



Full wwPDB EM Validation Report ⓘ

May 4, 2026 – 05:22 PM JST

PDB ID : 9KDW / pdb_00009kdw
EMDB ID : EMD-62288
Title : Cryo-EM structure of 80S ribosome
Authors : Lu, Y.; Wang, X.; Qin, Y.; Cao, Y.
Deposited on : 2024-11-04
Resolution : 2.67 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

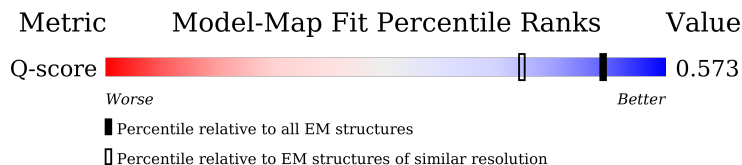
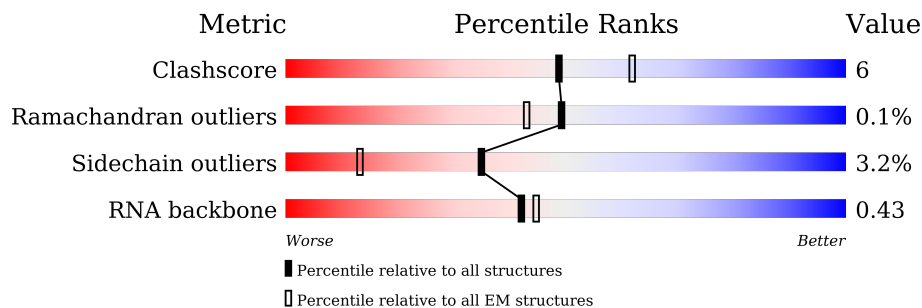
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.67 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.









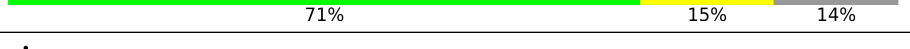
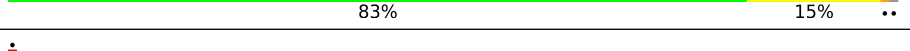
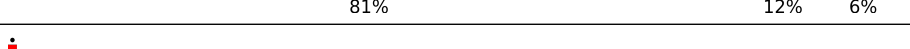
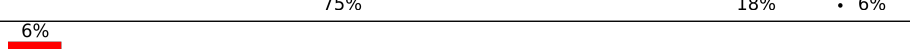


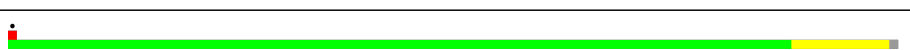

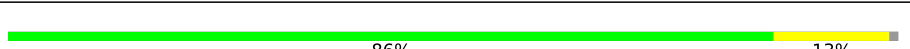






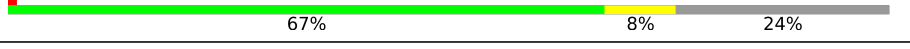



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9182 (2.17 - 3.17)

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	L5	4731	
2	L7	120	
3	L8	158	







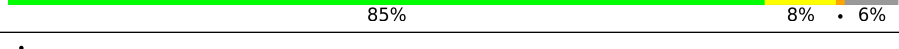
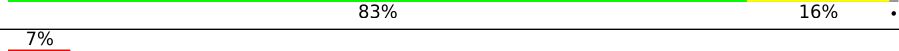
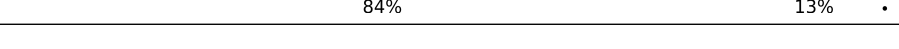
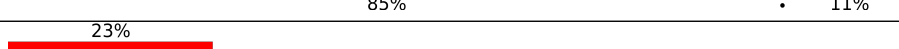
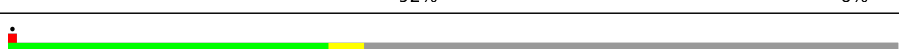
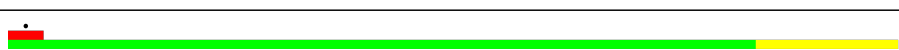

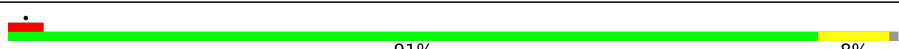

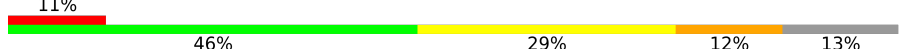

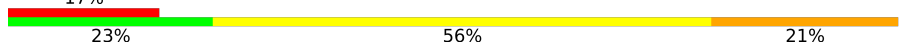

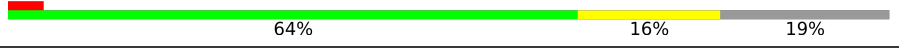
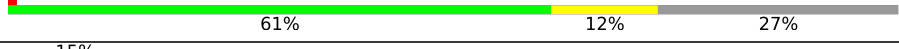



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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	419	
7	LD	297	
8	LE	296	
9	LF	270	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	217	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
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	
47	S7	75	
48	SA	295	
49	SB	264	
50	SC	293	
51	SD	243	
52	SE	263	

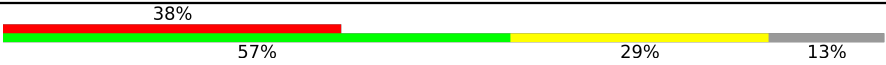
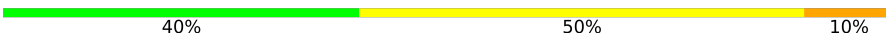
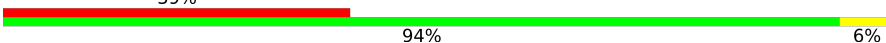
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Mol	Chain	Length	Quality of chain
53	SF	204	
54	SG	249	
55	SH	194	
56	SI	208	
57	SJ	194	
58	SK	165	
59	SL	158	
60	SN	151	
61	SO	151	
62	SP	145	
63	SQ	146	
64	SR	135	
65	SS	152	
66	ST	145	
67	SU	119	
68	SV	83	
69	SW	130	
70	SX	143	
71	SY	133	
72	SZ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

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Mol	Chain	Length	Quality of chain
78	Sg	317	
79	Sx	10	
80	Z	18	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 204125 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called Mus musculus 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3399	Total	C	N	O	P	0	0
			72884	32460	13325	23701	3398		

- Molecule 2 is a RNA chain called Mus musculus 5S ribosomal RNA.

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

- Molecule 3 is a RNA chain called Mus musculus 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	151	Total	C	N	O	P	0	0
			3210	1433	567	1060	150		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	357	Total	C	N	O	S	0	0
			2857	1797	571	474	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		

- 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 Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	229	Total	C	N	O	S	0	0
			1848	1179	354	311	4		

- 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		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	201	Total	C	N	O	S	0	0
			1631	1037	316	267	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	167	Total	C	N	O	S	0	0
			1340	848	250	236	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	206	Total	C	N	O	S	0	0
			1667	1043	343	277	4		

- 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 Large ribosomal subunit protein eL15.

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 Large ribosomal subunit protein uL13.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	154	Total	C	N	O	S	0	0
			1251	782	243	217	9		

- Molecule 19 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	174	Total	C	N	O	S	0	0
			1457	901	316	231	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		

- 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		

- 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 Large ribosomal subunit protein uL14.

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 Large ribosomal subunit protein eL24.

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		

- Molecule 27 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	132	Total	C	N	O	S	0	0
			1102	692	223	184	3		

- Molecule 28 is a protein called Large ribosomal subunit protein eL27.

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 Large ribosomal subunit protein uL15.

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	99	Total	C	N	O	S	0	0
			807	505	174	124	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		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	108	Total	C	N	O	S	0	0
			896	566	172	156	2		

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

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 Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	110	Total	C	N	O	S	0	0
			873	546	180	141	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 37 is a protein called Large ribosomal subunit protein eL36.

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 Large ribosomal subunit protein eL37.

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		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			438	279	93	64	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 42 is a protein called Small ribosomal subunit protein eS32.

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 Large ribosomal subunit protein eL42.

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 Large ribosomal subunit protein eL43.

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	124	Total	C	N	O	S	0	0
			994	616	206	167	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1628	Total	C	N	O	P	0	0
			34749	15516	6241	11365	1627		

- Molecule 47 is a RNA chain called A/P, P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		
47	S7	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 48 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	207	Total	C	N	O	S	0	0
			1636	1042	288	298	8		

- Molecule 49 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 50 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	215	Total	C	N	O	S	0	0
			1665	1080	285	291	9		

- Molecule 51 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	209	Total	C	N	O	S	0	0
			1626	1036	296	287	7		

- Molecule 52 is a protein called Small ribosomal subunit protein eS4.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 54 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SG	204	Total	C	N	O	S	0	0
			1645	1029	330	280	6		

- Molecule 55 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SH	180	Total	C	N	O	S	0	0
			1449	924	266	258	1		

- Molecule 56 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SI	183	Total	C	N	O	S	0	0
			1499	943	293	258	5		

- Molecule 57 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SJ	138	Total	C	N	O	S	0	0
			1162	743	230	187	2		

- Molecule 58 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SK	90	Total	C	N	O	S	0	0
			760	495	135	124	6		

- Molecule 59 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SL	135	Total	C	N	O	S	0	0
			1110	708	207	189	6		

- Molecule 60 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 61 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 62 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SP	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 63 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 64 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 66 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SU	95	Total	C	N	O	S	0	0
			753	471	142	136	4		

- Molecule 68 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SV	81	Total	C	N	O	S	0	0
			619	379	116	119	5		

- Molecule 69 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 71 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SY	110	Total	C	N	O	S	0	0
			891	565	173	149	4		

- Molecule 72 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 73 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sa	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 74 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sc	54	Total	C	N	O	S	0	0
			416	257	80	77	2		

- Molecule 76 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sd	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 77 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Se	48	Total	C	N	O	S	0	0
			384	234	86	63	1		

- Molecule 78 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sg	276	Total	C	N	O	S	0	0
			2148	1357	378	401	12		

- Molecule 79 is a RNA chain called RNA (5'-R(P*AP*UP*CP*AP*UP*GP*AP*AP*GP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sx	10	Total	C	N	O	P	0	0
			214	96	39	69	10		

- Molecule 80 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	Z	18	Total	C	N	O	0	0
			89	53	18	18		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
81	L5	94	Total	Mg	0
			94	94	
81	L7	1	Total	Mg	0
			1	1	
81	LN	1	Total	Mg	0
			1	1	
81	LP	1	Total	Mg	0
			1	1	

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	Lj	1	Total	Zn	0
			1	1	
82	Lm	1	Total	Zn	0
			1	1	

Continued on next page...

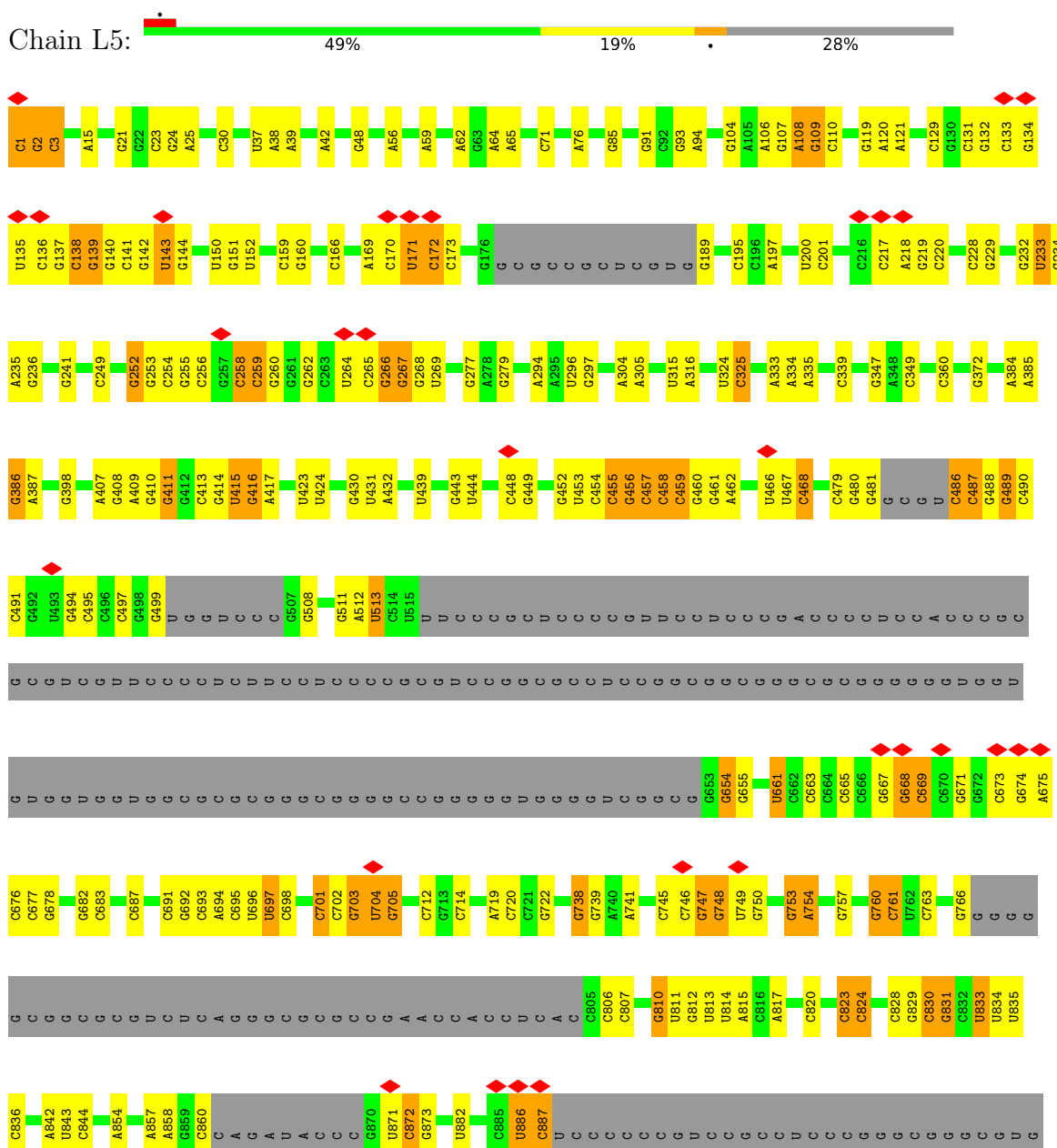
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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
82	Lp	1	1	1	0

3 Residue-property plots

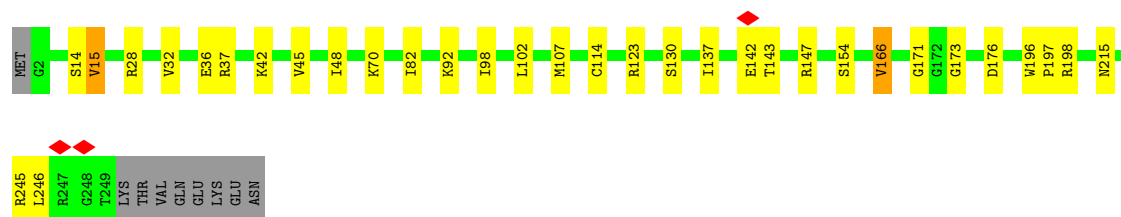
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Mus musculus 28S ribosomal RNA

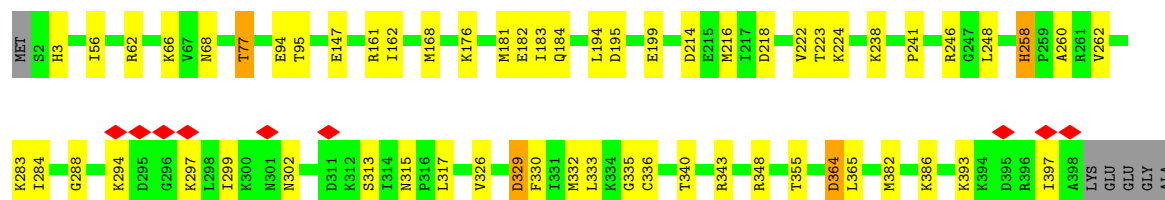
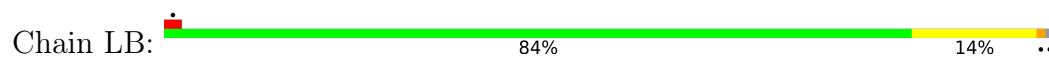




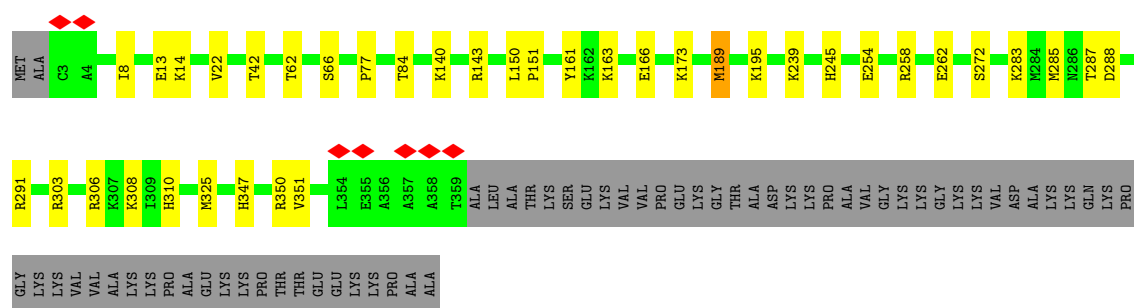
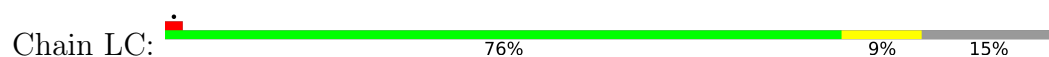




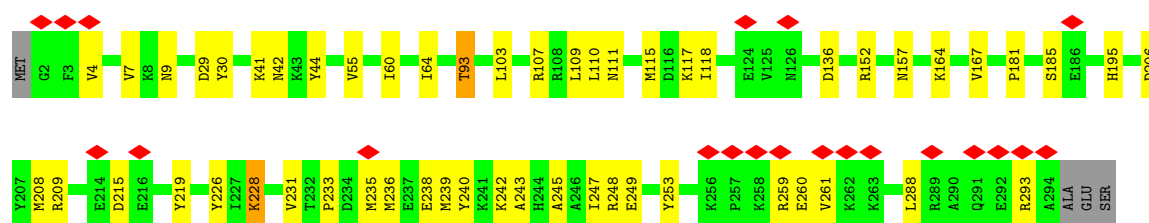
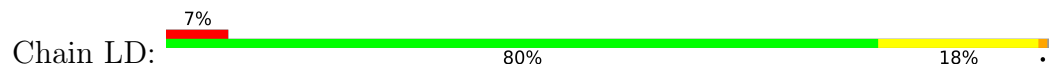
- Molecule 5: Large ribosomal subunit protein uL3



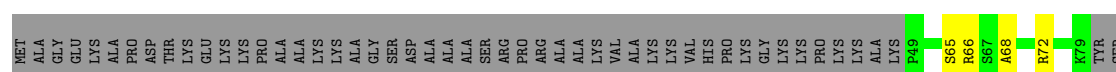
- Molecule 6: Large ribosomal subunit protein uL4

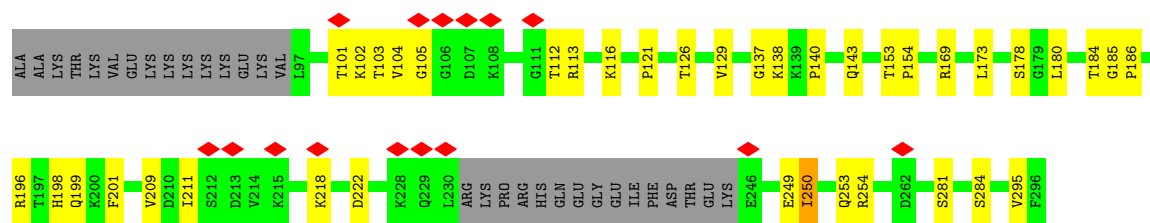


- Molecule 7: Large ribosomal subunit protein uL18



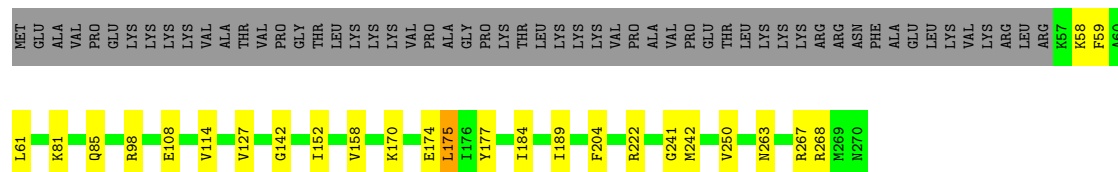
- Molecule 8: Large ribosomal subunit protein eL6





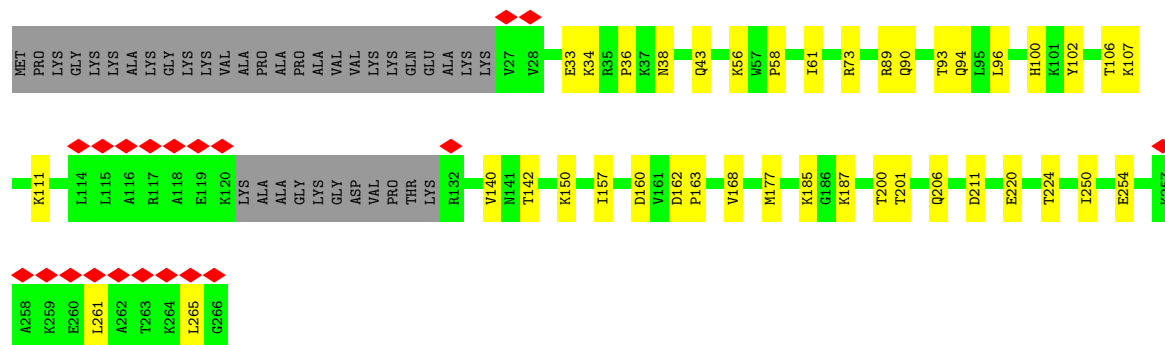
• Molecule 9: Large ribosomal subunit protein uL30

Chain LF: 70% 9% 21%



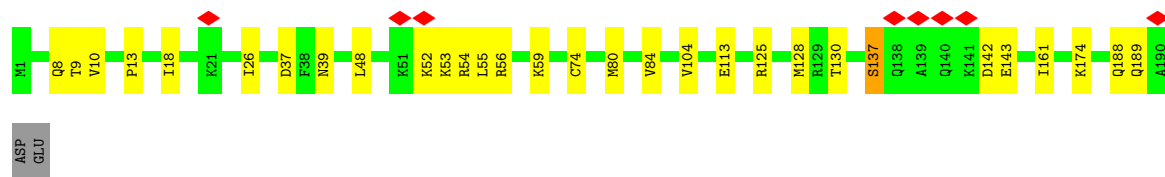
• Molecule 10: Large ribosomal subunit protein eL8

Chain LG: 8% 71% 15% 14%



• Molecule 11: Large ribosomal subunit protein uL6

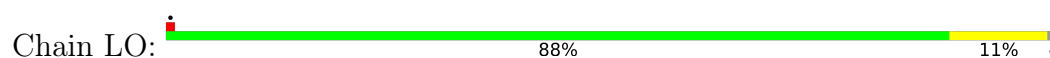
Chain LH: 83% 15% 2%



• Molecule 12: Large ribosomal subunit protein uL16-like

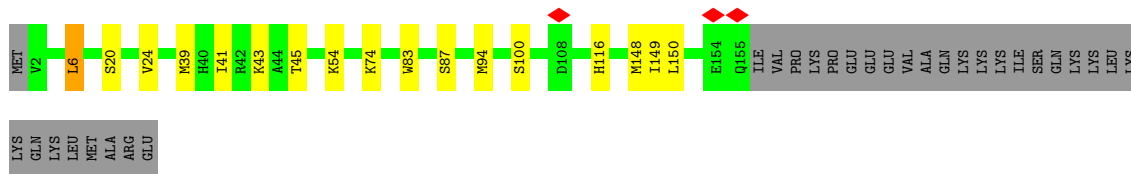
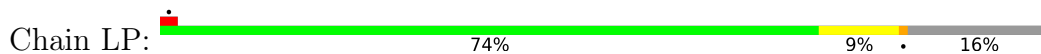
Chain LI: 81% 12% 6%







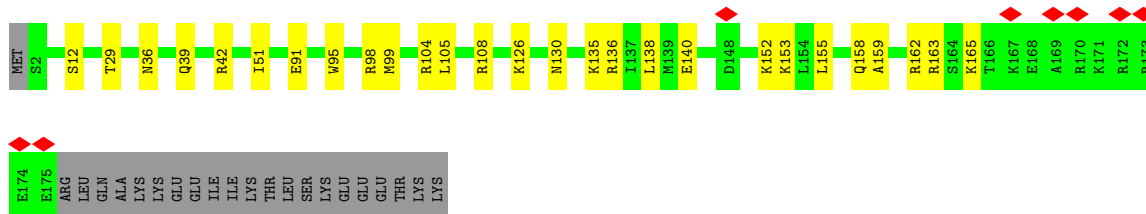
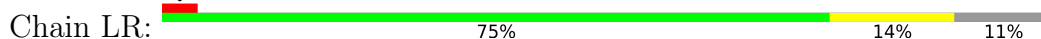
- Molecule 18: Large ribosomal subunit protein uL22



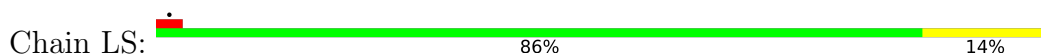
- Molecule 19: Large ribosomal subunit protein eL18



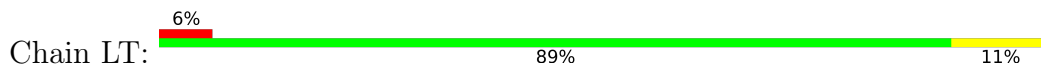
- Molecule 20: Large ribosomal subunit protein eL19



- Molecule 21: Large ribosomal subunit protein eL20

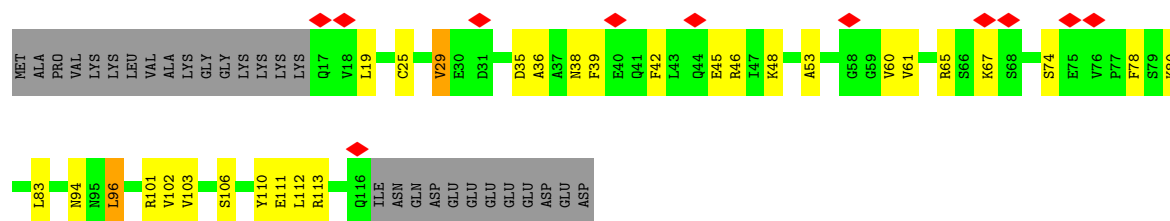


- Molecule 22: Large ribosomal subunit protein eL21



- Molecule 23: Large ribosomal subunit protein eL22





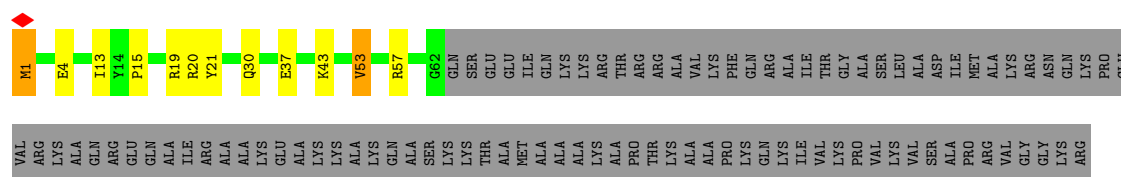
- Molecule 24: Large ribosomal subunit protein uL14

Chain LV: 82% 9% 7%



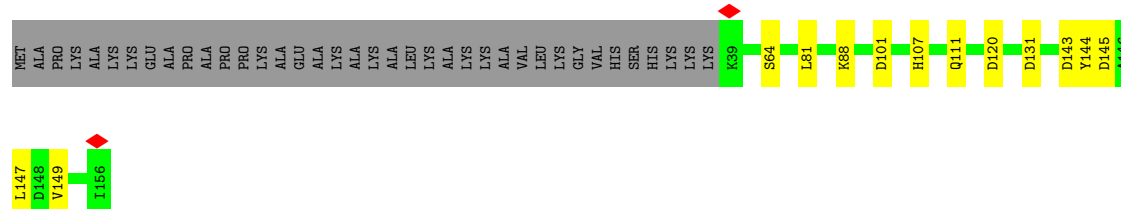
- Molecule 25: Large ribosomal subunit protein eL24

Chain LW: 32% 6% 61%



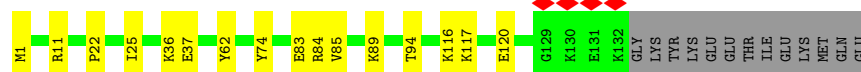
- Molecule 26: Large ribosomal subunit protein uL23

Chain LX: 67% 8% 24%



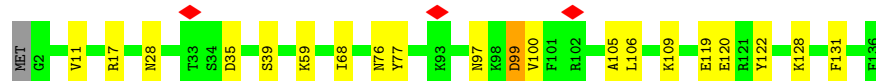
- Molecule 27: Large ribosomal subunit protein uL24

Chain LY: 80% 11% 9%




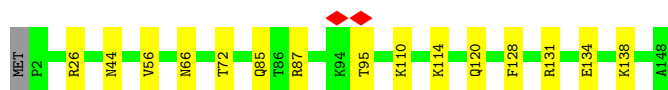
- Molecule 28: Large ribosomal subunit protein eL27

Chain LZ: 85% 14% ..



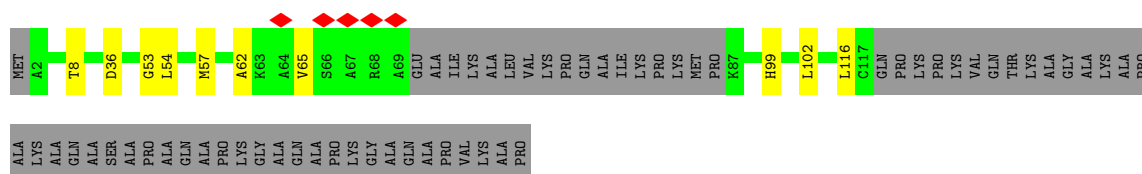
- Molecule 29: Large ribosomal subunit protein uL15

Chain La:  89% 10%



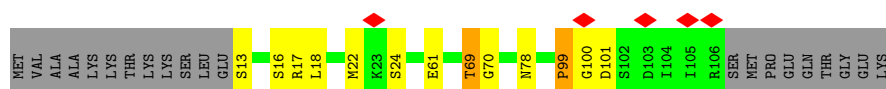
- Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:  56% 6% 38%




- Molecule 31: Large ribosomal subunit protein eL30

Chain Lc:  70% 10% 18%




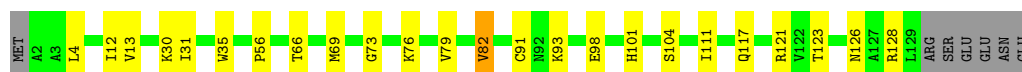
- Molecule 32: Large ribosomal subunit protein eL31

Chain Ld:  7% 77% 10% 14%




- Molecule 33: Large ribosomal subunit protein eL32

Chain Le:  77% 17% 5%




- Molecule 34: Large ribosomal subunit protein eL33

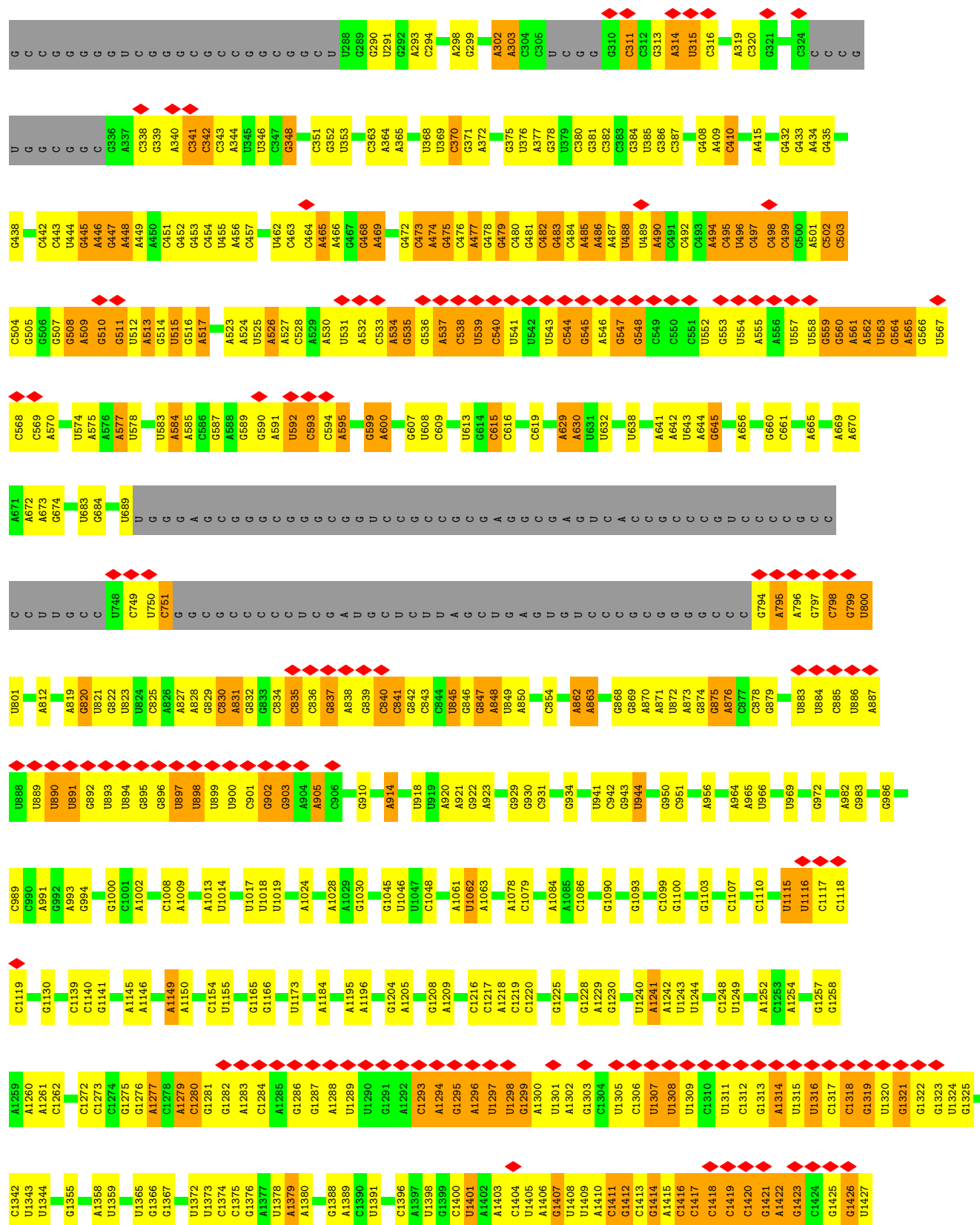
Chain Lf:  85% 14%

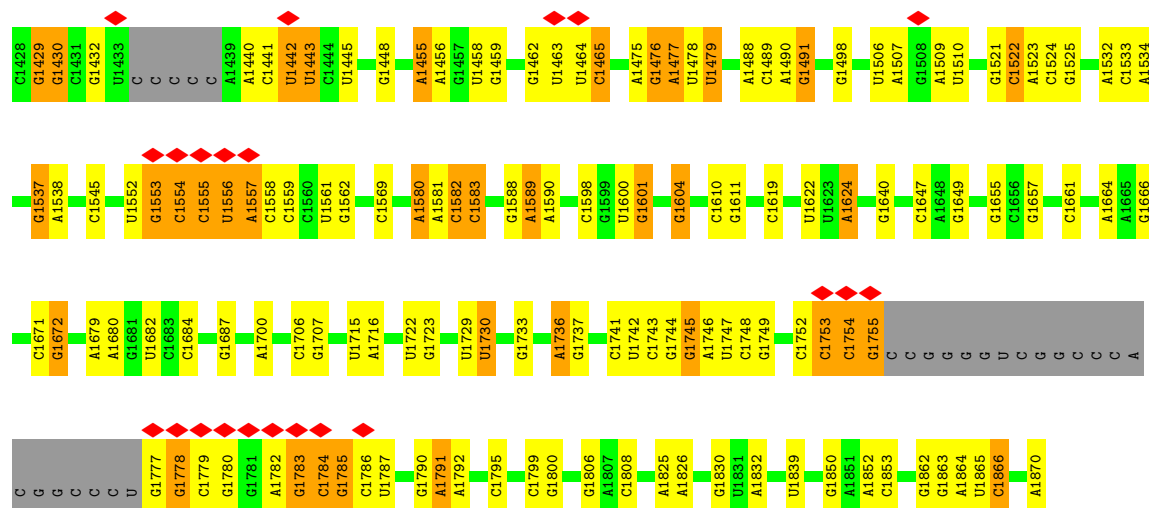


- Molecule 35: Large ribosomal subunit protein eL34

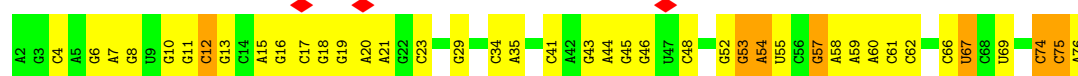
Chain Lg:  6% 85% 8% 6%

- [illegible]

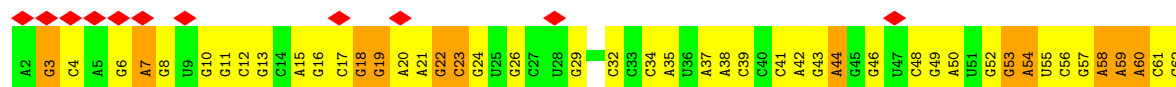




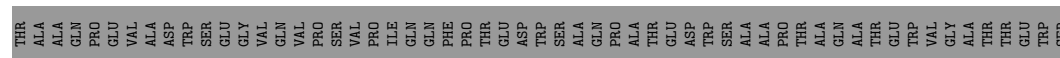
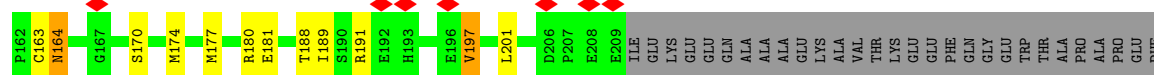
• Molecule 47: A/P, P/E tRNA



• Molecule 47: A/P, P/E tRNA



• Molecule 48: Small ribosomal subunit protein uS2



• Molecule 49: Small ribosomal subunit protein eS1

Frequency	Percentage
Daily	64%
Weekly	16%
Monthly	19%



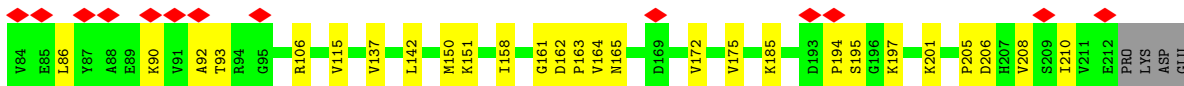
THR GLY ALA LYS VAL GLU ARG ALA ASP GLY TYR GLU PRO PRO VAL GLN GLU SER VAL

Frequency	Percentage
Daily	61%
Weekly	12%
Monthly	27%



Q267	E268	F269	T270	D271	H272	L273	V274	LYS	THR	HIS	THR	ARG	VAL	SER	VAL	GLN	ARG	THR	GLN	ALA	PRO	ALA	VAL	ALA	THR	THR
------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

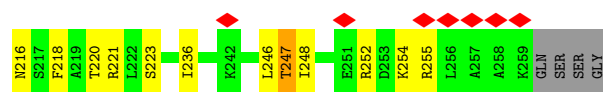
Frequency	Percentage
Daily	64%
Weekly	21%
Monthly	14%
Other	1%



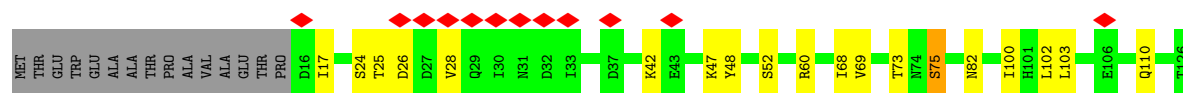
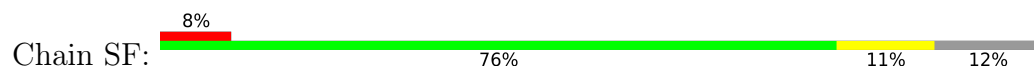
ILE	LEU	PRO	THR	THR	PRO	ILE	SER	GLU	GLN	LYS	GLY	GLY	LYS	PRO	GLU	PRO	PRO	ALA	MET	PRO	PRO	GLN	PRO	VAL	PRO	THR	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Category	Percentage
Very bad	7%
Bad	68%
Good	29%

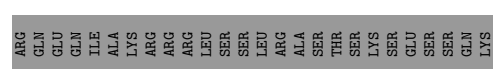
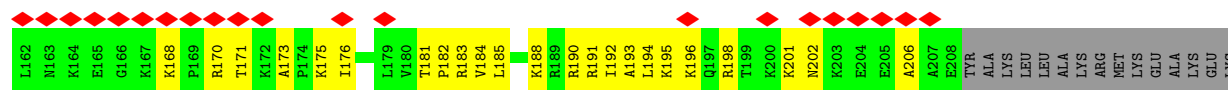
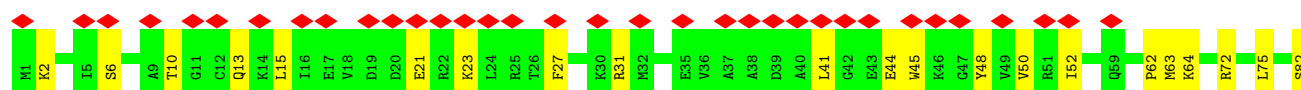




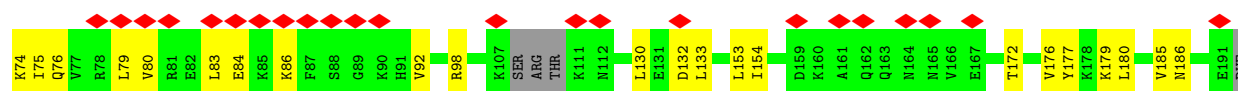
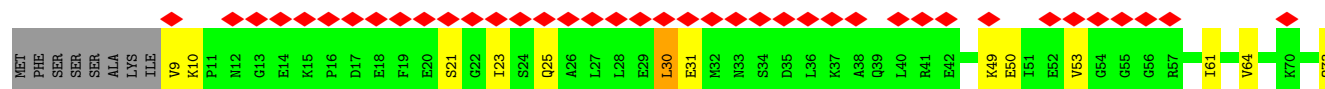
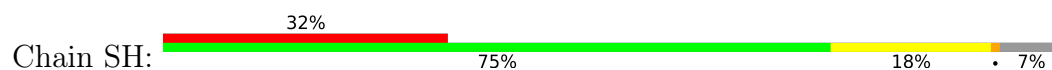
- Molecule 53: Small ribosomal subunit protein uS7



