



Full wwPDB EM Validation Report ⓘ

May 4, 2026 – 05:27 PM JST

PDB ID : 9KDU / pdb_00009kdu
EMDB ID : EMD-62286
Title : Cryo-EM structure of 80S ribosome
Authors : Lu, Y.; Wang, X.; Qin, Y.; Cao, Y.
Deposited on : 2024-11-04
Resolution : 2.96 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

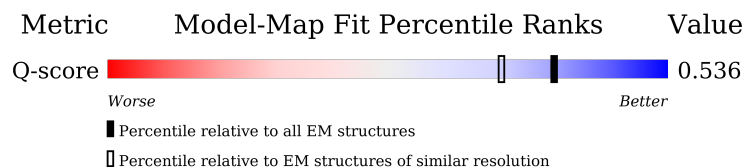
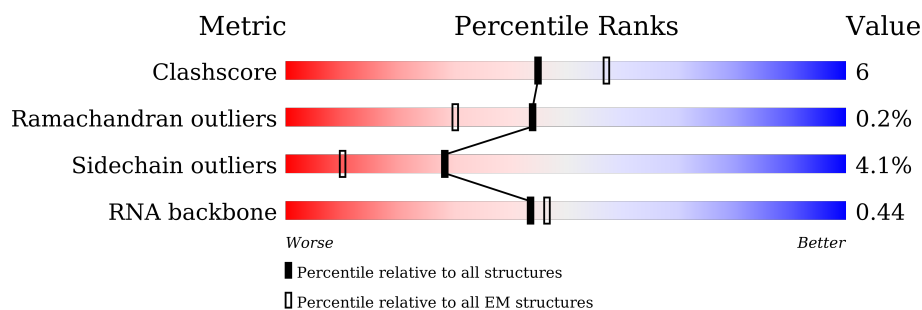
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	

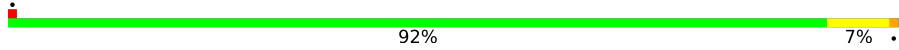


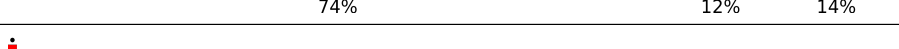

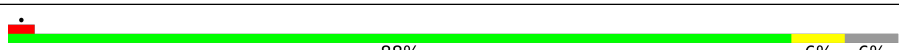



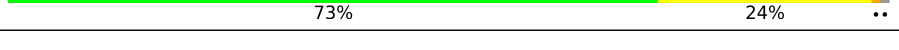
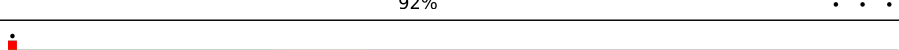
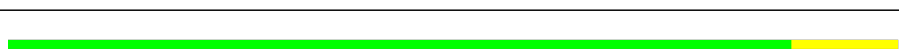



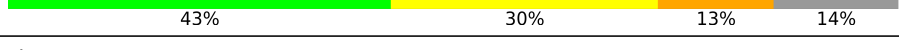
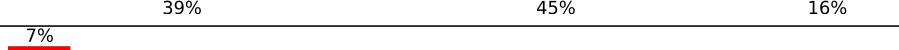




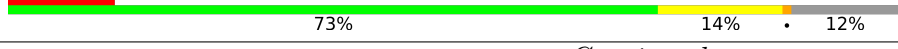



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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	419	
7	LD	297	
8	LE	296	
9	LF	270	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	217	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	





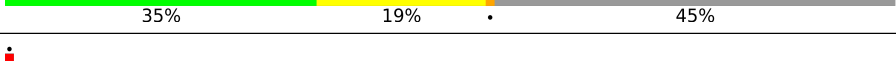
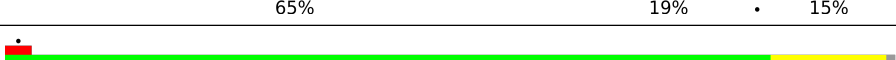
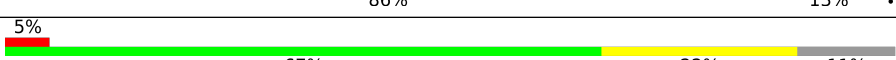
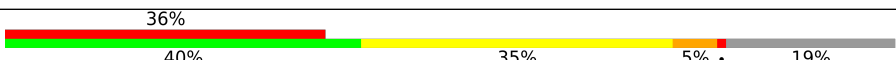
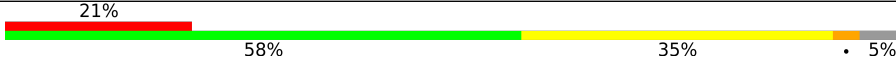





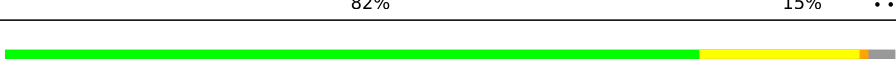
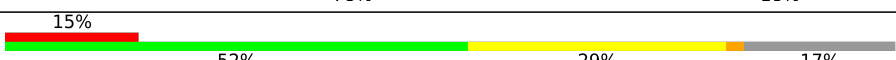
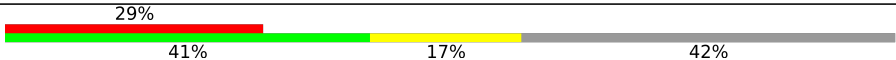

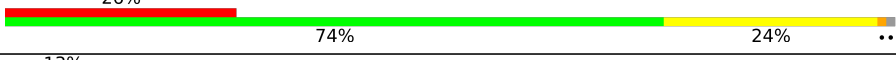
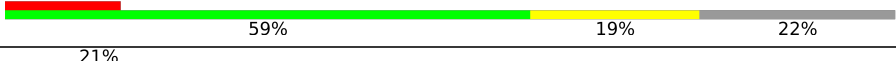


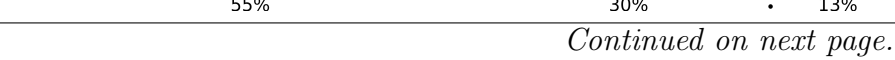


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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	160	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1870	
47	S7	75	
48	SA	295	
49	SB	264	
50	SC	293	
51	SD	243	
52	SE	263	
53	SF	204	

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Mol	Chain	Length	Quality of chain
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	
78	Sg	317	

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Mol	Chain	Length	Quality of chain
79	Sx	10	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>30%60%30%10%</div>
80	Z	7	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>29%71%</div>

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 202023 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	3392	Total	C	N	O	P	0	0
			72739	32395	13303	23650	3391		

- 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	1614	Total	C	N	O	P	0	0
			34451	15383	6189	11266	1613		

- Molecule 47 is a RNA chain called P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
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	7	Total	C	N	O	0	0
			34	20	7	7		

- 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	

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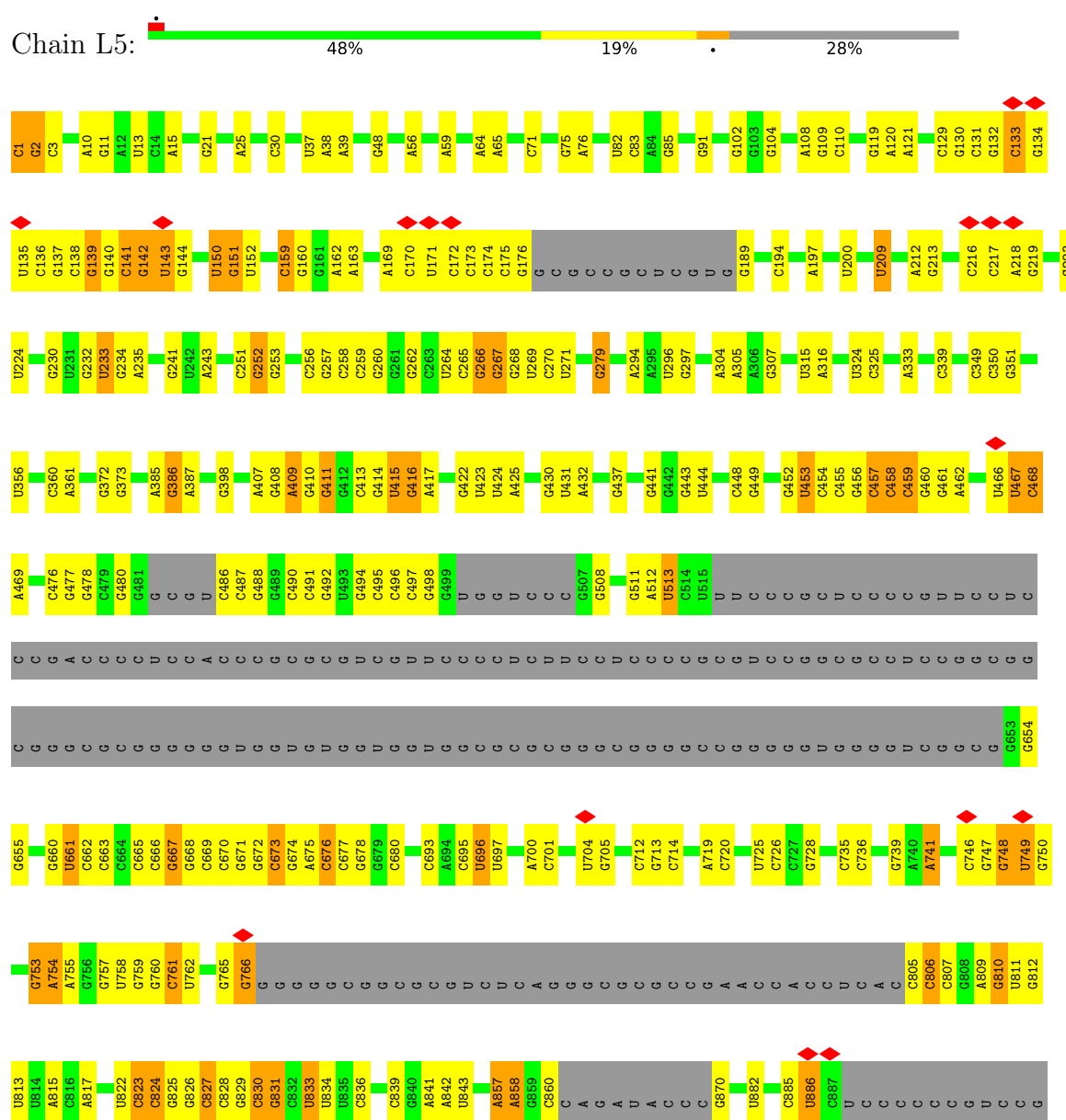
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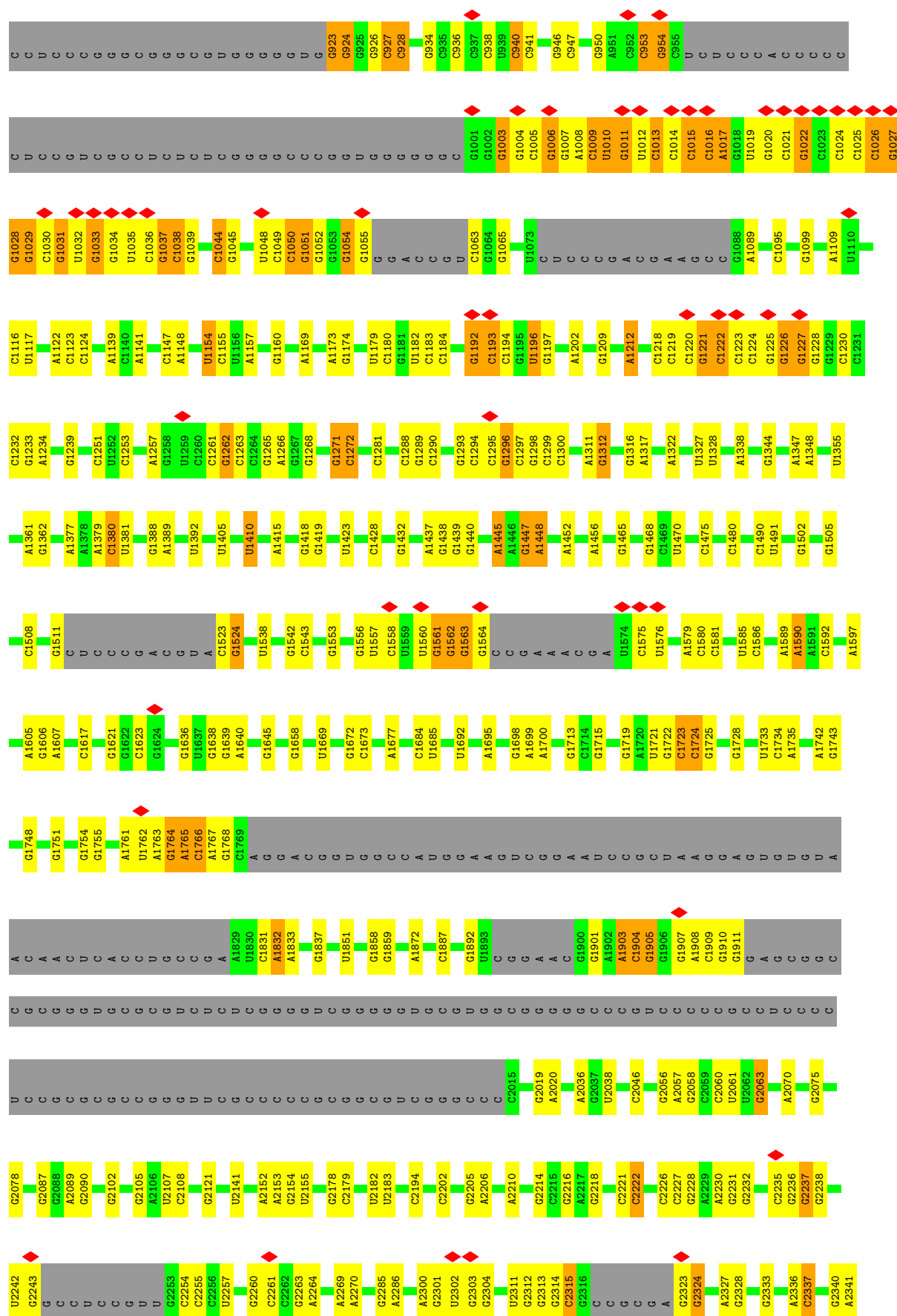
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
82	Lp	1	1	1	0

3 Residue-property plots

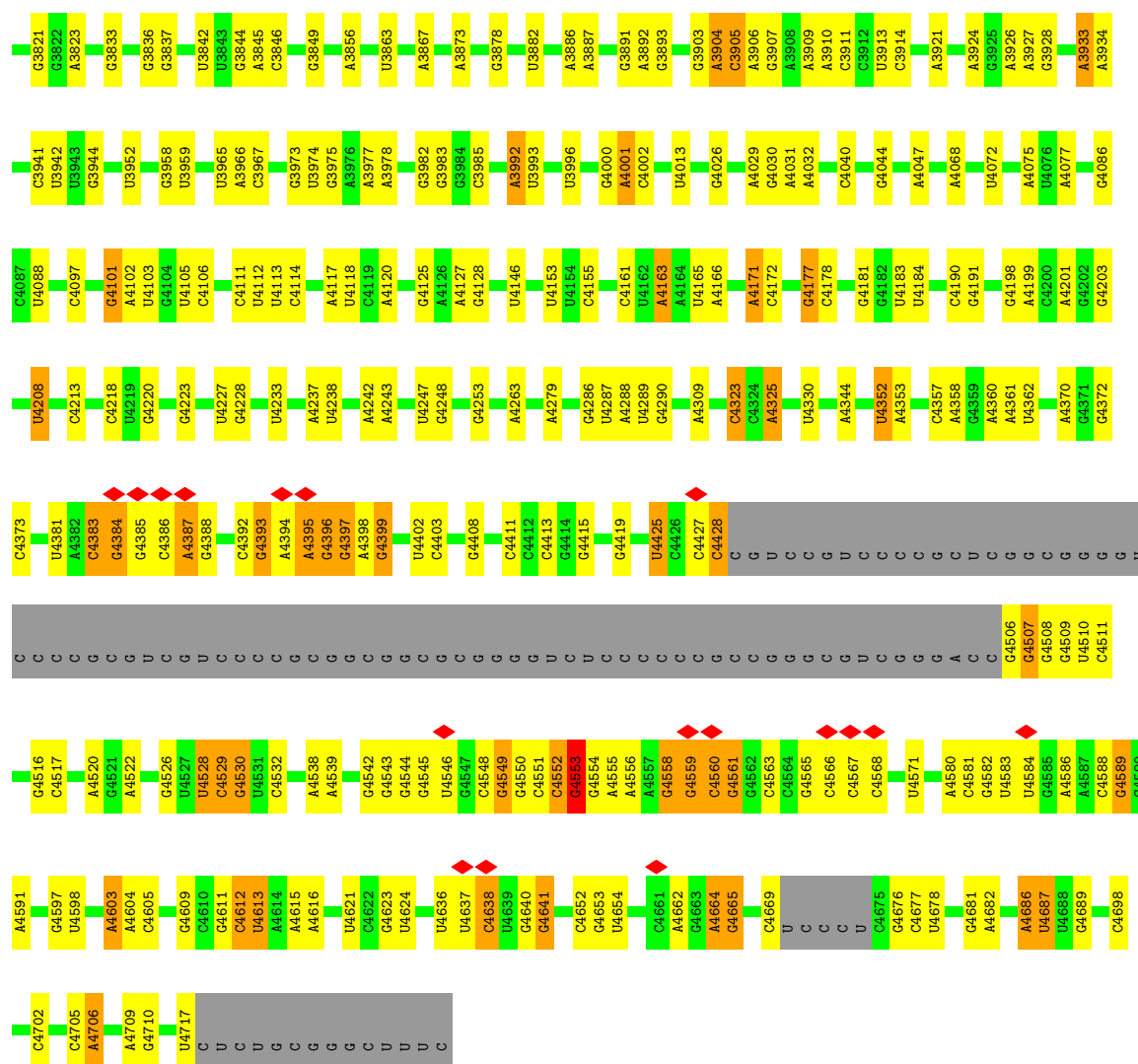
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

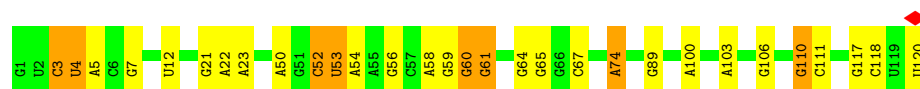
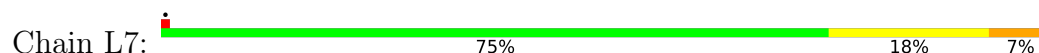




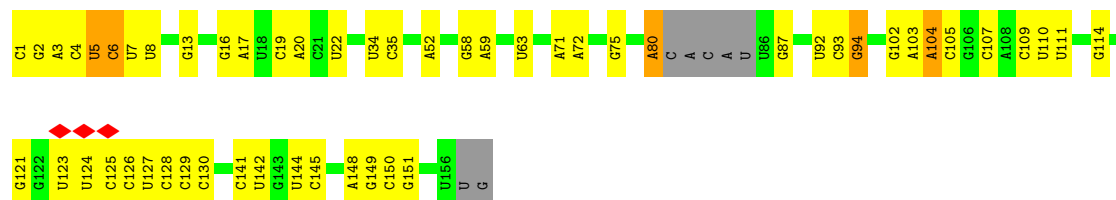





• Molecule 2: Mus musculus 5S ribosomal RNA



• Molecule 3: Mus musculus 5.8S ribosomal RNA




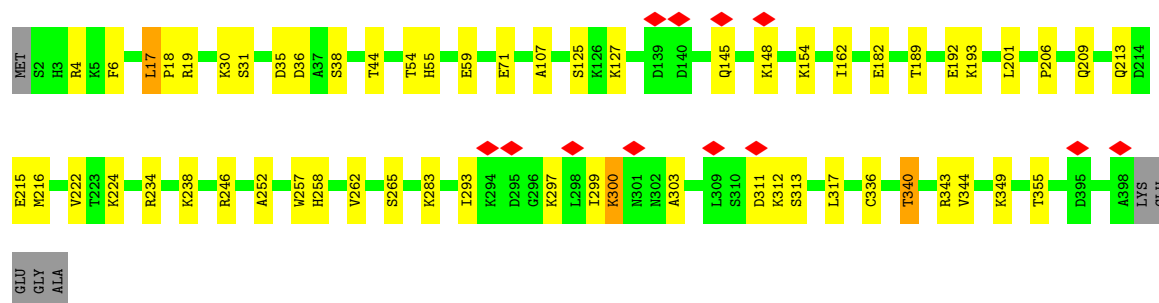
• Molecule 4: Large ribosomal subunit protein uL2

Chain LA:  85% 10% . .




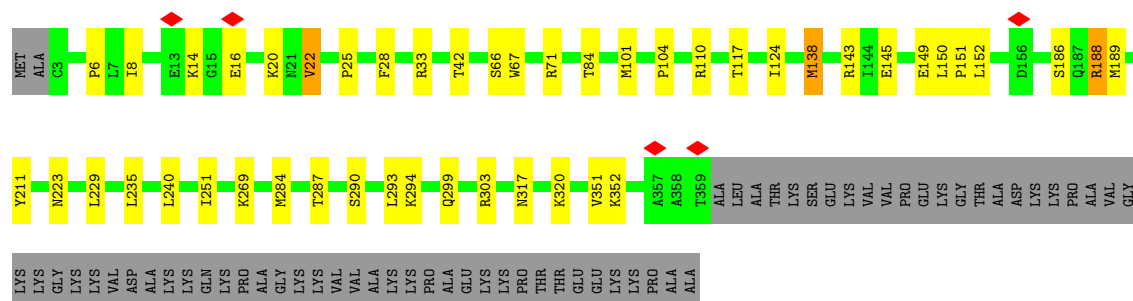
- Molecule 5: Large ribosomal subunit protein uL3

Chain LB:  84% 14% ..




