



Full wwPDB EM Validation Report ⓘ

Jul 8, 2026 – 02:29 pm BST

PDB ID : 9T5C / pdb_00009t5c
EMDB ID : EMD-55100
Title : Naked mole-rat 80S ribosome in post-translocation non-rotated state
Authors : Gul, M.; Kudryashev, M.
Deposited on : 2025-11-05
Resolution : 2.89 Å(reported)
Based on initial model : 7CPU

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:

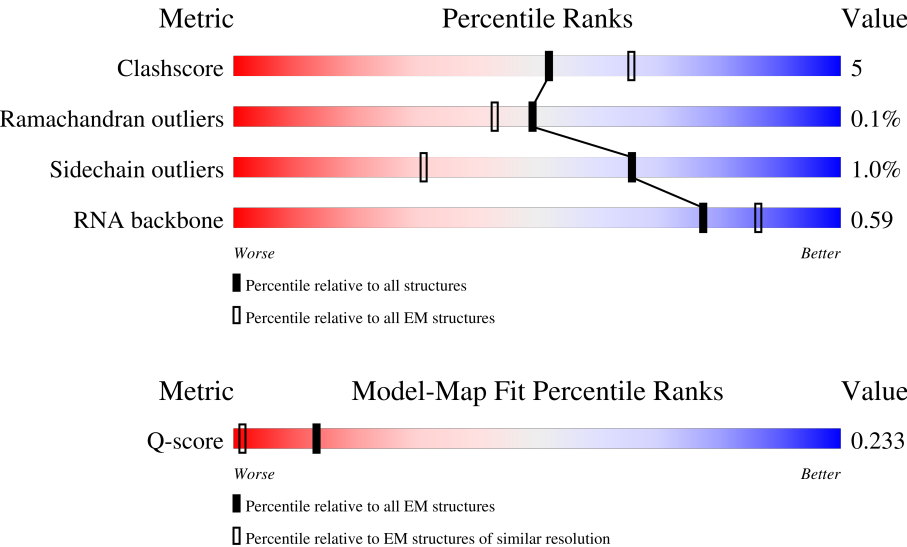
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.89 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	12148 (2.39 - 3.39)

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	B	10	
2	L5	4731	
3	L7	120	

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Mol	Chain	Length	Quality of chain
4	L8	158	
5	LA	257	
6	LC	419	
7	LD	297	
8	LE	296	
9	LF	270	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	217	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	160	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1870	
47	S6	75	
48	S7	75	
49	SA	295	
50	SB	264	
51	SC	293	
52	SD	243	
53	SE	263	

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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SG	249	
56	SH	194	
57	SI	208	
58	SJ	194	
59	SK	165	
60	SL	158	
61	SN	151	
62	SO	151	
63	SP	145	
64	SQ	146	
65	SR	135	
66	SS	152	
67	ST	145	
68	SU	119	
69	SV	83	
70	SW	130	
71	SX	143	
72	SY	133	
73	SZ	125	
74	Sa	115	
75	Sb	84	
76	Sc	69	
77	Sd	56	
78	Se	133	

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Mol	Chain	Length	Quality of chain
79	Sg	317	50% 66% 26% 8%
80	LB	403	80% 18%

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 206721 atoms, of which 38 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 RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	10	Total	C	N	O	P	0	0
			208	94	32	72	10		

- Molecule 2 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	L5	3455	Total	C	H	N	O	P	0	0
			74122	32996	35	13550	24087	3454		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 4 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 5 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	358	Total	C	N	O	S	0	0
			2862	1800	572	475	15		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2389	1509	441	425	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LD	19	ARG	LYS	conflict	UNP A0AAX6P0W2
LD	126	ASN	THR	conflict	UNP A0AAX6P0W2
LD	128	GLY	ASP	conflict	UNP A0AAX6P0W2
LD	191	ASN	SER	conflict	UNP A0AAX6P0W2

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	216	Total	C	N	O	S	0	0
			1743	1115	332	292	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	214	Total	C	N	O	S	0	0
			1771	1139	337	287	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	224	Total	C	N	O	S	0	0
			1813	1156	349	304	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LG	24	ALA	THR	conflict	UNP A0A0P6K8Y4
LG	131	LYS	ARG	conflict	UNP A0A0P6K8Y4

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1519	956	284	273	6		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	14	GLU	LYS	conflict	UNP G5C3U8
LH	17	GLU	ASP	conflict	UNP G5C3U8
LH	130	THR	ALA	conflict	UNP G5C3U8
LH	190	ALA	PRO	conflict	UNP G5C3U8

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	201	Total	C	N	O	S	0	0
			1633	1037	316	268	12		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	168	Total	C	N	O	S	0	0
			1349	853	251	239	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	205	Total	C	N	O	S	0	0
			1660	1038	342	276	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	20	GLN	ARG	conflict	UNP A0AAX6P3F5
LL	23	ASP	ALA	conflict	UNP A0AAX6P3F5
LL	168	VAL	ILE	conflict	UNP A0AAX6P3F5

- Molecule 15 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	136	Total	C	N	O	S	0	0
			1125	721	218	179	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LO	100	GLU	ASP	conflict	UNP A0AAX6Q4S4
LO	105	LEU	PHE	conflict	UNP A0AAX6Q4S4
LO	166	MET	ILE	conflict	UNP A0AAX6Q4S4
LO	175	LEU	MET	conflict	UNP A0AAX6Q4S4
LO	190	CYS	SER	conflict	UNP A0AAX6Q4S4
LO	199	ASN	HIS	conflict	UNP A0AAX6Q4S4

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	152	Total	C	N	O	S	0	0
			1231	770	238	214	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LP	40	ASP	HIS	conflict	UNP A0A0P6JH89

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1515	948	314	249	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LQ	92	ILE	VAL	conflict	UNP G5B890
LQ	129	GLU	ASP	conflict	UNP G5B890
LQ	134	ARG	HIS	conflict	UNP G5B890

- Molecule 20 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	178	Total	C	N	O	S	0	0
			1490	921	324	236	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1451	924	283	234	10		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LS	23	HIS	ARG	conflict	UNP A0A0P6JCV6
LS	135	GLY	SER	conflict	UNP A0A0P6JCV6
LS	161	ARG	HIS	conflict	UNP A0A0P6JCV6

- Molecule 22 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	160	Total	C	N	O	S	0	0
			1307	829	253	218	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LT	75	ILE	VAL	conflict	UNP G5ATV5

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	100	Total	C	N	O	S	0	0
			817	523	143	149	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LX	32	VAL	ILE	conflict	UNP A0AAX6PQW7

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	131	Total	C	N	O	S	0	0
			1093	686	221	183	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	97	Total	C	N	O	S	0	0
			794	497	171	122	4		

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lc	4	ALA	THR	conflict	UNP G5BJ16
Lc	5	LYS	GLU	conflict	UNP G5BJ16
Lc	70	GLY	ALA	conflict	UNP G5BJ16
Lc	90	ARG	THR	conflict	UNP G5BJ16

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	111	Total	C	N	O	S	0	0
			878	549	181	142	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lg	71	GLN	LYS	conflict	UNP A0AAX6Q439

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	121	Total	C	N	O	S	0	0
			1009	640	203	165	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lh	96	THR	ASN	conflict	UNP A0AAX6PDT5
Lh	105	LYS	ASN	conflict	UNP A0AAX6PDT5
Lh	119	TYR	PHE	conflict	UNP A0AAX6PDT5

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	68	ASP	GLU	conflict	UNP A0A0P6IYP5

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	123	Total	C	N	O	S	0	0
			987	611	205	166	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lr	9	VAL	ILE	conflict	UNP G5BVZ2
Lr	125	VAL	MET	conflict	UNP G5BVZ2
Lr	137	SER	ALA	conflict	UNP G5BVZ2

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
46	S2	1656	Total	C	H	N	O	P	0	0
			35239	15727	3	6309	11545	1655		

- Molecule 47 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S6	75	Total	C	N	O	P	0	0
			1596	714	291	517	74		

- Molecule 48 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S7	74	Total	C	N	O	P	0	0
			1570	702	280	515	73		

- Molecule 49 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SA	239	THR	ALA	conflict	UNP A0A0P6K1L6
SA	290	ALA	THR	conflict	UNP A0A0P6K1L6

- Molecule 50 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SB	236	GLY	SER	conflict	UNP G5C1K3
SB	242	ALA	THR	conflict	UNP G5C1K3

- Molecule 51 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SC	220	Total	C	N	O	S	0	0
			1690	1095	290	296	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SC	19	LEU	THR	conflict	UNP A0AAX6QEX7
SC	100	ALA	THR	conflict	UNP A0AAX6QEX7

- Molecule 52 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SD	222	Total	C	N	O	S	0	0
			1726	1100	310	309	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SD	235	ALA	VAL	conflict	UNP G5AS76

- Molecule 53 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SE	258	Total	C	N	O	S	0	0
			2050	1311	381	350	8		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SE	76	VAL	ILE	conflict	UNP A0A0P6JF61
SE	111	VAL	ILE	conflict	UNP A0A0P6JF61
SE	165	GLU	ASP	conflict	UNP A0A0P6JF61
SE	213	ALA	THR	conflict	UNP A0A0P6JF61
SE	260	GLN	HIS	conflict	UNP A0A0P6JF61

- Molecule 54 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SF	179	Total	C	N	O	S	0	0
			1416	888	262	259	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SF	6	ALA	THR	conflict	UNP G5B7K7
SF	8	THR	ALA	conflict	UNP G5B7K7

- Molecule 55 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG	220	Total	C	N	O	S	0	0
			1725	1077	346	296	6		

- Molecule 56 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SH	183	Total	C	N	O	S	0	0
			1457	929	267	260	1		

- Molecule 57 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SI	202	Total	C	N	O	S	0	0
			1593	999	312	277	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SI	40	PRO	ILE	conflict	UNP G5ARV4
SI	91	VAL	ILE	conflict	UNP G5ARV4
SI	175	ILE	VAL	conflict	UNP G5ARV4

- Molecule 58 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SJ	155	Total	C	N	O	S	0	0
			1258	806	246	204	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SJ	115	LEU	PHE	conflict	UNP A0AAX6Q606

- Molecule 59 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SK	96	Total	C	N	O	S	0	0
			789	513	141	129	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SK	109	PRO	VAL	conflict	UNP A0A0P6IZJ7
SK	115	ALA	MET	conflict	UNP A0A0P6IZJ7
SK	117	PHE	LEU	conflict	UNP A0A0P6IZJ7

- Molecule 60 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SL	134	Total	C	N	O	S	0	0
			1105	705	206	188	6		

- Molecule 61 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 62 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 63 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SP	124	Total	C	N	O	S	0	0
			997	632	186	172	7		

- Molecule 64 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SQ	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 65 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SR	131	Total	C	N	O	S	0	0
			1064	668	198	194	4		

- Molecule 66 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SS	140	Total	C	N	O	S	0	0
			1157	728	231	197	1		

- Molecule 67 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	ST	140	Total	C	N	O	S	0	0
			1090	681	212	195	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ST	88	ARG	MET	conflict	UNP A0AAX6QEV3

- Molecule 68 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SU	98	Total	C	N	O	S	0	0
			776	488	145	138	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SU	18	CYS	HIS	conflict	UNP A0AAX6QEN2
SU	19	LEU	ARG	conflict	UNP A0AAX6QEN2
SU	23	ILE	THR	conflict	UNP A0AAX6QEN2

- Molecule 69 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SV	83	Total	C	N	O	S	0	0
			639	393	118	123	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SV	25	ALA	GLY	conflict	UNP G5C8F1
SV	41	ARG	LYS	conflict	UNP G5C8F1
SV	42	THR	VAL	conflict	UNP G5C8F1
SV	54	GLY	ALA	conflict	UNP G5C8F1
SV	79	ILE	VAL	conflict	UNP G5C8F1
SV	82	ASP	ASN	conflict	UNP G5C8F1

- Molecule 70 is a protein called 40S ribosomal protein S15a isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 71 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SX	139	Total	C	N	O	S	0	0
			1081	682	215	181	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SX	23	ARG	HIS	conflict	UNP A0AAX6P1S3

- Molecule 72 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SY	119	Total	C	N	O	S	0	0
			979	623	190	161	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SY	10	GLN	ARG	conflict	UNP A0AAX6PA11
SY	15	LYS	ASN	conflict	UNP A0AAX6PA11

- Molecule 73 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SZ	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SZ	124	ASP	GLU	conflict	UNP A0AAX6PPX8
SZ	125	ALA	PRO	conflict	UNP A0AAX6PPX8

- Molecule 74 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sa	99	Total	C	N	O	S	0	0
			793	492	165	131	5		

- Molecule 75 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 76 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sc	62	Total	C	N	O	S	0	0
			454	279	88	85	2		

- Molecule 77 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 78 is a protein called Ubiquitin-like protein fubi and ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Se	49	Total	C	N	O	S	0	0
			384	234	87	62	1		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Se	9	GLU	ASP	conflict	UNP A0AAX6PHM7
Se	13	LEU	ILE	conflict	UNP A0AAX6PHM7
Se	18	GLN	HIS	conflict	UNP A0AAX6PHM7
Se	26	ASP	ALA	conflict	UNP A0AAX6PHM7
Se	27	HIS	GLN	conflict	UNP A0AAX6PHM7
Se	46	SER	LYS	conflict	UNP A0AAX6PHM7
Se	51	GLU	ASP	conflict	UNP A0AAX6PHM7
Se	63	THR	GLY	conflict	UNP A0AAX6PHM7

- Molecule 79 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sg	291	Total	C	N	O	S	0	0
			2271	1437	396	426	12		

- Molecule 80 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	LB	397	Total	C	N	O	S	0	0
			3202	2039	603	546	14		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LB	37	ALA	PRO	conflict	UNP A0A0P6IYN5
LB	41	VAL	ILE	conflict	UNP A0A0P6IYN5
LB	101	THR	SER	conflict	UNP A0A0P6IYN5
LB	141	THR	MET	conflict	UNP A0A0P6IYN5
LB	147	GLU	ASP	conflict	UNP A0A0P6IYN5
LB	151	ASN	SER	conflict	UNP A0A0P6IYN5
LB	205	VAL	ILE	conflict	UNP A0A0P6IYN5
LB	208	ASN	SER	conflict	UNP A0A0P6IYN5
LB	331	ILE	VAL	conflict	UNP A0A0P6IYN5
LB	382	MET	ILE	conflict	UNP A0A0P6IYN5

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	B	1	Total	Mg	0
			1	1	
81	L5	226	Total	Mg	0
			226	226	
81	L7	4	Total	Mg	0
			4	4	
81	L8	3	Total	Mg	0
			3	3	
81	LI	1	Total	Mg	0
			1	1	
81	LN	1	Total	Mg	0
			1	1	
81	LP	1	Total	Mg	0
			1	1	
81	Le	2	Total	Mg	0
			2	2	

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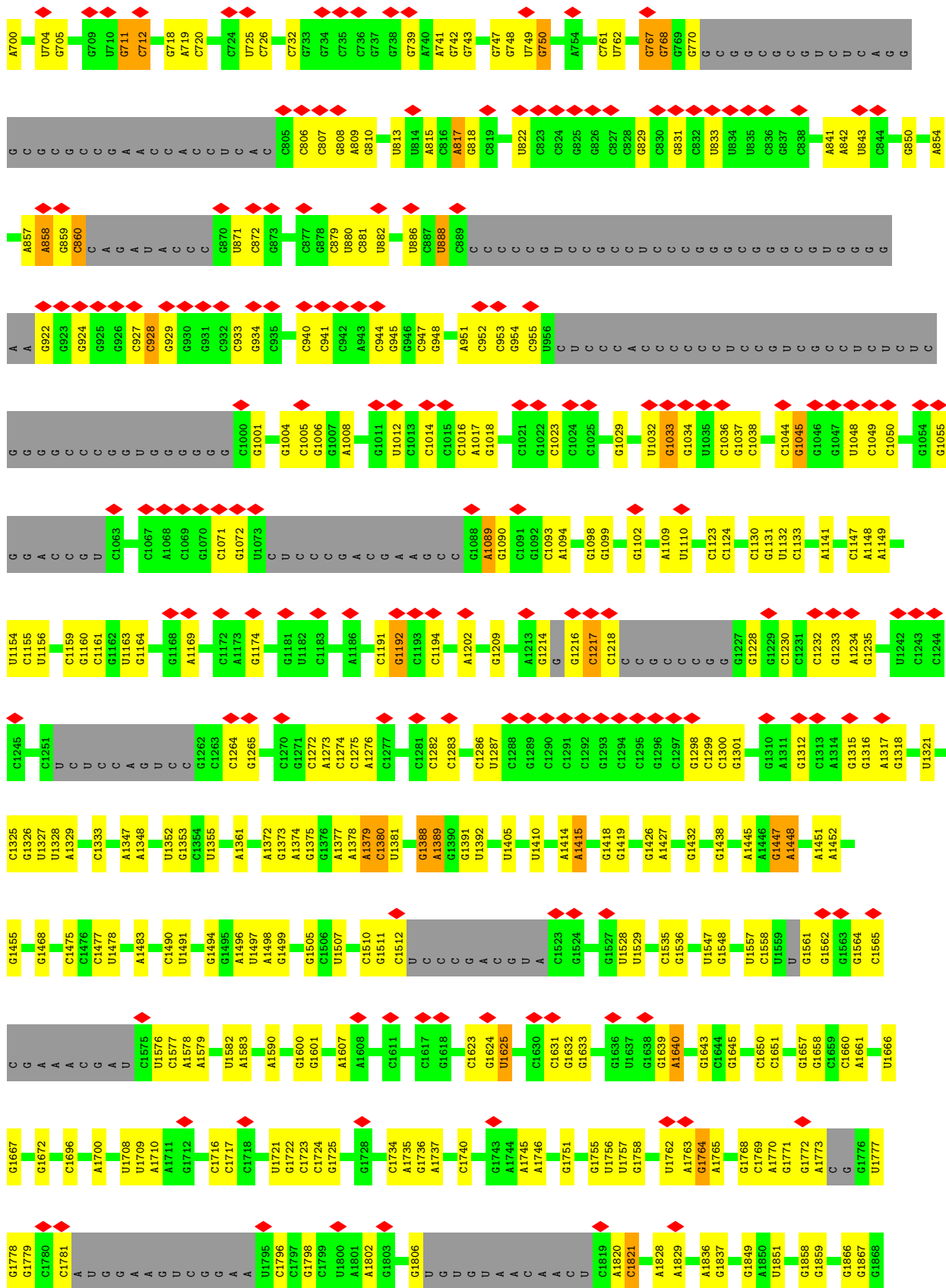
Mol	Chain	Residues	Atoms		AltConf
81	Lg	1	Total 1	Mg 1	0
81	S2	86	Total 86	Mg 86	0
81	SO	1	Total 1	Mg 1	0
81	LB	1	Total 1	Mg 1	0

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

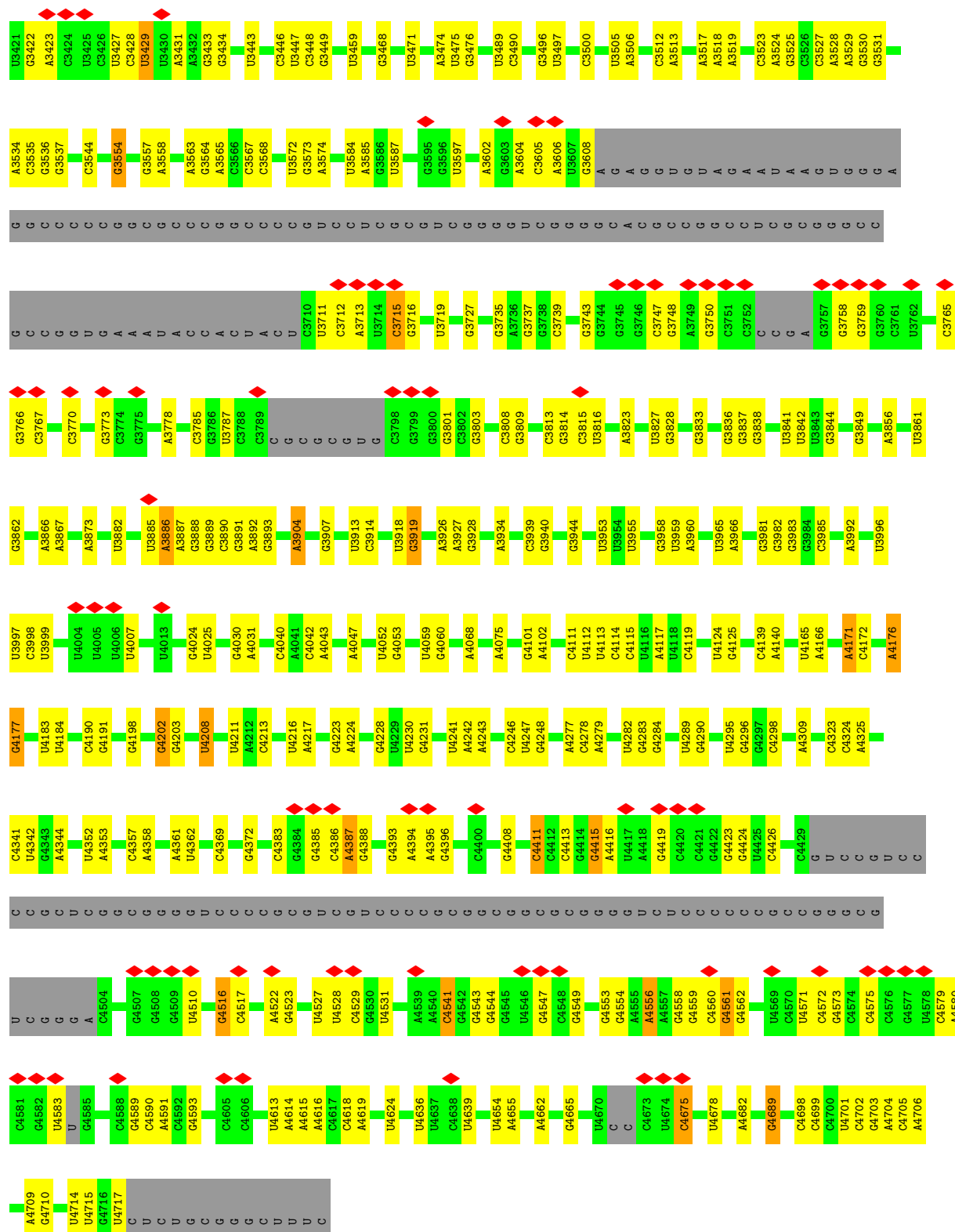
Mol	Chain	Residues	Atoms		AltConf
82	Lg	1	Total 1	Zn 1	0
82	Lp	1	Total 1	Zn 1	0
82	Sa	1	Total 1	Zn 1	0

- Molecule 83 is water.

Mol	Chain	Residues	Atoms		AltConf
83	L5	3	Total 3	O 3	0
83	La	1	Total 1	O 1	0
83	S2	2	Total 2	O 2	0



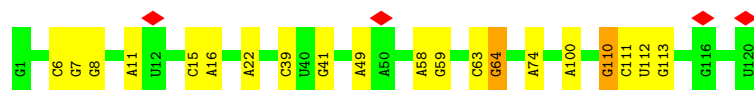




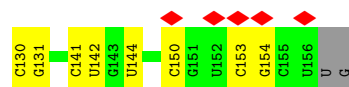
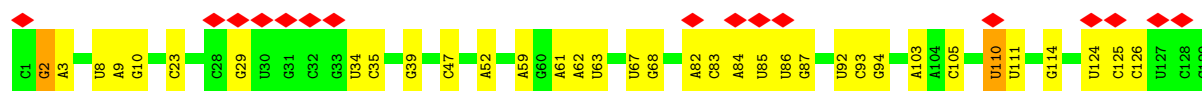
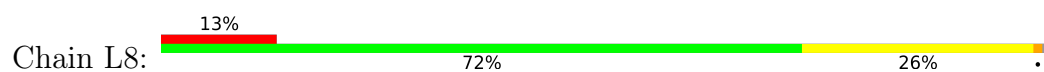
• Molecule 3: 5S ribosomal RNA

Chain L7:

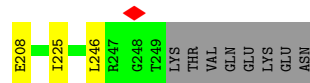
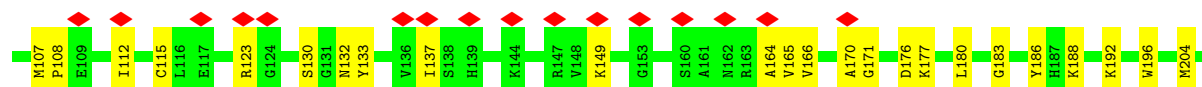
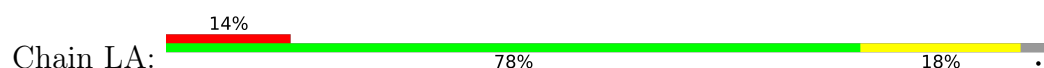




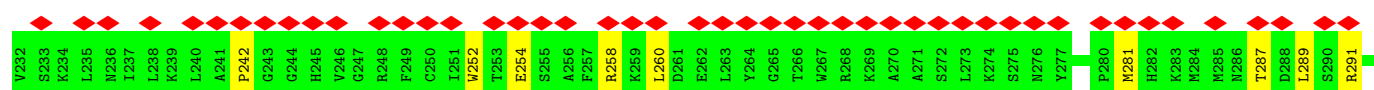
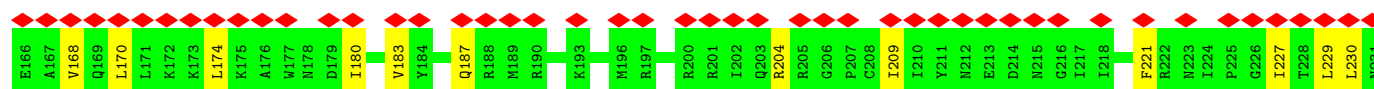
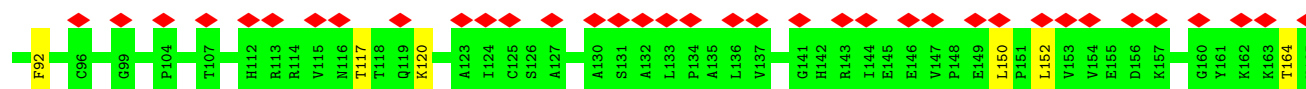
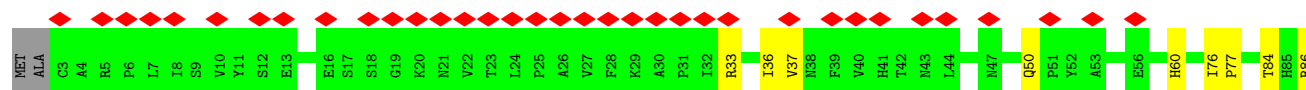
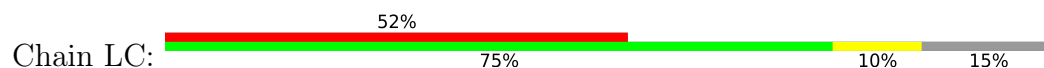
• Molecule 4: 5.8S ribosomal RNA



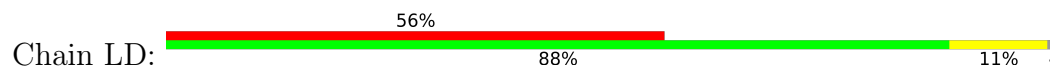
• Molecule 5: Large ribosomal subunit protein uL2



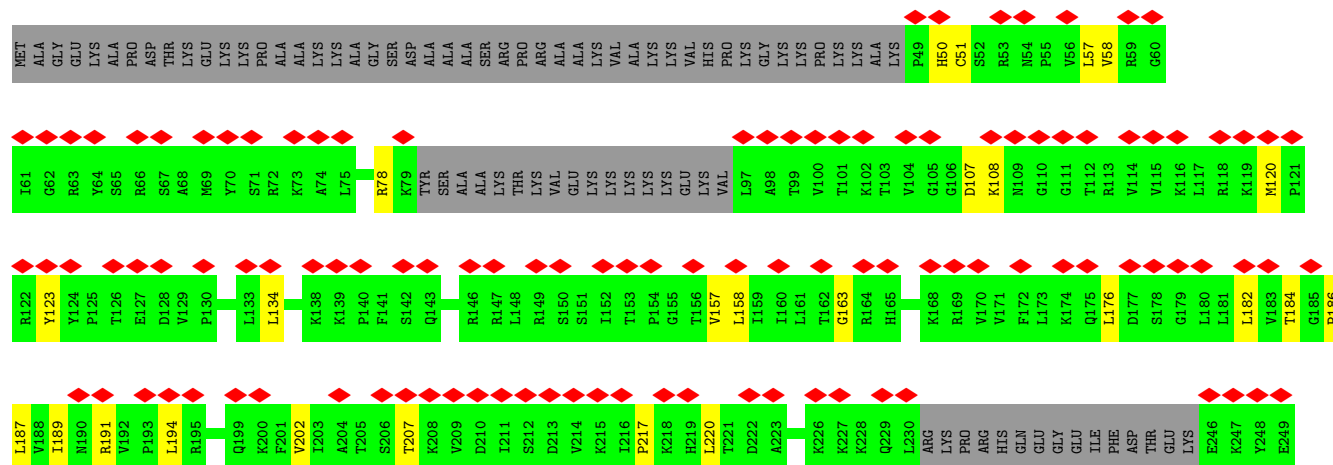
• Molecule 6: Large ribosomal subunit protein uL4

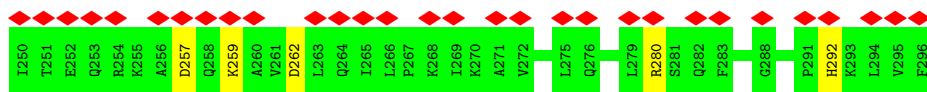


- Molecule 7: Large ribosomal subunit protein uL18

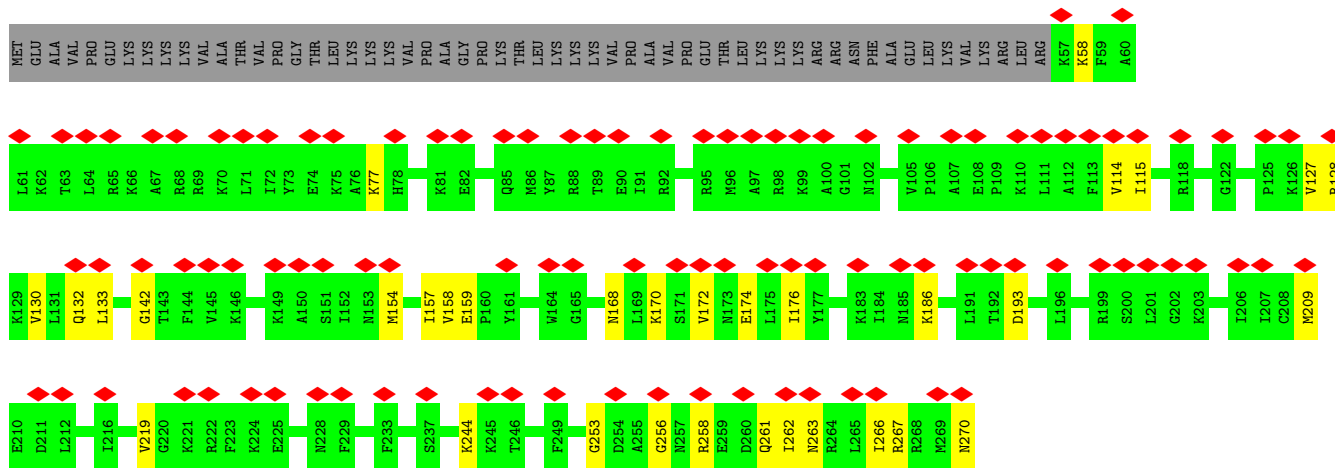
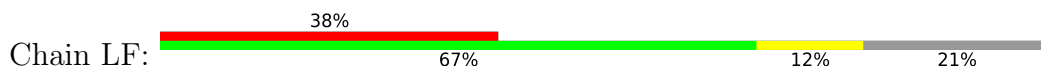


- Molecule 8: Large ribosomal subunit protein eL6

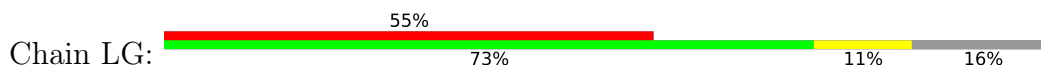




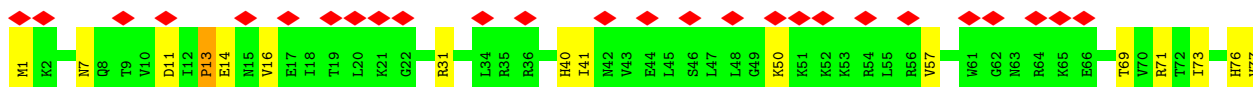
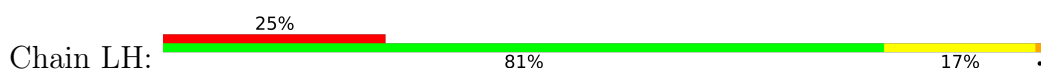
• Molecule 9: Large ribosomal subunit protein uL30

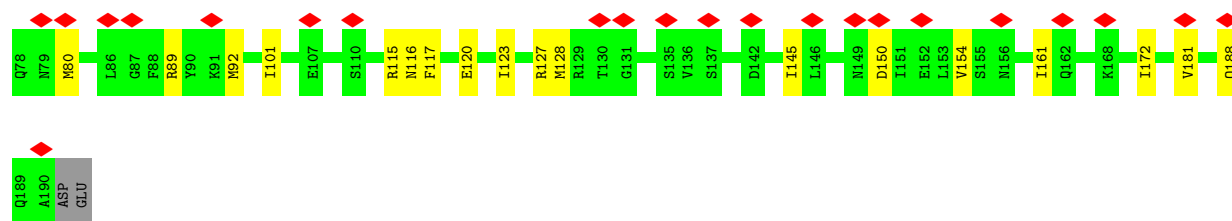


• Molecule 10: 60S ribosomal protein L7a

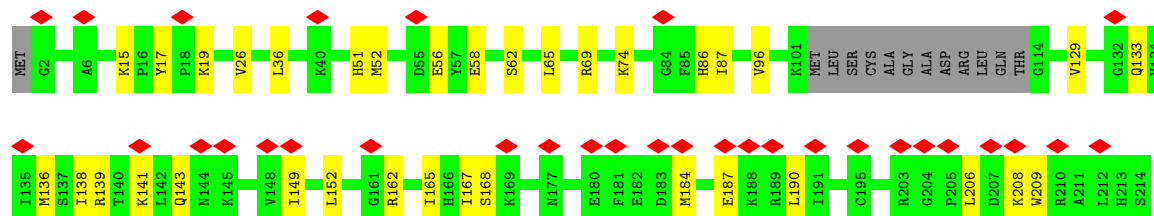
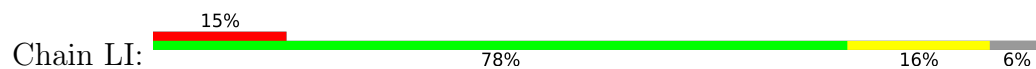


• Molecule 11: Large ribosomal subunit protein uL6

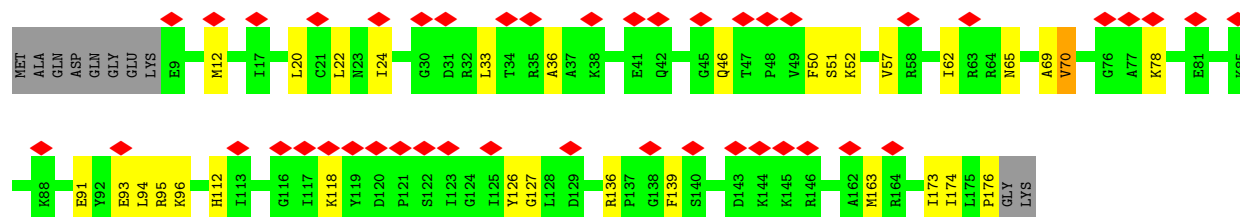
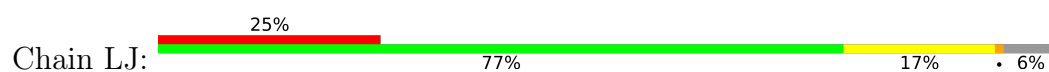




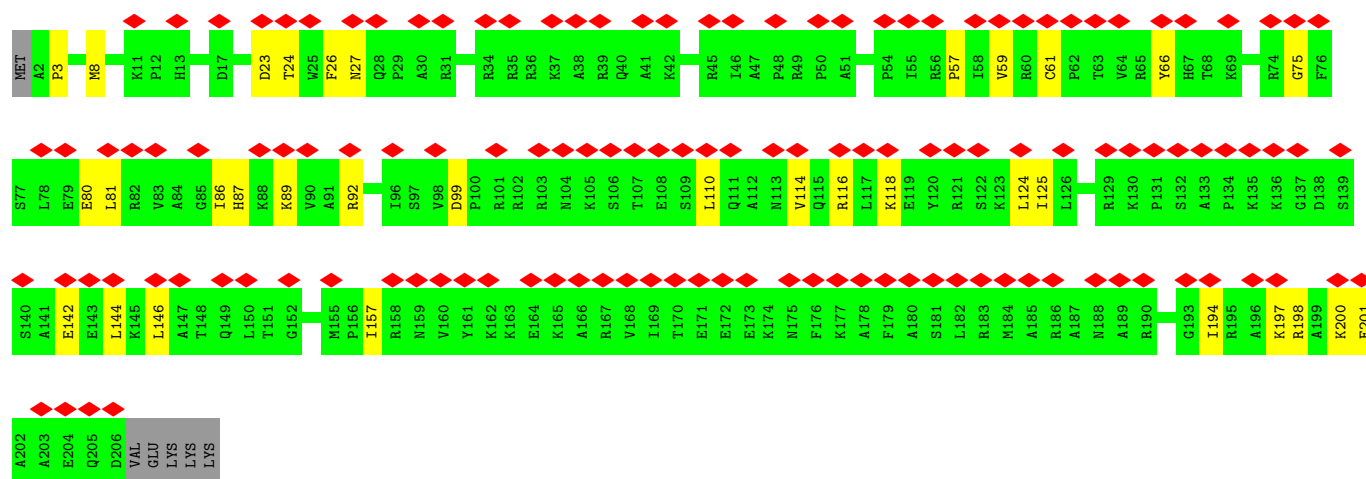
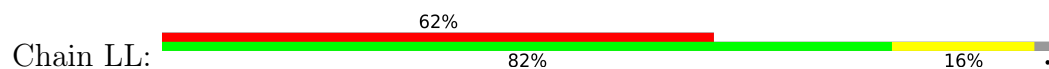
- Molecule 12: 60S ribosomal protein L10



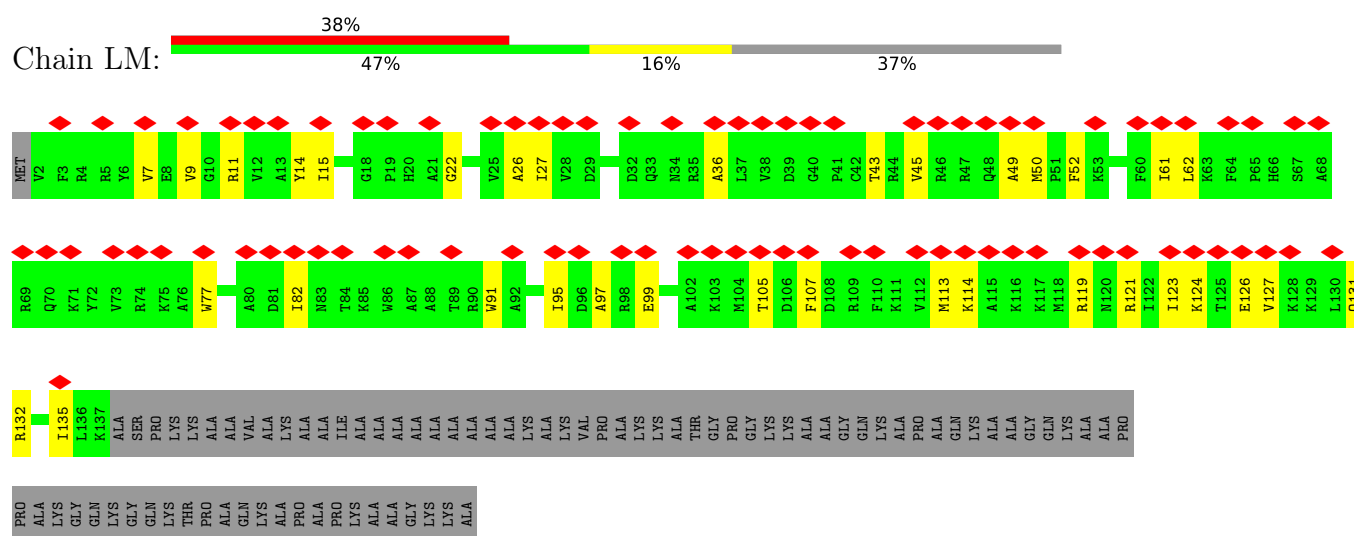
- Molecule 13: Large ribosomal subunit protein uL5



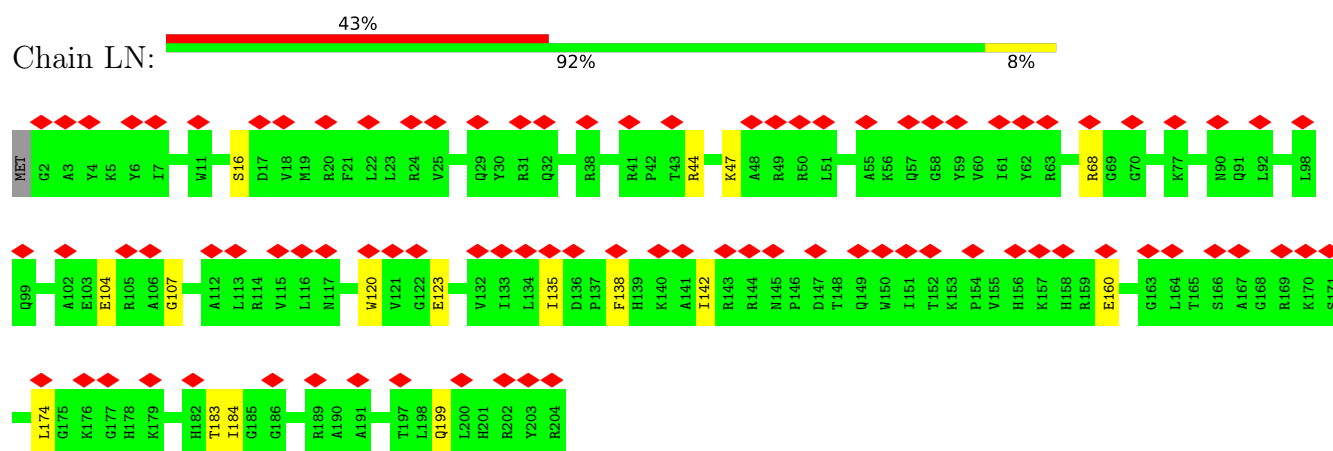
- Molecule 14: 60S ribosomal protein L13



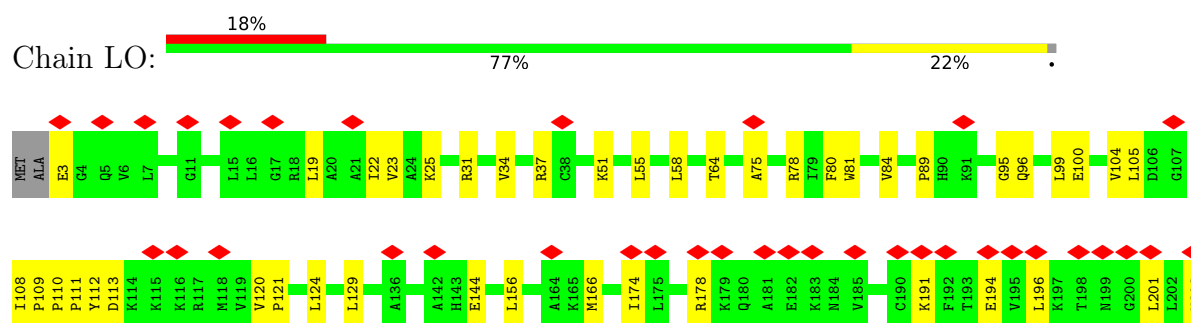
- Molecule 15: Large ribosomal subunit protein eL14



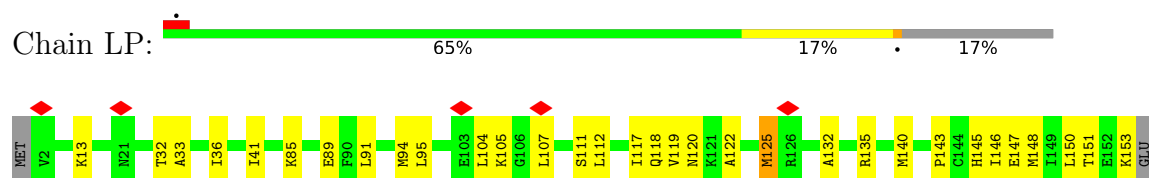
- Molecule 16: 60S ribosomal protein L15