- Molecule 54: Small ribosomal subunit protein eS6

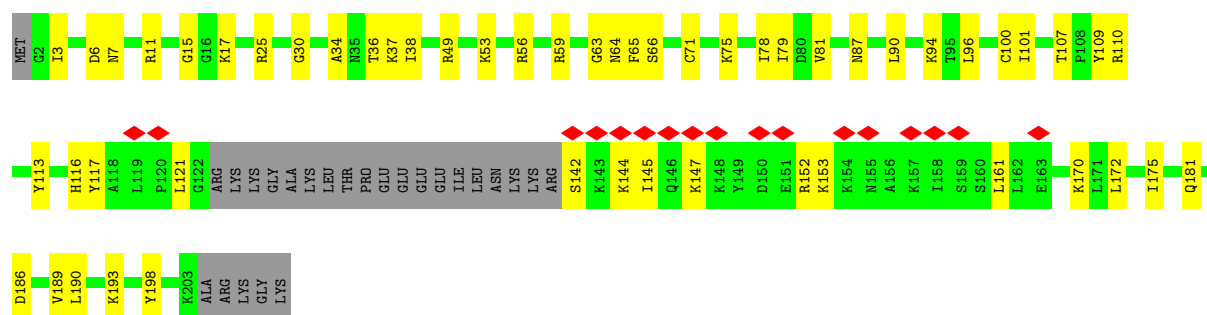


- Molecule 55: Small ribosomal subunit protein eS7

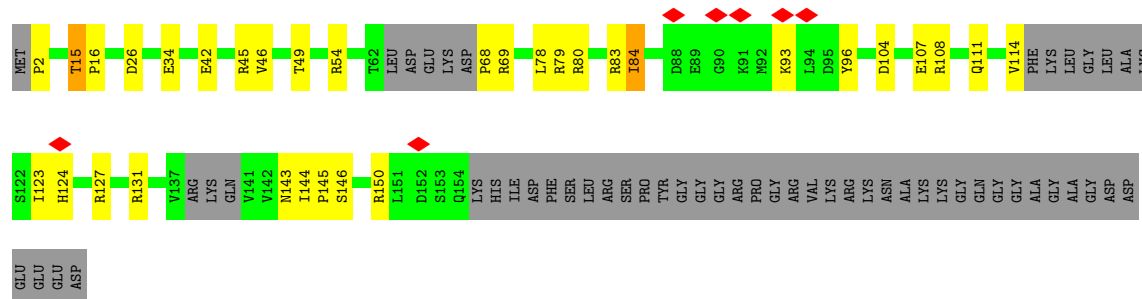


- Molecule 56: Small ribosomal subunit protein eS8

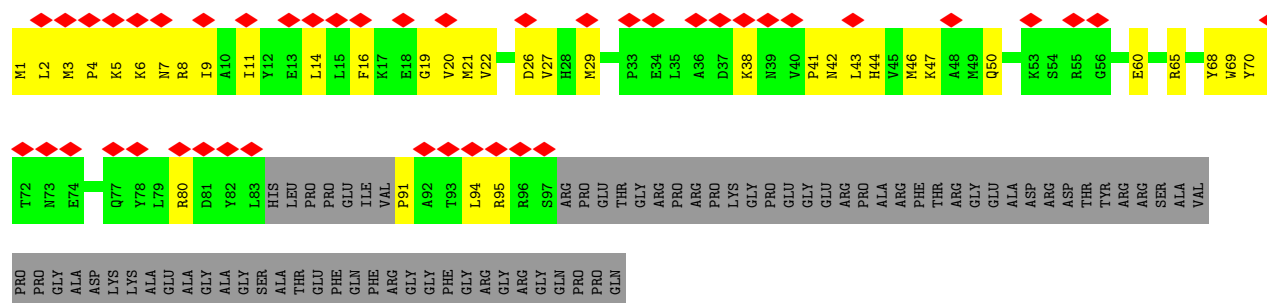
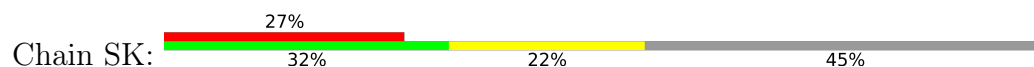




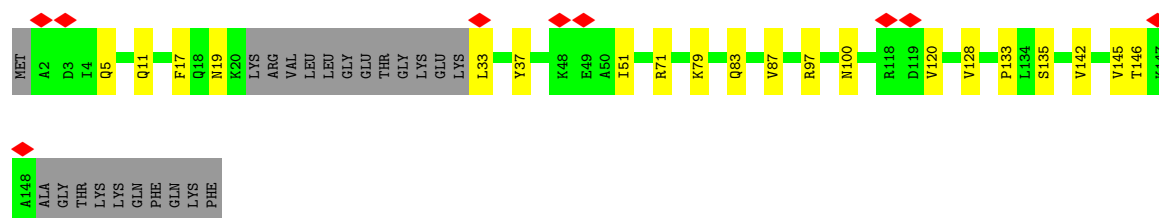
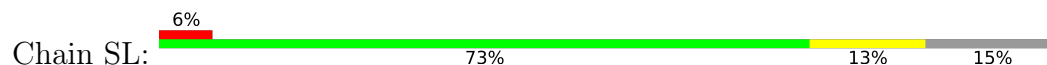
- Molecule 57: Small ribosomal subunit protein uS4



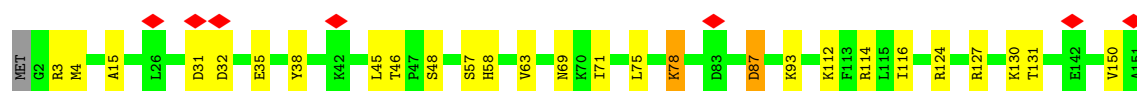
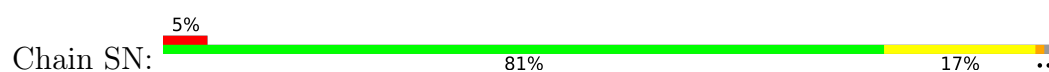
- Molecule 58: Small ribosomal subunit protein eS10



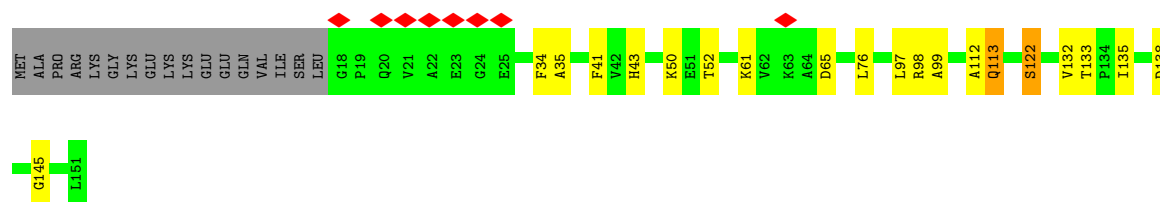
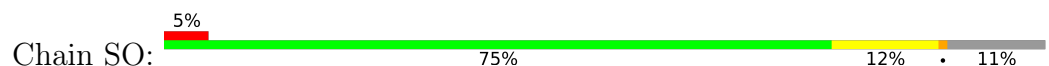
- Molecule 59: Small ribosomal subunit protein uS17



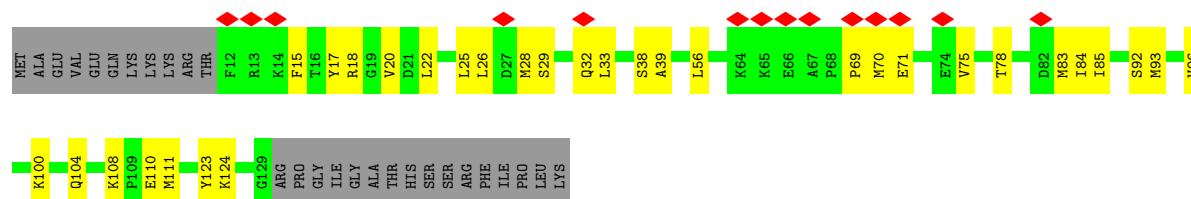
- Molecule 60: Small ribosomal subunit protein uS15



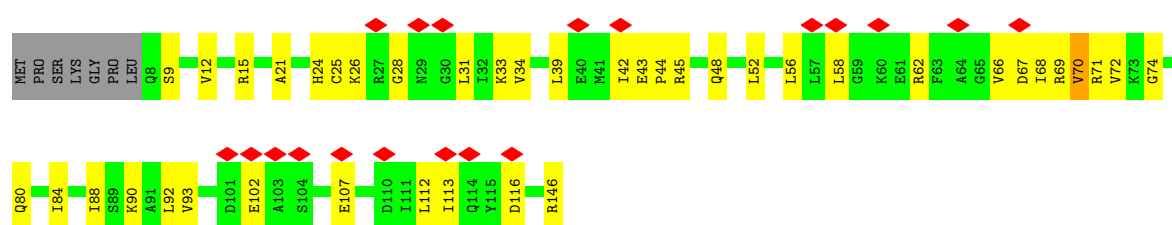
- Molecule 61: Small ribosomal subunit protein uS11



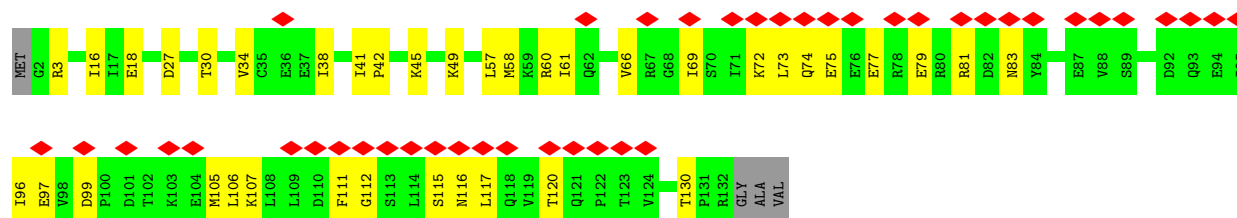
- Molecule 62: Small ribosomal subunit protein uS19



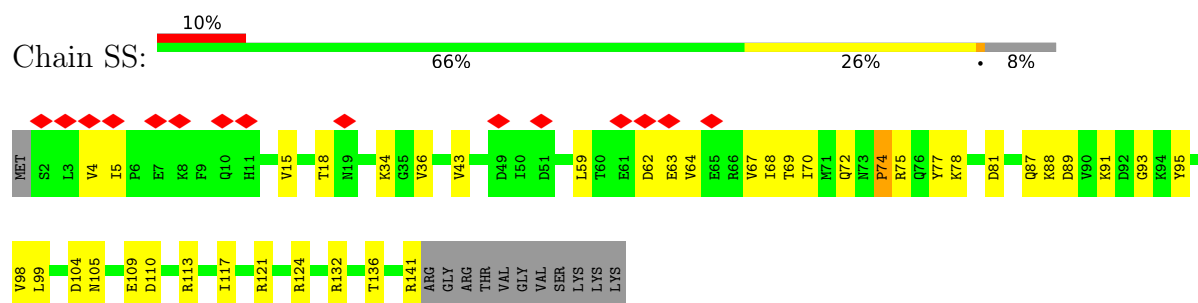
- Molecule 63: Small ribosomal subunit protein uS9



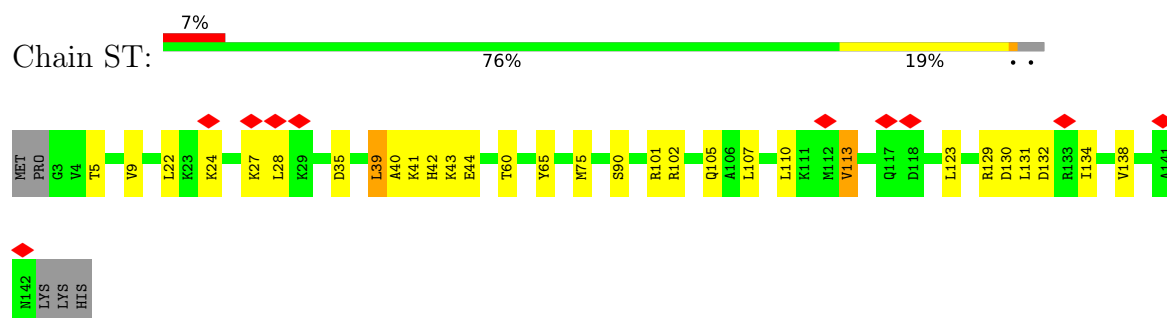
- Molecule 64: Small ribosomal subunit protein eS17



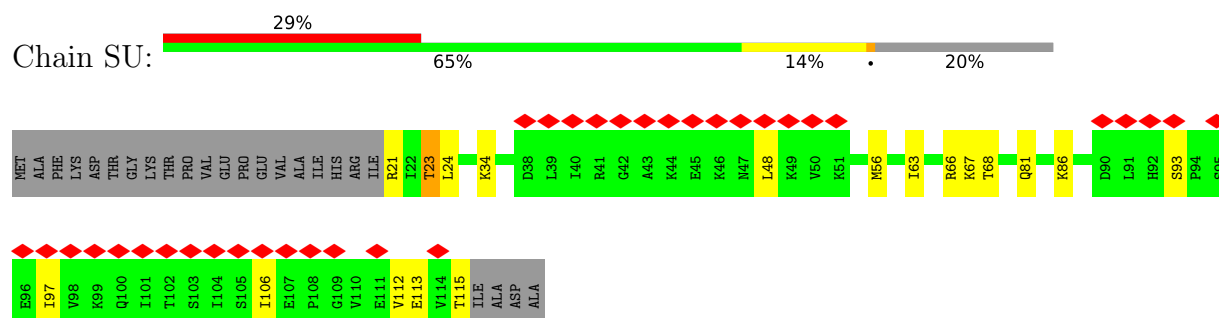
- Molecule 65: Small ribosomal subunit protein uS13



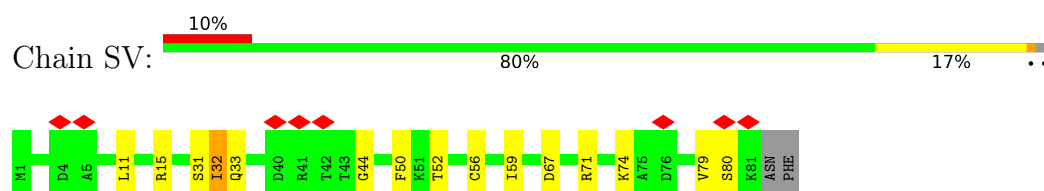
- Molecule 66: Small ribosomal subunit protein eS19



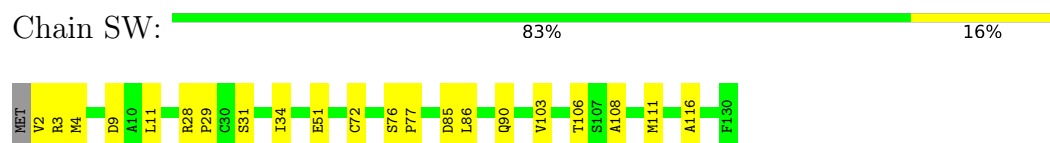
- Molecule 67: Small ribosomal subunit protein uS10




- Molecule 68: Small ribosomal subunit protein eS21

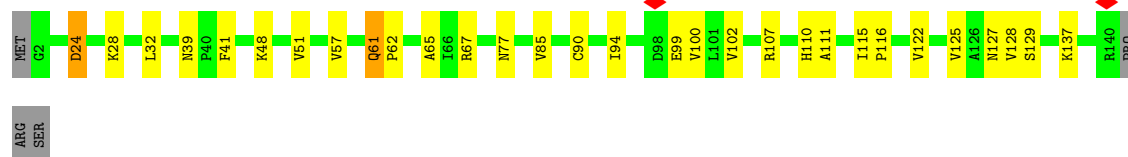


- Molecule 69: Small ribosomal subunit protein uS8



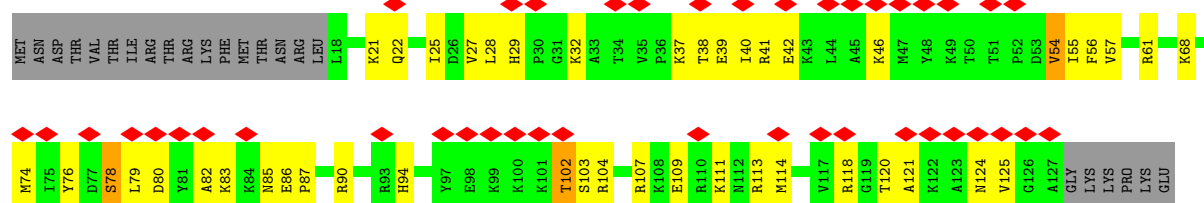
- Molecule 70: Small ribosomal subunit protein uS12

Chain SX:  76% 20% ..

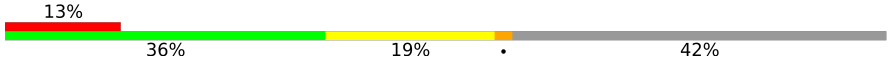


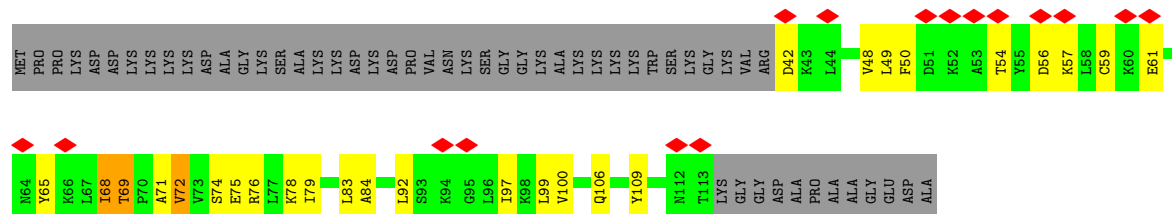
- Molecule 71: Small ribosomal subunit protein eS24

Chain SY:  32% 49% 32% 17%




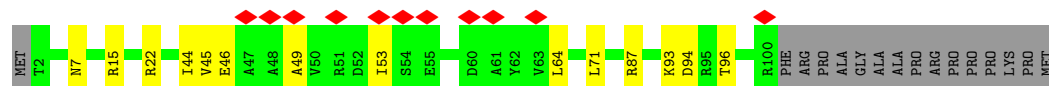
- Molecule 72: Small ribosomal subunit protein eS25

Chain SZ:  13% 36% 19% 42%




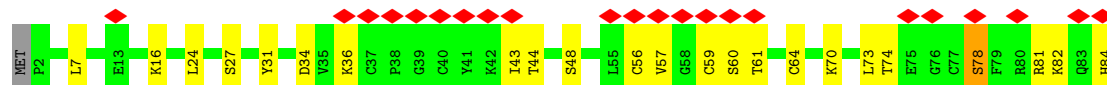
- Molecule 73: Small ribosomal subunit protein eS26

Chain Sa:  10% 74% 12% 14%



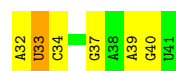
- Molecule 74: Small ribosomal subunit protein eS27

Chain Sb:  26% 71% 26% ..

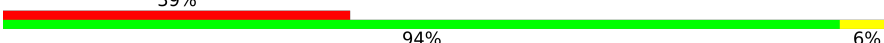


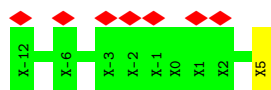
- Molecule 75: Small ribosomal subunit protein eS28

Chain Sc:  16% 58% 20% 22%



- Molecule 80: Nascent peptide

Chain Z:  39% 94% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97838	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.233	Depositor
Minimum map value	-2.071	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	616.0, 616.0, 616.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	L5	0.25	0/81527	0.36	1/127149 (0.0%)
2	L7	0.23	0/2858	0.38	2/4455 (0.0%)
3	L8	0.24	0/3584	0.34	0/5582
4	LA	0.24	0/1936	0.47	0/2596
5	LB	0.22	0/3269	0.45	0/4375
6	LC	0.24	0/2911	0.45	0/3907
7	LD	0.23	0/2435	0.46	1/3260 (0.0%)
8	LE	0.21	0/1775	0.46	0/2381
9	LF	0.24	0/1805	0.40	0/2408
10	LG	0.21	0/1880	0.45	0/2531
11	LH	0.20	0/1537	0.44	0/2065
12	LI	0.19	0/1669	0.40	0/2227
13	LJ	0.28	1/1363 (0.1%)	0.61	3/1824 (0.2%)
14	LL	0.22	0/1698	0.44	0/2274
15	LM	0.23	0/1146	0.44	0/1531
16	LN	0.25	0/1746	0.45	0/2338
17	LO	0.23	0/1670	0.45	0/2232
18	LP	0.23	0/1277	0.42	0/1712
19	LQ	0.24	0/1539	0.44	0/2053
20	LR	0.21	0/1473	0.39	0/1947
21	LS	0.22	0/1491	0.42	0/2000
22	LT	0.21	0/1335	0.40	0/1781
23	LU	0.20	0/831	0.49	0/1115
24	LV	0.20	0/987	0.39	0/1324
25	LW	0.22	0/532	0.42	0/708
26	LX	0.20	0/984	0.41	0/1323
27	LY	0.21	0/1119	0.41	0/1488
28	LZ	0.20	0/1130	0.41	1/1507 (0.1%)
29	La	0.24	0/1193	0.39	0/1593
30	Lb	0.21	0/821	0.46	0/1082
31	Lc	0.21	0/742	0.41	0/996
32	Ld	0.22	0/911	0.40	0/1227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.23	0/1071	0.37	0/1429
34	Lf	0.24	0/895	0.42	0/1198
35	Lg	0.21	0/883	0.42	0/1178
36	Lh	0.22	0/1023	0.42	0/1350
37	Li	0.20	0/843	0.46	0/1115
38	Lj	0.25	0/720	0.42	0/952
39	Lk	0.20	0/574	0.43	0/760
40	Ll	0.24	0/448	0.34	0/592
41	Lm	0.20	0/425	0.39	0/564
42	Ln	0.23	0/240	0.40	0/305
43	Lo	0.30	0/855	0.58	1/1128 (0.1%)
44	Lp	0.22	0/718	0.44	0/953
45	Lr	0.22	0/1009	0.41	0/1353
46	S2	0.20	0/38859	0.34	0/60556
47	S6	0.16	0/1795	0.30	0/2798
47	S7	0.14	0/1795	0.33	0/2798
48	SA	0.20	0/1673	0.43	0/2275
49	SB	0.20	0/1756	0.45	1/2350 (0.0%)
50	SC	0.20	0/1701	0.41	0/2300
51	SD	0.19	0/1651	0.44	0/2219
52	SE	0.18	0/2092	0.48	0/2816
53	SF	0.18	0/1436	0.41	0/1930
54	SG	0.17	0/1666	0.42	0/2222
55	SH	0.19	0/1470	0.48	0/1968
56	SI	0.20	0/1526	0.42	0/2038
57	SJ	0.19	0/1178	0.47	0/1574
58	SK	0.19	0/780	0.47	0/1046
59	SL	0.19	0/1130	0.43	0/1514
60	SN	0.20	0/1232	0.39	0/1656
61	SO	0.21	0/1015	0.47	0/1361
62	SP	0.18	0/1000	0.37	0/1335
63	SQ	0.19	0/1126	0.45	0/1506
64	SR	0.19	0/1078	0.45	0/1447
65	SS	0.21	0/1175	0.46	2/1575 (0.1%)
66	ST	0.19	0/1108	0.42	0/1486
67	SU	0.20	0/762	0.43	0/1023
68	SV	0.17	0/625	0.35	0/836
69	SW	0.20	0/1051	0.39	0/1406
70	SX	0.20	0/1097	0.50	0/1464
71	SY	0.20	0/907	0.55	0/1204
72	SZ	0.18	0/580	0.51	0/780
73	Sa	0.25	0/805	0.45	0/1079
74	Sb	0.19	0/665	0.43	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Sc	0.20	0/418	0.44	0/562
76	Sd	0.18	0/466	0.40	0/618
77	Se	0.19	0/386	0.44	0/504
78	Sg	0.18	0/2199	0.48	0/2989
79	Sx	0.21	0/239	0.34	0/370
All	All	0.23	1/219320 (0.0%)	0.39	12/322364 (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
8	LE	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	LJ	176	PRO	CG-CD	-7.10	1.26	1.50

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	LJ	176	PRO	N-CD-CG	-12.51	84.43	103.20
43	Lo	75	PRO	CA-N-CD	-11.21	96.31	112.00
13	LJ	176	PRO	CA-N-CD	-9.78	98.30	112.00
2	L7	48	G	OP1-P-O3'	-9.29	80.14	108.00
7	LD	233	PRO	CA-N-CD	-7.93	100.90	112.00
13	LJ	176	PRO	CA-CB-CG	-7.66	89.95	104.50
2	L7	48	G	OP2-P-O3'	-7.64	85.08	108.00
65	SS	74	PRO	CA-N-CD	-6.08	103.49	112.00
49	SB	24	PRO	CA-N-CD	-6.00	103.60	112.00
1	L5	4549	G	N9-C1'-C2'	5.52	122.28	114.00
28	LZ	35	ASP	N-CA-C	-5.16	107.65	114.04
65	SS	74	PRO	N-CD-CG	-5.04	95.64	103.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	LE	137	GLY	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	L5	72884	0	36804	388	0
2	L7	2558	0	1296	10	0
3	L8	3210	0	1630	9	0
4	LA	1898	0	1993	16	0
5	LB	3202	0	3347	37	0
6	LC	2857	0	3030	21	0
7	LD	2389	0	2420	39	0
8	LE	1743	0	1880	27	0
9	LF	1771	0	1886	15	0
10	LG	1848	0	1981	24	0
11	LH	1519	0	1603	14	0
12	LI	1631	0	1682	14	0
13	LJ	1340	0	1377	17	0
14	LL	1667	0	1771	20	0
15	LM	1125	0	1202	20	0
16	LN	1701	0	1749	17	0
17	LO	1640	0	1792	17	0
18	LP	1251	0	1282	8	0
19	LQ	1515	0	1639	16	0
20	LR	1457	0	1601	13	0
21	LS	1451	0	1488	14	0
22	LT	1307	0	1380	13	0
23	LU	817	0	839	19	0
24	LV	973	0	1034	13	0
25	LW	519	0	533	9	0
26	LX	967	0	1040	6	0
27	LY	1102	0	1189	12	0
28	LZ	1107	0	1182	12	0
29	La	1164	0	1213	10	0
30	Lb	807	0	875	4	0
31	Lc	732	0	769	6	0
32	Ld	896	0	941	5	0
33	Le	1053	0	1147	15	0
34	Lf	876	0	912	10	0
35	Lg	873	0	961	7	0
36	Lh	1015	0	1156	14	0
37	Li	832	0	917	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	705	0	737	3	0
39	Lk	568	0	635	9	0
40	Ll	438	0	474	2	0
41	Lm	419	0	452	3	0
42	Ln	239	0	289	4	0
43	Lo	842	0	916	11	0
44	Lp	708	0	756	6	0
45	Lr	994	0	1057	10	0
46	S2	34749	0	17548	472	0
47	S6	1604	0	816	17	0
47	S7	1604	0	816	29	0
48	SA	1636	0	1641	30	0
49	SB	1729	0	1803	25	0
50	SC	1665	0	1753	20	0
51	SD	1626	0	1714	37	0
52	SE	2050	0	2156	50	0
53	SF	1416	0	1458	13	0
54	SG	1645	0	1780	54	0
55	SH	1449	0	1539	23	0
56	SI	1499	0	1561	35	0
57	SJ	1162	0	1252	26	0
58	SK	760	0	783	30	0
59	SL	1110	0	1165	15	0
60	SN	1208	0	1294	14	0
61	SO	1002	0	1023	15	0
62	SP	981	0	1026	22	0
63	SQ	1109	0	1174	34	0
64	SR	1064	0	1118	25	0
65	SS	1157	0	1213	27	0
66	ST	1090	0	1116	18	0
67	SU	753	0	815	8	0
68	SV	619	0	620	12	0
69	SW	1034	0	1080	15	0
70	SX	1080	0	1147	22	0
71	SY	891	0	948	37	0
72	SZ	574	0	627	17	0
73	Sa	792	0	845	13	0
74	Sb	651	0	672	13	0
75	Sc	416	0	445	8	0
76	Sd	455	0	449	9	0
77	Se	384	0	422	11	0
78	Sg	2148	0	2108	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	Sx	214	0	108	6	0
80	Z	89	0	26	1	0
81	L5	94	0	0	0	0
81	L7	1	0	0	0	0
81	LN	1	0	0	0	0
81	LP	1	0	0	0	0
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lp	1	0	0	0	0
All	All	204125	0	150918	2005	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 6.