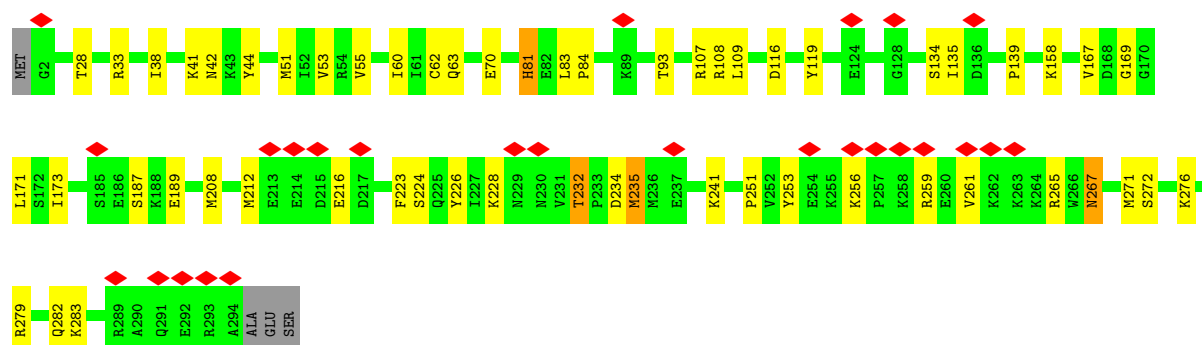
- Molecule 6: Large ribosomal subunit protein uL4

Chain LC:  74% 11% . 15%



- Molecule 7: Large ribosomal subunit protein uL18

Chain LD:  9% 80% 18% ..



- Molecule 8: Large ribosomal subunit protein eL6

Frequency	Percentage
Daily	62%
Weekly	10%
Monthly	27%
Other	1%



Device Type	Percentage
Smartphones	70%
Tablets	9%
Other mobile devices	21%



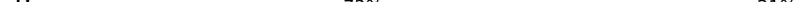
Frequency	Percentage
10%	10%
73%	73%
13%	13%
14%	14%




Frequency	Percentage
5%	5%
79%	79%
18%	18%



M144	M147	R154	S168	M177	E180	F181	E182	D183	K184	V185	R189	L190	I191	F192	D193	G194	C195	E202	S214																												
Met	G2	R3	R4	V26	P27	D28	D35	L36	G37	R38	C49	G50	H51	H52	V53	S79	C80	D83	H86	I87	R88	L91	I99	N100	K101	Met	Leu	Ser	Cys	Ala	Gly	Ala	Asp	Arg	Leu	Gln	Thr	G114	T125	V129	Q133	V134	R139	T140	K141	L142	G143

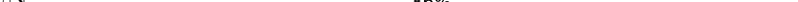
- Chain LJ: 

MET	ALA	GLN	ASP	GLN	GLY	GLU	LYS	GLU	N10	P11	M12	R13	E14	K38	E41	Q42	Q45	Q46	P47	P48	S51	Y55	T56	R63	R64	N65	E66	K67	C72	T73	E84	K85	K88	E93	L94	R95	N98	H112	I113	D114	L115	Y119	D120	P121	S122	E123
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- Chain LL: 


- Chain LM:  52% 11% 37%

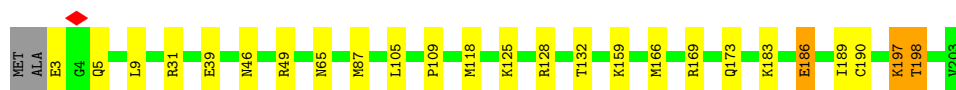
[illegible]

- Chain LN:  86% 13%

ME1	G2	A3	Y4		L10		K14		M19		R26		R38		T43	R44	P45		R49		R68		R73	P74		T80		K83	P84	V85		E104		R108		D124	S125		H158	R159	E160	M161		S171		K179		T197		P204
-----	----	----	----	--	-----	--	-----	--	-----	--	-----	--	-----	--	-----	-----	-----	--	-----	--	-----	--	-----	-----	--	-----	--	-----	-----	-----	--	------	--	------	--	------	------	--	------	------	------	------	--	------	--	------	--	------	--	------

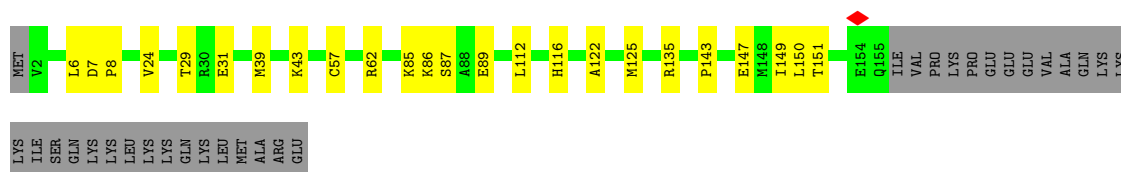
- Molecule 17: Large ribosomal subunit protein uL13

Chain LO:  87% 11% ..




- Molecule 18: Large ribosomal subunit protein uL22

Chain LP:  71% 13% 16%




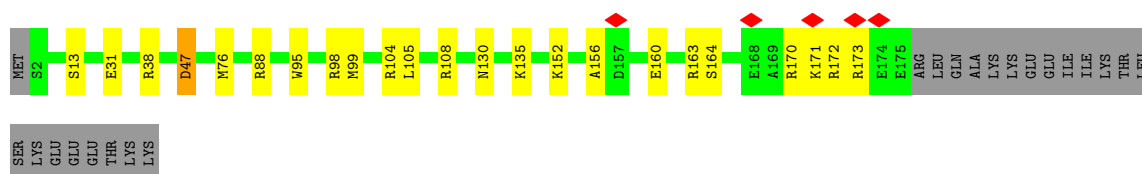
- Molecule 19: Large ribosomal subunit protein eL18

Chain LQ:  86% 13% ..



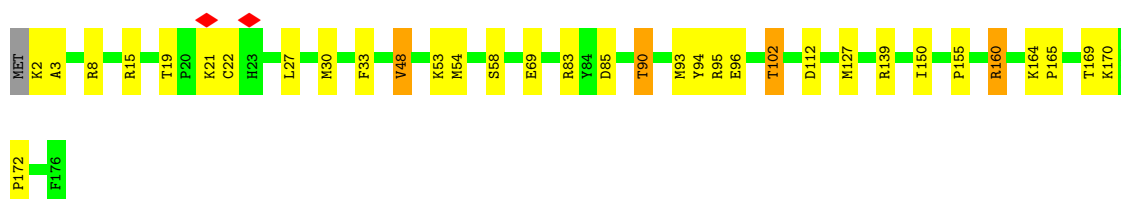
- Molecule 20: Large ribosomal subunit protein eL19

Chain LR:  77% 11% 11%



- Molecule 21: Large ribosomal subunit protein eL20

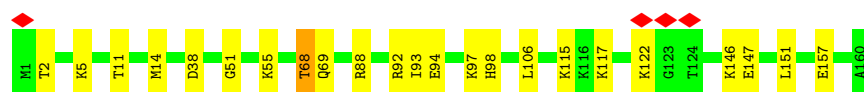
Chain LS:  80% 17% ..



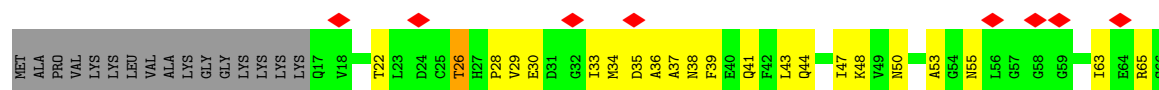
- Molecule 22: Large ribosomal subunit protein eL21

Chain LT:  86% 14%

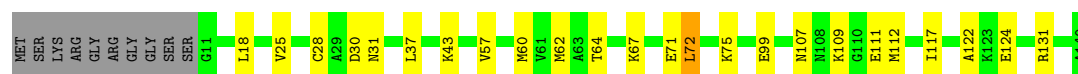
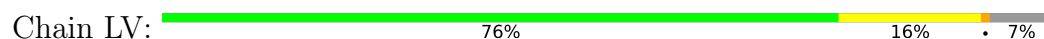




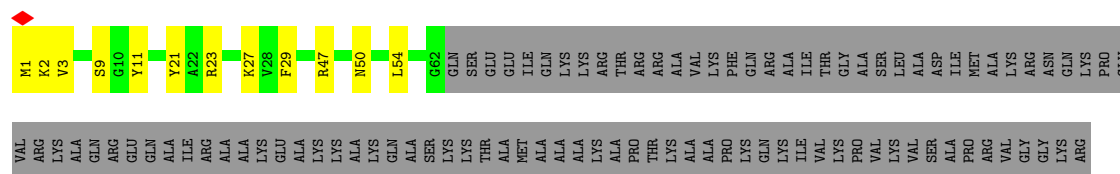
- Molecule 23: Large ribosomal subunit protein eL22



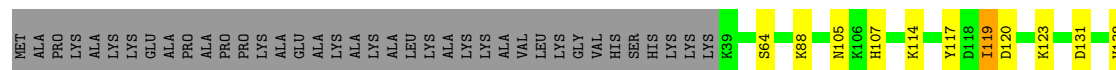
- Molecule 24: Large ribosomal subunit protein uL14



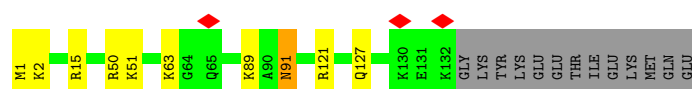
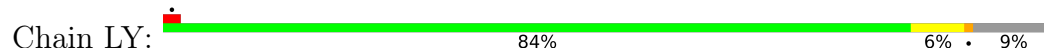
- Molecule 25: Large ribosomal subunit protein eL24




- Molecule 26: Large ribosomal subunit protein uL23



- Molecule 27: Large ribosomal subunit protein uL24




- Molecule 28: Large ribosomal subunit protein eL27

Chain LZ:  82% 16% ..



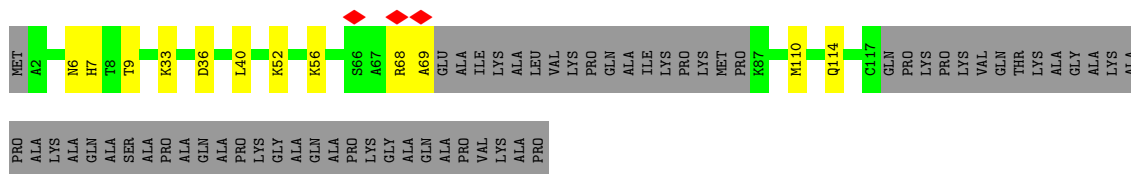
- Molecule 29: Large ribosomal subunit protein uL15

Chain La:  92% 7% ..



- Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:  54% 8% 38%




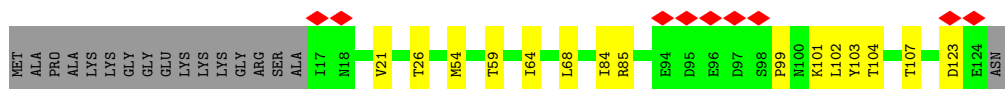
- Molecule 31: Large ribosomal subunit protein eL30

Chain Lc:  66% 14% 18%




- Molecule 32: Large ribosomal subunit protein eL31

Chain Ld:  7% 74% 12% 14%




- Molecule 33: Large ribosomal subunit protein eL32

Chain Le:  84% 10% 5%

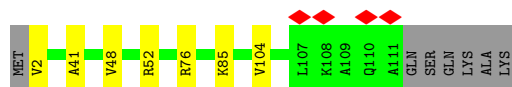


- Molecule 34: Large ribosomal subunit protein eL33

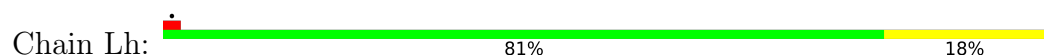
Chain Lf:  85% 14%



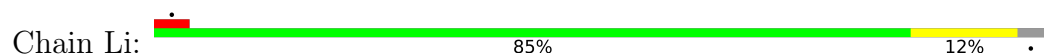
- Molecule 35: Large ribosomal subunit protein eL34



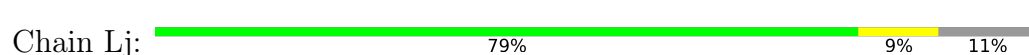
- Molecule 36: Large ribosomal subunit protein uL29



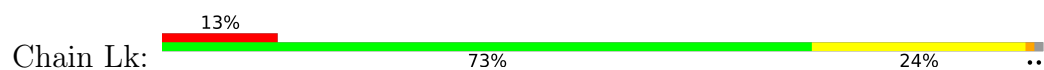
- Molecule 37: Large ribosomal subunit protein eL36



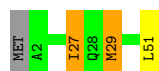
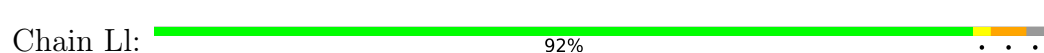
- Molecule 38: Large ribosomal subunit protein eL37



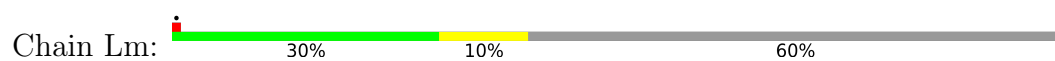
- Molecule 39: Large ribosomal subunit protein eL38



- Molecule 40: Large ribosomal subunit protein eL39-like



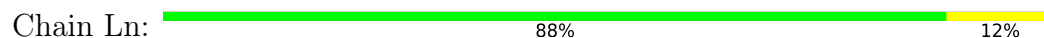
- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein



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

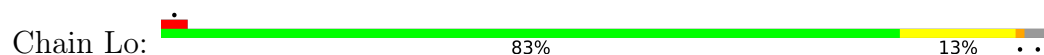
ILE GLN LYS SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY I77 I78 L82 L85 M94 I95 C99 Y100 P105 R111 K114 S24 K124 V127 LYS

- Molecule 42: Small ribosomal subunit protein eS32



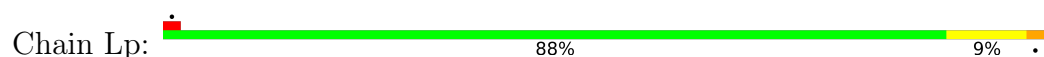
K1 K8 R12 R23 R25

- Molecule 43: Large ribosomal subunit protein eL42



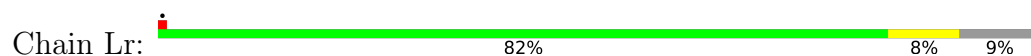
MET V2 V3 V4 Y26 D31 R39 I55 K59 I66 N76 M82 C88 K89 H90 L93 D96 R99 V103 I104 GLN PHE

- Molecule 44: Large ribosomal subunit protein eL43



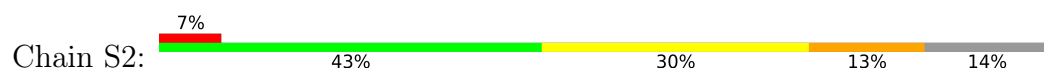
MET A2 S21 L22 V26 T38 T45 M61 T74 S75 L86 K87 E88 D91 Q92

- Molecule 45: Large ribosomal subunit protein eL28



MET S2 T27 E28 E52 K65 R71 T89 S92 M96 I97 R98 Y102 L118 V124 V125 VAL LYS ARG LYS THR ARG PRO THR LYS SER SER

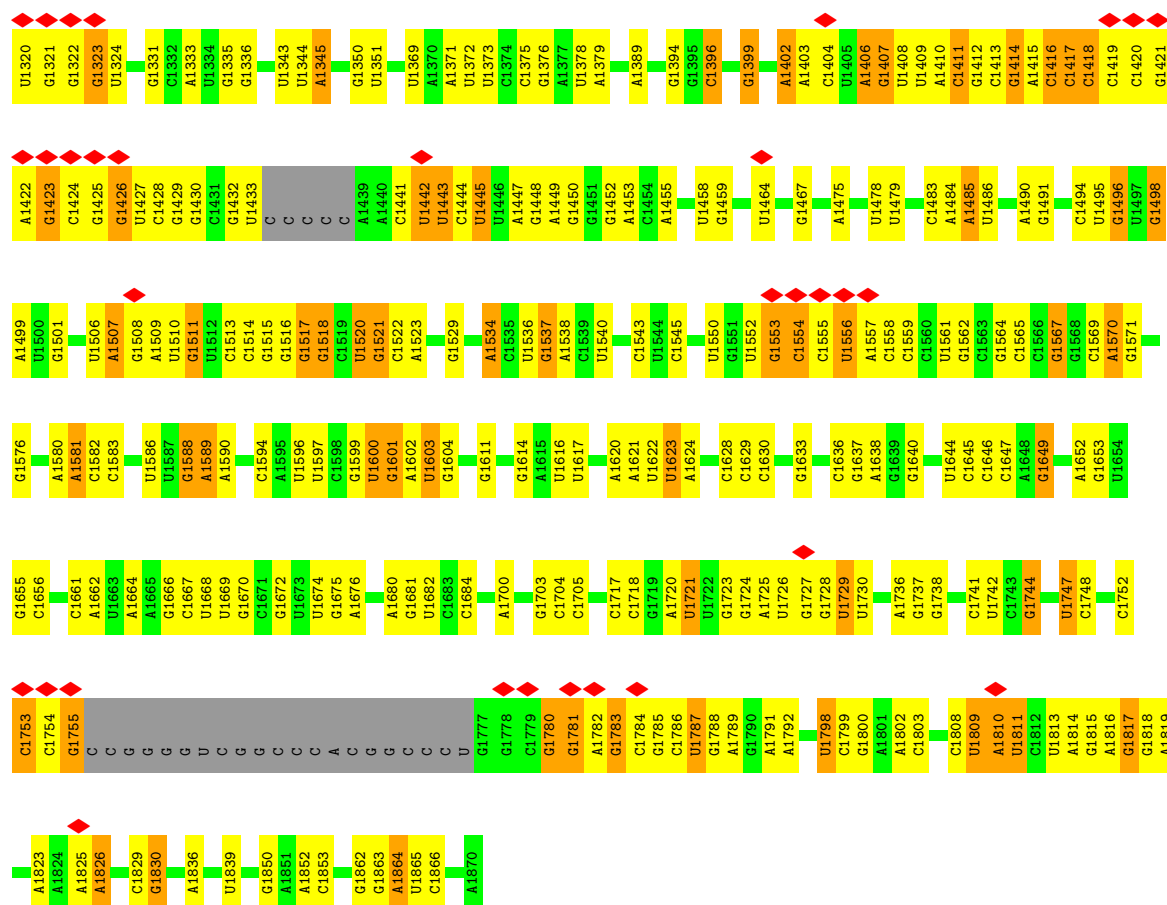
- Molecule 46: Mus musculus 18S ribosomal RNA



U1 A2 C3 G16 C17 G20 U26 A27 U28 G29 C30 U31 U32 G33 A39 A40 A41 A42 A43 U44 A45 A46 A47 C48 C49 U55 U56 U57 C58 U59 A60 A61 G62 U63 A64 C65 C66 C67 U68 C69 G70 G71 C72 C73 G74 G75 U76 A77 C78 A79 G80 U81 G82 A83 A84

A85 C86 U87 G88 C89 G90 A91 G94 G95 C96 U97 C98 A99 U100 A103 A104 U105 C106 A107 G108 A111 U112 G113 U114 G115 U116 C117 U121 G126 C127 U128 C129 G C C C C U A141 C142 U143 U144 G145 A147 U148 A149 A150 C151 U152





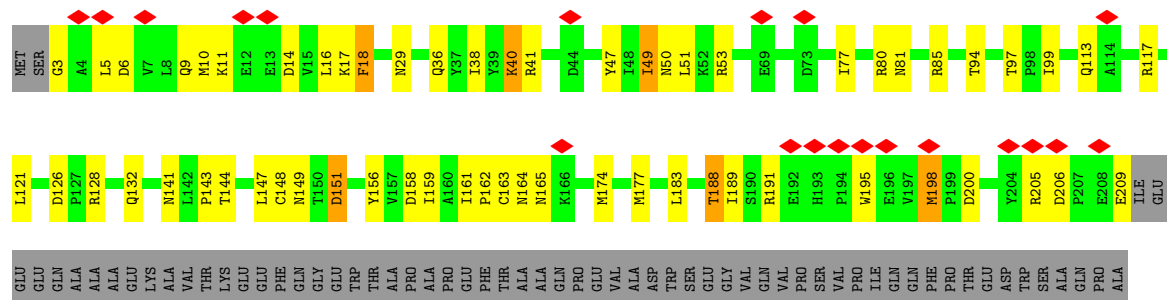
• Molecule 47: P tRNA

Chain S7: 39% 45% 16%

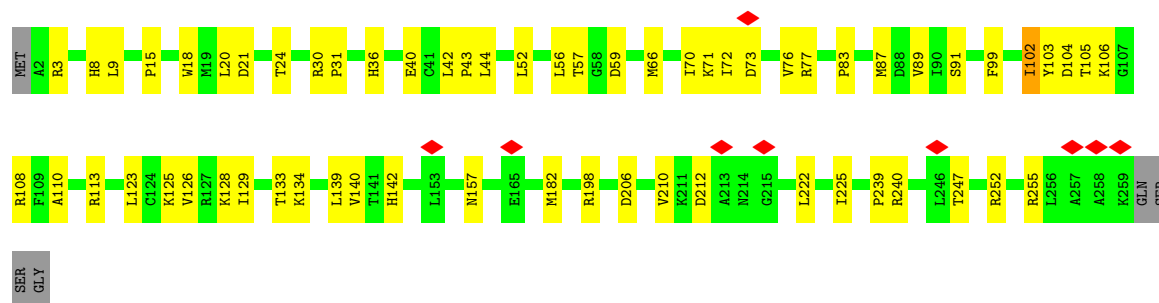


• Molecule 48: Small ribosomal subunit protein uS2

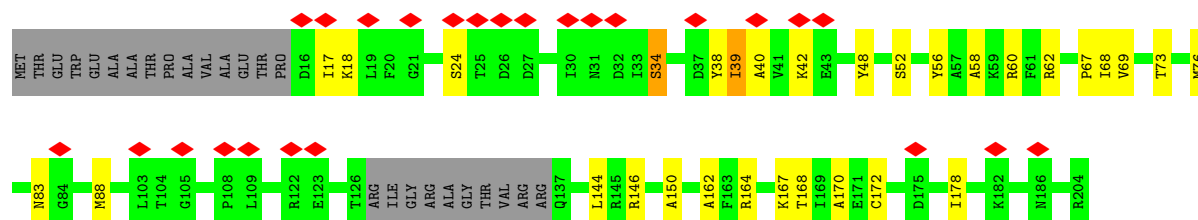
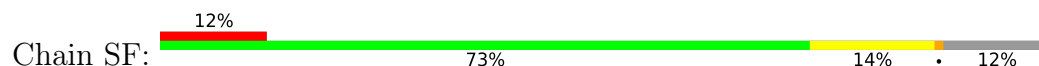
Chain SA: 7% 50% 18% 30%