- Molecule 17: 60S ribosomal protein L13a isoform X1

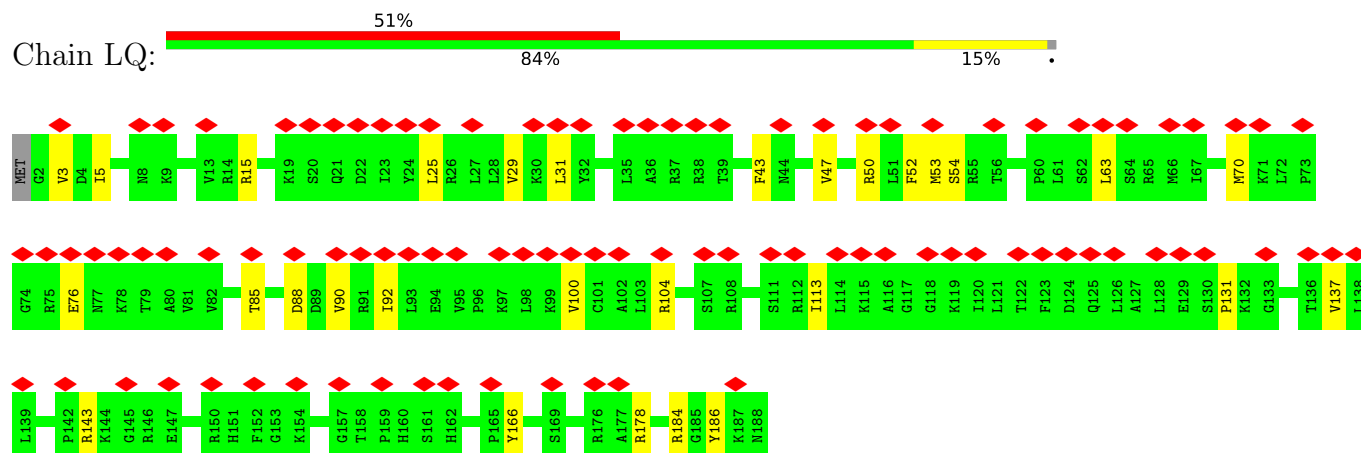


- Molecule 18: Large ribosomal subunit protein uL22

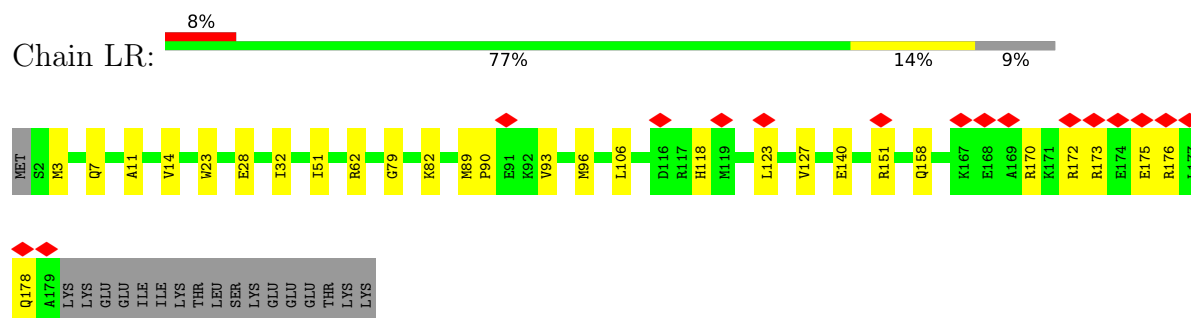


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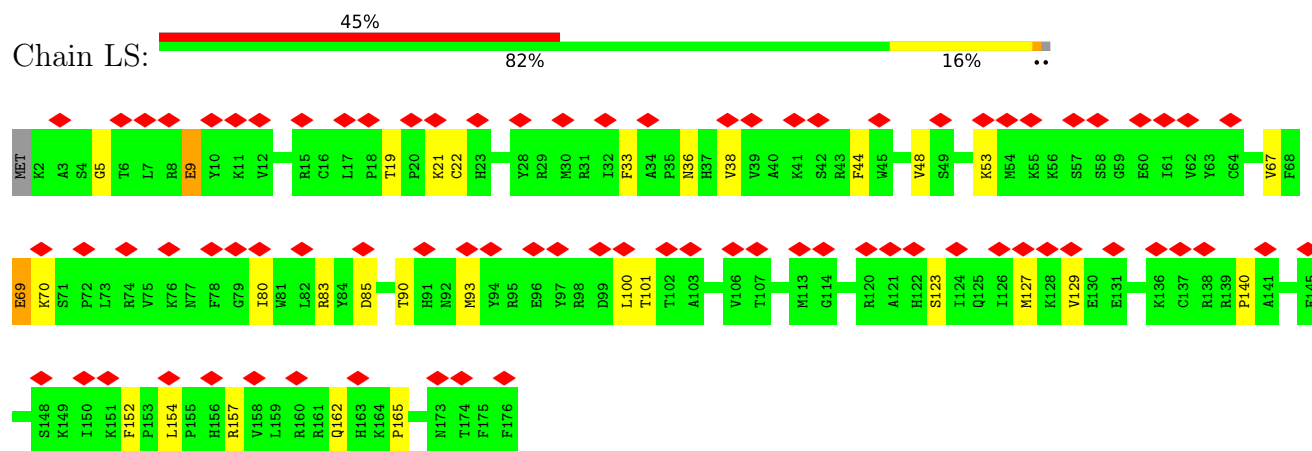
• Molecule 19: 60S ribosomal protein L18



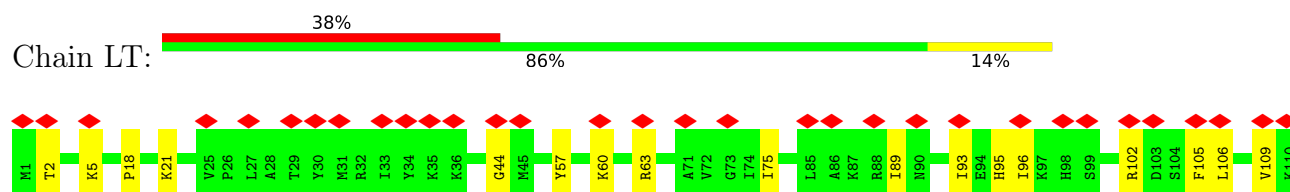
• Molecule 20: Ribosomal protein L19

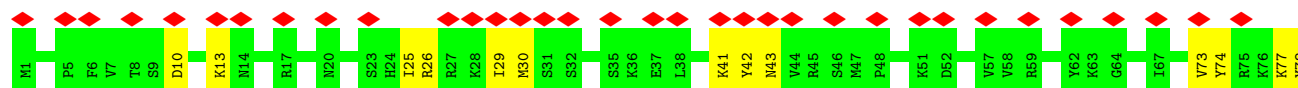


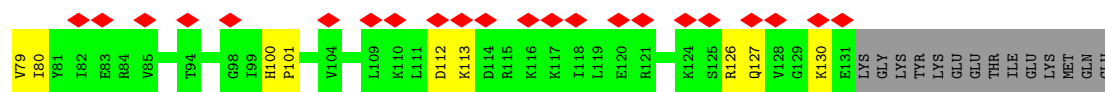
• Molecule 21: Large ribosomal subunit protein eL20



• Molecule 22: Large ribosomal subunit protein eL21

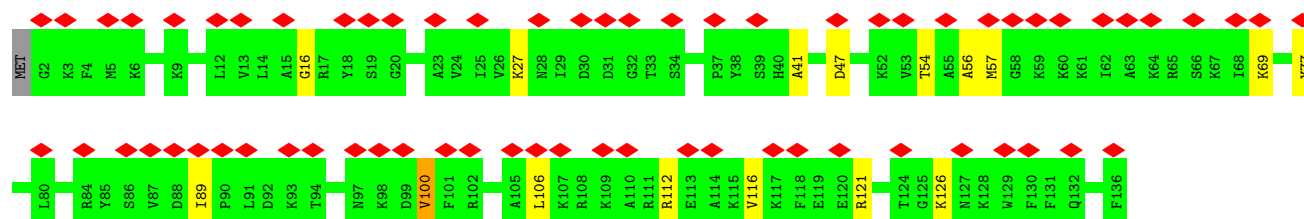






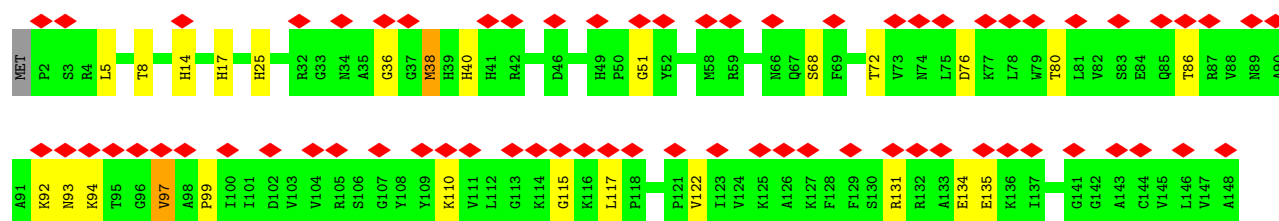
- Molecule 28: 60S ribosomal protein L27

Chain LZ:



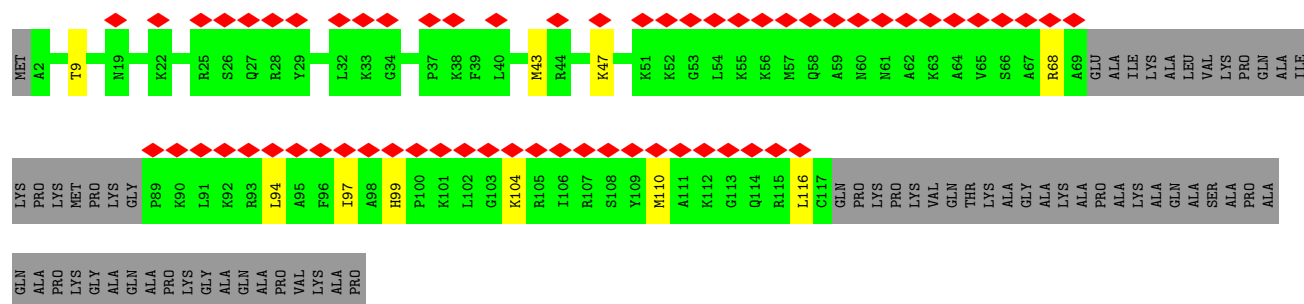
- Molecule 29: 60S ribosomal protein L27a

Chain La:



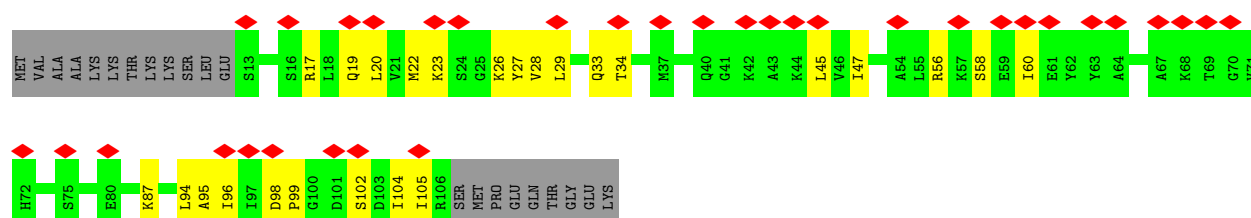
- Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:

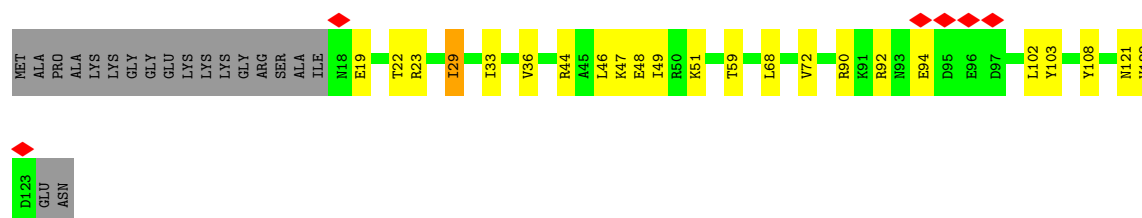


- Molecule 31: Large ribosomal subunit protein eL30

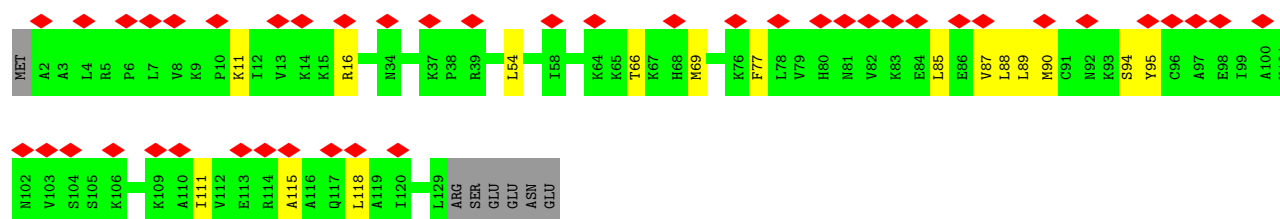
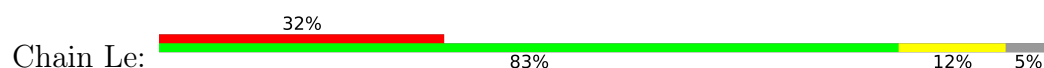
Chain Lc:



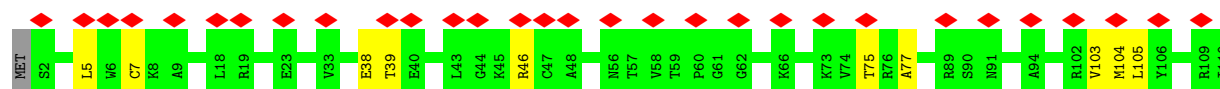
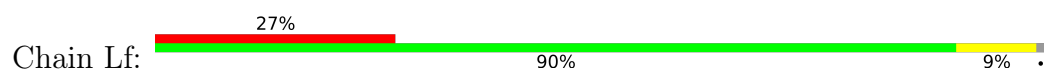
- Molecule 32: Large ribosomal subunit protein eL31



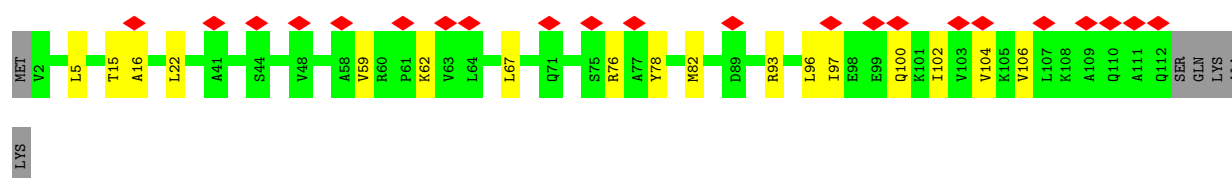
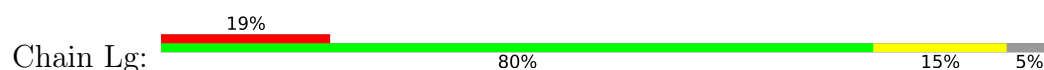
- Molecule 33: 60S ribosomal protein L32



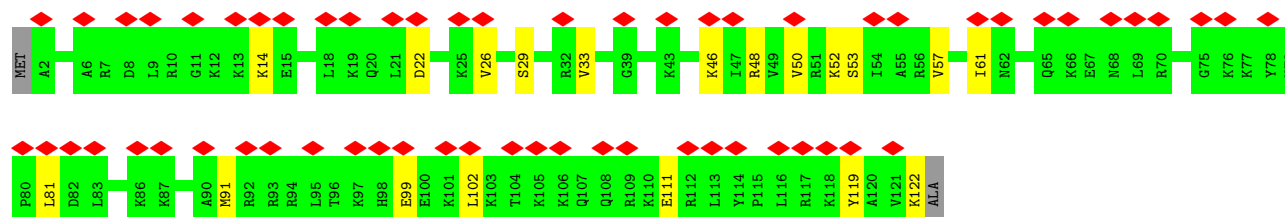
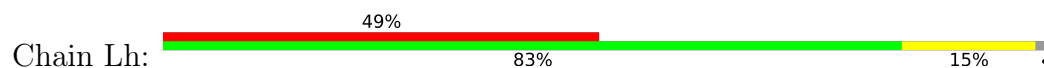
- Molecule 34: Large ribosomal subunit protein eL33



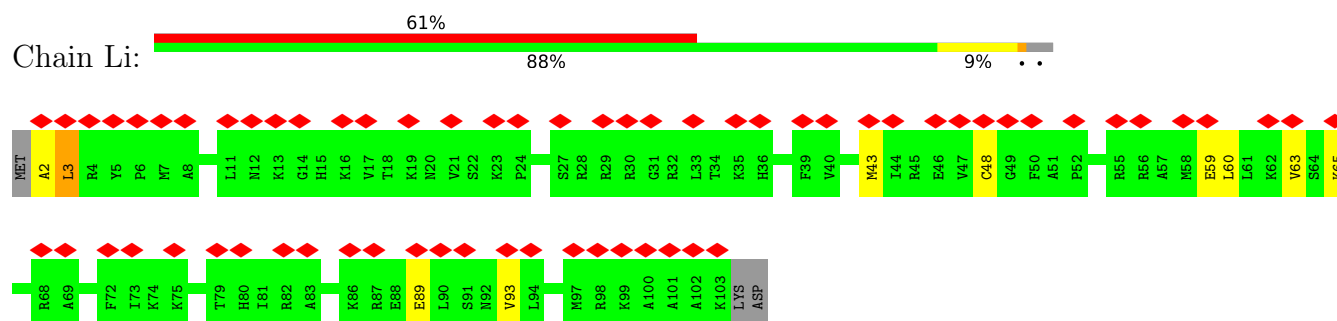
- Molecule 35: 60S ribosomal protein L34



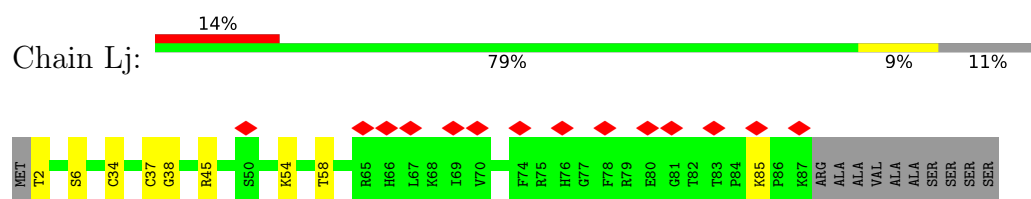
- Molecule 36: Large ribosomal subunit protein uL29



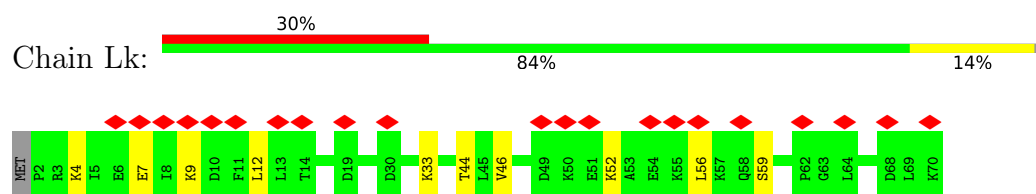
- Molecule 37: 60S ribosomal protein L36



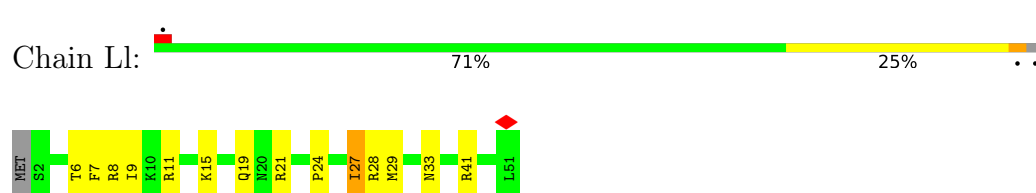
- Molecule 38: Ribosomal protein L37



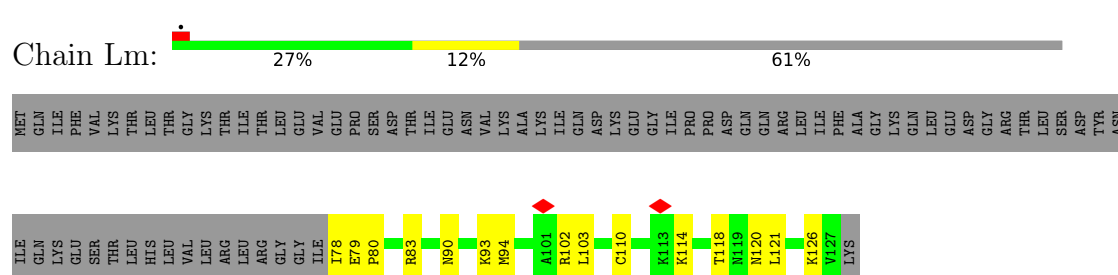
- Molecule 39: Large ribosomal subunit protein eL38



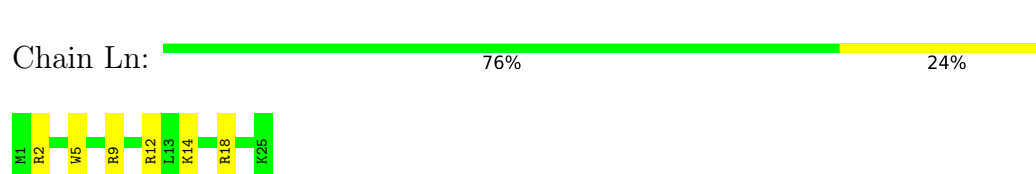
- Molecule 40: Large ribosomal subunit protein eL39

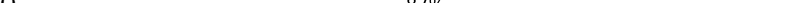


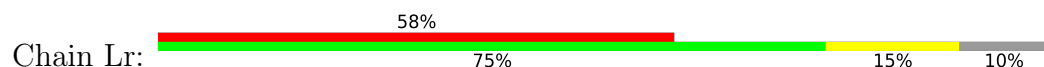
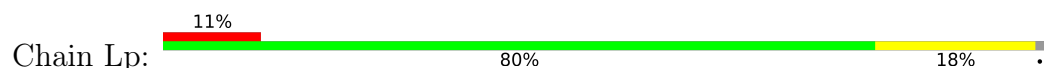
- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein

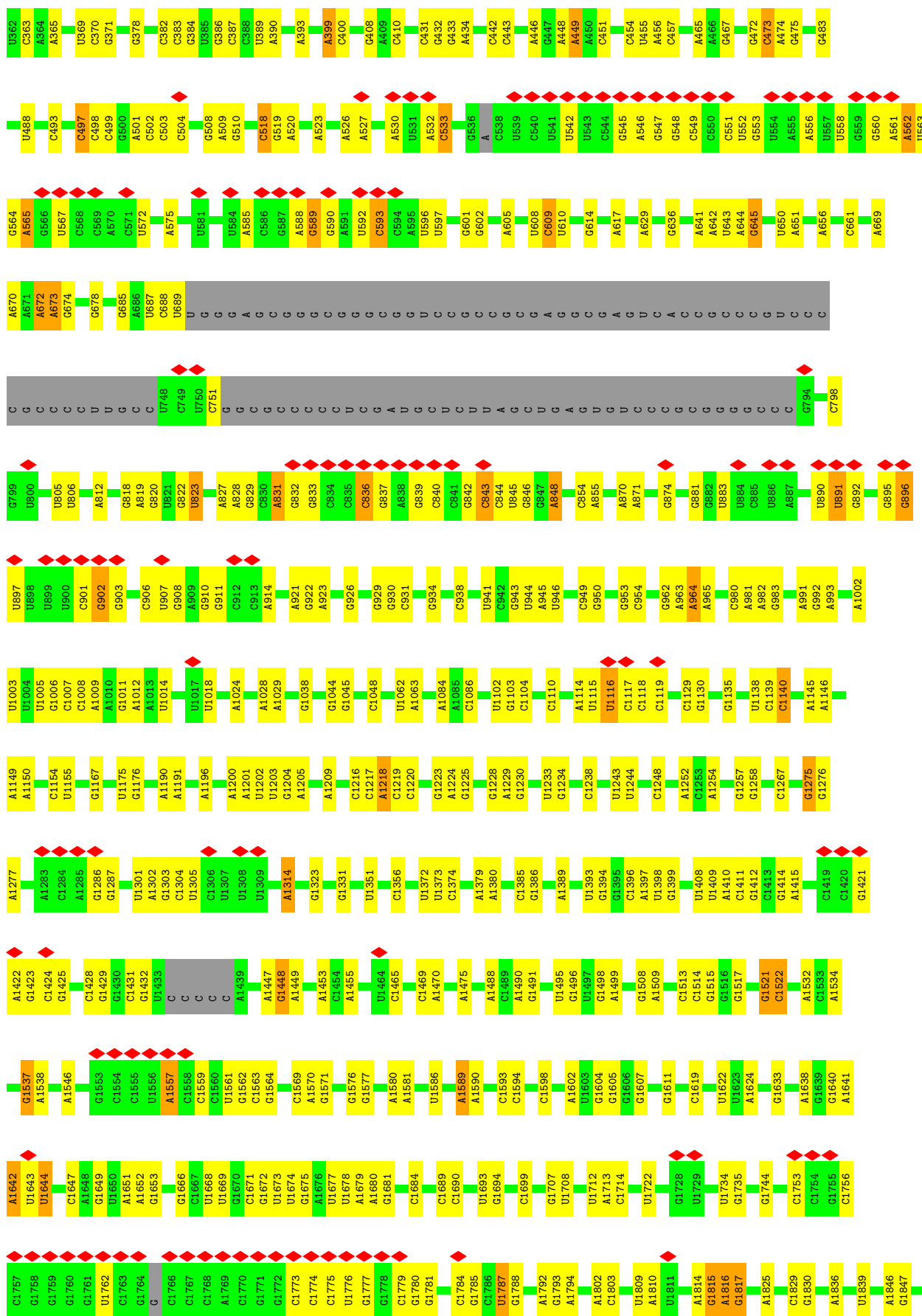


- Molecule 42: 60S ribosomal protein L41



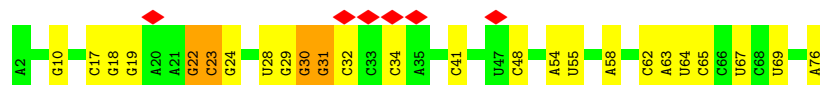
- Chain Lo: 



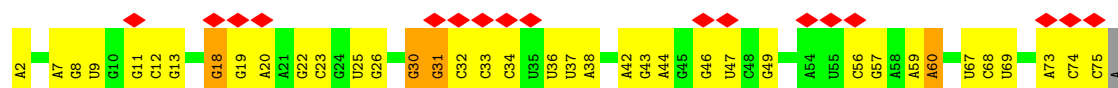




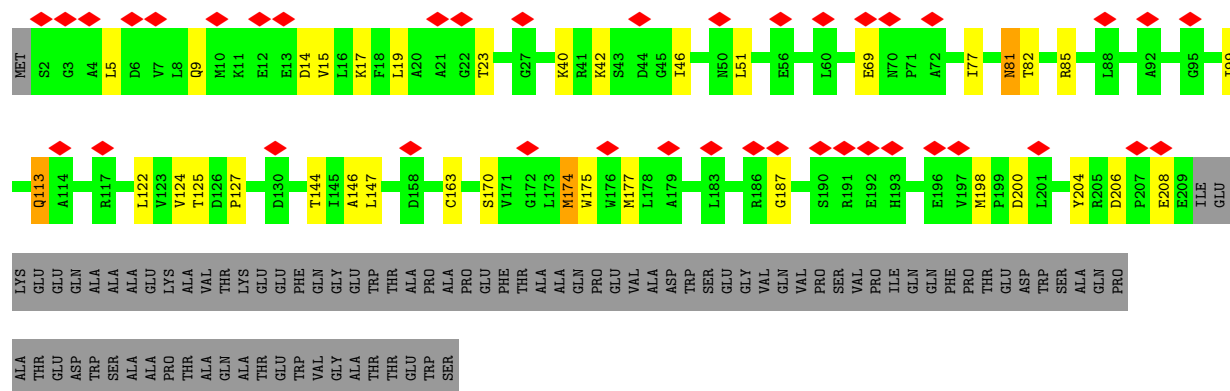
• Molecule 47: tRNA



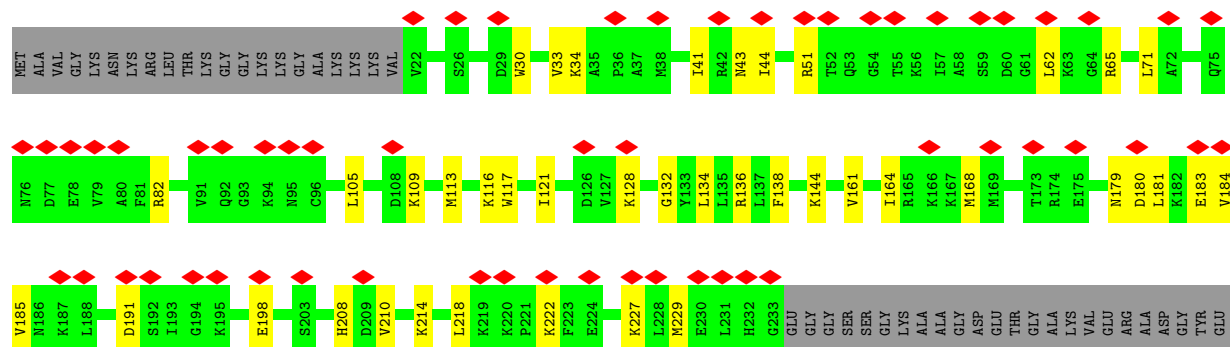
• Molecule 48: tRNA



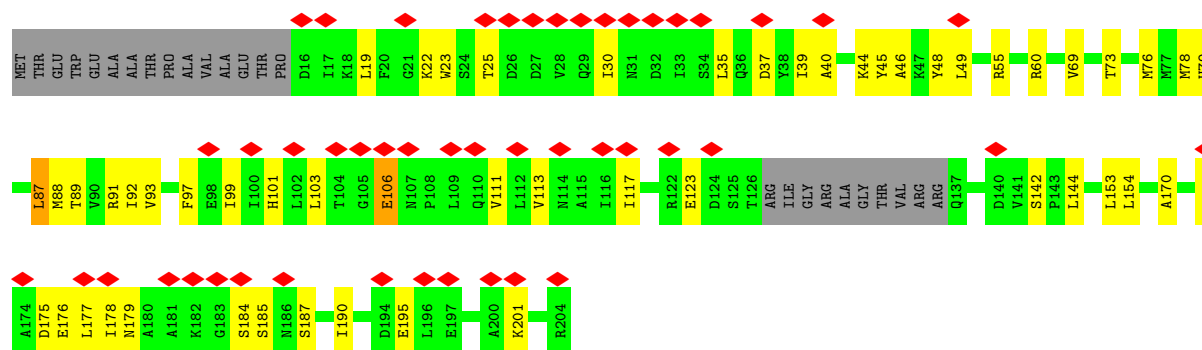
• Molecule 49: Small ribosomal subunit protein uS2



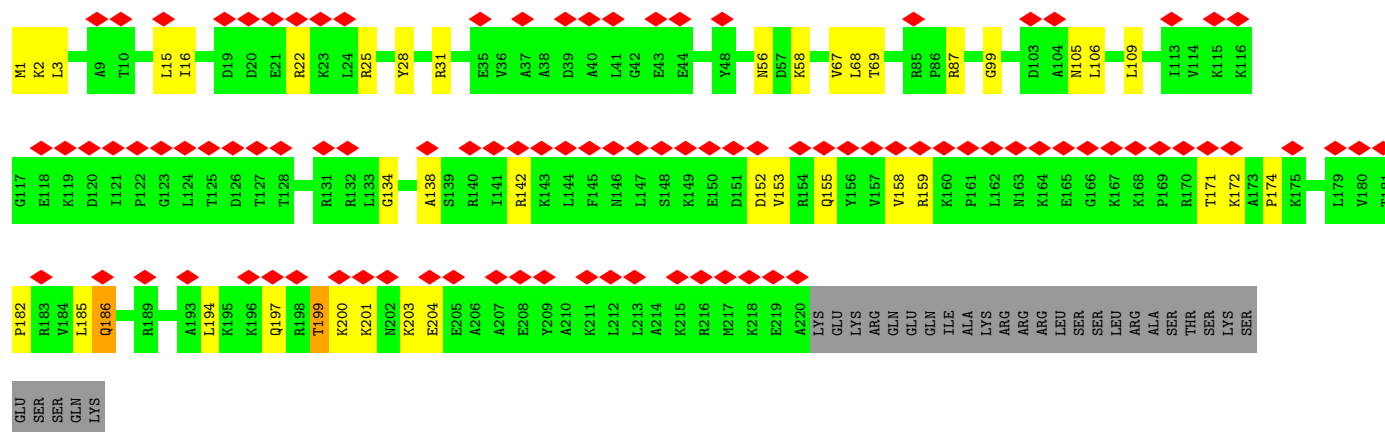
• Molecule 50: Small ribosomal subunit protein eS1



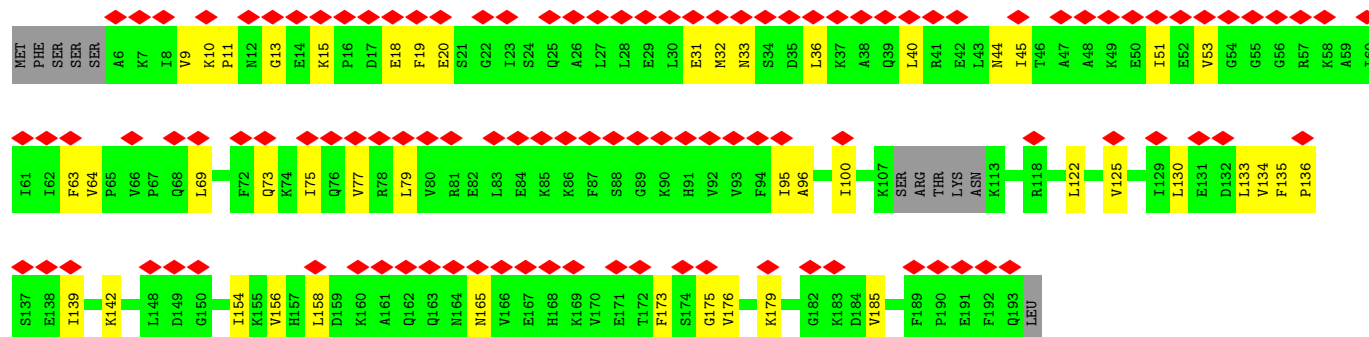
Chain SF: 23% 62% 25% 12%



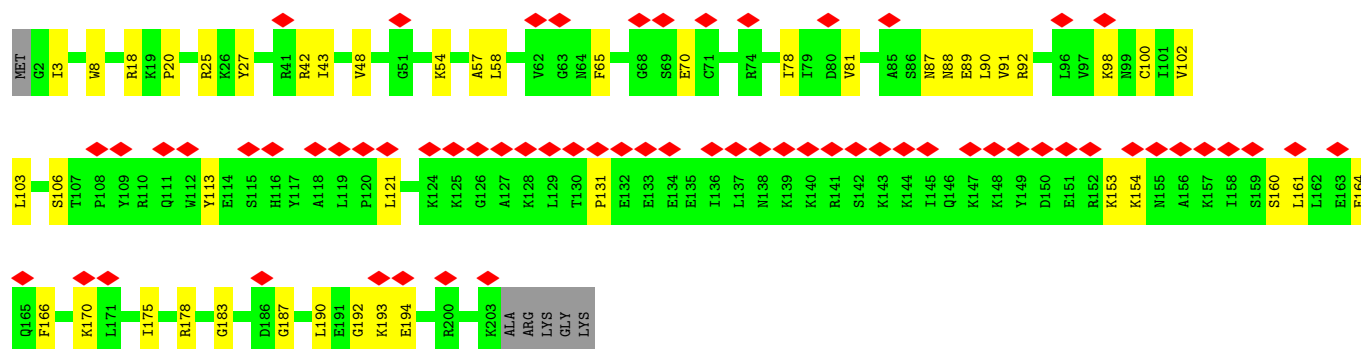
Chain SG:



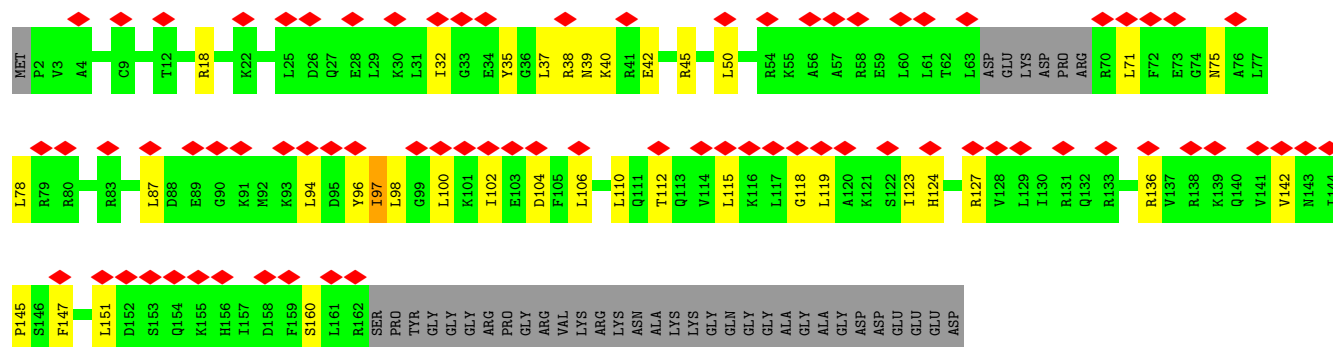
Chain SH: 57% 71% 23% 6%



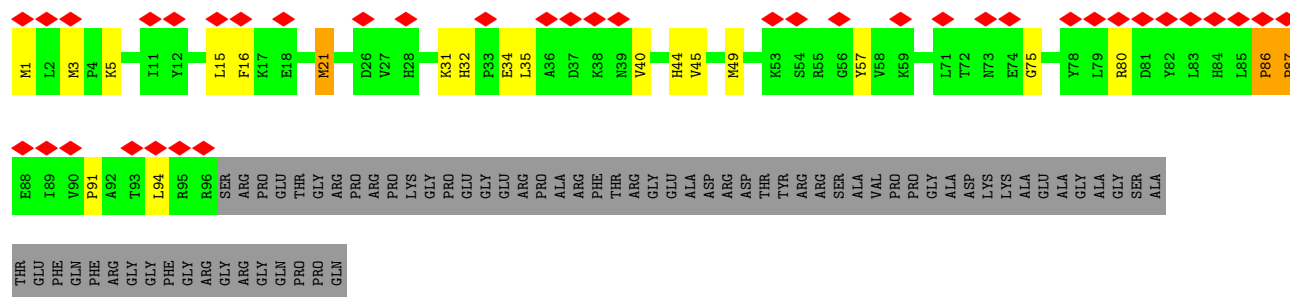
Chain SI:



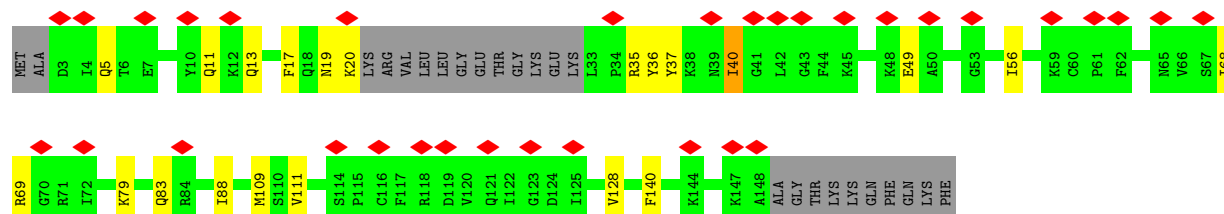
• Molecule 58: 40S ribosomal protein S9



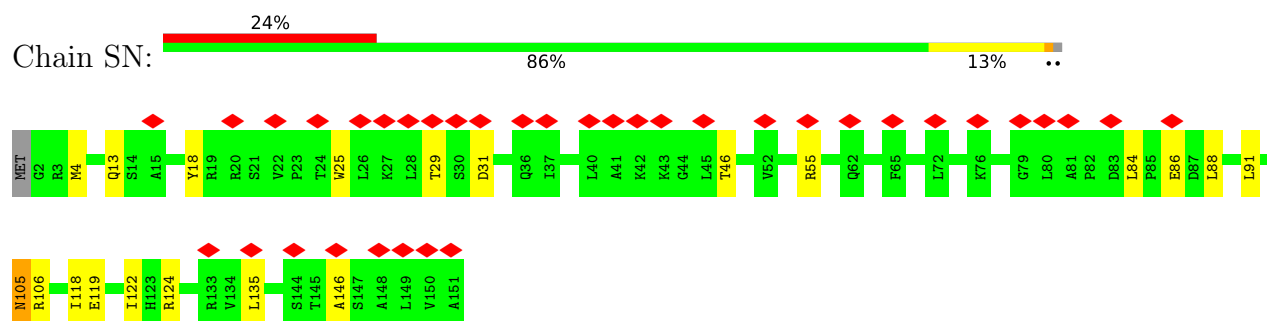
• Molecule 59: Small ribosomal subunit protein eS10



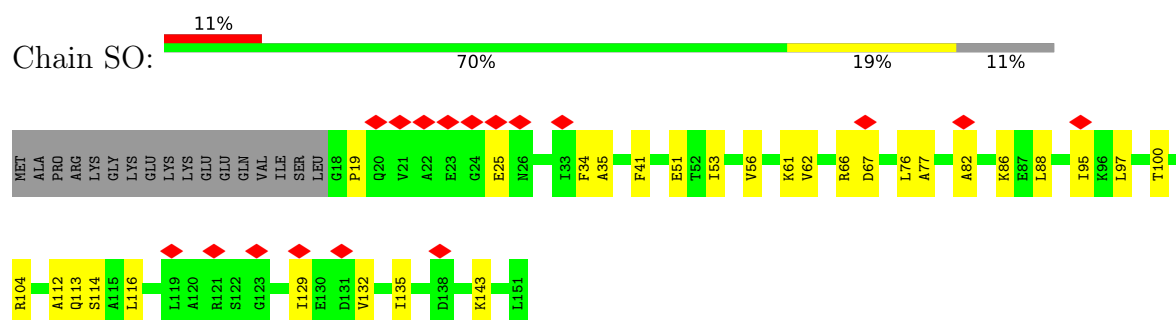
• Molecule 60: Small ribosomal subunit protein uS17



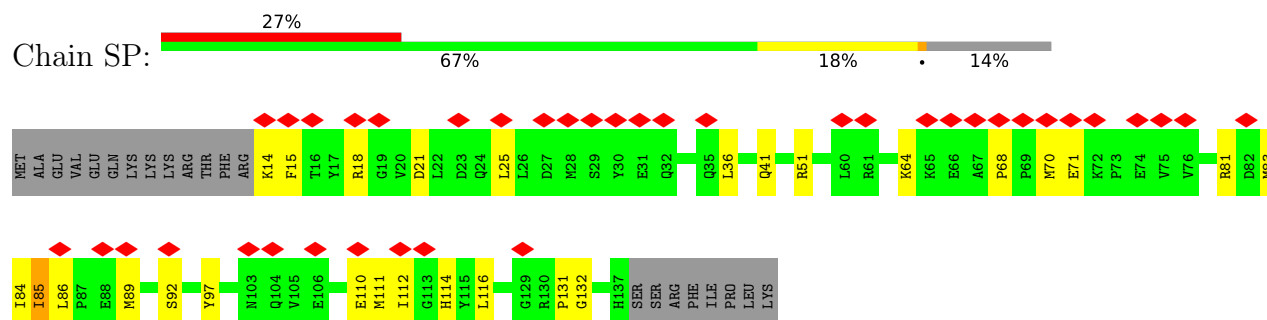
- Molecule 61: 40S ribosomal protein S13



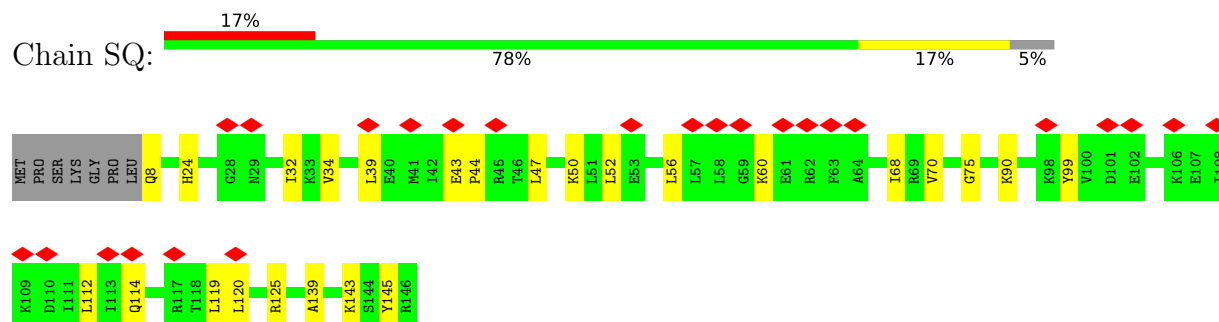
- Molecule 62: Small ribosomal subunit protein uS11



