



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 07:32 PM UTC

PDB ID : 9YF5 / pdb_00009yf5
EMDB ID : EMD-72877
Title : N4 Empty Particle C6 Tail
Authors : Bellis, N.F.; Cingolani, G.
Deposited on : 2025-09-25
Resolution : 3.65 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:

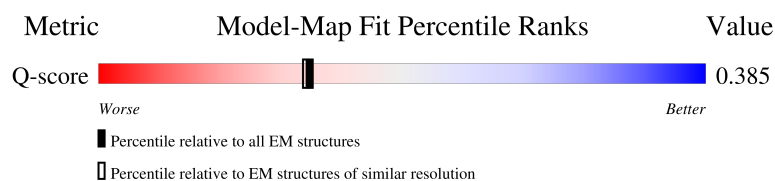
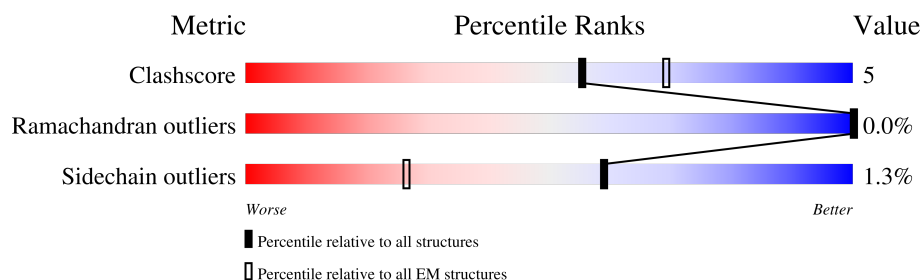
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.65 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	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11564 (3.15 - 4.15)

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 $\leq 5\%$. 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	236	17% 91% 8%
1	AB	236	20% 88% 12%
1	AC	236	16% 90% 9%
1	AD	236	19% 90% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	AE	236	16% 92% 8%
1	AF	236	18% 88% 11%
1	AG	236	17% 91% 9%
1	AH	236	20% 88% 11%
1	AI	236	16% 91% 8%
1	AJ	236	19% 89% 11%
1	AK	236	16% 90% 9%
1	AL	236	18% 89% 11%
2	LA	1382	70% 70% 15% 15%
2	LB	1382	70% 69% 16% 15%
2	LC	1382	70% 69% 16% 15%
2	LD	1382	70% 69% 16% 15%
2	LE	1382	70% 70% 15% 15%
2	LF	1382	70% 70% 15% 15%
3	SA	417	78% 83% 15% .
3	SB	417	79% 84% 15% .
3	SC	417	79% 86% 13% .
3	SD	417	78% 84% 15% .
3	SE	417	79% 85% 14% .
3	SF	417	79% 85% 14% .
4	TA	299	25% 87% 13%
4	TB	299	25% 87% 13%
4	TC	299	23% 88% 12%
4	TD	299	26% 87% 13%
4	TE	299	25% 88% 11%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	TF	299	24% 87% 13%
4	TG	299	25% 88% 12%
4	TH	299	25% 87% 13%
4	TI	299	23% 87% 12%
4	TJ	299	26% 86% 14%
4	TK	299	25% 87% 12%
4	TL	299	24% 85% 14%
5	XA	556	6% 10% 87%
5	XB	556	5% 11% 87%
5	XC	556	6% 10% 87%
5	XD	556	11% 87%
5	XE	556	6% 9% 87%
5	XF	556	11% 87%
5	XG	556	5% 10% 87%
5	XH	556	5% 11% 87%
5	XI	556	5% 10% 87%
5	XJ	556	11% 87%
5	XK	556	6% 10% 87%
5	XL	556	12% 87%
5	YA	556	5% 10% 88%
5	YB	556	5% 10% 88%
5	YC	556	5% 10% 88%
5	YD	556	5% 10% 88%
5	YE	556	10% 88%
5	YF	556	6% 10% 88%

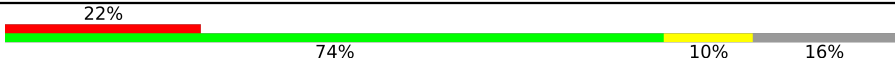
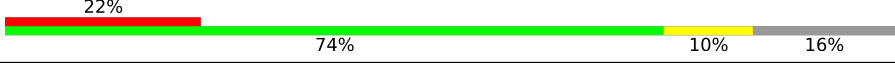
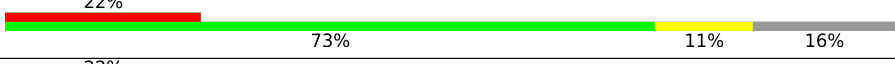
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	YG	556	
5	YH	556	
5	YI	556	
5	YJ	556	
5	YK	556	
5	YL	556	
5	ZA	556	
5	ZB	556	
5	ZC	556	
5	ZD	556	
5	ZE	556	
5	ZF	556	
5	ZG	556	
5	ZH	556	
5	ZI	556	
5	ZJ	556	
5	ZK	556	
5	ZL	556	
6	PA	763	
6	PB	763	
6	PC	763	
6	PD	763	
6	PE	763	
6	PF	763	
6	PG	763	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
6	PH	763	
6	PI	763	
6	PJ	763	
6	PK	763	
6	PL	763	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 207084 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 30 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AB	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AC	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AD	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AE	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AF	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AG	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AH	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AI	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AJ	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AK	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AL	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		

- Molecule 2 is a protein called Non-contractile tail sheath.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LA	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LB	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LC	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LD	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LE	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LF	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		

- Molecule 3 is a protein called Gp64.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
3	SB	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
3	SC	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
3	SD	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
3	SE	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
3	SF	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		

- Molecule 4 is a protein called Gp54.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	TA	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TB	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TC	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TD	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TE	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TF	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TG	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TH	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
4	TI	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TJ	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TK	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TL	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		

- Molecule 5 is a protein called 60 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	XA	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XB	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YA	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YB	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZA	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZB	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XC	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XD	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YC	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YD	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZC	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZD	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XE	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XF	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YE	68	Total	C	N	O	S	0	0
			543	355	89	96	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	YF	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZE	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZF	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XG	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XH	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YG	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YH	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZG	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZH	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XI	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XJ	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YI	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YJ	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZI	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZJ	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XK	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XL	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YK	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YL	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZK	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZL	63	Total	C	N	O	S	0	0
			508	330	82	93	3		

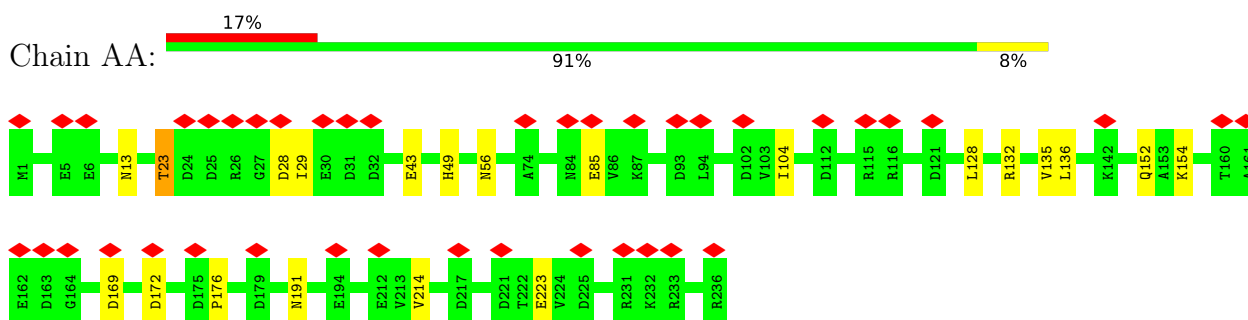
- Molecule 6 is a protein called Probable portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	PA	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PB	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PC	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PD	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PE	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PF	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PG	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PH	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PI	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PJ	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PK	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PL	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		

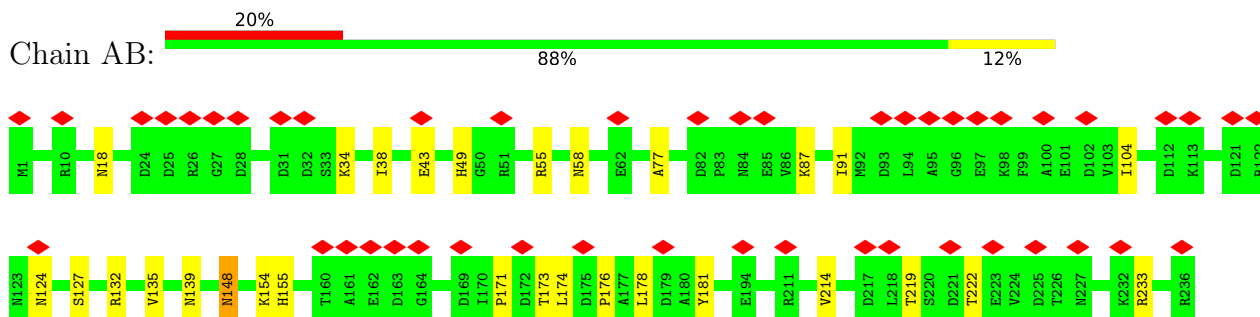
3 Residue-property plots

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.

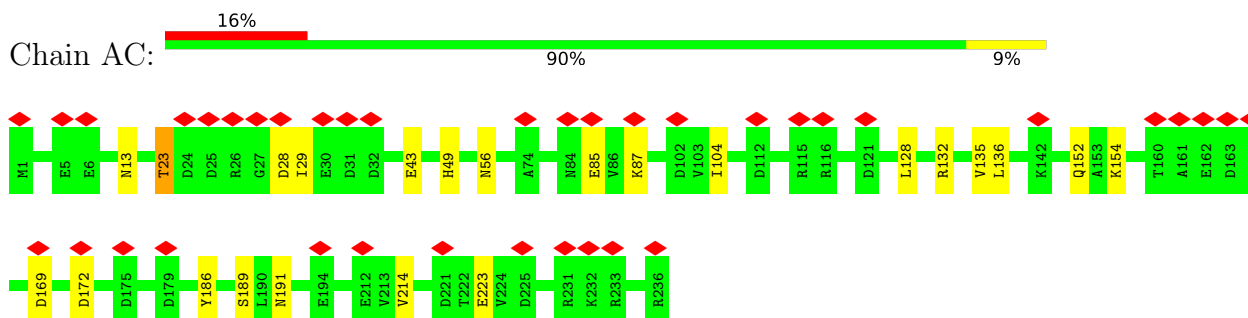
- Molecule 1: 30 kDa protein



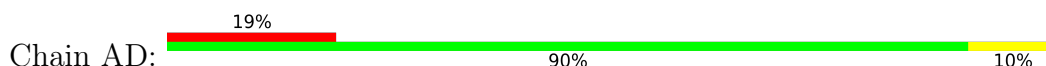
- Molecule 1: 30 kDa protein

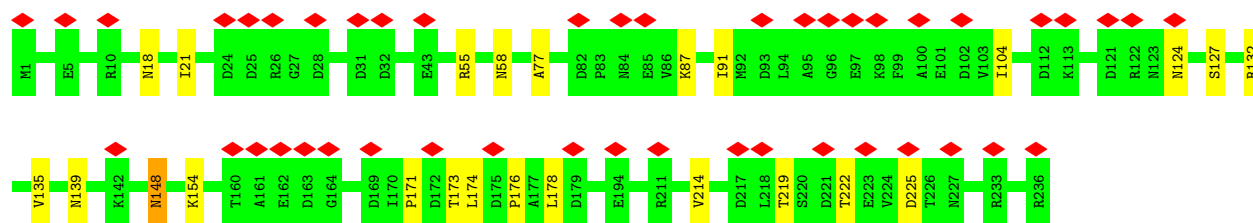


- Molecule 1: 30 kDa protein

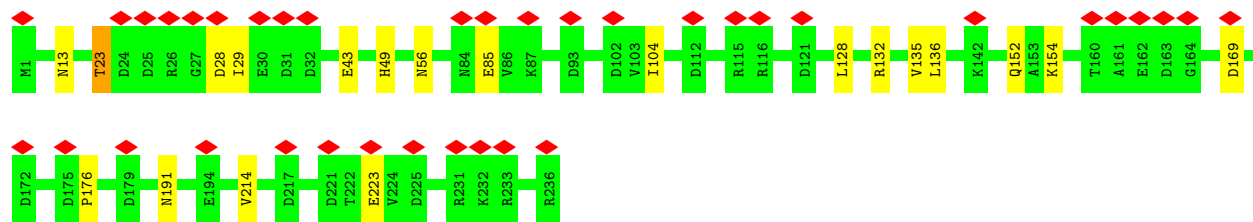


- Molecule 1: 30 kDa protein

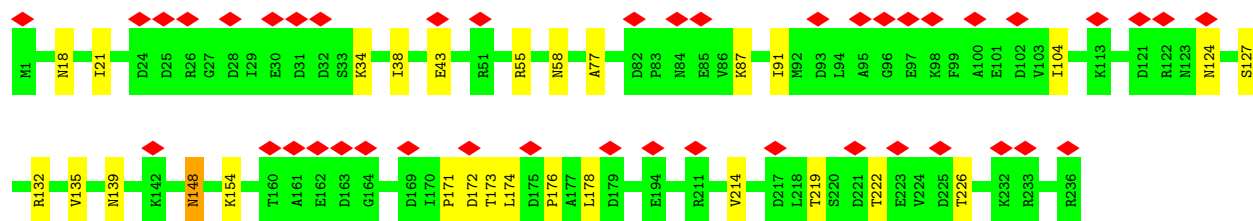
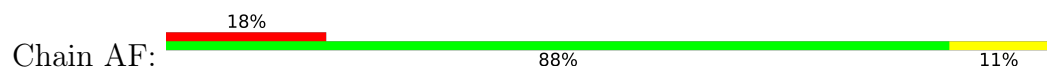




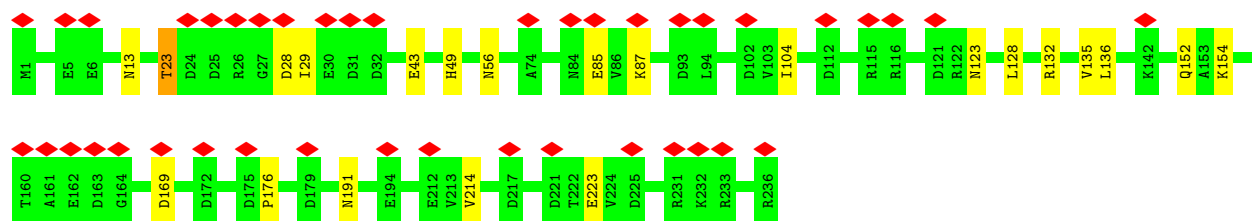
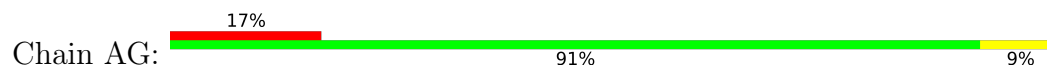
- Molecule 1: 30 kDa protein



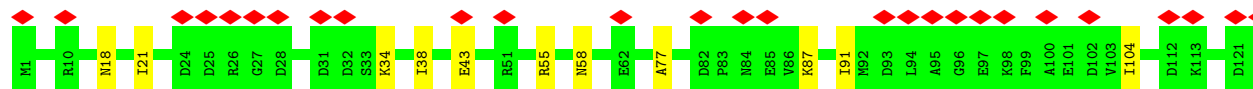
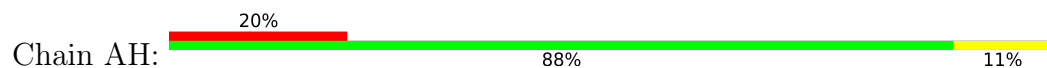
- Molecule 1: 30 kDa protein

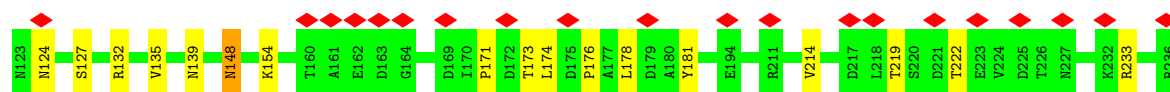


- Molecule 1: 30 kDa protein

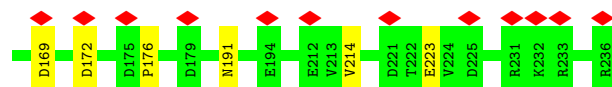
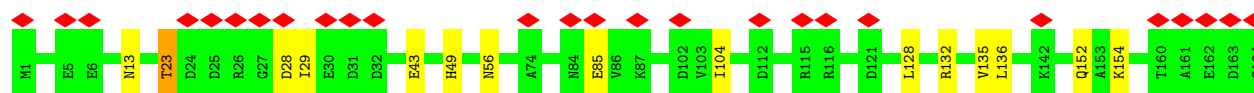


- Molecule 1: 30 kDa protein

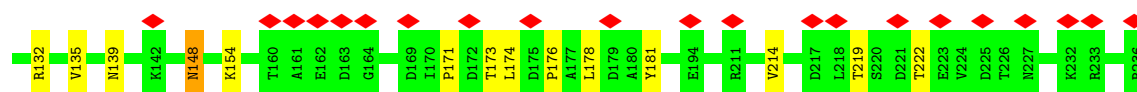
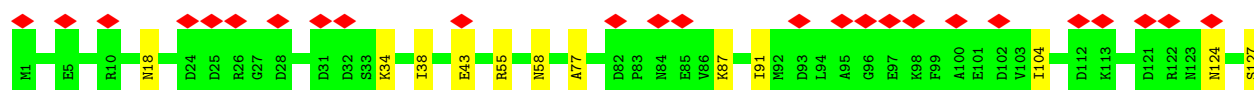
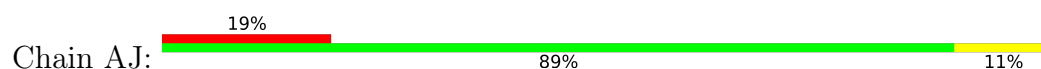




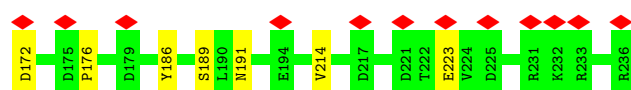
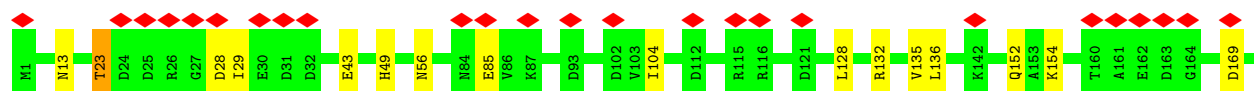
- Molecule 1: 30 kDa protein



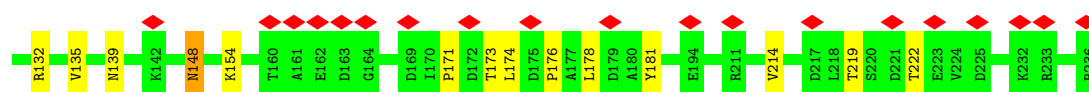
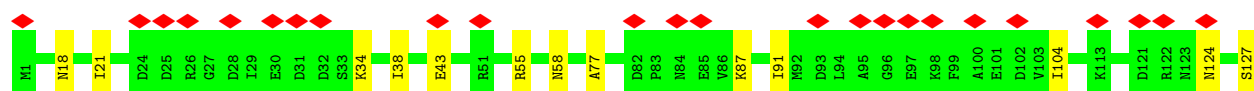
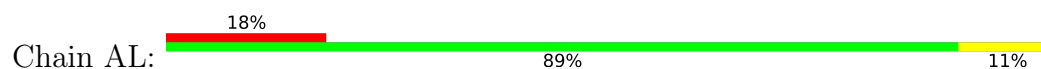
- Molecule 1: 30 kDa protein



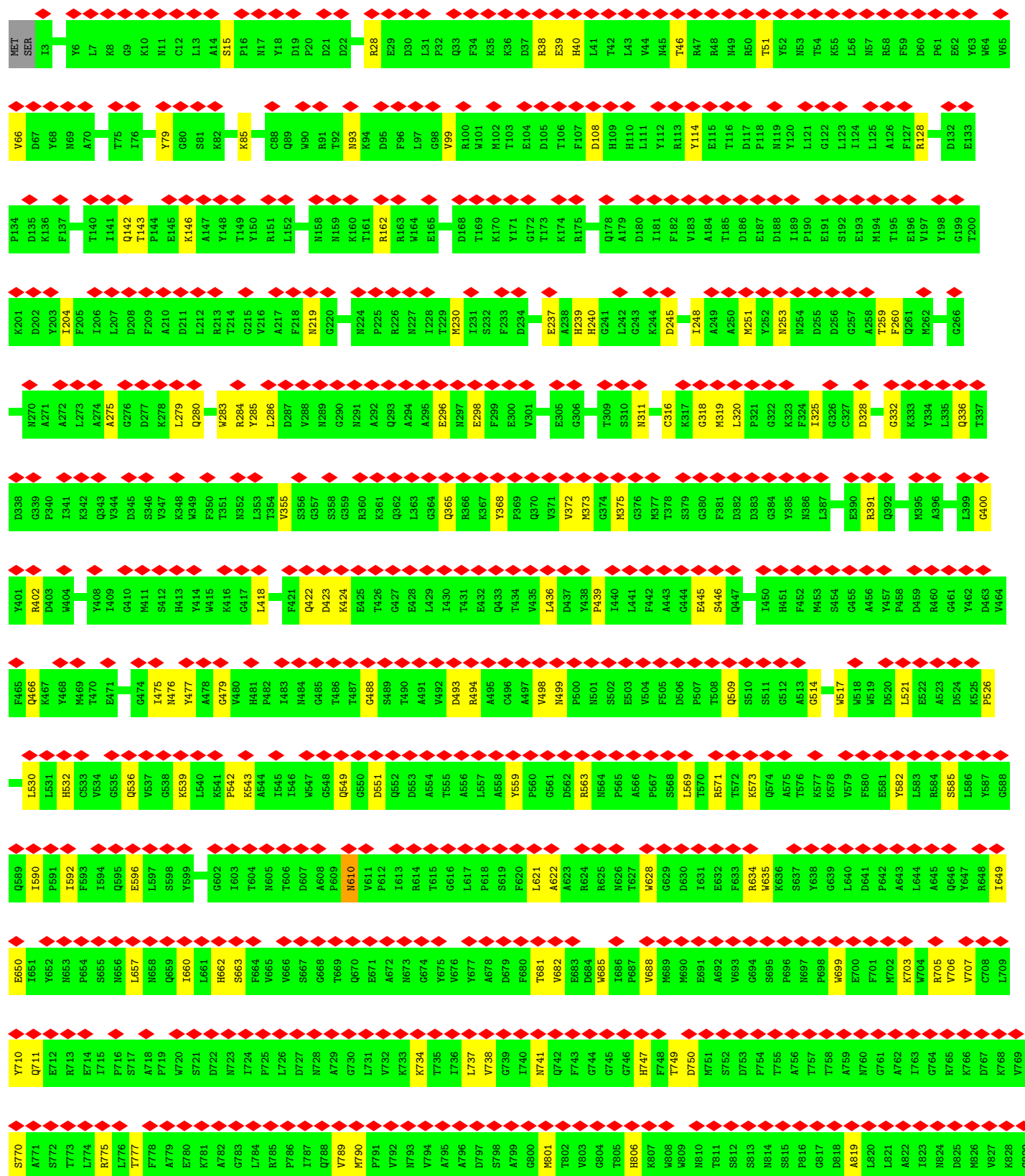
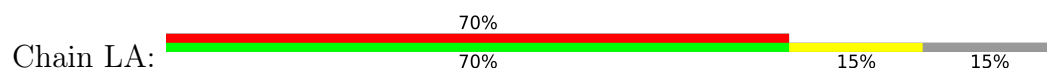
- Molecule 1: 30 kDa protein



- Molecule 1: 30 kDa protein



- Molecule 2: Non-contractile tail sheath

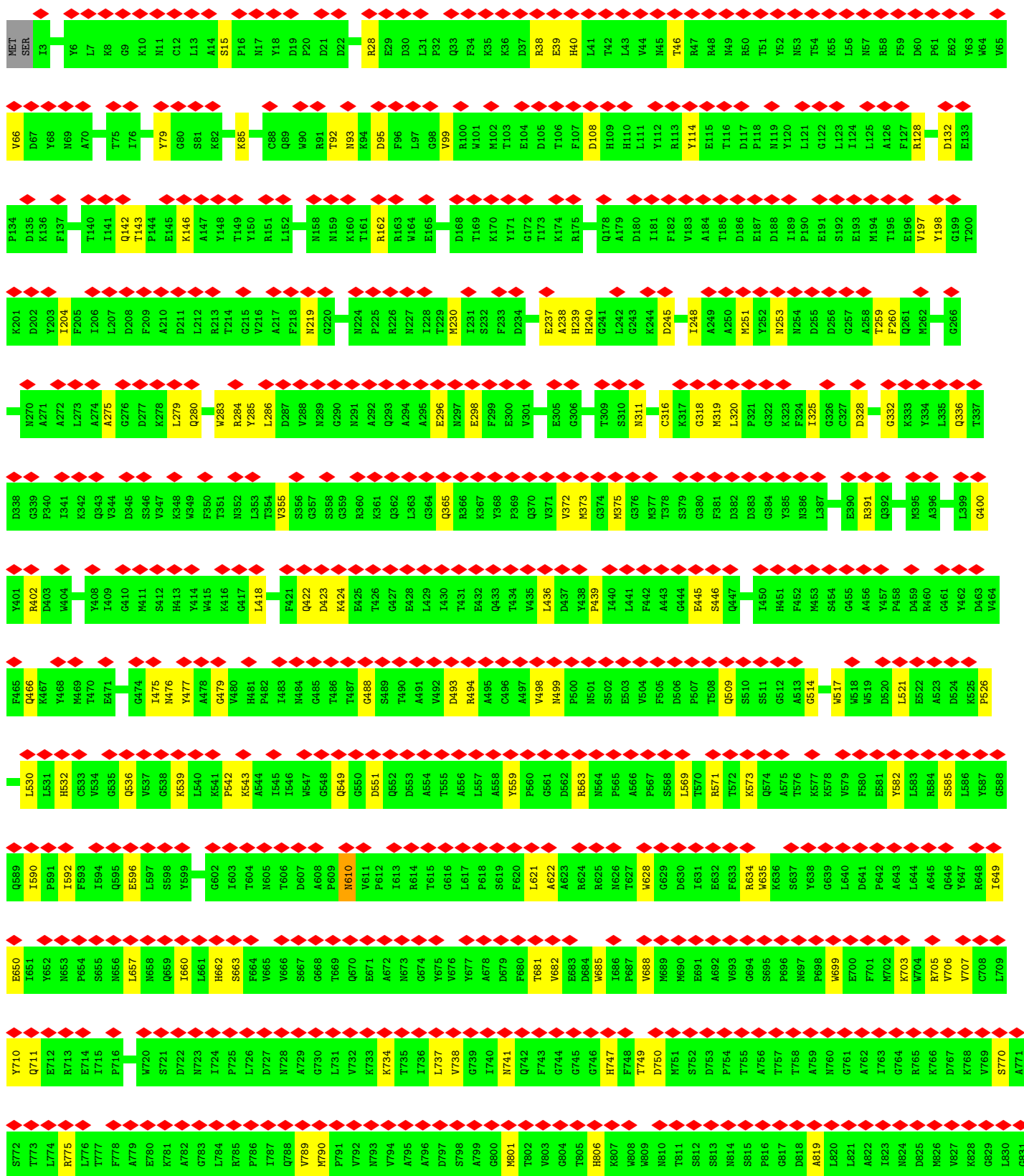


T1019	A959	P899	E339	A779	F719	Q659	S599	G539	I475	G410	K342	A271
T1020	I960	P900	A840	E780	W720	L660	Y599	K539	N476	M411	Q343	A272
G1021	E961	D902	N841	K781	S721	L661	G602	L540	Y477	S412	V344	L273
E1023	G963	D903	P842	A782	D722	H662	T603	K541	A478	H413	D345	A274
I1024	E964	N904	W843	G783	W723	H663	T604	P842	G479	K416	S346	G276
S1025	A965	S905	T845	R785	I724	H664	N605	A544	V480	G417	V347	D277
S1026	L966	E906	N846	P786	W725	V665	T606	I545	H481	L418	K348	K278
G1027	A967	A907	W847	I787	L726	V666	T607	I546	P482	G417	K348	L279
I1028	L968	T908	N848	Q788	D727	S667	D607	I547	I483	L418	K348	Q280
L1029	N969	V909	K849	W789	W728	V668	A608	Q548	N484	F421	N352	W283
T1030	I970	T910	D850	W790	G730	Q670	N610	Q549	I484	F422	L353	R284
S1031	N971	V911	W851	F791	L731	E671	G510	G550	H485	Q423	T354	Y285
E1033	A973	R912	N852	W792	W732	A672	P612	D551	G488	K424	V355	L286
Y1034	T974	D913	H853	M793	K733	N673	I613	Q552	T490	E425	S356	D287
V1035	N975	K914	S854	W794	W734	O674	R614	D553	A491	G426	G357	V288
F1036	N976	T915	T855	A795	W735	V675	T615	I555	V492	E427	G360	N289
P1037	P977	Q917	P857	A796	L737	V677	G616	T555	I430	E428	K361	G290
D1038	N978	H918	P858	D797	L737	V677	L617	A556	D493	I430	L363	G291
L1039	W979	A919	L859	S798	W738	A678	P618	L557	R494	T431	G364	N291
Q1040	S980	T920	N860	A799	G739	D679	S619	A558	A495	E432	Q365	A292
Q1041	Y981	A921	T861	G800	L740	F680	F620	Y559	C496	Q433	R366	Q293
N1043	L982	N922	H862	H801	W741	T681	L621	P560	A497	T434	K367	A294
A1044	R983	I923	Q863	T802	Q742	V682	A623	G561	V498	V435	Y368	A295
Y1045	E984	G924	E864	W803	F743	H683	R624	D562	N499	L436	P369	E296
N1046	S985	F925	S865	G804	G744	H684	R625	R563	P500	D437	Q370	N297
G1047	A986	K926	S866	T805	G745	W685	N626	N564	N501	Y438	V371	E298
L1048	N987	L927	P867	H806	G746	H686	T627	P565	S502	P439	W372	F299
T1049	Q988	Q928	N868	R807	H747	V688	W628	P567	V504	L441	M373	E300
L1050	Q989	F930	K868	W808	F748	H689	G629	S568	F505	F442	G374	V301
N1051	G990	N931	N870	H810	D750	N690	D630	L569	F506	A443	M375	E305
M1052	R991	V932	L871	T811	W751	E591	T631	T570	P507	G444	M377	G306
S1053	L993	E933	A872	S812	S752	A692	G632	R571	T508	E445	T378	T309
F1054	A994	S934	W873	S813	D753	G694	F633	T572	Q509	S446	G380	S310
S1055	T995	N935	N874	N814	T755	S695	W635	K573	S510	Q447	F381	N311
V1056	R996	L936	R875	S815	T757	P696	G637	A575	G512	I450	D382	C316
S1057	N997	Q937	T876	P816	T757	N697	Y638	T576	G513	H451	D383	K317
E1058	D997	T938	N877	C817	T758	P698	Y639	K577	G514	F452	G384	G318
Y1059	I998	A939	W878	D818	T759	N699	G639	K578	M454	M454	Y385	M319
A1060	K999	Y940	C879	A819	A759	E700	L640	V579	W517	G455	N386	L320
A1061	M1000	R941	N880	L820	W760	F701	D641	F580	W518	A456	L387	P321
T1062	T1001	N942	P881	L821	G761	W702	P642	W702	N519	A457	E390	G322
S1063	V1002	N882	N882	A822	A762	E581	A643	Y582	D520	Y457	R391	K323
G1064	D1003	E944	L883	T823	I763	K703	L644	L583	L521	D459	Q392	F324
A1065	N1004	S945	E884	N824	G764	W705	A645	R584	E522	P458	G392	I325
V1066	R1005	S946	T885	D825	W765	V706	Q646	S585	A523	G460	M395	D328
G1067	A1006	W947	W886	N826	K766	V707	Y647	L586	D524	G461	A396	G332
A1068	I1007	T948	N887	W827	D767	C708	R648	Y587	K525	Y462	L399	K333
S1069	T1008	Q949	Q888	K828	K768	L709	I649	G588	P526	V464	G400	Y334
S1070	Y950	Y950	C889	C829	W769	Y710	E650	Q589	L530	F465	L335	Q336
T1071	H1010	T951	G890	L830	S770	Q711	I651	I590	L531	Q466	Y401	T337
S1072	W1011	V952	N891	T891	A771	E712	Y652	H532	H532	K467	R402	Q337
V1073	K1012	E953	T892	T892	S772	R713	N653	I592	C533	Y468	T337	D338
G1074	Y1013	A954	W893	K833	T773	I714	P654	F593	V534	E471	Y408	I341
V1075	A1014	P894	W894	P834	L774	I715	S655	I594	G535	G474	I409	
V1076	N1015	H956	F895	D836	R775	F716	N656	Q595	Q536			
Q1077	N1016	A957	C896	Y836	L776	S717	L657	E596	V537			
N1078	H1017	T958	W897	F837	T777	A718	N658	L597				
	V1018		A898	T838								

ASN	ALA	ASN	P1085	S1025	A965	S905	T945	R785	F725	S663	I603	P542
ILE	GLN	ILE	T1086	S1026	L966	E906	M946	P786	L726	F664	T604	K543
LYS	GLU	LYS	Q1087	G1027	A967	A907	Y947	T787	D727	V665	T605	A544
TRP	ASP	TRP	L1088	I1028	L968	T908	M948	T788	N728	V666	T606	I545
ASP	ASP	ASP	K1089	I1029	N969	T909	K949	T789	N729	S667	D607	I546
LYS	LYS	LYS	A1090	T1030	N970	V911	D950	T790	A730	G668	A608	W547
PRO	ASP	PRO	A1091	S1031	N971	V912	V951	T791	L731	T669	P609	G548
GLY	P1032	GLY	K1092	E1032	R972	R912	N952	T792	V732	Q670	N610	Q549
GLY	E1033	GLY	E1093	E1033	A973	D913	S953	T793	K733	G671	V611	G550
ARG	E1034	ARG	L1094	E1034	T974	K914	S954	T794	K734	A672	P612	D551
ASP	V1035	ASP	N975	Q915	N975	Q915	T955	A795	T735	N673	I613	Q552
VAL	F1036	VAL	P976	I916	P976	I916	W956	A796	I736	G674	R614	D553
VAL	P1037	VAL	P977	Q917	P977	Q917	P957	A797	L737	G675	T615	A554
ARG	L1038	ARG	D978	N918	A958	N918	A958	S798	L738	V676	G616	T555
ILE	N1039	ILE	W979	A919	L959	A919	L959	A799	G739	Y677	L617	A556
ALA	D1040	ALA	N980	T920	M960	T920	M960	A799	I740	A678	P618	L557
THR	Q1041	THR	Y981	A921	T961	N922	T961	G800	G739	D679	S619	L557
THR	Q1042	THR	L982	N922	A962	N922	A962	M801	I741	F680	F620	Y559
ASN	A1043	ASN	R983	T923	F963	T923	F963	T902	Q742	T681	L621	P560
THR	P984	THR	P984	G924	E964	G924	E964	G804	F743	A622	A622	G561
ALA	Y1045	ALA	P985	F925	S965	F925	S965	T905	G744	E683	A623	D562
ALA	N1046	ALA	K926	S966	S966	K926	S966	H906	G745	D684	R624	R563
GLY	G1047	GLY	L927	N967	N967	L927	N967	K907	H747	W686	R625	N564
ILE	I1048	ILE	G928	K968	K968	G928	K968	W908	F748	I686	N626	P565
ASP	T1049	ASP	S929	A969	A969	S929	A969	W909	T749	P687	T627	A566
GLN	L1050	GLN	F930	M970	M970	F930	M970	W910	D750	V688	W628	P567
GLN	M1051	GLN	V931	L871	L871	V931	L871	N911	M751	M689	G629	S568
THR	S1052	THR	P932	A872	A872	P932	A872	S912	S752	E691	D630	L569
ASN	F1054	ASN	G933	W873	W873	G933	W873	S913	D753	A692	I631	T570
LEU	E1055	LEU	S934	M874	M874	S934	M874	N914	P754	G693	F633	R571
VAL	V1056	VAL	N935	R875	R875	N935	R875	S915	T755	G694	R634	K573
VAL	S1057	VAL	L936	T876	T876	L936	T876	P916	A756	S695	W635	Q574
THR	E1058	THR	Y937	N877	N877	Y937	N877	G917	T757	P696	K636	A575
GLY	Y1059	GLY	T938	W878	W878	T938	W878	D918	T758	N697	Y638	T576
GLU	A1060	GLU	A939	G879	G879	A939	G879	A919	A759	P698	G639	K577
GLN	A1061	GLN	Y940	N880	N880	Y940	N880	L920	M760	W699	L640	K578
ALA	D1062	ALA	R941	P881	P881	R941	P881	L921	G761	E700	D641	V579
ALA	S1063	ALA	N942	N882	N882	N942	N882	A922	A762	D642	P642	F580
ALA	G1064	ALA	Y943	L883	L883	Y943	L883	I923	I763	F701	A643	E581
ALA	A1065	ALA	E944	E884	E884	E944	E884	N924	G764	M702	L644	Y582
ALA	V1066	ALA	S945	I885	I885	S945	I885	D925	T765	K703	L644	L583
ALA	G1067	ALA	S946	W886	W886	S946	W886	M926	K766	W704	A645	R584
ALA	A1068	ALA	W947	F887	F887	W947	F887	V927	D767	V706	Q646	R585
ALA	S1069	ALA	Y949	Q888	Q888	Y949	Q888	K928	K768	V707	Y687	L586
GLY	S1070	GLY	T950	G889	G889	T950	G889	G929	V769	C708	G588	L586
LEU	S1071	LEU	V951	A890	A890	V951	A890	L930	S770	L709	I649	Q589
TYR	F1072	TYR	V952	T891	T891	V952	T891	G931	A771	Y710	E650	I590
ALA	E1133	ALA	E963	W993	W993	E963	W993	V932	T772	Q711	I651	F591
PHE	G1074	PHE	A954	N894	N894	A954	N894	K933	T773	E712	Y652	I592
THR	V1075	THR	F955	F995	F995	F955	F995	D935	L774	R713	N653	F593
ASP	V1076	ASP	H956	G996	G996	H956	G996	Y936	R775	E714	P654	I594
ASP	Q1077	ASP	A957	V997	V997	A957	V997	F937	L776	I715	S655	Q595
GLY	N1078	GLY	T958	N997	N997	T958	N997	I938	F778	P716	N656	Q596
ASN	G1079	ASN	A959	A998	A998	A959	A998	I939	A779	W720	L657	L597
ASN	S1080	ASN	T960	P999	P999	T960	P999	E939	A780	S721	N658	S598
ARG	Y1081	ARG	E961	N901	N901	E961	N901	A940	K781	D722	I660	Y599
GLY	N1082	GLY	L962	D902	D902	L962	D902	N941	A782	N723	L661	G602
GLY	Q1083	GLY	G963	L903	L903	G963	L903	P943	G783	I724	H662	
ASN	T1084	ASN	E964	N904	N904	E964	N904	E944	L784			

- Molecule 2: Non-contractile tail sheath

Chain LD: 



R1016	H956	G896	H836	F716	H656	Q956	G536	E471	T407	D338	G266
H1017	A957	V897	F837	S717	L657	E596	Q536	G474	Y408	I341	N270
V1018	T958	A898	I838	A718	N658	L597	V537	I475	I409	K342	A271
T1019	P899	A779	E839	F719	Q659	S598	G538	N476	G410	Q343	A272
T1020	F900	E780	A840	W720	Q659	Y599	K539	Y477	M411	Q344	L273
G1021	N901	K781	N841	S721	L661	G602	L540	A478	N413	D345	A274
A1022	D902	A782	F842	D722	H662	I603	P542	G479	K416	S346	A275
E1023	L962	G783	W843	W723	S663	T604	K543	V480	G417	V347	G276
E1024	E964	L784	F785	F725	F664	N605	A544	H481	L418	K348	D277
I1025	A965	K785	W786	W726	V666	T606	I545	I483	N352	L353	K278
S1026	L966	F787	Q788	D727	S667	D607	I546	N484	F421	T354	Q280
A1027	A967	W789	Q789	W728	G668	P609	N547	T486	Q422	V355	N283
I1028	L968	N790	H790	A729	T669	N610	G548	T487	Q423	S356	R284
T1030	N970	F911	W851	G730	Q670	V611	G550	K424	D424	S357	Y285
N971	N971	F791	E671	L731	E671	P612	D551	E425	E425	S358	L286
N972	N972	W792	A672	W732	A672	I613	Q552	T426	E426	G359	D287
A973	N912	K793	N673	K733	N673	R614	D553	G427	E427	R360	V288
E974	K914	W794	G674	W734	G674	T615	A554	E428	E428	K361	N289
V1035	Q915	A795	V675	T735	V675	G616	T555	V492	L429	Q362	G290
N975	N916	A796	V676	I736	V676	L617	A556	D493	T430	L363	N291
P976	N917	A797	V677	L737	V677	P618	L557	A495	E432	Q365	A292
P977	N918	S798	A678	W738	A678	S619	A558	C496	Q433	R366	Q293
L1038	N919	A799	D679	G739	D679	F620	Y559	A497	T434	K367	A294
N1039	T920	G800	F680	I740	F680	L621	P560	V498	L436	Y368	A295
D1040	N801	H801	T681	N741	T681	A622	G561	N499	D437	Q370	E296
G1041	T802	T802	V682	Q742	V682	Q623	D562	P500	Y438	V371	N297
N1043	F863	F863	E683	F743	E683	R624	R563	N501	I440	V372	E298
A1044	G804	G804	D684	G744	D684	R625	N564	S502	L441	M373	F299
Y1045	T805	T805	W685	G745	W685	N626	P565	E503	F442	G374	E300
N1046	G806	H806	L686	G746	L686	T927	A566	V504	E445	M375	E301
G1047	N807	K807	V688	W747	V688	W628	P567	F505	L444	G376	V301
D1048	W808	W808	N689	F748	N689	G629	S568	D506	F445	M377	E305
T1049	A869	W809	N690	T749	N690	D630	L569	F507	G444	T378	G306
L1050	N870	N810	E691	D750	E691	I631	T570	T508	E446	S379	T309
N1051	L871	T811	A692	W751	A692	E632	R571	Q509	S446	G380	S310
M1052	A872	S813	V693	S752	V693	F633	T572	S510	Q447	F381	N311
S1053	W873	N814	G694	F754	G694	R634	K573	S511	I450	D382	C316
F1054	N875	S815	S695	T755	S695	W635	Q574	G512	H451	D383	K317
S1055	T876	P816	P696	A756	P696	S637	A576	A513	F452	G384	G318
V1056	N877	G817	N697	T757	N697	Y638	K577	A514	M453	Y385	M319
S1057	W878	D818	P698	W758	P698	G639	K578	G514	S454	N386	L320
E1058	N699	W699	N699	A759	N699	L640	V579	W517	G455	L387	P321
Y1059	G879	L820	E700	N760	E700	D641	F580	N518	A456	P322	G322
A1060	K899	L821	F701	G761	F701	P642	E581	N519	Y457	E390	K323
M1061	N882	A822	W702	A762	W702	A643	Y582	D520	P458	Q392	F324
D1062	T823	I823	K703	I763	K703	L644	L583	E522	D459	K391	I325
S1063	E944	L883	W704	G764	W704	A645	R584	R460	G461	M395	D328
G1064	S945	T825	R705	G765	R705	Q646	S585	E523	Y462	A396	G332
A1065	S946	D825	V706	R766	V706	Y647	L586	D524	D463	L399	K333
V1066	N947	N826	W707	G766	W707	G648	Y587	K525	Y464	G400	Y334
A1067	T948	W827	C708	D767	C708	I649	G588	P526	F465	Y401	L335
I1068	Y949	K828	L709	K768	L709	E650	Y587	L530	K466	R402	Q336
S1069	G889	G829	W710	V769	W710	T651	Q589	L531	Y468		T337
T1070	N951	L830	Q711	S770	Q711	Y652	I590	H532			
H1010	W1011	G831	E712	A771	E712	N653	I592	C533			
S1071	E953	T892	R713	S772	R713	P654	F593	V534			
F1072	K1012	W832	E714	T773	E714	S655	I594				
V1073	A954	F955		L774							
G1074	A1014			R775							
V1075	N1015										

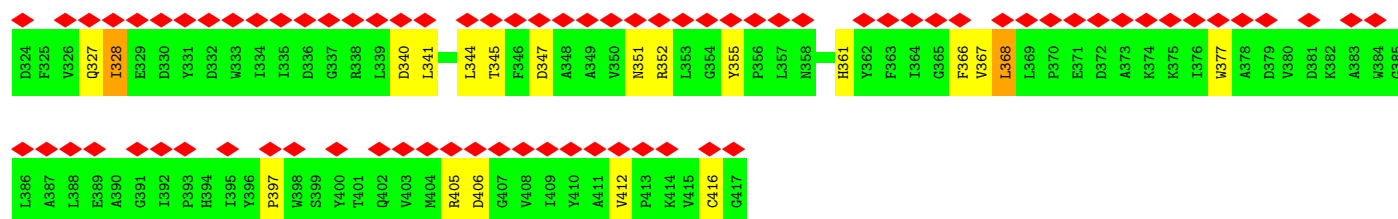
- Molecule 3: Gp64

Opinion	Percentage
Good job	78%
Bad job	83%

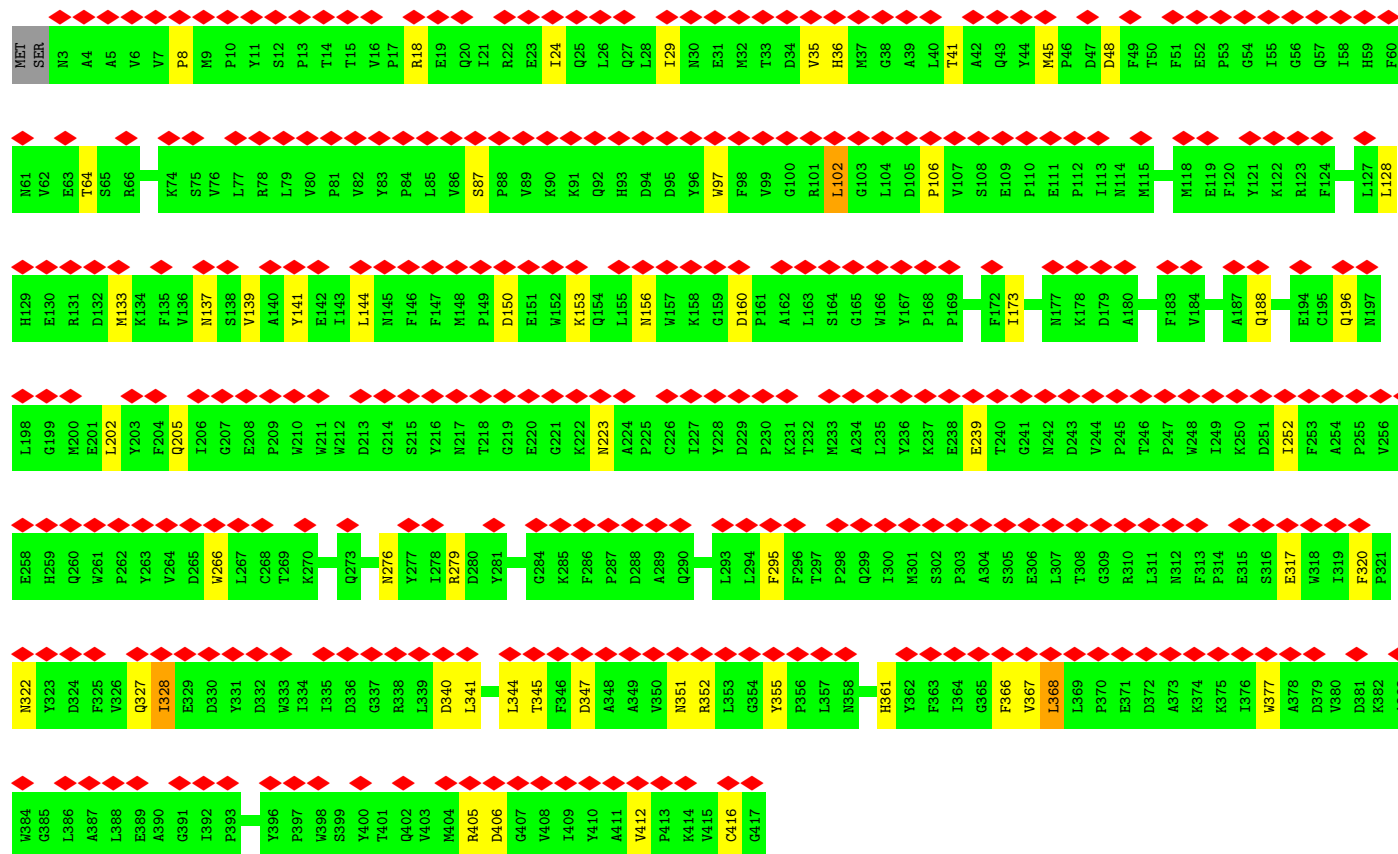
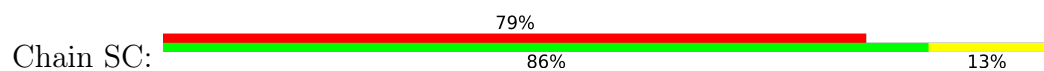