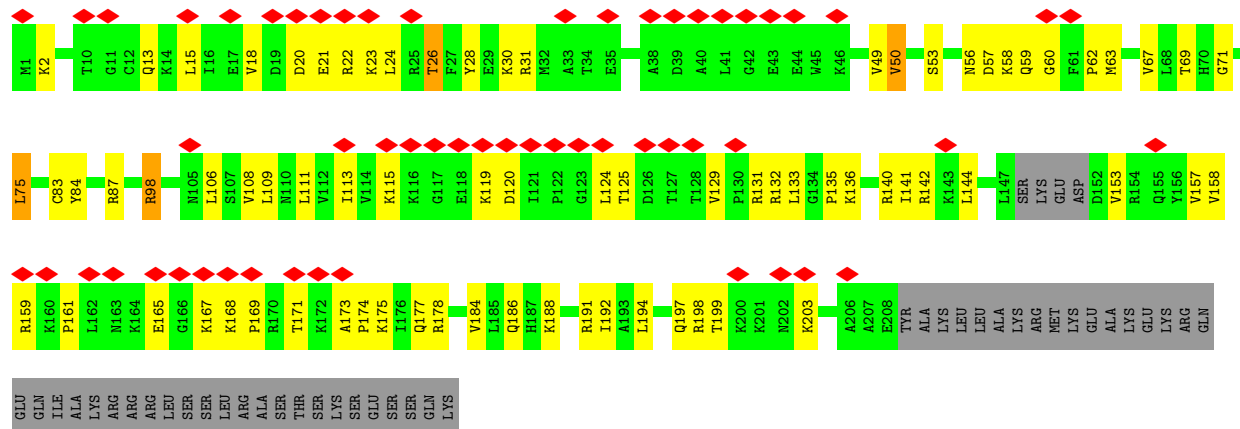
Chain SE:



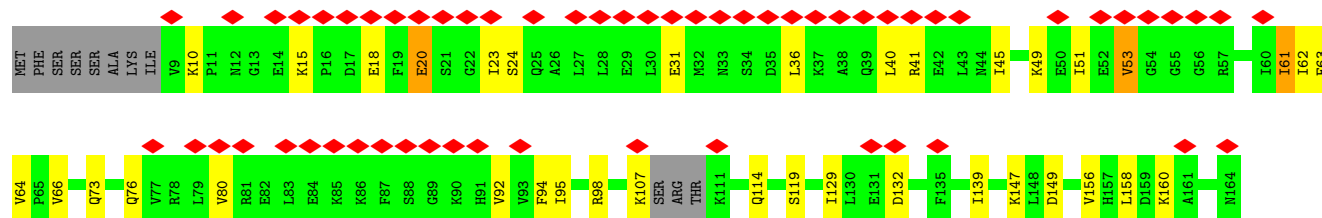
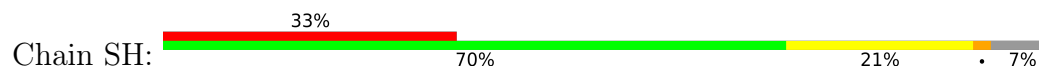
- Molecule 53: Small ribosomal subunit protein uS7



- Molecule 54: Small ribosomal subunit protein eS6

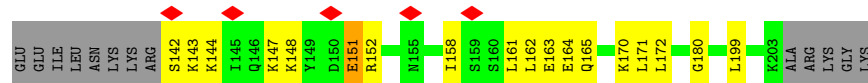


- Molecule 55: Small ribosomal subunit protein eS7

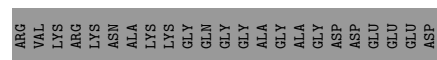
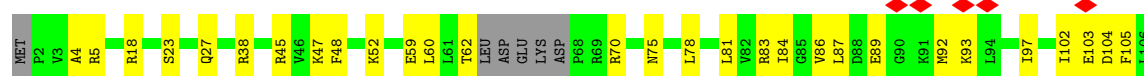




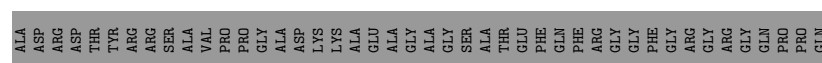
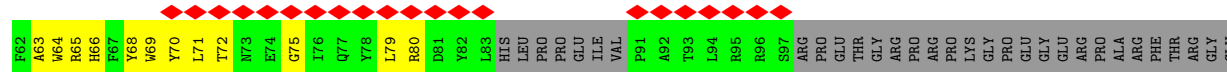
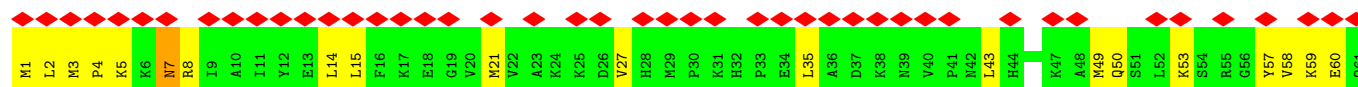
- Molecule 56: Small ribosomal subunit protein eS8



- Molecule 57: Small ribosomal subunit protein uS4



- Molecule 58: Small ribosomal subunit protein eS10



- Molecule 59: Small ribosomal subunit protein uS17





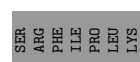
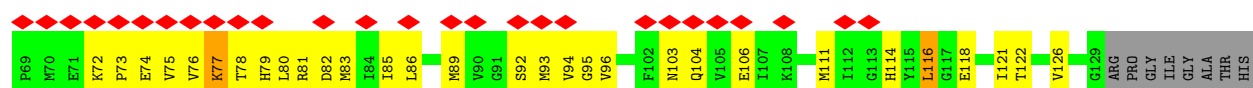
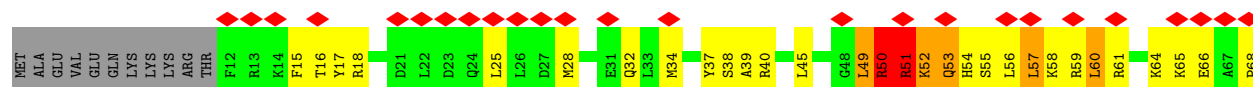
- Molecule 60: Small ribosomal subunit protein uS15



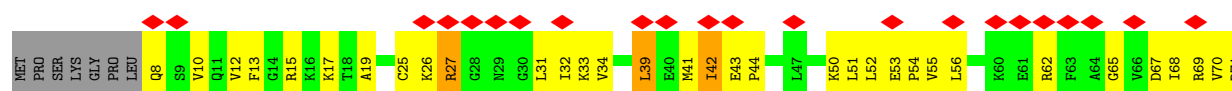
- Molecule 61: Small ribosomal subunit protein uS11



- Molecule 62: Small ribosomal subunit protein uS19

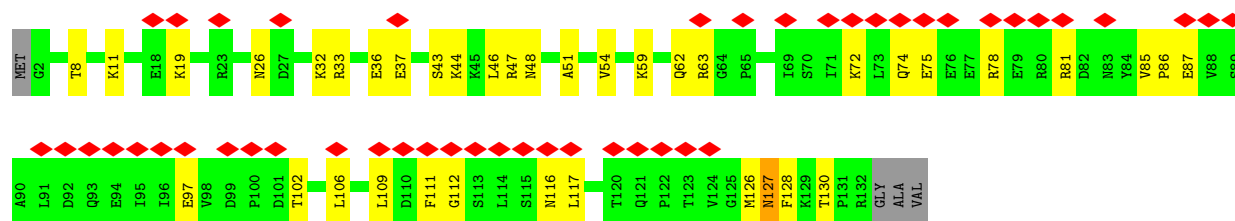


- Molecule 63: Small ribosomal subunit protein uS9

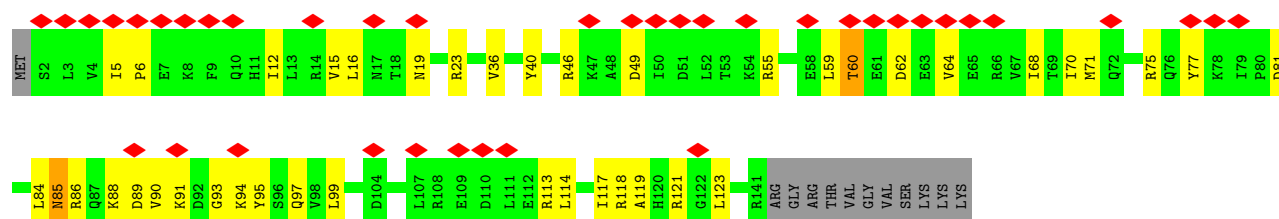


- Molecule 64: Small ribosomal subunit protein eS17

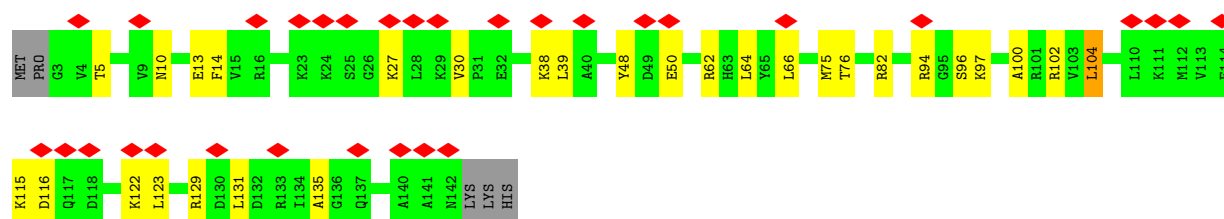
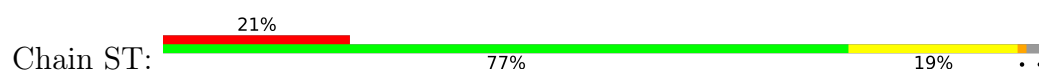




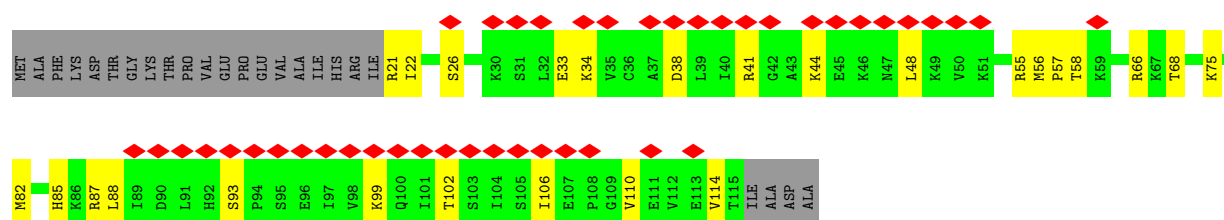
- Molecule 65: Small ribosomal subunit protein uS13



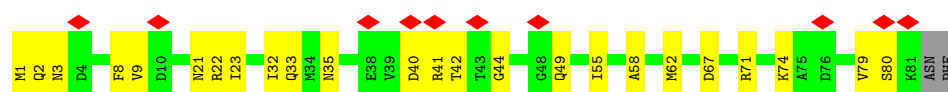
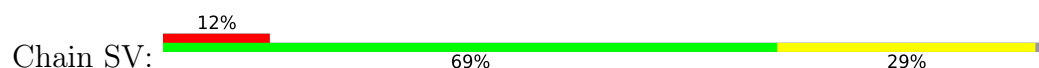
- Molecule 66: Small ribosomal subunit protein eS19




- Molecule 67: Small ribosomal subunit protein uS10



- Molecule 68: Small ribosomal subunit protein eS21




- Molecule 69: Small ribosomal subunit protein uS8

Chain SW:  82% 15% ..



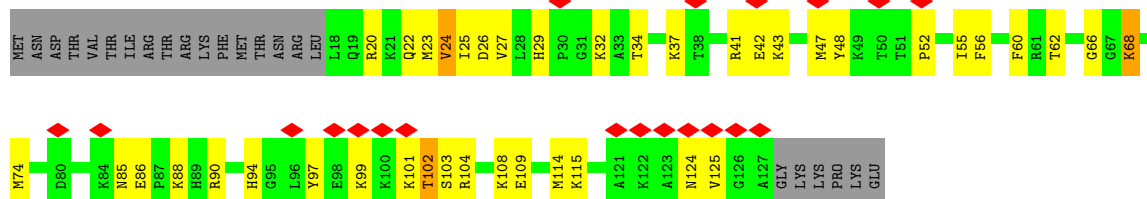
- Molecule 70: Small ribosomal subunit protein uS12

Chain SX:  78% 18% ..



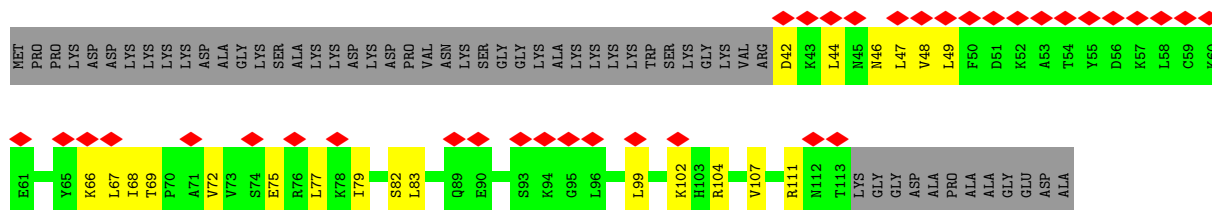
- Molecule 71: Small ribosomal subunit protein eS24

Chain SY:  15% 52% 29% . 17%



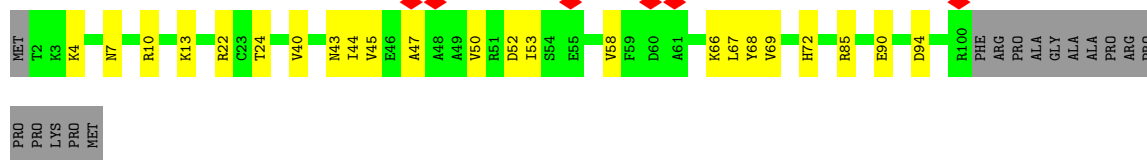
- Molecule 72: Small ribosomal subunit protein eS25

Chain SZ:  29% 41% 17% 42%




- Molecule 73: Small ribosomal subunit protein eS26

Chain Sa:  5% 66% 20% 14%

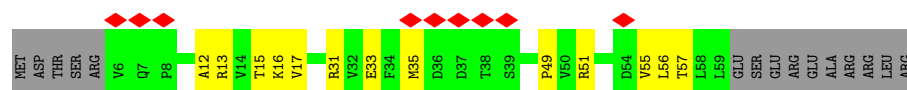


- Molecule 74: Small ribosomal subunit protein eS27

Chain Sb:  26% 74% 24% ..



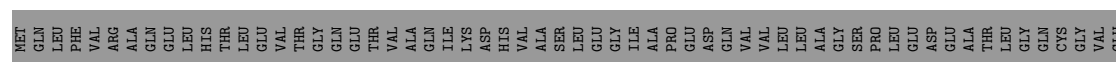
- Molecule 75: Small ribosomal subunit protein eS28



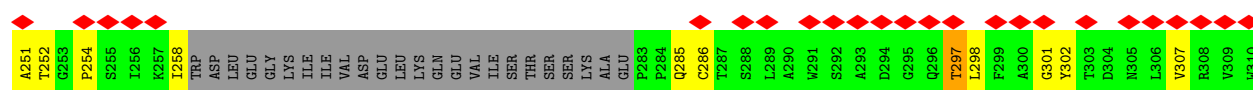
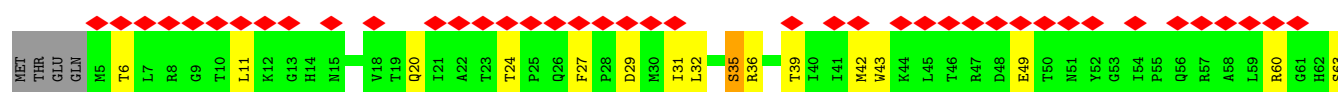
- Molecule 76: Small ribosomal subunit protein uS14



- Molecule 77: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

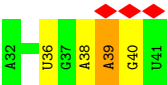


- Molecule 78: Small ribosomal subunit protein RACK1

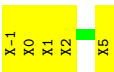
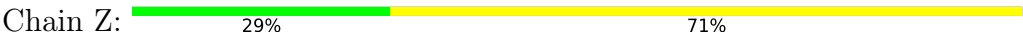


GLN
VAL
THR
ILE
GLY
THR
ARG

● Molecule 79: RNA (5'-R(P*AP*UP*CP*AP*UP*GP*AP*AP*GP*U)-3')



● Molecule 80: Nascent peptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38804	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	2.579	Depositor
Minimum map value	-0.891	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.38	Depositor
Map size (\AA)	616.0, 616.0, 616.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.25	0/81366	0.35	7/126899 (0.0%)
2	L7	0.21	0/2858	0.31	0/4455
3	L8	0.23	0/3584	0.32	0/5582
4	LA	0.24	0/1936	0.41	0/2596
5	LB	0.22	0/3269	0.41	0/4375
6	LC	0.23	0/2911	0.39	0/3907
7	LD	0.19	0/2435	0.39	0/3260
8	LE	0.20	0/1775	0.41	0/2381
9	LF	0.24	0/1805	0.38	1/2408 (0.0%)
10	LG	0.20	0/1880	0.36	0/2531
11	LH	0.20	0/1537	0.36	0/2065
12	LI	0.17	0/1669	0.33	0/2227
13	LJ	0.16	0/1363	0.39	0/1824
14	LL	0.22	0/1698	0.37	0/2274
15	LM	0.19	0/1146	0.36	0/1531
16	LN	0.24	0/1746	0.35	0/2338
17	LO	0.23	0/1670	0.43	1/2232 (0.0%)
18	LP	0.23	0/1277	0.37	0/1712
19	LQ	0.23	0/1539	0.34	0/2053
20	LR	0.21	0/1473	0.35	0/1947
21	LS	0.37	0/1491	0.65	2/2000 (0.1%)
22	LT	0.20	0/1335	0.31	0/1781
23	LU	0.18	0/831	0.44	0/1115
24	LV	0.21	0/987	0.38	0/1324
25	LW	0.22	0/532	0.35	0/708
26	LX	0.21	0/984	0.37	0/1323
27	LY	0.21	0/1119	0.34	0/1488
28	LZ	0.19	0/1130	0.36	0/1507
29	La	0.23	0/1193	0.35	0/1593
30	Lb	0.17	0/821	0.31	0/1082
31	Lc	0.24	0/742	0.36	0/996
32	Ld	0.23	0/911	0.38	1/1227 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.26	0/1071	0.41	0/1429
34	Lf	0.25	0/895	0.36	0/1198
35	Lg	0.22	0/883	0.35	0/1178
36	Lh	0.20	0/1023	0.30	0/1350
37	Li	0.20	0/843	0.42	0/1115
38	Lj	0.27	0/720	0.37	0/952
39	Lk	0.18	0/574	0.40	0/760
40	Ll	0.23	0/448	0.35	0/592
41	Lm	0.18	0/425	0.40	0/564
42	Ln	0.19	0/240	0.28	0/305
43	Lo	0.22	0/855	0.41	0/1128
44	Lp	0.23	0/718	0.37	0/953
45	Lr	0.22	0/1009	0.33	0/1353
46	S2	0.22	2/38525 (0.0%)	0.36	5/60033 (0.0%)
47	S7	0.16	0/1795	0.33	0/2798
48	SA	0.18	0/1673	0.42	0/2275
49	SB	0.19	0/1756	0.43	0/2350
50	SC	0.19	0/1701	0.39	0/2300
51	SD	0.17	0/1651	0.39	0/2219
52	SE	0.19	0/2092	0.42	0/2816
53	SF	0.14	0/1436	0.36	0/1930
54	SG	0.22	0/1666	0.47	0/2222
55	SH	0.18	0/1470	0.46	0/1968
56	SI	0.20	0/1526	0.40	0/2038
57	SJ	0.20	0/1178	0.48	0/1574
58	SK	0.15	0/780	0.41	0/1046
59	SL	0.22	0/1130	0.40	0/1514
60	SN	0.19	0/1232	0.32	0/1656
61	SO	0.19	0/1015	0.44	0/1361
62	SP	0.59	1/1000 (0.1%)	0.82	1/1335 (0.1%)
63	SQ	0.25	0/1126	0.51	0/1506
64	SR	0.18	0/1078	0.43	0/1447
65	SS	0.15	0/1175	0.35	0/1575
66	ST	0.16	0/1108	0.39	0/1486
67	SU	0.19	0/762	0.44	0/1023
68	SV	0.19	0/625	0.43	0/836
69	SW	0.20	0/1051	0.37	0/1406
70	SX	0.20	0/1097	0.43	0/1464
71	SY	0.37	0/907	0.73	1/1204 (0.1%)
72	SZ	0.38	0/580	0.66	1/780 (0.1%)
73	Sa	0.20	0/805	0.40	0/1079
74	Sb	0.19	0/665	0.43	0/891
75	Sc	0.21	0/418	0.65	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sd	0.18	0/466	0.39	0/618
77	Se	0.22	0/386	0.60	0/504
78	Sg	0.24	0/2199	0.54	1/2989 (0.0%)
79	Sx	0.15	0/239	0.33	0/370
All	All	0.23	3/217030 (0.0%)	0.38	21/318793 (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
55	SH	0	1
62	SP	0	1
66	ST	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	SP	50	ARG	C-O	6.14	1.31	1.24
46	S2	1817	G	P-O5'	5.44	1.68	1.59
46	S2	1817	G	O5'-C5'	5.35	1.50	1.42

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	1817	G	C2'-C3'-O3'	-11.26	96.80	113.70
21	LS	155	PRO	N-CA-C	8.47	125.58	113.47
46	S2	315	U	C4'-C3'-O3'	8.20	121.71	109.40
46	S2	56	G	C1'-O4'-C4'	-7.57	102.33	109.90
1	L5	667	G	C3'-C2'-C1'	-7.53	93.97	101.50
1	L5	458	C	C2'-C3'-O3'	7.36	124.73	113.70
1	L5	4553	G	C1'-O4'-C4'	-7.35	102.35	109.70
1	L5	4549	G	C3'-C2'-C1'	-6.41	95.09	101.50
1	L5	4549	G	C4'-C3'-O3'	5.89	118.24	109.40
62	SP	68	PRO	N-CA-C	-5.87	104.84	110.47
1	L5	4549	G	N9-C1'-C2'	5.85	122.78	114.00
78	Sg	94	THR	CB-CA-C	5.76	120.07	111.89
21	LS	172	PRO	N-CA-C	5.72	120.27	111.57
1	L5	453	U	P-O3'-C3'	5.56	128.53	120.20
71	SY	48	TYR	CB-CA-C	5.47	120.23	109.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	55	U	C2'-C3'-O3'	5.40	117.60	109.50
46	S2	1817	G	C4'-C3'-O3'	5.35	121.03	113.00
9	LF	120	ILE	N-CA-C	5.31	111.89	106.21
17	LO	186	GLU	CA-CB-CG	5.24	124.58	114.10
32	Ld	99	PRO	CA-N-CD	-5.16	104.78	112.00
72	SZ	75	GLU	N-CA-C	-5.11	105.88	112.68