All (2005) 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)
47:S7:76:A:O3'	80:Z:5:UNK:C	2.06	1.03
46:S2:160:U:H3	46:S2:469:A:HO2'	1.10	0.96
46:S2:516:G:H5''	46:S2:517:A:H5'	1.53	0.91
46:S2:889:U:H4'	46:S2:890:U:H5'	1.55	0.89
46:S2:1506:U:H4'	46:S2:1509:A:H1'	1.53	0.88
39:Lk:40:ARG:NH1	39:Lk:41:TYR:OH	2.07	0.87
1:L5:950:G:H22	1:L5:1035:U:H3	1.22	0.86
52:SE:166:THR:HG22	52:SE:168:LYS:HG3	1.55	0.86
46:S2:1736:A:H2	46:S2:1800:G:H21	1.23	0.86
52:SE:108:ARG:H	52:SE:108:ARG:HD2	1.42	0.84
58:SK:26:ASP:HB3	58:SK:29:MET:HE1	1.59	0.84
46:S2:116:U:H5'	46:S2:382:C:H1'	1.59	0.83
46:S2:1262:C:O2	76:Sd:10:HIS:NE2	2.12	0.81
46:S2:1426:G:OP1	63:SQ:69:ARG:NH1	2.13	0.81
46:S2:1093:G:H4'	69:SW:2:VAL:HG13	1.63	0.80
46:S2:1416:C:H3'	66:ST:129:ARG:HH12	1.44	0.80
66:ST:65:TYR:HB2	66:ST:123:LEU:HD22	1.64	0.80
46:S2:483:G:N2	46:S2:485:A:OP2	2.14	0.79
46:S2:1276:G:H5'	46:S2:1277:A:H5'	1.64	0.79
51:SD:42:THR:HG22	51:SD:44:THR:H	1.47	0.79
1:L5:4664:A:H2	1:L5:4681:G:H21	1.30	0.79
51:SD:74:GLN:HE22	51:SD:81:GLU:HA	1.48	0.78
46:S2:1442:U:N3	46:S2:1445:U:O4	2.16	0.78
62:SP:29:SER:H	62:SP:32:GLN:HE22	1.29	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:488:U:HO2'	46:S2:508:G:H1	1.32	0.77
78:Sg:57:ARG:HG3	78:Sg:59:LEU:HD23	1.66	0.77
46:S2:72:C:O2'	46:S2:74:G:N2	2.18	0.77
46:S2:539:U:O2	46:S2:547:G:N2	2.18	0.77
46:S2:492:C:O2'	46:S2:494:A:N6	2.18	0.76
46:S2:124:U:O2	46:S2:341:C:N4	2.18	0.76
51:SD:70:THR:HB	51:SD:86:LEU:HD23	1.66	0.76
70:SX:127:ASN:O	70:SX:127:ASN:ND2	2.19	0.75
14:LL:154:VAL:HG12	14:LL:155:MET:HG3	1.66	0.75
46:S2:95:G:O6	46:S2:435:G:N1	2.16	0.75
1:L5:189:G:H1	1:L5:252:G:H1	1.30	0.75
1:L5:4594:U:HO2'	34:Lf:2:SER:N	1.84	0.74
54:SG:193:ALA:HA	54:SG:196:LYS:HD2	1.70	0.74
46:S2:1489:C:O2'	46:S2:1491:G:OP2	2.06	0.74
1:L5:1013:C:OP1	1:L5:1015:C:N4	2.21	0.74
36:Lh:15:GLU:OE1	36:Lh:15:GLU:N	2.21	0.74
1:L5:3873:A:OP2	22:LT:2:THR:OG1	2.06	0.73
1:L5:4553:G:H2'	1:L5:4554:G:C8	2.22	0.73
7:LD:238:GLU:OE2	7:LD:238:GLU:N	2.21	0.73
46:S2:1611:G:OP1	65:SS:121:ARG:NH1	2.20	0.73
77:Se:99:LYS:O	77:Se:101:LYS:NZ	2.21	0.73
1:L5:2237:G:N2	1:L5:2238:G:O6	2.17	0.73
1:L5:3326:G:H21	1:L5:3329:G:N2	1.86	0.73
53:SF:75:SER:OG	53:SF:155:CYS:SG	2.46	0.73
1:L5:138:C:H2'	1:L5:139:G:H8	1.53	0.73
46:S2:1455:A:OP2	64:SR:3:ARG:NH1	2.22	0.73
66:ST:60:THR:HG23	66:ST:75:MET:HE3	1.69	0.73
1:L5:1562:G:H22	1:L5:1576:U:H3	1.34	0.73
78:Sg:114:SER:O	78:Sg:117:ASN:ND2	2.22	0.72
10:LG:157:ILE:HG22	10:LG:201:THR:HG23	1.71	0.72
18:LP:94:MET:HE2	18:LP:148:MET:HE3	1.70	0.72
46:S2:482:C:O2'	46:S2:485:A:OP1	2.07	0.72
46:S2:160:U:N3	46:S2:469:A:O2'	2.17	0.72
55:SH:73:GLN:NE2	55:SH:132:ASP:OD1	2.23	0.72
21:LS:21:LYS:NZ	21:LS:22:CYS:SG	2.62	0.72
47:S7:18:G:O2'	47:S7:57:G:N2	2.21	0.72
1:L5:3326:G:H21	1:L5:3329:G:H21	1.36	0.71
78:Sg:124:SER:OG	78:Sg:126:ASP:OD1	2.07	0.71
46:S2:96:C:H42	46:S2:434:A:H61	1.39	0.71
44:Lp:84:ARG:HG2	44:Lp:84:ARG:HH11	1.55	0.71
46:S2:834:C:H3'	46:S2:835:C:H4'	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sg:220:ASP:HB2	78:Sg:224:GLY:H	1.55	0.71
24:LV:71:GLU:O	24:LV:75:LYS:NZ	2.22	0.71
46:S2:497:C:H2'	46:S2:498:C:C2	2.26	0.71
46:S2:95:G:H1	46:S2:435:G:H22	1.38	0.71
52:SE:199:GLU:HB2	52:SE:207:VAL:HG12	1.72	0.71
56:SI:117:TYR:O	56:SI:153:LYS:NZ	2.24	0.71
11:LH:104:VAL:HG22	11:LH:113:GLU:HB2	1.73	0.71
46:S2:1407:G:H22	46:S2:1440:A:H2	1.36	0.71
46:S2:1422:A:H2'	46:S2:1423:G:H8	1.54	0.71
46:S2:52:G:N2	46:S2:508:G:N7	2.38	0.70
65:SS:105:ASN:O	65:SS:109:GLU:HG2	1.89	0.70
1:L5:1743:G:N2	1:L5:4087:C:OP1	2.23	0.70
46:S2:50:A:OP2	46:S2:473:C:N4	2.25	0.70
47:S6:13:G:H1	47:S6:23:C:H42	1.38	0.70
46:S2:482:C:N4	46:S2:486:A:OP2	2.24	0.70
48:SA:34:MET:HE3	48:SA:154:LEU:HD11	1.73	0.70
46:S2:146:G:N2	46:S2:174:C:N3	2.38	0.70
53:SF:47:LYS:NZ	63:SQ:116:ASP:OD1	2.24	0.70
46:S2:315:U:H2'	46:S2:316:C:C6	2.27	0.70
63:SQ:26:LYS:NZ	63:SQ:67:ASP:OD2	2.25	0.70
68:SV:74:LYS:HD3	68:SV:79:VAL:HG21	1.72	0.70
61:SO:61:LYS:HD3	61:SO:76:LEU:HB3	1.74	0.70
46:S2:145:G:H2'	46:S2:146:G:C8	2.27	0.69
52:SE:104:ASP:HB2	52:SE:110:ALA:HB2	1.73	0.69
1:L5:2019:G:OP2	45:Lr:98:ARG:NH2	2.22	0.69
10:LG:162:ASP:HB2	10:LG:163:PRO:HD3	1.74	0.69
46:S2:1421:G:H1'	46:S2:1422:A:H4'	1.74	0.69
65:SS:64:VAL:O	65:SS:68:ILE:HG12	1.93	0.69
46:S2:569:C:H1'	46:S2:584:A:H61	1.58	0.69
1:L5:4199:A:N7	4:LA:215:ASN:ND2	2.41	0.69
1:L5:386:G:O2'	1:L5:411:G:O6	2.06	0.69
12:LI:30:LYS:HG3	12:LI:63:GLU:HG3	1.75	0.69
20:LR:98:ARG:NH2	20:LR:130:ASN:OD1	2.24	0.69
46:S2:487:A:H2	46:S2:513:A:H61	1.41	0.69
74:Sb:36:LYS:HB2	74:Sb:43:ILE:HD13	1.75	0.69
1:L5:2342:C:OP1	1:L5:2522:C:O2'	2.11	0.69
48:SA:163:CYS:O	48:SA:164:ASN:ND2	2.18	0.69
56:SI:116:HIS:O	56:SI:152:ARG:NH1	2.25	0.69
46:S2:1406:A:H61	46:S2:1441:C:H42	1.41	0.68
46:S2:534:A:H2'	46:S2:535:G:C8	2.28	0.68
9:LF:127:VAL:HG13	9:LF:158:VAL:HG12	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sg:286:CYS:HA	78:Sg:302:TYR:HA	1.76	0.68
46:S2:515:U:H2'	46:S2:516:G:O4'	1.94	0.68
71:SY:38:THR:HG23	71:SY:39:GLU:OE2	1.94	0.68
46:S2:66:G:P	46:S2:82:G:H22	2.17	0.68
46:S2:92:A:H62	46:S2:445:G:H8	1.41	0.68
46:S2:869:G:N2	46:S2:869:G:OP2	2.27	0.68
1:L5:1909:C:O2'	1:L5:1910:G:N7	2.27	0.67
51:SD:195:SER:HB3	51:SD:201:LYS:HE2	1.75	0.67
54:SG:181:THR:HG22	54:SG:183:ARG:H	1.60	0.67
8:LE:169:ARG:NH1	8:LE:281:SER:OG	2.27	0.67
46:S2:1279:A:N1	46:S2:1321:G:N2	2.43	0.67
78:Sg:245:ARG:HD2	78:Sg:246:TYR:H	1.59	0.67
52:SE:57:THR:HG22	52:SE:59:ASP:H	1.58	0.67
1:L5:138:C:H2'	1:L5:139:G:C8	2.30	0.67
46:S2:538:C:H42	46:S2:547:G:H1	1.40	0.67
9:LF:108:GLU:OE2	22:LT:136:ARG:NH1	2.28	0.67
46:S2:558:U:H2'	46:S2:559:G:C8	2.29	0.67
48:SA:191:ARG:NH2	68:SV:44:GLY:O	2.28	0.67
33:Le:30:LYS:HG3	33:Le:31:ILE:HD12	1.75	0.67
20:LR:136:ARG:O	20:LR:140:GLU:HG2	1.94	0.66
46:S2:982:A:H2'	46:S2:983:G:C8	2.29	0.66
46:S2:1729:U:O2'	46:S2:1730:U:O5'	2.09	0.66
52:SE:9:LEU:HB3	52:SE:28:ALA:HB3	1.78	0.66
54:SG:120:ASP:HB3	54:SG:125:THR:HG21	1.75	0.66
58:SK:1:MET:HE2	58:SK:47:LYS:HB2	1.76	0.66
34:Lf:36:ARG:NH1	34:Lf:79:GLY:O	2.27	0.66
2:L7:4:U:OP1	2:L7:25:G:N2	2.28	0.66
7:LD:293:ARG:O	7:LD:293:ARG:HD3	1.95	0.66
21:LS:81:TRP:HZ3	21:LS:130:GLU:HG3	1.61	0.66
64:SR:27:ASP:OD2	64:SR:30:THR:OG1	2.13	0.66
67:SU:56:MET:HB2	67:SU:86:LYS:HB3	1.77	0.66
71:SY:41:ARG:HH12	71:SY:57:VAL:H	1.42	0.66
9:LF:241:GLY:O	9:LF:268:ARG:NH2	2.29	0.66
46:S2:92:A:OP1	52:SE:3:ARG:NH2	2.26	0.66
50:SC:200:ARG:O	57:SJ:54:ARG:NH1	2.25	0.66
1:L5:4423:G:OP1	17:LO:176:ARG:NH1	2.29	0.66
50:SC:266:TYR:O	50:SC:270:THR:OG1	2.14	0.66
59:SL:97:ARG:O	59:SL:97:ARG:NH1	2.27	0.66
13:LJ:55:TYR:HA	13:LJ:64:ARG:HG2	1.77	0.65
78:Sg:34:ALA:HB1	78:Sg:66:VAL:HG23	1.78	0.65
1:L5:761:C:H5	1:L5:810:G:H1	1.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:68:ALA:O	8:LE:72:ARG:HG3	1.97	0.65
24:LV:31:ASN:C	24:LV:31:ASN:HD22	2.03	0.65
46:S2:873:A:O2'	46:S2:875:G:OP2	2.14	0.65
46:S2:477:A:H4'	46:S2:488:U:H2'	1.76	0.65
46:S2:569:C:O2'	46:S2:584:A:N1	2.30	0.65
78:Sg:99:ARG:HD3	78:Sg:100:ARG:O	1.96	0.65
5:LB:222:VAL:O	5:LB:343:ARG:NH1	2.30	0.65
8:LE:140:PRO:HG2	8:LE:143:GLN:HG3	1.79	0.65
47:S6:34:C:H42	79:Sx:37:G:H1	1.44	0.65
46:S2:554:U:H2'	46:S2:555:A:H2'	1.78	0.65
71:SY:121:ALA:HA	71:SY:124:ASN:HB2	1.77	0.65
12:LI:87:ILE:HG12	12:LI:138:ILE:HG12	1.77	0.65
1:L5:753:G:O2'	1:L5:754:A:OP1	2.12	0.65
1:L5:4399:G:H1	1:L5:4603:A:H62	1.43	0.65
60:SN:87:ASP:OD1	60:SN:87:ASP:N	2.30	0.65
29:La:72:THR:HG22	29:La:110:LYS:HB3	1.79	0.64
62:SP:83:MET:HE3	62:SP:84:ILE:O	1.97	0.64
46:S2:311:C:O2'	46:S2:341:C:O4'	2.16	0.64
46:S2:944:U:OP1	49:SB:214:LYS:NZ	2.30	0.64
1:L5:4573:G:OP2	1:L5:4573:G:N2	2.23	0.64
58:SK:91:PRO:HB2	58:SK:94:LEU:HD23	1.79	0.64
64:SR:72:LYS:NZ	64:SR:75:GLU:OE1	2.31	0.64
47:S7:7:A:N6	47:S7:68:C:N3	2.45	0.64
6:LC:189:MET:HE3	6:LC:195:LYS:HD2	1.79	0.64
46:S2:994:G:N7	73:Sa:15:ARG:NH1	2.45	0.64
46:S2:1792:A:H5''	54:SG:75:LEU:HD11	1.80	0.64
47:S6:7:A:H62	47:S6:67:U:H3	1.45	0.64
65:SS:89:ASP:HB3	65:SS:93:GLY:H	1.59	0.64
24:LV:97:TYR:OH	25:LW:37:GLU:OE2	2.10	0.64
72:SZ:79:ILE:HG21	72:SZ:84:ALA:HB2	1.79	0.64
1:L5:3904:A:H5''	13:LJ:108:GLY:HA3	1.79	0.64
16:LN:116:LEU:HD22	16:LN:135:ILE:HD11	1.79	0.64
46:S2:1294:A:H2'	46:S2:1295:G:C8	2.33	0.64
46:S2:57:U:H3	46:S2:88:G:H1	1.45	0.64
78:Sg:92:LEU:HG	78:Sg:93:THR:HG23	1.78	0.64
4:LA:28:ARG:HG3	4:LA:123:ARG:HH11	1.62	0.63
18:LP:39:MET:HG2	18:LP:43:LYS:HD3	1.79	0.63
46:S2:862:A:O2'	46:S2:863:A:OP2	2.12	0.63
46:S2:914:A:N6	55:SH:98:ARG:O	2.24	0.63
58:SK:3:MET:SD	58:SK:7:ASN:ND2	2.72	0.63
1:L5:2083:G:OP2	33:Le:101:HIS:ND1	2.20	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:473:C:OP1	46:S2:475:G:N2	2.31	0.63
46:S2:583:U:H2'	46:S2:584:A:C8	2.34	0.63
62:SP:18:ARG:NH1	65:SS:88:LYS:O	2.31	0.63
71:SY:120:THR:O	71:SY:124:ASN:HB2	1.99	0.63
78:Sg:168:CYS:SG	78:Sg:198:VAL:HG13	2.39	0.63
46:S2:496:U:H2'	46:S2:497:C:C2	2.34	0.63
47:S7:34:C:H42	79:Sx:40:G:H1	1.44	0.63
54:SG:191:ARG:HB3	54:SG:195:LYS:HZ2	1.63	0.63
57:SJ:84:ILE:O	57:SJ:108:ARG:NH1	2.31	0.63
9:LF:170:LYS:O	9:LF:174:GLU:HG2	1.99	0.63
39:Lk:13:LEU:HD23	39:Lk:16:ARG:HH12	1.63	0.63
46:S2:589:G:OP2	46:S2:589:G:N2	2.31	0.63
50:SC:263:LYS:HE2	50:SC:268:GLU:HG2	1.81	0.63
78:Sg:11:LEU:HB2	78:Sg:307:VAL:HB	1.81	0.63
22:LT:103:ASP:O	22:LT:107:LYS:HG2	1.99	0.63
46:S2:613:U:H4'	77:Se:89:GLN:HE22	1.64	0.63
47:S7:54:A:O2'	47:S7:58:A:N1	2.32	0.63
51:SD:35:SER:OG	51:SD:51:LEU:O	2.16	0.63
70:SX:61:GLN:HB3	70:SX:62:PRO:HD3	1.80	0.63
78:Sg:130:LYS:HD3	78:Sg:141:THR:HB	1.81	0.63
46:S2:351:C:O2'	46:S2:384:G:N1	2.30	0.63
46:S2:1555:C:H2'	46:S2:1556:U:C4	2.33	0.63
78:Sg:245:ARG:HD2	78:Sg:246:TYR:N	2.13	0.63
1:L5:2075:G:N2	1:L5:2078:G:OP2	2.24	0.62
14:LL:170:THR:HG22	14:LL:173:GLU:HG2	1.81	0.62
24:LV:111:GLU:HG2	24:LV:131:ARG:HH11	1.63	0.62
5:LB:216:MET:HE2	5:LB:283:LYS:HD3	1.81	0.62
46:S2:456:A:O2'	46:S2:1736:A:H8	1.81	0.62
46:S2:564:G:H2'	46:S2:565:A:C8	2.34	0.62
14:LL:63:THR:HG22	14:LL:65:ARG:H	1.64	0.62
1:L5:4560:C:H2'	1:L5:4561:G:C8	2.35	0.62
51:SD:172:VAL:HG22	51:SD:185:LYS:HD2	1.80	0.62
1:L5:2164:G:H22	40:Ll:51:LEU:HD22	1.65	0.62
49:SB:113:MET:HE3	49:SB:142:PHE:HE2	1.65	0.62
1:L5:4425:U:H3	1:L5:4509:G:H1	1.47	0.62
1:L5:3443:U:OP1	1:L5:4203:G:O2'	2.17	0.62
5:LB:329:ASP:OD1	5:LB:329:ASP:N	2.32	0.62
46:S2:1422:A:H2'	46:S2:1423:G:C8	2.32	0.62
78:Sg:21:ILE:HD13	78:Sg:33:SER:HB3	1.82	0.62
14:LL:63:THR:HG21	29:La:66:ASN:HB3	1.82	0.62
46:S2:52:G:H2'	46:S2:53:C:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:462:U:H3	46:S2:469:A:H61	1.47	0.62
33:Le:98:GLU:OE2	33:Le:123:THR:OG1	2.18	0.62
46:S2:525:U:H3	46:S2:595:A:H2	1.46	0.62
65:SS:36:VAL:HG23	65:SS:99:LEU:HD22	1.82	0.62
78:Sg:220:ASP:H	78:Sg:224:GLY:HA2	1.65	0.62
1:L5:4387:A:H1'	1:L5:4388:G:C8	2.34	0.61
70:SX:24:ASP:OD1	70:SX:24:ASP:N	2.32	0.61
1:L5:189:G:H22	1:L5:252:G:H22	1.49	0.61
1:L5:3815:C:H5	10:LG:73:ARG:HH12	1.47	0.61
46:S2:126:G:N7	46:S2:180:G:N2	2.48	0.61
46:S2:1406:A:O2'	46:S2:1445:U:O2	2.12	0.61
64:SR:79:GLU:OE2	64:SR:83:ASN:ND2	2.32	0.61
11:LH:18:ILE:HG23	11:LH:26:ILE:HB	1.80	0.61
46:S2:47:G:H22	46:S2:479:G:N2	1.97	0.61
56:SI:113:TYR:HD2	56:SI:121:LEU:HD22	1.65	0.61
6:LC:14:LYS:N	6:LC:14:LYS:HD3	2.16	0.61
56:SI:36:THR:HB	56:SI:96:LEU:HB2	1.81	0.61
28:LZ:59:LYS:H	28:LZ:59:LYS:HD3	1.66	0.61
74:Sb:81:ARG:HH12	74:Sb:84:HIS:HA	1.65	0.61
1:L5:2314:G:H1	1:L5:2324:G:H22	1.47	0.61
46:S2:847:G:N3	52:SE:19:MET:HG2	2.15	0.61
63:SQ:45:ARG:HH12	63:SQ:48:GLN:HG3	1.66	0.61
1:L5:1168:G:N7	19:LQ:104:ARG:NH2	2.49	0.61
1:L5:4178:C:OP1	5:LB:246:ARG:NH1	2.34	0.61
1:L5:407:A:O2'	1:L5:410:G:OP2	2.18	0.61
71:SY:104:ARG:HD2	71:SY:104:ARG:H	1.65	0.61
1:L5:458:C:O2'	1:L5:459:C:OP1	2.19	0.61
1:L5:4559:G:O2'	1:L5:4560:C:O4'	2.13	0.61
46:S2:1240:U:H5''	62:SP:124:LYS:HE2	1.83	0.61
46:S2:820:G:H1	46:S2:830:C:H41	1.49	0.61
47:S6:29:G:H1	47:S6:41:C:H5	1.47	0.61
58:SK:42:ASN:OD1	58:SK:46:MET:HE3	2.01	0.61
46:S2:1745:G:O2'	46:S2:1791:A:N6	2.33	0.60
61:SO:145:GLY:O	73:Sa:22:ARG:NH2	2.33	0.60
23:LU:102:VAL:O	23:LU:102:VAL:HG12	2.01	0.60
53:SF:17:ILE:HA	53:SF:48:TYR:HE1	1.66	0.60
65:SS:5:ILE:HB	72:SZ:49:LEU:HB3	1.82	0.60
71:SY:54:VAL:HG12	71:SY:79:LEU:HD13	1.83	0.60
14:LL:47:ALA:HB3	14:LL:48:PRO:HD3	1.83	0.60
47:S7:53:G:H2'	47:S7:54:A:H8	1.66	0.60
61:SO:43:HIS:NE2	61:SO:52:THR:HG23	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Sc:15:THR:HG22	75:Sc:16:LYS:H	1.67	0.60
1:L5:3256:A:H2'	1:L5:3257:G:C8	2.36	0.60
46:S2:523:A:OP1	57:SJ:146:SER:OG	2.15	0.60
46:S2:1229:A:H2'	46:S2:1230:G:C8	2.36	0.60
71:SY:41:ARG:HH21	71:SY:94:HIS:HD2	1.49	0.60
46:S2:126:G:OP1	54:SG:198:ARG:NH1	2.34	0.60
46:S2:641:A:H2'	46:S2:642:A:C8	2.36	0.60
46:S2:1316:U:OP1	58:SK:1:MET:N	2.34	0.60
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.83	0.60
22:LT:41:ASP:OD1	22:LT:99:SER:OG	2.20	0.60
46:S2:540:C:OP1	46:S2:548:G:N2	2.35	0.60
46:S2:1747:U:OP1	54:SG:31:ARG:NH2	2.35	0.60
51:SD:68:GLU:O	51:SD:72:VAL:HG23	2.00	0.60
62:SP:75:VAL:HG12	62:SP:93:MET:HG2	1.83	0.60
1:L5:508:G:H1	1:L5:661:U:H3	1.50	0.60
46:S2:875:G:H2'	46:S2:876:A:H8	1.67	0.60
51:SD:194:PRO:O	51:SD:197:LYS:NZ	2.35	0.60
71:SY:37:LYS:HD2	71:SY:57:VAL:HG23	1.84	0.60
1:L5:2602:G:O2'	1:L5:3495:U:O4	2.17	0.60
46:S2:800:U:OP2	46:S2:868:G:N2	2.34	0.60
48:SA:31:ASP:OD1	48:SA:32:PHE:N	2.34	0.60
63:SQ:74:GLY:O	63:SQ:80:GLN:NE2	2.35	0.60
46:S2:831:A:OP2	46:S2:846:G:N2	2.35	0.60
46:S2:1103:G:OP2	49:SB:151:ARG:NH2	2.35	0.60
46:S2:1411:C:O2'	46:S2:1412:G:O5'	2.19	0.60
50:SC:135:GLY:O	50:SC:136:HIS:ND1	2.35	0.60
7:LD:238:GLU:O	7:LD:242:LYS:HG2	2.01	0.59
43:Lo:75:PRO:HD2	43:Lo:76:ASN:N	2.16	0.59
46:S2:1753:C:H3'	46:S2:1754:C:H4'	1.83	0.59
54:SG:2:LYS:HG2	54:SG:15:LEU:HD21	1.83	0.59
1:L5:3374:A:H2'	1:L5:3375:A:C8	2.36	0.59
16:LN:145:ASN:HB3	16:LN:148:THR:HG22	1.84	0.59
46:S2:498:C:H1'	46:S2:499:C:C6	2.36	0.59
52:SE:35:PRO:HD2	52:SE:83:PRO:HG2	1.84	0.59
70:SX:41:PHE:HZ	70:SX:102:VAL:HG12	1.67	0.59
1:L5:3530:G:H2'	1:L5:3531:G:C8	2.37	0.59
1:L5:4233:U:O2'	5:LB:182:GLU:OE2	2.17	0.59
46:S2:351:C:HO2'	46:S2:384:G:H1	1.50	0.59
46:S2:526:A:H2'	46:S2:527:A:C8	2.37	0.59
54:SG:191:ARG:O	54:SG:195:LYS:HG3	2.02	0.59
1:L5:4640:G:H2'	1:L5:4641:G:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:37:ASP:OD1	11:LH:39:ASN:ND2	2.34	0.59
46:S2:58:C:N4	46:S2:62:G:N7	2.48	0.59
1:L5:3773:G:N1	35:Lg:98:GLU:OE2	2.34	0.59
52:SE:90:ILE:HG23	52:SE:99:PHE:HB2	1.84	0.59
58:SK:19:GLY:HA2	58:SK:71:LEU:HD12	1.85	0.59
60:SN:4:MET:HE2	60:SN:124:ARG:NH2	2.17	0.59
77:Se:101:LYS:HD2	77:Se:101:LYS:H	1.67	0.59
1:L5:189:G:N2	1:L5:252:G:H22	2.01	0.59
63:SQ:12:VAL:HG11	63:SQ:90:LYS:HB3	1.83	0.59
69:SW:106:THR:HG22	69:SW:108:ALA:H	1.66	0.59
1:L5:457:C:OP1	8:LE:121:PRO:HA	2.02	0.59
1:L5:703:G:H3'	1:L5:704:U:H4'	1.85	0.59
1:L5:1558:C:H41	1:L5:1579:A:H2	1.50	0.59
1:L5:3787:U:O4	1:L5:3801:G:O6	2.21	0.59
64:SR:72:LYS:NZ	64:SR:72:LYS:O	2.34	0.59
46:S2:538:C:H5'	46:S2:539:U:H5	1.68	0.58
46:S2:845:U:N3	46:S2:846:G:O6	2.36	0.58
46:S2:846:G:H3'	46:S2:847:G:C8	2.38	0.58
76:Sd:12:ARG:HB3	76:Sd:18:SER:HB3	1.84	0.58
75:Sc:31:ARG:HA	75:Sc:43:ILE:HA	1.85	0.58
1:L5:936:C:N4	1:L5:1054:G:O6	2.35	0.58
54:SG:27:PHE:HE2	54:SG:111:LEU:HD11	1.68	0.58
78:Sg:251:ALA:HB2	78:Sg:289:LEU:HD22	1.85	0.58
1:L5:3904:A:H4'	1:L5:3905:C:OP1	2.02	0.58
35:Lg:99:GLU:OE1	35:Lg:99:GLU:HA	2.02	0.58
41:Lm:83:ARG:O	41:Lm:87:GLN:HG3	2.03	0.58
46:S2:221:U:H2'	46:S2:222:U:O4'	2.04	0.58
46:S2:1680:A:H2'	53:SF:60:ARG:HD2	1.83	0.58
66:ST:9:VAL:HG21	66:ST:138:VAL:HG13	1.85	0.58
36:Lh:96:THR:HG22	36:Lh:98:HIS:H	1.68	0.58
46:S2:509:A:H5''	46:S2:510:G:H8	1.68	0.58
46:S2:561:A:H2'	46:S2:562:A:C8	2.39	0.58
47:S7:53:G:O2'	47:S7:54:A:OP1	2.18	0.58
54:SG:6:SER:HA	54:SG:13:GLN:HB3	1.86	0.58
1:L5:953:C:H2'	1:L5:954:G:C8	2.39	0.58
1:L5:2499:A:H2'	1:L5:2500:A:C8	2.38	0.58
21:LS:147:ASP:HB3	21:LS:150:ILE:HB	1.85	0.58
27:LY:116:LYS:O	27:LY:120:GLU:HG2	2.02	0.58
48:SA:188:THR:HG22	48:SA:189:ILE:HG12	1.84	0.58
50:SC:116:THR:OG1	50:SC:119:GLY:O	2.20	0.58
71:SY:46:LYS:HD3	71:SY:46:LYS:N	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1388:G:N2	51:SD:206:ASP:OD1	2.36	0.58
46:S2:1730:U:OP1	56:SI:17:LYS:NZ	2.34	0.58
1:L5:3480:G:OP2	1:L5:3480:G:N2	2.26	0.58
53:SF:25:THR:OG1	53:SF:26:ASP:OD1	2.21	0.58
1:L5:1338:A:H62	1:L5:1465:G:H1	1.52	0.58
1:L5:3783:U:H3	1:L5:3805:G:H1	1.49	0.58
27:LY:37:GLU:OE1	27:LY:37:GLU:N	2.30	0.58
46:S2:1414:G:H2'	46:S2:1415:A:C8	2.39	0.58
51:SD:210:ILE:HG12	64:SR:16:ILE:HD11	1.85	0.58
61:SO:122:SER:O	61:SO:122:SER:OG	2.20	0.58
5:LB:315:ASN:HD21	5:LB:326:VAL:H	1.52	0.58
46:S2:480:C:H3'	46:S2:481:G:H8	1.69	0.58
14:LL:176:PHE:O	29:La:138:LYS:NZ	2.31	0.57
17:LO:3:GLU:HG2	17:LO:31:ARG:HH22	1.68	0.57
46:S2:499:C:N4	46:S2:505:G:H1	2.01	0.57
46:S2:1778:G:H2'	46:S2:1779:C:O4'	2.04	0.57
47:S7:13:G:H1	47:S7:23:C:H42	1.50	0.57
55:SH:133:LEU:HD11	55:SH:176:VAL:HG13	1.85	0.57
78:Sg:72:SER:OG	78:Sg:73:SER:N	2.37	0.57
1:L5:1014:C:H5''	1:L5:1015:C:C5	2.39	0.57
47:S7:29:G:H22	47:S7:41:C:H5	1.51	0.57
47:S7:43:G:H2'	47:S7:44:A:C8	2.38	0.57
54:SG:10:THR:HG22	54:SG:128:THR:HG22	1.85	0.57
54:SG:72:ARG:HH11	54:SG:72:ARG:HG3	1.69	0.57
53:SF:75:SER:HG	53:SF:155:CYS:HG	1.46	0.57
78:Sg:201:SER:OG	78:Sg:203:ASP:O	2.22	0.57
62:SP:28:MET:HG2	62:SP:32:GLN:HE21	1.69	0.57
1:L5:687:C:OP1	45:Lr:84:LYS:NZ	2.36	0.57
1:L5:3967:C:O2'	30:Lb:36:ASP:OD1	2.21	0.57
63:SQ:34:VAL:HG12	63:SQ:70:VAL:HB	1.86	0.57
1:L5:1470:U:OP2	29:La:26:ARG:NH2	2.38	0.57
1:L5:4677:C:HO2'	1:L5:4678:U:H6	1.53	0.57
1:L5:4551:C:O2'	1:L5:4552:C:O5'	2.23	0.57
34:Lf:106:TYR:O	34:Lf:108:SER:N	2.37	0.57
46:S2:64:A:O2'	46:S2:66:G:OP2	2.20	0.57
46:S2:1204:G:H2'	46:S2:1205:A:C8	2.40	0.57
69:SW:28:ARG:HB3	69:SW:29:PRO:HD3	1.87	0.57
46:S2:524:A:OP2	57:SJ:127:ARG:NH2	2.37	0.57
47:S6:43:G:H2'	47:S6:44:A:C8	2.40	0.57
47:S6:66:C:HO2'	47:S6:67:U:H6	1.51	0.57
1:L5:4556:A:H4'	5:LB:95:THR:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LM:24:LEU:O	15:LM:43:THR:HG21	2.04	0.57
1:L5:494:G:H1	1:L5:668:G:H1	1.50	0.56
6:LC:13:GLU:HG3	6:LC:14:LYS:HD3	1.87	0.56
14:LL:150:LEU:HD11	36:Lh:123:ALA:HB3	1.87	0.56
51:SD:55:THR:HB	51:SD:90:LYS:HE3	1.87	0.56
1:L5:4171:A:H5''	1:L5:4173:G:H4'	1.87	0.56
8:LE:249:GLU:OE2	8:LE:249:GLU:N	2.34	0.56
48:SA:177:MET:O	48:SA:181:GLU:HG3	2.05	0.56
49:SB:169:MET:O	49:SB:173:THR:HG22	2.04	0.56
72:SZ:56:ASP:OD1	72:SZ:57:LYS:N	2.38	0.56
1:L5:267:G:H2'	1:L5:268:G:H8	1.71	0.56
1:L5:1031:G:H2'	1:L5:1033:G:C8	2.41	0.56
43:Lo:14:LYS:HD2	43:Lo:77:CYS:HB2	1.87	0.56
46:S2:830:C:H5'	52:SE:21:ASP:HB2	1.86	0.56
46:S2:989:C:H5''	49:SB:116:LYS:HG2	1.88	0.56
51:SD:40:ARG:NH1	51:SD:47:GLU:OE2	2.38	0.56
1:L5:1218:C:H2'	1:L5:1219:C:C6	2.41	0.56
1:L5:2656:G:N2	1:L5:3255:C:N3	2.53	0.56
25:LW:53:VAL:O	25:LW:57:ARG:HG3	2.05	0.56
39:Lk:52:LYS:H	39:Lk:52:LYS:HD2	1.70	0.56
46:S2:509:A:H2	57:SJ:2:PRO:HB2	1.70	0.56
53:SF:28:VAL:HG23	53:SF:110:GLN:HG2	1.87	0.56
1:L5:1218:C:C4	1:L5:1219:C:N4	2.74	0.56
1:L5:4612:C:H2'	1:L5:4613:U:C6	2.39	0.56
7:LD:235:MET:SD	7:LD:242:LYS:NZ	2.78	0.56
46:S2:57:U:OP1	71:SY:111:LYS:NZ	2.31	0.56
46:S2:1445:U:OP1	63:SQ:15:ARG:NH2	2.38	0.56
46:S2:1755:G:H1	46:S2:1780:G:H1'	1.71	0.56
53:SF:69:VAL:O	53:SF:73:THR:HG23	2.05	0.56
66:ST:113:VAL:HG12	66:ST:123:LEU:HD12	1.88	0.56
1:L5:254:C:H2'	1:L5:255:G:C8	2.41	0.56
46:S2:77:A:H4'	54:SG:176:ILE:HG12	1.88	0.56
63:SQ:28:GLY:HA3	63:SQ:67:ASP:HB3	1.87	0.56
71:SY:21:LYS:HE3	71:SY:22:GLN:H	1.70	0.56
1:L5:1008:A:H3'	1:L5:1009:C:H5''	1.86	0.56
1:L5:1222:C:O2'	1:L5:1226:G:N3	2.35	0.56
1:L5:1258:G:H1	1:L5:1904:C:H42	1.54	0.56
1:L5:4323:C:O2'	1:L5:4325:A:OP2	2.20	0.56
52:SE:198:ARG:HG3	52:SE:208:VAL:HG22	1.86	0.56
65:SS:62:ASP:OD1	65:SS:63:GLU:N	2.39	0.56
1:L5:385:A:OP2	27:LY:89:LYS:NZ	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1323:G:OP2	46:S2:1323:G:N2	2.37	0.56
46:S2:1777:G:H5'	46:S2:1778:G:N7	2.21	0.56
71:SY:56:PHE:N	71:SY:74:MET:SD	2.79	0.56
46:S2:90:G:O6	54:SG:88:ARG:NE	2.39	0.55
66:ST:39:LEU:HD12	66:ST:40:ALA:H	1.71	0.55
1:L5:459:C:H2'	1:L5:460:G:H8	1.71	0.55
46:S2:34:U:O2'	46:S2:35:C:OP1	2.21	0.55
71:SY:80:ASP:OD1	71:SY:83:LYS:NZ	2.37	0.55
13:LJ:48:PRO:HB2	13:LJ:70:VAL:HG22	1.89	0.55
48:SA:85:ARG:NH2	64:SR:81:ARG:O	2.40	0.55
75:Sc:14:VAL:HG22	75:Sc:32:VAL:HG12	1.88	0.55
1:L5:1255:C:N3	1:L5:1256:C:N4	2.50	0.55
7:LD:41:LYS:HB2	22:LT:68:THR:O	2.05	0.55
14:LL:107:THR:HG22	37:Li:20:ASN:HB2	1.88	0.55
62:SP:110:GLU:HB2	65:SS:117:ILE:HD11	1.88	0.55
1:L5:1294:C:O2'	1:L5:1296:G:OP2	2.24	0.55
1:L5:1902:A:H2'	1:L5:1903:A:C8	2.40	0.55
6:LC:163:LYS:HB2	6:LC:166:GLU:HG3	1.89	0.55
7:LD:152:ARG:O	7:LD:157:ASN:ND2	2.39	0.55
27:LY:37:GLU:H	27:LY:37:GLU:CD	2.12	0.55
42:Ln:10:MET:HE2	46:S2:1173:U:H4'	1.89	0.55
46:S2:540:C:H4'	46:S2:548:G:H22	1.69	0.55
52:SE:183:VAL:HG21	52:SE:218:PHE:HE2	1.71	0.55
67:SU:66:ARG:HG3	67:SU:68:THR:HG22	1.87	0.55
1:L5:4108:G:OP1	5:LB:3:HIS:HB2	2.07	0.55
39:Lk:10:ASP:N	39:Lk:10:ASP:OD1	2.32	0.55
44:Lp:84:ARG:HG2	44:Lp:84:ARG:NH1	2.18	0.55
46:S2:58:C:O2'	46:S2:59:U:O5'	2.25	0.55
46:S2:217:G:H2'	46:S2:218:C:O4'	2.07	0.55
46:S2:384:G:H21	59:SL:133:PRO:HG2	1.71	0.55
1:L5:2214:G:HO2'	1:L5:3329:G:H8	1.55	0.55
46:S2:219:A:C6	46:S2:220:U:C4	2.94	0.55
60:SN:127:ARG:O	60:SN:131:THR:HG23	2.06	0.55
1:L5:455:C:O2'	1:L5:456:G:H8	1.90	0.55
1:L5:923:G:O2'	1:L5:924:G:OP1	2.24	0.55
12:LI:66:GLU:OE1	12:LI:69:ARG:NH1	2.40	0.55
51:SD:142:LEU:HD22	51:SD:150:MET:HE3	1.89	0.55
72:SZ:72:VAL:O	72:SZ:76:ARG:HG2	2.06	0.55
1:L5:828:C:H3'	1:L5:829:G:H21	1.71	0.55
31:Lc:13:SER:O	31:Lc:17:ARG:HD3	2.07	0.55
46:S2:1280:C:H2'	46:S2:1281:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SC:79:GLU:OE1	68:SV:11:LEU:HB3	2.07	0.55
63:SQ:9:SER:HB2	63:SQ:24:HIS:HE1	1.71	0.55
1:L5:760:G:O2'	1:L5:761:C:OP1	2.25	0.54
6:LC:283:LYS:HD3	19:LQ:103:LEU:HD22	1.88	0.54
46:S2:90:G:H2'	46:S2:91:A:H5'	1.89	0.54
51:SD:74:GLN:HE22	51:SD:81:GLU:CA	2.18	0.54
72:SZ:57:LYS:HZ3	72:SZ:61:GLU:HG3	1.71	0.54
78:Sg:57:ARG:HD2	78:Sg:94:THR:HG22	1.89	0.54
46:S2:562:A:H2'	46:S2:563:U:C6	2.42	0.54
73:Sa:46:GLU:O	73:Sa:49:ALA:N	2.40	0.54
1:L5:719:A:H2'	1:L5:720:C:C6	2.42	0.54
5:LB:393:LYS:O	5:LB:397:ILE:HG23	2.07	0.54
33:Le:76:LYS:NZ	33:Le:98:GLU:OE1	2.27	0.54
36:Lh:29:SER:O	36:Lh:33:VAL:HG23	2.07	0.54
46:S2:619:C:H41	70:SX:67:ARG:HH22	1.55	0.54
62:SP:29:SER:H	62:SP:32:GLN:NE2	2.01	0.54
72:SZ:79:ILE:CD1	72:SZ:83:LEU:HD23	2.38	0.54
1:L5:738:G:OP2	9:LF:98:ARG:NE	2.38	0.54
1:L5:3787:U:H3	1:L5:3801:G:H1	1.55	0.54
1:L5:4552:C:H2'	1:L5:4553:G:H4'	1.88	0.54
1:L5:3718:U:H2'	1:L5:3719:U:C6	2.43	0.54
46:S2:501:A:O2'	46:S2:502:C:O4'	2.17	0.54
1:L5:139:G:H2'	1:L5:140:G:C8	2.42	0.54
1:L5:1523:C:H3'	1:L5:1524:G:C8	2.42	0.54
7:LD:55:VAL:HG12	7:LD:60:ILE:HG12	1.89	0.54
7:LD:164:LYS:HD3	7:LD:195:HIS:NE2	2.23	0.54
40:Ll:9:ILE:HG23	40:Ll:51:LEU:HD11	1.89	0.54
46:S2:290:G:OP1	52:SE:155:LYS:NZ	2.24	0.54
46:S2:1556:U:N3	76:Sd:19:ARG:HA	2.22	0.54
49:SB:137:LEU:HG	49:SB:215:VAL:HG22	1.89	0.54
46:S2:1532:A:H2'	46:S2:1533:C:C6	2.42	0.54
47:S7:65:C:O2'	47:S7:66:C:H5'	2.08	0.54
56:SI:153:LYS:N	56:SI:153:LYS:HD3	2.23	0.54
1:L5:294:A:OP2	43:Lo:39:ARG:NH1	2.35	0.54
46:S2:535:G:H2'	46:S2:536:G:H8	1.73	0.54
1:L5:479:C:OP1	45:Lr:67:ARG:NH1	2.41	0.54
1:L5:1034:G:H2'	1:L5:1035:U:C6	2.43	0.54
1:L5:1164:G:H5'	19:LQ:19:LYS:HG2	1.90	0.54
46:S2:683:U:O2'	69:SW:4:MET:SD	2.65	0.54
46:S2:1418:C:O2'	46:S2:1419:C:O5'	2.26	0.54
3:L8:62:A:OP1	36:Lh:51:ARG:NH2	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:29:ALA:O	12:LI:32:ARG:NH2	2.37	0.53
13:LJ:31:ASP:O	13:LJ:35:ARG:HG3	2.08	0.53
46:S2:66:G:N2	46:S2:68:A:O4'	2.41	0.53
46:S2:92:A:N6	46:S2:445:G:H8	2.06	0.53
46:S2:527:A:H5''	77:Se:109:ARG:NH1	2.23	0.53
46:S2:1318:C:H2'	46:S2:1319:G:C8	2.43	0.53
47:S6:53:G:O2'	47:S6:54:A:OP1	2.26	0.53
52:SE:55:ALA:HB1	52:SE:60:GLU:HB2	1.90	0.53
1:L5:682:G:H2'	1:L5:683:C:C6	2.44	0.53
1:L5:2565:G:N1	1:L5:2568:C:OP2	2.29	0.53
6:LC:308:LYS:HD3	6:LC:310:HIS:NE2	2.23	0.53
46:S2:509:A:H5''	46:S2:510:G:C8	2.43	0.53
46:S2:1277:A:H61	46:S2:1323:G:H8	1.57	0.53
62:SP:69:PRO:O	62:SP:70:MET:HG3	2.08	0.53
64:SR:116:ASN:OD1	64:SR:117:LEU:N	2.35	0.53
71:SY:111:LYS:O	71:SY:114:MET:HB2	2.08	0.53
1:L5:511:G:O2'	1:L5:513:U:OP2	2.26	0.53
1:L5:1009:C:H42	1:L5:1017:A:N6	2.07	0.53
46:S2:1416:C:H1'	46:S2:1417:C:C5	2.44	0.53
46:S2:1715:U:H2'	46:S2:1716:A:C8	2.44	0.53
47:S7:26:G:H1	47:S7:44:A:H2	1.55	0.53
13:LJ:158:SER:OG	13:LJ:161:GLU:OE1	2.26	0.53
16:LN:45:PRO:O	16:LN:49:ARG:HG3	2.08	0.53
52:SE:120:LYS:HD3	52:SE:120:LYS:N	2.23	0.53
53:SF:184:SER:OG	53:SF:185:SER:N	2.41	0.53
71:SY:78:SER:OG	71:SY:79:LEU:N	2.41	0.53
10:LG:90:GLN:O	10:LG:94:GLN:HG2	2.09	0.53
20:LR:105:LEU:HD13	20:LR:135:LYS:HE3	1.90	0.53
46:S2:76:U:H2'	54:SG:173:ALA:HB3	1.89	0.53
46:S2:1522:C:H2'	65:SS:136:THR:HG22	1.90	0.53
65:SS:74:PRO:HD2	65:SS:75:ARG:H	1.73	0.53
1:L5:3288:U:H3	1:L5:3487:A:H62	1.56	0.53
22:LT:158:PHE:CD1	22:LT:158:PHE:O	2.62	0.53
23:LU:25:CYS:O	23:LU:29:VAL:HB	2.08	0.53
46:S2:1537:G:H2'	46:S2:1538:A:C8	2.43	0.53
57:SJ:111:GLN:HG3	57:SJ:145:PRO:HB3	1.90	0.53
63:SQ:21:ALA:HB2	63:SQ:72:VAL:HG23	1.88	0.53
72:SZ:50:PHE:HD1	72:SZ:54:THR:HG23	1.72	0.53
1:L5:1043:U:O2'	1:L5:1045:G:O4'	2.26	0.53
10:LG:160:ASP:OD1	10:LG:160:ASP:N	2.42	0.53
13:LJ:144:LYS:O	13:LJ:148:THR:OG1	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1229:A:H2'	46:S2:1230:G:H8	1.74	0.53
46:S2:1298:U:H2'	46:S2:1299:G:H8	1.73	0.53
47:S7:29:G:H1	47:S7:41:C:H41	1.56	0.53
54:SG:192:ILE:HA	54:SG:195:LYS:HD2	1.91	0.53
63:SQ:39:LEU:HA	63:SQ:42:ILE:HD11	1.91	0.53
78:Sg:59:LEU:HB3	78:Sg:90:TRP:HZ3	1.73	0.53
1:L5:316:A:N1	1:L5:4013:U:H5	2.06	0.53
46:S2:55:U:H3'	46:S2:452:G:C5	2.44	0.53
46:S2:86:C:O2'	46:S2:171:A:N1	2.31	0.53
1:L5:189:G:H22	1:L5:252:G:N2	2.06	0.53
1:L5:747:G:O2'	1:L5:748:G:H8	1.92	0.53
1:L5:830:C:H4'	1:L5:831:G:O5'	2.08	0.53
1:L5:4286:G:O2'	1:L5:4288:A:OP2	2.26	0.53
62:SP:108:LYS:H	62:SP:111:MET:HE3	1.74	0.53
23:LU:48:LYS:HG2	23:LU:53:ALA:HB2	1.90	0.53
46:S2:47:G:H1	46:S2:479:G:H22	1.57	0.53
46:S2:537:A:N7	46:S2:538:C:O2'	2.41	0.53
46:S2:1014:U:OP1	46:S2:1130:G:O2'	2.27	0.53
46:S2:1478:U:O2'	46:S2:1479:U:O5'	2.27	0.53
49:SB:125:VAL:HG22	49:SB:172:MET:HE3	1.91	0.53
54:SG:44:GLU:H	54:SG:44:GLU:CD	2.17	0.53
69:SW:111:MET:HE3	69:SW:116:ALA:HA	1.90	0.53
6:LC:150:LEU:HB3	6:LC:151:PRO:HD3	1.91	0.52
6:LC:288:ASP:OD2	6:LC:291:ARG:HB2	2.09	0.52
10:LG:220:GLU:O	10:LG:224:THR:HG23	2.08	0.52
14:LL:194:ILE:O	14:LL:198:ARG:HG3	2.08	0.52
47:S7:22:G:N7	47:S7:46:G:O6	2.41	0.52
66:ST:130:ASP:O	66:ST:134:ILE:HG12	2.09	0.52
21:LS:81:TRP:CZ3	21:LS:130:GLU:HG3	2.43	0.52
23:LU:38:ASN:OD1	23:LU:39:PHE:N	2.42	0.52
51:SD:92:ALA:O	51:SD:93:THR:OG1	2.20	0.52
51:SD:162:ASP:OD1	51:SD:165:ASN:ND2	2.41	0.52
64:SR:45:LYS:O	64:SR:49:LYS:HG3	2.10	0.52
68:SV:74:LYS:HA	68:SV:79:VAL:HG21	1.91	0.52
78:Sg:197:THR:HG21	78:Sg:239:LEU:H	1.73	0.52
1:L5:3355:G:OP2	4:LA:245:ARG:NH2	2.42	0.52
1:L5:4111:C:H2'	1:L5:4112:U:C6	2.44	0.52
52:SE:29:PRO:HG2	52:SE:46:ILE:HD11	1.92	0.52
56:SI:65:PHE:O	56:SI:109:TYR:OH	2.27	0.52
63:SQ:43:GLU:HB3	63:SQ:44:PRO:HD2	1.91	0.52
68:SV:31:SER:O	68:SV:32:ILE:HD13	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SW:76:SER:HB3	69:SW:77:PRO:HD3	1.91	0.52
78:Sg:166:VAL:HG12	78:Sg:176:VAL:HG13	1.91	0.52
46:S2:482:C:H4'	46:S2:483:G:H5''	1.90	0.52
61:SO:135:ILE:HD12	61:SO:135:ILE:O	2.10	0.52
72:SZ:48:VAL:HG22	72:SZ:49:LEU:HD13	1.90	0.52
1:L5:121:A:H62	1:L5:152:U:H3	1.57	0.52
1:L5:304:A:OP1	37:Li:76:ARG:NH1	2.42	0.52
6:LC:254:GLU:O	6:LC:258:ARG:HG3	2.09	0.52
7:LD:231:VAL:O	7:LD:231:VAL:HG12	2.10	0.52
46:S2:66:G:H3'	46:S2:68:A:H62	1.74	0.52
46:S2:538:C:H3'	46:S2:539:U:H6	1.74	0.52
52:SE:31:PRO:HG3	52:SE:43:PRO:HG3	1.92	0.52
54:SG:48:TYR:OH	54:SG:119:LYS:O	2.21	0.52
64:SR:30:THR:O	64:SR:34:VAL:HG23	2.10	0.52
1:L5:1761:A:O2'	1:L5:1764:G:N2	2.37	0.52
1:L5:2314:G:H22	1:L5:2324:G:N2	2.07	0.52
1:L5:4247:U:H2'	1:L5:4248:G:H8	1.74	0.52
2:L7:120:U:H4'	7:LD:260:GLU:HG3	1.91	0.52
22:LT:38:ASP:OD1	22:LT:38:ASP:N	2.32	0.52
30:Lb:62:ALA:HA	30:Lb:65:VAL:HG12	1.92	0.52
46:S2:510:G:OP1	57:SJ:2:PRO:HD2	2.10	0.52
53:SF:185:SER:O	53:SF:185:SER:OG	2.24	0.52
56:SI:7:ASN:OD1	56:SI:7:ASN:N	2.42	0.52
63:SQ:80:GLN:O	63:SQ:84:ILE:HG12	2.09	0.52
1:L5:1009:C:H42	1:L5:1017:A:H61	1.58	0.52
1:L5:2332:G:N7	28:LZ:17:ARG:NH1	2.57	0.52
1:L5:3298:U:H5	1:L5:3303:A:N7	2.08	0.52
46:S2:41:G:H22	46:S2:481:G:N2	2.07	0.52
55:SH:53:VAL:HG21	55:SH:172:THR:HA	1.92	0.52
1:L5:143:U:OP2	10:LG:111:LYS:NZ	2.42	0.52
1:L5:3346:G:O2'	1:L5:3475:U:OP2	2.28	0.52
6:LC:303:ARG:O	19:LQ:38:ARG:NH2	2.32	0.52
16:LN:96:ARG:NH1	16:LN:100:SER:OG	2.43	0.52
46:S2:1320:U:H3'	46:S2:1321:G:O4'	2.10	0.52
46:S2:1407:G:H2'	46:S2:1408:U:C6	2.45	0.52
46:S2:1462:G:N1	46:S2:1465:C:OP2	2.41	0.52
46:S2:1598:C:H4'	46:S2:1604:G:O6	2.10	0.52
57:SJ:79:ARG:HB2	57:SJ:79:ARG:HH11	1.74	0.52
58:SK:16:PHE:CE1	58:SK:91:PRO:HD3	2.45	0.52
71:SY:94:HIS:ND1	71:SY:94:HIS:O	2.39	0.52
5:LB:195:ASP:O	5:LB:199:GLU:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LD:226:TYR:O	7:LD:228:LYS:N	2.43	0.52
20:LR:39:GLN:OE1	20:LR:42:ARG:NH1	2.43	0.52
25:LW:4:GLU:HG3	25:LW:13:ILE:HB	1.91	0.52
33:Le:117:GLN:O	45:Lr:119:ARG:NH2	2.43	0.52
46:S2:1115:U:O2'	46:S2:1116:U:O5'	2.25	0.52
47:S6:15:A:H2'	47:S6:16:G:O4'	2.10	0.52
57:SJ:111:GLN:NE2	57:SJ:127:ARG:HG2	2.25	0.52
64:SR:60:ARG:HG3	64:SR:66:VAL:HG21	1.92	0.52
1:L5:1221:G:H21	1:L5:1227:G:H1	1.58	0.52
46:S2:158:A:H5'	46:S2:465:A:C6	2.45	0.52
46:S2:311:C:HO2'	46:S2:341:C:C1'	2.22	0.52
46:S2:1013:A:OP1	60:SN:3:ARG:NH1	2.42	0.52
66:ST:35:ASP:OD1	66:ST:35:ASP:N	2.43	0.52
6:LC:262:GLU:HG2	6:LC:272:SER:HB3	1.92	0.51
9:LF:81:LYS:O	9:LF:85:GLN:HG3	2.10	0.51
46:S2:341:C:H3'	46:S2:342:C:H6	1.74	0.51
54:SG:190:ARG:O	54:SG:194:LEU:HG	2.10	0.51
58:SK:11:ILE:HA	58:SK:14:LEU:HD12	1.92	0.51
79:Sx:33:U:H2'	79:Sx:34:C:C6	2.46	0.51
1:L5:829:G:C2'	1:L5:830:C:H5'	2.39	0.51
1:L5:1293:G:H2'	1:L5:1294:C:C6	2.45	0.51
15:LM:50:MET:HB3	15:LM:55:MET:HE1	1.92	0.51
46:S2:144:U:H2'	46:S2:145:G:C8	2.45	0.51
47:S7:13:G:H1	47:S7:23:C:N4	2.08	0.51
57:SJ:111:GLN:HE21	57:SJ:127:ARG:HG2	1.75	0.51
60:SN:93:LYS:HG3	60:SN:150:VAL:HG11	1.91	0.51
50:SC:92:GLU:OE1	50:SC:92:GLU:N	2.43	0.51
51:SD:62:LYS:HG2	58:SK:95:ARG:HH21	1.75	0.51
56:SI:87:ASN:HB3	56:SI:90:LEU:HG	1.92	0.51
60:SN:31:ASP:OD1	60:SN:32:ASP:N	2.43	0.51
76:Sd:33:LYS:O	76:Sd:36:LEU:HD12	2.10	0.51
9:LF:114:VAL:O	9:LF:142:GLY:HA2	2.10	0.51
19:LQ:50:ARG:HA	19:LQ:53:MET:HE3	1.91	0.51
23:LU:101:ARG:O	23:LU:112:LEU:HA	2.10	0.51
46:S2:34:U:HO2'	46:S2:35:C:P	2.33	0.51
46:S2:492:C:H1'	46:S2:511:G:N2	2.26	0.51
46:S2:497:C:H5'	46:S2:498:C:OP2	2.09	0.51
46:S2:514:G:H3'	46:S2:515:U:H6	1.76	0.51
62:SP:93:MET:SD	62:SP:104:GLN:NE2	2.73	0.51
1:L5:62:A:OP1	16:LN:169:ARG:NH2	2.44	0.51
1:L5:499:G:H1	1:L5:663:C:H5	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:934:G:H1	1:L5:1063:C:H42	1.57	0.51
1:L5:2063:G:OP1	33:Le:128:ARG:NH1	2.43	0.51
1:L5:2236:G:H3'	1:L5:2237:G:H8	1.76	0.51
16:LN:68:ARG:NH1	16:LN:124:ASP:O	2.36	0.51
46:S2:1277:A:O2'	58:SK:50:GLN:OE1	2.25	0.51
47:S7:3:G:OP2	47:S7:3:G:H8	1.93	0.51
52:SE:246:LEU:HD11	52:SE:254:LYS:HD2	1.92	0.51
54:SG:161:PRO:HA	54:SG:171:THR:HA	1.93	0.51
63:SQ:58:LEU:HD21	63:SQ:112:LEU:HD21	1.91	0.51
64:SR:34:VAL:HG12	64:SR:38:ILE:HD13	1.92	0.51
1:L5:1745:A:H2'	1:L5:1746:A:C8	2.44	0.51
1:L5:3927:A:H2'	1:L5:3928:G:C8	2.46	0.51
5:LB:77:THR:OG1	5:LB:335:GLY:O	2.28	0.51
20:LR:95:TRP:CH2	20:LR:99:MET:HE3	2.46	0.51
46:S2:480:C:H3'	46:S2:481:G:C8	2.45	0.51
46:S2:498:C:H4'	46:S2:499:C:OP1	2.09	0.51
46:S2:1752:C:N4	46:S2:1783:G:O6	2.38	0.51
55:SH:179:LYS:HD2	55:SH:179:LYS:O	2.10	0.51
73:Sa:45:VAL:HG21	73:Sa:53:ILE:HG21	1.92	0.51
1:L5:1523:C:H2'	1:L5:1524:G:C5	2.45	0.51
1:L5:2656:G:H3'	1:L5:2657:G:N2	2.25	0.51
1:L5:4125:G:O2'	41:Lm:100:TYR:O	2.29	0.51
5:LB:315:ASN:ND2	5:LB:326:VAL:H	2.08	0.51
46:S2:47:G:H22	46:S2:479:G:H22	1.57	0.51
57:SJ:83:ARG:HE	57:SJ:150:ARG:HD3	1.75	0.51
1:L5:1365:C:H2'	1:L5:1366:G:O4'	2.11	0.51
1:L5:1542:G:H2'	1:L5:1543:C:C6	2.46	0.51
8:LE:180:LEU:HD23	8:LE:196:ARG:HG3	1.93	0.51
18:LP:116:HIS:HB3	18:LP:149:ILE:HB	1.93	0.51
46:S2:1396:C:H1'	46:S2:1475:A:C5	2.46	0.51
47:S6:29:G:H22	47:S6:41:C:H5	1.59	0.51
78:Sg:99:ARG:NH1	78:Sg:100:ARG:H	2.08	0.51
1:L5:233:U:O2'	1:L5:2061:U:O4	2.29	0.51
1:L5:424:U:H4'	18:LP:6:LEU:HD11	1.93	0.51
32:Ld:26:THR:OG1	32:Ld:85:ARG:NH1	2.43	0.51
32:Ld:44:ARG:O	32:Ld:48:GLU:HG2	2.11	0.51
48:SA:197:VAL:HG23	48:SA:201:LEU:HD13	1.93	0.51
65:SS:78:LYS:NZ	65:SS:78:LYS:HB3	2.26	0.51
70:SX:77:ASN:O	70:SX:77:ASN:ND2	2.40	0.51
1:L5:1447:G:H5'	1:L5:1448:A:OP1	2.11	0.51
1:L5:3606:A:N6	1:L5:3714:U:H3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4392:C:H1'	1:L5:4609:G:C2	2.46	0.51
1:L5:4544:G:H2'	1:L5:4545:G:C8	2.46	0.51
12:LI:53:VAL:HG12	12:LI:134:VAL:HG22	1.93	0.51
46:S2:380:C:OP2	56:SI:181:GLN:NE2	2.38	0.51
46:S2:495:C:H3'	46:S2:496:U:C5	2.46	0.51
46:S2:944:U:O2'	61:SO:135:ILE:O	2.28	0.51
46:S2:1745:G:HO2'	46:S2:1791:A:N6	2.08	0.51
1:L5:2449:A:H4'	1:L5:2450:A:H5'	1.93	0.50
21:LS:13:VAL:HG22	21:LS:29:ARG:HG3	1.93	0.50
23:LU:111:GLU:OE1	23:LU:113:ARG:NE	2.40	0.50
37:Li:66:ASP:OD1	37:Li:66:ASP:N	2.39	0.50
50:SC:69:LEU:HD21	50:SC:273:LEU:HD11	1.91	0.50
51:SD:158:ILE:HG13	51:SD:164:VAL:HG22	1.93	0.50
54:SG:23:LYS:HB3	54:SG:41:LEU:HD13	1.91	0.50
2:L7:3:C:H2'	2:L7:4:U:H6	1.76	0.50
4:LA:173:GLY:O	4:LA:176:ASP:HB2	2.11	0.50
10:LG:89:ARG:O	10:LG:93:THR:HG23	2.12	0.50
21:LS:84:TYR:CE1	21:LS:93:MET:HE3	2.46	0.50
46:S2:57:U:H3	46:S2:88:G:H22	1.59	0.50
1:L5:2394:G:H2'	1:L5:2395:A:C8	2.46	0.50
4:LA:14:SER:OG	4:LA:15:VAL:N	2.42	0.50
35:Lg:94:ALA:O	35:Lg:98:GLU:HG2	2.11	0.50
46:S2:87:U:H3	46:S2:501:A:H2	1.59	0.50
46:S2:1729:U:O2'	46:S2:1730:U:O4'	2.29	0.50
47:S6:35:A:OP2	63:SQ:146:ARG:NH2	2.42	0.50
50:SC:188:CYS:O	50:SC:191:VAL:HG12	2.12	0.50
61:SO:98:ARG:HB2	61:SO:132:VAL:HG23	1.92	0.50
13:LJ:29:SER:OG	13:LJ:66:GLU:OE1	2.29	0.50
20:LR:36:ASN:OD1	20:LR:36:ASN:N	2.43	0.50
23:LU:102:VAL:HG22	23:LU:112:LEU:HD23	1.92	0.50
52:SE:99:PHE:HE1	52:SE:113:ARG:HB3	1.76	0.50
54:SG:181:THR:HB	54:SG:184:VAL:HG23	1.93	0.50
56:SI:34:ALA:HB2	56:SI:56:ARG:HD3	1.94	0.50
71:SY:41:ARG:HH12	71:SY:57:VAL:N	2.10	0.50
46:S2:514:G:H3'	46:S2:515:U:C6	2.47	0.50
46:S2:535:G:H2'	46:S2:536:G:C8	2.46	0.50
50:SC:179:THR:HG22	50:SC:221:ASP:HB2	1.92	0.50
78:Sg:212:LYS:HG3	78:Sg:235:ILE:HG12	1.92	0.50
1:L5:951:A:H2	1:L5:1034:G:H1	1.60	0.50
1:L5:4507:G:HO2'	1:L5:4508:G:H8	1.57	0.50
23:LU:94:ASN:O	23:LU:96:LEU:HD13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:171:A:OP1	46:S2:173:A:N6	2.44	0.50
48:SA:177:MET:HE3	48:SA:180:ARG:NH2	2.27	0.50
59:SL:17:PHE:CZ	59:SL:19:ASN:HB2	2.47	0.50
72:SZ:42:ASP:N	72:SZ:42:ASP:OD1	2.43	0.50
78:Sg:240:CYS:SG	78:Sg:249:CYS:HB3	2.51	0.50
1:L5:1012:U:H3'	1:L5:1013:C:O4'	2.12	0.50
1:L5:1012:U:HO2'	1:L5:1015:C:N4	2.10	0.50
1:L5:1179:U:OP2	14:LL:36:ARG:NH2	2.41	0.50
1:L5:1418:G:H2'	1:L5:1419:G:C8	2.47	0.50
7:LD:185:SER:O	7:LD:185:SER:OG	2.25	0.50
20:LR:105:LEU:HD23	20:LR:138:LEU:HD23	1.92	0.50
23:LU:78:PHE:HE2	23:LU:83:LEU:HD21	1.77	0.50
46:S2:219:A:C5	46:S2:220:U:C5	3.00	0.50
46:S2:434:A:OP1	56:SI:25:ARG:NH2	2.41	0.50
46:S2:1476:G:O2'	46:S2:1477:A:OP1	2.25	0.50
54:SG:191:ARG:HB3	54:SG:195:LYS:NZ	2.24	0.50
67:SU:23:THR:HG22	67:SU:113:GLU:HB2	1.94	0.50
71:SY:76:TYR:OH	71:SY:85:ASN:OD1	2.20	0.50
5:LB:218:ASP:OD2	5:LB:348:ARG:NH2	2.43	0.50
8:LE:101:THR:O	8:LE:101:THR:HG22	2.12	0.50
35:Lg:46:CYS:HB3	35:Lg:48:VAL:HG22	1.94	0.50
46:S2:118:C:H1'	46:S2:446:A:C5	2.46	0.50
46:S2:146:G:H1	46:S2:174:C:H42	1.58	0.50
46:S2:218:C:C4	46:S2:219:A:N7	2.80	0.50
46:S2:438:G:OP1	46:S2:474:A:N6	2.44	0.50
46:S2:929:G:H2'	46:S2:930:G:C8	2.46	0.50
46:S2:1753:C:H5''	46:S2:1754:C:H4'	1.93	0.50
49:SB:107:ARG:NH2	61:SO:133:THR:O	2.36	0.50
54:SG:27:PHE:CE2	54:SG:111:LEU:HD11	2.45	0.50
55:SH:75:ILE:HG13	55:SH:79:LEU:HD11	1.92	0.50
55:SH:179:LYS:HD2	55:SH:179:LYS:C	2.36	0.50
70:SX:110:HIS:HD2	70:SX:111:ALA:H	1.58	0.50
1:L5:1261:C:C2	1:L5:1262:G:C8	3.00	0.50
1:L5:2599:A:H61	1:L5:3500:C:H42	1.59	0.50
8:LE:138:LYS:HD3	8:LE:138:LYS:N	2.27	0.50
16:LN:101:VAL:O	16:LN:104:GLU:HG3	2.12	0.50
17:LO:105:LEU:HD22	17:LO:109:PRO:HG2	1.94	0.50
54:SG:52:ILE:H	54:SG:52:ILE:HD12	1.77	0.50
70:SX:100:VAL:HG12	70:SX:125:VAL:HG23	1.94	0.50
18:LP:41:ILE:HD13	18:LP:150:LEU:HD21	1.94	0.49
42:Ln:20:MET:N	42:Ln:20:MET:SD	2.85	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:456:A:H2'	46:S2:457:C:H6	1.76	0.49
46:S2:532:A:N1	46:S2:554:U:N3	2.58	0.49
46:S2:1589:A:H2'	46:S2:1590:A:C8	2.47	0.49
1:L5:3367:G:H1'	1:L5:3368:A:C8	2.47	0.49
46:S2:218:C:C2	46:S2:219:A:C8	3.00	0.49
55:SH:73:GLN:HA	55:SH:76:GLN:HB2	1.93	0.49
1:L5:443:G:H2'	1:L5:444:U:C6	2.47	0.49
1:L5:2017:C:OP1	8:LE:116:LYS:NZ	2.42	0.49
5:LB:258:HIS:C	5:LB:260:ALA:N	2.70	0.49
7:LD:103:LEU:HG	7:LD:247:ILE:HD11	1.94	0.49
46:S2:141:A:N6	46:S2:314:A:N1	2.59	0.49
46:S2:487:A:O2'	46:S2:488:U:O4'	2.22	0.49
46:S2:795:A:O2'	46:S2:796:A:O4'	2.18	0.49
46:S2:1294:A:H2'	46:S2:1295:G:H8	1.76	0.49
46:S2:1746:A:O3'	54:SG:31:ARG:NH1	2.45	0.49
57:SJ:15:THR:HG22	57:SJ:16:PRO:HD2	1.93	0.49
59:SL:120:VAL:HG22	59:SL:145:VAL:HG21	1.93	0.49
19:LQ:75:ARG:HA	19:LQ:78:LYS:HD2	1.94	0.49
33:Le:91:CYS:O	33:Le:93:LYS:N	2.46	0.49
39:Lk:33:LYS:HG2	39:Lk:46:VAL:HG22	1.95	0.49
46:S2:561:A:H2'	46:S2:562:A:H8	1.77	0.49
49:SB:113:MET:HE3	49:SB:142:PHE:CE2	2.47	0.49
52:SE:252:ARG:HA	52:SE:255:ARG:HH21	1.77	0.49
60:SN:71:ILE:O	60:SN:75:LEU:HG	2.12	0.49
70:SX:61:GLN:CB	70:SX:62:PRO:HD3	2.42	0.49
70:SX:128:VAL:HG13	70:SX:129:SER:N	2.26	0.49
71:SY:102:THR:OG1	71:SY:103:SER:N	2.42	0.49
1:L5:1054:G:O2'	1:L5:1055:G:O5'	2.28	0.49
1:L5:4549:G:H4'	1:L5:4550:G:OP1	2.12	0.49
19:LQ:72:LEU:HB2	19:LQ:75:ARG:HD2	1.93	0.49
42:Ln:22:GLN:O	42:Ln:22:GLN:HG2	2.12	0.49
46:S2:1316:U:H2'	46:S2:1317:C:C6	2.48	0.49
55:SH:176:VAL:O	55:SH:180:LEU:HD23	2.13	0.49
78:Sg:87:LEU:HB2	78:Sg:101:PHE:HB2	1.93	0.49
79:Sx:33:U:H2'	79:Sx:34:C:H6	1.77	0.49
14:LL:80:GLU:HG3	14:LL:110:LEU:HD12	1.94	0.49
36:Lh:6:ALA:O	36:Lh:10:ARG:HG3	2.13	0.49
46:S2:158:A:H2	46:S2:463:C:H2'	1.78	0.49
56:SI:64:ASN:HB3	56:SI:186:ASP:OD1	2.13	0.49
57:SJ:93:LYS:HB2	57:SJ:96:TYR:HE1	1.77	0.49
70:SX:85:VAL:HG22	70:SX:122:VAL:HG11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SZ:99:LEU:HA	72:SZ:109:TYR:HD1	1.77	0.49
77:Se:96:GLN:HG2	77:Se:98:LYS:HE2	1.94	0.49
1:L5:833:U:C2	15:LM:44:ARG:HG2	2.48	0.49
1:L5:2652:G:H2'	1:L5:2653:C:C6	2.48	0.49
1:L5:3369:A:C5	1:L5:3370:U:H1'	2.48	0.49
8:LE:295:VAL:O	15:LM:109:ARG:NH2	2.45	0.49
12:LI:189:ARG:HH11	12:LI:189:ARG:HG3	1.77	0.49
46:S2:97:U:H4'	46:S2:98:C:OP2	2.12	0.49
46:S2:120:U:H1'	52:SE:33:THR:HG23	1.94	0.49
46:S2:964:A:H2'	46:S2:965:A:C8	2.48	0.49
46:S2:1411:C:O2'	46:S2:1412:G:H8	1.95	0.49
46:S2:1458:U:H2'	46:S2:1459:G:H8	1.78	0.49
50:SC:132:ASP:OD1	50:SC:133:TYR:N	2.46	0.49
50:SC:176:LYS:HD3	50:SC:177:PRO:HD2	1.93	0.49
56:SI:37:LYS:HB2	56:SI:59:ARG:HG2	1.94	0.49
78:Sg:251:ALA:HB1	78:Sg:286:CYS:SG	2.52	0.49
1:L5:1031:G:H2'	1:L5:1033:G:H8	1.78	0.49
15:LM:78:GLU:OE1	15:LM:78:GLU:HA	2.13	0.49
58:SK:6:LYS:HE3	58:SK:38:LYS:HZ3	1.77	0.49
74:Sb:16:LYS:HD2	74:Sb:16:LYS:C	2.37	0.49
78:Sg:166:VAL:HG23	78:Sg:198:VAL:HG21	1.95	0.49
1:L5:443:G:H2'	1:L5:444:U:H6	1.78	0.49
6:LC:285:MET:HE3	19:LQ:122:THR:HG21	1.95	0.49
34:Lf:106:TYR:HB2	34:Lf:107:PRO:HD3	1.94	0.49
46:S2:68:A:N6	46:S2:82:G:H21	2.11	0.49
46:S2:1389:A:C2	51:SD:205:PRO:HG2	2.48	0.49
46:S2:1416:C:O2	46:S2:1417:C:N4	2.46	0.49
47:S7:62:C:H2'	47:S7:63:A:H8	1.77	0.49
52:SE:149:TYR:OH	54:SG:206:ALA:HA	2.12	0.49
1:L5:415:U:O2'	1:L5:416:G:OP1	2.26	0.49
1:L5:1005:C:O2'	1:L5:1006:G:O5'	2.25	0.49
1:L5:4352:U:H1'	1:L5:4353:A:H5''	1.94	0.49
8:LE:253:GLN:HG3	8:LE:254:ARG:N	2.28	0.49
46:S2:158:A:H5'	46:S2:465:A:C5	2.48	0.49
46:S2:448:A:H4'	52:SE:3:ARG:HG2	1.94	0.49
48:SA:56:GLU:OE2	68:SV:80:SER:OG	2.23	0.49
77:Se:85:LYS:O	77:Se:89:GLN:HG3	2.12	0.49
1:L5:1192:G:H5''	1:L5:1193:C:OP2	2.13	0.48
9:LF:184:ILE:HB	9:LF:189:ILE:HD12	1.95	0.48
46:S2:1293:C:H42	46:S2:1309:U:H3	1.61	0.48
54:SG:50:VAL:HB	54:SG:111:LEU:HD22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SG:105:ASN:O	54:SG:106:LEU:HD23	2.13	0.48
7:LD:41:LYS:HE3	22:LT:93:ILE:HD13	1.95	0.48
7:LD:107:ARG:HH21	7:LD:110:LEU:HD12	1.78	0.48
28:LZ:100:VAL:HG23	28:LZ:106:LEU:HB3	1.94	0.48
46:S2:185:G:H2'	46:S2:186:C:O4'	2.12	0.48
46:S2:1671:C:H2'	46:S2:1672:G:C8	2.47	0.48
48:SA:177:MET:HE3	48:SA:180:ARG:HH22	1.78	0.48
70:SX:94:ILE:HG23	70:SX:125:VAL:HG21	1.94	0.48
71:SY:41:ARG:NH1	71:SY:57:VAL:HG22	2.28	0.48
78:Sg:7:LEU:HB2	78:Sg:310:TRP:HZ3	1.78	0.48
78:Sg:201:SER:HB3	78:Sg:241:PHE:CD2	2.48	0.48
79:Sx:32:A:O2'	79:Sx:33:U:OP2	2.24	0.48
1:L5:747:G:O2'	1:L5:748:G:O4'	2.32	0.48
1:L5:951:A:H2	1:L5:1034:G:H22	1.62	0.48
11:LH:8:GLN:NE2	11:LH:74:CYS:SG	2.73	0.48
23:LU:65:ARG:HD2	23:LU:67:LYS:H	1.76	0.48
45:Lr:85:ASN:O	45:Lr:89:THR:OG1	2.20	0.48
46:S2:70:G:H1'	46:S2:80:G:N2	2.28	0.48
1:L5:955:C:H1'	1:L5:1029:G:O6	2.13	0.48
1:L5:3714:U:O2'	1:L5:3715:C:O2	2.19	0.48
13:LJ:151:ILE:HD11	13:LJ:156:ARG:HG2	1.96	0.48
14:LL:135:LYS:O	14:LL:136:LYS:HD2	2.13	0.48
24:LV:31:ASN:C	24:LV:31:ASN:ND2	2.71	0.48
46:S2:456:A:H2'	46:S2:457:C:C6	2.48	0.48
49:SB:164:ILE:O	49:SB:168:MET:HG2	2.13	0.48
52:SE:57:THR:O	52:SE:61:VAL:HG23	2.12	0.48
62:SP:56:LEU:HD11	62:SP:78:THR:HG21	1.95	0.48
1:L5:654:G:H2'	1:L5:655:G:O4'	2.14	0.48
1:L5:753:G:H2'	1:L5:754:A:C8	2.48	0.48
1:L5:2313:G:H2'	1:L5:2314:G:C8	2.48	0.48
1:L5:3366:U:H3	1:L5:3368:A:H62	1.61	0.48
46:S2:163:U:O3'	54:SG:83:CYS:HA	2.14	0.48
46:S2:956:A:N1	46:S2:969:U:O2'	2.43	0.48
52:SE:151:ASP:HB3	52:SE:154:ILE:HG13	1.94	0.48
1:L5:2236:G:H3'	1:L5:2237:G:C8	2.49	0.48
1:L5:3326:G:N2	1:L5:3329:G:H21	2.09	0.48
5:LB:355:THR:O	5:LB:355:THR:OG1	2.29	0.48
12:LI:183:ASP:N	12:LI:183:ASP:OD1	2.46	0.48
32:Ld:93:ASN:HB2	32:Ld:103:TYR:HD1	1.79	0.48
46:S2:225:C:O2'	46:S2:226:A:H8	1.96	0.48
46:S2:1388:G:H22	51:SD:206:ASP:CG	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1426:G:H4'	63:SQ:33:LYS:HD2	1.95	0.48
46:S2:1799:C:H2'	46:S2:1800:G:O4'	2.14	0.48
47:S6:13:G:H1	47:S6:23:C:N4	2.07	0.48
49:SB:38:MET:HG2	49:SB:182:LYS:HE3	1.95	0.48
52:SE:106:LYS:HB2	52:SE:108:ARG:CD	2.44	0.48
69:SW:2:VAL:HG12	69:SW:3:ARG:N	2.28	0.48
72:SZ:74:SER:OG	72:SZ:79:ILE:O	2.24	0.48
1:L5:266:G:H2'	1:L5:267:G:H8	1.78	0.48
1:L5:950:G:H2'	1:L5:951:A:C8	2.48	0.48
1:L5:1183:C:H1'	27:LY:1:MET:HE2	1.95	0.48
1:L5:4428:C:N3	1:L5:4506:G:N2	2.61	0.48
9:LF:204:PHE:CD1	9:LF:222:ARG:HD2	2.48	0.48
23:LU:42:PHE:HA	23:LU:45:GLU:OE1	2.13	0.48
46:S2:47:G:N2	46:S2:479:G:H22	2.12	0.48
46:S2:835:C:H2'	46:S2:840:C:O2	2.13	0.48
55:SH:86:LYS:HD2	55:SH:86:LYS:O	2.14	0.48
57:SJ:26:ASP:OD1	57:SJ:26:ASP:N	2.47	0.48
78:Sg:130:LYS:HD2	78:Sg:132:TRP:HZ3	1.79	0.48
1:L5:4333:G:H2'	1:L5:4334:A:C8	2.49	0.48
7:LD:93:THR:O	7:LD:93:THR:OG1	2.30	0.48
7:LD:208:MET:HE3	7:LD:208:MET:HB2	1.61	0.48
7:LD:208:MET:HG3	7:LD:219:TYR:HE1	1.78	0.48
12:LI:181:PHE:O	12:LI:185:VAL:HG23	2.14	0.48
16:LN:104:GLU:HA	16:LN:160:GLU:HG3	1.95	0.48
46:S2:115:U:H4'	46:S2:116:U:OP1	2.14	0.48
46:S2:368:U:H4'	46:S2:372:A:C8	2.48	0.48
46:S2:496:U:H2'	46:S2:497:C:O2	2.13	0.48
46:S2:1784:C:H4'	46:S2:1785:G:O5'	2.14	0.48
52:SE:212:ASP:OD1	52:SE:216:ASN:HB2	2.14	0.48
54:SG:133:LEU:HD12	54:SG:134:GLY:H	1.79	0.48
58:SK:6:LYS:HG2	58:SK:38:LYS:NZ	2.29	0.48
71:SY:41:ARG:HH21	71:SY:94:HIS:CD2	2.29	0.48
1:L5:949:C:H2'	1:L5:950:G:C8	2.49	0.48
1:L5:4414:G:H2'	1:L5:4415:G:O4'	2.14	0.48
12:LI:36:LEU:HD11	12:LI:69:ARG:HE	1.78	0.48
21:LS:139:ARG:O	21:LS:143:LYS:HG3	2.13	0.48
24:LV:111:GLU:HA	24:LV:131:ARG:HD3	1.94	0.48
46:S2:1582:C:H5''	46:S2:1583:C:H5	1.79	0.48
54:SG:192:ILE:HG22	54:SG:196:LYS:HE2	1.95	0.48
55:SH:49:LYS:HB2	55:SH:61:ILE:HG12	1.96	0.48
57:SJ:124:HIS:HD2	77:Se:109:ARG:NH2	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SV:67:ASP:OD1	68:SV:71:ARG:NH2	2.47	0.48
69:SW:85:ASP:N	69:SW:85:ASP:OD1	2.47	0.48
69:SW:86:LEU:O	69:SW:90:GLN:HG3	2.14	0.48
75:Sc:28:THR:HG23	75:Sc:46:VAL:HG23	1.95	0.48
76:Sd:5:GLN:O	76:Sd:9:SER:HB2	2.13	0.48
78:Sg:217:MET:HE3	78:Sg:219:TRP:CH2	2.49	0.48
1:L5:4131:G:O2'	1:L5:4255:A:N1	2.44	0.48
5:LB:299:ILE:HG23	5:LB:313:SER:HB3	1.96	0.48
7:LD:181:PRO:HG2	7:LD:195:HIS:HD1	1.78	0.48
27:LY:83:GLU:OE2	27:LY:84:ARG:NH2	2.47	0.48
52:SE:99:PHE:CE1	52:SE:113:ARG:HB3	2.49	0.48
70:SX:28:LYS:O	70:SX:32:LEU:HB2	2.14	0.48
1:L5:2512:G:O2'	1:L5:2519:A:N3	2.46	0.47
1:L5:4257:G:OP1	11:LH:174:LYS:NZ	2.47	0.47
16:LN:140:LYS:HG2	16:LN:144:ARG:NH2	2.29	0.47
43:Lo:83:LEU:HD12	43:Lo:83:LEU:HA	1.77	0.47
46:S2:514:G:H2'	46:S2:514:G:N3	2.29	0.47
46:S2:1314:A:H4'	46:S2:1315:U:H5''	1.95	0.47
47:S7:37:A:H2'	47:S7:38:A:O4'	2.14	0.47
62:SP:17:TYR:CE2	62:SP:18:ARG:HG3	2.49	0.47
71:SY:74:MET:HE3	71:SY:76:TYR:HD1	1.79	0.47
72:SZ:69:THR:H	72:SZ:72:VAL:HG12	1.79	0.47
76:Sd:19:ARG:HD2	76:Sd:32:ARG:HD3	1.96	0.47
78:Sg:59:LEU:HB3	78:Sg:90:TRP:CZ3	2.49	0.47
1:L5:468:C:N3	8:LE:113:ARG:NH2	2.61	0.47
1:L5:2296:C:H2'	1:L5:2297:C:C6	2.49	0.47
10:LG:162:ASP:OD1	10:LG:187:LYS:NZ	2.33	0.47
46:S2:170:A:H2'	46:S2:171:A:C8	2.49	0.47
57:SJ:80:ARG:O	57:SJ:84:ILE:HG22	2.14	0.47
46:S2:834:C:C5	46:S2:835:C:H1'	2.49	0.47
46:S2:1145:A:H2'	46:S2:1146:A:C8	2.50	0.47
46:S2:1425:G:H2'	46:S2:1426:G:C8	2.50	0.47
1:L5:1157:A:OP1	16:LN:204:ARG:HD2	2.15	0.47
1:L5:2406:G:C5	35:Lg:50:PRO:HG3	2.48	0.47
4:LA:48:ILE:HG22	44:Lp:54:ILE:HG12	1.97	0.47
15:LM:81:ASP:C	15:LM:81:ASP:OD1	2.57	0.47
24:LV:99:GLU:HG3	25:LW:21:TYR:OH	2.13	0.47
34:Lf:35:ALA:HB3	34:Lf:38:GLU:OE1	2.13	0.47
43:Lo:59:LYS:HD3	43:Lo:60:ALA:N	2.29	0.47
46:S2:315:U:H2'	46:S2:316:C:H6	1.78	0.47
51:SD:18:LYS:HE3	51:SD:39:VAL:HG11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70: SX:65:ALA:HB3	70: SX:67:ARG:NH1	2.29	0.47
74: Sb:36:LYS:H	74: Sb:78:SER:HB2	1.79	0.47
1: L5:940:C:H2'	1: L5:941:C:H6	1.79	0.47
17: LO:165:LYS:HE3	17: LO:169:ARG:HH21	1.78	0.47
46: S2:84:A:H2'	46: S2:85:A:C8	2.50	0.47
46: S2:172:U:P	46: S2:316:C:H5'	2.54	0.47
63: SQ:62:ARG:NH2	63: SQ:107:GLU:OE1	2.45	0.47
1: L5:952:C:H2'	1: L5:953:C:C6	2.49	0.47
1: L5:2060:C:H5''	33: Le:104:SER:HB3	1.96	0.47
1: L5:2655:G:N2	1: L5:3256:A:N3	2.63	0.47
5: LB:241:PRO:O	5: LB:248:LEU:HD11	2.14	0.47
7: LD:118:ILE:H	7: LD:118:ILE:HD12	1.80	0.47
8: LE:65:SER:OG	8: LE:66:ARG:N	2.48	0.47
21: LS:84:TYR:HE1	21: LS:93:MET:HE3	1.80	0.47
29: La:134:GLU:O	29: La:138:LYS:HG3	2.15	0.47
51: SD:50:ILE:HD11	51: SD:58:VAL:HG11	1.95	0.47
55: SH:130:LEU:HG	55: SH:177:TYR:CE1	2.49	0.47
58: SK:21:MET:HE2	58: SK:21:MET:HB3	1.67	0.47
59: SL:97:ARG:NH1	59: SL:100:ASN:OD1	2.47	0.47
63: SQ:52:LEU:O	63: SQ:56:LEU:HD12	2.15	0.47
73: Sa:45:VAL:HG11	73: Sa:64:LEU:HD23	1.96	0.47
78: Sg:130:LYS:HD3	78: Sg:141:THR:CB	2.44	0.47
1: L5:1715:G:N2	17: LO:87:MET:HE2	2.29	0.47
1: L5:1766:C:H2'	1: L5:1767:A:C8	2.50	0.47
1: L5:3907:G:H2'	1: L5:3907:G:N3	2.29	0.47
1: L5:4247:U:H2'	1: L5:4248:G:C8	2.50	0.47
1: L5:4651:U:H2'	1: L5:4652:C:C6	2.49	0.47
4: LA:130:SER:HB2	4: LA:171:GLY:HA3	1.96	0.47
8: LE:154:PRO:HB3	8: LE:211:ILE:HD11	1.97	0.47
10: LG:38:ASN:ND2	10: LG:43:GLN:HG2	2.30	0.47
10: LG:150:LYS:HD2	10: LG:177:MET:HE3	1.95	0.47
21: LS:113:MET:HE3	21: LS:113:MET:HB3	1.79	0.47
37: Li:38:LYS:HB3	37: Li:38:LYS:HE2	1.60	0.47
46: S2:19:A:H5'	70: SX:107:ARG:HH11	1.79	0.47
46: S2:66:G:N2	71: SY:121:ALA:HB3	2.30	0.47
46: S2:302:A:H5'	46: S2:303:A:OP2	2.14	0.47