Response	Percentage
U.S. is a threat to their country's security	79%
U.S. is not a threat to their country's security	84%

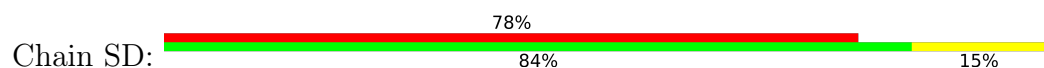


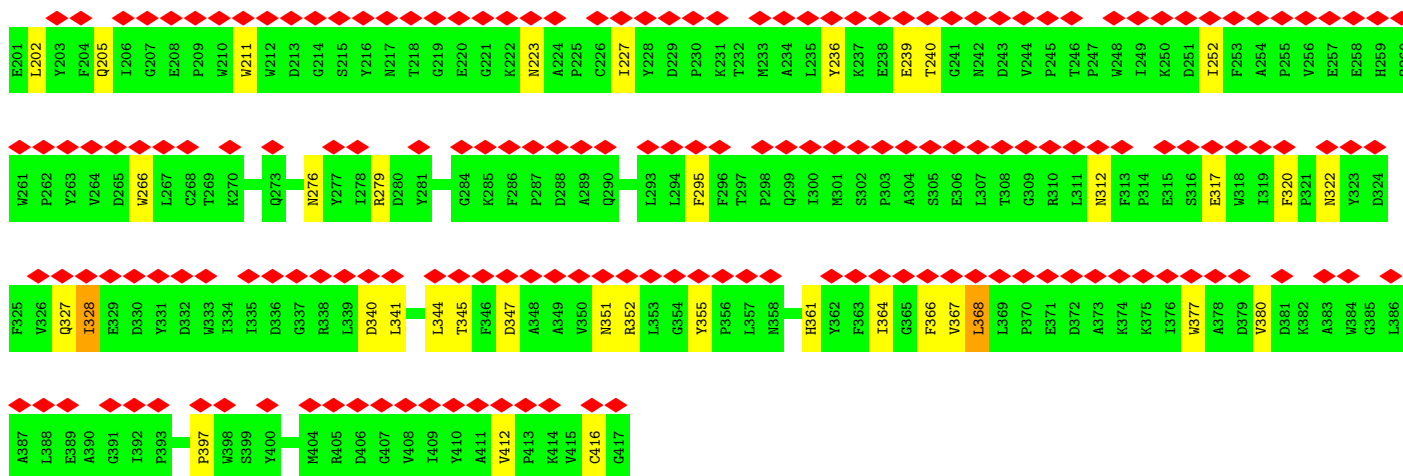


• Molecule 3: Gp64

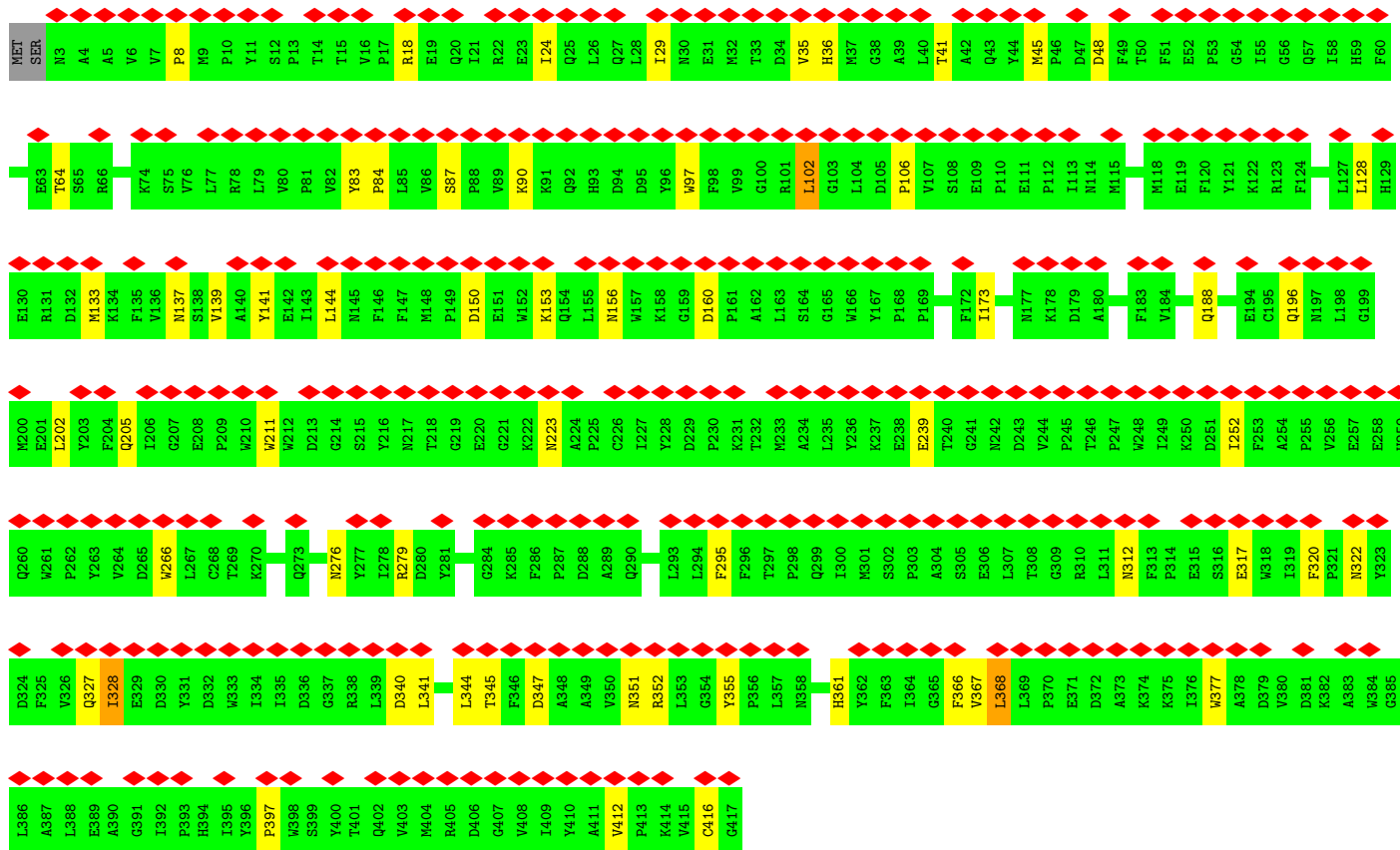
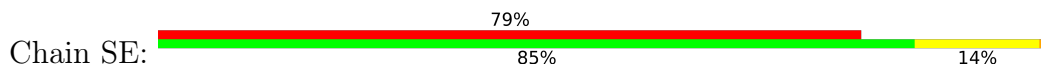


• Molecule 3: Gp64

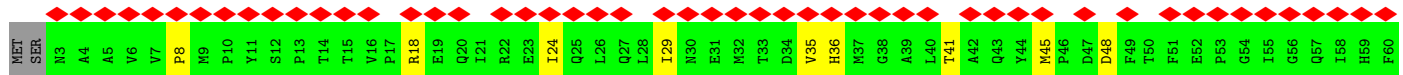
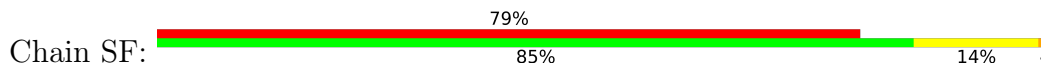


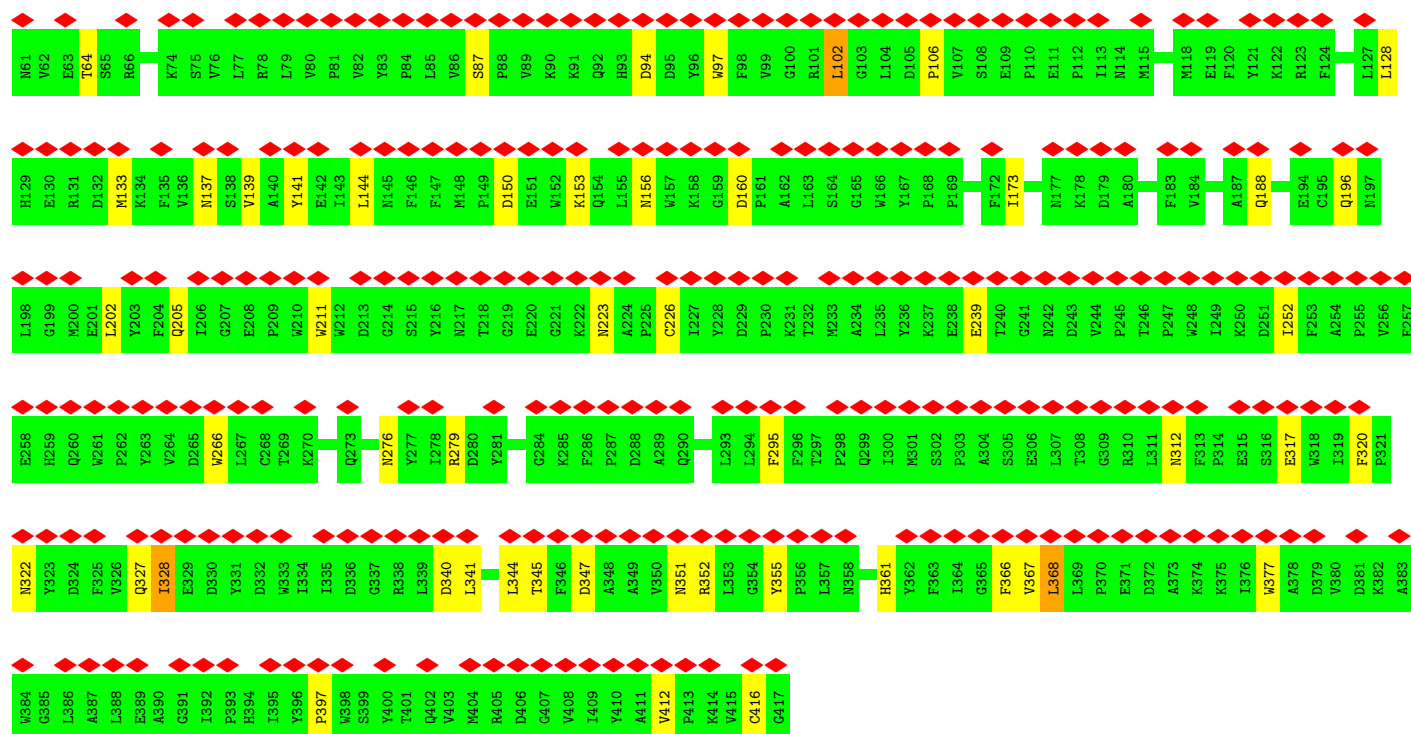


• Molecule 3: Gp64

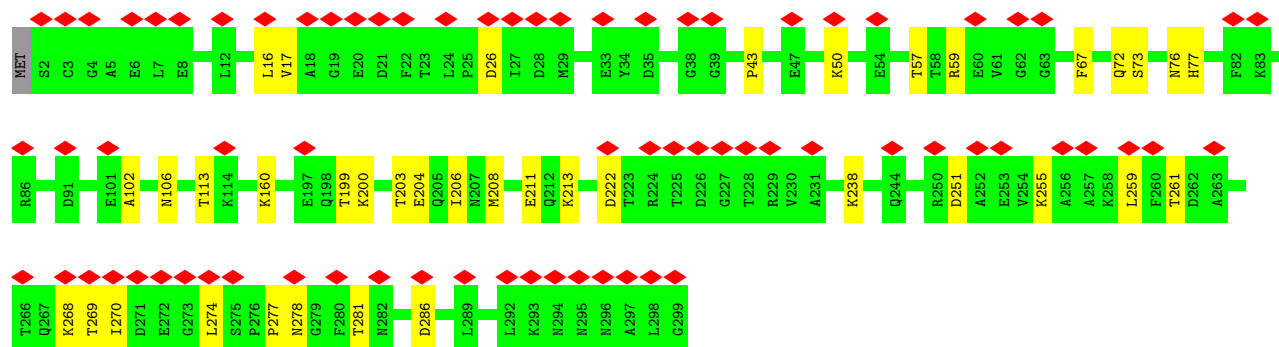
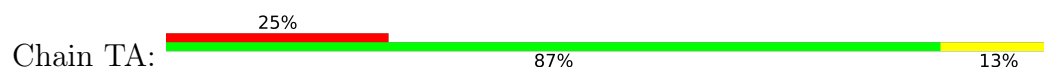


• Molecule 3: Gp64

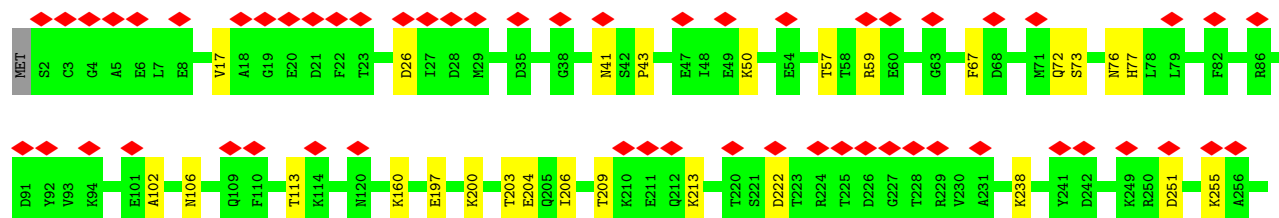
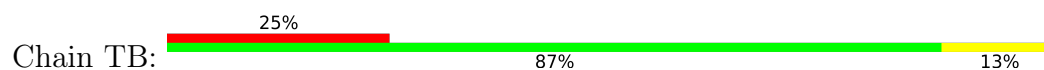


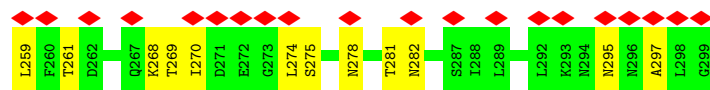


• Molecule 4: Gp54

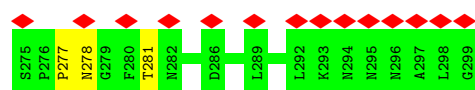
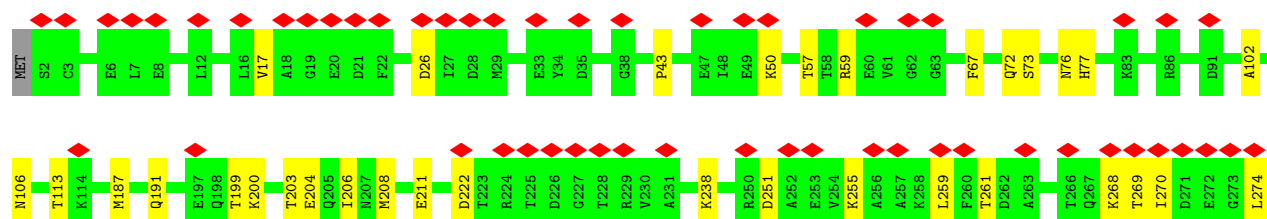
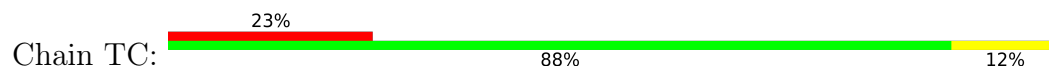


• Molecule 4: Gp54

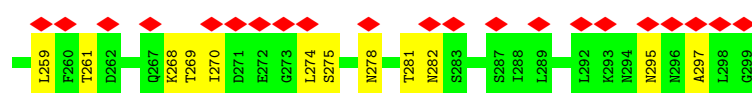
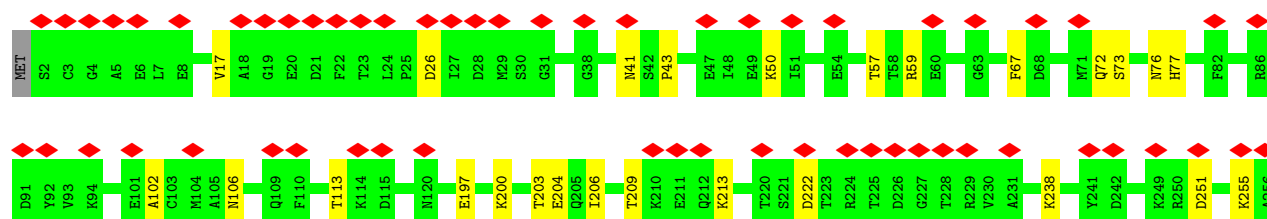
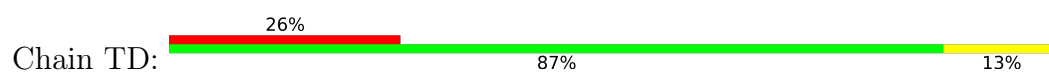




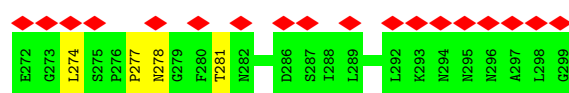
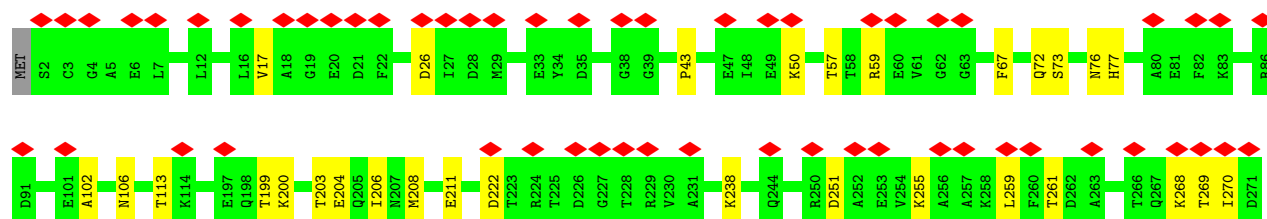
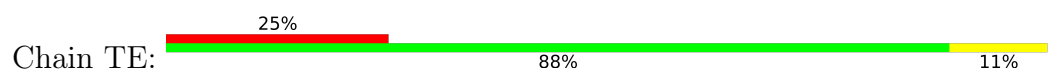
• Molecule 4: Gp54



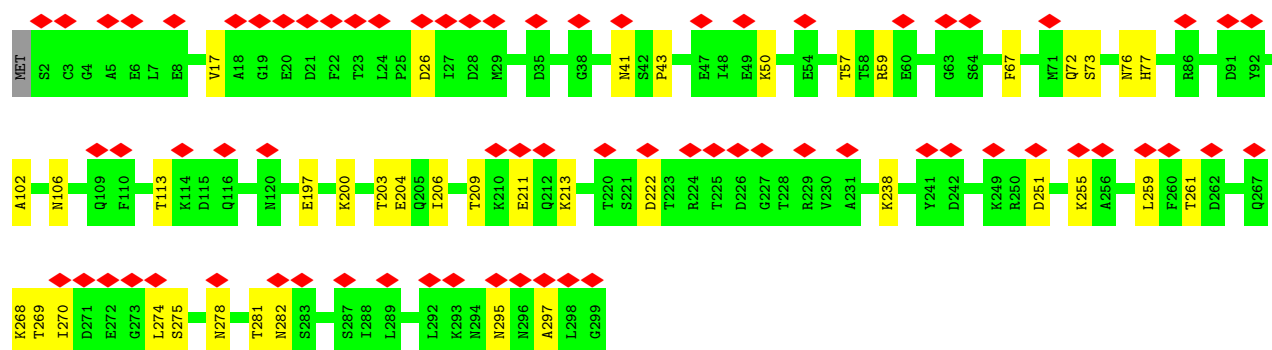
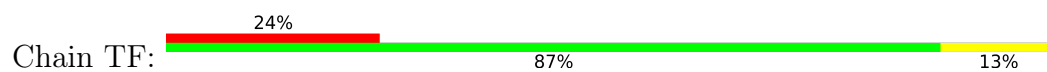
• Molecule 4: Gp54



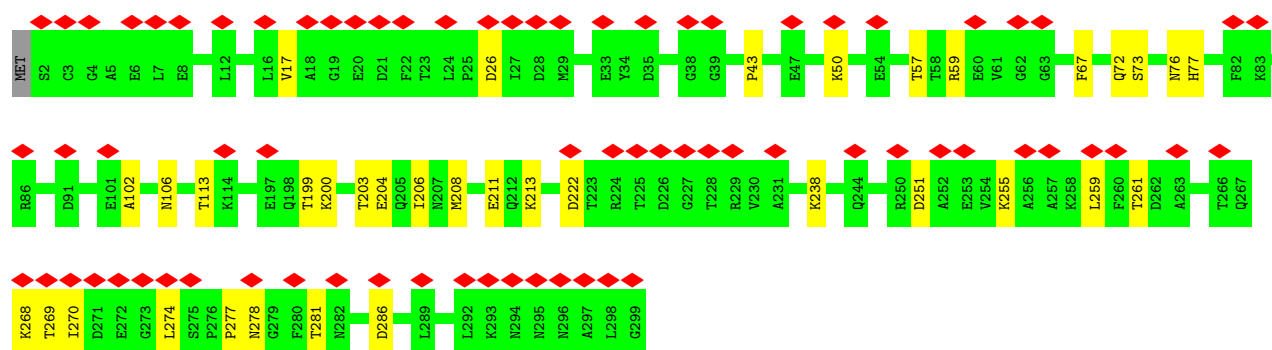
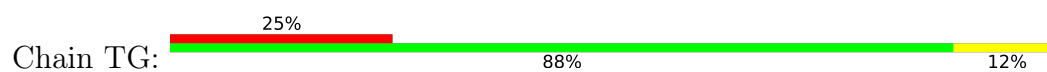
• Molecule 4: Gp54



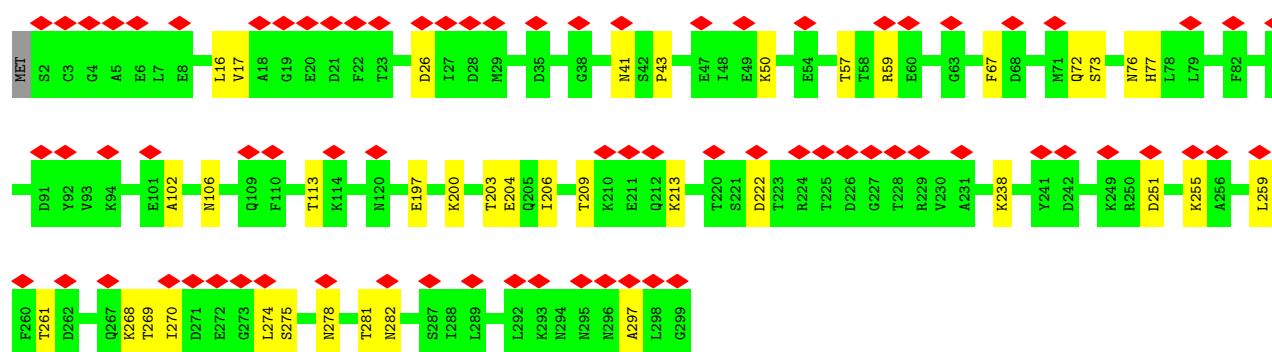
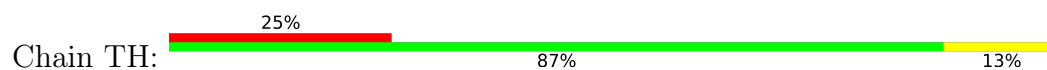
• Molecule 4: Gp54



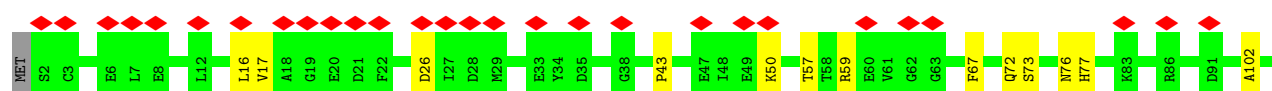
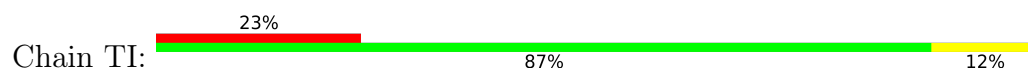
• Molecule 4: Gp54

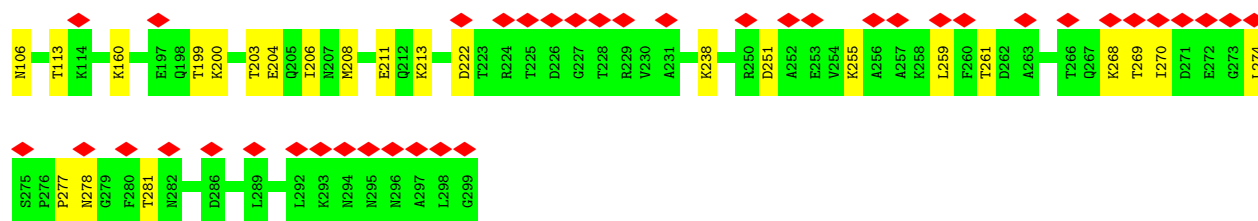


• Molecule 4: Gp54

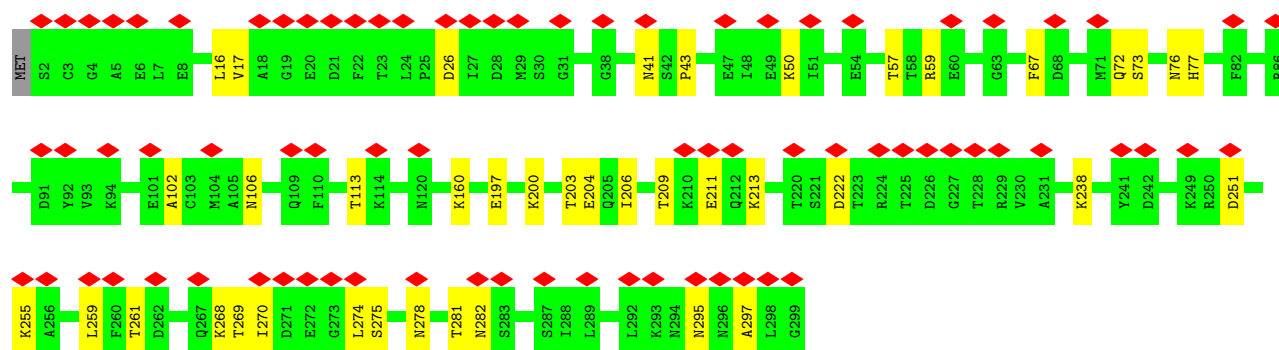
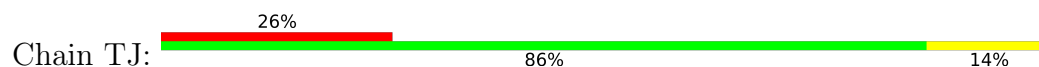


• Molecule 4: Gp54

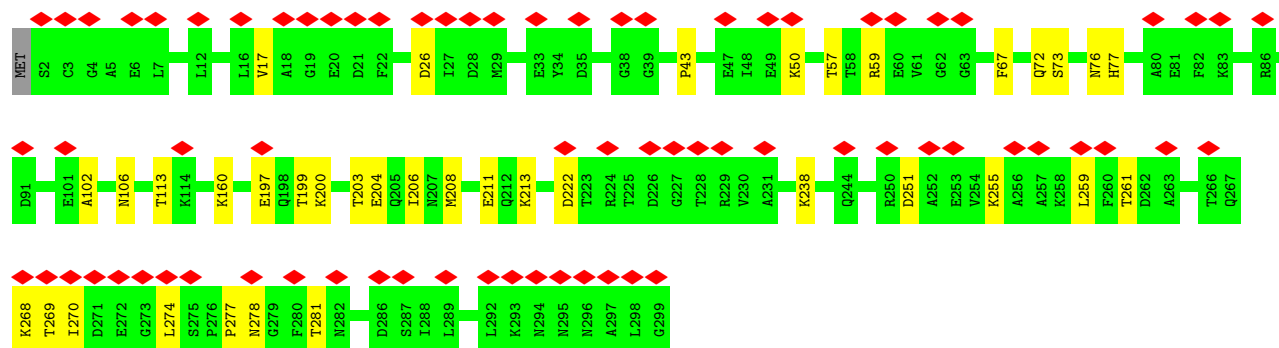




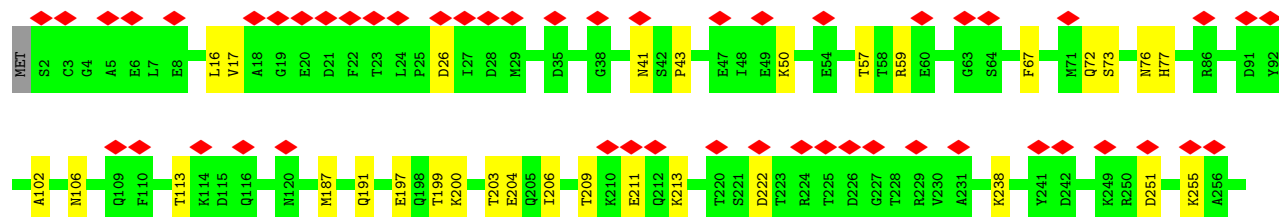
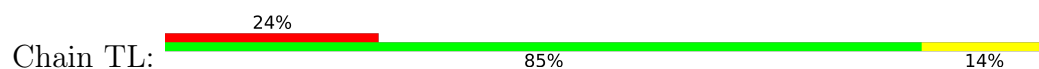
• Molecule 4: Gp54

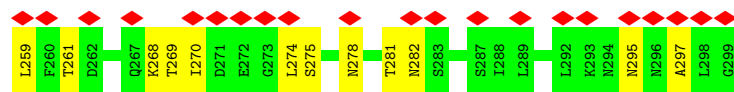


• Molecule 4: Gp54

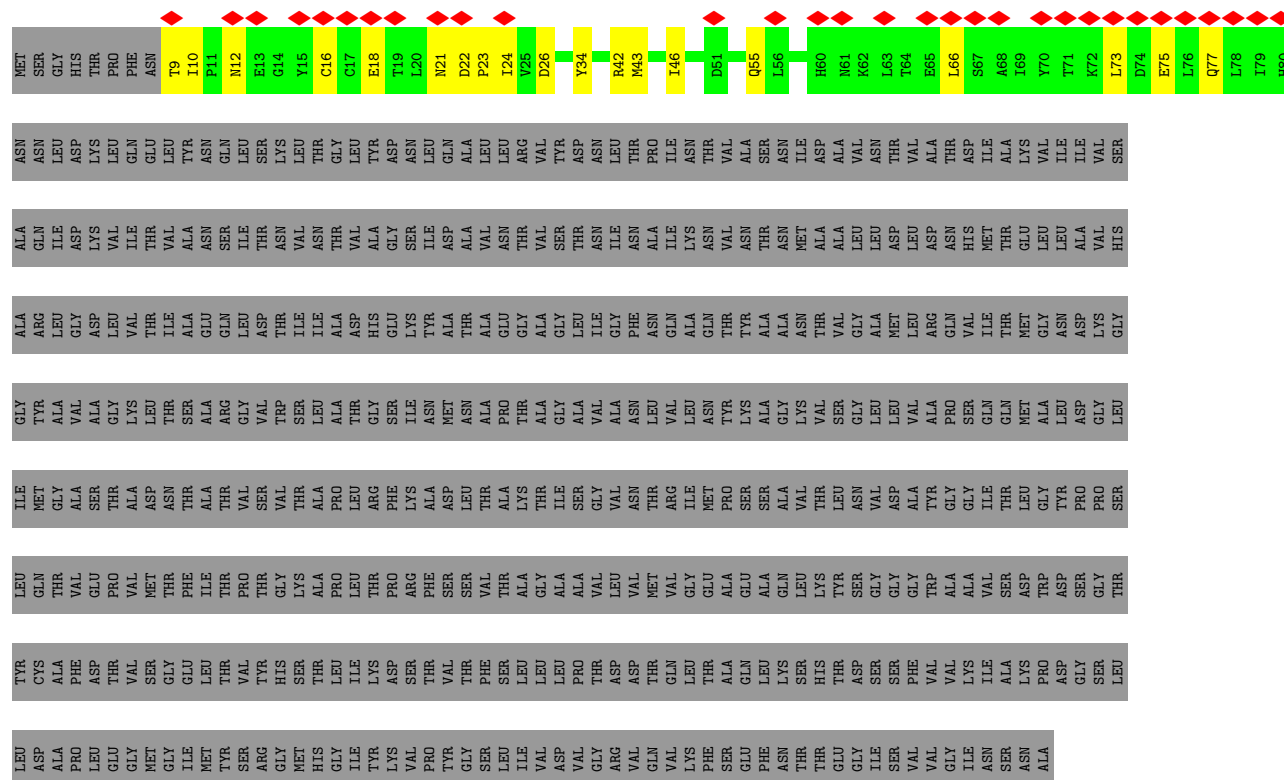


• Molecule 4: Gp54

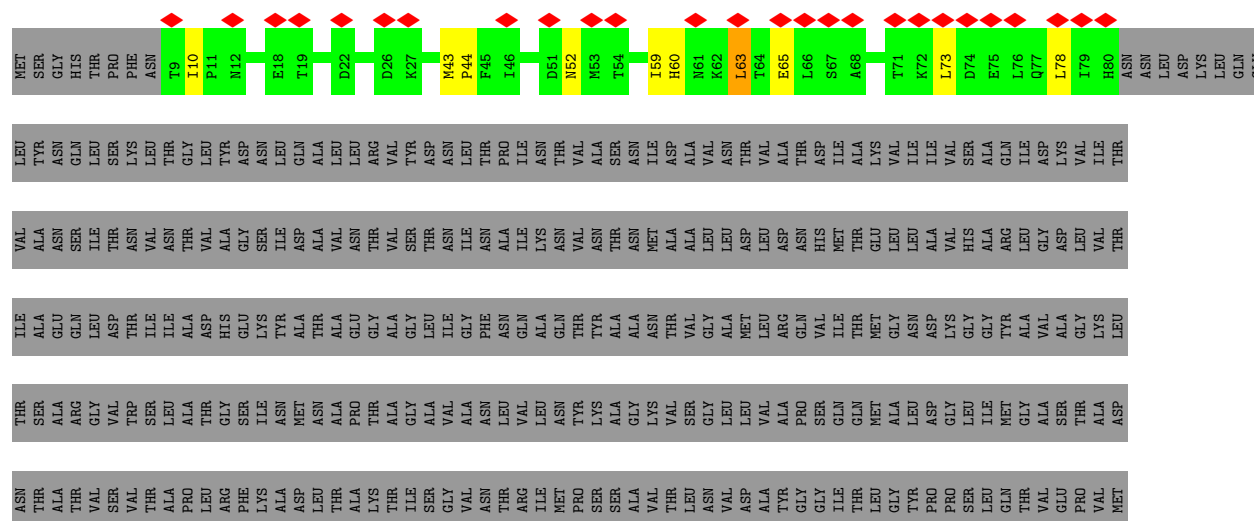




• Molecule 5: 60 kDa protein



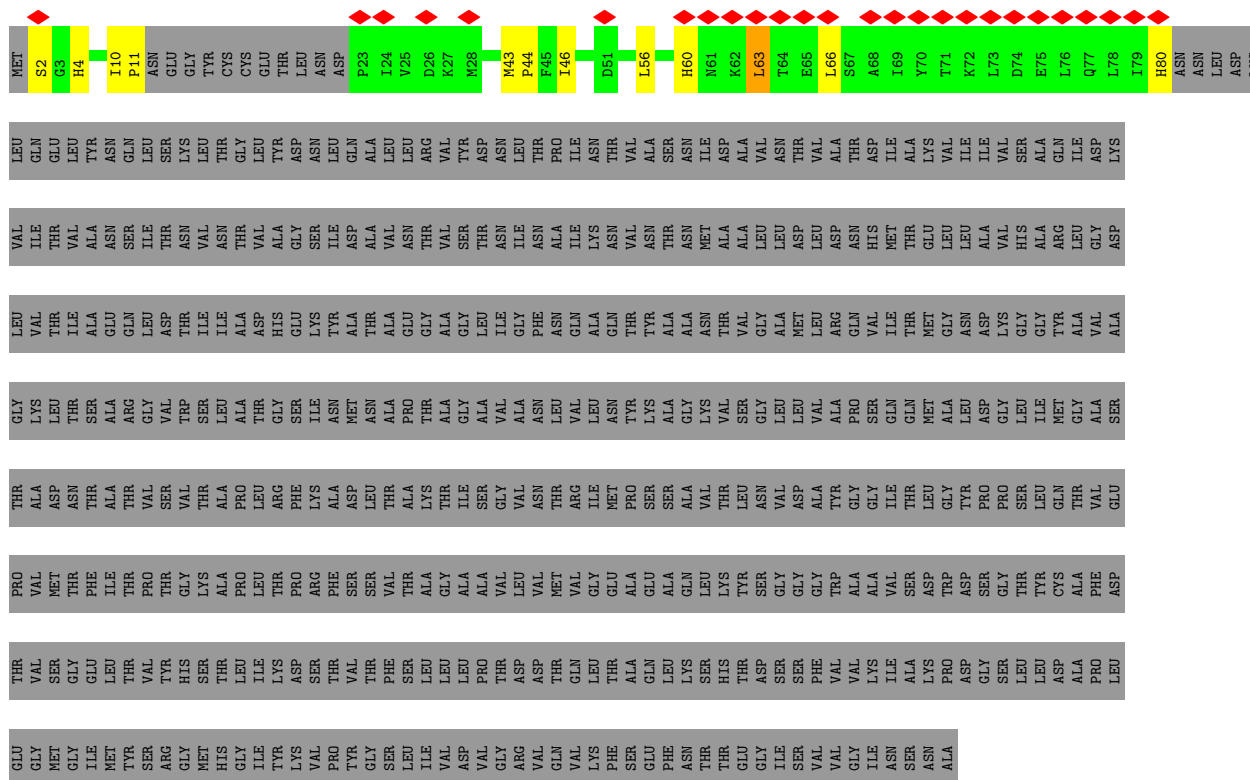
• Molecule 5: 60 kDa protein



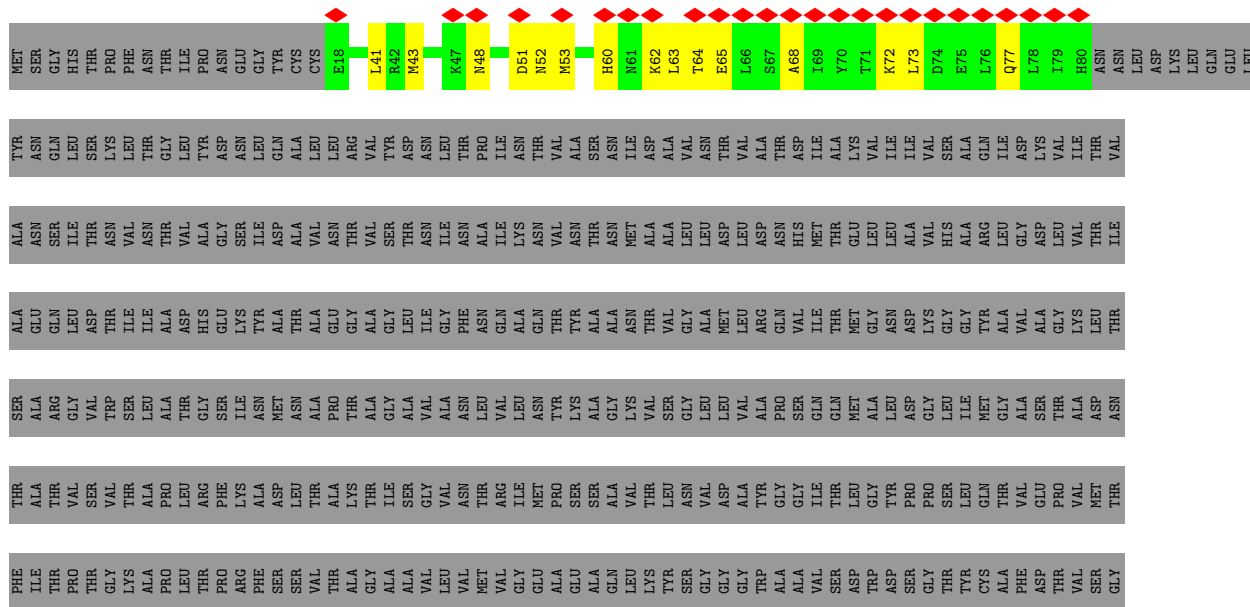
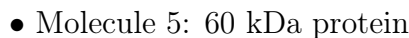


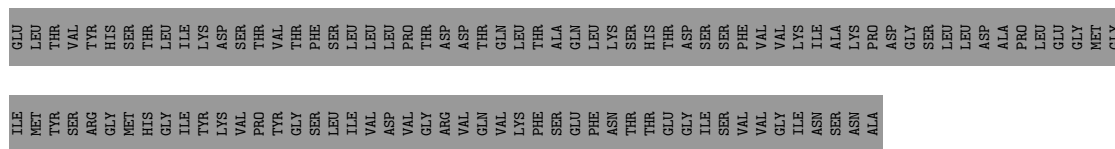


- Molecule 5: 60 kDa protein

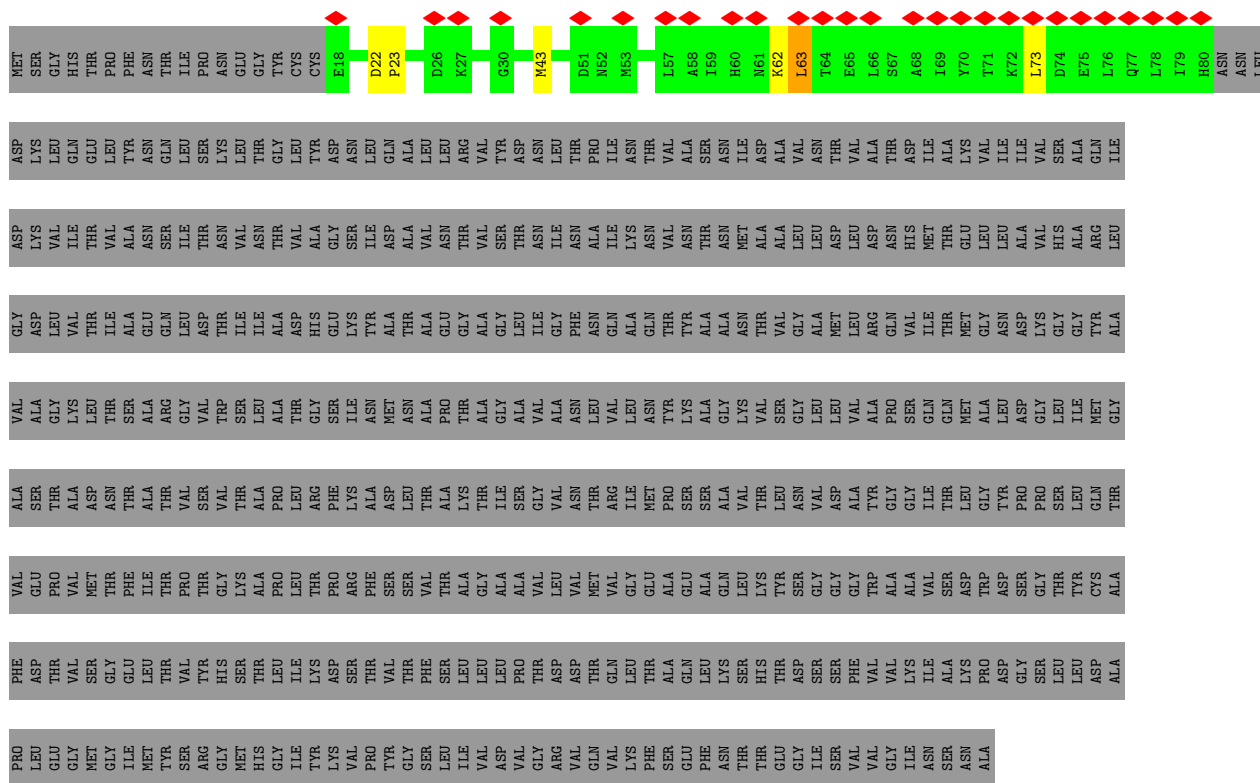


Chain YD:

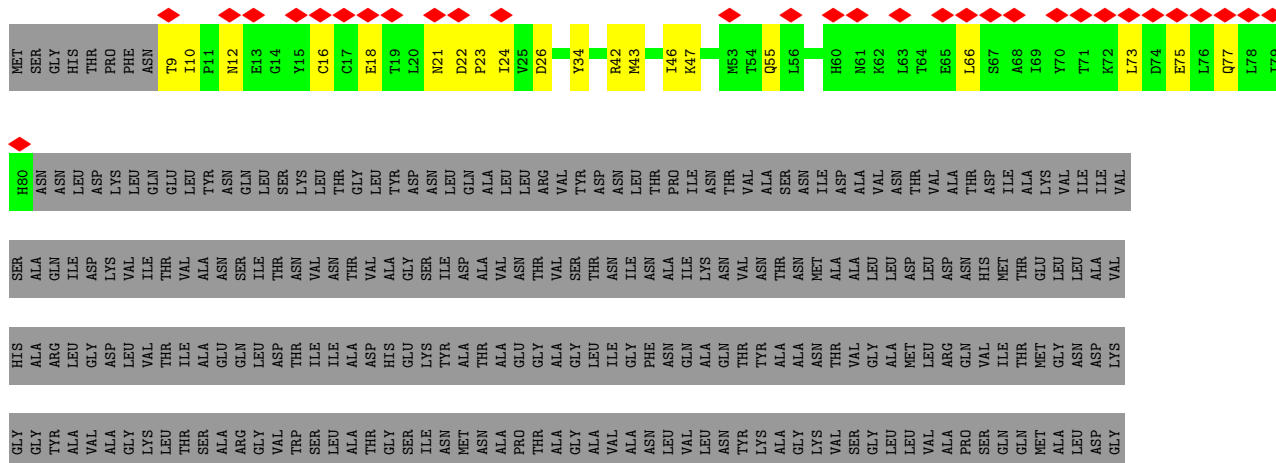


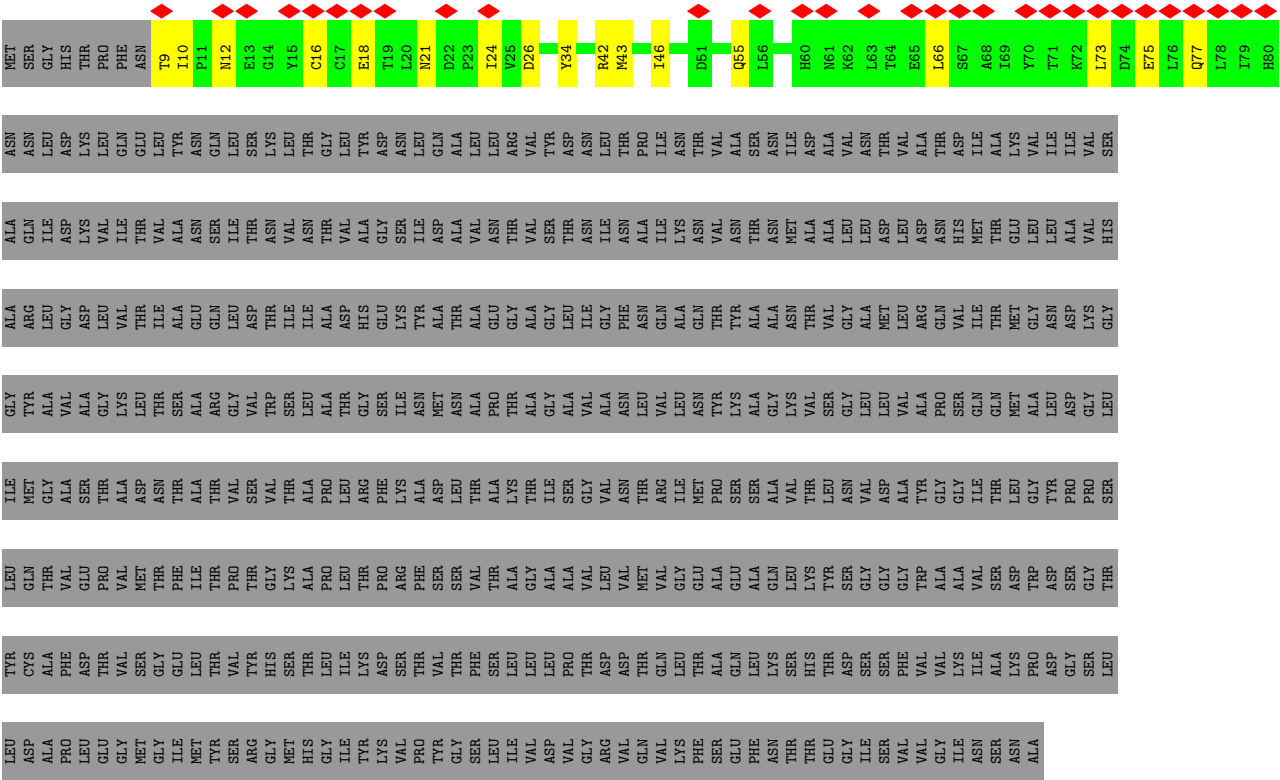


- Molecule 5: 60 kDa protein

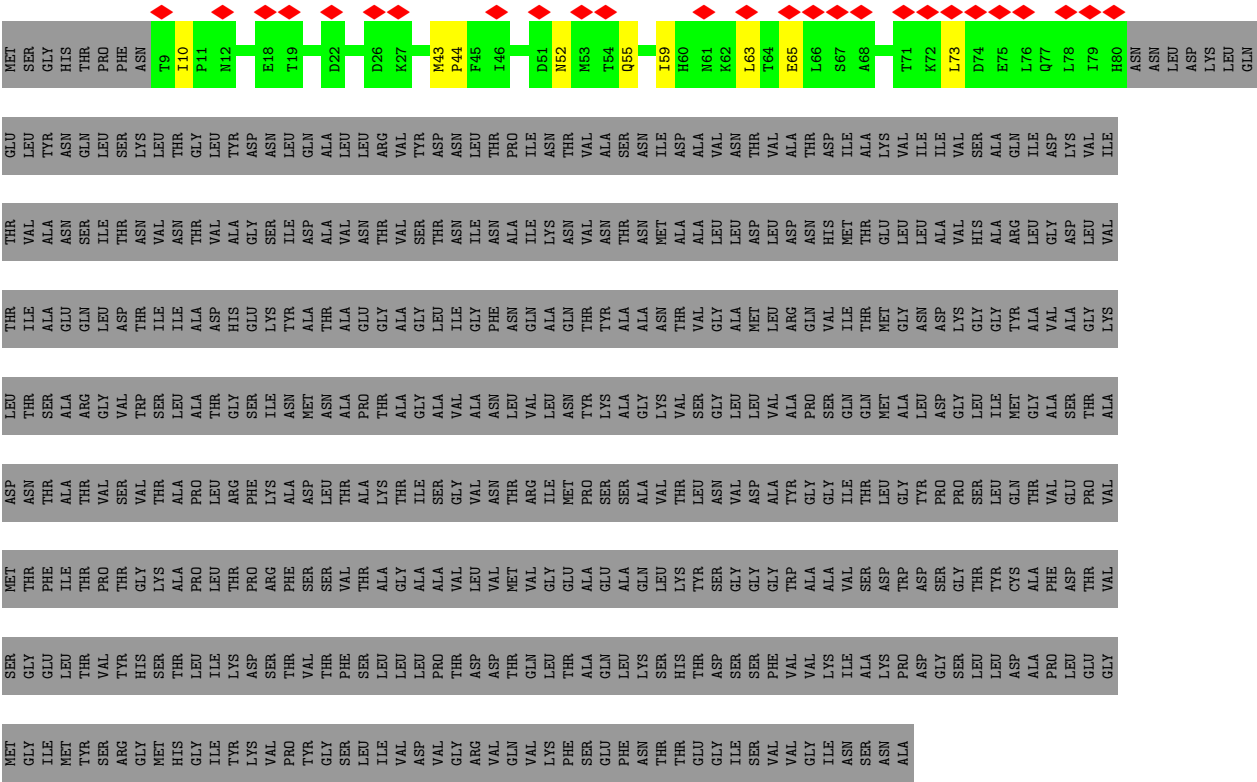


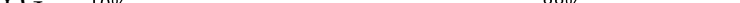
- Molecule 5: 60 kDa protein





● Molecule 5: 60 kDa protein



- Chain YG:  5% 10% 88%



VAL	ILE	THR	VAL	ALA	ASN	SER	THR	VAL	ASN	THR	VAL	ALA	GLY	ILE	ASP	VAL	ASN	THR	SER	THR	ASN	ILE	ALA	LYS	ASN	VAL	ASN	THR	THR	ASN	MET	ALA	ALA	LEU	LEU	ASP	LEU	ASP	ASN	ASN	HIS	ALA	VAL	LEU	LEU	LEU	ARG	GLY	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

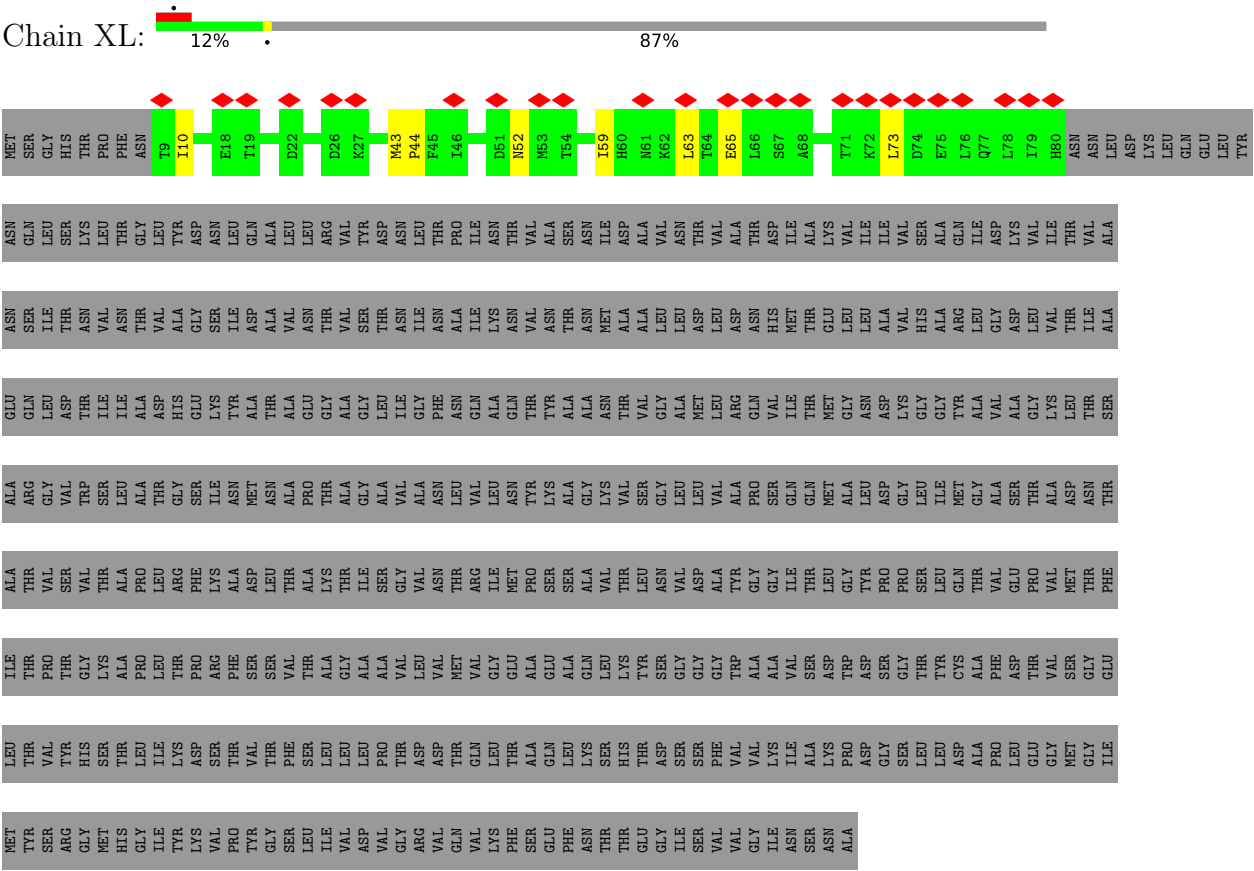
PRO	LEU	GLU	GLY	MET	GLY	ILE	GLY	THR	THR	VAL	PHE
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR	THR	THR	ASP
MET	GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
TYR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
CYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
CYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
E18	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
D22	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
P23	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
D26	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
K27	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
G30	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
M43	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
D51	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
M52	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
M53	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L57	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
A58	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
I59	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
H60	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
N61	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
K62	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L63	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
T64	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
E65	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L66	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
S67	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
A68	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
I69	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
Y70	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
T71	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
K72	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L73	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
D74	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
E75	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L76	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
Q77	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L78	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
I79	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
H80	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

● Molecule 5: 60 kDa protein

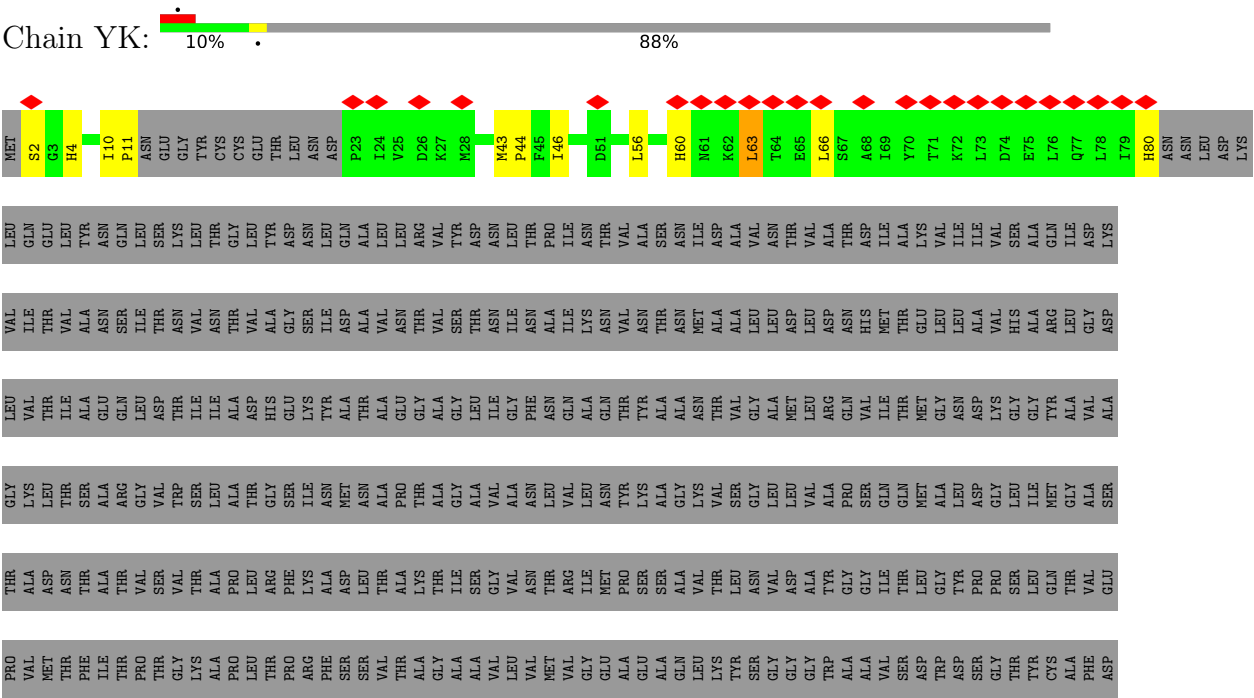


MET	SER	GLY	HIS	THR	PRO	PHE	ASN	T9	N12	E13	G14	Y15	C16	C17	E18	T19	L20	N21	D22	I24	V25	D26	Y34	R42	M43	P44	F45	I46	M53	T54	Q55	L56	H60	N61	K62	L63	T64	E65	L66	S67	A68	I69	Y70	T71	K72	L73	D74	E75	L76	Q77	L78	I79	H80
ASN	ASN	GLN	ASP	LYS	LEU	GLN	LEU	TYR	ASN	GLN	SER	LYS	LEU	THR	GLY	LEU	ASP	ASN	GLN	ALA	LEU	LEU	ARG	VAL	ASN	ASN	THR	PRO	ILE	ASN	VAL	VAL	ASN	ASP	ALA	ALA	VAL	ASN	THR	VAL	VAL	ASP	ALA	THR	ILE	ALA	LYS	VAL	VAL	ILE	VAL	SER	
ALA	GLN	ILE	ASP	LYS	VAL	ILE	THR	VAL	ASN	THR	ASN	VAL	VAL	ASN	THR	ALA	GLY	SER	ILE	ASP	VAL	THR	VAL	VAL	ASN	ASN	ALA	ALA	ILE	ASN	THR	ASN	THR	ASN	ALA	ALA	VAL	LEU	LEU	ASP	HIS	THR	THR	THR	GLY	LEU	LEU	ILE	ASN	VAL	ALA	HIS	
ARG	LEU	GLY	ASP	LEU	VAL	THR	THR	ILE	ALA	GLU	GLN	THR	THR	ILE	ALA	HIS	GLY	LYS	TYR	THR	ASP	ALA	GLY	ALA	GLY	PHE	ASN	GLN	GLN	THR	TYR	ALA	ALA	THR	VAL	GLY	THR	VAL	ARG	GLN	VAL	ILE	THR	MET	GLY	ASN	ASP	LYS	GLY	GLY			
GLY	TYR	ALA	VAL	GLY	LYS	LEU	THR	SER	SER	ARG	VAL	TRP	SER	THR	THR	THR	ILE	ASN	MET	THR	ALA	ALA	GLY	ALA	ASN	LEU	VAL	ASN	ASN	LYS	ALA	GLY	LYS	VAL	SER	GLY	ALA	MET	GLY	THR	GLN	GLN	MET	ALA	GLY	THR	THR	GLY	ASP	LEU			
ILE	MET	GLY	ALA	SER	THR	VAL	ASN	THR	THR	THR	VAL	VAL	THR	ALA	PRO	PHE	ARG	LYS	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	PRO	THR	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER		
LEU	GLN	THR	VAL	GLU	PRO	MET	THR	PHE	ILE	THR	PRO	GLY	LYS	ALA	LEU	THR	ARG	THR	PHE	SER	THR	GLY	ALA	VAL	VAL	VAL	GLY	ALA	ALA	ALA	ALA	GLY	ALA	ALA	VAL	ALA	ALA	ALA	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			
CYS	TYR	ALA	PHE	ASP	THR	SER	GLY	GLU	LEU	THR	VAL	HIS	SER	THR	ILE	LYS	ASP	SER	THR	THR	SER	LEU	LEU	LEU	THR	ASP	THR	GLN	LEU	GLN	LEU	LYS	THR	HIS	THR	TYR	SER	GLY	GLY	ALA	ALA	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR		
LEU	ASP	ALA	PRO	LEU	GLU	GLY	MET	ILE	MET	TYR	SER	ARG	MET	THR	ILE	TYR	LYS	VAL	THR	GLY	THR	THR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	

● Molecule 5: 60 kDa protein



● Molecule 5: 60 kDa protein



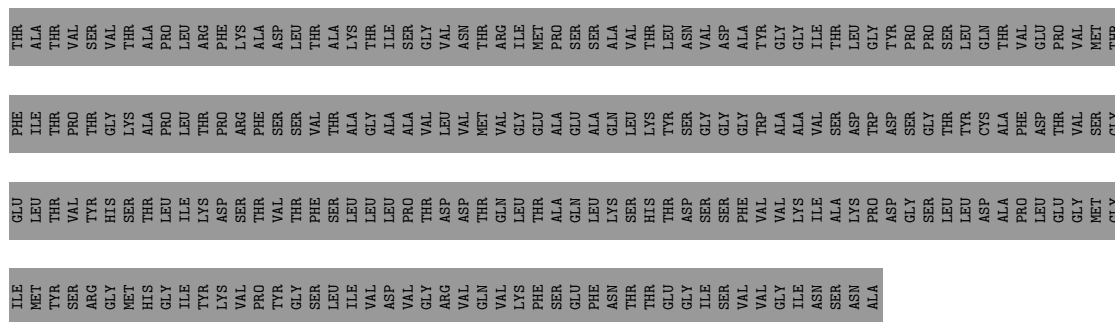
[illegible]

- Molecule 5: 60 kDa protein

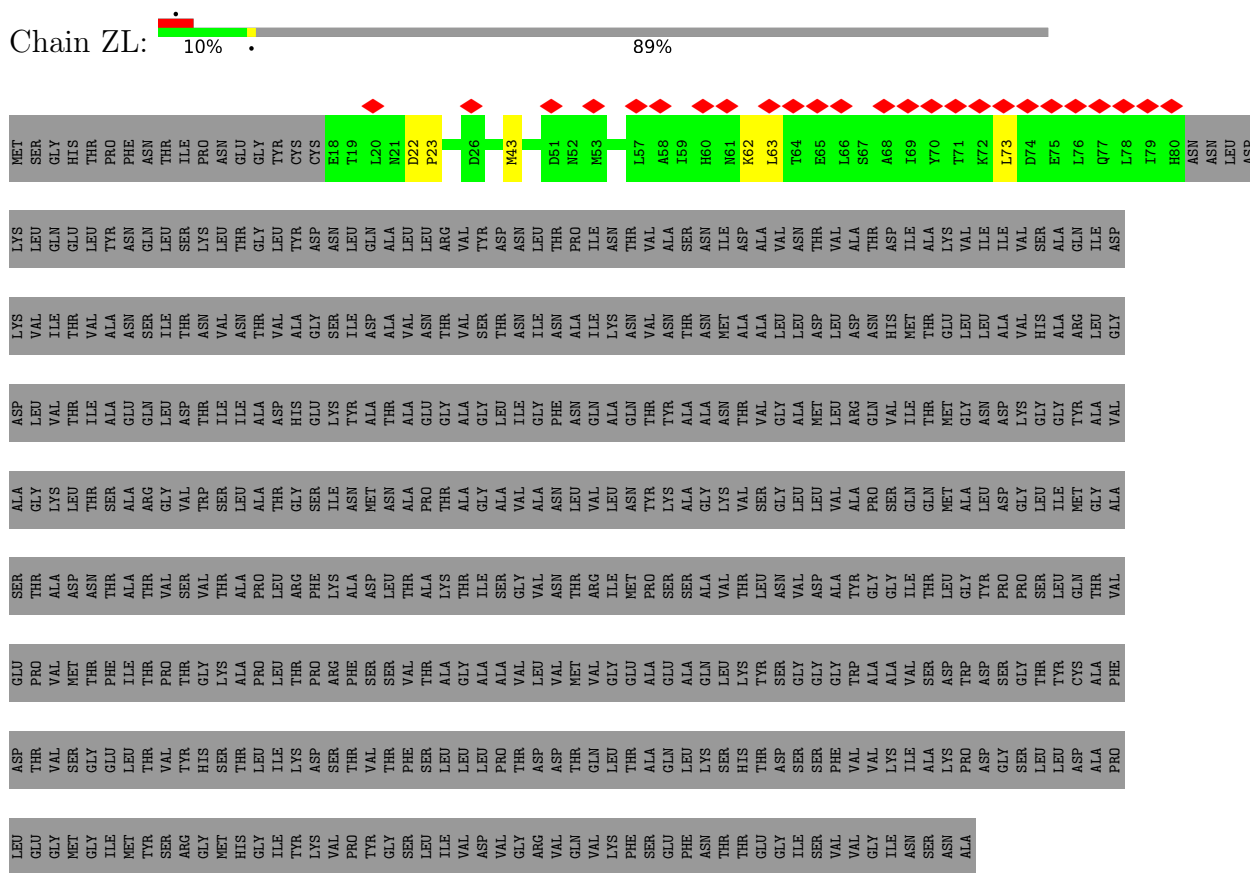
[illegible]

- Molecule 5: 60 kDa protein

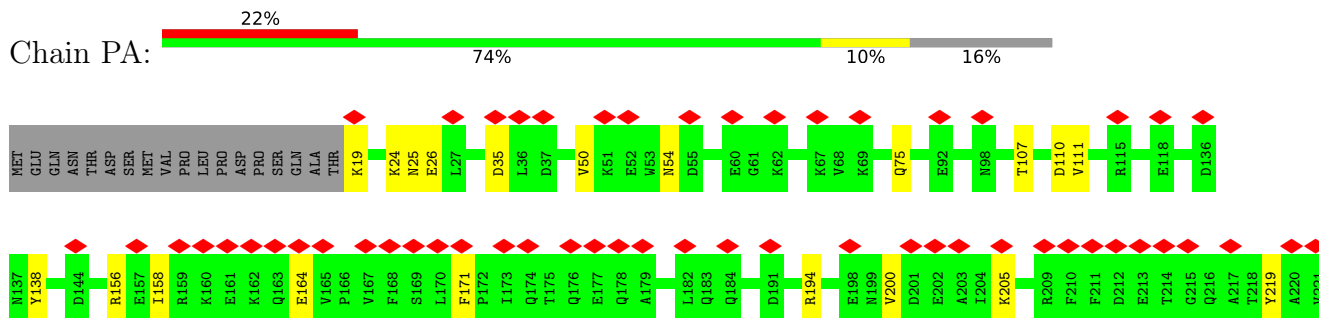
[illegible]



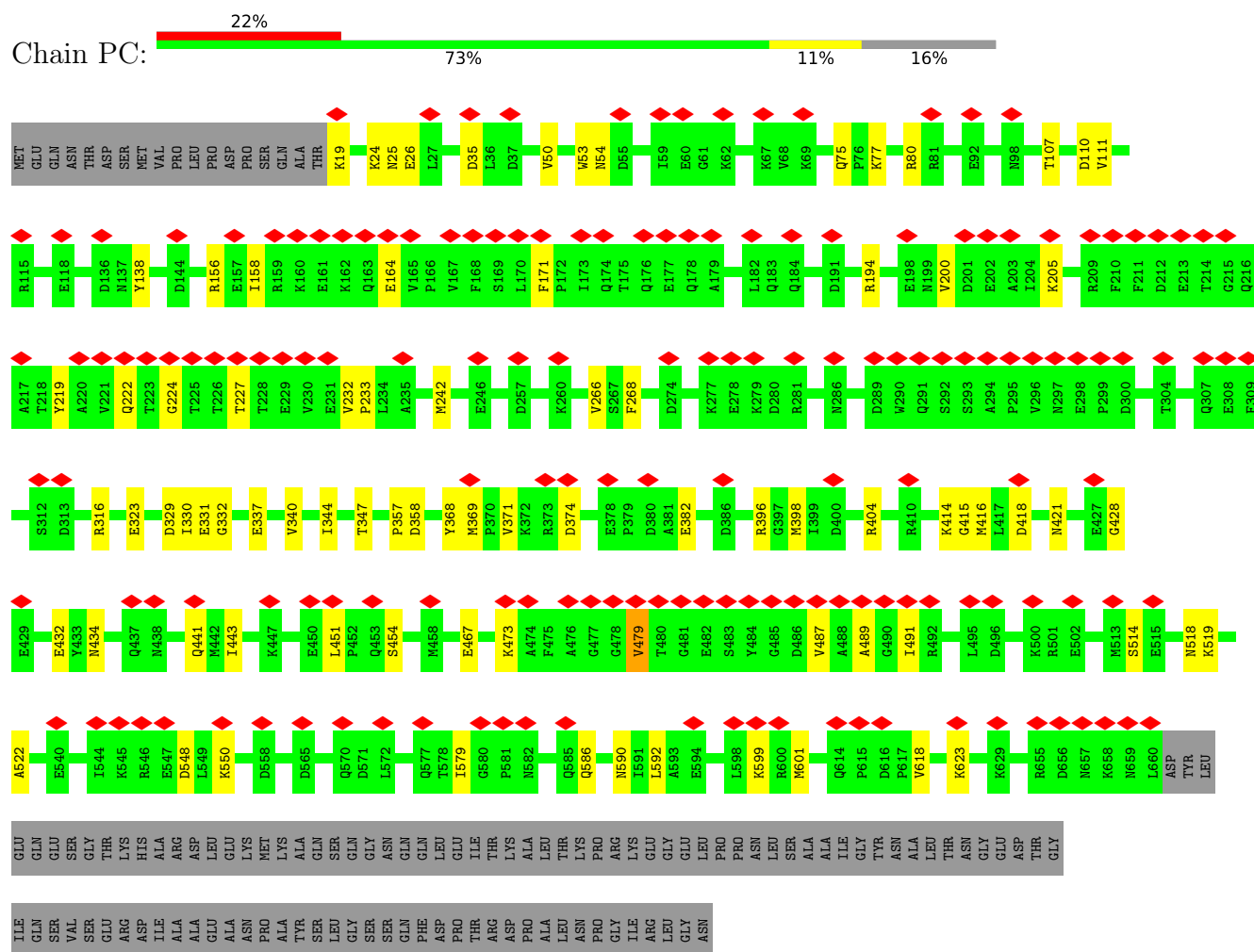
- Molecule 5: 60 kDa protein



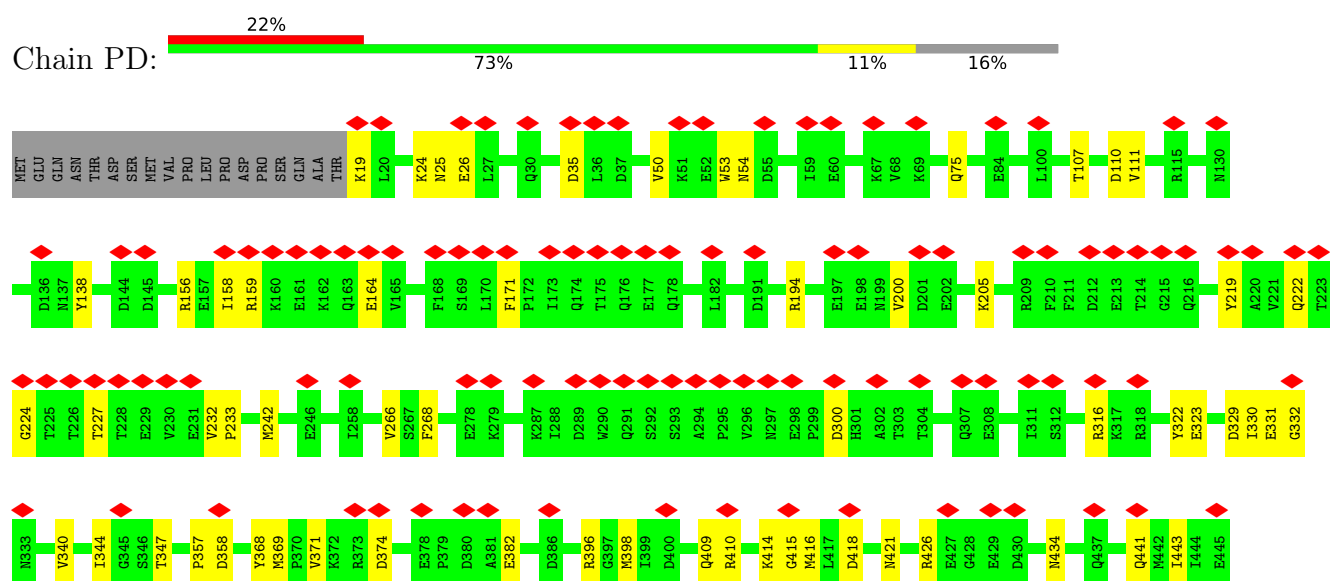
- Molecule 6: Probable portal protein

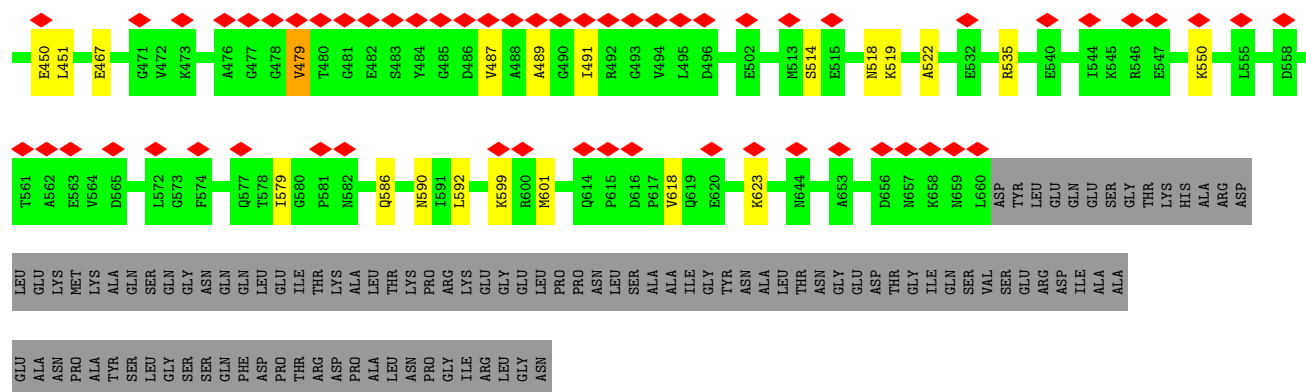


- Molecule 6: Probable portal protein

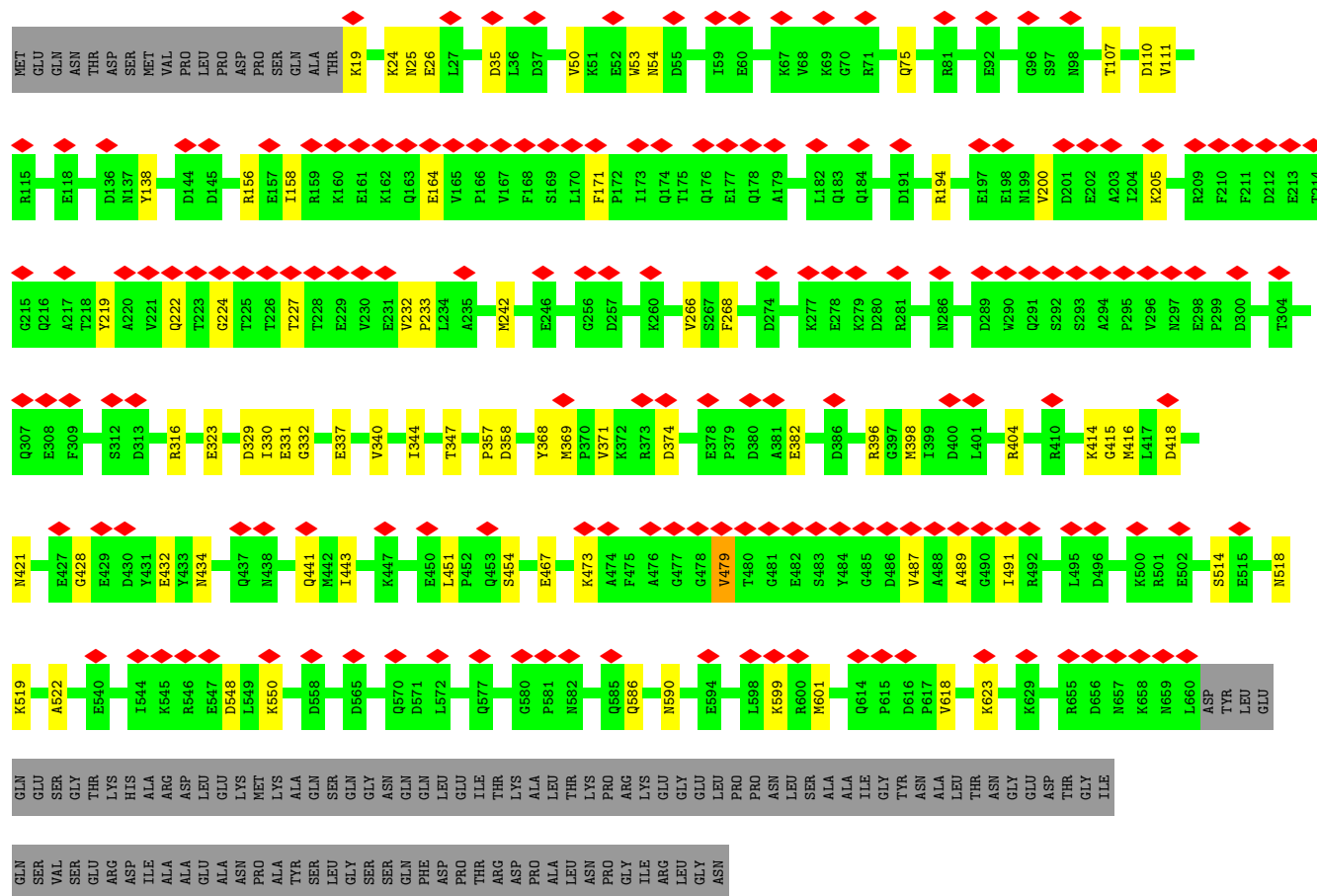
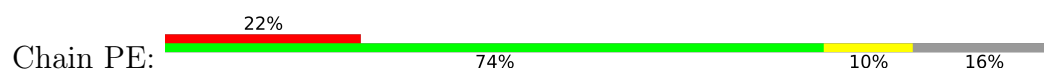


- Molecule 6: Probable portal protein

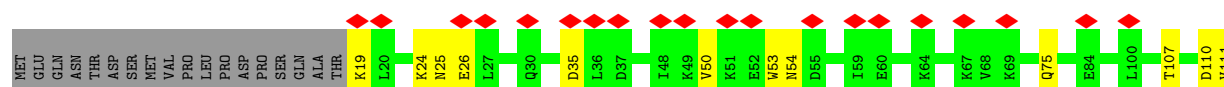
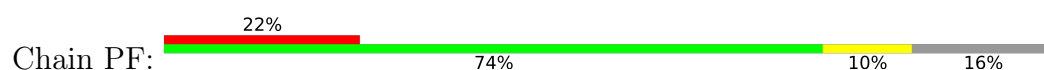


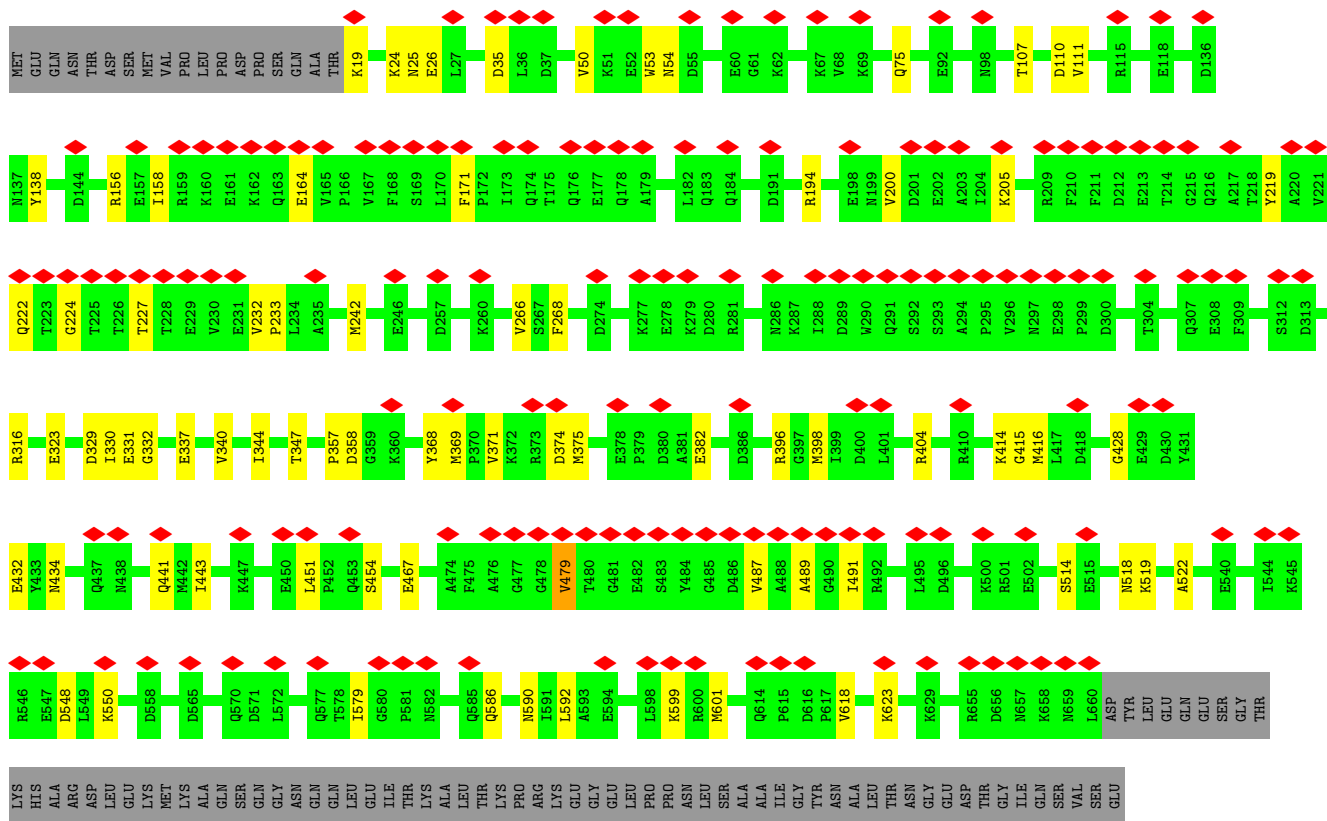


• Molecule 6: Probable portal protein



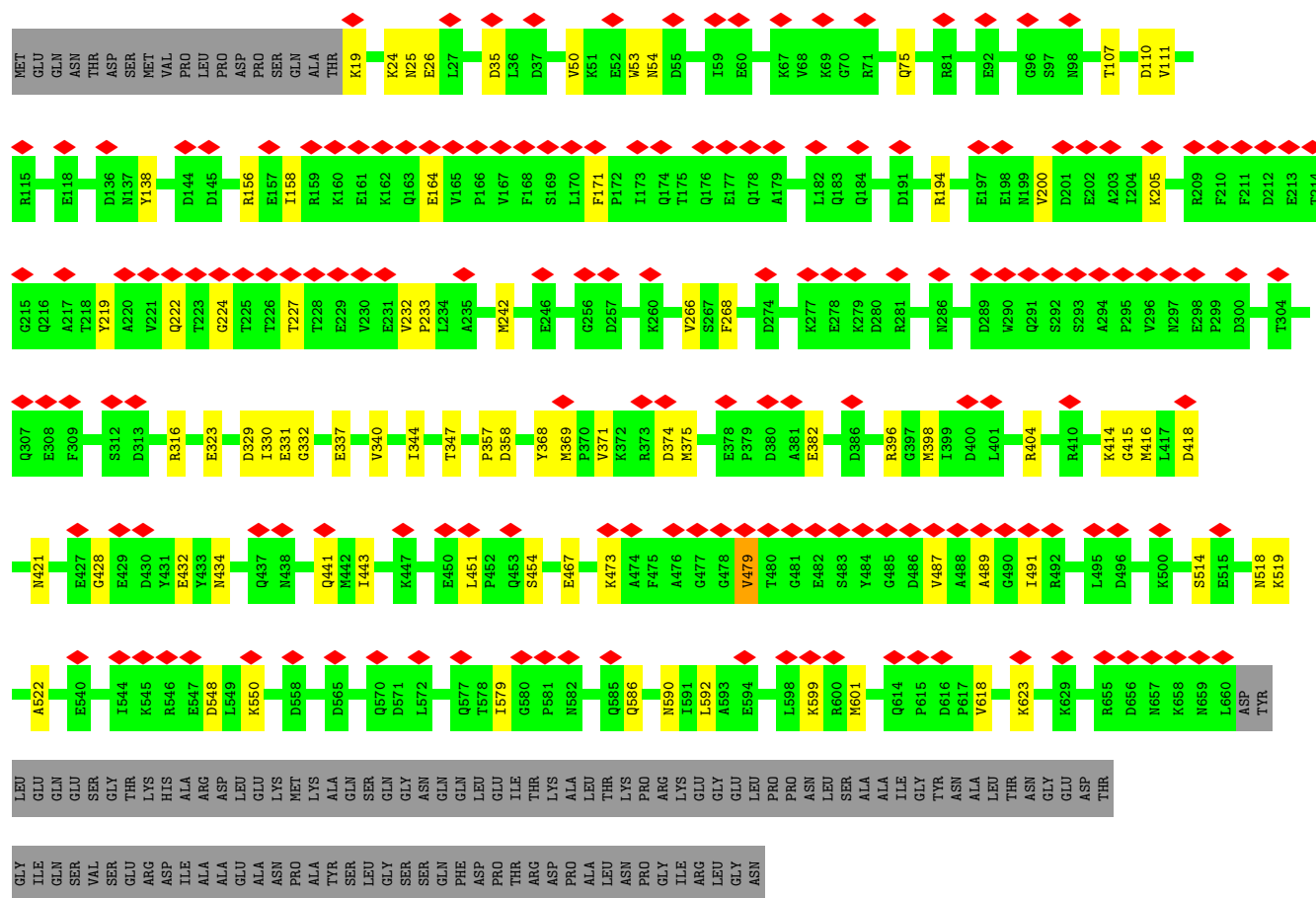
• Molecule 6: Probable portal protein



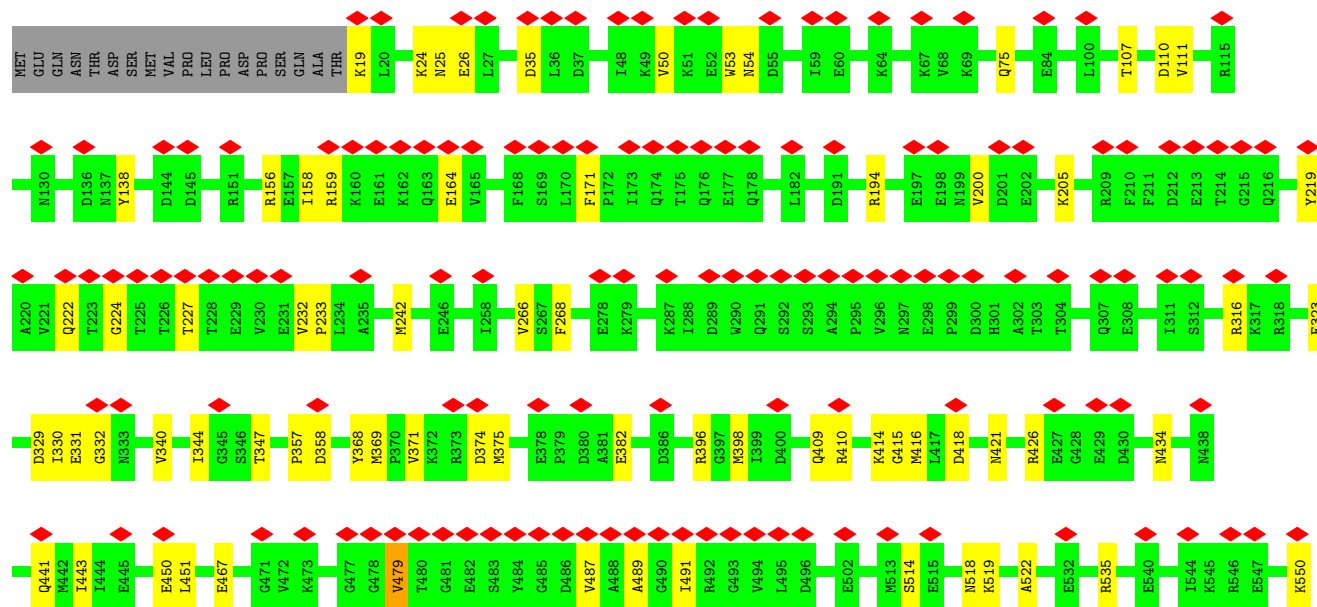
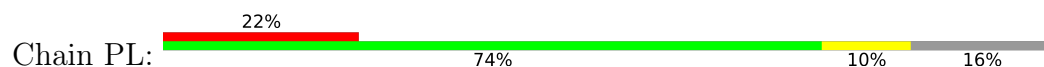


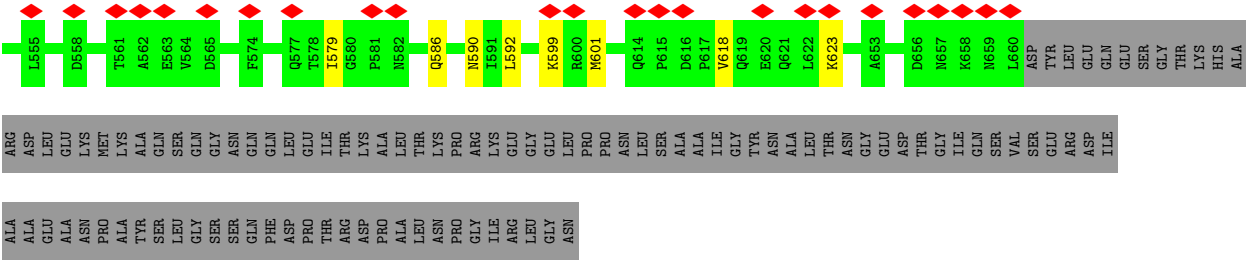
[illegible]





• Molecule 6: Probable portal protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	10265	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.443	Depositor
Minimum map value	-0.141	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	266.262, 268.65, 456.108	wwPDB
Map dimensions	382, 225, 223	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.194, 1.194, 1.194	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	0.07	0/1953	0.19	0/2654
1	AB	0.07	0/1953	0.19	0/2654
1	AC	0.07	0/1953	0.18	0/2654
1	AD	0.07	0/1953	0.19	0/2654
1	AE	0.07	0/1953	0.19	0/2654
1	AF	0.07	0/1953	0.19	0/2654
1	AG	0.07	0/1953	0.19	0/2654
1	AH	0.07	0/1953	0.19	0/2654
1	AI	0.07	0/1953	0.19	0/2654
1	AJ	0.07	0/1953	0.19	0/2654
1	AK	0.07	0/1953	0.19	0/2654
1	AL	0.07	0/1953	0.19	0/2654
2	LA	0.07	0/9606	0.22	0/13093
2	LB	0.07	0/9606	0.22	0/13093
2	LC	0.07	0/9606	0.22	0/13093
2	LD	0.07	0/9606	0.22	0/13093
2	LE	0.07	0/9606	0.22	0/13093
2	LF	0.07	0/9606	0.22	0/13093
3	SA	0.07	0/3498	0.22	0/4781
3	SB	0.07	0/3498	0.22	0/4781
3	SC	0.07	0/3498	0.22	0/4781
3	SD	0.07	0/3498	0.22	0/4781
3	SE	0.07	0/3498	0.22	0/4781
3	SF	0.07	0/3498	0.22	0/4781
4	TA	0.06	0/2290	0.17	0/3103
4	TB	0.06	0/2290	0.17	0/3103
4	TC	0.06	0/2290	0.17	0/3103
4	TD	0.06	0/2290	0.17	0/3103
4	TE	0.06	0/2290	0.17	0/3103
4	TF	0.06	0/2290	0.17	0/3103
4	TG	0.06	0/2290	0.17	0/3103
4	TH	0.06	0/2290	0.17	0/3103
4	TI	0.06	0/2290	0.17	0/3103
4	TJ	0.06	0/2290	0.17	0/3103

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	TK	0.06	0/2290	0.17	0/3103
4	TL	0.06	0/2290	0.17	0/3103
5	XA	0.08	0/585	0.21	0/794
5	XB	0.07	0/585	0.19	0/794
5	XC	0.08	0/585	0.21	0/794
5	XD	0.07	0/585	0.19	0/794
5	XE	0.08	0/585	0.21	0/794
5	XF	0.07	0/585	0.19	0/794
5	XG	0.08	0/585	0.21	0/794
5	XH	0.07	0/585	0.19	0/794
5	XI	0.08	0/585	0.21	0/794
5	XJ	0.07	0/585	0.19	0/794
5	XK	0.08	0/585	0.21	0/794
5	XL	0.07	0/585	0.19	0/794
5	YA	0.08	0/554	0.24	0/750
5	YB	0.07	0/554	0.21	0/750
5	YC	0.07	0/554	0.24	0/750
5	YD	0.07	0/554	0.21	0/750
5	YE	0.08	0/554	0.24	0/750
5	YF	0.07	0/554	0.21	0/750
5	YG	0.08	0/554	0.24	0/750
5	YH	0.07	0/554	0.21	0/750
5	YI	0.08	0/554	0.24	0/750
5	YJ	0.07	0/554	0.21	0/750
5	YK	0.08	0/554	0.24	0/750
5	YL	0.07	0/554	0.21	0/750
5	ZA	0.07	0/516	0.21	0/699
5	ZB	0.07	0/516	0.21	0/699
5	ZC	0.08	0/516	0.20	0/699
5	ZD	0.07	0/516	0.21	0/699
5	ZE	0.08	0/516	0.20	0/699
5	ZF	0.07	0/516	0.21	0/699
5	ZG	0.07	0/516	0.21	0/699
5	ZH	0.07	0/516	0.21	0/699
5	ZI	0.07	0/516	0.20	0/699
5	ZJ	0.07	0/516	0.21	0/699
5	ZK	0.07	0/516	0.21	0/699
5	ZL	0.07	0/516	0.21	0/699
6	PA	0.07	0/5188	0.18	0/7024
6	PB	0.07	0/5188	0.18	0/7024
6	PC	0.07	0/5188	0.18	0/7024
6	PD	0.07	0/5188	0.18	0/7024
6	PE	0.07	0/5188	0.18	0/7024

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	PF	0.07	0/5188	0.18	0/7024
6	PG	0.07	0/5188	0.18	0/7024
6	PH	0.07	0/5188	0.18	0/7024
6	PI	0.07	0/5188	0.18	0/7024
6	PJ	0.07	0/5188	0.18	0/7024
6	PK	0.07	0/5188	0.18	0/7024
6	PL	0.07	0/5188	0.18	0/7024
All	All	0.07	0/211656	0.20	0/287532

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1912	0	1842	17	0
1	AB	1912	0	1843	21	0
1	AC	1912	0	1842	18	0
1	AD	1912	0	1843	18	0
1	AE	1912	0	1842	16	0
1	AF	1912	0	1843	21	0
1	AG	1912	0	1842	18	0
1	AH	1912	0	1843	21	0
1	AI	1912	0	1842	17	0
1	AJ	1912	0	1843	19	0
1	AK	1912	0	1842	18	0
1	AL	1912	0	1843	20	0
2	LA	9341	0	8931	124	0
2	LB	9341	0	8931	132	0
2	LC	9341	0	8931	128	0
2	LD	9341	0	8931	128	0
2	LE	9341	0	8931	125	0
2	LF	9341	0	8931	125	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	SA	3383	0	3269	41	0
3	SB	3383	0	3269	43	0
3	SC	3383	0	3269	37	0
3	SD	3383	0	3269	43	0
3	SE	3383	0	3269	39	0
3	SF	3383	0	3269	38	0
4	TA	2263	0	2258	28	0
4	TB	2263	0	2258	29	0
4	TC	2263	0	2258	25	0
4	TD	2263	0	2258	28	0
4	TE	2263	0	2258	24	0
4	TF	2263	0	2258	29	0
4	TG	2263	0	2258	26	0
4	TH	2263	0	2258	29	0
4	TI	2263	0	2258	27	0
4	TJ	2263	0	2258	32	0
4	TK	2263	0	2258	28	0
4	TL	2263	0	2258	32	0
5	XA	575	0	586	13	0
5	XB	575	0	586	10	0
5	XC	575	0	586	12	0
5	XD	575	0	586	10	0
5	XE	575	0	586	14	0
5	XF	575	0	586	10	0
5	XG	575	0	586	11	0
5	XH	575	0	586	9	0
5	XI	575	0	586	13	0
5	XJ	575	0	586	11	0
5	XK	575	0	586	13	0
5	XL	575	0	586	7	0
5	YA	543	0	563	9	0
5	YB	543	0	563	10	0
5	YC	543	0	563	9	0
5	YD	543	0	563	10	0
5	YE	543	0	563	9	0
5	YF	543	0	563	9	0
5	YG	543	0	563	10	0
5	YH	543	0	563	9	0
5	YI	543	0	563	10	0
5	YJ	543	0	563	9	0
5	YK	543	0	563	10	0
5	YL	543	0	563	8	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	ZA	508	0	528	11	0
5	ZB	508	0	528	5	0
5	ZC	508	0	528	12	0
5	ZD	508	0	528	5	0
5	ZE	508	0	528	10	0
5	ZF	508	0	528	4	0
5	ZG	508	0	528	11	0
5	ZH	508	0	528	3	0
5	ZI	508	0	528	11	0
5	ZJ	508	0	528	4	0
5	ZK	508	0	528	11	0
5	ZL	508	0	528	4	0
6	PA	5094	0	5082	51	0
6	PB	5094	0	5082	54	0
6	PC	5094	0	5082	53	0
6	PD	5094	0	5082	55	0
6	PE	5094	0	5082	50	0
6	PF	5094	0	5082	53	0
6	PG	5094	0	5082	51	0
6	PH	5094	0	5082	53	0
6	PI	5094	0	5082	52	0
6	PJ	5094	0	5082	52	0
6	PK	5094	0	5082	53	0
6	PL	5094	0	5082	55	0
All	All	207084	0	203514	2067	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 5.