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
55	SH	15	LYS	Peptide
62	SP	49	LEU	Mainchain
66	ST	38	LYS	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	72739	0	36729	452	0
2	L7	2558	0	1296	15	0
3	L8	3210	0	1630	25	0
4	LA	1898	0	1993	20	0
5	LB	3202	0	3347	34	0
6	LC	2857	0	3030	32	0
7	LD	2389	0	2420	38	0
8	LE	1743	0	1880	24	0
9	LF	1771	0	1886	16	0
10	LG	1848	0	1981	24	0
11	LH	1519	0	1603	22	0
12	LI	1631	0	1682	18	0
13	LJ	1340	0	1377	26	0
14	LL	1667	0	1771	21	0
15	LM	1125	0	1202	11	0
16	LN	1701	0	1749	20	0
17	LO	1640	0	1792	18	0
18	LP	1251	0	1282	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	LQ	1515	0	1639	18	0
20	LR	1457	0	1601	19	0
21	LS	1451	0	1488	22	0
22	LT	1307	0	1380	19	0
23	LU	817	0	839	21	0
24	LV	973	0	1034	18	0
25	LW	519	0	533	8	0
26	LX	967	0	1040	8	0
27	LY	1102	0	1189	9	0
28	LZ	1107	0	1182	11	0
29	La	1164	0	1213	9	0
30	Lb	807	0	875	9	0
31	Lc	732	0	769	11	0
32	Ld	896	0	941	5	0
33	Le	1053	0	1147	11	0
34	Lf	876	0	912	9	0
35	Lg	873	0	961	3	0
36	Lh	1015	0	1156	14	0
37	Li	832	0	917	12	0
38	Lj	705	0	737	7	0
39	Lk	568	0	635	12	0
40	Ll	438	0	474	3	0
41	Lm	419	0	452	9	0
42	Ln	239	0	289	2	0
43	Lo	842	0	916	9	0
44	Lp	708	0	756	7	0
45	Lr	994	0	1057	7	0
46	S2	34451	0	17399	493	0
47	S7	1604	0	816	23	0
48	SA	1636	0	1641	39	0
49	SB	1729	0	1803	26	0
50	SC	1665	0	1753	27	0
51	SD	1626	0	1714	45	0
52	SE	2050	0	2156	41	0
53	SF	1416	0	1458	23	0
54	SG	1645	0	1780	55	0
55	SH	1449	0	1539	25	0
56	SI	1499	0	1561	32	0
57	SJ	1162	0	1252	34	0
58	SK	760	0	783	22	0
59	SL	1110	0	1165	18	0
60	SN	1208	0	1294	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	SO	1002	0	1023	20	0
62	SP	981	0	1026	45	0
63	SQ	1109	0	1174	35	0
64	SR	1064	0	1118	28	0
65	SS	1157	0	1213	35	0
66	ST	1090	0	1116	21	0
67	SU	753	0	815	17	0
68	SV	619	0	620	22	0
69	SW	1034	0	1080	19	0
70	SX	1080	0	1147	19	0
71	SY	891	0	948	29	0
72	SZ	574	0	627	10	0
73	Sa	792	0	845	17	0
74	Sb	651	0	672	13	0
75	Sc	416	0	445	12	0
76	Sd	455	0	449	15	0
77	Se	384	0	422	12	0
78	Sg	2148	0	2108	68	0
79	Sx	214	0	108	3	0
80	Z	34	0	11	7	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	202023	0	149863	2178	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 (2178) 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	2.00	1.09
46:S2:313:G:N1	46:S2:337:A:C2	2.21	1.07
46:S2:313:G:N1	46:S2:337:A:H2	1.52	1.06
46:S2:70:G:N2	46:S2:79:A:H62	1.55	1.02
46:S2:70:G:H21	46:S2:79:A:N6	1.57	1.01
78:Sg:157:SER:HG	78:Sg:164:ILE:N	1.57	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1288:A:H62	46:S2:1313:G:N2	1.61	0.98
47:S7:76:A:O3'	80:Z:5:UNK:O	1.83	0.97
5:LB:145:GLN:HA	5:LB:148:LYS:HZ3	1.29	0.95
46:S2:1288:A:N6	46:S2:1313:G:H21	1.68	0.92
47:S7:76:A:HO3'	80:Z:5:UNK:C	1.79	0.89
46:S2:116:U:H3	46:S2:348:G:H1	1.17	0.89
46:S2:1288:A:H62	46:S2:1313:G:H21	0.94	0.89
46:S2:483:G:N1	46:S2:485:A:N7	2.20	0.88
1:L5:508:G:H1	1:L5:661:U:H3	1.20	0.88
74:Sb:78:SER:HB3	74:Sb:80:ARG:HH12	1.39	0.87
5:LB:107:ALA:HB2	5:LB:201:LEU:HD22	1.57	0.86
1:L5:1009:C:H42	1:L5:1017:A:H61	1.18	0.86
62:SP:60:LEU:HD11	62:SP:76:VAL:HG13	1.55	0.85
52:SE:9:LEU:HB2	52:SE:30:ARG:HB2	1.59	0.85
46:S2:1616:U:O4	62:SP:40:ARG:NH1	2.10	0.85
64:SR:106:LEU:HB3	64:SR:112:GLY:HA3	1.60	0.83
46:S2:62:G:HO2'	46:S2:172:U:H3	1.26	0.83
46:S2:97:U:H3	46:S2:433:G:H1	1.23	0.83
46:S2:156:G:N3	54:SG:59:GLN:N	2.27	0.83
46:S2:1682:U:O2	46:S2:1684:C:N4	2.12	0.83
51:SD:194:PRO:HG3	51:SD:198:ILE:HD12	1.61	0.82
46:S2:94:G:H21	46:S2:475:G:H5'	1.44	0.82
12:LI:80:CYS:SG	12:LI:144:ASN:ND2	2.51	0.82
46:S2:536:G:N7	46:S2:538:C:N4	2.29	0.81
73:Sa:44:ILE:HG22	73:Sa:67:LEU:HG	1.63	0.81
46:S2:70:G:H21	46:S2:79:A:H62	0.83	0.78
46:S2:554:U:H2'	46:S2:555:A:H2'	1.63	0.78
1:L5:3337:U:OP1	4:LA:54:ARG:NH2	2.15	0.78
46:S2:879:G:H1	46:S2:909:A:H61	1.31	0.78
23:LU:65:ARG:HE	23:LU:67:LYS:H	1.31	0.78
46:S2:1287:G:C2	46:S2:1314:A:N6	2.51	0.78
75:Sc:15:THR:HG22	75:Sc:16:LYS:H	1.48	0.78
55:SH:160:LYS:NZ	55:SH:190:PRO:O	2.17	0.78
21:LS:21:LYS:NZ	21:LS:22:CYS:SG	2.57	0.78
62:SP:76:VAL:HB	62:SP:94:VAL:HG22	1.65	0.78
1:L5:3374:A:OP2	1:L5:3392:G:N2	2.17	0.78
23:LU:75:GLU:N	23:LU:75:GLU:OE1	2.17	0.78
46:S2:1290:U:H1'	46:S2:1312:C:H41	1.47	0.78
1:L5:1013:C:N3	7:LD:282:GLN:NE2	2.32	0.77
1:L5:3417:A:N7	46:S2:1826:A:N6	2.30	0.77
46:S2:1726:U:O2	46:S2:1810:A:N6	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:SB:107:ARG:NH2	61:SO:133:THR:O	2.18	0.77
24:LV:43:LYS:HG3	24:LV:60:MET:HG2	1.67	0.77
46:S2:498:C:H5''	52:SE:30:ARG:HB3	1.66	0.77
69:SW:2:VAL:HG12	69:SW:3:ARG:HG3	1.66	0.77
46:S2:833:G:H1	46:S2:842:G:H22	1.30	0.76
46:S2:1287:G:N2	46:S2:1314:A:N6	2.33	0.76
46:S2:1288:A:O2'	46:S2:1316:U:O2	2.02	0.76
68:SV:49:GLN:OE1	68:SV:49:GLN:N	2.18	0.76
5:LB:224:LYS:HG3	5:LB:340:THR:HG22	1.65	0.76
64:SR:97:GLU:OE1	64:SR:97:GLU:N	2.19	0.76
6:LC:101:MET:HE3	6:LC:104:PRO:HA	1.66	0.76
46:S2:1753:C:N4	46:S2:1755:G:N7	2.34	0.76
1:L5:209:U:OP1	27:LY:63:LYS:NZ	2.19	0.75
16:LN:68:ARG:NH1	16:LN:124:ASP:O	2.17	0.75
46:S2:313:G:O6	46:S2:337:A:N1	2.20	0.75
63:SQ:32:ILE:HD13	63:SQ:39:LEU:HB2	1.69	0.75
48:SA:198:MET:HE2	64:SR:85:VAL:HG22	1.69	0.74
52:SE:31:PRO:HG3	52:SE:43:PRO:HG3	1.69	0.74
46:S2:1744:G:H21	46:S2:1792:A:H62	1.34	0.74
1:L5:2513:G:H21	1:L5:2518:A:H62	1.35	0.74
65:SS:84:LEU:HD22	65:SS:97:GLN:HG2	1.69	0.74
50:SC:80:GLU:N	50:SC:80:GLU:OE2	2.19	0.74
1:L5:2328:G:OP2	28:LZ:67:LYS:NZ	2.21	0.74
46:S2:65:C:O2'	46:S2:67:C:OP1	2.05	0.73
16:LN:158:HIS:HB3	16:LN:161:MET:HG3	1.70	0.73
74:Sb:74:THR:OG1	74:Sb:77:CYS:SG	2.44	0.73
7:LD:223:PHE:HB3	7:LD:226:TYR:HB2	1.69	0.73
1:L5:766:G:H22	1:L5:805:C:H42	1.32	0.73
20:LR:31:GLU:N	20:LR:31:GLU:OE2	2.22	0.73
3:L8:58:G:N7	38:Lj:63:ARG:NH2	2.36	0.72
22:LT:146:LYS:NZ	22:LT:147:GLU:O	2.22	0.72
46:S2:1155:U:OP2	50:SC:187:ARG:NH2	2.22	0.72
1:L5:3408:G:H21	1:L5:3432:A:H8	1.37	0.72
48:SA:143:PRO:HG3	68:SV:32:ILE:HD11	1.71	0.72
17:LO:166:MET:SD	17:LO:169:ARG:NH2	2.60	0.72
46:S2:565:A:O2'	46:S2:566:G:O5'	2.07	0.72
61:SO:84:ARG:NH1	61:SO:87:GLU:OE1	2.22	0.72
1:L5:3787:U:H3	1:L5:3801:G:H1	1.36	0.72
48:SA:205:ARG:NH2	48:SA:206:ASP:OD1	2.23	0.72
63:SQ:12:VAL:HG21	63:SQ:91:ALA:HA	1.72	0.71
68:SV:74:LYS:HG2	68:SV:79:VAL:HG21	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LF:127:VAL:HG13	9:LF:158:VAL:HG12	1.70	0.71
46:S2:158:A:H2'	46:S2:159:A:C8	2.25	0.71
46:S2:313:G:H1	46:S2:337:A:H2	0.81	0.71
46:S2:177:G:H21	46:S2:178:C:H41	1.36	0.71
46:S2:61:A:N6	46:S2:503:C:OP2	2.24	0.71
1:L5:1636:G:N2	1:L5:1638:G:O4'	2.24	0.71
79:Sx:39:A:H2'	79:Sx:40:G:C8	2.26	0.71
1:L5:511:G:O2'	1:L5:513:U:OP2	2.07	0.70
46:S2:497:C:O2'	46:S2:498:C:OP1	2.07	0.70
60:SN:99:ARG:NH1	60:SN:119:GLU:OE1	2.23	0.70
62:SP:73:PRO:HB2	62:SP:93:MET:HE1	1.73	0.70
63:SQ:31:LEU:HD11	63:SQ:33:LYS:HD2	1.73	0.70
46:S2:879:G:N2	46:S2:909:A:N1	2.37	0.70
59:SL:97:ARG:O	59:SL:97:ARG:NH1	2.21	0.70
1:L5:676:C:H5'	6:LC:6:PRO:HB3	1.73	0.70
46:S2:156:G:N7	54:SG:56:ASN:ND2	2.36	0.70
71:SY:29:HIS:HB2	71:SY:32:LYS:HB2	1.72	0.70
76:Sd:17:GLY:O	76:Sd:27:ARG:NH2	2.25	0.70
1:L5:2019:G:OP2	45:Lr:98:ARG:NH2	2.24	0.70
46:S2:845:U:O2'	46:S2:846:G:OP2	2.08	0.70
63:SQ:34:VAL:HG12	63:SQ:70:VAL:HB	1.73	0.70
46:S2:1423:G:H1'	46:S2:1425:G:H1'	1.73	0.69
1:L5:1733:U:OP2	17:LO:49:ARG:NH1	2.23	0.69
14:LL:107:THR:HG22	37:Li:20:ASN:HB2	1.73	0.69
46:S2:353:U:O2	59:SL:71:ARG:NH1	2.25	0.69
57:SJ:143:ASN:O	57:SJ:144:ILE:HD13	1.93	0.69
48:SA:128:ARG:NH2	48:SA:151:ASP:O	2.25	0.69
78:Sg:64:HIS:HB3	78:Sg:83:TRP:HB2	1.74	0.69
46:S2:64:A:OP2	46:S2:83:A:N6	2.26	0.69
46:S2:156:G:N3	54:SG:60:GLY:N	2.40	0.69
46:S2:635:A:OP1	77:Se:87:ARG:NH1	2.26	0.69
1:L5:3326:G:H21	1:L5:3329:G:N2	1.91	0.69
62:SP:80:LEU:HD23	62:SP:82:ASP:H	1.58	0.69
78:Sg:220:ASP:HB2	78:Sg:224:GLY:H	1.57	0.69
6:LC:33:ARG:NH2	19:LQ:22:ASP:OD2	2.26	0.68
8:LE:285:LEU:HA	8:LE:289:MET:HE2	1.75	0.68
46:S2:1415:A:N6	46:S2:1416:C:N3	2.42	0.68
47:S7:35:A:H62	79:Sx:36:U:H3	1.40	0.68
55:SH:10:LYS:HD2	55:SH:45:ILE:HG12	1.74	0.68
1:L5:1470:U:OP2	29:La:26:ARG:NH2	2.25	0.68
50:SC:268:GLU:OE2	50:SC:268:GLU:N	2.21	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LM:96:ASP:OD2	15:LM:100:ARG:NH2	2.26	0.68
1:L5:1562:G:H22	1:L5:1576:U:H3	1.40	0.68
1:L5:2237:G:N2	1:L5:2238:G:O6	2.26	0.68
41:Lm:77:ILE:HG22	41:Lm:78:ILE:HG13	1.75	0.68
1:L5:461:G:H2'	1:L5:462:A:C8	2.29	0.68
7:LD:108:ARG:NH1	7:LD:251:PRO:O	2.25	0.68
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.76	0.68
46:S2:464:C:O2'	46:S2:466:A:N7	2.24	0.68
48:SA:14:ASP:HA	48:SA:17:LYS:HZ3	1.58	0.68
1:L5:3264:U:OP1	20:LR:88:ARG:NH1	2.27	0.68
46:S2:95:G:N2	46:S2:435:G:H22	1.91	0.68
78:Sg:217:MET:HA	78:Sg:217:MET:HE3	1.75	0.68
46:S2:434:A:OP1	56:SI:25:ARG:NH2	2.27	0.68
35:Lg:85:LYS:HD3	35:Lg:85:LYS:N	2.09	0.68
39:Lk:51:GLU:OE2	39:Lk:51:GLU:N	2.22	0.67
1:L5:3298:U:OP2	1:L5:3303:A:N6	2.27	0.67
1:L5:3326:G:H21	1:L5:3329:G:H21	1.40	0.67
46:S2:1649:G:N2	46:S2:1676:A:OP2	2.26	0.67
72:SZ:48:VAL:HG13	72:SZ:83:LEU:HB2	1.74	0.67
54:SG:21:GLU:HG3	54:SG:22:ARG:HH12	1.60	0.67
37:Li:58:MET:HE1	37:Li:90:LEU:HD22	1.75	0.67
9:LF:120:ILE:HG21	19:LQ:4:ASP:HB2	1.76	0.67
39:Lk:29:LYS:H	39:Lk:29:LYS:HD3	1.58	0.67
46:S2:1680:A:OP1	53:SF:60:ARG:NH2	2.26	0.67
10:LG:162:ASP:HB2	10:LG:163:PRO:HD3	1.76	0.67
5:LB:215:GLU:OE2	5:LB:349:LYS:NZ	2.27	0.67
1:L5:176:G:OP1	36:Lh:101:LYS:NZ	2.28	0.67
48:SA:188:THR:HG22	48:SA:189:ILE:HG13	1.76	0.67
35:Lg:41:ALA:O	35:Lg:52:ARG:NH1	2.26	0.66
51:SD:16:ILE:HD13	76:Sd:22:ARG:HH12	1.60	0.66
78:Sg:69:VAL:HG12	78:Sg:80:SER:HB3	1.75	0.66
46:S2:1402:A:N6	46:S2:1442:U:O4	2.27	0.66
46:S2:1416:C:O2'	46:S2:1417:C:H5'	1.95	0.66
49:SB:189:ILE:HB	49:SB:190:PRO:HD3	1.77	0.66
51:SD:6:SER:HB2	51:SD:9:ARG:HG3	1.77	0.66
48:SA:209:GLU:N	48:SA:209:GLU:OE1	2.28	0.66
1:L5:294:A:OP2	43:Lo:39:ARG:NH1	2.29	0.66
46:S2:60:A:H3'	46:S2:61:A:H5'	1.77	0.66
46:S2:1620:A:O2'	62:SP:82:ASP:OD2	2.13	0.66
1:L5:385:A:OP2	27:LY:89:LYS:NZ	2.28	0.66
18:LP:122:ALA:HB3	18:LP:143:PRO:HB2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:75:G:H1	54:SG:171:THR:H	1.44	0.66
19:LQ:94:GLU:N	19:LQ:94:GLU:OE1	2.29	0.66
46:S2:156:G:C2	54:SG:57:ASP:HB3	2.31	0.66
60:SN:35:GLU:N	60:SN:35:GLU:OE2	2.29	0.66
1:L5:3346:G:O2'	1:L5:3475:U:OP2	2.14	0.65
8:LE:149:ARG:NH2	8:LE:199:GLN:O	2.29	0.65
37:Li:23:LYS:HE2	37:Li:23:LYS:HA	1.78	0.65
37:Li:23:LYS:HD3	37:Li:24:PRO:HD2	1.77	0.65
46:S2:820:G:H1	46:S2:830:C:H5	1.43	0.65
46:S2:914:A:N6	55:SH:98:ARG:O	2.27	0.65
4:LA:109:GLU:OE1	4:LA:109:GLU:N	2.29	0.65
23:LU:48:LYS:HG2	23:LU:53:ALA:HB2	1.78	0.65
63:SQ:89:SER:HB3	63:SQ:112:LEU:HD13	1.78	0.65
1:L5:223:G:N3	6:LC:223:ASN:ND2	2.43	0.65
1:L5:2327:A:H62	1:L5:2515:U:H5	1.44	0.65
1:L5:4323:C:O2'	1:L5:4325:A:OP2	2.13	0.65
16:LN:104:GLU:HA	16:LN:160:GLU:HG3	1.79	0.65
1:L5:1003:G:O6	1:L5:1024:C:N4	2.30	0.65
53:SF:58:ALA:HB3	53:SF:62:ARG:HE	1.61	0.65
1:L5:858:A:H3'	1:L5:870:G:H22	1.61	0.65
12:LI:38:ARG:HD3	12:LI:83:ASP:HB3	1.78	0.65
48:SA:40:LYS:HD3	48:SA:41:ARG:H	1.62	0.65
70:SX:54:LYS:NZ	70:SX:94:ILE:O	2.23	0.65
1:L5:1027:G:H2'	1:L5:1028:G:C5	2.32	0.65
46:S2:64:A:O2'	46:S2:66:G:OP2	2.15	0.65
46:S2:1594:C:OP2	72:SZ:104:ARG:NH2	2.30	0.65
46:S2:1754:C:OP2	46:S2:1783:G:N2	2.29	0.65
78:Sg:87:LEU:HB2	78:Sg:101:PHE:HB2	1.79	0.65
1:L5:3439:C:OP1	42:Ln:23:ARG:NH2	2.29	0.64
39:Lk:23:VAL:HG23	39:Lk:64:LEU:HD11	1.78	0.64
46:S2:627:G:H5'	46:S2:628:U:H5'	1.79	0.64
46:S2:1278:C:N4	46:S2:1323:G:H8	1.95	0.64
13:LJ:65:ASN:HB2	43:Lo:103:VAL:HA	1.79	0.64
46:S2:641:A:H2'	46:S2:642:A:C8	2.33	0.64
46:S2:838:A:H61	71:SY:26:ASP:H	1.44	0.64
1:L5:4528:U:OP1	15:LM:117:LYS:NZ	2.29	0.64
1:L5:4664:A:H2	1:L5:4681:G:H21	1.46	0.64
46:S2:501:A:H3'	46:S2:502:C:H6	1.63	0.64
67:SU:21:ARG:N	67:SU:21:ARG:HD3	2.13	0.64
46:S2:1093:G:H4'	69:SW:2:VAL:HG13	1.78	0.64
5:LB:216:MET:HE2	5:LB:283:LYS:HD3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1233:U:H2'	46:S2:1234:G:H8	1.62	0.64
54:SG:62:PRO:HG2	54:SG:83:CYS:HB3	1.79	0.64
8:LE:209:VAL:HG23	8:LE:211:ILE:HD11	1.80	0.64
