY GLN PRO THR GLN THR PRO GLU GLU GLU ARG ARG


LEU MET LEU ALA GLY THR PHE SER LEU HIS GLN ALA ARG L674 A686 L689 R694 L695 E706 Y727 L753 E754 G755 L770 R776 Y780 I787 V788 E789 N790 T791 A800 A801 G802 N803 R804 L807 P810 I811 M812 R813 V814 H817 S825 L826
A827 F842 K845 I848 L865 F873 L884 V908 L917 M938 T945 T948 S949 G950 V951 Q952 R982 V988 T989 H990 P991 D992 T993 D1014 R1017 F1018 V1019 GLN ARG ASP LYS ALA LEU PRO SER ALA ALA SER ALA PHE ASP LEU THR THR ARG ALA
SER SER GLN ILE SER VAL SER ARG GLN SER HIS ARG PRO GLY ASP PHE PHE TYR GLU GLU ALA ASP GLY ALA ALA SER SER ASP ARG GLY ARG ARG GLY SER LEU ASP PHE ALA ASP ALA SER ILE LEU PRO THR VAL ARG LEU LEU LYS PRO ALA ALA ALA ALA THR LEU GLU ALA TYR ARG GLN
ARG HIS ALA ALA CYS GLY TRP THR GLN PRO LEU ARG GLU LYS SER HIS PHE HIS SER VAL ALA ARG VAL ARG ALA ALA LEU TYR GLY GLU GLU TRP ARG SER LEU MET VAL PRO SER ALA ALA ILE LEU PRO TYR VAL ASP VAL GLU VAL THR GLY PRO ASP THR LEU LYS LEU ALA PRO GLU CYS
PHE GLN PHE GLN GLU ALA LEU ALA VAL ASP ARG PRO THR LEU PRO VAL VAL ASN VAL PRO GLN ILE GLU ARG GLY GLU ALA VAL LEU GLU GLN GLY HIS PRO HIS MET VAL LEU SER PRO ASP ALA ALA GLU LEU LEU SER GLN TRP GLY VAL ALA ALA LEU PRO GLU VAL ASP GLU LYS GLY
GLN VAL ILE ASN ARG GLU ALA LYS LEU GLU LYS HIS GLY ARG ARG LEU PHE LEU PRO LEU VAL ASP PRO SER THR ASN GLN PRO PHE LEU GLY PHE TYR GLY GLU PRO VAL MET VAL PRO ASN PRO ASP ALA VAL TYR HIS SER VAL ILE ALA PRO ALA ALA ILE LEU ALA TYR ALA ARG ARG GLN ALA
ALA LEU VAL ASP ARG ALA LYS ASN ALA VAL GLY PRO ALA GLN LYS GLN ARG SER ALA MET VAL GLN GLY LYS ALA LYS LYS LEU GLY ALA LYS GLY LYS ALA GLY ALA LYS THR PRO ALA GLN ASP ALA SER LEU PRO ARG LYS VAL SER GLU LEU PRO ALA LYS LYS SER LEU
PRO ALA THR ALA ALA PRO ALA ALA LYS GLU GLY GLY ALA PRO GLU THR ALA GLU ASN ALA PRO PRO LYS VAL GLU ALA ALA ALA ALA PRO ASP LYS GLY LYS GLU GLU SER VAL GLU LYS LYS GLU GLU ALA SER PRO SER LEU LEU PRO ARG LYS VAL SER GLU LEU PRO ALA LYS LYS SER LEU
LEU ARG SER LYS ALA SER GLN GLU ILE LEU PRO LYS ALA PRO PRO LEU LYS ASP ASP SER SER ALA PRO GLU SER GLY SER ASP SER GLY ALA SER ARG LYS ARG SER PRO SER LEU SER THR LYS LYS SER PHE ALA LYS LYS THR SER ALA ASP ARG GLY GLU GLY
ALA THR ALA ASP GLY LYS PRO LYS SER LEU LEU GLY SER GLY ALA LYS LYS PHE ASP PRO SER ALA ALA TYR LYS ALA LYS SER VAL LYS ALA GLY PRO ALA PRO GLY LYS ALA LEU SER PHE ARG ALA THR PRO LYS HIS ALA ALA LYS LYS THR SER ALA ALA LEU PRO PRO PRO GLU ALA THR
LEU SER ASP PRO ASP ALA ILE LEU GLU GLN HIS GLU ALA SER ARG THR LYS ALA GLN THR THR THR ALA ASP SER HIS GLU LEU GLU GLY ARG ASN ASP MET LEU GLU GLU ARG GLU GLU GLU GLY ASP GLY GLY GLU GLU GLY LEU ALA LYS ARG LYS LYS VAL VAL PHE GLN LYS ASN VAL
GLU LYS LYS GLY ARG LYS VAL SER GLU GLN HIS GLU ALA SER ARG SER ALA ASP GLY ARG VAL GLY LYS ASN GLN GLN GLY PRO ALA ALA GLY ARG HIS GLY LEU LYS ALA LYS LYS LEU ASN ALA GLU THR GLU ARG ASN SER GLU SER GLU GLU LYS SER SER CYS GLY PHE ALA ALA
PRO GLN SER SER CYS THR ARG LYS ARG GLU GLY SER PRO GLU THR ARG CYS ILE ASN VAL GLU SER VAL PRO GLN PRO GLN GLU GLY PRO ASP GLY SER ARG ASP THR THR LEU ALA SER LEU SER PRO PRO SER SER SER LEU ARG CYS LYS LYS ALA SER SER LYS LEU GLU
LEU SER VAL GLU CYS SER ALA ASP ARG ARG GLU GLU GLU ASN ARG ARG GLU GLU ARG ARG GLU LYS THR ARG ARG ASP PHE LYS ALA LEU LEU LEU LEU LYS LYS GLN ARG SER LEU LEU SER PRO PRO ASP SER SER SER SER GLU THR LEU MET SER GLU LYS GLN LYS SER GLU
GLU ALA SER GLU CYS LYS ILE PHE LEU LYS MET GLN ARG SER LEU GLU GLU ARG LYS ASP GLU VAL GLY LEU PHE PHE PRO ARG ALA SER GLY ASN GLN THR THR PRO ALA ALA PHE GLN ARG ALA SER TRP GLN ALA ALA ALA LEU ALA GLY HIS LEU ARG SER SER LYS GLU THR ASP ARG
SER LEU TRP THR ARG GLY GLU GLU THR ALA GLU GLU GLU GLU GLU ARG LYS ARG VAL ARG GLU LEU LEU GLY CYS ASP THR ARG ALA SER HIS ARG GLU THR SER LEU GLY LEU PHE
ALA LEU ASP ARG GLU ALA GLN ARG PRO ALA GLU GLU ASN ARG CYS VAL SER SER SER PRO ARG LYS ALA ILE ASP GLN VAL PRO ASP LEU ASN CYS ARG ALA ALA LEU ASP PRO GLU ARG LYS SER PHE SER PRO GLU THR SER ILE ALA LEU
CYS ARG ARG ARG VAL SER GLY PRO SER PRO ARG TRP ARG GLY ASP ARG ARG ASN ALA SER SER ARG PRO THR LEU ASP TRP CYS LEU SER GLN GLN GLY ASN ALA THR GLU SER SER PRO HIS ARG GLU ASP ARG THR THR SER ARG ALA PRO ASP SER ARG
HIS VAL LYS ALA ALA SER LYS GLU SER ASN PHE LEU VAL PRO LEU ALA MET PRO PHE LEU ALA ALA ALA PRO PRO PRO LEU GLY LEU PHE SER PRO TRP ALA SER VAL ASN SER ASP GLY ASN GLY ASP THR GLU GLY LEU TRP ASP GLU GLY GLY ALA GLY SER SER LEU THR

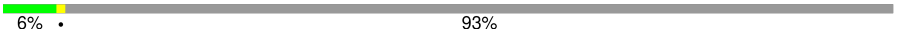

ARG ARG THR ARG SER SER GLU ARG SER LEU GLU LYS ARG SER VAL ARG GLN LYS ALA PRO SER GLN VAL SER GLU ALA ARG GLY LEU GLU ALA LYS LYS THR ARG ALA ASP GLU ARG ARG ASP ILE GLY THR VAL PHE CYS LEU SER ASP SER
ARG ASP THR GLU VAL LYS PRO GLY GLU GLU THR LEU PHE GLN SER ALA ALA GLY GLU SER TRP GLY VAL ASP ARG ARG TYR VAL GLU ALA GLU ARG GLU ARG ARG ASP ALA ASP ILE ARG ARG ARG ALA ASP PRO GLY GLY ARG GLY ARG THR
GLY SER ARG GLY GLU ALA SER THR TRP ARG ARG GLU SER THR SER SER ALA ALA THR GLU ALA GLU ARG GLU ARG VAL GLU GLN SER ARG PRO ASP SER GLY ARG GLN GLU ALA GLU ASN ARG VAL SER ARG GLY GLU ALA VAL ALA GLN GLY LYS ASP PHE ARG ARG GLU THR SER ARG ALA ASP GLY
ARG THR GLU GLY VAL ALA VAL LEU GLY GLN GLU ARG ARG ARG CYS VAL ASP ALA ARG ARG ASN GLU ALA GLU ASP GLU GLY GLU ASP LEU GLY LYS ASP PHE ASP SER PHE SER ASP SER GLY GLN GLU LYS ASP PHE ASP GLU GLU
ASP ASN GLU GLU ASP GLY GLU GLU ALA GLU LEU PHE SER THR ASN GLU VAL GLU THR ASP THR LEU GLU ARG SER GLY ARG VAL SER GLN HIS SER VAL SER SER SER PRO SER PRO TRP ARG VAL GLY ALA ASP ARG THR ARG SER ALA SER PRO GLU GLU
LEU SER GLY MET ARG THR SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER SER ALA SER ARG SER SER SER ARG ARG GLU LEU GLN LEU LYS ARG THR ARG LYS GLN LYS VAL ARG VAL GLY SER ARG GLU GLU GLY
ASN ALA GLN ARG SER PRO GLY ASN ARG ARG ARG ASP LYS LYS GLY GLN THR GLU GLY ARG ARG ARG GLY ASP TRP GLY ARG ALA TYR LEU GLU ARG LEU VAL VAL GLY GLN GLU THR ASP SER GLU ILE ALA THR LEU GLU ASP LEU GLN LYS ARG VAL ALA ASP ARG THR GLU LEU PRO ARG VAL VAL
SER PRO GLN THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ASP THR GLU THR ASP CYS LEU PHE SER THR PRO ARG LEU PRO VAL SER ASN ALA ASP PRO GLN ALA SER LYS THR HIS SER GLU ALA ASP GLU TYR VAL VAL SER PHE ALA SER GLN SER SER ALA ALA ARG SER
SER SER CYS TYR PRO SER ARG SER PRO SER CYS SER ALA LEU SER LEU SER PHE SER ASP SER THR VAL GLY ALA GLU SER ALA THR GLY ARG GLU ARG THR VAL HIS LEU LEU ARG PRO THR SER SER SER VAL SER SER ILE SER PRO THR SER SER ASP CYS GLY ARG LEU
ASP SER GLU LEU ASP ALA LEU PRO GLY PRO GLY LEU GLY LYS CYS THR LEU PHE SER ALA PRO GLU ALA VAL HIS ALA ARG PRO LEU ALA SER PRO SER PHE ARG GLN ARG LEU PHE SER ARG ARG ARG ASP SER GLY ALA GLU ARG ALA SER PHE ASP SER GLY PRO THR
SER ALA GLY ALA GLY SER ARG VAL GLU CYS GLY SER ASN VAL SER SER ARG GLY ARG VAL SER LEU LYS ALA ALA PHE SER ARG HIS SER GLU ASN SER SER ASN GLU ARG LEU GLY LEU GLY GLY LEU LYS ALA ALA PHE ASP SER GLU THR SER ARG LYS
GLY PRO LEU ALA VAL SER ARG LEU VAL HIS SER ARG SER SER LEU GLN GLU LEU GLY GLU ALA GLU SER ARG GLU ASP ASP SER GLN GLU ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU THR ARG GLU
THR PRO ASN GLY TRP ALA GLY VAL GLY GLY LEU GLU VAL SER ALA GLY GLU ASP SER ARG GLU LEU ARG LYS GLU CYS GLU LEU GLY GLU ARG THR PRO LEU LYS GLU ARG ARG PHE SER PHE SER SER ASP GLU ARG ARG PRO ARG ARG THR LEU SER
ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG ARG VAL LYS LYS LYS GLU GLY GLU GLU GLN GLU SER ASP GLU ARG GLU ARG ARG ASP GLU GLY GLU GLN GLU SER GLU ARG GLU ARG ASP GLU GLY GLN
GLU SER GLU ARG GLU ARG GLU ASP GLU GLN GLY GLY GLU LEU GLN GLU ALA GLU HIS GLU SER GLU ARG GLU GLU ARG ASP ASP GLU ARG GLN GLY GLU GLY GLU GLN GLU SER GLU ARG GLU GLU ARG ARG ASP GLU GLY GLN GLU
GLU ARG GLU ARG GLU GLN GLY GLY GLU LEU GLN GLY GLU ASN GLU GLN GLU ALA ALA GLU GLN ALA VAL GLY GLU GLU ALA ARG GLU GLN GLY GLY GLU GLY GLU GLU GLY GLU GLY GLU GLN ARG SER GLU SER GLU CYS GLU GLN GLN
GLN ALA GLU LYS GLU LYS SER SER LYS GLY GLU GLU SER ARG GLU GLY VAL ARG ALA ALA ASP ASN GLN ALA SER GLY GLU GLU GLN GLU GLN SER GLY SER SER SER ARG PHE SER GLN LEU LEU GLU LYS TRP ALA ARG MET
SER GLY GLY ALA THR PRO LYS GLN ILE GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY TRP ARG TRP ARG LYS ASP MET GLY ILE LEU LYS ASP SER GLU GLU GLU SER LEU ILE GLY LYS GLU GLY ILE SER GLN ARG LEU THR ASP ALA ASP THR GLY THR GLU LYS TRP ARG GLU
ALA GLN ARG GLU ASP ALA SER GLU ARG ASP ARG ARG ALA LEU GLY THR THR VAL SER LEU GLU SER LEU CYS ALA VAL GLY SER SER GLU SER HIS LEU GLU LYS LEU GLY SER GLY GLY GLY ASP GLU ASN ASP THR GLY ARG ASP ALA SER GLU GLU
THR LYS GLN GLY HIS CYS CYS GLU ASP ARG SER LEU ARG GLU LYS GLN VAL SER ALA ARG GLY VAL GLU THR PRO GLU THR LYS GLU GLU LEU PRO ALA SER PRO LEU SER GLY ASP SER SER SER

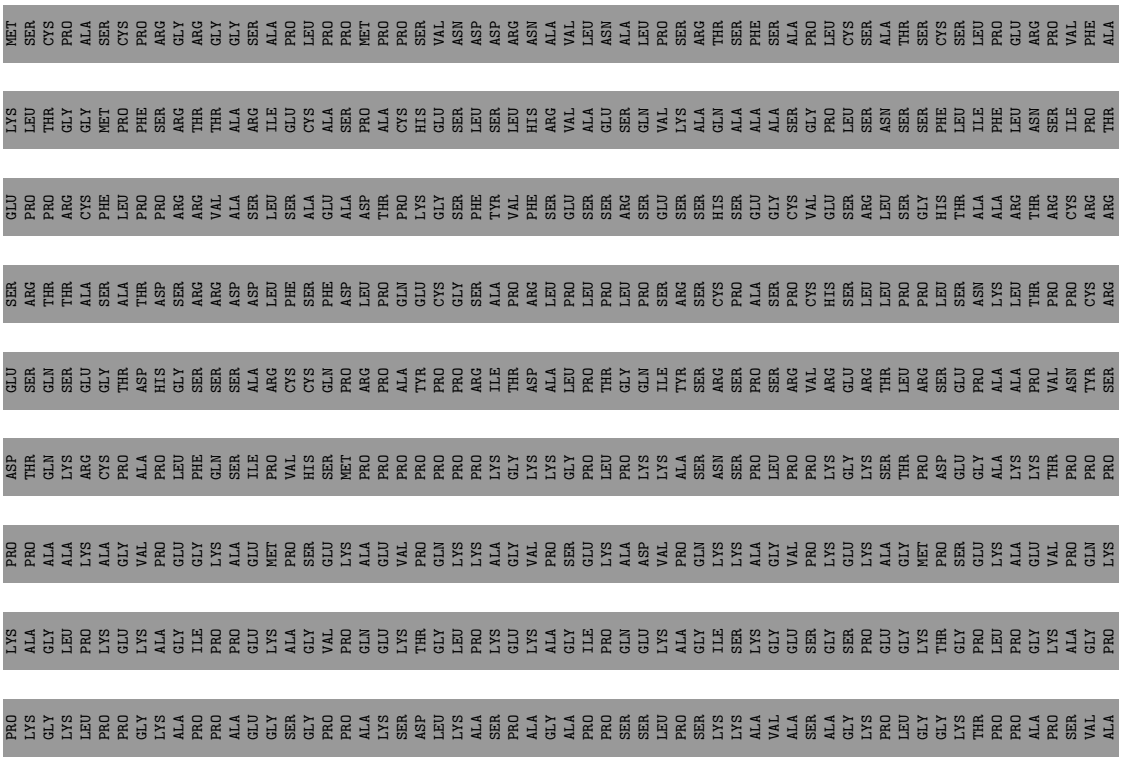

PRO LEU ALA GLY SER ALA SER ASN VAL PHE PRO ALA ARG LYS ARG LEU PHE SER SER ARG ARG MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS ALA ASP LYS PRO GLY SER PRO SER ASP ALA GLN ASN SER ALA VAL SER PRO SER PHE GLN LEU SER ARG
ALA GLU ALA ALA THR GLY GLY PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA VAL LEU SER GLY ALA LEU GLU VAL GLN THR HIS TRP ALA SER PRO SER PHE HIS SER LEU PHE SER ARG ARG PHE SER LEU
ARG ASP ARG LEU ARG ARG SER SER ALA SER SER MET THR VAL LEU ASP MET GLU GLU ASN LYS SER LEU ASP ALA LEU SER VAL ASP MET PRO ALA THR GLU PRO GLN ARG PRO LEU ALA SER VAL SER ASP SER LEU VAL PHE SER THR GLN GLN LYS TYR ARG THR SER GLU GLY LEU SER PHE SER ARG SER CYS VAL ASP
PRO VAL SER ASP PHE GLY ASP ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER GLU VAL PRO CYS ALA GLY GLY ALA ARG ARG HIS SER PHE VAL PHE ARG THR THR GLN GLN LYS TYR ARG THR GLU SER ARG
ASP ASN ARG GLY ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LYS VAL SER LEU ARG LYS ASP ARG GLU GLU ASP ASP ARG ASP ARG GLU GLU GLY LYS ALA LYS ASP ASP GLU
GLU LYS GLN THR GLY LYS ARG GLU GLY LYS ARG HIS LEU SER ALA GLU ARG LEU ILE PRO ARG GLY LEU VAL LYS SER PRO GLU ARG GLN ILE LEU ARG GLU GLU THR ASN LYS VAL CYS LYS ARG GLU GLY LYS ALA GLN ASP PRO PRO LEU PRO PRO GLU GLN ALA SER LEU PRO PRO HIS GLY ALA SER ARG LEU ARG LYS ASP LEU ARG
ALA ALA ALA SER PHE SER ARG LEU ARG ARG SER GLN SER SER VAL ASN ARG GLY LYS LYS GLU ALA ILE GLU ILE GLU LYS MET GLU GLU GLU THR LYS GLN ASN GLU ILE LYS HIS GLU ARG LYS SER GLU LEU LYS GLN GLU MET LYS GLU
VAL ASP GLU ILE LYS GLN GLU GLU VAL LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLU ASN VAL ASP GLU ILE LYS GLN GLU ARG LYS SER GLU LEU LYS ALA GLN ASN GLU ILE LYS HIS GLU ASP VAL ASP GLU MET LYS GLN GLU GLU ARG
LYS GLN GLU GLU VAL ASP GLU ILE LYS GLN GLU THR PRO GLU THR VAL PRO LEU TRP GLU PRO SER ILE THR SER HIS LEU SER ASP SER CYS GLY GLU ASP VAL ALA ILE PHE ALA VAL GLU ALA CYS VAL ARG ALA ALA ARG THR TRP GLN LYS
GLU ASP GLU THR LEU GLY ARG GLY ALA GLU ASP GLU ASP GLU CYS VAL ASP ARG GLY ASP ALA LEU THR GLY GLN ASP ASN ALA GLU GLU THR SER GLN ARG CYS SER CYS SER GLU ASP SER PRO GLU GLY VAL ALA GLU ARG GLU TRP MET GLY GLY SER
SER ASP GLY ALA GLU ILE HIS LEU LEU PRO GLU ALA ASP THR SER ASP GLU GLU GLU ASP GLU CYS VAL ASP GLY GLU GLU GLU

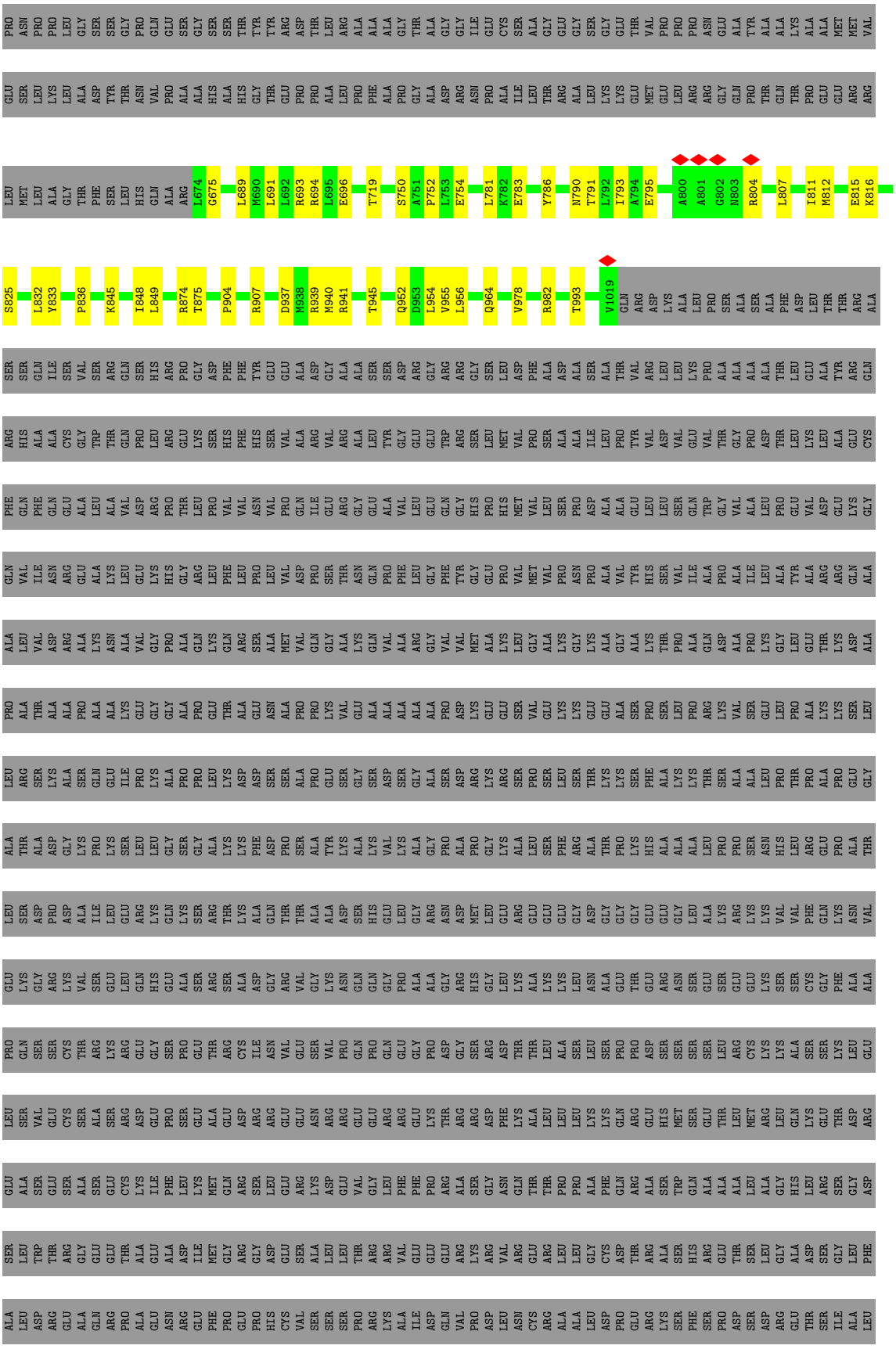


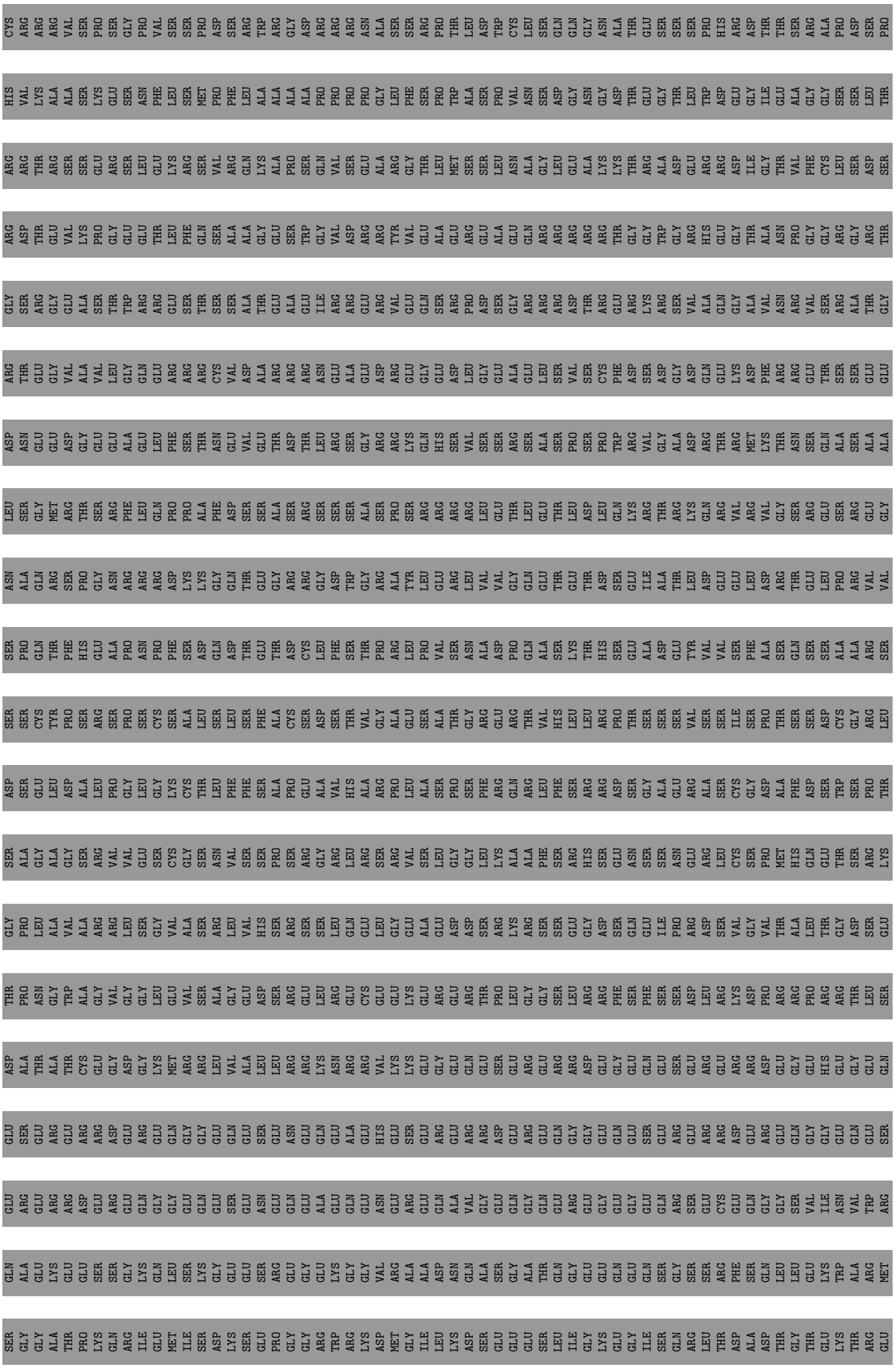
• Molecule 3: Formin 1

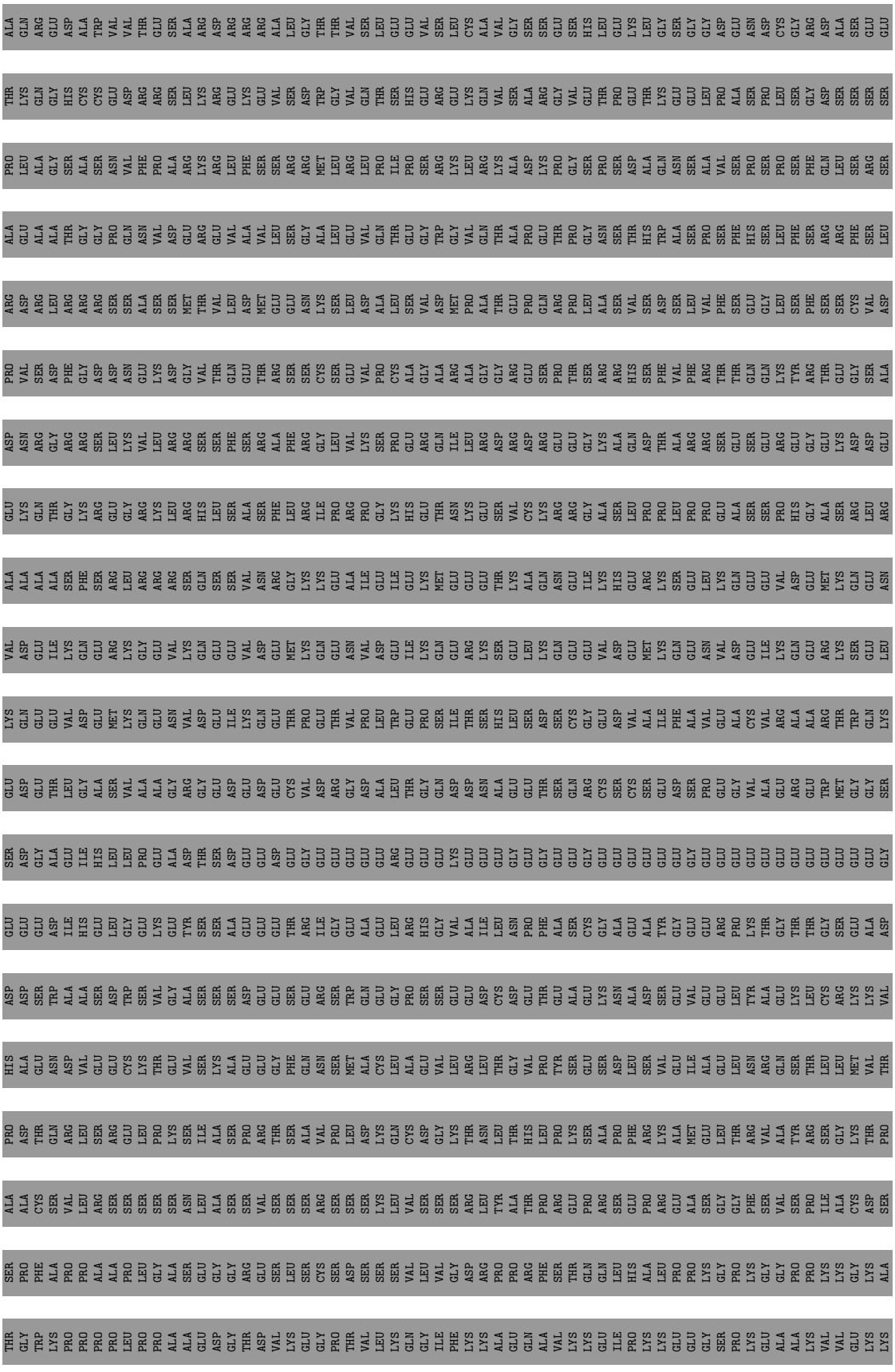
Chain BC:

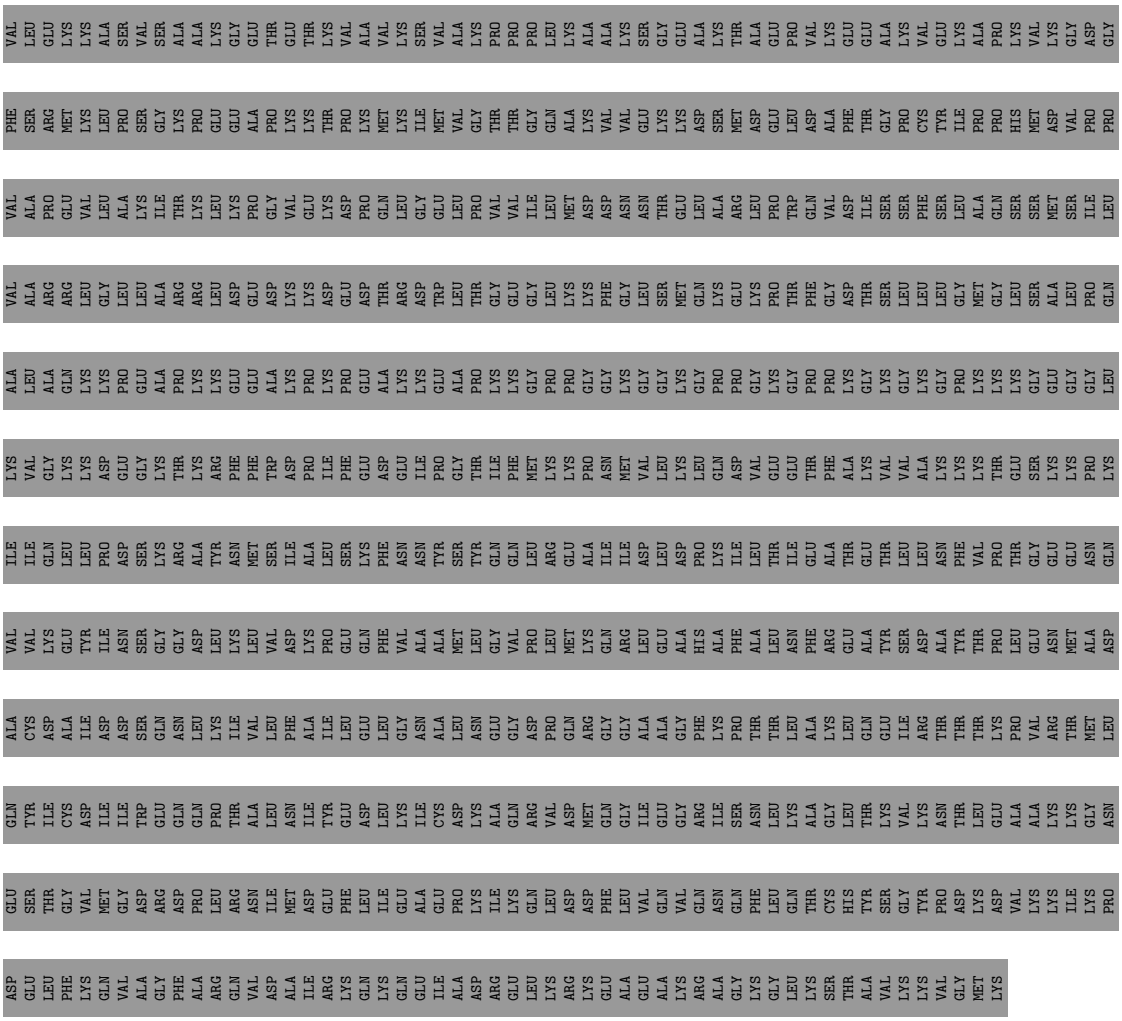





PRO ASN PRO PRO LEU GLY SER SER GLY PRO GLN GLU SER GLY SER SER THR TYR TYR ARG ASP THR LEU ARG ALA ALA ALA GLY THR ALA GLY GLY ILE GLU CYS SER ALA GLY GLU GLY SER GLY GLU THR VAL PRO PRO ASN GLU ALA TYR ALA ALA LYS ALA ALA MET MET VAL
GLU SER LEU LYS LEU ALA ASP TYR THR ASN VAL PRO ALA ALA HIS ALA HIS GLY THR GLU PRO ALA LEU PRO PHE ALA PRO GLY ALA ASP ARG ASN PRO ALA ILE LEU THR ARG ALA LEU LYS LYS GLU MET GLU LEU ARG ARG GLY GLN PRO THR GLN THR PRO GLU GLU ARG ARG
LEU MET LEU ALA GLY THR PHE SER LEU HIS GLN ALA ARG L674 G675 L689 M690 L691 L692 R693 R694 L695 E696 T719 S750 A751 P752 L753 E754 L781 K782 E783 Y786 N790 T791 L792 I793 A794 E795 A800 A801 G802 N803 R804 L807 I811 M812 E815 K816
S825 L832 Y833 P836 K845 I848 L849 R874 T875 P904 R907 D937 M938 R939 M940 R941 T945 Q952 D953 L954 V955 L956 Q964 V978 R982 T993 Y1019 GLN ARG ASP LYS ALA LEU PRO SER ALA SER ALA PHE ASP LEU THR THR ARG ALA
SER SER GLN ILE SER VAL SER ARG GLN SER HIS ARG PRO GLY ASP PHE PHE TYR GLU GLU ALA ASP GLY ALA ALA SER SER ASP ARG GLY ARG ARG GLY SER LEU ASP PHE ALA ASP ALA SER ALA THR VAL ARG LEU LEU LYS PRO ALA ALA ALA ALA THR LEU GLU ALA TYR ARG GLN
ARG HIS ALA ALA CYS GLY TRP THR GLN PRO LEU ARG GLU LYS SER HIS PHE HIS SER VAL ALA ARG VAL ARG ALA LEU TYR GLY GLU GLU TRP ARG SER LEU MET VAL PRO SER ALA ALA ILE LEU PRO TYR VAL ASP VAL GLU VAL THR GLY PRO ASP THR LEU LYS LEU ALA GLU CYS
PHE GLN PHE GLN GLU ALA LEU ALA VAL ASP ARG PRO THR LEU PRO VAL VAL ASN VAL PRO GLN ILE GLU ARG GLY GLU ALA VAL LEU GLU GLN GLY HIS PRO HIS MET VAL LEU SER PRO ASP ALA ALA GLU LEU LEU SER GLN TRP GLY VAL ALA LEU PRO GLU VAL ASP GLU LYS GLY
GLN VAL ILE ASN ARG GLU ALA LYS LEU GLU LYS HIS GLY ARG LEU PHE LEU GLY PHE TYR GLY GLU PRO VAL MET VAL LEU PRO ASN PRO VAL SER ILE ALA PRO ALA ILE LEU LEU ALA TYR ALA ARG ARG GLN ALA
ALA LEU VAL ASP ARG ALA LYS ASN ALA VAL GLY GLY PRO ALA GLN LYS GLN ARG SER ALA MET VAL GLN GLY ALA LYS GLN VAL ALA ARG GLY VAL MET ALA LYS LEU GLY ALA LYS GLY LYS GLY LYS ALA GLY ALA LYS THR PRO ALA GLN ASP ASP ALA
PRO ALA THR ALA ALA PRO ALA ALA LYS GLU GLY GLY GLY ALA PRO GLU THR ALA GLU ASN ALA ALA PRO PRO LYS VAL GLU ALA ALA ALA ALA ALA PRO ASP LYS GLU GLU SER VAL GLU LYS LYS GLU GLU ALA SER PRO SER LEU PRO ARG LYS VAL SER GLU LEU PRO ALA LYS LYS SER LEU
LEU ARG SER LYS ALA ALA SER GLN GLU ILE PRO LYS ALA PRO PRO LEU LYS ASP ASP SER SER ALA PRO GLU SER GLY SER ASP SER GLY ALA SER ASP ARG LYS GLU SER ARG PRO SER LEU SER THR LYS LYS SER PHE ALA LYS LYS THR SER ALA ALA LEU LEU PRO THR PRO ALA PRO GLU GLY
ALA THR ALA ASP GLY LYS PRO LYS SER LEU VAL LYS ALA TYR LYS ALA LYS VAL ALA PRO ALA ALA GLY PRO ALA PRO GLY LYS ALA LEU SER PHE ARG ALA THR PRO LYS HIS ALA LYS ALA ALA LEU PRO PRO SER ASN HIS LEU ARG GLU PRO ALA THR
LEU SER ASP PRO ASP ALA ILE LEU GLU ARG LYS GLN LYS SER THR ALA ALA GLN THR ALA ASP SER HIS GLU LEU GLU ARG ASN ASP MET LEU GLU GLU ARG GLU GLU GLU GLY ASP GLY GLY GLY GLU GLU GLY LEU ALA LYS ARG LYS LYS VAL VAL PHE GLN LYS ASN VAL
GLU LYS GLY ARG LYS VAL GLY LYS ASN GLN GLN GLY PRO ALA ALA GLY ARG HIS GLY LEU LYS ALA LYS LYS LEU ASN ALA GLU THR GLU ARG ASN SER GLU SER GLU LYS SER SER CYS GLY PHE ALA ALA
PRO GLN SER SER CYS THR ARG LYS ARG GLU GLY SER PRO GLU THR ARG CYS ILE ASN VAL GLU SER VAL PRO GLN PRO GLN GLU GLY PRO ASP GLY SER ARG ASP THR THR LEU ALA SER LEU LEU SER PRO PRO ASP SER SER SER SER LEU ARG CYS LYS LYS ALA SER SER LEU LEU GLU
LEU SER VAL GLU CYS SER ALA ARG ASP ARG GLU GLU LYS THR ARG ARG ASP PHE LYS ALA LEU LEU LEU LEU LYS LYS GLN ARG GLU ARG HIS GLU THR ASP ARG
GLU ALA SER GLU CYS LYS ILE PHE LEU LYS MET GLN ARG GLY ASP LEU GLU LYS ARG LEU GLY ASN GLN THR THR PRO PRO ALA PHE GLN ARG ALA SER TRP GLN ALA ALA ALA LEU ALA GLY HIS LEU ARG SER GLY ASP
SER LEU TRP THR ARG GLY GLU GLU THR ARG ARG VAL GLU GLU ARG LYS VAL PRO ASP LEU LEU GLY CYS ASP THR ARG ALA SER HIS ARG GLU THR SER LEU GLY ALA ASP SER GLY LEU PHE
ALA LEU ASP ARG GLU ALA GLN ARG PRO HIS CYS VAL SER SER SER PRO ARG LYS ALA ILE ASP GLN VAL PRO ASP LEU ASN CYS ARG ALA ALA LEU ASP PRO GLU ARG GLU VAL ASP PHE SER PRO GLN ASP ARG GLU VAL THR SER ILE ALA LEU

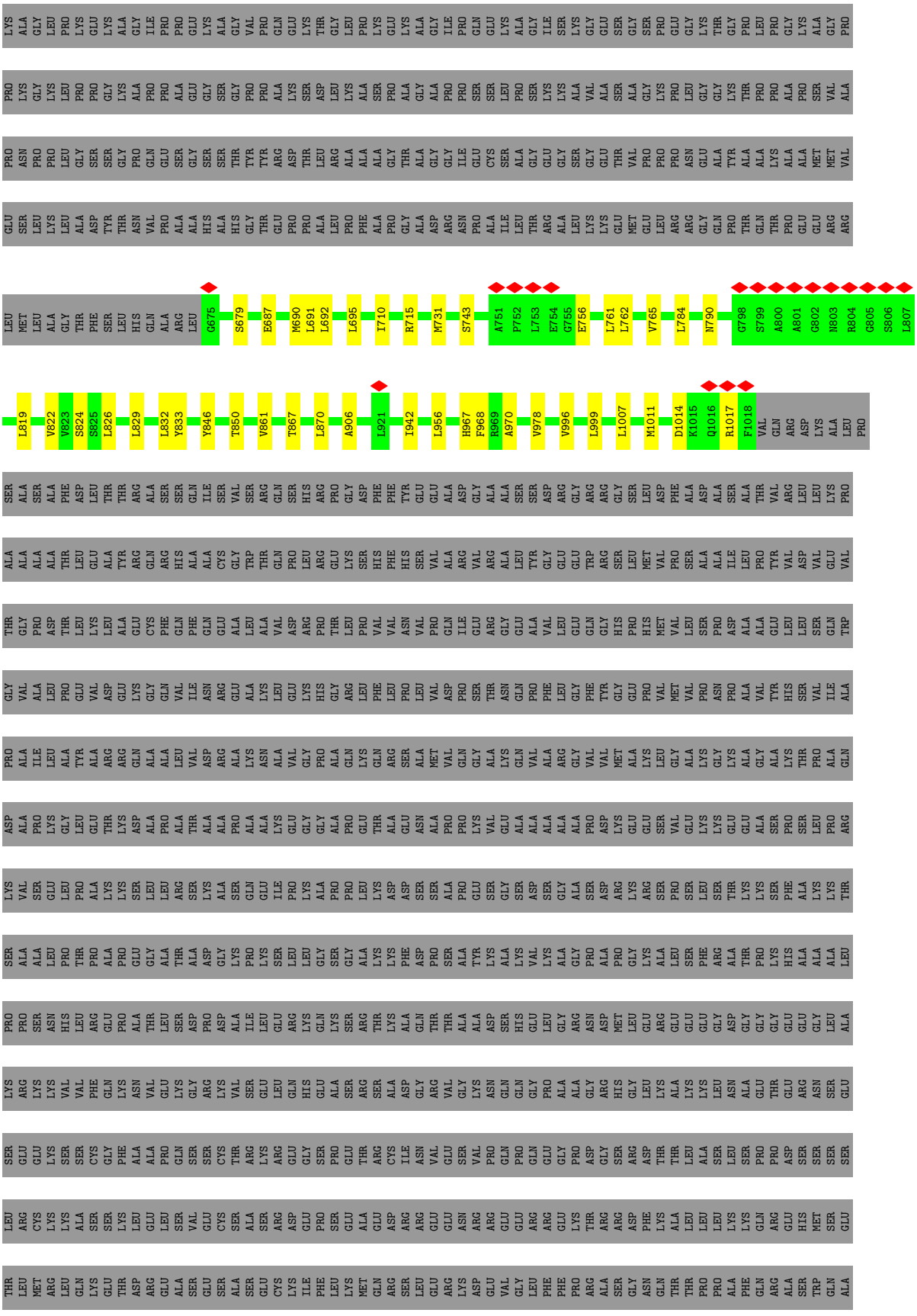

CYS ARG ARG ARG VAL SER PRO SER GLY PRO VAL SER SER PRO ASP SER ARG TRP ARG GLY ASP ARG ARG ARG ASN ALA SER SER ARG PRO THR LEU ASP TRP CYS LEU SER GLN GLN GLY ASN ALA THR GLU SER SER SER PRO HIS ARG ASP THR THR SER ARG ALA PRO ASP SER PRO
HIS VAL LYS ALA ALA SER LYS GLU SER ASN PHE LEU SER MET PRO PHE LEU ALA ALA ALA PRO PRO PRO PRO GLY LEU PHE SER PRO TRP ALA SER PRO VAL ASN SER ASP GLY ASN GLY ASP THR GLU GLY THR LEU TRP ASP GLU GLY GLY ILE GLU ALA GLY ALA LYS GLY GLY SER SER LEU THR
ARG ARG THR ARG SER SER GLU GLU LYS ARG SER VAL ARG GLN LYS ALA PRO SER GLN VAL SER GLU ALA ARG GLY THR LEU MET SER SER LEU ASN ALA GLY LEU GLU ASP ASP ILE GLY THR VAL PHE CYS LEU SER ASP ALA ARG ARG ARG ASP GLU ARG ALA ARG ARG SER
ARG ASP THR GLU VAL LYS PRO GLY GLU GLU THR LEU PHE GLN SER ALA ALA GLY GLU SER TRP GLY VAL ASP ARG ARG TYR VAL GLU ALA GLU ALA ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG THR
GLY SER ARG GLY GLU ALA SER THR TRP ARG GLU ILE ARG ARG GLU ALA GLU ILE ARG ARG GLU ARG VAL GLU GLN SER ARG PRO ASP SER GLY ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG ARG GLY
ARG THR GLU GLY VAL ALA VAL LEU GLY GLN GLU ARG ARG ARG CYS VAL ASP ALA ARG GLU ASP ARG ALA ASP ARG ASP LEU GLY GLU ALA LEU GLU THR THR GLU ASP SER CYS PHE ASP SER ASP GLY ASP GLN GLU LYS THR SER SER GLU GLU GLU
ASP ASN GLU GLU GLU ALA GLU LEU PHE SER THR ASN GLU VAL GLU THR ASP THR LEU ARG SER GLY ARG ARG LYS GLN HIS SER VAL SER SER ARG GLU GLY GLU GLN HIS SER ARG PRO ASP SER ALA SER PRO SER PRO TRP ARG VAL GLY ALA ASP ARG THR ARG MET LYS THR ASN SER GLN ALA SER ALA ALA
LEU SER GLY MET ARG THR SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER ALA SER ARG SER SER SER ARG ARG ARG LEU GLU THR LEU ASP LEU GLN LYS ARG THR ARG LYS GLN ARG VAL ARG VAL GLY SER ARG GLU SER ARG GLU GLU GLY
ASN ALA GLN ARG SER PRO GLY ASN ARG ARG ARG ASP LYS LYS GLY GLN THR GLU GLY ARG ARG ALA TYR LEU GLU ARG LEU VAL VAL GLY GLN GLU THR THR ASP SER GLU ILE ALA THR LEU GLU ASP ARG THR ARG VAL ASP GLU GLU LEU VAL ARG VAL
SER PRO GLN THR PHE HIS GLU ALA PRO ASN PRO PRO PHE SER ASP GLN ASP THR GLU THR ASP PHE SER THR PRO ARG LEU PRO VAL SER ASN ALA ASP PRO GLN ALA SER LYS THR HIS SER GLU ALA ASP GLU TYR VAL VAL SER PHE ALA SER GLN SER SER ASP ARG PRO ARG
SER SER CYS TYR PRO SER ARG SER PRO SER CYS SER ALA LEU SER LEU SER PHE ALA CYS SER ASP SER THR VAL GLY ALA GLU SER ALA THR GLY ARG GLU ARG LEU ARG PRO THR SER SER SER VAL SER SER ILE SER PRO THR SER SER ASP ARG LEU
ASP SER GLU LEU ASP ALA LEU PRO GLY LEU GLY GLY LYS CYS THR LEU PHE PHE SER ALA PRO GLU ALA VAL HIS ALA ARG PRO LEU ALA SER PRO SER PHE ARG GLN ARG ARG ASP SER GLN GLU ASN SER GLY ALA GLU ARG ALA SER CYS GLY ASP ALA PHE SER ASP ASP SER TRP SER PRO THR
SER ALA GLY ALA GLY SER ASN VAL SER SER CYS GLY SER ASN VAL SER SER ARG GLY ARG LEU ARG SER ARG VAL SER LEU GLY GLY LEU LYS ALA ALA PHE SER ARG HIS SER GLU ASN SER SER ASN GLU ARG LEU GLU ASP SER VAL SER ILE PRO MET HIS GLN GLU THR SER ARG LYS
GLY PRO LEU ALA VAL ALA ARG LEU SER GLY VAL ALA SER ARG SER SER LEU GLN GLU LEU GLY GLU ALA GLU ASP ASP SER ARG LYS ARG SER GLN GLU ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU GLU THR ASP
THR PRO ASN GLY TRP ALA GLY GLY LEU GLU VAL SER ALA GLY GLU LEU GLU ARG GLU ARG THR PRO LEU GLY GLY SER LEU ARG ARG PHE SER SER SER ASP LEU ARG ARG PRO ARG ARG PRO ARG THR SER
ASP ALA THR CYS GLU GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG LYS ASN ARG VAL LYS LYS GLU GLY GLU GLU ARG GLU ARG ASP GLU GLY GLN GLU SER GLU GLU GLY GLU GLU GLU GLU ARG ARG ASP ASP GLU GLY GLU GLN
GLU SER GLU ARG GLU GLN GLU GLU ALA GLU HIS GLU SER GLU ARG GLU GLU ARG ARG ASP GLU GLN GLU SER GLU ARG GLU ARG ASP GLU GLN GLN GLY GLU GLN GLU SER GLU ARG GLU GLU GLN GLY
GLU ARG GLU ARG GLU GLN GLY GLY GLY GLU GLN GLU SER GLU GLN ALA VAL GLY GLU GLN GLY GLY GLU GLY GLU GLN GLU GLY GLU GLN GLU GLN GLY GLY GLY SER VAL ILE ASN VAL TRP ARG
GLN ALA GLU LYS GLU SER SER LYS GLY GLY VAL ARG ALA ALA ASP ASN GLN ALA SER GLY ALA THR GLN GLY GLU GLU GLN GLN SER GLY SER SER ARG GLN LEU LEU GLU LYS TRP ALA ARG MET
SER GLY GLY ALA THR PRO LYS GLN ARG TRP ARG LYS ASP MET GLY ILE LEU LYS ASP SER GLU GLU SER LEU ILE GLY LYS GLU GLY ILE SER GLN ARG LEU THR ASP ALA ASP THR GLY THR GLU LYS THR ARG GLU

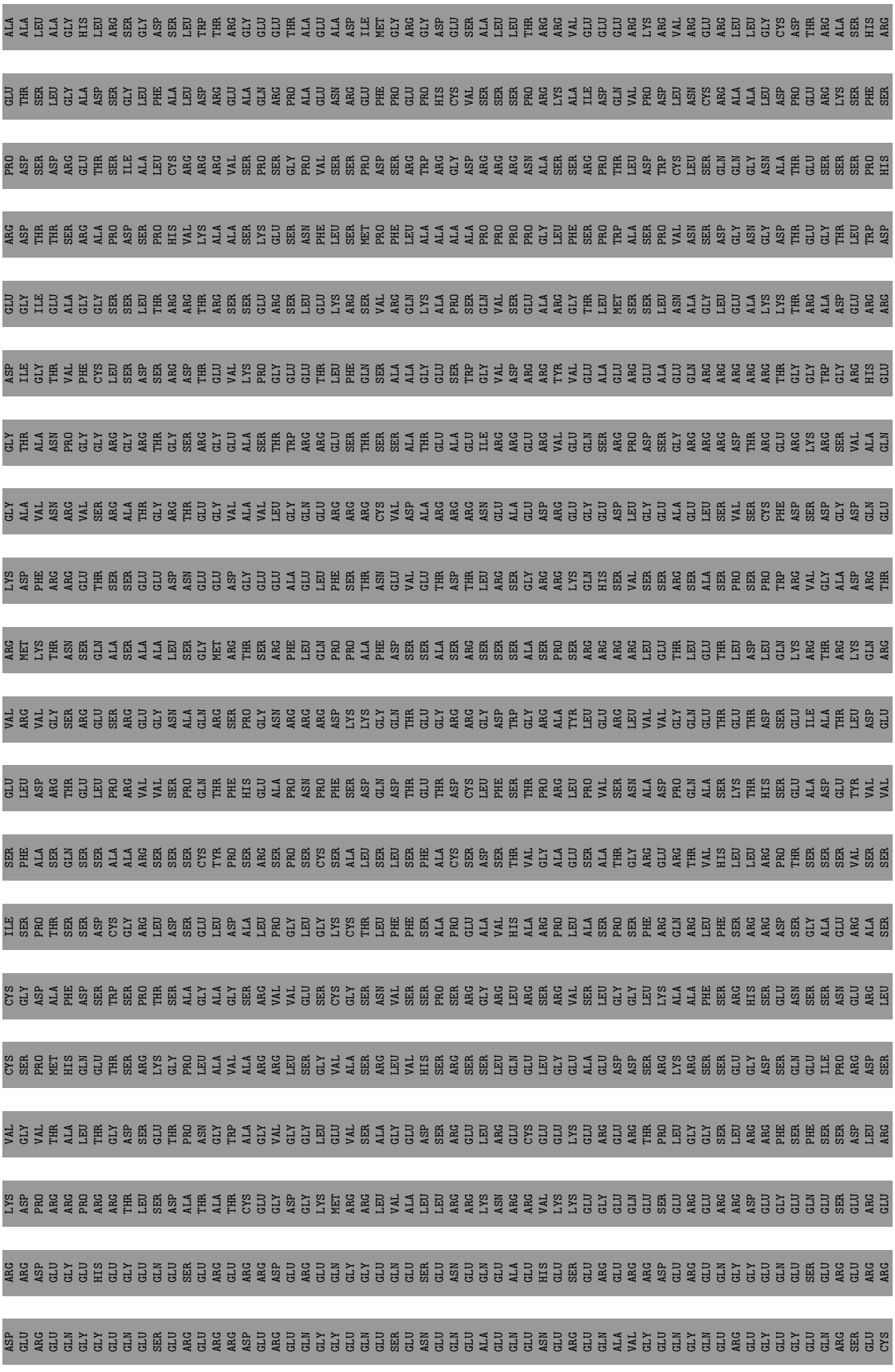

ALA GLN ARG GLU ASP ALA TRP VAL VAL THR GLU SER ALA ARG ASP ARG ARG ARG ALA LEU GLY THR THR VAL SER LEU GLU GLU VAL SER LEU CYS ALA VAL GLY SER SER GLU SER HIS LEU GLU LYS LEU GLY SER GLY GLY ASP GLU ASN ASP CYS GLY ARG ASP ALA SER GLU GLU
THR LYS GLN GLY HIS CYS CYS GLU ASP ARG SER LEU LYS ARG GLU LYS GLU VAL SER ASP TRP GLY VAL GLN THR SER HIS GLU ARG GLU LYS GLN VAL SER ALA ARG GLY VAL GLU THR PRO GLU THR LYS GLU GLU LEU PRO ALA SER PRO LEU SER GLY ASP SER SER SER SER
PRO LEU ALA GLY SER ALA SER ASN VAL PHE PRO ALA ARG LYS ARG LEU PHE SER SER ARG ARG MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS ALA ASP LYS PRO GLY SER PRO SER PHE SER GLN LEU SER ARG SER
ALA GLU ALA ALA THR GLY GLY PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA VAL LEU SER GLY ALA LEU GLU VAL GLN THR GLU GLY TRP GLY VAL GLN THR PRO GLU THR PRO GLY SER PRO SER PHE SER ARG ARG LEU SER LEU
ARG ASP ARG LEU ARG ARG SER SER ALA SER MET THR VAL LEU ASP MET GLU GLU ASN LYS SER LEU ASP ALA LEU SER VAL ASP SER LEU VAL PHE SER GLU HIS LEU SER GLU LEU PHE SER GLN ARG PHE SER SER CYS VAL ASP
PRO VAL SER ASP ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER GLU VAL PRO CYS ALA GLY GLY ALA ARG ALA GLY GLY GLN ARG GLU SER PRO THR SER ARG ARG HIS SER PHE VAL PHE ARG THR THR GLN GLN LYS TYR ARG THR GLU GLY GLY SER ALA
ASP ASN ARG GLY ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LEU VAL LYS SER PRO GLU GLU ASP ARG ARG ASP ALA ALA GLY GLU GLU ASP ARG ILE LEU ARG ASP ARG GLN ILE LEU ARG GLU GLU SER GLU GLU ARG ARG SER GLU GLU LYS ASP ASP GLU
GLU LYS GLN THR GLY LYS ARG GLU GLY ARG LYS LEU ARG HIS LEU SER ALA SER PHE LEU ARG ILE PRO ARG PRO GLY LYS HIS GLU THR ASN LYS GLU SER VAL CYS LYS ARG ARG GLY ALA SER LEU PRO LEU PRO PRO GLU ALA SER ALA LEU ARG
ALA ALA ALA SER PHE SER ARG ARG LEU ARG ARG SER GLN SER SER VAL ASN ARG GLY LYS LYS GLU ALA ILE GLU LYS MET GLU GLU ILE GLU LYS THR LYS ALA GLN ASN GLU ILE LYS HIS GLU ARG LYS SER GLU LEU LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU ASN
VAL ASP GLU ILE LYS GLY GLU GLU VAL LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLU VAL ASN VAL ASP GLU ILE LYS GLN GLU ARG LYS SER GLU LEU LYS GLN GLU ARG LYS SER GLU LEU
LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLU THR PRO GLU THR VAL PRO LEU TRP GLU PRO SER ILE THR SER HIS LEU SER ASP SER CYS GLY GLU ASP VAL ALA ILE PHE ALA VAL GLU ALA CYS ARG THR TRP GLN LYS
GLU ASP GLU THR LEU ARG GLY GLU ASP GLU ASP GLU CYS VAL ASP ARG GLY ASP ALA LEU THR GLY GLN ASP ASP ASN ALA GLU GLU THR SER GLN ARG CYS SER CYS SER GLU ASP SER PRO GLU GLY VAL ALA ALA GLU GLY ARG GLU TRP MET GLY GLY SER
SER ASP GLY ALA GLU ILE HIS LEU LEU PRO GLU GLU GLU GLU GLU GLU ARG GLU GLU HIS GLU LYS GLU GLU GLU GLU GLU GLY GLU GLU GLU GLU GLU GLU

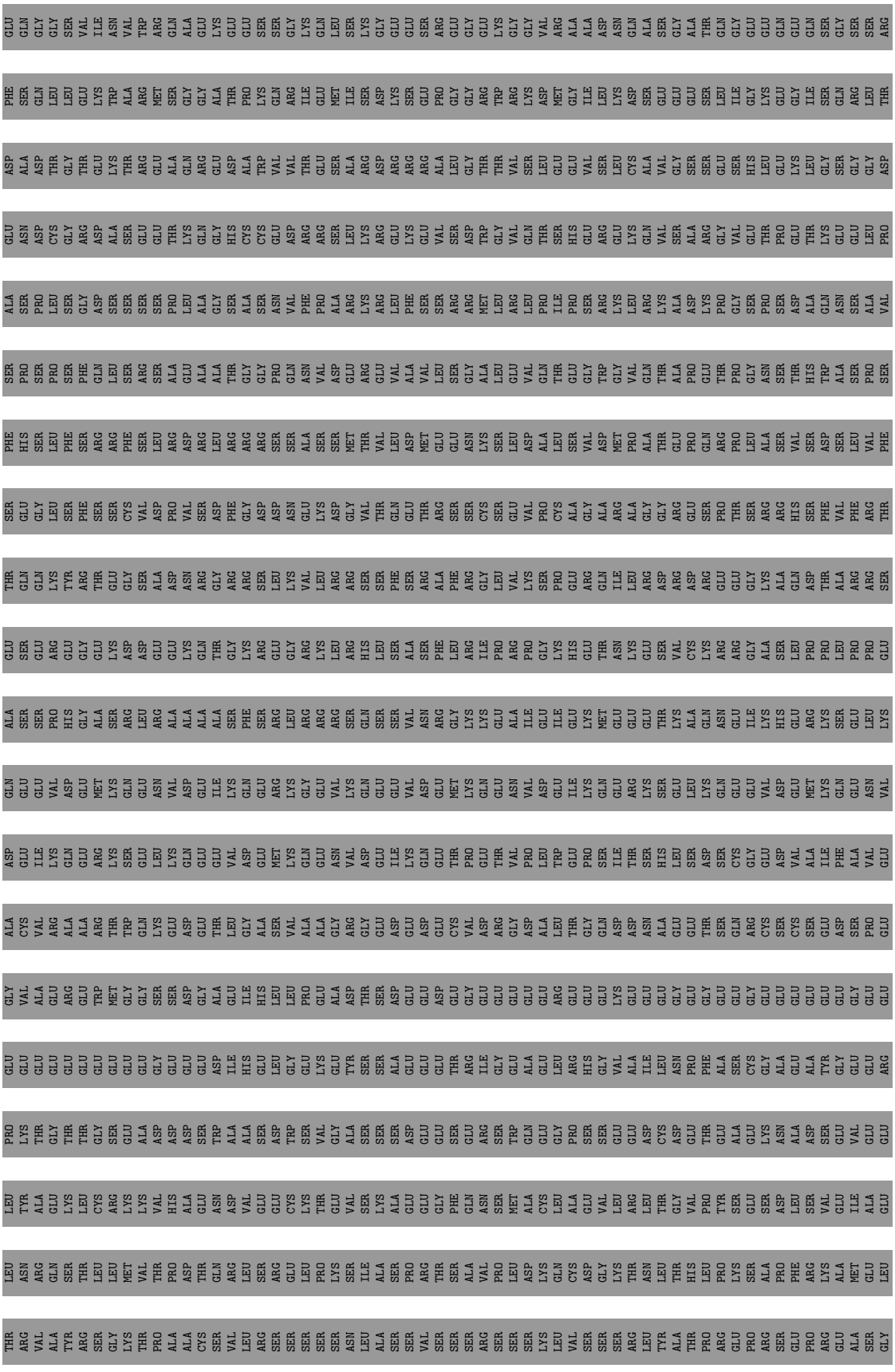


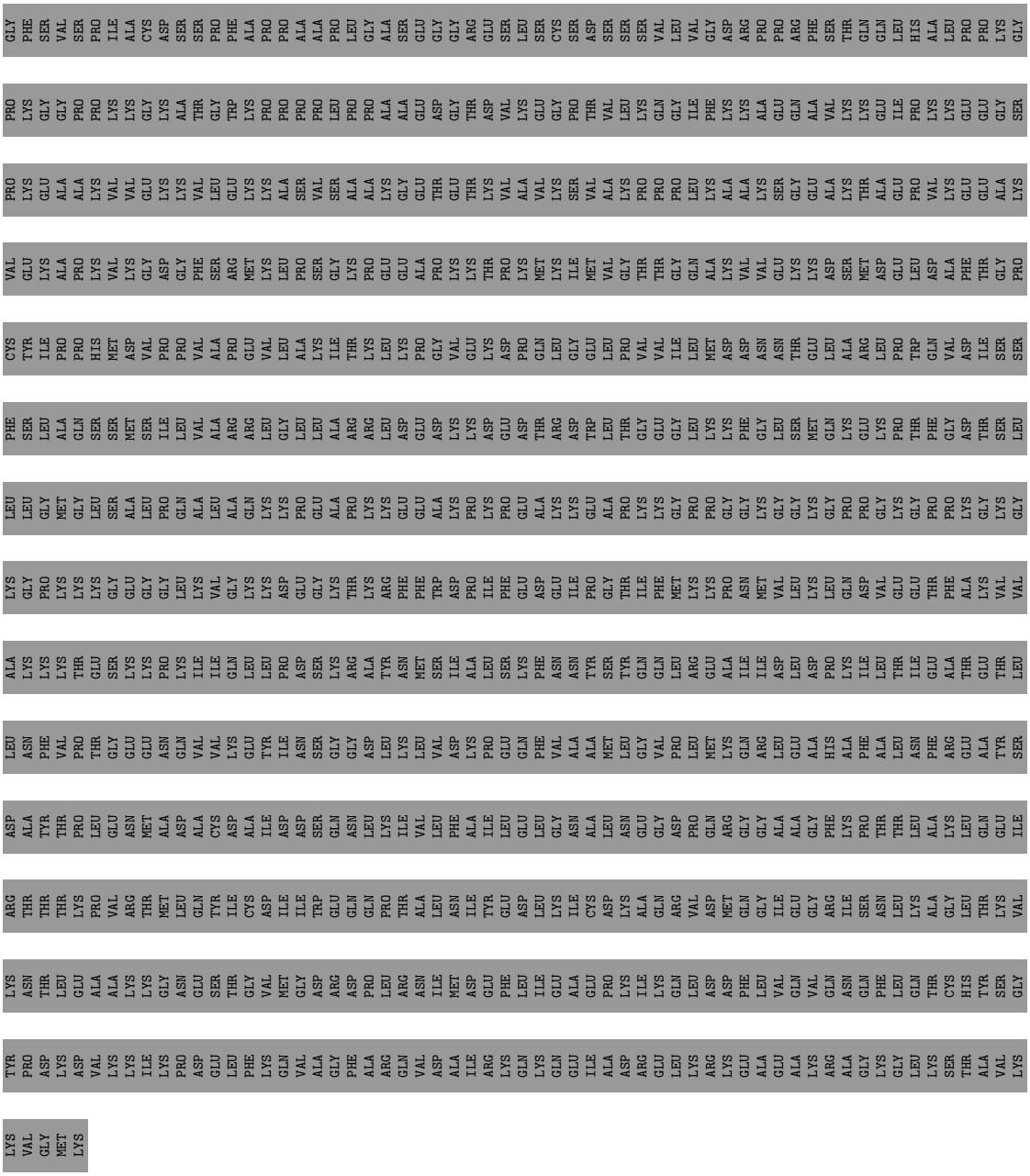
• Molecule 3: Formin 1

Chain CA: 6% 93%


G675
S679
E687
M690
L691
L692
L695
I710
R715
M731
S743
A751
P752
L753
E754
G755
E756
L761
L762
V765
L784
N790
G798
S799
A800
A801
G802
N803
R804
G805
S806
L807
L819
V822
V823
S824
S825
L826
L829
L832
Y833
Y846
T850
V861
T867
L870
A906
L921
I942
L956
H967
F968
R969
A970
V978
V996
L999
L1007
M1011
D1014
K1015
Q1016
R1017
F1018

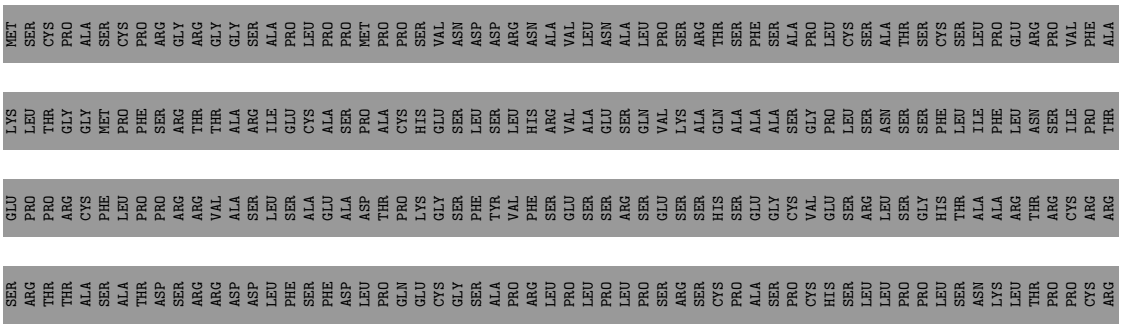


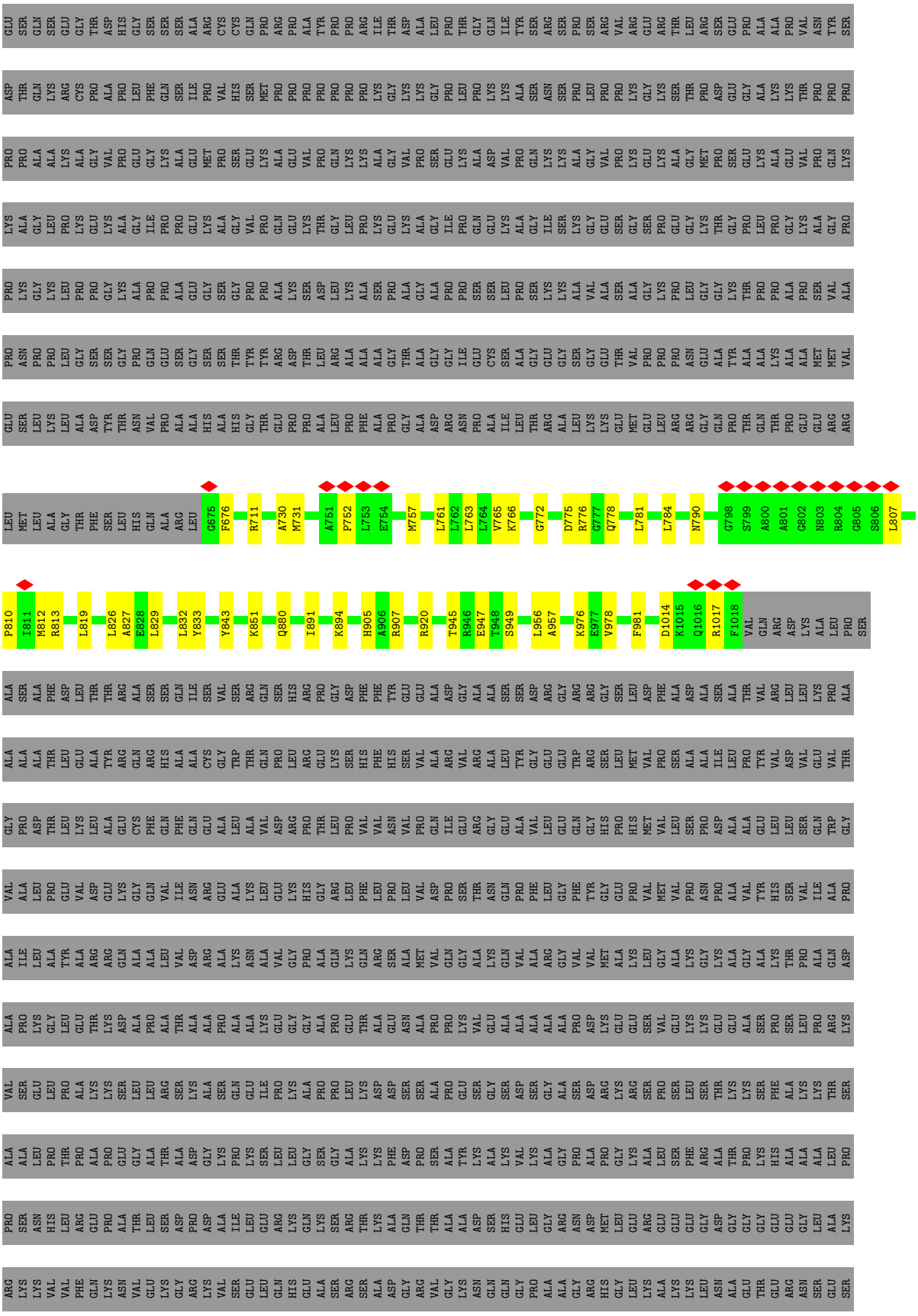

GLU GLN GLY GLY SER VAL ILE ASN VAL TRP ARG GLN ALA GLU LYS GLU GLU SER SER GLY LYS GLN LEU SER LYS GLY GLU GLU SER ARG GLU GLY GLU LYS GLY GLY VAL ARG ALA ALA ASP ASN GLN ALA SER GLY ALA THR GLN GLY GLU GLN GLU GLN SER GLY SER ARG
PHE SER GLN LEU LEU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ARG ILE GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY ARG TRP ARG LYS ASP MET GLY ILE LEU LYS ASP SER GLU GLU GLU SER LEU ILE GLY LYS GLU GLY ILE SER GLN ARG LEU THR
ASP ALA ASP THR GLY THR GLU LYS THR ARG GLU ALA GLN ARG GLU ASP ALA TRP VAL VAL THR GLU SER ALA ARG ASP ARG ARG ALA LEU GLU VAL SER LEU CYS ALA VAL GLY SER SER GLU SER LEU ILE GLY LYS LEU GLU LYS LEU GLY SER ASP GLY
GLU ASN ASP CYS GLY ARG ASP ALA SER GLU GLU THR LYS GLN GLY HIS CYS CYS GLU ASP ARG ARG SER LEU LYS ARG GLU LYS GLN VAL SER ALA ARG GLY VAL GLU THR PRO GLU THR LYS GLU GLU LEU PRO
ALA SER PRO LEU SER GLY ASP SER SER SER PRO LEU ALA GLY SER ALA ALA ARG LYS ARG LEU PHE SER SER ARG MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS ALA ASP LYS PRO GLY SER PRO SER ASP ALA GLN ASN SER ALA VAL
SER PRO SER PRO SER PHE GLN LEU SER ARG SER VAL ASP GLU ARG GLU VAL THR GLN GLU THR ARG SER GLU GLY VAL THR GLN GLU GLY TRP GLY VAL GLN THR ALA PRO GLU THR PRO GLY SER PRO SER PRO GLU ASN SER THR HIS TRP ALA SER PRO VAL SER
PHE HIS SER LEU PHE SER ARG ARG PHE SER LEU ARG ASP ARG LEU ARG ARG SER SER ALA SER SER MET THR VAL LEU ASP MET GLU GLU ASN LYS SER LEU ASP ALA LEU SER VAL ASP MET PRO ALA THR GLU PRO GLN ARG PRO LEU ALA SER VAL SER ASP PRO GLY SER VAL PHE
SER GLU GLY LEU SER PHE SER SER CYS VAL ASP PRO VAL SER ASP PHE GLY ASP ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER GLU VAL PRO CYS ALA GLY ALA ARG ALA GLY GLY ALA GLU SER PRO THR SER ARG ARG HIS SER PHE VAL PHE ARG THR
THR GLN GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASN ARG GLY ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LEU GLU VAL LYS SER PRO GLU ARG GLN ILE LEU ARG ASP ARG GLU GLU GLY GLY LYS ALA GLN ASP THR ALA ARG ARG SER
GLU SER GLU ARG GLU GLY LYS ASP ASP GLU GLU LYS GLN THR GLY LYS ARG GLU GLY LYS LEU ARG HIS LEU SER ALA SER PHE LEU ARG ILE PRO ARG PRO GLY LYS HIS GLU THR ASN LYS GLU SER VAL CYS LYS ARG ARG GLY ALA SER LEU PRO LEU PRO PRO GLU
ALA SER SER PRO HIS GLY ALA ARG ARG SER GLN SER SER SER VAL ASN ARG GLY LYS LYS GLU ALA ILE GLU ILE GLU LYS MET GLU GLU GLU THR LYS ALA GLN ASN GLU ILE LYS HIS GLU LEU GLU
GLN GLU GLU VAL ASP GLU ILE LYS GLN GLU VAL LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLY GLU VAL LYS GLY GLU ILE LYS GLN GLU ARG LYS SER GLU LEU GLU ASN VAL
ASP GLU ILE LYS GLN GLU GLU VAL ASP GLU LEU LYS GLN GLU GLU MET LYS GLN GLU ASP GLU ILE LYS GLN GLU ASN VAL ASP GLU ILE LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLU VAL ASP GLU MET

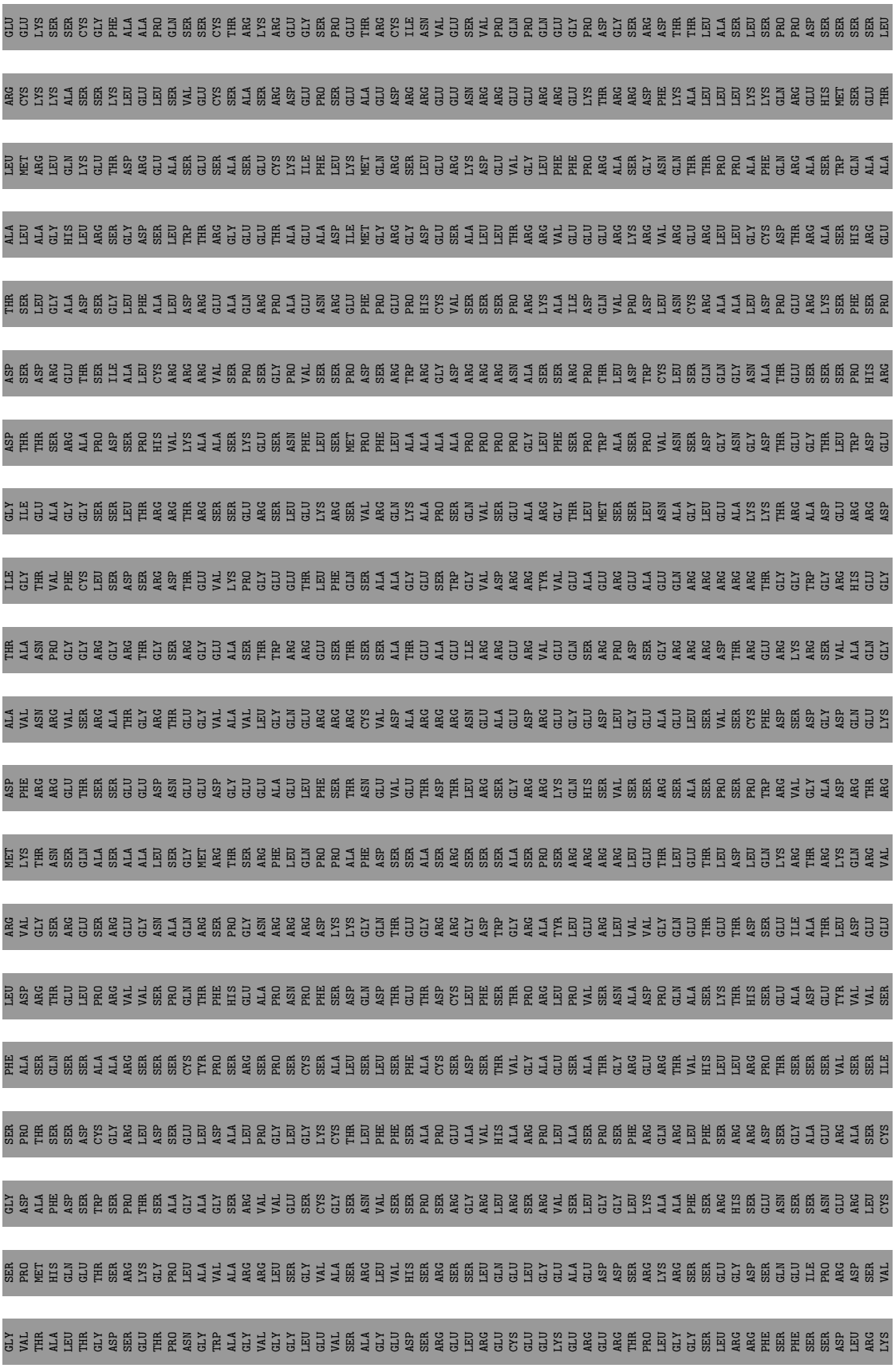


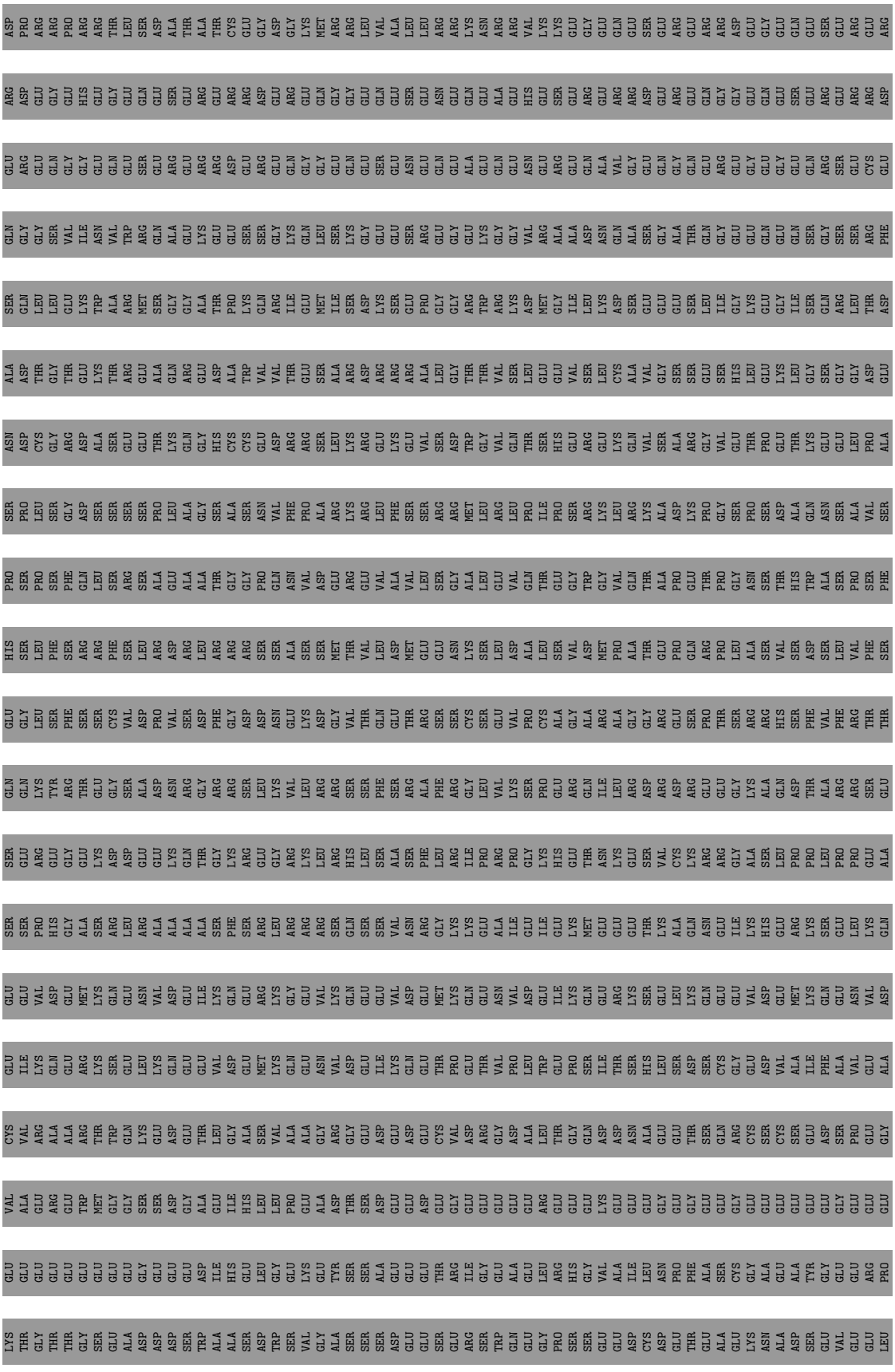
• Molecule 3: Formin 1

Chain CB: 6% • 93%




G675
F676
R711
A730
M731
A751
P752
L753
E754
M757
L761
L762
L763
L764
V765
K766
G772
D775
R776
G777
Q778
L781
L784
N790
G798
S799
A800
A801
G802
N803
R804
G805
S806
L807
P810
I811
M812
R813
L819
L826
A827
E828
L829
L832
Y833
Y843
K851
Q880
I891
K894
H905
A906
R907
R920
T945
R946
E947
T948
S949
L956
A957
K976
E977
V978
F981
D1014
K1015
Q1016
R1017
F1018


GLU GLU LYS SER SER CYS GLY PHE ALA ALA PRO GLN SER SER CYS THR ARG LYS ARG GLU GLY SER PRO GLU THR ARG CYS ILE ASN VAL GLU SER VAL PRO GLN PRO GLN SER SER CYS GLY SER ARG ASP THR THR LEU ALA SER LEU SER PRO PRO ASP SER SER LEU
ARG CYS LYS LYS ALA SER SER LYS LEU GLU LEU SER VAL GLU CYS SER ALA SER ARG ASP GLU PRO SER GLU ALA GLU ASP ARG ARG GLU GLU GLU ARG GLU LYS THR ARG ARG ASP PHE LYS ALA LEU LEU LEU LEU LYS LYS GLN ARG GLU HIS MET SER GLU THR
LEU MET ARG LEU GLN LYS GLU THR ASP ARG GLU ALA SER GLU CYS LYS ILE PHE LEU LYS MET GLN ARG SER LEU GLU ARG LYS ASP GLU VAL GLY LEU PHE PHE PRO ARG GLY ALA SER GLY ASN GLN THR THR PRO PRO ALA PHE GLN ARG ALA SER TRP HIS GLN ALA ALA
ALA LEU ALA GLY HIS LEU ARG SER GLY ASP SER LEU TRP ARG GLY GLU GLU THR ARG ARG VAL GLU GLU GLU ARG LYS ARG ARG ALA SER GLY ASN ASP ILE MET GLY ARG GLY ASP GLU SER ALA LEU LEU THR ARG ARG VAL GLU GLU ARG LEU LEU GLY CYS ASP THR ARG ALA SER HIS ARG GLU
THR SER LEU GLY ALA ASP SER GLY LEU PHE ALA LEU ASP ARG GLU ALA GLN ARG PRO ALA GLU ASN ARG GLU PHE PRO GLU PRO HIS CYS VAL SER SER SER PRO ARG LYS ALA ILE ASP GLN VAL PRO ASP LEU ASN CYS ARG ALA ALA LEU ASP PRO GLU ARG LYS SER PRO
ASP SER ASP ARG GLU THR SER ILE ALA LEU CYS ARG ARG ARG VAL SER SER SER PRO ASP SER ARG TRP HIS CYS VAL ARG GLY ASP ARG ARG ARG ARG SER SER ARG PRO THR LEU ASP TRP CYS LEU SER GLN GLN GLY ASN ALA THR GLU SER GLY SER
ASP THR THR SER ARG ALA PRO ASP SER PRO HIS VAL LYS ALA ALA SER LYS GLU SER ASN PHE LEU ALA ALA ALA ALA PRO PRO PRO GLY LEU PHE SER PRO TRP ALA SER PRO VAL ASN SER ASP GLY ASN GLY ASP THR GLU GLY THR LEU TRP ASP GLU
GLY ILE GLU ALA GLY GLY SER SER LEU THR ARG ARG THR ARG SER SER GLU ARG GLU LYS ARG SER VAL ARG GLN LYS ALA PRO SER GLN VAL SER GLY THR LEU MET SER SER LEU ASN ALA ALA GLY LEU GLU ALA LYS LYS THR ARG ALA ASP GLU ARG ARG ASP
ILE GLY THR VAL PHE CYS LEU SER ASP SER ARG ASP THR GLU VAL LYS PRO GLY GLU GLU THR LEU PHE GLN SER ALA ALA GLY GLU SER TRP GLY VAL ASP ARG ARG TYR VAL GLU ALA GLU GLN ARG ARG ARG THR GLY GLY TRP GLY ARG HIS GLU GLY
THR ALA ASN PRO GLY GLY ARG GLY ARG THR GLY GLY SER ARG GLY GLU ALA SER THR TRP ARG ARG GLU SER THR SER SER ALA ALA THR GLU ALA GLU ILE ARG ARG GLU GLY ARG ARG ASP THR ARG GLU LYS ARG SER VAL ALA GLN GLY
ALA VAL ASN ARG VAL SER ARG ALA THR GLY GLY VAL ALA VAL LEU GLY GLN GLU ARG ARG CYS VAL ASP ALA ARG ARG ARG ASN GLU ALA GLY GLU ASP ARG GLU GLY GLU ASP LEU GLY GLU ALA GLU LEU SER VAL ASP PRO ASP SER GLY GLU ASP GLY GLU LYS
ASP PHE ARG ARG GLU THR SER GLU GLU ASP ASN GLU GLU GLU ASP GLY GLU GLU ALA GLU LEU PHE SER THR ASN GLU VAL GLU THR ASP THR LEU LEU ARG SER GLY SER LYS GLN HIS SER SER VAL SER SER ARG SER ALA SER PRO SER ASP THR LEU ASP SER ARG
MET LYS THR ASN SER GLN ALA SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER ARG SER SER SER SER ARG ARG ARG ARG LEU GLU THR LEU GLU THR LEU ASP SER ARG ARG
ARG VAL GLY SER ARG GLU GLY ASN ARG ARG ARG ASP ASP LYS LYS GLY GLN THR GLU GLY ARG ARG GLY ASP TRP GLY ARG ALA TYR LEU GLU ARG LEU VAL VAL GLY GLN GLU THR GLU THR ASP SER GLU ILE ALA THR LEU ASP VAL
LEU ASP ARG THR GLU LEU PRO ARG VAL VAL SER PRO GLN THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ALA CYS LEU PHE SER THR ASP CYS LEU PHE SER THR VAL PRO ARG LEU PRO VAL SER ASN ALA SER LYS THR HIS SER GLU GLU ALA ASP GLU LYS SER
PHE ALA SER ARG ALA ALA LEU SER LEU SER PHE ALA CYS SER ASP SER ARG GLU ALA VAL GLY ALA GLU SER ALA THR GLY ARG GLU ARG THR VAL HIS LEU LEU SER LEU LEU ARG SER SER SER ILE
SER PRO THR SER SER ASP CYS GLY ARG LEU ASP SER ALA LEU PRO GLU ALA VAL HIS ALA ALA ARG PRO LEU ALA SER PRO SER PHE ARG GLN ARG LEU PHE SER ARG ARG ASP SER GLY ALA GLU ARG ALA SER CYS
GLY ASP ALA PHE ASP SER TRP SER PRO THR SER ARG GLY ARG LEU GLU VAL SER SER PRO SER ARG GLY ARG LEU VAL SER LEU GLY GLY SER PHE SER ARG HIS SER GLU SER ASN SER LEU CYS
SER PRO MET HIS GLN GLU THR SER ARG LEU VAL HIS SER SER ARG SER SER GLY GLU LEU ARG GLU GLN GLU LEU GLY ARG SER GLU GLY ASP SER GLN GLU ILE PRO ARG ASP SER VAL
GLY VAL THR ALA LEU THR GLY ASP SER GLU LEU GLY GLU ALA GLY VAL GLY GLY LEU GLU VAL SER ALA GLY GLU ARG THR PRO LEU GLY GLY SER LEU ARG ARG PHE SER PHE SER ASP LEU ARG LYS
TRP ALA GLY VAL GLY GLY LYS GLU ARG GLU CYS GLU GLU LEU GLU ARG GLU SER ASP SER ARG
ASN GLY GLU LEU SER GLU GLU ASP ARG ASP ARG
PRO ALA VAL GLY GLY ARG ARG
LEU ALA GLU ALA ALA ARG
ALA ALA ALA ALA
ALA ALA ALA
ALA ALA
ALA


ASP PRO ARG ARG PRO ARG ARG THR LEU SER ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG LYS ASN ARG ARG VAL LYS LYS GLU GLY GLU GLN GLN GLU SER GLU ARG
ARG ASP GLU GLY GLU HIS GLU GLY GLU GLN GLU SER GLU ARG GLU ARG ASP GLU ARG GLU GLN GLY GLY GLU GLU ASN GLU GLN GLU ALA GLU HIS GLU SER GLU ARG GLU ARG ASP
GLU ARG GLU GLN GLY GLU GLN GLU SER GLU ARG GLU ARG ARG ASP GLU ARG GLU GLN GLY GLY GLU GLU SER GLU ARG GLU GLN GLU GLN GLU ALA GLU GLN GLU ALA GLU ASN GLU ARG SER GLU CYS GLU
GLN GLY GLY SER VAL ILE ASN VAL TRP ARG GLN ALA GLU LYS GLU GLU SER SER GLY LYS GLN LEU SER LYS GLY GLU SER ARG GLU GLY GLY VAL ARG ALA ALA ASP ASN GLN ALA VAL GLY GLU GLN GLY GLN GLN SER GLY SER SER ARG PHE
SER GLN LEU LEU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ILE MET ILE SER ASP SER LYS GLY GLU GLY ARG ILE GLU MET ILE SER ASP LYS ASP SER GLU GLU GLU GLU SER LEU ILE GLY LYS GLU GLU GLY ILE SER GLN ARG LEU THR ASP
ALA ASP THR GLY THR LYS THR ARG GLU ALA ALA LEU GLY THR THR VAL SER LEU CYS ALA VAL GLY SER SER GLU SER HIS LEU GLU LYS LEU GLY SER GLY GLY GLU ASP GLU
ASN ASP CYS GLY ARG ALA SER GLU GLU LYS ARG GLU LYS GLU VAL SER ALA ARG GLY VAL GLU THR PRO GLU LYS GLU GLU LEU PRO ALA
SER PRO LEU SER GLY ASP SER SER SER PRO LEU PRO ALA ARG LYS ARG LEU PHE SER SER ARG LYS LEU ARG LYS ALA ASP LYS PRO GLY SER PRO SER ASP ALA GLN ASN SER ALA VAL SER
PRO SER PRO SER PHE GLN LEU SER ARG SER ALA GLU ALA ALA THR GLY GLY PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA VAL LEU SER GLY ALA LEU GLU VAL GLN THR GLU GLY TRP GLY VAL GLN THR ALA PRO GLU THR PRO GLY SER THR HIS TRP ALA SER PRO PHE
HIS SER LEU PHE SER ARG ARG PHE SER LEU ARG ASP ARG LEU ARG ARG ARG PHE SER SER ALA SER SER MET THR VAL LEU ASP MET GLU GLU ASN LYS SER LEU ASP ALA LEU SER VAL ASP MET PRO ALA THR GLU PRO GLN ARG PRO LEU SER ASP SER LEU VAL PHE SER
GLU GLY LEU SER PHE SER SER CYS VAL ASP PRO VAL SER ASP PHE GLY GLY ASP ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER GLU VAL PRO CYS ALA GLY ALA ARG ALA GLY GLY ARG GLU SER PRO THR SER ARG ARG HIS SER PHE VAL PHE ARG THR THR
GLN GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASP ASN ARG GLY ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LEU ARG ARG ARG SER GLU LYS VAL LEU ARG ARG SER GLU ILE LEU ARG ASP ARG GLN ILE GLU ARG ASP ASP ARG GLU ARG ASP ASP ARG GLU SER GLU
SER GLU ARG GLU GLY GLU LYS ASP GLU ASP GLU ARG GLU GLY ARG LYS LEU ARG ARG SER GLU ARG ILE PRO ARG PRO LEU ARG LYS HIS GLU THR ASN LYS GLU SER VAL CYS LYS ARG GLY ALA SER LEU PRO PRO LEU PRO PRO GLU ALA
SER SER PRO HIS GLY ALA SER ARG LEU SER SER GLN SER SER VAL ASN ARG GLY LYS LYS GLU ALA ALA ILE GLU ILE GLU LYS MET GLU GLU GLU THR LYS ALA GLN ASN GLU ILE LYS HIS GLU LEU SER LYS GLN
GLU GLU VAL ASP GLU ASN VAL ASP GLU MET LYS GLN GLU VAL ASP GLU ILE LYS GLN GLU GLU LYS SER ASP GLU ILE LYS GLN GLU GLU VAL ASP GLU GLU MET LYS GLN GLU
GLU ILE LYS GLN GLU LEU LYS GLN GLU MET LYS GLN GLU GLU ASP VAL PRO LEU TRP GLU PRO SER ILE THR SER HIS LEU SER ASP SER CYS GLY GLU ASP VAL ALA ILE PHE ALA VAL GLU ALA
CYS VAL ARG ALA ALA ARG THR TRP GLN LYS GLU ASP GLU CYS VAL ASP ARG GLY GLU ASP ALA LEU THR GLY GLN ASP ASP ALA GLU ARG GLN SER ILE CYS SER GLN ARG CYS SER CYS SER GLU ASP SER GLY
VAL ALA GLU ARG GLU TRP MET GLY GLY SER SER ASP GLY GLU ASP GLU GLY GLU GLU ARG GLU ASP GLU GLU GLU LYS GLU GLU GLU GLU GLU GLU GLU GLU GLY GLU GLY GLU GLU GLU GLU GLU GLU GLU
GLU GLU GLU GLU GLY GLU GLU GLU THR ARG ILE GLY GLU ALA GLU LEU ARG HIS GLY VAL ALA ILE LEU ASN PRO PHE ALA SER CYS GLY ALA GLU ALA TYR GLY GLU ARG PRO
LYS THR GLY THR THR GLY SER GLU ALA ASP ASP ASP SER TRP ALA ALA SER ASP SER SER SER ASP GLU GLU SER GLU ARG GLU GLN TRP SER VAL GLY ALA SER SER GLU GLU ALA ASP SER GLU VAL GLU GLU LEU

TYR ALA GLU LYS LEU CYS ARG LYS LYS VAL HIS ALA GLU ASN ASP VAL GLU GLU CYS LYS THR GLU VAL SER LYS ALA GLU GLU GLY PHE GLN ASN SER MET ALA CYS LEU ALA GLU VAL LEU ARG LEU THR GLY VAL PRO TYR SER GLU SER ASP LEU SER VAL GLU ILE ALA GLU LEU

ASN ARG GLN SER THR LEU LEU MET VAL THR PRO ASP THR GLN ARG LEU SER ARG GLU LEU PRO LYS SER ILE ALA SER PRO ARG THR SER ALA VAL PRO LEU ASP LYS GLN CYS ASP GLY LYS THR ASN LEU THR HIS LEU PRO LYS SER ALA PRO PHE ARG LYS ALA MET GLU LEU THR

ARG VAL ALA TYR ARG SER GLY LYS THR PRO ALA ALA CYS SER VAL LEU ARG SER SER SER SER SER ASN LEU ALA SER SER ARG LEU TYR ALA THR PRO ARG GLU PRO ARG SER GLU PRO ALA GLY LEU ALA SER SER SER VAL SER SER SER SER SER SER SER SER SER LYS LEU VAL SER SER ARG LEU GLU ALA SER GLY GLY

PHE SER VAL SER PRO ILE ALA CYS ASP SER SER PRO PHE ALA PRO PRO ALA ALA PRO LEU GLY ALA SER GLU GLY GLY ARG GLU SER LEU SER CYS SER ASP SER VAL LEU VAL GLY ASP ARG PRO PRO ARG PHE SER THR GLN GLN LEU HIS ALA LEU PRO PRO ARG GLY PRO

LYS GLY GLY PRO PRO LYS LYS GLY LYS ALA THR GLY TRP LYS PRO PRO PRO ALA PRO LEU PRO LYS GLN GLY ILE PHE LYS LYS ALA GLU GLN ALA VAL LYS LYS GLU GLY PRO THR VAL LEU LYS GLN GLY ILE PRO LYS LYS GLU GLU GLY SER PRO

LYS GLU ALA ALA LYS VAL VAL GLU LYS LYS LYS VAL LEU GLU LYS LYS ALA SER VAL SER ALA ALA LYS GLY GLU THR GLU THR LYS VAL ALA ALA LYS PRO PRO PRO LEU LYS ALA LYS SER GLY GLU GLY GLU ALA LYS LYS VAL

GLU LYS ALA PRO LYS VAL LYS GLY ASP GLY PHE SER ARG MET LYS LEU PRO SER GLY LYS PRO GLU GLU ALA PRO LYS LYS THR PRO VAL LYS MET LYS ILE MET VAL GLY THR THR GLY GLN ALA LYS VAL VAL GLU LYS LYS ASP SER MET ASP GLU LEU ASP ALA PHE THR GLY PRO CYS

TYR ILE PRO PRO HIS MET ASP VAL PRO PRO VAL ALA PRO GLU VAL LEU ALA LYS ILE THR LYS LEU LYS PRO GLY VAL GLU LYS ASP PRO GLN LEU GLY GLU LEU PRO VAL VAL ILE LEU MET ASP ASP ASN ASN THR GLU LEU ALA ARG LEU PRO TRP GLN VAL ASP ILE SER SER PHE

SER LEU ALA GLN SER SER MET SER ILE LEU VAL ALA ALA ARG ARG ARG LEU GLY LEU LEU LEU ALA ARG ARG LEU ASP GLU ASP LYS LYS ASP GLU ASP THR ARG ASP TRP LEU THR GLY GLU GLY LEU LYS LYS PHE GLY LEU SER MET GLN LYS GLU LYS PRO THR PHE GLY ASP THR SER LEU LEU

LEU GLY MET GLY LEU SER ALA LEU PRO GLN ALA LEU ALA GLN LYS LYS PRO GLU ALA ALA PRO LYS LYS GLU GLU ALA LYS PRO LYS PRO GLU ALA LYS LYS GLU LYS PRO PRO GLY GLY LYS GLY GLY LYS GLY PRO GLY PRO PRO LYS GLY LYS GLY LYS GLY

GLY PRO LYS LYS LYS GLY GLU GLU GLY GLY LEU LYS VAL GLY LYS LYS GLU GLY LYS THR LYS ARG PHE PHE TRP ASP PRO ILE PHE PHE GLU ASP GLU ILE PRO GLY THR ILE PHE MET LYS LYS PRO ASN MET VAL LEU LYS LEU GLN ASP VAL GLU THR PHE ALA LYS VAL VAL ALA

LYS LYS LYS THR GLU SER LYS LYS PRO LYS ILE ILE GLN LEU LEU LEU PRO ASP SER LYS ARG ALA TYR ASN MET SER ILE ALA LEU SER LYS PHE ASN ASN TYR SER TYR GLN GLN LEU ARG GLU ALA ILE ILE ASP LEU ASP PRO LYS ILE LEU THR ILE GLU ASP ALA LEU LEU

ASN PHE VAL PRO THR GLY GLU GLU ASN GLN VAL VAL LYS GLU GLY ASP LEU LYS LEU VAL ASP ASP LYS PRO GLU GLN PHE VAL ALA ALA MET LEU GLY VAL PRO LEU MET LYS GLN ARG LEU GLU ALA HIS ALA PHE ALA LEU ASN PHE ARG GLU ALA TYR SER ASP

ALA TYR THR PRO LEU GLU ASN MET ALA ASP ALA CYS ASP ALA ILE ASP ASP SER GLN ASN LEU LYS ILE VAL LEU PHE ALA ILE LEU GLU LEU GLY ASN ALA LEU ASN GLU GLY ASP PRO GLN ARG GLY GLY ALA ALA GLY PHE LYS PRO THR THR LEU LEU ALA LYS LEU GLN GLU ILE ARG

THR THR THR LYS PRO VAL ARG THR MET LEU GLN TYR ILE CYS ASP ILE ILE ILE TRP GLU GLN GLN PRO THR ALA LEU ASN ILE TYR GLU ASP LEU LYS ILE CYS ASP LYS ALA GLN ARG VAL ASP MET GLN GLY ILE GLU GLY ARG ILE SER ASN LEU LYS ALA GLY LEU THR LYS VAL LYS

ASN THR LEU GLU ALA ALA LYS LYS GLY ASN GLU SER THR GLY VAL MET GLY ASP ARG ASP PRO LEU ARG ASN ILE MET ASP GLU PHE LEU ILE GLU ALA GLU PRO LYS ILE LYS GLN LEU ASP PHE LEU VAL GLN VAL ASN ASN GLN PHE LEU GLU LEU LYS GLN LEU GLY GLY LEU ASP

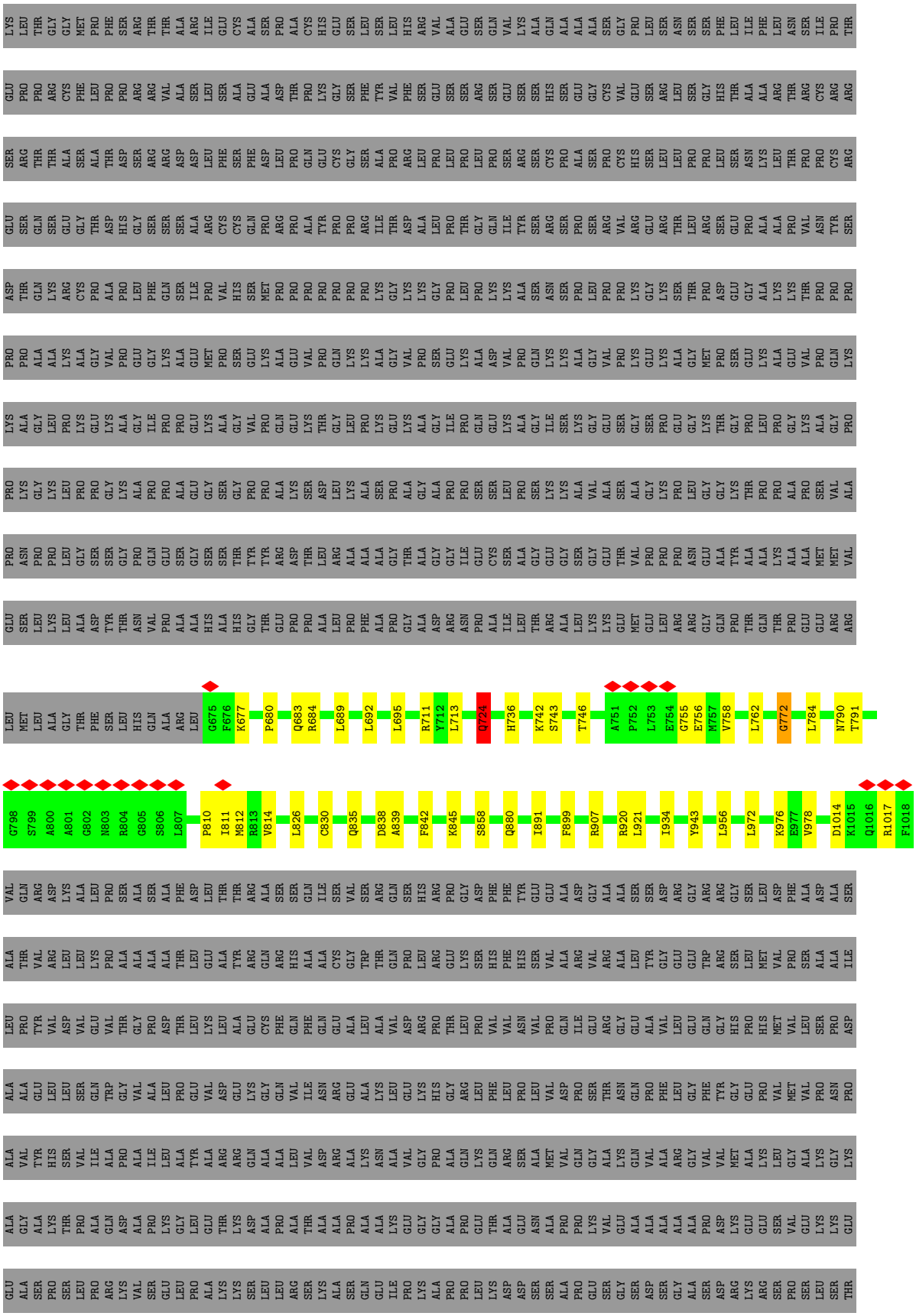
PRO ASP LYS ASP VAL LYS ILE PRO ASP GLU LEU PHE LYS GLN VAL ALA GLY PHE ALA ARG GLN VAL ASP ALA ILE ARG LYS GLN GLU ILE ALA ASP ARG GLU LEU LYS ARG GLU ALA GLU ALA ALA LYS ARG ALA GLY LYS SER THR ALA VAL LYS LYS

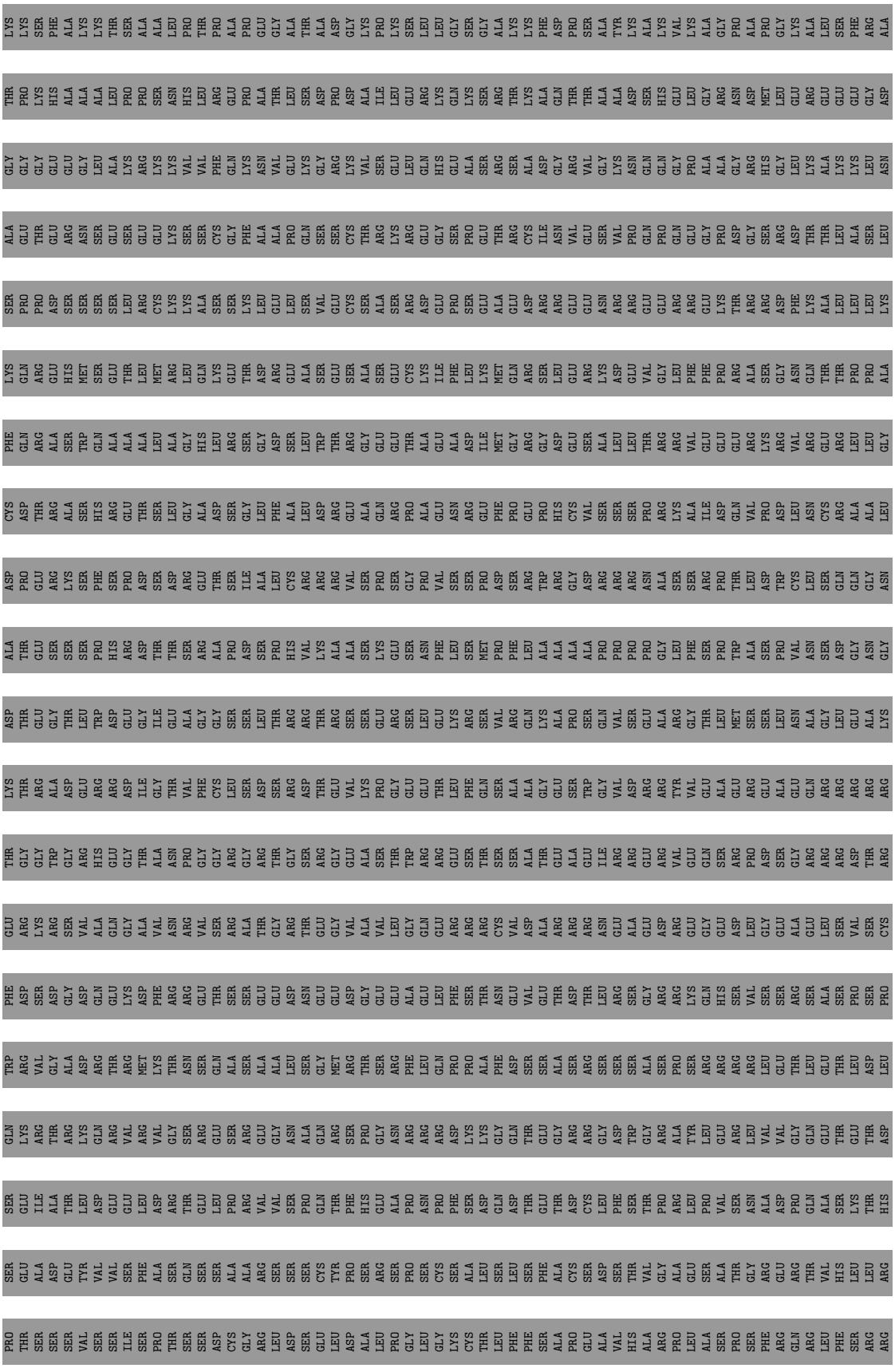
VAL GLY MET LYS

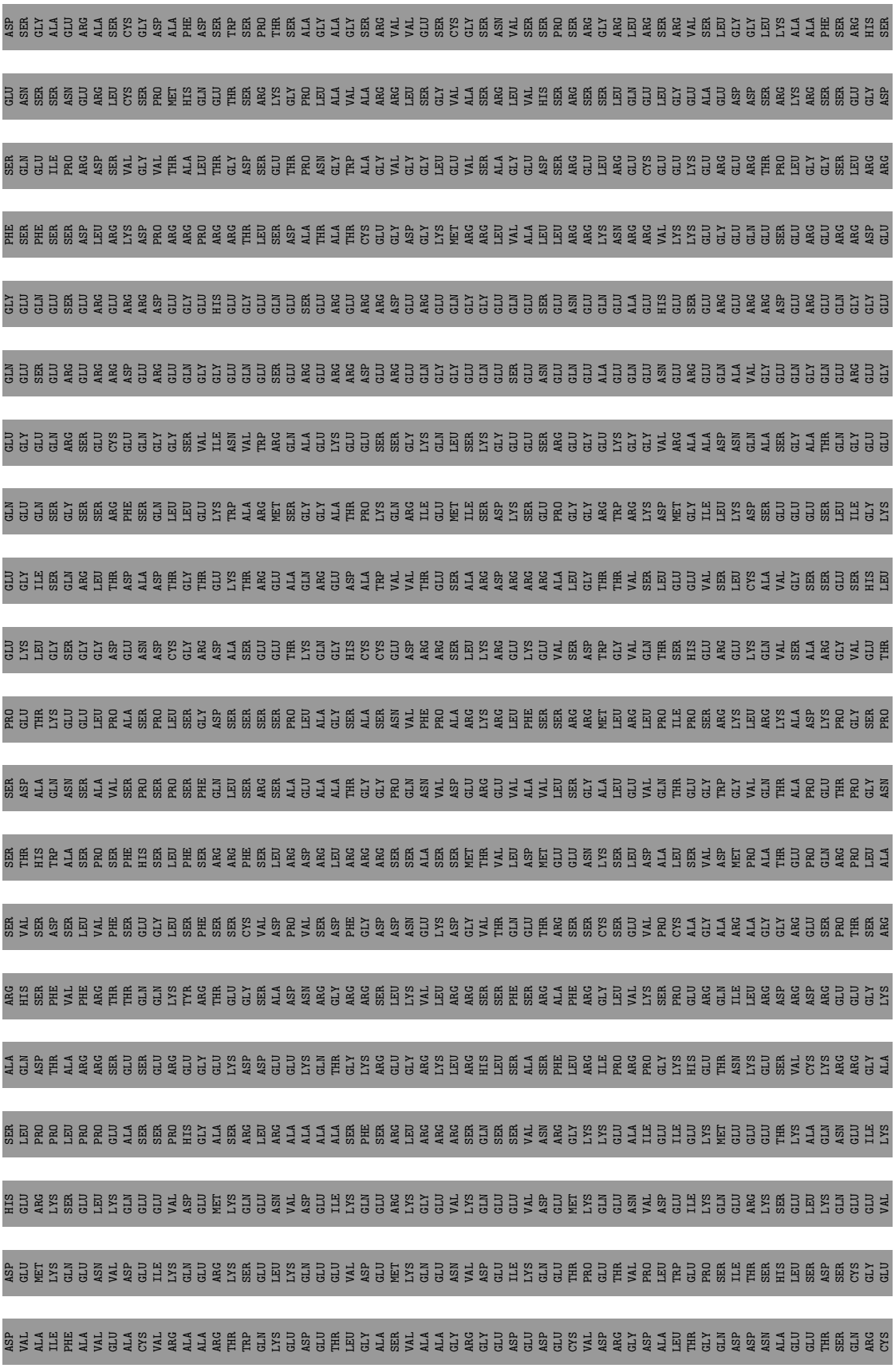
- Molecule 3: Formin 1

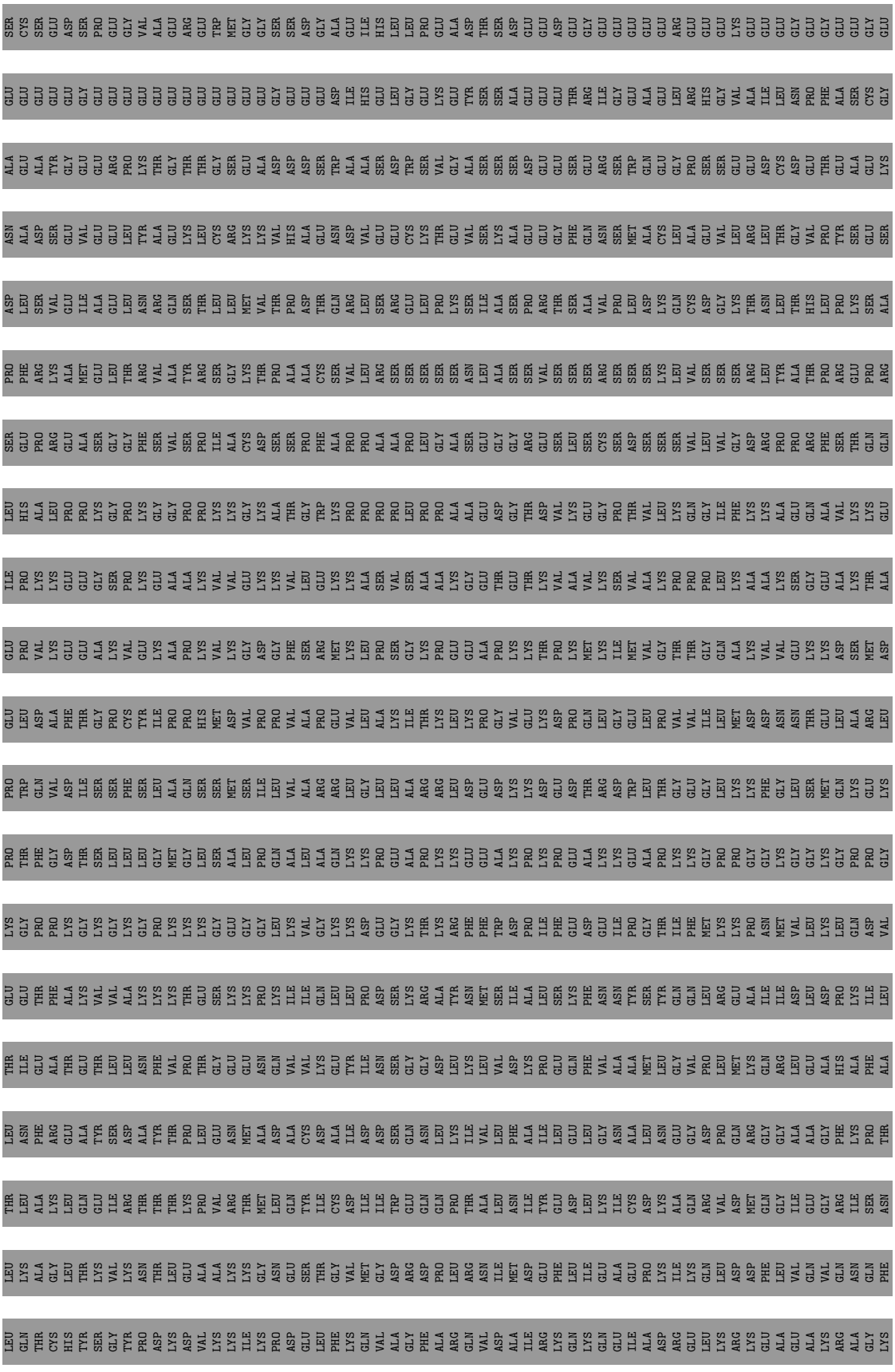
Chain CC: 6% 93%

MET SER CYS PRO ALA SER CYS PRO ARG GLY ARG GLY GLY SER ALA PRO LEU PRO PRO MET PRO PRO PRO SER VAL ASN ASP ASP ARG ASN ALA VAL LEU ASN ALA LEU PRO SER ARG THR SER PHE SER ALA PRO LEU CYS SER ALA THR SER CYS SER LEU PRO GLU ARG PRO VAL PHE ALA


G675 F676 K677 P680 Q683 R684 L689 L692 L695 R711 Y712 L713 Q724 H736 K742 S743 T746 A751 P752 L753 E754 G755 E756 M757 V758 L762 G772 L784 N790 T791
G798 S799 A800 A801 G802 N803 R804 G805 S806 L807 P810 I811 M812 R813 V814 L826 C830 Q835 D838 A839 F842 K845 S858 Q880 I891 F899 R907 R920 L921 I934 Y943 L956 L972 K976 E977 V978 D1014 K1015 Q1016 R1017 F1018


LYS LYS SER PHE ALA LYS LYS THR SER ALA ALA LEU PRO THR PRO ALA PRO GLU GLY ALA THR ALA ASP PRO GLY LYS PRO LYS SER LEU LEU GLY SER GLY ALA LYS LYS PHE ASP PRO SER ALA TYR LYS ALA LYS VAL LYS ALA GLY PRO ALA PRO GLY LYS ALA LEU SER PHE ARG ALA
THR PRO LYS HIS ALA ALA ALA LEU PRO PRO SER ASN HIS LEU ARG GLU PRO ALA THR LEU SER ASP PRO ASP ALA ILE LEU GLU ARG LYS GLN LYS SER ARG THR LYS ALA GLN THR THR ALA ALA ALA ASP SER HIS GLU LEU GLY ARG ASN ASP MET LEU GLU ARG GLU GLU LEU
GLY GLY GLY GLU GLU GLY LEU ALA LYS ARG LYS LYS VAL VAL PHE GLN LYS ASN VAL GLU LYS GLY ARG GLN ARG VAL GLY LYS ASN GLN GLN GLY PRO ALA ALA GLY ARG HIS GLY LEU LYS ASN LYS LYS LEU ASN
ALA GLU THR GLU ARG ASN SER GLU GLU GLU LYS SER SER CYS GLY PHE ALA ALA PRO GLN SER SER CYS THR ARG LYS ARG GLU GLY SER PRO GLU THR ARG CYS ILE ASN VAL GLU SER VAL PRO GLN PRO GLN GLU GLY PRO ASP GLY ASP ARG ASP THR THR LEU GLU LEU
SER PRO PRO ASP SER SER SER SER LEU ARG GLU CYS LYS LYS SER ALA SER SER LYS LEU GLU LEU SER VAL GLU GLU CYS SER ALA SER GLU GLU ASP ARG ARG GLU ARG GLU LYS THR ARG ARG ASP PHE LYS ALA LEU LEU LEU LYS
LYS GLN ARG GLU HIS MET SER GLU THR LEU MET ARG LEU GLN LYS GLU THR ASP ARG GLU SER ALA SER GLU CYS LYS ILE PHE LEU LYS SER GLU GLU ARG ASP ARG LEU GLN ARG GLN LYS ASP GLU VAL GLY LEU ASN GLN THR THR LEU PRO LEU ALA
PHE GLN ARG ALA SER TRP GLN ALA ALA LEU ALA GLY HIS LEU ARG SER GLY ASP SER LEU TRP THR ARG GLY GLU ALA SER GLU LEU THR ARG ARG VAL GLU VAL SER SER THR ARG GLU GLU ALA ASP GLU SER ALA ALA ILE ASP GLN VAL PRO ARG GLU GLU ARG LYS ARG VAL LEU ASP LEU GLY
CYS ASP THR ARG ALA SER HIS ARG GLU THR SER LEU GLY ALA ASP SER GLY LEU PHE ALA LEU ASP ARG GLU ALA GLN ARG PRO ALA GLU ASN ARG GLU PHE PRO GLU PRO HIS CYS VAL SER SER SER PRO ARG LYS ALA ILE ASP GLN VAL PRO ASP LEU ASN CYS ARG ALA ALA LEU
ASP PRO GLU ARG ARG SER PHE SER PRO SER GLY PRO VAL SER SER PRO ARG ASP SER ARG TRP GLY ASP ARG ARG ASN ALA SER SER ARG PRO THR LEU ASP TRP CYS LEU SER GLN GLN GLY ASN
ALA THR GLU SER SER PRO HIS ARG ASP THR THR SER ARG ALA PRO ASP SER PRO HIS VAL LYS ALA ALA SER LYS GLU SER ASN PHE LEU SER MET PRO PHE LEU ALA ALA ALA ALA PRO PRO PRO PRO GLY LEU PHE SER PRO TRP ALA SER PRO VAL ASN SER ASP GLY ASN GLY
ASP THR GLU GLY THR LEU GLU ILE GLU ALA GLY GLY SER SER LEU THR ARG SER SER GLU GLU ARG SER LEU GLU LYS ARG SER VAL ARG GLN LYS ALA PRO SER GLN VAL SER GLU ALA ARG GLY THR LEU MET SER SER LEU ASN ALA GLY LEU GLU GLU ALA LYS
LYS THR ARG ALA ASP GLU ARG ARG ASP ASP THR GLU VAL LYS PRO GLY GLU GLU THR LEU PHE GLN SER ALA ALA GLY GLU SER TRP GLY VAL ASP ARG ARG TYR VAL GLU ALA GLU GLU ARG GLU ALA GLU GLN ARG ARG ARG ARG ARG
THR GLY GLY TRP GLY ARG HIS GLU GLY THR ALA ASN PRO GLY GLY GLY ARG GLY GLY GLU ALA SER THR TRP ARG GLU SER THR ARG GLU ALA GLU ILE ARG ARG GLU ARG VAL GLU GLN SER ARG ASP ASP LEU ARG ARG
GLU ARG LYS ARG SER VAL ALA VAL ASN ARG GLY GLU GLN GLU ARG ARG ARG CYS VAL ASP ALA ARG ARG ARG ASN GLU ALA GLU ASP ARG GLU GLY GLU ALA GLU LEU ASP LEU GLY GLU ALA GLU LEU SER VAL SER CYS
PHE ASP SER ASP GLY ASP GLN GLU ASP ASP GLY GLU GLU LYS ASP PHE ARG ARG GLU ASP GLU ALA GLU LEU PHE SER THR ASN GLU VAL GLU THR ASP THR LEU ARG SER GLY GLU SER THR HIS SER VAL SER SER GLY ARG SER ALA SER PRO SER
TRP ARG VAL GLY ALA ASP ARG THR MET ARG THR SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER ALA LEU SER ARG SER SER ALA SER ARG SER SER SER ALA SER PRO SER ARG ARG ARG GLU LEU GLU THR LEU ASP LEU
GLN LYS ARG THR ARG VAL ARG VAL GLU GLY SER ARG GLU ALA ASN GLN ARG VAL GLY ASN ARG ARG ARG ASP LYS LYS GLY GLN THR GLU GLY ARG GLY SER TRP GLY ARG ALA TYR LEU GLU ARG LEU GLU VAL VAL GLY GLN GLU GLU THR ASP
SER GLU ILE ALA THR LEU ASP GLU GLU LEU ASP ARG VAL VAL SER PRO GLN THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ASP THR GLU THR ASP CYS LEU PHE SER THR PRO ARG LEU PRO VAL SER ASN HIS ALA ALA ASP PRO ILE HIS
SER GLU ALA ASP ALA ARG VAL SER LEU ALA ARG ALA SER SER SER LEU ARG LEU PHE SER ALA LEU SER PHE ALA CYS SER ASP SER THR VAL GLY ARG ALA GLU SER ALA THR ARG GLN ARG LEU ARG
PRO THR SER SER VAL SER ILE SER PRO THR SER SER ASP CYS GLY ARG LEU ASP ALA LEU PRO GLY LEU GLY LYS CYS THR LEU PHE PHE SER ALA PRO GLU ALA VAL HIS ALA ARG PRO LEU ALA SER PRO SER PHE ARG GLN ARG LEU PHE SER ARG LEU


ASP SER GLY ALA GLU ARG ALA SER CYS GLY ASP ALA PHE ASP SER TRP SER PRO THR SER ALA GLY ALA GLY SER ARG LEU ARG SER ARG VAL VAL GLU SER CYS GLY VAL ALA SER ASN VAL SER SER PRO SER ARG GLY LEU LYS ALA ALA PHE SER ARG HIS SER
GLU ASN SER SER ASN GLU ARG LEU CYS SER PRO MET HIS GLN GLU THR SER ARG LYS GLY PRO LEU ALA VAL ALA ARG ARG LEU SER GLY VAL ALA SER ARG LEU VAL HIS SER ARG SER SER LEU GLN GLU LEU GLY GLU ALA GLU ASP ASP SER ARG LYS ARG SER SER GLU GLY ASP
SER GLN GLU ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU THR GLY ASP SER GLU THR PRO ASN GLY TRP ALA GLY VAL GLY GLY LEU GLU VAL SER GLU ALA GLU LEU ARG GLU CYS GLU GLU LYS GLU ARG GLU ASP ASP SER ARG GLU SER LEU GLY GLY SER LEU ARG ARG
PHE SER PHE SER SER ASP LEU ARG LYS ASP PRO ARG ARG ARG PRO ARG ARG THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU LEU ARG ARG LYS ASN ARG GLY GLU ARG GLU ARG ARG ASP
GLY GLU GLN GLU SER GLU ARG ARG ASP GLU GLY GLU GLU SER ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU LEU ARG ARG LYS ASN ARG GLY GLU ARG GLU ARG ASP
GLN GLU SER GLU ARG GLU ARG ARG ASP GLU GLN GLU GLU SER GLU ASP SER GLU ARG GLU ARG GLU ARG ASP GLU GLY GLN GLU SER GLU ARG GLU ARG ASP
GLU GLY GLU GLN ARG SER GLU CYS GLU GLN GLY GLY SER VAL ILE ASN VAL TRP ARG GLN ALA GLU LYS GLU GLU SER SER GLY LYS GLN LEU SER LYS GLY GLU GLU SER GLU SER ARG GLU GLY GLY GLU GLN GLU GLU
GLN GLU SER GLY SER SER ARG PHE SER GLN LEU LEU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ILE GLU MET ILE SER ASP LYS SER GLU SER ARG GLU PRO GLY GLY ARG TRP ARG LYS GLY GLY VAL ARG ALA ALA THR GLN LEU LEU LYS ASP MET GLY ILE LEU LEU LYS ASP SER GLU GLU SER LEU ILE GLY LYS
GLU GLY ILE SER GLN ARG LEU THR ASP ALA ASP THR GLY THR GLU ARG GLU ALA GLN ARG GLU ASP ALA TRP VAL VAL THR GLU SER ALA ARG ASP ARG ARG ARG ALA LEU GLY THR THR VAL SER LEU GLU GLU VAL SER LEU CYS ALA VAL GLY SER SER GLU HIS LEU
GLU LYS LEU GLY SER GLY ASP GLU ASN ASP CYS GLY ARG ASP ALA SER GLU GLU THR LYS GLN GLY HIS CYS CYS GLU ASP ARG ARG SER LEU LYS ARG GLU LYS GLU VAL SER ASP TRP GLY VAL GLN THR SER HIS GLU ARG GLU LYS LEU GLY SER ALA ARG GLY VAL GLU THR
PRO GLU THR LYS GLU GLU LEU PRO ALA SER PRO PRO LEU SER GLY ASP SER SER SER SER PRO LEU PRO ALA ALA GLY SER ALA SER ASN VAL PHE PRO ALA ARG LYS ARG LEU PHE SER SER ARG ARG MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS ASP LYS PRO GLY SER PRO
SER ASP ALA GLN ASN SER PRO SER PRO HIS GLN ALA GLU ALA ALA THR GLY GLY PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA LEU GLU VAL GLN THR GLU GLY TRP GLY VAL GLN THR ALA PRO GLU THR PRO GLY ASN
SER THR HIS TRP ALA SER PRO SER PHE HIS SER LEU PHE SER ARG ARG PHE SER LEU ARG ARG ARG SER SER ALA SER SER MET THR VAL LEU ASP MET GLU GLU ASN LYS SER LEU ASP ALA LEU SER VAL LEU PHE GLU PRO GLN ARG PRO LEU ALA
SER VAL SER ASP SER LEU VAL PHE SER GLU GLY LEU SER PHE SER SER SER VAL ASP PRO VAL SER ASP PHE GLY ASP ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER GLU VAL PRO CYS ALA GLY ALA ARG ALA GLY GLY ARG GLU SER PRO THR SER ARG
ARG HIS SER PHE VAL PHE ARG THR THR GLN GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASN ARG GLY ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LEU VAL LYS SER PRO GLU GLN ILE LEU ARG ASP ARG ASP ASP ARG GLU GLU GLY LYS
ALA GLN ASP THR ALA ARG ARG SER GLU GLU ARG GLU LYS GLN THR GLY LYS ARG GLU GLY LEU ARG LYS ASP ASP GLU LYS GLU GLY ARG SER ALA PHE LEU ARG ILE PRO ARG PRO GLY LYS HIS GLU THR ASN LYS HIS SER VAL CYS LYS ARG ARG GLY ALA
SER LEU PRO PRO LEU PRO PRO GLU ALA SER SER ARG LEU ARG ARG SER GLN SER SER VAL SER ARG GLY GLY LYS LYS GLU ILE GLU LYS MET GLU GLU GLU ILE LYS GLN GLU ASN ARG GLU GLU ILE
HIS GLU ARG LYS SER GLU LEU LYS GLN GLU GLU VAL LYS GLN GLU VAL LYS GLY GLU VAL LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU ASN VAL ASP GLU ILE LYS GLN GLU ARG LYS SER GLU LEU LYS GLN GLU GLU VAL
ASP GLU MET LYS GLN GLU ASN VAL ASP GLU ILE LYS GLN GLU THR PRO GLU THR VAL ASP GLU TRP LEU SER GLU HIS LEU SER ASP SER CYS GLY GLU
ASP VAL ALA ILE PHE ALA CYS VAL GLU ALA ALA ARG THR TRP GLN LYS GLU ASP GLU THR LEU GLY ALA SER VAL ALA ALA GLY ARG GLY GLU ASP GLU CYS VAL ASP ARG GLY ASP ALA LEU THR GLY GLN ASP ASP ASN ALA GLU GLU THR SER GLN ARG CYS


SER CYS SER GLU ASP SER PRO GLU GLY VAL ALA GLU ARG GLU TRP MET GLY GLY SER SER ASP GLY ALA GLU ILE HIS LEU LEU PRO GLU ALA ASP THR SER ASP GLU GLU GLU GLU GLU ARG GLU GLU GLY GLU GLY GLU
GLU GLU GLU GLU GLY GLU GLU GLU GLU GLU

GLY LEU LYS SER THR ALA VAL LYS LYS VAL GLY MET LYS

• Molecule 3: Formin 1

Chain CE: 95%

MET SER CYS PRO ALA SER CYS PRO ARG GLY ARG GLY GLY SER ALA PRO LEU PRO PRO MET PRO PRO SER VAL ASN ASP ASP ARG ASN ALA VAL LEU ASN ALA LEU PRO SER ARG THR SER PHE SER ALA PRO LEU CYS SER ALA THR SER CYS SER LEU PRO GLU ARG PRO VAL PHE ALA

LYS LEU THR GLY GLY MET PRO PHE SER ARG THR THR ALA ARG ILE GLU CYS ALA SER PRO ALA CYS HIS GLU SER LEU SER LEU HIS ARG VAL ALA GLU SER GLN VAL LYS ALA GLN ALA ALA ALA SER GLY PRO LEU SER ASN SER SER PHE LEU ILE PHE LEU ASN SER ILE PRO THR

GLU PRO PRO ARG CYS PHE LEU PRO PRO PRO ARG ARG VAL ALA SER LEU SER ALA GLU ALA ASP THR PRO LYS GLY SER PHE TYR VAL PHE SER GLU SER SER SER ARG SER GLU SER SER HIS SER GLU GLY CYS VAL GLU SER ARG LEU SER GLY HIS THR ALA ALA ARG THR ARG CYS ARG ARG

SER ARG THR THR ALA SER ALA THR ASP SER ARG ARG ARG ASP ASP LEU PHE SER PHE ASP LEU PRO GLN GLU CYS GLY SER ALA ASP PRO ARG LEU PRO LEU PRO LEU PRO PRO SER ARG SER CYS PRO ALA SER PRO CYS HIS SER LEU LEU PRO PRO LEU SER ASN LYS LEU THR PRO PRO CYS ARG

GLU SER GLN SER GLU GLY THR ASP HIS GLY SER SER SER ALA ARG CYS CYS GLN PRO ARG PRO TYR PRO PRO ARG ILE THR ASP ALA LEU PRO THR GLY GLN ILE TYR SER ARG SER PRO ALA SER PRO CYS VAL ARG GLU ARG THR LEU ARG SER GLU PRO ALA ALA PRO VAL ASN TYR SER

ASP THR GLN LYS ARG CYS PRO ALA PRO LEU PHE GLN SER ILE PRO VAL HIS SER MET PRO PRO PRO PRO PRO PRO PRO PRO PRO LYS GLY LYS LYS GLY PRO LEU PRO LYS LYS ALA SER ASN SER PRO LEU PRO LYS GLY LYS SER THR PRO ASP GLU GLY ALA LYS LYS THR PRO PRO PRO

PRO PRO ALA ALA LYS ALA GLY VAL PRO GLU GLY LYS ALA GLU MET PRO SER GLU LYS ALA GLU VAL PRO GLN LYS ALA GLY VAL PRO GLN LYS LYS ALA GLY VAL PRO LYS GLU LYS ALA GLY MET PRO SER GLU GLU LYS ALA LYS GLU VAL PRO GLN LYS

LYS ALA GLY LEU PRO LYS GLU ILE PRO PRO GLU LYS ALA GLY VAL PRO GLN LYS LEU PRO LYS GLU LYS ALA GLY ILE PRO GLN GLU LYS ALA GLY ILE PRO GLN GLU LYS ALA GLY ILE PRO GLN GLU LYS ALA GLY GLU SER GLY SER PRO GLU GLY LYS THR GLY PRO LEU PRO GLY LYS ALA GLY PRO

PRO LYS GLY LYS LEU PRO PRO GLY LYS ALA GLU GLY SER GLY PRO ALA LYS SER ASP LEU LYS ALA SER PRO ALA GLY ALA PRO PRO SER LYS LYS ALA VAL ALA SER ALA GLY LYS PRO LEU GLY LYS THR PRO PRO ALA PRO SER VAL ALA

PRO ASN PRO PRO LEU GLY SER SER GLY PRO GLN GLU SER GLY SER SER THR TYR TYR ARG ASP THR LEU ARG ALA ALA ALA GLY THR ALA GLY ALA PRO GLU SER ALA GLY GLU GLY SER GLY GLU THR VAL PRO PRO PRO ASN GLU ALA TYR ALA ALA LYS ALA MET MET VAL

GLU SER LEU LYS LEU ALA ASP TYR THR ASN VAL PRO ALA HIS ALA HIS GLY THR GLU PRO PRO ALA LEU PRO PHE ALA PRO GLY ALA ASP ARG ASN PRO ALA ILE LEU THR ARG ALA LEU LYS LYS GLU MET GLU LEU ARG ARG ARG GLY GLN PRO THR GLN THR PRO GLU ARG ARG

LEU MET LEU ALA GLY THR PHE PHE SER LEU HIS HIS GLN ALA ARG LEU GLY PHE LYS LEU SER PRO GLU GLU ASP PHE ARG GLY SER VAL GLN ALA GLY GLU VAL GLN ARG ILE ARG TYR LEU LEU ARG VAL GLY GLU THR GLU

ALA PHE SER GLN GLN ARG TYR SER ASP ALA MET LEU GLN ALA LEU HIS SER TYR LEU LEU ALA LYS SER TYR TYR THR ALA TYR GLN SER ALA PRO LEU GLU GLY GLU MET VAL PRO GLU LEU LEU LEU LEU VAL LYS CYS CYS GLY LEU LEU ALA GLY CYS PRO ASP ARG GLY GLN GLU TYR

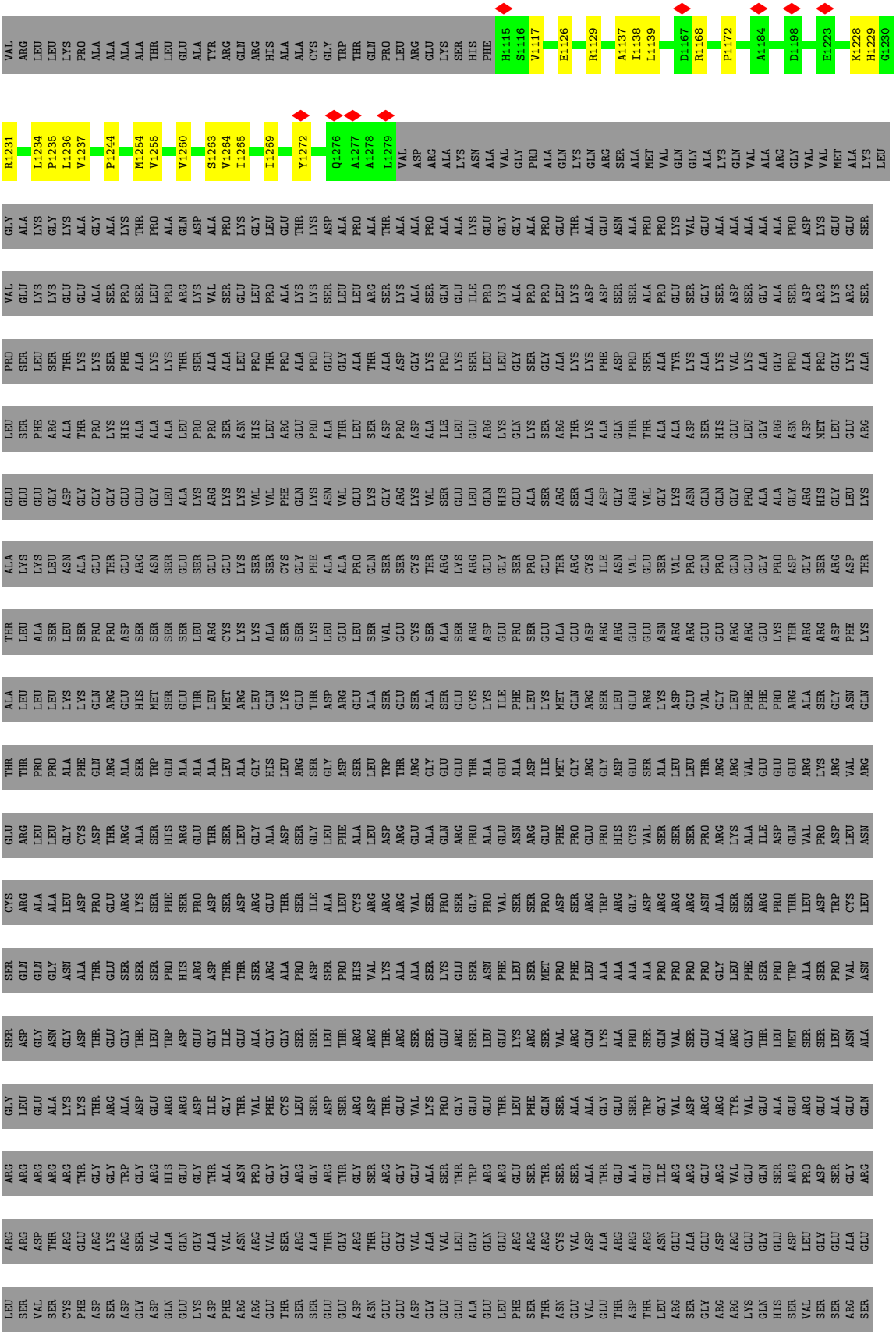
LEU LYS GLU LEU ARG TYR ILE VAL GLU ASN THR LEU ILE ALA GLU ALA ASP GLY ASN ARG GLY SER LEU VAL GLY PRO ILE MET ARG VAL GLU LYS HIS VAL LEU ALA SER VAL VAL SER SER LEU VAL ASN GLN PRO ASP ASP ALA ARG

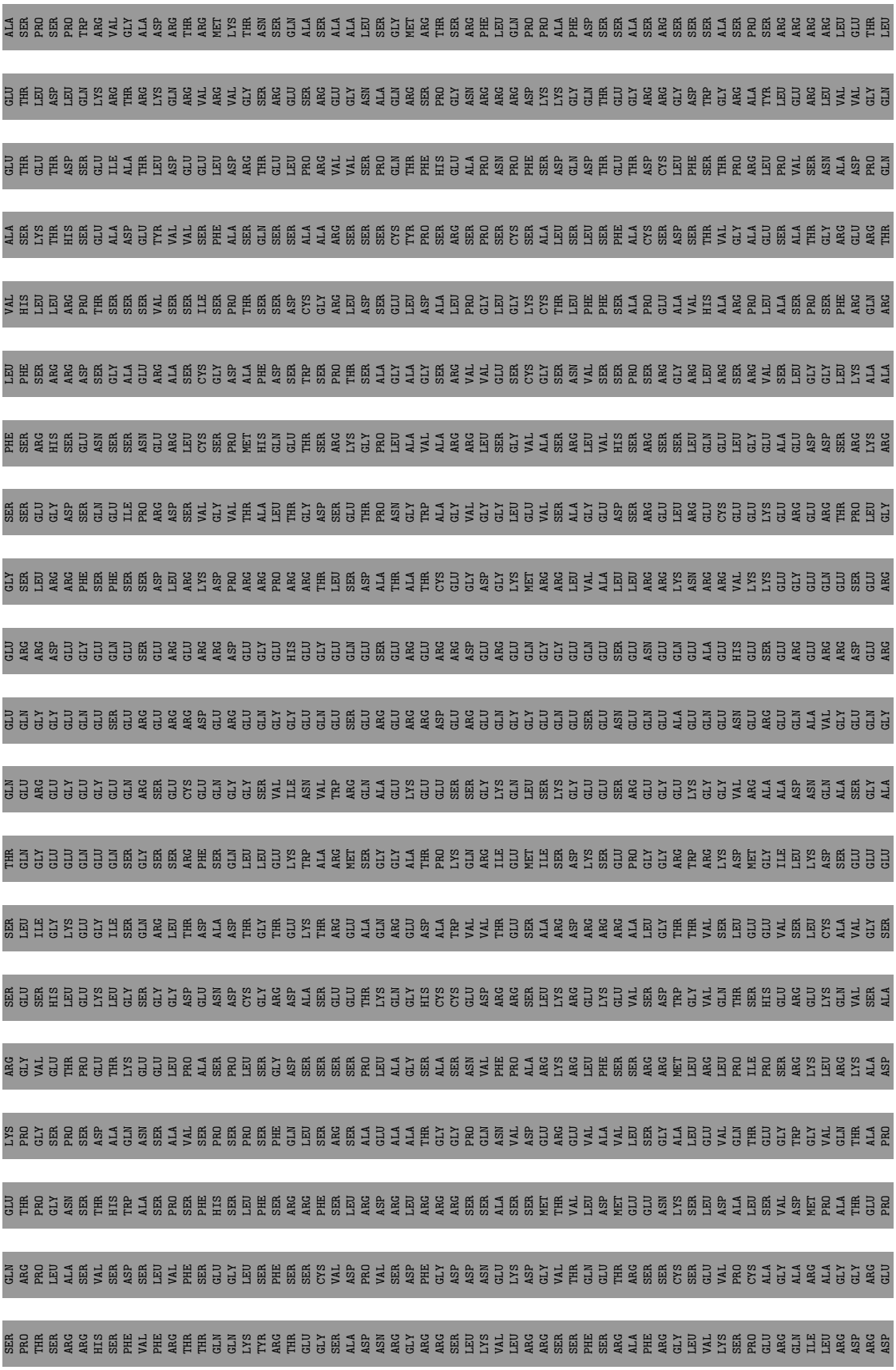
LEU PHE TYR GLU LYS TYR VAL ILE LEU LEU THR LYS ASP VAL TYR GLY ALA ASP SER LEU ALA VAL SER ASP ALA LEU ASN THR VAL ALA LEU TYR PHE PHE ARG GLN TYR GLY GLN ALA LEU PRO LEU VAL GLU GLN VAL LEU GLU CYS SER LEU TYR TYR ASN GLN PRO ASP GLY PHE ASP

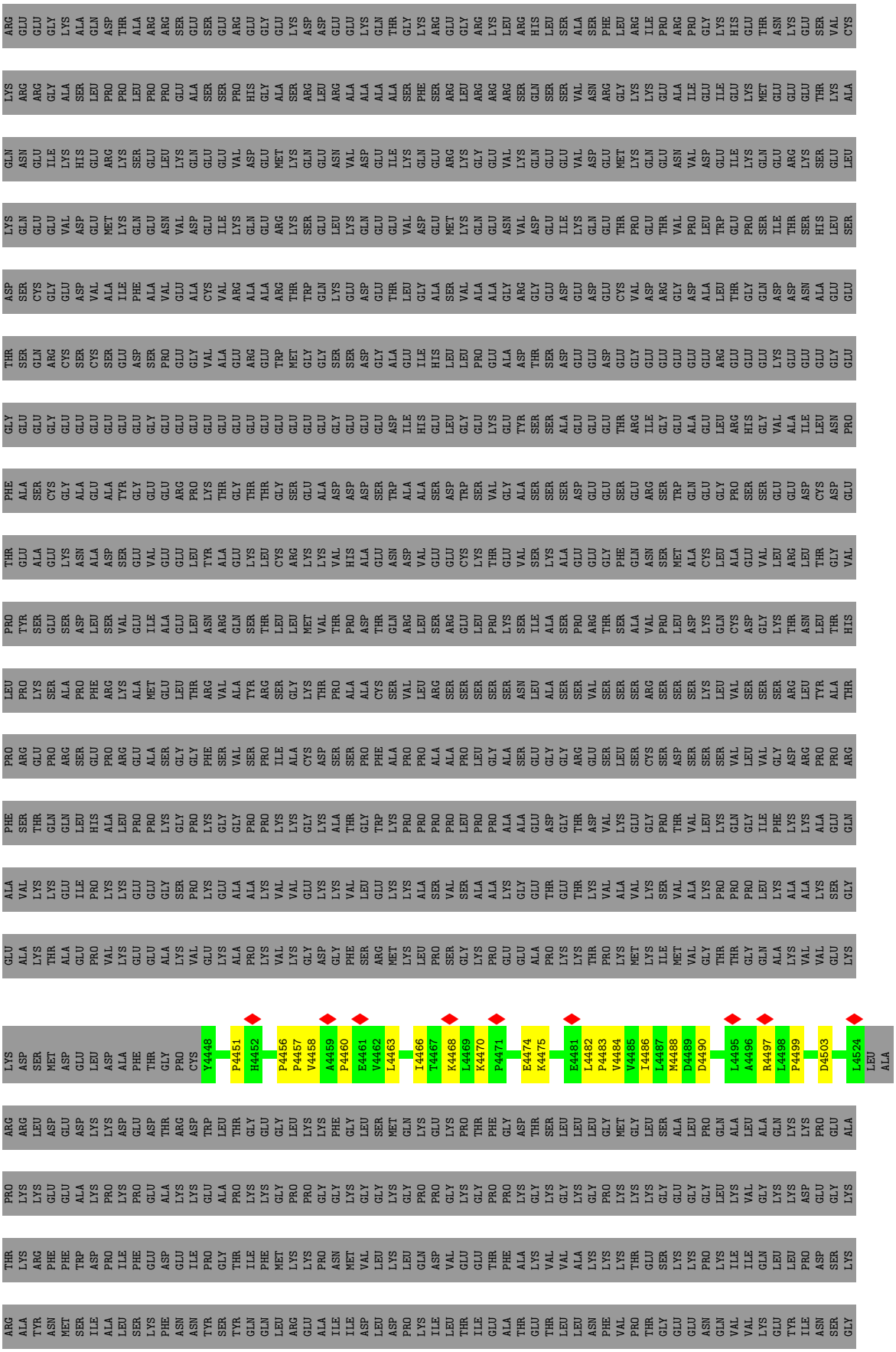
ALA ALA GLU PRO HIS ALA ARG VAL ALA ASP CYS TYR ALA ASN ILE GLY LEU LEU HIS ARG LEU LEU ASP MET ARG MET ARG ILE TYR GLN THR ARG GLU THR SER GLY VAL GLN ASP LEU VAL LEU GLY LEU ALA GLY CYS

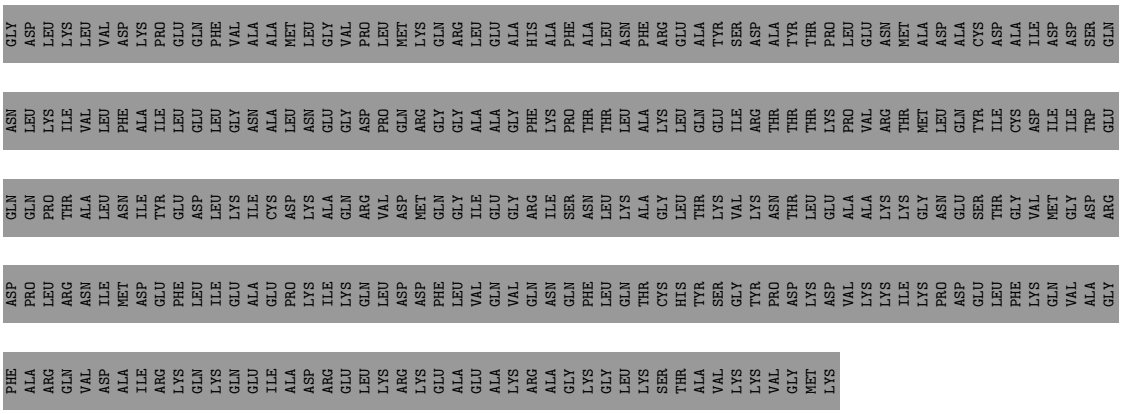
LEU GLN HIS GLN ALA GLY HIS PHE ARG ALA ALA LEU GLU VAL TRP THR PHE ARG ASN ASN THR LEU GLY VAL THR HIS PRO ASP THR HIS VAL ASN VAL GLU LEU LEU LEU ARG GLN LEU GLU LYS ASP GLU LEU ALA ALA GLN MET LYS ASP LEU GLU ALA ALA GLN ARG GLY ASP PHE VAL

ARG ASP LYS ALA LEU PRO SER ALA SER LEU GLN ILE SER VAL SER ARG GLN SER HIS ARG PRO GLY ASP PHE PHE TYR GLU GLU ALA ASP GLY ALA ALA SER SER ASP ARG GLY ARG ARG GLY SER LEU ASP PHE ALA ASP ALA SER THR


H1115
S1116
V1117
E1126
R1129
A1137
I1138
L1139
D1167
R1168
P1172
A1184
D1198
E1223
K1228
H1229
G1230
R1231
L1234
P1235
L1236
V1237
P1244
M1254
V1255
V1260
S1263
V1264
I1265
I1269
Y1272
Q1276
A1277
A1278
L1279

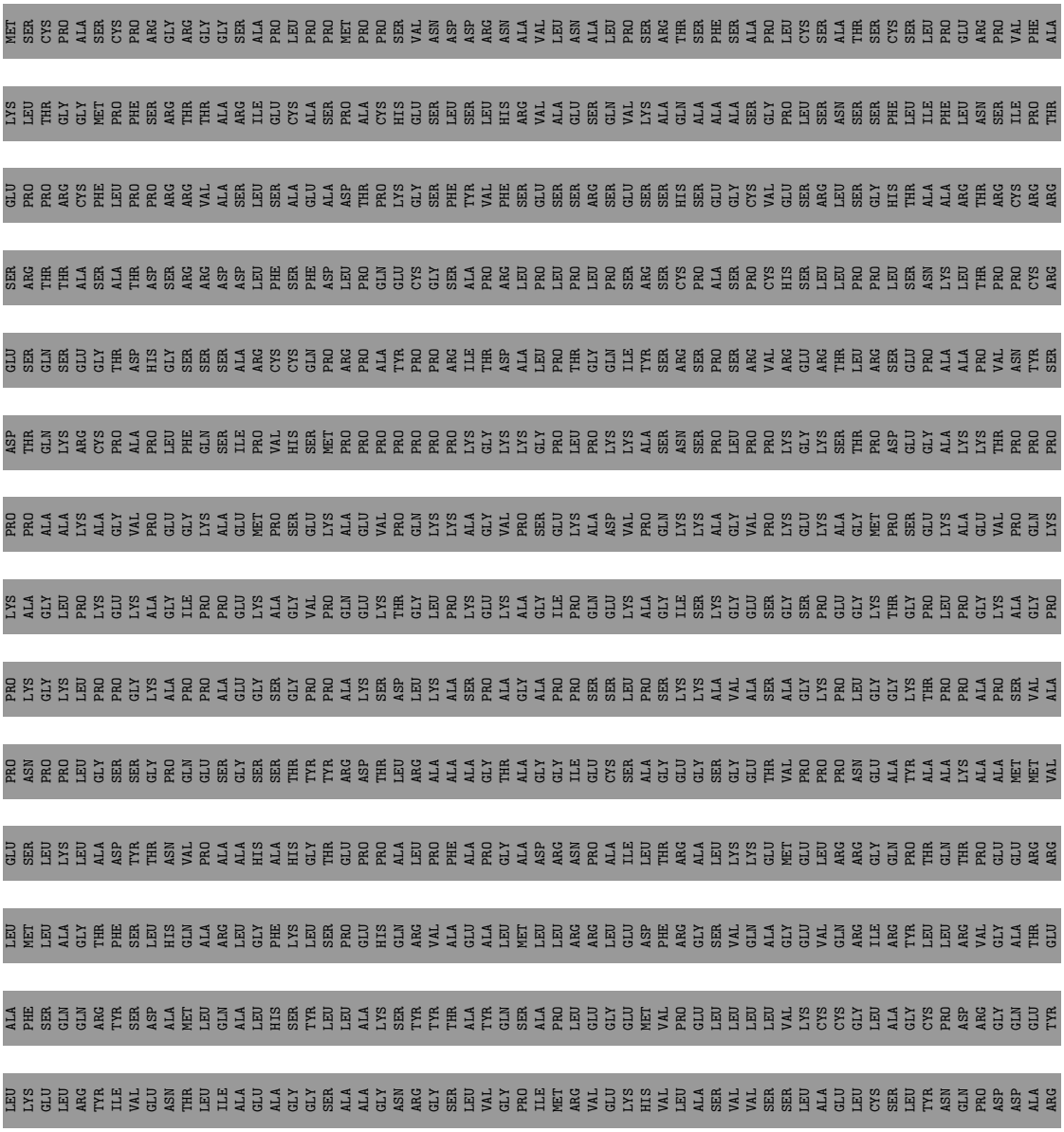

ALA SER PRO SER PRO TRP ARG VAL GLY ALA ASP ARG THR ARG MET LYS THR ASN SER GLN ALA SER ALA ALA LEU SER GLY MET ARG THR SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER ALA SER ARG SER SER ALA SER ARG SER SER
GLU THR LEU ASP LEU GLN LYS ARG THR ARG LYS GLN ARG VAL ARG VAL GLY SER ARG GLU SER ARG GLU GLY ASN ALA GLN ARG SER PRO GLY ASN ARG ARG GLY ASP TRP GLY ARG ALA TYR LEU GLU ARG LEU GLN ARG ARG ASP LYS GLY GLN THR GLU GLY ARG ARG GLY ASP ARG LEU VAL VAL GLY GLN
GLU THR GLU THR ASP SER GLU ILE ALA THR LEU ASP GLU GLU LEU ASP ARG THR GLU LEU PRO ARG VAL VAL SER PRO GLN THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ASP THR GLU THR ASP CYS LEU PHE SER THR PRO ARG LEU PRO VAL SER ASN ALA ASP PRO GLN
ALA SER LYS THR HIS SER GLU ALA ASP GLU TYR VAL VAL SER PHE ALA SER GLN SER SER ALA ALA ARG SER SER CYS TYR PRO SER ARG SER CYS SER SER PHE ALA CYS SER ASP SER THR VAL GLY ALA GLU SER ALA THR GLY ARG GLU ARG THR
VAL HIS LEU LEU ARG PRO THR SER SER SER VAL SER SER ILE SER PRO THR SER SER ASP SER CYS GLY ARG LEU ASP SER SER ALA PHE SER LEU SER PHE ALA CYS SER ASP ALA LEU PRO GLY GLU LEU ASP ALA LEU PRO GLY LEU SER PHE SER ALA VAL HIS ALA ARG PRO LEU ALA SER PRO SER PHE ARG GLN ARG
LEU PHE SER ARG ARG ASP SER GLY ALA GLU ARG ARG ALA SER CYS GLY ASP ALA PHE ASP SER TRP SER PRO THR SER ALA GLY ALA GLY SER ARG VAL SER SER PRO SER ARG GLY ARG LEU ARG SER GLY GLY LEU LYS ALA ALA
PHE SER ARG HIS SER SER ASN SER SER GLU ASN GLU ARG LEU CYS SER PRO MET HIS GLN GLU THR SER ARG LYS GLY PRO LEU ALA VAL ALA SER ARG LEU VAL LEU SER ARG SER SER LEU GLN LEU ALA GLU ALA ASP ARG
SER SER GLU GLY ASP SER GLN GLU ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU THR GLY ASP SER GLU THR PRO ASN GLY TRP ALA GLY VAL GLY GLY LEU GLU VAL SER ALA GLY GLU ASP SER ARG GLU LEU GLN GLU LEU GLY GLU ALA GLU ASP ARG GLU
GLY SER LEU ARG ARG PHE SER SER ASP LEU ARG LYS ASP PRO ARG ARG PRO ARG ARG ARG THR LEU SER ASP ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG ARG LEU LYS LYS GLU GLY GLU GLN GLU SER GLU ARG
GLU ARG ARG ASP GLU GLY GLU SER GLU GLU ARG GLU ARG ASP GLU ARG GLU ARG ASP GLU GLN GLU SER GLU ASN GLU GLN GLU ALA GLU HIS GLU SER GLU GLY GLU GLN GLU ARG GLU ARG ASP GLU
GLU GLN GLY GLY GLU GLN GLU SER GLU ARG GLU ARG ASP GLU ARG GLU GLN GLY GLY GLU GLU SER GLU ASN GLU GLN GLU ALA GLU GLN GLU ASN GLU ARG GLU GLY GLU GLN
GLN GLU ARG GLU GLY GLU GLN ARG SER GLU CYS GLU GLN ARG GLU VAL ILE ASN VAL TRP ARG GLN ALA GLU LYS GLU GLU SER SER GLU GLU GLY GLU GLU LYS GLY VAL GLY ALA
THR GLN GLY GLU GLU GLN GLY SER SER SER GLY SER GLN LEU LEU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ARG ARG ILE GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY ARG TRP ARG LYS ASP SER GLU GLU GLU
SER LEU ILE GLY LYS GLU GLY ILE SER GLN ARG LEU THR ASP ALA ASP THR GLY THR GLU LYS ARG GLU ASP ALA TRP VAL VAL THR GLU SER ALA ARG ASP ARG ARG ARG ALA LEU GLY THR THR VAL SER LEU GLU GLU VAL SER LEU CYS ALA VAL GLY
SER GLU SER HIS LEU GLU LYS GLY GLY ASP GLU ASP ASP CYS GLY ARG ASP GLU ASP ASP ARG SER LEU LYS ARG GLU LYS GLU VAL SER ARG GLU ARG GLU LYS GLN VAL SER
ARG GLY VAL GLU THR PRO GLU GLU PRO LEU SER PRO SER LEU GLY ARG GLU ASP ALA SER SER SER SER PRO LEU ALA LEU PRO PHE PRO ALA ARG LYS ARG LEU PHE SER SER ARG MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS ALA ASP
LYS PRO GLY SER PRO SER ASP ALA GLN SER ALA SER PRO SER PRO SER PHE GLN LEU SER ARG SER ALA GLU GLU ALA ALA THR GLY GLY PRO GLN ASN SER ALA VAL ALA GLU VAL ALA VAL LEU SER GLY ALA LEU GLU VAL GLN THR LEU GLU GLY TRP GLY VAL THR THR ALA PRO
GLU THR PRO GLY ASN SER THR HIS TRP ALA SER PRO SER PHE HIS SER LEU PHE SER ARG ARG ASP ARG LEU PHE SER ARG ARG ARG SER SER SER ALA SER SER MET THR VAL LEU ASP MET GLU GLU ASN LYS SER LEU ASP ALA LEU SER VAL ASP MET PRO ALA THR GLU PRO
GLN ARG PRO LEU ALA SER LEU GLY ASP PHE GLY ASP ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER GLU VAL PRO CYS ALA GLY ALA ARG ALA GLY GLY ARG GLU GLU
SER PRO THR SER ARG HIS SER PHE VAL PHE ARG THR THR GLN GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASN ARG GLY ARG ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LEU VAL LYS SER PRO GLU GLN ILE LEU ARG ASP ASP

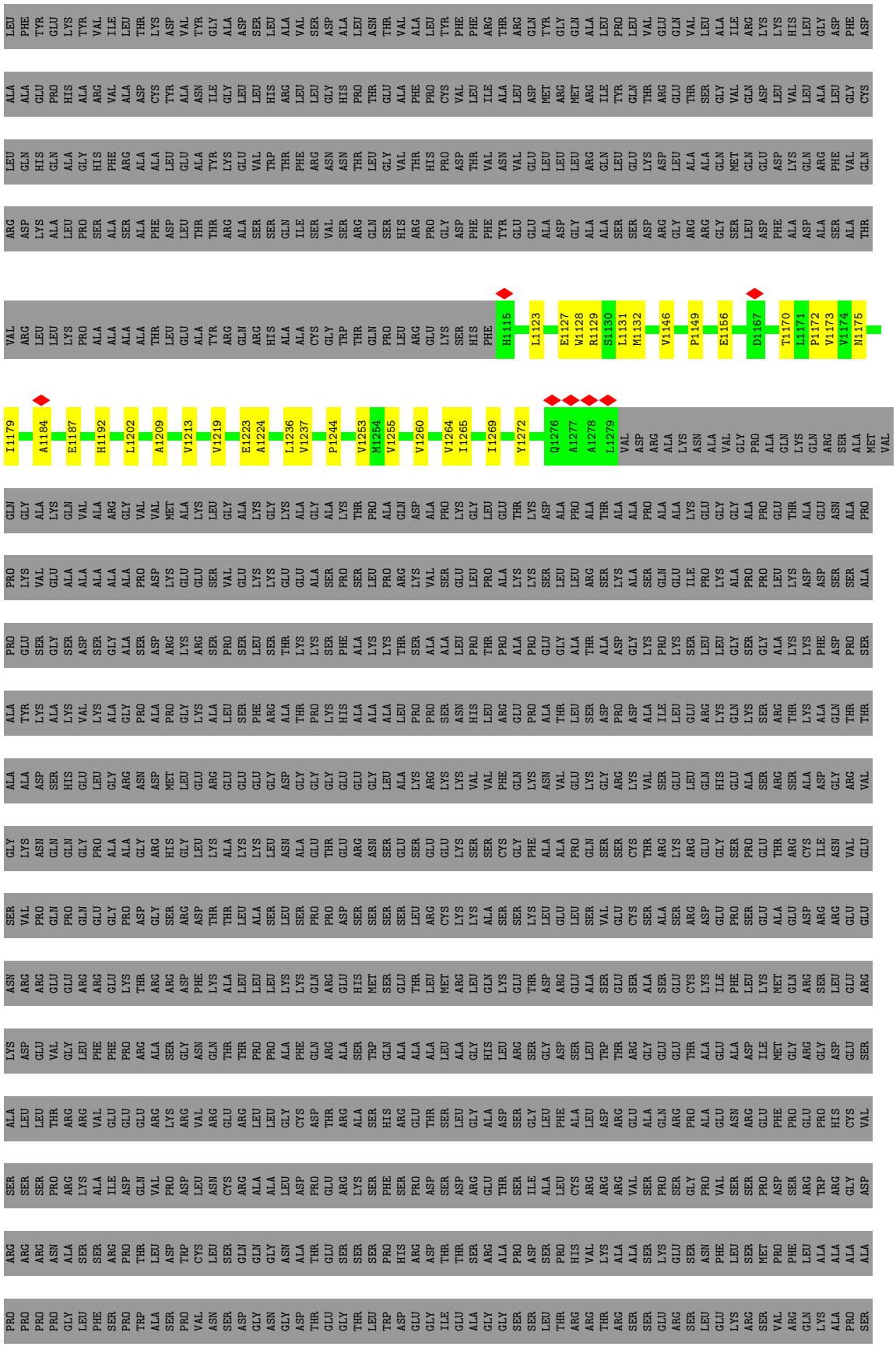

Y4448
P4451
H4452
P4456
P4457
V4458
A4459
P4460
E4461
V4462
L4463
I4466
T4467
K4468
L4469
K4470
P4471
E4474
K4475
E4481
L4482
P4483
V4484
V4485
I4486
L4487
M4488
D4489
D4490
L4495
A4496
R4497
L4498
P4499
D4503
L4524

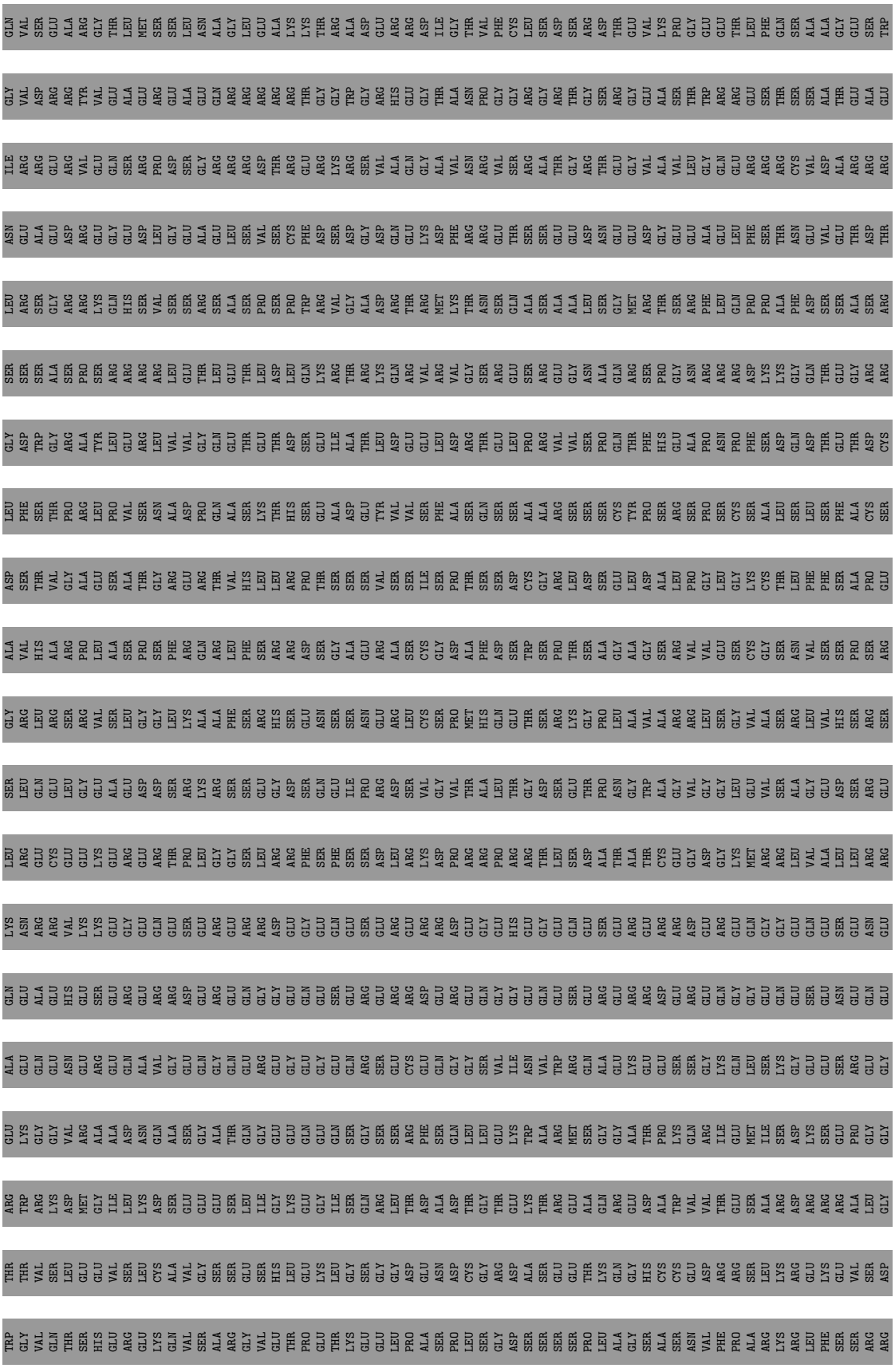


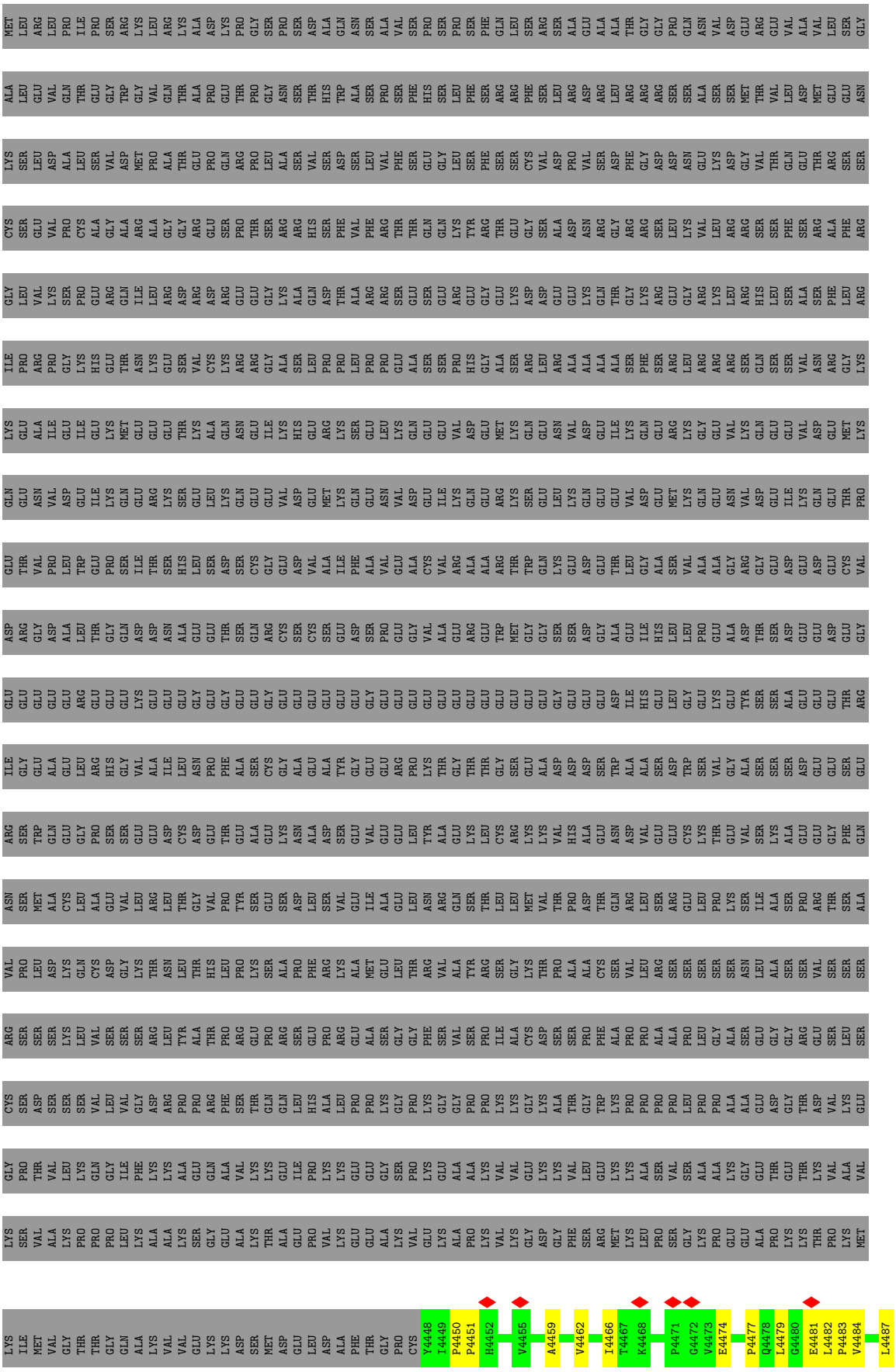
• Molecule 3: Formin 1

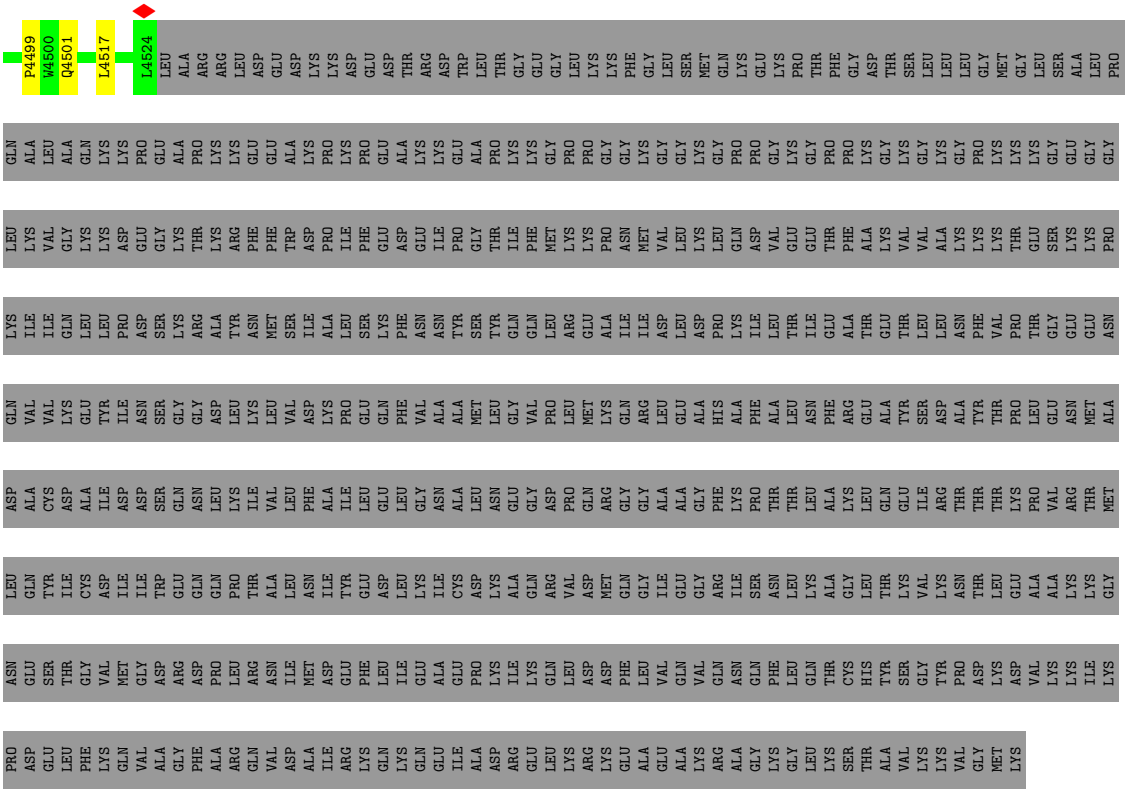
Chain CF: 95%




H1115
L1123
E1127
W1128
R1129
S1130
L1131
M1132
V1146
P1149
E1156
D1167
T1170
L1171
P1172
V1173
V1174
N1175
I1179
A1184
E1187
H1192
L1202
A1209
V1213
V1219
E1223
A1224
L1236
V1237
P1244
V1253
M1254
V1255
V1260
V1264
I1265
I1269
Y1272
Q1276
A1277
A1278
L1279

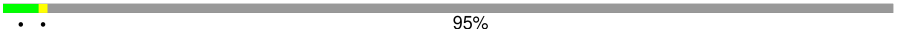

GLN VAL SER GLU ALA ARG GLY THR LEU MET SER SER LEU ASN ALA GLY LEU GLU ALA LYS LYS THR ARG ALA ASP GLU ARG ARG ASP ILE GLY THR VAL PHE CYS LEU SER ASP SER ARG ASP THR GLU VAL LYS PRO GLY GLU GLU THR LEU PHE GLN SER ALA ARG TRP
GLY VAL ASP ARG ARG TYR VAL GLU ALA GLU ARG GLU ALA GLU GLN ARG ARG ARG ARG THR GLY GLY TRP GLY ARG HIS GLU GLY THR ALA ASN PRO GLY GLY ARG GLU GLY GLU ALA SER THR TRP ARG ARG GLU SER THR SER SER ARG ALA THR GLU ALA GLU
ILE ARG ARG GLU ARG VAL GLU GLN SER ARG PRO ASP SER GLY ARG ARG ARG ASP THR ARG GLU ARG LYS ARG SER VAL ALA GLN GLY ALA VAL ASN ARG VAL SER ARG ALA THR GLY ARG THR GLU GLY GLU VAL ALA VAL LEU GLY GLN GLU ARG ARG ARG CYS VAL ASP ALA THR ARG ARG
ASN GLU ALA GLU ASP ARG GLU GLY GLU ASP LEU GLY GLU ALA GLU LEU SER VAL SER CYS PHE ASP SER ASP GLY ASP GLN GLU LYS ASP PHE ARG ARG GLU THR SER SER GLU ASP ASN GLU GLU ASP GLY GLU GLU ALA GLU LEU ASP PHE SER THR ASN GLU VAL GLU THR ASP ARG
LEU ARG SER GLY ARG ARG LYS GLN HIS SER VAL SER SER ARG SER PRO SER PRO TRP ARG VAL GLY ALA ASP ARG THR ARG MET LYS THR ASN SER GLN ALA SER ALA ALA LEU SER GLY MET ARG THR SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER ARG
SER SER SER ALA SER PRO SER ARG ARG ARG ARG GLU LEU GLU THR LEU GLU THR LEU ASP LEU GLN LYS LYS ARG THR ARG LYS GLN ARG ARG VAL GLY SER GLN GLU GLY ASN ALA GLN ARG SER SER PRO GLY ASN ARG ARG ARG ASP LYS LYS GLY GLN THR GLU GLY ARG ARG
GLY ASP TRP GLY ARG TYR LEU GLU ARG LEU VAL VAL GLY GLN GLU THR GLU ILE ALA THR LEU ASP GLU GLU LEU ASP ARG GLU VAL VAL SER PRO ARG VAL VAL SER PRO GLN GLN THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ASP PRO ARG VAL SER ASP CYS
LEU PHE SER THR PRO ARG LEU PRO VAL SER ASN ALA ASP PRO GLN ALA SER LYS THR HIS SER GLU ALA ASP GLU TYR VAL VAL SER PHE ALA SER GLN SER SER ALA ALA ARG SER SER CYS TYR PRO SER ARG SER PRO SER CYS SER ALA LEU SER LEU PHE ALA CYS SER
ASP SER THR VAL GLY ALA GLU SER ALA THR GLY ARG GLU ARG THR VAL HIS LEU LEU ARG ARG PRO THR SER SER SER VAL SER SER ILE SER PRO THR SER SER ASP CYS GLY ARG LEU ASP SER ALA LEU PRO PRO GLY LEU GLY LYS CYS THR LEU PHE SER ALA PRO GLU
ALA VAL HIS ALA ARG PRO LEU ALA SER PRO PHE ARG GLN ARG LEU PHE SER ARG ARG ASP SER GLY ALA GLU ARG ALA SER CYS GLY ASP ALA PHE ASP SER TRP SER PRO THR SER ALA GLY ALA GLU ARG ALA GLY SER ARG VAL GLU SER CYS SER GLY VAL ALA SER ARG
GLY ARG LEU ARG SER LEU GLY GLY LEU LYS LYS ALA ALA PHE SER ARG HIS SER GLU ASN SER SER ASN GLU ARG LEU CYS SER PRO MET HIS GLN GLU GLU THR SER ARG LYS GLY PRO LEU ALA VAL LEU SER GLY VAL ALA SER ARG LEU VAL SER HIS SER ARG
SER LEU GLN GLU GLU ILE PRO ARG ASP SER GLN GLU SER GLU GLY ASP SER GLU ARG GLY VAL THR ALA LEU THR GLY ASP SER GLU THR PRO ASN GLY TRP ALA SER GLY VAL GLY GLY LEU GLU LEU GLU VAL SER ALA GLY GLU ASP SER ARG GLU
LEU ARG GLU CYS GLU GLU LYS GLU ARG GLU ARG THR PRO LEU GLY GLY SER LEU ARG ARG PHE SER PHE SER SER ASP LEU ARG LYS ASP PRO ARG ARG ARG THR LEU SER ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG
LYS ASN ARG VAL LYS LYS GLU GLY GLU GLU ARG GLU ARG ARG ASP GLU GLY GLY GLU HIS GLU GLY GLY GLU GLU SER GLU ARG GLU ARG ASP GLU ARG GLU GLN GLY GLY GLY GLU SER GLU ASN GLU
GLN GLU ALA GLU HIS GLU SER GLU ARG GLU ARG ARG ASP GLU ARG GLY GLY GLU GLU ARG GLU ARG ARG ASP GLU ARG GLU GLN GLY GLY GLY GLU GLU GLN GLU SER GLU GLN GLU
ALA GLU GLN GLU ASN GLU ARG GLU ALA VAL GLY GLU GLN GLY GLU GLY GLU GLY GLU ARG GLN GLU ARG SER GLU CYS SER GLN GLN ILE VAL GLY LYS GLN LEU SER LYS GLY GLU GLU SER ARG GLU GLY
GLU LYS GLY GLY VAL ARG ALA ALA ASP ASN GLN ASN SER GLY SER GLY GLN GLU GLU GLN GLU GLN SER GLY SER SER ARG PHE SER GLN LEU GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY
ARG TRP ARG LYS ASP MET GLY ILE SER LEU LYS ASP SER GLU GLU LEU ILE GLY LYS GLU GLU GLN ARG LEU THR ASP ALA ASP THR GLY THR GLU LYS THR ARG GLU ALA GLN ARG GLU ASP ALA TRP VAL VAL THR GLU SER ALA ARG ASP ARG ARG ARG LEU GLY
THR THR VAL SER LEU GLU VAL ALA GLY SER GLU HIS LEU GLU LYS LEU GLY SER GLY CYS ASP GLU ASN ASP CYS GLY ARG ASP ALA SER GLU GLU GLY HIS CYS CYS GLU ASP ARG ARG SER LEU LYS ARG GLU LYS GLU SER VAL SER ASP
TRP GLY VAL GLN THR SER HIS GLU ARG GLU VAL THR PRO GLU THR LYS GLU GLU LEU PRO ALA SER PRO LEU SER GLY ASP SER SER SER PRO LEU ALA GLY SER ALA SER ASN VAL PHE PRO ALA ARG LYS ARG LEU PHE SER ARG ARG ARG

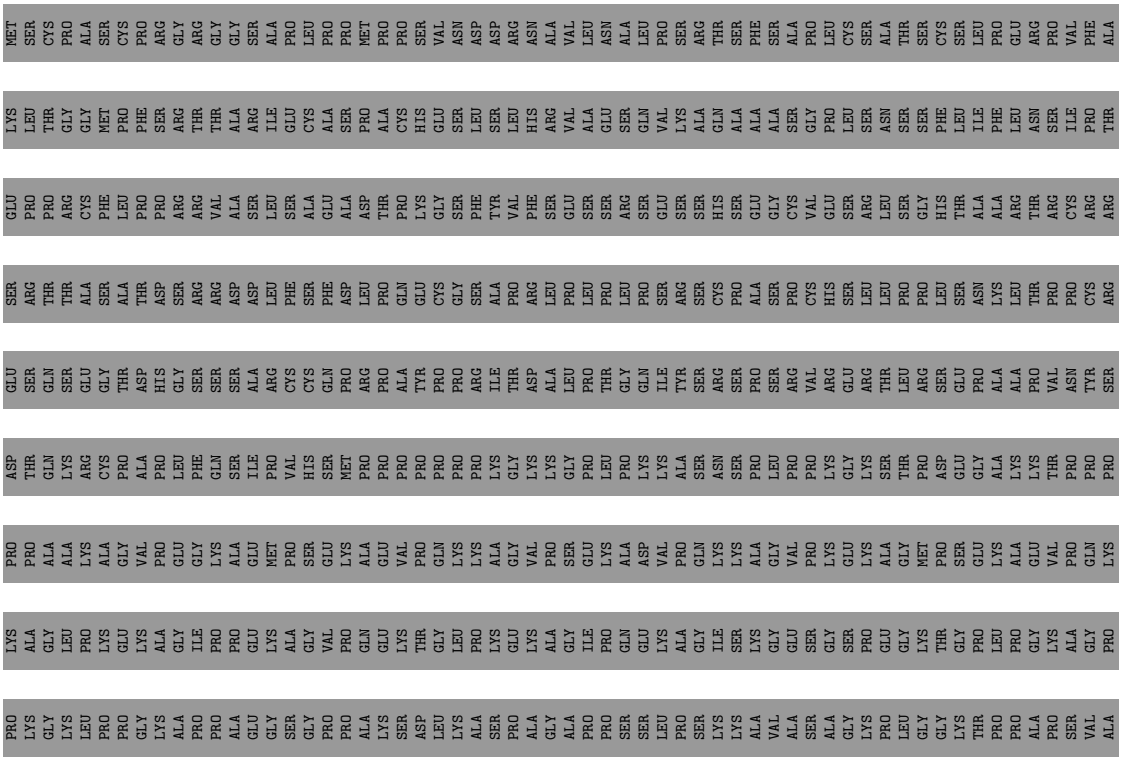

MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU LEU ARG LYS ALA ASP LYS PRO GLY SER PRO SER ASP ALA GLN ASN SER ALA VAL SER PRO SER PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA LEU ARG GLY PRO GLN ASN SER SER SER MET THR VAL LEU ASP MET GLU GLU ASN
ALA LEU GLU VAL GLN THR GLU GLY TRP GLY VAL GLN THR ALA PRO GLU THR PRO GLY ASN SER THR HIS TRP ALA SER PRO SER PHE HIS SER LEU PHE SER ARG ARG PHE SER LEU ARG ASP ARG LEU ARG ARG ARG SER SER SER ALA SER SER ARG GLU ASN
LYS SER LEU ASP ALA LEU SER VAL ASP MET PRO ALA THR GLU PRO GLN ARG PRO LEU ALA SER VAL SER ASP SER LEU VAL PHE SER GLU GLY LEU SER PHE SER SER CYS VAL ASP PRO VAL SER ASP ASN GLU LYS ASP PHE SER ARG GLU
CYS SER GLU VAL PRO CYS ALA GLY ALA ARG ALA GLY ALA ARG GLU SER PRO THR SER ARG ARG HIS SER PHE VAL PHE ARG THR THR GLN GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASN ARG GLY ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE GLN GLU THR ARG ALA PHE
GLY LEU VAL LYS SER PRO GLU ARG GLN ILE LEU ARG ASP ARG ASP ARG GLU GLU GLY LYS ALA GLN ASP THR ALA ARG ARG SER GLU SER GLU GLU LYS GLN THR GLY LYS ARG GLU GLU ARG HIS LEU SER ALA SER PHE LEU ARG
ILE PRO ARG PRO GLY LYS HIS GLU THR ASN LYS GLU SER VAL CYS LYS ARG ARG GLY ALA SER LEU PRO PRO LEU PRO PRO GLU ALA ALA SER SER PRO HIS GLY ALA ALA ALA SER ARG LEU ASN VAL ASP GLU MET LYS ARG GLY
LYS GLU ALA ILE GLU ILE GLU LYS MET GLU GLU GLU THR LYS ALA GLN ASN GLU ILE LYS HIS GLU ARG LYS SER GLU LEU LYS GLN GLU ASN VAL ASP GLU MET LYS GLN GLU GLU VAL ASP GLU MET LYS
GLN GLU ASN VAL ASP GLU ILE LYS GLN GLU ARG LYS SER GLU LEU LYS GLN GLU VAL ASP GLU MET LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLU VAL LYS GLN GLU THR PRO
GLU THR VAL PRO LEU TRP GLU PRO SER ILE THR SER HIS LEU SER ASP SER CYS GLY GLU ASP VAL ALA ALA ILE PHE ALA VAL GLU ALA CYS VAL ARG ALA ALA ARG THR TRP GLN LYS GLU ASP GLU THR LEU GLY ALA SER VAL ALA ALA GLY ARG GLY GLU ASP GLU CYS VAL
ASP ARG GLY ASP ALA LEU THR GLY GLN ASP ASP ASN ALA GLU GLU GLU THR SER GLN ARG CYS SER CYS SER GLU ASP SER PRO GLU GLY VAL ALA GLU ARG GLU GLU TRP MET GLY GLY SER SER ASP GLY ALA GLU ILE HIS LEU LEU PRO GLU GLU ASP GLU ASP GLU GLY
GLU GLU GLU GLU GLU ARG GLU GLU LYS LYS GLU GLU GLY GLU GLU GLU GLU GLU GLU GLU GLY GLU GLU GLU GLU GLU GLU GLU

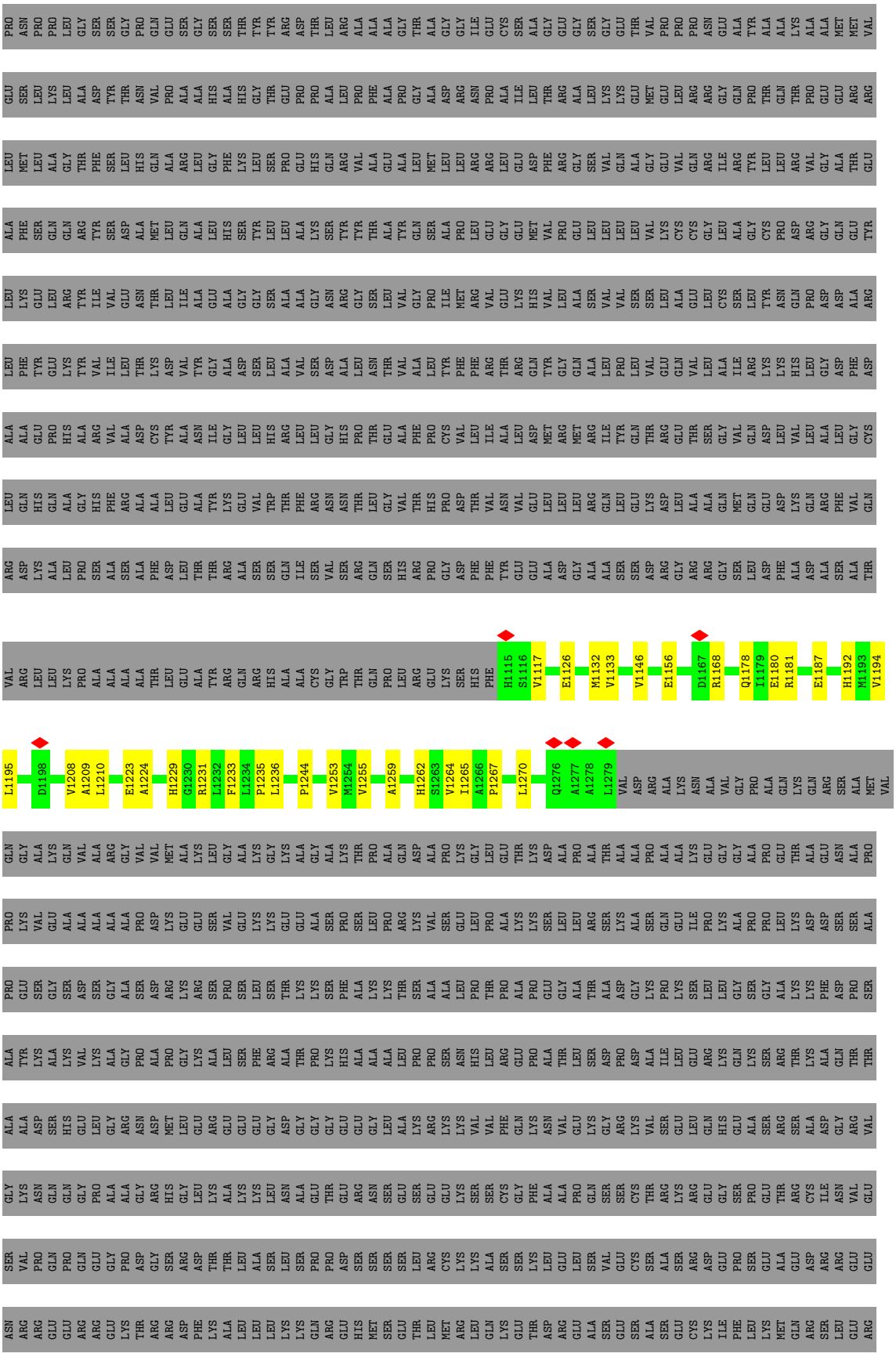


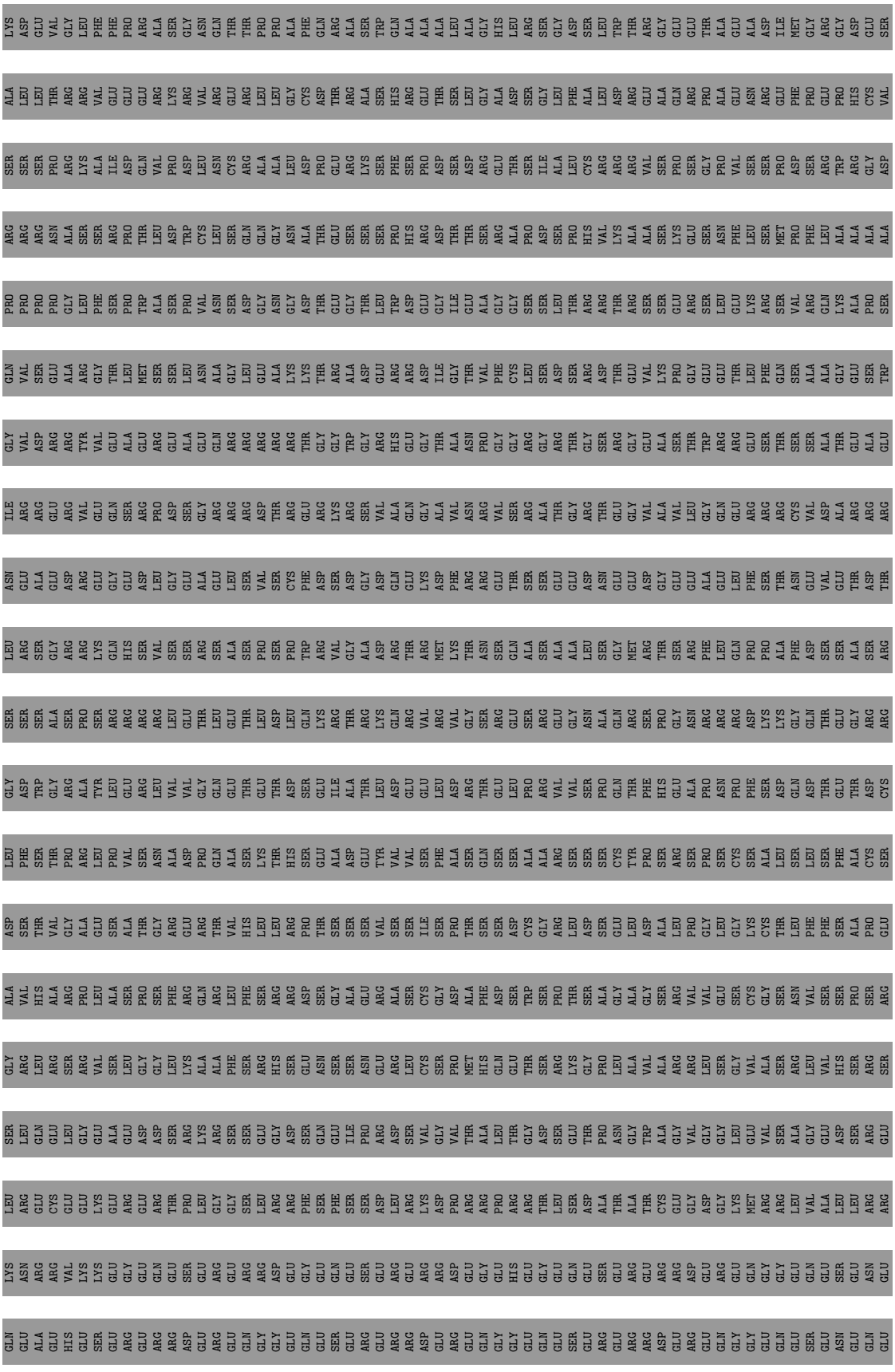
• Molecule 3: Formin 1

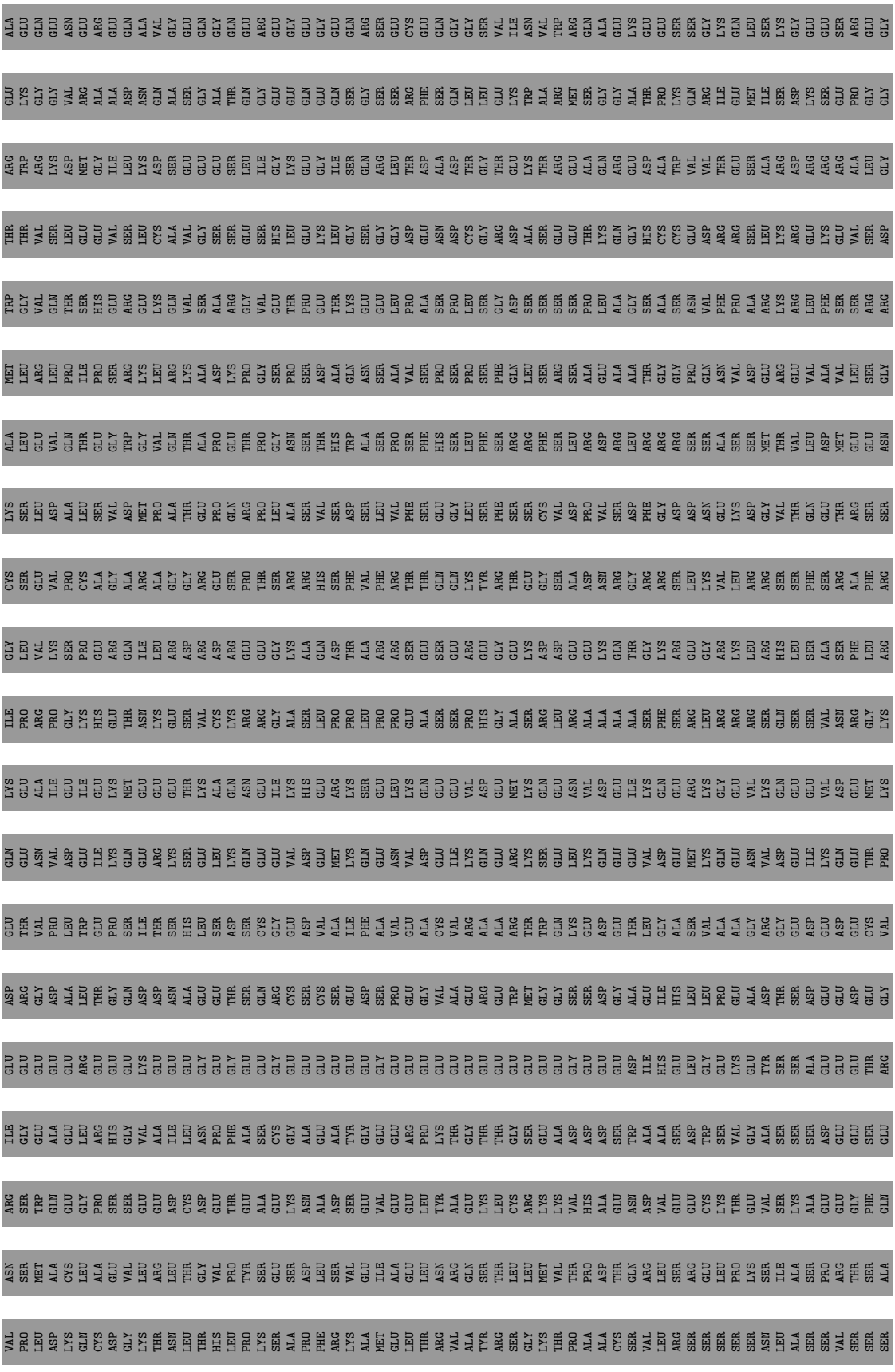
Chain CG:

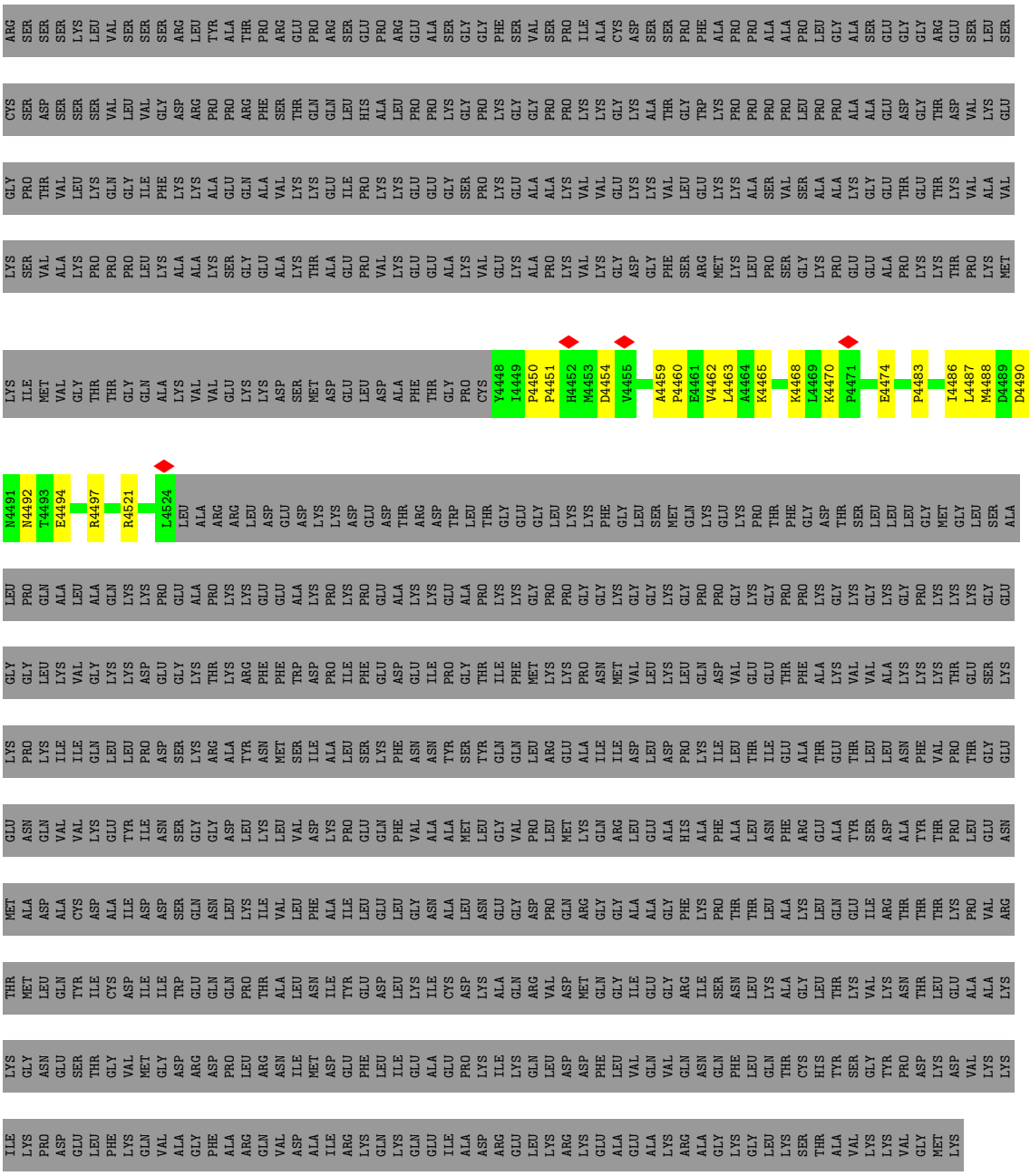





H1115
S1116
V1117
E1126
M1132
V1133
V1146
E1156
D1167
R1168
Q1178
I1179
E1180
R1181
E1187
H1192
N1193
V1194
L1196
D1198
V1208
A1209
L1210
E1223
A1224
H1229
G1230
R1231
L1232
F1233
L1234
P1235
L1236
P1244
V1253
M1254
V1255
A1259
H1262
S1263
V1264
I1265
A1266
P1267
L1270
Q1276
A1277
A1278
L1279

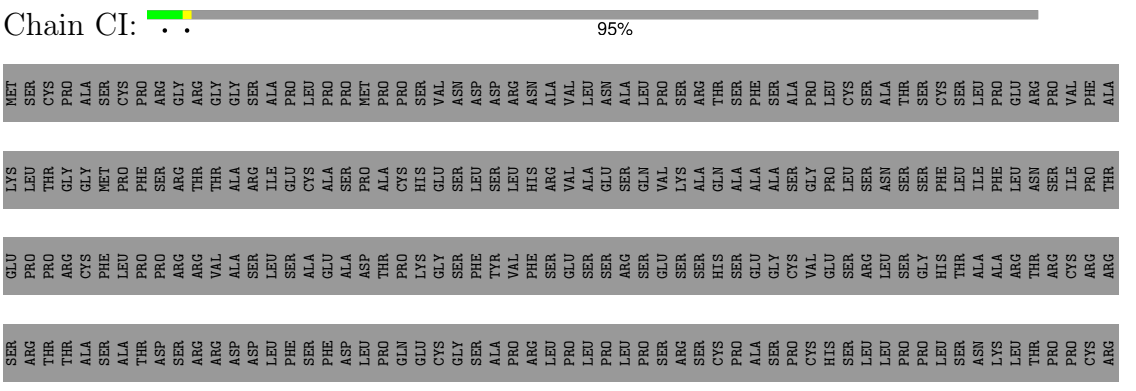

LYS ASP GLU VAL GLY LEU PHE PHE PRO ARG ALA SER GLY ASN GLN THR THR PRO PRO ALA PHE GLN ARG ALA SER TRP GLN ALA ALA ALA LEU ALA GLY HIS LEU ARG SER GLY ASP SER LEU TRP THR ARG GLY GLU GLU THR ALA GLU ALA ASP ILE MET GLY ARG GLY ASP GLU SER
ALA LEU LEU THR ARG ARG VAL GLU GLU ARG LYS ARG VAL ARG GLU ARG LEU LEU GLY CYS ASP THR ARG ALA SER HIS ARG GLU THR SER LEU GLY ALA ASP SER LEU ASP ARG GLU GLN ARG ALA GLU GLN ARG PRO ALA GLU ASN ARG GLU PHE PRO ALA CYS VAL
SER SER SER PRO ARG LYS ALA ILE ASP GLN VAL PRO ASP LEU ASN CYS ARG ALA ALA LEU ASP PRO GLU ARG LYS SER PHE SER PRO ASP SER ASP ARG GLU THR SER ILE ASP PRO ASP ARG GLU PRO ASP SER ARG TRP GLY ASP
ARG ARG ARG ASN ALA SER SER ARG PRO THR LEU ASP TRP CYS LEU SER GLN GLN GLY ASN ALA THR GLU SER SER SER PRO THR ARG ASP THR HIS ARG GLY ASP ASP THR HIS SER ILE ALA LEU PHE SER ASP SER PRO HIS ALA ALA ALA
PRO PRO PRO PRO GLY LEU PHE SER PRO TRP ALA SER PRO VAL ASN SER ASP GLY ASN GLY THR LEU TRP ASP GLU GLY GLY ILE GLU ALA GLY GLY SER GLU LEU THR ARG ARG ASP THR ARG SER LEU GLU GLU LYS ARG SER VAL ARG GLN LYS ALA PRO SER
GLN VAL SER GLU ALA ARG GLY THR LEU MET SER SER LEU ASN ALA GLY LEU GLU GLU ALA ASP GLU ARG ARG ASP ILE GLY THR ALA ASN PRO GLY GLY THR VAL PHE CYS LEU SER ASP SER ARG ASP THR GLU VAL GLU GLU THR LEU PHE GLN SER ALA ALA GLY GLU SER TRP
GLY VAL ASP ARG ARG TYR VAL GLU ALA GLU ARG GLU ALA GLU GLN ARG ARG ARG ARG THR GLY GLY TRP GLY ARG HIS GLU GLY THR ALA ASN PRO GLY CYS GLY ARG GLY GLY ALA SER THR TRP ARG ARG GLU SER THR SER GLU ALA ALA GLU
ILE ARG ARG GLU ARG VAL GLU GLN SER ARG PRO ASP SER GLY ARG GLN ARG ARG ASP THR ARG GLU ARG LYS ARG SER VAL ALA GLN GLY ALA VAL SER ARG THR GLY ARG THR GLY VAL LEU GLY GLN GLU ARG ARG CYS VAL ASP ARG ARG ARG
ASN GLU ALA GLU ASP ARG GLU GLY GLU ASP LEU SER VAL SER CYS PHE ASP SER ASP GLY ASP GLN GLU LYS ASP PHE ARG ARG GLU GLU ASP ASN GLU GLU ASP GLY GLU GLU ALA GLU LEU PHE SER THR GLU VAL THR ASP THR
LEU ARG SER GLY ARG ARG ARG SER ARG SER ALA GLU LEU SER PRO TRP ARG VAL GLY ALA ASP ARG THR ARG MET LYS THR ASN SER GLN ALA SER ALA ALA LEU SER GLY MET ARG THR SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER ALA SER ARG
SER SER SER ALA SER PRO SER ARG THR LEU GLU GLU THR LEU ASP LEU PRO ARG VAL GLY SER ARG GLU GLY ASN ALA GLN ARG SER PRO GLY ASN ASN ARG ARG ARG ASP ARG GLU GLU GLU GLN THR GLU GLY GLN THR GLU GLY ARG ARG
GLY ASP TRP GLY ARG ALA TYR LEU GLU ARG GLU LEU VAL VAL GLY GLN GLU THR GLU THR HIS SER GLU ILE ALA THR LEU ASP GLU GLU LEU ASP ARG GLU ALA PRO GLN PRO THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ASP THR GLU THR ASP CYS
LEU PHE SER THR PRO VAL SER ASN ALA ASP PRO GLN ALA SER LYS THR HIS SER GLU ALA ASP GLU TYR VAL VAL SER PHE ALA SER GLN SER SER ASP SER CYS TYR PRO SER ARG PRO SER CYS SER ALA LEU SER LEU PHE SER PHE ALA CYS SER
ASP SER THR VAL GLY ALA GLU SER ALA THR GLY ARG GLU ARG THR HIS LEU LEU ARG PRO THR SER SER SER ASP CYS GLY ARG LEU ASP SER GLU LEU ASP PRO GLY LEU GLY LYS CYS THR LEU PHE SER ALA LEU ASP GLY SER GLU
ALA VAL HIS ALA ARG PRO SER PHE ARG GLN ARG LEU PHE SER ARG ARG ASP SER GLY ALA GLU ARG ALA SER CYS GLY ASP ALA PHE ASP SER TRP SER PRO THR SER ALA GLY ALA GLY SER ARG VAL GLU SER CYS SER ASN VAL SER SER ARG
GLY ARG LEU ARG SER LEU GLY GLY LEU LYS ALA GLU SER ARG HIS SER GLU ASN SER SER ASN GLU ARG LEU CYS SER PRO MET HIS GLN GLU GLU THR SER ARG LYS GLY PRO LEU ALA VAL ARG LEU SER GLY VAL ALA ALA SER ARG LEU VAL HIS SER ARG SER
SER LEU GLN GLU LEU GLY GLU ALA ASP ASP SER ARG LYS ARG PRO GLN GLU GLU ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU THR THR GLY ASP SER GLU THR PRO ASN GLY TRP ALA GLY VAL GLY GLY LEU GLU SER GLY LEU GLU GLY ASP SER ALA GLY GLU ASP SER
LEU ARG GLU CYS GLU LYS GLU ARG GLU ARG THR PRO LEU GLY GLY SER LEU GLU ARG PHE SER SER ASP LEU ARG ARG LYS ASP PRO ARG ARG PRO ARG ARG THR LEU SER ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG
LYS ASN ARG ARG VAL LYS GLU GLN GLU SER GLU GLY GLU GLN GLU SER GLU ARG GLU ARG ARG ASP GLU ARG GLU ARG ASP ARG GLU GLN GLY GLN GLU SER GLU ASN GLU
GLN GLU ALA GLU HIS GLU SER GLU ARG GLU GLU ARG GLU ARG ARG ASP GLU ARG GLU GLN GLY GLY GLU GLN GLU SER GLU ASN GLU GLN