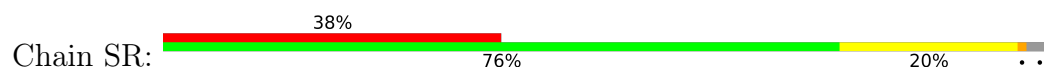
- Molecule 63: 40S ribosomal protein S15

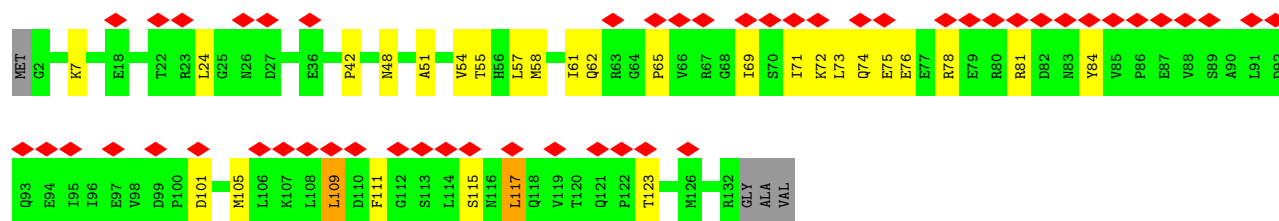


- Molecule 64: 40S ribosomal protein S16

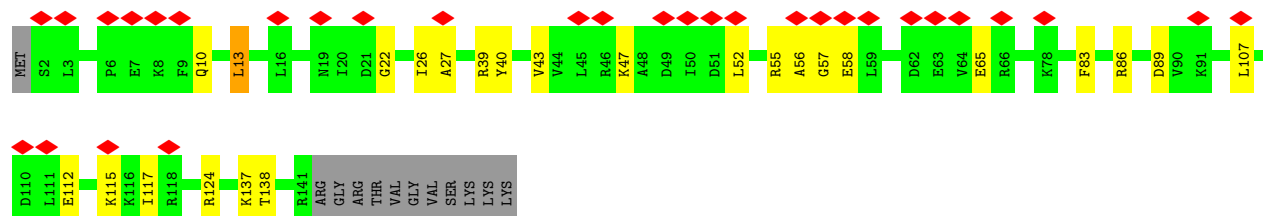
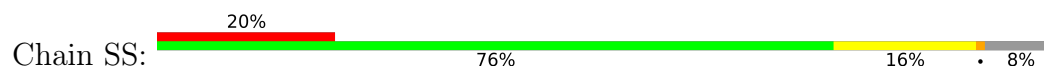


- Molecule 65: 40S ribosomal protein S17

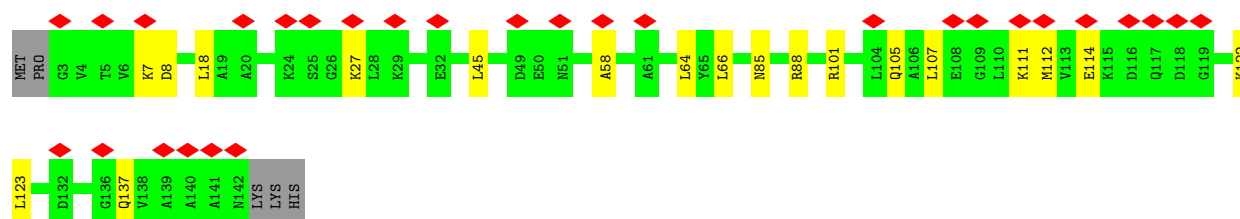
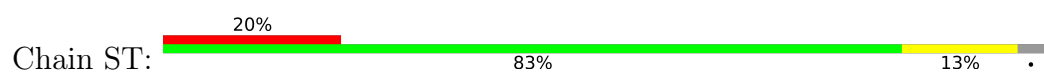




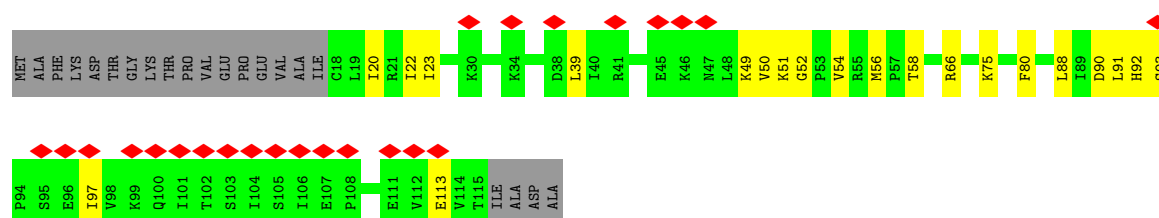
- Molecule 66: 40S ribosomal protein S18



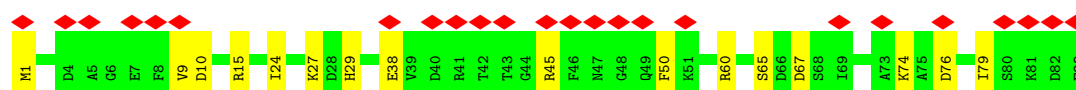
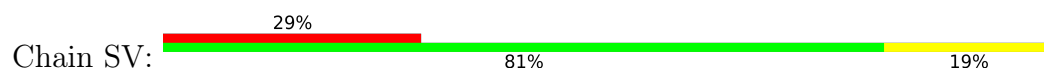
- Molecule 67: 40S ribosomal protein S19



- Molecule 68: 40S ribosomal protein S20

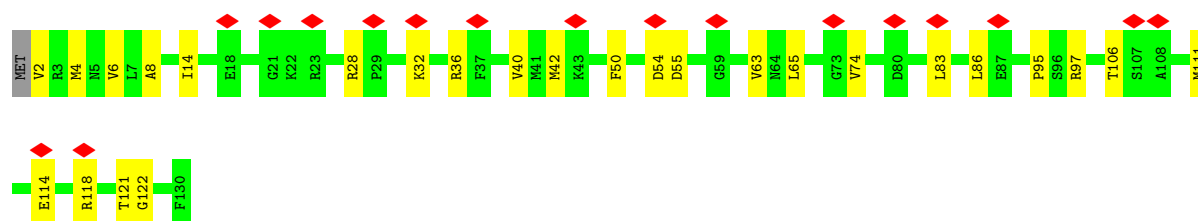


- Molecule 69: 40S ribosomal protein S21



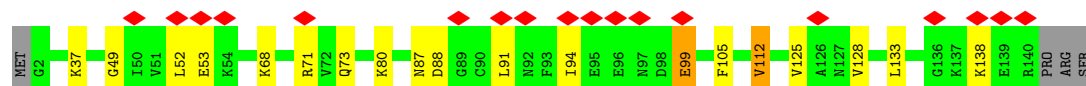
- Molecule 70: 40S ribosomal protein S15a isoform X1

Chain SW: 



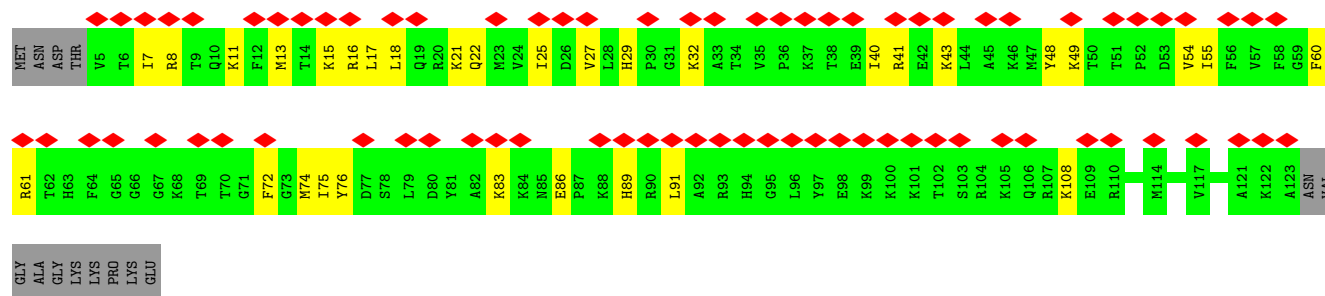
- Molecule 71: 40S ribosomal protein S23

Chain SX: 

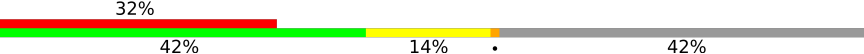


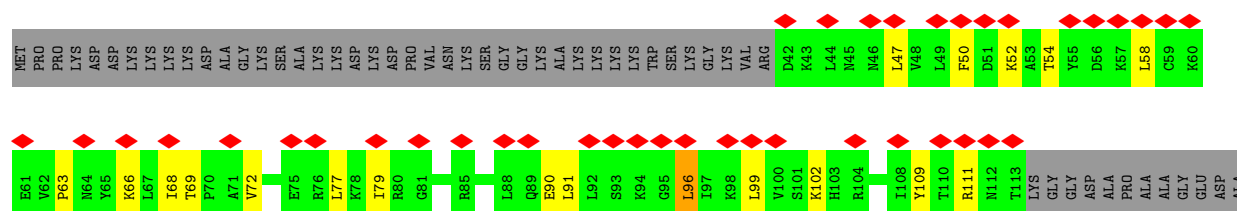
- Molecule 72: 40S ribosomal protein S24

Chain SY: 



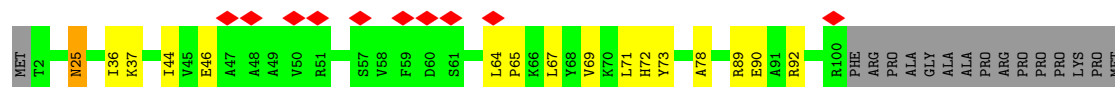
- Molecule 73: 40S ribosomal protein S25

Chain SZ: 

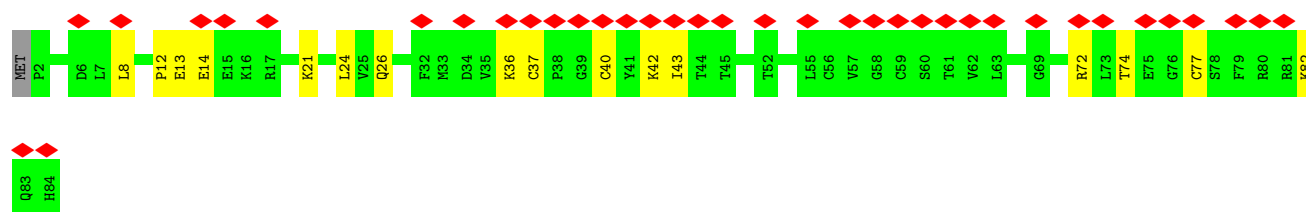
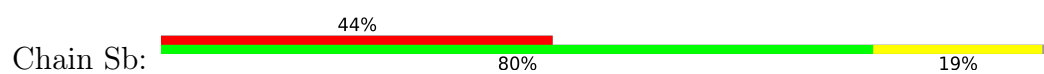


- Molecule 74: 40S ribosomal protein S26

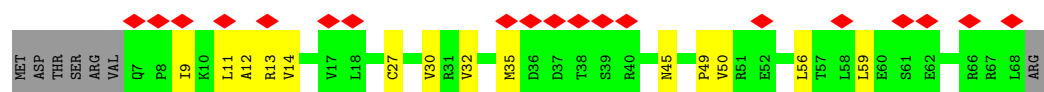
Chain Sa: 



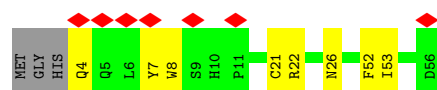
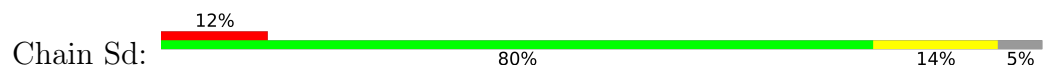
- Molecule 75: 40S ribosomal protein S27



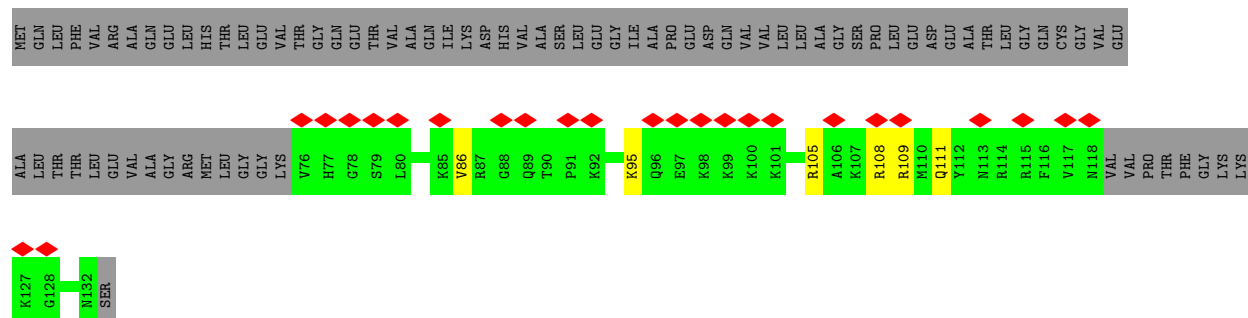
- Molecule 76: Small ribosomal subunit protein eS28



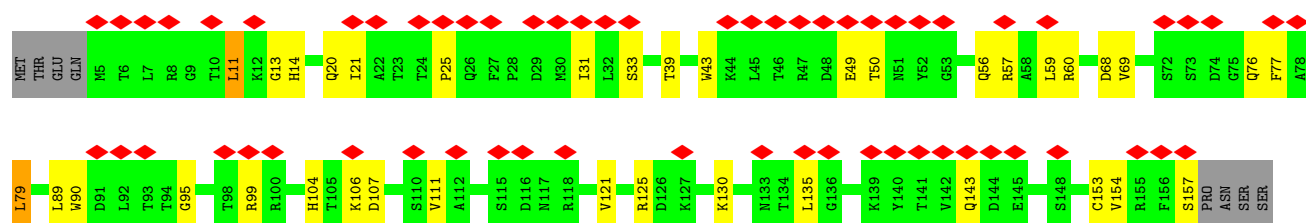
- Molecule 77: 40S ribosomal protein S29

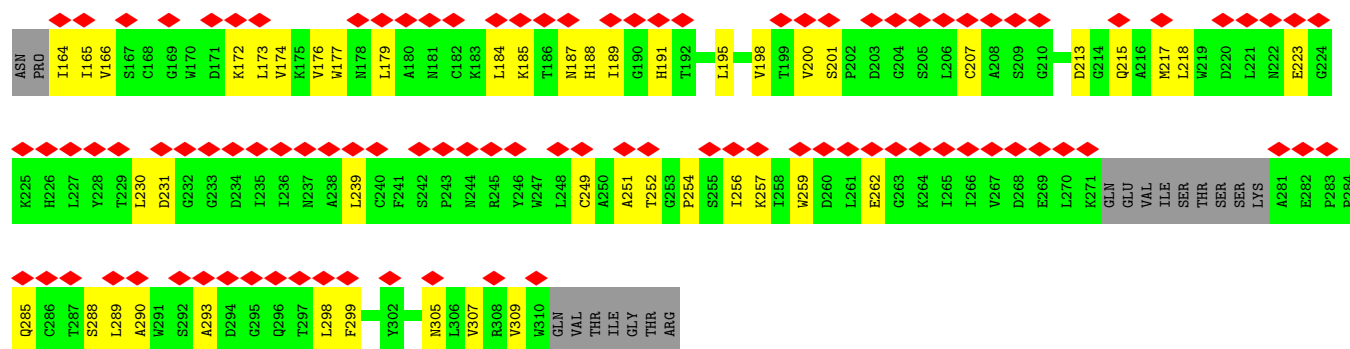


- Molecule 78: Ubiquitin-like protein fubi and ribosomal protein S30



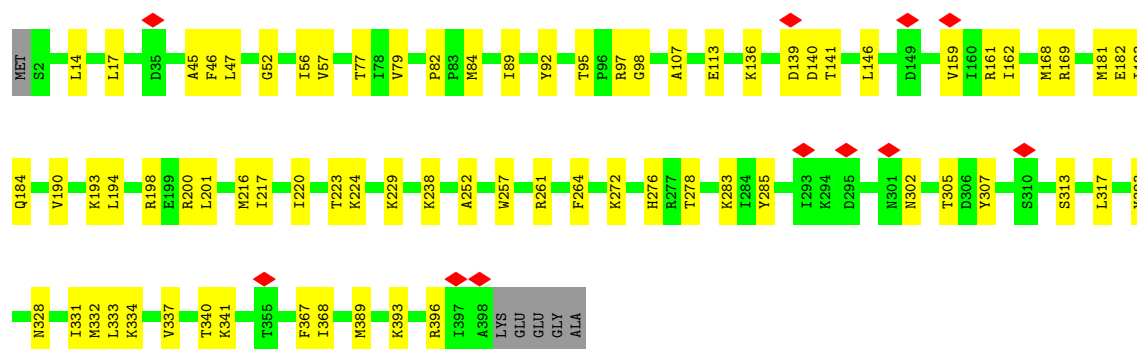
- Molecule 79: Small ribosomal subunit protein RACK1





- Molecule 80: Large ribosomal subunit protein uL3

Chain LB: 80% 18%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	118185	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.04	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.956	Depositor
Minimum map value	-1.484	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.147	Depositor
Recommended contour level	0.584	Depositor
Map size ($\text{\AA}$)	528.0, 528.0, 528.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	B	0.15	0/231	0.35	0/356
2	L5	0.16	0/82867	0.22	0/129223
3	L7	0.16	0/2858	0.20	0/4455
4	L8	0.15	0/3701	0.19	0/5766
5	LA	0.22	0/1936	0.46	0/2596
6	LC	0.19	0/2916	0.40	0/3914
7	LD	0.19	0/2435	0.39	0/3260
8	LE	0.18	0/1775	0.38	0/2381
9	LF	0.20	0/1805	0.38	0/2408
10	LG	0.18	0/1844	0.39	0/2483
11	LH	0.18	0/1537	0.37	0/2065
12	LI	0.20	0/1671	0.42	0/2230
13	LJ	0.18	0/1372	0.43	0/1836
14	LL	0.18	0/1691	0.39	0/2264
15	LM	0.20	0/1146	0.50	0/1531
16	LN	0.21	0/1746	0.40	0/2338
17	LO	0.22	0/1670	0.50	0/2232
18	LP	0.23	0/1256	0.48	0/1684
19	LQ	0.19	0/1539	0.40	0/2053
20	LR	0.19	0/1506	0.42	0/1991
21	LS	0.21	0/1491	0.39	0/2000
22	LT	0.19	0/1335	0.41	0/1781
23	LU	0.34	1/831 (0.1%)	0.60	0/1115
24	LV	0.21	0/987	0.39	0/1324
25	LW	0.19	0/532	0.39	0/708
26	LX	0.18	0/984	0.42	0/1323
27	LY	0.21	0/1110	0.49	0/1477
28	LZ	0.19	0/1130	0.39	0/1507
29	La	0.23	0/1193	0.51	2/1593 (0.1%)
30	Lb	0.18	0/808	0.45	0/1065
31	Lc	0.18	0/742	0.41	0/996
32	Ld	0.23	0/894	0.46	0/1204

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.19	0/1071	0.36	0/1429
34	Lf	0.20	0/895	0.41	0/1198
35	Lg	0.19	0/888	0.39	0/1185
36	Lh	0.19	0/1017	0.39	0/1343
37	Li	0.21	0/843	0.50	0/1115
38	Lj	0.20	0/720	0.38	0/952
39	Lk	0.20	0/574	0.47	0/760
40	Ll	0.20	0/454	0.44	0/599
41	Lm	0.22	0/417	0.49	0/553
42	Ln	0.18	0/240	0.31	0/305
43	Lo	0.18	0/855	0.36	0/1128
44	Lp	0.19	0/718	0.42	0/953
45	Lr	0.17	0/1002	0.38	0/1343
46	S2	0.17	0/39392	0.22	0/61373
47	S6	0.11	0/1784	0.27	0/2779
48	S7	0.12	0/1753	0.27	0/2730
49	SA	0.23	0/1679	0.44	0/2283
50	SB	0.20	0/1749	0.43	0/2340
51	SC	0.21	0/1726	0.44	0/2335
52	SD	0.18	0/1754	0.40	0/2362
53	SE	0.21	0/2092	0.48	1/2816 (0.0%)
54	SF	0.21	0/1436	0.50	0/1930
55	SG	0.25	0/1747	0.50	3/2337 (0.1%)
56	SH	0.21	0/1478	0.46	0/1981
57	SI	0.22	0/1621	0.57	1/2172 (0.0%)
58	SJ	0.23	0/1275	0.51	0/1710
59	SK	0.34	0/810	0.63	2/1091 (0.2%)
60	SL	0.21	0/1125	0.43	0/1507
61	SN	0.26	0/1232	0.43	0/1656
62	SO	0.22	0/1015	0.47	0/1361
63	SP	0.27	0/1015	0.54	2/1357 (0.1%)
64	SQ	0.24	0/1126	0.49	0/1506
65	SR	0.23	0/1078	0.50	0/1447
66	SS	0.22	0/1175	0.48	0/1575
67	ST	0.24	0/1108	0.55	1/1486 (0.1%)
68	SU	0.22	0/785	0.44	0/1054
69	SV	0.21	0/646	0.48	0/864
70	SW	0.21	0/1051	0.47	0/1406
71	SX	0.21	0/1097	0.46	0/1463
72	SY	0.21	0/996	0.50	0/1321
73	SZ	0.21	0/580	0.56	0/780
74	Sa	0.22	0/806	0.41	0/1080
75	Sb	0.22	0/665	0.53	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sc	0.20	0/456	0.52	0/615
77	Sd	0.21	0/455	0.47	0/603
78	Se	0.18	0/386	0.37	0/505
79	Sg	0.20	0/2324	0.52	2/3159 (0.1%)
80	LB	0.19	0/3269	0.43	0/4375
All	All	0.18	1/221919 (0.0%)	0.32	14/326272 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	LM	0	1
19	LQ	0	1
20	LR	0	1
62	SO	0	1
75	Sb	0	1
79	Sg	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	LU	30	GLU	CB-CG	-5.06	1.37	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SK	87	PRO	N-CA-CB	7.40	111.02	103.25
59	SK	86	PRO	N-CA-CB	7.38	110.24	103.08
57	SI	131	PRO	N-CA-CB	7.21	110.82	103.25
63	SP	131	PRO	N-CA-CB	6.78	110.49	103.38
29	La	38	MET	CA-C-N	-6.49	112.82	122.56
29	La	38	MET	C-N-CA	-6.49	112.82	122.56
53	SE	66	MET	CA-CB-CG	6.25	126.61	114.10
55	SG	186	GLN	CA-CB-CG	5.80	125.70	114.10
67	ST	8	ASP	N-CA-C	-5.70	108.12	114.62
55	SG	185	LEU	CA-C-N	5.66	128.91	120.31
55	SG	185	LEU	C-N-CA	5.66	128.91	120.31
79	Sg	143	GLN	CA-C-N	5.25	131.56	121.54
79	Sg	143	GLN	C-N-CA	5.25	131.56	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	SP	132	GLY	CA-C-O	-5.03	116.59	121.93

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	LM	9	VAL	Peptide
19	LQ	184	ARG	Peptide
20	LR	151	ARG	Sidechain
62	SO	25	GLU	Peptide
75	Sb	72	ARG	Sidechain
79	Sg	262	GLU	Peptide