23:LU:63:ILE:HG13	23:LU:72:VAL:HG22	1.80	0.64
3:L8:1:C:O5'	3:L8:2:G:N2	2.31	0.63
46:S2:58:C:H5''	46:S2:501:A:N7	2.12	0.63
49:SB:89:GLU:OE2	49:SB:99:ASN:HB3	1.97	0.63
58:SK:65:ARG:NH1	76:Sd:21:CYS:O	2.31	0.63
38:Lj:14:LYS:NZ	40:Ll:51:LEU:OXT	2.31	0.63
65:SS:75:ARG:HH22	65:SS:95:TYR:HB2	1.62	0.63
65:SS:84:LEU:HA	65:SS:97:GLN:HE21	1.64	0.63
2:L7:7:G:OP1	7:LD:33:ARG:NH1	2.32	0.63
36:Lh:63:GLN:O	36:Lh:67:GLU:HG2	1.99	0.63
56:SI:144:LYS:HA	56:SI:147:LYS:HE3	1.81	0.63
1:L5:230:G:OP1	27:LY:15:ARG:NH1	2.31	0.63
1:L5:441:G:OP1	34:Lf:68:ARG:NH1	2.31	0.63
15:LM:123:ILE:HD11	17:LO:189:ILE:HD13	1.80	0.63
48:SA:191:ARG:NH2	68:SV:44:GLY:O	2.31	0.63
63:SQ:32:ILE:HD12	63:SQ:32:ILE:O	1.98	0.63
70:SX:61:GLN:HG2	70:SX:62:PRO:HD2	1.79	0.63
1:L5:4560:C:H2'	1:L5:4561:G:C8	2.33	0.63
22:LT:94:GLU:N	22:LT:94:GLU:OE1	2.31	0.63
58:SK:63:ALA:HB2	58:SK:68:TYR:HE1	1.62	0.63
66:ST:116:ASP:HB3	66:ST:122:LYS:HB2	1.81	0.63
1:L5:2214:G:HO2'	1:L5:3329:G:H8	1.47	0.63
46:S2:890:U:O4	46:S2:899:U:N3	2.31	0.63
57:SJ:47:LYS:HG3	57:SJ:102:ILE:HD11	1.81	0.63
1:L5:1557:U:H3	1:L5:1579:A:H61	1.44	0.63
46:S2:503:C:H41	52:SE:66:MET:HE1	1.63	0.63
1:L5:3904:A:H4'	1:L5:3905:C:OP1	1.99	0.63
52:SE:206:ASP:HB2	52:SE:222:LEU:HD12	1.79	0.63
59:SL:103:GLU:OE2	70:SX:11:ARG:NH1	2.32	0.63
2:L7:23:A:N3	2:L7:118:C:O2'	2.30	0.62
53:SF:39:ILE:O	53:SF:42:LYS:NZ	2.32	0.62
62:SP:80:LEU:HD23	62:SP:81:ARG:H	1.64	0.62
1:L5:2599:A:H61	1:L5:3500:C:H42	1.46	0.62
8:LE:169:ARG:NH1	8:LE:281:SER:OG	2.32	0.62
46:S2:515:U:H2'	46:S2:516:G:C8	2.35	0.62
46:S2:560:G:O2'	46:S2:561:A:O5'	2.17	0.62
1:L5:766:G:H22	1:L5:805:C:N4	1.96	0.62
24:LV:71:GLU:O	24:LV:75:LYS:NZ	2.26	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:219:A:H3'	46:S2:220:U:H4'	1.81	0.62
62:SP:75:VAL:HB	62:SP:77:LYS:HE3	1.80	0.62
1:L5:407:A:O2'	1:L5:410:G:OP2	2.17	0.62
54:SG:31:ARG:H	54:SG:31:ARG:HD2	1.62	0.62
32:Ld:59:THR:HG21	32:Ld:103:TYR:HA	1.81	0.62
46:S2:321:G:O6	54:SG:186:GLN:NE2	2.32	0.62
46:S2:488:U:H4'	46:S2:490:A:C8	2.35	0.62
46:S2:1262:C:O2	76:Sd:10:HIS:NE2	2.33	0.62
73:Sa:7:ASN:ND2	73:Sa:10:ARG:O	2.33	0.62
1:L5:3716:G:H2'	1:L5:3717:U:C6	2.34	0.62
46:S2:313:G:C6	46:S2:337:A:N1	2.67	0.62
46:S2:833:G:H1	46:S2:842:G:N2	1.97	0.62
52:SE:57:THR:HG22	52:SE:59:ASP:H	1.65	0.62
62:SP:85:ILE:HA	62:SP:89:MET:HE2	1.81	0.62
54:SG:20:ASP:OD2	54:SG:23:LYS:NZ	2.32	0.62
19:LQ:154:LYS:HE3	19:LQ:158:THR:HG21	1.83	0.61
21:LS:94:TYR:OH	21:LS:96:GLU:OE2	2.13	0.61
13:LJ:55:TYR:HA	13:LJ:64:ARG:HG2	1.82	0.61
22:LT:88:ARG:NH1	30:Lb:33:LYS:O	2.33	0.61
46:S2:1227:G:N1	46:S2:1640:G:OP2	2.32	0.61
46:S2:1403:A:O2'	46:S2:1406:A:N6	2.34	0.61
46:S2:1131:G:OP2	46:S2:1131:G:N2	2.30	0.61
46:S2:94:G:N2	46:S2:475:G:H5'	2.16	0.61
47:S7:2:A:H2'	47:S7:3:G:H8	1.66	0.61
54:SG:26:THR:O	54:SG:30:LYS:NZ	2.32	0.61
46:S2:516:G:H5''	46:S2:517:A:H5'	1.83	0.61
57:SJ:59:GLU:OE2	57:SJ:59:GLU:N	2.25	0.61
59:SL:49:GLU:HB3	59:SL:118:ARG:NH2	2.15	0.61
64:SR:127:ASN:OD1	64:SR:127:ASN:N	2.34	0.61
46:S2:156:G:O2'	46:S2:157:U:O4'	2.17	0.61
46:S2:920:A:H5'	69:SW:57:ARG:HH21	1.65	0.61
50:SC:199:PRO:O	50:SC:202:THR:OG1	2.17	0.61
33:Le:91:CYS:O	33:Le:93:LYS:N	2.33	0.61
53:SF:168:THR:HG22	53:SF:170:ALA:H	1.64	0.61
1:L5:3374:A:H2'	1:L5:3375:A:C8	2.36	0.61
60:SN:56:ASP:OD2	74:Sb:52:THR:OG1	2.19	0.61
65:SS:118:ARG:HG2	65:SS:123:LEU:HD21	1.83	0.61
51:SD:105:LEU:HD12	51:SD:122:VAL:HG21	1.83	0.60
1:L5:4218:C:OP1	17:LO:65:ASN:ND2	2.34	0.60
46:S2:1308:U:O2'	46:S2:1309:U:O4'	2.19	0.60
62:SP:93:MET:N	62:SP:93:MET:HE3	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sg:124:SER:OG	78:Sg:126:ASP:OD1	2.14	0.60
2:L7:74:A:O2'	21:LS:53:LYS:NZ	2.34	0.60
62:SP:37:TYR:O	65:SS:88:LYS:NZ	2.34	0.60
11:LH:151:ILE:O	11:LH:155:SER:OG	2.16	0.60
15:LM:32:ASP:OD1	15:LM:34:ASN:N	2.31	0.60
22:LT:38:ASP:OD2	22:LT:98:HIS:NE2	2.30	0.60
46:S2:66:G:O5'	46:S2:68:A:N6	2.35	0.60
56:SI:3:ILE:O	56:SI:30:GLY:N	2.34	0.60
76:Sd:12:ARG:NH1	76:Sd:17:GLY:O	2.35	0.60
65:SS:71:MET:HG3	65:SS:99:LEU:HD13	1.83	0.60
78:Sg:246:TYR:HD1	78:Sg:247:TRP:H	1.50	0.60
1:L5:1013:C:OP1	1:L5:1015:C:N4	2.35	0.60
1:L5:3417:A:N6	46:S2:1826:A:N1	2.49	0.60
46:S2:1240:U:H2'	46:S2:1241:A:H2'	1.83	0.60
54:SG:23:LYS:H	54:SG:23:LYS:HD2	1.67	0.60
56:SI:56:ARG:NH1	56:SI:180:GLY:O	2.33	0.60
1:L5:950:G:H22	1:L5:1035:U:H3	1.50	0.60
1:L5:2342:C:OP1	1:L5:2522:C:O2'	2.19	0.60
46:S2:168:C:H4'	54:SG:131:ARG:HD2	1.83	0.60
1:L5:3466:G:OP2	1:L5:3466:G:N2	2.27	0.60
11:LH:95:VAL:HG12	41:Lm:82:LEU:HD23	1.84	0.60
23:LU:65:ARG:HE	23:LU:67:LYS:N	2.00	0.60
71:SY:102:THR:OG1	71:SY:103:SER:N	2.34	0.60
18:LP:24:VAL:HG12	18:LP:86:LYS:HD3	1.83	0.60
70:SX:61:GLN:CG	70:SX:62:PRO:HD2	2.31	0.60
70:SX:128:VAL:HG13	70:SX:129:SER:H	1.66	0.60
12:LI:53:VAL:HG12	12:LI:134:VAL:HG22	1.84	0.60
18:LP:116:HIS:HB3	18:LP:149:ILE:HB	1.84	0.60
46:S2:1281:G:C2	46:S2:1282:G:H1'	2.36	0.60
46:S2:1333:A:O2'	51:SD:145:GLN:O	2.15	0.60
78:Sg:149:GLU:HB3	78:Sg:170:TRP:HB2	1.84	0.60
78:Sg:227:LEU:HG	78:Sg:228:TYR:H	1.67	0.60
1:L5:1410:U:O2'	18:LP:135:ARG:NH2	2.32	0.59
63:SQ:68:ILE:HG21	63:SQ:88:ILE:HG13	1.84	0.59
65:SS:84:LEU:HD12	65:SS:95:TYR:HB3	1.84	0.59
46:S2:1561:U:O2	46:S2:1576:G:O6	2.20	0.59
46:S2:1792:A:H5''	54:SG:75:LEU:HD11	1.82	0.59
46:S2:95:G:H22	46:S2:435:G:H22	1.49	0.59
1:L5:3426:C:HO2'	1:L5:3427:U:H6	1.50	0.59
46:S2:1569:C:OP1	66:ST:96:SER:OG	2.20	0.59
51:SD:70:THR:HB	51:SD:86:LEU:HG	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SR:46:LEU:HD12	64:SR:46:LEU:H	1.68	0.59
71:SY:99:LYS:NZ	71:SY:101:LYS:O	2.36	0.59
1:L5:3815:C:H5	10:LG:73:ARG:HH12	1.50	0.59
46:S2:1552:U:OP2	46:S2:1580:A:N6	2.34	0.59
63:SQ:39:LEU:HD21	63:SQ:51:LEU:HG	1.83	0.59
1:L5:934:G:H1	1:L5:1063:C:H42	1.51	0.59
1:L5:4553:G:H2'	1:L5:4554:G:C8	2.38	0.59
8:LE:128:ASP:OD1	8:LE:128:ASP:N	2.34	0.59
13:LJ:85:LYS:HE2	13:LJ:115:LEU:HA	1.83	0.59
46:S2:1556:U:C4	76:Sd:19:ARG:HG3	2.38	0.59
61:SO:145:GLY:O	73:Sa:22:ARG:NH2	2.35	0.59
63:SQ:39:LEU:HA	63:SQ:42:ILE:HD11	1.85	0.59
1:L5:833:U:O2'	15:LM:44:ARG:NH2	2.34	0.59
46:S2:161:U:H1'	54:SG:87:ARG:HH22	1.68	0.59
46:S2:1652:A:O2'	53:SF:83:ASN:OD1	2.19	0.59
51:SD:14:ASP:O	51:SD:18:LYS:NZ	2.36	0.59
1:L5:3443:U:OP1	1:L5:4203:G:O2'	2.20	0.59
69:SW:94:LEU:HD21	69:SW:102:ILE:HG13	1.85	0.59
46:S2:313:G:C2	46:S2:337:A:H2	2.18	0.59
10:LG:165:GLU:OE2	16:LN:26:ARG:NH2	2.30	0.58
18:LP:39:MET:HG2	18:LP:43:LYS:HD3	1.84	0.58
42:Ln:8:LYS:HE3	42:Ln:12:ARG:HH21	1.68	0.58
71:SY:86:GLU:OE1	71:SY:90:ARG:NH1	2.35	0.58
1:L5:3269:C:H1'	1:L5:4664:A:C8	2.37	0.58
1:L5:1028:G:O2'	1:L5:1029:G:N2	2.36	0.58
31:Lc:78:ASN:OD1	31:Lc:78:ASN:N	2.36	0.58
1:L5:409:A:O2'	1:L5:413:C:O2'	2.20	0.58
1:L5:1010:U:H4'	7:LD:279:ARG:HD3	1.86	0.58
50:SC:84:PHE:CD2	50:SC:265:PRO:HD3	2.39	0.58
67:SU:66:ARG:HG3	67:SU:68:THR:HG22	1.85	0.58
1:L5:3380:A:OP2	37:Li:68:ARG:NH2	2.37	0.58
1:L5:4427:C:N4	1:L5:4508:G:N3	2.50	0.58
46:S2:222:U:H2'	46:S2:223:A:H8	1.68	0.58
48:SA:3:GLY:O	68:SV:80:SER:OG	2.20	0.58
76:Sd:22:ARG:HG3	76:Sd:23:VAL:HG23	1.85	0.58
46:S2:1744:G:N2	46:S2:1792:A:H62	2.02	0.58
78:Sg:157:SER:OG	78:Sg:164:ILE:N	2.32	0.58
1:L5:1447:G:H5'	1:L5:1448:A:OP1	2.04	0.58
46:S2:847:G:OP1	52:SE:106:LYS:NZ	2.32	0.58
46:S2:1307:U:H3'	46:S2:1308:U:H5''	1.86	0.58
46:S2:1409:U:H2'	46:S2:1410:A:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SI:161:LEU:O	56:SI:165:GLN:NE2	2.37	0.58
1:L5:266:G:H2'	1:L5:267:G:H8	1.68	0.58
1:L5:437:G:N2	34:Lf:23:GLU:OE2	2.36	0.58
1:L5:4111:C:H2'	1:L5:4112:U:C6	2.39	0.58
46:S2:833:G:H22	46:S2:842:G:H22	1.52	0.58
48:SA:163:CYS:SG	48:SA:164:ASN:N	2.77	0.58
78:Sg:197:THR:HG21	78:Sg:238:ALA:HA	1.85	0.58
13:LJ:56:THR:HG22	13:LJ:63:ARG:HA	1.86	0.57
17:LO:105:LEU:HD22	17:LO:109:PRO:HG2	1.86	0.57
22:LT:68:THR:HG22	22:LT:69:GLN:H	1.69	0.57
65:SS:23:ARG:O	65:SS:55:ARG:NE	2.34	0.57
7:LD:216:GLU:HG3	7:LD:216:GLU:O	2.04	0.57
12:LI:189:ARG:NH1	12:LI:202:GLU:OE2	2.37	0.57
73:Sa:47:ALA:HA	73:Sa:50:VAL:HB	1.86	0.57
1:L5:2020:A:O2'	8:LE:128:ASP:OD2	2.20	0.57
8:LE:138:LYS:HD3	8:LE:138:LYS:N	2.19	0.57
45:Lr:65:LYS:O	45:Lr:102:TYR:OH	2.21	0.57
72:SZ:99:LEU:HD21	72:SZ:102:LYS:HB2	1.85	0.57
1:L5:468:C:H2'	1:L5:469:A:H8	1.68	0.57
1:L5:2333:G:N2	1:L5:2336:A:OP2	2.29	0.57
1:L5:3873:A:OP2	22:LT:2:THR:OG1	2.19	0.57
1:L5:4127:A:OP2	41:Lm:124:LYS:NZ	2.37	0.57
12:LI:79:SER:OG	12:LI:147:HIS:ND1	2.36	0.57
46:S2:49:C:O2	46:S2:477:A:N6	2.38	0.57
47:S7:2:A:H2'	47:S7:3:G:C8	2.39	0.57
75:Sc:56:LEU:HD12	75:Sc:57:THR:H	1.69	0.57
1:L5:150:U:OP2	10:LG:200:THR:OG1	2.22	0.57
1:L5:151:G:OP2	16:LN:4:TYR:OH	2.23	0.57
1:L5:409:A:HO2'	1:L5:413:C:HO2'	1.49	0.57
4:LA:108:PRO:O	4:LA:111:THR:OG1	2.23	0.57
24:LV:112:MET:HE1	24:LV:117:ILE:HD11	1.86	0.57
39:Lk:61:PRO:HG2	39:Lk:64:LEU:HD23	1.86	0.57
52:SE:40:GLU:OE1	52:SE:40:GLU:N	2.27	0.57
61:SO:34:PHE:HB3	61:SO:41:PHE:HB2	1.86	0.57
1:L5:3904:A:N6	13:LJ:127:GLY:O	2.37	0.57
10:LG:110:LYS:O	10:LG:114:LEU:HD23	2.05	0.57
46:S2:1399:G:H1'	78:Sg:63:SER:HB2	1.86	0.57
61:SO:75:MET:O	61:SO:79:GLN:NE2	2.37	0.57
78:Sg:238:ALA:H	78:Sg:251:ALA:HB3	1.69	0.57
8:LE:138:LYS:HD3	8:LE:138:LYS:H	1.70	0.57
46:S2:1396:C:H1'	46:S2:1475:A:C5	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1506:U:H4'	46:S2:1509:A:H1'	1.85	0.57
46:S2:1543:C:OP1	66:ST:62:ARG:NE	2.38	0.57
1:L5:1219:C:H2'	1:L5:1220:C:C6	2.40	0.57
46:S2:322:C:H2'	46:S2:323:C:C6	2.40	0.57
46:S2:1211:G:OP1	73:Sa:85:ARG:NH1	2.35	0.57
52:SE:21:ASP:OD2	52:SE:24:THR:HG23	2.05	0.57
63:SQ:8:GLN:HB2	63:SQ:99:TYR:CZ	2.40	0.57
1:L5:1009:C:H42	1:L5:1017:A:N6	1.96	0.57
1:L5:1605:A:H5''	1:L5:1606:G:H5'	1.87	0.57
3:L8:141:C:OP1	16:LN:38:ARG:NH1	2.37	0.57
46:S2:494:A:H61	46:S2:510:G:H1'	1.70	0.57
52:SE:71:LYS:HG2	52:SE:76:VAL:HG22	1.86	0.57
65:SS:60:THR:OG1	65:SS:62:ASP:OD1	2.22	0.57
28:LZ:57:MET:HE2	28:LZ:61:LYS:HD3	1.87	0.56
46:S2:1537:G:H2'	46:S2:1538:A:C8	2.39	0.56
1:L5:267:G:H2'	1:L5:268:G:H8	1.70	0.56
1:L5:1380:C:H2'	1:L5:1381:U:C6	2.39	0.56
1:L5:3345:U:OP2	4:LA:198:ARG:NH1	2.35	0.56
4:LA:28:ARG:HG3	4:LA:123:ARG:HH11	1.70	0.56
9:LF:241:GLY:O	9:LF:268:ARG:NH2	2.38	0.56
24:LV:109:LYS:NZ	24:LV:111:GLU:HB2	2.20	0.56
46:S2:492:C:O2'	46:S2:575:A:N1	2.37	0.56
46:S2:873:A:O2'	46:S2:875:G:OP2	2.23	0.56
46:S2:904:A:H2'	46:S2:905:A:C8	2.40	0.56
49:SB:117:TRP:HB3	49:SB:153:THR:HG22	1.86	0.56
52:SE:125:LYS:O	52:SE:142:HIS:N	2.38	0.56
21:LS:19:THR:HG23	21:LS:22:CYS:H	1.70	0.56
46:S2:421:G:O2'	46:S2:661:C:N3	2.38	0.56
46:S2:637:C:H5''	77:Se:98:LYS:NZ	2.20	0.56
46:S2:833:G:H1	46:S2:842:G:H1	1.53	0.56
46:S2:1496:G:N2	76:Sd:45:GLN:OE1	2.38	0.56
52:SE:72:ILE:HD12	52:SE:77:ARG:HG3	1.86	0.56
55:SH:20:GLU:O	55:SH:24:SER:OG	2.24	0.56
61:SO:151:LEU:HD23	61:SO:151:LEU:H	1.69	0.56
69:SW:112:ASP:N	69:SW:112:ASP:OD1	2.30	0.56
1:L5:3374:A:H2'	1:L5:3375:A:H8	1.71	0.56
1:L5:4101:G:H5''	1:L5:4102:A:H5''	1.87	0.56
46:S2:57:U:H3	46:S2:88:G:H22	1.53	0.56
1:L5:2314:G:H1	1:L5:2324:G:H22	1.53	0.56
46:S2:77:A:O2'	46:S2:78:C:OP1	2.22	0.56
46:S2:1287:G:N2	46:S2:1314:A:H62	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1452:G:H21	46:S2:1475:A:H61	1.53	0.56
63:SQ:70:VAL:HG21	63:SQ:88:ILE:HD11	1.87	0.56
1:L5:102:G:O2'	1:L5:1196:U:O2'	2.22	0.56
8:LE:180:LEU:HD23	8:LE:196:ARG:HG3	1.88	0.56
46:S2:509:A:O2'	46:S2:510:G:H8	1.89	0.56
46:S2:982:A:H2'	46:S2:983:G:C8	2.40	0.56
69:SW:23:ARG:HH21	74:Sb:3:LEU:HB3	1.71	0.56
78:Sg:39:THR:HB	78:Sg:60:ARG:HB3	1.87	0.56
1:L5:4352:U:OP2	41:Lm:111:ARG:NH2	2.25	0.56
46:S2:158:A:H2'	46:S2:159:A:H8	1.70	0.56
57:SJ:104:ASP:OD1	57:SJ:105:PHE:N	2.39	0.56
46:S2:965:A:H2'	46:S2:966:U:H6	1.71	0.56
46:S2:1864:A:OP2	73:Sa:4:LYS:NZ	2.30	0.56
56:SI:116:HIS:O	56:SI:152:ARG:NH1	2.37	0.56
71:SY:41:ARG:HA	71:SY:55:ILE:HG21	1.88	0.56
1:L5:761:C:H5	1:L5:810:G:H1	1.52	0.56
1:L5:3913:U:H2'	1:L5:3914:C:C6	2.41	0.56
1:L5:4370:A:OP2	5:LB:30:LYS:NZ	2.31	0.56
14:LL:170:THR:HG23	14:LL:173:GLU:HG2	1.87	0.56
15:LM:39:ASP:O	15:LM:41:PRO:HD3	2.05	0.56
46:S2:1611:G:OP1	65:SS:121:ARG:NH1	2.39	0.56
54:SG:161:PRO:HA	54:SG:171:THR:HA	1.87	0.56
55:SH:49:LYS:HB2	55:SH:61:ILE:HG13	1.88	0.56