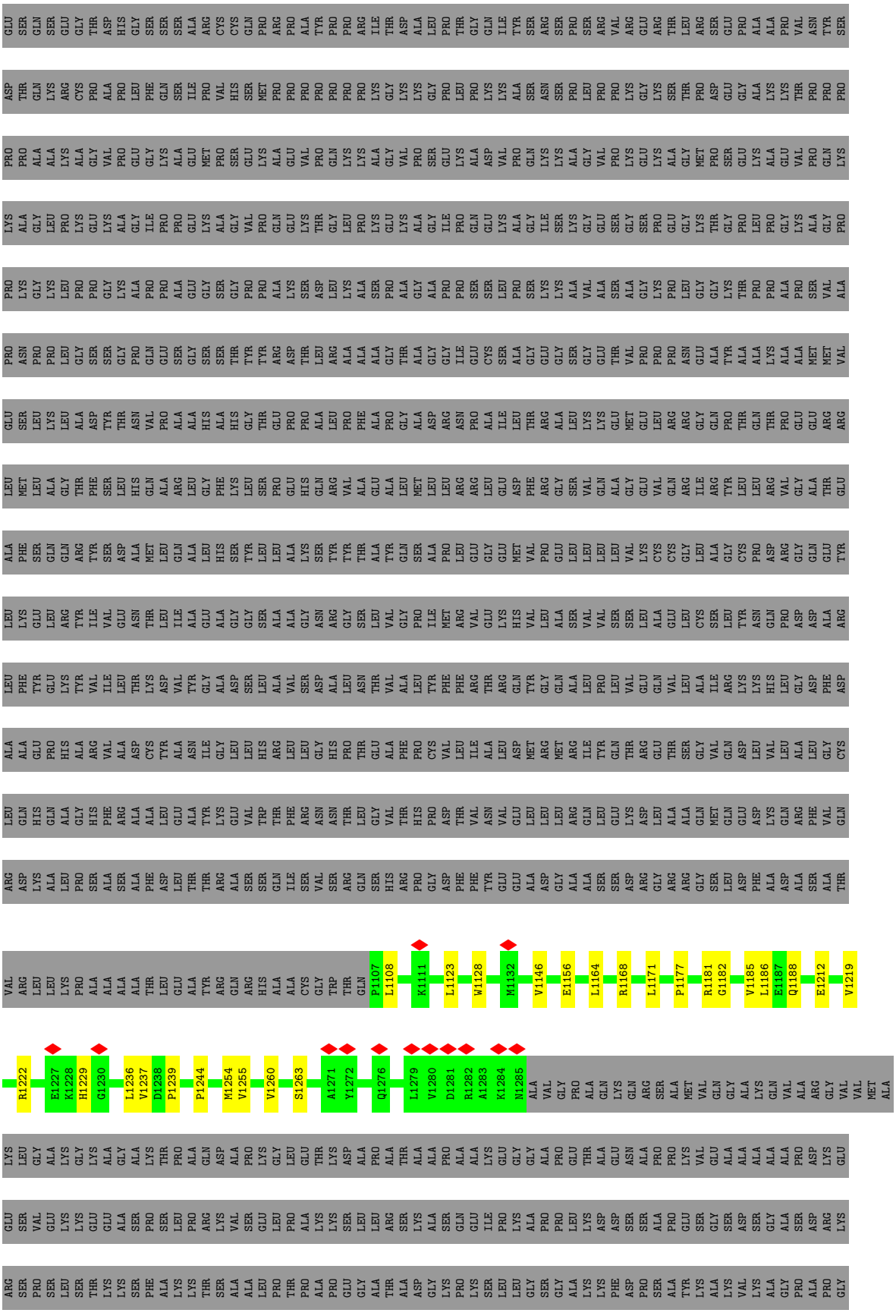

ALA GLU GLN GLU ASN GLU ARG GLU GLN ALA VAL GLY GLU GLN GLY GLN GLU ARG GLU GLY GLU GLY GLU GLN ARG SER GLU CYS GLU GLN GLY GLY SER VAL ILE ASN VAL TRP ARG GLN ALA GLU LYS GLU GLU SER SER GLY LYS GLY GLU GLU SER ARG GLU GLY
GLU LYS GLY GLY VAL ARG ALA ASP ASN GLN ALA SER GLY ALA THR GLN GLY ALA GLN SER GLY SER SER ARG PHE SER GLN LEU LEU GLU LEU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ARG ILE GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY
ARG TRP ARG LYS ASP MET GLY ILE LEU LYS ASP SER GLU GLU GLU SER LEU ILE GLY LYS GLU GLY ILE SER GLN ARG LEU THR ASP ALA ASP THR GLU LYS THR ARG GLU ARG ARG ASP ARG GLU LYS ARG ARG ARG ALA LEU GLY
THR THR VAL SER LEU GLU VAL SER LEU CYS ALA VAL GLY SER SER GLU SER LEU ILE GLY LYS GLU LYS LEU GLY SER GLN GLY ASN ASP CYS GLY ARG ASP ALA SER GLN GLY HIS CYS CYS GLU ASP ARG GLU LEU SER ASP
TRP GLY VAL GLN THR SER HIS GLU ARG GLU LYS GLN VAL SER ALA ARG GLY VAL GLU THR PRO GLU THR LYS GLU GLU LEU PRO ALA SER ASN VAL PHE PRO ALA GLY SER ARG SER SER PRO LEU ALA GLY HIS SER ALA SER ASN VAL PHE PRO ALA ARG LYS ARG LEU PHE SER SER ARG
MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS ALA ASP LYS PRO GLY SER PRO SER ASP ALA GLN ASN SER GLU VAL SER PRO SER PRO LEU PRO SER ARG SER ALA ALA THR GLY GLY PRO GLN ASN VAL PHE PRO ALA ARG GLU VAL ALA LEU GLU SER
ALA LEU GLU VAL GLN THR GLU GLY VAL GLN THR ALA PRO GLU THR PRO GLY ASN SER THR HIS TRP ALA SER PRO SER PHE HIS SER LEU PHE SER ARG ASP ARG PHE SER LEU ARG ASP ARG LEU ARG ARG ARG SER SER SER ALA GLU ASP MET GLU GLU ASN
LYS SER LEU ASP ALA LEU SER VAL SER ASP SER LEU VAL PHE SER GLU GLY LEU PHE SER CYS VAL ASP PRO VAL SER ASP PHE GLY ASP ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ASN SER
CYS SER GLU VAL PRO CYS ALA GLY ALA ARG ALA GLY GLY ARG GLU SER PRO THR SER ARG ARG HIS SER PHE VAL PHE ARG THR THR GLN GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASN ARG GLY ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE SER ARG ALA PHE ARG
GLY LEU VAL LYS SER PRO GLU ARG GLN ILE LEU ARG ASP ARG ASP ARG GLU GLU GLY LYS ALA GLN ASP THR ALA ARG ARG SER GLU ARG GLY GLU LYS ASP ASP GLU GLU LYS GLN THR GLY LYS ARG GLU GLY ARG LYS LEU ARG HIS LEU SER ALA SER PHE LEU ARG
ILE PRO ARG PRO GLY LYS HIS GLU THR ASN LYS GLU SER VAL CYS LYS ARG ARG GLY ALA SER LEU PRO PRO PRO LEU PRO PRO PRO GLU ALA SER SER PRO HIS GLY ALA SER ARG LEU ARG ALA ALA ALA ALA SER PHE SER ARG GLU GLY LYS
LYS GLU ALA ILE GLU ILE GLU LYS MET GLU GLU GLU VAL LYS HIS GLU ARG LYS SER GLU LEU LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU ASN VAL ASP GLU ILE ILE LYS GLN GLU ARG LYS GLY GLU VAL GLU LYS GLN GLU GLU VAL ASP GLU MET LYS
GLN GLU ASN VAL ASP GLU ILE LYS GLN GLU ARG LYS SER GLU LEU LYS GLN GLU ASN VAL ASP GLU ILE LYS GLN GLU ARG LYS SER GLU LEU LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU ASN VAL ASP GLU ILE LYS GLN GLU THR PRO
GLU THR VAL PRO LEU TRP GLU PRO SER ILE THR SER HIS LEU SER ASP SER CYS GLY GLU ASP VAL ALA ILE PHE ALA VAL GLU ALA CYS VAL ARG ALA ALA ARG THR TRP GLN LYS GLU ASP GLU THR LEU GLY ALA SER VAL ALA ALA GLY ARG GLY GLU ASP GLU CYS VAL
ASP ARG GLY ASP ALA LEU THR GLN GLN ASP ASN ALA GLU SER CYS SER GLU ASP PRO GLU GLY VAL ALA GLU ARG GLU TRP MET GLY GLY SER SER ASP GLY ALA GLU ILE LEU PRO GLU ALA ASP THR SER ASP GLU GLU ASP
GLU GLU GLU GLU GLU LYS GLU GLU GLU GLU GLU

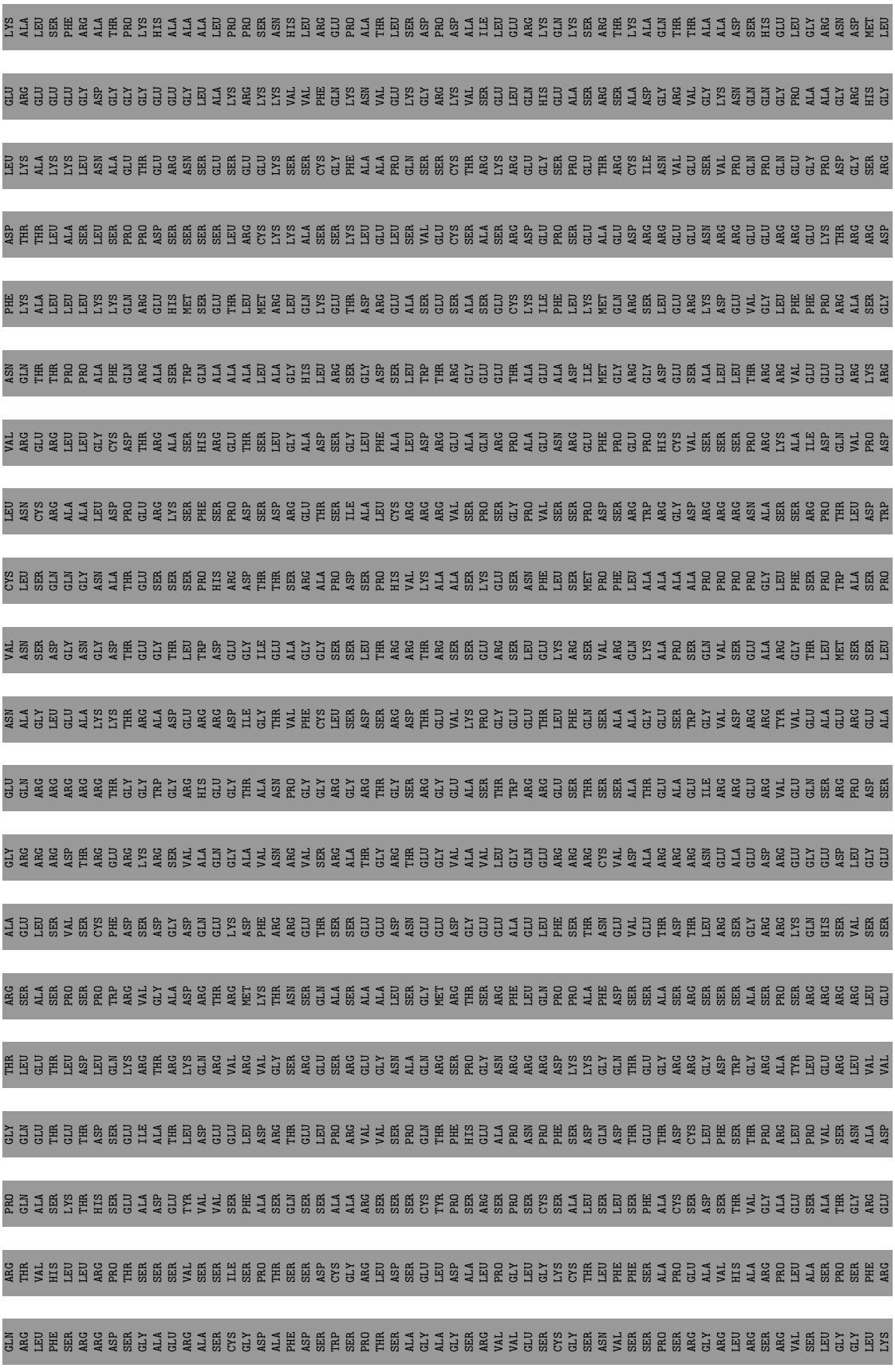


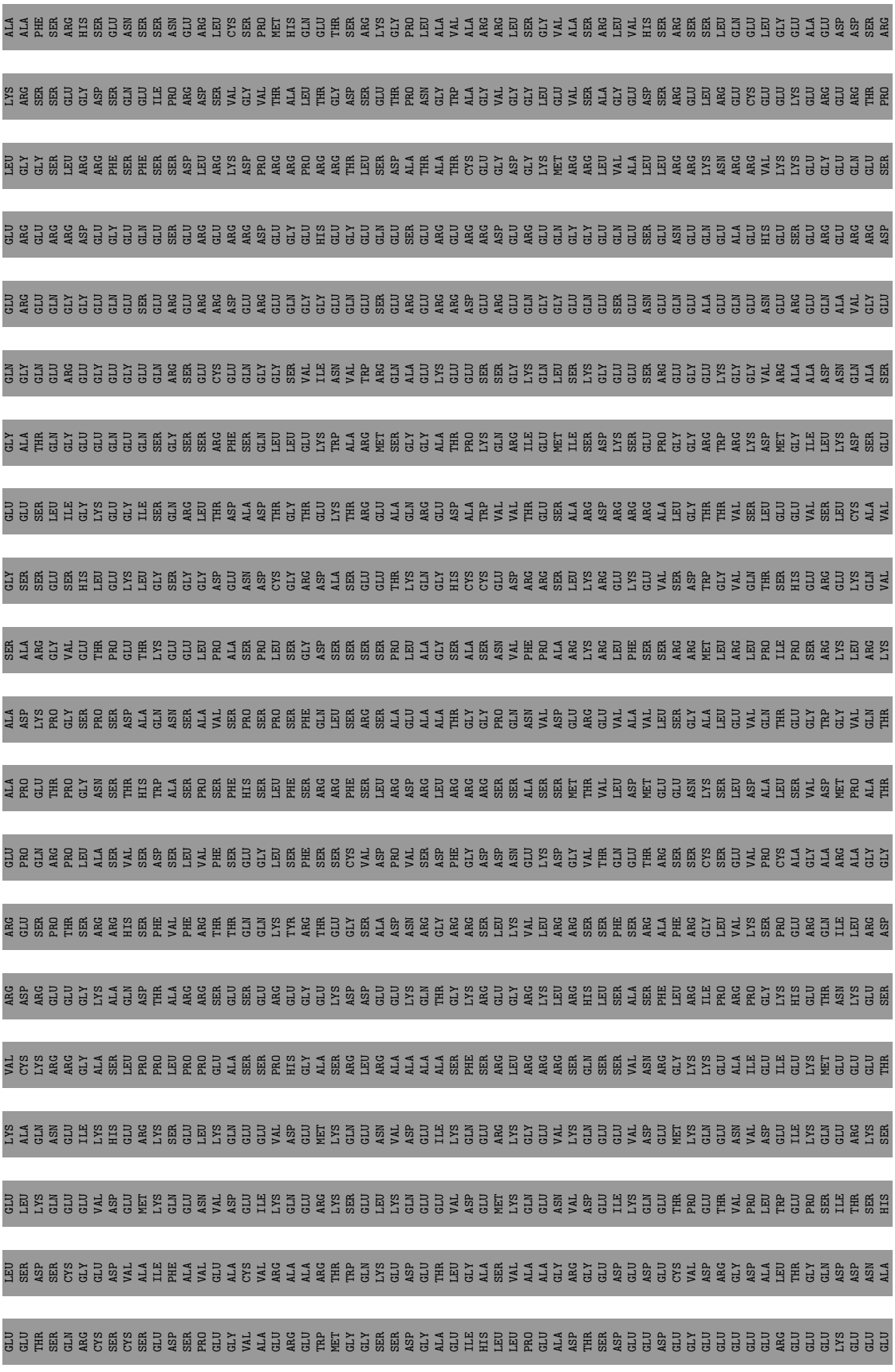
• Molecule 3: Formin 1

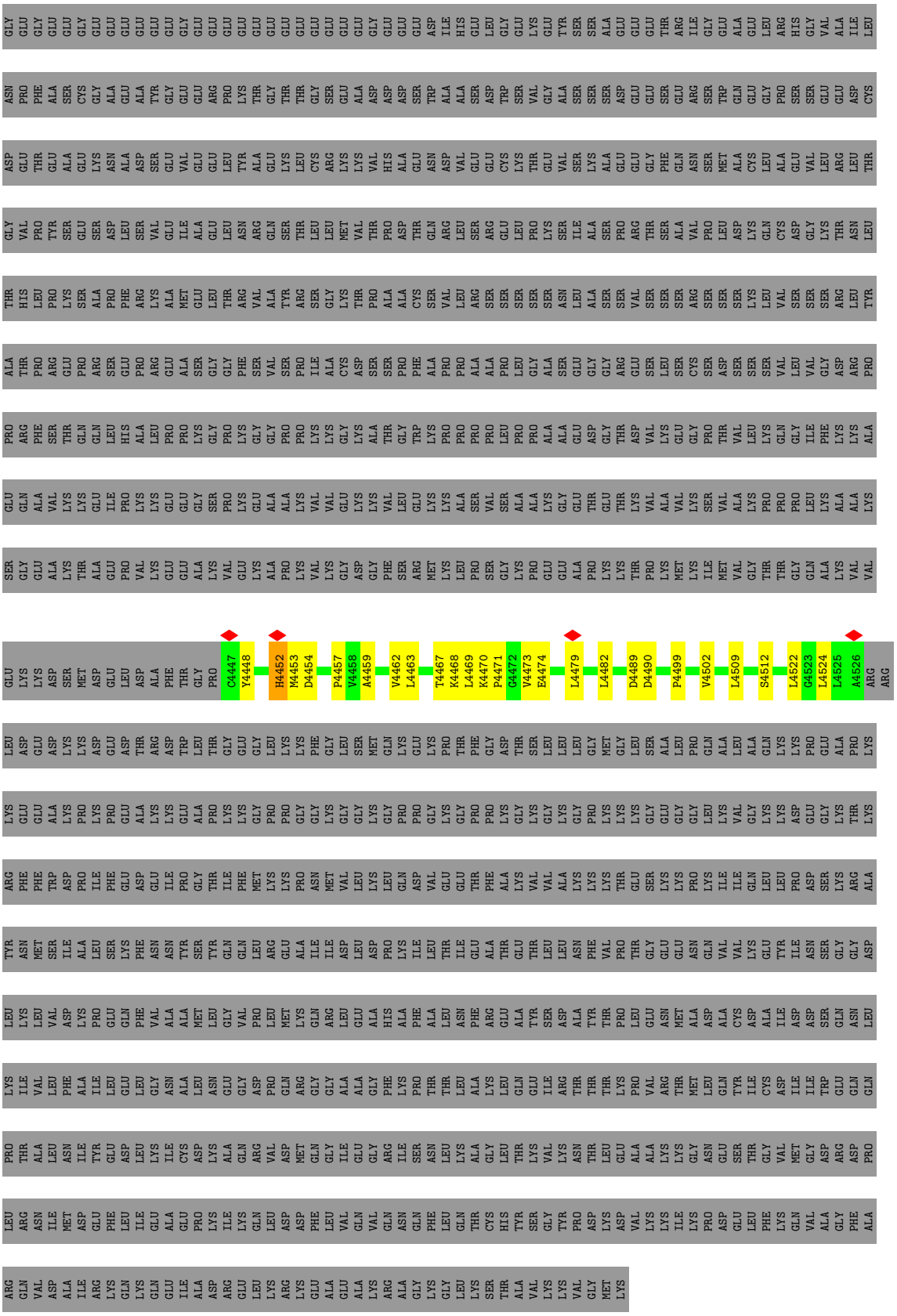
Chain CI: 95%




P1107
L1108
K1111
L1123
W1128
M1132
V1146
E1156
L1164
R1168
L1171
P1177
R1181
G1182
V1185
L1186
E1187
Q1188
E1212
V1219
R1222
E1227
K1228
H1229
G1230
L1236
V1237
D1238
P1239
P1244
M1254
V1255
V1260
S1263
A1271
Y1272
Q1276
L1279
V1280
D1281
R1282
A1283
K1284
N1285

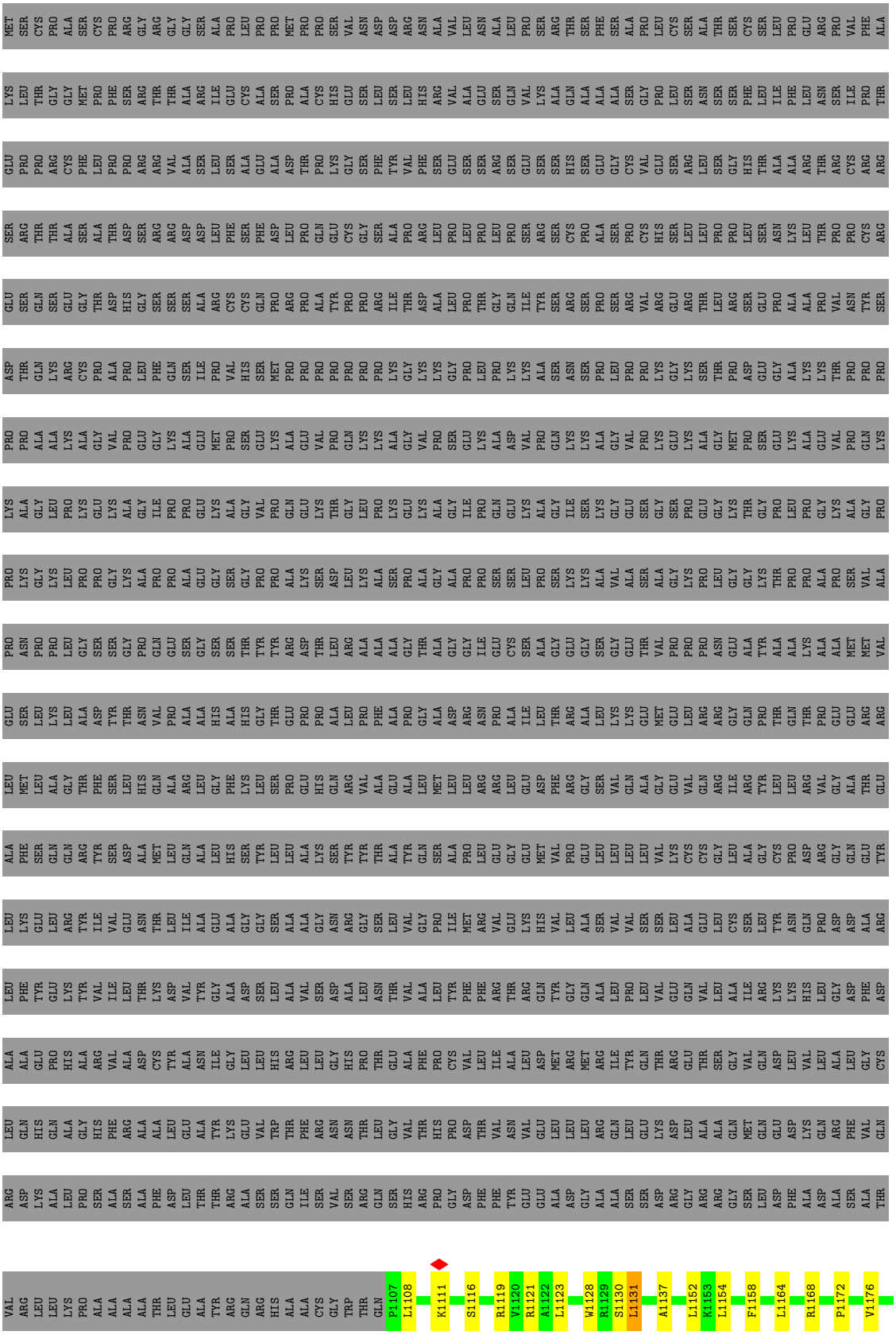

LYS ALA LEU SER PHE ARG ALA THR PRO LYS HIS ALA ALA ALA LEU PRO PRO SER ASN HIS LEU ARG GLU PRO ALA THR LEU SER ASP PRO ASP ALA ILE LEU GLU GLU ARG LYS GLN LYS SER ARG THR LYS ALA GLN THR THR ALA ALA ASP SER HIS GLU GLU LEU GLY ARG ASN ASP MET LEU
GLU ARG GLU GLU GLU GLY ASP GLY GLY GLY GLU GLU GLY LEU ALA LYS ARG LYS LYS VAL PHE GLN LYS ASN VAL GLU LYS GLY ARG LYS VAL SER GLU LEU GLN HIS GLU GLA SER ARG SER ALA ASP GLY ARG VAL GLY LYS ASN GLN GLN GLY PRO ALA ALA GLY ARG HIS GLY
LEU LYS ALA LYS LYS LEU ASN ALA GLU THR GLU ARG ASN SER GLU SER GLU GLU LYS SER SER SER CYS GLY PHE ALA ALA PRO GLN SER SER SER CYS THR ARG LYS ARG GLU LEU GLN HIS GLU GLY SER PRO GLU THR ARG CYS ILE ASN VAL GLU SER VAL PRO GLN PRO GLN GLU GLY PRO ALA ALA GLY ARG HIS GLY
ASP THR THR LEU ALA SER LEU SER PRO PRO ASP SER SER SER LEU CYS ASP ARG CYS LYS LYS ALA SER SER SER LYS LEU GLU LEU SER VAL GLU CYS SER ALA SER ARG ASP GLU PRO SER GLU ALA GLU ASP ARG ARG GLU GLU ASN GLU ARG GLU GLU ARG ARG GLU LYS THR ARG ARG ASP
PHE LYS ALA LEU LEU LEU LYS LYS GLN ARG GLU HIS MET SER GLU THR LEU MET ARG LEU GLN LYS GLU THR ASP ARG GLU ALA ILE LEU PHE LEU LYS MET GLN ARG SER LEU GLY ARG GLY ASP GLU VAL GLY LEU PHE PHE PRO ARG ALA SER GLY
ASN GLN THR THR PRO PRO ALA PHE GLN ARG ALA SER TRP GLN ALA ALA ALA LEU ALA GLY HIS LEU ARG SER GLY ASP SER LEU TRP GLU ARG GLY ASP GLY ILE MET GLY ARG GLY ASP GLU GLU GLU ARG LYS ARG
VAL ARG GLU ARG LEU LEU GLY CYS ASP THR ARG ALA SER HIS ARG GLU THR SER LEU GLY ALA ASP SER GLY LEU PHE ALA LEU ASP ARG GLU ALA GLN ARG PRO ALA GLU ASN ARG GLU PHE PRO GLU PRO HIS CYS VAL SER SER PRO ARG LYS ALA ILE ASP GLN VAL PRO ASP
LEU ASN CYS ARG ALA ALA LEU ASP PRO GLU ARG LYS SER PHE SER PRO ASP SER ASP ARG GLU THR SER ILE ALA LEU CYS ARG ARG ARG VAL SER PRO SER GLY PRO VAL SER SER PRO ASP SER ARG TRP ARG GLY ASP ARG ARG ARG ASN ALA SER SER PRO THR LEU ASP TRP
CYS LEU SER GLN GLN GLY ASN ALA THR GLU SER SER SER PRO HIS ARG ASP THR THR SER ARG ALA PRO ASP SER PRO HIS VAL LYS ALA ALA SER LYS GLU SER ASN PHE LEU SER MET PRO PHE LEU ALA ALA PRO PRO PRO GLY LEU PHE SER PRO TRP ALA SER PRO
VAL ASN SER ASP GLY ASN GLY ASP THR GLU GLY GLY THR LEU TRP ASP GLU GLY ILE GLU ALA GLY GLY SER SER SER LEU THR ARG ARG THR ARG SER SER GLU LEU GLU LYS ARG SER VAL ARG GLN LYS ALA PRO SER GLN VAL GLN LYS ALA ARG GLY THR LEU MET SER SER LEU
ASN ALA GLY LEU GLU ALA LYS THR ARG ALA ASP GLU ARG ARG ASP ILE GLY THR VAL PHE CYS LEU SER ASP SER ARG ASP THR GLU VAL LYS PRO GLY GLU GLU THR LEU PHE GLN SER ALA ALA GLY GLU SER TRP GLY VAL ASP GLU GLU ARG GLU ALA GLU ARG GLU ALA
GLU GLN ARG ARG ARG ARG ARG THR GLY GLY THR TRP ALA ASN PRO GLY GLY ARG GLY ARG THR GLY SER ARG GLY GLU ALA SER THR TRP ARG ARG GLU SER SER ALA THR GLU ALA ALA GLU ILE ARG ARG GLU ARG ASP SER
GLY ARG ARG ASP THR ARG GLU ARG LYS ASP GLU GLY ALA VAL ASN ARG VAL SER ARG ALA THR GLY ARG THR GLU GLY VAL ALA ALA VAL LEU GLY GLN GLU ARG ARG ARG ARG CYS VAL ASP ALA ARG GLU ALA THR GLU ALA ARG ARG ASN GLU ALA GLU ASP ARG GLU GLY GLU ASP LEU GLY GLU
ALA GLU LEU SER VAL SER CYS PHE ASP SER ASP GLY GLN GLU ASP GLY GLU LEU PHE SER THR ASN GLU VAL GLU THR ASP THR LEU ARG SER GLY ARG ARG LYS GLN HIS SER VAL SER SER
ARG SER ALA SER PRO TRP ARG VAL GLY MET ARG THR SER ARG PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER SER ARG ALA SER PRO SER ARG PRO ALA SER ARG ARG LEU GLU
THR LEU GLU THR LEU ASP LEU ARG THR ARG LYS ARG VAL ARG VAL GLY SER ARG GLU TRP SER ARG GLU VAL ARG GLN SER ARG ASN ALA GLN ARG SER PRO GLY ASN ALA GLN ARG SER THR GLU GLY GLY ARG ARG ARG ARG ASP LYS LYS GLY GLN THR GLU GLY GLY ASP TRP GLY ARG ALA TYR LEU GLU VAL
GLY GLN GLU THR GLU THR ASP SER GLU ILE ALA THR LEU GLU LEU PRO ARG VAL SER PRO GLN THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ASP GLU THR ASP CYS LEU PHE SER THR VAL PRO ARG LEU PRO VAL SER ASN ALA ASP
PRO GLN ALA SER GLU ALA ALA ARG SER SER SER SER CYS TYR PRO SER ARG SER CYS SER ALA LEU SER LEU SER PHE ALA CYS SER ASP SER THR VAL HIS ALA GLU SER ALA THR ARG GLY
ARG THR VAL HIS LEU LEU SER SER SER ILE SER PRO THR SER ASP CYS GLY ARG LEU ASP SER ALA LEU ASP PRO GLY LEU LYS CYS THR LEU PHE PHE SER ALA PRO GLU ALA VAL HIS ALA ARG PRO LEU ALA SER PRO SER ARG
GLN ARG LEU PHE SER ARG ASP SER ALA PHE ASP SER TRP SER PRO THR SER ALA GLY ALA GLY SER ARG GLU LEU SER SER PRO SER ARG GLY ARG LEU SER VAL ASN SER CYS GLY SER ASN VAL SER SER PRO SER ARG GLY ARG LEU GLY GLY LEU LYS

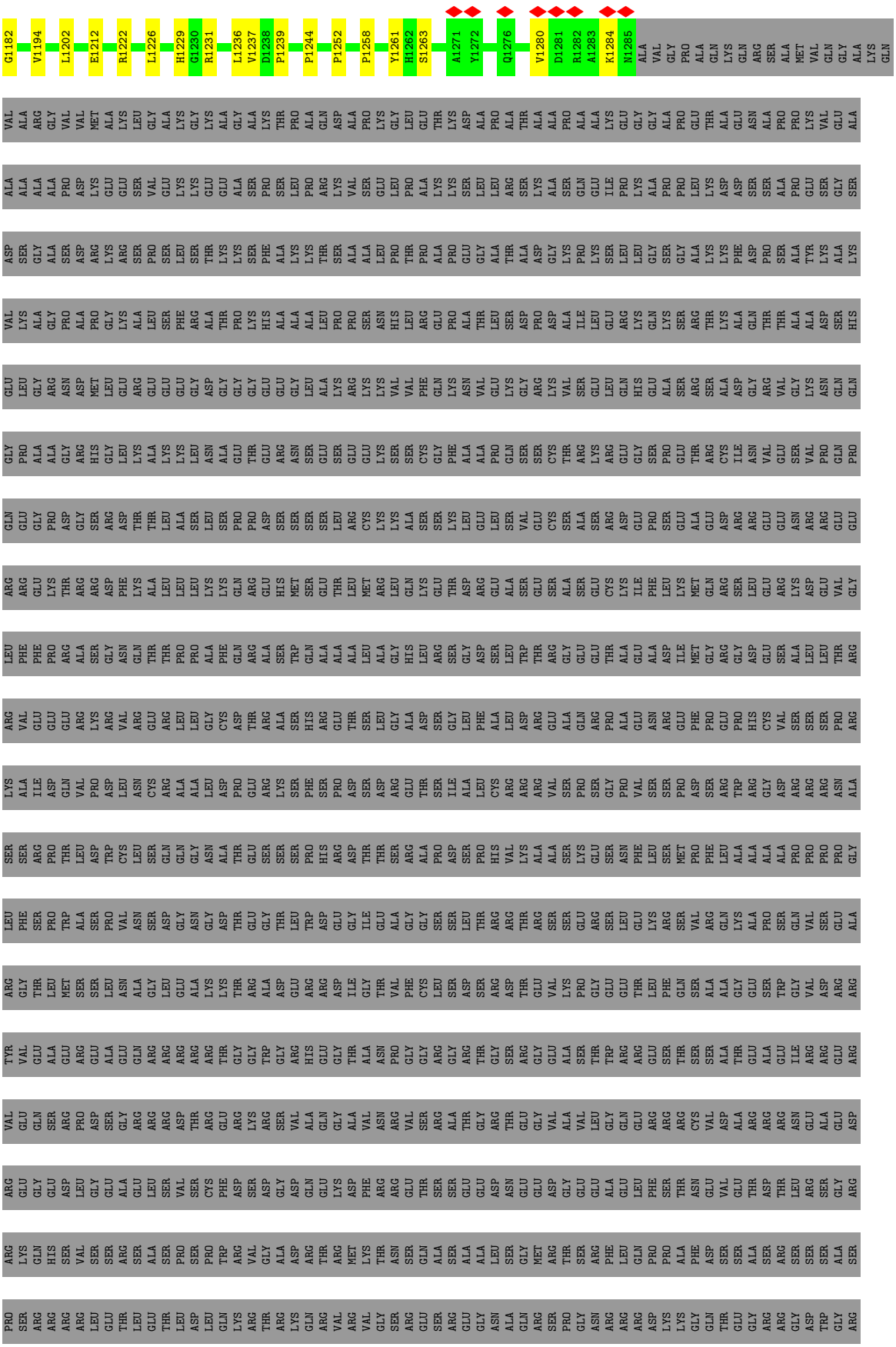

ALA ALA PHE SER ARG HIS SER GLU ASN SER SER ASN GLU ARG LEU CYS SER PRO MET HIS GLN GLU THR SER ARG LYS GLY PRO LEU ALA VAL ARG ARG LEU SER ARG GLU ASP ASP SER ARG
LYS ARG SER SER GLU GLY ASP SER GLN GLU ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU THR GLY ASP SER GLU THR PRO ASN GLY TRP ALA GLY VAL GLY GLY LEU GLU ASP SER ALA GLY GLU ASP SER ARG LEU GLY GLY ASP PRO ARG ARG PRO ARG ARG THR LEU SER ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU ARG ARG LYS ASN ARG ARG VAL LYS LYS GLU GLY GLY
LEU GLY GLY SER LEU ARG ARG PHE SER PHE SER SER ASP LEU ARG LYS ASP PRO ARG ARG PRO ARG ARG THR LEU SER ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG ARG LYS ASN ARG ARG VAL LYS LYS GLU GLY GLU GLN GLU SER
GLU ARG GLU ARG ARG ASP GLU GLY GLN GLU SER GLU ARG GLU ARG GLU ASP ASP GLU GLY GLU GLN GLY GLY GLU GLN GLU SER GLU ASN SER GLU ARG GLU ASP GLY GLY GLY GLU GLN GLU ALA GLU HIS GLU SER GLU ARG GLU ARG ASP
GLU ARG GLU GLN GLY GLY GLU GLN GLU SER GLU GLU ARG GLU ARG ASP GLU GLU GLN GLY GLY GLU GLN GLU SER GLU ASN GLU GLN GLU GLU ALA GLU GLN GLU ASN GLU GLY ASN GLU GLU ARG GLU ALA GLU GLN ALA VAL GLY GLU
GLN GLY GLN GLU ARG GLU GLY GLU GLN GLU GLY GLU GLN ARG SER GLU GLN ARG GLY SER SER VAL ILE ASN VAL TRP ARG GLN ALA ALA GLU GLU LYS GLU GLY GLY LYS GLN LEU SER LYS GLY GLU GLU SER GLU ASN GLU GLN GLU GLY GLY LYS LYS GLY GLY VAL ARG ALA ASP ASN GLN ALA SER
GLY ALA THR GLN GLY GLU GLU GLN GLU GLN SER SER ARG PHE SER GLN LEU LEU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ARG ILE GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY ARG TRP ARG LYS ASP MET GLY ILE LEU LYS ASP SER GLU
GLU GLU SER LEU ILE GLY LYS GLU GLY ILE SER GLN ARG LEU THR ASP ALA ASP THR GLY THR GLU LYS THR ARG GLU ALA GLN ARG GLU ASP ALA THR VAL VAL THR GLU SER ALA ARG ASP ARG ARG ARG ALA LEU GLY THR THR VAL SER LEU GLU GLU VAL SER LEU CYS ALA VAL
GLY SER SER GLU HIS LEU GLU LYS LEU GLY SER GLY GLY ASP GLU ASN ASP CYS GLY ASP ALA SER GLU GLU GLY HIS CYS CYS GLU ASP ARG ARG SER LEU LYS ARG GLU LYS LYS GLY ARG GLU LYS GLN VAL
SER ALA ARG GLY VAL GLU THR PRO GLU GLU THR LYS GLN LEU GLU PRO ALA SER PRO LEU SER SER SER PRO LEU ALA GLY SER ALA SER ASN VAL PHE PRO ALA ARG LYS ARG LEU PHE SER SER ARG MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS
ALA ASP LYS PRO GLY SER PRO SER ASP GLN ASN SER ALA VAL SER PRO SER PRO SER PHE GLN LEU SER ARG SER ALA GLU GLU ALA ALA THR GLY GLY PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA VAL LEU SER GLY ALA LEU GLU VAL GLU THR GLY TRP GLY VAL GLN THR
ALA PRO GLU THR PRO GLY ASN SER THR HIS HIS TRP ALA SER PRO PHE HIS SER LEU PHE SER ARG PHE SER LEU ARG ASP ARG LEU ARG ARG ARG SER SER ALA SER SER MET THR VAL LEU ASP MET GLU GLU ASN LYS SER LEU GLU VAL ASP MET PRO ALA THR
GLU PRO GLN ARG PRO LEU ALA SER VAL SER ASP SER ASP PRO VAL SER ASP PHE GLY ASP ASP SER LEU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER GLU VAL ALA PRO ALA CYS GLY GLY
ARG GLU SER PRO THR SER ARG ARG HIS SER PHE VAL PHE ARG THR THR GLN GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASN ARG GLY ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LEU VAL LYS SER PRO GLU ARG ILE LEU ARG ASP
ARG ASP ARG GLU GLU SER GLU ASP ASP GLU LYS ASP THR ASP ASP GLY LYS ARG GLU GLY ARG LYS LEU ARG HIS SER LEU SER SER CYS ALA GLY ALA ARG GLN ILE LEU ARG ASP
VAL CYS LYS ARG ARG LEU PRO PRO LEU PRO PRO GLU ALA SER SER PRO HIS GLY ALA ALA SER LEU ARG ALA ALA ALA ALA SER PHE ARG LEU ARG ARG SER VAL ASN ARG GLY LYS LYS GLU LEU ARG ARG SER ARG GLU GLU GLU THR
LYS ALA GLN ASN GLU ILE LYS HIS GLU ASP ARG LYS SER GLU LEU LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU LEU ARG ILE LYS GLN GLU ARG LYS GLY GLU VAL LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU ASN GLU GLU ILE LYS GLN GLU ARG LYS SER
GLU LEU LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU GLU ILE LYS GLN GLU GLU VAL ASP GLU MET LYS GLN GLU ASN VAL ASP GLU GLU THR PRO GLU THR VAL ASP ARG GLY ASP PRO SER ILE THR SER HIS
LEU SER ASP SER CYS GLY VAL ALA ILE PHE ALA VAL ALA ALA ARG THR TRP GLN LYS GLU THR LEU GLY ALA ALA GLY ARG THR GLY GLU ASP GLU ASP CYS VAL ASP ARG GLY ASP ALA LEU THR GLY GLN ASP ALA ASN
GLU GLU THR SER GLN GLU VAL ALA GLU ARG GLU ARG ALA TRP MET GLY GLY SER SER ASP GLY ALA GLU ILE HIS LEU LEU PRO GLU ALA ASP THR SER ASP GLU GLU GLU GLU GLU GLU ARG GLU GLU GLU LYS GLU GLU GLU

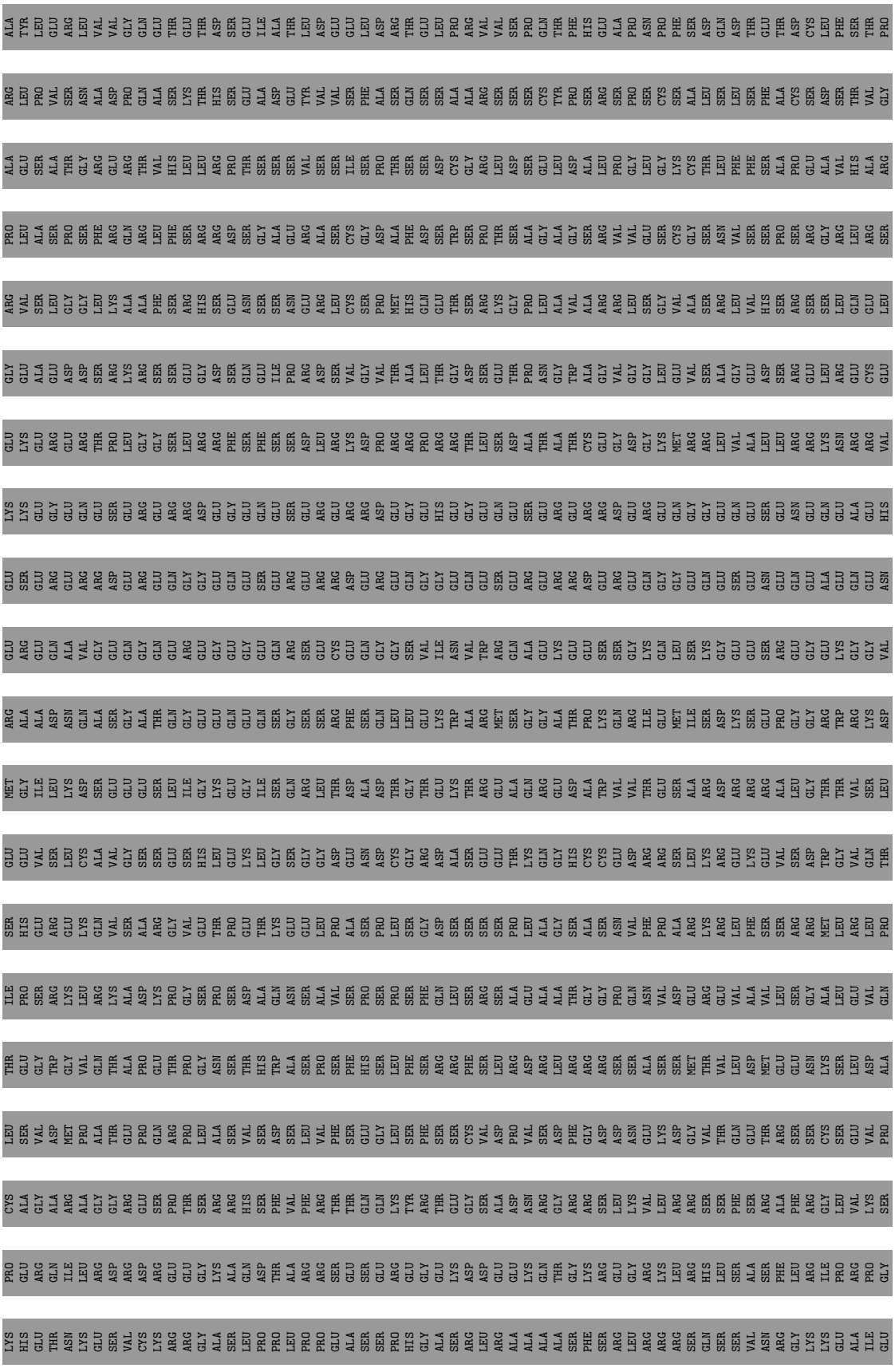


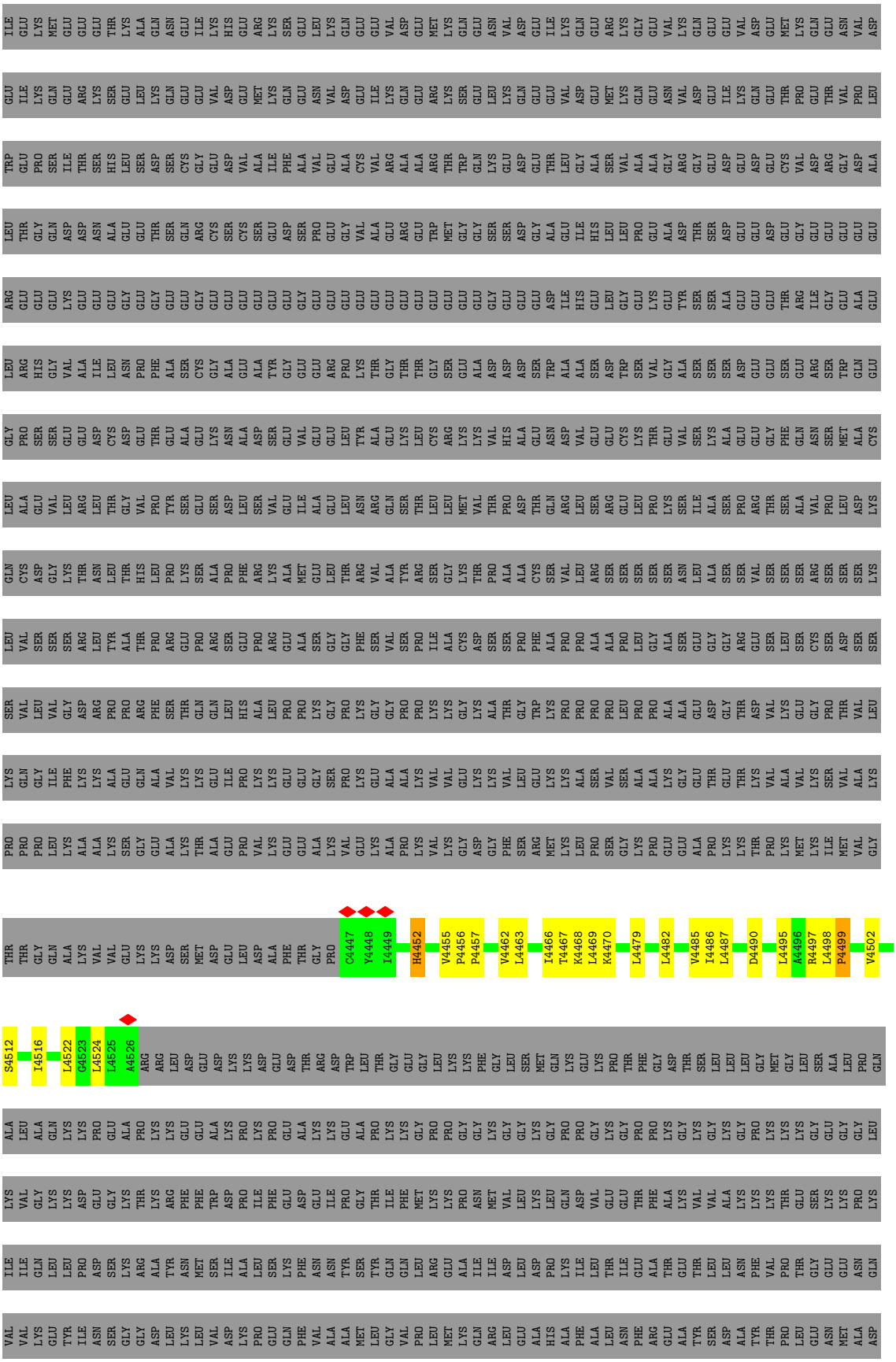
• Molecule 3: Formin 1

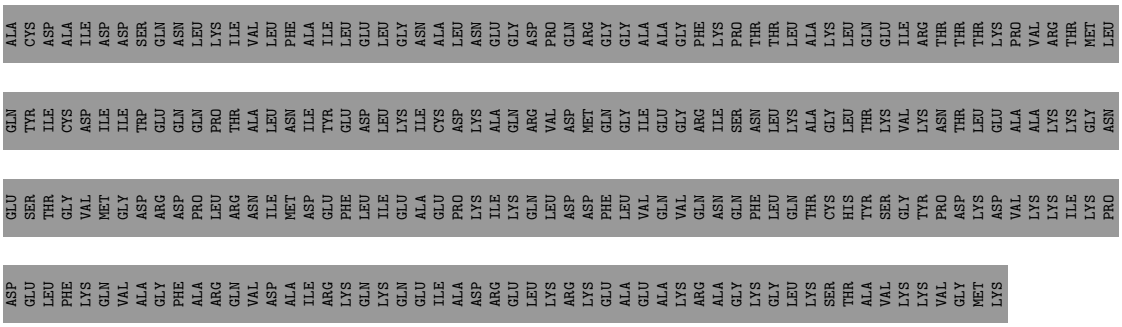
Chain CJ: 95%


P1107
L1108
K1111
S1116
R1119
V1120
R1121
A1122
L1123
W1128
R1129
S1130
L1131
A1137
L1152
K1153
L1154
F1158
L1164
R1168
P1172
V1176


G1182 V1194 L1202 E1212 R1222 L1226 H1229 G1230 R1231 L1236 V1237 D1238 P1239 P1244 P1252 P1258 Y1261 H1262 S1263 A1271 Y1272 Q1276 V1280 D1281 R1282 A1283 K1284 N1285
VAL ALA ARG GLY VAL VAL MET ALA LYS LEU GLY ALA LYS GLY LYS ALA GLY ALA LYS THR PRO ALA GLN ASP ALA PRO LYS GLY LEU GLU THR LYS ASP ALA PRO ALA THR ALA ALA PRO ALA ALA ALA LYS GLU GLY ALA GLY ALA ALA PRO GLU THR ALA GLU ASN ALA PRO PRO LYS VAL GLU ALA
ALA ALA ALA ALA PRO ASP LYS GLU GLU SER VAL GLU LYS LYS GLU GLU ALA GLY SER PRO SER LEU PRO ARG LYS VAL SER GLU LEU PRO THR LYS LYS LYS SER LEU ARG SER LYS ALA SER GLN GLU ILE PRO LYS ALA PRO PRO LEU LYS ASP ASP SER SER ALA PRO GLU SER GLY SER
ASP SER GLY ALA SER ASP ARG LYS ARG SER PRO SER LEU SER THR LYS LYS SER PHE ALA LYS LYS THR SER ALA LEU PRO THR PRO ALA PRO GLU GLY ALA THR LEU SER ASP PRO ALA THR ALA ASP GLY LYS PRO LYS SER LEU LEU GLY SER GLY ALA LYS LYS PHE ASP PRO SER ALA ALA TYR LYS ALA LYS
VAL LYS ALA GLY PRO ALA PRO GLY LYS ALA LEU SER PHE ARG ALA THR PRO LYS HIS ALA ALA ALA LEU PRO SER ASN HIS LEU ARG GLU PRO ALA THR LEU SER ASP PRO ASP ALA ILE LEU GLU ARG LYS HIS GLN LYS SER ARG THR LYS ALA GLN THR THR ALA ALA ALA SER HIS
GLU LEU GLY ARG ASN ASP MET LEU GLU ARG GLU GLU GLU GLY ASP GLY GLY GLY GLU GLY GLY LEU ALA LYS ARG LYS LYS VAL PHE GLN LYS ASN VAL GLU LYS GLY ARG LYS VAL SER GLU LEU GLN HIS GLU ALA SER ARG SER ALA ASP GLY ARG VAL GLY LYS ASN SER GLN GLN
GLY PRO ALA ALA GLY ARG HIS GLY LEU LYS ALA ALA LYS LYS LEU ASN ALA GLU GLU THR GLU ARG ASN SER GLU SER CYS GLY PHE ALA ALA PRO GLN SER SER CYS THR ARG LYS SER GLU LEU GLN HIS GLY SER PRO GLU THR ARG CYS ILE ASN VAL GLU SER VAL PRO GLN PRO
GLN GLU GLY PRO ASP GLY SER ARG ASP PHE LYS ALA LEU LEU LEU LYS LYS GLN ARG GLU HIS MET SER GLU THR LEU MET ARG LEU GLN LYS GLU THR ASP ARG GLU LEU SER GLU CYS SER ALA SER GLU CYS ARG ASP GLU ALA GLU ALA PRO SER GLU ALA ASP ILE MET GLY ARG GLY GLU ASP ARG GLU GLU ASN ARG ARG GLU GLU
ARG ARG GLU LYS THR ARG ARG ASP PHE LYS ALA LEU LEU LEU LYS LYS GLN ARG GLU HIS MET SER GLU THR LEU MET ARG LEU GLN LYS GLU THR ASP ARG GLU LEU SER GLU CYS SER ALA SER GLU CYS LYS ILE PHE LEU LYS MET GLN ARG SER LEU GLU ARG ARG GLU GLU VAL GLY
LEU PHE PHE PRO ARG ALA SER GLY ASN GLN THR THR PRO PRO ALA PHE GLN ARG GLN ALA ALA ALA LEU ALA GLY HIS LEU ARG SER GLY ASP SER LEU TRP THR ARG GLY GLU GLU THR ALA GLU ALA ASP ILE MET GLY ARG GLY ASP ARG GLU LEU GLU ARG LYS ASP GLU VAL THR ARG
ARG VAL GLU GLU GLU ARG VAL ARG GLU ARG LEU GLY CYS ASP THR ARG ALA SER HIS ARG GLU THR SER LEU GLY ALA ASP SER GLY LEU ASP ARG GLU ALA GLN ARG PRO ALA GLU ASN ARG GLU PHE PRO GLU PRO ARG PRO HIS CYS VAL SER SER SER PRO ARG
LYS ALA ILE ASP GLN VAL PRO ASP LEU ASN CYS ARG ALA ALA LEU ASP PRO GLU ARG LYS SER PHE SER PRO ASP SER ASP ARG GLU THR SER ILE ALA LEU CYS ARG ARG ARG VAL SER PRO GLY PRO VAL SER SER PRO ASP SER ARG TRP ARG GLY ASP ARG ARG ARG ASN ALA
SER SER ARG PRO THR LEU ASP TRP CYS LEU SER GLN GLN GLY ASN ALA THR GLU SER SER SER PRO HIS ARG ASP THR THR SER ARG ALA PRO ASP SER PRO HIS VAL LYS ALA ALA SER LYS GLU SER PHE LEU SER MET PRO PHE LEU ALA ALA ALA ALA PRO PRO PRO GLY
LEU PHE SER PRO TRP ALA VAL PRO VAL ASN SER ASP GLY ASN GLY ASP THR GLU GLY THR ALA ASP GLU GLY ILE GLU THR ARG GLY GLY SER SER LEU SER THR ARG THR ARG SER VAL ARG GLN LYS ALA PRO SER GLN VAL SER GLU ALA
ARG GLY THR LEU MET SER SER LEU ASN ALA GLY GLY GLY SER LEU SER ASP SER ARG ASP THR GLU VAL LYS PRO GLY GLU GLU THR LEU PHE GLN SER ALA ALA GLY GLU SER TRP GLY VAL ASP ARG ARG
TYR VAL GLU ALA GLU GLN ARG GLU GLY THR ALA ASN PRO GLY GLY ARG GLY ARG THR GLY SER ARG GLY GLU ALA SER THR TRP ARG ARG GLU SER THR SER ALA ALA THR GLU ALA GLU ILE ARG GLU ARG
VAL GLU GLN SER ARG GLY ASP ARG ARG ARG

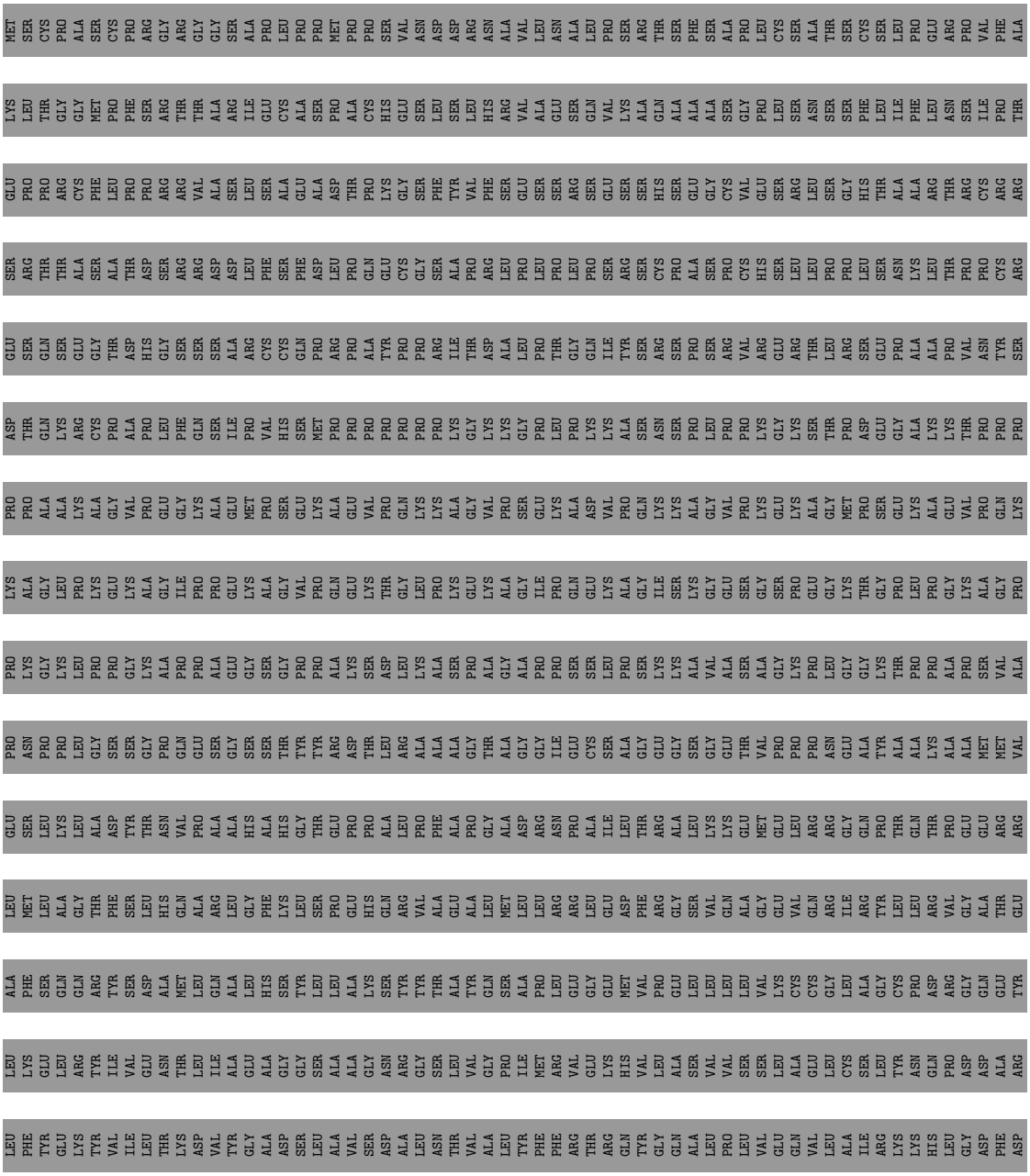

ALA TYR LEU GLU ARG LEU VAL VAL GLY GLN GLU THR GLU THR ASP SER GLU ILE ALA THR LEU ASP GLU GLU LEU ASP ARG THR GLU LEU PRO ARG VAL VAL SER PRO GLN THR PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN ASP THR GLU THR ASP CYS LEU PHE SER THR PRO
ARG LEU PRO VAL SER ASN ALA ASP PRO GLN GLN ALA SER LYS THR HIS SER GLU ALA ASP GLU TYR VAL VAL SER PHE ALA SER GLN SER SER SER ALA LEU SER LEU SER PHE SER ALA ALA PRO GLU ALA VAL HIS SER PRO SER ASP SER THR LEU SER ALA PRO THR VAL GLY
ALA GLU SER ALA THR GLY ARG GLU ARG THR VAL HIS LEU LEU ARG PRO THR SER SER ASP CYS GLY ARG LEU ASP SER GLU LEU ASP ALA LEU PRO GLY LEU GLY LYS CYS THR LEU PHE PHE SER ALA PRO GLU ALA ARG
PRO LEU ALA SER PRO SER PHE ARG GLN ARG LEU PHE SER ARG ARG ASP SER GLY ALA GLU ARG ALA SER CYS GLY ASP ALA PHE ASP SER CYS GLY SER ASN VAL VAL GLU SER CYS GLY SER ARG GLY ARG ARG SER
ARG VAL SER LEU GLY LEU LYS ALA ALA PHE SER ARG HIS SER GLU ASN SER SER ASN GLU ARG CYS LEU CYS SER PRO MET HIS GLN GLU THR SER ARG LYS GLY PRO LEU ALA VAL ALA ARG LEU SER GLY VAL ALA SER ARG LEU VAL GLN LEU
GLY GLU ALA GLU ASP ASP SER ARG LYS ALA SER GLN GLU ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU THR GLY ASP SER GLU THR PRO ASN GLY TRP ALA GLY VAL GLY GLY LEU GLU VAL SER ALA GLY GLU LEU ARG GLU CYS GLU
GLU LYS GLU ARG GLU ARG THR PRO LEU GLY GLY SER LEU ARG ARG PHE SER SER SER ASP LEU ARG LYS ASP PRO ARG ARG PRO ARG THR LEU SER ASP ALA THR ALA THR CYS GLU GLY ASP GLY LYS MET ARG ARG LEU VAL ALA LEU LEU ARG ARG LYS ASN ARG ARG VAL
LYS LYS GLU GLY GLU GLN GLU SER GLU GLN GLU SER GLU ARG GLU ARG ARG ASP GLU GLY GLU HIS GLU GLY GLU GLN GLU SER GLU ARG ASP GLU ARG ARG ASP GLU ARG GLU GLN GLY GLY GLU GLN GLU SER GLU ASN GLU GLN GLU ALA GLU GLN HIS
GLU SER GLU ARG GLU ARG ASP GLU ARG GLU GLN GLY GLY GLU GLN GLU SER GLU ARG GLU GLN GLY GLY GLU GLN GLU SER GLU ASN GLU GLU ALA GLU GLN GLU GLN ASN
GLU ARG GLU GLN ALA VAL GLY GLN GLY GLY GLN GLU ARG GLU GLN GLY GLY SER GLY VAL ILE ASN VAL TRP ARG GLN ALA GLU LYS GLU GLU SER ARG GLU GLY GLY LYS GLY GLY VAL
ARG ALA ALA ASP ASN GLN ALA SER GLY ALA THR GLN GLU GLU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ARG ILE GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY ARG TRP ARG LYS ASP
MET GLY ILE LEU LYS ASP SER GLU GLU GLY ILE SER GLN ARG LEU THR ASP ALA ASP THR GLY THR GLU LYS THR ARG GLU ALA GLN ARG GLU ASP ALA TRP VAL VAL THR GLU SER ALA ARG ASP ARG ARG GLU ASP SER ALA LEU GLY THR THR THR LEU SER
GLU GLU VAL SER LEU GLU SER SER GLU LEU GLY SER GLY ASP GLU ASN ASP CYS GLY ARG ASP ALA SER GLU THR CYS GLY GLU ASP ARG ARG SER LEU LYS ARG GLU LYS GLU VAL SER ARG VAL GLN THR
SER HIS GLU ARG GLU LYS GLN VAL GLU THR PRO GLU THR LYS GLU GLU LEU PRO ALA SER PRO LEU SER GLY ASP SER SER SER SER PRO LEU ALA GLY SER ALA SER ASN VAL PHE PRO ALA ARG LYS ARG LEU PHE SER SER ARG ARG MET LEU ARG LEU PRO
ILE PRO SER ARG LYS LEU ASP LYS PRO GLY SER PRO SER ASP ALA ASN SER ALA VAL PRO SER PRO SER PRO GLN LEU SER ARG SER ALA GLU ALA ALA THR GLY GLY PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA VAL LEU SER GLY ALA LEU GLU VAL GLN
THR GLU GLY TRP GLY VAL GLN THR ALA PRO GLU THR PRO GLY ASN SER THR HIS TRP ALA SER PRO SER PHE HIS SER LEU PHE SER ARG ARG PHE SER LEU ARG ARG ASP ARG LEU ARG ARG SER SER ALA SER SER MET THR VAL LEU ASP MET LEU SER ASN LYS SER LEU GLU ASP ALA
LEU SER VAL ASP MET PRO PRO GLN ARG PRO LEU ALA SER VAL PHE SER GLU GLY LEU SER PHE SER SER CYS VAL ASP PRO VAL SER ASP PHE GLY ASP ASN GLU LYS ASP GLY VAL THR GLN GLU THR ARG SER SER CYS SER LEU GLU VAL PRO
CYS ALA GLY ALA ARG ALA GLY GLY ARG GLU GLN SER PRO THR SER ARG HIS GLY GLN LYS TYR ARG THR GLU GLY SER ALA ASP ASN ARG GLY ARG ARG SER LEU LYS VAL LEU ARG ARG SER SER PHE SER ARG ALA PHE ARG GLY LEU VAL LYS SER
PRO GLU ARG GLN ILE LEU ARG ASP GLU GLU LYS ASP ASP GLU GLU LYS GLN THR GLY LYS ARG GLU GLY LYS LEU ARG HIS LEU SER ALA SER PHE LEU ARG ILE PRO ARG LEU GLY
LYS HIS GLU THR ASN LYS GLU SER VAL CYS LYS ARG ARG GLY ALA SER LEU PRO PRO GLU ALA SER SER PRO HIS GLY ALA SER ARG LEU ARG ALA ALA ALA SER PHE SER ARG LEU ARG ARG SER GLN SER SER VAL ASN ARG GLY LYS LYS GLU ALA ILE GLU

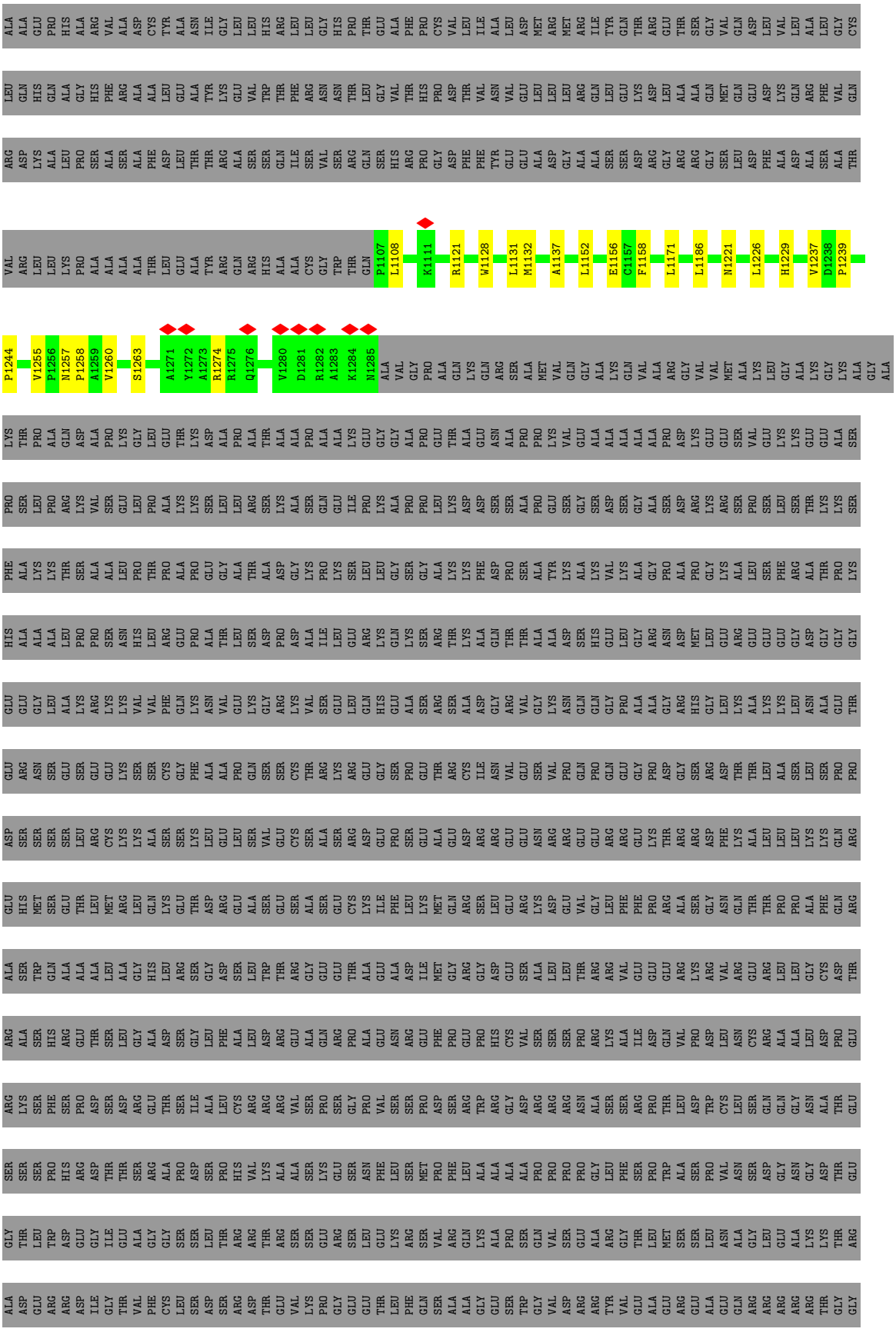

C4447
Y4448
I4449
H4452
V4455
P4456
P4457
V4462
L4463
T4466
T4467
K4468
L4469
K4470
L4479
L4482
V4485
I4486
I4487
D4490
L4495
A4496
R4497
L4498
P4499
V4502
S4512
I4516
L4522
G4523
L4524
L4525
A4526

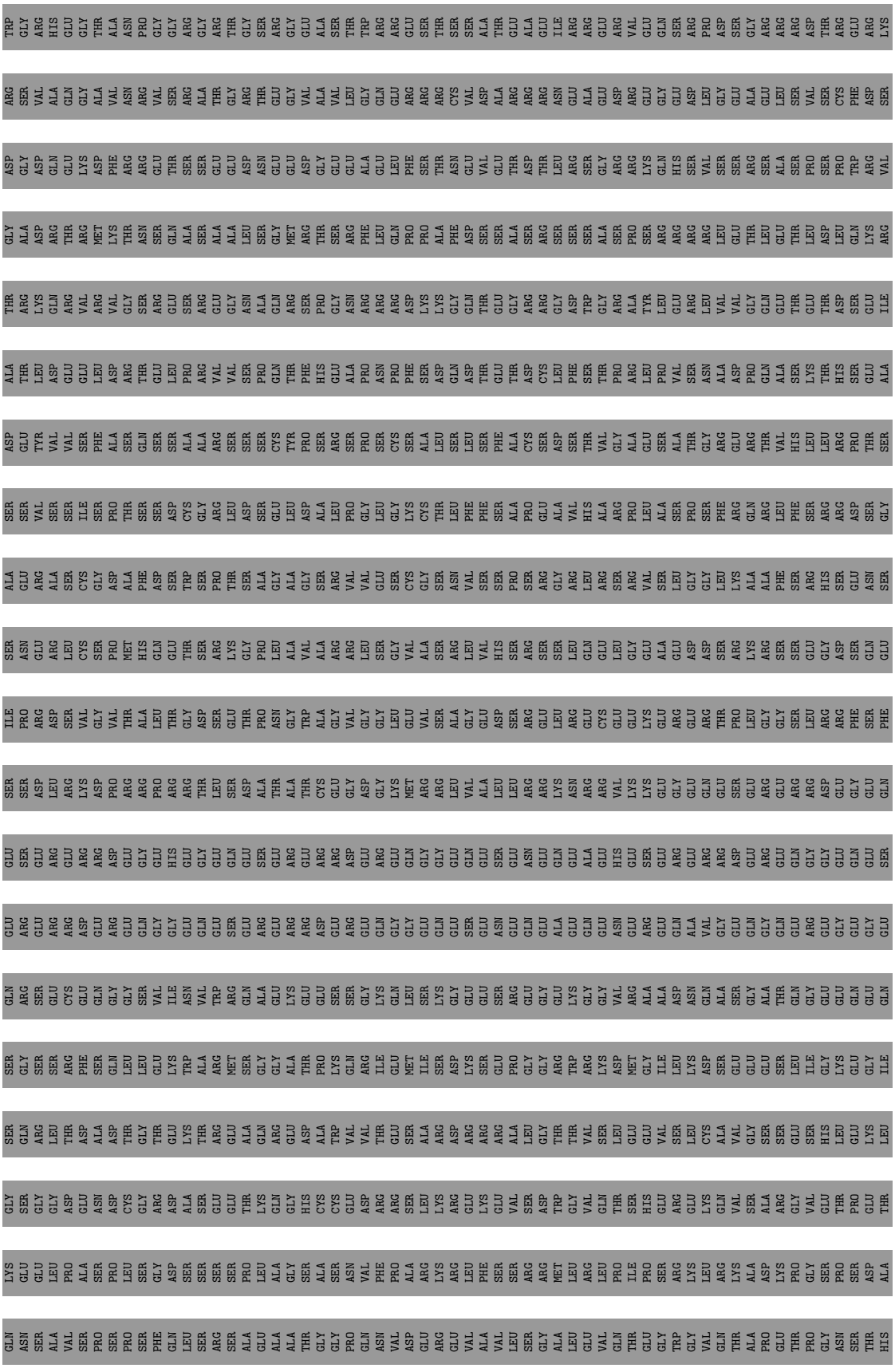


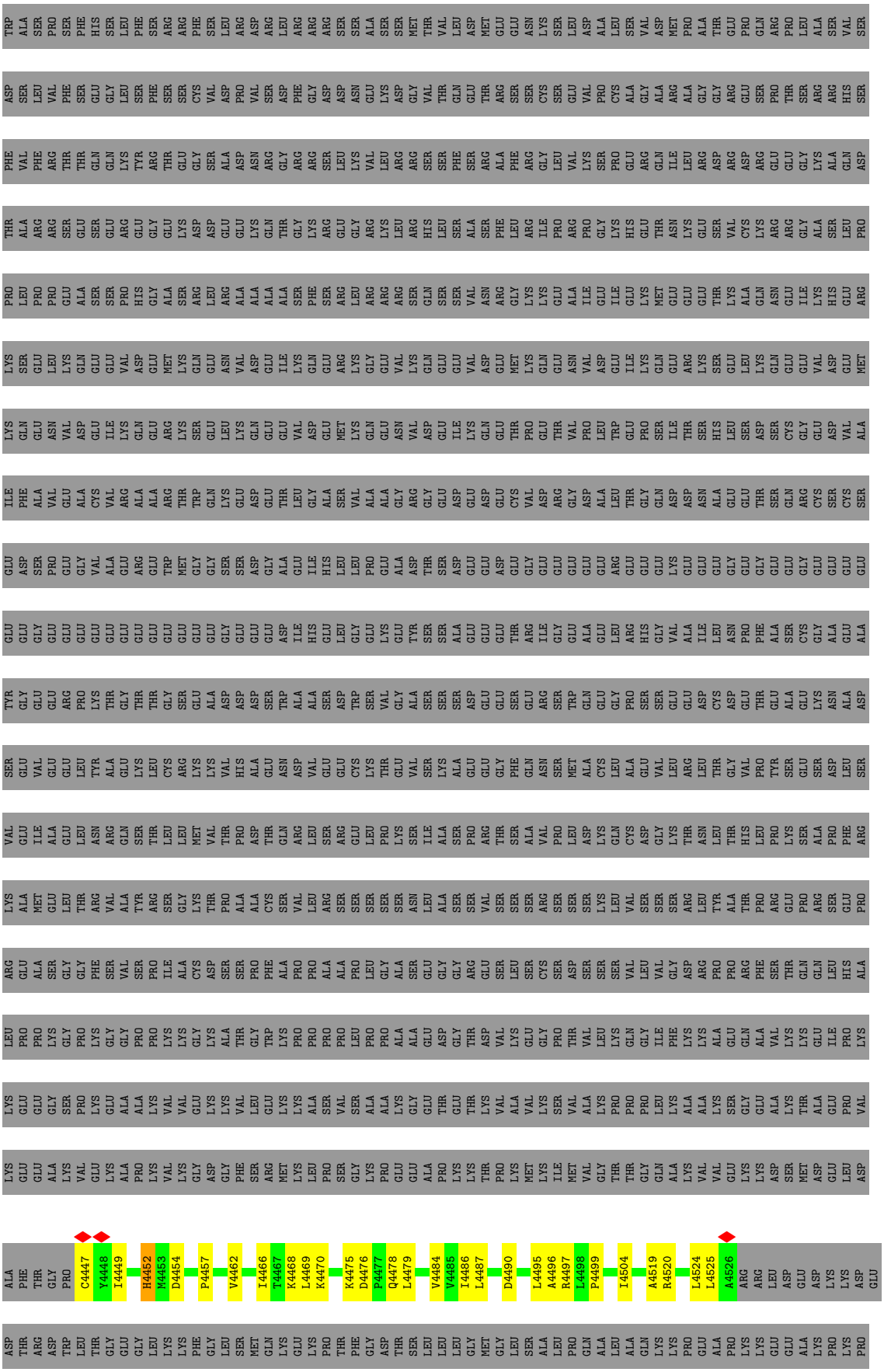
• Molecule 3: Formin 1

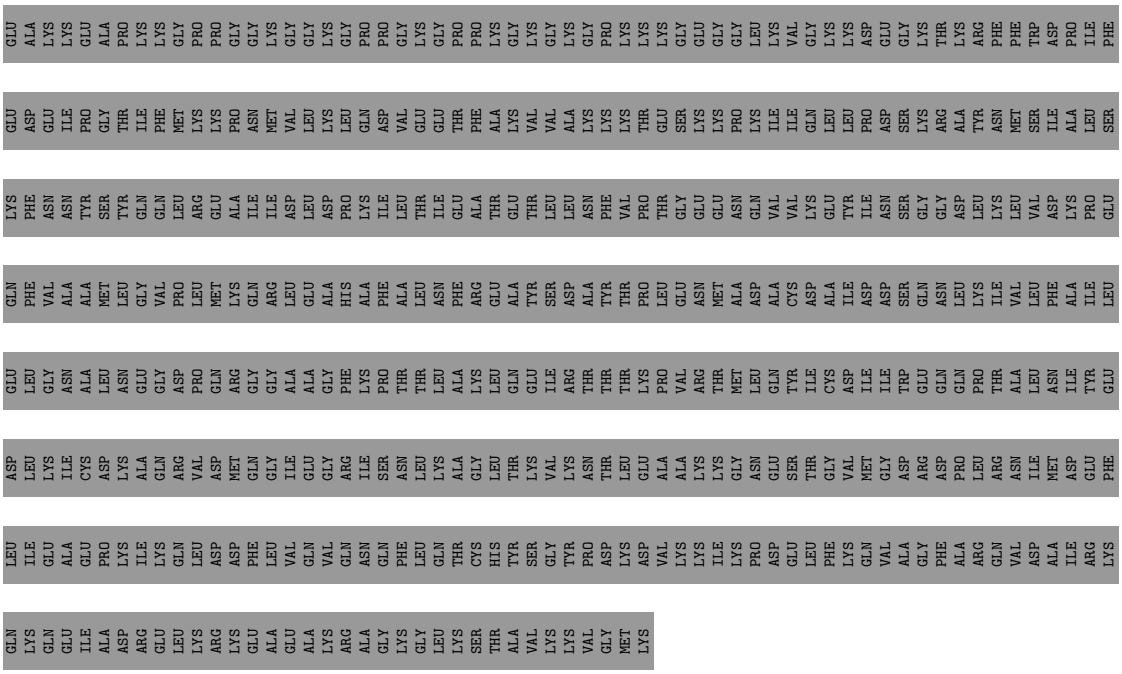
Chain CL: 95%




P1107
L1108
K1111
R1121
W1128
L1131
M1132
A1137
L1152
E1156
C1157
F1158
L1171
L1186
N1221
L1226
H1229
V1237
D1238
P1239
P1244
V1255
P1256
N1257
P1258
A1259
V1260
S1263
A1271
Y1272
A1273
R1274
R1275
Q1276
V1280
D1281
R1282
A1283
K1284
N1285

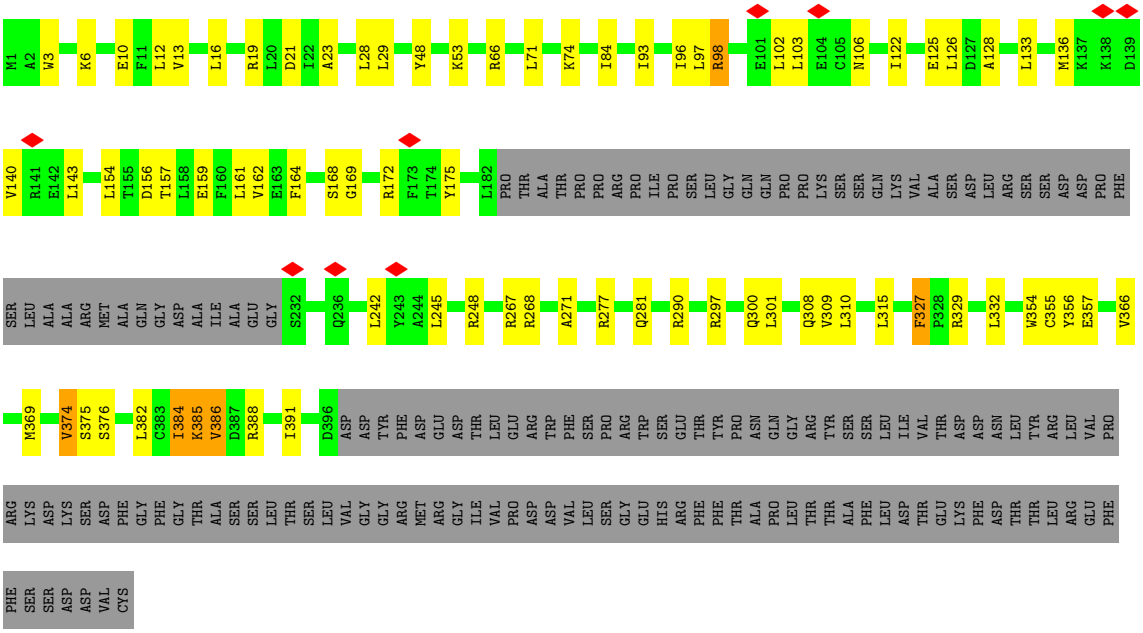

TRP GLY ARG HIS GLU GLY THR ALA ASN PRO GLY GLY ARG GLY ARG THR GLY ARG GLY GLU ALA SER THR TRP ARG ARG GLU SER SER ALA THR GLU ALA GLU ARG ARG GLU ARG VAL GLU GLN SER ARG PRO ASP SER GLY ARG ARG ARG
ARG SER VAL ALA GLN GLY ALA VAL ASN ARG VAL SER ARG ALA THR GLY ARG THR GLU GLU ASP PHE ARG ARG GLU THR SER SER GLU GLU ASP ASN GLU GLU GLY VAL ALA VAL LEU GLY GLN GLU ARG GLU ARG ARG CYS VAL ASP ALA ARG ARG ARG GLU ASP ARG GLU GLY GLU ALA GLU LEU SER VAL SER ARG ALA SER CYS PHE ASP SER
ASP GLY ASP GLN GLU LYS ASP PHE ARG ARG GLU THR SER SER GLU GLU ASP ASN GLU GLU GLY ASP GLY GLU GLU ALA GLU LEU PHE SER THR ASN GLU VAL GLU THR ASP THR LEU ARG SER GLY ARG ARG LYS GLN HIS SER VAL SER SER GLU ALA SER PRO SER PRO TRP ARG VAL
GLY ALA ASP ARG THR ARG MET LYS THR ASN SER GLN ALA SER ALA ALA ALA LEU SER GLY MET ARG THR SER GLY PHE LEU GLN PRO PRO ALA PHE ASP SER SER SER ALA ARG ARG ARG LEU GLU GLU THR LEU ARG SER ALA PHE ASP SER GLY ARG ARG LEU GLU GLY THR LEU GLU GLU THR LEU ASP PRO SER PRO SER ARG SER SER SER ALA SER PRO SER ARG ARG ARG LEU GLN LYS ARG
THR ARG LYS GLN ARG VAL ARG VAL GLY SER ARG GLU SER ARG GLU GLY ASN ALA GLN ARG ARG ASP TRP LYS LYS GLY GLN THR GLU GLY ARG ARG GLY ASP TRP GLY ARG ALA TYR LEU GLU ARG LEU VAL GLY GLN GLU THR GLU THR ASP ASP ARG
ALA THR LEU ASP GLU GLU LEU ASP ARG THR GLU VAL VAL SER PRO GLN THR ARG ASP CYS LEU PHE HIS GLU ALA PRO ASN PRO PHE SER ASP GLN GLN THR THR PHE SER THR PRO ARG LEU PRO VAL SER ASN ALA ASP PRO GLN ALA ALA SER HIS THR HIS SER GLU GLU ALA
ASP GLU TYR VAL SER PHE ALA SER GLN SER SER CYS TYR PRO SER ARG SER PRO SER CYS SER ALA LEU SER LEU SER PHE PHE SER ALA CYS SER ASP SER THR VAL GLY ALA GLU SER ALA THR GLY ARG GLU ARG THR VAL HIS LEU LEU LEU ARG PRO THR SER
SER SER VAL SER SER ILE SER PRO THR SER SER ASP CYS GLY ARG LEU ASP SER GLU LEU ASP ALA LEU PRO GLY LEU GLY LYS CYS THR LEU PHE PHE SER ALA CYS SER ASP SER ALA LEU ARG PRO GLU ALA VAL HIS ALA ARG PRO LEU ALA SER PRO SER PHE ARG GLU ARG THR VAL HIS LEU LEU ARG ARG ASP THR SER
ALA GLU ARG ALA SER CYS GLY ASP ALA PHE ASP SER GLY ALA ARG VAL VAL GLU SER CYS GLY SER ASN VAL SER SER GLU ARG VAL GLY GLY LEU LYS ALA ALA PHE SER ARG HIS SER GLU ASN SER
SER ASN GLU ARG LEU CYS SER PRO MET HIS GLN GLU THR SER ARG LYS GLY PRO LEU ALA VAL ALA ARG ARG LEU SER GLY VAL ALA SER ARG LEU VAL HIS SER ARG SER LEU GLN LEU GLU ASP ASP SER ARG LYS ARG SER SER GLU GLY ASP SER GLN GLU
ILE PRO ARG ASP SER VAL GLY VAL THR ALA LEU THR GLY ASP SER GLU THR PRO ASN GLY TRP ALA GLY VAL GLY GLY LEU GLU VAL SER ALA GLY GLU ASP ARG THR PRO LEU GLY GLY SER LEU ARG ARG PHE SER PHE
SER SER ASP LEU ARG LEU ASP ARG ARG THR LEU SER ASP ALA THR CYS GLU GLY ASP GLY LYS MET ARG LEU VAL ALA LEU LEU ARG ARG LYS ASN ARG ARG VAL LYS LYS GLU GLY GLU GLN GLU SER GLU ASP GLU GLU
GLU SER GLU ARG GLU GLY GLU HIS GLU GLY GLU GLN GLU SER GLU ARG GLU ARG ASP GLU ARG GLU GLN GLY GLY GLU GLN GLU SER GLU ARG GLU GLN GLU ASN GLU GLN GLU GLN GLU ALA GLU HIS GLU SER GLU ASP GLN GLY GLY GLU
GLU ARG GLU ARG ARG ASP GLU GLN GLY GLY GLU GLN GLU SER GLU ASN GLU GLN GLU ASN GLU ARG GLN GLU GLN ALA GLU GLN GLU VAL GLY GLU GLN GLU GLY GLU GLY GLU
GLN ARG SER GLU CYS GLU GLN GLY GLY SER VAL ILE ASN VAL TRP ARG GLN ALA GLU LYS GLU GLU SER LYS GLY GLU GLU SER ARG GLU GLY GLU LYS GLY VAL ARG ALA ALA ASP ASN GLN ALA SER GLY ALA THR GLN GLN GLU GLN
SER GLY SER SER ARG PHE SER GLN LEU LEU GLU LYS TRP ALA ARG MET SER GLY GLY ALA THR PRO LYS GLN ARG ILE GLU MET ILE SER ASP LYS SER GLU PRO GLY GLY ARG TRP ARG LYS ASP MET GLY ILE LEU LYS ASP SER GLU SER LEU ILE GLY LYS GLU GLY ILE
SER GLN ARG LEU THR ASP ALA ASP THR GLU LYS GLN ALA GLU ARG GLU ALA ALA TRP VAL VAL THR GLU SER ALA ARG ASP ARG ARG ARG GLY THR THR THR VAL SER LEU GLU GLU VAL SER ALA LEU CYS ALA VAL GLY GLU SER GLU SER GLU LEU SER HIS LEU GLU LYS LEU
GLY SER GLY GLY ASP GLU ASN ASP CYS GLY ARG GLU GLU CYS ASP ARG ARG SER GLU LEU LYS ARG GLU LYS GLU VAL SER ASP TRP GLY VAL GLN THR SER HIS GLU ARG GLU LYS GLN VAL SER ALA ARG GLY VAL GLU THR PRO GLU THR
LYS GLU GLU LEU PRO GLY ASP SER SER GLY ALA ALA GLY SER PRO LEU ALA ALA GLY PHE SER SER ARG MET LEU ARG LEU PRO ILE PRO SER ARG LYS LEU ARG LYS ALA ASP LYS PRO GLY SER PRO SER ASP ALA
GLN ASN SER ALA VAL SER PRO GLN ASN VAL ASP GLU ARG GLU VAL ALA LEU GLU VAL GLN THR GLU GLY TRP GLY VAL GLN THR ALA PRO GLU THR PRO GLY ASN SER THR HIS


C4447
Y4448
I4449
H4452
M4453
D4454
P4457
V4462
I4466
T4467
K4468
L4469
K4470
K4475
D4476
P4477
Q4478
L4479
V4484
V4485
I4486
L4487
D4490
L4495
A4496
R4497
L4498
P4499
I4504
A4519
R4520
L4524
L4525
A4526



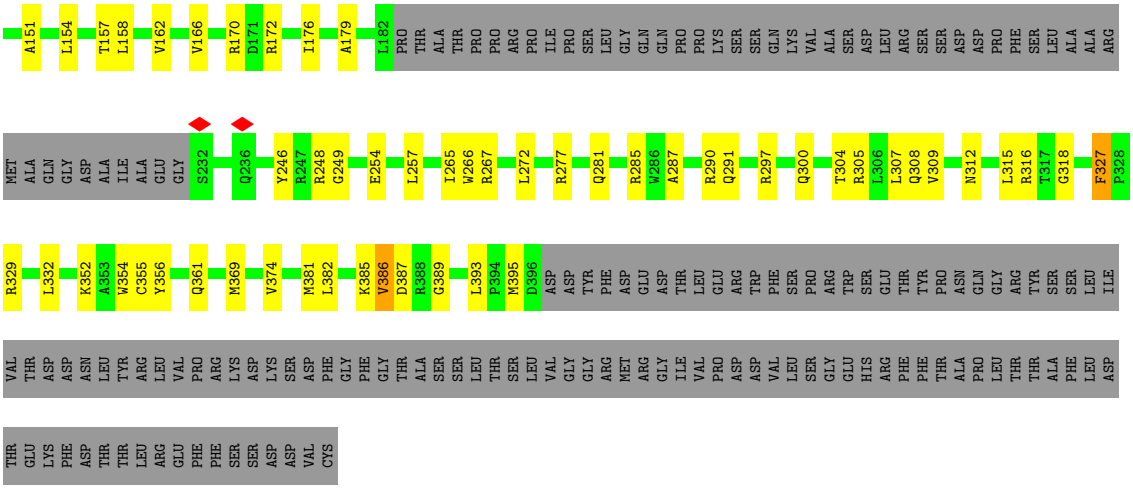
• Molecule 4: PCR11, TGME49_209490

Chain DA:



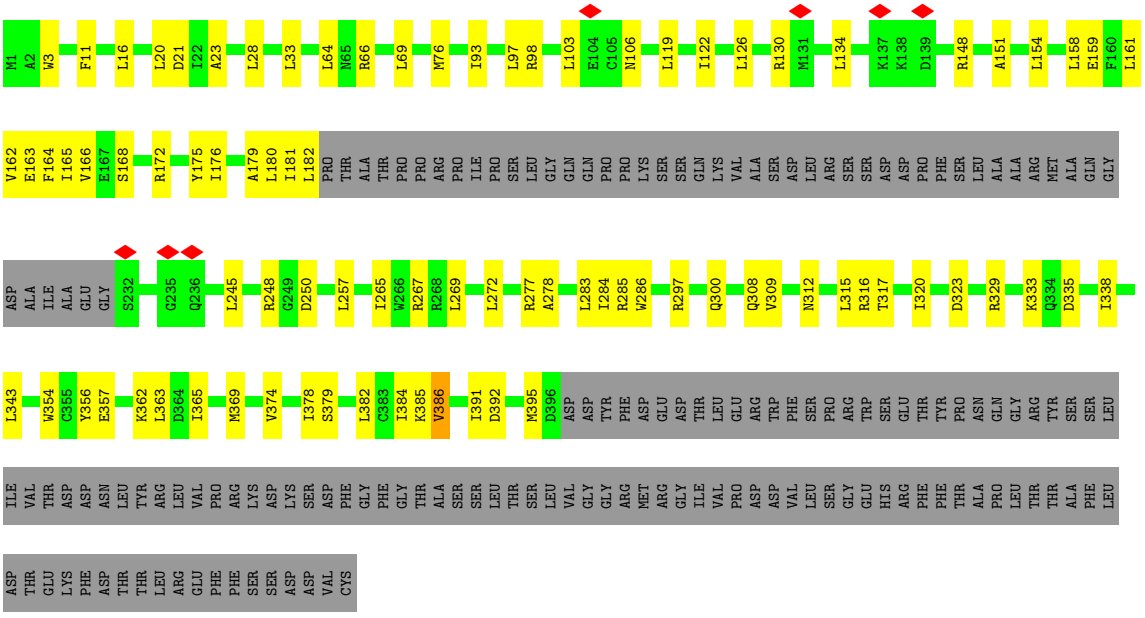
• Molecule 4: PCR11, TGME49_209490

Chain DB:



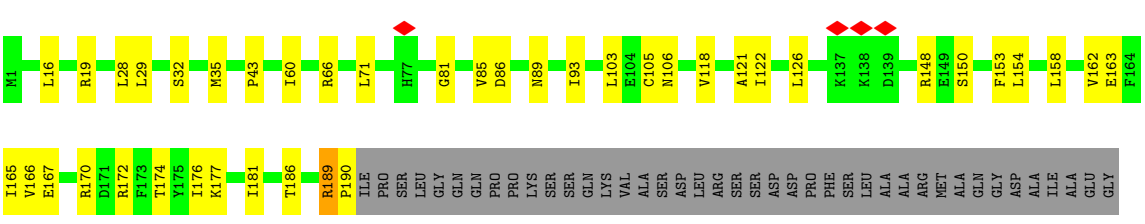
• Molecule 4: PCR11, TGME49_209490

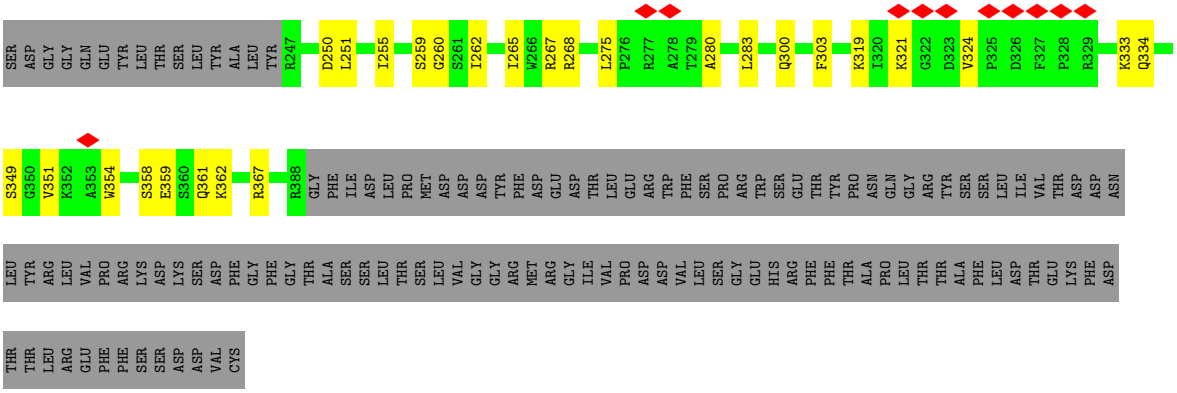
Chain DC:



• Molecule 4: PCR11, TGME49_209490

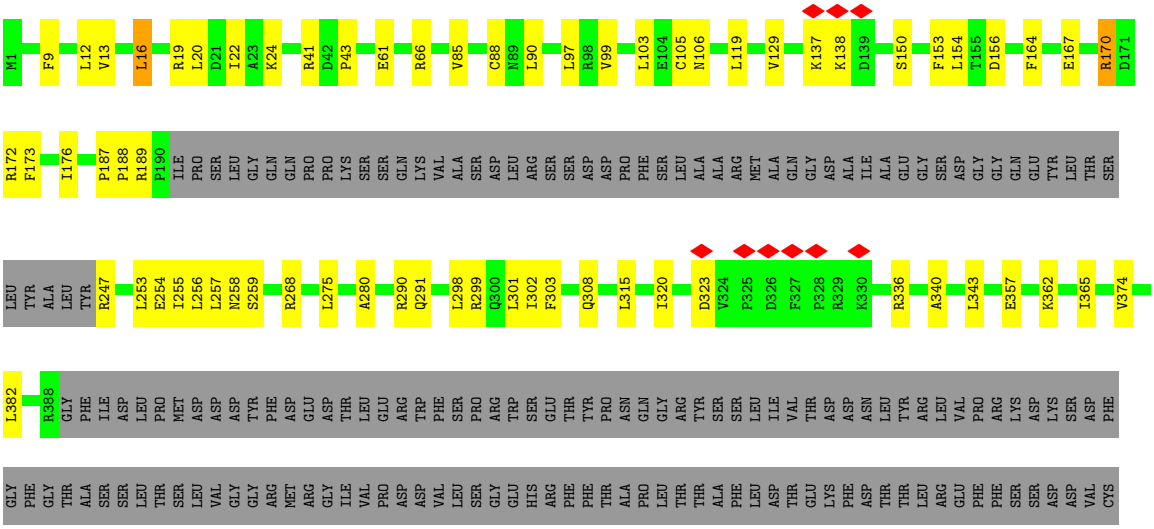
Chain DD:





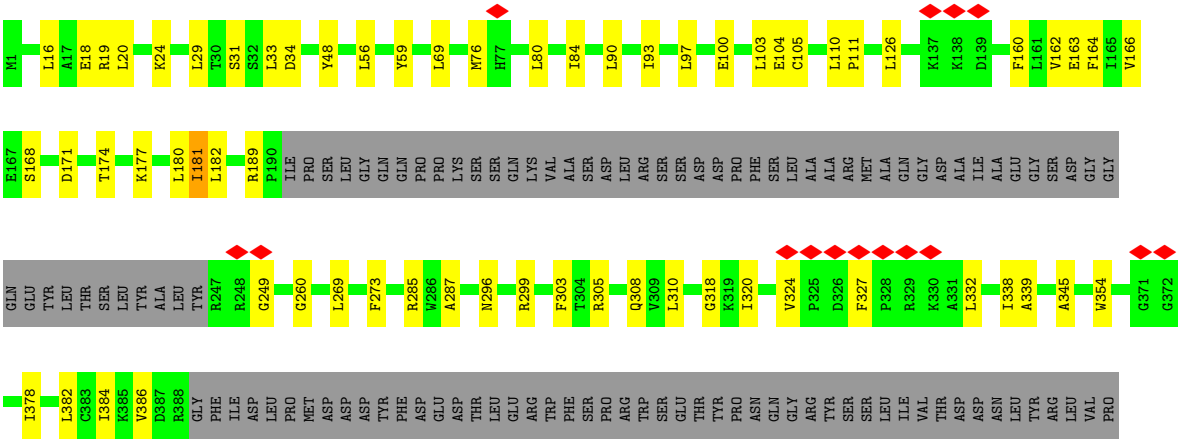
• Molecule 4: PCR11, TGME49_209490

Chain DE:



• Molecule 4: PCR11, TGME49_209490

Chain DF:



ARG LYS ASP LYS SER ASP PHE GLY PHE GLY THR ALA SER SER LEU THR SER LEU VAL GLY GLY ARG MET ARG GLY ILE VAL PRO ASP ASP VAL LEU SER GLY GLU HIS ARG PHE PHE THR ALA PRO LEU THR THR ALA PHE LEU ASP THR GLU LYS PHE ASP THR THR LEU ARG GLU GLU PHE

PHE SER SER ASP ASP VAL CYS

• Molecule 5: CGP, TGME49_240380

Chain EA: 22% 5% 73%

MET GLU GLY GLU ASP LYS ARG GLU ARG ASP GLU ASP GLN ALA GLU LYS ASP MET ALA SER THR THR GLU GLU GLN GLU GLN ILE PRO GLN GLY MET ASN THR GLY GLU ARG GLY ARG LYS SER ARG GLU ALA PHE PRO SER GLU ALA GLU PRO GLY ARG PRO GLN ASP ARG GLU ARG GLU GLU HIS VAL PRO HIS ASP LEU PHE ALA CYS ASP ARG PRO PHE SER LEU SER LYS GLY VAL PRO ALA ARG ALA THR GLN GLU ALA LYS GLN HIS THR PHE LEU HIS LEU CYS SER PRO

LEU PHE SER GLU SER ALA GLY THR ARG SER VAL ASN PRO ASP ASP ASN GLU GLY SER GLN SER ASP THR GLU GLY GLY GLU GLY GLY ALA GLN ASP GLY ARG ILE ARG VAL SER GLY VAL ARG ARG ALA LYS GLU ALA LEU GLU SER GLN ARG SER ILE ALA GLY PRO SER PHE GLN

GLN ASP ASP PRO THR GLU SER HIS GLU LEU GLU ARG GLU VAL ASN GLU ASP ALA PHE HIS PRO SER GLY ARG THR SER LEU SER SER LEU PRO SER LEU GLY HIS ILE PRO LEU VAL GLU SER GLN TRP PHE SER GLY ARG PRO LEU HIS PHE GLN THR GLN ASN ASP LEU ARG

LEU PHE PRO VAL SER PRO PRO LEU SER PHE SER SER PRO GLY LEU LYS ARG LYS GLU ARG GLY LYS SER GLY LEU THR LEU PRO VAL ARG GLU PRO GLU GLU GLY GLU LYS GLN LEU ASP ILE VAL ALA SER PHE ALA ARG LEU ILE LYS ASP ILE GLY ARG ARG THR SER THR ARG LEU

SER ARG THR ASP GLN GLY GLU PRO ALA SER VAL GLY GLU GLY ARG ILE GLY LEU ARG TRP GLY THR PRO GLY SER ILE GLY THR GLU SER SER GLU GLU GLY ASN SER THR TRP ARG GLU GLU VAL GLY GLU GLU PRO ASN GLU ARG ARG VAL GLY GLU SER LEU LYS ASN LEU

SER GLU LEU TYR LEU ASP PRO SER LEU SER ASP MET ARG TRP GLU GLU ASN ARG ARG GLU ARG SER LEU GLU ALA PRO LYS LEU SER LYS GLU ALA SER HIS GLY ALA ASN PRO GLU ASP GLN GLU GLN ARG GLN GLU THR ARG ALA GLN GLY GLU SER ARG ASP GLY ALA SER ALA THR LEU

GLN ARG ILE ARG ARG THR GLY ILE GLU GLY THR MET PRO TYR ARG GLY ASN GLU VAL THR THR HIS THR LEU GLU SER VAL GLN GLU GLN GLY ASP ARG ASP ALA SER SER PHE THR PHE GLN LYS GLU THR PRO PHE PHE THR LEU PHE CYS GLN GLU LEU ASN ALA CYS GLY ARG

VAL ARG GLY GLY THR GLY LYS GLY GLU PRO VAL GLU ASN VAL MET SER GLU CYS ARG ARG ASN THR ARG SER SER SER LEU PRO ALA CYS SER SER SER SER SER SER ARG ILE PHE SER ASP SER PRO LEU ALA ARG PHE PRO ARG LEU GLU GLU THR ARG HIS PRO GLY GLY ILE THR SER ARG

SER SER GLN LEU PRO ALA LEU LEU SER SER PHE PRO PRO ARG ILE ALA THR GLN SER PHE ARG PHE ARG ARG ARG TYR SER HIS GLY ASN VAL PRO GLU ASP ILE ILE SER ALA PRO SER PRO ALA SER ALA SER SER PRO PRO CYS SER PHE ALA SER PRO PHE ARG CYS HIS LYS

SER ARG GLY SER LEU CYS SER THR CYS PRO ILE PRO SER SER SER VAL SER ARG CYS THR ASP SER PRO ARG ARG THR GLY GLY SER GLU SER ASP PRO CYS ARG LEU SER PRO ALA ALA SER SER LEU ALA LEU LEU LEU SER PRO SER SER SER SER SER PRO ARG ILE VAL LEU HIS

VAL GLU ALA LEU SER GLU SER TYR LYS GLU PRO GLU GLY GLY LEU SER SER ALA ALA SER SER PHE HIS SER ALA SER PRO GLU SER THR CYS ALA VAL SER ARG THR ARG LEU ARG ARG THR GLU ARG ARG GLY GLU SER ILE ARG ARG SER SER GLY ASN THR GLY ARG ILE VAL LEU SER

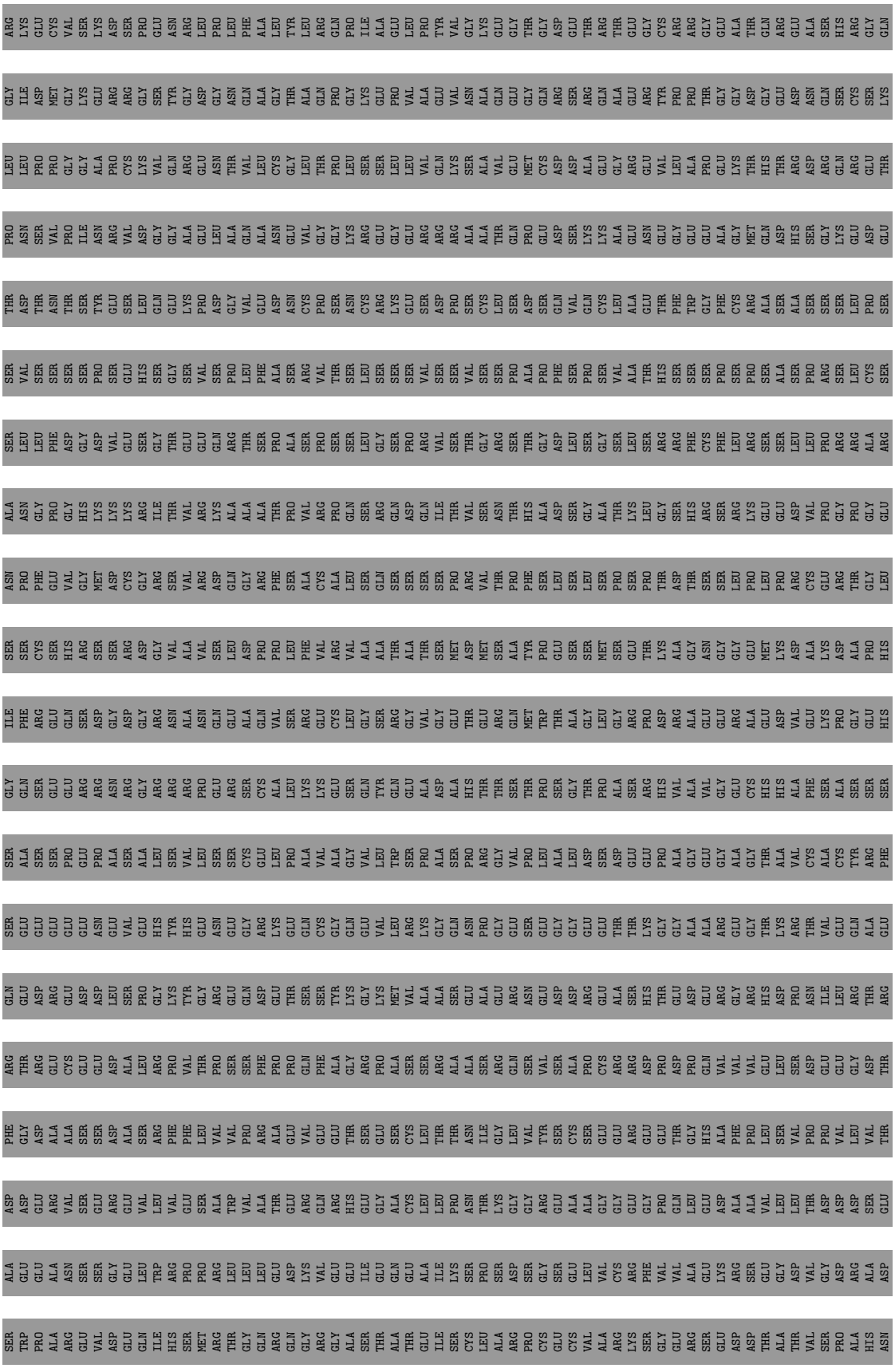
GLN LEU SER ARG ALA SER ARG ARG ARG SER GLY ARG ILE ARG ARG ARG SER GLY ASP ALA LEU GLY GLU HIS ARG THR GLU ALA GLU PRO ARG GLN PRO PRO ARG GLY ARG ARG GLU ARG THR ASP SER ALA ARG GLY SER THR ASP LYS GLU GLU ILE ARG ARG SER SER ALA ARG GLY

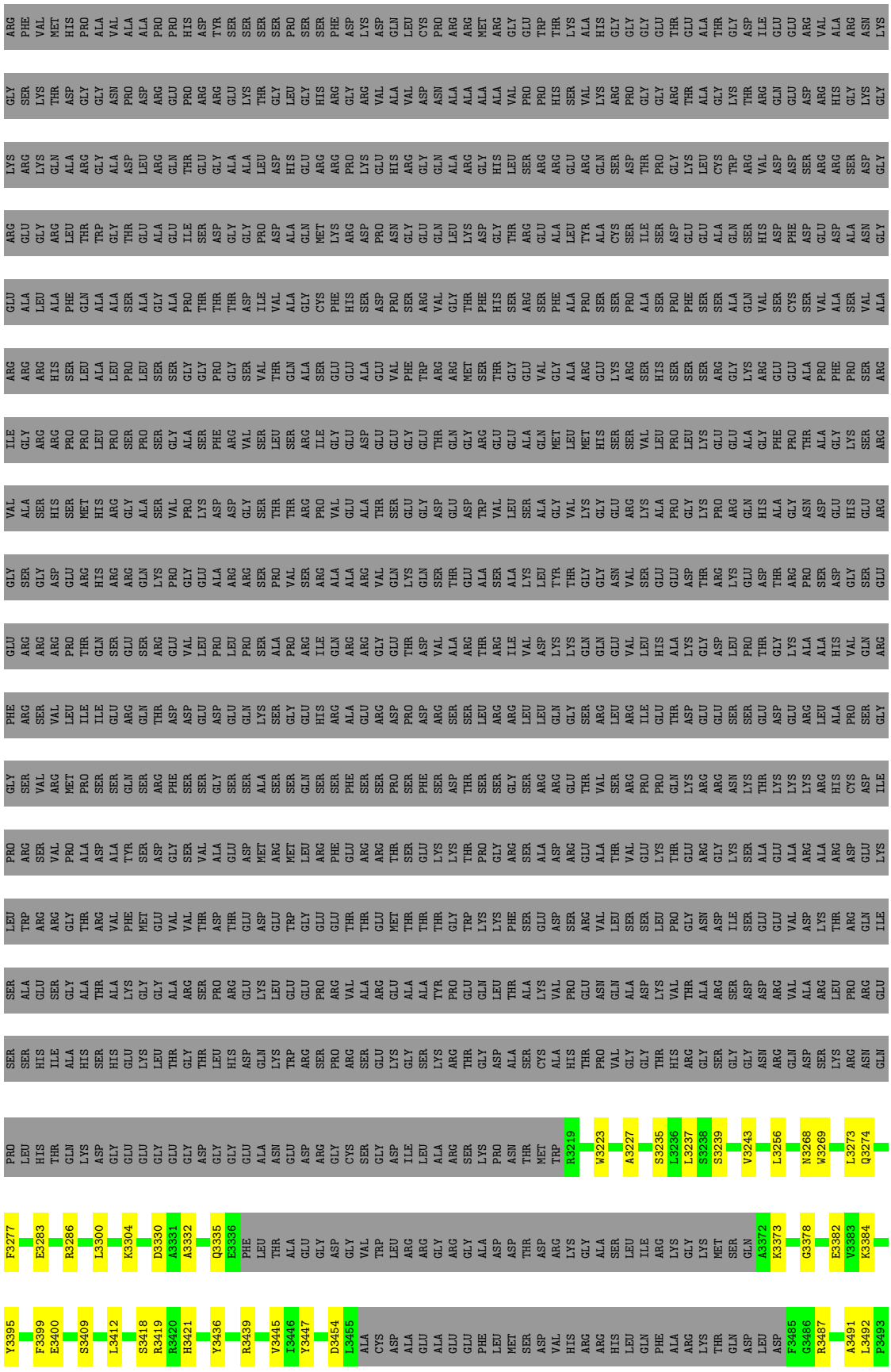
HIS ALA THR ARG PRO LEU PHE GLU GLY ARG PRO LEU ARG LEU SER SER LEU ALA VAL ASP LYS VAL SER ALA VAL GLY GLU SER ASP ARG GLU VAL GLU ASN TYR GLN LYS THR THR SER ALA SER GLU VAL ALA GLY GLN ILE SER GLY PHE LYS GLU LYS ASP ILE TYR VAL LEU GLU ARG

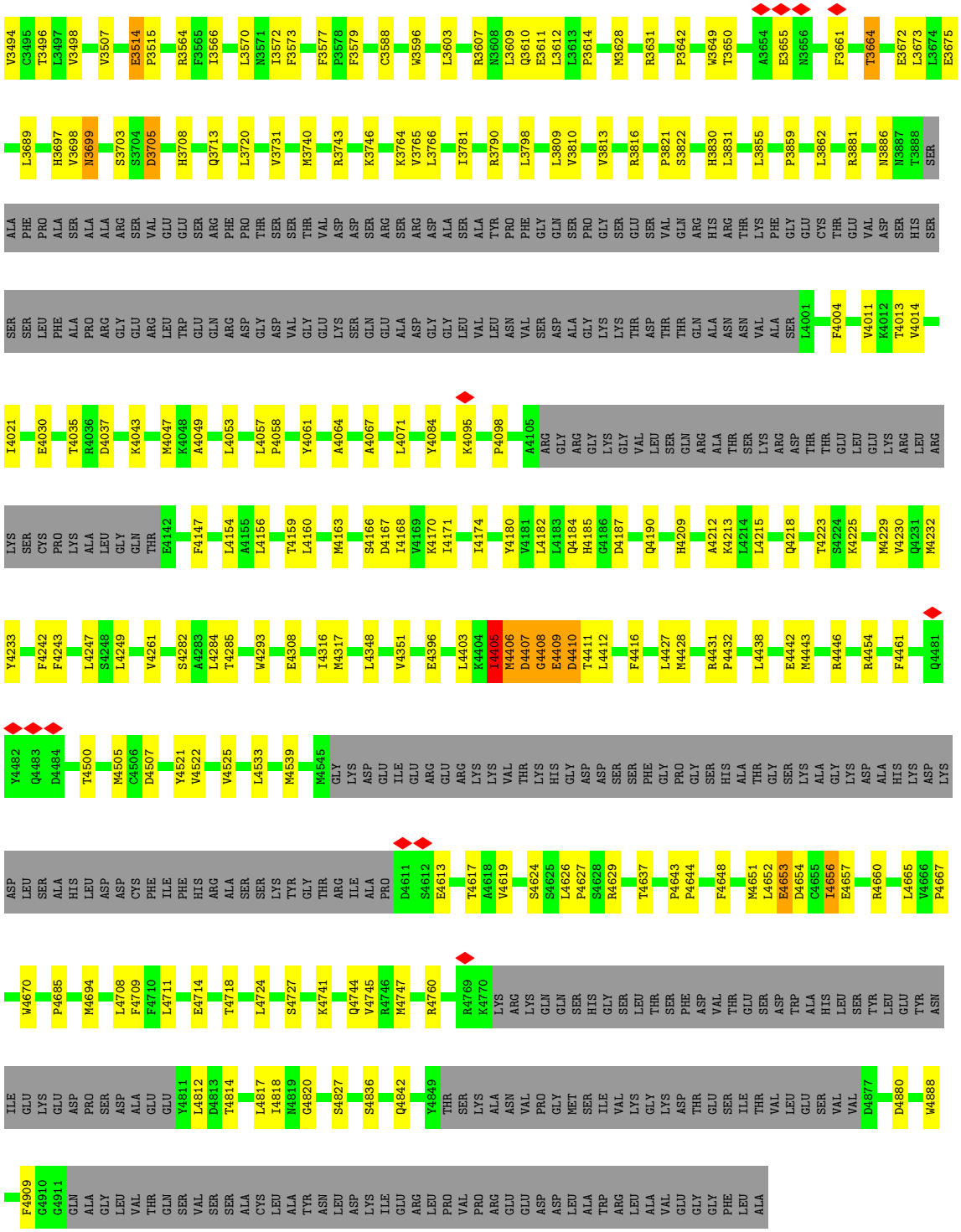
HIS SER GLY GLU GLU ASN HIS ALA ALA SER SER PRO SER SER HIS SER HIS THR PRO VAL SER THR PRO GLU VAL PRO ALA THR ALA GLY GLY SER GLU CYS PHE HIS ASN GLY ARG THR ARG VAL LEU SER LEU CYS ARG GLU THR GLY ALA ASN SER GLN LYS PRO PHE THR LEU ILE

PRO ALA PRO LYS GLU GLY LYS TRP LYS GLU ALA ALA VAL GLN LYS TYR GLU ARG VAL GLY PRO HIS VAL SER LEU SER LYS GLU GLU LEU GLU GLY VAL GLY THR GLU ARG GLU ASN MET GLY GLY CYS THR VAL LEU

VAL LYS LYS PRO SER VAL SER THR PRO ASP GLU GLY LEU PHE PRO PHE PRO CYS SER ASN ARG PRO GLN GLU ARG ASN LYS ILE GLU ASP GLY GLN GLY LYS PRO GLU ARG GLU GLU HIS GLY GLU SER SER TRP LYS GLN PRO GLY SER GLU THR ASP GLU HIS LEU VAL

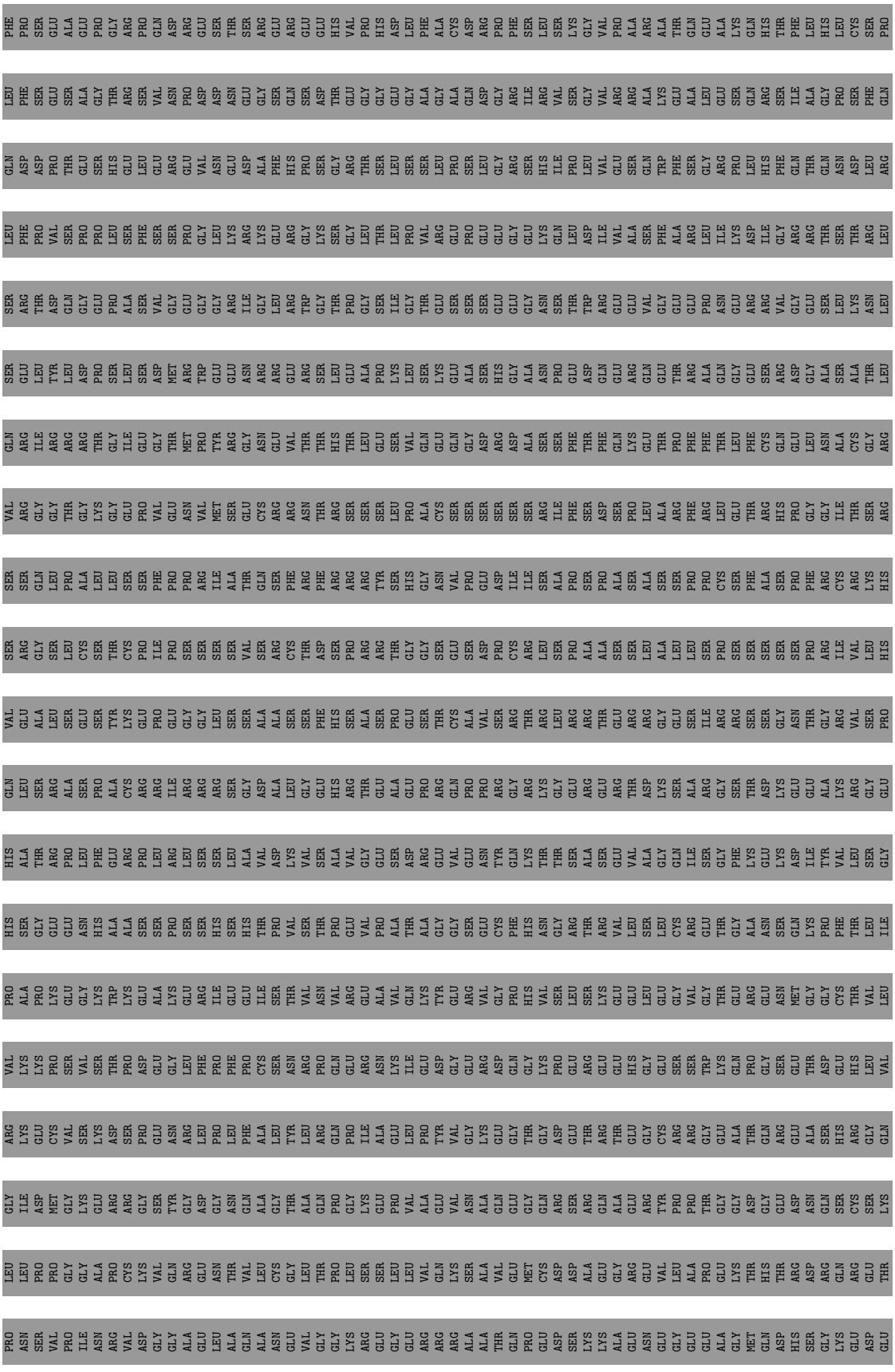

ARG LYS GLU CYS VAL SER LYS ASP SER PRO GLU ASN ARG LEU PRO LEU PHE ALA LEU TYR LEU ARG GLN PRO ILE ALA GLU LEU PRO TYR VAL GLY LYS GLU GLY THR GLY ASP GLU THR ARG THR GLU GLY CYS ARG ARG GLY GLU ALA THR GLN ARG GLU ALA SER HIS ARG GLY GLN
GLY ILE ASP MET GLY LYS GLU ARG ARG GLY SER TYR GLY ASP GLY ASN GLN ALA GLY THR ALA GLN PRO GLY LYS GLU PRO VAL ALA GLU VAL ASN ALA GLN GLU GLY GLU GLN ARG ASP SER ARG GLN ALA GLU ARG GLY ARG PRO TYR PRO PRO GLY GLY ASP ASN GLN SER CYS SER LYS
LEU LEU PRO PRO GLY GLY ALA PRO CYS LYS VAL GLN ARG GLU ASN THR VAL LEU CYS GLY LEU THR PRO LEU SER SER LEU LEU VAL GLN LYS SER ALA VAL GLU MET CYS ASP ASP ALA GLU GLY GLY ARG ASP ARG GLN ARG GLU THR
PRO ASN SER VAL PRO ILE ASN ARG VAL ASP GLY GLY ALA GLU LEU ALA GLN LEU ALA ASN GLU VAL GLY LYS ARG GLU GLY GLU ARG ARG ARG ALA ALA THR GLN PRO GLU ASP SER LYS LYS ALA GLU ASN GLU GLY GLU ALA GLY MET GLN ASP HIS SER GLY LYS GLU ASP GLU
THR ASP THR ASN THR SER TYR GLU SER LEU GLN GLU LYS PRO ASP GLY VAL GLU ASP ASN CYS PRO SER ASN CYS ARG LYS GLU SER ASP PRO SER CYS LEU ALA GLU ASN GLU THR PHE TRP GLY PHE CYS ARG ALA SER ALA ALA SER SER SER LEU PRO SER
SER VAL SER SER SER PRO PRO SER GLU HIS SER GLY SER VAL SER PRO LEU PHE ALA SER ARG VAL THR SER LEU SER SER SER VAL SER SER PRO PHE SER PRO SER VAL ALA THR HIS SER SER PRO SER ARG SER LEU CYS SER
SER LEU LEU PHE ASP GLY ASP VAL GLU GLY SER ASP ARG THR SER PRO ALA SER PRO SER LEU GLY SER LEU SER GLY SER LEU SER ARG ARG PHE CYS PHE LEU ARG SER SER LEU ARG LEU PRO ARG ARG ALA
ALA ASN GLY PRO GLY HIS LYS LYS LYS ARG ILE THR VAL ARG LYS ALA ALA ALA THR PRO VAL ARG PRO GLN SER ARG GLN ASP GLN ILE THR VAL SER ASN THR HIS ALA ASP SER GLY ALA THR LYS LEU GLY SER HIS ARG SER ARG LYS LEU GLU GLU ASP VAL PRO GLY GLY GLU
ASN PRO PHE GLU VAL GLY MET ASP CYS GLY ARG SER VAL ARG ASP GLN GLY ARG PHE SER ALA CYS ALA LEU SER GLN SER SER SER SER PRO ARG VAL THR PRO PHE SER LEU SER LEU SER PRO SER PRO THR ASP THR SER SER LEU PRO LEU PRO ARG CYS GLU ARG THR GLY LEU
SER SER CYS SER HIS ARG SER SER ARG ASP GLY VAL ALA VAL ARG VAL ALA ALA THR ALA THR SER MET ASP MET SER ALA TYR PRO GLU SER SER MET SER GLU THR LYS ALA GLY ASN GLY GLY GLU MET LYS ASP ALA LYS ASP ALA PRO HIS
ILE PHE ARG GLU GLN SER ASP GLY ASP GLY ARG GLY ASN ALA ASN GLN GLU ALA GLN VAL SER ARG GLU CYS LEU GLY SER ARG GLY VAL GLY GLU THR ARG GLU GLN SER ASP ARG ALA GLU GLU ARG GLY GLU ASP VAL GLU LYS PRO GLY GLU HIS
GLY GLN SER GLU GLU ARG GLY ARG ARG PRO GLU ARG SER CYS ALA LEU LYS LYS GLU SER GLN TYR GLN GLU ALA ASP ALA HIS THR THR GLU THR THR PRO SER GLY THR PRO ALA SER ARG PRO ASP ARG ALA GLU GLU GLY GLY CYS ARG ARG ARG PHE SER SER SER
SER ALA SER SER PRO GLU PRO ALA SER ALA LEU SER SER CYS GLU LEU PRO ALA VAL ALA GLY VAL LEU TRP SER PRO ALA SER PRO ARG GLY VAL PRO LEU ALA LEU ASP SER ASP GLU GLU PRO ALA ALA GLY GLU GLY GLY VAL PHE SER ALA ALA ALA
SER GLU GLU GLU GLU GLU ASN GLU VAL GLU HIS TYR HIS GLU ASN GLU GLY ARG LYS GLU GLN CYS GLY GLN GLU VAL LEU LEU ARG LYS GLY GLN ASN PRO GLY GLU SER GLU GLY GLY THR THR LYS GLY GLY ALA ALA ALA ARG GLU GLY THR LYS ARG THR VAL GLU ARG
GLN GLU ASP ARG GLU ASP LEU SER PRO GLY LYS TYR GLY ARG GLU GLN ASP GLU THR SER SER SER TYR LYS GLY LYS MET VAL ALA ALA SER GLU GLU ALA ASP ARG ASN GLU ASP ASP ARG GLU ALA SER HIS THR GLU ASP GLU ARG GLY ARG ASP PRO ASN PRO VAL
ARG THR ARG GLU CYS GLU GLU ASP ALA LEU ARG PRO VAL THR PRO SER SER PHE PRO PRO GLN PHE ALA GLY ARG PRO ALA SER SER ARG ALA LEU ARG GLN SER VAL SER ALA PRO CYS ARG ARG ASP PRO GLN VAL VAL LEU GLU LEU SER ASP GLU GLU ARG THR
PHE GLY ASP ALA ALA SER ARG SER SER VAL PRO ARG ALA GLU VAL GLU GLU THR SER GLU GLU SER CYS LEU THR THR ASN ILE GLY LEU VAL TYR SER CYS SER GLU GLU GLU ARG GLU GLU THR GLY HIS ALA PHE PRO LEU SER VAL PRO PRO VAL LEU VAL THR
ASP ASP GLU ARG VAL SER GLU LEU LEU LEU PRO ASN THR LYS GLY GLY ARG GLU ALA GLN GLY GLY GLU GLY GLY PRO GLN LEU LEU GLU ASP ALA ALA VAL LEU LEU THR ASP ASP ASP SER GLU
ALA GLU ALA ASN SER TRP GLU LYS SER PRO SER ASP SER GLY GLU VAL ALA CYS ARG PHE VAL VAL ALA GLU LYS ARG SER GLU ASP ASP ASP ARG ALA ASP
SER TRP PRO ALA ARG GLU GLN ILE HIS SER CYS LEU ALA ARG PRO CYS GLU CYS VAL ALA ARG LYS SER GLY GLU ARG SER GLU ASP ASP THR ALA VAL GLY ARG HIS ALA

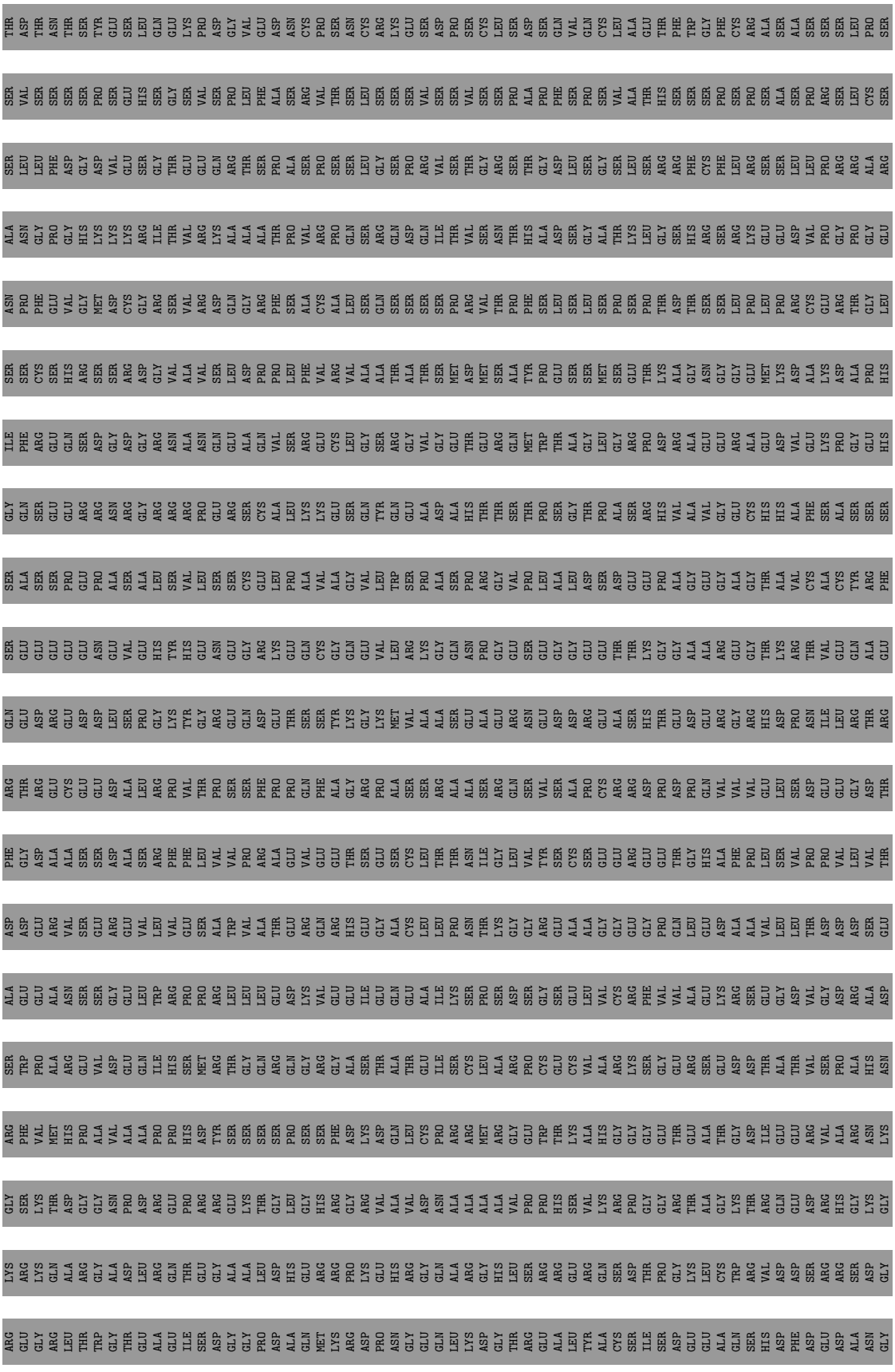

ARG PHE VAL MET HIS PRO ALA VAL ALA ALA ALA PRO PRO HIS ASP TYR SER SER SER SER PRO SER SER PHE ASP LYS ASP GLN LEU CYS PRO ARG ARG MET ARG GLY GLU TRP THR LYS ALA HIS GLY GLY GLU THR GLU ALA THR GLY ASP ILE GLU GLU ARG VAL ALA ARG GLN
GLY SER LYS THR ASP GLY GLY ASN PRO ASP ARG GLU PRO ARG ARG GLU LYS THR GLY LEU GLY HIS ARG GLY ARG VAL ALA VAL ASP ASN ALA ALA ALA VAL PRO PRO HIS SER VAL LYS ARG PRO GLY GLY ARG THR ALA GLY LYS THR GLY ARG GLN GLU ASP ARG HIS GLY LYS GLY
LYS ARG LYS GLN ALA ARG GLY ALA ASP LEU ARG GLN THR GLU GLY ALA LEU ASP HIS GLU ARG ARG PRO LYS GLU GLN ALA ARG GLY HIS GLU ARG GLY GLN ALA ARG GLY GLN LEU CYS TRP ARG VAL ASP ASP SER ARG ARG ARG HIS SER ASP THR PRO GLY LYS LEU CYS TRP ARG GLN
ARG GLU GLY ARG LEU THR GLU GLU ALA ALA GLU ILE SER ASP GLY GLY PRO ASP ALA ALA GLN MET LYS ARG ASP PRO ASN GLY GLU GLN LEU LYS ASP GLY THR ARG GLU ALA LEU TYR ALA CYS SER ILE SER ASP GLU GLU ALA GLN SER ARG GLU ASP PHE ASP GLU ALA GLY
GLU ALA LEU PHE GLN ALA ALA LEU SER ASP PRO THR THR ASP ILE VAL ALA GLY CYS PHE HIS SER ASP PRO SER ARG VAL GLY THR PHE TRP HIS SER PRO PHE SER SER PRO ALA SER PRO GLU VAL ALA
ARG ARG ARG HIS SER LEU ALA LEU PRO LEU PRO ALA GLU GLU GLU ALA GLU VAL SER THR GLN ALA SER GLU GLU GLU ARG SER VAL GLY GLY ALA ARG GLU GLU LYS ARG SER HIS SER SER SER ARG GLY LYS ARG GLN GLU GLU GLU SER ARG
ILE GLY ARG PRO PRO LEU PRO SER PRO SER GLY GLU ASP GLU GLU GLY GLU THR GLN GLY GLU GLU ALA GLN MET LEU MET HIS SER SER VAL LEU PRO LEU LYS GLU GLY ALA GLY PHE PRO THR ALA GLY LYS SER SER ARG
VAL ALA SER HIS SER MET HIS ARG GLY ALA SER VAL PRO LYS ASP ASP GLY SER THR THR ARG PRO VAL GLU ALA THR SER GLU GLY ASP GLU ASP TRP VAL LEU SER ALA GLY VAL LYS GLY GLU ARG LYS ALA PRO GLY LYS GLN HIS ALA GLY ASN ASP GLU HIS SER ARG
GLY SER GLY ASP GLU ARG HIS ARG ARG GLN LYS PRO GLY GLU GLN LYS GLN SER THR GLU ALA SER ALA LYS LEU TYR THR GLY GLY ASN VAL SER GLU GLU ASP THR ARG LYS GLU ASP THR GLY GLU SER GLU
GLU ARG ARG PRO THR GLN SER GLU ARG ASP VAL ALA ARG GLY GLU THR ASP VAL ALA ARG ILE VAL ASP LYS LYS GLN GLN GLU VAL LEU HIS ALA LYS GLY ASP LEU PRO THR GLY LYS ALA ALA HIS VAL GLN ARG
PHE ARG SER VAL LEU ILE ILE GLU ARG GLN THR ASP GLU GLU GLN LYS SER GLY GLU HIS ASP GLU ASP PRO ASP ARG ALA GLU ARG ASP PRO ASP ARG SER SER LEU ARG ARG ARG LEU LEU LEU GLN GLY SER ARG LEU ILE GLU THR ASP GLU GLU SER ARG LEU ALA PRO SER SER GLY
GLY SER VAL ARG MET PRO SER SER GLN SER SER GLY SER SER ALA SER SER SER PHE SER SER ASP THR SER PRO SER PHE SER ASP THR SER ARG ARG GLU THR VAL SER ARG PRO PRO GLN THR LYS ARG ARG ASN LYS THR SER GLU VAL LEU ILE GLU LYS ASP GLY ASP LEU PRO LEU GLY LYS LYS GLN GLN GLU ASP SER
PRO ARG SER VAL PRO ALA ASP ALA TYR SER ASP ALA MET ARG MET LEU ARG PHE GLU ARG ARG THR SER GLU LYS LYS THR PRO GLY ARG SER ALA ASP ARG GLU THR VAL ALA THR VAL GLU LYS THR GLU GLY ASN ASP ILE SER LEU PRO GLY ASN ILE SER GLU GLU VAL ALA GLU LYS
LEU TRP ARG ARG GLY THR ARG VAL PHE MET GLU VAL VAL THR ASP THR GLU ASP GLU TRP GLY GLU THR THR GLU MET THR THR THR THR GLY TRP LYS LYS PHE SER GLU ASP SER ARG VAL LEU SER SER LEU PRO GLY ASN ASP ILE SER GLU GLU VAL ASP LYS THR GLN ILE
SER ALA GLU SER GLY ALA ALA TYR PRO GLU GLN ALA LEU GLU THR ALA ALA ARG GLU ALA ASP LYS VAL THR ARG GLN GLN LEU THR ALA ARG SER ASP ASP ARG VAL ASN ARG
SER SER HIS ILE ALA HIS GLU ILE LYS GLY THR HIS SER LYS ARG THR GLY ASP GLN ALA CYS ALA HIS THR PRO VAL GLY GLY THR HIS ARG GLY SER GLY GLY ASN ARG GLN ASP ARG SER LYS ARG ASN GLN
PRO LEU HIS THR GLN LYS ASP GLY GLU GLU GLY GLU GLY GLU GLY GLY CYS SER GLY ASP ILE LEU ALA ARG SER LYS PRO ASN THR MET TRP R3219 W3223 A3227 S3235 L3236 L3237 S3238 S3239 V3243 L3256 N3268 W3269 L3273 Q3274
F3277 E3283 R3286 L3300 K3304 D3330 A3331 A3332 Q3335 E3336 PHE LEU THR ALA GLU GLY ASP GLY ALA GLU ARG GLY ARG GLY ALA ASP ASP THR ASP ARG LYS GLY ALA SER LEU ILE ARG LYS MET SER GLN A3372 K3373 G3378 E3382 V3383 K3384
Y3395 F3399 E3400 S3409 L3412 S3418 R3419 R3420 H3421 Y3436 R3439 V3445 I3446 Y3447 D3454 L3455 ALA CYS ASP ALA GLU GLU ALA GLU GLU PHE LEU MET SER ASP VAL HIS ARG ARG HIS LEU GLN PHE ALA ARG LYS THR GLN ASP LEU F3485 G3486 R3487 A3491 L3492 P3493

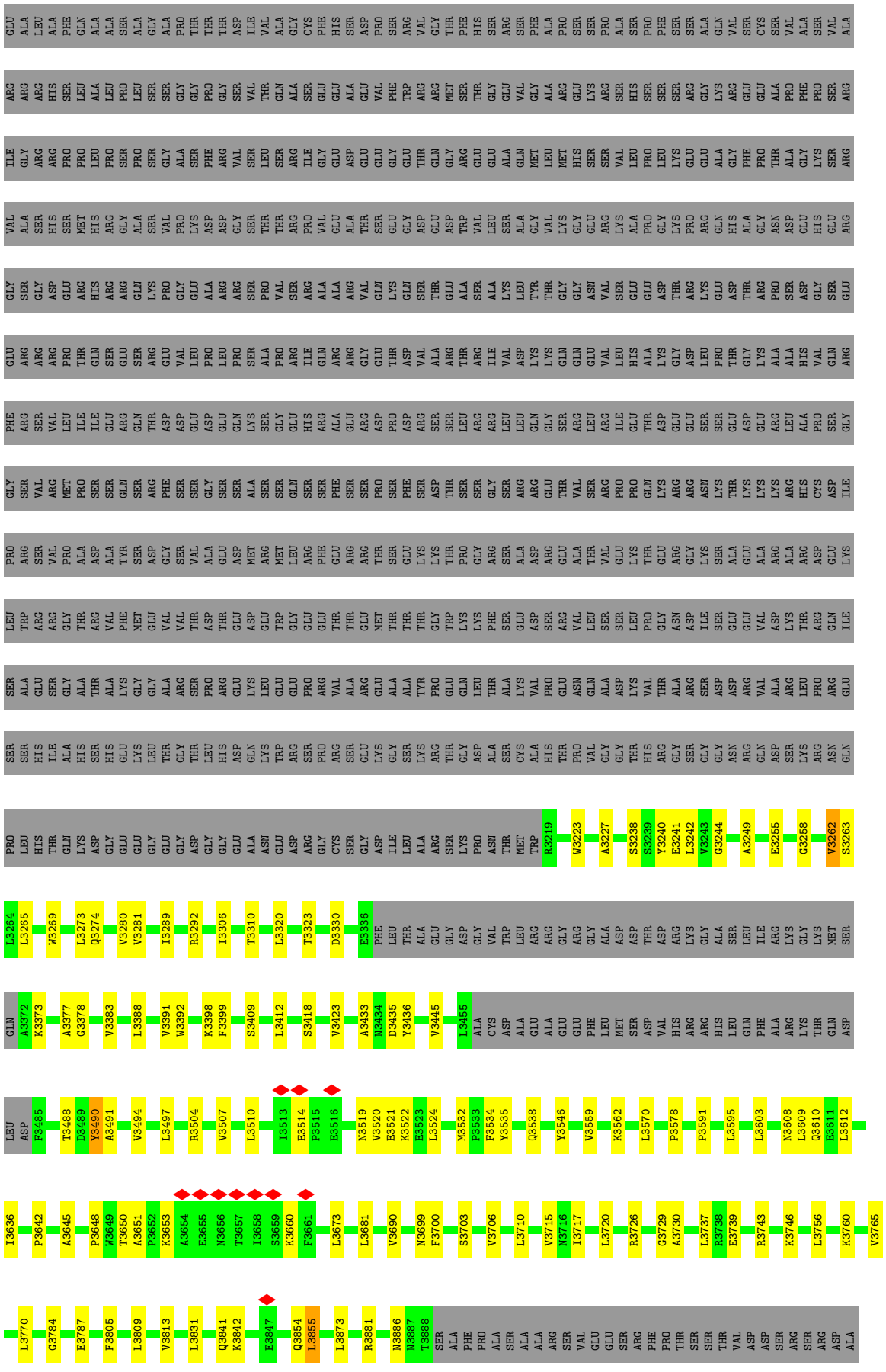


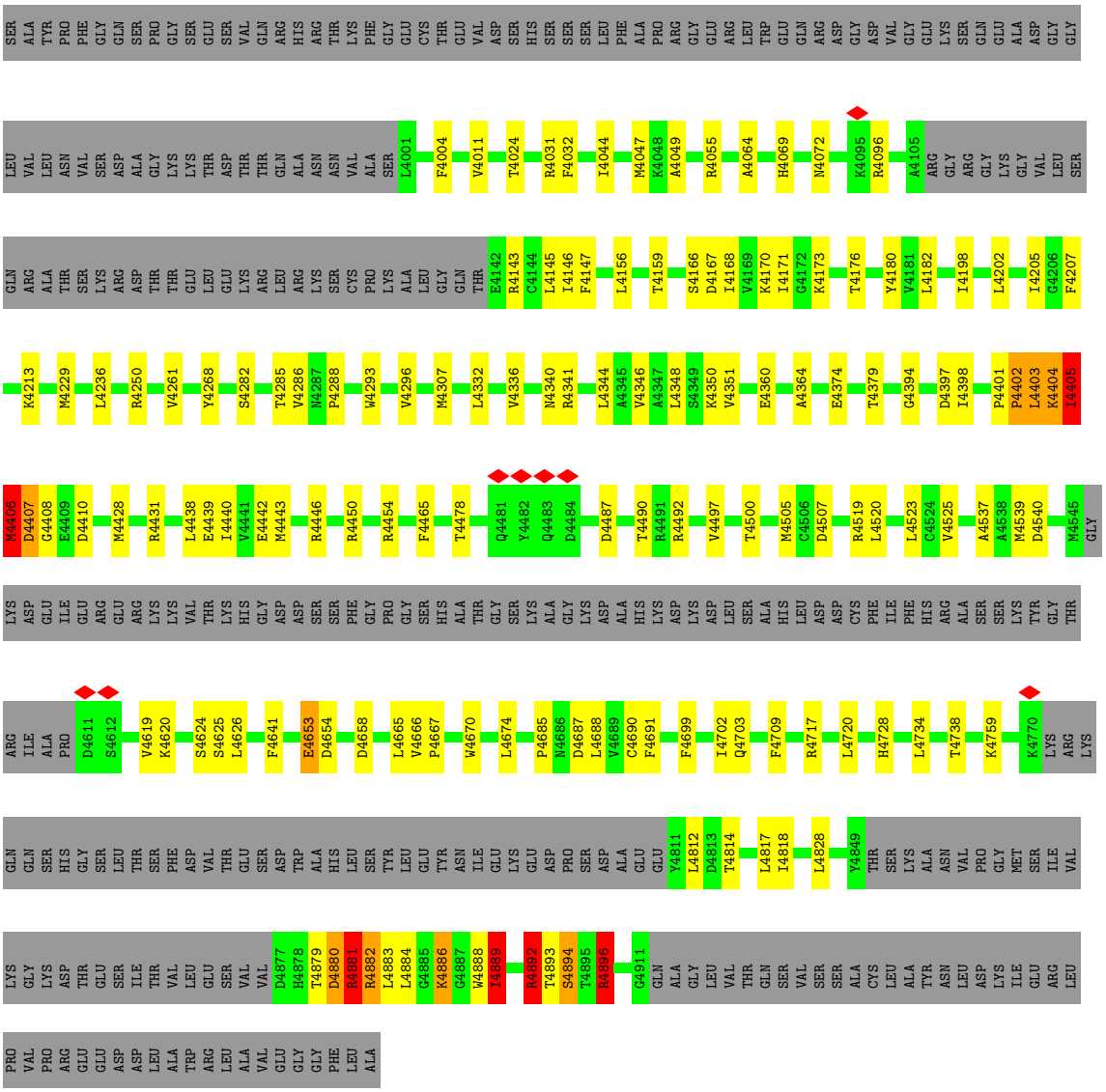
• Molecule 5: CGP, TGME49_240380

Chain EB:


PHE PRO SER GLU ALA GLU PRO GLY ARG PRO GLN ASP ARG GLU SER THR SER ARG GLU ARG GLU GLU HIS VAL PRO HIS ASP LEU PHE ALA CYS ASP ARG PRO PHE SER LEU SER LYS GLY VAL PRO ALA ARG ALA THR GLN GLU ALA LYS GLN HIS THR PHE LEU HIS LEU CYS SER PRO
LEU PHE SER GLU SER ALA GLY THR ARG SER VAL ASN PRO ASP ASP ASN GLU GLU GLY SER GLN SER ASP THR GLU GLY GLY GLU GLY GLY ALA GLY ALA GLN ASP GLY ARG ILE ARG VAL SER GLY VAL ARG ARG ALA LYS GLU ALA LEU GLU SER GLN ARG SER ILE ALA GLY PRO SER PHE GLN
GLN ASP ASP PRO THR GLU SER HIS GLU LEU GLU ARG GLU VAL ASN GLU ASP ALA PHE HIS PRO SER GLY ARG THR SER LEU SER SER LEU PRO SER LEU GLU GLN ILE ARG SER HIS ILE PRO LEU VAL GLU SER GLN TRP PHE SER GLY ARG LEU GLU ALA GLY ARG PRO LEU HIS PHE GLN THR GLN ASN ASP ARG
LEU PHE PRO VAL SER PRO PRO LEU SER PHE SER SER PRO GLU LYS GLU GLY LYS SER GLY LEU THR LEU PRO VAL ARG GLU PRO GLU GLU GLY GLU LYS GLN LEU ASP ILE VAL ALA SER GLN VAL ARG ARG ILE LYS ASP ILE GLY ARG ARG THR SER THR ARG LEU
SER ARG THR ASP GLN GLY GLU PRO ALA SER ARG GLY GLU ARG ILE GLY LEU ARG TRP GLY THR PRO GLY SER ILE GLY THR GLU SER SER SER GLU GLY GLY ASN SER THR TRP ARG GLU GLU VAL GLY GLU GLU PRO ASN GLU GLY ARG ARG VAL GLY GLU ARG ASP GLY SER THR ASN LEU
SER GLU LEU TYR LEU ASP PRO SER LEU SER ASP MET ARG TRP GLU GLU ASN ARG GLU ARG SER LEU GLU ALA PRO LYS LEU SER SER LYS GLU ALA ASN SER HIS GLY GLY ALA ASN PRO GLU ASP GLN GLU GLY GLU SER ARG ASP GLY ALA GLU ASP ASP GLN GLU GLY GLY ALA SER ALA THR LEU
GLN ARG ILE ARG ARG THR GLY ILE GLU GLY THR MET PRO TYR ARG GLY ASN GLU VAL THR THR HIS THR LEU GLU ALA GLN GLU GLN GLY ASP ARG ASP ALA SER SER PHE THR PHE GLN LYS GLU THR PRO PHE PHE PHE THR LEU PHE CYS GLN GLU LEU GLU THR ARG HIS PRO GLY GLY ILE THR SER ARG
VAL ARG GLY GLY THR GLY LYS GLY GLU PRO VAL GLU ASN VAL MET SER GLU CYS ARG ARG ASN THR ARG SER SER SER LEU PRO ALA CYS SER GLN SER SER SER SER SER ARG ILE PHE SER ASP SER PRO LEU ALA ARG PHE PHE ARG LEU GLU THR ARG HIS PRO GLY GLY ILE THR SER ARG
SER SER GLN LEU PRO ALA ALA LEU LEU SER SER PHE PRO PRO ARG ILE ALA THR GLN SER PHE ARG ARG ARG TYR SER HIS GLY ASN VAL PRO GLU ASP ILE ILE SER ALA PRO SER PRO PRO CYS SER PHE ALA SER PRO PHE ARG CYS ARG LYS HIS
SER ARG GLY SER LEU CYS SER THR CYS PRO ILE PRO SER SER SER VAL SER ARG CYS THR ASP SER PRO ARG ARG THR GLY GLY SER GLU SER ASP PRO CYS ARG LEU SER PRO ALA ALA SER SER LEU ALA LEU LEU SER PRO SER SER SER SER PRO PRO ARG ILE VAL LEU HIS
VAL GLU ALA LEU SER GLU SER TYR LYS GLU PRO GLU GLY GLY LEU SER SER PHE HIS SER ALA SER PRO GLU GLU ALA ALA SER SER GLU SER PRO GLU SER THR CYS ALA VAL SER ARG THR ARG LEU SER PRO ARG ARG THR GLU GLU ARG ARG GLY GLU SER ILE ARG ARG SER SER GLY ASN THR GLY LEU ARG VAL SER
GLN LEU SER ARG ALA ARG ARG ILE ARG ARG ARG ARG ARG ALA ALA SER ALA CYS ALA GLN PRO ARG GLN PRO PRO ARG GLY ARG ARG GLU ARG ARG THR ASP LYS SER ALA GLU ARG GLU ARG GLY GLU GLU SER ILE ARG ALA SER GLY ARG GLY GLU
HIS ALA THR ARG PRO LEU PHE GLU ARG PRO LEU LEU ARG LEU SER SER HIS ALA VAL ASP LYS VAL SER ALA VAL GLY GLU SER ASP ARG GLU VAL PRO GLU ASN TYR GLN LYS THR THR SER ALA SER GLU VAL ALA GLY GLN ILE SER GLY PHE LYS GLU LYS ASP ILE TYR VAL LEU SER GLY
HIS SER GLY GLU GLU ASN HIS ALA ALA SER SER PRO SER SER HIS SER HIS THR PRO VAL PRO GLU VAL PRO ALA THR ALA GLY GLY SER GLU ASN GLY ARG THR ARG VAL LEU SER LEU CYS ARG GLU THR GLY ALA ASN SER GLN LYS PRO PHE THR LEU ILE
PRO ALA PRO LYS GLU GLY LYS GLU ALA LYS GLU ALA VAL GLN LYS TYR GLU ARG VAL GLY PRO HIS VAL SER LEU SER LYS GLU GLU LEU GLU GLY VAL GLY THR GLU ARG GLU ASN MET GLY GLY CYS THR VAL LEU
VAL LYS LYS PRO SER VAL SER THR PRO ASP GLU GLU GLY LEU PHE PRO PHE PRO CYS SER ASN ARG PRO GLN GLN ARG ASN LYS ILE GLU GLU ASP GLN GLY LYS PRO GLU ARG CYS GLU GLU HIS GLY GLU SER GLU GLY SER GLU THR ASP GLU HIS LEU VAL
ARG LYS GLU CYS VAL SER LYS ASP SER PRO GLU GLU ASN ARG LEU PRO LEU PHE ALA LEU TYR LEU ARG GLN PRO ILE ALA GLU LEU PRO TYR VAL GLY LYS GLU GLY THR GLY ASP GLU THR ARG THR GLU GLY CYS ARG ARG GLY GLU GLY ALA THR GLN ARG GLU ALA SER HIS ARG GLY GLN
GLY ILE ASP MET GLY LYS GLU SER TYR GLY ARG ASP GLY ASN ARG GLY THR ALA GLY GLN ARG SER GLN ALA GLN GLU GLY GLN ARG GLN ALA GLU ARG TYR PRO PRO THR GLY GLY ASP GLY GLU ASP ASN GLN SER CYS SER LYS
LEU LEU PRO PRO GLY GLY LYS VAL CYS GLN VAL GLN LYS SER ALA ALA VAL GLU MET CYS ASP ASP ALA GLU GLY ARG GLU VAL LEU ALA PRO GLU LYS THR HIS THR ARG GLU GLU THR
PRO ASN SER VAL PRO ILE ASN ARG VAL GLY GLY LEU ALA ALA GLN ALA ALA ASN GLU VAL GLY LYS ARG GLU GLY GLU ARG ARG ALA ALA THR GLN PRO GLU ASP SER LYS LYS ALA GLU ASN GLU GLY GLU GLU ALA GLY MET GLN ASP HIS SER GLY LYS GLU ASP GLU

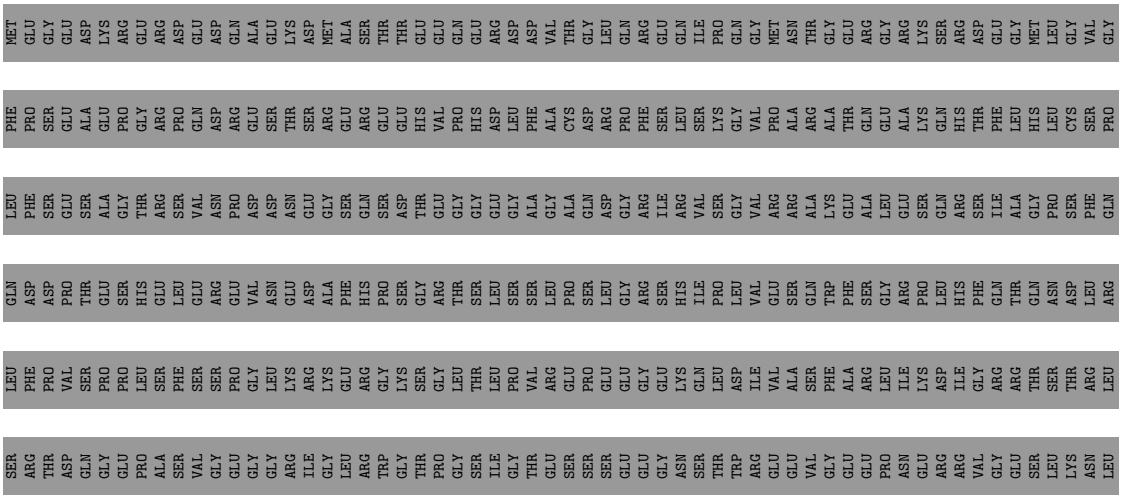

THR ASP THR ASN THR SER TYR GLU SER LEU GLN GLU LYS PRO ASP GLY VAL GLU ASP ASN CYS PRO SER ASN CYS ARG LYS GLU SER ASP PRO SER CYS LEU SER ASP SER GLN VAL GLN CYS LEU ALA GLU THR PHE TRP GLY PHE CYS ARG ALA SER ALA SER SER SER
SER VAL SER SER SER SER PRO SER GLU HIS SER GLY SER VAL SER PRO LEU PHE ALA SER ARG VAL THR SER LEU SER ARG SER SER SER VAL SER SER VAL SER SER PRO ALA PRO PHE SER PRO SER VAL ALA THR HIS SER SER SER PRO SER ALA SER PRO ARG SER LEU CYS SER
SER LEU LEU PHE ASP GLY ASP VAL GLU GLY SER VAL SER PRO LEU PHE SER PRO ALA SER PRO SER GLY SER LEU GLY SER PRO ARG VAL SER THR GLY ARG SER THR GLY ASP LEU SER GLY ALA THR LYS LEU SER ARG ARG PHE CYS PHE LEU ARG SER ARG LYS ARG SER ALA SER LEU LEU LEU PRO ARG ARG ARG ALA ARG
ALA ASN GLY PRO GLY HIS LYS LYS LYS ARG ILE THR VAL ARG LYS ALA ALA ALA THR PRO VAL ARG PRO GLN SER ARG GLN ASP GLN ILE THR VAL SER ASN THR HIS ALA ASP SER GLY ALA THR LYS LEU SER GLY ALA ASP VAL PRO GLY PRO GLY GLU
ASN PRO PHE GLU VAL GLY MET ASP CYS GLY ARG ARG SER VAL ARG ASP GLN GLY GLY ARG PHE SER ALA CYS ALA LEU SER GLN SER SER SER PRO ARG VAL ALA LEU SER LEU SER PRO SER PRO ARG CYS GLU ARG THR GLY GLY LEU
SER SER CYS SER HIS ARG SER SER ARG ASP GLY ASP PRO PRO LEU PHE VAL ARG VAL ALA ALA THR THR SER MET ASP MET SER ALA TYR PRO GLU GLY SER SER MET SER GLU THR LYS ALA ASP PRO ALA PRO HIS
ILE PHE ARG GLU GLN SER ASP GLY ASP GLN ALA GLN VAL SER ARG GLU CYS LEU GLY SER ARG GLY VAL GLY GLU THR ARG GLN MET TRP THR ALA GLY LEU GLY ARG PRO ASP ARG ALA ALA GLU GLU GLY ASP VAL GLU LYS PRO GLY GLU HIS
GLY GLN SER GLU GLU ARG ARG ASN ARG GLY ARG ARG ARG PRO GLU ARG SER CYS ALA LEU LYS LYS GLU SER GLN TYR GLN GLU ALA ASP ALA HIS THR THR SER THR PRO SER GLY THR PRO ALA SER ARG HIS VAL ALA ALA GLU GLU ARG CYS HIS HIS ALA PHE SER ALA SER SER SER
SER ALA SER SER PRO GLU PRO ALA SER ALA LEU LEU TRP SER PRO ALA SER PRO ARG GLY VAL PRO LEU ALA LEU ASP SER ASP GLU GLU PRO ALA GLY GLU GLY ALA GLY PRO ALA GLY GLU GLY GLU CYS HIS HIS ALA PHE SER ALA CYS TYR ARG PHE
SER GLU GLU GLU GLU GLU ASN GLU GLY GLY GLN CYS GLY GLN GLU VAL LEU ARG LYS GLY GLN ASN PRO GLY GLU SER GLU GLY GLY GLU GLU CYS THR THR LYS GLY GLY ALA ALA ARG GLU GLY THR LYS ARG THR VAL GLU GLN ALA GLU
GLN GLU ASP ARG GLU GLN ASP GLU THR SER GLY LYS TYR GLY ARG GLU GLN ASP GLU THR SER SER TYR LYS GLY LYS MET VAL ALA ALA SER GLU ALA GLU GLU ASP ASP ARG GLU ALA SER HIS THR GLU ASP PRO GLU ARG GLY LYS ARG HIS VAL ASP PRO ASN ILE LEU ARG THR ARG
ARG THR ARG GLU CYS GLU GLU ASP ALA LEU GLU ARG PRO VAL THR PRO SER SER SER PHE PRO PRO PRO GLN PHE ALA GLY ARG PRO ALA SER SER ARG ALA ARG ALA SER ARG GLN LEU SER SER ALA PRO CYS GLU ARG ASP PRO ASP PRO GLN VAL VAL VAL VAL LEU GLU ASP THR
PHE GLY ASP ALA ALA SER SER ASP ALA SER ARG PHE PHE LEU VAL VAL PRO ARG ALA GLU VAL GLU GLU THR SER GLU ARG SER CYS LEU THR THR ASN ILE GLY LEU VAL TYR SER CYS SER GLU GLU ARG GLU GLU THR GLY HIS ALA PHE PRO LEU SER VAL PRO PRO VAL LEU VAL THR
ASP ASP GLU ARG VAL SER GLU ARG GLN ARG HIS GLU GLY ALA CYS LEU LEU PRO ASN THR LYS GLY GLY ARG GLU ALA ALA GLY GLY GLU GLY PRO GLN LEU GLU GLU ASP ALA ALA VAL LEU LEU LEU THR ASP ASP SER
ALA GLU GLU ALA ASN SER GLY LEU TRP LEU GLU ASP ILE LYS SER PRO SER ASP SER GLY SER GLU LEU VAL CYS ARG PHE VAL VAL ALA GLU LYS ARG SER PRO VAL ASP ARG ALA
SER TRP PRO ALA ARG GLU VAL ASP GLU HIS SER MET ARG THR GLY GLN ARG GLN GLY ARG GLY ALA SER THR ALA THR GLU ILE SER CYS LEU ALA ARG PRO CYS GLU CYS VAL ALA ARG LYS SER GLY GLU ARG ASP THR ALA HIS ASN
ARG PHE VAL MET HIS PRO ALA VAL ALA ALA PRO PRO HIS ASP TYR SER SER SER SER PRO SER PHE ASP LYS ASP GLN LEU CYS PRO ARG ARG MET ARG GLY GLU TRP THR LYS ALA HIS GLY GLY GLU THR CYS ALA ARG ARG GLU ALA THR GLY ASP LYS ARG ASN
GLY SER LYS THR ASP GLY GLY ARG GLU PRO ARG ARG GLU VAL ALA VAL ASP ASN ALA ALA ALA ALA VAL PRO PRO HIS SER VAL LYS ARG PRO GLY GLY GLU GLY ARG THR ALA GLY LYS THR ARG GLN GLU ASP ARG HIS GLY LYS GLY
LYS ARG LYS GLN ALA ALA ASP LEU ARG GLY GLN ALA ARG GLY HIS ARG GLY GLN LEU SER ARG GLU HIS ARG GLU ARG ARG GLU ARG GLN SER ASP THR PRO LYS LEU CYS TRP ARG VAL ASP ASP SER ARG ARG SER ASP GLY
ARG GLU GLY ARG LEU GLU THR TRP GLY ALA GLY PRO ASP ASN GLY GLU GLN LEU LYS ASP GLY THR ARG GLU ALA LEU TYR ALA CYS SER ILE SER ASP GLU GLU ALA GLN SER HIS ASP PHE ASP GLU ASP ALA ASN GLY

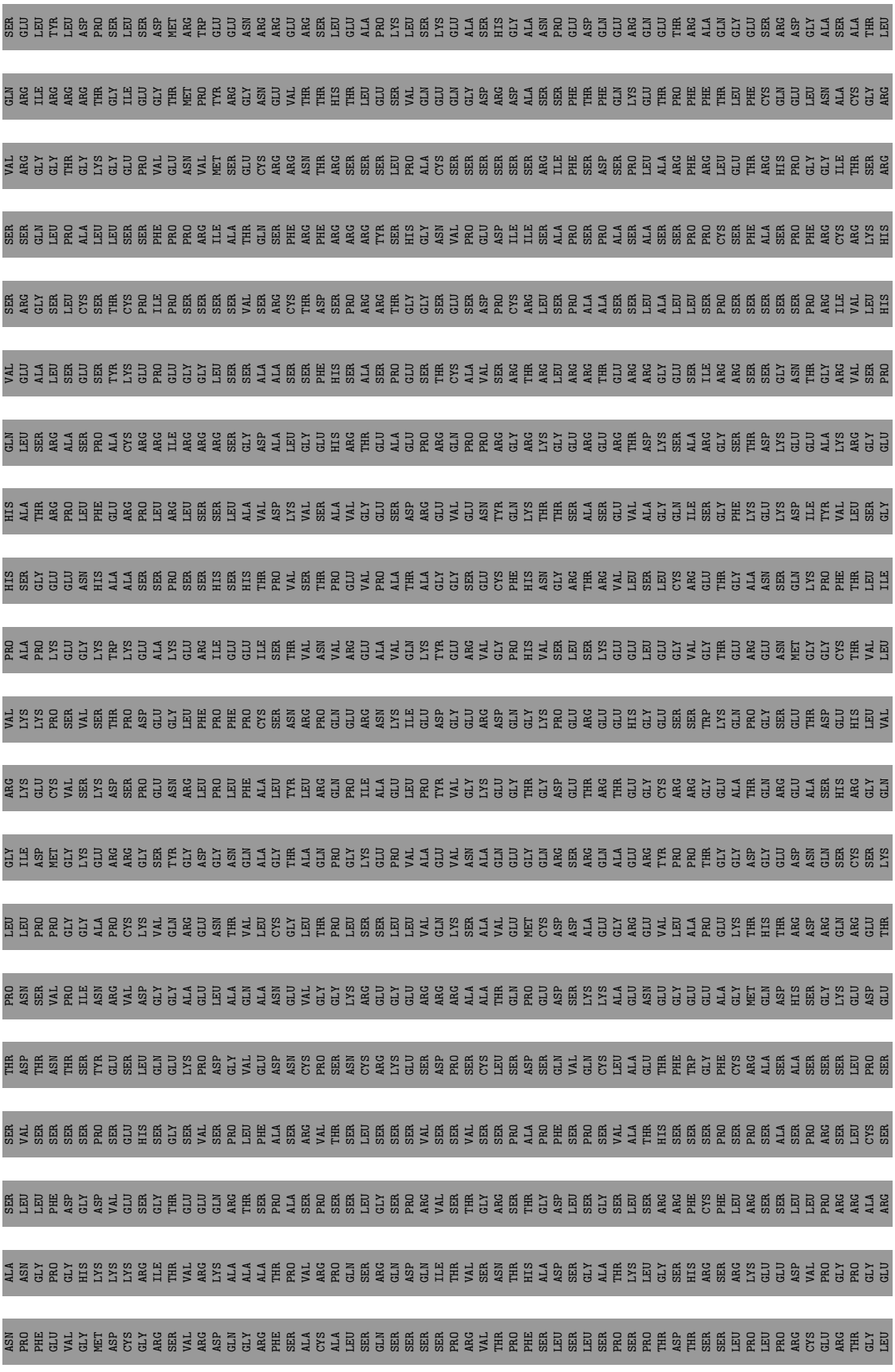


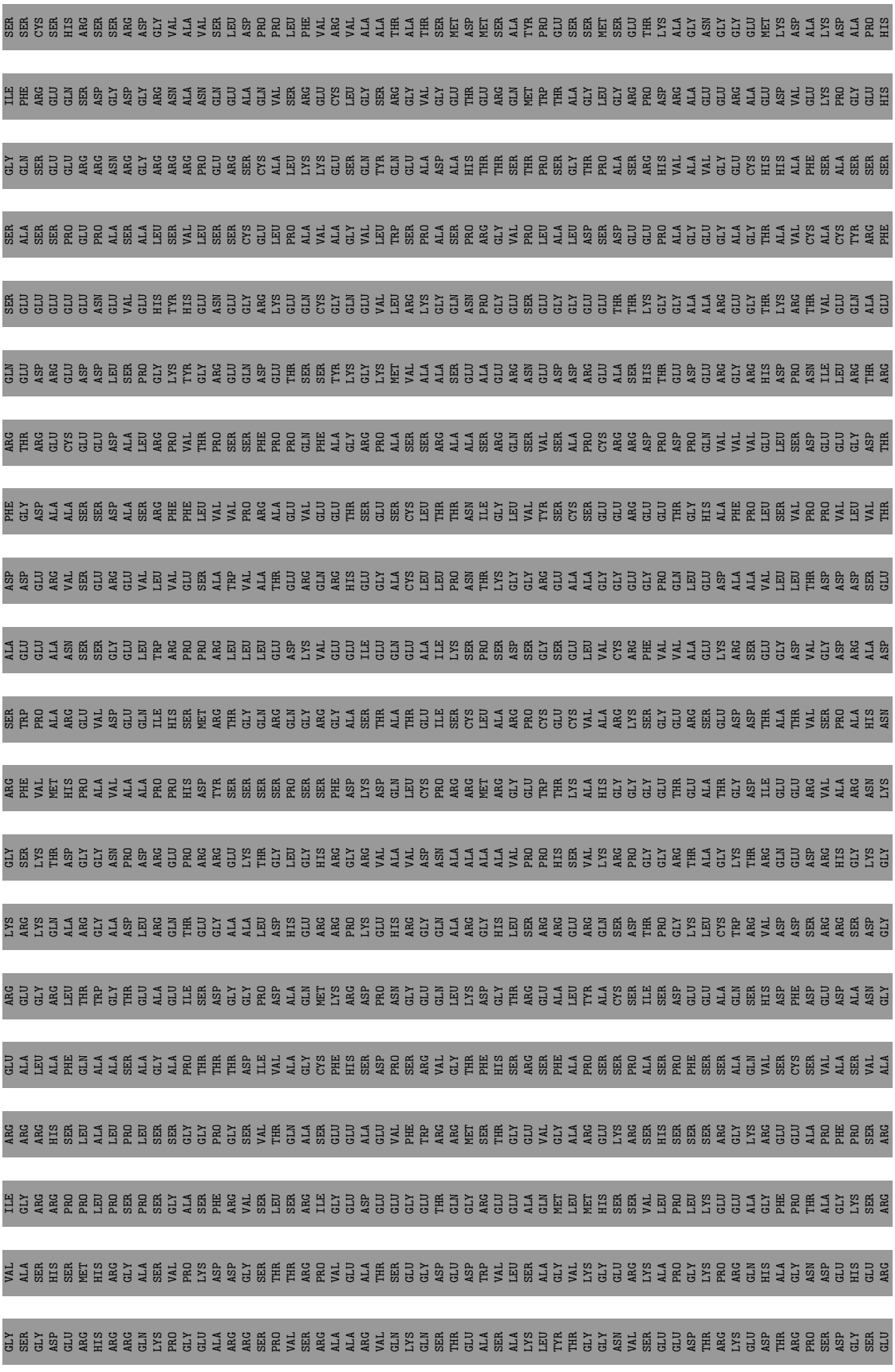


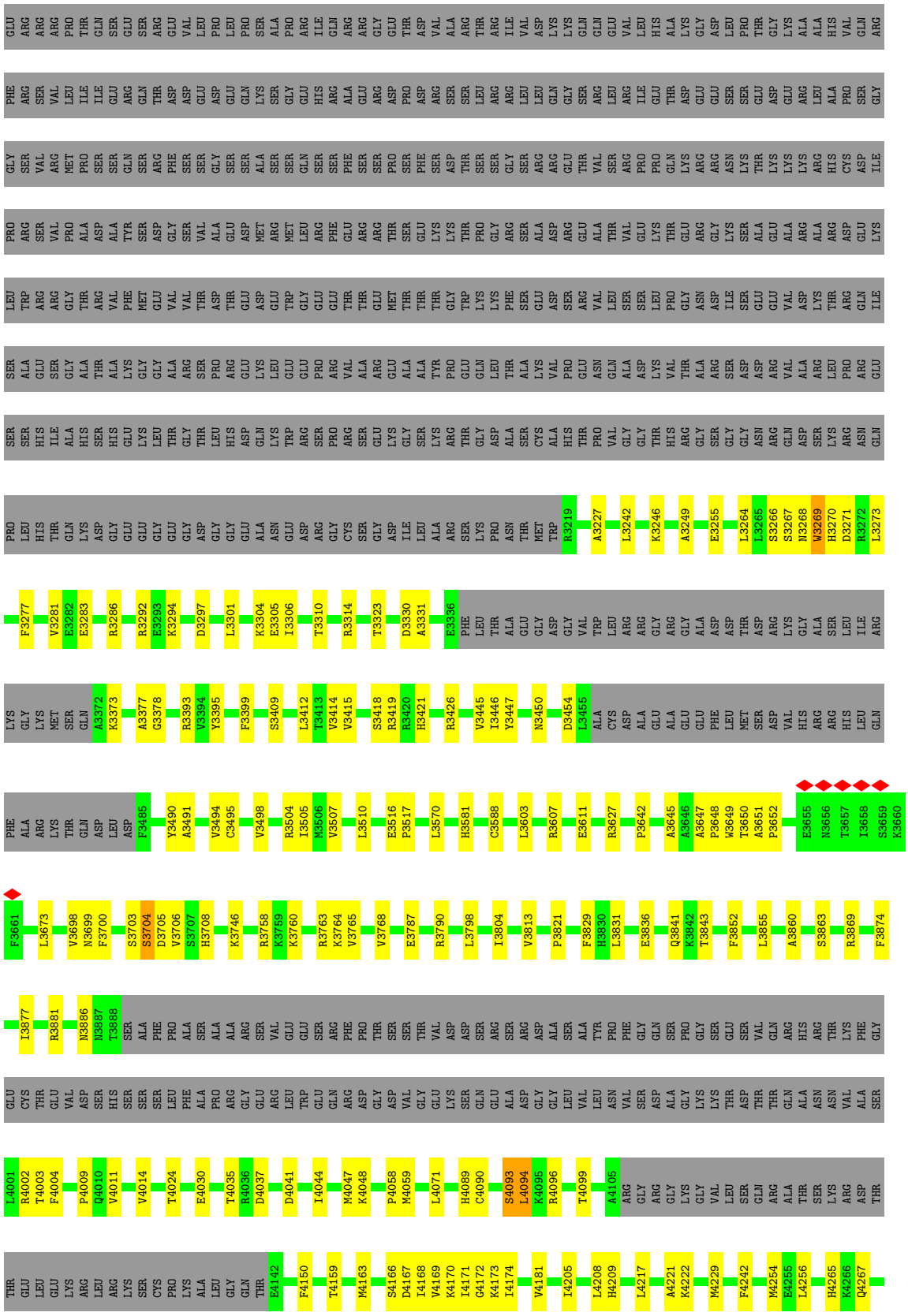
• Molecule 5: CGP, TGME49_240380

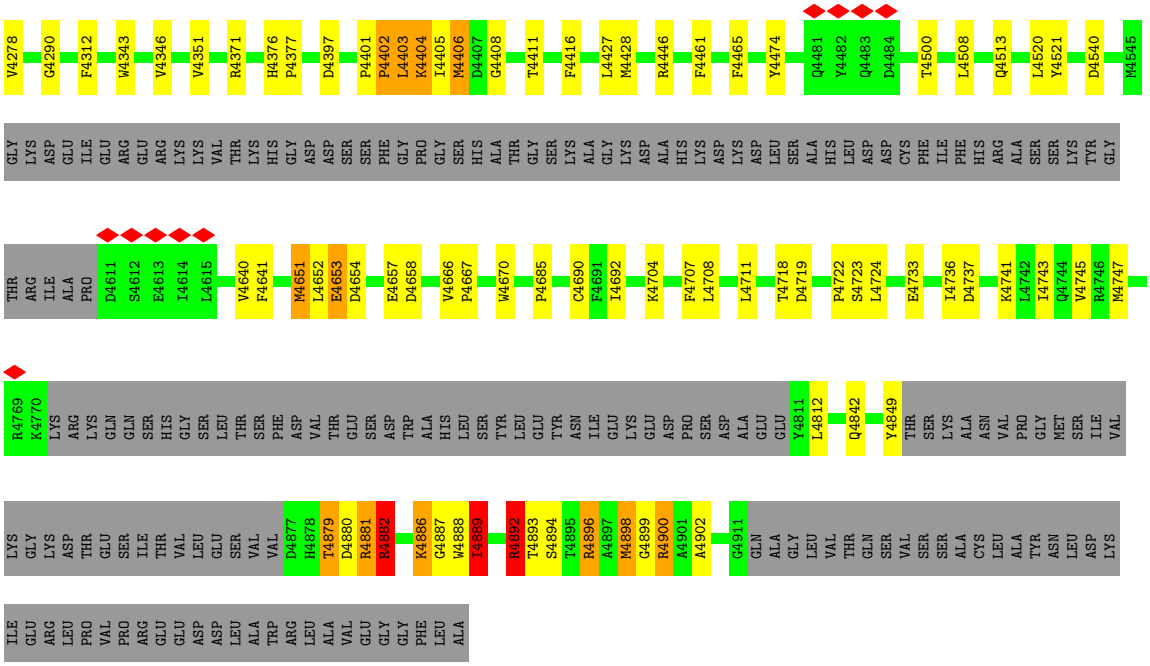
Chain EC:




SER GLU LEU TYR LEU ASP PRO SER LEU SER ASP MET ARG TRP GLU GLU ASN ARG ARG GLU ARG SER LEU GLU ALA PRO LYS LEU SER LYS GLU ALA SER HIS GLY ALA ASN PRO GLU ASP GLN GLU GLY GLY ALA SER ARG ASP GLY ALA SER ALA THR LEU
GLN ARG ILE ARG ARG ARG THR GLY ILE GLU GLY THR MET PRO TYR ARG GLY ASN GLU VAL THR THR HIS THR LEU GLU ALA PRO GLU GLN GLU GLN GLY GLU SER VAL GLN GLU GLN GLY ASP ARG ASP ALA SER SER PHE THR PHE GLN LYS GLU THR PRO PHE PHE THR LEU PHE CYS GLN GLU LEU ASN ALA CYS GLY ARG
VAL ARG GLY GLY THR GLY LYS GLY GLU PRO VAL GLU ASN VAL MET SER GLU CYS ARG ASN THR ARG SER SER LEU PRO ALA CYS SER SER SER ASP SER PRO LEU ALA ARG PHE ARG PHE CYS LEU GLU LEU PHE THR LEU PHE GLY GLU ILE THR SER ARG
SER SER GLN LEU PRO ALA LEU LEU SER SER PHE PRO PRO ARG ILE ALA THR GLN SER PHE ARG ARG ARG TYR SER HIS GLY ASN VAL PRO GLU ASP ILE ILE SER ALA SER PRO SER PRO ALA ALA SER SER PRO CYS SER PHE ALA SER PRO PHE ARG CYS ARG HIS PRO GLY GLY ILE THR ARG
SER ARG GLY SER LEU CYS SER THR CYS PRO ILE PRO SER SER SER VAL SER ARG CYS THR ASP SER PRO GLY GLY SER GLU SER ASP PRO CYS ARG LEU SER PRO LEU LEU SER PRO CYS SER PRO PRO ARG ILE ARG VAL SER PRO ARG ILE LEU VAL LEU HIS
VAL GLU ALA LEU SER TYR LYS GLU PRO GLU GLY GLY LEU SER SER HIS SER ALA SER PRO GLU GLU ALA SER ALA SER ARG GLY GLU SER ILE ARG ARG SER SER GLY ASN THR GLY ARG LEU SER PRO
GLN LEU SER ARG ALA CYS ARG ARG ILE ARG ARG ARG SER GLY ASP ALA LEU GLY GLU HIS ARG THR GLU ALA GLU PRO ARG GLN PRO PRO ARG GLY GLU ARG THR ASP LYS SER ALA ARG GLY GLU
HIS ALA THR ARG PRO LEU PHE GLU ARG PRO LEU ARG LEU SER SER LEU ALA ALA VAL ASP LYS VAL SER ALA ALA VAL GLY GLU SER ASP ARG GLU VAL GLU ASN TYR GLN LYS THR THR SER ALA SER GLU VAL ALA GLY GLN ILE SER GLY PHE LYS GLU LYS ASP ILE TYR VAL LEU SER GLY
HIS SER GLY GLU GLU ASN HIS ALA ALA SER SER PRO SER SER HIS SER HIS THR PRO VAL SER THR PRO GLU VAL PRO ALA THR ALA GLY GLY SER GLU CYS PHE HIS ASN GLY ARG THR ARG VAL LEU SER LEU CYS ARG GLU THR GLY PHE LYS ALA ASN SER GLN LYS PRO PHE THR LEU ILE
PRO ALA PRO LYS GLU GLY LYS TRP LYS GLU ALA LYS GLU ARG ILE GLU GLU ILE SER THR VAL ASN VAL ARG GLU ALA VAL GLN LYS TYR GLU ARG VAL GLY PRO HIS VAL SER LEU SER LYS GLU GLY VAL GLY THR GLU ARG GLU ASN MET GLY GLY CYS THR VAL LEU
VAL LYS LYS PRO SER VAL SER THR PRO ASP GLU GLY LEU PHE PRO PHE PRO PRO CYS SER ASN ARG PRO GLN GLU ARG ASN LYS ILE GLU ASP GLY GLU GLN GLY LYS PRO GLU ARG ASP GLN GLY VAL SER LEU GLU GLU LEU GLU GLY VAL SER SER TRP LYS GLN PRO GLY SER GLU THR ASP HIS LEU VAL
ARG LYS GLU CYS VAL SER LYS ASP SER PRO GLU LEU ARG LEU PRO LEU PHE ALA LEU TYR LEU ARG GLN PRO ILE ALA GLU LEU PRO PRO TYR VAL GLY GLU ASN ALA GLN GLU GLU GLY THR GLY ASP GLU THR ARG GLN ALA GLU GLY GLY CYS ARG ARG GLY GLU ALA THR ARG GLN HIS ARG GLY GLN
GLY ILE ASP MET GLY LYS GLU ARG GLY ASP GLY ASN GLN ALA GLY THR ALA GLN PRO GLY LYS GLU PRO VAL ALA GLU VAL ASN ALA GLN GLU GLY GLY THR GLY ARG GLN ALA GLU GLY GLN ARG SER ARG GLN ALA GLU ARG TYR PRO PRO THR GLY GLU ALA ASP GLY GLU ASN GLN SER CYS SER LYS
LEU LEU PRO PRO GLY GLY VAL GLN LYS SER SER LEU LEU VAL ALA GLN LYS SER ALA VAL GLU MET CYS ASP ASP ALA GLU GLY ARG GLU VAL LEU ALA PRO GLU LYS THR HIS THR ARG ASP ARG GLN ARG GLU THR
PRO ASN SER VAL PRO ILE ASN ARG VAL ASP GLY GLY ALA GLU LEU ASN GLY GLU ARG ARG ARG ALA ALA THR GLN PRO GLU ASP SER LYS LYS ALA GLU ASN GLU GLY GLY GLU ALA LYS MET GLN ARG GLU ASP GLU
THR ASP THR ASN THR SER TYR GLU SER LEU GLN GLU LYS PRO ASP GLY VAL ASP ASN CYS PRO SER ASN CYS ARG LYS GLU SER PRO SER SER LEU GLN LEU SER ASP PRO SER SER CYS LEU ALA GLU ASN SER LEU PRO
SER VAL SER SER HIS SER GLY SER VAL PRO ALA SER ARG VAL THR SER LEU SER SER SER VAL SER SER VAL SER SER PRO PRO SER VAL ALA THR HIS SER SER PRO SER PRO SER ARG SER LEU
SER LEU LEU PHE ASP GLY ASP VAL GLU SER GLY THR GLU GLU GLN ARG THR SER PRO ALA SER PRO SER SER GLU GLY SER THR GLY ARG SER THR GLY ASP LEU SER GLY ALA SER LEU SER ARG ARG PHE CYS PHE LEU ARG SER LEU LEU PRO ARG ARG
ALA ASN GLY PRO GLY HIS LYS LYS LYS ARG ILE THR VAL ARG LYS ALA ALA ALA THR PRO VAL ARG PRO GLN SER ARG GLN ASP GLN ILE THR VAL SER ASN THR HIS ALA ASP SER GLY ALA THR LYS LEU GLY SER HIS ARG SER SER ARG GLU GLU ASP VAL PRO GLY PRO GLY GLU
ASN PRO PHE GLU VAL GLY MET ASP CYS GLY ARG PHE SER ALA CYS ALA LEU SER GLN SER SER SER SER PRO ARG VAL THR PRO PHE PRO SER LEU SER PRO SER PRO THR ASP THR SER SER LEU PRO LEU PRO ARG CYS GLU ARG THR GLY LEU

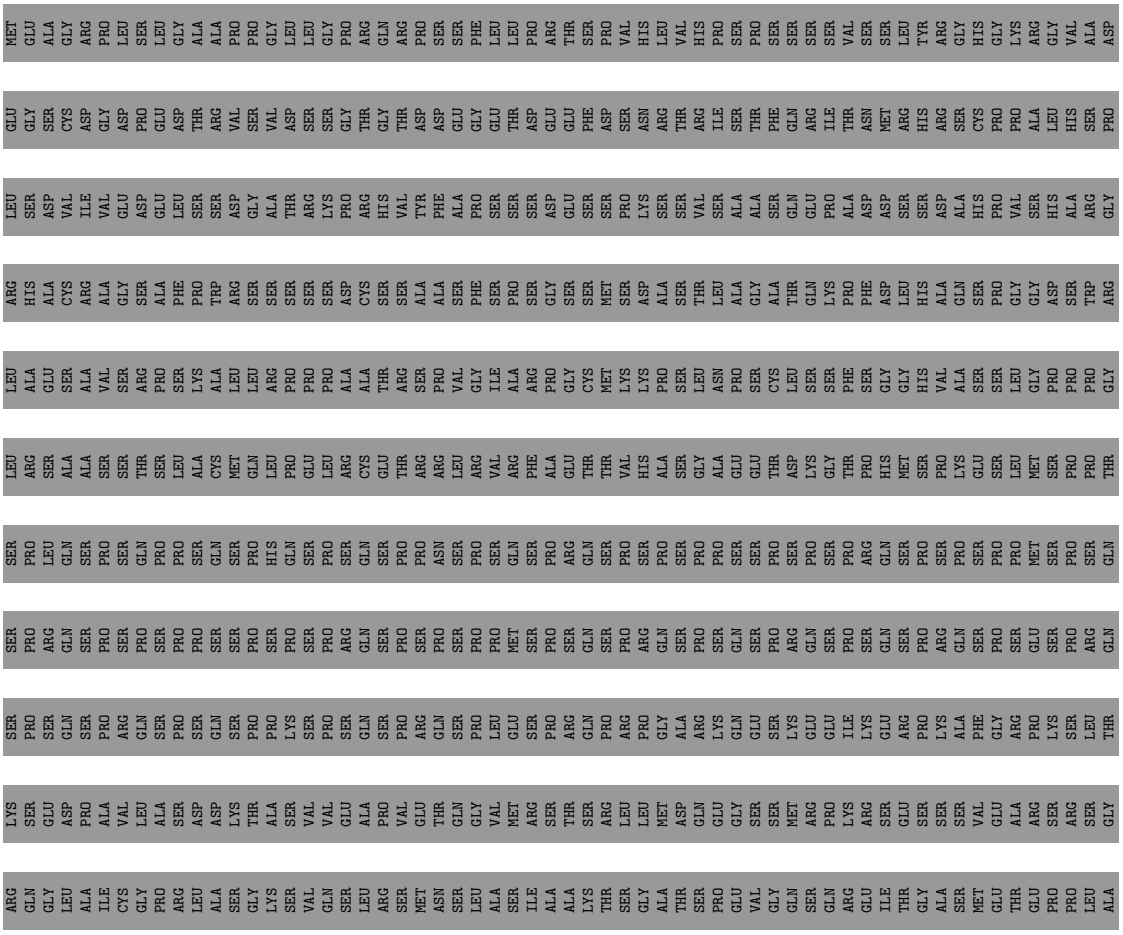

SER SER CYS SER HIS ARG SER SER ARG ASP GLY VAL ALA VAL SER LEU ASP PRO PRO LEU PHE VAL ARG VAL ALA ALA THR ALA THR SER MET ASP MET SER ALA TYR PRO GLU SER SER MET SER GLU THR LYS ALA GLY ASN GLY GLY GLU MET LYS ASP ALA LYS ASP ALA PRO HIS
ILE PHE ARG GLU GLN SER ASP GLY ASP GLY ARG ASN ALA ASN GLN GLU ALA GLN VAL SER ARG GLU CYS LEU GLY SER ARG GLY VAL GLY GLU THR GLU ARG GLN MET TRP THR ALA GLY LEU GLY ARG PRO ASP PRO ALA GLU ASP VAL GLU LYS PRO GLY GLU HIS
GLY GLN SER GLU GLU ARG ARG ASN ARG GLY ARG ARG ARG ARG PRO GLU ARG SER CYS ALA LEU LYS LYS GLU SER GLN TYR GLN GLU ALA ASP ALA HIS THR THR SER THR PRO SER GLY THR PRO ALA SER ARG HIS VAL ALA VAL GLY GLU GLY ALA CYS HIS HIS ALA PHE SER ALA SER SER
SER ALA SER SER PRO GLU PRO ALA SER ALA LEU SER SER SER CYS GLU LEU PRO ALA GLY VAL LEU TRP SER PRO ALA SER PRO ARG GLY VAL PRO LEU ALA LEU ASP SER ASP SER GLU GLU PRO ALA SER ARG PRO ALA GLY GLU GLY ALA GLY THR ALA ALA VAL CYS ALA CYS TYR ARG PHE
SER GLU GLU GLU GLU ASN GLU VAL GLU HIS TYR HIS GLU ASN GLU GLY ARG LYS GLU GLN CYS GLY GLN GLU VAL LEU ARG LYS GLY GLN ASN PRO GLY GLU SER GLU GLY GLY GLU GLU THR THR LYS GLY GLY ALA ALA ALA ARG GLU GLY THR LYS ARG THR VAL GLU GLN ALA GLU
GLN GLU ASP ARG GLU ASP ASP LEU SER PRO GLY LYS TYR GLY ARG GLU GLN ASP GLU THR SER SER TYR LYS GLY VAL LYS MET VAL ALA ALA SER GLU ALA GLU ARG ASN GLU ASP ASP ARG GLU ALA SER HIS THR GLU ASP GLU ARG GLY HIS ASP PRO ASN ILE LEU ARG THR ARG
ARG THR ARG GLU CYS GLU GLU ASP ALA LEU ARG PRO VAL THR PRO SER SER PHE PRO PRO GLN PHE ALA GLY ARG PRO ALA SER SER ARG ALA ALA GLU SER VAL SER ALA PRO CYS ARG ARG ASP PRO ASP PRO GLN VAL VAL VAL GLU LEU SER ASP GLU GLU GLY LEU VAL THR
PHE GLY ASP ALA ALA SER SER ASP ALA SER ARG PHE PHE LEU VAL VAL PRO ARG ALA GLU VAL GLU GLU THR SER GLU ASP ALA SER CYS LEU THR THR ASN ILE GLY LEU VAL TYR SER CYS SER GLU GLU GLU ARG GLU PRO LEU SER VAL PRO GLU PRO ASP VAL VAL LEU VAL THR
ASP ASP GLU ARG GLU VAL LEU LEU VAL GLU SER ALA TRP VAL ALA THR GLU GLN ARG HIS GLU GLY ALA CYS LEU LEU PRO ASN THR LYS GLY GLY ARG GLU GLY GLY PRO GLN LEU GLU ASP ALA ALA VAL LEU LEU THR ASP ASP ASP SER GLU
ALA GLU GLU ALA ASN SER GLY GLU LEU TRP ARG PRO PRO ARG LEU LEU LEU GLU ASP LYS VAL GLU GLU ILE GLU GLN GLU ALA ILE LYS SER PRO SER ASP SER GLY SER GLU LEU VAL CYS ARG PHE VAL VAL ALA GLU LYS ARG SER GLU GLY ASP ASP ARG ALA ASP
SER TRP PRO ALA ARG GLU VAL ASP GLU GLN ILE HIS SER MET ARG THR GLY GLN ARG GLN GLY ARG GLY ALA SER THR ALA THR GLU ILE SER CYS LEU ALA ARG PRO CYS GLU CYS VAL VAL ALA ARG LYS SER GLY GLU ARG GLU ASP THR ALA THR VAL SER PRO ALA HIS ASN
ARG PHE VAL MET HIS PRO ALA VAL ALA ALA PRO PRO HIS ASP TYR SER SER SER SER PRO SER SER PHE ASP LYS ASP GLN ARG ARG MET ARG ARG GLU GLY GLU TRP THR LYS ALA HIS GLY GLY GLY GLU THR GLU ALA THR ARG VAL LYS ARG PRO GLY GLY HIS SER VAL LYS ARG ASN LYS
GLY SER LYS THR ASP GLY GLY ASN PRO ASP ARG GLU PRO ARG ARG GLU LYS THR GLY LEU GLY HIS ARG GLY ARG VAL ALA VAL ASP ASN ALA ALA ALA ARG PRO HIS SER VAL LYS ARG PRO GLY GLY ARG THR ALA GLY LYS THR ARG ARG GLN GLU ASP HIS GLY LYS GLY
LYS ARG LYS GLN ALA ARG GLY ALA ASP LEU ARG GLN THR GLU GLY ALA ALA LEU ASP HIS ARG GLU PRO LYS GLU HIS ARG GLY GLN ALA ARG GLY HIS LEU SER ARG ARG GLU ARG GLN SER ASP THR PRO GLY LYS LEU CYS TRP ARG VAL ASP ASP SER ARG ARG ARG SER ASP GLY
ARG GLU GLY ARG LEU THR GLU ALA GLU ILE SER ASP GLY GLU GLN GLN LEU LYS ASP GLY THR ARG GLU ALA LEU TYR ALA CYS SER ILE SER ASP GLU GLU ALA GLN SER HIS ASP PHE ASP GLU ASP GLY ALA
GLU ALA LEU ALA ALA GLY THR PHE GLN ALA GLY ALA PRO THR THR THR ASP ILE VAL ALA GLY CYS PHE HIS SER ASP PRO SER ARG VAL GLY THR PHE HIS SER ARG SER PHE ALA PRO SER SER SER PRO ALA SER PRO PHE SER SER ALA GLN VAL SER CYS SER VAL ALA
ARG ARG ARG HIS SER LEU ALA LEU PRO LEU SER SER GLY GLY PRO GLY SER VAL THR GLN ALA SER GLU VAL PHE TRP ARG ARG MET SER THR GLY GLU VAL GLY ALA ARG GLU LYS ARG SER HIS SER SER SER ARG GLY LYS ARG GLU GLU GLU ARG
ILE GLY ARG PRO PRO LEU PRO SER PRO SER GLY SER VAL PHE SER ARG ILE GLY GLU ASP GLU GLU GLY GLY GLU THR GLN GLY GLY ARG GLU GLU ALA GLN MET LEU MET HIS SER SER VAL LEU PRO LEU LYS GLU GLU ALA GLY PHE PRO THR ALA PRO SER ARG
VAL ALA SER HIS SER LEU SER PRO ARG GLY SER GLU GLY ASP GLU ALA THR SER ALA GLY ASP TRP VAL LEU SER ALA GLY VAL LYS GLY GLU ARG LYS ALA PRO GLY LYS SER ASP GLU HIS GLU ARG
GLY SER GLY ASP GLU ARG GLN SER THR GLU ALA SER ALA LYS LEU TYR THR GLY GLY ASN VAL SER GLU GLU ASP THR ARG LYS GLU ASP THR ARG PRO SER ASP GLY SER GLU

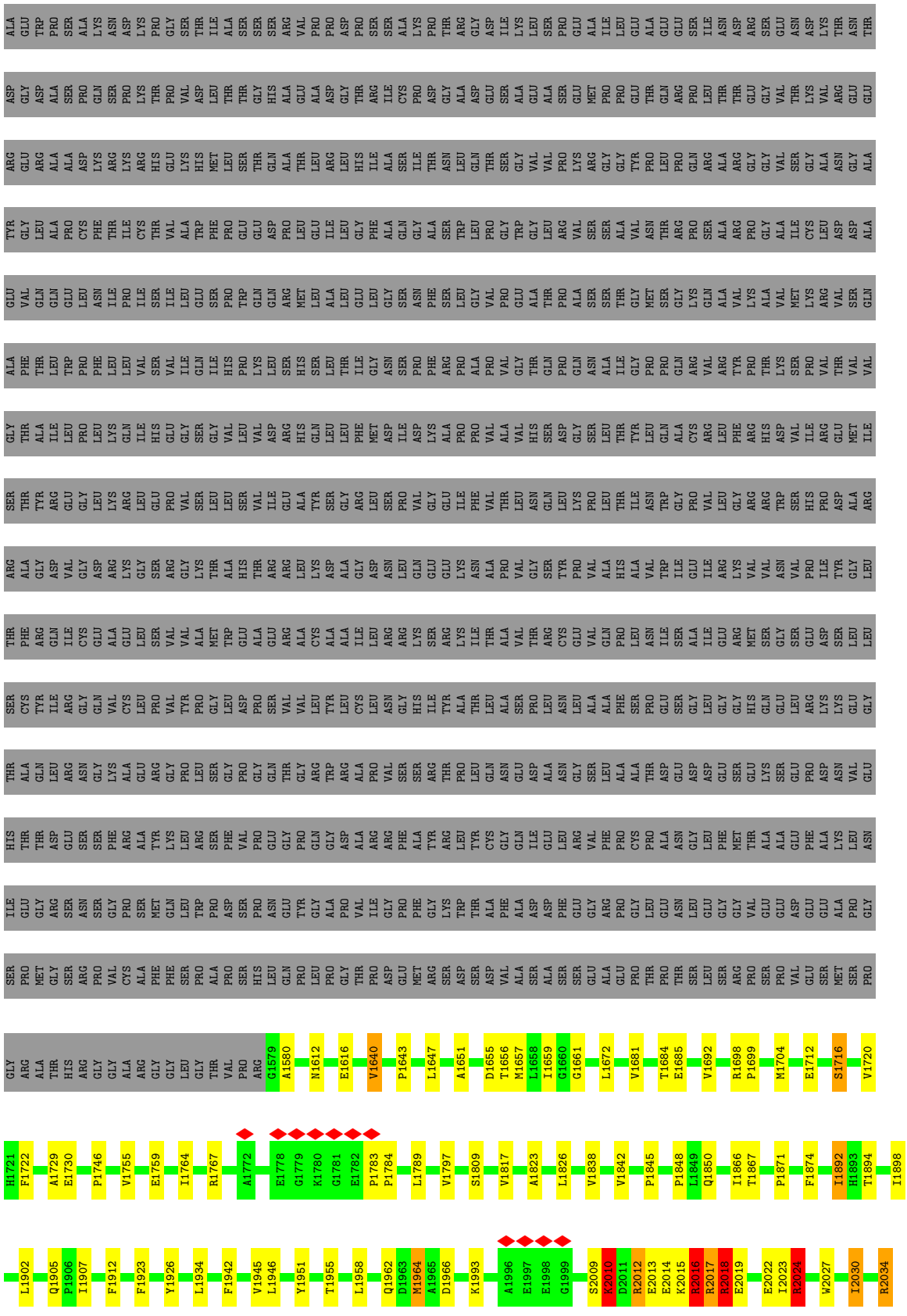

GLU ARG ARG ARG PRO THR GLN SER GLU SER ARG GLU VAL LEU PRO LEU PRO SER ALA PRO ARG ILE GLN ARG ARG GLY GLU THR ASP VAL ALA ARG THR ARG ILE VAL ASP LYS LYS GLN GLN GLU VAL LEU HIS ALA LYS GLY ASP LEU PRO THR GLY LYS ALA ALA HIS VAL GLN ARG
PHE ARG SER VAL LEU ILE ILE GLU ARG GLN THR ASP ASP GLU GLN LYS SER GLY GLU HIS ARG ALA GLU ARG ASP PRO ASP ARG GLN SER LEU ARG ARG LEU LEU GLN GLY SER ARG LEU ARG ILE GLU THR ASP GLU GLU SER SER SER GLU ASP GLU ARG LEU LEU ALA PRO SER GLY
GLY SER VAL ARG MET PRO SER SER GLN SER ARG PHE SER SER GLY SER SER ALA SER SER GLN SER SER PHE SER SER ASP THR SER SER GLY GLY SER ARG GLN GLU THR VAL SER ARG PRO PRO GLN LYS ARG ARG ASN LYS THR LYS LYS LYS LYS ARG HIS CYS ASP ILE
PRO ARG SER VAL PRO ALA ASP ALA TYR SER ASP GLY SER VAL ALA GLU ASP MET ARG MET LEU ARG PHE GLU ARG ARG THR SER GLU ALA THR VAL GLU LYS THR GLU GLY ARG GLY LYS LYS THR PRO GLY ARG SER ALA ASP ARG GLU ALA THR VAL LEU SER ARG PRO GLU ALA GLU ALA ARG ALA ARG ASP GLU LYS
LEU TRP ARG GLY THR ARG VAL PHE MET GLU VAL VAL THR ASP THR GLU GLU ASP GLU TRP GLY GLU GLU THR THR GLU MET THR THR THR GLY TRP LYS LYS PHE SER GLU ASP SER ARG VAL LEU SER SER LEU PRO GLY ASN ASP ILE SER GLU GLU VAL ASP LYS THR ARG GLN ILE
SER ALA GLU SER GLY ALA THR GLY GLY GLU LYS LEU GLU GLU PRO ARG GLU VAL ALA ALA TYR PRO GLN GLN ASN GLN ALA ASP LYS ASP ASP ARG VAL ALA ARG LEU ARG GLU
SER SER HIS ILE ALA HIS SER HIS GLU LYS LEU THR GLY THR LEU HIS ASP GLN LYS TRP ARG SER PRO ARG SER GLU LYS GLY SER LYS ARG THR GLY ASP ALA SER CYS ALA HIS THR PRO VAL GLY GLY THR HIS ARG GLY SER GLY GLY SER ARG GLN ASP SER ARG ASN GLN
PRO LEU HIS THR GLN LYS ASP GLY GLU GLY GLU GLY GLY ASP GLY GLY GLU ALA ASN GLU GLY CYS SER GLY ASP ILE LEU ALA ARG SER LYS PRO ASN THR MET TRP R3219 A3227 L3242 K3246 A3249 E3255 L3264 L3265 S3266 S3267 N3268 W3269 H3270 D3271 R3272 L3273
F3277 V3281 E3282 E3283 R3286 R3292 E3293 K3294 D3297 L3301 K3304 E3305 I3306 T3310 R3314 T3323 D3330 A3331 E3336 PHE LEU THR ALA GLU GLY ASP GLY VAL TRP LEU ARG ARG GLY ARG GLY ALA ASP ASP THR ASP ARG LYS GLY ALA SER LEU ILE ARG
LYS GLY LYS MET SER GLN A3372 K3373 A3377 G3378 R3393 V3394 Y3395 F3399 S3409 L3412 T3413 V3414 V3415 S3418 R3419 R3420 H3421 R3426 V3445 I3446 Y3447 N3450 D3454 L3455 ALA CYS ASP ALA GLU ALA GLU GLU PHE LEU MET SER ASP VAL HIS ARG ARG HIS LEU GLN
PHE ALA ARG LYS THR GLN ASP LEU ASP F3485 Y3490 A3491 V3494 C3495 V3498 R3504 I3505 M3506 V3507 L3510 E3516 P3517 L3570 H3581 C3588 L3603 R3607 E3611 R3627 P3642 A3645 A3646 A3647 P3648 W3649 T3650 A3651 P3652 E3655 N3656 T3657 I3658 S3659 K3660
F3661 L3673 V3698 N3699 F3700 S3703 S3704 D3705 V3706 S3707 H3708 K3746 R3758 K3759 K3760 R3763 K3764 V3765 V3768 E3787 R3790 L3798 I3804 V3813 P3821 F3829 H3830 L3831 E3836 Q3841 K3842 T3843 F3852 L3855 A3860 S3863 R3869 F3874
I3877 R3881 N3886 N3887 T3888 SER ALA PHE PRO ALA SER ALA ALA ARG SER VAL GLU GLU SER ARG PHE PRO THR SER SER THR VAL ASP ASP SER ARG SER ARG ASP ALA SER ALA TYR PRO PHE GLY GLN SER PRO GLY SER GLU SER VAL GLN ARG HIS ARG THR LYS PHE GLY
GLU CYS THR GLU VAL ASP SER SER HIS SER ARG GLN GLU ARG LEU TRP GLU GLN ARG ASP GLY ASP VAL GLY LYS GLU LYS SER GLN GLU SER ALA GLY GLY LEU VAL LEU ASN VAL SER ASP ALA GLY LYS LYS THR ASP THR THR GLN ALA ASN ASN VAL ALA SER
L4001 R4002 T4003 F4004 P4009 Q4010 V4011 V4014 T4024 E4030 T4035 R4036 D4037 D4041 I4044 M4047 K4048 P4058 M4059 L4071 H4089 C4090 S4093 L4094 K4095 R4096 T4099 A4105 ARG GLY ARG GLY LYS GLY VAL LEU SER GLN ARG ARG ALA THR SER LYS ARG ASP THR
THR GLU LEU GLU LYS ARG LYS SER CYS PRO LYS ALA LEU GLY GLN THR E4142 F4150 T4159 M4163 S4166 D4167 I4168 V4169 K4170 I4171 G4172 K4173 I4174 V4181 I4205 L4208 H4209 L4217 A4221 K4222 M4229 F4242 M4254 E4255 L4256 H4265 K4266 Q4267

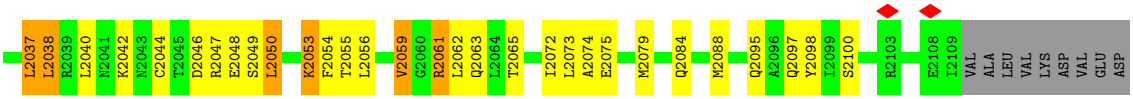


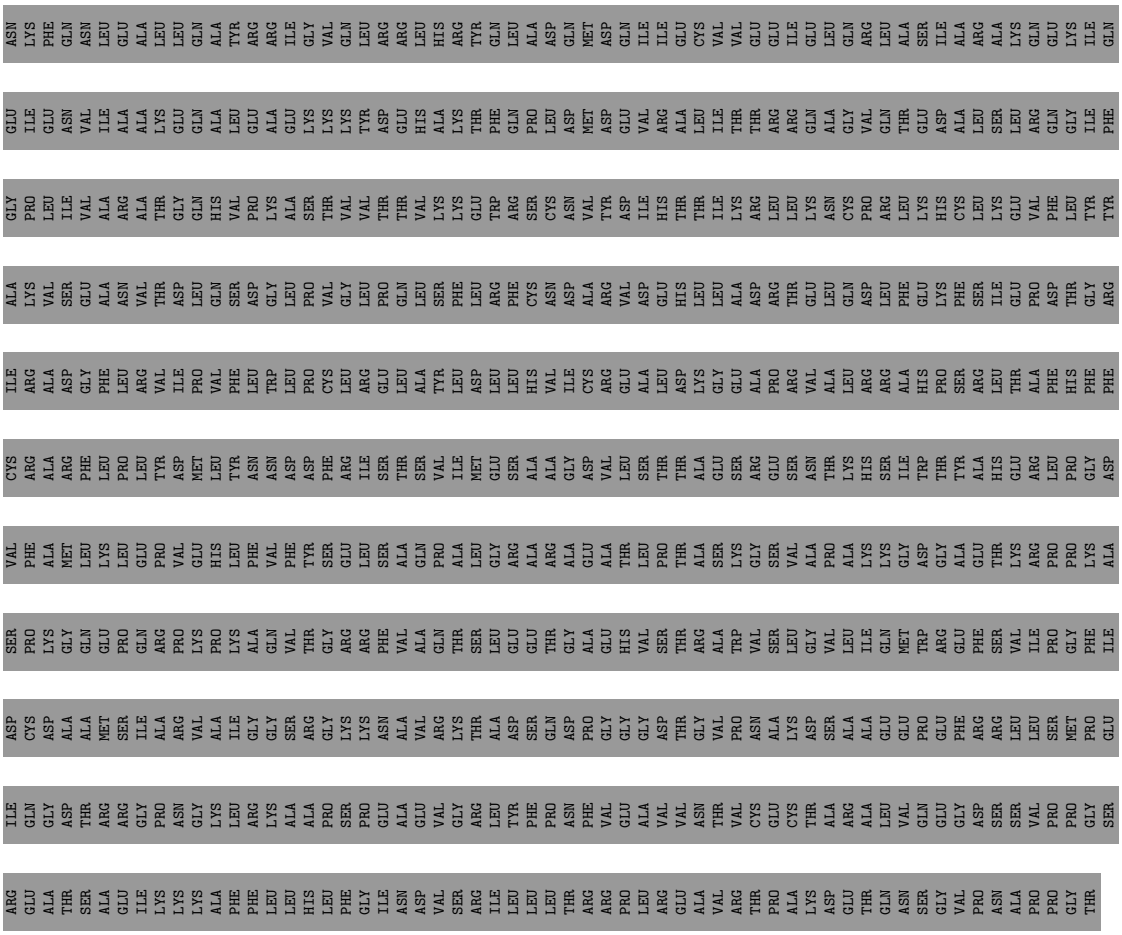
• Molecule 6: FLM1, TGME49_271780

Chain FA:



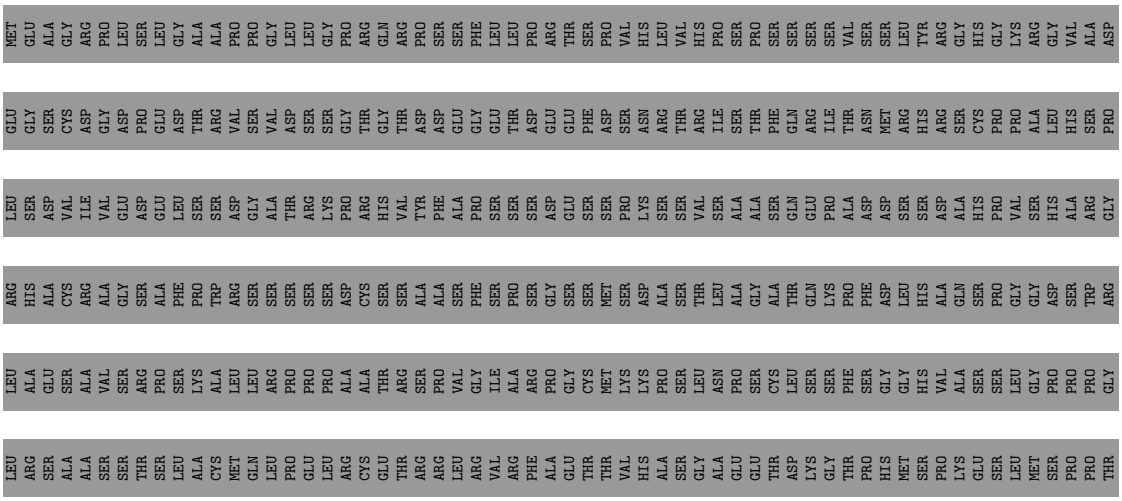

ALA GLU TRP PRO SER ALA LYS ASN ASP LYS PRO GLY SER THR ILE ALA SER SER SER ARG VAL PRO PRO ASP PRO SER SER SER ALA LYS PRO THR ARG GLY ASP ILE LYS LEU SER PRO GLU ALA ILE LEU LEU GLU ALA GLU SER ILE SER GLU ASP ARG SER GLU GLU ASN ASP LYS THR ASN THR
ASP GLY ASP ALA SER PRO GLN SER PRO LYS THR PRO VAL ASP LEU THR THR GLY HIS ALA GLU ALA ASP GLY THR ARG ILE CYS PRO ASP GLY ALA ASP GLU SER ALA GLU ALA SER GLU MET PRO PRO GLU THR GLN ARG PRO LEU PRO GLN ARG THR THR GLU GLY GLY VAL THR LYS LYS VAL ARG GLU GLU
ARG GLU ARG ALA ALA ASP LYS ARG LYS ARG HIS GLU LYS HIS MET LEU SER THR GLN ALA THR LEU ARG LEU HIS ILE ALA SER ILE THR ASN LEU GLN THR SER GLY VAL VAL PRO LYS ARG GLY GLY ARG GLY GLY VAL SER GLY ILE ALA
TYR GLY LEU ALA PRO CYS PHE THR ILE CYS THR VAL ALA TRP PHE PRO GLU GLU ASP PRO LEU GLU ILE LEU GLY PHE ALA GLN GLY ALA SER TRP LEU PRO GLY TRP GLY VAL ALA ILE CYS LEU ASP ALA
GLU VAL GLN GLN GLU LEU ASN ILE PRO ILE SER LEU GLN GLN ARG MET LEU ALA LEU GLU LEU GLY SER ASN PHE SER LEU GLY VAL PRO GLU ALA THR PRO GLN ALA SER SER THR GLY ALA VAL ASN THR ARG PRO SER ALA ARG PRO GLY LYS ARG VAL SER GLN
ALA PHE THR LEU TRP PRO PHE LEU LEU VAL SER VAL ILE GLN ILE HIS PRO LYS LEU SER HIS SER LEU LEU THR ILE GLY ASN SER PRO PHE ARG PRO ALA PRO VAL THR GLN PRO GLN ASN ALA ILE GLY PRO PRO GLN ARG VAL ARG TYR PRO THR LYS SER PRO VAL THR VAL VAL
GLY THR ALA ILE LEU LEU PRO LEU LYS GLN ILE HIS GLU GLY SER GLY VAL LEU VAL ASP ARG HIS GLN LEU LEU LEU PHE MET ASP ILE ASP LYS ALA PRO PRO VAL ALA ALA VAL HIS SER ASP GLY SER LEU THR TYR LEU GLN ALA CYS ARG VAL ARG LEU PHE ARG HIS ASP VAL ILE ARG GLU MET ILE
SER THR TYR ARG GLU GLY LEU LYS ARG LEU GLU GLU PRO VAL SER LEU LEU SER VAL ILE GLU GLU ALA TYR SER GLY ARG LEU SER PRO VAL GLY GLU ILE PHE VAL THR LEU ASN GLN LEU LYS PRO LEU THR ILE ASN TRP GLY PRO VAL LEU LEU GLY ARG ARG TRP SER HIS PRO ASP ALA
ARG ALA GLY ASP VAL GLY ARG LYS GLY SER ARG GLY LYS THR ALA HIS THR ARG ARG LEU LYS ASP ALA GLY ASP ASN LEU GLN GLU GLU LYS ASN ALA PRO VAL GLY SER TYR PRO VAL ALA HIS ALA VAL TRP ILE GLU ILE ARG LYS VAL VAL ASN VAL PRO ILE TYR GLY LEU
THR PHE ARG GLN ILE CYS GLU ALA GLU LEU SER VAL VAL ALA MET TRP GLU ALA GLU ARG ALA ALA CYS GLU TYR ALA ALA ALA ILE LEU ARG ARG LYS SER ARG LYS ILE THR ALA VAL THR ARG CYS GLU VAL GLN PRO LEU ASN ILE SER ALA ILE GLU ILE ARG MET SER GLY SER GLU ASP SER LEU LEU
SER CYS TYR ILE ARG GLY GLN VAL CYS LEU PRO VAL TYR PRO GLY LEU ASP PRO SER VAL VAL LEU TYR LEU CYS LEU LEU ASN GLY HIS ILE TYR ALA THR LEU ALA SER PRO LEU GLN GLU VAL ALA ALA PHE SER PRO GLU SER GLY LEU GLY GLY HIS GLN GLU LEU ARG LYS LYS GLU GLY
THR ALA GLN LEU ARG GLU ARG GLY PRO LEU SER GLY PRO GLY GLN THR GLY ARG TRP ARG ALA PRO VAL SER SER ARG THR PRO LEU GLN GLY ARG ASN GLU ASP ALA ASN GLY SER LEU ALA THR ASP GLU ASP GLU GLU SER ASP GLU GLY PRO ASP ASN VAL GLU
HIS THR THR ASP GLU SER SER PHE ARG ALA TYR ARG LEU LYS ALA PHE VAL PRO GLU GLY PRO GLN GLY ASP ALA ARG ARG PHE ALA TYR ARG LEU TYR CYS GLY GLN ILE GLU LEU ARG VAL PHE PRO CYS PRO ALA ASN GLY LEU GLU GLY PHE MET THR ALA ALA GLU PHE ALA LYS LEU ASN
ILE GLU GLY ARG SER ASN SER MET GLN LEU TRP PRO ASP SER PRO ASN GLU GLY TYR GLY ALA PRO VAL ILE GLY PRO PHE GLY LYS TRP THR ALA PHE ALA ASP ASP PHE GLU GLY ARG PRO GLY LEU GLU GLY GLY VAL GLU GLU GLU ASP GLU GLU PRO GLY
SER PRO MET GLY SER ARG PRO VAL CYS ALA PHE PHE SER PRO ALA PRO SER HIS LEU GLN PRO LEU PRO GLY THR PRO ASP GLU MET ARG SER ASP SER ASP VAL ALA SER ALA SER SER GLU ALA GLU PRO THR PRO THR SER LEU SER ARG PRO SER PRO VAL GLU SER MET SER PRO
GLY ARG ALA THR HIS ARG GLY GLY GLY LEU GLY THR VAL PRO ARG G1579 A1580 N1612 E1616 V1640 P1643 L1647 A1651 D1655 T1656 M1657 L1658 I1659 G1660 G1661 L1672 V1681 T1684 E1685 V1692 R1698 P1699 M1704 E1712 S1716 V1720
H1721 F1722 A1729 E1730 P1746 V1755 E1759 I1764 R1767 A1772 E1778 G1779 K1780 G1781 E1782 P1783 P1784 L1789 V1797 S1809 V1817 A1823 L1826 V1838 V1842 P1845 P1848 L1849 Q1850 I1866 T1867 P1871 F1874 I1892 H1893 T1894 I1898
L1902 Q1905 P1906 I1907 F1912 F1923 Y1926 L1934 F1942 V1945 L1946 Y1951 T1955 L1958 Q1962 D1963 M1964 A1965 D1966 K1993 A1996 E1997 E1998 G1999 S2009 K2010 D2011 R2012 E2013 E2014 K2015 R2016 R2017 R2018 E2019 E2022 I2023 R2024 W2027 I2030 R2034