All (2067) 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)
2:LA:840:ALA:HA	2:LA:888:GLN:HB3	1.64	0.80
2:LD:840:ALA:HA	2:LD:888:GLN:HB3	1.64	0.80
2:LE:840:ALA:HA	2:LE:888:GLN:HB3	1.64	0.80
6:PA:24:LYS:HE2	6:PA:332:GLY:H	1.48	0.79
2:LB:840:ALA:HA	2:LB:888:GLN:HB3	1.64	0.79
6:PI:24:LYS:HE2	6:PI:332:GLY:H	1.48	0.79
6:PE:24:LYS:HE2	6:PE:332:GLY:H	1.48	0.79
6:PG:24:LYS:HE2	6:PG:332:GLY:H	1.48	0.79
6:PK:24:LYS:HE2	6:PK:332:GLY:H	1.48	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PB:24:LYS:HE2	6:PB:332:GLY:H	1.48	0.78
6:PD:24:LYS:HE2	6:PD:332:GLY:H	1.48	0.78
6:PH:24:LYS:HE2	6:PH:332:GLY:H	1.48	0.78
2:LF:840:ALA:HA	2:LF:888:GLN:HB3	1.64	0.78
6:PF:24:LYS:HE2	6:PF:332:GLY:H	1.48	0.78
6:PJ:24:LYS:HE2	6:PJ:332:GLY:H	1.48	0.78
2:LC:840:ALA:HA	2:LC:888:GLN:HB3	1.64	0.77
6:PL:24:LYS:HE2	6:PL:332:GLY:H	1.48	0.77
6:PC:24:LYS:HE2	6:PC:332:GLY:H	1.48	0.76
2:LF:445:GLU:HG2	2:LF:551:ASP:HB2	1.73	0.70
2:LA:445:GLU:HG2	2:LA:551:ASP:HB2	1.73	0.70
2:LC:445:GLU:HG2	2:LC:551:ASP:HB2	1.73	0.70
2:LD:445:GLU:HG2	2:LD:551:ASP:HB2	1.73	0.70
6:PL:158:ILE:HG22	6:PL:233:PRO:HA	1.75	0.69
6:PA:158:ILE:HG22	6:PA:233:PRO:HA	1.75	0.69
2:LE:445:GLU:HG2	2:LE:551:ASP:HB2	1.73	0.69
6:PD:158:ILE:HG22	6:PD:233:PRO:HA	1.75	0.69
6:PI:158:ILE:HG22	6:PI:233:PRO:HA	1.75	0.69
6:PB:158:ILE:HG22	6:PB:233:PRO:HA	1.75	0.69
6:PK:158:ILE:HG22	6:PK:233:PRO:HA	1.75	0.69
2:LB:445:GLU:HG2	2:LB:551:ASP:HB2	1.73	0.69
6:PC:158:ILE:HG22	6:PC:233:PRO:HA	1.75	0.69
6:PJ:158:ILE:HG22	6:PJ:233:PRO:HA	1.75	0.69
6:PF:158:ILE:HG22	6:PF:233:PRO:HA	1.75	0.68
6:PG:158:ILE:HG22	6:PG:233:PRO:HA	1.75	0.68
6:PH:158:ILE:HG22	6:PH:233:PRO:HA	1.75	0.68
6:PG:194:ARG:NH1	6:PH:110:ASP:OD1	2.27	0.68
6:PE:158:ILE:HG22	6:PE:233:PRO:HA	1.75	0.68
6:PI:194:ARG:NH1	6:PJ:110:ASP:OD1	2.27	0.68
6:PA:194:ARG:NH1	6:PB:110:ASP:OD1	2.27	0.67
6:PC:194:ARG:NH1	6:PD:110:ASP:OD1	2.27	0.67
6:PK:194:ARG:NH1	6:PL:110:ASP:OD1	2.27	0.67
2:LA:526:PRO:HB3	2:LA:530:LEU:HD23	1.77	0.67
6:PC:548:ASP:OD2	6:PF:535:ARG:NH1	2.26	0.67
6:PG:548:ASP:OD2	6:PJ:535:ARG:NH1	2.26	0.67
2:LD:559:TYR:O	2:LD:563:ARG:NH2	2.28	0.67
2:LD:526:PRO:HB3	2:LD:530:LEU:HD23	1.77	0.66
6:PE:194:ARG:NH1	6:PF:110:ASP:OD1	2.27	0.66
3:SE:279:ARG:NH1	3:SE:322:ASN:O	2.29	0.66
2:LB:108:ASP:OD1	2:LB:391:ARG:NH1	2.29	0.66
2:LC:559:TYR:O	2:LC:563:ARG:NH2	2.29	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SD:327:GLN:HG2	3:SD:361:HIS:HB2	1.78	0.66
3:SF:279:ARG:NH1	3:SF:322:ASN:O	2.29	0.66
3:SA:279:ARG:NH1	3:SA:322:ASN:O	2.29	0.66
2:LD:1039:ASN:O	2:LD:1043:ASN:ND2	2.29	0.66
2:LF:526:PRO:HB3	2:LF:530:LEU:HD23	1.77	0.66
3:SB:279:ARG:NH1	3:SB:322:ASN:O	2.29	0.66
2:LA:108:ASP:OD1	2:LA:391:ARG:NH1	2.29	0.65
6:PA:586:GLN:O	6:PA:590:ASN:ND2	2.30	0.65
2:LB:526:PRO:HB3	2:LB:530:LEU:HD23	1.77	0.65
3:SD:279:ARG:NH1	3:SD:322:ASN:O	2.29	0.65
2:LE:526:PRO:HB3	2:LE:530:LEU:HD23	1.77	0.65
2:LC:108:ASP:OD1	2:LC:391:ARG:NH1	2.29	0.65
2:LF:1039:ASN:O	2:LF:1043:ASN:ND2	2.29	0.65
2:LA:1039:ASN:O	2:LA:1043:ASN:ND2	2.29	0.65
3:SC:279:ARG:NH1	3:SC:322:ASN:O	2.29	0.65
3:SA:327:GLN:HG2	3:SA:361:HIS:HB2	1.78	0.65
2:LB:1039:ASN:O	2:LB:1043:ASN:ND2	2.29	0.65
3:SB:327:GLN:HG2	3:SB:361:HIS:HB2	1.78	0.65
2:LE:1039:ASN:O	2:LE:1043:ASN:ND2	2.29	0.65
3:SF:327:GLN:HG2	3:SF:361:HIS:HB2	1.78	0.65
2:LC:526:PRO:HB3	2:LC:530:LEU:HD23	1.78	0.65
2:LD:108:ASP:OD1	2:LD:391:ARG:NH1	2.29	0.65
3:SC:327:GLN:HG2	3:SC:361:HIS:HB2	1.78	0.65
6:PI:548:ASP:OD2	6:PL:535:ARG:NH1	2.26	0.65
2:LC:1039:ASN:O	2:LC:1043:ASN:ND2	2.29	0.65
6:PC:586:GLN:O	6:PC:590:ASN:ND2	2.30	0.65
2:LA:559:TYR:O	2:LA:563:ARG:NH2	2.28	0.64
6:PL:586:GLN:O	6:PL:590:ASN:ND2	2.30	0.64
3:SE:327:GLN:HG2	3:SE:361:HIS:HB2	1.78	0.64
2:LB:559:TYR:O	2:LB:563:ARG:NH2	2.28	0.64
2:LE:108:ASP:OD1	2:LE:391:ARG:NH1	2.29	0.64
2:LF:108:ASP:OD1	2:LF:391:ARG:NH1	2.29	0.64
2:LF:559:TYR:O	2:LF:563:ARG:NH2	2.28	0.64
6:PB:586:GLN:O	6:PB:590:ASN:ND2	2.29	0.64
2:LE:253:ASN:HD21	2:LE:320:LEU:HB2	1.63	0.64
2:LA:253:ASN:HD21	2:LA:320:LEU:HB2	1.63	0.63
2:LE:559:TYR:O	2:LE:563:ARG:NH2	2.28	0.63
6:PE:514:SER:O	6:PE:518:ASN:ND2	2.31	0.63
6:PH:514:SER:O	6:PH:518:ASN:ND2	2.31	0.63
2:LB:1179:GLN:NE2	4:TL:275:SER:OG	2.32	0.63
4:TK:102:ALA:O	4:TK:106:ASN:ND2	2.31	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PA:548:ASP:OD2	6:PD:535:ARG:NH1	2.26	0.63
6:PE:586:GLN:O	6:PE:590:ASN:ND2	2.30	0.63
6:PF:514:SER:O	6:PF:518:ASN:ND2	2.31	0.63
6:PG:514:SER:O	6:PG:518:ASN:ND2	2.31	0.63
2:LA:1179:GLN:NE2	4:TJ:275:SER:OG	2.32	0.63
4:TA:102:ALA:O	4:TA:106:ASN:ND2	2.31	0.63
4:TD:275:SER:OG	2:LD:1179:GLN:NE2	2.32	0.63
4:TF:275:SER:OG	2:LE:1179:GLN:NE2	2.32	0.63
2:LD:253:ASN:HD21	2:LD:320:LEU:HB2	1.63	0.63
6:PG:586:GLN:O	6:PG:590:ASN:ND2	2.30	0.63
6:PJ:586:GLN:O	6:PJ:590:ASN:ND2	2.30	0.63
4:TB:275:SER:OG	2:LC:1179:GLN:NE2	2.32	0.63
4:TJ:59:ARG:O	4:TK:76:ASN:ND2	2.32	0.63
2:LF:253:ASN:HD21	2:LF:320:LEU:HB2	1.63	0.63
4:TF:102:ALA:O	4:TF:106:ASN:ND2	2.31	0.63
6:PA:514:SER:O	6:PA:518:ASN:ND2	2.31	0.63
4:TC:222:ASP:OD1	4:TC:238:LYS:NZ	2.32	0.63
4:TK:222:ASP:OD1	4:TK:238:LYS:NZ	2.32	0.63
6:PC:514:SER:O	6:PC:518:ASN:ND2	2.31	0.63
4:TI:102:ALA:O	4:TI:106:ASN:ND2	2.31	0.63
6:PI:454:SER:HB2	6:PL:451:LEU:HG	1.81	0.63
6:PJ:514:SER:O	6:PJ:518:ASN:ND2	2.31	0.63
6:PA:454:SER:HB2	6:PD:451:LEU:HG	1.81	0.62
6:PB:451:LEU:HG	6:PK:454:SER:HB2	1.81	0.62
6:PI:514:SER:O	6:PI:518:ASN:ND2	2.31	0.62
4:TD:222:ASP:OD1	4:TD:238:LYS:NZ	2.32	0.62
4:TL:222:ASP:OD1	4:TL:238:LYS:NZ	2.32	0.62
6:PB:514:SER:O	6:PB:518:ASN:ND2	2.31	0.62
6:PB:535:ARG:NH1	6:PK:548:ASP:OD2	2.26	0.62
2:LC:253:ASN:HD21	2:LC:320:LEU:HB2	1.63	0.62
4:TG:222:ASP:OD1	4:TG:238:LYS:NZ	2.32	0.62
4:TH:275:SER:OG	2:LF:1179:GLN:NE2	2.32	0.62
1:AI:214:VAL:O	6:PL:414:LYS:NZ	2.28	0.62
6:PD:514:SER:O	6:PD:518:ASN:ND2	2.31	0.62
6:PH:222:GLN:NE2	6:PH:224:GLY:O	2.33	0.62
6:PI:222:GLN:NE2	6:PI:224:GLY:O	2.33	0.62
6:PJ:24:LYS:NZ	6:PJ:331:GLU:OE1	2.32	0.62
6:PG:24:LYS:NZ	6:PG:331:GLU:OE1	2.32	0.62
6:PG:222:GLN:NE2	6:PG:224:GLY:O	2.33	0.62
4:TA:76:ASN:ND2	4:TL:59:ARG:O	2.32	0.62
4:TD:102:ALA:O	4:TD:106:ASN:ND2	2.31	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:TE:59:ARG:NH1	4:TF:72:GLN:OE1	2.32	0.62
6:PD:586:GLN:O	6:PD:590:ASN:ND2	2.30	0.62
6:PE:222:GLN:NE2	6:PE:224:GLY:O	2.33	0.62
6:PJ:222:GLN:NE2	6:PJ:224:GLY:O	2.33	0.62
3:SF:276:ASN:OD1	3:SF:279:ARG:NH2	2.32	0.62
6:PF:222:GLN:NE2	6:PF:224:GLY:O	2.33	0.62
2:LE:738:VAL:HA	2:LE:838:ILE:HB	1.81	0.62
2:LF:738:VAL:HA	2:LF:838:ILE:HB	1.81	0.62
6:PC:222:GLN:NE2	6:PC:224:GLY:O	2.33	0.62
6:PC:454:SER:HB2	6:PF:451:LEU:HG	1.81	0.62
6:PG:454:SER:HB2	6:PJ:451:LEU:HG	1.81	0.62
6:PL:222:GLN:NE2	6:PL:224:GLY:O	2.33	0.62
1:AB:77:ALA:HA	1:AB:91:ILE:HB	1.82	0.62
4:TA:222:ASP:OD1	4:TA:238:LYS:NZ	2.32	0.62
2:LB:253:ASN:HD21	2:LB:320:LEU:HB2	1.63	0.62
3:SC:223:ASN:HB3	3:SC:252:ILE:HG12	1.82	0.62
1:AC:169:ASP:OD2	1:AD:132:ARG:NH2	2.33	0.62
1:AD:77:ALA:HA	1:AD:91:ILE:HB	1.82	0.62
3:SB:223:ASN:HB3	3:SB:252:ILE:HG12	1.82	0.62
4:TC:102:ALA:O	4:TC:106:ASN:ND2	2.31	0.62
1:AE:169:ASP:OD2	1:AF:132:ARG:NH2	2.33	0.62
3:SC:276:ASN:OD1	3:SC:279:ARG:NH2	2.32	0.62
4:TH:222:ASP:OD1	4:TH:238:LYS:NZ	2.32	0.62
6:PH:586:GLN:O	6:PH:590:ASN:ND2	2.29	0.62
1:AG:169:ASP:OD2	1:AH:132:ARG:NH2	2.33	0.62
4:TG:59:ARG:NH1	4:TH:72:GLN:OE1	2.32	0.62
6:PE:548:ASP:OD2	6:PH:535:ARG:NH1	2.26	0.62
6:PK:514:SER:O	6:PK:518:ASN:ND2	2.31	0.62
3:SA:276:ASN:OD1	3:SA:279:ARG:NH2	2.33	0.61
6:PC:24:LYS:NZ	6:PC:331:GLU:OE1	2.32	0.61
6:PI:586:GLN:O	6:PI:590:ASN:ND2	2.30	0.61
3:SA:223:ASN:HB3	3:SA:252:ILE:HG12	1.82	0.61
4:TF:59:ARG:O	4:TG:76:ASN:ND2	2.32	0.61
1:AL:77:ALA:HA	1:AL:91:ILE:HB	1.82	0.61
6:PD:222:GLN:NE2	6:PD:224:GLY:O	2.33	0.61
1:AC:214:VAL:O	6:PF:414:LYS:NZ	2.28	0.61
3:SB:276:ASN:OD1	3:SB:279:ARG:NH2	2.32	0.61
6:PH:24:LYS:NZ	6:PH:331:GLU:OE1	2.32	0.61
1:AE:104:ILE:HD11	1:AE:154:LYS:HB3	1.83	0.61
2:LC:738:VAL:HA	2:LC:838:ILE:HB	1.81	0.61
3:SD:223:ASN:HB3	3:SD:252:ILE:HG12	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:169:ASP:OD2	1:AJ:132:ARG:NH2	2.33	0.61
1:AA:169:ASP:OD2	1:AB:132:ARG:NH2	2.33	0.61
4:TA:59:ARG:NH1	4:TB:72:GLN:OE1	2.32	0.61
4:TE:222:ASP:OD1	4:TE:238:LYS:NZ	2.32	0.61
3:SE:276:ASN:OD1	3:SE:279:ARG:NH2	2.32	0.61
1:AK:104:ILE:HD11	1:AK:154:LYS:HB3	1.83	0.61
6:PE:337:GLU:OE2	6:PH:159:ARG:NH1	2.34	0.61
4:TC:59:ARG:NH1	4:TD:72:GLN:OE1	2.32	0.61
3:SD:276:ASN:OD1	3:SD:279:ARG:NH2	2.33	0.61
1:AK:169:ASP:OD2	1:AL:132:ARG:NH2	2.33	0.61
6:PE:454:SER:HB2	6:PH:451:LEU:HG	1.81	0.61
6:PK:222:GLN:NE2	6:PK:224:GLY:O	2.33	0.61
6:PK:586:GLN:O	6:PK:590:ASN:ND2	2.30	0.61
6:PA:414:LYS:NZ	1:AL:214:VAL:O	2.31	0.61
6:PA:222:GLN:NE2	6:PA:224:GLY:O	2.33	0.61
2:LB:738:VAL:HA	2:LB:838:ILE:HB	1.81	0.61
1:AF:77:ALA:HA	1:AF:91:ILE:HB	1.82	0.61
5:ZE:48:ASN:O	5:ZE:52:ASN:ND2	2.33	0.61
2:LD:738:VAL:HA	2:LD:838:ILE:HB	1.81	0.61
4:TG:102:ALA:O	4:TG:106:ASN:ND2	2.31	0.61
2:LF:849:LYS:NZ	2:LF:850:ASP:OD1	2.34	0.61
2:LA:849:LYS:NZ	2:LA:850:ASP:OD1	2.33	0.61
6:PA:337:GLU:OE2	6:PD:159:ARG:NH1	2.33	0.61
3:SF:223:ASN:HB3	3:SF:252:ILE:HG12	1.82	0.61
6:PC:337:GLU:OE2	6:PF:159:ARG:NH1	2.34	0.61
6:PG:337:GLU:OE2	6:PJ:159:ARG:NH1	2.34	0.61
6:PL:514:SER:O	6:PL:518:ASN:ND2	2.31	0.61
2:LC:521:LEU:HD12	2:LC:571:ARG:HG3	1.83	0.61
2:LE:849:LYS:NZ	2:LE:850:ASP:OD1	2.34	0.61
2:LA:573:LYS:HE3	3:SA:24:ILE:HG23	1.83	0.60
2:LD:39:GLU:HA	3:SD:412:VAL:HA	1.83	0.60
2:LA:681:THR:OG1	2:LA:775:ARG:NH2	2.34	0.60
2:LA:738:VAL:HA	2:LA:838:ILE:HB	1.81	0.60
4:TB:222:ASP:OD1	4:TB:238:LYS:NZ	2.32	0.60
2:LB:681:THR:OG1	2:LB:775:ARG:NH2	2.34	0.60
2:LD:521:LEU:HD12	2:LD:571:ARG:HG3	1.83	0.60
2:LE:521:LEU:HD12	2:LE:571:ARG:HG3	1.83	0.60
4:TJ:102:ALA:O	4:TJ:106:ASN:ND2	2.31	0.60
1:AC:104:ILE:HD11	1:AC:154:LYS:HB3	1.83	0.60
2:LB:573:LYS:HE3	3:SB:24:ILE:HG23	1.83	0.60
1:AH:77:ALA:HA	1:AH:91:ILE:HB	1.82	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:681:THR:OG1	2:LD:775:ARG:NH2	2.34	0.60
2:LD:849:LYS:NZ	2:LD:850:ASP:OD1	2.33	0.60
4:TH:59:ARG:O	4:TI:76:ASN:ND2	2.32	0.60
2:LE:681:THR:OG1	2:LE:775:ARG:NH2	2.34	0.60
3:SE:223:ASN:HB3	3:SE:252:ILE:HG12	1.82	0.60
4:TI:222:ASP:OD1	4:TI:238:LYS:NZ	2.32	0.60
4:TK:59:ARG:NH1	4:TL:72:GLN:OE1	2.32	0.60
6:PB:222:GLN:NE2	6:PB:224:GLY:O	2.33	0.60
2:LA:521:LEU:HD12	2:LA:571:ARG:HG3	1.83	0.60
4:TD:59:ARG:O	4:TE:76:ASN:ND2	2.32	0.60
1:AG:104:ILE:HD11	1:AG:154:LYS:HB3	1.83	0.60
1:AG:214:VAL:O	6:PJ:414:LYS:NZ	2.28	0.60
6:PB:50:VAL:O	6:PB:54:ASN:ND2	2.35	0.60
6:PJ:416:MET:HE1	6:PJ:443:ILE:HD11	1.84	0.60
1:AI:104:ILE:HD11	1:AI:154:LYS:HB3	1.83	0.60
4:TI:59:ARG:NH1	4:TJ:72:GLN:OE1	2.32	0.60
2:LF:521:LEU:HD12	2:LF:571:ARG:HG3	1.83	0.60
5:ZK:48:ASN:O	5:ZK:52:ASN:ND2	2.33	0.60
6:PD:200:VAL:O	6:PD:205:LYS:NZ	2.35	0.60
6:PF:586:GLN:O	6:PF:590:ASN:ND2	2.30	0.60
6:PA:35:ASP:OD2	6:PD:316:ARG:NH2	2.35	0.60
2:LD:573:LYS:HE3	3:SD:24:ILE:HG23	1.83	0.60
4:TH:102:ALA:O	4:TH:106:ASN:ND2	2.31	0.60
1:AJ:77:ALA:HA	1:AJ:91:ILE:HB	1.82	0.60
6:PG:416:MET:HE1	6:PG:443:ILE:HD11	1.84	0.60
6:PI:50:VAL:O	6:PI:54:ASN:ND2	2.35	0.60
2:LB:521:LEU:HD12	2:LB:571:ARG:HG3	1.83	0.60
4:TL:102:ALA:O	4:TL:106:ASN:ND2	2.31	0.60
6:PB:159:ARG:NH1	6:PK:337:GLU:OE2	2.34	0.60
6:PA:50:VAL:O	6:PA:54:ASN:ND2	2.35	0.60
2:LC:39:GLU:HA	3:SC:412:VAL:HA	1.83	0.60
2:LC:1018:VAL:HG13	2:LC:1019:THR:HG23	1.84	0.60
2:LE:573:LYS:HE3	3:SE:24:ILE:HG23	1.83	0.60
6:PB:24:LYS:NZ	6:PB:331:GLU:OE1	2.32	0.60
6:PB:200:VAL:O	6:PB:205:LYS:NZ	2.35	0.60
6:PE:24:LYS:NZ	6:PE:331:GLU:OE1	2.32	0.60
6:PH:416:MET:HE1	6:PH:443:ILE:HD11	1.84	0.60
6:PK:24:LYS:NZ	6:PK:331:GLU:OE1	2.32	0.60
6:PK:200:VAL:O	6:PK:205:LYS:NZ	2.35	0.60
6:PL:50:VAL:O	6:PL:54:ASN:ND2	2.35	0.60
6:PA:24:LYS:NZ	6:PA:331:GLU:OE1	2.32	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:214:VAL:O	6:PH:414:LYS:NZ	2.28	0.60
2:LC:681:THR:OG1	2:LC:775:ARG:NH2	2.34	0.60
1:AJ:214:VAL:O	6:PK:414:LYS:NZ	2.31	0.60
2:LF:39:GLU:HA	3:SF:412:VAL:HA	1.83	0.60
2:LF:681:THR:OG1	2:LF:775:ARG:NH2	2.34	0.60
6:PD:24:LYS:NZ	6:PD:331:GLU:OE1	2.32	0.60
6:PI:200:VAL:O	6:PI:205:LYS:NZ	2.35	0.60
6:PI:337:GLU:OE2	6:PL:159:ARG:NH1	2.34	0.60
6:PI:416:MET:HE1	6:PI:443:ILE:HD11	1.84	0.60
6:PJ:200:VAL:O	6:PJ:205:LYS:NZ	2.35	0.60
4:TF:222:ASP:OD1	4:TF:238:LYS:NZ	2.32	0.60
6:PF:200:VAL:O	6:PF:205:LYS:NZ	2.35	0.60
2:LC:493:ASP:OD1	2:LC:494:ARG:N	2.35	0.59
2:LD:128:ARG:HG2	2:LD:204:ILE:HG22	1.84	0.59
2:LE:128:ARG:HG2	2:LE:204:ILE:HG22	1.84	0.59
6:PE:35:ASP:OD2	6:PH:316:ARG:NH2	2.35	0.59
6:PE:200:VAL:O	6:PE:205:LYS:NZ	2.35	0.59
6:PH:200:VAL:O	6:PH:205:LYS:NZ	2.35	0.59
1:AA:104:ILE:HD11	1:AA:154:LYS:HB3	1.83	0.59
2:LC:573:LYS:HE3	3:SC:24:ILE:HG23	1.83	0.59
6:PB:316:ARG:NH2	6:PK:35:ASP:OD2	2.35	0.59
6:PL:200:VAL:O	6:PL:205:LYS:NZ	2.35	0.59
2:LA:493:ASP:OD1	2:LA:494:ARG:N	2.36	0.59
6:PA:200:VAL:O	6:PA:205:LYS:NZ	2.35	0.59
2:LE:446:SER:HB3	2:LE:488:GLY:HA2	1.85	0.59
6:PC:35:ASP:OD2	6:PF:316:ARG:NH2	2.35	0.59
6:PG:35:ASP:OD2	6:PJ:316:ARG:NH2	2.35	0.59
6:PL:24:LYS:NZ	6:PL:331:GLU:OE1	2.32	0.59
6:PL:416:MET:HE1	6:PL:443:ILE:HD11	1.84	0.59
2:LA:446:SER:HB3	2:LA:488:GLY:HA2	1.84	0.59
5:YB:28:MET:N	5:YB:28:MET:SD	2.76	0.59
2:LB:446:SER:HB3	2:LB:488:GLY:HA2	1.85	0.59
2:LB:493:ASP:OD1	2:LB:494:ARG:N	2.36	0.59
2:LD:446:SER:HB3	2:LD:488:GLY:HA2	1.84	0.59
2:LE:39:GLU:HA	3:SE:412:VAL:HA	1.83	0.59
2:LF:446:SER:HB3	2:LF:488:GLY:HA2	1.84	0.59
5:YL:28:MET:N	5:YL:28:MET:SD	2.76	0.59
6:PE:416:MET:HE1	6:PE:443:ILE:HD11	1.84	0.59
1:AL:58:ASN:HB2	1:AL:148:ASN:HD21	1.68	0.59
6:PJ:50:VAL:O	6:PJ:54:ASN:ND2	2.34	0.59
4:TB:102:ALA:O	4:TB:106:ASN:ND2	2.31	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:TE:102:ALA:O	4:TE:106:ASN:ND2	2.31	0.59
1:AH:58:ASN:HB2	1:AH:148:ASN:HD21	1.68	0.59
6:PC:200:VAL:O	6:PC:205:LYS:NZ	2.35	0.59
2:LC:128:ARG:HG2	2:LC:204:ILE:HG22	1.85	0.59
2:LC:446:SER:HB3	2:LC:488:GLY:HA2	1.85	0.59
2:LC:849:LYS:NZ	2:LC:850:ASP:OD1	2.34	0.59
2:LD:1018:VAL:HG13	2:LD:1019:THR:HG23	1.84	0.59
2:LF:573:LYS:HE3	3:SF:24:ILE:HG23	1.83	0.59
6:PG:467:GLU:HB3	6:PJ:479:VAL:HG12	1.84	0.59
5:YD:28:MET:N	5:YD:28:MET:SD	2.76	0.59
2:LE:852:ASN:OD1	2:LE:854:SER:OG	2.20	0.59
2:LF:493:ASP:OD1	2:LF:494:ARG:N	2.36	0.59
6:PG:200:VAL:O	6:PG:205:LYS:NZ	2.35	0.59
6:PI:35:ASP:OD2	6:PL:316:ARG:NH2	2.35	0.59
6:PI:467:GLU:HB3	6:PL:479:VAL:HG12	1.84	0.59
2:LA:39:GLU:HA	3:SA:412:VAL:HA	1.83	0.59
6:PA:467:GLU:HB3	6:PD:479:VAL:HG12	1.85	0.59
2:LD:466:GLN:NE2	2:LD:477:TYR:O	2.31	0.59
2:LF:1018:VAL:HG13	2:LF:1019:THR:HG23	1.84	0.59
6:PK:416:MET:HE1	6:PK:443:ILE:HD11	1.84	0.59
4:TB:59:ARG:O	4:TC:76:ASN:ND2	2.32	0.59
2:LE:493:ASP:OD1	2:LE:494:ARG:N	2.35	0.59
5:YJ:28:MET:N	5:YJ:28:MET:SD	2.76	0.59
4:TK:59:ARG:O	4:TL:76:ASN:ND2	2.36	0.59
6:PF:416:MET:HE1	6:PF:443:ILE:HD11	1.84	0.59
2:LF:128:ARG:HG2	2:LF:204:ILE:HG22	1.85	0.58
1:AB:214:VAL:O	6:PC:414:LYS:NZ	2.31	0.58
5:ZC:48:ASN:O	5:ZC:52:ASN:ND2	2.33	0.58
4:TJ:222:ASP:OD1	4:TJ:238:LYS:NZ	2.32	0.58
6:PB:479:VAL:HG12	6:PK:467:GLU:HB3	1.84	0.58
6:PC:50:VAL:O	6:PC:54:ASN:ND2	2.35	0.58
6:PC:467:GLU:HB3	6:PF:479:VAL:HG12	1.84	0.58
6:PF:50:VAL:O	6:PF:54:ASN:ND2	2.35	0.58
6:PK:50:VAL:O	6:PK:54:ASN:ND2	2.34	0.58
2:LB:39:GLU:HA	3:SB:412:VAL:HA	1.83	0.58
6:PD:50:VAL:O	6:PD:54:ASN:ND2	2.35	0.58
6:PF:358:ASP:O	6:PF:550:LYS:NZ	2.37	0.58
6:PG:358:ASP:O	6:PG:550:LYS:NZ	2.37	0.58
4:TG:59:ARG:O	4:TH:76:ASN:ND2	2.36	0.58
2:LF:852:ASN:OD1	2:LF:854:SER:OG	2.21	0.58
6:PB:416:MET:HE1	6:PB:443:ILE:HD11	1.84	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PE:50:VAL:O	6:PE:54:ASN:ND2	2.34	0.58
5:XF:65:GLU:OE1	5:XF:65:GLU:N	2.34	0.58
5:YF:28:MET:SD	5:YF:28:MET:N	2.76	0.58
2:LD:493:ASP:OD1	2:LD:494:ARG:N	2.36	0.58
5:ZI:48:ASN:O	5:ZI:52:ASN:ND2	2.33	0.58
6:PC:416:MET:HE1	6:PC:443:ILE:HD11	1.84	0.58
6:PI:24:LYS:NZ	6:PI:331:GLU:OE1	2.32	0.58
5:XF:59:ILE:HD11	5:YF:60:HIS:HB2	1.86	0.58
5:YH:28:MET:N	5:YH:28:MET:SD	2.76	0.58
1:AJ:58:ASN:HB2	1:AJ:148:ASN:HD21	1.68	0.58
2:LF:466:GLN:NE2	2:LF:477:TYR:O	2.31	0.58
6:PG:618:VAL:HG21	6:PH:623:LYS:HE3	1.86	0.58
2:LA:128:ARG:HG2	2:LA:204:ILE:HG22	1.84	0.58
2:LA:1018:VAL:HG13	2:LA:1019:THR:HG23	1.84	0.58
6:PA:416:MET:HE1	6:PA:443:ILE:HD11	1.84	0.58
1:AD:58:ASN:HB2	1:AD:148:ASN:HD21	1.68	0.58
2:LB:1082:MET:HB2	2:LB:1171:SER:HB3	1.86	0.58
6:PD:416:MET:HE1	6:PD:443:ILE:HD11	1.84	0.58
6:PH:50:VAL:O	6:PH:54:ASN:ND2	2.35	0.58
2:LE:1018:VAL:HG13	2:LE:1019:THR:HG23	1.84	0.58
3:SE:156:ASN:HD21	3:SE:160:ASP:HB3	1.69	0.58
5:XJ:65:GLU:OE1	5:XJ:65:GLU:N	2.34	0.58
6:PE:467:GLU:HB3	6:PH:479:VAL:HG12	1.84	0.58
6:PJ:358:ASP:O	6:PJ:550:LYS:NZ	2.37	0.58
6:PL:415:GLY:O	6:PL:434:ASN:ND2	2.37	0.58
2:LA:1082:MET:HB2	2:LA:1171:SER:HB3	1.86	0.58
2:LB:128:ARG:HG2	2:LB:204:ILE:HG22	1.85	0.58
2:LB:1018:VAL:HG13	2:LB:1019:THR:HG23	1.84	0.58
5:XD:59:ILE:HD11	5:YD:60:HIS:HB2	1.86	0.58
2:LE:318:GLY:O	2:LF:162:ARG:NH1	2.37	0.58
6:PH:415:GLY:O	6:PH:434:ASN:ND2	2.37	0.58
6:PK:415:GLY:O	6:PK:434:ASN:ND2	2.37	0.58
1:AB:58:ASN:HB2	1:AB:148:ASN:HD21	1.68	0.57
1:AH:214:VAL:O	6:PI:414:LYS:NZ	2.31	0.57
2:LE:280:GLN:HG3	2:LE:298:GLU:HG2	1.86	0.57
3:SF:156:ASN:HD21	3:SF:160:ASP:HB3	1.69	0.57
6:PE:415:GLY:O	6:PE:434:ASN:ND2	2.37	0.57
6:PG:50:VAL:O	6:PG:54:ASN:ND2	2.35	0.57
6:PG:415:GLY:O	6:PG:434:ASN:ND2	2.37	0.57
1:AD:222:THR:HG21	6:PH:421:ASN:HD21	1.70	0.57
5:ZG:48:ASN:O	5:ZG:52:ASN:ND2	2.33	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PE:358:ASP:O	6:PE:550:LYS:NZ	2.37	0.57
6:PI:415:GLY:O	6:PI:434:ASN:ND2	2.37	0.57
1:AH:222:THR:HG21	6:PL:421:ASN:HD21	1.69	0.57
3:SD:156:ASN:HD21	3:SD:160:ASP:HB3	1.69	0.57
6:PB:415:GLY:O	6:PB:434:ASN:ND2	2.37	0.57
1:AB:222:THR:HG21	6:PF:421:ASN:HD21	1.69	0.57
2:LA:318:GLY:O	2:LB:162:ARG:NH1	2.37	0.57
4:TA:59:ARG:O	4:TB:76:ASN:ND2	2.36	0.57
1:AF:58:ASN:HB2	1:AF:148:ASN:HD21	1.68	0.57
2:LD:318:GLY:O	2:LE:162:ARG:NH1	2.37	0.57
2:LD:1082:MET:HB2	2:LD:1171:SER:HB3	1.86	0.57
5:XL:65:GLU:OE1	5:XL:65:GLU:N	2.34	0.57
6:PI:618:VAL:HG21	6:PJ:623:LYS:HE3	1.86	0.57
6:PJ:415:GLY:O	6:PJ:434:ASN:ND2	2.37	0.57
6:PA:415:GLY:O	6:PA:434:ASN:ND2	2.37	0.57
2:LB:318:GLY:O	2:LC:162:ARG:NH1	2.37	0.57
1:AF:222:THR:HG21	6:PJ:421:ASN:HD21	1.70	0.57
5:XH:59:ILE:HD11	5:YH:60:HIS:HB2	1.86	0.57
2:LF:280:GLN:HG3	2:LF:298:GLU:HG2	1.87	0.57
6:PC:415:GLY:O	6:PC:434:ASN:ND2	2.37	0.57
6:PD:415:GLY:O	6:PD:434:ASN:ND2	2.37	0.57
6:PF:24:LYS:NZ	6:PF:331:GLU:OE1	2.32	0.57
6:PL:330:ILE:HG13	6:PL:331:GLU:HG2	1.87	0.57
2:LD:280:GLN:HG3	2:LD:298:GLU:HG2	1.86	0.57
6:PB:330:ILE:HG13	6:PB:331:GLU:HG2	1.87	0.57
6:PF:415:GLY:O	6:PF:434:ASN:ND2	2.37	0.57
6:PK:330:ILE:HG13	6:PK:331:GLU:HG2	1.87	0.57
3:SA:156:ASN:HD21	3:SA:160:ASP:HB3	1.69	0.57
6:PA:330:ILE:HG13	6:PA:331:GLU:HG2	1.87	0.57
2:LB:466:GLN:NE2	2:LB:477:TYR:O	2.31	0.57
6:PC:618:VAL:HG21	6:PD:623:LYS:HE3	1.86	0.57
6:PE:618:VAL:HG21	6:PF:623:LYS:HE3	1.86	0.57
2:LA:162:ARG:NH1	2:LF:318:GLY:O	2.37	0.57
2:LA:280:GLN:HG3	2:LA:298:GLU:HG2	1.86	0.57
6:PA:358:ASP:O	6:PA:550:LYS:NZ	2.37	0.57
2:LC:1082:MET:HB2	2:LC:1171:SER:HB3	1.86	0.57
2:LE:1082:MET:HB2	2:LE:1171:SER:HB3	1.86	0.57
6:PD:330:ILE:HG13	6:PD:331:GLU:HG2	1.87	0.57
6:PI:330:ILE:HG13	6:PI:331:GLU:HG2	1.87	0.57
6:PA:618:VAL:HG21	6:PB:623:LYS:HE3	1.86	0.57
2:LB:498:VAL:HG11	2:LB:509:GLN:HE22	1.70	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:222:THR:HG21	6:PB:421:ASN:HD21	1.70	0.57
6:PC:330:ILE:HG13	6:PC:331:GLU:HG2	1.87	0.56
2:LA:852:ASN:OD1	2:LA:854:SER:OG	2.20	0.56
3:SC:156:ASN:HD21	3:SC:160:ASP:HB3	1.69	0.56
2:LD:93:ASN:ND2	2:LD:239:HIS:O	2.38	0.56
2:LE:466:GLN:NE2	2:LE:477:TYR:O	2.31	0.56
2:LA:498:VAL:HG11	2:LA:509:GLN:HE22	1.70	0.56
5:XB:59:ILE:HD11	5:YB:60:HIS:HB2	1.86	0.56
5:XB:65:GLU:OE1	5:XB:65:GLU:N	2.34	0.56
5:ZA:48:ASN:O	5:ZA:52:ASN:ND2	2.33	0.56
1:AD:214:VAL:O	6:PE:414:LYS:NZ	2.31	0.56
2:LB:849:LYS:NZ	2:LB:850:ASP:OD1	2.34	0.56
2:LE:245:ASP:OD2	2:LE:539:LYS:NZ	2.37	0.56
2:LE:494:ARG:HG2	2:LE:517:TRP:CD2	2.41	0.56
1:AL:222:THR:HG21	6:PD:421:ASN:HD21	1.70	0.56
2:LF:806:HIS:HB3	2:LF:819:ALA:HB2	1.88	0.56
6:PJ:330:ILE:HG13	6:PJ:331:GLU:HG2	1.87	0.56
6:PK:358:ASP:O	6:PK:550:LYS:NZ	2.37	0.56
6:PK:618:VAL:HG21	6:PL:623:LYS:HE3	1.86	0.56
2:LB:806:HIS:HB3	2:LB:819:ALA:HB2	1.88	0.56
2:LC:318:GLY:O	2:LD:162:ARG:NH1	2.37	0.56
2:LD:494:ARG:HG2	2:LD:517:TRP:CD2	2.40	0.56
6:PD:358:ASP:O	6:PD:550:LYS:NZ	2.37	0.56
6:PI:358:ASP:O	6:PI:550:LYS:NZ	2.37	0.56
2:LA:494:ARG:HG2	2:LA:517:TRP:CD2	2.40	0.56
2:LB:280:GLN:HG3	2:LB:298:GLU:HG2	1.86	0.56
3:SB:156:ASN:HD21	3:SB:160:ASP:HB3	1.69	0.56
2:LC:498:VAL:HG11	2:LC:509:GLN:HE22	1.70	0.56
2:LC:806:HIS:HB3	2:LC:819:ALA:HB2	1.88	0.56
6:PB:358:ASP:O	6:PB:550:LYS:NZ	2.37	0.56
6:PF:330:ILE:HG13	6:PF:331:GLU:HG2	1.87	0.56
2:LA:891:THR:HG21	2:LA:950:TYR:HE1	1.71	0.56
1:AF:214:VAL:O	6:PG:414:LYS:NZ	2.31	0.56
2:LC:93:ASN:ND2	2:LC:239:HIS:O	2.38	0.56
2:LB:93:ASN:ND2	2:LB:239:HIS:O	2.38	0.56
2:LB:891:THR:HG21	2:LB:950:TYR:HE1	1.71	0.56
2:LC:494:ARG:HG2	2:LC:517:TRP:CD2	2.41	0.56
5:XJ:59:ILE:HD11	5:YJ:60:HIS:HB2	1.86	0.56
2:LF:93:ASN:ND2	2:LF:239:HIS:O	2.38	0.56
2:LF:494:ARG:HG2	2:LF:517:TRP:CD2	2.40	0.56
2:LC:280:GLN:HG3	2:LC:298:GLU:HG2	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:498:VAL:HG11	2:LD:509:GLN:HE22	1.70	0.56
2:LE:93:ASN:ND2	2:LE:239:HIS:O	2.38	0.56
6:PG:330:ILE:HG13	6:PG:331:GLU:HG2	1.87	0.56
2:LA:93:ASN:ND2	2:LA:239:HIS:O	2.38	0.56
2:LB:494:ARG:HG2	2:LB:517:TRP:CD2	2.41	0.56
4:TC:50:LYS:HE3	4:TD:43:PRO:HB2	1.88	0.56
2:LC:245:ASP:OD2	2:LC:539:LYS:NZ	2.37	0.56
2:LC:931:VAL:HG23	2:LC:934:SER:HB2	1.87	0.56
6:PL:358:ASP:O	6:PL:550:LYS:NZ	2.37	0.56
2:LB:245:ASP:OD2	2:LB:539:LYS:NZ	2.37	0.56
2:LC:860:MET:HB3	2:LC:914:LYS:HE3	1.88	0.56
4:TE:59:ARG:O	4:TF:76:ASN:ND2	2.36	0.56
2:LE:931:VAL:HG23	2:LE:934:SER:HB2	1.87	0.56
5:XL:59:ILE:HD11	5:YL:60:HIS:HB2	1.86	0.56
5:YA:60:HIS:HA	5:YA:63:LEU:HD23	1.88	0.55
6:PA:19:LYS:N	6:PA:26:GLU:OE1	2.40	0.55
2:LB:931:VAL:HG23	2:LB:934:SER:HB2	1.87	0.55
2:LC:628:TRP:HB2	2:LC:790:MET:HG2	1.88	0.55
2:LD:628:TRP:HB2	2:LD:790:MET:HG2	1.89	0.55
6:PE:330:ILE:HG13	6:PE:331:GLU:HG2	1.87	0.55
6:PF:19:LYS:N	6:PF:26:GLU:OE1	2.40	0.55
6:PH:330:ILE:HG13	6:PH:331:GLU:HG2	1.87	0.55
6:PH:358:ASP:O	6:PH:550:LYS:NZ	2.37	0.55
6:PK:164:GLU:OE1	6:PK:227:THR:OG1	2.21	0.55
2:LA:1156:VAL:O	2:LA:1178:GLY:N	2.40	0.55
6:PA:473:LYS:NZ	6:PD:479:VAL:O	2.36	0.55
5:YC:60:HIS:HA	5:YC:63:LEU:HD23	1.88	0.55
4:TF:59:ARG:NH1	4:TG:72:GLN:OE1	2.37	0.55
4:TI:59:ARG:O	4:TJ:76:ASN:ND2	2.36	0.55
2:LF:891:THR:HG21	2:LF:950:TYR:HE1	1.71	0.55
2:LF:1082:MET:HB2	2:LF:1171:SER:HB3	1.86	0.55
2:LD:806:HIS:HB3	2:LD:819:ALA:HB2	1.88	0.55
5:YI:60:HIS:HA	5:YI:63:LEU:HD23	1.88	0.55
2:LF:931:VAL:HG23	2:LF:934:SER:HB2	1.87	0.55
6:PB:19:LYS:N	6:PB:26:GLU:OE1	2.40	0.55
6:PE:19:LYS:N	6:PE:26:GLU:OE1	2.40	0.55
4:TE:50:LYS:HE3	4:TF:43:PRO:HB2	1.88	0.55
2:LE:628:TRP:HB2	2:LE:790:MET:HG2	1.89	0.55
2:LA:806:HIS:HB3	2:LA:819:ALA:HB2	1.88	0.55
2:LB:860:MET:HB3	2:LB:914:LYS:HE3	1.88	0.55
2:LC:891:THR:HG21	2:LC:950:TYR:HE1	1.71	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:860:MET:HB3	2:LD:914:LYS:HE3	1.88	0.55
2:LD:931:VAL:HG23	2:LD:934:SER:HB2	1.87	0.55
6:PB:344:ILE:O	6:PB:347:THR:OG1	2.25	0.55
6:PE:428:GLY:HA2	6:PF:409:GLN:NE2	2.22	0.55
2:LA:1179:GLN:H	2:LA:1179:GLN:CD	2.15	0.55
4:TA:50:LYS:HE3	4:TB:43:PRO:HB2	1.88	0.55
4:TB:59:ARG:NH1	4:TC:72:GLN:OE1	2.37	0.55
5:XG:66:LEU:HD11	5:YG:66:LEU:HD13	1.88	0.55
2:LE:806:HIS:HB3	2:LE:819:ALA:HB2	1.88	0.55
2:LF:498:VAL:HG11	2:LF:509:GLN:HE22	1.70	0.55
6:PC:19:LYS:N	6:PC:26:GLU:OE1	2.40	0.55
6:PC:358:ASP:OD2	6:PC:519:LYS:NZ	2.40	0.55
6:PD:344:ILE:O	6:PD:347:THR:OG1	2.25	0.55
6:PL:358:ASP:OD2	6:PL:519:LYS:NZ	2.40	0.55
4:TD:59:ARG:NH1	4:TE:72:GLN:OE1	2.37	0.55
2:LE:498:VAL:HG11	2:LE:509:GLN:HE22	1.70	0.55
6:PC:428:GLY:HA2	6:PD:409:GLN:NE2	2.22	0.55
6:PD:19:LYS:N	6:PD:26:GLU:OE1	2.39	0.55
6:PI:358:ASP:OD2	6:PI:519:LYS:NZ	2.40	0.55
6:PL:344:ILE:O	6:PL:347:THR:OG1	2.25	0.55
2:LA:860:MET:HB3	2:LA:914:LYS:HE3	1.88	0.55
5:XC:66:LEU:HD11	5:YC:66:LEU:HD13	1.88	0.55
3:SD:351:ASN:OD1	3:SD:352:ARG:N	2.40	0.55
5:YK:60:HIS:HA	5:YK:63:LEU:HD23	1.88	0.55
6:PG:19:LYS:N	6:PG:26:GLU:OE1	2.40	0.55
6:PH:358:ASP:OD2	6:PH:519:LYS:NZ	2.40	0.55
6:PI:19:LYS:N	6:PI:26:GLU:OE1	2.40	0.55
6:PJ:19:LYS:N	6:PJ:26:GLU:OE1	2.40	0.55
6:PK:358:ASP:OD2	6:PK:519:LYS:NZ	2.40	0.55
6:PL:19:LYS:N	6:PL:26:GLU:OE1	2.39	0.55
2:LA:245:ASP:OD2	2:LA:539:LYS:NZ	2.37	0.55
2:LB:628:TRP:HB2	2:LB:790:MET:HG2	1.89	0.55
3:SB:351:ASN:OD1	3:SB:352:ARG:N	2.40	0.55
5:YG:60:HIS:HA	5:YG:63:LEU:HD23	1.88	0.55
6:PD:358:ASP:OD2	6:PD:519:LYS:NZ	2.40	0.55
6:PF:358:ASP:OD2	6:PF:519:LYS:NZ	2.40	0.55
6:PG:428:GLY:HA2	6:PH:409:GLN:NE2	2.22	0.55
6:PH:164:GLU:OE1	6:PH:227:THR:OG1	2.21	0.55
2:LA:466:GLN:NE2	2:LA:477:TYR:O	2.31	0.54
3:SA:351:ASN:OD1	3:SA:352:ARG:N	2.40	0.54
2:LB:1179:GLN:CD	2:LB:1179:GLN:H	2.15	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LF:628:TRP:HB2	2:LF:790:MET:HG2	1.89	0.54
3:SF:351:ASN:OD1	3:SF:352:ARG:N	2.40	0.54
6:PC:358:ASP:O	6:PC:550:LYS:NZ	2.37	0.54
6:PF:344:ILE:O	6:PF:347:THR:OG1	2.25	0.54
6:PI:428:GLY:HA2	6:PJ:409:GLN:NE2	2.22	0.54
1:AB:104:ILE:HD11	1:AB:154:LYS:HB3	1.90	0.54
2:LA:917:GLN:HA	2:LA:920:THR:HG22	1.90	0.54
1:AC:13:ASN:ND2	3:SB:416:CYS:SG	2.81	0.54
2:LD:891:THR:HG21	2:LD:950:TYR:HE1	1.71	0.54
4:TG:50:LYS:HE3	4:TH:43:PRO:HB2	1.88	0.54
1:AL:104:ILE:HD11	1:AL:154:LYS:HB3	1.90	0.54
6:PE:75:GLN:OE1	6:PE:396:ARG:NH1	2.40	0.54
6:PJ:358:ASP:OD2	6:PJ:519:LYS:NZ	2.40	0.54
6:PK:428:GLY:HA2	6:PL:409:GLN:NE2	2.22	0.54
6:PA:358:ASP:OD2	6:PA:519:LYS:NZ	2.40	0.54
1:AD:104:ILE:HD11	1:AD:154:LYS:HB3	1.90	0.54
1:AE:13:ASN:ND2	3:SC:416:CYS:SG	2.81	0.54
2:LD:245:ASP:OD2	2:LD:539:LYS:NZ	2.37	0.54
2:LE:860:MET:HB3	2:LE:914:LYS:HE3	1.88	0.54
6:PB:358:ASP:OD2	6:PB:519:LYS:NZ	2.40	0.54
1:AA:191:ASN:ND2	1:AL:18:ASN:OD1	2.41	0.54
2:LA:628:TRP:HB2	2:LA:790:MET:HG2	1.89	0.54
3:SC:351:ASN:OD1	3:SC:352:ARG:N	2.40	0.54
2:LD:845:THR:HG22	2:LD:911:VAL:HG21	1.90	0.54
5:XH:65:GLU:OE1	5:XH:65:GLU:N	2.34	0.54
5:XI:66:LEU:HD11	5:YI:66:LEU:HD13	1.88	0.54
6:PE:358:ASP:OD2	6:PE:519:LYS:NZ	2.40	0.54
6:PK:19:LYS:N	6:PK:26:GLU:OE1	2.40	0.54
1:AB:18:ASN:OD1	1:AC:191:ASN:ND2	2.41	0.54
4:TB:268:LYS:NZ	4:TB:274:LEU:O	2.40	0.54
5:XA:66:LEU:HD11	5:YA:66:LEU:HD13	1.88	0.54
6:PA:428:GLY:HA2	6:PB:409:GLN:NE2	2.22	0.54
2:LC:917:GLN:HA	2:LC:920:THR:HG22	1.90	0.54
2:LD:917:GLN:HA	2:LD:920:THR:HG22	1.90	0.54
1:AJ:104:ILE:HD11	1:AJ:154:LYS:HB3	1.90	0.54
2:LE:917:GLN:HA	2:LE:920:THR:HG22	1.90	0.54
1:AK:13:ASN:ND2	3:SF:416:CYS:SG	2.81	0.54
2:LF:801:MET:SD	2:LF:801:MET:N	2.73	0.54
2:LF:917:GLN:HA	2:LF:920:THR:HG22	1.90	0.54
2:LB:852:ASN:OD1	2:LB:854:SER:OG	2.20	0.54
2:LB:1156:VAL:O	2:LB:1178:GLY:N	2.40	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:XE:66:LEU:HD11	5:YE:66:LEU:HD13	1.88	0.54
2:LD:248:ILE:HG21	2:LD:251:MET:HE3	1.90	0.54
1:AJ:18:ASN:OD1	1:AK:191:ASN:ND2	2.41	0.54
2:LE:248:ILE:HG21	2:LE:251:MET:HE3	1.90	0.54
2:LE:1179:GLN:CD	2:LE:1179:GLN:H	2.15	0.54
3:SE:351:ASN:OD1	3:SE:352:ARG:N	2.40	0.54
4:TI:50:LYS:HE3	4:TJ:43:PRO:HB2	1.88	0.54
4:TJ:50:LYS:HE3	4:TK:43:PRO:HB2	1.89	0.54
2:LF:860:MET:HB3	2:LF:914:LYS:HE3	1.88	0.54
3:SF:341:LEU:HA	3:SF:344:LEU:HD13	1.90	0.54
4:TK:50:LYS:HE3	4:TL:43:PRO:HB2	1.88	0.54
6:PD:25:ASN:ND2	6:PD:329:ASP:O	2.36	0.54
6:PG:344:ILE:O	6:PG:347:THR:OG1	2.25	0.54
6:PG:358:ASP:OD2	6:PG:519:LYS:NZ	2.40	0.54
6:PH:19:LYS:N	6:PH:26:GLU:OE1	2.40	0.54
2:LB:917:GLN:HA	2:LB:920:THR:HG22	1.90	0.54
4:TD:50:LYS:HE3	4:TE:43:PRO:HB2	1.89	0.54
2:LC:253:ASN:HA	2:LC:260:PHE:HB2	1.90	0.54
2:LC:466:GLN:NE2	2:LC:477:TYR:O	2.31	0.54
2:LC:845:THR:HG22	2:LC:911:VAL:HG21	1.90	0.54
3:SC:341:LEU:HA	3:SC:344:LEU:HD13	1.90	0.54
4:TH:59:ARG:NH1	4:TI:72:GLN:OE1	2.37	0.54
2:LE:845:THR:HG22	2:LE:911:VAL:HG21	1.90	0.54
1:AA:13:ASN:ND2	3:SA:416:CYS:SG	2.81	0.54
1:AA:214:VAL:O	6:PD:414:LYS:NZ	2.28	0.54
5:XF:73:LEU:HD11	5:ZF:62:LYS:HD2	1.90	0.54
1:AG:13:ASN:ND2	3:SD:416:CYS:SG	2.81	0.54
2:LE:662:HIS:HB2	2:LE:688:VAL:HG21	1.90	0.54
2:LE:891:THR:HG21	2:LE:950:TYR:HE1	1.71	0.54
2:LF:662:HIS:HB2	2:LF:688:VAL:HG21	1.89	0.54
2:LA:931:VAL:HG23	2:LA:934:SER:HB2	1.87	0.54
1:AD:18:ASN:OD1	1:AE:191:ASN:ND2	2.41	0.54
5:YE:60:HIS:HA	5:YE:63:LEU:HD23	1.88	0.54
2:LD:852:ASN:OD1	2:LD:854:SER:OG	2.20	0.54
1:AI:13:ASN:ND2	3:SE:416:CYS:SG	2.81	0.54
6:PC:25:ASN:ND2	6:PC:329:ASP:O	2.36	0.54
2:LA:439:PRO:HB2	2:LA:542:PRO:HA	1.90	0.54
4:TA:251:ASP:OD2	4:TA:255:LYS:NZ	2.41	0.53
4:TB:251:ASP:OD2	4:TB:255:LYS:NZ	2.41	0.53
6:PA:25:ASN:ND2	6:PA:329:ASP:O	2.37	0.53
3:SB:341:LEU:HA	3:SB:344:LEU:HD13	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:TC:251:ASP:OD2	4:TC:255:LYS:NZ	2.41	0.53
4:TD:251:ASP:OD2	4:TD:255:LYS:NZ	2.41	0.53
2:LD:1156:VAL:O	2:LD:1178:GLY:N	2.40	0.53
4:TJ:59:ARG:NH1	4:TK:72:GLN:OE1	2.37	0.53
4:TL:251:ASP:OD2	4:TL:255:LYS:NZ	2.41	0.53
6:PK:25:ASN:ND2	6:PK:329:ASP:O	2.36	0.53
5:XD:73:LEU:HD11	5:ZD:62:LYS:HD2	1.90	0.53
2:LC:439:PRO:HB2	2:LC:542:PRO:HA	1.90	0.53
1:AH:18:ASN:OD1	1:AI:191:ASN:ND2	2.41	0.53
2:LE:275:ALA:O	2:LE:336:GLN:NE2	2.41	0.53
2:LF:1156:VAL:O	2:LF:1178:GLY:N	2.40	0.53
4:TK:251:ASP:OD2	4:TK:255:LYS:NZ	2.41	0.53
6:PF:25:ASN:ND2	6:PF:329:ASP:O	2.36	0.53
4:TC:59:ARG:O	4:TD:76:ASN:ND2	2.36	0.53
5:XH:73:LEU:HD11	5:ZH:62:LYS:HD2	1.90	0.53
2:LE:475:ILE:HD12	2:LE:479:GLY:HA3	1.91	0.53
6:PI:344:ILE:O	6:PI:347:THR:OG1	2.25	0.53
4:TB:50:LYS:HE3	4:TC:43:PRO:HB2	1.90	0.53
2:LB:439:PRO:HB2	2:LB:542:PRO:HA	1.90	0.53
4:TE:251:ASP:OD2	4:TE:255:LYS:NZ	2.41	0.53
2:LD:275:ALA:O	2:LD:336:GLN:NE2	2.41	0.53
4:TH:50:LYS:HE3	4:TI:43:PRO:HB2	1.89	0.53
4:TJ:268:LYS:NZ	4:TJ:274:LEU:O	2.40	0.53
2:LF:248:ILE:HG21	2:LF:251:MET:HE3	1.90	0.53
4:TK:268:LYS:NZ	4:TK:274:LEU:O	2.40	0.53
6:PC:164:GLU:OE1	6:PC:227:THR:OG1	2.21	0.53
3:SA:341:LEU:HA	3:SA:344:LEU:HD13	1.90	0.53
4:TA:72:GLN:OE1	4:TL:59:ARG:NH1	2.37	0.53
6:PA:171:PHE:O	6:PA:219:TYR:N	2.40	0.53
1:AF:104:ILE:HD11	1:AF:154:LYS:HB3	1.90	0.53
1:AH:104:ILE:HD11	1:AH:154:LYS:HB3	1.90	0.53
2:LD:475:ILE:HD12	2:LD:479:GLY:HA3	1.91	0.53
3:SE:341:LEU:HA	3:SE:344:LEU:HD13	1.90	0.53
4:TJ:251:ASP:OD2	4:TJ:255:LYS:NZ	2.41	0.53
2:LF:253:ASN:HA	2:LF:260:PHE:HB2	1.90	0.53
6:PG:25:ASN:ND2	6:PG:329:ASP:O	2.36	0.53
2:LA:253:ASN:HA	2:LA:260:PHE:HB2	1.90	0.53
2:LC:248:ILE:HG21	2:LC:251:MET:HE3	1.90	0.53
2:LE:1156:VAL:O	2:LE:1178:GLY:N	2.40	0.53
6:PC:473:LYS:NZ	6:PF:479:VAL:O	2.35	0.53
2:LB:475:ILE:HD12	2:LB:479:GLY:HA3	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:TF:251:ASP:OD2	4:TF:255:LYS:NZ	2.41	0.53
4:TH:251:ASP:OD2	4:TH:255:LYS:NZ	2.41	0.53
2:LE:253:ASN:HA	2:LE:260:PHE:HB2	1.90	0.53
1:AK:214:VAL:O	6:PB:414:LYS:NZ	2.28	0.53
2:LF:1179:GLN:H	2:LF:1179:GLN:CD	2.15	0.53
4:TL:268:LYS:NZ	4:TL:274:LEU:O	2.40	0.53
6:PH:344:ILE:O	6:PH:347:THR:OG1	2.25	0.53
4:TC:204:GLU:HG3	4:TD:206:ILE:HG23	1.91	0.53
2:LD:499:ASN:HB3	2:LD:514:GLY:HA2	1.91	0.53
5:XJ:73:LEU:HD11	5:ZJ:62:LYS:HD2	1.90	0.53
6:PB:25:ASN:ND2	6:PB:329:ASP:O	2.36	0.53
2:LC:499:ASN:HB3	2:LC:514:GLY:HA2	1.91	0.53
2:LD:1179:GLN:H	2:LD:1179:GLN:CD	2.15	0.53
2:LE:801:MET:SD	2:LE:801:MET:N	2.73	0.53
4:TI:204:GLU:HG3	4:TJ:206:ILE:HG23	1.91	0.53
4:TI:268:LYS:NZ	4:TI:274:LEU:O	2.40	0.53
2:LF:439:PRO:HB2	2:LF:542:PRO:HA	1.90	0.53
6:PH:75:GLN:OE1	6:PH:396:ARG:NH1	2.40	0.53
2:LA:662:HIS:HB2	2:LA:688:VAL:HG21	1.90	0.53
4:TA:43:PRO:HB2	4:TL:50:LYS:HE3	1.89	0.53
4:TA:204:GLU:HG3	4:TB:206:ILE:HG23	1.91	0.53
2:LB:845:THR:HG22	2:LB:911:VAL:HG21	1.90	0.53
2:LC:475:ILE:HD12	2:LC:479:GLY:HA3	1.91	0.53
4:TF:50:LYS:HE3	4:TG:43:PRO:HB2	1.89	0.53
2:LD:662:HIS:HB2	2:LD:688:VAL:HG21	1.90	0.53
2:LF:1138:THR:HG23	2:LF:1141:GLU:HG2	1.91	0.53
5:XK:66:LEU:HD11	5:YK:66:LEU:HD13	1.88	0.53
6:PB:164:GLU:OE1	6:PB:227:THR:OG1	2.21	0.53
6:PK:344:ILE:O	6:PK:347:THR:OG1	2.25	0.53
6:PL:25:ASN:ND2	6:PL:329:ASP:O	2.36	0.53
2:LA:423:ASP:OD1	2:LA:424:LYS:N	2.42	0.52
4:TA:268:LYS:NZ	4:TA:274:LEU:O	2.40	0.52
2:LB:275:ALA:O	2:LB:336:GLN:NE2	2.41	0.52
4:TD:268:LYS:NZ	4:TD:274:LEU:O	2.40	0.52
1:AF:18:ASN:OD1	1:AG:191:ASN:ND2	2.41	0.52
2:LC:423:ASP:OD1	2:LC:424:LYS:N	2.42	0.52
2:LC:662:HIS:HB2	2:LC:688:VAL:HG21	1.89	0.52
2:LF:845:THR:HG22	2:LF:911:VAL:HG21	1.90	0.52
4:TK:204:GLU:HG3	4:TL:206:ILE:HG23	1.91	0.52
6:PB:75:GLN:OE1	6:PB:396:ARG:NH1	2.40	0.52
2:LA:248:ILE:HG21	2:LA:251:MET:HE3	1.90	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:XB:73:LEU:HD11	5:ZB:62:LYS:HD2	1.90	0.52
2:LD:439:PRO:HB2	2:LD:542:PRO:HA	1.90	0.52
3:SD:341:LEU:HA	3:SD:344:LEU:HD13	1.90	0.52
2:LE:1138:THR:HG23	2:LE:1141:GLU:HG2	1.91	0.52
6:PE:25:ASN:ND2	6:PE:329:ASP:O	2.36	0.52
6:PG:164:GLU:OE1	6:PG:227:THR:OG1	2.21	0.52
4:TF:204:GLU:HG3	4:TG:206:ILE:HG23	1.92	0.52
4:TG:251:ASP:OD2	4:TG:255:LYS:NZ	2.41	0.52
4:TI:251:ASP:OD2	4:TI:255:LYS:NZ	2.41	0.52
6:PK:75:GLN:OE1	6:PK:396:ARG:NH1	2.40	0.52
2:LA:475:ILE:HD12	2:LA:479:GLY:HA3	1.91	0.52
2:LA:1138:THR:HG23	2:LA:1141:GLU:HG2	1.92	0.52
2:LB:248:ILE:HG21	2:LB:251:MET:HE3	1.90	0.52
2:LB:253:ASN:HA	2:LB:260:PHE:HB2	1.90	0.52
2:LC:1179:GLN:H	2:LC:1179:GLN:CD	2.15	0.52
2:LD:1138:THR:HG23	2:LD:1141:GLU:HG2	1.92	0.52