46: S2:599:G:O2'	46: S2:600:A:OP1	2.30	0.47
46: S2:1298:U:C4	46: S2:1300:A:N7	2.82	0.47
46: S2:1601:G:H2'	46: S2:1601:G:N3	2.29	0.47
52: SE:63:LYS:HA	52: SE:63:LYS:HD2	1.68	0.47
64: SR:73:LEU:O	64: SR:77:GLU:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:ST:41:LYS:HB2	66:ST:41:LYS:HE2	1.80	0.47
1:L5:150:U:OP2	10:LG:200:THR:OG1	2.29	0.47
1:L5:494:G:N2	1:L5:669:C:N3	2.62	0.47
1:L5:1050:C:H2'	1:L5:1051:G:H8	1.79	0.47
1:L5:1132:U:H2'	1:L5:1133:C:C6	2.49	0.47
1:L5:3366:U:H3	1:L5:3368:A:N6	2.12	0.47
78:Sg:147:HIS:CE1	78:Sg:175:LYS:HD2	2.49	0.47
1:L5:694:A:H4'	8:LE:105:GLY:HA3	1.96	0.47
1:L5:2236:G:N3	1:L5:2236:G:H2'	2.30	0.47
1:L5:4602:G:H2'	1:L5:4603:A:N3	2.29	0.47
3:L8:92:U:H2'	3:L8:93:C:O4'	2.15	0.47
7:LD:239:MET:HG3	7:LD:240:TYR:N	2.30	0.47
15:LM:55:MET:HE2	15:LM:55:MET:HB3	1.68	0.47
20:LR:104:ARG:O	20:LR:108:ARG:HG3	2.15	0.47
22:LT:75:ILE:HD13	22:LT:88:ARG:HG2	1.97	0.47
33:Le:82:VAL:HG12	33:Le:111:ILE:HG12	1.96	0.47
46:S2:922:G:C6	69:SW:28:ARG:HD2	2.50	0.47
46:S2:1296:A:C6	46:S2:1297:U:H1'	2.50	0.47
46:S2:1537:G:H2'	46:S2:1538:A:H8	1.79	0.47
55:SH:9:VAL:HG13	55:SH:10:LYS:HE2	1.97	0.47
65:SS:87:GLN:HB3	65:SS:95:TYR:CE2	2.50	0.47
1:L5:1193:C:OP1	1:L5:1193:C:H4'	2.15	0.47
1:L5:1564:G:H1	1:L5:1575:C:H1'	1.80	0.47
1:L5:2314:G:H22	1:L5:2324:G:H22	1.62	0.47
45:Lr:19:LYS:HG2	45:Lr:24:THR:HG23	1.97	0.47
46:S2:220:U:N3	46:S2:221:U:C5	2.82	0.47
46:S2:473:C:P	46:S2:475:G:H21	2.38	0.47
46:S2:1476:G:HO2'	46:S2:1477:A:P	2.38	0.47
56:SI:193:LYS:HE2	56:SI:193:LYS:H	1.80	0.47
57:SJ:104:ASP:HA	57:SJ:107:GLU:HG2	1.97	0.47
1:L5:1460:A:O2'	38:Lj:49:TRP:O	2.29	0.46
1:L5:4686:A:O2'	1:L5:4687:U:OP1	2.31	0.46
8:LE:222:ASP:N	8:LE:222:ASP:OD1	2.48	0.46
11:LH:80:MET:O	11:LH:84:VAL:HG22	2.14	0.46
30:Lb:99:HIS:CG	30:Lb:102:LEU:HD12	2.50	0.46
46:S2:41:G:N2	46:S2:481:G:H22	2.13	0.46
46:S2:538:C:N4	46:S2:547:G:H1	2.12	0.46
46:S2:1279:A:N6	46:S2:1321:G:H1	2.13	0.46
46:S2:1379:A:H4'	46:S2:1380:A:O5'	2.15	0.46
46:S2:1416:C:HO2'	46:S2:1417:C:H5	1.60	0.46
56:SI:11:ARG:NH1	56:SI:15:GLY:O	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SO:113:GLN:OE1	73:Sa:46:GLU:HG2	2.15	0.46
71:SY:55:ILE:C	71:SY:55:ILE:HD12	2.40	0.46
73:Sa:87:ARG:NH1	73:Sa:94:ASP:OD1	2.48	0.46
78:Sg:131:LEU:CD2	78:Sg:140:TYR:HB3	2.44	0.46
1:L5:258:C:H2'	1:L5:259:C:C6	2.49	0.46
1:L5:1012:U:HO2'	1:L5:1013:C:P	2.35	0.46
1:L5:2311:U:O4	1:L5:2518:A:H5''	2.15	0.46
13:LJ:88:LYS:HB2	13:LJ:88:LYS:HE3	1.61	0.46
31:Lc:24:SER:O	31:Lc:24:SER:OG	2.28	0.46
46:S2:72:C:H42	54:SG:170:ARG:HG3	1.80	0.46
46:S2:1561:U:H2'	46:S2:1562:G:H8	1.80	0.46
56:SI:110:ARG:HG2	56:SI:121:LEU:HD21	1.98	0.46
58:SK:16:PHE:HZ	58:SK:80:ARG:HG2	1.81	0.46
62:SP:29:SER:O	62:SP:33:LEU:HB2	2.15	0.46
1:L5:423:U:H2'	1:L5:424:U:C6	2.49	0.46
1:L5:1018:G:O2'	1:L5:1019:U:H6	1.98	0.46
1:L5:1122:A:H2'	1:L5:1123:C:C6	2.51	0.46
1:L5:4218:C:OP1	17:LO:65:ASN:ND2	2.44	0.46
2:L7:111:C:H2'	2:L7:112:U:O4'	2.14	0.46
22:LT:111:GLU:N	22:LT:111:GLU:OE2	2.49	0.46
42:Ln:15:ARG:NH2	46:S2:1184:A:OP1	2.48	0.46
46:S2:825:C:C2	57:SJ:144:ILE:HD13	2.50	0.46
46:S2:1624:A:C6	65:SS:132:ARG:HG2	2.50	0.46
49:SB:171:ILE:HD13	49:SB:196:ASP:OD1	2.16	0.46
55:SH:30:LEU:O	55:SH:30:LEU:HD13	2.15	0.46
1:L5:2214:G:O2'	1:L5:3329:G:H8	1.97	0.46
17:LO:198:THR:O	17:LO:198:THR:OG1	2.34	0.46
23:LU:35:ASP:OD1	23:LU:36:ALA:N	2.45	0.46
46:S2:116:U:H3	46:S2:348:G:H1	1.64	0.46
46:S2:1441:C:H2'	46:S2:1442:U:C6	2.51	0.46
52:SE:87:MET:HG3	52:SE:87:MET:O	2.15	0.46
52:SE:114:ILE:HD11	52:SE:118:GLU:CD	2.41	0.46
67:SU:24:LEU:HD23	67:SU:112:VAL:HG22	1.97	0.46
1:L5:151:G:OP2	16:LN:4:TYR:OH	2.29	0.46
1:L5:925:G:H2'	1:L5:926:G:H5'	1.97	0.46
1:L5:1497:U:OP1	29:La:44:ASN:ND2	2.46	0.46
1:L5:4510:U:H2'	1:L5:4511:C:C6	2.51	0.46
4:LA:142:GLU:O	4:LA:143:THR:OG1	2.29	0.46
28:LZ:59:LYS:HD3	28:LZ:59:LYS:N	2.28	0.46
34:Lf:29:LYS:HB2	34:Lf:83:MET:HE3	1.97	0.46
39:Lk:24:LYS:HB3	39:Lk:69:LEU:HD11	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:SB:122:GLU:HG3	49:SB:140:VAL:HG23	1.96	0.46
51:SD:115:VAL:HG11	51:SD:142:LEU:HD23	1.96	0.46
52:SE:246:LEU:O	52:SE:247:THR:HB	2.16	0.46
56:SI:38:ILE:HD11	56:SI:78:ILE:HG13	1.98	0.46
62:SP:32:GLN:OE1	62:SP:32:GLN:N	2.33	0.46
65:SS:67:VAL:HG23	65:SS:68:ILE:HD13	1.98	0.46
1:L5:3298:U:OP2	1:L5:3303:A:N6	2.49	0.46
7:LD:64:ILE:HD13	7:LD:109:LEU:HD22	1.98	0.46
13:LJ:65:ASN:HB2	43:Lo:103:VAL:HA	1.97	0.46
19:LQ:99:LYS:HE3	19:LQ:99:LYS:HB2	1.67	0.46
23:LU:25:CYS:HA	23:LU:112:LEU:HD12	1.97	0.46
26:LX:64:SER:HB2	36:Lh:69:LEU:HD13	1.98	0.46
46:S2:68:A:H2'	46:S2:69:C:O4'	2.16	0.46
46:S2:1298:U:H2'	46:S2:1299:G:C8	2.49	0.46
52:SE:61:VAL:HG12	52:SE:80:ILE:HD11	1.97	0.46
54:SG:188:LYS:O	54:SG:192:ILE:HG13	2.15	0.46
63:SQ:9:SER:HB2	63:SQ:24:HIS:CE1	2.49	0.46
70:SX:128:VAL:HG13	70:SX:129:SER:H	1.79	0.46
78:Sg:35:SER:OG	78:Sg:36:ARG:N	2.49	0.46
1:L5:1585:U:H2'	1:L5:1586:C:O2	2.16	0.46
1:L5:3374:A:H2'	1:L5:3375:A:H8	1.79	0.46
1:L5:4634:G:H5''	5:LB:176:LYS:HG3	1.98	0.46
15:LM:39:ASP:C	15:LM:41:PRO:HD3	2.40	0.46
36:Lh:122:LYS:HB3	36:Lh:122:LYS:HE3	1.75	0.46
46:S2:1308:U:O2'	46:S2:1309:U:O4'	2.34	0.46
55:SH:23:ILE:HD11	55:SH:50:GLU:OE2	2.16	0.46
59:SL:37:TYR:CD1	59:SL:37:TYR:C	2.93	0.46
1:L5:3287:A:N1	1:L5:3488:U:H5	2.14	0.46
23:LU:42:PHE:CE1	23:LU:46:ARG:HG3	2.50	0.46
46:S2:89:C:H2'	46:S2:90:G:O4'	2.16	0.46
46:S2:158:A:H2'	46:S2:159:A:C8	2.51	0.46
46:S2:820:G:H22	46:S2:830:C:H5	1.64	0.46
1:L5:489:G:H2'	1:L5:490:C:C6	2.51	0.46
1:L5:2221:C:O2'	1:L5:2222:C:H6	1.99	0.46
6:LC:140:LYS:HE3	6:LC:245:HIS:HB2	1.98	0.46
11:LH:59:LYS:HA	11:LH:59:LYS:HD2	1.69	0.46
24:LV:72:LEU:HA	24:LV:75:LYS:NZ	2.31	0.46
46:S2:17:C:O2'	46:S2:1195:A:N1	2.49	0.46
47:S6:74:C:H5'	47:S6:75:C:OP2	2.16	0.46
47:S7:15:A:H2'	47:S7:16:G:O4'	2.15	0.46
49:SB:189:ILE:HB	49:SB:190:PRO:HD3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SE:127:ARG:HG3	52:SE:142:HIS:HA	1.98	0.46
1:L5:416:G:OP1	1:L5:2066:G:N2	2.49	0.46
1:L5:1219:C:H2'	1:L5:1220:C:C6	2.51	0.46
1:L5:2345:A:H2'	1:L5:2346:U:H6	1.80	0.46
1:L5:2377:A:OP1	23:LU:101:ARG:NH1	2.48	0.46
1:L5:3861:U:OP1	1:L5:3987:U:O2'	2.32	0.46
6:LC:66:SER:HA	6:LC:77:PRO:HA	1.98	0.46
10:LG:102:TYR:OH	10:LG:211:ASP:OD2	2.33	0.46
46:S2:302:A:O2'	56:SI:71:CYS:O	2.31	0.46
46:S2:1099:C:H2'	46:S2:1100:G:C8	2.50	0.46
46:S2:1442:U:H4'	46:S2:1443:U:OP2	2.13	0.46
58:SK:1:MET:HE1	58:SK:44:HIS:HA	1.97	0.46
58:SK:68:TYR:HD1	58:SK:68:TYR:H	1.63	0.46
62:SP:85:ILE:HD13	62:SP:85:ILE:HA	1.83	0.46
65:SS:74:PRO:HD2	65:SS:75:ARG:N	2.31	0.46
78:Sg:104:HIS:CD2	78:Sg:104:HIS:H	2.33	0.46
1:L5:93:G:H2'	1:L5:94:A:C8	2.51	0.45
1:L5:1004:G:H22	1:L5:1022:G:H1	1.63	0.45
1:L5:3269:C:H1'	1:L5:4664:A:C8	2.51	0.45
8:LE:138:LYS:HD3	8:LE:138:LYS:H	1.80	0.45
11:LH:9:THR:HA	11:LH:55:LEU:O	2.16	0.45
19:LQ:61:LEU:HD11	19:LQ:66:MET:HB2	1.98	0.45
32:Ld:19:GLU:OE1	32:Ld:92:ARG:NH1	2.49	0.45
37:Li:16:LYS:HD3	37:Li:16:LYS:HA	1.75	0.45
46:S2:128:U:H4'	46:S2:217:G:H5'	1.98	0.45
46:S2:1316:U:H2'	46:S2:1317:C:H6	1.81	0.45
70:SX:137:LYS:HE2	70:SX:137:LYS:HB2	1.80	0.45
78:Sg:133:ASN:OD1	78:Sg:139:LYS:HG2	2.16	0.45
1:L5:417:A:C2	3:L8:17:A:H1'	2.51	0.45
1:L5:3256:A:H2'	1:L5:3257:G:H8	1.78	0.45
1:L5:3903:G:O2'	13:LJ:129:ASP:OD1	2.10	0.45
7:LD:164:LYS:HA	7:LD:167:VAL:HG22	1.97	0.45
46:S2:54:A:H2'	46:S2:54:A:N3	2.30	0.45
46:S2:86:C:O2	46:S2:86:C:H2'	2.15	0.45
46:S2:1425:G:H2'	46:S2:1426:G:H8	1.81	0.45
47:S6:19:G:O4'	47:S6:57:G:N2	2.39	0.45
78:Sg:27:PHE:HE1	78:Sg:75:GLY:HA3	1.81	0.45
78:Sg:38:LYS:HG2	78:Sg:64:HIS:O	2.15	0.45
78:Sg:131:LEU:HD21	78:Sg:140:TYR:HB3	1.98	0.45
78:Sg:147:HIS:NE2	78:Sg:168:CYS:O	2.50	0.45
1:L5:833:U:O2	15:LM:44:ARG:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LM:75:LYS:HB2	15:LM:75:LYS:HE3	1.79	0.45
28:LZ:120:GLU:OE1	28:LZ:120:GLU:N	2.49	0.45
32:Ld:64:ILE:HG23	32:Ld:68:LEU:HD23	1.98	0.45
45:Lr:7:TRP:O	45:Lr:11:ARG:HB2	2.16	0.45
46:S2:481:G:H2'	46:S2:482:C:H5''	1.97	0.45
46:S2:965:A:H2'	46:S2:966:U:H6	1.82	0.45
46:S2:1553:G:H22	76:Sd:32:ARG:HB3	1.81	0.45
50:SC:75:ILE:HG12	50:SC:80:GLU:OE1	2.16	0.45
60:SN:130:LYS:HB2	60:SN:130:LYS:HE3	1.77	0.45
62:SP:20:VAL:HG23	62:SP:25:LEU:HG	1.97	0.45
63:SQ:92:LEU:HD12	63:SQ:92:LEU:HA	1.81	0.45
78:Sg:104:HIS:NE2	78:Sg:122:SER:OG	2.41	0.45
1:L5:1035:U:H2'	1:L5:1037:G:O4'	2.16	0.45
9:LF:58:LYS:HA	9:LF:58:LYS:HD3	1.78	0.45
15:LM:131:GLN:OE1	17:LO:174:ILE:HD11	2.16	0.45
16:LN:159:ARG:HB3	16:LN:164:LEU:HB2	1.98	0.45
26:LX:120:ASP:HB2	26:LX:144:TYR:CE1	2.51	0.45
46:S2:1378:U:H3'	48:SA:102:ARG:HH12	1.82	0.45
46:S2:1736:A:H3'	46:S2:1737:G:H8	1.81	0.45
47:S6:59:A:H2'	47:S6:59:A:N3	2.31	0.45
47:S7:53:G:H2'	47:S7:54:A:C8	2.51	0.45
52:SE:72:ILE:HG13	52:SE:77:ARG:HG3	1.98	0.45
1:L5:1536:G:N3	1:L5:3867:A:H2'	2.32	0.45
1:L5:4278:C:O2'	1:L5:4279:A:H5'	2.17	0.45
12:LI:121:LYS:HE2	47:S7:3:G:OP1	2.16	0.45
46:S2:82:G:OP2	46:S2:82:G:H8	1.99	0.45
46:S2:488:U:H1'	46:S2:508:G:H22	1.81	0.45
46:S2:1745:G:HO2'	46:S2:1791:A:H61	1.63	0.45
78:Sg:7:LEU:HD23	78:Sg:9:GLY:H	1.82	0.45
2:L7:117:G:OP1	7:LD:253:TYR:OH	2.30	0.45
45:Lr:107:ARG:O	45:Lr:111:ILE:HG12	2.16	0.45
46:S2:107:A:H2'	46:S2:108:G:C8	2.52	0.45
46:S2:111:A:O2'	46:S2:112:U:H5'	2.16	0.45
46:S2:150:A:OP2	46:S2:151:C:N4	2.36	0.45
46:S2:442:C:H2'	46:S2:443:C:C6	2.52	0.45
51:SD:72:VAL:HG11	58:SK:68:TYR:HD2	1.82	0.45
52:SE:51:ARG:HA	52:SE:51:ARG:HD3	1.48	0.45
52:SE:87:MET:HE2	52:SE:87:MET:HB2	1.83	0.45
60:SN:114:ARG:HD3	60:SN:114:ARG:HA	1.67	0.45
65:SS:75:ARG:NH2	65:SS:81:ASP:OD2	2.50	0.45
1:L5:461:G:H2'	1:L5:462:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:19:C:H2'	3:L8:20:A:C8	2.51	0.45
3:L8:80:A:C8	36:Lh:46:LYS:HG3	2.51	0.45
5:LB:56:ILE:HD13	5:LB:365:LEU:HD22	1.98	0.45
14:LL:51:ALA:HB2	14:LL:149:GLN:NE2	2.31	0.45
21:LS:21:LYS:HG3	21:LS:22:CYS:N	2.32	0.45
46:S2:106:C:OP1	46:S2:432:G:O2'	2.34	0.45
46:S2:509:A:C2	57:SJ:2:PRO:HB2	2.51	0.45
46:S2:897:U:H5'	46:S2:898:U:OP2	2.16	0.45
46:S2:923:A:OP1	69:SW:28:ARG:NH2	2.49	0.45
46:S2:1315:U:H6	58:SK:8:ARG:NH2	2.14	0.45
46:S2:1429:G:H4'	46:S2:1430:G:H5''	1.98	0.45
52:SE:18:TRP:C	52:SE:18:TRP:CD1	2.94	0.45
52:SE:52:LEU:HA	52:SE:52:LEU:HD23	1.81	0.45
57:SJ:124:HIS:HD2	77:Se:109:ARG:HH21	1.64	0.45
64:SR:96:ILE:O	64:SR:96:ILE:HG13	2.16	0.45
1:L5:266:G:H2'	1:L5:267:G:C8	2.51	0.45
1:L5:1088:G:P	9:LF:59:PHE:HZ	2.39	0.45
1:L5:3389:A:H2'	1:L5:3390:A:C8	2.52	0.45
7:LD:29:ASP:O	7:LD:30:TYR:HB2	2.16	0.45
8:LE:284:SER:OG	34:Lf:3:GLY:HA2	2.17	0.45
46:S2:1306:C:H2'	46:S2:1307:U:C6	2.52	0.45
46:S2:1747:U:H5'	54:SG:31:ARG:HH12	1.80	0.45
49:SB:227:LYS:HE2	49:SB:227:LYS:HB2	1.70	0.45
50:SC:269:PHE:O	50:SC:273:LEU:HD12	2.17	0.45
58:SK:47:LYS:HD3	58:SK:47:LYS:HA	1.80	0.45
60:SN:38:TYR:CZ	60:SN:78:LYS:HD2	2.52	0.45
70:SX:110:HIS:CD2	70:SX:111:ALA:H	2.33	0.45
5:LB:238:LYS:HB2	5:LB:238:LYS:HE2	1.74	0.45
10:LG:107:LYS:HA	10:LG:107:LYS:HD3	1.81	0.45
18:LP:94:MET:HE2	18:LP:148:MET:CE	2.43	0.45
46:S2:638:U:OP2	77:Se:98:LYS:NZ	2.50	0.45
46:S2:834:C:N4	46:S2:835:C:O2	2.50	0.45
46:S2:986:G:H4'	61:SO:138:ASP:OD2	2.17	0.45
46:S2:1140:C:H2'	46:S2:1141:G:O4'	2.17	0.45
46:S2:1415:A:H3'	46:S2:1416:C:C5'	2.47	0.45
52:SE:18:TRP:CD1	52:SE:20:LEU:HD13	2.51	0.45
56:SI:100:CYS:SG	56:SI:101:ILE:N	2.90	0.45
64:SR:106:LEU:HB3	64:SR:112:GLY:HA3	1.99	0.45
1:L5:108:A:H4'	1:L5:109:G:OP1	2.17	0.45
1:L5:823:C:O2'	1:L5:824:C:OP1	2.32	0.45
1:L5:4291:U:H2'	1:L5:4292:G:N3	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4528:U:OP1	15:LM:117:LYS:NZ	2.49	0.45
7:LD:228:LYS:H	7:LD:228:LYS:HZ3	1.64	0.45
21:LS:21:LYS:HE2	21:LS:21:LYS:HB2	1.75	0.45
31:Lc:18:LEU:O	31:Lc:22:MET:HG2	2.17	0.45
46:S2:38:A:N1	46:S2:516:G:H2'	2.32	0.45
46:S2:71:G:H2'	46:S2:72:C:H4'	1.98	0.45
46:S2:536:G:C6	46:S2:538:C:C2	3.05	0.45
46:S2:796:A:H2'	46:S2:797:G:C4	2.52	0.45
46:S2:1400:C:H2'	46:S2:1401:U:C6	2.52	0.45
51:SD:72:VAL:HG21	58:SK:70:TYR:HE1	1.80	0.45
52:SE:44:LEU:HD21	52:SE:72:ILE:HD11	1.99	0.45
54:SG:45:TRP:NE1	54:SG:121:ILE:HG13	2.32	0.45
54:SG:201:LYS:HZ2	54:SG:202:ASN:HA	1.82	0.45
59:SL:79:LYS:HE2	59:SL:87:VAL:HG11	1.97	0.45
1:L5:1212:A:C8	29:La:114:LYS:HD2	2.52	0.44
1:L5:3736:A:C5	10:LG:56:LYS:HD3	2.52	0.44
1:L5:4549:G:O6	1:L5:4565:G:H1'	2.17	0.44
5:LB:161:ARG:HG2	5:LB:184:GLN:HA	1.99	0.44
7:LD:215:ASP:OD1	7:LD:215:ASP:N	2.47	0.44
24:LV:62:MET:HE3	24:LV:76:VAL:HG12	1.98	0.44
46:S2:153:G:H1'	54:SG:13:GLN:OE1	2.17	0.44
46:S2:1866:C:H6	73:Sa:7:ASN:HB2	1.82	0.44
49:SB:66:VAL:HG11	49:SB:85:LYS:HE2	1.98	0.44
63:SQ:43:GLU:O	63:SQ:45:ARG:NH2	2.50	0.44
73:Sa:45:VAL:HG22	73:Sa:45:VAL:O	2.16	0.44
78:Sg:125:ARG:HD2	78:Sg:150:TRP:CE2	2.53	0.44
78:Sg:254:PRO:HA	78:Sg:285:GLN:HA	1.98	0.44
1:L5:4161:C:H5''	24:LV:43:LYS:HE3	1.97	0.44
3:L8:128:C:H2'	3:L8:129:C:C6	2.52	0.44
6:LC:173:LYS:HD3	6:LC:173:LYS:HA	1.63	0.44
7:LD:245:ALA:O	7:LD:249:GLU:HG2	2.18	0.44
25:LW:43:LYS:NZ	25:LW:43:LYS:HB3	2.31	0.44
46:S2:80:G:H2'	46:S2:81:U:C6	2.52	0.44
46:S2:226:A:H2'	46:S2:227:G:C8	2.53	0.44
46:S2:922:G:C5	69:SW:28:ARG:HD2	2.52	0.44
56:SI:38:ILE:HD12	56:SI:38:ILE:HA	1.82	0.44
63:SQ:102:GLU:OE1	63:SQ:102:GLU:N	2.50	0.44
1:L5:171:U:H5''	1:L5:172:C:C5	2.52	0.44
1:L5:2133:A:H2'	1:L5:2134:C:C6	2.52	0.44
1:L5:2644:C:O2'	1:L5:4664:A:N6	2.50	0.44
8:LE:103:THR:OG1	8:LE:104:VAL:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:168:C:H4'	54:SG:131:ARG:HB3	2.00	0.44
46:S2:527:A:H5''	77:Se:109:ARG:HH11	1.82	0.44
46:S2:643:U:O2'	46:S2:645:G:H4'	2.17	0.44
46:S2:1281:G:H2'	46:S2:1282:G:H8	1.80	0.44
63:SQ:9:SER:HB3	63:SQ:26:LYS:HG2	1.99	0.44
66:ST:102:ARG:HD3	66:ST:102:ARG:HA	1.59	0.44
70:SX:65:ALA:HB3	70:SX:67:ARG:HH11	1.83	0.44
74:Sb:34:ASP:OD1	74:Sb:82:LYS:HD2	2.18	0.44
1:L5:704:U:O2'	1:L5:705:G:OP1	2.35	0.44
1:L5:2655:G:N2	1:L5:3256:A:C2	2.86	0.44
11:LH:48:LEU:HD11	11:LH:56:ARG:HB2	1.99	0.44
15:LM:97:ALA:HB2	17:LO:203:VAL:HG23	1.99	0.44
19:LQ:115:LYS:HE3	19:LQ:115:LYS:HB3	1.67	0.44
33:Le:69:MET:HE3	33:Le:73:GLY:HA2	1.99	0.44
46:S2:468:G:H5'	54:SG:72:ARG:HH21	1.82	0.44
46:S2:929:G:H1	46:S2:1014:U:H3	1.65	0.44
46:S2:1423:G:C5	46:S2:1425:G:H1'	2.52	0.44
46:S2:1554:C:H2'	46:S2:1555:C:C6	2.52	0.44
49:SB:142:PHE:HD2	49:SB:209:ASP:HB2	1.83	0.44
51:SD:151:LYS:HB3	51:SD:151:LYS:HE2	1.81	0.44
54:SG:168:LYS:HB3	54:SG:170:ARG:HH11	1.82	0.44
55:SH:80:VAL:O	55:SH:84:GLU:HG2	2.18	0.44
74:Sb:64:CYS:HB3	74:Sb:73:LEU:HD12	1.99	0.44
1:L5:1050:C:H2'	1:L5:1051:G:C8	2.52	0.44
5:LB:288:GLY:HA3	5:LB:330:PHE:CE2	2.53	0.44
7:LD:136:ASP:OD1	7:LD:136:ASP:N	2.51	0.44
46:S2:163:U:O2'	54:SG:62:PRO:HG3	2.17	0.44
46:S2:525:U:H5'	46:S2:526:A:O4'	2.18	0.44
48:SA:128:ARG:HE	48:SA:153:PRO:HD3	1.82	0.44
48:SA:158:ASP:N	48:SA:158:ASP:OD1	2.50	0.44
50:SC:161:SER:O	50:SC:161:SER:OG	2.26	0.44
55:SH:153:LEU:HD11	55:SH:186:ASN:OD1	2.18	0.44
57:SJ:68:PRO:HB2	57:SJ:69:ARG:H	1.64	0.44
62:SP:15:PHE:CE2	62:SP:17:TYR:HB2	2.52	0.44
78:Sg:226:HIS:C	78:Sg:227:LEU:HD22	2.43	0.44
78:Sg:286:CYS:HB3	78:Sg:302:TYR:CZ	2.53	0.44
1:L5:106:A:H2'	1:L5:107:G:O4'	2.17	0.44
1:L5:1154:U:H2'	1:L5:1155:C:C6	2.53	0.44
1:L5:3345:U:OP2	4:LA:198:ARG:NH2	2.50	0.44
11:LH:113:GLU:HG2	11:LH:125:ARG:HG2	1.98	0.44
13:LJ:87:LEU:HD21	13:LJ:166:PHE:HE1	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LM:62:LEU:HD21	15:LM:82:ILE:HD11	1.99	0.44
19:LQ:49:LYS:HE2	19:LQ:49:LYS:HB3	1.69	0.44
20:LR:126:LYS:HE2	20:LR:126:LYS:HB3	1.80	0.44
46:S2:83:A:H2'	46:S2:84:A:C8	2.53	0.44
46:S2:159:A:O2'	46:S2:160:U:H5'	2.18	0.44
46:S2:375:G:H1'	59:SL:83:GLN:HE21	1.82	0.44
46:S2:547:G:H1'	46:S2:548:G:N7	2.33	0.44
46:S2:943:G:H2'	46:S2:944:U:C6	2.53	0.44
46:S2:1464:U:H5''	46:S2:1465:C:C5	2.52	0.44
54:SG:10:THR:HG21	54:SG:125:THR:HA	1.98	0.44
66:ST:101:ARG:O	66:ST:105:GLN:HG2	2.18	0.44
67:SU:48:LEU:HD13	67:SU:93:SER:OG	2.17	0.44
71:SY:85:ASN:O	71:SY:86:GLU:HG2	2.17	0.44
2:L7:110:G:H2'	2:L7:111:C:C6	2.52	0.44
5:LB:181:MET:HE2	5:LB:183:ILE:HG12	1.99	0.44
6:LC:13:GLU:OE2	6:LC:161:TYR:OH	2.34	0.44
7:LD:208:MET:HE1	7:LD:226:TYR:HE2	1.82	0.44
14:LL:17:ASP:OD1	14:LL:17:ASP:O	2.36	0.44
14:LL:87:HIS:HB3	14:LL:90:VAL:HG23	2.00	0.44
15:LM:29:ASP:OD1	15:LM:30:VAL:N	2.47	0.44
26:LX:107:HIS:O	26:LX:111:GLN:HG3	2.18	0.44
45:Lr:56:ASP:OD1	45:Lr:57:GLY:N	2.50	0.44
47:S6:12:C:H2'	47:S6:13:G:H8	1.81	0.44
47:S7:69:U:H2'	47:S7:70:G:C8	2.52	0.44
57:SJ:42:GLU:OE2	57:SJ:45:ARG:NH2	2.51	0.44
58:SK:41:PRO:HD2	58:SK:44:HIS:ND1	2.33	0.44
68:SV:74:LYS:HE3	68:SV:74:LYS:HB2	1.79	0.44
71:SY:29:HIS:HB3	71:SY:32:LYS:HB2	2.00	0.44
1:L5:37:U:H2'	1:L5:38:A:O4'	2.18	0.44
1:L5:1005:C:HO2'	1:L5:1006:G:P	2.38	0.44
1:L5:4148:G:H2'	1:L5:4149:A:H8	1.81	0.44
1:L5:4357:C:H2'	1:L5:4358:A:C8	2.53	0.44
1:L5:4386:C:H4'	1:L5:4387:A:H5'	1.99	0.44
1:L5:4551:C:HO2'	1:L5:4552:C:P	2.41	0.44
5:LB:382:MET:O	5:LB:386:LYS:HG3	2.17	0.44
7:LD:117:LYS:HA	7:LD:117:LYS:HD2	1.75	0.44
7:LD:206:ASP:OD1	7:LD:209:ARG:NH2	2.51	0.44
7:LD:243:ALA:O	7:LD:247:ILE:HG23	2.18	0.44
11:LH:128:MET:HE1	11:LH:161:ILE:HD11	2.00	0.44
11:LH:142:ASP:OD1	11:LH:142:ASP:O	2.36	0.44
13:LJ:169:LYS:HB2	13:LJ:169:LYS:HE2	1.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S7:34:C:H2'	47:S7:35:A:C8	2.52	0.44
48:SA:44:ASP:OD1	48:SA:44:ASP:N	2.51	0.44
48:SA:55:TRP:HZ3	48:SA:177:MET:HE2	1.82	0.44
51:SD:106:ARG:HG3	51:SD:175:VAL:HB	2.00	0.44
56:SI:81:VAL:HG21	56:SI:94:LYS:HA	2.00	0.44
61:SO:65:ASP:C	61:SO:65:ASP:OD1	2.61	0.44
69:SW:9:ASP:OD1	69:SW:9:ASP:N	2.38	0.44
1:L5:2172:U:H2'	1:L5:2173:G:C8	2.53	0.44
37:Li:70:LEU:HD12	37:Li:70:LEU:HA	1.84	0.44
46:S2:75:G:H1	54:SG:170:ARG:HB3	1.82	0.44
46:S2:592:U:O4'	46:S2:593:C:H3'	2.17	0.44
56:SI:66:SER:O	56:SI:189:VAL:HG23	2.18	0.44
63:SQ:24:HIS:O	63:SQ:68:ILE:HA	2.18	0.44
71:SY:109:GLU:HG3	71:SY:113:ARG:HH12	1.82	0.44
1:L5:1182:U:O2'	1:L5:1184:C:OP2	2.35	0.43
12:LI:189:ARG:HG3	12:LI:189:ARG:NH1	2.33	0.43
15:LM:40:GLY:HA3	15:LM:45:VAL:HB	2.00	0.43
46:S2:1061:A:H4'	46:S2:1062:U:H5''	1.99	0.43
63:SQ:45:ARG:HA	63:SQ:45:ARG:CZ	2.48	0.43
72:SZ:68:ILE:HG23	72:SZ:109:TYR:HB2	1.99	0.43
73:Sa:45:VAL:HG11	73:Sa:64:LEU:CD2	2.48	0.43
78:Sg:217:MET:HE3	78:Sg:219:TRP:CZ2	2.53	0.43
1:L5:682:G:H2'	1:L5:683:C:H6	1.83	0.43
1:L5:3786:G:H5'	1:L5:3787:U:OP2	2.18	0.43
10:LG:206:GLN:H	10:LG:206:GLN:HG2	1.60	0.43
20:LR:158:GLN:OE1	20:LR:162:ARG:NH1	2.51	0.43
46:S2:819:A:H2'	46:S2:820:G:H8	1.83	0.43
49:SB:36:PRO:HG2	49:SB:39:PHE:HE2	1.83	0.43
57:SJ:131:ARG:NH1	57:SJ:143:ASN:O	2.44	0.43
1:L5:831:G:N2	1:L5:836:C:H2'	2.33	0.43
1:L5:3984:G:H3'	1:L5:3985:C:H5'	2.00	0.43
2:L7:58:A:H2'	2:L7:59:G:H8	1.83	0.43
4:LA:98:ILE:HA	4:LA:166:VAL:HG22	2.00	0.43
5:LB:317:LEU:HD23	5:LB:317:LEU:HA	1.80	0.43
8:LE:153:THR:HG22	8:LE:154:PRO:HD2	2.00	0.43
10:LG:33:GLU:OE1	28:LZ:128:LYS:HE3	2.19	0.43
15:LM:63:LYS:HA	15:LM:63:LYS:HD2	1.84	0.43
19:LQ:71:LYS:HB2	19:LQ:71:LYS:HE2	1.80	0.43
23:LU:60:VAL:HG23	23:LU:61:VAL:HG23	1.99	0.43
38:Lj:79:ARG:O	38:Lj:80:GLU:HG3	2.18	0.43
49:SB:103:MET:HE2	49:SB:103:MET:HB3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SJ:123:ILE:O	57:SJ:123:ILE:HG13	2.17	0.43
58:SK:60:GLU:CD	58:SK:69:TRP:HE1	2.25	0.43
74:Sb:31:TYR:O	74:Sb:48:SER:OG	2.23	0.43
74:Sb:34:ASP:OD1	74:Sb:34:ASP:N	2.51	0.43
74:Sb:81:ARG:NH1	74:Sb:84:HIS:HA	2.31	0.43
78:Sg:212:LYS:O	78:Sg:212:LYS:HG2	2.17	0.43
1:L5:1736:G:H2'	1:L5:1737:A:C8	2.54	0.43
1:L5:2345:A:H2'	1:L5:2346:U:C6	2.53	0.43
1:L5:3432:A:H2'	1:L5:3433:G:O4'	2.18	0.43
1:L5:4071:G:O6	1:L5:4074:C:H2'	2.19	0.43
3:L8:75:G:OP2	27:LY:74:TYR:OH	2.36	0.43
24:LV:87:SER:OG	25:LW:19:ARG:NH1	2.51	0.43
28:LZ:99:ASP:N	28:LZ:99:ASP:OD1	2.51	0.43
37:Li:3:LEU:O	37:Li:4:ARG:HB2	2.17	0.43
46:S2:174:C:H3'	46:S2:175:A:C8	2.53	0.43
46:S2:353:U:O2	59:SL:71:ARG:NH1	2.51	0.43
46:S2:538:C:H3'	46:S2:539:U:C6	2.53	0.43
47:S7:62:C:H2'	47:S7:63:A:C8	2.53	0.43
49:SB:76:ASN:OD1	49:SB:76:ASN:N	2.48	0.43
52:SE:46:ILE:O	52:SE:50:ASN:HB2	2.18	0.43
60:SN:57:SER:HB2	60:SN:58:HIS:ND1	2.34	0.43
63:SQ:72:VAL:HB	63:SQ:84:ILE:HD11	2.00	0.43
66:ST:27:LYS:NZ	66:ST:110:LEU:HA	2.33	0.43
1:L5:23:C:H2'	1:L5:24:G:O4'	2.18	0.43
1:L5:229:G:OP1	27:LY:11:ARG:HD2	2.18	0.43
1:L5:811:U:H2'	1:L5:812:G:O4'	2.18	0.43
29:La:110:LYS:HG3	29:La:128:PHE:HB2	2.00	0.43
34:Lf:33:VAL:HG13	34:Lf:38:GLU:HB2	2.00	0.43
34:Lf:43:LEU:HD12	34:Lf:43:LEU:HA	1.68	0.43
46:S2:55:U:H4'	46:S2:56:G:OP1	2.18	0.43
46:S2:84:A:HO2'	71:SY:118:ARG:HE	1.60	0.43
46:S2:98:C:H1'	46:S2:410:C:OP1	2.18	0.43
46:S2:1318:C:H2'	46:S2:1319:G:H8	1.81	0.43
55:SH:154:ILE:HB	55:SH:185:VAL:HG23	2.00	0.43
60:SN:112:LYS:O	60:SN:116:ILE:HG13	2.19	0.43
62:SP:123:TYR:OH	65:SS:124:ARG:NH1	2.52	0.43
1:L5:871:U:H5''	1:L5:872:C:OP1	2.18	0.43
1:L5:939:U:O4	1:L5:1050:C:N4	2.52	0.43
1:L5:3885:U:H5'	43:Lo:3:ASN:HB3	1.99	0.43
29:La:87:ARG:HG3	29:La:120:GLN:HE22	1.84	0.43
36:Lh:97:LYS:HD3	36:Lh:97:LYS:C	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lp:84:ARG:HH22	44:Lp:85:ARG:HH21	1.64	0.43
46:S2:1379:A:OP2	48:SA:102:ARG:NH1	2.51	0.43
46:S2:1679:A:O2'	46:S2:1680:A:H5'	2.19	0.43
56:SI:147:LYS:HA	56:SI:147:LYS:HD3	1.78	0.43
1:L5:761:C:H5	1:L5:810:G:N1	2.12	0.43
1:L5:1723:C:H3'	1:L5:1724:C:H5''	2.00	0.43
1:L5:1745:A:H2'	1:L5:1746:A:H8	1.83	0.43
1:L5:2314:G:H1	1:L5:2324:G:N2	2.16	0.43
1:L5:3383:A:H2'	1:L5:3384:A:C8	2.54	0.43
1:L5:3826:G:H2'	1:L5:3827:U:C6	2.53	0.43
1:L5:4630:A:OP1	18:LP:74:LYS:NZ	2.45	0.43
5:LB:302:ASN:HB2	5:LB:313:SER:HA	2.00	0.43
20:LR:165:LYS:HB3	20:LR:165:LYS:HE3	1.69	0.43
26:LX:88:LYS:HE2	26:LX:88:LYS:HB2	1.72	0.43
28:LZ:76:ASN:OD1	28:LZ:77:TYR:N	2.52	0.43
31:Lc:99:PRO:HB2	31:Lc:100:GLY:H	1.55	0.43
46:S2:315:U:P	46:S2:315:U:H6	2.42	0.43
46:S2:444:U:H2'	46:S2:445:G:O4'	2.18	0.43
46:S2:574:U:H1'	46:S2:577:A:N7	2.34	0.43
46:S2:1420:C:H2'	46:S2:1421:G:C5	2.54	0.43
46:S2:1458:U:H2'	46:S2:1459:G:C8	2.54	0.43
50:SC:180:VAL:HG23	50:SC:197:PRO:HG3	2.01	0.43
59:SL:79:LYS:HB2	59:SL:87:VAL:HG12	2.00	0.43
63:SQ:43:GLU:CB	63:SQ:44:PRO:HD2	2.49	0.43
70:SX:115:ILE:HA	70:SX:116:PRO:HD3	1.88	0.43
78:Sg:155:ARG:HD2	78:Sg:198:VAL:O	2.19	0.43
1:L5:297:G:OP1	16:LN:179:LYS:HD3	2.18	0.43
1:L5:1766:C:H2'	1:L5:1767:A:H8	1.84	0.43
1:L5:2406:G:N2	44:Lp:58:GLY:O	2.52	0.43
1:L5:3577:U:H2'	1:L5:3578:U:C6	2.53	0.43
1:L5:4279:A:OP2	5:LB:224:LYS:NZ	2.46	0.43
13:LJ:57:VAL:HG12	13:LJ:59:SER:H	1.84	0.43
15:LM:39:ASP:O	15:LM:41:PRO:HD3	2.19	0.43
27:LY:36:LYS:HE2	27:LY:36:LYS:HB3	1.70	0.43
28:LZ:28:ASN:HB2	28:LZ:77:TYR:OH	2.18	0.43
28:LZ:68:ILE:HG13	28:LZ:119:GLU:HG3	2.01	0.43
46:S2:66:G:O5'	46:S2:82:G:N2	2.37	0.43
46:S2:797:G:H2'	46:S2:798:C:H4'	2.01	0.43
46:S2:836:C:H4'	46:S2:837:G:N7	2.33	0.43
46:S2:1425:G:C2	46:S2:1426:G:N7	2.86	0.43
54:SG:182:PRO:HA	54:SG:185:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SI:6:ASP:OD1	56:SI:6:ASP:N	2.50	0.43
78:Sg:236:ILE:HD13	78:Sg:239:LEU:HD23	2.01	0.43
1:L5:760:G:HO2'	1:L5:761:C:P	2.41	0.43
1:L5:4560:C:H2'	1:L5:4561:G:H8	1.83	0.43
8:LE:218:LYS:HA	8:LE:218:LYS:HD2	1.85	0.43
10:LG:160:ASP:O	10:LG:187:LYS:HE2	2.18	0.43
17:LO:201:LEU:HD12	17:LO:201:LEU:H	1.84	0.43
46:S2:159:A:C2	46:S2:468:G:N2	2.87	0.43
46:S2:172:U:H5'	46:S2:315:U:O3'	2.19	0.43
46:S2:536:G:H2'	46:S2:538:C:H1'	1.99	0.43
46:S2:559:G:H1'	46:S2:560:G:C8	2.54	0.43
46:S2:878:C:H2'	46:S2:879:G:C8	2.54	0.43
46:S2:1296:A:C5	46:S2:1297:U:H1'	2.53	0.43
47:S7:35:A:N1	79:Sx:39:A:N1	2.67	0.43
48:SA:16:LEU:HD23	48:SA:16:LEU:HA	1.87	0.43
48:SA:51:LEU:HD13	64:SR:105:MET:HE1	2.00	0.43
50:SC:142:LYS:HG3	50:SC:143:CYS:N	2.32	0.43
51:SD:194:PRO:HB2	51:SD:197:LYS:HG2	1.99	0.43
52:SE:18:TRP:NE1	52:SE:20:LEU:HD22	2.33	0.43
54:SG:145:PHE:HD2	54:SG:156:TYR:HB3	1.84	0.43
56:SI:79:ILE:HD12	56:SI:170:LYS:HD2	2.01	0.43
58:SK:5:LYS:O	58:SK:9:ILE:HG23	2.19	0.43
73:Sa:94:ASP:OD1	73:Sa:94:ASP:C	2.61	0.43
74:Sb:24:LEU:HD12	74:Sb:24:LEU:HA	1.83	0.43
78:Sg:285:GLN:O	78:Sg:303:THR:N	2.50	0.43
1:L5:953:C:H2'	1:L5:954:G:H8	1.82	0.43
1:L5:1025:C:H2'	1:L5:1026:C:H5''	2.01	0.43
1:L5:4581:C:H2'	1:L5:4582:G:C8	2.53	0.43
5:LB:294:LYS:HE3	5:LB:294:LYS:HB2	1.80	0.43
10:LG:34:LYS:HG3	10:LG:36:PRO:HD3	2.00	0.43
30:Lb:53:GLY:O	30:Lb:57:MET:HG3	2.18	0.43
45:Lr:82:ILE:HG23	45:Lr:84:LYS:HZ3	1.84	0.43
46:S2:849:U:H2'	46:S2:850:A:H8	1.83	0.43
46:S2:1426:G:C6	46:S2:1427:U:C4	3.07	0.43
48:SA:40:LYS:HG3	48:SA:41:ARG:N	2.34	0.43
50:SC:259:THR:HG21	68:SV:15:ARG:HA	2.01	0.43
51:SD:162:ASP:N	51:SD:163:PRO:HD2	2.34	0.43
63:SQ:84:ILE:O	63:SQ:88:ILE:HG12	2.19	0.43
1:L5:3313:A:H2'	1:L5:3314:U:H6	1.84	0.42
2:L7:58:A:H2'	2:L7:59:G:C8	2.54	0.42
6:LC:8:ILE:N	6:LC:22:VAL:O	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LC:143:ARG:HE	6:LC:143:ARG:HB3	1.64	0.42
22:LT:113:ASP:N	22:LT:113:ASP:OD1	2.52	0.42
25:LW:20:ARG:HE	25:LW:20:ARG:HB2	1.61	0.42
36:Lh:82:ASP:OD1	36:Lh:82:ASP:N	2.44	0.42
43:Lo:73:VAL:HG22	43:Lo:74:GLU:OE1	2.19	0.42
46:S2:84:A:C6	46:S2:85:A:C6	3.07	0.42
46:S2:1389:A:H61	51:SD:161:GLY:HA3	1.84	0.42
46:S2:1741:C:H42	46:S2:1795:C:H42	1.67	0.42
52:SE:88:ASP:OD1	52:SE:122:LYS:NZ	2.52	0.42
75:Sc:43:ILE:H	75:Sc:43:ILE:HG13	1.70	0.42
1:L5:384:A:N3	1:L5:386:G:H5''	2.34	0.42
1:L5:923:G:HO2'	1:L5:924:G:P	2.42	0.42
1:L5:1865:C:O2'	21:LS:5:GLY:HA2	2.19	0.42
10:LG:185:LYS:HE2	10:LG:185:LYS:HB2	1.82	0.42
13:LJ:38:LYS:HE2	13:LJ:38:LYS:HB3	1.77	0.42
19:LQ:70:MET:HE1	19:LQ:78:LYS:O	2.19	0.42
19:LQ:88:ASP:HB2	19:LQ:109:ALA:HB2	2.01	0.42
37:Li:13:LYS:HB3	37:Li:13:LYS:HE3	1.83	0.42
46:S2:175:A:H2'	46:S2:176:U:O4'	2.19	0.42
46:S2:224:U:O2'	46:S2:225:C:H5'	2.18	0.42
46:S2:1165:G:O2'	46:S2:1166:G:H5'	2.19	0.42
48:SA:10:MET:O	48:SA:11:LYS:HB2	2.18	0.42
52:SE:106:LYS:HB2	52:SE:108:ARG:HD3	2.00	0.42
52:SE:252:ARG:HE	52:SE:252:ARG:HB3	1.59	0.42
54:SG:98:ARG:CZ	54:SG:106:LEU:HD21	2.48	0.42
55:SH:83:LEU:HB3	55:SH:92:VAL:HG21	2.02	0.42
78:Sg:156:PHE:HA	78:Sg:164:ILE:O	2.19	0.42
1:L5:753:G:HO2'	1:L5:754:A:P	2.38	0.42
5:LB:147:GLU:OE2	5:LB:147:GLU:HA	2.19	0.42
5:LB:332:MET:HE3	5:LB:332:MET:HB2	1.93	0.42
46:S2:52:G:H8	46:S2:52:G:OP2	2.02	0.42
46:S2:514:G:C5	46:S2:515:U:C4	3.08	0.42
46:S2:883:U:H3	46:S2:905:A:N6	2.16	0.42
56:SI:3:ILE:O	56:SI:30:GLY:N	2.53	0.42
65:SS:70:ILE:HG13	65:SS:77:TYR:CG	2.54	0.42
78:Sg:5:MET:HE2	78:Sg:5:MET:HB2	1.83	0.42
78:Sg:7:LEU:HB2	78:Sg:310:TRP:CZ3	2.54	0.42
78:Sg:31:ILE:HG23	78:Sg:45:LEU:HD21	2.01	0.42
1:L5:3601:G:H1	1:L5:3720:U:H3	1.65	0.42
8:LE:102:LYS:O	8:LE:112:THR:OG1	2.21	0.42
12:LI:184:LYS:HZ2	12:LI:190:LEU:HD11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LS:21:LYS:HG3	21:LS:22:CYS:H	1.83	0.42
24:LV:109:LYS:HD2	24:LV:109:LYS:HA	1.89	0.42
36:Lh:14:LYS:HE2	36:Lh:18:LEU:HD11	2.01	0.42
46:S2:66:G:C8	46:S2:82:G:N2	2.87	0.42
46:S2:147:A:H2'	46:S2:148:U:C6	2.55	0.42
46:S2:1220:C:H4'	75:Sc:24:GLN:HE21	1.83	0.42
46:S2:1410:A:O2'	46:S2:1411:C:H5'	2.20	0.42
47:S6:12:C:H2'	47:S6:13:G:C8	2.54	0.42
47:S7:18:G:H21	47:S7:58:A:H5'	1.83	0.42
50:SC:166:ARG:HB2	50:SC:248:TYR:CE2	2.55	0.42
56:SI:63:GLY:O	56:SI:75:LYS:HG2	2.19	0.42
57:SJ:78:LEU:HD12	57:SJ:78:LEU:HA	1.90	0.42
59:SL:128:VAL:HG12	59:SL:142:VAL:HA	2.01	0.42
78:Sg:191:HIS:CG	78:Sg:195:LEU:HD21	2.53	0.42
1:L5:2:G:H2'	1:L5:3:C:C6	2.54	0.42
1:L5:3787:U:C4	1:L5:3801:G:O6	2.72	0.42
23:LU:61:VAL:HG22	23:LU:74:SER:HB2	2.01	0.42
46:S2:369:U:H2'	46:S2:370:C:C5	2.55	0.42
46:S2:497:C:H2'	46:S2:498:C:N1	2.34	0.42
46:S2:502:C:H2'	46:S2:503:C:C5'	2.50	0.42
46:S2:1426:G:C2	66:ST:5:THR:HG21	2.54	0.42
51:SD:39:VAL:HG23	51:SD:48:ILE:HG12	2.01	0.42
56:SI:172:LEU:HD13	56:SI:190:LEU:HD12	2.02	0.42
58:SK:4:PRO:HG2	58:SK:7:ASN:OD1	2.19	0.42
71:SY:102:THR:HG23	71:SY:107:ARG:HG3	2.02	0.42
78:Sg:14:HIS:CD2	78:Sg:35:SER:HB2	2.55	0.42
1:L5:1589:A:H2'	1:L5:1592:C:C5	2.54	0.42
1:L5:3567:C:H2'	1:L5:3568:C:C6	2.55	0.42
17:LO:168:TYR:CE2	17:LO:172:LYS:HD2	2.55	0.42
19:LQ:70:MET:HE2	19:LQ:80:ALA:HB2	2.00	0.42
21:LS:15:ARG:HB3	21:LS:27:LEU:HD13	2.01	0.42
46:S2:62:G:H1'	46:S2:172:U:O4	2.19	0.42
46:S2:91:A:H61	54:SG:88:ARG:HG2	1.84	0.42
46:S2:177:G:O6	46:S2:314:A:H5'	2.20	0.42
46:S2:629:A:O2'	46:S2:630:A:OP1	2.31	0.42
46:S2:1280:C:H2'	46:S2:1281:G:H8	1.85	0.42
54:SG:137:ARG:HG2	54:SG:140:ARG:HH21	1.84	0.42
54:SG:159:ARG:NH1	54:SG:171:THR:HG23	2.35	0.42
71:SY:87:PRO:HG2	71:SY:90:ARG:HB2	2.01	0.42
74:Sb:59:CYS:SG	74:Sb:60:SER:N	2.92	0.42
1:L5:334:A:H2'	1:L5:335:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2450:A:C6	39:Lk:69:LEU:HD13	2.54	0.42
1:L5:4154:U:H3'	1:L5:4155:C:O2	2.19	0.42
12:LI:91:LEU:HD23	12:LI:91:LEU:HA	1.92	0.42
13:LJ:40:LEU:HD23	13:LJ:40:LEU:HA	1.83	0.42
15:LM:32:ASP:OD1	15:LM:32:ASP:C	2.62	0.42
20:LR:159:ALA:O	20:LR:163:ARG:HG3	2.19	0.42
37:Li:3:LEU:HD23	37:Li:3:LEU:HA	1.87	0.42
37:Li:67:LYS:HD3	37:Li:71:LYS:NZ	2.35	0.42
46:S2:41:G:N2	46:S2:481:G:N2	2.67	0.42
46:S2:74:G:H4'	46:S2:75:G:H5'	2.02	0.42
46:S2:448:A:OP1	56:SI:49:ARG:NH2	2.52	0.42
46:S2:1553:G:H5''	46:S2:1557:A:N3	2.35	0.42
46:S2:1610:C:OP2	65:SS:132:ARG:HD2	2.19	0.42
49:SB:195:LYS:O	49:SB:199:LYS:HG2	2.20	0.42
54:SG:136:LYS:NZ	54:SG:175:LYS:HG3	2.35	0.42
56:SI:53:LYS:HE2	56:SI:53:LYS:HB2	1.88	0.42
61:SO:98:ARG:HG3	61:SO:99:ALA:O	2.19	0.42
65:SS:67:VAL:O	65:SS:70:ILE:HG22	2.20	0.42
68:SV:56:CYS:SG	68:SV:59:ILE:HG12	2.59	0.42
69:SW:11:LEU:HB3	69:SW:72:CYS:O	2.19	0.42
73:Sa:93:LYS:HE2	73:Sa:93:LYS:HB3	1.77	0.42
78:Sg:11:LEU:HB3	78:Sg:43:TRP:CH2	2.55	0.42
1:L5:4506:G:O2'	1:L5:4507:G:H5'	2.20	0.42
4:LA:32:VAL:HA	4:LA:36:GLU:OE1	2.20	0.42
5:LB:168:MET:HE3	5:LB:168:MET:HB3	1.87	0.42
5:LB:214:ASP:HA	5:LB:284:ILE:O	2.20	0.42
13:LJ:167:GLN:HA	13:LJ:171:ASP:O	2.20	0.42
26:LX:145:ASP:O	26:LX:149:VAL:HG23	2.20	0.42
33:Le:66:THR:O	33:Le:66:THR:HG22	2.19	0.42
36:Lh:28:LEU:O	36:Lh:32:ARG:HG3	2.20	0.42
39:Lk:52:LYS:HD2	39:Lk:52:LYS:N	2.35	0.42
46:S2:59:U:O2'	46:S2:60:A:O5'	2.36	0.42
48:SA:143:PRO:HG3	68:SV:32:ILE:HG23	2.01	0.42
64:SR:97:GLU:HB3	64:SR:120:THR:HG21	2.02	0.42
65:SS:91:LYS:NZ	65:SS:113:ARG:HG3	2.35	0.42
66:ST:22:LEU:HD22	66:ST:28:LEU:HD12	2.01	0.42
75:Sc:14:VAL:HG12	75:Sc:52:GLU:HA	2.01	0.42
1:L5:697:U:H2'	1:L5:698:C:C6	2.55	0.42
1:L5:701:C:H2'	1:L5:702:C:H6	1.83	0.42
1:L5:1523:C:H2'	1:L5:1524:G:C4	2.54	0.42
1:L5:3605:C:C2	1:L5:3606:A:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3606:A:N7	1:L5:3607:U:C5	2.88	0.42
1:L5:4686:A:HO2'	1:L5:4687:U:P	2.42	0.42
4:LA:137:ILE:HG12	4:LA:147:ARG:O	2.20	0.42
35:Lg:88:ARG:HG3	35:Lg:88:ARG:HH11	1.84	0.42
37:Li:85:ARG:O	37:Li:88:GLU:HG3	2.19	0.42
46:S2:177:G:H1	46:S2:314:A:H5'	1.85	0.42
46:S2:381:G:P	56:SI:56:ARG:HH22	2.43	0.42
46:S2:465:A:H8	46:S2:465:A:OP1	2.03	0.42
58:SK:27:VAL:HG22	58:SK:43:LEU:HD12	2.02	0.42
68:SV:33:GLN:HE21	68:SV:52:THR:HG21	1.84	0.42
78:Sg:241:PHE:HA	78:Sg:248:LEU:HD22	2.02	0.42
1:L5:1:C:H1'	1:L5:2:G:C8	2.54	0.42
1:L5:171:U:H3'	1:L5:172:C:C6	2.54	0.42
1:L5:1768:G:H2'	1:L5:1769:C:C6	2.55	0.42
1:L5:3739:C:OP1	4:LA:37:ARG:NH1	2.53	0.42
1:L5:4637:U:O2'	1:L5:4638:C:H5''	2.20	0.42
27:LY:62:TYR:CD2	27:LY:85:VAL:HG13	2.55	0.42
31:Lc:78:ASN:OD1	31:Lc:78:ASN:N	2.51	0.42
46:S2:375:G:H2'	46:S2:376:U:C6	2.54	0.42
46:S2:1107:C:H5''	74:Sb:70:LYS:HE2	2.00	0.42
46:S2:1423:G:N1	46:S2:1425:G:O2'	2.43	0.42
46:S2:1624:A:C5	65:SS:132:ARG:HG2	2.55	0.42
52:SE:220:THR:OG1	52:SE:221:ARG:N	2.52	0.42
53:SF:137:GLN:HA	53:SF:137:GLN:OE1	2.20	0.42
55:SH:21:SER:O	55:SH:25:GLN:HG3	2.20	0.42
65:SS:104:ASP:OD1	65:SS:104:ASP:N	2.52	0.42
74:Sb:56:CYS:SG	74:Sb:57:VAL:N	2.93	0.42
77:Se:99:LYS:HA	77:Se:99:LYS:HD3	1.82	0.42
1:L5:2519:A:H4'	1:L5:2520:A:OP1	2.20	0.41
1:L5:3607:U:N3	1:L5:3608:G:O6	2.53	0.41
5:LB:62:ARG:H	5:LB:68:ASN:HD22	1.67	0.41
46:S2:67:C:H4'	46:S2:68:A:N7	2.35	0.41
46:S2:800:U:H2'	46:S2:801:U:C6	2.55	0.41
46:S2:1008:C:H2'	46:S2:1009:A:C8	2.54	0.41
58:SK:2:LEU:HD12	58:SK:2:LEU:HA	1.78	0.41
66:ST:40:ALA:HB3	66:ST:43:LYS:HG2	2.02	0.41
71:SY:40:ILE:H	71:SY:40:ILE:HG12	1.66	0.41
76:Sd:54:LYS:HD3	76:Sd:54:LYS:C	2.45	0.41
1:L5:2316:G:H21	1:L5:2323:G:H1	1.68	0.41
1:L5:2512:G:H2'	1:L5:2513:G:N7	2.35	0.41
1:L5:3900:G:H4'	7:LD:4:VAL:HG11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LW:4:GLU:OE2	25:LW:30:GLN:HG2	2.20	0.41
33:Le:12:ILE:HD11	33:Le:69:MET:HE2	2.02	0.41
46:S2:847:G:O5'	46:S2:848:A:H5''	2.20	0.41
51:SD:28:GLU:HA	51:SD:28:GLU:OE2	2.21	0.41
53:SF:42:LYS:HD3	53:SF:42:LYS:HA	1.58	0.41
54:SG:63:MET:SD	54:SG:98:ARG:NH1	2.94	0.41
55:SH:75:ILE:O	55:SH:79:LEU:HD12	2.20	0.41
58:SK:21:MET:HG2	58:SK:22:VAL:N	2.33	0.41
58:SK:80:ARG:HD2	58:SK:80:ARG:HA	1.79	0.41
66:ST:42:HIS:CE1	66:ST:43:LYS:HE3	2.55	0.41
1:L5:1476:C:H2'	1:L5:1477:C:C6	2.54	0.41
1:L5:2258:C:H2'	1:L5:2259:G:O4'	2.19	0.41
1:L5:3605:C:H2'	1:L5:3606:A:N3	2.35	0.41
1:L5:4286:G:O3'	1:L5:4287:U:H3'	2.20	0.41
7:LD:247:ILE:HG13	7:LD:248:ARG:N	2.35	0.41
11:LH:52:LYS:N	11:LH:52:LYS:HD3	2.35	0.41
16:LN:36:LEU:HD13	16:LN:64:ILE:HD13	2.02	0.41
46:S2:97:U:H3	46:S2:433:G:H1	1.67	0.41
46:S2:146:G:H2'	46:S2:147:A:C4	2.54	0.41
46:S2:563:U:H2'	46:S2:564:G:O4'	2.20	0.41
46:S2:1312:C:H2'	46:S2:1313:G:O4'	2.20	0.41
46:S2:1553:G:H5''	46:S2:1557:A:C2	2.55	0.41
47:S6:53:G:HO2'	47:S6:54:A:P	2.42	0.41
60:SN:63:VAL:HG11	60:SN:71:ILE:HD11	2.01	0.41
64:SR:99:ASP:OD1	64:SR:120:THR:OG1	2.38	0.41
65:SS:68:ILE:HG22	65:SS:72:GLN:OE1	2.20	0.41
65:SS:110:ASP:OD1	65:SS:113:ARG:NH2	2.53	0.41
67:SU:66:ARG:O	67:SU:67:LYS:HB3	2.19	0.41
78:Sg:91:ASP:O	78:Sg:95:GLY:HA2	2.21	0.41
1:L5:665:C:O2	1:L5:665:C:H2'	2.20	0.41
1:L5:936:C:H2'	1:L5:937:C:O4'	2.19	0.41
4:LA:196:TRP:HB3	4:LA:197:PRO:HD3	2.02	0.41
14:LL:108:GLU:OE1	14:LL:108:GLU:N	2.42	0.41
15:LM:81:ASP:O	15:LM:85:LYS:HG3	2.20	0.41
17:LO:181:ALA:O	17:LO:185:VAL:HG22	2.21	0.41
26:LX:131:ASP:C	26:LX:131:ASP:OD1	2.63	0.41
39:Lk:64:LEU:HD12	39:Lk:64:LEU:HA	1.93	0.41
46:S2:62:G:H2'	46:S2:62:G:N3	2.35	0.41
46:S2:1276:G:H4'	46:S2:1277:A:C8	2.56	0.41
46:S2:1682:U:O2	46:S2:1684:C:N4	2.48	0.41
62:SP:38:SER:OG	62:SP:39:ALA:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SY:25:ILE:HD12	71:SY:25:ILE:N	2.36	0.41
71:SY:28:LEU:HD13	71:SY:68:LYS:HD2	2.02	0.41
1:L5:106:A:OP1	14:LL:39:ARG:HD3	2.19	0.41
1:L5:1001:G:H2'	1:L5:1002:G:H8	1.84	0.41
1:L5:4190:C:H2'	1:L5:4191:G:C8	2.56	0.41
1:L5:4652:C:H2'	1:L5:4653:G:O4'	2.21	0.41
2:L7:3:C:H2'	2:L7:4:U:C6	2.56	0.41
4:LA:28:ARG:HB2	4:LA:123:ARG:HD3	2.03	0.41
4:LA:102:LEU:HB2	4:LA:107:MET:HE3	2.02	0.41
8:LE:198:HIS:HB3	8:LE:201:PHE:HD1	1.85	0.41
14:LL:42:LYS:O	14:LL:46:ILE:HG12	2.20	0.41
14:LL:179:PHE:CD2	29:La:131:ARG:HG3	2.55	0.41
31:Lc:69:THR:OG1	31:Lc:70:GLY:N	2.53	0.41
35:Lg:19:LYS:HD2	35:Lg:19:LYS:HA	1.77	0.41
46:S2:446:A:H2'	46:S2:447:G:O4'	2.21	0.41
46:S2:1366:G:H2'	46:S2:1367:G:C8	2.56	0.41
49:SB:168:MET:O	49:SB:172:MET:HG2	2.20	0.41
58:SK:65:ARG:HD2	76:Sd:22:ARG:O	2.21	0.41
67:SU:34:LYS:HB3	67:SU:34:LYS:HE3	1.88	0.41
71:SY:121:ALA:O	71:SY:125:VAL:HG12	2.20	0.41
72:SZ:48:VAL:HG22	72:SZ:49:LEU:N	2.35	0.41
1:L5:139:G:H2'	1:L5:140:G:H8	1.83	0.41
1:L5:886:U:O4	1:L5:887:C:N4	2.54	0.41
1:L5:1670:A:H2'	1:L5:1671:A:C8	2.56	0.41
1:L5:2512:G:H2'	1:L5:2513:G:C8	2.55	0.41
1:L5:3885:U:O2'	43:Lo:97:LYS:NZ	2.51	0.41
2:L7:60:G:HO2'	2:L7:61:G:P	2.44	0.41
6:LC:325:MET:HE1	9:LF:177:TYR:CZ	2.55	0.41
10:LG:96:LEU:HD23	10:LG:96:LEU:HA	1.82	0.41
11:LH:137:SER:HB3	11:LH:143:GLU:HG3	2.03	0.41
17:LO:122:ALA:O	17:LO:128:ARG:HD3	2.21	0.41
20:LR:153:LYS:HD2	20:LR:153:LYS:C	2.46	0.41
22:LT:111:GLU:O	22:LT:115:LYS:HG3	2.21	0.41
43:Lo:93:LEU:HD23	43:Lo:93:LEU:HA	1.94	0.41
46:S2:28:U:H2'	46:S2:29:G:H8	1.84	0.41
46:S2:553:G:H2'	46:S2:554:U:O4'	2.20	0.41
46:S2:751:C:N4	46:S2:794:G:H2'	2.35	0.41
46:S2:1706:C:H2'	46:S2:1707:G:C8	2.55	0.41
48:SA:10:MET:HB3	64:SR:111:PHE:HE2	1.85	0.41
56:SI:144:LYS:HE3	56:SI:144:LYS:HB2	1.65	0.41
57:SJ:34:GLU:HG2	57:SJ:34:GLU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SO:34:PHE:HB3	61:SO:41:PHE:HB2	2.02	0.41
63:SQ:25:CYS:SG	63:SQ:68:ILE:HG12	2.60	0.41
64:SR:74:GLN:HA	64:SR:77:GLU:HG2	2.03	0.41
64:SR:112:GLY:HA2	64:SR:115:SER:HB2	2.01	0.41
71:SY:61:ARG:HE	71:SY:61:ARG:HB3	1.73	0.41
1:L5:432:A:C2	1:L5:3524:A:H4'	2.55	0.41
1:L5:1710:A:H2'	1:L5:1711:A:C8	2.55	0.41
1:L5:2260:G:O2'	1:L5:2262:C:OP1	2.28	0.41
1:L5:3434:G:O2'	1:L5:3472:G:O6	2.33	0.41
1:L5:3913:U:H2'	1:L5:3914:C:C6	2.55	0.41
1:L5:4611:G:C6	1:L5:4612:C:N4	2.88	0.41
16:LN:16:SER:O	16:LN:20:ARG:HB2	2.20	0.41
17:LO:125:LYS:HE3	17:LO:125:LYS:HB3	1.86	0.41
17:LO:187:LYS:HA	17:LO:187:LYS:HD2	1.63	0.41
28:LZ:105:ALA:O	28:LZ:109:LYS:HG3	2.20	0.41
28:LZ:122:TYR:HB2	28:LZ:131:PHE:CE1	2.56	0.41
46:S2:1017:U:H5'	60:SN:15:ALA:O	2.20	0.41
46:S2:1426:G:H4'	63:SQ:33:LYS:CD	2.50	0.41
48:SA:85:ARG:HA	64:SR:81:ARG:HH21	1.85	0.41
51:SD:61:GLU:OE1	51:SD:61:GLU:N	2.53	0.41
53:SF:102:LEU:HD11	72:SZ:100:VAL:HG21	2.03	0.41
55:SH:74:LYS:HD3	55:SH:74:LYS:HA	1.80	0.41
78:Sg:109:LEU:HD21	78:Sg:125:ARG:HE	1.86	0.41
1:L5:1148:A:H2'	1:L5:1149:A:C8	2.56	0.41
1:L5:3718:U:H2'	1:L5:3719:U:H6	1.84	0.41
10:LG:254:GLU:C	10:LG:254:GLU:OE1	2.63	0.41
24:LV:31:ASN:ND2	24:LV:31:ASN:O	2.39	0.41
27:LY:22:PRO:HG2	27:LY:25:ILE:HD12	2.03	0.41
46:S2:834:C:N4	46:S2:841:C:H41	2.18	0.41
46:S2:902:G:H2'	46:S2:903:G:C5	2.56	0.41
46:S2:1241:A:C6	62:SP:100:LYS:HB2	2.56	0.41
48:SA:58:LEU:HD12	48:SA:161:ILE:HD13	2.03	0.41
59:SL:37:TYR:CE2	59:SL:51:ILE:HD12	2.56	0.41
62:SP:22:LEU:O	62:SP:26:LEU:HG	2.20	0.41
66:ST:24:LYS:HD2	66:ST:24:LYS:HA	1.76	0.41
1:L5:1:C:H4'	1:L5:2:G:OP1	2.21	0.41
1:L5:189:G:C4	1:L5:253:G:N2	2.88	0.41
1:L5:486:C:O2'	1:L5:487:C:P	2.79	0.41
1:L5:1901:G:H2'	1:L5:1902:A:C8	2.56	0.41
1:L5:2222:C:H2'	1:L5:2223:G:O4'	2.21	0.41
1:L5:2355:A:N6	1:L5:2498:A:OP2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB:62:ARG:H	5:LB:68:ASN:ND2	2.19	0.41
16:LN:165:THR:O	16:LN:169:ARG:HG2	2.21	0.41
22:LT:103:ASP:OD1	22:LT:104:SER:N	2.54	0.41
23:LU:101:ARG:HG2	23:LU:103:VAL:HG22	2.03	0.41
25:LW:1:MET:HE3	25:LW:15:PRO:HB3	2.02	0.41
46:S2:92:A:H4'	46:S2:93:U:OP2	2.20	0.41
46:S2:220:U:C4	46:S2:221:U:C5	3.08	0.41
46:S2:483:G:H3'	46:S2:483:G:N3	2.36	0.41
46:S2:1281:G:H2'	46:S2:1282:G:C8	2.56	0.41
46:S2:1525:G:OP2	65:SS:141:ARG:NH1	2.54	0.41
48:SA:147:LEU:HD12	48:SA:147:LEU:HA	1.86	0.41
51:SD:31:GLU:OE1	51:SD:31:GLU:N	2.52	0.41
51:SD:66:ILE:O	51:SD:70:THR:HG22	2.21	0.41
52:SE:111:VAL:O	52:SE:111:VAL:HG23	2.21	0.41
52:SE:211:LYS:HB3	52:SE:211:LYS:HE2	1.81	0.41
55:SH:31:GLU:H	55:SH:31:GLU:HG2	1.71	0.41
56:SI:198:TYR:HD1	56:SI:198:TYR:HA	1.80	0.41
59:SL:5:GLN:HE22	59:SL:11:GLN:H	1.68	0.41
61:SO:35:ALA:CB	61:SO:112:ALA:HB2	2.50	0.41
69:SW:31:SER:HB2	69:SW:34:ILE:HG13	2.01	0.41
71:SY:42:GLU:OE1	71:SY:42:GLU:N	2.53	0.41
72:SZ:56:ASP:HA	72:SZ:59:CYS:SG	2.60	0.41
75:Sc:32:VAL:HG11	75:Sc:56:LEU:HD12	2.02	0.41
1:L5:940:C:H2'	1:L5:941:C:C6	2.54	0.41
1:L5:1558:C:H5''	1:L5:1559:U:C5	2.56	0.41
1:L5:1562:G:N2	1:L5:1576:U:H3	2.12	0.41
1:L5:2205:G:H2'	1:L5:2206:A:C8	2.56	0.41
1:L5:2388:C:H2'	1:L5:2389:U:C6	2.56	0.41
1:L5:3417:A:H4'	1:L5:3418:C:O5'	2.20	0.41
3:L8:94:G:C5	38:Lj:84:PRO:HG3	2.56	0.41
5:LB:224:LYS:HG3	5:LB:340:THR:HG22	2.03	0.41
5:LB:297:LYS:HE3	5:LB:297:LYS:HB3	1.74	0.41
5:LB:364:ASP:OD1	5:LB:364:ASP:N	2.53	0.41
9:LF:175:LEU:HD12	9:LF:175:LEU:HA	1.92	0.41
10:LG:261:LEU:HG	10:LG:265:LEU:HB2	2.03	0.41
17:LO:188:LYS:HE3	17:LO:188:LYS:HB3	1.74	0.41
41:Lm:97:ARG:HB2	41:Lm:120:ASN:O	2.21	0.41
46:S2:537:A:H3'	46:S2:538:C:C5'	2.51	0.41
46:S2:890:U:H2'	46:S2:891:U:H5''	2.03	0.41
46:S2:950:G:H2'	46:S2:951:C:C6	2.56	0.41
46:S2:1218:A:H2'	46:S2:1219:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1426:G:H5''	63:SQ:31:LEU:HD11	2.02	0.41
48:SA:108:PHE:HB2	48:SA:136:GLU:HG2	2.02	0.41
49:SB:86:LEU:HA	49:SB:99:ASN:O	2.21	0.41
51:SD:40:ARG:HH21	67:SU:106:ILE:HG21	1.86	0.41
64:SR:18:GLU:HG2	64:SR:69:ILE:HG23	2.03	0.41
72:SZ:71:ALA:O	72:SZ:75:GLU:HG3	2.21	0.41
78:Sg:142:VAL:HG11	78:Sg:177:TRP:CH2	2.56	0.41
78:Sg:172:LYS:HE3	78:Sg:172:LYS:HB2	1.77	0.41
1:L5:1661:A:H2'	1:L5:1662:C:H6	1.85	0.40
1:L5:3892:A:H2'	1:L5:3893:G:C8	2.56	0.40
6:LC:347:HIS:O	6:LC:351:VAL:HG13	2.20	0.40
14:LL:111:GLN:OE1	14:LL:111:GLN:HA	2.21	0.40
46:S2:47:G:H1	46:S2:479:G:H1	1.69	0.40
46:S2:222:U:H3'	46:S2:223:A:H8	1.86	0.40
46:S2:226:A:O2'	46:S2:227:G:O5'	2.37	0.40
46:S2:339:G:H2'	46:S2:340:A:O4'	2.21	0.40
46:S2:488:U:H4'	46:S2:490:A:C8	2.56	0.40
46:S2:1293:C:N4	46:S2:1309:U:H3	2.19	0.40
46:S2:1755:G:N1	46:S2:1780:G:H1'	2.35	0.40
47:S7:19:G:N2	47:S7:56:C:C2	2.89	0.40
56:SI:142:SER:N	56:SI:145:ILE:HD11	2.36	0.40
78:Sg:38:LYS:HD3	78:Sg:63:SER:C	2.46	0.40
1:L5:747:G:O2'	1:L5:748:G:O5'	2.29	0.40
1:L5:1675:G:O2'	1:L5:3872:A:N3	2.49	0.40
1:L5:2499:A:H2'	1:L5:2500:A:H8	1.84	0.40
1:L5:4423:G:H5''	17:LO:176:ARG:HD3	2.03	0.40
3:L8:80:A:H1'	36:Lh:46:LYS:HE3	2.02	0.40
8:LE:173:LEU:HD11	8:LE:184:THR:HG22	2.04	0.40
34:Lf:83:MET:HB3	34:Lf:83:MET:HE2	1.87	0.40
43:Lo:75:PRO:HD2	43:Lo:76:ASN:H	1.85	0.40
46:S2:96:C:O2'	46:S2:97:U:O5'	2.37	0.40
46:S2:170:A:H2'	46:S2:171:A:H8	1.86	0.40
46:S2:497:C:H2'	46:S2:498:C:N3	2.37	0.40
46:S2:615:C:H4'	46:S2:616:C:H6	1.86	0.40
47:S7:59:A:H2'	47:S7:60:A:H5'	2.03	0.40
48:SA:10:MET:HE1	48:SA:51:LEU:HB3	2.03	0.40
48:SA:57:LYS:HA	48:SA:57:LYS:HD2	1.74	0.40
49:SB:133:TYR:CE1	49:SB:181:LEU:HD12	2.56	0.40
54:SG:64:LYS:HE3	54:SG:82:SER:HB3	2.02	0.40
71:SY:82:ALA:O	71:SY:86:GLU:HB2	2.20	0.40
1:L5:458:C:HO2'	1:L5:459:C:P	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LC:350:ARG:HE	6:LC:350:ARG:HB2	1.72	0.40
7:LD:236:MET:HA	7:LD:239:MET:HG2	2.03	0.40
8:LE:178:SER:O	8:LE:178:SER:OG	2.37	0.40
9:LF:61:LEU:HD23	9:LF:61:LEU:HA	1.87	0.40
33:Le:35:TRP:CZ2	33:Le:56:PRO:HD2	2.56	0.40
44:Lp:45:THR:O	44:Lp:45:THR:HG22	2.20	0.40
46:S2:1355:G:N2	46:S2:1358:A:OP2	2.38	0.40
51:SD:137:VAL:HG22	51:SD:151:LYS:HG2	2.03	0.40
61:SO:97:LEU:CD2	73:Sa:44:ILE:HD11	2.52	0.40
63:SQ:72:VAL:HG21	63:SQ:80:GLN:HG2	2.04	0.40
64:SR:57:LEU:O	64:SR:61:ILE:HG13	2.21	0.40
1:L5:1123:C:H2'	1:L5:1124:C:C6	2.56	0.40
1:L5:1296:G:OP2	1:L5:1296:G:H8	2.04	0.40
1:L5:1378:A:N6	46:S2:1030:G:O2'	2.55	0.40
1:L5:2327:A:H62	1:L5:2515:U:H5	1.68	0.40
7:LD:9:ASN:OD1	7:LD:9:ASN:N	2.55	0.40
7:LD:288:LEU:HD23	7:LD:288:LEU:HA	1.87	0.40
8:LE:185:GLY:O	8:LE:186:PRO:C	2.64	0.40
8:LE:250:ILE:H	8:LE:250:ILE:HG13	1.67	0.40
9:LF:263:ASN:O	9:LF:267:ARG:HG2	2.21	0.40
12:LI:86:HIS:HB3	12:LI:139:ARG:HG2	2.03	0.40
18:LP:54:LYS:HA	18:LP:83:TRP:CD1	2.56	0.40
23:LU:80:LYS:HE2	23:LU:110:TYR:CZ	2.56	0.40
33:Le:4:LEU:O	33:Le:121:ARG:NH1	2.55	0.40
46:S2:66:G:N2	46:S2:68:A:OP1	2.53	0.40
46:S2:494:A:H1'	46:S2:575:A:C8	2.56	0.40
46:S2:799:G:N3	46:S2:799:G:H2'	2.37	0.40
46:S2:819:A:H2'	46:S2:820:G:C8	2.56	0.40
46:S2:941:U:H2'	46:S2:942:C:C6	2.56	0.40
47:S7:65:C:C2'	47:S7:66:C:H5'	2.51	0.40
48:SA:174:MET:HE3	48:SA:174:MET:HB3	1.81	0.40
49:SB:85:LYS:HB3	49:SB:101:HIS:HB3	2.03	0.40
59:SL:5:GLN:NE2	59:SL:5:GLN:HA	2.37	0.40
70:SX:39:ASN:OD1	70:SX:39:ASN:C	2.64	0.40
1:L5:324:U:H2'	1:L5:325:C:C6	2.56	0.40
1:L5:1906:G:H2'	1:L5:1907:G:H8	1.86	0.40
7:LD:259:ARG:HA	7:LD:259:ARG:HD2	1.89	0.40
16:LN:99:GLN:HG3	16:LN:130:PHE:CE1	2.57	0.40
27:LY:117:LYS:HE3	27:LY:117:LYS:HB3	1.81	0.40
33:Le:91:CYS:C	33:Le:93:LYS:H	2.29	0.40
46:S2:226:A:H2	46:S2:298:A:N1	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:544:C:H3'	46:S2:545:G:C8	2.57	0.40
46:S2:583:U:H2'	46:S2:584:A:H8	1.82	0.40
46:S2:1149:A:H4'	46:S2:1150:A:O4'	2.22	0.40
46:S2:1321:G:C2	46:S2:1322:G:N7	2.90	0.40
46:S2:1359:U:H5'	50:SC:114:LYS:HD2	2.03	0.40
46:S2:1375:C:H2'	46:S2:1376:G:O4'	2.21	0.40
46:S2:1408:U:H4'	63:SQ:71:ARG:CZ	2.51	0.40
46:S2:1552:U:OP2	46:S2:1580:A:N6	2.55	0.40
46:S2:1741:C:H2'	46:S2:1742:U:C6	2.56	0.40
59:SL:79:LYS:HB2	59:SL:87:VAL:CG1	2.51	0.40
64:SR:41:ILE:HA	64:SR:42:PRO:HD3	1.94	0.40
66:ST:132:ASP:OD1	66:ST:132:ASP:N	2.55	0.40
70:SX:48:LYS:HD3	70:SX:99:GLU:OE2	2.22	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	
4	LA	246/257 (96%)	228 (93%)	18 (7%)	0	100	100
5	LB	395/403 (98%)	370 (94%)	25 (6%)	0	100	100
6	LC	355/419 (85%)	337 (95%)	18 (5%)	0	100	100
7	LD	291/297 (98%)	268 (92%)	23 (8%)	0	100	100
8	LE	210/296 (71%)	197 (94%)	13 (6%)	0	100	100
9	LF	212/270 (78%)	201 (95%)	11 (5%)	0	100	100
10	LG	225/266 (85%)	217 (96%)	8 (4%)	0	100	100
11	LH	188/192 (98%)	175 (93%)	10 (5%)	3 (2%)	7	18
12	LI	197/214 (92%)	194 (98%)	3 (2%)	0	100	100
13	LJ	165/178 (93%)	159 (96%)	5 (3%)	1 (1%)	21	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	LL	204/211 (97%)	193 (95%)	11 (5%)	0	100	100
15	LM	134/217 (62%)	125 (93%)	9 (7%)	0	100	100
16	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	LO	199/203 (98%)	189 (95%)	10 (5%)	0	100	100
18	LP	152/184 (83%)	148 (97%)	4 (3%)	0	100	100
19	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
20	LR	172/196 (88%)	170 (99%)	2 (1%)	0	100	100
21	LS	173/176 (98%)	168 (97%)	5 (3%)	0	100	100
22	LT	158/160 (99%)	154 (98%)	4 (2%)	0	100	100
23	LU	98/128 (77%)	85 (87%)	13 (13%)	0	100	100
24	LV	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
25	LW	60/157 (38%)	59 (98%)	1 (2%)	0	100	100
26	LX	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
27	LY	130/145 (90%)	130 (100%)	0	0	100	100
28	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
29	La	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
30	Lb	95/160 (59%)	93 (98%)	2 (2%)	0	100	100
31	Lc	92/115 (80%)	91 (99%)	0	1 (1%)	11	26
32	Ld	106/125 (85%)	102 (96%)	4 (4%)	0	100	100
33	Le	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	Lf	107/110 (97%)	103 (96%)	4 (4%)	0	100	100
35	Lg	108/117 (92%)	107 (99%)	1 (1%)	0	100	100
36	Lh	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
37	Li	100/105 (95%)	91 (91%)	9 (9%)	0	100	100
38	Lj	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
39	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	49/128 (38%)	48 (98%)	1 (2%)	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	95 (94%)	5 (5%)	1 (1%)	12	28
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	Lr	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
48	SA	205/295 (70%)	191 (93%)	14 (7%)	0	100	100
49	SB	211/264 (80%)	201 (95%)	10 (5%)	0	100	100
50	SC	213/293 (73%)	206 (97%)	6 (3%)	1 (0%)	24	45
51	SD	207/243 (85%)	195 (94%)	12 (6%)	0	100	100
52	SE	256/263 (97%)	233 (91%)	22 (9%)	1 (0%)	30	51
53	SF	175/204 (86%)	164 (94%)	11 (6%)	0	100	100
54	SG	200/249 (80%)	188 (94%)	12 (6%)	0	100	100
55	SH	176/194 (91%)	161 (92%)	15 (8%)	0	100	100
56	SI	179/208 (86%)	168 (94%)	11 (6%)	0	100	100
57	SJ	130/194 (67%)	119 (92%)	11 (8%)	0	100	100
58	SK	86/165 (52%)	75 (87%)	11 (13%)	0	100	100
59	SL	131/158 (83%)	128 (98%)	3 (2%)	0	100	100
60	SN	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
61	SO	132/151 (87%)	121 (92%)	11 (8%)	0	100	100
62	SP	116/145 (80%)	113 (97%)	3 (3%)	0	100	100
63	SQ	137/146 (94%)	122 (89%)	15 (11%)	0	100	100
64	SR	129/135 (96%)	120 (93%)	9 (7%)	0	100	100
65	SS	138/152 (91%)	127 (92%)	11 (8%)	0	100	100
66	ST	138/145 (95%)	132 (96%)	6 (4%)	0	100	100
67	SU	93/119 (78%)	89 (96%)	4 (4%)	0	100	100
68	SV	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
69	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
70	SX	137/143 (96%)	127 (93%)	9 (7%)	1 (1%)	18	37
71	SY	108/133 (81%)	98 (91%)	10 (9%)	0	100	100
72	SZ	70/125 (56%)	62 (89%)	8 (11%)	0	100	100
73	Sa	97/115 (84%)	89 (92%)	8 (8%)	0	100	100
74	Sb	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
75	Sc	52/69 (75%)	44 (85%)	7 (14%)	1 (2%)	6	15
76	Sd	52/56 (93%)	51 (98%)	1 (2%)	0	100	100
77	Se	44/133 (33%)	39 (89%)	5 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	Sg	270/317 (85%)	229 (85%)	41 (15%)	0	100	100
All	All	10626/12499 (85%)	10031 (94%)	585 (6%)	10 (0%)	49	71