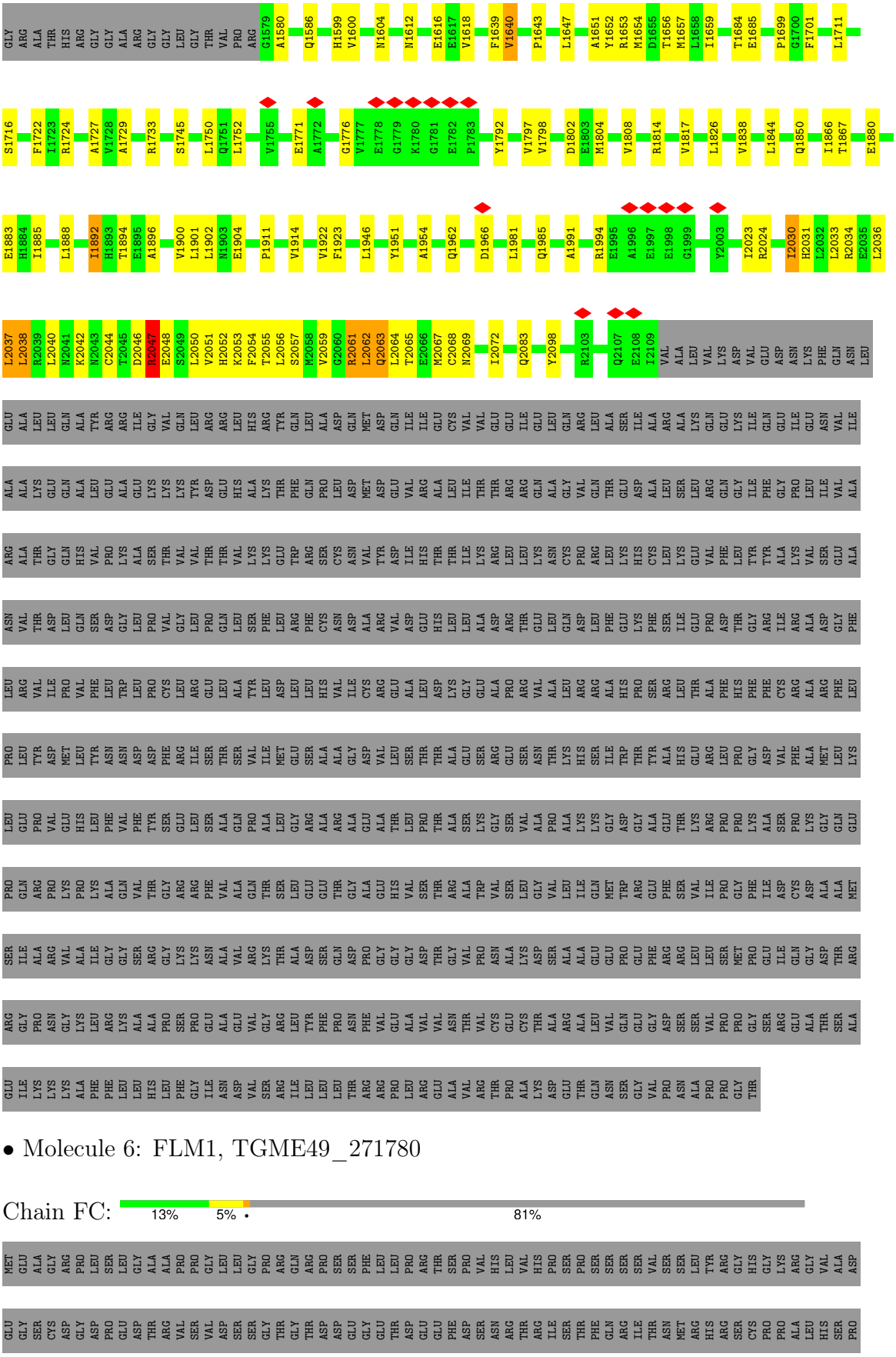




• Molecule 6: FLM1, TGME49_271780

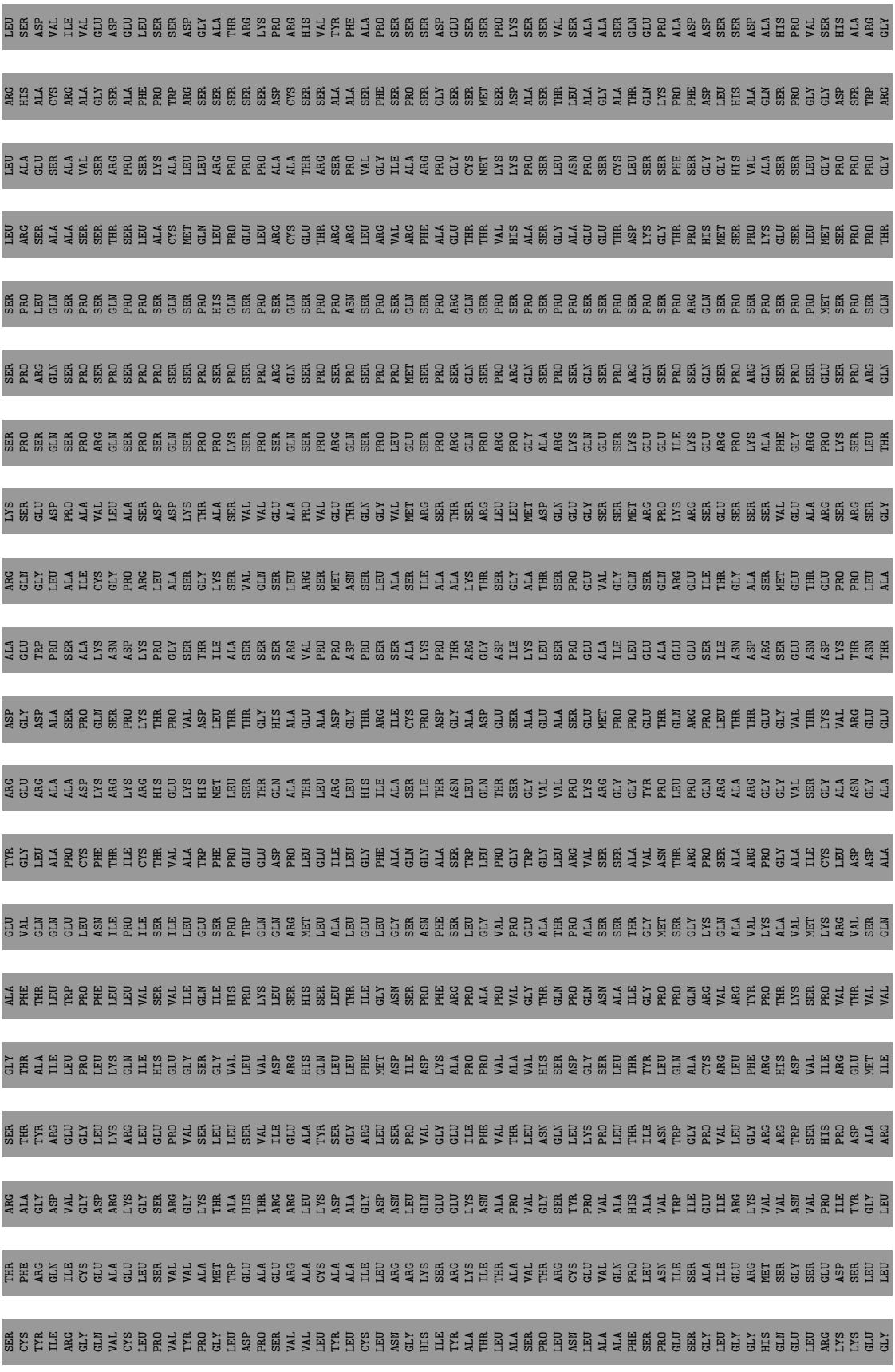
Chain FB:

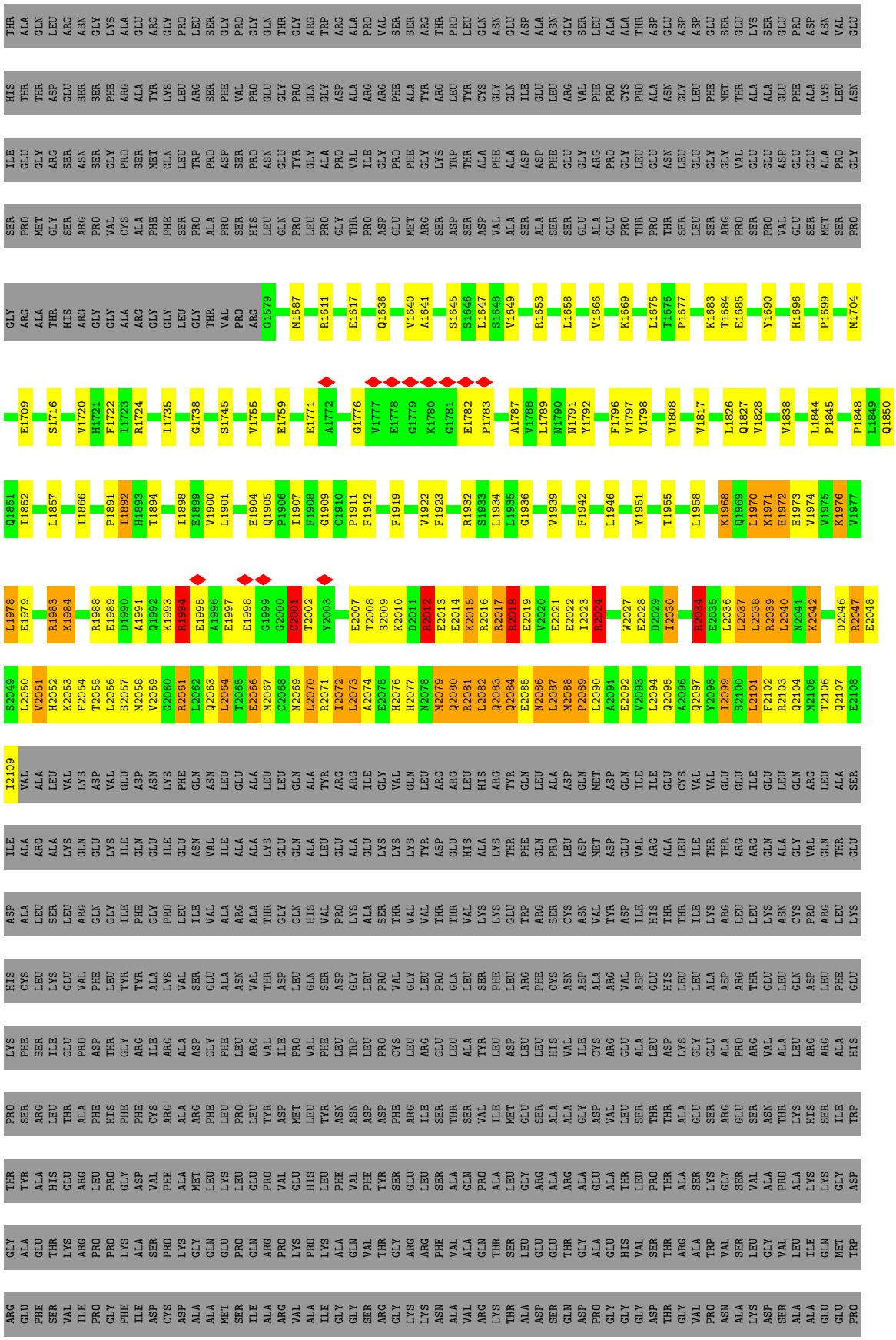


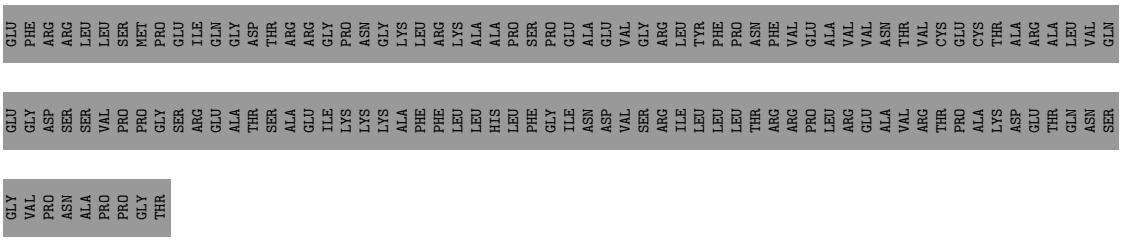


• Molecule 6: FLM1, TGME49_271780

Chain FC:

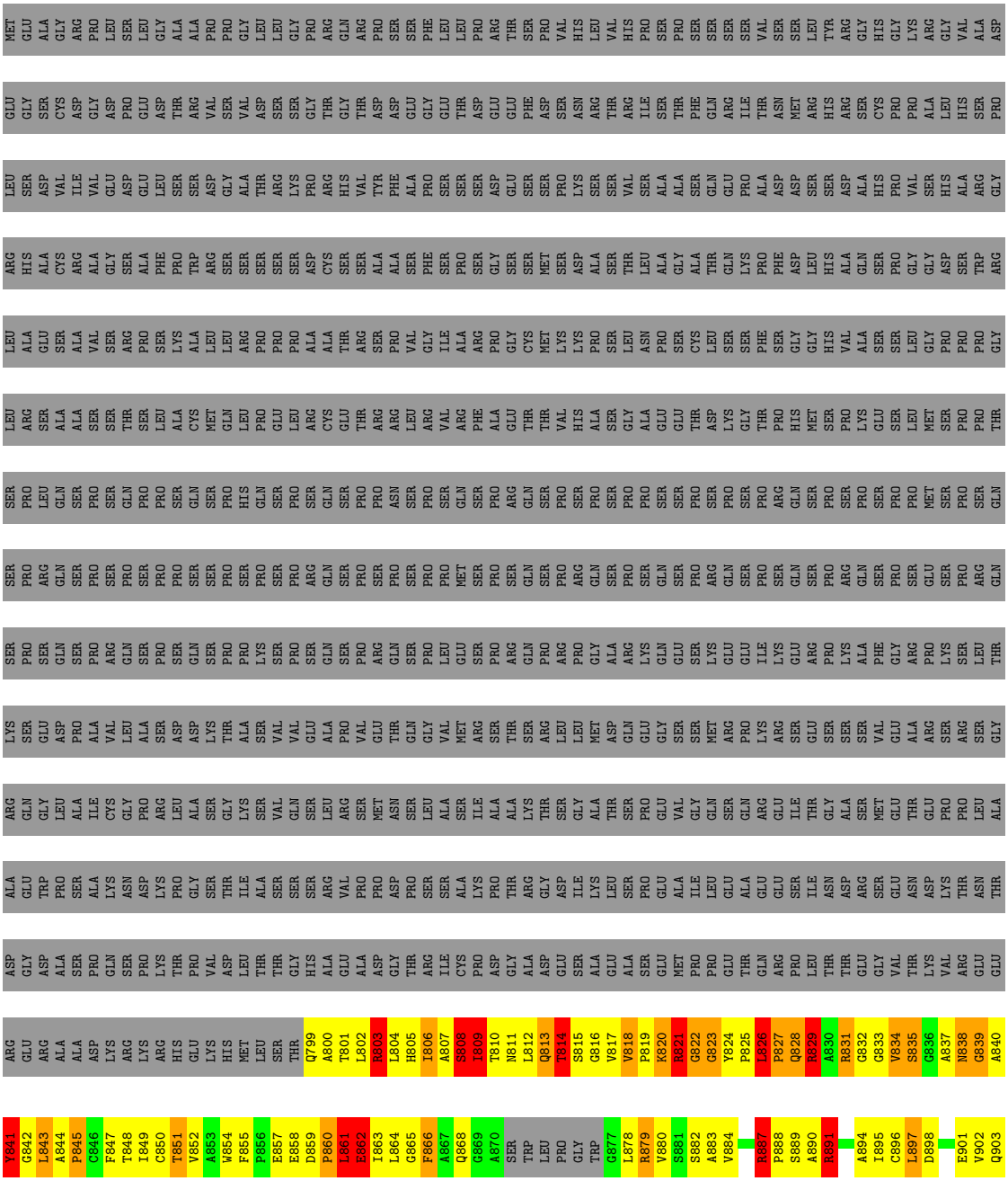

LEU SER ASP VAL ILE VAL GLU ASP GLU LEU SER SER ASP GLY ALA THR ARG LYS PRO ARG HIS VAL TYR PHE ALA PRO SER SER SER ASP GLU SER SER SER PRO LYS SER SER VAL SER ALA ALA SER GLN GLU PRO ALA ASP ASP SER SER ASP GLY ALA HIS PRO VAL SER HIS ALA ARG GLY
ARG HIS ALA CYS ARG ALA GLY SER ALA PHE PRO TRP ARG SER SER SER SER ARG ASP CYS SER SER SER ALA ALA SER PHE SER PRO SER SER GLY SER SER MET SER ASP ALA SER THR LEU ALA ALA GLY ALA THR GLN LYS PRO PHE ASP LEU HIS ALA GLN SER PRO GLY SER ASP GLY GLY ASP SER TRP ARG
LEU ALA GLU SER ALA VAL SER ARG PRO PRO PRO ALA ALA THR ARG SER PRO VAL GLY ILE ALA ARG PRO GLY CYS MET LYS LYS PRO SER LEU ASN PRO SER CYS LEU GLY SER SER PHE SER GLY GLY HIS VAL ALA SER SER PRO GLY LEU GLY GLY ASP PRO GLY
LEU ARG SER ALA ALA SER SER THR SER LEU ALA CYS MET GLN LEU PRO GLU LEU ARG CYS GLU THR ARG ARG ARG LEU ARG VAL ARG PHE ALA GLU THR THR VAL HIS ALA SER GLY ALA GLU GLU THR ASP LYS PRO SER GLY THR THR THR VAL HIS ALA SER LEU MET SER PRO PRO THR
SER PRO LEU GLN SER PRO PRO SER GLN PRO SER GLN SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN
SER PRO ARG GLN SER PRO SER PRO PRO SER PRO SER PRO ARG GLN SER PRO SER PRO MET SER PRO SER GLN SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN SER PRO SER PRO ARG GLN
SER PRO SER GLN SER PRO PRO LYS SER PRO SER GLN SER PRO ARG GLN SER PRO LEU GLU SER PRO ARG GLN PRO ARG PRO GLY ALA ARG LYS GLN GLU SER LYS GLU GLU ILE LYS GLU ARG PRO LYS ALA PHE GLY ARG PRO LYS SER LEU THR
LYS SER GLU ASP PRO ALA VAL LEU ALA SER ASP ASP LYS THR ALA SER VAL VAL GLU ALA PRO VAL GLU THR GLN GLY VAL MET ARG SER THR SER ARG LEU LEU MET ASP GLN GLU GLY SER SER MET ARG PRO LYS ARG GLU VAL GLU VAL ALA ARG SER ARG SER VAL GLY
ARG GLN GLY LEU ALA ILE CYS GLY PRO ARG LEU ALA LYS SER VAL VAL GLN SER LEU ARG SER MET ASN SER LEU ALA SER ILE ALA ALA LYS THR SER GLY ALA THR SER PRO GLU VAL GLY GLN SER GLN ARG GLU ILE THR GLY ALA SER MET GLU THR GLU PRO PRO LEU ALA
ALA GLU TRP PRO SER ALA LYS ASN ASP LYS PRO GLY SER THR ILE ALA SER SER SER ARG VAL PRO PRO ASP PRO SER SER SER ALA LYS PRO THR ARG GLY ASP GLU ILE LYS LEU SER PRO GLU ALA ILE LEU GLU ALA GLU ASN ASP ARG SER GLU ASN ASP LYS THR ASN THR
ASP GLY ASP ALA SER PRO GLN SER PRO LYS THR PRO VAL ASP LEU GLU ALA ASP GLY THR ARG ILE CYS PRO ASP GLY ALA ASP GLU SER ALA GLU ALA SER GLU MET PRO PRO GLU THR GLN ARG PRO LEU THR ARG GLU GLY
ARG GLU ARG ALA ALA ASP LYS ARG LYS HIS ILE ALA SER ILE THR ASN LEU GLN THR SER GLY VAL VAL PRO LYS ARG GLY GLY TYR PRO LEU PRO GLN ARG GLN ALA ARG GLY GLY GLY VAL SER GLY ALA ASN GLY ALA
TYR GLY LEU ALA PRO CYS PHE THR ILE CYS THR VAL ALA TRP PHE PRO GLU GLU ASP PRO LEU GLU ILE LEU GLY PHE ALA GLN GLY ALA SER TRP LEU PRO GLY GLY ALA ILE CYS LEU ASP ALA
GLU VAL GLN GLN GLU LEU ASN ILE PRO LEU GLU LEU GLY SER SER ASN PHE SER LEU GLY VAL PRO GLU ALA THR PRO ALA SER SER THR GLY MET SER GLY LYS GLN ALA VAL LYS ALA VAL ALA SER GLN
ALA PHE THR LEU TRP PRO PHE LEU LEU LEU VAL SER VAL ILE LEU GLN ILE HIS PRO LYS LEU SER HIS SER LEU LEU THR ILE GLY ASN SER PRO PHE ARG PRO ALA PRO VAL GLY THR GLN PRO GLN ASN ALA ILE GLY PRO PRO GLN GLN ARG VAL ARG TYR PRO THR LYS ALA VAL MET SER GLN
GLY THR ALA ILE LEU LYS GLN ILE HIS GLU GLY SER VAL LEU GLU ASP ARG HIS GLN LEU LEU PHE MET ASP ILE ASP LYS ALA PRO VAL ALA VAL HIS SER ASP GLY SER LEU THR TYR LEU GLN ALA CYS ARG LEU PHE ARG HIS ASP VAL ILE ARG GLU VAL SER
SER THR TYR ARG GLU ALA TYR SER GLY ARG LEU SER PRO VAL GLY GLU ILE PHE VAL THR LEU ASN GLN LEU LYS PRO VAL LEU THR ILE ASN TRP GLY PRO VAL LEU GLY ARG HIS PRO ASP ASP ARG
ARG ALA GLY ASP ASN LEU GLN GLU GLU LYS ASN ALA PRO VAL GLY SER TYR PRO VAL ALA HIS ALA VAL TRP ILE GLU ILE ARG LYS VAL VAL ASN VAL PRO ILE TYR GLY LEU
THR PHE ARG GLN ILE CYS GLU ALA ALA ALA ILE LEU ARG ARG LYS SER ARG LYS ILE THR ALA VAL THR ARG CYS GLU VAL GLN PRO LEU ASN ILE SER ALA ILE GLU GLU ARG MET SER GLY SER ASP SER LEU LEU
SER CYS TYR ILE ARG GLY HIS ILE TYR ALA THR LEU ALA SER PRO LEU ASN LEU ALA ALA PHE SER PRO GLU SER GLY LEU GLY GLY HIS GLN GLU LEU ARG LYS LYS GLU GLY

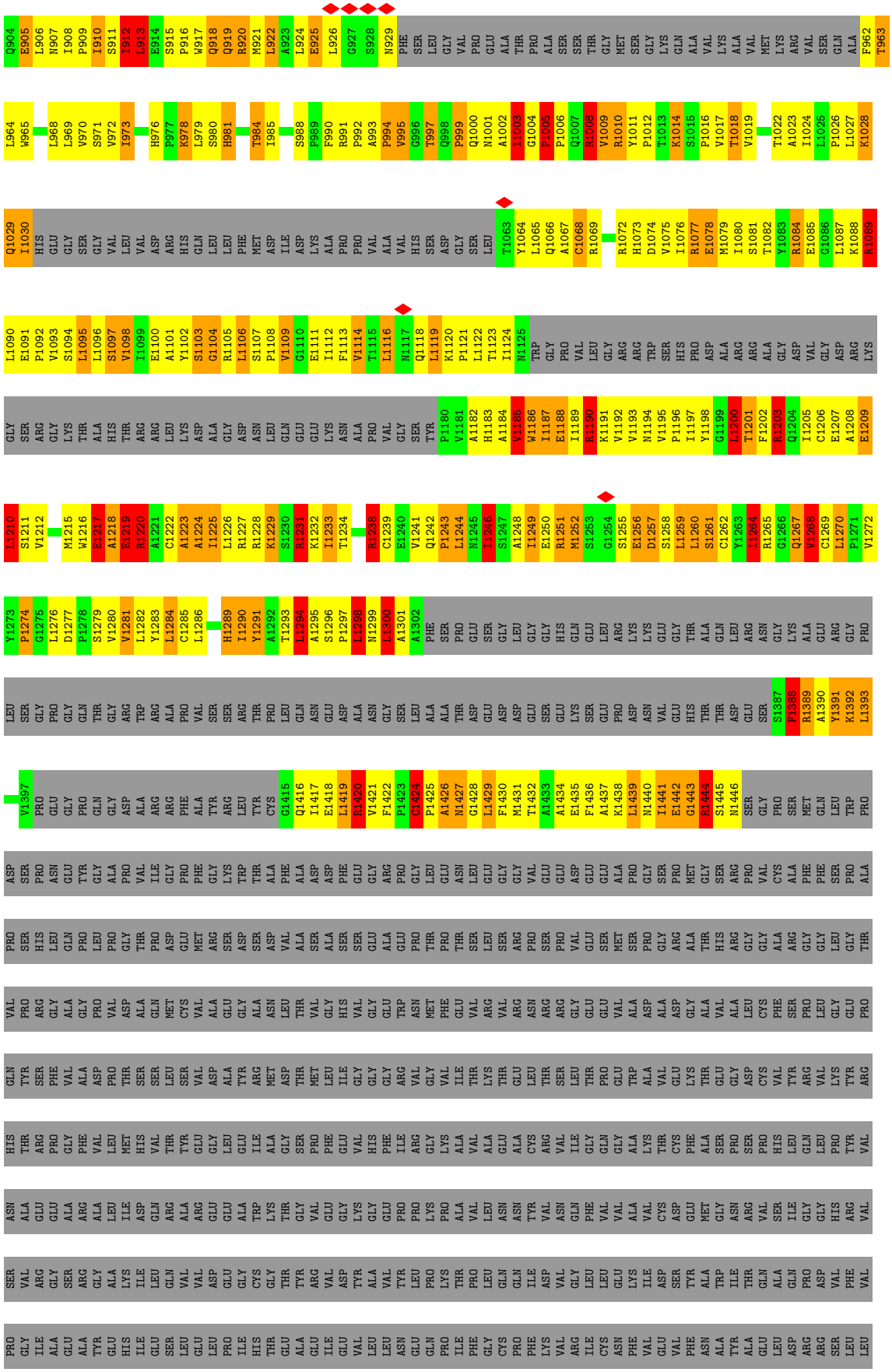

THR ALA GLN LEU ARG ASN GLY LYS ALA GLU ARG GLY PRO LEU SER GLY PRO GLY GLN THR GLY ARG TRP ARG ALA PRO VAL SER SER ARG THR PRO LEU GLN ASN GLU ASP ALA ASN GLY SER LEU ALA ALA THR ASP GLU ASP ASP GLU SER GLU LYS SER GLU PRO ASP ASN VAL GLU
HIS THR THR ASP GLU SER SER PHE ARG ALA TYR LYS LEU ARG SER PHE VAL PRO GLU GLY PRO GLN ALA GLU ARG ASP ALA ARG PHE ARG ALA TYR ARG LEU TYR CYS GLY GLN ILE GLU LEU ARG VAL PHE PRO CYS ARG ILE GLU ASP ALA ALA GLU PHE GLY ARG LEU ASN
ILE GLU GLY ARG SER ASN SER GLY PRO SER MET GLN LEU TRP PRO ASP SER PRO ASN GLU GLY TYR GLY ALA PRO VAL ILE GLY PRO PHE GLY LYS TRP THR ALA PHE ALA ASP PHE GLU GLY ARG PRO GLY LEU GLU ASN LEU GLU GLY GLY VAL GLU ASP GLU GLU PRO ALA LYS LEU
SER PRO MET GLY SER ARG PRO VAL CYS ALA PHE PHE SER PRO ALA PRO SER HIS LEU GLN PRO LEU PRO GLY THR PRO ASP GLU MET ARG SER ASP SER ASP VAL ALA SER ALA SER SER GLU GLY ALA GLU PRO THR PRO THR SER LEU SER ARG PRO SER PRO VAL GLU SER MET SER PRO
GLY ARG ALA THR HIS ARG GLY GLY GLY ALA ARG GLY GLY LEU GLY THR VAL PRO ARG G1579 M1587 R1611 E1617 Q1636 V1640 A1641 S1645 S1646 L1647 S1648 V1649 R1653 L1658 V1666 K1669 L1675 T1676 P1677 K1683 T1684 E1685 Y1690 H1696 P1699 M1704
E1709 S1716 V1720 H1721 F1722 I1723 R1724 I1735 G1738 S1745 V1755 E1759 E1771 A1772 G1776 V1777 E1778 G1779 K1780 G1781 E1782 P1783 A1787 V1788 L1789 N1790 N1791 Y1792 F1796 V1797 V1798 V1808 V1817 L1826 Q1827 V1828 V1838 L1844 P1845 P1848 L1849 Q1850
Q1851 I1852 L1857 I1866 P1891 I1892 H1893 T1894 I1898 E1899 V1900 L1901 E1904 Q1905 P1906 I1907 F1908 G1909 G1910 P1911 F1912 F1919 V1922 F1923 R1932 S1933 L1934 L1935 G1936 V1939 F1942 L1946 Y1951 T1955 L1958 K1968 Q1969 L1970 K1971 E1972 E1973 V1974 V1975 K1976 V1977
L1978 E1979 R1983 K1984 R1988 E1989 D1990 A1991 Q1992 K1993 R1994 E1995 A1996 E1997 E1998 G1999 G2000 C2001 T2002 Y2003 E2007 T2008 S2009 K2010 D2011 R2012 E2013 E2014 K2015 R2016 R2017 R2018 E2019 W2020 E2021 E2022 I2023 R2024 W2027 E2028 D2029 I2030 R2034 E2035 L2036 L2037 L2038 R2039 L2040 N2041 K2042 D2046 R2047 E2048
S2049 L2050 V2051 H2052 K2053 F2054 T2055 L2056 S2057 M2058 V2059 G2060 R2061 L2062 Q2063 L2064 T2065 E2066 M2067 C2068 N2069 L2070 R2071 I2072 L2073 A2074 E2075 H2076 H2077 N2078 M2079 Q2080 R2081 L2082 Q2083 Q2084 E2085 N2086 L2087 M2088 P2089 L2090 A2091 E2092 V2093 L2094 Q2095 A2096 Q2097 Y2098 I2099 S2100 L2101 F2102 R2103 Q2104 M2105 T2106 Q2107 E2108
I2109 VAL ALA LEU VAL LYS ASP VAL GLU ASP ASN LYS PHE GLN ASN LEU GLU ALA LEU LEU GLN ALA TYR ARG ARG ILE GLY VAL GLN LEU ARG GLN LEU ASP MET ASP GLU GLN ILE ILE GLU CYS VAL VAL GLU ILE THR THR ARG ARG GLN ALA GLY VAL LEU THR SER
ILE ALA ARG ALA LYS GLN GLU LYS ILE GLN GLU ILE GLU ASN VAL ILE ALA ALA LYS GLU GLN ALA LEU GLU ALA LYS LYS TYR ASP GLU HIS ALA LYS THR PHE GLN PRO LEU ASP MET ASP GLU VAL ARG ALA LEU ILE THR THR ARG ARG GLN ALA GLY VAL LEU GLN ARG
ASP ALA LEU SER LEU ARG GLN GLY ILE PHE GLY PRO LEU ILE VAL ALA ARG ALA THR GLY GLN HIS VAL PRO LYS ALA SER THR VAL VAL THR THR VAL LYS GLU TRP ARG SER CYS ASN VAL TYR ASP ILE HIS THR THR ILE LYS ARG LEU LEU LYS ASN CYS PRO ARG LEU LYS
HIS CYS LEU LYS GLU VAL PHE LEU TYR TYR ALA LYS VAL SER GLU ALA ASN VAL THR ASP LEU GLN SER ASP GLY LEU PRO VAL GLY LEU PRO GLN LEU LEU SER PHE LEU ARG PHE CYS ASN ASP ALA ARG VAL ASP GLU HIS LEU LEU ALA ASP ARG THR GLU LEU GLN ASP LEU GLU HIS
LYS PHE SER ILE GLU PRO ASP THR GLY ARG PHE LEU LEU ARG VAL ILE PRO VAL PHE LEU TRP LEU PRO CYS LEU ARG GLU GLU LEU ALA TYR LEU ASP LEU LEU HIS VAL ILE CYS ARG GLU ALA LEU ASP LYS GLY GLU GLN ALA PRO ARG GLU LEU ARG VAL ALA LEU ASP
PRO SER ARG LEU THR ALA PHE HIS PHE PHE CYS ARG ILE SER THR SER VAL ILE MET GLU SER ALA ALA ALA GLY ASP VAL LEU SER THR THR ALA GLU SER ARG GLU SER VAL ASN THR LYS HIS SER ILE TRP
THR TYR ALA HIS GLU ARG LEU PRO GLY ASP VAL PHE HIS LEU LYS LEU GLU PRO VAL GLU HIS LEU PHE VAL PHE TYR SER GLU LEU SER ALA GLN PRO ALA LEU GLY ARG ALA ARG ALA GLU ALA THR LEU PRO THR THR ALA SER LYS GLY SER VAL ALA PRO ALA LYS LYS GLY ASP
GLY ALA GLU THR LYS ARG GLY GLN GLU PRO PRO LYS ALA SER GLN VAL THR GLY ARG ARG PHE VAL VAL ALA GLN THR SER LEU GLU GLU THR GLY ALA GLU HIS VAL SER THR ARG ALA TRP VAL SER LEU LEU GLY VAL LEU ILE GLN MET TRP
ARG GLU PHE SER VAL ILE ASP CYS ASP ASP SER ARG GLY LYS LYS ASN ALA VAL ARG LYS THR ALA ASP SER GLN ASP PRO GLY GLY SER ARG GLY ASP THR GLY VAL PRO ASN ALA LYS ASP SER ALA ALA GLU GLU PRO



• Molecule 6: FLM1, TGME49_271780

Chain FD: 7% 85%


MET GLU ALA GLY ARG PRO LEU SER LEU GLY ALA ALA PRO PRO GLY LEU LEU GLY PRO ARG GLN ARG PRO SER SER PHE LEU LEU PRO ARG THR SER PRO VAL HIS LEU VAL HIS PRO SER PRO SER SER SER VAL SER SER LEU TYR ARG GLY HIS GLY LYS ARG GLY VAL ALA ASP
GLU GLY SER CYS ASP GLY ASP PRO GLU ASP THR ARG VAL SER VAL ASP SER SER GLY THR GLY THR ASP ASP GLU GLY GLU THR ASP GLU GLU PHE ASP SER ASN ARG THR ARG ILE SER THR PHE GLN ARG ILE THR ASN MET ARG HIS ARG SER CYS PRO PRO ALA LEU HIS SER PRO
LEU SER ASP VAL ILE VAL GLU LEU SER SER ASP GLY ALA THR ARG LYS PRO ARG HIS VAL TYR PHE ALA PRO SER SER SER ASP GLU SER SER PRO LYS SER SER VAL SER ALA ALA ALA SER GLN GLU PRO ALA ALA ASP ASP SER SER ASP ALA HIS PRO VAL SER HIS ALA ARG GLY
ARG HIS ALA CYS ARG ALA GLY SER ALA PHE PRO TRP ARG SER SER SER SER ASP CYS SER SER SER ALA ALA SER PHE SER PRO SER SER GLY SER SER MET SER ASP ALA SER THR LEU ALA ALA GLY ALA THR GLN LYS PRO PHE ASP LEU HIS ALA GLN SER PRO GLY GLY ASP SER TRP ARG
LEU ALA GLU SER ALA VAL SER ARG PRO SER LYS ALA LEU LEU ARG PRO PRO PRO ALA ALA THR ARG SER PRO VAL GLY ILE ALA ARG PRO GLY CYS MET LYS LYS PRO SER LEU ASN PRO SER CYS LEU SER SER PHE SER GLY GLY HIS VAL ALA SER SER LEU GLY PRO PRO PRO GLY
LEU ARG SER ALA ALA SER SER THR SER LEU ALA CYS MET GLN LEU PRO GLU LEU ARG CYS GLU THR ARG ARG LEU ARG VAL ARG PHE ALA GLU THR THR VAL HIS ALA SER GLY ALA GLU GLU THR ASP LYS GLY THR PRO HIS MET SER PRO LYS GLU SER LEU MET SER PRO PRO THR
SER PRO LEU GLN SER PRO PRO SER GLN PRO PRO SER GLN SER PRO ASN SER PRO SER GLN SER PRO ARG GLN SER PRO SER PRO SER PRO ARG GLN SER PRO SER PRO SER PRO


Q904 E905 L906 N907 I908 P909 I910 S911 I912 L913 E914 S915 P916 W917 Q918 Q919 R920 M921 L922 A923 L924 E925 L926 G927 S928 N929 PHE SER LEU GLY VAL PRO GLU ALA THR PRO ALA SER SER THR GLY MET SER GLY LYS GLN ALA VAL LYS ALA VAL MET LYS ARG VAL SER GLN ALA F962 T963
L964 W965 L968 L969 V970 S971 V972 I973 H976 P977 K978 L979 S980 H981 T984 I985 S988 P989 F990 R991 P992 A993 P994 V995 G996 T997 Q998 P999 Q1000 N1001 A1002 I1003 G1004 P1005 P1006 Q1007 R1008 V1009 R1010 Y1011 P1012 T1013 K1014 S1015 P1016 V1017 T1018 V1019 T1022 A1023 I1024 L1025 P1026 L1027 K1028
Q1029 I1030 HIS GLU GLY SER GLY VAL LEU VAL ASP ARG HIS GLN LEU LEU PHE MET ASP ILE ASP LYS ALA PRO PRO VAL ALA VAL HIS SER ASP GLY SER LEU T1063 Y1064 L1065 Q1066 A1067 C1068 R1069 R1072 H1073 D1074 V1075 I1076 R1077 E1078 M1079 I1080 S1081 T1082 Y1083 R1084 E1085 G1086 L1087 K1088 R1089
L1090 E1091 P1092 V1093 S1094 L1095 L1096 S1097 V1098 I1099 E1100 A1101 Y1102 S1103 G1104 R1105 L1106 S1107 P1108 V1109 G1110 E1111 I1112 F1113 V1114 T1115 L1116 N1117 Q1118 L1119 K1120 P1121 L1122 T1123 I1124 N1125 TRP GLY PRO VAL LEU GLY ARG ARG TRP SER HIS PRO ASP ALA ARG ALA GLY ASP VAL GLY ARG LYS
GLY SER ARG GLY LYS THR ALA HIS THR ARG ARG ARG LEU LYS ASP ALA GLY ASP ASN LEU GLN GLU GLU LYS ASN ALA PRO VAL GLY SER TYR P1180 V1181 A1182 H1183 A1184 V1185 W1186 I1187 E1188 I1189 R1190 K1191 V1192 V1193 N1194 V1195 P1196 I1197 Y1198 G1199 L1200 T1201 F1202 R1203 Q1204 I1205 C1206 E1207 A1208 E1209
L1210 S1211 V1212 M1215 W1216 E1217 A1218 E1219 R1220 A1221 C1222 A1223 A1224 I1225 L1226 R1227 R1228 K1229 S1230 R1231 K1232 I1233 T1234 R1238 C1239 E1240 V1241 Q1242 P1243 L1244 N1245 I1246 S1247 A1248 I1249 E1250 R1251 M1252 S1253 G1254 S1255 E1256 D1257 S1258 L1259 L1260 S1261 C1262 Y1263 T1264 R1265 G1266 Q1267 V1268 C1269 L1270 P1271 V1272
Y1273 P1274 G1275 L1276 D1277 P1278 S1279 V1280 V1281 L1282 Y1283 L1284 C1285 L1286 H1289 I1290 Y1291 A1292 T1293 L1294 A1295 S1296 P1297 L1298 N1299 L1300 A1301 A1302 PHE SER PRO GLU SER GLY LEU GLY GLY HIS GLN GLU LEU ARG LYS LYS GLU GLY THR ALA GLN LEU GLU ASP PRO LYS ALA GLU PRO GLY
LEU SER GLY PRO GLY GLN THR GLY ARG TRP ARG ALA PRO VAL SER SER ARG LEU THR PRO LEU GLN ASN GLU ASP ALA ASN GLY SER LEU ALA ALA THR ASP GLU ASP ASP GLU SER GLU LYS SER GLU PRO ASP ASN VAL GLU HIS THR THR GLU ASP GLU SER S1387 F1388 R1389 A1390 Y1391 K1392 L1393
V1397 PRO GLU GLY PRO GLN GLY ASP ALA ARG PHE ALA TYR ARG LEU TYR CYS G1415 Q1416 I1417 E1418 L1419 R1420 V1421 F1422 P1423 C1424 P1425 A1426 N1427 G1428 L1429 F1430 M1431 T1432 A1433 A1434 E1435 F1436 A1437 K1438 L1439 N1440 I1441 E1442 G1443 R1444 S1445 N1446 SER GLY PRO SER MET GLN LEU TRP PRO
ASP SER PRO ASN GLU TYR GLY ALA PRO VAL ILE GLY PRO PHE GLY LYS TRP THR ALA PHE GLU GLY ARG PRO GLY LEU GLU ASN LEU GLU GLU GLY GLY VAL GLU GLU GLU ASP GLU GLU ALA PRO GLY SER PRO MET GLY SER ARG PRO VAL CYS ALA PHE PHE GLY PRO PHE
PRO SER HIS LEU GLN PRO LEU PRO GLY THR PRO ASP GLU MET ARG SER ASP SER ASP VAL ALA SER ALA SER SER GLU ALA GLU THR PRO THR PRO THR SER LEU SER ARG PRO SER PRO VAL GLU SER MET SER PRO GLY ALA THR HIS ARG GLY GLY ALA ARG GLY GLY PRO GLY THR
VAL PRO ARG GLY ALA GLY PRO VAL ALA GLN MET CYS VAL ALA GLU GLY ALA ASN LEU THR VAL GLY HIS VAL GLY GLU TRP ASN MET PHE GLU VAL ARG VAL ARG ASN ARG ARG GLY GLU GLU SER GLU GLU VAL ALA ASP ALA ASP GLY ALA VAL PHE CYS PHE SER PRO LEU GLY GLU PRO
GLN TYR SER PHE VAL ALA ASP PRO THR SER SER LEU GLY ILE GLY GLY GLY ARG VAL GLY VAL ILE ILE THR LYS THR GLU LEU THR SER LEU THR PRO GLU TRP ALA VAL GLU LYS THR GLU VAL CYS VAL TYR ARG VAL TYR ARG
HIS THR ARG PRO GLY PHE VAL LEU MET HIS VAL THR TYR GLU GLY GLU LEU GLU ILE ALA GLY SER PRO PHE GLU VAL HIS PHE ILE ARG GLY LYS ALA VAL ALA ALA GLU GLY ALA CYS ARG VAL ILE GLY GLN GLY PHE ALA SER PRO SER PRO HIS LEU GLN LEU PRO TYR PRO
ASN ALA GLU GLU ALA ARG GLU GLU ALA TRP LYS THR GLY VAL GLU GLY LYS GLY GLU PRO PRO LYS PRO ALA VAL LEU ASN ASN TYR VAL ASN GLN PHE VAL ALA ALA VAL CYS ASP GLU MET GLY GLY ASN ARG VAL GLY GLY LEU HIS ASP PRO
SER VAL ARG GLY SER ARG VAL GLU GLY GLN PRO LYS THR PRO LEU GLN GLN ASN GLY PRO ILE ASP VAL GLY LEU LEU GLU LYS ASP SER TYR ALA TRP ILE THR ASP ARG
PRO GLY ILE ALA GLU ALA GLU ILE GLU VAL LEU ASN GLU PRO ILE PHE GLY CYS PRO PHE LYS VAL ARG ILE CYS ASN PHE VAL GLU VAL ASN ALA TYR ARG ARG SER LEU

GLY GLN GLN VAL CYS ALA PHE GLU ARG VAL LEU GLU LEU GLU GLY ASN TYR GLU GLU ALA THR SER MET LEU TRP LYS VAL GLN ASP MET ALA ASP GLU LYS GLN LEU LYS GLU GLU VAL VAL LYS VAL LEU GLU ASN LEU VAL ARG LYS GLN LEU GLU ARG GLU ASP ALA GLN LYS ARG GLU

ALA GLU GLU GLY GLY CYS THR TYR LEU LEU GLU GLU GLU THR SER LYS ASP ARG GLU GLU LYS ARG ARG GLU VAL GLU GLU THR GLU GLU ILE ARG SER GLN TRP GLU ASP ILE HIS LEU GLU LEU ARG GLU LEU LEU LEU ARG LEU ASN LYS ASN CYS THR ASP ARG GLU SER LEU VAL HIS LYS PHE THR

LEU SER MET VAL GLY ARG LEU GLN LEU THR GLU MET CYS ASN LEU ARG ILE LEU ALA GLU GLY HIS HIS ASN MET GLN ARG LEU GLN GLN GLU ASN LEU MET PRO LEU ALA GLU VAL LEU GLN ALA GLN GLU ILE VAL ALA ARG ASP LYS GLN

VAL GLU ASP ASN LYS PHE GLN ASN LEU GLU ALA LEU LEU GLN ALA TYR ARG ARG ILE GLY VAL GLN LEU ARG ARG LEU HIS ARG TYR GLN LEU ALA ASP GLN MET ASP GLN ILE ILE GLU CYS VAL VAL GLU GLU ILE GLU GLN GLN ARG LEU ALA SER ILE ALA ARG ALA LYS GLN GLU

LYS ILE GLN GLU ILE GLU ASN VAL ILE ALA ALA ALA LYS GLU GLN ALA LEU GLU ALA GLU LYS LYS LYS LYS TYR ASP GLU HIS ALA LYS THR PHE GLN PRO LEU ASP MET ASP GLU VAL ARG ALA LEU ILE LEU THR THR ARG ARG GLN ALA GLY VAL GLN THR GLU ASP ALA LEU SER LEU ARG GLN

GLY ILE PHE GLY PRO LEU ILE VAL ALA ARG ALA THR GLY GLN HIS VAL PRO LYS ALA SER THR VAL VAL THR THR VAL LYS LYS GLU TRP ARG SER CYS ASN VAL TYR ASP ILE HIS THR THR ILE LYS ARG LEU LEU LYS ASN CYS PRO ARG LEU LYS HIS CYS LEU LYS GLU VAL PHE

LEU TYR TYR ALA LYS VAL SER GLU ALA ASN VAL THR ASP LEU GLN SER ASP GLY LEU PRO VAL GLY LEU PRO GLN LEU SER PHE LEU ARG PHE CYS ASN ASP ALA ARG VAL ASP GLU HIS LEU LEU ALA ASP ARG THR GLU LEU GLN ASP LEU PHE GLU LYS PHE SER ILE GLU PRO ASP

THR GLY ARG ILE ARG ALA ASP GLY PHE LEU ARG VAL ILE PRO VAL PHE LEU TRP LEU PRO CYS LEU ARG GLU LEU ALA TYR LEU ASP LEU LEU HIS VAL ILE CYS ARG GLU ALA LEU ASP LYS GLY GLU ALA ASP ARG THR GLU LEU GLN GLU ASP LEU PHE GLU LYS HIS PRO SER ARG LEU THR ALA PHE

HIS PHE PHE CYS ARG ALA ARG PHE LEU PRO LEU TYR ASP MET LEU TYR ASN ASN ASP ASP PHE ARG ILE SER THR SER VAL ILE MET GLU SER ALA ALA GLY ASP VAL LEU SER THR THR ALA GLU SER ARG GLU SER ASN THR LYS HIS SER ILE TRP THR TYR ALA HIS GLU ARG LEU

PRO GLY ASP VAL PHE ALA MET LEU LYS LEU GLU GLU PRO VAL GLU HIS LEU PHE VAL PHE TYR SER GLU LEU SER ALA GLN PRO ALA LEU GLY ARG ALA ARG GLU GLU ALA THR LEU PRO THR ALA SER LYS GLY SER VAL ALA PRO ALA LYS LYS GLY ASP GLY ALA GLU THR LYS ARG PRO

PRO LYS ALA SER PRO LYS GLY GLN GLU PRO GLN ARG PRO LYS PRO LYS ALA GLN VAL THR GLY ARG ARG PHE VAL ALA GLN THR SER LEU GLU GLU GLU THR GLY GLU ALA GLU HIS VAL SER THR ARG ALA TRP VAL SER LEU GLY VAL LEU ILE GLN MET TRP ARG GLU PHE SER VAL ILE PRO

GLY PHE ILE ASP CYS ASP ALA ALA MET SER ILE ALA ARG VAL ALA ILE GLY GLY SER ARG GLY LYS LYS ASN ALA VAL ARG LYS THR ALA ASP SER GLN ASP PRO GLY GLY GLY ASP THR GLY VAL PRO ASN ALA LYS ASP SER ALA ALA GLU GLU PRO GLU PHE ARG ARG LEU LEU SER

MET PRO GLU ILE GLN GLY ASP THR ARG ARG GLY PRO ASN GLY LYS LEU ARG LYS ALA ALA PRO SER PRO GLU ALA GLU VAL GLY LEU TYR PHE PRO ASN PHE VAL GLU ALA VAL VAL ASN THR VAL CYS GLU CYS THR ALA ARG ALA LEU VAL GLN PRO GLU GLY ASP SER SER VAL PRO

PRO GLY SER ARG GLU ALA THR SER ALA GLU ILE LYS LYS ALA PHE PHE LEU LEU HIS LEU PHE GLY ILE ASN ASP VAL SER ARG ILE LEU LEU LEU LEU THR ARG ARG PRO LEU ARG GLU ALA VAL ARG THR PRO ALA LYS ASP GLU THR GLN ASN SER GLY VAL PRO ASN ALA PRO PRO

GLY THR

- Molecule 6: FLM1, TGME49_271780

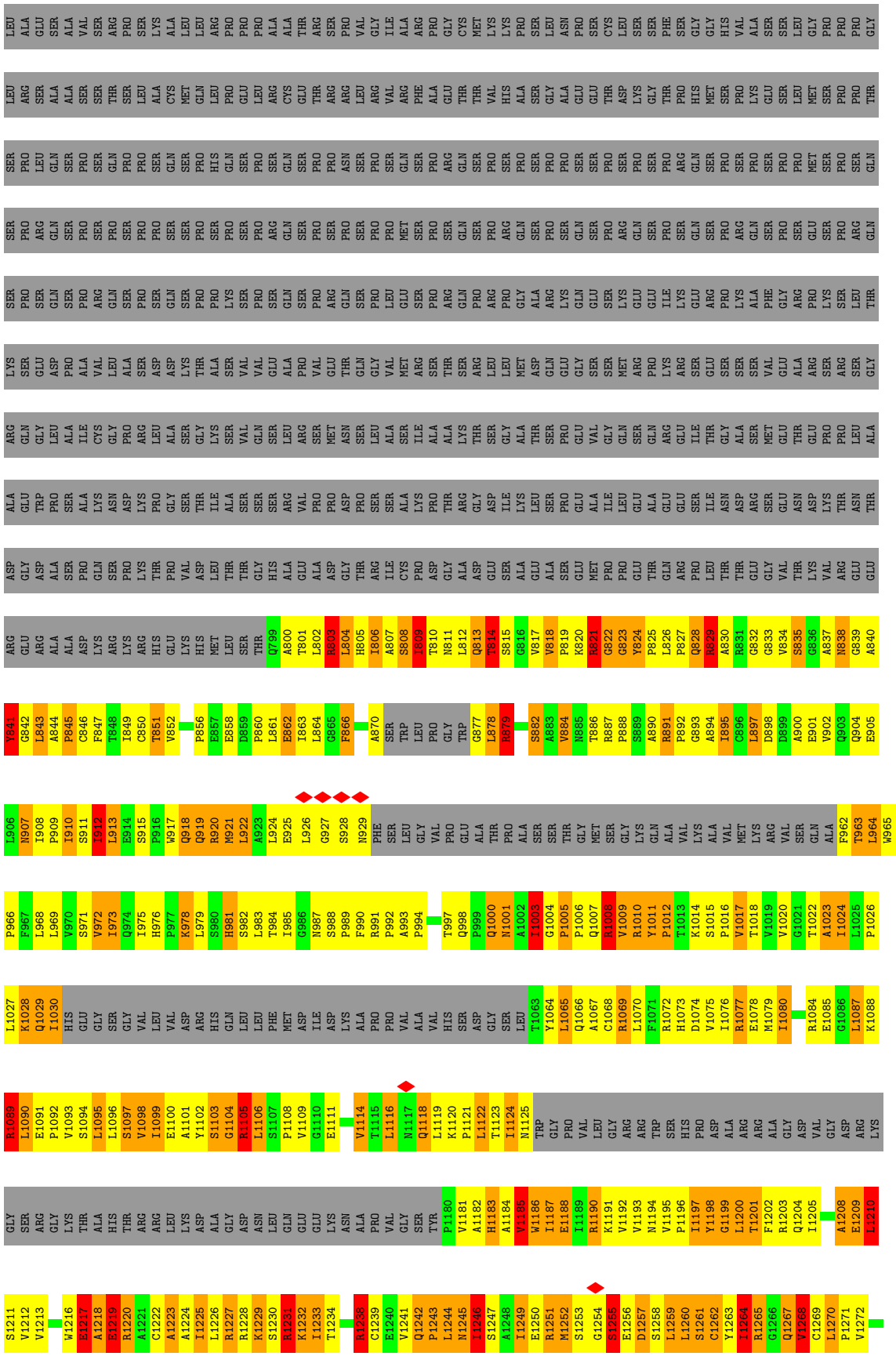
Chain FE: 7% 85%

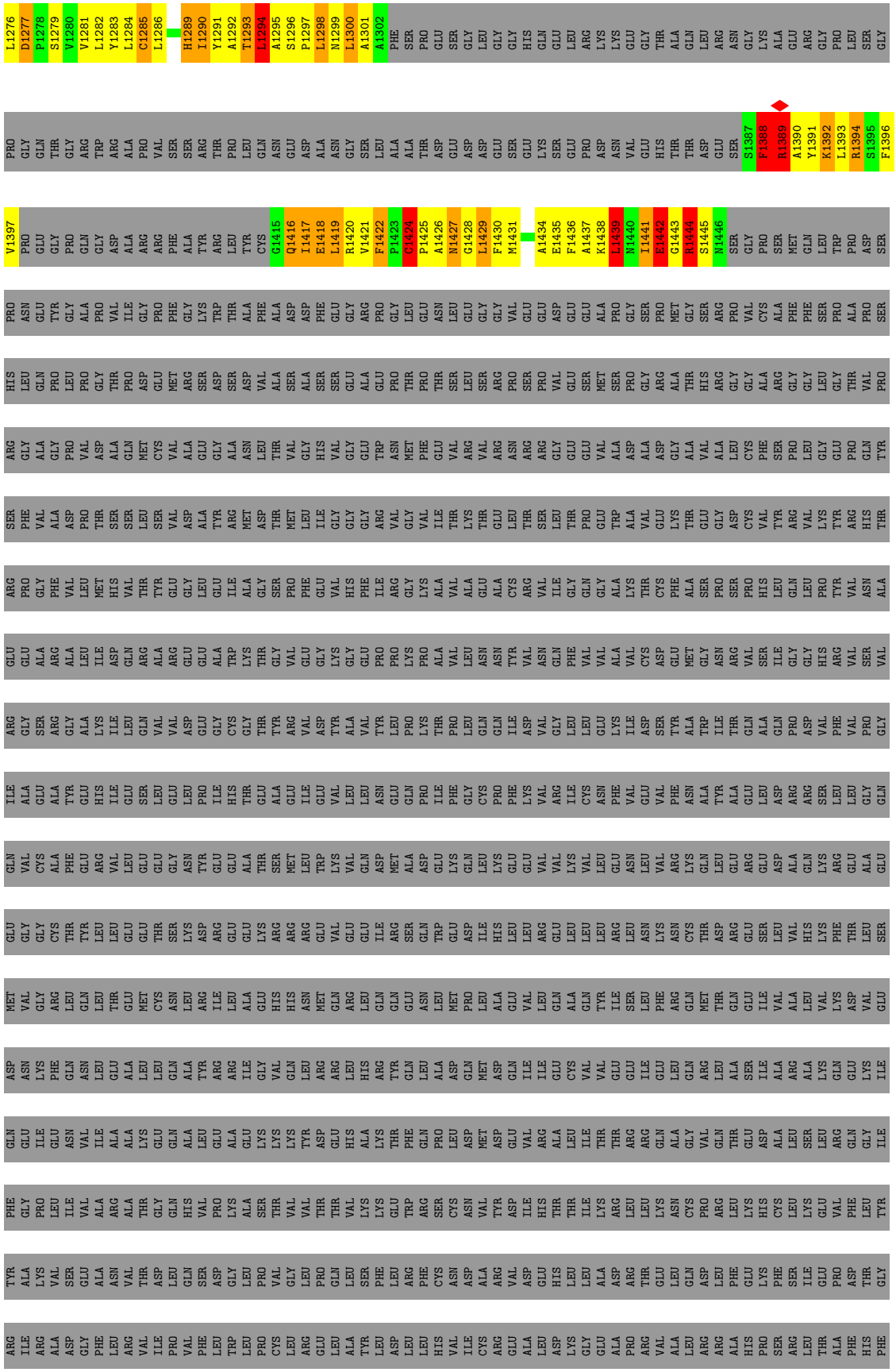
MET GLU ALA GLY ARG PRO LEU SER LEU GLY ALA ALA PRO PRO GLY LEU LEU GLY PRO ARG ARG GLN ARG PRO PRO SER SER PHE LEU LEU PRO ARG THR SER PRO VAL HIS LEU VAL HIS PRO SER PRO SER SER SER SER VAL SER SER LEU TYR ARG GLY HIS GLY LYS ARG GLY VAL ALA ASP

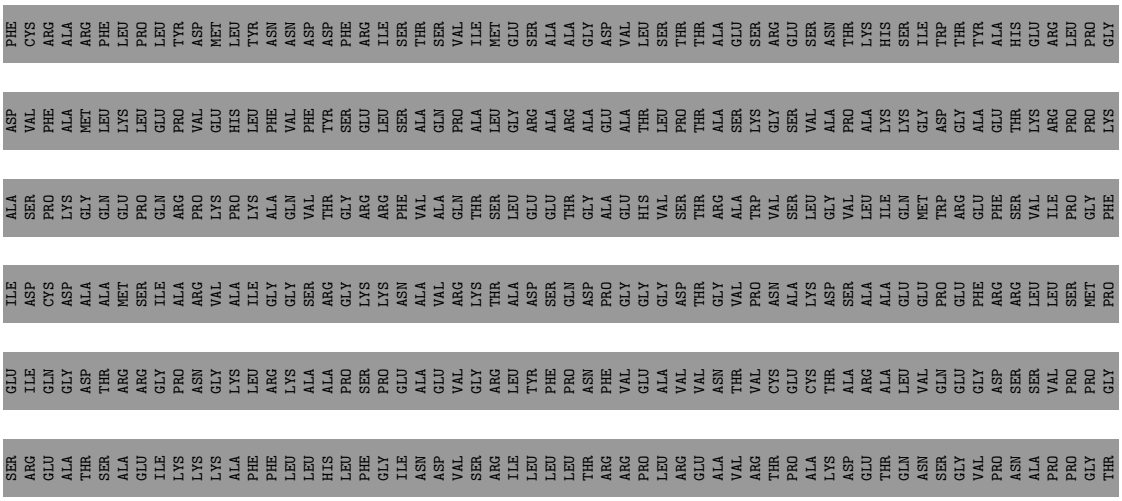
GLU GLY SER CYS ASP GLY ASP PRO GLU GLY ASP THR ARG VAL SER VAL ASP SER SER GLY THR GLY THR ASP ASP GLU GLY GLU PHE ASP SER ASN ARG THR ARG ILE SER THR PHE GLN ARG ILE THR ASN MET ARG HIS ARG SER CYS PRO PRO ALA LEU HIS SER PRO

LEU SER ASP VAL ILE VAL GLU ASP GLU LEU SER SER ASP GLY ALA THR ARG LYS PRO ARG HIS VAL TYR PHE ALA PRO SER SER SER ASP GLU SER SER PRO LYS SER SER VAL SER ALA ALA SER GLN GLU PRO ALA ASP ASP SER SER SER ASP ALA ALA HIS PRO VAL SER HIS ALA SER GLY

ARG HIS ALA CYS ARG ALA ALA PHE PRO TRP ARG SER SER SER SER ASP CYS SER SER ALA ALA ALA SER PHE SER PRO SER GLY SER SER MET SER ASP ALA SER THR LEU ALA ALA GLY ALA THR GLN LYS PRO PHE ASP LEU HIS ALA GLN SER PRO GLY GLY ASP SER TRP ARG

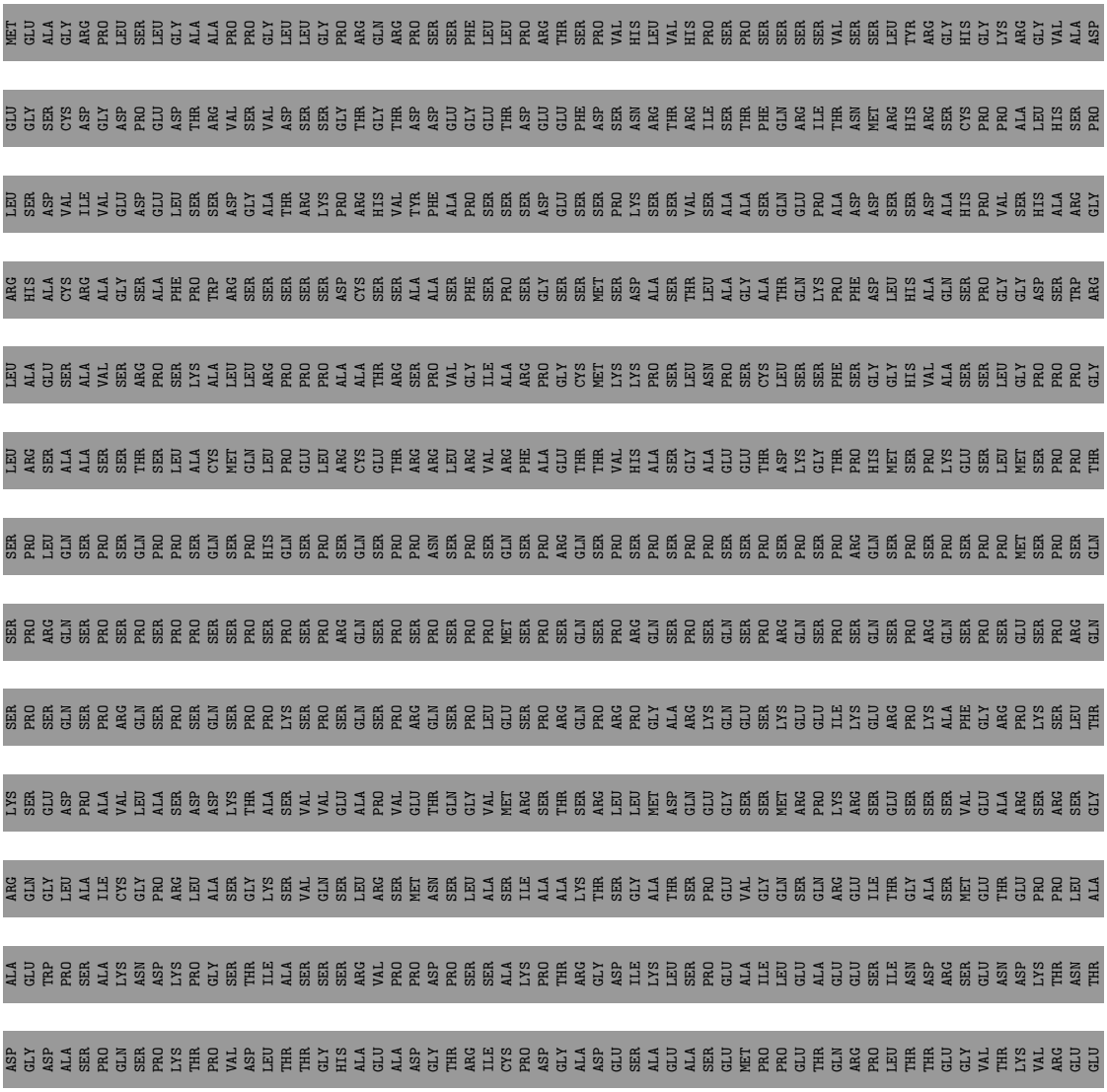


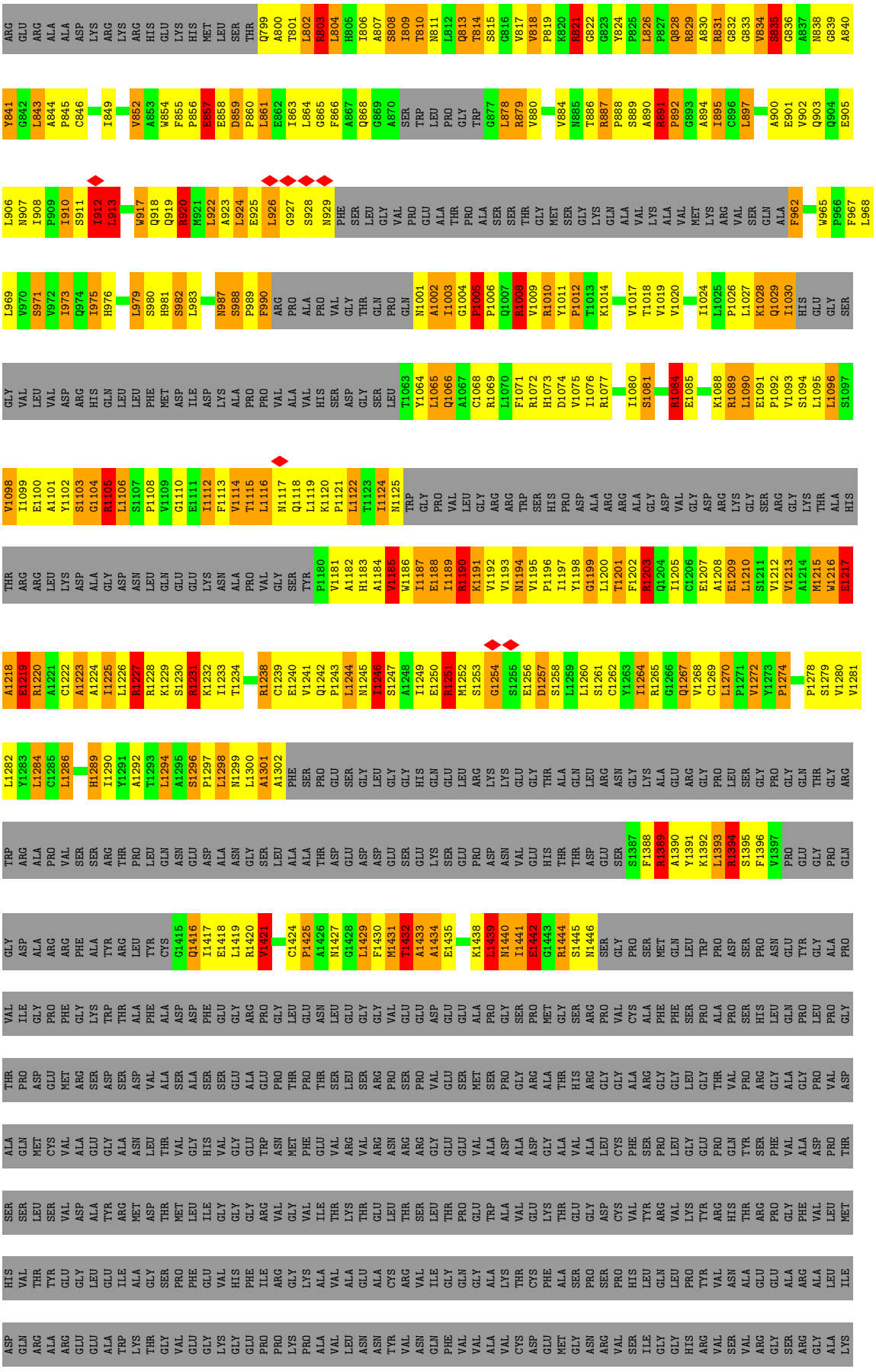

L1276 D1277 P1278 S1279 V1280 V1281 L1282 Y1283 L1284 C1285 L1286 H1289 I1290 Y1291 A1292 T1293 L1294 A1295 S1296 P1297 L1298 N1299 L1300 A1301 A1302 F1387 F1388 R1389 A1390 Y1391 K1392 L1393 R1394 S1395 F1396
V1397 G1415 Q1416 I1417 E1418 L1419 R1420 V1421 F1422 P1423 C1424 P1425 A1426 N1427 G1428 L1429 F1430 M1431 A1434 E1435 F1436 A1437 K1438 L1439 N1440 I1441 E1442 G1443 R1444 S1445 N1446

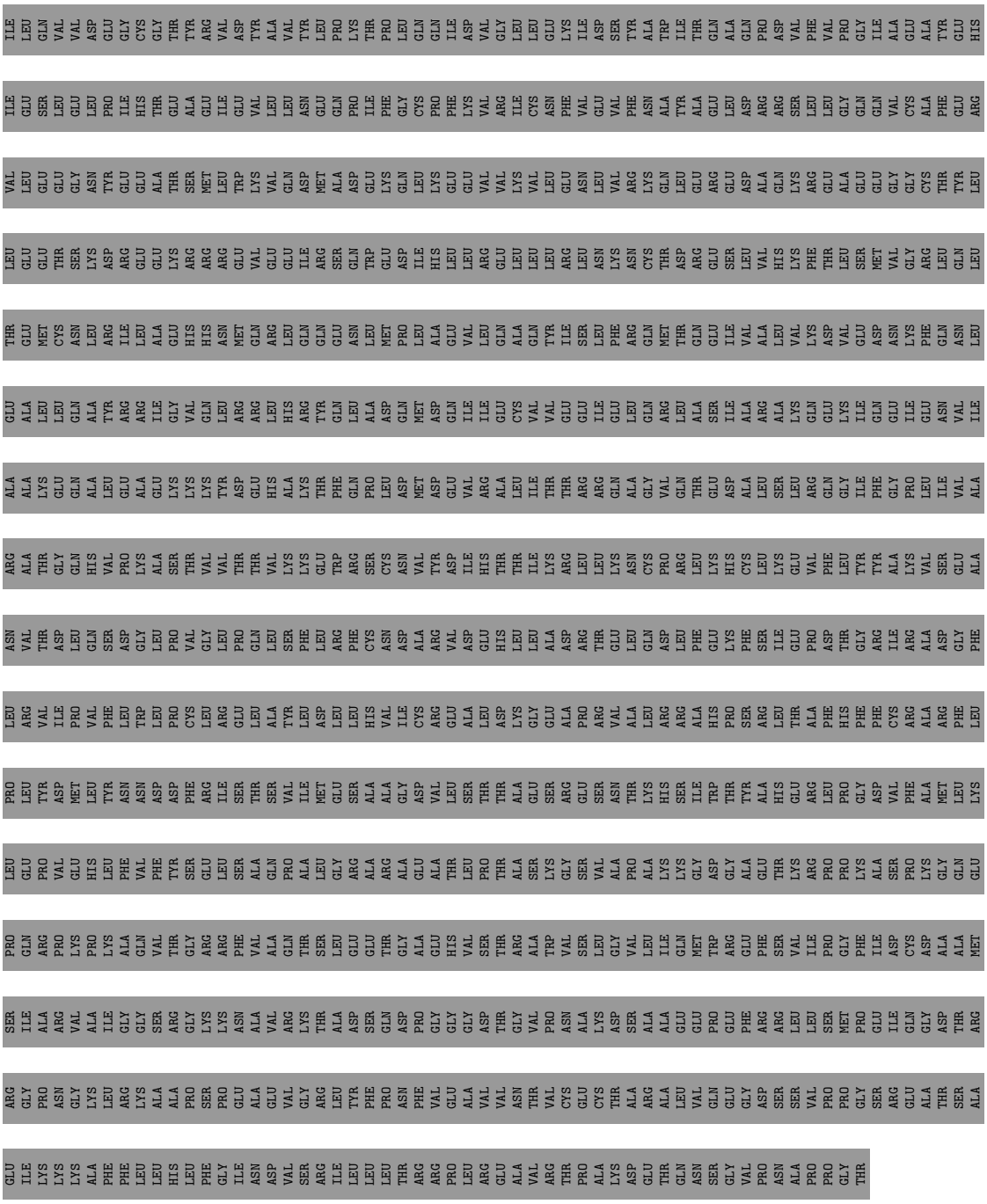


• Molecule 6: FLM1, TGME49_271780

Chain FF: 7% 85%

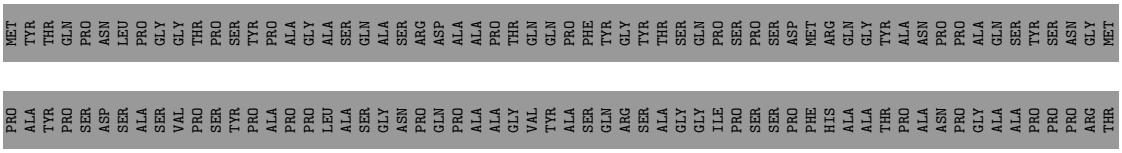

MET GLU ALA GLY ARG PRO LEU SER LEU GLY ALA ALA PRO PRO GLY LEU LEU GLY PRO ARG GLN ARG PRO SER SER PHE LEU LEU PRO ARG THR SER PRO VAL HIS LEU VAL HIS PRO SER PRO SER SER SER VAL SER SER LEU TYR ARG GLY HIS GLY LYS ARG GLY VAL ALA ASP
GLU GLY SER CYS ASP GLY ASP PRO GLU ASP THR ARG VAL SER VAL ASP SER SER GLY THR GLY THR ASP ASP GLU GLY GLU THR ASP GLU GLU PHE ASP SER ASN ARG THR ARG ILE SER THR PHE GLN ARG ILE THR ASN MET ARG HIS ARG SER CYS PRO PRO ALA LEU HIS SER PRO
LEU SER ASP VAL ILE VAL GLU ASP GLU LEU SER SER SER ARG LYS PRO ARG HIS VAL TYR PHE ALA PRO SER SER SER ASP GLU SER SER PRO LYS SER SER VAL SER ALA ALA SER GLN GLU PRO ALA ASP ASP SER SER ASP HIS PRO VAL SER HIS ALA ARG GLY
ARG HIS ALA CYS ARG ALA GLY SER ALA PHE PRO TRP ARG SER SER SER SER SER ASP CYS SER SER ALA ALA ALA SER PHE SER PRO SER GLY GLY SER SER MET SER ASP ALA SER THR LEU ALA GLY ALA THR GLN LYS PRO PHE SER ASP LEU HIS ALA GLN SER PRO PRO GLY GLY ASP SER TRP ARG
LEU ALA GLU SER ALA VAL SER ARG PRO SER LYS ALA LEU LEU ARG PRO PRO PRO ALA ALA THR ARG SER PRO VAL GLY ILE ALA ARG PRO GLY CYS MET LYS LYS PRO SER LEU LEU ASN PRO SER CYS LEU SER SER PHE SER GLY GLY HIS VAL ALA SER SER LEU LEU GLY PRO PRO PRO GLY
LEU ARG SER SER THR SER LEU LEU ALA CYS MET GLN LEU PRO GLU LEU ARG CYS GLU THR ARG ARG LEU ARG VAL ARG PHE ALA GLU THR THR VAL HIS ALA SER GLY ALA GLU GLU THR ASP LYS GLY LYS GLY THR PRO PRO HIS MET SER PRO LYS GLU SER LEU MET SER PRO PRO THR
SER PRO LEU GLN SER PRO PRO SER GLN SER PRO HIS GLN SER PRO SER GLN SER PRO SER PRO SER PRO ARG GLN SER PRO SER PRO SER PRO

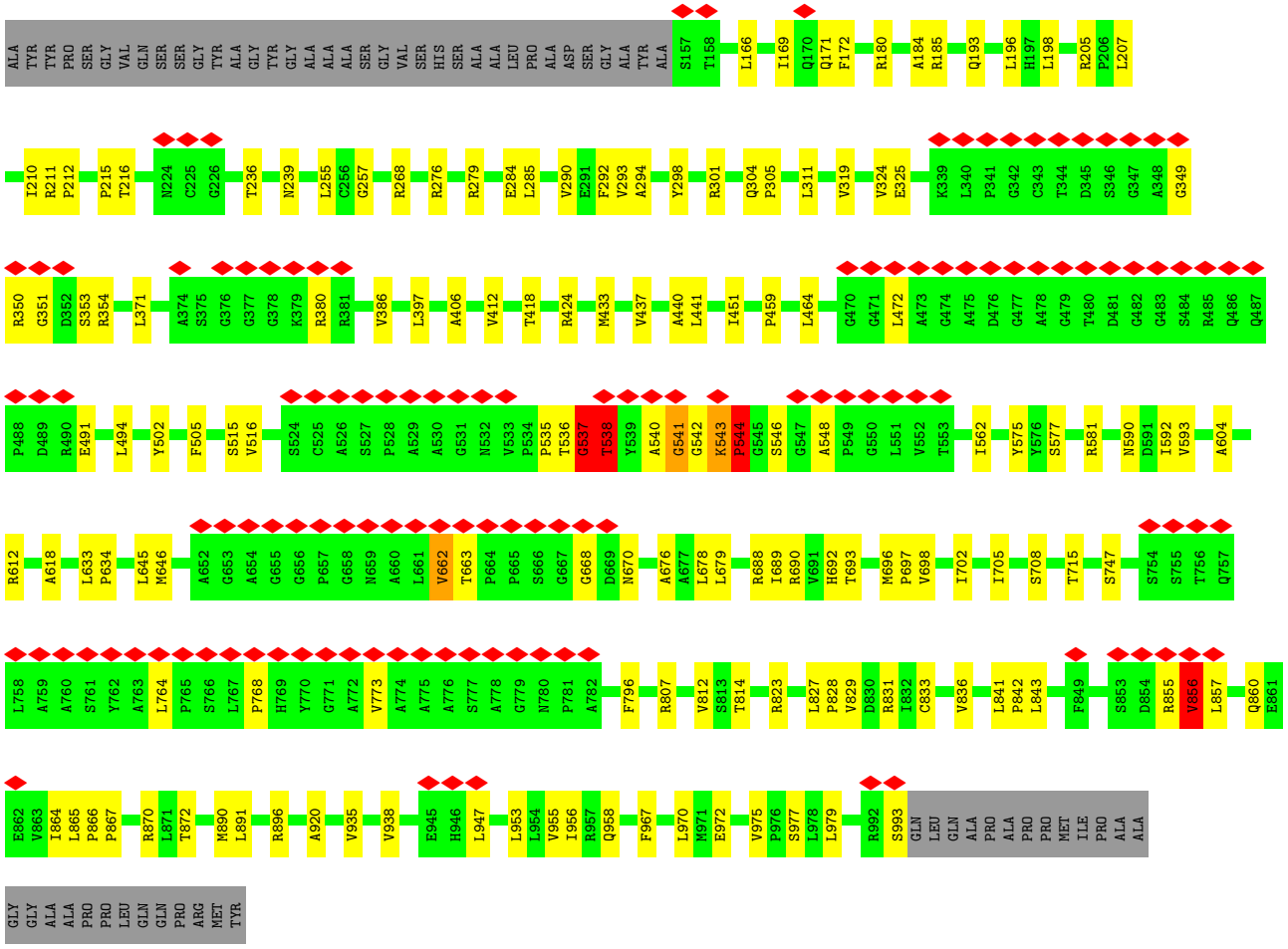




• Molecule 7: Transport protein Sec24

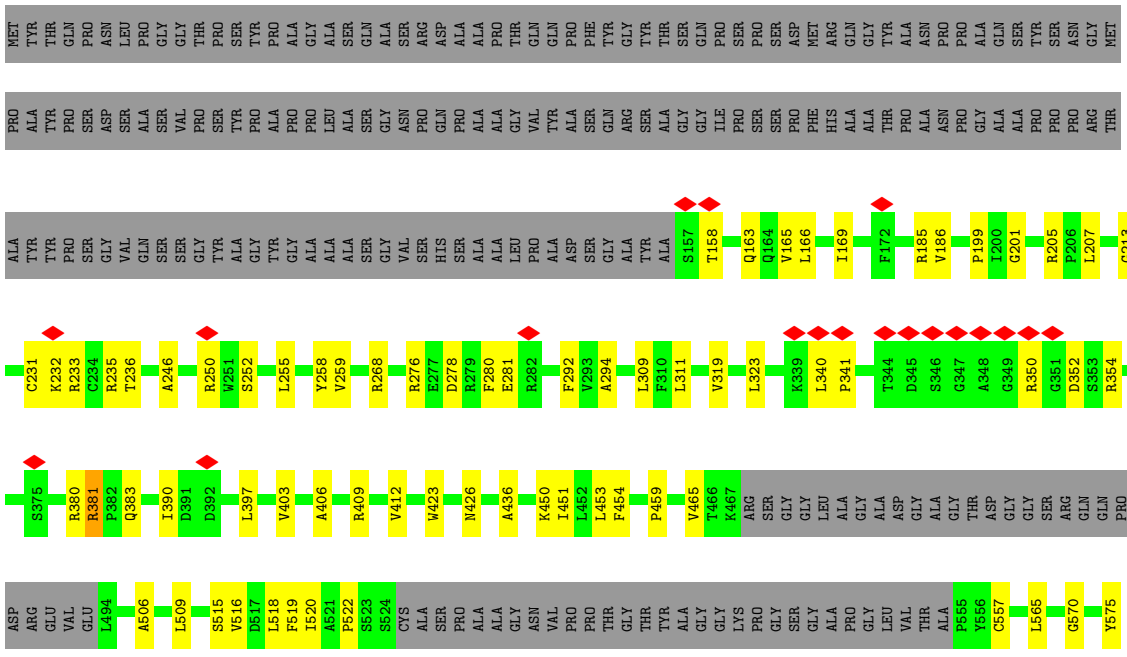
Chain GA:

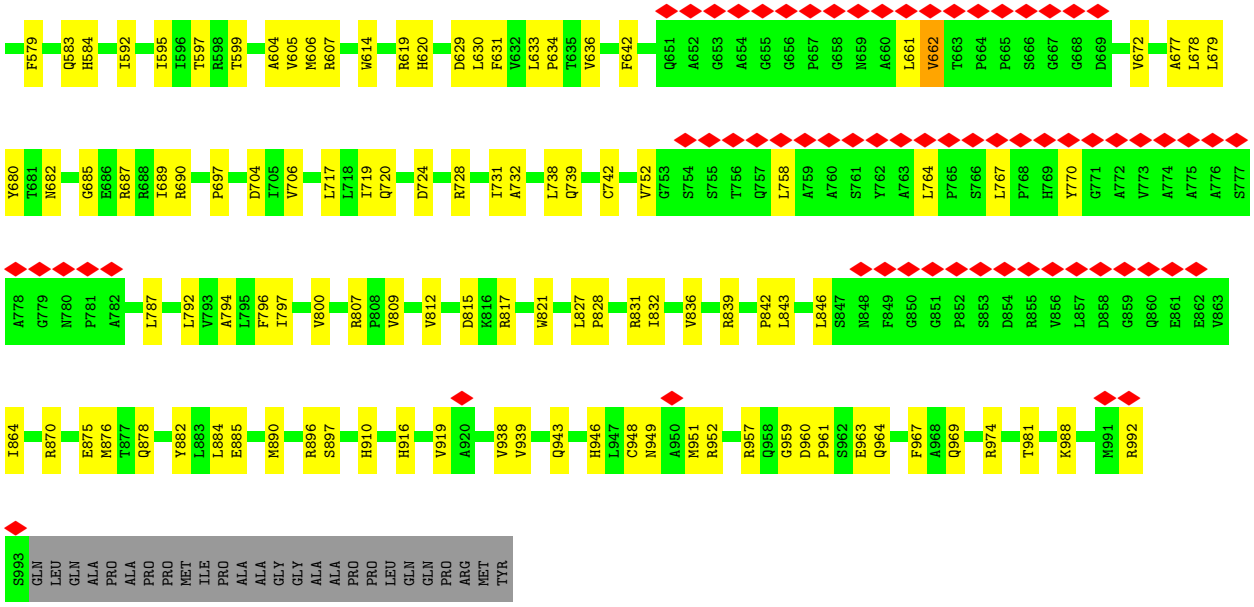




• Molecule 7: Transport protein Sec24

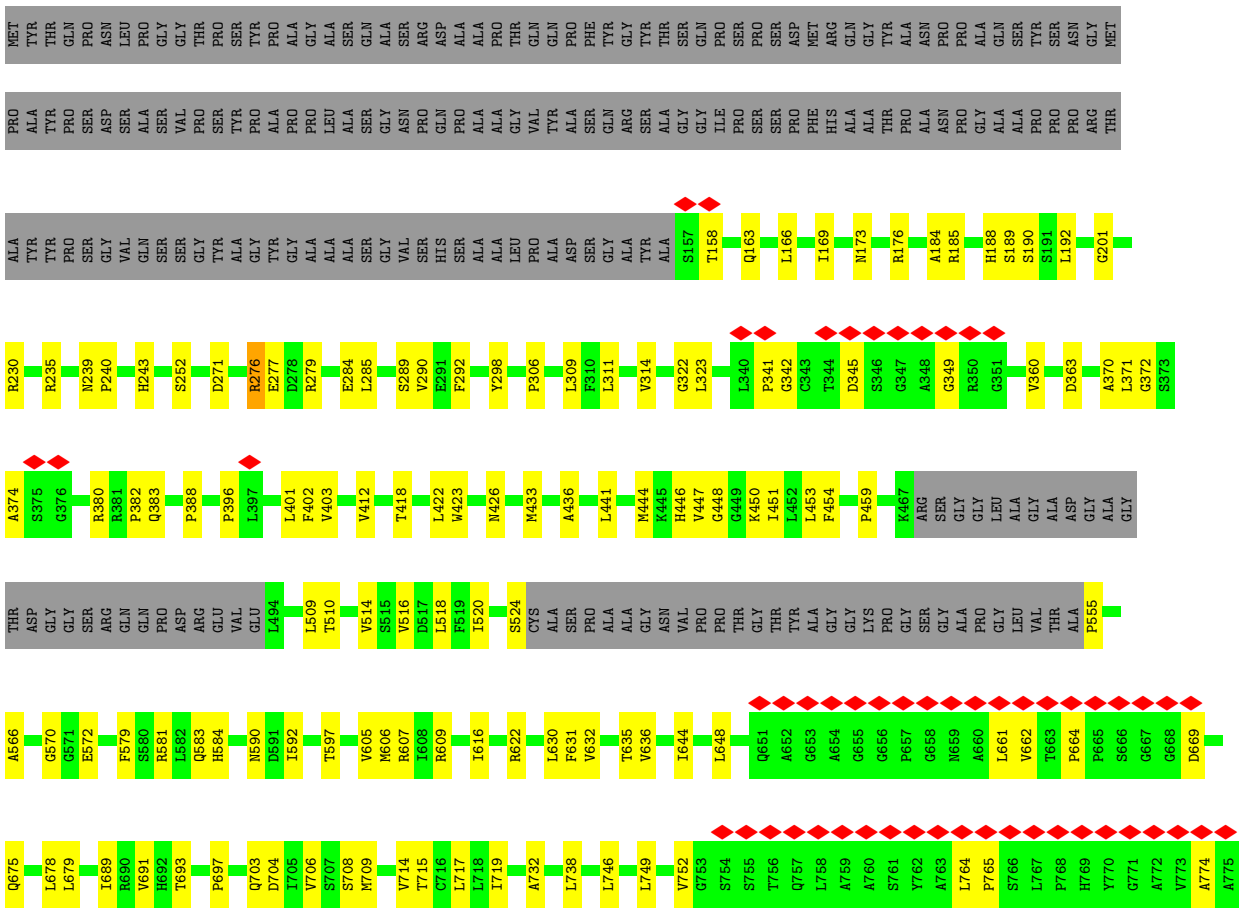
Chain GC:

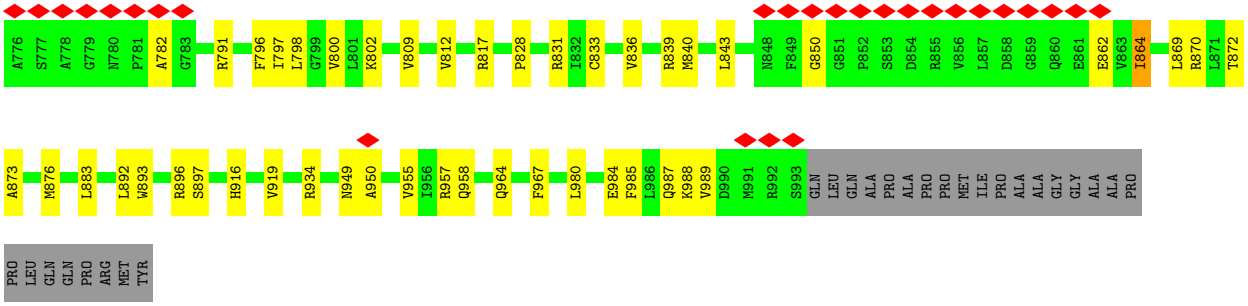




• Molecule 7: Transport protein Sec24

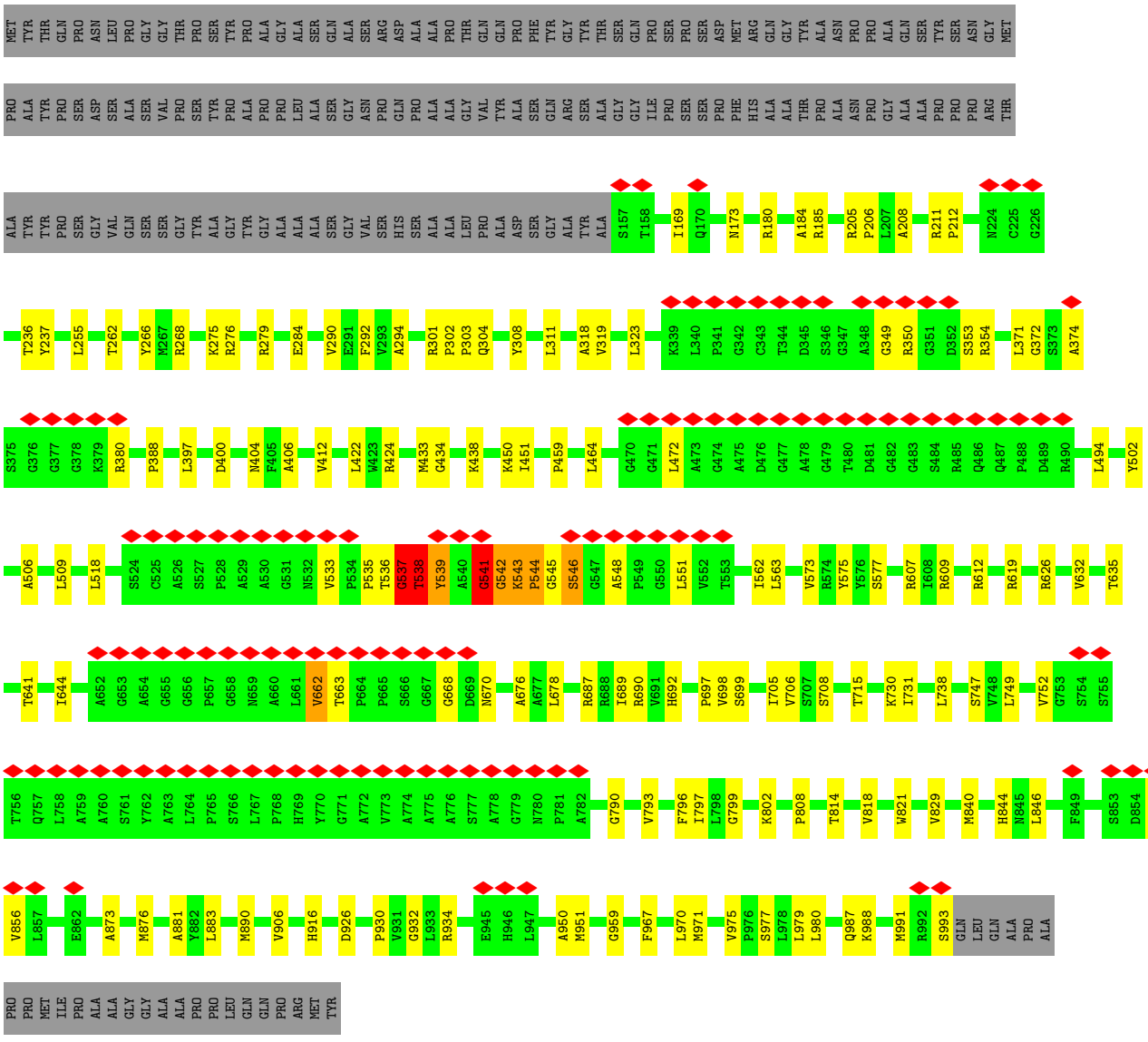
Chain GE:





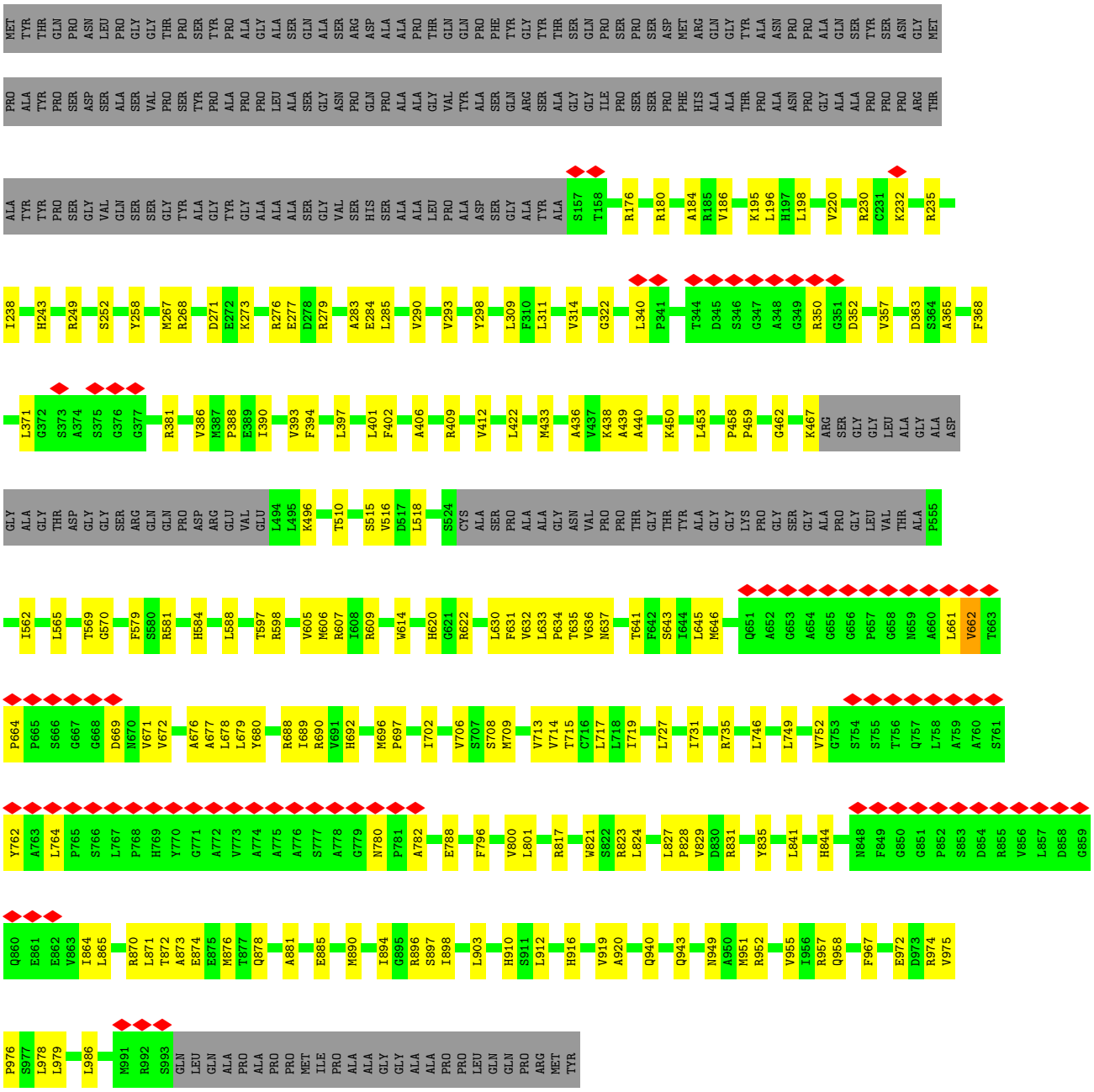
• Molecule 7: Transport protein Sec24

Chain GG:



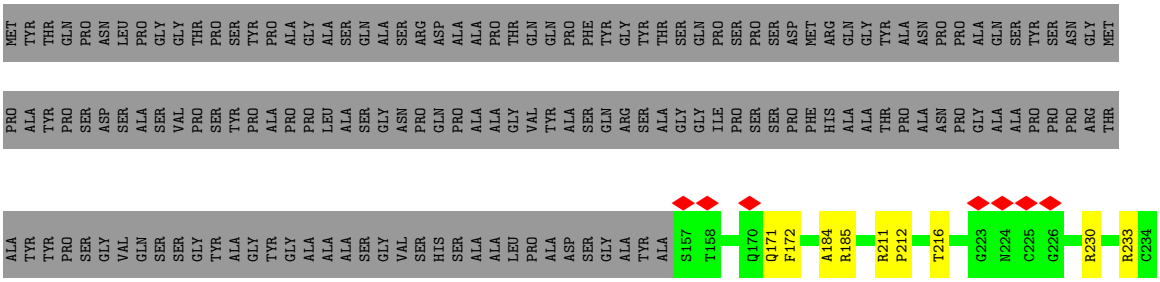
• Molecule 7: Transport protein Sec24

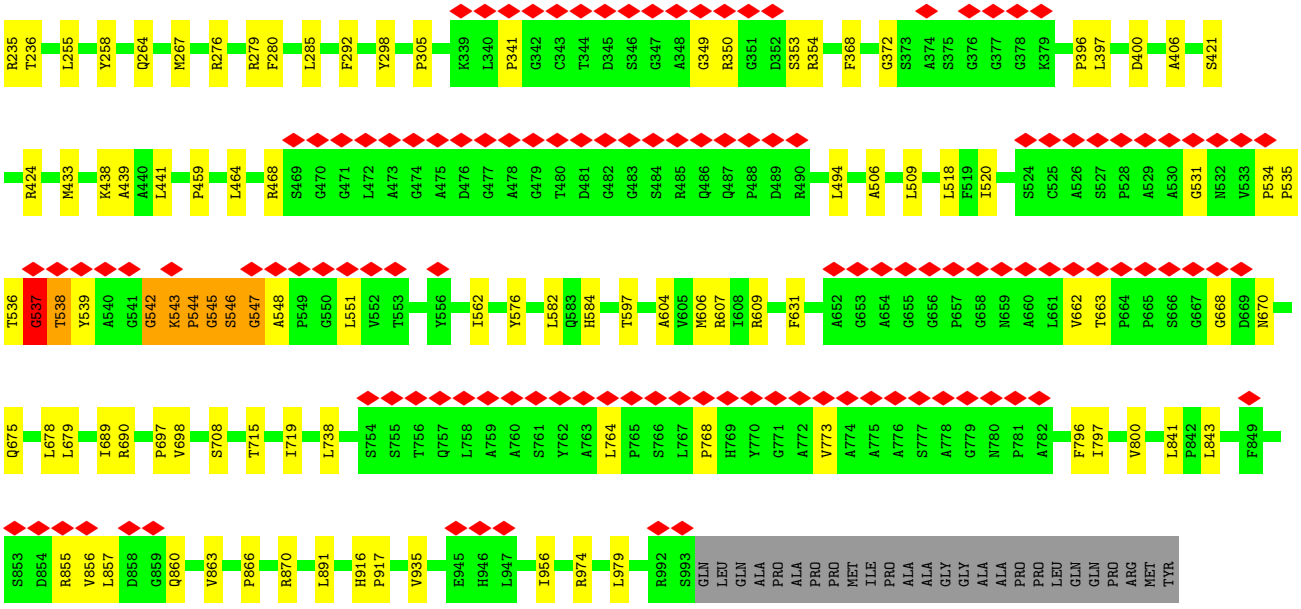
Chain GI:



• Molecule 7: Transport protein Sec24

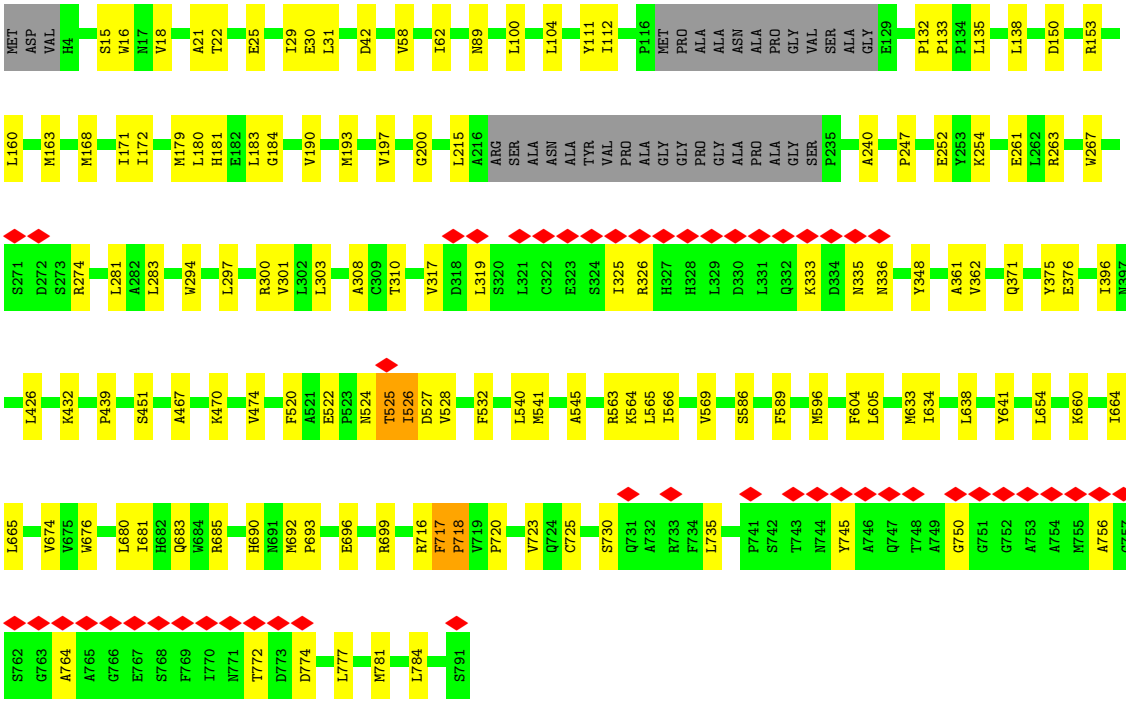
Chain GK:





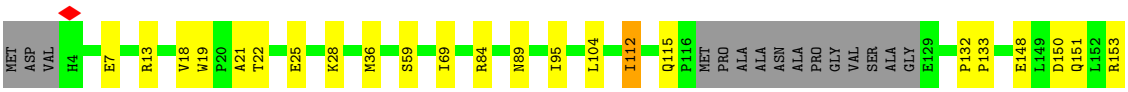
• Molecule 8: Protein transport protein SEC23

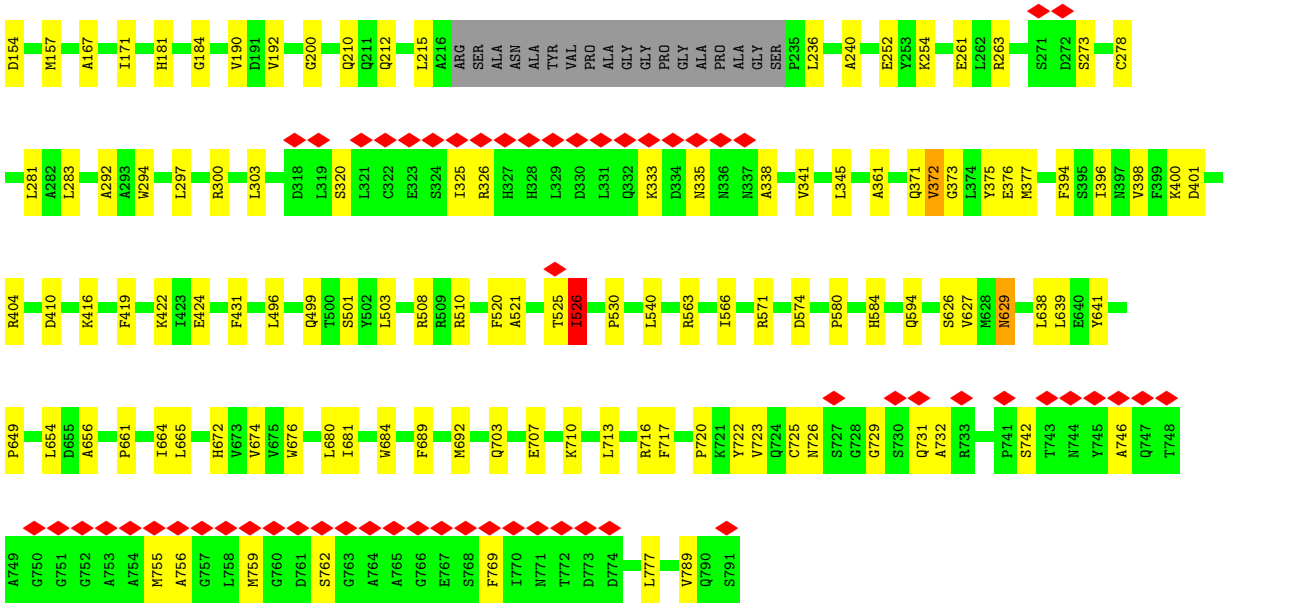
Chain GB:



• Molecule 8: Protein transport protein SEC23

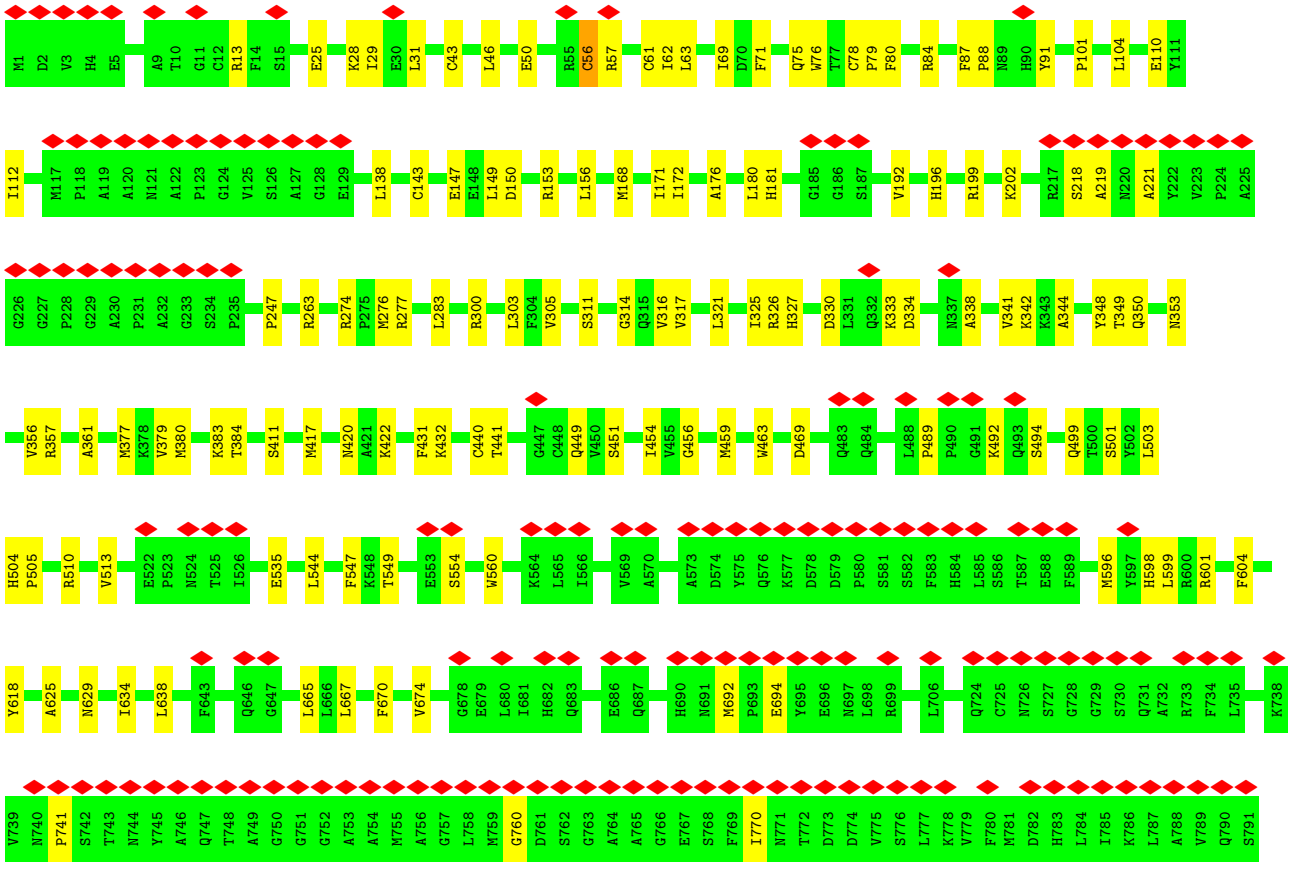
Chain GD:





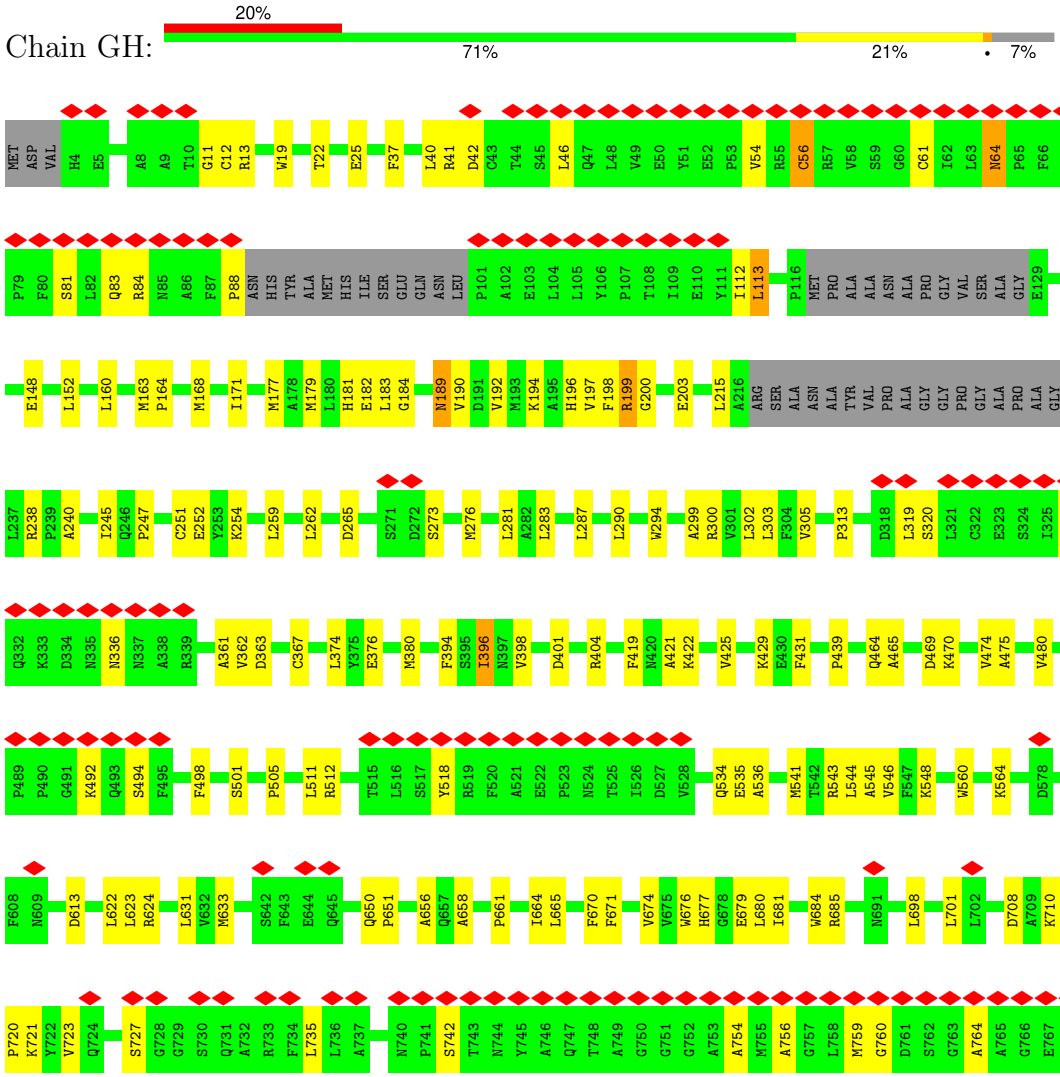
• Molecule 8: Protein transport protein SEC23

Chain GF:



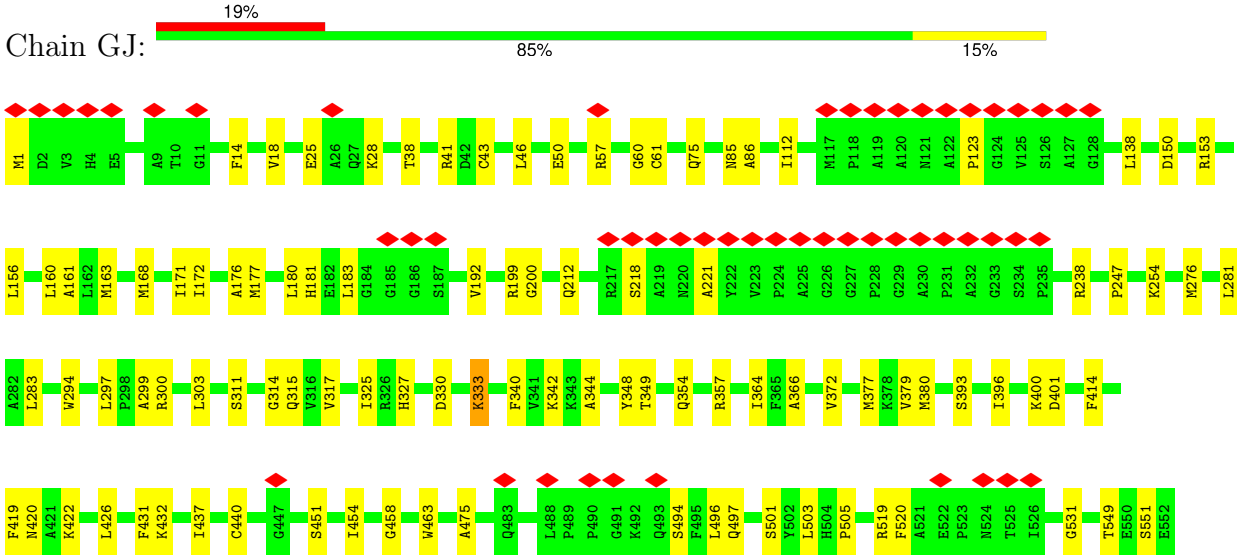
• Molecule 8: Protein transport protein SEC23

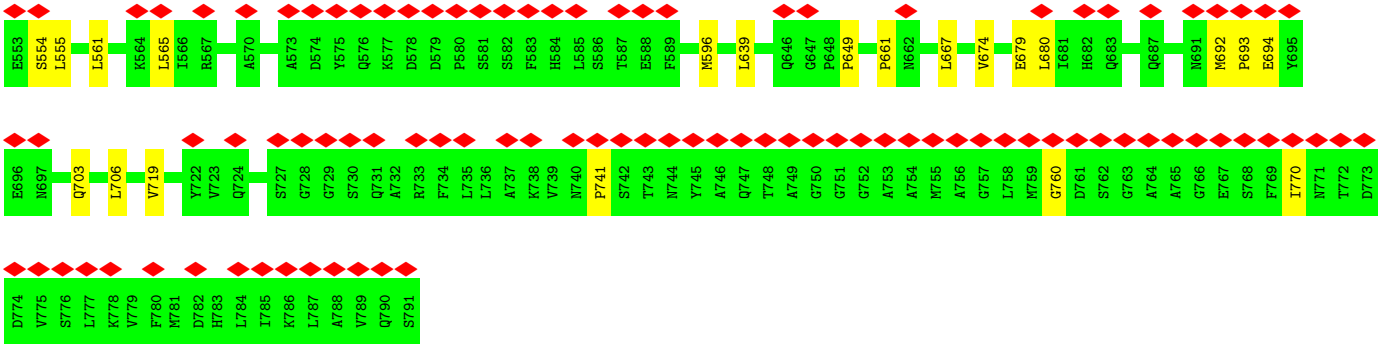
Chain GH:



• Molecule 8: Protein transport protein SEC23

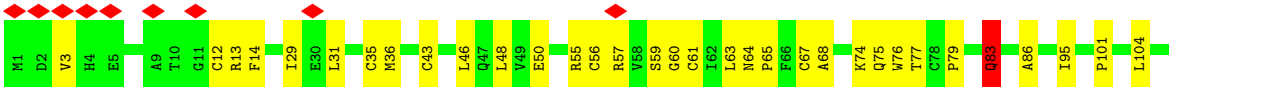
Chain GJ:

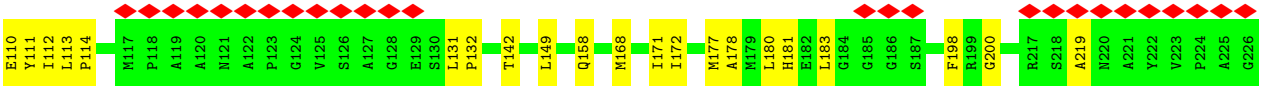


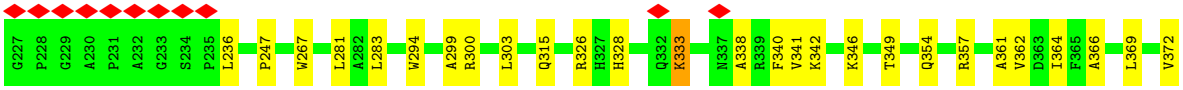


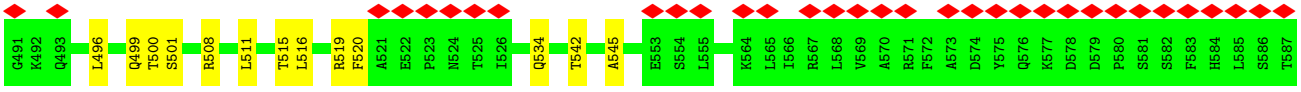
• Molecule 8: Protein transport protein SEC23

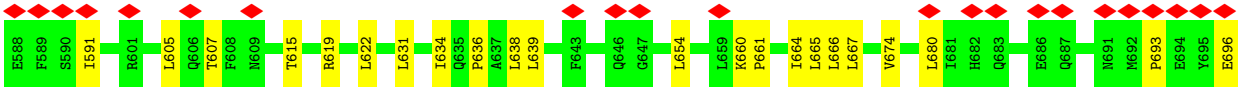
Chain GL:

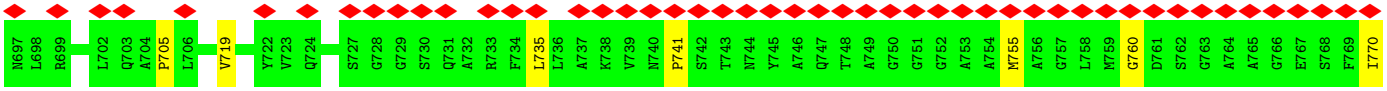


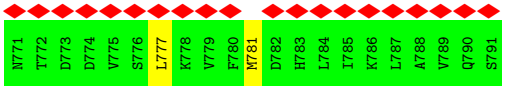






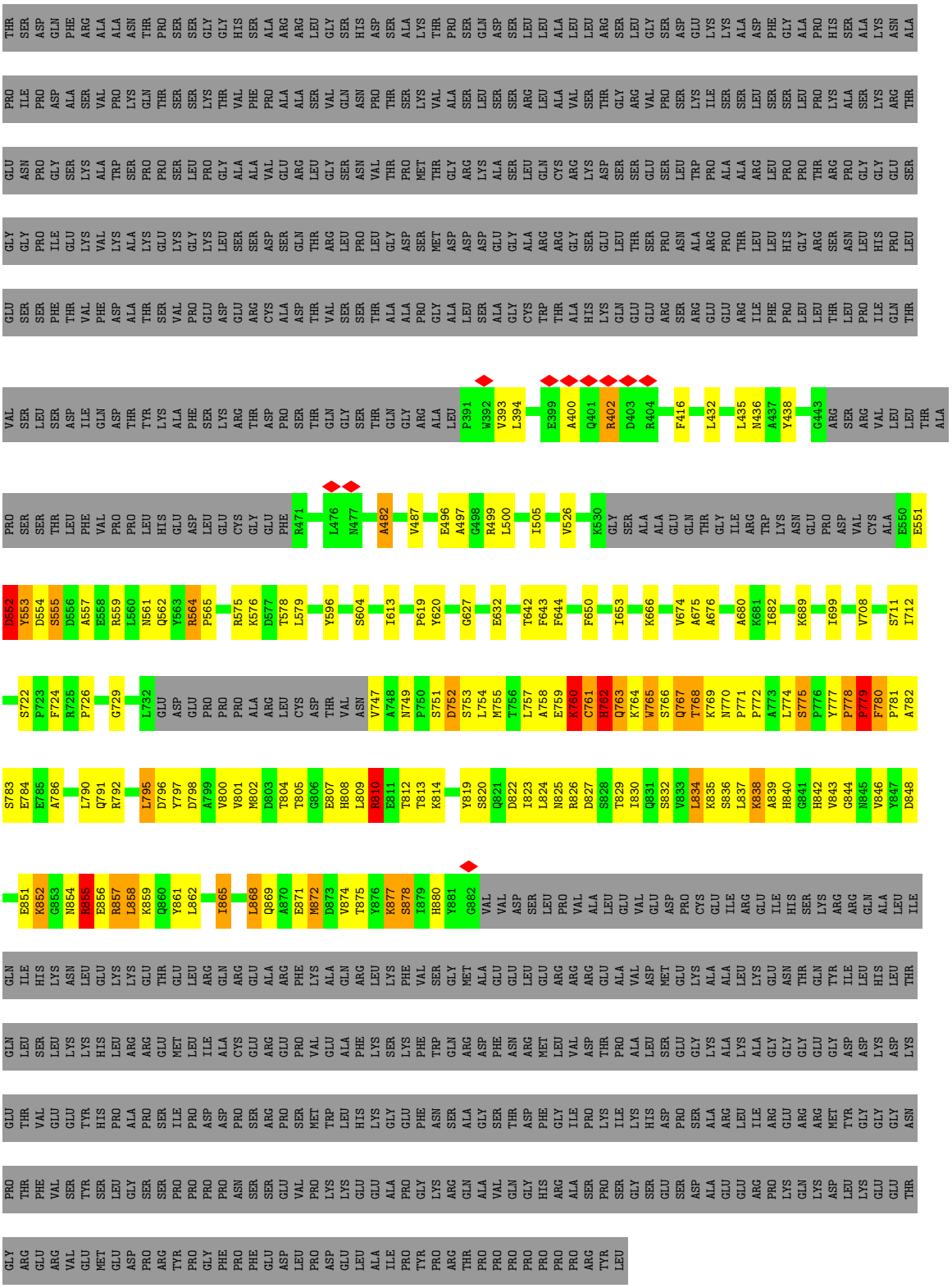






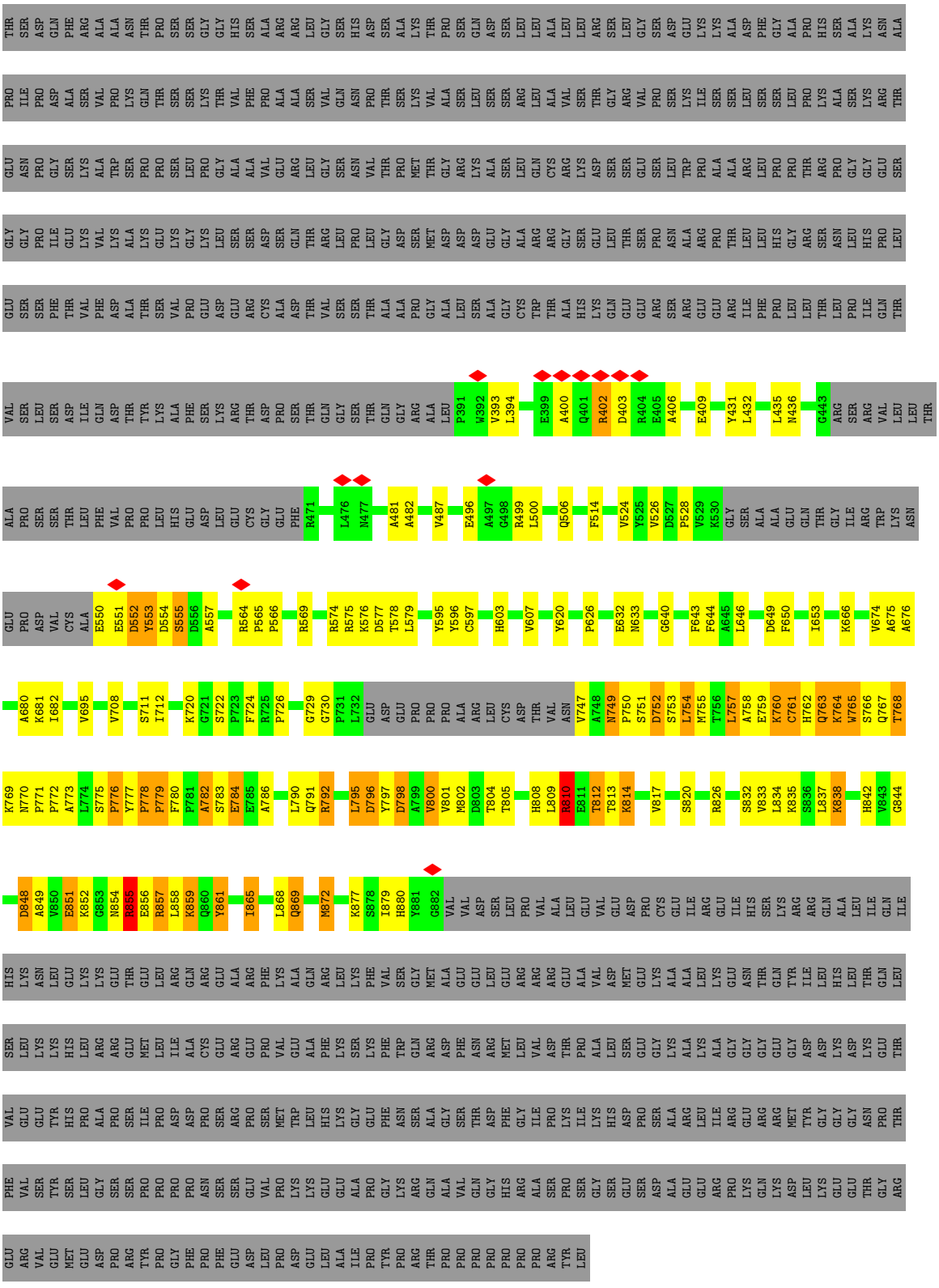
• Molecule 9: FLM2, TGME49_285990

Chain HA:



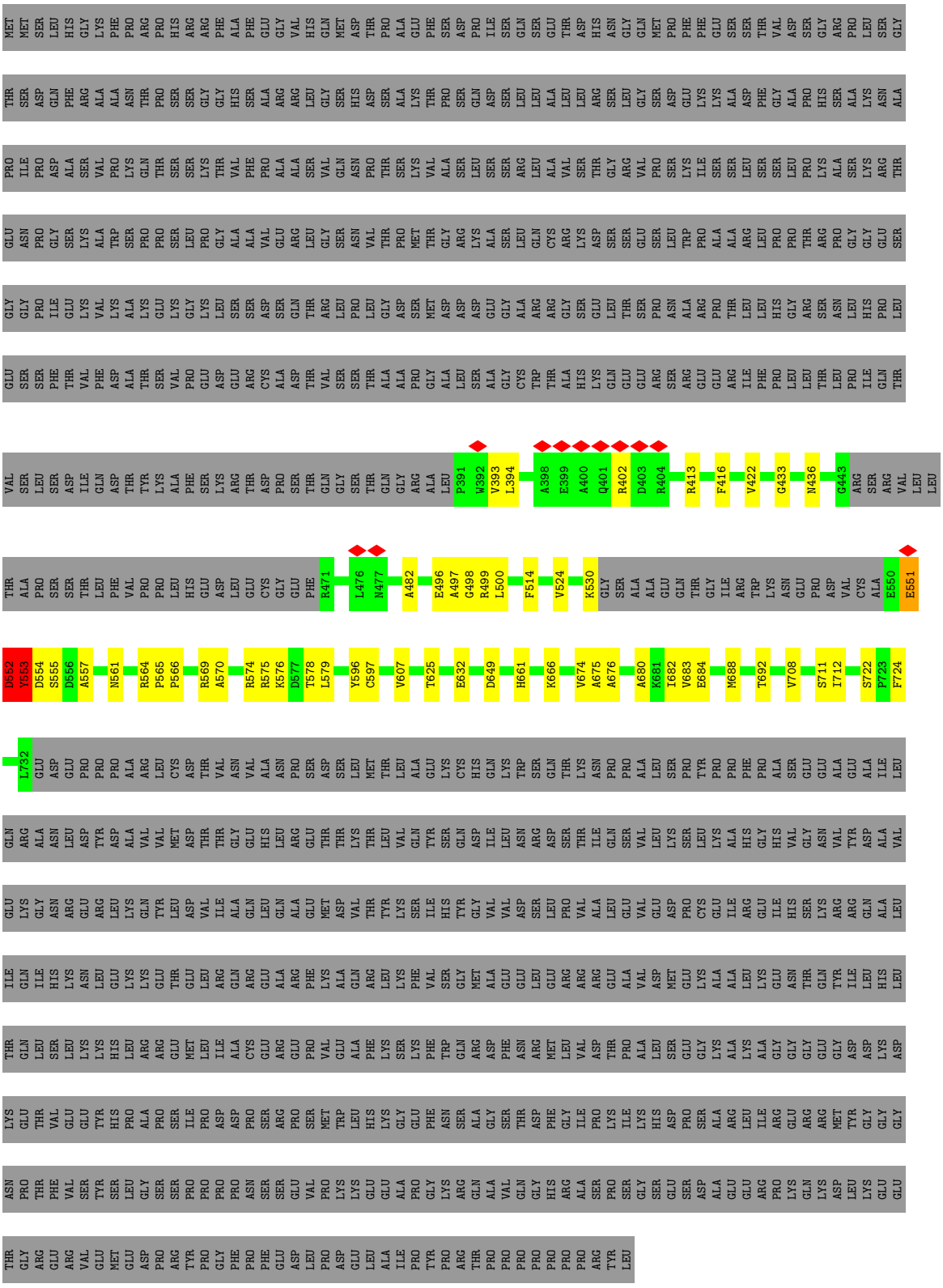
• Molecule 9: FLM2, TGME49_285990

Chain HB:



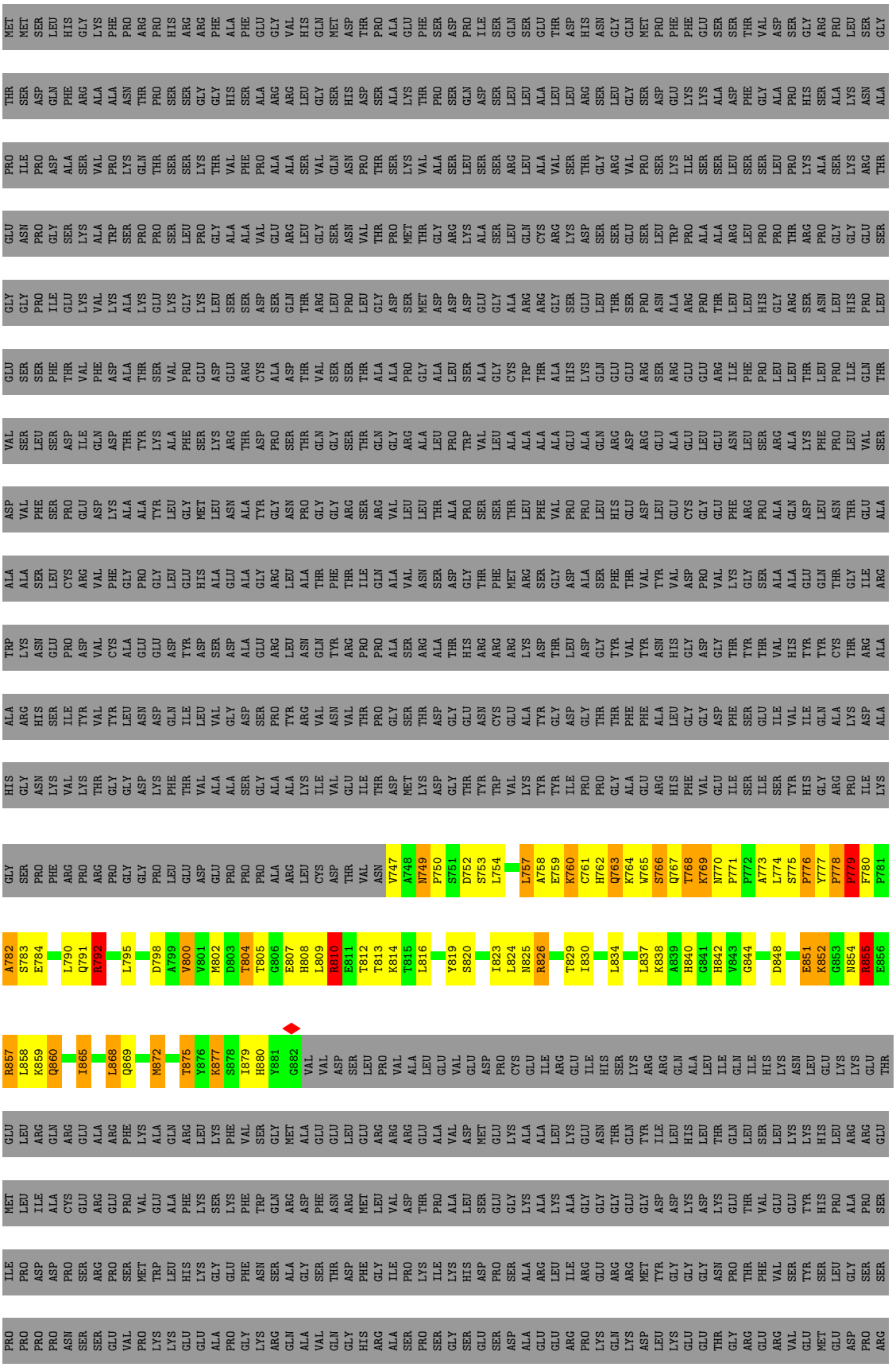
• Molecule 9: FLM2, TGME49_285990

Chain HC:



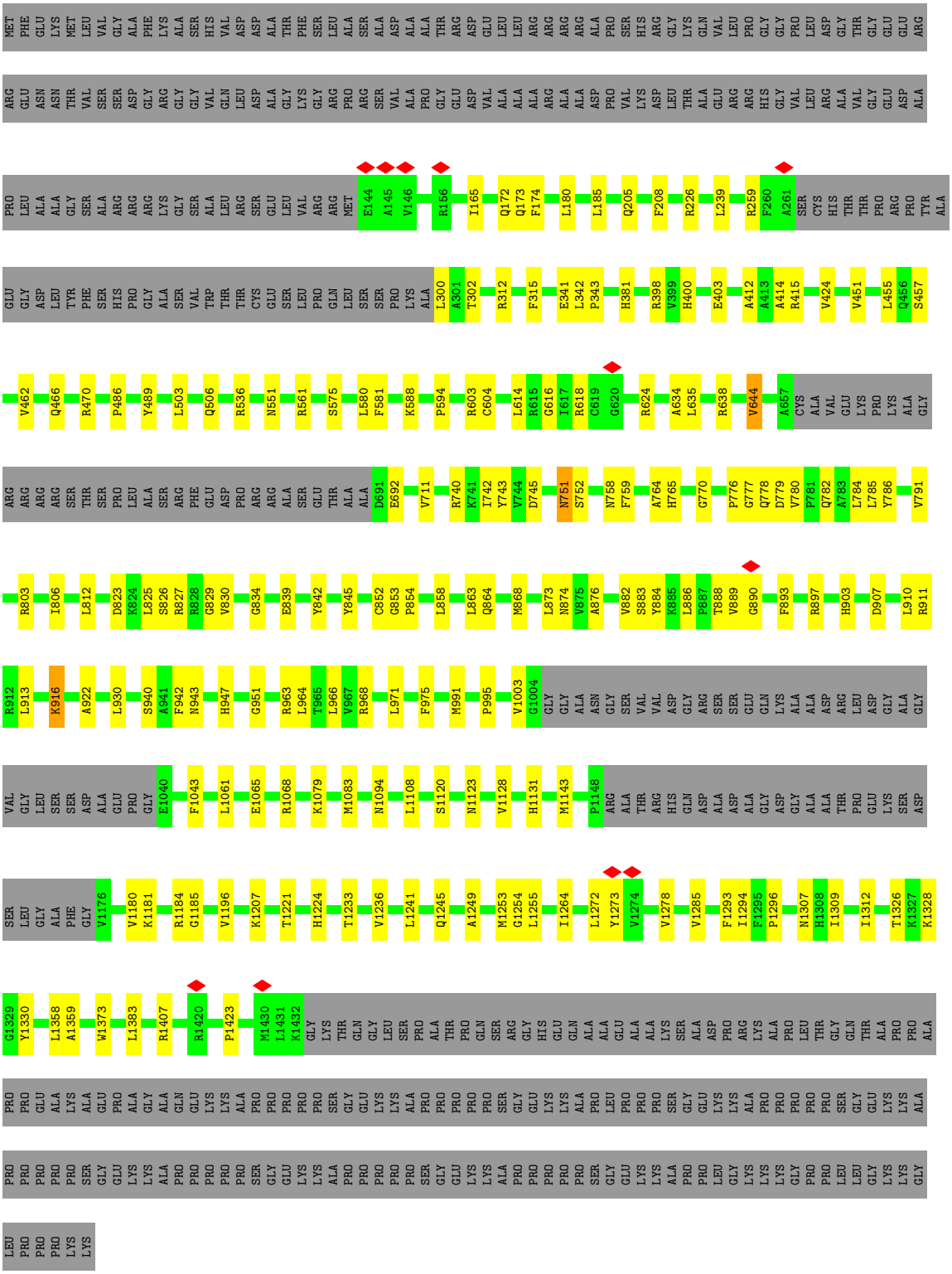
• Molecule 9: FLM2, TGME49_285990

Chain HD: 5% 5% • 89%


MET MET SER LEU HIS GLY LYS PHE PRO ARG PRO HIS ARG ARG PHE ALA PHE GLU GLY VAL HIS GLN MET ASP THR PRO ALA GLU PHE SER ASP PRO ILE SER GLN SER GLU THR ASP HIS ASN GLY GLN MET PRO PHE PHE GLU SER SER THR VAL ASP SER GLY ARG PRO
THR SER ASP GLN PHE ARG ALA ALA ASN THR PRO SER GLN ASP SER LEU LEU LEU ARG SER LEU GLY SER ASP GLU LYS LYS ALA SER ALA PRO HIS SER ALA LYS ASN ALA
PRO ILE PRO ASP ALA SER VAL PRO LYS GLN THR SER SER GLY GLY HIS SER ARG ALA LEU GLY SER GLN ASN PRO THR SER LYS VAL ALA SER LEU SER SER LEU LEU PRO LYS ALA SER LYS ARG THR
GLU ASN PRO GLY SER ALA TRP SER PRO PRO SER LEU PRO GLY ALA ALA VAL GLU ARG LEU GLY SER ASN VAL THR PRO MET THR GLY ARG LYS ALA SER LEU GLN CYS ARG LYS ASP SER SER GLU SER LEU TRP PRO ALA ALA ARG LEU HIS GLY GLU SER
GLY GLY PRO ILE GLU LYS VAL LYS ALA LYS GLU GLU LYS GLY LYS LEU SER SER ASP GLU ARG GLN THR ARG LEU PRO LEU GLY ASP SER MET ASP ASP GLU GLY ALA ARG ARG ASP LEU THR SER PRO ASN ALA ARG PRO THR LEU LEU HIS GLY ARG SER ASN LEU HIS PRO LEU
GLU SER SER PHE THR VAL PHE ASP ALA THR ALA ASP THR VAL SER SER THR ALA ALA PRO GLY ALA LEU ASP PRO GLY GLN GLU GLU ARG GLN LEU THR LEU LEU ILE GLN THR
VAL SER LEU SER ASP ILE GLN ASP THR TYR LYS ALA PHE SER LYS ARG THR ASP PRO SER THR GLN GLY SER THR GLN GLY ARG ALA LEU PRO TRP VAL THR ALA ASP ARG GLN ASP ARG GLU ALA GLU LEU GLU GLU ASN LEU ARG ILE PHE PRO LEU VAL SER
ASP VAL PHE SER PRO GLU ASP LYS ALA ALA TYR GLY ASN PRO GLY GLY ARG SER ARG VAL LEU LEU THR ALA PRO SER THR PHE MET LEU ASN ALA TYR LEU LEU GLY MET LEU ASN PRO GLY GLY ARG SER THR LEU PHE VAL PRO PRO LEU HIS GLU ASP LEU ASP GLY ARG PHE VAL PRO ALA GLU CYS GLY GLU PHE PRO ARG PRO ALA GLU ASN LEU GLU GLU ASP
ALA ALA SER LEU CYS ARG VAL PHE GLY PRO GLY LEU GLU HIS ALA GLU ALA GLY ARG LEU ALA THR PHE THR ILE GLN ALA VAL ASN SER ASP GLY THR PHE MET ARG SER GLY ASP ALA SER PHE THR VAL TYR VAL ASP PRO VAL LYS GLY PHE ARG PRO ALA ALA GLN GLU GLU ARG ILE
TRP LYS ASN GLU PRO ASP VAL CYS ALA GLU GLU GLU ASP TYR ASP SER ASP ALA GLU ARG LEU ASN GLN TYR ARG PRO PRO ALA SER ARG ALA THR HIS ARG ARG ARG LYS ASP THR LEU ASP GLY TYR VAL TYR ASN HIS GLY GLY ASP GLY THR TYR THR VAL HIS TYR TYR CYS THR ARG ALA
ALA ARG HIS SER ILE TYR VAL TYR LEU ASN ASP GLN ILE LEU VAL GLY ASP SER PRO TYR ARG VAL ASN VAL THR PRO GLY SER THR ASP GLY GLU GLY GLU ASN CYS GLU ALA TYR GLY ASP GLY THR THR PHE PHE ALA LEU GLY GLY GLY ASP PHE SER GLU ILE SER VAL ILE GLN LYS ASP ILE
HIS GLY ASN LYS VAL LYS THR GLY GLY ASP LYS PHE THR VAL ALA ALA SER GLY ALA ALA LYS ILE VAL GLU ILE THR ASP MET LYS ASP GLY THR TYR TRP VAL LYS TYR TYR ILE PRO PRO GLY ALA GLU ARG HIS PHE VAL GLU ILE SER ILE ILE SER TYR HIS GLY ARG PRO ILE LYS
GLY SER PRO PHE ARG PRO ARG PRO GLY GLY PRO PRO LEU GLU ASP GLU PRO PRO PRO ALA ARG LEU CYS ASP THR VAL ASN V747 A748 N749 P750 S751 D752 S753 L754 L757 A758 E759 K760 C761 H762 Q763 K764 W765 S766 Q767 T768 K769 N770 P771 P772 A773 L774 S775 P776 Y777 P778 P779 F780 P781
A782 S783 E784 L790 Q791 R792 L795 D798 A799 V800 V801 M802 D803 T804 T805 G806 E807 H808 L809 R810 E811 T812 T813 K814 T815 L816 Y819 S820 I823 L824 N825 R826 T829 I830 L834 L837 K838 A839 H840 G841 H842 V843 G844 D848 E851 K852 G853 N854 R855 E856
R857 L858 K859 Q860 I865 L868 Q869 M872 T875 Y876 K877 S878 I879 H880 Y881 G882 VAL VAL ASP SER LEU PRO VAL ALA ALA LEU GLU VAL GLU ASP GLU ASP PRO CYS GLU ILE ARG GLU ILE HIS SER LYS ARG ARG GLN ALA LEU GLN TYR ILE LEU HIS LEU THR GLN LEU SER LEU LYS LYS HIS LEU ARG ARG GLU
GLU LEU ARG GLN ARG GLU ALA ARG PHE LYS ALA GLN ARG LEU LYS PHE VAL SER GLY MET ALA GLU GLU LEU GLU ARG ARG ARG GLU ALA GLU ASP MET GLU LYS ALA ALA LEU LYS GLU ASN THR GLN TYR ILE LEU HIS LEU THR GLN LEU SER LEU LEU LYS LYS HIS LEU ARG ARG GLU
MET LEU ILE ALA CYS GLU ARG GLU PRO VAL GLU GLU ALA PHE LYS SER LYS PHE TRP GLN ARG ASP PHE ASN ARG MET LEU VAL ASP THR PRO ALA LEU SER GLU GLY LYS ALA ALA LYS ALA GLY GLY GLY GLU GLY THR VAL GLU GLU TYR HIS PRO ALA PRO SER
ILE PRO ASP PRO PRO SER ARG PRO SER MET TRP LEU HIS LYS GLY GLU PHE ASN SER ALA GLY PRO PHE GLY ILE PRO LYS ILE LYS HIS ASP PRO SER ALA ARG LEU ILE ARG GLU ARG MET TYR GLY GLY GLY ASN PRO THR PHE VAL SER TYR SER LEU GLY LEU SER
PRO PRO PRO PRO ASN SER SER GLU VAL GLN GLY HIS ARG ALA SER PRO SER GLY SER GLU SER ASP ALA ALA GLU GLU ARG PRO LYS GLN LYS ASP LEU LYS LYS GLU GLU THR GLY GLU ARG GLU ARG VAL GLU MET GLU ILE ASP PRO ARG

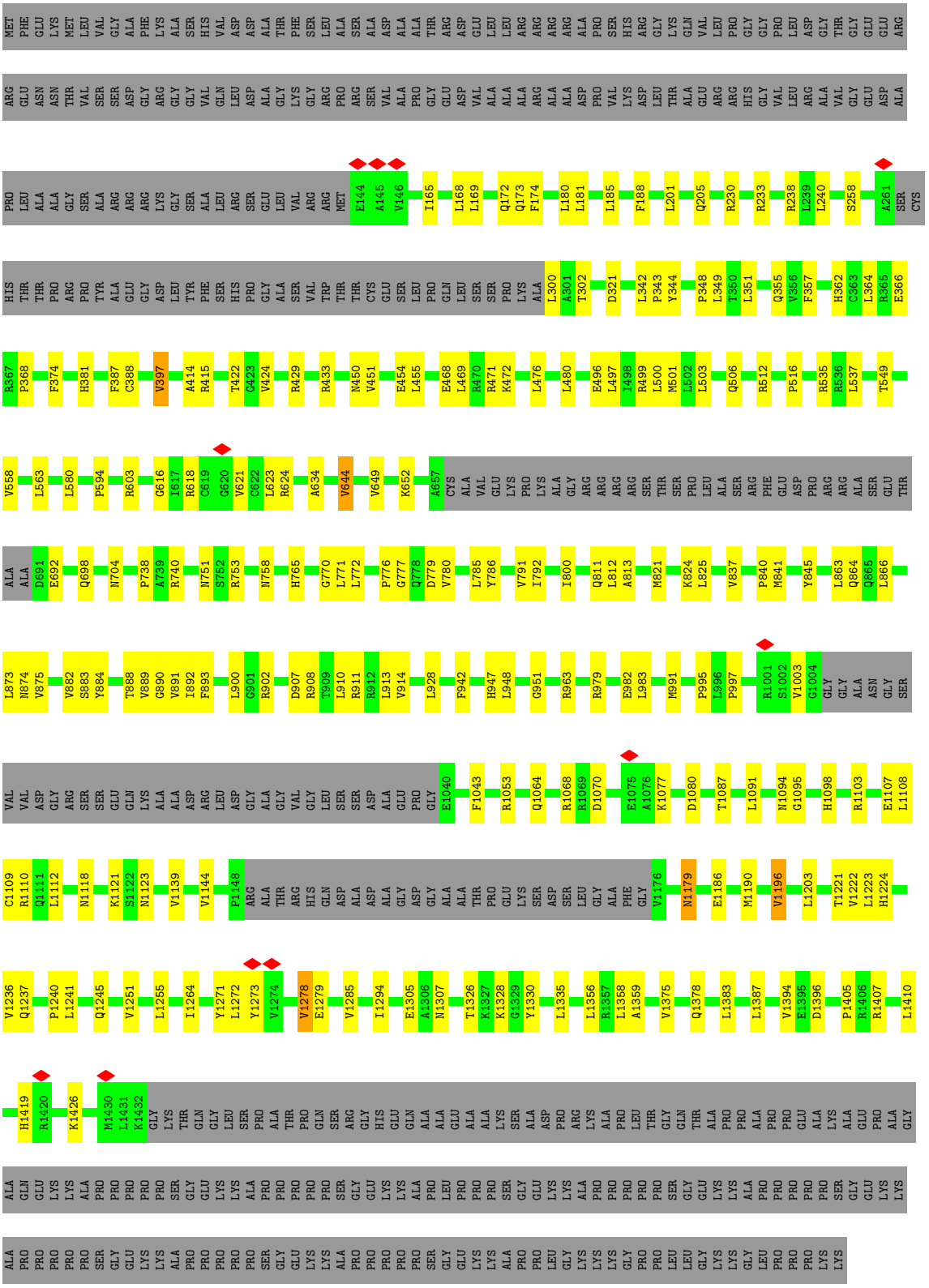
• Molecule 10: PCR12, TGME49_292170

Chain IA:



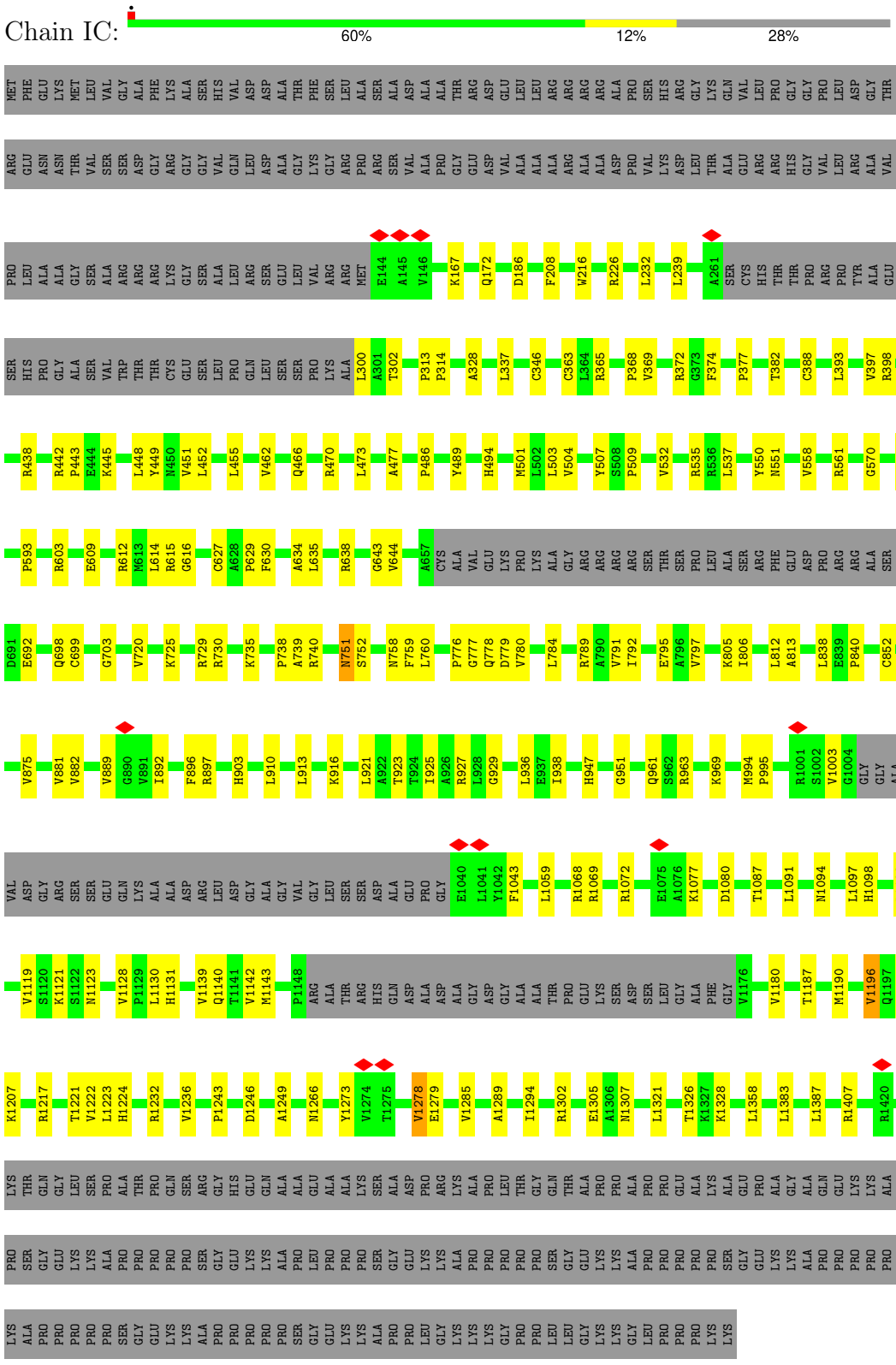
• Molecule 10: PCR12, TGME49_292170

Chain IB:



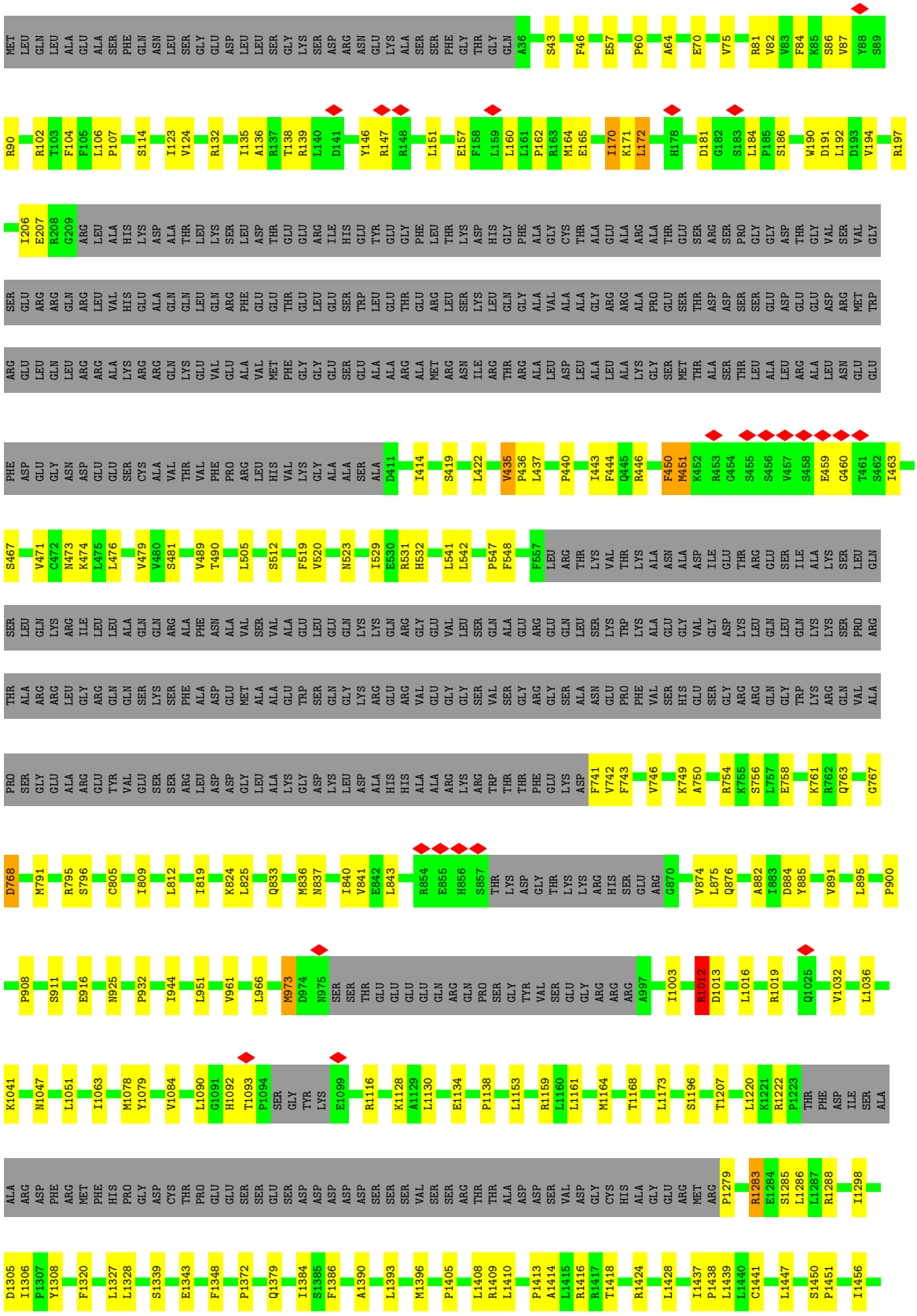
• Molecule 10: PCR12, TGME49_292170

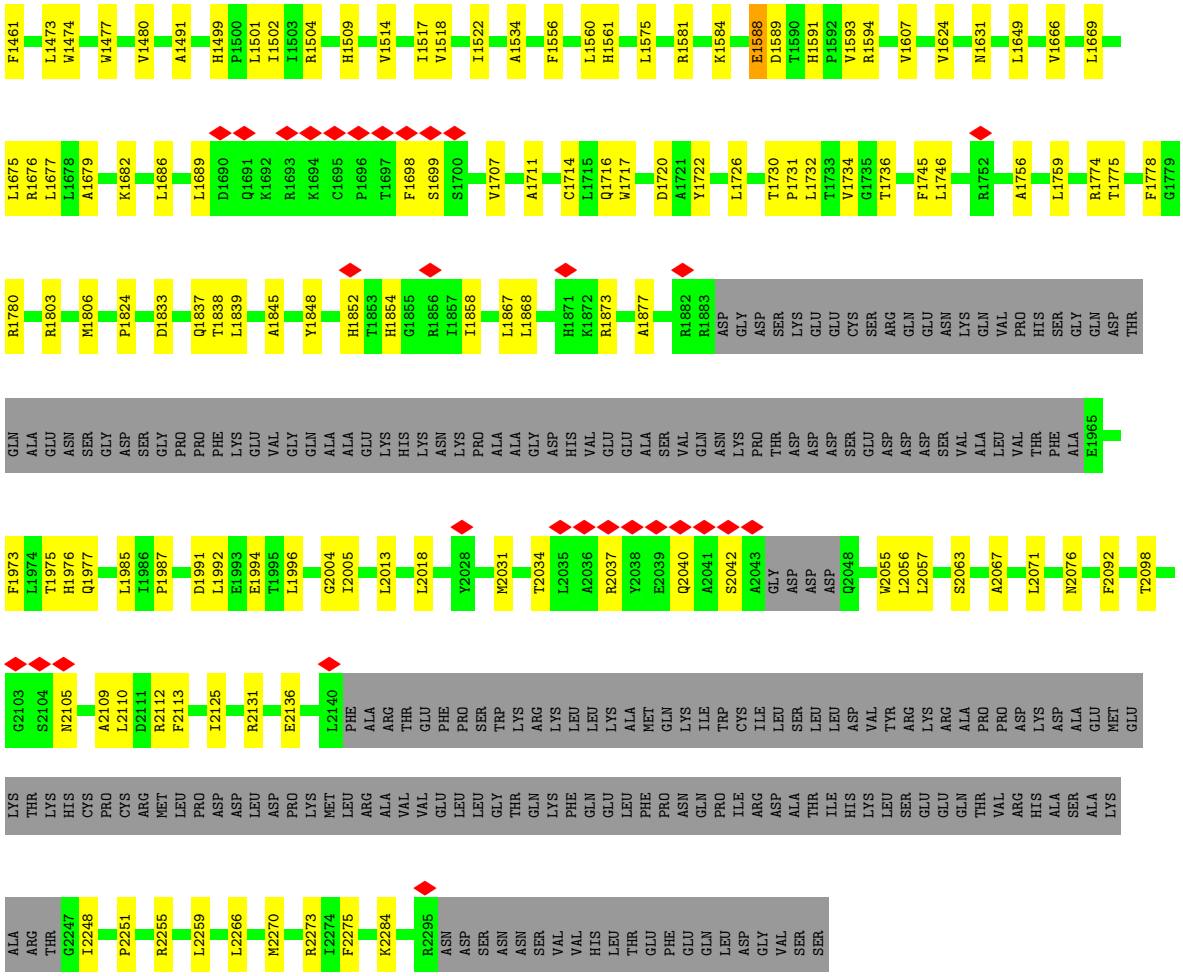
Chain IC:



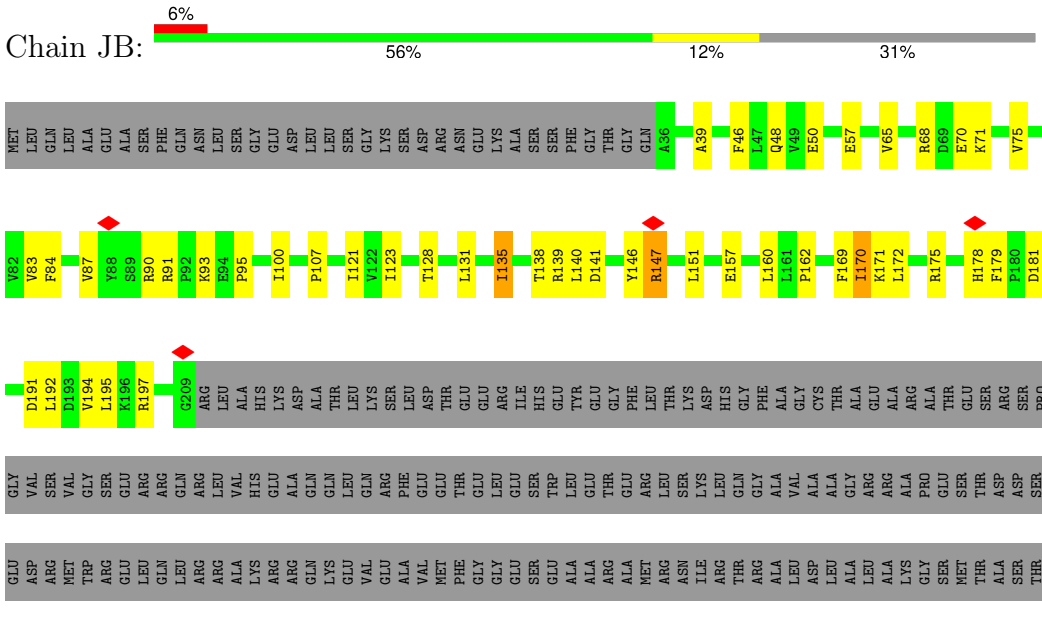
• Molecule 11: PCR10, TGME49_298010

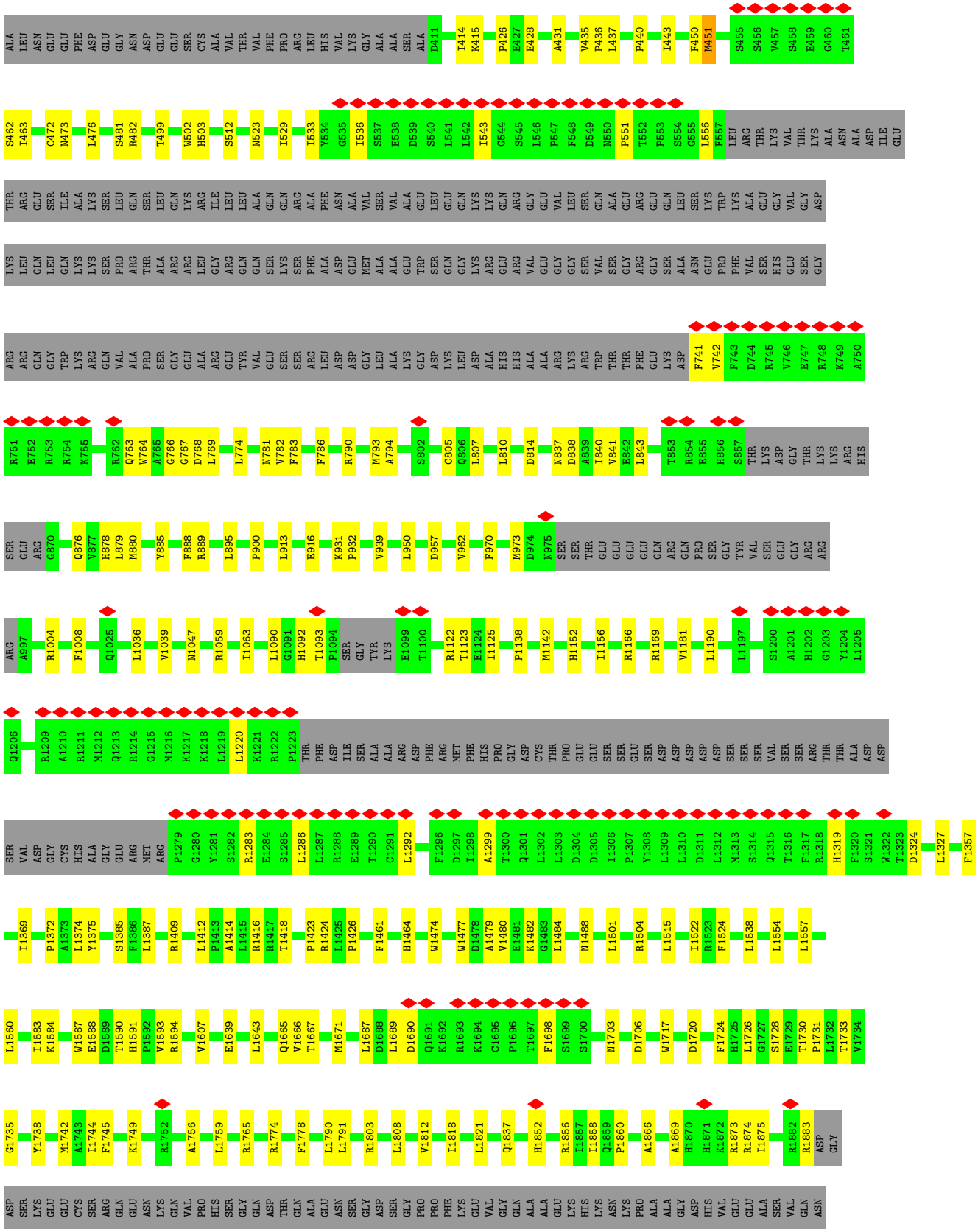
Chain JA:

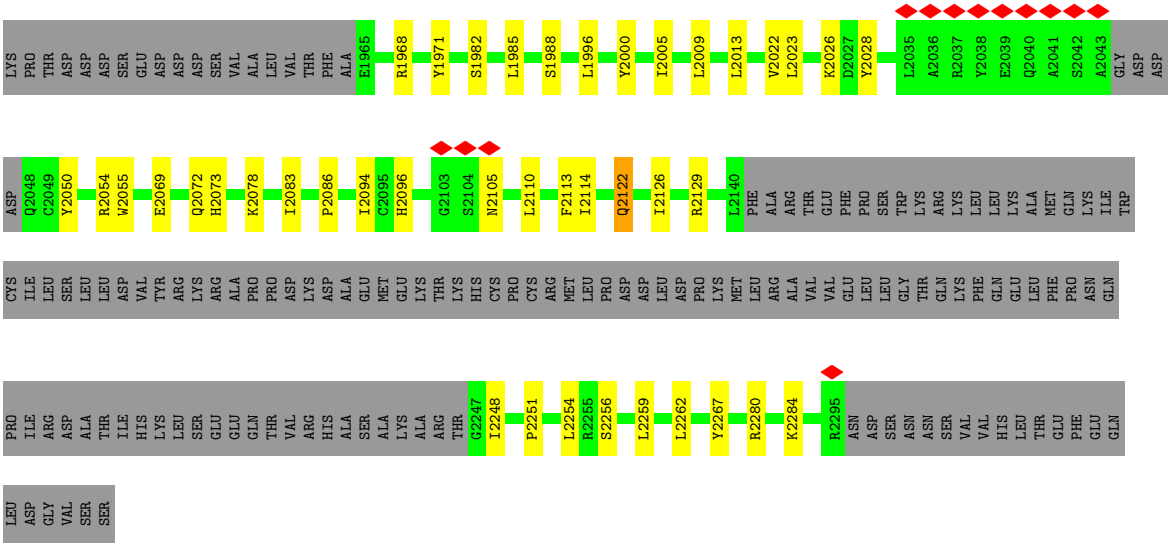




• Molecule 11: PCR10, TGME49_298010

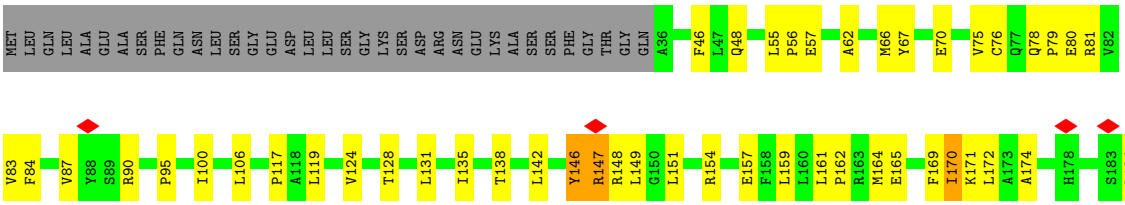


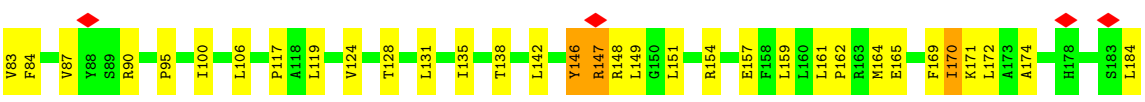


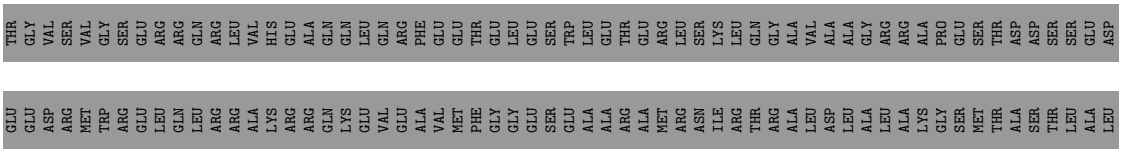


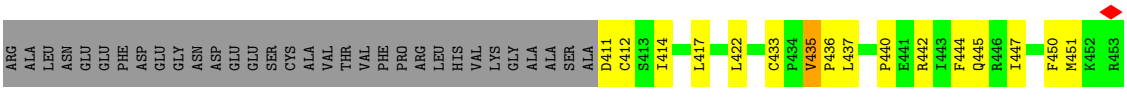
• Molecule 11: PCR10, TGME49_298010

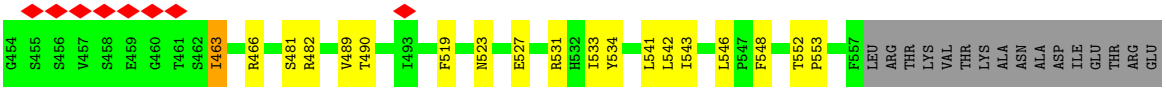
Chain JC:

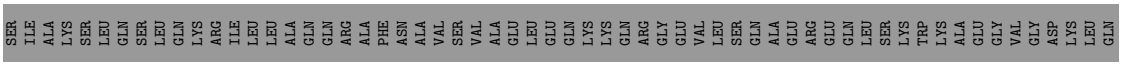


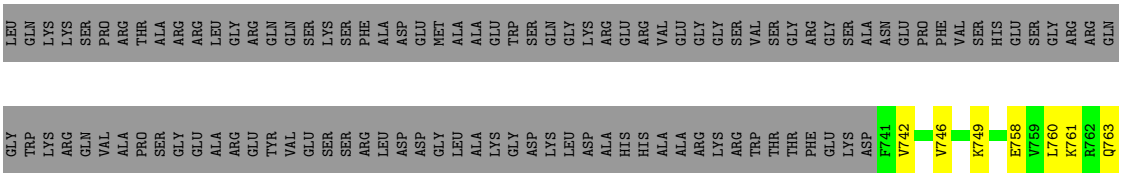


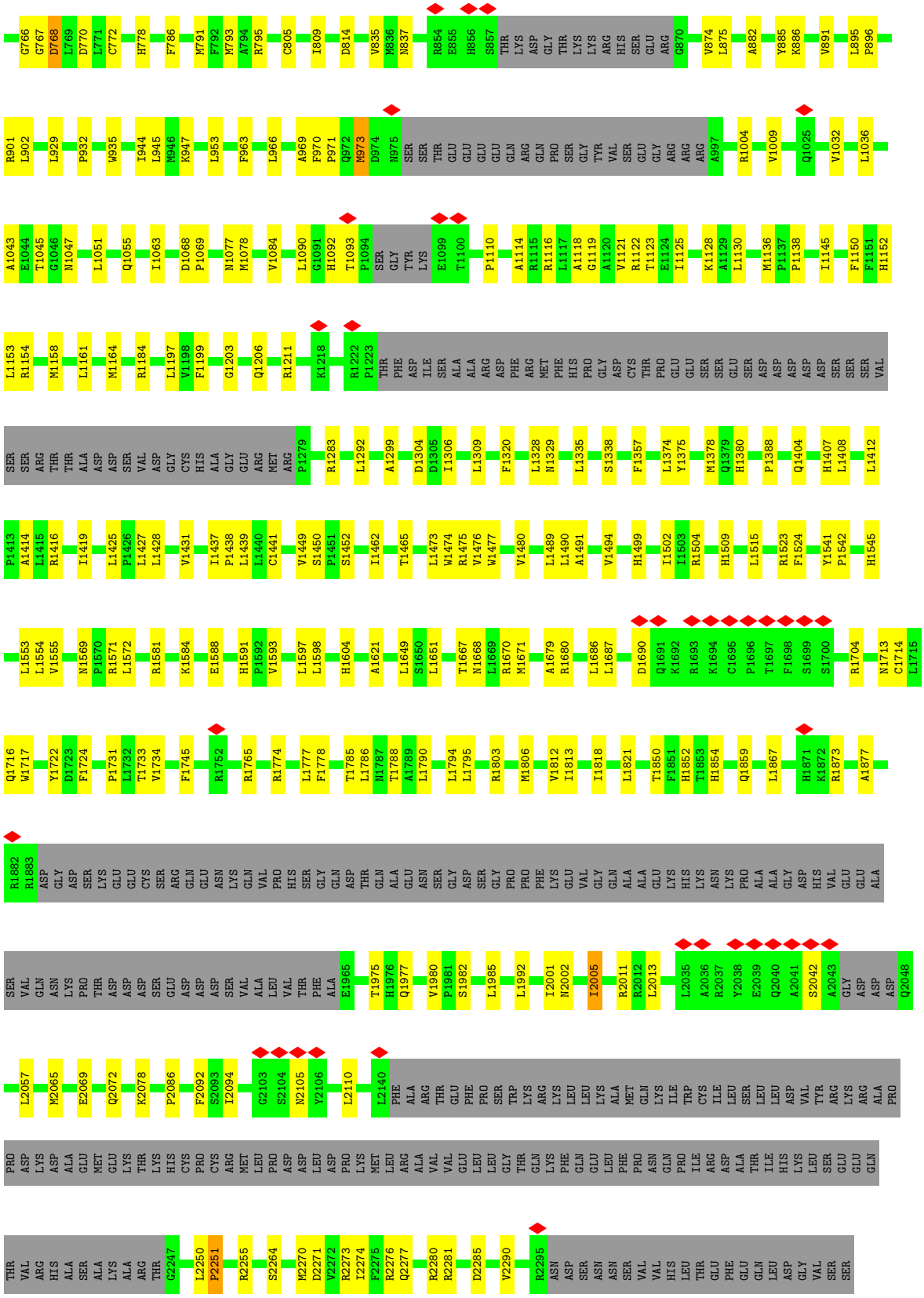






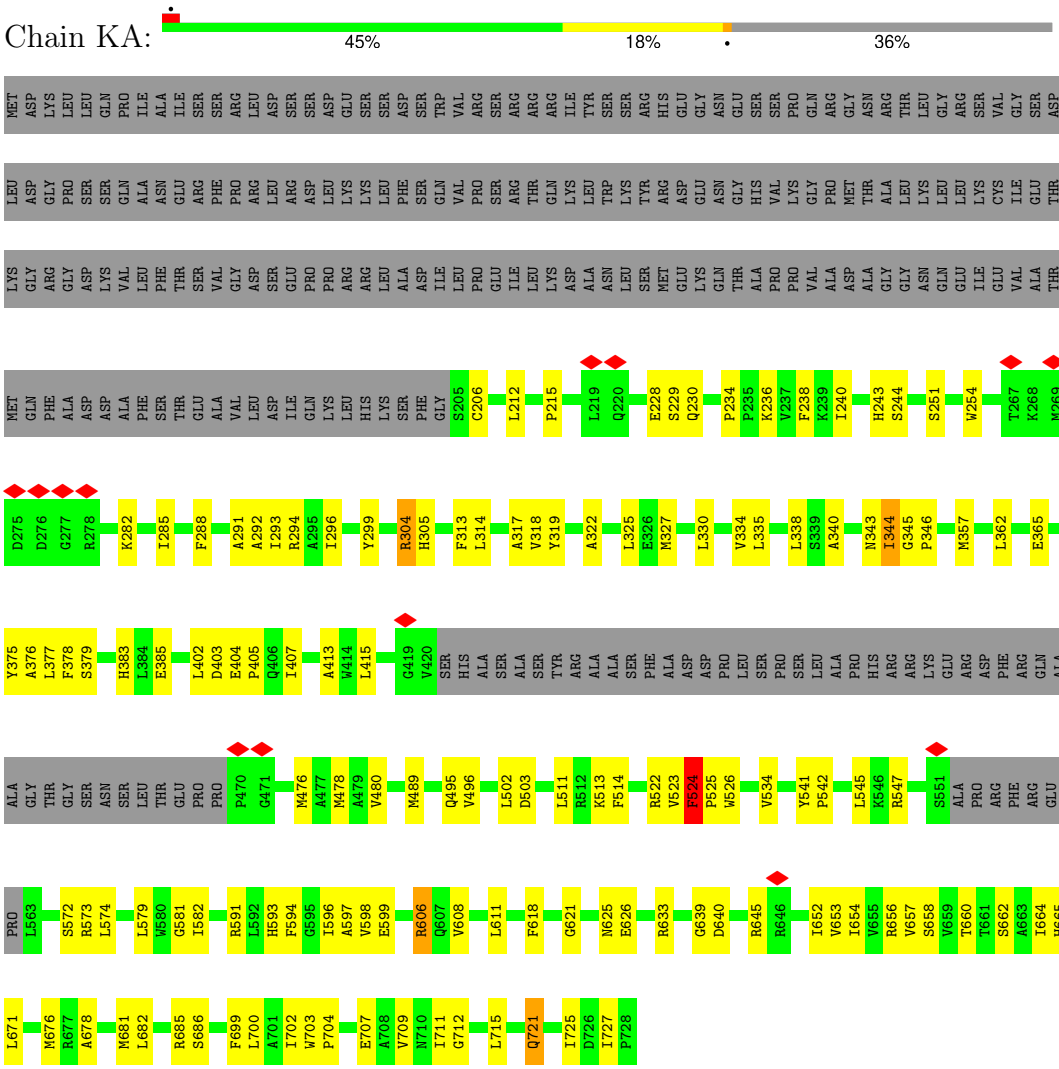






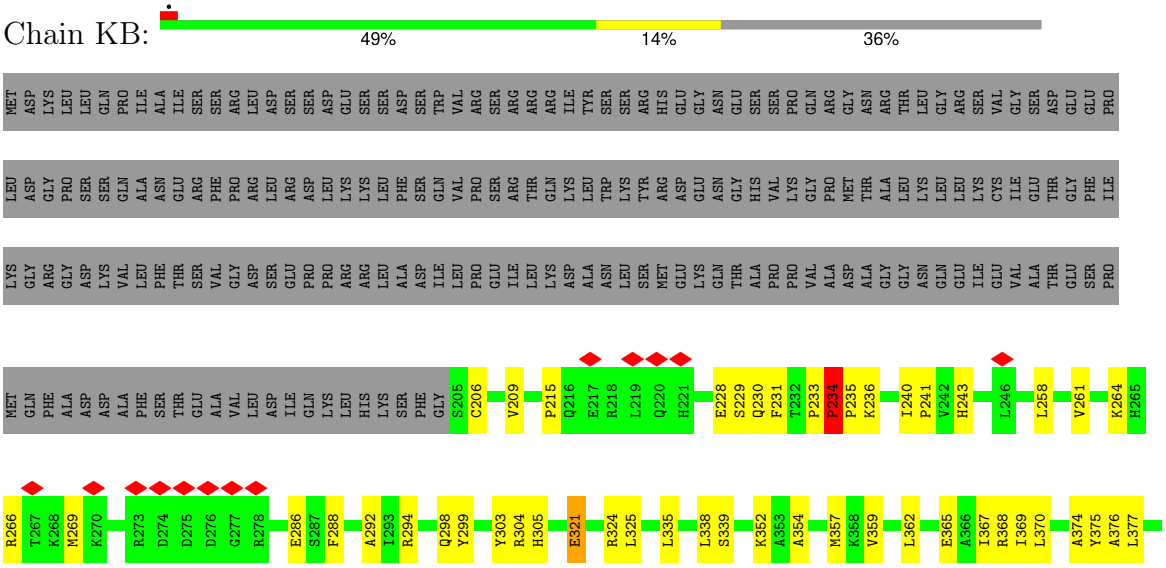
• Molecule 12: PCR14, TGME49_311880

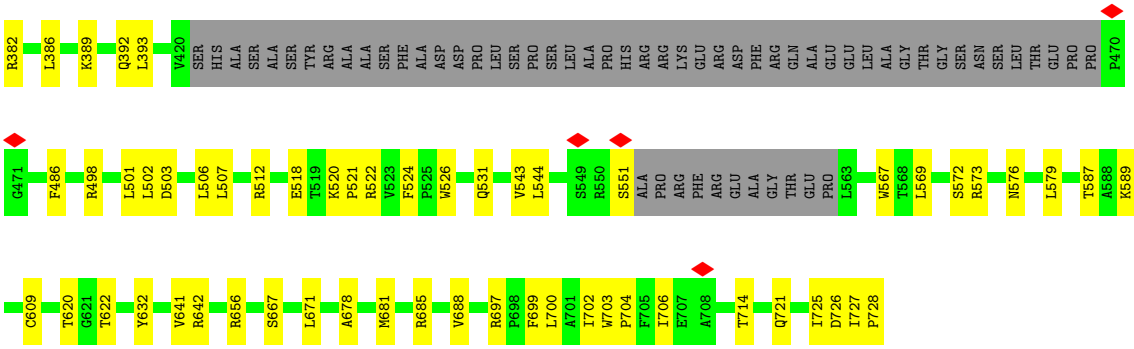
Chain KA:



• Molecule 12: PCR14, TGME49_311880

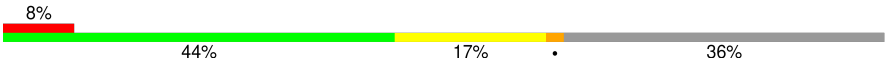
Chain KB:

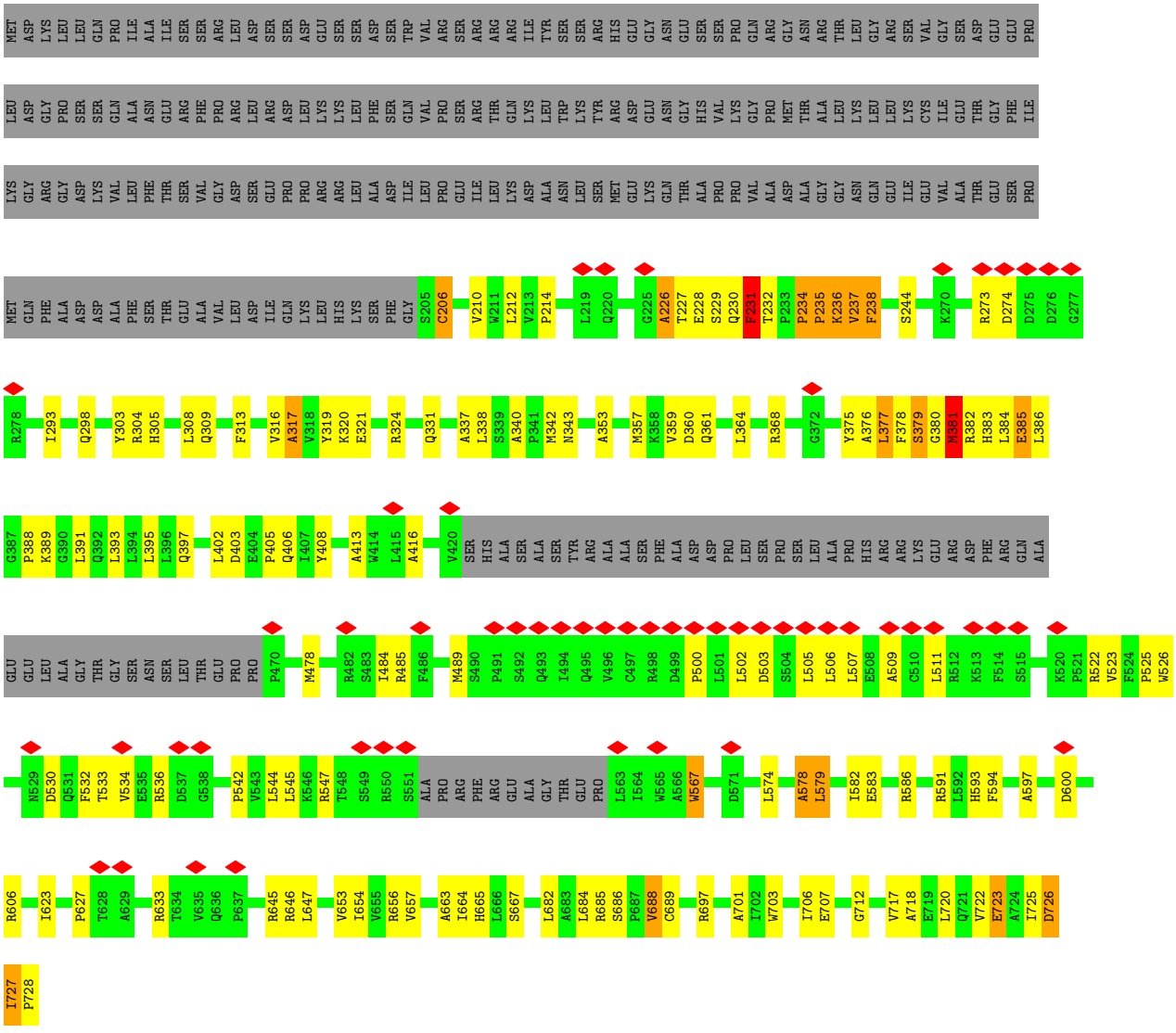




• Molecule 12: PCR14, TGME49_311880

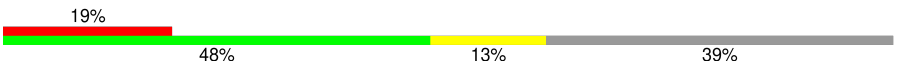
Chain KC:

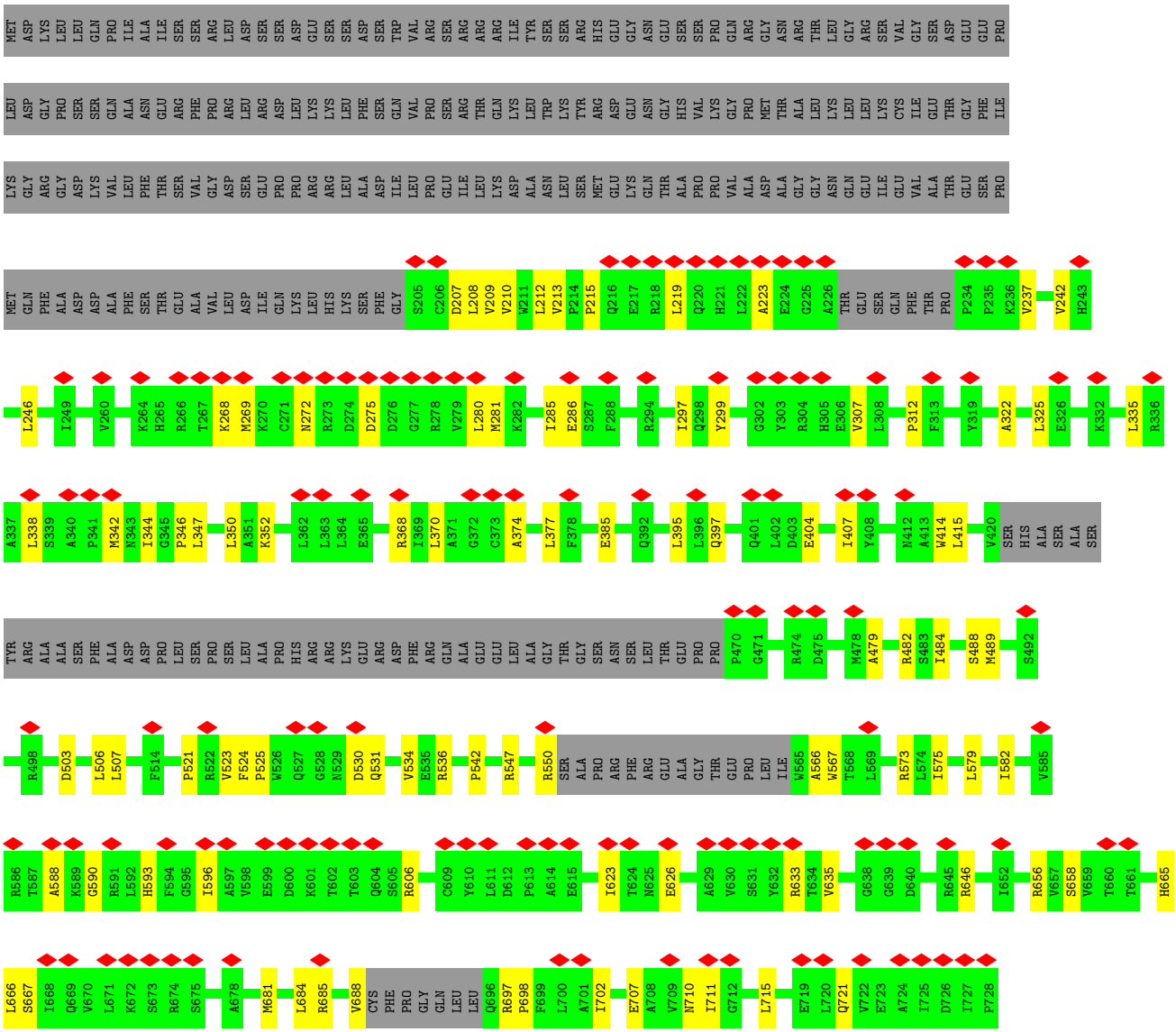




• Molecule 12: PCR14, TGME49_311880

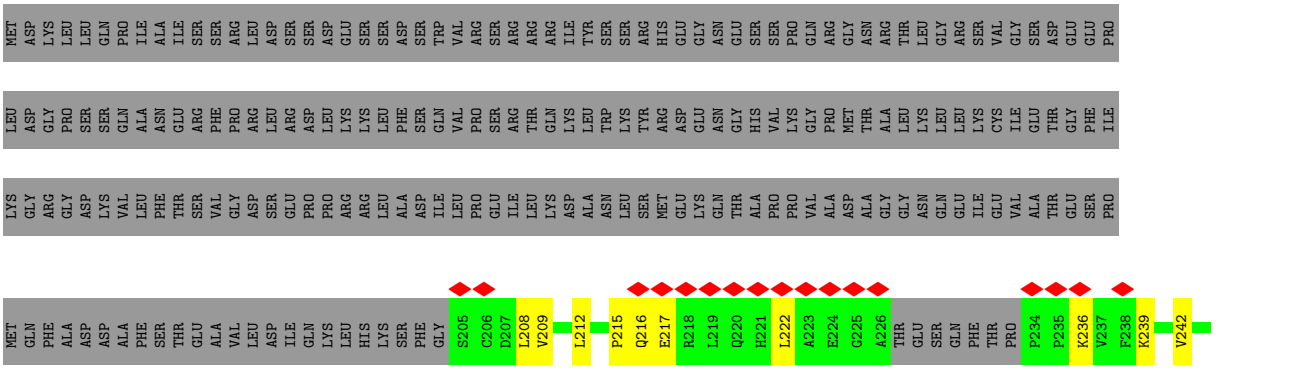
Chain KE:

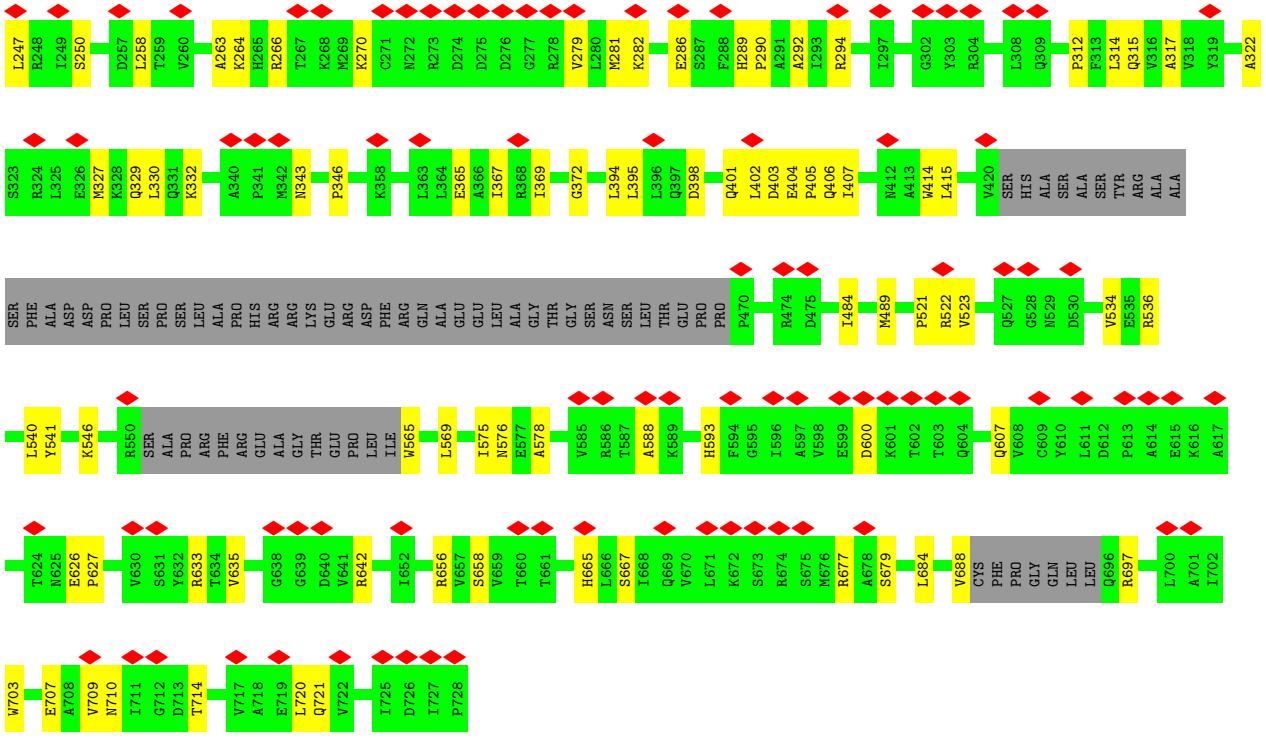




• Molecule 12: PCR14, TGME49_311880

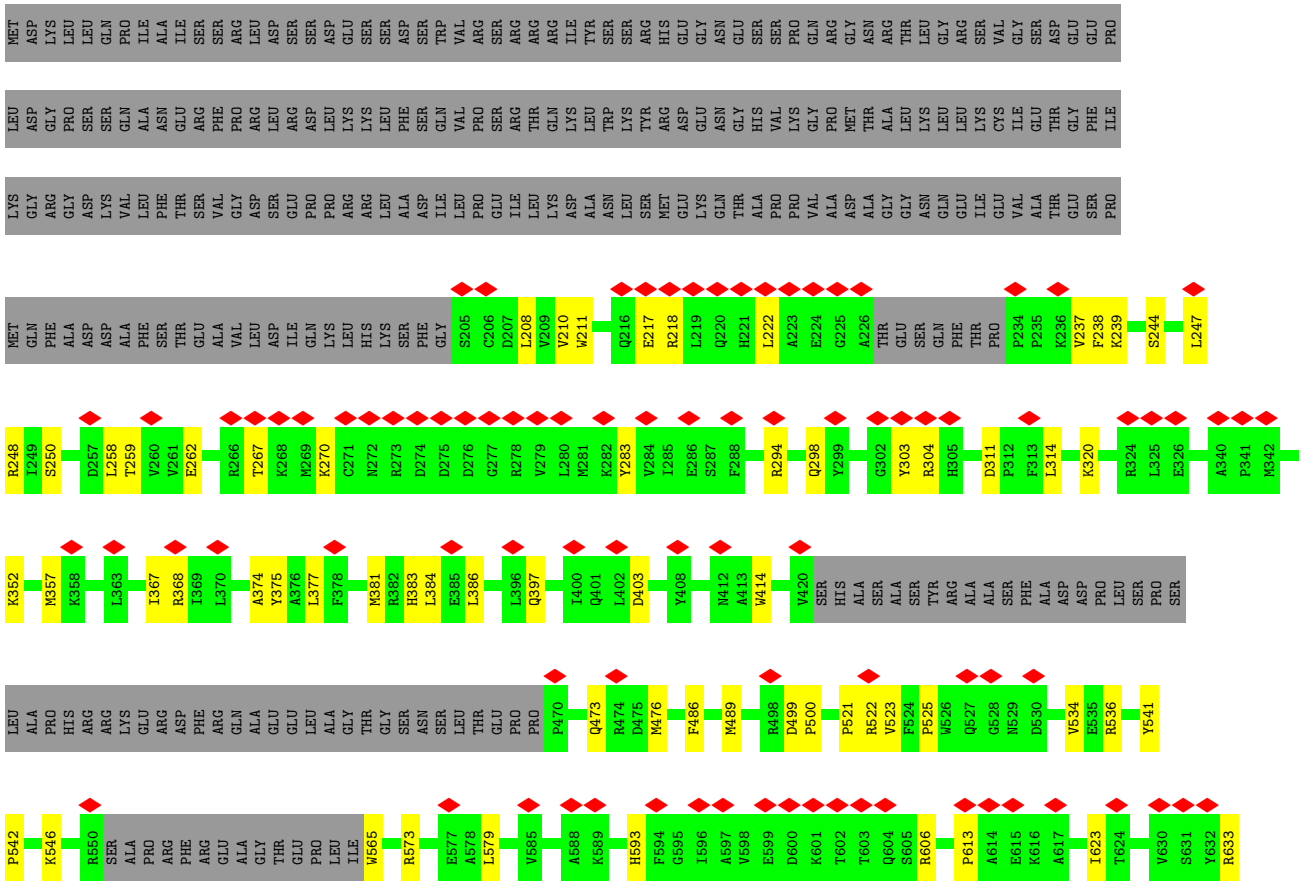
Chain KF:

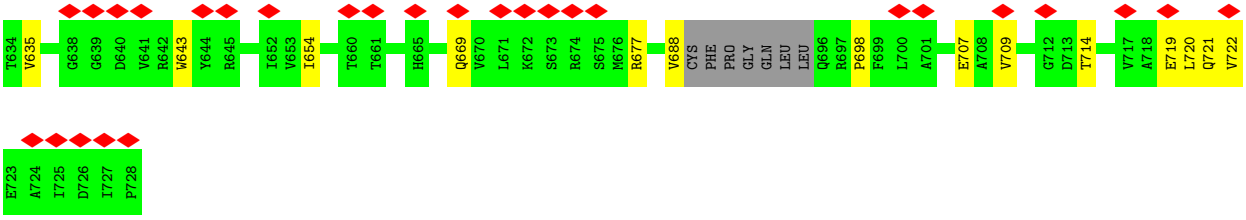




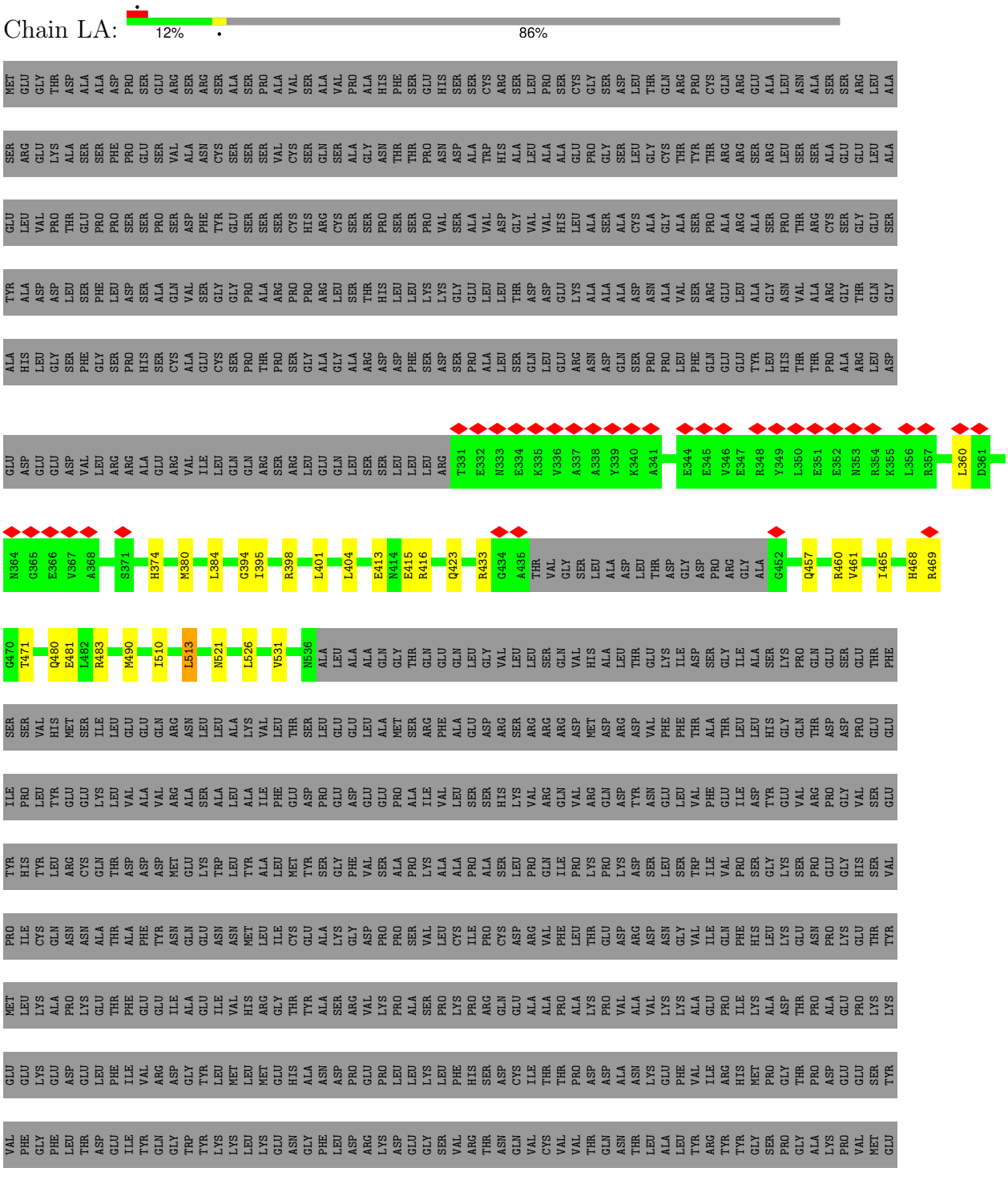
• Molecule 12: PCR14, TGME49_311880

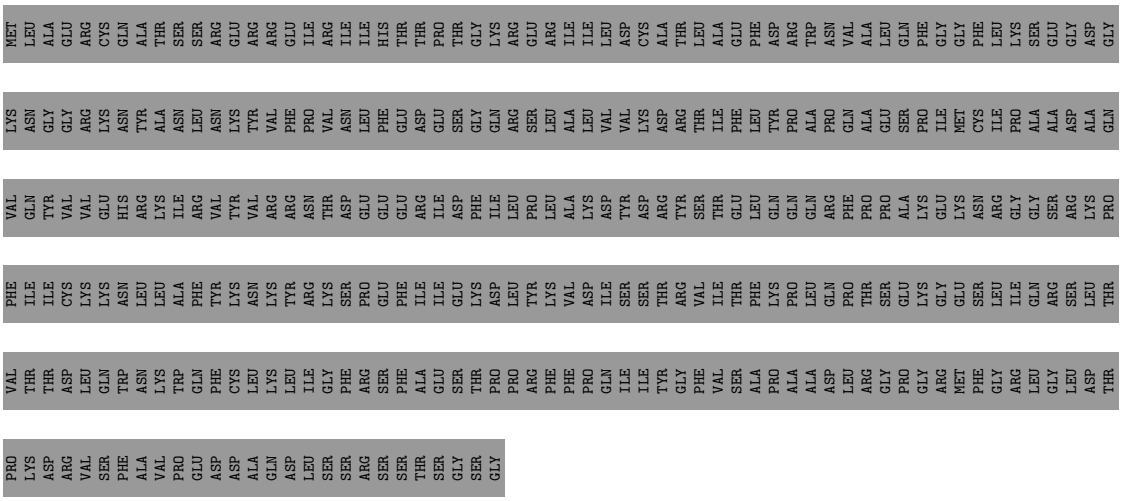
Chain KG:





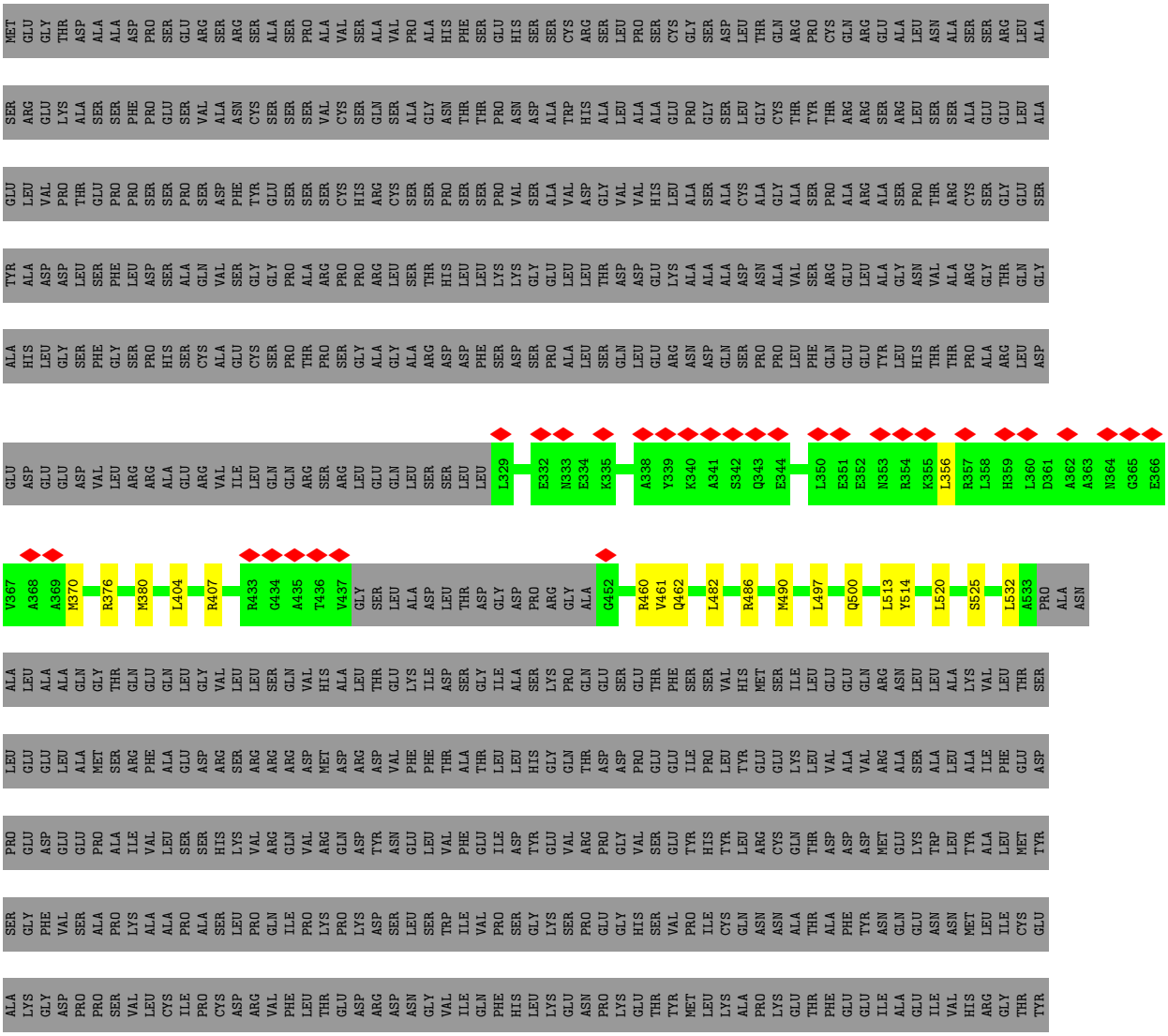
• Molecule 13: ICAP16, TGME49_202120

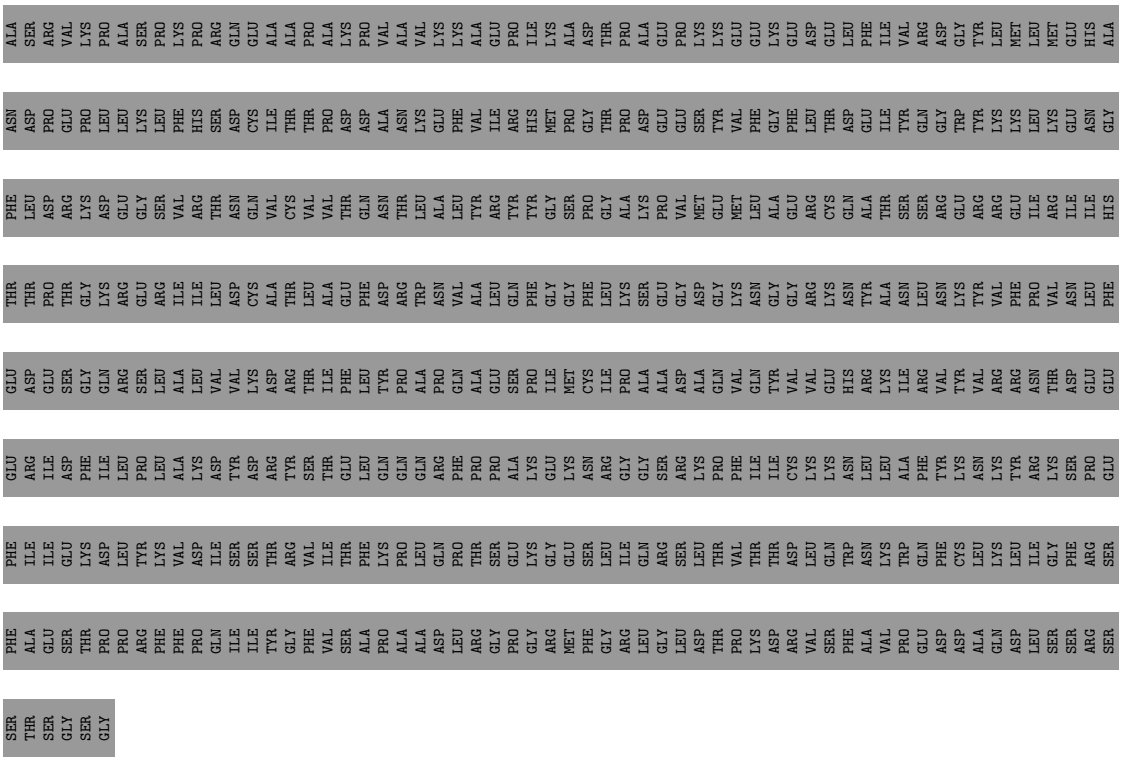




• Molecule 13: ICAP16, TGME49_202120

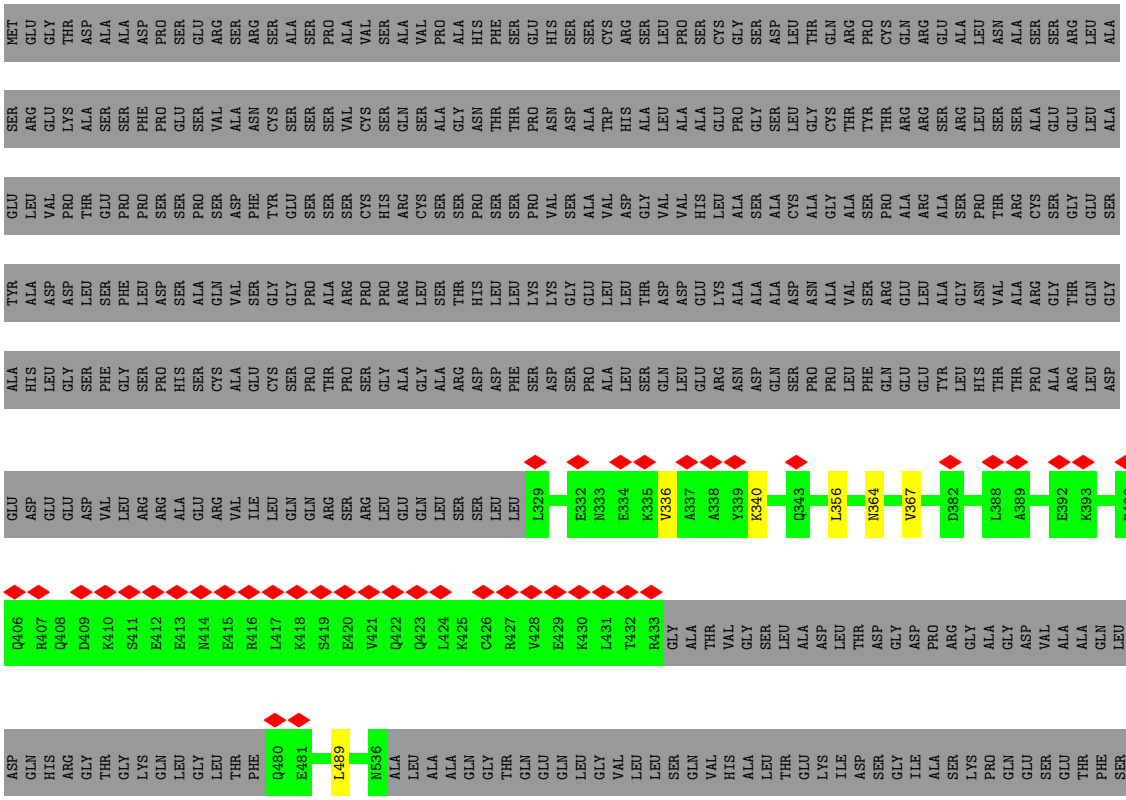
Chain LB:

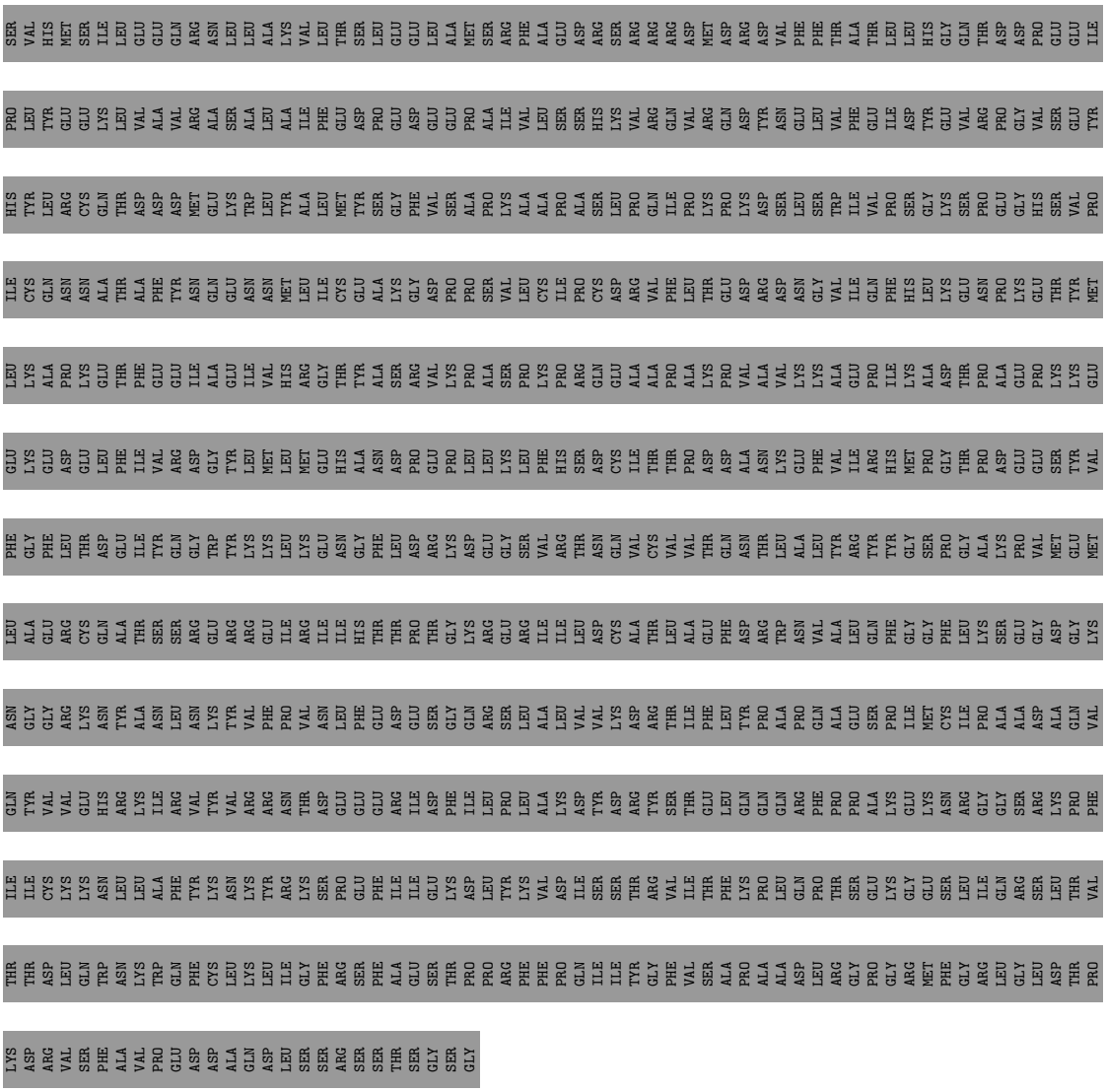




• Molecule 13: ICAP16, TGME49_202120

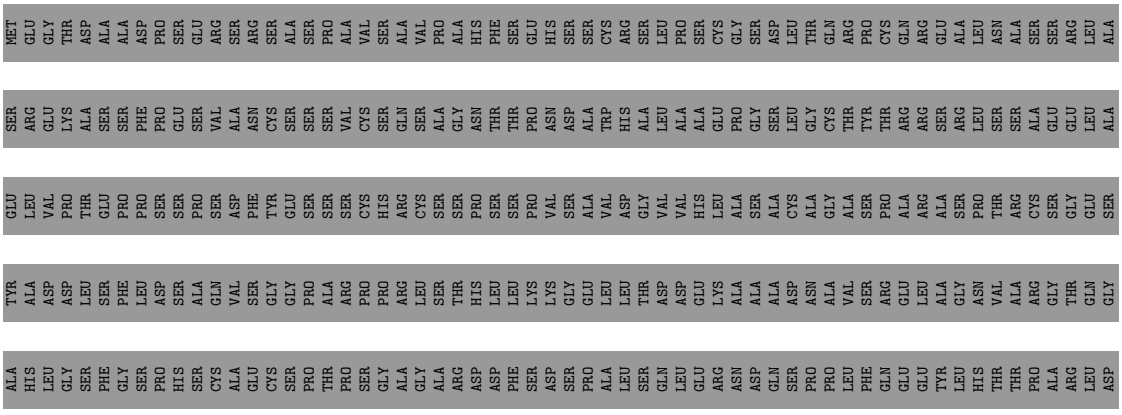
Chain LC:

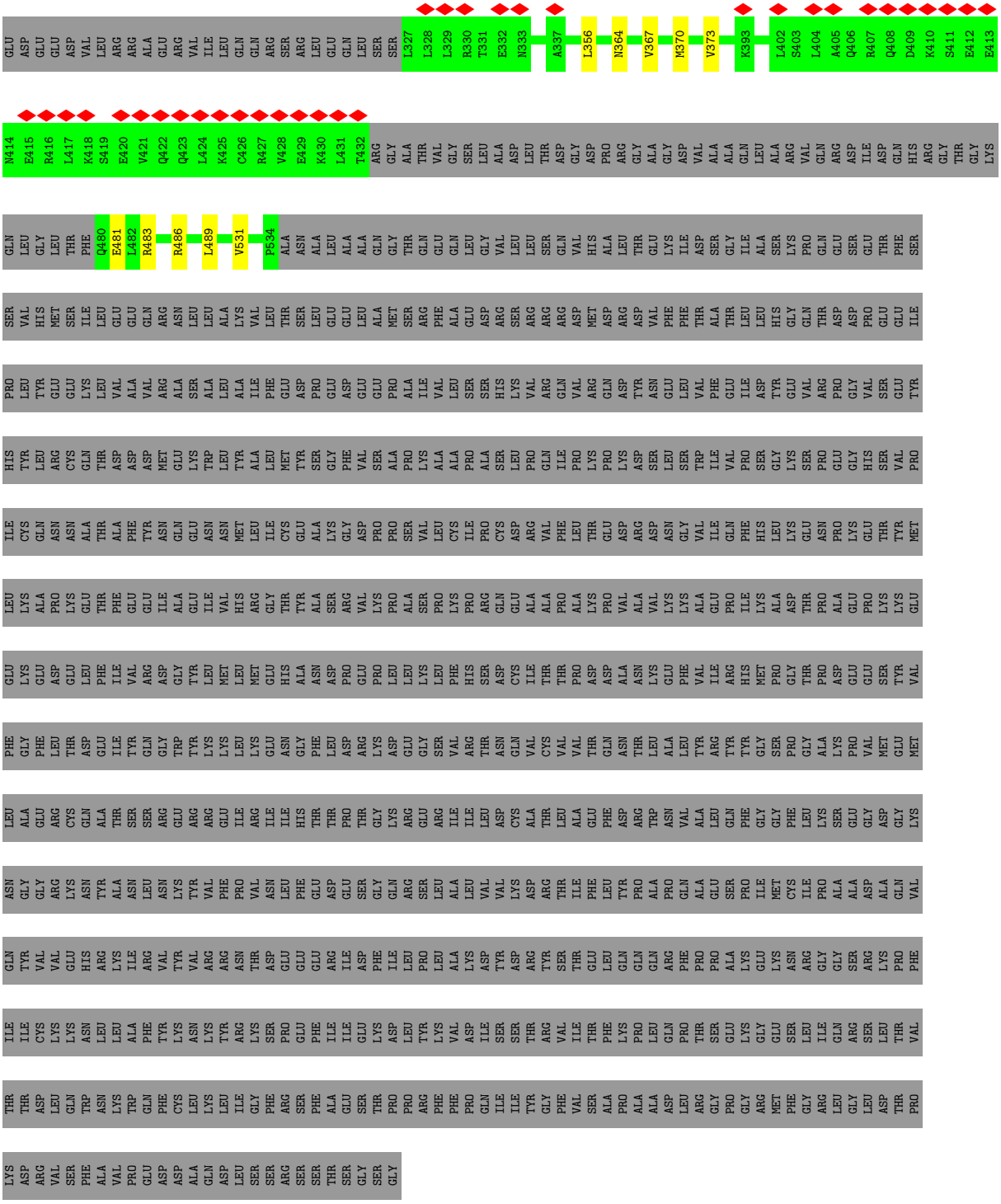




• Molecule 13: ICAP16, TGME49_202120

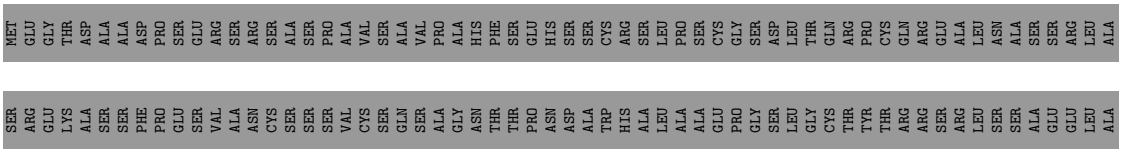
Chain LD:

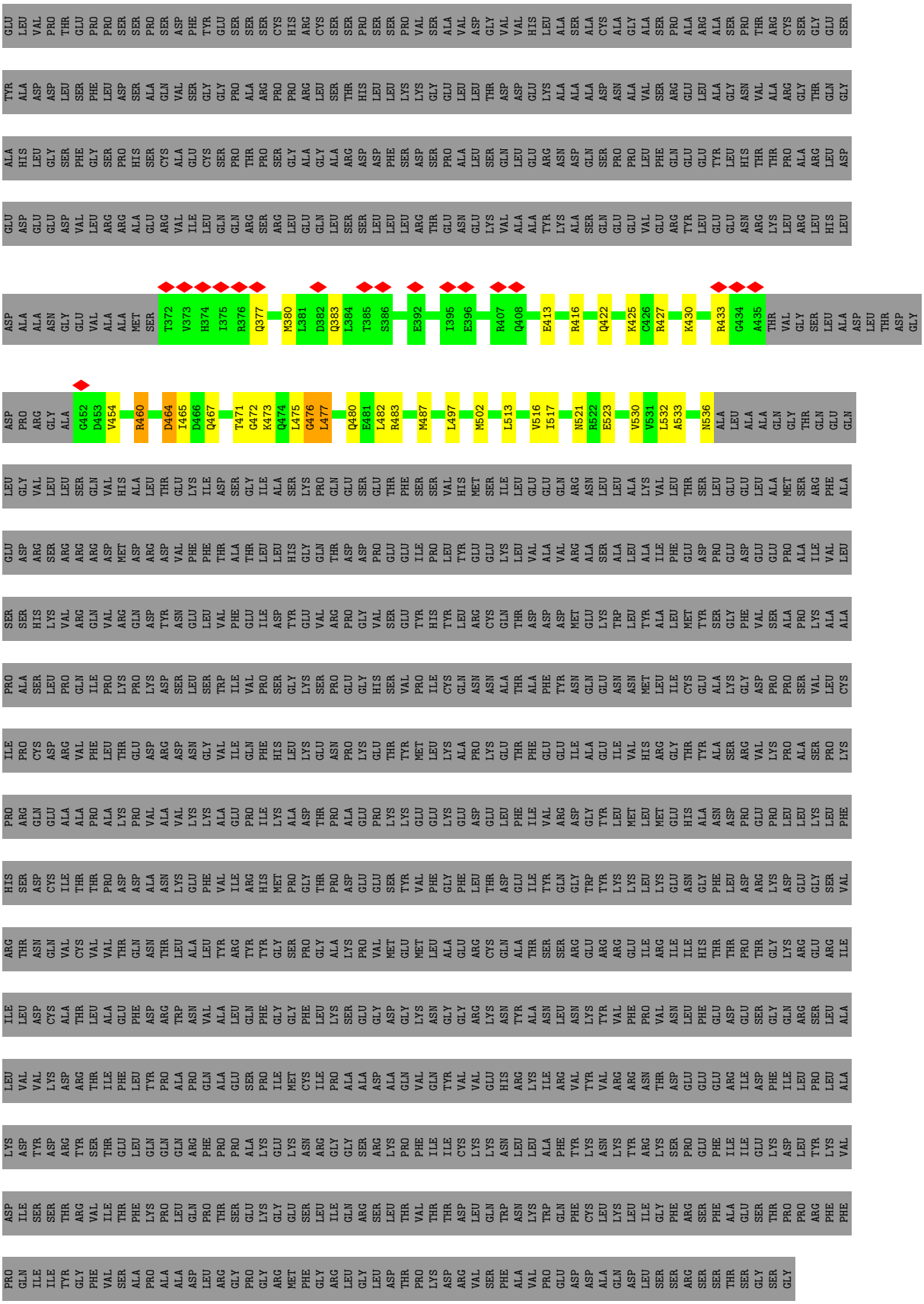




• Molecule 13: ICAP16, TGME49_202120

Chain LE:

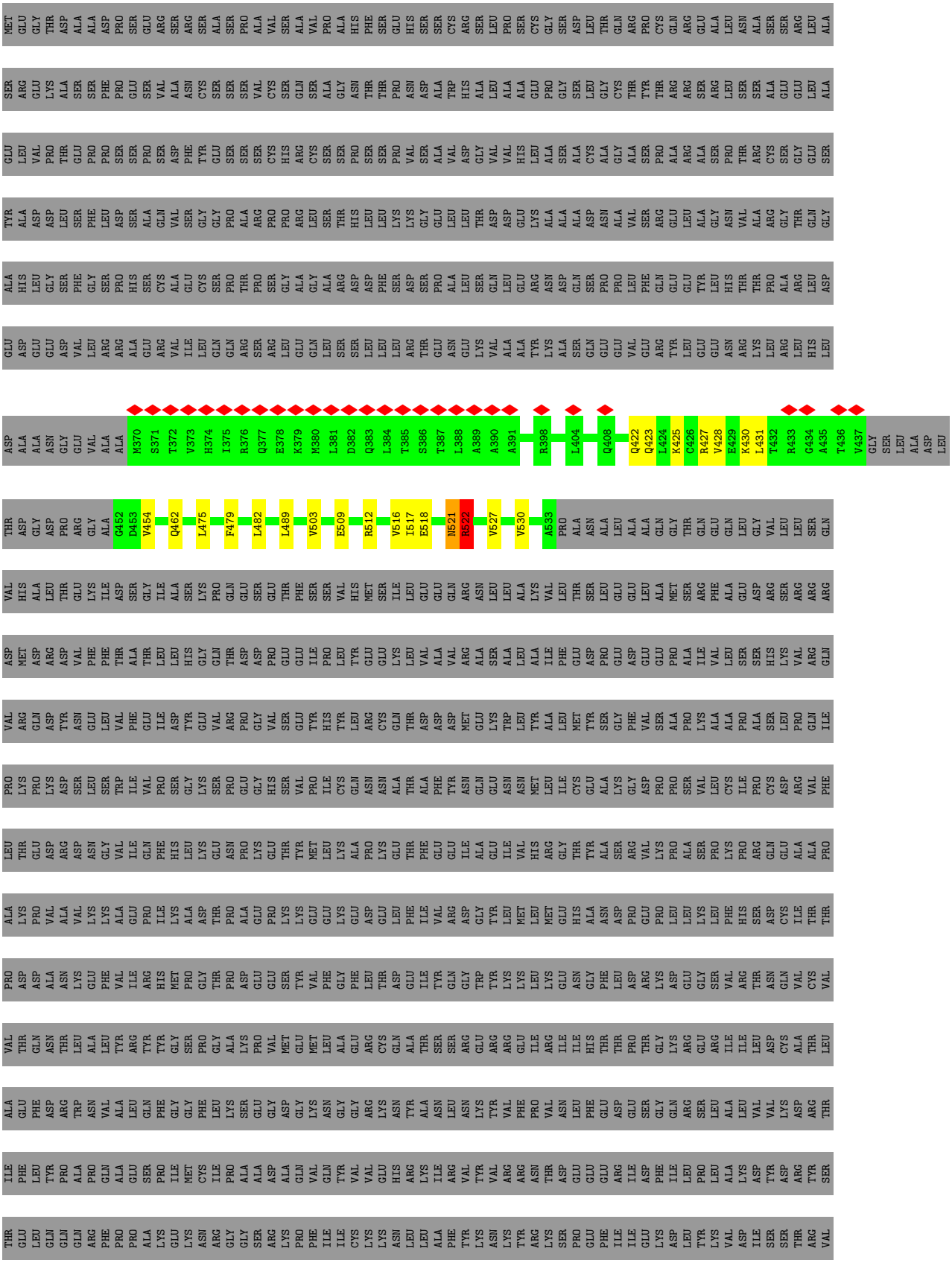


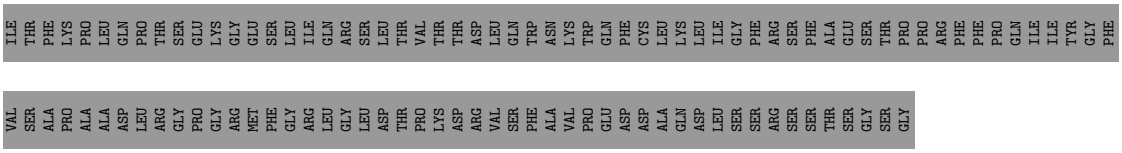


- Molecule 13: ICAP16, TGME49_202120

Chain LF:

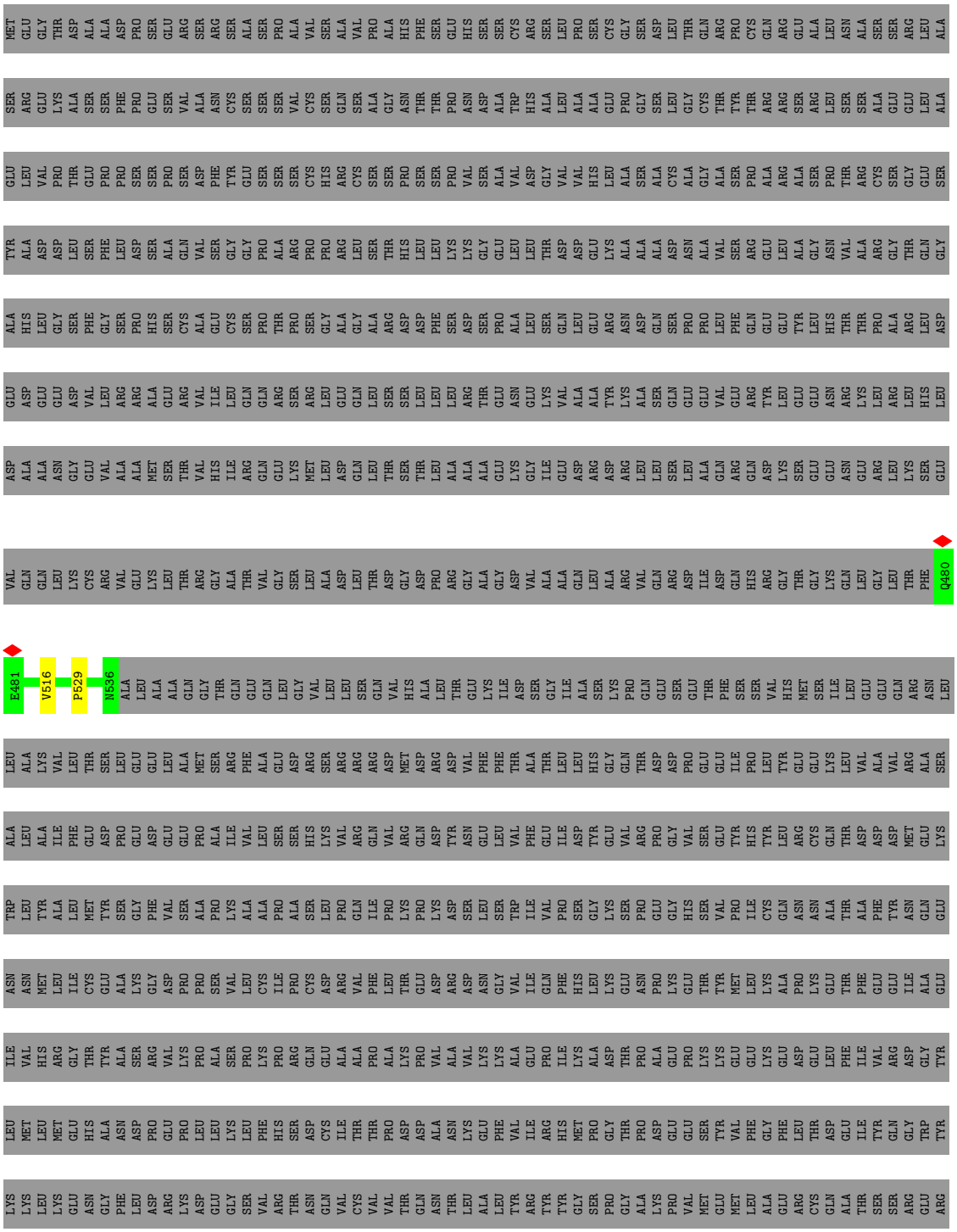
10%
89%

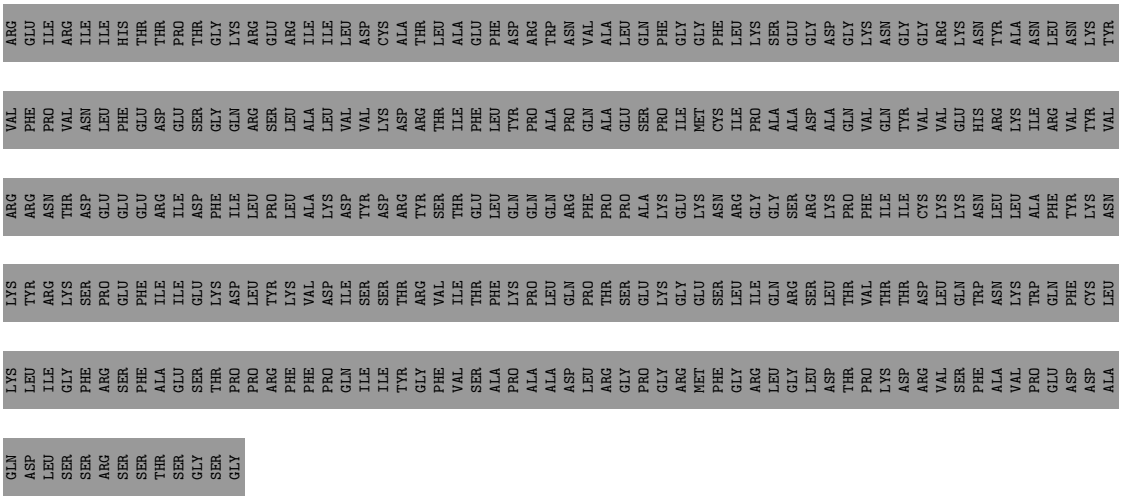

M370
S371
T372
V373
H374
I375
R376
Q377
E378
K379
M380
L381
D382
Q383
L384
T385
S386
T387
L388
A389
A390
A391
R398
L404
Q408
Q422
Q423
L424
K425
C426
R427
V428
E429
K430
L431
T432
R433
G434
A435
T436
V437
G452
D453
V454
Q462
L475
F479
L482
L489
V503
E509
R512
V516
I517
E518
N521
R522
V527
V530
A533



• Molecule 13: ICAP16, TGME49_202120

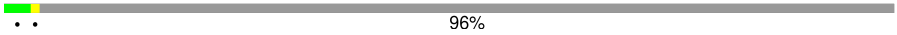
Chain LG: 96%

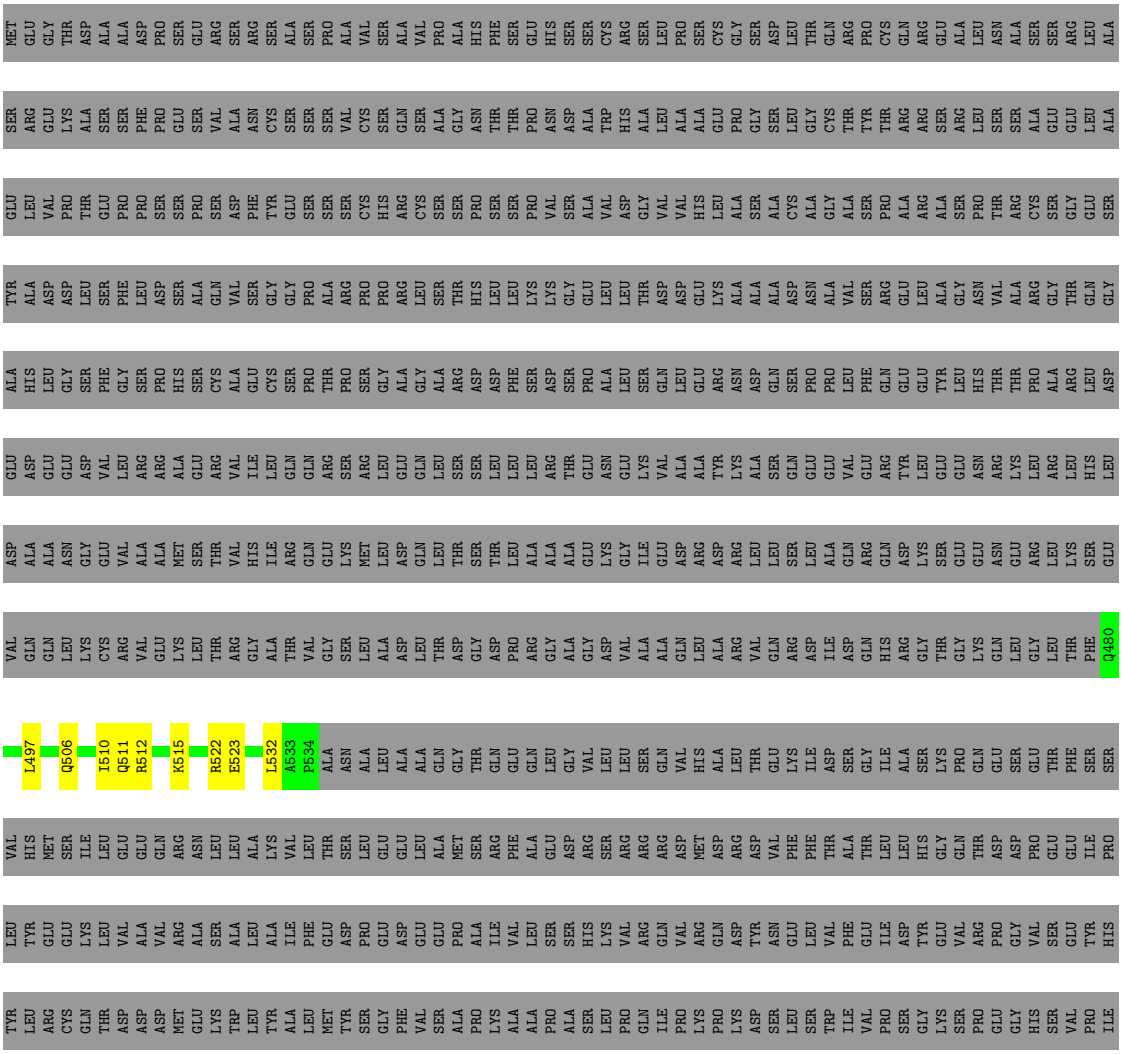


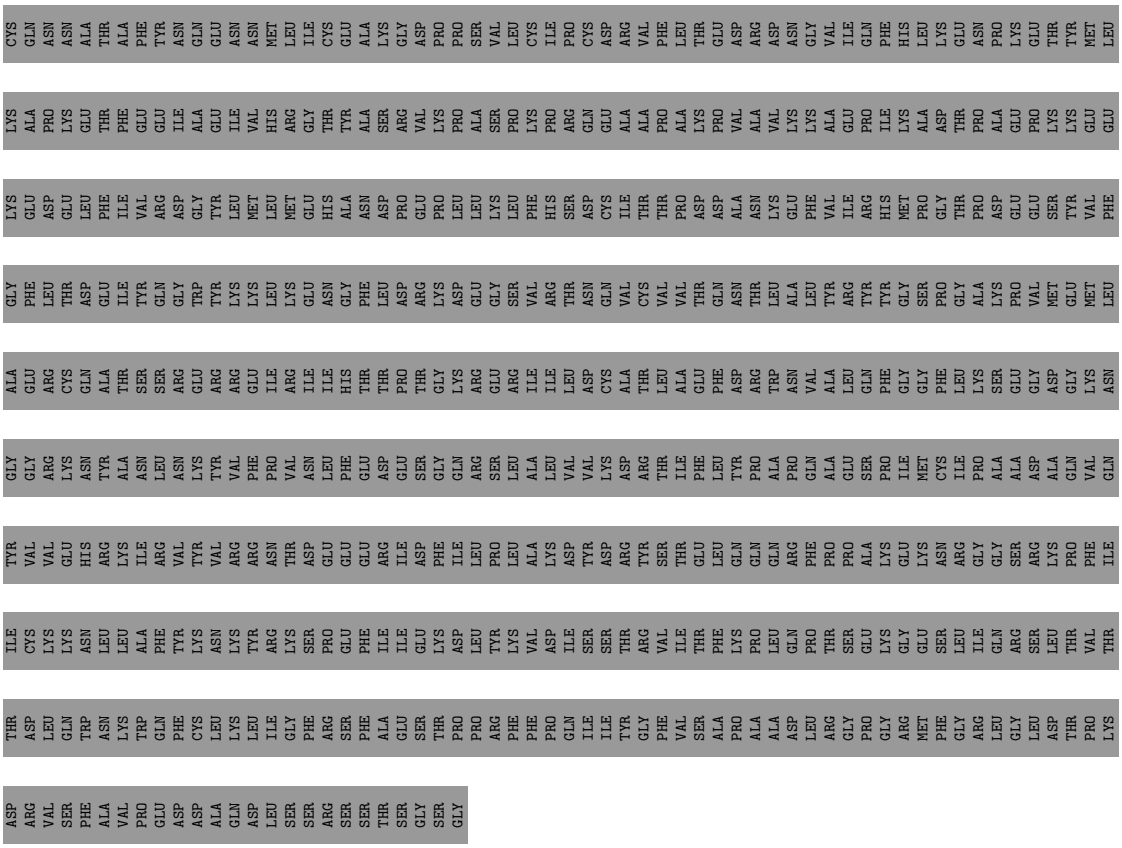


• Molecule 13: ICAP16, TGME49_202120

Chain LH:

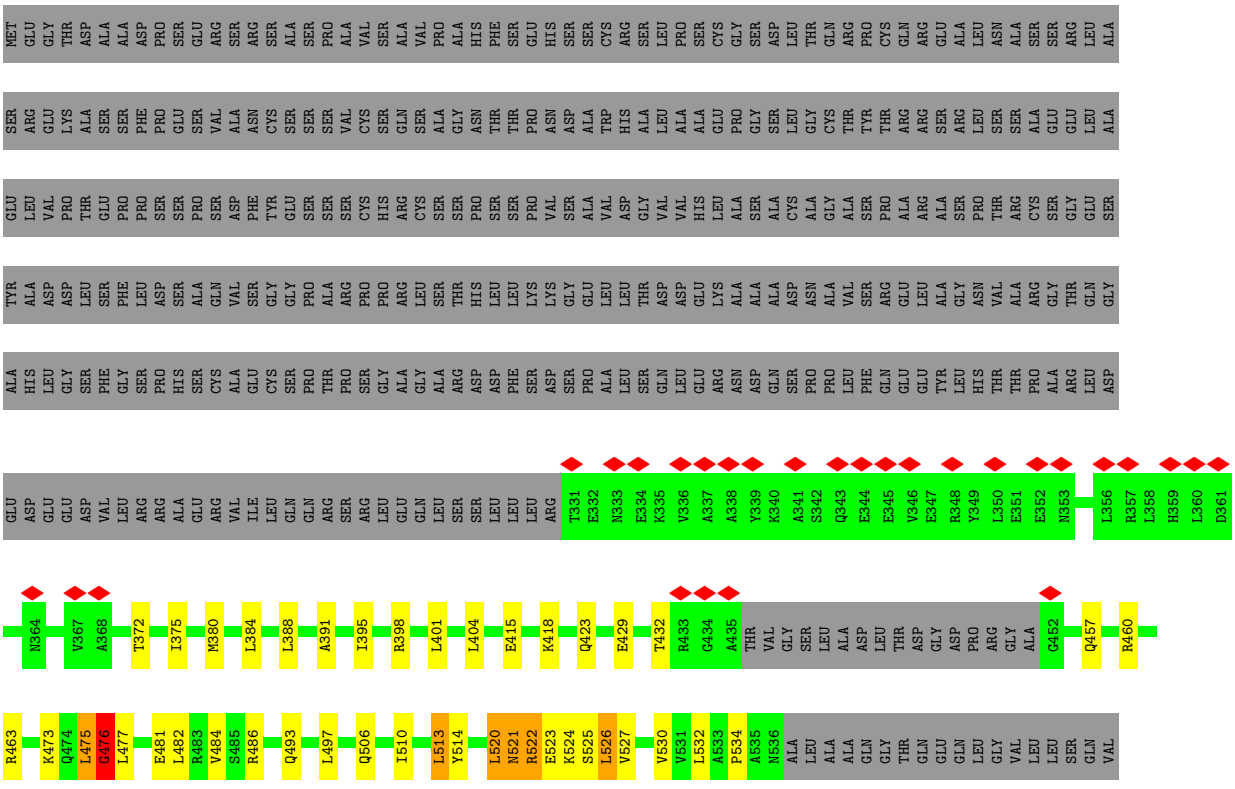


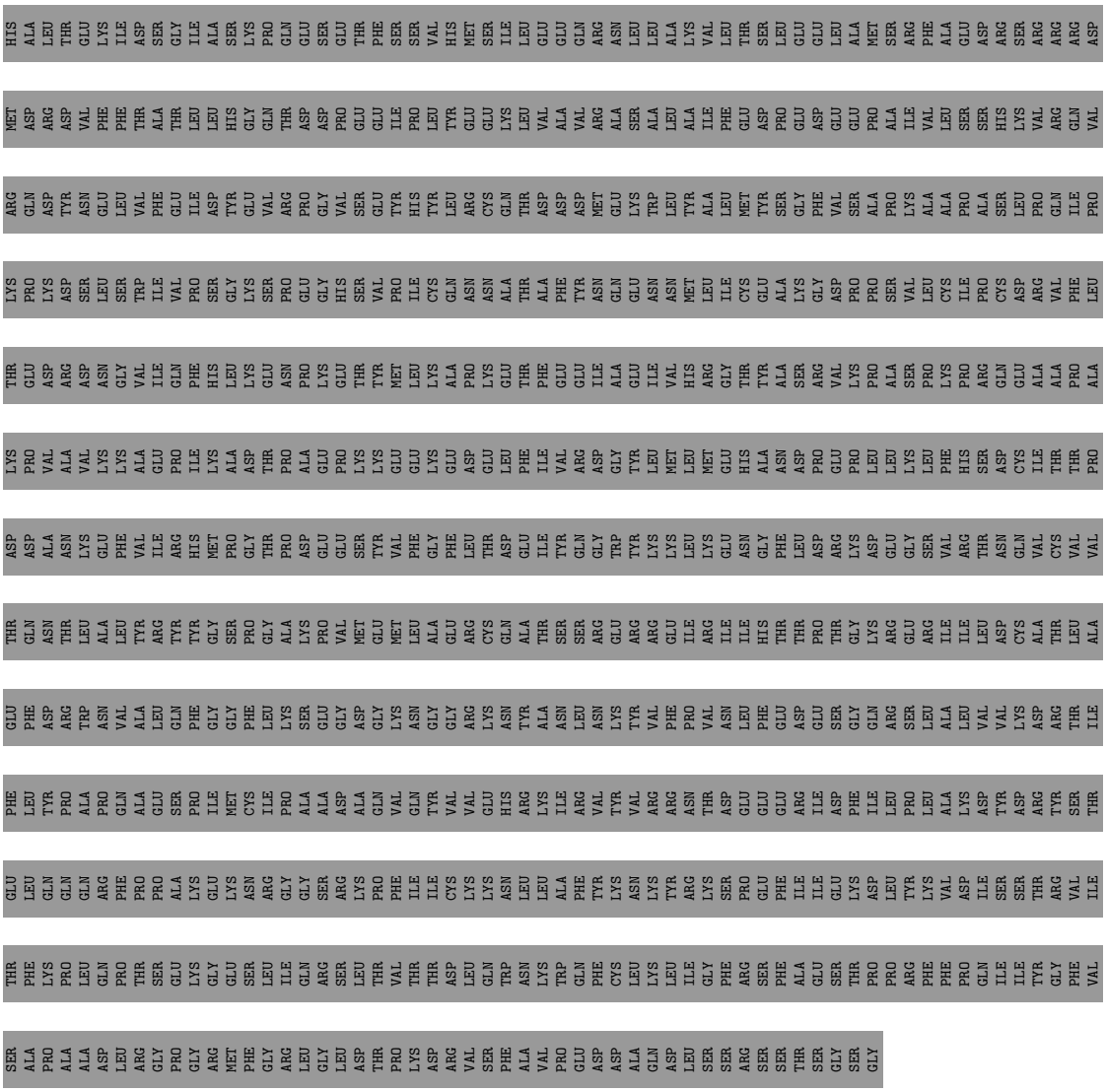




• Molecule 13: ICAP16, TGME49_202120

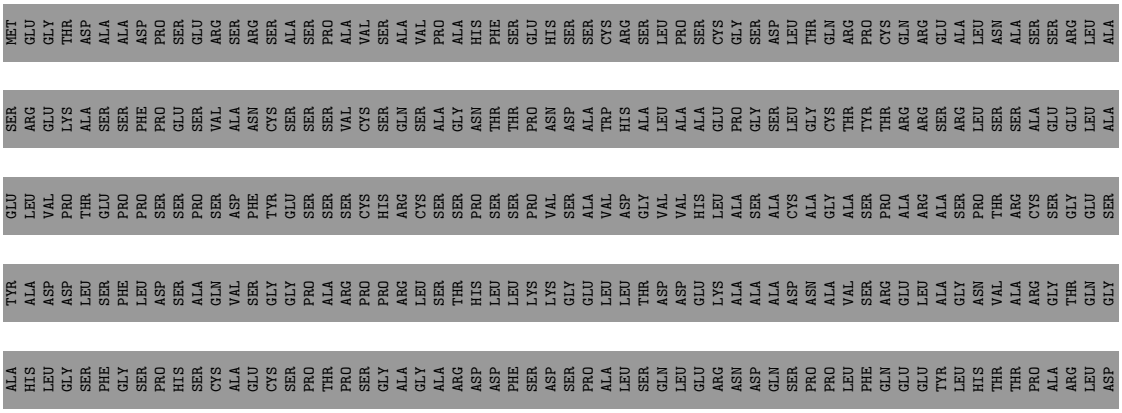
Chain LI:

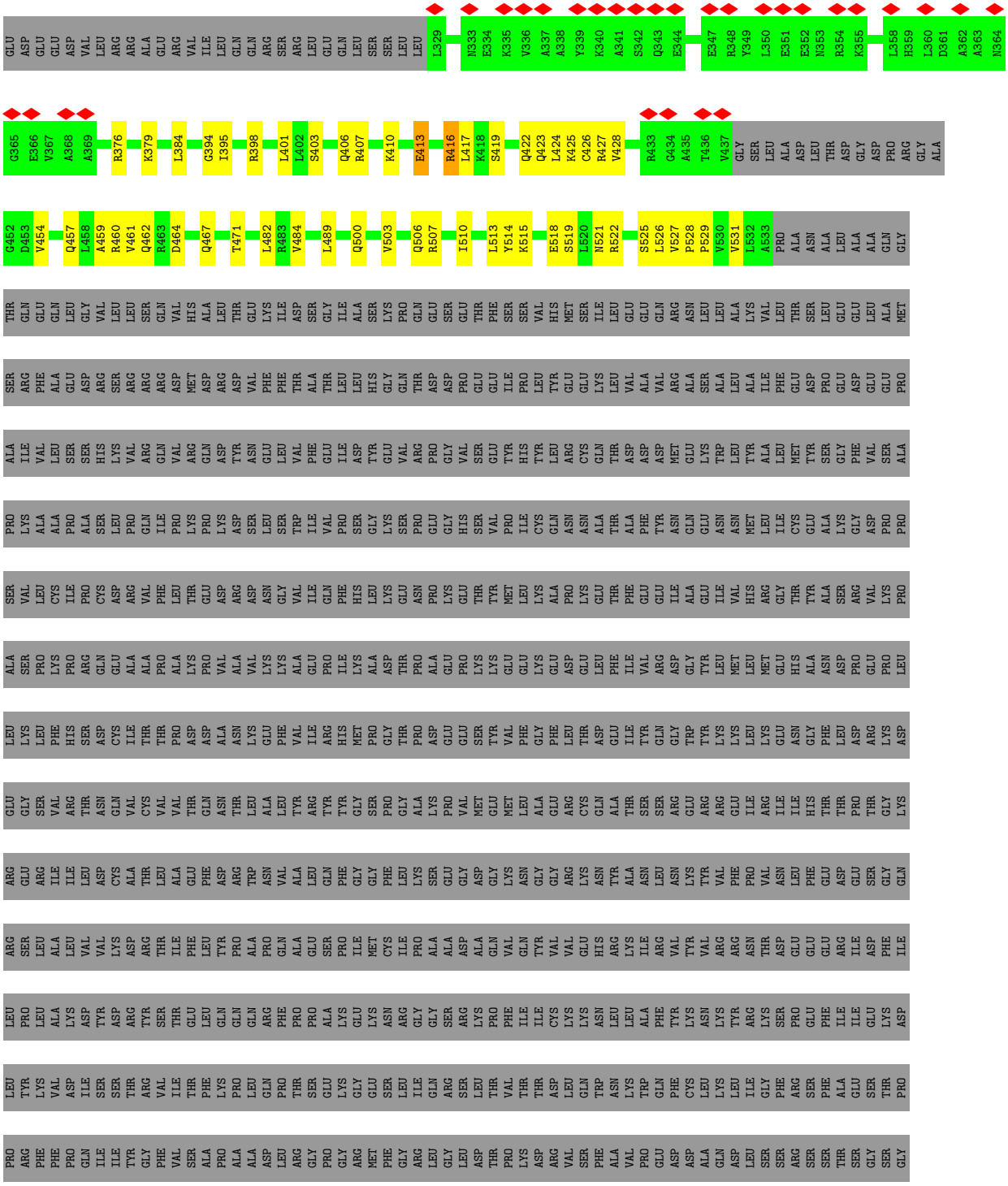




• Molecule 13: ICAP16, TGME49_202120

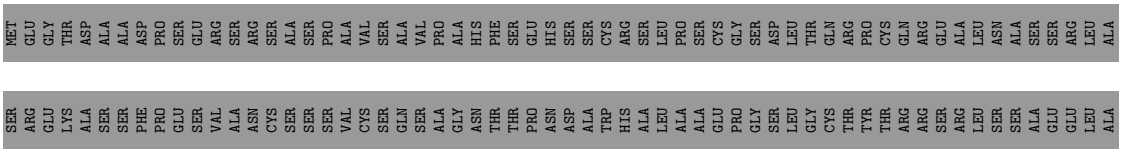
Chain LJ:

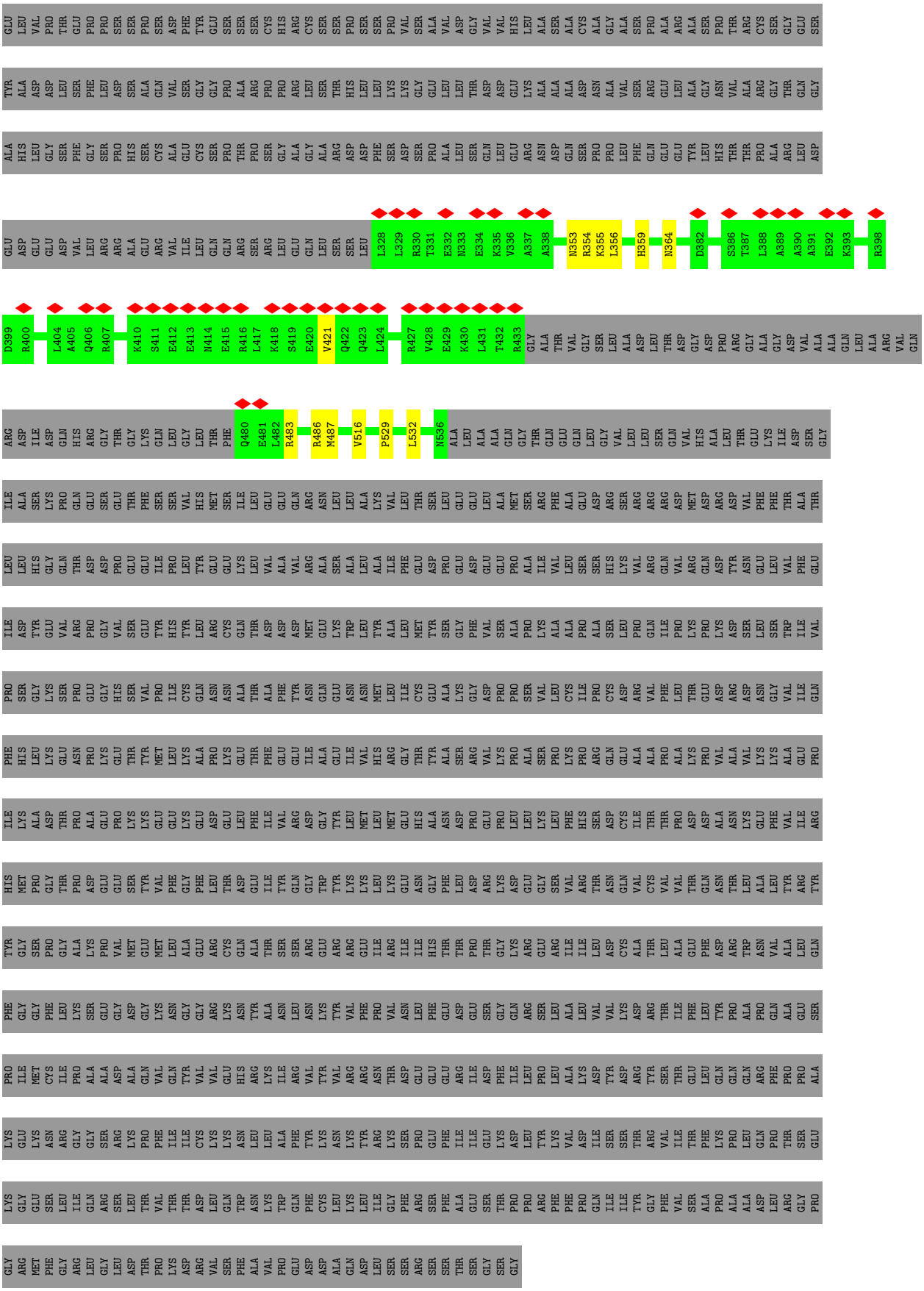




• Molecule 13: ICAP16, TGME49_202120

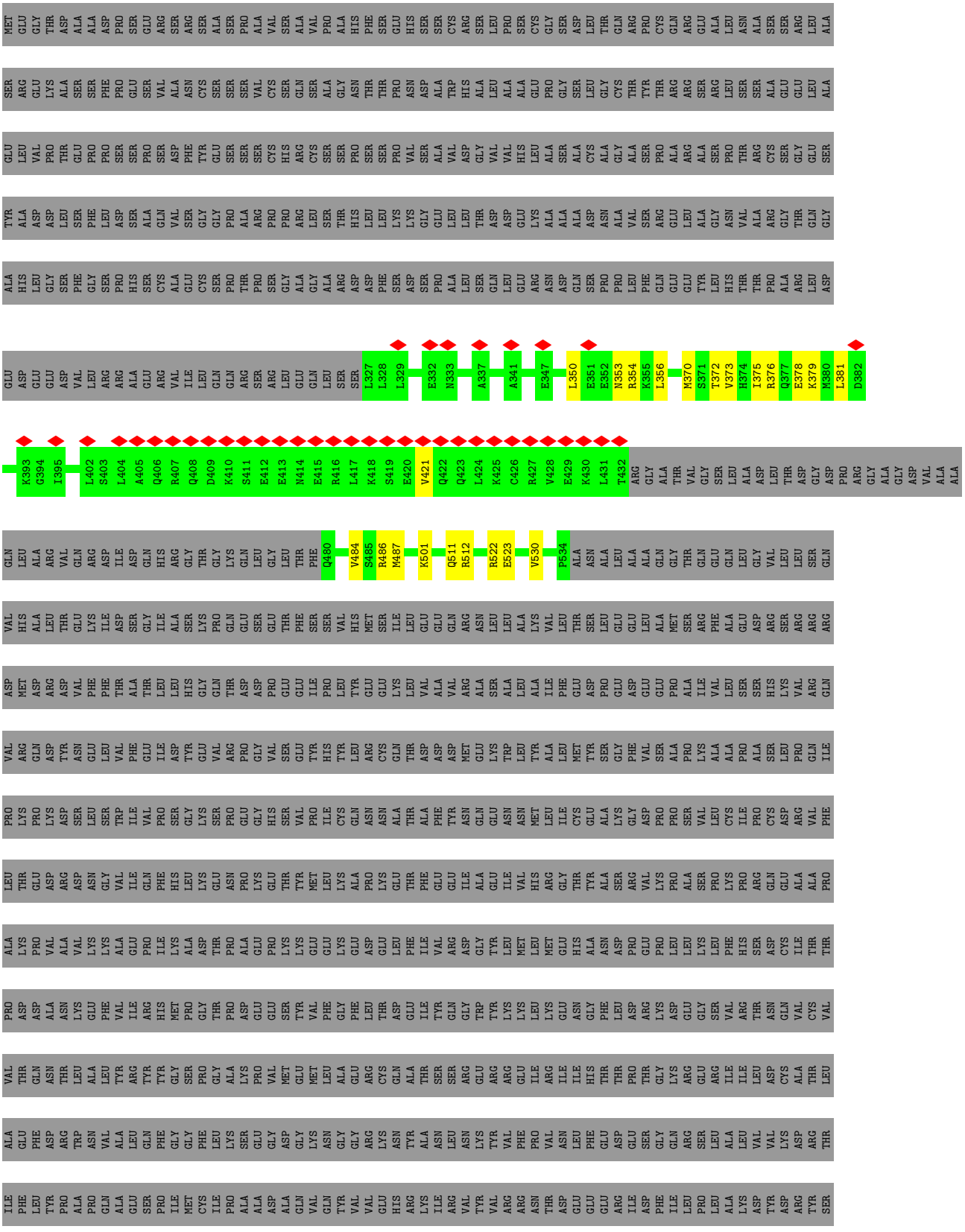
Chain LK:

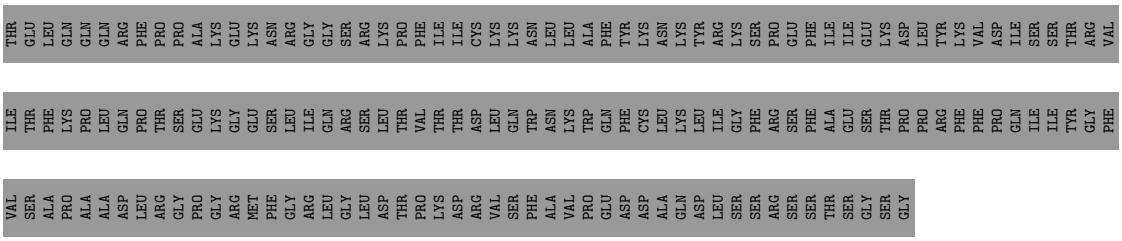



L328 L329 R330 T331 E332 N333 E334 K335 V336 A337 A338 N353 R354 K355 L356 H359 N364 D382 S386 T387 L388 A389 A390 A391 E392 K393 R398
D399 R400 L404 A405 Q406 R407 K410 S411 E412 E413 N414 E415 R416 L417 K418 S419 E420 V421 Q422 Q423 L424 R427 V428 E429 K430 L431 T432 R433
Q480 E481 L482 R483 R486 M487 V516 P529 L532 N536

• Molecule 13: ICAP16, TGME49_202120

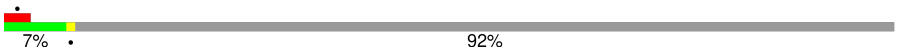
Chain LL:

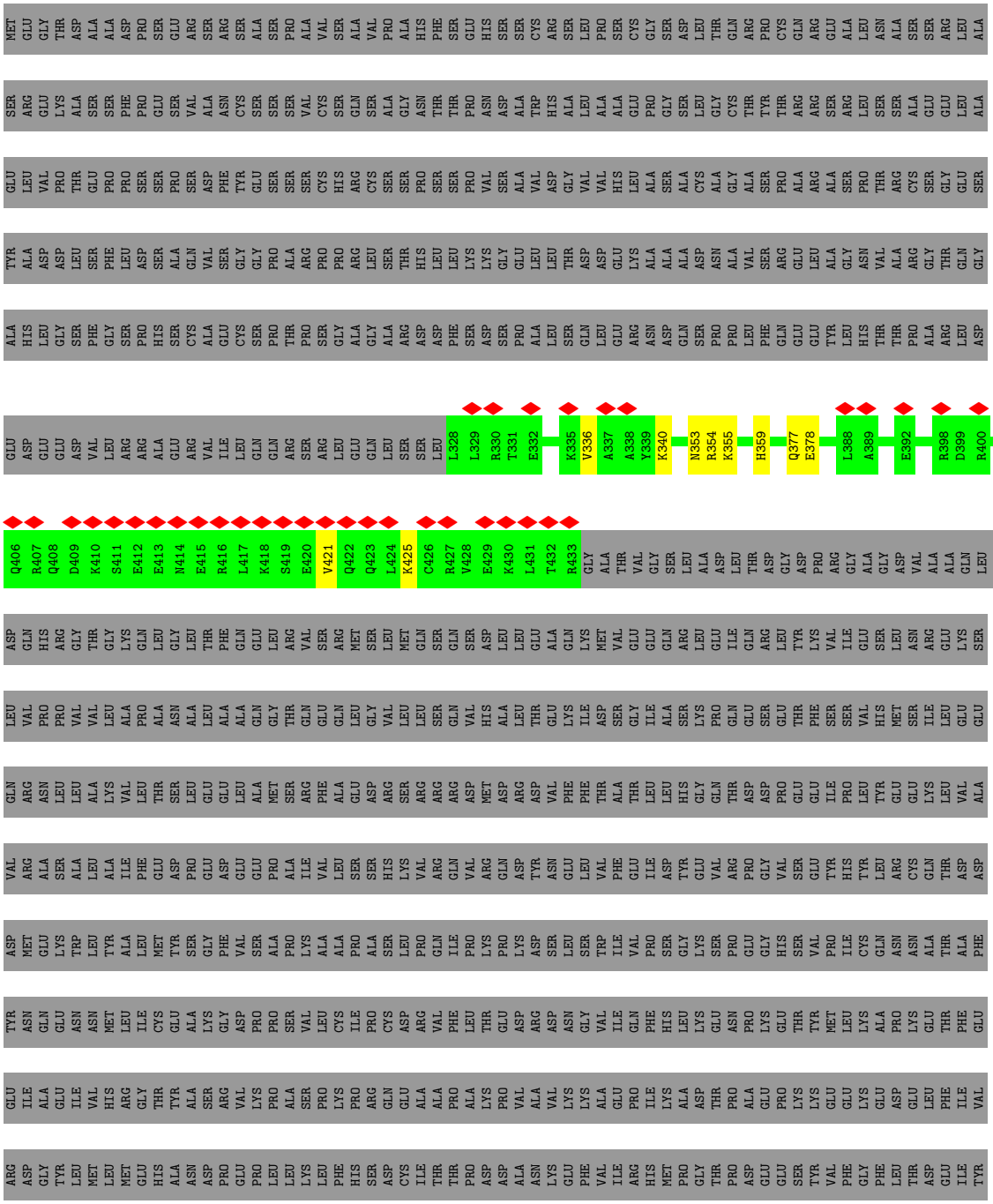


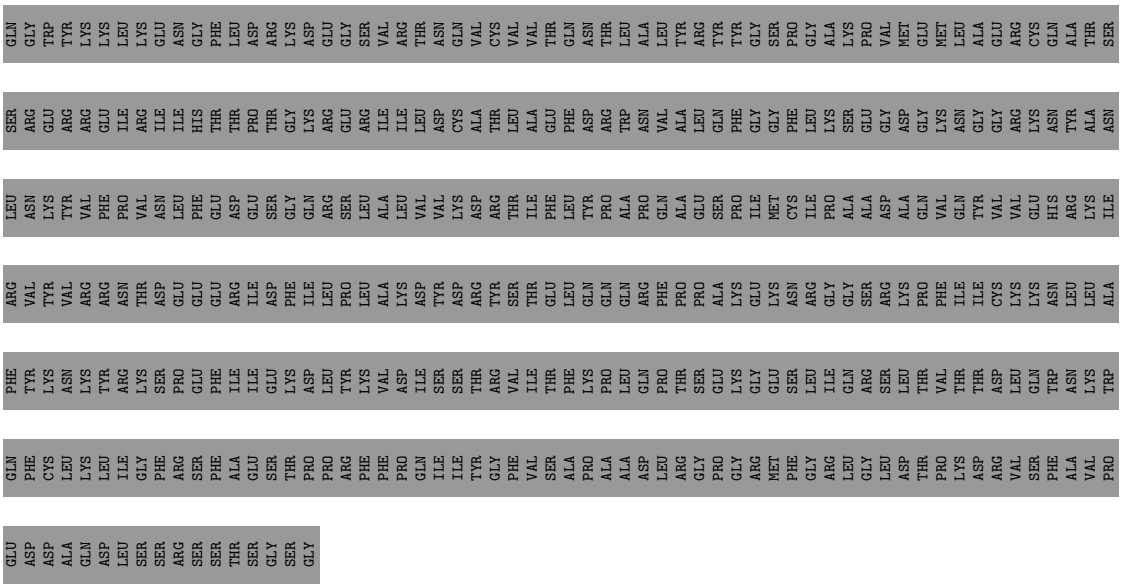


• Molecule 13: ICAP16, TGME49_202120

Chain LM:

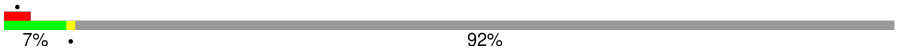


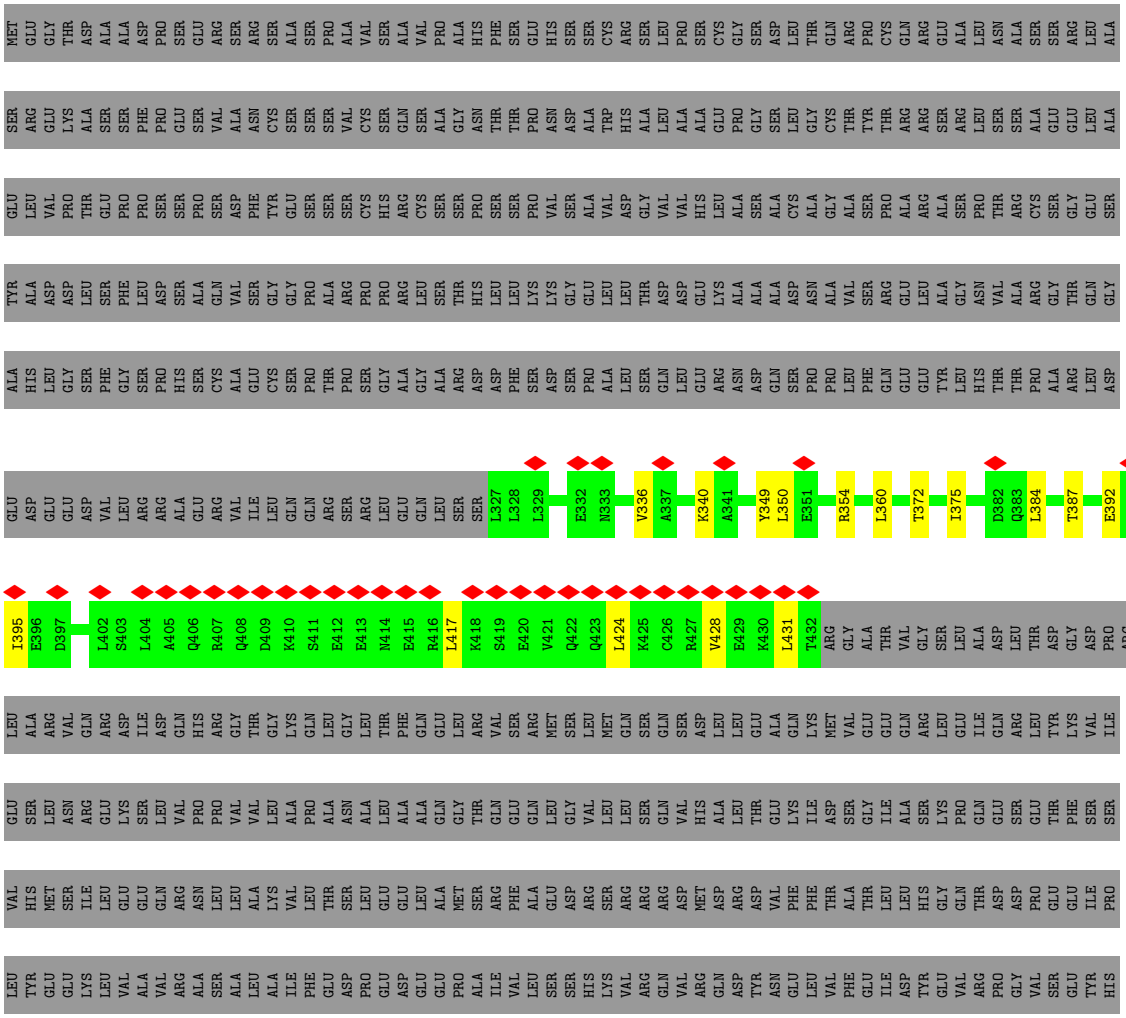


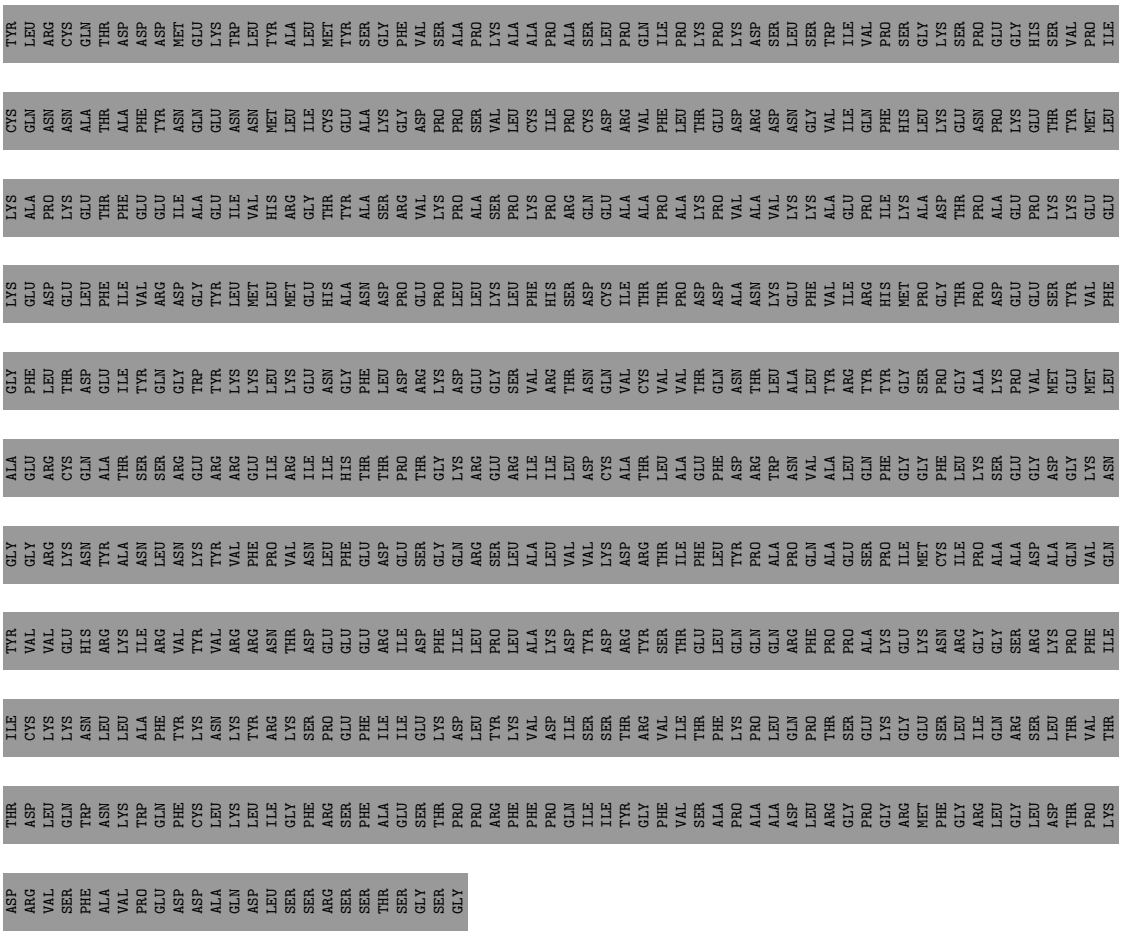


• Molecule 13: ICAP16, TGME49_202120

Chain LN:

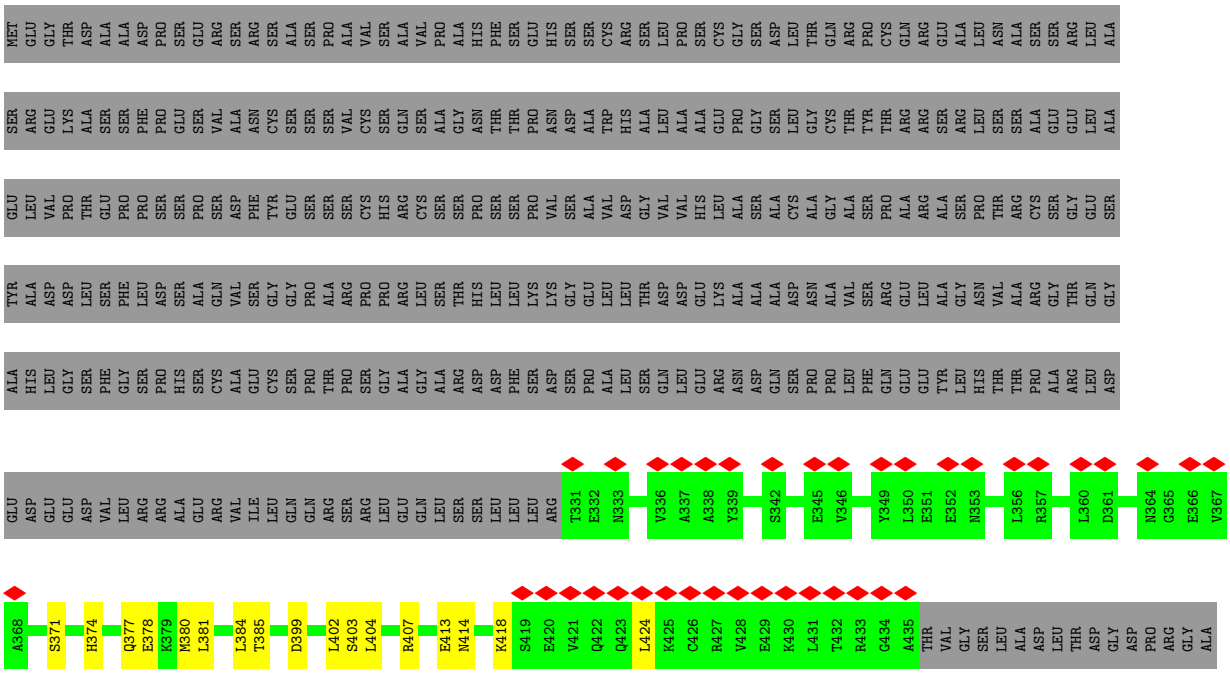


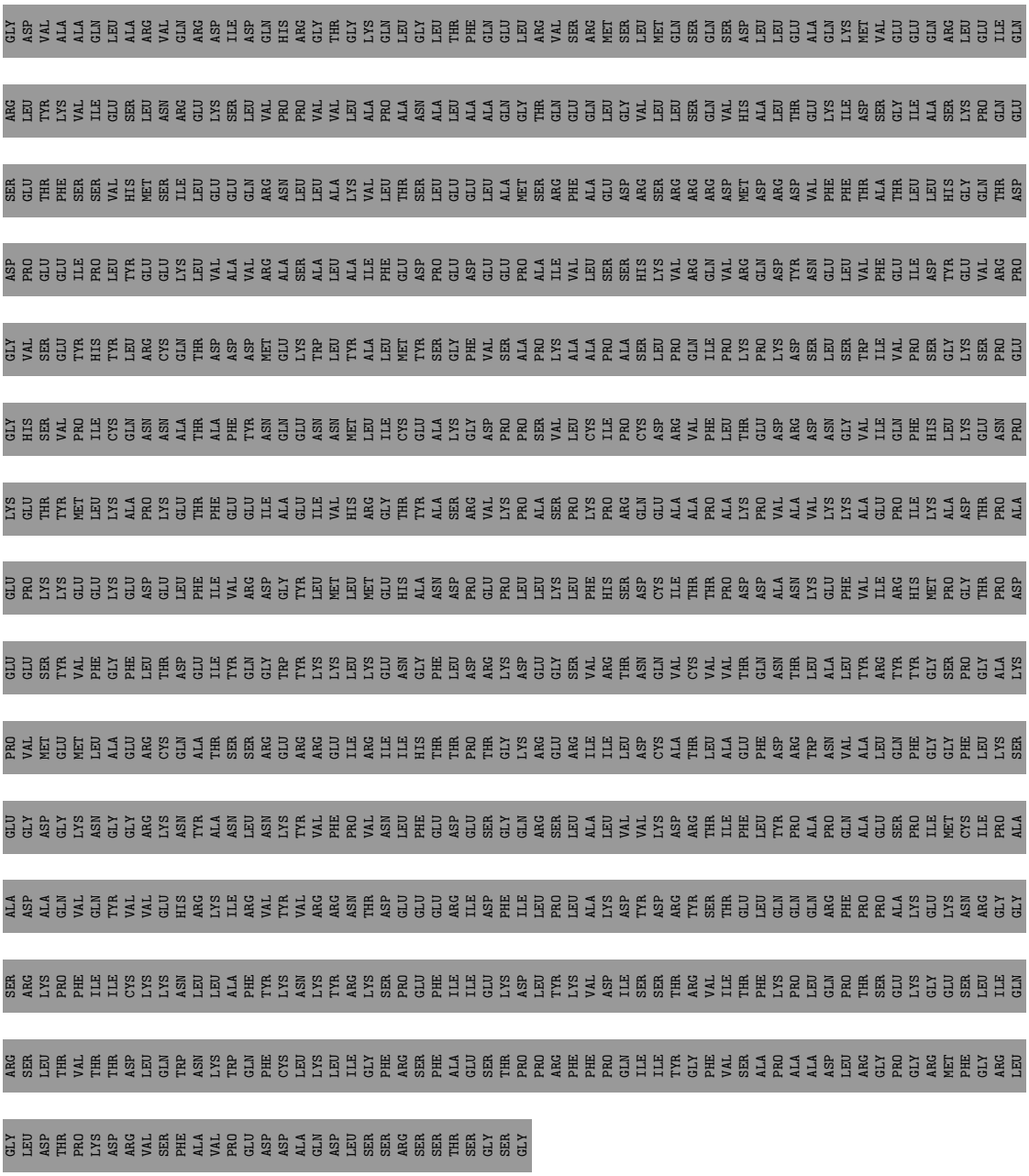




• Molecule 13: ICAP16, TGME49_202120

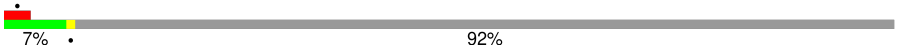
Chain LO: 7% 92%

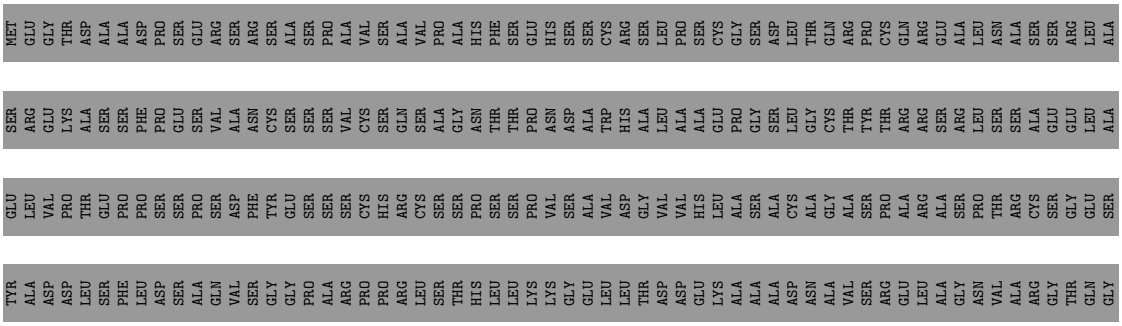


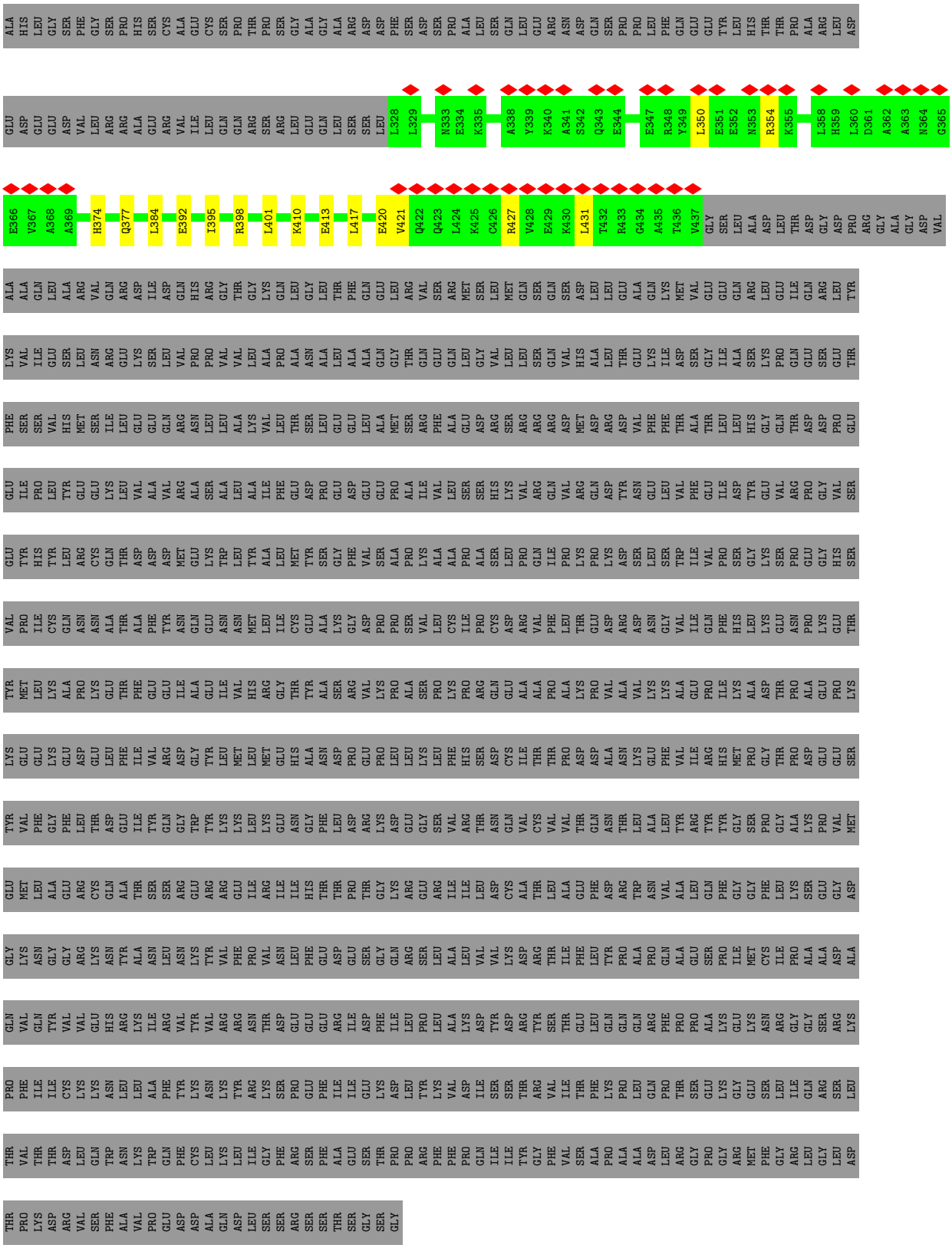


• Molecule 13: ICAP16, TGME49_202120

Chain LP:



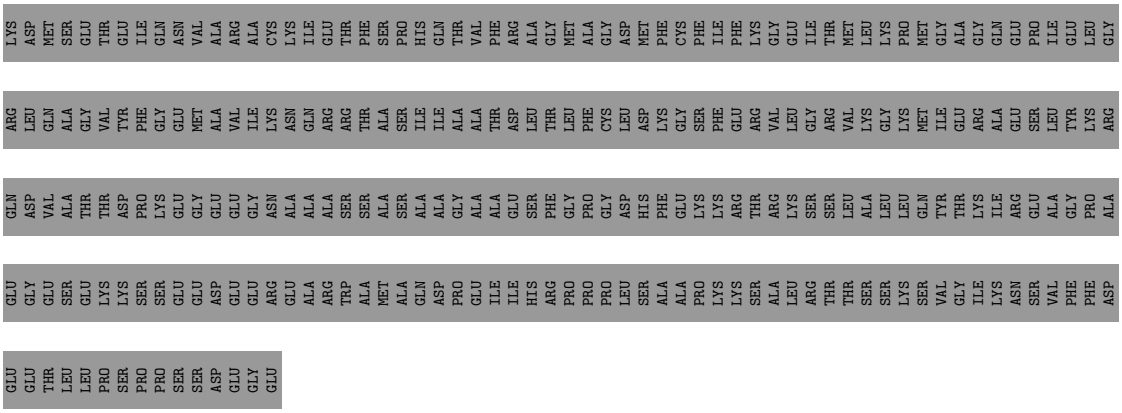




• Molecule 14: PCR12, TGME49_219070

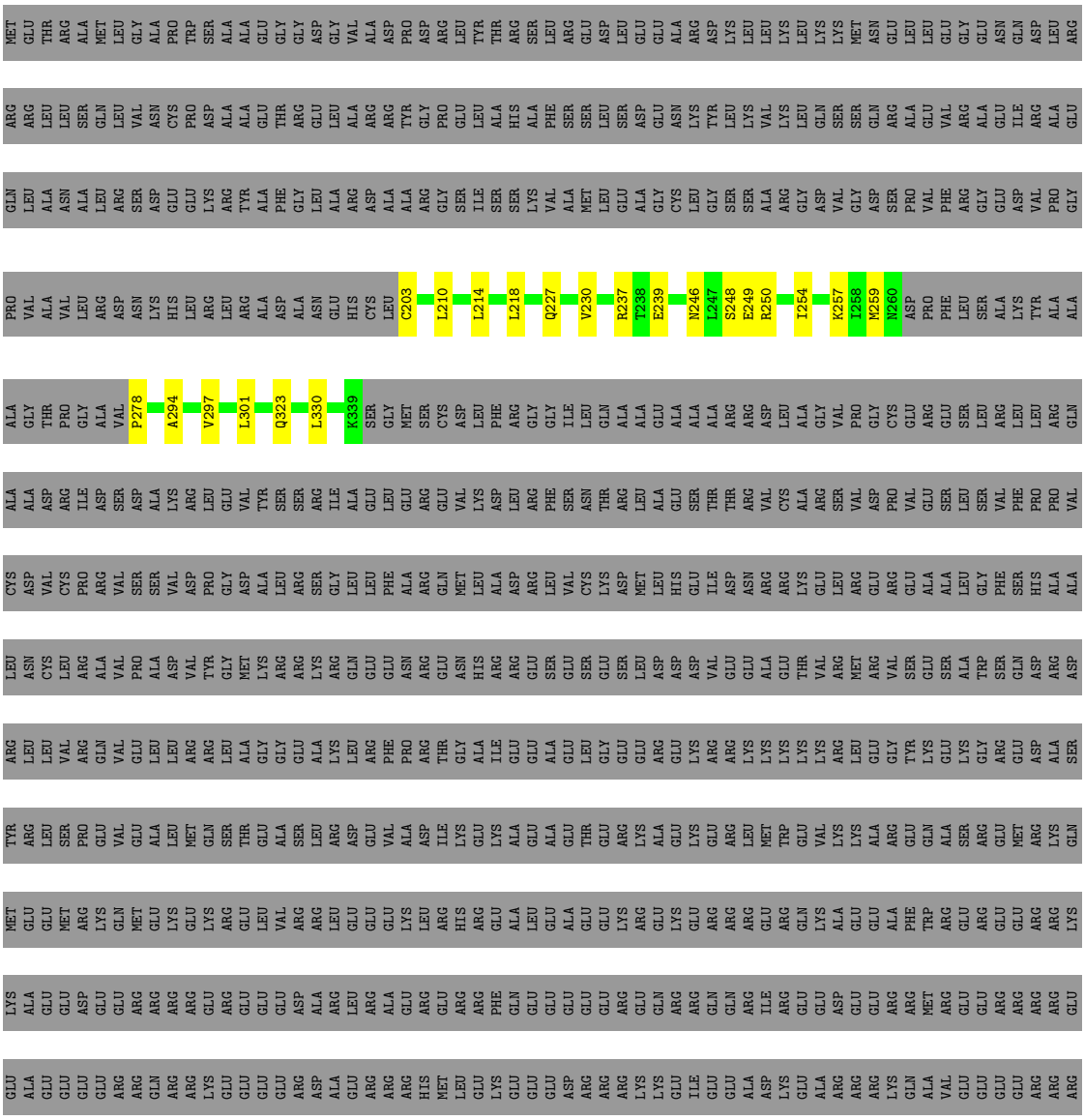
Chain MA: 95%

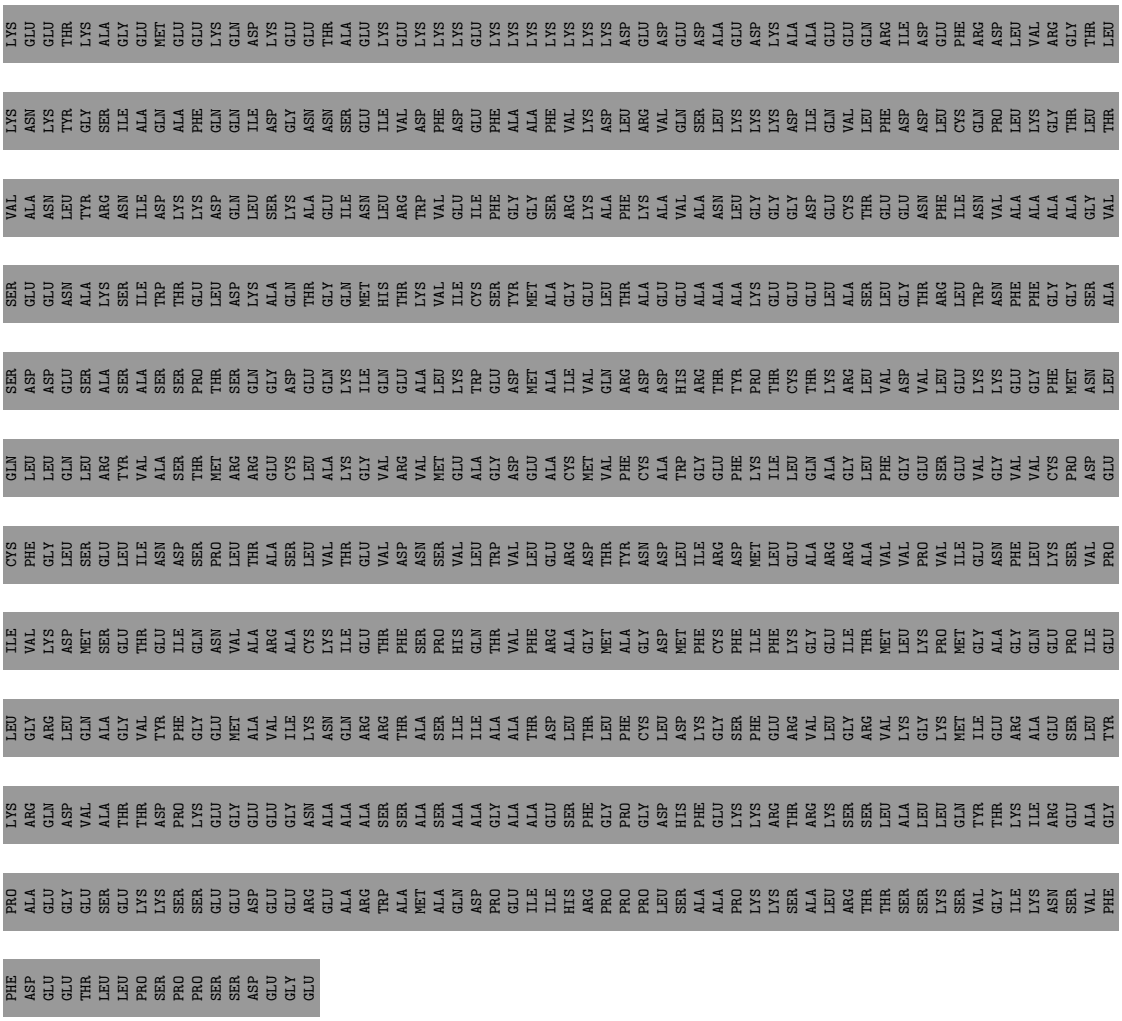
E199
C203
M211
L214
K219
R223
L233
E236
L240
K243
L247
L251
I258
M259
L264
S265
T273
V277
Q283
L284
R285
A292
E295
S296
V297
L301
R304
R313
Q316
T317
R320
R324
E325
L326
R327
S340



• Molecule 14: PCR12, TGME49_219070

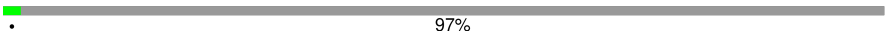
Chain MB: 96%

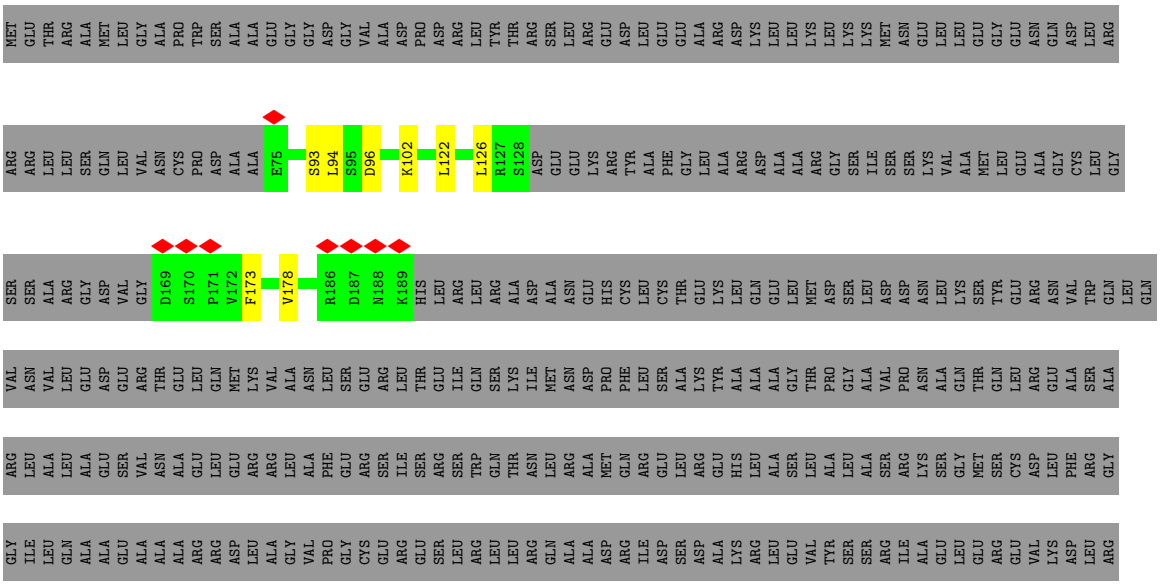


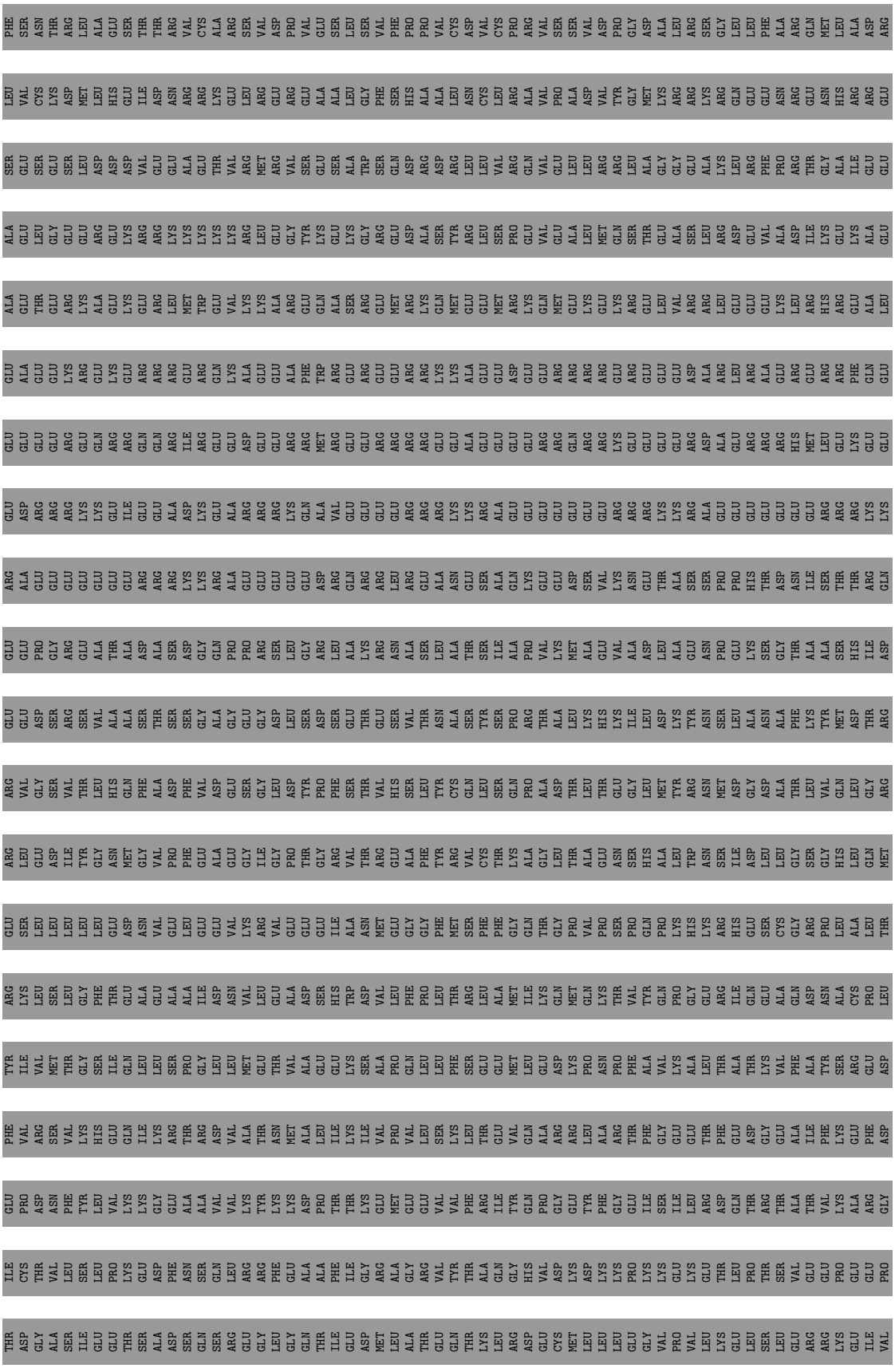


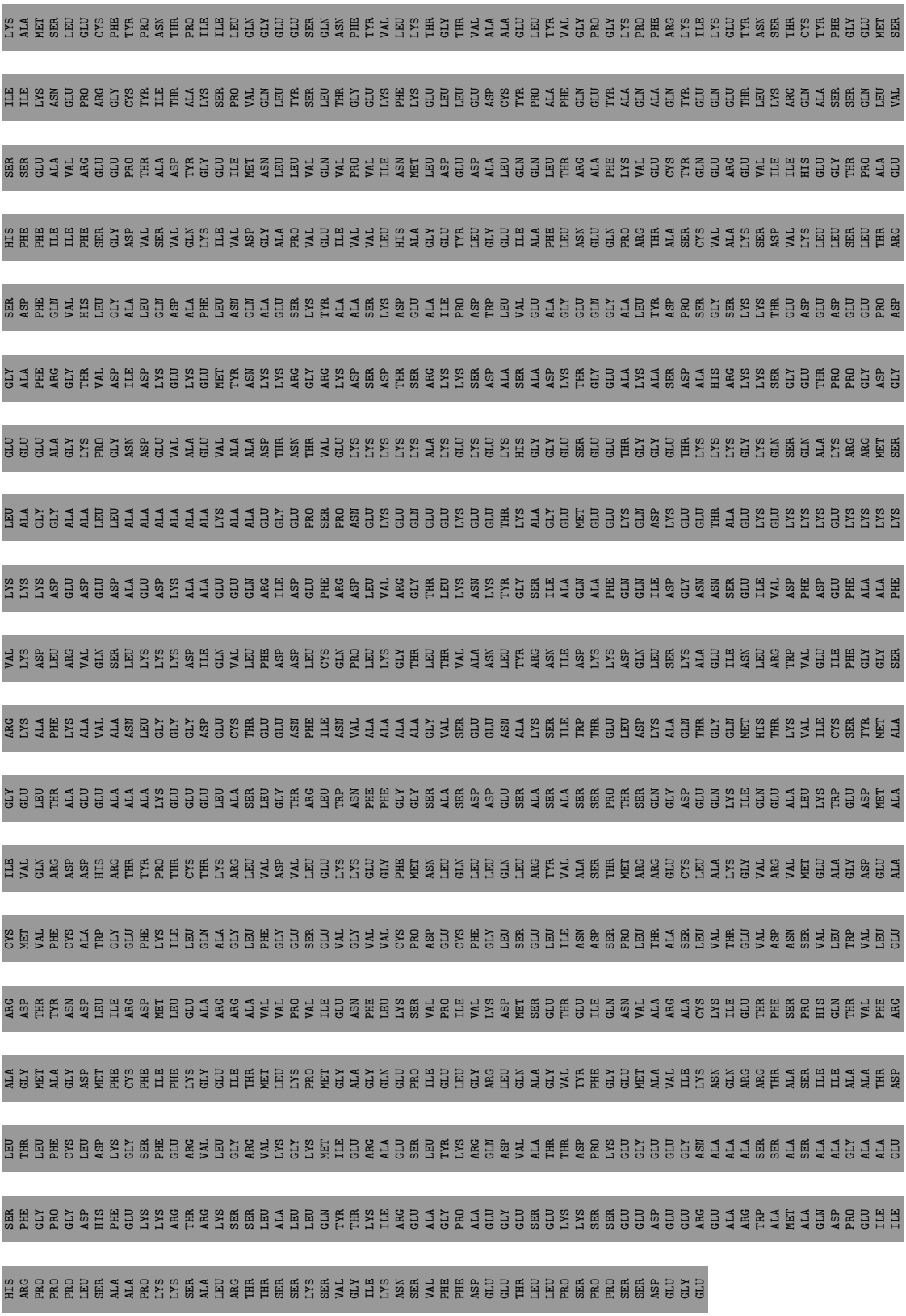
• Molecule 14: PCR12, TGME49_219070

Chain MC:



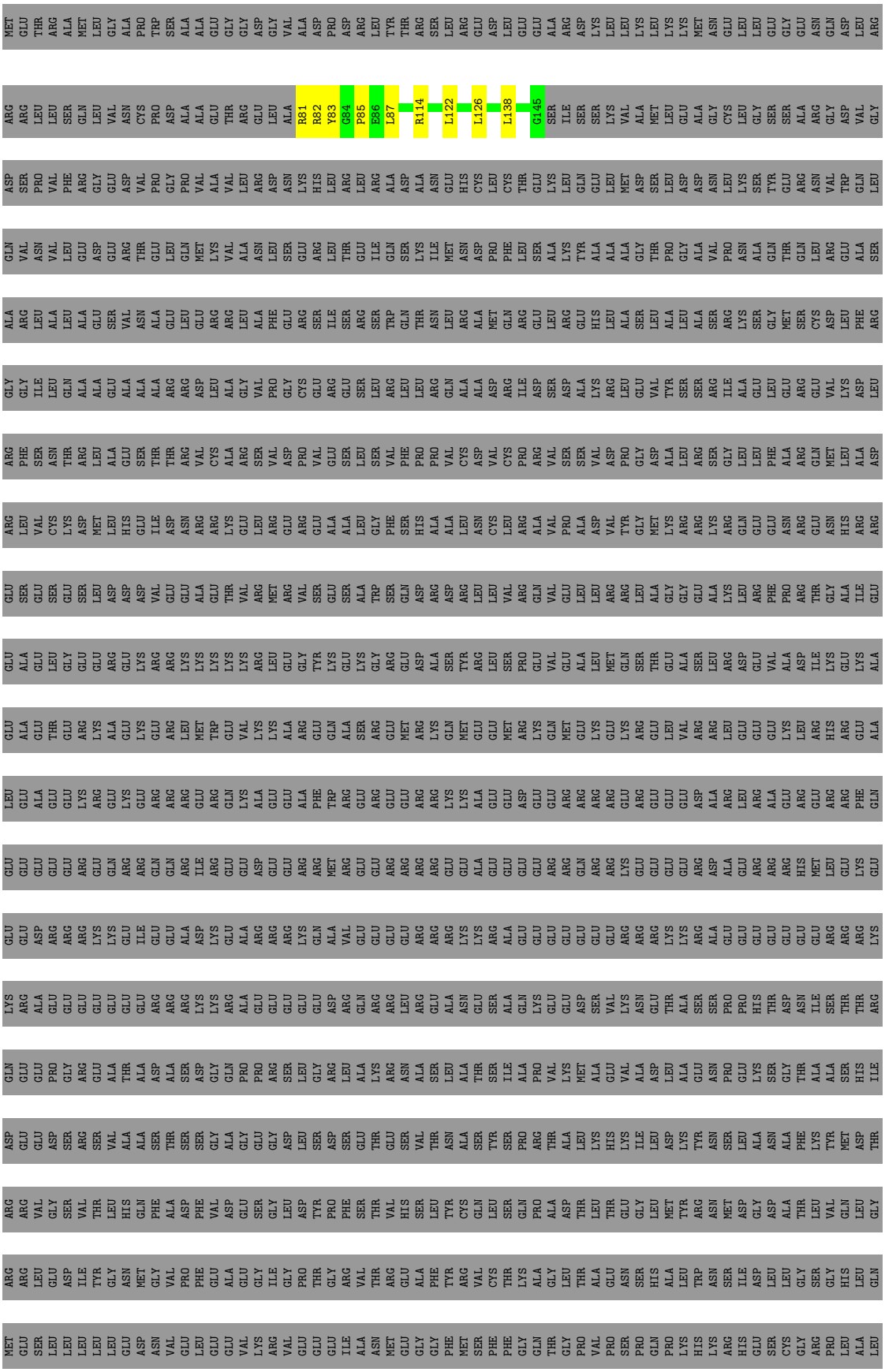


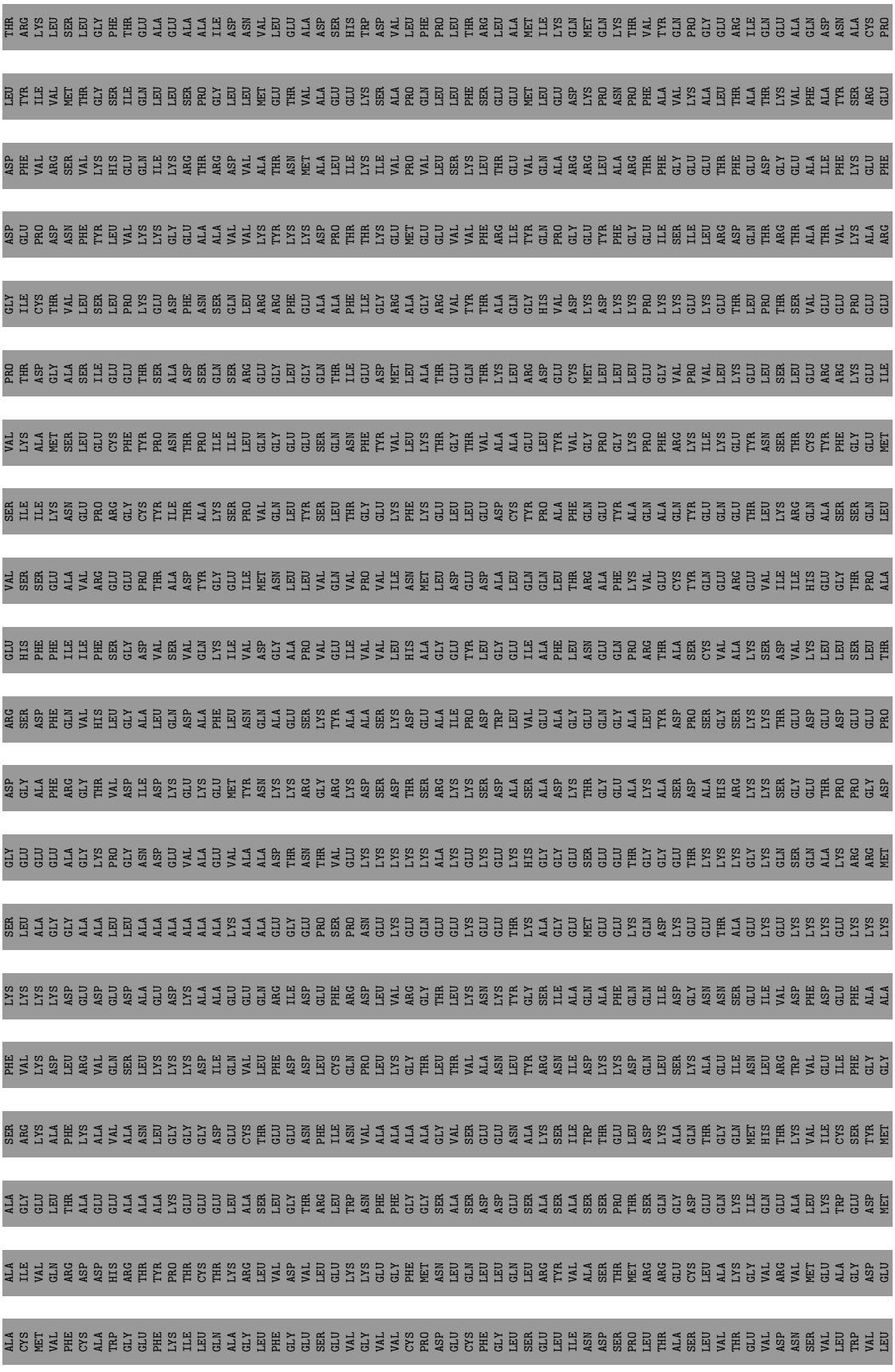

PHE SER ASN THR ARG LEU ALA GLU SER THR ARG VAL CYS ALA ARG SER VAL ASP PRO VAL GLU SER LEU SER VAL ASP PRO GLY ASP ALA LEU ARG SER GLY LEU LEU PHE ALA ARG GLN MET LEU ALA ASP ARG
LEU VAL CYS LYS ASP MET LEU HIS GLU ILE ASP ASN ARG ARG LYS GLU LEU ARG GLU ARG GLU ALA LEU GLY PHE SER HIS ALA ALA LEU ASN CYS LEU ARG ALA VAL PRO ALA ASP VAL TYR GLY MET LYS ARG ARG LYS ARG GLN GLU GLU ARG GLU ASN HIS ARG ARG GLU
SER GLU SER GLU SER LEU ASP ASP ASP VAL GLU GLU ALA GLU THR VAL ARG MET ARG VAL SER GLU SER ALA TRP SER GLN ASP ARG ASP ARG LEU LEU VAL ARG GLN VAL GLU LEU LEU ARG ARG LEU ALA ALA GLY GLY GLU ALA LYS LEU ARG PHE PRO ARG THR GLY ALA ILE GLU GLU
ALA GLU LEU GLY GLU GLU ARG GLU LYS ARG GLU LYS LYS LYS LYS ARG LEU GLU GLY TYR LYS GLU LYS GLY ARG GLU ASP ALA SER TYR ARG LEU SER PRO GLU VAL GLU ALA LEU MET GLN SER THR GLU ALA SER LEU ARG ASP GLU VAL GLU LEU ALA ASP ILE LYS GLU VAL GLU ALA
ALA GLU THR GLU ARG ARG GLU LYS GLU ARG LEU MET TRP GLU VAL LYS LYS ALA ARG GLU GLN LYS ALA SER ARG GLU MET ARG LYS GLN MET GLU ARG LYS GLN MET GLU GLU GLU MET ARG LYS GLN MET GLU GLU LYS LEU ARG HIS ARG GLU ALA LEU
GLU ALA GLU GLU LYS GLU ARG ARG ARG GLU ALA ALA PHE TRP ARG GLU ARG GLU GLU GLU ARG ARG ARG ARG ARG GLU ARG GLU GLU GLU GLU ASP ALA ARG LEU GLU ARG GLU GLU ALA GLU ARG GLU GLN
GLU GLU GLU GLU ARG GLN ARG ARG GLN GLN ARG ILE ARG GLU ASP GLU ARG ARG MET ARG GLU GLU GLU ALA GLU GLU GLU ARG ARG ARG GLN ARG ARG LYS GLU GLU GLU ARG ASP ALA GLU LEU GLU GLU ARG HIS MET LEU GLU LYS GLU GLU
GLU ASP ARG ARG ARG LYS LYS GLU ILE GLU GLU ALA ASP LYS GLU ALA ARG ARG LYS GLN ALA VAL GLU GLU GLU ARG ARG ARG LYS LYS ARG ALA GLU GLU GLU ARG ARG ARG LYS LYS ARG ALA GLU GLU GLU ARG ARG ARG LYS LYS
ARG ALA GLU GLU GLU GLU GLU GLU ARG ARG GLN ARG ARG LEU ARG GLU GLU ALA ALA SER VAL THR GLU ALA ALA SER SER PRO PRO HIS THR ASP ASN ILE SER THR THR ARG GLN
GLU GLU PRO GLY ARG GLU ALA THR ALA ASP ALA SER ARG GLN PRO PRO ARG SER LEU GLY ARG LEU ALA LYS ARG ASN ALA SER LEU ALA THR SER ILE ALA PRO VAL LYS MET ALA GLU VAL ALA ASP LEU ALA GLU ASN PRO GLU LYS SER GLY THR ALA SER HIS ILE ASP
GLU GLU ASP SER ARG SER VAL ALA ALA SER ASP SER GLU THR GLU SER VAL THR ASN ALA SER LEU ALA THR SER GLN PRO ARG THR ALA LEU LYS HIS LYS ILE LEU ASP TYR LYS TYR ASN SER LEU LEU ALA GLU PHE LYS TYR MET ASP THR ARG
ARG VAL GLY SER VAL THR LEU HIS GLN PHE ALA ASP PHE VAL ASP GLU SER GLY LEU ASP TYR PRO PHE SER THR VAL HIS SER LEU TYR CYS GLN LEU SER GLN PRO ALA ASP THR LEU THR GLU GLY LEU MET TYR ARG ASN MET ASP GLY ASP ALA THR LEU VAL GLN LEU GLY ARG
ARG LEU GLU ASP ILE TYR GLY ASN MET GLY VAL PRO PHE GLU ALA GLU GLY ILE GLY PRO THR GLY ARG VAL THR ARG GLU ALA PHE TYR ARG CYS VAL CYS THR LYS ALA GLY LEU THR ALA GLU GLU ASN SER HIS ALA LEU TRP ASN SER ILE ASP LEU LEU GLY GLY SER GLY HIS LEU GLN MET
GLU SER LEU LEU LEU LEU GLU ASP ASN VAL GLU LEU GLU VAL LYS ARG VAL GLU GLU ALA ILE ALA ASN MET GLU GLY PHE MET SER PHE PHE GLY GLN THR GLY PRO VAL PRO SER PRO GLN PRO LYS HIS LYS ARG HIS GLU SER CYS GLY ARG PRO LEU ALA LEU THR
ARG LYS LEU SER LEU ALA GLU ASP ASN VAL LEU GLU ALA ILE ASP SER HIS TRP ASP VAL LEU PHE PRO LEU THR ARG LEU ALA MET ILE LYS GLN MET GLN LYS THR VAL TYR GLN PRO GLY GLU ARG ILE GLN GLU ALA GLN ASP ASN ALA CYS PRO LEU
TYR ILE VAL MET THR GLY SER ILE GLN LEU LEU LEU SER PRO GLY LEU LEU MET GLU THR VAL ALA GLU GLU LYS SER ALA PRO GLN LEU LEU PHE SER GLU GLU MET LEU GLU GLU ASP LYS PRO ASN PRO PHE ALA LEU THR ALA THR LYS VAL PHE ALA TYR SER ARG GLU ASP
PHE VAL ARG SER VAL ASP LYS ILE ARG ASP VAL ALA THR ASN MET ALA LEU ILE LYS ILE GLU GLN ARG THR ARG ASP VAL ALA LEU ILE LYS LEU GLU VAL GLN ALA ALA ARG ARG LEU GLU VAL LEU SER LYS LEU THR GLU VAL GLN ALA ARG ARG LEU ALA ILE PHE GLY GLU ILE SER ILE LEU LEU ARG ASP PHE GLU GLN THR ARG THR ALA ILE PHE
GLU PRO ASP ASN PHE TYR LEU VAL LYS ARG ILE LYS ASP PRO THR THR THR LYS GLU MET ARG VAL PHE ARG ILE TYR GLN PRO GLY GLU TYR PHE GLY GLU ILE SER ILE LEU LEU ARG ASP GLN THR ARG THR ALA THR VAL LYS ALA ARG
ILE CYS THR VAL LEU SER LEU PRO LYS GLU ASP PHE ASN SER ARG ALA ALA PHE ILE GLY ARG VAL TYR THR ALA GLN GLY HIS VAL ASP LYS ASP LYS LYS PRO LYS LYS GLU LYS GLU THR LEU LYS GLU LEU PRO THR SER VAL GLU GLU GLU GLU PRO
THR ASP GLY ALA SER ILE GLU GLY GLN SER ARG GLU GLY LEU GLY GLN THR ILE GLU ASP MET LEU ALA THR GLU GLN THR LYS LEU ARG ASP GLU CYS MET LEU LEU LEU GLU GLY VAL PRO VAL LEU LYS GLU LEU GLU ARG ARG LYS GLU ILE GLU VAL

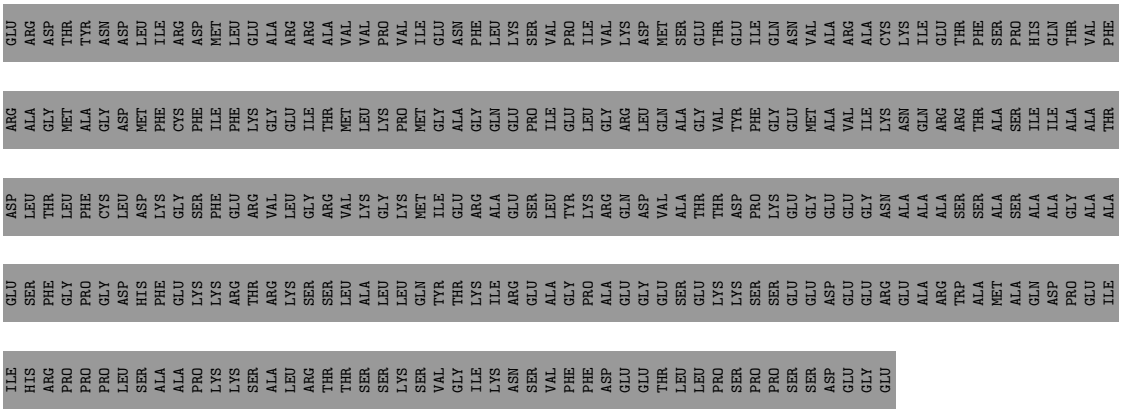


• Molecule 14: PCR12, TGME49_219070

Chain MD: 98%

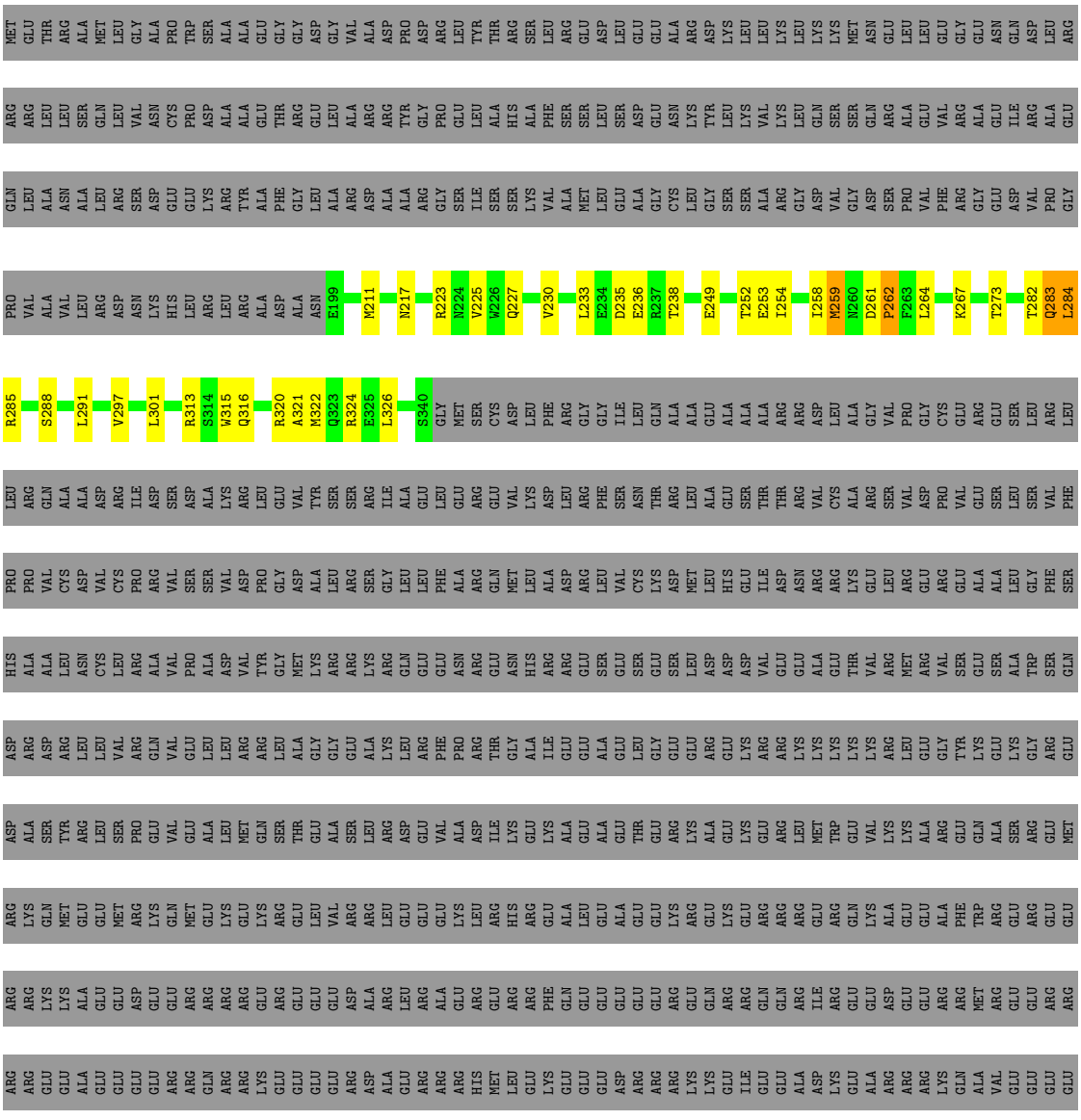

R81
R82
Y83
G84
P85
E86
L87
R114
L122
L126
L138
G145

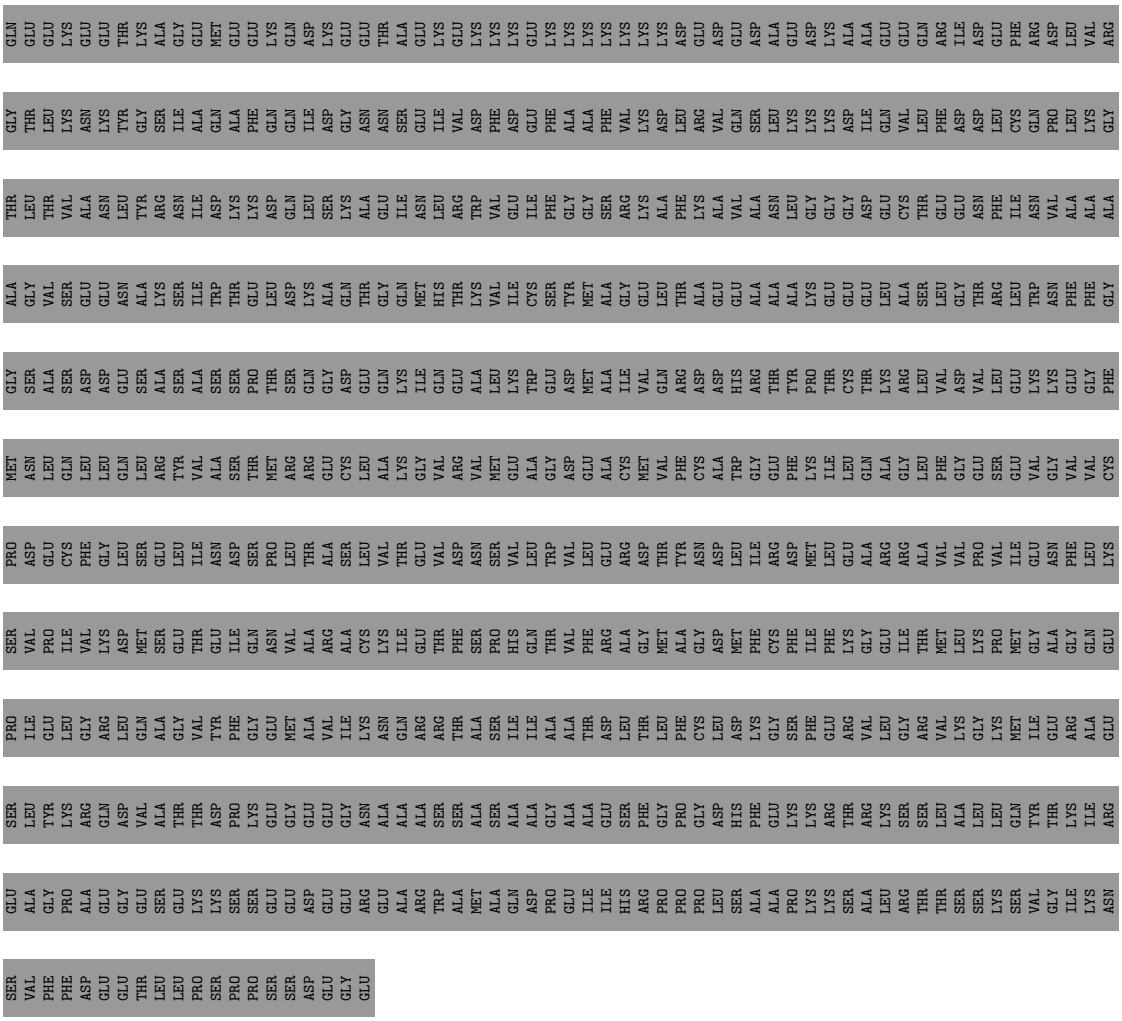

THR ARG LYS LEU SER LEU GLY PHE THR GLU ALA GLU ALA ALA ILE ASP ASN VAL LEU GLU ALA ASP SER HIS TRP ASP VAL LEU PHE PRO LEU THR ARG LEU ALA MET ILE LYS GLN MET GLN LYS THR VAL TYR GLN PRO GLY GLU ARG ILE GLN GLU ALA GLN ASP ASN ALA CYS PRO
LEU TYR ILE VAL MET THR GLY SER ILE GLN LEU LEU LEU SER PRO GLY LEU LEU MET GLU THR VAL ALA GLU GLU LYS SER ALA PRO GLN LEU PHE SER GLU GLU MET GLN ASN PRO PHE ALA VAL LYS ALA LEU THR ALA THR LYS VAL PHE ALA TYR SER ARG GLU
ASP PHE VAL ARG SER VAL LYS HIS GLU GLN ILE LYS ARG THR ARG ASP VAL ALA THR ASN MET ALA LEU ILE LYS ILE VAL PRO VAL LEU SER LYS LEU THR GLU VAL GLN ALA ARG ARG LEU ALA GLY GLU ALA ILE PHE LYS GLU PHE
ASP GLU PRO ASP ASN PHE TYR LEU VAL LYS LYS GLY GLU ALA ALA VAL VAL LYS TYR LYS LYS ASP PRO THR THR LYS GLU GLU VAL VAL PHE ARG ILE TYR GLN PRO GLY GLU TYR PHE GLY GLU ILE SER ILE LEU ARG GLY GLU THR ARG THR PHE ALA ARG
GLY ILE CYS THR VAL LEU SER LEU PRO LYS GLU GLY ASP PHE GLU ALA ALA PHE ILE GLY ARG ALA GLY ARG VAL TYR THR ALA GLN GLY HIS VAL ASP LYS ASP LYS LYS GLU GLY LYS GLU THR LEU PRO THR SER VAL GLU GLU LYS LYS GLU
PRO THR ASP GLY ALA SER ILE GLU GLU ASP SER SER GLN SER ARG GLU GLY LEU GLY GLN THR ILE GLU GLU ASP MET LEU ALA ALA THR GLU GLN THR LYS LEU LEU ARG ASP GLU CYS MET LEU LEU LEU LEU GLU GLY VAL PRO VAL LEU LYS GLU GLU ARG ARG GLU GLU ILE
VAL LYS ALA MET SER LEU GLU CYS PHE TYR PRO ASN THR PRO ILE ILE LEU GLN GLY GLU GLU SER GLN ASN PHE TYR VAL LEU LYS THR GLY THR VAL ALA ALA GLU LEU TYR VAL GLY PRO GLY LYS PRO PHE ARG LYS ILE LYS GLU TYR ASN SER THR CYS TYR PHE GLY GLU MET
SER ILE ILE LYS ASN GLU PRO ARG GLY CYS TYR ILE THR ALA LYS SER PRO VAL GLN LEU TYR SER LEU THR GLY GLU LYS PHE LYS GLU LEU LEU GLU ASP CYS TYR PRO ALA PHE GLN GLU TYR ALA GLN ALA GLN TYR GLU GLN GLU THR LEU LEU LYS ARG GLN ALA SER SER GLN LEU
VAL SER SER GLU ALA VAL ARG GLU GLU PRO THR ALA ASP TYR GLY GLU ILE MET ASN LEU LEU VAL GLN VAL PRO VAL ILE ASN MET LEU ASP GLU ASP ALA LEU GLN GLN GLU ARG GLU VAL ILE ILE HIS GLU GLY THR PRO ALA
GLU HIS PHE PHE ILE ILE PHE SER GLY ASP VAL SER VAL GLN LYS ILE VAL ASP GLY ALA PRO VAL GLU ILE VAL VAL LEU HIS ALA GLY GLU TYR LEU GLY GLU ILE ALA PHE LEU ASN GLU GLN PRO ARG THR ALA SER CYS VAL ALA LYS SER ASP VAL LYS LEU LEU SER LEU THR
ARG SER ASP PHE GLN VAL GLY LEU ALA ASN LEU GLN ASP ALA PHE LEU ASN GLN GLN ALA GLU LYS SER LYS TYR ALA ALA SER LYS ASP GLU ALA ILE PRO ASP TRP LEU VAL GLU ALA GLY GLU GLN GLY ALA LEU TYR ASP PRO SER GLY SER LYS LYS THR GLU ASP GLU GLU PRO
ASP GLY ALA PHE ARG GLY THR VAL ASP ILE ASP ASP LYS GLU LYS ASP SER ASP ARG LYS LYS SER ASP ALA SER ARG GLY LYS SER ASP THR SER ARG GLY GLU ALA GLU ALA LYS ASP THR GLY GLU ALA LYS ALA SER ASP ALA HIS ARG LYS LYS SER GLY GLU THR PRO PRO GLY ASP
GLY GLU GLU GLU ALA GLY LYS PRO GLY ASN ASP GLU VAL ALA ALA ASP THR ASN THR VAL GLU LYS LYS LYS ALA LYS GLU VAL ALA ALA ASP THR ASN THR VAL GLU LYS LYS LYS GLU GLU LYS HIS GLY GLY GLU SER GLU GLU LYS LYS GLY THR GLY GLY LYS LYS GLN SER GLN ALA LYS GLU ARG ARG MET
SER LEU ALA GLY GLY ALA ALA ALA ALA ALA LYS ALA ALA ALA GLU GLY GLU PRO SER PRO ASN GLU LYS GLU GLN GLU GLU LYS GLU GLU THR LYS ALA GLU GLY GLU MET GLU GLU LYS GLN ASP LYS GLU GLU THR ALA GLU LYS LYS GLU LYS LYS ALA
LYS LYS LYS ASP GLU ASP ALA ALA ALA ALA GLU ASP LYS ALA ASP GLU PHE ARG ASP LEU VAL ARG GLY THR LEU LYS ASN LYS TYR GLY SER ILE ALA GLN ALA PHE GLN GLN ILE ASP GLY ASN ASN SER GLU ILE VAL ASP PHE ASP GLU PHE ALA ALA
PHE VAL LYS ASP LEU ARG VAL GLN SER LEU LYS LYS LYS ASP ILE GLN LEU VAL LEU PHE ASP ASP PHE CYS GLN PRO LEU LYS GLY THR LEU THR VAL ALA ALA ASN LEU TYR ARG ASN ILE ASP LYS LYS ASP GLN LEU SER LYS ALA GLU ILE ASP ILE LEU ARG TRP VAL GLU ILE PHE GLY GLY
SER ARG LYS ALA PHE LYS ALA VAL ALA GLY VAL SER GLU GLU ASN ALA LYS SER ILE TRP THR GLU LEU ASP GLN ALA GLN THR GLY GLN MET HIS THR LYS VAL ILE CYS SER TYR MET
ALA GLY GLU LEU THR ALA GLU GLU ALA GLU ALA ALA SER GLU GLU ALA SER ALA SER SER PRO THR GLU ASP SER ALA GLN GLY ASP GLU GLN LYS ILE ALA GLN LEU GLU ALA ALA LEU LYS TRP GLU VAL
ALA ILE VAL GLN ARG THR TYR PRO THR CYS THR LYS ARG LEU VAL ASP VAL LEU GLU LYS LYS GLU GLY PHE MET ASN LEU GLN LEU LEU GLN LEU ARG TYR VAL ALA SER THR MET ARG ARG GLU CYS LEU ALA LYS GLY VAL ARG GLU GLU
ALA CYS MET VAL PHE CYS ALA TRP GLY GLU PHE LYS ILE LEU GLN ALA GLY LEU PHE GLY GLU SER GLU VAL VAL CYS PRO ASP GLU CYS PHE GLY LEU SER GLU VAL ILE ASN ASP SER PRO LEU THR ALA SER LEU VAL THR GLU VAL ASP ASN SER VAL LEU TRP VAL LEU



• Molecule 14: PCR12, TGME49_219070

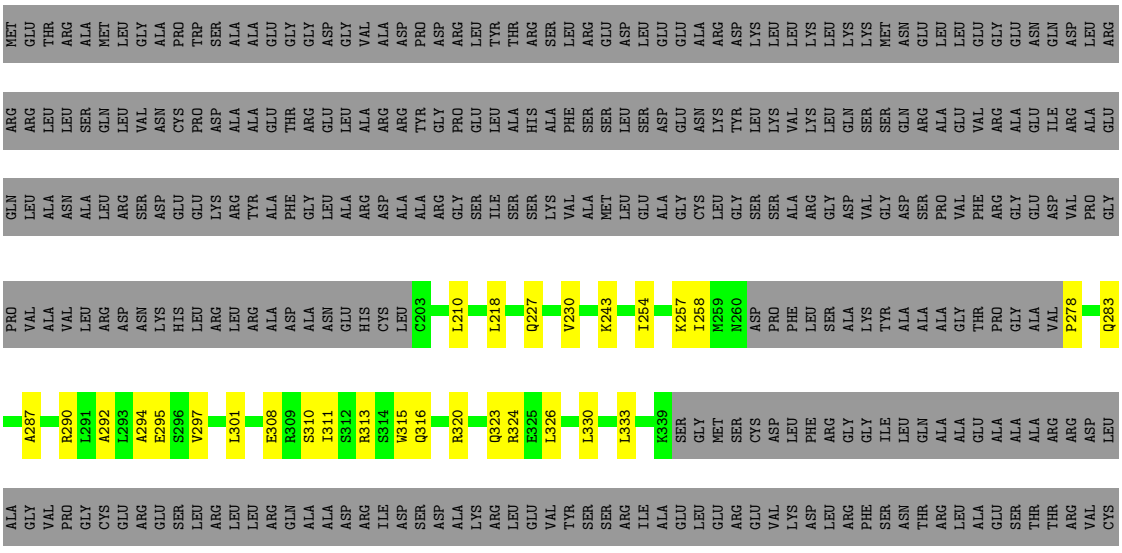
Chain ME: 95%

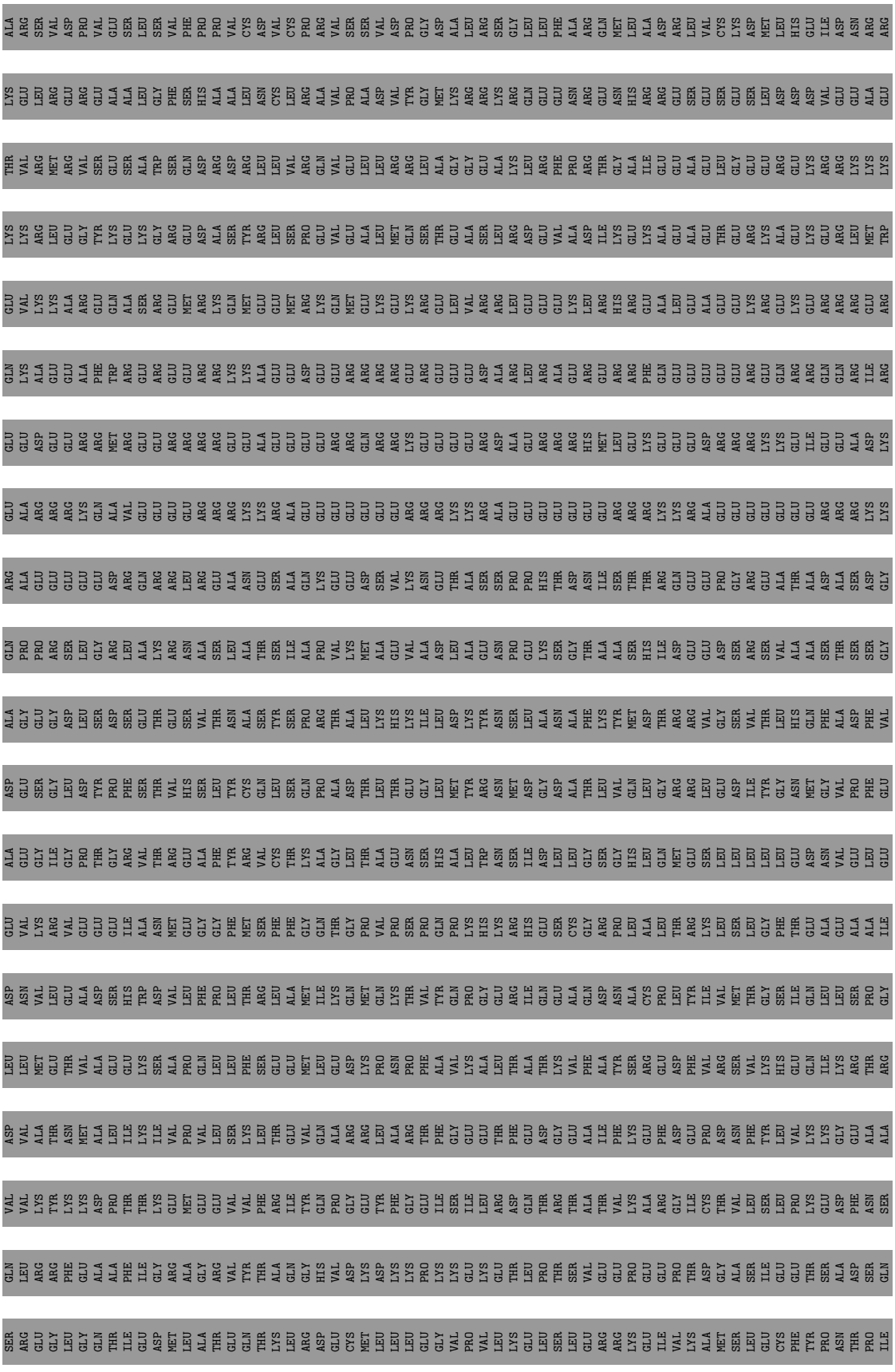


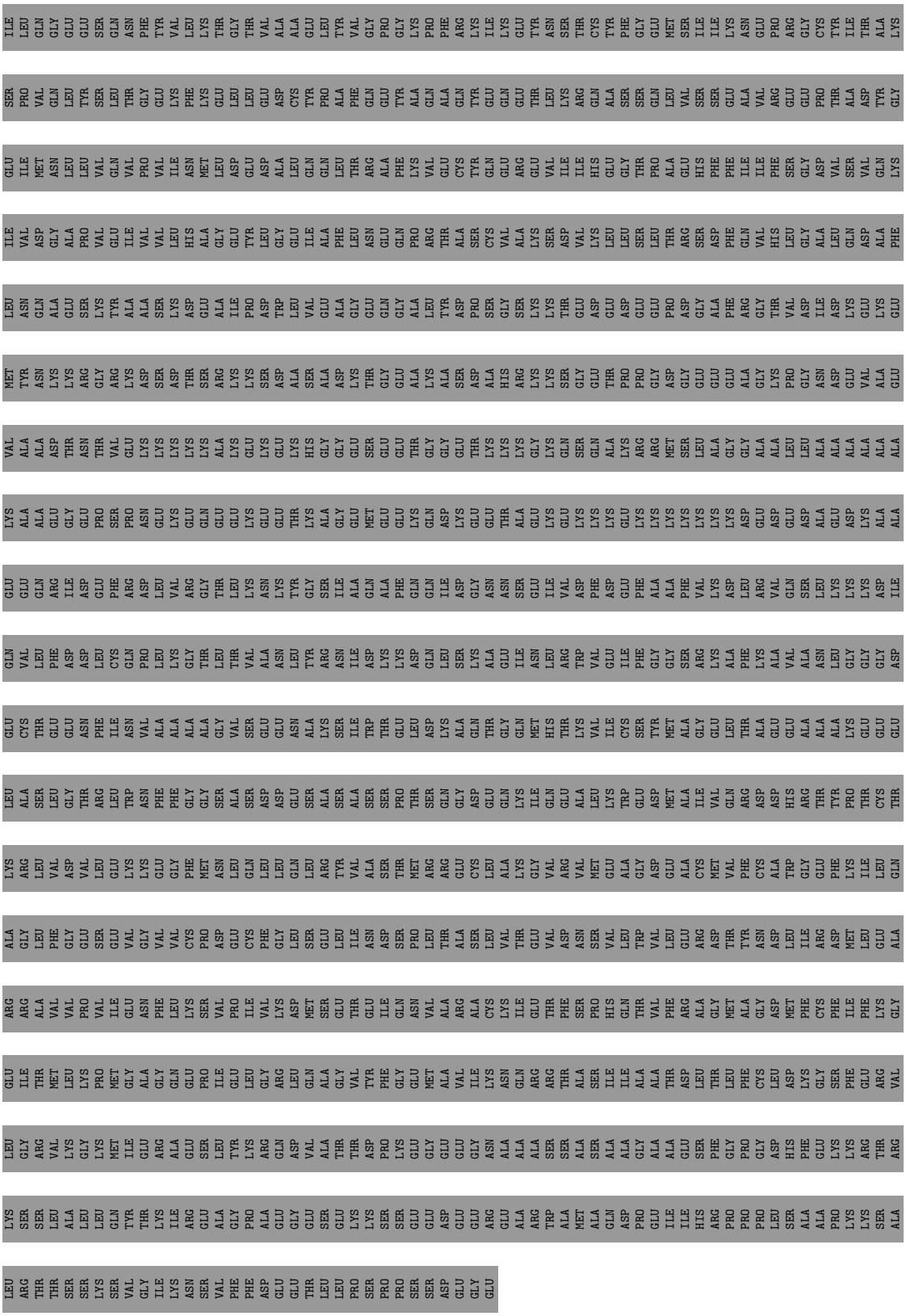


• Molecule 14: PCR12, TGME49_219070

Chain MF: 96%

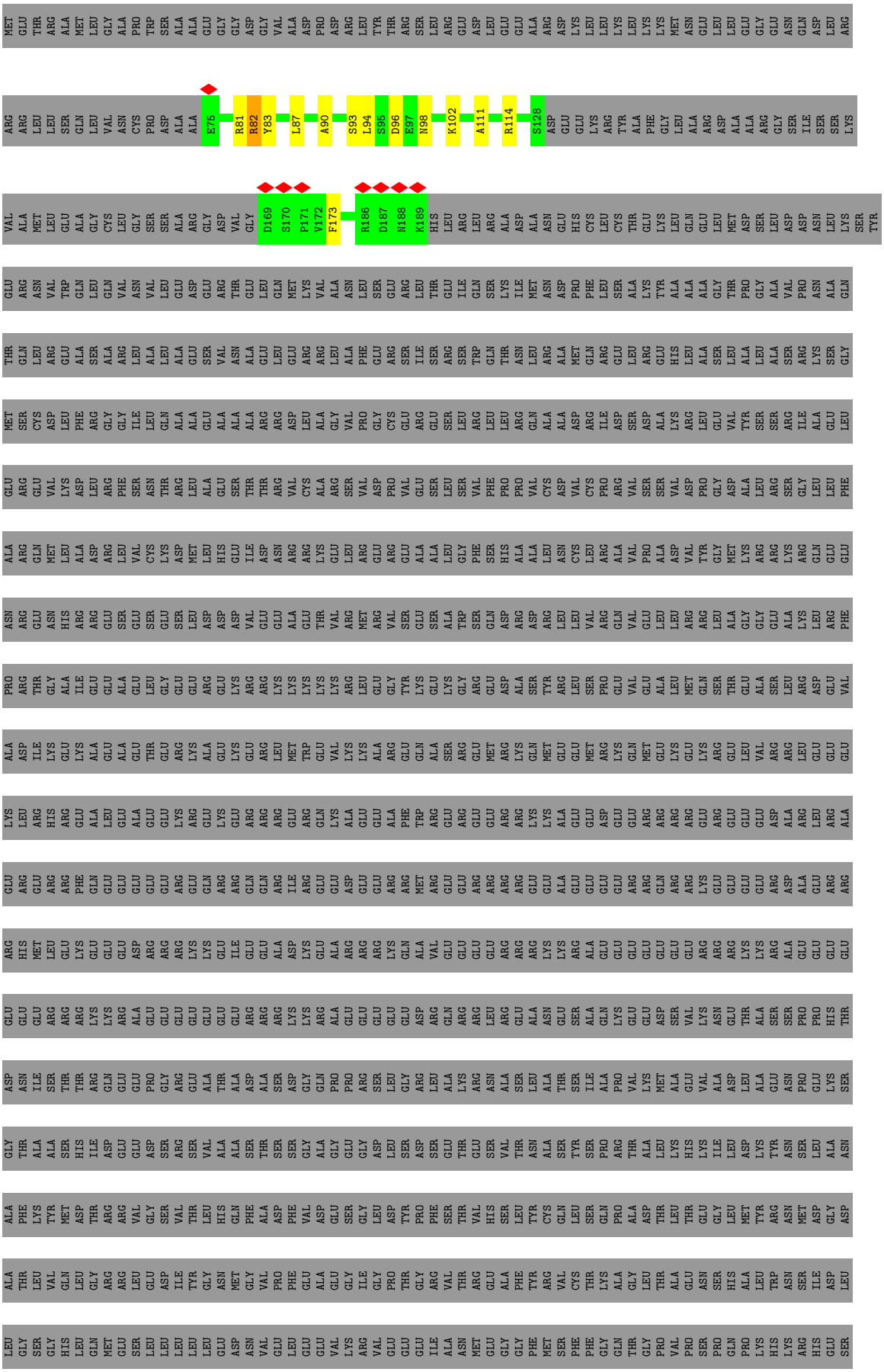


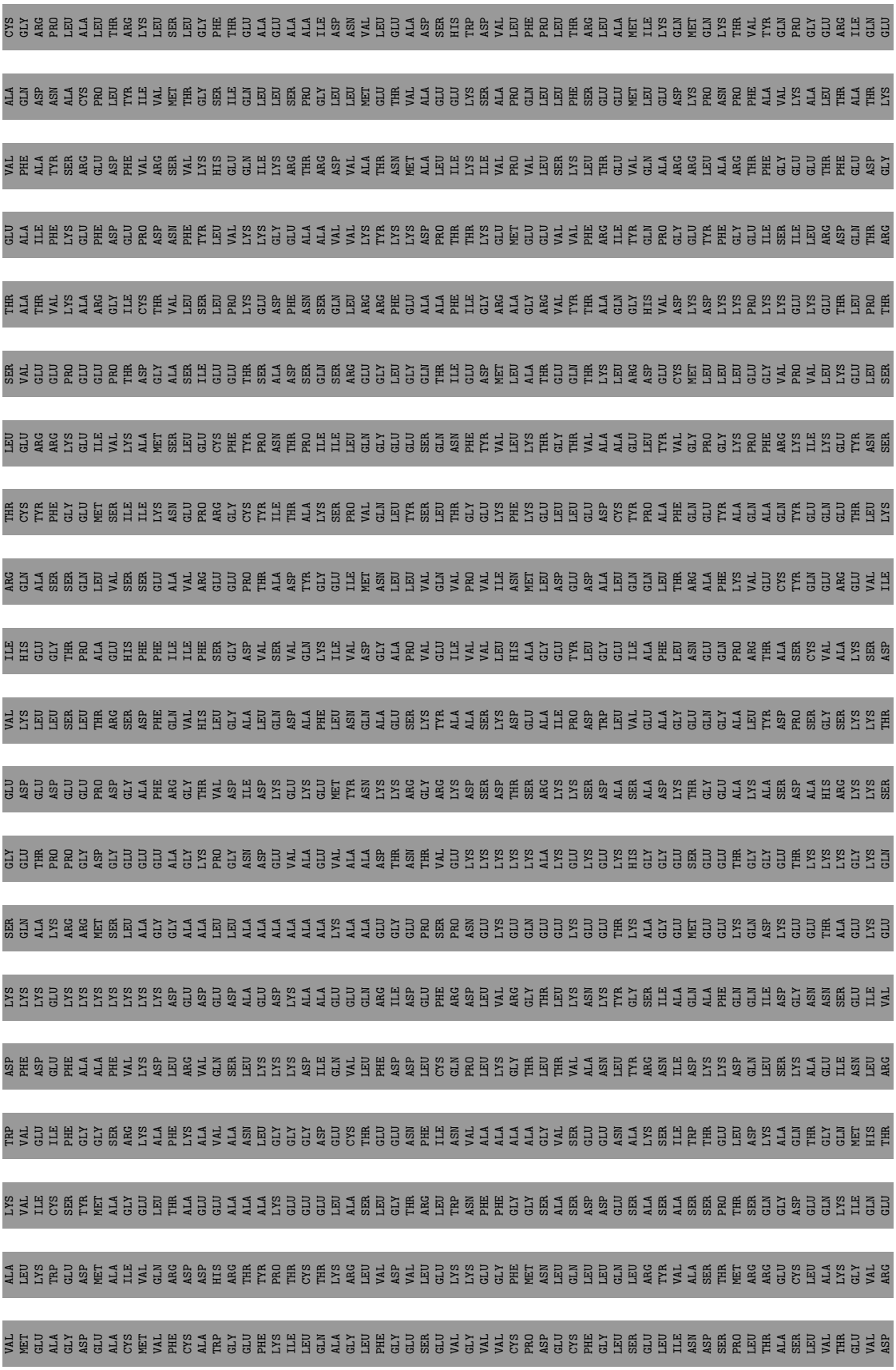


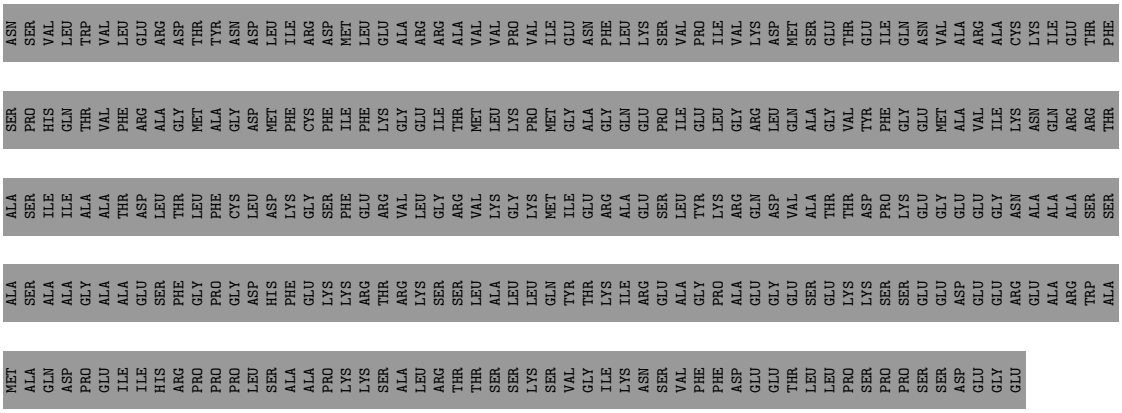


• Molecule 14: PCR12, TGME49_219070

Chain MG: 97%

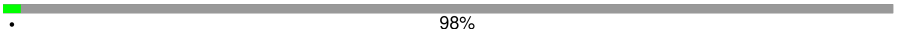

E75
R81
R82
Y83
L87
A90
S93
L94
S95
D96
E97
N98
K102
A111
R114
S128
D169
S170
P171
V172
F173
R186
D187
N188
K189

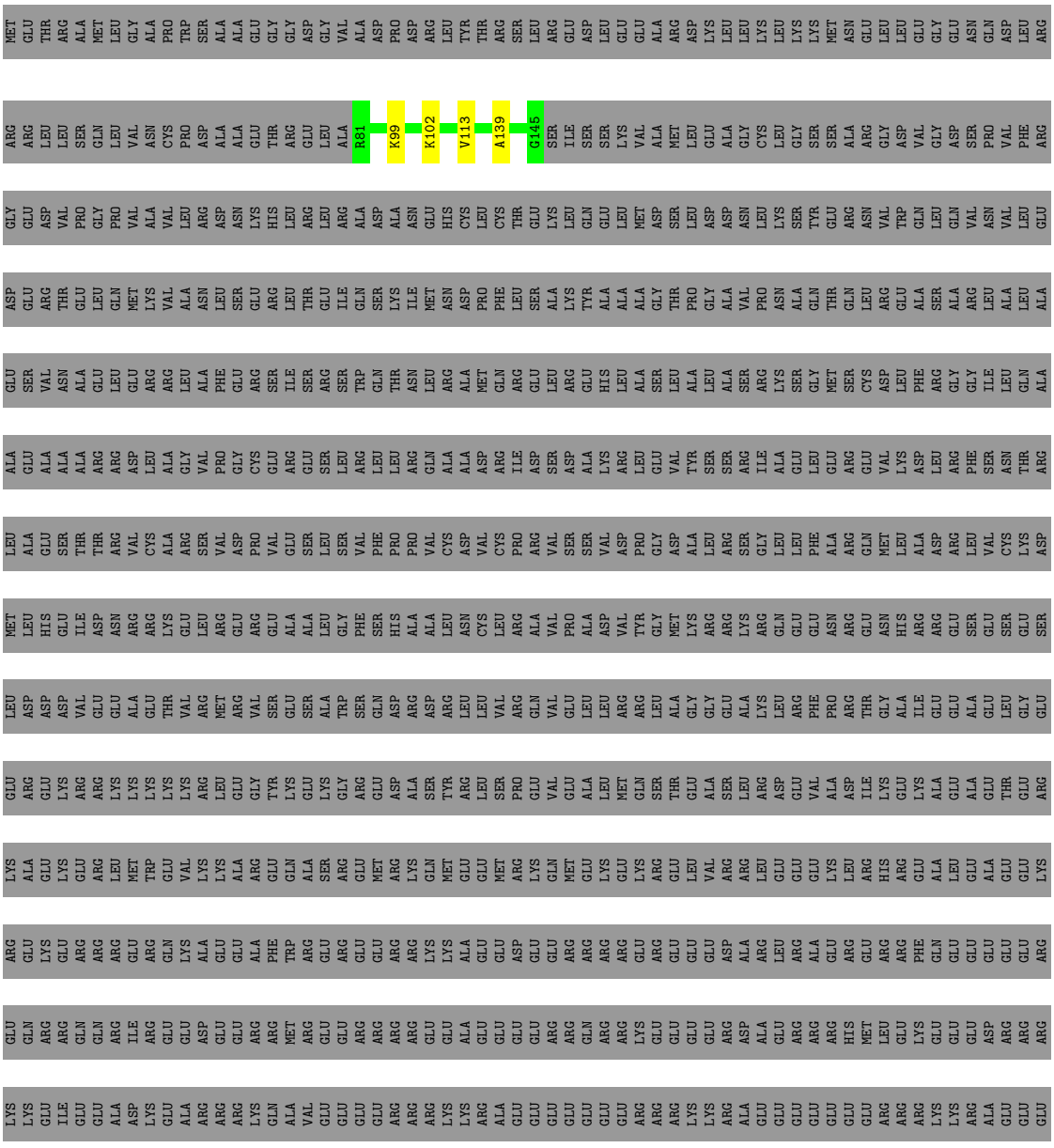


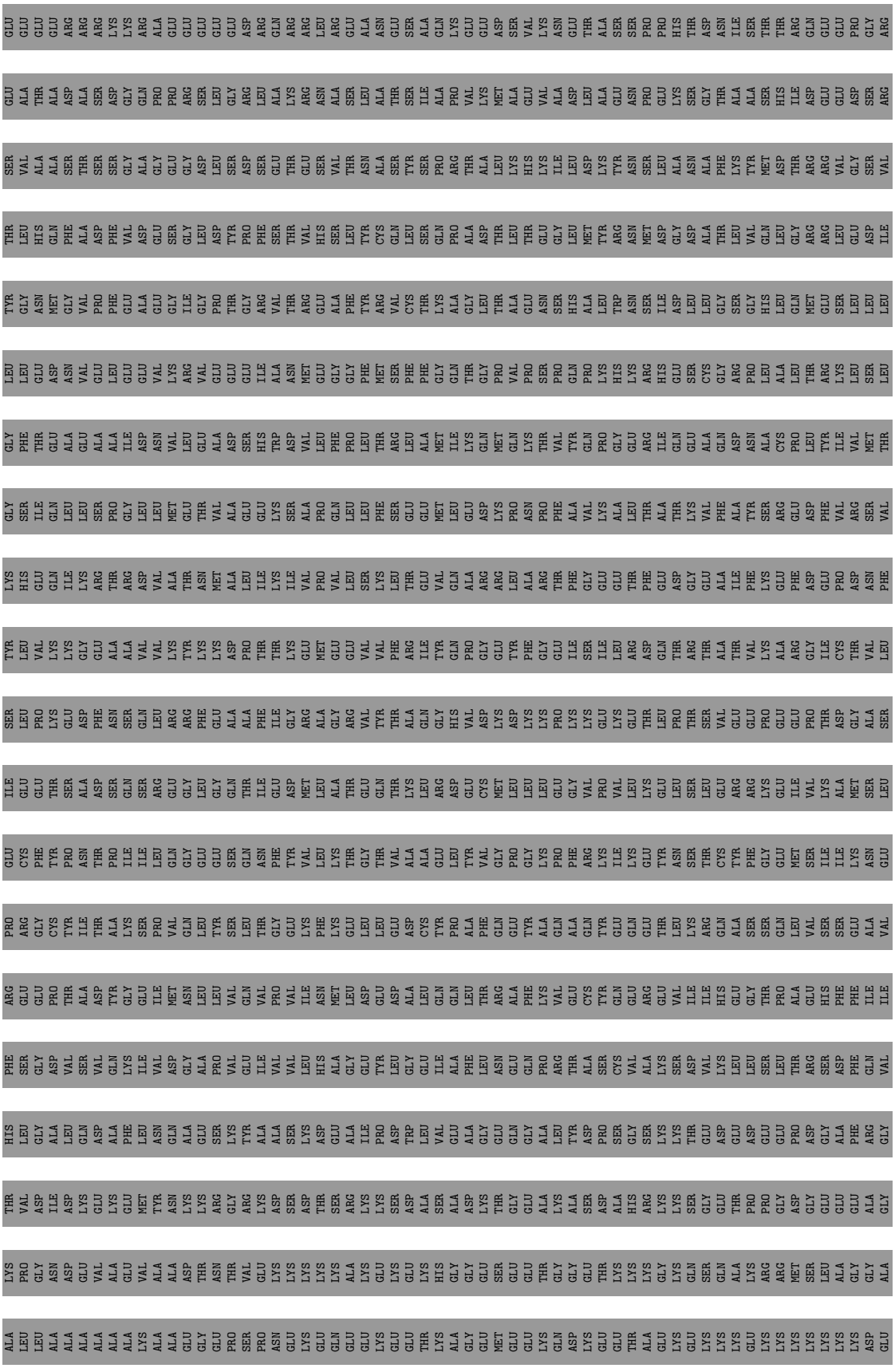


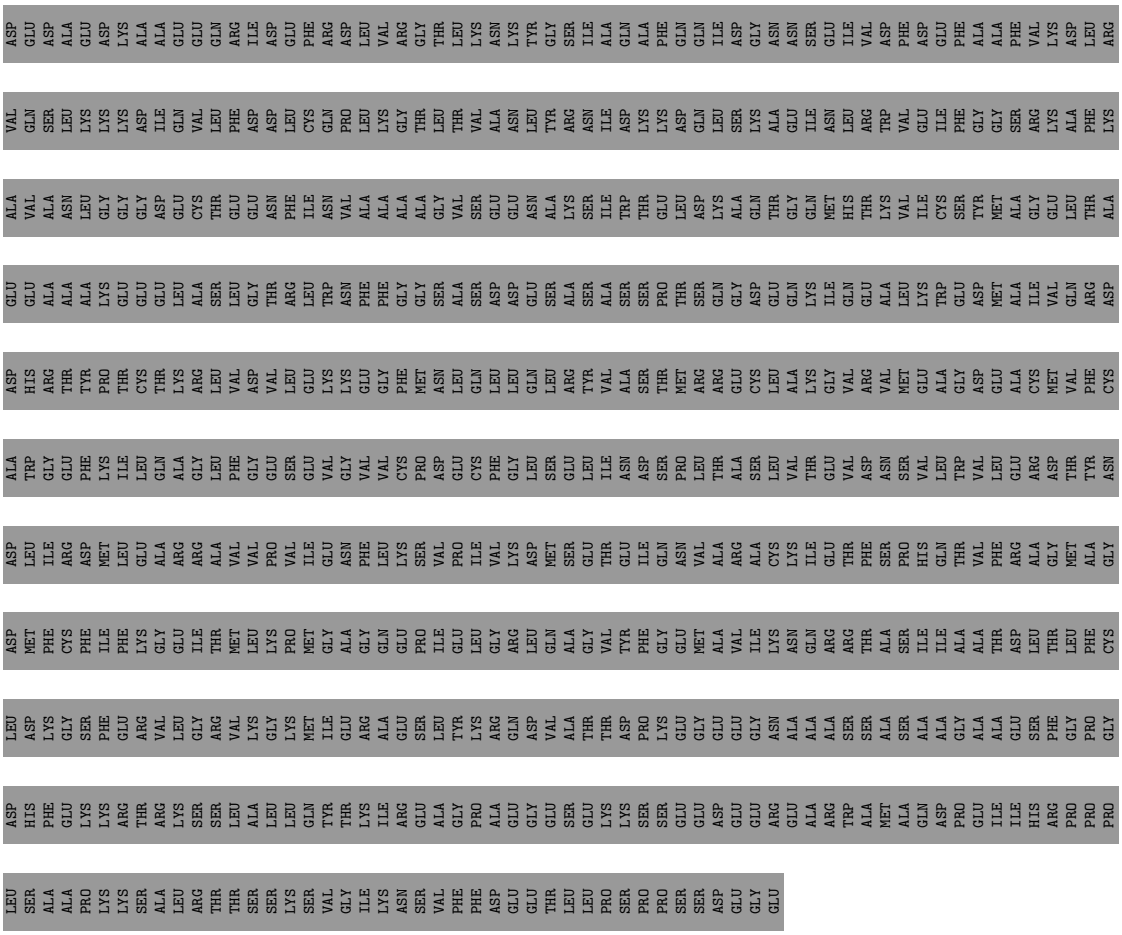
• Molecule 14: PCR12, TGME49_219070

Chain MH:



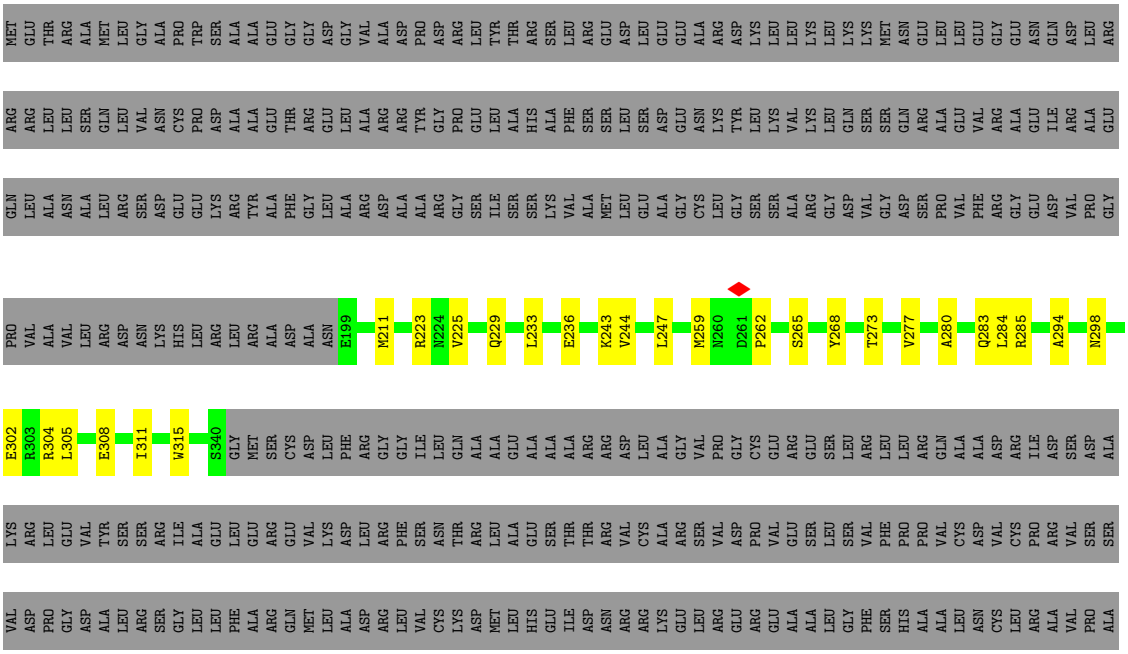

MET GLU THR ARG ALA MET LEU GLY ALA PRO TRP SER ALA ALA GLU GLY GLY ASP GLY VAL ALA ASP PRO ASP ARG LEU TYR THR ARG SER LEU ARG GLU ASP LEU LEU GLU GLU ALA ARG ASP LYS LEU LEU LYS LEU LYS LYS MET ASN GLU LEU LEU GLU GLU GLY GLU ASN GLN ASP LEU ARG
ARG ARG LEU LEU SER GLN LEU VAL ASN CYS PRO ASP ALA ALA GLU THR ARG GLU LEU ALA R81 K99 K102 V113 A139 G145 SER ILE SER SER LYS VAL ALA MET LEU GLU GLU ALA GLY CYS LEU GLY SER SER ALA ARG GLY ASP VAL GLY ASP SER PRO VAL PHE ARG
GLY GLU ASP VAL PRO GLY PRO VAL ALA VAL LEU LEU ARG ASP ASN LYS HIS LEU ARG LEU ARG ALA ASP ALA ASN GLU HIS CYS LEU CYS THR GLU LYS LEU GLN GLU GLU LEU MET ASP SER LEU ASP ASP ASN LEU LYS SER TYR GLU ARG ASN VAL TRP GLN LEU GLN VAL ASN VAL LEU GLU
ASP GLU ARG THR GLU LEU GLN MET LYS VAL ALA ASN LEU SER GLU ARG LEU THR GLU ILE GLN SER LYS ILE MET ASN ASP PRO PHE LEU SER ALA LYS TYR ALA ALA ALA GLY THR PRO GLY ALA VAL PRO ASN ALA GLN THR GLN LEU GLN ARG GLU ALA SER ALA ARG LEU ALA LEU GLU ALA
GLU SER VAL ASN ALA GLU LEU GLU ARG ARG LEU ALA PHE GLU ARG SER ILE SER ARG SER TRP GLN THR ASN LEU ARG GLN MET GLN ARG GLU LEU ARG GLU HIS LEU ALA SER LEU ALA LEU LEU ALA SER ARG LYS SER GLY MET SER CYS ASP LEU PHE ARG GLY GLY ILE LEU GLN ALA
ALA GLU ALA ALA ARG ARG ASP LEU ALA GLY VAL PRO GLY CYS GLU ARG LEU ARG GLN ALA ALA ASP ARG ILE ASP SER ASP ALA LYS ARG LEU GLU VAL TYR SER SER ARG ILE ALA GLU LEU GLU ARG GLU VAL LYS ASP LEU ARG PHE SER ASN THR ARG
LEU ALA GLU SER THR THR ARG VAL CYS ALA ARG SER VAL ASP PRO VAL GLU SER LEU SER VAL PHE PRO PRO VAL CYS ASP VAL CYS PRO ARG VAL SER SER VAL ASP PRO GLY ASP ALA LEU ARG SER GLY LEU LEU PHE ALA ARG GLN MET LEU ALA ASP ARG LEU VAL CYS LYS ASP
MET LEU HIS GLU ILE ASP ASN ARG LYS GLU LEU ARG GLU GLU ARG GLU ARG LYS ARG LEU GLY PHE SER HIS ALA ALA LEU ASN CYS LEU ARG ALA VAL PRO ALA ASP VAL TYR GLY MET LYS ARG ARG LYS ARG GLN GLU GLU ASN ARG GLU ASN HIS ARG ARG GLU SER GLU SER GLU
LEU ASP ASP VAL GLU GLU ALA GLU THR VAL ARG MET ARG VAL SER GLU SER ALA TRP SER GLN ASP ARG ASP ARG LEU LEU VAL ARG GLN VAL GLU LEU ARG ARG LEU ALA GLY GLY GLU ALA LYS LEU ARG PHE PRO ARG THR GLY ALA ILE GLU GLU ALA GLU LEU LEU GLY GLU
GLU ARG GLU LYS ARG LYS LYS LYS LYS ARG LEU GLU GLY TYR LYS GLU LYS GLY ARG GLU ASP ALA SER TYR ARG LEU SER PRO GLU VAL GLU ALA LEU MET GLN SER THR GLU ALA SER LEU ARG ASP GLU VAL ALA ASP ILE LYS GLU LYS GLU VAL GLU ALA GLU THR GLU ARG
LYS ALA GLU LYS GLU ARG LEU MET TRP GLU VAL LYS LYS ALA ARG GLU GLN ALA SER ARG GLU GLU MET ARG LYS GLN MET GLU GLU LYS GLU LYS ARG LEU GLU GLU GLU LYS LEU ARG HIS ARG GLU ALA LEU GLU GLU ALA GLU GLU LYS
ARG GLU LYS GLU ARG GLN LYS ALA GLU GLU PHE TRP ARG GLU ARG GLU GLU ASP GLU GLU ARG ARG ARG ARG GLU ARG GLU GLU ASP ALA ARG LEU ARG GLU ALA GLU GLU ARG PHE GLN GLU GLU GLU GLU ARG
GLU GLN ARG GLN GLN ARG ILE ARG GLU MET ARG GLU GLU ASP GLU ARG GLN ARG ARG LYS GLU GLU ARG ASP ALA GLU ARG ARG HIS MET LEU GLU LYS GLU GLU ASP ARG ARG ARG
LYS LYS GLU ILE GLU GLU ALA ASP LYS GLN ALA VAL GLU GLU GLU GLU

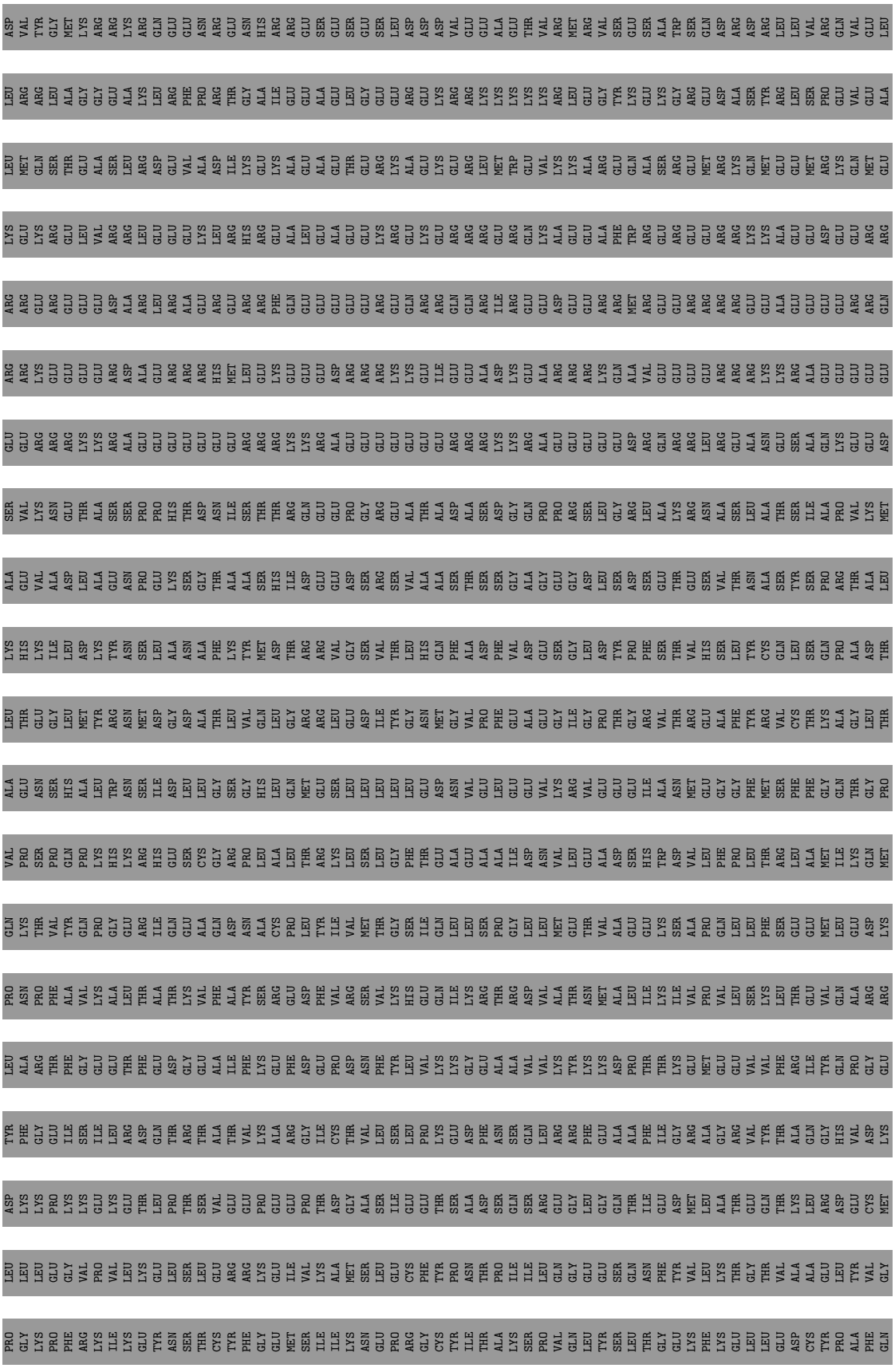

GLU GLU GLU GLU ARG ARG ARG ARG LYS LYS LYS ARG ALA GLU GLU GLU GLU GLU GLU ASP ARG GLN ARG ARG LEU ARG GLU ALA ASN GLU SER ALA GLN LYS GLU GLU ASP SER VAL LYS ASN GLU THR ALA SER SER PRO PRO HIS THR ASP ASN ILE SER THR THR ARG GLN GLU GLU ASP GLU ARG
GLU ALA THR ALA ASP ALA SER ASP GLY GLN PRO PRO ARG SER LEU GLY ARG LEU ALA LYS ARG ASN ALA SER LEU ALA THR SER ILE ALA PRO VAL LYS MET ALA GLU VAL ALA ASP LEU ALA GLU ASN PRO GLU LYS SER GLY THR ALA ALA SER HIS ILE ASP GLU GLU ASP SER VAL
SER VAL ALA ALA SER THR SER SER GLY ALA GLY GLU GLY ASP LEU SER ASP SER GLU THR GLU SER VAL THR ASN ALA SER TYR SER PRO ARG THR ALA LEU LYS HIS LYS ILE LEU ASP THR ASP ASN ALA PHE LYS TYR MET HIS ARG ARG VAL GLY SER VAL
THR LEU HIS GLN PHE ALA ASP PHE VAL ASP GLU SER GLY LEU ASP TYR PRO PHE SER THR VAL HIS SER LEU TYR CYS GLN LEU SER GLN PRO ALA ASP THR LEU THR GLU GLY LEU ASP GLN LEU GLY MET ARG ARG LEU GLU ASP ILE
TYR GLY ASN MET GLY VAL PRO PHE GLU ALA GLY GLY ILE GLY PRO THR GLY ARG VAL THR ARG GLU ALA PHE TYR ARG VAL CYS THR LYS ALA GLY LEU THR ALA GLU ASN SER HIS ALA LEU TRP ASN SER ILE ASP LEU LEU GLY SER LEU LEU LEU
LEU LEU GLU ASP ASN VAL GLU LEU GLU GLU VAL LYS ARG VAL GLU GLU GLU ILE ALA ASN MET GLU GLY PHE MET SER PHE GLY GLN THR GLY PRO VAL PRO SER PRO GLN GLN PRO LYS HIS LYS ARG HIS GLU SER CYS GLY ARG PRO LEU ALA LEU THR ARG LYS LEU SER LEU
GLY PHE THR GLU ALA GLU ALA ALA ILE ASP ASN VAL LEU GLU ASP SER HIS TRP ASP VAL LEU PHE PRO LEU THR ARG LEU GLU ALA MET ILE LYS GLN MET GLN LYS THR VAL TYR GLN PRO GLY GLU ARG GLN ILE GLN GLU ALA GLN ASP ASN ALA CYS PRO LEU TYR ILE VAL MET THR
GLY SER ILE GLN LEU LEU SER PRO GLY LEU LEU MET GLU THR VAL ALA GLU GLU LYS SER ALA PRO GLN LEU LEU PHE SER GLU GLU MET LEU GLU ASP LYS PRO ASN PRO PHE ALA VAL LYS ALA LEU THR ALA THR LYS VAL PHE ALA GLU ARG GLU ASP PHE VAL ARG SER VAL
LYS HIS GLU GLN ILE LYS ARG THR ARG ASP VAL ALA THR ASN MET ALA LEU ILE LYS ILE VAL PRO VAL LEU GLN VAL ARG ALA THR PHE GLY GLU GLU THR PHE GLU ASP GLY GLU ALA LYS PHE GLU PHE ASP GLU PRO ASP ASN PHE
TYR LEU VAL LYS LYS GLY GLU ALA ALA VAL LYS TYR LYS LYS ASP PRO THR THR LYS GLU MET GLU GLU VAL VAL PHE ARG ILE TYR GLN PRO GLY GLU TYR PHE GLY GLU GLU ILE SER ILE LEU ARG ASP GLN THR ARG THR ALA THR ARG ASP VAL LYS GLU ALA ARG GLY ILE CYS THR VAL LEU
SER LEU PRO LYS GLU ASP PHE ASN SER GLN LEU ARG ARG PHE GLU ALA ALA PHE ILE GLY ARG ALA ALA GLY ARG VAL TYR THR ALA GLN GLY HIS VAL ASP LYS ASP LYS LYS PRO LYS LYS GLU LYS GLU THR LEU PRO THR SER VAL GLU PRO THR ARG THR ALA LEU ARG ASP ALA SER
ILE GLU GLU THR SER GLN GLN THR ILE GLU ASP MET LEU ASP SER GLN THR GLU GLN THR ILE GLU ASP CYS MET LEU LEU LEU GLU GLY VAL PRO VAL LEU LYS GLU LYS GLU LEU SER LEU GLU ARG GLN ARG LYS VAL LYS ALA MET SER LEU
GLU CYS PHE TYR PRO ASN THR PRO ILE ILE LEU GLN GLY GLU GLU SER GLN ASN PHE TYR VAL LEU LYS THR GLY THR VAL ALA ALA GLU LEU TYR VAL PRO PHE ARG LYS ILE LYS GLU TYR ASN SER THR CYS TYR PHE GLY GLU MET SER ILE ILE LYS ASN GLU
PRO ARG GLY CYS TYR ILE THR ALA LYS SER PRO VAL GLN LEU TYR SER LEU THR GLY GLU LYS LEU GLU LEU GLU ASP CYS TYR PRO ALA PHE GLN GLU TYR ALA ALA GLN GLN GLU THR LEU LYS ARG GLN ALA SER SER GLN GLU VAL SER SER ILE ALA VAL
ARG GLU GLU PRO THR ALA ASP TYR GLY GLU ILE MET ASN LEU LEU LEU VAL GLN VAL PRO VAL ILE ASN MET LEU ASP GLU ASP ASP ALA LEU GLN GLN LEU THR ARG ALA PHE LYS VAL GLU CYS TYR GLN GLU ARG GLU VAL ILE ILE HIS GLU GLY THR PRO ALA GLU HIS PHE PHE ILE
PHE SER GLY ASP VAL SER ILE VAL GLN GLY ALA PRO VAL GLU ILE VAL VAL LEU HIS ALA GLY GLU TYR LEU GLU GLU ILE ALA PHE LEU LEU ASN GLU GLN PRO ARG THR ALA SER CYS VAL ALA LYS SER ASP VAL LYS LEU LEU SER LEU THR ARG SER ASP SER PHE GLN VAL
HIS LEU GLY ALA LEU GLN ASP ALA PHE GLU ASP GLU ALA ILE PRO ASP TRP LEU VAL GLU ALA ALA GLY ALA GLU GLN GLY ALA LEU TYR ASP PRO SER GLY SER LYS LYS THR GLU ASP GLU GLU GLU PRO ASP GLY ALA PHE ARG GLY
THR VAL ASP ILE ASP LYS GLU LYS GLU MET TYR ASN LYS LYS ARG GLY LYS ASP SER ASP THR SER ARG LYS LYS SER ASP ALA ALA SER ALA SER ALA LYS LYS THR LYS ALA ASP LYS THR GLY GLU ALA LYS ALA SER ASP ALA HIS ARG LYS LYS SER GLY GLU THR PRO PRO GLY ASP GLY GLU GLU GLU ALA GLY
LYS PRO GLY ASN ASP GLU VAL ALA ALA GLU LYS LYS LYS LYS ALA LYS GLU LYS LYS HIS GLY GLY GLU GLU THR LYS LYS LYS GLY GLY GLU THR GLY GLY GLU THR LYS GLU GLN SER GLN ALA LYS ARG MET SER LEU ALA GLY GLY ALA
ALA LEU LEU ALA ALA ALA ALA ALA LYS ALA ALA ALA GLU GLY GLU PRO SER PRO ASN GLU LYS GLU GLU GLU LYS GLU GLN GLU GLU LYS GLU THR LYS ALA GLY GLU MET GLU GLU LYS GLN ASP LYS GLU GLU THR ALA GLU LYS LYS LYS LYS



• Molecule 14: PCR12, TGME49_219070

Chain MI: 95%




ASP VAL TYR GLY MET LYS ARG ARG LYS ARG GLN GLU GLU ASN ARG GLU ASN HIS ARG ARG GLU SER GLU SER GLU SER LEU ASP ASP ASP VAL GLU GLU ALA GLU THR VAL ARG MET ARG VAL SER GLU SER ALA TRP SER GLN ASP ARG ASP ARG LEU LEU LEU VAL ARG GLN VAL GLU LEU
LEU ARG ARG LEU ALA GLY GLY GLU ALA LYS LEU ARG PHE PRO ARG THR GLY ALA GLU ALA GLU LEU GLY GLY GLU GLU LYS ARG GLU LYS LYS LYS LYS LYS LYS ARG LEU GLU GLY TYR LYS GLU LYS GLY ARG GLU ASP ALA SER TYR ARG LEU SER PRO GLU VAL GLU ALA
LEU MET GLN SER THR GLU ALA SER LEU ARG ASP GLU VAL ALA ASP ILE LYS GLU LYS ALA GLU ALA GLU ALA GLU THR GLU GLU ARG GLN GLN LYS LYS ALA ARG GLU GLN GLU LYS GLU ARG LEU MET TRP GLU VAL LYS LYS LYS ALA ARG GLU LYS GLN MET GLU GLU MET ARG LYS GLN MET GLU
LYS GLU LYS ARG GLU LEU VAL ARG ARG LEU GLU GLU GLU LYS LEU ARG HIS ARG GLU ALA LEU GLU ALA GLU GLU LYS GLU ARG GLN LYS ALA GLU GLU ALA PHE TRP ARG GLU ARG GLU GLU ARG ARG LYS LYS ALA GLU GLU ASP GLU ARG ARG
ARG ARG GLU ARG GLU GLU GLU GLU ASP ALA ARG LEU GLU ARG ALA GLU ARG GLN ARG ARG GLU ASP ALA ARG GLU GLN GLN ARG ILE ARG GLU GLU ASP GLU GLU ARG ARG GLU GLU ALA ALA GLU GLU ARG ARG MET ARG GLU GLU ARG ARG ARG ARG GLU LYS LYS ALA GLU GLU GLN
ARG ARG LYS GLU GLU GLU GLU GLU ARG ARG ASP ALA GLU ARG ARG HIS MET LEU GLU LYS GLU GLU GLU ASP GLU ARG ARG PHE GLN GLU GLU GLU ASP ASP ARG ARG GLU ARG ARG LYS LYS ILE GLU GLU GLU ALA ASP LYS GLU ALA ASP ARG LYS GLN ALA VAL GLU GLU GLU GLU GLU GLU GLU GLU
GLU GLU ARG ARG LYS LYS ARG ALA GLU GLU GLU GLU GLU GLU GLU ARG ARG ARG ARG LYS LYS ARG ALA GLU GLU GLU GLU GLU GLU ARG ARG ARG ARG ARG ARG ARG ALA ASP ARG GLU ALA GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU ASP ARG GLN LYS GLU GLU GLU ASP
SER VAL LYS ASN GLU THR ALA SER SER PRO PRO HIS THR ASP ASN ILE SER THR THR ARG GLN GLU GLU PRO GLY ARG GLU ALA THR ALA ASP ALA SER ASP GLY GLN PRO PRO ARG SER LEU GLY ARG LEU ALA LYS ARG ASN ALA SER LEU ALA THR SER ILE ALA PRO VAL LYS MET
ALA GLU VAL ALA ASP LEU ALA GLU ASN PRO GLU LYS GLU ALA ALA GLU ASP SER ARG GLU SER VAL ALA ALA SER THR SER SER GLY GLY ALA GLY GLU GLY ASP LEU SER ASP SER GLU THR THR GLU SER VAL THR ASN ALA SER LEU ALA SER TYR SER PRO ARG THR ALA LEU
LYS HIS LYS ILE LEU ASP TYR ASN SER LEU ALA ASN ALA PHE LYS TYR MET ASP THR ARG ARG VAL GLY SER VAL THR LEU HIS GLN PHE ALA ASP PHE VAL ASP GLU SER GLY LEU ASP TYR PRO PHE SER THR VAL HIS SER LEU TYR CYS GLN LEU SER GLN PRO ALA ASP THR
LEU THR GLU GLY LEU MET TYR ARG ASN MET ASP GLY ASP ALA THR LEU VAL GLN LEU GLY ARG ARG LEU GLU ASP ILE TYR GLY ASN MET GLY VAL PRO PHE GLU ALA GLU GLY ILE GLY PRO THR GLY ARG VAL THR ARG GLU ALA PHE TYR ARG VAL CYS THR LYS ALA GLY LEU THR
ALA GLU ASN SER HIS ALA LEU TRP ASN SER ILE ASP LEU GLN MET GLU SER LEU LEU LEU LEU LEU GLU GLU ASP ASN VAL GLU LEU GLU GLU VAL LYS ARG VAL GLU GLU ILE ALA ASN MET GLU GLY GLY PHE MET SER PHE PHE GLY GLN THR GLY PRO
VAL PRO SER PRO GLN PRO LYS HIS LYS ARG HIS GLU SER CYS GLY ARG PRO LEU ALA LEU THR ARG LYS LEU SER LEU GLY PHE THR GLU ALA ALA ASP GLU ILE ILE GLN LEU LEU SER LEU MET THR GLY SER ILE GLN LEU GLU ALA GLU LEU SER PRO ILE ASP ASN VAL LEU GLU ALA ASP SER HIS TRP ASP VAL LEU PHE PRO LEU THR ARG LEU ALA MET GLU LEU PHE PRO GLN LEU LEU LEU PHE SER GLU GLU MET ILE LYS GLN MET
GLN LYS THR VAL TYR GLN PRO GLY GLU ARG ILE GLN GLU ALA GLN ASP ASN ALA CYS PRO LEU TYR ILE VAL MET THR GLY SER ILE GLN LEU LEU SER PRO GLY LEU LEU MET GLU THR VAL ALA GLU GLU LYS SER ALA PRO GLN LEU LEU LEU PHE SER GLU GLU MET LEU GLU ASP LYS
PRO ASN PRO PHE ALA VAL LYS ALA LEU LEU THR ALA ALA THR LYS VAL PHE ALA PHE SER ARG GLU ASP PHE VAL ARG SER VAL LYS HIS GLU GLN ILE LYS ARG THR ARG ASP VAL ALA THR ASN MET ALA LEU ILE LYS ARG LEU ALA ARG
LEU ALA ARG THR PHE GLY GLU GLU THR PHE GLU ASP GLY GLU PHE ASP GLU PRO ASP ASN PHE TYR LEU VAL LYS LYS GLY GLU ALA ALA VAL LYS TYR LYS LYS ASP PRO THR THR LYS GLU MET ALA LEU ILE LYS ILE GLY GLU
TYR PHE GLY GLU ILE SER ILE LEU ARG THR ARG THR ALA THR VAL LYS ALA ARG GLY ILE CYS THR VAL LEU SER LEU PRO LYS GLU ASP PHE ASN SER GLN LEU ARG ARG PHE GLU ALA ALA PHE ILE GLY ARG GLY ARG ILE TYR GLN PRO ASP
ASP LYS LYS PRO LYS THR LEU PRO GLU GLU THR SER ALA ASP SER GLN SER ARG GLU GLY GLN THR ILE GLU ASP MET LEU ALA THR GLU GLN LYS THR ARG ASP VAL GLY
LEU LEU LEU GLU LYS GLU VAL LEU GLU CYS PHE TYR PRO ASN THR PRO ILE ILE ILE LEU GLN GLY GLU GLU SER GLN ASN PHE TYR VAL LEU LYS THR GLY THR VAL ALA GLY LEU
PRO GLY LYS PRO PHE ARG ILE LYS GLU GLU PRO ARG GLY CYS TYR ILE THR ALA LYS SER PRO VAL GLN LEU TYR SER LEU THR GLY GLU LYS PHE LYS GLU LEU LEU GLU TYR VAL LYS GLY

GLU TYR ALA GLN ALA GLN TYR GLU GLN GLU GLU THR LEU LYS ARG GLN ALA SER SER GLN LEU VAL SER SER GLU ALA VAL ARG GLU GLU PRO THR ALA ASP TYR GLY GLU ILE MET ASN LEU LEU VAL GLN VAL PRO VAL ILE ASN MET LEU ASP GLU ASP ALA LEU GLN GLN LEU THR ARG

ALA PHE LYS VAL GLU CYS TYR GLN GLU ARG GLU VAL ILE ILE HIS GLU GLY THR PRO ALA GLU HIS PHE PHE ILE ILE PHE SER GLY ASP VAL SER VAL GLN LYS ILE VAL ASP GLY ALA PRO VAL GLU ILE VAL VAL LEU HIS ALA GLY GLU TYR LEU GLY GLU ILE ALA PHE LEU ASN

GLU GLN PRO ARG THR ALA SER CYS VAL ALA LYS SER ASP VAL LYS LEU LEU SER LEU THR ARG SER ASP PHE GLN VAL HIS LEU GLY ALA LEU GLN ASP GLN ALA GLU SER LYS TYR ALA ALA SER LYS ASP GLU ALA ILE GLY GLU LEU VAL GLU ALA GLY

GLN GLY ALA LEU TYR ASP PRO SER GLY SER LYS LYS THR GLU ASP GLU ASP GLU GLU PRO ASP GLY ALA PHE ARG GLY THR VAL ASP ILE ASP LYS GLU LYS GLU MET TYR ASN LYS LYS ARG GLY ARG LYS ASP SER ASP ALA SER ALA ASP LYS THR

GLY GLU ALA LYS ALA SER ASP ALA HIS ARG LYS LYS SER GLY GLU GLU THR PRO PRO GLY ASP GLY GLU GLU GLU GLY ALA GLY LYS PRO GLY ASN ASP GLU VAL ALA ALA ASP THR ASN THR VAL GLU LYS LYS LYS LYS LYS ALA LYS GLU GLU GLY SER

GLU GLU THR GLY GLY GLU THR LYS LYS GLY LYS GLN SER GLN ALA LYS ARG ARG MET SER LEU ALA CYS GLY GLY ALA ALA LEU LEU ALA ALA ALA ALA ALA LYS ALA ALA GLU GLY GLU PRO SER PRO ASN GLU LYS GLU GLN GLN GLU GLU LYS GLU GLU THR LYS ALA GLY GLU MET

GLU GLU LYS GLN ASP LYS GLU GLU THR GLU LYS LYS LYS LYS LYS LYS LYS LYS ASP GLU ASP GLU ASP ALA GLU ASP GLU ALA ALA ILE ASP GLU PHE ARG ASP LEU VAL LYS ASN THR LEU GLY SER GLN LEU SER ILE ALA

ALA PHE GLN GLN ILE ASP GLY ASN ASN SER GLU ILE VAL ASP PHE ASP GLU GLU PHE ALA ALA PHE VAL LYS ASP LEU ARG VAL GLN SER LEU LYS LYS LYS ASP ILE GLN VAL LEU PHE ASP ASP LEU CYS GLN PRO LEU LYS GLY THR LEU THR VAL ALA ASN LEU TYR ARG ASN ILE ASP

LYS LYS ASP GLN LEU SER LYS ALA GLU ILE ASN LEU GLU ILE PHE GLY GLY SER ARG LYS ALA PHE LYS ALA VAL ALA ASN LEU GLY GLY GLY ASP GLU CYS THR GLU GLU ASP GLY PHE ILE ASN VAL ALA ALA ALA ALA ALA GLY VAL SER GLU GLU GLU ASN ALA LYS SER ILE TRP

THR GLU LEU ASP LYS ALA GLN THR GLY GLN MET HIS THR LYS VAL ILE CYS SER TYR MET ALA GLY GLU LEU THR ALA GLU GLU ALA ALA LYS GLU GLU GLU GLU LEU ALA SER LEU GLY THR ARG LEU TRP ASN PHE PHE GLY GLY SER ALA SER ASP ASP GLU SER ALA SER ALA SER

SER PRO THR SER GLN GLY ASP GLU GLN LYS ILE GLN GLU ALA LEU LYS TRP GLU ASP MET ALA ILE VAL GLN ARG ASP ASP HIS ARG THR TYR PRO THR CYS THR LYS ARG LEU VAL ASP VAL LEU GLU LYS LYS GLU GLY PHE MET ASN LEU GLN LEU LEU GLN LEU GLU ARG TYR VAL ALA

SER THR MET ARG ARG GLU CYS LEU ALA LYS GLY VAL ARG VAL MET GLU ALA GLY ASP GLU GLU ALA CYS MET VAL PHE CYS ALA TRP GLY GLU PHE LYS ILE LEU GLN ALA GLY LEU PHE GLY GLU SER GLU VAL GLY VAL VAL CYS PRO ASP GLU CYS PHE GLY LEU SER GLU ILE LEU

ASP SER PRO LEU THR ALA SER LEU VAL THR GLU VAL ASP ASN SER VAL LEU TRP VAL LEU GLU ARG ASP THR TYR ASN ASP LEU ILE ARG ASP MET LEU GLU ALA ARG ALA VAL VAL PRO VAL ILE GLU ASN PHE LEU LYS SER VAL PRO ILE VAL LYS ASP MET SER GLU THR GLU

ILE GLN ASN VAL ALA ARG ALA CYS LYS ILE GLU GLU THR PHE SER PRO HIS GLN THR VAL PHE ARG ALA GLY MET ALA GLY ASP MET PHE CYS PHE ILE PHE LYS GLY GLU ILE THR MET LEU LYS PRO MET GLY ALA GLY GLN GLU PRO ILE GLU LEU LEU GLY ARG LEU GLN GLN ALA GLY THR VAL TYR

PHE GLY GLU MET ALA VAL ILE LYS ASN GLN ARG ARG THR ALA SER ILE ILE ALA ALA THR ASP LEU THR LEU PHE CYS LEU ASP LYS GLY SER PHE GLU ARG VAL LEU GLY ARG VAL LYS GLY LYS MET ILE GLU GLU TYR LYS ARG VAL ARG GLN ASP VAL ALA THR ASP

PRO LYS GLU GLY GLU GLY ASN ALA ALA ALA SER SER ALA SER ALA ALA ALA GLY ALA ALA GLU SER PHE GLY PRO GLY ASP HIS PHE GLU LYS ARG THR ARG LYS SER SER LEU ALA LEU LEU LEU GLN TYR THR LYS ILE ARG GLU ALA GLY LEU GLY GLU SER LYS LYS

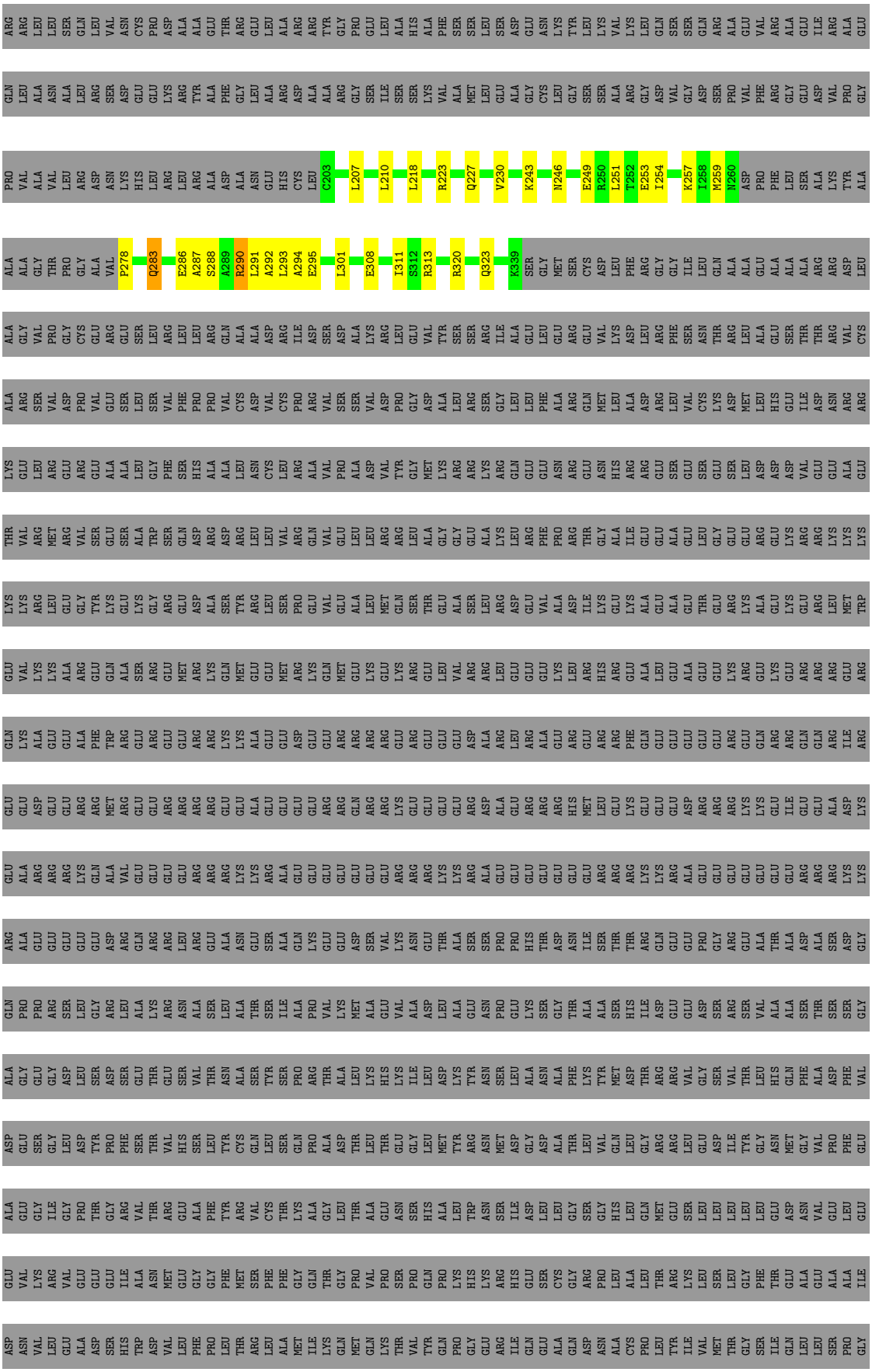
SER SER GLU GLU ASP GLU GLU ARG GLU TRP ALA MET ALA GLN ASP PRO GLU ILE ILE HIS ARG PRO PRO PRO LEU SER ALA ALA PRO LYS LYS ARG LEU ARG THR THR SER SER LYS SER VAL GLY ILE LYS ASN SER VAL PHE PHE ASP GLU GLU THR LEU LEU PRO SER

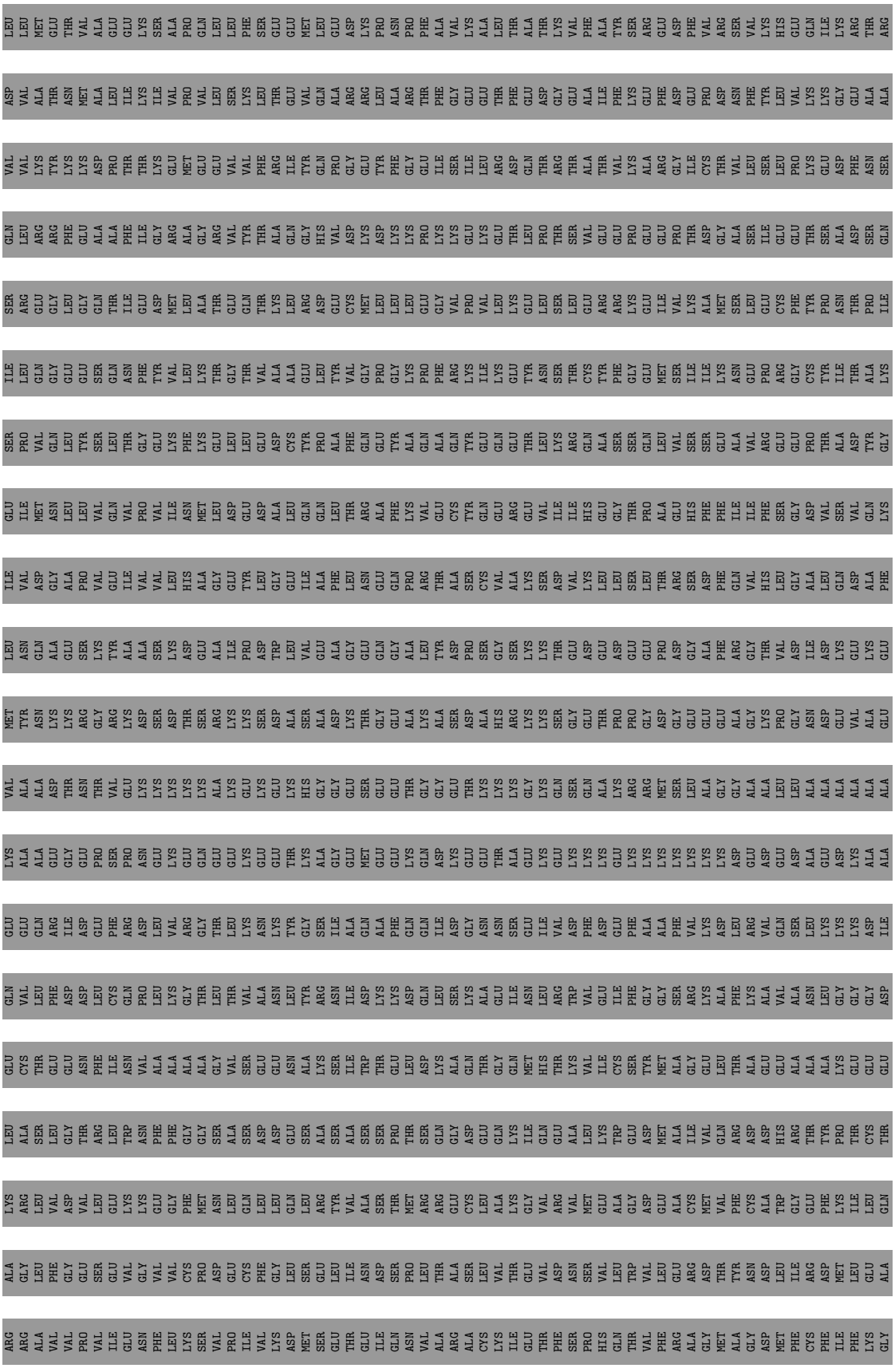
PRO PRO SER SER ASP GLU GLY GLU

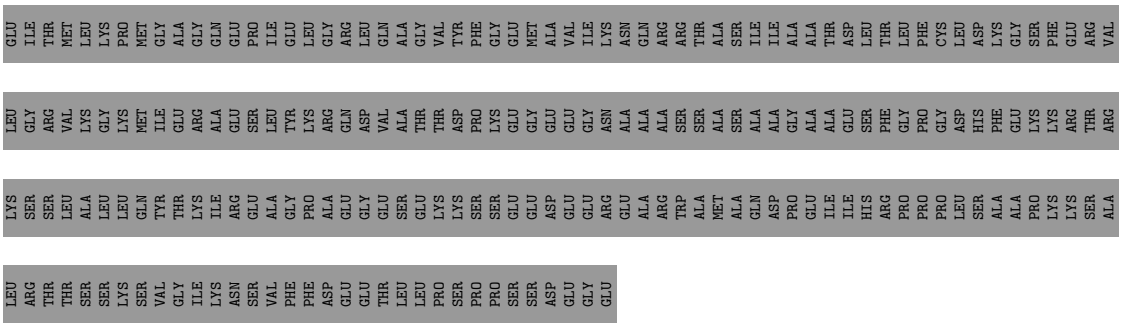
- Molecule 14: PCR12, TGME49_219070

Chain MJ: 96%

MET GLU THR ARG ALA MET LEU GLY ALA PRO TRP SER ALA ALA GLU GLY GLY ASP GLY VAL ALA ASP PRO ASP ARG LEU TYR THR ARG SER LEU ARG GLU ASP LEU GLU GLU ALA ARG ASP LYS LEU LEU LYS LEU LYS LYS MET ASN GLU LEU GLU GLY GLU ASN GLN ASP LEU ARG

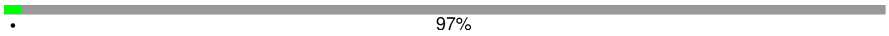

C203
L207
L210
L218
R223
Q227
V230
K243
N246
E249
R250
L251
T252
E253
I254
K257
Y258
M259
N260
P278
Q283
E286
A287
S288
A289
R290
L291
A292
L293
A294
E296
L301
E308
I311
S312
R313
R320
Q323
K339

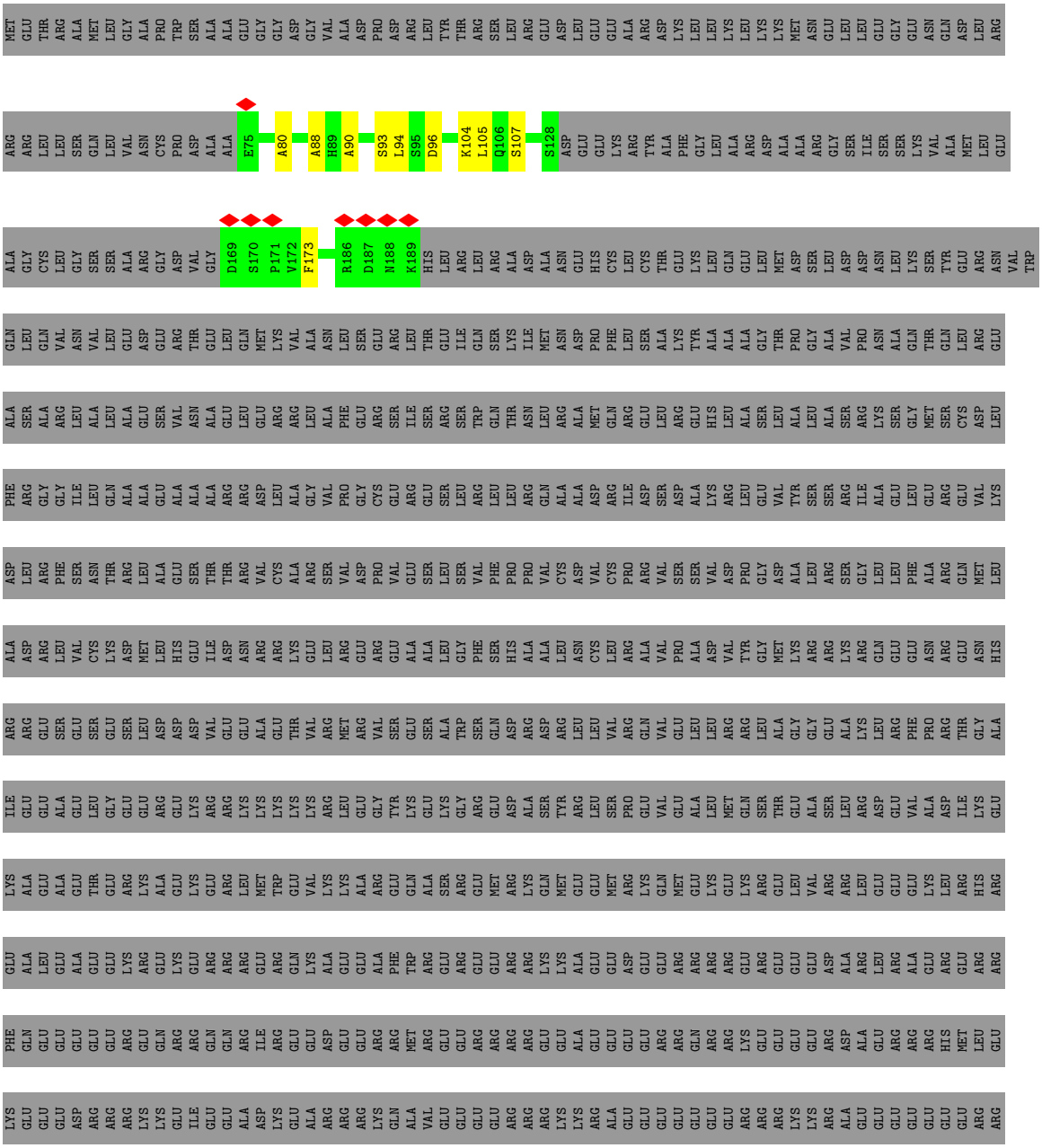

LEU LEU MET GLU THR VAL ALA GLU GLU LYS SER ALA PRO GLN LEU LEU PHE SER GLU GLU MET LEU GLU GLU ASP LYS PRO ASN PRO PHE ALA VAL LYS ALA LEU THR ALA THR LYS VAL PHE ALA TYR SER ARG GLU ASP PHE VAL ARG SER VAL LYS HIS GLU GLN ILE LYS ARG THR ARG
ASP VAL ALA THR ASN MET ALA LEU ILE LYS ILE VAL PRO VAL LEU SER LYS LEU THR GLU VAL ALA ARG ARG LEU ALA ARG THR PHE GLY GLU GLU THR PHE GLU ASP GLY GLU ALA ILE PHE LYS GLU PHE ASP GLU PRO ASP ASN PHE TYR LEU VAL LYS LYS GLY GLU ALA ALA
VAL VAL LYS TYR LYS LYS ASP PRO THR THR LYS GLU MET GLU GLU VAL VAL PHE ARG ILE TYR GLN PRO GLY GLU TYR PHE GLY GLU ILE SER ILE GLU ILE LEU ARG ASP GLN THR ARG GLY GLU ALA THR VAL LYS GLU ALA ILE CYS THR VAL LEU SER LEU VAL LYS LYS GLU ASP PHE ASN SER
GLN LEU ARG ARG PHE GLU ALA ALA PHE ILE GLY ARG VAL TYR THR ALA GLN GLY HIS VAL ASP LYS ASP LYS LYS PRO LYS LYS GLU GLU THR LEU PRO THR SER VAL GLU GLU PRO THR ASP THR GLY GLU GLU THR GLU GLN LEU GLU GLU PRO GLU GLU LYS ASP LYS LYS LYS GLU GLU GLY VAL PRO VAL LEU LYS GLU GLU CYS PHE TYR PRO ASN THR PRO ILE
SER ARG GLU GLY LEU GLY GLN THR ILE GLU ASP MET LEU ALA THR GLU GLN THR LYS LEU GLN ARG ASP GLU CYS MET LEU LEU LEU GLY VAL PRO VAL LEU LYS GLU TYR LEU SER LEU GLU ARG ARG LYS LEU GLU ARG LYS ALA LYS ALA LEU GLU ALA MET SER LEU GLU GLU GLU PRO ASP ALA ASP SER GLN
ILE LEU GLN GLY GLU GLU SER GLN ASN PHE TYR VAL LEU LYS THR GLY THR VAL ALA GLU LEU TYR VAL GLY PRO GLY LYS PRO PHE ARG LYS ILE LYS GLU TYR ASN SER THR CYS TYR PHE GLY GLU MET SER ILE ILE LYS ASN GLU PRO ALA GLU HIS GLU GLY THR PRO ALA THR ILE ILE HIS GLU GLY THR PRO ALA GLU HIS PHE PHE ILE ILE PHE SER GLY ASP VAL SER ILE ALA LYS
SER PRO VAL GLN LEU TYR SER LEU THR ILE GLU ASP CYS TYR PRO ALA PHE GLN GLU TYR ALA GLN GLN GLU THR LEU LYS ARG GLN ALA ALA SER SER GLN LEU VAL SER SER GLU GLN ALA VAL ARG GLU GLU PRO ALA GLU HIS ILE LYS ASN GLU PRO THR ALA ASP TYR GLY
GLU ILE MET ASN LEU LEU VAL GLN VAL PRO VAL ILE ASN MET LEU ASP GLU ASP ALA LEU GLN LEU THR ARG ALA PHE LYS VAL GLU CYS TYR GLN GLU GLN GLU ARG GLU VAL ILE ILE HIS GLU GLY THR PRO ALA GLU HIS PHE PHE ILE ILE PHE SER GLY ASP VAL SER VAL GLN LEU
ILE VAL ASP GLY ALA PRO VAL GLU GLU ILE GLU LEU GLU GLU LEU GLY ASN GLU GLN LEU ASN GLU GLN GLY LEU LEU SER LEU GLN LEU LEU LYS ALA LYS SER ASP VAL LYS LEU LEU LEU SER LEU THR ARG SER VAL LEU GLY ALA LEU GLN ASP ALA PHE
LEU ASN GLN ALA GLU SER LYS TYR ALA ALA SER LYS ASP GLU ALA ILE PRO ASP TRP LEU VAL GLU ALA GLY GLU GLN GLY ALA LEU TYR ASP PRO SER GLY SER LYS LYS THR GLU ASP GLU ASP GLU GLU PRO ASP GLY ALA PHE ARG GLY THR VAL ASP ILE ASP LYS LYS GLU LYS
MET TYR ASN LYS LYS ARG GLY ARG LYS ASP SER ASP THR SER ARG LYS LYS SER ASP ALA SER ALA ASP LYS THR GLY GLU ALA LYS GLU ALA SER ARG LYS LYS SER ASP ALA LYS SER GLY GLU THR PRO PRO GLY ASP GLY GLU GLU GLU ALA GLY LYS PRO GLY ASN ASP GLU VAL ALA GLU
VAL ALA ALA ASP THR ASN GLU LYS LYS LYS LYS ALA LYS GLU GLU LYS GLU GLU GLY GLU THR LYS LYS GLY LYS GLN SER GLN ALA LYS ARG ARG MET SER LEU LEU ALA GLY GLY ALA LEU LEU LEU ALA ALA ALA ALA ALA
LYS ALA ALA GLU GLY GLU PRO SER PRO ASN GLU LYS GLN ASP LYS GLU GLU THR LYS GLU GLU MET GLU GLU LYS GLN GLN ILE ASP GLY ASN ASN SER GLU ILE VAL ASP PHE ASP GLU PHE ALA ALA PHE VAL LYS ASP LEU ARG VAL GLN SER LEU LYS LYS ASP GLU ALA ILE
GLU GLU GLN ARG ILE ASP GLU PHE ARG ASP LEU VAL ARG GLY THR LEU LYS ASN LYS TYR GLY SER ILE ALA GLN ALA PHE GLN GLN ILE ASP GLY ASN ASN SER GLU ILE VAL ASP PHE ASP GLU PHE ALA ALA PHE VAL LYS ASP LEU ARG VAL GLN SER LEU LYS LYS ASP GLU ALA
GLN VAL LEU PHE ASP ASP PRO LEU LYS GLY THR LEU THR VAL ALA ASN LEU TYR ARG ASN ILE ASP LYS LYS ASP GLN LEU SER LYS ALA GLU ILE ASN LEU ARG TRP VAL GLU ILE PHE GLY GLY SER ARG LYS ALA VAL GLN SER LEU LYS LYS ASP GLY GLY
GLU CYS THR GLU GLU ALA ALA ALA GLY VAL SER ASP ASN SER ILE TRP THR GLU LEU ASP LYS ALA GLN THR GLU ILE ASN MET HIS THR LYS VAL ILE CYS SER TYR MET ALA GLY GLU LEU THR ALA GLU GLU GLN ALA ALA ALA ASN LEU GLY GLY GLU
LEU ALA SER LEU GLY GLY THR ARG LEU TRP ASN PHE PHE GLY ASP GLU GLU SER ALA SER SER ASP GLU GLU ALA SER SER ALA SER SER ILE ALA SER SER PRO THR SER GLN GLY ASP GLU LEU LYS ILE GLN GLU LEU ALA LEU LYS TRP GLU ALA GLY ASP MET ALA ILE VAL CYS THR
LYS ARG LEU VAL ALA GLU GLU LYS GLU GLY PHE MET ASN LEU GLN LEU GLN LEU ARG TYR VAL ALA SER THR MET ARG ARG GLU CYS LEU ALA LYS GLY VAL ARG VAL MET GLU ALA GLY ASP GLU ALA CYS MET VAL PHE CYS ALA TRP GLY GLU PHE LYS ILE LEU GLN
ALA GLY LEU PHE GLY GLU VAL VAL CYS PRO ASP GLU CYS PHE GLY LEU SER GLU LEU ILE ASN ASP SER PRO LEU THR ALA SER LEU VAL THR GLU VAL ASP ASN SER VAL LEU TRP VAL LEU GLU ARG ASP THR TYR ASN ASP HIS ILE ARG ASP MET GLU VAL
ARG ARG ALA VAL PRO ILE GLU VAL LYS SER VAL PRO ILE GLU THR VAL LYS ASP MET SER GLU LEU THR GLU ILE GLN ASN VAL ALA ARG ALA CYS LYS ILE GLU THR PHE SER PRO HIS GLN THR VAL PHE ARG ALA GLY MET ALA CYS PHE ILE PHE LYS GLY

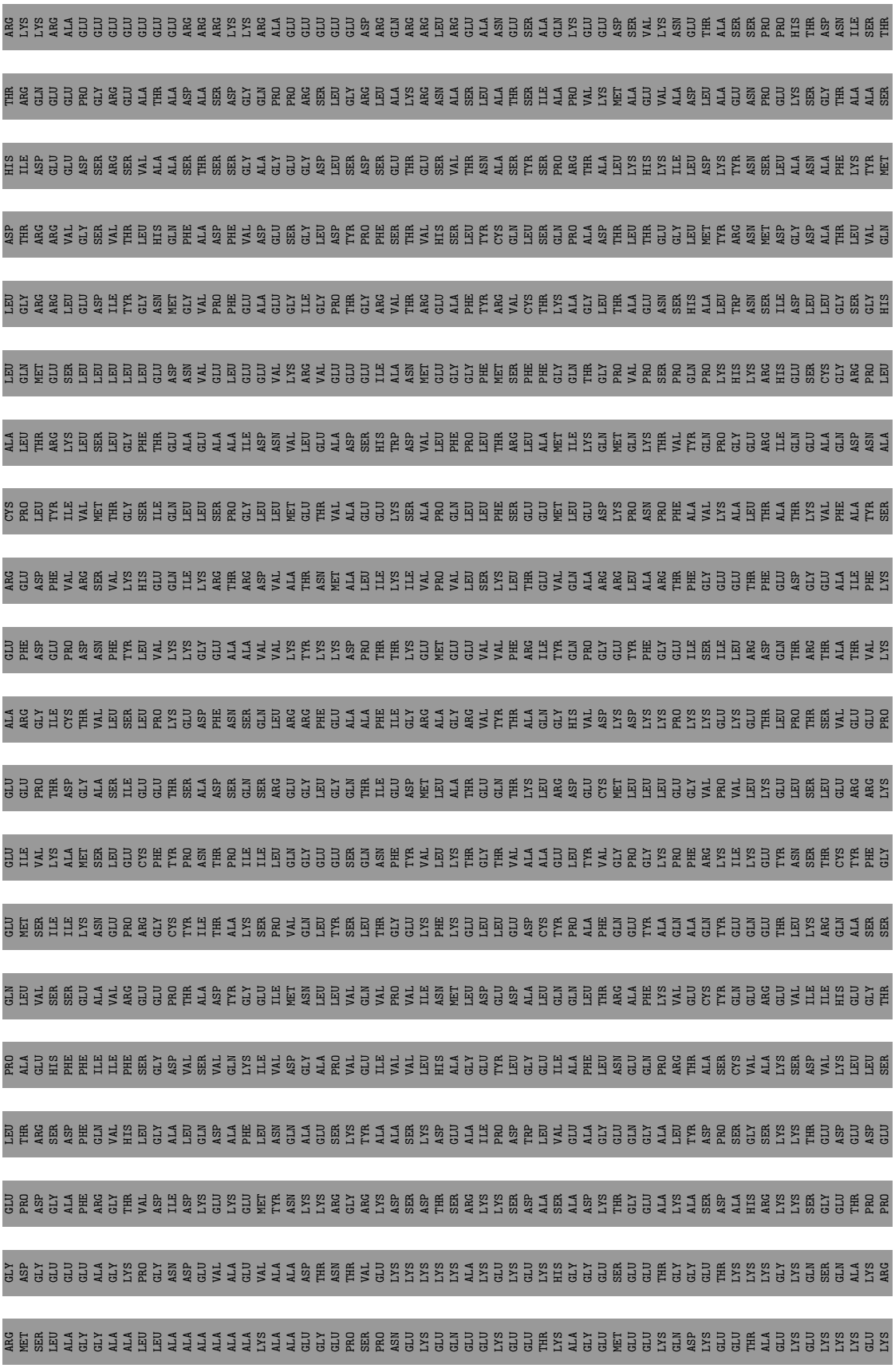


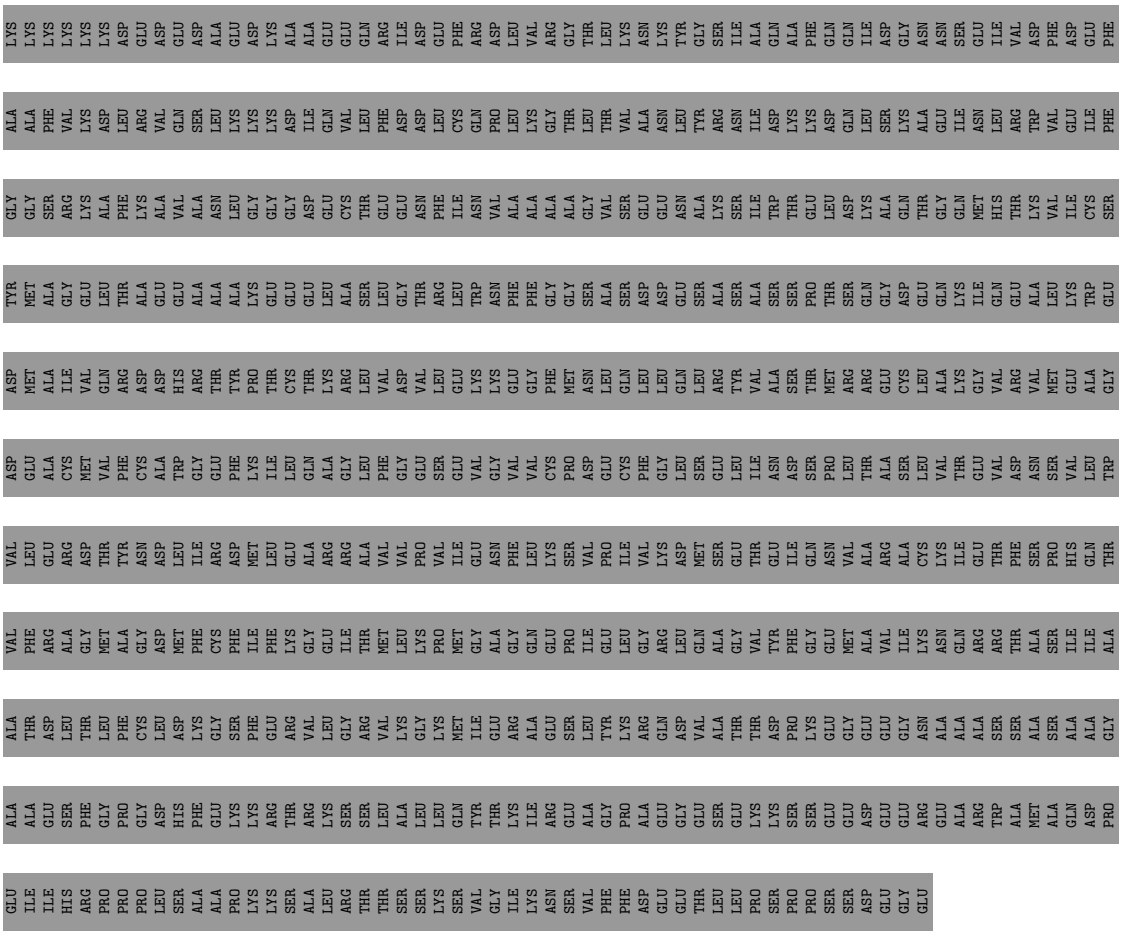
• Molecule 14: PCR12, TGME49_219070

Chain MK:



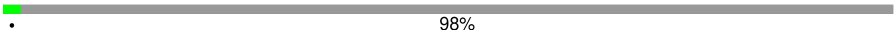


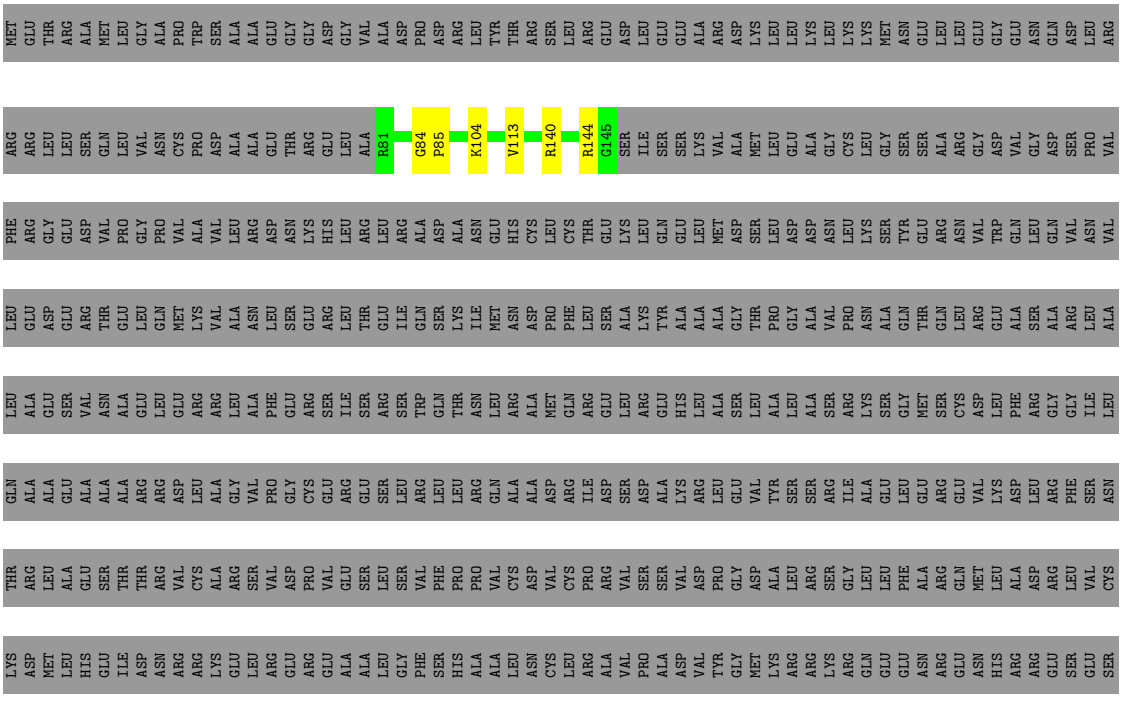

ARG LYS LYS ARG ALA GLU GLU GLU GLU GLU GLU GLU ARG ARG ARG LYS LYS ARG ALA GLU GLU GLU GLU GLU GLU GLU ASP ARG GLN ARG ARG LEU ARG GLU GLN ALA ASN GLU SER ALA GLN LYS GLU GLU ASP SER VAL LYS ASN GLU THR ALA SER ASP HIS THR ASP ASN ILE SER THR
THR ARG GLN GLU GLU PRO GLY ARG GLU ALA THR ALA ASP ALA SER ASP GLY GLN PRO PRO ARG SER LEU GLY ARG LEU ALA LYS ARG ASN ALA SER LEU ALA THR SER ILE ALA PRO VAL LYS MET ALA GLU VAL ALA ASP LEU ALA GLU ASN SER LEU ALA PRO GLU LYS SER GLY THR ALA SER
HIS ILE ASP GLU GLU ASP SER ARG SER VAL ALA ALA ALA SER THR SER SER GLY ALA GLY GLU GLY ASP LEU SER ASP SER GLU THR GLU SER VAL THR ASN ALA SER TYR SER PRO ARG THR ALA LEU LYS HIS LYS ILE LEU ASP LYS TYR ASN ASP PHE LYS MET
ASP THR ARG ARG VAL GLY SER VAL THR LEU HIS GLN PHE ALA ASP PHE VAL ASP GLU SER GLY LEU ASP TYR PRO PHE SER THR LEU THR VAL HIS SER LEU TYR CYS GLN LEU SER GLN PRO ALA ASP THR LEU THR GLU GLY LEU MET TYR ARG ASN MET ASP GLY ASP ALA THR LEU VAL GLN
LEU GLY ARG ARG LEU GLU ASP ILE TYR GLY ASN MET GLY VAL PRO PHE GLU GLU ALA GLU GLY ILE GLY PRO THR GLY ARG VAL THR ARG GLU GLU PHE TYR ARG VAL CYS THR LYS ALA GLY LEU THR ALA GLU ASN SER HIS ALA LEU TRP ASN SER ILE ASP LEU LEU GLY SER VAL GLN
LEU GLN MET GLU SER LEU LEU LEU LEU GLU GLU ASP ASN VAL GLU LEU GLU GLU VAL LYS ARG VAL GLU GLU GLU ILE ALA ASN MET GLU GLY PHE MET SER PHE PHE GLY GLN THR GLY PRO VAL PRO SER PRO GLN PRO LYS HIS LYS ARG HIS GLU SER CYS GLY ARG PRO LEU
ALA LEU THR ARG LYS LEU GLY PHE THR GLU ALA GLU ALA ALA ILE ASP ASN VAL LEU GLU ALA ASP SER HIS TRP ASP VAL LEU PHE PRO LEU THR ARG LEU ALA MET ILE LYS GLN MET GLN LYS THR VAL TYR GLN PRO GLY GLU ARG ILE GLN ILE ALA ASP ASN ALA
CYS PRO LEU TYR ILE VAL MET THR GLY SER ILE GLN LEU LEU SER PRO GLY LEU LEU MET GLU THR VAL ALA GLU GLU LYS SER ALA PRO GLN LEU LEU PHE SER GLU GLU MET LEU GLU ASP LYS PRO ASN PRO PHE ALA VAL LYS ALA LEU THR ALA THR LYS VAL PHE ALA TYR SER
ARG GLU ASP PHE VAL ARG SER VAL LYS HIS GLU GLN ILE LYS ARG THR ARG ASP VAL ALA THR ASN MET ALA LEU ILE LYS ARG VAL LEU PRO VAL LEU SER LYS LEU THR GLU VAL GLN ALA ARG ARG LEU ALA ARG THR PHE GLY GLU GLU THR PHE GLU GLY ASP GLY GLU ALA ILE PHE LYS
GLU PHE ASP GLU PRO ASP ASN PHE TYR LEU VAL LYS LYS GLY GLU ALA ALA VAL VAL LYS TYR LYS LYS ASP PRO THR THR THR LYS GLU MET GLU GLU VAL VAL PHE ARG ILE TYR GLN PRO GLY GLU TYR PHE GLY GLU ILE SER ILE LEU ARG ASP GLN THR ARG THR ALA THR VAL LYS
ALA ARG GLY ILE CYS THR VAL LEU SER LEU PRO LYS GLU ASP PHE ASN SER GLN LEU ARG ARG PHE GLU ALA ALA PHE ILE GLY ARG ALA GLY ARG VAL TYR THR ALA GLN GLY HIS VAL ASP LYS ASP LYS LYS PRO LYS LYS GLU GLU LYS GLU ILE PRO THR SER VAL GLU GLU PRO
GLU GLU PRO THR ASP GLY ALA SER GLN SER ILE GLU ASP MET LEU ALA THR GLU GLN THR LYS LEU GLU GLY ARG ASP GLY VAL PRO VAL LEU LEU LEU GLU GLY VAL PRO GLY LYS LYS GLU ILE LEU GLN THR ARG THR ALA VAL GLU PRO
GLU ILE VAL LYS ALA MET SER LEU GLU CYS PHE TYR PRO ASN THR PRO ILE ILE LEU GLN GLY GLU GLU SER GLN ASN PHE TYR VAL LEU LYS THR GLY THR VAL ALA ALA GLU LEU TYR VAL GLY PRO GLY LYS PRO PHE ARG LYS ILE LYS GLU LEU GLY VAL PRO VAL LEU LYS GLU GLY
GLU MET SER ILE ILE LYS ASN GLU PRO ARG GLY CYS TYR ILE THR ALA LYS SER PRO VAL GLN LEU TYR SER LEU THR GLY GLU LYS PHE LYS GLU LEU LEU GLU GLU ASP CYS TYR PRO ALA PHE GLN GLU TYR ALA GLN ALA GLN TYR GLU GLN GLU TYR THR LEU LYS ARG GLN ALA SER SER
GLN LEU VAL SER SER GLU ALA GLU GLU PRO THR ALA ASP TYR GLY GLU ILE MET ASN LEU LEU VAL GLN VAL PRO VAL ILE ASN MET LEU ASP GLU ASP ALA LEU GLN GLN LEU THR ARG ALA PHE LYS VAL CYS TYR GLN GLU GLN GLU ARG GLU VAL ILE ILE HIS GLU GLY THR
PRO ALA GLU HIS PHE SER GLY ASP VAL SER VAL GLN LYS ILE PHE VAL ASP GLY ALA PRO VAL GLU ILE VAL VAL LEU HIS ALA GLY GLU TYR LEU GLY ASP ILE ALA PHE LEU ASN GLU GLN PRO ARG THR ALA SER CYS VAL ILE LEU LEU SER
LEU THR ARG SER ASP PHE GLN VAL HIS LEU GLY ALA LEU GLN ASP PHE LEU ASN GLN ALA ALA SER LYS TYR ALA ALA SER LYS ASP GLU ALA ILE PRO ASP TRP LEU VAL GLU ALA ALA GLY GLU GLN GLY ALA LEU TYR ASP PRO SER GLY SER LYS LYS THR GLU ASP ASP
GLU PRO ASP GLY ALA PHE ARG GLY THR VAL ASP ILE ASP LYS GLU MET TYR ASN LYS LYS ARG GLY LYS ARG GLY LYS ASP SER ASP THR SER ARG LYS LYS SER ASP ALA SER ALA ASP LYS THR GLY GLU ALA LYS ALA SER ASP ALA HIS ARG LYS LYS SER GLY GLU THR PRO PRO
GLY ASP GLY GLU GLU ALA GLY LYS GLU VAL LYS ASN GLU ALA ALA ASP THR ASN THR VAL GLU LYS LYS LYS LYS LYS ALA LYS GLU VAL ALA ALA ASP THR ASN GLY ARG LYS LYS LYS LYS GLU LYS LYS GLU GLU SER GLU GLU LYS HIS GLY GLY GLU SER GLU GLU THR GLY GLY GLU THR LYS LYS LYS LYS GLY LYS GLN SER GLN ALA LYS ARG
ARG MET SER LEU ALA GLY GLY ALA ALA ALA LEU LEU GLY SER PRO ASN GLU LYS GLU GLN GLU GLU LYS GLU GLU THR LYS ALA GLY GLU MET GLU GLU LYS GLN ASP LYS GLU GLU THR ALA GLU LYS LYS GLU LYS LYS GLU GLY