1:L5:1755:G:H4'	21:LS:93:MET:HG2	1.86	0.56
78:Sg:175:LYS:HB3	78:Sg:184:LEU:HD11	1.88	0.55
1:L5:1226:G:O2'	1:L5:1227:G:O4'	2.16	0.55
56:SI:164:GLU:H	56:SI:164:GLU:CD	2.15	0.55
1:L5:1293:G:H2'	1:L5:1294:C:C6	2.41	0.55
1:L5:4425:U:H3	1:L5:4509:G:H1	1.54	0.55
47:S7:10:G:H21	47:S7:45:G:H3'	1.71	0.55
1:L5:3933:A:N6	7:LD:28:THR:O	2.39	0.55
1:L5:4612:C:H2'	1:L5:4613:U:C6	2.41	0.55
27:LY:91:ASN:N	27:LY:91:ASN:OD1	2.39	0.55
46:S2:56:G:H3'	71:SY:115:LYS:HZ1	1.70	0.55
54:SG:53:SER:O	54:SG:53:SER:OG	2.21	0.55
63:SQ:74:GLY:O	63:SQ:80:GLN:NE2	2.38	0.55
68:SV:21:ASN:C	68:SV:22:ARG:HD2	2.31	0.55
1:L5:422:G:OP1	18:LP:62:ARG:NH1	2.39	0.55
1:L5:1621:G:O2'	1:L5:1623:C:OP2	2.21	0.55
1:L5:3480:G:OP2	1:L5:3480:G:N2	2.27	0.55
10:LG:180:PRO:HD3	10:LG:223:ARG:HH21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:368:U:H4'	46:S2:372:A:C8	2.41	0.55
46:S2:405:G:O3'	46:S2:1810:A:O2'	2.21	0.55
48:SA:10:MET:O	48:SA:10:MET:HE3	2.05	0.55
56:SI:105:ASP:OD1	56:SI:106:SER:N	2.39	0.55
5:LB:71:GLU:HB2	25:LW:1:MET:HE3	1.87	0.55
1:L5:162:A:H2'	1:L5:163:A:C8	2.42	0.55
1:L5:2063:G:OP1	33:Le:128:ARG:NH1	2.40	0.55
6:LC:284:MET:HE2	6:LC:287:THR:HA	1.88	0.55
11:LH:11:ASP:OD1	11:LH:54:ARG:HG2	2.07	0.55
46:S2:95:G:H22	46:S2:435:G:N2	2.03	0.55
46:S2:615:C:H2'	46:S2:627:G:C8	2.42	0.55
46:S2:629:A:H61	46:S2:1501:G:H21	1.55	0.55
65:SS:86:ARG:NH2	65:SS:89:ASP:OD1	2.39	0.55
1:L5:671:G:H2'	1:L5:672:G:C8	2.42	0.55
1:L5:3368:A:H1'	46:S2:971:G:C4	2.42	0.55
46:S2:1427:U:H3	66:ST:5:THR:HG21	1.71	0.55
62:SP:89:MET:O	62:SP:92:SER:OG	2.23	0.55
63:SQ:19:ALA:HB2	63:SQ:75:GLY:HA3	1.88	0.55
78:Sg:254:PRO:HA	78:Sg:285:GLN:HA	1.88	0.55
1:L5:671:G:H2'	1:L5:672:G:H8	1.72	0.55
21:LS:15:ARG:HB3	21:LS:27:LEU:HD23	1.89	0.55
46:S2:497:C:H5	46:S2:506:G:H1	1.54	0.55
51:SD:66:ILE:HG23	51:SD:67:ARG:HD3	1.88	0.55
52:SE:73:ASP:HA	52:SE:89:VAL:HG23	1.88	0.55
58:SK:7:ASN:OD1	58:SK:7:ASN:N	2.23	0.55
1:L5:3996:U:O2'	43:Lo:31:ASP:OD2	2.25	0.55
8:LE:100:VAL:HG23	8:LE:115:VAL:HB	1.89	0.55
46:S2:177:G:H21	46:S2:178:C:N4	2.04	0.55
46:S2:845:U:HO2'	46:S2:846:G:P	2.28	0.55
49:SB:229:MET:HE3	49:SB:229:MET:C	2.32	0.55
52:SE:240:ARG:NH1	52:SE:240:ARG:HA	2.22	0.55
23:LU:28:PRO:HB2	23:LU:34:MET:HG2	1.88	0.54
25:LW:2:LYS:HD2	25:LW:3:VAL:H	1.71	0.54
46:S2:1534:A:N7	46:S2:1603:U:O4	2.40	0.54
47:S7:51:U:H2'	47:S7:52:G:H8	1.71	0.54
1:L5:4428:C:N4	1:L5:4507:G:N3	2.55	0.54
1:L5:4586:A:OP1	8:LE:191:ARG:NH2	2.33	0.54
46:S2:66:G:H8	46:S2:82:G:H21	1.55	0.54
46:S2:882:G:H21	46:S2:907:U:H3	1.54	0.54
51:SD:135:GLU:HG2	51:SD:153:VAL:HG22	1.89	0.54
1:L5:477:G:H2'	1:L5:478:G:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4393:G:H1'	1:L5:4396:G:H5''	1.89	0.54
15:LM:51:PRO:HG2	15:LM:54:CYS:SG	2.48	0.54
16:LN:14:LYS:HA	16:LN:19:MET:HG2	1.90	0.54
52:SE:126:VAL:HG22	52:SE:139:LEU:HD13	1.90	0.54
1:L5:102:G:HO2'	1:L5:1196:U:HO2'	1.55	0.54
1:L5:143:U:O3'	10:LG:108:GLN:NE2	2.40	0.54
1:L5:2512:G:O2'	1:L5:2519:A:N3	2.40	0.54
46:S2:524:A:OP2	57:SJ:127:ARG:NH2	2.40	0.54
46:S2:1216:C:O2'	46:S2:1646:C:OP2	2.21	0.54
46:S2:1260:A:H62	46:S2:1520:U:H5'	1.73	0.54
62:SP:93:MET:HA	62:SP:106:GLU:HA	1.89	0.54
74:Sb:78:SER:HB3	74:Sb:80:ARG:NH1	2.18	0.54
1:L5:4068:A:OP1	12:LI:154:ARG:NH1	2.41	0.54
7:LD:93:THR:O	7:LD:158:LYS:NZ	2.41	0.54
46:S2:59:U:OP1	46:S2:502:C:O2'	2.26	0.54
46:S2:522:A:OP1	57:SJ:45:ARG:NH1	2.32	0.54
78:Sg:109:LEU:HD11	78:Sg:125:ARG:HD3	1.90	0.54
5:LB:299:ILE:HG23	5:LB:313:SER:HB3	1.90	0.54
28:LZ:17:ARG:NH2	28:LZ:18:TYR:OH	2.41	0.54
46:S2:85:A:O2'	46:S2:86:C:O5'	2.23	0.54
46:S2:833:G:H22	46:S2:842:G:N2	2.04	0.54
52:SE:252:ARG:HH12	57:SJ:75:ASN:HD22	1.55	0.54
62:SP:78:THR:O	62:SP:80:LEU:N	2.40	0.54
1:L5:1011:G:H5''	7:LD:283:LYS:HE3	1.90	0.54
48:SA:5:LEU:O	48:SA:9:GLN:NE2	2.40	0.54
1:L5:1212:A:HO2'	1:L5:1281:C:HO2'	1.55	0.54
1:L5:3389:A:H2'	1:L5:3390:A:C8	2.43	0.54
46:S2:222:U:H2'	46:S2:223:A:C8	2.42	0.54
46:S2:586:C:O2'	46:S2:587:G:O5'	2.23	0.54
69:SW:76:SER:HB3	69:SW:77:PRO:HD3	1.90	0.54
11:LH:129:ARG:HE	11:LH:153:LEU:HD22	1.72	0.54
45:Lr:92:SER:O	45:Lr:96:MET:HG3	2.08	0.54
46:S2:76:U:H5	54:SG:173:ALA:HB3	1.73	0.54
46:S2:95:G:H1	46:S2:435:G:H1	1.56	0.54
46:S2:629:A:N6	46:S2:1501:G:H21	2.05	0.54
1:L5:1008:A:H3'	1:L5:1009:C:H5''	1.89	0.54
1:L5:1012:U:O2'	1:L5:1013:C:OP1	2.24	0.54
5:LB:303:ALA:HB3	5:LB:312:LYS:HG3	1.90	0.54
34:Lf:106:TYR:HB2	34:Lf:107:PRO:HD3	1.90	0.54
44:Lp:38:THR:HA	44:Lp:45:THR:HA	1.90	0.54
46:S2:1599:G:N2	46:S2:1600:U:O4	2.34	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SE:44:LEU:HD21	52:SE:70:ILE:HG21	1.89	0.54
1:L5:1418:G:H2'	1:L5:1419:G:C8	2.44	0.53
7:LD:116:ASP:OD1	7:LD:116:ASP:N	2.38	0.53
16:LN:19:MET:HA	16:LN:19:MET:HE3	1.89	0.53
27:LY:1:MET:HE3	27:LY:2:LYS:O	2.08	0.53
59:SL:104:LYS:O	70:SX:11:ARG:NH2	2.30	0.53
24:LV:109:LYS:HZ2	24:LV:111:GLU:HB2	1.73	0.53
28:LZ:121:ARG:NH1	28:LZ:127:ASN:OD1	2.41	0.53
33:Le:91:CYS:C	33:Le:93:LYS:H	2.16	0.53
46:S2:497:C:H2'	46:S2:499:C:C6	2.43	0.53
46:S2:1649:G:O2'	46:S2:1675:G:O6	2.22	0.53
57:SJ:83:ARG:HE	57:SJ:150:ARG:HD3	1.74	0.53
1:L5:2337:C:OP2	35:Lg:76:ARG:NH2	2.28	0.53
46:S2:515:U:H2'	46:S2:516:G:H8	1.71	0.53
46:S2:1229:A:H2'	46:S2:1230:G:C8	2.44	0.53
48:SA:41:ARG:HD3	48:SA:47:TYR:CZ	2.43	0.53
58:SK:60:GLU:CD	58:SK:69:TRP:HE1	2.16	0.53
1:L5:386:G:O2'	1:L5:411:G:O6	2.17	0.53
1:L5:2499:A:H2'	1:L5:2500:A:C8	2.44	0.53
1:L5:3913:U:H2'	1:L5:3914:C:H6	1.73	0.53
15:LM:29:ASP:OD1	15:LM:30:VAL:N	2.41	0.53
21:LS:96:GLU:HG3	21:LS:139:ARG:HG2	1.90	0.53
46:S2:885:C:O2'	46:S2:903:G:O6	2.18	0.53
46:S2:1314:A:H5'	46:S2:1315:U:C4	2.43	0.53
1:L5:753:G:O2'	1:L5:754:A:OP1	2.21	0.53
1:L5:761:C:H2'	1:L5:762:U:C6	2.42	0.53
52:SE:99:PHE:HE1	52:SE:113:ARG:HB3	1.74	0.53
54:SG:71:GLY:H	54:SG:98:ARG:NH1	2.06	0.53
68:SV:40:ASP:OD1	68:SV:42:THR:N	2.31	0.53
1:L5:4544:G:H2'	1:L5:4545:G:C8	2.43	0.53
6:LC:152:LEU:HD23	6:LC:251:ILE:HG12	1.90	0.53
20:LR:152:LYS:HA	20:LR:152:LYS:HE2	1.90	0.53
24:LV:99:GLU:HG3	25:LW:21:TYR:OH	2.08	0.53
46:S2:161:U:H1'	54:SG:87:ARG:HH12	1.72	0.53
78:Sg:110:SER:HB3	78:Sg:153:CYS:HA	1.91	0.53
78:Sg:171:ASP:O	78:Sg:172:LYS:HG2	2.09	0.53
78:Sg:191:HIS:CG	78:Sg:195:LEU:HD21	2.44	0.53
1:L5:224:U:HO2'	1:L5:243:A:HO2'	1.55	0.53
1:L5:3718:U:O2'	1:L5:3719:U:H5'	2.09	0.53
11:LH:153:LEU:O	11:LH:157:SER:OG	2.27	0.53
46:S2:565:A:O2'	46:S2:566:G:H8	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:838:A:H61	71:SY:26:ASP:HB2	1.74	0.53
46:S2:1409:U:H2'	46:S2:1410:A:C8	2.44	0.53
51:SD:51:LEU:HD11	51:SD:91:VAL:HA	1.91	0.53
1:L5:1031:G:H2'	1:L5:1033:G:C8	2.44	0.53
23:LU:41:GLN:O	23:LU:44:GLN:NE2	2.41	0.53
46:S2:572:U:O2'	71:SY:60:PHE:O	2.26	0.53
51:SD:132:LYS:HD3	51:SD:191:PRO:HA	1.91	0.53
65:SS:15:VAL:HG13	65:SS:16:LEU:H	1.74	0.53
72:SZ:42:ASP:N	72:SZ:42:ASP:OD1	2.41	0.53
1:L5:3719:U:HO2'	1:L5:3720:U:H6	1.57	0.53
1:L5:3975:G:N2	1:L5:3978:A:OP2	2.35	0.53
46:S2:836:C:O2'	46:S2:838:A:OP2	2.27	0.53
46:S2:891:U:C5	46:S2:898:U:H5''	2.43	0.53
47:S7:43:G:H2'	47:S7:44:A:C8	2.44	0.53
46:S2:225:C:O2'	46:S2:226:A:H8	1.91	0.53
50:SC:74:LYS:HB3	50:SC:269:PHE:CE2	2.44	0.53
4:LA:14:SER:OG	4:LA:15:VAL:N	2.41	0.52
23:LU:26:THR:O	23:LU:30:GLU:HG2	2.08	0.52
46:S2:586:C:O2'	46:S2:587:G:H8	1.91	0.52
48:SA:151:ASP:OD1	48:SA:151:ASP:N	2.41	0.52
67:SU:99:LYS:O	67:SU:102:THR:OG1	2.23	0.52
1:L5:4125:G:O2'	41:Lm:100:TYR:O	2.28	0.52
7:LD:70:GLU:OE1	7:LD:70:GLU:N	2.39	0.52
28:LZ:97:ASN:HB2	28:LZ:100:VAL:HG13	1.90	0.52
51:SD:74:GLN:NE2	51:SD:79:PHE:O	2.32	0.52
56:SI:164:GLU:OE1	56:SI:164:GLU:N	2.33	0.52
1:L5:1377:A:P	1:L5:1377:A:H8	2.33	0.52
1:L5:2393:U:O2'	1:L5:2448:G:O6	2.19	0.52
1:L5:4397:G:H2'	1:L5:4398:A:C8	2.44	0.52
11:LH:31:ARG:O	11:LH:149:ASN:ND2	2.43	0.52
13:LJ:113:ILE:HD12	13:LJ:119:TYR:HD2	1.74	0.52
46:S2:1515:G:H2'	46:S2:1516:G:H8	1.75	0.52
50:SC:266:TYR:O	50:SC:270:THR:HG23	2.08	0.52
57:SJ:78:LEU:HG	57:SJ:92:MET:HG2	1.92	0.52
70:SX:63:ASN:ND2	70:SX:114:ASP:OD2	2.36	0.52
71:SY:24:VAL:C	71:SY:25:ILE:HD13	2.35	0.52
75:Sc:31:ARG:NH1	75:Sc:31:ARG:O	2.42	0.52
78:Sg:131:LEU:HD21	78:Sg:140:TYR:HB3	1.91	0.52
79:Sx:38:A:H2'	79:Sx:39:A:C8	2.44	0.52
1:L5:828:C:H3'	1:L5:829:G:H21	1.73	0.52
46:S2:76:U:C5	54:SG:173:ALA:HB3	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:876:A:H1'	55:SH:114:GLN:NE2	2.24	0.52
46:S2:1561:U:H2'	46:S2:1562:G:H8	1.74	0.52
61:SO:76:LEU:HA	61:SO:79:GLN:NE2	2.24	0.52
1:L5:132:G:H3'	1:L5:133:C:H4'	1.90	0.52
1:L5:1218:C:H2'	1:L5:1219:C:C6	2.44	0.52
23:LU:102:VAL:O	23:LU:102:VAL:HG12	2.10	0.52
46:S2:797:G:H2'	46:S2:798:C:H4'	1.91	0.52
49:SB:147:ASN:N	49:SB:147:ASN:OD1	2.41	0.52
60:SN:29:THR:OG1	60:SN:30:SER:N	2.40	0.52
60:SN:93:LYS:HG3	60:SN:150:VAL:HG11	1.92	0.52
1:L5:1212:A:O2'	1:L5:1281:C:O2'	2.27	0.52
1:L5:4637:U:H1'	1:L5:4638:C:H5	1.75	0.52
46:S2:75:G:O2'	54:SG:159:ARG:NH1	2.40	0.52
46:S2:595:A:N6	46:S2:643:U:O2'	2.43	0.52
46:S2:888:U:H2'	46:S2:889:U:H2'	1.91	0.52
65:SS:114:LEU:O	65:SS:118:ARG:N	2.43	0.52
73:Sa:66:LYS:HG3	73:Sa:68:TYR:HE1	1.74	0.52
1:L5:4279:A:OP2	5:LB:224:LYS:NZ	2.29	0.52
34:Lf:56:ASN:OD1	34:Lf:66:LYS:NZ	2.41	0.52
53:SF:17:ILE:HA	53:SF:48:TYR:HE1	1.75	0.52
56:SI:158:ILE:HD11	56:SI:163:GLU:HG3	1.91	0.52
1:L5:351:G:O2'	3:L8:22:U:O4	2.28	0.52
1:L5:1179:U:OP2	14:LL:36:ARG:NH2	2.21	0.52
46:S2:143:U:H5'	54:SG:178:ARG:HE	1.75	0.52
46:S2:448:A:H4'	52:SE:3:ARG:HG2	1.92	0.52
19:LQ:39:THR:HG22	19:LQ:41:SER:H	1.75	0.52
21:LS:21:LYS:HG3	21:LS:22:CYS:H	1.75	0.52
28:LZ:88:ASP:OD1	28:LZ:88:ASP:N	2.36	0.52
34:Lf:106:TYR:O	34:Lf:108:SER:N	2.43	0.52
46:S2:107:A:H2'	46:S2:108:G:C8	2.45	0.52
13:LJ:14:GLU:OE1	13:LJ:14:GLU:N	2.43	0.52
46:S2:464:C:H2'	46:S2:466:A:H62	1.75	0.52
46:S2:507:G:OP1	71:SY:108:LYS:NZ	2.43	0.52
50:SC:72:ASP:HB2	50:SC:74:LYS:HG2	1.92	0.52
61:SO:122:SER:O	61:SO:122:SER:OG	2.20	0.52
70:SX:96:GLU:N	70:SX:96:GLU:OE1	2.43	0.52
71:SY:20:ARG:HD3	71:SY:20:ARG:N	2.25	0.52
78:Sg:168:CYS:SG	78:Sg:198:VAL:HG13	2.50	0.52
8:LE:284:SER:HB2	34:Lf:3:GLY:HA3	1.93	0.51
46:S2:168:C:O2'	54:SG:133:LEU:O	2.28	0.51
46:S2:569:C:H2'	46:S2:570:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SZ:77:LEU:HD12	72:SZ:79:ILE:HD11	1.92	0.51
73:Sa:44:ILE:HG23	73:Sa:66:LYS:HA	1.91	0.51
1:L5:468:C:H2'	1:L5:469:A:C8	2.44	0.51
46:S2:571:C:O2'	71:SY:34:THR:O	2.27	0.51
46:S2:944:U:O2'	61:SO:135:ILE:O	2.29	0.51
52:SE:72:ILE:HB	52:SE:77:ARG:HG3	1.91	0.51
54:SG:120:ASP:HB2	54:SG:125:THR:HG21	1.91	0.51
64:SR:37:GLU:HG2	78:Sg:150:TRP:CZ2	2.44	0.51
1:L5:279:G:H5''	16:LN:14:LYS:NZ	2.25	0.51
1:L5:1004:G:H22	1:L5:1022:G:H1	1.58	0.51
6:LC:293:LEU:O	6:LC:299:GLN:NE2	2.38	0.51
46:S2:156:G:H1'	54:SG:60:GLY:N	2.24	0.51
46:S2:1534:A:H2	46:S2:1537:G:N3	2.09	0.51
48:SA:198:MET:O	48:SA:200:ASP:N	2.41	0.51
57:SJ:84:ILE:HD11	57:SJ:148:ILE:HG21	1.92	0.51
1:L5:857:A:C8	8:LE:131:ARG:HG2	2.44	0.51
1:L5:950:G:C2	1:L5:1037:G:C2	2.98	0.51
1:L5:1013:C:O2'	1:L5:1016:C:N4	2.33	0.51
1:L5:4640:G:H2'	1:L5:4641:G:C8	2.45	0.51
3:L8:52:A:H62	40:L1:27:ILE:HD13	1.76	0.51
12:LI:129:VAL:HG23	12:LI:133:GLN:HG2	1.93	0.51
14:LL:77:SER:OG	14:LL:80:GLU:OE2	2.22	0.51
18:LP:7:ASP:OD1	18:LP:8:PRO:HD2	2.10	0.51
46:S2:609:C:O4'	77:Se:132:ASN:ND2	2.44	0.51
59:SL:47:PRO:HB2	59:SL:49:GLU:OE1	2.11	0.51
78:Sg:24:THR:HG23	78:Sg:71:ILE:HD12	1.92	0.51
1:L5:940:C:H2'	1:L5:941:C:C6	2.46	0.51
1:L5:3967:C:O2'	30:Lb:36:ASP:OD1	2.28	0.51
1:L5:4559:G:O2'	1:L5:4560:C:O4'	2.22	0.51
46:S2:128:U:OP1	46:S2:129:C:N4	2.44	0.51
46:S2:1253:C:OP1	67:SU:75:LYS:NZ	2.44	0.51
48:SA:50:ASN:HB3	48:SA:53:ARG:HG2	1.92	0.51
65:SS:89:ASP:HB3	65:SS:93:GLY:H	1.76	0.51
1:L5:4552:C:H2'	1:L5:4553:G:H4'	1.93	0.51
20:LR:98:ARG:NH2	20:LR:130:ASN:OD1	2.39	0.51
46:S2:145:G:H2'	46:S2:146:G:C8	2.45	0.51
54:SG:191:ARG:HA	54:SG:194:LEU:HD12	1.93	0.51
63:SQ:104:SER:O	63:SQ:108:ILE:HG12	2.10	0.51
1:L5:4522:A:C2	21:LS:165:PRO:HD3	2.46	0.51
23:LU:105:ASN:HD22	23:LU:111:GLU:HB2	1.74	0.51
29:La:134:GLU:HA	29:La:134:GLU:OE2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lf:36:ARG:NH1	34:Lf:79:GLY:O	2.40	0.51