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	LH	13	PRO
31	Lc	99	PRO
70	SX	61	GLN
75	Sc	51	ARG
11	LH	189	GLN
43	Lo	59	LYS
50	SC	172	ASN
11	LH	53	LYS
13	LJ	171	ASP
52	SE	247	THR

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	
4	LA	190/199 (96%)	180 (95%)	10 (5%)	20	43
5	LB	344/348 (99%)	332 (96%)	12 (4%)	32	58
6	LC	301/348 (86%)	294 (98%)	7 (2%)	44	71
7	LD	246/249 (99%)	238 (97%)	8 (3%)	33	60
8	LE	194/256 (76%)	189 (97%)	5 (3%)	40	68
9	LF	185/234 (79%)	181 (98%)	4 (2%)	45	72
10	LG	197/223 (88%)	191 (97%)	6 (3%)	36	63
11	LH	169/171 (99%)	164 (97%)	5 (3%)	36	63
12	LI	170/180 (94%)	163 (96%)	7 (4%)	27	52
13	LJ	141/149 (95%)	136 (96%)	5 (4%)	32	58
14	LL	173/178 (97%)	171 (99%)	2 (1%)	63	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	LM	116/157 (74%)	116 (100%)	0	100	100
16	LN	171/172 (99%)	169 (99%)	2 (1%)	63	82
17	LO	172/173 (99%)	170 (99%)	2 (1%)	63	82
18	LP	135/163 (83%)	129 (96%)	6 (4%)	25	50
19	LQ	164/165 (99%)	159 (97%)	5 (3%)	36	63
20	LR	154/175 (88%)	148 (96%)	6 (4%)	28	54
21	LS	155/156 (99%)	147 (95%)	8 (5%)	21	43
22	LT	140/140 (100%)	137 (98%)	3 (2%)	47	73
23	LU	90/114 (79%)	86 (96%)	4 (4%)	25	50
24	LV	100/107 (94%)	96 (96%)	4 (4%)	28	53
25	LW	54/126 (43%)	52 (96%)	2 (4%)	30	56
26	LX	106/133 (80%)	102 (96%)	4 (4%)	29	55
27	LY	123/135 (91%)	122 (99%)	1 (1%)	73	87
28	LZ	117/118 (99%)	113 (97%)	4 (3%)	32	59
29	La	120/121 (99%)	117 (98%)	3 (2%)	42	69
30	Lb	83/124 (67%)	80 (96%)	3 (4%)	31	57
31	Lc	79/97 (81%)	75 (95%)	4 (5%)	21	44
32	Ld	99/110 (90%)	97 (98%)	2 (2%)	48	74
33	Le	114/121 (94%)	110 (96%)	4 (4%)	32	58
34	Lf	88/89 (99%)	86 (98%)	2 (2%)	44	71
35	Lg	94/100 (94%)	91 (97%)	3 (3%)	34	61
36	Lh	109/110 (99%)	107 (98%)	2 (2%)	51	76
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	82
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	61 (95%)	3 (5%)	23	47
40	Ll	46/47 (98%)	45 (98%)	1 (2%)	45	72
41	Lm	47/116 (40%)	47 (100%)	0	100	100
42	Ln	24/24 (100%)	24 (100%)	0	100	100
43	Lo	91/94 (97%)	89 (98%)	2 (2%)	45	72
44	Lp	74/75 (99%)	72 (97%)	2 (3%)	39	67
45	Lr	108/121 (89%)	105 (97%)	3 (3%)	38	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	SA	173/242 (72%)	163 (94%)	10 (6%)	18	39
49	SB	194/229 (85%)	188 (97%)	6 (3%)	35	62
50	SC	181/224 (81%)	177 (98%)	4 (2%)	45	72
51	SD	173/202 (86%)	166 (96%)	7 (4%)	28	53
52	SE	221/225 (98%)	205 (93%)	16 (7%)	13	29
53	SF	152/170 (89%)	144 (95%)	8 (5%)	20	43
54	SG	178/218 (82%)	174 (98%)	4 (2%)	45	72
55	SH	161/174 (92%)	159 (99%)	2 (1%)	63	82
56	SI	159/180 (88%)	156 (98%)	3 (2%)	50	75
57	SJ	126/168 (75%)	121 (96%)	5 (4%)	28	53
58	SK	81/136 (60%)	80 (99%)	1 (1%)	63	82
59	SL	123/142 (87%)	120 (98%)	3 (2%)	43	70
60	SN	130/131 (99%)	123 (95%)	7 (5%)	20	42
61	SO	104/119 (87%)	101 (97%)	3 (3%)	37	64
62	SP	107/130 (82%)	104 (97%)	3 (3%)	38	65
63	SQ	115/121 (95%)	111 (96%)	4 (4%)	32	58
64	SR	119/121 (98%)	116 (98%)	3 (2%)	42	69
65	SS	122/132 (92%)	114 (93%)	8 (7%)	15	33
66	ST	110/115 (96%)	104 (94%)	6 (6%)	19	41
67	SU	88/107 (82%)	82 (93%)	6 (7%)	14	32
68	SV	65/67 (97%)	63 (97%)	2 (3%)	35	62
69	SW	112/113 (99%)	110 (98%)	2 (2%)	51	76
70	SX	111/115 (96%)	107 (96%)	4 (4%)	31	57
71	SY	93/115 (81%)	89 (96%)	4 (4%)	26	51
72	SZ	64/103 (62%)	56 (88%)	8 (12%)	4	10
73	Sa	86/98 (88%)	84 (98%)	2 (2%)	44	71
74	Sb	75/76 (99%)	69 (92%)	6 (8%)	11	25
75	Sc	48/62 (77%)	46 (96%)	2 (4%)	26	52
76	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	73
77	Se	39/106 (37%)	38 (97%)	1 (3%)	40	68
78	Sg	237/275 (86%)	233 (98%)	4 (2%)	53	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9301/10617 (88%)	8999 (97%)	302 (3%)	35 61