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	B	208	0	105	1	0
2	L5	74087	35	37416	478	0
3	L7	2558	0	1296	11	0
4	L8	3314	0	1683	17	0
5	LA	1898	0	1993	34	0
6	LC	2862	0	3035	29	0
7	LD	2389	0	2420	23	0
8	LE	1743	0	1880	19	0
9	LF	1771	0	1886	20	0
10	LG	1813	0	1944	18	0
11	LH	1519	0	1603	20	0
12	LI	1633	0	1679	21	0
13	LJ	1349	0	1383	17	0
14	LL	1660	0	1762	24	0
15	LM	1125	0	1202	23	0
16	LN	1701	0	1749	11	0
17	LO	1640	0	1792	30	0
18	LP	1231	0	1265	23	0
19	LQ	1515	0	1639	21	0
20	LR	1490	0	1638	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	LS	1451	0	1488	20	0
22	LT	1307	0	1380	15	0
23	LU	817	0	839	16	0
24	LV	973	0	1034	11	0
25	LW	519	0	533	10	0
26	LX	967	0	1040	8	0
27	LY	1093	0	1176	16	0
28	LZ	1107	0	1182	11	0
29	La	1164	0	1213	17	0
30	Lb	794	0	860	6	0
31	Lc	732	0	769	15	0
32	Ld	879	0	924	13	0
33	Le	1053	0	1147	12	0
34	Lf	876	0	912	7	0
35	Lg	878	0	961	11	0
36	Lh	1009	0	1151	11	0
37	Li	832	0	917	6	0
38	Lj	705	0	741	5	0
39	Lk	568	0	635	7	0
40	Ll	444	0	483	12	0
41	Lm	411	0	445	11	0
42	Ln	239	0	289	3	0
43	Lo	842	0	916	6	0
44	Lp	708	0	756	15	0
45	Lr	987	0	1048	16	0
46	S2	35236	3	17778	264	0
47	S6	1596	0	815	13	0
48	S7	1570	0	802	17	0
49	SA	1642	0	1646	28	0
50	SB	1722	0	1794	26	0
51	SC	1690	0	1763	30	0
52	SD	1726	0	1816	32	0
53	SE	2050	0	2156	36	0
54	SF	1416	0	1458	37	0
55	SG	1725	0	1822	28	0
56	SH	1457	0	1533	28	0
57	SI	1593	0	1603	30	0
58	SJ	1258	0	1333	24	0
59	SK	789	0	790	16	0
60	SL	1105	0	1160	17	0
61	SN	1208	0	1294	16	0
62	SO	1002	0	1023	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	SP	997	0	1024	17	0
64	SQ	1109	0	1174	17	0
65	SR	1064	0	1118	29	0
66	SS	1157	0	1213	17	0
67	ST	1090	0	1116	14	0
68	SU	776	0	846	12	0
69	SV	639	0	635	10	0
70	SW	1034	0	1080	18	0
71	SX	1081	0	1153	12	0
72	SY	979	0	1055	25	0
73	SZ	574	0	627	12	0
74	Sa	793	0	841	13	0
75	Sb	651	0	668	14	0
76	Sc	454	0	457	11	0
77	Sd	445	0	442	5	0
78	Se	384	0	415	7	0
79	Sg	2271	0	2226	57	0
80	LB	3202	0	3347	47	0
81	B	1	0	0	0	0
81	L5	226	0	0	0	0
81	L7	4	0	0	0	0
81	L8	3	0	0	0	0
81	LB	1	0	0	0	0
81	LI	1	0	0	0	0
81	LN	1	0	0	0	0
81	LP	1	0	0	0	0
81	Le	2	0	0	0	0
81	Lg	1	0	0	0	0
81	S2	86	0	0	0	0
81	SO	1	0	0	0	0
82	Lg	1	0	0	0	0
82	Lp	1	0	0	0	0
82	Sa	1	0	0	0	0
83	L5	3	0	0	0	0
83	La	1	0	0	0	0
83	S2	2	0	0	0	0
All	All	206683	38	152232	1927	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 (1927) 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)
46:S2:70:G:H21	46:S2:79:A:H62	1.20	0.86
2:L5:1895:G:N2	2:L5:1896:G:C4	2.45	0.84
71:SX:94:ILE:HG22	71:SX:125:VAL:HG21	1.58	0.83
2:L5:176:G:H1	2:L5:260:G:H1	1.22	0.82
54:SF:35:LEU:HD13	54:SF:117:ILE:HG22	1.60	0.82
50:SB:62:LEU:HA	50:SB:65:ARG:HE	1.44	0.82
49:SA:14:ASP:HB2	49:SA:177:MET:HE1	1.61	0.80
7:LD:65:ALA:HB2	7:LD:74:ILE:HD13	1.65	0.79
2:L5:4575:C:H5''	15:LM:114:LYS:HD2	1.63	0.78
50:SB:229:MET:HA	50:SB:229:MET:HE3	1.66	0.78
2:L5:1895:G:C2	2:L5:1896:G:C4	2.72	0.78
49:SA:198:MET:HG3	49:SA:200:ASP:H	1.49	0.78
57:SI:190:LEU:HD22	57:SI:194:GLU:HG2	1.65	0.77
18:LP:111:SER:HB3	18:LP:153:LYS:HG2	1.65	0.77
79:Sg:157:SER:HA	79:Sg:200:VAL:HG11	1.65	0.77
55:SG:22:ARG:HA	55:SG:25:ARG:HE	1.49	0.77
2:L5:4553:G:H2'	2:L5:4559:G:H22	1.48	0.77
49:SA:77:ILE:HD11	49:SA:124:VAL:HG12	1.65	0.77
2:L5:1415:A:H61	2:L5:4208:U:H3	1.34	0.76
28:LZ:54:THR:HG22	28:LZ:56:ALA:H	1.51	0.76
52:SD:127:MET:HA	52:SD:127:MET:HE3	1.67	0.76
29:La:94:LYS:HA	29:La:94:LYS:HE3	1.68	0.76
54:SF:185:SER:HA	54:SF:190:ILE:HD11	1.68	0.75
73:SZ:52:LYS:HA	73:SZ:52:LYS:HE2	1.68	0.75
75:Sb:36:LYS:HE3	75:Sb:43:ILE:HG13	1.66	0.75
61:SN:13:GLN:HG3	75:Sb:21:LYS:HE3	1.69	0.75
36:Lh:99:GLU:HA	36:Lh:102:LEU:HD12	1.68	0.74
79:Sg:31:ILE:HG23	79:Sg:43:TRP:HB2	1.69	0.74
46:S2:1223:G:H5''	54:SF:78:MET:HE1	1.69	0.74
46:S2:70:G:N2	46:S2:79:A:H62	1.84	0.74
2:L5:1355:U:H3	2:L5:1432:G:H1	1.36	0.74
45:Lr:58:LYS:H	45:Lr:58:LYS:HE2	1.53	0.74
79:Sg:77:PHE:HB2	79:Sg:89:LEU:HD11	1.70	0.73
46:S2:1145:A:H5'	46:S2:1356:C:H41	1.53	0.73
19:LQ:178:ARG:H	29:La:51:GLY:HA2	1.53	0.73
71:SX:49:GLY:O	71:SX:99:GLU:HA	1.87	0.73
79:Sg:176:VAL:HG23	79:Sg:185:LYS:HB2	1.70	0.73
7:LD:200:MET:HA	7:LD:200:MET:HE3	1.70	0.73
47:S6:29:G:H1	47:S6:41:C:H5	1.35	0.73
65:SR:69:ILE:HG23	65:SR:74:GLN:HE21	1.53	0.73
2:L5:189:G:H1	2:L5:252:G:H22	1.37	0.72
30:Lb:110:MET:HE2	30:Lb:110:MET:HA	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3787:U:H3	2:L5:3801:G:H1	1.37	0.72
46:S2:155:G:H2'	46:S2:156:G:H8	1.54	0.72
2:L5:513:U:H5'	29:La:86:THR:HG22	1.71	0.72
48:S7:13:G:H1	48:S7:23:C:H42	1.37	0.71
18:LP:140:MET:HA	18:LP:140:MET:HE3	1.71	0.71
79:Sg:20:GLN:HE21	79:Sg:68:ASP:HB2	1.56	0.70
11:LH:31:ARG:HD2	11:LH:188:GLN:HE22	1.55	0.70
6:LC:170:LEU:HD23	6:LC:174:LEU:HD22	1.73	0.70
25:LW:13:ILE:HD11	25:LW:32:LEU:HA	1.74	0.70
45:Lr:58:LYS:HE2	45:Lr:58:LYS:N	2.07	0.69
49:SA:163:CYS:HB2	49:SA:174:MET:HE3	1.73	0.69
49:SA:77:ILE:HG22	49:SA:99:ILE:HB	1.74	0.69
53:SE:65:CYS:HA	53:SE:70:ILE:HD12	1.74	0.69
79:Sg:166:VAL:HG12	79:Sg:176:VAL:HG12	1.75	0.69
2:L5:2236:G:H1	2:L5:2256:C:H42	1.40	0.69
34:Lf:104:MET:HA	34:Lf:104:MET:HE3	1.75	0.69
2:L5:2327:A:H1'	28:LZ:112:ARG:HH22	1.54	0.69
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.74	0.69
14:LL:142:GLU:HA	14:LL:146:LEU:HD12	1.75	0.69
28:LZ:54:THR:HB	28:LZ:57:MET:HE3	1.75	0.69
76:Sc:13:ARG:HH11	76:Sc:13:ARG:HG2	1.57	0.69
53:SE:112:HIS:HD1	53:SE:112:HIS:C	2.00	0.69
46:S2:70:G:H21	46:S2:79:A:N6	1.91	0.68
53:SE:64:ILE:HD11	72:SY:18:LEU:HG	1.75	0.68
59:SK:16:PHE:HZ	59:SK:80:ARG:HD2	1.58	0.68
65:SR:58:MET:HE3	65:SR:61:ILE:HD11	1.74	0.68
55:SG:2:LYS:HB3	55:SG:15:LEU:HD21	1.75	0.68
2:L5:1044:C:H5'	2:L5:1045:G:H5''	1.76	0.68
17:LO:105:LEU:HD13	17:LO:109:PRO:HG2	1.76	0.68
52:SD:101:GLN:HG3	52:SD:126:ILE:HD11	1.74	0.68
72:SY:29:HIS:HB2	72:SY:32:LYS:HG3	1.76	0.68
2:L5:3602:A:H61	2:L5:3719:U:H3	1.40	0.67
37:Li:60:LEU:HD23	37:Li:65:LYS:HE3	1.77	0.67
2:L5:762:U:H3	2:L5:809:A:H61	1.42	0.67
2:L5:1147:C:H2'	2:L5:1148:A:H8	1.58	0.67
62:SO:34:PHE:HB3	62:SO:41:PHE:HB2	1.76	0.67
5:LA:46:LYS:HE3	5:LA:62:VAL:HG11	1.77	0.67
46:S2:1642:A:N7	48:S7:31:G:H5'	2.09	0.67
80:LB:220:ILE:HG12	80:LB:278:THR:HG23	1.77	0.67
2:L5:1557:U:H3	2:L5:1579:A:H61	1.43	0.66
72:SY:41:ARG:HH11	72:SY:41:ARG:HG3	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LA:108:PRO:HB2	44:Lp:86:LEU:HD23	1.77	0.66
40:Ll:29:MET:HE2	40:Ll:29:MET:HA	1.77	0.66
2:L5:1708:U:H3	2:L5:1874:A:H61	1.42	0.66
33:Le:66:THR:HA	33:Le:69:MET:HE3	1.78	0.66
58:SJ:110:LEU:HD13	58:SJ:147:PHE:HB3	1.78	0.66
2:L5:1378:A:H2'	2:L5:1379:A:H5''	1.78	0.66
2:L5:1895:G:N1	2:L5:1896:G:C5	2.64	0.66
46:S2:378:G:H5'	57:SI:98:LYS:HB3	1.76	0.66
70:SW:50:PHE:HB3	70:SW:63:VAL:HG13	1.76	0.66
4:L8:84:A:H62	27:LY:113:LYS:HB2	1.61	0.66
2:L5:711:G:H2'	2:L5:712:C:H4'	1.76	0.65
51:SC:210:PRO:HD3	51:SC:236:PHE:HE2	1.62	0.65
53:SE:127:ARG:HD2	53:SE:142:HIS:HA	1.77	0.65
53:SE:234:PRO:HG3	53:SE:238:LEU:HD21	1.78	0.65
62:SO:61:LYS:HE2	62:SO:76:LEU:HB3	1.79	0.65
55:SG:200:LYS:HE2	55:SG:200:LYS:HA	1.77	0.65
8:LE:176:LEU:HD21	8:LE:182:LEU:HB2	1.79	0.65
46:S2:1744:G:H21	46:S2:1792:A:H62	1.43	0.65
23:LU:25:CYS:HB3	23:LU:112:LEU:HD13	1.78	0.65
52:SD:131:ALA:HA	52:SD:191:PRO:HG3	1.77	0.65
2:L5:4190:C:H2'	2:L5:4191:G:H8	1.61	0.64
7:LD:156:GLY:HA2	7:LD:181:PRO:HG3	1.79	0.64
2:L5:299:A:H2'	2:L5:300:G:H8	1.63	0.64
46:S2:1233:U:H2'	46:S2:1234:G:H8	1.62	0.64
2:L5:1660:C:H2'	2:L5:1661:A:H8	1.63	0.64
2:L5:2237:G:H1	2:L5:2255:C:H42	1.46	0.64
50:SB:180:ASP:O	50:SB:184:VAL:HG23	1.97	0.64
56:SH:154:ILE:HB	56:SH:185:VAL:HG22	1.79	0.64
25:LW:4:GLU:HB2	25:LW:13:ILE:HB	1.78	0.64
46:S2:1641:A:C5	48:S7:30:G:H4'	2.32	0.64
65:SR:84:TYR:HD2	65:SR:84:TYR:O	1.81	0.64
2:L5:4387:A:H1'	2:L5:4388:G:C8	2.32	0.64
6:LC:60:HIS:HA	6:LC:92:PHE:HE1	1.63	0.64
10:LG:180:PRO:HG3	10:LG:219:VAL:HG13	1.80	0.64
53:SE:45:ILE:HD12	53:SE:80:ILE:HD12	1.78	0.64
46:S2:165:G:H2'	46:S2:166:A:H8	1.63	0.63
79:Sg:251:ALA:HA	79:Sg:256:ILE:HG22	1.80	0.63
32:Ld:36:VAL:HG21	32:Ld:44:ARG:HG2	1.79	0.63
53:SE:44:LEU:HD21	53:SE:72:ILE:HD11	1.80	0.63
57:SI:78:ILE:HD11	57:SI:102:VAL:HG11	1.79	0.63
59:SK:57:TYR:HD1	59:SK:75:GLY:HA2	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:La:93:ASN:HD22	29:La:97:VAL:HG12	1.64	0.63
46:S2:1414:G:H2'	46:S2:1415:A:H8	1.63	0.63
63:SP:41:GLN:HG3	63:SP:84:ILE:HD13	1.81	0.63
72:SY:13:MET:N	72:SY:13:MET:HE3	2.14	0.63
2:L5:2499:A:H2'	2:L5:2500:A:H8	1.64	0.63
59:SK:91:PRO:HD2	59:SK:94:LEU:HB2	1.79	0.63
72:SY:48:TYR:C	72:SY:49:LYS:HD3	2.23	0.63
53:SE:100:ARG:HB2	53:SE:114:ILE:HD13	1.81	0.63
2:L5:4699:C:H5''	80:LB:323:TYR:O	1.99	0.62
68:SU:66:ARG:HH22	68:SU:75:LYS:HD3	1.64	0.62
12:LI:87:ILE:HG12	12:LI:138:ILE:HG12	1.81	0.62
56:SH:45:ILE:HG22	56:SH:64:VAL:HG12	1.79	0.62
5:LA:54:ARG:HG2	5:LA:56:ALA:H	1.64	0.62
20:LR:89:MET:HE3	20:LR:90:PRO:HD2	1.80	0.62
46:S2:891:U:C4	46:S2:896:G:C6	2.88	0.62
52:SD:205:PRO:HA	65:SR:42:PRO:HG2	1.81	0.62
2:L5:3422:G:N2	2:L5:3423:A:H62	1.97	0.62
66:SS:27:ALA:HB2	66:SS:52:LEU:HD12	1.82	0.62
2:L5:750:G:H1	2:L5:822:U:H3	1.48	0.62
40:LI:28:ARG:HA	40:LI:33:ASN:ND2	2.15	0.62
46:S2:16:G:H21	46:S2:1196:A:H62	1.47	0.62
49:SA:122:LEU:HB3	49:SA:144:THR:HG22	1.80	0.62
70:SW:2:VAL:HG12	70:SW:4:MET:HE3	1.82	0.62
79:Sg:11:LEU:HD11	79:Sg:307:VAL:HB	1.82	0.62
31:Lc:58:SER:HB3	35:Lg:96:LEU:HD13	1.82	0.62
48:S7:2:A:H2	48:S7:73:A:H62	1.48	0.62
65:SR:61:ILE:HD12	65:SR:62:GLN:N	2.15	0.62
74:Sa:44:ILE:HG13	74:Sa:65:PRO:HG2	1.80	0.62
24:LV:107:ASN:HD21	24:LV:111:GLU:HB2	1.64	0.62
35:Lg:15:THR:HG22	35:Lg:16:ALA:H	1.63	0.62
75:Sb:36:LYS:HE2	75:Sb:36:LYS:HA	1.82	0.62
18:LP:33:ALA:HB1	18:LP:117:ILE:HG12	1.81	0.61
46:S2:509:A:H3'	46:S2:510:G:H8	1.66	0.61
55:SG:67:VAL:HB	55:SG:99:GLY:HA2	1.81	0.61
63:SP:70:MET:HE2	63:SP:70:MET:H	1.65	0.61
2:L5:181:A:H8	2:L5:257:G:H1	1.49	0.61
46:S2:1514:C:H2'	46:S2:1515:G:H8	1.66	0.61
63:SP:85:ILE:HD13	63:SP:112:ILE:HA	1.81	0.61
53:SE:137:PRO:HG2	53:SE:150:PRO:HD2	1.81	0.61
46:S2:926:G:H1	46:S2:1018:U:H3	1.49	0.61
60:SL:111:VAL:HG12	60:SL:140:PHE:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SU:50:VAL:HG22	68:SU:52:GLY:H	1.65	0.61
79:Sg:184:LEU:HD21	79:Sg:187:ASN:HD21	1.65	0.61
64:SQ:43:GLU:CD	64:SQ:44:PRO:HD2	2.26	0.61
11:LH:73:ILE:O	11:LH:77:VAL:HG23	2.01	0.61
17:LO:178:ARG:NH1	17:LO:178:ARG:HB3	2.15	0.61
34:Lf:46:ARG:HB2	34:Lf:104:MET:HB2	1.82	0.61
11:LH:89:ARG:HG3	11:LH:145:ILE:HG23	1.83	0.61
46:S2:106:C:H2'	46:S2:107:A:H8	1.66	0.61
46:S2:1641:A:C4	48:S7:30:G:H4'	2.35	0.61
54:SF:178:ILE:HD12	54:SF:179:ASN:H	1.66	0.61
58:SJ:75:ASN:HA	58:SJ:78:LEU:HG	1.81	0.61
46:S2:963:A:H3'	62:SO:66:ARG:HH11	1.67	0.60
79:Sg:173:LEU:HD22	79:Sg:189:ILE:HD12	1.82	0.60
10:LG:147:VAL:HG13	10:LG:179:VAL:HG11	1.83	0.60
46:S2:650:U:H2'	46:S2:651:A:H8	1.67	0.60
54:SF:178:ILE:HD12	54:SF:179:ASN:N	2.16	0.60
33:Le:95:TYR:HE1	45:Lr:23:GLN:HG2	1.67	0.60
51:SC:211:LYS:O	51:SC:215:MET:HG2	2.00	0.60
63:SP:18:ARG:HG3	63:SP:36:LEU:HB2	1.83	0.60
9:LF:128:ARG:O	9:LF:132:GLN:HG3	2.00	0.60
49:SA:85:ARG:NH1	65:SR:81:ARG:HH22	1.99	0.60
52:SD:163:PRO:O	52:SD:167:TYR:HB2	2.02	0.60
52:SD:108:LYS:HE2	52:SD:108:LYS:N	2.16	0.60
79:Sg:13:GLY:HA3	79:Sg:43:TRP:HH2	1.66	0.60
2:L5:3861:U:H2'	2:L5:3862:G:H8	1.67	0.60
6:LC:298:ILE:HG22	19:LQ:131:PRO:HB3	1.83	0.60
66:SS:10:GLN:HG3	66:SS:57:GLY:HA2	1.83	0.60
7:LD:212:MET:HA	7:LD:212:MET:HE3	1.84	0.60
49:SA:125:THR:HG22	49:SA:175:TRP:HE1	1.66	0.60
46:S2:575:A:H4'	72:SY:89:HIS:HB2	1.83	0.60
2:L5:3384:A:H2'	2:L5:3385:A:C8	2.37	0.59
9:LF:244:LYS:HB2	9:LF:253:GLY:HA2	1.83	0.59
79:Sg:49:GLU:HG2	79:Sg:50:THR:HG23	1.83	0.59
10:LG:187:LYS:HD3	10:LG:198:THR:HG23	1.83	0.59
13:LJ:96:LYS:HD2	13:LJ:163:MET:HE1	1.83	0.59
21:LS:9:GLU:HB3	21:LS:67:VAL:HG22	1.83	0.59
58:SJ:112:THR:HG22	58:SJ:123:ILE:HD11	1.84	0.59
63:SP:110:GLU:HG2	66:SS:117:ILE:HD11	1.82	0.59
2:L5:1154:U:H2'	2:L5:1155:C:C6	2.37	0.59
50:SB:41:ILE:HD12	50:SB:41:ILE:H	1.66	0.59
8:LE:158:LEU:HB3	8:LE:202:VAL:HG11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L1:21:ARG:HH12	40:L1:24:PRO:HD3	1.67	0.59
58:SJ:127:ARG:HD3	78:Se:105:ARG:HE	1.67	0.59
10:LG:48:LYS:HD2	26:LX:42:THR:HG23	1.85	0.59
10:LG:143:VAL:O	10:LG:147:VAL:HG23	2.03	0.59
62:SO:82:ALA:O	62:SO:86:LYS:HG2	2.03	0.59
63:SP:64:LYS:HE3	63:SP:92:SER:HB3	1.84	0.59
8:LE:189:ILE:HG23	8:LE:280:ARG:HG3	1.85	0.59
46:S2:941:U:H3	46:S2:1003:U:H3	1.50	0.59
50:SB:134:LEU:HG	50:SB:218:LEU:HD12	1.85	0.59
2:L5:2132:A:H2'	2:L5:2133:A:H8	1.68	0.59
2:L5:3866:A:H5''	2:L5:3867:A:H5'	1.85	0.59
8:LE:186:PRO:HG2	8:LE:189:ILE:HD12	1.84	0.59
16:LN:104:GLU:HA	16:LN:160:GLU:HG3	1.85	0.59
19:LQ:178:ARG:N	29:La:51:GLY:HA2	2.18	0.59
80:LB:95:THR:HG22	80:LB:97:ARG:H	1.68	0.59
5:LA:45:VAL:HG22	5:LA:61:VAL:HG22	1.83	0.59
16:LN:174:LEU:HA	16:LN:183:THR:HG21	1.84	0.59
46:S2:306:U:H6	57:SI:43:ILE:HD13	1.66	0.59
46:S2:1314:A:H5'	59:SK:5:LYS:NZ	2.18	0.59
54:SF:175:ASP:HA	54:SF:178:ILE:HD11	1.85	0.59
55:SG:153:VAL:HA	55:SG:155:GLN:HE22	1.68	0.59
2:L5:1895:G:C2	2:L5:1896:G:C5	2.91	0.58
17:LO:81:TRP:HB2	17:LO:104:VAL:HG21	1.85	0.58
18:LP:13:LYS:HA	18:LP:107:LEU:HD21	1.85	0.58
64:SQ:24:HIS:O	64:SQ:68:ILE:HA	2.03	0.58
39:Lk:33:LYS:HG2	39:Lk:46:VAL:HG12	1.85	0.58
46:S2:964:A:H5''	62:SO:66:ARG:NH2	2.17	0.58
2:L5:176:G:H22	2:L5:260:G:H22	1.51	0.58
2:L5:462:A:H61	2:L5:700:A:H61	1.51	0.58
52:SD:42:THR:OG1	52:SD:45:ARG:HG3	2.03	0.58
27:LY:30:MET:HB3	27:LY:101:PRO:HG3	1.86	0.58
46:S2:1537:G:H2'	46:S2:1538:A:H8	1.68	0.58
67:ST:107:LEU:HD22	67:ST:112:MET:HE2	1.85	0.58
17:LO:121:PRO:HA	17:LO:124:LEU:HD12	1.83	0.58
23:LU:28:PRO:HB2	23:LU:34:MET:HB3	1.85	0.58
23:LU:100:LEU:HD11	23:LU:112:LEU:HB3	1.86	0.58
71:SX:52:LEU:HD11	71:SX:73:GLN:HB3	1.85	0.58
4:L8:47:C:H1'	4:L8:61:A:H2'	1.84	0.58
5:LA:130:SER:HB2	5:LA:171:GLY:HA3	1.84	0.58
38:Lj:37:CYS:HA	38:Lj:45:ARG:HB3	1.85	0.58
46:S2:1802:A:H2'	46:S2:1803:C:H6	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SI:103:LEU:HD22	57:SI:170:LYS:HB3	1.86	0.58
66:SS:22:GLY:HA2	66:SS:56:ALA:HB3	1.86	0.58
46:S2:1229:A:H2'	46:S2:1230:G:C8	2.39	0.58
32:Ld:29:ILE:O	32:Ld:33:ILE:HG12	2.04	0.58
46:S2:155:G:H2'	46:S2:156:G:C8	2.39	0.58
46:S2:1374:C:OP1	65:SR:7:LYS:HG3	2.04	0.58
56:SH:142:LYS:HB3	70:SW:54:ASP:HB3	1.86	0.58
7:LD:117:LYS:HE3	7:LD:117:LYS:HA	1.84	0.57
14:LL:197:LYS:HA	14:LL:200:LYS:HE3	1.86	0.57
19:LQ:25:LEU:O	19:LQ:29:VAL:HG23	2.04	0.57
79:Sg:20:GLN:HA	79:Sg:288:SER:OG	2.03	0.57
46:S2:1115:U:H3'	46:S2:1116:U:H5''	1.86	0.57
46:S2:1589:A:H2'	46:S2:1590:A:C8	2.38	0.57
57:SI:57:ALA:HB2	57:SI:183:GLY:HA2	1.86	0.57
61:SN:46:THR:HB	61:SN:86:GLU:OE2	2.04	0.57
15:LM:7:VAL:HG23	15:LM:27:ILE:HD13	1.85	0.57
24:LV:35:LYS:HG3	24:LV:67:LYS:HG2	1.86	0.57
41:Lm:103:LEU:HD12	41:Lm:121:LEU:HD11	1.85	0.57
46:S2:301:U:H2'	46:S2:302:A:C8	2.40	0.57
67:ST:85:ASN:HB2	67:ST:88:ARG:HB2	1.85	0.57
2:L5:2020:A:H5''	45:Lr:108:MET:HE2	1.86	0.57
51:SC:78:LEU:HD12	51:SC:81:ILE:HD12	1.86	0.57
2:L5:1008:A:H2	2:L5:1018:G:H22	1.52	0.57
52:SD:157:MET:HE2	52:SD:157:MET:HA	1.87	0.57
55:SG:199:THR:O	55:SG:203:LYS:HG2	2.05	0.57
2:L5:4171:A:OP2	80:LB:257:TRP:HB3	2.05	0.57
2:L5:3419:U:H2'	2:L5:3420:A:C8	2.39	0.57
32:Ld:90:ARG:HD2	32:Ld:102:LEU:HD13	1.85	0.57
47:S6:22:G:H2'	47:S6:23:C:C6	2.40	0.57
51:SC:196:ILE:HB	51:SC:223:TYR:HB2	1.87	0.57
80:LB:92:TYR:HB2	80:LB:159:VAL:HB	1.87	0.57
2:L5:455:C:H2'	2:L5:456:G:H8	1.69	0.57
2:L5:2227:C:H1'	10:LG:59:ARG:HH12	1.70	0.57
46:S2:1546:A:H4'	64:SQ:75:GLY:H	1.70	0.57
18:LP:132:ALA:HB3	18:LP:135:ARG:HH21	1.68	0.56
70:SW:32:LYS:O	70:SW:36:ARG:HG2	2.05	0.56
79:Sg:191:HIS:CD2	79:Sg:195:LEU:HD21	2.40	0.56
9:LF:258:ARG:HB2	9:LF:261:GLN:HB2	1.87	0.56
13:LJ:112:HIS:NE2	13:LJ:126:TYR:HB2	2.21	0.56
18:LP:118:GLN:HB3	18:LP:147:GLU:HG2	1.88	0.56
46:S2:1537:G:H2'	46:S2:1538:A:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2054:G:H4'	6:LC:242:PRO:HB2	1.88	0.56
2:L5:3523:C:H42	2:L5:3537:G:H1	1.52	0.56
2:L5:4068:A:H4'	12:LI:74:LYS:HD3	1.86	0.56
11:LH:92:MET:HG2	11:LH:181:VAL:HA	1.86	0.56
14:LL:110:LEU:O	14:LL:114:VAL:HG23	2.04	0.56
29:La:99:PRO:HG2	29:La:122:VAL:HG23	1.87	0.56
50:SB:109:LYS:O	50:SB:113:MET:HG3	2.05	0.56
33:Le:87:VAL:HG23	45:Lr:34:ALA:HB1	1.87	0.56
79:Sg:99:ARG:HG2	79:Sg:99:ARG:HH11	1.70	0.56
46:S2:1779:C:H2'	46:S2:1780:G:C8	2.41	0.56
2:L5:719:A:H2'	2:L5:720:C:C6	2.41	0.56
2:L5:2244:G:H1	2:L5:2250:G:H1	1.52	0.56
15:LM:43:THR:HG22	15:LM:45:VAL:HG23	1.87	0.56
2:L5:3927:A:H2'	2:L5:3928:G:C8	2.41	0.56
33:Le:89:LEU:HD13	33:Le:118:LEU:HD23	1.87	0.56
48:S7:8:G:H22	48:S7:67:U:H1'	1.70	0.56
54:SF:73:THR:HG23	54:SF:89:THR:HB	1.87	0.56
57:SI:81:VAL:HG22	57:SI:102:VAL:HG12	1.87	0.56
61:SN:105:ASN:N	61:SN:105:ASN:OD1	2.37	0.56
71:SX:68:LYS:HD2	71:SX:91:LEU:HD22	1.88	0.56
2:L5:4424:G:H22	2:L5:4510:U:H3	1.54	0.56
7:LD:51:MET:HE3	7:LD:105:LEU:HD23	1.88	0.56
37:Li:89:GLU:O	37:Li:93:VAL:HG23	2.06	0.56
2:L5:1147:C:H2'	2:L5:1148:A:C8	2.40	0.55
46:S2:1809:U:H2'	46:S2:1810:A:C8	2.40	0.55
79:Sg:191:HIS:NE2	79:Sg:217:MET:HG3	2.21	0.55
49:SA:69:GLU:HG2	51:SC:270:THR:HG21	1.87	0.55
54:SF:23:TRP:HZ3	54:SF:101:HIS:ND1	2.04	0.55
54:SF:39:ILE:HG21	54:SF:113:VAL:HG23	1.87	0.55
61:SN:106:ARG:HA	61:SN:106:ARG:HE	1.71	0.55
63:SP:85:ILE:HD11	63:SP:114:HIS:H	1.71	0.55
10:LG:215:LEU:O	10:LG:219:VAL:HG23	2.06	0.55
20:LR:173:ARG:HG2	20:LR:176:ARG:HG2	1.88	0.55
49:SA:85:ARG:HG2	49:SA:204:TYR:HA	1.88	0.55
77:Sd:4:GLN:HE21	77:Sd:7:TYR:HD1	1.55	0.55
2:L5:1894:C:O2	2:L5:1894:C:O4'	2.23	0.55
12:LI:19:LYS:HG3	12:LI:26:VAL:HG21	1.89	0.55
45:Lr:52:GLU:HG2	45:Lr:61:VAL:HB	1.87	0.55
59:SK:21:MET:HE2	59:SK:21:MET:HA	1.88	0.55
2:L5:4113:U:H2'	2:L5:4114:C:H6	1.71	0.55
8:LE:57:LEU:HD12	8:LE:58:VAL:HG22	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Lo:69:ARG:HE	43:Lo:80:LYS:HD3	1.72	0.55
46:S2:1814:A:H2'	46:S2:1815:G:C8	2.41	0.55
46:S2:1229:A:H2'	46:S2:1230:G:H8	1.71	0.55
51:SC:130:ILE:HD11	51:SC:162:ILE:HD11	1.89	0.55
51:SC:168:GLY:HA2	69:SV:1:MET:HE1	1.88	0.55
56:SH:69:LEU:HD22	56:SH:96:ALA:HB2	1.89	0.55
72:SY:15:LYS:HD2	72:SY:21:LYS:HD3	1.88	0.55
36:Lh:53:SER:O	36:Lh:57:VAL:HG23	2.06	0.55
66:SS:10:GLN:NE2	66:SS:13:LEU:HD23	2.21	0.55
46:S2:383:C:H2'	46:S2:384:G:H8	1.72	0.55
46:S2:944:U:H2'	46:S2:945:A:C8	2.42	0.55
47:S6:23:C:H2'	47:S6:24:G:C8	2.42	0.55
2:L5:2168:C:H2'	2:L5:2169:A:H8	1.71	0.55
2:L5:4705:C:H2'	2:L5:4706:A:C8	2.42	0.55
6:LC:281:MET:HA	6:LC:281:MET:HE3	1.87	0.55
12:LI:62:SER:HA	12:LI:65:LEU:HD12	1.89	0.55
32:Ld:22:THR:HG22	32:Ld:122:VAL:HB	1.88	0.55
40:Ll:15:LYS:O	40:Ll:19:GLN:HG2	2.07	0.55
43:Lo:77:CYS:C	43:Lo:78:ARG:HD2	2.32	0.55
46:S2:1779:C:H2'	46:S2:1780:G:H8	1.71	0.55
66:SS:137:LYS:HG2	66:SS:138:THR:HG23	1.89	0.55
79:Sg:153:CYS:SG	79:Sg:198:VAL:HG22	2.47	0.55
2:L5:4572:C:H3'	2:L5:4573:G:H21	1.72	0.54
8:LE:259:LYS:HA	8:LE:262:ASP:OD1	2.06	0.54
46:S2:224:U:H5''	60:SL:17:PHE:CE1	2.42	0.54
50:SB:164:ILE:HG22	50:SB:168:MET:HE3	1.89	0.54
51:SC:210:PRO:HD3	51:SC:236:PHE:CE2	2.42	0.54
63:SP:14:LYS:HZ2	63:SP:15:PHE:H	1.55	0.54
14:LL:114:VAL:HG12	14:LL:118:LYS:HE2	1.89	0.54
15:LM:127:VAL:O	15:LM:131:GLN:HG2	2.07	0.54
46:S2:118:C:H1'	46:S2:446:A:C4	2.42	0.54
80:LB:89:ILE:HD12	80:LB:162:ILE:HA	1.88	0.54
2:L5:3873:A:P	22:LT:2:THR:HG21	2.48	0.54
23:LU:41:GLN:HA	23:LU:44:GLN:OE1	2.07	0.54
45:Lr:32:LEU:HD12	45:Lr:106:LEU:HD23	1.87	0.54
46:S2:641:A:H2'	46:S2:642:A:C8	2.42	0.54
45:Lr:32:LEU:HD22	45:Lr:110:ALA:HA	1.88	0.54
50:SB:128:LYS:HE2	50:SB:132:GLY:HA2	1.88	0.54
53:SE:45:ILE:HG13	53:SE:61:VAL:HG11	1.89	0.54
53:SE:87:MET:HE1	53:SE:123:LEU:H	1.72	0.54
64:SQ:39:LEU:HD23	64:SQ:52:LEU:HD23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1562:G:H1	2:L5:1576:U:H3	1.55	0.54
5:LA:107:MET:HE2	5:LA:166:VAL:HG22	1.88	0.54
8:LE:107:ASP:O	8:LE:108:LYS:HG2	2.07	0.54
17:LO:196:LEU:HB3	17:LO:201:LEU:HB2	1.88	0.54
57:SI:87:ASN:HB3	57:SI:90:LEU:HG	1.90	0.54
60:SL:49:GLU:HA	60:SL:49:GLU:OE2	2.06	0.54
2:L5:1562:G:H22	2:L5:1576:U:H3	1.56	0.54
2:L5:3927:A:H2'	2:L5:3928:G:H8	1.73	0.54
2:L5:4190:C:H2'	2:L5:4191:G:C8	2.42	0.54
2:L5:4615:A:H2'	2:L5:4616:A:H8	1.73	0.54
14:LL:124:LEU:HD11	36:Lh:119:TYR:HB2	1.88	0.54
21:LS:85:ASP:HB2	21:LS:123:SER:HB3	1.89	0.54
28:LZ:41:ALA:HB2	28:LZ:77:TYR:HE1	1.73	0.54
40:Ll:28:ARG:HA	40:Ll:33:ASN:HD21	1.71	0.54
57:SI:48:VAL:HG11	57:SI:54:LYS:HD2	1.88	0.54
73:SZ:50:PHE:HE1	73:SZ:79:ILE:HG21	1.72	0.54
79:Sg:20:GLN:NE2	79:Sg:69:VAL:H	2.04	0.54
14:LL:80:GLU:HG3	14:LL:110:LEU:HD12	1.89	0.54
31:Lc:102:SER:HB2	31:Lc:105:ILE:HD11	1.89	0.54
46:S2:225:C:H2'	46:S2:226:A:C8	2.43	0.54
46:S2:1011:G:H2'	46:S2:1012:A:H8	1.73	0.54
2:L5:3321:G:H2'	2:L5:3322:G:H8	1.73	0.54
14:LL:116:ARG:HH12	14:LL:157:ILE:HG12	1.71	0.54
47:S6:62:C:H2'	47:S6:63:A:H8	1.71	0.54
2:L5:176:G:H22	2:L5:260:G:N2	2.06	0.54
2:L5:948:G:H1	2:L5:1038:C:H42	1.54	0.54
2:L5:2018:G:H4'	8:LE:120:MET:HE1	1.89	0.54
21:LS:154:LEU:HB3	21:LS:157:ARG:HD3	1.89	0.54
46:S2:1780:G:H2'	46:S2:1781:G:C8	2.43	0.54
79:Sg:104:HIS:CE1	79:Sg:130:LYS:HG3	2.43	0.54
46:S2:944:U:H2'	46:S2:945:A:H8	1.73	0.54
67:ST:18:LEU:HB3	67:ST:58:ALA:HB1	1.90	0.53
24:LV:33:GLY:HA3	24:LV:69:LYS:HD2	1.91	0.53
31:Lc:26:LYS:HD2	31:Lc:98:ASP:HB3	1.89	0.53
35:Lg:100:GLN:O	35:Lg:104:VAL:HG23	2.08	0.53
46:S2:1267:C:H42	46:S2:1517:G:H1	1.55	0.53
52:SD:123:LEU:HD22	52:SD:152:PHE:HB3	1.88	0.53
76:Sc:32:VAL:HG11	76:Sc:56:LEU:HD12	1.91	0.53
2:L5:1164:G:H1	2:L5:1321:U:H3	1.57	0.53
11:LH:1:MET:HE2	21:LS:140:PRO:HB2	1.91	0.53
46:S2:533:C:H41	46:S2:551:C:H42	1.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SR:109:LEU:HD12	65:SR:111:PHE:HD2	1.74	0.53
72:SY:83:LYS:HA	72:SY:91:LEU:HD11	1.91	0.53
76:Sc:11:LEU:HB3	76:Sc:35:MET:HG3	1.90	0.53
2:L5:4615:A:H2'	2:L5:4616:A:C8	2.43	0.53
46:S2:1233:U:H2'	46:S2:1234:G:C8	2.43	0.53
74:Sa:36:ILE:HD12	74:Sa:36:ILE:O	2.08	0.53
80:LB:56:ILE:HG22	80:LB:368:ILE:HA	1.89	0.53
2:L5:1352:U:H2'	2:L5:1353:G:H8	1.74	0.53
31:Lc:20:LEU:H	31:Lc:20:LEU:HD12	1.73	0.53
35:Lg:93:ARG:O	35:Lg:97:ILE:HG13	2.09	0.53
36:Lh:46:LYS:O	36:Lh:50:VAL:HG23	2.08	0.53
41:Lm:78:ILE:HG12	41:Lm:83:ARG:HH21	1.74	0.53
51:SC:104:ASP:HB2	51:SC:130:ILE:HG22	1.90	0.53
79:Sg:56:GLN:HG3	79:Sg:57:ARG:HG2	1.91	0.53
18:LP:94:MET:HG2	18:LP:148:MET:SD	2.49	0.53
47:S6:23:C:H2'	47:S6:24:G:H8	1.72	0.53
47:S6:30:G:C2	47:S6:31:G:H1'	2.44	0.53
53:SE:70:ILE:HG12	53:SE:92:ILE:HD11	1.90	0.53
57:SI:8:TRP:CZ3	57:SI:20:PRO:HB3	2.44	0.53
2:L5:3419:U:H2'	2:L5:3420:A:H8	1.72	0.53
5:LA:29:LEU:H	5:LA:123:ARG:HB3	1.74	0.53
48:S7:26:G:H1	48:S7:44:A:H61	1.57	0.53
5:LA:101:VAL:HG22	5:LA:165:VAL:HG22	1.91	0.53
23:LU:48:LYS:HG2	23:LU:53:ALA:HB2	1.91	0.53
53:SE:31:PRO:HG3	53:SE:43:PRO:HG3	1.90	0.53
53:SE:123:LEU:HD22	53:SE:159:THR:HG22	1.91	0.53
53:SE:256:LEU:HD23	53:SE:256:LEU:H	1.73	0.53
76:Sc:27:CYS:HB3	76:Sc:45:ASN:HB3	1.91	0.53
2:L5:2446:U:H4'	39:Lk:44:THR:HG21	1.91	0.53
2:L5:4344:A:H4'	11:LH:71:ARG:HB3	1.90	0.53
46:S2:456:A:H2'	46:S2:457:C:H6	1.74	0.53
65:SR:71:ILE:O	65:SR:75:GLU:HG2	2.08	0.53
76:Sc:14:VAL:HG13	76:Sc:30:VAL:HB	1.91	0.53
2:L5:3374:A:H2'	2:L5:3375:A:H8	1.73	0.53
3:L7:49:A:H5''	7:LD:224:SER:HB2	1.90	0.53
6:LC:117:THR:HA	6:LC:120:LYS:HE3	1.90	0.53
15:LM:105:THR:HG23	15:LM:107:PHE:H	1.73	0.53
56:SH:134:VAL:O	56:SH:134:VAL:HG23	2.09	0.53
72:SY:40:ILE:HA	72:SY:43:LYS:HE2	1.90	0.53
6:LC:164:THR:O	6:LC:168:VAL:HG23	2.09	0.52
12:LI:206:LEU:HD12	12:LI:209:TRP:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SQ:32:ILE:HD11	64:SQ:39:LEU:HD13	1.91	0.52
80:LB:17:LEU:HD21	80:LB:264:PHE:HD2	1.74	0.52
26:LX:120:ASP:HB3	26:LX:141:ALA:HB2	1.90	0.52
33:Le:90:MET:HA	33:Le:90:MET:HE3	1.91	0.52
50:SB:222:LYS:H	50:SB:222:LYS:HD3	1.74	0.52
2:L5:2415:U:C2	20:LR:118:HIS:CE1	2.97	0.52
7:LD:236:MET:HA	7:LD:239:MET:HG2	1.92	0.52
21:LS:80:ILE:HG23	21:LS:129:VAL:HG22	1.91	0.52
35:Lg:5:LEU:HD11	35:Lg:22:LEU:HD11	1.91	0.52
46:S2:16:G:H2'	46:S2:17:C:C6	2.44	0.52
46:S2:306:U:O2	46:S2:306:U:H3'	2.09	0.52
46:S2:389:U:H2'	46:S2:390:A:H8	1.74	0.52
46:S2:1204:G:H2'	46:S2:1205:A:C8	2.45	0.52
79:Sg:164:ILE:HA	79:Sg:179:LEU:HB3	1.89	0.52
16:LN:135:ILE:HG23	16:LN:142:ILE:HD13	1.91	0.52
19:LQ:53:MET:HE1	19:LQ:143:ARG:NH2	2.24	0.52
31:Lc:17:ARG:HA	31:Lc:20:LEU:CD1	2.40	0.52
51:SC:176:LYS:HG3	51:SC:177:PRO:HD2	1.92	0.52
54:SF:201:LYS:NZ	54:SF:201:LYS:HB3	2.25	0.52
65:SR:65:PRO:HA	65:SR:73:LEU:HD13	1.90	0.52
80:LB:57:VAL:HG12	80:LB:367:PHE:HB3	1.91	0.52
2:L5:173:C:H2'	2:L5:174:C:C6	2.45	0.52
2:L5:2194:C:H42	26:LX:89:LYS:HZ3	1.56	0.52
2:L5:4111:C:H2'	2:L5:4112:U:C6	2.44	0.52
21:LS:19:THR:HG23	21:LS:22:CYS:H	1.74	0.52
46:S2:819:A:H2'	46:S2:820:G:H8	1.75	0.52
46:S2:1218:A:H2'	46:S2:1219:C:H6	1.73	0.52
2:L5:684:C:H2'	2:L5:685:G:H8	1.75	0.52
2:L5:3861:U:H2'	2:L5:3862:G:C8	2.44	0.52
22:LT:105:PHE:O	22:LT:109:VAL:HG23	2.10	0.52
46:S2:636:G:H5'	78:Se:95:LYS:HD2	1.91	0.52
55:SG:58:LYS:HE2	55:SG:105:ASN:HB2	1.91	0.52
67:ST:88:ARG:HH11	67:ST:88:ARG:HG3	1.74	0.52
46:S2:1447:A:H5''	68:SU:58:THR:HG23	1.92	0.52
71:SX:53:GLU:HG3	71:SX:71:ARG:HB2	1.91	0.52
79:Sg:99:ARG:HH12	79:Sg:135:LEU:HD13	1.75	0.52
20:LR:170:ARG:O	20:LR:170:ARG:HD3	2.10	0.52
23:LU:44:GLN:NE2	23:LU:63:ILE:HG21	2.25	0.52
45:Lr:92:SER:O	45:Lr:96:MET:HG3	2.09	0.52
68:SU:80:PHE:HB3	77:Sd:52:PHE:HB3	1.90	0.52
79:Sg:59:LEU:HD23	79:Sg:90:TRP:CG	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:56:GLU:HB2	12:LI:58:GLU:HG2	1.90	0.52
23:LU:65:ARG:HH11	23:LU:65:ARG:HG3	1.75	0.52
38:Lj:85:LYS:O	38:Lj:85:LYS:HD2	2.09	0.52
46:S2:455:U:H2'	46:S2:456:A:H8	1.75	0.52
65:SR:84:TYR:O	65:SR:84:TYR:CD2	2.63	0.52
67:ST:101:ARG:O	67:ST:105:GLN:HG3	2.09	0.52
46:S2:1414:G:H2'	46:S2:1415:A:C8	2.45	0.52
46:S2:1642:A:HO2'	46:S2:1643:U:H6	1.56	0.52
52:SD:98:ALA:HB2	52:SD:188:ILE:HG22	1.92	0.52
2:L5:182:A:H62	2:L5:255:G:H1	1.58	0.51
2:L5:2018:G:H2'	2:L5:2019:G:H21	1.75	0.51
2:L5:4654:U:H4'	2:L5:4655:A:H5'	1.92	0.51
19:LQ:63:LEU:HD23	19:LQ:92:ILE:HD11	1.93	0.51
33:Le:85:LEU:HD22	33:Le:111:ILE:HG23	1.92	0.51
46:S2:832:G:H2'	46:S2:833:G:C8	2.45	0.51
46:S2:963:A:H3'	62:SO:66:ARG:NH1	2.25	0.51
55:SG:134:GLY:HA3	55:SG:158:VAL:HG11	1.92	0.51
2:L5:262:G:O2'	2:L5:263:C:H5''	2.09	0.51
9:LF:266:ILE:O	9:LF:270:ASN:HB2	2.10	0.51
50:SB:198:GLU:HG3	50:SB:210:VAL:HB	1.92	0.51
76:Sc:12:ALA:HB1	76:Sc:32:VAL:HB	1.92	0.51
2:L5:1391:G:O2'	2:L5:1426:G:H4'	2.11	0.51
2:L5:4689:G:C6	80:LB:389:MET:HE2	2.45	0.51
45:Lr:89:THR:O	45:Lr:93:ILE:HG13	2.10	0.51
53:SE:192:ILE:HB	53:SE:243:GLY:HA3	1.91	0.51
71:SX:128:VAL:HG13	71:SX:138:LYS:HE2	1.91	0.51
2:L5:254:C:H2'	2:L5:255:G:H8	1.75	0.51
11:LH:117:PHE:O	11:LH:120:GLU:HG3	2.11	0.51
16:LN:16:SER:HB2	37:Li:48:CYS:HB3	1.91	0.51
17:LO:178:ARG:HB3	17:LO:178:ARG:HH11	1.74	0.51
26:LX:57:GLN:O	26:LX:57:GLN:HG3	2.11	0.51
46:S2:527:A:H5''	78:Se:109:ARG:HH12	1.76	0.51
2:L5:165:A:H2'	2:L5:166:C:H5''	1.92	0.51
2:L5:1745:A:H2'	2:L5:1746:A:C8	2.46	0.51
20:LR:170:ARG:HH21	46:S2:910:G:P	2.33	0.51
46:S2:929:G:H2'	46:S2:930:G:C8	2.45	0.51
46:S2:1514:C:H2'	46:S2:1515:G:C8	2.44	0.51
52:SD:107:TYR:HA	52:SD:110:LEU:HD12	1.92	0.51
55:SG:182:PRO:O	55:SG:186:GLN:HB3	2.11	0.51
63:SP:83:MET:HB3	63:SP:116:LEU:HD12	1.90	0.51
2:L5:2479:A:H1'	20:LR:93:VAL:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3374:A:H2'	2:L5:3375:A:C8	2.46	0.51
46:S2:1138:U:H3	46:S2:1149:A:H62	1.59	0.51
46:S2:1238:C:H42	46:S2:1521:G:H1	1.58	0.51
47:S6:22:G:H2'	47:S6:23:C:H6	1.76	0.51
4:L8:8:U:H2'	4:L8:9:A:H8	1.76	0.51
10:LG:143:VAL:HG13	10:LG:203:ALA:HB2	1.92	0.51
10:LG:229:ARG:O	10:LG:233:ILE:HG13	2.11	0.51
46:S2:1114:A:H2'	46:S2:1115:U:C6	2.46	0.51
46:S2:1707:G:H2'	46:S2:1708:U:H6	1.75	0.51
47:S6:62:C:H2'	47:S6:63:A:C8	2.46	0.51
53:SE:94:LYS:HG3	53:SE:95:THR:HG23	1.93	0.51
79:Sg:39:THR:HG22	79:Sg:60:ARG:HG2	1.93	0.51
2:L5:1895:G:N2	2:L5:1896:G:N9	2.58	0.51
2:L5:2092:C:H2'	2:L5:2093:G:H8	1.74	0.51
44:Lp:84:ARG:HH11	44:Lp:84:ARG:HG3	1.74	0.51
62:SO:129:ILE:HG21	74:Sa:44:ILE:HG21	1.92	0.51
17:LO:22:ILE:HD13	17:LO:120:VAL:HG11	1.92	0.51
18:LP:85:LYS:O	18:LP:89:GLU:HG3	2.11	0.51
18:LP:94:MET:HE1	18:LP:146:ILE:HG23	1.92	0.51
46:S2:552:U:H2'	46:S2:553:G:C8	2.46	0.51
46:S2:1569:C:H2'	46:S2:1570:A:C8	2.46	0.51
46:S2:1744:G:N2	46:S2:1792:A:H62	2.09	0.51
51:SC:204:ILE:HG13	51:SC:220:ASP:O	2.11	0.51
55:SG:3:LEU:HD13	55:SG:109:LEU:HB3	1.92	0.51
57:SI:42:ARG:HG2	57:SI:58:LEU:HB2	1.91	0.51
72:SY:21:LYS:HG3	72:SY:75:ILE:HG13	1.92	0.51
2:L5:674:G:H21	45:Lr:46:ARG:H	1.59	0.51
2:L5:4247:U:H2'	2:L5:4248:G:H8	1.75	0.51
17:LO:19:LEU:O	17:LO:23:VAL:HG23	2.11	0.51
46:S2:1802:A:H2'	46:S2:1803:C:C6	2.46	0.51
72:SY:55:ILE:HG13	72:SY:75:ILE:HG22	1.93	0.51
75:Sb:74:THR:HB	75:Sb:77:CYS:SG	2.51	0.51
2:L5:1736:G:H2'	2:L5:1737:A:C8	2.46	0.50
2:L5:3264:U:H2'	2:L5:3265:A:H8	1.76	0.50
2:L5:4246:C:H2'	2:L5:4247:U:H6	1.75	0.50
2:L5:4675:C:H41	57:SI:170:LYS:NZ	2.09	0.50
3:L7:7:G:H2'	3:L7:8:G:H8	1.76	0.50
51:SC:87:PRO:HG3	69:SV:29:HIS:HD1	1.76	0.50
51:SC:108:LYS:HG2	51:SC:233:LEU:HD22	1.92	0.50
69:SV:15:ARG:HH21	69:SV:24:ILE:HG21	1.75	0.50
2:L5:888:U:C5	2:L5:922:G:C2	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1895:G:C2	2:L5:1896:G:N9	2.79	0.50
2:L5:2599:A:H61	2:L5:3500:C:H42	1.58	0.50
19:LQ:3:VAL:HG13	19:LQ:5:ILE:HG22	1.93	0.50
36:Lh:22:ASP:O	36:Lh:26:VAL:HG23	2.11	0.50
46:S2:929:G:H1	46:S2:1014:U:H3	1.58	0.50
46:S2:1048:C:H5'	62:SO:143:LYS:HB2	1.92	0.50
2:L5:1325:C:H2'	2:L5:1326:G:H8	1.77	0.50
4:L8:67:U:H2'	4:L8:68:G:H8	1.76	0.50
46:S2:221:U:H2'	46:S2:222:U:H6	1.76	0.50
46:S2:1277:A:C5	46:S2:1323:G:H1'	2.47	0.50
80:LB:216:MET:HE2	80:LB:283:LYS:HB2	1.94	0.50
19:LQ:90:VAL:HB	29:La:80:THR:HG21	1.94	0.50
43:Lo:22:LYS:HD2	43:Lo:73:VAL:HG12	1.92	0.50
65:SR:72:LYS:NZ	65:SR:76:GLU:HB2	2.26	0.50
71:SX:68:LYS:HB3	71:SX:91:LEU:HD13	1.93	0.50
2:L5:2316:G:H1'	2:L5:2323:G:H22	1.77	0.50
2:L5:4112:U:H2'	2:L5:4113:U:C6	2.46	0.50
13:LJ:20:LEU:HD23	13:LJ:22:LEU:HD11	1.92	0.50
15:LM:26:ALA:HB2	15:LM:77:TRP:HZ3	1.76	0.50
17:LO:194:GLU:H	17:LO:194:GLU:CD	2.20	0.50
29:La:5:LEU:HD23	29:La:5:LEU:H	1.76	0.50
63:SP:68:PRO:HG2	63:SP:71:GLU:OE2	2.11	0.50
2:L5:2277:C:H2'	2:L5:2278:G:C8	2.47	0.50
2:L5:3587:U:H3	2:L5:3833:G:H1	1.59	0.50
19:LQ:70:MET:HE1	19:LQ:137:VAL:HB	1.93	0.50
46:S2:4:C:H1'	58:SJ:18:ARG:HH22	1.76	0.50
46:S2:126:G:N3	46:S2:181:A:H1'	2.27	0.50
55:SG:22:ARG:HB3	55:SG:25:ARG:HH21	1.76	0.50
56:SH:51:ILE:HG21	56:SH:179:LYS:HG2	1.93	0.50
59:SK:1:MET:HE1	59:SK:44:HIS:HA	1.93	0.50
18:LP:32:THR:O	18:LP:36:ILE:HG23	2.11	0.50
20:LR:7:GLN:HG2	20:LR:32:ILE:HG22	1.94	0.50
46:S2:1218:A:H2'	46:S2:1219:C:C6	2.47	0.50
46:S2:1408:U:H2'	46:S2:1409:U:C6	2.46	0.50
2:L5:681:C:H2'	2:L5:682:G:H8	1.77	0.50
2:L5:2499:A:H2'	2:L5:2500:A:C8	2.44	0.50
9:LF:176:ILE:HG22	9:LF:209:MET:HE3	1.94	0.50
46:S2:51:U:H2'	46:S2:52:G:H8	1.77	0.50
54:SF:179:ASN:OD1	54:SF:184:SER:HB3	2.12	0.50
56:SH:69:LEU:O	56:SH:73:GLN:HG2	2.12	0.50
58:SJ:42:GLU:OE2	58:SJ:42:GLU:N	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:17:C:H2'	46:S2:18:C:H6	1.77	0.50
46:S2:532:A:H3'	46:S2:533:C:H5''	1.94	0.50
46:S2:1671:C:H2'	46:S2:1672:G:C8	2.47	0.50
58:SJ:42:GLU:HA	58:SJ:45:ARG:HB3	1.93	0.50
2:L5:254:C:H2'	2:L5:255:G:C8	2.47	0.49
2:L5:761:C:H42	2:L5:810:G:H1	1.58	0.49
2:L5:767:G:H2'	2:L5:768:G:H4'	1.94	0.49
6:LC:289:LEU:HD21	19:LQ:31:LEU:HB2	1.93	0.49
10:LG:244:PRO:HA	10:LG:247:VAL:HG22	1.93	0.49
12:LI:187:GLU:N	12:LI:187:GLU:OE2	2.44	0.49
15:LM:95:ILE:O	15:LM:99:GLU:HG2	2.12	0.49
22:LT:57:TYR:HA	22:LT:60:LYS:HG3	1.94	0.49
22:LT:102:ARG:O	22:LT:106:LEU:HD23	2.12	0.49
58:SJ:37:LEU:HB3	58:SJ:42:GLU:OE1	2.12	0.49
58:SJ:115:LEU:HD22	58:SJ:123:ILE:HD12	1.94	0.49
58:SJ:124:HIS:CE1	78:Se:109:ARG:HD3	2.47	0.49
61:SN:4:MET:HE3	61:SN:124:ARG:HH11	1.75	0.49
62:SO:97:LEU:HD21	74:Sa:44:ILE:HG23	1.93	0.49
2:L5:30:C:H2'	2:L5:31:U:C6	2.47	0.49
2:L5:407:A:H4'	2:L5:408:G:H3'	1.94	0.49
2:L5:1017:A:H2'	2:L5:1018:G:C8	2.47	0.49
12:LI:141:LYS:HE3	12:LI:143:GLN:HE21	1.76	0.49
43:Lo:33:LEU:HA	43:Lo:38:LYS:HG2	1.95	0.49
49:SA:77:ILE:HG13	49:SA:122:LEU:HD11	1.94	0.49
4:L8:52:A:H62	40:Ll:27:ILE:HD13	1.77	0.49
7:LD:111:ASN:HD21	7:LD:252:VAL:HG22	1.78	0.49
12:LI:17:TYR:O	12:LI:96:VAL:HG12	2.12	0.49
56:SH:15:LYS:H	56:SH:15:LYS:HD3	1.78	0.49
79:Sg:213:ASP:HB3	79:Sg:215:GLN:NE2	2.26	0.49
2:L5:4554:G:H21	2:L5:4559:G:H5'	1.78	0.49
5:LA:180:LEU:HD21	44:Lp:22:LEU:HB3	1.94	0.49
6:LC:150:LEU:O	6:LC:152:LEU:HD12	2.13	0.49
13:LJ:57:VAL:HG23	13:LJ:62:ILE:HD11	1.94	0.49
17:LO:96:GLN:O	17:LO:100:GLU:HG3	2.12	0.49
46:S2:498:C:H2'	46:S2:499:C:C6	2.48	0.49
46:S2:1431:C:H2'	46:S2:1432:G:H8	1.77	0.49
56:SH:100:ILE:HG12	56:SH:125:VAL:HG21	1.94	0.49
72:SY:16:ARG:HG2	72:SY:17:LEU:N	2.27	0.49
2:L5:1016:C:C2	2:L5:1017:A:C8	3.00	0.49
2:L5:1191:C:H3'	2:L5:1192:G:C8	2.47	0.49
2:L5:4202:G:H2'	2:L5:4203:G:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Lg:102:ILE:O	35:Lg:106:VAL:HG23	2.13	0.49
46:S2:399:A:H5''	46:S2:400:C:H3'	1.93	0.49
46:S2:982:A:H2'	46:S2:983:G:C8	2.47	0.49
46:S2:1448:G:H2'	46:S2:1449:A:H8	1.78	0.49
49:SA:85:ARG:CZ	65:SR:81:ARG:HH22	2.26	0.49
49:SA:85:ARG:HD2	65:SR:81:ARG:HH12	1.78	0.49
52:SD:57:ASN:C	52:SD:57:ASN:HD22	2.20	0.49
2:L5:2029:C:H2'	2:L5:2030:G:H8	1.78	0.49
6:LC:254:GLU:O	6:LC:258:ARG:HG3	2.13	0.49
12:LI:184:MET:HE2	12:LI:190:LEU:HD13	1.94	0.49
23:LU:100:LEU:HG	23:LU:112:LEU:HD23	1.95	0.49
41:Lm:103:LEU:HD11	41:Lm:110:CYS:HA	1.95	0.49
46:S2:65:C:H4'	55:SG:172:LYS:HD3	1.93	0.49
46:S2:221:U:H2'	46:S2:222:U:C6	2.47	0.49
46:S2:1409:U:H2'	46:S2:1410:A:H8	1.77	0.49
61:SN:91:LEU:HB3	61:SN:122:ILE:HG12	1.94	0.49
69:SV:38:GLU:HG3	69:SV:50:PHE:HA	1.94	0.49
79:Sg:57:ARG:HH21	79:Sg:95:GLY:HA3	1.77	0.49
2:L5:455:C:H2'	2:L5:456:G:C8	2.47	0.49
17:LO:89:PRO:O	17:LO:95:GLY:HA3	2.13	0.49
19:LQ:100:VAL:HG21	19:LQ:113:ILE:HD13	1.95	0.49
21:LS:44:PHE:O	21:LS:48:VAL:HG23	2.13	0.49
46:S2:1301:U:H2'	63:SP:51:ARG:NH1	2.27	0.49
52:SD:105:LEU:HD13	52:SD:122:VAL:HG21	1.94	0.49
56:SH:9:VAL:HG13	56:SH:10:LYS:HG2	1.94	0.49
73:SZ:99:LEU:HD21	73:SZ:102:LYS:HB2	1.94	0.49
2:L5:1578:A:H2'	2:L5:1579:A:H8	1.77	0.49
2:L5:3827:U:H2'	2:L5:3828:G:H8	1.77	0.49
30:Lb:9:THR:HG22	30:Lb:9:THR:O	2.12	0.49
46:S2:601:G:H2'	46:S2:602:G:H8	1.77	0.49
46:S2:1224:A:H61	46:S2:1644:U:H3	1.60	0.49
46:S2:498:C:H2'	46:S2:499:C:H6	1.78	0.49
46:S2:1140:C:H5	46:S2:1150:A:H62	1.61	0.49
46:S2:1846:A:H2'	46:S2:1847:G:C8	2.48	0.49
2:L5:492:G:H1	2:L5:670:C:H42	1.61	0.49
2:L5:508:G:H1	2:L5:661:U:H3	1.61	0.49
2:L5:4298:C:H3'	20:LR:62:ARG:HH22	1.78	0.49
5:LA:137:ILE:HD11	5:LA:149:LYS:HB2	1.95	0.49
13:LJ:95:ARG:HH21	13:LJ:176:PRO:HG3	1.78	0.49
28:LZ:47:ASP:HB3	28:LZ:69:LYS:HD3	1.93	0.49
46:S2:833:G:H1	46:S2:843:C:N4	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:S7:18:G:H4'	48:S7:60:A:N7	2.28	0.49
54:SF:111:VAL:HG21	54:SF:178:ILE:HG22	1.94	0.49
73:SZ:54:THR:HG23	73:SZ:77:LEU:HD23	1.95	0.49
2:L5:1216:G:H4'	2:L5:1217:C:H4'	1.94	0.48
2:L5:3711:U:H2'	2:L5:3713:A:H62	1.78	0.48
4:L8:8:U:H2'	4:L8:9:A:C8	2.48	0.48
27:LY:74:TYR:CE2	27:LY:77:LYS:HE2	2.48	0.48
38:Lj:54:LYS:O	38:Lj:58:THR:HG23	2.12	0.48
46:S2:449:A:H5''	57:SI:25:ARG:HA	1.95	0.48
55:SG:56:ASN:O	55:SG:106:LEU:HD22	2.13	0.48
80:LB:161:ARG:HG2	80:LB:184:GLN:HA	1.95	0.48
2:L5:2163:G:H1'	2:L5:2545:C:H5''	1.94	0.48
2:L5:3489:U:H2'	2:L5:3490:C:H6	1.79	0.48
2:L5:4541:C:H6	15:LM:132:ARG:HD2	1.78	0.48
23:LU:87:THR:O	23:LU:91:LEU:HD13	2.14	0.48
24:LV:106:VAL:HG12	24:LV:112:MET:HA	1.95	0.48
46:S2:1018:U:H5'	61:SN:55:ARG:HD3	1.94	0.48
74:Sa:25:ASN:HD21	74:Sa:73:TYR:HD2	1.59	0.48
2:L5:100:C:H2'	2:L5:101:A:H8	1.79	0.48
2:L5:4531:U:H3	2:L5:4580:A:H61	1.59	0.48
17:LO:51:LYS:HE3	17:LO:144:GLU:HB3	1.95	0.48
46:S2:1672:G:H2'	46:S2:1673:U:H6	1.78	0.48
50:SB:227:LYS:O	50:SB:227:LYS:HG3	2.12	0.48
56:SH:19:PHE:CD1	56:SH:19:PHE:O	2.66	0.48
79:Sg:259:TRP:CE3	79:Sg:259:TRP:HA	2.48	0.48
80:LB:45:ALA:HB3	80:LB:183:ILE:HG23	1.95	0.48
2:L5:673:C:H2'	45:Lr:67:ARG:HH21	1.79	0.48
2:L5:3604:A:H62	2:L5:3715:C:H42	1.61	0.48
5:LA:188:LYS:HZ2	5:LA:192:LYS:HE3	1.79	0.48
15:LM:123:ILE:O	15:LM:127:VAL:HG23	2.14	0.48
41:Lm:126:LYS:N	41:Lm:126:LYS:HD2	2.27	0.48
46:S2:12:U:H2'	46:S2:13:C:C6	2.48	0.48
56:SH:75:ILE:O	56:SH:79:LEU:HD12	2.13	0.48
61:SN:18:TYR:HE1	70:SW:55:ASP:HA	1.78	0.48
67:ST:64:LEU:HB3	67:ST:123:LEU:HD11	1.95	0.48
2:L5:2168:C:H2'	2:L5:2169:A:C8	2.49	0.48
2:L5:3384:A:H2'	2:L5:3385:A:H8	1.76	0.48
2:L5:4052:U:C2	2:L5:4053:G:C8	3.02	0.48
2:L5:4341:C:H2'	2:L5:4342:U:C6	2.48	0.48
28:LZ:89:ILE:HG22	28:LZ:121:ARG:CZ	2.44	0.48
46:S2:563:U:H2'	46:S2:564:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SB:34:LYS:HE2	50:SB:43:ASN:OD1	2.14	0.48
77:Sd:53:ILE:C	77:Sd:53:ILE:HD12	2.38	0.48
80:LB:79:VAL:HB	80:LB:331:ILE:HG22	1.95	0.48
2:L5:2170:U:H2'	2:L5:2171:G:H8	1.78	0.48
16:LN:107:GLY:HA3	16:LN:160:GLU:OE2	2.13	0.48
26:LX:62:ARG:HG3	36:Lh:81:LEU:HD23	1.96	0.48
55:SG:138:ALA:O	55:SG:142:ARG:HG3	2.14	0.48
57:SI:8:TRP:HA	57:SI:18:ARG:HH11	1.78	0.48
2:L5:473:C:H2'	2:L5:474:G:H8	1.79	0.48
2:L5:1391:G:N2	44:Lp:17:ARG:HD2	2.29	0.48
4:L8:153:C:H2'	4:L8:154:G:H8	1.78	0.48
7:LD:219:TYR:CE2	7:LD:227:ILE:HD11	2.49	0.48
61:SN:4:MET:HE3	61:SN:124:ARG:NH1	2.28	0.48
70:SW:111:MET:HE2	70:SW:111:MET:HB3	1.76	0.48
80:LB:77:THR:HG21	80:LB:337:VAL:HG22	1.96	0.48
2:L5:1326:G:H2'	2:L5:1327:U:H6	1.79	0.48
2:L5:3518:A:H2'	2:L5:3519:A:H8	1.78	0.48
2:L5:4113:U:H2'	2:L5:4114:C:C6	2.49	0.48
2:L5:4423:G:H2'	2:L5:4424:G:C8	2.49	0.48
14:LL:8:MET:HB2	19:LQ:166:TYR:HB3	1.96	0.48
52:SD:162:ASP:N	52:SD:163:PRO:HD2	2.29	0.48
53:SE:44:LEU:HD23	53:SE:65:CYS:SG	2.53	0.48
53:SE:71:LYS:HB3	53:SE:91:SER:O	2.12	0.48
72:SY:25:ILE:HD12	72:SY:25:ILE:O	2.14	0.48
77:Sd:7:TYR:C	77:Sd:8:TRP:HD1	2.21	0.48
79:Sg:31:ILE:HG13	79:Sg:31:ILE:O	2.12	0.48
79:Sg:99:ARG:HG2	79:Sg:135:LEU:O	2.13	0.48
2:L5:1333:C:H5	29:La:25:HIS:HD1	1.62	0.48
2:L5:1895:G:C2	2:L5:1896:G:C8	3.01	0.48
2:L5:3512:C:H2'	2:L5:3513:A:H8	1.79	0.48
2:L5:4705:C:H2'	2:L5:4706:A:H8	1.79	0.48
5:LA:30:ARG:NH1	5:LA:41:ILE:HG21	2.29	0.48
5:LA:70:LYS:HD3	5:LA:72:ARG:HE	1.79	0.48
5:LA:115:CYS:O	5:LA:164:ALA:HA	2.14	0.48
22:LT:157:GLU:HA	22:LT:157:GLU:OE2	2.13	0.48
41:Lm:79:GLU:OE1	41:Lm:80:PRO:HD2	2.14	0.48
46:S2:17:C:H2'	46:S2:18:C:C6	2.49	0.48
52:SD:50:ILE:HD11	52:SD:86:LEU:HD12	1.96	0.48
25:LW:43:LYS:HE2	25:LW:43:LYS:HB2	1.70	0.48
32:Ld:46:LEU:HD23	32:Ld:49:ILE:HD12	1.96	0.48
46:S2:1640:G:H21	48:S7:43:G:H4'	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SN:25:TRP:CD1	75:Sb:82:LYS:HD3	2.49	0.48
62:SO:132:VAL:HG12	62:SO:132:VAL:O	2.13	0.48
79:Sg:25:PRO:HA	79:Sg:293:ALA:HB2	1.96	0.48
2:L5:952:C:H2'	2:L5:953:C:C6	2.49	0.47
2:L5:3996:U:H2'	2:L5:3997:U:H6	1.79	0.47
8:LE:292:HIS:CD2	34:Lf:38:GLU:HG2	2.49	0.47
9:LF:168:ASN:O	9:LF:172:VAL:HG23	2.14	0.47
27:LY:73:VAL:HG13	27:LY:80:ILE:HG22	1.96	0.47
40:Ll:24:PRO:HG2	40:Ll:27:ILE:HD12	1.96	0.47
46:S2:1275:G:H5''	59:SK:1:MET:HG3	1.95	0.47
55:SG:194:LEU:HA	55:SG:197:GLN:CD	2.39	0.47
60:SL:88:ILE:HG13	60:SL:109:MET:HG2	1.96	0.47
70:SW:8:ALA:HA	70:SW:74:VAL:HG11	1.96	0.47
79:Sg:106:LYS:HB3	79:Sg:125:ARG:HB2	1.96	0.47
79:Sg:256:ILE:HD12	79:Sg:256:ILE:O	2.14	0.47
2:L5:3892:A:H2'	2:L5:3893:G:C8	2.49	0.47
6:LC:183:VAL:O	6:LC:187:GLN:HG2	2.14	0.47
8:LE:123:TYR:HD2	45:Lr:115:SER:HB3	1.78	0.47
11:LH:128:MET:HE1	11:LH:161:ILE:HD11	1.95	0.47
25:LW:6:CYS:HB3	25:LW:10:GLY:H	1.77	0.47
46:S2:1469:C:H2'	46:S2:1470:A:H8	1.78	0.47
51:SC:130:ILE:C	51:SC:130:ILE:HD12	2.39	0.47
54:SF:187:SER:HB2	54:SF:190:ILE:HG12	1.96	0.47
56:SH:31:GLU:C	56:SH:32:MET:HE3	2.39	0.47
58:SJ:118:GLY:O	58:SJ:119:LEU:HD23	2.14	0.47
59:SK:35:LEU:HD12	59:SK:40:VAL:HB	1.97	0.47
2:L5:2274:A:H5'	35:Lg:62:LYS:HD3	1.96	0.47
46:S2:601:G:H2'	46:S2:602:G:C8	2.49	0.47
46:S2:1448:G:H2'	46:S2:1449:A:C8	2.49	0.47
54:SF:142:SER:HB2	76:Sc:50:VAL:HG13	1.96	0.47
54:SF:195:GLU:HA	54:SF:195:GLU:OE1	2.13	0.47
57:SI:154:LYS:HE2	57:SI:154:LYS:N	2.30	0.47
2:L5:1660:C:H2'	2:L5:1661:A:C8	2.48	0.47
2:L5:4415:G:H2'	2:L5:4416:A:H8	1.79	0.47
8:LE:220:LEU:HD21	8:LE:257:ASP:OD1	2.14	0.47
11:LH:172:ILE:HD12	41:Lm:90:ASN:HB3	1.96	0.47
13:LJ:136:ARG:HB2	13:LJ:139:PHE:CE1	2.49	0.47
24:LV:65:VAL:HG21	24:LV:72:LEU:HD12	1.96	0.47
41:Lm:93:LYS:HD3	41:Lm:102:ARG:HG2	1.96	0.47
46:S2:225:C:H2'	46:S2:226:A:H8	1.79	0.47
53:SE:195:ILE:HD13	53:SE:210:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SL:13:GLN:OE1	60:SL:36:TYR:HB3	2.14	0.47
62:SO:100:THR:HG23	62:SO:104:ARG:HG3	1.95	0.47
79:Sg:107:ASP:HB2	79:Sg:125:ARG:HH11	1.79	0.47
2:L5:2224:U:H4'	2:L5:2225:U:H5'	1.97	0.47
2:L5:3429:U:H2'	2:L5:3433:G:O6	2.14	0.47
2:L5:3913:U:H2'	2:L5:3914:C:H6	1.80	0.47
18:LP:41:ILE:HD13	18:LP:150:LEU:HD21	1.96	0.47
20:LR:123:LEU:O	20:LR:127:VAL:HG23	2.14	0.47
31:Lc:19:GLN:O	31:Lc:23:LYS:HG2	2.14	0.47
46:S2:65:C:C6	55:SG:174:PRO:HB3	2.49	0.47
46:S2:836:C:N4	72:SY:8:ARG:HD2	2.30	0.47
51:SC:183:LYS:HD2	70:SW:95:PRO:HA	1.95	0.47
56:SH:77:VAL:HG22	56:SH:135:PHE:CE2	2.50	0.47
57:SI:100:CYS:O	57:SI:175:ILE:HG22	2.15	0.47
2:L5:172:C:H4'	2:L5:173:C:C6	2.50	0.47
17:LO:166:MET:HA	17:LO:166:MET:HE3	1.96	0.47
49:SA:187:GLY:HA2	69:SV:45:ARG:CZ	2.45	0.47
54:SF:30:ILE:HG12	54:SF:113:VAL:HG21	1.96	0.47
56:SH:13:GLY:H	56:SH:15:LYS:HZ3	1.63	0.47
73:SZ:69:THR:HG22	73:SZ:72:VAL:HG13	1.95	0.47
2:L5:260:G:C2	2:L5:261:G:C8	3.03	0.47
2:L5:418:A:H2'	2:L5:419:A:H8	1.78	0.47
2:L5:659:C:H2'	2:L5:660:G:H8	1.78	0.47
2:L5:1757:U:H2'	2:L5:1758:G:H8	1.79	0.47
2:L5:3939:C:H2'	2:L5:3940:G:C8	2.50	0.47
4:L8:83:C:H1'	27:LY:113:LYS:HE3	1.96	0.47
4:L8:130:C:H2'	4:L8:131:G:H8	1.80	0.47
15:LM:49:ALA:HB2	21:LS:100:LEU:HD11	1.97	0.47
15:LM:126:GLU:OE1	15:LM:126:GLU:C	2.58	0.47
46:S2:533:C:N4	46:S2:551:C:H42	2.13	0.47
46:S2:678:G:H21	46:S2:1029:A:H62	1.63	0.47
46:S2:1513:C:H2'	46:S2:1514:C:C6	2.50	0.47
47:S6:64:U:H2'	47:S6:65:C:C6	2.49	0.47
50:SB:82:ARG:NH2	50:SB:191:ASP:HB2	2.29	0.47
53:SE:9:LEU:HB2	53:SE:30:ARG:HD3	1.97	0.47
80:LB:393:LYS:HA	80:LB:396:ARG:NH1	2.30	0.47
2:L5:1160:G:H2'	2:L5:1161:C:C6	2.50	0.47
2:L5:1696:C:H1'	2:L5:1740:C:O2	2.14	0.47
23:LU:30:GLU:HG3	23:LU:31:ASP:N	2.28	0.47
26:LX:90:ILE:HG22	26:LX:147:LEU:HD22	1.95	0.47
41:Lm:118:THR:HG23	41:Lm:120:ASN:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Ln:14:LYS:O	42:Ln:18:ARG:HG3	2.14	0.47
51:SC:263:LYS:HE3	51:SC:267:GLN:HG2	1.97	0.47
71:SX:128:VAL:HG11	71:SX:133:LEU:HD21	1.95	0.47
80:LB:107:ALA:HB2	80:LB:201:LEU:HD22	1.96	0.47
2:L5:1388:G:H4'	2:L5:1389:A:OP1	2.13	0.47
11:LH:50:LYS:HD3	11:LH:50:LYS:H	1.79	0.47
40:Ll:6:THR:HB	40:Ll:9:ILE:HG12	1.96	0.47
45:Lr:33:LYS:HD3	45:Lr:35:ARG:HH21	1.78	0.47
46:S2:930:G:H2'	46:S2:931:C:O4'	2.15	0.47
46:S2:1411:C:H2'	46:S2:1412:G:H8	1.80	0.47
46:S2:1607:G:N2	46:S2:1633:G:H1'	2.30	0.47
59:SK:32:HIS:CE1	59:SK:34:GLU:HB3	2.49	0.47
60:SL:128:VAL:CG1	60:SL:140:PHE:HB3	2.45	0.47
65:SR:51:ALA:O	65:SR:55:THR:HG22	2.14	0.47
66:SS:10:GLN:NE2	66:SS:57:GLY:HA2	2.30	0.47
79:Sg:207:CYS:O	79:Sg:218:LEU:HA	2.15	0.47
2:L5:2313:G:C2	2:L5:2314:G:N7	2.83	0.47
2:L5:2513:G:O2'	2:L5:2514:G:H5'	2.15	0.47
2:L5:4613:U:H4'	2:L5:4614:A:H5'	1.97	0.47
11:LH:127:ARG:HG2	11:LH:127:ARG:HH11	1.80	0.47
40:Ll:7:PHE:CE2	40:Ll:11:ARG:HD2	2.50	0.47
43:Lo:4:VAL:HG11	43:Lo:68:LEU:HD21	1.97	0.47
46:S2:455:U:H2'	46:S2:456:A:C8	2.49	0.47
46:S2:1224:A:O2'	46:S2:1652:A:H4'	2.15	0.47
46:S2:1408:U:H2'	46:S2:1409:U:H6	1.80	0.47
55:SG:31:ARG:HD3	55:SG:68:LEU:HD11	1.97	0.47
55:SG:159:ARG:HE	55:SG:171:THR:HB	1.80	0.47
56:SH:51:ILE:HD11	56:SH:176:VAL:HG22	1.97	0.47
72:SY:86:GLU:HG2	72:SY:91:LEU:HG	1.97	0.47
2:L5:218:A:H2'	2:L5:219:G:C8	2.50	0.46
2:L5:807:C:H2'	2:L5:808:G:C8	2.49	0.46
2:L5:850:G:H4'	34:Lf:75:THR:HG22	1.97	0.46
2:L5:3885:U:H4'	2:L5:3886:A:O4'	2.15	0.46
25:LW:53:VAL:O	25:LW:57:ARG:HG3	2.14	0.46
31:Lc:99:PRO:HG3	31:Lc:104:ILE:HD11	1.97	0.46
44:Lp:23:ARG:HA	44:Lp:26:VAL:HG12	1.97	0.46
46:S2:28:U:H2'	46:S2:29:G:H8	1.80	0.46
46:S2:120:U:H1'	53:SE:33:THR:O	2.15	0.46
46:S2:564:G:H1	46:S2:593:C:H5	1.63	0.46
46:S2:1220:C:H5''	47:S6:34:C:H5'	1.97	0.46
2:L5:858:A:H8	8:LE:134:LEU:HD12	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1017:A:H2'	2:L5:1018:G:H8	1.80	0.46
2:L5:3276:G:H4'	20:LR:79:GLY:O	2.15	0.46
2:L5:3527:C:H2'	2:L5:3528:A:H8	1.80	0.46
3:L7:6:C:H4'	7:LD:52:ILE:HG21	1.97	0.46
23:LU:65:ARG:HG3	23:LU:65:ARG:NH1	2.30	0.46
27:LY:10:ASP:HB2	27:LY:13:LYS:HB2	1.97	0.46
80:LB:305:THR:HG23	80:LB:307:TYR:H	1.80	0.46
2:L5:305:A:H2'	2:L5:306:A:C8	2.50	0.46
2:L5:3530:G:H2'	2:L5:3531:G:C8	2.50	0.46
2:L5:4527:U:C4	15:LM:113:MET:HE2	2.51	0.46
3:L7:112:U:H2'	3:L7:113:G:H8	1.78	0.46
5:LA:13:GLY:O	5:LA:17:ARG:HG3	2.16	0.46
7:LD:111:ASN:ND2	7:LD:252:VAL:HG22	2.29	0.46
23:LU:20:LYS:NZ	23:LU:71:THR:HB	2.30	0.46
24:LV:75:LYS:HB3	24:LV:75:LYS:HE2	1.78	0.46
27:LY:41:LYS:HD3	27:LY:42:TYR:CZ	2.51	0.46
42:Ln:9:ARG:HA	42:Ln:12:ARG:HD2	1.97	0.46
46:S2:49:C:H2'	46:S2:473:C:H41	1.79	0.46
46:S2:456:A:H2'	46:S2:457:C:C6	2.50	0.46
49:SA:14:ASP:HA	49:SA:17:LYS:HE2	1.96	0.46
49:SA:147:LEU:HD21	49:SA:174:MET:HB3	1.96	0.46
50:SB:30:TRP:CE2	62:SO:19:PRO:HG3	2.50	0.46
51:SC:133:TYR:CD1	51:SC:216:MET:HA	2.51	0.46
52:SD:142:LEU:HD12	52:SD:148:LYS:HG3	1.97	0.46
56:SH:134:VAL:HG21	56:SH:158:LEU:HD22	1.97	0.46
70:SW:106:THR:HG21	70:SW:121:THR:HG23	1.98	0.46
2:L5:3264:U:H2'	2:L5:3265:A:C8	2.50	0.46
2:L5:3505:U:H2'	2:L5:3506:A:H8	1.80	0.46
2:L5:4295:U:H2'	2:L5:4296:G:H8	1.79	0.46
5:LA:171:GLY:O	44:Lp:68:ALA:HB2	2.16	0.46
6:LC:84:THR:HG23	6:LC:86:ARG:H	1.80	0.46
46:S2:145:G:H2'	46:S2:146:G:C8	2.51	0.46
46:S2:943:G:H2'	46:S2:944:U:C6	2.51	0.46
50:SB:33:VAL:HG13	50:SB:44:ILE:HB	1.97	0.46
52:SD:59:LEU:HD23	52:SD:66:ILE:HB	1.96	0.46
59:SK:16:PHE:CZ	59:SK:80:ARG:HD2	2.46	0.46
2:L5:1895:G:N2	2:L5:1896:G:N3	2.63	0.46
2:L5:3517:A:OP1	18:LP:140:MET:HB2	2.16	0.46
5:LA:112:ILE:HG23	5:LA:133:TYR:HB2	1.97	0.46
10:LG:139:GLY:O	10:LG:143:VAL:HG23	2.15	0.46
19:LQ:50:ARG:HA	19:LQ:53:MET:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LU:23:LEU:HD23	23:LU:110:TYR:HB2	1.97	0.46
25:LW:1:MET:HE3	25:LW:1:MET:HB2	1.76	0.46
46:S2:503:C:C6	53:SE:66:MET:HE1	2.50	0.46
46:S2:617:A:N3	78:Se:86:VAL:HG21	2.30	0.46
56:SH:133:LEU:HD21	56:SH:173:PHE:CD1	2.51	0.46
79:Sg:188:HIS:C	79:Sg:189:ILE:HD13	2.40	0.46
2:L5:204:U:H2'	2:L5:205:C:C6	2.51	0.46
28:LZ:100:VAL:HG22	28:LZ:106:LEU:HB3	1.97	0.46
46:S2:1190:A:H2'	46:S2:1191:A:H8	1.81	0.46
50:SB:181:LEU:O	50:SB:185:VAL:HG23	2.16	0.46
56:SH:33:ASN:HB2	56:SH:36:LEU:HD12	1.98	0.46
2:L5:807:C:H2'	2:L5:808:G:H8	1.80	0.46
2:L5:933:C:H2'	2:L5:934:G:C8	2.51	0.46
2:L5:1507:U:H5'	19:LQ:143:ARG:HH12	1.81	0.46
44:Lp:61:MET:HE3	44:Lp:61:MET:HB3	1.82	0.46
46:S2:162:C:H5''	55:SG:87:ARG:HH22	1.79	0.46
46:S2:906:C:H2'	46:S2:907:U:C6	2.51	0.46
46:S2:1145:A:H2'	46:S2:1146:A:C8	2.51	0.46
48:S7:25:U:C2	48:S7:26:G:C8	3.03	0.46
64:SQ:8:GLN:HE21	64:SQ:99:TYR:HB3	1.81	0.46
2:L5:175:C:H2'	2:L5:176:G:C8	2.50	0.46
2:L5:181:A:H8	2:L5:257:G:N1	2.14	0.46
2:L5:1004:G:N2	2:L5:1023:C:H42	2.13	0.46
2:L5:2131:A:H2'	2:L5:2132:A:H8	1.80	0.46
2:L5:2285:G:H4'	2:L5:2537:A:H4'	1.98	0.46
2:L5:2312:G:H22	28:LZ:112:ARG:HH21	1.63	0.46
2:L5:4177:G:N3	80:LB:252:ALA:HB1	2.31	0.46