4:TH:204:GLU:HG3	4:TI:206:ILE:HG23	1.92	0.52
2:LE:499:ASN:HB3	2:LE:514:GLY:HA2	1.91	0.52
2:LE:622:ALA:HB3	2:LE:634:ARG:HB2	1.92	0.52
6:PG:171:PHE:O	6:PG:219:TYR:N	2.40	0.52
6:PJ:171:PHE:O	6:PJ:219:TYR:N	2.40	0.52
6:PJ:344:ILE:O	6:PJ:347:THR:OG1	2.25	0.52
2:LA:622:ALA:HB3	2:LA:634:ARG:HB2	1.92	0.52
2:LA:845:THR:HG22	2:LA:911:VAL:HG21	1.90	0.52
6:PA:344:ILE:O	6:PA:347:THR:OG1	2.25	0.52
2:LC:1138:THR:HG23	2:LC:1141:GLU:HG2	1.91	0.52
2:LC:1156:VAL:O	2:LC:1178:GLY:N	2.40	0.52
4:TE:204:GLU:HG3	4:TF:206:ILE:HG23	1.91	0.52
2:LD:253:ASN:HA	2:LD:260:PHE:HB2	1.90	0.52
2:LD:660:ILE:HD11	2:LD:663:SER:HB3	1.92	0.52
5:XL:73:LEU:HD11	5:ZL:62:LYS:HD2	1.90	0.52
6:PA:75:GLN:OE1	6:PA:396:ARG:NH1	2.40	0.52
2:LB:499:ASN:HB3	2:LB:514:GLY:HA2	1.91	0.52
2:LB:1138:THR:HG23	2:LB:1141:GLU:HG2	1.91	0.52
4:TD:204:GLU:HG3	4:TE:206:ILE:HG23	1.92	0.52
2:LD:622:ALA:HB3	2:LD:634:ARG:HB2	1.92	0.52
4:TG:204:GLU:HG3	4:TH:206:ILE:HG23	1.91	0.52
2:LF:423:ASP:OD1	2:LF:424:LYS:N	2.42	0.52
4:TB:204:GLU:HG3	4:TC:206:ILE:HG23	1.92	0.52
2:LB:423:ASP:OD1	2:LB:424:LYS:N	2.42	0.52
2:LB:622:ALA:HB3	2:LB:634:ARG:HB2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LB:662:HIS:HB2	2:LB:688:VAL:HG21	1.90	0.52
2:LD:423:ASP:OD1	2:LD:424:LYS:N	2.42	0.52
2:LF:622:ALA:HB3	2:LF:634:ARG:HB2	1.92	0.52
2:LF:1004:ASN:OD1	2:LF:1005:ARG:N	2.42	0.52
2:LA:1004:ASN:OD1	2:LA:1005:ARG:N	2.42	0.52
2:LC:1004:ASN:OD1	2:LC:1005:ARG:N	2.42	0.52
4:TJ:204:GLU:HG3	4:TK:206:ILE:HG23	1.92	0.52
1:AK:49:HIS:O	1:AK:152:GLN:NE2	2.43	0.52
6:PH:25:ASN:ND2	6:PH:329:ASP:O	2.36	0.52
6:PI:171:PHE:O	6:PI:219:TYR:N	2.40	0.52
1:AA:49:HIS:O	1:AA:152:GLN:NE2	2.43	0.52
2:LB:660:ILE:HD11	2:LB:663:SER:HB3	1.92	0.52
2:LB:1004:ASN:OD1	2:LB:1005:ARG:N	2.42	0.52
6:PI:25:ASN:ND2	6:PI:329:ASP:O	2.36	0.52
6:PL:75:GLN:OE1	6:PL:396:ARG:NH1	2.40	0.52
2:LA:660:ILE:HD11	2:LA:663:SER:HB3	1.92	0.52
3:SA:236:TYR:O	3:SA:240:THR:OG1	2.25	0.52
4:TA:206:ILE:HG23	4:TL:204:GLU:HG3	1.92	0.52
4:TA:286:ASP:OD2	2:LC:1177:THR:OG1	2.26	0.52
2:LB:650:GLU:OE1	2:LB:705:ARG:NH2	2.40	0.52
2:LC:622:ALA:HB3	2:LC:634:ARG:HB2	1.92	0.52
2:LC:660:ILE:HD11	2:LC:663:SER:HB3	1.92	0.52
2:LC:852:ASN:OD1	2:LC:854:SER:OG	2.20	0.52
2:LD:650:GLU:OE1	2:LD:705:ARG:NH2	2.40	0.52
4:TG:286:ASP:OD2	2:LF:1177:THR:OG1	2.26	0.52
2:LF:219:ASN:O	4:TL:41:ASN:ND2	2.43	0.52
6:PC:344:ILE:O	6:PC:347:THR:OG1	2.25	0.52
6:PD:171:PHE:O	6:PD:219:TYR:N	2.40	0.52
6:PH:171:PHE:O	6:PH:219:TYR:N	2.40	0.52
5:XG:21:ASN:O	5:XG:42:ARG:NH1	2.43	0.51
2:LE:439:PRO:HB2	2:LE:542:PRO:HA	1.90	0.51
2:LA:275:ALA:O	2:LA:336:GLN:NE2	2.41	0.51
4:TH:268:LYS:NZ	4:TH:274:LEU:O	2.40	0.51
2:LF:499:ASN:HB3	2:LF:514:GLY:HA2	1.91	0.51
6:PJ:25:ASN:ND2	6:PJ:329:ASP:O	2.36	0.51
2:LA:499:ASN:HB3	2:LA:514:GLY:HA2	1.91	0.51
5:XE:21:ASN:O	5:XE:42:ARG:NH1	2.43	0.51
5:YE:56:LEU:HD11	5:ZE:53:MET:HE1	1.93	0.51
6:PB:618:VAL:HG21	6:PK:623:LYS:HE3	1.92	0.51
6:PE:623:LYS:HE3	6:PH:618:VAL:HG21	1.92	0.51
2:LA:219:ASN:O	4:TB:41:ASN:ND2	2.43	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LA:649:ILE:HG12	2:LA:706:VAL:HG22	1.93	0.51
5:XD:65:GLU:OE1	5:XD:65:GLU:N	2.34	0.51
2:LD:219:ASN:O	4:TH:41:ASN:ND2	2.43	0.51
1:AL:43:GLU:OE2	1:AL:181:TYR:OH	2.25	0.51
2:LF:475:ILE:HD12	2:LF:479:GLY:HA3	1.91	0.51
2:LF:660:ILE:HD11	2:LF:663:SER:HB3	1.92	0.51
6:PD:75:GLN:OE1	6:PD:396:ARG:NH1	2.40	0.51
2:LB:649:ILE:HG12	2:LB:706:VAL:HG22	1.93	0.51
3:SC:340:ASP:OD1	3:SC:340:ASP:N	2.44	0.51
2:LE:1004:ASN:OD1	2:LE:1005:ARG:N	2.42	0.51
2:LF:649:ILE:HG12	2:LF:706:VAL:HG22	1.93	0.51
3:SF:150:ASP:HA	3:SF:153:LYS:HE2	1.93	0.51
5:YC:56:LEU:HD11	5:ZC:53:MET:HE1	1.93	0.51
2:LC:219:ASN:O	4:TF:41:ASN:ND2	2.43	0.51
3:SC:150:ASP:HA	3:SC:153:LYS:HE2	1.93	0.51
2:LF:424:LYS:NZ	3:SF:94:ASP:O	2.31	0.51
6:PF:75:GLN:OE1	6:PF:396:ARG:NH1	2.40	0.51
2:LB:887:PHE:O	2:LB:928:GLY:N	2.44	0.51
1:AI:49:HIS:O	1:AI:152:GLN:NE2	2.43	0.51
2:LE:423:ASP:OD1	2:LE:424:LYS:N	2.42	0.51
5:XI:21:ASN:O	5:XI:42:ARG:NH1	2.43	0.51
2:LF:245:ASP:OD2	2:LF:539:LYS:NZ	2.38	0.51
6:PG:623:LYS:HE3	6:PJ:618:VAL:HG21	1.92	0.51
2:LA:734:LYS:HB2	2:LA:789:VAL:HG12	1.93	0.51
1:AC:49:HIS:O	1:AC:152:GLN:NE2	2.43	0.51
5:XC:21:ASN:O	5:XC:42:ARG:NH1	2.43	0.51
2:LE:219:ASN:O	4:TJ:41:ASN:ND2	2.43	0.51
2:LE:649:ILE:HG12	2:LE:706:VAL:HG22	1.93	0.51
6:PL:171:PHE:O	6:PL:219:TYR:N	2.40	0.51
6:PA:623:LYS:HE3	6:PD:618:VAL:HG21	1.92	0.51
2:LB:142:GLN:HB3	2:LB:230:MET:HG2	1.93	0.51
2:LB:219:ASN:O	4:TD:41:ASN:ND2	2.43	0.51
2:LB:734:LYS:HB2	2:LB:789:VAL:HG12	1.93	0.51
2:LC:649:ILE:HG12	2:LC:706:VAL:HG22	1.93	0.51
3:SD:150:ASP:HA	3:SD:153:LYS:HE2	1.93	0.51
3:SD:340:ASP:OD1	3:SD:340:ASP:N	2.44	0.51
2:LE:660:ILE:HD11	2:LE:663:SER:HB3	1.92	0.51
2:LF:610:ASN:O	2:LF:610:ASN:ND2	2.42	0.51
2:LA:995:THR:OG1	2:LA:997:ASP:OD1	2.27	0.51
2:LB:582:TYR:O	2:LB:585:SER:OG	2.24	0.51
1:AE:49:HIS:O	1:AE:152:GLN:NE2	2.43	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SE:150:ASP:HA	3:SE:153:LYS:HE2	1.93	0.51
5:XI:12:ASN:HD21	5:XI:18:GLU:HG2	1.76	0.51
5:XK:12:ASN:HD21	5:XK:18:GLU:HG2	1.76	0.51
6:PI:75:GLN:OE1	6:PI:396:ARG:NH1	2.40	0.51
6:PI:623:LYS:HE3	6:PL:618:VAL:HG21	1.92	0.51
5:XA:21:ASN:O	5:XA:42:ARG:NH1	2.43	0.50
5:XC:73:LEU:HD13	5:ZC:62:LYS:HZ1	1.76	0.50
2:LC:142:GLN:HB3	2:LC:230:MET:HG2	1.93	0.50
1:AG:49:HIS:O	1:AG:152:GLN:NE2	2.43	0.50
2:LD:649:ILE:HG12	2:LD:706:VAL:HG22	1.93	0.50
5:YG:56:LEU:HD11	5:ZG:53:MET:HE1	1.93	0.50
6:PE:171:PHE:O	6:PE:219:TYR:N	2.40	0.50
2:LA:887:PHE:O	2:LA:928:GLY:N	2.44	0.50
2:LC:801:MET:SD	2:LC:801:MET:N	2.73	0.50
3:SD:141:TYR:HB3	3:SD:173:ILE:HG12	1.93	0.50
5:XG:26:ASP:OD1	5:XG:34:TYR:OH	2.28	0.50
6:PC:75:GLN:OE1	6:PC:396:ARG:NH1	2.40	0.50
6:PJ:164:GLU:OE1	6:PJ:227:THR:OG1	2.21	0.50
2:LB:681:THR:OG1	2:LB:682:VAL:N	2.45	0.50
3:SB:239:GLU:OE2	3:SB:266:TRP:NE1	2.38	0.50
2:LD:582:TYR:O	2:LD:585:SER:OG	2.24	0.50
2:LD:610:ASN:O	2:LD:610:ASN:ND2	2.42	0.50
2:LE:681:THR:OG1	2:LE:682:VAL:N	2.45	0.50
2:LE:922:ASN:OD1	2:LE:923:ILE:N	2.44	0.50
6:PD:164:GLU:OE1	6:PD:227:THR:OG1	2.21	0.50
2:LA:142:GLN:HB3	2:LA:230:MET:HG2	1.93	0.50
2:LA:681:THR:OG1	2:LA:682:VAL:N	2.45	0.50
2:LC:143:THR:HG23	2:LC:146:LYS:H	1.76	0.50
2:LD:681:THR:OG1	2:LD:682:VAL:N	2.45	0.50
2:LE:286:LEU:HB2	2:LE:325:ILE:HD11	1.93	0.50
5:XK:21:ASN:O	5:XK:42:ARG:NH1	2.43	0.50
4:TB:297:ALA:HA	2:LD:1042:GLN:HE21	1.77	0.50
2:LB:286:LEU:HB2	2:LB:325:ILE:HD11	1.93	0.50
5:XC:12:ASN:HD21	5:XC:18:GLU:HG2	1.76	0.50
5:XC:26:ASP:OD1	5:XC:34:TYR:OH	2.28	0.50
2:LC:681:THR:OG1	2:LC:682:VAL:N	2.45	0.50
4:TF:297:ALA:HA	2:LF:1042:GLN:HE21	1.77	0.50
3:SD:317:GLU:O	3:SD:322:ASN:ND2	2.45	0.50
6:PE:344:ILE:O	6:PE:347:THR:OG1	2.25	0.50
2:LA:143:THR:HG23	2:LA:146:LYS:H	1.76	0.50
2:LB:1042:GLN:HE21	4:TJ:297:ALA:HA	1.77	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:TD:297:ALA:HA	2:LE:1042:GLN:HE21	1.77	0.50
2:LC:734:LYS:HB2	2:LC:789:VAL:HG12	1.93	0.50
2:LD:1004:ASN:OD1	2:LD:1005:ARG:N	2.42	0.50
5:XG:73:LEU:HD13	5:ZG:62:LYS:HZ1	1.77	0.50
2:LF:143:THR:HG23	2:LF:146:LYS:H	1.76	0.50
6:PC:171:PHE:O	6:PC:219:TYR:N	2.40	0.50
2:LA:848:MET:HA	2:LA:851:VAL:HG22	1.94	0.50
2:LA:1042:GLN:HE21	4:TH:297:ALA:HA	1.77	0.50
3:SA:340:ASP:OD1	3:SA:340:ASP:N	2.44	0.50
5:XA:73:LEU:HD13	5:ZA:62:LYS:HZ1	1.77	0.50
5:YA:56:LEU:HD11	5:ZA:53:MET:HE1	1.93	0.50
2:LB:1105:ARG:NH1	2:LB:1106:PRO:HD2	2.27	0.50
4:TC:268:LYS:NZ	4:TC:274:LEU:O	2.40	0.50
2:LE:610:ASN:O	2:LE:610:ASN:ND2	2.42	0.50
5:XI:26:ASP:OD1	5:XI:34:TYR:OH	2.28	0.50
2:LF:887:PHE:O	2:LF:928:GLY:N	2.44	0.50
5:XK:73:LEU:HD13	5:ZK:62:LYS:HZ1	1.77	0.50
2:LA:922:ASN:OD1	2:LA:923:ILE:N	2.44	0.50
3:SA:150:ASP:HA	3:SA:153:LYS:HE2	1.93	0.50
4:TB:282:ASN:HD21	4:TC:277:PRO:HA	1.77	0.50
2:LB:143:THR:HG23	2:LB:146:LYS:H	1.76	0.50
2:LC:286:LEU:HB2	2:LC:325:ILE:HD11	1.93	0.50
3:SC:317:GLU:O	3:SC:322:ASN:ND2	2.45	0.50
2:LD:38:ARG:HG2	2:LD:40:HIS:CE1	2.47	0.50
2:LD:143:THR:HG23	2:LD:146:LYS:H	1.76	0.50
4:TH:282:ASN:HD21	4:TI:277:PRO:HA	1.77	0.50
2:LE:734:LYS:HB2	2:LE:789:VAL:HG12	1.93	0.50
2:LE:887:PHE:O	2:LE:928:GLY:N	2.44	0.50
5:YI:56:LEU:HD11	5:ZI:53:MET:HE1	1.93	0.50
2:LF:142:GLN:HB3	2:LF:230:MET:HG2	1.93	0.50
2:LF:922:ASN:OD1	2:LF:923:ILE:N	2.44	0.50
6:PC:623:LYS:HE3	6:PF:618:VAL:HG21	1.92	0.50
2:LB:38:ARG:HG2	2:LB:40:HIS:CE1	2.47	0.50
2:LC:275:ALA:O	2:LC:336:GLN:NE2	2.41	0.50
2:LE:848:MET:HA	2:LE:851:VAL:HG22	1.94	0.50
3:SE:317:GLU:O	3:SE:322:ASN:ND2	2.45	0.50
2:LF:734:LYS:HB2	2:LF:789:VAL:HG12	1.93	0.50
6:PK:171:PHE:O	6:PK:219:TYR:N	2.40	0.50
3:SB:150:ASP:HA	3:SB:153:LYS:HE2	1.93	0.49
3:SB:317:GLU:O	3:SB:322:ASN:ND2	2.45	0.49
4:TF:282:ASN:HD21	4:TG:277:PRO:HA	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:142:GLN:HB3	2:LD:230:MET:HG2	1.93	0.49
2:LD:286:LEU:HB2	2:LD:325:ILE:HD11	1.93	0.49
2:LD:922:ASN:OD1	2:LD:923:ILE:N	2.44	0.49
2:LD:1105:ARG:NH1	2:LD:1106:PRO:HD2	2.27	0.49
5:XG:12:ASN:HD21	5:XG:18:GLU:HG2	1.76	0.49
2:LF:38:ARG:HG2	2:LF:40:HIS:CE1	2.47	0.49
2:LA:38:ARG:HG2	2:LA:40:HIS:CE1	2.47	0.49
2:LD:848:MET:HA	2:LD:851:VAL:HG22	1.94	0.49
2:LE:650:GLU:OE1	2:LE:705:ARG:NH2	2.40	0.49
4:TJ:200:LYS:O	4:TJ:203:THR:OG1	2.30	0.49
6:PJ:75:GLN:OE1	6:PJ:396:ARG:NH1	2.40	0.49
2:LA:650:GLU:OE1	2:LA:705:ARG:NH2	2.40	0.49
3:SA:141:TYR:HB3	3:SA:173:ILE:HG12	1.93	0.49
2:LC:1042:GLN:HE21	4:TL:297:ALA:HA	1.77	0.49
6:PC:110:ASP:OD1	6:PF:194:ARG:NH1	2.46	0.49
6:PD:487:VAL:HG22	6:PD:489:ALA:H	1.78	0.49
6:PE:53:TRP:NE1	6:PE:382:GLU:OE1	2.39	0.49
6:PE:110:ASP:OD1	6:PH:194:ARG:NH1	2.45	0.49
2:LA:286:LEU:HB2	2:LA:325:ILE:HD11	1.93	0.49
3:SA:317:GLU:O	3:SA:322:ASN:ND2	2.45	0.49
5:XA:12:ASN:HD21	5:XA:18:GLU:HG2	1.76	0.49
5:XA:26:ASP:OD1	5:XA:34:TYR:OH	2.28	0.49
6:PA:110:ASP:OD1	6:PD:194:ARG:NH1	2.45	0.49
2:LB:891:THR:HG21	2:LB:950:TYR:CE1	2.48	0.49
4:TD:282:ASN:HD21	4:TE:277:PRO:HA	1.77	0.49
3:SD:102:LEU:HB3	3:SD:106:PRO:HB3	1.95	0.49
4:TG:268:LYS:NZ	4:TG:274:LEU:O	2.40	0.49
2:LE:142:GLN:HB3	2:LE:230:MET:HG2	1.93	0.49
3:SF:317:GLU:O	3:SF:322:ASN:ND2	2.45	0.49
6:PB:487:VAL:HG22	6:PB:489:ALA:H	1.78	0.49
6:PF:164:GLU:OE1	6:PF:227:THR:OG1	2.21	0.49
6:PK:487:VAL:HG22	6:PK:489:ALA:H	1.78	0.49
6:PL:487:VAL:HG22	6:PL:489:ALA:H	1.78	0.49
2:LA:891:THR:HG21	2:LA:950:TYR:CE1	2.48	0.49
4:TA:277:PRO:HA	4:TL:282:ASN:HD21	1.77	0.49
6:PA:487:VAL:HG22	6:PA:489:ALA:H	1.78	0.49
2:LB:922:ASN:OD1	2:LB:923:ILE:N	2.44	0.49
2:LC:38:ARG:HG2	2:LC:40:HIS:CE1	2.47	0.49
3:SC:141:TYR:HB3	3:SC:173:ILE:HG12	1.93	0.49
5:XE:73:LEU:HD13	5:ZE:62:LYS:HZ1	1.77	0.49
2:LE:143:THR:HG23	2:LE:146:LYS:H	1.76	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SE:141:TYR:HB3	3:SE:173:ILE:HG12	1.93	0.49
3:SF:102:LEU:HB3	3:SF:106:PRO:HB3	1.95	0.49
4:TK:26:ASP:OD1	4:TK:26:ASP:N	2.46	0.49
5:YK:56:LEU:HD11	5:ZK:53:MET:HE1	1.93	0.49
2:LB:532:HIS:CE1	2:LB:536:GLN:HE21	2.31	0.49
3:SB:141:TYR:HB3	3:SB:173:ILE:HG12	1.93	0.49
5:XE:12:ASN:HD21	5:XE:18:GLU:HG2	1.77	0.49
2:LE:1105:ARG:NH1	2:LE:1106:PRO:HD2	2.27	0.49
4:TJ:282:ASN:HD21	4:TK:277:PRO:HA	1.77	0.49
1:AK:23:THR:OG1	1:AK:28:ASP:O	2.29	0.49
3:SF:141:TYR:HB3	3:SF:173:ILE:HG12	1.93	0.49
4:TL:26:ASP:OD1	4:TL:26:ASP:N	2.46	0.49
6:PB:194:ARG:NH1	6:PK:110:ASP:OD1	2.45	0.49
6:PB:479:VAL:O	6:PK:473:LYS:NZ	2.35	0.49
6:PC:487:VAL:HG22	6:PC:489:ALA:H	1.78	0.49
2:LD:734:LYS:HB2	2:LD:789:VAL:HG12	1.93	0.49
3:SE:102:LEU:HB3	3:SE:106:PRO:HB3	1.95	0.49
3:SE:347:ASP:OD1	3:SE:351:ASN:ND2	2.41	0.49
2:LF:275:ALA:O	2:LF:336:GLN:NE2	2.41	0.49
2:LF:532:HIS:CE1	2:LF:536:GLN:HE21	2.31	0.49
2:LF:848:MET:HA	2:LF:851:VAL:HG22	1.94	0.49
4:TK:200:LYS:O	4:TK:203:THR:OG1	2.30	0.49
6:PF:487:VAL:HG22	6:PF:489:ALA:H	1.78	0.49
6:PI:487:VAL:HG22	6:PI:489:ALA:H	1.78	0.49
6:PJ:487:VAL:HG22	6:PJ:489:ALA:H	1.78	0.49
2:LA:1105:ARG:NH1	2:LA:1106:PRO:HD2	2.27	0.49
2:LB:848:MET:HA	2:LB:851:VAL:HG22	1.94	0.49
2:LC:532:HIS:CE1	2:LC:536:GLN:HE21	2.31	0.49
3:SC:102:LEU:HB3	3:SC:106:PRO:HB3	1.95	0.49
2:LE:532:HIS:CE1	2:LE:536:GLN:HE21	2.31	0.49
4:TI:57:THR:HB	4:TI:67:PHE:HB3	1.95	0.49
6:PC:53:TRP:NE1	6:PC:382:GLU:OE1	2.39	0.49
4:TC:57:THR:HB	4:TC:67:PHE:HB3	1.95	0.49
2:LD:532:HIS:CE1	2:LD:536:GLN:HE21	2.31	0.49
2:LD:887:PHE:O	2:LD:928:GLY:N	2.44	0.49
2:LE:38:ARG:HG2	2:LE:40:HIS:CE1	2.47	0.49
2:LF:286:LEU:HB2	2:LF:325:ILE:HD11	1.93	0.49
2:LF:984:PRO:HD3	2:LF:1068:ALA:HB3	1.95	0.49
6:PF:171:PHE:O	6:PF:219:TYR:N	2.40	0.49
3:SA:347:ASP:OD1	3:SA:351:ASN:ND2	2.41	0.49
4:TB:200:LYS:O	4:TB:203:THR:OG1	2.30	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LC:922:ASN:OD1	2:LC:923:ILE:N	2.44	0.49
2:LC:1105:ARG:NH1	2:LC:1106:PRO:HD2	2.27	0.49
5:YF:10:ILE:HD12	5:YF:11:PRO:HD2	1.95	0.49
1:AI:23:THR:OG1	1:AI:28:ASP:O	2.29	0.49
2:LF:681:THR:OG1	2:LF:682:VAL:N	2.45	0.49
3:SA:102:LEU:HB3	3:SA:106:PRO:HB3	1.95	0.48
2:LB:424:LYS:NZ	3:SB:94:ASP:O	2.31	0.48
2:LB:984:PRO:HD3	2:LB:1068:ALA:HB3	1.95	0.48
1:AE:23:THR:OG1	1:AE:28:ASP:O	2.29	0.48
4:TG:26:ASP:OD1	4:TG:26:ASP:N	2.46	0.48
4:TH:26:ASP:OD1	4:TH:26:ASP:N	2.46	0.48
3:SE:340:ASP:N	3:SE:340:ASP:OD1	2.44	0.48
4:TL:57:THR:HB	4:TL:67:PHE:HB3	1.95	0.48
2:LD:551:ASP:OD1	3:SD:18:ARG:NH1	2.33	0.48
2:LD:1116:THR:HB	2:LD:1157:ILE:HB	1.95	0.48
5:XI:73:LEU:HD13	5:ZI:62:LYS:HZ1	1.77	0.48
1:AL:139:ASN:OD1	5:YK:4:HIS:ND1	2.46	0.48
6:PE:487:VAL:HG22	6:PE:489:ALA:H	1.78	0.48
6:PG:75:GLN:OE1	6:PG:396:ARG:NH1	2.40	0.48
6:PI:110:ASP:OD1	6:PL:194:ARG:NH1	2.46	0.48
4:TB:57:THR:HB	4:TB:67:PHE:HB3	1.95	0.48
5:YB:46:ILE:HD11	5:ZB:43:MET:HE1	1.95	0.48
2:LC:984:PRO:HD3	2:LC:1068:ALA:HB3	1.95	0.48
5:XE:73:LEU:HB3	5:ZE:62:LYS:HZ1	1.78	0.48
2:LD:801:MET:SD	2:LD:801:MET:N	2.73	0.48
2:LE:891:THR:HG21	2:LE:950:TYR:CE1	2.48	0.48
2:LF:279:LEU:HD22	2:LF:332:GLY:HA2	1.96	0.48
2:LF:582:TYR:O	2:LF:585:SER:OG	2.24	0.48
2:LF:650:GLU:OE1	2:LF:705:ARG:NH2	2.40	0.48
5:XK:73:LEU:HB3	5:ZK:62:LYS:HZ1	1.79	0.48
5:YL:46:ILE:HD11	5:ZL:43:MET:HE1	1.95	0.48
6:PE:473:LYS:NZ	6:PH:479:VAL:O	2.35	0.48
6:PG:110:ASP:OD1	6:PJ:194:ARG:NH1	2.45	0.48
6:PG:487:VAL:HG22	6:PG:489:ALA:H	1.78	0.48
6:PH:487:VAL:HG22	6:PH:489:ALA:H	1.78	0.48
2:LA:532:HIS:CE1	2:LA:536:GLN:HE21	2.31	0.48
4:TC:200:LYS:O	4:TC:203:THR:OG1	2.30	0.48
2:LC:1116:THR:HB	2:LC:1157:ILE:HB	1.95	0.48
2:LE:1116:THR:HB	2:LE:1157:ILE:HB	1.95	0.48
4:TJ:57:THR:HB	4:TJ:67:PHE:HB3	1.95	0.48
5:XJ:73:LEU:HD21	5:ZJ:62:LYS:HZ3	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PB:171:PHE:O	6:PB:219:TYR:N	2.40	0.48
2:LA:259:THR:O	2:LB:162:ARG:NH2	2.43	0.48
2:LA:424:LYS:NZ	3:SA:94:ASP:O	2.31	0.48
2:LA:984:PRO:HD3	2:LA:1068:ALA:HB3	1.95	0.48
4:TA:26:ASP:OD1	4:TA:26:ASP:N	2.46	0.48
5:YB:10:ILE:HD12	5:YB:11:PRO:HD2	1.95	0.48
6:PA:164:GLU:OE1	6:PA:227:THR:OG1	2.21	0.48
2:LC:569:LEU:HD23	3:SC:24:ILE:HD11	1.95	0.48
4:TF:57:THR:HB	4:TF:67:PHE:HB3	1.95	0.48
2:LF:891:THR:HG21	2:LF:950:TYR:CE1	2.48	0.48
1:AD:139:ASN:OD1	5:YC:4:HIS:ND1	2.46	0.48
3:SB:102:LEU:HB3	3:SB:106:PRO:HB3	1.95	0.48
4:TD:73:SER:O	4:TD:77:HIS:ND1	2.43	0.48
2:LC:891:THR:HG21	2:LC:950:TYR:CE1	2.48	0.48
2:LE:984:PRO:HD3	2:LE:1068:ALA:HB3	1.95	0.48
2:LF:1105:ARG:NH1	2:LF:1106:PRO:HD2	2.27	0.48
6:PI:164:GLU:OE1	6:PI:227:THR:OG1	2.21	0.48
5:XA:75:GLU:OE2	5:YA:80:HIS:NE2	2.45	0.48
6:PA:599:LYS:HB3	6:PA:601:MET:HE3	1.96	0.48
2:LC:848:MET:HA	2:LC:851:VAL:HG22	1.94	0.48
2:LD:891:THR:HG21	2:LD:950:TYR:CE1	2.48	0.48
2:LD:1082:MET:HE2	2:LD:1162:GLU:HG2	1.96	0.48
3:SE:239:GLU:OE2	3:SE:266:TRP:NE1	2.38	0.48
4:TK:57:THR:HB	4:TK:67:PHE:HB3	1.95	0.48
6:PL:599:LYS:HB3	6:PL:601:MET:HE3	1.96	0.48
4:TA:57:THR:HB	4:TA:67:PHE:HB3	1.95	0.48
2:LB:801:MET:SD	2:LB:801:MET:N	2.73	0.48
4:TC:26:ASP:OD1	4:TC:26:ASP:N	2.46	0.48
4:TD:200:LYS:O	4:TD:203:THR:OG1	2.30	0.48
5:YD:46:ILE:HD11	5:ZD:43:MET:HE1	1.95	0.48
4:TE:268:LYS:NZ	4:TE:274:LEU:O	2.40	0.48
4:TG:57:THR:HB	4:TG:67:PHE:HB3	1.95	0.48
5:YH:10:ILE:HD12	5:YH:11:PRO:HD2	1.95	0.48
2:LE:279:LEU:HD22	2:LE:332:GLY:HA2	1.96	0.48
6:PD:599:LYS:HB3	6:PD:601:MET:HE3	1.96	0.48
6:PI:599:LYS:HB3	6:PI:601:MET:HE3	1.96	0.48
6:PK:599:LYS:HB3	6:PK:601:MET:HE3	1.96	0.48
1:AA:223:GLU:HG3	6:PD:426:ARG:HH12	1.79	0.48
1:AB:139:ASN:OD1	5:YA:4:HIS:ND1	2.46	0.48
1:AC:223:GLU:HG3	6:PF:426:ARG:HH12	1.79	0.48
3:SC:347:ASP:OD1	3:SC:351:ASN:ND2	2.41	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:46:ILE:HD11	5:ZF:43:MET:HE1	1.95	0.48
1:AH:139:ASN:OD1	5:YG:4:HIS:ND1	2.46	0.48
2:LD:984:PRO:HD3	2:LD:1068:ALA:HB3	1.95	0.48
4:TH:57:THR:HB	4:TH:67:PHE:HB3	1.95	0.48
1:AI:223:GLU:HG3	6:PL:426:ARG:HH12	1.79	0.48
5:XI:73:LEU:HB3	5:ZI:62:LYS:HZ1	1.79	0.48
1:AK:223:GLU:HG3	6:PB:426:ARG:HH12	1.79	0.48
5:XL:73:LEU:HD21	5:ZL:62:LYS:HZ3	1.79	0.48
6:PB:599:LYS:HB3	6:PB:601:MET:HE3	1.96	0.48
2:LC:1082:MET:HE2	2:LC:1162:GLU:HG2	1.96	0.48
5:XB:73:LEU:HD21	5:ZB:62:LYS:HZ3	1.79	0.47
2:LB:1116:THR:HB	2:LB:1157:ILE:HB	1.95	0.47
4:TD:26:ASP:OD1	4:TD:26:ASP:N	2.46	0.47
2:LC:650:GLU:OE1	2:LC:705:ARG:NH2	2.40	0.47
4:TE:57:THR:HB	4:TE:67:PHE:HB3	1.95	0.47
4:TF:26:ASP:OD1	4:TF:26:ASP:N	2.46	0.47
2:LE:569:LEU:HD23	3:SE:24:ILE:HD11	1.95	0.47
5:YJ:46:ILE:HD11	5:ZJ:43:MET:HE1	1.95	0.47
5:XA:73:LEU:HB3	5:ZA:62:LYS:HZ1	1.78	0.47
2:LB:569:LEU:HD23	3:SB:24:ILE:HD11	1.95	0.47
4:TD:57:THR:HB	4:TD:67:PHE:HB3	1.95	0.47
3:SC:239:GLU:OE2	3:SC:266:TRP:NE1	2.38	0.47
4:TE:200:LYS:O	4:TE:203:THR:OG1	2.30	0.47
5:YH:46:ILE:HD11	5:ZH:43:MET:HE1	1.95	0.47
2:LF:1116:THR:HB	2:LF:1157:ILE:HB	1.95	0.47
6:PC:599:LYS:HB3	6:PC:601:MET:HE3	1.96	0.47
6:PJ:599:LYS:HB3	6:PJ:601:MET:HE3	1.96	0.47
2:LA:436:LEU:HD11	3:SA:87:SER:HB3	1.97	0.47
2:LB:436:LEU:HD11	3:SB:87:SER:HB3	1.97	0.47
2:LC:114:TYR:HA	2:LC:365:GLN:HA	1.97	0.47
2:LA:279:LEU:HD22	2:LA:332:GLY:HA2	1.96	0.47
5:XC:73:LEU:HB3	5:ZC:62:LYS:HZ1	1.79	0.47
5:XE:26:ASP:OD1	5:XE:34:TYR:OH	2.28	0.47
2:LD:569:LEU:HD23	3:SD:24:ILE:HD11	1.95	0.47
2:LE:1082:MET:HE2	2:LE:1162:GLU:HG2	1.96	0.47
5:YJ:10:ILE:HD12	5:YJ:11:PRO:HD2	1.95	0.47
5:XC:75:GLU:OE2	5:YC:80:HIS:NE2	2.45	0.47
1:AF:139:ASN:OD1	5:YE:4:HIS:ND1	2.46	0.47
2:LC:436:LEU:HD11	3:SC:87:SER:HB3	1.97	0.47
2:LC:927:LEU:HD21	2:LC:930:PHE:CZ	2.50	0.47
4:TF:268:LYS:NZ	4:TF:274:LEU:O	2.40	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:927:LEU:HD21	2:LD:930:PHE:CZ	2.50	0.47
1:AJ:139:ASN:OD1	5:YI:4:HIS:ND1	2.46	0.47
3:SE:328:ILE:HD12	3:SE:345:THR:HG22	1.96	0.47
6:PH:53:TRP:NE1	6:PH:382:GLU:OE1	2.39	0.47
2:LA:569:LEU:HD23	3:SA:24:ILE:HD11	1.95	0.47
5:YD:10:ILE:HD12	5:YD:11:PRO:HD2	1.95	0.47
4:TF:200:LYS:O	4:TF:203:THR:OG1	2.30	0.47
3:SD:128:LEU:HG	3:SD:133:MET:HE3	1.97	0.47
2:LE:927:LEU:HD21	2:LE:930:PHE:CZ	2.49	0.47
3:SE:48:ASP:HB3	3:SE:64:THR:HG21	1.97	0.47
2:LF:436:LEU:HD11	3:SF:87:SER:HB3	1.97	0.47
2:LF:927:LEU:HD21	2:LF:930:PHE:CZ	2.50	0.47
5:YL:10:ILE:HD12	5:YL:11:PRO:HD2	1.95	0.47
2:LB:551:ASP:OD1	3:SB:18:ARG:NH1	2.33	0.47
2:LB:747:HIS:ND1	2:LB:770:SER:OG	2.46	0.47
2:LB:1082:MET:HE2	2:LB:1162:GLU:HG2	1.96	0.47
3:SB:328:ILE:HD12	3:SB:345:THR:HG22	1.96	0.47
1:AG:23:THR:OG1	1:AG:28:ASP:O	2.29	0.47
1:AG:223:GLU:HG3	6:PJ:426:ARG:HH12	1.79	0.47
2:LD:436:LEU:HD11	3:SD:87:SER:HB3	1.97	0.47
2:LE:436:LEU:HD11	3:SE:87:SER:HB3	1.97	0.47
4:TJ:16:LEU:O	4:TK:160:LYS:NZ	2.44	0.47
3:SF:239:GLU:OE2	3:SF:266:TRP:NE1	2.38	0.47
4:TK:261:THR:HG21	4:TL:259:LEU:HD12	1.97	0.47
5:XK:75:GLU:OE2	5:YK:80:HIS:NE2	2.45	0.47
6:PF:599:LYS:HB3	6:PF:601:MET:HE3	1.96	0.47
6:PG:599:LYS:HB3	6:PG:601:MET:HE3	1.96	0.47
4:TA:261:THR:HG21	4:TB:259:LEU:HD12	1.97	0.47
2:LB:927:LEU:HD21	2:LB:930:PHE:CZ	2.50	0.47
2:LC:279:LEU:HD22	2:LC:332:GLY:HA2	1.96	0.47
4:TF:269:THR:HG23	4:TF:270:ILE:HG12	1.97	0.47
3:SF:366:PHE:CZ	3:SF:368:LEU:HB2	2.50	0.47
2:LA:927:LEU:HD21	2:LA:930:PHE:CZ	2.50	0.47
3:SA:366:PHE:CZ	3:SA:368:LEU:HB2	2.50	0.47
4:TA:200:LYS:O	4:TA:203:THR:OG1	2.30	0.47
2:LD:279:LEU:HD22	2:LD:332:GLY:HA2	1.96	0.47
2:LD:935:ASN:OD1	2:LD:935:ASN:N	2.48	0.47
3:SD:328:ILE:HD12	3:SD:345:THR:HG22	1.96	0.47
2:LF:66:VAL:HG12	2:LF:99:VAL:HG22	1.97	0.47
3:SF:328:ILE:HD12	3:SF:345:THR:HG22	1.96	0.47
4:TK:278:ASN:HA	4:TK:281:THR:HG23	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PL:164:GLU:OE1	6:PL:227:THR:OG1	2.21	0.47
1:AA:23:THR:OG1	1:AA:28:ASP:O	2.29	0.47
1:AD:124:ASN:HB3	1:AD:127:SER:HB2	1.97	0.47
1:AE:223:GLU:HG3	6:PH:426:ARG:HH12	1.79	0.47
4:TE:26:ASP:OD1	4:TE:26:ASP:N	2.46	0.47
4:TI:269:THR:HG23	4:TI:270:ILE:HG12	1.97	0.47
4:TL:73:SER:O	4:TL:77:HIS:ND1	2.43	0.47
6:PE:599:LYS:HB3	6:PE:601:MET:HE3	1.96	0.47
2:LA:935:ASN:OD1	2:LA:935:ASN:N	2.48	0.46
4:TB:278:ASN:HA	4:TB:281:THR:HG23	1.97	0.46
2:LB:279:LEU:HD22	2:LB:332:GLY:HA2	1.96	0.46
4:TC:261:THR:HG21	4:TD:259:LEU:HD12	1.97	0.46
4:TC:278:ASN:HA	4:TC:281:THR:HG23	1.97	0.46
2:LC:887:PHE:O	2:LC:928:GLY:N	2.44	0.46
3:SC:366:PHE:CZ	3:SC:368:LEU:HB2	2.50	0.46
3:SD:236:TYR:O	3:SD:240:THR:OG1	2.25	0.46
3:SD:347:ASP:OD1	3:SD:351:ASN:ND2	2.41	0.46
2:LF:569:LEU:HD23	3:SF:24:ILE:HD11	1.95	0.46
2:LF:1082:MET:HE2	2:LF:1162:GLU:HG2	1.96	0.46
4:TL:278:ASN:HA	4:TL:281:THR:HG23	1.97	0.46
6:PH:599:LYS:HB3	6:PH:601:MET:HE3	1.96	0.46
1:AB:124:ASN:HB3	1:AB:127:SER:HB2	1.97	0.46
4:TB:26:ASP:OD1	4:TB:26:ASP:N	2.46	0.46
1:AD:171:PRO:HG2	1:AD:174:LEU:HD23	1.98	0.46
3:SB:366:PHE:CZ	3:SB:368:LEU:HB2	2.50	0.46
1:AF:171:PRO:HG2	1:AF:174:LEU:HD23	1.98	0.46
4:TG:200:LYS:O	4:TG:203:THR:OG1	2.30	0.46
1:AL:124:ASN:HB3	1:AL:127:SER:HB2	1.97	0.46
3:SF:48:ASP:HB3	3:SF:64:THR:HG21	1.97	0.46
2:LA:1082:MET:HE2	2:LA:1162:GLU:HG2	1.96	0.46
2:LA:1116:THR:HB	2:LA:1157:ILE:HB	1.95	0.46
4:TC:73:SER:O	4:TC:77:HIS:ND1	2.43	0.46
4:TE:269:THR:HG23	4:TE:270:ILE:HG12	1.97	0.46
3:SD:48:ASP:HB3	3:SD:64:THR:HG21	1.97	0.46
2:LE:114:TYR:HA	2:LE:365:GLN:HA	1.97	0.46
5:XI:75:GLU:OE2	5:YI:80:HIS:NE2	2.45	0.46
4:TB:261:THR:HG21	4:TC:259:LEU:HD12	1.98	0.46
1:AD:176:PRO:HG3	1:AE:43:GLU:HG3	1.98	0.46
2:LB:114:TYR:HA	2:LB:365:GLN:HA	1.97	0.46
1:AH:124:ASN:HB3	1:AH:127:SER:HB2	1.97	0.46
4:TH:269:THR:HG23	4:TH:270:ILE:HG12	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:124:ASN:HB3	1:AJ:127:SER:HB2	1.98	0.46
2:LE:66:VAL:HG12	2:LE:99:VAL:HG22	1.97	0.46
1:AL:171:PRO:HG2	1:AL:174:LEU:HD23	1.98	0.46
1:AB:171:PRO:HG2	1:AB:174:LEU:HD23	1.98	0.46
4:TA:269:THR:HG23	4:TA:270:ILE:HG12	1.97	0.46
5:YB:55:GLN:OE1	5:YB:55:GLN:N	2.45	0.46
1:AF:124:ASN:HB3	1:AF:127:SER:HB2	1.98	0.46
2:LC:596:GLU:OE2	3:SC:41:THR:N	2.43	0.46
2:LC:995:THR:OG1	2:LC:997:ASP:OD1	2.27	0.46
3:SC:328:ILE:HD12	3:SC:345:THR:HG22	1.96	0.46
2:LE:935:ASN:OD1	2:LE:935:ASN:N	2.48	0.46
3:SE:211:TRP:N	3:SE:312:ASN:OD1	2.44	0.46
4:TI:261:THR:HG21	4:TJ:259:LEU:HD12	1.97	0.46
4:TL:269:THR:HG23	4:TL:270:ILE:HG12	1.97	0.46
3:SD:239:GLU:OE2	3:SD:266:TRP:NE1	2.38	0.46
3:SD:366:PHE:CZ	3:SD:368:LEU:HB2	2.50	0.46
4:TG:269:THR:HG23	4:TG:270:ILE:HG12	1.97	0.46
3:SE:366:PHE:CZ	3:SE:368:LEU:HB2	2.50	0.46
4:TJ:261:THR:HG21	4:TK:259:LEU:HD12	1.98	0.46
2:LF:873:TRP:O	2:LF:877:ASN:ND2	2.27	0.46
3:SF:128:LEU:HG	3:SF:133:MET:HE3	1.97	0.46
2:LA:66:VAL:HG12	2:LA:99:VAL:HG22	1.97	0.46
2:LA:657:LEU:HB3	2:LA:703:LYS:HE2	1.98	0.46
2:LA:801:MET:SD	2:LA:801:MET:N	2.73	0.46
4:TA:259:LEU:HD12	4:TL:261:THR:HG21	1.98	0.46
2:LB:66:VAL:HG12	2:LB:99:VAL:HG22	1.97	0.46
2:LD:114:TYR:HA	2:LD:365:GLN:HA	1.97	0.46
3:SE:128:LEU:HG	3:SE:133:MET:HE3	1.97	0.46
2:LF:422:GLN:HG3	3:SF:97:TRP:HB2	1.98	0.46
4:TK:73:SER:O	4:TK:77:HIS:ND1	2.43	0.46
6:PE:164:GLU:OE1	6:PE:227:THR:OG1	2.21	0.46
3:SA:48:ASP:HB3	3:SA:64:THR:HG21	1.97	0.46
3:SA:328:ILE:HD12	3:SA:345:THR:HG22	1.96	0.46
1:AC:23:THR:OG1	1:AC:28:ASP:O	2.29	0.46
1:AF:176:PRO:HG3	1:AG:43:GLU:HG3	1.98	0.46
2:LC:445:GLU:HB2	2:LC:549:GLN:HA	1.98	0.46
3:SC:367:VAL:HG21	3:SC:377:TRP:CE2	2.51	0.46
4:TH:261:THR:HG21	4:TI:259:LEU:HD12	1.98	0.46
1:AJ:171:PRO:HG2	1:AJ:174:LEU:HD23	1.98	0.46
4:TK:269:THR:HG23	4:TK:270:ILE:HG12	1.97	0.46
6:PB:451:LEU:H	6:PK:454:SER:HB3	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:367:VAL:HG21	3:SA:377:TRP:CE2	2.51	0.46
3:SC:128:LEU:HG	3:SC:133:MET:HE3	1.97	0.46
4:TG:261:THR:HG21	4:TH:259:LEU:HD12	1.97	0.46
4:TH:278:ASN:HA	4:TH:281:THR:HG23	1.97	0.46
2:LE:422:GLN:HG3	3:SE:97:TRP:HB2	1.98	0.46
4:TI:278:ASN:HA	4:TI:281:THR:HG23	1.97	0.46
2:LF:114:TYR:HA	2:LF:365:GLN:HA	1.97	0.46
2:LF:657:LEU:HB3	2:LF:703:LYS:HE2	1.98	0.46
6:PB:156:ARG:HE	6:PB:158:ILE:HD13	1.81	0.46
6:PI:156:ARG:HE	6:PI:158:ILE:HD13	1.81	0.46
6:PI:454:SER:HB3	6:PL:451:LEU:H	1.81	0.46
2:LC:422:GLN:HG3	3:SC:97:TRP:HB2	1.98	0.46
2:LC:935:ASN:OD1	2:LC:935:ASN:N	2.48	0.46
1:AH:171:PRO:HG2	1:AH:174:LEU:HD23	1.98	0.46
2:LD:422:GLN:HG3	3:SD:97:TRP:HB2	1.98	0.46
2:LD:445:GLU:HB2	2:LD:549:GLN:HA	1.98	0.46
5:XG:75:GLU:OE2	5:YG:80:HIS:NE2	2.45	0.46
2:LE:445:GLU:HB2	2:LE:549:GLN:HA	1.98	0.46
3:SF:367:VAL:HG21	3:SF:377:TRP:CE2	2.51	0.46
6:PG:454:SER:HB3	6:PJ:451:LEU:H	1.81	0.46
4:TB:269:THR:HG23	4:TB:270:ILE:HG12	1.97	0.45
2:LB:445:GLU:HB2	2:LB:549:GLN:HA	1.98	0.45
2:LB:657:LEU:HB3	2:LB:703:LYS:HE2	1.98	0.45
4:TC:269:THR:HG23	4:TC:270:ILE:HG12	1.97	0.45
4:TD:261:THR:HG21	4:TE:259:LEU:HD12	1.98	0.45
2:LC:66:VAL:HG12	2:LC:99:VAL:HG22	1.97	0.45
2:LC:259:THR:O	2:LD:162:ARG:NH2	2.43	0.45
1:AH:176:PRO:HG3	1:AI:43:GLU:HG3	1.98	0.45
2:LD:873:TRP:O	2:LD:877:ASN:ND2	2.27	0.45
5:XG:77:GLN:NE2	5:ZG:65:GLU:OE2	2.48	0.45
1:AJ:176:PRO:HG3	1:AK:43:GLU:HG3	1.98	0.45
4:TJ:73:SER:O	4:TJ:77:HIS:ND1	2.43	0.45
4:TJ:278:ASN:HA	4:TJ:281:THR:HG23	1.97	0.45
3:SA:128:LEU:HG	3:SA:133:MET:HE3	1.97	0.45
5:XC:43:MET:HE3	5:XC:46:ILE:HB	1.98	0.45
2:LC:747:HIS:ND1	2:LC:770:SER:OG	2.46	0.45
4:TE:278:ASN:HA	4:TE:281:THR:HG23	1.97	0.45
1:AH:43:GLU:OE2	1:AH:181:TYR:OH	2.25	0.45
3:SD:367:VAL:HG21	3:SD:377:TRP:CE2	2.51	0.45
4:TH:200:LYS:O	4:TH:203:THR:OG1	2.30	0.45
5:XJ:55:GLN:OE1	5:XJ:55:GLN:N	2.43	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LF:445:GLU:HB2	2:LF:549:GLN:HA	1.98	0.45
6:PG:156:ARG:HE	6:PG:158:ILE:HD13	1.81	0.45
2:LA:114:TYR:HA	2:LA:365:GLN:HA	1.97	0.45
2:LA:162:ARG:NH2	2:LF:259:THR:O	2.43	0.45
2:LA:445:GLU:HB2	2:LA:549:GLN:HA	1.98	0.45
3:SB:367:VAL:HG21	3:SB:377:TRP:CE2	2.51	0.45
4:TE:208:MET:HE3	4:TF:209:THR:HG23	1.99	0.45
4:TE:261:THR:HG21	4:TF:259:LEU:HD12	1.97	0.45
4:TF:261:THR:HG21	4:TG:259:LEU:HD12	1.98	0.45
2:LD:66:VAL:HG12	2:LD:99:VAL:HG22	1.97	0.45
3:SF:340:ASP:OD1	3:SF:340:ASP:N	2.44	0.45
6:PJ:156:ARG:HE	6:PJ:158:ILE:HD13	1.81	0.45
6:PL:156:ARG:HE	6:PL:158:ILE:HD13	1.81	0.45
4:TA:278:ASN:HA	4:TA:281:THR:HG23	1.97	0.45
2:LB:995:THR:OG1	2:LB:997:ASP:OD1	2.27	0.45
3:SB:128:LEU:HG	3:SB:133:MET:HE3	1.97	0.45
2:LC:284:ARG:NH1	2:LC:328:ASP:OD1	2.50	0.45
5:XF:55:GLN:OE1	5:XF:55:GLN:N	2.43	0.45
5:XF:73:LEU:HD21	5:ZF:62:LYS:HZ3	1.82	0.45
5:YG:10:ILE:HD12	5:YG:11:PRO:HD2	1.99	0.45
4:TI:73:SER:O	4:TI:77:HIS:ND1	2.43	0.45
4:TI:208:MET:HE3	4:TJ:209:THR:HG23	1.99	0.45
4:TJ:269:THR:HG23	4:TJ:270:ILE:HG12	1.97	0.45
6:PB:53:TRP:NE1	6:PB:382:GLU:OE1	2.39	0.45
6:PD:53:TRP:NE1	6:PD:382:GLU:OE1	2.39	0.45
6:PH:156:ARG:HE	6:PH:158:ILE:HD13	1.81	0.45
6:PK:156:ARG:HE	6:PK:158:ILE:HD13	1.81	0.45
5:YC:10:ILE:HD12	5:YC:11:PRO:HD2	1.99	0.45
2:LC:494:ARG:NH2	2:LC:500:PRO:O	2.40	0.45
3:SC:48:ASP:HB3	3:SC:64:THR:HG21	1.97	0.45
4:TG:208:MET:HE3	4:TH:209:THR:HG23	1.99	0.45
2:LE:259:THR:O	2:LF:162:ARG:NH2	2.43	0.45
2:LE:657:LEU:HB3	2:LE:703:LYS:HE2	1.98	0.45
2:LF:935:ASN:OD1	2:LF:935:ASN:N	2.48	0.45
5:XK:26:ASP:OD1	5:XK:34:TYR:OH	2.28	0.45
6:PF:53:TRP:NE1	6:PF:382:GLU:OE1	2.39	0.45
5:XE:75:GLU:OE2	5:YE:80:HIS:NE2	2.45	0.45
2:LD:284:ARG:NH1	2:LD:328:ASP:OD1	2.50	0.45
6:PI:473:LYS:NZ	6:PL:479:VAL:O	2.35	0.45
2:LA:741:ASN:HD21	2:LA:843:TRP:HB2	1.82	0.45
6:PA:156:ARG:HE	6:PA:158:ILE:HD13	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LC:93:ASN:O	2:LC:240:HIS:ND1	2.50	0.45
2:LC:582:TYR:O	2:LC:585:SER:OG	2.24	0.45
4:TF:278:ASN:HA	4:TF:281:THR:HG23	1.97	0.45
6:PC:156:ARG:HE	6:PC:158:ILE:HD13	1.81	0.45
5:YA:10:ILE:HD12	5:YA:11:PRO:HD2	1.99	0.45
6:PA:454:SER:HB3	6:PD:451:LEU:H	1.82	0.45
3:SB:48:ASP:HB3	3:SB:64:THR:HG21	1.97	0.45
5:XD:73:LEU:HD21	5:ZD:62:LYS:HZ3	1.82	0.45
1:AG:28:ASP:OD1	1:AG:29:ILE:N	2.50	0.45
1:AI:28:ASP:OD1	1:AI:29:ILE:N	2.50	0.45
5:XI:77:GLN:NE2	5:ZI:65:GLU:OE2	2.48	0.45
5:YI:10:ILE:HD12	5:YI:11:PRO:HD2	1.99	0.45
5:XK:77:GLN:NE2	5:ZK:65:GLU:OE2	2.48	0.45
6:PG:432:GLU:OE1	6:PH:414:LYS:HG2	2.17	0.45
2:LB:284:ARG:NH1	2:LB:328:ASP:OD1	2.50	0.45
4:TD:269:THR:HG23	4:TD:270:ILE:HG12	1.97	0.45
2:LE:741:ASN:HD21	2:LE:843:TRP:HB2	1.82	0.45
1:AK:186:TYR:O	1:AK:189:SER:OG	2.29	0.45
5:XL:10:ILE:HD11	5:ZK:41:LEU:HA	1.99	0.45
6:PH:398:MET:HE3	6:PH:451:LEU:HD13	1.99	0.45
1:AA:43:GLU:HG3	1:AL:176:PRO:HG3	1.98	0.45
2:LB:741:ASN:HD21	2:LB:843:TRP:HB2	1.82	0.45
4:TE:211:GLU:HG3	4:TF:213:LYS:HG3	1.99	0.45
4:TH:73:SER:O	4:TH:77:HIS:ND1	2.43	0.45
5:XI:43:MET:HE3	5:XI:46:ILE:HB	1.98	0.45
5:XJ:10:ILE:HD11	5:ZI:41:LEU:HA	1.99	0.45
1:AL:148:ASN:HB2	5:YL:7:PHE:CD2	2.52	0.45
6:PC:432:GLU:OE1	6:PD:414:LYS:HG2	2.17	0.45
6:PE:398:MET:HE3	6:PE:451:LEU:HD13	1.99	0.45
6:PG:398:MET:HE3	6:PG:451:LEU:HD13	1.99	0.45
1:AD:148:ASN:HB2	5:YD:7:PHE:CD2	2.52	0.44
4:TC:208:MET:HE3	4:TD:209:THR:HG23	1.99	0.44
4:TD:278:ASN:HA	4:TD:281:THR:HG23	1.97	0.44
4:TG:278:ASN:HA	4:TG:281:THR:HG23	1.97	0.44
5:XG:43:MET:HE3	5:XG:46:ILE:HB	1.98	0.44
5:XH:10:ILE:HD11	5:ZG:41:LEU:HA	1.99	0.44
2:LE:284:ARG:NH1	2:LE:328:ASP:OD1	2.50	0.44
2:LE:551:ASP:OD1	3:SE:18:ARG:NH1	2.33	0.44
2:LF:143:THR:OG1	2:LF:145:GLU:OE1	2.31	0.44
4:TK:208:MET:HE3	4:TL:209:THR:HG23	1.99	0.44
6:PE:454:SER:HB3	6:PH:451:LEU:H	1.81	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PI:398:MET:HE3	6:PI:451:LEU:HD13	1.99	0.44
1:AB:43:GLU:OE2	1:AB:181:TYR:OH	2.25	0.44
5:XA:43:MET:HE3	5:XA:46:ILE:HB	1.98	0.44
6:PA:432:GLU:OE1	6:PB:414:LYS:HG2	2.17	0.44
5:XF:10:ILE:HD11	5:ZE:41:LEU:HA	1.99	0.44
4:TG:211:GLU:HG3	4:TH:213:LYS:HG3	1.99	0.44
5:XH:55:GLN:OE1	5:XH:55:GLN:N	2.43	0.44
3:SE:367:VAL:HG21	3:SE:377:TRP:CE2	2.51	0.44
2:LF:596:GLU:OE2	3:SF:41:THR:N	2.43	0.44
2:LF:741:ASN:HD21	2:LF:843:TRP:HB2	1.82	0.44
6:PF:156:ARG:HE	6:PF:158:ILE:HD13	1.81	0.44
1:AA:56:ASN:ND2	5:YA:2:SER:O	2.51	0.44
1:AB:176:PRO:HG3	1:AC:43:GLU:HG3	1.98	0.44
4:TA:73:SER:O	4:TA:77:HIS:ND1	2.43	0.44
1:AJ:148:ASN:HB2	5:YJ:7:PHE:CD2	2.52	0.44
1:AK:28:ASP:OD1	1:AK:29:ILE:N	2.50	0.44
6:PC:454:SER:HB3	6:PF:451:LEU:H	1.81	0.44
2:LA:93:ASN:O	2:LA:240:HIS:ND1	2.50	0.44
2:LB:143:THR:OG1	2:LB:145:GLU:OE1	2.31	0.44
2:LB:888:GLN:HE21	2:LB:931:VAL:HG13	1.83	0.44
2:LE:888:GLN:HE21	2:LE:931:VAL:HG13	1.83	0.44
2:LF:894:TRP:HB2	2:LF:947:TRP:HB2	2.00	0.44
6:PJ:398:MET:HE3	6:PJ:451:LEU:HD13	1.99	0.44
2:LA:422:GLN:HG3	3:SA:97:TRP:HB2	1.98	0.44
2:LA:888:GLN:HE21	2:LA:931:VAL:HG13	1.83	0.44
2:LA:894:TRP:HB2	2:LA:947:TRP:HB2	2.00	0.44
2:LB:422:GLN:HG3	3:SB:97:TRP:HB2	1.98	0.44
1:AE:28:ASP:OD1	1:AE:29:ILE:N	2.50	0.44
1:AF:148:ASN:HB2	5:YF:7:PHE:CD2	2.52	0.44
2:LC:551:ASP:OD1	3:SC:18:ARG:NH1	2.33	0.44
1:AH:148:ASN:HB2	5:YH:7:PHE:CD2	2.53	0.44
2:LD:747:HIS:ND1	2:LD:770:SER:OG	2.46	0.44
2:LF:93:ASN:O	2:LF:240:HIS:ND1	2.50	0.44
6:PD:156:ARG:HE	6:PD:158:ILE:HD13	1.81	0.44
6:PE:156:ARG:HE	6:PE:158:ILE:HD13	1.81	0.44
2:LA:284:ARG:NH1	2:LA:328:ASP:OD1	2.50	0.44
2:LA:968:LEU:O	2:LA:969:ASN:ND2	2.51	0.44
2:LB:610:ASN:O	2:LB:610:ASN:ND2	2.42	0.44
3:SB:340:ASP:OD1	3:SB:340:ASP:N	2.44	0.44
2:LC:657:LEU:HB3	2:LC:703:LYS:HE2	1.98	0.44
2:LC:888:GLN:HE21	2:LC:931:VAL:HG13	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:311:ASN:O	2:LD:476:ASN:ND2	2.50	0.44
2:LD:657:LEU:HB3	2:LD:703:LYS:HE2	1.98	0.44
2:LD:888:GLN:HE21	2:LD:931:VAL:HG13	1.83	0.44
6:PE:107:THR:OG1	6:PE:110:ASP:OD2	2.36	0.44
6:PF:398:MET:HE3	6:PF:451:LEU:HD13	1.99	0.44
6:PL:398:MET:HE3	6:PL:451:LEU:HD13	1.99	0.44
2:LB:968:LEU:O	2:LB:969:ASN:ND2	2.51	0.44
2:LC:311:ASN:O	2:LC:476:ASN:ND2	2.50	0.44
2:LD:995:THR:OG1	2:LD:997:ASP:OD1	2.27	0.44
5:XH:73:LEU:HD21	5:ZH:62:LYS:HZ3	1.83	0.44
2:LE:311:ASN:O	2:LE:476:ASN:ND2	2.50	0.44
2:LF:311:ASN:O	2:LF:476:ASN:ND2	2.50	0.44
5:XK:43:MET:HE3	5:XK:46:ILE:HB	1.98	0.44
6:PC:107:THR:OG1	6:PC:110:ASP:OD2	2.36	0.44
6:PI:432:GLU:OE1	6:PJ:414:LYS:HG2	2.17	0.44
6:PK:432:GLU:OE1	6:PL:414:LYS:HG2	2.17	0.44
3:SA:239:GLU:OE2	3:SA:266:TRP:NE1	2.38	0.44
4:TA:208:MET:HE3	4:TB:209:THR:HG23	1.99	0.44
4:TB:73:SER:O	4:TB:77:HIS:ND1	2.43	0.44
4:TC:211:GLU:HG3	4:TD:213:LYS:HG3	1.99	0.44
5:XE:43:MET:HE3	5:XE:46:ILE:HB	1.98	0.44
1:AG:56:ASN:ND2	5:YG:2:SER:O	2.51	0.44
2:LD:968:LEU:O	2:LD:969:ASN:ND2	2.51	0.44
2:LE:894:TRP:HB2	2:LE:947:TRP:HB2	2.00	0.44
2:LF:284:ARG:NH1	2:LF:328:ASP:OD1	2.50	0.44
2:LF:968:LEU:O	2:LF:969:ASN:ND2	2.51	0.44
4:TK:211:GLU:HG3	4:TL:213:LYS:HG3	1.99	0.44
6:PF:107:THR:OG1	6:PF:110:ASP:OD2	2.36	0.44
2:LB:311:ASN:O	2:LB:476:ASN:ND2	2.50	0.44
2:LC:237:GLU:OE1	2:LC:239:HIS:N	2.34	0.44
2:LC:741:ASN:HD21	2:LC:843:TRP:HB2	1.82	0.44
4:TI:200:LYS:O	4:TI:203:THR:OG1	2.30	0.44
5:YK:10:ILE:HD12	5:YK:11:PRO:HD2	1.99	0.44
1:AB:148:ASN:HB2	5:YB:7:PHE:CD2	2.53	0.43
2:LA:311:ASN:O	2:LA:476:ASN:ND2	2.50	0.43
6:PA:454:SER:HB3	6:PD:450:GLU:HA	2.00	0.43
2:LB:237:GLU:OE1	2:LB:239:HIS:N	2.34	0.43
5:YD:55:GLN:OE1	5:YD:55:GLN:N	2.45	0.43
5:YH:55:GLN:OE1	5:YH:55:GLN:N	2.45	0.43
2:LE:747:HIS:ND1	2:LE:770:SER:OG	2.46	0.43
6:PC:454:SER:HB3	6:PF:450:GLU:HA	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PD:107:THR:OG1	6:PD:110:ASP:OD2	2.36	0.43