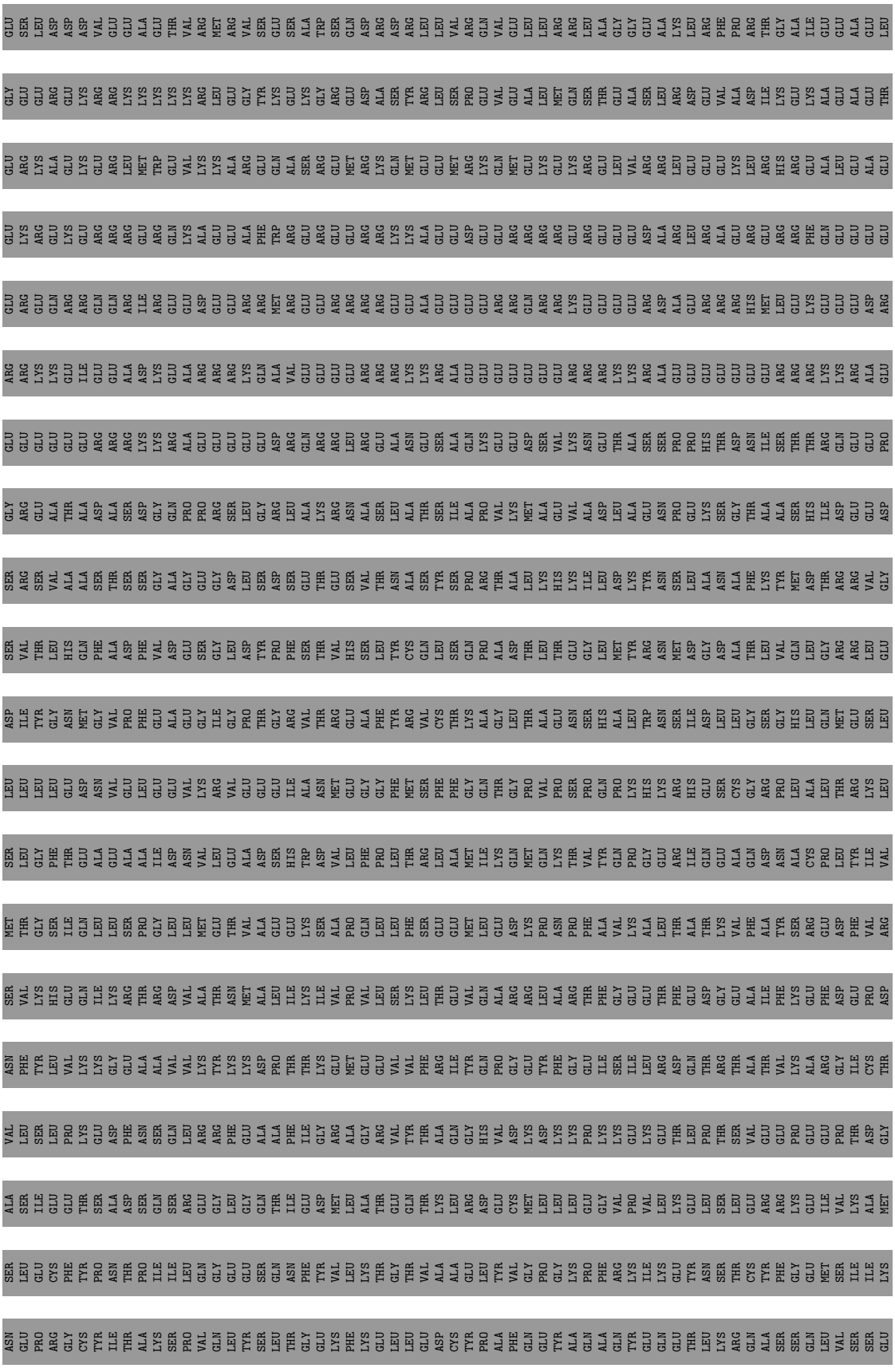


• Molecule 14: PCR12, TGME49_219070

Chain ML:






GLU SER LEU ASP ASP ASP VAL GLU GLU ALA GLU THR VAL ARG MET ARG VAL SER GLU SER ALA TRP SER GLN ASP ARG ASP ARG LEU LEU VAL ARG GLN VAL GLU LEU LEU ARG GLY GLU ALA LYS LEU ARG PHE PRO ARG THR GLY ALA ILE GLU GLU LEU GLU
GLY GLU GLU ARG GLU LYS ARG LYS LYS LYS LYS ARG LEU GLU GLY TYR LYS GLU LYS GLY ARG GLU ASP ALA SER TYR ARG LEU SER PRO GLU VAL GLU ALA LEU MET GLN SER THR GLU ALA SER LEU ARG ASP GLU VAL ALA ASP ILE LYS GLU LYS ALA GLU GLU THR
GLU ARG LYS ALA GLU LYS GLU ARG LEU MET TRP GLU VAL LYS LYS ALA ARG GLU GLN LYS ALA SER ARG GLU MET ARG LYS GLN MET GLU GLU MET ARG LYS GLN MET GLU LYS GLU LYS ARG GLU LEU VAL ARG ARG LEU GLU GLU ALA GLU
GLU LYS ARG GLU LYS GLU ARG ARG ARG GLN LYS ALA GLU GLU ALA PHE TRP ARG GLU ARG ARG GLU GLU ARG LYS LYS GLU ASP GLU GLU ARG GLU ARG ARG ARG GLU GLU ARG ALA GLU GLU ARG HIS ARG GLU ALA LEU GLU ALA
GLU ARG GLU GLN ARG ARG GLN GLN ARG ILE ARG GLU GLU ASP ARG GLN ARG ARG ARG GLU GLU ARG ARG GLU GLU ARG ARG ARG

ALA VAL ARG GLU GLU PRO THR ALA ASP TYR GLY GLU ILE MET ASN LEU LEU VAL GLN VAL PRO VAL ILE ASN MET LEU ASP GLU ASP ALA LEU GLN GLN LEU THR ARG ALA PHE LYS VAL GLU CYS TYR GLN GLU ARG GLU VAL ILE HIS GLU GLY THR PRO ALA GLU HIS PHE PHE

ILE ILE PHE SER GLY ASP VAL SER VAL GLN LYS ILE VAL ASP GLY ALA PRO VAL GLU ILE VAL ALA VAL VAL LEU HIS ALA GLY GLU TYR LEU GLY GLU ILE ALA PHE LEU LEU ASN GLU GLN PRO ARG THR ALA SER CYS VAL ALA ALA LYS SER ASP VAL LYS LEU LEU SER LEU THR ARG SER ASP PHE

GLN VAL HIS LEU GLY ALA LEU GLN ASP ALA PHE LEU ASN GLN ALA GLU SER LYS TYR ALA ALA ALA SER LYS ASP GLU ALA ILE PRO ASP TRP LEU VAL GLU ALA GLY GLU GLN GLN GLY GLY ALA LEU TYR ASP PRO SER GLY SER LYS LYS THR GLY GLU GLU ASP GLU GLU PRO GLY ASP GLY ALA PHE

ARG GLY THR VAL ASP ILE ASP LYS GLU LYS GLU MET TYR ASN LYS LYS ARG GLY ARG LYS ASP SER ASP THR SER ARG GLY GLU LYS SER ASP ALA SER ALA ASP LYS THR GLY GLU GLN GLY GLU ALA LYS ALA SER ASP ALA HIS ARG LYS LYS SER GLY GLU THR PRO PRO GLY ASP GLU GLU ASP GLU

ALA GLY LYS PRO GLY ASN ASP GLU VAL ALA GLU VAL ALA ALA ASP THR ASN THR VAL GLU LYS LYS LYS LYS GLU LYS GLU LYS ALA LYS GLU GLU LYS HIS GLY LYS GLY GLU GLU SER GLU GLU LYS GLN LYS GLY GLU THR GLY ALA LYS LYS LYS GLY LYS GLN SER GLN ALA LYS ARG ARG MET SER LEU ALA GLY

GLY ALA ALA LEU LEU ALA ALA ALA ALA ALA ALA LYS ALA ALA ALA GLU GLY GLU PRO SER PRO ASN GLU LYS LYS GLU GLU GLN GLN GLU GLU GLU LYS GLU GLU GLU MET GLU GLU LYS GLN ASP LYS GLU GLU THR ALA GLU GLU LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS LYS

ASP GLU ASP GLU ASP GLU ALA GLU ASP LYS ALA ALA GLU GLN ARG ILE ASP GLU PHE ARG ASP LEU VAL ARG GLY THR LEU THR VAL ALA ASN LYS TYR GLY SER ILE ALA GLN ALA PHE GLN GLN ILE ASP LYS GLU GLU ASN ASN SER GLU ILE VAL ASP PHE ASP GLU PHE ALA ALA PHE VAL LYS ASP

LEU ARG VAL GLN SER LEU LYS LYS LYS ASP ILE GLN VAL LEU PHE ASP ASP LEU CYS GLN PRO LEU LYS GLY THR LEU THR VAL ALA ASN LEU TYR ARG ASN ILE ASP LYS LYS ASP GLN LEU SER LYS ALA GLU ILE ASN LEU ARG TRP VAL GLU ILE PHE GLY GLY SER ARG LYS ALA

PHE LYS ALA VAL ALA ASN LEU GLY GLY GLY ASP GLU CYS THR GLU GLU ASN PHE ILE ASN VAL ALA ALA ALA ALA ALA GLY VAL SER GLU GLU GLU ASN ALA LYS SER ILE TRP THR GLU LEU ASP LYS ALA GLN HIS MET HIS THR LYS VAL ILE CYS SER TYR MET ALA GLY GLU LEU

THR ALA GLU GLU ALA ALA LYS GLU GLU LEU ALA SER LEU GLY THR ARG LEU TRP ASN PHE PHE GLY GLY SER ALA SER ASP ASP GLU SER ALA SER SER PRO THR SER GLN GLY ASP GLU GLN LYS ILE GLN GLU ALA LEU LYS TRP GLU ASP MET ALA ILE VAL GLN

ARG ASP ASP HIS ARG THR TYR PRO THR CYS THR LYS ARG LEU VAL ASP VAL LEU GLU LYS LYS GLU GLY PHE MET ASN LEU GLN LEU LEU LEU GLN GLU LEU ARG TYR VAL ALA SER THR MET ARG ARG GLU CYS LEU LEU ALA LYS GLY VAL ARG VAL MET GLU ALA GLY ASP GLU ALA CYS MET VAL

PHE CYS ALA TRP GLY GLU PHE LYS ILE LEU GLN GLN ALA GLY LEU PHE GLY GLU SER GLU VAL VAL GLY VAL VAL CYS PRO ASP GLU CYS PHE GLY LEU SER SER GLU LEU ILE ASN ASP SER PRO LEU THR ALA SER LEU VAL THR GLU VAL ASP ASN SER LEU TRP VAL LEU LEU GLU ARG ASP THR

TYR ASN ASP LEU ILE ARG ASP MET LEU GLU ALA ARG ARG ALA VAL VAL PRO VAL ILE GLU ASN PHE LEU LYS SER VAL PRO ILE VAL LYS ASP MET SER GLU THR GLU ILE GLN ASN VAL ALA ARG ALA CYS LYS ILE GLU THR PHE SER PRO HIS GLN THR VAL LEU TRP ALA ASP LEU THR

ALA GLY ASP MET PHE CYS PHE ILE PHE LYS GLY GLU ILE THR MET LEU LYS PRO MET GLY ALA GLY GLN GLU PRO ILE GLU LEU GLY ARG LEU GLN ALA GLY VAL TYR PHE GLY GLU MET ALA VAL ILE LYS ASN GLN ARG ARG THR ALA SER ILE ILE ALA ALA THR ASP LEU LEU THR LEU

PHE CYS LEU ASP LYS GLY SER PHE GLU ARG VAL LEU GLY ARG VAL LYS GLY LYS MET ILE GLU GLU ARG VAL LYS GLY LYS LEU TYR LYS ARG GLN ASP VAL ALA THR THR ASP PRO LYS GLU GLY GLU GLU GLY ASN ALA SER ALA ALA ILE LEU GLY ALA ALA GLU ALA PHE SER

PRO GLY ASP HIS PHE GLU LYS LYS ARG THR ARG LYS SER SER LEU ALA LEU LEU LEU GLN TYR THR LYS ILE ARG GLU ALA GLY PRO ALA GLU GLY GLU SER GLU LYS LYS SER SER GLU GLU GLU ASP GLU GLU ARG GLU ALA ARG TRP ALA MET ALA GLN ASP PRO GLU ILE ILE HIS ARG PRO

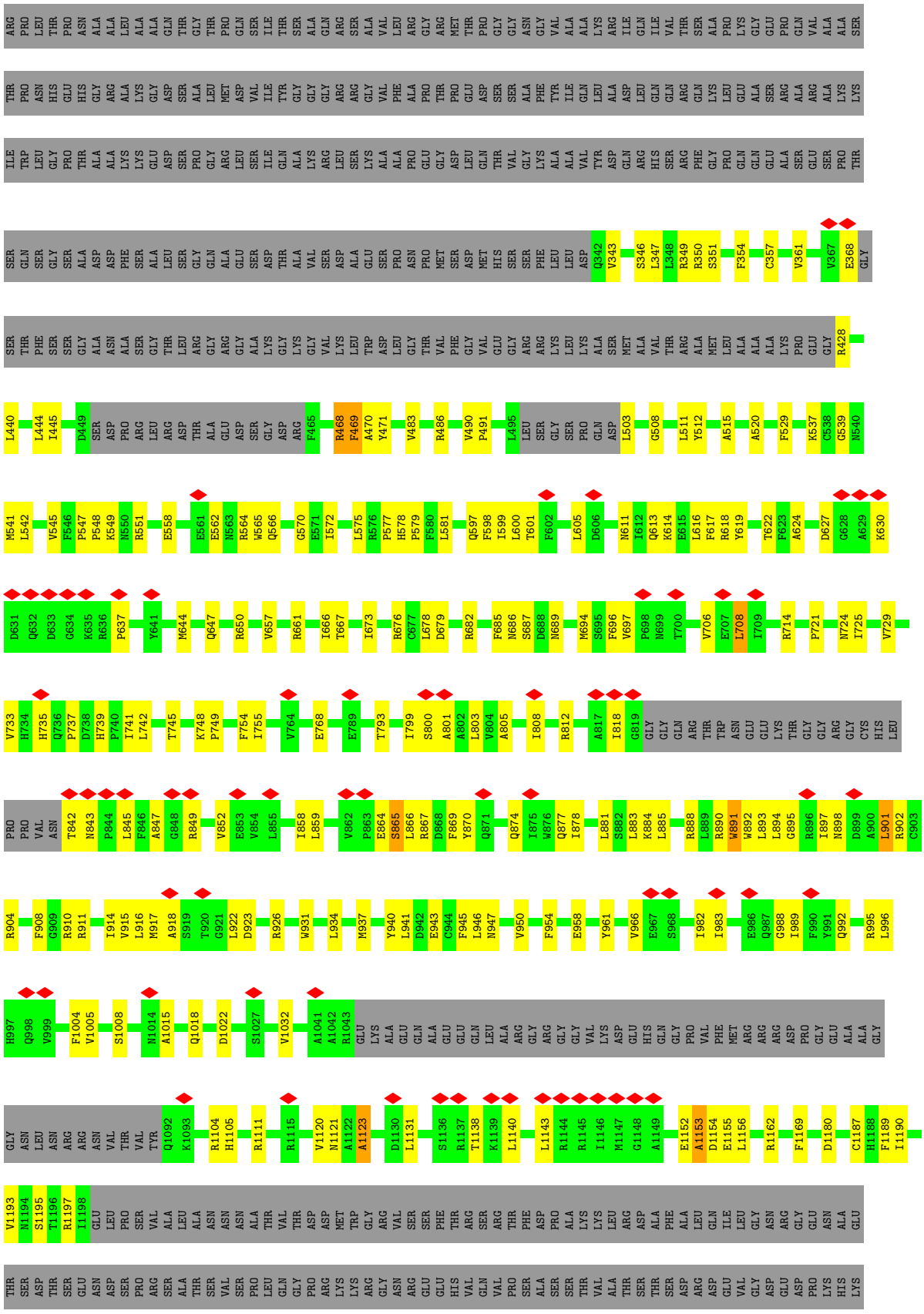
PRO PRO LEU SER ALA ALA PRO LYS LYS SER ALA LEU ARG THR THR SER SER LYS SER VAL GLY ILE LYS ASN SER VAL PHE PHE ASP GLU GLU THR LEU LEU PRO SER PRO PRO SER SER ASP GLU GLY

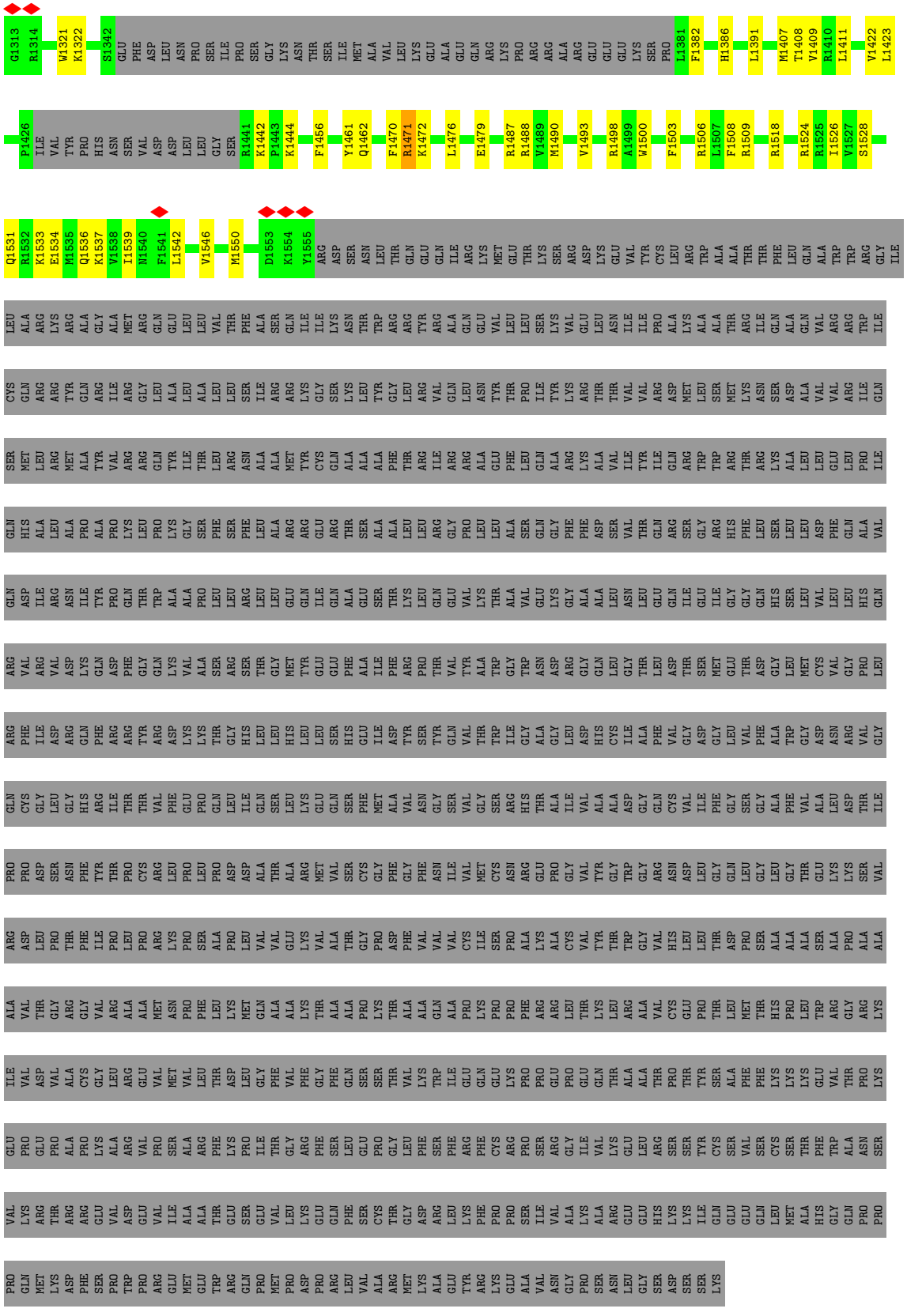
• Molecule 15: myosin L, TGME49_291020

Chain NA:

MET ASP ALA SER ARG LYS GLY ARG ARG ARG ARG PRO LEU SER PRO LEU ASP SER VAL ASP PHE SER SER VAL THR SER SER SER ALA CYS ALA SER SER GLU LEU ARG TYR PRO ALA VAL PRO ARG PRO SER ASP PHE ALA ALA PHE SER GLY PHE PRO LYS SER ASP SER ARG SER SER

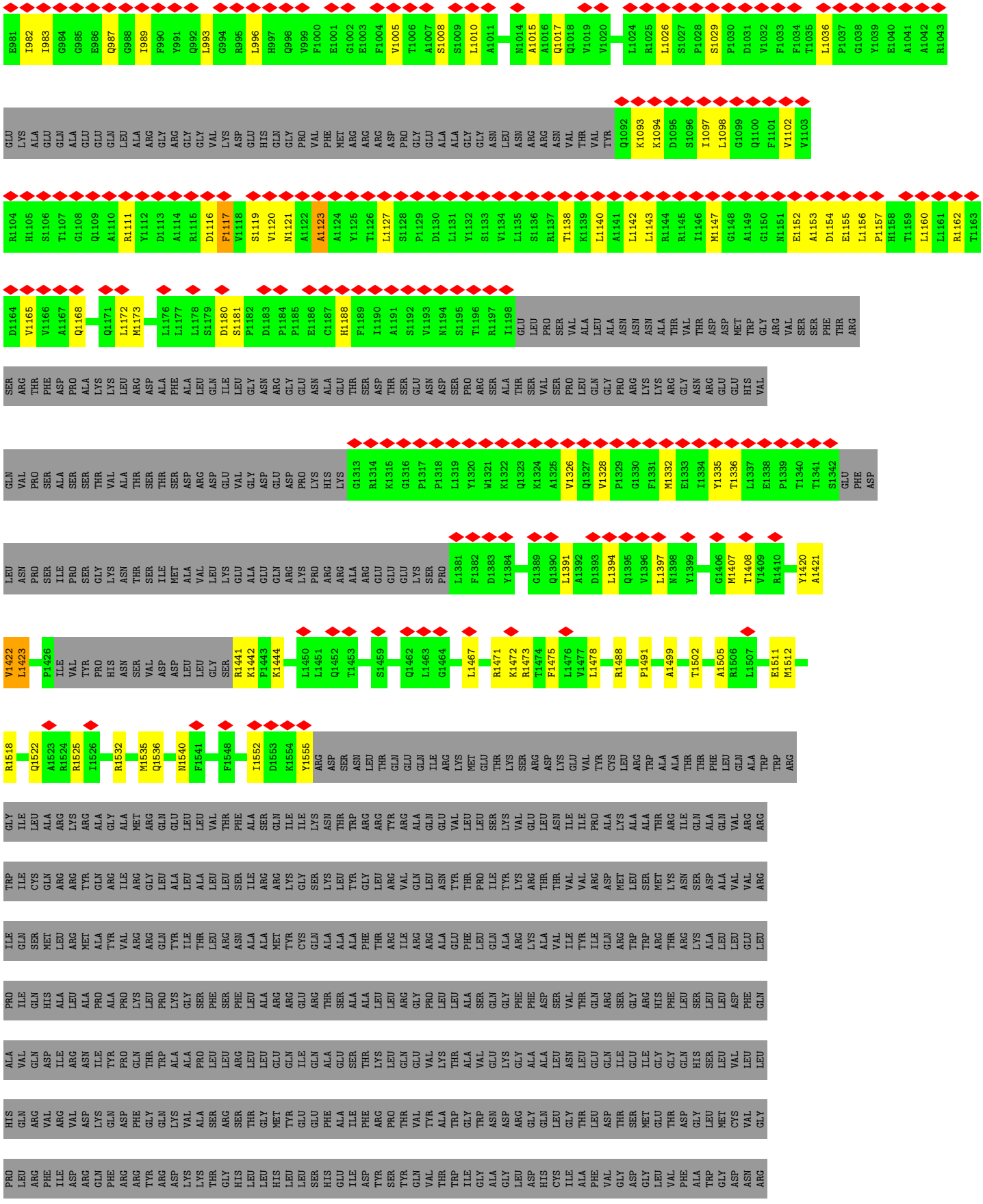
ALA SER ASN HIS THR SER ALA SER VAL ASP ALA ARG THR ARG LEU LEU ARG SER SER ASP ALA GLN SER LEU PRO VAL ALA PHE SER SER VAL ALA CYS LEU GLY ARG PRO ASN SER GLY GLU ALA SER GLY LYS ASP THR PRO GLU PRO GLY PRO SER THR ASN ALA ALA SER ALA PHE

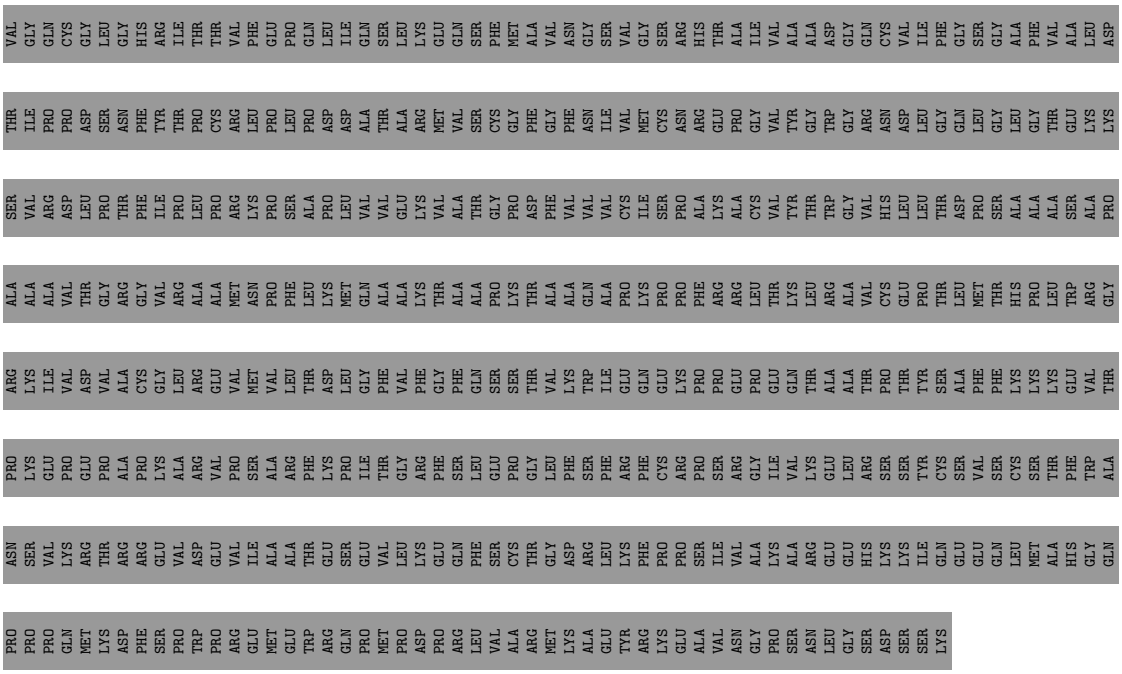




• Molecule 15: myosin L, TGME49_291020

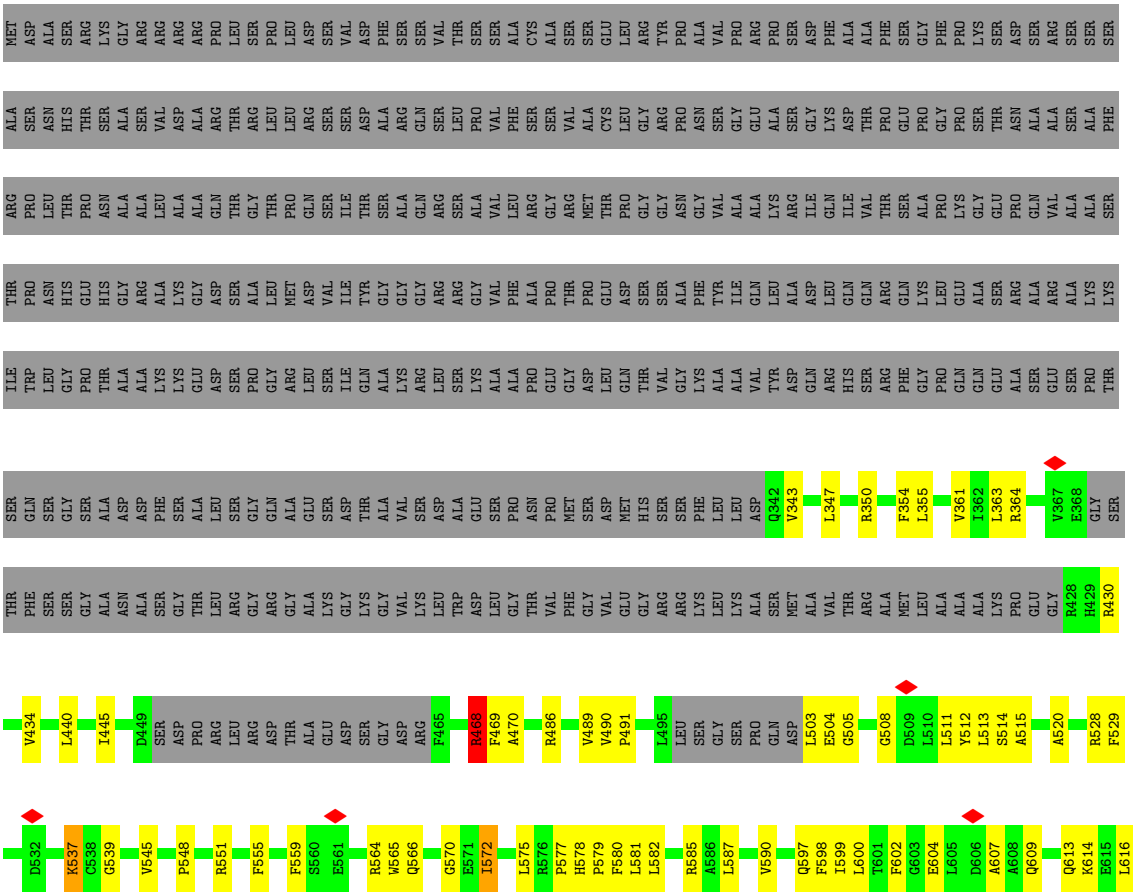
Chain NB:

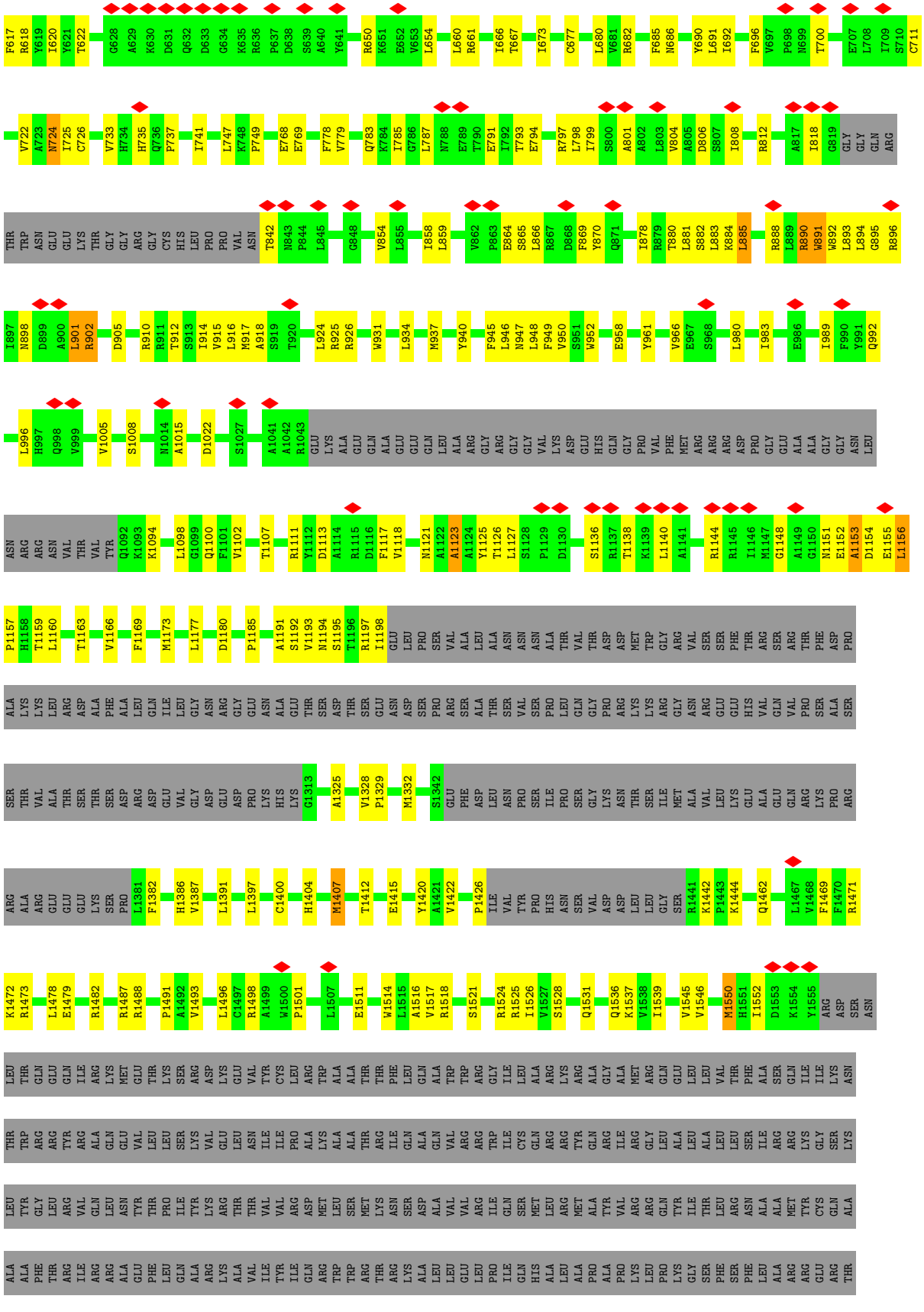

E981 I982 I983 G984 G985 E986 Q987 G988 I989 F990 Y991 Q992 L993 G994 R995 L996 H997 Q998 V999 F1000 E1001 G1002 E1003 F1004 V1005 T1006 A1007 S1008 S1009 L1010 A1011 N1014 A1015 A1016 Q1017 Q1018 V1019 V1020 L1024 R1025 L1026 S1027 P1028 S1029 P1030 D1031 V1032 F1033 F1034 T1035 L1036 P1037 G1038 Y1039 E1040 A1041 A1042 R1043
GLU LYS ALA GLU GLN ALA GLU GLU GLN LEU ALA ARG GLY ARG GLY GLY VAL LYS ASP GLU HIS GLN GLY PRO VAL PHE MET ARG ARG ARG ASP PRO GLY GLU ALA ALA GLY GLY ASN LEU ASN ARG ARG ASN VAL THR VAL TYR Q1092 K1093 K1094 D1095 S1096 I1097 L1098 G1099 Q1100 F1101 V1102 V1103
R1104 H1105 S1106 T1107 G1108 Q1109 A1110 R1111 Y1112 D1113 A1114 R1115 D1116 F1117 V1118 S1119 V1120 N1121 A1122 A1123 A1124 Y1125 T1126 L1127 S1128 P1129 D1130 L1131 Y1132 S1133 V1134 L1135 S1136 R1137 T1138 K1139 L1140 A1141 L1142 L1143 R1144 R1145 I1146 M1147 G1148 A1149 G1150 N1151 E1152 A1153 D1154 E1155 L1156 P1157 H1158 T1159 L1160 L1161 R1162 T1163
D1164 V1165 V1166 A1167 Q1168 Q1171 L1172 M1173 L1176 L1177 L1178 S1179 D1180 S1181 P1182 D1183 P1184 P1185 E1186 C1187 H1188 F1189 I1190 A1191 S1192 V1193 N1194 S1195 T1196 R1197 I1198 GLU LEU PRO SER VAL ALA LEU ALA ASN ASN ASN ALA THR VAL THR ASP ASP MET TRP GLY ARG VAL SER SER PHE THR ARG
SER ARG THR PHE ASP PRO ALA LYS LYS LEU ARG ASP ALA PHE ALA LEU GLN ILE LEU GLY ASN ARG GLY GLU ASN ALA GLU THR SER ASP THR SER GLU ASN ASP SER PRO ARG SER ALA THR SER VAL SER PRO LEU GLN GLY PRO ARG LYS LYS ARG GLY ASN ARG GLU GLU HIS VAL
GLN VAL PRO SER ALA SER SER THR VAL ALA THR SER THR SER ASP ARG ASP GLU VAL GLY ASP GLU ASP PRO LYS HIS LYS G1313 R1314 K1315 G1316 P1317 P1318 L1319 Y1320 W1321 K1322 Q1323 K1324 A1325 V1326 Q1327 V1328 P1329 G1330 F1331 M1332 E1333 I1334 Y1335 T1336 L1337 E1338 P1339 T1340 T1341 S1342 GLU PHE ASP
LEU ASN PRO SER ILE PRO SER GLY LYS ASN THR SER ILE MET ALA VAL LEU LEU LYS GLU ALA GLU GLN ARG LYS PRO ARG ARG ARG ALA ARG GLU GLU GLN LYS SER PRO L1381 F1382 D1383 Y1384 G1389 Q1390 L1391 A1392 D1393 L1394 Q1395 V1396 L1397 N1398 Y1399 G1406 M1407 T1408 V1409 R1410 Y1420 A1421
V1422 L1423 P1426 ILE VAL TYR PRO HIS ASN SER VAL ASP ASP LEU LEU GLY SER R1441 K1442 P1443 K1444 L1450 L1451 Q1452 T1453 S1459 Q1462 L1463 G1464 L1467 R1471 K1472 R1473 T1474 F1475 L1476 V1477 L1478 R1488 P1491 A1499 T1502 A1505 R1506 L1507 E1511 M1512
R1518 Q1522 A1523 R1524 R1525 I1526 R1532 M1535 Q1536 N1540 F1541 F1548 I1552 D1553 K1554 Y1555 ARG ASP SER ASN LEU THR GLN GLU GLN ILE ARG LYS MET GLU THR LYS SER ARG ASP LYS GLU VAL TYR CYS LEU ARG TRP ALA ALA THR THR PHE LEU GLN ALA TRP TRP ARG
GLY ILE LEU ALA ARG LYS ARG ALA GLY ALA MET ARG GLN GLU LEU LEU LEU VAL THR PHE ALA SER GLN ILE ILE LYS ASN THR TRP ARG ARG TYR ARG ALA GLN GLU VAL LEU LEU SER LYS VAL GLU LEU ASN ILE ILE PRO PRO ALA LYS ALA ALA ALA THR ARG ARG ILE GLN ALA ALA GLN VAL ARG ARG
TRP ILE CYS GLN ARG ARG TYR GLN ARG ILE ARG GLY LEU ALA LEU ALA LEU LEU LEU SER ILE ARG ARG LYS GLY SER LYS LEU GLY LEU ARG VAL LEU GLN LEU ASN TYR THR PRO ILE TYR LYS ARG THR THR VAL VAL ARG ASP MET LEU SER MET LYS ASN SER ASP ALA VAL VAL ARG
ILE GLN SER MET LEU ARG MET ALA TYR VAL ARG ARG GLN TYR ILE THR LEU ARG ASN ALA ALA MET TYR CYS GLN ALA ALA ALA PHE THR ARG ILE ARG ARG ALA GLU PHE LEU GLN ALA ALA GLU VAL ILE TYR ILE GLN ARG TRP TRP ARG THR ARG LYS ALA LEU LEU GLU LEU
PRO ILE GLN HIS ALA LEU ALA PRO LYS LEU PRO LYS GLY SER PHE SER PHE LEU ALA ARG GLU ARG THR SER ALA ALA LEU LEU ARG GLY PRO LEU LEU ALA SER GLN GLY PHE PHE ASP SER VAL THR GLN ARG SER GLY ARG HIS PHE LEU SER LEU LEU ASP PHE GLN
ALA VAL GLN ASP ILE ARG ASN ILE TYR PRO GLN THR TRP ALA ALA PRO LEU LEU ARG LEU LEU LEU GLU GLN ILE GLN ALA GLU ALA LEU THR LYS LEU GLN GLN GLU VAL LYS THR ALA VAL GLU LYS GLY GLY ALA ALA LEU ASN LEU GLU GLU GLN ILE GLU ILE GLY GLY GLN HIS SER LEU VAL LEU LEU
HIS GLN ARG VAL ARG VAL ASP LYS GLN ILE PHE GLY GLN LYS VAL ALA SER ARG SER THR GLY MET TYR GLU GLU PHE ALA ILE PHE ARG PRO THR VAL TYR ALA TRP GLY TRP ASN ASP ARG GLY GLN LEU GLY THR LEU ASP THR SER MET GLU THR ASP GLY LEU MET CYS VAL GLY
PRO LEU ARG PHE ILE ASP ARG GLN PHE ARG ARG TYR ARG ASP LYS LYS THR GLY HIS LEU LEU HIS LEU LEU LEU SER HIS GLU ILE ASP TYR SER TYR GLN VAL THR TRP ILE GLY ALA ASP GLY LEU ASP HIS CYS ILE ALA PHE VAL GLY ASP GLY LEU VAL PHE ALA TRP GLY ASP ASN ARG

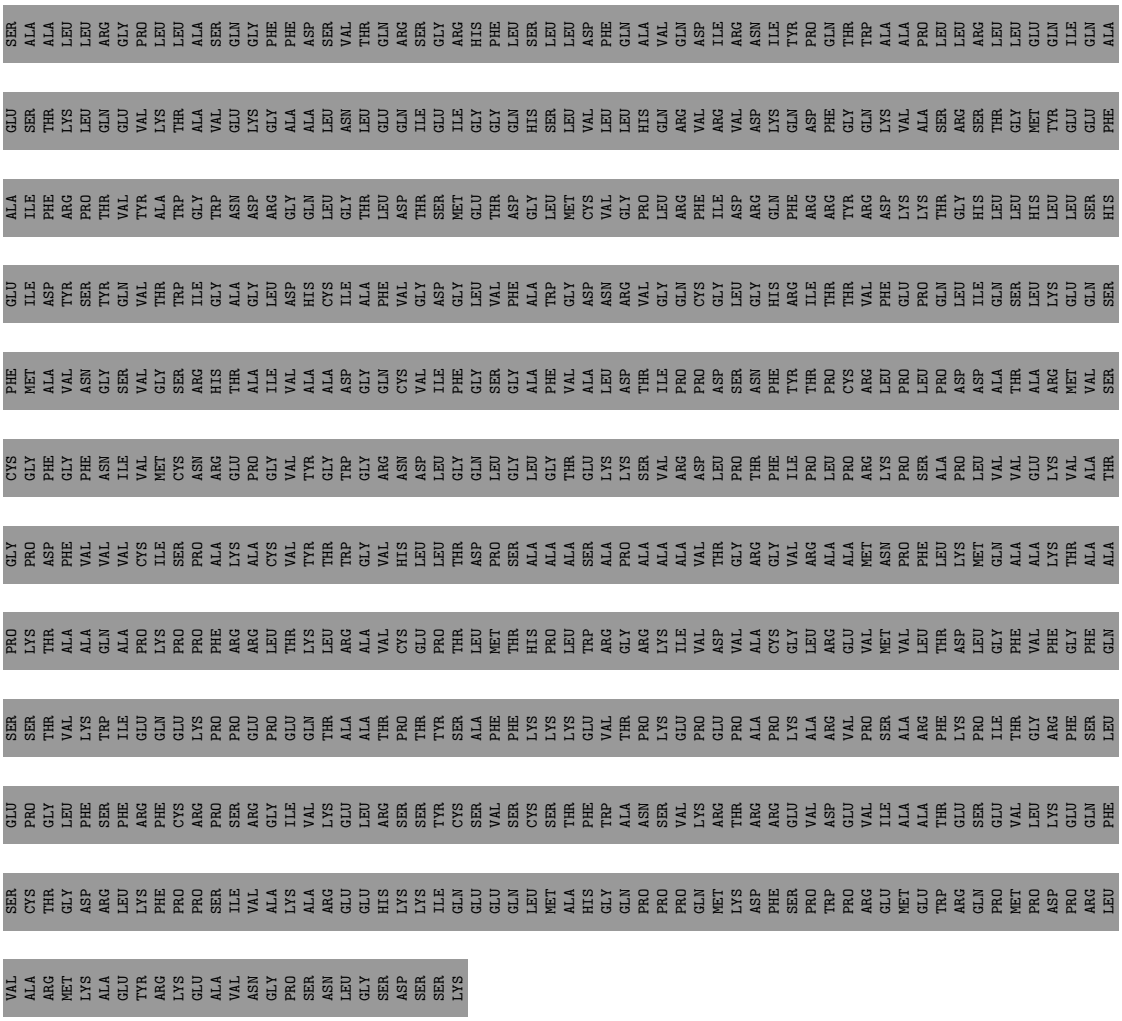


• Molecule 15: myosin L, TGME49_291020

Chain NC:

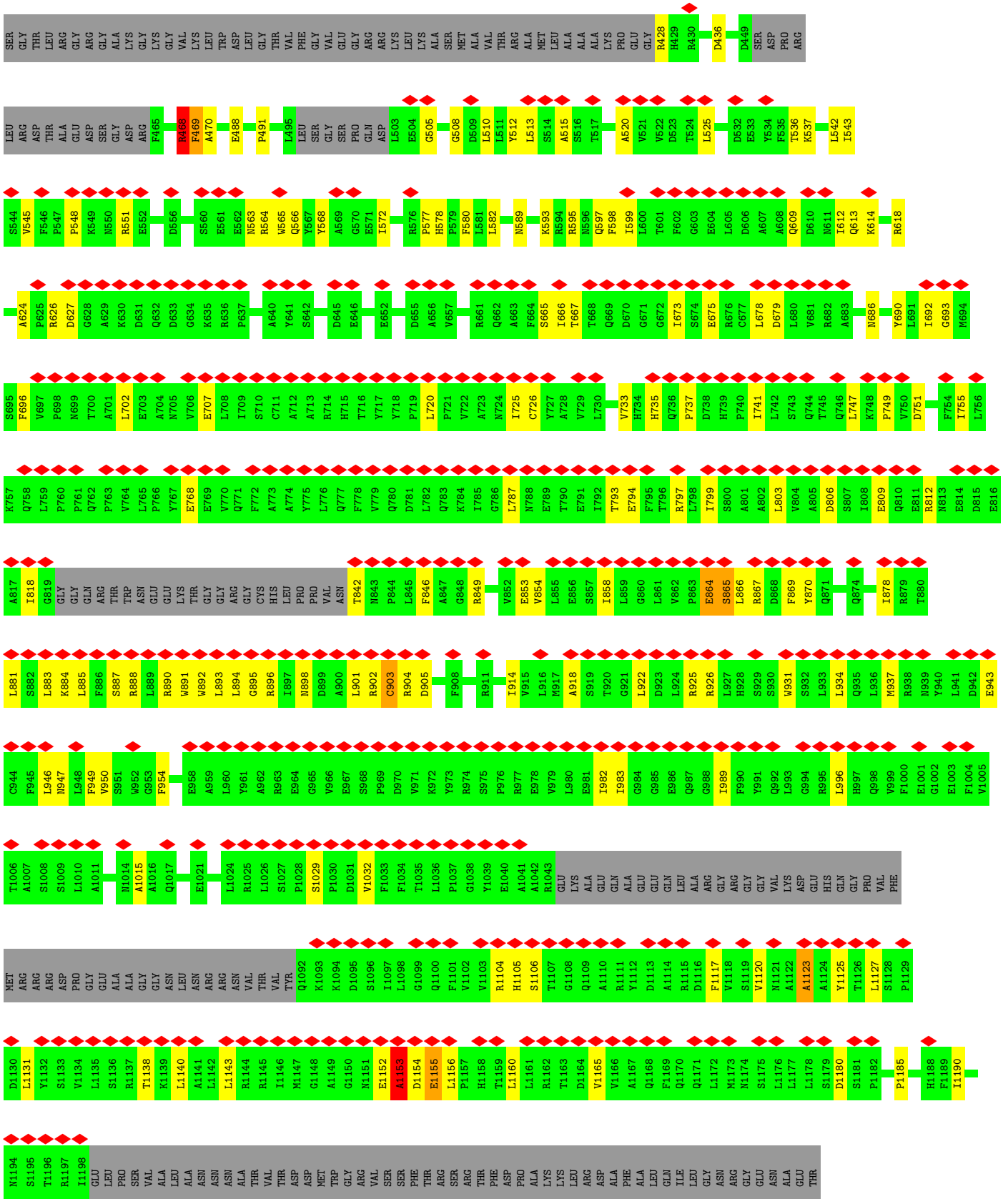


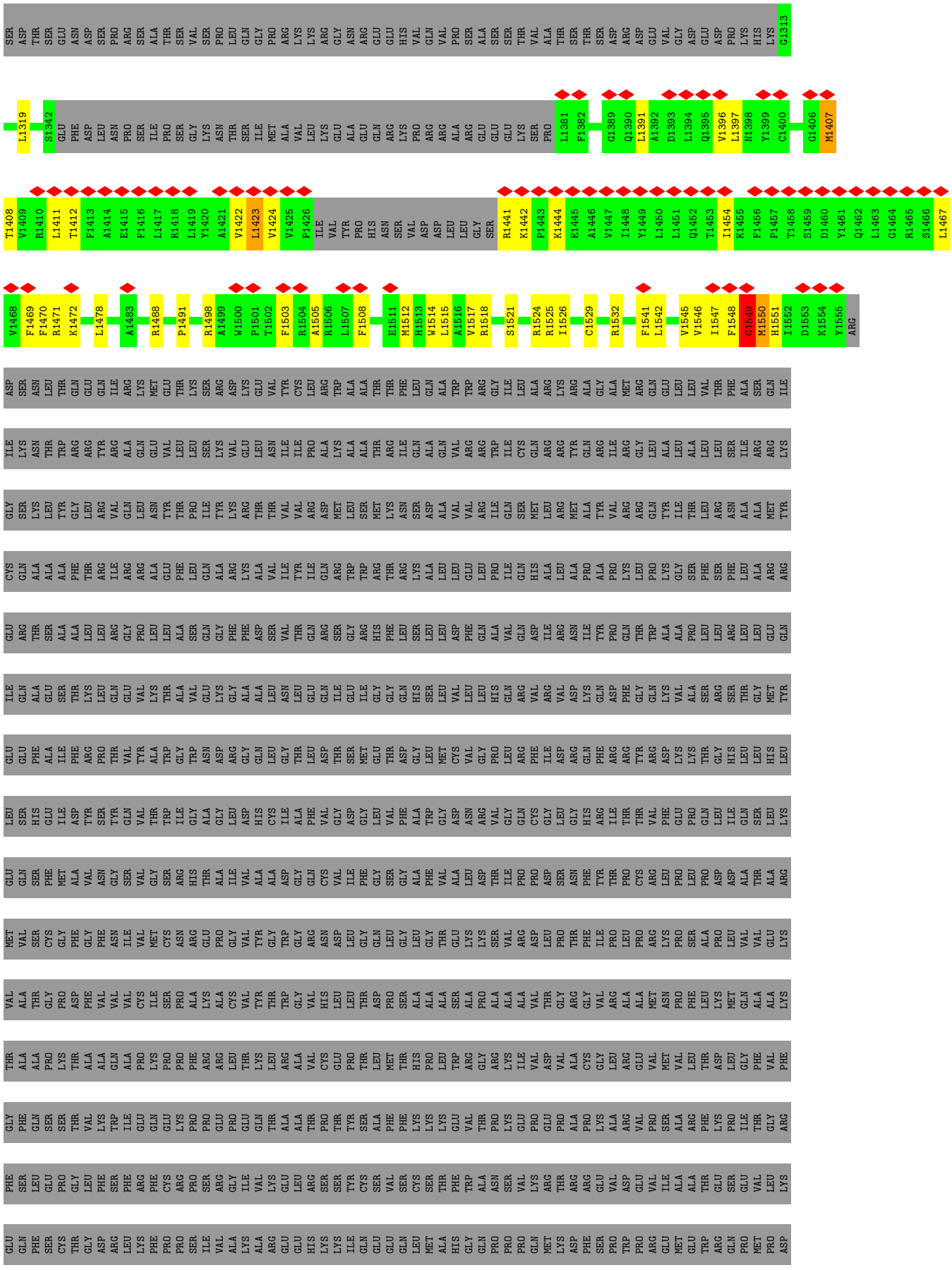


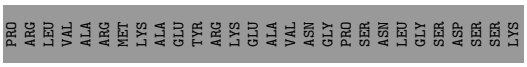


• Molecule 15: myosin L, TGME49_291020

Chain ND:

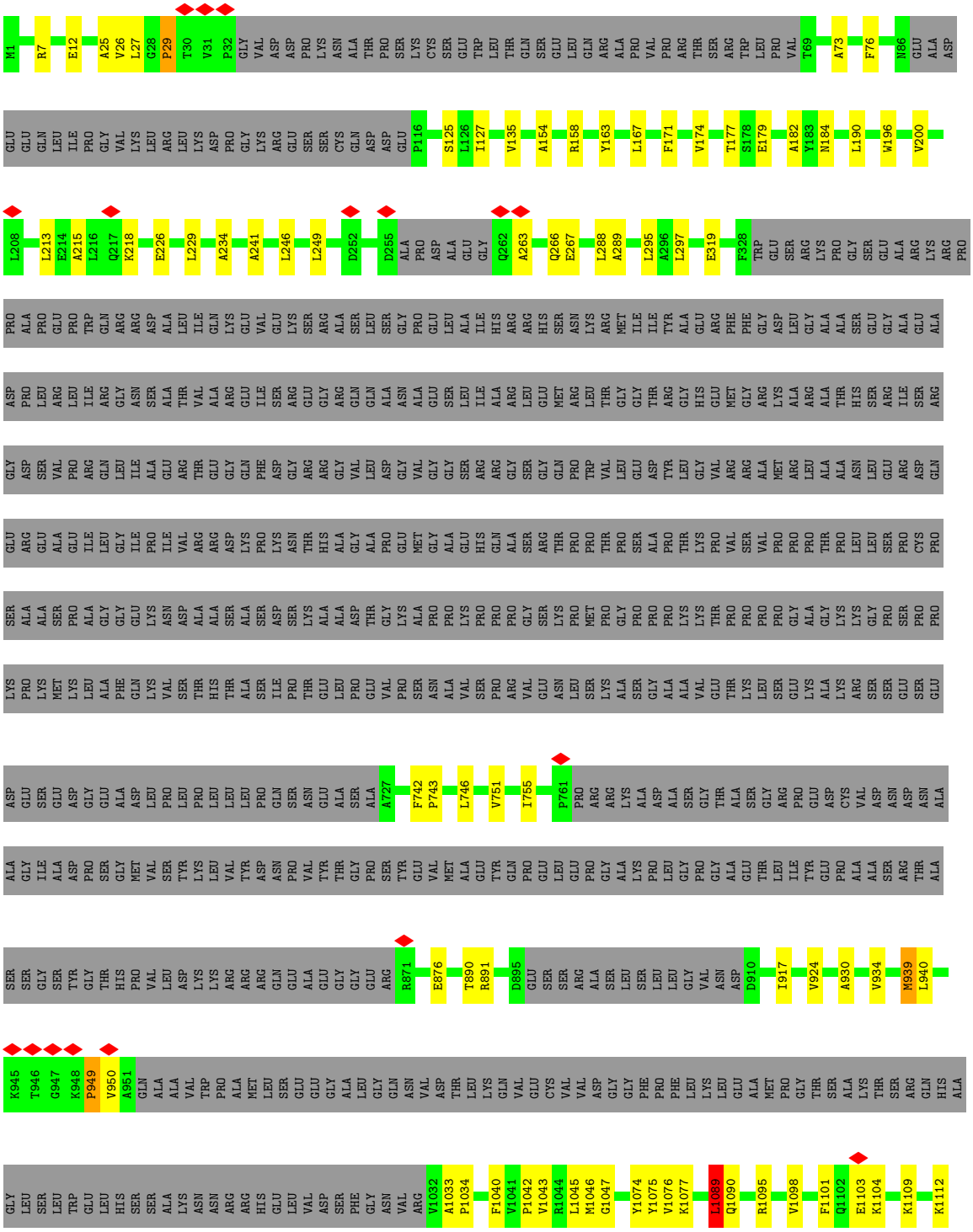

SER GLY THR LEU ARG GLY ARG GLY ALA LYS GLY LYS GLY VAL LYS LEU TRP ASP LEU GLY THR VAL PHE GLY VAL GLU GLY ARG ARG LYS LEU LYS ALA SER MET ALA VAL THR ARG ALA MET LEU ALA ALA ALA LYS PRO GLU GLY R428 H429 R430 D436 D449 SER ASP PRO ARG
LEU ARG ASP THR ALA GLU ASP SER GLY ASP ARG F465 R468 F469 A470 E488 P491 L495 LEU SER GLY SER PRO GLN ASP L503 E504 G505 G508 D509 L510 L511 Y512 L513 S514 A515 S516 T517 A520 V521 V522 D523 T524 L525 D532 E533 Y534 F535 T536 K537 L542 I543
S544 V545 F546 P547 P548 K549 N550 R551 E552 D556 S560 E561 E562 N563 R564 W565 Q566 Y567 Y568 A569 G570 E571 I572 R576 P577 H578 P579 F580 L581 L582 N589 K593 R594 R595 N596 Q597 F598 I599 L600 T601 F602 G603 E604 L605 D606 A607 A608 Q609 D610 N611 I612 Q613 K614 R618
A624 P625 R626 D627 G628 A629 K630 D631 Q632 D633 G634 K635 R636 P637 A640 Y641 S642 D645 E646 E652 D655 A656 V657 R661 Q662 A663 F664 S665 I666 T667 T668 Q669 D670 G671 G672 I673 S674 E675 R676 C677 L678 D679 L680 V681 R682 A683 M686 Y690 L691 I692 G693 M694
S695 F696 V697 P698 N699 T700 A701 L702 E703 A704 N705 V706 E707 L708 I709 S710 C711 A712 A713 R714 H715 T716 Y717 Y718 P719 L720 P721 V722 A723 N724 I725 C726 Y727 A728 V729 L730 V733 H734 H735 Q736 P737 D738 H739 P740 I741 L742 S743 Q744 T745 Q746 L747 K748 P749 V750 D751 F754 I755 L756
K757 Q758 L759 P760 P761 Q762 P763 V764 L765 P766 Y767 E768 E769 V770 Q771 F772 A773 A774 Y775 L776 Q777 F778 V779 Q780 D781 L782 Q783 K784 I785 G786 L787 N788 E789 T790 E791 I792 T793 E794 F795 T796 R797 L798 I799 S800 A801 A802 L803 V804 A805 D806 S807 I808 E809 Q810 E811 R812 N813 E814 D815 E816
A817 I818 G819 GLY GLY GLN GLN ARG THR TRP ASN GLU GLU LYS THR GLY GLY ARG GLY CYS HIS LEU PRO PRO VAL ASN T842 N843 P844 L845 F846 A847 G848 R849 V852 E853 V854 L855 E856 S857 I858 L859 G860 L861 V862 P863 E864 S865 L866 R867 D868 F869 Y870 Q871 Q874 I878 R879 T880
L881 S882 L883 K884 L885 F886 S887 R888 L889 R890 W891 W892 L893 L894 G895 R896 I897 N898 D899 A900 L901 R902 C903 R904 D905 F908 R911 I914 V915 L916 M917 A918 S919 T920 G921 L922 D923 L924 R925 R926 L927 H928 S929 S930 W931 S932 L933 L934 Q935 L936 M937 R938 N939 Y940 L941 D942 E943
C944 F945 L946 N947 L948 F949 V950 S951 W952 G953 F954 E958 A959 L960 Y961 A962 R963 E964 G965 V966 E967 S968 P969 D970 V971 K972 Y973 R974 S975 P976 R977 E978 V979 L980 E981 I982 I983 G984 G985 E986 Q987 G988 I989 F990 Y991 Q992 L993 G994 R995 L996 H997 Q998 V999 F1000 E1001 G1002 E1003 F1004 V1005
T1006 A1007 S1008 S1009 L1010 A1011 N1014 A1015 A1016 Q1017 E1021 L1024 R1025 L1026 S1027 P1028 S1029 P1030 D1031 V1032 F1033 F1034 T1035 L1036 P1037 G1038 Y1039 E1040 A1041 A1042 R1043 GLU LYS ALA GLU GLN ALA GLU GLU GLN LEU ALA ARG GLY ARG GLY GLY VAL LYS ASP GLU HIS GLN GLY PRO VAL PHE
MET ARG ARG ASP PRO GLY GLU ALA ALA GLY GLY ASN LEU ASN ARG ARG ASN VAL THR VAL TYR Q1092 K1093 K1094 D1095 S1096 I1097 L1098 G1099 Q1100 F1101 V1102 V1103 R1104 H1105 S1106 T1107 G1108 Q1109 A1110 R1111 Y1112 D1113 A1114 R1115 D1116 F1117 V1118 S1119 V1120 N1121 A1122 A1123 A1124 Y1125 T1126 L1127 S1128 P1129
D1130 L1131 Y1132 S1133 V1134 L1135 S1136 R1137 T1138 K1139 L1140 A1141 L1142 L1143 R1144 R1145 I1146 M1147 G1148 A1149 G1150 N1151 E1152 A1153 D1154 E1155 L1156 P1157 H1158 T1159 L1160 L1161 R1162 T1163 D1164 V1165 V1166 A1167 Q1168 F1169 Q1170 Q1171 L1172 M1173 N1174 S1175 L1176 L1177 L1178 S1179 D1180 S1181 P1182 P1185 H1188 F1189 I1190
N1194 S1195 T1196 R1197 I1198 GLU LEU PRO SER VAL ALA LEU ALA ASN ASN ASN ALA THR VAL THR ASP ASP MET TRP GLY ARG VAL SER SER PHE THR ARG SER ARG THR PHE ASP PRO ALA LYS LYS LEU ARG ASP ALA PHE ALA ALA LEU GLN ILE LEU GLY ASN ARG GLY GLU ASN ALA GLU THR


SER ASP THR SER GLU ASN ASP SER PRO ARG SER ALA THR SER VAL SER PRO LEU GLN GLY PRO ARG LYS LYS ARG GLY ASN ARG GLU GLU GLU HIS VAL GLN VAL PRO SER ALA SER SER THR VAL ALA THR SER THR SER ASP ARG ASP GLU VAL GLY ASP GLU ASP PRO LYS HIS LYS G1313
L1319 S1342 GLU PHE ASP LEU ASN PRO SER ILE PRO SER GLY LYS ASN THR SER ILE MET ALA VAL LEU LYS GLU ALA GLU GLN ARG LYS PRO ARG ARG ALA ARG GLU GLU GLU LYS SER PRO L1381 F1382 G1389 Q1390 L1391 A1392 D1393 L1394 Q1395 V1396 L1397 N1398 Y1399 C1400 G1406 M1407
T1408 V1409 R1410 L1411 T1412 F1413 A1414 E1415 F1416 L1417 R1418 L1419 Y1420 A1421 V1422 L1423 V1424 V1425 P1426 ILE VAL TYR PRO HIS ASN SER VAL ASP ASP LEU LEU GLY SER R1441 K1442 P1443 K1444 E1445 A1446 V1447 I1448 Y1449 L1450 L1451 Q1452 T1453 I1454 K1455 F1456 P1457 T1458 S1459 D1460 Y1461 Q1462 L1463 G1464 R1465 S1466 L1467
V1468 F1469 F1470 R1471 K1472 L1478 A1483 R1488 P1491 R1498 A1499 W1500 P1501 T1502 F1503 R1504 A1505 R1506 L1507 F1508 E1511 M1512 H1513 W1514 L1515 A1516 V1517 R1518 S1521 R1524 R1525 I1526 C1529 R1532 F1541 L1542 V1545 V1546 I1547 F1548 G1549 M1550 H1551 I1552 D1553 K1554 Y1555 ARG
ASP SER ASN LEU THR GLN GLU GLN ILE ARG LYS MET GLU THR LYS SER ARG ASP LYS GLU VAL TYR CYS LEU ARG TRP ALA ALA THR THR PHE LEU GLN LEU ALA ARG LYS ARG ALA GLY ALA MET ARG GLN GLU LEU LEU VAL THR PHE ALA SER GLN ILE
ILE LYS ASN THR TRP ARG ARG TYR ARG ALA GLN GLU VAL LEU LEU SER LYS VAL GLU LEU ASN ILE ILE PRO ALA LYS ALA ALA THR ARG ILE GLN ALA GLN VAL ARG ARG TRP ILE CYS GLN ARG ARG TYR GLN ARG ILE ARG GLY LEU ALA LEU ALA LEU LEU SER ILE ARG ARG LYS
GLY SER LYS LEU TYR GLY LEU ARG VAL GLN LEU ASN TYR THR PRO ILE TYR LYS ARG THR THR VAL VAL ARG ASP MET LEU SER MET LYS ASN SER ASP ALA VAL VAL ARG ILE GLN SER MET LEU ARG MET ALA TYR VAL ARG ARG GLN TYR ILE THR LEU ARG ASN ALA ALA MET TYR
CYS GLN ALA ALA ALA PHE THR ARG ILE ARG ARG GLU PHE LEU GLN ALA ARG LYS ALA VAL ILE TYR ILE GLN ARG TRP TRP ARG THR ARG LYS ALA LEU LEU GLU LEU PRO ILE GLN HIS ALA LEU ARG PRO ALA PRO LYS LEU PRO LYS GLY SER PHE SER PHE LEU ARG ARG
GLU ARG THR SER ALA ALA LEU LEU ARG GLY PRO LEU LEU ALA SER GLN GLY PHE PHE ASP SER VAL THR GLN ARG SER GLY ARG HIS PHE LEU SER LEU LEU ASP PHE GLN ALA VAL GLN ASP ILE ARG ASN ILE TYR PRO GLN THR TRP ALA ALA PRO LEU LEU ARG LEU LEU GLU GLN
ILE GLN ALA GLU SER THR LYS LEU GLN GLU VAL VAL LYS GLY ALA ALA LEU ASN LEU GLU GLN ILE GLU ILE GLY GLY GLN HIS SER LEU VAL LEU LEU HIS GLN ARG VAL ASP LYS GLN ASP PHE GLY GLN LYS VAL ALA SER ARG SER THR GLY MET TYR
GLU GLU PHE ALA ILE PHE ARG PRO THR VAL TYR ALA TRP GLY TRP ASN ASP ARG GLY GLN LEU GLY THR LEU ASP THR SER MET GLU THR ASP GLY LEU MET CYS VAL GLY PRO LEU ARG PHE ILE ASP ARG GLN PHE ARG ARG TYR ARG ASP LYS LYS THR GLY HIS LEU LEU HIS LEU
LEU SER HIS GLU ILE ASP TYR SER TYR GLN VAL THR TRP ILE GLY ALA GLY LEU ASP HIS CYS ILE ALA PHE VAL GLY ASP GLY LEU VAL PHE ALA TRP GLY ASP ASN ARG VAL GLY GLN CYS GLY LEU GLY HIS ARG ILE THR VAL THR VAL PHE GLU PRO GLN LEU ILE GLN SER LEU LYS
GLU GLN SER PHE MET ALA VAL ASN GLY SER VAL GLY ARG GLN CYS VAL ILE PHE GLY GLN SER GLY ALA PHE VAL ALA ASP ARG ALA ALA ASP GLY ASP PRO PRO ASP SER ASN PHE TYR THR PRO CYS ARG LEU PRO LEU PRO PRO LEU PRO ASP ASP ALA THR ALA ARG
MET VAL SER CYS GLY PHE GLY PHE ASN ILE VAL MET CYS ASN ARG GLU PRO GLY VAL TYR GLY TRP GLY ARG ASN ASP LEU GLY GLN LEU GLY LEU GLY GLN LEU GLY LEU ASP THR PHE ILE PRO LEU PRO ARG LYS PRO SER ALA PRO LEU VAL VAL GLU LYS
VAL ALA THR GLY PRO ASP PHE VAL VAL HIS LEU LEU LEU THR ASP PRO SER ALA ALA PRO ALA ALA VAL THR GLY ARG GLY VAL ARG ALA ALA MET ASN PRO PHE LEU LYS MET GLN ALA ALA LYS
THR ALA ALA PRO LYS THR ALA ALA GLN PRO PRO PHE ARG ALA ARG LEU THR LYS LEU ARG ALA ALA VAL CYS GLU PRO THR LEU MET THR HIS PRO LEU TRP ARG GLY ARG LYS ILE VAL ASP VAL ALA CYS GLY LEU ARG GLU VAL MET VAL LEU THR ASP LEU GLY PHE
GLY PHE GLN SER SER THR VAL LYS TRP GLN GLU GLN GLU PRO GLU GLN LYS PRO PRO PRO GLU GLU ALA ALA THR PRO THR TYR SER ALA PHE PHE LYS LYS LYS LYS GLU VAL PRO GLU PRO ALA PRO ALA ALA ARG VAL PRO SER PRO ILE THR GLY ARG GLY
PHE SER LEU GLU PRO GLY PHE LEU GLU ARG SER SER TYR CYS SER VAL SER CYS SER THR PHE TRP ALA ASN SER VAL LYS ARG THR ARG GLU VAL ASP VAL ILE ALA ARG GLU VAL ASP PRO ALA ARG PHE SER VAL PHE
GLU GLN PHE SER LYS LYS ILE GLN GLU GLU GLU GLN LEU MET ALA HIS GLY GLN PRO PRO PRO GLN MET LYS ASP PHE SER PRO TRP PRO ARG GLN PRO MET PRO ASP



• Molecule 16: PCR13, TGME49_284620

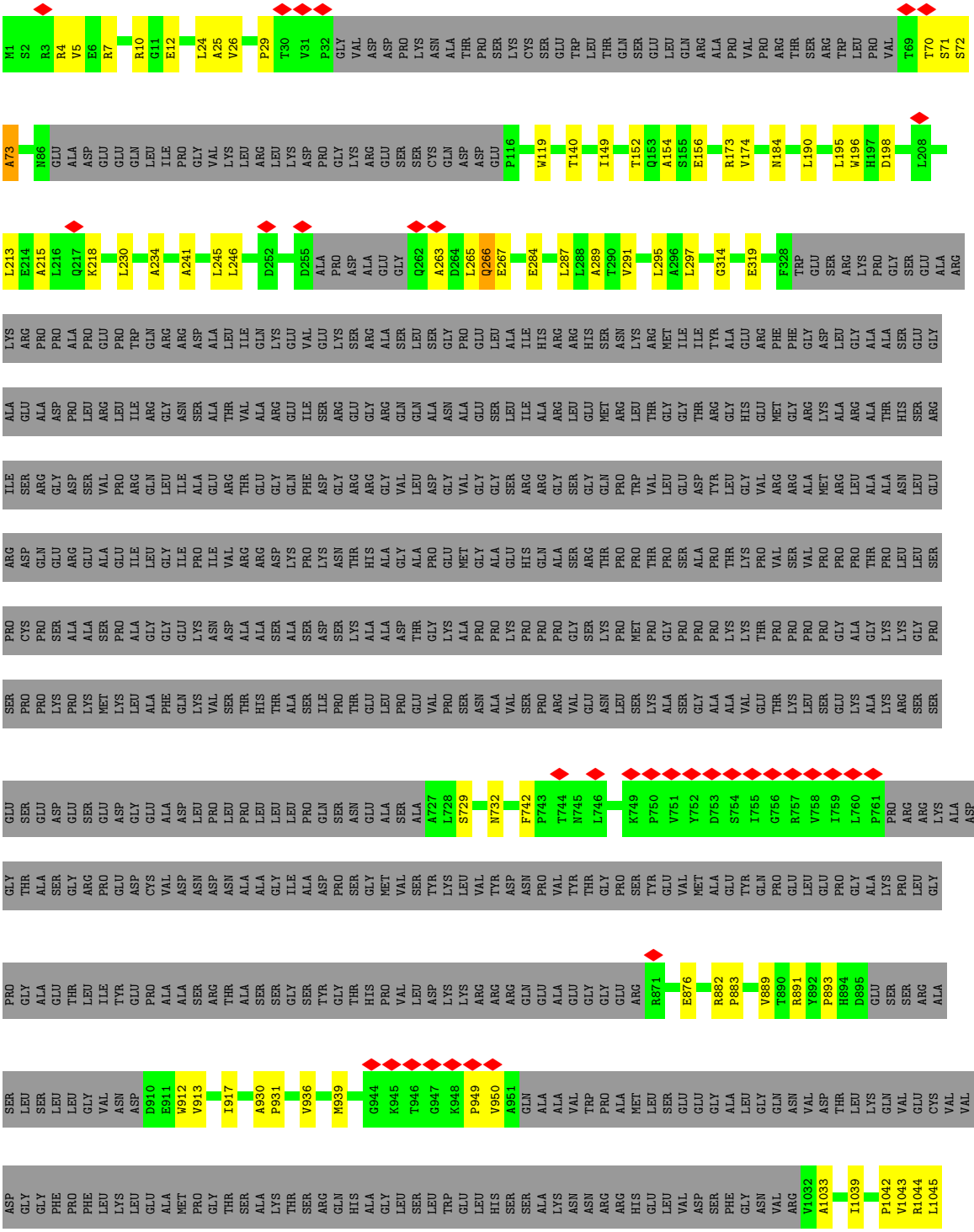
Chain OA:



A1113
R1114
E1118
R1119
A1120

• Molecule 16: PCR13, TGME49_284620

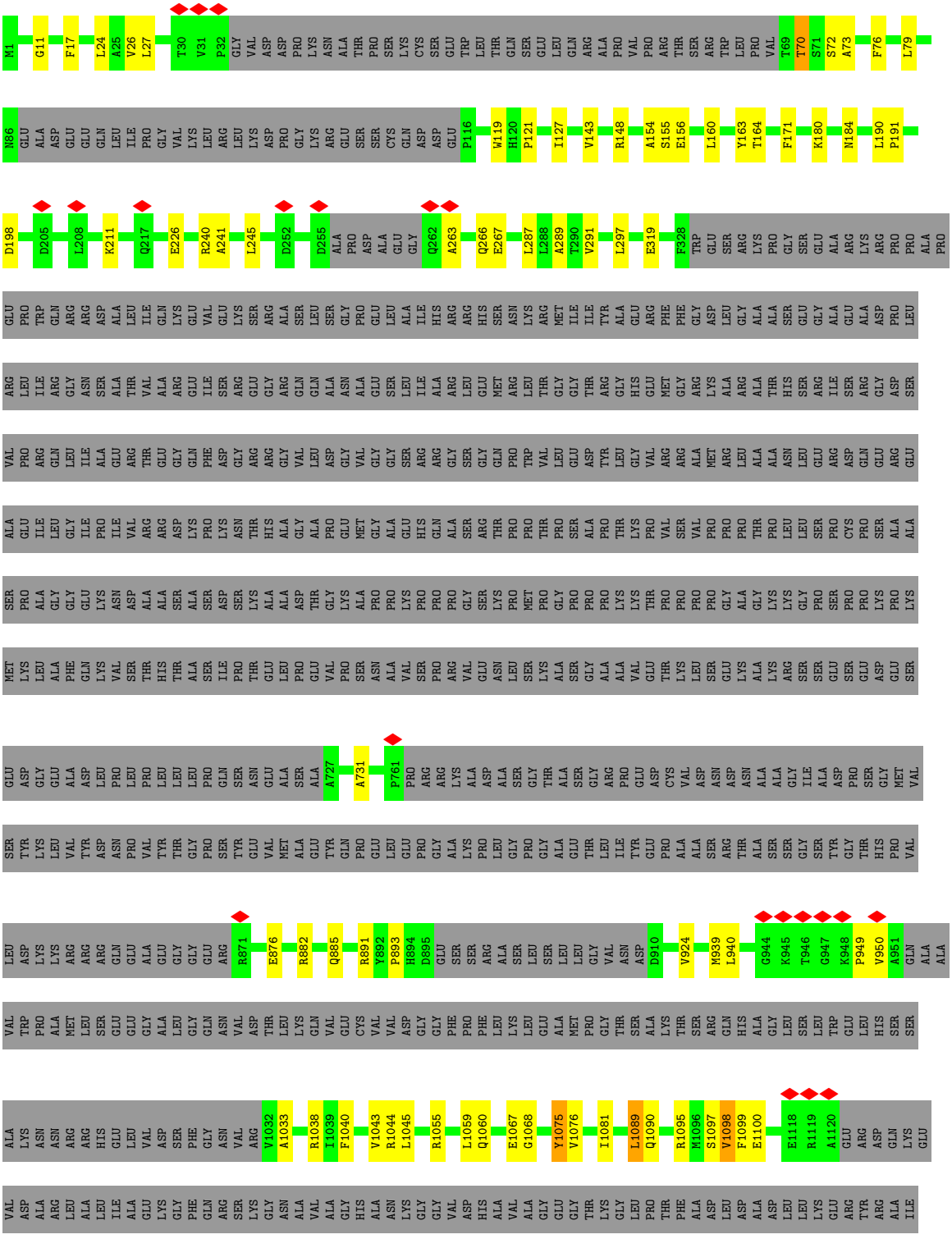
Chain OB:

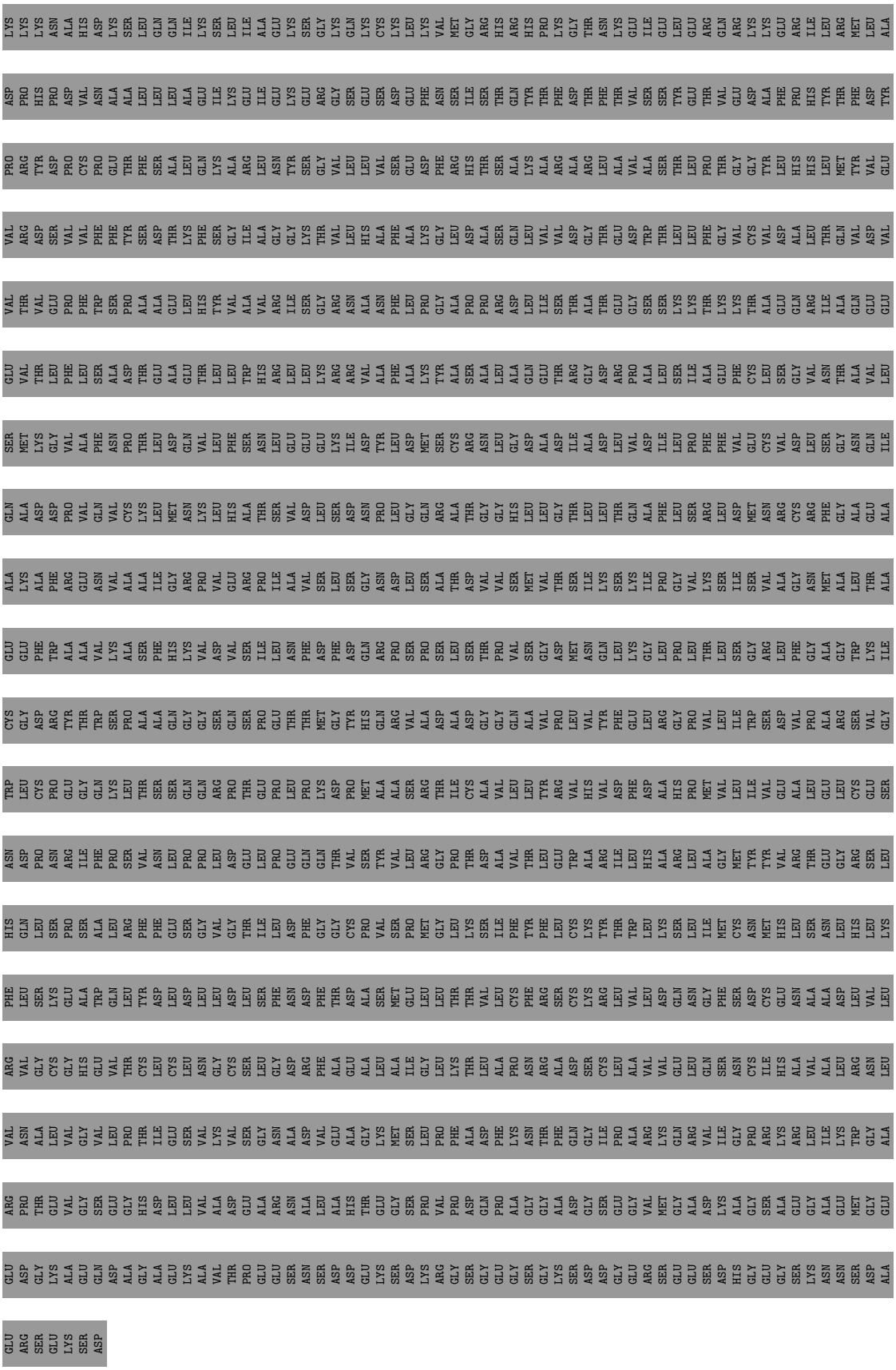


M1046
G1047
T1053
R1062
Y1074
Y1075
V1076
K1077
A1078
A1079
D1080
I1081
R1085
L1089
Q1090
A1091
R1092
M1096
F1101
E1118
R1119
A1120

• Molecule 16: PCR13, TGME49_284620

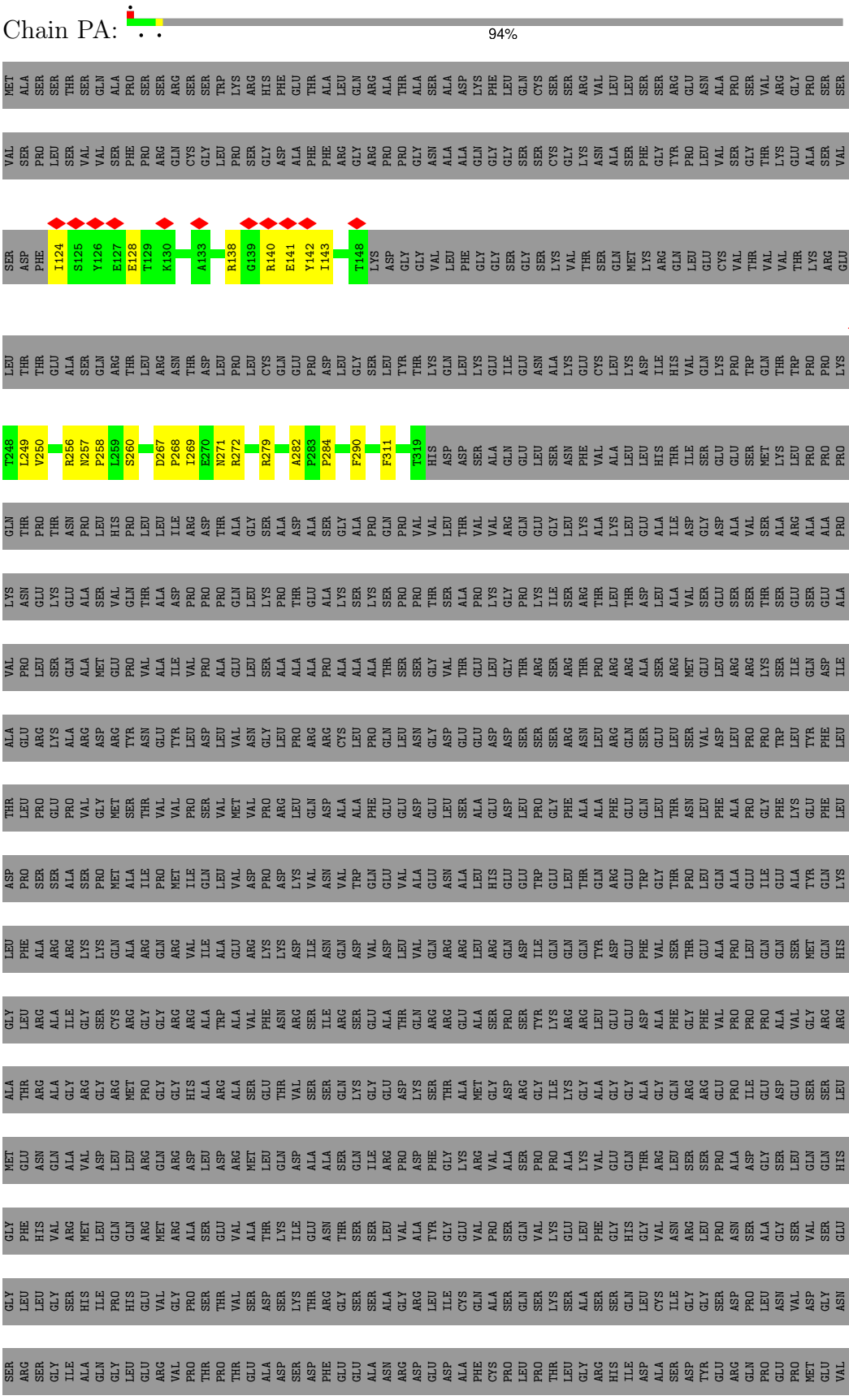
Chain OC:

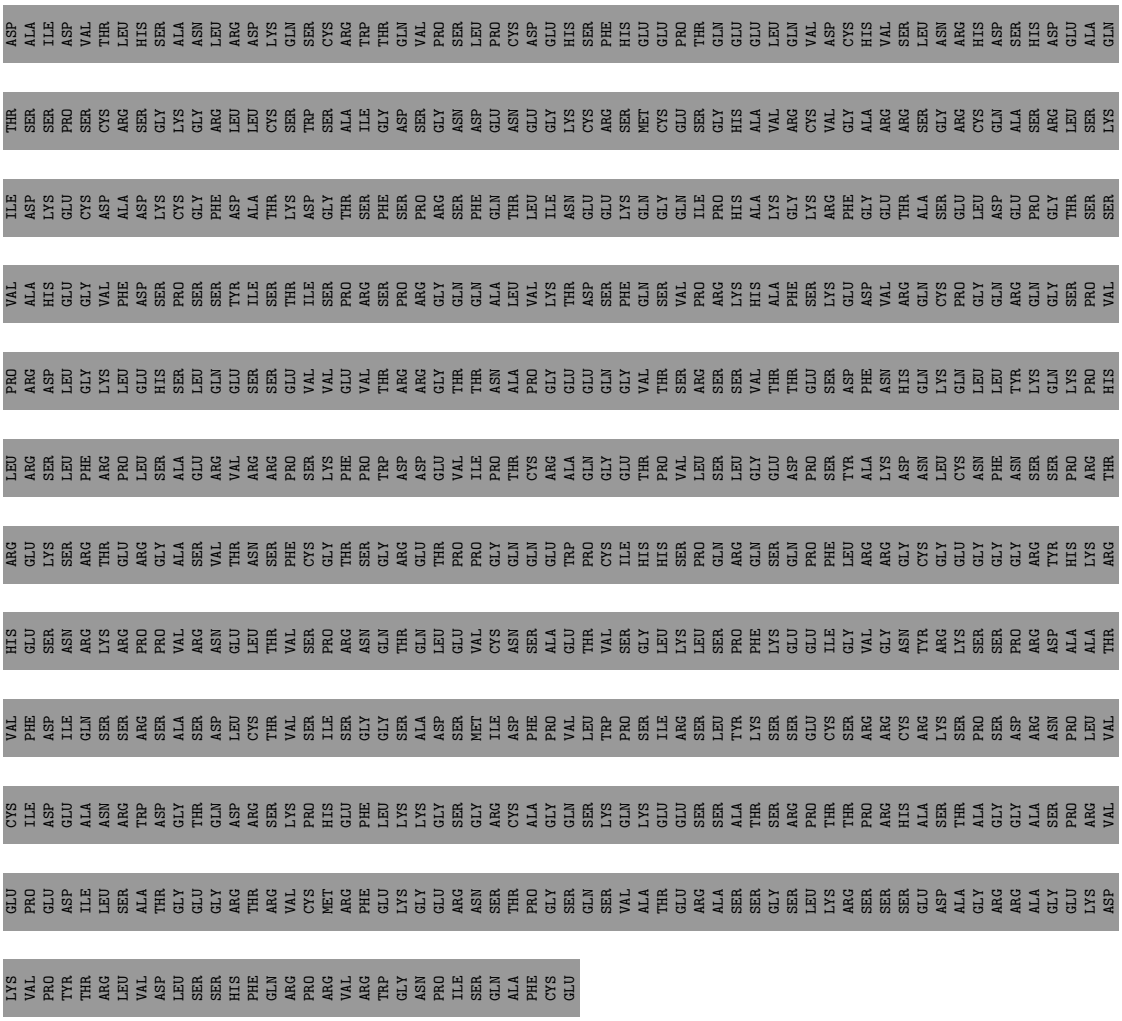




• Molecule 17: PCR15, TGME49_232560

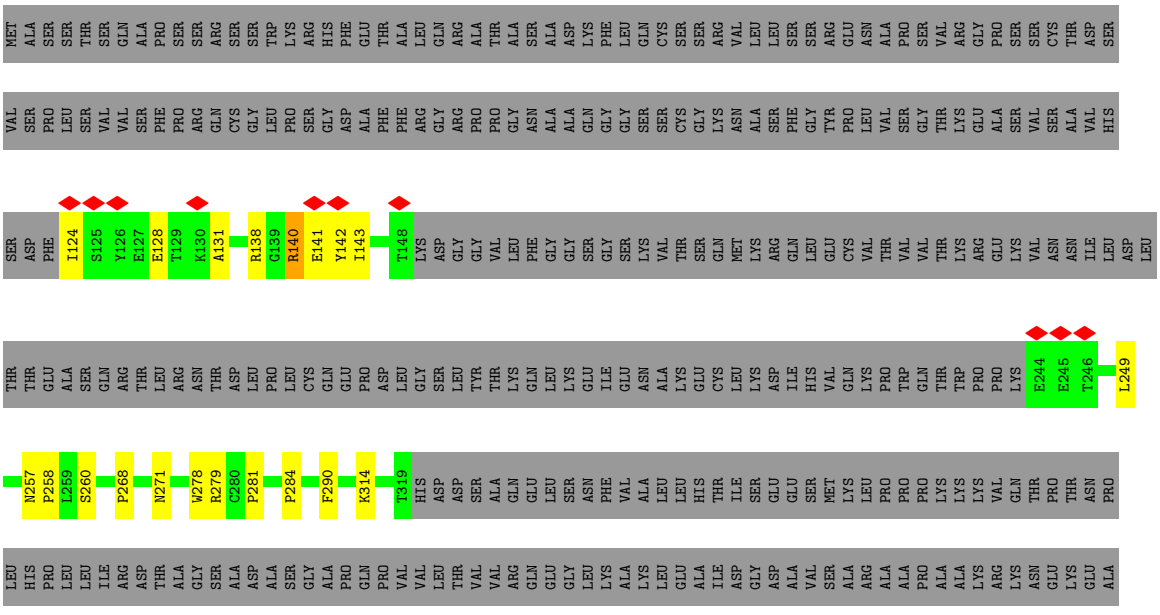
Chain PA:

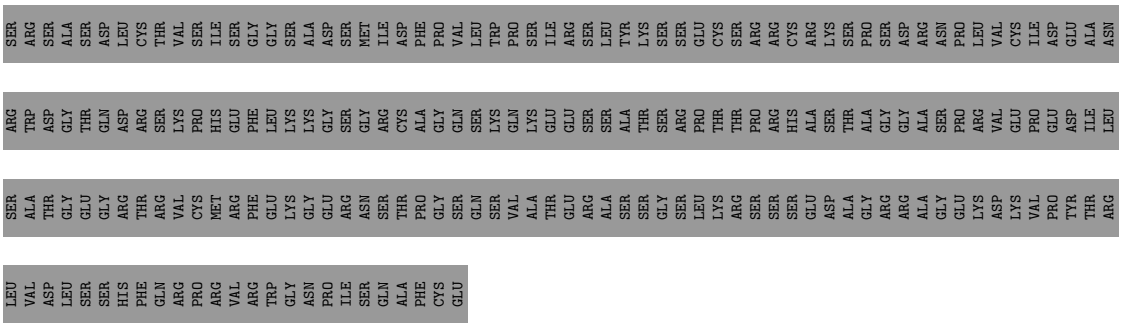

94%
MET ALA SER SER THR SER GLN ALA PRO SER SER ARG SER SER TRP LYS ARG HIS PHE GLU THR ALA LEU GLN ARG ALA THR ALA SER ALA ASP LYS PHE LEU GLN CYS SER SER ARG VAL LEU LEU SER SER ARG GLU ASN ALA PRO SER VAL ARG GLY PRO SER
VAL SER PRO LEU SER VAL VAL SER PHE PRO ARG GLN CYS GLY LEU PRO SER GLY ASP ALA PHE PHE ARG GLY ARG PRO PRO GLY ASN ALA ALA GLN GLY GLY SER SER CYS GLY LYS ASN ALA SER PHE GLY TYR PRO LEU VAL SER GLY THR LYS GLU ALA SER VAL SER ALA VAL HIS
SER ASP PHE I124 S125 Y126 E127 E128 T129 K130 A133 R138 G139 R140 E141 Y142 I143 T148 LYS ASP GLY GLY VAL LEU PHE GLY GLY SER GLY SER LYS VAL THR SER GLN MET LYS ARG GLN LEU GLU CYS VAL THR VAL VAL THR LYS ARG GLU LYS VAL ASN ASN ILE LEU ASP
LEU THR THR GLU ALA SER GLN ARG THR LEU ARG ARG ASN THR ASP LEU PRO LEU CYS GLN GLU GLU PRO ASP LEU GLY SER LEU TYR THR LYS GLN LEU LYS LYS GLU ILE GLU GLU ASN ALA LYS GLU CYS LEU LYS ASP ILE HIS VAL GLN LYS PRO TRP GLN THR TRP PRO PRO LYS E244 E245 T246 L247
T248 L249 V250 R256 N257 P258 L259 S260 D267 P268 I269 E270 N271 R272 R279 A282 P283 P284 F290 F311 T319 HIS ASP ASP SER ALA GLN GLU LEU SER ASN PHE VAL ALA LEU LEU HIS THR ILE SER GLU GLU SER MET LYS LEU PRO PRO PRO LYS LYS LYS VAL
GLN THR PRO THR ASN PRO LEU HIS PRO LEU LEU ILE ARG ASP THR ALA GLY SER ALA ASP ALA SER GLY ALA PRO GLN PRO VAL VAL LEU THR VAL VAL ARG GLN GLU GLY LEU LYS ALA LYS LEU GLU ALA ILE ASP GLY ASP ALA VAL SER GLU SER SER THR SER GLU ALA PRO ALA ALA ALA PRO ALA ALA LYS ARG
LYS ASN GLU LYS GLU ALA SER VAL GLN THR ALA ASP PRO PRO PRO GLN LEU LYS PRO THR GLU ALA LYS SER LYS SER PRO PRO THR SER ALA PRO VAL THR LEU THR ASP LEU ALA VAL SER GLU SER SER THR SER GLU SER GLU ALA PRO SER PRO ARG LEU
VAL PRO LEU SER GLN ALA MET GLU PRO VAL ALA ALA ILE VAL PRO ALA GLU LEU SER ALA ALA ALA PRO ALA ALA ALA THR SER SER GLY VAL THR GLU LEU GLY THR ARG SER ARG THR PRO ARG ARG ALA SER ARG MET GLU LEU ARG ARG LYS SER ILE GLN ASP ILE GLU PRO ARG ALA ILE
ALA GLU ARG LYS ALA ARG ASP ARG TYR ASN GLU TYR LEU ASP LEU VAL ASN GLY PRO ARG ARG CYS LEU PRO GLN LEU ASN GLY ASP GLU GLU ASP ASP SER SER SER ARG ASN LEU ARG GLN SER GLU LEU SER VAL ASP LEU PRO PRO TRP LEU TYR PHE LEU ASP THR HIS THR
THR LEU PRO GLU PRO VAL GLY MET SER THR VAL VAL PRO SER VAL MET VAL PRO ARG LEU LEU GLN ASP ALA ALA PHE GLU GLU GLU ASP GLU LEU SER ALA GLU ASP LEU PRO GLY PHE ALA ALA PHE GLU GLN LEU THR ASN LEU PHE ALA PRO GLY PHE LYS GLU PHE LEU TYR PRO GLU TYR
ASP PRO SER SER ALA SER PRO MET ALA ILE PRO MET ILE GLN LEU VAL ASP PRO ASP LYS VAL ASN VAL TRP GLN GLU VAL ALA GLU ASN ALA LEU HIS GLU GLU GLU TRP GLU LEU THR GLN ARG GLU TRP GLY THR PRO LEU GLN ALA GLU ILE GLU ALA TYR GLN LYS LEU GLU GLU ARG LYS
LEU PHE ALA ARG ARG LYS LYS GLN ALA ARG GLN ARG VAL ILE ALA GLU ARG LYS LYS ASP ILE ASN GLN GLN ASP VAL ASP LEU VAL GLN ARG ARG LEU ARG GLN ASP ILE GLN GLN GLN TYR ASP GLU PHE VAL SER THR GLU ALA PRO LEU GLN GLN GLN SER MET GLN HIS GLU LEU ASN LYS
GLY LEU ARG ALA ILE GLY SER CYS ARG GLY GLY ARG ARG ALA TRP ALA VAL PHE ASN ARG SER ILE ARG SER GLU ALA THR GLN ARG ARG GLU ALA LEU SER PRO SER TYR LYS ARG ARG LEU GLU GLU ASP ALA PHE GLY PHE VAL PRO PRO LEU GLN ILE GLU ALA VAL GLY ARG CYS GLY ARG GLN
ALA THR ARG ALA GLY ARG MET PRO GLY GLY HIS ALA ARG ALA ALA SER GLU THR VAL SER SER GLN LYS GLY GLU ASP LYS SER THR ALA MET GLY ASP ARG GLY ILE LYS GLY ALA GLY GLN ARG ARG GLU PRO ILE GLU ASP GLU SER LEU THR SER GLU GLU
MET GLU ASN GLN ALA VAL ASP LEU LEU ARG GLN ARG ASP LEU ASP ARG MET LEU GLN ASP ALA ALA SER GLN ILE ARG PRO ASP PHE GLY LYS ARG VAL ALA SER PRO PRO ALA LYS VAL GLU GLN THR ARG LEU SER SER PRO ALA ASP GLY SER LEU GLN GLN HIS ASP ALA ASP ASN
GLY PHE HIS VAL ARG MET LEU GLN GLN ARG MET ARG ALA SER GLU VAL ALA THR LYS ILE GLU LEU ASN THR SER SER LEU VAL ALA TYR GLY GLU VAL ARG VAL PRO SER GLN VAL LYS GLU LEU PHE GLY HIS GLY VAL ASN ARG LEU SER PRO ALA ASP SER LEU GLN SER ALA GLY SER VAL SER GLU ASN ALA PHE VAL
GLY LEU LEU GLY SER HIS VAL GLN ARG VAL LYS THR ARG GLY SER SER LEU ALA GLY ARG LEU ILE CYS GLN ALA SER GLN SER LYS SER ALA SER SER GLN LEU CYS ILE GLY GLY SER ASP PRO LEU ASN VAL ASP GLY ASN GLU ASP ASN
SER ARG SER GLY ILE ALA GLN ARG VAL PRO THR PRO THR GLU ALA ASP SER PHE GLU GLU ALA ASN ARG ASP GLU ASP ALA PHE CYS PRO LEU PRO THR LEU GLY ARG HIS ILE ASP ALA SER ASP TYR GLU ARG GLN PRO GLU PRO MET GLU VAL ILE THR SER LYS



• Molecule 17: PCR15, TGME49_232560

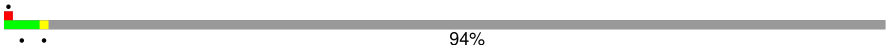
Chain PB: 94%

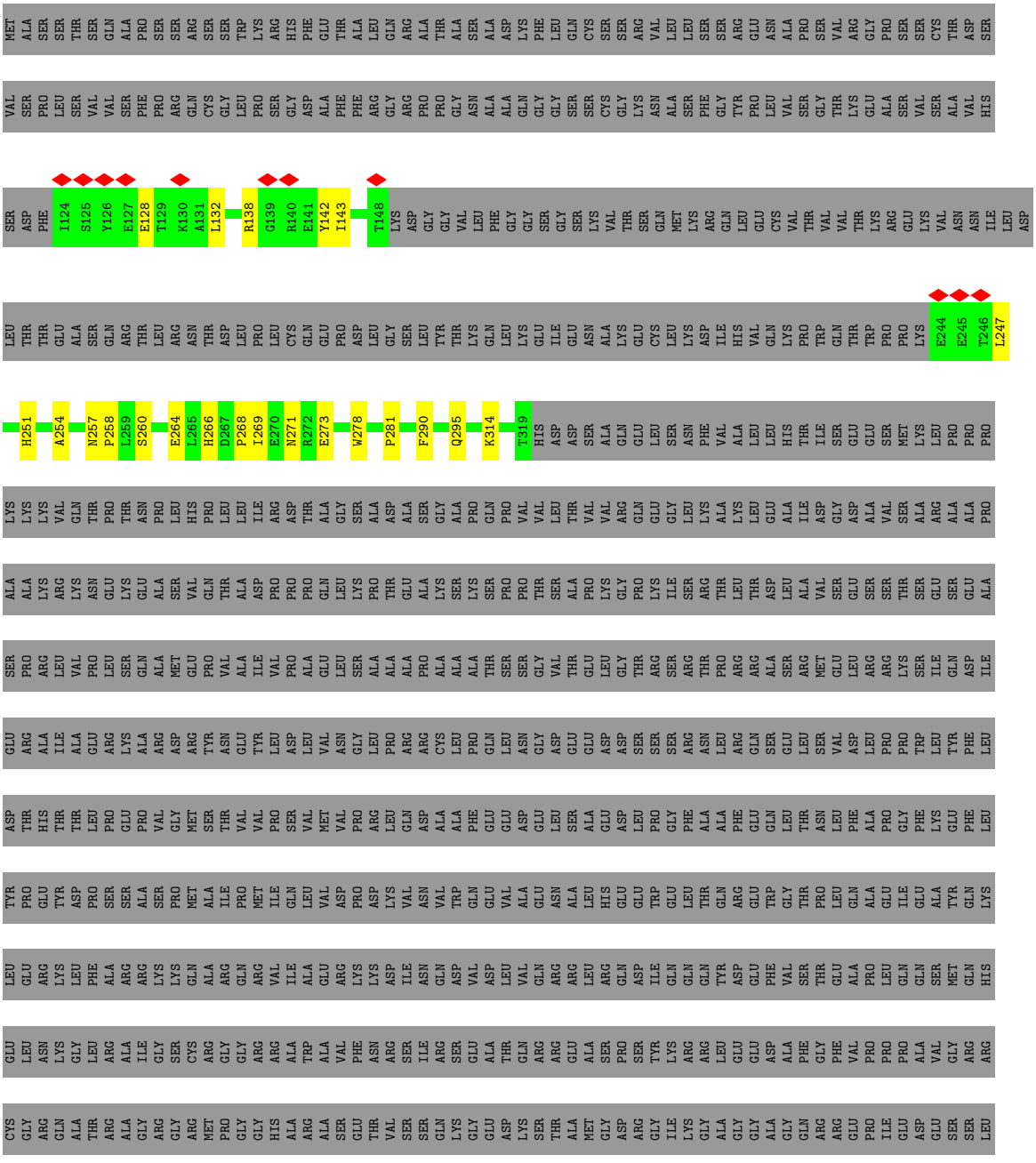


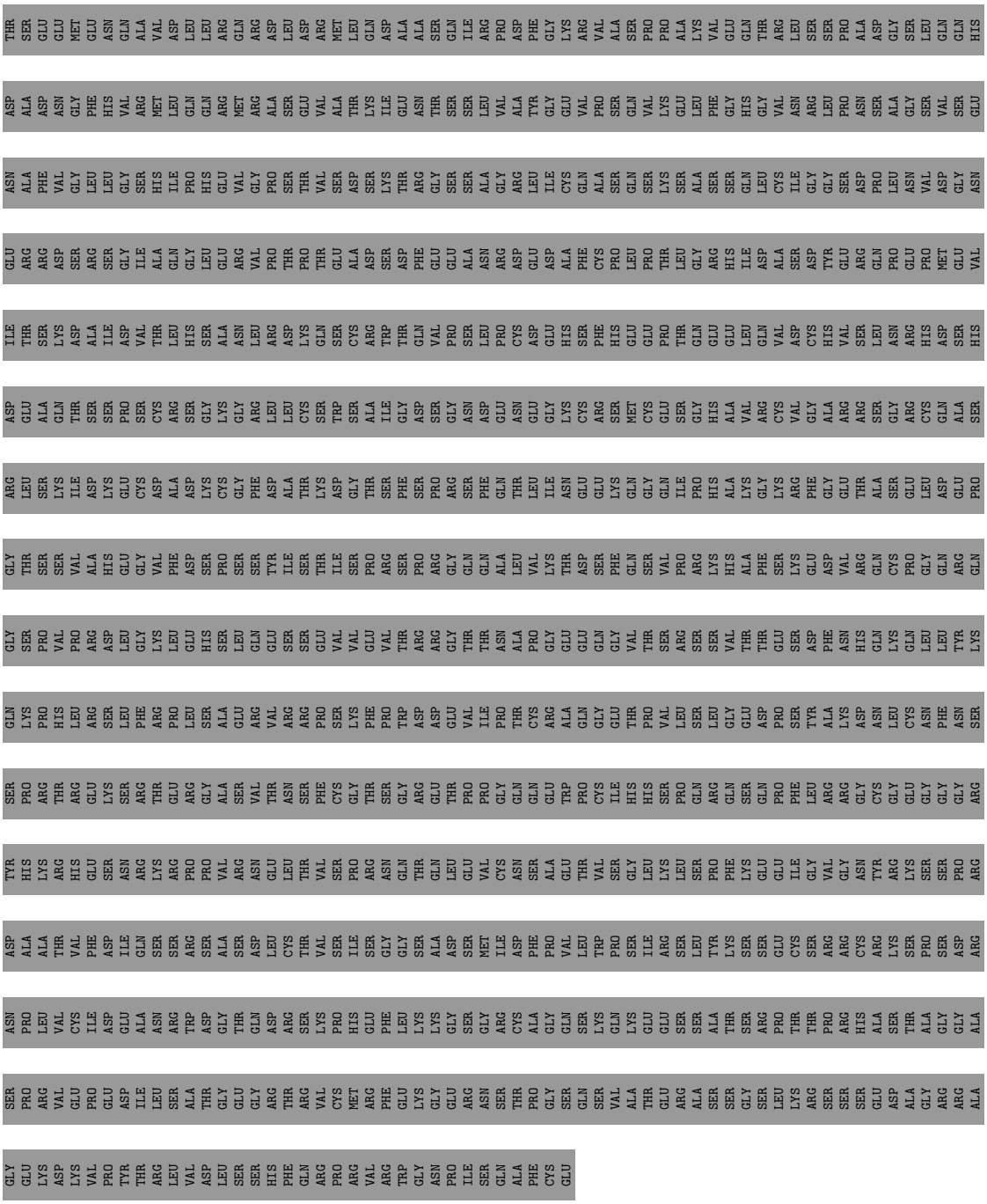


• Molecule 17: PCR15, TGME49_232560

Chain PC:

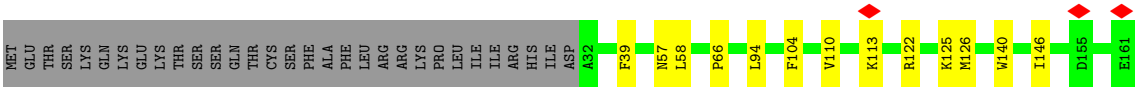


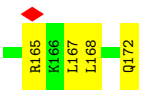




• Molecule 18: MLC4, TGME49_294390

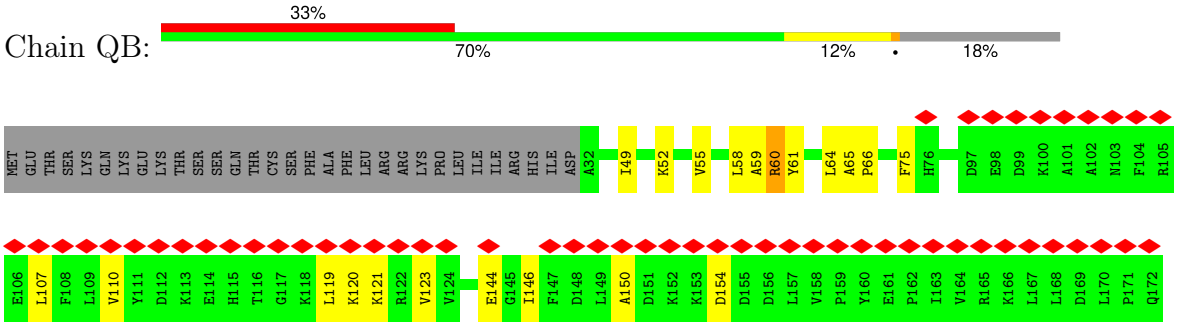
Chain QA:





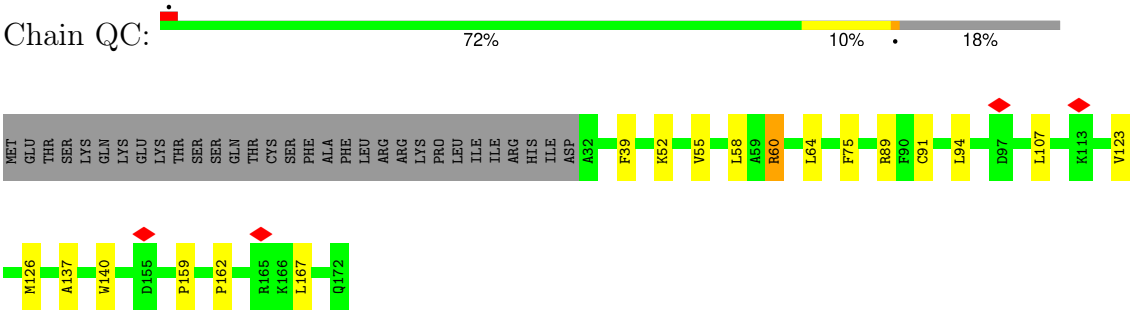
• Molecule 18: MLC4, TGME49_294390

Chain QB:



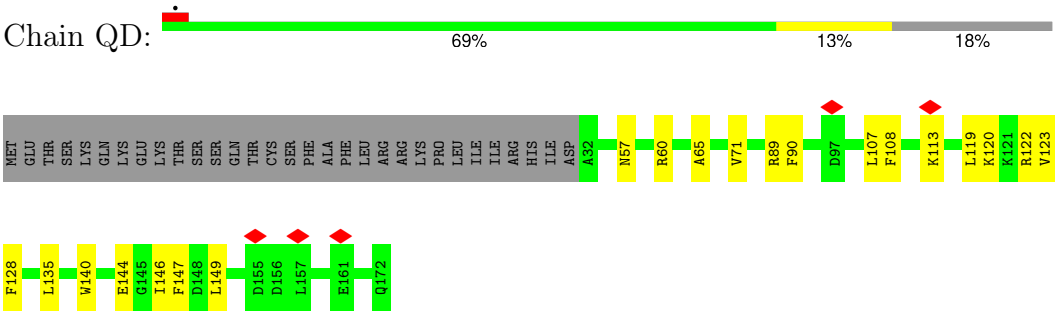
• Molecule 18: MLC4, TGME49_294390

Chain QC:



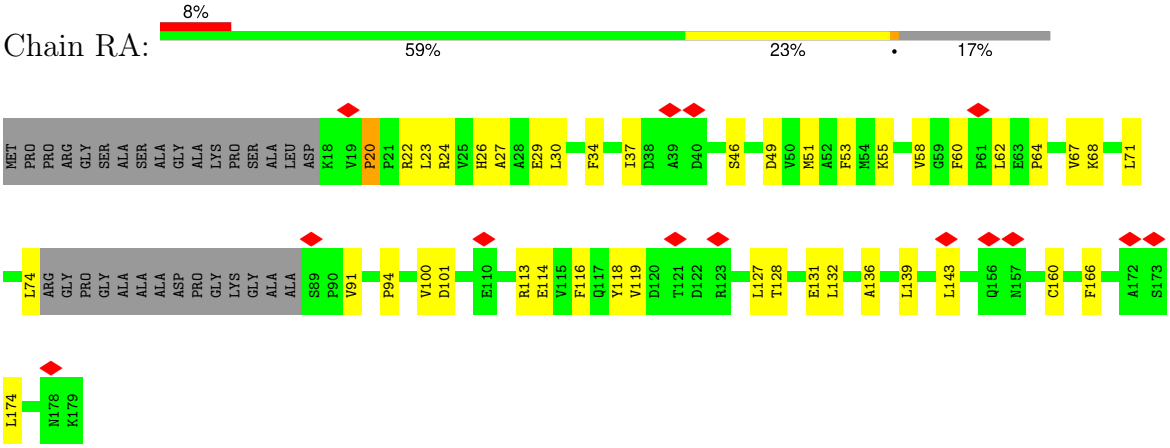
• Molecule 18: MLC4, TGME49_294390

Chain QD:



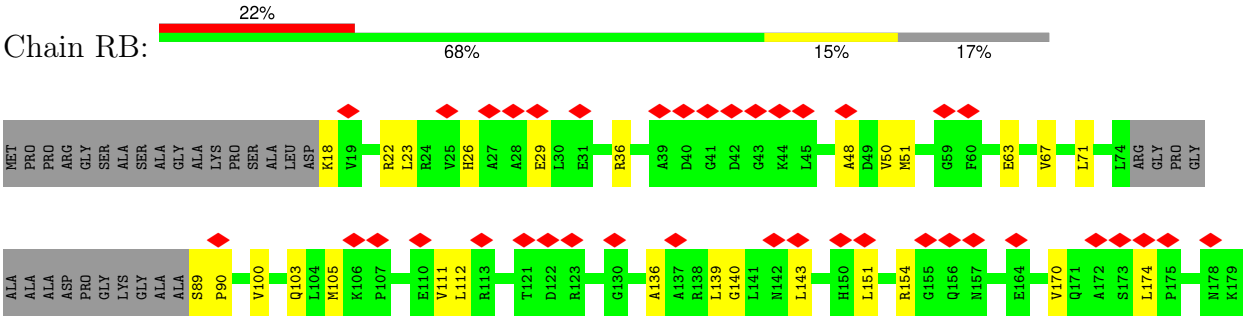
• Molecule 19: Calmodulin

Chain RA:



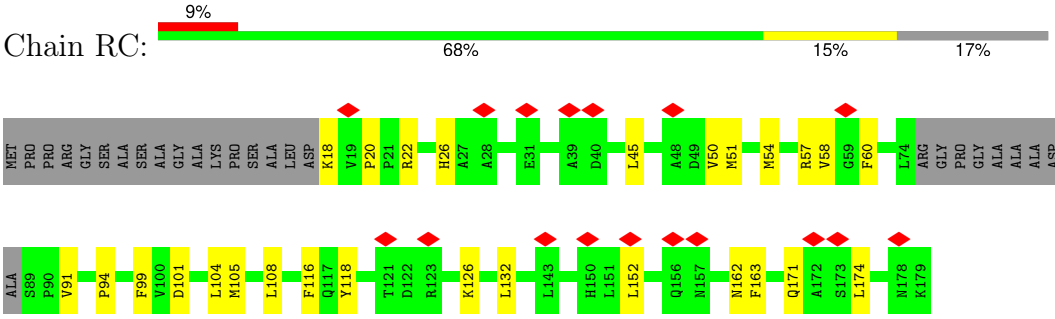
• Molecule 19: Calmodulin

Chain RB:



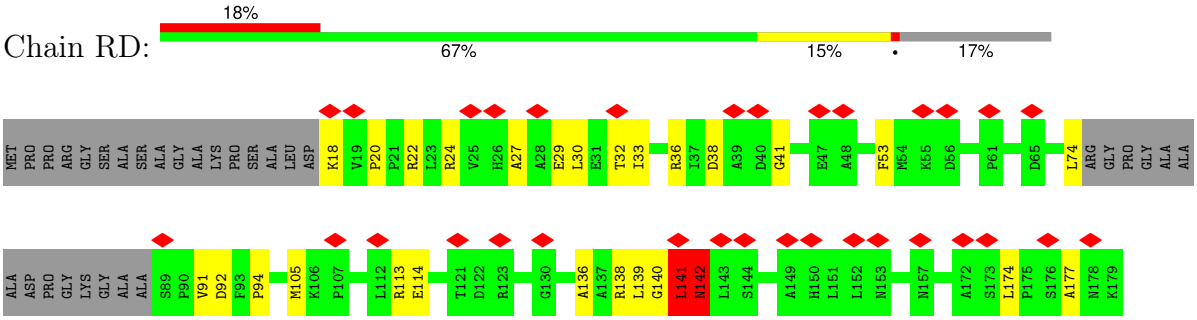
• Molecule 19: Calmodulin

Chain RC:



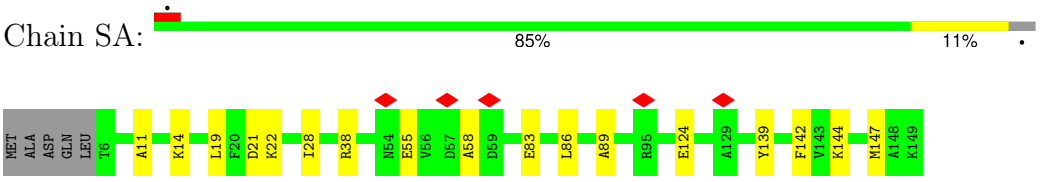
• Molecule 19: Calmodulin

Chain RD:



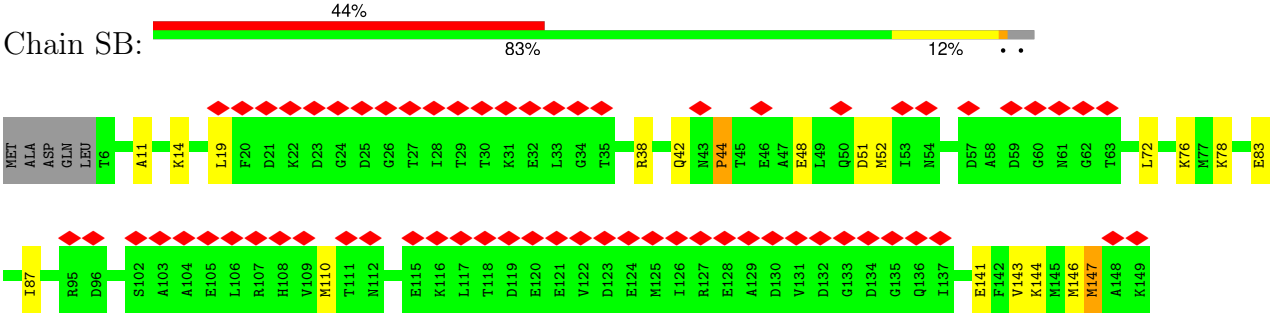
• Molecule 20: Calmodulin

Chain SA:



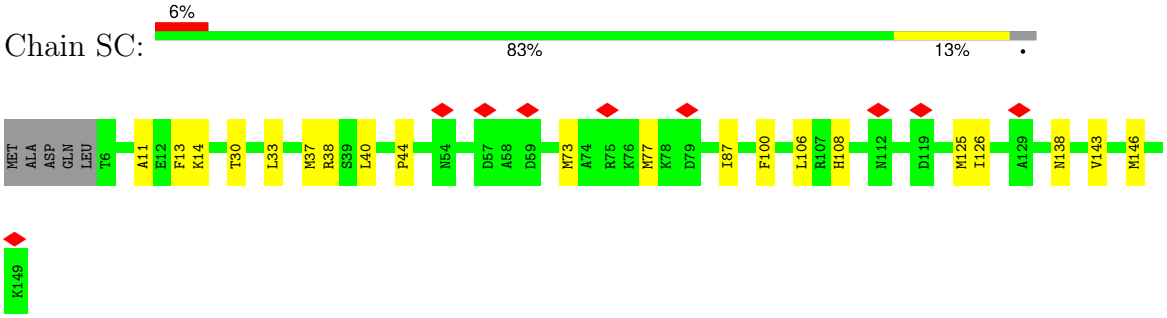
• Molecule 20: Calmodulin

Chain SB:



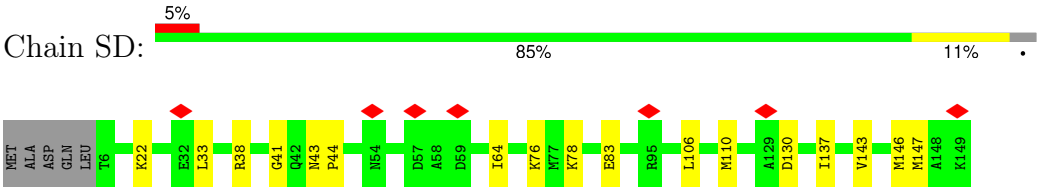
• Molecule 20: Calmodulin

Chain SC:



• Molecule 20: Calmodulin

Chain SD:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	131707	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.073	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	686.08, 686.08, 686.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	AA	0.24	1/6682 (0.0%)	0.65	5/9057 (0.1%)
1	AD	0.22	0/6958	0.58	0/9433
1	AE	0.24	0/6682	0.67	4/9057 (0.0%)
1	AH	0.22	0/6958	0.59	3/9433 (0.0%)
1	AI	0.24	0/6682	0.64	3/9057 (0.0%)
1	AL	0.23	0/6958	0.57	0/9433
2	AB	0.34	1/3898 (0.0%)	0.66	4/5265 (0.1%)
2	AC	0.20	0/3926	0.51	0/5305
2	AF	0.25	0/3898	0.65	3/5265 (0.1%)
2	AG	0.21	0/3926	0.54	0/5305
2	AJ	0.23	0/3892	0.60	2/5258 (0.0%)
2	AK	0.22	0/3926	0.57	1/5305 (0.0%)
3	BA	0.22	0/2777	0.60	0/3759
3	BB	0.23	0/2777	0.62	0/3759
3	BC	0.22	0/2777	0.64	0/3759
3	CA	0.23	0/2762	0.60	1/3738 (0.0%)
3	CB	0.23	0/2762	0.62	0/3738
3	CC	0.22	0/2762	0.61	1/3738 (0.0%)
3	CE	0.24	0/1921	0.66	0/2628
3	CF	0.28	0/1921	0.74	0/2628
3	CG	0.32	0/1921	0.74	0/2628
3	CI	0.23	0/2062	0.68	0/2816
3	CJ	0.25	0/2062	0.67	1/2816 (0.0%)
3	CL	0.24	0/2062	0.69	0/2816
4	DA	0.27	0/2795	0.74	6/3763 (0.2%)
4	DB	0.25	0/2795	0.70	2/3763 (0.1%)
4	DC	0.26	0/2795	0.73	2/3763 (0.1%)
4	DD	0.23	0/2672	0.63	3/3600 (0.1%)
4	DE	0.24	0/2672	0.69	3/3600 (0.1%)
4	DF	0.25	0/2672	0.68	0/3600
5	EA	0.24	0/10890	0.64	2/14730 (0.0%)
5	EB	0.28	0/10890	0.66	4/14730 (0.0%)
5	EC	0.28	0/10886	0.67	7/14726 (0.0%)
6	FA	0.39	0/4286	0.77	2/5798 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
6	FB	0.34	0/4286	0.70	0/5798
6	FC	0.57	0/4286	0.89	1/5798 (0.0%)
6	FD	0.98	0/3323	1.16	4/4521 (0.1%)
6	FE	0.98	0/3329	1.12	3/4528 (0.1%)
6	FF	0.98	0/3245	1.11	2/4410 (0.0%)
7	GA	0.25	0/6456	0.59	10/8779 (0.1%)
7	GC	0.25	1/6087 (0.0%)	0.61	0/8272
7	GE	0.24	0/6087	0.62	0/8272
7	GG	0.24	0/6456	0.61	11/8779 (0.1%)
7	GI	0.24	0/6087	0.64	0/8272
7	GK	0.23	0/6456	0.58	9/8779 (0.1%)
8	GB	0.23	0/6087	0.61	3/8257 (0.0%)
8	GD	0.23	0/6087	0.61	1/8257 (0.0%)
8	GF	0.19	0/6301	0.52	2/8556 (0.0%)
8	GH	0.24	0/5913	0.66	5/8019 (0.1%)
8	GJ	0.21	0/6301	0.55	0/8556
8	GL	0.21	0/6301	0.59	3/8556 (0.0%)
9	HA	0.67	3/3439 (0.1%)	0.95	7/4668 (0.1%)
9	HB	0.66	1/3439 (0.0%)	0.93	9/4668 (0.2%)
9	HC	0.27	0/2345	0.73	7/3182 (0.2%)
9	HD	1.11	1/1094 (0.1%)	1.24	0/1486
10	IA	0.22	0/9289	0.59	6/12571 (0.0%)
10	IB	0.22	0/9289	0.61	6/12571 (0.0%)
10	IC	0.22	1/9289 (0.0%)	0.60	4/12571 (0.0%)
11	JA	0.25	0/12997	0.67	16/17611 (0.1%)
11	JB	0.23	0/12997	0.66	18/17611 (0.1%)
11	JC	0.24	0/12997	0.68	9/17611 (0.1%)
12	KA	0.29	0/3752	0.83	5/5093 (0.1%)
12	KB	0.29	0/3752	0.79	2/5093 (0.0%)
12	KC	0.39	0/3746	0.90	7/5086 (0.1%)
12	KE	0.18	0/3616	0.52	0/4901
12	KF	0.18	0/3616	0.49	0/4901
12	KG	0.20	0/3616	0.55	0/4901
13	LA	0.18	0/1524	0.51	1/2040 (0.0%)
13	LB	0.17	0/1536	0.51	0/2055
13	LC	0.18	0/1318	0.47	0/1763
13	LD	0.16	0/1310	0.51	0/1753
13	LE	0.24	0/1195	0.70	5/1598 (0.3%)
13	LF	0.22	0/1202	0.66	3/1606 (0.2%)
13	LG	0.21	0/464	0.53	0/623
13	LH	0.22	0/451	0.70	0/605
13	LI	0.38	0/1524	0.77	2/2040 (0.1%)
13	LJ	0.26	0/1536	0.74	3/2055 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
13	LK	0.15	0/1326	0.50	0/1774
13	LL	0.21	0/1310	0.58	1/1753 (0.1%)
13	LM	0.16	0/862	0.50	0/1151
13	LN	0.17	0/859	0.55	0/1148
13	LO	0.16	0/844	0.55	0/1127
13	LP	0.18	0/885	0.56	0/1183
14	MA	0.27	0/1144	0.80	2/1541 (0.1%)
14	MB	0.24	0/981	0.72	1/1315 (0.1%)
14	MC	0.17	0/601	0.51	0/807
14	MD	0.16	0/527	0.40	0/703
14	ME	0.30	0/1144	0.85	2/1541 (0.1%)
14	MF	0.27	0/981	0.83	1/1315 (0.1%)
14	MG	0.21	0/601	0.59	0/807
14	MH	0.17	0/527	0.52	0/703
14	MI	0.26	0/1144	0.78	0/1541
14	MJ	0.32	0/981	0.88	3/1315 (0.2%)
14	MK	0.18	0/601	0.51	0/807
14	ML	0.30	0/527	0.61	0/703
15	NA	0.27	0/7422	0.71	9/10053 (0.1%)
15	NB	0.24	0/7422	0.64	4/10053 (0.0%)
15	NC	0.28	0/7422	0.74	6/10053 (0.1%)
15	ND	0.27	0/7422	0.72	17/10053 (0.2%)
16	OA	0.24	0/3570	0.69	4/4821 (0.1%)
16	OB	0.24	0/3570	0.70	3/4821 (0.1%)
16	OC	0.25	0/3570	0.72	4/4821 (0.1%)
17	PA	0.26	0/831	0.74	2/1127 (0.2%)
17	PB	0.28	0/831	0.77	2/1127 (0.2%)
17	PC	0.25	0/831	0.69	0/1127
18	QA	0.22	0/1151	0.59	0/1548
18	QB	0.20	0/1151	0.52	0/1548
18	QC	0.21	0/1151	0.58	0/1548
18	QD	0.25	0/1151	0.59	0/1548
19	RA	0.28	0/1163	0.71	0/1573
19	RB	0.22	0/1163	0.63	0/1573
19	RC	0.24	0/1163	0.65	0/1573
19	RD	0.27	0/1163	0.86	7/1573 (0.4%)
20	SA	0.25	0/1146	0.65	0/1536
20	SB	0.19	0/1146	0.56	1/1536 (0.1%)
20	SC	0.23	0/1146	0.65	0/1536
20	SD	0.23	0/1146	0.64	0/1536
All	All	0.31	9/423302 (0.0%)	0.67	292/573059 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	3
1	AE	0	5
1	AI	0	3
1	AL	0	2
2	AB	0	3
2	AC	0	1
2	AK	0	1
3	BC	0	1
3	CB	0	1
3	CC	0	1
3	CF	0	2
3	CG	0	1
3	CL	0	1
4	DC	0	1
4	DD	0	1
5	EA	0	5
5	EB	0	6
5	EC	0	7
6	FA	0	8
6	FB	0	3
6	FC	0	13
6	FD	0	26
6	FE	0	22
6	FF	0	26
7	GA	0	6
7	GC	0	1
7	GE	0	1
7	GG	0	8
7	GI	0	1
7	GK	0	7
8	GB	0	4
8	GD	0	4
8	GF	0	1
8	GH	0	6
8	GJ	0	4
8	GL	0	4
9	HA	0	8
9	HB	0	7
9	HC	0	2
9	HD	0	5

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
10	IA	0	2
10	IB	0	1
10	IC	0	1
11	JA	0	10
11	JB	0	7
11	JC	0	10
12	KA	0	5
12	KB	0	4
12	KC	0	5
12	KE	0	1
12	KF	0	1
12	KG	0	2
13	LE	0	4
13	LF	0	1
13	LI	0	3
13	LJ	0	2
13	LO	0	1
14	MC	0	1
14	ME	0	3
14	MG	0	1
14	MI	0	2
14	MJ	0	2
14	MK	0	1
15	NA	0	5
15	NB	0	5
15	NC	0	10
15	ND	0	7
16	OA	0	3
16	OB	0	2
16	OC	0	1
17	PB	0	1
18	QB	0	1
18	QC	0	1
19	RA	0	1
19	RB	0	1
19	RD	0	4
20	SB	0	1
All	All	0	325

All (9) bond length outliers are listed below:

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	415	HIS	C-O	8.28	1.33	1.24
9	HA	749	ASN	C-O	6.18	1.31	1.24
9	HB	749	ASN	C-O	6.12	1.31	1.24
9	HD	749	ASN	C-O	5.95	1.31	1.24
1	AA	714	PHE	CA-C	5.84	1.60	1.52
9	HA	763	GLN	C-O	5.43	1.30	1.24
9	HA	760	LYS	C-O	5.31	1.30	1.24
7	GC	875	GLU	CA-CB	5.19	1.61	1.52
10	IC	593	PRO	CA-C	-5.02	1.49	1.51

All (292) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
19	RD	141	LEU	CA-CB-CG	10.66	153.62	116.30
19	RD	141	LEU	CB-CA-C	9.90	130.13	110.42
7	GK	546	SER	N-CA-C	9.12	121.58	110.91
7	GA	543	LYS	N-CA-C	8.84	129.34	109.81
7	GG	543	LYS	N-CA-C	8.81	129.28	109.81
11	JB	767	GLY	CA-C-N	8.56	137.89	121.54
11	JB	767	GLY	C-N-CA	8.56	137.89	121.54
11	JC	767	GLY	CA-C-N	8.53	137.83	121.54
11	JC	767	GLY	C-N-CA	8.53	137.83	121.54
15	ND	1550	MET	CB-CG-SD	8.36	137.79	112.70
7	GK	547	GLY	N-CA-C	8.20	120.54	111.85
1	AH	735	LEU	CA-C-N	7.97	131.81	120.49
1	AH	735	LEU	C-N-CA	7.97	131.81	120.49
7	GA	542	GLY	CA-C-N	7.90	141.09	121.80
7	GA	542	GLY	C-N-CA	7.90	141.09	121.80
5	EC	3704	SER	CA-C-N	7.88	136.59	121.54
5	EC	3704	SER	C-N-CA	7.88	136.59	121.54
9	HB	553	TYR	CA-CB-CG	7.74	127.83	113.90
1	AE	640	GLN	CA-CB-CG	7.56	129.22	114.10
11	JA	1012	ARG	CG-CD-NE	-7.36	95.80	112.00
15	ND	1153	ALA	N-CA-C	7.35	123.75	108.53
9	HB	649	ASP	CA-C-N	7.34	135.57	121.54
9	HB	649	ASP	C-N-CA	7.34	135.57	121.54
11	JA	1305	ASP	CA-C-N	7.28	124.83	120.24
11	JA	1305	ASP	C-N-CA	7.28	124.83	120.24
4	DE	170	ARG	CA-CB-CG	7.24	128.59	114.10
8	GH	671	PHE	N-CA-C	-7.24	105.36	114.56

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
14	MJ	286	GLU	CA-C-N	7.24	135.36	121.54
14	MJ	286	GLU	C-N-CA	7.24	135.36	121.54
7	GK	543	LYS	N-CA-C	7.19	125.69	109.81
4	DA	308	GLN	CA-C-N	7.01	134.58	121.97
4	DA	308	GLN	C-N-CA	7.01	134.58	121.97
13	LI	513	LEU	CB-CG-CD2	-6.98	89.75	110.70
5	EC	4651	MET	CB-CG-SD	-6.97	91.79	112.70
7	GA	855	ARG	CA-C-N	6.94	134.47	121.97
7	GA	855	ARG	C-N-CA	6.94	134.47	121.97
9	HC	649	ASP	CA-C-N	6.94	134.80	121.54
9	HC	649	ASP	C-N-CA	6.94	134.80	121.54
19	RD	141	LEU	CB-CG-CD1	6.94	131.51	110.70
12	KC	377	LEU	N-CA-C	-6.92	104.71	113.01
5	EB	3262	VAL	N-CA-C	-6.87	107.18	113.71
7	GG	542	GLY	CA-C-N	6.87	138.56	121.80
7	GG	542	GLY	C-N-CA	6.87	138.56	121.80
14	MB	278	PRO	N-CA-CB	6.87	110.55	103.00
14	MJ	278	PRO	N-CA-CB	6.83	110.51	103.00
11	JC	969	ALA	CA-C-N	6.83	133.91	120.94
11	JC	969	ALA	C-N-CA	6.83	133.91	120.94
19	RD	142	ASN	N-CA-CB	6.80	121.98	110.49
6	FD	862	GLU	N-CA-C	-6.79	106.89	114.62
14	MF	278	PRO	N-CA-CB	6.76	110.44	103.00
9	HC	551	GLU	CA-C-N	6.72	134.38	121.54
9	HC	551	GLU	C-N-CA	6.72	134.38	121.54
20	SB	147	MET	CA-CB-CG	6.67	127.44	114.10
11	JB	1875	ILE	N-CA-C	-6.64	106.52	111.90
2	AB	419	LYS	O-C-N	-6.63	113.69	121.32
6	FA	2010	LYS	N-CA-C	-6.54	104.07	111.07
10	IA	1068	ARG	CB-CG-CD	6.53	126.33	111.30
10	IC	779	ASP	CA-C-N	6.48	134.11	122.13
10	IC	779	ASP	C-N-CA	6.48	134.11	122.13
15	NA	468	ARG	CA-C-N	6.44	133.84	121.54
15	NA	468	ARG	C-N-CA	6.44	133.84	121.54
4	DA	98	ARG	CA-CB-CG	6.44	126.98	114.10
9	HA	553	TYR	CA-CB-CG	6.35	125.33	113.90
15	NC	1153	ALA	N-CA-C	6.35	120.67	112.41
8	GL	77	THR	CA-C-N	6.35	137.29	121.80
8	GL	77	THR	C-N-CA	6.35	137.29	121.80
12	KB	671	LEU	CA-C-N	6.33	133.62	121.54
12	KB	671	LEU	C-N-CA	6.33	133.62	121.54
19	RD	141	LEU	CA-C-O	-6.32	111.48	120.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	ND	1549	GLY	N-CA-C	6.30	128.12	113.18
6	FC	1709	GLU	CA-CB-CG	6.29	126.69	114.10
10	IB	779	ASP	CA-C-N	6.28	133.75	122.13
10	IB	779	ASP	C-N-CA	6.28	133.75	122.13
11	JB	135	ILE	N-CA-C	-6.27	107.39	113.53
16	OA	1089	LEU	CA-C-N	6.23	133.44	121.54
16	OA	1089	LEU	C-N-CA	6.23	133.44	121.54
10	IA	779	ASP	CA-C-N	6.23	133.65	122.13
10	IA	779	ASP	C-N-CA	6.23	133.65	122.13
7	GA	537	GLY	N-CA-C	6.22	127.93	113.18
11	JB	451	MET	CA-CB-CG	6.19	126.48	114.10
8	GF	56	CYS	CA-C-N	6.19	133.36	121.54
8	GF	56	CYS	C-N-CA	6.19	133.36	121.54
4	DA	385	LYS	N-CA-C	6.18	118.68	108.48
7	GG	539	TYR	N-CA-C	6.18	116.02	107.73
9	HA	551	GLU	CA-C-N	6.18	133.35	121.54
9	HA	551	GLU	C-N-CA	6.18	133.35	121.54
11	JA	1588	GLU	CA-C-N	6.17	133.31	121.54
11	JA	1588	GLU	C-N-CA	6.17	133.31	121.54
15	ND	1155	GLU	CA-C-N	6.17	136.84	121.80
15	ND	1155	GLU	C-N-CA	6.17	136.84	121.80
10	IB	397	VAL	N-CA-C	-6.16	107.86	113.71
8	GH	199	ARG	CB-CG-CD	-6.15	97.16	111.30
7	GA	538	THR	N-CA-C	6.13	123.86	110.80
15	NB	468	ARG	CA-C-N	6.12	133.23	121.54
15	NB	468	ARG	C-N-CA	6.12	133.23	121.54
10	IA	711	VAL	N-CA-C	-6.08	107.57	113.53
1	AA	670	ASP	N-CA-C	-6.08	97.85	110.80
6	FF	913	LEU	N-CA-C	-6.06	104.75	111.36
15	NA	1153	ALA	N-CA-C	6.04	120.26	112.41
12	KA	685	ARG	CA-C-N	6.04	136.53	121.80
12	KA	685	ARG	C-N-CA	6.04	136.53	121.80
7	GK	542	GLY	CA-C-N	6.03	136.51	121.80
7	GK	542	GLY	C-N-CA	6.03	136.51	121.80
4	DB	308	GLN	CA-C-N	6.03	132.82	121.97
4	DB	308	GLN	C-N-CA	6.03	132.82	121.97
7	GG	546	SER	N-CA-C	6.03	123.64	110.80
7	GA	541	GLY	N-CA-C	6.01	127.42	113.18
7	GK	545	GLY	N-CA-C	6.01	127.42	113.18
11	JA	741	PHE	CA-C-N	6.00	132.78	121.97
11	JA	741	PHE	C-N-CA	6.00	132.78	121.97
16	OC	1089	LEU	CA-C-N	6.00	133.01	121.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	OC	1089	LEU	C-N-CA	6.00	133.01	121.54
11	JC	147	ARG	N-CA-C	-5.98	103.91	111.92
4	DA	384	ILE	CA-C-N	-5.97	114.47	121.64
4	DA	384	ILE	C-N-CA	-5.97	114.47	121.64
9	HB	750	PRO	N-CA-C	-5.97	105.15	113.81
9	HC	552	ASP	N-CA-C	5.97	123.51	110.80
7	GG	545	GLY	CA-C-N	5.96	132.93	121.54
7	GG	545	GLY	C-N-CA	5.96	132.93	121.54
7	GK	537	GLY	N-CA-C	5.95	127.28	113.18
15	ND	1408	THR	N-CA-C	5.95	119.36	111.75
16	OB	1089	LEU	CA-C-N	5.93	132.87	121.54
16	OB	1089	LEU	C-N-CA	5.93	132.87	121.54
4	DE	16	LEU	CA-CB-CG	5.92	137.02	116.30
11	JC	135	ILE	N-CA-C	-5.92	107.73	113.53
8	GH	189	ASN	CA-C-N	5.89	132.58	121.97
8	GH	189	ASN	C-N-CA	5.89	132.58	121.97
7	GK	538	THR	N-CA-C	5.89	123.35	110.80
11	JB	450	PHE	CA-C-N	5.89	132.79	121.54
11	JB	450	PHE	C-N-CA	5.89	132.79	121.54
14	MA	283	GLN	N-CA-C	-5.88	107.34	114.75
12	KC	382	ARG	N-CA-C	-5.86	106.09	113.18
11	JA	1092	HIS	CA-C-N	5.84	136.05	121.80
11	JA	1092	HIS	C-N-CA	5.84	136.05	121.80
15	ND	468	ARG	CA-CB-CG	5.83	125.77	114.10
11	JB	147	ARG	N-CA-C	-5.83	104.11	111.92
4	DD	85	VAL	N-CA-C	-5.82	106.73	111.91
5	EC	4652	LEU	CA-C-N	5.81	132.63	121.54
5	EC	4652	LEU	C-N-CA	5.81	132.63	121.54
11	JC	1092	HIS	CA-C-N	5.81	135.97	121.80
11	JC	1092	HIS	C-N-CA	5.81	135.97	121.80
16	OB	882	ARG	CA-CB-CG	5.81	125.72	114.10
15	ND	1153	ALA	CA-C-N	5.79	132.68	121.63
15	ND	1153	ALA	C-N-CA	5.79	132.68	121.63
3	CJ	1131	LEU	CA-CB-CG	5.76	136.46	116.30
15	ND	1550	MET	N-CA-C	5.76	120.84	113.18
9	HA	552	ASP	N-CA-C	5.75	123.06	110.80
4	DD	189	ARG	CG-CD-NE	-5.75	99.35	112.00
14	MA	259	MET	CA-CB-CG	5.75	125.59	114.10
13	LF	521	ASN	CA-C-N	5.75	132.51	121.54
13	LF	521	ASN	C-N-CA	5.75	132.51	121.54
13	LF	522	ARG	N-CA-C	5.74	123.02	110.80
11	JB	178	HIS	CA-C-N	5.73	135.79	121.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	JB	178	HIS	C-N-CA	5.73	135.79	121.80
7	GG	538	THR	N-CA-C	5.73	123.01	110.80
8	GL	83	GLN	CB-CG-CD	5.73	122.34	112.60
7	GG	537	GLY	N-CA-C	5.72	126.75	113.18
4	DC	308	GLN	CA-C-N	5.70	132.23	121.97
4	DC	308	GLN	C-N-CA	5.70	132.23	121.97
9	HC	553	TYR	CA-CB-CG	5.70	124.16	113.90
11	JB	1092	HIS	CA-C-N	5.70	135.70	121.80
11	JB	1092	HIS	C-N-CA	5.70	135.70	121.80
11	JA	450	PHE	CA-C-N	5.69	132.40	121.54
11	JA	450	PHE	C-N-CA	5.69	132.40	121.54
11	JB	415	LYS	CA-CB-CG	5.68	125.47	114.10
2	AJ	344	GLU	CA-C-N	5.67	128.73	120.51
2	AJ	344	GLU	C-N-CA	5.67	128.73	120.51
15	NA	891	TRP	N-CA-C	5.67	117.70	110.61
11	JB	462	SER	CA-C-N	5.66	132.15	121.97
11	JB	462	SER	C-N-CA	5.66	132.15	121.97
7	GK	542	GLY	N-CA-C	5.65	126.58	113.18
17	PB	140	ARG	CA-C-N	5.64	132.31	121.54
17	PB	140	ARG	C-N-CA	5.64	132.31	121.54
11	JA	767	GLY	CA-C-N	5.62	132.28	121.54
11	JA	767	GLY	C-N-CA	5.62	132.28	121.54
6	FF	1005	PRO	CB-CA-C	5.62	117.78	110.92
13	LJ	416	ARG	CA-CB-CG	5.62	125.33	114.10
9	HB	553	TYR	CB-CA-C	-5.61	99.26	110.42
13	LE	464	ASP	CA-C-N	5.60	132.06	121.97
13	LE	464	ASP	C-N-CA	5.60	132.06	121.97
6	FE	1011	TYR	CB-CA-C	5.60	116.47	110.65
11	JA	451	MET	CA-CB-CG	5.59	125.28	114.10
10	IC	172	GLN	CB-CA-C	-5.59	110.12	116.54
15	NA	1423	LEU	CB-CA-C	-5.59	109.14	115.79
13	LA	513	LEU	CB-CG-CD2	-5.58	93.94	110.70
17	PA	140	ARG	CA-C-N	5.58	132.20	121.54
17	PA	140	ARG	C-N-CA	5.58	132.20	121.54
15	NC	691	LEU	N-CA-C	5.54	117.39	110.91
7	GG	542	GLY	N-CA-C	5.54	126.30	113.18
11	JA	2004	GLY	CA-C-N	5.54	131.93	121.97
11	JA	2004	GLY	C-N-CA	5.54	131.93	121.97
12	KC	359	VAL	CA-C-N	5.51	132.06	121.54
12	KC	359	VAL	C-N-CA	5.51	132.06	121.54
1	AA	43	ASP	CA-C-N	5.49	128.40	120.38
1	AA	43	ASP	C-N-CA	5.49	128.40	120.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	ND	468	ARG	CA-C-N	5.48	132.01	121.54
15	ND	468	ARG	C-N-CA	5.48	132.01	121.54
15	ND	1423	LEU	CB-CA-C	-5.48	109.27	115.79
13	LJ	413	GLU	CA-CB-CG	5.46	125.02	114.10
12	KC	633	ARG	CB-CA-C	-5.46	109.29	115.79
7	GA	544	PRO	N-CA-C	5.44	120.85	111.77
15	NA	1408	THR	N-CA-C	5.44	118.71	111.75
6	FA	1964	MET	CB-CG-SD	-5.43	96.40	112.70
9	HB	481	ALA	CA-C-N	5.43	131.91	121.54
9	HB	481	ALA	C-N-CA	5.43	131.91	121.54
1	AA	898	PRO	N-CA-C	5.41	123.62	112.47
13	LE	467	GLN	N-CA-C	-5.38	107.37	114.31
4	DD	16	LEU	CA-CB-CG	5.38	135.12	116.30
3	CA	1011	MET	CB-CG-SD	5.37	128.81	112.70
15	NA	1471	ARG	CA-C-N	5.37	131.79	121.54
15	NA	1471	ARG	C-N-CA	5.37	131.79	121.54
2	AK	50	ILE	N-CA-C	-5.37	107.89	113.10
9	HC	551	GLU	N-CA-C	5.36	116.88	109.54
19	RD	141	LEU	N-CA-CB	-5.34	101.46	110.49
13	LE	472	GLY	N-CA-C	-5.33	105.36	110.21
6	FD	829	ARG	N-CA-C	-5.32	107.81	114.56
15	NC	468	ARG	CA-C-N	5.32	131.69	121.54
15	NC	468	ARG	C-N-CA	5.32	131.69	121.54
13	LL	522	ARG	CA-CB-CG	5.31	124.73	114.10
2	AF	541	PRO	CA-C-N	5.31	131.69	121.54
2	AF	541	PRO	C-N-CA	5.31	131.69	121.54
7	GG	541	GLY	N-CA-C	5.31	125.77	113.18
5	EB	4653	GLU	CB-CA-C	-5.30	109.49	115.79
10	IB	357	PHE	CA-C-N	5.29	132.70	123.91
10	IB	357	PHE	C-N-CA	5.29	132.70	123.91
13	LJ	531	VAL	N-CA-C	-5.29	108.68	113.71
10	IA	916	LYS	CA-C-N	5.25	126.90	122.28
10	IA	916	LYS	C-N-CA	5.25	126.90	122.28
15	ND	1524	ARG	CA-CB-CG	5.24	124.58	114.10
6	FE	913	LEU	N-CA-C	-5.24	106.84	114.12
12	KC	388	PRO	CA-C-N	5.22	131.51	121.54
12	KC	388	PRO	C-N-CA	5.22	131.51	121.54
16	OA	1103	GLU	CA-C-N	-5.21	112.90	121.92
16	OA	1103	GLU	C-N-CA	-5.21	112.90	121.92
5	EB	3809	LEU	CA-CB-CG	5.21	134.54	116.30
8	GB	30	GLU	N-CA-CB	-5.21	108.23	114.17
15	ND	1550	MET	CA-CB-CG	5.20	124.51	114.10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	AB	113	LEU	CA-CB-CG	5.20	134.51	116.30
1	AE	237	VAL	CA-C-N	5.20	131.76	122.09
1	AE	237	VAL	C-N-CA	5.20	131.76	122.09
15	NC	891	TRP	CA-C-N	5.20	131.46	121.54
15	NC	891	TRP	C-N-CA	5.20	131.46	121.54
1	AH	264	ARG	N-CA-C	-5.19	107.97	114.56
15	ND	1550	MET	CB-CA-C	-5.19	101.09	110.23
6	FD	913	LEU	N-CA-C	-5.19	106.35	113.30
9	HA	760	LYS	N-CA-C	-5.17	105.08	111.33
12	KA	282	LYS	CA-CB-CG	5.15	124.41	114.10
2	AB	541	PRO	CA-C-N	5.14	131.35	121.54
2	AB	541	PRO	C-N-CA	5.14	131.35	121.54
11	JB	931	LYS	CB-CG-CD	5.13	123.10	111.30
5	EB	4892	ARG	N-CA-C	-5.12	107.19	112.93
10	IC	778	GLN	CA-CB-CG	5.11	124.32	114.10
5	EC	4718	THR	CA-C-N	5.10	129.37	122.07
5	EC	4718	THR	C-N-CA	5.10	129.37	122.07
6	FD	1005	PRO	CB-CA-C	5.10	117.14	110.92
3	CC	724	GLN	CB-CG-CD	5.10	121.27	112.60
2	AF	376	ARG	CB-CG-CD	-5.10	99.58	111.30
15	NA	469	PHE	N-CA-C	5.10	121.66	110.80
1	AI	816	ARG	CA-CB-CG	5.09	124.29	114.10
10	IB	321	ASP	CB-CA-C	-5.09	110.68	116.54
15	NB	1421	ALA	CA-C-N	5.09	131.13	121.97
15	NB	1421	ALA	C-N-CA	5.09	131.13	121.97
1	AI	343	SER	CA-C-N	5.07	134.18	121.80
1	AI	343	SER	C-N-CA	5.07	134.18	121.80
4	DE	85	VAL	N-CA-C	-5.07	107.40	111.91
6	FE	1118	GLN	N-CA-C	-5.06	107.78	114.31
1	AA	259	ASP	CB-CA-C	-5.06	110.72	116.54
5	EA	4718	THR	CA-C-N	5.06	131.20	121.54
5	EA	4718	THR	C-N-CA	5.06	131.20	121.54
8	GH	56	CYS	CA-CB-SG	5.06	126.04	114.40
14	ME	259	MET	CB-CG-SD	5.05	127.84	112.70
13	LI	423	GLN	CA-CB-CG	5.05	124.19	114.10
12	KA	304	ARG	CA-C-N	5.04	131.17	121.54
12	KA	304	ARG	C-N-CA	5.04	131.17	121.54
19	RD	142	ASN	CB-CA-C	-5.04	100.39	110.42
1	AE	898	PRO	N-CA-C	5.04	122.84	112.47
13	LE	471	THR	CA-C-O	5.04	125.52	119.43
16	OC	1075	TYR	CA-C-N	5.04	131.03	121.97
16	OC	1075	TYR	C-N-CA	5.04	131.03	121.97

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	JB	741	PHE	CA-C-N	5.03	131.02	121.97
11	JB	741	PHE	C-N-CA	5.03	131.02	121.97
15	ND	903	CYS	N-CA-C	5.03	114.67	108.19
7	GA	542	GLY	N-CA-C	5.02	125.08	113.18
8	GD	372	VAL	N-CA-C	-5.02	107.94	112.96
9	HA	551	GLU	N-CA-C	5.02	116.47	110.44
8	GB	525	THR	CA-C-N	5.02	131.00	121.97
8	GB	525	THR	C-N-CA	5.02	131.00	121.97
9	HA	653	ILE	CG1-CB-CG2	-5.00	95.69	110.70
9	HB	551	GLU	CA-C-N	5.00	130.48	122.93
9	HB	551	GLU	C-N-CA	5.00	130.48	122.93
11	JC	1850	THR	N-CA-C	5.00	116.54	111.14
14	ME	284	LEU	CA-CB-CG	5.00	133.80	116.30

There are no chirality outliers.