30:Lb:94:LEU:HA	30:Lb:97:ILE:HD12	1.97	0.46
32:Ld:44:ARG:O	32:Ld:48:GLU:HG2	2.15	0.46
32:Ld:68:LEU:O	32:Ld:72:VAL:HG23	2.16	0.46
34:Lf:39:THR:HG21	34:Lf:77:ALA:HB2	1.97	0.46
68:SU:49:LYS:HE3	68:SU:92:HIS:CD2	2.50	0.46
2:L5:1163:U:H2'	2:L5:1164:G:H8	1.80	0.46
2:L5:3383:A:H2'	2:L5:3384:A:C8	2.51	0.46
2:L5:4703:G:H2'	2:L5:4704:A:H8	1.81	0.46
6:LC:287:THR:HG21	45:Lr:5:LEU:HB2	1.98	0.46
7:LD:113:PHE:HE2	7:LD:142:PHE:HE2	1.63	0.46
9:LF:130:VAL:HG13	9:LF:154:MET:HE3	1.97	0.46
15:LM:97:ALA:HB2	17:LO:203:VAL:HB	1.96	0.46
49:SA:15:VAL:O	49:SA:19:LEU:HD23	2.16	0.46
54:SF:106:GLU:OE1	54:SF:106:GLU:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SG:201:LYS:HA	55:SG:204:GLU:HG3	1.98	0.46
57:SI:3:ILE:H	57:SI:3:ILE:HD12	1.81	0.46
79:Sg:21:ILE:HG23	79:Sg:33:SER:OG	2.15	0.46
79:Sg:249:CYS:SG	79:Sg:289:LEU:HD13	2.56	0.46
2:L5:166:C:H2'	2:L5:167:C:O4'	2.16	0.46
2:L5:421:C:H2'	2:L5:422:G:H8	1.81	0.46
2:L5:3904:A:C2	13:LJ:127:GLY:HA3	2.51	0.46
3:L7:58:A:H2'	3:L7:59:G:H8	1.81	0.46
5:LA:83:HIS:HB3	44:Lp:64:VAL:HG22	1.97	0.46
6:LC:180:ILE:O	6:LC:183:VAL:HG22	2.16	0.46
6:LC:335:MET:HB3	6:LC:335:MET:HE2	1.84	0.46
12:LI:129:VAL:HG23	12:LI:133:GLN:HG2	1.98	0.46
16:LN:120:TRP:HE1	16:LN:123:GLU:HB3	1.81	0.46
39:Lk:56:LEU:HD12	39:Lk:59:SER:HB3	1.97	0.46
46:S2:519:G:H2'	46:S2:520:A:H8	1.81	0.46
46:S2:1204:G:H2'	46:S2:1205:A:H8	1.81	0.46
46:S2:1576:G:H2'	46:S2:1577:G:H8	1.81	0.46
49:SA:51:LEU:HD13	49:SA:51:LEU:HA	1.78	0.46
51:SC:80:GLU:H	51:SC:80:GLU:CD	2.24	0.46
76:Sc:9:ILE:HD12	76:Sc:59:LEU:HD23	1.98	0.46
79:Sg:79:LEU:HD12	79:Sg:89:LEU:HB2	1.98	0.46
2:L5:132:G:H4'	2:L5:177:G:H4'	1.98	0.45
2:L5:667:G:H2'	2:L5:668:G:C8	2.51	0.45
2:L5:1033:G:H2'	2:L5:1034:G:H8	1.80	0.45
2:L5:2394:G:H2'	2:L5:2395:A:H8	1.81	0.45
2:L5:4618:C:C2	2:L5:4619:A:C8	3.04	0.45
31:Lc:22:MET:HA	31:Lc:27:TYR:CE2	2.50	0.45
46:S2:1522:C:N4	66:SS:137:LYS:HD3	2.31	0.45
49:SA:85:ARG:HG2	49:SA:204:TYR:CA	2.45	0.45
52:SD:131:ALA:HB1	52:SD:188:ILE:HD11	1.98	0.45
56:SH:135:PHE:CG	56:SH:136:PRO:HD3	2.51	0.45
2:L5:99:A:H5''	16:LN:184:ILE:HD12	1.97	0.45
2:L5:1317:A:H4'	2:L5:1318:G:H5'	1.98	0.45
2:L5:2598:A:O2'	2:L5:4284:G:H4'	2.17	0.45
2:L5:3997:U:H2'	2:L5:3998:C:C6	2.51	0.45
11:LH:115:ARG:HD3	11:LH:123:ILE:HG12	1.98	0.45
20:LR:11:ALA:HA	20:LR:14:VAL:HG22	1.99	0.45
20:LR:23:TRP:HB3	20:LR:51:ILE:HD12	1.98	0.45
20:LR:173:ARG:CG	20:LR:176:ARG:HG2	2.45	0.45
21:LS:69:GLU:HG3	21:LS:101:THR:HB	1.97	0.45
39:Lk:12:LEU:HD21	39:Lk:56:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:501:A:H3'	46:S2:502:C:H6	1.81	0.45
70:SW:14:ILE:HG23	70:SW:65:LEU:HD21	1.98	0.45
75:Sb:37:CYS:HB2	75:Sb:40:CYS:HB2	1.41	0.45
76:Sc:13:ARG:HG2	76:Sc:13:ARG:NH1	2.27	0.45
80:LB:216:MET:HE2	80:LB:283:LYS:HD2	1.97	0.45
2:L5:947:C:H2'	2:L5:948:G:H8	1.81	0.45
2:L5:3347:U:H2'	2:L5:3348:G:O4'	2.17	0.45
3:L7:110:G:H2'	3:L7:111:C:C6	2.51	0.45
6:LC:33:ARG:O	6:LC:37:VAL:HG23	2.16	0.45
9:LF:170:LYS:O	9:LF:174:GLU:HG3	2.16	0.45
37:Li:43:MET:HG3	37:Li:43:MET:O	2.17	0.45
46:S2:29:G:H2'	46:S2:30:C:C6	2.51	0.45
46:S2:306:U:O2	46:S2:306:U:C3'	2.64	0.45
46:S2:1006:G:H2'	46:S2:1007:C:H6	1.82	0.45
46:S2:1385:C:C2	46:S2:1386:G:C8	3.04	0.45
55:SG:16:ILE:HD12	55:SG:16:ILE:O	2.16	0.45
2:L5:74:G:H5'	14:LL:59:VAL:HG13	1.98	0.45
2:L5:1755:G:O2'	21:LS:93:MET:HG2	2.17	0.45
20:LR:28:GLU:OE1	20:LR:28:GLU:N	2.50	0.45
27:LY:74:TYR:HB3	27:LY:79:VAL:HG23	1.98	0.45
46:S2:518:C:H2'	46:S2:519:G:O4'	2.17	0.45
46:S2:1513:C:H2'	46:S2:1514:C:H6	1.81	0.45
47:S6:28:U:H2'	47:S6:29:G:C8	2.52	0.45
51:SC:187:ARG:HE	51:SC:192:LEU:HD12	1.81	0.45
57:SI:164:GLU:OE1	57:SI:164:GLU:C	2.59	0.45
63:SP:70:MET:HE2	63:SP:70:MET:N	2.30	0.45
2:L5:204:U:H2'	2:L5:205:C:H6	1.82	0.45
2:L5:947:C:H2'	2:L5:948:G:C8	2.51	0.45
2:L5:2638:G:H2'	2:L5:2639:A:H8	1.80	0.45
2:L5:3292:A:C8	2:L5:3349:A:C8	3.04	0.45
2:L5:3313:A:H2'	2:L5:3314:U:H6	1.82	0.45
5:LA:30:ARG:HH12	5:LA:41:ILE:HD13	1.80	0.45
19:LQ:15:ARG:HD2	19:LQ:52:PHE:HB3	1.99	0.45
19:LQ:63:LEU:HB2	19:LQ:88:ASP:HA	1.99	0.45
27:LY:26:ARG:O	27:LY:30:MET:HG3	2.17	0.45
27:LY:41:LYS:HD3	27:LY:42:TYR:CE2	2.51	0.45
27:LY:130:LYS:HA	27:LY:130:LYS:HD3	1.67	0.45
31:Lc:56:ARG:O	31:Lc:60:ILE:HG12	2.16	0.45
46:S2:1351:U:H3	46:S2:1380:A:H61	1.64	0.45
50:SB:138:PHE:CD2	50:SB:214:LYS:HB3	2.51	0.45
57:SI:89:GLU:O	57:SI:92:ARG:HG2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SR:75:GLU:OE1	65:SR:75:GLU:HA	2.17	0.45
70:SW:114:GLU:O	70:SW:118:ARG:HG3	2.15	0.45
2:L5:67:C:H41	2:L5:325:C:H5'	1.80	0.45
4:L8:141:C:H2'	4:L8:142:U:C6	2.52	0.45
24:LV:87:SER:HA	24:LV:97:TYR:HB3	1.99	0.45
34:Lf:7:CYS:SG	34:Lf:105:LEU:HD21	2.56	0.45
53:SE:112:HIS:C	53:SE:112:HIS:ND1	2.64	0.45
58:SJ:94:LEU:H	58:SJ:96:TYR:HE2	1.64	0.45
62:SO:51:GLU:OE1	62:SO:51:GLU:N	2.50	0.45
65:SR:57:LEU:O	65:SR:61:ILE:HG13	2.16	0.45
75:Sb:37:CYS:HB3	75:Sb:40:CYS:H	1.81	0.45
2:L5:176:G:N2	2:L5:260:G:H22	2.12	0.45
2:L5:1762:U:H4'	2:L5:1764:G:H5''	1.98	0.45
2:L5:4282:U:C2	2:L5:4283:G:C8	3.05	0.45
2:L5:4522:A:OP2	21:LS:165:PRO:HG3	2.17	0.45
3:L7:15:C:H2'	3:L7:16:A:H8	1.82	0.45
6:LC:183:VAL:HG12	6:LC:204:ARG:HB3	1.97	0.45
15:LM:119:ARG:O	15:LM:123:ILE:HG12	2.17	0.45
32:Ld:47:LYS:O	32:Ld:51:LYS:HG3	2.17	0.45
46:S2:964:A:H5''	62:SO:66:ARG:HH22	1.82	0.45
46:S2:1175:U:H2'	46:S2:1176:G:H8	1.81	0.45
46:S2:1713:A:H2'	46:S2:1714:C:C6	2.52	0.45
50:SB:136:ARG:HB2	50:SB:218:LEU:HD21	1.98	0.45
54:SF:87:LEU:HD11	64:SQ:47:LEU:HG	1.98	0.45
57:SI:70:GLU:N	57:SI:70:GLU:OE2	2.49	0.45
58:SJ:142:VAL:HG11	58:SJ:147:PHE:CG	2.52	0.45
60:SL:40:ILE:HG21	60:SL:68:ILE:HB	1.98	0.45
66:SS:10:GLN:CG	66:SS:57:GLY:HA2	2.47	0.45
74:Sa:89:ARG:HG3	74:Sa:92:ARG:HH12	1.81	0.45
2:L5:684:C:H2'	2:L5:685:G:C8	2.51	0.45
2:L5:1497:U:H2'	2:L5:1498:A:H8	1.82	0.45
2:L5:3341:G:H2'	2:L5:3342:C:C6	2.52	0.45
2:L5:3904:A:N1	13:LJ:127:GLY:HA3	2.31	0.45
2:L5:3997:U:H2'	2:L5:3998:C:H6	1.80	0.45
5:LA:48:ILE:HD13	44:Lp:65:ALA:HB2	1.99	0.45
8:LE:184:THR:OG1	8:LE:194:LEU:HD22	2.17	0.45
11:LH:69:THR:O	11:LH:73:ILE:HG13	2.17	0.45
14:LL:125:ILE:HG12	14:LL:142:GLU:HG2	1.99	0.45
21:LS:70:LYS:HD3	21:LS:70:LYS:HA	1.63	0.45
46:S2:836:C:H42	72:SY:8:ARG:HD2	1.82	0.45
56:SH:63:PHE:HA	56:SH:95:ILE:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1447:G:H5'	2:L5:1448:A:OP1	2.17	0.45
2:L5:1561:G:H2'	2:L5:1562:G:O4'	2.17	0.45
2:L5:3939:C:H2'	2:L5:3940:G:H8	1.82	0.45
2:L5:3996:U:H2'	2:L5:3997:U:C6	2.52	0.45
2:L5:4590:C:H5''	8:LE:163:GLY:HA2	1.98	0.45
10:LG:29:ASN:OD1	10:LG:31:LEU:HD12	2.15	0.45
18:LP:132:ALA:HB3	18:LP:135:ARG:NH2	2.31	0.45
46:S2:1576:G:H2'	46:S2:1577:G:C8	2.52	0.45
46:S2:1641:A:H1'	48:S7:42:A:H1'	1.99	0.45
50:SB:229:MET:HA	50:SB:229:MET:CE	2.43	0.45
51:SC:133:TYR:HD1	51:SC:216:MET:HA	1.82	0.45
71:SX:73:GLN:HB2	71:SX:80:LYS:HG2	1.99	0.45
79:Sg:13:GLY:HA3	79:Sg:43:TRP:CH2	2.51	0.45
79:Sg:230:LEU:HD21	79:Sg:259:TRP:NE1	2.32	0.45
80:LB:302:ASN:HB3	80:LB:313:SER:HA	1.98	0.45
2:L5:189:G:H22	2:L5:252:G:N2	2.15	0.45
2:L5:940:C:H2'	2:L5:941:C:C6	2.52	0.45
2:L5:1528:U:H2'	2:L5:1529:U:H6	1.81	0.45
2:L5:2277:C:H2'	2:L5:2278:G:H8	1.82	0.45
4:L8:67:U:H2'	4:L8:68:G:C8	2.52	0.45
17:LO:55:LEU:HD23	17:LO:58:LEU:HD12	1.98	0.45
38:Lj:34:CYS:HB3	38:Lj:38:GLY:H	1.82	0.45
46:S2:523:A:H5''	58:SJ:145:PRO:HD2	1.99	0.45
46:S2:902:G:H2'	46:S2:903:G:C8	2.51	0.45
46:S2:1228:G:C2	46:S2:1229:A:C8	3.05	0.45
46:S2:1680:A:H2'	54:SF:60:ARG:HD2	1.99	0.45
54:SF:25:THR:HG21	54:SF:46:ALA:HB2	1.99	0.45
2:L5:674:G:H2'	6:LC:291:ARG:HH11	1.82	0.44
2:L5:1347:A:H5''	2:L5:1451:A:H62	1.83	0.44
2:L5:3339:A:H5''	5:LA:132:ASN:ND2	2.33	0.44
2:L5:3873:A:OP2	22:LT:2:THR:HG21	2.17	0.44
10:LG:87:LEU:HD21	10:LG:182:CYS:HB2	1.99	0.44
11:LH:150:ASP:O	11:LH:154:VAL:HG23	2.17	0.44
29:La:8:THR:HG23	29:La:17:HIS:CE1	2.53	0.44
41:Lm:94:MET:HE2	41:Lm:94:MET:HA	1.99	0.44
46:S2:1103:G:H2'	46:S2:1104:C:C6	2.51	0.44
46:S2:1563:C:H2'	46:S2:1564:G:H8	1.81	0.44
46:S2:1593:C:H2'	46:S2:1594:C:C6	2.52	0.44
48:S7:68:C:H2'	48:S7:69:U:C6	2.53	0.44
52:SD:61:GLU:O	52:SD:62:LYS:HG2	2.18	0.44
52:SD:93:THR:HG21	52:SD:96:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SE:66:MET:SD	53:SE:66:MET:O	2.75	0.44
54:SF:48:TYR:CZ	64:SQ:56:LEU:HD23	2.52	0.44
55:SG:194:LEU:O	55:SG:197:GLN:HG2	2.16	0.44
80:LB:113:GLU:OE1	80:LB:169:ARG:HG3	2.17	0.44
2:L5:656:G:H2'	2:L5:657:A:H8	1.81	0.44
2:L5:1004:G:H22	2:L5:1023:C:H42	1.65	0.44
2:L5:1328:U:H2'	2:L5:1329:A:C8	2.52	0.44
2:L5:1477:C:H2'	2:L5:1478:U:H6	1.83	0.44
2:L5:1547:U:C2	2:L5:1548:G:C8	3.06	0.44
2:L5:2296:C:H2'	2:L5:2297:C:C6	2.52	0.44
7:LD:135:ILE:HG13	7:LD:138:GLN:HB2	1.99	0.44
24:LV:42:VAL:HA	24:LV:61:VAL:HG12	1.99	0.44
46:S2:848:A:H4'	53:SE:106:LYS:HD3	2.00	0.44
46:S2:1652:A:H2'	46:S2:1653:G:H8	1.83	0.44
58:SJ:35:TYR:HD2	58:SJ:106:LEU:HD13	1.81	0.44
68:SU:54:VAL:HB	68:SU:88:LEU:HB2	1.99	0.44
80:LB:317:LEU:HD12	80:LB:317:LEU:HA	1.81	0.44
2:L5:1755:G:H2'	2:L5:1756:U:H6	1.81	0.44
4:L8:9:A:H2'	4:L8:10:G:H8	1.83	0.44
13:LJ:33:LEU:HD23	13:LJ:50:PHE:HD1	1.82	0.44
15:LM:7:VAL:HG12	21:LS:152:PHE:O	2.17	0.44
15:LM:62:LEU:HD21	15:LM:82:ILE:HD11	1.98	0.44
44:Lp:75:SER:O	44:Lp:79:VAL:HG23	2.17	0.44
44:Lp:83:ILE:HD13	44:Lp:83:ILE:HA	1.85	0.44
46:S2:650:U:H2'	46:S2:651:A:C8	2.48	0.44
46:S2:1428:C:H5'	46:S2:1429:G:OP1	2.18	0.44
46:S2:1431:C:H2'	46:S2:1432:G:C8	2.52	0.44
46:S2:1561:U:H2'	46:S2:1562:G:H8	1.82	0.44
46:S2:1598:C:H4'	46:S2:1604:G:C6	2.53	0.44
54:SF:40:ALA:HB1	54:SF:45:TYR:CG	2.52	0.44
54:SF:92:ILE:HG23	54:SF:170:ALA:HA	1.98	0.44
58:SJ:71:LEU:HD23	58:SJ:71:LEU:HA	1.84	0.44
58:SJ:136:ARG:HG3	58:SJ:160:SER:HA	1.98	0.44
64:SQ:112:LEU:HD22	64:SQ:119:LEU:HD13	1.98	0.44
79:Sg:252:THR:CG2	79:Sg:257:LYS:HG3	2.48	0.44
80:LB:285:TYR:CE1	80:LB:334:LYS:HB2	2.52	0.44
2:L5:175:C:H2'	2:L5:176:G:H8	1.82	0.44
2:L5:1089:A:H2'	2:L5:1090:G:C8	2.52	0.44
2:L5:1709:U:H2'	2:L5:1710:A:H8	1.82	0.44
2:L5:4216:U:H2'	2:L5:4217:A:H8	1.82	0.44
2:L5:4278:C:O2'	2:L5:4279:A:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:29:G:H5''	14:LL:27:ASN:HB3	1.98	0.44
15:LM:121:ARG:O	15:LM:124:LYS:HG2	2.16	0.44
79:Sg:21:ILE:HG13	79:Sg:288:SER:OG	2.17	0.44
2:L5:477:G:H2'	2:L5:478:G:H8	1.82	0.44
2:L5:1666:U:OP1	12:LI:15:LYS:HG3	2.18	0.44
6:LC:33:ARG:HB3	6:LC:36:ILE:HG13	1.98	0.44
7:LD:55:VAL:HG13	7:LD:60:ILE:HG12	1.99	0.44
46:S2:442:C:H2'	46:S2:443:C:C6	2.52	0.44
46:S2:1409:U:H2'	46:S2:1410:A:C8	2.52	0.44
50:SB:51:ARG:H	50:SB:51:ARG:HG3	1.58	0.44
54:SF:19:LEU:HD23	54:SF:97:PHE:HE2	1.82	0.44
62:SO:56:VAL:HG23	62:SO:77:ALA:HB1	1.99	0.44
80:LB:95:THR:HB	80:LB:98:GLY:O	2.18	0.44
2:L5:423:U:H2'	2:L5:424:U:C6	2.53	0.44
2:L5:1132:U:H2'	2:L5:1133:C:C6	2.53	0.44
2:L5:2271:G:H5''	35:Lg:15:THR:HG21	1.99	0.44
2:L5:3913:U:H2'	2:L5:3914:C:C6	2.53	0.44
2:L5:4183:U:H2'	2:L5:4184:U:H2'	1.98	0.44
5:LA:204:MET:HE3	5:LA:208:GLU:HG2	1.99	0.44
11:LH:50:LYS:H	11:LH:50:LYS:CD	2.30	0.44
13:LJ:52:LYS:HE2	13:LJ:65:ASN:HB3	2.00	0.44
29:La:36:GLY:HA3	29:La:40:HIS:NE2	2.33	0.44
33:Le:85:LEU:HD21	33:Le:115:ALA:HB2	1.98	0.44
46:S2:1423:G:H2'	46:S2:1423:G:N3	2.31	0.44
46:S2:1809:U:H2'	46:S2:1810:A:H8	1.83	0.44
52:SD:131:ALA:CB	52:SD:188:ILE:HD11	2.47	0.44
58:SJ:38:ARG:HG3	78:Se:105:ARG:HB3	1.99	0.44
70:SW:42:MET:HE2	70:SW:42:MET:HB3	1.76	0.44
80:LB:46:PHE:CE1	80:LB:84:MET:HG3	2.51	0.44
2:L5:453:U:H2'	2:L5:454:C:H6	1.83	0.44
2:L5:951:A:H2	2:L5:1034:G:H22	1.66	0.44
2:L5:1511:G:H2'	2:L5:1512:C:C6	2.53	0.44
2:L5:1866:G:H5'	21:LS:5:GLY:HA2	1.99	0.44
2:L5:3396:C:C2	2:L5:3397:G:C8	3.06	0.44
8:LE:50:HIS:CD2	8:LE:51:CYS:H	2.35	0.44
10:LG:175:ARG:HE	10:LG:230:TYR:HB3	1.82	0.44
17:LO:191:LYS:HA	17:LO:191:LYS:HD3	1.67	0.44
33:Le:11:LYS:HB2	33:Le:11:LYS:HE3	1.73	0.44
46:S2:76:U:O2'	46:S2:77:A:H5''	2.18	0.44
46:S2:609:C:H2'	46:S2:610:U:C6	2.53	0.44
46:S2:1011:G:H2'	46:S2:1012:A:C8	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1642:A:O2'	46:S2:1643:U:H5''	2.17	0.44
56:SH:100:ILE:HD13	56:SH:122:LEU:HD12	1.98	0.44
57:SI:113:TYR:CE2	57:SI:121:LEU:HD13	2.52	0.44
2:L5:928:C:H2'	2:L5:929:G:C8	2.53	0.44
2:L5:944:C:H2'	2:L5:945:G:H8	1.83	0.44
2:L5:1717:C:H4'	17:LO:89:PRO:HD3	1.99	0.44
3:L7:74:A:H1'	21:LS:53:LYS:NZ	2.33	0.44
4:L8:110:U:H5''	40:L1:8:ARG:HH12	1.82	0.44
46:S2:687:U:OP1	70:SW:32:LYS:HG3	2.18	0.44
46:S2:1453:A:H5''	65:SR:48:ASN:ND2	2.32	0.44
46:S2:1693:U:H2'	46:S2:1694:G:H8	1.82	0.44
47:S6:63:A:H2'	47:S6:64:U:C6	2.53	0.44
49:SA:51:LEU:HD23	65:SR:105:MET:HE1	1.99	0.44
49:SA:206:ASP:HB3	49:SA:208:GLU:OE1	2.18	0.44
52:SD:194:PRO:HG2	52:SD:199:GLY:HA3	2.00	0.44
2:L5:465:A:H2'	2:L5:466:U:C6	2.53	0.44
2:L5:718:G:H2'	2:L5:719:A:H8	1.83	0.44
2:L5:1558:C:H41	2:L5:1579:A:H2	1.64	0.44
2:L5:1643:G:H1'	9:LF:133:LEU:HD23	1.99	0.44
2:L5:2276:U:H1'	2:L5:2277:C:C6	2.53	0.44
2:L5:3808:C:H2'	2:L5:3809:G:O4'	2.17	0.44
2:L5:4277:A:H5'	80:LB:223:THR:CG2	2.48	0.44
2:L5:4701:U:H3'	2:L5:4702:C:C6	2.53	0.44
7:LD:280:VAL:HG12	7:LD:284:LYS:HE2	2.00	0.44
21:LS:9:GLU:HG2	21:LS:33:PHE:CE1	2.53	0.44
46:S2:949:C:H2'	46:S2:950:G:H8	1.82	0.44
46:S2:1642:A:C8	48:S7:31:G:H5'	2.52	0.44
49:SA:23:THR:HG22	49:SA:170:SER:OG	2.18	0.44
53:SE:175:PHE:HE2	53:SE:198:ARG:HE	1.66	0.44
54:SF:144:LEU:HD12	76:Sc:49:PRO:HG2	1.99	0.44
59:SK:15:LEU:HD22	59:SK:49:MET:SD	2.58	0.44
62:SO:53:ILE:HG23	62:SO:88:LEU:HD23	1.98	0.44
80:LB:229:LYS:HG3	80:LB:272:LYS:HD3	2.00	0.44
2:L5:18:C:H4'	16:LN:138:PHE:CD2	2.53	0.43
2:L5:1418:G:H2'	2:L5:1419:G:C8	2.53	0.43
2:L5:2445:U:C2	2:L5:2446:U:C5	3.06	0.43
2:L5:4216:U:C2	2:L5:4217:A:C8	3.06	0.43
9:LF:172:VAL:O	9:LF:176:ILE:HG13	2.17	0.43
22:LT:93:ILE:HA	22:LT:96:ILE:HG12	1.99	0.43
25:LW:51:TRP:CD1	25:LW:51:TRP:H	2.35	0.43
25:LW:58:LYS:HE3	25:LW:58:LYS:HB2	1.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lh:14:LYS:HE2	36:Lh:61:ILE:HG23	2.00	0.43
46:S2:992:G:C6	46:S2:1135:G:H4'	2.53	0.43
49:SA:42:LYS:HG3	49:SA:46:ILE:O	2.17	0.43
53:SE:36:HIS:CG	53:SE:85:GLY:HA3	2.53	0.43
67:ST:88:ARG:HG3	67:ST:88:ARG:NH1	2.31	0.43
74:Sa:64:LEU:HA	74:Sa:64:LEU:HD23	1.76	0.43
2:L5:439:U:H2'	2:L5:440:G:H8	1.83	0.43
2:L5:1275:C:H2'	2:L5:1276:A:H8	1.82	0.43
2:L5:3841:U:H2'	2:L5:3842:U:C6	2.53	0.43
6:LC:331:TYR:CZ	9:LF:77:LYS:HG3	2.54	0.43
9:LF:186:LYS:HE2	9:LF:186:LYS:HB2	1.61	0.43
23:LU:44:GLN:HA	23:LU:56:LEU:HD11	2.00	0.43
33:Le:16:ARG:NH1	33:Le:54:LEU:HD12	2.33	0.43
38:Lj:2:THR:HB	38:Lj:6:SER:HB3	1.99	0.43
46:S2:51:U:H2'	46:S2:52:G:C8	2.53	0.43
46:S2:805:U:H2'	46:S2:806:U:C6	2.52	0.43
47:S6:31:G:C2	47:S6:32:C:C5	3.06	0.43
51:SC:104:ASP:OD2	51:SC:104:ASP:C	2.61	0.43
51:SC:130:ILE:CD1	51:SC:162:ILE:HD11	2.48	0.43
54:SF:55:ARG:HD3	64:SQ:125:ARG:NH1	2.33	0.43
62:SO:62:VAL:HG11	62:SO:67:ASP:HB2	2.00	0.43
70:SW:86:LEU:HD12	70:SW:86:LEU:HA	1.88	0.43
80:LB:168:MET:HE3	80:LB:168:MET:HB3	1.89	0.43
80:LB:217:ILE:HD11	80:LB:333:LEU:HD21	1.99	0.43
2:L5:324:U:H2'	2:L5:325:C:C6	2.52	0.43
2:L5:424:U:H2'	2:L5:425:A:H8	1.83	0.43
2:L5:460:G:H2'	2:L5:461:G:C8	2.53	0.43
2:L5:677:C:H2'	2:L5:678:G:C8	2.53	0.43
2:L5:881:C:H41	8:LE:78:ARG:NH1	2.17	0.43
2:L5:1372:A:H2'	2:L5:1373:G:H8	1.83	0.43
2:L5:2021:C:H2'	2:L5:2022:G:O4'	2.18	0.43
6:LC:252:TRP:CZ3	6:LC:260:LEU:HD11	2.54	0.43
32:Ld:92:ARG:HG2	32:Ld:94:GLU:HG3	2.00	0.43
42:Ln:2:ARG:HD3	42:Ln:5:TRP:NE1	2.33	0.43
46:S2:431:C:C2	46:S2:432:G:C8	3.06	0.43
46:S2:561:A:H61	46:S2:589:G:H1	1.66	0.43
46:S2:881:G:H8	46:S2:908:G:N1	2.16	0.43
60:SL:56:ILE:O	60:SL:56:ILE:HD12	2.18	0.43
66:SS:55:ARG:HB2	66:SS:58:GLU:OE2	2.17	0.43
2:L5:1600:G:C2	2:L5:1601:G:C8	3.07	0.43
2:L5:3257:G:H2'	2:L5:3258:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LA:80:GLU:HB2	5:LA:170:ALA:HA	2.00	0.43
7:LD:64:ILE:HG12	7:LD:105:LEU:HD21	2.00	0.43
25:LW:47:ARG:HG2	25:LW:58:LYS:HD2	2.00	0.43
39:Lk:7:GLU:OE1	39:Lk:9:LYS:HG2	2.18	0.43
54:SF:123:GLU:HB2	76:Sc:59:LEU:HD12	2.00	0.43
57:SI:153:LYS:C	57:SI:154:LYS:HE2	2.44	0.43
2:L5:1377:A:H2'	2:L5:1378:A:O4'	2.19	0.43
2:L5:3584:U:H2'	2:L5:3585:A:H8	1.84	0.43
2:L5:3998:C:H2'	2:L5:3999:U:H6	1.83	0.43
5:LA:246:LEU:O	5:LA:246:LEU:HG	2.19	0.43
6:LC:221:PHE:HB2	6:LC:229:LEU:HD21	2.01	0.43
9:LF:127:VAL:HG13	9:LF:158:VAL:HG12	2.01	0.43
13:LJ:36:ALA:HB2	13:LJ:126:TYR:CZ	2.53	0.43
15:LM:14:TYR:CE2	15:LM:22:GLY:HA2	2.54	0.43
15:LM:15:ILE:HD12	15:LM:50:MET:SD	2.59	0.43
29:La:76:ASP:OD1	29:La:115:GLY:HA2	2.19	0.43
46:S2:1005:U:H2'	46:S2:1006:G:H8	1.83	0.43
48:S7:56:C:H2'	48:S7:57:G:C8	2.53	0.43
52:SD:193:ASP:N	52:SD:194:PRO:HD2	2.34	0.43
60:SL:69:ARG:HD3	60:SL:69:ARG:N	2.33	0.43
68:SU:113:GLU:C	68:SU:113:GLU:OE2	2.61	0.43
73:SZ:66:LYS:HB2	73:SZ:66:LYS:HE3	1.79	0.43
2:L5:473:C:H2'	2:L5:474:G:C8	2.54	0.43
2:L5:1716:C:H5''	17:LO:25:LYS:HD3	2.00	0.43
9:LF:115:ILE:HD12	9:LF:262:ILE:HD11	1.99	0.43
18:LP:120:ASN:HB2	18:LP:145:HIS:HB2	2.00	0.43
22:LT:137:GLU:HA	22:LT:137:GLU:OE2	2.18	0.43
28:LZ:27:LYS:HA	28:LZ:27:LYS:HD2	1.70	0.43
39:Lk:52:LYS:HE2	39:Lk:52:LYS:HB2	1.93	0.43
46:S2:1793:G:H2'	46:S2:1794:A:H8	1.84	0.43
50:SB:121:ILE:HG12	50:SB:161:VAL:HG13	2.00	0.43
58:SJ:97:ILE:HD12	58:SJ:98:LEU:N	2.34	0.43
65:SR:78:ARG:HH11	65:SR:81:ARG:HG2	1.83	0.43
74:Sa:36:ILE:CD1	74:Sa:73:TYR:HB2	2.48	0.43
75:Sb:24:LEU:HD12	75:Sb:24:LEU:HA	1.86	0.43
2:L5:50:C:C2	2:L5:51:A:C8	3.06	0.43
2:L5:954:G:H2'	2:L5:955:C:C6	2.54	0.43
2:L5:1640:A:H5'	22:LT:129:LYS:HE3	2.00	0.43
2:L5:2315:C:C2	2:L5:2316:G:C8	3.06	0.43
2:L5:3813:C:H2'	2:L5:3814:G:C8	2.53	0.43
20:LR:170:ARG:NH1	20:LR:172:ARG:HH21	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1589:A:H2'	46:S2:1590:A:H8	1.83	0.43
46:S2:1642:A:OP2	48:S7:31:G:H5''	2.19	0.43
52:SD:132:LYS:HD2	52:SD:191:PRO:HA	2.01	0.43
54:SF:173:LEU:O	54:SF:177:LEU:HD23	2.19	0.43
56:SH:18:GLU:C	56:SH:20:GLU:H	2.25	0.43
57:SI:98:LYS:HB2	57:SI:178:ARG:HG2	2.00	0.43
60:SL:79:LYS:HE3	60:SL:79:LYS:HB2	1.91	0.43
67:ST:7:LYS:HE2	67:ST:66:LEU:CD2	2.48	0.43
68:SU:51:LYS:HA	68:SU:51:LYS:HD2	1.79	0.43
72:SY:54:VAL:HB	72:SY:76:TYR:HB2	2.01	0.43
74:Sa:37:LYS:HG2	74:Sa:72:HIS:ND1	2.34	0.43
75:Sb:12:PRO:HG2	75:Sb:13:GLU:OE2	2.19	0.43
79:Sg:254:PRO:HA	79:Sg:285:GLN:HA	2.00	0.43
2:L5:391:U:H1'	18:LP:104:LEU:HD11	2.00	0.43
2:L5:1148:A:H2'	2:L5:1149:A:C8	2.54	0.43
2:L5:1497:U:H2'	2:L5:1498:A:C8	2.54	0.43
2:L5:3276:G:O2'	20:LR:82:LYS:HE3	2.18	0.43
2:L5:3518:A:H2'	2:L5:3519:A:C8	2.54	0.43
8:LE:187:LEU:O	8:LE:191:ARG:HD2	2.19	0.43
14:LL:75:GLY:HA3	14:LL:99:ASP:HB2	2.00	0.43
29:La:117:LEU:HD23	29:La:117:LEU:HA	1.87	0.43
31:Lc:29:LEU:HD11	31:Lc:87:LYS:HE3	2.01	0.43
33:Le:77:PHE:HD2	33:Le:88:LEU:HD11	1.84	0.43
49:SA:127:PRO:HG3	49:SA:146:ALA:HB1	2.00	0.43
54:SF:78:MET:O	54:SF:79:HIS:HB2	2.18	0.43
65:SR:58:MET:HE3	65:SR:58:MET:HA	2.00	0.43
69:SV:76:ASP:C	69:SV:76:ASP:OD1	2.62	0.43
79:Sg:76:GLN:OE1	79:Sg:77:PHE:HD1	2.02	0.43
2:L5:322:C:H2'	2:L5:323:A:H8	1.84	0.43
2:L5:806:C:H2'	2:L5:807:C:C6	2.54	0.43
2:L5:860:C:H4'	9:LF:58:LYS:NZ	2.34	0.43
2:L5:3313:A:H2'	2:L5:3314:U:C6	2.54	0.43
2:L5:3955:U:H4'	22:LT:5:LYS:HD2	2.01	0.43
2:L5:4675:C:H41	57:SI:170:LYS:HZ2	1.66	0.43
6:LC:347:HIS:O	6:LC:351:VAL:HG22	2.18	0.43
7:LD:113:PHE:HE2	7:LD:142:PHE:CE2	2.36	0.43
14:LL:125:ILE:HD11	36:Lh:122:LYS:HE3	2.01	0.43
24:LV:75:LYS:HG3	24:LV:77:HIS:CE1	2.53	0.43
27:LY:43:ASN:O	27:LY:126:ARG:HD3	2.19	0.43
36:Lh:29:SER:O	36:Lh:33:VAL:HG23	2.18	0.43
46:S2:1651:A:H5''	64:SQ:139:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SC:253:PRO:HA	51:SC:256:TRP:CE2	2.54	0.43
54:SF:91:ARG:HG3	54:SF:92:ILE:N	2.33	0.43
65:SR:78:ARG:NH1	65:SR:81:ARG:HG2	2.34	0.43
2:L5:652:G:H1'	2:L5:653:G:C8	2.54	0.43
2:L5:685:G:H2'	2:L5:686:C:H6	1.84	0.43
2:L5:3255:C:H2'	2:L5:3256:A:C8	2.53	0.43
2:L5:3489:U:H2'	2:L5:3490:C:C6	2.54	0.43
2:L5:3529:A:H2'	2:L5:3530:G:H8	1.84	0.43
6:LC:209:ILE:HD13	6:LC:227:ILE:HG23	1.99	0.43
8:LE:157:VAL:HG23	8:LE:207:THR:HB	2.01	0.43
12:LI:149:ILE:HD11	12:LI:167:ILE:HD11	2.01	0.43
14:LL:87:HIS:CE1	14:LL:89:LYS:HG3	2.54	0.43
15:LM:11:ARG:CZ	15:LM:61:ILE:HD11	2.49	0.43
17:LO:80:PHE:O	17:LO:84:VAL:HG23	2.19	0.43
46:S2:454:C:H2'	46:S2:455:U:H6	1.84	0.43
46:S2:831:A:C6	46:S2:846:G:C5	3.07	0.43
46:S2:1038:G:H4'	46:S2:1846:A:H4'	2.00	0.43
53:SE:122:LYS:HD2	53:SE:164:LEU:HD21	2.01	0.43
67:ST:27:LYS:HA	67:ST:27:LYS:HD2	1.82	0.43
2:L5:231:U:H4'	27:LY:100:HIS:CD2	2.54	0.42
2:L5:732:C:OP1	6:LC:350:ARG:HD2	2.18	0.42
2:L5:1155:C:H2'	2:L5:1156:U:H6	1.84	0.42
2:L5:1866:G:H2'	2:L5:1867:G:C8	2.54	0.42
2:L5:2512:G:H1'	2:L5:2520:A:H1'	2.01	0.42
2:L5:2518:A:H2'	2:L5:2519:A:H8	1.83	0.42
2:L5:3567:C:H2'	2:L5:3568:C:H6	1.82	0.42
5:LA:112:ILE:HD12	5:LA:133:TYR:CD2	2.54	0.42
5:LA:188:LYS:NZ	5:LA:192:LYS:HE3	2.33	0.42
5:LA:225:ILE:HD12	5:LA:225:ILE:HA	1.88	0.42
11:LH:76:HIS:O	11:LH:80:MET:HG3	2.19	0.42
17:LO:75:ALA:HB3	17:LO:78:ARG:HG3	2.01	0.42
22:LT:111:GLU:O	22:LT:115:LYS:HG3	2.18	0.42
23:LU:30:GLU:HG3	23:LU:31:ASP:H	1.84	0.42
35:Lg:78:TYR:HB3	35:Lg:82:MET:HB3	2.01	0.42
46:S2:107:A:H2'	46:S2:108:G:C8	2.54	0.42
46:S2:672:A:H4'	46:S2:673:A:H5''	2.00	0.42
46:S2:910:G:H2'	46:S2:911:G:C8	2.54	0.42
46:S2:1044:G:H2'	46:S2:1045:G:O4'	2.18	0.42
51:SC:195:LEU:HD11	51:SC:244:ILE:HG22	2.01	0.42
72:SY:22:GLN:HB2	72:SY:72:PHE:CE1	2.53	0.42
77:Sd:21:CYS:HB3	77:Sd:26:ASN:H	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2446:U:H5'	39:Lk:4:LYS:HE3	2.00	0.42
2:L5:3597:U:H5''	10:LG:75:LYS:HE2	2.02	0.42
12:LI:52:MET:HE3	12:LI:136:MET:HB2	2.00	0.42
13:LJ:51:SER:HB2	13:LJ:69:ALA:HB3	2.00	0.42
17:LO:109:PRO:HB2	17:LO:111:PRO:HD2	2.01	0.42
29:La:14:HIS:ND1	29:La:14:HIS:N	2.67	0.42
37:Li:2:ALA:O	37:Li:3:LEU:HB2	2.18	0.42
41:Lm:94:MET:HB3	41:Lm:121:LEU:HD12	2.01	0.42
46:S2:854:C:C2	46:S2:855:A:C8	3.07	0.42
46:S2:1816:A:H3'	46:S2:1817:G:O4'	2.19	0.42
50:SB:116:LYS:HG3	50:SB:117:TRP:H	1.84	0.42
54:SF:99:ILE:O	54:SF:103:LEU:HB2	2.19	0.42
59:SK:32:HIS:CD2	59:SK:45:VAL:HG21	2.54	0.42
59:SK:94:LEU:HD23	59:SK:94:LEU:HA	1.87	0.42
62:SO:135:ILE:HD12	62:SO:135:ILE:O	2.20	0.42
68:SU:23:ILE:HB	68:SU:113:GLU:OE1	2.19	0.42
80:LB:238:LYS:HE2	80:LB:238:LYS:HB2	1.87	0.42
2:L5:425:A:H2'	2:L5:426:A:C8	2.54	0.42
2:L5:817:A:H2'	2:L5:818:G:O4'	2.19	0.42
2:L5:1325:C:H2'	2:L5:1326:G:C8	2.53	0.42
2:L5:2351:G:H2'	2:L5:2352:A:H8	1.83	0.42
2:L5:2444:C:H2'	2:L5:2445:U:H6	1.85	0.42
2:L5:3341:G:H2'	2:L5:3342:C:H6	1.83	0.42
2:L5:3349:A:C2	44:Lp:19:GLY:HA2	2.55	0.42
2:L5:3890:C:H2'	2:L5:3891:G:H8	1.84	0.42
2:L5:4059:U:C2	2:L5:4060:G:C8	3.07	0.42
3:L7:63:C:H5'	3:L7:64:G:H5''	2.01	0.42
7:LD:51:MET:HE1	7:LD:166:ALA:HB2	2.01	0.42
13:LJ:93:GLU:OE1	13:LJ:173:ILE:HD11	2.19	0.42
17:LO:3:GLU:HB3	17:LO:31:ARG:HH22	1.84	0.42
18:LP:125:MET:HA	18:LP:125:MET:HE3	2.01	0.42
46:S2:643:U:P	58:SJ:39:ASN:HB2	2.60	0.42
46:S2:953:G:H2'	46:S2:954:C:C6	2.54	0.42
54:SF:176:GLU:OE1	54:SF:176:GLU:HA	2.20	0.42
57:SI:192:GLY:HA3	60:SL:19:ASN:HB3	2.02	0.42
61:SN:84:LEU:HD23	61:SN:84:LEU:HA	1.94	0.42
70:SW:36:ARG:O	70:SW:40:VAL:HG23	2.18	0.42
73:SZ:68:ILE:HB	73:SZ:109:TYR:HB2	2.01	0.42
79:Sg:121:VAL:HG11	79:Sg:165:ILE:HD11	2.01	0.42
80:LB:52:GLY:HA2	80:LB:341:LYS:HE3	2.01	0.42
1:B:4:A:H1'	1:B:5:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:221:C:H2'	2:L5:222:C:C6	2.54	0.42
2:L5:933:C:H2'	2:L5:934:G:H8	1.84	0.42
2:L5:1159:C:H2'	2:L5:1160:G:H8	1.85	0.42
2:L5:1328:U:H2'	2:L5:1329:A:H8	1.84	0.42
2:L5:3573:G:H2'	2:L5:3574:A:H8	1.85	0.42
5:LA:176:ASP:C	5:LA:176:ASP:OD2	2.62	0.42
9:LF:263:ASN:O	9:LF:267:ARG:HG2	2.19	0.42
46:S2:922:G:C6	70:SW:28:ARG:HD3	2.54	0.42
46:S2:964:A:H2'	46:S2:965:A:C8	2.55	0.42
50:SB:138:PHE:HD2	50:SB:214:LYS:HB3	1.83	0.42
52:SD:113:LEU:HD12	52:SD:114:ALA:H	1.84	0.42
53:SE:19:MET:HB2	53:SE:51:ARG:HH22	1.84	0.42
56:SH:11:PRO:HD3	56:SH:44:ASN:HB2	2.02	0.42
59:SK:31:LYS:HD3	59:SK:31:LYS:HA	1.82	0.42
67:ST:137:GLN:C	67:ST:137:GLN:OE1	2.62	0.42
2:L5:109:G:H5'	14:LL:92:ARG:NH1	2.34	0.42
2:L5:287:G:H2'	2:L5:288:C:C6	2.54	0.42
2:L5:725:U:H2'	2:L5:726:C:C6	2.54	0.42
2:L5:1623:C:H2'	2:L5:1625:U:H5''	2.01	0.42
2:L5:2131:A:H2'	2:L5:2132:A:C8	2.55	0.42
2:L5:4042:C:H2'	2:L5:4043:A:C8	2.54	0.42
2:L5:4411:C:H42	2:L5:4561:G:H4'	1.84	0.42
2:L5:4516:G:H5''	15:LM:91:TRP:CZ2	2.55	0.42
3:L7:39:C:O2'	13:LJ:46:GLN:HB3	2.19	0.42
6:LC:150:LEU:HD12	6:LC:150:LEU:HA	1.83	0.42
12:LI:208:LYS:HD2	12:LI:209:TRP:N	2.34	0.42
13:LJ:91:GLU:HG2	13:LJ:93:GLU:HG2	2.02	0.42
17:LO:34:VAL:HG21	17:LO:112:TYR:OH	2.20	0.42
18:LP:105:LYS:HE2	18:LP:105:LYS:HB3	1.90	0.42
22:LT:44:GLY:HA2	22:LT:95:HIS:HB3	2.01	0.42
26:LX:128:ILE:HD13	40:LI:7:PHE:HE1	1.85	0.42
31:Lc:45:LEU:HB3	31:Lc:96:ILE:HD12	2.00	0.42
37:Li:59:GLU:O	37:Li:63:VAL:HG22	2.19	0.42
2:L5:698:C:H2'	2:L5:699:C:C6	2.55	0.42
2:L5:1286:C:H2'	2:L5:1287:U:C6	2.55	0.42
2:L5:1496:A:H5''	14:LL:3:PRO:O	2.19	0.42
2:L5:2031:C:H2'	2:L5:2032:G:C8	2.54	0.42
2:L5:2394:G:H2'	2:L5:2395:A:C8	2.55	0.42
2:L5:2437:C:H2'	2:L5:2438:C:C6	2.55	0.42
2:L5:3326:G:H21	2:L5:3329:G:N2	2.17	0.42
2:L5:3505:U:H2'	2:L5:3506:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3953:U:H4'	22:LT:89:ILE:HG22	2.00	0.42
2:L5:4223:G:C2	2:L5:4224:A:C8	3.08	0.42
12:LI:36:LEU:HD11	12:LI:69:ARG:HD2	2.02	0.42
19:LQ:43:PHE:O	19:LQ:47:VAL:HG23	2.20	0.42
24:LV:88:TYR:HE1	24:LV:124:GLU:OE1	2.02	0.42
40:Ll:41:ARG:HA	40:Ll:41:ARG:HD2	1.64	0.42
46:S2:29:G:H2'	46:S2:30:C:H6	1.85	0.42
46:S2:126:G:H8	55:SG:199:THR:HG21	1.85	0.42
46:S2:828:A:C4	46:S2:829:G:C8	3.07	0.42
46:S2:1642:A:H2'	48:S7:32:C:OP2	2.20	0.42
49:SA:81:ASN:ND2	49:SA:82:THR:N	2.67	0.42
55:SG:16:ILE:HD12	55:SG:16:ILE:C	2.45	0.42
56:SH:139:ILE:HG23	56:SH:156:VAL:HG13	2.01	0.42
65:SR:54:VAL:O	65:SR:58:MET:HG2	2.19	0.42
80:LB:181:MET:HG2	80:LB:182:GLU:N	2.34	0.42
2:L5:177:G:H2'	2:L5:178:A:C8	2.54	0.42
2:L5:1093:C:H2'	2:L5:1094:A:O4'	2.19	0.42
4:L8:92:U:H2'	4:L8:93:C:O4'	2.20	0.42
9:LF:193:ASP:OD2	9:LF:193:ASP:C	2.62	0.42
12:LI:152:LEU:HB3	12:LI:165:ILE:HD12	2.02	0.42
14:LL:198:ARG:HA	14:LL:201:GLU:HG2	2.01	0.42
19:LQ:85:THR:HA	19:LQ:104:ARG:O	2.20	0.42
43:Lo:66:ILE:O	43:Lo:66:ILE:HD12	2.20	0.42
46:S2:1668:U:H2'	46:S2:1669:U:C6	2.54	0.42
56:SH:18:GLU:O	56:SH:19:PHE:HB3	2.18	0.42
62:SO:95:ILE:HG13	62:SO:116:LEU:HD11	2.00	0.42
65:SR:72:LYS:HZ1	65:SR:76:GLU:HB2	1.83	0.42
66:SS:86:ARG:HG3	66:SS:89:ASP:OD1	2.19	0.42
68:SU:93:SER:HB2	68:SU:97:ILE:HD12	2.01	0.42
2:L5:344:C:H2'	2:L5:345:G:C8	2.55	0.42
2:L5:4124:U:H2'	2:L5:4125:G:H8	1.85	0.42
7:LD:99:TYR:HE1	7:LD:164:LYS:HG3	1.83	0.42
9:LF:130:VAL:HG21	9:LF:157:ILE:HD11	2.01	0.42
11:LH:13:PRO:HB2	11:LH:14:GLU:H	1.63	0.42
19:LQ:76:GLU:N	19:LQ:76:GLU:OE2	2.53	0.42
22:LT:63:ARG:CZ	22:LT:75:ILE:HD11	2.49	0.42
46:S2:1393:U:H2'	46:S2:1394:G:C8	2.55	0.42
54:SF:49:LEU:HD12	64:SQ:50:LYS:HG2	2.02	0.42
57:SI:65:PHE:HA	57:SI:187:GLY:O	2.20	0.42
58:SJ:100:LEU:HD22	58:SJ:104:ASP:CG	2.45	0.42
62:SO:113:GLN:HG3	74:Sa:46:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:ST:111:LYS:HD3	67:ST:111:LYS:N	2.35	0.42
70:SW:83:LEU:HD23	70:SW:83:LEU:HA	1.84	0.42
73:SZ:90:GLU:OE2	73:SZ:90:GLU:C	2.63	0.42
75:Sb:21:LYS:HD3	75:Sb:26:GLN:OE1	2.20	0.42
79:Sg:259:TRP:HA	79:Sg:259:TRP:HE3	1.85	0.42
2:L5:93:G:H2'	2:L5:94:A:C8	2.55	0.42
2:L5:189:G:H22	2:L5:252:G:H22	1.66	0.42
2:L5:879:C:H2'	2:L5:880:U:C6	2.55	0.42
2:L5:1317:A:H1'	2:L5:1318:G:C8	2.54	0.42
2:L5:2233:G:H2'	2:L5:2234:A:C8	2.55	0.42
2:L5:2569:A:H2'	2:L5:2570:G:H8	1.84	0.42
2:L5:3525:G:H22	2:L5:3557:G:H1'	1.83	0.42
2:L5:4024:G:H1'	2:L5:4025:U:C6	2.55	0.42
2:L5:4357:C:H2'	2:L5:4358:A:H8	1.84	0.42
17:LO:25:LYS:HD2	17:LO:25:LYS:HA	1.89	0.42
18:LP:122:ALA:HB3	18:LP:143:PRO:HB2	2.02	0.42
21:LS:83:ARG:HG2	21:LS:127:MET:HE2	2.01	0.42
54:SF:89:THR:O	54:SF:93:VAL:HG23	2.20	0.42
55:SG:25:ARG:HA	55:SG:28:TYR:CD2	2.55	0.42
67:ST:45:LEU:HD23	67:ST:45:LEU:HA	1.89	0.42
78:Se:108:ARG:HD3	78:Se:111:GLN:NE2	2.35	0.42
80:LB:136:LYS:HA	80:LB:139:ASP:OD2	2.20	0.42
2:L5:456:G:H2'	2:L5:457:C:H6	1.85	0.42
2:L5:697:U:H2'	2:L5:698:C:C6	2.55	0.42
2:L5:742:G:C2	2:L5:743:G:C8	3.07	0.42
2:L5:1633:G:H4'	30:Lb:68:ARG:HH22	1.85	0.42
2:L5:1666:U:H2'	2:L5:1667:G:H8	1.85	0.42
2:L5:1895:G:H21	2:L5:1896:G:H1'	1.85	0.42
2:L5:3787:U:O2	2:L5:3801:G:N2	2.39	0.42
18:LP:95:LEU:HD23	18:LP:95:LEU:HA	1.82	0.42
20:LR:175:GLU:O	20:LR:178:GLN:HG3	2.20	0.42
35:Lg:59:VAL:HG21	35:Lg:67:LEU:HD11	2.02	0.42
46:S2:382:C:N4	57:SI:27:TYR:HB2	2.35	0.42
46:S2:389:U:H2'	46:S2:390:A:C8	2.55	0.42
46:S2:497:C:H2'	46:S2:498:C:C6	2.54	0.42
46:S2:818:G:H2'	46:S2:819:A:H8	1.85	0.42
46:S2:1202:U:H2'	46:S2:1203:U:C6	2.55	0.42
46:S2:1396:C:O2'	46:S2:1397:A:H5'	2.20	0.42
48:S7:12:C:H2'	48:S7:13:G:C8	2.55	0.42
51:SC:177:PRO:CD	69:SV:9:VAL:HG21	2.50	0.42
51:SC:194:ARG:O	51:SC:224:THR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SE:70:ILE:HA	53:SE:92:ILE:HD13	2.02	0.42
57:SI:88:ASN:O	57:SI:91:VAL:HG22	2.20	0.42
57:SI:106:SER:HB3	57:SI:166:PHE:CD1	2.55	0.42
61:SN:29:THR:HG23	61:SN:31:ASP:H	1.85	0.42
64:SQ:143:LYS:HG2	64:SQ:145:TYR:CE1	2.55	0.42
66:SS:65:GLU:OE1	66:SS:65:GLU:HA	2.20	0.42
2:L5:1264:C:H2'	2:L5:1265:G:O4'	2.20	0.41
6:LC:353:LYS:HB2	6:LC:353:LYS:HE2	1.79	0.41
14:LL:61:CYS:HB2	14:LL:66:TYR:O	2.20	0.41
33:Le:94:SER:C	33:Le:95:TYR:HD2	2.28	0.41
46:S2:1674:U:H2'	46:S2:1675:G:O4'	2.19	0.41
52:SD:113:LEU:HD12	52:SD:114:ALA:N	2.35	0.41
54:SF:76:MET:HE3	54:SF:76:MET:HB3	1.78	0.41
54:SF:153:LEU:HD23	54:SF:153:LEU:HA	1.94	0.41
63:SP:21:ASP:O	63:SP:25:LEU:HB2	2.20	0.41
72:SY:91:LEU:HD23	72:SY:91:LEU:HA	1.89	0.41
79:Sg:290:ALA:O	79:Sg:298:LEU:HD12	2.20	0.41
2:L5:1300:C:H2'	2:L5:1301:G:H8	1.85	0.41
2:L5:2628:U:H1'	44:Lp:20:ALA:HB2	2.03	0.41
2:L5:3271:G:H2'	2:L5:3274:G:N2	2.36	0.41
2:L5:3529:A:H2'	2:L5:3530:G:C8	2.56	0.41
2:L5:3785:C:H42	2:L5:3803:G:H1	1.69	0.41
2:L5:3892:A:H2'	2:L5:3893:G:H8	1.83	0.41
2:L5:3965:U:H2'	2:L5:3966:A:C8	2.55	0.41
5:LA:80:GLU:HG3	44:Lp:66:GLY:HA2	2.02	0.41
7:LD:164:LYS:HD3	7:LD:164:LYS:HA	1.88	0.41
18:LP:91:LEU:HD21	18:LP:146:ILE:HG12	2.01	0.41
20:LR:106:LEU:HD23	20:LR:106:LEU:HA	1.92	0.41
32:Ld:19:GLU:HB2	32:Ld:102:LEU:HD11	2.02	0.41
46:S2:1389:A:H61	52:SD:161:GLY:CA	2.33	0.41
49:SA:113:GLN:H	49:SA:113:GLN:HG2	1.72	0.41
63:SP:85:ILE:HA	63:SP:89:MET:SD	2.60	0.41
79:Sg:223:GLU:OE1	79:Sg:223:GLU:N	2.44	0.41
79:Sg:239:LEU:HD23	79:Sg:239:LEU:HA	1.90	0.41
80:LB:136:LYS:HG3	80:LB:146:LEU:HD11	2.02	0.41
2:L5:173:C:H2'	2:L5:174:C:H6	1.84	0.41
2:L5:425:A:H2'	2:L5:426:A:H8	1.85	0.41
2:L5:1582:U:H2'	2:L5:1583:A:C8	2.55	0.41
2:L5:1757:U:H2'	2:L5:1758:G:C8	2.54	0.41
2:L5:2439:C:H2'	2:L5:2440:G:O4'	2.21	0.41
2:L5:4176:A:H1'	2:L5:4211:U:C4	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LA:177:LYS:HB2	44:Lp:29:ILE:HG21	2.02	0.41
10:LG:107:LYS:HE2	10:LG:107:LYS:HB2	1.83	0.41
17:LO:174:ILE:O	17:LO:178:ARG:HG3	2.20	0.41
21:LS:85:ASP:OD1	21:LS:90:THR:HG22	2.20	0.41
32:Ld:59:THR:HG21	32:Ld:103:TYR:HA	2.01	0.41
36:Lh:48:ARG:O	36:Lh:52:LYS:HG2	2.21	0.41
46:S2:980:C:H2'	46:S2:981:A:C8	2.56	0.41
46:S2:1653:G:H1	46:S2:1673:U:H3	1.69	0.41
49:SA:40:LYS:HE3	65:SR:101:ASP:OD1	2.20	0.41
51:SC:240:THR:O	51:SC:244:ILE:HG23	2.20	0.41
51:SC:242:ASP:OD2	51:SC:242:ASP:C	2.62	0.41
58:SJ:32:ILE:HD11	58:SJ:40:LYS:HD3	2.02	0.41
60:SL:37:TYR:C	60:SL:37:TYR:CD2	2.98	0.41
65:SR:24:LEU:HD12	65:SR:24:LEU:HA	1.90	0.41
79:Sg:172:LYS:HE2	79:Sg:172:LYS:HB2	1.90	0.41
2:L5:191:G:H2'	2:L5:192:G:H8	1.85	0.41
2:L5:217:C:H5''	2:L5:218:A:H4'	2.02	0.41
2:L5:2359:G:H2'	2:L5:2360:G:H8	1.85	0.41
2:L5:2409:C:H2'	2:L5:2410:U:C6	2.55	0.41
2:L5:2421:C:O4'	20:LR:96:MET:HG3	2.20	0.41
2:L5:4246:C:H2'	2:L5:4247:U:C6	2.54	0.41
2:L5:4556:A:C8	17:LO:156:LEU:HD13	2.54	0.41
12:LI:51:HIS:CD2	12:LI:168:SER:HB2	2.55	0.41
12:LI:190:LEU:HD12	12:LI:190:LEU:HA	1.90	0.41
14:LL:24:THR:HB	14:LL:26:PHE:CD2	2.55	0.41
15:LM:36:ALA:HB2	15:LM:52:PHE:CZ	2.56	0.41
24:LV:30:ASP:OD1	24:LV:30:ASP:N	2.53	0.41
29:La:92:LYS:H	29:La:92:LYS:HG3	1.66	0.41
46:S2:1829:C:H2'	46:S2:1830:G:O4'	2.20	0.41
53:SE:29:PRO:HG2	53:SE:46:ILE:HD11	2.02	0.41
61:SN:25:TRP:HB2	75:Sb:82:LYS:HZ3	1.84	0.41
61:SN:135:LEU:HD23	61:SN:135:LEU:HA	1.91	0.41
66:SS:39:ARG:HB3	66:SS:83:PHE:CZ	2.55	0.41
72:SY:61:ARG:HD3	72:SY:61:ARG:HA	1.80	0.41
73:SZ:63:PRO:O	73:SZ:111:ARG:HG2	2.21	0.41
74:Sa:36:ILE:HD11	74:Sa:78:ALA:HB2	2.02	0.41
75:Sb:8:LEU:HD23	75:Sb:8:LEU:HA	1.93	0.41
79:Sg:299:PHE:CD1	79:Sg:309:VAL:HG12	2.55	0.41
80:LB:139:ASP:O	80:LB:141:THR:N	2.53	0.41
80:LB:200:ARG:CZ	80:LB:200:ARG:HB3	2.51	0.41
2:L5:301:C:H5''	16:LN:68:ARG:HH21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:422:G:H2'	2:L5:423:U:C6	2.55	0.41
2:L5:1510:C:C2	2:L5:1511:G:C8	3.09	0.41
2:L5:1745:A:H2'	2:L5:1746:A:H8	1.83	0.41
2:L5:2080:C:H2'	2:L5:2081:C:H6	1.85	0.41
2:L5:2377:A:H2'	2:L5:2378:G:H8	1.85	0.41
2:L5:2519:A:H2'	2:L5:2520:A:C8	2.55	0.41
6:LC:76:ILE:HD12	6:LC:77:PRO:HD2	2.01	0.41
21:LS:36:ASN:ND2	21:LS:38:VAL:HB	2.35	0.41
22:LT:18:PRO:HB2	22:LT:21:LYS:HB2	2.02	0.41
46:S2:562:A:H2'	46:S2:563:U:O4'	2.20	0.41
46:S2:819:A:H2'	46:S2:820:G:C8	2.55	0.41
46:S2:1008:C:H2'	46:S2:1009:A:C8	2.56	0.41
46:S2:1677:U:C4	46:S2:1678:U:C4	3.09	0.41
50:SB:179:ASN:HD22	50:SB:183:GLU:HG3	1.85	0.41
51:SC:179:THR:HG23	51:SC:180:VAL:O	2.20	0.41
53:SE:45:ILE:HA	53:SE:61:VAL:HG11	2.03	0.41
53:SE:92:ILE:HD13	53:SE:92:ILE:HA	1.86	0.41
54:SF:22:LYS:HG3	54:SF:23:TRP:CE2	2.55	0.41
55:SG:15:LEU:HD23	55:SG:16:ILE:N	2.35	0.41
58:SJ:50:LEU:HD23	58:SJ:102:ILE:HD13	2.03	0.41
66:SS:40:TYR:HA	66:SS:43:VAL:HG22	2.02	0.41
68:SU:90:ASP:O	68:SU:91:LEU:HD23	2.20	0.41
71:SX:37:LYS:HE3	71:SX:37:LYS:HB2	1.88	0.41
72:SY:11:LYS:HA	72:SY:11:LYS:HD3	1.94	0.41
75:Sb:14:GLU:C	75:Sb:14:GLU:OE1	2.64	0.41
79:Sg:165:ILE:HG23	79:Sg:177:TRP:HB2	2.02	0.41
79:Sg:174:VAL:HG23	79:Sg:188:HIS:HB2	2.01	0.41
80:LB:194:LEU:O	80:LB:198:ARG:HG2	2.20	0.41
2:L5:1159:C:H2'	2:L5:1160:G:C8	2.55	0.41
2:L5:1272:C:C2	2:L5:1273:A:C8	3.09	0.41
2:L5:1282:C:C2	2:L5:1283:C:C5	3.08	0.41
2:L5:1577:C:H2'	2:L5:1578:A:H8	1.86	0.41
2:L5:1820:A:H5''	2:L5:1821:C:H5	1.85	0.41
2:L5:2295:U:H2'	2:L5:2296:C:C6	2.56	0.41
2:L5:2387:U:H2'	2:L5:2388:C:H6	1.86	0.41
2:L5:3321:G:H2'	2:L5:3322:G:C8	2.53	0.41
7:LD:69:ILE:HD13	7:LD:69:ILE:HA	1.92	0.41
8:LE:217:PRO:HG2	8:LE:220:LEU:HG	2.01	0.41
15:LM:91:TRP:O	15:LM:95:ILE:HG13	2.20	0.41
18:LP:112:LEU:HA	18:LP:151:THR:O	2.21	0.41
23:LU:100:LEU:HD12	23:LU:113:ARG:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Lc:47:ILE:HD12	31:Lc:94:LEU:HD22	2.03	0.41
46:S2:643:U:H4'	46:S2:645:G:H4'	2.02	0.41
52:SD:108:LYS:O	52:SD:113:LEU:HB3	2.21	0.41
52:SD:133:GLY:HA3	52:SD:156:LEU:O	2.20	0.41
60:SL:20:LYS:HB3	60:SL:20:LYS:HE3	1.75	0.41
61:SN:88:LEU:HD12	61:SN:88:LEU:HA	1.90	0.41
63:SP:111:MET:HG3	66:SS:117:ILE:HD12	2.02	0.41
67:ST:114:GLU:HB2	67:ST:122:LYS:HB3	2.02	0.41
71:SX:105:PHE:CE2	71:SX:112:VAL:HG12	2.56	0.41
80:LB:162:ILE:O	80:LB:182:GLU:HA	2.21	0.41
2:L5:146:G:H4'	4:L8:144:U:OP1	2.21	0.41
2:L5:507:G:H2'	2:L5:508:G:C8	2.56	0.41
2:L5:1326:G:H2'	2:L5:1327:U:C6	2.56	0.41
2:L5:2070:A:H5'	2:L5:2071:G:OP2	2.21	0.41
2:L5:2315:C:H2'	2:L5:2316:G:O4'	2.21	0.41
2:L5:3267:A:H2'	2:L5:3268:A:H8	1.85	0.41
2:L5:3919:G:H2'	2:L5:3919:G:N3	2.35	0.41
3:L7:58:A:H2'	3:L7:59:G:C8	2.55	0.41
6:LC:230:LEU:HD23	6:LC:230:LEU:HA	1.89	0.41
9:LF:114:VAL:O	9:LF:142:GLY:HA2	2.19	0.41
14:LL:142:GLU:O	14:LL:146:LEU:HB2	2.20	0.41
18:LP:94:MET:HE3	18:LP:94:MET:HB2	1.76	0.41
29:La:72:THR:HG22	29:La:110:LYS:HB3	2.03	0.41
30:Lb:43:MET:O	30:Lb:47:LYS:HG3	2.20	0.41
46:S2:945:A:H2'	46:S2:946:U:C6	2.56	0.41
46:S2:1393:U:H2'	46:S2:1394:G:H8	1.85	0.41
46:S2:1712:U:H2'	46:S2:1713:A:C8	2.55	0.41
50:SB:71:LEU:HD22	50:SB:82:ARG:HD2	2.02	0.41
51:SC:108:LYS:HD2	51:SC:233:LEU:HD13	2.03	0.41
62:SO:35:ALA:HB3	62:SO:112:ALA:HB2	2.01	0.41
62:SO:113:GLN:OE1	62:SO:113:GLN:HA	2.21	0.41
72:SY:55:ILE:HD12	72:SY:55:ILE:H	1.86	0.41
73:SZ:68:ILE:O	73:SZ:109:TYR:HB2	2.21	0.41
80:LB:285:TYR:HB2	80:LB:332:MET:HG2	2.02	0.41
2:L5:1771:G:H2'	2:L5:1772:G:C2	2.56	0.41
2:L5:2388:C:H2'	2:L5:2389:U:H6	1.85	0.41
2:L5:3422:G:N2	2:L5:3423:A:N6	2.68	0.41
2:L5:3554:G:H2'	2:L5:4177:G:OP1	2.21	0.41
2:L5:3886:A:C5	2:L5:3888:G:C8	3.09	0.41
2:L5:4139:C:H2'	2:L5:4140:A:O4'	2.21	0.41
2:L5:4241:U:H5'	80:LB:14:LEU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4295:U:H2'	2:L5:4296:G:C8	2.56	0.41
7:LD:108:ARG:NE	7:LD:253:TYR:HB2	2.35	0.41
26:LX:145:ASP:O	26:LX:149:VAL:HG23	2.21	0.41
32:Ld:23:ARG:HD3	32:Ld:121:ASN:OD1	2.21	0.41
34:Lf:7:CYS:HB2	34:Lf:103:VAL:HB	2.03	0.41
46:S2:26:U:H2'	46:S2:27:A:C8	2.55	0.41
46:S2:383:C:H2'	46:S2:384:G:C8	2.54	0.41
46:S2:1200:A:H2'	46:S2:1201:A:C8	2.55	0.41
46:S2:1679:A:O2'	46:S2:1680:A:H5'	2.21	0.41
50:SB:144:LYS:HD3	50:SB:208:HIS:HB3	2.03	0.41
53:SE:108:ARG:HE	53:SE:108:ARG:HB2	1.67	0.41
53:SE:112:HIS:ND1	53:SE:112:HIS:O	2.41	0.41
65:SR:115:SER:O	65:SR:117:LEU:HD22	2.20	0.41
71:SX:87:ASN:HB3	71:SX:88:ASP:H	1.61	0.41
2:L5:299:A:H2'	2:L5:300:G:C8	2.51	0.41
2:L5:1130:C:H2'	2:L5:1131:G:H8	1.84	0.41
2:L5:1427:A:H5'	5:LA:183:GLY:HA2	2.02	0.41
2:L5:2187:C:H2'	2:L5:2188:A:H8	1.85	0.41
2:L5:3567:C:H2'	2:L5:3568:C:C6	2.56	0.41
2:L5:3889:G:H4'	2:L5:3981:G:O2'	2.21	0.41
4:L8:2:G:H5''	4:L8:3:A:H8	1.86	0.41
5:LA:186:TYR:HB2	5:LA:196:TRP:CZ3	2.56	0.41
11:LH:101:ILE:HA	11:LH:116:ASN:O	2.21	0.41
14:LL:57:PRO:HG3	14:LL:75:GLY:O	2.20	0.41
14:LL:194:ILE:HD12	14:LL:194:ILE:HA	1.97	0.41
29:La:131:ARG:HG2	29:La:135:GLU:OE2	2.21	0.41
30:Lb:104:LYS:HB2	30:Lb:104:LYS:HE3	1.92	0.41
31:Lc:23:LYS:HB2	31:Lc:23:LYS:HE3	1.82	0.41
31:Lc:34:THR:HG23	31:Lc:95:ALA:HB2	2.02	0.41
32:Ld:68:LEU:HD13	32:Ld:108:TYR:HB2	2.01	0.41
41:Lm:114:LYS:H	41:Lm:114:LYS:HG2	1.66	0.41
46:S2:28:U:H2'	46:S2:29:G:C8	2.56	0.41
46:S2:107:A:H2'	46:S2:108:G:H8	1.85	0.41
46:S2:526:A:H2'	46:S2:527:A:C8	2.56	0.41
46:S2:823:U:H3	46:S2:827:A:H62	1.67	0.41
46:S2:1787:U:H2'	46:S2:1788:G:C8	2.56	0.41
56:SH:130:LEU:HD12	56:SH:130:LEU:HA	1.90	0.41
58:SJ:87:LEU:O	58:SJ:151:LEU:HG	2.21	0.41
59:SK:57:TYR:CD1	59:SK:75:GLY:HA2	2.49	0.41
62:SO:88:LEU:HD12	62:SO:88:LEU:HA	1.75	0.41
66:SS:112:GLU:HA	66:SS:115:LYS:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SV:27:LYS:HA	69:SV:27:LYS:HD3	1.92	0.41
69:SV:60:ARG:HA	69:SV:65:SER:HB2	2.03	0.41
70:SW:106:THR:HG22	70:SW:122:GLY:C	2.45	0.41
79:Sg:14:HIS:O	79:Sg:305:ASN:HB3	2.20	0.41
79:Sg:68:ASP:OD1	79:Sg:111:VAL:HG22	2.21	0.41
80:LB:224:LYS:HG2	80:LB:340:THR:HG22	2.03	0.41
2:L5:132:G:H2'	2:L5:133:C:O4'	2.20	0.41
2:L5:1154:U:H2'	2:L5:1155:C:H6	1.83	0.41
2:L5:1483:A:H4'	2:L5:1499:G:N2	2.36	0.41
5:LA:36:GLU:HG3	5:LA:91:GLY:HA2	2.02	0.41
9:LF:159:GLU:HG3	9:LF:256:GLY:HA2	2.03	0.41
27:LY:25:ILE:O	27:LY:29:ILE:HG13	2.21	0.41
46:S2:572:U:O3'	72:SY:60:PHE:HB2	2.21	0.41
46:S2:1557:A:H2'	46:S2:1557:A:N3	2.36	0.41
46:S2:1689:C:H2'	46:S2:1690:C:C6	2.56	0.41
52:SD:123:LEU:HD12	52:SD:123:LEU:HA	1.88	0.41
57:SI:161:LEU:HD23	57:SI:161:LEU:HA	1.90	0.41
65:SR:78:ARG:HD2	65:SR:78:ARG:HA	1.87	0.41
68:SU:66:ARG:HH12	68:SU:75:LYS:HD2	1.86	0.41
2:L5:439:U:H2'	2:L5:440:G:C8	2.57	0.40
2:L5:1164:G:OP2	19:LQ:54:SER:HB2	2.21	0.40
2:L5:1274:C:H2'	2:L5:1275:C:H6	1.86	0.40
2:L5:1380:C:H2'	2:L5:1381:U:H6	1.86	0.40
2:L5:1882:G:H2'	2:L5:1883:U:C6	2.56	0.40
2:L5:2170:U:H2'	2:L5:2171:G:C8	2.56	0.40
2:L5:2526:C:C2	2:L5:2527:G:C8	3.09	0.40
2:L5:4704:A:H2'	2:L5:4705:C:C6	2.56	0.40
10:LG:164:ILE:O	10:LG:168:VAL:HG13	2.21	0.40
11:LH:7:ASN:HA	11:LH:57:VAL:O	2.21	0.40
12:LI:162:ARG:HD3	12:LI:162:ARG:C	2.46	0.40
13:LJ:94:LEU:HD23	13:LJ:94:LEU:HA	1.86	0.40
14:LL:81:LEU:HD23	14:LL:86:ILE:HB	2.02	0.40
18:LP:119:VAL:HG22	18:LP:146:ILE:HD13	2.02	0.40
46:S2:1129:C:H2'	46:S2:1130:G:C8	2.57	0.40
46:S2:1409:U:C2	46:S2:1410:A:C8	3.10	0.40
46:S2:1734:U:H2'	46:S2:1735:G:O4'	2.21	0.40
55:SG:155:GLN:CD	55:SG:155:GLN:N	2.78	0.40
59:SK:3:MET:HB2	59:SK:3:MET:HE2	1.87	0.40
60:SL:11:GLN:HB3	60:SL:56:ILE:HG12	2.03	0.40
61:SN:118:ILE:O	61:SN:122:ILE:HG13	2.20	0.40
64:SQ:8:GLN:HA	64:SQ:99:TYR:CZ	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SQ:112:LEU:HB2	64:SQ:120:LEU:HD21	2.03	0.40
73:SZ:47:LEU:HD12	73:SZ:47:LEU:O	2.20	0.40
73:SZ:91:LEU:HD22	73:SZ:96:LEU:HD11	2.03	0.40
80:LB:82:PRO:HB3	80:LB:328:ASN:ND2	2.36	0.40
2:L5:741:A:H61	2:L5:829:G:N2	2.19	0.40
2:L5:3427:U:H2'	2:L5:3428:C:O4'	2.21	0.40
2:L5:4114:C:C2	2:L5:4115:C:C5	3.10	0.40
2:L5:4543:G:H2'	2:L5:4544:G:O4'	2.21	0.40
11:LH:40:HIS:ND1	11:LH:41:ILE:HG13	2.36	0.40
12:LI:86:HIS:HB3	12:LI:139:ARG:CG	2.51	0.40
13:LJ:24:ILE:HB	13:LJ:70:VAL:HG13	2.03	0.40
17:LO:81:TRP:CZ2	17:LO:99:LEU:HD21	2.57	0.40
27:LY:30:MET:SD	27:LY:78:TYR:HA	2.61	0.40
31:Lc:28:VAL:HG13	31:Lc:33:GLN:HB3	2.03	0.40
36:Lh:91:MET:HE3	36:Lh:91:MET:HB3	1.90	0.40
46:S2:53:C:O3'	72:SY:108:LYS:HD2	2.21	0.40
46:S2:567:U:H3	46:S2:585:A:H61	1.69	0.40
46:S2:1301:U:H2'	63:SP:51:ARG:HH12	1.84	0.40
56:SH:53:VAL:HG12	56:SH:175:GLY:HA3	2.03	0.40
60:SL:13:GLN:HE22	60:SL:35:ARG:NH1	2.19	0.40
65:SR:7:LYS:HB2	65:SR:7:LYS:HE2	1.91	0.40
74:Sa:90:GLU:N	74:Sa:90:GLU:CD	2.79	0.40
2:L5:158:A:H5''	2:L5:159:C:H2'	2.03	0.40
2:L5:421:C:H2'	2:L5:422:G:C8	2.57	0.40
2:L5:1768:G:C2	2:L5:1769:C:H5	2.39	0.40
2:L5:3838:G:OP1	5:LA:2:GLY:HA3	2.21	0.40
2:L5:4230:U:H2'	2:L5:4231:G:C8	2.56	0.40
2:L5:4424:G:H1	2:L5:4510:U:H3	1.68	0.40
16:LN:44:ARG:NH1	16:LN:47:LYS:HG2	2.36	0.40
17:LO:37:ARG:HD2	17:LO:108:ILE:HD11	2.03	0.40
17:LO:64:THR:HG21	80:LB:261:ARG:HB2	2.02	0.40
27:LY:112:ASP:C	27:LY:112:ASP:OD2	2.64	0.40
28:LZ:112:ARG:O	28:LZ:116:VAL:HG23	2.22	0.40
45:Lr:108:MET:HG3	45:Lr:112:ARG:HE	1.87	0.40
46:S2:433:G:H2'	46:S2:434:A:C8	2.56	0.40
46:S2:564:G:O2'	46:S2:565:A:H8	2.04	0.40
46:S2:1102:U:H2'	46:S2:1103:G:C8	2.56	0.40
46:S2:1522:C:P	66:SS:124:ARG:HH22	2.44	0.40
46:S2:1652:A:H2'	46:S2:1653:G:C8	2.56	0.40
49:SA:5:LEU:O	49:SA:9:GLN:HG2	2.21	0.40
63:SP:81:ARG:HD2	63:SP:97:TYR:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SV:74:LYS:HG3	69:SV:79:ILE:HG22	2.02	0.40
80:LB:190:VAL:HA	80:LB:193:LYS:HD2	2.02	0.40
2:L5:1631:C:H2'	2:L5:1632:G:H8	1.86	0.40
2:L5:2031:C:H2'	2:L5:2032:G:H8	1.86	0.40
2:L5:3960:A:H4'	19:LQ:186:TYR:CG	2.56	0.40
2:L5:4572:C:H3'	2:L5:4573:G:N2	2.36	0.40
14:LL:23:ASP:OD1	16:LN:199:GLN:HA	2.21	0.40
17:LO:110:PRO:HA	17:LO:113:ASP:OD2	2.21	0.40
25:LW:2:LYS:HA	25:LW:2:LYS:HD2	1.97	0.40
28:LZ:16:GLY:O	35:Lg:76:ARG:HG3	2.22	0.40
33:Le:77:PHE:CD2	33:Le:88:LEU:HD11	2.57	0.40
46:S2:393:A:H1'	60:SL:83:GLN:HE21	1.86	0.40
52:SD:126:ILE:HG21	52:SD:134:CYS:SG	2.61	0.40
55:SG:69:THR:O	55:SG:99:GLY:HA3	2.21	0.40
64:SQ:90:LYS:HE2	64:SQ:90:LYS:HB3	1.75	0.40
72:SY:7:ILE:HD11	72:SY:27:VAL:HG12	2.02	0.40
74:Sa:36:ILE:HD11	74:Sa:73:TYR:HB2	2.04	0.40
75:Sb:40:CYS:HB3	75:Sb:42:LYS:HG3	2.03	0.40
79:Sg:252:THR:HG21	79:Sg:257:LYS:HG3	2.03	0.40
2:L5:443:G:H2'	2:L5:444:U:C6	2.56	0.40
2:L5:481:G:H2'	2:L5:486:C:C6	2.55	0.40
2:L5:871:U:H4'	2:L5:872:C:H6	1.86	0.40
2:L5:1123:C:H2'	2:L5:1124:C:C6	2.57	0.40
2:L5:1374:A:H2'	2:L5:1375:G:H8	1.86	0.40
2:L5:1535:C:H2'	2:L5:1536:G:C8	2.57	0.40
2:L5:1650:C:H2'	2:L5:1651:C:C6	2.57	0.40
2:L5:2359:G:H2'	2:L5:2360:G:C8	2.56	0.40
2:L5:3573:G:H2'	2:L5:3574:A:C8	2.56	0.40
2:L5:4369:C:H5''	80:LB:276:HIS:O	2.21	0.40
2:L5:4423:G:H2'	2:L5:4424:G:H8	1.85	0.40
2:L5:4714:U:H2'	2:L5:4715:U:C6	2.57	0.40
21:LS:21:LYS:C	21:LS:21:LYS:HD2	2.47	0.40
46:S2:12:U:H2'	46:S2:13:C:H6	1.87	0.40
46:S2:596:U:H2'	46:S2:597:U:C6	2.56	0.40
52:SD:135:GLU:HG3	52:SD:153:VAL:HG22	2.03	0.40
60:SL:5:GLN:OE1	60:SL:11:GLN:HG2	2.22	0.40
64:SQ:34:VAL:HG12	64:SQ:70:VAL:HB	2.03	0.40
67:ST:66:LEU:HD23	67:ST:66:LEU:HA	1.82	0.40
79:Sg:230:LEU:HD23	79:Sg:231:ASP:O	2.21	0.40
80:LB:47:LEU:HG	80:LB:181:MET:HE2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
5	LA	246/257 (96%)	228 (93%)	18 (7%)	0	100	100
6	LC	356/419 (85%)	338 (95%)	18 (5%)	0	100	100
7	LD	291/297 (98%)	284 (98%)	7 (2%)	0	100	100
8	LE	210/296 (71%)	193 (92%)	17 (8%)	0	100	100
9	LF	212/270 (78%)	205 (97%)	6 (3%)	1 (0%)	24	54
10	LG	220/266 (83%)	215 (98%)	5 (2%)	0	100	100
11	LH	188/192 (98%)	177 (94%)	10 (5%)	1 (0%)	24	54
12	LI	197/214 (92%)	193 (98%)	4 (2%)	0	100	100
13	LJ	166/178 (93%)	147 (89%)	16 (10%)	3 (2%)	6	25
14	LL	203/211 (96%)	192 (95%)	11 (5%)	0	100	100
15	LM	134/217 (62%)	125 (93%)	9 (7%)	0	100	100
16	LN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
17	LO	199/203 (98%)	189 (95%)	10 (5%)	0	100	100
18	LP	150/184 (82%)	142 (95%)	8 (5%)	0	100	100
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	176/196 (90%)	166 (94%)	10 (6%)	0	100	100
21	LS	173/176 (98%)	165 (95%)	8 (5%)	0	100	100
22	LT	158/160 (99%)	150 (95%)	8 (5%)	0	100	100
23	LU	98/128 (77%)	86 (88%)	12 (12%)	0	100	100
24	LV	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
25	LW	60/157 (38%)	58 (97%)	2 (3%)	0	100	100
26	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
27	LY	129/145 (89%)	127 (98%)	2 (2%)	0	100	100
28	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	Lb	93/160 (58%)	90 (97%)	3 (3%)	0	100	100
31	Lc	92/115 (80%)	91 (99%)	1 (1%)	0	100	100
32	Ld	104/125 (83%)	100 (96%)	4 (4%)	0	100	100
33	Le	126/135 (93%)	121 (96%)	5 (4%)	0	100	100
34	Lf	107/110 (97%)	102 (95%)	4 (4%)	1 (1%)	14	41
35	Lg	109/117 (93%)	108 (99%)	1 (1%)	0	100	100
36	Lh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	96 (96%)	3 (3%)	1 (1%)	12	39
38	Lj	84/97 (87%)	76 (90%)	8 (10%)	0	100	100
39	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	48/128 (38%)	46 (96%)	2 (4%)	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Lr	121/137 (88%)	118 (98%)	3 (2%)	0	100	100
49	SA	206/295 (70%)	198 (96%)	8 (4%)	0	100	100
50	SB	210/264 (80%)	208 (99%)	2 (1%)	0	100	100
51	SC	218/293 (74%)	206 (94%)	12 (6%)	0	100	100
52	SD	220/243 (90%)	209 (95%)	11 (5%)	0	100	100
53	SE	256/263 (97%)	242 (94%)	14 (6%)	0	100	100
54	SF	175/204 (86%)	160 (91%)	15 (9%)	0	100	100
55	SG	218/249 (88%)	201 (92%)	16 (7%)	1 (0%)	24	54
56	SH	179/194 (92%)	162 (90%)	17 (10%)	0	100	100
57	SI	200/208 (96%)	182 (91%)	18 (9%)	0	100	100
58	SJ	151/194 (78%)	137 (91%)	14 (9%)	0	100	100
59	SK	94/165 (57%)	81 (86%)	11 (12%)	2 (2%)	5	21
60	SL	130/158 (82%)	117 (90%)	13 (10%)	0	100	100
61	SN	148/151 (98%)	146 (99%)	1 (1%)	1 (1%)	18	48
62	SO	132/151 (87%)	119 (90%)	13 (10%)	0	100	100
63	SP	122/145 (84%)	119 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	SQ	137/146 (94%)	127 (93%)	10 (7%)	0	100	100
65	SR	129/135 (96%)	118 (92%)	11 (8%)	0	100	100
66	SS	138/152 (91%)	135 (98%)	3 (2%)	0	100	100
67	ST	138/145 (95%)	131 (95%)	7 (5%)	0	100	100
68	SU	96/119 (81%)	93 (97%)	3 (3%)	0	100	100
69	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
70	SW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
71	SX	137/143 (96%)	133 (97%)	4 (3%)	0	100	100
72	SY	117/133 (88%)	114 (97%)	3 (3%)	0	100	100
73	SZ	70/125 (56%)	66 (94%)	4 (6%)	0	100	100
74	Sa	97/115 (84%)	93 (96%)	4 (4%)	0	100	100
75	Sb	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
76	Sc	60/69 (87%)	53 (88%)	7 (12%)	0	100	100
77	Sd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
78	Se	45/133 (34%)	45 (100%)	0	0	100	100
79	Sg	285/317 (90%)	253 (89%)	31 (11%)	1 (0%)	30	59
80	LB	395/403 (98%)	373 (94%)	21 (5%)	1 (0%)	36	65
All	All	10748/12499 (86%)	10172 (95%)	563 (5%)	13 (0%)	49	77