6:PH:107:THR:OG1	6:PH:110:ASP:OD2	2.36	0.43
6:PH:371:VAL:HB	6:PH:374:ASP:HB3	2.00	0.43
6:PI:371:VAL:HB	6:PI:374:ASP:HB3	2.00	0.43
6:PK:398:MET:HE3	6:PK:451:LEU:HD13	1.99	0.43
1:AF:173:THR:HG23	1:AF:174:LEU:HD22	2.00	0.43
2:LC:92:THR:OG1	2:LC:95:ASP:OD1	2.36	0.43
2:LC:543:LYS:HA	2:LC:590:ILE:HG21	2.00	0.43
1:AG:85:GLU:N	1:AG:85:GLU:OE1	2.51	0.43
4:TG:73:SER:O	4:TG:77:HIS:ND1	2.43	0.43
6:PC:371:VAL:HB	6:PC:374:ASP:HB3	2.00	0.43
6:PG:53:TRP:NE1	6:PG:382:GLU:OE1	2.39	0.43
6:PG:107:THR:OG1	6:PG:110:ASP:OD2	2.36	0.43
5:ZA:73:LEU:O	5:ZA:77:GLN:HG2	2.19	0.43
2:LB:682:VAL:HA	2:LB:685:TRP:NE1	2.34	0.43
1:AE:85:GLU:OE1	1:AE:85:GLU:N	2.51	0.43
2:LE:543:LYS:HA	2:LE:590:ILE:HG21	2.00	0.43
2:LE:968:LEU:O	2:LE:969:ASN:ND2	2.51	0.43
5:ZI:73:LEU:O	5:ZI:77:GLN:HG2	2.19	0.43
1:AK:85:GLU:OE1	1:AK:85:GLU:N	2.51	0.43
2:LF:92:THR:OG1	2:LF:95:ASP:OD1	2.36	0.43
2:LF:543:LYS:HA	2:LF:590:ILE:HG21	2.00	0.43
3:SF:347:ASP:OD1	3:SF:351:ASN:ND2	2.41	0.43
6:PB:371:VAL:HB	6:PB:374:ASP:HB3	2.00	0.43
6:PC:398:MET:HE3	6:PC:451:LEU:HD13	1.99	0.43
6:PE:432:GLU:OE1	6:PF:414:LYS:HG2	2.17	0.43
6:PA:107:THR:OG1	6:PA:110:ASP:OD2	2.36	0.43
2:LC:968:LEU:O	2:LC:969:ASN:ND2	2.51	0.43
2:LD:1125:ILE:HG12	2:LD:1145:PHE:CZ	2.54	0.43
1:AI:56:ASN:ND2	5:YI:2:SER:O	2.51	0.43
1:AI:85:GLU:OE1	1:AI:85:GLU:N	2.52	0.43
1:AA:28:ASP:OD1	1:AA:29:ILE:N	2.50	0.43
4:TA:211:GLU:HG3	4:TB:213:LYS:HG3	1.99	0.43
1:AC:28:ASP:OD1	1:AC:29:ILE:N	2.50	0.43
2:LB:543:LYS:HA	2:LB:590:ILE:HG21	2.00	0.43
2:LB:894:TRP:HB2	2:LB:947:TRP:HB2	2.00	0.43
2:LB:935:ASN:OD1	2:LB:935:ASN:N	2.48	0.43
3:SB:347:ASP:OD1	3:SB:351:ASN:ND2	2.41	0.43
5:XD:10:ILE:HD11	5:ZC:41:LEU:HA	1.99	0.43
2:LC:610:ASN:O	2:LC:610:ASN:ND2	2.42	0.43
5:YE:10:ILE:HD12	5:YE:11:PRO:HD2	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:682:VAL:HA	2:LD:685:TRP:NE1	2.34	0.43
2:LD:741:ASN:HD21	2:LD:843:TRP:HB2	1.82	0.43
5:ZG:73:LEU:O	5:ZG:77:GLN:HG2	2.19	0.43
2:LE:93:ASN:O	2:LE:240:HIS:ND1	2.50	0.43
2:LE:259:THR:HG1	2:LE:316:CYS:C	2.24	0.43
4:TI:211:GLU:HG3	4:TJ:213:LYS:HG3	1.99	0.43
1:AK:56:ASN:ND2	5:YK:2:SER:O	2.51	0.43
2:LF:888:GLN:HE21	2:LF:931:VAL:HG13	1.83	0.43
2:LF:940:TYR:HA	2:LF:950:TYR:HA	2.01	0.43
2:LF:1125:ILE:HG12	2:LF:1145:PHE:CZ	2.54	0.43
1:AA:85:GLU:N	1:AA:85:GLU:OE1	2.51	0.43
2:LA:551:ASP:OD1	3:SA:18:ARG:NH1	2.33	0.43
2:LB:93:ASN:O	2:LB:240:HIS:ND1	2.50	0.43
5:ZC:73:LEU:O	5:ZC:77:GLN:HG2	2.19	0.43
2:LE:1125:ILE:HG12	2:LE:1145:PHE:CZ	2.54	0.43
3:SF:320:PHE:HA	3:SF:355:TYR:CZ	2.54	0.43
6:PB:398:MET:HE3	6:PB:451:LEU:HD13	1.99	0.43
6:PF:371:VAL:HB	6:PF:374:ASP:HB3	2.00	0.43
2:LA:259:THR:HG1	2:LA:316:CYS:C	2.24	0.43
2:LA:747:HIS:ND1	2:LA:770:SER:OG	2.46	0.43
3:SB:87:SER:O	3:SB:90:LYS:NZ	2.47	0.43
1:AE:56:ASN:ND2	5:YE:2:SER:O	2.50	0.43
2:LC:682:VAL:HA	2:LC:685:TRP:NE1	2.34	0.43
3:SD:211:TRP:N	3:SD:312:ASN:OD1	2.44	0.43
3:SE:320:PHE:HA	3:SE:355:TYR:CZ	2.54	0.43
6:PD:357:PRO:HG2	6:PD:522:ALA:HB1	2.01	0.43
6:PD:398:MET:HE3	6:PD:451:LEU:HD13	1.99	0.43
6:PK:371:VAL:HB	6:PK:374:ASP:HB3	2.00	0.43
6:PL:107:THR:OG1	6:PL:110:ASP:OD2	2.36	0.43
1:AB:173:THR:HG23	1:AB:174:LEU:HD22	2.00	0.43
2:LA:237:GLU:OE1	2:LA:239:HIS:N	2.34	0.43
2:LA:873:TRP:O	2:LA:877:ASN:ND2	2.27	0.43
6:PA:398:MET:HE3	6:PA:451:LEU:HD13	1.99	0.43
1:AD:173:THR:HG23	1:AD:174:LEU:HD22	2.00	0.43
2:LC:1125:ILE:HG12	2:LC:1145:PHE:CZ	2.54	0.43
5:ZE:73:LEU:O	5:ZE:77:GLN:HG2	2.19	0.43
3:SE:8:PRO:HB2	3:SE:45:MET:HE2	2.01	0.43
3:SE:196:GLN:HG3	3:SE:202:LEU:HD11	2.01	0.43
4:TJ:26:ASP:OD1	4:TJ:26:ASP:N	2.46	0.43
1:AL:173:THR:HG23	1:AL:174:LEU:HD22	2.00	0.43
6:PE:454:SER:HB3	6:PH:450:GLU:HA	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PJ:371:VAL:HB	6:PJ:374:ASP:HB3	2.00	0.43
1:AA:132:ARG:HB2	1:AA:135:VAL:HB	2.01	0.43
1:AF:87:LYS:HE3	2:LC:15:SER:HB3	2.01	0.43
2:LE:749:THR:OG1	2:LE:750:ASP:N	2.52	0.43
2:LE:940:TYR:HA	2:LE:950:TYR:HA	2.01	0.43
6:PB:450:GLU:HA	6:PK:454:SER:HB3	2.00	0.43
6:PJ:107:THR:OG1	6:PJ:110:ASP:OD2	2.36	0.43
2:LA:682:VAL:HA	2:LA:685:TRP:NE1	2.34	0.43
2:LA:1125:ILE:HG12	2:LA:1145:PHE:CZ	2.54	0.43
5:XB:10:ILE:HD11	5:ZA:41:LEU:HA	1.99	0.43
1:AC:85:GLU:OE1	1:AC:85:GLU:N	2.52	0.43
1:AC:132:ARG:HB2	1:AC:135:VAL:HB	2.01	0.43
2:LB:1125:ILE:HG12	2:LB:1145:PHE:CZ	2.54	0.43
2:LC:894:TRP:HB2	2:LC:947:TRP:HB2	2.00	0.43
3:SD:8:PRO:HB2	3:SD:45:MET:HE2	2.01	0.43
5:XH:43:MET:N	5:XH:44:PRO:HD2	2.34	0.43
2:LE:991:ARG:HD2	2:LE:1077:GLN:HB3	2.01	0.43
2:LF:991:ARG:HD2	2:LF:1077:GLN:HB3	2.01	0.43
5:ZK:73:LEU:O	5:ZK:77:GLN:HG2	2.19	0.43
6:PB:107:THR:OG1	6:PB:110:ASP:OD2	2.36	0.43
6:PG:371:VAL:HB	6:PG:374:ASP:HB3	2.01	0.43
6:PK:107:THR:OG1	6:PK:110:ASP:OD2	2.36	0.43
6:PL:53:TRP:NE1	6:PL:382:GLU:OE1	2.39	0.43
2:LA:582:TYR:O	2:LA:585:SER:OG	2.24	0.42
2:LA:610:ASN:O	2:LA:610:ASN:ND2	2.42	0.42
6:PA:371:VAL:HB	6:PA:374:ASP:HB3	2.00	0.42
3:SB:405:ARG:NE	3:SB:406:ASP:OD1	2.48	0.42
5:XE:77:GLN:NE2	5:ZE:65:GLU:OE2	2.48	0.42
2:LD:543:LYS:HA	2:LD:590:ILE:HG21	2.00	0.42
4:TH:213:LYS:HE2	4:TH:213:LYS:HB3	1.88	0.42
1:AI:128:LEU:HD23	1:AI:136:LEU:HD11	2.01	0.42
2:LE:582:TYR:O	2:LE:585:SER:OG	2.24	0.42
1:AK:128:LEU:HD23	1:AK:136:LEU:HD11	2.02	0.42
2:LF:747:HIS:ND1	2:LF:770:SER:OG	2.46	0.42
3:SF:8:PRO:HB2	3:SF:45:MET:HE2	2.01	0.42
3:SF:137:ASN:O	3:SF:205:GLN:N	2.52	0.42
5:XL:43:MET:N	5:XL:44:PRO:HD2	2.34	0.42
6:PE:371:VAL:HB	6:PE:374:ASP:HB3	2.00	0.42
6:PI:107:THR:OG1	6:PI:110:ASP:OD2	2.36	0.42
6:PL:371:VAL:HB	6:PL:374:ASP:HB3	2.00	0.42
1:AA:128:LEU:HD23	1:AA:136:LEU:HD11	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LA:940:TYR:HA	2:LA:950:TYR:HA	2.01	0.42
3:SA:320:PHE:HA	3:SA:355:TYR:CZ	2.54	0.42
5:XB:43:MET:N	5:XB:44:PRO:HD2	2.34	0.42
2:LB:51:THR:O	2:LB:368:TYR:OH	2.35	0.42
1:AE:132:ARG:HB2	1:AE:135:VAL:HB	2.01	0.42
2:LC:991:ARG:HD2	2:LC:1077:GLN:HB3	2.01	0.42
5:XE:9:THR:OG1	5:XE:10:ILE:N	2.51	0.42
1:AG:128:LEU:HD23	1:AG:136:LEU:HD11	2.01	0.42
1:AK:132:ARG:HB2	1:AK:135:VAL:HB	2.01	0.42
6:PD:371:VAL:HB	6:PD:374:ASP:HB3	2.00	0.42
6:PK:53:TRP:NE1	6:PK:382:GLU:OE1	2.39	0.42
2:LA:543:LYS:HA	2:LA:590:ILE:HG21	2.00	0.42
3:SA:137:ASN:O	3:SA:205:GLN:N	2.52	0.42
1:AD:87:LYS:HE3	2:LB:15:SER:HB3	2.01	0.42
2:LB:886:TRP:HE3	2:LB:928:GLY:HA2	1.84	0.42
5:XC:77:GLN:NE2	5:ZC:65:GLU:OE2	2.48	0.42
2:LC:737:LEU:O	2:LC:838:ILE:N	2.51	0.42
3:SC:8:PRO:HB2	3:SC:45:MET:HE2	2.01	0.42
1:AH:173:THR:HG23	1:AH:174:LEU:HD22	2.00	0.42
2:LD:894:TRP:HB2	2:LD:947:TRP:HB2	2.00	0.42
2:LE:494:ARG:NH2	2:LE:500:PRO:O	2.40	0.42
2:LE:596:GLU:OE2	3:SE:41:THR:N	2.43	0.42
2:LE:682:VAL:HA	2:LE:685:TRP:NE1	2.34	0.42
2:LF:710:TYR:O	2:LF:711:GLN:HG3	2.19	0.42
2:LA:710:TYR:O	2:LA:711:GLN:HG3	2.19	0.42
2:LA:886:TRP:HE3	2:LA:928:GLY:HA2	1.84	0.42
3:SA:8:PRO:HB2	3:SA:45:MET:HE2	2.01	0.42
5:XA:9:THR:OG1	5:XA:10:ILE:N	2.51	0.42
2:LB:1050:LEU:HG	2:LB:1075:VAL:HG23	2.02	0.42
3:SB:8:PRO:HB2	3:SB:45:MET:HE2	2.01	0.42
3:SB:137:ASN:O	3:SB:205:GLN:N	2.52	0.42
2:LC:873:TRP:O	2:LC:877:ASN:ND2	2.27	0.42
5:XF:43:MET:N	5:XF:44:PRO:HD2	2.34	0.42
2:LD:1089:LYS:HE2	2:LD:1089:LYS:HB2	1.90	0.42
3:SE:137:ASN:O	3:SE:205:GLN:N	2.52	0.42
2:LF:259:THR:HG1	2:LF:316:CYS:C	2.24	0.42
6:PE:357:PRO:HG2	6:PE:522:ALA:HB1	2.01	0.42
6:PF:268:PHE:HE1	6:PF:323:GLU:HG3	1.85	0.42
6:PI:479:VAL:HG12	6:PJ:467:GLU:HB3	2.01	0.42
6:PK:357:PRO:HG2	6:PK:522:ALA:HB1	2.01	0.42
5:XA:77:GLN:NE2	5:ZA:65:GLU:OE2	2.48	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:XB:52:ASN:ND2	5:YB:53:MET:SD	2.93	0.42
2:LB:749:THR:OG1	2:LB:750:ASP:N	2.52	0.42
2:LB:1088:LEU:HD13	2:LB:1102:TRP:HB3	2.02	0.42
5:XC:9:THR:OG1	5:XC:10:ILE:N	2.51	0.42
5:XD:43:MET:N	5:XD:44:PRO:HD2	2.34	0.42
3:SC:139:VAL:HG22	3:SC:188:GLN:NE2	2.35	0.42
3:SC:320:PHE:HA	3:SC:355:TYR:CZ	2.54	0.42
2:LE:995:THR:OG1	2:LE:997:ASP:OD1	2.27	0.42
3:SE:87:SER:O	3:SE:90:LYS:NZ	2.47	0.42
5:XJ:43:MET:N	5:XJ:44:PRO:HD2	2.34	0.42
6:PB:357:PRO:HG2	6:PB:522:ALA:HB1	2.01	0.42
6:PC:268:PHE:HE1	6:PC:323:GLU:HG3	1.85	0.42
6:PC:357:PRO:HG2	6:PC:522:ALA:HB1	2.01	0.42
6:PC:487:VAL:O	6:PC:491:ILE:HG12	2.20	0.42
6:PF:357:PRO:HG2	6:PF:522:ALA:HB1	2.01	0.42
6:PI:454:SER:HB3	6:PL:450:GLU:HA	2.00	0.42
6:PL:374:ASP:OD1	6:PL:375:MET:N	2.52	0.42
2:LA:1050:LEU:HG	2:LA:1075:VAL:HG23	2.02	0.42
6:PA:487:VAL:O	6:PA:491:ILE:HG12	2.20	0.42
3:SB:320:PHE:HA	3:SB:355:TYR:CZ	2.54	0.42
5:XD:52:ASN:ND2	5:YD:53:MET:SD	2.93	0.42
2:LC:143:THR:OG1	2:LC:145:GLU:OE1	2.31	0.42
5:XF:52:ASN:ND2	5:YF:53:MET:SD	2.93	0.42
2:LD:737:LEU:O	2:LD:838:ILE:N	2.51	0.42
2:LE:92:THR:OG1	2:LE:95:ASP:OD1	2.36	0.42
3:SE:139:VAL:HG22	3:SE:188:GLN:NE2	2.35	0.42
1:AL:87:LYS:HE3	2:LF:15:SER:HB3	2.01	0.42
6:PF:487:VAL:O	6:PF:491:ILE:HG12	2.20	0.42
6:PG:454:SER:HB3	6:PJ:450:GLU:HA	2.00	0.42
6:PI:53:TRP:NE1	6:PI:382:GLU:OE1	2.39	0.42
1:AA:172:ASP:OD1	1:AA:172:ASP:N	2.52	0.42
6:PA:357:PRO:HG2	6:PA:522:ALA:HB1	2.01	0.42
6:PA:404:ARG:O	6:PD:410:ARG:NH2	2.53	0.42
1:AE:128:LEU:HD23	1:AE:136:LEU:HD11	2.01	0.42
2:LC:1050:LEU:HG	2:LC:1075:VAL:HG23	2.02	0.42
1:AG:132:ARG:HB2	1:AG:135:VAL:HB	2.01	0.42
2:LD:1117:SER:OG	2:LD:1120:ASP:O	2.38	0.42
3:SD:320:PHE:HA	3:SD:355:TYR:CZ	2.54	0.42
1:AJ:173:THR:HG23	1:AJ:174:LEU:HD22	2.00	0.42
2:LE:1039:ASN:N	2:LE:1039:ASN:OD1	2.52	0.42
2:LF:886:TRP:HE3	2:LF:928:GLY:HA2	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PB:410:ARG:NH2	6:PK:404:ARG:O	2.53	0.42
6:PE:268:PHE:HE1	6:PE:323:GLU:HG3	1.85	0.42
6:PI:374:ASP:OD1	6:PI:375:MET:N	2.52	0.42
2:LA:749:THR:OG1	2:LA:750:ASP:N	2.52	0.42
2:LA:1088:LEU:HD13	2:LA:1102:TRP:HB3	2.02	0.42
3:SC:405:ARG:NE	3:SC:406:ASP:OD1	2.48	0.42
2:LD:400:GLY:HA2	2:LD:402:ARG:HE	1.85	0.42
2:LD:749:THR:OG1	2:LD:750:ASP:N	2.52	0.42
1:AI:132:ARG:HB2	1:AI:135:VAL:HB	2.01	0.42
2:LE:710:TYR:O	2:LE:711:GLN:HG3	2.19	0.42
2:LE:932:PRO:HG2	2:LE:957:ALA:HB1	2.02	0.42
4:TI:26:ASP:OD1	4:TI:26:ASP:N	2.46	0.42
2:LF:551:ASP:OD1	3:SF:18:ARG:NH1	2.33	0.42
2:LF:621:LEU:HD13	2:LF:635:TRP:HB3	2.02	0.42
2:LF:913:ASP:OD2	2:LF:983:ARG:NH2	2.53	0.42
3:SF:196:GLN:HG3	3:SF:202:LEU:HD11	2.01	0.42
6:PG:479:VAL:HG12	6:PH:467:GLU:HB3	2.01	0.42
6:PK:374:ASP:OD1	6:PK:375:MET:N	2.52	0.42
6:PK:479:VAL:HG12	6:PL:467:GLU:HB3	2.01	0.42
2:LA:913:ASP:OD2	2:LA:983:ARG:NH2	2.53	0.42
2:LA:991:ARG:HD2	2:LA:1077:GLN:HB3	2.01	0.42
3:SA:196:GLN:HG3	3:SA:202:LEU:HD11	2.01	0.42
1:AD:132:ARG:HB2	1:AD:135:VAL:HB	2.02	0.42
3:SB:196:GLN:HG3	3:SB:202:LEU:HD11	2.01	0.42
1:AF:132:ARG:HB2	1:AF:135:VAL:HB	2.02	0.42
2:LC:886:TRP:HE3	2:LC:928:GLY:HA2	1.84	0.42
3:SC:137:ASN:O	3:SC:205:GLN:N	2.52	0.42
5:YF:55:GLN:OE1	5:YF:55:GLN:N	2.45	0.42
1:AH:233:ARG:HA	1:AH:233:ARG:HD3	1.95	0.42
2:LD:940:TYR:HA	2:LD:950:TYR:HA	2.01	0.42
5:ZG:62:LYS:HB2	5:ZG:65:GLU:CD	2.45	0.42
2:LE:142:GLN:O	2:LE:229:THR:OG1	2.26	0.42
6:PF:368:TYR:CD2	6:PF:369:MET:HG3	2.55	0.42
6:PH:487:VAL:O	6:PH:491:ILE:HG12	2.20	0.42
6:PI:579:ILE:HG12	6:PL:592:LEU:HD13	2.02	0.42
1:AC:128:LEU:HD23	1:AC:136:LEU:HD11	2.01	0.42
1:AC:186:TYR:O	1:AC:189:SER:OG	2.29	0.42
2:LB:596:GLU:OE2	3:SB:41:THR:N	2.43	0.42
2:LB:913:ASP:OD2	2:LB:983:ARG:NH2	2.53	0.42
2:LC:932:PRO:HG2	2:LC:957:ALA:HB1	2.02	0.42
4:TF:73:SER:O	4:TF:77:HIS:ND1	2.43	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SD:139:VAL:HG22	3:SD:188:GLN:NE2	2.35	0.42
1:AJ:132:ARG:HB2	1:AJ:135:VAL:HB	2.02	0.42
5:ZI:62:LYS:HB2	5:ZI:65:GLU:CD	2.45	0.42
1:AK:172:ASP:OD1	1:AK:172:ASP:N	2.52	0.42
2:LF:30:ASP:OD1	2:LF:31:LEU:N	2.53	0.42
3:SF:211:TRP:N	3:SF:312:ASN:OD1	2.44	0.42
6:PC:404:ARG:O	6:PF:410:ARG:NH2	2.53	0.42
6:PD:487:VAL:O	6:PD:491:ILE:HG12	2.20	0.42
6:PI:357:PRO:HG2	6:PI:522:ALA:HB1	2.01	0.42
6:PI:404:ARG:O	6:PL:410:ARG:NH2	2.53	0.42
6:PJ:374:ASP:OD1	6:PJ:375:MET:N	2.52	0.42
4:TB:197:GLU:HG3	4:TC:199:THR:HG23	2.02	0.41
6:PA:579:ILE:HG12	6:PD:592:LEU:HD13	2.02	0.41
1:AC:56:ASN:ND2	5:YC:2:SER:O	2.51	0.41
2:LC:901:ASN:CG	2:LC:905:SER:HB3	2.45	0.41
2:LC:1039:ASN:OD1	2:LC:1039:ASN:N	2.52	0.41
3:SC:196:GLN:HG3	3:SC:202:LEU:HD11	2.01	0.41
1:AH:87:LYS:HE3	2:LD:15:SER:HB3	2.01	0.41
2:LD:886:TRP:HE3	2:LD:928:GLY:HA2	1.84	0.41
2:LD:913:ASP:OD2	2:LD:983:ARG:NH2	2.53	0.41
4:TH:197:GLU:HG3	4:TI:199:THR:HG23	2.02	0.41
5:YJ:43:MET:N	5:YJ:44:PRO:HD2	2.35	0.41
6:PD:268:PHE:HE1	6:PD:323:GLU:HG3	1.85	0.41
6:PE:487:VAL:O	6:PE:491:ILE:HG12	2.20	0.41
6:PH:268:PHE:HE1	6:PH:323:GLU:HG3	1.85	0.41
6:PH:368:TYR:CD2	6:PH:369:MET:HG3	2.55	0.41
1:AB:132:ARG:HB2	1:AB:135:VAL:HB	2.02	0.41
1:AB:233:ARG:HA	1:AB:233:ARG:HD3	1.95	0.41
2:LA:400:GLY:HA2	2:LA:402:ARG:HE	1.85	0.41
2:LA:932:PRO:HG2	2:LA:957:ALA:HB1	2.02	0.41
4:TA:199:THR:HG23	4:TL:197:GLU:HG3	2.02	0.41
2:LB:1039:ASN:OD1	2:LB:1039:ASN:N	2.52	0.41
5:YD:43:MET:N	5:YD:44:PRO:HD2	2.35	0.41
4:TF:197:GLU:HG3	4:TG:199:THR:HG23	2.02	0.41
1:AH:55:ARG:NH2	1:AI:132:ARG:HH21	2.18	0.41
1:AH:132:ARG:HB2	1:AH:135:VAL:HB	2.02	0.41
2:LD:710:TYR:O	2:LD:711:GLN:HG3	2.19	0.41
2:LD:932:PRO:HG2	2:LD:957:ALA:HB1	2.02	0.41
2:LD:991:ARG:HD2	2:LD:1077:GLN:HB3	2.01	0.41
1:AJ:87:LYS:HE3	2:LE:15:SER:HB3	2.01	0.41
2:LE:621:LEU:HD13	2:LE:635:TRP:HB3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YL:43:MET:N	5:YL:44:PRO:HD2	2.35	0.41
6:PD:368:TYR:CD2	6:PD:369:MET:HG3	2.55	0.41
6:PG:357:PRO:HG2	6:PG:522:ALA:HB1	2.01	0.41
6:PJ:357:PRO:HG2	6:PJ:522:ALA:HB1	2.01	0.41
6:PK:368:TYR:CD2	6:PK:369:MET:HG3	2.55	0.41
2:LA:621:LEU:HD13	2:LA:635:TRP:HB3	2.02	0.41
3:SA:29:ILE:HG23	3:SA:36:HIS:HB2	2.02	0.41
2:LB:710:TYR:O	2:LB:711:GLN:HG3	2.19	0.41
2:LB:737:LEU:O	2:LB:838:ILE:N	2.52	0.41
2:LB:940:TYR:HA	2:LB:950:TYR:HA	2.01	0.41
3:SB:29:ILE:HG23	3:SB:36:HIS:HB2	2.02	0.41
4:TD:295:ASN:ND2	2:LE:1046:ASN:OD1	2.54	0.41
5:YC:43:MET:N	5:YC:44:PRO:HD2	2.35	0.41
1:AF:55:ARG:NH2	1:AG:132:ARG:HH21	2.18	0.41
2:LC:913:ASP:OD2	2:LC:983:ARG:NH2	2.53	0.41
3:SD:87:SER:O	3:SD:90:LYS:NZ	2.47	0.41
5:XH:52:ASN:ND2	5:YH:53:MET:SD	2.93	0.41
2:LE:901:ASN:CG	2:LE:905:SER:HB3	2.45	0.41
4:TI:213:LYS:HE2	4:TI:213:LYS:HB3	1.88	0.41
1:AL:132:ARG:HB2	1:AL:135:VAL:HB	2.02	0.41
2:LF:400:GLY:HA2	2:LF:402:ARG:HE	1.85	0.41
2:LF:682:VAL:HA	2:LF:685:TRP:NE1	2.34	0.41
3:SF:139:VAL:HG22	3:SF:188:GLN:NE2	2.35	0.41
4:TL:200:LYS:O	4:TL:203:THR:OG1	2.30	0.41
5:ZK:62:LYS:HB2	5:ZK:65:GLU:CD	2.45	0.41
6:PE:368:TYR:CD2	6:PE:369:MET:HG3	2.55	0.41
6:PG:368:TYR:CD2	6:PG:369:MET:HG3	2.55	0.41
6:PL:368:TYR:CD2	6:PL:369:MET:HG3	2.55	0.41
1:AB:87:LYS:HE3	2:LA:15:SER:HB3	2.01	0.41
2:LA:596:GLU:OE2	3:SA:41:THR:N	2.43	0.41
5:YA:43:MET:N	5:YA:44:PRO:HD2	2.36	0.41
2:LB:991:ARG:HD2	2:LB:1077:GLN:HB3	2.01	0.41
4:TD:197:GLU:HG3	4:TE:199:THR:HG23	2.02	0.41
5:ZC:62:LYS:HB2	5:ZC:65:GLU:CD	2.45	0.41
2:LC:1046:ASN:OD1	4:TL:295:ASN:ND2	2.54	0.41
1:AI:172:ASP:OD1	1:AI:172:ASP:N	2.52	0.41
2:LE:400:GLY:HA2	2:LE:402:ARG:HE	1.85	0.41
1:AK:176:PRO:HG3	1:AL:43:GLU:HG3	2.02	0.41
5:XL:52:ASN:ND2	5:YL:53:MET:SD	2.93	0.41
6:PB:374:ASP:OD1	6:PB:375:MET:N	2.52	0.41
6:PE:404:ARG:O	6:PH:410:ARG:NH2	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PG:404:ARG:O	6:PJ:410:ARG:NH2	2.53	0.41
6:PI:268:PHE:HE1	6:PI:323:GLU:HG3	1.85	0.41
6:PI:487:VAL:O	6:PI:491:ILE:HG12	2.20	0.41
6:PL:268:PHE:HE1	6:PL:323:GLU:HG3	1.85	0.41
5:ZA:62:LYS:HB2	5:ZA:65:GLU:CD	2.45	0.41
6:PA:138:TYR:HA	6:PA:242:MET:SD	2.61	0.41
6:PA:268:PHE:HE1	6:PA:323:GLU:HG3	1.85	0.41
6:PA:368:TYR:CD2	6:PA:369:MET:HG3	2.55	0.41
1:AD:21:ILE:HD12	1:AD:21:ILE:HA	1.96	0.41
2:LB:92:THR:OG1	2:LB:95:ASP:OD1	2.36	0.41
2:LB:621:LEU:HD13	2:LB:635:TRP:HB3	2.02	0.41
2:LB:932:PRO:HG2	2:LB:957:ALA:HB1	2.02	0.41
2:LC:400:GLY:HA2	2:LC:402:ARG:HE	1.85	0.41
5:YG:43:MET:N	5:YG:44:PRO:HD2	2.36	0.41
6:PC:368:TYR:CD2	6:PC:369:MET:HG3	2.55	0.41
6:PC:479:VAL:HG12	6:PD:467:GLU:HB3	2.01	0.41
6:PC:579:ILE:HG12	6:PF:592:LEU:HD13	2.02	0.41
6:PE:479:VAL:HG12	6:PF:467:GLU:HB3	2.01	0.41
6:PH:357:PRO:HG2	6:PH:522:ALA:HB1	2.01	0.41
6:PI:368:TYR:CD2	6:PI:369:MET:HG3	2.55	0.41
6:PJ:487:VAL:O	6:PJ:491:ILE:HG12	2.20	0.41
6:PK:268:PHE:HE1	6:PK:323:GLU:HG3	1.85	0.41
6:PL:357:PRO:HG2	6:PL:522:ALA:HB1	2.01	0.41
2:LA:283:TRP:CZ3	2:LA:285:TYR:HB3	2.56	0.41
2:LA:737:LEU:O	2:LA:838:ILE:N	2.51	0.41
2:LB:777:THR:HG21	2:LB:960:ILE:HA	2.03	0.41
2:LB:873:TRP:O	2:LB:877:ASN:ND2	2.27	0.41
5:XC:12:ASN:ND2	5:XC:18:GLU:HG2	2.35	0.41
2:LC:710:TYR:O	2:LC:711:GLN:HG3	2.19	0.41
2:LC:940:TYR:HA	2:LC:950:TYR:HA	2.01	0.41
3:SC:156:ASN:ND2	3:SC:160:ASP:HB3	2.36	0.41
2:LD:596:GLU:OE2	3:SD:41:THR:N	2.43	0.41
2:LD:979:TRP:CD1	2:LD:979:TRP:H	2.39	0.41
2:LE:913:ASP:OD2	2:LE:983:ARG:NH2	2.53	0.41
2:LE:1088:LEU:HD13	2:LE:1102:TRP:HB3	2.02	0.41
4:TJ:211:GLU:HG3	4:TK:213:LYS:HG3	2.02	0.41
2:LF:901:ASN:CG	2:LF:905:SER:HB3	2.46	0.41
2:LF:1050:LEU:HG	2:LF:1075:VAL:HG23	2.02	0.41
5:XK:55:GLN:HG3	5:YK:60:HIS:CE1	2.56	0.41
6:PB:487:VAL:O	6:PB:491:ILE:HG12	2.20	0.41
6:PC:138:TYR:HA	6:PC:242:MET:SD	2.61	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PJ:368:TYR:CD2	6:PJ:369:MET:HG3	2.55	0.41
2:LA:777:THR:HG21	2:LA:960:ILE:HA	2.03	0.41
3:SB:139:VAL:HG22	3:SB:188:GLN:NE2	2.35	0.41
2:LC:979:TRP:CD1	2:LC:979:TRP:H	2.39	0.41
2:LC:1088:LEU:HD13	2:LC:1102:TRP:HB3	2.02	0.41
2:LD:283:TRP:CZ3	2:LD:285:TYR:HB3	2.56	0.41
2:LD:621:LEU:HD13	2:LD:635:TRP:HB3	2.02	0.41
2:LD:901:ASN:CG	2:LD:905:SER:HB3	2.45	0.41
2:LD:1039:ASN:OD1	2:LD:1039:ASN:N	2.52	0.41
2:LE:886:TRP:HE3	2:LE:928:GLY:HA2	1.84	0.41
5:XI:55:GLN:HG3	5:YI:60:HIS:CE1	2.56	0.41
5:YJ:55:GLN:OE1	5:YJ:55:GLN:N	2.45	0.41
2:LF:1039:ASN:OD1	2:LF:1039:ASN:N	2.52	0.41
6:PB:268:PHE:HE1	6:PB:323:GLU:HG3	1.85	0.41
6:PD:138:TYR:HA	6:PD:242:MET:SD	2.61	0.41
6:PG:138:TYR:HA	6:PG:242:MET:SD	2.61	0.41
6:PG:374:ASP:OD1	6:PG:375:MET:N	2.52	0.41
6:PJ:53:TRP:NE1	6:PJ:382:GLU:OE1	2.39	0.41
6:PK:487:VAL:O	6:PK:491:ILE:HG12	2.20	0.41
3:SA:139:VAL:HG22	3:SA:188:GLN:NE2	2.35	0.41
4:TB:295:ASN:ND2	2:LD:1046:ASN:OD1	2.54	0.41
5:XA:12:ASN:ND2	5:XA:18:GLU:HG2	2.35	0.41
5:YB:43:MET:N	5:YB:44:PRO:HD2	2.35	0.41
6:PA:479:VAL:HG12	6:PB:467:GLU:HB3	2.01	0.41
2:LB:1089:LYS:HE2	2:LB:1089:LYS:HB2	1.90	0.41
5:XD:60:HIS:HA	5:XD:63:LEU:HD23	2.03	0.41
2:LC:259:THR:HG1	2:LC:316:CYS:C	2.25	0.41
5:XE:12:ASN:ND2	5:XE:18:GLU:HG2	2.35	0.41
5:XE:55:GLN:HG3	5:YE:60:HIS:CE1	2.56	0.41
1:AH:21:ILE:HD12	1:AH:21:ILE:HA	1.95	0.41
2:LD:894:TRP:CD1	2:LD:899:PRO:HG2	2.56	0.41
3:SD:156:ASN:OD1	3:SD:160:ASP:N	2.54	0.41
3:SD:196:GLN:HG3	3:SD:202:LEU:HD11	2.01	0.41
5:YH:43:MET:N	5:YH:44:PRO:HD2	2.35	0.41
1:AJ:55:ARG:NH2	1:AK:132:ARG:HH21	2.18	0.41
2:LE:283:TRP:CZ3	2:LE:285:TYR:HB3	2.56	0.41
4:TI:16:LEU:O	4:TJ:160:LYS:NZ	2.40	0.41
4:TJ:197:GLU:HG3	4:TK:199:THR:HG23	2.02	0.41
5:XJ:52:ASN:ND2	5:YJ:53:MET:SD	2.93	0.41
1:AL:34:LYS:O	1:AL:38:ILE:HG12	2.21	0.41
2:LF:777:THR:HG21	2:LF:960:ILE:HA	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LF:932:PRO:HG2	2:LF:957:ALA:HB1	2.02	0.41
6:PG:268:PHE:HE1	6:PG:323:GLU:HG3	1.85	0.41
6:PJ:138:TYR:HA	6:PJ:242:MET:SD	2.61	0.41
1:AB:55:ARG:NH2	1:AC:132:ARG:HH21	2.18	0.41
2:LA:51:THR:O	2:LA:368:TYR:OH	2.35	0.41
2:LA:79:TYR:CD1	2:LA:85:LYS:HG3	2.56	0.41
2:LA:901:ASN:CG	2:LA:905:SER:HB3	2.45	0.41
3:SA:87:SER:O	3:SA:90:LYS:NZ	2.47	0.41
3:SA:405:ARG:NE	3:SA:406:ASP:OD1	2.48	0.41
5:ZB:22:ASP:N	5:ZB:23:PRO:HD2	2.36	0.41
1:AD:55:ARG:NH2	1:AE:132:ARG:HH21	2.19	0.41
3:SB:156:ASN:ND2	3:SB:160:ASP:HB3	2.36	0.41
3:SB:211:TRP:N	3:SB:312:ASN:OD1	2.44	0.41
1:AF:226:THR:O	1:AG:123:ASN:ND2	2.46	0.41
2:LC:30:ASP:OD1	2:LC:31:LEU:N	2.53	0.41
2:LC:132:ASP:OD2	2:LC:238:ALA:N	2.54	0.41
2:LC:621:LEU:HD13	2:LC:635:TRP:HB3	2.02	0.41
3:SC:295:PHE:HB2	3:SC:328:ILE:HG22	2.03	0.41
4:TF:295:ASN:ND2	2:LF:1046:ASN:OD1	2.54	0.41
5:ZE:62:LYS:HB2	5:ZE:65:GLU:CD	2.45	0.41
2:LD:93:ASN:O	2:LD:240:HIS:ND1	2.50	0.41
2:LD:197:VAL:HG22	2:LD:198:TYR:CD2	2.56	0.41
2:LD:1088:LEU:HD13	2:LD:1102:TRP:HB3	2.02	0.41
4:TH:16:LEU:O	4:TI:160:LYS:NZ	2.44	0.41
2:LE:979:TRP:CD1	2:LE:979:TRP:H	2.39	0.41
2:LE:1050:LEU:HG	2:LE:1075:VAL:HG23	2.02	0.41
5:XI:12:ASN:ND2	5:XI:18:GLU:HG2	2.35	0.41
5:YI:43:MET:N	5:YI:44:PRO:HD2	2.35	0.41
5:YI:46:ILE:HD11	5:ZI:43:MET:HE1	2.03	0.41
1:AL:21:ILE:HD12	1:AL:21:ILE:HA	1.95	0.41
2:LF:894:TRP:CD1	2:LF:899:PRO:HG2	2.56	0.41
4:TK:213:LYS:HE2	4:TK:213:LYS:HB3	1.88	0.41
5:XK:12:ASN:ND2	5:XK:18:GLU:HG2	2.35	0.41
5:ZL:22:ASP:N	5:ZL:23:PRO:HD2	2.36	0.41
6:PB:138:TYR:HA	6:PB:242:MET:SD	2.61	0.41
6:PB:592:LEU:HD13	6:PK:579:ILE:HG12	2.02	0.41
6:PE:418:ASP:OD2	6:PE:421:ASN:ND2	2.54	0.41
6:PG:579:ILE:HG12	6:PJ:592:LEU:HD13	2.02	0.41
6:PJ:268:PHE:HE1	6:PJ:323:GLU:HG3	1.85	0.41
6:PK:592:LEU:HD13	6:PL:579:ILE:HG12	2.03	0.41
6:PL:138:TYR:HA	6:PL:242:MET:SD	2.61	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:PL:487:VAL:O	6:PL:491:ILE:HG12	2.20	0.41
2:LA:894:TRP:CD1	2:LA:899:PRO:HG2	2.56	0.41
4:TA:213:LYS:HG3	4:TL:211:GLU:HG3	2.02	0.41
5:XA:22:ASP:HB2	5:XA:23:PRO:HD3	2.03	0.41
5:XB:60:HIS:HA	5:XB:63:LEU:HD23	2.03	0.41
6:PA:374:ASP:OD1	6:PA:375:MET:N	2.52	0.41
6:PA:418:ASP:OD2	6:PA:421:ASN:ND2	2.54	0.41
2:LB:132:ASP:OD2	2:LB:238:ALA:N	2.54	0.41
2:LB:727:ASP:N	2:LB:727:ASP:OD1	2.54	0.41
5:XC:22:ASP:HB2	5:XC:23:PRO:HD3	2.03	0.41
1:AF:34:LYS:O	1:AF:38:ILE:HG12	2.21	0.41
2:LC:283:TRP:CZ3	2:LC:285:TYR:HB3	2.56	0.41
1:AH:34:LYS:O	1:AH:38:ILE:HG12	2.21	0.41
2:LD:92:THR:OG1	2:LD:95:ASP:OD1	2.36	0.41
2:LD:237:GLU:OE1	2:LD:239:HIS:N	2.34	0.41
2:LD:259:THR:HG1	2:LD:316:CYS:C	2.24	0.41
2:LD:375:MET:HE2	3:SD:397:PRO:HD3	2.03	0.41
2:LD:919:ALA:O	2:LD:971:ASN:ND2	2.54	0.41
3:SD:156:ASN:ND2	3:SD:160:ASP:HB3	2.36	0.41
1:AJ:34:LYS:O	1:AJ:38:ILE:HG12	2.21	0.41
2:LE:197:VAL:HG22	2:LE:198:TYR:CD2	2.56	0.41
2:LE:894:TRP:CD1	2:LE:899:PRO:HG2	2.56	0.41
3:SE:29:ILE:HG23	3:SE:36:HIS:HB2	2.02	0.41
3:SF:29:ILE:HG23	3:SF:36:HIS:HB2	2.02	0.41
5:YK:46:ILE:HD11	5:ZK:43:MET:HE1	2.03	0.41
6:PB:368:TYR:CD2	6:PB:369:MET:HG3	2.55	0.41
6:PD:300:ASP:OD2	6:PD:322:TYR:OH	2.37	0.41
6:PI:316:ARG:NH2	6:PJ:35:ASP:OD2	2.55	0.41
6:PK:418:ASP:OD2	6:PK:421:ASN:ND2	2.54	0.41
1:AA:176:PRO:HG3	1:AB:43:GLU:HG3	2.02	0.40
4:TA:160:LYS:NZ	4:TL:16:LEU:O	2.44	0.40
2:LB:181:ILE:HD12	2:LB:181:ILE:HA	1.97	0.40
2:LB:259:THR:O	2:LC:162:ARG:NH2	2.43	0.40
2:LB:1117:SER:OG	2:LB:1120:ASP:O	2.38	0.40
5:YC:46:ILE:HD11	5:ZC:43:MET:HE1	2.03	0.40
5:ZC:60:HIS:HA	5:ZC:63:LEU:HB2	2.03	0.40
2:LC:79:TYR:CD1	2:LC:85:LYS:HG3	2.56	0.40
3:SC:29:ILE:HG12	3:SC:36:HIS:HB2	2.03	0.40
4:TF:211:GLU:HG3	4:TG:213:LYS:HG3	2.02	0.40
5:XF:62:LYS:NZ	5:YF:63:LEU:HG	2.37	0.40
5:YF:43:MET:N	5:YF:44:PRO:HD2	2.35	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:1050:LEU:HG	2:LD:1075:VAL:HG23	2.02	0.40
3:SD:364:ILE:HG21	3:SD:380:VAL:HG13	2.04	0.40
5:XG:9:THR:OG1	5:XG:10:ILE:N	2.51	0.40
5:XG:12:ASN:ND2	5:XG:18:GLU:HG2	2.35	0.40
5:XG:55:GLN:HG3	5:YG:60:HIS:CE1	2.56	0.40
5:ZG:51:ASP:OD1	5:ZG:52:ASN:ND2	2.54	0.40
1:AJ:43:GLU:OE2	1:AJ:181:TYR:OH	2.25	0.40
2:LE:375:MET:HE2	3:SE:397:PRO:HD3	2.03	0.40
4:TJ:213:LYS:HE2	4:TJ:213:LYS:HB3	1.88	0.40
5:XJ:59:ILE:HD13	5:YJ:56:LEU:HD12	2.03	0.40
2:LF:741:ASN:HA	2:LF:796:ALA:O	2.21	0.40
2:LF:1088:LEU:HD13	2:LF:1102:TRP:HB3	2.02	0.40
5:YL:55:GLN:OE1	5:YL:55:GLN:N	2.45	0.40
5:ZK:51:ASP:OD1	5:ZK:52:ASN:ND2	2.54	0.40
5:ZK:60:HIS:HA	5:ZK:63:LEU:HB2	2.03	0.40
6:PD:418:ASP:OD2	6:PD:421:ASN:ND2	2.54	0.40
6:PE:316:ARG:NH2	6:PF:35:ASP:OD2	2.54	0.40
6:PF:138:TYR:HA	6:PF:242:MET:SD	2.61	0.40
6:PF:418:ASP:OD2	6:PF:421:ASN:ND2	2.54	0.40
1:AB:34:LYS:O	1:AB:38:ILE:HG12	2.21	0.40
3:SA:211:TRP:CE3	3:SA:227:ILE:HG22	2.57	0.40
3:SA:364:ILE:HG21	3:SA:380:VAL:HG13	2.04	0.40
5:ZA:60:HIS:HA	5:ZA:63:LEU:HB2	2.03	0.40
5:ZA:68:ALA:O	5:ZA:72:LYS:HG2	2.21	0.40
1:AD:225:ASP:OD1	1:AD:225:ASP:N	2.54	0.40
2:LB:901:ASN:CG	2:LB:905:SER:HB3	2.45	0.40
3:SB:211:TRP:CE3	3:SB:227:ILE:HG22	2.57	0.40
5:ZD:22:ASP:N	5:ZD:23:PRO:HD2	2.36	0.40
3:SC:156:ASN:OD1	3:SC:160:ASP:N	2.54	0.40
5:XE:22:ASP:HB2	5:XE:23:PRO:HD3	2.03	0.40
5:YE:46:ILE:HD11	5:ZE:43:MET:HE1	2.03	0.40
5:ZE:60:HIS:HA	5:ZE:63:LEU:HB2	2.03	0.40
1:AG:176:PRO:HG3	1:AH:43:GLU:HG3	2.02	0.40
2:LD:79:TYR:CD1	2:LD:85:LYS:HG3	2.56	0.40
5:YG:46:ILE:HD11	5:ZG:43:MET:HE1	2.03	0.40
2:LE:373:MET:HE1	2:LE:400:GLY:HA3	2.04	0.40
5:XI:22:ASP:HB2	5:XI:23:PRO:HD3	2.03	0.40
5:ZI:68:ALA:O	5:ZI:72:LYS:HG2	2.21	0.40
2:LF:283:TRP:CZ3	2:LF:285:TYR:HB3	2.56	0.40
2:LF:375:MET:HE2	3:SF:397:PRO:HD3	2.03	0.40
2:LF:919:ALA:O	2:LF:971:ASN:ND2	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:XK:20:LEU:O	5:XK:23:PRO:HD2	2.21	0.40
5:YK:43:MET:N	5:YK:44:PRO:HD2	2.36	0.40
6:PB:418:ASP:OD2	6:PB:421:ASN:ND2	2.54	0.40
6:PC:316:ARG:NH2	6:PD:35:ASP:OD2	2.55	0.40
6:PC:418:ASP:OD2	6:PC:421:ASN:ND2	2.54	0.40
6:PC:592:LEU:HD13	6:PD:579:ILE:HG12	2.03	0.40
6:PE:138:TYR:HA	6:PE:242:MET:SD	2.61	0.40
6:PG:592:LEU:HD13	6:PH:579:ILE:HG12	2.03	0.40
6:PL:418:ASP:OD2	6:PL:421:ASN:ND2	2.54	0.40
1:AA:132:ARG:HH21	1:AL:55:ARG:NH2	2.18	0.40
2:LA:375:MET:HE2	3:SA:397:PRO:HD3	2.03	0.40
6:PA:592:LEU:HD13	6:PB:579:ILE:HG12	2.02	0.40
2:LB:375:MET:HE2	3:SB:397:PRO:HD3	2.03	0.40
2:LB:741:ASN:HA	2:LB:796:ALA:O	2.21	0.40
4:TC:187:MET:SD	4:TC:191:GLN:NE2	2.95	0.40
5:ZC:68:ALA:O	5:ZC:72:LYS:HG2	2.21	0.40
5:ZD:63:LEU:HD12	5:ZD:63:LEU:HA	1.96	0.40
1:AE:176:PRO:HG3	1:AF:43:GLU:HG3	2.02	0.40
2:LC:18:TYR:O	5:XE:47:LYS:NZ	2.46	0.40
2:LC:894:TRP:CD1	2:LC:899:PRO:HG2	2.56	0.40
2:LC:1130:TRP:CD2	2:LC:1135:LEU:HD12	2.57	0.40
5:XF:60:HIS:HA	5:XF:63:LEU:HD23	2.03	0.40
2:LD:132:ASP:OD2	2:LD:238:ALA:N	2.54	0.40
3:SD:29:ILE:HG12	3:SD:36:HIS:HB2	2.03	0.40
3:SD:295:PHE:HB2	3:SD:328:ILE:HG22	2.04	0.40
1:AI:176:PRO:HG3	1:AJ:43:GLU:HG3	2.02	0.40
2:LE:130:ASN:OD1	2:LE:130:ASN:N	2.55	0.40
2:LE:727:ASP:OD1	2:LE:727:ASP:N	2.54	0.40
3:SE:156:ASN:OD1	3:SE:160:ASP:N	2.54	0.40
5:XI:20:LEU:O	5:XI:23:PRO:HD2	2.22	0.40
5:XJ:22:ASP:H	5:XJ:42:ARG:HH21	1.69	0.40
5:ZI:51:ASP:OD1	5:ZI:52:ASN:ND2	2.54	0.40
2:LF:373:MET:HE1	2:LF:400:GLY:HA3	2.04	0.40
5:XK:43:MET:N	5:XK:44:PRO:HD2	2.37	0.40
6:PG:316:ARG:NH2	6:PH:35:ASP:OD2	2.55	0.40
6:PH:374:ASP:OD1	6:PH:375:MET:N	2.52	0.40
6:PH:418:ASP:OD2	6:PH:421:ASN:ND2	2.54	0.40
2:LA:979:TRP:CD1	2:LA:979:TRP:H	2.39	0.40
2:LA:1130:TRP:CD2	2:LA:1135:LEU:HD12	2.57	0.40
3:SA:156:ASN:HA	3:SA:226:CYS:HA	2.04	0.40
4:TA:16:LEU:O	4:TB:160:LYS:NZ	2.40	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:XA:55:GLN:HG3	5:YA:60:HIS:CE1	2.56	0.40
5:XB:59:ILE:HD13	5:YB:56:LEU:HD12	2.04	0.40
5:ZA:51:ASP:OD1	5:ZA:52:ASN:ND2	2.54	0.40
2:LB:30:ASP:OD1	2:LB:31:LEU:N	2.53	0.40
2:LB:283:TRP:CZ3	2:LB:285:TYR:HB3	2.56	0.40
2:LB:376:GLY:O	3:SB:397:PRO:HD2	2.22	0.40
2:LB:1046:ASN:OD1	4:TJ:295:ASN:ND2	2.54	0.40
2:LB:1130:TRP:CD2	2:LB:1135:LEU:HD12	2.57	0.40
3:SB:156:ASN:OD1	3:SB:160:ASP:N	2.54	0.40
1:AF:21:ILE:HD12	1:AF:21:ILE:HA	1.96	0.40
1:AF:172:ASP:OD1	1:AF:172:ASP:N	2.54	0.40
5:ZF:34:TYR:CE1	1:AG:87:LYS:HE3	2.57	0.40
2:LD:373:MET:HE1	2:LD:400:GLY:HA3	2.04	0.40
3:SD:137:ASN:O	3:SD:205:GLN:N	2.52	0.40
5:XH:59:ILE:HD13	5:YH:56:LEU:HD12	2.04	0.40
2:LE:1057:SER:HB2	2:LE:1069:SER:HA	2.04	0.40
3:SE:295:PHE:HB2	3:SE:328:ILE:HG22	2.03	0.40
5:XJ:60:HIS:HA	5:XJ:63:LEU:HD23	2.03	0.40
5:ZJ:22:ASP:N	5:ZJ:23:PRO:HD2	2.36	0.40
6:PG:487:VAL:O	6:PG:491:ILE:HG12	2.20	0.40
6:PI:138:TYR:HA	6:PI:242:MET:SD	2.61	0.40
6:PI:418:ASP:OD2	6:PI:421:ASN:ND2	2.54	0.40
6:PK:138:TYR:HA	6:PK:242:MET:SD	2.61	0.40
1:AB:49:HIS:CE1	1:AB:155:HIS:HB2	2.57	0.40
2:LA:373:MET:HE1	2:LA:400:GLY:HA3	2.04	0.40
5:XB:78:LEU:HD12	5:YB:80:HIS:NE2	2.37	0.40
5:ZB:34:TYR:CE1	1:AC:87:LYS:HE3	2.57	0.40
1:AC:172:ASP:OD1	1:AC:172:ASP:N	2.52	0.40
2:LB:259:THR:HG1	2:LB:316:CYS:C	2.24	0.40
2:LB:373:MET:HE1	2:LB:400:GLY:HA3	2.04	0.40
3:SB:295:PHE:HB2	3:SB:328:ILE:HG22	2.03	0.40
5:XD:59:ILE:HD13	5:YD:56:LEU:HD12	2.04	0.40
5:XD:62:LYS:NZ	5:YD:63:LEU:HG	2.37	0.40
5:ZC:51:ASP:OD1	5:ZC:52:ASN:ND2	2.54	0.40
2:LC:197:VAL:HG22	2:LC:198:TYR:CD2	2.56	0.40
4:TE:73:SER:O	4:TE:77:HIS:ND1	2.43	0.40
2:LD:259:THR:O	2:LE:162:ARG:NH2	2.43	0.40
3:SD:29:ILE:HG23	3:SD:36:HIS:HB2	2.02	0.40
3:SD:211:TRP:CE3	3:SD:227:ILE:HG22	2.57	0.40
5:ZG:60:HIS:HA	5:ZG:63:LEU:HB2	2.03	0.40
5:ZG:68:ALA:O	5:ZG:72:LYS:HG2	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SE:83:TYR:HA	3:SE:84:PRO:HD3	1.92	0.40
2:LF:79:TYR:CD1	2:LF:85:LYS:HG3	2.56	0.40
3:SF:156:ASN:HA	3:SF:226:CYS:HA	2.04	0.40
3:SF:295:PHE:HB2	3:SF:328:ILE:HG22	2.03	0.40
4:TK:197:GLU:HG3	4:TL:199:THR:HG23	2.04	0.40
4:TL:187:MET:SD	4:TL:191:GLN:NE2	2.95	0.40
6:PC:77:LYS:HB3	6:PC:80:ARG:HB3	2.04	0.40
6:PK:316:ARG:NH2	6:PL:35:ASP:OD2	2.55	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	234/236 (99%)	234 (100%)	0	0	100	100
1	AB	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AC	234/236 (99%)	234 (100%)	0	0	100	100
1	AD	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AE	234/236 (99%)	234 (100%)	0	0	100	100
1	AF	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AG	234/236 (99%)	234 (100%)	0	0	100	100
1	AH	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AI	234/236 (99%)	234 (100%)	0	0	100	100
1	AJ	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AK	234/236 (99%)	234 (100%)	0	0	100	100
1	AL	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
2	LA	1179/1382 (85%)	1155 (98%)	24 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	LB	1179/1382 (85%)	1154 (98%)	25 (2%)	0	100	100
2	LC	1179/1382 (85%)	1155 (98%)	24 (2%)	0	100	100
2	LD	1179/1382 (85%)	1155 (98%)	24 (2%)	0	100	100
2	LE	1179/1382 (85%)	1153 (98%)	26 (2%)	0	100	100
2	LF	1179/1382 (85%)	1153 (98%)	26 (2%)	0	100	100
3	SA	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SB	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SC	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SD	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SE	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SF	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
4	TA	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TB	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TC	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TD	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TE	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TF	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TG	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TH	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TI	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TJ	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TK	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TL	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
5	XA	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XB	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XC	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XD	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XE	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XF	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XG	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XH	70/556 (13%)	69 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	XI	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XJ	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XK	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XL	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	YA	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YB	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YC	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YD	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YE	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YF	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YG	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YH	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YI	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YJ	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YK	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YL	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	ZA	61/556 (11%)	61 (100%)	0	0	100	100
5	ZB	61/556 (11%)	61 (100%)	0	0	100	100
5	ZC	61/556 (11%)	61 (100%)	0	0	100	100
5	ZD	61/556 (11%)	61 (100%)	0	0	100	100
5	ZE	61/556 (11%)	61 (100%)	0	0	100	100
5	ZF	61/556 (11%)	61 (100%)	0	0	100	100
5	ZG	61/556 (11%)	61 (100%)	0	0	100	100
5	ZH	61/556 (11%)	61 (100%)	0	0	100	100
5	ZI	61/556 (11%)	61 (100%)	0	0	100	100
5	ZJ	61/556 (11%)	61 (100%)	0	0	100	100
5	ZK	61/556 (11%)	61 (100%)	0	0	100	100
5	ZL	61/556 (11%)	61 (100%)	0	0	100	100
6	PA	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PB	640/763 (84%)	633 (99%)	7 (1%)	0	100	100
6	PC	640/763 (84%)	631 (99%)	9 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	PD	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PE	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PF	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PG	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PH	640/763 (84%)	633 (99%)	7 (1%)	0	100	100
6	PI	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PJ	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PK	640/763 (84%)	633 (99%)	7 (1%)	0	100	100
6	PL	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
All	All	25932/46386 (56%)	25539 (98%)	387 (2%)	6 (0%)	100	100