46:S2:56:G:H3'	71:SY:115:LYS:NZ	2.26	0.51
46:S2:116:U:H5'	46:S2:382:C:H1'	1.93	0.51
46:S2:1553:G:C5	51:SD:9:ARG:HD2	2.45	0.51
56:SI:36:THR:HB	56:SI:96:LEU:HB2	1.92	0.51
1:L5:719:A:H2'	1:L5:720:C:C6	2.45	0.51
1:L5:4686:A:O2'	1:L5:4687:U:OP1	2.28	0.51
4:LA:104:VAL:HA	4:LA:107:MET:HG3	1.92	0.51
7:LD:226:TYR:O	7:LD:228:LYS:N	2.44	0.51
44:Lp:45:THR:O	44:Lp:45:THR:OG1	2.29	0.51
50:SC:213:LEU:HD23	50:SC:213:LEU:H	1.75	0.51
52:SE:240:ARG:HA	52:SE:240:ARG:CZ	2.41	0.51
54:SG:142:ARG:HE	54:SG:153:VAL:HG22	1.75	0.51
64:SR:126:MET:HB3	64:SR:128:PHE:HE1	1.75	0.51
73:Sa:45:VAL:HG11	73:Sa:50:VAL:HG23	1.92	0.51
1:L5:1157:A:OP1	16:LN:204:ARG:HD2	2.10	0.51
1:L5:3594:C:H1'	16:LN:125:SER:HB3	1.91	0.51
5:LB:4:ARG:HH12	5:LB:6:PHE:HB2	1.74	0.51
7:LD:41:LYS:HE3	22:LT:93:ILE:HD13	1.92	0.51
21:LS:69:GLU:OE1	21:LS:102:THR:OG1	2.27	0.51
46:S2:41:G:N2	46:S2:481:G:H22	2.08	0.51
46:S2:503:C:N4	52:SE:66:MET:HE1	2.26	0.51
53:SF:18:LYS:HE3	53:SF:24:SER:HB2	1.92	0.51
62:SP:93:MET:HE3	62:SP:93:MET:H	1.76	0.51
62:SP:114:HIS:ND1	62:SP:118:GLU:OE2	2.43	0.51
78:Sg:188:HIS:NE2	78:Sg:224:GLY:O	2.32	0.51
1:L5:194:C:O2	27:LY:121:ARG:NH1	2.44	0.51
21:LS:95:ARG:NH2	21:LS:112:ASP:OD2	2.44	0.51
48:SA:85:ARG:NH2	64:SR:81:ARG:O	2.44	0.51
51:SD:106:ARG:HG3	51:SD:175:VAL:HG22	1.93	0.51
52:SE:103:TYR:HB2	52:SE:182:MET:HE3	1.92	0.51
55:SH:129:ILE:HG21	55:SH:180:LEU:HD11	1.93	0.51
63:SQ:69:ARG:HH12	63:SQ:71:ARG:HG2	1.76	0.51
30:Lb:6:ASN:OD1	30:Lb:7:HIS:N	2.45	0.50
46:S2:1233:U:H2'	46:S2:1234:G:C8	2.44	0.50
47:S7:65:C:H2'	47:S7:66:C:C6	2.46	0.50
1:L5:1005:C:O2'	1:L5:1006:G:O5'	2.30	0.50
2:L7:3:C:H2'	2:L7:4:U:H6	1.76	0.50
7:LD:119:TYR:OH	7:LD:139:PRO:O	2.27	0.50
46:S2:156:G:H1'	54:SG:60:GLY:H	1.77	0.50
46:S2:603:G:H3'	46:S2:604:C:H2'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SF:76:MET:O	53:SF:76:MET:HE3	2.11	0.50
62:SP:111:MET:HE2	65:SS:117:ILE:HG23	1.94	0.50
64:SR:116:ASN:OD1	64:SR:117:LEU:N	2.38	0.50
76:Sd:33:LYS:HG2	76:Sd:34:TYR:CD2	2.46	0.50
1:L5:316:A:N1	1:L5:4013:U:H5	2.09	0.50
11:LH:141:LYS:HG3	11:LH:142:ASP:N	2.26	0.50
26:LX:148:ASP:OD1	26:LX:149:VAL:N	2.45	0.50
46:S2:71:G:H2'	46:S2:72:C:O4'	2.10	0.50
46:S2:305:C:O2'	46:S2:310:G:N7	2.45	0.50
46:S2:1413:C:N4	46:S2:1414:G:O6	2.45	0.50
62:SP:94:VAL:HG11	62:SP:116:LEU:HD23	1.93	0.50
1:L5:1561:G:H2'	1:L5:1562:G:O4'	2.11	0.50
1:L5:3368:A:H1'	46:S2:971:G:N3	2.27	0.50
12:LI:143:GLN:HG2	12:LI:144:ASN:OD1	2.11	0.50
13:LJ:72:CYS:SG	13:LJ:73:THR:N	2.84	0.50
19:LQ:35:LEU:O	19:LQ:39:THR:HB	2.11	0.50
46:S2:482:C:O2'	46:S2:483:G:N2	2.44	0.50
46:S2:1266:A:H5'	46:S2:1267:C:OP2	2.12	0.50
46:S2:1741:C:H2'	46:S2:1742:U:C6	2.46	0.50
52:SE:87:MET:HE2	52:SE:123:LEU:H	1.77	0.50
53:SF:34:SER:HA	75:Sc:55:VAL:HB	1.93	0.50
60:SN:26:LEU:HD13	60:SN:28:LEU:H	1.75	0.50
1:L5:831:G:N2	1:L5:836:C:H2'	2.27	0.50
1:L5:1562:G:H3'	1:L5:1563:G:C8	2.46	0.50
46:S2:1242:A:N1	46:S2:1518:G:H5'	2.27	0.50
52:SE:128:LYS:HB3	52:SE:140:VAL:HG12	1.94	0.50
1:L5:811:U:H2'	1:L5:812:G:O4'	2.10	0.50
1:L5:1355:U:H3	1:L5:1432:G:H1	1.58	0.50
1:L5:1380:C:H2'	1:L5:1381:U:H6	1.75	0.50
1:L5:3927:A:H2'	1:L5:3928:G:C8	2.47	0.50
1:L5:4544:G:H2'	1:L5:4545:G:H8	1.77	0.50
14:LL:80:GLU:HG3	14:LL:110:LEU:HD12	1.93	0.50
20:LR:171:LYS:HD2	20:LR:171:LYS:C	2.36	0.50
46:S2:111:A:O2'	46:S2:112:U:H5'	2.11	0.50
46:S2:997:A:H2'	46:S2:998:A:C8	2.47	0.50
46:S2:1453:A:H5''	64:SR:48:ASN:ND2	2.27	0.50
48:SA:144:THR:OG1	48:SA:156:TYR:O	2.27	0.50
49:SB:139:CYS:HB2	49:SB:172:MET:HE1	1.94	0.50
50:SC:166:ARG:HH21	68:SV:1:MET:HE1	1.77	0.50
54:SG:63:MET:HA	54:SG:98:ARG:HB2	1.94	0.50
61:SO:61:LYS:HZ2	61:SO:77:ALA:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:138:C:H2'	1:L5:139:G:C8	2.46	0.50
1:L5:415:U:O2'	1:L5:416:G:OP1	2.27	0.50
1:L5:2056:G:O6	6:LC:188:ARG:NH2	2.45	0.50
47:S7:51:U:H2'	47:S7:52:G:C8	2.47	0.50
50:SC:108:LYS:HD3	50:SC:233:LEU:HD13	1.92	0.50
50:SC:116:THR:OG1	50:SC:117:ARG:N	2.45	0.50
51:SD:21:LEU:HD13	51:SD:48:ILE:HD12	1.93	0.50
64:SR:32:LYS:HE3	64:SR:47:ARG:CZ	2.42	0.50
72:SZ:66:LYS:HA	72:SZ:111:ARG:HD2	1.94	0.50
1:L5:761:C:H2'	1:L5:762:U:H6	1.75	0.50
1:L5:830:C:H4'	1:L5:831:G:O5'	2.11	0.50
1:L5:3427:U:OP1	47:S7:24:G:O2'	2.18	0.50
7:LD:208:MET:O	7:LD:212:MET:HG3	2.12	0.50
29:La:110:LYS:HG3	29:La:128:PHE:HB2	1.93	0.50
46:S2:1553:G:C6	51:SD:9:ARG:HB3	2.46	0.50
50:SC:196:ILE:HB	50:SC:223:TYR:HB2	1.93	0.50
61:SO:102:GLY:O	61:SO:106:LYS:NZ	2.39	0.50
63:SQ:52:LEU:O	63:SQ:55:VAL:HG12	2.12	0.50
5:LB:206:PRO:HG2	5:LB:209:GLN:HG3	1.94	0.49
23:LU:41:GLN:HA	23:LU:44:GLN:HG3	1.94	0.49
46:S2:510:G:H2'	46:S2:511:G:C8	2.47	0.49
46:S2:835:C:N4	46:S2:836:C:H41	2.10	0.49
46:S2:1099:C:H2'	46:S2:1100:G:C8	2.47	0.49
53:SF:40:ALA:HB3	53:SF:67:PRO:HA	1.93	0.49
55:SH:53:VAL:HG22	55:SH:175:GLY:HA3	1.93	0.49
55:SH:62:ILE:HD12	55:SH:94:PHE:HE1	1.77	0.49
62:SP:60:LEU:CD1	62:SP:76:VAL:HG13	2.35	0.49
1:L5:1013:C:OP1	1:L5:1013:C:H4'	2.12	0.49
1:L5:1222:C:N4	1:L5:1227:G:N3	2.59	0.49
1:L5:4559:G:O2'	1:L5:4560:C:OP2	2.29	0.49
8:LE:53:ARG:HH11	8:LE:73:LYS:HG2	1.77	0.49
11:LH:137:SER:HB3	11:LH:143:GLU:HG3	1.94	0.49
46:S2:143:U:H4'	46:S2:144:U:H5'	1.94	0.49
46:S2:514:G:H5'	46:S2:515:U:C5	2.48	0.49
54:SG:106:LEU:HD21	54:SG:109:LEU:HD13	1.94	0.49
76:Sd:6:LEU:HA	76:Sd:9:SER:HB2	1.95	0.49
1:L5:2565:G:N1	1:L5:2568:C:OP2	2.36	0.49
3:L8:6:C:H2'	3:L8:7:U:H6	1.78	0.49
24:LV:107:ASN:HD21	24:LV:111:GLU:HB3	1.77	0.49
32:Ld:64:ILE:HG23	32:Ld:68:LEU:HD23	1.93	0.49
46:S2:175:A:N6	46:S2:314:A:N7	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1736:A:H2'	46:S2:1737:G:O4'	2.12	0.49
64:SR:43:SER:HB3	64:SR:46:LEU:CD1	2.42	0.49
46:S2:104:A:H62	46:S2:357:C:H5	1.59	0.49
46:S2:1521:G:H21	62:SP:126:VAL:HG11	1.77	0.49
50:SC:105:GLU:HA	50:SC:105:GLU:OE2	2.12	0.49
58:SK:49:MET:N	58:SK:49:MET:SD	2.85	0.49
68:SV:67:ASP:O	68:SV:71:ARG:HG2	2.13	0.49
73:Sa:24:THR:HG23	73:Sa:72:HIS:O	2.12	0.49
1:L5:1523:C:H2'	1:L5:1524:G:C8	2.48	0.49
1:L5:3368:A:H1'	46:S2:971:G:C2	2.48	0.49
1:L5:4510:U:H2'	1:L5:4511:C:C6	2.47	0.49
17:LO:118:MET:SD	21:LS:169:THR:HG22	2.52	0.49
20:LR:170:ARG:HG2	20:LR:170:ARG:HH11	1.77	0.49
25:LW:47:ARG:HG3	25:LW:54:LEU:HD23	1.95	0.49
46:S2:47:G:H22	46:S2:479:G:N2	2.10	0.49
55:SH:51:ILE:HD11	55:SH:176:VAL:HG12	1.94	0.49
60:SN:28:LEU:HD22	60:SN:32:ASP:HB2	1.93	0.49
78:Sg:301:GLY:HA2	78:Sg:307:VAL:HG22	1.94	0.49
1:L5:1192:G:H5''	1:L5:1193:C:OP2	2.12	0.49
1:L5:1293:G:H21	14:LL:184:MET:HE3	1.76	0.49
1:L5:4178:C:OP1	5:LB:246:ARG:NH1	2.33	0.49
46:S2:605:A:N3	46:S2:640:C:O2'	2.38	0.49
46:S2:1452:G:N2	46:S2:1475:A:H61	2.10	0.49
46:S2:1485:A:H2'	46:S2:1486:U:H6	1.78	0.49
46:S2:1670:G:OP2	63:SQ:130:LYS:HD3	2.12	0.49
1:L5:1010:U:H4'	7:LD:279:ARG:HH11	1.77	0.49
3:L8:94:G:N3	38:Lj:82:THR:OG1	2.43	0.49
16:LN:45:PRO:O	16:LN:49:ARG:HG3	2.13	0.49
46:S2:85:A:HO2'	46:S2:86:C:P	2.36	0.49
46:S2:905:A:H2'	46:S2:906:C:C6	2.48	0.49
50:SC:183:LYS:HE2	69:SW:95:PRO:HA	1.95	0.49
63:SQ:17:LYS:O	63:SQ:126:ARG:NH2	2.45	0.49
65:SS:75:ARG:NH2	65:SS:81:ASP:OD2	2.46	0.49
1:L5:267:G:H2'	1:L5:268:G:C8	2.47	0.49
1:L5:1271:G:O2'	1:L5:1272:C:O5'	2.28	0.49
1:L5:1903:A:H8	1:L5:1903:A:OP2	1.96	0.49
1:L5:3952:U:OP1	30:Lb:33:LYS:NZ	2.45	0.49
5:LB:145:GLN:HA	5:LB:148:LYS:NZ	2.13	0.49
6:LC:150:LEU:HB3	6:LC:151:PRO:HD3	1.95	0.49
9:LF:114:VAL:O	9:LF:142:GLY:HA2	2.12	0.49
46:S2:483:G:H4'	70:SX:76:LYS:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:946:U:H2'	46:S2:947:U:C6	2.47	0.49
46:S2:1637:G:O2'	53:SF:164:ARG:NH1	2.45	0.49
48:SA:143:PRO:CG	68:SV:32:ILE:HD11	2.40	0.49
52:SE:102:ILE:HD12	52:SE:239:PRO:HD3	1.94	0.49
60:SN:13:GLN:HG3	74:Sb:21:LYS:HE3	1.93	0.49
1:L5:831:G:H8	1:L5:831:G:OP1	1.96	0.49
1:L5:3992:A:H2'	1:L5:3993:U:H6	1.77	0.49
1:L5:4171:A:OP2	5:LB:258:HIS:HB2	2.12	0.49
2:L7:117:G:OP1	7:LD:253:TYR:OH	2.27	0.49
46:S2:583:U:H2'	46:S2:584:A:H5''	1.93	0.49
46:S2:619:C:H41	70:SX:67:ARG:HH22	1.60	0.49
46:S2:891:U:H5	46:S2:898:U:H5''	1.77	0.49
46:S2:1442:U:H4'	46:S2:1443:U:OP2	2.12	0.49
55:SH:31:GLU:HG2	55:SH:41:ARG:NH2	2.28	0.49
71:SY:104:ARG:HH21	71:SY:108:LYS:HZ1	1.61	0.49
78:Sg:132:TRP:HA	78:Sg:138:CYS:HA	1.94	0.49
1:L5:923:G:O2'	1:L5:924:G:OP1	2.27	0.49
1:L5:1377:A:H61	46:S2:1029:A:H2	1.58	0.49
6:LC:66:SER:O	6:LC:67:TRP:HB2	2.13	0.49
9:LF:218:THR:O	9:LF:218:THR:OG1	2.30	0.49
10:LG:209:SER:HA	10:LG:212:LYS:HD3	1.95	0.49
22:LT:14:MET:HE1	22:LT:55:LYS:HB2	1.95	0.49
31:Lc:75:SER:O	31:Lc:75:SER:OG	2.28	0.49
46:S2:573:U:OP2	71:SY:37:LYS:NZ	2.46	0.49
46:S2:820:G:H4'	52:SE:255:ARG:HH22	1.78	0.49
46:S2:1458:U:H2'	46:S2:1459:G:H8	1.78	0.49
77:Se:89:GLN:OE1	77:Se:89:GLN:O	2.31	0.49
1:L5:3259:C:H2'	1:L5:3260:G:C8	2.49	0.48
6:LC:25:PRO:HG2	6:LC:28:PHE:CE2	2.47	0.48
18:LP:85:LYS:O	18:LP:89:GLU:HG2	2.13	0.48
46:S2:62:G:N1	46:S2:86:C:O2	2.46	0.48
46:S2:1319:G:H2'	46:S2:1320:U:C6	2.48	0.48
46:S2:1780:G:H2'	46:S2:1781:G:C4	2.48	0.48
46:S2:1802:A:H2'	46:S2:1803:C:C6	2.47	0.48
57:SJ:48:PHE:CE2	57:SJ:52:LYS:HD2	2.48	0.48
69:SW:28:ARG:HB3	69:SW:29:PRO:HD3	1.94	0.48
74:Sb:34:ASP:HB2	74:Sb:80:ARG:HG3	1.94	0.48
1:L5:766:G:N2	1:L5:805:C:H42	2.06	0.48
4:LA:242:ARG:NH2	4:LA:243:THR:O	2.46	0.48
11:LH:120:GLU:HG2	11:LH:122:TYR:H	1.78	0.48
13:LJ:167:GLN:HA	13:LJ:171:ASP:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:63:U:O2	46:S2:85:A:H2	1.96	0.48
46:S2:877:C:H2'	46:S2:878:C:C6	2.47	0.48
65:SS:59:LEU:HD23	65:SS:59:LEU:H	1.78	0.48
1:L5:459:C:H2'	1:L5:460:G:H8	1.79	0.48
7:LD:107:ARG:NH1	7:LD:169:GLY:O	2.46	0.48
14:LL:178:ALA:HB3	29:La:134:GLU:OE1	2.13	0.48
46:S2:558:U:O2'	46:S2:559:G:O5'	2.30	0.48
57:SJ:59:GLU:O	57:SJ:62:THR:OG1	2.27	0.48
57:SJ:86:VAL:HG13	57:SJ:104:ASP:OD2	2.13	0.48
66:ST:76:THR:HB	66:ST:94:ARG:HB3	1.95	0.48
67:SU:34:LYS:HB3	67:SU:34:LYS:HE2	1.50	0.48
1:L5:270:C:H2'	1:L5:271:U:O2	2.13	0.48
1:L5:1012:U:H3'	1:L5:1013:C:H5''	1.94	0.48
1:L5:2540:C:O2'	1:L5:2541:A:OP2	2.27	0.48
1:L5:3267:A:H2'	1:L5:3268:A:H8	1.78	0.48
1:L5:3410:G:H5''	1:L5:3433:G:C8	2.48	0.48
8:LE:250:ILE:H	8:LE:250:ILE:HD12	1.79	0.48
9:LF:89:THR:O	9:LF:93:MET:HG2	2.13	0.48
46:S2:49:C:C2	46:S2:477:A:N6	2.81	0.48
50:SC:161:SER:O	50:SC:161:SER:OG	2.31	0.48
61:SO:96:LYS:HE3	61:SO:132:VAL:HG11	1.95	0.48
63:SQ:13:PHE:HE2	63:SQ:15:ARG:HE	1.60	0.48
1:L5:417:A:C2	3:L8:17:A:H1'	2.47	0.48
2:L7:12:U:OP2	2:L7:67:C:O2'	2.31	0.48
46:S2:157:U:H6	46:S2:157:U:O5'	1.97	0.48
46:S2:464:C:O2'	46:S2:465:A:O5'	2.31	0.48
48:SA:149:ASN:ND2	48:SA:165:ASN:HB2	2.28	0.48
49:SB:197:ILE:HB	49:SB:210:VAL:HG11	1.96	0.48
59:SL:3:ASP:OD1	59:SL:3:ASP:N	2.30	0.48
59:SL:119:ASP:OD1	59:SL:119:ASP:O	2.32	0.48
63:SQ:104:SER:HA	63:SQ:107:GLU:OE1	2.14	0.48
78:Sg:187:ASN:OD1	78:Sg:187:ASN:N	2.45	0.48
1:L5:1:C:H4'	1:L5:2:G:OP1	2.13	0.48
1:L5:927:C:O2'	1:L5:928:C:OP1	2.28	0.48
1:L5:4387:A:H1'	1:L5:4388:G:C8	2.48	0.48
6:LC:71:ARG:HD2	6:LC:71:ARG:N	2.29	0.48
19:LQ:115:LYS:HE3	19:LQ:115:LYS:HB3	1.67	0.48
21:LS:48:VAL:HG11	21:LS:54:MET:HE2	1.96	0.48
46:S2:311:C:H2'	46:S2:312:C:C6	2.49	0.48
46:S2:895:G:H5''	46:S2:896:G:C8	2.48	0.48
46:S2:965:A:H2'	46:S2:966:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1747:U:H5	46:S2:1789:A:N1	2.11	0.48
51:SD:7:LYS:HE2	51:SD:7:LYS:HB3	1.66	0.48
57:SJ:153:SER:O	57:SJ:153:SER:OG	2.25	0.48
63:SQ:27:ARG:HA	63:SQ:65:GLY:O	2.13	0.48
1:L5:4120:A:O2'	1:L5:4163:A:N3	2.45	0.48
1:L5:4392:C:H1'	1:L5:4609:G:C2	2.49	0.48
7:LD:42:ASN:ND2	22:LT:69:GLN:OE1	2.32	0.48
24:LV:71:GLU:OE1	24:LV:71:GLU:N	2.47	0.48
46:S2:494:A:N6	46:S2:510:G:H1'	2.27	0.48
46:S2:1586:U:O2'	46:S2:1588:G:OP2	2.22	0.48
52:SE:104:ASP:HB2	52:SE:110:ALA:HB2	1.96	0.48
56:SI:143:LYS:HD2	56:SI:144:LYS:N	2.28	0.48
57:SJ:81:LEU:HB3	57:SJ:87:LEU:HB2	1.96	0.48
65:SS:85:ASN:OD1	65:SS:97:GLN:NE2	2.39	0.48
72:SZ:48:VAL:HG12	72:SZ:49:LEU:H	1.78	0.48
75:Sc:13:ARG:HG3	75:Sc:35:MET:HE2	1.96	0.48
7:LD:109:LEU:HD23	7:LD:171:LEU:HD11	1.96	0.48
11:LH:91:LYS:HB2	11:LH:183:GLU:HG3	1.95	0.48
11:LH:91:LYS:HE2	11:LH:183:GLU:OE2	2.14	0.48
11:LH:142:ASP:OD1	11:LH:142:ASP:O	2.32	0.48
13:LJ:136:ARG:NH2	13:LJ:156:ARG:O	2.47	0.48