All (302) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	15	VAL
4	LA	42	LYS
4	LA	45	VAL
4	LA	70	LYS
4	LA	82	ILE
4	LA	92	LYS
4	LA	114	CYS
4	LA	154	SER
4	LA	166	VAL
4	LA	246	LEU
5	LB	66	LYS
5	LB	77	THR
5	LB	94	GLU
5	LB	162	ILE
5	LB	194	LEU
5	LB	223	THR
5	LB	258	HIS
5	LB	262	VAL
5	LB	329	ASP
5	LB	333	LEU
5	LB	336	CYS
5	LB	364	ASP
6	LC	42	THR
6	LC	62	THR
6	LC	84	THR
6	LC	189	MET
6	LC	239	LYS
6	LC	287	THR
6	LC	306	ARG
7	LD	7	VAL
7	LD	42	ASN
7	LD	44	TYR
7	LD	93	THR
7	LD	111	ASN
7	LD	115	MET
7	LD	228	LYS
7	LD	261	VAL

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Mol	Chain	Res	Type
8	LE	126	THR
8	LE	129	VAL
8	LE	199	GLN
8	LE	209	VAL
8	LE	250	ILE
9	LF	152	ILE
9	LF	175	LEU
9	LF	242	MET
9	LF	250	VAL
10	LG	100	HIS
10	LG	106	THR
10	LG	140	VAL
10	LG	142	THR
10	LG	168	VAL
10	LG	250	ILE
11	LH	10	VAL
11	LH	54	ARG
11	LH	130	THR
11	LH	137	SER
11	LH	188	GLN
12	LI	43	VAL
12	LI	51	HIS
12	LI	61	SER
12	LI	77	VAL
12	LI	133	GLN
12	LI	183	ASP
12	LI	197	VAL
13	LJ	47	THR
13	LJ	52	LYS
13	LJ	73	THR
13	LJ	132	VAL
13	LJ	150	CYS
14	LL	59	VAL
14	LL	168	VAL
16	LN	104	GLU
16	LN	132	VAL
17	LO	187	LYS
17	LO	202	LEU
18	LP	6	LEU
18	LP	20	SER
18	LP	24	VAL
18	LP	45	THR

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Mol	Chain	Res	Type
18	LP	87	SER
18	LP	100	SER
19	LQ	14	ARG
19	LQ	82	VAL
19	LQ	100	VAL
19	LQ	119	LYS
19	LQ	183	SER
20	LR	12	SER
20	LR	29	THR
20	LR	51	ILE
20	LR	91	GLU
20	LR	152	LYS
20	LR	155	LEU
21	LS	48	VAL
21	LS	66	GLN
21	LS	88	SER
21	LS	90	THR
21	LS	102	THR
21	LS	158	VAL
21	LS	168	THR
21	LS	174	THR
22	LT	29	THR
22	LT	76	VAL
22	LT	111	GLU
23	LU	19	LEU
23	LU	29	VAL
23	LU	96	LEU
23	LU	106	SER
24	LV	22	VAL
24	LV	31	ASN
24	LV	48	ARG
24	LV	72	LEU
25	LW	1	MET
25	LW	53	VAL
26	LX	81	LEU
26	LX	101	ASP
26	LX	143	ASP
26	LX	147	LEU
27	LY	94	THR
28	LZ	11	VAL
28	LZ	39	SER
28	LZ	97	ASN

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Mol	Chain	Res	Type
28	LZ	99	ASP
29	La	56	VAL
29	La	85	GLN
29	La	95	THR
30	Lb	8	THR
30	Lb	54	LEU
30	Lb	116	LEU
31	Lc	16	SER
31	Lc	61	GLU
31	Lc	69	THR
31	Lc	101	ASP
32	Ld	29	ILE
32	Ld	94	GLU
33	Le	13	VAL
33	Le	79	VAL
33	Le	82	VAL
33	Le	126	ASN
34	Lf	25	THR
34	Lf	57	THR
35	Lg	17	SER
35	Lg	20	THR
35	Lg	46	CYS
36	Lh	81	LEU
36	Lh	109	ARG
37	Li	81	ILE
39	Lk	23	VAL
39	Lk	59	SER
39	Lk	67	LYS
40	Ll	27	ILE
43	Lo	33	LEU
43	Lo	73	VAL
44	Lp	26	VAL
44	Lp	52	VAL
45	Lr	60	VAL
45	Lr	78	VAL
45	Lr	115	SER
48	SA	10	MET
48	SA	28	THR
48	SA	66	VAL
48	SA	94	THR
48	SA	112	ILE
48	SA	131	HIS