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	SA	368	LEU
3	SB	368	LEU
3	SC	368	LEU
3	SD	368	LEU
3	SE	368	LEU
3	SF	368	LEU

5.3.2 Protein sidechains ⓘ

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	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AB	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AC	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AD	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AE	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AF	209/209 (100%)	206 (99%)	3 (1%)	59	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AG	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AH	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AI	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AJ	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AK	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AL	209/209 (100%)	206 (99%)	3 (1%)	59	68
2	LA	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LB	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LC	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LD	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LE	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LF	989/1155 (86%)	971 (98%)	18 (2%)	51	65
3	SA	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SB	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SC	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SD	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SE	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SF	369/371 (100%)	365 (99%)	4 (1%)	65	71
4	TA	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TB	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TC	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TD	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TE	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TF	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TG	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TH	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TI	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TJ	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TK	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TL	243/244 (100%)	241 (99%)	2 (1%)	73	74
5	XA	66/455 (14%)	64 (97%)	2 (3%)	36	56

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	XB	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XC	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XD	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XE	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XF	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XG	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XH	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XI	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XJ	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XK	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XL	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	YA	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YB	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YC	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YD	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YE	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YF	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YG	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YH	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YI	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YJ	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YK	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YL	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	ZA	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZB	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZC	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZD	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZE	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZF	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZG	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZH	58/455 (13%)	56 (97%)	2 (3%)	32	53

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	ZI	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZJ	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZK	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZL	58/455 (13%)	56 (97%)	2 (3%)	32	53
6	PA	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PB	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PC	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PD	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PE	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PF	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PG	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PH	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PI	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PJ	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PK	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PL	551/652 (84%)	545 (99%)	6 (1%)	65	71
All	All	22416/38796 (58%)	22116 (99%)	300 (1%)	59	69