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
55	SG	152	ASP
59	SK	87	PRO
80	LB	140	ASP
11	LH	13	PRO
13	LJ	78	LYS
61	SN	146	ALA
13	LJ	118	LYS
37	Li	3	LEU
34	Lf	5	LEU
59	SK	86	PRO
13	LJ	174	ILE
9	LF	219	VAL
79	Sg	201	SER

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	
5	LA	190/199 (96%)	190 (100%)	0	100	100
6	LC	301/348 (86%)	300 (100%)	1 (0%)	86	96
7	LD	246/249 (99%)	245 (100%)	1 (0%)	84	94
8	LE	194/256 (76%)	194 (100%)	0	100	100
9	LF	185/234 (79%)	185 (100%)	0	100	100
10	LG	193/223 (86%)	191 (99%)	2 (1%)	68	89
11	LH	169/171 (99%)	167 (99%)	2 (1%)	63	86
12	LI	171/181 (94%)	171 (100%)	0	100	100
13	LJ	142/149 (95%)	140 (99%)	2 (1%)	59	85
14	LL	172/178 (97%)	171 (99%)	1 (1%)	78	93
15	LM	116/157 (74%)	115 (99%)	1 (1%)	70	90
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	172/173 (99%)	171 (99%)	1 (1%)	78	93
18	LP	133/163 (82%)	132 (99%)	1 (1%)	73	90
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	157/175 (90%)	154 (98%)	3 (2%)	50	79
21	LS	155/156 (99%)	152 (98%)	3 (2%)	50	79
22	LT	140/140 (100%)	140 (100%)	0	100	100
23	LU	90/114 (79%)	88 (98%)	2 (2%)	45	77
24	LV	100/107 (94%)	100 (100%)	0	100	100
25	LW	54/126 (43%)	54 (100%)	0	100	100
26	LX	106/133 (80%)	105 (99%)	1 (1%)	70	90
27	LY	122/135 (90%)	121 (99%)	1 (1%)	73	90
28	LZ	117/118 (99%)	115 (98%)	2 (2%)	53	82
29	La	120/121 (99%)	116 (97%)	4 (3%)	33	67
30	Lb	82/124 (66%)	80 (98%)	2 (2%)	43	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	Lc	79/97 (81%)	79 (100%)	0	100	100
32	Ld	97/110 (88%)	96 (99%)	1 (1%)	68	89
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	94/100 (94%)	94 (100%)	0	100	100
36	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	90
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	46 (98%)	1 (2%)	47	77
41	Lm	46/116 (40%)	46 (100%)	0	100	100
42	Ln	24/24 (100%)	24 (100%)	0	100	100
43	Lo	91/94 (97%)	91 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	107/121 (88%)	107 (100%)	0	100	100
49	SA	174/242 (72%)	171 (98%)	3 (2%)	53	82
50	SB	193/229 (84%)	192 (100%)	1 (0%)	81	93
51	SC	181/224 (81%)	178 (98%)	3 (2%)	53	82
52	SD	186/202 (92%)	186 (100%)	0	100	100
53	SE	221/225 (98%)	218 (99%)	3 (1%)	59	85
54	SF	152/170 (89%)	145 (95%)	7 (5%)	24	57
55	SG	178/218 (82%)	176 (99%)	2 (1%)	65	88
56	SH	159/174 (91%)	157 (99%)	2 (1%)	61	86
57	SI	159/180 (88%)	157 (99%)	2 (1%)	61	86
58	SJ	130/168 (77%)	129 (99%)	1 (1%)	73	90
59	SK	80/136 (59%)	79 (99%)	1 (1%)	61	86
60	SL	123/142 (87%)	122 (99%)	1 (1%)	73	90
61	SN	130/131 (99%)	128 (98%)	2 (2%)	57	84
62	SO	104/119 (87%)	103 (99%)	1 (1%)	68	89
63	SP	105/130 (81%)	103 (98%)	2 (2%)	50	79
64	SQ	115/121 (95%)	113 (98%)	2 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	SR	119/121 (98%)	116 (98%)	3 (2%)	42	74
66	SS	122/132 (92%)	118 (97%)	4 (3%)	33	67
67	ST	110/115 (96%)	110 (100%)	0	100	100
68	SU	91/107 (85%)	87 (96%)	4 (4%)	25	59
69	SV	67/67 (100%)	65 (97%)	2 (3%)	36	70
70	SW	112/113 (99%)	110 (98%)	2 (2%)	51	80
71	SX	111/115 (96%)	109 (98%)	2 (2%)	51	80
72	SY	104/115 (90%)	103 (99%)	1 (1%)	68	89
73	SZ	64/103 (62%)	62 (97%)	2 (3%)	35	69
74	Sa	87/99 (88%)	83 (95%)	4 (5%)	24	57
75	Sb	75/76 (99%)	75 (100%)	0	100	100
76	Sc	47/62 (76%)	47 (100%)	0	100	100
77	Sd	47/49 (96%)	46 (98%)	1 (2%)	47	77
78	Se	37/106 (35%)	37 (100%)	0	100	100
79	Sg	250/275 (91%)	247 (99%)	3 (1%)	63	86
80	LB	344/348 (99%)	344 (100%)	0	100	100
All	All	9332/10620 (88%)	9238 (99%)	94 (1%)	65	89