All (325) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	136	PHE	Peptide
1	AA	715	LEU	Peptide
1	AA	897	PRO	Peptide
2	AB	207	GLU	Peptide
2	AB	295	PHE	Peptide
2	AB	419	LYS	Mainchain
2	AC	517	ARG	Sidechain
1	AE	1025	ARG	Sidechain
1	AE	136	PHE	Peptide
1	AE	274	ARG	Peptide
1	AE	715	LEU	Peptide
1	AE	897	PRO	Peptide
1	AI	136	PHE	Peptide
1	AI	245	PRO	Peptide
1	AI	897	PRO	Peptide
2	AK	24	ASP	Peptide
1	AL	1028	ARG	Sidechain
1	AL	886	ARG	Sidechain
3	BC	691	LEU	Peptide
3	CB	772	GLY	Peptide
3	CC	772	GLY	Peptide
3	CF	4450	PRO	Peptide
3	CF	4487	LEU	Peptide
3	CG	4450	PRO	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
3	CL	4476	ASP	Peptide
4	DC	175	TYR	Peptide
4	DD	19	ARG	Sidechain
5	EA	3419	ARG	Sidechain
5	EA	3514	GLU	Peptide
5	EA	3705	ASP	Peptide
5	EA	3855	LEU	Peptide
5	EA	4013	THR	Peptide
5	EB	3514	GLU	Peptide
5	EB	3855	LEU	Peptide
5	EB	4881	ARG	Sidechain
5	EB	4882	ARG	Sidechain
5	EB	4892	ARG	Sidechain
5	EB	4896	ARG	Sidechain
5	EC	3855	LEU	Peptide
5	EC	4096	ARG	Sidechain
5	EC	4881	ARG	Sidechain
5	EC	4882	ARG	Sidechain
5	EC	4892	ARG	Sidechain
5	EC	4896	ARG	Sidechain
5	EC	4900	ARG	Sidechain
6	FA	1716	SER	Peptide
6	FA	2012	ARG	Sidechain
6	FA	2016	ARG	Sidechain
6	FA	2017	ARG	Sidechain
6	FA	2018	ARG	Sidechain
6	FA	2024	ARG	Sidechain
6	FA	2034	ARG	Sidechain
6	FA	2061	ARG	Sidechain
6	FB	1716	SER	Peptide
6	FB	2034	ARG	Sidechain
6	FB	2047	ARG	Sidechain
6	FC	1716	SER	Peptide
6	FC	1983	ARG	Sidechain
6	FC	1988	ARG	Sidechain
6	FC	1994	ARG	Sidechain
6	FC	2012	ARG	Sidechain
6	FC	2016	ARG	Sidechain
6	FC	2018	ARG	Sidechain
6	FC	2024	ARG	Sidechain
6	FC	2034	ARG	Sidechain
6	FC	2039	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
6	FC	2047	ARG	Sidechain
6	FC	2071	ARG	Sidechain
6	FC	2081	ARG	Sidechain
6	FD	1008	ARG	Sidechain
6	FD	1069	ARG	Sidechain
6	FD	1072	ARG	Sidechain
6	FD	1077	ARG	Sidechain
6	FD	1084	ARG	Sidechain
6	FD	1089	ARG	Sidechain
6	FD	1190	ARG	Sidechain
6	FD	1203	ARG	Sidechain
6	FD	1220	ARG	Sidechain
6	FD	1227	ARG	Sidechain
6	FD	1228	ARG	Sidechain
6	FD	1231	ARG	Sidechain
6	FD	1238	ARG	Sidechain
6	FD	1251	ARG	Sidechain
6	FD	1265	ARG	Sidechain
6	FD	1389	ARG	Sidechain
6	FD	1420	ARG	Sidechain
6	FD	1444	ARG	Sidechain
6	FD	803	ARG	Sidechain
6	FD	821	ARG	Sidechain
6	FD	829	ARG	Sidechain
6	FD	831	ARG	Sidechain
6	FD	879	ARG	Sidechain
6	FD	887	ARG	Sidechain
6	FD	891	ARG	Sidechain
6	FD	920	ARG	Sidechain
6	FE	1008	ARG	Sidechain
6	FE	1010	ARG	Sidechain
6	FE	1069	ARG	Sidechain
6	FE	1072	ARG	Sidechain
6	FE	1077	ARG	Sidechain
6	FE	1089	ARG	Sidechain
6	FE	1105	ARG	Sidechain
6	FE	1220	ARG	Sidechain
6	FE	1227	ARG	Sidechain
6	FE	1231	ARG	Sidechain
6	FE	1238	ARG	Sidechain
6	FE	1251	ARG	Sidechain
6	FE	1265	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
6	FE	1389	ARG	Sidechain
6	FE	1444	ARG	Sidechain
6	FE	803	ARG	Sidechain
6	FE	821	ARG	Sidechain
6	FE	829	ARG	Sidechain
6	FE	879	ARG	Sidechain
6	FE	887	ARG	Sidechain
6	FE	920	ARG	Sidechain
6	FE	991	ARG	Sidechain
6	FF	1008	ARG	Sidechain
6	FF	1010	ARG	Sidechain
6	FF	1072	ARG	Sidechain
6	FF	1077	ARG	Sidechain
6	FF	1084	ARG	Sidechain
6	FF	1089	ARG	Sidechain
6	FF	1105	ARG	Sidechain
6	FF	1190	ARG	Sidechain
6	FF	1203	ARG	Sidechain
6	FF	1220	ARG	Sidechain
6	FF	1227	ARG	Sidechain
6	FF	1228	ARG	Sidechain
6	FF	1231	ARG	Sidechain
6	FF	1238	ARG	Sidechain
6	FF	1251	ARG	Sidechain
6	FF	1265	ARG	Sidechain
6	FF	1389	ARG	Sidechain
6	FF	1394	ARG	Sidechain
6	FF	803	ARG	Sidechain
6	FF	821	ARG	Sidechain
6	FF	829	ARG	Sidechain
6	FF	831	ARG	Sidechain
6	FF	879	ARG	Sidechain
6	FF	887	ARG	Sidechain
6	FF	891	ARG	Sidechain
6	FF	920	ARG	Sidechain
7	GA	350	ARG	Peptide
7	GA	537	GLY	Peptide
7	GA	538	THR	Peptide
7	GA	541	GLY	Peptide
7	GA	544	PRO	Peptide
7	GA	856	VAL	Peptide
8	GB	112	ILE	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
8	GB	525	THR	Peptide
8	GB	717	PHE	Peptide
8	GB	764	ALA	Peptide
7	GC	381	ARG	Peptide
8	GD	112	ILE	Peptide
8	GD	525	THR	Peptide
8	GD	526	ILE	Peptide
8	GD	717	PHE	Peptide
7	GE	276	ARG	Sidechain
8	GF	760	GLY	Peptide
7	GG	350	ARG	Peptide
7	GG	537	GLY	Peptide
7	GG	538	THR	Peptide
7	GG	541	GLY	Peptide
7	GG	542	GLY	Peptide
7	GG	544	PRO	Peptide
7	GG	855	ARG	Peptide
7	GG	856	VAL	Peptide
8	GH	112	ILE	Peptide
8	GH	396	ILE	Peptide
8	GH	717	PHE	Peptide
8	GH	759	MET	Peptide
8	GH	760	GLY	Peptide
8	GH	764	ALA	Peptide
7	GI	397	LEU	Peptide
8	GJ	333	LYS	Peptide
8	GJ	60	GLY	Peptide
8	GJ	61	CYS	Peptide
8	GJ	760	GLY	Peptide
7	GK	350	ARG	Peptide
7	GK	396	PRO	Peptide
7	GK	537	GLY	Peptide
7	GK	538	THR	Peptide
7	GK	542	GLY	Peptide
7	GK	544	PRO	Peptide
7	GK	856	VAL	Peptide
8	GL	333	LYS	Peptide
8	GL	660	LYS	Peptide
8	GL	760	GLY	Peptide
8	GL	83	GLN	Peptide
9	HA	552	ASP	Peptide
9	HA	564	ARG	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
9	HA	565	PRO	Peptide
9	HA	792	ARG	Sidechain
9	HA	810	ARG	Sidechain
9	HA	826	ARG	Sidechain
9	HA	855	ARG	Sidechain
9	HA	857	ARG	Sidechain
9	HB	552	ASP	Peptide
9	HB	565	PRO	Peptide
9	HB	792	ARG	Sidechain
9	HB	810	ARG	Sidechain
9	HB	826	ARG	Sidechain
9	HB	855	ARG	Sidechain
9	HB	857	ARG	Sidechain
9	HC	552	ASP	Peptide
9	HC	564	ARG	Peptide
9	HD	792	ARG	Sidechain
9	HD	810	ARG	Sidechain
9	HD	826	ARG	Sidechain
9	HD	855	ARG	Sidechain
9	HD	857	ARG	Sidechain
10	IA	312	ARG	Peptide
10	IA	776	PRO	Peptide
10	IB	381	HIS	Peptide
10	IC	776	PRO	Peptide
11	JA	1012	ARG	Sidechain
11	JA	1450	SER	Peptide
11	JA	146	TYR	Peptide
11	JA	170	ILE	Peptide
11	JA	172	LEU	Peptide
11	JA	184	LEU	Peptide
11	JA	2248	ILE	Peptide
11	JA	2251	PRO	Peptide
11	JA	435	VAL	Peptide
11	JA	481	SER	Peptide
11	JB	146	TYR	Peptide
11	JB	170	ILE	Peptide
11	JB	184	LEU	Peptide
11	JB	2251	PRO	Peptide
11	JB	435	VAL	Peptide
11	JB	481	SER	Peptide
11	JB	482	ARG	Peptide
11	JC	1450	SER	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
11	JC	146	TYR	Peptide
11	JC	1680	ARG	Sidechain
11	JC	170	ILE	Peptide
11	JC	184	LEU	Peptide
11	JC	2251	PRO	Peptide
11	JC	433	CYS	Peptide
11	JC	435	VAL	Peptide
11	JC	481	SER	Peptide
11	JC	482	ARG	Peptide
12	KA	344	ILE	Peptide
12	KA	524	PHE	Peptide
12	KA	606	ARG	Sidechain
12	KA	626	GLU	Peptide
12	KA	727	ILE	Peptide
12	KB	234	PRO	Peptide
12	KB	321	GLU	Peptide
12	KB	374	ALA	Peptide
12	KB	642	ARG	Peptide
12	KC	317	ALA	Peptide
12	KC	342	MET	Peptide
12	KC	500	PRO	Peptide
12	KC	509	ALA	Peptide
12	KC	578	ALA	Peptide
12	KE	721	GLN	Peptide
12	KF	721	GLN	Peptide
12	KG	304	ARG	Peptide
12	KG	721	GLN	Peptide
13	LE	460	ARG	Sidechain
13	LE	464	ASP	Peptide
13	LE	475	LEU	Peptide
13	LE	476	GLY	Peptide
13	LF	521	ASN	Peptide
13	LI	475	LEU	Peptide
13	LI	476	GLY	Peptide
13	LI	522	ARG	Sidechain
13	LJ	514	TYR	Peptide
13	LJ	521	ASN	Peptide
13	LO	413	GLU	Peptide
14	MC	173	PHE	Peptide
14	ME	223	ARG	Sidechain
14	ME	282	THR	Peptide
14	ME	283	GLN	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
14	MG	173	PHE	Peptide
14	MI	223	ARG	Sidechain
14	MI	268	TYR	Peptide
14	MJ	283	GLN	Peptide
14	MJ	290	ARG	Peptide
14	MK	173	PHE	Peptide
15	NA	468	ARG	Peptide
15	NA	470	ALA	Peptide
15	NA	708	LEU	Peptide
15	NA	901	LEU	Peptide
15	NA	902	ARG	Peptide
15	NB	468	ARG	Peptide
15	NB	470	ALA	Peptide
15	NB	901	LEU	Peptide
15	NB	902	ARG	Peptide
15	NB	937	MET	Peptide
15	NC	1156	LEU	Peptide
15	NC	1407	MET	Peptide
15	NC	1550	MET	Peptide
15	NC	468	ARG	Peptide
15	NC	470	ALA	Peptide
15	NC	537	LYS	Peptide
15	NC	885	LEU	Peptide
15	NC	890	ARG	Sidechain
15	NC	901	LEU	Peptide
15	NC	902	ARG	Peptide
15	ND	1153	ALA	Peptide
15	ND	1407	MET	Peptide
15	ND	1551	HIS	Peptide
15	ND	468	ARG	Peptide
15	ND	470	ALA	Peptide
15	ND	565	TRP	Peptide
15	ND	902	ARG	Peptide
16	OA	1089	LEU	Peptide
16	OA	1095	ARG	Peptide
16	OA	939	MET	Peptide
16	OB	1089	LEU	Peptide
16	OB	883	PRO	Peptide
16	OC	1089	LEU	Peptide
17	PB	140	ARG	Peptide
18	QB	60	ARG	Sidechain
18	QC	60	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
19	RA	20	PRO	Peptide
19	RB	63	GLU	Peptide
19	RD	140	GLY	Peptide
19	RD	141	LEU	Peptide,Mainchain
19	RD	142	ASN	Peptide
20	SB	44	PRO	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	6540	0	6548	95	0
1	AD	6810	0	6785	85	0
1	AE	6540	0	6548	107	0
1	AH	6810	0	6785	81	0
1	AI	6540	0	6548	91	0
1	AL	6810	0	6785	84	0
2	AB	3821	0	3771	71	0
2	AC	3847	0	3808	65	0
2	AF	3821	0	3771	61	0
2	AG	3847	0	3808	61	0
2	AJ	3815	0	3760	43	0
2	AK	3847	0	3808	56	0
3	BA	2727	0	2744	42	0
3	BB	2727	0	2744	37	0
3	BC	2727	0	2744	33	0
3	CA	2712	0	2724	24	0
3	CB	2712	0	2724	29	0
3	CC	2712	0	2724	30	0
3	CE	1874	0	1903	32	0
3	CF	1874	0	1903	29	0
3	CG	1874	0	1903	33	0
3	CI	2012	0	2046	31	0
3	CJ	2012	0	2046	40	0
3	CL	2012	0	2046	32	0
4	DA	2753	0	2847	60	0
4	DB	2753	0	2847	57	0
4	DC	2753	0	2847	58	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	DD	2631	0	2743	40	0
4	DE	2631	0	2743	45	0
4	DF	2631	0	2743	39	0
5	EA	10670	0	10838	157	0
5	EB	10670	0	10838	169	0
5	EC	10666	0	10827	146	0
6	FA	4210	0	4162	97	0
6	FB	4210	0	4162	72	0
6	FC	4210	0	4162	136	0
6	FD	3255	0	3343	295	0
6	FE	3261	0	3354	271	0
6	FF	3182	0	3272	236	0
7	GA	6320	0	6301	101	0
7	GC	5960	0	5962	130	0
7	GE	5960	0	5962	113	0
7	GG	6320	0	6301	102	0
7	GI	5960	0	5962	123	0
7	GK	6320	0	6301	78	0
8	GB	5949	0	5884	85	0
8	GD	5949	0	5884	84	0
8	GF	6155	0	6082	83	0
8	GH	5781	0	5723	114	0
8	GJ	6155	0	6081	68	0
8	GL	6155	0	6082	97	0
9	HA	3361	0	3225	143	0
9	HB	3361	0	3225	153	0
9	HC	2288	0	2172	45	0
9	HD	1073	0	1053	59	0
10	IA	9113	0	9248	120	0
10	IB	9113	0	9248	139	0
10	IC	9113	0	9248	134	0
11	JA	12718	0	12853	190	0
11	JB	12718	0	12853	168	0
11	JC	12718	0	12853	201	0
12	KA	3674	0	3771	97	0
12	KB	3674	0	3771	73	0
12	KC	3668	0	3760	101	0
12	KE	3544	0	3640	55	0
12	KF	3544	0	3640	53	0
12	KG	3544	0	3640	41	0
13	LA	1516	0	1551	30	0
13	LB	1529	0	1573	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	LC	1312	0	1352	6	0
13	LD	1304	0	1350	9	0
13	LE	1190	0	1235	34	0
13	LF	1198	0	1247	19	0
13	LG	461	0	486	2	0
13	LH	448	0	475	8	0
13	LI	1516	0	1551	35	0
13	LJ	1529	0	1573	43	0
13	LK	1320	0	1363	16	0
13	LL	1304	0	1350	18	0
13	LM	859	0	877	10	0
13	LN	856	0	875	10	0
13	LO	841	0	850	11	0
13	LP	882	0	901	10	0
14	MA	1132	0	1134	24	0
14	MB	976	0	982	15	0
14	MC	594	0	593	6	0
14	MD	521	0	517	7	0
14	ME	1132	0	1134	27	0
14	MF	976	0	982	23	0
14	MG	594	0	593	7	0
14	MH	521	0	517	4	0
14	MI	1132	0	1135	22	0
14	MJ	976	0	983	28	0
14	MK	594	0	593	5	0
14	ML	521	0	517	7	0
15	NA	7263	0	7230	177	0
15	NB	7263	0	7230	161	0
15	NC	7263	0	7230	190	0
15	ND	7263	0	7230	155	0
16	OA	3510	0	3532	55	0
16	OB	3510	0	3532	59	0
16	OC	3510	0	3532	50	0
17	PA	807	0	769	23	0
17	PB	807	0	769	18	0
17	PC	807	0	769	21	0
18	QA	1129	0	1127	12	0
18	QB	1129	0	1127	18	0
18	QC	1129	0	1127	16	0
18	QD	1129	0	1127	19	0
19	RA	1143	0	1133	33	0
19	RB	1143	0	1133	16	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	RC	1143	0	1133	19	0
19	RD	1143	0	1133	27	0
20	SA	1134	0	1074	12	0
20	SB	1134	0	1074	14	0
20	SC	1134	0	1074	12	0
20	SD	1134	0	1074	11	0
All	All	415078	0	416877	6651	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (6651) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FD:1002:ALA:HB3	6:FD:1010:ARG:NH1	1.37	1.36
6:FD:803:ARG:CG	6:FD:1118:GLN:HG3	1.76	1.14
6:FD:1002:ALA:CB	6:FD:1010:ARG:HH11	1.60	1.14
9:HB:776:PRO:HA	13:LE:521:ASN:HD21	1.09	1.13
6:FD:803:ARG:HG2	6:FD:1118:GLN:HE21	1.10	1.11
6:FD:803:ARG:HG3	6:FD:1118:GLN:CG	1.79	1.11
6:FF:1425:PRO:HD2	6:FF:1429:LEU:HD12	1.18	1.11
6:FD:861:LEU:H	6:FD:861:LEU:CD2	1.67	1.05
6:FF:1425:PRO:CD	6:FF:1429:LEU:HD12	1.86	1.05
6:FD:861:LEU:H	6:FD:861:LEU:HD23	0.90	1.04
6:FC:2030:ILE:HD11	9:HB:813:THR:HG22	1.42	1.01
6:FD:861:LEU:HD23	6:FD:861:LEU:N	1.74	1.00
15:ND:892:TRP:H	15:ND:1154:ASP:H	1.02	1.00
6:FE:1424:CYS:HB2	6:FE:1425:PRO:HD3	1.44	1.00
6:FD:1424:CYS:HB2	6:FD:1425:PRO:HD3	1.43	1.00
6:FE:993:ALA:HB3	12:KB:229:SER:HB3	1.45	0.98
9:HB:808:HIS:O	9:HB:812:THR:HG23	1.65	0.97
6:FE:992:PRO:HB3	12:KB:231:PHE:CE1	2.02	0.95
15:NC:892:TRP:H	15:NC:1154:ASP:H	0.99	0.94
6:FD:895:ILE:HG21	7:GC:967:PHE:HZ	1.32	0.93
6:FF:1098:VAL:HA	6:FF:1101:ALA:HB3	1.50	0.93
6:FD:803:ARG:HG2	6:FD:1118:GLN:NE2	1.83	0.92
6:FD:1098:VAL:HA	6:FD:1101:ALA:HB3	1.52	0.92
6:FE:983:LEU:HB3	12:KB:725:ILE:HD11	1.50	0.92
6:FF:983:LEU:HD21	12:KC:656:ARG:HD2	1.52	0.92
6:FC:2083:GLN:HA	6:FC:2087:LEU:HB2	1.52	0.91
6:FF:1425:PRO:HD2	6:FF:1429:LEU:CD1	2.01	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1187:ILE:HG23	6:FE:1419:LEU:HD13	1.54	0.90
8:GF:61:CYS:HG	8:GF:80:PHE:HD2	1.11	0.90
6:FD:981:HIS:HA	12:KA:656:ARG:HH22	1.36	0.90
15:NA:892:TRP:H	15:NA:1154:ASP:H	0.92	0.90
9:HB:776:PRO:HA	13:LE:521:ASN:ND2	1.87	0.90
16:OC:882:ARG:HE	16:OC:885:GLN:HE21	1.18	0.89
9:HB:776:PRO:CA	13:LE:521:ASN:HD21	1.84	0.89
6:FE:884:VAL:HG21	6:FE:902:VAL:HA	1.51	0.89
9:HA:795:LEU:HD13	9:HA:797:TYR:CE2	2.07	0.88
9:HB:795:LEU:HD13	9:HB:797:TYR:CE2	2.07	0.88
6:FC:2024:ARG:HA	9:HB:778:PRO:HG2	1.54	0.88
6:FD:803:ARG:HG3	6:FD:1118:GLN:HG3	0.90	0.87
6:FA:2095:GLN:HE22	9:HA:875:THR:HG21	1.39	0.87
6:FF:1103:SER:HB2	9:HC:393:VAL:HG21	1.56	0.87
6:FE:1182:ALA:HB2	6:FE:1429:LEU:HB2	1.53	0.87
6:FD:1182:ALA:HB2	6:FD:1429:LEU:HB2	1.56	0.87
15:NA:892:TRP:H	15:NA:1154:ASP:N	1.73	0.86
6:FA:2024:ARG:HA	9:HA:778:PRO:HG2	1.57	0.86
12:KF:365:GLU:HB3	12:KF:697:ARG:HH22	1.40	0.86
6:FD:884:VAL:HG21	6:FD:902:VAL:HA	1.57	0.85
6:FD:888:PRO:HG2	7:GC:897:SER:HB3	1.58	0.85
6:FF:884:VAL:HG21	6:FF:902:VAL:HA	1.59	0.85
15:ND:881:LEU:HA	15:ND:884:LYS:HB2	1.58	0.85
6:FF:1182:ALA:HB2	6:FF:1429:LEU:HB2	1.57	0.85
8:GF:61:CYS:SG	8:GF:80:PHE:CD2	2.70	0.85
15:NB:892:TRP:H	15:NB:1154:ASP:N	1.73	0.85
15:NB:892:TRP:N	15:NB:1154:ASP:H	1.73	0.84
6:FF:803:ARG:HG3	6:FF:1118:GLN:HG3	1.59	0.84
8:GF:61:CYS:SG	8:GF:80:PHE:HD2	2.00	0.84
15:NB:892:TRP:H	15:NB:1154:ASP:H	0.87	0.84
6:FE:992:PRO:HA	12:KB:230:GLN:O	1.76	0.84
12:KC:234:PRO:HD2	12:KC:235:PRO:HD2	1.59	0.84
15:NA:892:TRP:N	15:NA:1154:ASP:H	1.76	0.83
1:AL:968:ASN:HB2	1:AL:971:GLU:HG2	1.61	0.82
15:NC:892:TRP:H	15:NC:1154:ASP:N	1.74	0.82
6:FD:1211:SER:HA	6:FD:1234:THR:HA	1.61	0.82
6:FA:2075:GLU:HB3	9:HA:858:LEU:HD11	1.62	0.81
6:FE:1098:VAL:HA	6:FE:1101:ALA:HB3	1.61	0.80
6:FE:893:GLY:HA2	7:GE:873:ALA:O	1.80	0.80
6:FE:1388:PHE:HB2	6:FE:1418:GLU:HB3	1.63	0.80
2:AB:415:HIS:HB2	6:FC:2077:HIS:HB2	1.61	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:SA:83:GLU:HG2	20:SA:147:MET:HG3	1.63	0.80
6:FE:846:CYS:HB3	12:KB:305:HIS:CE1	2.16	0.80
11:JA:1581:ARG:HH22	15:NC:354:PHE:HB3	1.47	0.79
8:GL:519:ARG:HH21	8:GL:520:PHE:HB2	1.48	0.79
2:AB:412:ALA:HB2	6:FC:2074:ALA:HB2	1.64	0.79
6:FF:822:GLY:HA2	7:GI:976:PRO:HB3	1.63	0.79
5:EB:4405:ILE:HG13	5:EB:4428:MET:HE1	1.63	0.79
6:FD:981:HIS:HA	12:KA:656:ARG:NH2	1.98	0.79
6:FA:2079:MET:CE	9:HA:865:ILE:HG12	2.13	0.79
14:MI:285:ARG:HH12	14:MJ:257:LYS:HA	1.44	0.79
2:AG:558:ARG:HD3	11:JC:1116:ARG:HH12	1.48	0.78
3:CF:1132:MET:HG2	10:IB:1237:GLN:HE21	1.48	0.78
7:GC:584:HIS:HA	7:GC:952:ARG:HH22	1.48	0.78
10:IA:943:ASN:HD22	16:OA:1034:PRO:HG3	1.48	0.78
7:GG:546:SER:HB3	9:HA:496:GLU:HA	1.64	0.78
2:AB:113:LEU:HD12	2:AB:208:GLU:HG2	1.63	0.77
8:GD:526:ILE:HG13	14:MA:324:ARG:HH22	1.48	0.77
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CD2	2.37	0.77
5:EA:4760:ARG:HH12	11:JA:743:PHE:HA	1.48	0.77
7:GK:546:SER:HB3	9:HC:496:GLU:HA	1.65	0.77
15:NC:892:TRP:N	15:NC:1154:ASP:H	1.78	0.77
6:FF:1190:ARG:HB2	6:FF:1418:GLU:HB2	1.67	0.77
7:GE:240:PRO:HA	7:GE:285:LEU:HD13	1.67	0.77
15:ND:894:LEU:HD23	15:ND:1153:ALA:HB3	1.65	0.77
5:EA:4167:ASP:HB3	5:EA:4170:LYS:HB2	1.66	0.76
6:FD:1187:ILE:HG23	6:FD:1419:LEU:HD13	1.65	0.76
6:FD:895:ILE:HG21	7:GC:967:PHE:CZ	2.17	0.76
10:IA:580:LEU:HB3	10:IA:603:ARG:HH12	1.51	0.76
6:FC:1978:LEU:HD11	9:HB:817:VAL:HG22	1.65	0.76
6:FA:2095:GLN:NE2	9:HA:875:THR:HG21	2.00	0.76
15:NC:1328:VAL:HG13	15:NC:1332:MET:HE2	1.68	0.76
12:KB:573:ARG:HH22	12:KB:704:PRO:HG3	1.51	0.76
3:BC:689:LEU:HG	17:PC:258:PRO:HG2	1.66	0.76
6:FD:1002:ALA:CB	6:FD:1010:ARG:NH1	2.32	0.76
11:JC:1852:HIS:HD2	11:JC:1985:LEU:HG	1.50	0.75
15:ND:892:TRP:H	15:ND:1154:ASP:N	1.82	0.75
6:FE:888:PRO:HG2	7:GE:897:SER:HB3	1.69	0.75
7:GA:864:ILE:HG22	7:GA:866:PRO:HD3	1.68	0.75
15:NC:686:ASN:HD22	15:NC:905:ASP:HB3	1.50	0.75
6:FF:988:SER:HB3	12:KC:313:PHE:CZ	2.21	0.75
12:KG:368:ARG:HD2	12:KG:397:GLN:HE22	1.51	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:892:TRP:HB3	15:NC:1154:ASP:HB2	1.68	0.75
7:GC:878:GLN:HE21	7:GC:896:ARG:HG2	1.52	0.74
7:GA:211:ARG:HE	7:GA:212:PRO:HD2	1.52	0.74
7:GG:541:GLY:H	9:HA:579:LEU:HD21	1.52	0.74
15:NB:881:LEU:HA	15:NB:884:LYS:HB2	1.68	0.74
15:ND:1550:MET:H	19:RD:142:ASN:HB3	1.52	0.74
1:AD:233:VAL:HB	10:IB:1271:TYR:HB2	1.69	0.74
6:FF:918:GLN:HB3	6:FF:922:LEU:HG	1.70	0.74
7:GK:678:LEU:HB3	7:GK:690:ARG:HB3	1.69	0.74
15:ND:892:TRP:N	15:ND:1154:ASP:H	1.83	0.74
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CE3	2.40	0.74
1:AD:310:CYS:H	1:AD:313:CYS:HB2	1.53	0.74
6:FF:925:GLU:HG2	6:FF:1092:PRO:HB2	1.70	0.74
6:FE:1391:TYR:HB2	6:FE:1417:ILE:HG23	1.69	0.73
4:DB:329:ARG:HH12	8:GL:48:LEU:HD22	1.53	0.73
6:FF:1441:ILE:HB	6:FF:1444:ARG:HB2	1.69	0.73
8:GD:294:TRP:HB3	8:GD:297:LEU:HB2	1.70	0.73
12:KE:404:GLU:HB2	12:KE:489:MET:HE1	1.70	0.73
7:GG:275:LYS:HE3	7:GG:279:ARG:HH22	1.53	0.73
9:HA:781:PRO:HG3	13:LA:531:VAL:HG12	1.68	0.73
4:DC:267:ARG:HH22	14:MI:294:ALA:HA	1.54	0.73
3:CG:4488:MET:HE3	3:CG:4492:ASN:H	1.51	0.73
6:FD:1198:TYR:HA	6:FD:1257:ASP:HA	1.70	0.73
6:FF:1005:PRO:HB2	6:FF:1006:PRO:HD3	1.70	0.73
8:GD:746:ALA:HA	8:GJ:342:LYS:HE2	1.69	0.73
11:JA:1480:VAL:HG13	15:NC:440:LEU:HD12	1.71	0.73
1:AI:315:LEU:HD23	1:AI:316:ILE:HG12	1.70	0.73
3:CJ:4467:THR:HG23	3:CJ:4468:LYS:HG3	1.70	0.73
6:FD:980:SER:HA	12:KA:343:ASN:HB2	1.70	0.73
6:FD:999:PRO:CA	12:KA:229:SER:HA	2.18	0.73
10:IB:740:ARG:HH12	10:IB:777:GLY:HA3	1.54	0.73
20:SA:21:ASP:HA	20:SA:28:ILE:HD13	1.71	0.73
6:FD:803:ARG:CG	6:FD:1118:GLN:CG	2.52	0.73
7:GA:546:SER:HB3	9:HB:496:GLU:HA	1.68	0.73
15:NC:1407:MET:HG3	15:NC:1471:ARG:HG3	1.71	0.73
6:FF:1280:VAL:HG13	6:FF:1300:LEU:HD11	1.70	0.73
12:KC:383:HIS:HA	12:KC:386:LEU:HD23	1.70	0.73
1:AL:310:CYS:H	1:AL:313:CYS:HB2	1.54	0.72
6:FE:1283:TYR:HB3	6:FE:1290:ILE:HG23	1.70	0.72
15:NC:1102:VAL:HG22	15:NC:1111:ARG:HG2	1.71	0.72
1:AL:987:LEU:HD13	7:GK:424:ARG:HH22	1.53	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AK:427:ARG:HH21	1:AL:456:VAL:HG22	1.54	0.72
8:GH:665:LEU:HB2	8:GH:676:TRP:HB3	1.71	0.72
15:NB:696:PHE:HB2	15:NB:894:LEU:HD11	1.72	0.72
1:AE:442:HIS:HB2	2:AF:368:HIS:HB2	1.70	0.72
8:GJ:519:ARG:HH21	8:GJ:520:PHE:HB2	1.52	0.72
3:BB:982:ARG:HB3	3:BB:993:THR:HG22	1.71	0.72
3:BC:964:GLN:HE21	16:OC:127:ILE:HG21	1.52	0.72
4:DC:297:ARG:HE	4:DC:391:ILE:HD13	1.54	0.72
15:NA:881:LEU:HA	15:NA:884:LYS:HB2	1.71	0.72
11:JC:772:CYS:HB2	11:JC:793:MET:HB2	1.72	0.72
12:KA:415:LEU:HD11	12:KA:480:VAL:HG21	1.70	0.72
12:KC:231:PHE:CZ	12:KC:313:PHE:CG	2.78	0.72
2:AG:448:ASN:HD21	1:AH:472:LYS:HA	1.55	0.71
6:FE:962:PHE:CE2	6:FE:965:TRP:HB2	2.25	0.71
7:GI:570:GLY:HA2	7:GI:622:ARG:HB3	1.72	0.71
12:KC:304:ARG:HE	12:KC:305:HIS:H	1.38	0.71
5:EC:4405:ILE:HG23	5:EC:4411:THR:HG21	1.72	0.71
6:FE:1424:CYS:HB2	6:FE:1425:PRO:CD	2.20	0.71
6:FE:870:ALA:HB3	12:KB:235:PRO:HD2	1.73	0.71
6:FF:1112:ILE:HG13	6:FF:1114:VAL:HG22	1.71	0.71
12:KC:579:LEU:HD12	12:KC:654:ILE:HG21	1.72	0.71
3:BC:982:ARG:HB3	3:BC:993:THR:HG22	1.71	0.71
6:FD:888:PRO:HD3	12:KA:305:HIS:ND1	2.05	0.71
7:GC:988:LYS:HD2	9:HB:402:ARG:HE	1.54	0.71
15:ND:1512:MET:HA	15:ND:1515:LEU:HB2	1.71	0.71
4:DC:33:LEU:HB3	4:DC:103:LEU:HA	1.73	0.71
8:GJ:422:LYS:HB3	8:GJ:501:SER:HB3	1.73	0.71
10:IC:616:GLY:H	10:IC:758:ASN:HD21	1.36	0.71
6:FF:818:VAL:HG12	6:FF:819:PRO:HD2	1.73	0.71
17:PB:257:ASN:HB3	17:PB:260:SER:HB3	1.71	0.71
1:AL:376:LEU:HD11	11:JB:1639:GLU:HG3	1.72	0.70
6:FE:879:ARG:HE	6:FE:908:ILE:HG23	1.56	0.70
7:GA:185:ARG:HB2	7:GA:705:ILE:HG22	1.73	0.70
4:DB:277:ARG:HD3	4:DB:281:GLN:HE22	1.55	0.70
6:FA:2079:MET:HE1	9:HA:865:ILE:HG12	1.73	0.70
6:FF:852:VAL:HG12	6:FF:880:VAL:HG22	1.73	0.70
11:JA:791:MET:HG2	11:JA:809:ILE:HG12	1.73	0.70
5:EB:3873:LEU:HD21	5:EB:4205:ILE:HD11	1.72	0.70
6:FC:1677:PRO:HG3	6:FC:1696:HIS:HD2	1.55	0.70
8:GH:13:ARG:HE	8:GH:536:ALA:HB2	1.56	0.70
19:RD:138:ARG:HG3	19:RD:139:LEU:HD12	1.72	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FD:831:ARG:HG3	6:FD:979:LEU:HD21	1.73	0.70
6:FF:1424:CYS:HB2	6:FF:1425:PRO:HD3	1.73	0.70
12:KC:533:THR:HG22	12:KC:534:VAL:HG13	1.71	0.70
11:JA:1379:GLN:HE22	11:JA:1386:PHE:HB2	1.56	0.70
11:JC:523:ASN:HD21	11:JC:766:GLY:H	1.38	0.70
11:JA:882:ALA:HB3	11:JA:1416:ARG:HB3	1.74	0.70
15:ND:1548:PHE:H	19:RD:141:LEU:HD12	1.56	0.70
3:CF:1236:LEU:HD21	3:CF:1255:VAL:HG13	1.74	0.70
4:DC:250:ASP:HB2	4:DC:283:LEU:HD23	1.74	0.70
6:FC:2055:THR:HG22	9:HB:837:LEU:HD11	1.74	0.70
11:JC:489:VAL:HG13	11:JC:490:THR:HG23	1.74	0.70
6:FC:2085:GLU:O	6:FC:2089:PRO:HD2	1.91	0.70
6:FF:988:SER:HB3	12:KC:313:PHE:HZ	1.55	0.70
15:ND:1488:ARG:HH12	15:ND:1491:PRO:HD2	1.56	0.70
4:DA:248:ARG:HE	4:DA:290:ARG:HH12	1.40	0.69
10:IA:616:GLY:H	10:IA:758:ASN:HD21	1.39	0.69
3:CC:684:ARG:HD2	3:CC:713:LEU:HB3	1.74	0.69
4:DE:61:GLU:HA	4:DE:66:ARG:HH22	1.56	0.69
6:FE:1425:PRO:HD2	6:FE:1429:LEU:HD12	1.75	0.69
10:IC:609:GLU:HG2	10:IC:614:LEU:HG	1.74	0.69
4:DF:110:LEU:HD12	4:DF:111:PRO:HD2	1.75	0.69
9:HB:848:ASP:C	9:HB:848:ASP:OD1	2.36	0.69
4:DE:129:VAL:HG13	4:DE:154:LEU:HD21	1.75	0.69
9:HA:766:SER:O	9:HA:768:THR:N	2.26	0.69
10:IB:174:PHE:HB3	10:IB:205:GLN:HE21	1.58	0.69
10:IB:1064:GLN:HB3	10:IB:1068:ARG:HH12	1.57	0.69
15:NC:505:GLY:H	15:NC:512:TYR:HB2	1.57	0.69
7:GA:828:PRO:HG2	7:GA:831:ARG:HG2	1.74	0.69
8:GB:526:ILE:HB	14:ME:321:ALA:HB2	1.74	0.69
7:GG:539:TYR:HB2	9:HA:576:LYS:HG2	1.74	0.69
7:GG:670:ASN:HB3	7:GG:698:VAL:HB	1.75	0.69
7:GI:510:THR:HG23	7:GI:632:VAL:HG11	1.75	0.69
14:MI:244:VAL:HG13	14:MJ:243:LYS:HZ1	1.57	0.69
7:GG:808:PRO:HD2	7:GG:977:SER:HB2	1.75	0.69
10:IA:883:SER:HB3	16:OA:1045:LEU:HD11	1.74	0.69
6:FF:836:GLY:HA3	6:FF:840:ALA:HB3	1.73	0.69
11:JC:1489:LEU:HD11	15:NA:483:VAL:HG23	1.76	0.69
15:NA:614:LYS:HB3	15:NA:678:LEU:HD22	1.74	0.69
15:ND:1498:ARG:HE	20:SB:38:ARG:HD2	1.58	0.69
20:SB:42:GLN:HB2	20:SB:78:LYS:HB2	1.75	0.69
1:AL:988:GLN:HA	1:AL:991:LEU:HD23	1.75	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GB:326:ARG:HH12	8:GB:375:TYR:HB3	1.58	0.68
10:IA:165:ILE:HD11	10:IA:180:LEU:HD22	1.74	0.68
10:IB:616:GLY:H	10:IB:758:ASN:HD21	1.41	0.68
11:JB:192:LEU:HB3	11:JB:1063:ILE:HD13	1.74	0.68
5:EB:4307:MET:HE1	5:EB:4346:VAL:HG12	1.74	0.68
15:ND:679:ASP:HB2	15:ND:696:PHE:HB3	1.75	0.68
6:FF:923:ALA:HB1	6:FF:928:SER:HA	1.74	0.68
14:MJ:290:ARG:HA	14:MJ:293:LEU:HD23	1.74	0.68
6:FD:995:VAL:N	12:KA:385:GLU:OE2	2.24	0.68
9:HB:778:PRO:HB2	9:HB:779:PRO:HD3	1.75	0.68
1:AI:248:LEU:HB2	1:AI:258:CYS:HA	1.75	0.68
7:GG:353:SER:HB3	7:GG:406:ALA:HB2	1.74	0.68
8:GL:131:LEU:HD12	8:GL:132:PRO:HD2	1.74	0.68
11:JC:770:ASP:HB2	11:JC:795:ARG:HB2	1.75	0.68
15:NA:892:TRP:HB2	15:NA:1155:GLU:HB2	1.75	0.68
3:CA:867:THR:HA	3:CA:870:LEU:HD23	1.76	0.68
4:DE:254:GLU:HG2	4:DE:291:GLN:HE22	1.58	0.68
6:FE:971:SER:HB3	6:FE:1022:THR:HG23	1.76	0.68
6:FF:808:SER:HB3	6:FF:1113:PHE:HB2	1.73	0.68
8:GB:294:TRP:HB3	8:GB:297:LEU:HB2	1.76	0.68
7:GG:538:THR:HG23	9:HA:555:SER:HB3	1.75	0.68
12:KB:367:ILE:HD13	12:KB:393:LEU:HB2	1.76	0.68
6:FE:1005:PRO:HB2	6:FE:1006:PRO:HD3	1.76	0.68
6:FF:1188:GLU:HG3	6:FF:1267:GLN:HB3	1.73	0.68
9:HA:676:ALA:HB2	9:HA:682:ILE:HG12	1.74	0.68
11:JB:162:PRO:HD2	11:JB:169:PHE:HA	1.76	0.68
3:CE:1260:VAL:HG21	3:CE:4466:ILE:HD13	1.74	0.68
11:JA:1078:MET:HB2	11:JA:1509:HIS:HD2	1.58	0.68
12:KC:380:GLY:HA3	12:KC:723:GLU:O	1.94	0.68
1:AH:228:PRO:HG2	10:IA:1254:GLY:HA2	1.74	0.68
12:KC:273:ARG:HD2	12:KC:274:ASP:HB2	1.76	0.68
5:EA:4095:LYS:HB3	9:HB:796:ASP:OD1	1.94	0.67
8:GB:171:ILE:HG22	8:GB:183:LEU:HD21	1.76	0.67
7:GE:764:LEU:HD13	7:GE:870:ARG:HD2	1.75	0.67
12:KE:209:VAL:HG23	12:KE:280:LEU:HB2	1.75	0.67
1:AE:460:VAL:HG13	1:AE:465:MET:HE1	1.75	0.67
1:AH:990:LYS:HB3	7:GG:424:ARG:HH12	1.59	0.67
5:EC:3491:ALA:HB2	5:EC:3603:LEU:HD13	1.74	0.67
6:FD:1182:ALA:HB2	6:FD:1430:PHE:H	1.58	0.67
6:FD:1187:ILE:HG21	6:FD:1282:LEU:HD21	1.76	0.67
6:FE:1030:ILE:HG23	6:FE:1116:LEU:HD13	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:91:ILE:HB	2:AJ:528:LEU:HG	1.76	0.67
6:FC:1653:ARG:HD3	6:FC:1658:LEU:HD13	1.76	0.67
7:GG:543:LYS:H	9:HA:596:TYR:HB3	1.59	0.67
15:ND:895:GLY:HA2	15:ND:898:ASN:HB2	1.75	0.67
5:EC:3698:VAL:HG13	5:EC:4059:MET:HE1	1.75	0.67
6:FD:825:PRO:O	6:FD:826:LEU:C	2.36	0.67
8:GB:750:GLY:H	8:GF:334:ASP:HB2	1.60	0.67
7:GG:397:LEU:HD21	8:GJ:176:ALA:HB3	1.76	0.67
4:DF:104:GLU:HA	4:DF:260:GLY:HA3	1.77	0.67
6:FA:2098:TYR:CE2	9:HA:875:THR:HG22	2.29	0.67
3:CC:784:LEU:HD22	3:CC:826:LEU:HD13	1.76	0.67
6:FA:2009:SER:HA	6:FA:2012:ARG:HG2	1.76	0.67
6:FF:799:GLN:HB3	6:FF:911:SER:HA	1.77	0.67
11:JC:1572:LEU:HD13	11:JC:1604:HIS:HE1	1.60	0.67
16:OB:876:GLU:HB2	16:OB:939:MET:HG3	1.76	0.67
4:DB:18:GLU:HG2	14:ME:283:GLN:HE21	1.57	0.67
7:GC:614:TRP:HE1	7:GC:661:LEU:HD21	1.59	0.67
13:LN:350:LEU:HB3	13:LN:354:ARG:HH12	1.60	0.67
15:NC:680:LEU:HB3	15:NC:682:ARG:HH12	1.59	0.67
16:OC:191:PRO:HD3	16:OC:245:LEU:HD12	1.75	0.67
2:AC:514:ALA:HA	2:AC:517:ARG:HD2	1.77	0.67
4:DC:11:PHE:HE1	14:MJ:288:SER:HB3	1.59	0.67
6:FD:999:PRO:HA	12:KA:229:SER:HA	1.76	0.67
8:GF:61:CYS:HB2	8:GF:78:CYS:SG	2.35	0.67
12:KA:524:PHE:H	12:KA:525:PRO:HD3	1.58	0.67
6:FC:2048:GLU:HG2	9:HB:765:TRP:CD1	2.30	0.67
6:FF:834:VAL:HG12	6:FF:981:HIS:HB2	1.77	0.67
11:JB:774:LEU:HD21	11:JB:793:MET:HG3	1.77	0.67
11:JC:963:PHE:HB3	11:JC:966:LEU:HD21	1.77	0.67
12:KA:523:VAL:HG11	12:KA:573:ARG:HE	1.60	0.67
1:AE:248:LEU:HB2	1:AE:258:CYS:HA	1.76	0.66
3:BA:711:ARG:HH12	3:BA:756:GLU:HG2	1.60	0.66
3:BB:695:LEU:HD21	17:PB:290:PHE:HB3	1.77	0.66
6:FD:808:SER:O	6:FD:809:ILE:C	2.37	0.66
6:FF:1251:ARG:HE	11:JB:774:LEU:H	1.42	0.66
7:GA:353:SER:HB3	7:GA:406:ALA:HB2	1.76	0.66
8:GB:150:ASP:HA	8:GB:153:ARG:HD3	1.77	0.66
8:GJ:414:PHE:HB3	8:GJ:505:PRO:HB2	1.77	0.66
15:NC:787:LEU:HD22	15:NC:791:GLU:HG3	1.77	0.66
9:HA:758:ALA:HA	9:HA:761:CYS:SG	2.35	0.66
14:MI:302:GLU:HA	14:MI:305:LEU:HD23	1.77	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:301:VAL:HG23	1:AH:332:THR:HG22	1.77	0.66
4:DC:317:THR:H	14:MJ:246:ASN:HD21	1.43	0.66
6:FC:2009:SER:HA	6:FC:2012:ARG:HE	1.60	0.66
6:FF:819:PRO:HG3	6:FF:895:ILE:HD13	1.77	0.66
8:GL:422:LYS:HB3	8:GL:501:SER:HB3	1.76	0.66
10:IA:1094:ASN:HA	10:IA:1123:ASN:HD22	1.60	0.66
11:JA:124:VAL:HB	11:JA:132:ARG:HG3	1.77	0.66
1:AA:769:LEU:HD12	13:LL:375:ILE:HG12	1.78	0.66
5:EA:3491:ALA:HB2	5:EA:3603:LEU:HB3	1.77	0.66
6:FC:2059:VAL:HG22	9:HB:754:LEU:HB3	1.78	0.66
6:FD:842:GLY:HA2	7:GC:959:GLY:HA3	1.77	0.66
5:EC:3269:TRP:HD1	5:EC:3409:SER:HB3	1.60	0.66
9:HD:778:PRO:HB2	9:HD:779:PRO:HD3	1.76	0.66
11:JA:1220:LEU:HD23	11:JA:1283:ARG:HH21	1.59	0.66
11:JB:160:LEU:HB2	11:JB:171:LYS:HG2	1.78	0.66
4:DB:386:VAL:HG13	4:DB:387:ASP:H	1.60	0.66
5:EB:4728:HIS:HB2	5:EB:4817:LEU:HD13	1.78	0.66
8:GD:148:GLU:HB2	8:GD:394:PHE:HB2	1.77	0.66
9:HB:757:LEU:HD11	9:HB:833:VAL:HG13	1.78	0.66
15:NC:895:GLY:HA2	15:NC:898:ASN:HB2	1.77	0.66
1:AD:991:LEU:HD13	7:GA:424:ARG:HH12	1.60	0.66
3:CC:758:VAL:HG21	3:CC:812:MET:HE1	1.77	0.66
5:EC:4461:PHE:HB3	5:EC:4500:THR:HG22	1.76	0.66
6:FD:844:ALA:C	7:GC:896:ARG:HH12	2.04	0.66
6:FD:850:CYS:HB3	6:FD:973:ILE:HG12	1.77	0.66
6:FD:992:PRO:HD3	12:KA:313:PHE:CE1	2.31	0.66
8:GF:489:PRO:HD2	8:GF:492:LYS:HD2	1.78	0.66
1:AD:736:LEU:HD23	1:AD:738:GLY:H	1.59	0.66
1:AH:151:LEU:HD13	1:AH:210:LEU:HD21	1.78	0.66
5:EC:4446:ARG:HH12	17:PC:143:ILE:HD11	1.61	0.66
6:FD:1210:LEU:HD23	6:FD:1286:LEU:HD23	1.78	0.66
11:JB:1560:LEU:HD21	11:JB:1607:VAL:HG11	1.76	0.66
12:KB:685:ARG:HH11	12:KB:700:LEU:HD12	1.60	0.66
16:OC:731:ALA:HB2	20:SA:144:LYS:HE3	1.77	0.66
5:EA:4827:SER:HB3	11:JA:1343:GLU:HG2	1.78	0.66
5:EC:4405:ILE:CG2	5:EC:4427:LEU:HB3	2.25	0.66
6:FD:860:PRO:HG2	6:FD:861:LEU:CD2	2.26	0.66
6:FE:894:ALA:HB1	6:FE:897:LEU:HB2	1.78	0.66
10:IB:342:LEU:HD12	10:IB:343:PRO:HD2	1.78	0.66
15:NB:943:GLU:HA	15:NB:946:LEU:HG	1.76	0.66
1:AA:411:LEU:HB3	1:AA:458:VAL:HG11	1.78	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:52:TYR:HB2	2:AF:517:ARG:HE	1.59	0.66
9:HA:778:PRO:HB2	9:HA:779:PRO:HD3	1.78	0.66
15:NC:812:ARG:HE	15:NC:870:TYR:HB2	1.59	0.66
3:BA:791:THR:HG22	3:BA:811:ILE:HG13	1.78	0.65
5:EA:4071:LEU:HD13	5:EA:4218:GLN:HB3	1.77	0.65
6:FE:1203:ARG:HB2	11:JC:901:ARG:NH1	2.10	0.65
8:GD:132:PRO:HG3	8:GD:236:LEU:HG	1.77	0.65
7:GG:802:LYS:HB2	7:GG:971:MET:HE1	1.78	0.65
11:JA:57:GLU:HA	11:JA:90:ARG:HH21	1.61	0.65
11:JC:437:LEU:HB2	11:JC:1465:THR:HG21	1.78	0.65
15:NB:1102:VAL:HG22	15:NB:1111:ARG:HG2	1.77	0.65
3:BB:754:GLU:HA	17:PB:278:TRP:HH2	1.60	0.65
4:DC:180:LEU:HD12	4:DC:181:ILE:HG13	1.77	0.65
5:EB:3841:GLN:HG3	5:EB:3854:GLN:HE22	1.60	0.65
5:EB:4167:ASP:HB2	5:EB:4171:ILE:HG12	1.78	0.65
5:EC:3652:PRO:HG3	9:HA:500:LEU:HB2	1.77	0.65
6:FF:1300:LEU:O	6:FF:1301:ALA:C	2.38	0.65
7:GE:374:ALA:HB2	7:GE:380:ARG:HE	1.60	0.65
11:JB:1324:ASP:HA	11:JB:1327:LEU:HD12	1.78	0.65
15:NB:964:GLU:HG3	15:NB:1467:LEU:HG	1.79	0.65
6:FA:1612:ASN:HD21	6:FA:1616:GLU:HB2	1.61	0.65
7:GE:518:LEU:HD23	7:GE:566:ALA:HB2	1.78	0.65
11:JB:71:LYS:HE2	11:JB:191:ASP:HA	1.77	0.65
11:JC:66:MET:HE1	11:JC:75:VAL:HG11	1.78	0.65
11:JC:791:MET:HG2	11:JC:809:ILE:HG12	1.79	0.65
15:ND:726:CYS:HB3	15:ND:803:LEU:HD12	1.77	0.65
3:BC:694:ARG:HD2	17:PC:290:PHE:HE1	1.61	0.65
6:FE:1244:LEU:HB3	6:FE:1249:ILE:HG12	1.79	0.65
10:IC:725:LYS:HB3	10:IC:729:ARG:HH12	1.61	0.65
15:NA:894:LEU:H	15:NA:1153:ALA:H	1.42	0.65
1:AD:396:MET:HE3	5:EA:4617:THR:HG22	1.79	0.65
11:JB:2110:LEU:HD12	11:JB:2113:PHE:HB3	1.77	0.65
12:KB:382:ARG:HG2	12:KB:727:ILE:HG21	1.79	0.65
12:KB:503:ASP:HA	12:KB:506:LEU:HB3	1.78	0.65
12:KE:368:ARG:HD3	12:KE:397:GLN:HE22	1.61	0.65
13:LL:350:LEU:HG	13:LL:354:ARG:HE	1.62	0.65
14:MI:233:LEU:HD23	14:MI:236:GLU:HG3	1.77	0.65
1:AE:382:ILE:HG21	2:AF:464:ILE:HD11	1.78	0.65
5:EC:3283:GLU:HA	5:EC:3286:ARG:HE	1.61	0.65
6:FD:1210:LEU:HD22	6:FD:1284:LEU:HD21	1.79	0.65
14:MJ:292:ALA:HA	14:MJ:295:GLU:HB2	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:442:HIS:HB2	2:AB:368:HIS:HB2	1.77	0.65
4:DC:23:ALA:HA	4:DC:28:LEU:HD12	1.79	0.65
5:EC:3331:ALA:HA	5:EC:3763:ARG:HA	1.78	0.65
5:EC:3419:ARG:HH22	5:EC:3758:ARG:HA	1.61	0.65
6:FD:971:SER:HA	6:FD:1022:THR:HA	1.78	0.65
6:FD:1231:ARG:HB3	6:FD:1270:LEU:HD21	1.79	0.65
9:HA:675:ALA:HB3	9:HA:711:SER:HB2	1.77	0.65
9:HB:795:LEU:HD13	9:HB:797:TYR:HE2	1.61	0.65
14:MI:285:ARG:HH22	14:MJ:257:LYS:HG2	1.60	0.65
2:AB:66:ARG:HG2	2:AB:172:GLY:HA3	1.77	0.65
6:FB:1901:LEU:HB3	6:FB:1904:GLU:HA	1.78	0.65
6:FE:1253:SER:HB3	11:JC:778:HIS:CD2	2.32	0.65
8:GD:132:PRO:HG2	8:GD:297:LEU:HD12	1.78	0.65
7:GE:738:LEU:HD12	7:GE:797:ILE:HG23	1.79	0.65
8:GF:199:ARG:HE	8:GF:202:LYS:HD3	1.62	0.65
11:JB:426:PRO:HB3	11:JB:1524:PHE:HB3	1.77	0.65
11:JC:2065:MET:HE1	11:JC:2276:ARG:HE	1.62	0.65
12:KA:721:GLN:HE22	12:KA:725:ILE:HG23	1.61	0.65
14:MI:247:LEU:HD11	14:MJ:251:LEU:HD21	1.79	0.65
15:NA:1526:ILE:HG21	18:QA:146:ILE:HG13	1.79	0.65
15:NC:1138:THR:HG23	15:NC:1140:LEU:H	1.61	0.65
2:AF:63:THR:HA	2:AF:66:ARG:HD2	1.79	0.65
6:FF:890:ALA:O	6:FF:891:ARG:C	2.40	0.65
7:GC:767:LEU:HB3	7:GC:839:ARG:HH12	1.61	0.65
8:GH:148:GLU:HB2	8:GH:394:PHE:HB2	1.77	0.65
18:QD:122:ARG:HA	18:QD:125:LYS:HE2	1.78	0.65
6:FE:1217:GLU:O	6:FE:1218:ALA:C	2.40	0.65
11:JA:746:VAL:HA	11:JA:749:LYS:HG2	1.78	0.65
15:ND:751:ASP:HB3	15:ND:849:ARG:HD3	1.79	0.65
1:AL:405:LEU:HD11	16:OB:24:LEU:HD22	1.76	0.64
6:FE:826:LEU:HB2	6:FE:841:TYR:HE2	1.62	0.64
8:GJ:349:THR:HG22	8:GJ:379:VAL:HG21	1.79	0.64
9:HB:777:TYR:H	13:LE:521:ASN:ND2	1.95	0.64
10:IB:740:ARG:HD2	10:IB:772:LEU:HG	1.78	0.64
11:JA:1975:THR:HG23	11:JA:1977:GLN:H	1.61	0.64
15:NA:1550:MET:HE3	19:RC:174:LEU:HD21	1.79	0.64
2:AB:408:LYS:HB3	2:AB:409:PRO:HD3	1.78	0.64
6:FD:826:LEU:HD21	6:FD:843:LEU:HD23	1.78	0.64
6:FE:823:GLY:C	6:FE:825:PRO:HD3	2.22	0.64
8:GJ:661:PRO:HB2	8:GJ:680:LEU:HB2	1.79	0.64
10:IC:813:ALA:HB2	10:IC:840:PRO:HB2	1.79	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:882:ALA:HB3	11:JC:1416:ARG:HB3	1.77	0.64
12:KG:238:PHE:HB3	12:KG:294:ARG:HH22	1.62	0.64
19:RA:23:LEU:HA	19:RA:26:HIS:HB2	1.77	0.64
3:CB:945:THR:HG22	3:CB:947:GLU:H	1.61	0.64
3:CG:1187:GLU:HB2	3:CG:1192:HIS:HB3	1.80	0.64
5:EC:3649:TRP:HE1	5:EC:3673:LEU:HD22	1.61	0.64
6:FF:1187:ILE:HG23	6:FF:1419:LEU:HD13	1.78	0.64
7:GE:184:ALA:HB3	7:GE:708:SER:HB2	1.80	0.64
7:GI:284:GLU:HA	7:GI:290:VAL:HG11	1.79	0.64
15:NA:570:GLY:HA3	15:NA:575:LEU:HD21	1.79	0.64
15:NB:1511:GLU:HB3	18:QC:107:LEU:HD11	1.80	0.64
4:DC:257:LEU:HD23	4:DC:265:ILE:HD13	1.79	0.64
8:GJ:426:LEU:HB2	8:GJ:497:GLN:HB3	1.77	0.64
15:ND:947:ASN:HA	15:ND:950:VAL:HB	1.78	0.64
2:AG:544:ARG:HH21	1:AH:485:PRO:HD3	1.63	0.64
8:GJ:393:SER:HB3	8:GJ:396:ILE:HG12	1.80	0.64
9:HC:574:ARG:HB3	9:HC:578:THR:HG21	1.80	0.64
11:JC:758:GLU:HA	11:JC:761:LYS:HB3	1.79	0.64
15:NB:1472:LYS:HA	15:NB:1475:PHE:HB3	1.80	0.64
6:FC:2051:VAL:O	6:FC:2055:THR:HG23	1.98	0.64
8:GH:396:ILE:HG22	8:GH:721:LYS:HZ1	1.63	0.64
10:IB:634:ALA:HB2	10:IB:692:GLU:HB3	1.78	0.64
12:KC:308:LEU:HD13	12:KC:337:ALA:HB2	1.78	0.64
1:AL:801:ARG:HE	1:AL:996:SER:HB3	1.63	0.64
4:DD:35:MET:HG2	4:DD:106:ASN:HB2	1.79	0.64
5:EA:3273:LEU:HD13	5:EA:3494:VAL:HG11	1.80	0.64
7:GA:538:THR:HG23	9:HB:555:SER:HB3	1.78	0.64
7:GE:606:MET:HB3	7:GE:631:PHE:HB2	1.79	0.64
8:GH:283:LEU:HD21	8:GH:303:LEU:HD22	1.79	0.64
10:IA:551:ASN:HD21	10:IA:803:ARG:HH21	1.43	0.64
19:RC:58:VAL:HG13	19:RC:60:PHE:H	1.62	0.64
5:EB:3258:GLY:HA3	5:EB:3263:SER:HB3	1.80	0.64
5:EC:3705:ASP:HA	5:EC:3708:HIS:HB3	1.79	0.64
6:FD:832:GLY:HA3	6:FD:844:ALA:HB2	1.79	0.64
12:KG:218:ARG:HB3	12:KG:222:LEU:H	1.61	0.64
2:AG:115:ARG:HH11	16:OC:148:ARG:H	1.46	0.64
6:FF:818:VAL:HG23	6:FF:821:ARG:HG2	1.80	0.64
7:GG:987:GLN:HB3	7:GG:991:MET:HE1	1.79	0.64
11:JA:422:LEU:HD23	11:JA:1441:CYS:HB3	1.79	0.64
11:JB:1717:TRP:HB3	16:OB:931:PRO:HG3	1.80	0.64
15:NB:1017:GLN:HG3	15:NB:1094:LYS:HG3	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:QC:123:VAL:HA	18:QC:126:MET:HE3	1.80	0.64
3:CB:757:MET:HB3	3:CB:761:LEU:HD23	1.81	0.63
5:EC:4653:GLU:HG3	5:EC:4654:ASP:H	1.62	0.63
6:FF:894:ALA:HB1	6:FF:897:LEU:HB2	1.80	0.63
12:KF:395:LEU:HD13	12:KF:484:ILE:HD11	1.80	0.63
14:MC:126:LEU:HD22	14:MD:126:LEU:HD12	1.78	0.63
2:AG:548:ARG:HD2	5:EB:4620:LYS:HZ1	1.62	0.63
6:FE:839:GLY:HA3	12:KB:681:MET:HE3	1.80	0.63
8:GJ:43:CYS:HB2	8:GJ:46:LEU:HB2	1.80	0.63
9:HB:554:ASP:HB2	9:HB:557:ALA:HB3	1.80	0.63
11:JA:1852:HIS:HB2	11:JA:1985:LEU:HD22	1.78	0.63
13:LE:502:MET:HG3	13:LF:503:VAL:HG21	1.79	0.63
14:MI:243:LYS:HE2	14:MI:247:LEU:HD22	1.79	0.63
15:NA:812:ARG:HH21	15:NA:878:ILE:HD12	1.63	0.63
15:NA:1524:ARG:HE	18:QA:57:ASN:HD22	1.47	0.63
15:NC:1528:SER:HA	15:NC:1531:GLN:HG3	1.80	0.63
15:ND:892:TRP:HB2	15:ND:1155:GLU:HB2	1.78	0.63
2:AC:175:VAL:HG21	16:OA:29:PRO:HG3	1.81	0.63
1:AI:239:GLU:HB2	1:AI:257:LEU:HD12	1.80	0.63
6:FC:2052:HIS:HE1	9:HB:762:HIS:HB2	1.63	0.63
7:GE:370:ALA:HB3	7:GE:383:GLN:HB2	1.79	0.63
10:IC:936:LEU:HD21	10:IC:969:LYS:HB3	1.79	0.63
16:OA:742:PHE:HA	18:QD:89:ARG:HH12	1.62	0.63
17:PC:257:ASN:HB2	17:PC:260:SER:HB3	1.80	0.63
2:AC:554:ASP:HB3	1:AD:471:GLU:HG2	1.80	0.63
6:FC:2001:CYS:O	6:FC:2002:THR:C	2.42	0.63
11:JC:422:LEU:HD23	11:JC:1441:CYS:HB3	1.79	0.63
12:KF:367:ILE:HD11	12:KF:394:LEU:HB2	1.81	0.63
2:AK:32:LEU:HD21	1:AL:451:ILE:HD11	1.80	0.63
1:AL:376:LEU:HB3	11:JB:1643:LEU:HD22	1.81	0.63
6:FA:2059:VAL:CG2	9:HA:754:LEU:HB2	2.28	0.63
6:FF:1222:CYS:HB3	6:FF:1225:ILE:HG13	1.80	0.63
8:GB:300:ARG:HG2	8:GB:361:ALA:HB3	1.81	0.63
8:GF:349:THR:HG22	8:GF:379:VAL:HG21	1.81	0.63
7:GG:506:ALA:HA	7:GG:509:LEU:HD12	1.81	0.63
11:JB:1744:ILE:HD11	11:JB:1759:LEU:HB3	1.79	0.63
15:NB:982:ILE:HD11	15:NB:1029:SER:H	1.63	0.63
20:SB:83:GLU:HA	20:SB:147:MET:HE1	1.79	0.63
1:AH:405:LEU:HD11	16:OC:24:LEU:HB3	1.79	0.63
6:FD:1429:LEU:HD23	6:FD:1430:PHE:CD2	2.33	0.63
8:GD:372:VAL:HG12	8:GD:377:MET:HE1	1.81	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GE:433:MET:HE2	7:GE:459:PRO:HD3	1.80	0.63
7:GG:311:LEU:HD13	7:GG:451:ILE:HG23	1.80	0.63
10:IA:864:GLN:HB3	10:IA:1241:LEU:HD22	1.80	0.63
16:OA:1101:PHE:HA	16:OA:1104:LYS:HZ1	1.64	0.63
3:BC:956:LEU:HD13	3:BC:978:VAL:HG21	1.79	0.63
6:FB:2055:THR:HG22	9:HD:837:LEU:HD11	1.81	0.63
7:GI:406:ALA:HA	7:GI:409:ARG:HB2	1.79	0.63
9:HA:554:ASP:HB2	9:HA:557:ALA:HB3	1.81	0.63
11:JA:1746:LEU:HD21	11:JA:1854:HIS:HE1	1.63	0.63
5:EA:3798:LEU:HD23	5:EA:3810:VAL:HA	1.80	0.63
6:FE:1190:ARG:HB2	6:FE:1418:GLU:HB2	1.81	0.63
8:GB:756:ALA:HB3	8:GF:333:LYS:HD2	1.81	0.63
8:GD:665:LEU:HB2	8:GD:676:TRP:HB3	1.80	0.63
8:GH:203:GLU:HB2	8:GH:313:PRO:HG3	1.81	0.63
8:GL:112:ILE:HD11	8:GL:508:ARG:HB2	1.80	0.63
10:IA:888:THR:HG21	15:NA:565:TRP:HD1	1.64	0.63
12:KE:524:PHE:HD1	12:KE:573:ARG:HH22	1.46	0.63
12:KE:606:ARG:HE	12:KE:623:ILE:HG13	1.62	0.63
13:LA:521:ASN:HB3	13:LB:520:LEU:HD13	1.80	0.63
15:ND:894:LEU:H	15:ND:1153:ALA:H	1.44	0.63
5:EA:3514:GLU:HG2	5:EA:3515:PRO:HD3	1.80	0.63
6:FC:2048:GLU:HG2	9:HB:765:TRP:NE1	2.14	0.63
6:FD:1432:THR:HB	6:FD:1435:GLU:HB2	1.80	0.63
8:GD:338:ALA:HA	8:GD:341:VAL:HG12	1.80	0.63
7:GG:169:ILE:HG23	7:GG:173:ASN:HD22	1.64	0.63
8:GH:773:ASP:H	8:GL:346:LYS:HD2	1.63	0.63
10:IA:968:ARG:HE	10:IA:1061:LEU:HD21	1.64	0.63
11:JB:48:GLN:HA	11:JB:95:PRO:HB3	1.80	0.63
19:RC:57:ARG:HH12	19:RC:118:TYR:HB3	1.64	0.63
1:AL:429:ARG:HH22	16:OB:5:VAL:HG21	1.62	0.62
3:CC:972:LEU:HD11	3:CF:1149:PRO:HG3	1.79	0.62
5:EA:3798:LEU:HB3	5:EA:3810:VAL:HG22	1.81	0.62
5:EB:4398:ILE:HG22	5:EB:4703:GLN:HE21	1.63	0.62
6:FC:1724:ARG:HE	6:FC:1808:VAL:HG13	1.64	0.62
6:FD:1233:ILE:HD11	6:FD:1268:VAL:HG22	1.80	0.62
6:FE:918:GLN:HB3	6:FE:922:LEU:HG	1.81	0.62
7:GA:284:GLU:HB3	7:GA:290:VAL:HG21	1.81	0.62
7:GG:844:HIS:HD2	7:GG:881:ALA:H	1.47	0.62
9:HB:643:PHE:HB2	9:HB:729:GLY:HA2	1.81	0.62
9:HC:675:ALA:HB3	9:HC:711:SER:HB2	1.80	0.62
10:IC:921:LEU:HD21	10:IC:938:ILE:HD13	1.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JA:2076:ASN:HD21	11:JA:2255:ARG:HH12	1.47	0.62
11:JC:541:LEU:HD11	11:JC:548:PHE:HA	1.79	0.62
1:AA:303:MET:HE2	1:AA:345:PRO:HD2	1.81	0.62
6:FD:813:GLN:O	6:FD:814:THR:C	2.41	0.62
6:FE:1244:LEU:O	6:FE:1246:ILE:N	2.33	0.62
7:GE:309:LEU:HD22	7:GE:444:MET:HE3	1.80	0.62
7:GI:371:LEU:HD12	7:GI:412:VAL:HG22	1.80	0.62
5:EA:4064:ALA:HB1	5:EA:4180:TYR:HD2	1.65	0.62
6:FD:1238:ARG:HH21	6:FD:1238:ARG:HA	1.64	0.62
15:NC:350:ARG:HE	15:NC:486:ARG:HD3	1.62	0.62
4:DA:356:TYR:HB3	4:DA:382:LEU:HD22	1.82	0.62
6:FD:997:THR:CG2	12:KA:230:GLN:HE22	2.11	0.62
6:FE:917:TRP:HD1	6:FE:918:GLN:HE21	1.46	0.62
8:GD:326:ARG:HH12	8:GD:375:TYR:HB3	1.63	0.62
7:GE:185:ARG:HH21	7:GE:704:ASP:HB2	1.64	0.62
7:GG:397:LEU:HD11	8:GJ:177:MET:H	1.64	0.62
8:GH:171:ILE:HG23	8:GH:181:HIS:HB2	1.80	0.62
10:IC:643:GLY:HA3	16:OC:1075:TYR:H	1.65	0.62
11:JA:1873:ARG:HH21	11:JA:1877:ALA:HB2	1.63	0.62
15:NB:1512:MET:HG2	18:QC:107:LEU:HD22	1.81	0.62
1:AH:310:CYS:H	1:AH:313:CYS:HB2	1.63	0.62
1:AL:462:LEU:HA	1:AL:465:MET:HG2	1.82	0.62
3:CB:711:ARG:HH12	3:CB:757:MET:HE1	1.64	0.62
4:DD:105:CYS:H	4:DD:260:GLY:HA2	1.64	0.62
6:FC:1755:VAL:HB	6:FC:1759:GLU:HG3	1.81	0.62
6:FD:888:PRO:HG2	7:GC:897:SER:CB	2.28	0.62
6:FD:1283:TYR:HB3	6:FD:1290:ILE:HG23	1.82	0.62
6:FE:1222:CYS:HB3	6:FE:1225:ILE:HB	1.81	0.62
6:FF:1433:ALA:O	6:FF:1434:ALA:C	2.42	0.62
8:GF:218:SER:HB3	8:GF:221:ALA:HB2	1.81	0.62
7:GG:535:PRO:HG2	9:HA:553:TYR:CD1	2.35	0.62
7:GK:353:SER:HB3	7:GK:406:ALA:HB2	1.80	0.62
11:JC:57:GLU:HA	11:JC:90:ARG:HH21	1.63	0.62
12:KE:207:ASP:HA	12:KE:280:LEU:HB3	1.81	0.62
1:AE:1025:ARG:HD2	14:ML:85:PRO:HD2	1.80	0.62
2:AK:378:ASN:HB3	5:EA:4396:GLU:HG3	1.82	0.62
11:JB:1982:SER:HA	11:JB:1985:LEU:HD23	1.81	0.62
15:NB:1536:GLN:HB2	19:RB:111:VAL:HG23	1.81	0.62
15:NC:1498:ARG:HH12	15:NC:1501:PRO:HG2	1.64	0.62
1:AA:64:HIS:HB2	1:AA:229:LEU:HD21	1.82	0.62
1:AE:728:VAL:HG13	1:AE:729:THR:HG23	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EC:3498:VAL:HG12	5:EC:4011:VAL:HG22	1.81	0.62
9:HA:777:TYR:CD1	9:HA:778:PRO:HD2	2.35	0.62
9:HB:810:ARG:HA	9:HB:813:THR:HG23	1.81	0.62
10:IC:784:LEU:HD23	11:JC:2057:LEU:HD21	1.81	0.62
11:JB:1749:LYS:HE2	11:JB:1858:ILE:HD11	1.81	0.62
11:JB:1818:ILE:HA	11:JB:1821:LEU:HD23	1.81	0.62
13:LI:526:LEU:HG	13:LJ:525:SER:HB3	1.81	0.62
15:NB:707:GLU:HB2	15:NB:934:LEU:HD21	1.81	0.62
15:NC:1526:ILE:HG21	18:QD:146:ILE:HG21	1.82	0.62
15:ND:1160:LEU:HD12	15:ND:1165:VAL:HG11	1.81	0.62
1:AD:228:PRO:HD2	10:IB:1251:VAL:HA	1.81	0.62
4:DA:126:LEU:HD21	4:DA:157:THR:HG22	1.82	0.62
4:DB:130:ARG:HH21	4:DB:154:LEU:HD12	1.63	0.62
5:EC:4879:THR:HG22	5:EC:4892:ARG:HB3	1.81	0.62
5:EC:4882:ARG:HG3	5:EC:4887:GLY:HA2	1.81	0.62
6:FE:808:SER:O	6:FE:809:ILE:C	2.42	0.62
6:FF:828:GLN:HA	6:FF:831:ARG:HG2	1.81	0.62
8:GF:422:LYS:HB2	8:GF:501:SER:HB2	1.80	0.62
7:GG:536:THR:HA	9:HA:553:TYR:HB2	1.80	0.62
8:GH:674:VAL:HG12	8:GH:723:VAL:HB	1.81	0.62
11:JB:1852:HIS:HB2	11:JB:1985:LEU:HD12	1.82	0.62
12:KF:588:ALA:HB3	12:KF:710:ASN:HD21	1.65	0.62
15:NC:1126:THR:H	15:NC:1159:THR:HA	1.65	0.62
15:ND:922:LEU:HD21	15:ND:1106:SER:HB3	1.81	0.62
2:AB:177:VAL:HG11	2:AB:183:ALA:HB2	1.82	0.62
2:AG:27:ALA:HB1	1:AH:443:LYS:HG2	1.81	0.62
1:AL:1046:THR:HG22	1:AL:1048:ALA:H	1.65	0.62
3:CJ:1154:LEU:HG	3:CJ:1158:PHE:HE2	1.65	0.62
6:FD:993:ALA:HB2	12:KA:230:GLN:HB2	1.80	0.62
6:FF:1217:GLU:O	6:FF:1218:ALA:C	2.42	0.62
9:HB:552:ASP:HB2	9:HB:576:LYS:HD3	1.82	0.62
11:JC:46:PHE:H	11:JC:170:ILE:HG21	1.63	0.62
12:KA:296:ILE:HD11	12:KA:318:VAL:HG13	1.81	0.62
12:KA:660:THR:HG22	12:KA:662:SER:H	1.65	0.62
14:MK:105:LEU:HD21	14:ML:104:LYS:HD2	1.80	0.62
15:ND:468:ARG:HD3	15:ND:469:PHE:HD1	1.65	0.62
1:AE:44:LEU:HD11	17:PC:268:PRO:HB2	1.81	0.62
1:AI:64:HIS:HB2	1:AI:229:LEU:HD21	1.82	0.62
3:BA:808:VAL:HG22	17:PA:279:ARG:HH21	1.64	0.62
3:BB:694:ARG:HD2	17:PB:290:PHE:HE2	1.65	0.62
4:DB:154:LEU:HA	4:DB:157:THR:HG22	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DE:336:ARG:HH12	4:DE:340:ALA:HB2	1.65	0.62
5:EB:4405:ILE:HG23	5:EB:4431:ARG:HD3	1.82	0.62
7:GC:606:MET:HE2	7:GC:678:LEU:HD13	1.82	0.62
8:GF:544:LEU:HG	8:GF:560:TRP:HH2	1.65	0.62
7:GI:746:LEU:HA	7:GI:749:LEU:HD12	1.82	0.62
9:HA:761:CYS:O	9:HA:762:HIS:C	2.43	0.62
12:KE:374:ALA:HA	12:KE:377:LEU:HB3	1.82	0.62
12:KF:642:ARG:HE	12:KF:677:ARG:HB3	1.65	0.62
15:NB:685:PHE:HE2	15:NB:689:ASN:HA	1.65	0.62
1:AD:22:PHE:HB3	1:AD:25:ALA:HB3	1.82	0.61
2:AG:168:GLN:HG3	2:AG:280:ARG:HD2	1.80	0.61
2:AK:489:ILE:HG23	1:AL:354:ARG:HH12	1.65	0.61
5:EC:4167:ASP:HB2	5:EC:4171:ILE:HG12	1.82	0.61
6:FE:807:ALA:O	6:FE:808:SER:HB2	1.98	0.61
11:JA:1168:THR:HG21	11:JA:1173:LEU:HB3	1.80	0.61
11:JC:805:CYS:HB2	11:JC:895:LEU:HB3	1.82	0.61
15:NC:925:ARG:HE	15:NC:926:ARG:H	1.47	0.61
1:AL:38:VAL:HG12	1:AL:111:ILE:HD12	1.82	0.61
5:EB:3445:VAL:HG21	5:EB:3570:LEU:HD23	1.80	0.61
6:FE:1218:ALA:O	6:FE:1219:GLU:C	2.41	0.61
14:ML:140:ARG:HB2	14:ML:144:ARG:HH12	1.63	0.61
16:OB:1042:PRO:HB3	16:OB:1044:ARG:HH21	1.65	0.61
3:BB:948:THR:HG22	3:BB:950:GLY:H	1.65	0.61
6:FC:1892:ILE:HG22	6:FC:1894:THR:H	1.65	0.61
6:FD:803:ARG:HB3	6:FD:907:ASN:HD22	1.65	0.61
6:FD:918:GLN:O	6:FD:919:GLN:C	2.43	0.61
6:FD:1217:GLU:O	6:FD:1218:ALA:C	2.43	0.61
6:FE:918:GLN:O	6:FE:919:GLN:C	2.43	0.61
7:GC:185:ARG:HH21	7:GC:704:ASP:HB2	1.65	0.61
10:IC:791:VAL:HG21	10:IC:812:LEU:HD22	1.82	0.61
15:NA:708:LEU:HB3	15:NA:714:ARG:HH11	1.65	0.61
15:NA:1197:ARG:HD2	15:NA:1386:HIS:HB2	1.82	0.61
6:FF:833:GLY:H	6:FF:979:LEU:HD23	1.66	0.61
7:GA:543:LYS:H	9:HB:596:TYR:HB3	1.64	0.61
7:GA:823:ARG:HE	7:GA:827:LEU:HD11	1.65	0.61
15:NA:558:GLU:HB2	15:NA:578:HIS:HE2	1.64	0.61
15:NA:922:LEU:HD11	15:NA:1105:HIS:HE1	1.65	0.61
1:AA:460:VAL:HG23	1:AA:465:MET:HE3	1.81	0.61
2:AB:41:ARG:HG2	2:AB:291:LEU:HB2	1.81	0.61
6:FD:971:SER:HB3	6:FD:1022:THR:HG23	1.82	0.61
6:FE:1292:ALA:HB1	6:FE:1393:LEU:HG	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GB:745:TYR:HB3	8:GF:342:LYS:HG3	1.82	0.61
7:GI:606:MET:HB3	7:GI:631:PHE:HB2	1.81	0.61
12:KE:503:ASP:HA	12:KE:506:LEU:HD13	1.82	0.61
15:NC:983:ILE:HG23	15:NC:989:ILE:HB	1.82	0.61
15:ND:505:GLY:H	15:ND:512:TYR:HB2	1.65	0.61
1:AL:632:LEU:HD23	1:AL:633:MET:HG3	1.83	0.61
4:DB:93:ILE:HG23	4:DB:97:LEU:HD12	1.83	0.61
5:EC:4041:ASP:HB3	5:EC:4371:ARG:HH21	1.65	0.61
6:FF:1193:VAL:HB	6:FF:1416:GLN:HB3	1.82	0.61
8:GF:327:HIS:H	8:GF:330:ASP:HB2	1.65	0.61
8:GL:415:LEU:HB3	8:GL:417:MET:HE2	1.82	0.61
9:HB:848:ASP:OD1	9:HB:849:ALA:N	2.34	0.61
12:KF:656:ARG:HB3	12:KF:667:SER:HB3	1.83	0.61
13:LP:410:LYS:HG3	13:LP:413:GLU:HB3	1.81	0.61
14:ME:326:LEU:HD13	14:MF:326:LEU:HD11	1.82	0.61
19:RC:18:LYS:HB3	19:RC:105:MET:HA	1.81	0.61
5:EA:4745:VAL:HG13	5:EA:4842:GLN:HE22	1.66	0.61
5:EC:4640:VAL:HG21	5:EC:4708:LEU:HD21	1.83	0.61
6:FD:962:PHE:CE2	6:FD:965:TRP:HB2	2.35	0.61
6:FD:1218:ALA:O	6:FD:1219:GLU:C	2.44	0.61
6:FD:1222:CYS:O	6:FD:1223:ALA:C	2.43	0.61
6:FE:1185:VAL:O	6:FE:1186:TRP:C	2.44	0.61
6:FE:1188:GLU:HG3	6:FE:1267:GLN:HB3	1.82	0.61
7:GI:350:ARG:HH12	7:GI:352:ASP:HB2	1.65	0.61
11:JC:1581:ARG:HH22	15:NA:354:PHE:HB3	1.64	0.61
12:KA:534:VAL:HG13	12:KA:542:PRO:HB3	1.83	0.61
12:KC:727:ILE:HB	12:KC:728:PRO:HD3	1.82	0.61
6:FD:1424:CYS:HB2	6:FD:1425:PRO:CD	2.24	0.61
8:GJ:440:CYS:HB2	8:GJ:463:TRP:HB3	1.83	0.61
11:JA:1591:HIS:HD2	11:JA:1593:VAL:HG22	1.65	0.61
11:JC:1818:ILE:HA	11:JC:1821:LEU:HD23	1.82	0.61
12:KC:377:LEU:HD23	12:KC:377:LEU:H	1.65	0.61
1:AA:366:ARG:HH12	1:AA:370:GLN:HG2	1.65	0.61
2:AK:50:ILE:HD11	2:AK:282:PHE:HB2	1.81	0.61
5:EC:3445:VAL:HG21	5:EC:3570:LEU:HG	1.83	0.61
6:FB:1962:GLN:HG2	6:FB:2047:ARG:HD2	1.82	0.61
6:FD:1388:PHE:HD1	6:FD:1418:GLU:HA	1.66	0.61
6:FE:1222:CYS:O	6:FE:1223:ALA:C	2.44	0.61
6:FE:1393:LEU:HD13	6:FE:1417:ILE:HG21	1.82	0.61
7:GA:239:ASN:HD22	7:GA:693:THR:HG21	1.65	0.61
7:GA:301:ARG:HH12	7:GA:304:GLN:HB3	1.64	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:433:MET:HE2	7:GG:459:PRO:HD3	1.82	0.61
8:GL:385:GLY:HA2	8:GL:439:PRO:HB2	1.82	0.61
10:IA:940:SER:HA	10:IA:975:PHE:HZ	1.65	0.61
15:NC:515:ALA:HB3	15:NC:520:ALA:HB2	1.81	0.61
15:NC:787:LEU:HD21	15:NC:896:ARG:HD3	1.83	0.61
3:BB:791:THR:HG21	3:BB:812:MET:HG2	1.82	0.61
3:CC:842:PHE:HA	3:CC:845:LYS:HE2	1.83	0.61
5:EA:3650:THR:HG23	9:HC:499:ARG:HA	1.81	0.61
5:EA:3705:ASP:HA	5:EA:3708:HIS:HB3	1.83	0.61
6:FD:1002:ALA:HB3	6:FD:1010:ARG:HH11	0.67	0.61
7:GI:605:VAL:HB	7:GI:630:LEU:HD11	1.82	0.61
10:IA:174:PHE:HB3	10:IA:205:GLN:HE21	1.65	0.61
11:JA:1327:LEU:HD21	11:JA:1384:ILE:HG12	1.83	0.61
12:KC:402:LEU:HD11	12:KC:720:LEU:HD21	1.82	0.61
13:LA:374:HIS:HE1	13:LB:370:MET:HB2	1.65	0.61
15:NA:741:ILE:HG23	15:NA:793:THR:HG22	1.83	0.61
2:AC:192:TRP:HE1	5:EA:4613:GLU:HG2	1.66	0.60
3:BA:982:ARG:HB3	3:BA:993:THR:HG22	1.82	0.60
3:CJ:1182:GLY:H	3:CJ:4512:SER:HB2	1.66	0.60
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CE2	2.53	0.60
5:EC:3760:LYS:HG3	5:EC:3763:ARG:HG3	1.81	0.60
6:FB:2072:ILE:HG21	9:HD:854:ASN:HB3	1.83	0.60
7:GA:807:ARG:HG3	7:GA:977:SER:HB3	1.83	0.60
7:GC:916:HIS:HB3	7:GC:919:VAL:HG12	1.83	0.60
9:HB:646:LEU:HD13	9:HB:730:GLY:H	1.66	0.60
10:IB:644:VAL:H	16:OB:1074:TYR:HB2	1.66	0.60
10:IB:813:ALA:HB2	10:IB:840:PRO:HB2	1.82	0.60
11:JB:1583:ILE:HG21	11:JB:1594:ARG:HB2	1.83	0.60
15:NA:515:ALA:HB3	15:NA:520:ALA:HB2	1.83	0.60
15:NB:925:ARG:HE	15:NB:926:ARG:H	1.47	0.60
15:NC:725:ILE:HG13	15:NC:799:ILE:HG21	1.83	0.60
2:AJ:209:SER:HB3	2:AJ:259:VAL:HA	1.83	0.60
4:DC:300:GLN:HE21	4:DC:354:TRP:HA	1.65	0.60
5:EB:3242:LEU:HD23	5:EB:3249:ALA:HA	1.83	0.60
5:EC:4641:PHE:HE1	5:EC:4704:LYS:HB3	1.66	0.60
5:EC:4651:MET:HE3	5:EC:4657:GLU:HB3	1.83	0.60
7:GA:535:PRO:HG2	9:HB:553:TYR:CD1	2.36	0.60
7:GI:196:LEU:HB3	7:GI:198:LEU:HD23	1.81	0.60
7:GK:171:GLN:HG3	7:GK:172:PHE:HD2	1.67	0.60
8:GL:300:ARG:HG2	8:GL:361:ALA:HB3	1.83	0.60
9:HB:681:LYS:HE2	13:LD:483:ARG:NH1	2.17	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1003:VAL:HB	10:IC:1043:PHE:HB2	1.84	0.60
11:JA:1032:VAL:HG21	11:JA:1063:ILE:HG12	1.82	0.60
11:JA:1676:ARG:HD3	11:JA:1736:THR:HG22	1.83	0.60
11:JC:147:ARG:HA	11:JC:151:LEU:HD22	1.84	0.60
13:LJ:459:ALA:HA	13:LJ:462:GLN:HB2	1.82	0.60
2:AG:44:LEU:HD21	2:AG:47:ALA:HB2	1.83	0.60
1:AH:58:LEU:HB3	3:CE:1117:VAL:HG11	1.82	0.60
3:CA:996:VAL:HA	3:CA:999:LEU:HD12	1.83	0.60
4:DC:16:LEU:HD22	4:DC:97:LEU:HD12	1.83	0.60
6:FD:842:GLY:N	7:GC:957:ARG:HH21	1.98	0.60
7:GA:890:MET:HE3	7:GA:953:LEU:HB2	1.82	0.60
8:GH:160:LEU:HA	8:GH:163:MET:HG2	1.83	0.60
10:IC:838:LEU:HD11	10:IC:875:VAL:HG11	1.83	0.60
10:IC:1232:ARG:HG2	10:IC:1302:ARG:HH22	1.65	0.60
11:JA:84:PHE:HB3	11:JA:2092:PHE:HZ	1.66	0.60
11:JC:1078:MET:HG2	11:JC:1509:HIS:HD2	1.65	0.60
15:NB:564:ARG:HH21	15:NB:619:TYR:HA	1.67	0.60
19:RD:24:ARG:HA	19:RD:27:ALA:HB2	1.83	0.60
4:DD:126:LEU:HD23	4:DD:158:LEU:HA	1.83	0.60
6:FD:978:LYS:HZ1	6:FD:984:THR:H	1.49	0.60
6:FE:1003:ILE:HG13	6:FE:1009:VAL:HG13	1.84	0.60
7:GI:715:THR:HG21	7:GI:796:PHE:HB3	1.83	0.60
12:KC:298:GLN:HB3	12:KC:303:TYR:HB2	1.83	0.60
13:LE:427:ARG:HE	13:LE:430:LYS:HZ1	1.49	0.60
15:NB:735:HIS:HD2	15:NB:768:GLU:HG2	1.65	0.60
3:CI:4467:THR:HG23	3:CI:4468:LYS:HG3	1.82	0.60
4:DB:327:PHE:HE1	14:ME:259:MET:HG2	1.67	0.60
6:FC:1991:ALA:HA	6:FC:1994:ARG:HE	1.64	0.60
6:FE:803:ARG:HB3	6:FE:1118:GLN:HG3	1.82	0.60
6:FF:1189:ILE:HD11	6:FF:1282:LEU:HD13	1.83	0.60
7:GG:319:VAL:HG13	7:GG:424:ARG:HG2	1.83	0.60
8:GJ:315:GLN:HG2	8:GJ:340:PHE:HB3	1.82	0.60
12:KA:206:CYS:HA	12:KA:243:HIS:HA	1.84	0.60
12:KG:534:VAL:HG13	12:KG:536:ARG:HH12	1.65	0.60
14:ME:285:ARG:HH12	14:MF:257:LYS:HA	1.66	0.60
3:CL:1263:SER:HA	3:CL:4457:PRO:HG3	1.83	0.60
5:EB:3765:VAL:HG12	11:JA:932:PRO:HG2	1.84	0.60
6:FC:2009:SER:HA	6:FC:2012:ARG:NE	2.17	0.60
6:FD:1102:TYR:O	6:FD:1103:SER:C	2.44	0.60
6:FE:837:ALA:O	6:FE:838:ASN:C	2.44	0.60
6:FE:993:ALA:HB3	12:KB:229:SER:CB	2.27	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:464:LEU:HB3	7:GG:502:TYR:HE1	1.67	0.60
8:GJ:50:GLU:H	14:MI:259:MET:HE1	1.67	0.60
12:KC:231:PHE:HZ	12:KC:313:PHE:CG	2.18	0.60
15:NB:947:ASN:HA	15:NB:950:VAL:HG22	1.83	0.60
1:AE:64:HIS:HE1	17:PC:268:PRO:HD2	1.65	0.60
4:DB:329:ARG:HA	4:DB:332:LEU:HB2	1.84	0.60
5:EB:4438:LEU:HD11	5:EB:4709:PHE:HE2	1.66	0.60
5:EC:3765:VAL:HG12	11:JC:932:PRO:HG2	1.82	0.60
6:FC:1955:THR:HG21	9:HB:838:LYS:HA	1.82	0.60
6:FD:1190:ARG:HB2	6:FD:1418:GLU:HB2	1.83	0.60
6:FD:1209:GLU:O	6:FD:1210:LEU:C	2.44	0.60
8:GF:43:CYS:HB2	8:GF:46:LEU:HB2	1.82	0.60
7:GI:314:VAL:HG23	7:GI:363:ASP:HB3	1.84	0.60
9:HB:675:ALA:HB3	9:HB:711:SER:HB2	1.83	0.60
10:IA:634:ALA:HB2	10:IA:692:GLU:HB3	1.83	0.60
12:KA:335:LEU:HD23	12:KA:338:LEU:HD22	1.83	0.60
12:KF:593:HIS:HB2	12:KF:707:GLU:HB3	1.83	0.60
15:NA:508:GLY:HA3	15:NA:577:PRO:HG3	1.83	0.60
15:NC:696:PHE:HB2	15:NC:894:LEU:HD22	1.83	0.60
15:ND:686:ASN:HB2	15:ND:692:ILE:HG22	1.83	0.60
2:AB:159:ARG:HG3	5:EA:4626:LEU:HD22	1.82	0.60
2:AB:507:PRO:HG3	3:BA:750:SER:HB2	1.83	0.60
4:DB:8:GLU:HA	4:DB:11:PHE:HD1	1.67	0.60
6:FA:1661:GLY:HA2	6:FA:1809:SER:HB2	1.83	0.60
6:FD:844:ALA:O	7:GC:896:ARG:NH2	2.33	0.60
6:FF:1108:PRO:HD3	9:HC:394:LEU:HG	1.84	0.60
8:GD:716:ARG:HH11	8:GD:720:PRO:HG3	1.67	0.60
7:GE:423:TRP:HB3	7:GE:426:ASN:HD22	1.65	0.60
9:HA:761:CYS:HA	9:HA:765:TRP:CD2	2.36	0.60
11:JB:46:PHE:H	11:JB:170:ILE:HG21	1.66	0.60
15:NC:1518:ARG:HH21	18:QD:65:ALA:HB2	1.67	0.60
15:ND:1526:ILE:HD13	18:QB:146:ILE:HG13	1.84	0.60
1:AA:666:LEU:HB3	1:AA:720:LEU:HD11	1.83	0.60
1:AE:633:MET:HE3	7:GG:930:PRO:HG3	1.84	0.60
1:AH:835:ALA:HB2	1:AH:918:VAL:HG21	1.84	0.60
6:FB:1750:LEU:HD13	6:FB:1752:LEU:HD23	1.84	0.60
8:GL:315:GLN:HG2	8:GL:340:PHE:HB3	1.83	0.60
9:HB:680:ALA:HB2	9:HB:708:VAL:HG13	1.83	0.60
10:IC:995:PRO:HA	10:IC:1103:ARG:HD2	1.84	0.60
11:JA:147:ARG:HA	11:JA:151:LEU:HD22	1.83	0.60
13:LN:336:VAL:HG12	13:LN:340:LYS:HE2	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:1548:PHE:N	19:RD:141:LEU:HD12	2.16	0.60
2:AF:177:VAL:HG11	2:AF:183:ALA:HB2	1.83	0.60
1:AH:912:SER:HB2	13:LI:486:ARG:HG2	1.83	0.60
1:AI:382:ILE:HG21	2:AJ:464:ILE:HD11	1.84	0.60
2:AJ:299:LEU:HA	2:AJ:307:PRO:HA	1.84	0.60
7:GA:807:ARG:HD2	7:GA:812:VAL:HG23	1.82	0.60
7:GC:890:MET:HE2	7:GC:951:MET:HB2	1.84	0.60
11:JC:2001:ILE:HG22	11:JC:2270:MET:HG3	1.84	0.60
12:KF:292:ALA:HB2	12:KF:314:LEU:HD22	1.83	0.60
15:NA:729:VAL:HG11	15:NA:800:SER:HB3	1.83	0.60
15:NA:895:GLY:HA2	15:NA:898:ASN:HB2	1.83	0.60
2:AG:376:ARG:HH22	5:EC:4405:ILE:HD13	1.67	0.59
3:CG:1133:VAL:HG11	10:IC:1094:ASN:HD21	1.67	0.59
4:DC:335:ASP:HA	4:DC:338:ILE:HG12	1.84	0.59
5:EC:3581:HIS:HD2	5:EC:3647:ALA:HA	1.67	0.59
6:FB:2083:GLN:HG3	9:HD:865:ILE:HD11	1.83	0.59
6:FC:1704:MET:HE3	6:FC:1720:VAL:HG21	1.83	0.59
6:FD:844:ALA:O	6:FD:845:PRO:C	2.44	0.59
6:FF:1009:VAL:HG21	6:FF:1219:GLU:HA	1.84	0.59
9:HD:875:THR:O	9:HD:879:ILE:HG13	2.02	0.59
11:JA:1220:LEU:HD21	11:JA:1286:LEU:HD12	1.83	0.59
14:MI:211:MET:HE1	14:MJ:210:LEU:HD13	1.83	0.59
15:NB:614:LYS:HB3	15:NB:678:LEU:HD22	1.84	0.59
18:QA:125:LYS:HG2	18:QA:140:TRP:HZ2	1.66	0.59
1:AD:632:LEU:HD23	1:AD:633:MET:HG3	1.84	0.59
1:AE:73:THR:HG22	1:AE:75:ALA:H	1.67	0.59
4:DA:66:ARG:HD3	4:DA:71:LEU:HA	1.83	0.59
6:FC:2080:GLN:HB3	9:HB:861:TYR:HE2	1.66	0.59
6:FE:1211:SER:HA	6:FE:1234:THR:HA	1.84	0.59
8:GD:725:CYS:HB3	8:GD:732:ALA:HB2	1.84	0.59
8:GH:670:PHE:HA	8:GH:720:PRO:HG3	1.84	0.59
10:IA:342:LEU:HD12	10:IA:343:PRO:HD2	1.84	0.59
10:IC:614:LEU:HD21	10:IC:797:VAL:HG21	1.84	0.59
11:JA:435:VAL:HA	11:JA:437:LEU:HD12	1.83	0.59
11:JB:1474:TRP:HA	11:JB:1477:TRP:HB2	1.83	0.59
11:JB:1666:VAL:HG22	16:OB:917:ILE:HD11	1.85	0.59
14:MA:258:ILE:HG13	14:MA:264:LEU:HG	1.83	0.59
15:NC:1511:GLU:HB2	18:QD:107:LEU:HD21	1.84	0.59
2:AB:317:ALA:HB2	1:AI:274:ARG:HH22	1.66	0.59
1:AE:131:ARG:HD3	1:AE:132:PRO:HD2	1.83	0.59
1:AE:1005:LEU:HD13	1:AE:1007:LYS:HZ3	1.67	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:4468:LYS:HB2	3:CE:4488:MET:HB2	1.85	0.59
3:CF:4477:PRO:HG2	3:CF:4479:LEU:HG	1.84	0.59
3:CG:1146:VAL:HG23	3:CL:1137:ALA:HB2	1.84	0.59
4:DE:150:SER:HA	4:DE:153:PHE:HB3	1.84	0.59
5:EC:4030:GLU:HB3	5:EC:4058:PRO:HB3	1.84	0.59
6:FD:833:GLY:H	6:FD:979:LEU:HD23	1.67	0.59
6:FF:808:SER:CB	6:FF:1113:PHE:HB2	2.31	0.59
6:FF:1184:ALA:N	6:FF:1424:CYS:HB3	2.17	0.59
8:GD:115:GLN:HE22	8:GD:508:ARG:HD2	1.67	0.59
7:GE:605:VAL:HB	7:GE:630:LEU:HD11	1.84	0.59
11:JA:46:PHE:H	11:JA:170:ILE:HG21	1.67	0.59
11:JA:1138:PRO:HG3	11:JA:1837:GLN:HB3	1.83	0.59
12:KB:234:PRO:HG2	12:KB:236:LYS:HE2	1.84	0.59
12:KG:606:ARG:HG3	12:KG:623:ILE:HG13	1.85	0.59
13:LA:395:ILE:HD13	13:LA:398:ARG:HH12	1.67	0.59
16:OA:171:PHE:HA	16:OA:182:ALA:HA	1.84	0.59
1:AE:654:LEU:HD13	1:AE:662:LEU:HD13	1.84	0.59
3:CI:1171:LEU:HD22	3:CI:4502:VAL:HG12	1.84	0.59
3:CJ:1244:PRO:HB2	3:CJ:1252:PRO:HB3	1.84	0.59
4:DA:28:LEU:HD13	4:DA:154:LEU:HD11	1.84	0.59
7:GE:276:ARG:NH2	7:GE:285:LEU:HG	2.16	0.59
7:GI:458:PRO:HB3	7:GI:562:ILE:HD11	1.83	0.59
11:JB:57:GLU:HA	11:JB:90:ARG:HH21	1.67	0.59
12:KF:677:ARG:HH12	12:KF:679:SER:HB3	1.66	0.59
12:KG:217:GLU:HG3	12:KG:218:ARG:H	1.66	0.59
13:LI:523:GLU:C	13:LI:525:SER:H	2.09	0.59
15:NC:579:PRO:HB2	15:NC:616:LEU:HD21	1.84	0.59
18:QB:121:LYS:HD3	18:QB:154:ASP:HA	1.85	0.59
1:AA:301:VAL:HG23	1:AA:332:THR:HG22	1.85	0.59
5:EB:4641:PHE:HB3	5:EB:4812:LEU:HD23	1.84	0.59
5:EC:3268:ASN:HA	5:EC:3271:ASP:HB2	1.84	0.59
6:FB:1656:THR:HB	6:FB:1659:ILE:HD13	1.84	0.59
6:FF:834:VAL:O	6:FF:835:SER:C	2.45	0.59
6:FF:895:ILE:HG12	7:GI:967:PHE:HE2	1.66	0.59
9:HB:762:HIS:HD2	9:HB:763:GLN:HE22	1.49	0.59
12:KG:320:LYS:HE3	12:KG:357:MET:HB2	1.84	0.59
15:NA:1138:THR:HG23	15:NA:1140:LEU:H	1.67	0.59
15:NC:361:VAL:HG11	15:NC:445:ILE:HD11	1.84	0.59
2:AB:46:GLN:HB2	5:EA:4522:VAL:HG21	1.83	0.59
4:DA:21:ASP:HB3	14:MA:277:VAL:HG13	1.84	0.59
6:FD:844:ALA:C	7:GC:896:ARG:HH22	2.10	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1209:GLU:O	6:FE:1210:LEU:C	2.45	0.59
7:GE:988:LYS:HD2	9:HA:402:ARG:HE	1.67	0.59
15:NC:604:GLU:HG3	15:NC:1198:ILE:HG21	1.84	0.59
15:NC:866:LEU:HD23	15:NC:869:PHE:HD2	1.68	0.59
1:AE:121:ARG:HB3	1:AE:213:ALA:HB2	1.84	0.59
1:AE:988:GLN:HA	1:AE:991:LEU:HG	1.84	0.59
4:DE:105:CYS:HA	4:DE:259:SER:HB2	1.83	0.59
5:EC:3255:GLU:HG3	7:GE:732:ALA:HB2	1.85	0.59
6:FA:2062:LEU:HA	6:FA:2065:THR:HG22	1.83	0.59
8:GD:13:ARG:HG3	8:GD:627:VAL:HG11	1.84	0.59
8:GH:287:LEU:HA	8:GH:290:LEU:HD23	1.85	0.59
8:GH:362:VAL:HG21	8:GH:380:MET:HE3	1.84	0.59
8:GH:469:ASP:HB2	8:GH:624:ARG:HH22	1.67	0.59
11:JA:1410:LEU:HD22	11:JA:1502:ILE:HD11	1.84	0.59
11:JC:1515:LEU:HD22	11:JC:1554:LEU:HD12	1.84	0.59
11:JC:1980:VAL:HG12	11:JC:1982:SER:H	1.67	0.59
2:AG:555:SER:HA	2:AG:558:ARG:HG2	1.84	0.59
3:BA:694:ARG:HD2	17:PA:290:PHE:HE1	1.67	0.59
3:CJ:1263:SER:HA	3:CJ:4457:PRO:HG3	1.85	0.59
6:FD:1182:ALA:CB	6:FD:1429:LEU:HB2	2.31	0.59
6:FE:1301:ALA:HA	6:FE:1430:PHE:HB3	1.85	0.59
6:FE:1436:PHE:O	6:FE:1437:ALA:C	2.45	0.59
6:FF:888:PRO:HG2	7:GI:897:SER:HB3	1.84	0.59
7:GG:747:SER:HB3	7:GG:993:SER:HB2	1.83	0.59
8:GH:656:ALA:HB3	8:GH:742:SER:H	1.68	0.59
8:GL:639:LEU:HD12	8:GL:666:LEU:HD23	1.83	0.59
16:OA:289:ALA:HB1	16:OA:297:LEU:HD21	1.85	0.59
18:QA:39:PHE:HA	18:QA:58:LEU:HD21	1.85	0.59
1:AD:71:LEU:HD11	1:AD:218:PRO:HB2	1.83	0.59
2:AG:178:GLU:HG3	2:AG:179:ASP:H	1.67	0.59
1:AI:243:VAL:HG21	19:RA:94:PRO:HG3	1.85	0.59
2:AJ:114:MET:HE1	2:AJ:143:ARG:HG3	1.84	0.59
4:DE:299:ARG:HD3	4:DE:302:ILE:HD13	1.84	0.59
5:EA:3650:THR:HG22	9:HC:500:LEU:HD22	1.83	0.59
5:EB:3255:GLU:HG2	7:GC:732:ALA:HB2	1.85	0.59
6:FB:1599:HIS:H	6:FB:1604:ASN:HD21	1.50	0.59
8:GD:526:ILE:HG12	8:GD:530:PRO:HD3	1.84	0.59
7:GE:980:LEU:HD12	7:GE:984:GLU:HG3	1.83	0.59
9:HA:795:LEU:HD13	9:HA:797:TYR:HE2	1.62	0.59
11:JA:900:PRO:HB2	11:JA:951:LEU:HD12	1.85	0.59
11:JB:68:ARG:HG3	11:JB:140:LEU:HD11	1.83	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:1555:VAL:HG11	15:NA:349:ARG:HH21	1.67	0.59
15:NA:564:ARG:HH22	15:NA:619:TYR:HA	1.67	0.59
15:ND:887:SER:HB2	15:ND:1156:LEU:HD12	1.85	0.59
1:AA:382:ILE:HG21	2:AB:464:ILE:HD11	1.84	0.59
3:CJ:1154:LEU:HD13	3:CJ:4516:ILE:HA	1.84	0.59
4:DD:43:PRO:HG3	8:GD:680:LEU:HD21	1.85	0.59
4:DF:56:LEU:HD23	4:DF:162:VAL:HG23	1.85	0.59
6:FC:1771:GLU:HG2	6:FC:1776:GLY:HA3	1.83	0.59
6:FD:1223:ALA:O	6:FD:1224:ALA:C	2.46	0.59
8:GD:762:SER:HA	8:GJ:555:LEU:HB3	1.85	0.59
11:JB:78:GLN:HE22	11:JB:80:GLU:HB3	1.67	0.59
11:JC:1032:VAL:HG21	11:JC:1063:ILE:HG23	1.85	0.59
11:JC:1412:LEU:HB3	11:JC:1504:ARG:HB2	1.85	0.59
12:KG:383:HIS:HA	12:KG:386:LEU:HD23	1.84	0.59
15:NA:983:ILE:HG23	15:NA:989:ILE:HB	1.85	0.59
15:NB:794:GLU:HG3	15:NB:797:ARG:HH11	1.67	0.59
15:NC:607:ALA:HB3	15:NC:609:GLN:HE22	1.67	0.59
3:BC:939:ARG:HH11	3:BC:954:LEU:HD11	1.68	0.58
3:CG:1236:LEU:HD21	3:CG:1255:VAL:HG13	1.85	0.58
5:EC:3611:GLU:HA	5:EC:3627:ARG:HH21	1.67	0.58
6:FB:1701:PHE:HZ	13:LL:484:VAL:HG11	1.68	0.58
6:FD:1184:ALA:N	6:FD:1424:CYS:HB3	2.18	0.58
6:FD:1233:ILE:HD11	6:FD:1268:VAL:CG2	2.33	0.58
6:FF:1388:PHE:HD1	6:FF:1418:GLU:HA	1.68	0.58
7:GG:548:ALA:HB1	9:HA:666:LYS:HG2	1.85	0.58
9:HB:798:ASP:OD2	13:LE:536:ASN:ND2	2.36	0.58
10:IA:466:GLN:HA	10:IA:638:ARG:HH21	1.68	0.58
15:NB:898:ASN:HA	15:NB:901:LEU:HB3	1.84	0.58
15:NB:1138:THR:HG23	15:NB:1140:LEU:H	1.68	0.58
15:NC:893:LEU:H	15:NC:1154:ASP:N	1.99	0.58
15:NC:910:ARG:HH12	15:NC:912:THR:HB	1.67	0.58
15:NC:931:TRP:HB2	15:NC:934:LEU:HB2	1.85	0.58
16:OB:289:ALA:HB1	16:OB:297:LEU:HD21	1.84	0.58
2:AB:336:ARG:HH12	1:AI:254:ARG:HG3	1.68	0.58
1:AE:411:LEU:HB3	1:AE:458:VAL:HG11	1.85	0.58
3:CI:1237:VAL:HA	3:CI:1244:PRO:HA	1.83	0.58
4:DE:255:ILE:HD11	8:GB:759:MET:HG3	1.85	0.58
4:DE:308:GLN:HA	4:DE:365:ILE:HD11	1.85	0.58
5:EB:4049:ALA:HA	6:FA:1905:GLN:HG2	1.86	0.58
6:FD:1184:ALA:HB3	6:FD:1424:CYS:HA	1.85	0.58
6:FF:1441:ILE:O	6:FF:1442:GLU:C	2.46	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GH:600:ARG:HH22	8:GH:605:LEU:HD22	1.68	0.58
12:KB:369:ILE:HG23	12:KB:576:ASN:HB3	1.85	0.58
3:BC:791:THR:HG21	3:BC:812:MET:HG2	1.85	0.58
4:DB:126:LEU:HD22	4:DB:158:LEU:HB3	1.84	0.58
5:EC:4405:ILE:HG21	5:EC:4427:LEU:HB3	1.85	0.58
6:FB:2051:VAL:O	6:FB:2055:THR:HG23	2.04	0.58
6:FC:2024:ARG:HA	9:HB:778:PRO:CG	2.29	0.58
6:FF:1073:HIS:O	6:FF:1074:ASP:C	2.46	0.58
8:GL:43:CYS:HB2	8:GL:46:LEU:HB2	1.85	0.58
15:NA:579:PRO:HB3	15:NA:616:LEU:HD12	1.83	0.58
15:NA:667:THR:HA	15:NA:673:ILE:HG23	1.85	0.58
3:CF:1175:ASN:HD21	3:CF:1253:VAL:HA	1.68	0.58
6:FC:2034:ARG:HG2	6:FC:2034:ARG:NH1	2.19	0.58
6:FD:1301:ALA:HA	6:FD:1430:PHE:HB3	1.85	0.58
7:GE:840:MET:HE1	7:GE:869:LEU:HD23	1.84	0.58
8:GF:377:MET:HB2	8:GF:380:MET:HE1	1.85	0.58
9:HB:808:HIS:O	9:HB:812:THR:CG2	2.44	0.58
10:IA:886:LEU:HD23	10:IA:888:THR:H	1.68	0.58
10:IA:910:LEU:HA	10:IA:913:LEU:HD13	1.86	0.58
10:IC:1236:VAL:HG22	10:IC:1285:VAL:HG12	1.83	0.58
11:JB:1873:ARG:HG3	11:JB:1874:ARG:HE	1.69	0.58
15:NA:613:GLN:HG2	15:NA:918:ALA:HB2	1.84	0.58
1:AI:157:LEU:HD12	1:AI:180:PHE:HD2	1.68	0.58
1:AI:429:ARG:HH21	2:AJ:417:ALA:HB1	1.67	0.58
1:AL:918:VAL:HB	1:AL:982:VAL:HG21	1.85	0.58
4:DA:133:LEU:HA	4:DA:136:MET:HE3	1.86	0.58
6:FE:968:LEU:HB2	6:FE:1027:LEU:HD11	1.85	0.58
6:FE:1108:PRO:HD3	9:HA:394:LEU:HG	1.85	0.58
7:GE:675:GLN:HE22	7:GE:691:VAL:HG13	1.67	0.58
8:GL:64:ASN:HD22	8:GL:515:THR:HG21	1.68	0.58
8:GL:111:TYR:HB2	8:GL:511:LEU:HB3	1.84	0.58
8:GL:374:LEU:HA	8:GL:377:MET:HB2	1.86	0.58
9:HA:758:ALA:O	9:HA:761:CYS:HB2	2.04	0.58
10:IC:1140:GLN:HA	10:IC:1143:MET:HG2	1.84	0.58
12:KC:593:HIS:HB2	12:KC:707:GLU:HB3	1.85	0.58
15:NB:1138:THR:HG21	15:NB:1143:LEU:HB3	1.85	0.58
15:ND:1138:THR:HG23	15:ND:1140:LEU:H	1.68	0.58
15:ND:1546:VAL:HG11	19:RD:174:LEU:HD21	1.85	0.58
2:AB:415:HIS:O	2:AB:418:LYS:HB3	2.03	0.58
2:AG:180:GLU:HA	2:AG:183:ALA:HB3	1.85	0.58
3:BA:964:GLN:HE21	16:OA:127:ILE:HG21	1.68	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:920:ARG:HH12	16:OB:266:GLN:HG3	1.69	0.58
4:DB:356:TYR:HB3	4:DB:382:LEU:HD22	1.86	0.58
4:DF:69:LEU:HB3	4:DF:76:MET:HG3	1.86	0.58
6:FA:2059:VAL:HG22	9:HA:754:LEU:HB2	1.85	0.58
7:GA:747:SER:HB3	7:GA:993:SER:HB2	1.86	0.58
7:GC:278:ASP:HB2	7:GC:281:GLU:HB3	1.84	0.58
7:GG:180:ARG:HD3	7:GG:829:VAL:HG21	1.84	0.58
8:GJ:327:HIS:H	8:GJ:330:ASP:HB2	1.68	0.58
9:HA:760:LYS:O	9:HA:763:GLN:HG2	2.04	0.58
11:JB:1319:HIS:HA	15:NB:1326:VAL:HG21	1.86	0.58
11:JC:1571:ARG:HH22	15:NA:346:SER:HB2	1.69	0.58
14:ME:217:ASN:HB3	14:ME:322:MET:HE1	1.85	0.58
15:NA:937:MET:HA	15:NA:940:TYR:HB3	1.84	0.58
2:AC:521:LEU:HD21	1:AD:56:LEU:HD22	1.86	0.58
1:AL:301:VAL:HG23	1:AL:332:THR:HG22	1.83	0.58
3:CG:1259:ALA:HB2	3:CG:4487:LEU:HD13	1.86	0.58
4:DE:275:LEU:HB2	4:DE:280:ALA:HB2	1.86	0.58
6:FD:806:ILE:HG23	6:FD:1112:ILE:HD11	1.85	0.58
7:GE:572:GLU:HA	7:GE:622:ARG:HH21	1.68	0.58
8:GF:13:ARG:HH22	8:GF:535:GLU:HB2	1.67	0.58
9:HB:553:TYR:HE1	9:HB:575:ARG:HH21	1.50	0.58
16:OC:289:ALA:HB1	16:OC:297:LEU:HD21	1.85	0.58
1:AL:345:PRO:HA	1:AL:348:GLU:HB3	1.85	0.58
3:CB:812:MET:HG3	3:CB:819:LEU:HD13	1.86	0.58
6:FA:2024:ARG:HA	9:HA:778:PRO:CG	2.30	0.58
6:FA:2030:ILE:HD11	9:HA:813:THR:HG22	1.85	0.58
7:GA:920:ALA:HB3	7:GA:955:VAL:HG11	1.86	0.58
7:GC:185:ARG:HG2	7:GC:697:PRO:HG2	1.84	0.58
7:GC:236:THR:HG21	7:GC:255:LEU:HD13	1.86	0.58
11:JA:805:CYS:HB3	11:JA:895:LEU:HB3	1.85	0.58
13:LK:353:ASN:HA	13:LK:356:LEU:HG	1.85	0.58
1:AL:793:LEU:HG	1:AL:988:GLN:HG3	1.86	0.58
3:BC:693:ARG:HA	3:BC:696:GLU:HG3	1.86	0.58
3:CB:761:LEU:HB3	3:CB:784:LEU:HD12	1.86	0.58
3:CI:1229:HIS:HB2	3:CI:4463:LEU:HB3	1.86	0.58
5:EB:3373:LYS:HG3	5:EB:3378:GLY:HA2	1.86	0.58
5:EC:4474:TYR:HB3	13:LK:532:LEU:HD12	1.86	0.58
6:FC:1684:THR:HG22	6:FC:1685:GLU:H	1.69	0.58
6:FD:1103:SER:O	6:FD:1104:GLY:C	2.47	0.58
8:GH:398:VAL:HG23	8:GH:721:LYS:HZ2	1.69	0.58
8:GJ:703:GLN:HA	8:GJ:706:LEU:HD23	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JA:489:VAL:HG11	11:JA:1439:LEU:HD23	1.85	0.58
11:JB:523:ASN:HD21	11:JB:766:GLY:H	1.52	0.58
15:NB:512:TYR:HA	15:NB:1473:ARG:HH22	1.69	0.58
15:NC:1118:VAL:HA	15:NC:1121:ASN:HB2	1.85	0.58
16:OA:184:ASN:HA	16:OA:295:LEU:HD11	1.86	0.58
5:EB:4405:ILE:HG13	5:EB:4428:MET:CE	2.33	0.58
6:FE:962:PHE:HE2	6:FE:965:TRP:HB2	1.68	0.58
6:FF:1103:SER:O	6:FF:1104:GLY:C	2.46	0.58
6:FF:1284:LEU:HB3	6:FF:1292:ALA:HB3	1.84	0.58
6:FF:1432:THR:O	6:FF:1433:ALA:C	2.47	0.58
7:GG:284:GLU:HA	7:GG:290:VAL:HG11	1.84	0.58
8:GH:78:CYS:HB3	8:GH:83:GLN:H	1.67	0.58
11:JA:81:ARG:HG3	11:JA:106:LEU:HD11	1.84	0.58
15:NA:733:VAL:HB	15:NA:742:LEU:HD13	1.84	0.58
15:ND:347:LEU:HB3	15:ND:491:PRO:HD2	1.85	0.58
2:AK:448:ASN:C	2:AK:448:ASN:HD22	2.12	0.57
3:CG:1195:LEU:HD22	3:CG:1210:LEU:HD11	1.86	0.57
5:EA:3283:GLU:HG2	5:EA:3286:ARG:HH21	1.68	0.57
6:FD:1200:LEU:HB3	6:FD:1205:ILE:HG12	1.85	0.57
6:FF:1213:VAL:HA	6:FF:1231:ARG:O	2.04	0.57
7:GA:166:LEU:HA	7:GA:169:ILE:HD12	1.86	0.57
7:GG:967:PHE:HA	7:GG:970:LEU:HD23	1.86	0.57
8:GH:64:ASN:C	8:GH:64:ASN:HD22	2.10	0.57
8:GH:179:MET:HG2	8:GH:197:VAL:HG12	1.86	0.57
7:GI:940:GLN:HA	7:GI:943:GLN:HB2	1.86	0.57
9:HD:766:SER:O	9:HD:768:THR:N	2.37	0.57
12:KB:512:ARG:HB3	12:KB:518:GLU:HG3	1.86	0.57
5:EB:4881:ARG:HB2	5:EB:4886:LYS:HB2	1.86	0.57
6:FE:1216:TRP:O	6:FE:1217:GLU:C	2.46	0.57
10:IA:414:ALA:HB2	10:IA:424:VAL:HG11	1.86	0.57
10:IC:627:CYS:HA	10:IC:699:CYS:HA	1.87	0.57
11:JA:192:LEU:HB3	11:JA:1063:ILE:HD13	1.85	0.57
12:KA:319:TYR:HB2	12:KA:334:VAL:HG11	1.84	0.57
14:ME:249:GLU:HA	14:ME:252:THR:HG22	1.85	0.57
15:NA:885:LEU:HA	15:NA:888:ARG:HB2	1.86	0.57
15:NB:647:GLN:HA	15:NB:650:ARG:HD2	1.85	0.57
16:OB:284:GLU:HA	16:OB:287:LEU:HD23	1.85	0.57
1:AI:240:MET:HA	19:RA:24:ARG:HD2	1.86	0.57
5:EA:4648:PHE:HA	5:EA:4651:MET:HE3	1.86	0.57
5:EC:3273:LEU:HD23	5:EC:3494:VAL:HG21	1.87	0.57
6:FE:1097:SER:O	6:FE:1101:ALA:N	2.37	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GF:172:ILE:HG12	8:GF:180:LEU:HA	1.86	0.57
10:IB:1053:ARG:HG2	10:IB:1107:GLU:HG2	1.85	0.57
1:AD:107:LEU:HD13	1:AD:221:VAL:HG11	1.86	0.57
1:AI:247:THR:HG23	1:AI:248:LEU:HD12	1.86	0.57
3:CG:4468:LYS:HB2	3:CG:4488:MET:HB3	1.86	0.57
5:EB:3238:SER:H	5:EB:3241:GLU:HG3	1.70	0.57
5:EB:4207:PHE:HB3	5:EB:4250:ARG:HH22	1.68	0.57
5:EC:3227:ALA:HB2	5:EC:4159:THR:HG22	1.85	0.57
6:FC:1844:LEU:HD12	6:FC:1922:VAL:HG21	1.86	0.57
6:FE:822:GLY:O	6:FE:823:GLY:C	2.47	0.57
6:FE:1187:ILE:HG21	6:FE:1282:LEU:HD21	1.87	0.57
6:FF:1218:ALA:HA	6:FF:1220:ARG:HH21	1.69	0.57
7:GC:738:LEU:HD12	7:GC:797:ILE:HG13	1.85	0.57
7:GG:294:ALA:HB3	7:GG:687:ARG:HB3	1.85	0.57
7:GG:502:TYR:HE2	7:GG:562:ILE:HG22	1.69	0.57
10:IB:169:LEU:HD11	10:IB:201:LEU:HA	1.86	0.57
11:JB:1726:LEU:HB3	11:JB:1730:THR:HG21	1.87	0.57
12:KC:378:PHE:O	12:KC:379:SER:C	2.47	0.57
15:NA:679:ASP:HB2	15:NA:696:PHE:HB3	1.85	0.57
15:NB:737:PRO:HG3	15:NB:749:PRO:HD3	1.86	0.57
15:NC:343:VAL:HG21	15:NC:490:VAL:HG11	1.87	0.57
1:AL:25:ALA:HB1	15:NB:1336:THR:HG22	1.87	0.57
4:DC:297:ARG:HA	4:DC:300:GLN:HB3	1.85	0.57
5:EC:4044:ILE:HG22	5:EC:4048:LYS:HE3	1.86	0.57
6:FD:994:PRO:HD2	12:KA:230:GLN:NE2	2.19	0.57
6:FE:1104:GLY:N	9:HA:393:VAL:HG11	2.19	0.57
7:GC:319:VAL:HG21	7:GC:426:ASN:HD21	1.70	0.57
11:JB:147:ARG:HA	11:JB:151:LEU:HD22	1.87	0.57
11:JC:1130:LEU:HD21	11:JC:1164:MET:HG2	1.86	0.57
11:JC:2276:ARG:HB3	11:JC:2280:ARG:HH12	1.68	0.57
12:KC:526:TRP:HZ2	12:KC:582:ILE:HG23	1.70	0.57
12:KE:525:PRO:HA	12:KE:542:PRO:HG3	1.86	0.57
15:NC:622:THR:HG23	15:NC:650:ARG:HH12	1.70	0.57
2:AK:5:VAL:HA	2:AK:84:LEU:HB3	1.86	0.57
4:DC:69:LEU:HB3	4:DC:76:MET:HG3	1.86	0.57
5:EA:4095:LYS:HB3	9:HB:796:ASP:CG	2.30	0.57
5:EA:4629:ARG:HH21	5:EA:4714:GLU:HB3	1.70	0.57
8:GF:143:CYS:HB2	8:GF:277:ARG:HD3	1.86	0.57
12:KB:370:LEU:HD13	12:KB:377:LEU:HD11	1.87	0.57
15:NC:883:LEU:HD23	15:NC:1123:ALA:HB1	1.84	0.57
15:ND:597:GLN:HB2	15:ND:914:ILE:HG22	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:869:PHE:HE2	15:ND:1131:LEU:HD13	1.70	0.57
1:AL:728:VAL:HG13	1:AL:729:THR:HG23	1.85	0.57
4:DF:269:LEU:HD13	4:DF:338:ILE:HG21	1.86	0.57
5:EC:3399:PHE:HB3	5:EC:3418:SER:HB2	1.86	0.57
6:FF:922:LEU:O	6:FF:925:GLU:HB2	2.05	0.57
7:GA:670:ASN:HB3	7:GA:698:VAL:HB	1.87	0.57
8:GB:100:LEU:HD12	8:GB:104:LEU:HD12	1.86	0.57
8:GD:150:ASP:HA	8:GD:153:ARG:HD3	1.87	0.57
9:HD:852:LYS:HD3	9:HD:855:ARG:HH11	1.70	0.57
13:LC:489:LEU:HD22	13:LD:489:LEU:HD13	1.87	0.57
15:NC:1493:VAL:HG12	15:NC:1496:LEU:HD12	1.86	0.57
19:RD:32:THR:HG22	19:RD:36:ARG:HH12	1.70	0.57
1:AA:437:PHE:HB3	2:AB:410:TYR:HE1	1.69	0.57
1:AD:212:ARG:HH12	11:JA:1339:SER:N	2.02	0.57
2:AG:200:GLU:HG3	2:AG:201:LYS:H	1.70	0.57
3:BB:753:LEU:HD22	3:BB:787:ILE:HD11	1.87	0.57
4:DE:13:VAL:HA	4:DE:16:LEU:HD23	1.85	0.57
5:EC:4312:PHE:HB3	5:EC:4351:VAL:HG22	1.87	0.57
6:FF:1071:PHE:HB2	6:FF:1076:ILE:HD11	1.87	0.57
7:GA:305:PRO:HB3	7:GA:354:ARG:HG2	1.86	0.57
7:GC:350:ARG:HH12	7:GC:352:ASP:HB2	1.69	0.57
7:GG:236:THR:HG21	7:GG:255:LEU:HD13	1.87	0.57
10:IB:882:VAL:HG12	16:OB:1044:ARG:HH22	1.70	0.57
11:JA:541:LEU:HD11	11:JA:548:PHE:HA	1.86	0.57
12:KB:215:PRO:HG2	12:KB:288:PHE:HB3	1.87	0.57
15:NA:618:ARG:HH21	15:NA:661:ARG:HH22	1.53	0.57
15:NA:725:ILE:HG13	15:NA:799:ILE:HG21	1.85	0.57
15:NB:791:GLU:HG2	15:NB:1142:LEU:HD21	1.87	0.57
16:OC:70:THR:HG23	16:OC:72:SER:H	1.70	0.57
1:AD:227:LYS:HB2	10:IB:1251:VAL:HG13	1.87	0.57
4:DC:356:TYR:HB3	4:DC:382:LEU:HD22	1.87	0.57
6:FB:1729:ALA:HA	6:FB:1902:LEU:HD23	1.86	0.57
6:FD:1222:CYS:HB3	6:FD:1225:ILE:HD12	1.87	0.57
6:FD:1425:PRO:HD2	6:FD:1429:LEU:HD12	1.86	0.57
6:FE:1282:LEU:HD11	6:FE:1419:LEU:HD22	1.86	0.57
8:GD:7:GLU:HB2	8:GD:13:ARG:HD3	1.86	0.57
7:GE:311:LEU:HD11	7:GE:436:ALA:HB1	1.86	0.57
7:GI:293:VAL:HA	7:GI:688:ARG:HG3	1.87	0.57
7:GK:536:THR:HA	9:HC:553:TYR:HB2	1.86	0.57
11:JA:157:GLU:HB3	11:JA:172:LEU:HD11	1.87	0.57
12:KE:212:LEU:HD22	12:KE:285:ILE:HG12	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:ME:313:ARG:HD3	14:ME:316:GLN:HE22	1.69	0.57
15:NB:866:LEU:HD23	15:NB:869:PHE:HD2	1.70	0.57
15:ND:613:GLN:HG2	15:ND:918:ALA:HB2	1.87	0.57
2:AB:371:VAL:HG13	2:AB:375:CYS:HB3	1.87	0.57
1:AH:1046:THR:HG22	1:AH:1048:ALA:H	1.70	0.57
5:EC:3412:LEU:HG	5:EC:3507:VAL:HG22	1.86	0.57
6:FC:1942:PHE:HZ	6:FC:2050:LEU:HD11	1.70	0.57
6:FC:2104:GLN:HA	6:FC:2107:GLN:HE21	1.70	0.57
6:FD:837:ALA:O	6:FD:838:ASN:C	2.48	0.57
7:GI:516:VAL:HG11	7:GI:565:LEU:HG	1.85	0.57
8:GJ:218:SER:HB3	8:GJ:221:ALA:HB2	1.86	0.57
10:IC:725:LYS:HB3	10:IC:729:ARG:NH1	2.19	0.57
11:JB:1687:LEU:HA	11:JB:1690:ASP:HB2	1.86	0.57
4:DA:277:ARG:HG2	4:DA:281:GLN:HE22	1.69	0.56
6:FD:809:ILE:HD13	6:FD:972:VAL:HG21	1.87	0.56
6:FD:1185:VAL:O	6:FD:1186:TRP:C	2.48	0.56
6:FE:1182:ALA:HA	6:FE:1425:PRO:HD3	1.87	0.56
6:FF:1004:GLY:O	6:FF:1005:PRO:C	2.48	0.56
6:FF:1182:ALA:HB2	6:FF:1430:PHE:H	1.68	0.56
7:GA:464:LEU:HB3	7:GA:502:TYR:HE2	1.69	0.56
11:JC:1813:ILE:HG23	11:JC:1992:LEU:HD22	1.87	0.56
11:JC:1852:HIS:CD2	11:JC:1985:LEU:HG	2.37	0.56
12:KC:606:ARG:HB2	12:KC:623:ILE:HB	1.87	0.56
14:MD:82:ARG:HG2	14:MD:87:LEU:HD22	1.87	0.56
15:NA:541:MET:HE1	15:NA:1189:PHE:HD2	1.69	0.56
1:AA:248:LEU:HB2	1:AA:258:CYS:HA	1.86	0.56
1:AE:316:ILE:CD1	9:HD:872:MET:HG2	2.35	0.56
1:AE:815:LEU:HD13	13:LM:354:ARG:HG3	1.87	0.56
1:AH:63:LEU:HD12	1:AH:226:MET:HE2	1.85	0.56
6:FD:807:ALA:O	6:FD:808:SER:HB2	2.03	0.56
6:FE:1095:LEU:O	6:FE:1096:LEU:C	2.48	0.56
6:FE:1249:ILE:HG13	6:FE:1250:GLU:N	2.19	0.56
7:GA:764:LEU:HD12	7:GA:870:ARG:HE	1.69	0.56
7:GC:885:GLU:HA	7:GC:890:MET:HG2	1.86	0.56
8:GH:133:PRO:HD2	8:GH:294:TRP:HH2	1.70	0.56
10:IB:233:ARG:HH11	10:IB:785:LEU:HD11	1.71	0.56
11:JC:148:ARG:HG3	11:JC:149:LEU:H	1.70	0.56
15:NC:924:LEU:HB3	15:NC:1107:THR:HG23	1.85	0.56
2:AC:29:LEU:HD13	2:AC:283:LEU:HD21	1.87	0.56
1:AH:408:LYS:HE3	16:OC:24:LEU:HD13	1.88	0.56
3:CB:790:ASN:HD22	3:CB:807:LEU:HB3	1.71	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:4484:VAL:HA	3:CE:4499:PRO:HA	1.87	0.56
4:DB:179:ALA:HB3	4:DE:189:ARG:HH12	1.70	0.56
4:DC:316:ARG:HB2	14:MJ:246:ASN:ND2	2.20	0.56
5:EA:4167:ASP:HB2	5:EA:4171:ILE:HG12	1.87	0.56
5:EB:3642:PRO:HD3	5:EB:3673:LEU:HD23	1.85	0.56
5:EC:4898:MET:HG3	5:EC:4902:ALA:HB3	1.88	0.56
6:FD:861:LEU:CD2	6:FD:861:LEU:N	2.46	0.56
6:FD:973:ILE:HG22	6:FD:1019:VAL:HG22	1.88	0.56
6:FE:825:PRO:O	6:FE:826:LEU:C	2.48	0.56
6:FE:842:GLY:N	7:GE:957:ARG:HH21	2.04	0.56
6:FF:803:ARG:HB3	6:FF:907:ASN:HA	1.86	0.56
7:GC:605:VAL:HB	7:GC:679:LEU:HB3	1.86	0.56
8:GD:112:ILE:HG22	8:GD:510:ARG:HG2	1.86	0.56
7:GE:828:PRO:HG2	7:GE:831:ARG:HG2	1.88	0.56
8:GH:77:THR:HB	8:GH:84:ARG:HH11	1.70	0.56
7:GK:518:LEU:HD23	7:GK:520:ILE:HD11	1.86	0.56
7:GK:543:LYS:H	9:HC:596:TYR:HB3	1.70	0.56
9:HC:674:VAL:HG13	9:HC:712:ILE:HG12	1.87	0.56
10:IA:341:GLU:HG3	10:IA:536:ARG:HD3	1.86	0.56
11:JA:75:VAL:HG23	11:JA:81:ARG:HD2	1.86	0.56
11:JC:1425:LEU:HB3	11:JC:1428:LEU:HD23	1.87	0.56
14:ME:301:LEU:HB3	14:MF:301:LEU:HD22	1.87	0.56
15:NA:893:LEU:H	15:NA:1154:ASP:N	2.03	0.56
15:NB:812:ARG:HD2	15:NB:870:TYR:HB2	1.87	0.56
15:NB:894:LEU:HB2	15:NB:1152:GLU:HB3	1.86	0.56
15:NC:578:HIS:CE1	15:NC:580:PHE:HB2	2.41	0.56
15:ND:666:ILE:HG21	15:ND:720:LEU:HD13	1.86	0.56
15:ND:818:ILE:HB	15:ND:842:THR:HA	1.86	0.56
19:RD:139:LEU:HB2	19:RD:141:LEU:HD23	1.88	0.56
3:CC:791:THR:HG22	3:CC:811:ILE:HA	1.88	0.56
3:CE:1231:ARG:H	3:CE:4466:ILE:HD11	1.70	0.56
6:FD:1190:ARG:HE	6:FD:1420:ARG:HD3	1.69	0.56
7:GA:207:LEU:HD13	7:GA:690:ARG:HH21	1.71	0.56
8:GB:665:LEU:HB2	8:GB:676:TRP:HB3	1.88	0.56
7:GE:276:ARG:HH21	7:GE:285:LEU:HG	1.69	0.56
8:GJ:160:LEU:HA	8:GJ:163:MET:HE3	1.87	0.56
2:AB:29:LEU:HD13	2:AB:283:LEU:HD21	1.87	0.56
3:BA:917:LEU:HD21	16:OA:174:VAL:HG21	1.88	0.56
4:DF:327:PHE:HB3	4:DF:332:LEU:HD22	1.88	0.56
5:EA:3609:LEU:HD23	5:EA:3612:LEU:HD22	1.86	0.56
6:FD:822:GLY:O	6:FD:823:GLY:C	2.48	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:918:GLN:O	6:FF:919:GLN:C	2.48	0.56
7:GA:371:LEU:HD13	7:GA:412:VAL:HG22	1.88	0.56
15:NA:1546:VAL:HG12	15:NA:1550:MET:HE1	1.88	0.56
15:NC:880:THR:HB	15:NC:884:LYS:HE3	1.88	0.56
15:ND:537:LYS:HA	15:ND:542:LEU:HD12	1.87	0.56
19:RB:50:VAL:HG21	19:RB:71:LEU:HD11	1.86	0.56
1:AA:994:LEU:HA	7:GA:215:PRO:HA	1.88	0.56
5:EC:4376:HIS:HD2	5:EC:4377:PRO:HD2	1.71	0.56
6:FC:1901:LEU:HB3	6:FC:1904:GLU:HA	1.87	0.56
6:FC:2087:LEU:HD13	9:HB:872:MET:HE1	1.87	0.56
6:FD:854:TRP:CD1	6:FD:854:TRP:H	2.24	0.56
6:FD:1223:ALA:HA	6:FD:1226:LEU:HD12	1.87	0.56
6:FE:992:PRO:HB3	12:KB:231:PHE:CZ	2.39	0.56
6:FE:1103:SER:O	6:FE:1104:GLY:C	2.48	0.56
6:FE:1223:ALA:O	6:FE:1226:LEU:N	2.35	0.56
6:FF:866:PHE:HB3	6:FF:1274:PRO:HD2	1.88	0.56
6:FF:990:PHE:HB2	12:KC:313:PHE:HE2	1.70	0.56
9:HB:761:CYS:O	9:HB:762:HIS:C	2.49	0.56
11:JA:837:ASN:HA	11:JA:840:ILE:HG22	1.87	0.56
11:JC:542:LEU:HD11	11:JC:1320:PHE:HB2	1.87	0.56
11:JC:1873:ARG:HH21	11:JC:1877:ALA:HB2	1.69	0.56
12:KE:215:PRO:HB3	12:KE:286:GLU:HB3	1.86	0.56
12:KF:521:PRO:HB2	12:KF:523:VAL:HG12	1.88	0.56
19:RC:126:LYS:HE3	19:RC:162:ASN:HB3	1.88	0.56
1:AI:159:LYS:HE2	1:AI:183:LEU:HD12	1.88	0.56
4:DA:385:LYS:HZ3	13:LB:461:VAL:HG23	1.70	0.56
4:DD:32:SER:HB2	4:DD:121:ALA:HB1	1.87	0.56
5:EB:3418:SER:HB3	5:EB:3423:VAL:HB	1.88	0.56
5:EC:3304:LYS:HD3	5:EC:4163:MET:HE3	1.88	0.56
6:FD:806:ILE:HD13	6:FD:1114:VAL:HG13	1.86	0.56
6:FD:1233:ILE:CD1	6:FD:1268:VAL:HG22	2.36	0.56
8:GB:310:THR:HB	8:GB:319:LEU:HA	1.86	0.56
8:GH:396:ILE:HG22	8:GH:721:LYS:NZ	2.20	0.56
8:GL:200:GLY:HA2	8:GL:281:LEU:HD22	1.88	0.56
9:HA:765:TRP:N	9:HA:765:TRP:HE3	2.04	0.56
10:IC:634:ALA:HB2	10:IC:692:GLU:HB3	1.87	0.56
11:JA:758:GLU:HA	11:JA:761:LYS:HB3	1.88	0.56
11:JA:1090:LEU:HB2	11:JA:1128:LYS:HZ3	1.69	0.56
12:KC:574:LEU:HA	12:KC:701:ALA:HA	1.88	0.56
12:KE:588:ALA:HB3	12:KE:710:ASN:HD21	1.71	0.56
1:AH:397:LYS:HE2	1:AH:401:THR:HG21	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CA:784:LEU:HD22	3:CA:826:LEU:HD13	1.87	0.56
4:DB:136:MET:HB3	4:DB:147:ARG:HH12	1.69	0.56
5:EC:3281:VAL:HG21	5:EC:3450:ASN:HB3	1.88	0.56
5:EC:4667:PRO:HA	5:EC:4670:TRP:HB3	1.86	0.56
6:FD:824:TYR:CE2	7:GC:963:GLU:HG2	2.41	0.56
6:FF:1424:CYS:SG	6:FF:1429:LEU:HG	2.46	0.56
11:JC:87:VAL:HG22	11:JC:90:ARG:HH12	1.70	0.56
13:LI:524:LYS:O	13:LJ:525:SER:HA	2.06	0.56
14:MF:254:ILE:HA	14:MF:257:LYS:HG2	1.87	0.56
15:ND:893:LEU:H	15:ND:1153:ALA:C	2.14	0.56
15:ND:1547:ILE:HB	19:RD:141:LEU:HD13	1.88	0.56
1:AI:266:HIS:HB3	1:AI:277:ARG:HH21	1.71	0.56
6:FD:887:ARG:HA	12:KA:305:HIS:ND1	2.21	0.56
6:FD:1022:THR:HG22	6:FD:1023:ALA:H	1.71	0.56
6:FD:1242:GLN:HB2	6:FD:1259:LEU:HD12	1.88	0.56
6:FD:1280:VAL:HG23	6:FD:1300:LEU:HD11	1.88	0.56
6:FF:1434:ALA:O	6:FF:1435:GLU:C	2.49	0.56
8:GB:545:ALA:HB1	8:GB:605:LEU:HD11	1.87	0.56
7:GC:516:VAL:HG11	7:GC:565:LEU:HB3	1.87	0.56
7:GG:518:LEU:HD12	7:GG:573:VAL:HG22	1.88	0.56
7:GG:537:GLY:H	9:HA:554:ASP:N	2.04	0.56
7:GK:607:ARG:HH12	7:GK:609:ARG:HE	1.53	0.56
9:HC:683:VAL:HG12	9:HC:684:GLU:HG2	1.88	0.56
9:HD:773:ALA:HB3	13:LJ:527:VAL:HG13	1.88	0.56
10:IB:1326:THR:HG23	10:IB:1328:LYS:H	1.71	0.56
10:IC:239:LEU:HD23	10:IC:792:ILE:HD11	1.87	0.56
12:KE:272:ASN:HD21	12:KE:275:ASP:HB2	1.71	0.56
12:KE:582:ILE:HD12	12:KE:715:LEU:HB3	1.88	0.56
14:MK:93:SER:HA	14:MK:96:ASP:HB2	1.87	0.56
2:AC:173:ARG:HH11	1:AD:407:VAL:HG22	1.71	0.56
1:AE:672:ASP:HB3	1:AE:676:ARG:HH21	1.71	0.56
2:AG:462:GLU:HG3	2:AG:466:GLN:HE21	1.71	0.56
6:FD:808:SER:HB3	6:FD:1113:PHE:HD2	1.70	0.56
6:FD:1203:ARG:HH21	6:FD:1207:GLU:HG3	1.71	0.56
7:GA:437:VAL:HG13	7:GA:505:PHE:HE2	1.71	0.56
8:GH:419:PHE:HE2	8:GH:505:PRO:HG3	1.71	0.56
8:GJ:432:LYS:HB2	8:GJ:451:SER:HB3	1.87	0.56
7:GK:184:ALA:HB3	7:GK:708:SER:HB2	1.88	0.56
10:IC:806:ILE:HG21	10:IC:858:LEU:HD21	1.88	0.56
11:JA:1726:LEU:HB3	11:JA:1730:THR:HG21	1.88	0.56
11:JB:2013:LEU:HD21	11:JB:2262:LEU:HD22	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:444:PHE:HA	11:JC:447:ILE:HG22	1.87	0.56
12:KF:404:GLU:HB2	12:KF:489:MET:HE1	1.88	0.56
12:KG:546:LYS:HG3	12:KG:714:THR:HG22	1.88	0.56
15:NA:892:TRP:HB3	15:NA:1154:ASP:HB2	1.88	0.56
19:RA:64:PRO:HA	19:RA:67:VAL:HG22	1.88	0.56
3:CC:689:LEU:HA	3:CC:692:LEU:HD12	1.88	0.55
3:CJ:4522:LEU:HB3	3:CJ:4524:LEU:HD23	1.88	0.55
5:EB:4198:ILE:HA	5:EB:4202:LEU:HD23	1.87	0.55
6:FD:1189:ILE:HG23	6:FD:1417:ILE:HD11	1.88	0.55
6:FE:983:LEU:HA	12:KB:726:ASP:OD1	2.06	0.55
6:FF:1425:PRO:HD3	6:FF:1429:LEU:HD12	1.85	0.55
7:GA:502:TYR:HE1	7:GA:562:ILE:HG22	1.71	0.55
8:GH:302:LEU:HA	8:GH:363:ASP:HB2	1.88	0.55
7:GI:598:ARG:HH22	7:GI:637:ASN:HD22	1.52	0.55
9:HB:640:GLY:HA3	9:HB:653:ILE:HG12	1.88	0.55
11:JA:446:ARG:HH12	11:JA:505:LEU:HD11	1.72	0.55
11:JA:542:LEU:HD11	11:JA:1320:PHE:HB2	1.89	0.55
11:JB:2023:LEU:HD13	11:JB:2129:ARG:HD2	1.88	0.55
11:JC:1084:VAL:HG11	11:JC:1153:LEU:HD23	1.88	0.55
11:JC:2271:ASP:HB3	11:JC:2274:ILE:HG22	1.88	0.55
12:KB:543:VAL:HG13	12:KB:544:LEU:HG	1.88	0.55
14:ME:288:SER:HA	14:ME:291:LEU:HB3	1.88	0.55
15:NC:667:THR:HA	15:NC:673:ILE:HG23	1.89	0.55
15:NC:812:ARG:HH21	15:NC:870:TYR:HD2	1.54	0.55
15:ND:892:TRP:N	15:ND:1155:GLU:H	2.03	0.55
15:ND:982:ILE:HD11	15:ND:1029:SER:H	1.71	0.55
19:RD:92:ASP:HB3	19:RD:94:PRO:HD2	1.88	0.55
20:SD:143:VAL:HA	20:SD:146:MET:HB2	1.87	0.55
2:AF:209:SER:HB3	2:AF:259:VAL:HA	1.87	0.55
1:AH:131:ARG:HG2	1:AH:205:ARG:HH12	1.71	0.55
3:CB:676:PHE:HA	17:PC:251:HIS:HB2	1.87	0.55
3:CE:1129:ARG:HD3	10:IA:1264:ILE:HD11	1.86	0.55
4:DA:6:LYS:HZ3	4:DD:181:ILE:HA	1.71	0.55
4:DA:300:GLN:HG3	4:DA:355:CYS:HB2	1.88	0.55
5:EA:4095:LYS:HD3	9:HB:796:ASP:OD2	2.07	0.55
5:EC:3267:SER:HB2	5:EC:3409:SER:HB2	1.87	0.55
6:FD:839:GLY:HA3	12:KA:681:MET:CE	2.36	0.55
6:FD:997:THR:HG23	12:KA:230:GLN:HE22	1.70	0.55
6:FE:1003:ILE:HG12	6:FE:1009:VAL:HG22	1.87	0.55
7:GA:515:SER:HB3	7:GA:634:PRO:HB2	1.88	0.55
8:GH:421:ALA:HB3	8:GH:465:ALA:HB3	1.87	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GL:534:GLN:HE22	8:GL:591:ILE:HD13	1.71	0.55
10:IC:1098:HIS:HE1	10:IC:1121:LYS:HG3	1.70	0.55
11:JA:440:PRO:HG2	11:JA:1477:TRP:HB3	1.88	0.55
12:KC:664:ILE:HB	12:KC:682:LEU:HB3	1.89	0.55
12:KG:298:GLN:HG3	12:KG:303:TYR:HB2	1.87	0.55
2:AC:464:ILE:HD11	1:AD:382:ILE:HG21	1.89	0.55
1:AE:38:VAL:HG11	1:AE:111:ILE:HG23	1.87	0.55
3:CC:695:LEU:HD22	3:CC:743:SER:HB2	1.88	0.55
5:EA:3445:VAL:HG21	5:EA:3570:LEU:HD23	1.88	0.55
5:EB:3650:THR:HG22	9:HB:500:LEU:HD22	1.87	0.55
6:FD:1005:PRO:HB2	6:FD:1006:PRO:HD3	1.88	0.55
6:FD:1186:TRP:CE3	6:FD:1267:GLN:HB2	2.41	0.55
6:FF:1124:ILE:O	6:FF:1125:ASN:C	2.50	0.55
8:GD:422:LYS:HB3	8:GD:501:SER:HB3	1.88	0.55
8:GJ:317:VAL:HG11	8:GJ:325:ILE:HG22	1.88	0.55
9:HA:782:ALA:O	9:HA:783:SER:C	2.49	0.55
11:JB:191:ASP:HB3	11:JB:194:VAL:HG12	1.88	0.55
14:MJ:288:SER:HA	14:MJ:291:LEU:HB3	1.88	0.55
2:AG:553:THR:HB	1:AH:471:GLU:HG2	1.89	0.55
2:AK:319:LEU:HD22	2:AK:327:ILE:HD11	1.89	0.55
1:AL:793:LEU:HD13	1:AL:801:ARG:HG3	1.88	0.55
3:CF:1173:VAL:HA	3:CF:1255:VAL:HG12	1.87	0.55
5:EA:3765:VAL:HG12	11:JB:932:PRO:HG2	1.89	0.55
6:FE:1193:VAL:HG21	6:FE:1416:GLN:HB3	1.89	0.55
8:GH:142:THR:HG23	8:GH:265:ASP:HB2	1.87	0.55
8:GH:215:LEU:HA	8:GH:238:ARG:HH22	1.70	0.55
7:GI:186:VAL:HG23	7:GI:696:MET:HG2	1.87	0.55
7:GK:236:THR:HG21	7:GK:255:LEU:HD13	1.88	0.55
9:HA:765:TRP:HE3	9:HA:765:TRP:H	1.52	0.55
10:IB:1294:ILE:HD12	10:IB:1358:LEU:HD11	1.88	0.55
11:JB:1869:ALA:HB2	11:JB:2072:GLN:HE22	1.72	0.55
15:NB:1160:LEU:HD12	15:NB:1165:VAL:HG11	1.89	0.55
19:RD:113:ARG:NH1	19:RD:114:GLU:HB3	2.22	0.55
1:AE:357:ILE:HG23	2:AF:485:LEU:HD12	1.88	0.55
2:AJ:92:LEU:HD23	2:AJ:277:VAL:HG11	1.89	0.55
3:CJ:4479:LEU:HB3	3:CJ:4482:LEU:HD23	1.88	0.55
5:EA:3436:TYR:HE1	5:EA:4014:VAL:HG22	1.72	0.55
6:FC:1968:LYS:HA	6:FC:1971:LYS:HD2	1.87	0.55
6:FD:1003:ILE:HG12	6:FD:1009:VAL:HG13	1.89	0.55
6:FE:817:VAL:O	6:FE:818:VAL:C	2.49	0.55
6:FE:1186:TRP:HE3	6:FE:1267:GLN:HB2	1.70	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:1026:PRO:HB2	6:FF:1029:GLN:HG2	1.88	0.55
7:GA:544:PRO:HD3	9:HB:596:TYR:HA	1.88	0.55
8:GB:168:MET:HG2	8:GB:247:PRO:HA	1.89	0.55
7:GE:292:PHE:HD2	7:GE:689:ILE:HD11	1.72	0.55
7:GG:169:ILE:HD11	7:GG:697:PRO:HD3	1.88	0.55
8:GH:374:LEU:HD23	8:GH:613:ASP:HB2	1.87	0.55
7:GI:176:ARG:HD3	7:GI:180:ARG:HH22	1.71	0.55
8:GJ:171:ILE:HG23	8:GJ:181:HIS:HB2	1.88	0.55
8:GJ:561:LEU:HD11	8:GJ:596:MET:HG3	1.89	0.55
9:HA:642:THR:HG22	9:HA:643:PHE:H	1.70	0.55
12:KB:240:ILE:HD11	12:KB:294:ARG:HH11	1.69	0.55
13:LK:483:ARG:HG2	13:LK:487:MET:HE1	1.87	0.55
1:AE:378:VAL:HG11	2:AF:543:MET:HE3	1.89	0.55
2:AF:213:HIS:HE1	2:AF:258:GLY:HA3	1.70	0.55
1:AH:91:ILE:HG21	1:AH:150:LYS:HZ2	1.72	0.55
1:AH:988:GLN:HA	1:AH:991:LEU:HD23	1.88	0.55
3:CE:1229:HIS:HB3	3:CE:4463:LEU:HD13	1.88	0.55
4:DF:378:ILE:HG23	4:DF:382:LEU:HD13	1.89	0.55
5:EC:4719:ASP:HA	5:EC:4722:PRO:HD2	1.89	0.55
7:GA:604:ALA:HB1	7:GA:678:LEU:HD11	1.88	0.55
8:GD:726:ASN:HB2	8:GD:729:GLY:HA3	1.89	0.55
8:GL:354:GLN:HA	8:GL:357:ARG:HG2	1.88	0.55
9:HA:496:GLU:HG3	9:HA:499:ARG:HH11	1.71	0.55
9:HB:722:SER:HA	9:HB:724:PHE:H	1.71	0.55
9:HB:778:PRO:HB2	9:HB:779:PRO:CD	2.37	0.55
10:IA:451:VAL:HG13	10:IA:455:LEU:HD12	1.89	0.55
10:IB:1139:VAL:HG13	10:IB:1203:LEU:HD22	1.88	0.55
11:JC:1499:HIS:HB3	11:JC:1502:ILE:HG22	1.89	0.55
12:KA:319:TYR:HE2	12:KA:357:MET:HE1	1.71	0.55
12:KC:383:HIS:O	12:KC:386:LEU:HD23	2.07	0.55
12:KC:502:LEU:HA	12:KC:505:LEU:HB2	1.87	0.55
12:KF:343:ASN:HB2	12:KF:346:PRO:HD2	1.89	0.55
12:KG:374:ALA:HA	12:KG:377:LEU:HB3	1.88	0.55
13:LJ:394:GLY:HA3	13:LJ:398:ARG:HH21	1.70	0.55
15:NA:892:TRP:N	15:NA:1155:GLU:H	2.05	0.55
1:AD:301:VAL:HG23	1:AD:332:THR:HG22	1.88	0.55
1:AH:488:VAL:HG12	1:AH:490:SER:H	1.71	0.55
1:AI:472:LYS:HD2	2:AJ:448:ASN:HD22	1.72	0.55
2:AK:145:LYS:HA	2:AK:148:ASP:HB2	1.89	0.55
3:CB:730:ALA:HB1	3:CB:763:LEU:HD21	1.87	0.55
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CZ3	2.59	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:4523:LEU:HA	5:EB:4537:ALA:HB1	1.89	0.55
6:FC:2023:ILE:HG22	9:HB:778:PRO:HB3	1.87	0.55
6:FD:1442:GLU:C	6:FD:1444:ARG:H	2.14	0.55
6:FE:826:LEU:HB2	6:FE:841:TYR:CE2	2.42	0.55
6:FE:1022:THR:HG22	6:FE:1023:ALA:H	1.72	0.55
6:FE:1208:ALA:HB3	6:FE:1286:LEU:HD22	1.88	0.55
7:GC:680:TYR:HE2	7:GC:690:ARG:HB2	1.72	0.55
8:GD:661:PRO:HB2	8:GD:680:LEU:HB2	1.89	0.55
7:GG:883:LEU:HD11	7:GG:890:MET:HE2	1.88	0.55
8:GH:681:ILE:HA	8:GH:684:TRP:HD1	1.72	0.55
10:IB:1236:VAL:HG22	10:IB:1285:VAL:HG12	1.89	0.55
11:JC:1867:LEU:HB3	11:JC:2273:ARG:HH12	1.70	0.55
13:LC:364:ASN:HA	13:LC:367:VAL:HG12	1.89	0.55
15:NC:363:LEU:HD11	15:NC:430:ARG:HD3	1.87	0.55
1:AL:763:LEU:HD13	1:AL:776:LEU:HD13	1.89	0.55
3:CL:4475:LYS:HE3	3:CL:4484:VAL:HG21	1.88	0.55
5:EC:3650:THR:HG23	9:HA:499:ARG:HA	1.88	0.55
7:GK:298:TYR:HB3	7:GK:679:LEU:HD11	1.89	0.55
10:IA:1128:VAL:HG12	10:IA:1131:HIS:CD2	2.41	0.55
11:JB:157:GLU:HB3	11:JB:172:LEU:HD11	1.89	0.55
11:JB:880:MET:HE2	11:JB:1418:THR:HG21	1.89	0.55
13:LI:520:LEU:O	13:LI:521:ASN:C	2.49	0.55
14:MI:280:ALA:HA	14:MI:283:GLN:HE22	1.71	0.55
14:MJ:253:GLU:O	14:MJ:257:LYS:HG3	2.07	0.55
1:AE:915:TRP:HB3	13:LM:355:LYS:HZ3	1.71	0.55
2:AG:538:ASN:HB3	5:EB:4818:ILE:HD12	1.89	0.55
1:AI:443:LYS:HD3	2:AJ:27:ALA:HB1	1.89	0.55
1:AI:995:GLU:HB3	7:GK:216:THR:HG22	1.89	0.55
3:CG:1178:GLN:HE22	3:CG:1180:GLU:HG2	1.71	0.55
3:CJ:1164:LEU:HD12	3:CJ:1168:ARG:HG2	1.89	0.55
5:EA:4814:THR:HA	5:EA:4817:LEU:HD21	1.88	0.55
5:EB:4738:THR:HG21	5:EB:4828:LEU:HD12	1.88	0.55
6:FE:1073:HIS:O	6:FE:1074:ASP:C	2.49	0.55
8:GF:317:VAL:HG11	8:GF:325:ILE:HG22	1.89	0.55
8:GF:440:CYS:HG	8:GF:463:TRP:CD1	2.25	0.55
7:GI:713:VAL:HG22	7:GI:829:VAL:HG11	1.87	0.55
8:GJ:18:VAL:HG12	8:GJ:531:GLY:HA3	1.89	0.55
8:GJ:401:ASP:HB2	8:GJ:719:VAL:HG11	1.89	0.55
8:GL:113:LEU:HD12	8:GL:114:PRO:HD2	1.89	0.55
10:IB:165:ILE:HD11	10:IB:180:LEU:HD22	1.88	0.55
10:IB:451:VAL:HG13	10:IB:455:LEU:HD12	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:698:GLN:HE21	16:OB:1081:ILE:HD11	1.72	0.55
12:KF:546:LYS:HG3	12:KF:714:THR:HG22	1.89	0.55
15:NB:794:GLU:HA	15:NB:797:ARG:HD2	1.89	0.55
15:NB:894:LEU:HB3	15:NB:898:ASN:HB3	1.87	0.55
15:NC:343:VAL:HG22	15:NC:364:ARG:HH21	1.71	0.55
15:NC:613:GLN:HG2	15:NC:918:ALA:HB2	1.88	0.55
1:AA:147:MET:HE1	1:AA:218:PRO:HB3	1.89	0.55
2:AC:327:ILE:HG22	1:AH:269:THR:HG21	1.89	0.55
2:AF:161:ILE:HG22	5:EB:4624:SER:HA	1.87	0.55
1:AH:288:GLY:HA3	1:AH:298:ILE:HD12	1.88	0.55
3:BC:781:LEU:HD22	3:BC:833:TYR:HD2	1.72	0.55
5:EB:3706:VAL:HG11	5:EB:3739:GLU:HG3	1.88	0.55
5:EB:4403:LEU:HB3	5:EB:4405:ILE:HD11	1.88	0.55
6:FA:1729:ALA:HA	6:FA:1902:LEU:HD23	1.89	0.55
6:FB:1612:ASN:HD21	6:FB:1616:GLU:HB3	1.71	0.55
6:FD:845:PRO:N	7:GC:896:ARG:HH12	2.04	0.55
6:FF:1184:ALA:HB3	6:FF:1424:CYS:HA	1.88	0.55
7:GG:268:ARG:HB2	7:GG:276:ARG:HH12	1.72	0.55
7:GK:539:TYR:HB2	9:HC:576:LYS:HG2	1.88	0.55
9:HD:809:LEU:O	9:HD:813:THR:HG23	2.07	0.55
10:IB:258:SER:HA	10:IB:979:ARG:HH12	1.72	0.55
11:JA:795:ARG:HE	11:JA:796:SER:H	1.55	0.55
11:JB:440:PRO:HG3	11:JB:1477:TRP:HB3	1.89	0.55
12:KA:403:ASP:HA	12:KA:541:TYR:HE1	1.72	0.55
12:KC:214:PRO:HG3	12:KC:236:LYS:HB3	1.89	0.55
12:KC:234:PRO:CD	12:KC:235:PRO:HD2	2.33	0.55
14:MI:225:VAL:HG21	14:MI:315:TRP:HE1	1.72	0.55
14:MJ:218:LEU:HD21	14:MJ:323:GLN:HB3	1.89	0.55
15:NA:577:PRO:HA	15:NA:581:LEU:HD12	1.87	0.55
15:NA:687:SER:HB2	15:NA:910:ARG:HD3	1.88	0.55
15:NA:735:HIS:HD2	15:NA:768:GLU:HG2	1.71	0.55
15:NA:1193:VAL:HG11	15:NA:1391:LEU:HD21	1.89	0.55
15:NB:983:ILE:HG23	15:NB:989:ILE:HB	1.89	0.55
15:NC:599:ILE:HB	15:NC:916:LEU:HA	1.89	0.55
15:ND:737:PRO:HG3	15:ND:749:PRO:HD3	1.89	0.55
1:AA:815:LEU:HD13	13:LK:354:ARG:HG3	1.88	0.54
1:AI:309:LEU:HD13	1:AI:314:ILE:HD13	1.87	0.54
1:AL:715:LEU:HD21	1:AL:839:GLU:HG2	1.88	0.54
5:EA:3373:LYS:HG3	5:EA:3378:GLY:HA2	1.89	0.54
6:FA:1656:THR:HB	6:FA:1659:ILE:HD13	1.88	0.54
6:FE:1012:PRO:HB2	6:FE:1016:PRO:HD3	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GE:189:SER:HB3	7:GE:192:LEU:HB2	1.89	0.54
7:GG:678:LEU:HB3	7:GG:690:ARG:HB3	1.89	0.54
7:GI:515:SER:HB3	7:GI:634:PRO:HB2	1.89	0.54
7:GI:873:ALA:HA	7:GI:876:MET:HE1	1.87	0.54
8:GJ:75:GLN:HG3	8:GJ:86:ALA:HA	1.89	0.54
12:KA:240:ILE:HD11	12:KA:294:ARG:HD2	1.89	0.54
12:KC:231:PHE:HZ	12:KC:313:PHE:CD1	2.25	0.54
12:KF:575:ILE:HD12	12:KF:578:ALA:HB2	1.88	0.54
15:NA:1409:VAL:HB	15:NA:1470:PHE:HB2	1.88	0.54
15:NC:618:ARG:HG2	15:NC:654:LEU:HD21	1.88	0.54
15:ND:548:PRO:HA	15:ND:551:ARG:HE	1.72	0.54
19:RA:27:ALA:HA	19:RA:30:LEU:HB3	1.89	0.54
1:AI:1001:SER:HA	7:GK:860:GLN:HG2	1.89	0.54
2:AK:157:GLY:HA3	2:AK:253:LYS:HE3	1.89	0.54
3:CJ:4469:LEU:HD11	3:CJ:4485:VAL:HB	1.89	0.54
3:CL:4519:ALA:HB1	3:CL:4525:LEU:HB2	1.88	0.54
4:DA:354:TRP:HB3	4:DA:382:LEU:HD23	1.90	0.54
5:EA:3227:ALA:HB2	5:EA:4159:THR:HG22	1.88	0.54
5:EB:3412:LEU:HG	5:EB:3507:VAL:HG22	1.89	0.54
5:EB:4893:THR:O	5:EB:4894:SER:C	2.49	0.54
6:FD:843:LEU:O	7:GC:896:ARG:NH1	2.40	0.54
6:FE:1196:PRO:O	6:FE:1197:ILE:C	2.50	0.54
6:FF:1431:MET:O	6:FF:1435:GLU:HB3	2.08	0.54
8:GH:721:LYS:HA	8:GH:721:LYS:HE3	1.89	0.54
13:LO:371:SER:HA	13:LO:374:HIS:CE1	2.42	0.54
15:ND:1546:VAL:HA	19:RD:142:ASN:H	1.72	0.54
16:OA:213:LEU:HB3	16:OA:246:LEU:HD21	1.89	0.54
19:RB:48:ALA:HA	19:RB:51:MET:HE3	1.88	0.54
1:AA:428:LEU:HD12	1:AA:432:LEU:HD11	1.87	0.54
4:DC:163:GLU:HA	4:DC:166:VAL:HG12	1.89	0.54
5:EA:3642:PRO:HD3	5:EA:3673:LEU:HD23	1.88	0.54
5:EB:4454:ARG:HD2	5:EB:4507:ASP:HB2	1.89	0.54
6:FB:1844:LEU:HD12	6:FB:1922:VAL:HG21	1.88	0.54
6:FD:1030:ILE:HG23	6:FD:1116:LEU:HD22	1.89	0.54
6:FD:1188:GLU:HG3	6:FD:1267:GLN:HB3	1.89	0.54
6:FF:1222:CYS:O	6:FF:1223:ALA:C	2.51	0.54
7:GE:719:ILE:HD11	7:GE:800:VAL:HG21	1.88	0.54
8:GH:300:ARG:HG2	8:GH:361:ALA:HB3	1.89	0.54
9:HA:643:PHE:HB3	9:HA:729:GLY:HA2	1.89	0.54
9:HA:809:LEU:O	9:HA:813:THR:HG23	2.07	0.54
10:IC:615:ARG:HG2	10:IC:759:PHE:HE1	1.71	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1326:THR:HG23	10:IC:1328:LYS:H	1.73	0.54
11:JB:2256:SER:HB3	11:JB:2259:LEU:HB2	1.89	0.54
11:JC:1136:MET:HE3	11:JC:1668:ASN:HD21	1.72	0.54
12:KC:578:ALA:HB3	12:KC:657:VAL:H	1.72	0.54
15:NA:755:ILE:HG21	15:NA:803:LEU:HD21	1.89	0.54
15:NB:794:GLU:HG2	15:NB:1140:LEU:HD13	1.88	0.54
15:NB:1005:VAL:H	15:NB:1008:SER:HB2	1.72	0.54
16:OB:1075:TYR:HE2	16:OB:1077:LYS:HB2	1.72	0.54
20:SC:87:ILE:HG13	20:SC:143:VAL:HG21	1.90	0.54
3:BA:718:ALA:HB2	3:BA:733:GLN:HB2	1.88	0.54
4:DE:362:LYS:HE2	4:DE:382:LEU:HD13	1.90	0.54
5:EA:3496:THR:HB	5:EA:3507:VAL:HB	1.89	0.54
5:EA:4095:LYS:HD3	9:HB:796:ASP:HA	1.89	0.54
6:FD:1223:ALA:O	6:FD:1226:LEU:N	2.39	0.54
7:GA:236:THR:HG21	7:GA:255:LEU:HD13	1.89	0.54
7:GA:967:PHE:HA	7:GA:970:LEU:HD23	1.90	0.54
8:GB:772:THR:HG23	8:GB:774:ASP:H	1.73	0.54
8:GD:278:CYS:HB3	8:GD:281:LEU:HB3	1.90	0.54
9:HB:776:PRO:HB3	13:LE:521:ASN:OD1	2.07	0.54
12:KA:291:ALA:HB3	12:KA:314:LEU:HD11	1.89	0.54
15:NC:741:ILE:HG23	15:NC:793:THR:HG22	1.88	0.54
3:BA:690:MET:HE1	17:PA:257:ASN:HA	1.89	0.54
3:BA:873:PHE:HZ	16:OA:174:VAL:HG22	1.71	0.54
4:DE:167:GLU:HA	4:DE:170:ARG:HB3	1.89	0.54
5:EC:4405:ILE:HG23	5:EC:4411:THR:CG2	2.37	0.54
6:FE:1223:ALA:HA	6:FE:1226:LEU:HD12	1.90	0.54
6:FF:1105:ARG:O	6:FF:1106:LEU:C	2.49	0.54
7:GC:232:LYS:HB3	7:GC:258:TYR:HE2	1.72	0.54
8:GD:574:ASP:HA	14:MA:320:ARG:HH21	1.72	0.54
8:GF:29:ILE:HG22	8:GF:31:LEU:H	1.72	0.54
8:GF:625:ALA:HB1	8:GF:629:ASN:HB2	1.89	0.54
8:GL:55:ARG:HD3	8:GL:60:GLY:HA2	1.90	0.54
8:GL:405:LYS:HA	8:GL:408:GLU:HB2	1.88	0.54
10:IC:466:GLN:HA	10:IC:638:ARG:HH21	1.72	0.54
10:IC:1221:THR:H	10:IC:1224:HIS:HB2	1.72	0.54
11:JA:1285:SER:HA	11:JA:1288:ARG:HD3	1.89	0.54
11:JB:138:THR:HA	11:JB:162:PRO:HA	1.88	0.54
11:JB:1480:VAL:HG13	15:NB:440:LEU:HD12	1.89	0.54
15:NA:748:LYS:HE2	15:NA:849:ARG:HH12	1.72	0.54
15:ND:1518:ARG:HH22	18:QB:65:ALA:HB2	1.73	0.54
18:QA:104:PHE:HD2	18:QA:168:LEU:HD11	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:762:LEU:HD23	3:CC:784:LEU:HD11	1.88	0.54
4:DD:93:ILE:HD13	4:DD:165:ILE:HG12	1.90	0.54
5:EA:3439:ARG:HH22	5:EA:3607:ARG:HH11	1.55	0.54
6:FA:2055:THR:HA	9:HA:837:LEU:HD21	1.89	0.54
6:FD:879:ARG:HE	6:FD:908:ILE:HG23	1.72	0.54
6:FD:1445:SER:O	6:FD:1446:ASN:C	2.51	0.54
8:GB:676:TRP:HB2	8:GB:735:LEU:HD13	1.89	0.54
7:GK:368:PHE:HZ	7:GK:439:ALA:HB1	1.72	0.54
10:IA:890:GLY:H	15:NA:566:GLN:HE22	1.53	0.54
14:MA:259:MET:HA	14:MA:265:SER:HB2	1.89	0.54
17:PA:257:ASN:HB2	17:PA:260:SER:HB2	1.89	0.54
1:AE:274:ARG:HG3	1:AE:275:HIS:H	1.72	0.54
3:BC:783:GLU:HA	3:BC:786:TYR:HD2	1.73	0.54
3:CF:1209:ALA:HB3	3:CF:1223:GLU:HA	1.90	0.54
4:DC:179:ALA:HB3	4:DF:189:ARG:HE	1.73	0.54
6:FD:799:GLN:HB3	6:FD:911:SER:HA	1.90	0.54
7:GC:371:LEU:HD12	7:GC:412:VAL:HG22	1.88	0.54
8:GD:18:VAL:HG13	8:GD:520:PHE:HA	1.89	0.54
8:GD:300:ARG:HG2	8:GD:361:ALA:HB3	1.88	0.54
8:GF:314:GLY:HA2	8:GF:344:ALA:HA	1.88	0.54
8:GL:283:LEU:HD22	8:GL:380:MET:HE1	1.89	0.54
9:HB:579:LEU:HD23	9:HB:595:TYR:HB2	1.90	0.54
10:IB:864:GLN:HB3	10:IB:1241:LEU:HD22	1.90	0.54
11:JA:1451:PRO:HB2	11:JA:1456:ILE:HD11	1.89	0.54
11:JA:1560:LEU:HD23	11:JA:1561:HIS:CD2	2.43	0.54
11:JC:896:PRO:HB3	11:JC:953:LEU:HD12	1.89	0.54
12:KF:534:VAL:HG13	12:KF:536:ARG:HH12	1.72	0.54
13:LB:500:GLN:HE21	14:MC:178:VAL:HG23	1.72	0.54
15:NC:1005:VAL:H	15:NC:1008:SER:HB3	1.73	0.54
15:ND:794:GLU:HA	15:ND:797:ARG:HB2	1.89	0.54
16:OC:190:LEU:HD23	16:OC:241:ALA:HB3	1.89	0.54
1:AA:632:LEU:HD22	7:GA:856:VAL:HG22	1.90	0.54
1:AD:229:LEU:HD11	10:IB:824:LYS:HB3	1.89	0.54
1:AH:713:LEU:HD12	13:LJ:484:VAL:HG13	1.90	0.54
1:AH:834:ILE:HD13	1:AH:989:LEU:HD23	1.89	0.54
4:DA:156:ASP:HA	4:DA:159:GLU:HG3	1.90	0.54
4:DC:126:LEU:HD22	4:DC:158:LEU:HD13	1.88	0.54
5:EC:4743:ILE:HG22	5:EC:4747:MET:HE2	1.89	0.54
6:FA:2084:GLN:HA	6:FA:2088:MET:HE1	1.90	0.54
6:FD:860:PRO:HD2	6:FD:861:LEU:HD23	1.90	0.54
6:FE:890:ALA:O	6:FE:891:ARG:C	2.50	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:967:PHE:CD2	6:FF:1095:LEU:HD23	2.43	0.54
9:HB:681:LYS:HB3	13:LD:483:ARG:HD2	1.88	0.54
12:KA:335:LEU:HD21	12:KA:362:LEU:HD11	1.90	0.54
14:MB:246:ASN:HA	14:MB:249:GLU:HG3	1.90	0.54
15:NA:1120:VAL:HA	15:NA:1123:ALA:HB2	1.89	0.54
15:NA:1442:LYS:HD3	15:NA:1444:LYS:H	1.73	0.54
15:NC:686:ASN:HB2	15:NC:692:ILE:HG22	1.89	0.54
15:NC:996:LEU:HD22	15:NC:1015:ALA:HB1	1.88	0.54
15:ND:515:ALA:HB3	15:ND:520:ALA:HB2	1.89	0.54
19:RB:151:LEU:HD23	19:RB:154:ARG:HH12	1.72	0.54
2:AK:331:ASN:HD22	2:AK:331:ASN:C	2.13	0.54
3:BB:908:VAL:HB	3:BB:938:MET:HE1	1.89	0.54
5:EB:3730:ALA:HB3	5:EB:4285:THR:HA	1.89	0.54
6:FE:1124:ILE:O	6:FE:1125:ASN:C	2.51	0.54
8:GB:586:SER:HB3	14:ME:320:ARG:HH22	1.73	0.54
11:JB:1414:ALA:HB2	11:JB:1504:ARG:HE	1.73	0.54
14:MH:99:LYS:HA	14:MH:102:LYS:HG2	1.90	0.54
15:NB:505:GLY:H	15:NB:512:TYR:HB2	1.73	0.54
15:ND:996:LEU:HD22	15:ND:1015:ALA:HB1	1.89	0.54
2:AC:368:HIS:HB2	1:AD:442:HIS:HB2	1.88	0.54
3:CI:1164:LEU:HB3	3:CI:1168:ARG:HB2	1.90	0.54
4:DC:285:ARG:HG3	4:DC:286:TRP:CD1	2.43	0.54
4:DC:385:LYS:HZ3	13:LJ:461:VAL:HG22	1.73	0.54
5:EB:3660:LYS:HZ1	5:EB:4055:ARG:HH22	1.54	0.54
6:FA:1958:LEU:HD22	6:FA:2054:PHE:CD2	2.43	0.54
6:FA:2079:MET:HE2	9:HA:865:ILE:HG12	1.87	0.54
6:FD:993:ALA:HA	12:KA:230:GLN:CG	2.38	0.54
6:FE:1026:PRO:HB2	6:FE:1029:GLN:HG2	1.90	0.54
6:FE:1231:ARG:HH21	6:FE:1271:PRO:HD2	1.73	0.54
7:GA:646:MET:HE1	7:GA:696:MET:HE1	1.90	0.54
8:GD:325:ILE:HD13	8:GD:371:GLN:HB2	1.90	0.54
7:GE:607:ARG:HB2	7:GE:609:ARG:HH22	1.72	0.54
8:GH:475:ALA:HB2	8:GH:543:ARG:HD2	1.90	0.54
9:HA:559:ARG:HA	9:HA:562:GLN:HG3	1.90	0.54
9:HA:804:THR:O	9:HA:805:THR:C	2.51	0.54
11:JC:1328:LEU:HD21	11:JC:1408:LEU:HD11	1.90	0.54
12:KB:609:CYS:HA	12:KB:620:THR:HG22	1.90	0.54
12:KB:656:ARG:HB3	12:KB:667:SER:HB2	1.90	0.54
15:NA:1121:ASN:HA	15:NA:1162:ARG:HE	1.73	0.54
2:AC:481:ARG:HH21	2:AC:533:SER:H	1.56	0.53
1:AL:1033:GLN:O	1:AL:1034:SER:C	2.51	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BB:754:GLU:HG2	17:PB:284:PRO:HB2	1.89	0.53
3:BB:1014:ASP:HA	3:BB:1017:ARG:HE	1.73	0.53
3:CL:1257:ASN:HB3	3:CL:1260:VAL:HG12	1.90	0.53
4:DF:31:SER:HB2	4:DF:48:TYR:HE2	1.72	0.53
6:FA:2098:TYR:HE1	9:HA:878:SER:HB2	1.73	0.53
6:FD:999:PRO:N	12:KA:229:SER:HA	2.24	0.53
6:FD:1186:TRP:HE3	6:FD:1267:GLN:HB2	1.72	0.53
6:FE:1085:GLU:HA	6:FE:1088:LYS:HB2	1.90	0.53
6:FE:1212:VAL:HG23	6:FE:1264:ILE:HD12	1.90	0.53
7:GA:268:ARG:HB2	7:GA:276:ARG:HH12	1.73	0.53
7:GA:279:ARG:HG3	7:GA:285:LEU:HB3	1.90	0.53
8:GF:62:ILE:HG21	8:GF:513:VAL:HG11	1.90	0.53
7:GK:576:TYR:HB3	7:GK:584:HIS:HD1	1.73	0.53
9:HB:766:SER:O	9:HB:768:THR:N	2.41	0.53
9:HB:777:TYR:CD1	9:HB:778:PRO:HD2	2.44	0.53
12:KC:525:PRO:HD2	12:KC:542:PRO:HD2	1.90	0.53
14:MA:240:LEU:HD22	14:MA:243:LYS:HZ3	1.73	0.53
15:NC:508:GLY:HA3	15:NC:577:PRO:HG3	1.89	0.53
19:RB:23:LEU:HA	19:RB:26:HIS:HB3	1.89	0.53
2:AC:456:CYS:SG	1:AD:389:LEU:HD22	2.49	0.53
1:AL:1026:ASP:OD2	1:AL:1032:PHE:N	2.41	0.53
6:FF:1102:TYR:O	6:FF:1103:SER:C	2.51	0.53
7:GC:519:PHE:HZ	7:GC:595:ILE:HG13	1.72	0.53
7:GC:633:LEU:HD23	7:GC:636:VAL:HG12	1.90	0.53
8:GF:432:LYS:HB2	8:GF:451:SER:HB2	1.91	0.53
8:GF:596:MET:HA	8:GF:599:LEU:HB3	1.91	0.53
11:JC:84:PHE:HB3	11:JC:2092:PHE:HZ	1.73	0.53
14:ME:284:LEU:HD13	14:MF:283:GLN:NE2	2.23	0.53
15:NB:667:THR:HA	15:NB:673:ILE:HG23	1.89	0.53
15:NB:892:TRP:N	15:NB:1155:GLU:H	2.06	0.53
15:NB:931:TRP:CD1	15:NB:934:LEU:HB2	2.43	0.53
15:NC:682:ARG:HE	15:NC:917:MET:HE1	1.73	0.53
15:NC:818:ILE:HB	15:NC:842:THR:HA	1.88	0.53
2:AG:438:VAL:HG11	1:AH:408:LYS:HB2	1.90	0.53
1:AI:97:ASP:HB3	1:AI:100:GLU:HB2	1.90	0.53
4:DA:356:TYR:CZ	4:DA:385:LYS:HG3	2.44	0.53
6:FD:806:ILE:HG21	6:FD:851:THR:HG21	1.89	0.53
6:FD:1073:HIS:O	6:FD:1074:ASP:C	2.50	0.53
6:FE:1011:TYR:O	6:FE:1012:PRO:C	2.52	0.53
6:FF:1218:ALA:O	6:FF:1219:GLU:C	2.51	0.53
7:GC:246:ALA:HB2	7:GC:250:ARG:HE	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:HA:754:LEU:HG	9:HA:840:HIS:CD2	2.43	0.53
9:HD:777:TYR:CD1	9:HD:778:PRO:HD2	2.44	0.53
10:IB:1094:ASN:HA	10:IB:1123:ASN:HD22	1.72	0.53
11:JA:414:ILE:HD11	11:JA:437:LEU:HB3	1.89	0.53
11:JC:1975:THR:HG23	11:JC:1977:GLN:H	1.73	0.53
12:KB:298:GLN:HB3	12:KB:303:TYR:HB2	1.90	0.53
12:KG:259:THR:HA	12:KG:262:GLU:HG2	1.90	0.53
15:NB:1407:MET:HA	15:NB:1471:ARG:HD3	1.90	0.53
15:NC:895:GLY:H	15:NC:1152:GLU:HB3	1.72	0.53
16:OB:213:LEU:HD13	16:OB:246:LEU:HD13	1.89	0.53
5:EB:3227:ALA:HB2	5:EB:4159:THR:HG22	1.91	0.53
6:FD:1436:PHE:O	6:FD:1437:ALA:C	2.50	0.53
6:FE:1182:ALA:CB	6:FE:1429:LEU:HB2	2.34	0.53
6:FF:908:ILE:HD13	6:FF:968:LEU:HD21	1.90	0.53
7:GE:441:LEU:HD13	7:GE:509:LEU:HD23	1.90	0.53
9:HA:644:PHE:HD2	9:HA:726:PRO:HB2	1.73	0.53
9:HB:762:HIS:HD2	9:HB:763:GLN:NE2	2.06	0.53
10:IB:891:VAL:HG13	10:IB:892:ILE:HG23	1.90	0.53
11:JA:1078:MET:HB2	11:JA:1509:HIS:CD2	2.42	0.53
11:JB:1369:ILE:HG21	11:JB:1374:LEU:HD22	1.90	0.53
12:KA:234:PRO:HG2	12:KA:236:LYS:HE2	1.89	0.53
12:KB:382:ARG:HH12	12:KB:728:PRO:HD3	1.72	0.53
13:LO:377:GLN:HA	13:LO:380:MET:HB3	1.90	0.53
13:LP:350:LEU:HB3	13:LP:354:ARG:HH21	1.73	0.53
15:NB:948:LEU:HD21	15:NB:1173:MET:HE1	1.91	0.53
15:NB:1165:VAL:HA	15:NB:1168:GLN:HG2	1.89	0.53
15:NC:614:LYS:HD2	15:NC:661:ARG:HH12	1.73	0.53
1:AD:25:ALA:HB2	11:JA:1306:ILE:HG23	1.90	0.53
2:AG:115:ARG:HD2	16:OC:148:ARG:HG3	1.89	0.53
2:AG:442:LEU:HD23	2:AG:446:ARG:HH12	1.74	0.53
3:BC:904:PRO:HG3	3:BC:941:ARG:HH11	1.72	0.53
3:CG:1132:MET:HE1	10:IC:1243:PRO:HG3	1.90	0.53
3:CL:4520:ARG:HH22	3:CL:4525:LEU:HD22	1.73	0.53
4:DA:297:ARG:HD2	13:LA:460:ARG:HH22	1.72	0.53
6:FE:1182:ALA:HB2	6:FE:1430:PHE:H	1.73	0.53
6:FE:1202:PHE:CE1	6:FE:1243:PRO:HA	2.43	0.53
7:GC:311:LEU:HD11	7:GC:436:ALA:HB1	1.88	0.53
8:GH:22:THR:HG23	8:GH:25:GLU:H	1.72	0.53
8:GH:603:HIS:HA	8:GH:606:GLN:HG2	1.90	0.53
9:HA:761:CYS:HA	9:HA:765:TRP:CE3	2.43	0.53
10:IA:400:HIS:HA	10:IA:403:GLU:HB3	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1094:ASN:HA	10:IC:1123:ASN:HD22	1.72	0.53
11:JB:91:ARG:HE	11:JB:93:LYS:HE2	1.74	0.53
13:LF:422:GLN:HA	13:LF:425:LYS:HZ3	1.73	0.53
15:NA:890:ARG:HD2	15:NA:1156:LEU:HD21	1.89	0.53
15:NC:892:TRP:HB2	15:NC:1155:GLU:OE1	2.09	0.53
15:ND:564:ARG:HH12	15:ND:618:ARG:HB2	1.73	0.53
2:AG:368:HIS:HB2	1:AH:442:HIS:HB2	1.90	0.53
3:BC:719:THR:HG22	16:OC:287:LEU:HD13	1.91	0.53
4:DC:159:GLU:HA	4:DC:162:VAL:HG12	1.90	0.53
5:EC:4265:HIS:HB2	5:EC:4267:GLN:HE22	1.73	0.53
6:FB:2098:TYR:CD1	9:HD:879:ILE:HG12	2.44	0.53
6:FD:1105:ARG:O	6:FD:1106:LEU:C	2.52	0.53
6:FF:855:PHE:O	6:FF:857:GLU:N	2.42	0.53
7:GE:284:GLU:HA	7:GE:290:VAL:HG21	1.91	0.53
7:GG:184:ALA:HB3	7:GG:708:SER:HB2	1.89	0.53
8:GJ:38:THR:HB	8:GJ:41:ARG:HG2	1.90	0.53
7:GK:670:ASN:HB3	7:GK:698:VAL:HB	1.89	0.53
9:HD:778:PRO:HB2	9:HD:779:PRO:CD	2.38	0.53
10:IA:1245:GLN:HA	10:IA:1272:LEU:HD22	1.89	0.53
11:JA:1518:VAL:HG21	11:JA:1534:ALA:HB2	1.89	0.53
11:JA:2018:LEU:HD13	11:JA:2067:ALA:HB2	1.91	0.53
11:JB:2280:ARG:HG2	11:JB:2284:LYS:HE3	1.90	0.53
12:KA:299:TYR:HA	12:KA:304:ARG:HG3	1.91	0.53
12:KB:359:VAL:HG11	12:KB:362:LEU:HD23	1.91	0.53
15:NA:676:ARG:HH22	15:NA:706:VAL:HG23	1.74	0.53
15:NA:894:LEU:H	15:NA:1153:ALA:N	2.06	0.53
15:NC:885:LEU:HA	15:NC:888:ARG:HB2	1.91	0.53
1:AA:229:LEU:HG	17:PA:272:ARG:HD3	1.89	0.53
2:AK:455:ARG:HB2	1:AL:475:LEU:HD23	1.90	0.53
3:CI:1108:LEU:HD22	3:CI:1128:TRP:HE1	1.74	0.53
4:DD:167:GLU:HA	4:DD:170:ARG:HB3	1.89	0.53
5:EA:4521:TYR:HB2	5:EA:4711:LEU:HD21	1.91	0.53
5:EB:4442:GLU:HB3	5:EB:4446:ARG:HH11	1.73	0.53
6:FE:813:GLN:O	6:FE:814:THR:C	2.50	0.53
7:GA:540:ALA:HA	9:HB:577:ASP:HA	1.91	0.53
8:GB:215:LEU:HA	8:GB:240:ALA:HB1	1.90	0.53
7:GG:434:GLY:HA3	7:GG:464:LEU:HB2	1.89	0.53
8:GL:83:GLN:O	8:GL:83:GLN:NE2	2.41	0.53
10:IB:368:PRO:HD2	10:IB:388:CYS:HB2	1.90	0.53
11:JC:1687:LEU:HA	11:JC:1690:ASP:HB2	1.91	0.53
12:KG:384:LEU:HA	12:KG:414:TRP:HD1	1.72	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:958:GLU:HA	15:NC:961:TYR:HB2	1.90	0.53
1:AE:732:LYS:HE3	1:AE:852:ARG:HB2	1.91	0.53
2:AF:299:LEU:HA	2:AF:307:PRO:HA	1.91	0.53
3:CI:4479:LEU:HB3	3:CI:4482:LEU:HD23	1.90	0.53
4:DD:250:ASP:HB2	4:DD:283:LEU:HB3	1.91	0.53
5:EB:3399:PHE:HB3	5:EB:3418:SER:HB2	1.90	0.53
6:FA:1684:THR:HG22	6:FA:1685:GLU:H	1.73	0.53
6:FC:2077:HIS:O	6:FC:2080:GLN:HG3	2.09	0.53
6:FE:1238:ARG:CZ	6:FE:1238:ARG:HA	2.37	0.53
6:FF:819:PRO:HA	6:FF:824:TYR:OH	2.09	0.53
8:GB:638:LEU:HD22	8:GB:654:LEU:HA	1.91	0.53
8:GB:696:GLU:HA	8:GB:699:ARG:HG2	1.91	0.53
7:GC:292:PHE:HB2	7:GC:689:ILE:HB	1.91	0.53
7:GI:614:TRP:HE3	7:GI:646:MET:HG2	1.74	0.53
10:IB:349:LEU:HA	10:IB:422:THR:HG21	1.91	0.53
10:IB:883:SER:HB3	16:OB:1045:LEU:HD11	1.90	0.53
10:IC:442:ARG:HD3	10:IC:443:PRO:HD2	1.89	0.53
11:JA:908:PRO:HG2	11:JA:911:SER:HB3	1.90	0.53
11:JB:128:THR:HG21	11:JB:2086:PRO:HB2	1.91	0.53
11:JC:1717:TRP:HZ3	16:OC:940:LEU:HD12	1.74	0.53
12:KA:322:ALA:HA	12:KA:327:MET:HB2	1.89	0.53
12:KC:236:LYS:C	12:KC:238:PHE:H	2.17	0.53
14:MI:298:ASN:HD21	14:MJ:294:ALA:HA	1.73	0.53
15:NC:1514:TRP:HA	15:NC:1517:VAL:HG22	1.91	0.53
15:ND:1521:SER:HB3	18:QB:60:ARG:HH21	1.73	0.53
15:ND:1550:MET:HG3	19:RD:29:GLU:HG2	1.89	0.53
2:AC:427:ARG:HE	1:AD:452:PHE:HB3	1.74	0.53
3:CL:1274:ARG:HH11	3:CL:4449:ILE:HB	1.74	0.53
4:DA:242:LEU:HD12	4:DA:245:LEU:HD11	1.91	0.53
4:DB:305:ARG:HE	4:DB:361:GLN:HE22	1.56	0.53
6:FD:1087:LEU:HD23	6:FD:1092:PRO:HB3	1.90	0.53
6:FE:833:GLY:O	6:FE:979:LEU:HB3	2.09	0.53
6:FE:1184:ALA:N	6:FE:1424:CYS:HB3	2.24	0.53
8:GD:410:ASP:HB3	8:GD:416:LYS:HD3	1.91	0.53
7:GE:798:LEU:HG	7:GE:802:LYS:NZ	2.23	0.53
9:HB:778:PRO:O	9:HB:779:PRO:C	2.52	0.53
11:JB:1004:ARG:HH22	11:JB:1152:HIS:HB3	1.74	0.53
12:KC:526:TRP:HE1	12:KC:706:ILE:HG21	1.74	0.53
13:LO:378:GLU:HG3	13:LP:377:GLN:HE22	1.73	0.53
15:ND:755:ILE:HD12	15:ND:846:PHE:HE2	1.74	0.53
15:ND:881:LEU:HD22	15:ND:884:LYS:HD2	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:16:LEU:HD22	2:AC:50:ILE:HA	1.91	0.53
1:AE:275:HIS:HB3	1:AE:277:ARG:HH21	1.73	0.53
1:AH:630:PRO:HA	13:LL:512:ARG:HH22	1.74	0.53
1:AH:687:SER:HA	1:AH:1005:LEU:HD11	1.90	0.53
3:BC:675:GLY:HA3	17:PC:264:GLU:HA	1.91	0.53
3:CF:1223:GLU:CD	3:CF:1224:ALA:H	2.17	0.53
4:DA:267:ARG:HE	14:MA:297:VAL:HG21	1.73	0.53
4:DB:248:ARG:HE	4:DB:290:ARG:HH12	1.56	0.53
6:FA:1942:PHE:HA	6:FA:1945:VAL:HG12	1.91	0.53
6:FF:888:PRO:HG3	7:GI:896:ARG:HD2	1.91	0.53
7:GA:171:GLN:HG3	7:GA:172:PHE:HD2	1.74	0.53
8:GB:42:ASP:H	8:GB:470:LYS:HD2	1.74	0.53
7:GC:604:ALA:HB1	7:GC:678:LEU:HD11	1.91	0.53
8:GL:393:SER:HB3	8:GL:396:ILE:HG13	1.90	0.53
9:HB:777:TYR:O	9:HB:778:PRO:C	2.52	0.53
9:HB:804:THR:O	9:HB:805:THR:C	2.50	0.53
10:IC:698:GLN:HE21	10:IC:703:GLY:HA2	1.74	0.53
10:IC:1266:ASN:HD21	10:IC:1289:ALA:HA	1.74	0.53
11:JB:1220:LEU:HD21	11:JB:1286:LEU:HD12	1.89	0.53
11:JC:81:ARG:HG3	11:JC:106:LEU:HD11	1.90	0.53
12:KB:335:LEU:HD23	12:KB:338:LEU:HD21	1.91	0.53
13:LP:427:ARG:HH11	13:LP:431:LEU:HD12	1.73	0.53
14:MJ:254:ILE:HD12	14:MJ:257:LYS:HD3	1.90	0.53
15:NA:898:ASN:HA	15:NA:901:LEU:HB3	1.91	0.53
2:AB:41:ARG:HD2	2:AB:289:PRO:HA	1.91	0.52
3:CI:1263:SER:HA	3:CI:4457:PRO:HG3	1.91	0.52
3:CJ:1108:LEU:HD22	3:CJ:1128:TRP:HE1	1.74	0.52
5:EA:4229:MET:HE3	5:EA:4261:VAL:HG11	1.90	0.52
6:FB:2069:ASN:HA	6:FB:2072:ILE:HD12	1.92	0.52
6:FD:827:PRO:C	6:FD:829:ARG:H	2.18	0.52
6:FE:1223:ALA:O	6:FE:1224:ALA:C	2.52	0.52
8:GD:212:GLN:HB3	7:GE:388:PRO:HB2	1.92	0.52
8:GL:56:CYS:HB3	8:GL:60:GLY:H	1.74	0.52
8:GL:423:ILE:HD11	8:GL:468:LEU:HD11	1.91	0.52
10:IA:462:VAL:HG12	10:IA:470:ARG:HG3	1.92	0.52
10:IA:1326:THR:HG22	10:IA:1330:TYR:H	1.74	0.52
11:JC:489:VAL:HG11	11:JC:1439:LEU:HD23	1.90	0.52
13:LJ:376:ARG:HA	13:LJ:379:LYS:HD2	1.90	0.52
13:LO:404:LEU:HD23	13:LO:407:ARG:HD2	1.91	0.52
15:NA:931:TRP:NE1	15:NA:934:LEU:HB2	2.24	0.52
2:AF:115:ARG:HH22	11:JC:1651:LEU:HD13	1.74	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AK:438:VAL:HG22	1:AL:460:VAL:HG21	1.90	0.52
3:CA:761:LEU:HB3	3:CA:784:LEU:HD12	1.90	0.52
3:CF:1237:VAL:HA	3:CF:1244:PRO:HA	1.91	0.52
3:CL:1108:LEU:HD22	3:CL:1128:TRP:HE1	1.74	0.52
4:DA:175:TYR:HB3	4:DD:189:ARG:CZ	2.39	0.52
5:EB:3521:GLU:HB3	5:EB:3546:TYR:HE1	1.74	0.52
6:FD:860:PRO:C	6:FD:862:GLU:H	2.17	0.52
7:GA:975:VAL:HG23	7:GA:977:SER:H	1.74	0.52
8:GB:604:PHE:HZ	8:GB:633:MET:HG2	1.73	0.52
7:GC:731:ILE:HD13	7:GC:821:TRP:HZ2	1.74	0.52
8:GD:672:HIS:HB3	8:GD:674:VAL:HG13	1.91	0.52
9:HB:773:ALA:HB3	13:LF:527:VAL:CG1	2.39	0.52
10:IB:549:THR:HG23	10:IB:563:LEU:HD11	1.91	0.52
10:IB:888:THR:HA	15:NC:566:GLN:HE22	1.73	0.52
13:LI:395:ILE:HG23	13:LJ:398:ARG:HH12	1.74	0.52
13:LJ:413:GLU:HA	13:LJ:416:ARG:HD3	1.91	0.52
15:NA:511:LEU:HB2	15:NA:539:GLY:HA2	1.92	0.52
15:NA:1407:MET:HG3	15:NA:1471:ARG:HB2	1.91	0.52
15:NB:811:GLU:HA	15:NB:814:GLU:HB2	1.91	0.52
15:NB:933:LEU:HD11	15:NB:1117:PHE:HD1	1.74	0.52
15:ND:667:THR:HA	15:ND:673:ILE:HG23	1.91	0.52
1:AE:98:LEU:HD23	1:AE:145:HIS:HB3	1.92	0.52
3:BC:689:LEU:HD13	3:CB:731:MET:HG2	1.90	0.52
4:DB:119:LEU:HD12	4:DB:122:ILE:HD12	1.92	0.52
5:EA:3395:TYR:HA	5:EA:3607:ARG:HH21	1.73	0.52
5:EC:3323:THR:HB	5:EC:3377:ALA:HB2	1.91	0.52
5:EC:4540:ASP:HA	5:EC:4685:PRO:HD3	1.91	0.52
6:FB:1653:ARG:HH21	6:FB:1657:MET:HG3	1.73	0.52
6:FB:2030:ILE:HD11	9:HD:813:THR:HG22	1.90	0.52
6:FD:891:ARG:HH11	6:FD:891:ARG:HB2	1.73	0.52
6:FE:1212:VAL:O	6:FE:1233:ILE:HD12	2.09	0.52
6:FE:1242:GLN:HB2	6:FE:1259:LEU:HD12	1.90	0.52
7:GE:798:LEU:HG	7:GE:802:LYS:HZ1	1.73	0.52
7:GG:799:GLY:HA2	7:GG:971:MET:HE2	1.91	0.52
10:IA:834:GLY:HA2	10:IA:873:LEU:HD13	1.91	0.52
10:IC:1198:ARG:HG2	10:IC:1305:GLU:HB2	1.90	0.52
11:JA:489:VAL:HG13	11:JA:490:THR:HG23	1.91	0.52
11:JA:824:LYS:HE2	11:JA:1159:ARG:HH21	1.73	0.52
11:JA:1196:SER:HA	11:JA:1207:THR:HG21	1.91	0.52
11:JB:1142:MET:HG2	11:JB:1593:VAL:HG21	1.91	0.52
11:JB:1738:TYR:HB2	11:JB:1774:ARG:HH12	1.74	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:2072:GLN:HA	11:JB:2267:TYR:HE1	1.73	0.52
13:LI:418:LYS:HG3	13:LJ:417:LEU:HD21	1.91	0.52
14:ME:211:MET:HE1	14:MF:210:LEU:HD13	1.91	0.52
14:MI:305:LEU:HD21	14:MJ:301:LEU:HD22	1.91	0.52
15:NC:512:TYR:HA	15:NC:1473:ARG:HH12	1.73	0.52
15:NC:598:PHE:HB2	15:NC:1185:PRO:HB2	1.91	0.52
16:OA:190:LEU:HD11	16:OA:234:ALA:HB1	1.91	0.52
18:QC:64:LEU:HB3	18:QC:94:LEU:HD22	1.90	0.52
2:AB:259:VAL:HB	2:AB:297:VAL:HB	1.91	0.52
1:AI:751:LEU:HD13	1:AI:903:MET:HG3	1.92	0.52
2:AK:544:ARG:HE	1:AL:484:ALA:HB2	1.75	0.52
4:DC:97:LEU:HD11	4:DC:164:PHE:HE1	1.75	0.52
4:DC:312:ASN:ND2	4:DC:315:LEU:HB2	2.24	0.52
5:EA:4047:MET:HG3	13:LG:516:VAL:HG21	1.90	0.52
6:FA:1640:VAL:HG12	6:FA:1651:ALA:HB3	1.91	0.52
6:FC:2087:LEU:HD21	9:HB:869:GLN:NE2	2.25	0.52
6:FE:1244:LEU:HA	6:FE:1259:LEU:HD11	1.92	0.52
6:FF:1185:VAL:HG23	6:FF:1270:LEU:H	1.73	0.52
8:GB:172:ILE:HD12	8:GB:180:LEU:HD13	1.92	0.52
7:GC:169:ILE:HG13	7:GC:697:PRO:HD3	1.91	0.52
8:GD:273:SER:HA	8:GD:320:SER:HA	1.92	0.52
7:GE:812:VAL:HG11	7:GE:817:ARG:HE	1.73	0.52
7:GI:975:VAL:HG23	7:GI:978:LEU:H	1.75	0.52
10:IB:889:VAL:HG21	10:IB:914:VAL:HG21	1.92	0.52
10:IB:1003:VAL:HB	10:IB:1043:PHE:HB2	1.91	0.52
10:IB:1190:MET:HG2	10:IB:1222:VAL:HA	1.91	0.52
11:JB:194:VAL:HA	11:JB:197:ARG:HG2	1.91	0.52
12:KE:575:ILE:HD11	12:KE:702:ILE:HD12	1.92	0.52
12:KG:211:TRP:HE1	12:KG:239:LYS:HE3	1.74	0.52
14:MF:320:ARG:HH22	14:MF:324:ARG:HH22	1.56	0.52
15:NB:1391:LEU:HD23	15:NB:1397:LEU:HG	1.91	0.52
15:ND:891:TRP:HA	15:ND:1152:GLU:O	2.10	0.52
2:AC:522:ARG:HD3	1:AD:350:LEU:HD13	1.92	0.52
1:AD:137:GLU:HB2	10:IB:928:LEU:HD21	1.90	0.52
1:AH:879:THR:HB	13:LJ:515:LYS:HG3	1.92	0.52
3:CI:1156:GLU:HA	10:IA:398:ARG:HH22	1.74	0.52
5:EC:3494:VAL:HA	5:EC:4014:VAL:HG11	1.92	0.52
6:FB:1798:VAL:HG21	6:FB:1900:VAL:HG11	1.90	0.52
6:FB:1946:LEU:HD21	6:FB:2054:PHE:CE2	2.44	0.52
6:FC:1958:LEU:HD22	6:FC:2054:PHE:CD2	2.45	0.52
6:FC:2059:VAL:O	6:FC:2063:GLN:HG2	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1103:SER:HB2	9:HA:393:VAL:HG21	1.92	0.52
7:GC:506:ALA:HA	7:GC:509:LEU:HD12	1.92	0.52
7:GC:974:ARG:HH21	7:GC:981:THR:HG23	1.73	0.52
7:GE:590:ASN:HD22	7:GE:950:ALA:HB3	1.74	0.52
8:GF:420:ASN:HB2	8:GF:503:LEU:HD23	1.92	0.52
8:GH:398:VAL:HG23	8:GH:721:LYS:NZ	2.25	0.52
8:GL:283:LEU:HD11	8:GL:303:LEU:HD22	1.90	0.52
9:HA:778:PRO:HB2	9:HA:779:PRO:CD	2.39	0.52
9:HB:869:GLN:HA	9:HB:872:MET:HE2	1.90	0.52
11:JB:556:LEU:HD21	11:JB:810:LEU:HD23	1.90	0.52
11:JB:1538:LEU:HD12	15:NB:349:ARG:HH22	1.74	0.52
11:JC:786:PHE:HB3	11:JC:814:ASP:HB2	1.91	0.52
12:KA:547:ARG:HG2	12:KA:711:ILE:HA	1.92	0.52
12:KB:685:ARG:HH22	12:KB:688:VAL:HG23	1.73	0.52
15:NB:528:ARG:HH21	15:NB:533:GLU:HB3	1.73	0.52
16:OB:230:LEU:HD21	16:OB:245:LEU:HB3	1.90	0.52
1:AD:686:ASN:HB2	1:AD:734:MET:HE1	1.90	0.52
2:AF:412:ALA:HB2	6:FA:2074:ALA:HB2	1.92	0.52
2:AG:421:HIS:CE1	2:AG:423:VAL:HG12	2.44	0.52
1:AI:486:TYR:HE1	6:FC:1645:SER:HA	1.74	0.52
5:EB:3398:LYS:HA	5:EB:3591:PRO:HD2	1.91	0.52
6:FE:1293:THR:HG23	6:FE:1394:ARG:HG2	1.90	0.52
6:FF:980:SER:C	6:FF:982:SER:H	2.16	0.52
8:GB:21:ALA:HB3	8:GB:25:GLU:HG3	1.90	0.52
7:GC:354:ARG:HH12	7:GC:685:GLY:HA3	1.74	0.52
7:GE:892:LEU:HD23	7:GE:955:VAL:HG12	1.92	0.52
10:IC:1077:LYS:HG3	10:IC:1080:ASP:H	1.74	0.52
11:JA:1631:ASN:HB2	16:OA:934:VAL:HG21	1.91	0.52
11:JA:2018:LEU:HD11	11:JA:2063:SER:HB2	1.91	0.52
11:JB:2069:GLU:HA	11:JB:2072:GLN:HB2	1.90	0.52
12:KA:215:PRO:HG3	12:KA:288:PHE:HB3	1.91	0.52
12:KC:383:HIS:CA	12:KC:386:LEU:HD23	2.39	0.52
12:KE:404:GLU:HA	12:KE:407:ILE:HB	1.90	0.52
12:KF:216:GLN:HA	12:KF:222:LEU:HD23	1.91	0.52
15:NA:1539:ILE:HG21	19:RC:99:PHE:HE1	1.75	0.52
15:NC:347:LEU:HD22	15:NC:491:PRO:HG2	1.92	0.52
16:OB:215:ALA:HA	16:OB:218:LYS:HE3	1.90	0.52
2:AB:417:ALA:O	2:AB:418:LYS:C	2.52	0.52
3:BB:917:LEU:HD21	16:OB:174:VAL:HG21	1.91	0.52
5:EA:3790:ARG:HH12	5:EA:3816:ARG:HH22	1.56	0.52
5:EC:3581:HIS:CD2	5:EC:3647:ALA:HA	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FA:1955:THR:HG21	9:HA:838:LYS:HA	1.90	0.52
6:FB:2055:THR:O	6:FB:2059:VAL:HG23	2.10	0.52
6:FE:1102:TYR:O	6:FE:1103:SER:C	2.52	0.52
8:GB:58:VAL:HG13	14:MH:139:ALA:HB2	1.92	0.52
8:GD:36:MET:HE2	8:GD:540:LEU:HG	1.92	0.52
8:GH:140:VAL:HG13	8:GH:152:LEU:HD21	1.92	0.52
12:KC:403:ASP:H	12:KC:717:VAL:HG11	1.73	0.52
15:NA:696:PHE:H	15:NA:894:LEU:HD21	1.74	0.52
15:NA:996:LEU:HD22	15:NA:1015:ALA:HB1	1.91	0.52
15:NB:891:TRP:H	15:NB:1155:GLU:N	2.06	0.52
15:NC:881:LEU:HA	15:NC:884:LYS:HB2	1.92	0.52
2:AJ:263:TYR:HE2	16:OB:73:ALA:HA	1.75	0.52
4:DC:316:ARG:HB2	14:MJ:246:ASN:HD22	1.73	0.52
4:DD:105:CYS:HA	4:DD:259:SER:HB2	1.92	0.52
5:EC:4343:TRP:HA	5:EC:4346:VAL:HG12	1.91	0.52
6:FE:1439:LEU:HB3	6:FE:1441:ILE:HG12	1.92	0.52
6:FF:1424:CYS:HB2	6:FF:1425:PRO:CD	2.40	0.52
7:GG:537:GLY:H	9:HA:554:ASP:H	1.57	0.52
8:GH:12:CYS:HA	8:GH:37:PHE:HA	1.90	0.52
7:GI:268:ARG:HB2	7:GI:276:ARG:HH11	1.75	0.52
7:GI:680:TYR:HE2	7:GI:690:ARG:HB2	1.74	0.52
8:GL:366:ALA:HB1	8:GL:372:VAL:HG21	1.91	0.52
10:IA:784:LEU:HD23	11:JA:2057:LEU:HD21	1.91	0.52
10:IB:982:GLU:HG2	10:IB:983:LEU:HD12	1.91	0.52
11:JA:206:ILE:HG23	11:JA:1051:LEU:HD12	1.92	0.52
11:JB:414:ILE:HG12	11:JB:437:LEU:HD22	1.91	0.52
12:KB:572:SER:HB2	12:KB:703:TRP:HE1	1.74	0.52
15:NC:711:CYS:HB2	15:NC:806:ASP:HB2	1.92	0.52
2:AC:551:ILE:HG13	1:AD:475:LEU:HD13	1.92	0.52
1:AD:99:ASN:HD22	10:IB:902:ARG:HA	1.75	0.52
3:BA:693:ARG:HH11	17:PA:256:ARG:HG2	1.75	0.52
3:BB:991:PRO:HG2	16:OB:173:ARG:HH12	1.75	0.52
3:CE:4460:PRO:HA	3:CE:4463:LEU:HD23	1.92	0.52
4:DA:122:ILE:HA	4:DA:125:GLU:HG2	1.92	0.52
4:DE:41:ARG:HH21	8:GB:660:LYS:HE2	1.75	0.52
6:FD:1218:ALA:O	6:FD:1220:ARG:HB2	2.10	0.52
7:GC:450:LYS:HG2	7:GC:515:SER:HB3	1.91	0.52
7:GG:450:LYS:HG2	7:GG:635:THR:HG21	1.92	0.52
9:HD:778:PRO:O	9:HD:779:PRO:C	2.53	0.52
10:IA:259:ARG:HH22	10:IA:854:PRO:HB2	1.74	0.52
10:IA:1181:LYS:HD2	10:IA:1185:GLY:HA2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JA:548:PHE:HB3	11:JA:1288:ARG:HG3	1.92	0.52
11:JA:2013:LEU:HD21	11:JA:2266:LEU:HD21	1.91	0.52
12:KA:270:LYS:HD2	12:KE:269:MET:HE1	1.92	0.52
12:KF:600:ASP:HB2	12:KF:607:GLN:HG2	1.92	0.52
15:NB:1540:ASN:HD21	19:RB:112:LEU:HD13	1.75	0.52
15:ND:702:LEU:HB3	15:ND:937:MET:HB3	1.92	0.52
18:QD:146:ILE:HG13	18:QD:147:PHE:HD1	1.74	0.52
20:SD:83:GLU:HA	20:SD:147:MET:HE3	1.92	0.52
3:CB:766:LYS:HG2	3:CB:829:LEU:HD21	1.90	0.52
3:CB:826:LEU:HA	3:CB:829:LEU:HB2	1.92	0.52
3:CC:907:ARG:HH12	17:PB:314:LYS:HE2	1.74	0.52
3:CF:1260:VAL:HG21	3:CF:4466:ILE:HD13	1.92	0.52
4:DF:18:GLU:HB3	4:DF:320:ILE:HD11	1.90	0.52
5:EA:4405:ILE:HD13	5:EA:4431:ARG:HD3	1.91	0.52
5:EA:4656:ILE:HD11	5:EA:4660:ARG:HE	1.74	0.52
6:FE:1202:PHE:HE1	6:FE:1243:PRO:HA	1.74	0.52
7:GA:433:MET:HE3	7:GA:459:PRO:HD3	1.92	0.52
7:GE:679:LEU:HA	7:GE:689:ILE:HG22	1.91	0.52
8:GJ:177:MET:HE2	8:GJ:199:ARG:HA	1.92	0.52
9:HA:680:ALA:HB2	9:HA:708:VAL:HG13	1.92	0.52
9:HB:506:GLN:HG2	9:HB:514:PHE:CE2	2.44	0.52
10:IB:468:GLU:HA	10:IB:471:ARG:HG2	1.91	0.52
11:JA:1560:LEU:HD21	11:JA:1607:VAL:HG11	1.91	0.52
12:KA:645:ARG:H	12:KA:676:MET:HE3	1.75	0.52
12:KB:544:LEU:HB3	12:KB:714:THR:HG22	1.91	0.52
12:KF:633:ARG:HH22	12:KF:635:VAL:HG23	1.74	0.52
19:RC:20:PRO:HG3	19:RC:104:LEU:HD13	1.90	0.52
4:DA:16:LEU:HD22	4:DA:97:LEU:HD12	1.92	0.51
4:DD:255:ILE:HD11	8:GD:759:MET:HG3	1.92	0.51
6:FA:1704:MET:HE3	6:FA:1720:VAL:HG21	1.91	0.51
6:FB:2023:ILE:HG22	9:HD:778:PRO:HB3	1.90	0.51
6:FE:812:LEU:HG	6:FE:813:GLN:H	1.74	0.51
6:FE:818:VAL:O	6:FE:819:PRO:C	2.53	0.51
6:FE:1186:TRP:CE3	6:FE:1267:GLN:HB2	2.45	0.51
7:GA:663:THR:HG23	7:GA:668:GLY:HA2	1.90	0.51
7:GE:166:LEU:HA	7:GE:169:ILE:HG12	1.92	0.51
7:GG:205:ARG:HG2	7:GG:641:THR:HG22	1.91	0.51
7:GG:676:ALA:HB3	7:GG:692:HIS:HB2	1.92	0.51
7:GI:579:PHE:HZ	7:GI:588:LEU:HD22	1.75	0.51
7:GK:537:GLY:H	9:HC:554:ASP:N	2.08	0.51
9:HB:506:GLN:HG2	9:HB:514:PHE:HE2	1.74	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:HC:524:VAL:HG22	9:HC:607:VAL:HG22	1.92	0.51
10:IA:208:PHE:HB2	10:IA:239:LEU:HD13	1.92	0.51
10:IA:888:THR:HG21	15:NA:565:TRP:CD1	2.45	0.51
11:JC:78:GLN:HE22	11:JC:80:GLU:HG3	1.74	0.51
11:JC:119:LEU:HB2	11:JC:142:LEU:HD21	1.92	0.51
14:MA:214:LEU:HD11	14:MB:214:LEU:HD21	1.91	0.51
15:NA:735:HIS:CD2	15:NA:768:GLU:HG2	2.46	0.51
15:ND:1442:LYS:HD3	15:ND:1444:LYS:H	1.74	0.51
2:AG:509:ALA:HB1	1:AH:231:ILE:HD11	1.91	0.51
1:AI:157:LEU:HB3	1:AI:183:LEU:HD13	1.93	0.51
5:EB:3292:ARG:HH12	9:HB:436:ASN:HA	1.75	0.51
6:FA:2018:ARG:HH22	6:FA:2022:GLU:HB2	1.74	0.51
6:FD:1012:PRO:HB2	6:FD:1016:PRO:HD3	1.91	0.51
7:GA:169:ILE:HD11	7:GA:697:PRO:HD3	1.93	0.51
8:GB:132:PRO:HG3	8:GB:297:LEU:HD22	1.92	0.51
8:GF:499:GLN:HG3	8:GF:513:VAL:HG22	1.91	0.51
7:GK:547:GLY:H	9:HC:625:THR:HG23	1.75	0.51
11:JB:443:ILE:HD12	11:JB:1474:TRP:HH2	1.75	0.51
11:JB:543:ILE:HD11	15:NB:1328:VAL:HG22	1.92	0.51
12:KE:352:LYS:HE2	12:KE:385:GLU:HB3	1.92	0.51
13:LI:415:GLU:HA	13:LI:418:LYS:HB2	1.91	0.51
15:NA:818:ILE:HB	15:NA:842:THR:HA	1.91	0.51
15:NB:881:LEU:HD22	15:NB:884:LYS:HD2	1.92	0.51
15:NC:597:GLN:HB2	15:NC:914:ILE:HG22	1.92	0.51
18:QD:123:VAL:HA	18:QD:126:MET:HE3	1.91	0.51
19:RB:136:ALA:HA	19:RB:139:LEU:HB2	1.91	0.51
1:AE:237:VAL:HG23	1:AE:238:CYS:H	1.76	0.51
2:AG:108:LEU:HD21	2:AG:285:PHE:HE2	1.75	0.51
1:AH:799:THR:HG22	1:AH:999:LYS:H	1.75	0.51
1:AH:815:LEU:HD12	1:AH:830:THR:HG21	1.92	0.51
2:AJ:178:GLU:HG3	2:AJ:179:ASP:H	1.75	0.51
2:AK:332:ARG:NH2	11:JB:2284:LYS:HG3	2.26	0.51
1:AL:257:LEU:HD23	1:AL:261:CYS:HB3	1.91	0.51
4:DF:181:ILE:HG22	4:DF:182:LEU:HG	1.93	0.51
5:EC:3495:CYS:H	5:EC:4014:VAL:HG11	1.74	0.51
6:FE:1203:ARG:HD2	11:JC:901:ARG:HH12	1.75	0.51
8:GB:16:TRP:HZ2	8:GB:31:LEU:HB2	1.74	0.51
7:GG:846:LEU:HD13	7:GG:934:ARG:HG2	1.91	0.51
7:GG:975:VAL:HG23	7:GG:977:SER:H	1.76	0.51
10:IC:896:PHE:HE1	10:IC:921:LEU:HD22	1.74	0.51
11:JA:60:PRO:HB3	11:JA:86:SER:HA	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:553:PRO:HG2	11:JC:1199:PHE:HE1	1.75	0.51
15:NB:893:LEU:H	15:NB:1154:ASP:N	2.09	0.51
15:NC:733:VAL:HG21	15:NC:747:LEU:HD13	1.92	0.51
15:NC:888:ARG:HD2	15:NC:1156:LEU:HD12	1.91	0.51
15:ND:367:VAL:HG23	15:ND:428:ARG:HE	1.74	0.51
15:ND:665:SER:HB2	15:ND:675:GLU:HA	1.92	0.51
16:OA:200:VAL:HG22	17:PA:282:ALA:HB2	1.91	0.51
1:AA:243:VAL:HG21	19:RC:94:PRO:HG3	1.92	0.51
1:AE:84:ALA:HA	1:AE:87:LEU:HB2	1.91	0.51
2:AF:416:MET:HE3	6:FA:2073:LEU:HD21	1.92	0.51
3:BA:870:LEU:HD11	16:OA:167:LEU:HD11	1.91	0.51
3:CC:956:LEU:HB2	3:CC:978:VAL:HG11	1.92	0.51
6:FA:2016:ARG:O	6:FA:2019:GLU:HG3	2.10	0.51
6:FE:841:TYR:H	7:GE:957:ARG:NH2	2.08	0.51
6:FE:994:PRO:HB3	12:KB:382:ARG:CD	2.41	0.51
6:FE:1184:ALA:HB3	6:FE:1424:CYS:HA	1.93	0.51
6:FF:1209:GLU:O	6:FF:1210:LEU:C	2.54	0.51
6:FF:1282:LEU:HD11	6:FF:1419:LEU:HD22	1.91	0.51
7:GE:230:ARG:HE	7:GE:235:ARG:HD2	1.74	0.51
7:GE:636:VAL:HG21	7:GE:678:LEU:HD21	1.92	0.51
8:GH:19:TRP:HE1	8:GH:518:TYR:HB2	1.75	0.51
8:GH:546:VAL:HG11	8:GH:623:LEU:HD21	1.92	0.51
10:IA:644:VAL:H	16:OA:1074:TYR:HB2	1.75	0.51
11:JA:1222:ARG:HH12	11:JA:1279:PRO:HG3	1.76	0.51
12:KA:593:HIS:HB2	12:KA:707:GLU:HB3	1.90	0.51
12:KC:380:GLY:O	12:KC:381:MET:C	2.53	0.51
15:NA:685:PHE:HB2	15:NA:914:ILE:HG12	1.92	0.51
15:NC:1442:LYS:HD3	15:NC:1444:LYS:H	1.76	0.51
1:AA:60:THR:HG22	3:BA:806:SER:HB2	1.93	0.51
1:AA:274:ARG:HG3	1:AA:275:HIS:H	1.76	0.51
2:AG:434:ARG:HE	1:AH:456:VAL:HG21	1.76	0.51
1:AI:743:LEU:HA	1:AI:746:VAL:HG12	1.93	0.51
2:AK:197:ALA:HB3	2:AK:270:VAL:HB	1.92	0.51
3:CI:1177:PRO:HD2	3:CI:4509:LEU:HG	1.93	0.51
3:CI:4459:ALA:HB3	3:CI:4462:VAL:HG22	1.92	0.51
4:DB:94:PHE:HZ	4:DB:103:LEU:HD21	1.74	0.51
4:DC:362:LYS:HZ1	4:DC:379:SER:HA	1.74	0.51
5:EA:3572:ILE:HD11	5:EA:3614:PRO:HD3	1.93	0.51
5:EB:4096:ARG:HD3	5:EB:4478:THR:HA	1.93	0.51
6:FD:817:VAL:O	6:FD:818:VAL:C	2.52	0.51
6:FD:1426:ALA:O	6:FD:1427:ASN:OD1	2.28	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:1104:GLY:O	6:FF:1105:ARG:C	2.54	0.51
7:GA:292:PHE:HB2	7:GA:689:ILE:HB	1.93	0.51
7:GA:451:ILE:HD13	7:GA:516:VAL:HG22	1.93	0.51
8:GH:492:LYS:HG2	8:GH:494:SER:H	1.75	0.51
7:GI:230:ARG:HH21	7:GI:235:ARG:HB3	1.75	0.51
8:GL:326:ARG:HH21	8:GL:375:TYR:HB3	1.74	0.51
9:HB:765:TRP:N	9:HB:765:TRP:HE3	2.08	0.51
10:IA:575:SER:HB3	10:IA:580:LEU:HD21	1.91	0.51
12:KC:338:LEU:HD23	12:KC:697:ARG:HH12	1.75	0.51
13:LA:513:LEU:HD22	13:LB:513:LEU:HB3	1.91	0.51
13:LB:404:LEU:HD23	13:LB:407:ARG:HE	1.75	0.51
14:MF:310:SER:HA	14:MF:313:ARG:HB3	1.93	0.51
15:NA:801:ALA:HB2	15:NA:859:LEU:HD21	1.93	0.51
15:NA:992:GLN:HE22	15:NA:1022:ASP:HB2	1.75	0.51
15:NC:575:LEU:HD12	15:NC:581:LEU:HD21	1.93	0.51
15:ND:983:ILE:HG23	15:ND:989:ILE:HB	1.92	0.51
16:OB:742:PHE:HA	18:QC:89:ARG:HH22	1.75	0.51
3:BC:874:ARG:HD2	16:OC:163:TYR:HB3	1.92	0.51
3:CJ:1168:ARG:HH21	3:CJ:4499:PRO:HB3	1.76	0.51
4:DA:366:VAL:HG12	4:DA:375:SER:HB2	1.93	0.51
5:EA:3256:LEU:HD12	5:EA:3268:ASN:HA	1.91	0.51
5:EA:4067:ALA:HB1	5:EA:4293:TRP:HZ2	1.75	0.51
5:EB:4497:VAL:HG23	5:EB:4667:PRO:HG3	1.92	0.51
8:GD:28:LYS:HB3	8:GD:571:ARG:HH12	1.74	0.51
8:GJ:366:ALA:HB1	8:GJ:372:VAL:HG21	1.92	0.51
7:GK:292:PHE:HB2	7:GK:689:ILE:HB	1.92	0.51
10:IB:1375:VAL:HG11	16:OA:755:ILE:HG23	1.92	0.51
11:JA:87:VAL:HG22	11:JA:90:ARG:HH12	1.76	0.51
11:JA:450:PHE:HE2	11:JA:474:LYS:HE2	1.76	0.51
11:JC:835:VAL:HG11	11:JC:1009:VAL:HG21	1.93	0.51
12:KA:526:TRP:HB3	12:KA:545:LEU:HD11	1.91	0.51
12:KG:208:LEU:HD13	12:KG:244:SER:HA	1.91	0.51
12:KG:267:THR:HA	12:KG:270:LYS:HG2	1.91	0.51
15:NA:503:LEU:HB3	15:NA:512:TYR:HB3	1.92	0.51
15:NA:1546:VAL:HG22	19:RC:26:HIS:CE1	2.46	0.51
15:NB:1407:MET:HG3	15:NB:1471:ARG:HB2	1.92	0.51
15:ND:853:GLU:HB2	15:ND:867:ARG:HH12	1.76	0.51
1:AE:414:GLU:HB3	2:AF:67:LEU:HD11	1.93	0.51
1:AI:247:THR:H	1:AI:258:CYS:HB3	1.75	0.51
2:AK:459:ILE:HG12	11:JB:1166:ARG:HG3	1.92	0.51
3:CE:1126:GLU:HB3	10:IA:995:PRO:HG2	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CG:1229:HIS:HB3	3:CG:4463:LEU:HD22	1.92	0.51
5:EC:3787:GLU:HG2	5:EC:3790:ARG:HH12	1.75	0.51
5:EC:4888:TRP:O	5:EC:4889:ILE:C	2.53	0.51
6:FD:1082:THR:O	6:FD:1085:GLU:HG3	2.11	0.51
6:FE:910:ILE:HG12	6:FE:962:PHE:CE2	2.45	0.51
6:FF:807:ALA:O	6:FF:808:SER:HB2	2.10	0.51
7:GC:742:CYS:HB2	7:GC:797:ILE:HD13	1.92	0.51
7:GI:368:PHE:HB3	7:GI:401:LEU:HD11	1.92	0.51
7:GI:731:ILE:HD13	7:GI:817:ARG:HH12	1.76	0.51
8:GL:349:THR:HG22	8:GL:379:VAL:HG21	1.93	0.51
8:GL:369:LEU:HD23	8:GL:392:ASP:HB3	1.93	0.51
10:IB:480:LEU:HD23	10:IB:497:LEU:HD21	1.92	0.51
10:IB:1179:ASN:HD22	10:IB:1179:ASN:C	2.18	0.51
10:IC:1087:THR:HG21	10:IC:1091:LEU:HD12	1.92	0.51
11:JA:529:ILE:HD13	11:JA:885:TYR:HD2	1.76	0.51
14:MA:301:LEU:HB3	14:MB:301:LEU:HD22	1.93	0.51
15:ND:593:LYS:HG2	15:ND:595:ARG:HG2	1.92	0.51
15:ND:725:ILE:HG23	15:ND:799:ILE:HD11	1.91	0.51
16:OB:889:VAL:HG21	16:OB:913:VAL:HG21	1.93	0.51
2:AC:373:ARG:HH11	5:EB:4404:LYS:HG3	1.76	0.51
2:AC:535:LEU:HD22	5:EA:4820:GLY:HA3	1.91	0.51
1:AE:1025:ARG:NH1	14:ML:84:GLY:HA3	2.26	0.51
2:AF:94:ILE:HG13	2:AF:99:MET:HE2	1.92	0.51
1:AI:805:TYR:HE2	1:AI:994:LEU:HB2	1.75	0.51
3:CC:724:GLN:O	3:CC:724:GLN:NE2	2.44	0.51
3:CF:1172:PRO:HD2	3:CF:1202:LEU:HD22	1.92	0.51
3:CL:1221:ASN:HD21	3:CL:1226:LEU:HD12	1.75	0.51
5:EA:4405:ILE:HG22	5:EA:4427:LEU:HD12	1.93	0.51
5:EB:3491:ALA:HB2	5:EB:3603:LEU:HB3	1.92	0.51
6:FC:1817:VAL:HG11	6:FC:1838:VAL:HG11	1.92	0.51
6:FD:1216:TRP:O	6:FD:1217:GLU:C	2.54	0.51
6:FE:833:GLY:H	6:FE:979:LEU:HD23	1.76	0.51
6:FE:917:TRP:CD1	6:FE:918:GLN:HE21	2.26	0.51
8:GL:178:ALA:HB3	8:GL:198:PHE:HB2	1.91	0.51
10:IB:1095:GLY:H	10:IB:1098:HIS:HD2	1.59	0.51
10:IB:1419:HIS:HA	10:IB:1426:LYS:HZ1	1.76	0.51
11:JB:503:HIS:HE1	11:JB:1426:PRO:HB2	1.75	0.51
11:JB:512:SER:HB3	11:JB:1474:TRP:HZ3	1.76	0.51
11:JC:1553:LEU:HD21	11:JC:1597:LEU:HD13	1.92	0.51
11:JC:1765:ARG:HH12	16:OC:893:PRO:CD	2.23	0.51
12:KG:579:LEU:HD11	12:KG:654:ILE:HG22	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LD:481:GLU:HB3	13:LD:486:ARG:HD3	1.92	0.51
18:QB:49:ILE:HG21	18:QB:55:VAL:HB	1.91	0.51
1:AD:309:LEU:HD12	1:AD:329:LEU:HD21	1.93	0.51
2:AK:424:LEU:HD12	1:AL:418:ILE:HB	1.93	0.51
3:BC:750:SER:H	17:PC:254:ALA:HB1	1.76	0.51
3:CE:4474:GLU:CD	3:CE:4475:LYS:H	2.19	0.51
4:DA:140:VAL:HB	4:DA:143:LEU:HB2	1.92	0.51
5:EA:4461:PHE:HB3	5:EA:4500:THR:HG22	1.92	0.51
5:EB:3383:VAL:HG12	5:EB:3392:TRP:HE3	1.75	0.51
5:EC:4169:VAL:HB	5:EC:4205:ILE:HD11	1.93	0.51
6:FB:1727:ALA:HA	6:FB:1802:ASP:HA	1.92	0.51
6:FE:803:ARG:CB	6:FE:1118:GLN:HG3	2.41	0.51
6:FE:844:ALA:O	7:GE:896:ARG:NH2	2.43	0.51
6:FE:852:VAL:HG11	6:FE:864:LEU:HG	1.92	0.51
6:FF:1239:CYS:HB3	6:FF:1260:LEU:HD11	1.93	0.51
8:GH:273:SER:HA	8:GH:320:SER:HA	1.93	0.51
7:GI:184:ALA:HB3	7:GI:708:SER:HB2	1.91	0.51
8:GL:326:ARG:HB3	8:GL:338:ALA:HB2	1.93	0.51
11:JA:1666:VAL:HG13	16:OA:917:ILE:HD11	1.92	0.51
11:JC:1794:LEU:HD21	11:JC:1859:GLN:HG2	1.93	0.51
12:KE:246:LEU:HD13	12:KE:297:ILE:HG23	1.92	0.51
12:KE:596:ILE:HG12	12:KE:666:LEU:HD11	1.92	0.51
13:LD:370:MET:HA	13:LD:373:VAL:HG22	1.93	0.51
15:NA:805:ALA:HB2	15:NA:885:LEU:HD12	1.92	0.51
19:RA:22:ARG:HG2	19:RA:174:LEU:HD12	1.93	0.51
1:AA:38:VAL:HG21	1:AA:111:ILE:HG23	1.92	0.51
2:AG:300:CYS:HB2	2:AG:320:CYS:HB3	1.93	0.51
1:AI:148:VAL:HG23	1:AI:219:THR:HB	1.91	0.51
3:BB:788:VAL:HG21	3:BB:826:LEU:HD22	1.92	0.51
3:CG:1236:LEU:HD23	3:CG:1253:VAL:HG23	1.93	0.51
5:EA:4412:LEU:HD13	5:EA:4416:PHE:HE2	1.75	0.51
5:EB:4814:THR:HG22	5:EB:4817:LEU:HD21	1.93	0.51
5:EC:4172:GLY:HA3	5:EC:4208:LEU:HD21	1.93	0.51
5:EC:4893:THR:O	5:EC:4894:SER:C	2.54	0.51
6:FC:2080:GLN:O	6:FC:2083:GLN:HG3	2.11	0.51
6:FF:1429:LEU:HD23	6:FF:1430:PHE:CD2	2.46	0.51
8:GB:401:ASP:HA	8:GB:404:ARG:HG2	1.93	0.51
7:GI:709:MET:HE2	7:GI:714:VAL:HG21	1.92	0.51
9:HA:674:VAL:HG22	9:HA:712:ILE:HG23	1.92	0.51
9:HA:778:PRO:O	9:HA:779:PRO:C	2.54	0.51
10:IC:1097:LEU:HA	10:IC:1112:LEU:HD13	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:KA:375:TYR:HD1	12:KA:402:LEU:HD11	1.76	0.51
15:NB:1442:LYS:HG3	15:NB:1444:LYS:H	1.75	0.51
15:ND:1518:ARG:HH21	18:QB:60:ARG:NH2	2.08	0.51
20:SC:30:THR:HA	20:SC:33:LEU:HD23	1.93	0.51
20:SD:130:ASP:HB2	20:SD:137:ILE:HD11	1.91	0.51
2:AC:517:ARG:HH12	1:AD:48:ALA:HB1	1.76	0.50
1:AE:65:ILE:HG12	1:AE:222:LEU:HB3	1.94	0.50
2:AG:319:LEU:HD21	2:AG:327:ILE:HD12	1.93	0.50
3:BA:791:THR:HG21	3:BA:812:MET:SD	2.51	0.50
3:CF:4484:VAL:HG12	3:CF:4499:PRO:HA	1.91	0.50
3:CI:1239:PRO:HG3	3:CI:4471:PRO:HD2	1.92	0.50
3:CJ:1152:LEU:HD23	10:IB:397:VAL:HG13	1.93	0.50
4:DA:376:SER:HA	13:LA:433:ARG:HH22	1.75	0.50
4:DB:10:GLU:HA	4:DB:13:VAL:HB	1.93	0.50
4:DB:385:LYS:HZ1	13:LF:462:GLN:HA	1.76	0.50
4:DD:162:VAL:HA	4:DD:165:ILE:HD12	1.92	0.50
5:EA:4741:LYS:HD2	5:EA:4836:SER:HA	1.94	0.50
5:EC:3292:ARG:HH22	9:HA:436:ASN:N	2.09	0.50
6:FD:993:ALA:HA	12:KA:230:GLN:HG2	1.93	0.50
7:GA:768:PRO:HG2	7:GA:773:VAL:HG22	1.92	0.50
8:GD:7:GLU:HB2	8:GD:13:ARG:HH11	1.76	0.50
7:GE:396:PRO:HD2	7:GE:401:LEU:HD11	1.93	0.50
8:GF:101:PRO:HD2	8:GF:104:LEU:HD12	1.93	0.50
8:GH:199:ARG:NH2	7:GI:394:PHE:HB2	2.26	0.50
8:GL:416:LYS:HB3	8:GL:470:LYS:HG2	1.93	0.50
9:HB:574:ARG:HG3	9:HB:578:THR:HB	1.93	0.50
10:IC:615:ARG:HB2	10:IC:629:PRO:HG3	1.92	0.50
11:JA:874:VAL:HG12	11:JA:961:VAL:HG22	1.93	0.50
11:JA:1720:ASP:HB3	16:OA:930:ALA:HA	1.93	0.50
11:JC:1734:VAL:HG11	11:JC:1774:ARG:HG3	1.92	0.50
12:KA:370:LEU:HD22	12:KA:377:LEU:HD11	1.93	0.50
12:KC:591:ARG:H	12:KC:646:ARG:HH22	1.59	0.50
12:KE:344:ILE:HA	12:KE:347:LEU:HD12	1.93	0.50
14:MF:287:ALA:HA	14:MF:290:ARG:HB2	1.92	0.50
15:NC:355:LEU:HD22	15:NC:434:VAL:HG21	1.92	0.50
16:OA:177:THR:HG23	16:OA:179:GLU:HG3	1.92	0.50
16:OC:1097:SER:H	16:OC:1100:GLU:HB3	1.76	0.50
2:AK:193:GLU:HG3	1:AL:466:PRO:HG3	1.92	0.50
3:BB:951:VAL:HG13	3:BB:952:GLN:HE21	1.75	0.50
5:EC:4745:VAL:HG13	5:EC:4842:GLN:HE22	1.76	0.50
6:FB:1640:VAL:HG13	6:FB:1643:PRO:HB3	1.91	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FC:1970:LEU:HD12	6:FC:2040:LEU:HD22	1.93	0.50
7:GA:386:VAL:HB	8:GF:196:HIS:HA	1.91	0.50
8:GH:544:LEU:HD23	8:GH:548:LYS:HZ3	1.77	0.50
8:GJ:57:ARG:HH21	8:GJ:85:ASN:HA	1.76	0.50
7:GK:551:LEU:HB2	9:HC:666:LYS:HD2	1.93	0.50
9:HC:575:ARG:H	9:HC:578:THR:HB	1.76	0.50
10:IA:1294:ILE:HD12	10:IA:1358:LEU:HD11	1.92	0.50
10:IB:1245:GLN:HA	10:IB:1272:LEU:HD12	1.94	0.50
11:JB:1856:ARG:HH21	11:JB:1860:PRO:HD3	1.77	0.50
12:KA:582:ILE:HG23	12:KA:653:VAL:HG13	1.93	0.50
12:KA:598:VAL:HG12	12:KA:702:ILE:HG22	1.93	0.50
13:LA:398:ARG:HA	13:LA:401:LEU:HB2	1.93	0.50
13:LJ:489:LEU:HG	14:ML:113:VAL:HG21	1.92	0.50
15:NA:343:VAL:HG21	15:NA:490:VAL:HG11	1.91	0.50
15:NA:617:PHE:HD1	15:NA:916:LEU:HD22	1.77	0.50
15:NA:891:TRP:H	15:NA:1154:ASP:C	2.20	0.50
15:NB:598:PHE:HZ	15:NB:948:LEU:HD13	1.76	0.50
15:NB:621:TYR:HB2	15:NB:626:ARG:HH22	1.76	0.50
16:OC:1059:LEU:HD12	16:OC:1060:GLN:HG2	1.93	0.50
1:AL:588:ILE:HD11	1:AL:594:TYR:HE1	1.77	0.50
1:AL:852:ARG:HG2	1:AL:853:TYR:H	1.75	0.50
3:BB:817:HIS:CE1	16:OB:241:ALA:HB2	2.46	0.50
3:CE:1236:LEU:HD21	3:CE:1255:VAL:HG13	1.93	0.50
3:CG:4486:ILE:HD12	3:CG:4494:GLU:HG3	1.92	0.50
4:DC:93:ILE:HD12	4:DC:164:PHE:HB3	1.94	0.50
5:EA:4652:LEU:H	5:EA:4657:GLU:HB2	1.75	0.50
5:EB:4167:ASP:HB3	5:EB:4170:LYS:HB3	1.92	0.50
5:EB:4394:GLY:HA2	5:EB:4450:ARG:HB3	1.92	0.50
6:FB:1724:ARG:HE	6:FB:1808:VAL:HG13	1.77	0.50
6:FD:826:LEU:HB3	6:FD:841:TYR:HE2	1.77	0.50
6:FD:1026:PRO:HB2	6:FD:1029:GLN:HG2	1.93	0.50
6:FD:1200:LEU:H	6:FD:1256:GLU:HG3	1.74	0.50
6:FE:878:LEU:HB3	6:FE:907:ASN:H	1.76	0.50
6:FE:917:TRP:O	6:FE:918:GLN:C	2.54	0.50
8:GH:192:VAL:HG11	7:GI:422:LEU:HD11	1.93	0.50
7:GI:762:TYR:HA	7:GI:986:LEU:HD11	1.92	0.50
7:GI:764:LEU:HD13	7:GI:870:ARG:HD2	1.93	0.50
8:GJ:25:GLU:HA	8:GJ:28:LYS:HG2	1.93	0.50
7:GK:606:MET:HB2	7:GK:631:PHE:HB2	1.92	0.50
9:HA:759:GLU:O	9:HA:760:LYS:C	2.54	0.50
9:HD:777:TYR:O	9:HD:778:PRO:C	2.55	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:791:VAL:HG21	10:IB:812:LEU:HD22	1.92	0.50
11:JA:2125:ILE:HD11	11:JA:2259:LEU:HD11	1.93	0.50
12:KC:231:PHE:CE1	12:KC:313:PHE:CD2	3.00	0.50
12:KF:212:LEU:HD11	12:KF:294:ARG:HD2	1.92	0.50
12:KG:593:HIS:HB2	12:KG:707:GLU:HB3	1.93	0.50
13:LI:429:GLU:HA	13:LI:432:THR:HG22	1.92	0.50
14:MF:330:LEU:HD13	14:MF:333:LEU:HD12	1.92	0.50
15:NB:1422:VAL:HB	20:SC:108:HIS:CE1	2.46	0.50
20:SC:73:MET:HA	20:SC:77:MET:HE3	1.93	0.50
1:AA:240:MET:HE1	1:AA:265:VAL:HG11	1.93	0.50
1:AA:241:CYS:HB3	1:AA:243:VAL:HG23	1.92	0.50
1:AA:648:ARG:HE	1:AA:688:PHE:HE2	1.59	0.50
1:AL:62:ASP:HA	1:AL:228:PRO:HB3	1.93	0.50
3:BA:724:GLN:HG3	3:BA:725:GLN:H	1.77	0.50
3:CE:1237:VAL:HG21	3:CE:4468:LYS:HD2	1.92	0.50
4:DA:315:LEU:HD21	14:MB:239:GLU:HB3	1.93	0.50
4:DD:28:LEU:HG	4:DD:29:LEU:HG	1.92	0.50
4:DE:308:GLN:HE22	4:DE:315:LEU:HD21	1.76	0.50
5:EA:4539:MET:HB2	5:EA:4685:PRO:HA	1.93	0.50
5:EB:3265:LEU:HA	5:EB:3510:LEU:HD21	1.93	0.50
6:FE:846:CYS:HB3	12:KB:305:HIS:NE2	2.25	0.50
7:GC:518:LEU:HB3	7:GC:520:ILE:HG12	1.94	0.50
7:GE:276:ARG:HB3	7:GE:276:ARG:CZ	2.41	0.50
7:GE:372:GLY:HA3	7:GE:403:VAL:HG11	1.91	0.50
8:GH:773:ASP:HB2	8:GL:346:LYS:HD3	1.93	0.50
7:GI:309:LEU:HB3	7:GI:402:PHE:HE1	1.76	0.50
7:GI:919:VAL:HB	12:KC:684:LEU:HD22	1.92	0.50
7:GK:544:PRO:HG3	9:HC:596:TYR:HA	1.93	0.50
7:GK:843:LEU:HD13	7:GK:935:VAL:HG13	1.94	0.50
10:IA:922:ALA:HB2	10:IA:942:PHE:HD2	1.75	0.50
11:JB:1169:ARG:HH21	11:JB:1665:GLN:HA	1.77	0.50
12:KA:599:GLU:HA	12:KA:606:ARG:NH2	2.26	0.50
12:KC:305:HIS:HB2	12:KC:309:GLN:HB2	1.93	0.50
12:KC:376:ALA:HB2	12:KC:725:ILE:HD11	1.93	0.50
15:NB:467:ASP:HB2	15:NB:469:PHE:CZ	2.47	0.50
15:NC:801:ALA:HA	15:NC:804:VAL:HG12	1.93	0.50
15:NC:894:LEU:H	15:NC:1153:ALA:H	1.59	0.50
2:AG:53:PRO:HB2	5:EC:4290:GLY:HA2	1.94	0.50
2:AG:548:ARG:HD2	5:EB:4620:LYS:NZ	2.27	0.50
1:AI:1046:THR:HG22	1:AI:1048:ALA:H	1.75	0.50
3:CB:920:ARG:HH12	3:CB:957:ALA:HA	1.75	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FB:1647:LEU:HD22	6:FB:1797:VAL:HG23	1.94	0.50
6:FC:1845:PRO:HB2	6:FC:1848:PRO:HD2	1.94	0.50
6:FE:910:ILE:HD11	6:FE:965:TRP:CD1	2.46	0.50
6:FF:861:LEU:HA	6:FF:864:LEU:HD12	1.94	0.50
7:GA:536:THR:HA	9:HB:553:TYR:HB2	1.93	0.50
8:GD:154:ASP:HA	8:GD:157:MET:HG2	1.93	0.50
7:GK:531:GLY:HA2	9:HC:530:LYS:HB2	1.93	0.50
9:HB:856:GLU:HA	9:HB:859:LYS:HD2	1.93	0.50
10:IB:1087:THR:HG21	10:IB:1091:LEU:HD12	1.92	0.50
11:JB:786:PHE:HB3	11:JB:814:ASP:HB2	1.93	0.50
11:JC:131:LEU:HD11	11:JC:1821:LEU:HD13	1.94	0.50
12:KA:285:ILE:HG21	12:KA:293:ILE:HG12	1.92	0.50
12:KE:530:ASP:HA	12:KE:550:ARG:HD2	1.94	0.50
15:NA:368:GLU:HG2	15:NA:428:ARG:HH21	1.76	0.50
1:AA:266:HIS:HA	1:AA:272:LEU:HD12	1.94	0.50
1:AA:731:SER:H	1:AA:735:LEU:HD23	1.77	0.50
2:AG:376:ARG:HH22	5:EC:4405:ILE:CD1	2.25	0.50
2:AJ:140:LYS:HD3	2:AJ:143:ARG:NH2	2.26	0.50
2:AK:63:THR:HG21	2:AK:170:GLY:HA3	1.93	0.50
3:CG:1133:VAL:HG11	10:IC:1094:ASN:ND2	2.26	0.50
5:EA:4724:LEU:HG	5:EA:4812:LEU:HD11	1.93	0.50
5:EC:4217:LEU:HD13	5:EC:4254:MET:HE2	1.94	0.50
5:EC:4403:LEU:HD12	5:EC:4428:MET:HE1	1.93	0.50
6:FB:1653:ARG:HH12	6:FB:1733:ARG:HH21	1.57	0.50
6:FC:1755:VAL:HG21	6:FC:1934:LEU:HB3	1.93	0.50
7:GA:418:THR:HG21	8:GF:192:VAL:HG21	1.94	0.50
8:GD:526:ILE:HG21	14:MA:317:THR:HB	1.94	0.50
8:GL:661:PRO:HB2	8:GL:680:LEU:H	1.77	0.50
9:HA:854:ASN:HA	9:HA:857:ARG:HE	1.77	0.50
10:IC:929:GLY:H	10:IC:963:ARG:HE	1.60	0.50
11:JA:836:MET:HG3	11:JA:966:LEU:HD13	1.93	0.50
11:JC:1803:ARG:HA	11:JC:1806:MET:HB3	1.92	0.50
12:KC:534:VAL:HB	12:KC:536:ARG:HG2	1.93	0.50
15:NB:1532:ARG:HA	15:NB:1535:MET:HE2	1.94	0.50
15:ND:885:LEU:HA	15:ND:888:ARG:HB2	1.94	0.50
16:OB:70:THR:HG22	16:OB:71:SER:H	1.76	0.50
18:QB:144:GLU:HB3	18:QB:150:ALA:HB2	1.93	0.50
1:AA:382:ILE:HG23	2:AB:460:LEU:HD12	1.94	0.50
2:AB:303:CYS:HB2	2:AB:323:CYS:HB3	1.94	0.50
1:AD:131:ARG:HG2	1:AD:205:ARG:HH12	1.76	0.50
1:AD:231:ILE:HA	10:IB:825:LEU:HD11	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:967:ARG:HD3	14:MC:94:LEU:HD13	1.92	0.50
3:BB:810:PRO:HA	17:PB:278:TRP:CZ3	2.47	0.50
4:DA:329:ARG:HA	4:DA:332:LEU:HB2	1.94	0.50
4:DB:304:THR:HG22	4:DB:307:LEU:HD12	1.93	0.50
4:DC:134:LEU:HA	4:DC:148:ARG:HH22	1.76	0.50
4:DE:88:CYS:HB2	4:DE:172:ARG:HH22	1.77	0.50
6:FB:2044:CYS:HB3	9:HD:826:ARG:HH21	1.76	0.50
6:FF:1217:GLU:O	6:FF:1219:GLU:N	2.44	0.50
8:GF:61:CYS:CB	8:GF:78:CYS:SG	2.99	0.50
7:GG:494:LEU:HB3	7:GG:814:THR:HG21	1.93	0.50
11:JC:1427:LEU:HD12	11:JC:1462:ILE:HD11	1.94	0.50
12:KA:621:GLY:HA3	12:KA:633:ARG:HE	1.77	0.50
12:KB:498:ARG:HE	12:KE:507:LEU:HD22	1.76	0.50
16:OA:7:ARG:HD2	16:OA:12:GLU:HB2	1.94	0.50
16:OA:1046:MET:HG3	16:OA:1047:GLY:H	1.77	0.50
19:RD:22:ARG:HH21	19:RD:177:ALA:HB2	1.77	0.50
1:AD:908:ARG:HB3	13:LA:490:MET:HB3	1.94	0.50
2:AF:207:GLU:HG2	2:AF:208:GLU:HG3	1.93	0.50
1:AH:99:ASN:HD21	1:AH:134:PHE:HB3	1.75	0.50
2:AK:263:TYR:HD1	1:AL:423:THR:HB	1.76	0.50
4:DB:110:LEU:HG	4:DB:114:VAL:HG13	1.94	0.50
5:EA:3304:LYS:HD3	5:EA:4163:MET:HB2	1.92	0.50
5:EC:3836:GLU:HG2	5:EC:3863:SER:HA	1.94	0.50
6:FA:2063:GLN:OE1	9:HA:751:SER:HB2	2.12	0.50
6:FB:1850:GLN:HA	6:FB:1923:PHE:HE1	1.77	0.50
6:FB:2037:LEU:HD23	9:HD:816:LEU:HD22	1.93	0.50
6:FD:852:VAL:HG12	6:FD:880:VAL:HG22	1.93	0.50
6:FD:1441:ILE:O	6:FD:1444:ARG:N	2.44	0.50
6:FE:829:ARG:HB2	6:FE:976:HIS:CD2	2.46	0.50
6:FF:895:ILE:HG12	7:GI:967:PHE:CE2	2.46	0.50
6:FF:981:HIS:NE2	12:KC:667:SER:HB2	2.27	0.50
8:GF:316:VAL:HG23	8:GF:341:VAL:HG12	1.94	0.50
8:GL:379:VAL:HA	8:GL:382:GLU:HG2	1.94	0.50
11:JC:138:THR:HA	11:JC:162:PRO:HA	1.94	0.50
12:KF:414:TRP:HE3	12:KF:415:LEU:HD22	1.77	0.50
13:LF:489:LEU:HB3	14:MH:113:VAL:HG21	1.92	0.50
13:LJ:464:ASP:HA	13:LJ:467:GLN:HB3	1.93	0.50
15:NA:575:LEU:HD12	15:NA:581:LEU:HD21	1.94	0.50
15:NA:1005:VAL:H	15:NA:1008:SER:HB3	1.77	0.50
15:NB:864:GLU:HA	15:NB:867:ARG:HE	1.77	0.50
16:OA:891:ARG:HH12	16:OA:924:VAL:HG22	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:259:VAL:HG21	2:AB:307:PRO:HB3	1.93	0.50
1:AE:429:ARG:HE	2:AF:417:ALA:HB1	1.77	0.50
2:AF:72:PHE:HB3	2:AF:164:TYR:HD2	1.76	0.50
1:AI:303:MET:HB2	1:AI:328:PRO:HG2	1.94	0.50
2:AK:373:ARG:HE	2:AK:374:LEU:HD22	1.77	0.50
2:AK:495:SER:HB2	2:AK:518:HIS:HE1	1.76	0.50
3:BA:812:MET:HA	16:OA:196:TRP:HZ3	1.76	0.50
3:CL:1152:LEU:HD23	10:IC:397:VAL:HG13	1.94	0.50
4:DD:174:THR:HA	4:DD:177:LYS:HZ2	1.77	0.50
5:EA:4454:ARG:HD2	5:EA:4507:ASP:HB2	1.94	0.50
5:EC:3426:ARG:HH22	5:EC:3804:ILE:HG13	1.77	0.50
6:FD:909:PRO:O	6:FD:911:SER:N	2.45	0.50
6:FE:1285:CYS:O	6:FE:1286:LEU:C	2.53	0.50
6:FF:886:THR:HG22	6:FF:900:ALA:HB2	1.92	0.50
7:GC:620:HIS:CD2	7:GC:720:GLN:HB3	2.47	0.50
8:GD:283:LEU:HD21	8:GD:303:LEU:HD22	1.94	0.50
8:GH:374:LEU:HB2	8:GH:613:ASP:HA	1.93	0.50
9:HD:779:PRO:O	9:HD:780:PHE:C	2.54	0.50
10:IA:827:ARG:HE	11:JA:2055:TRP:HE1	1.60	0.50
11:JA:107:PRO:HB3	11:JA:186:SER:HA	1.94	0.50
11:JA:1679:ALA:HB2	11:JA:1714:CYS:HB2	1.94	0.50
11:JB:131:LEU:HD21	11:JB:1821:LEU:HA	1.94	0.50
11:JB:841:VAL:HG13	11:JB:1424:ARG:HB2	1.94	0.50
11:JC:761:LYS:HD2	11:JC:768:ASP:HA	1.94	0.50
11:JC:1542:PRO:HD2	11:JC:1545:HIS:CD2	2.47	0.50
11:JC:1569:ASN:HB2	11:JC:1572:LEU:HG	1.94	0.50
15:NA:864:GLU:HA	15:NA:867:ARG:HD2	1.93	0.50
15:NA:1508:PHE:HB2	20:SA:19:LEU:HD11	1.94	0.50
15:NC:980:LEU:HD13	15:NC:983:ILE:HD12	1.94	0.50
2:AG:332:ARG:HH12	2:AG:336:ARG:HE	1.60	0.49
3:BB:790:ASN:HB3	3:BB:811:ILE:HG22	1.94	0.49
3:BB:825:SER:HB2	16:OB:291:VAL:HG12	1.92	0.49
3:CC:680:PRO:HA	3:CC:683:GLN:HB2	1.94	0.49
4:DF:285:ARG:HE	4:DF:345:ALA:HB2	1.77	0.49
5:EB:3488:THR:HG22	5:EB:3559:VAL:HG22	1.94	0.49
6:FD:834:VAL:O	6:FD:835:SER:C	2.55	0.49
8:GH:336:ASN:HA	8:GL:219:ALA:HA	1.93	0.49
9:HA:552:ASP:HB2	9:HA:576:LYS:HG3	1.94	0.49
9:HA:761:CYS:HA	9:HA:765:TRP:CE2	2.47	0.49
9:HB:801:VAL:HA	13:LE:532:LEU:O	2.11	0.49
11:JA:139:ARG:HH11	11:JA:160:LEU:HD11	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:KA:314:LEU:HD13	12:KA:317:ALA:HB3	1.92	0.49
12:KC:503:ASP:H	12:KC:506:LEU:HD23	1.77	0.49
12:KF:398:ASP:HA	12:KF:522:ARG:HD2	1.94	0.49
13:LE:513:LEU:HA	13:LE:516:VAL:HG12	1.94	0.49
15:NA:1503:PHE:HD1	15:NA:1506:ARG:HH22	1.59	0.49
15:NB:608:ALA:H	15:NB:676:ARG:HH22	1.60	0.49
15:NB:1036:LEU:HD11	15:NB:1097:ILE:HB	1.94	0.49
15:ND:1140:LEU:HD12	15:ND:1143:LEU:HD22	1.94	0.49
16:OB:184:ASN:HA	16:OB:295:LEU:HD11	1.93	0.49
18:QA:165:ARG:HE	18:QA:172:GLN:HA	1.77	0.49
18:QC:55:VAL:HA	18:QC:58:LEU:HB3	1.94	0.49
1:AA:399:ARG:HD2	6:FA:1672:LEU:HD11	1.94	0.49
1:AH:389:LEU:HA	5:EB:4619:VAL:HG11	1.93	0.49
1:AI:44:LEU:HD22	17:PB:268:PRO:HB2	1.94	0.49
2:AK:12:SER:HB2	6:FC:1911:PRO:HD2	1.95	0.49
5:EA:4727:SER:HB2	5:EA:4817:LEU:HD12	1.94	0.49
5:EB:4397:ASP:OD1	5:EB:4402:PRO:HD3	2.12	0.49
6:FA:2012:ARG:HH21	6:FA:2012:ARG:HB3	1.77	0.49
6:FE:841:TYR:C	7:GE:957:ARG:HH21	2.20	0.49
6:FF:917:TRP:O	6:FF:918:GLN:C	2.55	0.49
6:FF:923:ALA:C	6:FF:928:SER:H	2.20	0.49
7:GA:604:ALA:HB3	7:GA:633:LEU:HB2	1.95	0.49
7:GC:884:LEU:HD21	7:GC:969:GLN:HB2	1.94	0.49
8:GH:251:CYS:HA	8:GH:254:LYS:HE2	1.93	0.49
10:IC:374:PHE:HB3	10:IC:393:LEU:HD12	1.94	0.49
11:JB:769:LEU:HD12	11:JB:794:ALA:HB1	1.93	0.49
11:JB:1125:ILE:HG22	11:JB:1156:ILE:HD11	1.95	0.49
11:JC:1138:PRO:HA	11:JC:1670:ARG:HH12	1.76	0.49
13:LO:404:LEU:HA	13:LO:407:ARG:HG2	1.94	0.49
15:NA:545:VAL:HG22	15:NA:1195:SER:HA	1.94	0.49
2:AB:408:LYS:HA	2:AB:411:GLN:HE21	1.76	0.49
1:AE:443:LYS:HG2	2:AF:27:ALA:HB1	1.94	0.49
2:AG:145:LYS:HA	2:AG:148:ASP:HB2	1.94	0.49
3:BA:904:PRO:HG3	3:BA:941:ARG:HG2	1.94	0.49
5:EB:3273:LEU:HD23	5:EB:3494:VAL:HG11	1.94	0.49
6:FF:800:ALA:HB3	6:FF:910:ILE:HG23	1.94	0.49
6:FF:895:ILE:C	7:GI:878:GLN:HE22	2.19	0.49
6:FF:1001:ASN:O	6:FF:1009:VAL:HA	2.12	0.49
7:GC:372:GLY:HA3	7:GC:403:VAL:HG11	1.94	0.49
7:GG:959:GLY:HA2	9:HA:689:LYS:NZ	2.27	0.49
11:JA:1594:ARG:HD3	11:JA:1624:VAL:HG11	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:1703:ASN:HA	11:JB:1706:ASP:HB2	1.94	0.49
11:JC:882:ALA:HA	11:JC:891:VAL:HG12	1.94	0.49
12:KF:212:LEU:HD22	12:KF:290:PRO:HB2	1.94	0.49
14:MF:308:GLU:HA	14:MF:311:ILE:HG22	1.95	0.49
15:NB:1518:ARG:HG3	18:QC:167:LEU:HB3	1.94	0.49
16:OA:190:LEU:HD23	16:OA:229:LEU:HD13	1.93	0.49
17:PA:124:ILE:HG23	17:PA:128:GLU:HB2	1.94	0.49
19:RA:136:ALA:HA	19:RA:139:LEU:HB2	1.95	0.49
1:AE:289:SER:H	17:PC:271:ASN:HD22	1.60	0.49
3:CJ:1212:GLU:HB2	3:CJ:1222:ARG:HH22	1.76	0.49
4:DA:48:TYR:HE1	4:DA:128:ALA:HB3	1.78	0.49
4:DB:48:TYR:CD1	4:DB:125:GLU:HA	2.47	0.49
4:DD:150:SER:HA	4:DD:153:PHE:HB3	1.94	0.49
4:DF:105:CYS:H	4:DF:260:GLY:H	1.60	0.49
5:EA:4667:PRO:HA	5:EA:4670:TRP:HB3	1.92	0.49
5:EC:3273:LEU:HD12	5:EC:3305:GLU:HG3	1.93	0.49
6:FA:2059:VAL:HG23	9:HA:754:LEU:CB	2.43	0.49
6:FD:1212:VAL:HG23	6:FD:1264:ILE:HD12	1.94	0.49
6:FD:1244:LEU:HB3	6:FD:1249:ILE:HG12	1.95	0.49
6:FE:1064:TYR:O	6:FE:1065:LEU:C	2.55	0.49
6:FF:1186:TRP:CE3	6:FF:1269:CYS:HB2	2.47	0.49
8:GD:184:GLY:H	8:GD:254:LYS:HG3	1.76	0.49
9:HD:782:ALA:O	9:HD:783:SER:C	2.55	0.49
10:IA:740:ARG:HH12	10:IA:777:GLY:HA3	1.77	0.49
10:IA:791:VAL:HG11	10:IA:812:LEU:HD22	1.94	0.49
10:IB:1307:ASN:HA	10:IB:1383:LEU:HD13	1.93	0.49
10:IC:1196:VAL:HG12	10:IC:1305:GLU:HG2	1.94	0.49
11:JA:1686:LEU:HD12	11:JA:1707:VAL:HG13	1.94	0.49
11:JB:533:ILE:HG21	11:JB:888:PHE:HE2	1.77	0.49
12:KA:574:LEU:HD12	12:KA:699:PHE:HB3	1.95	0.49
13:LI:482:LEU:HD13	13:LJ:482:LEU:HD22	1.93	0.49
15:NB:884:LYS:HD3	15:NB:1127:LEU:HD12	1.93	0.49
15:ND:950:VAL:HA	15:ND:954:PHE:HD2	1.77	0.49
1:AA:146:VAL:HB	1:AA:224:PHE:HE2	1.78	0.49
1:AD:470:SER:HB3	11:JA:1019:ARG:HH21	1.78	0.49
1:AE:203:ALA:HB2	3:BC:804:ARG:HB2	1.94	0.49
1:AE:648:ARG:HD2	1:AE:688:PHE:HE1	1.76	0.49
2:AK:427:ARG:HB2	1:AL:418:ILE:HD13	1.94	0.49
3:CJ:1237:VAL:HA	3:CJ:1244:PRO:HA	1.94	0.49
4:DF:310:LEU:HB3	4:DF:339:ALA:HB2	1.94	0.49
6:FF:1184:ALA:O	6:FF:1424:CYS:SG	2.69	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GB:541:MET:HE2	8:GB:564:LYS:HG2	1.94	0.49
7:GG:731:ILE:HD13	7:GG:821:TRP:HZ2	1.77	0.49
8:GL:68:ALA:HB3	8:GL:76:TRP:HA	1.94	0.49
9:HA:835:LYS:O	9:HA:838:LYS:HB2	2.11	0.49
9:HB:676:ALA:HB2	9:HB:682:ILE:HG12	1.93	0.49
9:HB:773:ALA:HB3	13:LF:527:VAL:HG13	1.94	0.49
9:HB:792:ARG:HD3	13:LG:529:PRO:HD3	1.94	0.49
9:HB:809:LEU:O	9:HB:813:THR:HG23	2.12	0.49
11:JC:162:PRO:HD2	11:JC:170:ILE:H	1.76	0.49
11:JC:414:ILE:HD13	11:JC:417:LEU:HD12	1.93	0.49
12:KA:299:TYR:CE2	12:KA:330:LEU:HD13	2.47	0.49
12:KB:576:ASN:HB2	12:KB:699:PHE:HE1	1.78	0.49
12:KF:405:PRO:HD3	12:KF:489:MET:HE1	1.95	0.49
12:KF:684:LEU:HD13	12:KF:688:VAL:H	1.77	0.49
13:LA:374:HIS:CE1	13:LB:370:MET:HB2	2.45	0.49
14:MA:211:MET:HE3	14:MB:210:LEU:HD22	1.94	0.49
15:NA:562:GLU:O	15:NA:566:GLN:HG2	2.12	0.49
15:NA:1539:ILE:HA	15:NA:1542:LEU:HD12	1.93	0.49
1:AA:415:MET:HE3	2:AB:431:LEU:HD11	1.95	0.49
2:AC:180:GLU:HA	2:AC:183:ALA:HB3	1.93	0.49
2:AF:143:ARG:HD3	2:AF:210:LEU:HD11	1.93	0.49
1:AH:139:ASN:HD21	10:IA:874:ASN:HD21	1.59	0.49
3:BB:827:ALA:HB2	3:BB:842:PHE:HB2	1.93	0.49
5:EB:3717:ILE:HG12	5:EB:3743:ARG:HH22	1.77	0.49
5:EC:3700:PHE:HA	5:EC:3706:VAL:HG22	1.94	0.49
6:FA:1850:GLN:HA	6:FA:1923:PHE:HE1	1.78	0.49
6:FD:1095:LEU:O	6:FD:1096:LEU:C	2.56	0.49
6:FD:1103:SER:HB2	9:HB:393:VAL:HG21	1.94	0.49
6:FD:1442:GLU:HG3	6:FD:1444:ARG:HB2	1.93	0.49
7:GC:311:LEU:HD23	7:GC:453:LEU:HD13	1.95	0.49
7:GG:551:LEU:HB2	9:HA:666:LYS:HD3	1.94	0.49
7:GG:612:ARG:HH21	7:GG:662:VAL:HG13	1.78	0.49
8:GH:135:LEU:HB3	8:GH:299:ALA:HA	1.93	0.49
9:HA:497:ALA:HB2	9:HA:627:GLY:HA3	1.95	0.49
9:HC:722:SER:HA	9:HC:724:PHE:H	1.78	0.49
9:HD:810:ARG:HA	9:HD:813:THR:HG23	1.93	0.49
10:IA:412:ALA:HA	10:IA:415:ARG:HE	1.78	0.49
11:JA:1285:SER:HA	11:JA:1288:ARG:HH11	1.77	0.49
11:JB:473:ASN:HB3	11:JB:876:GLN:HE21	1.76	0.49
12:KF:250:SER:HB2	12:KF:327:MET:HE1	1.95	0.49
12:KG:210:VAL:HG12	12:KG:283:TYR:H	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LJ:422:GLN:HG3	13:LJ:425:LYS:HZ3	1.77	0.49
14:MA:304:ARG:NH1	14:MB:237:ARG:HH12	2.09	0.49
15:NA:1476:LEU:HA	15:NA:1479:GLU:HG2	1.94	0.49
15:NA:1533:LYS:O	15:NA:1537:LYS:HG2	2.13	0.49
15:NC:891:TRP:H	15:NC:1154:ASP:C	2.20	0.49
15:NC:891:TRP:CD1	15:NC:1151:ASN:HA	2.47	0.49
15:NC:1521:SER:HA	18:QD:60:ARG:HD3	1.95	0.49
15:ND:741:ILE:HG23	15:ND:793:THR:HG22	1.93	0.49
18:QA:113:LYS:HE3	20:SA:22:LYS:HE2	1.93	0.49
1:AE:176:ILE:HG21	1:AE:211:LYS:HG3	1.94	0.49
1:AE:243:VAL:HG12	1:AE:244:LEU:HB2	1.93	0.49
2:AF:92:LEU:HD23	2:AF:277:VAL:HG11	1.95	0.49
1:AI:395:ALA:HB2	6:FC:1669:LYS:HG3	1.95	0.49
3:CA:715:ARG:HH12	3:CA:756:GLU:HG2	1.78	0.49
3:CJ:4466:ILE:HD11	3:CJ:4487:LEU:HB3	1.94	0.49
4:DE:320:ILE:HD12	4:DE:323:ASP:HB3	1.95	0.49
5:EA:3399:PHE:HB3	5:EA:3418:SER:HB3	1.94	0.49
5:EB:3520:VAL:HG21	5:EB:3595:LEU:HD23	1.95	0.49
6:FA:1755:VAL:HB	6:FA:1759:GLU:HG3	1.93	0.49
6:FB:1771:GLU:HG2	6:FB:1776:GLY:HA3	1.94	0.49
6:FB:1885:ILE:HD13	6:FB:1888:LEU:HD12	1.93	0.49
6:FC:2034:ARG:HD2	9:HB:772:PRO:O	2.13	0.49
6:FE:809:ILE:HD11	6:FE:812:LEU:HD22	1.95	0.49
6:FE:1105:ARG:O	6:FE:1106:LEU:C	2.55	0.49
6:FF:1189:ILE:HG23	6:FF:1417:ILE:HD11	1.95	0.49
7:GA:325:GLU:HG3	7:GA:581:ARG:HD2	1.93	0.49
7:GC:294:ALA:HB3	7:GC:687:ARG:HB3	1.94	0.49
8:GF:76:TRP:HZ3	8:GF:79:PRO:HD3	1.77	0.49
7:GG:237:TYR:HE1	7:GG:607:ARG:HH22	1.60	0.49
8:GH:756:ALA:HB3	8:GL:333:LYS:HD2	1.94	0.49
7:GI:249:ARG:HH22	7:GI:267:MET:HA	1.77	0.49
8:GL:741:PRO:HB3	8:GL:770:ILE:HB	1.95	0.49
11:JA:2110:LEU:HD12	11:JA:2113:PHE:HB3	1.94	0.49
11:JB:1522:ILE:HD13	11:JB:1557:LEU:HD22	1.94	0.49
11:JC:128:THR:HG21	11:JC:2086:PRO:HB2	1.94	0.49
12:KB:700:LEU:HD22	12:KB:702:ILE:HG22	1.94	0.49
12:KC:395:LEU:HD12	12:KC:484:ILE:HA	1.94	0.49
12:KE:521:PRO:HB2	12:KE:523:VAL:HG12	1.94	0.49
13:LI:401:LEU:HD13	13:LI:404:LEU:HD23	1.95	0.49
15:NB:614:LYS:HE3	15:NB:678:LEU:HB2	1.95	0.49
15:NB:925:ARG:HH22	15:NB:1111:ARG:HD2	1.78	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RC:20:PRO:HD2	19:RC:101:ASP:HA	1.94	0.49
1:AD:168:ASP:HA	1:AD:185:ARG:HH22	1.77	0.49
2:AF:259:VAL:HG11	2:AF:307:PRO:HG3	1.95	0.49
1:AI:270:ARG:NH2	16:OA:746:LEU:H	2.11	0.49
1:AL:741:SER:O	1:AL:745:GLN:HG3	2.13	0.49
4:DA:48:TYR:CD1	4:DA:125:GLU:HA	2.47	0.49
4:DA:267:ARG:HH12	4:DA:271:ALA:HB2	1.77	0.49
4:DE:19:ARG:HH22	4:DE:156:ASP:HB3	1.76	0.49
5:EA:4035:THR:HG22	5:EA:4037:ASP:H	1.78	0.49
5:EA:4213:LYS:HB3	5:EA:4232:MET:SD	2.53	0.49
5:EC:3395:TYR:HE1	5:EC:3510:LEU:HD12	1.77	0.49
6:FA:2072:ILE:HD12	9:HA:855:ARG:N	2.27	0.49
6:FE:1255:SER:C	6:FE:1257:ASP:H	2.21	0.49
6:FF:878:LEU:HD12	6:FF:906:LEU:HA	1.95	0.49
7:GA:171:GLN:HG3	7:GA:172:PHE:CD2	2.48	0.49
8:GF:638:LEU:HD11	8:GF:665:LEU:HB3	1.94	0.49
7:GG:472:LEU:HB3	7:GG:494:LEU:HD11	1.95	0.49
7:GI:676:ALA:HB3	7:GI:692:HIS:HB2	1.95	0.49
7:GK:768:PRO:HG2	7:GK:773:VAL:HG22	1.94	0.49
9:HB:674:VAL:HG13	9:HB:712:ILE:HG12	1.95	0.49
9:HB:676:ALA:HB1	9:HB:681:LYS:HA	1.94	0.49
9:HB:765:TRP:HE3	9:HB:765:TRP:H	1.59	0.49
10:IB:947:HIS:HB3	10:IB:951:GLY:H	1.78	0.49
11:JA:519:PHE:HE2	11:JA:1473:LEU:HD13	1.78	0.49
12:KF:289:HIS:CE1	12:KF:317:ALA:HB1	2.48	0.49
13:LO:424:LEU:HD11	13:LP:421:VAL:HG13	1.94	0.49
14:ME:235:ASP:HA	14:ME:238:THR:HG22	1.95	0.49
15:NA:1518:ARG:HG3	18:QA:167:LEU:HB3	1.95	0.49
15:ND:883:LEU:HD23	15:ND:1123:ALA:HB1	1.93	0.49
19:RD:74:LEU:HG	19:RD:91:VAL:HG11	1.95	0.49
1:AE:670:ASP:HB3	1:AE:673:GLN:HB2	1.94	0.49
1:AH:99:ASN:HA	1:AH:104:PRO:HB3	1.95	0.49
2:AK:483:LEU:HD13	1:AL:158:ALA:H	1.78	0.49
3:CE:1231:ARG:HD2	3:CE:1234:LEU:HB3	1.95	0.49
5:EC:3877:ILE:HG13	5:EC:3881:ARG:HE	1.78	0.49
5:EC:4658:ASP:HA	5:EC:4690:CYS:SG	2.53	0.49
6:FB:2059:VAL:HG12	6:FB:2063:GLN:HE22	1.78	0.49
6:FC:2085:GLU:O	6:FC:2089:PRO:CD	2.61	0.49
6:FD:850:CYS:HB3	6:FD:973:ILE:CG1	2.41	0.49
6:FD:1294:LEU:O	6:FD:1295:ALA:C	2.56	0.49
7:GA:196:LEU:HB3	7:GA:198:LEU:HD23	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GE:746:LEU:HD21	7:GE:989:VAL:HG23	1.94	0.49
7:GE:809:VAL:HG12	7:GE:817:ARG:HH22	1.78	0.49
8:GJ:123:PRO:HD2	8:GJ:238:ARG:HH12	1.78	0.49
8:GL:519:ARG:HE	8:GL:520:PHE:N	2.11	0.49
10:IB:621:VAL:HG11	10:IB:704:ASN:HD22	1.77	0.49
10:IB:1394:VAL:HG22	10:IB:1396:ASP:H	1.78	0.49
10:IC:910:LEU:HD12	10:IC:913:LEU:HD13	1.93	0.49
11:JA:840:ILE:HD13	11:JA:875:LEU:HD23	1.95	0.49
12:KA:405:PRO:HD3	12:KA:489:MET:HE1	1.95	0.49
12:KG:381:MET:HE3	12:KG:722:VAL:HG11	1.95	0.49
15:NB:1391:LEU:HD12	15:NB:1394:LEU:HD11	1.94	0.49
16:OA:158:ARG:HA	16:OA:163:TYR:HB2	1.95	0.49
1:AA:915:TRP:CZ2	13:LK:355:LYS:HG3	2.48	0.49
1:AE:743:LEU:HA	1:AE:746:VAL:HG22	1.95	0.49
2:AG:68:LEU:HD13	1:AH:457:ARG:HD3	1.94	0.49
3:BA:689:LEU:HB3	17:PA:258:PRO:HG2	1.94	0.49
3:CC:943:TYR:HE2	10:IB:1405:PRO:HD3	1.77	0.49
4:DA:327:PHE:HE1	14:MA:259:MET:HE2	1.78	0.49
4:DC:20:LEU:HB3	4:DC:98:ARG:HH22	1.77	0.49
6:FC:1951:TYR:CE2	9:HB:844:GLY:HA3	2.48	0.49
6:FF:981:HIS:HA	12:KC:656:ARG:NH1	2.28	0.49
8:GB:439:PRO:HD2	8:GB:474:VAL:HG22	1.95	0.49
8:GF:300:ARG:HD2	8:GF:361:ALA:HB3	1.95	0.49
8:GH:276:MET:HE1	8:GH:319:LEU:HB2	1.95	0.49
8:GH:534:GLN:HG3	8:GH:591:ILE:HB	1.93	0.49
7:GI:453:LEU:HD23	7:GI:518:LEU:HG	1.95	0.49
7:GI:706:VAL:HG11	7:GI:752:VAL:HG21	1.95	0.49
8:GJ:50:GLU:HB3	8:GJ:112:ILE:HB	1.95	0.49
7:GK:841:LEU:HB3	7:GK:866:PRO:HG2	1.94	0.49
8:GL:638:LEU:HD11	8:GL:665:LEU:HB3	1.95	0.49
11:JA:2098:THR:HG23	11:JA:2109:ALA:HB2	1.94	0.49
12:KF:209:VAL:HG13	12:KF:239:LYS:HA	1.95	0.49
13:LC:356:LEU:HD13	13:LD:356:LEU:HD11	1.94	0.49
15:NB:600:LEU:HD13	15:NB:917:MET:HB2	1.94	0.49
15:NB:725:ILE:HG13	15:NB:799:ILE:HG21	1.95	0.49
15:NC:797:ARG:HD3	15:NC:859:LEU:HD13	1.94	0.49
15:ND:542:LEU:HD23	15:ND:1190:ILE:HD12	1.95	0.49
15:ND:598:PHE:HB2	15:ND:1185:PRO:HB2	1.95	0.49
15:ND:864:GLU:CD	15:ND:865:SER:H	2.21	0.49
19:RB:112:LEU:HD11	19:RB:170:VAL:HG21	1.94	0.49
1:AD:665:LEU:HB3	1:AD:1019:TYR:HE2	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:169:VAL:HG23	2:AJ:277:VAL:HG22	1.94	0.48
3:BA:955:VAL:HG13	3:BA:978:VAL:HG22	1.94	0.48
3:CA:762:LEU:HD11	3:CA:822:VAL:HG23	1.95	0.48
3:CF:1264:VAL:HG13	3:CF:1265:ILE:HD12	1.94	0.48
3:CL:4452:HIS:CE1	3:CL:4454:ASP:HB2	2.48	0.48
4:DC:300:GLN:HG3	4:DC:354:TRP:CE2	2.48	0.48
4:DF:384:ILE:HG22	4:DF:386:VAL:HG23	1.94	0.48
5:EA:3237:LEU:HD21	5:EA:3243:VAL:HG12	1.95	0.48
5:EB:4031:ARG:HG3	5:EB:4032:PHE:CD1	2.48	0.48
5:EB:4064:ALA:HB1	5:EB:4180:TYR:HE2	1.77	0.48
5:EC:4724:LEU:HD23	5:EC:4812:LEU:HD21	1.94	0.48
6:FD:1293:THR:O	6:FD:1295:ALA:N	2.46	0.48
6:FE:846:CYS:HB3	12:KB:305:HIS:HE1	1.72	0.48
6:FE:860:PRO:C	6:FE:862:GLU:H	2.21	0.48
8:GB:184:GLY:HA2	8:GB:254:LYS:HG3	1.95	0.48
8:GF:741:PRO:HB3	8:GF:770:ILE:HB	1.95	0.48
8:GH:664:ILE:HD12	8:GH:677:HIS:HD2	1.78	0.48
7:GI:881:ALA:HA	7:GI:894:ILE:HA	1.95	0.48
8:GJ:420:ASN:HB2	8:GJ:503:LEU:HD23	1.95	0.48
8:GJ:431:PHE:HE1	8:GJ:494:SER:HB3	1.77	0.48
8:GL:545:ALA:HB1	8:GL:605:LEU:HD21	1.95	0.48
10:IA:916:LYS:HE3	11:JA:2042:SER:HA	1.94	0.48
11:JC:463:ILE:H	11:JC:466:ARG:NH2	2.11	0.48
11:JC:760:LEU:HB2	11:JC:1491:ALA:HB1	1.95	0.48
12:KF:403:ASP:HB3	12:KF:541:TYR:CZ	2.48	0.48
15:NA:597:GLN:HB2	15:NA:914:ILE:HG22	1.95	0.48
15:NA:611:ASN:HA	15:NA:614:LYS:HG2	1.95	0.48
15:NB:893:LEU:HB3	15:NB:1153:ALA:HB3	1.95	0.48
15:NB:1120:VAL:HA	15:NB:1123:ALA:HB2	1.95	0.48
2:AC:502:LEU:HA	2:AC:505:VAL:HG12	1.94	0.48
1:AD:157:LEU:HB2	1:AD:180:PHE:CD2	2.48	0.48
2:AG:452:GLU:HA	2:AG:455:ARG:HG2	1.94	0.48
1:AH:381:ARG:HH22	5:EB:4625:SER:HA	1.79	0.48
1:AI:660:ILE:HG13	1:AI:661:PRO:HD3	1.94	0.48
4:DA:84:ILE:HD13	4:DA:169:GLY:HA3	1.95	0.48
5:EC:3768:VAL:HG11	5:EC:4003:THR:HA	1.93	0.48
6:FD:860:PRO:O	6:FD:862:GLU:N	2.46	0.48
6:FE:814:THR:O	6:FE:815:SER:C	2.56	0.48
6:FF:813:GLN:O	6:FF:814:THR:C	2.56	0.48
6:FF:975:ILE:O	6:FF:976:HIS:C	2.56	0.48
6:FF:990:PHE:HB2	12:KC:313:PHE:CE2	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:1122:LEU:HD22	6:FF:1122:LEU:HA	1.71	0.48
7:GA:537:GLY:H	9:HB:554:ASP:H	1.59	0.48
7:GE:798:LEU:HD13	7:GE:985:PHE:CG	2.48	0.48
11:JA:547:PRO:HB3	11:JA:1286:LEU:HD23	1.95	0.48
11:JA:1868:LEU:HD22	11:JA:2270:MET:HG2	1.94	0.48
11:JB:437:LEU:HD11	11:JB:1461:PHE:HB3	1.95	0.48
11:JB:1190:LEU:HD11	11:JB:1327:LEU:HD23	1.95	0.48
11:JC:1731:PRO:HB3	11:JC:1778:PHE:HZ	1.76	0.48
12:KB:389:LYS:HA	12:KB:392:GLN:HE22	1.78	0.48
12:KC:583:GLU:HG2	12:KC:718:ALA:HA	1.95	0.48
13:LE:473:LYS:O	13:LE:476:GLY:HA3	2.13	0.48
14:ME:225:VAL:HG21	14:ME:315:TRP:HE1	1.78	0.48
15:NA:347:LEU:HD22	15:NA:491:PRO:HG2	1.95	0.48
15:NB:709:ILE:HA	15:NB:714:ARG:HD3	1.95	0.48
15:NB:819:GLY:H	15:NB:842:THR:HA	1.77	0.48
15:ND:812:ARG:HH21	15:ND:870:TYR:HD2	1.60	0.48
15:ND:891:TRP:H	15:ND:1155:GLU:N	2.11	0.48
2:AB:298:PRO:HG2	2:AB:318:ARG:HD2	1.95	0.48
1:AD:157:LEU:HB2	1:AD:180:PHE:HD2	1.79	0.48
1:AE:850:ILE:HG22	1:AE:895:ARG:HH22	1.78	0.48
2:AK:448:ASN:C	2:AK:448:ASN:ND2	2.71	0.48
1:AL:656:ASP:HA	9:HC:514:PHE:CE1	2.48	0.48
3:BC:816:LYS:HE2	3:BC:849:LEU:HD11	1.94	0.48
3:CE:1269:ILE:HA	3:CE:1272:TYR:HB3	1.96	0.48
4:DB:356:TYR:CZ	4:DB:385:LYS:HG2	2.47	0.48
4:DD:66:ARG:HG3	4:DD:71:LEU:HA	1.96	0.48
5:EA:3689:LEU:HD13	5:EA:3713:GLN:HG3	1.95	0.48
5:EB:4147:PHE:HE1	5:EB:4182:LEU:HA	1.78	0.48
6:FA:1962:GLN:HG2	9:HA:834:LEU:HD21	1.95	0.48
6:FB:1892:ILE:HG22	6:FB:1894:THR:H	1.77	0.48
6:FD:888:PRO:HD3	12:KA:305:HIS:CE1	2.49	0.48
6:FD:1212:VAL:O	6:FD:1233:ILE:HD12	2.14	0.48
6:FD:1217:GLU:O	6:FD:1219:GLU:N	2.46	0.48
6:FD:1244:LEU:O	6:FD:1246:ILE:N	2.41	0.48
6:FE:824:TYR:N	6:FE:825:PRO:HD3	2.28	0.48
6:FE:1201:THR:O	6:FE:1202:PHE:C	2.56	0.48
6:FF:1064:TYR:O	6:FF:1065:LEU:HB2	2.13	0.48
6:FF:1216:TRP:CZ3	6:FF:1300:LEU:HD13	2.48	0.48
8:GF:75:GLN:HG2	8:GF:84:ARG:HE	1.78	0.48
7:GG:354:ARG:HA	7:GG:404:ASN:HD21	1.79	0.48
7:GG:371:LEU:HD13	7:GG:412:VAL:HG22	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GI:496:LYS:HB2	7:GI:496:LYS:HE3	1.59	0.48
7:GK:264:GLN:HA	7:GK:267:MET:HE3	1.95	0.48
7:GK:397:LEU:HD12	8:GL:177:MET:HE3	1.94	0.48
10:IB:414:ALA:HB2	10:IB:424:VAL:HG11	1.95	0.48
10:IB:910:LEU:HA	10:IB:913:LEU:HD13	1.94	0.48
10:IC:612:ARG:HD3	10:IC:797:VAL:HG23	1.95	0.48
12:KC:226:ALA:HB1	12:KC:232:THR:HG23	1.96	0.48
15:NA:950:VAL:HG13	15:NA:954:PHE:HD2	1.77	0.48
15:ND:925:ARG:HE	15:ND:926:ARG:H	1.60	0.48
15:ND:1407:MET:HG3	15:ND:1469:PHE:HB3	1.94	0.48
2:AB:481:ARG:HE	2:AB:537:ARG:HH22	1.61	0.48
1:AD:99:ASN:HA	1:AD:104:PRO:HB3	1.94	0.48
2:AG:441:MET:HE2	1:AH:404:LEU:HD11	1.93	0.48
2:AK:14:LYS:HG2	6:FC:1911:PRO:HD3	1.95	0.48
3:CA:679:SER:HB3	17:PA:250:VAL:HG21	1.94	0.48
3:CG:1267:PRO:HA	3:CG:1270:LEU:HG	1.95	0.48
3:CG:4460:PRO:HA	3:CG:4463:LEU:HG	1.95	0.48
3:CJ:1280:VAL:HG13	3:CJ:1284:LYS:HD2	1.95	0.48
4:DA:98:ARG:HH22	4:DA:102:LEU:HD22	1.79	0.48
5:EA:4316:ILE:HG22	5:EA:4317:MET:HE2	1.95	0.48
5:EA:4438:LEU:HD11	5:EA:4709:PHE:HE1	1.78	0.48
5:EB:3269:TRP:HD1	5:EB:3409:SER:HB2	1.78	0.48
6:FA:2059:VAL:CG2	9:HA:754:LEU:CB	2.91	0.48
6:FD:1075:VAL:HG13	6:FD:1105:ARG:HB2	1.94	0.48
6:FE:1439:LEU:O	6:FE:1441:ILE:N	2.46	0.48
6:FF:1223:ALA:HA	6:FF:1226:LEU:HD12	1.95	0.48
8:GB:333:LYS:HE2	8:GB:335:ASN:HD21	1.78	0.48
8:GF:168:MET:HE1	8:GF:247:PRO:HG3	1.95	0.48
8:GH:54:VAL:HG11	8:GH:88:PRO:HD3	1.95	0.48
8:GH:303:LEU:HD11	8:GH:305:VAL:HB	1.96	0.48
8:GH:545:ALA:HA	8:GH:548:LYS:HZ1	1.78	0.48
8:GJ:172:ILE:HG12	8:GJ:180:LEU:HA	1.95	0.48
7:GK:535:PRO:HB2	9:HC:553:TYR:N	2.27	0.48
9:HB:777:TYR:N	13:LE:521:ASN:HD21	2.11	0.48
10:IC:328:ALA:HB3	10:IC:570:GLY:H	1.79	0.48
11:JA:1675:LEU:HD21	11:JA:1717:TRP:HE3	1.79	0.48
11:JB:499:THR:HG23	11:JB:502:TRP:H	1.78	0.48
12:KG:473:GLN:HA	12:KG:476:MET:HE2	1.95	0.48
15:NA:866:LEU:HD23	15:NA:869:PHE:HD2	1.79	0.48
15:ND:1542:LEU:HA	15:ND:1545:VAL:HG23	1.96	0.48
17:PC:268:PRO:HG2	17:PC:269:ILE:HD12	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:32:LEU:HD11	1:AD:451:ILE:HD11	1.95	0.48
2:AG:50:ILE:HD11	2:AG:282:PHE:HB2	1.94	0.48
1:AI:629:LEU:HA	1:AI:632:LEU:HD23	1.95	0.48
2:AJ:145:LYS:HA	2:AJ:148:ASP:HB3	1.95	0.48
2:AK:553:THR:HB	1:AL:471:GLU:HG3	1.95	0.48
3:CF:1187:GLU:HB3	3:CF:1192:HIS:HB3	1.96	0.48
3:CF:4459:ALA:HB3	3:CF:4462:VAL:HG23	1.94	0.48
3:CJ:1226:LEU:HG	3:CJ:1231:ARG:HH21	1.77	0.48
3:CL:4487:LEU:HB2	3:CL:4496:ALA:HB3	1.95	0.48
6:FB:2023:ILE:CG2	9:HD:778:PRO:HB3	2.43	0.48
6:FE:809:ILE:HG23	6:FE:900:ALA:O	2.14	0.48
6:FE:1441:ILE:O	6:FE:1444:ARG:N	2.36	0.48
6:FF:1431:MET:O	6:FF:1432:THR:C	2.57	0.48
8:GF:25:GLU:HA	8:GF:28:LYS:HE3	1.94	0.48
8:GL:14:PHE:HZ	8:GL:496:LEU:HD11	1.78	0.48
8:GL:693:PRO:HA	8:GL:696:GLU:HG3	1.94	0.48
9:HD:792:ARG:HD3	13:LK:529:PRO:HD3	1.95	0.48
10:IC:1128:VAL:HG11	10:IC:1180:VAL:HG11	1.94	0.48
11:JA:443:ILE:HG23	11:JA:444:PHE:HD2	1.79	0.48
11:JB:1292:LEU:HD21	11:JB:1299:ALA:HB1	1.94	0.48
11:JC:161:LEU:HD12	11:JC:169:PHE:HB3	1.96	0.48
11:JC:543:ILE:HD11	11:JC:546:LEU:HD12	1.96	0.48
14:MA:233:LEU:HA	14:MA:236:GLU:HG2	1.96	0.48
1:AA:403:TYR:HE1	2:AB:193:GLU:HB3	1.78	0.48
1:AA:507:LEU:HD11	6:FA:1826:LEU:HB3	1.95	0.48
1:AH:234:ARG:HG3	10:IA:778:GLN:HB2	1.95	0.48
2:AJ:29:LEU:HD13	2:AJ:283:LEU:HD21	1.94	0.48
1:AL:421:MET:HB3	1:AL:444:PHE:HE1	1.79	0.48
3:BB:990:HIS:HB3	3:BB:993:THR:HG23	1.94	0.48
3:CF:1269:ILE:HA	3:CF:1272:TYR:HB3	1.96	0.48
3:CL:1239:PRO:HB3	3:CL:4470:LYS:HE2	1.95	0.48
4:DA:66:ARG:HH22	4:DA:74:LYS:HD2	1.79	0.48
4:DD:251:LEU:HD11	8:GD:755:MET:HG2	1.95	0.48
5:EB:4403:LEU:H	5:EB:4440:ILE:HD13	1.79	0.48
5:EC:4150:PHE:HE2	5:EC:4181:VAL:HG21	1.77	0.48
6:FB:1640:VAL:HG12	6:FB:1651:ALA:HB3	1.94	0.48
6:FC:1787:ALA:N	6:FC:1932:ARG:HH12	2.12	0.48
6:FD:1004:GLY:O	6:FD:1005:PRO:C	2.56	0.48
6:FE:998:GLN:C	12:KB:229:SER:OG	2.57	0.48
8:GD:594:GLN:HG3	8:GD:777:LEU:HD21	1.95	0.48
7:GE:188:HIS:HA	7:GE:661:LEU:HD22	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:372:GLY:H	7:GG:400:ASP:HB3	1.77	0.48
8:GH:200:GLY:HA2	8:GH:281:LEU:HD23	1.96	0.48
7:GI:232:LYS:HB3	7:GI:258:TYR:HE2	1.78	0.48
7:GI:894:ILE:HD11	7:GI:912:LEU:HD11	1.95	0.48
8:GJ:1:MET:HE1	8:GJ:531:GLY:HA2	1.94	0.48
11:JB:1720:ASP:HB3	16:OB:930:ALA:HA	1.95	0.48
11:JC:1414:ALA:HB2	11:JC:1504:ARG:HE	1.77	0.48
11:JC:2094:ILE:HD11	11:JC:2110:LEU:HD13	1.96	0.48
12:KA:251:SER:HB3	12:KA:254:TRP:HB2	1.94	0.48
12:KC:688:VAL:HG22	12:KC:689:CYS:H	1.78	0.48
12:KG:248:ARG:HD2	12:KG:258:LEU:HD13	1.95	0.48
13:LA:510:ILE:HD13	13:LA:513:LEU:HD12	1.95	0.48
13:LJ:398:ARG:HA	13:LJ:401:LEU:HG	1.96	0.48
15:NA:614:LYS:HE3	15:NA:678:LEU:HB2	1.94	0.48
15:NA:1500:TRP:CZ2	20:SA:124:GLU:HG3	2.48	0.48
15:NB:511:LEU:HD11	15:NB:1472:LYS:HD3	1.94	0.48
15:NC:806:ASP:HB3	15:NC:882:SER:HB2	1.95	0.48
15:NC:1100:GLN:HG3	15:NC:1113:ASP:HB3	1.96	0.48
15:ND:468:ARG:HH11	15:ND:469:PHE:HB3	1.79	0.48
15:ND:893:LEU:H	15:ND:1154:ASP:N	2.10	0.48
1:AA:425:PHE:HA	1:AA:428:LEU:HD23	1.96	0.48
2:AB:427:ARG:HA	2:AB:430:GLU:HB3	1.94	0.48
2:AC:332:ARG:HH12	11:JA:2284:LYS:HG3	1.77	0.48
2:AF:548:ARG:HE	2:AF:551:ILE:HG21	1.79	0.48
2:AG:332:ARG:HH22	11:JC:2285:ASP:HB2	1.79	0.48
2:AJ:177:VAL:HG21	2:AJ:183:ALA:HB2	1.94	0.48
2:AK:44:LEU:HD12	2:AK:285:PHE:HB3	1.94	0.48
4:DF:174:THR:HA	4:DF:177:LYS:HE3	1.96	0.48
5:EA:3400:GLU:H	5:EA:3418:SER:HB3	1.78	0.48
6:FA:1958:LEU:HD22	6:FA:2054:PHE:HD2	1.77	0.48
6:FC:2037:LEU:HD21	9:HB:820:SER:HB3	1.95	0.48
6:FE:1066:GLN:N	6:FE:1114:VAL:O	2.47	0.48
6:FE:1293:THR:O	6:FE:1294:LEU:C	2.56	0.48
6:FF:1210:LEU:HD23	6:FF:1286:LEU:HA	1.95	0.48
7:GA:537:GLY:H	9:HB:554:ASP:N	2.12	0.48
8:GB:336:ASN:HA	8:GF:219:ALA:HA	1.95	0.48
7:GE:451:ILE:HB	7:GE:516:VAL:HG23	1.95	0.48
7:GE:870:ARG:HG2	7:GE:872:THR:HG23	1.95	0.48
7:GG:206:PRO:HB2	7:GG:678:LEU:HD22	1.96	0.48
8:GJ:741:PRO:HB3	8:GJ:770:ILE:HB	1.96	0.48
10:IC:477:ALA:CB	10:IC:494:HIS:HE1	2.26	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:477:ALA:HB3	10:IC:494:HIS:HE1	1.79	0.48
11:JA:444:PHE:HE2	11:JA:512:SER:HB2	1.79	0.48
11:JC:1116:ARG:HA	11:JC:1119:GLY:H	1.79	0.48
12:KF:569:LEU:HD13	12:KF:703:TRP:HE3	1.77	0.48
14:MB:210:LEU:HD12	14:MB:330:LEU:HD13	1.96	0.48
15:NA:350:ARG:HE	15:NA:486:ARG:HD3	1.79	0.48
15:NC:661:ARG:HB3	15:NC:677:CYS:HB2	1.96	0.48
18:QD:120:LYS:HB3	18:QD:123:VAL:HG23	1.95	0.48
19:RA:23:LEU:HD12	19:RA:30:LEU:HD12	1.95	0.48
1:AD:892:GLU:HA	1:AD:895:ARG:HH12	1.77	0.48
1:AE:915:TRP:HB3	13:LM:355:LYS:NZ	2.29	0.48
3:CL:4462:VAL:HG13	3:CL:4495:LEU:HD13	1.95	0.48
3:CL:4466:ILE:HG12	3:CL:4487:LEU:HD23	1.95	0.48
5:EB:3519:ASN:HB2	5:EB:3522:LYS:H	1.79	0.48
5:EC:3843:THR:HG23	5:EC:3852:PHE:CE1	2.49	0.48
6:FC:1611:ARG:HG2	6:FC:1617:GLU:H	1.78	0.48
6:FC:2089:PRO:O	6:FC:2092:GLU:HG3	2.14	0.48
6:FD:1079:MET:HG2	6:FD:1102:TYR:HD2	1.77	0.48
7:GC:199:PRO:HB2	7:GC:717:LEU:HD13	1.96	0.48
7:GE:314:VAL:HG23	7:GE:363:ASP:HB3	1.96	0.48
9:HA:575:ARG:H	9:HA:578:THR:HG23	1.79	0.48
9:HA:765:TRP:N	9:HA:765:TRP:CE3	2.81	0.48
9:HC:554:ASP:HB2	9:HC:557:ALA:HB3	1.95	0.48
9:HD:773:ALA:HB3	13:LJ:527:VAL:CG1	2.43	0.48
11:JA:1745:PHE:HE2	11:JA:1858:ILE:HG21	1.78	0.48
11:JB:878:HIS:HB2	11:JB:962:VAL:HB	1.96	0.48
11:JC:192:LEU:HA	11:JC:195:LEU:HD23	1.96	0.48
11:JC:1553:LEU:HD11	11:JC:1597:LEU:HD22	1.95	0.48
11:JC:2078:LYS:H	11:JC:2264:SER:HB3	1.79	0.48
12:KC:375:TYR:O	12:KC:379:SER:HB3	2.13	0.48
12:KE:395:LEU:HD21	12:KE:484:ILE:HG13	1.95	0.48
12:KF:327:MET:HB3	12:KF:330:LEU:HB2	1.95	0.48
14:MK:104:LYS:HA	14:MK:107:SER:HB3	1.96	0.48
15:NA:666:ILE:HG23	15:NA:721:PRO:HG2	1.96	0.48
15:NB:1420:TYR:HE2	15:NB:1478:LEU:HD23	1.78	0.48
15:NC:768:GLU:OE1	15:NC:769:GLU:HG2	2.13	0.48
16:OB:198:ASP:HB3	17:PB:290:PHE:CD1	2.49	0.48
1:AD:60:THR:HG22	1:AD:62:ASP:H	1.78	0.48
1:AD:747:MET:HE1	1:AD:784:PHE:HE1	1.79	0.48
1:AE:1025:ARG:HG2	1:AE:1025:ARG:HH11	1.78	0.48
1:AH:745:GLN:NE2	7:GG:916:HIS:HB2	2.29	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:908:ARG:HH12	13:LI:497:LEU:HD12	1.78	0.48
3:CG:1168:ARG:HH11	3:CG:4483:PRO:HD2	1.79	0.48
3:CJ:1229:HIS:HB2	3:CJ:4463:LEU:HB3	1.96	0.48
3:CL:1171:LEU:HD11	3:CL:1258:PRO:HD3	1.96	0.48
4:DB:312:ASN:HD21	4:DB:315:LEU:HD23	1.77	0.48
4:DC:21:ASP:HB3	14:MI:277:VAL:HG13	1.94	0.48
5:EB:3306:ILE:O	5:EB:3310:THR:HG23	2.14	0.48
6:FA:1647:LEU:HD22	6:FA:1797:VAL:HG23	1.96	0.48
6:FD:1216:TRP:CZ2	6:FD:1272:VAL:HG22	2.49	0.48
6:FD:1289:HIS:O	6:FD:1290:ILE:C	2.57	0.48
6:FE:983:LEU:HA	12:KB:726:ASP:CG	2.39	0.48
6:FF:1182:ALA:CB	6:FF:1429:LEU:HB2	2.38	0.48
6:FF:1393:LEU:O	6:FF:1394:ARG:C	2.57	0.48
8:GB:18:VAL:HG13	8:GB:520:PHE:HA	1.96	0.48
8:GD:345:LEU:HD23	8:GD:376:GLU:HA	1.96	0.48
7:GG:544:PRO:HD3	9:HA:596:TYR:HA	1.96	0.48
8:GH:42:ASP:HB3	8:GH:470:LYS:HZ1	1.78	0.48
8:GH:698:LEU:HA	8:GH:701:LEU:HB3	1.96	0.48
7:GI:450:LYS:HG3	7:GI:635:THR:HG21	1.95	0.48
7:GI:636:VAL:HG11	7:GI:678:LEU:HD21	1.94	0.48
8:GL:398:VAL:HA	8:GL:719:VAL:HG13	1.94	0.48
10:IC:1294:ILE:HD12	10:IC:1358:LEU:HD11	1.96	0.48
11:JB:160:LEU:HD22	11:JB:171:LYS:HD2	1.96	0.48
11:JB:440:PRO:HB3	11:JB:1474:TRP:CE2	2.48	0.48
11:JB:913:LEU:HD21	11:JB:950:LEU:HD13	1.95	0.48
11:JC:157:GLU:HB3	11:JC:172:LEU:HD11	1.96	0.48
11:JC:190:TRP:HB3	11:JC:195:LEU:HD21	1.94	0.48
11:JC:973:MET:HB2	11:JC:1118:ALA:HB2	1.95	0.48
11:JC:1474:TRP:HA	11:JC:1477:TRP:HB2	1.96	0.48
11:JC:2069:GLU:HA	11:JC:2072:GLN:HB3	1.96	0.48
12:KC:313:PHE:HA	12:KC:316:VAL:HG12	1.94	0.48
12:KG:403:ASP:HB3	12:KG:541:TYR:CZ	2.48	0.48
13:LE:532:LEU:HD21	13:LF:530:VAL:HG23	1.95	0.48
15:NB:682:ARG:HH22	15:NB:1172:LEU:HG	1.78	0.48
15:NC:1488:ARG:HH12	15:NC:1491:PRO:HG2	1.78	0.48
15:ND:931:TRP:CD1	15:ND:934:LEU:HB2	2.48	0.48
15:ND:1514:TRP:HA	15:ND:1517:VAL:HG12	1.96	0.48
2:AB:209:SER:HB3	2:AB:259:VAL:HA	1.95	0.48
2:AG:492:MET:HE1	1:AH:354:ARG:HE	1.79	0.48
1:AI:181:THR:HB	1:AI:215:GLN:HE22	1.78	0.48
1:AI:238:CYS:HB3	1:AI:242:GLU:H	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:259:VAL:HB	2:AJ:297:VAL:HB	1.95	0.48
1:AL:804:LEU:HD22	1:AL:837:CYS:HB2	1.94	0.48
4:DA:384:ILE:HG21	13:LA:457:GLN:HE22	1.78	0.48
6:FD:1293:THR:O	6:FD:1294:LEU:C	2.57	0.48
6:FE:1393:LEU:HD12	6:FE:1393:LEU:HA	1.78	0.48
8:GB:15:SER:HG	8:GB:16:TRP:CD1	2.32	0.48
8:GB:586:SER:HB3	14:ME:320:ARG:HH12	1.78	0.48
7:GC:201:GLY:HA3	7:GC:717:LEU:HD11	1.95	0.48
7:GG:663:THR:HG23	7:GG:668:GLY:HA2	1.96	0.48
7:GI:273:LYS:HE2	7:GI:279:ARG:HH21	1.79	0.48
7:GK:663:THR:HG23	7:GK:668:GLY:HA2	1.95	0.48
9:HB:777:TYR:N	13:LE:521:ASN:ND2	2.61	0.48
10:IA:782:GLN:HA	10:IA:785:LEU:HD13	1.96	0.48
10:IB:740:ARG:HD3	10:IB:771:LEU:HB3	1.96	0.48
10:IB:864:GLN:HG3	10:IB:1240:PRO:HB2	1.96	0.48
10:IC:438:ARG:HH22	10:IC:448:LEU:HB3	1.78	0.48
11:JA:194:VAL:HG23	11:JA:197:ARG:HH11	1.78	0.48
12:KA:671:LEU:HD21	12:KA:725:ILE:HG22	1.95	0.48
12:KB:206:CYS:HA	12:KB:243:HIS:HA	1.96	0.48
12:KB:526:TRP:CD1	12:KB:706:ILE:HG12	2.49	0.48
12:KF:263:ALA:HA	12:KF:266:ARG:HG2	1.96	0.48
13:LA:481:GLU:HG3	13:LB:482:LEU:HD11	1.96	0.48
16:OA:190:LEU:HB3	16:OA:241:ALA:HB1	1.96	0.48
16:OB:1089:LEU:HB3	16:OB:1092:ARG:HH21	1.79	0.48
1:AA:715:LEU:HB3	13:LK:364:ASN:ND2	2.29	0.47
2:AC:49:HIS:HE2	2:AC:51:ALA:HB3	1.79	0.47
1:AE:49:GLN:HG2	2:AF:520:ARG:NH2	2.29	0.47
1:AE:757:ILE:HD11	1:AE:779:PRO:HB2	1.96	0.47
1:AI:289:SER:N	17:PB:271:ASN:HD22	2.12	0.47
1:AI:1004:VAL:HG13	1:AI:1006:ARG:HH22	1.79	0.47
2:AJ:113:LEU:HD22	2:AJ:208:GLU:HG2	1.96	0.47
2:AJ:314:ALA:HB3	2:AJ:337:HIS:HD2	1.78	0.47
2:AK:494:TRP:HZ2	1:AL:57:SER:HA	1.79	0.47
1:AL:298:ILE:HG22	1:AL:332:THR:HG21	1.95	0.47
3:CJ:1123:LEU:HG	10:IB:811:GLN:HG3	1.95	0.47
4:DD:60:ILE:HG21	4:DD:81:GLY:HA2	1.96	0.47
5:EB:3710:LEU:HD12	5:EB:3717:ILE:HD12	1.97	0.47
5:EB:4332:LEU:HD13	5:EB:4336:VAL:HG11	1.96	0.47
6:FC:2015:LYS:HE2	6:FC:2015:LYS:HB2	1.42	0.47
6:FC:2101:LEU:O	6:FC:2104:GLN:HG3	2.14	0.47
6:FD:895:ILE:HG12	7:GC:876:MET:HE2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1231:ARG:HE	6:FE:1231:ARG:HB3	1.50	0.47
7:GA:180:ARG:HD3	7:GA:829:VAL:HG21	1.95	0.47
7:GC:406:ALA:HA	7:GC:409:ARG:HB2	1.96	0.47
7:GI:645:LEU:HG	7:GI:717:LEU:HD12	1.95	0.47
8:GL:432:LYS:HB2	8:GL:451:SER:HB3	1.96	0.47
9:HB:674:VAL:HG22	9:HB:712:ILE:HG23	1.95	0.47
9:HB:674:VAL:HG11	9:HB:695:VAL:HG21	1.94	0.47
10:IC:1113:ILE:HD12	10:IC:1119:VAL:HG22	1.96	0.47
11:JB:2078:LYS:HB2	11:JB:2083:ILE:HD13	1.96	0.47
11:JC:1306:ILE:HA	11:JC:1309:LEU:HB2	1.95	0.47
12:KB:365:GLU:HG2	12:KB:368:ARG:HH12	1.79	0.47
12:KE:335:LEU:HD23	12:KE:338:LEU:HD21	1.94	0.47
15:NC:609:GLN:HG3	15:NC:1192:SER:HB3	1.95	0.47
1:AA:289:SER:N	17:PA:271:ASN:HD22	2.12	0.47
2:AG:379:HIS:HB3	2:AG:382:ALA:HB2	1.96	0.47
1:AI:310:CYS:H	1:AI:313:CYS:HB2	1.78	0.47
1:AI:841:LEU:HA	1:AI:845:PHE:HD2	1.79	0.47
1:AL:157:LEU:HB2	1:AL:180:PHE:CD2	2.49	0.47
1:AL:908:ARG:HH12	13:LE:497:LEU:HD12	1.78	0.47
3:BB:812:MET:HG3	3:BB:814:VAL:HG22	1.95	0.47
3:CB:781:LEU:HD22	3:CB:833:TYR:HD2	1.79	0.47
3:CE:1263:SER:HB2	3:CE:4458:VAL:HB	1.94	0.47
3:CF:4479:LEU:HD11	3:CF:4482:LEU:HD22	1.96	0.47
4:DA:10:GLU:HA	4:DA:13:VAL:HG12	1.96	0.47
4:DB:130:ARG:HD3	4:DB:134:LEU:HG	1.96	0.47
6:FC:1850:GLN:HA	6:FC:1923:PHE:HE1	1.79	0.47
6:FD:814:THR:O	6:FD:815:SER:C	2.57	0.47
6:FE:834:VAL:O	6:FE:835:SER:C	2.56	0.47
6:FE:863:ILE:HA	6:FE:866:PHE:CE2	2.49	0.47
6:FE:1213:VAL:HG11	6:FE:1226:LEU:HA	1.95	0.47
6:FE:1222:CYS:O	6:FE:1224:ALA:N	2.47	0.47
6:FF:962:PHE:HE2	6:FF:965:TRP:HB2	1.79	0.47
6:FF:1244:LEU:HD13	6:FF:1257:ASP:HB2	1.96	0.47
6:FF:1300:LEU:HB3	6:FF:1430:PHE:CE2	2.49	0.47
7:GC:662:VAL:HG21	7:GC:672:VAL:HA	1.95	0.47
7:GI:677:ALA:HB1	7:GI:689:ILE:HD11	1.96	0.47
7:GI:823:ARG:HG2	7:GI:827:LEU:HD11	1.96	0.47
7:GI:824:LEU:HD21	7:GI:835:TYR:HD1	1.79	0.47
7:GK:545:GLY:O	9:HC:497:ALA:HB2	2.13	0.47
9:HA:487:VAL:HG12	9:HA:505:ILE:HG12	1.96	0.47
11:JA:1013:ASP:HA	11:JA:1016:LEU:HB2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:1571:ARG:NH2	15:NA:346:SER:HB2	2.29	0.47
12:KE:370:LEU:HD22	12:KE:377:LEU:HD13	1.96	0.47
13:LE:413:GLU:HA	13:LE:416:ARG:HB2	1.96	0.47
14:MG:111:ALA:HA	14:MG:114:ARG:HB2	1.95	0.47
15:NA:1506:ARG:HA	15:NA:1509:ARG:HB3	1.96	0.47
15:NC:555:PHE:HA	15:NC:559:PHE:HD2	1.79	0.47
15:NC:582:LEU:HG	15:NC:585:ARG:HH21	1.79	0.47
15:NC:735:HIS:CD2	15:NC:768:GLU:HG2	2.49	0.47
15:ND:1529:CYS:HA	15:ND:1532:ARG:HG2	1.96	0.47
16:OB:190:LEU:HD11	16:OB:234:ALA:HB1	1.95	0.47
1:AA:799:THR:HB	1:AA:1000:PHE:HE2	1.79	0.47
2:AB:421:HIS:CE1	2:AB:423:VAL:HG12	2.49	0.47
1:AD:830:THR:HG23	1:AD:833:ALA:H	1.79	0.47
1:AE:237:VAL:HG12	17:PC:247:LEU:HD21	1.95	0.47
1:AE:367:GLN:HE22	1:AE:371:LEU:HD22	1.79	0.47
1:AE:668:ALA:HB1	1:AE:1032:PHE:HZ	1.79	0.47
1:AE:683:ASN:HD21	1:AE:1008:ALA:HB1	1.80	0.47
1:AI:246:ALA:HA	1:AI:258:CYS:SG	2.54	0.47
3:CE:1172:PRO:HA	3:CE:4503:ASP:HB3	1.97	0.47
3:CG:1181:ARG:CZ	10:IC:452:LEU:HB2	2.45	0.47
4:DB:32:SER:HB2	4:DB:122:ILE:HA	1.96	0.47
5:EA:4407:ASP:O	5:EA:4409:GLU:N	2.47	0.47
5:EC:3763:ARG:HB2	5:EC:3764:LYS:NZ	2.29	0.47
5:EC:4733:GLU:HA	5:EC:4736:ILE:HG12	1.97	0.47
6:FE:1283:TYR:CD1	6:FE:1293:THR:HB	2.49	0.47
7:GC:341:PRO:HD3	7:GC:597:THR:HA	1.96	0.47
8:GD:261:GLU:HA	8:GD:263:ARG:NH1	2.30	0.47
8:GF:46:LEU:HD11	8:GF:110:GLU:HB2	1.96	0.47
7:GG:738:LEU:HD22	7:GG:797:ILE:HD12	1.96	0.47
8:GH:604:PHE:HE1	8:GH:622:LEU:HD13	1.79	0.47
9:HA:763:GLN:HG2	9:HA:764:LYS:H	1.78	0.47
10:IB:506:GLN:HB3	10:IB:594:PRO:HD2	1.95	0.47
11:JA:520:VAL:HA	11:JA:523:ASN:HB2	1.96	0.47
11:JA:885:TYR:HD1	11:JA:1413:PRO:HB3	1.78	0.47
11:JB:1039:VAL:HG21	11:JB:1059:ARG:HH12	1.79	0.47
11:JB:2022:VAL:HG13	11:JB:2055:TRP:HH2	1.79	0.47
11:JB:2073:HIS:HB2	11:JB:2248:ILE:HD12	1.95	0.47
12:KA:658:SER:HB2	12:KA:665:HIS:HB2	1.97	0.47
15:NB:1017:GLN:HE22	15:NB:1098:LEU:HB3	1.78	0.47
15:NC:891:TRP:HD1	15:NC:1151:ASN:HA	1.79	0.47
15:ND:614:LYS:HB3	15:ND:678:LEU:HD22	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:707:GLU:HG2	15:ND:883:LEU:HD11	1.95	0.47
2:AC:361:GLU:HB2	5:EB:4406:MET:SD	2.55	0.47
1:AH:716:HIS:CG	13:LI:493:GLN:HE22	2.32	0.47
1:AH:878:ARG:HD3	1:AH:881:LEU:HD23	1.95	0.47
3:BB:791:THR:HG22	3:BB:812:MET:H	1.79	0.47
4:DA:297:ARG:HA	4:DA:300:GLN:HB2	1.97	0.47
4:DC:245:LEU:HD12	4:DC:248:ARG:HD2	1.96	0.47
5:EA:3764:LYS:HG3	5:EA:3765:VAL:HG13	1.95	0.47
5:EA:4443:MET:HE1	17:PB:143:ILE:HD13	1.97	0.47
5:EC:3642:PRO:HD3	5:EC:3673:LEU:HD23	1.96	0.47
6:FA:2062:LEU:O	6:FA:2063:GLN:C	2.54	0.47
6:FC:1976:LYS:HB2	6:FC:1976:LYS:HE2	1.70	0.47
6:FD:912:ILE:HG21	6:FD:1425:PRO:O	2.14	0.47
6:FD:922:LEU:O	6:FD:925:GLU:HB2	2.14	0.47
6:FD:1097:SER:O	6:FD:1101:ALA:N	2.47	0.47
6:FD:1285:CYS:O	6:FD:1286:LEU:C	2.57	0.47
6:FE:1008:ARG:O	6:FE:1009:VAL:C	2.57	0.47
7:GA:184:ALA:HB3	7:GA:708:SER:HB2	1.96	0.47
7:GC:309:LEU:HD23	7:GC:309:LEU:H	1.78	0.47
7:GC:952:ARG:HA	7:GC:952:ARG:HD3	1.75	0.47
7:GE:518:LEU:HD12	7:GE:520:ILE:HD11	1.96	0.47
7:GG:464:LEU:HB3	7:GG:502:TYR:CE1	2.47	0.47
9:HA:561:ASN:HB2	9:HA:564:ARG:HB2	1.97	0.47
9:HB:644:PHE:HD2	9:HB:726:PRO:HB2	1.78	0.47
9:HD:804:THR:O	9:HD:805:THR:C	2.56	0.47
10:IB:800:ILE:HD12	16:OB:1062:ARG:HG2	1.97	0.47
10:IB:1222:VAL:HG13	10:IB:1223:LEU:HD12	1.96	0.47
11:JA:1689:LEU:HB3	11:JA:1698:PHE:HB3	1.96	0.47
11:JB:1501:LEU:HB3	15:NB:440:LEU:HD11	1.96	0.47
11:JC:1374:LEU:HG	11:JC:1378:MET:HE1	1.96	0.47
11:JC:1584:LYS:HA	11:JC:1588:GLU:HA	1.95	0.47
11:JC:1598:LEU:HD13	11:JC:1621:ALA:HA	1.97	0.47
12:KA:365:GLU:HG3	12:KA:368:ARG:HH12	1.79	0.47
12:KC:206:CYS:H	12:KC:244:SER:HB3	1.80	0.47
15:NC:779:VAL:HG12	15:NC:783:GLN:HE22	1.79	0.47
15:NC:1537:LYS:HA	19:RA:114:GLU:HG2	1.96	0.47
16:OB:7:ARG:HD2	16:OB:12:GLU:HB2	1.97	0.47
19:RD:20:PRO:HB2	19:RD:22:ARG:HG2	1.97	0.47
3:CA:691:LEU:HD22	3:CA:710:ILE:HD13	1.97	0.47
4:DF:168:SER:HA	4:DF:171:ASP:HB3	1.94	0.47
5:EA:3731:VAL:HG21	5:EA:4249:LEU:HB2	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EA:4011:VAL:HB	5:EA:4166:SER:HB2	1.96	0.47
5:EB:3609:LEU:HD22	5:EB:3612:LEU:HD13	1.94	0.47
6:FA:1871:PRO:HD2	6:FA:1874:PHE:CE2	2.49	0.47
6:FA:2030:ILE:HD13	6:FA:2030:ILE:HA	1.69	0.47
6:FE:922:LEU:O	6:FE:925:GLU:HB2	2.15	0.47
6:FF:854:TRP:CD1	6:FF:854:TRP:H	2.32	0.47
6:FF:1186:TRP:HE3	6:FF:1267:GLN:HB2	1.79	0.47
7:GC:636:VAL:HG21	7:GC:678:LEU:HD21	1.96	0.47
7:GE:201:GLY:HA3	7:GE:717:LEU:HD21	1.95	0.47
7:GE:709:MET:HG2	7:GE:714:VAL:HG21	1.96	0.47
8:GJ:354:GLN:HA	8:GJ:357:ARG:HG2	1.95	0.47
8:GL:300:ARG:HD2	8:GL:419:PHE:HE1	1.79	0.47
9:HA:771:PRO:HG3	9:HA:819:TYR:CE1	2.49	0.47
10:IA:1326:THR:HG23	10:IA:1328:LYS:H	1.79	0.47
10:IC:398:ARG:H	10:IC:398:ARG:HG2	1.51	0.47
11:JA:1372:PRO:HB2	11:JA:1390:ALA:HB1	1.96	0.47
11:JC:62:ALA:HB3	11:JC:124:VAL:HB	1.96	0.47
12:KE:656:ARG:HB3	12:KE:667:SER:HB3	1.95	0.47
15:NA:627:ASP:HB2	15:NA:904:ARG:HB2	1.96	0.47
15:NC:891:TRP:HA	15:NC:1152:GLU:O	2.15	0.47
15:ND:1454:ILE:HD12	15:ND:1478:LEU:HD11	1.96	0.47
1:AA:768:ILE:HA	1:AA:776:LEU:HD21	1.95	0.47
2:AB:113:LEU:HD23	11:JA:1649:LEU:HD21	1.96	0.47
1:AI:650:LEU:HD22	1:AI:1013:THR:HG23	1.97	0.47
3:CB:956:LEU:HB2	3:CB:978:VAL:HG21	1.97	0.47
3:CL:1121:ARG:HH12	3:CL:1131:LEU:HD13	1.79	0.47
4:DB:249:GLY:HA3	4:DB:287:ALA:HB2	1.97	0.47
4:DC:277:ARG:HD2	4:DC:278:ALA:H	1.79	0.47
6:FC:2079:MET:HE3	6:FC:2083:GLN:HG2	1.95	0.47
6:FE:814:THR:OG1	6:FE:815:SER:N	2.46	0.47
6:FF:913:LEU:HD12	6:FF:913:LEU:HA	1.70	0.47
6:FF:1098:VAL:C	6:FF:1101:ALA:H	2.23	0.47
7:GA:891:LEU:HB3	7:GA:956:ILE:HD12	1.97	0.47
7:GE:583:GLN:HG2	7:GE:584:HIS:ND1	2.30	0.47
8:GF:25:GLU:HA	8:GF:28:LYS:HG2	1.97	0.47
8:GL:401:ASP:HB2	8:GL:719:VAL:HG11	1.96	0.47
10:IC:881:VAL:HA	16:OC:1045:LEU:HD13	1.96	0.47
10:IC:889:VAL:HA	10:IC:892:ILE:HB	1.97	0.47
11:JB:1856:ARG:NH1	11:JB:1988:SER:H	2.13	0.47
11:JC:2277:GLN:NE2	11:JC:2281:ARG:HH12	2.12	0.47
12:KA:524:PHE:H	12:KA:525:PRO:CD	2.27	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LA:468:HIS:HA	13:LA:471:THR:HG22	1.97	0.47
14:MA:292:ALA:HA	14:MA:295:GLU:HG2	1.97	0.47
15:NB:818:ILE:HB	15:NB:842:THR:HA	1.96	0.47
15:ND:806:ASP:HA	15:ND:809:GLU:HG2	1.96	0.47
15:ND:1120:VAL:HA	15:ND:1123:ALA:HB2	1.96	0.47
19:RD:30:LEU:HD13	19:RD:33:ILE:HD12	1.97	0.47
1:AA:56:LEU:HD22	2:AB:521:LEU:HD21	1.97	0.47
1:AA:107:LEU:HD13	1:AA:221:VAL:HG11	1.96	0.47
1:AA:816:ARG:HH22	1:AA:828:HIS:H	1.61	0.47
2:AB:52:THR:HG22	2:AB:54:HIS:H	1.79	0.47
1:AE:1021:LEU:HB3	14:ML:85:PRO:HG3	1.97	0.47
1:AH:38:VAL:HG11	11:JA:2031:MET:HE1	1.97	0.47
1:AH:603:THR:HB	1:AH:608:LEU:HD11	1.97	0.47
1:AI:787:ARG:HG3	1:AI:790:ARG:HH21	1.78	0.47
1:AL:703:LEU:HA	1:AL:706:VAL:HG12	1.96	0.47
3:BB:988:VAL:HG13	3:BB:989:THR:HG23	1.95	0.47
3:CA:956:LEU:HB2	3:CA:978:VAL:HG21	1.97	0.47
3:CF:1123:LEU:HD11	10:IB:997:PRO:HA	1.95	0.47
3:CJ:4452:HIS:CE1	3:CJ:4499:PRO:HG3	2.50	0.47
4:DB:385:LYS:NZ	13:LF:462:GLN:HA	2.30	0.47
4:DC:300:GLN:NE2	4:DC:354:TRP:HA	2.28	0.47
4:DE:256:LEU:HD11	4:DE:268:ARG:HG2	1.96	0.47
5:EA:3274:GLN:HE22	5:EA:3492:LEU:HB3	1.79	0.47
5:EA:4098:PRO:HG3	9:HB:797:TYR:CE2	2.49	0.47
5:EB:4405:ILE:HD13	5:EB:4431:ARG:HD3	1.96	0.47
6:FA:2061:ARG:NH1	6:FA:2065:THR:HB	2.30	0.47
6:FB:2038:LEU:HD13	6:FB:2038:LEU:HA	1.76	0.47
6:FC:1978:LEU:HD11	9:HB:817:VAL:CG2	2.42	0.47
6:FC:2037:LEU:HD13	6:FC:2037:LEU:HA	1.73	0.47
6:FC:2099:ILE:HA	6:FC:2102:PHE:CD2	2.50	0.47
6:FD:818:VAL:O	6:FD:821:ARG:N	2.46	0.47
6:FD:834:VAL:O	6:FD:840:ALA:HB3	2.15	0.47
6:FD:1285:CYS:HB2	6:FD:1289:HIS:H	1.80	0.47
6:FE:963:THR:O	6:FE:964:LEU:C	2.57	0.47
6:FE:1067:ALA:HB1	6:FE:1111:GLU:OE2	2.14	0.47
6:FE:1393:LEU:HD22	6:FE:1417:ILE:HB	1.96	0.47
6:FF:980:SER:HA	12:KC:343:ASN:HB2	1.96	0.47
8:GB:777:LEU:HD23	8:GB:781:MET:HE2	1.96	0.47
7:GC:252:SER:HB2	7:GC:259:VAL:HG12	1.97	0.47
7:GE:746:LEU:HA	7:GE:749:LEU:HD12	1.97	0.47
8:GF:56:CYS:SG	8:GF:61:CYS:HB2	2.55	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:422:LEU:HD11	8:GJ:192:VAL:HG11	1.95	0.47
7:GG:790:GLY:HA2	7:GG:793:VAL:HG12	1.96	0.47
8:GH:439:PRO:HD2	8:GH:474:VAL:HG22	1.96	0.47
7:GI:357:VAL:HG13	7:GI:371:LEU:HD11	1.96	0.47
8:GJ:294:TRP:CE3	8:GJ:297:LEU:HD23	2.50	0.47
8:GJ:314:GLY:HA2	8:GJ:344:ALA:HA	1.96	0.47
7:GK:372:GLY:H	7:GK:400:ASP:HB3	1.79	0.47
8:GL:661:PRO:HB2	8:GL:680:LEU:HB2	1.96	0.47
9:HA:758:ALA:HA	9:HA:761:CYS:HB2	1.97	0.47
9:HA:766:SER:O	9:HA:767:GLN:C	2.58	0.47
9:HB:758:ALA:O	9:HB:761:CYS:HB2	2.15	0.47
9:HB:813:THR:OG1	9:HB:814:LYS:N	2.47	0.47
9:HD:765:TRP:O	9:HD:766:SER:C	2.58	0.47
9:HD:807:GLU:OE2	9:HD:807:GLU:N	2.44	0.47
10:IA:561:ARG:HH22	10:IA:853:GLY:HA2	1.79	0.47
10:IA:893:PHE:HZ	10:IA:907:ASP:HA	1.80	0.47
10:IA:1143:MET:HE1	10:IA:1207:LYS:HE2	1.97	0.47
10:IB:351:LEU:HD21	10:IB:355:GLN:HB2	1.96	0.47
10:IC:346:CYS:HB3	10:IC:532:VAL:HG12	1.97	0.47
11:JB:843:LEU:HD21	11:JB:916:GLU:HB3	1.97	0.47
11:JC:1667:THR:HG22	11:JC:1671:MET:HE3	1.97	0.47
12:KA:327:MET:HB3	12:KA:330:LEU:HB3	1.96	0.47
12:KE:534:VAL:HG13	12:KE:536:ARG:HH12	1.79	0.47
12:KF:212:LEU:HD12	12:KF:236:LYS:HB2	1.97	0.47
12:KG:669:GLN:HB3	12:KG:677:ARG:HH11	1.79	0.47
13:LB:486:ARG:HH12	13:LB:490:MET:HE2	1.79	0.47
15:NA:564:ARG:HH12	15:NA:619:TYR:HB2	1.80	0.47
15:NA:943:GLU:HA	15:NA:946:LEU:HB2	1.97	0.47
15:NA:1531:GLN:HA	15:NA:1534:GLU:HG3	1.95	0.47
15:NB:627:ASP:HB2	15:NB:904:ARG:HB2	1.96	0.47
15:NC:572:ILE:HG23	15:NC:581:LEU:HD22	1.96	0.47
15:NC:1479:GLU:HA	15:NC:1482:ARG:HG2	1.97	0.47
15:ND:733:VAL:HG21	15:ND:747:LEU:HD13	1.97	0.47
15:ND:1125:TYR:HE1	15:ND:1156:LEU:HD13	1.79	0.47
20:SC:100:PHE:HE1	20:SC:138:ASN:HB3	1.79	0.47
1:AA:393:LEU:HD11	1:AA:475:LEU:HD13	1.97	0.47
2:AB:415:HIS:HA	2:AB:418:LYS:HE3	1.96	0.47
2:AC:182:GLU:HA	2:AC:187:ARG:HD2	1.97	0.47
2:AC:190:LEU:HD21	2:AC:195:ASP:HA	1.97	0.47
1:AE:185:ARG:HB3	1:AE:207:LEU:HB2	1.97	0.47
2:AF:44:LEU:HD21	2:AF:47:ALA:HB2	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:830:THR:HG23	1:AH:833:ALA:H	1.80	0.47
1:AL:1025:ARG:O	1:AL:1029:GLU:HG3	2.14	0.47
3:CC:899:PHE:HE1	3:CC:934:ILE:HB	1.79	0.47
3:CL:4486:ILE:HG22	3:CL:4497:ARG:HE	1.77	0.47
4:DA:357:GLU:HA	4:DA:386:VAL:HB	1.96	0.47
4:DF:19:ARG:HD3	4:DF:19:ARG:HA	1.75	0.47
5:EA:3746:LYS:HA	5:EA:3831:LEU:HD13	1.96	0.47
5:EB:4520:LEU:HD11	5:EB:4691:PHE:HE2	1.80	0.47
6:FA:2010:LYS:HE2	6:FA:2010:LYS:HB2	1.44	0.47
6:FC:1636:GLN:HB2	6:FC:1666:VAL:HG13	1.97	0.47
6:FC:1798:VAL:HG21	6:FC:1900:VAL:HG11	1.97	0.47
6:FC:2055:THR:HA	9:HB:837:LEU:HD21	1.97	0.47
6:FD:1297:PRO:C	6:FD:1299:ASN:H	2.23	0.47
7:GC:706:VAL:HG11	7:GC:752:VAL:HG11	1.96	0.47
8:GD:563:ARG:HA	8:GD:566:ILE:HG22	1.97	0.47
7:GE:163:GLN:HA	7:GE:166:LEU:HG	1.97	0.47
7:GE:893:TRP:HE1	7:GE:958:GLN:HB2	1.80	0.47
7:GG:185:ARG:HB2	7:GG:705:ILE:HD13	1.97	0.47
7:GG:262:THR:HG23	7:GG:266:TYR:HD2	1.79	0.47
8:GH:238:ARG:HH11	8:GH:240:ALA:HB3	1.79	0.47
7:GI:311:LEU:HD11	7:GI:436:ALA:HB1	1.96	0.47
8:GL:362:VAL:HG11	8:GL:380:MET:HG2	1.97	0.47
10:IA:226:ARG:HG2	10:IA:226:ARG:HH11	1.80	0.47
10:IB:841:MET:HB3	10:IB:866:LEU:HD13	1.96	0.47
11:JC:1745:PHE:HB2	11:JC:1795:LEU:HD21	1.97	0.47
11:JC:1786:LEU:HD12	11:JC:1812:VAL:HG13	1.97	0.47
12:KC:304:ARG:NH2	12:KC:308:LEU:HD23	2.29	0.47
12:KE:488:SER:C	12:KE:489:MET:HE2	2.39	0.47
13:LI:506:GLN:HE22	13:LJ:507:ARG:HE	1.63	0.47
15:NA:983:ILE:HG12	15:NA:989:ILE:HD12	1.97	0.47
15:NB:717:TYR:HE1	15:NB:927:LEU:HD22	1.79	0.47
15:NC:947:ASN:HA	15:NC:950:VAL:HB	1.97	0.47
15:ND:468:ARG:NH1	15:ND:469:PHE:HB3	2.30	0.47
2:AB:284:LEU:HD22	5:EA:4533:LEU:HD11	1.96	0.47
2:AC:114:MET:HE2	16:OA:135:VAL:HG21	1.96	0.47
1:AE:131:ARG:N	1:AE:205:ARG:HH12	2.12	0.47
1:AE:132:PRO:HA	1:AE:133:PRO:HD3	1.84	0.47
3:CI:1181:ARG:HB2	3:CI:4512:SER:HA	1.97	0.47
5:EA:3859:PRO:HA	5:EA:3862:LEU:HD13	1.96	0.47
5:EB:4539:MET:HE3	5:EB:4688:LEU:HD21	1.97	0.47
6:FA:1699:PRO:HA	6:FA:1722:PHE:HB3	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FA:1898:ILE:HB	6:FA:1912:PHE:HB2	1.96	0.47
6:FD:1030:ILE:HG13	6:FD:1116:LEU:HB2	1.96	0.47
6:FE:971:SER:HA	6:FE:1022:THR:HA	1.96	0.47
6:FF:864:LEU:O	6:FF:865:GLY:C	2.57	0.47
6:FF:1075:VAL:HG13	6:FF:1105:ARG:HB2	1.97	0.47
8:GD:326:ARG:HH21	8:GD:373:GLY:HA2	1.79	0.47
8:GD:419:PHE:HB2	8:GD:503:LEU:HB3	1.97	0.47
7:GI:633:LEU:HD23	7:GI:636:VAL:HB	1.96	0.47
7:GI:903:LEU:HD11	7:GI:912:LEU:HD13	1.97	0.47
7:GI:910:HIS:HE1	12:KC:340:ALA:HA	1.80	0.47
8:GJ:437:ILE:HB	8:GJ:475:ALA:HB3	1.97	0.47
7:GK:534:PRO:HA	7:GK:535:PRO:HD3	1.64	0.47
8:GL:46:LEU:HD11	8:GL:110:GLU:HG2	1.97	0.47
8:GL:638:LEU:HD21	8:GL:665:LEU:HD13	1.97	0.47
11:JA:1079:TYR:HB3	11:JA:1428:LEU:HD12	1.97	0.47
11:JB:107:PRO:HB3	11:JB:186:SER:HA	1.97	0.47
11:JC:1051:LEU:HA	11:JC:1055:GLN:HB2	1.96	0.47
12:KC:532:PHE:HB2	12:KC:547:ARG:HA	1.97	0.47
12:KF:329:GLN:HA	12:KF:332:LYS:HE3	1.95	0.47
13:LC:336:VAL:HG13	13:LC:340:LYS:HE2	1.96	0.47
13:LF:425:LYS:HA	13:LF:428:VAL:HG12	1.95	0.47
15:NA:947:ASN:HA	15:NA:950:VAL:HB	1.95	0.47
15:NB:644:MET:HE3	15:NB:648:ASN:HD21	1.80	0.47
15:NB:794:GLU:HA	15:NB:797:ARG:HB2	1.96	0.47
16:OA:215:ALA:HA	16:OA:218:LYS:HE3	1.97	0.47
1:AA:497:PRO:HG3	6:FA:1789:LEU:HD13	1.97	0.47
1:AE:421:MET:HE1	1:AE:451:ILE:HG21	1.96	0.47
2:AF:177:VAL:HG21	2:AF:197:ALA:HB1	1.97	0.47
1:AL:730:SER:HB3	1:AL:852:ARG:HD2	1.96	0.47
1:AL:793:LEU:HB3	1:AL:801:ARG:HG3	1.96	0.47
3:CA:870:LEU:HD22	17:PA:311:PHE:HE2	1.80	0.47
3:CB:784:LEU:HD22	3:CB:826:LEU:HD13	1.97	0.47
3:CG:4486:ILE:HG22	3:CG:4497:ARG:HA	1.97	0.47
4:DA:385:LYS:HZ1	13:LB:462:GLN:HG3	1.79	0.47
4:DE:137:LYS:HG3	4:DE:138:LYS:H	1.80	0.47
4:DE:343:LEU:HB3	4:DE:374:VAL:HG21	1.97	0.47
6:FA:2061:ARG:HH11	6:FA:2065:THR:HB	1.80	0.47
6:FB:2098:TYR:CG	9:HD:879:ILE:HG12	2.50	0.47
6:FE:965:TRP:CD1	6:FE:965:TRP:H	2.33	0.47
6:FE:1441:ILE:O	6:FE:1442:GLU:C	2.58	0.47
6:FE:1441:ILE:C	6:FE:1442:GLU:HG3	2.39	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:804:LEU:HD13	6:FF:804:LEU:HA	1.74	0.47
6:FF:814:THR:O	6:FF:815:SER:C	2.57	0.47
6:FF:1009:VAL:CG2	6:FF:1219:GLU:HA	2.44	0.47
7:GI:662:VAL:HG21	7:GI:672:VAL:HA	1.96	0.47
7:GK:341:PRO:HD3	7:GK:597:THR:HA	1.96	0.47
8:GL:294:TRP:CD1	8:GL:299:ALA:HB2	2.49	0.47
10:IA:581:PHE:CE2	10:IA:759:PHE:HA	2.50	0.47
10:IC:486:PRO:HA	10:IC:489:TYR:CZ	2.50	0.47
11:JA:1677:LEU:HD21	11:JA:1833:ASP:HB2	1.97	0.47
11:JB:1873:ARG:HG3	11:JB:1874:ARG:HG2	1.96	0.47
11:JC:76:CYS:HB3	11:JC:84:PHE:HZ	1.80	0.47
13:LJ:403:SER:HA	13:LJ:406:GLN:HG2	1.96	0.47
15:NA:754:PHE:HB3	15:NA:847:ALA:HB2	1.97	0.47
15:NB:891:TRP:HA	15:NB:1152:GLU:O	2.15	0.47
15:NC:866:LEU:HD22	15:NC:878:ILE:HG12	1.96	0.47
15:ND:627:ASP:HB2	15:ND:904:ARG:HB2	1.97	0.47
2:AB:415:HIS:CB	6:FC:2077:HIS:HB2	2.38	0.46
2:AC:558:ARG:HH11	5:EB:3787:GLU:HB3	1.79	0.46
1:AD:139:ASN:HD21	10:IB:874:ASN:HD21	1.63	0.46
2:AF:208:GLU:OE2	11:JC:1649:LEU:HD11	2.15	0.46
2:AG:428:ARG:HH12	1:AH:419:GLU:HG3	1.79	0.46
1:AH:654:LEU:HG	1:AH:662:LEU:HB2	1.97	0.46
1:AI:446:LEU:HD21	2:AJ:24:ASP:HA	1.97	0.46
2:AK:169:VAL:HG12	2:AK:171:VAL:HG23	1.95	0.46
3:CB:810:PRO:HB2	3:CB:813:ARG:HG3	1.97	0.46
3:CL:4466:ILE:HD11	3:CL:4487:LEU:HB3	1.97	0.46
5:EA:3649:TRP:HZ2	5:EA:3655:GLU:HG3	1.80	0.46
5:EB:4401:PRO:HD2	5:EB:4702:ILE:HG21	1.96	0.46
5:EB:4667:PRO:HA	5:EB:4670:TRP:HB3	1.97	0.46
6:FB:2030:ILE:HD13	6:FB:2030:ILE:HA	1.74	0.46
6:FC:1971:LYS:HG2	6:FC:1972:GLU:N	2.31	0.46
6:FC:2086:ASN:O	6:FC:2087:LEU:C	2.58	0.46
6:FD:1249:ILE:HG13	6:FD:1250:GLU:N	2.27	0.46
6:FE:1103:SER:O	6:FE:1105:ARG:N	2.47	0.46
6:FE:1203:ARG:HB2	11:JC:901:ARG:HH12	1.76	0.46
7:GA:294:ALA:HB1	7:GA:298:TYR:HD2	1.80	0.46
8:GB:200:GLY:HA2	8:GB:281:LEU:HD22	1.96	0.46
7:GE:243:HIS:CE1	7:GE:252:SER:HB3	2.50	0.46
7:GE:984:GLU:HA	7:GE:987:GLN:HB2	1.97	0.46
7:GG:211:ARG:HE	7:GG:212:PRO:HD2	1.79	0.46
7:GI:433:MET:HE3	7:GI:453:LEU:HD21	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GI:727:LEU:HD13	7:GI:821:TRP:HZ3	1.80	0.46
7:GK:518:LEU:HD21	7:GK:562:ILE:HG13	1.96	0.46
10:IB:900:LEU:HD12	10:IB:902:ARG:HH21	1.80	0.46
10:IC:455:LEU:HD21	10:IC:535:ARG:HH12	1.80	0.46
10:IC:882:VAL:HA	16:OC:1044:ARG:HH21	1.81	0.46
11:JB:139:ARG:HG2	11:JB:140:LEU:H	1.80	0.46
11:JC:1431:VAL:HG22	11:JC:1462:ILE:HG23	1.97	0.46
12:KB:359:VAL:HG12	12:KB:362:LEU:H	1.79	0.46
12:KB:622:THR:HG22	12:KB:632:TYR:HB2	1.96	0.46
12:KC:582:ILE:HB	12:KC:653:VAL:HG13	1.98	0.46
13:LD:367:VAL:HA	13:LD:370:MET:HG2	1.97	0.46
14:MI:284:LEU:HG	14:MJ:283:GLN:HE22	1.80	0.46
16:OB:742:PHE:HA	18:QC:89:ARG:NH2	2.30	0.46
20:SC:106:LEU:HD23	20:SC:126:ILE:HG12	1.98	0.46
1:AD:667:LYS:HD3	1:AD:1036:THR:HG21	1.95	0.46
1:AE:107:LEU:HD22	1:AE:145:HIS:CE1	2.50	0.46
2:AF:75:THR:HG23	2:AF:84:LEU:HD21	1.97	0.46
2:AG:332:ARG:HH21	11:JC:2281:ARG:HG3	1.80	0.46
1:AH:157:LEU:HB2	1:AH:180:PHE:CD2	2.51	0.46
2:AK:265:PHE:HZ	2:AK:267:HIS:CE1	2.33	0.46
1:AL:799:THR:HG22	1:AL:998:LEU:HA	1.97	0.46
3:BB:865:LEU:HD12	3:BB:884:LEU:HG	1.97	0.46
3:CJ:1172:PRO:HD3	3:CJ:1202:LEU:HD13	1.98	0.46
4:DA:301:LEU:HD22	4:DA:357:GLU:HG2	1.98	0.46
4:DB:170:ARG:HH12	4:DE:173:PHE:HD2	1.63	0.46
4:DF:100:GLU:HG2	4:DF:103:LEU:HD12	1.95	0.46
4:DF:296:ASN:H	4:DF:299:ARG:HB2	1.79	0.46
5:EB:3532:MET:HG3	5:EB:3535:TYR:HB3	1.98	0.46
5:EB:4443:MET:HE2	17:PA:143:ILE:HD12	1.97	0.46
6:FC:1974:VAL:CG2	6:FC:2036:LEU:HB3	2.45	0.46
6:FC:2070:LEU:HD22	6:FC:2070:LEU:HA	1.73	0.46
6:FD:817:VAL:HG11	6:FD:826:LEU:HD12	1.98	0.46
6:FE:911:SER:C	6:FE:912:ILE:HG23	2.40	0.46
6:FF:926:LEU:H	6:FF:926:LEU:HG	1.56	0.46
6:FF:990:PHE:C	12:KC:313:PHE:CE2	2.93	0.46
7:GA:210:ILE:HD13	7:GA:216:THR:HA	1.96	0.46
7:GC:233:ARG:HE	7:GC:258:TYR:HB2	1.80	0.46
7:GC:606:MET:HB3	7:GC:631:PHE:HB2	1.97	0.46
7:GC:680:TYR:HE1	7:GC:682:ASN:HB3	1.79	0.46
7:GC:758:LEU:HD22	7:GC:787:LEU:HD22	1.95	0.46
8:GF:326:ARG:HB3	8:GF:338:ALA:HB2	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GH:46:LEU:HD13	8:GH:512:ARG:HH12	1.80	0.46
8:GL:667:LEU:HB3	8:GL:674:VAL:HB	1.97	0.46
9:HD:773:ALA:CB	13:LJ:527:VAL:HG13	2.45	0.46
10:IA:889:VAL:HG12	10:IA:893:PHE:HE1	1.80	0.46
10:IA:889:VAL:H	10:IA:911:ARG:NH2	2.14	0.46
11:JC:1679:ALA:HB2	11:JC:1714:CYS:HB2	1.98	0.46
12:KA:596:ILE:HD13	12:KA:657:VAL:HG11	1.97	0.46
12:KB:567:TRP:HZ3	12:KB:569:LEU:HB2	1.80	0.46
13:LE:523:GLU:HG2	13:LH:522:ARG:HD2	1.97	0.46
13:LI:523:GLU:C	13:LI:525:SER:N	2.72	0.46
14:MJ:227:GLN:HA	14:MJ:230:VAL:HG12	1.97	0.46
15:NC:545:VAL:HG22	15:NC:1195:SER:HA	1.97	0.46
15:NC:1545:VAL:HG11	19:RA:139:LEU:HG	1.96	0.46
2:AC:68:LEU:HD13	1:AD:457:ARG:HD3	1.97	0.46
1:AE:728:VAL:HG23	1:AE:734:MET:HE2	1.98	0.46
1:AI:237:VAL:HG23	1:AI:238:CYS:H	1.80	0.46
3:BB:807:LEU:HD23	17:PB:279:ARG:HH22	1.80	0.46
3:CA:765:VAL:HG13	3:CA:833:TYR:HE1	1.81	0.46
6:FE:994:PRO:HB3	12:KB:382:ARG:HD3	1.97	0.46
6:FF:1213:VAL:HG11	6:FF:1226:LEU:HA	1.97	0.46
7:GA:494:LEU:HB3	7:GA:814:THR:HG21	1.98	0.46
7:GE:616:ILE:HG23	7:GE:644:ILE:HG23	1.96	0.46
7:GE:703:GLN:HG3	7:GE:752:VAL:HG13	1.97	0.46
8:GF:283:LEU:HD11	8:GF:303:LEU:HD22	1.97	0.46
8:GF:692:MET:HE1	8:GF:694:GLU:HB2	1.97	0.46
7:GI:220:VAL:HG22	7:GI:283:ALA:HB3	1.98	0.46
7:GK:715:THR:HG21	7:GK:796:PHE:HB3	1.97	0.46
7:GK:916:HIS:HD2	7:GK:917:PRO:HD2	1.80	0.46
8:GL:35:CYS:C	8:GL:36:MET:HE2	2.40	0.46
8:GL:171:ILE:HG22	8:GL:183:LEU:HD21	1.97	0.46
9:HB:783:SER:O	9:HB:784:GLU:C	2.58	0.46
10:IB:348:PRO:HB3	10:IB:364:LEU:HD11	1.97	0.46
11:JB:1803:ARG:NH2	16:OB:4:ARG:HH12	2.13	0.46
11:JC:154:ARG:HG3	11:JC:174:ALA:HB3	1.98	0.46
12:KE:335:LEU:HD13	12:KE:697:ARG:HH22	1.79	0.46
14:MF:294:ALA:HA	14:MF:297:VAL:HG12	1.97	0.46
15:ND:866:LEU:HD23	15:ND:869:PHE:HD2	1.80	0.46
16:OB:1096:MET:HE3	16:OB:1096:MET:HB3	1.82	0.46
19:RA:20:PRO:HB3	19:RA:22:ARG:HD3	1.98	0.46
20:SA:139:TYR:HA	20:SA:142:PHE:HB3	1.97	0.46
1:AA:705:TRP:HZ2	1:AA:1037:PRO:HD2	1.80	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:331:ASN:HD21	1:AH:265:VAL:HG13	1.80	0.46
1:AE:465:MET:HG2	1:AE:469:MET:HG3	1.97	0.46
3:CG:4470:LYS:HB2	3:CG:4486:ILE:HG13	1.97	0.46
4:DD:28:LEU:HD11	4:DD:154:LEU:HD13	1.96	0.46
6:FA:1657:MET:HE1	6:FA:1698:ARG:HD3	1.98	0.46
6:FD:813:GLN:O	6:FD:815:SER:N	2.48	0.46
6:FD:1189:ILE:CD1	6:FD:1233:ILE:HD13	2.45	0.46
6:FF:1191:LYS:HG3	6:FF:1418:GLU:HG3	1.96	0.46
6:FF:1439:LEU:O	6:FF:1440:ASN:HB3	2.15	0.46
7:GG:979:LEU:HB3	9:HA:650:PHE:HB2	1.97	0.46
8:GL:417:MET:HG3	8:GL:469:ASP:HB3	1.98	0.46
9:HA:650:PHE:HE1	13:LL:486:ARG:HH21	1.63	0.46
9:HA:779:PRO:O	9:HA:780:PHE:C	2.58	0.46
10:IB:888:THR:HA	15:NC:566:GLN:NE2	2.29	0.46
11:JC:1790:LEU:HD21	11:JC:1859:GLN:HG3	1.96	0.46
12:KE:207:ASP:HB2	12:KE:281:MET:HG3	1.97	0.46
12:KG:613:PRO:HG3	12:KG:643:TRP:HZ3	1.81	0.46
13:LA:360:LEU:HD22	13:LB:356:LEU:HD22	1.98	0.46
13:LI:523:GLU:O	13:LI:525:SER:N	2.46	0.46
14:MC:93:SER:HA	14:MC:96:ASP:HB3	1.98	0.46
14:ME:253:GLU:HG2	14:ME:254:ILE:HD12	1.97	0.46
15:NC:564:ARG:HA	15:NC:580:PHE:CZ	2.50	0.46
15:NC:1550:MET:HE2	19:RA:29:GLU:HB3	1.96	0.46
16:OB:729:SER:HA	16:OB:732:ASN:HB2	1.96	0.46
1:AA:419:GLU:HB3	16:OA:76:PHE:HD1	1.81	0.46
1:AA:801:ARG:HD2	1:AA:996:SER:HB2	1.98	0.46
2:AC:190:LEU:HD22	2:AC:272:TYR:HD2	1.80	0.46
1:AE:314:ILE:HD12	1:AE:319:HIS:HB3	1.97	0.46
1:AE:1036:THR:HG21	1:AE:1039:LEU:HD23	1.96	0.46
3:BC:754:GLU:HA	17:PC:278:TRP:HH2	1.80	0.46
3:BC:793:ILE:HG21	3:BC:807:LEU:HA	1.98	0.46
3:BC:904:PRO:HG2	3:BC:941:ARG:HG2	1.97	0.46
3:CI:1156:GLU:HA	10:IA:398:ARG:NH2	2.30	0.46
4:DA:159:GLU:HA	4:DA:162:VAL:HG22	1.98	0.46
4:DF:90:LEU:HA	4:DF:93:ILE:HG22	1.98	0.46
5:EB:4143:ARG:HD2	5:EB:4143:ARG:HA	1.72	0.46
6:FA:1817:VAL:HG11	6:FA:1838:VAL:HG11	1.98	0.46
6:FD:803:ARG:CG	6:FD:1118:GLN:NE2	2.69	0.46
6:FD:1078:GLU:O	6:FD:1081:SER:HB3	2.15	0.46
6:FD:1103:SER:OG	6:FD:1104:GLY:N	2.48	0.46
6:FE:832:GLY:HA3	6:FE:844:ALA:HB2	1.95	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GC:570:GLY:HA3	7:GC:633:LEU:HD11	1.98	0.46
7:GE:570:GLY:HA2	7:GE:622:ARG:HB3	1.96	0.46
7:GK:233:ARG:HE	7:GK:258:TYR:HB2	1.81	0.46
7:GK:543:LYS:N	9:HC:596:TYR:HB3	2.30	0.46
8:GL:341:VAL:HG13	8:GL:342:LYS:HD3	1.97	0.46
9:HB:762:HIS:CD2	9:HB:763:GLN:NE2	2.83	0.46
10:IB:455:LEU:HD21	10:IB:535:ARG:HH12	1.80	0.46
11:JA:191:ASP:HB3	11:JA:194:VAL:HG12	1.97	0.46
11:JB:889:ARG:HH21	11:JB:1416:ARG:HH12	1.64	0.46
11:JC:171:LYS:HG2	11:JC:172:LEU:H	1.81	0.46
11:JC:202:LEU:HD23	11:JC:1043:ALA:HB3	1.98	0.46
11:JC:2011:ARG:HH12	11:JC:2290:VAL:HG12	1.81	0.46
12:KA:618:PHE:HD2	12:KA:639:GLY:HA2	1.79	0.46
13:LK:532:LEU:HD23	13:LL:530:VAL:HG23	1.98	0.46
13:LP:392:GLU:HA	13:LP:395:ILE:HG12	1.98	0.46
14:MF:227:GLN:HA	14:MF:230:VAL:HG12	1.98	0.46
15:NA:682:ARG:HD2	15:NA:917:MET:HE1	1.96	0.46
15:NA:1498:ARG:CZ	20:SA:38:ARG:HD2	2.46	0.46
15:NA:1528:SER:HA	15:NA:1531:GLN:HG3	1.96	0.46
15:NB:512:TYR:HA	15:NB:1473:ARG:NH2	2.31	0.46
15:NC:937:MET:HA	15:NC:940:TYR:HB3	1.96	0.46
1:AA:265:VAL:HB	2:AF:331:ASN:HD21	1.81	0.46
1:AA:431:SER:HB2	2:AB:296:ALA:H	1.80	0.46
1:AD:918:VAL:HB	1:AD:982:VAL:HG21	1.97	0.46
1:AD:1030:GLY:HA3	8:GD:84:ARG:HH21	1.79	0.46
2:AG:446:ARG:HD2	2:AG:450:ARG:HH21	1.80	0.46
1:AI:397:LYS:HD2	1:AI:397:LYS:HA	1.77	0.46
3:BA:792:LEU:HD13	3:BA:845:LYS:HG2	1.97	0.46
3:BC:825:SER:HB3	16:OC:291:VAL:HG12	1.96	0.46
3:CE:1263:SER:HA	3:CE:4457:PRO:HB3	1.96	0.46
4:DC:28:LEU:HD13	4:DC:154:LEU:HD11	1.97	0.46
5:EC:3270:HIS:CE1	5:EC:3603:LEU:HD11	2.51	0.46
5:EC:4047:MET:HG3	13:LK:516:VAL:HG21	1.97	0.46
6:FA:1759:GLU:HB3	6:FA:1934:LEU:HG	1.98	0.46
6:FA:1962:GLN:O	6:FA:2047:ARG:HD2	2.16	0.46
6:FA:2034:ARG:HE	9:HA:774:LEU:HG	1.80	0.46
6:FC:1946:LEU:HD11	6:FC:2054:PHE:CE1	2.51	0.46
6:FD:993:ALA:CB	12:KA:230:GLN:HB2	2.46	0.46
6:FD:1008:ARG:HD3	6:FD:1008:ARG:HA	1.35	0.46
6:FD:1190:ARG:NH2	6:FD:1418:GLU:HB3	2.30	0.46
6:FE:819:PRO:HG3	6:FE:895:ILE:HB	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:864:LEU:HD11	6:FF:973:ILE:HD12	1.97	0.46
6:FF:1184:ALA:H	6:FF:1424:CYS:HB3	1.79	0.46
7:GC:522:PRO:HG3	7:GC:575:TYR:HE1	1.80	0.46
7:GE:862:GLU:HG3	7:GE:864:ILE:HG23	1.96	0.46
8:GF:63:LEU:HD21	8:GF:87:PHE:HE1	1.81	0.46
8:GF:667:LEU:HB3	8:GF:674:VAL:HB	1.98	0.46
7:GG:374:ALA:HB2	7:GG:380:ARG:HB2	1.98	0.46
8:GH:152:LEU:HB2	8:GH:394:PHE:CD2	2.50	0.46
8:GH:681:ILE:HG22	8:GH:685:ARG:HH21	1.81	0.46
7:GI:458:PRO:HB2	7:GI:467:LYS:NZ	2.30	0.46
7:GK:891:LEU:HB3	7:GK:956:ILE:HD12	1.96	0.46
8:GL:168:MET:HE1	8:GL:247:PRO:HG3	1.97	0.46
9:HA:807:GLU:HG3	9:HA:810:ARG:HH21	1.80	0.46
10:IC:372:ARG:HD2	10:IC:1217:ARG:HH21	1.81	0.46
10:IC:473:LEU:HD13	10:IC:501:MET:HE2	1.98	0.46
11:JA:1731:PRO:HB3	11:JA:1778:PHE:HZ	1.80	0.46
11:JC:159:LEU:HD21	11:JC:169:PHE:HB2	1.97	0.46
11:JC:1090:LEU:HB2	11:JC:1128:LYS:HZ3	1.81	0.46
12:KA:376:ALA:HB2	12:KA:579:LEU:HD11	1.97	0.46
12:KA:594:PHE:H	12:KA:611:LEU:HB3	1.80	0.46
14:MC:122:LEU:HD22	14:MD:122:LEU:HB3	1.97	0.46
15:NB:885:LEU:HD23	15:NB:888:ARG:HD3	1.98	0.46
15:NC:1148:GLY:HA2	15:NC:1157:PRO:HA	1.97	0.46
15:ND:1125:TYR:CE1	15:ND:1156:LEU:HD13	2.49	0.46
15:ND:1423:LEU:HB3	15:ND:1424:VAL:H	1.57	0.46
16:OA:1033:ALA:HA	16:OA:1034:PRO:HD3	1.83	0.46
2:AC:371:VAL:HG12	2:AC:379:HIS:CE1	2.51	0.46
1:AE:157:LEU:HB2	1:AE:180:PHE:HD2	1.80	0.46
2:AF:481:ARG:HH22	2:AF:532:PRO:HB2	1.80	0.46
2:AG:354:ARG:HG3	2:AG:355:HIS:CE1	2.51	0.46
3:CA:906:ALA:HB2	3:CA:942:ILE:HG12	1.97	0.46
3:CC:755:GLY:HA2	3:CC:810:PRO:HG3	1.97	0.46
5:EA:3436:TYR:CE1	5:EA:4014:VAL:HG22	2.49	0.46
5:EA:3720:LEU:HD23	5:EA:3740:MET:HG3	1.97	0.46
5:EA:3821:PRO:HG2	5:EA:4242:PHE:CZ	2.51	0.46
6:FD:1208:ALA:HB3	6:FD:1286:LEU:HD22	1.98	0.46
6:FD:1443:GLY:O	6:FD:1444:ARG:C	2.59	0.46
6:FE:1247:SER:HB2	11:JC:795:ARG:HD2	1.97	0.46
6:FF:843:LEU:HB3	7:GI:958:GLN:OE1	2.15	0.46
6:FF:1198:TYR:O	6:FF:1199:GLY:C	2.59	0.46
6:FF:1429:LEU:HD22	6:FF:1429:LEU:N	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GD:396:ILE:HG23	8:GD:398:VAL:HG12	1.98	0.46
8:GD:424:GLU:HB3	8:GD:499:GLN:HB2	1.96	0.46
8:GF:604:PHE:HE1	8:GF:618:TYR:HB3	1.80	0.46
7:GI:243:HIS:CE1	7:GI:252:SER:HB3	2.51	0.46
7:GK:433:MET:HE3	7:GK:459:PRO:HD3	1.97	0.46
9:HD:774:LEU:C	13:LJ:526:LEU:HD23	2.40	0.46
10:IB:1196:VAL:HG12	10:IB:1305:GLU:HG2	1.97	0.46
10:IC:537:LEU:HD22	10:IC:558:VAL:HG11	1.97	0.46
11:JA:476:LEU:HA	11:JA:479:VAL:HG12	1.97	0.46
11:JA:1328:LEU:HD21	11:JA:1408:LEU:HD11	1.98	0.46
11:JA:1676:ARG:NH2	11:JA:1833:ASP:HA	2.31	0.46
11:JA:1716:GLN:NE2	16:OA:890:THR:HG23	2.31	0.46
11:JB:1735:GLY:HA2	11:JB:1774:ARG:HH22	1.81	0.46
11:JC:55:LEU:HD12	11:JC:56:PRO:HD2	1.98	0.46
12:KA:212:LEU:HB2	12:KA:238:PHE:HB2	1.97	0.46
12:KA:513:LYS:HE2	12:KA:513:LYS:HB2	1.74	0.46
12:KC:402:LEU:HD13	12:KC:406:GLN:HG3	1.97	0.46
12:KF:208:LEU:HB2	12:KF:281:MET:HE3	1.97	0.46
13:LF:423:GLN:HG3	13:LF:427:ARG:HH22	1.81	0.46
15:ND:890:ARG:C	15:ND:1153:ALA:HA	2.40	0.46
16:OB:152:THR:HG22	16:OB:156:GLU:HB3	1.98	0.46
20:SD:106:LEU:HB3	20:SD:110:MET:HE2	1.98	0.46
2:AB:323:CYS:O	2:AB:327:ILE:HG12	2.16	0.46
2:AG:14:LYS:HG3	6:FB:1911:PRO:HD3	1.98	0.46
2:AG:114:MET:HE1	16:OC:143:VAL:HG13	1.97	0.46
1:AH:965:ALA:HB1	1:AH:967:ARG:NH1	2.31	0.46
5:EB:3651:ALA:H	9:HB:499:ARG:HD2	1.80	0.46
5:EB:3842:LYS:H	11:JA:1041:LYS:HE3	1.81	0.46
5:EB:4540:ASP:H	5:EB:4685:PRO:HD3	1.80	0.46
5:EB:4674:LEU:HD21	5:EB:4690:CYS:HB3	1.98	0.46
6:FD:888:PRO:HB3	7:GC:896:ARG:HG3	1.97	0.46
6:FF:1201:THR:O	6:FF:1202:PHE:C	2.59	0.46
6:FF:1210:LEU:HD23	6:FF:1286:LEU:HD23	1.98	0.46
7:GA:397:LEU:HD21	8:GF:176:ALA:HB3	1.97	0.46
7:GA:548:ALA:HB3	9:HB:626:PRO:HG2	1.98	0.46
8:GB:22:THR:H	8:GB:25:GLU:HB2	1.81	0.46
7:GC:323:LEU:HA	7:GC:579:PHE:HE2	1.80	0.46
7:GC:619:ARG:HD3	7:GC:631:PHE:CE1	2.51	0.46
8:GF:504:HIS:CD2	8:GF:505:PRO:HD2	2.51	0.46
7:GI:311:LEU:HD23	7:GI:453:LEU:HD13	1.98	0.46
7:GK:276:ARG:HD3	7:GK:285:LEU:HD21	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:HA:777:TYR:O	9:HA:778:PRO:C	2.58	0.46
10:IC:1068:ARG:HH22	10:IC:1072:ARG:HD3	1.81	0.46
11:JA:1669:LEU:HD11	11:JA:1726:LEU:HD13	1.98	0.46
11:JB:970:PHE:HD1	11:JB:1008:PHE:HD2	1.64	0.46
11:JB:1745:PHE:HE2	11:JB:1858:ILE:HG12	1.81	0.46
12:KC:413:ALA:HA	12:KC:416:ALA:HB3	1.98	0.46
12:KC:582:ILE:HG21	12:KC:594:PHE:HE2	1.81	0.46
12:KC:600:ASP:HB2	12:KC:685:ARG:HB2	1.97	0.46
12:KE:219:LEU:HD22	12:KE:223:ALA:HA	1.98	0.46
13:LI:520:LEU:O	13:LI:523:GLU:N	2.49	0.46
15:NC:355:LEU:HB3	15:NC:434:VAL:HG11	1.96	0.46
15:NC:503:LEU:HB2	15:NC:514:SER:HB2	1.97	0.46
15:ND:903:CYS:SG	15:ND:904:ARG:HG2	2.56	0.46
16:OA:1109:LYS:HA	16:OA:1112:LYS:HE2	1.98	0.46
2:AC:145:LYS:HA	2:AC:148:ASP:HB2	1.98	0.46
2:AC:147:LEU:HA	2:AC:150:ALA:HB3	1.98	0.46
3:BC:875:THR:HB	16:OC:154:ALA:HA	1.97	0.46
5:EA:4431:ARG:HH11	5:EA:4432:PRO:HD2	1.81	0.46
5:EB:3690:VAL:HG11	5:EB:3726:ARG:HG3	1.98	0.46
5:EB:4348:LEU:HA	5:EB:4351:VAL:HG12	1.97	0.46
6:FB:1684:THR:HG22	6:FB:1685:GLU:H	1.80	0.46
6:FC:2052:HIS:CE1	9:HB:762:HIS:HB2	2.47	0.46
6:FD:865:GLY:HA2	6:FD:868:GLN:HE21	1.81	0.46
6:FD:963:THR:HA	6:FD:1028:LYS:HD3	1.98	0.46
6:FD:1182:ALA:HB1	6:FD:1424:CYS:SG	2.56	0.46
6:FE:1001:ASN:HD22	6:FE:1001:ASN:H	1.62	0.46
7:GA:298:TYR:HB3	7:GA:679:LEU:HD11	1.97	0.46
8:GB:716:ARG:HH11	8:GB:720:PRO:HG3	1.81	0.46
7:GE:916:HIS:HB3	7:GE:919:VAL:HG12	1.98	0.46
7:GG:438:LYS:HE2	7:GG:464:LEU:HG	1.98	0.46
7:GG:690:ARG:HA	7:GG:690:ARG:HD3	1.74	0.46
9:HC:676:ALA:HB2	9:HC:682:ILE:HG12	1.98	0.46
10:IA:561:ARG:HH12	10:IA:853:GLY:HA2	1.80	0.46
10:IA:947:HIS:HB3	10:IA:951:GLY:H	1.81	0.46
11:JA:123:ILE:HB	11:JA:135:ILE:HB	1.98	0.46
11:JA:1584:LYS:HA	11:JA:1588:GLU:HA	1.97	0.46
11:JA:1838:THR:HG22	11:JA:1839:LEU:HD12	1.97	0.46
11:JB:529:ILE:HG21	11:JB:885:TYR:HD2	1.81	0.46
11:JC:1152:HIS:CE1	11:JC:1158:MET:HB2	2.51	0.46
13:LI:510:ILE:HD13	13:LI:513:LEU:HD12	1.98	0.46
13:LK:483:ARG:HA	13:LK:486:ARG:HG2	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NA:542:LEU:HB3	15:NA:1190:ILE:HG13	1.98	0.46
15:NA:548:PRO:HA	15:NA:551:ARG:HE	1.81	0.46
15:NA:657:VAL:HG21	15:NA:897:ILE:HD12	1.97	0.46
15:NC:537:LYS:NZ	15:NC:578:HIS:H	2.13	0.46
15:NC:1526:ILE:HG21	18:QD:146:ILE:HD13	1.98	0.46
15:NC:1550:MET:HE1	19:RA:26:HIS:HA	1.97	0.46
15:ND:468:ARG:HG2	15:ND:469:PHE:H	1.80	0.46
15:ND:1498:ARG:HH12	20:SB:44:PRO:HD3	1.80	0.46
20:SB:11:ALA:HA	20:SB:14:LYS:HE3	1.98	0.46
20:SD:33:LEU:HD13	20:SD:64:ILE:HG12	1.98	0.46
1:AA:777:PHE:HB3	1:AA:780:ALA:HB3	1.96	0.46
1:AH:811:VAL:HG21	1:AH:836:THR:HG21	1.98	0.46
1:AI:1026:ASP:HB3	1:AI:1032:PHE:HB2	1.97	0.46
3:CA:850:THR:HG23	3:CA:861:VAL:HG23	1.97	0.46
3:CG:1126:GLU:HB3	10:IC:995:PRO:HG2	1.97	0.46
4:DA:19:ARG:HH12	4:DA:156:ASP:CG	2.24	0.46
4:DB:395:MET:HA	14:MF:320:ARG:NH2	2.31	0.46
4:DC:3:TRP:CH2	14:MJ:293:LEU:HD22	2.51	0.46
5:EA:3445:VAL:HG11	5:EA:3566:ILE:HA	1.98	0.46
5:EA:3881:ARG:HG2	5:EA:4004:PHE:HE2	1.81	0.46
5:EC:3246:LYS:HB3	5:EC:3301:LEU:HD21	1.98	0.46
6:FA:2037:LEU:HD13	6:FA:2037:LEU:HA	1.70	0.46
6:FC:1974:VAL:HG21	6:FC:2040:LEU:HD23	1.98	0.46
6:FC:2064:LEU:HD12	6:FC:2064:LEU:HA	1.73	0.46
6:FE:821:ARG:O	6:FE:823:GLY:N	2.49	0.46
6:FE:1190:ARG:CZ	6:FE:1388:PHE:HB3	2.46	0.46
8:GD:69:ILE:HD11	8:GD:104:LEU:HD21	1.98	0.46
7:GG:292:PHE:HB2	7:GG:689:ILE:HB	1.98	0.46
7:GK:506:ALA:HA	7:GK:509:LEU:HD12	1.98	0.46
8:GL:63:LEU:HD21	8:GL:104:LEU:HD22	1.98	0.46
9:HA:496:GLU:HG3	9:HA:499:ARG:HD2	1.98	0.46
10:IC:1223:LEU:HD23	10:IC:1387:LEU:HD22	1.98	0.46
11:JA:1556:PHE:HA	11:JA:1575:LEU:HD13	1.98	0.46
11:JB:837:ASN:HA	11:JB:840:ILE:HG22	1.98	0.46
11:JB:1412:LEU:HB3	11:JB:1504:ARG:HB2	1.98	0.46
11:JC:1765:ARG:HH22	16:OC:893:PRO:HD2	1.81	0.46
12:KB:261:VAL:HA	12:KB:264:LYS:HG2	1.98	0.46
12:KF:312:PRO:HA	12:KF:315:GLN:HB2	1.98	0.46
13:LB:497:LEU:HD11	14:MD:114:ARG:HD3	1.98	0.46
13:LI:380:MET:HE3	13:LI:384:LEU:HB2	1.98	0.46
15:NB:780:GLN:HA	15:NB:783:GLN:NE2	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NB:891:TRP:H	15:NB:1154:ASP:C	2.24	0.46
15:ND:1441:ARG:HA	15:ND:1441:ARG:HD2	1.83	0.46
19:RD:53:PHE:HE1	19:RD:139:LEU:HD21	1.80	0.46
1:AA:389:LEU:HD11	2:AB:549:VAL:HG11	1.97	0.45
2:AC:200:GLU:HG3	2:AC:201:LYS:H	1.80	0.45
3:CG:4462:VAL:HG12	3:CG:4465:LYS:HD3	1.98	0.45
3:CL:1131:LEU:O	3:CL:1132:MET:HE2	2.16	0.45
4:DB:393:LEU:HD13	14:MF:316:GLN:HG3	1.98	0.45
4:DC:343:LEU:HD13	4:DC:374:VAL:HG11	1.97	0.45
4:DE:173:PHE:HA	4:DE:176:ILE:HG12	1.98	0.45
5:EA:4408:GLY:O	5:EA:4410:ASP:N	2.47	0.45
5:EB:4072:ASN:HB3	5:EB:4293:TRP:HH2	1.81	0.45
6:FC:2083:GLN:HG3	6:FC:2084:GLN:H	1.80	0.45
6:FE:1193:VAL:HG12	6:FE:1194:ASN:HD22	1.81	0.45
6:FF:976:HIS:O	6:FF:987:ASN:ND2	2.49	0.45
6:FF:1216:TRP:CZ2	6:FF:1272:VAL:HG22	2.51	0.45
6:FF:1216:TRP:O	6:FF:1217:GLU:C	2.59	0.45
7:GA:294:ALA:HB2	7:GA:689:ILE:HG12	1.97	0.45
8:GB:664:ILE:HD11	8:GB:681:ILE:HG21	1.97	0.45
7:GE:276:ARG:HH22	7:GE:279:ARG:HG2	1.81	0.45
7:GE:839:ARG:HA	7:GE:839:ARG:HD3	1.83	0.45
7:GG:715:THR:HG21	7:GG:796:PHE:HB3	1.97	0.45
7:GI:898:ILE:HG23	7:GI:903:LEU:HD21	1.98	0.45
9:HA:872:MET:HB2	9:HA:872:MET:HE2	1.58	0.45
9:HB:854:ASN:HA	9:HB:857:ARG:HE	1.80	0.45
10:IB:649:VAL:HA	10:IB:652:LYS:HG2	1.98	0.45
10:IB:1095:GLY:H	10:IB:1098:HIS:CD2	2.34	0.45
10:IC:615:ARG:HD3	10:IC:629:PRO:HG3	1.97	0.45
10:IC:1059:LEU:HD22	10:IC:1111:GLN:HG3	1.97	0.45
10:IC:1278:VAL:HG23	10:IC:1279:GLU:H	1.81	0.45
11:JA:64:ALA:HB2	11:JA:82:VAL:HG23	1.98	0.45
11:JA:1437:ILE:HA	11:JA:1438:PRO:HD3	1.81	0.45
11:JB:1515:LEU:HD22	11:JB:1554:LEU:HD22	1.98	0.45
11:JC:162:PRO:HD2	11:JC:169:PHE:HA	1.98	0.45
11:JC:945:LEU:HD23	11:JC:947:LYS:H	1.81	0.45
11:JC:1687:LEU:HG	11:JC:1854:HIS:CE1	2.50	0.45
12:KA:495:GLN:NE2	12:KA:496:VAL:HG23	2.31	0.45
15:NC:504:GLU:HA	15:NC:514:SER:H	1.81	0.45
15:NC:1163:THR:HA	15:NC:1166:VAL:HG22	1.98	0.45
15:ND:508:GLY:HA3	15:ND:577:PRO:HG3	1.97	0.45
19:RC:108:LEU:HD22	19:RC:171:GLN:HE21	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:SB:52:MET:HG2	20:SB:72:LEU:HD11	1.98	0.45
1:AA:289:SER:H	17:PA:271:ASN:HD22	1.63	0.45
2:AF:502:LEU:HD23	2:AF:514:ALA:HB1	1.99	0.45
1:AH:291:PRO:HB3	10:IA:826:SER:HA	1.97	0.45
1:AL:795:ASP:HB3	7:GK:582:LEU:HD22	1.98	0.45
5:EB:3729:GLY:HA2	5:EB:4288:PRO:HD3	1.98	0.45
5:EB:3881:ARG:HA	5:EB:4004:PHE:HE2	1.82	0.45
5:EB:4229:MET:HE1	5:EB:4261:VAL:HG21	1.97	0.45
5:EC:4256:LEU:HD12	5:EC:4278:VAL:HG11	1.97	0.45
6:FA:1946:LEU:HD22	6:FA:2054:PHE:CE1	2.51	0.45
6:FB:1643:PRO:HG2	6:FB:1652:TYR:HD2	1.81	0.45
6:FF:912:ILE:H	6:FF:912:ILE:HG12	1.43	0.45
8:GB:565:LEU:HD22	8:GB:596:MET:HG2	1.98	0.45
8:GD:133:PRO:HB2	8:GD:167:ALA:HA	1.98	0.45
8:GD:674:VAL:HG12	8:GD:723:VAL:HB	1.98	0.45
7:GI:641:THR:HG21	7:GI:828:PRO:HA	1.99	0.45
7:GI:885:GLU:HA	7:GI:890:MET:HG3	1.98	0.45
8:GJ:565:LEU:HD13	8:GJ:596:MET:HE3	1.98	0.45
7:GK:535:PRO:HB3	9:HC:551:GLU:O	2.16	0.45
10:IA:506:GLN:HB3	10:IA:594:PRO:HD2	1.98	0.45
10:IA:893:PHE:O	10:IA:897:ARG:HG2	2.17	0.45
13:LA:526:LEU:HD11	13:LB:525:SER:HB3	1.97	0.45
13:LM:353:ASN:HD22	13:LN:349:TYR:HE1	1.63	0.45
14:ME:285:ARG:HH22	14:MF:257:LYS:HD2	1.81	0.45
15:NA:361:VAL:HG11	15:NA:445:ILE:HD11	1.96	0.45
15:NA:812:ARG:CZ	15:NA:870:TYR:HA	2.45	0.45
15:NA:893:LEU:HG	15:NA:1154:ASP:CG	2.42	0.45
15:NA:1487:ARG:HB3	15:NA:1488:ARG:H	1.52	0.45
15:NB:629:ALA:HB2	15:NB:646:GLU:HG3	1.99	0.45
15:ND:536:THR:HB	15:ND:543:ILE:HB	1.98	0.45
15:ND:1412:THR:HG22	15:ND:1467:LEU:HG	1.98	0.45
15:ND:1488:ARG:NH1	15:ND:1491:PRO:HD2	2.28	0.45
19:RA:37:ILE:HG22	19:RA:53:PHE:CD1	2.52	0.45
1:AA:237:VAL:HG11	17:PA:249:LEU:HD13	1.97	0.45
1:AE:850:ILE:HG21	1:AE:904:ASP:HB2	1.98	0.45
2:AG:521:LEU:HD21	1:AH:56:LEU:HD22	1.99	0.45
3:BA:952:GLN:HA	3:BA:955:VAL:HG12	1.97	0.45
3:CB:776:ARG:HD2	3:CB:776:ARG:HA	1.73	0.45
4:DB:300:GLN:HG3	4:DB:355:CYS:HB2	1.98	0.45
4:DB:354:TRP:HB2	4:DB:381:MET:HE2	1.98	0.45
4:DC:267:ARG:NH2	14:MI:294:ALA:HA	2.26	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DC:269:LEU:HD13	4:DC:284:ILE:HD12	1.98	0.45
4:DE:103:LEU:HB2	4:DE:106:ASN:ND2	2.31	0.45
5:EA:3631:ARG:HH21	5:EA:4057:LEU:HD13	1.81	0.45
5:EA:4247:LEU:HD11	5:EA:4284:LEU:HB3	1.97	0.45
5:EB:4888:TRP:O	5:EB:4889:ILE:C	2.60	0.45
5:EC:4024:THR:HG23	9:HA:438:TYR:HD2	1.81	0.45
6:FE:851:THR:HG23	6:FE:972:VAL:HG13	1.98	0.45
6:FE:1000:GLN:HG3	6:FE:1444:ARG:HG2	1.98	0.45
8:GD:580:PRO:HG3	8:GD:789:VAL:HG11	1.98	0.45
7:GE:322:GLY:HA3	7:GE:581:ARG:HD3	1.98	0.45
8:GH:501:SER:HB3	8:GH:511:LEU:HD13	1.99	0.45
7:GI:871:LEU:O	7:GI:972:GLU:HG2	2.16	0.45
10:IC:1128:VAL:HG12	10:IC:1131:HIS:ND1	2.31	0.45
11:JA:2071:LEU:HD13	11:JA:2266:LEU:HB3	1.97	0.45
11:JB:1765:ARG:NH2	16:OB:893:PRO:HD2	2.32	0.45
12:KA:511:LEU:H	12:KA:514:PHE:HD2	1.65	0.45
12:KB:377:LEU:HD12	12:KB:386:LEU:HD11	1.99	0.45
12:KC:319:TYR:HE1	12:KC:331:GLN:HE22	1.64	0.45
12:KG:633:ARG:HH22	12:KG:635:VAL:HG23	1.81	0.45
15:NB:693:GLY:HA2	15:NB:901:LEU:HD23	1.97	0.45
15:NB:801:ALA:HA	15:NB:804:VAL:HG12	1.99	0.45
15:NB:805:ALA:HB2	15:NB:885:LEU:HD12	1.98	0.45
15:NB:1156:LEU:HD13	15:NB:1160:LEU:HD21	1.98	0.45
16:OA:1075:TYR:HE2	16:OA:1077:LYS:HB3	1.82	0.45
19:RA:20:PRO:HB3	19:RA:22:ARG:HB2	1.98	0.45
19:RA:116:PHE:HE1	19:RA:166:PHE:HB3	1.82	0.45
19:RC:51:MET:HA	19:RC:54:MET:HE2	1.98	0.45
2:AB:373:ARG:HG3	2:AB:374:LEU:HD12	1.97	0.45
2:AC:273:ASP:HB3	2:AC:276:GLN:HG3	1.97	0.45
1:AE:654:LEU:HB3	1:AE:662:LEU:HB2	1.99	0.45
2:AF:61:ARG:HG2	6:FB:1711:LEU:HD11	1.99	0.45
1:AH:966:LEU:HD12	1:AH:971:GLU:HB3	1.98	0.45
2:AK:164:TYR:HB2	2:AK:285:PHE:HE1	1.82	0.45
1:AL:725:LEU:HA	1:AL:728:VAL:HG12	1.98	0.45
3:CC:835:GLN:HB3	3:CC:838:ASP:HB2	1.99	0.45
3:CE:1228:LYS:HE3	3:CE:1228:LYS:HB3	1.83	0.45
4:DB:103:LEU:HB3	4:DB:106:ASN:HB3	1.97	0.45
4:DB:352:LYS:HZ3	13:LE:454:VAL:HG23	1.80	0.45
4:DD:163:GLU:HA	4:DD:166:VAL:HG23	1.97	0.45
5:EB:3223:TRP:HZ2	5:EB:4182:LEU:HD21	1.80	0.45
5:EB:3258:GLY:HA2	5:EB:3262:VAL:HG13	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:3648:PRO:HB2	7:GA:543:LYS:NZ	2.31	0.45
5:EC:3498:VAL:HG23	5:EC:3505:ILE:HB	1.98	0.45
5:EC:3874:PHE:HD1	5:EC:4009:PRO:HD3	1.82	0.45
5:EC:3881:ARG:HA	5:EC:4004:PHE:CZ	2.51	0.45
5:EC:4035:THR:HG22	5:EC:4037:ASP:H	1.82	0.45
6:FA:1951:TYR:CE2	9:HA:844:GLY:HA3	2.51	0.45
6:FA:2038:LEU:HD22	9:HA:771:PRO:HG2	1.99	0.45
6:FB:1880:GLU:HA	6:FB:1883:GLU:HB2	1.98	0.45
6:FB:1951:TYR:CE1	9:HD:844:GLY:HA3	2.51	0.45
6:FC:1828:VAL:HG13	6:FC:1838:VAL:HG22	1.97	0.45
6:FC:1936:GLY:HA2	6:FC:1939:VAL:HB	1.99	0.45
6:FC:2042:LYS:HZ2	6:FC:2042:LYS:HG3	1.68	0.45
6:FD:845:PRO:N	7:GC:896:ARG:NH1	2.64	0.45
6:FD:860:PRO:HG2	6:FD:861:LEU:HD22	1.98	0.45
6:FE:1230:SER:C	6:FE:1232:LYS:H	2.24	0.45
6:FE:1233:ILE:HG12	6:FE:1268:VAL:HG22	1.98	0.45
6:FF:811:ASN:O	6:FF:1110:GLY:HA2	2.17	0.45
6:FF:912:ILE:HD11	6:FF:965:TRP:HZ2	1.81	0.45
8:GB:261:GLU:HG3	8:GB:263:ARG:HH22	1.81	0.45
7:GC:185:ARG:NH2	7:GC:704:ASP:HB2	2.31	0.45
7:GC:280:PHE:HE1	12:KE:626:GLU:HB3	1.82	0.45
8:GD:151:GLN:HB3	8:GD:400:LYS:HZ3	1.82	0.45
7:GE:706:VAL:HG21	7:GE:752:VAL:HG21	1.98	0.45
7:GG:575:TYR:HE1	7:GG:577:SER:HB2	1.80	0.45
7:GG:607:ARG:HD2	7:GG:609:ARG:NH2	2.31	0.45
7:GK:397:LEU:HB3	8:GL:267:TRP:HE1	1.81	0.45
12:KA:545:LEU:HD12	12:KA:715:LEU:HD11	1.98	0.45
12:KB:339:SER:HA	12:KB:697:ARG:HD3	1.98	0.45
15:NA:357:CYS:O	15:NA:471:TYR:HB3	2.17	0.45
15:NA:564:ARG:NH2	15:NA:619:TYR:HA	2.31	0.45
15:NA:1138:THR:HG21	15:NA:1143:LEU:HB3	1.99	0.45
15:NB:685:PHE:HB3	15:NB:912:THR:HG23	1.98	0.45
15:NC:893:LEU:HB2	15:NC:1154:ASP:CG	2.41	0.45
15:ND:1521:SER:HB3	18:QB:60:ARG:NH2	2.32	0.45
18:QB:55:VAL:HG23	18:QB:58:LEU:HD23	1.98	0.45
1:AE:423:THR:HG21	2:AF:263:TYR:HD1	1.80	0.45
2:AG:176:VAL:HG13	16:OC:27:LEU:HA	1.99	0.45
1:AH:416:LEU:HD12	16:OC:17:PHE:HB3	1.97	0.45
1:AI:203:ALA:HB2	3:BB:804:ARG:HB2	1.97	0.45
1:AI:628:ASN:HB2	1:AI:630:PRO:HD2	1.99	0.45
1:AI:709:LEU:HD21	1:AI:1037:PRO:HG2	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:338:MET:HE2	1:AL:344:SER:HB2	1.99	0.45
3:BA:875:THR:HB	16:OA:154:ALA:HA	1.98	0.45
3:CA:1014:ASP:HA	3:CA:1017:ARG:HG2	1.97	0.45
3:CJ:1116:SER:HA	3:CJ:1119:ARG:HG2	1.98	0.45
3:CL:1239:PRO:HA	3:CL:4470:LYS:HD3	1.98	0.45
5:EC:4222:LYS:HE2	5:EC:4222:LYS:HB3	1.86	0.45
5:EC:4404:LYS:H	5:EC:4404:LYS:HG2	1.65	0.45
6:FA:1681:VAL:HG22	6:FA:1692:VAL:HG22	1.98	0.45
6:FA:1730:GLU:HA	6:FA:1907:ILE:HA	1.98	0.45
6:FA:1962:GLN:HG2	9:HA:834:LEU:CD2	2.47	0.45
6:FB:1699:PRO:HA	6:FB:1722:PHE:HB3	1.99	0.45
6:FC:2063:GLN:NE2	9:HB:751:SER:HB2	2.32	0.45
6:FD:887:ARG:CZ	6:FD:889:SER:HA	2.46	0.45
6:FD:992:PRO:O	12:KA:230:GLN:HB3	2.17	0.45
6:FD:1098:VAL:C	6:FD:1101:ALA:H	2.25	0.45
6:FE:841:TYR:N	7:GE:957:ARG:NH2	2.64	0.45
6:FE:1260:LEU:HG	6:FE:1261:SER:N	2.32	0.45
6:FF:1105:ARG:H	6:FF:1105:ARG:HG2	1.43	0.45
6:FF:1210:LEU:HD23	6:FF:1210:LEU:HA	1.77	0.45
8:GB:317:VAL:HB	8:GB:325:ILE:HG13	1.99	0.45
7:GC:268:ARG:HB2	7:GC:276:ARG:CZ	2.47	0.45
7:GC:370:ALA:HB3	7:GC:383:GLN:HB2	1.99	0.45
8:GD:626:SER:HB3	8:GD:629:ASN:HB2	1.99	0.45
7:GG:730:LYS:HA	7:GG:730:LYS:HE3	1.99	0.45
8:GH:40:LEU:HG	8:GH:470:LYS:HD3	1.98	0.45
8:GH:708:ASP:O	8:GH:712:ILE:HG12	2.16	0.45
7:GI:872:THR:HG22	7:GI:972:GLU:HG3	1.98	0.45
8:GJ:667:LEU:HB3	8:GJ:674:VAL:HB	1.99	0.45
7:GK:607:ARG:HH22	7:GK:609:ARG:HH21	1.64	0.45
8:GL:383:LYS:HE2	8:GL:441:THR:HG22	1.97	0.45
9:HA:722:SER:HA	9:HA:724:PHE:H	1.81	0.45
9:HB:783:SER:O	9:HB:786:ALA:N	2.49	0.45
9:HC:566:PRO:HA	9:HC:569:ARG:HB3	1.98	0.45
11:JB:783:PHE:HD1	11:JB:807:LEU:HD11	1.82	0.45
11:JC:837:ASN:HB3	11:JC:1419:ILE:HD11	1.98	0.45
11:JC:1161:LEU:HB2	11:JC:1357:PHE:HB3	1.98	0.45
11:JC:1388:PRO:HG3	11:JC:1407:HIS:HD2	1.81	0.45
11:JC:1722:TYR:HB3	11:JC:1733:THR:HG22	1.98	0.45
12:KE:414:TRP:HE3	12:KE:415:LEU:HD23	1.80	0.45
14:MA:320:ARG:HH22	14:MA:327:ARG:HH21	1.64	0.45
15:NC:948:LEU:HD21	15:NC:1173:MET:HE1	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:88:LYS:HD3	2:AB:535:LEU:HD13	1.98	0.45
1:AA:148:VAL:HG23	1:AA:219:THR:HB	1.98	0.45
1:AD:245:PRO:HG3	10:IB:776:PRO:HG2	1.98	0.45
1:AE:507:LEU:HD21	6:FB:1826:LEU:HD13	1.97	0.45
1:AH:663:LEU:HD21	1:AH:698:LEU:HA	1.98	0.45
2:AK:190:LEU:HD22	2:AK:272:TYR:HD2	1.82	0.45
1:AL:600:GLU:CD	13:LH:511:GLN:HE22	2.25	0.45
1:AL:851:LEU:HD23	1:AL:896:VAL:HG11	1.99	0.45
3:CF:1127:GLU:HB2	3:CF:1128:TRP:CE3	2.51	0.45
3:CL:4478:GLN:HG2	3:CL:4479:LEU:HG	1.98	0.45
4:DA:103:LEU:HB2	4:DA:106:ASN:HB2	1.99	0.45
4:DB:266:TRP:CD1	4:DB:316:ARG:HH22	2.35	0.45
4:DE:301:LEU:HD11	4:DE:357:GLU:HB2	1.97	0.45
4:DF:16:LEU:HD13	4:DF:160:PHE:CD2	2.52	0.45
5:EA:4403:LEU:HD13	5:EA:4405:ILE:HD11	1.98	0.45
6:FC:2009:SER:HA	6:FC:2012:ARG:CZ	2.47	0.45
6:FC:2027:TRP:HB2	9:HB:778:PRO:HD3	1.98	0.45
6:FC:2085:GLU:O	6:FC:2086:ASN:C	2.59	0.45
6:FD:860:PRO:CD	6:FD:861:LEU:HD23	2.47	0.45
6:FD:1028:LYS:HA	6:FD:1028:LYS:HD2	1.55	0.45
6:FE:1075:VAL:O	6:FE:1076:ILE:C	2.58	0.45
6:FE:1276:LEU:O	6:FE:1277:ASP:C	2.60	0.45
8:GB:432:LYS:HE2	8:GB:451:SER:HB3	1.99	0.45
7:GG:706:VAL:HG11	7:GG:752:VAL:HG11	1.99	0.45
8:GH:56:CYS:HB3	8:GH:61:CYS:HB2	1.36	0.45
8:GH:184:GLY:HA2	8:GH:254:LYS:HE3	1.98	0.45
8:GH:236:LEU:HB3	8:GH:294:TRP:HE1	1.80	0.45
9:HD:800:VAL:O	13:LI:534:PRO:HD2	2.17	0.45
10:IA:172:GLN:HB3	10:IA:173:GLN:H	1.59	0.45
10:IB:1121:LYS:HA	10:IB:1121:LYS:HD3	1.79	0.45
10:IC:938:ILE:HA	16:OC:1040:PHE:HE1	1.82	0.45
11:JA:1393:LEU:HA	11:JA:1396:MET:HE2	1.98	0.45
11:JB:1584:LYS:HB2	11:JB:1584:LYS:HE2	1.77	0.45
12:KG:486:PHE:HA	12:KG:489:MET:HE1	1.98	0.45
13:LA:401:LEU:HD23	13:LA:404:LEU:HD21	1.99	0.45
13:LA:513:LEU:HD21	13:LB:514:TYR:CD1	2.52	0.45
13:LJ:503:VAL:O	13:LJ:507:ARG:HG2	2.16	0.45
13:LJ:506:GLN:O	13:LJ:510:ILE:HG12	2.17	0.45
15:NA:676:ARG:O	15:NA:676:ARG:HD2	2.17	0.45
15:NB:503:LEU:HB3	15:NB:512:TYR:HB3	1.99	0.45
15:NC:898:ASN:HA	15:NC:901:LEU:HB3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:1412:THR:HG23	15:NC:1415:GLU:H	1.80	0.45
19:RA:58:VAL:HA	19:RA:118:TYR:OH	2.17	0.45
20:SD:76:LYS:HZ1	20:SD:78:LYS:HG3	1.82	0.45
1:AE:815:LEU:HD23	1:AE:830:THR:HG21	1.98	0.45
2:AG:94:ILE:HG12	2:AG:274:SER:HA	1.99	0.45
2:AK:515:TRP:HE3	2:AK:516:LEU:HD22	1.81	0.45
1:AL:593:GLU:HG2	1:AL:594:TYR:HD2	1.82	0.45
3:BA:693:ARG:HB2	17:PA:258:PRO:HG3	1.97	0.45
3:BA:731:MET:HE2	3:BA:776:ARG:HH12	1.82	0.45
3:BA:845:LYS:HB2	3:BA:845:LYS:HE2	1.70	0.45
4:DB:28:LEU:HD13	4:DB:154:LEU:HD11	1.98	0.45
4:DC:103:LEU:HB2	4:DC:106:ASN:HB2	1.99	0.45
4:DD:275:LEU:HB2	4:DD:280:ALA:HB2	1.99	0.45
5:EA:4505:MET:HE1	5:EA:4694:MET:HB3	1.99	0.45
6:FB:1817:VAL:HG11	6:FB:1838:VAL:HG11	1.99	0.45
6:FB:2031:HIS:CE1	13:LJ:519:SER:HG	2.35	0.45
6:FC:2038:LEU:HD13	9:HB:771:PRO:HG2	1.99	0.45
6:FD:843:LEU:HB3	7:GC:896:ARG:CZ	2.47	0.45
6:FD:1119:LEU:HD12	6:FD:1119:LEU:HA	1.87	0.45
6:FE:983:LEU:HA	12:KB:726:ASP:OD2	2.16	0.45
6:FE:1245:ASN:HB3	6:FE:1249:ILE:HG23	1.98	0.45
6:FE:1293:THR:HG22	6:FE:1396:PHE:HB2	1.99	0.45
6:FF:990:PHE:CB	12:KC:313:PHE:HE2	2.30	0.45
7:GA:543:LYS:HA	7:GA:544:PRO:HD3	1.92	0.45
8:GB:674:VAL:HG12	8:GB:723:VAL:HB	1.99	0.45
8:GD:681:ILE:HA	8:GD:684:TRP:CD1	2.51	0.45
8:GF:276:MET:SD	8:GF:311:SER:HB3	2.57	0.45
7:GG:318:ALA:HB1	7:GG:323:LEU:HB3	1.99	0.45
7:GG:626:ARG:HH12	7:GG:632:VAL:HG21	1.82	0.45
9:HA:808:HIS:O	9:HA:812:THR:HG23	2.17	0.45
9:HA:865:ILE:HD12	9:HA:865:ILE:HA	1.83	0.45
10:IA:829:GLY:HA2	11:JA:2037:ARG:HH12	1.82	0.45
10:IB:1077:LYS:HG3	10:IB:1080:ASP:H	1.82	0.45
11:JA:467:SER:O	11:JA:471:VAL:HG23	2.17	0.45
11:JA:1867:LEU:HB3	11:JA:2273:ARG:HH12	1.82	0.45
11:JC:552:THR:HG21	11:JC:1203:GLY:HA3	1.99	0.45
12:KA:664:ILE:HB	12:KA:682:LEU:HB3	1.98	0.45
12:KE:658:SER:HB3	12:KE:665:HIS:HB2	1.99	0.45
12:KF:215:PRO:HB3	12:KF:286:GLU:HB3	1.98	0.45
13:LP:417:LEU:HA	13:LP:420:GLU:HG2	1.99	0.45
15:NA:890:ARG:O	15:NA:891:TRP:HD1	2.00	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NB:679:ASP:HB2	15:NB:696:PHE:HB3	1.99	0.45
15:NB:698:PRO:HB3	15:NB:890:ARG:NH2	2.31	0.45
15:NB:937:MET:HE1	15:NB:1162:ARG:HH22	1.81	0.45
15:NB:1499:ALA:HA	20:SC:38:ARG:CZ	2.47	0.45
15:ND:609:GLN:HA	15:ND:612:ILE:HG22	1.99	0.45
15:ND:884:LYS:HZ3	15:ND:1127:LEU:HD13	1.80	0.45
15:ND:1391:LEU:HG	15:ND:1396:VAL:HB	1.97	0.45
16:OA:1075:TYR:CE2	16:OA:1077:LYS:HB3	2.51	0.45
16:OB:1077:LYS:NZ	16:OB:1079:ALA:H	2.15	0.45
1:AA:834:ILE:HG23	1:AA:985:CYS:HB2	1.98	0.45
1:AD:993:ARG:HD3	1:AD:993:ARG:HA	1.68	0.45
3:CE:1168:ARG:HH21	3:CE:4482:LEU:HD22	1.82	0.45
4:DC:357:GLU:HA	4:DC:386:VAL:HB	1.98	0.45
6:FD:813:GLN:O	6:FD:816:GLY:N	2.49	0.45
6:FD:818:VAL:O	6:FD:819:PRO:C	2.60	0.45
6:FD:819:PRO:HG3	6:FD:895:ILE:HD13	1.98	0.45
6:FD:829:ARG:HB2	6:FD:976:HIS:CD2	2.51	0.45
6:FD:1196:PRO:O	6:FD:1197:ILE:C	2.58	0.45
6:FD:1251:ARG:HD3	6:FD:1252:MET:HE1	1.97	0.45
6:FF:1429:LEU:HD23	6:FF:1430:PHE:CE2	2.52	0.45
7:GA:319:VAL:HG12	7:GA:324:VAL:HG11	1.98	0.45
8:GB:717:PHE:CD2	8:GB:718:PRO:HD3	2.52	0.45
8:GD:19:TRP:H	8:GD:520:PHE:HB2	1.82	0.45
8:GF:454:ILE:HD11	8:GF:459:MET:HE3	1.98	0.45
8:GH:600:ARG:NH2	8:GH:605:LEU:HD22	2.32	0.45
8:GJ:150:ASP:HA	8:GJ:153:ARG:HB3	1.97	0.45
7:GK:544:PRO:HD3	9:HC:596:TYR:HD1	1.81	0.45
8:GL:615:THR:O	8:GL:619:ARG:HG2	2.17	0.45
8:GL:631:LEU:HA	8:GL:634:ILE:HG22	1.99	0.45
9:HA:699:ILE:HD12	9:HA:708:VAL:HG21	1.98	0.45
9:HC:680:ALA:HB2	9:HC:708:VAL:HG13	1.99	0.45
10:IA:1307:ASN:HA	10:IA:1383:LEU:HD13	1.99	0.45
10:IB:765:HIS:HD2	10:IB:786:TYR:HA	1.82	0.45
10:IC:363:CYS:O	10:IC:365:ARG:HG3	2.17	0.45
10:IC:427:PHE:HD1	10:IC:504:VAL:HG21	1.81	0.45
11:JB:75:VAL:HB	11:JB:81:ARG:HD2	1.99	0.45
11:JB:1138:PRO:HG3	11:JB:1837:GLN:HB3	1.99	0.45
11:JC:1475:ARG:HG3	11:JC:1476:VAL:HG13	1.98	0.45
12:KB:215:PRO:HA	12:KB:286:GLU:OE2	2.17	0.45
12:KB:587:THR:HG23	12:KB:589:LYS:H	1.81	0.45
14:MA:258:ILE:HA	14:MA:264:LEU:HD23	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:OA:263:ALA:HB1	16:OA:267:GLU:HB2	1.98	0.45
19:RC:22:ARG:HE	19:RC:174:LEU:HB3	1.81	0.45
20:SB:48:GLU:HA	20:SB:51:ASP:HB3	1.99	0.45
1:AA:1021:LEU:HB3	14:MD:85:PRO:HG3	1.99	0.45
1:AE:403:TYR:HE1	1:AE:466:PRO:HD2	1.81	0.45
1:AE:424:PHE:CD2	2:AF:35:MET:HG3	2.52	0.45
3:CE:1168:ARG:HE	3:CE:4483:PRO:HD2	1.82	0.45
4:DD:333:LYS:HE2	4:DD:334:GLN:HE22	1.82	0.45
5:EB:4519:ARG:HA	5:EB:4519:ARG:HD2	1.75	0.45
5:EC:4093:SER:OG	5:EC:4094:LEU:N	2.49	0.45
6:FA:2034:ARG:HD2	9:HA:772:PRO:O	2.15	0.45
6:FB:2052:HIS:CE1	9:HD:762:HIS:HB2	2.51	0.45
6:FD:838:ASN:O	6:FD:839:GLY:C	2.59	0.45
6:FD:997:THR:HG21	12:KA:230:GLN:HE22	1.81	0.45
6:FD:1088:LYS:HD3	6:FD:1233:ILE:HG23	1.97	0.45
6:FD:1106:LEU:HD23	6:FD:1106:LEU:HA	1.84	0.45
6:FE:805:HIS:O	6:FE:806:ILE:C	2.60	0.45
6:FE:989:PRO:HG2	6:FE:990:PHE:CE2	2.52	0.45
6:FE:1229:LYS:H	6:FE:1229:LYS:HG3	1.62	0.45
6:FF:891:ARG:O	6:FF:892:PRO:C	2.59	0.45
6:FF:1196:PRO:O	6:FF:1197:ILE:C	2.60	0.45
6:FF:1216:TRP:HZ3	6:FF:1300:LEU:HD13	1.80	0.45
7:GA:380:ARG:HD2	8:GF:263:ARG:HH22	1.82	0.45
8:GF:549:THR:HG22	8:GF:554:SER:HA	1.98	0.45
8:GH:259:LEU:HA	8:GH:262:LEU:HD23	1.99	0.45
7:GI:607:ARG:HB3	7:GI:609:ARG:NH1	2.32	0.45
8:GL:50:GLU:HB3	8:GL:112:ILE:HG23	1.97	0.45
10:IB:1070:ASP:HB3	10:IB:1077:LYS:NZ	2.31	0.45
10:IC:216:TRP:NE1	10:IC:232:LEU:HD11	2.31	0.45
10:IC:630:PHE:HE2	10:IC:698:GLN:HB3	1.82	0.45
10:IC:1232:ARG:H	10:IC:1302:ARG:HH22	1.65	0.45
11:JB:1756:ALA:HA	11:JB:1759:LEU:HD23	1.99	0.45
11:JC:1077:ASN:HB3	11:JC:1084:VAL:HG22	1.98	0.45
12:KA:378:PHE:HA	12:KA:383:HIS:HD2	1.81	0.45
12:KB:321:GLU:HB3	12:KB:325:LEU:HD12	1.97	0.45
12:KE:665:HIS:CD2	12:KE:681:MET:HE1	2.50	0.45
12:KF:576:ASN:ND2	12:KF:697:ARG:HB3	2.32	0.45
12:KF:658:SER:HB3	12:KF:665:HIS:HB3	1.98	0.45
13:LM:359:HIS:HD2	13:LN:360:LEU:HD11	1.82	0.45
14:ME:264:LEU:HD23	14:ME:267:LYS:HG3	1.98	0.45
14:MJ:320:ARG:HA	14:MJ:323:GLN:HB2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NA:599:ILE:HB	15:NA:916:LEU:HG	1.99	0.45
15:NC:528:ARG:NH2	15:NC:577:PRO:HG2	2.32	0.45
15:ND:854:VAL:O	15:ND:858:ILE:HG12	2.17	0.45
16:OB:1085:ARG:H	16:OB:1085:ARG:HG2	1.61	0.45
18:QC:137:ALA:HA	18:QC:140:TRP:HB3	1.99	0.45
1:AA:290:CYS:HA	1:AA:298:ILE:HD11	1.99	0.45
2:AB:425:ALA:HA	2:AB:428:ARG:HB3	1.98	0.45
2:AC:505:VAL:HG22	10:IB:1255:LEU:HD23	1.99	0.45
1:AI:39:SER:HB3	1:AI:70:ASN:HB3	1.98	0.45
1:AL:622:ALA:HA	1:AL:625:ARG:HB2	1.99	0.45
1:AL:692:PRO:HG3	1:AL:998:LEU:HD12	1.99	0.45
3:CA:967:HIS:HB3	3:CA:970:ALA:HB3	1.99	0.45
4:DD:103:LEU:HD13	4:DD:106:ASN:HB3	1.98	0.45
4:DF:29:LEU:HD21	4:DF:126:LEU:HG	1.98	0.45
5:EB:3490:TYR:HE2	5:EB:3562:LYS:HB3	1.81	0.45
6:FA:2059:VAL:HG23	9:HA:754:LEU:HB3	1.98	0.45
6:FE:921:MET:HG3	6:FE:1092:PRO:HG3	1.97	0.45
6:FE:1197:ILE:HG13	6:FE:1260:LEU:HD22	1.98	0.45
6:FE:1289:HIS:O	6:FE:1291:TYR:N	2.50	0.45
6:FF:840:ALA:HB2	12:KC:665:HIS:HE1	1.82	0.45
7:GA:472:LEU:HB3	7:GA:494:LEU:HD21	1.99	0.45
8:GB:171:ILE:HG23	8:GB:181:HIS:HB2	1.97	0.45
8:GB:348:TYR:HD2	8:GB:376:GLU:HB3	1.82	0.45
8:GH:135:LEU:HD12	8:GH:168:MET:HE3	1.99	0.45
8:GH:541:MET:HE1	8:GH:544:LEU:HD22	1.99	0.45
7:GI:719:ILE:HD11	7:GI:800:VAL:HG21	1.99	0.45
8:GJ:168:MET:HE1	8:GJ:247:PRO:HG3	1.98	0.45
10:IA:742:ILE:HA	10:IA:745:ASP:HB3	1.99	0.45
10:IB:181:LEU:HD12	10:IB:201:LEU:HD22	1.98	0.45
10:IB:240:LEU:HD13	10:IB:792:ILE:HG13	1.99	0.45
10:IB:616:GLY:H	10:IB:758:ASN:ND2	2.11	0.45
11:JB:87:VAL:HG22	11:JB:90:ARG:HH12	1.81	0.45
11:JB:1689:LEU:HB3	11:JB:1698:PHE:HB3	1.98	0.45
13:LJ:403:SER:HB2	13:LJ:407:ARG:HH12	1.82	0.45
13:LN:384:LEU:HA	13:LN:387:THR:HG22	1.99	0.45
15:NA:1411:LEU:HD23	15:NA:1470:PHE:HE2	1.82	0.45
15:NC:735:HIS:HD2	15:NC:768:GLU:HG2	1.82	0.45
15:NC:881:LEU:HD12	15:NC:884:LYS:HB2	1.99	0.45
15:NC:1420:TYR:HE1	15:NC:1478:LEU:HB3	1.81	0.45
15:ND:624:ALA:O	15:ND:626:ARG:HG3	2.17	0.45
1:AA:121:ARG:HB3	1:AA:213:ALA:HB2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:141:SER:HA	1:AA:226:MET:HB3	1.99	0.44
2:AB:63:THR:HA	2:AB:66:ARG:HD2	1.98	0.44
2:AB:506:LEU:HD13	2:AB:510:ASP:HB3	1.99	0.44
1:AD:133:PRO:O	1:AD:136:PHE:HB2	2.17	0.44
1:AE:316:ILE:HD13	9:HD:872:MET:HG2	1.99	0.44
1:AE:403:TYR:CZ	1:AE:465:MET:HG3	2.52	0.44
1:AI:127:SER:HB3	1:AI:206:VAL:HG23	1.98	0.44
3:BA:920:ARG:HH22	16:OA:177:THR:HG21	1.82	0.44
3:BC:937:ASP:HA	3:BC:940:MET:HB2	1.99	0.44
3:CG:1209:ALA:HB3	3:CG:1223:GLU:HA	1.99	0.44
4:DA:3:TRP:CD1	4:DA:3:TRP:H	2.35	0.44
4:DC:93:ILE:HD11	4:DC:168:SER:HB2	1.99	0.44
4:DD:86:ASP:HB3	4:DD:89:ASN:HB2	2.00	0.44
5:EB:4341:ARG:HG2	5:EB:4364:ALA:HB2	1.98	0.44
5:EB:4405:ILE:O	5:EB:4406:MET:C	2.60	0.44
5:EB:4500:THR:HG21	5:EB:4667:PRO:HG2	1.99	0.44
5:EB:4658:ASP:HB3	5:EB:4670:TRP:HZ2	1.83	0.44
5:EC:3373:LYS:HG3	5:EC:3378:GLY:HA2	1.98	0.44
6:FA:2098:TYR:CZ	9:HA:875:THR:HG22	2.51	0.44
6:FB:2062:LEU:HG	9:HD:750:PRO:HG2	1.98	0.44
6:FD:843:LEU:C	7:GC:896:ARG:NH1	2.75	0.44
6:FD:1089:ARG:O	6:FD:1090:LEU:C	2.60	0.44
6:FD:1434:ALA:O	6:FD:1435:GLU:C	2.60	0.44
6:FE:1198:TYR:O	6:FE:1199:GLY:C	2.59	0.44
6:FE:1232:LYS:C	6:FE:1233:ILE:HG13	2.42	0.44
8:GB:267:TRP:CZ2	7:GC:397:LEU:HA	2.52	0.44
8:GH:11:GLY:HA3	8:GH:41:ARG:HG2	1.98	0.44
7:GI:614:TRP:CE3	7:GI:646:MET:HG2	2.51	0.44
9:HC:553:TYR:HD1	9:HC:575:ARG:HE	1.66	0.44
10:IC:698:GLN:NE2	10:IC:703:GLY:HA2	2.32	0.44
11:JA:2131:ARG:HH11	11:JA:2136:GLU:HG2	1.82	0.44
12:KC:364:LEU:O	12:KC:368:ARG:HG2	2.17	0.44
12:KC:405:PRO:HA	12:KC:408:TYR:HB3	1.99	0.44
12:KE:342:MET:SD	12:KE:346:PRO:HB2	2.57	0.44
13:LJ:422:GLN:HA	13:LJ:425:LYS:NZ	2.32	0.44
13:LM:336:VAL:O	13:LM:340:LYS:HG2	2.17	0.44
15:NA:745:THR:HB	15:NA:858:ILE:HG23	1.99	0.44
15:NC:854:VAL:O	15:NC:858:ILE:HG12	2.17	0.44
15:NC:1524:ARG:HH21	18:QD:57:ASN:CG	2.25	0.44
15:ND:1032:VAL:HG23	15:ND:1104:ARG:HB3	1.99	0.44
16:OB:195:LEU:HB2	16:OB:284:GLU:HG2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RC:22:ARG:HE	19:RC:174:LEU:HD22	1.82	0.44
1:AD:799:THR:HG22	1:AD:998:LEU:HA	1.98	0.44
2:AF:61:ARG:NH1	6:FB:1586:GLN:HE22	2.16	0.44
1:AH:73:THR:HG22	1:AH:75:ALA:H	1.82	0.44
2:AK:176:VAL:HG11	16:OB:25:ALA:HB1	1.99	0.44
1:AL:364:LYS:HD3	1:AL:364:LYS:HA	1.80	0.44
3:CE:4468:LYS:HE2	3:CE:4490:ASP:HA	1.99	0.44
3:CJ:1123:LEU:HA	10:IB:770:GLY:HA3	1.98	0.44
3:CL:1158:PHE:CE1	3:CL:4504:ILE:HG23	2.52	0.44
3:CL:1274:ARG:HH22	3:CL:4447:CYS:N	2.15	0.44
4:DB:76:MET:HB3	4:DE:9:PHE:HZ	1.81	0.44
4:DF:20:LEU:O	4:DF:24:LYS:HG2	2.17	0.44
5:EA:4348:LEU:HA	5:EA:4351:VAL:HG12	2.00	0.44
5:EB:3636:ILE:HG23	5:EB:4055:ARG:NH2	2.32	0.44
5:EB:4817:LEU:HD23	5:EB:4817:LEU:H	1.81	0.44
6:FA:1746:PRO:HB3	6:FA:1926:TYR:HE2	1.81	0.44
6:FA:2053:LYS:HE3	6:FA:2053:LYS:HB3	1.30	0.44
6:FB:2033:LEU:HD23	9:HD:816:LEU:HD13	2.00	0.44
6:FC:1699:PRO:HA	6:FC:1722:PHE:HB3	1.98	0.44
6:FC:2072:ILE:HG12	9:HB:855:ARG:HG3	2.00	0.44
6:FD:911:SER:C	6:FD:912:ILE:HG23	2.42	0.44
6:FD:916:PRO:O	6:FD:917:TRP:C	2.60	0.44
6:FD:1294:LEU:HD11	6:FD:1391:TYR:CD1	2.53	0.44
6:FD:1441:ILE:O	6:FD:1443:GLY:N	2.50	0.44
6:FE:800:ALA:HB3	6:FE:910:ILE:O	2.17	0.44
6:FE:813:GLN:O	6:FE:815:SER:N	2.50	0.44
6:FE:1217:GLU:O	6:FE:1219:GLU:N	2.50	0.44
6:FE:1293:THR:O	6:FE:1295:ALA:N	2.50	0.44
6:FF:800:ALA:HB2	6:FF:913:LEU:HD11	1.99	0.44
7:GA:833:CYS:HA	7:GA:836:VAL:HG22	1.98	0.44
7:GC:454:PHE:HZ	7:GC:592:ILE:HD12	1.81	0.44
8:GD:215:LEU:HA	8:GD:240:ALA:HB1	1.99	0.44
7:GE:309:LEU:HD11	7:GE:360:VAL:HG23	1.99	0.44
7:GE:510:THR:HB	7:GE:632:VAL:HG11	1.98	0.44
8:GH:163:MET:HE3	8:GH:164:PRO:HD2	1.98	0.44
8:GH:192:VAL:HG21	7:GI:422:LEU:HD11	1.99	0.44
7:GI:176:ARG:HE	7:GI:180:ARG:HH12	1.64	0.44
7:GI:515:SER:HA	7:GI:569:THR:HB	1.98	0.44
7:GI:620:HIS:HB2	7:GI:643:SER:HB3	1.99	0.44
9:HA:858:LEU:HD23	9:HA:858:LEU:HA	1.78	0.44
9:HB:526:VAL:HB	9:HB:579:LEU:HB2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:890:GLY:HA2	10:IB:893:PHE:CZ	2.53	0.44
10:IB:1109:CYS:HA	10:IB:1112:LEU:HD12	1.99	0.44
11:JC:1004:ARG:HH12	11:JC:1152:HIS:CG	2.36	0.44
12:KG:521:PRO:O	12:KG:522:ARG:HD3	2.17	0.44
13:LA:513:LEU:HD21	13:LB:514:TYR:CE1	2.53	0.44
13:LI:395:ILE:HD12	13:LJ:398:ARG:HH22	1.80	0.44
14:MI:262:PRO:HA	14:MI:265:SER:HB3	1.98	0.44
15:NB:605:LEU:HB2	15:NB:923:ASP:HB2	2.00	0.44
15:NB:937:MET:HA	15:NB:940:TYR:HB3	1.99	0.44
15:ND:922:LEU:HD11	15:ND:1105:HIS:CD2	2.52	0.44
3:BC:790:ASN:HB3	3:BC:811:ILE:HG22	1.99	0.44
3:BC:795:GLU:HB2	3:BC:816:LYS:HE3	1.99	0.44
3:CA:687:GLU:HA	3:CA:690:MET:HE3	1.99	0.44
3:CB:891:ILE:HA	3:CB:894:LYS:HE2	1.98	0.44
3:CL:1152:LEU:HD21	10:IC:377:PRO:HG3	1.99	0.44
4:DD:359:GLU:HA	4:DD:362:LYS:NZ	2.32	0.44
6:FC:1745:SER:HB3	6:FC:1792:TYR:H	1.82	0.44
6:FC:2066:GLU:HG3	6:FC:2067:MET:N	2.32	0.44
6:FD:962:PHE:HE2	6:FD:965:TRP:HB2	1.78	0.44
6:FE:886:THR:HA	6:FE:900:ALA:HB2	1.98	0.44
6:FE:1079:MET:HG2	6:FE:1102:TYR:HD2	1.82	0.44
6:FF:1203:ARG:HA	6:FF:1203:ARG:HD2	1.67	0.44
7:GA:536:THR:CA	9:HB:553:TYR:H	2.30	0.44
7:GG:275:LYS:HB3	7:GG:279:ARG:NH2	2.32	0.44
8:GH:367:CYS:HB3	8:GH:394:PHE:CE1	2.52	0.44
8:GH:676:TRP:HB2	8:GH:735:LEU:HD13	2.00	0.44
7:GI:365:ALA:HB1	7:GI:388:PRO:HA	1.99	0.44
7:GI:368:PHE:HZ	7:GI:439:ALA:HB1	1.83	0.44
7:GK:438:LYS:HE2	7:GK:464:LEU:HG	1.98	0.44
9:HB:800:VAL:O	13:LE:533:ALA:HA	2.16	0.44
10:IB:991:MET:HE1	10:IB:1108:LEU:HD11	1.99	0.44
10:IC:167:LYS:HB3	10:IC:167:LYS:HE2	1.81	0.44
11:JA:1130:LEU:O	11:JA:1134:GLU:HG2	2.18	0.44
11:JA:1414:ALA:HB2	11:JA:1504:ARG:HE	1.82	0.44
11:JC:442:ARG:HA	11:JC:445:GLN:HB3	1.99	0.44
11:JC:1591:HIS:CE1	11:JC:1593:VAL:HG13	2.52	0.44
12:KA:581:GLY:HA2	12:KA:654:ILE:HG22	2.00	0.44
12:KA:668:ILE:HB	12:KA:678:ALA:HB3	1.99	0.44
12:KC:405:PRO:HD3	12:KC:489:MET:HG3	1.99	0.44
12:KC:579:LEU:HD21	12:KC:726:ASP:OD2	2.18	0.44
12:KF:270:LYS:HD2	12:KF:270:LYS:HA	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LO:384:LEU:HB3	13:LP:384:LEU:HD22	1.98	0.44
14:MB:227:GLN:HA	14:MB:230:VAL:HG12	1.98	0.44
14:MG:83:TYR:HB3	14:MG:87:LEU:HD23	1.99	0.44
14:MJ:246:ASN:O	14:MJ:249:GLU:HB2	2.17	0.44
15:NB:698:PRO:HG2	15:NB:890:ARG:O	2.18	0.44
15:NB:1332:MET:HA	15:NB:1335:TYR:HD2	1.81	0.44
15:NC:545:VAL:HG23	15:NC:1193:VAL:HG23	1.98	0.44
15:NC:952:TRP:HZ2	15:NC:1177:LEU:HD13	1.82	0.44
15:ND:1508:PHE:O	15:ND:1512:MET:HG3	2.18	0.44
1:AD:243:VAL:HG12	10:IB:738:PRO:HG3	1.98	0.44
1:AE:728:VAL:HA	1:AE:734:MET:HG2	1.99	0.44
3:BA:785:ARG:HD2	3:BA:804:ARG:HH12	1.83	0.44
3:BB:787:ILE:HG12	3:BB:810:PRO:HB2	1.99	0.44
3:CC:830:CYS:HB2	3:CC:839:ALA:HB2	2.00	0.44
5:EA:4406:MET:N	5:EA:4406:MET:SD	2.91	0.44
5:EA:4817:LEU:HD23	5:EA:4817:LEU:H	1.82	0.44
5:EB:4665:LEU:HD23	5:EB:4665:LEU:HA	1.82	0.44
5:EC:4416:PHE:HZ	5:EC:4723:SER:HA	1.83	0.44
6:FE:822:GLY:O	6:FE:824:TYR:N	2.50	0.44
6:FE:1295:ALA:HB3	6:FE:1392:LYS:HB3	2.00	0.44
6:FF:1208:ALA:HB3	6:FF:1286:LEU:HD22	1.98	0.44
7:GI:322:GLY:HA3	7:GI:581:ARG:HD2	1.99	0.44
8:GJ:300:ARG:HD2	8:GJ:419:PHE:HE1	1.81	0.44
8:GL:75:GLN:HG3	8:GL:86:ALA:HA	1.98	0.44
9:HA:400:ALA:HA	9:HA:402:ARG:NH1	2.33	0.44
10:IA:886:LEU:HD12	16:OA:1040:PHE:HE1	1.82	0.44
10:IA:897:ARG:HB2	10:IA:903:HIS:HA	1.99	0.44
10:IA:1221:THR:H	10:IA:1224:HIS:HB2	1.82	0.44
10:IB:1221:THR:H	10:IB:1224:HIS:HB2	1.82	0.44
10:IC:897:ARG:HD2	10:IC:903:HIS:HA	1.98	0.44
11:JA:756:SER:HB3	11:JA:1491:ALA:HA	2.00	0.44
11:JA:843:LEU:HD21	11:JA:916:GLU:HB2	1.99	0.44
11:JB:1667:THR:HG23	11:JB:1671:MET:HE3	1.98	0.44
11:JC:874:VAL:O	11:JC:875:LEU:HD12	2.17	0.44
12:KA:524:PHE:HZ	12:KA:704:PRO:HD2	1.82	0.44
12:KB:352:LYS:HE3	12:KB:386:LEU:HA	2.00	0.44
15:NA:685:PHE:CE2	15:NA:689:ASN:HA	2.53	0.44
15:NB:702:LEU:HD12	15:NB:703:GLU:HB3	1.99	0.44
1:AH:666:LEU:HD23	1:AH:720:LEU:HD13	2.00	0.44
1:AI:829:VAL:HG11	1:AI:989:LEU:HB3	2.00	0.44
2:AJ:160:ARG:HD2	2:AJ:160:ARG:HA	1.78	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:1031:THR:O	1:AL:1032:PHE:C	2.60	0.44
5:EA:3661:PHE:HD1	5:EA:3664:THR:H	1.66	0.44
5:EC:4094:LEU:HD13	5:EC:4094:LEU:HA	1.73	0.44
5:EC:4167:ASP:HB3	5:EC:4170:LYS:HG2	2.00	0.44
6:FA:1764:ILE:HG12	6:FA:1767:ARG:HH21	1.82	0.44
6:FD:1094:SER:O	6:FD:1095:LEU:C	2.60	0.44
6:FD:1225:ILE:HG23	6:FD:1231:ARG:HD3	1.99	0.44
6:FD:1242:GLN:HB3	6:FD:1243:PRO:HD2	2.00	0.44
6:FE:1095:LEU:HD13	6:FE:1095:LEU:HA	1.79	0.44
6:FF:854:TRP:CD2	6:FF:860:PRO:HD3	2.53	0.44
6:FF:1185:VAL:O	6:FF:1186:TRP:C	2.61	0.44
6:FF:1390:ALA:HA	6:FF:1416:GLN:HG2	1.99	0.44
8:GB:138:LEU:HB2	8:GB:171:ILE:HD12	1.99	0.44
8:GB:300:ARG:HH11	8:GB:467:ALA:HB3	1.81	0.44
8:GD:756:ALA:HB3	8:GJ:333:LYS:HD2	1.98	0.44
8:GF:56:CYS:O	8:GF:57:ARG:HD3	2.17	0.44
7:GI:230:ARG:HE	7:GI:235:ARG:HB3	1.81	0.44
8:GJ:183:LEU:HA	8:GJ:254:LYS:HD2	1.99	0.44
8:GJ:692:MET:HA	8:GJ:693:PRO:HD3	1.87	0.44
8:GL:638:LEU:HD22	8:GL:654:LEU:HD23	2.00	0.44
10:IB:362:HIS:HD2	10:IB:429:ARG:HH22	1.65	0.44
11:JB:2094:ILE:HD11	11:JB:2110:LEU:HB2	1.99	0.44
11:JB:2254:LEU:HA	11:JB:2254:LEU:HD23	1.80	0.44
12:KA:591:ARG:HB2	12:KA:709:VAL:HB	1.98	0.44
12:KB:370:LEU:HD22	12:KB:377:LEU:HD21	2.00	0.44
12:KB:531:GLN:HE22	12:KB:551:SER:H	1.64	0.44
12:KC:321:GLU:HA	12:KC:324:ARG:HB3	1.99	0.44
12:KC:526:TRP:HB3	12:KC:545:LEU:HD13	1.99	0.44
12:KF:521:PRO:HD3	12:KF:540:LEU:HD23	1.99	0.44
13:LB:376:ARG:O	13:LB:380:MET:HG3	2.17	0.44
15:NA:622:THR:HG23	15:NA:650:ARG:HH12	1.81	0.44
15:NA:843:ASN:HB3	15:NA:845:LEU:HD23	1.98	0.44
15:NA:1456:PHE:HE2	15:NA:1461:TYR:HB2	1.82	0.44
15:NB:564:ARG:HH22	15:NB:622:THR:HB	1.82	0.44
15:NB:591:TRP:HB3	15:NB:592:LEU:HD12	2.00	0.44
15:NC:891:TRP:HA	15:NC:1152:GLU:C	2.43	0.44
16:OA:743:PRO:HD2	18:QD:89:ARG:HH12	1.83	0.44
16:OB:263:ALA:HB1	16:OB:267:GLU:HB2	1.99	0.44
16:OC:263:ALA:HB1	16:OC:267:GLU:HB2	2.00	0.44
19:RA:34:PHE:HA	19:RA:37:ILE:HG12	1.99	0.44
1:AA:915:TRP:CE2	13:LK:359:HIS:HB2	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:171:PHE:HB2	1:AD:185:ARG:HH21	1.82	0.44
1:AE:715:LEU:HD12	1:AE:715:LEU:HA	1.89	0.44
2:AF:428:ARG:HH21	2:AF:432:GLU:CD	2.25	0.44
2:AF:502:LEU:HG	2:AF:506:LEU:HD12	1.98	0.44
2:AJ:44:LEU:HD23	2:AJ:285:PHE:HB3	1.99	0.44
2:AK:147:LEU:HA	2:AK:150:ALA:HB3	1.99	0.44
2:AK:190:LEU:HD11	2:AK:195:ASP:HA	2.00	0.44
2:AK:509:ALA:HB1	1:AL:231:ILE:HD11	1.99	0.44
3:BB:706:GLU:OE1	10:IB:1378:GLN:HG2	2.18	0.44
3:CB:775:ASP:HA	3:CB:778:GLN:HB2	1.99	0.44
3:CI:1237:VAL:HG21	3:CI:4468:LYS:HG2	2.00	0.44
3:CI:4473:VAL:HG23	3:CI:4474:GLU:H	1.82	0.44
3:CJ:1258:PRO:HA	3:CJ:1261:TYR:HB2	1.98	0.44
4:DA:16:LEU:HD11	4:DA:161:LEU:HD23	2.00	0.44
4:DC:64:LEU:HD23	4:DC:64:LEU:HA	1.87	0.44
4:DC:119:LEU:HA	4:DC:122:ILE:HD12	1.99	0.44
5:EA:4154:LEU:HD22	5:EA:4174:ILE:HD11	1.98	0.44
5:EC:3841:GLN:HE22	11:JC:1045:THR:HG21	1.81	0.44
6:FC:2101:LEU:HD22	6:FC:2104:GLN:HE21	1.82	0.44
6:FE:1089:ARG:O	6:FE:1090:LEU:C	2.61	0.44
6:FE:1389:ARG:HE	6:FE:1389:ARG:HB3	1.53	0.44
7:GA:193:GLN:HA	7:GA:196:LEU:HD12	2.00	0.44
7:GG:906:VAL:HG22	7:GG:932:GLY:HA2	2.00	0.44
8:GH:560:TRP:CZ2	8:GH:564:LYS:HD2	2.53	0.44
8:GJ:639:LEU:HB3	8:GJ:649:PRO:HB2	2.00	0.44
7:GK:185:ARG:HG2	7:GK:697:PRO:HG2	2.00	0.44
7:GK:764:LEU:HD13	7:GK:870:ARG:HD3	1.98	0.44
10:IA:315:PHE:HZ	10:IA:536:ARG:HH21	1.66	0.44
10:IA:551:ASN:ND2	10:IA:803:ARG:HH21	2.14	0.44
11:JA:750:ALA:O	11:JA:754:ARG:HG2	2.18	0.44
11:JA:825:LEU:HD12	11:JA:825:LEU:HA	1.85	0.44
11:JC:195:LEU:HD12	11:JC:1036:LEU:HG	1.99	0.44
11:JC:489:VAL:HG22	11:JC:490:THR:H	1.83	0.44
12:KC:379:SER:HA	12:KC:720:LEU:HB3	1.98	0.44
12:KC:523:VAL:HG23	12:KC:525:PRO:HG3	1.99	0.44
12:KE:479:ALA:HA	12:KE:482:ARG:HG2	1.98	0.44
15:NB:683:ALA:HB3	15:NB:915:VAL:HA	2.00	0.44
15:NB:721:PRO:HD3	15:NB:762:GLN:HE21	1.81	0.44
15:NC:565:TRP:HZ2	16:OB:1039:ILE:HA	1.82	0.44
15:NC:666:ILE:HA	15:NC:724:ASN:HB2	1.99	0.44
15:ND:626:ARG:HD3	15:ND:690:TYR:HA	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:OB:1047:GLY:HA2	16:OB:1053:THR:HG22	2.00	0.44
19:RD:38:ASP:HB3	19:RD:41:GLY:H	1.82	0.44
20:SC:11:ALA:HA	20:SC:14:LYS:HD3	1.99	0.44
2:AC:558:ARG:HA	11:JA:1116:ARG:NH2	2.33	0.44
1:AD:41:ILE:HG22	1:AD:47:LEU:HG	2.00	0.44
1:AE:419:GLU:HB3	16:OC:76:PHE:HD2	1.83	0.44
2:AF:507:PRO:HG3	3:BC:752:PRO:HD3	1.99	0.44
1:AI:274:ARG:HG3	1:AI:275:HIS:H	1.83	0.44
1:AL:38:VAL:HG23	1:AL:39:SER:H	1.83	0.44
3:BB:845:LYS:HA	3:BB:848:ILE:HG22	1.99	0.44
3:CI:1186:LEU:HD21	10:IA:1423:PRO:HG3	2.00	0.44
4:DD:319:LYS:HA	4:DD:324:VAL:HG22	1.98	0.44
4:DE:9:PHE:CD2	4:DE:12:LEU:HD12	2.53	0.44
4:DF:34:ASP:HB3	4:DF:104:GLU:OE2	2.18	0.44
5:EA:4049:ALA:HA	6:FC:1905:GLN:HG2	2.00	0.44
5:EB:4653:GLU:HB3	5:EB:4654:ASP:H	1.66	0.44
5:EC:3651:ALA:H	9:HA:499:ARG:HG2	1.83	0.44
5:EC:3860:ALA:HA	5:EC:4002:ARG:HH12	1.82	0.44
5:EC:4403:LEU:HD23	5:EC:4403:LEU:HA	1.82	0.44
6:FB:2062:LEU:HD13	6:FB:2062:LEU:HA	1.76	0.44
6:FC:1828:VAL:HG22	6:FC:1838:VAL:HG13	1.98	0.44
6:FD:1027:LEU:O	6:FD:1028:LYS:C	2.60	0.44
6:FD:1098:VAL:O	6:FD:1101:ALA:N	2.50	0.44
6:FE:1016:PRO:HG2	6:FE:1017:VAL:HG12	1.99	0.44
6:FF:832:GLY:HA3	6:FF:844:ALA:HB2	1.99	0.44
7:GA:424:ARG:HD2	7:GA:424:ARG:HA	1.85	0.44
7:GC:423:TRP:HB3	7:GC:426:ASN:ND2	2.32	0.44
7:GC:764:LEU:HD21	7:GC:767:LEU:HD11	2.00	0.44
8:GD:59:SER:HA	14:MD:138:LEU:HD21	2.00	0.44
8:GD:192:VAL:HG22	7:GE:382:PRO:HG2	1.98	0.44
7:GE:524:SER:HB3	7:GE:555:PRO:HD3	1.99	0.44
8:GF:321:LEU:HD11	13:LA:415:GLU:HG3	1.98	0.44
8:GF:380:MET:O	8:GF:384:THR:HG22	2.17	0.44
7:GG:535:PRO:HB2	9:HA:553:TYR:N	2.32	0.44
8:GH:192:VAL:HG22	7:GI:381:ARG:HH12	1.81	0.44
8:GL:423:ILE:HG12	8:GL:500:THR:HG23	2.00	0.44
9:HA:754:LEU:HD21	9:HA:840:HIS:HB2	2.00	0.44
9:HB:566:PRO:HB3	9:HB:569:ARG:HH22	1.83	0.44
9:HB:762:HIS:O	9:HB:763:GLN:C	2.59	0.44
10:IC:208:PHE:HB2	10:IC:239:LEU:HD13	2.00	0.44
11:JB:57:GLU:HB3	11:JB:90:ARG:HE	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:782:VAL:HG21	11:JB:900:PRO:HB2	1.99	0.44
11:JC:1554:LEU:HD23	11:JC:1554:LEU:HA	1.86	0.44
11:JC:2250:LEU:HD12	11:JC:2251:PRO:HD2	2.00	0.44
13:LE:482:LEU:HD13	13:LF:482:LEU:HD22	2.00	0.44
13:LI:391:ALA:O	13:LI:395:ILE:HG12	2.18	0.44
15:NA:931:TRP:CD1	15:NA:934:LEU:HB2	2.53	0.44
15:NA:966:VAL:HA	15:NA:1462:GLN:NE2	2.32	0.44
15:NB:808:ILE:HA	15:NB:811:GLU:HB2	2.00	0.44
15:NC:1387:VAL:HA	15:NC:1391:LEU:HD23	1.98	0.44
15:ND:895:GLY:HA3	15:ND:1152:GLU:HG3	2.00	0.44
19:RA:58:VAL:HG12	19:RA:60:PHE:H	1.82	0.44
1:AA:381:ARG:HD2	1:AA:381:ARG:HA	1.83	0.44
2:AC:49:HIS:CD2	2:AC:51:ALA:H	2.35	0.44
1:AD:266:HIS:HA	1:AD:272:LEU:HB3	2.00	0.44
1:AI:715:LEU:HB2	13:LC:364:ASN:ND2	2.33	0.44
1:AI:715:LEU:HB2	13:LC:364:ASN:HD21	1.82	0.44
2:AK:66:ARG:NH1	2:AK:173:ARG:HD3	2.33	0.44
3:CB:827:ALA:HB1	3:CB:843:TYR:CE1	2.53	0.44
3:CI:1219:VAL:HB	3:CI:1254:MET:HE3	1.99	0.44
5:EA:3300:LEU:HD13	5:EA:4160:LEU:HD12	2.00	0.44
5:EC:3651:ALA:O	9:HA:499:ARG:HD3	2.18	0.44
5:EC:4089:HIS:CG	5:EC:4090:CYS:H	2.35	0.44
6:FE:837:ALA:O	6:FE:839:GLY:N	2.51	0.44
6:FE:964:LEU:HB2	6:FE:965:TRP:H	1.62	0.44
6:FF:1011:TYR:O	6:FF:1012:PRO:C	2.60	0.44
7:GA:676:ALA:HB3	7:GA:692:HIS:HB2	1.99	0.44
7:GC:205:ARG:HD2	7:GC:828:PRO:HB3	2.00	0.44
8:GF:138:LEU:HD13	8:GF:156:LEU:HD22	2.00	0.44
8:GJ:138:LEU:HD13	8:GJ:156:LEU:HD22	2.00	0.44
8:GL:74:LYS:HG2	8:GL:95:ILE:HG21	2.00	0.44
9:HB:403:ASP:HA	9:HB:406:ALA:HB3	2.00	0.44
9:HD:868:LEU:HD22	9:HD:868:LEU:HA	1.68	0.44
10:IA:991:MET:HE1	10:IA:1108:LEU:HD11	2.00	0.44
10:IC:208:PHE:HB3	10:IC:239:LEU:HB2	2.00	0.44
11:JA:437:LEU:HD11	11:JA:1461:PHE:HB3	1.99	0.44
11:JB:1742:MET:HE2	11:JB:1791:LEU:HD22	2.00	0.44
11:JB:1968:ARG:HH22	11:JB:1971:TYR:HB3	1.83	0.44
11:JC:1523:ARG:HH11	11:JC:1524:PHE:HE2	1.66	0.44
12:KB:228:GLU:HB2	12:KB:230:GLN:HG2	2.00	0.44
12:KE:531:GLN:HG3	12:KE:566:ALA:HB1	2.00	0.44
12:KG:565:TRP:CE3	12:KG:709:VAL:HG23	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NA:808:ILE:HG22	15:NA:878:ILE:HG21	1.98	0.44
15:NC:1325:ALA:HB3	15:NC:1328:VAL:HB	1.99	0.44
16:OA:742:PHE:HA	18:QD:89:ARG:NH1	2.31	0.44
19:RA:127:LEU:HB3	19:RA:132:LEU:HD11	1.98	0.44
19:RB:51:MET:HE2	19:RB:67:VAL:HG11	2.00	0.44
1:AA:893:ARG:CZ	1:AA:894:SER:HB3	2.47	0.44
2:AB:72:PHE:HB3	2:AB:164:TYR:HD2	1.83	0.44
1:AE:338:MET:HA	1:AE:341:GLN:HG3	1.99	0.44
2:AF:361:GLU:HG3	2:AF:373:ARG:HB3	1.99	0.44
2:AF:501:TYR:HD2	2:AF:502:LEU:HD12	1.83	0.44
3:CJ:1121:ARG:CZ	3:CJ:1131:LEU:HD22	2.48	0.44
3:CL:4504:ILE:HD12	3:CL:4524:LEU:HD21	1.99	0.44
4:DA:12:LEU:HB3	4:DA:164:PHE:CZ	2.53	0.44
4:DB:162:VAL:O	4:DB:166:VAL:HG23	2.18	0.44
4:DC:181:ILE:HG22	4:DC:182:LEU:HG	2.00	0.44
4:DC:329:ARG:HB3	4:DC:333:LYS:NZ	2.33	0.44
5:EA:3596:TRP:CD1	5:EA:3607:ARG:HG3	2.53	0.44
5:EA:4230:VAL:HA	5:EA:4233:TYR:HB3	2.00	0.44
5:EC:4221:ALA:HB2	5:EC:4229:MET:HE1	1.99	0.44
5:EC:4886:LYS:HB2	5:EC:4887:GLY:H	1.65	0.44
6:FD:1238:ARG:HA	6:FD:1238:ARG:HD3	1.67	0.44
6:FD:1441:ILE:O	6:FD:1442:GLU:C	2.59	0.44
6:FE:907:ASN:HD22	6:FE:907:ASN:HA	1.71	0.44
6:FE:1075:VAL:HG13	6:FE:1105:ARG:HB2	2.00	0.44
6:FE:1231:ARG:HB3	6:FE:1270:LEU:HD21	1.99	0.44
6:FE:1294:LEU:HD22	6:FE:1294:LEU:HA	1.86	0.44
6:FE:1443:GLY:C	6:FE:1445:SER:H	2.26	0.44
6:FF:917:TRP:CG	6:FF:918:GLN:N	2.85	0.44
6:FF:1219:GLU:H	6:FF:1219:GLU:HG2	1.42	0.44
7:GC:807:ARG:HB3	7:GC:812:VAL:HG21	1.98	0.44
7:GE:715:THR:HG21	7:GE:796:PHE:HB3	2.00	0.44
7:GE:850:GLY:HA3	7:GE:934:ARG:HE	1.83	0.44
7:GG:308:TYR:CE1	7:GG:450:LYS:HD3	2.53	0.44
7:GG:612:ARG:HB2	7:GG:662:VAL:HG22	2.00	0.44
7:GI:780:ASN:HD22	7:GI:788:GLU:HG2	1.82	0.44
7:GK:543:LYS:HD3	9:HC:661:HIS:CD2	2.52	0.44
7:GK:604:ALA:HB1	7:GK:678:LEU:HD11	2.00	0.44
8:GL:132:PRO:HD3	8:GL:236:LEU:HD22	2.00	0.44
9:HA:852:LYS:HA	9:HA:852:LYS:HD3	1.73	0.44
9:HB:528:PRO:HB3	9:HB:603:HIS:CE1	2.52	0.44
9:HC:496:GLU:HG3	9:HC:499:ARG:HD2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IA:1003:VAL:HB	10:IA:1043:PHE:HB2	2.00	0.44
10:IC:368:PRO:HD3	10:IC:388:CYS:HB2	2.00	0.44
11:JA:1499:HIS:CE1	11:JA:1501:LEU:HD23	2.53	0.44
11:JB:1372:PRO:HA	11:JB:1375:TYR:HB3	1.99	0.44
11:JC:746:VAL:HA	11:JC:749:LYS:HG2	1.99	0.44
12:KB:520:LYS:HD2	12:KB:521:PRO:HD2	1.99	0.44
12:KC:319:TYR:CE2	12:KC:353:ALA:HB1	2.53	0.44
12:KG:375:TYR:HE1	12:KG:719:GLU:HA	1.83	0.44
12:KG:525:PRO:HA	12:KG:542:PRO:HG3	1.99	0.44
13:LL:376:ARG:HA	13:LL:379:LYS:HE2	1.99	0.44
14:MD:81:ARG:HG3	14:MD:83:TYR:HD1	1.83	0.44
15:NA:694:MET:HE3	15:NA:694:MET:HB2	1.87	0.44
15:NB:726:CYS:HB3	15:NB:803:LEU:HD12	2.00	0.44
15:NB:745:THR:HB	15:NB:858:ILE:HG13	1.99	0.44
15:NC:528:ARG:HH22	15:NC:577:PRO:HG2	1.82	0.44
15:NC:600:LEU:HD11	15:NC:945:PHE:HB3	2.00	0.44
15:ND:866:LEU:HD22	15:ND:878:ILE:HG12	2.00	0.44
17:PB:124:ILE:HG23	17:PB:128:GLU:HB3	2.00	0.44
18:QC:52:LYS:HD2	18:QC:75:PHE:HE2	1.83	0.44
19:RC:58:VAL:HG22	19:RC:60:PHE:HD2	1.83	0.44
2:AB:327:ILE:HD13	1:AI:271:MET:HE2	2.00	0.43
2:AC:45:LEU:HD23	2:AC:286:GLU:HB2	2.00	0.43
2:AC:438:VAL:HG22	1:AD:460:VAL:HG21	2.00	0.43
2:AC:542:ASP:HA	5:EA:4627:PRO:HB3	1.99	0.43
1:AE:749:PRO:HB2	1:AE:787:ARG:HD2	2.00	0.43
2:AG:188:PHE:HD1	2:AG:190:LEU:H	1.66	0.43
2:AG:355:HIS:CE1	2:AG:375:CYS:HB3	2.53	0.43
2:AG:528:LEU:HD22	1:AH:91:ILE:HB	1.99	0.43
1:AH:212:ARG:HH12	11:JC:1338:SER:HA	1.82	0.43
2:AJ:319:LEU:HD13	2:AJ:324:ASP:HA	1.98	0.43
1:AL:993:ARG:HD3	1:AL:993:ARG:HA	1.70	0.43
3:BA:694:ARG:HD2	17:PA:290:PHE:CE1	2.50	0.43
3:BC:832:LEU:HD22	16:OC:164:THR:HG23	2.00	0.43
4:DA:172:ARG:HH12	4:DD:190:PRO:HD3	1.83	0.43
4:DF:16:LEU:HD13	4:DF:160:PHE:HD2	1.82	0.43
5:EA:3277:PHE:HE1	5:EA:3447:TYR:HD1	1.65	0.43
5:EB:3737:LEU:HD11	5:EB:3813:VAL:HG21	2.00	0.43
5:EB:4011:VAL:HB	5:EB:4166:SER:HB2	1.99	0.43
5:EB:4374:GLU:HA	5:EB:4379:THR:HG21	2.00	0.43
5:EB:4882:ARG:HH12	5:EB:4888:TRP:HE3	1.65	0.43
5:EC:4849:TYR:HB2	15:ND:1319:LEU:HD21	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FD:803:ARG:HH11	6:FD:905:GLU:HB3	1.82	0.43
6:FD:837:ALA:HA	12:KA:640:ASP:OD2	2.18	0.43
6:FD:1014:LYS:HB2	6:FD:1014:LYS:HE2	1.41	0.43
6:FD:1267:GLN:HB3	6:FD:1267:GLN:HE21	1.61	0.43
6:FF:924:LEU:HB3	6:FF:1092:PRO:HD2	2.00	0.43
7:GE:448:GLY:HA2	7:GE:514:VAL:HG22	2.00	0.43
8:GF:417:MET:HG2	8:GF:469:ASP:HB3	2.00	0.43
7:GK:441:LEU:HD13	7:GK:509:LEU:HD23	2.00	0.43
7:GK:855:ARG:HA	7:GK:855:ARG:HD3	1.84	0.43
8:GL:328:HIS:CG	8:GL:607:THR:HB	2.53	0.43
8:GL:426:LEU:HD13	8:GL:499:GLN:HE22	1.83	0.43
9:HA:604:SER:HB2	9:HA:619:PRO:HB2	1.99	0.43
9:HB:633:ASN:HA	9:HB:720:LYS:HE2	1.99	0.43
9:HB:759:GLU:O	9:HB:760:LYS:C	2.61	0.43
10:IB:884:TYR:HB2	10:IB:942:PHE:HE1	1.82	0.43
11:JA:882:ALA:HA	11:JA:891:VAL:HG12	2.00	0.43
11:JA:884:ASP:HB2	11:JA:1414:ALA:HB3	2.00	0.43
11:JA:2076:ASN:HD21	11:JA:2255:ARG:NH1	2.15	0.43
11:JC:164:MET:HA	11:JC:165:GLU:HA	1.82	0.43
11:JC:902:LEU:HB3	11:JC:935:TRP:CD1	2.53	0.43
12:KA:572:SER:HA	12:KA:703:TRP:CD1	2.53	0.43
12:KB:501:LEU:HD22	12:KB:502:LEU:HD23	2.00	0.43
12:KB:579:LEU:HD12	12:KB:656:ARG:HB2	2.00	0.43
12:KC:385:GLU:H	12:KC:385:GLU:HG2	1.70	0.43
12:KC:597:ALA:O	12:KC:703:TRP:HB2	2.18	0.43
12:KE:322:ALA:HA	12:KE:325:LEU:HD12	1.99	0.43
13:LO:381:LEU:O	13:LO:385:THR:HG23	2.18	0.43
15:NC:564:ARG:NH2	15:NC:622:THR:HB	2.33	0.43
16:OB:119:TRP:HB2	16:OB:149:ILE:HB	2.00	0.43
16:OC:1067:GLU:HG3	16:OC:1068:GLY:H	1.83	0.43
19:RA:71:LEU:HD23	19:RA:74:LEU:HD12	2.00	0.43
1:AA:236:PRO:HG2	1:AA:256:GLN:HG3	2.00	0.43
1:AA:238:CYS:HB3	1:AA:242:GLU:H	1.84	0.43
2:AC:296:ALA:H	1:AD:431:SER:HB2	1.83	0.43
1:AE:338:MET:HA	1:AE:341:GLN:HE21	1.83	0.43
2:AF:355:HIS:HA	2:AF:356:PRO:HD3	1.86	0.43
2:AG:19:VAL:HB	2:AG:47:ALA:HB3	2.00	0.43
1:AH:878:ARG:HH22	6:FB:2036:LEU:HD21	1.83	0.43
1:AI:636:LEU:HD11	7:GK:857:LEU:HD13	2.00	0.43
2:AK:178:GLU:CD	2:AK:179:ASP:H	2.25	0.43
3:CB:832:LEU:HA	17:PC:295:GLN:HE21	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DD:303:PHE:HB3	4:DD:354:TRP:HZ2	1.82	0.43
5:EA:3698:VAL:HG23	5:EA:3699:ASN:H	1.82	0.43
5:EA:4637:THR:HG22	5:EA:4708:LEU:HD13	1.99	0.43
5:EC:4405:ILE:HG22	5:EC:4406:MET:H	1.83	0.43
6:FA:2038:LEU:HD13	6:FA:2038:LEU:HA	1.73	0.43
6:FB:1580:ALA:HA	6:FB:1618:VAL:HG12	1.99	0.43
6:FC:1984:LYS:HA	6:FC:1984:LYS:HD2	1.65	0.43
6:FC:2088:MET:O	6:FC:2089:PRO:C	2.61	0.43
6:FD:809:ILE:HD11	6:FD:812:LEU:HD22	1.99	0.43
6:FD:1291:TYR:HD1	6:FD:1291:TYR:HA	1.75	0.43
6:FF:859:ASP:N	6:FF:859:ASP:OD2	2.51	0.43
6:FF:1300:LEU:O	6:FF:1302:ALA:N	2.50	0.43
6:FF:1390:ALA:O	6:FF:1391:TYR:C	2.62	0.43
7:GC:842:PRO:HA	7:GC:882:TYR:CD1	2.53	0.43
7:GC:843:LEU:HG	7:GC:846:LEU:HD11	2.01	0.43
8:GD:641:TYR:HB2	8:GD:664:ILE:HB	2.00	0.43
7:GE:323:LEU:HA	7:GE:579:PHE:HE2	1.83	0.43
8:GH:326:ARG:HH22	8:GH:376:GLU:N	2.17	0.43
7:GI:309:LEU:HD11	7:GI:440:ALA:HB1	2.00	0.43
8:GJ:276:MET:HE3	8:GJ:311:SER:HB3	2.01	0.43
7:GK:230:ARG:HD3	7:GK:235:ARG:NH2	2.33	0.43
7:GK:279:ARG:HG2	7:GK:280:PHE:HD1	1.82	0.43
10:IB:1070:ASP:HB3	10:IB:1077:LYS:HZ3	1.83	0.43
10:IB:1405:PRO:HG2	10:IB:1410:LEU:HD11	2.00	0.43
10:IC:698:GLN:HG3	16:OC:1081:ILE:HD11	1.99	0.43
10:IC:795:GLU:HG3	10:IC:805:LYS:NZ	2.33	0.43
11:JA:1803:ARG:HA	11:JA:1806:MET:HB2	1.99	0.43
11:JB:65:VAL:HG12	11:JB:121:ILE:HG12	2.00	0.43
11:JB:1584:LYS:HA	11:JB:1588:GLU:HA	1.99	0.43
12:KA:664:ILE:HD11	12:KA:700:LEU:HD13	2.00	0.43
12:KF:404:GLU:HA	12:KF:407:ILE:HB	2.00	0.43
12:KG:720:LEU:HD23	12:KG:720:LEU:HA	1.85	0.43
13:LL:378:GLU:HA	13:LL:381:LEU:HG	1.99	0.43
15:NB:613:GLN:HG3	15:NB:918:ALA:HB2	2.00	0.43
15:NB:702:LEU:HB3	15:NB:937:MET:SD	2.58	0.43
15:NB:922:LEU:HD23	15:NB:1394:LEU:HD22	2.00	0.43
15:ND:787:LEU:HD21	15:ND:896:ARG:HG3	1.99	0.43
17:PC:138:ARG:HG2	17:PC:142:TYR:CZ	2.53	0.43
19:RB:89:SER:HA	19:RB:90:PRO:HD3	1.90	0.43
1:AA:705:TRP:HE1	1:AA:1036:THR:HG23	1.83	0.43
1:AD:65:ILE:HD11	1:AD:222:LEU:HD22	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:261:CYS:HA	1:AD:264:ARG:HG2	1.99	0.43
1:AD:831:SER:HB3	1:AD:918:VAL:HG22	1.99	0.43
1:AE:131:ARG:HB2	1:AE:205:ARG:HH22	1.83	0.43
2:AF:259:VAL:HG23	2:AF:297:VAL:HB	1.99	0.43
2:AG:311:TRP:CD2	2:AG:345:MET:HG3	2.53	0.43
1:AH:231:ILE:HG22	10:IA:825:LEU:HD11	2.00	0.43
1:AH:282:HIS:CE1	10:IA:1359:ALA:HB2	2.53	0.43
1:AH:882:VAL:HG11	13:LJ:518:GLU:HG2	2.00	0.43
3:CE:1137:ALA:HA	10:IA:1184:ARG:HH21	1.83	0.43
3:CL:1156:GLU:HA	10:IC:398:ARG:HH12	1.83	0.43
4:DA:13:VAL:HG23	4:DA:97:LEU:HD13	2.00	0.43
5:EB:4717:ARG:NH1	5:EB:4720:LEU:HB2	2.33	0.43
5:EC:3395:TYR:HE2	5:EC:3607:ARG:HD3	1.81	0.43
5:EC:3787:GLU:HG2	5:EC:3790:ARG:NH1	2.33	0.43
5:EC:3798:LEU:HD11	5:EC:3813:VAL:HB	1.99	0.43
5:EC:4896:ARG:HH11	5:EC:4899:GLY:HA2	1.83	0.43
6:FA:1955:THR:HG21	9:HA:838:LYS:CA	2.48	0.43
6:FC:1683:LYS:HG3	6:FC:1690:TYR:CZ	2.53	0.43
6:FC:1907:ILE:HD11	6:FC:1912:PHE:HZ	1.84	0.43
6:FC:2018:ARG:HE	6:FC:2018:ARG:HB2	1.59	0.43
6:FD:1201:THR:O	6:FD:1202:PHE:C	2.61	0.43
6:FE:895:ILE:HG21	7:GE:967:PHE:CZ	2.52	0.43
6:FF:1213:VAL:HG12	6:FF:1231:ARG:HB2	2.00	0.43
6:FF:1392:LYS:HE3	6:FF:1392:LYS:HB3	1.82	0.43
7:GA:843:LEU:HD13	7:GA:935:VAL:HG13	2.00	0.43
8:GB:18:VAL:HG11	8:GB:527:ASP:HB3	2.01	0.43
8:GB:325:ILE:HD13	8:GB:371:GLN:HB2	2.00	0.43
8:GD:639:LEU:HD12	8:GD:649:PRO:HB2	2.00	0.43
7:GE:306:PRO:HG3	7:GE:342:GLY:HA3	2.00	0.43
7:GE:873:ALA:HA	7:GE:876:MET:HG2	2.00	0.43
8:GF:599:LEU:HA	8:GF:634:ILE:HD11	2.00	0.43
8:GH:182:GLU:HB3	8:GH:194:LYS:HB2	1.99	0.43
7:GI:890:MET:HE1	7:GI:951:MET:HB2	2.00	0.43
7:GK:576:TYR:HB3	7:GK:584:HIS:ND1	2.33	0.43
9:HB:779:PRO:O	9:HB:780:PHE:C	2.60	0.43
9:HD:761:CYS:HB3	9:HD:765:TRP:NE1	2.34	0.43
9:HD:762:HIS:O	9:HD:763:GLN:C	2.61	0.43
10:IB:618:ARG:HB2	10:IB:753:ARG:HA	1.99	0.43
10:IC:730:ARG:HB3	10:IC:739:ALA:HB2	2.00	0.43
11:JA:114:SER:HB3	11:JA:190:TRP:HH2	1.82	0.43
11:JB:1181:VAL:HG23	11:JB:1357:PHE:HD2	1.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LI:475:LEU:HD22	13:LJ:471:THR:HG22	2.01	0.43
14:MA:251:LEU:HD21	14:MB:250:ARG:HH21	1.83	0.43
14:ME:291:LEU:HD21	14:MF:290:ARG:NH1	2.33	0.43
14:MJ:308:GLU:HA	14:MJ:311:ILE:HG22	2.00	0.43
15:NA:881:LEU:HD22	15:NA:1131:LEU:HD21	2.00	0.43
15:NB:548:PRO:HG3	15:NB:551:ARG:HH21	1.82	0.43
15:NB:1525:ARG:HE	18:QC:60:ARG:NH1	2.16	0.43
15:NC:1094:LYS:HB3	15:NC:1098:LEU:HD13	2.00	0.43
15:NC:1498:ARG:NH1	20:SD:38:ARG:HB3	2.33	0.43
15:ND:1498:ARG:NH1	20:SB:44:PRO:HD3	2.33	0.43
16:OB:265:LEU:HB3	16:OB:266:GLN:H	1.66	0.43
19:RD:18:LYS:HB2	19:RD:105:MET:HB2	2.00	0.43
2:AB:160:ARG:HB3	5:EA:4624:SER:HB2	2.00	0.43
2:AB:501:TYR:CZ	2:AB:505:VAL:HG21	2.53	0.43
1:AH:993:ARG:HA	1:AH:993:ARG:HD3	1.74	0.43
1:AI:153:LEU:HB2	1:AI:182:ALA:HB2	1.99	0.43
1:AL:248:LEU:HD21	1:AL:277:ARG:HG2	1.99	0.43
1:AL:405:LEU:HD12	1:AL:405:LEU:HA	1.80	0.43
1:AL:906:LEU:HD11	1:AL:973:PHE:HE2	1.84	0.43
3:CF:1131:LEU:HB3	10:IB:1091:LEU:HD11	2.00	0.43
3:CG:1156:GLU:HG2	10:IC:411:MET:HE2	2.00	0.43
3:CI:1146:VAL:HG22	10:IA:381:HIS:HE1	1.83	0.43
4:DA:332:LEU:HB3	8:GF:411:SER:HB2	2.01	0.43
4:DC:395:MET:HA	14:MJ:320:ARG:HH12	1.82	0.43
4:DF:303:PHE:HB3	4:DF:354:TRP:HZ2	1.83	0.43
5:EA:4407:ASP:O	5:EA:4408:GLY:C	2.62	0.43
5:EB:3323:THR:HB	5:EB:3377:ALA:HB2	2.00	0.43
5:EB:4505:MET:HG3	5:EB:4699:PHE:CE1	2.54	0.43
5:EC:3821:PRO:HG2	5:EC:4242:PHE:CZ	2.53	0.43
6:FA:2072:ILE:HG21	9:HA:855:ARG:HG3	2.01	0.43
6:FC:1649:VAL:HG12	6:FC:1735:ILE:HD13	2.00	0.43
6:FC:2076:HIS:HE1	9:HB:857:ARG:HB3	1.82	0.43
6:FD:888:PRO:O	6:FD:889:SER:C	2.61	0.43
6:FD:965:TRP:CD1	6:FD:965:TRP:H	2.36	0.43
6:FD:1229:LYS:H	6:FD:1229:LYS:HG3	1.54	0.43
6:FE:850:CYS:HB3	6:FE:973:ILE:HG12	1.99	0.43
6:FE:864:LEU:HD11	6:FE:973:ILE:HD12	2.00	0.43
6:FE:992:PRO:CA	12:KB:230:GLN:O	2.58	0.43
6:FE:1251:ARG:HD3	6:FE:1252:MET:HE1	2.01	0.43
6:FE:1253:SER:O	6:FE:1254:GLY:C	2.60	0.43
6:FE:1389:ARG:O	6:FE:1390:ALA:C	2.61	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:962:PHE:CE2	6:FF:965:TRP:HB2	2.53	0.43
6:FF:1244:LEU:C	6:FF:1246:ILE:H	2.27	0.43
8:GH:326:ARG:HH22	8:GH:376:GLU:H	1.64	0.43
8:GJ:200:GLY:HA2	8:GJ:281:LEU:HD22	2.01	0.43
8:GL:171:ILE:HG23	8:GL:181:HIS:HB2	2.00	0.43
8:GL:499:GLN:HB2	8:GL:511:LEU:HD11	2.00	0.43
8:GL:777:LEU:HG	8:GL:781:MET:HE1	2.01	0.43
9:HA:564:ARG:HD2	9:HA:564:ARG:HA	1.78	0.43
9:HD:795:LEU:HD23	9:HD:795:LEU:HA	1.83	0.43
10:IA:830:VAL:HG22	11:JA:2040:GLN:HB2	1.99	0.43
10:IA:839:GLU:HA	10:IA:842:TYR:HD2	1.82	0.43
10:IA:1236:VAL:HG22	10:IA:1285:VAL:HG22	2.00	0.43
10:IA:1249:ALA:HB1	10:IA:1253:MET:HE2	2.01	0.43
10:IB:821:MET:HE1	10:IB:1251:VAL:HG21	2.00	0.43
10:IC:393:LEU:O	10:IC:397:VAL:HB	2.19	0.43
10:IC:455:LEU:HB3	10:IC:507:TYR:HE2	1.83	0.43
11:JA:2270:MET:HE2	11:JA:2275:PHE:HB2	1.99	0.43
12:KC:375:TYR:CD2	12:KC:725:ILE:HD13	2.54	0.43
13:LI:398:ARG:HA	13:LI:401:LEU:HB2	2.00	0.43
15:NC:884:LYS:HZ3	15:NC:1127:LEU:HD12	1.83	0.43
15:NC:1197:ARG:HA	15:NC:1386:HIS:ND1	2.33	0.43
18:QD:113:LYS:HE3	20:SD:22:LYS:HE2	1.99	0.43
1:AA:249:TYR:HE2	1:AA:284:PRO:HD2	1.83	0.43
2:AB:53:PRO:HA	2:AB:56:VAL:HG12	2.00	0.43
1:AE:424:PHE:CG	2:AF:35:MET:HG3	2.53	0.43
1:AE:660:ILE:HD13	1:AE:663:LEU:HD21	2.00	0.43
2:AF:63:THR:HG21	2:AF:170:GLY:HA3	2.01	0.43
1:AI:105:GLN:HG2	1:AI:109:ASN:HB3	1.99	0.43
1:AI:301:VAL:HG11	1:AI:335:ALA:HB2	1.99	0.43
2:AJ:203:ALA:HB1	2:AJ:266:ARG:HE	1.83	0.43
3:CC:812:MET:HB3	3:CC:814:VAL:HG22	2.00	0.43
3:CI:1229:HIS:HE2	3:CI:1260:VAL:HG13	1.82	0.43
4:DA:388:ARG:HA	4:DA:391:ILE:HG12	1.98	0.43
4:DE:97:LEU:HG	4:DE:99:VAL:HG23	2.00	0.43
4:DE:258:ASN:HA	4:DE:299:ARG:HD2	1.98	0.43
4:DF:318:GLY:HA2	4:DF:324:VAL:HG22	2.01	0.43
5:EB:4173:LYS:HA	5:EB:4176:THR:HG22	2.00	0.43
5:EC:4150:PHE:HD2	5:EC:4181:VAL:HG11	1.82	0.43
6:FC:1898:ILE:HB	6:FC:1912:PHE:HB2	2.00	0.43
6:FE:978:LYS:NZ	6:FE:984:THR:H	2.16	0.43
6:FE:1294:LEU:O	6:FE:1295:ALA:C	2.61	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:841:TYR:C	6:FF:841:TYR:CD2	2.95	0.43
7:GA:896:ARG:HG2	7:GA:958:GLN:HB3	2.00	0.43
8:GB:62:ILE:HG21	8:GB:111:TYR:HE2	1.82	0.43
8:GF:147:GLU:HG3	13:LA:423:GLN:HG3	2.00	0.43
8:GF:356:VAL:HG23	8:GF:357:ARG:HD2	1.99	0.43
7:GG:301:ARG:HE	7:GG:304:GLN:HG2	1.84	0.43
7:GG:619:ARG:HG3	7:GG:644:ILE:HG22	2.00	0.43
7:GG:749:LEU:HD23	7:GG:749:LEU:HA	1.81	0.43
7:GI:671:VAL:HG22	7:GI:697:PRO:HA	2.00	0.43
7:GI:870:ARG:HH21	7:GI:874:GLU:HG2	1.83	0.43
7:GI:912:LEU:HD12	7:GI:912:LEU:HA	1.75	0.43
7:GI:920:ALA:HB3	7:GI:955:VAL:HG11	2.01	0.43
7:GK:468:ARG:HH12	7:GK:494:LEU:HA	1.83	0.43
9:HD:774:LEU:O	13:LJ:526:LEU:HD23	2.19	0.43
9:HD:854:ASN:HA	9:HD:857:ARG:HE	1.84	0.43
10:IA:823:ASP:HB2	11:JA:2056:LEU:HD22	2.00	0.43
10:IB:185:LEU:HD21	10:IB:624:ARG:HG3	2.00	0.43
10:IC:1068:ARG:HH21	10:IC:1069:ARG:HG2	1.84	0.43
11:JA:459:GLU:HG2	11:JA:460:GLY:H	1.84	0.43
11:JA:841:VAL:HG13	11:JA:1424:ARG:HB3	2.01	0.43
11:JB:805:CYS:HB2	11:JB:895:LEU:HD22	1.99	0.43
11:JC:67:TYR:CE1	11:JC:106:LEU:HD23	2.53	0.43
12:KA:522:ARG:HD2	12:KA:522:ARG:HA	1.88	0.43
12:KE:590:GLY:HA3	12:KE:646:ARG:HG2	2.00	0.43
13:LE:480:GLN:HE21	14:MH:102:LYS:NZ	2.17	0.43
13:LJ:410:LYS:HB3	13:LJ:413:GLU:OE1	2.18	0.43
14:MF:218:LEU:HD21	14:MF:323:GLN:HB3	2.00	0.43
15:NA:1032:VAL:HG22	15:NA:1104:ARG:HB3	1.99	0.43
15:NB:884:LYS:HZ3	15:NB:1127:LEU:HG	1.83	0.43
15:NB:1147:MET:O	15:NB:1157:PRO:HA	2.19	0.43
19:RC:45:LEU:HD12	19:RC:91:VAL:HB	2.01	0.43
19:RD:22:ARG:HH12	19:RD:174:LEU:HB3	1.83	0.43
2:AF:374:LEU:HD11	5:EB:4439:GLU:HA	1.99	0.43
2:AG:5:VAL:HG12	2:AG:84:LEU:HD23	2.01	0.43
1:AI:249:TYR:HD1	1:AI:256:GLN:HG2	1.83	0.43
1:AI:269:THR:OG1	1:AI:271:MET:HB2	2.18	0.43
3:CG:1181:ARG:NH1	10:IC:452:LEU:HB2	2.33	0.43
3:CJ:1176:VAL:HG13	3:CJ:1194:VAL:HG13	2.00	0.43
5:EA:3223:TRP:HH2	5:EA:4182:LEU:HD21	1.83	0.43
5:EA:3332:ALA:HB3	5:EA:3766:LEU:HA	2.00	0.43
5:EA:4405:ILE:H	5:EA:4405:ILE:HG12	1.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:3240:TYR:O	5:EB:3242:LEU:HD12	2.18	0.43
5:EB:3524:LEU:HD21	5:EB:3559:VAL:HG11	1.99	0.43
5:EB:3700:PHE:HA	5:EB:3706:VAL:HG22	2.01	0.43
5:EC:4900:ARG:HD2	5:EC:4900:ARG:HA	1.79	0.43
6:FA:2098:TYR:CE1	9:HA:878:SER:HB2	2.52	0.43
6:FC:1675:LEU:HD12	6:FC:1696:HIS:HE2	1.84	0.43
6:FC:1857:LEU:HB3	6:FC:1919:PHE:HB3	2.00	0.43
6:FD:820:LYS:O	6:FD:821:ARG:NH1	2.52	0.43
6:FD:1298:LEU:O	6:FD:1299:ASN:C	2.61	0.43
6:FF:1098:VAL:O	6:FF:1099:ILE:C	2.62	0.43
6:FF:1289:HIS:O	6:FF:1290:ILE:C	2.61	0.43
7:GA:843:LEU:HD21	7:GA:938:VAL:HG11	1.98	0.43
8:GD:574:ASP:HB2	8:GD:584:HIS:HB3	2.01	0.43
7:GE:450:LYS:HB3	7:GE:635:THR:HG21	2.00	0.43
8:GH:422:LYS:HD2	8:GH:464:GLN:HA	2.01	0.43
8:GH:781:MET:O	8:GH:785:ILE:HG13	2.18	0.43
7:GI:664:PRO:HD2	7:GI:669:ASP:HB2	2.00	0.43
7:GI:735:ARG:HG3	7:GI:801:LEU:HD11	1.99	0.43
9:HA:868:LEU:HA	9:HA:868:LEU:HD22	1.67	0.43
10:IA:806:ILE:HG21	10:IA:858:LEU:HD21	2.01	0.43
10:IC:313:PRO:HA	10:IC:314:PRO:HD3	1.82	0.43
10:IC:451:VAL:HG12	10:IC:503:LEU:HD13	2.01	0.43
11:JB:805:CYS:HB2	11:JB:895:LEU:HB3	2.01	0.43
11:JC:527:GLU:HB2	11:JC:531:ARG:HD3	2.00	0.43
11:JC:885:TYR:CD2	11:JC:886:LYS:HG2	2.53	0.43
11:JC:1541:TYR:HD1	11:JC:1545:HIS:HD2	1.66	0.43
12:KA:523:VAL:HG12	12:KA:524:PHE:HD1	1.83	0.43
12:KB:354:ALA:HA	12:KB:357:MET:HG2	1.99	0.43
12:KC:567:TRP:CD2	12:KC:627:PRO:HA	2.54	0.43
12:KG:499:ASP:HA	12:KG:500:PRO:HD3	1.90	0.43
13:LN:392:GLU:HA	13:LN:395:ILE:HD12	2.00	0.43
14:MA:203:CYS:HB2	14:MB:203:CYS:HB3	1.49	0.43
15:NA:926:ARG:HG3	15:NA:1111:ARG:HB2	2.00	0.43
15:NB:1422:VAL:HG23	15:NB:1423:LEU:H	1.82	0.43
15:NC:685:PHE:HB2	15:NC:914:ILE:HG12	1.99	0.43
15:NC:966:VAL:HG22	15:NC:1462:GLN:HE22	1.84	0.43
16:OC:119:TRP:CZ3	16:OC:121:PRO:HG3	2.53	0.43
16:OC:156:GLU:O	16:OC:160:LEU:HG	2.19	0.43
1:AA:632:LEU:HD12	7:GA:857:LEU:HD12	2.01	0.43
2:AC:89:ARG:HG3	2:AC:90:ARG:HG3	2.01	0.43
2:AC:330:GLN:HG2	2:AC:331:ASN:H	1.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:285:LEU:HD22	1:AE:297:MET:HB2	2.01	0.43
1:AE:315:LEU:HD12	1:AE:316:ILE:HB	2.01	0.43
1:AE:698:LEU:HA	1:AE:701:TYR:CE1	2.53	0.43
2:AG:540:PHE:HE2	5:EB:4818:ILE:HD11	1.83	0.43
3:CC:711:ARG:HH12	3:CC:756:GLU:HB2	1.84	0.43
3:CE:1138:ILE:HG22	10:IA:1184:ARG:HH22	1.83	0.43
3:CE:4456:PRO:HA	3:CE:4457:PRO:HD3	1.84	0.43
3:CJ:1111:LYS:HA	3:CJ:1111:LYS:HD2	1.87	0.43
4:DB:318:GLY:H	14:MF:243:LYS:HZ2	1.65	0.43
4:DD:172:ARG:O	4:DD:176:ILE:HG12	2.19	0.43
4:DD:349:SER:HB3	4:DD:351:VAL:HG23	2.01	0.43
5:EA:4021:ILE:HB	5:EA:4160:LEU:HD22	2.00	0.43
5:EA:4043:LYS:HD3	5:EA:4053:LEU:HD21	2.01	0.43
5:EA:4084:TYR:CE1	5:EA:4184:GLN:HG3	2.53	0.43
5:EC:3746:LYS:HA	5:EC:3831:LEU:HD21	2.00	0.43
6:FC:1974:VAL:HG23	6:FC:2036:LEU:HB3	2.00	0.43
6:FC:2048:GLU:OE2	9:HB:765:TRP:CD2	2.71	0.43
6:FD:1030:ILE:HD12	6:FD:1030:ILE:HA	1.75	0.43
6:FD:1205:ILE:HG22	6:FD:1260:LEU:HD13	2.01	0.43
6:FD:1270:LEU:HD22	6:FD:1270:LEU:HA	1.79	0.43
6:FD:1301:ALA:HA	6:FD:1430:PHE:CB	2.47	0.43
6:FD:1429:LEU:O	6:FD:1430:PHE:HB2	2.18	0.43
8:GB:133:PRO:HG2	8:GB:168:MET:HE2	2.00	0.43
7:GC:207:LEU:HD13	7:GC:599:THR:HG22	2.01	0.43
7:GC:809:VAL:HG12	7:GC:817:ARG:HH22	1.84	0.43
7:GE:169:ILE:O	7:GE:173:ASN:HB2	2.19	0.43
7:GE:271:ASP:HB3	7:GE:277:GLU:HA	2.01	0.43
7:GE:833:CYS:HA	7:GE:836:VAL:HG22	1.99	0.43
8:GF:431:PHE:HE1	8:GF:494:SER:HB3	1.83	0.43
8:GH:113:LEU:HD12	8:GH:113:LEU:HA	1.82	0.43
8:GL:664:ILE:HG21	8:GL:705:PRO:HG3	1.99	0.43
9:HB:861:TYR:HD1	9:HB:861:TYR:HA	1.69	0.43
9:HD:860:GLN:OE1	9:HD:860:GLN:HA	2.18	0.43
10:IA:1128:VAL:HG11	10:IA:1180:VAL:HG11	2.00	0.43
10:IB:300:LEU:HD23	10:IB:302:THR:H	1.83	0.43
10:IC:509:PRO:HB2	10:IC:550:TYR:CZ	2.54	0.43
10:IC:1190:MET:HG2	10:IC:1222:VAL:HA	2.01	0.43
11:JA:1717:TRP:HZ3	16:OA:940:LEU:HD12	1.82	0.43
11:JB:476:LEU:HD23	11:JB:476:LEU:HA	1.88	0.43
11:JC:117:PRO:HG3	11:JC:146:TYR:HD1	1.84	0.43
12:KC:376:ALA:HB2	12:KC:579:LEU:HD23	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LA:469:ARG:HH21	13:LB:460:ARG:HH22	1.65	0.43
13:LL:372:THR:HA	13:LL:375:ILE:HD12	2.00	0.43
14:ME:261:ASP:HA	14:ME:262:PRO:HD2	1.71	0.43
15:NA:982:ILE:O	15:NA:988:GLY:HA3	2.19	0.43
15:ND:563:ASN:HA	15:ND:566:GLN:NE2	2.33	0.43
15:ND:693:GLY:HA2	15:ND:901:LEU:O	2.19	0.43
15:ND:867:ARG:HA	15:ND:870:TYR:CE1	2.53	0.43
16:OB:931:PRO:HB2	16:OB:936:VAL:HB	2.00	0.43
16:OC:876:GLU:HG2	16:OC:939:MET:HB3	1.99	0.43
19:RB:36:ARG:HH12	19:RB:140:GLY:H	1.66	0.43
1:AA:715:LEU:HD22	13:LK:364:ASN:HD21	1.83	0.43
1:AE:716:HIS:HB3	1:AE:1037:PRO:HD3	2.01	0.43
1:AE:892:GLU:HA	1:AE:895:ARG:HB3	1.99	0.43
1:AE:1010:ASP:HA	1:AE:1013:THR:HG22	2.01	0.43
2:AG:506:LEU:HD13	10:IA:1255:LEU:HD11	2.01	0.43
1:AL:609:PRO:HG3	13:LH:497:LEU:HD12	2.00	0.43
4:DA:84:ILE:HA	4:DA:169:GLY:HA3	2.00	0.43
4:DA:384:ILE:HD11	13:LA:461:VAL:HG11	2.00	0.43
4:DC:161:LEU:O	4:DC:165:ILE:HG12	2.19	0.43
5:EA:3573:PHE:CZ	5:EA:3650:THR:HB	2.54	0.43
5:EA:4665:LEU:HD23	5:EA:4665:LEU:HA	1.91	0.43
5:EB:3274:GLN:NE2	5:EB:3491:ALA:HB1	2.34	0.43
5:EB:3388:LEU:HB3	5:EB:3391:VAL:HB	2.00	0.43
5:EC:4170:LYS:O	5:EC:4174:ILE:HG12	2.18	0.43
6:FC:2019:GLU:O	6:FC:2023:ILE:HG12	2.18	0.43
6:FD:821:ARG:HA	6:FD:821:ARG:HD3	1.60	0.43
6:FD:1241:VAL:HG22	6:FD:1260:LEU:HD12	2.00	0.43
6:FD:1392:LYS:HE3	6:FD:1392:LYS:HB3	1.43	0.43
6:FE:856:PRO:HA	6:FE:1080:ILE:HD11	2.01	0.43
6:FE:1181:VAL:O	6:FE:1425:PRO:HG2	2.18	0.43
6:FE:1295:ALA:HA	6:FE:1394:ARG:NE	2.34	0.43
6:FF:808:SER:O	6:FF:809:ILE:C	2.60	0.43
6:FF:1027:LEU:O	6:FF:1028:LYS:C	2.61	0.43
6:FF:1186:TRP:CD2	6:FF:1269:CYS:HB2	2.53	0.43
6:FF:1393:LEU:HD13	6:FF:1393:LEU:HA	1.77	0.43
7:GC:186:VAL:HG21	7:GC:672:VAL:HG21	2.01	0.43
7:GC:423:TRP:HB3	7:GC:426:ASN:HD22	1.84	0.43
8:GD:681:ILE:HD13	8:GD:684:TRP:HE1	1.84	0.43
8:GH:425:VAL:HG23	8:GH:498:PHE:HE1	1.84	0.43
7:GI:614:TRP:HE1	7:GI:661:LEU:HD13	1.83	0.43
8:GJ:294:TRP:CD1	8:GJ:299:ALA:HB2	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GK:544:PRO:HB3	9:HC:597:CYS:H	1.84	0.43
8:GL:636:PRO:HB2	8:GL:654:LEU:HD11	1.99	0.43
9:HB:432:LEU:HD13	9:HB:435:LEU:HD12	2.01	0.43
9:HB:765:TRP:N	9:HB:765:TRP:CE3	2.85	0.43
10:IB:188:PHE:HE1	11:JB:1883:ARG:HE	1.66	0.43
10:IB:450:ASN:O	10:IB:454:GLU:HB3	2.18	0.43
10:IC:462:VAL:HG12	10:IC:470:ARG:HG3	2.00	0.43
10:IC:581:PHE:CE2	10:IC:759:PHE:HA	2.54	0.43
11:JA:531:ARG:HG3	11:JA:532:HIS:CD2	2.54	0.43
11:JA:1084:VAL:HG11	11:JA:1153:LEU:HD23	2.00	0.43
11:JA:2109:ALA:HA	11:JA:2112:ARG:HE	1.84	0.43
11:JB:1790:LEU:HD13	11:JB:1812:VAL:HG11	2.01	0.43
11:JB:2110:LEU:O	11:JB:2114:ILE:HG12	2.18	0.43
11:JB:2280:ARG:O	11:JB:2284:LYS:HG2	2.19	0.43
12:KG:311:ASP:HB2	12:KG:314:LEU:HG	2.01	0.43
13:LE:473:LYS:O	13:LE:477:LEU:HD23	2.19	0.43
13:LE:530:VAL:HG11	13:LF:530:VAL:HB	2.00	0.43
13:LI:460:ARG:HG2	13:LI:463:ARG:HE	1.84	0.43
13:LJ:425:LYS:HA	13:LJ:428:VAL:HG12	2.01	0.43
13:LP:374:HIS:HA	13:LP:377:GLN:HB3	2.01	0.43
14:MG:93:SER:HA	14:MG:96:ASP:HB2	2.01	0.43
15:NA:600:LEU:HD11	15:NA:945:PHE:HB3	2.01	0.43
15:ND:364:ARG:HB2	15:ND:488:GLU:HG2	2.01	0.43
16:OC:882:ARG:NE	16:OC:885:GLN:HE21	2.00	0.43
18:QD:71:VAL:HG12	18:QD:90:PHE:HZ	1.83	0.43
19:RB:18:LYS:HB3	19:RB:105:MET:HA	2.01	0.43
20:SB:76:LYS:NZ	20:SB:78:LYS:HG2	2.33	0.43
1:AA:98:LEU:HD23	1:AA:145:HIS:HB3	2.01	0.43
1:AA:350:LEU:HD13	2:AB:522:ARG:HD3	2.01	0.43
2:AF:87:ILE:HD11	2:AF:279:PRO:HG3	2.01	0.43
1:AH:133:PRO:O	1:AH:136:PHE:HB2	2.19	0.43
1:AI:107:LEU:HD12	1:AI:221:VAL:HG11	2.00	0.43
1:AI:768:ILE:HA	1:AI:776:LEU:HD13	2.01	0.43
3:BA:873:PHE:HD2	3:BA:918:LEU:HD21	1.84	0.43
3:BC:845:LYS:HA	3:BC:848:ILE:HG22	2.01	0.43
3:CA:695:LEU:HD22	3:CA:743:SER:HB2	2.00	0.43
3:CC:858:SER:H	3:CC:891:ILE:HD11	1.84	0.43
3:CF:1156:GLU:HA	10:IB:415:ARG:HH22	1.84	0.43
4:DB:145:ASN:HA	4:DB:148:ARG:HG2	2.00	0.43
4:DE:90:LEU:HB3	4:DE:119:LEU:HD23	2.00	0.43
4:DF:180:LEU:HB2	4:DF:181:ILE:HD12	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EA:4030:GLU:HB2	5:EA:4058:PRO:HB3	2.00	0.43
5:EA:4212:ALA:HA	5:EA:4215:LEU:HD23	2.00	0.43
5:EB:4213:LYS:HB3	5:EB:4236:LEU:HD21	2.00	0.43
5:EC:4071:LEU:HD21	5:EC:4222:LYS:HG2	2.01	0.43
6:FE:1205:ILE:HG23	6:FE:1286:LEU:HD11	2.01	0.43
6:FF:806:ILE:HG23	6:FF:1112:ILE:HD11	2.00	0.43
6:FF:1065:LEU:HA	6:FF:1115:THR:CA	2.49	0.43
6:FF:1066:GLN:O	6:FF:1114:VAL:N	2.46	0.43
6:FF:1071:PHE:HD1	6:FF:1108:PRO:HA	1.84	0.43
8:GB:193:MET:HG3	7:GC:381:ARG:HH12	1.82	0.43
7:GC:719:ILE:HD11	7:GC:800:VAL:HG21	2.01	0.43
8:GD:707:GLU:HA	8:GD:710:LYS:HD2	1.99	0.43
7:GI:271:ASP:HB3	7:GI:277:GLU:HG3	2.01	0.43
7:GI:298:TYR:HB3	7:GI:679:LEU:HD21	2.00	0.43
9:HA:432:LEU:HD13	9:HA:435:LEU:HD12	2.01	0.43
9:HB:524:VAL:HG22	9:HB:607:VAL:HG22	2.01	0.43
9:HB:526:VAL:HB	9:HB:579:LEU:HD22	2.00	0.43
10:IA:551:ASN:ND2	10:IA:852:CYS:HA	2.32	0.43
10:IB:1278:VAL:HG23	10:IB:1279:GLU:H	1.83	0.43
11:JB:138:THR:HG22	11:JB:162:PRO:HG3	2.00	0.43
11:JC:1480:VAL:HG13	15:NA:440:LEU:HD11	2.00	0.43
11:JC:1765:ARG:HH12	16:OC:893:PRO:HD2	1.84	0.43
12:KE:593:HIS:HB2	12:KE:707:GLU:HB3	1.99	0.43
13:LN:428:VAL:HA	13:LN:431:LEU:HD12	2.01	0.43
14:ME:315:TRP:CZ3	14:MF:315:TRP:HA	2.54	0.43
15:NA:529:PHE:CD2	15:NA:1382:PHE:HB2	2.54	0.43
15:NA:685:PHE:HE2	15:NA:689:ASN:HA	1.83	0.43
15:NB:599:ILE:HB	15:NB:916:LEU:HG	2.01	0.43
15:NC:617:PHE:O	15:NC:620:ILE:HG12	2.19	0.43
15:NC:1487:ARG:HB3	15:NC:1488:ARG:H	1.62	0.43
19:RC:116:PHE:CE2	19:RC:163:PHE:HA	2.53	0.43
19:RC:132:LEU:HD21	19:RC:152:LEU:HD11	2.00	0.43
1:AA:73:THR:HG22	1:AA:75:ALA:H	1.83	0.43
1:AD:488:VAL:HG12	1:AD:490:SER:H	1.84	0.43
1:AL:71:LEU:HD11	1:AL:218:PRO:HB2	2.01	0.43
3:BA:963:HIS:HE1	16:OA:125:SER:HB3	1.83	0.43
4:DD:267:ARG:NH1	4:DD:268:ARG:HB2	2.34	0.43
4:DE:19:ARG:HD2	4:DE:22:ILE:HD11	2.01	0.43
5:EA:4522:VAL:HA	5:EA:4525:VAL:HG12	2.01	0.43
5:EB:3521:GLU:HB3	5:EB:3546:TYR:CE1	2.54	0.43
5:EB:3784:GLY:HA2	5:EB:3855:LEU:HD21	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:4880:ASP:OD1	5:EB:4880:ASP:N	2.52	0.43
5:EC:3648:PRO:HB2	7:GG:543:LYS:HZ2	1.84	0.43
6:FD:1068:CYS:HB3	6:FD:1112:ILE:HG23	2.01	0.43
6:FD:1089:ARG:HD2	6:FD:1089:ARG:HA	1.71	0.43
6:FE:1270:LEU:HD22	6:FE:1270:LEU:HA	1.81	0.43
6:FF:1065:LEU:HA	6:FF:1115:THR:HA	2.01	0.43
7:GA:872:THR:HB	7:GA:972:GLU:HB2	2.01	0.43
7:GC:724:ASP:HB3	7:GC:728:ARG:HH21	1.83	0.43
8:GH:664:ILE:HD11	8:GH:681:ILE:HG21	2.00	0.43
7:GK:211:ARG:HD3	7:GK:212:PRO:HD2	2.00	0.43
8:GL:142:THR:HA	8:GL:149:LEU:HD21	2.00	0.43
9:HA:761:CYS:SG	9:HA:765:TRP:CZ2	3.10	0.43
9:HB:487:VAL:HG21	9:HB:620:TYR:CZ	2.53	0.43
10:IA:457:SER:HB3	10:IA:503:LEU:HD21	2.01	0.43
10:IA:743:TYR:CD2	10:IA:764:ALA:HA	2.54	0.43
10:IB:344:TYR:CZ	10:IB:433:ARG:HG2	2.54	0.43
10:IB:893:PHE:HZ	10:IB:907:ASP:HA	1.83	0.43
10:IC:963:ARG:HD3	10:IC:963:ARG:HA	1.80	0.43
10:IC:1232:ARG:H	10:IC:1302:ARG:NH2	2.16	0.43
11:JA:812:LEU:HA	11:JA:819:ILE:HG23	2.00	0.43
11:JA:1447:LEU:HD11	11:JA:1976:HIS:HD2	1.84	0.43
11:JB:1385:SER:HB2	11:JB:1409:ARG:NH2	2.33	0.43
12:KC:536:ARG:NH2	12:KC:544:LEU:H	2.16	0.43
15:NC:808:ILE:HG22	15:NC:878:ILE:HG21	1.99	0.43
15:NC:915:VAL:HG12	15:NC:917:MET:HE3	2.01	0.43
18:QB:52:LYS:HA	18:QB:75:PHE:CE1	2.54	0.43
2:AC:161:ILE:HD11	6:FA:1874:PHE:HA	2.01	0.42
1:AD:282:HIS:CE1	10:IB:1359:ALA:HB2	2.53	0.42
1:AE:419:GLU:HG3	16:OC:79:LEU:HD11	2.00	0.42
1:AH:393:LEU:HA	1:AH:393:LEU:HD12	1.89	0.42
3:BA:850:THR:HA	3:BA:853:VAL:HG12	2.01	0.42
3:BB:689:LEU:HD23	17:PB:258:PRO:HB2	2.00	0.42
3:BB:755:GLY:HA2	3:BB:787:ILE:HD13	2.00	0.42
3:BB:873:PHE:HZ	16:OB:174:VAL:HG22	1.82	0.42
3:CJ:1116:SER:HB2	10:IB:512:ARG:HH22	1.84	0.42
3:CJ:1154:LEU:HD13	3:CJ:4516:ILE:HD12	2.01	0.42
3:CL:1186:LEU:HD13	10:IC:1423:PRO:HG3	2.00	0.42
4:DD:118:VAL:O	4:DD:122:ILE:HG12	2.19	0.42
5:EA:4308:GLU:H	5:EA:4308:GLU:HG2	1.69	0.42
5:EC:3242:LEU:HD23	5:EC:3249:ALA:HA	2.01	0.42
5:EC:3306:ILE:O	5:EC:3310:THR:HG23	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FA:2075:GLU:CB	9:HA:858:LEU:HD11	2.40	0.42
6:FC:1852:ILE:HD11	6:FC:1891:PRO:HD2	2.01	0.42
6:FD:854:TRP:CD1	6:FD:854:TRP:N	2.87	0.42
6:FD:993:ALA:HB1	12:KA:228:GLU:HG3	2.01	0.42
6:FD:1202:PHE:HE1	6:FD:1243:PRO:HA	1.84	0.42
6:FE:917:TRP:HA	6:FE:1422:PHE:HE2	1.84	0.42
6:FF:980:SER:C	6:FF:982:SER:N	2.77	0.42
6:FF:1246:ILE:HG23	6:FF:1247:SER:N	2.34	0.42
7:GA:311:LEU:HD11	7:GA:440:ALA:HB2	2.01	0.42
8:GB:532:PHE:HB3	8:GB:589:PHE:HE2	1.83	0.42
7:GC:792:LEU:HG	7:GC:796:PHE:HE2	1.83	0.42
8:GD:333:LYS:HE2	8:GD:335:ASN:HD21	1.83	0.42
8:GF:112:ILE:HD12	8:GF:510:ARG:HG2	2.00	0.42
8:GH:196:HIS:HA	7:GI:386:VAL:HB	2.01	0.42
8:GH:401:ASP:HA	8:GH:404:ARG:HG2	2.01	0.42
9:HA:836:SER:O	9:HA:839:ALA:N	2.51	0.42
9:HD:760:LYS:O	9:HD:761:CYS:C	2.61	0.42
10:IB:366:GLU:HB3	10:IB:516:PRO:HD2	2.01	0.42
10:IB:580:LEU:HG	10:IB:603:ARG:HH12	1.84	0.42
11:JA:138:THR:HG22	11:JA:162:PRO:HG3	2.01	0.42
11:JA:1824:PRO:HB2	11:JA:1973:PHE:CE1	2.54	0.42
11:JB:781:ASN:HD21	11:JB:939:VAL:HG11	1.84	0.42
12:KA:404:GLU:HA	12:KA:407:ILE:HD12	2.01	0.42
12:KA:652:ILE:HG22	12:KA:654:ILE:HG23	1.99	0.42
12:KE:567:TRP:HB3	12:KE:707:GLU:HG3	2.01	0.42
13:LI:398:ARG:HH21	13:LJ:395:ILE:HD13	1.83	0.42
14:MA:285:ARG:NH1	14:MB:257:LYS:HA	2.34	0.42
15:NA:630:LYS:HA	15:NA:637:PRO:HD3	2.00	0.42
15:NB:806:ASP:HB3	15:NB:882:SER:HB2	2.01	0.42
15:NB:993:LEU:HB3	15:NB:1121:ASN:HD21	1.84	0.42
15:NB:1010:LEU:HD22	15:NB:1093:LYS:HB2	2.01	0.42
15:NC:513:LEU:HB2	15:NC:1404:HIS:CD2	2.54	0.42
15:ND:1525:ARG:NH2	18:QB:60:ARG:HG3	2.34	0.42
16:OA:288:LEU:HD23	16:OA:288:LEU:HA	1.93	0.42
16:OB:10:ARG:HA	16:OB:10:ARG:HD3	1.77	0.42
16:OB:1077:LYS:HZ3	16:OB:1079:ALA:H	1.66	0.42
18:QD:128:PHE:HB2	18:QD:140:TRP:CH2	2.54	0.42
20:SA:55:GLU:HA	20:SA:58:ALA:HB2	2.00	0.42
20:SA:86:LEU:HD12	20:SA:89:ALA:HB3	2.00	0.42
1:AA:368:LEU:HB3	2:AC:153:GLN:HE21	1.84	0.42
2:AC:16:LEU:HD13	2:AC:50:ILE:HG22	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:176:VAL:HG11	16:OA:25:ALA:HB1	2.02	0.42
2:AC:364:CYS:SG	2:AC:381:HIS:HB2	2.58	0.42
2:AC:538:ASN:HB3	5:EA:4818:ILE:HD12	2.00	0.42
2:AF:559:ARG:HH21	13:LK:483:ARG:HB3	1.85	0.42
1:AI:418:ILE:HG23	2:AJ:424:LEU:HD22	2.01	0.42
2:AJ:288:ASP:HB3	2:AJ:291:LEU:HG	2.01	0.42
3:BC:907:ARG:CZ	16:OC:184:ASN:HD21	2.32	0.42
3:CE:4486:ILE:HG21	3:CE:4497:ARG:HH11	1.83	0.42
3:CJ:1168:ARG:HH12	3:CJ:4482:LEU:HB3	1.83	0.42
4:DC:363:LEU:HD21	8:GJ:161:ALA:HB1	2.00	0.42
5:EA:3743:ARG:HE	5:EA:3830:HIS:CE1	2.37	0.42
5:EB:3653:LYS:HD3	5:EB:3653:LYS:HA	1.81	0.42
5:EC:3314:ARG:HH22	5:EC:4166:SER:HA	1.84	0.42
6:FA:1759:GLU:OE2	6:FA:1964:MET:HG2	2.19	0.42
6:FB:1804:MET:HE2	6:FB:1804:MET:HB3	1.86	0.42
6:FC:1738:GLY:HA3	6:FC:1796:PHE:HB3	2.02	0.42
6:FD:993:ALA:HB1	12:KA:230:GLN:OE1	2.19	0.42
6:FD:1067:ALA:HB1	6:FD:1111:GLU:OE2	2.19	0.42
6:FD:1442:GLU:C	6:FD:1444:ARG:N	2.76	0.42
6:FE:811:ASN:HD21	6:FE:891:ARG:HD2	1.84	0.42
6:FF:830:ALA:HB1	6:FF:843:LEU:HD21	2.01	0.42
6:FF:975:ILE:H	6:FF:975:ILE:HG12	1.59	0.42
8:GB:326:ARG:NH1	8:GB:375:TYR:HB3	2.31	0.42
8:GD:431:PHE:HZ	8:GD:496:LEU:HD13	1.83	0.42
8:GF:88:PRO:HG2	8:GF:91:TYR:HB2	2.01	0.42
8:GF:348:TYR:HB3	8:GF:380:MET:SD	2.59	0.42
7:GG:699:SER:HB3	7:GG:705:ILE:HD11	2.01	0.42
7:GK:305:PRO:HA	7:GK:354:ARG:HH21	1.84	0.42
10:IA:930:LEU:H	10:IA:966:LEU:HD12	1.84	0.42
10:IC:1207:LYS:HD3	10:IC:1207:LYS:HA	1.83	0.42
11:JB:84:PHE:CE2	11:JB:2096:HIS:HB3	2.53	0.42
12:KF:247:LEU:HB3	12:KF:258:LEU:HD12	2.00	0.42
13:LE:483:ARG:O	13:LE:487:MET:HG2	2.19	0.42
13:LO:403:SER:HB2	13:LO:407:ARG:HH21	1.84	0.42
14:MK:80:ALA:HA	14:MK:88:ALA:HB2	2.00	0.42
15:NA:598:PHE:HB3	15:NA:1187:CYS:HA	2.01	0.42
15:NB:599:ILE:HD13	15:NB:1188:HIS:HB2	2.01	0.42
15:NC:946:LEU:HA	15:NC:949:PHE:CE1	2.53	0.42
2:AC:552:LEU:HD13	2:AC:557:LEU:HB2	2.01	0.42
1:AD:287:PHE:CZ	10:IB:1356:LEU:HD11	2.53	0.42
2:AF:300:CYS:HB2	2:AF:320:CYS:H	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:32:LEU:HD23	2:AJ:166:LEU:HD11	2.02	0.42
2:AJ:68:LEU:HB3	2:AJ:168:GLN:HE21	1.84	0.42
2:AK:267:HIS:HB3	2:AK:269:TYR:CE1	2.54	0.42
3:CB:1014:ASP:HA	3:CB:1017:ARG:HG2	2.01	0.42
3:CC:677:LYS:HB2	17:PB:249:LEU:HD22	2.01	0.42
3:CF:1213:VAL:HG22	3:CF:1219:VAL:HG12	2.01	0.42
3:CJ:4455:VAL:HA	3:CJ:4456:PRO:HD3	1.81	0.42
5:EA:3269:TRP:HD1	5:EA:3409:SER:HB2	1.84	0.42
5:EB:3660:LYS:NZ	5:EB:4055:ARG:HH22	2.18	0.42
5:EB:3746:LYS:HA	5:EB:3831:LEU:HD13	2.00	0.42
5:EB:4296:VAL:HG13	5:EB:4340:ASN:HD21	1.84	0.42
6:FA:1640:VAL:HG13	6:FA:1643:PRO:HB3	2.01	0.42
6:FD:799:GLN:HG3	6:FD:912:ILE:H	1.84	0.42
6:FD:855:PHE:C	6:FD:857:GLU:H	2.27	0.42
6:FE:830:ALA:HA	6:FE:847:PHE:CE1	2.53	0.42
6:FE:1008:ARG:HH11	6:FE:1009:VAL:HG23	1.84	0.42
7:GC:739:GLN:HB3	7:GC:992:ARG:HH22	1.83	0.42
7:GC:939:VAL:O	7:GC:943:GLN:HG2	2.19	0.42
7:GE:371:LEU:HD12	7:GE:412:VAL:HG22	2.00	0.42
7:GG:533:VAL:O	7:GG:535:PRO:HD3	2.20	0.42
7:GG:950:ALA:O	7:GG:951:MET:HE2	2.19	0.42
8:GH:661:PRO:HB2	8:GH:680:LEU:H	1.84	0.42
7:GK:433:MET:HE3	7:GK:433:MET:HB3	1.94	0.42
7:GK:548:ALA:HB1	9:HC:666:LYS:HG3	2.01	0.42
8:GL:101:PRO:HD2	8:GL:104:LEU:HD23	2.01	0.42
9:HA:786:ALA:HB1	9:HA:801:VAL:HG11	2.01	0.42
9:HA:825:ASN:O	9:HA:829:THR:HG23	2.20	0.42
9:HB:749:ASN:C	9:HB:751:SER:N	2.73	0.42
9:HB:786:ALA:HB1	9:HB:801:VAL:HG11	2.02	0.42
9:HC:552:ASP:HB2	9:HC:576:LYS:HB2	2.02	0.42
9:HD:771:PRO:HG3	9:HD:819:TYR:CZ	2.54	0.42
9:HD:816:LEU:HD23	9:HD:816:LEU:HA	1.89	0.42
10:IB:845:TYR:CZ	10:IB:863:LEU:HD22	2.55	0.42
10:IB:902:ARG:HH12	10:IB:910:LEU:HB3	1.84	0.42
11:JA:440:PRO:HG3	11:JA:1474:TRP:CZ3	2.54	0.42
11:JB:764:TRP:CD2	11:JB:1501:LEU:HD21	2.53	0.42
11:JC:78:GLN:HA	11:JC:79:PRO:HD3	1.92	0.42
11:JC:450:PHE:O	11:JC:451:MET:HE2	2.19	0.42
11:JC:1122:ARG:HG3	11:JC:1123:THR:HG23	2.01	0.42
12:KC:212:LEU:HD11	12:KC:293:ILE:HD11	2.01	0.42
12:KC:393:LEU:O	12:KC:397:GLN:HG2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:ML:140:ARG:HB2	14:ML:144:ARG:NH1	2.31	0.42
15:NB:893:LEU:HB2	15:NB:1154:ASP:CG	2.44	0.42
15:ND:510:LEU:O	15:ND:513:LEU:HG	2.19	0.42
15:ND:1407:MET:HE1	15:ND:1471:ARG:HD2	2.01	0.42
15:ND:1508:PHE:HZ	18:QB:110:VAL:HG11	1.84	0.42
17:PA:267:ASP:HB3	17:PA:269:ILE:HG22	2.00	0.42
18:QD:144:GLU:HB3	18:QD:149:LEU:C	2.45	0.42
1:AA:707:GLY:HA2	13:LK:354:ARG:HH12	1.83	0.42
1:AD:905:LYS:O	1:AD:909:GLN:HG3	2.19	0.42
2:AF:86:ASP:HB3	2:AF:90:ARG:NH1	2.35	0.42
1:AI:999:LYS:HE2	7:GK:860:GLN:HB3	2.02	0.42
2:AK:331:ASN:C	2:AK:331:ASN:ND2	2.77	0.42
3:BA:686:ALA:HA	3:BA:689:LEU:HD13	1.99	0.42
3:BA:754:GLU:HG2	17:PA:284:PRO:HB2	2.01	0.42
3:CF:4479:LEU:HD12	3:CF:4481:GLU:H	1.83	0.42
4:DB:170:ARG:HG2	4:DE:170:ARG:NH2	2.35	0.42
4:DC:312:ASN:O	4:DC:316:ARG:HG2	2.20	0.42
5:EA:4653:GLU:HB3	5:EA:4654:ASP:H	1.70	0.42
5:EB:3280:VAL:HG13	5:EB:3281:VAL:HG13	2.01	0.42
5:EB:3435:ASP:HA	5:EB:3610:GLN:HA	2.01	0.42
6:FB:2024:ARG:HH21	9:HD:779:PRO:HG2	1.84	0.42
6:FC:1647:LEU:HD22	6:FC:1797:VAL:HG23	2.01	0.42
6:FD:1108:PRO:HG3	9:HB:394:LEU:HG	2.00	0.42
6:FE:827:PRO:O	6:FE:829:ARG:N	2.48	0.42
6:FE:844:ALA:O	6:FE:845:PRO:C	2.62	0.42
6:FE:1106:LEU:HD23	6:FE:1106:LEU:HA	1.83	0.42
6:FE:1203:ARG:O	6:FE:1204:GLN:C	2.62	0.42
6:FF:807:ALA:HB2	6:FF:903:GLN:HA	1.99	0.42
7:GA:257:GLY:HA3	7:GA:612:ARG:HH21	1.84	0.42
7:GA:612:ARG:HB2	7:GA:662:VAL:HG22	2.01	0.42
8:GB:160:LEU:HA	8:GB:163:MET:HG2	2.01	0.42
7:GC:231:CYS:HB3	7:GC:236:THR:H	1.85	0.42
8:GH:177:MET:HB3	8:GH:198:PHE:O	2.19	0.42
9:HD:776:PRO:O	9:HD:777:TYR:C	2.62	0.42
10:IA:451:VAL:HG12	10:IA:503:LEU:HD13	2.01	0.42
10:IA:618:ARG:HH12	10:IA:752:SER:HB2	1.85	0.42
10:IA:886:LEU:HD12	16:OA:1040:PHE:CE1	2.54	0.42
10:IA:1296:PRO:HB3	10:IA:1373:TRP:CE2	2.54	0.42
11:JA:164:MET:HA	11:JA:165:GLU:HA	1.82	0.42
11:JC:1449:VAL:HG23	11:JC:1452:SER:HA	2.01	0.42
14:MA:313:ARG:HD2	14:MA:316:GLN:HE22	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:MA:326:LEU:HD23	14:MA:326:LEU:HA	1.93	0.42
14:MF:243:LYS:HD3	14:MF:243:LYS:HA	1.74	0.42
15:NA:349:ARG:HG3	15:NA:351:SER:H	1.84	0.42
15:NA:537:LYS:HB3	15:NA:577:PRO:HB2	2.00	0.42
15:NA:697:VAL:HG21	15:NA:1169:PHE:CE2	2.54	0.42
15:NB:891:TRP:HA	15:NB:1152:GLU:C	2.44	0.42
15:NB:1441:ARG:HB3	15:NB:1442:LYS:H	1.71	0.42
15:NB:1525:ARG:HG2	18:QC:60:ARG:NH1	2.34	0.42
15:NC:578:HIS:HD1	15:NC:580:PHE:HD2	1.68	0.42
15:ND:582:LEU:HD21	15:ND:599:ILE:HG23	2.01	0.42
15:ND:892:TRP:HE3	15:ND:1154:ASP:HB2	1.85	0.42
15:ND:1391:LEU:HD23	15:ND:1397:LEU:HG	2.00	0.42
16:OA:226:GLU:HB3	16:OA:249:LEU:HD11	2.01	0.42
17:PA:138:ARG:HB3	17:PA:142:TYR:CD2	2.54	0.42
18:QB:58:LEU:HA	18:QB:61:TYR:CD2	2.54	0.42
19:RA:119:VAL:O	19:RA:131:GLU:HG3	2.19	0.42
19:RB:22:ARG:HD2	19:RB:174:LEU:HD22	2.01	0.42
1:AA:243:VAL:HG12	17:PA:247:LEU:HB3	2.00	0.42
2:AB:19:VAL:HB	2:AB:47:ALA:HB3	2.01	0.42
1:AE:49:GLN:HG2	2:AF:520:ARG:HH21	1.84	0.42
1:AE:229:LEU:HB2	17:PC:273:GLU:O	2.20	0.42
2:AF:206:PRO:HD3	2:AF:266:ARG:HB2	2.00	0.42
1:AH:364:LYS:HD3	1:AH:364:LYS:HA	1.78	0.42
1:AH:783:LEU:HD21	7:GG:926:ASP:HB3	2.02	0.42
2:AK:446:ARG:HD2	2:AK:450:ARG:HH21	1.84	0.42
4:DA:374:VAL:HG13	4:DA:375:SER:H	1.82	0.42
4:DD:262:ILE:HA	4:DD:265:ILE:HG12	2.00	0.42
5:EA:3809:LEU:HD13	5:EA:3813:VAL:HG11	2.01	0.42
5:EC:3414:VAL:HG12	5:EC:3505:ILE:HD12	2.02	0.42
6:FB:1981:LEU:O	6:FB:1985:GLN:HG2	2.20	0.42
6:FD:844:ALA:C	7:GC:896:ARG:NH1	2.76	0.42
6:FD:978:LYS:NZ	6:FD:984:THR:H	2.17	0.42
6:FD:1088:LYS:C	6:FD:1090:LEU:H	2.27	0.42
6:FD:1217:GLU:HB3	6:FD:1218:ALA:H	1.58	0.42
6:FD:1218:ALA:HB3	6:FD:1276:LEU:HD13	2.02	0.42
6:FE:839:GLY:CA	12:KB:681:MET:HE3	2.49	0.42
6:FE:917:TRP:HA	6:FE:1422:PHE:CE2	2.54	0.42
6:FE:1230:SER:OG	6:FE:1231:ARG:N	2.53	0.42
6:FE:1293:THR:HG23	6:FE:1394:ARG:CG	2.49	0.42
6:FF:1391:TYR:HE2	6:FF:1419:LEU:HB3	1.84	0.42
7:GC:213:GLY:HA3	12:KE:685:ARG:HH12	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GC:232:LYS:HD3	7:GC:235:ARG:HH12	1.85	0.42
7:GC:827:LEU:HB3	7:GC:831:ARG:HB2	2.01	0.42
7:GE:572:GLU:HA	7:GE:622:ARG:NH2	2.34	0.42
9:HB:579:LEU:HD21	9:HB:597:CYS:HB3	2.01	0.42
9:HB:754:LEU:HD23	9:HB:754:LEU:HA	1.75	0.42
9:HB:761:CYS:HB3	9:HB:765:TRP:CE2	2.54	0.42
9:HC:579:LEU:HA	9:HC:579:LEU:HD23	1.85	0.42
10:IA:876:ALA:HB1	10:IA:947:HIS:HE2	1.84	0.42
10:IA:964:LEU:O	10:IA:968:ARG:HG2	2.19	0.42
10:IB:1186:GLU:HA	10:IB:1190:MET:HE3	2.01	0.42
10:IC:1094:ASN:HA	10:IC:1123:ASN:ND2	2.33	0.42
11:JA:102:ARG:HH21	11:JA:104:PHE:HE1	1.66	0.42
11:JA:1775:THR:HG23	11:JA:1780:ARG:HG2	2.00	0.42
11:JA:1987:PRO:HG2	11:JA:1992:LEU:HD21	2.00	0.42
11:JC:895:LEU:HD12	11:JC:896:PRO:HD2	2.01	0.42
12:KA:525:PRO:HD2	12:KA:541:TYR:CE2	2.55	0.42
12:KF:369:ILE:HD11	12:KF:697:ARG:HH21	1.84	0.42
13:LI:372:THR:HA	13:LI:375:ILE:HG12	2.00	0.42
13:LL:484:VAL:HA	13:LL:487:MET:HE2	2.00	0.42
14:MB:254:ILE:O	14:MB:257:LYS:HB2	2.20	0.42
14:ME:233:LEU:HA	14:ME:236:GLU:HG2	2.01	0.42
15:NA:644:MET:HE2	16:OA:1042:PRO:HD2	2.01	0.42
15:NA:686:ASN:HD21	15:NA:908:PHE:HA	1.85	0.42
15:NA:852:VAL:HG11	15:NA:867:ARG:HG3	2.02	0.42
15:NB:510:LEU:O	15:NB:513:LEU:HG	2.19	0.42
15:NC:564:ARG:CZ	15:NC:622:THR:HB	2.49	0.42
15:NC:1516:ALA:HB1	18:QD:135:LEU:HD21	2.01	0.42
15:ND:946:LEU:HA	15:ND:949:PHE:CE1	2.54	0.42
15:ND:1505:ALA:HA	20:SB:19:LEU:HD11	2.01	0.42
16:OC:226:GLU:HB3	16:OC:245:LEU:HD21	2.01	0.42
18:QA:165:ARG:HE	18:QA:172:GLN:HG2	1.84	0.42
18:QC:39:PHE:HD1	18:QC:58:LEU:HD21	1.84	0.42
19:RB:100:VAL:HA	19:RB:103:GLN:NE2	2.35	0.42
1:AA:246:ALA:HA	1:AA:258:CYS:SG	2.59	0.42
2:AB:44:LEU:HD21	2:AB:47:ALA:HB2	2.01	0.42
2:AB:366:ILE:HD12	2:AB:381:HIS:CG	2.55	0.42
1:AD:298:ILE:HG22	1:AD:332:THR:HG21	2.01	0.42
1:AI:465:MET:HE3	1:AI:465:MET:HB2	1.76	0.42
2:AJ:213:HIS:CD2	2:AJ:293:GLU:HB3	2.55	0.42
1:AL:967:ARG:H	1:AL:967:ARG:HG2	1.68	0.42
3:BA:793:ILE:HG21	3:BA:807:LEU:HA	1.99	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BC:952:GLN:HA	3:BC:955:VAL:HG12	2.02	0.42
3:CF:1146:VAL:HG13	3:CJ:1137:ALA:HB2	2.02	0.42
3:CF:4482:LEU:HA	3:CF:4483:PRO:HD3	1.88	0.42
3:CI:4452:HIS:CE1	3:CI:4454:ASP:HB2	2.54	0.42
3:CJ:4486:ILE:HA	3:CJ:4497:ARG:HH12	1.84	0.42
3:CL:1255:VAL:HG21	3:CL:4469:LEU:HD22	2.01	0.42
4:DA:93:ILE:HD11	4:DA:168:SER:HB2	2.02	0.42
4:DE:164:PHE:HA	4:DE:167:GLU:OE1	2.20	0.42
5:EA:3235:SER:HB2	9:HC:413:ARG:NH2	2.35	0.42
5:EB:4032:PHE:CD2	5:EB:4146:ILE:HG12	2.55	0.42
5:EB:4145:LEU:HD23	5:EB:4145:LEU:HA	1.91	0.42
5:EC:3304:LYS:HG2	9:HA:416:PHE:HE1	1.84	0.42
6:FA:1845:PRO:HB2	6:FA:1848:PRO:HD2	2.01	0.42
6:FD:800:ALA:HB2	6:FD:913:LEU:HD11	2.01	0.42
6:FD:1182:ALA:HB2	6:FD:1430:PHE:N	2.31	0.42
6:FE:877:GLY:HA3	6:FE:909:PRO:HG3	2.01	0.42
6:FE:1087:LEU:O	6:FE:1088:LYS:C	2.62	0.42
6:FE:1190:ARG:NH2	6:FE:1418:GLU:OE2	2.53	0.42
6:FF:810:THR:HB	6:FF:1113:PHE:HE2	1.84	0.42
6:FF:1181:VAL:O	6:FF:1425:PRO:HG3	2.19	0.42
7:GA:205:ARG:HH12	7:GA:947:LEU:HD11	1.85	0.42
7:GA:979:LEU:HB3	9:HB:650:PHE:HB2	2.00	0.42
7:GC:633:LEU:HD22	7:GC:642:PHE:HZ	1.85	0.42
8:GF:50:GLU:HB3	8:GF:112:ILE:CG2	2.50	0.42
9:HB:752:ASP:OD1	9:HB:752:ASP:N	2.53	0.42
10:IB:374:PHE:HB2	10:IB:387:PHE:HB2	2.00	0.42
10:IB:963:ARG:HD3	10:IB:963:ARG:HA	1.89	0.42
10:IC:720:VAL:HB	10:IC:760:LEU:HD13	2.01	0.42
10:IC:947:HIS:HB3	10:IC:951:GLY:H	1.84	0.42
10:IC:1246:ASP:HB3	10:IC:1249:ALA:H	1.85	0.42
11:JA:170:ILE:O	11:JA:171:LYS:HG2	2.19	0.42
11:JA:1682:LYS:HB2	11:JA:1711:ALA:HB2	2.01	0.42
11:JB:162:PRO:HD2	11:JB:170:ILE:H	1.84	0.42
11:JC:1197:LEU:HD12	11:JC:1197:LEU:HA	1.92	0.42
12:KE:312:PRO:HB3	12:KE:350:LEU:HB3	2.01	0.42
13:LM:377:GLN:NE2	13:LM:378:GLU:HG3	2.35	0.42
14:ME:227:GLN:HA	14:ME:230:VAL:HG22	2.02	0.42
14:MI:304:ARG:O	14:MI:308:GLU:HB3	2.18	0.42
15:NA:891:TRP:HA	15:NA:1152:GLU:C	2.43	0.42
15:NA:908:PHE:HD1	15:NA:911:ARG:HD3	1.85	0.42
15:NB:902:ARG:HA	15:NB:902:ARG:HD3	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:893:LEU:H	15:NC:1153:ALA:C	2.27	0.42
15:NC:1136:SER:HB2	15:NC:1144:ARG:HG2	2.01	0.42
15:ND:578:HIS:HB3	15:ND:580:PHE:HD1	1.84	0.42
15:ND:1548:PHE:N	19:RD:142:ASN:HA	2.34	0.42
18:QB:64:LEU:HD23	18:QB:64:LEU:HA	1.85	0.42
18:QC:159:PRO:HB2	18:QC:162:PRO:HD2	2.02	0.42
1:AA:298:ILE:HG22	1:AA:332:THR:HG21	2.00	0.42
1:AA:398:GLU:HA	1:AA:401:THR:HG22	2.01	0.42
1:AD:747:MET:HE1	1:AD:784:PHE:CE1	2.54	0.42
1:AE:186:ARG:HH21	1:AE:204:TYR:HE1	1.67	0.42
1:AE:384:GLU:OE1	6:FB:1654:MET:HE2	2.20	0.42
2:AF:150:ALA:HB2	2:AF:212:VAL:HG11	2.02	0.42
2:AF:161:ILE:HB	5:EB:4626:LEU:HD22	2.02	0.42
1:AH:798:CYS:HB2	1:AH:997:PRO:HD2	2.02	0.42
1:AI:279:PRO:HG3	16:OA:751:VAL:HB	2.02	0.42
1:AI:360:GLU:HB3	2:AJ:485:LEU:HD21	2.02	0.42
2:AK:24:ASP:HB2	1:AL:446:LEU:HG	2.02	0.42
3:BB:1018:PHE:HB2	16:OB:912:TRP:NE1	2.35	0.42
3:CA:819:LEU:HA	3:CA:822:VAL:HG12	2.02	0.42
3:CB:976:LYS:HG3	10:IC:382:THR:HG22	2.01	0.42
3:CI:4467:THR:HG22	3:CI:4489:ASP:HA	2.01	0.42
4:DD:300:GLN:HE21	4:DD:354:TRP:HA	1.85	0.42
4:DF:80:LEU:O	4:DF:84:ILE:HD12	2.18	0.42
5:EA:3496:THR:HG22	5:EA:3498:VAL:H	1.83	0.42
5:EB:3578:PRO:HD3	5:EB:3612:LEU:HD12	2.01	0.42
5:EB:4405:ILE:H	5:EB:4405:ILE:HG12	1.50	0.42
5:EB:4492:ARG:HA	5:EB:4492:ARG:HD2	1.76	0.42
5:EC:3421:HIS:CE1	5:EC:3588:CYS:HA	2.54	0.42
6:FB:1639:PHE:CE1	6:FB:1654:MET:HE1	2.55	0.42
6:FB:1991:ALA:HA	6:FB:1994:ARG:HG2	2.01	0.42
6:FD:968:LEU:HB2	6:FD:1027:LEU:HD11	2.01	0.42
6:FE:1184:ALA:H	6:FE:1424:CYS:HB3	1.85	0.42
6:FE:1429:LEU:O	6:FE:1430:PHE:HB2	2.20	0.42
6:FE:1434:ALA:O	6:FE:1435:GLU:C	2.61	0.42
6:FF:1223:ALA:O	6:FF:1224:ALA:C	2.62	0.42
8:GB:179:MET:HG3	8:GB:197:VAL:HG22	2.02	0.42
8:GF:274:ARG:NH1	8:GF:321:LEU:HA	2.35	0.42
8:GF:383:LYS:HE3	8:GF:441:THR:HG21	2.02	0.42
8:GF:629:ASN:HB3	8:GF:670:PHE:CE1	2.55	0.42
8:GH:64:ASN:C	8:GH:64:ASN:ND2	2.76	0.42
8:GH:152:LEU:HB2	8:GH:394:PHE:HD2	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GI:974:ARG:HB2	7:GI:979:LEU:HA	2.01	0.42
8:GJ:454:ILE:HG23	8:GJ:458:GLY:HA3	2.01	0.42
8:GJ:549:THR:HG22	8:GJ:554:SER:HA	2.02	0.42
10:IA:300:LEU:HD23	10:IA:302:THR:H	1.85	0.42
10:IB:875:VAL:HG13	10:IB:948:LEU:HD23	2.02	0.42
10:IC:927:ARG:HH12	10:IC:961:GLN:HE22	1.68	0.42
10:IC:1221:THR:HB	10:IC:1321:LEU:HD11	2.01	0.42
11:JA:973:MET:HG3	11:JA:1003:ILE:HG23	2.00	0.42
11:JA:1689:LEU:HD12	11:JA:1699:SER:HB2	2.02	0.42
11:JB:2122:GLN:NE2	11:JB:2126:ILE:HG12	2.35	0.42
12:KA:325:LEU:HD23	12:KA:327:MET:HE3	2.00	0.42
12:KB:299:TYR:HE1	12:KB:304:ARG:HG3	1.85	0.42
12:KF:372:GLY:HA2	12:KF:401:GLN:HE22	1.84	0.42
12:KF:402:LEU:HD21	12:KF:406:GLN:HB3	2.01	0.42
12:KG:688:VAL:HG23	12:KG:698:PRO:HB3	2.01	0.42
13:LJ:423:GLN:HA	13:LJ:426:CYS:HB3	2.02	0.42
13:LJ:500:GLN:HA	13:LJ:503:VAL:HG12	2.02	0.42
13:LM:421:VAL:HG21	13:LN:417:LEU:HD22	2.00	0.42
15:NB:626:ARG:HB3	15:NB:690:TYR:HA	2.01	0.42
15:NC:548:PRO:HD3	15:NC:1194:ASN:HB2	2.00	0.42
15:NC:1125:TYR:HB3	15:NC:1160:LEU:H	1.85	0.42
15:NC:1407:MET:O	15:NC:1469:PHE:HB3	2.19	0.42
16:OC:198:ASP:HB3	17:PC:290:PHE:CD2	2.54	0.42
18:QA:122:ARG:HH11	18:QA:126:MET:HE1	1.84	0.42
18:QB:59:ALA:HB3	18:QB:66:PRO:HG3	2.00	0.42
1:AA:39:SER:HB3	1:AA:70:ASN:HB3	2.01	0.42
2:AC:332:ARG:NH1	11:JA:2284:LYS:HG3	2.34	0.42
1:AD:774:ALA:HA	1:AD:906:LEU:HD13	2.00	0.42
1:AI:161:SER:HB3	1:AI:185:ARG:CZ	2.50	0.42
1:AI:746:VAL:HG13	1:AI:747:MET:HG2	2.02	0.42
2:AJ:312:CYS:HB3	2:AJ:315:ASP:HB2	2.02	0.42
3:BA:738:TYR:HD2	3:BA:739:LEU:HD22	1.84	0.42
3:BA:892:ARG:O	3:BA:896:LEU:HB2	2.20	0.42
3:BB:945:THR:HG23	16:OB:314:GLY:HA2	2.02	0.42
3:CI:1123:LEU:HA	10:IA:770:GLY:HA3	2.02	0.42
4:DA:355:CYS:HA	4:DA:384:ILE:O	2.20	0.42
4:DA:385:LYS:NZ	13:LB:461:VAL:HG23	2.34	0.42
4:DC:130:ARG:HH21	4:DC:151:ALA:HA	1.84	0.42
4:DF:273:PHE:HZ	4:DF:338:ILE:HD13	1.84	0.42
5:EA:3781:ILE:HD12	5:EA:3781:ILE:HA	1.91	0.42
5:EB:4044:ILE:HA	5:EB:4047:MET:HG3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:4687:ASP:HA	5:EB:4690:CYS:SG	2.60	0.42
5:EB:4734:LEU:HD21	5:EB:4828:LEU:HB3	2.02	0.42
5:EC:4173:LYS:HA	5:EC:4173:LYS:HD3	1.84	0.42
6:FC:2040:LEU:HA	6:FC:2040:LEU:HD13	1.68	0.42
6:FD:819:PRO:HA	6:FD:824:TYR:OH	2.20	0.42
6:FD:866:PHE:HB3	6:FD:1274:PRO:HD2	2.02	0.42
6:FD:910:ILE:HD11	6:FD:965:TRP:CD1	2.55	0.42
6:FD:1298:LEU:HD23	6:FD:1298:LEU:HA	1.91	0.42
6:FE:1004:GLY:O	6:FE:1005:PRO:C	2.63	0.42
6:FE:1095:LEU:HB3	6:FE:1099:ILE:HG12	2.02	0.42
8:GB:569:VAL:HG21	8:GB:784:LEU:HD21	2.02	0.42
7:GC:719:ILE:HD12	7:GC:800:VAL:HG11	2.00	0.42
7:GE:276:ARG:HH12	7:GE:279:ARG:HA	1.85	0.42
7:GG:980:LEU:HD21	7:GG:988:LYS:HE2	2.02	0.42
8:GH:168:MET:HG2	8:GH:247:PRO:HA	2.02	0.42
7:GI:279:ARG:HA	7:GI:285:LEU:HB3	2.01	0.42
8:GJ:283:LEU:HD11	8:GJ:303:LEU:HD22	2.02	0.42
7:GK:738:LEU:HD22	7:GK:797:ILE:HD12	2.01	0.42
8:GL:56:CYS:HB3	8:GL:59:SER:HB2	2.01	0.42
9:HA:760:LYS:HA	9:HA:763:GLN:CD	2.44	0.42
9:HB:764:LYS:HB2	9:HB:765:TRP:HE3	1.85	0.42
9:HD:757:LEU:O	9:HD:761:CYS:SG	2.75	0.42
9:HD:820:SER:O	9:HD:824:LEU:HG	2.20	0.42
9:HD:851:GLU:HB3	9:HD:855:ARG:CZ	2.50	0.42
10:IC:186:ASP:HB2	16:OC:1095:ARG:HH22	1.84	0.42
10:IC:916:LYS:HB2	11:JC:2042:SER:HB2	2.02	0.42
11:JA:419:SER:O	11:JA:490:THR:HG22	2.20	0.42
11:JB:1765:ARG:HH22	16:OB:891:ARG:HA	1.84	0.42
11:JB:1996:LEU:HG	11:JB:2000:TYR:CZ	2.54	0.42
11:JC:1206:GLN:HE21	11:JC:1211:ARG:HG2	1.85	0.42
11:JC:1335:LEU:HD21	11:JC:1375:TYR:HB2	2.02	0.42
11:JC:1437:ILE:HG22	11:JC:1439:LEU:HG	2.02	0.42
13:LA:394:GLY:O	13:LA:398:ARG:HG2	2.20	0.42
13:LA:531:VAL:HG23	13:LD:531:VAL:HG23	2.02	0.42
13:LF:430:LYS:HD3	13:LF:431:LEU:HD12	2.02	0.42
14:MJ:223:ARG:HE	14:MJ:223:ARG:HB2	1.75	0.42
15:NC:511:LEU:HD13	15:NC:539:GLY:HA3	2.01	0.42
15:NC:548:PRO:HA	15:NC:551:ARG:HE	1.85	0.42
16:OA:876:GLU:HG2	16:OA:939:MET:HB3	2.01	0.42
18:QC:64:LEU:HD11	18:QC:91:CYS:HA	2.00	0.42
19:RA:68:LYS:HA	19:RA:68:LYS:HD2	1.81	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RC:50:VAL:HG12	19:RC:54:MET:HE1	2.02	0.42
20:SB:141:GLU:HA	20:SB:144:LYS:HG3	2.02	0.42
2:AC:176:VAL:HG13	16:OA:27:LEU:HA	2.01	0.42
1:AH:612:THR:HG22	13:LL:501:LYS:HG3	2.02	0.42
1:AI:410:GLU:HG2	2:AJ:67:LEU:HD22	2.00	0.42
1:AI:491:LEU:HB3	6:FC:1791:ASN:HB2	2.02	0.42
1:AI:507:LEU:HD11	6:FC:1826:LEU:HB3	2.01	0.42
2:AJ:481:ARG:HD3	2:AJ:537:ARG:HH22	1.85	0.42
2:AK:9:VAL:HG21	6:FC:1909:GLY:HA3	2.02	0.42
2:AK:296:ALA:H	1:AL:431:SER:HB2	1.84	0.42
1:AL:663:LEU:HD21	1:AL:698:LEU:HA	2.02	0.42
1:AL:967:ARG:HD3	14:MG:94:LEU:HD13	2.02	0.42
3:CE:1237:VAL:HG21	3:CE:4468:LYS:HB3	2.02	0.42
3:CG:1194:VAL:HG22	3:CG:1195:LEU:H	1.85	0.42
3:CG:1235:PRO:HB2	3:CG:1244:PRO:HB3	2.01	0.42
3:CI:1236:LEU:HA	3:CI:4469:LEU:HB3	2.02	0.42
4:DB:267:ARG:HD2	14:ME:297:VAL:HG11	2.01	0.42
5:EB:3244:GLY:H	9:HB:409:GLU:HG3	1.83	0.42
5:EC:4520:LEU:HD11	5:EC:4692:ILE:HD11	2.02	0.42
6:FA:2012:ARG:HB3	6:FA:2012:ARG:NH2	2.35	0.42
6:FB:1814:ARG:NH1	13:LL:511:GLN:HA	2.35	0.42
6:FD:805:HIS:O	6:FD:806:ILE:C	2.62	0.42
6:FD:894:ALA:HB1	6:FD:897:LEU:HB2	2.01	0.42
6:FD:922:LEU:HD22	6:FD:922:LEU:HA	1.75	0.42
6:FD:976:HIS:CE1	6:FD:1018:THR:HG23	2.55	0.42
6:FE:824:TYR:HB2	7:GE:964:GLN:NE2	2.35	0.42
6:FE:1227:ARG:O	6:FE:1228:ARG:C	2.61	0.42
6:FF:830:ALA:HB1	6:FF:843:LEU:CD2	2.50	0.42
6:FF:975:ILE:HG21	6:FF:989:PRO:HD3	2.02	0.42
6:FF:1096:LEU:HD13	6:FF:1096:LEU:HA	1.90	0.42
6:FF:1217:GLU:HB3	6:FF:1218:ALA:H	1.69	0.42
6:FF:1218:ALA:O	6:FF:1220:ARG:N	2.53	0.42
6:FF:1296:SER:O	6:FF:1297:PRO:C	2.63	0.42
7:GA:441:LEU:HD22	7:GA:505:PHE:HE1	1.83	0.42
7:GC:605:VAL:HG13	7:GC:630:LEU:HD11	2.02	0.42
7:GC:794:ALA:HA	7:GC:797:ILE:HG22	2.02	0.42
7:GC:910:HIS:CE1	12:KA:340:ALA:HA	2.55	0.42
8:GD:171:ILE:HG23	8:GD:181:HIS:HB2	2.00	0.42
7:GE:341:PRO:HD3	7:GE:597:THR:HA	2.02	0.42
7:GE:454:PHE:HZ	7:GE:592:ILE:HD12	1.85	0.42
8:GH:133:PRO:HG2	8:GH:168:MET:HE2	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GH:535:GLU:HB3	8:GH:631:LEU:HD11	2.01	0.42
7:GI:390:ILE:HG22	7:GI:462:GLY:HA3	2.02	0.42
7:GI:870:ARG:HE	7:GI:872:THR:HG21	1.84	0.42
9:HA:771:PRO:HG3	9:HA:819:TYR:CZ	2.55	0.42
9:HA:836:SER:O	9:HA:837:LEU:C	2.63	0.42
9:HB:400:ALA:HA	9:HB:402:ARG:NH1	2.35	0.42
9:HB:782:ALA:O	9:HB:783:SER:C	2.62	0.42
9:HB:795:LEU:HD23	9:HB:795:LEU:HA	1.78	0.42
10:IB:500:LEU:HA	10:IB:503:LEU:HD12	2.01	0.42
10:IB:821:MET:HE2	10:IB:821:MET:HB2	1.97	0.42
10:IC:300:LEU:HD23	10:IC:302:THR:H	1.83	0.42
12:KC:308:LEU:HA	12:KC:337:ALA:HB2	2.01	0.42
12:KF:212:LEU:HD13	12:KF:290:PRO:HB2	2.02	0.42
13:LI:526:LEU:HD23	13:LI:526:LEU:HA	1.80	0.42
14:MJ:207:LEU:HD23	14:MJ:207:LEU:HA	1.95	0.42
15:NA:558:GLU:HB2	15:NA:578:HIS:NE2	2.32	0.42
15:NA:883:LEU:HD23	15:NA:1123:ALA:HB1	2.02	0.42
15:NB:996:LEU:HD13	15:NB:1015:ALA:HB1	2.02	0.42
15:NB:1180:ASP:HB3	15:NB:1181:SER:H	1.61	0.42
15:NC:1407:MET:HB3	15:NC:1469:PHE:HB3	2.02	0.42
15:NC:1521:SER:O	15:NC:1525:ARG:HG2	2.20	0.42
19:RB:26:HIS:CE1	19:RB:29:GLU:HB3	2.55	0.42
20:SD:106:LEU:O	20:SD:110:MET:HG2	2.19	0.42
2:AB:328:HIS:CD2	2:AB:337:HIS:HB2	2.55	0.42
1:AD:988:GLN:HA	1:AD:988:GLN:NE2	2.35	0.42
1:AE:655:SER:HA	1:AE:659:PHE:HD1	1.84	0.42
2:AG:105:ASN:HB2	2:AG:264:THR:HG23	2.02	0.42
1:AI:265:VAL:HG23	1:AI:266:HIS:CD2	2.55	0.42
1:AI:1004:VAL:HG23	1:AI:1008:ALA:HB3	2.01	0.42
1:AL:894:SER:O	13:LE:502:MET:HE1	2.20	0.42
3:CC:976:LYS:HA	3:CC:976:LYS:HD2	1.86	0.42
3:CF:1129:ARG:HD3	10:IB:1264:ILE:HD11	2.01	0.42
4:DA:175:TYR:HE2	4:DD:186:THR:OG1	2.03	0.42
4:DB:130:ARG:CZ	4:DB:151:ALA:HA	2.50	0.42
4:DC:365:ILE:HG21	4:DC:378:ILE:HG21	2.02	0.42
4:DE:299:ARG:HD3	4:DE:299:ARG:HA	1.81	0.42
5:EA:4282:SER:HA	5:EA:4285:THR:HG22	2.01	0.42
5:EB:3320:LEU:HD13	5:EB:3412:LEU:HD22	2.02	0.42
5:EB:3433:ALA:O	5:EB:3436:TYR:HB3	2.20	0.42
5:EB:4465:PHE:HD2	5:EB:4666:VAL:HG12	1.84	0.42
5:EB:4487:ASP:HA	5:EB:4490:THR:HG22	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EC:3704:SER:HB2	5:EC:3829:PHE:CE1	2.55	0.42
5:EC:4403:LEU:CB	5:EC:4405:ILE:HD11	2.50	0.42
5:EC:4405:ILE:HG22	5:EC:4406:MET:N	2.35	0.42
6:FA:1962:GLN:O	6:FA:1966:ASP:HB2	2.20	0.42
6:FD:824:TYR:HB2	7:GC:964:GLN:NE2	2.34	0.42
6:FD:841:TYR:CD2	6:FD:841:TYR:C	2.98	0.42
6:FE:895:ILE:HG12	7:GE:967:PHE:CZ	2.55	0.42
6:FE:1218:ALA:HB3	6:FE:1276:LEU:HD13	2.02	0.42
6:FF:1003:ILE:HG21	6:FF:1444:ARG:HH12	1.84	0.42
6:FF:1027:LEU:O	6:FF:1030:ILE:N	2.48	0.42
7:GA:538:THR:H	9:HB:554:ASP:C	2.28	0.42
8:GD:656:ALA:HB3	8:GD:742:SER:H	1.84	0.42
7:GE:239:ASN:HB2	7:GE:693:THR:HG21	2.01	0.42
7:GE:765:PRO:HB3	7:GE:791:ARG:HG3	2.02	0.42
7:GI:340:LEU:HA	7:GI:597:THR:HG22	2.00	0.42
7:GK:421:SER:HA	7:GK:424:ARG:NE	2.34	0.42
8:GL:29:ILE:HG22	8:GL:31:LEU:H	1.85	0.42
8:GL:342:LYS:HE2	8:GL:342:LYS:HB2	1.79	0.42
9:HA:674:VAL:HG13	9:HA:712:ILE:HG12	2.01	0.42
9:HA:843:VAL:O	9:HA:846:VAL:HB	2.20	0.42
9:HD:808:HIS:O	9:HD:812:THR:HG23	2.20	0.42
10:IA:588:LYS:HE2	10:IA:604:CYS:HB3	2.02	0.42
10:IB:893:PHE:CZ	10:IB:907:ASP:HA	2.55	0.42
10:IB:1223:LEU:HD23	10:IB:1387:LEU:HD22	2.02	0.42
11:JA:1991:ASP:HA	11:JA:1994:GLU:HB3	2.02	0.42
11:JB:83:VAL:HG21	11:JB:100:ILE:HD11	2.02	0.42
11:JB:472:CYS:HB3	11:JB:879:LEU:HD11	2.02	0.42
11:JB:1387:LEU:HG	11:JB:1409:ARG:HB2	2.02	0.42
11:JC:191:ASP:HB3	11:JC:194:VAL:HB	2.02	0.42
11:JC:533:ILE:HG22	11:JC:534:TYR:CD1	2.55	0.42
11:JC:1158:MET:HE2	11:JC:1161:LEU:HD21	2.02	0.42
12:KA:526:TRP:CE2	12:KA:582:ILE:HD13	2.54	0.42
12:KE:579:LEU:HD23	12:KE:656:ARG:HA	2.02	0.42
12:KF:279:VAL:HG11	12:KF:282:LYS:HD3	2.02	0.42
13:LI:527:VAL:HG11	13:LJ:528:PRO:HG3	2.01	0.42
15:NA:601:THR:HG23	15:NA:1190:ILE:HG23	2.01	0.42
15:NA:647:GLN:HE21	15:NA:647:GLN:HB3	1.74	0.42
15:NB:1116:ASP:HB2	15:NB:1119:SER:HB2	2.00	0.42
15:NC:1536:GLN:HE22	19:RA:113:ARG:HH21	1.68	0.42
15:ND:1548:PHE:HB3	19:RD:136:ALA:HA	2.02	0.42
16:OC:171:PHE:CG	16:OC:180:LYS:HD3	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:PC:128:GLU:HG3	17:PC:132:LEU:HD12	2.01	0.42
1:AA:683:ASN:C	1:AA:683:ASN:HD22	2.28	0.41
2:AC:528:LEU:HD22	1:AD:91:ILE:HB	2.01	0.41
1:AE:653:LEU:HD23	1:AE:653:LEU:HA	1.90	0.41
1:AE:1004:VAL:HG13	1:AE:1006:ARG:HH22	1.85	0.41
2:AF:45:LEU:HD13	5:EB:4525:VAL:HG11	2.01	0.41
3:CA:731:MET:HE2	3:CA:731:MET:HB2	1.93	0.41
3:CC:742:LYS:HA	3:CC:746:THR:HB	2.01	0.41
4:DB:75:TYR:HD1	4:DB:78:LYS:HZ3	1.68	0.41
5:EA:3610:GLN:HG2	5:EA:3611:GLU:HG2	2.00	0.41
5:EB:4156:LEU:HD12	9:HB:431:TYR:CE1	2.55	0.41
5:EB:4759:LYS:HB2	5:EB:4759:LYS:HE3	1.77	0.41
5:EC:4465:PHE:HD2	5:EC:4666:VAL:HG12	1.85	0.41
6:FA:2097:GLN:HA	6:FA:2100:SER:HB3	2.01	0.41
6:FC:2023:ILE:CG2	9:HB:778:PRO:HB3	2.49	0.41
6:FD:819:PRO:HG3	6:FD:895:ILE:CD1	2.50	0.41
6:FF:818:VAL:O	6:FF:821:ARG:HB2	2.19	0.41
7:GA:491:GLU:HA	7:GA:494:LEU:HD23	2.02	0.41
8:GB:135:LEU:HB2	8:GB:294:TRP:CZ3	2.55	0.41
7:GC:619:ARG:HH12	7:GC:629:ASP:HA	1.84	0.41
7:GE:176:ARG:HA	7:GE:176:ARG:HD2	1.93	0.41
10:IC:635:LEU:HD12	10:IC:638:ARG:HD3	2.02	0.41
11:JA:57:GLU:HB3	11:JA:90:ARG:HE	1.85	0.41
11:JA:1409:ARG:HG3	11:JA:1410:LEU:H	1.85	0.41
11:JA:1734:VAL:HG11	11:JA:1774:ARG:HG3	2.02	0.41
11:JB:838:ASP:OD1	11:JB:1423:PRO:HD2	2.20	0.41
11:JC:2255:ARG:HD3	11:JC:2255:ARG:HA	1.87	0.41
12:KB:258:LEU:HA	12:KB:261:VAL:HG12	2.01	0.41
12:KC:586:ARG:HH21	12:KC:712:GLY:HA2	1.84	0.41
13:LI:473:LYS:O	13:LI:476:GLY:HA3	2.20	0.41
13:LK:421:VAL:HG11	13:LL:421:VAL:HG22	2.02	0.41
14:MB:294:ALA:HA	14:MB:297:VAL:HG12	2.02	0.41
15:NA:622:THR:HG23	15:NA:650:ARG:HH22	1.85	0.41
15:NB:676:ARG:HA	15:NB:676:ARG:HD3	1.82	0.41
15:NC:1193:VAL:HG11	15:NC:1391:LEU:HD21	2.02	0.41
15:ND:525:LEU:HD21	15:ND:545:VAL:HG11	2.02	0.41
15:ND:542:LEU:HB3	15:ND:1190:ILE:HA	2.02	0.41
15:ND:568:TYR:HE2	16:OC:1038:ARG:HE	1.68	0.41
16:OC:1055:ARG:NH1	16:OC:1059:LEU:HD23	2.35	0.41
18:QB:119:LEU:HD22	18:QB:123:VAL:HG11	2.02	0.41
19:RA:20:PRO:HD2	19:RA:101:ASP:HA	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:89:GLY:HA3	1:AA:154:GLY:HA2	2.02	0.41
1:AA:418:ILE:O	1:AA:421:MET:HB2	2.20	0.41
1:AD:132:PRO:HA	1:AD:133:PRO:HD3	1.96	0.41
2:AF:29:LEU:HD13	2:AF:283:LEU:HD21	2.02	0.41
2:AG:428:ARG:HH11	1:AH:415:MET:HE3	1.85	0.41
2:AK:450:ARG:HD2	11:JB:1724:PHE:HE1	1.85	0.41
3:CB:765:VAL:HG12	3:CB:829:LEU:HD22	2.02	0.41
3:CF:1179:ILE:HD13	3:CF:4517:LEU:HD22	2.00	0.41
3:CL:1237:VAL:HA	3:CL:1244:PRO:HA	2.02	0.41
4:DA:310:LEU:HD23	4:DA:310:LEU:HA	1.87	0.41
5:EA:4209:HIS:O	5:EA:4213:LYS:HG2	2.20	0.41
5:EC:3446:ILE:HD12	5:EC:3490:TYR:HB3	2.01	0.41
6:FA:1823:ALA:HA	6:FA:1842:VAL:HA	2.01	0.41
6:FC:2042:LYS:HA	6:FC:2042:LYS:HD2	1.86	0.41
6:FC:2073:LEU:HD12	6:FC:2073:LEU:HA	1.75	0.41
6:FD:864:LEU:HD11	6:FD:973:ILE:HD12	2.02	0.41
6:FE:1241:VAL:HG22	6:FE:1260:LEU:HD12	2.01	0.41
6:FF:965:TRP:N	6:FF:965:TRP:CD1	2.88	0.41
6:FF:1194:ASN:HD22	6:FF:1194:ASN:HA	1.59	0.41
6:FF:1253:SER:O	6:FF:1254:GLY:C	2.62	0.41
7:GA:548:ALA:HB1	9:HB:666:LYS:HB2	2.02	0.41
8:GB:326:ARG:HH22	8:GB:375:TYR:H	1.68	0.41
8:GB:563:ARG:HA	8:GB:566:ILE:HG22	2.01	0.41
8:GD:200:GLY:HA2	8:GD:281:LEU:HD22	2.01	0.41
8:GD:689:PHE:HA	8:GD:692:MET:SD	2.60	0.41
7:GE:190:SER:HA	7:GE:648:LEU:HD13	2.02	0.41
7:GI:916:HIS:NE2	12:KC:663:ALA:HB2	2.35	0.41
8:GJ:348:TYR:HB3	8:GJ:380:MET:SD	2.60	0.41
7:GK:719:ILE:HG12	7:GK:800:VAL:HG11	2.02	0.41
8:GL:56:CYS:HB2	8:GL:61:CYS:HB2	2.02	0.41
9:HB:764:LYS:H	9:HB:764:LYS:HG2	1.61	0.41
9:HD:826:ARG:O	9:HD:830:ILE:HG13	2.21	0.41
10:IC:551:ASN:ND2	10:IC:852:CYS:HA	2.35	0.41
11:JA:1298:ILE:HG12	11:JA:1348:PHE:HB2	2.01	0.41
11:JA:1756:ALA:HA	11:JA:1759:LEU:HD23	2.02	0.41
11:JB:428:GLU:HA	11:JB:431:ALA:HB3	2.02	0.41
11:JB:1464:HIS:HD1	11:JB:1464:HIS:C	2.28	0.41
11:JC:48:GLN:HA	11:JC:95:PRO:HB3	2.02	0.41
11:JC:519:PHE:HE1	11:JC:1473:LEU:HD13	1.84	0.41
11:JC:2005:ILE:HD13	11:JC:2005:ILE:HA	1.91	0.41
12:KB:520:LYS:HG3	12:KB:522:ARG:H	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LF:509:GLU:HG2	13:LF:512:ARG:NH2	2.35	0.41
13:LJ:424:LEU:HA	13:LJ:427:ARG:NH1	2.35	0.41
15:NC:529:PHE:CD2	15:NC:1382:PHE:HB2	2.55	0.41
15:NC:898:ASN:HB3	15:NC:902:ARG:HE	1.85	0.41
15:NC:1426:PRO:HG2	16:OA:949:PRO:HB2	2.02	0.41
1:AA:315:LEU:HD12	1:AA:316:ILE:HB	2.03	0.41
2:AB:113:LEU:HG	11:JA:1649:LEU:HD11	2.01	0.41
2:AB:355:HIS:HA	2:AB:356:PRO:HD3	1.90	0.41
1:AE:51:GLU:HG3	1:AE:64:HIS:HA	2.03	0.41
1:AE:998:LEU:HD12	1:AE:998:LEU:HA	1.84	0.41
2:AG:263:TYR:CE1	16:OC:11:GLY:HA3	2.55	0.41
4:DB:281:GLN:HG3	4:DB:285:ARG:HH22	1.85	0.41
5:EA:3239:SER:HB2	5:EA:3268:ASN:HB3	2.02	0.41
5:EA:3382:GLU:OE1	5:EA:3384:LYS:HG2	2.20	0.41
5:EA:4446:ARG:NH2	17:PB:143:ILE:HD11	2.35	0.41
5:EA:4744:GLN:HA	5:EA:4747:MET:HG2	2.00	0.41
5:EB:3534:PHE:O	5:EB:3538:GLN:HG3	2.19	0.41
5:EB:4024:THR:HG21	9:HB:435:LEU:HD23	2.03	0.41
5:EB:4307:MET:HE3	5:EB:4350:LYS:HG3	2.03	0.41
6:FA:2040:LEU:HD23	6:FA:2040:LEU:HA	1.74	0.41
6:FC:2038:LEU:HD13	6:FC:2038:LEU:HA	1.87	0.41
6:FF:1203:ARG:HH22	11:JB:957:ASP:HA	1.85	0.41
7:GA:293:VAL:HG22	7:GA:688:ARG:HH12	1.85	0.41
8:GB:29:ILE:HG21	8:GB:528:VAL:HG21	2.01	0.41
8:GB:294:TRP:CG	8:GB:297:LEU:HD12	2.55	0.41
8:GB:725:CYS:HA	8:GB:730:SER:HB3	2.02	0.41
8:GD:22:THR:HG23	8:GD:25:GLU:H	1.85	0.41
7:GE:169:ILE:HD13	7:GE:697:PRO:HG3	2.02	0.41
7:GE:289:SER:HA	7:GE:691:VAL:O	2.20	0.41
7:GE:402:PHE:HE2	7:GE:447:VAL:HB	1.85	0.41
7:GE:446:HIS:CD2	7:GE:447:VAL:HG23	2.56	0.41
8:GF:149:LEU:HD12	8:GF:149:LEU:HA	1.90	0.41
8:GH:183:LEU:HD21	8:GH:245:ILE:HA	2.02	0.41
8:GH:710:LYS:HA	8:GH:710:LYS:HD3	1.69	0.41
7:GK:543:LYS:HA	7:GK:544:PRO:HD3	1.97	0.41
9:HA:526:VAL:O	9:HA:578:THR:HA	2.20	0.41
9:HA:824:LEU:O	9:HA:827:ASP:N	2.53	0.41
9:HD:758:ALA:O	9:HD:759:GLU:C	2.63	0.41
10:IA:486:PRO:HA	10:IA:489:TYR:CZ	2.56	0.41
10:IA:616:GLY:H	10:IA:758:ASN:ND2	2.14	0.41
10:IA:751:ASN:HB3	10:IA:752:SER:H	1.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IA:882:VAL:HB	10:IA:884:TYR:CE1	2.55	0.41
10:IB:230:ARG:HD3	11:JB:2054:ARG:HD2	2.02	0.41
10:IB:837:VAL:HB	10:IB:873:LEU:HD11	2.00	0.41
10:IC:740:ARG:HH12	10:IC:777:GLY:HA3	1.85	0.41
10:IC:789:ARG:HA	10:IC:792:ILE:HG22	2.02	0.41
11:JA:1514:VAL:HA	11:JA:1517:ILE:HG22	2.01	0.41
11:JB:1090:LEU:HD12	11:JB:1090:LEU:HA	1.92	0.41
11:JC:83:VAL:HG11	11:JC:100:ILE:HD11	2.01	0.41
12:KC:391:LEU:HA	12:KC:391:LEU:HD12	1.71	0.41
12:KE:633:ARG:HH12	12:KE:635:VAL:HG22	1.85	0.41
13:LF:530:VAL:HG21	13:LH:532:LEU:HD22	2.01	0.41
14:MA:247:LEU:HD11	14:MB:248:SER:HA	2.02	0.41
14:MF:292:ALA:HA	14:MF:295:GLU:HB2	2.02	0.41
15:NA:600:LEU:HD13	15:NA:917:MET:HB3	2.02	0.41
15:NB:729:VAL:HG11	15:NB:800:SER:HB3	2.03	0.41
15:NB:1552:ILE:HD12	19:RB:143:LEU:HA	2.02	0.41
15:NC:587:LEU:HA	15:NC:590:VAL:HB	2.03	0.41
15:NC:602:PHE:HD2	15:NC:1191:ALA:HB2	1.85	0.41
15:NC:1498:ARG:HD3	20:SD:41:GLY:HA2	2.01	0.41
15:ND:735:HIS:CE1	15:ND:768:GLU:HA	2.55	0.41
18:QB:120:LYS:HB2	18:QB:123:VAL:HG23	2.02	0.41
2:AB:374:LEU:HD23	5:EA:4442:GLU:HG3	2.02	0.41
1:AD:656:ASP:HA	9:HB:514:PHE:CD1	2.55	0.41
2:AF:169:VAL:HG12	2:AF:171:VAL:HG13	2.02	0.41
1:AL:987:LEU:HD13	7:GK:424:ARG:NH2	2.29	0.41
3:BA:731:MET:HE1	3:BA:768:CYS:SG	2.60	0.41
3:CC:689:LEU:HD12	3:CC:736:HIS:NE2	2.35	0.41
3:CF:1170:THR:HA	3:CF:4501:GLN:HB2	2.03	0.41
3:CG:1262:HIS:CE1	3:CG:4454:ASP:HA	2.54	0.41
3:CG:1264:VAL:HG13	3:CG:1265:ILE:HD12	2.01	0.41
3:CG:4521:ARG:HD3	3:CG:4521:ARG:HA	1.83	0.41
3:CI:4522:LEU:HB3	3:CI:4524:LEU:HD13	2.01	0.41
3:CJ:1236:LEU:HD11	3:CJ:4502:VAL:HG11	2.02	0.41
4:DC:66:ARG:HA	4:DC:66:ARG:HD2	1.87	0.41
4:DE:298:LEU:HD23	4:DE:298:LEU:HA	1.93	0.41
5:EA:3564:ARG:HA	5:EA:3564:ARG:HD3	1.83	0.41
5:EB:3720:LEU:HD12	5:EB:3805:PHE:HE2	1.85	0.41
5:EB:4401:PRO:O	5:EB:4402:PRO:C	2.63	0.41
5:EC:4892:ARG:O	5:EC:4893:THR:C	2.61	0.41
6:FA:1712:GLU:HG2	6:FA:1716:SER:HB2	2.02	0.41
6:FA:2023:ILE:HG22	9:HA:778:PRO:HB3	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FB:2069:ASN:O	6:FB:2072:ILE:N	2.53	0.41
6:FC:2055:THR:OG1	6:FC:2056:LEU:N	2.53	0.41
6:FC:2080:GLN:HB3	9:HB:861:TYR:CE2	2.51	0.41
6:FE:927:GLY:O	6:FE:928:SER:C	2.62	0.41
6:FE:1219:GLU:H	6:FE:1219:GLU:HG2	1.51	0.41
6:FF:925:GLU:CG	6:FF:1092:PRO:HB2	2.46	0.41
6:FF:1187:ILE:O	6:FF:1267:GLN:HA	2.21	0.41
6:FF:1215:MET:HG2	6:FF:1219:GLU:HG3	2.01	0.41
8:GB:263:ARG:HE	7:GC:380:ARG:NH2	2.18	0.41
8:GB:283:LEU:HD21	8:GB:303:LEU:HD22	2.01	0.41
7:GC:165:VAL:HB	7:GC:697:PRO:HG3	2.02	0.41
7:GC:340:LEU:HA	7:GC:597:THR:HG22	2.03	0.41
7:GC:451:ILE:HD11	7:GC:516:VAL:HG23	2.02	0.41
7:GC:607:ARG:HG3	7:GC:677:ALA:HB3	2.02	0.41
8:GD:638:LEU:HD22	8:GD:654:LEU:HA	2.02	0.41
8:GH:189:ASN:HD21	7:GI:422:LEU:HA	1.85	0.41
7:GK:974:ARG:HB3	7:GK:979:LEU:HA	2.02	0.41
9:HA:482:ALA:HB2	9:HA:613:ILE:HD12	2.02	0.41
9:HB:865:ILE:HA	9:HB:865:ILE:HD12	1.57	0.41
9:HD:769:LYS:HE2	9:HD:826:ARG:HD2	2.03	0.41
10:IA:614:LEU:HD21	10:IA:759:PHE:HB3	2.02	0.41
10:IA:1309:ILE:HA	10:IA:1312:ILE:HG22	2.03	0.41
10:IB:172:GLN:HB3	10:IB:173:GLN:H	1.58	0.41
10:IB:537:LEU:HD22	10:IB:558:VAL:HG11	2.01	0.41
10:IC:452:LEU:HD23	10:IC:503:LEU:HD12	2.03	0.41
10:IC:735:LYS:HG3	10:IC:738:PRO:HD2	2.02	0.41
10:IC:994:MET:HE2	10:IC:994:MET:HB2	1.80	0.41
11:JA:473:ASN:ND2	11:JA:876:GLN:HB3	2.35	0.41
11:JA:489:VAL:HG22	11:JA:490:THR:H	1.84	0.41
11:JB:123:ILE:HG13	11:JB:135:ILE:HB	2.02	0.41
11:JB:536:ILE:HD12	11:JB:551:PRO:HG2	2.01	0.41
11:JB:1587:TRP:HB3	11:JB:1591:HIS:HB2	2.02	0.41
11:JB:2009:LEU:HD23	11:JB:2009:LEU:HA	1.94	0.41
11:JC:1110:PRO:HA	11:JC:1114:ALA:HB3	2.02	0.41
12:KA:476:MET:O	12:KA:480:VAL:HG13	2.20	0.41
12:KB:486:PHE:HE2	12:KB:506:LEU:HD13	1.86	0.41
12:KC:361:GLN:HA	12:KC:364:LEU:HD23	2.01	0.41
12:KC:377:LEU:HD12	12:KC:383:HIS:CE1	2.54	0.41
12:KE:547:ARG:HG3	12:KE:711:ILE:HD13	2.01	0.41
12:KG:367:ILE:HG23	12:KG:397:GLN:NE2	2.35	0.41
13:LH:506:GLN:O	13:LH:510:ILE:HG12	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LJ:457:GLN:HA	13:LJ:460:ARG:NH1	2.35	0.41
13:LO:399:ASP:HA	13:LO:402:LEU:HB2	2.02	0.41
14:MG:98:ASN:O	14:MG:102:LYS:HG3	2.21	0.41
15:NA:682:ARG:NH1	15:NA:915:VAL:HG13	2.34	0.41
15:NA:739:HIS:HB3	15:NA:742:LEU:HB2	2.02	0.41
15:NA:1533:LYS:HA	15:NA:1536:GLN:HE21	1.84	0.41
15:NC:926:ARG:HD3	15:NC:1111:ARG:HB2	2.02	0.41
16:OB:1089:LEU:HD22	16:OB:1092:ARG:HH21	1.85	0.41
19:RA:62:LEU:HD23	19:RA:67:VAL:HG12	2.01	0.41
2:AB:108:LEU:HA	2:AB:108:LEU:HD23	1.77	0.41
2:AC:32:LEU:HD21	1:AD:451:ILE:HD11	2.01	0.41
1:AD:389:LEU:HD12	5:EA:4619:VAL:HG21	2.02	0.41
1:AE:399:ARG:HG2	1:AE:400:LYS:HG3	2.02	0.41
1:AE:669:SER:HB2	1:AE:674:ARG:HE	1.85	0.41
2:AG:90:ARG:HE	2:AG:90:ARG:HB2	1.70	0.41
1:AI:284:PRO:HA	1:AI:333:LEU:HD23	2.02	0.41
2:AJ:271:VAL:HG12	2:AJ:273:ASP:H	1.85	0.41
3:BA:880:GLN:O	3:BA:884:LEU:HD23	2.21	0.41
3:CE:1235:PRO:HA	3:CE:1254:MET:HA	2.01	0.41
3:CE:1264:VAL:HG13	3:CE:1265:ILE:HD12	2.03	0.41
3:CJ:4470:LYS:HB2	3:CJ:4470:LYS:HE3	1.84	0.41
4:DB:254:GLU:HB2	4:DB:291:GLN:NE2	2.35	0.41
4:DC:172:ARG:O	4:DC:176:ILE:HG12	2.21	0.41
4:DC:272:LEU:HD23	4:DC:272:LEU:HA	1.94	0.41
4:DE:253:LEU:HA	4:DE:256:LEU:HG	2.01	0.41
4:DF:59:TYR:CE2	4:DF:166:VAL:HG11	2.56	0.41
5:EA:3304:LYS:HG2	9:HC:416:PHE:HE1	1.86	0.41
5:EA:4223:THR:O	5:EA:4225:LYS:HG2	2.21	0.41
5:EC:4521:TYR:HB2	5:EC:4711:LEU:HD21	2.02	0.41
6:FB:1946:LEU:HD22	6:FB:1954:ALA:HB1	2.01	0.41
6:FC:2069:ASN:HB2	9:HB:851:GLU:CD	2.45	0.41
6:FD:1075:VAL:O	6:FD:1076:ILE:C	2.64	0.41
6:FE:882:SER:N	6:FE:904:GLN:OE1	2.51	0.41
6:FF:802:LEU:HD21	6:FF:968:LEU:HD22	2.01	0.41
6:FF:910:ILE:O	6:FF:910:ILE:HG13	2.19	0.41
6:FF:1095:LEU:O	6:FF:1096:LEU:C	2.64	0.41
6:FF:1096:LEU:O	6:FF:1099:ILE:HB	2.20	0.41
6:FF:1389:ARG:CZ	6:FF:1391:TYR:HA	2.50	0.41
6:FF:1394:ARG:O	6:FF:1396:PHE:N	2.53	0.41
6:FF:1420:ARG:O	6:FF:1421:VAL:C	2.63	0.41
8:GB:522:GLU:OE2	8:GB:524:ASN:HB2	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GC:827:LEU:HD12	7:GC:832:ILE:HD13	2.03	0.41
8:GD:401:ASP:HA	8:GD:404:ARG:HG2	2.02	0.41
8:GD:723:VAL:HG11	8:GD:731:GLN:HB2	2.02	0.41
7:GG:873:ALA:HA	7:GG:876:MET:HE3	2.02	0.41
8:GH:137:PHE:CE1	8:GH:245:ILE:HG21	2.55	0.41
8:GL:172:ILE:HG12	8:GL:180:LEU:HA	2.03	0.41
9:HA:822:ASP:O	9:HA:823:ILE:C	2.63	0.41
9:HD:877:LYS:HD3	9:HD:877:LYS:HA	1.60	0.41
10:IA:1079:LYS:HE3	10:IA:1083:MET:HE3	2.03	0.41
10:IB:238:ARG:HD3	11:JB:2050:TYR:HB3	2.03	0.41
11:JA:1996:LEU:HD23	11:JA:1996:LEU:HA	1.93	0.41
11:JB:1484:LEU:HB3	11:JB:1488:ASN:HB2	2.02	0.41
11:JB:1728:SER:HA	11:JB:1733:THR:HG21	2.02	0.41
11:JC:1068:ASP:HA	11:JC:1069:PRO:HD3	1.94	0.41
11:JC:1404:GLN:HB2	11:JC:1407:HIS:CE1	2.55	0.41
11:JC:1437:ILE:HA	11:JC:1438:PRO:HD3	1.89	0.41
12:KA:547:ARG:HB3	12:KA:712:GLY:H	1.85	0.41
12:KA:597:ALA:HB2	12:KA:608:VAL:HG12	2.02	0.41
12:KC:234:PRO:O	12:KC:235:PRO:C	2.64	0.41
12:KE:322:ALA:HA	12:KE:325:LEU:HB2	2.02	0.41
13:LA:513:LEU:HD23	13:LA:513:LEU:HA	1.80	0.41
13:LI:388:LEU:HD11	13:LJ:384:LEU:HD13	2.02	0.41
14:MI:225:VAL:HG21	14:MI:315:TRP:NE1	2.35	0.41
15:NA:867:ARG:HA	15:NA:870:TYR:CE1	2.55	0.41
15:NA:874:GLN:HB3	15:NA:877:GLN:HB2	2.01	0.41
15:NA:966:VAL:HG22	15:NA:1462:GLN:HE21	1.84	0.41
15:ND:686:ASN:ND2	15:ND:905:ASP:HB3	2.36	0.41
1:AA:835:ALA:HB1	1:AA:915:TRP:CZ3	2.55	0.41
2:AB:475:MET:HE3	2:AB:475:MET:HB3	1.76	0.41
1:AE:66:VAL:HG11	17:PC:266:HIS:HB3	2.02	0.41
1:AI:62:ASP:HB2	1:AI:228:PRO:HB3	2.02	0.41
2:AK:265:PHE:HD1	16:OB:140:THR:HG22	1.85	0.41
1:AL:615:ILE:HD13	1:AL:618:ARG:HE	1.85	0.41
3:CC:1014:ASP:HA	3:CC:1017:ARG:HG2	2.02	0.41
4:DB:272:LEU:HD23	4:DB:272:LEU:HA	1.92	0.41
4:DB:297:ARG:HH22	13:LE:460:ARG:NH2	2.18	0.41
4:DD:367:ARG:HD2	4:DD:367:ARG:HA	1.86	0.41
4:DF:97:LEU:HD21	4:DF:164:PHE:HE2	1.85	0.41
4:DF:163:GLU:O	4:DF:166:VAL:HG22	2.20	0.41
5:EA:3672:GLU:HA	5:EA:3675:GLU:HB2	2.02	0.41
5:EA:3822:SER:HB3	5:EA:4243:PHE:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:3681:LEU:HD11	5:EB:3715:VAL:HA	2.01	0.41
5:EB:4658:ASP:HA	5:EB:4690:CYS:SG	2.60	0.41
6:FA:1866:ILE:HG23	6:FA:1867:THR:HG23	2.03	0.41
6:FB:2040:LEU:HA	6:FB:2040:LEU:HD23	1.79	0.41
6:FC:1991:ALA:HA	6:FC:1994:ARG:NE	2.33	0.41
6:FD:842:GLY:O	6:FD:843:LEU:C	2.62	0.41
6:FD:1388:PHE:CE1	6:FD:1390:ALA:HA	2.56	0.41
6:FE:1181:VAL:HG22	6:FE:1182:ALA:H	1.86	0.41
6:FF:854:TRP:NE1	6:FF:971:SER:OG	2.50	0.41
8:GB:274:ARG:HH12	8:GB:308:ALA:HB3	1.85	0.41
8:GB:301:VAL:HB	8:GB:362:VAL:HG12	2.02	0.41
7:GC:309:LEU:HD21	7:GC:451:ILE:HG22	2.01	0.41
7:GC:946:HIS:CE1	7:GC:948:CYS:HB2	2.55	0.41
7:GG:535:PRO:HB2	9:HA:552:ASP:C	2.46	0.41
8:GL:667:LEU:HD22	8:GL:735:LEU:HA	2.02	0.41
9:HC:561:ASN:HD21	9:HC:570:ALA:HB3	1.85	0.41
10:IB:469:LEU:HA	10:IB:472:LYS:NZ	2.35	0.41
10:IC:337:LEU:HD13	10:IC:561:ARG:HE	1.84	0.41
11:JB:1122:ARG:HG3	11:JB:1123:THR:HG23	2.02	0.41
11:JB:1479:ALA:HA	11:JB:1482:LYS:HG2	2.02	0.41
11:JC:929:LEU:HD21	11:JC:966:LEU:HD11	2.02	0.41
11:JC:1150:PHE:HE1	11:JC:1154:ARG:HH21	1.68	0.41
11:JC:1553:LEU:HD23	11:JC:1553:LEU:HA	1.93	0.41
12:KA:345:GLY:HA3	12:KA:346:PRO:HD3	1.95	0.41
12:KC:236:LYS:C	12:KC:238:PHE:N	2.78	0.41
12:KF:322:ALA:HB1	12:KF:327:MET:HB2	2.03	0.41
13:LA:483:ARG:HH11	13:LA:483:ARG:HG3	1.85	0.41
13:LE:377:GLN:HA	13:LE:380:MET:HG2	2.02	0.41
13:LN:372:THR:HA	13:LN:375:ILE:HG22	2.01	0.41
15:NA:605:LEU:HB2	15:NA:923:ASP:HB2	2.02	0.41
15:NC:570:GLY:HA3	15:NC:575:LEU:HD21	2.02	0.41
15:NC:578:HIS:ND1	15:NC:580:PHE:HD2	2.19	0.41
15:NC:722:VAL:HG13	15:NC:726:CYS:HB2	2.03	0.41
15:ND:1541:PHE:O	15:ND:1545:VAL:HG23	2.21	0.41
19:RA:46:SER:H	19:RA:49:ASP:HB2	1.84	0.41
20:SC:143:VAL:O	20:SC:146:MET:HB2	2.21	0.41
1:AA:64:HIS:NE2	17:PA:268:PRO:HD2	2.36	0.41
2:AF:46:GLN:HB3	2:AF:48:TRP:CZ3	2.56	0.41
1:AI:91:ILE:HD12	1:AI:91:ILE:HG23	1.79	0.41
2:AK:380:LEU:HG	5:EA:4351:VAL:O	2.21	0.41
1:AL:628:ASN:HB3	13:LH:512:ARG:HG2	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:661:PRO:HB3	1:AL:1052:LEU:HD11	2.03	0.41
3:BB:727:TYR:HE1	3:BB:770:LEU:HD13	1.85	0.41
3:BB:812:MET:HA	16:OB:196:TRP:CZ3	2.56	0.41
3:BC:836:PRO:HG3	16:OC:155:SER:HB3	2.02	0.41
3:CB:905:HIS:NE2	3:CB:907:ARG:HG2	2.36	0.41
3:CL:1237:VAL:HG11	3:CL:4468:LYS:HD3	2.01	0.41
4:DA:53:LYS:HD2	4:DA:53:LYS:HA	1.87	0.41
4:DE:43:PRO:HG3	8:GB:680:LEU:HD22	2.03	0.41
4:DE:247:ARG:HD2	4:DE:290:ARG:NH1	2.35	0.41
4:DF:105:CYS:H	4:DF:260:GLY:N	2.19	0.41
5:EB:3289:ILE:HD11	9:HB:432:LEU:HB3	2.03	0.41
5:EB:3841:GLN:HB3	11:JA:1041:LYS:NZ	2.36	0.41
5:EB:4892:ARG:O	5:EB:4893:THR:C	2.63	0.41
5:EC:3393:ARG:HH21	5:EC:3516:GLU:HB3	1.86	0.41
5:EC:3415:VAL:HB	5:EC:3504:ARG:HB3	2.02	0.41
5:EC:4011:VAL:HG11	5:EC:4166:SER:HB2	2.01	0.41
6:FA:1892:ILE:HG22	6:FA:1894:THR:H	1.84	0.41
6:FA:2049:SER:O	6:FA:2050:LEU:C	2.64	0.41
6:FB:1612:ASN:HD22	6:FB:1618:VAL:HG13	1.85	0.41
6:FC:2087:LEU:HD22	6:FC:2087:LEU:HA	1.76	0.41
6:FE:804:LEU:HG	6:FE:1114:VAL:HG11	2.02	0.41
6:FE:1122:LEU:HD22	6:FE:1122:LEU:HA	1.82	0.41
6:FE:1427:ASN:C	6:FE:1429:LEU:HD13	2.46	0.41
6:FF:826:LEU:O	6:FF:831:ARG:NH2	2.53	0.41
6:FF:1081:SER:HA	6:FF:1084:ARG:HE	1.86	0.41
7:GA:860:GLN:H	7:GA:860:GLN:HG2	1.69	0.41
7:GC:770:TYR:OH	7:GC:839:ARG:HG2	2.19	0.41
7:GE:850:GLY:HA2	7:GE:934:ARG:HH21	1.86	0.41
8:GH:81:SER:HA	8:GH:429:LYS:HG2	2.02	0.41
7:GI:598:ARG:NH2	7:GI:637:ASN:HD22	2.18	0.41
7:GI:844:HIS:HB2	7:GI:881:ALA:H	1.85	0.41
8:GJ:364:ILE:HD13	8:GJ:377:MET:HG3	2.02	0.41
7:GK:609:ARG:HG3	7:GK:675:GLN:HE21	1.84	0.41
8:GL:3:VAL:HG23	8:GL:13:ARG:HH21	1.85	0.41
8:GL:400:LYS:HE2	8:GL:400:LYS:HB2	1.96	0.41
10:IB:623:LEU:HD12	10:IB:623:LEU:HA	1.86	0.41
10:IC:580:LEU:HD12	10:IC:587:ARG:HH12	1.85	0.41
10:IC:923:THR:O	10:IC:927:ARG:HG3	2.21	0.41
11:JA:1722:TYR:CD1	11:JA:1732:LEU:HB3	2.56	0.41
11:JB:39:ALA:HB3	11:JB:175:ARG:HB2	2.03	0.41
11:JB:2110:LEU:HD11	11:JB:2114:ILE:HG23	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:1777:LEU:HD23	11:JC:1777:LEU:HA	1.93	0.41
12:KC:319:TYR:CD2	12:KC:353:ALA:HB1	2.55	0.41
12:KF:208:LEU:HB3	12:KF:242:VAL:HG23	2.03	0.41
12:KG:381:MET:HE2	12:KG:383:HIS:HE1	1.86	0.41
12:KG:523:VAL:HA	12:KG:573:ARG:HH21	1.86	0.41
13:LA:380:MET:HE3	13:LA:384:LEU:HG	2.02	0.41
13:LE:517:ILE:HD12	13:LF:516:VAL:HG12	2.02	0.41
13:LJ:416:ARG:HA	13:LJ:419:SER:HB3	2.01	0.41
13:LP:398:ARG:HA	13:LP:401:LEU:HB2	2.03	0.41
15:NA:958:GLU:HA	15:NA:961:TYR:HD2	1.85	0.41
15:NA:1498:ARG:HB3	20:SA:38:ARG:HG3	2.01	0.41
15:NB:347:LEU:HD22	15:NB:491:PRO:HG2	2.03	0.41
15:NB:515:ALA:HB3	15:NB:520:ALA:HB2	2.03	0.41
15:NB:666:ILE:HG23	15:NB:721:PRO:HG2	2.02	0.41
15:NB:667:THR:HG23	15:NB:673:ILE:HG12	2.03	0.41
15:NB:685:PHE:HB2	15:NB:914:ILE:HG12	2.02	0.41
15:NB:892:TRP:CA	15:NB:1152:GLU:HB2	2.51	0.41
15:NC:682:ARG:HD2	15:NC:1169:PHE:CZ	2.56	0.41
15:ND:589:ASN:HB3	15:ND:593:LYS:HE2	2.03	0.41
15:ND:614:LYS:HE3	15:ND:678:LEU:HB2	2.02	0.41
15:ND:755:ILE:HD12	15:ND:846:PHE:CE2	2.55	0.41
18:QA:66:PRO:HB3	18:QA:94:LEU:HD21	2.02	0.41
20:SB:87:ILE:HD13	20:SB:143:VAL:HG21	2.01	0.41
2:AB:90:ARG:HH21	2:AB:93:LYS:HB3	1.85	0.41
2:AB:153:GLN:HE22	2:AB:155:LEU:HB2	1.85	0.41
2:AB:405:PRO:HG3	17:PB:131:ALA:HB3	2.02	0.41
2:AC:49:HIS:HD2	2:AC:51:ALA:H	1.69	0.41
2:AC:541:PRO:HG3	1:AD:370:GLN:HB3	2.02	0.41
1:AD:330:ILE:HD13	5:EA:4909:PHE:CZ	2.56	0.41
1:AD:892:GLU:HA	1:AD:895:ARG:NH1	2.35	0.41
1:AE:73:THR:HB	1:AE:76:GLN:HG3	2.02	0.41
2:AG:450:ARG:HD2	11:JC:1724:PHE:CE2	2.55	0.41
2:AJ:166:LEU:HD22	2:AJ:281:PHE:HD2	1.85	0.41
2:AK:300:CYS:HB2	2:AK:320:CYS:HB3	2.02	0.41
2:AK:543:MET:HE3	2:AK:543:MET:HB2	1.89	0.41
3:BA:873:PHE:CZ	16:OA:174:VAL:HG22	2.54	0.41
3:CE:1236:LEU:O	3:CE:1244:PRO:HA	2.21	0.41
3:CL:1229:HIS:HD2	3:CL:1260:VAL:HG23	1.86	0.41
4:DA:96:ILE:HG23	4:DA:97:LEU:HD22	2.02	0.41
4:DA:268:ARG:HD2	4:DA:268:ARG:HA	1.76	0.41
4:DB:69:LEU:HG	4:DE:9:PHE:HE2	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DC:392:ASP:HA	14:MJ:313:ARG:NH1	2.36	0.41
5:EB:4896:ARG:H	5:EB:4896:ARG:HG2	1.73	0.41
6:FA:2027:TRP:NE1	9:HA:775:SER:O	2.54	0.41
6:FB:1866:ILE:HG23	6:FB:1867:THR:HG23	2.02	0.41
6:FC:2061:ARG:HA	6:FC:2061:ARG:HD2	1.78	0.41
6:FD:1294:LEU:HD22	6:FD:1294:LEU:HA	1.80	0.41
6:FE:818:VAL:O	6:FE:820:LYS:N	2.53	0.41
6:FE:842:GLY:O	6:FE:843:LEU:C	2.64	0.41
6:FE:1427:ASN:HD22	6:FE:1427:ASN:HA	1.55	0.41
6:FF:854:TRP:CE2	6:FF:860:PRO:HD3	2.56	0.41
7:GA:590:ASN:HA	7:GA:593:VAL:HG12	2.01	0.41
7:GA:618:ALA:HB3	7:GA:645:LEU:HD22	2.03	0.41
8:GB:15:SER:HB3	8:GB:540:LEU:HD12	2.03	0.41
7:GC:459:PRO:HB2	7:GC:465:VAL:HG22	2.03	0.41
8:GD:210:GLN:HG2	8:GD:292:ALA:HB2	2.01	0.41
7:GE:298:TYR:HB3	7:GE:679:LEU:HD21	2.02	0.41
8:GH:431:PHE:HA	8:GH:480:VAL:HA	2.03	0.41
8:GH:721:LYS:HB3	8:GH:723:VAL:HG23	2.02	0.41
7:GI:872:THR:HA	7:GI:972:GLU:HB2	2.02	0.41
7:GK:543:LYS:HG2	9:HC:498:GLY:HA2	2.02	0.41
7:GK:857:LEU:HD21	7:GK:863:VAL:HA	2.00	0.41
8:GL:12:CYS:SG	8:GL:516:LEU:HD11	2.61	0.41
9:HA:487:VAL:HG21	9:HA:620:TYR:CZ	2.56	0.41
9:HA:762:HIS:O	9:HA:763:GLN:C	2.61	0.41
9:HD:754:LEU:HG	9:HD:840:HIS:CD2	2.55	0.41
10:IA:743:TYR:HD2	10:IA:764:ALA:HA	1.84	0.41
10:IA:971:LEU:HD22	10:IA:1065:GLU:HG2	2.03	0.41
10:IA:1120:SER:HA	10:IA:1128:VAL:HG23	2.03	0.41
10:IA:1233:THR:HG23	10:IA:1293:PHE:HZ	1.86	0.41
10:IC:580:LEU:HG	10:IC:603:ARG:HH12	1.86	0.41
10:IC:1224:HIS:HD1	10:IC:1326:THR:HB	1.85	0.41
11:JA:1036:LEU:HD12	11:JA:1036:LEU:HA	1.89	0.41
11:JA:1845:ALA:HA	11:JA:1848:TYR:HD2	1.86	0.41
12:KE:684:LEU:HD13	12:KE:688:VAL:H	1.86	0.41
13:LE:380:MET:HA	13:LE:383:GLN:HB2	2.01	0.41
13:LL:353:ASN:HA	13:LL:356:LEU:HD12	2.03	0.41
13:LO:414:ASN:O	13:LO:418:LYS:HG2	2.20	0.41
15:NA:1004:PHE:HA	15:NA:1008:SER:HB3	2.02	0.41
15:NB:686:ASN:HA	15:NB:911:ARG:HA	2.01	0.41
15:NC:486:ARG:HH11	15:NC:489:VAL:HG23	1.85	0.41
15:NC:660:LEU:HA	15:NC:778:PHE:HE2	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:983:ILE:HG12	15:ND:989:ILE:HD12	2.03	0.41
15:ND:1411:LEU:HB3	15:ND:1470:PHE:CE2	2.56	0.41
1:AA:176:ILE:HA	1:AA:177:PRO:HD3	1.84	0.41
1:AA:791:LEU:HD13	1:AA:796:PHE:HE1	1.85	0.41
1:AA:897:PRO:HD2	1:AA:900:TYR:HD2	1.86	0.41
2:AB:72:PHE:HB3	2:AB:164:TYR:CD2	2.56	0.41
1:AD:62:ASP:OD1	1:AD:228:PRO:HG3	2.21	0.41
2:AG:328:HIS:CD2	2:AG:339:ARG:HD3	2.55	0.41
1:AI:381:ARG:HH21	6:FC:1641:ALA:HA	1.84	0.41
1:AI:497:PRO:HG3	6:FC:1789:LEU:HD13	2.03	0.41
2:AJ:263:TYR:CE2	16:OB:73:ALA:HA	2.55	0.41
3:BA:693:ARG:NH1	17:PA:256:ARG:HG2	2.34	0.41
3:BB:776:ARG:HH11	3:BB:780:TYR:HE2	1.67	0.41
3:CB:949:SER:HA	3:CB:981:PHE:HE2	1.84	0.41
3:CI:1182:GLY:H	3:CI:4512:SER:HB2	1.85	0.41
3:CI:1185:VAL:HG23	3:CI:1188:GLN:H	1.84	0.41
3:CI:1255:VAL:HG21	3:CI:4469:LEU:HD22	2.02	0.41
3:CJ:1130:SER:O	3:CJ:1131:LEU:HD23	2.21	0.41
3:CJ:1239:PRO:HA	3:CJ:4470:LYS:HE2	2.02	0.41
3:CJ:1258:PRO:HB2	3:CJ:4498:LEU:HD23	2.02	0.41
4:DD:148:ARG:HA	4:DD:148:ARG:CZ	2.51	0.41
4:DD:358:SER:H	4:DD:361:GLN:HE22	1.69	0.41
4:DE:187:PRO:HA	4:DE:188:PRO:HD3	1.92	0.41
5:EA:4156:LEU:HD21	9:HC:422:VAL:HG11	2.03	0.41
5:EB:3650:THR:HG23	9:HB:499:ARG:HA	2.03	0.41
5:EC:4737:ASP:O	5:EC:4741:LYS:HG2	2.21	0.41
6:FA:1993:LYS:HD2	6:FA:1993:LYS:HA	1.76	0.41
6:FA:2048:GLU:HG3	9:HA:830:ILE:HG12	2.02	0.41
6:FB:1745:SER:HB3	6:FB:1792:TYR:H	1.84	0.41
6:FB:1966:ASP:HA	6:FB:2047:ARG:NH1	2.35	0.41
6:FC:2017:ARG:HH12	6:FC:2018:ARG:HG3	1.86	0.41
6:FD:803:ARG:HA	6:FD:906:LEU:O	2.21	0.41
6:FD:925:GLU:HG2	6:FD:1092:PRO:HG2	2.03	0.41
6:FD:1260:LEU:HG	6:FD:1261:SER:N	2.35	0.41
6:FD:1281:VAL:O	6:FD:1282:LEU:C	2.62	0.41
6:FD:1388:PHE:CD1	6:FD:1418:GLU:HA	2.50	0.41
6:FE:840:ALA:N	12:KB:681:MET:HE3	2.35	0.41
6:FE:845:PRO:HA	7:GE:896:ARG:HH12	1.86	0.41
6:FE:1075:VAL:HG11	6:FE:1106:LEU:N	2.36	0.41
6:FE:1094:SER:O	6:FE:1095:LEU:C	2.64	0.41
6:FE:1229:LYS:HB2	6:FE:1229:LYS:HE2	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1297:PRO:O	6:FE:1299:ASN:N	2.47	0.41
6:FE:1435:GLU:O	6:FE:1436:PHE:C	2.63	0.41
6:FF:839:GLY:O	7:GI:957:ARG:NH2	2.50	0.41
6:FF:1075:VAL:O	6:FF:1076:ILE:C	2.64	0.41
6:FF:1116:LEU:HB2	6:FF:1117:ASN:H	1.64	0.41
7:GC:163:GLN:HA	7:GC:166:LEU:HG	2.03	0.41
7:GC:764:LEU:HD13	7:GC:870:ARG:HE	1.85	0.41
8:GD:21:ALA:HB2	8:GD:521:ALA:HB1	2.03	0.41
8:GD:192:VAL:HG21	7:GE:418:THR:HG21	2.01	0.41
8:GD:254:LYS:HD2	8:GD:254:LYS:HA	1.86	0.41
7:GE:345:ASP:HA	7:GE:349:GLY:HA2	2.03	0.41
7:GE:843:LEU:HD11	7:GE:883:LEU:HB2	2.03	0.41
8:GF:171:ILE:HG23	8:GF:181:HIS:HB2	2.02	0.41
8:GF:350:GLN:HA	8:GF:353:ASN:HB2	2.02	0.41
7:GG:211:ARG:NE	7:GG:212:PRO:HD2	2.36	0.41
7:GG:388:PRO:HB2	8:GJ:212:GLN:HB3	2.02	0.41
8:GH:135:LEU:HD11	8:GH:245:ILE:HD12	2.03	0.41
8:GH:650:GLN:HA	8:GH:651:PRO:HD3	1.93	0.41
8:GH:679:GLU:N	8:GH:727:SER:HB2	2.35	0.41
7:GI:393:VAL:HG11	7:GI:438:LYS:HB2	2.02	0.41
8:GJ:661:PRO:HA	8:GJ:679:GLU:H	1.85	0.41
7:GK:562:ILE:HD12	7:GK:562:ILE:HA	1.95	0.41
8:GL:65:PRO:HA	8:GL:104:LEU:HD12	2.03	0.41
8:GL:364:ILE:HD13	8:GL:377:MET:HB3	2.03	0.41
9:HB:708:VAL:HG12	9:HB:726:PRO:HG2	2.02	0.41
10:IA:845:TYR:CZ	10:IA:863:LEU:HD22	2.56	0.41
10:IA:913:LEU:HA	10:IA:916:LYS:NZ	2.36	0.41
10:IA:963:ARG:HD3	10:IA:963:ARG:HA	1.84	0.41
10:IB:476:LEU:HD23	10:IB:501:MET:HE3	2.03	0.41
10:IB:891:VAL:HG11	15:NC:566:GLN:O	2.21	0.41
10:IB:1118:ASN:HB3	10:IB:1121:LYS:HB2	2.02	0.41
10:IC:445:LYS:HA	10:IC:449:TYR:CD2	2.56	0.41
10:IC:751:ASN:HB3	10:IC:752:SER:H	1.64	0.41
11:JA:136:ALA:HB1	11:JA:162:PRO:HB3	2.03	0.41
11:JA:761:LYS:HD2	11:JA:768:ASP:HA	2.03	0.41
11:JA:833:GLN:HB2	11:JA:1418:THR:HG21	2.03	0.41
11:JA:1161:LEU:HD23	11:JA:1164:MET:HE3	2.03	0.41
11:JA:2034:THR:HA	11:JA:2037:ARG:HG2	2.03	0.41
11:JC:875:LEU:HD23	11:JC:963:PHE:HE2	1.86	0.41
11:JC:1785:THR:HA	11:JC:1788:THR:HG22	2.02	0.41
12:KB:266:ARG:CZ	12:KB:269:MET:HE3	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:KE:299:TYR:HB2	12:KE:307:VAL:HG21	2.03	0.41
12:KF:565:TRP:CE3	12:KF:709:VAL:HG13	2.55	0.41
12:KG:352:LYS:HE3	12:KG:352:LYS:HB2	1.86	0.41
12:KG:523:VAL:O	12:KG:525:PRO:HD3	2.20	0.41
13:LA:461:VAL:O	13:LA:465:ILE:HG12	2.21	0.41
13:LF:475:LEU:HD12	13:LF:479:PHE:CE2	2.56	0.41
13:LI:481:GLU:HA	13:LI:484:VAL:HG12	2.02	0.41
13:LI:514:TYR:HE1	13:LJ:513:LEU:HD11	1.86	0.41
13:LJ:528:PRO:HA	13:LJ:529:PRO:HD3	1.94	0.41
13:LL:370:MET:HA	13:LL:373:VAL:HG12	2.03	0.41
14:ME:258:ILE:HG12	14:MF:258:ILE:HD11	2.02	0.41
14:MI:285:ARG:NH1	14:MJ:257:LYS:HA	2.23	0.41
15:NB:987:GLN:HG3	15:NB:1026:LEU:HD13	2.02	0.41
15:NB:1488:ARG:CZ	15:NB:1491:PRO:HG2	2.51	0.41
15:NC:434:VAL:HA	15:NC:445:ILE:HD12	2.03	0.41
15:NC:798:LEU:HD13	15:NC:885:LEU:HD12	2.03	0.41
15:NC:983:ILE:HG12	15:NC:989:ILE:HD12	2.01	0.41
15:NC:1329:PRO:HD2	15:NC:1332:MET:HE1	2.03	0.41
15:NC:1546:VAL:HG21	19:RA:23:LEU:HD11	2.03	0.41
15:NC:1552:ILE:HB	19:RA:143:LEU:HD23	2.03	0.41
15:ND:468:ARG:HD3	15:ND:469:PHE:CD1	2.51	0.41
15:ND:891:TRP:C	15:ND:1152:GLU:H	2.29	0.41
15:ND:1143:LEU:HD12	15:ND:1143:LEU:HA	1.91	0.41
15:ND:1503:PHE:CD1	20:SB:146:MET:HB3	2.56	0.41
15:ND:1512:MET:HB3	18:QB:107:LEU:HD22	2.03	0.41
1:AA:915:TRP:CZ2	13:LK:359:HIS:HB2	2.56	0.41
1:AD:418:ILE:HG22	1:AD:452:PHE:CE2	2.56	0.41
1:AE:1025:ARG:NE	1:AE:1025:ARG:HA	2.36	0.41
1:AH:747:MET:HE2	1:AH:850:ILE:HD11	2.03	0.41
1:AI:238:CYS:HB3	1:AI:241:CYS:H	1.86	0.41
1:AL:878:ARG:HH12	6:FC:2039:ARG:HE	1.69	0.41
3:CC:921:LEU:HD23	3:CC:921:LEU:HA	1.92	0.41
3:CE:1126:GLU:CD	3:CE:1129:ARG:HH21	2.28	0.41
3:CF:1184:ALA:HB2	3:CF:4517:LEU:HB2	2.03	0.41
3:CG:1208:VAL:HG22	3:CG:1209:ALA:H	1.86	0.41
3:CI:1212:GLU:HG2	3:CI:1222:ARG:HH12	1.86	0.41
4:DA:23:ALA:HB1	4:DA:29:LEU:HD23	2.02	0.41
4:DB:246:TYR:CZ	4:DE:189:ARG:HB3	2.56	0.41
5:EA:3412:LEU:HG	5:EA:3507:VAL:HG22	2.03	0.41
5:EA:3421:HIS:CE1	5:EA:3588:CYS:HA	2.55	0.41
5:EA:3614:PRO:HG2	5:EA:3628:MET:HE3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EA:4061:TYR:HB3	5:EA:4174:ILE:HD13	2.01	0.41
5:EA:4643:PRO:HA	5:EA:4644:PRO:HD3	1.92	0.41
5:EB:4344:LEU:HD23	5:EB:4360:GLU:HG2	2.03	0.41
5:EC:4513:GLN:HG2	5:EC:4707:PHE:HD1	1.86	0.41
6:FA:1655:ASP:OD1	6:FA:1657:MET:HG2	2.21	0.41
6:FA:1759:GLU:HA	6:FA:1964:MET:CE	2.51	0.41
6:FA:1764:ILE:HA	6:FA:1767:ARG:HG2	2.03	0.41
6:FC:1951:TYR:HE2	9:HB:844:GLY:HA3	1.86	0.41
7:GA:535:PRO:C	9:HB:550:GLU:HG2	2.46	0.41
7:GA:575:TYR:HE2	7:GA:577:SER:HB2	1.86	0.41
7:GA:702:ILE:HA	7:GA:705:ILE:HG12	2.03	0.41
8:GB:132:PRO:HA	8:GB:133:PRO:HD2	1.96	0.41
7:GC:960:ASP:HA	7:GC:961:PRO:HD3	1.95	0.41
8:GD:713:LEU:HD21	8:GD:722:TYR:HB2	2.02	0.41
8:GD:769:PHE:HB3	8:GJ:551:SER:HA	2.03	0.41
7:GE:664:PRO:HD2	7:GE:669:ASP:HB2	2.03	0.41
8:GF:305:VAL:HG11	8:GF:377:MET:HE1	2.03	0.41
7:GG:302:PRO:HA	7:GG:303:PRO:HD3	1.94	0.41
8:GH:754:ALA:H	8:GL:333:LYS:HE2	1.87	0.41
7:GI:232:LYS:HA	7:GI:232:LYS:HD3	1.91	0.41
7:GI:268:ARG:HD2	7:GI:268:ARG:HA	1.86	0.41
7:GI:584:HIS:HA	7:GI:952:ARG:HH12	1.86	0.41
7:GI:841:LEU:HD13	7:GI:865:LEU:HD12	2.03	0.41
9:HA:579:LEU:HA	9:HA:579:LEU:HD23	1.87	0.41
9:HC:433:GLY:HA2	9:HC:436:ASN:HD22	1.86	0.41
10:IA:968:ARG:NE	10:IA:1061:LEU:HD21	2.35	0.41
10:IC:1139:VAL:HG13	10:IC:1203:LEU:HD22	2.03	0.41
11:JA:925:ASN:HB3	11:JA:1012:ARG:HH12	1.85	0.41
11:JA:1308:TYR:HD1	11:JA:1405:PRO:HD3	1.86	0.41
11:JB:48:GLN:HG3	11:JB:50:GLU:OE1	2.21	0.41
11:JB:195:LEU:HG	11:JB:1036:LEU:HD11	2.02	0.41
11:JC:411:ASP:HB3	11:JC:412:CYS:H	1.66	0.41
11:JC:1121:VAL:HA	11:JC:1125:ILE:HB	2.03	0.41
11:JC:1304:ASP:H	11:JC:1329:ASN:HD21	1.69	0.41
12:KA:523:VAL:HG12	12:KA:524:PHE:CD1	2.56	0.41
12:KB:641:VAL:HG12	12:KB:678:ALA:HB1	2.02	0.41
12:KC:231:PHE:CZ	12:KC:313:PHE:CD2	3.09	0.41
12:KC:645:ARG:HH12	12:KC:647:LEU:HA	1.86	0.41
13:LA:413:GLU:HA	13:LA:416:ARG:HG2	2.02	0.41
15:NA:995:ARG:HH22	15:NA:1018:GLN:HG2	1.85	0.41
15:NB:933:LEU:O	15:NB:937:MET:HG3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NB:1552:ILE:HG13	15:NB:1555:TYR:HD2	1.86	0.41
15:NC:598:PHE:HD1	15:NC:915:VAL:HB	1.86	0.41
15:NC:785:ILE:HD13	15:NC:785:ILE:HA	1.96	0.41
15:NC:1397:LEU:HA	15:NC:1400:CYS:HB2	2.03	0.41
15:ND:898:ASN:HA	15:ND:901:LEU:HB3	2.02	0.41
15:ND:1545:VAL:HA	19:RD:141:LEU:HD22	2.03	0.41
16:OC:1098:VAL:HG13	16:OC:1099:PHE:H	1.85	0.41
2:AB:92:LEU:HD23	2:AB:277:VAL:HG11	2.02	0.40
2:AB:327:ILE:HA	1:AI:271:MET:HE2	2.02	0.40
1:AD:712:SER:HA	1:AD:915:TRP:CE2	2.56	0.40
1:AE:65:ILE:HG13	1:AE:224:PHE:HB3	2.03	0.40
1:AE:71:LEU:H	1:AE:220:ALA:HA	1.86	0.40
1:AI:120:TRP:CH2	1:AI:218:PRO:HG3	2.56	0.40
2:AJ:499:LEU:HD22	2:AJ:518:HIS:CD2	2.56	0.40
2:AK:471:THR:O	2:AK:475:MET:HG2	2.22	0.40
3:CA:790:ASN:C	3:CA:790:ASN:HD22	2.29	0.40
3:CB:851:LYS:HB2	3:CB:851:LYS:HE3	1.84	0.40
3:CC:790:ASN:C	3:CC:790:ASN:HD22	2.29	0.40
3:CE:1137:ALA:HB1	3:CE:1139:LEU:HD13	2.03	0.40
3:CG:1231:ARG:HG3	3:CG:1233:PHE:H	1.86	0.40
3:CI:4448:TYR:HE1	3:CI:4453:MET:HG2	1.87	0.40
4:DC:384:ILE:HD13	13:LI:457:GLN:HB3	2.03	0.40
5:EA:4187:ASP:OD1	5:EA:4190:GLN:HB2	2.21	0.40
5:EC:3650:THR:HG22	9:HA:500:LEU:HD22	2.03	0.40
6:FA:1783:PRO:HA	6:FA:1784:PRO:HD3	1.98	0.40
6:FB:1600:VAL:HB	6:FB:1724:ARG:HA	2.03	0.40
6:FB:1896:ALA:HB3	6:FB:1914:VAL:HG23	2.02	0.40
6:FC:1866:ILE:HD13	6:FC:1866:ILE:HA	1.96	0.40
6:FE:1027:LEU:O	6:FE:1028:LYS:C	2.64	0.40
6:FF:990:PHE:C	12:KC:313:PHE:HE2	2.29	0.40
6:FF:1002:ALA:HB2	6:FF:1009:VAL:HG13	2.03	0.40
8:GB:641:TYR:HB2	8:GB:664:ILE:HB	2.03	0.40
7:GC:796:PHE:HD1	7:GC:836:VAL:HG23	1.86	0.40
8:GF:456:GLY:HA2	8:GF:547:PHE:CZ	2.56	0.40
7:GI:433:MET:HB3	7:GI:459:PRO:HD3	2.04	0.40
7:GI:827:LEU:HB3	7:GI:831:ARG:HB3	2.02	0.40
9:HB:564:ARG:HD2	9:HB:564:ARG:HA	1.81	0.40
9:HC:565:PRO:HA	9:HC:566:PRO:HD3	1.77	0.40
9:HD:825:ASN:O	9:HD:829:THR:HG23	2.22	0.40
10:IA:185:LEU:HD21	10:IA:624:ARG:HB2	2.04	0.40
10:IB:908:ARG:HH21	10:IB:911:ARG:HH11	1.69	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:1330:TYR:HB3	10:IB:1335:LEU:HB2	2.03	0.40
10:IC:369:VAL:HB	10:IC:372:ARG:HB3	2.03	0.40
10:IC:868:MET:HE2	10:IC:868:MET:HB2	1.96	0.40
10:IC:1130:LEU:HD11	10:IC:1142:VAL:HG13	2.03	0.40
11:JA:207:GLU:HB3	11:JA:1051:LEU:HD11	2.04	0.40
11:JC:1292:LEU:HD21	11:JC:1299:ALA:HB1	2.03	0.40
11:JC:1489:LEU:HD22	15:NA:444:LEU:HD13	2.03	0.40
11:JC:1490:LEU:O	11:JC:1494:VAL:HG23	2.20	0.40
11:JC:1713:ASN:O	11:JC:1716:GLN:HB3	2.20	0.40
13:LD:364:ASN:HA	13:LD:367:VAL:HG12	2.02	0.40
13:LE:516:VAL:HG13	13:LF:517:ILE:HD13	2.03	0.40
14:MG:81:ARG:HG2	14:MG:82:ARG:H	1.86	0.40
15:NA:547:PRO:HG2	15:NA:549:LYS:HG2	2.04	0.40
15:NA:600:LEU:HB3	15:NA:1189:PHE:CE1	2.56	0.40
15:NB:933:LEU:HD13	15:NB:1120:VAL:HG21	2.03	0.40
15:ND:564:ARG:HH22	15:ND:618:ARG:HB2	1.86	0.40
15:ND:1549:GLY:H	19:RD:142:ASN:HB3	1.85	0.40
1:AA:132:PRO:HB3	3:BA:807:LEU:HD11	2.03	0.40
1:AA:408:LYS:HB2	2:AB:438:VAL:HG11	2.03	0.40
1:AA:793:LEU:HD23	1:AA:793:LEU:HA	1.91	0.40
1:AD:271:MET:HE2	1:AD:271:MET:HB2	1.99	0.40
1:AE:692:PRO:HG3	1:AE:998:LEU:HD23	2.02	0.40
2:AF:447:ARG:HD2	2:AF:450:ARG:HH21	1.87	0.40
1:AH:631:THR:HG23	13:LL:512:ARG:NH2	2.35	0.40
1:AI:775:LYS:HB3	1:AI:970:GLU:HG2	2.02	0.40
2:AJ:300:CYS:HB2	2:AJ:319:LEU:HA	2.02	0.40
1:AL:908:ARG:HH22	13:LE:497:LEU:HD12	1.85	0.40
3:BC:815:GLU:OE2	16:OC:240:ARG:HD3	2.21	0.40
3:CC:880:GLN:H	3:CC:880:GLN:HG3	1.71	0.40
3:CJ:4462:VAL:HG13	3:CJ:4495:LEU:HB3	2.04	0.40
4:DC:320:ILE:HG23	4:DC:323:ASP:HB2	2.03	0.40
4:DF:249:GLY:HA3	4:DF:287:ALA:HB2	2.02	0.40
5:EA:4147:PHE:HB2	5:EA:4185:HIS:CE1	2.56	0.40
5:EA:4405:ILE:HG13	5:EA:4428:MET:HE1	2.03	0.40
5:EA:4760:ARG:NH1	11:JA:743:PHE:HA	2.24	0.40
6:FC:1587:MET:HE2	6:FC:1587:MET:HB2	1.92	0.40
6:FC:1683:LYS:HD3	6:FC:1684:THR:O	2.21	0.40
6:FE:966:PRO:O	6:FE:1027:LEU:HB2	2.21	0.40
6:FF:923:ALA:O	6:FF:927:GLY:N	2.54	0.40
6:FF:1003:ILE:H	6:FF:1003:ILE:HG12	1.73	0.40
6:FF:1225:ILE:C	6:FF:1227:ARG:H	2.28	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GA:715:THR:HG21	7:GA:796:PHE:HB3	2.02	0.40
8:GB:426:LEU:HD23	8:GB:426:LEU:HA	1.87	0.40
8:GB:526:ILE:HD11	14:ME:324:ARG:HH11	1.85	0.40
7:GC:390:ILE:HD12	7:GC:390:ILE:HG23	1.78	0.40
7:GC:515:SER:HB2	7:GC:634:PRO:HB2	2.03	0.40
7:GC:583:GLN:HB3	7:GC:584:HIS:ND1	2.36	0.40
8:GF:598:HIS:HA	8:GF:601:ARG:HG2	2.02	0.40
7:GG:205:ARG:HB2	7:GG:208:ALA:HB2	2.04	0.40
8:GH:658:ALA:HB1	8:GH:665:LEU:HD21	2.03	0.40
8:GH:661:PRO:O	8:GH:681:ILE:HG12	2.21	0.40
7:GI:238:ILE:HG23	7:GI:284:GLU:HG3	2.04	0.40
8:GL:158:GLN:HE22	13:LE:433:ARG:HH12	1.68	0.40
9:HA:877:LYS:HA	9:HA:877:LYS:HD3	1.41	0.40
10:IA:893:PHE:CZ	10:IA:907:ASP:HA	2.56	0.40
10:IB:362:HIS:CD2	10:IB:429:ARG:HH22	2.38	0.40
10:IB:496:GLU:HA	10:IB:499:ARG:HG3	2.04	0.40
10:IB:1110:ARG:HB2	10:IB:1144:VAL:HG21	2.02	0.40
10:IC:921:LEU:O	10:IC:925:ILE:HG12	2.20	0.40
12:KA:721:GLN:NE2	12:KA:725:ILE:HG23	2.34	0.40
12:KC:485:ARG:HH21	12:KC:522:ARG:HG2	1.86	0.40
12:KC:536:ARG:NE	12:KC:542:PRO:HA	2.36	0.40
14:MB:218:LEU:HD21	14:MB:323:GLN:HB3	2.02	0.40
14:MI:229:GLN:HG3	14:MI:311:ILE:HD12	2.03	0.40
14:MK:90:ALA:O	14:MK:94:LEU:HD23	2.20	0.40
15:NA:864:GLU:HB3	15:NA:865:SER:H	1.70	0.40
15:NA:1321:TRP:HB3	15:NA:1322:LYS:H	1.72	0.40
15:NA:1490:MET:HA	15:NA:1493:VAL:HG22	2.02	0.40
15:NA:1508:PHE:HZ	18:QA:110:VAL:HG21	1.86	0.40
15:NC:737:PRO:HG2	15:NC:749:PRO:HD3	2.03	0.40
15:NC:992:GLN:HE22	15:NC:1022:ASP:HB2	1.86	0.40
15:ND:891:TRP:CD1	15:ND:1156:LEU:HD21	2.56	0.40
15:ND:943:GLU:HA	15:ND:946:LEU:HB2	2.03	0.40
17:PB:138:ARG:HB3	17:PB:142:TYR:CD2	2.56	0.40
19:RA:51:MET:HB3	19:RA:55:LYS:NZ	2.35	0.40
19:RA:74:LEU:HB3	19:RA:91:VAL:HG11	2.02	0.40
20:SC:37:MET:HE2	20:SC:44:PRO:HB3	2.03	0.40
1:AA:345:PRO:HA	1:AA:348:GLU:HB2	2.03	0.40
1:AA:437:PHE:CB	2:AB:410:TYR:HE1	2.33	0.40
2:AB:41:ARG:HH21	2:AB:293:GLU:HG3	1.86	0.40
2:AC:66:ARG:NH2	2:AC:173:ARG:HH21	2.20	0.40
1:AD:376:LEU:HA	1:AD:379:GLN:HB3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:915:TRP:CE3	13:LM:359:HIS:HB2	2.56	0.40
1:AH:629:LEU:C	13:LL:512:ARG:HH12	2.29	0.40
1:AI:442:HIS:HB2	2:AJ:368:HIS:HB2	2.04	0.40
1:AI:458:VAL:HB	2:AJ:434:ARG:HH11	1.86	0.40
1:AI:507:LEU:HD13	6:FC:1827:GLN:HE21	1.85	0.40
2:AJ:499:LEU:HD21	2:AJ:515:TRP:HD1	1.85	0.40
2:AK:494:TRP:CZ2	1:AL:56:LEU:HG	2.57	0.40
3:CA:824:SER:HB2	3:CA:846:TYR:CE1	2.56	0.40
3:CA:829:LEU:HA	3:CA:832:LEU:HB3	2.04	0.40
4:DB:33:LEU:HB2	4:DB:103:LEU:HD23	2.04	0.40
4:DB:257:LEU:HD23	4:DB:265:ILE:HD13	2.02	0.40
4:DF:260:GLY:HA2	4:DF:299:ARG:HH12	1.87	0.40
5:EA:3577:PHE:HB2	5:EA:3579:PHE:CE2	2.57	0.40
5:EB:3497:LEU:HD12	5:EB:3504:ARG:HD2	2.03	0.40
5:EB:4438:LEU:HD11	5:EB:4709:PHE:CE2	2.52	0.40
5:EC:3294:LYS:HA	5:EC:3297:ASP:OD1	2.21	0.40
5:EC:3516:GLU:HA	5:EC:3517:PRO:HD3	1.85	0.40
5:EC:4401:PRO:O	5:EC:4402:PRO:C	2.63	0.40
6:FB:2061:ARG:O	6:FB:2065:THR:HG23	2.22	0.40
6:FC:2080:GLN:HE21	6:FC:2080:GLN:HB2	1.57	0.40
6:FD:824:TYR:C	6:FD:826:LEU:H	2.29	0.40
6:FD:891:ARG:HB2	6:FD:891:ARG:NH1	2.36	0.40
6:FD:1095:LEU:HA	6:FD:1095:LEU:HD13	1.79	0.40
6:FD:1203:ARG:HA	6:FD:1203:ARG:HD2	1.35	0.40
6:FE:912:ILE:HG21	6:FE:1425:PRO:O	2.21	0.40
6:FF:1064:TYR:HB3	6:FF:1065:LEU:H	1.75	0.40
6:FF:1089:ARG:HA	6:FF:1089:ARG:HD2	1.78	0.40
7:GA:841:LEU:HD13	7:GA:865:LEU:HD22	2.02	0.40
8:GB:396:ILE:HG23	8:GB:398:VAL:HG12	2.02	0.40
7:GC:758:LEU:HB3	7:GC:787:LEU:HD22	2.04	0.40
7:GE:311:LEU:HD23	7:GE:453:LEU:HD13	2.02	0.40
7:GE:418:THR:HG22	7:GE:422:LEU:HB2	2.03	0.40
7:GG:563:LEU:HD11	7:GG:818:VAL:HG13	2.04	0.40
7:GG:840:MET:HE1	7:GG:970:LEU:HD11	2.03	0.40
8:GH:633:MET:HE1	8:GH:670:PHE:HB2	2.03	0.40
7:GI:195:LYS:NZ	7:GI:702:ILE:HD12	2.36	0.40
8:GJ:692:MET:HE1	8:GJ:694:GLU:HB2	2.02	0.40
8:GL:542:THR:HG22	8:GL:622:LEU:HD21	2.03	0.40
9:HA:575:ARG:HB2	9:HA:578:THR:HG23	2.03	0.40
10:IA:635:LEU:HD12	10:IA:638:ARG:HD3	2.03	0.40
11:JB:1587:TRP:HE3	11:JB:1590:THR:HG23	1.87	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:1808:LEU:HD12	11:JB:1808:LEU:HA	1.89	0.40
11:JB:2026:LYS:HB3	11:JB:2028:TYR:CZ	2.56	0.40
11:JC:970:PHE:HA	11:JC:971:PRO:HD3	1.92	0.40
11:JC:1145:ILE:HD11	11:JC:1380:HIS:HB3	2.03	0.40
11:JC:1161:LEU:HD11	11:JC:1184:ARG:HH11	1.87	0.40
11:JC:1581:ARG:NH2	15:NA:354:PHE:HB3	2.35	0.40
12:KG:247:LEU:HA	12:KG:250:SER:HB3	2.03	0.40
13:LE:523:GLU:OE2	13:LH:523:GLU:HA	2.20	0.40
15:NA:941:LEU:HD23	15:NA:941:LEU:HA	1.92	0.40
15:NB:444:LEU:HD21	15:NB:481:LEU:HD13	2.04	0.40
15:NB:702:LEU:HA	15:NB:934:LEU:HA	2.03	0.40
15:NB:885:LEU:HA	15:NB:888:ARG:HB2	2.04	0.40
15:NB:1522:GLN:HB3	18:QC:167:LEU:HD23	2.02	0.40
15:NC:690:TYR:HB2	15:NC:905:ASP:CG	2.45	0.40
19:RD:113:ARG:HH11	19:RD:114:GLU:HB3	1.85	0.40
20:SC:13:PHE:HD1	20:SC:40:LEU:HD11	1.86	0.40
2:AC:108:LEU:HB3	2:AC:162:PHE:HE2	1.86	0.40
2:AC:319:LEU:HD11	2:AC:327:ILE:HD11	2.03	0.40
2:AC:434:ARG:O	2:AC:438:VAL:HG23	2.20	0.40
1:AD:736:LEU:HA	1:AD:737:PRO:HD3	1.97	0.40
2:AF:64:GLN:H	2:AF:66:ARG:NH1	2.20	0.40
2:AF:159:ARG:O	5:EB:4626:LEU:HB3	2.22	0.40
1:AH:649:ARG:HA	1:AH:649:ARG:HD2	1.85	0.40
2:AJ:475:MET:HG3	2:AK:145:LYS:HB2	2.02	0.40
3:CA:692:LEU:HD23	3:CA:692:LEU:HA	1.97	0.40
3:CA:968:PHE:HB3	3:CA:1007:LEU:HD13	2.04	0.40
3:CB:907:ARG:HH22	17:PC:314:LYS:HB3	1.87	0.40
3:CB:920:ARG:NH1	3:CB:957:ALA:HA	2.37	0.40
3:CE:4470:LYS:HB2	3:CE:4486:ILE:HG13	2.03	0.40
3:CI:4470:LYS:HB2	3:CI:4470:LYS:HE3	1.87	0.40
4:DB:172:ARG:O	4:DB:176:ILE:HG12	2.22	0.40
5:EA:4403:LEU:CD1	5:EA:4405:ILE:HD11	2.51	0.40
5:EA:4880:ASP:CG	5:EA:4888:TRP:CZ3	3.00	0.40
5:EB:3591:PRO:HB2	5:EB:3608:ASN:ND2	2.36	0.40
5:EB:3760:LYS:HA	5:EB:3760:LYS:HD3	1.94	0.40
5:EB:4147:PHE:CE1	5:EB:4182:LEU:HA	2.56	0.40
5:EB:4282:SER:HA	5:EB:4285:THR:HG22	2.04	0.40
5:EC:3277:PHE:HE1	5:EC:3447:TYR:HD1	1.69	0.40
5:EC:3869:ARG:HD3	5:EC:4209:HIS:CE1	2.56	0.40
5:EC:4397:ASP:OD2	5:EC:4402:PRO:HD3	2.22	0.40
6:FC:2024:ARG:O	6:FC:2028:GLU:HG2	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FC:2103:ARG:O	6:FC:2106:THR:OG1	2.40	0.40
6:FD:859:ASP:OD2	6:FD:859:ASP:N	2.54	0.40
6:FD:1297:PRO:C	6:FD:1299:ASN:N	2.80	0.40
6:FD:1424:CYS:SG	6:FD:1429:LEU:HG	2.62	0.40
6:FE:1103:SER:OG	6:FE:1104:GLY:N	2.54	0.40
6:FE:1285:CYS:HB2	6:FE:1289:HIS:H	1.87	0.40
6:FE:1442:GLU:C	6:FE:1444:ARG:H	2.29	0.40
6:FF:803:ARG:CB	6:FF:907:ASN:HA	2.51	0.40
6:FF:1089:ARG:O	6:FF:1090:LEU:C	2.65	0.40
6:FF:1216:TRP:O	6:FF:1218:ALA:N	2.55	0.40
6:FF:1251:ARG:NE	11:JB:774:LEU:H	2.15	0.40
7:GA:592:ILE:HD13	7:GA:592:ILE:HA	1.89	0.40
8:GF:69:ILE:HB	8:GF:71:PHE:CE2	2.56	0.40
8:GF:150:ASP:HA	8:GF:153:ARG:HH11	1.86	0.40
8:GF:432:LYS:HD2	8:GF:449:GLN:HA	2.03	0.40
8:GJ:14:PHE:HZ	8:GJ:496:LEU:HD11	1.87	0.40
8:GJ:400:LYS:HE2	8:GJ:400:LYS:HB2	1.95	0.40
9:HA:752:ASP:OD1	9:HA:752:ASP:N	2.50	0.40
10:IA:868:MET:HE3	10:IA:1249:ALA:HB2	2.03	0.40
10:IB:165:ILE:HD13	10:IB:168:LEU:HD12	2.03	0.40
10:IC:1432:LYS:HA	10:IC:1432:LYS:HD3	1.91	0.40
11:JA:1518:VAL:O	11:JA:1522:ILE:HG12	2.21	0.40
11:JC:1686:LEU:HD11	11:JC:1704:ARG:HD3	2.02	0.40
12:KB:209:VAL:HG22	12:KB:241:PRO:HB3	2.02	0.40
12:KB:569:LEU:HD11	12:KB:703:TRP:HE3	1.86	0.40
12:KC:317:ALA:HA	12:KC:320:LYS:HE2	2.03	0.40
12:KC:723:GLU:H	12:KC:723:GLU:HG2	1.77	0.40
12:KE:213:VAL:HG12	12:KE:237:VAL:HG22	2.03	0.40
12:KE:268:LYS:HA	12:KE:268:LYS:HD3	1.81	0.40
13:LF:518:GLU:OE2	13:LF:522:ARG:HD3	2.21	0.40
13:LH:515:LYS:HE3	13:LH:515:LYS:HB2	1.93	0.40
13:LI:522:ARG:HB2	13:LL:523:GLU:OE2	2.21	0.40
13:LM:425:LYS:HZ3	13:LN:424:LEU:HD12	1.86	0.40
14:MA:219:LYS:O	14:MA:223:ARG:HG2	2.22	0.40
14:MC:102:LYS:HB2	14:MC:102:LYS:HE2	1.84	0.40
15:NB:801:ALA:HB2	15:NB:859:LEU:HD21	2.03	0.40
15:NB:1502:THR:HA	15:NB:1505:ALA:HB3	2.04	0.40
15:NC:794:GLU:HA	15:NC:797:ARG:HD2	2.02	0.40
15:NC:1539:ILE:HD11	19:RA:100:VAL:HA	2.03	0.40
16:OB:1096:MET:SD	16:OB:1101:PHE:HB2	2.61	0.40
16:OC:891:ARG:HH12	16:OC:924:VAL:HB	1.85	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:QD:108:PHE:HD1	18:QD:119:LEU:HD12	1.86	0.40
19:RA:128:THR:HG22	19:RA:160:CYS:HB3	2.02	0.40
1:AA:368:LEU:HB3	2:AC:153:GLN:NE2	2.37	0.40
2:AB:65:GLY:H	2:AB:66:ARG:HH11	1.69	0.40
2:AC:441:MET:HE2	1:AD:404:LEU:HD21	2.02	0.40
1:AE:289:SER:N	17:PC:271:ASN:HD22	2.19	0.40
1:AE:1026:ASP:HB3	1:AE:1032:PHE:HB2	2.04	0.40
1:AI:1058:ARG:HD3	14:MG:90:ALA:HB1	2.03	0.40
2:AJ:502:LEU:HA	2:AJ:505:VAL:HG12	2.04	0.40
3:CG:1223:GLU:HB3	3:CG:1224:ALA:H	1.67	0.40
4:DB:179:ALA:HB3	4:DE:189:ARG:NH1	2.35	0.40
4:DB:389:GLY:O	4:DB:393:LEU:HB2	2.22	0.40
4:DD:321:LYS:HD2	4:DD:321:LYS:HA	1.95	0.40
4:DE:20:LEU:O	4:DE:24:LYS:HG2	2.21	0.40
4:DE:257:LEU:HB3	4:DE:303:PHE:HZ	1.86	0.40
4:DF:33:LEU:HD12	4:DF:33:LEU:HA	1.91	0.40
4:DF:305:ARG:HH11	4:DF:308:GLN:HG2	1.86	0.40
5:EB:3409:SER:HA	5:EB:3510:LEU:HD22	2.02	0.40
5:EB:3756:LEU:HD22	5:EB:3770:LEU:HD21	2.03	0.40
5:EB:4285:THR:HG23	5:EB:4286:VAL:HG23	2.03	0.40
5:EC:4508:LEU:HD23	5:EC:4508:LEU:HA	1.95	0.40
6:FC:1782:GLU:HA	6:FC:1783:PRO:HD3	1.95	0.40
6:FC:2081:ARG:O	6:FC:2082:LEU:C	2.65	0.40
6:FD:843:LEU:HD22	6:FD:847:PHE:HZ	1.85	0.40
6:FD:1011:TYR:O	6:FD:1012:PRO:C	2.64	0.40
6:FD:1393:LEU:HD13	6:FD:1393:LEU:HA	1.86	0.40
6:FE:1001:ASN:HD22	6:FE:1001:ASN:N	2.19	0.40
6:FE:1298:LEU:HD23	6:FE:1298:LEU:HA	1.88	0.40
6:FF:1088:LYS:C	6:FF:1090:LEU:H	2.30	0.40
7:GA:842:PRO:HD2	7:GA:867:PRO:HG2	2.04	0.40
8:GB:604:PHE:HE2	8:GB:634:ILE:HD13	1.86	0.40
8:GB:685:ARG:HA	8:GB:690:HIS:CD2	2.57	0.40
8:GB:692:MET:HA	8:GB:693:PRO:HD3	1.84	0.40
7:GC:557:CYS:HB3	7:GC:815:ASP:OD2	2.21	0.40
7:GC:843:LEU:HD11	7:GC:938:VAL:HG11	2.04	0.40
8:GD:95:ILE:HD12	8:GD:95:ILE:HA	2.00	0.40
7:GI:943:GLN:HE22	7:GI:951:MET:H	1.69	0.40
8:GL:67:CYS:SG	8:GL:79:PRO:HD3	2.62	0.40
9:HC:688:MET:HB2	9:HC:692:THR:O	2.22	0.40
10:IA:765:HIS:HD2	10:IA:786:TYR:HA	1.87	0.40
10:IB:995:PRO:HA	10:IB:1103:ARG:HD2	2.04	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1187:THR:HG23	10:IC:1190:MET:HE2	2.04	0.40
10:IC:1307:ASN:HA	10:IC:1383:LEU:HD13	2.03	0.40
11:JB:556:LEU:HD23	11:JB:790:ARG:HG3	2.04	0.40
11:JB:1731:PRO:HB3	11:JB:1778:PHE:HZ	1.85	0.40
11:JB:2126:ILE:HD13	11:JB:2126:ILE:HA	1.89	0.40
11:JC:440:PRO:HG3	11:JC:1474:TRP:CZ3	2.57	0.40
11:JC:2002:ASN:O	11:JC:2274:ILE:HG12	2.22	0.40
11:JC:2013:LEU:HD23	11:JC:2013:LEU:HA	1.96	0.40
12:KA:383:HIS:HE1	12:KA:413:ALA:HB3	1.87	0.40
12:KC:383:HIS:C	12:KC:386:LEU:HD23	2.47	0.40
12:KE:208:LEU:HD12	12:KE:242:VAL:HG23	2.04	0.40
12:KF:264:LYS:HD3	12:KF:264:LYS:HA	1.85	0.40
12:KF:626:GLU:HA	12:KF:627:PRO:HD3	1.90	0.40
12:KF:720:LEU:HD23	12:KF:720:LEU:HA	1.77	0.40
13:LE:422:GLN:HA	13:LE:425:LYS:HE2	2.04	0.40
15:NA:737:PRO:HG2	15:NA:749:PRO:HD3	2.02	0.40
15:NC:700:THR:HG21	15:NC:890:ARG:HD2	2.02	0.40
15:ND:1155:GLU:O	15:ND:1156:LEU:HG	2.20	0.40
15:ND:1550:MET:N	19:RD:142:ASN:HB3	2.29	0.40
20:SA:11:ALA:HA	20:SA:14:LYS:NZ	2.36	0.40
20:SB:110:MET:HE2	20:SB:110:MET:HB3	1.88	0.40
20:SC:125:MET:HB2	20:SC:125:MET:HE3	1.79	0.40
20:SD:43:ASN:HA	20:SD:44:PRO:HD3	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	AA	817/1073 (76%)	730 (89%)	81 (10%)	6 (1%)	19 54
1	AD	851/1073 (79%)	782 (92%)	64 (8%)	5 (1%)	22 56