All (300) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	23	THR
1	AB	148	ASN
1	AB	178	LEU
1	AB	219	THR
2	LA	28	ARG
2	LA	46	THR
2	LA	296	GLU
2	LA	319	MET
2	LA	355	VAL
2	LA	372	VAL
2	LA	418	LEU
2	LA	592	ILE
2	LA	610	ASN
2	LA	699	TRP
2	LA	707	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LA	1038	LEU
2	LA	1039	ASN
2	LA	1105	ARG
2	LA	1113	VAL
2	LA	1136	THR
2	LA	1176	VAL
2	LA	1179	GLN
3	SA	35	VAL
3	SA	102	LEU
3	SA	144	LEU
3	SA	328	ILE
4	TA	17	VAL
4	TA	113	THR
4	TB	17	VAL
4	TB	113	THR
5	XA	16	CYS
5	XA	24	ILE
5	XB	63	LEU
5	YA	63	LEU
5	YB	25	VAL
5	ZA	64	THR
5	ZB	63	LEU
5	ZB	73	LEU
6	PA	111	VAL
6	PA	232	VAL
6	PA	266	VAL
6	PA	340	VAL
6	PA	441	GLN
6	PA	479	VAL
1	AC	23	THR
1	AD	148	ASN
1	AD	178	LEU
1	AD	219	THR
2	LB	28	ARG
2	LB	46	THR
2	LB	296	GLU
2	LB	319	MET
2	LB	355	VAL
2	LB	372	VAL
2	LB	418	LEU
2	LB	592	ILE
2	LB	610	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LB	699	TRP
2	LB	707	VAL
2	LB	1038	LEU
2	LB	1039	ASN
2	LB	1105	ARG
2	LB	1113	VAL
2	LB	1136	THR
2	LB	1176	VAL
2	LB	1179	GLN
3	SB	35	VAL
3	SB	102	LEU
3	SB	144	LEU
3	SB	328	ILE
4	TC	17	VAL
4	TC	113	THR
4	TD	17	VAL
4	TD	113	THR
5	XC	16	CYS
5	XC	24	ILE
5	XD	63	LEU
5	YC	63	LEU
5	YD	25	VAL
5	ZC	64	THR
5	ZD	63	LEU
5	ZD	73	LEU
1	AE	23	THR
1	AF	148	ASN
1	AF	178	LEU
1	AF	219	THR
2	LC	28	ARG
2	LC	46	THR
2	LC	296	GLU
2	LC	319	MET
2	LC	355	VAL
2	LC	372	VAL
2	LC	418	LEU
2	LC	592	ILE
2	LC	610	ASN
2	LC	699	TRP
2	LC	707	VAL
2	LC	1038	LEU
2	LC	1039	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LC	1105	ARG
2	LC	1113	VAL
2	LC	1136	THR
2	LC	1176	VAL
2	LC	1179	GLN
3	SC	35	VAL
3	SC	102	LEU
3	SC	144	LEU
3	SC	328	ILE
4	TE	17	VAL
4	TE	113	THR
4	TF	17	VAL
4	TF	113	THR
5	XE	16	CYS
5	XE	24	ILE
5	XF	63	LEU
5	YE	63	LEU
5	YF	25	VAL
5	ZE	64	THR
5	ZF	63	LEU
5	ZF	73	LEU
1	AG	23	THR
1	AH	148	ASN
1	AH	178	LEU
1	AH	219	THR
2	LD	28	ARG
2	LD	46	THR
2	LD	296	GLU
2	LD	319	MET
2	LD	355	VAL
2	LD	372	VAL
2	LD	418	LEU
2	LD	592	ILE
2	LD	610	ASN
2	LD	699	TRP
2	LD	707	VAL
2	LD	1038	LEU
2	LD	1039	ASN
2	LD	1105	ARG
2	LD	1113	VAL
2	LD	1136	THR
2	LD	1176	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LD	1179	GLN
3	SD	35	VAL
3	SD	102	LEU
3	SD	144	LEU
3	SD	328	ILE
4	TG	17	VAL
4	TG	113	THR
4	TH	17	VAL
4	TH	113	THR
5	XG	16	CYS
5	XG	24	ILE
5	XH	63	LEU
5	YG	63	LEU
5	YH	25	VAL
5	ZG	64	THR
5	ZH	63	LEU
5	ZH	73	LEU
1	AI	23	THR
1	AJ	148	ASN
1	AJ	178	LEU
1	AJ	219	THR
2	LE	28	ARG
2	LE	46	THR
2	LE	296	GLU
2	LE	319	MET
2	LE	355	VAL
2	LE	372	VAL
2	LE	418	LEU
2	LE	592	ILE
2	LE	610	ASN
2	LE	699	TRP
2	LE	707	VAL
2	LE	1038	LEU
2	LE	1039	ASN
2	LE	1105	ARG
2	LE	1113	VAL
2	LE	1136	THR
2	LE	1176	VAL
2	LE	1179	GLN
3	SE	35	VAL
3	SE	102	LEU
3	SE	144	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SE	328	ILE
4	TI	17	VAL
4	TI	113	THR
4	TJ	17	VAL
4	TJ	113	THR
5	XI	16	CYS
5	XI	24	ILE
5	XJ	63	LEU
5	YI	63	LEU
5	YJ	25	VAL
5	ZI	64	THR
5	ZJ	63	LEU
5	ZJ	73	LEU
1	AK	23	THR
1	AL	148	ASN
1	AL	178	LEU
1	AL	219	THR
2	LF	28	ARG
2	LF	46	THR
2	LF	296	GLU
2	LF	319	MET
2	LF	355	VAL
2	LF	372	VAL
2	LF	418	LEU
2	LF	592	ILE
2	LF	610	ASN
2	LF	699	TRP
2	LF	707	VAL
2	LF	1038	LEU
2	LF	1039	ASN
2	LF	1105	ARG
2	LF	1113	VAL
2	LF	1136	THR
2	LF	1176	VAL
2	LF	1179	GLN
3	SF	35	VAL
3	SF	102	LEU
3	SF	144	LEU
3	SF	328	ILE
4	TK	17	VAL
4	TK	113	THR
4	TL	17	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	TL	113	THR
5	XK	16	CYS
5	XK	24	ILE
5	XL	63	LEU
5	YK	63	LEU
5	YL	25	VAL
5	ZK	64	THR
5	ZL	63	LEU
5	ZL	73	LEU
6	PB	111	VAL
6	PB	232	VAL
6	PB	266	VAL
6	PB	340	VAL
6	PB	441	GLN
6	PB	479	VAL
6	PC	111	VAL
6	PC	232	VAL
6	PC	266	VAL
6	PC	340	VAL
6	PC	441	GLN
6	PC	479	VAL
6	PD	111	VAL
6	PD	232	VAL
6	PD	266	VAL
6	PD	340	VAL
6	PD	441	GLN
6	PD	479	VAL
6	PE	111	VAL
6	PE	232	VAL
6	PE	266	VAL
6	PE	340	VAL
6	PE	441	GLN
6	PE	479	VAL
6	PF	111	VAL
6	PF	232	VAL
6	PF	266	VAL
6	PF	340	VAL
6	PF	441	GLN
6	PF	479	VAL
6	PG	111	VAL
6	PG	232	VAL
6	PG	266	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	PG	340	VAL
6	PG	441	GLN
6	PG	479	VAL
6	PH	111	VAL
6	PH	232	VAL
6	PH	266	VAL
6	PH	340	VAL
6	PH	441	GLN
6	PH	479	VAL
6	PI	111	VAL
6	PI	232	VAL
6	PI	266	VAL
6	PI	340	VAL
6	PI	441	GLN
6	PI	479	VAL
6	PJ	111	VAL
6	PJ	232	VAL
6	PJ	266	VAL
6	PJ	340	VAL
6	PJ	441	GLN
6	PJ	479	VAL
6	PK	111	VAL
6	PK	232	VAL
6	PK	266	VAL
6	PK	340	VAL
6	PK	441	GLN
6	PK	479	VAL
6	PL	111	VAL
6	PL	232	VAL
6	PL	266	VAL
6	PL	340	VAL
6	PL	441	GLN
6	PL	479	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (340) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	64	GLN
1	AB	56	ASN
1	AB	134	ASN
1	AB	148	ASN
1	AB	191	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LA	11	ASN
2	LA	293	GLN
2	LA	297	ASN
2	LA	447	GLN
2	LA	509	GLN
2	LA	532	HIS
2	LA	882	ASN
2	LA	888	GLN
2	LA	969	ASN
2	LA	1042	GLN
2	LA	1093	GLN
2	LA	1179	GLN
3	SA	57	GLN
3	SA	205	GLN
3	SA	394	HIS
4	TA	116	GLN
4	TA	148	GLN
4	TA	194	GLN
4	TB	41	ASN
4	TB	116	GLN
4	TB	148	GLN
4	TB	194	GLN
4	TB	282	ASN
4	TB	295	ASN
5	XA	12	ASN
5	XA	80	HIS
5	XB	48	ASN
5	XB	77	GLN
5	YB	4	HIS
5	ZA	21	ASN
5	ZB	61	ASN
6	PA	82	GLN
6	PA	124	GLN
6	PA	291	GLN
6	PA	409	GLN
6	PA	441	GLN
6	PA	462	GLN
6	PA	524	ASN
6	PA	570	GLN
6	PA	619	GLN
1	AC	64	GLN
1	AD	56	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AD	134	ASN
1	AD	148	ASN
1	AD	191	ASN
2	LB	11	ASN
2	LB	293	GLN
2	LB	297	ASN
2	LB	447	GLN
2	LB	509	GLN
2	LB	532	HIS
2	LB	882	ASN
2	LB	888	GLN
2	LB	969	ASN
2	LB	1042	GLN
2	LB	1093	GLN
3	SB	57	GLN
3	SB	93	HIS
3	SB	205	GLN
3	SB	394	HIS
4	TC	116	GLN
4	TC	148	GLN
4	TC	194	GLN
4	TD	41	ASN
4	TD	116	GLN
4	TD	148	GLN
4	TD	194	GLN
4	TD	282	ASN
4	TD	295	ASN
5	XC	12	ASN
5	XC	80	HIS
5	XD	48	ASN
5	XD	77	GLN
5	YD	4	HIS
5	ZC	21	ASN
5	ZD	60	HIS
5	ZD	61	ASN
1	AE	64	GLN
1	AE	69	ASN
1	AF	56	ASN
1	AF	64	GLN
1	AF	134	ASN
1	AF	148	ASN
1	AF	191	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LC	11	ASN
2	LC	293	GLN
2	LC	297	ASN
2	LC	447	GLN
2	LC	509	GLN
2	LC	532	HIS
2	LC	662	HIS
2	LC	882	ASN
2	LC	888	GLN
2	LC	969	ASN
2	LC	1042	GLN
2	LC	1093	GLN
3	SC	57	GLN
3	SC	93	HIS
3	SC	394	HIS
4	TE	116	GLN
4	TE	134	ASN
4	TE	148	GLN
4	TE	194	GLN
4	TF	41	ASN
4	TF	116	GLN
4	TF	148	GLN
4	TF	194	GLN
4	TF	282	ASN
4	TF	295	ASN
5	XE	12	ASN
5	XF	48	ASN
5	XF	77	GLN
5	YF	4	HIS
5	ZE	21	ASN
5	ZF	61	ASN
1	AG	64	GLN
1	AG	69	ASN
1	AH	56	ASN
1	AH	64	GLN
1	AH	134	ASN
1	AH	148	ASN
1	AH	191	ASN
2	LD	11	ASN
2	LD	293	GLN
2	LD	297	ASN
2	LD	447	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LD	509	GLN
2	LD	532	HIS
2	LD	882	ASN
2	LD	888	GLN
2	LD	969	ASN
2	LD	1042	GLN
2	LD	1093	GLN
3	SD	57	GLN
3	SD	93	HIS
3	SD	205	GLN
3	SD	394	HIS
4	TG	116	GLN
4	TG	134	ASN
4	TG	148	GLN
4	TG	194	GLN
4	TH	41	ASN
4	TH	116	GLN
4	TH	148	GLN
4	TH	194	GLN
4	TH	282	ASN
4	TH	295	ASN
5	XG	12	ASN
5	XG	80	HIS
5	XH	48	ASN
5	XH	77	GLN
5	YH	4	HIS
5	ZG	21	ASN
5	ZH	60	HIS
5	ZH	61	ASN
1	AI	64	GLN
1	AI	69	ASN
1	AJ	56	ASN
1	AJ	64	GLN
1	AJ	134	ASN
1	AJ	148	ASN
1	AJ	191	ASN
2	LE	11	ASN
2	LE	293	GLN
2	LE	297	ASN
2	LE	447	GLN
2	LE	509	GLN
2	LE	532	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	LE	882	ASN
2	LE	888	GLN
2	LE	969	ASN
2	LE	1042	GLN
2	LE	1093	GLN
3	SE	57	GLN
3	SE	394	HIS
4	TI	116	GLN
4	TI	148	GLN
4	TI	194	GLN
4	TJ	41	ASN
4	TJ	116	GLN
4	TJ	148	GLN
4	TJ	194	GLN
4	TJ	282	ASN
4	TJ	295	ASN
5	XI	12	ASN
5	XI	80	HIS
5	XJ	48	ASN
5	YJ	4	HIS
5	ZI	21	ASN
5	ZJ	60	HIS
5	ZJ	61	ASN
1	AK	64	GLN
1	AL	56	ASN
1	AL	64	GLN
1	AL	134	ASN
1	AL	148	ASN
1	AL	191	ASN
2	LF	11	ASN
2	LF	293	GLN
2	LF	447	GLN
2	LF	509	GLN
2	LF	532	HIS
2	LF	882	ASN
2	LF	888	GLN
2	LF	969	ASN
2	LF	1042	GLN
2	LF	1093	GLN
3	SF	57	GLN
3	SF	93	HIS
3	SF	394	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	TK	116	GLN
4	TK	134	ASN
4	TK	148	GLN
4	TK	194	GLN
4	TL	41	ASN
4	TL	116	GLN
4	TL	148	GLN
4	TL	194	GLN
4	TL	282	ASN
4	TL	295	ASN
5	XK	12	ASN
5	XL	48	ASN
5	XL	77	GLN
5	YL	4	HIS
5	ZK	21	ASN
5	ZL	60	HIS
5	ZL	61	ASN
6	PB	82	GLN
6	PB	124	GLN
6	PB	291	GLN
6	PB	409	GLN
6	PB	441	GLN
6	PB	462	GLN
6	PB	524	ASN
6	PB	570	GLN
6	PB	606	HIS
6	PB	619	GLN
6	PC	82	GLN
6	PC	124	GLN
6	PC	291	GLN
6	PC	409	GLN
6	PC	441	GLN
6	PC	462	GLN
6	PC	524	ASN
6	PC	570	GLN
6	PD	82	GLN
6	PD	124	GLN
6	PD	291	GLN
6	PD	409	GLN
6	PD	441	GLN
6	PD	462	GLN
6	PD	524	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	PD	570	GLN
6	PD	606	HIS
6	PD	619	GLN
6	PE	82	GLN
6	PE	124	GLN
6	PE	291	GLN
6	PE	409	GLN
6	PE	441	GLN
6	PE	462	GLN
6	PE	524	ASN
6	PE	570	GLN
6	PE	619	GLN
6	PF	82	GLN
6	PF	124	GLN
6	PF	291	GLN
6	PF	409	GLN
6	PF	441	GLN
6	PF	524	ASN
6	PF	570	GLN
6	PF	606	HIS
6	PF	619	GLN
6	PG	82	GLN
6	PG	124	GLN
6	PG	291	GLN
6	PG	388	GLN
6	PG	409	GLN
6	PG	441	GLN
6	PG	462	GLN
6	PG	524	ASN
6	PG	570	GLN
6	PG	619	GLN
6	PH	82	GLN
6	PH	124	GLN
6	PH	291	GLN
6	PH	409	GLN
6	PH	441	GLN
6	PH	462	GLN
6	PH	524	ASN
6	PH	570	GLN
6	PH	606	HIS
6	PH	619	GLN
6	PI	82	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	PI	124	GLN
6	PI	291	GLN
6	PI	388	GLN
6	PI	409	GLN
6	PI	441	GLN
6	PI	462	GLN
6	PI	524	ASN
6	PI	570	GLN
6	PI	619	GLN
6	PJ	82	GLN
6	PJ	117	ASN
6	PJ	124	GLN
6	PJ	291	GLN
6	PJ	388	GLN
6	PJ	409	GLN
6	PJ	441	GLN
6	PJ	462	GLN
6	PJ	524	ASN
6	PJ	570	GLN
6	PJ	606	HIS
6	PJ	619	GLN
6	PJ	649	GLN
6	PK	82	GLN
6	PK	124	GLN
6	PK	291	GLN
6	PK	387	ASN
6	PK	409	GLN
6	PK	441	GLN
6	PK	524	ASN
6	PK	570	GLN
6	PK	619	GLN
6	PL	82	GLN
6	PL	124	GLN
6	PL	291	GLN
6	PL	409	GLN
6	PL	441	GLN
6	PL	462	GLN
6	PL	524	ASN
6	PL	570	GLN
6	PL	606	HIS
6	PL	619	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

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.

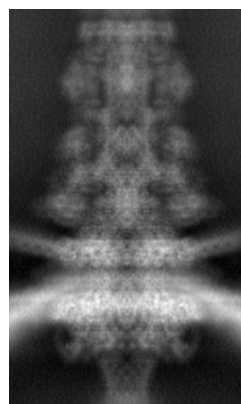
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72877. These allow visual inspection of the internal detail of the map and identification of artifacts.

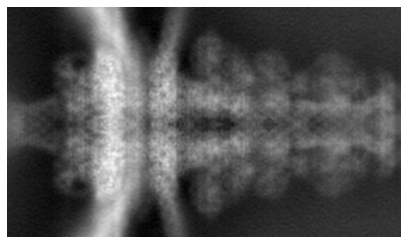
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

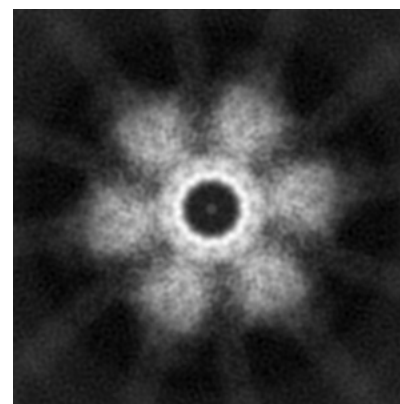
6.1.1 Primary map



X

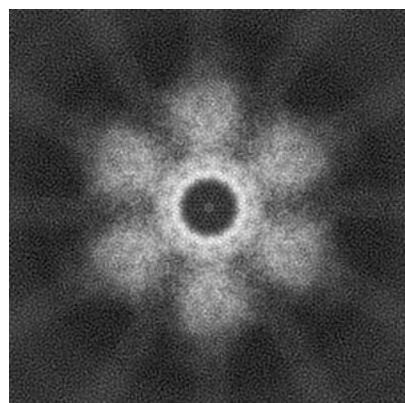


Y

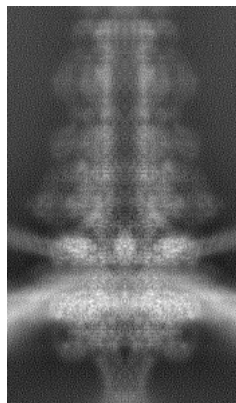


Z

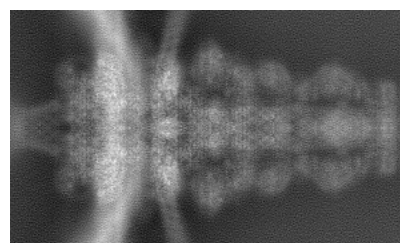
6.1.2 Raw map



X



Y

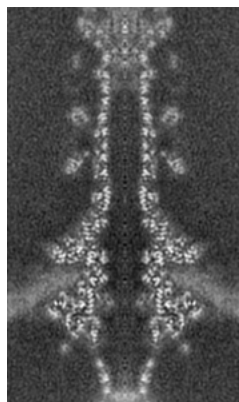


Z

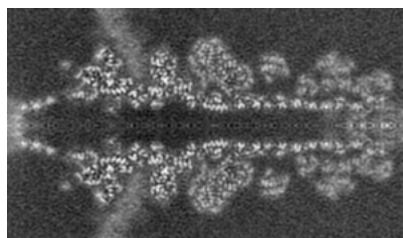
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

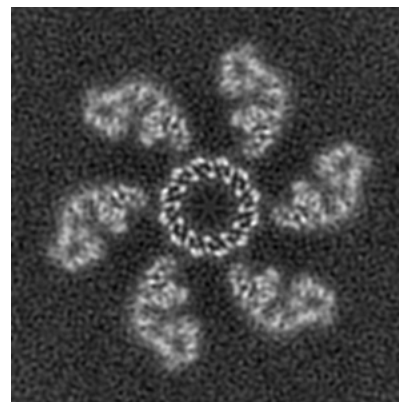
6.2.1 Primary map



X Index: 111

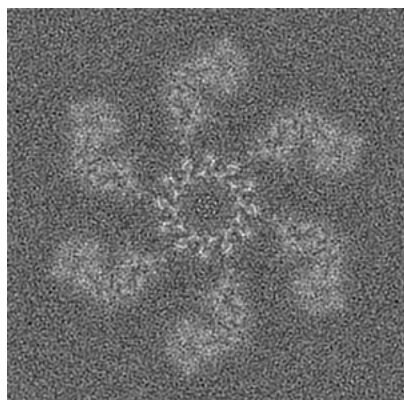


Y Index: 112

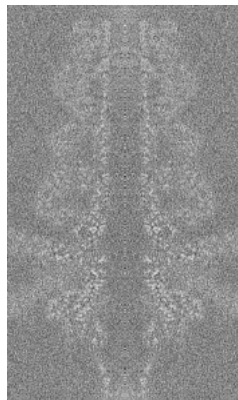


Z Index: 191

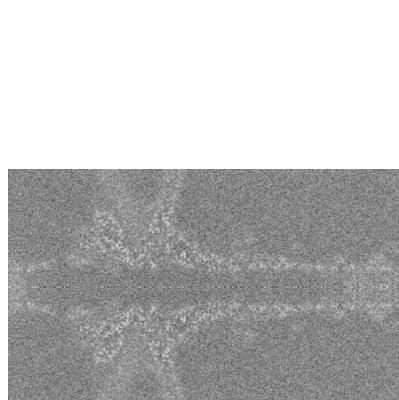
6.2.2 Raw map



X Index: 191



Y Index: 112



Z Index: 111

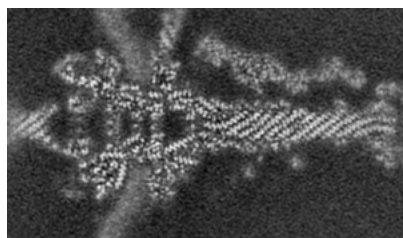
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

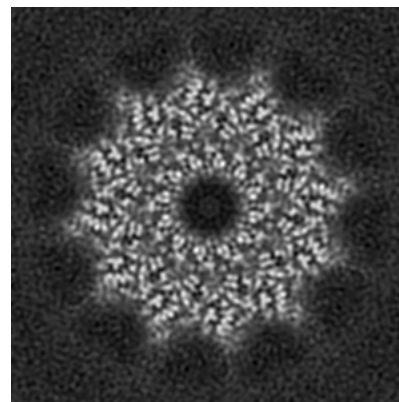
6.3.1 Primary map



X Index: 93

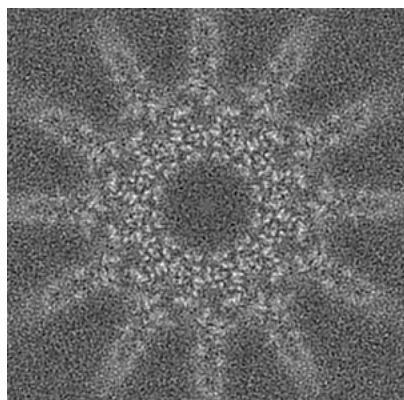


Y Index: 130

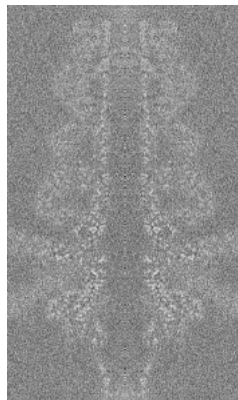


Z Index: 143

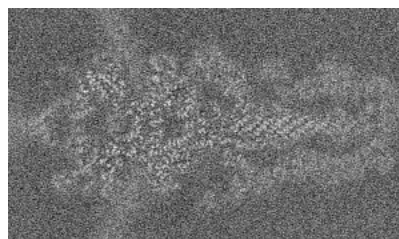
6.3.2 Raw map



X Index: 151



Y Index: 112

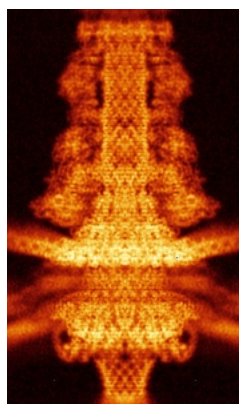


Z Index: 91

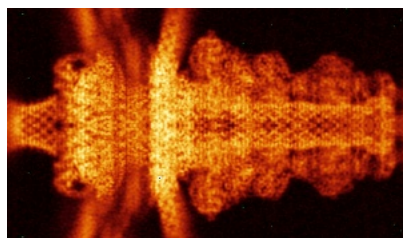
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

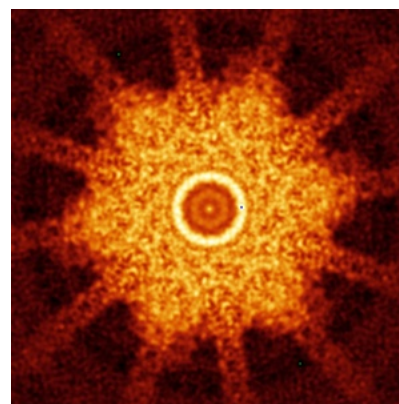
6.4.1 Primary map



X

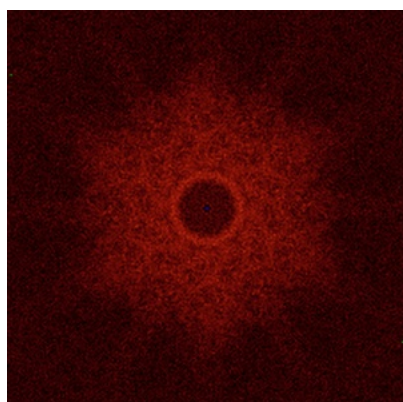


Y

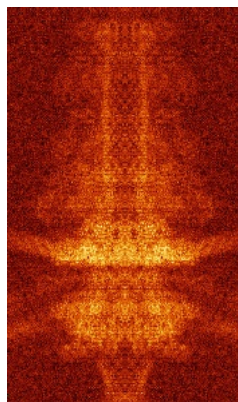


Z

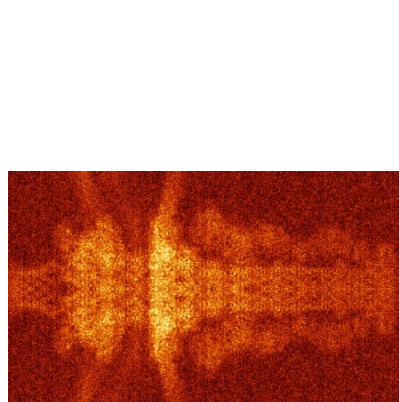
6.4.2 Raw map



X



Y

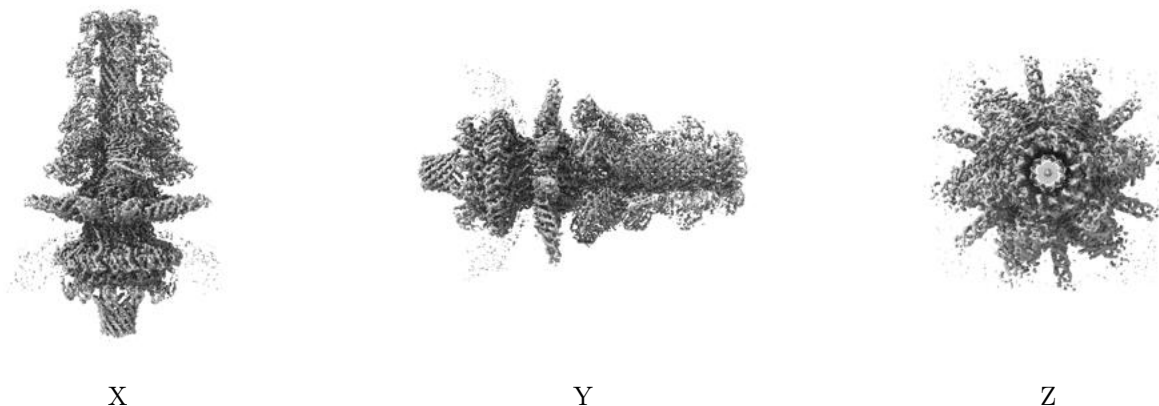


Z

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.

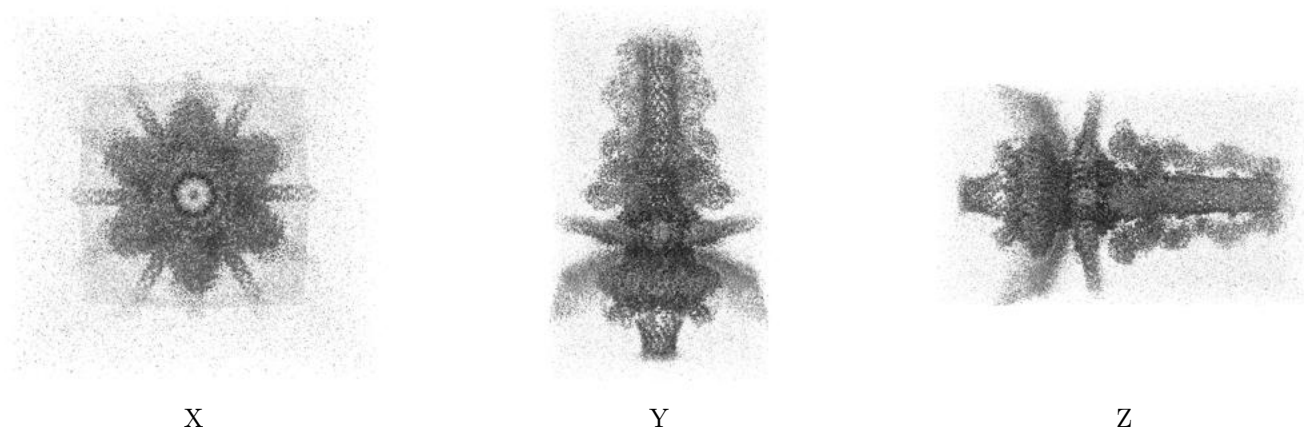
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.17. 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



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.

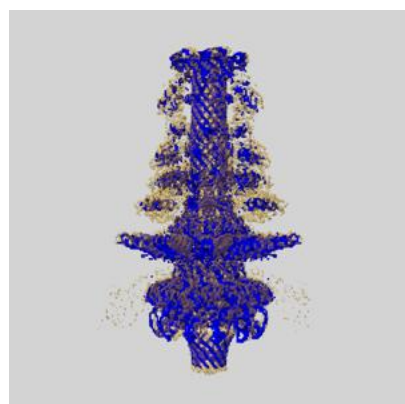
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

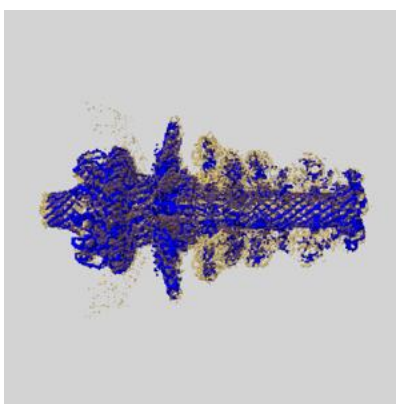
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

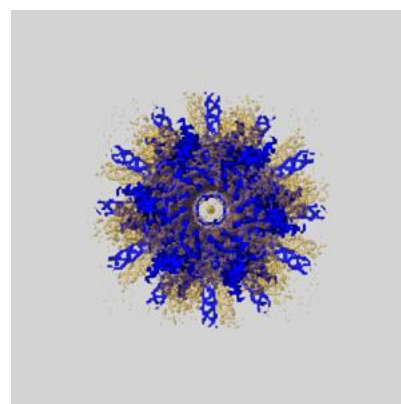
6.6.1 emd_72877_msk_1.map [i](#)



X



Y

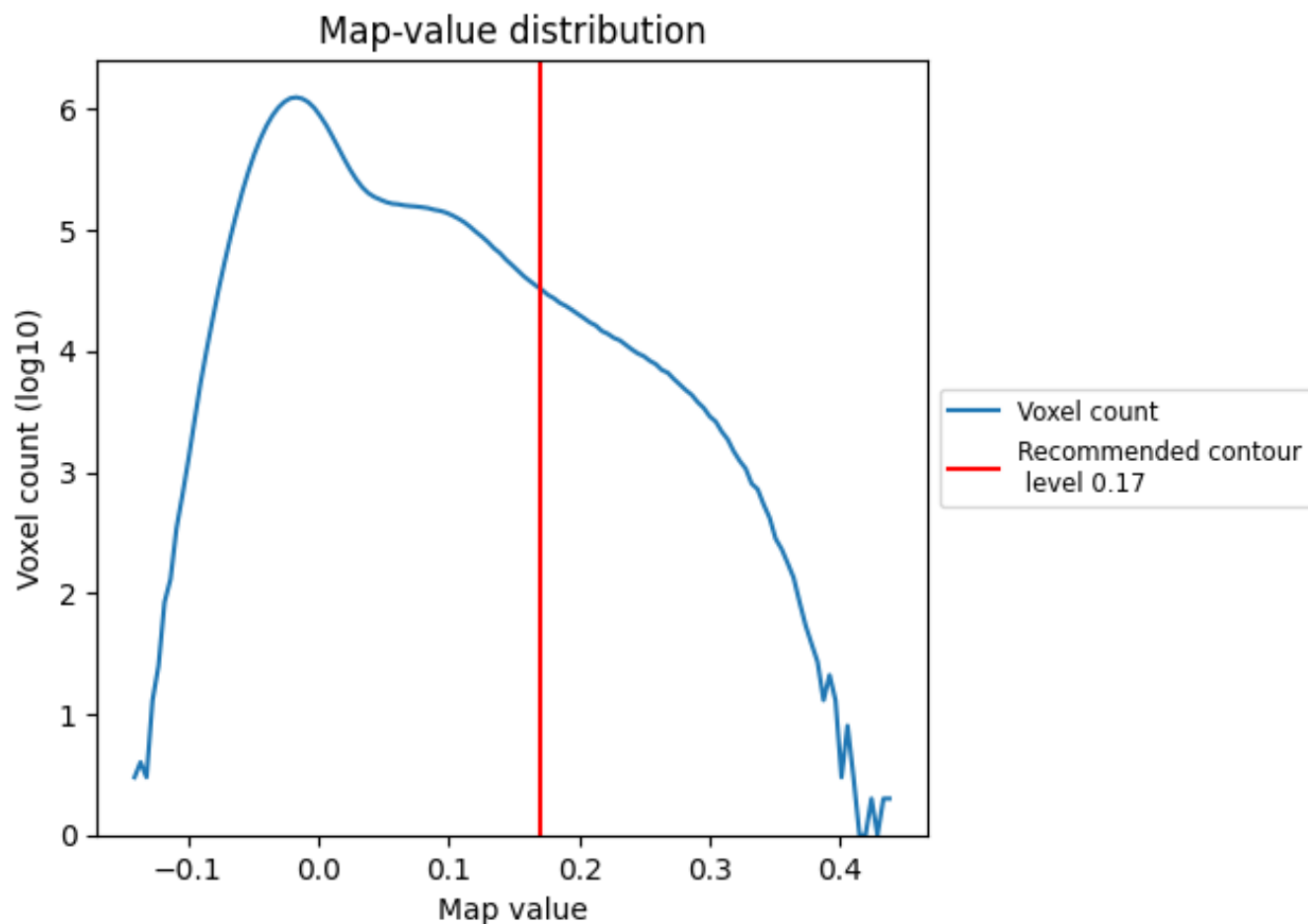


Z

7 Map analysis [i](#)

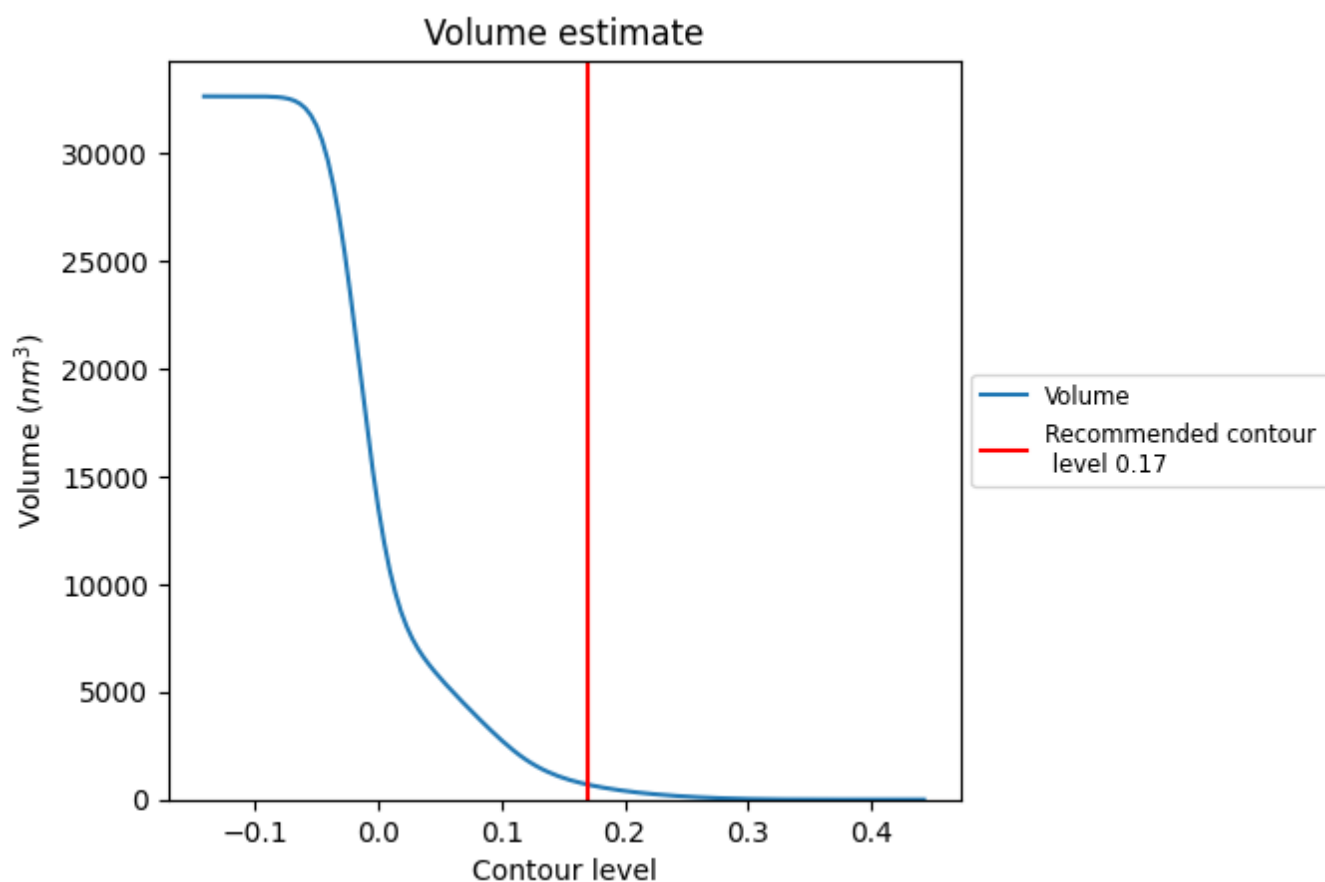
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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 [i](#)



The volume at the recommended contour level is 698 nm³; this corresponds to an approximate mass of 631 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

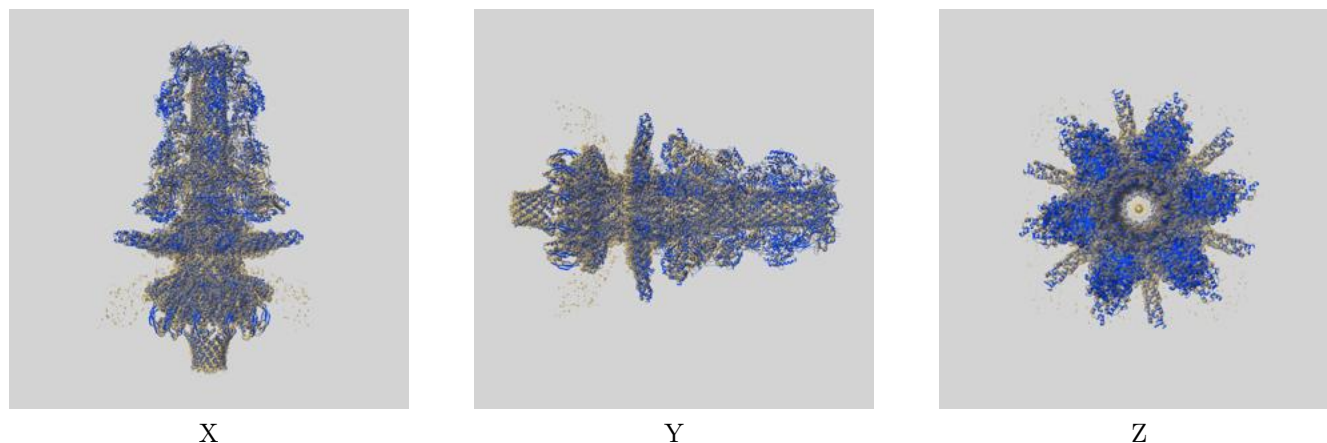
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

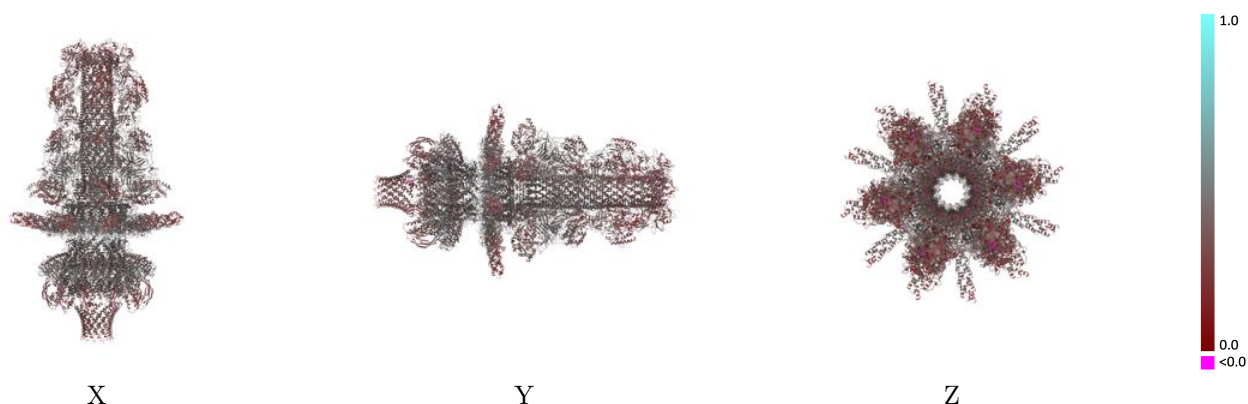
This section contains information regarding the fit between EMDB map EMD-72877 and PDB model 9YF5. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



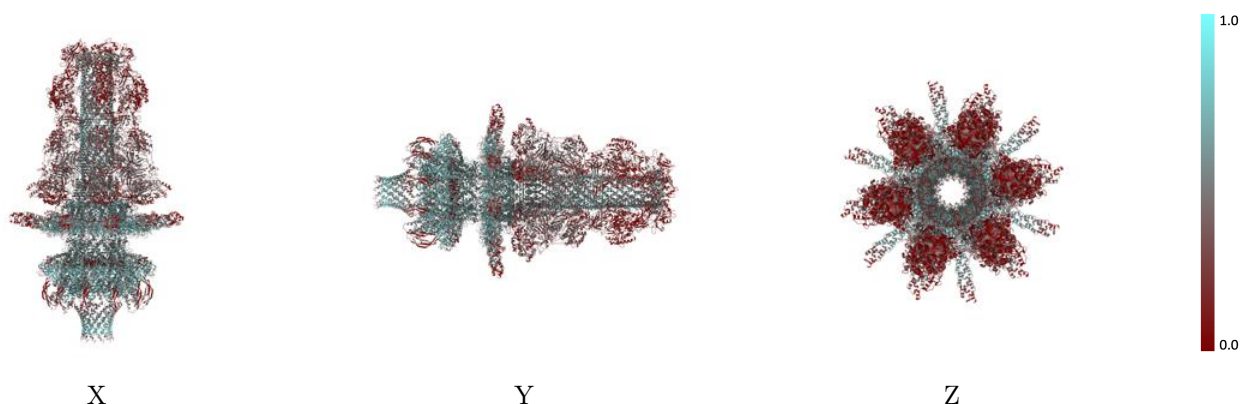
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



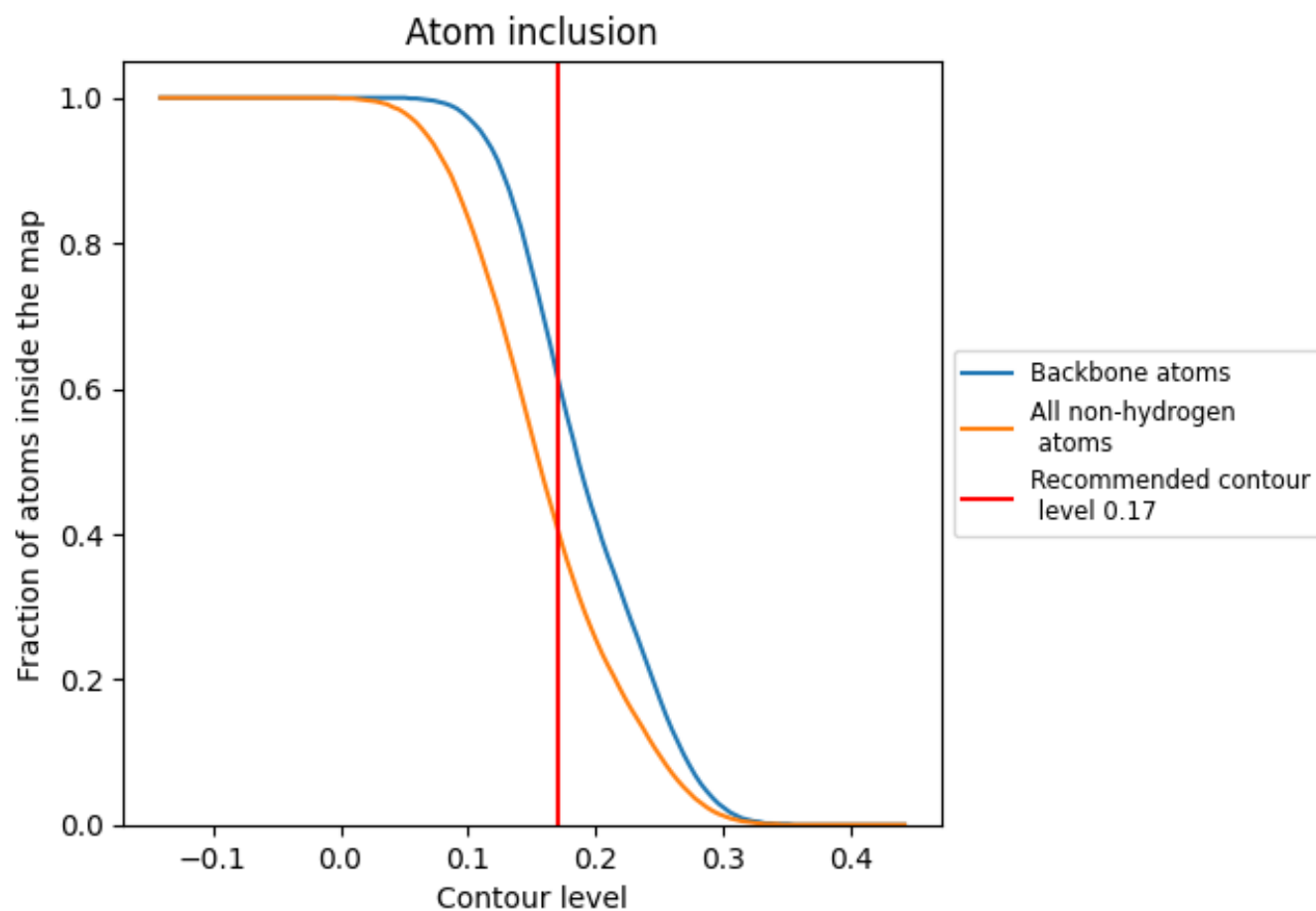
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 41% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4100	 0.3850
AA	 0.5740	 0.4470
AB	 0.5760	 0.4450
AC	 0.5740	 0.4440
AD	 0.5800	 0.4460
AE	 0.5800	 0.4450
AF	 0.5830	 0.4460
AG	 0.5740	 0.4470
AH	 0.5760	 0.4460
AI	 0.5740	 0.4460
AJ	 0.5810	 0.4470
AK	 0.5800	 0.4460
AL	 0.5830	 0.4460
LA	 0.2220	 0.3590
LB	 0.2220	 0.3590
LC	 0.2220	 0.3600
LD	 0.2220	 0.3600
LE	 0.2220	 0.3600
LF	 0.2220	 0.3610
PA	 0.5280	 0.3990
PB	 0.5190	 0.3980
PC	 0.5260	 0.3990
PD	 0.5210	 0.3990
PE	 0.5250	 0.3990
PF	 0.5230	 0.3960
PG	 0.5280	 0.3990
PH	 0.5200	 0.3960
PI	 0.5270	 0.3990
PJ	 0.5200	 0.3970
PK	 0.5250	 0.3990
PL	 0.5230	 0.3980
SA	 0.2420	 0.3550
SB	 0.2390	 0.3540
SC	 0.2350	 0.3560
SD	 0.2420	 0.3560



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SE	 0.2390	 0.3560
SF	 0.2350	 0.3550
TA	 0.4960	 0.3910
TB	 0.5020	 0.3920
TC	 0.5020	 0.3900
TD	 0.4970	 0.3910
TE	 0.5000	 0.3880
TF	 0.5030	 0.3890
TG	 0.4960	 0.3900
TH	 0.5020	 0.3900
TI	 0.5020	 0.3900
TJ	 0.4970	 0.3910
TK	 0.5010	 0.3900
TL	 0.5030	 0.3920
XA	 0.4530	 0.3640
XB	 0.4550	 0.3620
XC	 0.4500	 0.3670
XD	 0.4550	 0.3670
XE	 0.4430	 0.3640
XF	 0.4570	 0.3670
XG	 0.4550	 0.3680
XH	 0.4620	 0.3670
XI	 0.4520	 0.3650
XJ	 0.4530	 0.3620
XK	 0.4460	 0.3640
XL	 0.4570	 0.3610
YA	 0.4850	 0.3690
YB	 0.4460	 0.3700
YC	 0.4780	 0.3740
YD	 0.4480	 0.3740
YE	 0.4870	 0.3720
YF	 0.4500	 0.3750
YG	 0.4830	 0.3720
YH	 0.4500	 0.3770
YI	 0.4780	 0.3720
YJ	 0.4460	 0.3710
YK	 0.4870	 0.3710
YL	 0.4500	 0.3710
ZA	 0.4290	 0.3600
ZB	 0.4020	 0.3510
ZC	 0.4190	 0.3570
ZD	 0.4040	 0.3520

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
ZE	 0.4230	 0.3600
ZF	 0.4080	 0.3520
ZG	 0.4270	 0.3600
ZH	 0.4020	 0.3540
ZI	 0.4190	 0.3590
ZJ	 0.4040	 0.3560
ZK	 0.4230	 0.3590
ZL	 0.4080	 0.3520