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	LC	50	GLN
7	LD	235	MET
10	LG	54	PHE
10	LG	96	LEU
11	LH	11	ASP
11	LH	16	VAL
13	LJ	12	MET
13	LJ	70	VAL
14	LL	144	LEU
15	LM	135	ILE
17	LO	129	LEU
18	LP	125	MET
20	LR	3	MET
20	LR	140	GLU
20	LR	158	GLN

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Mol	Chain	Res	Type
21	LS	9	GLU
21	LS	69	GLU
21	LS	162	GLN
23	LU	30	GLU
23	LU	83	LEU
26	LX	91	GLU
27	LY	127	GLN
28	LZ	100	VAL
28	LZ	126	LYS
29	La	38	MET
29	La	68	SER
29	La	97	VAL
29	La	134	GLU
30	Lb	99	HIS
30	Lb	116	LEU
32	Ld	29	ILE
36	Lh	111	GLU
40	Li	27	ILE
49	SA	81	ASN
49	SA	113	GLN
49	SA	174	MET
50	SB	105	LEU
51	SC	120	GLN
51	SC	162	ILE
51	SC	216	MET
53	SE	19	MET
53	SE	112	HIS
53	SE	236	ILE
54	SF	37	ASP
54	SF	44	LYS
54	SF	69	VAL
54	SF	87	LEU
54	SF	88	MET
54	SF	106	GLU
54	SF	154	LEU
55	SG	1	MET
55	SG	199	THR
56	SH	40	LEU
56	SH	165	ASN
57	SI	160	SER
57	SI	193	LYS
58	SJ	97	ILE

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Mol	Chain	Res	Type
59	SK	21	MET
60	SL	40	ILE
61	SN	105	ASN
61	SN	119	GLU
62	SO	114	SER
63	SP	85	ILE
63	SP	86	LEU
64	SQ	60	LYS
64	SQ	114	GLN
65	SR	109	LEU
65	SR	117	LEU
65	SR	123	THR
66	SS	13	LEU
66	SS	26	ILE
66	SS	47	LYS
66	SS	107	LEU
68	SU	20	ILE
68	SU	22	ILE
68	SU	39	LEU
68	SU	56	MET
69	SV	10	ASP
69	SV	67	ASP
70	SW	6	VAL
70	SW	97	ARG
71	SX	99	GLU
71	SX	112	VAL
72	SY	74	MET
73	SZ	58	LEU
73	SZ	96	LEU
74	Sa	25	ASN
74	Sa	67	LEU
74	Sa	69	VAL
74	Sa	71	LEU
77	Sd	22	ARG
79	Sg	11	LEU
79	Sg	79	LEU
79	Sg	154	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
5	LA	22	HIS

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Mol	Chain	Res	Type
5	LA	83	HIS
5	LA	194	ASN
6	LC	41	HIS
6	LC	43	ASN
6	LC	215	ASN
6	LC	310	HIS
6	LC	329	ASN
7	LD	17	GLN
7	LD	131	ASN
7	LD	195	HIS
7	LD	202	GLN
8	LE	190	ASN
9	LF	263	ASN
9	LF	270	ASN
10	LG	46	GLN
10	LG	82	GLN
10	LG	100	HIS
10	LG	153	GLN
10	LG	206	GLN
10	LG	208	ASN
10	LG	225	ASN
11	LH	98	HIS
12	LI	73	ASN
12	LI	130	HIS
12	LI	147	HIS
13	LJ	71	HIS
13	LJ	167	GLN
14	LL	87	HIS
15	LM	20	HIS
15	LM	48	GLN
17	LO	42	ASN
19	LQ	125	GLN
20	LR	134	ASN
21	LS	144	GLN
23	LU	27	HIS
26	LX	111	GLN
29	La	19	HIS
30	Lb	6	ASN
30	Lb	12	GLN
31	Lc	51	ASN
32	Ld	18	ASN
32	Ld	34	HIS

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Mol	Chain	Res	Type
33	Le	57	ASN
33	Le	80	HIS
34	Lf	24	HIS
34	Lf	55	ASN
34	Lf	91	ASN
36	Lh	65	GLN
36	Lh	98	HIS
38	Lj	76	HIS
45	Lr	4	HIS
49	SA	81	ASN
49	SA	169	HIS
51	SC	120	GLN
52	SD	57	ASN
52	SD	101	GLN
53	SE	50	ASN
53	SE	67	GLN
53	SE	142	HIS
53	SE	161	GLN
54	SF	82	ASN
54	SF	95	HIS
54	SF	165	ASN
55	SG	56	ASN
55	SG	177	GLN
56	SH	39	GLN
56	SH	68	GLN
56	SH	157	HIS
56	SH	162	GLN
56	SH	165	ASN
56	SH	186	ASN
57	SI	165	GLN
59	SK	32	HIS
60	SL	83	GLN
60	SL	100	ASN
62	SO	103	ASN
63	SP	79	HIS
64	SQ	11	GLN
64	SQ	35	ASN
66	SS	73	ASN
66	SS	85	ASN
66	SS	134	GLN
69	SV	35	ASN
71	SX	16	HIS

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Mol	Chain	Res	Type
72	SY	106	GLN
73	SZ	46	ASN
77	Sd	4	GLN
79	Sg	20	GLN
79	Sg	187	ASN
79	Sg	305	ASN
80	LB	123	HIS
80	LB	145	GLN
80	LB	167	GLN
80	LB	175	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	9/10 (90%)	9 (100%)	1 (11%)
2	L5	3424/4731 (72%)	445 (12%)	7 (0%)
3	L7	119/120 (99%)	6 (5%)	0
4	L8	155/158 (98%)	22 (14%)	0
46	S2	1637/1870 (87%)	246 (15%)	3 (0%)
47	S6	74/75 (98%)	15 (20%)	2 (2%)
48	S7	73/75 (97%)	21 (28%)	0
All	All	5491/7039 (78%)	764 (13%)	13 (0%)

All (764) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	-2	U
1	B	-1	U
1	B	0	U
1	B	1	U
1	B	2	U
1	B	3	U
1	B	4	A
1	B	5	A
1	B	6	A
2	L5	21	G
2	L5	39	A
2	L5	42	A
2	L5	48	G
2	L5	56	A
2	L5	59	A

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Mol	Chain	Res	Type
2	L5	64	A
2	L5	65	A
2	L5	73	A
2	L5	91	G
2	L5	109	G
2	L5	110	C
2	L5	119	G
2	L5	120	A
2	L5	134	G
2	L5	136	C
2	L5	143	U
2	L5	144	G
2	L5	151	G
2	L5	159	C
2	L5	166	C
2	L5	171	U
2	L5	172	C
2	L5	200	U
2	L5	218	A
2	L5	220	C
2	L5	233	U
2	L5	246	G
2	L5	258	C
2	L5	263	C
2	L5	266	G
2	L5	279	G
2	L5	305	A
2	L5	309	G
2	L5	339	C
2	L5	362	A
2	L5	372	G
2	L5	386	G
2	L5	410	G
2	L5	411	G
2	L5	412	G
2	L5	432	A
2	L5	448	C
2	L5	449	G
2	L5	451	A
2	L5	452	G
2	L5	495	C
2	L5	513	U

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Mol	Chain	Res	Type
2	L5	651	C
2	L5	652	G
2	L5	673	C
2	L5	674	G
2	L5	675	A
2	L5	676	C
2	L5	677	C
2	L5	693	C
2	L5	704	U
2	L5	705	G
2	L5	711	G
2	L5	712	C
2	L5	739	G
2	L5	747	G
2	L5	748	G
2	L5	749	U
2	L5	750	G
2	L5	767	G
2	L5	768	G
2	L5	770	G
2	L5	813	U
2	L5	815	A
2	L5	817	A
2	L5	831	G
2	L5	833	U
2	L5	841	A
2	L5	842	A
2	L5	843	U
2	L5	854	A
2	L5	857	A
2	L5	858	A
2	L5	859	G
2	L5	860	C
2	L5	882	U
2	L5	886	U
2	L5	888	U
2	L5	924	G
2	L5	927	C
2	L5	928	C
2	L5	1001	G
2	L5	1005	C
2	L5	1006	G

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Mol	Chain	Res	Type
2	L5	1012	U
2	L5	1014	C
2	L5	1029	G
2	L5	1032	U
2	L5	1033	G
2	L5	1036	C
2	L5	1037	G
2	L5	1045	G
2	L5	1048	U
2	L5	1049	C
2	L5	1050	C
2	L5	1055	G
2	L5	1071	C
2	L5	1072	G
2	L5	1089	A
2	L5	1098	G
2	L5	1099	G
2	L5	1102	G
2	L5	1109	A
2	L5	1110	U
2	L5	1141	A
2	L5	1169	A
2	L5	1174	G
2	L5	1192	G
2	L5	1194	C
2	L5	1202	A
2	L5	1209	G
2	L5	1214	G
2	L5	1217	C
2	L5	1218	C
2	L5	1228	G
2	L5	1230	C
2	L5	1232	C
2	L5	1233	G
2	L5	1234	A
2	L5	1235	G
2	L5	1298	G
2	L5	1299	C
2	L5	1312	G
2	L5	1315	G
2	L5	1316	G
2	L5	1348	A

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Mol	Chain	Res	Type
2	L5	1361	A
2	L5	1379	A
2	L5	1380	C
2	L5	1388	G
2	L5	1389	A
2	L5	1392	U
2	L5	1405	U
2	L5	1410	U
2	L5	1414	A
2	L5	1415	A
2	L5	1438	G
2	L5	1445	A
2	L5	1447	G
2	L5	1448	A
2	L5	1452	A
2	L5	1455	G
2	L5	1468	G
2	L5	1475	C
2	L5	1490	C
2	L5	1491	U
2	L5	1494	G
2	L5	1505	G
2	L5	1564	G
2	L5	1565	C
2	L5	1590	A
2	L5	1607	A
2	L5	1624	G
2	L5	1625	U
2	L5	1639	G
2	L5	1640	A
2	L5	1645	G
2	L5	1657	G
2	L5	1658	G
2	L5	1672	G
2	L5	1700	A
2	L5	1721	U
2	L5	1722	G
2	L5	1723	C
2	L5	1724	C
2	L5	1725	G
2	L5	1734	C
2	L5	1735	A

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Mol	Chain	Res	Type
2	L5	1751	G
2	L5	1763	A
2	L5	1764	G
2	L5	1765	A
2	L5	1770	A
2	L5	1773	A
2	L5	1777	U
2	L5	1778	G
2	L5	1779	G
2	L5	1781	C
2	L5	1796	C
2	L5	1798	G
2	L5	1802	A
2	L5	1806	G
2	L5	1821	C
2	L5	1828	A
2	L5	1829	A
2	L5	1837	G
2	L5	1849	G
2	L5	1851	U
2	L5	1858	G
2	L5	1859	G
2	L5	1872	A
2	L5	1874	A
2	L5	1887	C
2	L5	1892	G
2	L5	1894	C
2	L5	2046	C
2	L5	2057	A
2	L5	2058	G
2	L5	2063	G
2	L5	2070	A
2	L5	2088	G
2	L5	2090	G
2	L5	2102	G
2	L5	2105	G
2	L5	2108	C
2	L5	2117	A
2	L5	2153	A
2	L5	2154	G
2	L5	2178	G
2	L5	2179	C

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Mol	Chain	Res	Type
2	L5	2182	U
2	L5	2194	C
2	L5	2222	C
2	L5	2228	G
2	L5	2231	G
2	L5	2232	G
2	L5	2242	U
2	L5	2243	G
2	L5	2245	C
2	L5	2246	C
2	L5	2247	U
2	L5	2260	G
2	L5	2269	A
2	L5	2270	A
2	L5	2271	G
2	L5	2277	C
2	L5	2301	G
2	L5	2303	G
2	L5	2318	C
2	L5	2319	G
2	L5	2321	G
2	L5	2323	G
2	L5	2337	C
2	L5	2341	A
2	L5	2343	C
2	L5	2356	G
2	L5	2392	G
2	L5	2406	G
2	L5	2416	G
2	L5	2423	C
2	L5	2429	G
2	L5	2441	U
2	L5	2448	G
2	L5	2449	A
2	L5	2450	A
2	L5	2463	C
2	L5	2464	C
2	L5	2465	G
2	L5	2480	G
2	L5	2481	C
2	L5	2493	C
2	L5	2497	A

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Mol	Chain	Res	Type
2	L5	2514	G
2	L5	2515	U
2	L5	2517	U
2	L5	2518	A
2	L5	2523	U
2	L5	2524	C
2	L5	2542	U
2	L5	2544	U
2	L5	2545	C
2	L5	2550	G
2	L5	2553	G
2	L5	2568	C
2	L5	2580	U
2	L5	2581	G
2	L5	2583	U
2	L5	2609	G
2	L5	3254	G
2	L5	3272	G
2	L5	3282	G
2	L5	3283	G
2	L5	3292	A
2	L5	3303	A
2	L5	3310	A
2	L5	3319	A
2	L5	3330	C
2	L5	3349	A
2	L5	3358	C
2	L5	3368	A
2	L5	3369	A
2	L5	3370	U
2	L5	3394	A
2	L5	3410	G
2	L5	3416	A
2	L5	3417	A
2	L5	3418	C
2	L5	3429	U
2	L5	3431	A
2	L5	3434	G
2	L5	3443	U
2	L5	3446	C
2	L5	3447	U
2	L5	3448	C

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Mol	Chain	Res	Type
2	L5	3449	G
2	L5	3459	U
2	L5	3468	G
2	L5	3471	U
2	L5	3474	A
2	L5	3475	U
2	L5	3476	G
2	L5	3496	G
2	L5	3497	U
2	L5	3524	A
2	L5	3534	A
2	L5	3535	C
2	L5	3536	G
2	L5	3544	C
2	L5	3554	G
2	L5	3558	A
2	L5	3563	A
2	L5	3564	G
2	L5	3565	A
2	L5	3572	U
2	L5	3605	C
2	L5	3606	A
2	L5	3608	G
2	L5	3712	C
2	L5	3715	C
2	L5	3716	G
2	L5	3727	G
2	L5	3735	G
2	L5	3737	G
2	L5	3739	C
2	L5	3743	G
2	L5	3747	C
2	L5	3748	G
2	L5	3750	G
2	L5	3758	G
2	L5	3759	G
2	L5	3765	C
2	L5	3766	G
2	L5	3767	C
2	L5	3770	C
2	L5	3773	G
2	L5	3778	A

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Mol	Chain	Res	Type
2	L5	3815	C
2	L5	3816	U
2	L5	3823	A
2	L5	3836	G
2	L5	3837	G
2	L5	3844	G
2	L5	3849	G
2	L5	3856	A
2	L5	3882	U
2	L5	3886	A
2	L5	3887	A
2	L5	3904	A
2	L5	3907	G
2	L5	3918	U
2	L5	3919	G
2	L5	3926	A
2	L5	3934	A
2	L5	3944	G
2	L5	3958	G
2	L5	3959	U
2	L5	3982	G
2	L5	3983	G
2	L5	3985	C
2	L5	3992	A
2	L5	4007	U
2	L5	4030	G
2	L5	4031	A
2	L5	4040	C
2	L5	4047	A
2	L5	4075	A
2	L5	4101	G
2	L5	4102	A
2	L5	4117	A
2	L5	4119	C
2	L5	4165	U
2	L5	4166	A
2	L5	4171	A
2	L5	4172	C
2	L5	4176	A
2	L5	4177	G
2	L5	4198	G
2	L5	4202	G

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Mol	Chain	Res	Type
2	L5	4208	U
2	L5	4213	C
2	L5	4228	G
2	L5	4242	A
2	L5	4243	A
2	L5	4289	U
2	L5	4290	G
2	L5	4309	A
2	L5	4323	C
2	L5	4324	C
2	L5	4325	A
2	L5	4353	A
2	L5	4361	A
2	L5	4362	U
2	L5	4372	G
2	L5	4383	C
2	L5	4385	G
2	L5	4386	C
2	L5	4387	A
2	L5	4393	G
2	L5	4394	A
2	L5	4395	A
2	L5	4396	G
2	L5	4408	G
2	L5	4411	C
2	L5	4413	C
2	L5	4415	G
2	L5	4419	G
2	L5	4426	C
2	L5	4516	G
2	L5	4517	C
2	L5	4523	G
2	L5	4528	U
2	L5	4529	C
2	L5	4541	C
2	L5	4547	G
2	L5	4549	G
2	L5	4556	A
2	L5	4558	G
2	L5	4560	C
2	L5	4561	G
2	L5	4562	G

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Mol	Chain	Res	Type
2	L5	4571	U
2	L5	4579	C
2	L5	4583	U
2	L5	4589	G
2	L5	4591	A
2	L5	4593	G
2	L5	4624	U
2	L5	4636	U
2	L5	4639	U
2	L5	4662	A
2	L5	4665	G
2	L5	4675	C
2	L5	4678	U
2	L5	4682	A
2	L5	4689	G
2	L5	4698	C
2	L5	4709	A
2	L5	4710	G
2	L5	4717	U
3	L7	11	A
3	L7	22	A
3	L7	41	G
3	L7	64	G
3	L7	100	A
3	L7	110	G
4	L8	2	G
4	L8	23	C
4	L8	34	U
4	L8	35	C
4	L8	39	G
4	L8	59	A
4	L8	62	A
4	L8	63	U
4	L8	82	A
4	L8	85	U
4	L8	86	U
4	L8	87	G
4	L8	94	G
4	L8	103	A
4	L8	105	C
4	L8	110	U
4	L8	111	U

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Mol	Chain	Res	Type
4	L8	114	G
4	L8	124	U
4	L8	125	C
4	L8	126	C
4	L8	150	C
46	S2	17	C
46	S2	26	U
46	S2	33	G
46	S2	41	G
46	S2	44	U
46	S2	46	A
46	S2	56	G
46	S2	66	G
46	S2	67	C
46	S2	68	A
46	S2	71	G
46	S2	73	C
46	S2	74	G
46	S2	75	G
46	S2	76	U
46	S2	92	A
46	S2	101	U
46	S2	102	A
46	S2	103	A
46	S2	113	G
46	S2	114	G
46	S2	115	U
46	S2	116	U
46	S2	126	G
46	S2	129	C
46	S2	143	U
46	S2	162	C
46	S2	168	C
46	S2	182	C
46	S2	183	G
46	S2	184	G
46	S2	185	G
46	S2	186	C
46	S2	306	U
46	S2	313	G
46	S2	320	C
46	S2	321	G

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Mol	Chain	Res	Type
46	S2	330	G
46	S2	357	C
46	S2	361	A
46	S2	363	C
46	S2	365	A
46	S2	369	U
46	S2	370	C
46	S2	371	G
46	S2	386	G
46	S2	387	C
46	S2	399	A
46	S2	408	G
46	S2	410	C
46	S2	448	A
46	S2	449	A
46	S2	451	C
46	S2	465	A
46	S2	467	G
46	S2	472	G
46	S2	473	C
46	S2	474	A
46	S2	475	G
46	S2	483	G
46	S2	488	U
46	S2	493	C
46	S2	497	C
46	S2	504	C
46	S2	508	G
46	S2	518	C
46	S2	530	A
46	S2	533	C
46	S2	542	U
46	S2	545	G
46	S2	547	G
46	S2	548	G
46	S2	549	C
46	S2	556	A
46	S2	558	U
46	S2	560	G
46	S2	562	A
46	S2	565	A
46	S2	588	A

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Mol	Chain	Res	Type
46	S2	589	G
46	S2	590	G
46	S2	592	U
46	S2	593	C
46	S2	605	A
46	S2	608	U
46	S2	609	C
46	S2	614	G
46	S2	629	A
46	S2	644	A
46	S2	645	G
46	S2	656	A
46	S2	661	C
46	S2	669	A
46	S2	670	A
46	S2	672	A
46	S2	673	A
46	S2	674	G
46	S2	685	G
46	S2	688	C
46	S2	689	U
46	S2	751	C
46	S2	798	C
46	S2	812	A
46	S2	822	G
46	S2	823	U
46	S2	831	A
46	S2	836	C
46	S2	837	G
46	S2	839	G
46	S2	840	C
46	S2	842	G
46	S2	843	C
46	S2	844	C
46	S2	845	U
46	S2	848	A
46	S2	870	A
46	S2	871	A
46	S2	874	G
46	S2	883	U
46	S2	890	U
46	S2	891	U

Continued on next page...