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AE	817/1073 (76%)	731 (90%)	82 (10%)	4 (0%)	25	59
1	AH	851/1073 (79%)	781 (92%)	65 (8%)	5 (1%)	22	56
1	AI	817/1073 (76%)	725 (89%)	88 (11%)	4 (0%)	25	59
1	AL	851/1073 (79%)	779 (92%)	65 (8%)	7 (1%)	16	51
2	AB	465/603 (77%)	406 (87%)	53 (11%)	6 (1%)	10	42
2	AC	471/603 (78%)	439 (93%)	30 (6%)	2 (0%)	30	63
2	AF	465/603 (77%)	411 (88%)	50 (11%)	4 (1%)	14	49
2	AG	471/603 (78%)	427 (91%)	43 (9%)	1 (0%)	44	74
2	AJ	465/603 (77%)	417 (90%)	46 (10%)	2 (0%)	30	63
2	AK	471/603 (78%)	427 (91%)	42 (9%)	2 (0%)	30	63
3	BA	344/5051 (7%)	313 (91%)	30 (9%)	1 (0%)	37	68
3	BB	344/5051 (7%)	308 (90%)	35 (10%)	1 (0%)	37	68
3	BC	344/5051 (7%)	312 (91%)	31 (9%)	1 (0%)	37	68
3	CA	342/5051 (7%)	313 (92%)	29 (8%)	0	100	100
3	CB	342/5051 (7%)	312 (91%)	29 (8%)	1 (0%)	37	68
3	CC	342/5051 (7%)	306 (90%)	35 (10%)	1 (0%)	37	68
3	CE	238/5051 (5%)	195 (82%)	42 (18%)	1 (0%)	30	63
3	CF	238/5051 (5%)	188 (79%)	48 (20%)	2 (1%)	16	51
3	CG	238/5051 (5%)	190 (80%)	43 (18%)	5 (2%)	5	33
3	CI	255/5051 (5%)	228 (89%)	24 (9%)	3 (1%)	11	44
3	CJ	255/5051 (5%)	224 (88%)	28 (11%)	3 (1%)	11	44
3	CL	255/5051 (5%)	222 (87%)	30 (12%)	3 (1%)	11	44
4	DA	343/505 (68%)	317 (92%)	21 (6%)	5 (2%)	8	39
4	DB	343/505 (68%)	322 (94%)	16 (5%)	5 (2%)	8	39
4	DC	343/505 (68%)	318 (93%)	22 (6%)	3 (1%)	14	49
4	DD	328/505 (65%)	317 (97%)	11 (3%)	0	100	100
4	DE	328/505 (65%)	316 (96%)	12 (4%)	0	100	100
4	DF	328/505 (65%)	316 (96%)	11 (3%)	1 (0%)	37	68
5	EA	1333/4956 (27%)	1186 (89%)	130 (10%)	17 (1%)	10	42
5	EB	1333/4956 (27%)	1175 (88%)	142 (11%)	16 (1%)	11	44
5	EC	1333/4956 (27%)	1168 (88%)	151 (11%)	14 (1%)	12	46