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Mol	Chain	Res	Type
48	SA	138	SER
48	SA	164	ASN
48	SA	170	SER
48	SA	197	VAL
49	SB	21	VAL
49	SB	32	ASP
49	SB	91	VAL
49	SB	154	SER
49	SB	169	MET
49	SB	203	SER
50	SC	75	ILE
50	SC	137	VAL
50	SC	254	ASP
50	SC	260	VAL
51	SD	14	ASP
51	SD	17	PHE
51	SD	32	ASP
51	SD	41	VAL
51	SD	50	ILE
51	SD	70	THR
51	SD	208	VAL
52	SE	18	TRP
52	SE	73	ASP
52	SE	76	VAL
52	SE	90	ILE
52	SE	115	THR
52	SE	117	GLU
52	SE	126	VAL
52	SE	153	LEU
52	SE	161	GLN
52	SE	162	ILE
52	SE	164	LEU
52	SE	182	MET
52	SE	210	VAL
52	SE	223	SER
52	SE	236	ILE
52	SE	248	ILE
53	SF	24	SER
53	SF	52	SER
53	SF	68	ILE
53	SF	75	SER
53	SF	82	ASN

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Mol	Chain	Res	Type
53	SF	100	ILE
53	SF	103	LEU
53	SF	147	VAL
54	SG	21	GLU
54	SG	116	LYS
54	SG	119	LYS
54	SG	153	VAL
55	SH	30	LEU
55	SH	64	VAL
56	SI	107	THR
56	SI	161	LEU
56	SI	175	ILE
57	SJ	15	THR
57	SJ	46	VAL
57	SJ	49	THR
57	SJ	84	ILE
57	SJ	114	VAL
58	SK	20	VAL
59	SL	33	LEU
59	SL	135	SER
59	SL	146	THR
60	SN	35	GLU
60	SN	45	LEU
60	SN	46	THR
60	SN	48	SER
60	SN	69	ASN
60	SN	78	LYS
60	SN	87	ASP
61	SO	50	LYS
61	SO	113	GLN
61	SO	122	SER
62	SP	71	GLU
62	SP	92	SER
62	SP	96	VAL
63	SQ	66	VAL
63	SQ	70	VAL
63	SQ	93	VAL
63	SQ	113	ILE
64	SR	58	MET
64	SR	107	LYS
64	SR	130	THR
65	SS	4	VAL

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Mol	Chain	Res	Type
65	SS	15	VAL
65	SS	18	THR
65	SS	34	LYS
65	SS	43	VAL
65	SS	59	LEU
65	SS	69	THR
65	SS	98	VAL
66	ST	39	LEU
66	ST	44	GLU
66	ST	90	SER
66	ST	107	LEU
66	ST	113	VAL
66	ST	131	LEU
67	SU	21	ARG
67	SU	23	THR
67	SU	63	ILE
67	SU	81	GLN
67	SU	97	ILE
67	SU	115	THR
68	SV	32	ILE
68	SV	50	PHE
69	SW	51	GLU
69	SW	103	VAL
70	SX	24	ASP
70	SX	51	VAL
70	SX	57	VAL
70	SX	90	CYS
71	SY	27	VAL
71	SY	54	VAL
71	SY	78	SER
71	SY	102	THR
72	SZ	65	TYR
72	SZ	68	ILE
72	SZ	69	THR
72	SZ	72	VAL
72	SZ	78	LYS
72	SZ	92	LEU
72	SZ	97	ILE
72	SZ	106	GLN
73	Sa	71	LEU
73	Sa	96	THR
74	Sb	7	LEU

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Mol	Chain	Res	Type
74	Sb	27	SER
74	Sb	44	THR
74	Sb	61	THR
74	Sb	74	THR
74	Sb	78	SER
75	Sc	6	VAL
75	Sc	38	THR
76	Sd	27	ARG
77	Se	117	VAL
78	Sg	59	LEU
78	Sg	111	VAL
78	Sg	113	PHE
78	Sg	120	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (87) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	86	GLN
4	LA	205	ASN
5	LB	123	HIS
5	LB	175	GLN
5	LB	184	GLN
5	LB	203	GLN
5	LB	328	ASN
6	LC	112	HIS
6	LC	198	ASN
7	LD	39	GLN
7	LD	122	GLN
7	LD	267	ASN
9	LF	121	ASN
9	LF	228	ASN
10	LG	206	GLN
12	LI	51	HIS
12	LI	147	HIS
13	LJ	110	GLN
14	LL	115	GLN
15	LM	20	HIS
15	LM	48	GLN
16	LN	29	GLN
16	LN	91	GLN
17	LO	42	ASN
17	LO	63	ASN

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Mol	Chain	Res	Type
18	LP	97	ASN
20	LR	30	ASN
20	LR	66	ASN
20	LR	86	ASN
21	LS	91	HIS
22	LT	66	ASN
22	LT	131	GLN
24	LV	31	ASN
25	LW	50	ASN
27	LY	20	ASN
27	LY	65	GLN
29	La	25	HIS
29	La	60	HIS
30	Lb	19	ASN
30	Lb	58	GLN
31	Lc	33	GLN
32	Ld	118	GLN
33	Le	23	HIS
34	Lf	21	GLN
40	Ll	33	ASN
41	Lm	109	ASN
42	Ln	22	GLN
45	Lr	4	HIS
45	Lr	36	ASN
48	SA	9	GLN
48	SA	165	ASN
49	SB	179	ASN
49	SB	186	ASN
50	SC	115	GLN
51	SD	74	GLN
52	SE	50	ASN
52	SE	188	ASN
52	SE	214	ASN
52	SE	216	ASN
52	SE	224	ASN
53	SF	83	ASN
53	SF	118	ASN
53	SF	149	GLN
54	SG	4	ASN
54	SG	81	HIS
55	SH	39	GLN
55	SH	163	GLN

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Mol	Chain	Res	Type
56	SI	87	ASN
56	SI	167	GLN
57	SJ	124	HIS
57	SJ	132	GLN
58	SK	32	HIS
60	SN	5	HIS
60	SN	105	ASN
61	SO	26	ASN
65	SS	73	ASN
65	SS	135	HIS
66	ST	42	HIS
67	SU	81	GLN
68	SV	33	GLN
69	SW	90	GLN
69	SW	113	HIS
70	SX	110	HIS
70	SX	127	ASN
73	Sa	25	ASN
77	Se	89	GLN
77	Se	111	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3378/4731 (71%)	767 (22%)	29 (0%)
2	L7	119/120 (99%)	13 (10%)	2 (1%)
3	L8	149/158 (94%)	30 (20%)	1 (0%)
46	S2	1618/1870 (86%)	495 (30%)	26 (1%)
47	S6	74/75 (98%)	26 (35%)	2 (2%)
47	S7	74/75 (98%)	40 (54%)	2 (2%)
79	Sx	9/10 (90%)	1 (11%)	0
All	All	5421/7039 (77%)	1372 (25%)	62 (1%)

All (1372) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	15	A
1	L5	21	G
1	L5	25	A

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Mol	Chain	Res	Type
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	71	C
1	L5	76	A
1	L5	85	G
1	L5	91	G
1	L5	104	G
1	L5	108	A
1	L5	109	G
1	L5	110	C
1	L5	119	G
1	L5	120	A
1	L5	129	C
1	L5	131	C
1	L5	132	G
1	L5	133	C
1	L5	134	G
1	L5	135	U
1	L5	136	C
1	L5	137	G
1	L5	138	C
1	L5	139	G
1	L5	141	C
1	L5	142	G
1	L5	143	U
1	L5	144	G
1	L5	159	C
1	L5	160	G
1	L5	166	C
1	L5	169	A
1	L5	170	C
1	L5	171	U
1	L5	172	C
1	L5	173	C
1	L5	195	C
1	L5	197	A

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Mol	Chain	Res	Type
1	L5	200	U
1	L5	201	C
1	L5	217	C
1	L5	218	A
1	L5	219	G
1	L5	220	C
1	L5	228	C
1	L5	232	G
1	L5	233	U
1	L5	234	G
1	L5	235	A
1	L5	236	G
1	L5	241	G
1	L5	249	C
1	L5	252	G
1	L5	256	C
1	L5	258	C
1	L5	259	C
1	L5	260	G
1	L5	262	G
1	L5	264	U
1	L5	265	C
1	L5	266	G
1	L5	267	G
1	L5	269	U
1	L5	277	G
1	L5	279	G
1	L5	296	U
1	L5	305	A
1	L5	315	U
1	L5	325	C
1	L5	333	A
1	L5	339	C
1	L5	347	G
1	L5	349	C
1	L5	360	C
1	L5	372	G
1	L5	386	G
1	L5	387	A
1	L5	398	G
1	L5	408	G
1	L5	409	A

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Mol	Chain	Res	Type
1	L5	411	G
1	L5	413	C
1	L5	414	G
1	L5	415	U
1	L5	416	G
1	L5	430	G
1	L5	431	U
1	L5	439	U
1	L5	448	C
1	L5	449	G
1	L5	452	G
1	L5	454	C
1	L5	455	C
1	L5	456	G
1	L5	457	C
1	L5	458	C
1	L5	459	C
1	L5	466	U
1	L5	467	U
1	L5	468	C
1	L5	480	G
1	L5	481	G
1	L5	487	C
1	L5	488	G
1	L5	489	G
1	L5	491	C
1	L5	495	C
1	L5	497	C
1	L5	512	A
1	L5	513	U
1	L5	654	G
1	L5	661	U
1	L5	667	G
1	L5	668	G
1	L5	669	C
1	L5	671	G
1	L5	673	C
1	L5	674	G
1	L5	675	A
1	L5	676	C
1	L5	677	C
1	L5	678	G

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Mol	Chain	Res	Type
1	L5	691	C
1	L5	692	G
1	L5	693	C
1	L5	695	C
1	L5	696	U
1	L5	697	U
1	L5	701	C
1	L5	703	G
1	L5	704	U
1	L5	705	G
1	L5	712	C
1	L5	714	C
1	L5	722	G
1	L5	738	G
1	L5	739	G
1	L5	741	A
1	L5	746	C
1	L5	747	G
1	L5	748	G
1	L5	749	U
1	L5	750	G
1	L5	754	A
1	L5	757	G
1	L5	761	C
1	L5	763	C
1	L5	766	G
1	L5	806	C
1	L5	807	C
1	L5	810	G
1	L5	813	U
1	L5	814	U
1	L5	815	A
1	L5	817	A
1	L5	820	C
1	L5	824	C
1	L5	830	C
1	L5	831	G
1	L5	833	U
1	L5	834	U
1	L5	835	U
1	L5	842	A
1	L5	843	U

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Mol	Chain	Res	Type
1	L5	844	C
1	L5	854	A
1	L5	857	A
1	L5	858	A
1	L5	860	C
1	L5	872	C
1	L5	873	G
1	L5	882	U
1	L5	886	U
1	L5	887	C
1	L5	924	G
1	L5	926	G
1	L5	927	C
1	L5	928	C
1	L5	936	C
1	L5	938	C
1	L5	940	C
1	L5	953	C
1	L5	954	G
1	L5	1003	G
1	L5	1005	C
1	L5	1006	G
1	L5	1007	G
1	L5	1008	A
1	L5	1009	C
1	L5	1011	G
1	L5	1012	U
1	L5	1013	C
1	L5	1014	C
1	L5	1015	C
1	L5	1016	C
1	L5	1017	A
1	L5	1019	U
1	L5	1021	C
1	L5	1022	G
1	L5	1026	C
1	L5	1027	G
1	L5	1028	G
1	L5	1029	G
1	L5	1031	G
1	L5	1032	U
1	L5	1033	G

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Mol	Chain	Res	Type
1	L5	1034	G
1	L5	1036	C
1	L5	1037	G
1	L5	1038	C
1	L5	1039	G
1	L5	1044	C
1	L5	1045	G
1	L5	1048	U
1	L5	1049	C
1	L5	1050	C
1	L5	1051	G
1	L5	1052	G
1	L5	1053	G
1	L5	1054	G
1	L5	1055	G
1	L5	1065	G
1	L5	1095	C
1	L5	1096	G
1	L5	1099	G
1	L5	1102	G
1	L5	1108	G
1	L5	1111	G
1	L5	1116	C
1	L5	1117	U
1	L5	1139	A
1	L5	1141	A
1	L5	1152	A
1	L5	1154	U
1	L5	1160	G
1	L5	1169	A
1	L5	1173	A
1	L5	1174	G
1	L5	1180	C
1	L5	1193	C
1	L5	1194	C
1	L5	1195	G
1	L5	1200	G
1	L5	1202	A
1	L5	1209	G
1	L5	1212	A
1	L5	1221	G
1	L5	1223	C

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Mol	Chain	Res	Type
1	L5	1224	C
1	L5	1225	G
1	L5	1226	G
1	L5	1227	G
1	L5	1228	G
1	L5	1229	G
1	L5	1230	C
1	L5	1232	C
1	L5	1234	A
1	L5	1239	G
1	L5	1242	U
1	L5	1256	C
1	L5	1261	C
1	L5	1263	C
1	L5	1266	A
1	L5	1272	C
1	L5	1290	C
1	L5	1295	C
1	L5	1296	G
1	L5	1297	C
1	L5	1298	G
1	L5	1299	C
1	L5	1311	A
1	L5	1312	G
1	L5	1316	G
1	L5	1317	A
1	L5	1326	G
1	L5	1328	U
1	L5	1329	A
1	L5	1344	G
1	L5	1348	A
1	L5	1351	A
1	L5	1352	U
1	L5	1361	A
1	L5	1380	C
1	L5	1389	A
1	L5	1392	U
1	L5	1400	G
1	L5	1405	U
1	L5	1410	U
1	L5	1427	A
1	L5	1428	C

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Mol	Chain	Res	Type
1	L5	1438	G
1	L5	1439	G
1	L5	1445	A
1	L5	1447	G
1	L5	1448	A
1	L5	1452	A
1	L5	1454	C
1	L5	1455	G
1	L5	1456	A
1	L5	1465	G
1	L5	1468	G
1	L5	1475	C
1	L5	1484	G
1	L5	1490	C
1	L5	1491	U
1	L5	1508	C
1	L5	1511	G
1	L5	1524	G
1	L5	1537	G
1	L5	1538	U
1	L5	1553	G
1	L5	1557	U
1	L5	1559	U
1	L5	1560	U
1	L5	1561	G
1	L5	1562	G
1	L5	1563	G
1	L5	1564	G
1	L5	1575	C
1	L5	1578	A
1	L5	1586	C
1	L5	1590	A
1	L5	1607	A
1	L5	1609	G
1	L5	1615	C
1	L5	1620	U
1	L5	1624	G
1	L5	1625	U
1	L5	1632	G
1	L5	1639	G
1	L5	1640	A
1	L5	1645	G

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Mol	Chain	Res	Type
1	L5	1658	G
1	L5	1670	A
1	L5	1672	G
1	L5	1673	C
1	L5	1681	G
1	L5	1685	U
1	L5	1692	U
1	L5	1695	A
1	L5	1696	C
1	L5	1700	A
1	L5	1713	G
1	L5	1715	G
1	L5	1721	U
1	L5	1722	G
1	L5	1723	C
1	L5	1724	C
1	L5	1725	G
1	L5	1728	G
1	L5	1733	U
1	L5	1734	C
1	L5	1735	A
1	L5	1739	C
1	L5	1743	G
1	L5	1751	G
1	L5	1754	G
1	L5	1762	U
1	L5	1763	A
1	L5	1764	G
1	L5	1765	A
1	L5	1766	C
1	L5	1767	A
1	L5	1768	G
1	L5	1831	C
1	L5	1832	A
1	L5	1847	U
1	L5	1851	U
1	L5	1858	G
1	L5	1859	G
1	L5	1872	A
1	L5	1874	A
1	L5	1878	G
1	L5	1887	C

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Mol	Chain	Res	Type
1	L5	1892	G
1	L5	1903	A
1	L5	1904	C
1	L5	1905	G
1	L5	1907	G
1	L5	1908	A
1	L5	1909	C
1	L5	1910	G
1	L5	2016	G
1	L5	2028	C
1	L5	2046	C
1	L5	2057	A
1	L5	2058	G
1	L5	2063	G
1	L5	2070	A
1	L5	2089	A
1	L5	2090	G
1	L5	2105	G
1	L5	2107	U
1	L5	2108	C
1	L5	2117	A
1	L5	2121	G
1	L5	2141	U
1	L5	2152	A
1	L5	2153	A
1	L5	2154	G
1	L5	2166	U
1	L5	2178	G
1	L5	2179	C
1	L5	2180	A
1	L5	2182	U
1	L5	2183	U
1	L5	2194	C
1	L5	2204	U
1	L5	2207	G
1	L5	2210	A
1	L5	2221	C
1	L5	2222	C
1	L5	2226	C
1	L5	2227	C
1	L5	2228	G
1	L5	2230	A

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Mol	Chain	Res	Type
1	L5	2231	G
1	L5	2232	G
1	L5	2235	C
1	L5	2236	G
1	L5	2237	G
1	L5	2238	G
1	L5	2242	U
1	L5	2243	G
1	L5	2254	C
1	L5	2255	C
1	L5	2260	G
1	L5	2261	C
1	L5	2262	C
1	L5	2263	G
1	L5	2264	A
1	L5	2269	A
1	L5	2270	A
1	L5	2271	G
1	L5	2274	A
1	L5	2285	G
1	L5	2300	A
1	L5	2301	G
1	L5	2302	U
1	L5	2303	G
1	L5	2304	G
1	L5	2311	U
1	L5	2312	G
1	L5	2315	C
1	L5	2324	G
1	L5	2337	C
1	L5	2341	A
1	L5	2343	C
1	L5	2346	U
1	L5	2350	G
1	L5	2355	A
1	L5	2356	G
1	L5	2392	G
1	L5	2400	C
1	L5	2406	G
1	L5	2407	C
1	L5	2414	A
1	L5	2415	U

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Mol	Chain	Res	Type
1	L5	2416	G
1	L5	2423	C
1	L5	2429	G
1	L5	2435	G
1	L5	2441	U
1	L5	2448	G
1	L5	2449	A
1	L5	2450	A
1	L5	2451	A
1	L5	2457	G
1	L5	2459	G
1	L5	2460	G
1	L5	2461	U
1	L5	2462	U
1	L5	2463	C
1	L5	2464	C
1	L5	2465	G
1	L5	2466	G
1	L5	2480	G
1	L5	2493	C
1	L5	2497	A
1	L5	2513	G
1	L5	2514	G
1	L5	2515	U
1	L5	2516	G
1	L5	2517	U
1	L5	2518	A
1	L5	2519	A
1	L5	2520	A
1	L5	2524	C
1	L5	2527	G
1	L5	2532	G
1	L5	2541	A
1	L5	2542	U
1	L5	2544	U
1	L5	2552	A
1	L5	2568	C
1	L5	2569	A
1	L5	2576	G
1	L5	2580	U
1	L5	2581	G
1	L5	2582	U

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Mol	Chain	Res	Type
1	L5	2587	A
1	L5	2609	G
1	L5	2646	C
1	L5	2650	G
1	L5	2651	G
1	L5	2653	C
1	L5	2657	G
1	L5	3263	U
1	L5	3272	G
1	L5	3273	U
1	L5	3275	C
1	L5	3283	G
1	L5	3292	A
1	L5	3319	A
1	L5	3321	G
1	L5	3330	C
1	L5	3367	G
1	L5	3368	A
1	L5	3375	A
1	L5	3407	G
1	L5	3418	C
1	L5	3431	A
1	L5	3434	G
1	L5	3441	A
1	L5	3443	U
1	L5	3446	C
1	L5	3449	G
1	L5	3459	U
1	L5	3468	G
1	L5	3469	C
1	L5	3471	U
1	L5	3474	A
1	L5	3475	U
1	L5	3476	G
1	L5	3495	U
1	L5	3496	G
1	L5	3497	U
1	L5	3524	A
1	L5	3534	A
1	L5	3535	C
1	L5	3536	G
1	L5	3544	C

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Mol	Chain	Res	Type
1	L5	3549	U
1	L5	3553	C
1	L5	3554	G
1	L5	3558	A
1	L5	3563	A
1	L5	3564	G
1	L5	3565	A
1	L5	3572	U
1	L5	3589	U
1	L5	3595	G
1	L5	3596	G
1	L5	3598	G
1	L5	3601	G
1	L5	3602	A
1	L5	3603	G
1	L5	3604	A
1	L5	3605	C
1	L5	3606	A
1	L5	3608	G
1	L5	3713	A
1	L5	3714	U
1	L5	3715	C
1	L5	3716	G
1	L5	3727	G
1	L5	3735	G
1	L5	3744	G
1	L5	3745	G
1	L5	3747	C
1	L5	3748	G
1	L5	3768	U
1	L5	3770	C
1	L5	3773	G
1	L5	3778	A
1	L5	3780	G
1	L5	3783	U
1	L5	3786	G
1	L5	3787	U
1	L5	3788	C
1	L5	3789	C
1	L5	3801	G
1	L5	3803	G
1	L5	3805	G

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Mol	Chain	Res	Type
1	L5	3815	C
1	L5	3816	U
1	L5	3823	A
1	L5	3836	G
1	L5	3837	G
1	L5	3844	G
1	L5	3849	G
1	L5	3856	A
1	L5	3858	A
1	L5	3878	G
1	L5	3881	G
1	L5	3882	U
1	L5	3885	U
1	L5	3886	A
1	L5	3903	G
1	L5	3904	A
1	L5	3905	C
1	L5	3907	G
1	L5	3909	A
1	L5	3910	A
1	L5	3911	C
1	L5	3921	A
1	L5	3924	A
1	L5	3926	A
1	L5	3933	A
1	L5	3934	A
1	L5	3944	G
1	L5	3945	A
1	L5	3958	G
1	L5	3959	U
1	L5	3967	C
1	L5	3977	A
1	L5	3983	G
1	L5	3985	C
1	L5	3992	A
1	L5	4020	G
1	L5	4021	G
1	L5	4026	G
1	L5	4029	A
1	L5	4030	G
1	L5	4031	A
1	L5	4040	C

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Mol	Chain	Res	Type
1	L5	4047	A
1	L5	4064	G
1	L5	4068	A
1	L5	4073	U
1	L5	4074	C
1	L5	4075	A
1	L5	4086	G
1	L5	4088	U
1	L5	4089	U
1	L5	4101	G
1	L5	4103	U
1	L5	4106	C
1	L5	4117	A
1	L5	4124	U
1	L5	4128	G
1	L5	4146	U
1	L5	4155	C
1	L5	4165	U
1	L5	4166	A
1	L5	4171	A
1	L5	4172	C
1	L5	4177	G
1	L5	4181	G
1	L5	4198	G
1	L5	4201	A
1	L5	4207	G
1	L5	4208	U
1	L5	4213	C
1	L5	4220	G
1	L5	4223	G
1	L5	4228	G
1	L5	4237	A
1	L5	4242	A
1	L5	4243	A
1	L5	4253	G
1	L5	4259	G
1	L5	4263	A
1	L5	4287	U
1	L5	4289	U
1	L5	4290	G
1	L5	4301	A
1	L5	4309	A

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Mol	Chain	Res	Type
1	L5	4310	U
1	L5	4323	C
1	L5	4325	A
1	L5	4326	U
1	L5	4353	A
1	L5	4355	G
1	L5	4360	A
1	L5	4361	A
1	L5	4362	U
1	L5	4372	G
1	L5	4373	C
1	L5	4381	U
1	L5	4383	C
1	L5	4384	G
1	L5	4386	C
1	L5	4387	A
1	L5	4393	G
1	L5	4394	A
1	L5	4395	A
1	L5	4396	G
1	L5	4397	G
1	L5	4399	G
1	L5	4404	G
1	L5	4408	G
1	L5	4411	C
1	L5	4413	C
1	L5	4415	G
1	L5	4419	G
1	L5	4425	U
1	L5	4428	C
1	L5	4507	G
1	L5	4516	G
1	L5	4517	C
1	L5	4523	G
1	L5	4526	G
1	L5	4528	U
1	L5	4529	C
1	L5	4532	C
1	L5	4546	U
1	L5	4550	G
1	L5	4552	C
1	L5	4553	G

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Mol	Chain	Res	Type
1	L5	4554	G
1	L5	4555	A
1	L5	4558	G
1	L5	4559	G
1	L5	4560	C
1	L5	4561	G
1	L5	4563	C
1	L5	4564	C
1	L5	4565	G
1	L5	4566	C
1	L5	4567	C
1	L5	4568	C
1	L5	4571	U
1	L5	4580	A
1	L5	4583	U
1	L5	4584	U
1	L5	4585	G
1	L5	4588	C
1	L5	4589	G
1	L5	4591	A
1	L5	4597	G
1	L5	4599	G
1	L5	4604	A
1	L5	4608	G
1	L5	4613	U
1	L5	4621	U
1	L5	4624	U
1	L5	4636	U
1	L5	4638	C
1	L5	4639	U
1	L5	4654	U
1	L5	4662	A
1	L5	4664	A
1	L5	4665	G
1	L5	4668	G
1	L5	4669	C
1	L5	4676	G
1	L5	4677	C
1	L5	4678	U
1	L5	4682	A
1	L5	4687	U
1	L5	4689	G

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Mol	Chain	Res	Type
1	L5	4698	C
1	L5	4702	C
1	L5	4706	A
1	L5	4709	A
1	L5	4710	G
1	L5	4717	U
2	L7	4	U
2	L7	22	A
2	L7	24	C
2	L7	30	C
2	L7	33	U
2	L7	53	U
2	L7	56	G
2	L7	61	G
2	L7	64	G
2	L7	100	A
2	L7	103	A
2	L7	110	G
2	L7	120	U
3	L8	2	G
3	L8	6	C
3	L8	7	U
3	L8	23	C
3	L8	34	U
3	L8	35	C
3	L8	51	U
3	L8	52	A
3	L8	57	C
3	L8	59	A
3	L8	60	G
3	L8	62	A
3	L8	63	U
3	L8	71	A
3	L8	72	A
3	L8	75	G
3	L8	80	A
3	L8	87	G
3	L8	94	G
3	L8	103	A
3	L8	105	C
3	L8	109	C
3	L8	110	U

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Mol	Chain	Res	Type
3	L8	111	U
3	L8	114	G
3	L8	121	G
3	L8	125	C
3	L8	126	C
3	L8	150	C
3	L8	151	G
46	S2	2	A
46	S2	4	C
46	S2	5	U
46	S2	17	C
46	S2	33	G
46	S2	35	C
46	S2	40	A
46	S2	41	G
46	S2	43	U
46	S2	44	U
46	S2	46	A
46	S2	49	C
46	S2	50	A
46	S2	51	U
46	S2	52	G
46	S2	54	A
46	S2	56	G
46	S2	57	U
46	S2	59	U
46	S2	60	A
46	S2	61	A
46	S2	62	G
46	S2	63	U
46	S2	65	C
46	S2	67	C
46	S2	68	A
46	S2	72	C
46	S2	73	C
46	S2	74	G
46	S2	76	U
46	S2	78	C
46	S2	79	A
46	S2	80	G
46	S2	82	G
46	S2	83	A

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Mol	Chain	Res	Type
46	S2	86	C
46	S2	87	U
46	S2	88	G
46	S2	90	G
46	S2	91	A
46	S2	92	A
46	S2	94	G
46	S2	95	G
46	S2	96	C
46	S2	97	U
46	S2	98	C
46	S2	99	A
46	S2	100	U
46	S2	103	A
46	S2	113	G
46	S2	115	U
46	S2	116	U
46	S2	117	C
46	S2	120	U
46	S2	122	G
46	S2	126	G
46	S2	127	C
46	S2	129	C
46	S2	142	C
46	S2	143	U
46	S2	145	G
46	S2	149	A
46	S2	151	C
46	S2	152	U
46	S2	155	G
46	S2	156	G
46	S2	158	A
46	S2	161	U
46	S2	162	C
46	S2	163	U
46	S2	165	G
46	S2	166	A
46	S2	167	G
46	S2	168	C
46	S2	169	U
46	S2	171	A
46	S2	173	A

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Mol	Chain	Res	Type
46	S2	177	G
46	S2	179	C
46	S2	181	A
46	S2	182	C
46	S2	220	U
46	S2	222	U
46	S2	225	C
46	S2	226	A
46	S2	291	U
46	S2	293	A
46	S2	294	C
46	S2	299	G
46	S2	302	A
46	S2	303	A
46	S2	311	C
46	S2	313	G
46	S2	314	A
46	S2	315	U
46	S2	319	A
46	S2	320	C
46	S2	338	C
46	S2	341	C
46	S2	342	C
46	S2	343	C
46	S2	344	A
46	S2	346	U
46	S2	348	G
46	S2	352	G
46	S2	363	C
46	S2	364	A
46	S2	365	A
46	S2	370	C
46	S2	371	G
46	S2	377	A
46	S2	378	G
46	S2	385	U
46	S2	386	G
46	S2	387	C
46	S2	408	G
46	S2	409	A
46	S2	410	C
46	S2	415	A

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Mol	Chain	Res	Type
46	S2	445	G
46	S2	447	G
46	S2	448	A
46	S2	449	A
46	S2	451	C
46	S2	453	G
46	S2	455	U
46	S2	464	C
46	S2	465	A
46	S2	466	A
46	S2	468	G
46	S2	469	A
46	S2	472	G
46	S2	473	C
46	S2	474	A
46	S2	475	G
46	S2	476	C
46	S2	477	A
46	S2	478	G
46	S2	479	G
46	S2	482	C
46	S2	483	G
46	S2	484	C
46	S2	485	A
46	S2	486	A
46	S2	488	U
46	S2	489	U
46	S2	490	A
46	S2	494	A
46	S2	495	C
46	S2	496	U
46	S2	497	C
46	S2	498	C
46	S2	499	C
46	S2	502	C
46	S2	503	C
46	S2	504	C
46	S2	507	G
46	S2	508	G
46	S2	509	A
46	S2	510	G
46	S2	511	G

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Mol	Chain	Res	Type
46	S2	512	U
46	S2	513	A
46	S2	515	U
46	S2	517	A
46	S2	526	A
46	S2	528	C
46	S2	530	A
46	S2	531	U
46	S2	533	C
46	S2	534	A
46	S2	535	G
46	S2	537	A
46	S2	538	C
46	S2	539	U
46	S2	540	C
46	S2	541	U
46	S2	543	U
46	S2	544	C
46	S2	545	G
46	S2	546	A
46	S2	547	G
46	S2	548	G
46	S2	552	U
46	S2	557	U
46	S2	559	G
46	S2	560	G
46	S2	561	A
46	S2	562	A
46	S2	563	U
46	S2	564	G
46	S2	565	A
46	S2	566	G
46	S2	567	U
46	S2	568	C
46	S2	570	A
46	S2	577	A
46	S2	578	U
46	S2	584	A
46	S2	585	A
46	S2	587	G
46	S2	590	G
46	S2	591	A

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Mol	Chain	Res	Type
46	S2	592	U
46	S2	593	C
46	S2	594	C
46	S2	595	A
46	S2	600	A
46	S2	607	G
46	S2	608	U
46	S2	609	C
46	S2	615	C
46	S2	629	A
46	S2	630	A
46	S2	632	U
46	S2	644	A
46	S2	645	G
46	S2	656	A
46	S2	660	G
46	S2	661	C
46	S2	665	A
46	S2	669	A
46	S2	670	A
46	S2	672	A
46	S2	673	A
46	S2	674	G
46	S2	684	G
46	S2	689	U
46	S2	749	C
46	S2	750	U
46	S2	751	C
46	S2	795	A
46	S2	798	C
46	S2	799	G
46	S2	800	U
46	S2	812	A
46	S2	820	G
46	S2	821	U
46	S2	822	G
46	S2	823	U
46	S2	827	A
46	S2	828	A
46	S2	829	G
46	S2	830	C
46	S2	831	A

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Mol	Chain	Res	Type
46	S2	832	G
46	S2	835	C
46	S2	837	G
46	S2	838	A
46	S2	839	G
46	S2	840	C
46	S2	841	C
46	S2	842	G
46	S2	843	C
46	S2	845	U
46	S2	847	G
46	S2	848	A
46	S2	854	C
46	S2	863	A
46	S2	870	A
46	S2	871	A
46	S2	872	U
46	S2	874	G
46	S2	875	G
46	S2	876	A
46	S2	884	U
46	S2	885	C
46	S2	886	U
46	S2	887	A
46	S2	890	U
46	S2	891	U
46	S2	892	G
46	S2	893	U
46	S2	894	U
46	S2	895	G
46	S2	896	G
46	S2	897	U
46	S2	898	U
46	S2	899	U
46	S2	900	U
46	S2	901	C
46	S2	902	G
46	S2	903	G
46	S2	905	A
46	S2	910	G
46	S2	914	A
46	S2	918	U

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Mol	Chain	Res	Type
46	S2	920	A
46	S2	921	A
46	S2	931	C
46	S2	934	G
46	S2	944	U
46	S2	972	G
46	S2	991	A
46	S2	993	A
46	S2	1000	G
46	S2	1002	A
46	S2	1018	U
46	S2	1019	U
46	S2	1024	A
46	S2	1028	A
46	S2	1045	G
46	S2	1046	U
46	S2	1048	C
46	S2	1062	U
46	S2	1063	A
46	S2	1078	A
46	S2	1079	C
46	S2	1084	A
46	S2	1086	C
46	S2	1090	G
46	S2	1110	C
46	S2	1115	U
46	S2	1116	U
46	S2	1117	C
46	S2	1118	C
46	S2	1119	C
46	S2	1139	C
46	S2	1149	A
46	S2	1154	C
46	S2	1155	U
46	S2	1196	A
46	S2	1208	G
46	S2	1209	A
46	S2	1216	C
46	S2	1217	C
46	S2	1225	G
46	S2	1228	G
46	S2	1241	A

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Mol	Chain	Res	Type
46	S2	1242	A
46	S2	1243	U
46	S2	1244	U
46	S2	1248	C
46	S2	1249	U
46	S2	1252	A
46	S2	1254	A
46	S2	1257	G
46	S2	1258	G
46	S2	1260	A
46	S2	1261	A
46	S2	1272	C
46	S2	1273	C
46	S2	1275	G
46	S2	1277	A
46	S2	1279	A
46	S2	1280	C
46	S2	1283	A
46	S2	1284	C
46	S2	1286	G
46	S2	1287	G
46	S2	1288	A
46	S2	1289	U
46	S2	1293	C
46	S2	1294	A
46	S2	1295	G
46	S2	1296	A
46	S2	1297	U
46	S2	1298	U
46	S2	1299	G
46	S2	1301	U
46	S2	1302	A
46	S2	1303	G
46	S2	1305	U
46	S2	1307	U
46	S2	1308	U
46	S2	1311	U
46	S2	1314	A
46	S2	1316	U
46	S2	1318	C
46	S2	1319	G
46	S2	1321	G

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Mol	Chain	Res	Type
46	S2	1324	U
46	S2	1325	G
46	S2	1342	C
46	S2	1343	U
46	S2	1344	U
46	S2	1365	U
46	S2	1372	U
46	S2	1373	U
46	S2	1374	C
46	S2	1379	A
46	S2	1391	U
46	S2	1398	U
46	S2	1401	U
46	S2	1403	A
46	S2	1404	C
46	S2	1405	U
46	S2	1407	G
46	S2	1409	U
46	S2	1411	C
46	S2	1412	G
46	S2	1413	C
46	S2	1414	G
46	S2	1416	C
46	S2	1417	C
46	S2	1418	C
46	S2	1419	C
46	S2	1420	C
46	S2	1421	G
46	S2	1422	A
46	S2	1423	G
46	S2	1426	G
46	S2	1429	G
46	S2	1430	G
46	S2	1432	G
46	S2	1442	U
46	S2	1443	U
46	S2	1448	G
46	S2	1455	A
46	S2	1456	A
46	S2	1463	U
46	S2	1465	C
46	S2	1477	A

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Mol	Chain	Res	Type
46	S2	1479	U
46	S2	1488	A
46	S2	1490	A
46	S2	1491	G
46	S2	1498	G
46	S2	1507	A
46	S2	1510	U
46	S2	1521	G
46	S2	1522	C
46	S2	1523	A
46	S2	1524	C
46	S2	1534	A
46	S2	1537	G
46	S2	1545	C
46	S2	1553	G
46	S2	1554	C
46	S2	1556	U
46	S2	1557	A
46	S2	1558	C
46	S2	1559	C
46	S2	1569	C
46	S2	1580	A
46	S2	1581	A
46	S2	1582	C
46	S2	1583	C
46	S2	1588	G
46	S2	1589	A
46	S2	1600	U
46	S2	1601	G
46	S2	1604	G
46	S2	1619	C
46	S2	1622	U
46	S2	1624	A
46	S2	1640	G
46	S2	1647	C
46	S2	1649	G
46	S2	1655	G
46	S2	1657	G
46	S2	1661	C
46	S2	1664	A
46	S2	1666	G
46	S2	1672	G

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Mol	Chain	Res	Type
46	S2	1687	G
46	S2	1700	A
46	S2	1722	U
46	S2	1723	G
46	S2	1730	U
46	S2	1733	G
46	S2	1736	A
46	S2	1743	C
46	S2	1744	G
46	S2	1745	G
46	S2	1748	C
46	S2	1749	G
46	S2	1753	C
46	S2	1754	C
46	S2	1755	G
46	S2	1778	G
46	S2	1782	A
46	S2	1783	G
46	S2	1784	C
46	S2	1785	G
46	S2	1786	C
46	S2	1787	U
46	S2	1790	G
46	S2	1791	A
46	S2	1806	G
46	S2	1808	C
46	S2	1825	A
46	S2	1826	A
46	S2	1830	G
46	S2	1832	A
46	S2	1839	U
46	S2	1850	G
46	S2	1852	A
46	S2	1853	C
46	S2	1862	G
46	S2	1863	G
46	S2	1864	A
46	S2	1865	U
46	S2	1866	C
46	S2	1870	A
47	S6	4	C
47	S6	6	G

Continued on next page...

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Mol	Chain	Res	Type
47	S6	8	G
47	S6	10	G
47	S6	11	G
47	S6	12	C
47	S6	17	C
47	S6	18	G
47	S6	20	A
47	S6	21	A
47	S6	45	G
47	S6	46	G
47	S6	48	C
47	S6	52	G
47	S6	54	A
47	S6	55	U
47	S6	57	G
47	S6	58	A
47	S6	60	A
47	S6	61	C
47	S6	62	C
47	S6	67	U
47	S6	69	U
47	S6	74	C
47	S6	75	C
47	S6	76	A
47	S7	3	G
47	S7	4	C
47	S7	6	G
47	S7	7	A
47	S7	8	G
47	S7	10	G
47	S7	11	G
47	S7	12	C
47	S7	17	C
47	S7	18	G
47	S7	19	G
47	S7	20	A
47	S7	21	A
47	S7	22	G
47	S7	23	C
47	S7	24	G
47	S7	32	C
47	S7	39	C

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Mol	Chain	Res	Type
47	S7	42	A
47	S7	44	A
47	S7	48	C
47	S7	49	G
47	S7	50	A
47	S7	52	G
47	S7	53	G
47	S7	54	A
47	S7	55	U
47	S7	58	A
47	S7	59	A
47	S7	60	A
47	S7	61	C
47	S7	63	A
47	S7	66	C
47	S7	67	U
47	S7	69	U
47	S7	71	C
47	S7	72	U
47	S7	73	A
47	S7	74	C
47	S7	76	A
79	Sx	33	U

All (62) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	1	C
1	L5	266	G
1	L5	415	U
1	L5	453	U
1	L5	458	C
1	L5	486	C
1	L5	745	C
1	L5	753	G
1	L5	760	G
1	L5	823	C
1	L5	830	C
1	L5	923	G
1	L5	1054	G
1	L5	1192	G
1	L5	1227	G

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Mol	Chain	Res	Type
1	L5	1271	G
1	L5	1447	G
1	L5	1563	G
1	L5	1585	U
1	L5	2345	A
1	L5	2519	A
1	L5	2540	C
1	L5	2649	A
1	L5	3417	A
1	L5	3904	A
1	L5	4352	U
1	L5	4549	G
1	L5	4612	C
1	L5	4686	A
2	L7	3	C
2	L7	60	G
3	L8	5	U
46	S2	34	U
46	S2	55	U
46	S2	94	G
46	S2	96	C
46	S2	115	U
46	S2	126	G
46	S2	172	U
46	S2	180	G
46	S2	293	A
46	S2	446	A
46	S2	454	C
46	S2	498	C
46	S2	565	A
46	S2	592	U
46	S2	599	G
46	S2	629	A
46	S2	842	G
46	S2	862	A
46	S2	1241	A
46	S2	1343	U
46	S2	1416	C
46	S2	1442	U
46	S2	1476	G
46	S2	1555	C
46	S2	1783	G

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Mol	Chain	Res	Type
46	S2	1784	C
47	S6	53	G
47	S6	54	A
47	S7	53	G
47	S7	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 100 ligands modelled in this entry, 100 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](#)

There are no chain breaks in this entry.

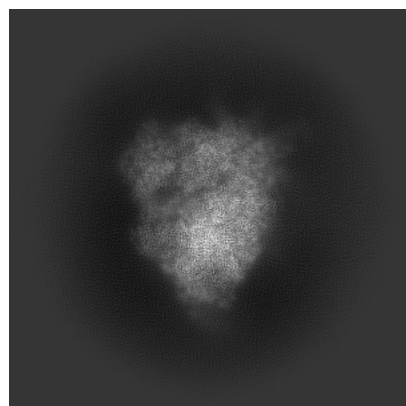
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62288. These allow visual inspection of the internal detail of the map and identification of artifacts.