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Mol	Chain	Res	Type
46	S2	892	G
46	S2	895	G
46	S2	896	G
46	S2	897	U
46	S2	901	C
46	S2	902	G
46	S2	914	A
46	S2	921	A
46	S2	923	A
46	S2	934	G
46	S2	938	C
46	S2	962	G
46	S2	964	A
46	S2	991	A
46	S2	993	A
46	S2	1002	A
46	S2	1024	A
46	S2	1028	A
46	S2	1062	U
46	S2	1063	A
46	S2	1084	A
46	S2	1086	C
46	S2	1110	C
46	S2	1116	U
46	S2	1117	C
46	S2	1119	C
46	S2	1139	C
46	S2	1140	C
46	S2	1154	C
46	S2	1155	U
46	S2	1167	G
46	S2	1209	A
46	S2	1216	C
46	S2	1217	C
46	S2	1218	A
46	S2	1225	G
46	S2	1243	U
46	S2	1244	U
46	S2	1248	C
46	S2	1252	A
46	S2	1254	A
46	S2	1257	G

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Mol	Chain	Res	Type
46	S2	1258	G
46	S2	1275	G
46	S2	1276	G
46	S2	1286	G
46	S2	1287	G
46	S2	1302	A
46	S2	1303	G
46	S2	1304	C
46	S2	1305	U
46	S2	1314	A
46	S2	1331	G
46	S2	1372	U
46	S2	1373	U
46	S2	1379	A
46	S2	1398	U
46	S2	1399	G
46	S2	1421	G
46	S2	1422	A
46	S2	1424	C
46	S2	1425	G
46	S2	1448	G
46	S2	1455	A
46	S2	1465	C
46	S2	1475	A
46	S2	1488	A
46	S2	1490	A
46	S2	1491	G
46	S2	1495	U
46	S2	1496	G
46	S2	1498	G
46	S2	1499	A
46	S2	1508	G
46	S2	1509	A
46	S2	1522	C
46	S2	1532	A
46	S2	1534	A
46	S2	1537	G
46	S2	1557	A
46	S2	1559	C
46	S2	1571	G
46	S2	1580	A
46	S2	1581	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	S2	1586	U
46	S2	1589	A
46	S2	1602	A
46	S2	1605	G
46	S2	1611	G
46	S2	1619	C
46	S2	1622	U
46	S2	1624	A
46	S2	1638	A
46	S2	1642	A
46	S2	1644	U
46	S2	1647	C
46	S2	1649	G
46	S2	1666	G
46	S2	1681	G
46	S2	1684	C
46	S2	1699	C
46	S2	1722	U
46	S2	1753	C
46	S2	1756	C
46	S2	1762	U
46	S2	1773	C
46	S2	1774	C
46	S2	1775	C
46	S2	1776	U
46	S2	1777	G
46	S2	1784	C
46	S2	1785	G
46	S2	1787	U
46	S2	1815	G
46	S2	1816	A
46	S2	1817	G
46	S2	1825	A
46	S2	1836	A
46	S2	1839	U
46	S2	1850	G
46	S2	1852	A
46	S2	1862	G
46	S2	1863	G
46	S2	1864	A
46	S2	1866	C
47	S6	10	G

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Mol	Chain	Res	Type
47	S6	17	C
47	S6	18	G
47	S6	19	G
47	S6	22	G
47	S6	23	C
47	S6	30	G
47	S6	31	G
47	S6	48	C
47	S6	54	A
47	S6	55	U
47	S6	58	A
47	S6	67	U
47	S6	69	U
47	S6	76	A
48	S7	7	A
48	S7	9	U
48	S7	11	G
48	S7	18	G
48	S7	19	G
48	S7	20	A
48	S7	22	G
48	S7	30	G
48	S7	31	G
48	S7	33	C
48	S7	34	C
48	S7	36	U
48	S7	37	U
48	S7	38	A
48	S7	46	G
48	S7	47	U
48	S7	49	G
48	S7	59	A
48	S7	60	A
48	S7	74	C
48	S7	75	C

All (13) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	B	3	U
2	L5	219	G
2	L5	1388	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	L5	1447	G
2	L5	1836	A
2	L5	2516	G
2	L5	3271	G
2	L5	4352	U
46	S2	546	A
46	S2	1118	C
46	S2	1521	G
47	S6	22	G
47	S6	54	A

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](#)

Of 331 ligands modelled in this entry, 331 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	L5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	183:A	O3'	189:G	P	5.53

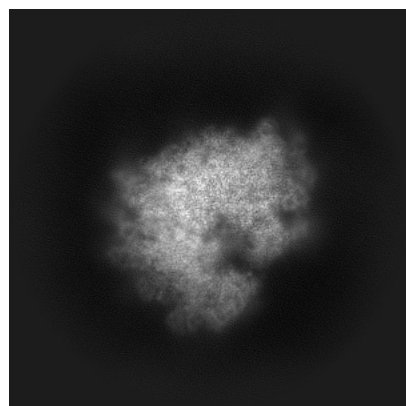
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55100. These allow visual inspection of the internal detail of the map and identification of artifacts.

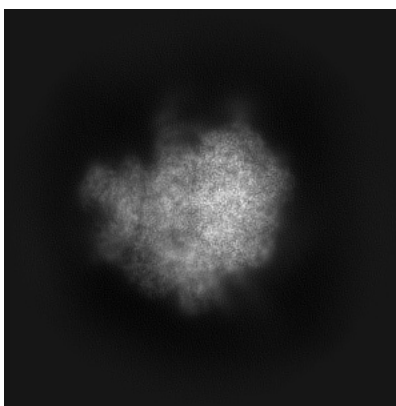
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

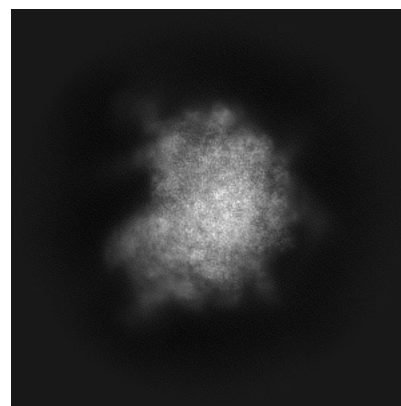
6.1.1 Primary map



X

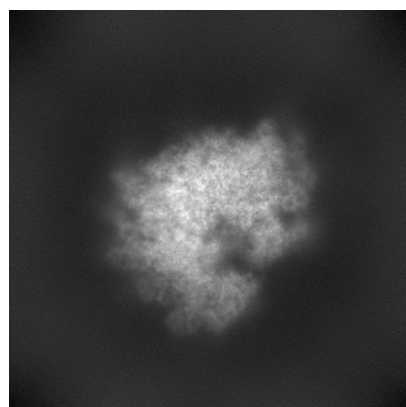


Y

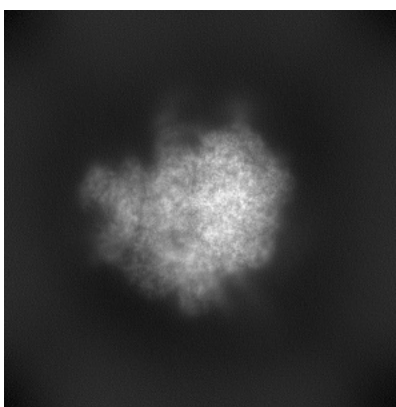


Z

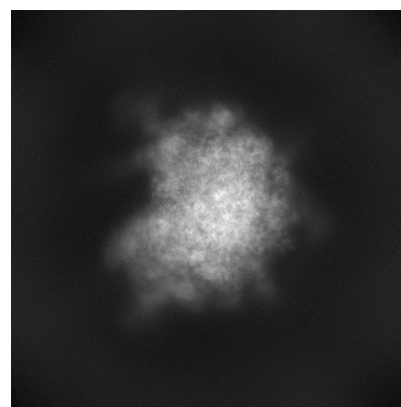
6.1.2 Raw map



X



Y

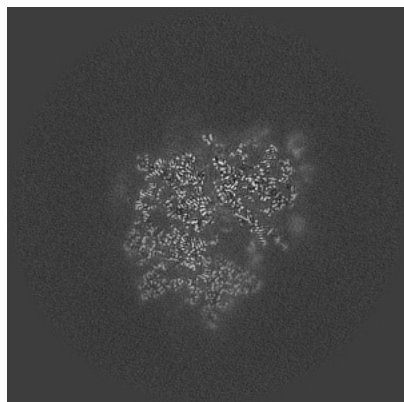


Z

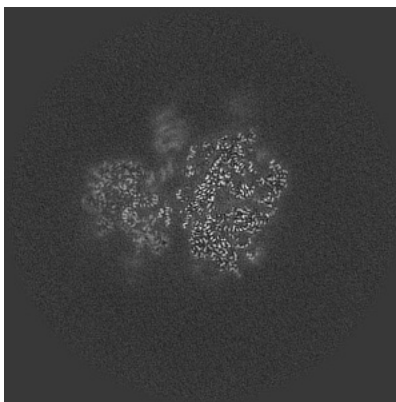
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

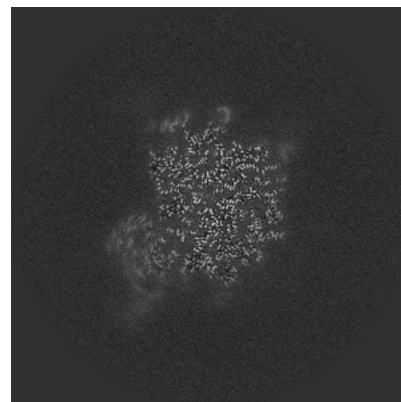
6.2.1 Primary map



X Index: 240

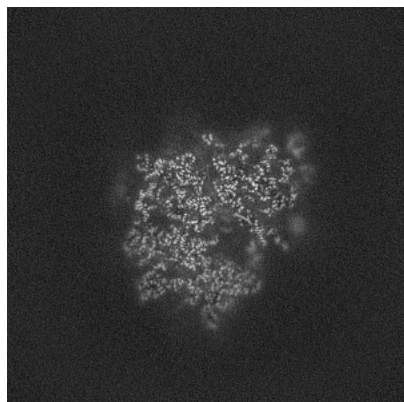


Y Index: 240

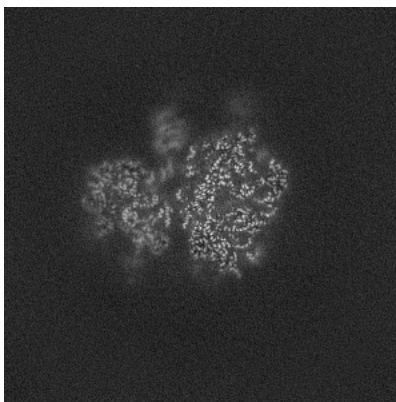


Z Index: 240

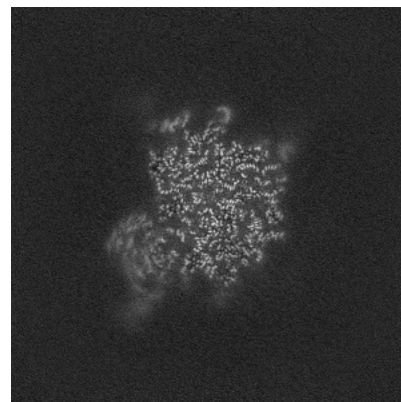
6.2.2 Raw map



X Index: 240



Y Index: 240

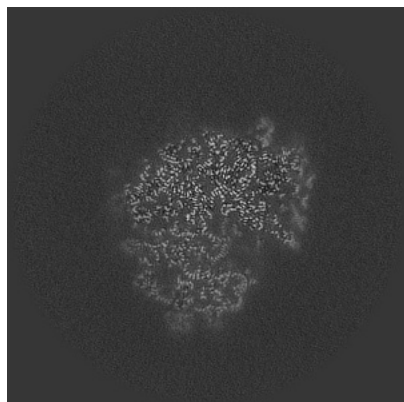


Z Index: 240

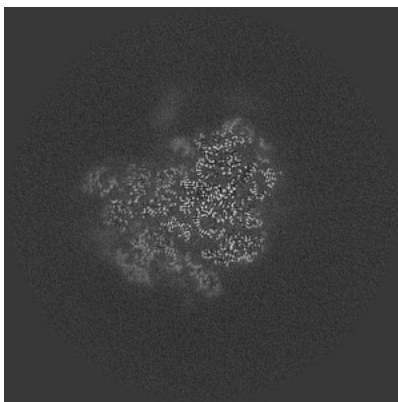
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

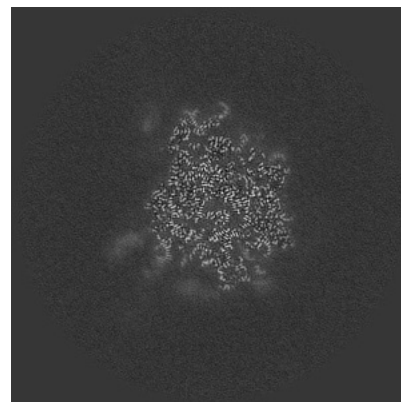
6.3.1 Primary map



X Index: 253

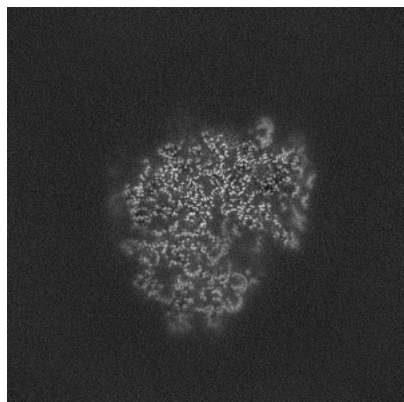


Y Index: 226

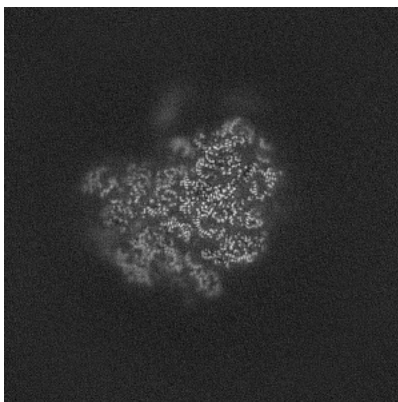


Z Index: 263

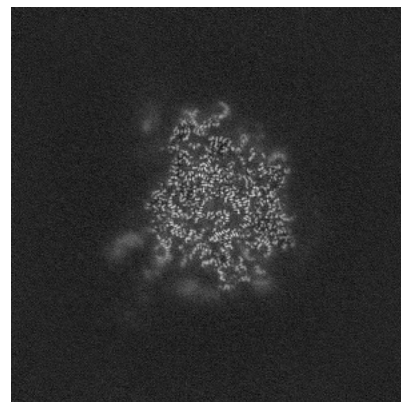
6.3.2 Raw map



X Index: 252



Y Index: 226

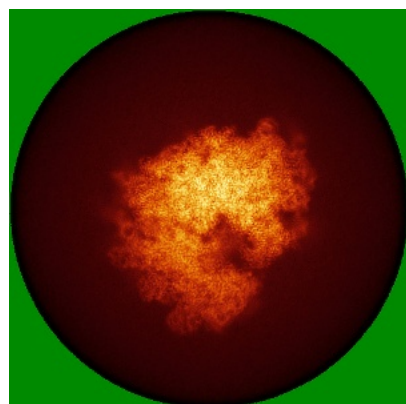


Z Index: 263

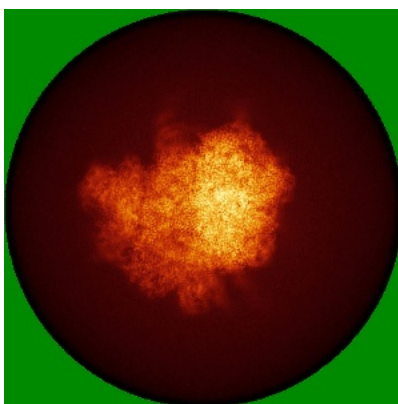
The images above show the largest variance slices of the map in three orthogonal directions.

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

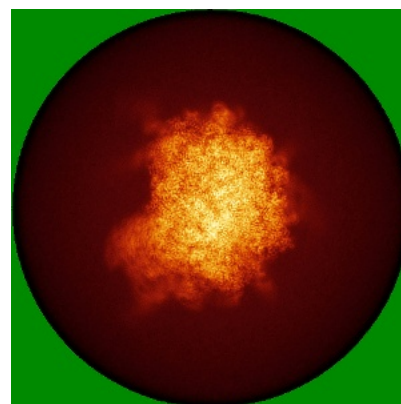
6.4.1 Primary map



X

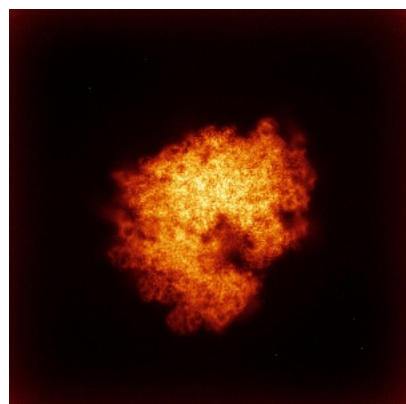


Y

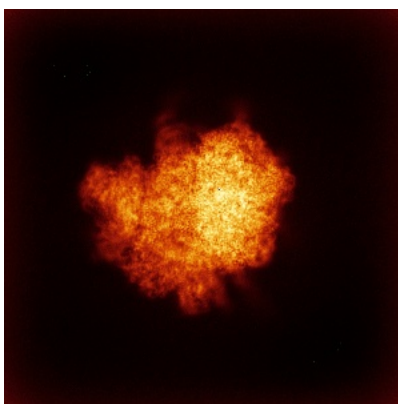


Z

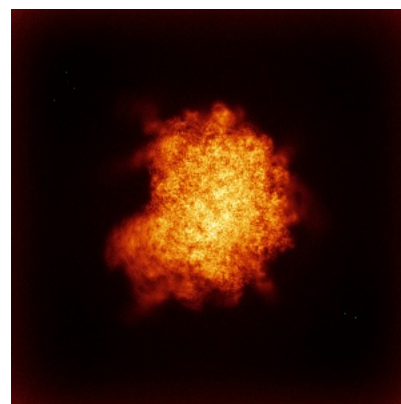
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

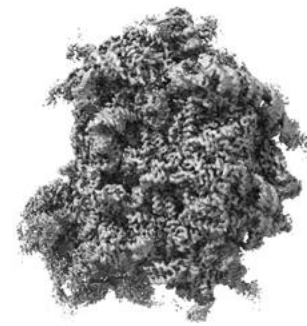
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.584. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

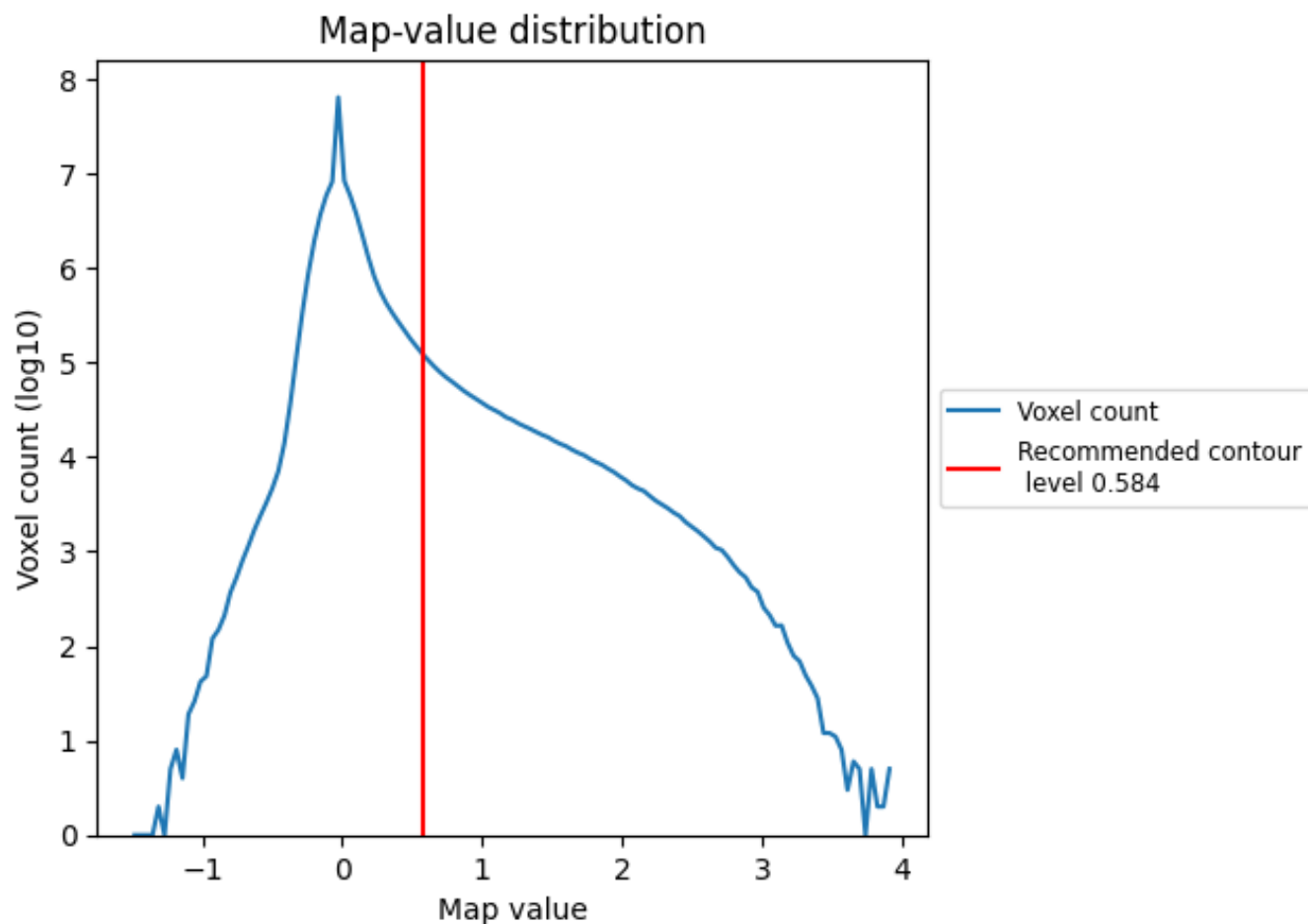
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

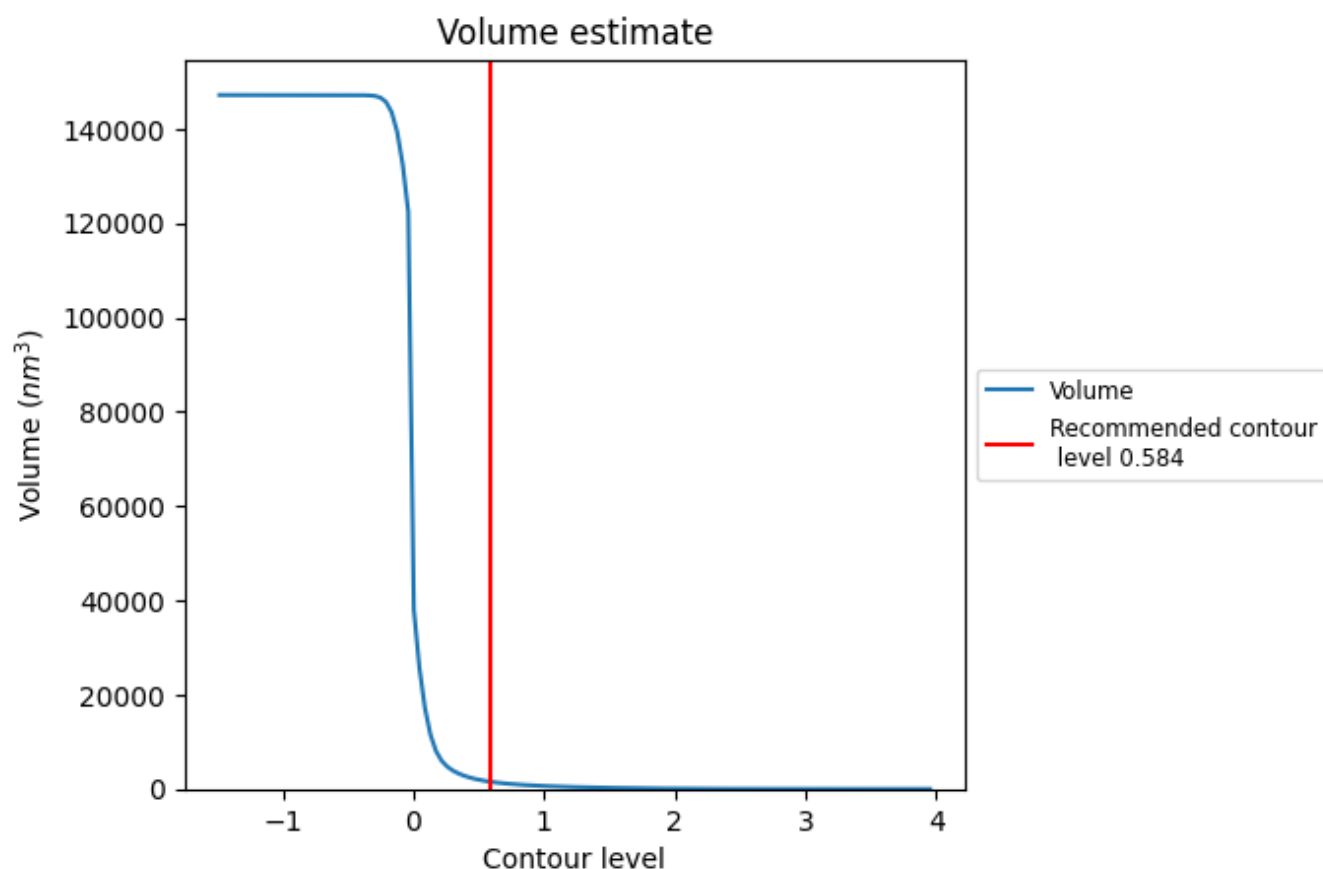
This section contains the results of statistical analysis of the map.

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.

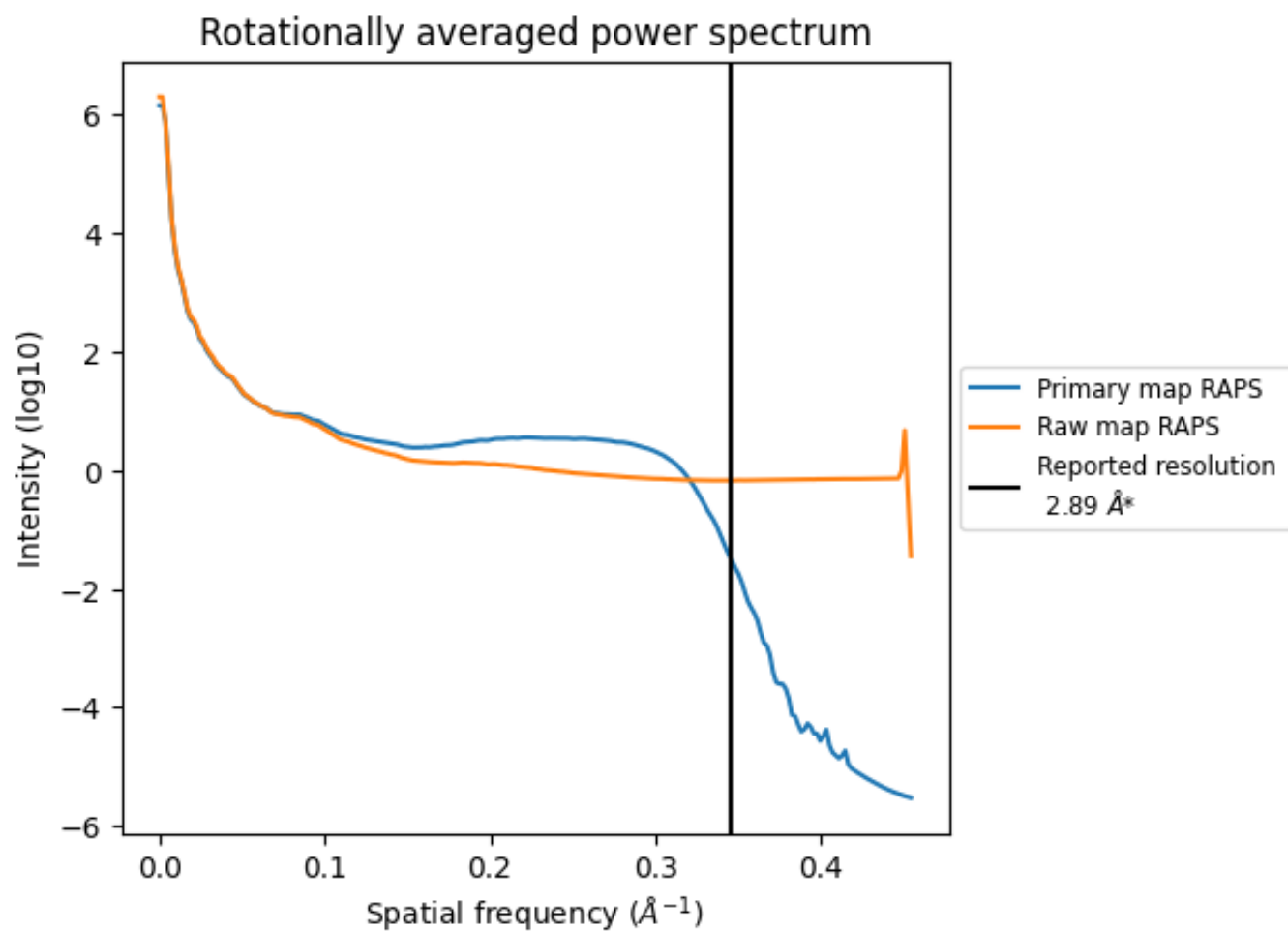
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1551 nm³; this corresponds to an approximate mass of 1401 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 ⓘ

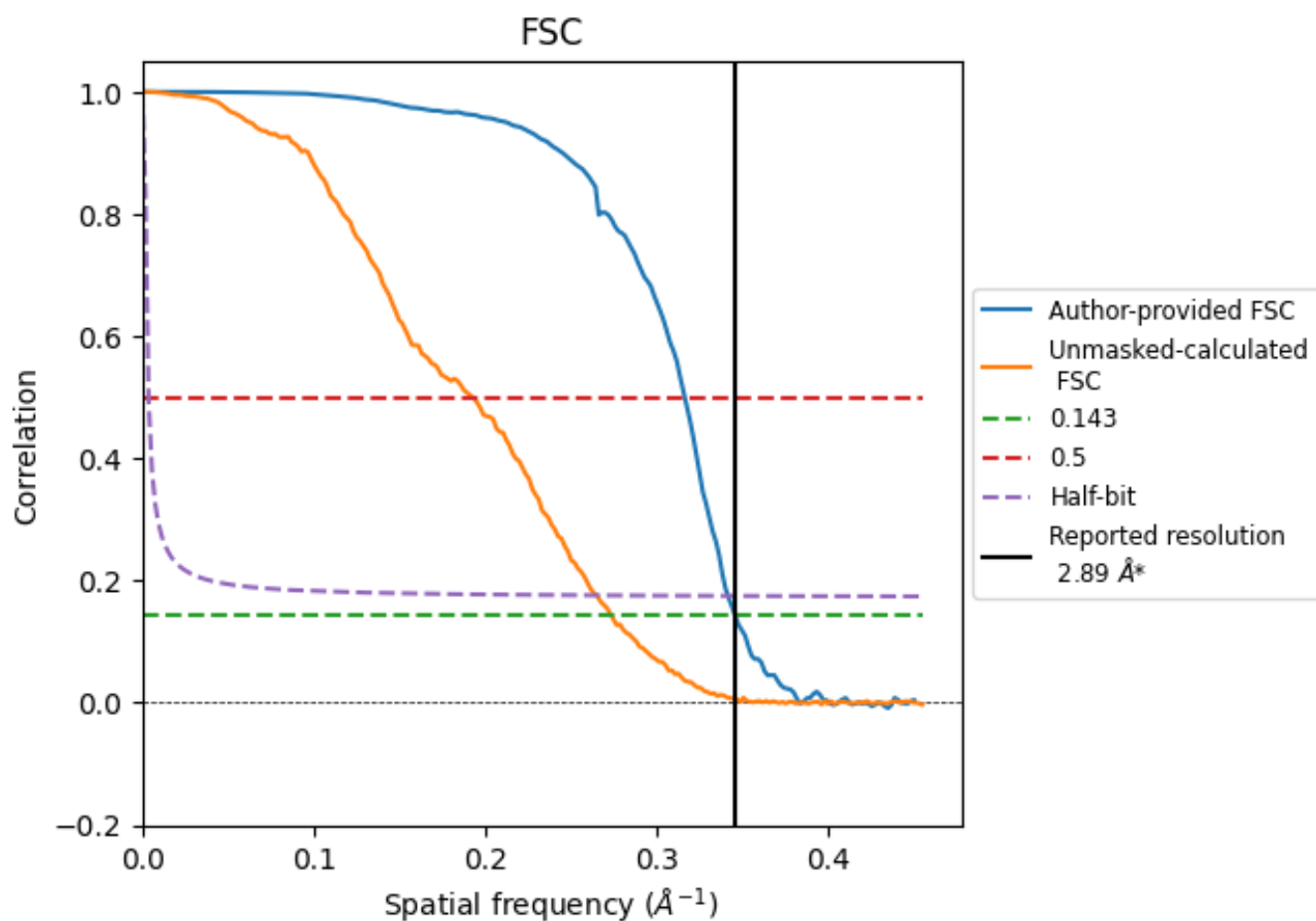


*Reported resolution corresponds to spatial frequency of $0.346 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.346 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

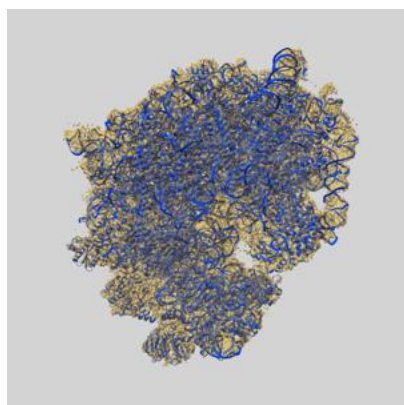
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.89	3.16	2.93
Unmasked-calculated*	3.66	5.19	3.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.66 differs from the reported value 2.89 by more than 10 %

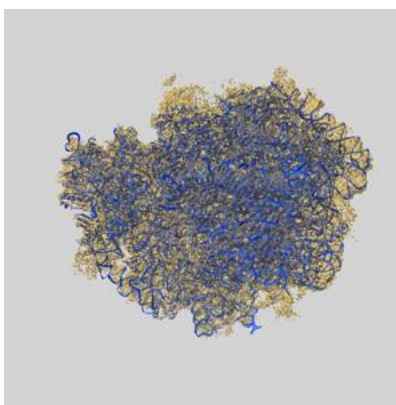
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55100 and PDB model 9T5C. Per-residue inclusion information can be found in [section 3](#) on [page 25](#).

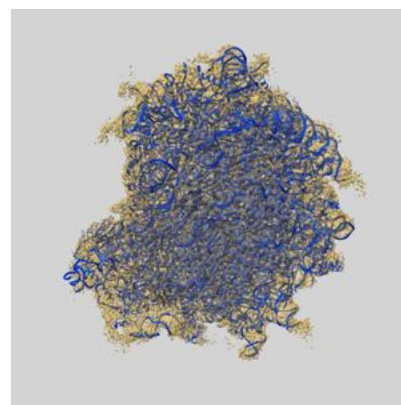
9.1 Map-model overlay [i](#)



X



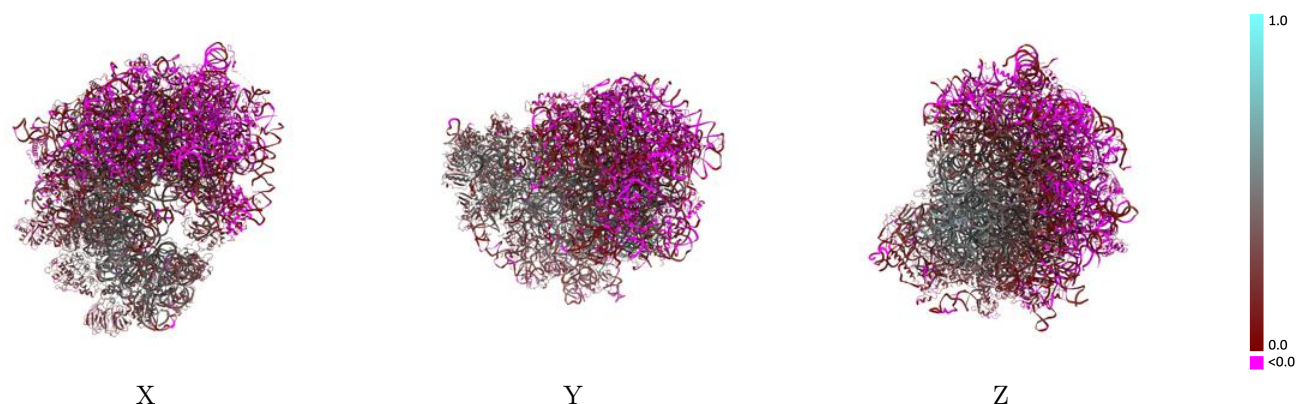
Y



Z

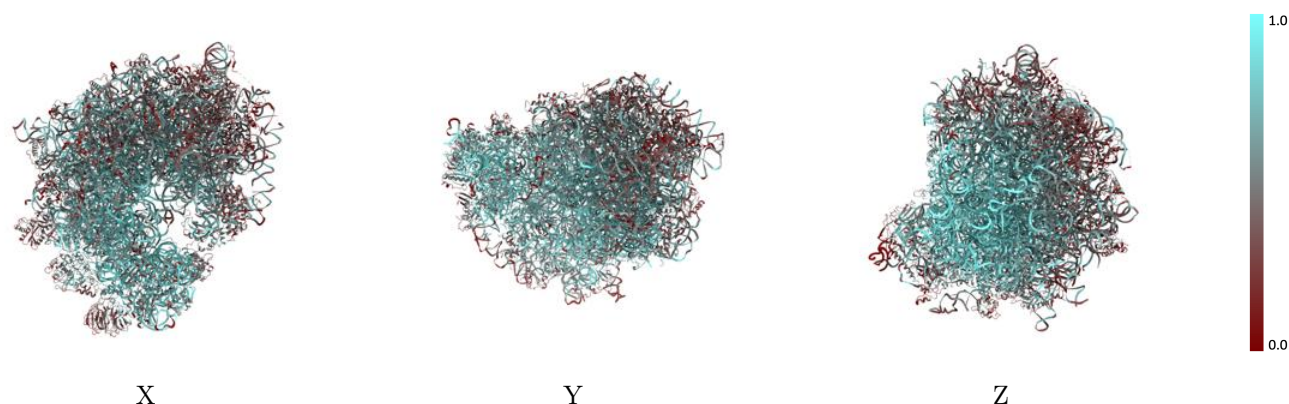
The images above show the 3D surface view of the map at the recommended contour level 0.584 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



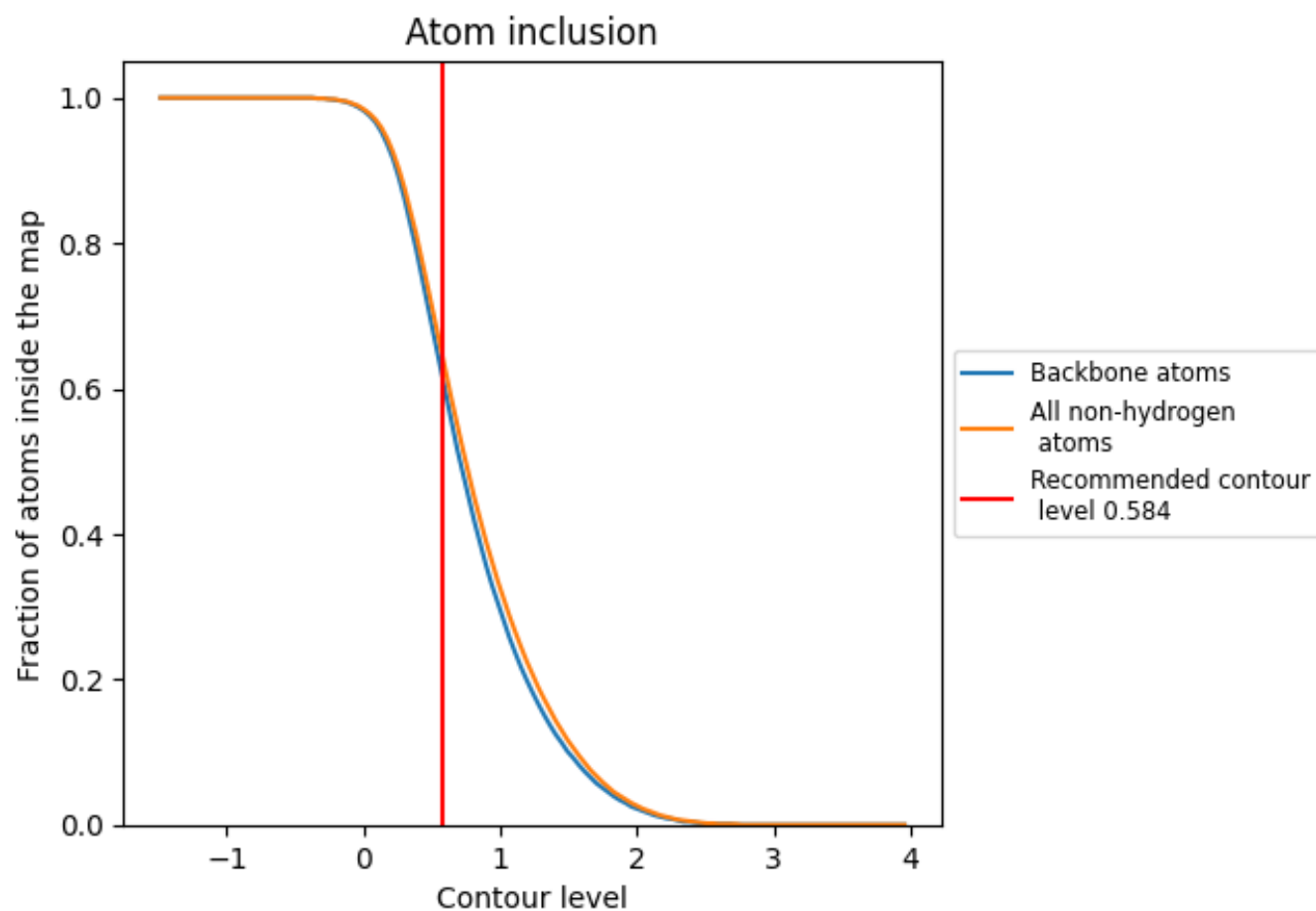
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.584).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 64% 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 (0.584) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6390	 0.2330
B	 0.2780	 0.0640
L5	 0.6960	 0.2130
L7	 0.6450	 0.1350
L8	 0.6200	 0.0880
LA	 0.6660	 0.2500
LB	 0.7980	 0.4400
LC	 0.3830	 -0.0020
LD	 0.3850	 0.0500
LE	 0.3230	 -0.0180
LF	 0.4260	 0.0220
LG	 0.3310	 -0.0220
LH	 0.5330	 0.1820
LI	 0.6320	 0.2520
LJ	 0.5590	 0.2390
LL	 0.3390	 -0.0130
LM	 0.3590	 -0.0150
LN	 0.4580	 0.0300
LO	 0.6360	 0.2190
LP	 0.8040	 0.3880
LQ	 0.4100	 0.0140
LR	 0.7190	 0.3630
LS	 0.4490	 0.0480
LT	 0.4620	 0.0840
LU	 0.6530	 0.3600
LV	 0.8430	 0.4900
LW	 0.8380	 0.4880
LX	 0.5680	 0.1680
LY	 0.4480	 0.0770
LZ	 0.4240	 0.0740
La	 0.4460	 0.0490
Lb	 0.3130	 0.0330
Lc	 0.5290	 0.1600
Ld	 0.8230	 0.5030
Le	 0.5300	 0.1090



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Chain	Atom inclusion	Q-score
Lf	 0.5300	 0.1280
Lg	 0.6510	 0.2230
Lh	 0.4500	 0.0600
Li	 0.3350	 -0.0070
Lj	 0.6500	 0.1880
Lk	 0.5070	 0.1800
Ll	 0.7260	 0.2870
Lm	 0.6780	 0.2640
Ln	 0.8940	 0.5200
Lo	 0.5530	 0.1750
Lp	 0.7000	 0.2860
Lr	 0.3520	 -0.0170
S2	 0.8020	 0.3560
S6	 0.6990	 0.2430
S7	 0.6030	 0.2580
SA	 0.5920	 0.3160
SB	 0.5360	 0.2580
SC	 0.6860	 0.3810
SD	 0.5610	 0.3620
SE	 0.3300	 0.1330
SF	 0.5910	 0.3310
SG	 0.4620	 0.2570
SH	 0.3440	 0.1710
SI	 0.5490	 0.2410
SJ	 0.4270	 0.1620
SK	 0.4900	 0.3070
SL	 0.5760	 0.2580
SN	 0.5800	 0.2530
SO	 0.6610	 0.3400
SP	 0.5550	 0.3200
SQ	 0.6550	 0.3780
SR	 0.4910	 0.3010
SS	 0.5670	 0.3090
ST	 0.6290	 0.3610
SU	 0.5930	 0.4010
SV	 0.5200	 0.3010
SW	 0.6310	 0.3110
SX	 0.7070	 0.3920
SY	 0.3220	 0.1640
SZ	 0.4120	 0.2720
Sa	 0.7520	 0.4110
Sb	 0.4180	 0.1970

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Chain	Atom inclusion	Q-score
Sc	 0.5750	 0.3450
Sd	 0.7450	 0.4380
Se	 0.4200	 0.2160
Sg	 0.3820	 0.2780