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
6	FA	529/2777 (19%)	484 (92%)	42 (8%)	3 (1%)	22 56
6	FB	529/2777 (19%)	477 (90%)	50 (10%)	2 (0%)	30 63
6	FC	529/2777 (19%)	472 (89%)	53 (10%)	4 (1%)	16 51
6	FD	409/2777 (15%)	236 (58%)	112 (27%)	61 (15%)	0 2
6	FE	409/2777 (15%)	214 (52%)	133 (32%)	62 (15%)	0 2
6	FF	397/2777 (14%)	215 (54%)	137 (34%)	45 (11%)	0 4
7	GA	835/1019 (82%)	784 (94%)	47 (6%)	4 (0%)	25 59
7	GC	775/1019 (76%)	712 (92%)	59 (8%)	4 (0%)	25 59
7	GE	775/1019 (76%)	702 (91%)	67 (9%)	6 (1%)	16 51
7	GG	835/1019 (82%)	781 (94%)	52 (6%)	2 (0%)	44 74
7	GI	775/1019 (76%)	706 (91%)	65 (8%)	4 (0%)	25 59
7	GK	835/1019 (82%)	781 (94%)	52 (6%)	2 (0%)	44 74
8	GB	752/791 (95%)	667 (89%)	80 (11%)	5 (1%)	19 54
8	GD	752/791 (95%)	661 (88%)	87 (12%)	4 (0%)	25 59
8	GF	789/791 (100%)	746 (95%)	43 (5%)	0	100 100
8	GH	728/791 (92%)	650 (89%)	75 (10%)	3 (0%)	30 63
8	GJ	789/791 (100%)	744 (94%)	45 (6%)	0	100 100
8	GL	789/791 (100%)	743 (94%)	44 (6%)	2 (0%)	37 68
9	HA	424/1192 (36%)	359 (85%)	56 (13%)	9 (2%)	5 33
9	HB	424/1192 (36%)	360 (85%)	54 (13%)	10 (2%)	5 30
9	HC	290/1192 (24%)	242 (83%)	43 (15%)	5 (2%)	7 37
9	HD	134/1192 (11%)	114 (85%)	15 (11%)	5 (4%)	2 22
10	IA	1146/1599 (72%)	1045 (91%)	94 (8%)	7 (1%)	22 56
10	IB	1146/1599 (72%)	1046 (91%)	93 (8%)	7 (1%)	22 56
10	IC	1146/1599 (72%)	1054 (92%)	84 (7%)	8 (1%)	19 54
11	JA	1573/2316 (68%)	1374 (87%)	182 (12%)	17 (1%)	12 46
11	JB	1573/2316 (68%)	1357 (86%)	199 (13%)	17 (1%)	12 46
11	JC	1573/2316 (68%)	1368 (87%)	191 (12%)	14 (1%)	14 49
12	KA	458/728 (63%)	355 (78%)	92 (20%)	11 (2%)	5 30
12	KB	458/728 (63%)	365 (80%)	84 (18%)	9 (2%)	6 34
12	KC	458/728 (63%)	334 (73%)	101 (22%)	23 (5%)	1 17

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
12	KE	437/728 (60%)	408 (93%)	27 (6%)	2 (0%)	25 59
12	KF	437/728 (60%)	408 (93%)	28 (6%)	1 (0%)	44 74
12	KG	437/728 (60%)	409 (94%)	27 (6%)	1 (0%)	44 74
13	LA	186/1322 (14%)	184 (99%)	2 (1%)	0	100 100
13	LB	187/1322 (14%)	184 (98%)	2 (1%)	1 (0%)	25 59
13	LC	158/1322 (12%)	158 (100%)	0	0	100 100
13	LD	157/1322 (12%)	155 (99%)	2 (1%)	0	100 100
13	LE	145/1322 (11%)	138 (95%)	5 (3%)	2 (1%)	9 41
13	LF	146/1322 (11%)	137 (94%)	7 (5%)	2 (1%)	9 41
13	LG	55/1322 (4%)	54 (98%)	1 (2%)	0	100 100
13	LH	53/1322 (4%)	52 (98%)	1 (2%)	0	100 100
13	LI	186/1322 (14%)	176 (95%)	7 (4%)	3 (2%)	8 38
13	LJ	187/1322 (14%)	179 (96%)	6 (3%)	2 (1%)	12 46
13	LK	159/1322 (12%)	156 (98%)	3 (2%)	0	100 100
13	LL	157/1322 (12%)	156 (99%)	1 (1%)	0	100 100
13	LM	104/1322 (8%)	104 (100%)	0	0	100 100
13	LN	104/1322 (8%)	104 (100%)	0	0	100 100
13	LO	103/1322 (8%)	102 (99%)	1 (1%)	0	100 100
13	LP	108/1322 (8%)	106 (98%)	2 (2%)	0	100 100
14	MA	140/2736 (5%)	128 (91%)	11 (8%)	1 (1%)	19 54
14	MB	116/2736 (4%)	109 (94%)	6 (5%)	1 (1%)	14 49
14	MC	71/2736 (3%)	65 (92%)	6 (8%)	0	100 100
14	MD	63/2736 (2%)	63 (100%)	0	0	100 100
14	ME	140/2736 (5%)	125 (89%)	13 (9%)	2 (1%)	9 41
14	MF	116/2736 (4%)	112 (97%)	4 (3%)	0	100 100
14	MG	71/2736 (3%)	65 (92%)	5 (7%)	1 (1%)	9 41
14	MH	63/2736 (2%)	60 (95%)	3 (5%)	0	100 100
14	MI	140/2736 (5%)	126 (90%)	13 (9%)	1 (1%)	19 54
14	MJ	116/2736 (4%)	108 (93%)	6 (5%)	2 (2%)	7 37
14	MK	71/2736 (3%)	66 (93%)	5 (7%)	0	100 100
14	ML	63/2736 (2%)	63 (100%)	0	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	NA	879/2484 (35%)	763 (87%)	107 (12%)	9 (1%)	13	47
15	NB	879/2484 (35%)	757 (86%)	107 (12%)	15 (2%)	7	37
15	NC	879/2484 (35%)	758 (86%)	110 (12%)	11 (1%)	10	42
15	ND	879/2484 (35%)	757 (86%)	111 (13%)	11 (1%)	10	42
16	OA	432/2333 (18%)	369 (85%)	51 (12%)	12 (3%)	4	27
16	OB	432/2333 (18%)	373 (86%)	45 (10%)	14 (3%)	3	25
16	OC	432/2333 (18%)	373 (86%)	46 (11%)	13 (3%)	3	27
17	PA	97/1822 (5%)	77 (79%)	19 (20%)	1 (1%)	13	47
17	PB	97/1822 (5%)	75 (77%)	20 (21%)	2 (2%)	5	33
17	PC	97/1822 (5%)	81 (84%)	15 (16%)	1 (1%)	13	47
18	QA	139/172 (81%)	136 (98%)	3 (2%)	0	100	100
18	QB	139/172 (81%)	137 (99%)	2 (1%)	0	100	100
18	QC	139/172 (81%)	135 (97%)	4 (3%)	0	100	100
18	QD	139/172 (81%)	135 (97%)	4 (3%)	0	100	100
19	RA	144/179 (80%)	135 (94%)	9 (6%)	0	100	100
19	RB	144/179 (80%)	130 (90%)	14 (10%)	0	100	100
19	RC	144/179 (80%)	135 (94%)	9 (6%)	0	100	100
19	RD	144/179 (80%)	136 (94%)	8 (6%)	0	100	100
20	SA	142/149 (95%)	133 (94%)	9 (6%)	0	100	100
20	SB	142/149 (95%)	137 (96%)	5 (4%)	0	100	100
20	SC	142/149 (95%)	138 (97%)	4 (3%)	0	100	100
20	SD	142/149 (95%)	138 (97%)	4 (3%)	0	100	100
All	All	51874/215354 (24%)	46217 (89%)	5060 (10%)	597 (1%)	14	44

All (597) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	174	CYS
1	AD	136	PHE
1	AD	460	VAL
1	AD	588	ILE
1	AE	137	GLU
1	AE	174	CYS
1	AE	829	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	AF	259	VAL
1	AH	136	PHE
1	AH	460	VAL
1	AI	174	CYS
1	AI	344	SER
1	AL	136	PHE
1	AL	460	VAL
1	AL	798	CYS
3	BB	686	ALA
3	CE	4451	PRO
3	CF	4451	PRO
3	CF	4474	GLU
3	CG	1117	VAL
3	CG	4451	PRO
3	CG	4459	ALA
3	CG	4474	GLU
4	DA	309	VAL
4	DA	327	PHE
4	DA	374	VAL
4	DB	309	VAL
4	DB	327	PHE
4	DB	369	MET
4	DB	374	VAL
4	DB	386	VAL
4	DC	369	MET
5	EA	3330	ASP
5	EA	3454	ASP
5	EA	3699	ASN
5	EB	3330	ASP
5	EB	3645	ALA
5	EB	3699	ASN
5	EB	3886	ASN
5	EB	4894	SER
5	EC	3330	ASP
5	EC	3454	ASP
5	EC	3645	ALA
5	EC	3699	ASN
5	EC	3886	ASN
5	EC	4653	GLU
6	FA	1580	ALA
6	FA	1640	VAL
6	FB	1640	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FC	1640	VAL
6	FD	808	SER
6	FD	809	ILE
6	FD	814	THR
6	FD	845	PRO
6	FD	981	HIS
6	FD	1185	VAL
6	FD	1218	ALA
6	FD	1269	CYS
6	FD	1442	GLU
6	FE	808	SER
6	FE	809	ILE
6	FE	981	HIS
6	FE	1003	ILE
6	FE	1121	PRO
6	FE	1185	VAL
6	FE	1218	ALA
6	FE	1243	PRO
6	FE	1246	ILE
6	FE	1290	ILE
6	FE	1424	CYS
6	FF	808	SER
6	FF	857	GLU
6	FF	1185	VAL
6	FF	1218	ALA
6	FF	1246	ILE
6	FF	1301	ALA
6	FF	1425	PRO
6	FF	1434	ALA
7	GA	856	VAL
8	GB	190	VAL
8	GB	252	GLU
8	GB	526	ILE
7	GC	949	ASN
8	GD	526	ILE
7	GE	864	ILE
7	GE	949	ASN
7	GI	864	ILE
7	GI	949	ASN
8	GL	57	ARG
8	GL	755	MET
9	HA	482	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HA	767	GLN
9	HB	482	ALA
9	HB	767	GLN
9	HB	778	PRO
9	HC	482	ALA
9	HD	767	GLN
9	HD	778	PRO
10	IA	780	VAL
10	IA	1273	TYR
10	IA	1278	VAL
10	IB	780	VAL
10	IB	1273	TYR
10	IB	1407	ARG
10	IC	780	VAL
10	IC	1273	TYR
10	IC	1278	VAL
11	JA	451	MET
11	JA	463	ILE
11	JA	742	VAL
11	JA	944	ILE
11	JA	1093	THR
11	JA	2005	ILE
11	JB	179	PHE
11	JB	181	ASP
11	JB	451	MET
11	JB	463	ILE
11	JB	742	VAL
11	JB	1093	THR
11	JB	1283	ARG
11	JB	1866	ALA
11	JC	463	ILE
11	JC	742	VAL
11	JC	973	MET
11	JC	1093	THR
12	KA	379	SER
12	KA	503	ASP
12	KA	524	PHE
12	KA	625	ASN
12	KA	686	SER
12	KA	721	GLN
12	KB	292	ALA
12	KB	375	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KB	524	PHE
12	KC	234	PRO
12	KC	235	PRO
12	KC	357	MET
12	KC	360	ASP
12	KC	507	LEU
12	KC	511	LEU
12	KC	688	VAL
12	KC	726	ASP
12	KE	698	PRO
13	LE	465	ILE
13	LE	477	LEU
13	LF	522	ARG
13	LI	477	LEU
13	LJ	522	ARG
14	MB	259	MET
14	ME	262	PRO
14	MG	82	ARG
15	NA	469	PHE
15	NA	1180	ASP
15	NB	469	PHE
15	NB	1422	VAL
15	NC	469	PHE
15	NC	1180	ASP
15	ND	469	PHE
15	ND	1123	ALA
15	ND	1180	ASP
16	OA	266	GLN
16	OA	949	PRO
16	OA	1098	VAL
16	OB	266	GLN
16	OB	949	PRO
16	OC	26	VAL
16	OC	949	PRO
16	OC	1076	VAL
16	OC	1098	VAL
17	PA	141	GLU
17	PB	141	GLU
1	AA	137	GLU
1	AA	829	VAL
2	AB	208	GLU
2	AB	343	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AD	15	THR
1	AH	15	THR
1	AI	137	GLU
1	AL	15	THR
1	AL	588	ILE
3	BA	945	THR
3	BC	945	THR
3	CJ	4490	ASP
3	CJ	4499	PRO
3	CL	4490	ASP
4	DC	309	VAL
4	DF	181	ILE
5	EA	4408	GLY
5	EA	4653	GLU
5	EB	3703	SER
5	EC	3264	LEU
5	EC	3703	SER
5	EC	4408	GLY
6	FA	1892	ILE
6	FB	1892	ILE
6	FC	1892	ILE
6	FC	2001	CYS
6	FC	2086	ASN
6	FD	823	GLY
6	FD	860	PRO
6	FD	910	ILE
6	FD	1103	SER
6	FD	1104	GLY
6	FD	1186	TRP
6	FD	1217	GLU
6	FD	1223	ALA
6	FD	1243	PRO
6	FD	1246	ILE
6	FD	1294	LEU
6	FE	814	THR
6	FE	822	GLY
6	FE	823	GLY
6	FE	838	ASN
6	FE	841	TYR
6	FE	912	ILE
6	FE	1097	SER
6	FE	1104	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1186	TRP
6	FE	1197	ILE
6	FE	1199	GLY
6	FE	1217	GLU
6	FE	1223	ALA
6	FE	1245	ASN
6	FE	1269	CYS
6	FE	1294	LEU
6	FE	1300	LEU
6	FE	1428	GLY
6	FE	1439	LEU
6	FF	987	ASN
6	FF	1002	ALA
6	FF	1005	PRO
6	FF	1104	GLY
6	FF	1199	GLY
6	FF	1217	GLU
6	FF	1264	ILE
6	FF	1298	LEU
6	FF	1299	ASN
6	FF	1395	SER
6	FF	1421	VAL
6	FF	1433	ALA
6	FF	1439	LEU
6	FF	1442	GLU
7	GC	864	ILE
8	GD	252	GLU
8	GH	252	GLU
7	GI	782	ALA
9	HA	402	ARG
9	HA	555	SER
9	HA	761	CYS
9	HA	778	PRO
9	HB	555	SER
9	HC	632	GLU
10	IA	644	VAL
10	IB	644	VAL
10	IB	751	ASN
10	IB	1278	VAL
11	JA	181	ASP
11	JA	1283	ARG
11	JC	768	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	JC	944	ILE
11	JC	1283	ARG
12	KA	244	SER
12	KA	292	ALA
12	KA	344	ILE
12	KA	478	MET
12	KB	376	ALA
12	KB	721	GLN
12	KC	237	VAL
12	KC	379	SER
12	KC	478	MET
12	KE	210	VAL
12	KG	237	VAL
13	LJ	454	VAL
14	MJ	287	ALA
15	NB	572	ILE
15	NB	724	ASN
15	NB	1117	PHE
15	NB	1123	ALA
15	NB	1408	THR
15	NC	1123	ALA
15	NC	1472	LYS
15	ND	1422	VAL
16	OA	73	ALA
16	OA	319	GLU
16	OA	1043	VAL
16	OA	1076	VAL
16	OA	1090	GLN
16	OB	73	ALA
16	OB	1076	VAL
16	OC	73	ALA
16	OC	266	GLN
16	OC	1043	VAL
16	OC	1090	GLN
2	AB	305	ASP
2	AB	418	LYS
2	AC	359	VAL
2	AC	534	MET
1	AD	39	SER
2	AF	115	ARG
2	AF	343	ASN
2	AG	359	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	AK	359	VAL
2	AK	534	MET
3	CJ	4452	HIS
4	DA	369	MET
5	EA	3487	ARG
5	EA	3664	THR
5	EA	3703	SER
5	EA	3886	ASN
5	EA	4407	ASP
5	EB	4407	ASP
5	EB	4408	GLY
5	EB	4410	ASP
5	EC	3269	TRP
5	EC	4402	PRO
6	FD	822	GLY
6	FD	827	PRO
6	FD	861	LEU
6	FD	883	ALA
6	FD	1121	PRO
6	FD	1210	LEU
6	FD	1300	LEU
6	FD	1424	CYS
6	FD	1426	ALA
6	FD	1439	LEU
6	FE	1009	VAL
6	FE	1012	PRO
6	FE	1070	LEU
6	FE	1268	VAL
6	FE	1426	ALA
6	FE	1442	GLU
6	FF	912	ILE
6	FF	1106	LEU
6	FF	1243	PRO
6	FF	1286	LEU
6	FF	1294	LEU
8	GB	89	ASN
7	GC	158	THR
8	GD	89	ASN
9	HA	632	GLU
9	HB	402	ARG
9	HB	632	GLU
9	HB	761	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HB	763	GLN
9	HC	402	ARG
9	HC	553	TYR
9	HC	555	SER
9	HD	766	SER
10	IA	1407	ARG
10	IC	226	ARG
10	IC	644	VAL
10	IC	751	ASN
11	JA	43	SER
11	JB	70	GLU
11	JB	2005	ILE
11	JC	2005	ILE
11	JC	2105	ASN
12	KB	233	PRO
12	KC	381	MET
12	KC	389	LYS
12	KC	567	TRP
12	KC	686	SER
12	KF	217	GLU
13	LF	454	VAL
13	LI	521	ASN
14	MJ	259	MET
15	NA	865	SER
15	NA	1123	ALA
15	NA	1422	VAL
15	NB	905	ASP
15	NC	865	SER
15	NC	1117	PHE
15	ND	1117	PHE
15	ND	1549	GLY
16	OA	1089	LEU
16	OB	319	GLU
16	OB	1043	VAL
16	OB	1090	GLN
1	AA	898	PRO
2	AF	208	GLU
1	AH	39	SER
1	AL	1034	SER
3	CI	4452	HIS
3	CL	4452	HIS
5	EA	3697	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	EA	4409	GLU
5	EA	4410	ASP
5	EA	4411	THR
5	EB	4168	ILE
5	EB	4405	ILE
5	EB	4406	MET
5	EC	3266	SER
6	FD	826	LEU
6	FD	828	GLN
6	FD	841	TYR
6	FD	890	ALA
6	FD	912	ILE
6	FD	963	THR
6	FD	1097	SER
6	FD	1200	LEU
6	FD	1296	SER
6	FE	1103	SER
6	FE	1106	LEU
6	FE	1183	HIS
6	FE	1200	LEU
6	FE	1209	GLU
6	FE	1219	GLU
6	FE	1255	SER
6	FE	1264	ILE
6	FE	1388	PHE
6	FF	835	SER
6	FF	856	PRO
6	FF	1216	TRP
6	FF	1219	GLU
6	FF	1440	ASN
7	GE	158	THR
7	GE	774	ALA
7	GE	782	ALA
10	IA	751	ASN
11	JA	763	GLN
11	JA	973	MET
11	JA	1047	ASN
11	JB	768	ASP
11	JB	973	MET
11	JC	763	GLN
12	KA	502	LEU
12	KB	507	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KC	238	PHE
13	LB	532	LEU
15	NA	572	ILE
15	NA	1472	LYS
15	NB	624	ALA
15	NB	768	GLU
15	NB	864	GLU
15	NB	1423	LEU
15	NC	572	ILE
15	NC	864	GLU
15	ND	572	ILE
16	OA	26	VAL
16	OA	950	VAL
16	OC	950	VAL
1	AH	588	ILE
3	CI	4490	ASP
5	EB	3490	TYR
5	EC	4889	ILE
6	FD	919	GLN
6	FD	1003	ILE
6	FD	1219	GLU
6	FD	1388	PHE
6	FD	1440	ASN
6	FD	1441	ILE
6	FE	919	GLN
6	FE	963	THR
6	FE	1198	TYR
6	FE	1208	ALA
6	FE	1210	LEU
6	FE	1262	CYS
6	FE	1296	SER
6	FE	1441	ILE
6	FF	920	ARG
6	FF	1223	ALA
6	FF	1432	THR
7	GC	662	VAL
7	GE	662	VAL
7	GI	662	VAL
9	HA	762	HIS
9	HD	782	ALA
11	JA	70	GLU
11	JA	768	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	JA	1589	ASP
11	JB	141	ASP
11	JB	436	PRO
11	JB	1047	ASN
12	KC	206	CYS
12	KC	210	VAL
12	KC	226	ALA
12	KC	231	PHE
12	KC	530	ASP
15	NA	624	ALA
15	NB	865	SER
15	NC	468	ARG
15	ND	436	ASP
15	ND	864	GLU
15	ND	1472	LYS
16	OA	29	PRO
16	OB	26	VAL
16	OB	72	SER
16	OB	950	VAL
16	OB	1089	LEU
16	OC	211	LYS
16	OC	319	GLU
1	AA	260	THR
2	AB	259	VAL
1	AI	829	VAL
2	AJ	343	ASN
1	AL	39	SER
3	CG	4490	ASP
3	CI	4499	PRO
3	CL	4499	PRO
5	EB	4268	TYR
5	EC	4168	ILE
6	FD	999	PRO
6	FD	1106	LEU
6	FD	1224	ALA
6	FD	1248	ALA
6	FD	1290	ILE
6	FD	1298	LEU
6	FE	828	GLN
6	FE	1023	ALA
6	FE	1024	ILE
6	FE	1256	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	892	PRO
6	FF	1008	ARG
6	FF	1103	SER
6	FF	1121	PRO
8	GD	190	VAL
9	HB	782	ALA
10	IC	1407	ARG
11	JA	2105	ASN
11	JB	763	GLN
11	JB	2105	ASN
11	JC	70	GLU
11	JC	1047	ASN
12	KB	234	PRO
12	KB	324	ARG
12	KC	579	LEU
14	ME	273	THR
15	NA	724	ASN
15	NB	930	SER
15	NC	724	ASN
15	NC	1422	VAL
15	ND	865	SER
16	OB	29	PRO
16	OB	154	ALA
16	OC	70	THR
2	AJ	259	VAL
5	EB	4402	PRO
6	FD	994	PRO
6	FD	1428	GLY
6	FE	806	ILE
9	HD	779	PRO
11	JC	436	PRO
12	KC	727	ILE
14	MI	273	THR
2	AB	541	PRO
5	EA	4168	ILE
6	FD	1443	GLY
6	FE	1005	PRO
9	HB	779	PRO
10	IA	1196	VAL
10	IC	1196	VAL
16	OB	1033	ALA
1	AE	898	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	CB	752	PRO
4	DA	386	VAL
5	EB	4889	ILE
6	FD	806	ILE
6	FD	839	GLY
6	FD	1264	ILE
6	FD	1268	VAL
6	FD	1274	PRO
6	FF	845	PRO
6	FF	1012	PRO
6	FF	1254	GLY
6	FF	1278	PRO
7	GA	662	VAL
8	GB	718	PRO
9	HA	779	PRO
17	PB	281	PRO
17	PC	281	PRO
1	AA	344	SER
3	CC	772	GLY
4	DC	386	VAL
6	FD	1005	PRO
6	FD	1109	VAL
6	FE	845	PRO
6	FE	910	ILE
6	FF	1274	PRO
6	FF	1296	SER
7	GA	351	GLY
7	GG	662	VAL
8	GH	190	VAL
7	GK	349	GLY
7	GK	662	VAL
10	IB	1196	VAL
11	JA	436	PRO
11	JC	435	VAL
14	MA	273	THR
15	NB	843	ASN
5	EA	4405	ILE
5	EA	4656	ILE
6	FE	892	PRO
7	GA	349	GLY
7	GG	349	GLY
8	GH	113	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	LI	476	GLY
16	OC	1033	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	718/908 (79%)	718 (100%)	0	100	100
1	AD	740/908 (82%)	739 (100%)	1 (0%)	92	97
1	AE	718/908 (79%)	718 (100%)	0	100	100
1	AH	740/908 (82%)	740 (100%)	0	100	100
1	AI	718/908 (79%)	717 (100%)	1 (0%)	92	97
1	AL	740/908 (82%)	736 (100%)	4 (0%)	86	93
2	AB	415/516 (80%)	410 (99%)	5 (1%)	67	83
2	AC	418/516 (81%)	418 (100%)	0	100	100
2	AF	415/516 (80%)	415 (100%)	0	100	100
2	AG	418/516 (81%)	418 (100%)	0	100	100
2	AJ	414/516 (80%)	414 (100%)	0	100	100
2	AK	418/516 (81%)	415 (99%)	3 (1%)	81	90
3	BA	286/4189 (7%)	286 (100%)	0	100	100
3	BB	286/4189 (7%)	286 (100%)	0	100	100
3	BC	286/4189 (7%)	286 (100%)	0	100	100
3	CA	284/4189 (7%)	284 (100%)	0	100	100
3	CB	284/4189 (7%)	283 (100%)	1 (0%)	89	95
3	CC	284/4189 (7%)	283 (100%)	1 (0%)	89	95
3	CE	206/4189 (5%)	206 (100%)	0	100	100
3	CF	206/4189 (5%)	206 (100%)	0	100	100
3	CG	206/4189 (5%)	206 (100%)	0	100	100
3	CI	221/4189 (5%)	221 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	CJ	221/4189 (5%)	221 (100%)	0	100 100
3	CL	221/4189 (5%)	221 (100%)	0	100 100
4	DA	297/435 (68%)	297 (100%)	0	100 100
4	DB	297/435 (68%)	297 (100%)	0	100 100
4	DC	297/435 (68%)	297 (100%)	0	100 100
4	DD	285/435 (66%)	285 (100%)	0	100 100
4	DE	285/435 (66%)	285 (100%)	0	100 100
4	DF	285/435 (66%)	285 (100%)	0	100 100
5	EA	1150/4160 (28%)	1147 (100%)	3 (0%)	91 96
5	EB	1150/4160 (28%)	1135 (99%)	15 (1%)	65 81
5	EC	1149/4160 (28%)	1135 (99%)	14 (1%)	67 83
6	FA	453/2343 (19%)	435 (96%)	18 (4%)	27 56
6	FB	453/2343 (19%)	436 (96%)	17 (4%)	28 57
6	FC	453/2343 (19%)	391 (86%)	62 (14%)	3 17
6	FD	356/2343 (15%)	189 (53%)	167 (47%)	0 0
6	FE	357/2343 (15%)	192 (54%)	165 (46%)	0 0
6	FF	348/2343 (15%)	184 (53%)	164 (47%)	0 0
7	GA	680/807 (84%)	680 (100%)	0	100 100
7	GC	647/807 (80%)	647 (100%)	0	100 100
7	GE	647/807 (80%)	647 (100%)	0	100 100
7	GG	680/807 (84%)	680 (100%)	0	100 100
7	GI	647/807 (80%)	647 (100%)	0	100 100
7	GK	680/807 (84%)	680 (100%)	0	100 100
8	GB	647/665 (97%)	646 (100%)	1 (0%)	92 97
8	GD	647/665 (97%)	645 (100%)	2 (0%)	91 96
8	GF	665/665 (100%)	665 (100%)	0	100 100
8	GH	629/665 (95%)	628 (100%)	1 (0%)	92 97
8	GJ	665/665 (100%)	665 (100%)	0	100 100
8	GL	665/665 (100%)	664 (100%)	1 (0%)	92 97
9	HA	353/1003 (35%)	306 (87%)	47 (13%)	3 18
9	HB	353/1003 (35%)	309 (88%)	44 (12%)	3 20

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
9	HC	234/1003 (23%)	234 (100%)	0	100 100
9	HD	119/1003 (12%)	77 (65%)	42 (35%)	0 1
10	IA	978/1309 (75%)	978 (100%)	0	100 100
10	IB	978/1309 (75%)	977 (100%)	1 (0%)	92 97
10	IC	978/1309 (75%)	978 (100%)	0	100 100
11	JA	1388/1993 (70%)	1388 (100%)	0	100 100
11	JB	1388/1993 (70%)	1387 (100%)	1 (0%)	92 97
11	JC	1388/1993 (70%)	1388 (100%)	0	100 100
12	KA	401/626 (64%)	401 (100%)	0	100 100
12	KB	401/626 (64%)	401 (100%)	0	100 100
12	KC	400/626 (64%)	388 (97%)	12 (3%)	36 63
12	KE	385/626 (62%)	385 (100%)	0	100 100
12	KF	385/626 (62%)	385 (100%)	0	100 100
12	KG	385/626 (62%)	385 (100%)	0	100 100
13	LA	165/1137 (14%)	164 (99%)	1 (1%)	84 92
13	LB	167/1137 (15%)	167 (100%)	0	100 100
13	LC	146/1137 (13%)	146 (100%)	0	100 100
13	LD	146/1137 (13%)	146 (100%)	0	100 100
13	LE	132/1137 (12%)	132 (100%)	0	100 100
13	LF	134/1137 (12%)	134 (100%)	0	100 100
13	LG	54/1137 (5%)	54 (100%)	0	100 100
13	LH	53/1137 (5%)	53 (100%)	0	100 100
13	LI	165/1137 (14%)	161 (98%)	4 (2%)	44 68
13	LJ	167/1137 (15%)	167 (100%)	0	100 100
13	LK	147/1137 (13%)	147 (100%)	0	100 100
13	LL	146/1137 (13%)	146 (100%)	0	100 100
13	LM	93/1137 (8%)	93 (100%)	0	100 100
13	LN	93/1137 (8%)	93 (100%)	0	100 100
13	LO	90/1137 (8%)	90 (100%)	0	100 100
13	LP	95/1137 (8%)	95 (100%)	0	100 100
14	MA	123/2310 (5%)	123 (100%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	MB	107/2310 (5%)	107 (100%)	0	100	100
14	MC	63/2310 (3%)	63 (100%)	0	100	100
14	MD	51/2310 (2%)	51 (100%)	0	100	100
14	ME	123/2310 (5%)	123 (100%)	0	100	100
14	MF	107/2310 (5%)	107 (100%)	0	100	100
14	MG	63/2310 (3%)	63 (100%)	0	100	100
14	MH	51/2310 (2%)	51 (100%)	0	100	100
14	MI	123/2310 (5%)	123 (100%)	0	100	100
14	MJ	107/2310 (5%)	107 (100%)	0	100	100
14	MK	63/2310 (3%)	63 (100%)	0	100	100
14	ML	51/2310 (2%)	51 (100%)	0	100	100
15	NA	785/2093 (38%)	785 (100%)	0	100	100
15	NB	785/2093 (38%)	785 (100%)	0	100	100
15	NC	785/2093 (38%)	785 (100%)	0	100	100
15	ND	785/2093 (38%)	785 (100%)	0	100	100
16	OA	370/1912 (19%)	370 (100%)	0	100	100
16	OB	370/1912 (19%)	370 (100%)	0	100	100
16	OC	370/1912 (19%)	370 (100%)	0	100	100
17	PA	88/1558 (6%)	88 (100%)	0	100	100
17	PB	88/1558 (6%)	88 (100%)	0	100	100
17	PC	88/1558 (6%)	88 (100%)	0	100	100
18	QA	120/150 (80%)	120 (100%)	0	100	100
18	QB	120/150 (80%)	120 (100%)	0	100	100
18	QC	120/150 (80%)	120 (100%)	0	100	100
18	QD	120/150 (80%)	120 (100%)	0	100	100
19	RA	123/139 (88%)	123 (100%)	0	100	100
19	RB	123/139 (88%)	123 (100%)	0	100	100
19	RC	123/139 (88%)	123 (100%)	0	100	100
19	RD	123/139 (88%)	122 (99%)	1 (1%)	79	88
20	SA	123/127 (97%)	123 (100%)	0	100	100
20	SB	123/127 (97%)	123 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
20	SC	123/127 (97%)	123 (100%)	0	100 100
20	SD	123/127 (97%)	123 (100%)	0	100 100
All	All	44894/180824 (25%)	44095 (98%)	799 (2%)	54 74

All (799) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	329	GLN
2	AB	408	LYS
2	AB	411	GLN
2	AB	414	LEU
2	AB	419	LYS
1	AD	988	GLN
1	AI	341	GLN
2	AK	331	ASN
2	AK	343	ASN
2	AK	448	ASN
1	AL	1027	MET
1	AL	1028	ARG
1	AL	1031	THR
1	AL	1033	GLN
3	CB	880	GLN
3	CC	724	GLN
5	EA	3335	GLN
5	EA	4405	ILE
5	EA	4406	MET
5	EB	4069	HIS
5	EB	4403	LEU
5	EB	4404	LYS
5	EB	4405	ILE
5	EB	4406	MET
5	EB	4407	ASP
5	EB	4879	THR
5	EB	4880	ASP
5	EB	4881	ARG
5	EB	4883	LEU
5	EB	4884	LEU
5	EB	4886	LYS
5	EB	4889	ILE
5	EB	4892	ARG
5	EB	4896	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	EC	4093	SER
5	EC	4094	LEU
5	EC	4099	THR
5	EC	4403	LEU
5	EC	4404	LYS
5	EC	4406	MET
5	EC	4879	THR
5	EC	4880	ASP
5	EC	4881	ARG
5	EC	4882	ARG
5	EC	4886	LYS
5	EC	4889	ILE
5	EC	4892	ARG
5	EC	4898	MET
6	FA	2010	LYS
6	FA	2013	GLU
6	FA	2014	GLU
6	FA	2015	LYS
6	FA	2016	ARG
6	FA	2017	ARG
6	FA	2018	ARG
6	FA	2024	ARG
6	FA	2030	ILE
6	FA	2037	LEU
6	FA	2038	LEU
6	FA	2042	LYS
6	FA	2044	CYS
6	FA	2046	ASP
6	FA	2050	LEU
6	FA	2053	LYS
6	FA	2056	LEU
6	FA	2059	VAL
6	FB	2030	ILE
6	FB	2037	LEU
6	FB	2038	LEU
6	FB	2042	LYS
6	FB	2046	ASP
6	FB	2047	ARG
6	FB	2048	GLU
6	FB	2050	LEU
6	FB	2053	LYS
6	FB	2056	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FB	2057	SER
6	FB	2061	ARG
6	FB	2062	LEU
6	FB	2063	GLN
6	FB	2064	LEU
6	FB	2067	MET
6	FB	2068	CYS
6	FC	1968	LYS
6	FC	1970	LEU
6	FC	1971	LYS
6	FC	1972	GLU
6	FC	1973	GLU
6	FC	1976	LYS
6	FC	1978	LEU
6	FC	1979	GLU
6	FC	1983	ARG
6	FC	1984	LYS
6	FC	1989	GLU
6	FC	1993	LYS
6	FC	1994	ARG
6	FC	1995	GLU
6	FC	1997	GLU
6	FC	1998	GLU
6	FC	2001	CYS
6	FC	2007	GLU
6	FC	2008	THR
6	FC	2010	LYS
6	FC	2012	ARG
6	FC	2013	GLU
6	FC	2014	GLU
6	FC	2015	LYS
6	FC	2017	ARG
6	FC	2018	ARG
6	FC	2021	GLU
6	FC	2022	GLU
6	FC	2024	ARG
6	FC	2030	ILE
6	FC	2034	ARG
6	FC	2037	LEU
6	FC	2038	LEU
6	FC	2040	LEU
6	FC	2042	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FC	2046	ASP
6	FC	2047	ARG
6	FC	2051	VAL
6	FC	2053	LYS
6	FC	2057	SER
6	FC	2058	MET
6	FC	2061	ARG
6	FC	2064	LEU
6	FC	2066	GLU
6	FC	2070	LEU
6	FC	2072	ILE
6	FC	2073	LEU
6	FC	2079	MET
6	FC	2080	GLN
6	FC	2082	LEU
6	FC	2083	GLN
6	FC	2084	GLN
6	FC	2087	LEU
6	FC	2088	MET
6	FC	2089	PRO
6	FC	2090	LEU
6	FC	2094	LEU
6	FC	2095	GLN
6	FC	2097	GLN
6	FC	2099	ILE
6	FC	2101	LEU
6	FC	2109	ILE
6	FD	801	THR
6	FD	802	LEU
6	FD	803	ARG
6	FD	804	LEU
6	FD	808	SER
6	FD	809	ILE
6	FD	810	THR
6	FD	811	ASN
6	FD	813	GLN
6	FD	814	THR
6	FD	818	VAL
6	FD	820	LYS
6	FD	821	ARG
6	FD	826	LEU
6	FD	828	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	829	ARG
6	FD	834	VAL
6	FD	835	SER
6	FD	838	ASN
6	FD	841	TYR
6	FD	843	LEU
6	FD	848	THR
6	FD	849	ILE
6	FD	851	THR
6	FD	858	GLU
6	FD	861	LEU
6	FD	862	GLU
6	FD	863	ILE
6	FD	866	PHE
6	FD	878	LEU
6	FD	882	SER
6	FD	887	ARG
6	FD	891	ARG
6	FD	896	CYS
6	FD	897	LEU
6	FD	898	ASP
6	FD	901	GLU
6	FD	903	GLN
6	FD	905	GLU
6	FD	912	ILE
6	FD	913	LEU
6	FD	915	SER
6	FD	918	GLN
6	FD	920	ARG
6	FD	921	MET
6	FD	922	LEU
6	FD	924	LEU
6	FD	925	GLU
6	FD	926	LEU
6	FD	929	ASN
6	FD	964	LEU
6	FD	969	LEU
6	FD	970	VAL
6	FD	973	ILE
6	FD	978	LYS
6	FD	984	THR
6	FD	985	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	988	SER
6	FD	990	PHE
6	FD	991	ARG
6	FD	995	VAL
6	FD	997	THR
6	FD	1000	GLN
6	FD	1001	ASN
6	FD	1003	ILE
6	FD	1008	ARG
6	FD	1009	VAL
6	FD	1010	ARG
6	FD	1014	LYS
6	FD	1017	VAL
6	FD	1018	THR
6	FD	1024	ILE
6	FD	1028	LYS
6	FD	1029	GLN
6	FD	1030	ILE
6	FD	1064	TYR
6	FD	1065	LEU
6	FD	1066	GLN
6	FD	1068	CYS
6	FD	1077	ARG
6	FD	1078	GLU
6	FD	1080	ILE
6	FD	1084	ARG
6	FD	1089	ARG
6	FD	1091	GLU
6	FD	1093	VAL
6	FD	1095	LEU
6	FD	1098	VAL
6	FD	1100	GLU
6	FD	1107	SER
6	FD	1109	VAL
6	FD	1114	VAL
6	FD	1116	LEU
6	FD	1119	LEU
6	FD	1120	LYS
6	FD	1122	LEU
6	FD	1123	THR
6	FD	1124	ILE
6	FD	1183	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	1185	VAL
6	FD	1187	ILE
6	FD	1188	GLU
6	FD	1190	ARG
6	FD	1191	LYS
6	FD	1192	VAL
6	FD	1193	VAL
6	FD	1194	ASN
6	FD	1195	VAL
6	FD	1200	LEU
6	FD	1201	THR
6	FD	1203	ARG
6	FD	1206	CYS
6	FD	1209	GLU
6	FD	1210	LEU
6	FD	1215	MET
6	FD	1217	GLU
6	FD	1219	GLU
6	FD	1220	ARG
6	FD	1225	ILE
6	FD	1229	LYS
6	FD	1231	ARG
6	FD	1232	LYS
6	FD	1233	ILE
6	FD	1238	ARG
6	FD	1239	CYS
6	FD	1244	LEU
6	FD	1246	ILE
6	FD	1249	ILE
6	FD	1252	MET
6	FD	1255	SER
6	FD	1256	GLU
6	FD	1257	ASP
6	FD	1258	SER
6	FD	1259	LEU
6	FD	1260	LEU
6	FD	1261	SER
6	FD	1262	CYS
6	FD	1264	ILE
6	FD	1267	GLN
6	FD	1268	VAL
6	FD	1270	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	1277	ASP
6	FD	1279	SER
6	FD	1281	VAL
6	FD	1284	LEU
6	FD	1289	HIS
6	FD	1291	TYR
6	FD	1294	LEU
6	FD	1298	LEU
6	FD	1300	LEU
6	FD	1388	PHE
6	FD	1389	ARG
6	FD	1391	TYR
6	FD	1392	LYS
6	FD	1393	LEU
6	FD	1416	GLN
6	FD	1419	LEU
6	FD	1420	ARG
6	FD	1421	VAL
6	FD	1422	PHE
6	FD	1424	CYS
6	FD	1427	ASN
6	FD	1429	LEU
6	FD	1431	MET
6	FD	1438	LYS
6	FD	1439	LEU
6	FD	1444	ARG
6	FE	801	THR
6	FE	802	LEU
6	FE	803	ARG
6	FE	804	LEU
6	FE	809	ILE
6	FE	810	THR
6	FE	813	GLN
6	FE	814	THR
6	FE	818	VAL
6	FE	821	ARG
6	FE	824	TYR
6	FE	828	GLN
6	FE	829	ARG
6	FE	835	SER
6	FE	841	TYR
6	FE	843	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	849	ILE
6	FE	851	THR
6	FE	858	GLU
6	FE	861	LEU
6	FE	862	GLU
6	FE	866	PHE
6	FE	878	LEU
6	FE	879	ARG
6	FE	882	SER
6	FE	884	VAL
6	FE	891	ARG
6	FE	895	ILE
6	FE	897	LEU
6	FE	898	ASP
6	FE	901	GLU
6	FE	905	GLU
6	FE	907	ASN
6	FE	912	ILE
6	FE	913	LEU
6	FE	915	SER
6	FE	918	GLN
6	FE	920	ARG
6	FE	921	MET
6	FE	922	LEU
6	FE	924	LEU
6	FE	926	LEU
6	FE	929	ASN
6	FE	964	LEU
6	FE	969	LEU
6	FE	972	VAL
6	FE	973	ILE
6	FE	975	ILE
6	FE	978	LYS
6	FE	981	HIS
6	FE	982	SER
6	FE	985	ILE
6	FE	987	ASN
6	FE	988	SER
6	FE	997	THR
6	FE	1000	GLN
6	FE	1001	ASN
6	FE	1003	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1007	GLN
6	FE	1008	ARG
6	FE	1010	ARG
6	FE	1014	LYS
6	FE	1015	SER
6	FE	1017	VAL
6	FE	1018	THR
6	FE	1020	VAL
6	FE	1024	ILE
6	FE	1028	LYS
6	FE	1029	GLN
6	FE	1030	ILE
6	FE	1065	LEU
6	FE	1068	CYS
6	FE	1069	ARG
6	FE	1077	ARG
6	FE	1078	GLU
6	FE	1080	ILE
6	FE	1084	ARG
6	FE	1087	LEU
6	FE	1089	ARG
6	FE	1090	LEU
6	FE	1091	GLU
6	FE	1093	VAL
6	FE	1095	LEU
6	FE	1098	VAL
6	FE	1099	ILE
6	FE	1100	GLU
6	FE	1105	ARG
6	FE	1109	VAL
6	FE	1114	VAL
6	FE	1116	LEU
6	FE	1119	LEU
6	FE	1120	LYS
6	FE	1122	LEU
6	FE	1123	THR
6	FE	1124	ILE
6	FE	1183	HIS
6	FE	1185	VAL
6	FE	1187	ILE
6	FE	1188	GLU
6	FE	1190	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1191	LYS
6	FE	1192	VAL
6	FE	1195	VAL
6	FE	1200	LEU
6	FE	1201	THR
6	FE	1210	LEU
6	FE	1217	GLU
6	FE	1219	GLU
6	FE	1220	ARG
6	FE	1225	ILE
6	FE	1229	LYS
6	FE	1231	ARG
6	FE	1232	LYS
6	FE	1233	ILE
6	FE	1238	ARG
6	FE	1239	CYS
6	FE	1242	GLN
6	FE	1244	LEU
6	FE	1246	ILE
6	FE	1249	ILE
6	FE	1252	MET
6	FE	1255	SER
6	FE	1257	ASP
6	FE	1258	SER
6	FE	1259	LEU
6	FE	1260	LEU
6	FE	1261	SER
6	FE	1262	CYS
6	FE	1263	TYR
6	FE	1264	ILE
6	FE	1265	ARG
6	FE	1267	GLN
6	FE	1268	VAL
6	FE	1270	LEU
6	FE	1272	VAL
6	FE	1277	ASP
6	FE	1279	SER
6	FE	1281	VAL
6	FE	1284	LEU
6	FE	1285	CYS
6	FE	1289	HIS
6	FE	1293	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1294	LEU
6	FE	1298	LEU
6	FE	1300	LEU
6	FE	1388	PHE
6	FE	1389	ARG
6	FE	1392	LYS
6	FE	1394	ARG
6	FE	1397	VAL
6	FE	1416	GLN
6	FE	1417	ILE
6	FE	1418	GLU
6	FE	1419	LEU
6	FE	1420	ARG
6	FE	1421	VAL
6	FE	1422	PHE
6	FE	1424	CYS
6	FE	1427	ASN
6	FE	1429	LEU
6	FE	1431	MET
6	FE	1438	LYS
6	FE	1439	LEU
6	FE	1442	GLU
6	FE	1444	ARG
6	FF	801	THR
6	FF	802	LEU
6	FF	803	ARG
6	FF	804	LEU
6	FF	809	ILE
6	FF	810	THR
6	FF	813	GLN
6	FF	814	THR
6	FF	817	VAL
6	FF	818	VAL
6	FF	821	ARG
6	FF	826	LEU
6	FF	828	GLN
6	FF	829	ARG
6	FF	834	VAL
6	FF	835	SER
6	FF	838	ASN
6	FF	841	TYR
6	FF	843	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	846	CYS
6	FF	849	ILE
6	FF	852	VAL
6	FF	857	GLU
6	FF	858	GLU
6	FF	859	ASP
6	FF	861	LEU
6	FF	863	ILE
6	FF	868	GLN
6	FF	878	LEU
6	FF	879	ARG
6	FF	887	ARG
6	FF	889	SER
6	FF	891	ARG
6	FF	895	ILE
6	FF	897	LEU
6	FF	901	GLU
6	FF	905	GLU
6	FF	910	ILE
6	FF	912	ILE
6	FF	913	LEU
6	FF	917	TRP
6	FF	920	ARG
6	FF	922	LEU
6	FF	924	LEU
6	FF	926	LEU
6	FF	929	ASN
6	FF	962	PHE
6	FF	969	LEU
6	FF	971	SER
6	FF	973	ILE
6	FF	975	ILE
6	FF	979	LEU
6	FF	982	SER
6	FF	988	SER
6	FF	990	PHE
6	FF	1003	ILE
6	FF	1008	ARG
6	FF	1010	ARG
6	FF	1014	LYS
6	FF	1017	VAL
6	FF	1018	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	1019	VAL
6	FF	1020	VAL
6	FF	1024	ILE
6	FF	1028	LYS
6	FF	1029	GLN
6	FF	1030	ILE
6	FF	1065	LEU
6	FF	1066	GLN
6	FF	1068	CYS
6	FF	1069	ARG
6	FF	1080	ILE
6	FF	1081	SER
6	FF	1084	ARG
6	FF	1085	GLU
6	FF	1090	LEU
6	FF	1091	GLU
6	FF	1093	VAL
6	FF	1094	SER
6	FF	1096	LEU
6	FF	1098	VAL
6	FF	1100	GLU
6	FF	1105	ARG
6	FF	1112	ILE
6	FF	1114	VAL
6	FF	1115	THR
6	FF	1116	LEU
6	FF	1119	LEU
6	FF	1120	LYS
6	FF	1122	LEU
6	FF	1124	ILE
6	FF	1183	HIS
6	FF	1185	VAL
6	FF	1187	ILE
6	FF	1188	GLU
6	FF	1189	ILE
6	FF	1190	ARG
6	FF	1191	LYS
6	FF	1192	VAL
6	FF	1194	ASN
6	FF	1195	VAL
6	FF	1200	LEU
6	FF	1201	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	1203	ARG
6	FF	1205	ILE
6	FF	1207	GLU
6	FF	1209	GLU
6	FF	1210	LEU
6	FF	1212	VAL
6	FF	1213	VAL
6	FF	1215	MET
6	FF	1217	GLU
6	FF	1219	GLU
6	FF	1225	ILE
6	FF	1227	ARG
6	FF	1229	LYS
6	FF	1230	SER
6	FF	1231	ARG
6	FF	1232	LYS
6	FF	1233	ILE
6	FF	1234	THR
6	FF	1238	ARG
6	FF	1240	GLU
6	FF	1241	VAL
6	FF	1242	GLN
6	FF	1244	LEU
6	FF	1245	ASN
6	FF	1246	ILE
6	FF	1249	ILE
6	FF	1250	GLU
6	FF	1251	ARG
6	FF	1252	MET
6	FF	1256	GLU
6	FF	1257	ASP
6	FF	1258	SER
6	FF	1261	SER
6	FF	1262	CYS
6	FF	1264	ILE
6	FF	1267	GLN
6	FF	1268	VAL
6	FF	1270	LEU
6	FF	1272	VAL
6	FF	1279	SER
6	FF	1281	VAL
6	FF	1284	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	1289	HIS
6	FF	1294	LEU
6	FF	1298	LEU
6	FF	1389	ARG
6	FF	1393	LEU
6	FF	1394	ARG
6	FF	1416	GLN
6	FF	1421	VAL
6	FF	1427	ASN
6	FF	1429	LEU
6	FF	1431	MET
6	FF	1432	THR
6	FF	1438	LYS
6	FF	1439	LEU
6	FF	1441	ILE
6	FF	1442	GLU
6	FF	1444	ARG
6	FF	1445	SER
6	FF	1446	ASN
8	GB	683	GLN
8	GD	629	ASN
8	GD	703	GLN
8	GH	64	ASN
8	GL	83	GLN
9	HA	747	VAL
9	HA	752	ASP
9	HA	753	SER
9	HA	755	MET
9	HA	757	LEU
9	HA	760	LYS
9	HA	762	HIS
9	HA	765	TRP
9	HA	768	THR
9	HA	769	LYS
9	HA	770	ASN
9	HA	775	SER
9	HA	779	PRO
9	HA	780	PHE
9	HA	784	GLU
9	HA	790	LEU
9	HA	791	GLN
9	HA	795	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HA	796	ASP
9	HA	798	ASP
9	HA	800	VAL
9	HA	802	MET
9	HA	810	ARG
9	HA	814	LYS
9	HA	820	SER
9	HA	832	SER
9	HA	834	LEU
9	HA	838	LYS
9	HA	842	HIS
9	HA	848	ASP
9	HA	851	GLU
9	HA	852	LYS
9	HA	855	ARG
9	HA	856	GLU
9	HA	858	LEU
9	HA	859	LYS
9	HA	861	TYR
9	HA	862	LEU
9	HA	865	ILE
9	HA	868	LEU
9	HA	869	GLN
9	HA	871	GLU
9	HA	872	MET
9	HA	874	VAL
9	HA	877	LYS
9	HA	878	SER
9	HA	880	HIS
9	HB	747	VAL
9	HB	752	ASP
9	HB	753	SER
9	HB	754	LEU
9	HB	755	MET
9	HB	757	LEU
9	HB	760	LYS
9	HB	764	LYS
9	HB	765	TRP
9	HB	768	THR
9	HB	769	LYS
9	HB	770	ASN
9	HB	775	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HB	776	PRO
9	HB	784	GLU
9	HB	790	LEU
9	HB	791	GLN
9	HB	795	LEU
9	HB	796	ASP
9	HB	798	ASP
9	HB	800	VAL
9	HB	802	MET
9	HB	810	ARG
9	HB	812	THR
9	HB	814	LYS
9	HB	832	SER
9	HB	834	LEU
9	HB	835	LYS
9	HB	838	LYS
9	HB	842	HIS
9	HB	848	ASP
9	HB	851	GLU
9	HB	852	LYS
9	HB	855	ARG
9	HB	858	LEU
9	HB	859	LYS
9	HB	861	TYR
9	HB	865	ILE
9	HB	868	LEU
9	HB	869	GLN
9	HB	872	MET
9	HB	877	LYS
9	HB	879	ILE
9	HB	880	HIS
9	HD	747	VAL
9	HD	749	ASN
9	HD	752	ASP
9	HD	753	SER
9	HD	757	LEU
9	HD	760	LYS
9	HD	763	GLN
9	HD	764	LYS
9	HD	768	THR
9	HD	769	LYS
9	HD	770	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HD	775	SER
9	HD	776	PRO
9	HD	779	PRO
9	HD	784	GLU
9	HD	790	LEU
9	HD	791	GLN
9	HD	792	ARG
9	HD	798	ASP
9	HD	800	VAL
9	HD	802	MET
9	HD	804	THR
9	HD	810	ARG
9	HD	814	LYS
9	HD	823	ILE
9	HD	834	LEU
9	HD	838	LYS
9	HD	842	HIS
9	HD	848	ASP
9	HD	851	GLU
9	HD	852	LYS
9	HD	855	ARG
9	HD	858	LEU
9	HD	859	LYS
9	HD	860	GLN
9	HD	865	ILE
9	HD	868	LEU
9	HD	869	GLN
9	HD	872	MET
9	HD	875	THR
9	HD	877	LYS
9	HD	880	HIS
10	IB	1179	ASN
11	JB	2122	GLN
12	KC	227	THR
12	KC	228	GLU
12	KC	229	SER
12	KC	230	GLN
12	KC	231	PHE
12	KC	236	LYS
12	KC	237	VAL
12	KC	381	MET
12	KC	384	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KC	385	GLU
12	KC	722	VAL
12	KC	723	GLU
13	LA	480	GLN
13	LI	520	LEU
13	LI	526	LEU
13	LI	530	VAL
13	LI	532	LEU
19	RD	142	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (520) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	76	GLN
1	AA	232	GLN
1	AA	256	GLN
1	AA	275	HIS
1	AA	372	HIS
1	AA	442	HIS
1	AA	673	GLN
1	AA	683	ASN
2	AB	153	GLN
2	AB	168	GLN
2	AB	267	HIS
2	AB	329	GLN
2	AB	415	HIS
2	AB	466	GLN
2	AB	518	HIS
2	AC	46	GLN
2	AC	82	ASN
2	AC	153	GLN
2	AC	415	HIS
1	AD	370	GLN
1	AD	716	HIS
1	AD	814	GLN
1	AD	909	GLN
1	AD	988	GLN
1	AE	442	HIS
1	AE	744	HIS
1	AE	909	GLN
2	AF	64	GLN
2	AF	136	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	AF	262	GLN
2	AF	304	GLN
2	AF	368	HIS
2	AF	381	HIS
2	AF	466	GLN
2	AF	482	GLN
2	AG	46	GLN
2	AG	49	HIS
2	AG	304	GLN
2	AG	355	HIS
2	AG	448	ASN
2	AG	518	HIS
1	AH	27	HIS
1	AH	232	GLN
1	AH	256	GLN
1	AH	450	ASN
1	AH	652	ASN
1	AI	145	HIS
1	AI	215	GLN
1	AI	379	GLN
1	AI	476	GLN
1	AI	504	ASN
1	AI	652	ASN
1	AI	686	ASN
2	AJ	168	GLN
2	AJ	213	HIS
2	AJ	304	GLN
2	AJ	337	HIS
2	AJ	411	GLN
2	AJ	518	HIS
2	AK	262	GLN
2	AK	329	GLN
2	AK	439	GLN
2	AK	518	HIS
1	AL	76	GLN
1	AL	145	HIS
1	AL	293	HIS
1	AL	628	ASN
1	AL	683	ASN
1	AL	762	HIS
1	AL	968	ASN
3	BA	725	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	BA	733	GLN
3	BA	817	HIS
3	BA	964	GLN
3	BA	967	HIS
3	BA	995	ASN
3	BB	736	HIS
3	BB	778	GLN
3	BB	952	GLN
3	BB	962	GLN
3	BB	995	ASN
3	BB	1012	GLN
3	BC	683	GLN
3	BC	708	GLN
3	BC	749	GLN
3	BC	790	ASN
3	BC	995	ASN
3	BC	1010	GLN
3	CA	733	GLN
3	CA	835	GLN
3	CB	790	ASN
3	CB	817	HIS
3	CC	683	GLN
3	CC	790	ASN
3	CC	895	HIS
3	CC	944	GLN
3	CC	962	GLN
3	CF	1192	HIS
3	CG	1178	GLN
3	CG	1192	HIS
3	CG	1257	ASN
3	CI	1242	ASN
3	CJ	1178	GLN
3	CJ	1205	GLN
3	CJ	1243	GLN
3	CJ	4511	GLN
3	CL	1221	ASN
3	CL	1242	ASN
3	CL	4492	ASN
4	DA	308	GLN
4	DA	334	GLN
4	DA	361	GLN
4	DB	63	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	DB	72	GLN
4	DB	291	GLN
4	DB	312	ASN
4	DB	361	GLN
4	DC	312	ASN
4	DC	361	GLN
4	DD	334	GLN
4	DE	281	GLN
4	DE	308	GLN
4	DF	252	GLN
4	DF	300	GLN
5	EA	3274	GLN
5	EA	3440	GLN
5	EA	3519	ASN
5	EA	3581	HIS
5	EA	3820	HIS
5	EA	3864	HIS
5	EA	3882	ASN
5	EA	4069	HIS
5	EA	4177	GLN
5	EA	4340	ASN
5	EA	4830	ASN
5	EB	3279	GLN
5	EB	3416	HIS
5	EB	3503	GLN
5	EB	3713	GLN
5	EB	3820	HIS
5	EB	3864	HIS
5	EB	4264	GLN
5	EB	4280	HIS
5	EB	4340	ASN
5	EB	4455	GLN
5	EB	4631	HIS
5	EB	4703	GLN
5	EB	4748	ASN
5	EB	4756	GLN
5	EB	4829	GLN
5	EB	4878	HIS
5	EC	3448	GLN
5	EC	3626	HIS
5	EC	3725	ASN
5	EC	3820	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	EC	4161	HIS
5	EC	4267	GLN
5	EC	4287	ASN
5	EC	4376	HIS
5	EC	4391	GLN
5	EC	4479	GLN
5	EC	4762	GLN
5	EC	4824	ASN
5	EC	4878	HIS
6	FA	1612	ASN
6	FA	1806	ASN
6	FA	1850	GLN
6	FA	1893	HIS
6	FA	1937	GLN
6	FA	2043	ASN
6	FA	2095	GLN
6	FB	1612	ASN
6	FB	1790	ASN
6	FB	1851	GLN
6	FB	2043	ASN
6	FB	2052	HIS
6	FB	2063	GLN
6	FB	2076	HIS
6	FB	2080	GLN
6	FC	1599	HIS
6	FC	1791	ASN
6	FC	1827	GLN
6	FC	1985	GLN
6	FC	2031	HIS
6	FC	2052	HIS
6	FC	2076	HIS
6	FC	2097	GLN
6	FC	2107	GLN
6	FD	799	GLN
6	FD	907	ASN
6	FD	1001	ASN
6	FD	1242	GLN
6	FD	1267	GLN
6	FD	1427	ASN
6	FE	811	ASN
6	FE	885	ASN
6	FE	903	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	907	ASN
6	FE	918	GLN
6	FE	1001	ASN
6	FE	1007	GLN
6	FE	1117	ASN
6	FE	1194	ASN
6	FE	1204	GLN
6	FE	1242	GLN
6	FE	1267	GLN
6	FE	1416	GLN
6	FE	1427	ASN
6	FF	811	ASN
6	FF	828	GLN
6	FF	907	ASN
6	FF	918	GLN
6	FF	919	GLN
6	FF	1007	GLN
6	FF	1194	ASN
6	FF	1242	GLN
6	FF	1245	ASN
7	GA	239	ASN
7	GA	721	GLN
7	GA	958	GLN
8	GB	47	GLN
8	GB	99	ASN
8	GB	336	ASN
7	GC	171	GLN
7	GC	260	ASN
7	GC	426	ASN
7	GC	586	GLN
7	GC	590	ASN
7	GC	670	ASN
7	GC	848	ASN
7	GC	964	GLN
8	GD	371	GLN
8	GD	484	GLN
8	GD	677	HIS
8	GD	731	GLN
8	GD	771	ASN
7	GE	197	HIS
7	GE	426	ASN
7	GE	590	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	GE	675	GLN
7	GE	878	GLN
7	GE	964	GLN
7	GE	969	GLN
8	GF	85	ASN
8	GF	90	HIS
8	GF	98	GLN
8	GF	158	GLN
8	GF	196	HIS
8	GF	328	HIS
8	GF	629	ASN
7	GG	173	ASN
7	GG	586	GLN
7	GG	845	ASN
7	GG	910	HIS
7	GG	943	GLN
8	GH	47	GLN
8	GH	115	GLN
8	GH	350	GLN
8	GH	484	GLN
8	GH	672	HIS
8	GH	683	GLN
8	GH	724	GLN
7	GI	620	HIS
7	GI	637	ASN
7	GI	670	ASN
7	GI	675	GLN
7	GI	848	ASN
7	GI	878	GLN
7	GI	910	HIS
8	GJ	115	GLN
8	GJ	211	GLN
8	GJ	327	HIS
8	GJ	336	ASN
8	GJ	397	ASN
8	GJ	482	ASN
8	GJ	724	GLN
7	GK	532	ASN
7	GK	837	HIS
7	GK	910	HIS
7	GK	969	GLN
8	GL	98	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	GL	196	HIS
8	GL	534	GLN
8	GL	683	GLN
8	GL	690	HIS
9	HA	603	HIS
9	HA	661	HIS
9	HA	791	GLN
9	HA	808	HIS
9	HA	840	HIS
9	HA	860	GLN
9	HB	401	GLN
9	HB	410	ASN
9	HB	661	HIS
9	HB	749	ASN
9	HB	762	HIS
9	HB	763	GLN
9	HB	791	GLN
9	HB	821	GLN
9	HB	860	GLN
9	HC	610	ASN
9	HC	612	GLN
9	HD	791	GLN
9	HD	808	HIS
10	IA	173	GLN
10	IA	311	GLN
10	IA	323	GLN
10	IA	336	GLN
10	IA	381	HIS
10	IA	494	HIS
10	IA	551	ASN
10	IA	757	ASN
10	IA	765	HIS
10	IA	874	ASN
10	IA	898	HIS
10	IA	943	ASN
10	IA	1123	ASN
10	IA	1212	ASN
10	IA	1237	GLN
10	IA	1257	HIS
10	IA	1320	GLN
10	IA	1411	GLN
10	IA	1417	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	IB	202	ASN
10	IB	205	GLN
10	IB	336	GLN
10	IB	396	ASN
10	IB	698	GLN
10	IB	757	ASN
10	IB	778	GLN
10	IB	864	GLN
10	IB	874	ASN
10	IB	943	ASN
10	IB	1055	GLN
10	IB	1098	HIS
10	IB	1123	ASN
10	IB	1179	ASN
10	IB	1212	ASN
10	IB	1417	GLN
10	IC	323	GLN
10	IC	355	GLN
10	IC	362	HIS
10	IC	400	HIS
10	IC	494	HIS
10	IC	765	HIS
10	IC	811	GLN
10	IC	943	ASN
10	IC	1094	ASN
10	IC	1111	GLN
10	IC	1123	ASN
10	IC	1212	ASN
10	IC	1245	GLN
10	IC	1266	ASN
10	IC	1378	GLN
11	JA	473	ASN
11	JA	915	GLN
11	JA	1072	HIS
11	JA	1213	GLN
11	JA	1539	ASN
11	JA	1591	HIS
11	JA	1638	ASN
11	JA	1781	GLN
11	JA	1799	GLN
11	JA	1854	HIS
11	JA	1871	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	JA	2003	HIS
11	JA	2076	ASN
11	JB	469	GLN
11	JB	503	HIS
11	JB	1468	GLN
11	JB	1604	HIS
11	JB	1656	GLN
11	JB	1657	GLN
11	JB	1781	GLN
11	JB	1799	GLN
11	JB	1802	HIS
11	JB	1870	HIS
11	JB	2072	GLN
11	JB	2122	GLN
11	JB	2268	HIS
11	JC	41	ASN
11	JC	101	ASN
11	JC	503	HIS
11	JC	523	ASN
11	JC	763	GLN
11	JC	1152	HIS
11	JC	1202	HIS
11	JC	1355	GLN
11	JC	1407	HIS
11	JC	1545	HIS
11	JC	1550	GLN
11	JC	1604	HIS
11	JC	1606	HIS
11	JC	1713	ASN
11	JC	1852	HIS
11	JC	1984	HIS
12	KA	216	GLN
12	KA	230	GLN
12	KA	298	GLN
12	KA	343	ASN
12	KA	383	HIS
12	KA	401	GLN
12	KA	593	HIS
12	KA	636	GLN
12	KA	696	GLN
12	KA	721	GLN
12	KB	669	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KB	710	ASN
12	KC	331	GLN
12	KC	383	HIS
12	KC	665	HIS
12	KE	298	GLN
12	KE	392	GLN
12	KE	473	GLN
12	KE	516	HIS
12	KE	636	GLN
12	KE	665	HIS
12	KE	710	ASN
12	KF	516	HIS
12	KF	604	GLN
12	KF	636	GLN
12	KF	696	GLN
12	KG	397	GLN
12	KG	418	GLN
12	KG	531	GLN
12	KG	576	ASN
12	KG	636	GLN
13	LA	374	HIS
13	LA	422	GLN
13	LA	467	GLN
13	LA	480	GLN
13	LA	493	GLN
13	LA	506	GLN
13	LB	377	GLN
13	LB	491	GLN
13	LC	353	ASN
13	LC	491	GLN
13	LC	493	GLN
13	LE	480	GLN
13	LE	521	ASN
13	LF	374	HIS
13	LG	491	GLN
13	LH	493	GLN
13	LI	343	GLN
13	LI	422	GLN
13	LI	468	HIS
13	LI	493	GLN
13	LI	506	GLN
13	LJ	521	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	LK	506	GLN
13	LL	343	GLN
13	LL	364	ASN
13	LL	493	GLN
13	LN	364	ASN
13	LO	374	HIS
14	MA	241	GLN
14	ME	208	GLN
14	ME	224	ASN
14	MF	229	GLN
14	MF	283	GLN
14	MF	323	GLN
14	MI	227	GLN
14	MJ	246	ASN
14	MJ	316	GLN
15	NA	589	ASN
15	NA	597	GLN
15	NA	686	ASN
15	NA	744	GLN
15	NA	810	GLN
15	NA	1158	HIS
15	NB	480	ASN
15	NB	609	GLN
15	NB	724	ASN
15	NB	735	HIS
15	NB	736	GLN
15	NB	1121	ASN
15	NB	1188	HIS
15	NB	1398	ASN
15	NB	1536	GLN
15	NB	1540	ASN
15	NC	566	GLN
15	NC	609	GLN
15	NC	758	GLN
15	NC	783	GLN
15	NC	810	GLN
15	NC	871	GLN
15	NC	1018	GLN
15	NC	1398	ASN
15	NC	1462	GLN
15	ND	540	ASN
15	ND	810	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	ND	871	GLN
15	ND	1105	HIS
15	ND	1403	GLN
15	ND	1452	GLN
16	OA	131	ASN
16	OA	197	HIS
16	OA	217	GLN
16	OA	266	GLN
16	OA	745	ASN
16	OB	308	GLN
16	OB	310	ASN
16	OB	745	ASN
16	OB	1086	GLN
16	OC	184	ASN
16	OC	745	ASN
16	OC	1060	GLN
17	PC	266	HIS
18	QA	172	GLN
18	QB	172	GLN
18	QD	76	HIS
19	RA	171	GLN
19	RB	26	HIS
19	RC	26	HIS
19	RC	133	GLN
19	RC	171	GLN
19	RD	133	GLN
20	SA	9	GLN
20	SB	112	ASN
20	SC	108	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

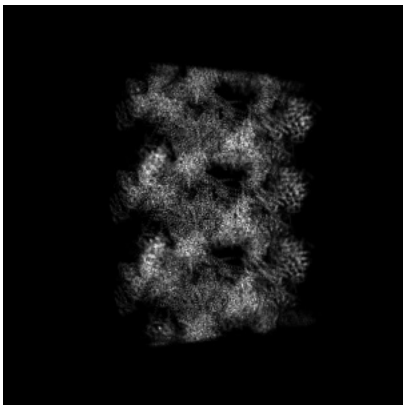
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-72716. These allow visual inspection of the internal detail of the map and identification of artifacts.

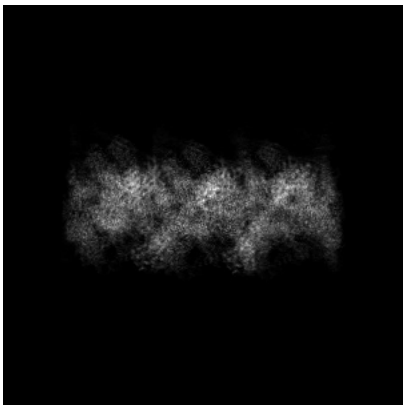
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

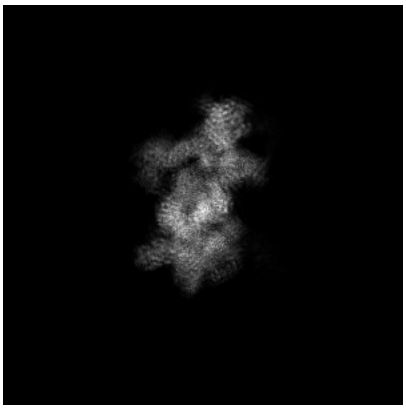
6.1.1 Primary map



X

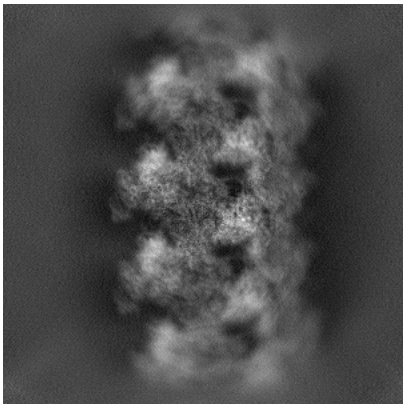


Y

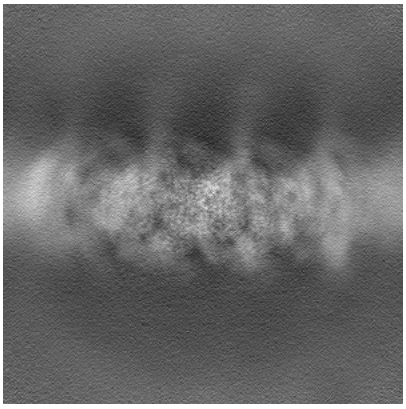


Z

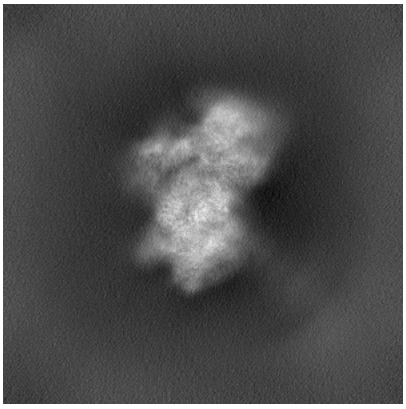
6.1.2 Raw map



X



Y



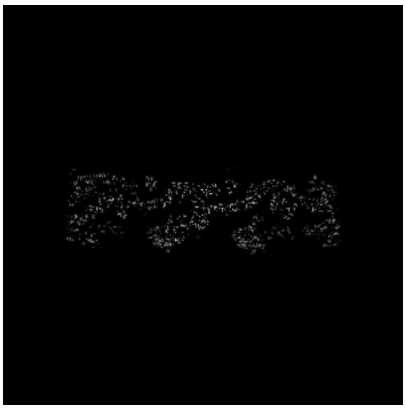
Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map

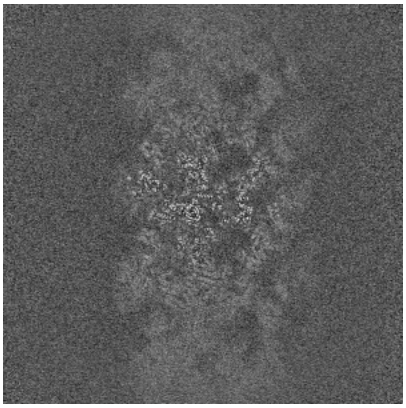
X Index: 256



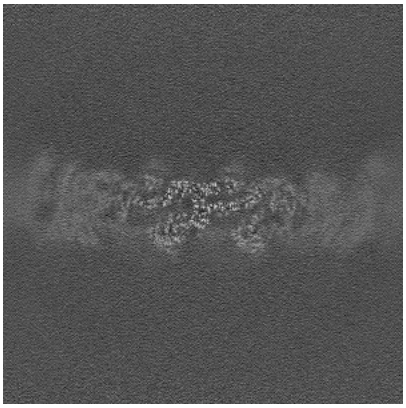
Y Index: 256

Z Index: 256

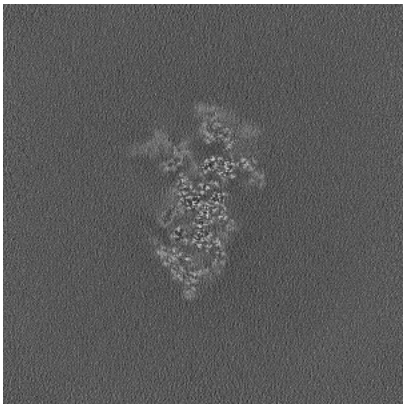
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

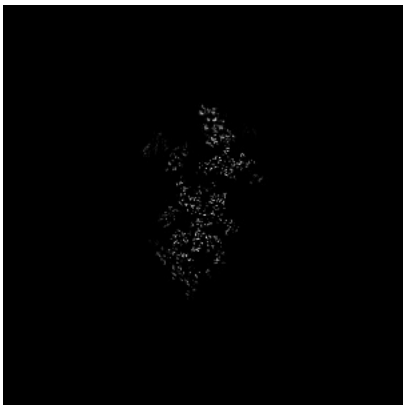
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

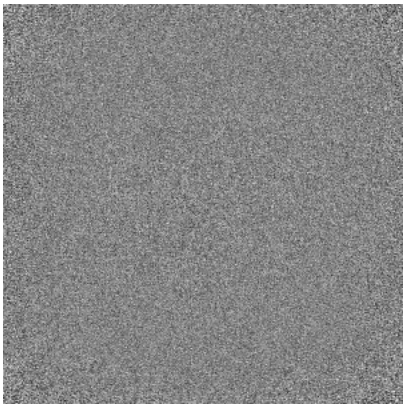
X Index: 279

Y Index: 249

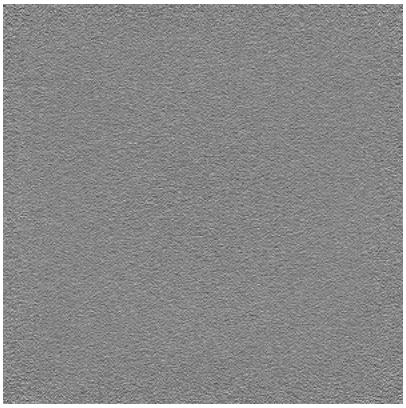


Z Index: 258

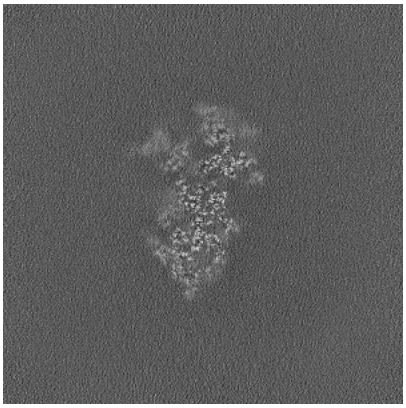
6.3.2 Raw map



X Index: 0



Y Index: 0

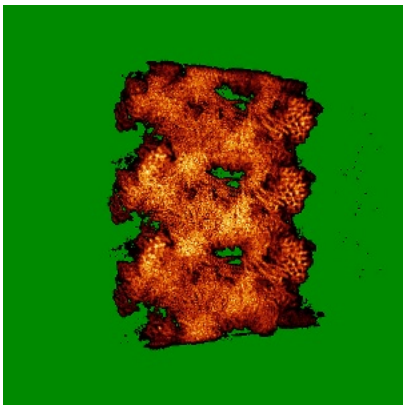


Z Index: 258

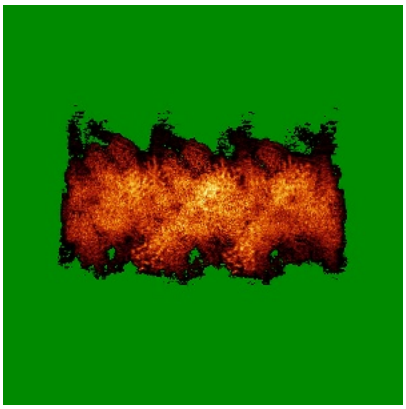
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

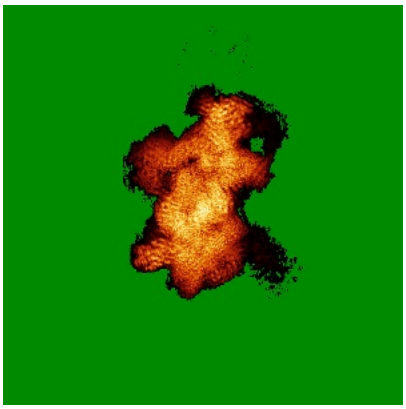
6.4.1 Primary map



X

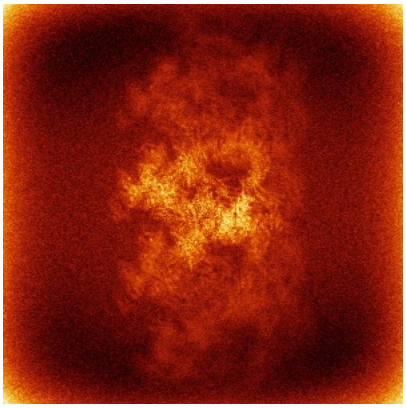


Y

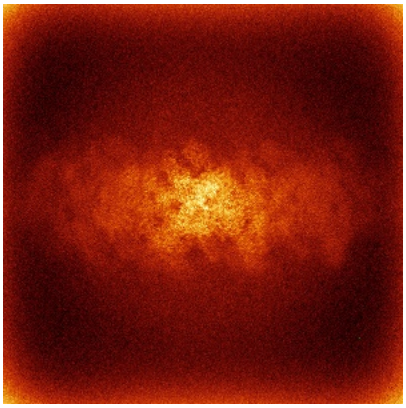


Z

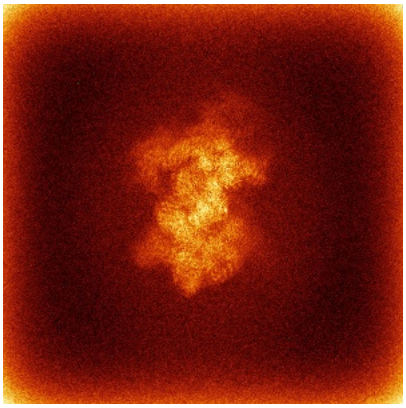
6.4.2 Raw map



X



Y

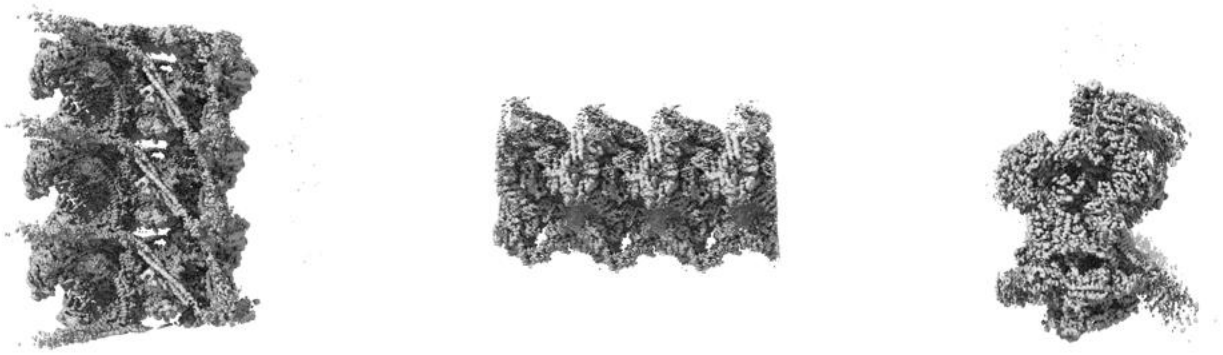


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

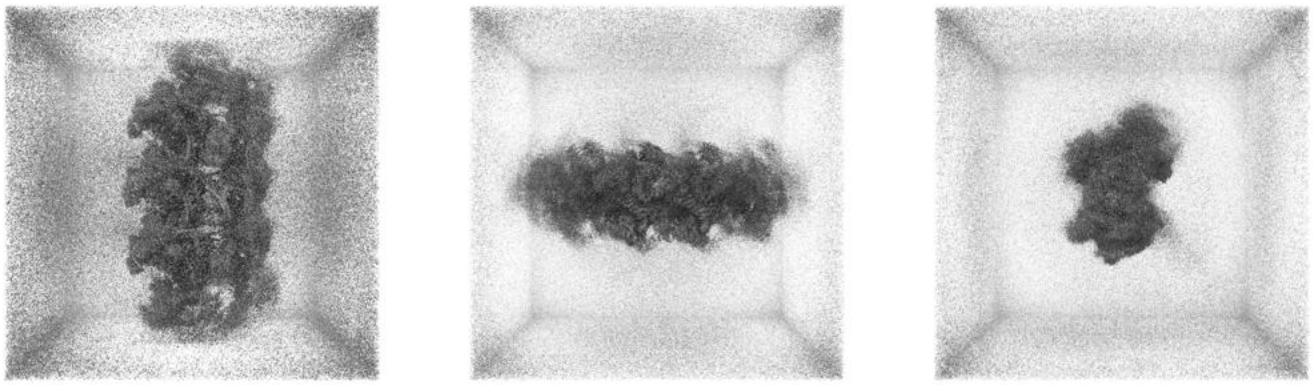
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

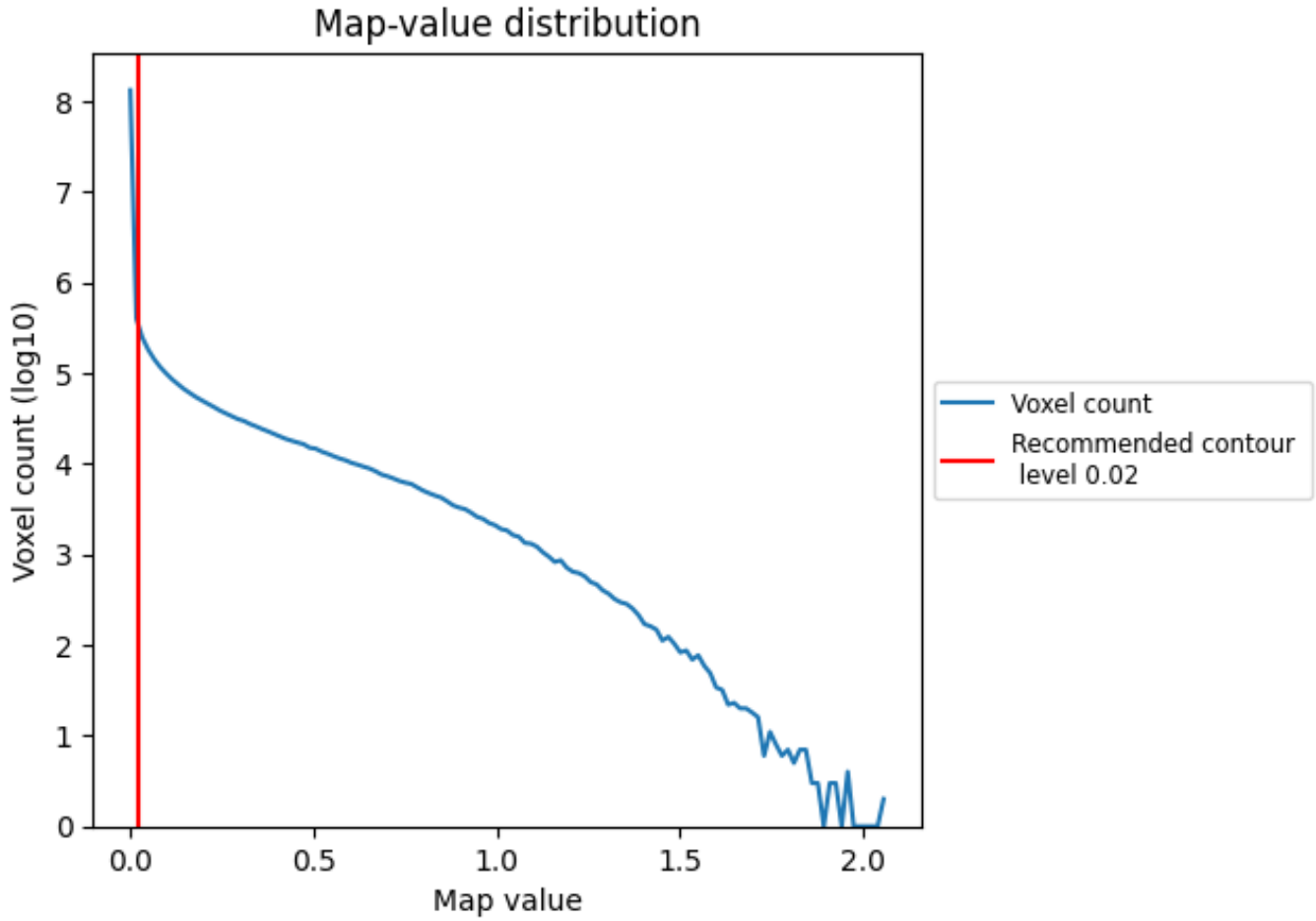
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

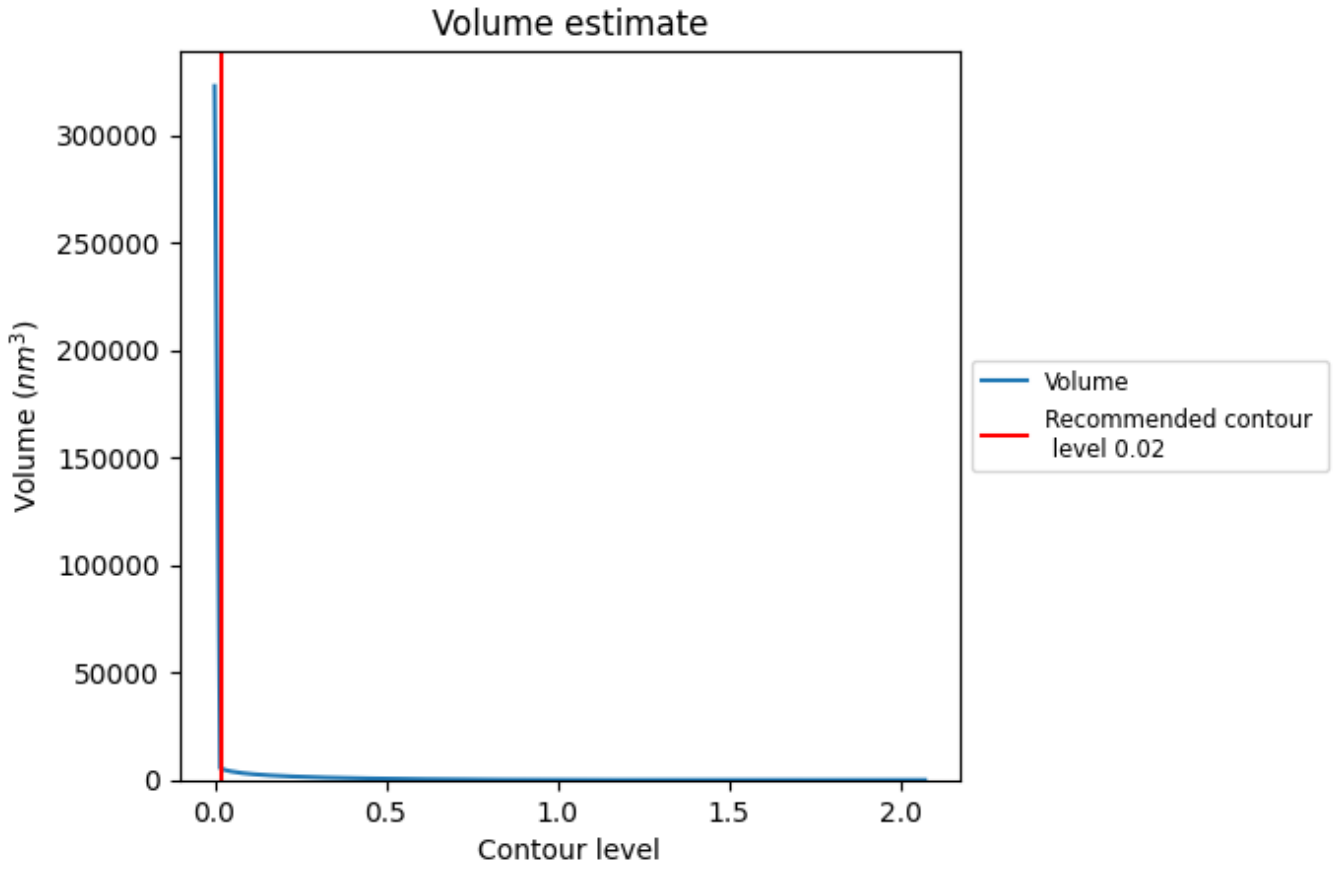
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

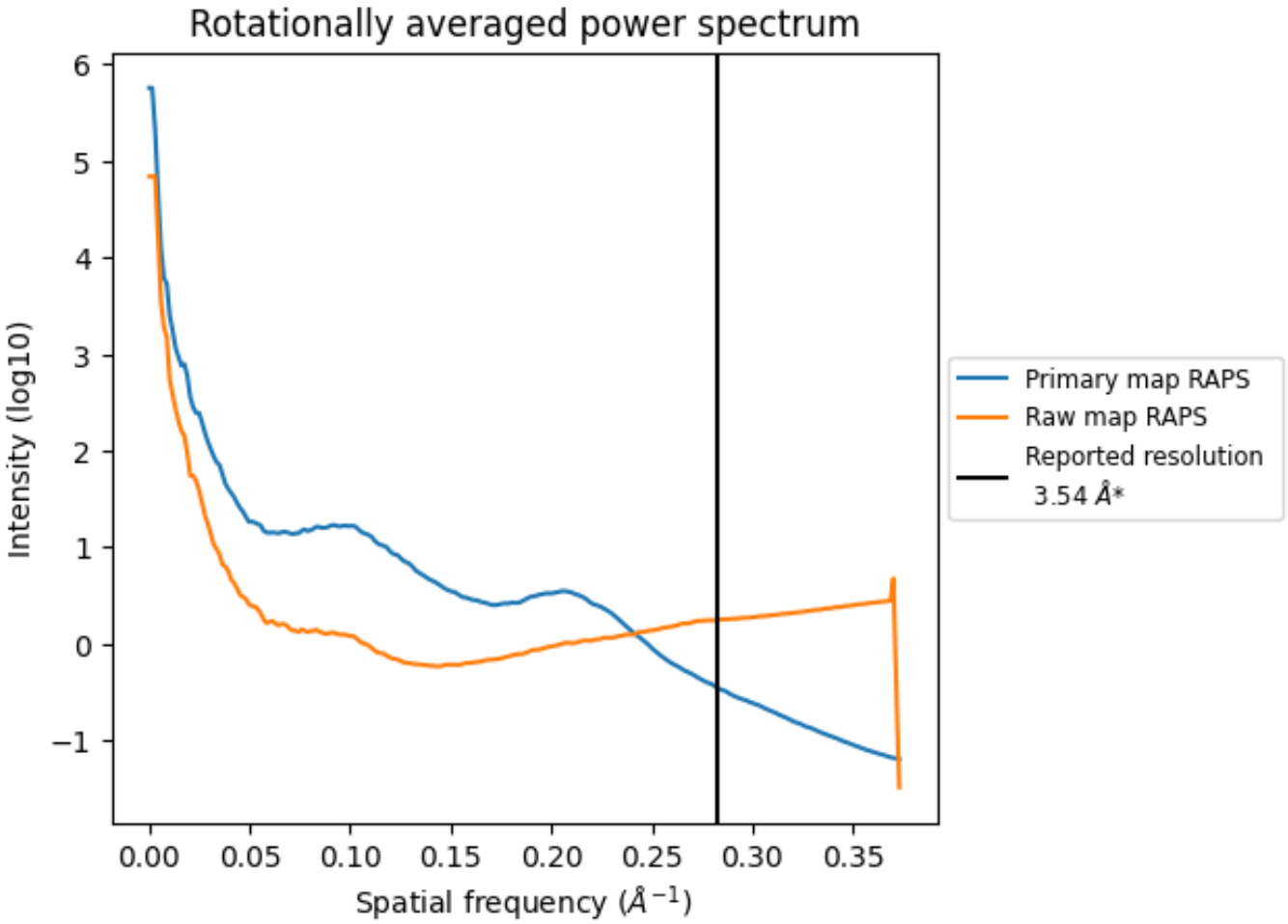
7.2 Volume estimate



The volume at the recommended contour level is 5300 nm^3; this corresponds to an approximate mass of 4787 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

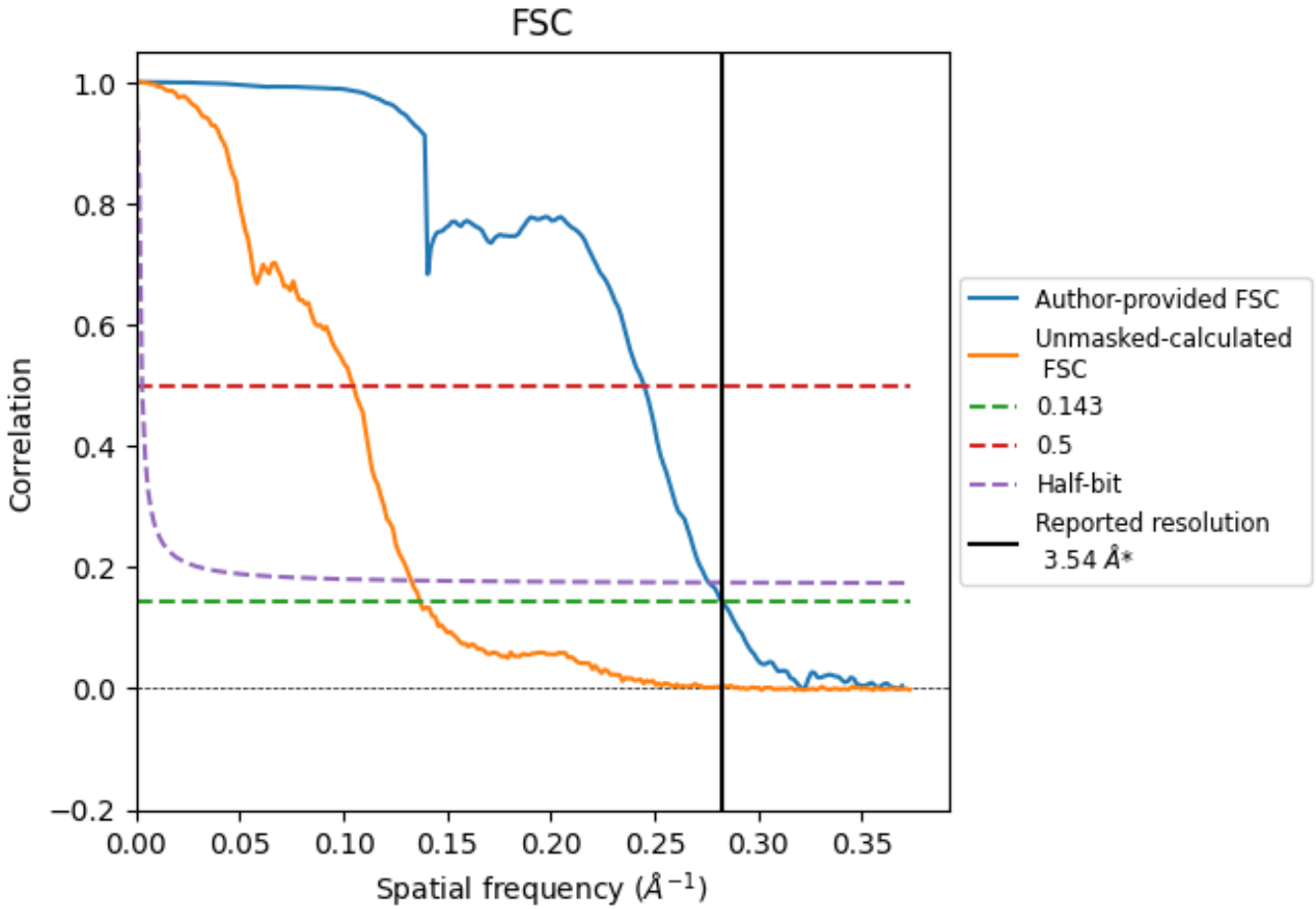


*Reported resolution corresponds to spatial frequency of 0.282 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.282 Å^{-1}

8.2 Resolution estimates (i)

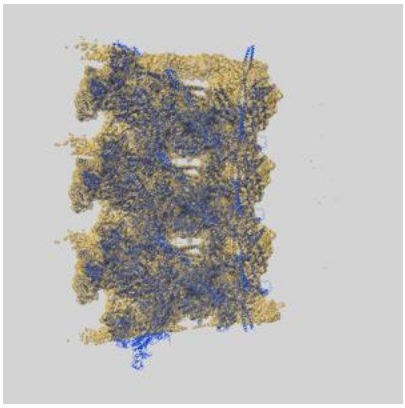
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	4.08	3.62
Unmasked-calculated*	7.30	9.55	7.53

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.30 differs from the reported value 3.54 by more than 10 %

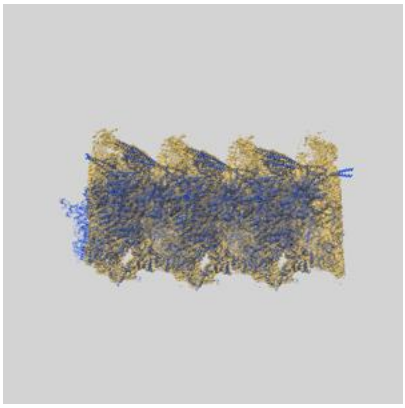
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-72716 and PDB model 9YA0. Per-residue inclusion information can be found in section 3 on page 21.

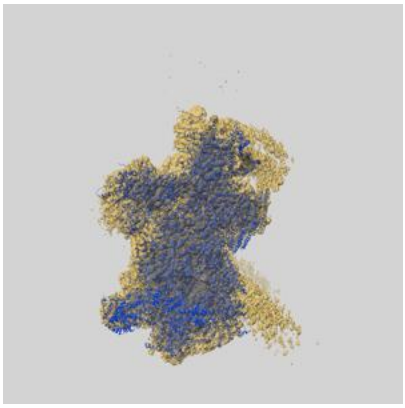
9.1 Map-model overlay



X



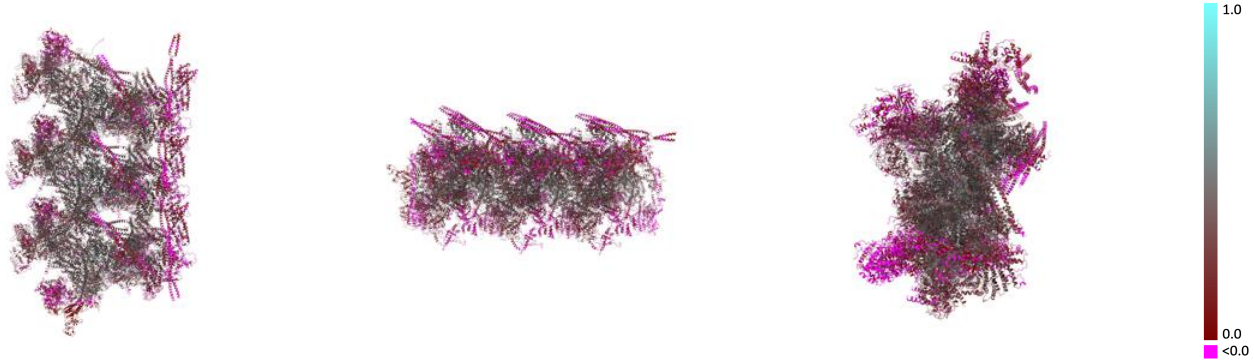
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

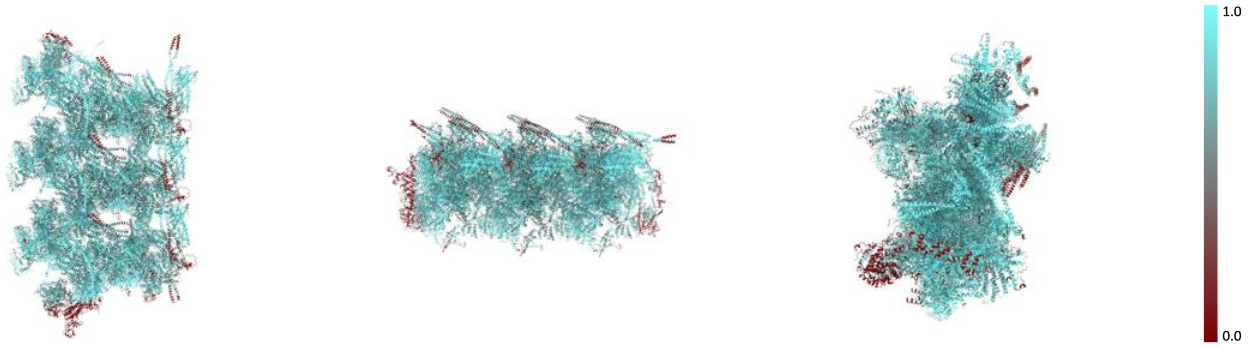
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

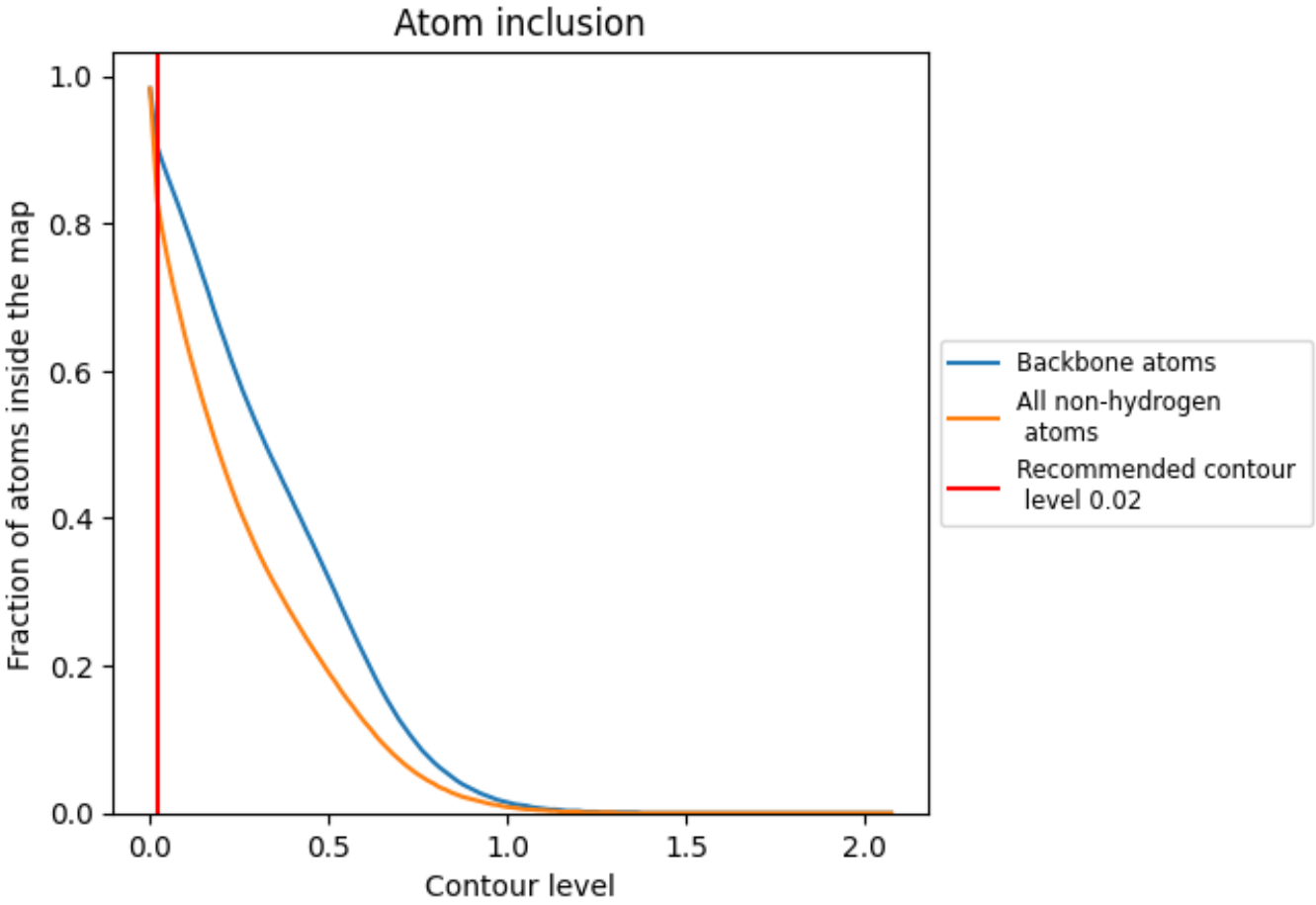
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8310	0.2630
AA	0.8810	0.3180
AB	0.9330	0.3690
AC	0.9200	0.3960
AD	0.9530	0.4090
AE	0.9020	0.3070
AF	0.9380	0.3630
AG	0.9310	0.3870
AH	0.9530	0.4060
AI	0.9070	0.3080
AJ	0.8560	0.3270
AK	0.8170	0.3280
AL	0.6320	0.2580
BA	0.9260	0.3830
BB	0.9490	0.3730
BC	0.9490	0.3730
CA	0.8220	0.2550
CB	0.8550	0.2550
CC	0.8530	0.2500
CE	0.7720	0.1770
CF	0.8240	0.1880
CG	0.8280	0.1920
CI	0.8090	0.2280
CJ	0.8350	0.2300
CL	0.8540	0.2330
DA	0.8870	0.1810
DB	0.9220	0.1760
DC	0.9110	0.1670
DD	0.8820	0.1360
DE	0.9150	0.1430
DF	0.9040	0.1420
EA	0.9520	0.3910
EB	0.9290	0.3910
EC	0.9460	0.3880
FA	0.9000	0.3750

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
FB	0.9120	0.3640
FC	0.9200	0.3610
FD	0.8650	0.2500
FE	0.8780	0.2470
FF	0.8540	0.2580
GA	0.8260	0.3120
GB	0.8810	0.2880
GC	0.8020	0.2430
GD	0.8730	0.2910
GE	0.8360	0.2410
GF	0.6990	0.1670
GG	0.8400	0.3030
GH	0.6860	0.1480
GI	0.8290	0.2390
GJ	0.7230	0.1710
GK	0.8290	0.3120
GL	0.7020	0.1710
HA	0.9060	0.3390
HB	0.8960	0.3370
HC	0.9100	0.3600
HD	0.8810	0.2960
IA	0.9190	0.3510
IB	0.9380	0.3420
IC	0.9350	0.3450
JA	0.8950	0.3330
JB	0.8520	0.3040
JC	0.9080	0.3230
KA	0.8400	0.1560
KB	0.8560	0.1610
KC	0.7530	0.1260
KE	0.5630	0.0310
KF	0.6210	0.0460
KG	0.6070	0.0470
LA	0.7380	0.1890
LB	0.7550	0.1940
LC	0.6430	0.1780
LD	0.6610	0.1620
LE	0.7910	0.2390
LF	0.7300	0.2020
LG	0.8930	0.3760
LH	0.9610	0.4310
LI	0.7700	0.1980

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LJ	0.7510	0.1710
LK	0.6280	0.1670
LL	0.6600	0.1590
LM	0.5200	0.0610
LN	0.5370	0.0240
LO	0.5640	0.0570
LP	0.5260	0.0490
MA	0.9030	0.2890
MB	0.9190	0.2890
MC	0.7890	0.3380
MD	0.9200	0.3960
ME	0.9190	0.2600
MF	0.9420	0.2670
MG	0.8140	0.3300
MH	0.9440	0.3720
MI	0.9240	0.2660
MJ	0.9220	0.2580
MK	0.8260	0.3310
ML	0.9420	0.3690
NA	0.8300	0.0930
NB	0.3040	0.0020
NC	0.8310	0.0940
ND	0.3900	0.0160
OA	0.8440	0.2900
OB	0.8390	0.2790
OC	0.8640	0.2850
PA	0.7550	0.2530
PB	0.7980	0.2450
PC	0.8120	0.2690
QA	0.8610	0.2020
QB	0.5000	0.1140
QC	0.8330	0.1740
QD	0.8350	0.2000
RA	0.7650	0.0940
RB	0.6230	0.0540
RC	0.7670	0.0940
RD	0.6930	0.1060
SA	0.8170	0.1530
SB	0.4520	0.0920
SC	0.7500	0.1340
SD	0.8090	0.1560