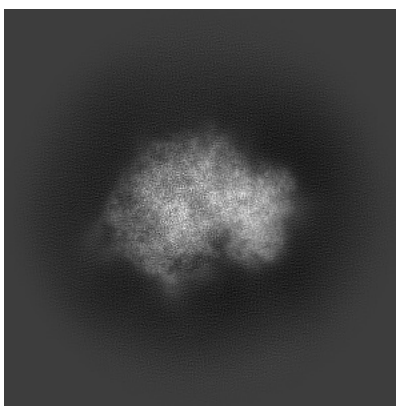
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

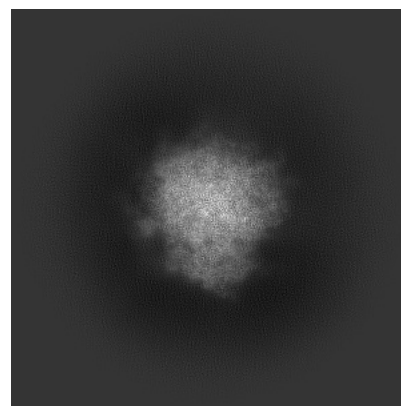
6.1.1 Primary map



X

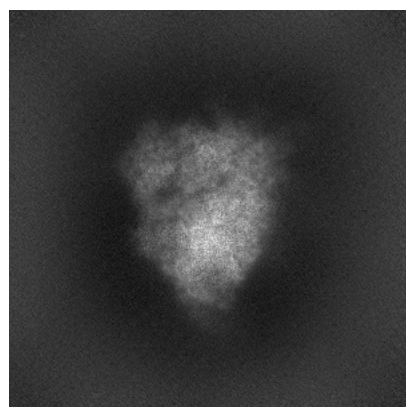


Y

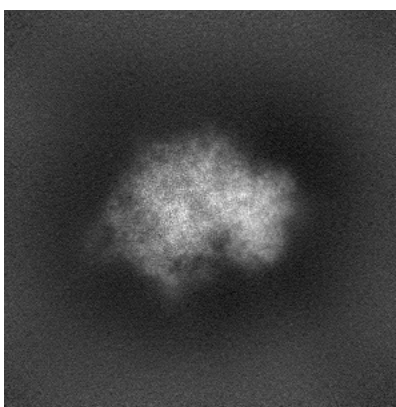


Z

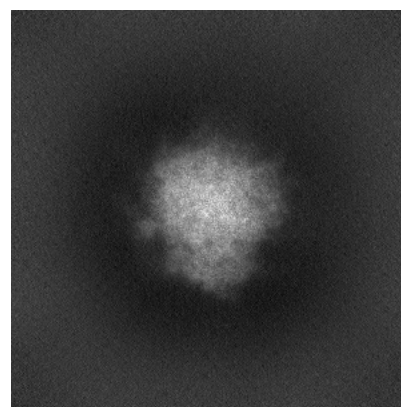
6.1.2 Raw map



X



Y

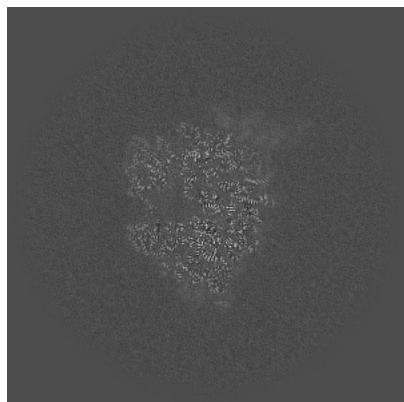


Z

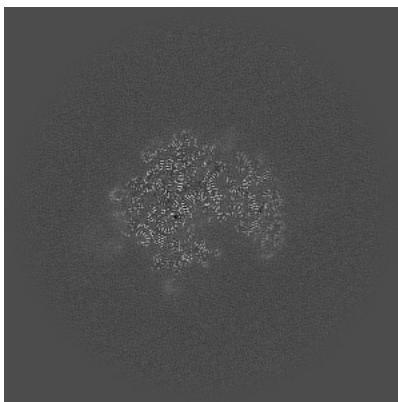
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

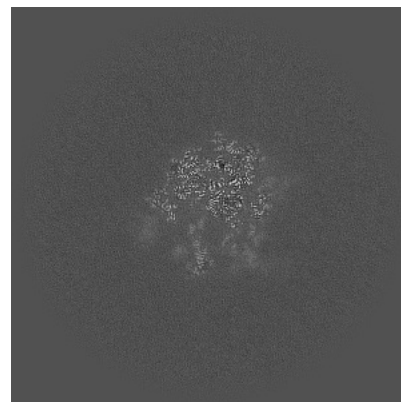
6.2.1 Primary map



X Index: 280

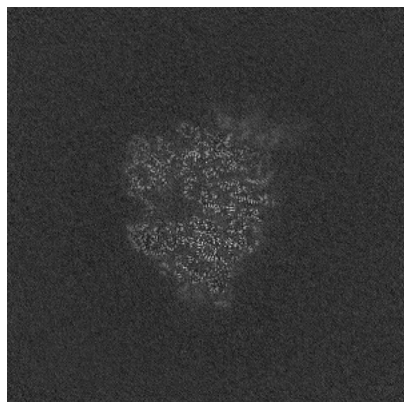


Y Index: 280

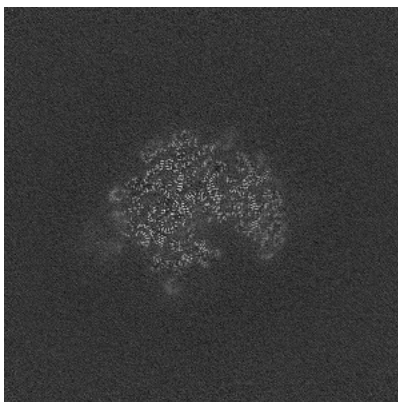


Z Index: 280

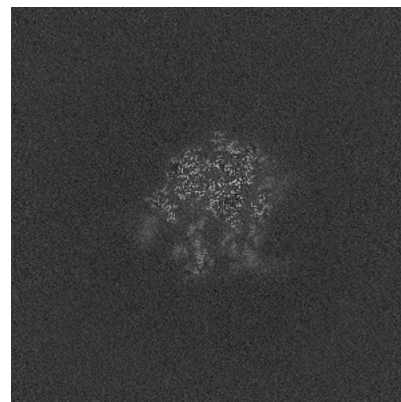
6.2.2 Raw map



X Index: 280



Y Index: 280

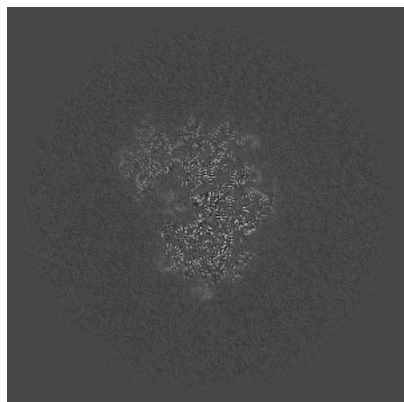


Z Index: 280

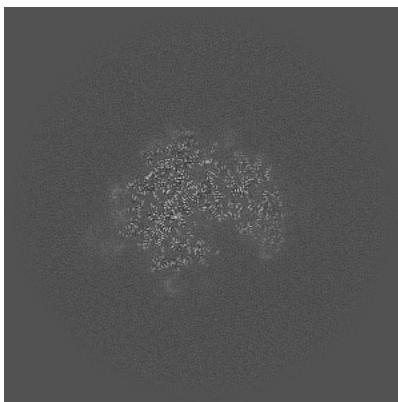
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

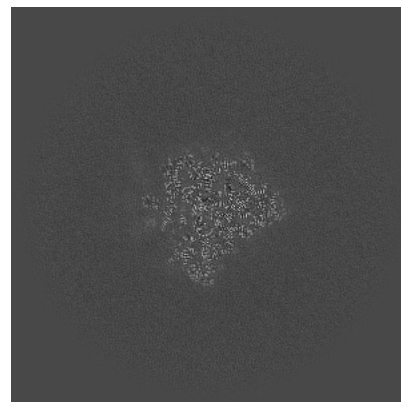
6.3.1 Primary map



X Index: 303

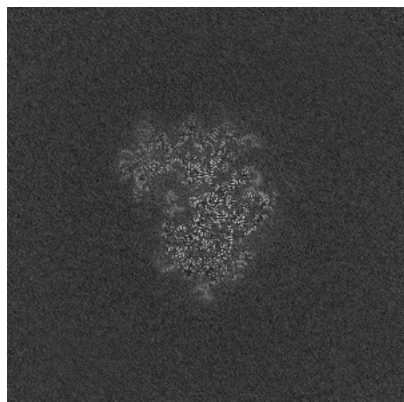


Y Index: 278

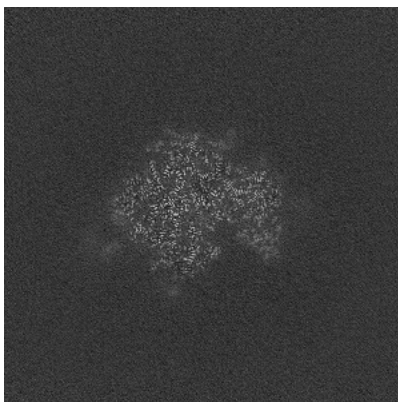


Z Index: 246

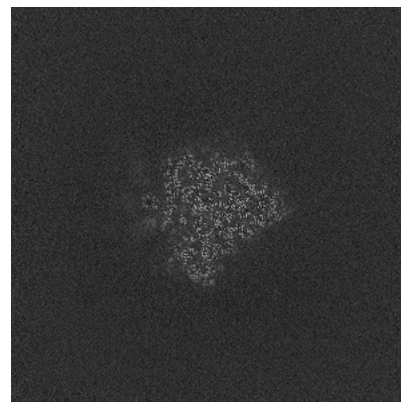
6.3.2 Raw map



X Index: 302



Y Index: 287

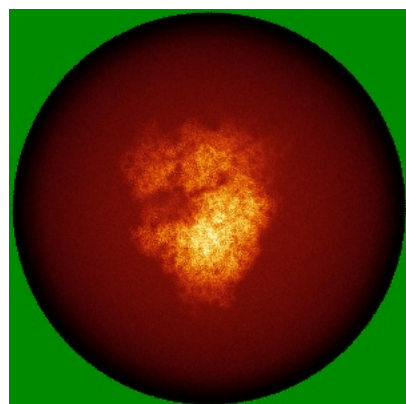


Z Index: 246

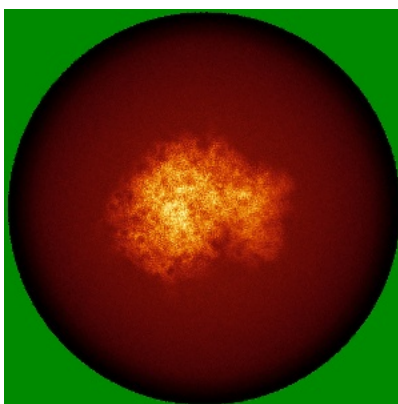
The images above show the largest variance slices of the map in three orthogonal directions.

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

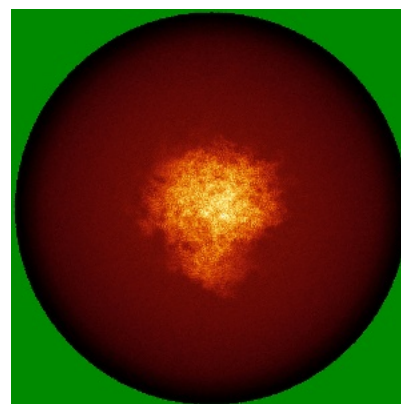
6.4.1 Primary map



X

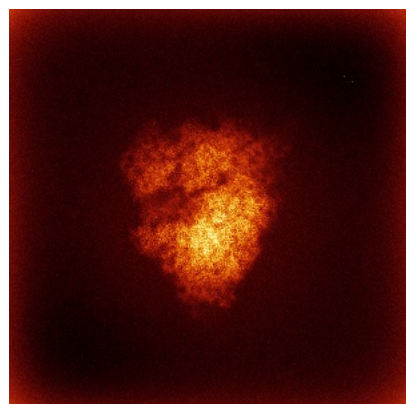


Y

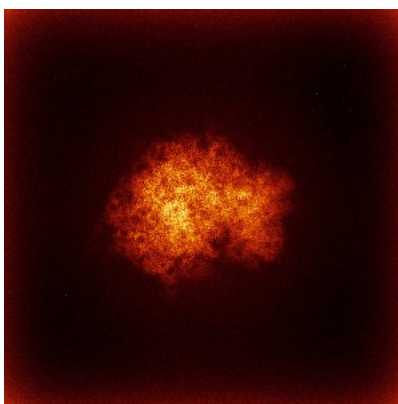


Z

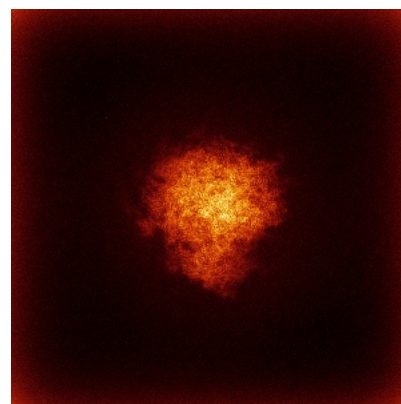
6.4.2 Raw map



X



Y

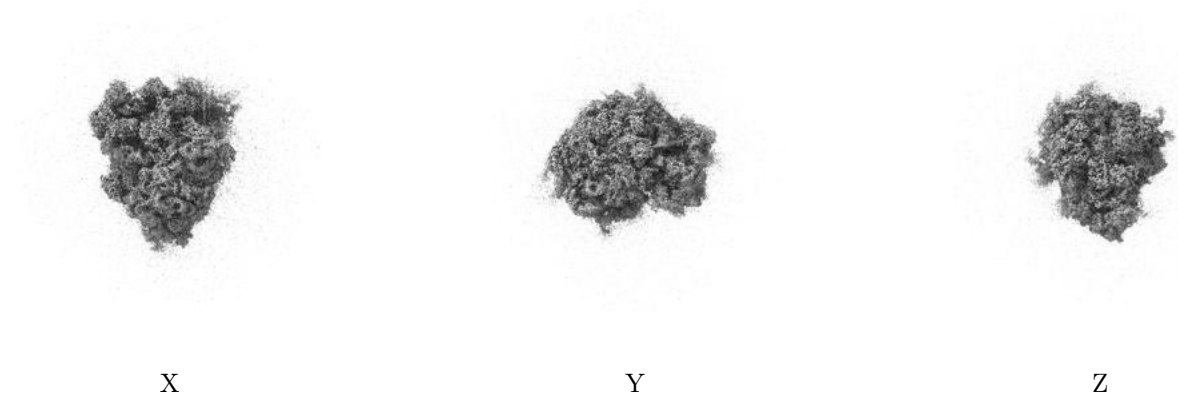


Z

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

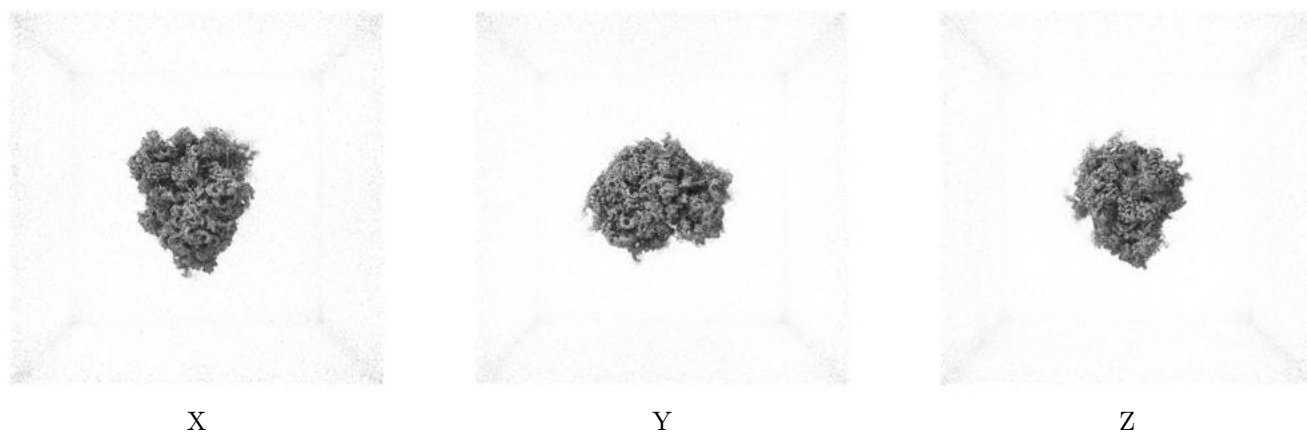
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

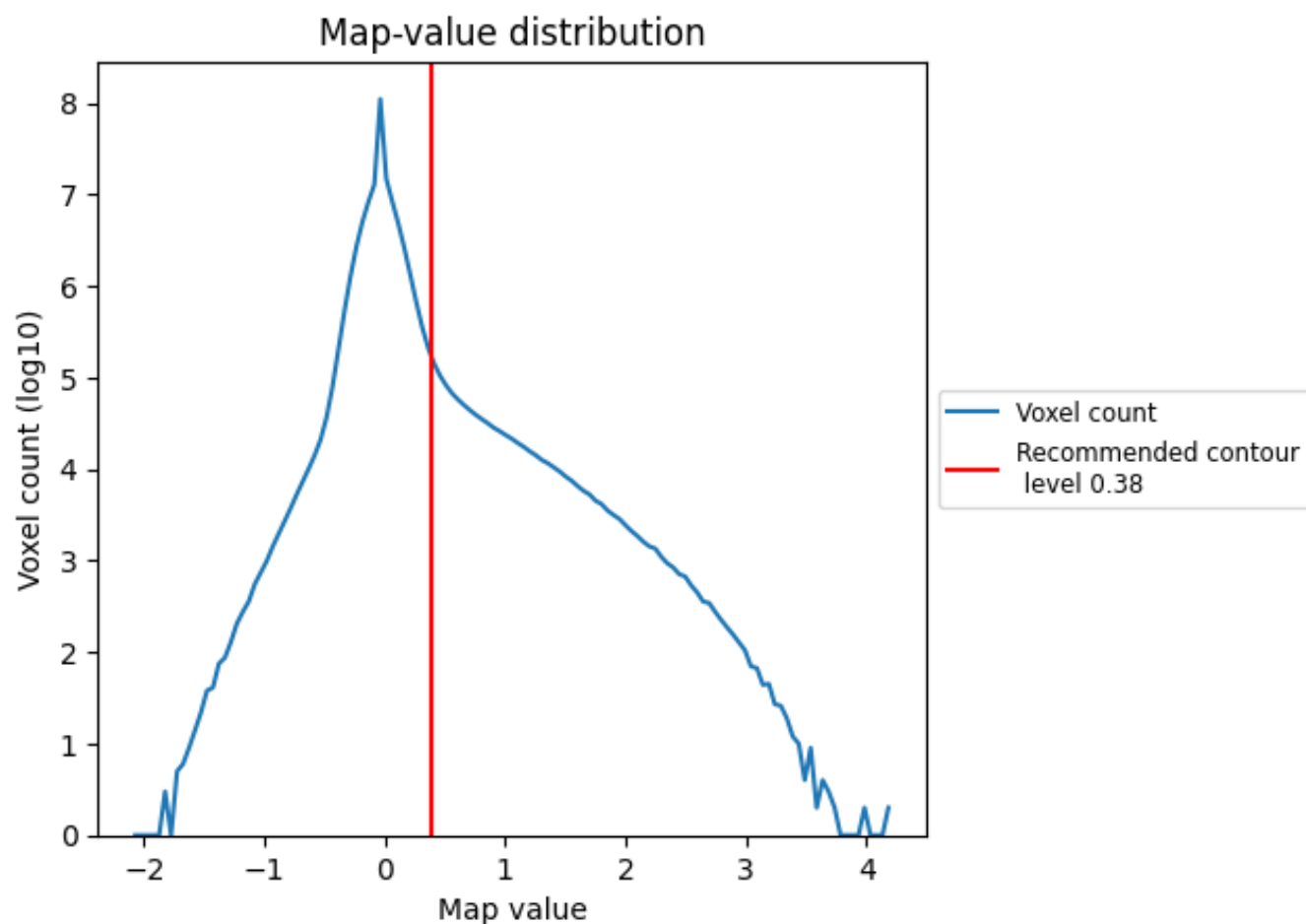
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

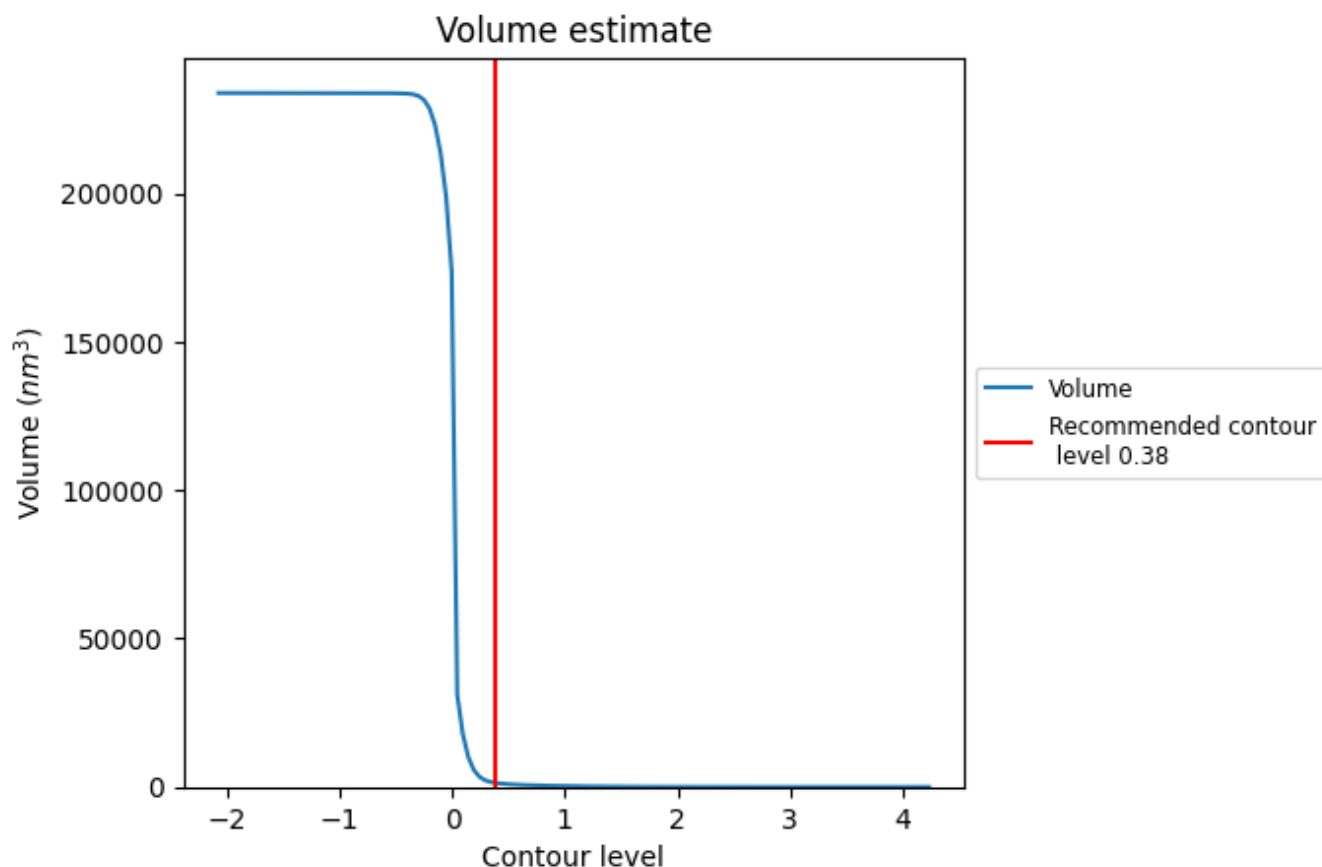
This section contains the results of statistical analysis of the map.

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.

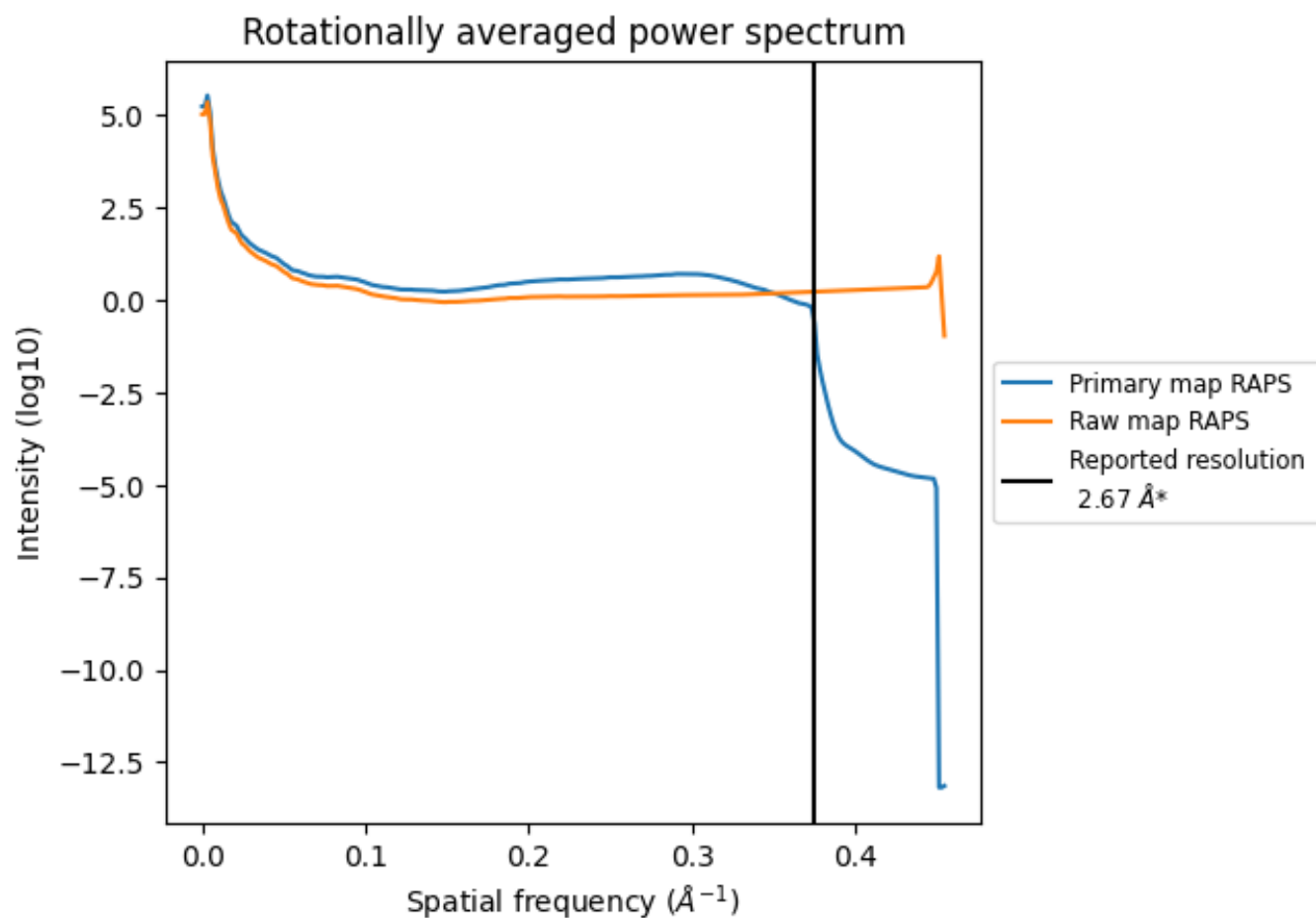
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1414 nm³; this corresponds to an approximate mass of 1278 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 ⓘ

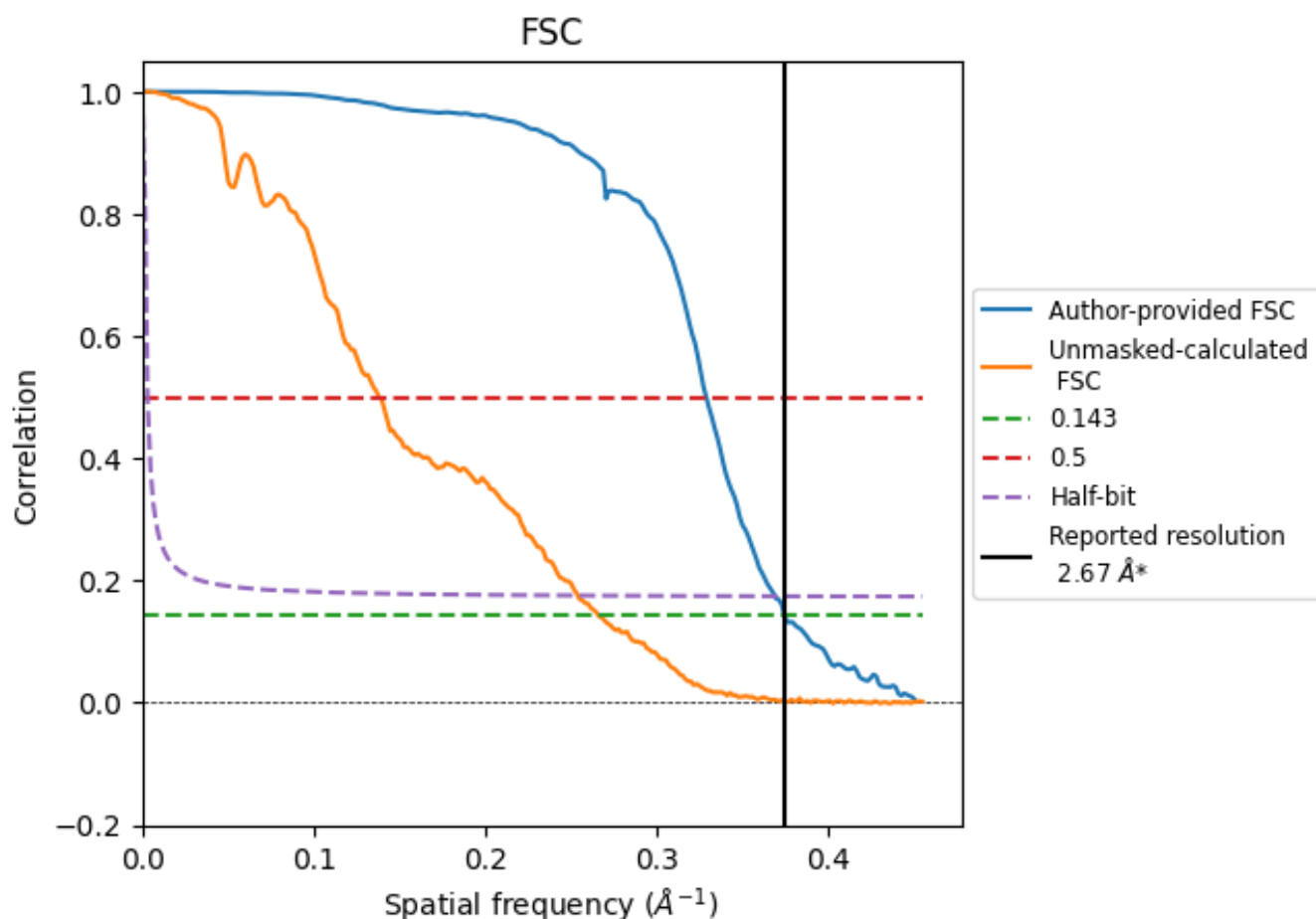


*Reported resolution corresponds to spatial frequency of 0.375 \AA^{-1}

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 0.375 Å⁻¹

8.2 Resolution estimates [i](#)

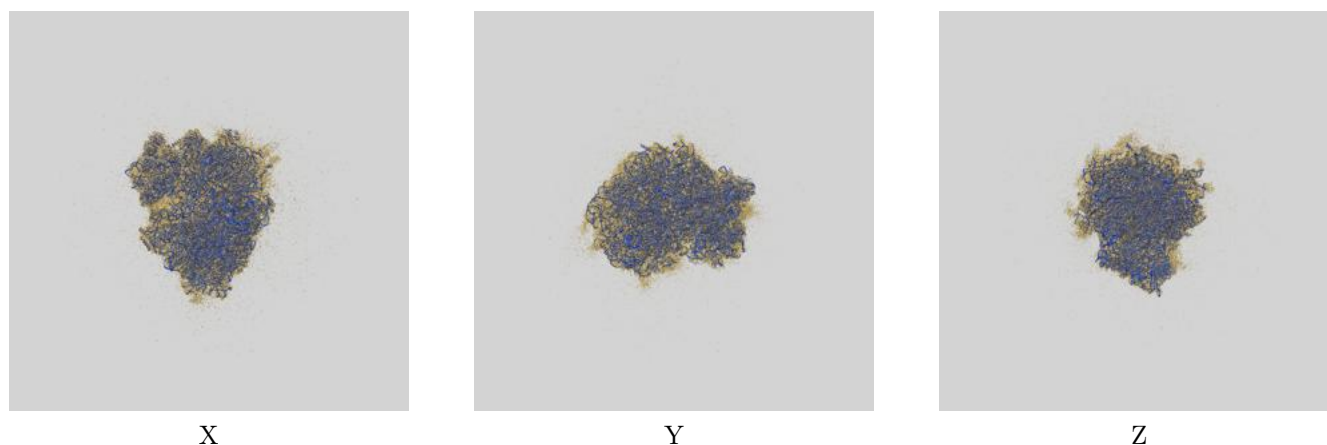
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.67	-	-
Author-provided FSC curve	2.67	3.04	2.71
Unmasked-calculated*	3.76	7.25	3.94

*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 3.76 differs from the reported value 2.67 by more than 10 %

9 Map-model fit [i](#)

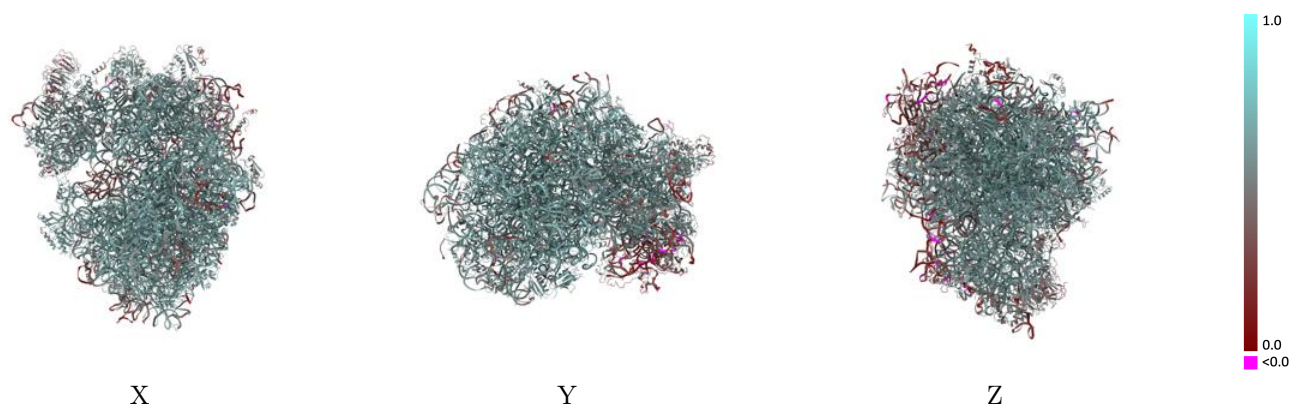
This section contains information regarding the fit between EMDB map EMD-62288 and PDB model 9KDW. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



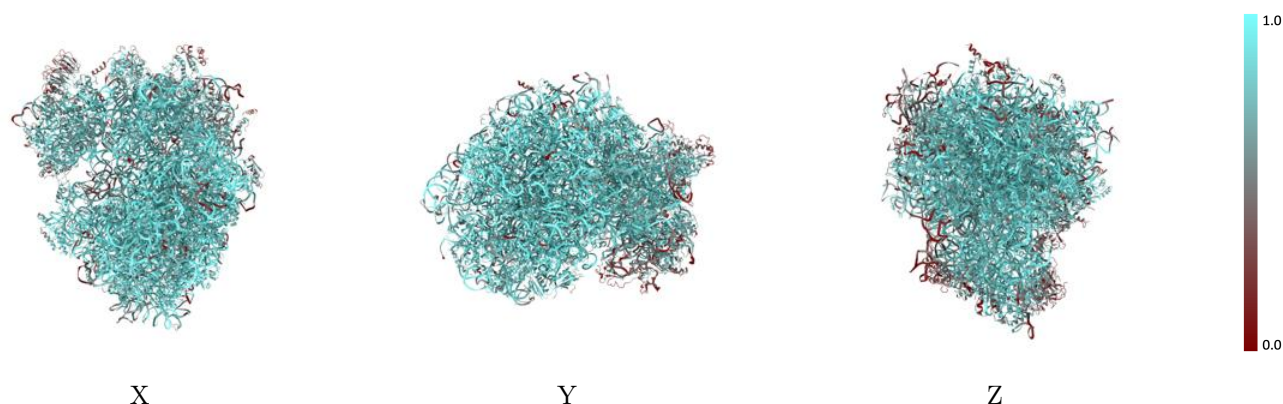
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



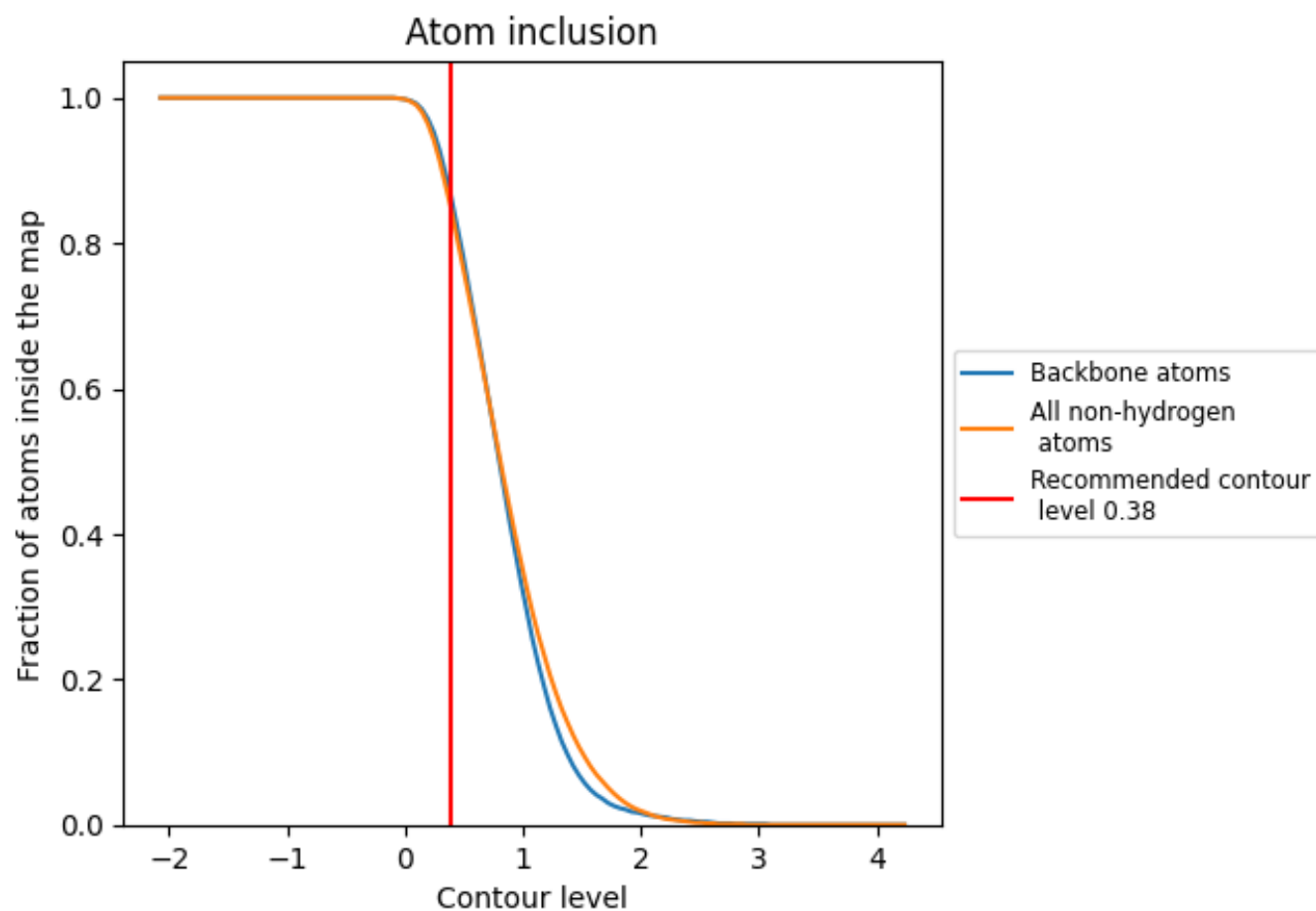
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.38).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 86% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8550	 0.5730
L5	 0.9140	 0.5940
L7	 0.9850	 0.6360
L8	 0.9420	 0.6120
LA	 0.9500	 0.6440
LB	 0.8990	 0.6270
LC	 0.9310	 0.6310
LD	 0.8190	 0.5830
LE	 0.8370	 0.5900
LF	 0.9550	 0.6410
LG	 0.8060	 0.5750
LH	 0.8450	 0.5980
LI	 0.8870	 0.6140
LJ	 0.8290	 0.5990
LL	 0.8580	 0.6070
LM	 0.9110	 0.6180
LN	 0.9750	 0.6550
LO	 0.9250	 0.6360
LP	 0.9270	 0.6350
LQ	 0.9430	 0.6430
LR	 0.8610	 0.5950
LS	 0.9330	 0.6310
LT	 0.8850	 0.6080
LU	 0.6950	 0.5150
LV	 0.9150	 0.6300
LW	 0.9240	 0.6380
LX	 0.8790	 0.6140
LY	 0.8830	 0.6140
LZ	 0.8580	 0.6050
La	 0.9400	 0.6440
Lb	 0.8440	 0.5850
Lc	 0.8630	 0.6050
Ld	 0.8450	 0.5980
Le	 0.9560	 0.6480
Lf	 0.9640	 0.6490













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Chain	Atom inclusion	Q-score
Lg	 0.8950	 0.6160
Lh	 0.8590	 0.6070
Li	 0.8180	 0.5930
Lj	 0.9700	 0.6480
Lk	 0.6850	 0.5490
Ll	 0.9530	 0.6300
Lm	 0.9110	 0.6290
Ln	 0.8940	 0.6160
Lo	 0.8900	 0.6210
Lp	 0.9160	 0.6330
Lr	 0.9360	 0.6290
S2	 0.8280	 0.5180
S6	 0.7820	 0.4740
S7	 0.6480	 0.4140
SA	 0.7960	 0.5780
SB	 0.7940	 0.5810
SC	 0.8380	 0.5850
SD	 0.6570	 0.5130
SE	 0.7190	 0.5120
SF	 0.7350	 0.5430
SG	 0.4740	 0.3840
SH	 0.5440	 0.4740
SI	 0.7550	 0.5240
SJ	 0.7770	 0.5410
SK	 0.4610	 0.4290
SL	 0.8750	 0.5910
SN	 0.8350	 0.5930
SO	 0.8140	 0.5800
SP	 0.7210	 0.5310
SQ	 0.7460	 0.5380
SR	 0.5860	 0.4890
SS	 0.7570	 0.5620
ST	 0.7550	 0.5480
SU	 0.5560	 0.4570
SV	 0.7740	 0.5690
SW	 0.9170	 0.6130
SX	 0.8460	 0.5840
SY	 0.4760	 0.3790
SZ	 0.6200	 0.4990
Sa	 0.8200	 0.5860
Sb	 0.6290	 0.5000
Sc	 0.6260	 0.4880

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Chain	Atom inclusion	Q-score
Sd	 0.7280	 0.4900
Se	 0.6530	 0.4680
Sg	 0.4370	 0.4130
Sx	 0.8740	 0.5500
Z	 0.5390	 0.4090