46:S2:60:A:C3'	46:S2:61:A:H5'	2.44	0.48
46:S2:486:A:H5''	46:S2:487:A:OP1	2.14	0.48
46:S2:838:A:N6	71:SY:26:ASP:HB2	2.28	0.48
47:S7:20:A:H2'	47:S7:21:A:H4'	1.95	0.48
60:SN:47:PRO:HG2	60:SN:86:GLU:CD	2.38	0.48
62:SP:95:GLY:HA2	62:SP:103:ASN:O	2.14	0.48
68:SV:32:ILE:HG22	68:SV:55:ILE:O	2.13	0.48
71:SY:104:ARG:HH21	71:SY:108:LYS:NZ	2.11	0.48
1:L5:822:U:H2'	1:L5:823:C:C6	2.48	0.48
33:Le:126:ASN:HD22	33:Le:126:ASN:C	2.20	0.48
46:S2:569:C:H2'	46:S2:570:A:H8	1.79	0.48
46:S2:885:C:O2	46:S2:902:G:N1	2.33	0.48
46:S2:1614:G:OP2	62:SP:39:ALA:N	2.46	0.48
51:SD:105:LEU:HD23	51:SD:184:ILE:HD12	1.96	0.48
56:SI:4:SER:HA	56:SI:29:LEU:HA	1.96	0.48
75:Sc:15:THR:HG22	75:Sc:16:LYS:HG2	1.96	0.48
78:Sg:297:THR:OG1	78:Sg:298:LEU:N	2.47	0.48
1:L5:1347:A:H5'	1:L5:1437:A:H61	1.79	0.48
2:L7:3:C:H2'	2:L7:4:U:C6	2.49	0.48
46:S2:530:A:C5	46:S2:531:U:H1'	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:637:C:H5''	77:Se:98:LYS:HZ3	1.76	0.48
46:S2:1554:C:H42	76:Sd:22:ARG:HE	1.62	0.48
53:SF:167:LYS:HE3	53:SF:172:CYS:SG	2.54	0.48
56:SI:162:LEU:HA	56:SI:165:GLN:NE2	2.28	0.48
20:LR:160:GLU:OE2	20:LR:163:ARG:NH2	2.47	0.47
36:Lh:35:LYS:HA	36:Lh:44:LEU:HD21	1.95	0.47
46:S2:39:A:H2'	46:S2:40:A:O4'	2.14	0.47
46:S2:1290:U:H3	46:S2:1311:U:H2'	1.79	0.47
67:SU:26:SER:HB3	67:SU:110:VAL:HA	1.96	0.47
1:L5:2313:G:H2'	1:L5:2314:G:C8	2.49	0.47
1:L5:4247:U:H2'	1:L5:4248:G:H8	1.78	0.47
1:L5:4392:C:H1'	1:L5:4609:G:N2	2.29	0.47
2:L7:61:G:H5''	7:LD:271:MET:SD	2.53	0.47
6:LC:14:LYS:NZ	6:LC:16:GLU:OE2	2.41	0.47
6:LC:303:ARG:O	19:LQ:38:ARG:NH2	2.35	0.47
7:LD:55:VAL:HG22	7:LD:60:ILE:HG12	1.94	0.47
18:LP:112:LEU:HD13	18:LP:150:LEU:HD23	1.96	0.47
19:LQ:122:THR:HB	19:LQ:125:GLN:HG3	1.95	0.47
32:Ld:101:LYS:HG3	32:Ld:102:LEU:HD22	1.96	0.47
43:Lo:26:TYR:CD1	43:Lo:82:MET:HE1	2.50	0.47
46:S2:115:U:HO2'	46:S2:116:U:H6	1.63	0.47
46:S2:501:A:H3'	46:S2:502:C:C6	2.48	0.47
8:LE:209:VAL:HG11	8:LE:275:LEU:HD21	1.97	0.47
14:LL:18:TRP:CD1	14:LL:18:TRP:H	2.31	0.47
20:LR:104:ARG:HG2	20:LR:108:ARG:HH21	1.79	0.47
46:S2:1567:G:O6	66:ST:97:LYS:HE3	2.14	0.47
51:SD:12:VAL:O	51:SD:16:ILE:HG13	2.15	0.47
60:SN:26:LEU:HD11	60:SN:28:LEU:HB2	1.96	0.47
62:SP:16:THR:HG23	62:SP:16:THR:O	2.13	0.47
75:Sc:31:ARG:HH11	75:Sc:31:ARG:C	2.22	0.47
78:Sg:206:LEU:HD12	78:Sg:219:TRP:O	2.15	0.47
1:L5:1026:C:H2'	1:L5:1027:G:H8	1.79	0.47
20:LR:172:ARG:HH22	46:S2:910:G:P	2.37	0.47
25:LW:9:SER:HB2	25:LW:11:TYR:HD1	1.79	0.47
48:SA:132:GLN:HA	48:SA:132:GLN:OE1	2.14	0.47
51:SD:16:ILE:HD13	76:Sd:22:ARG:NH1	2.29	0.47
57:SJ:89:GLU:OE1	57:SJ:89:GLU:N	2.47	0.47
1:L5:266:G:H2'	1:L5:267:G:C8	2.49	0.47
1:L5:2345:A:H2'	1:L5:2346:U:H6	1.79	0.47
1:L5:3941:C:O2'	1:L5:3974:U:OP1	2.28	0.47
1:L5:4357:C:H2'	1:L5:4358:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LD:272:SER:O	7:LD:276:LYS:HG3	2.15	0.47
22:LT:157:GLU:N	22:LT:157:GLU:OE1	2.48	0.47
33:Le:35:TRP:CZ2	33:Le:56:PRO:HD2	2.50	0.47
46:S2:540:C:H2'	46:S2:542:U:H5''	1.95	0.47
46:S2:1737:G:H2'	46:S2:1738:G:C8	2.49	0.47
50:SC:173:LYS:HD3	68:SV:3:ASN:HA	1.96	0.47
51:SD:67:ARG:HA	51:SD:70:THR:HG22	1.96	0.47
54:SG:188:LYS:O	54:SG:192:ILE:HG13	2.14	0.47
1:L5:174:C:H2'	1:L5:175:C:C6	2.50	0.47
1:L5:477:G:H2'	1:L5:478:G:C8	2.48	0.47
14:LL:62:PRO:O	14:LL:63:THR:OG1	2.26	0.47
43:Lo:99:ARG:NE	43:Lo:99:ARG:HA	2.29	0.47
46:S2:3:C:O2	57:SJ:18:ARG:NH2	2.34	0.47
46:S2:875:G:H2'	46:S2:876:A:H8	1.79	0.47
46:S2:1458:U:H2'	46:S2:1459:G:C8	2.50	0.47
46:S2:1717:C:H2'	46:S2:1718:C:C6	2.50	0.47
50:SC:135:GLY:O	50:SC:136:HIS:ND1	2.48	0.47
56:SI:142:SER:OG	56:SI:143:LYS:N	2.48	0.47
59:SL:120:VAL:HG22	59:SL:145:VAL:HG11	1.94	0.47
78:Sg:211:GLY:O	78:Sg:236:ILE:HG22	2.14	0.47
1:L5:138:C:H2'	1:L5:139:G:H8	1.79	0.47
1:L5:1004:G:N2	1:L5:1022:G:H22	2.12	0.47
1:L5:3530:G:H2'	1:L5:3531:G:C8	2.50	0.47
1:L5:4199:A:N7	4:LA:215:ASN:ND2	2.63	0.47
1:L5:4384:G:OP2	1:L5:4384:G:H8	1.97	0.47
2:L7:4:U:H2'	2:L7:5:A:H8	1.79	0.47
3:L8:141:C:H2'	3:L8:142:U:C6	2.50	0.47
5:LB:189:THR:O	5:LB:193:LYS:HG2	2.14	0.47
14:LL:21:ARG:O	16:LN:197:THR:OG1	2.29	0.47
19:LQ:99:LYS:HG3	19:LQ:119:LYS:HB3	1.97	0.47
46:S2:68:A:H2'	46:S2:69:C:O4'	2.14	0.47
46:S2:523:A:N7	57:SJ:38:ARG:NH2	2.63	0.47
46:S2:846:G:OP2	52:SE:108:ARG:NH2	2.29	0.47
46:S2:1254:A:H4'	46:S2:1255:C:H5''	1.95	0.47
46:S2:1287:G:N2	46:S2:1314:A:C6	2.83	0.47
50:SC:160:LEU:HD12	50:SC:160:LEU:HA	1.78	0.47
51:SD:35:SER:HB2	51:SD:51:LEU:O	2.14	0.47
57:SJ:4:ALA:O	57:SJ:5:ARG:HD2	2.14	0.47
68:SV:2:GLN:HG2	68:SV:8:PHE:CE1	2.49	0.47
71:SY:26:ASP:HB3	71:SY:68:LYS:NZ	2.29	0.47
1:L5:665:C:H2'	1:L5:666:C:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1221:G:H21	1:L5:1227:G:H1	1.63	0.47
3:L8:92:U:H2'	3:L8:93:C:O4'	2.15	0.47
25:LW:27:LYS:HE3	25:LW:29:PHE:HZ	1.80	0.47
46:S2:28:U:H2'	46:S2:29:G:H8	1.79	0.47
46:S2:82:G:OP2	46:S2:82:G:H8	1.98	0.47
59:SL:80:MET:HA	59:SL:86:ILE:HG22	1.97	0.47
78:Sg:20:GLN:HG3	78:Sg:68:ASP:HB2	1.97	0.47
1:L5:946:G:H2'	1:L5:947:C:C6	2.50	0.47
1:L5:1580:C:H2'	1:L5:1581:C:C6	2.50	0.47
4:LA:117:GLU:O	4:LA:162:ASN:ND2	2.40	0.47
4:LA:178:PRO:HD2	44:Lp:26:VAL:HG23	1.97	0.47
5:LB:125:SER:O	5:LB:127:LYS:NZ	2.47	0.47
6:LC:138:MET:HE1	6:LC:145:GLU:OE1	2.15	0.47
10:LG:145:THR:O	10:LG:149:ASN:ND2	2.47	0.47
20:LR:170:ARG:HG2	20:LR:170:ARG:NH1	2.30	0.47
24:LV:62:MET:HE3	24:LV:62:MET:HB3	1.73	0.47
46:S2:833:G:N2	46:S2:842:G:H22	2.12	0.47
46:S2:1320:U:H2'	46:S2:1321:G:C8	2.49	0.47
46:S2:1529:G:O2'	46:S2:1667:C:OP1	2.31	0.47
48:SA:38:ILE:HA	48:SA:49:ILE:HA	1.96	0.47
58:SK:53:LYS:HD3	58:SK:60:GLU:HG3	1.96	0.47
59:SL:90:ARG:HD3	59:SL:109:MET:HE3	1.95	0.47
61:SO:143:LYS:HE2	61:SO:143:LYS:HB2	1.62	0.47
1:L5:152:U:OP2	16:LN:49:ARG:NH2	2.44	0.47
1:L5:324:U:H2'	1:L5:325:C:C6	2.50	0.47
1:L5:490:C:H2'	1:L5:491:C:C6	2.50	0.47
1:L5:1261:C:H2'	1:L5:1262:G:C8	2.50	0.47
3:L8:19:C:H2'	3:L8:20:A:C8	2.50	0.47
20:LR:76:MET:HE3	20:LR:76:MET:HB3	1.80	0.47
20:LR:105:LEU:HD13	20:LR:135:LYS:HE3	1.96	0.47
30:Lb:110:MET:O	30:Lb:114:GLN:HG2	2.15	0.47
46:S2:805:U:H2'	46:S2:806:U:C6	2.50	0.47
46:S2:868:G:O2'	46:S2:869:G:H5'	2.15	0.47
51:SD:179:GLN:NE2	51:SD:179:GLN:O	2.48	0.47
54:SG:119:LYS:H	54:SG:119:LYS:HD2	1.80	0.47
63:SQ:31:LEU:HB3	63:SQ:67:ASP:HB3	1.97	0.47
63:SQ:113:ILE:HD13	63:SQ:120:LEU:HD12	1.97	0.47
68:SV:22:ARG:HD2	68:SV:22:ARG:N	2.30	0.47
1:L5:1147:C:H2'	1:L5:1148:A:H8	1.80	0.46
1:L5:1226:G:H2'	1:L5:1227:G:C8	2.51	0.46
1:L5:1233:G:OP1	19:LQ:71:LYS:NZ	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3267:A:H2'	1:L5:3268:A:C8	2.50	0.46
19:LQ:172:ARG:HA	19:LQ:176:ARG:HD2	1.96	0.46
46:S2:180:G:H2'	46:S2:180:G:N3	2.30	0.46
46:S2:947:U:H2'	46:S2:948:G:C8	2.51	0.46
47:S7:65:C:O2'	47:S7:66:C:H5'	2.15	0.46
56:SI:87:ASN:HB3	56:SI:90:LEU:HG	1.97	0.46
56:SI:164:GLU:CD	56:SI:164:GLU:N	2.73	0.46
65:SS:85:ASN:ND2	65:SS:97:GLN:OE1	2.48	0.46
66:ST:14:PHE:HE2	66:ST:135:ALA:HB2	1.80	0.46
73:Sa:43:ASN:OD1	73:Sa:44:ILE:N	2.48	0.46
1:L5:425:A:N1	3:L8:8:U:H5	2.12	0.46
1:L5:1154:U:H2'	1:L5:1155:C:C6	2.50	0.46
1:L5:1677:A:OP1	30:Lb:9:THR:HG23	2.15	0.46
1:L5:3420:A:O2'	1:L5:3421:U:H6	1.98	0.46
1:L5:4357:C:H2'	1:L5:4358:A:H8	1.80	0.46
2:L7:110:G:H2'	2:L7:111:C:C6	2.50	0.46
6:LC:25:PRO:HG2	6:LC:28:PHE:HE2	1.80	0.46
12:LI:177:ASN:HB2	12:LI:180:GLU:OE2	2.14	0.46
17:LO:5:GLN:OE1	17:LO:5:GLN:N	2.48	0.46
26:LX:117:TYR:O	26:LX:119:ILE:HG23	2.14	0.46
46:S2:488:U:H4'	46:S2:490:A:H8	1.80	0.46
46:S2:1291:G:N7	46:S2:1311:U:O2'	2.48	0.46
46:S2:1810:A:H3'	46:S2:1811:U:H5''	1.97	0.46
1:L5:748:G:H3'	1:L5:749:U:H5''	1.96	0.46
1:L5:1557:U:H3	1:L5:1579:A:N6	2.12	0.46
1:L5:2602:G:O2'	1:L5:3495:U:O4	2.32	0.46
3:L8:102:G:OP2	3:L8:104:A:O2'	2.26	0.46
4:LA:180:LEU:HD21	44:Lp:22:LEU:HB3	1.96	0.46
10:LG:140:VAL:O	10:LG:144:THR:OG1	2.24	0.46
11:LH:120:GLU:CD	11:LH:124:ARG:HH12	2.24	0.46
22:LT:97:LYS:HB3	22:LT:97:LYS:HE2	1.65	0.46
26:LX:88:LYS:HE3	26:LX:88:LYS:HB3	1.67	0.46
40:LI:29:MET:HE3	40:LI:29:MET:HB3	1.85	0.46
46:S2:1110:C:N3	64:SR:126:MET:HG3	2.30	0.46
51:SD:72:VAL:HG11	58:SK:70:TYR:HE1	1.80	0.46
57:SJ:107:GLU:O	57:SJ:112:THR:OG1	2.34	0.46
70:SX:99:GLU:OE1	70:SX:99:GLU:HA	2.15	0.46
78:Sg:212:LYS:HE3	78:Sg:212:LYS:HB2	1.74	0.46
1:L5:3430:U:H2'	1:L5:3432:A:H2	1.81	0.46
1:L5:4637:U:H1'	1:L5:4638:C:C5	2.50	0.46
13:LJ:84:GLU:HG3	13:LJ:170:TYR:HE2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LU:38:ASN:OD1	23:LU:39:PHE:N	2.48	0.46
46:S2:514:G:H5'	46:S2:515:U:H5	1.81	0.46
58:SK:57:TYR:O	58:SK:72:THR:OG1	2.31	0.46
62:SP:53:GLN:O	62:SP:54:HIS:C	2.59	0.46
63:SQ:129:SER:OG	63:SQ:130:LYS:N	2.47	0.46
65:SS:90:VAL:HG11	65:SS:113:ARG:HH11	1.81	0.46
78:Sg:72:SER:OG	78:Sg:73:SER:N	2.49	0.46
1:L5:4233:U:O2'	5:LB:182:GLU:OE2	2.26	0.46
10:LG:157:ILE:HG23	10:LG:201:THR:HG22	1.97	0.46
36:Lh:107:GLN:O	36:Lh:111:GLU:HG3	2.16	0.46
45:Lr:89:THR:HG21	45:Lr:118:LEU:HD11	1.97	0.46
48:SA:51:LEU:HB2	64:SR:109:LEU:HD11	1.96	0.46
78:Sg:194:TYR:CZ	78:Sg:212:LYS:HD2	2.50	0.46
1:L5:1122:A:H2'	1:L5:1123:C:C6	2.50	0.46
1:L5:2221:C:O2'	1:L5:2222:C:H6	1.99	0.46
1:L5:2345:A:H2'	1:L5:2346:U:C6	2.51	0.46
10:LG:96:LEU:HD22	10:LG:189:ARG:HH21	1.81	0.46
21:LS:8:ARG:O	21:LS:33:PHE:HA	2.15	0.46
46:S2:809:A:H2	46:S2:856:G:H22	1.62	0.46
49:SB:85:LYS:HB3	49:SB:101:HIS:HB3	1.98	0.46
51:SD:40:ARG:HH22	67:SU:106:ILE:HG21	1.81	0.46
54:SG:135:PRO:HB2	54:SG:141:ILE:HG22	1.96	0.46
56:SI:103:LEU:HD21	56:SI:170:LYS:HD3	1.96	0.46
62:SP:34:MET:SD	62:SP:45:LEU:HB3	2.56	0.46
62:SP:56:LEU:HD12	62:SP:56:LEU:HA	1.74	0.46
78:Sg:11:LEU:HD23	78:Sg:307:VAL:HG12	1.98	0.46
1:L5:142:G:H4'	1:L5:143:U:C5	2.51	0.46
1:L5:1050:C:O2'	1:L5:1051:G:O4'	2.26	0.46
1:L5:4506:G:O2'	1:L5:4507:G:H8	1.99	0.46
33:Le:124:ASN:OD1	33:Le:124:ASN:N	2.49	0.46
46:S2:1017:U:OP1	74:Sb:30:SER:OG	2.32	0.46
47:S7:18:G:N2	47:S7:58:A:OP2	2.47	0.46
51:SD:104:SER:HA	51:SD:107:TYR:CE2	2.51	0.46
63:SQ:53:GLU:HB2	63:SQ:54:PRO:HD3	1.97	0.46
68:SV:40:ASP:OD1	68:SV:41:ARG:N	2.49	0.46
77:Se:105:ARG:CZ	77:Se:105:ARG:HB3	2.45	0.46
1:L5:2214:G:O2'	1:L5:3329:G:H8	1.97	0.46
5:LB:59:GLU:HG3	5:LB:71:GLU:OE2	2.15	0.46
46:S2:614:G:OP2	46:S2:614:G:H8	1.98	0.46
46:S2:1724:G:H2'	46:S2:1725:A:C8	2.51	0.46
59:SL:55:TYR:CD2	59:SL:115:PRO:HG2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SL:100:ASN:O	59:SL:101:ARG:HG3	2.16	0.46
1:L5:490:C:H2'	1:L5:491:C:H6	1.80	0.46
1:L5:2075:G:N2	1:L5:2078:G:OP2	2.33	0.46
1:L5:4393:G:H1'	1:L5:4396:G:H8	1.80	0.46
6:LC:8:ILE:N	6:LC:22:VAL:O	2.34	0.46
16:LN:124:ASP:OD1	16:LN:125:SER:N	2.49	0.46
23:LU:43:LEU:O	23:LU:47:ILE:HG12	2.15	0.46
27:LY:50:ARG:HG2	27:LY:51:LYS:H	1.81	0.46
46:S2:943:G:H2'	46:S2:944:U:C6	2.50	0.46
46:S2:1093:G:O2'	69:SW:3:ARG:HG2	2.15	0.46
46:S2:1278:C:H42	46:S2:1323:G:H8	1.62	0.46
47:S7:62:C:H2'	47:S7:63:A:C8	2.51	0.46
49:SB:82:ARG:NH2	49:SB:191:ASP:HB2	2.31	0.46
59:SL:61:PRO:HA	59:SL:66:VAL:HG22	1.96	0.46
78:Sg:220:ASP:H	78:Sg:224:GLY:HA2	1.81	0.46
1:L5:416:G:O2'	3:L8:16:G:N2	2.38	0.46
1:L5:3973:G:H2'	1:L5:3974:U:C6	2.51	0.46
3:L8:80:A:H3'	36:Lh:2:ALA:HB3	1.98	0.46
23:LU:37:ALA:O	23:LU:41:GLN:HG2	2.16	0.46
46:S2:1674:U:H2'	46:S2:1675:G:O4'	2.15	0.46
48:SA:6:ASP:HA	48:SA:9:GLN:HG2	1.96	0.46
49:SB:71:LEU:HD12	49:SB:82:ARG:HD2	1.98	0.46
62:SP:86:LEU:O	62:SP:89:MET:HG2	2.16	0.46
62:SP:121:ILE:HD12	62:SP:121:ILE:HA	1.80	0.46
68:SV:1:MET:SD	68:SV:1:MET:N	2.73	0.46
78:Sg:238:ALA:N	78:Sg:251:ALA:HB3	2.31	0.46
1:L5:279:G:H5''	16:LN:14:LYS:HZ3	1.82	0.45
1:L5:1445:A:C2	4:LA:204:MET:HG2	2.51	0.45
1:L5:1669:U:OP1	12:LI:4:ARG:NH2	2.45	0.45
11:LH:120:GLU:OE2	11:LH:124:ARG:NH1	2.49	0.45
12:LI:49:CYS:HB3	12:LI:168:SER:HB3	1.98	0.45
46:S2:42:A:H4'	46:S2:97:U:OP1	2.17	0.45
47:S7:31:G:O2'	47:S7:32:C:O2	2.27	0.45
53:SF:38:TYR:HD2	53:SF:144:LEU:HD13	1.81	0.45
65:SS:40:TYR:OH	65:SS:97:GLN:HG3	2.16	0.45
65:SS:46:ARG:NH1	66:ST:50:GLU:OE2	2.48	0.45
1:L5:2656:G:H3'	1:L5:2657:G:N2	2.31	0.45
2:L7:50:A:OP1	7:LD:224:SER:OG	2.29	0.45
8:LE:292:HIS:CE1	34:Lf:33:VAL:HG22	2.51	0.45
13:LJ:160:GLU:HA	13:LJ:163:MET:HE2	1.98	0.45
46:S2:226:A:H2'	46:S2:227:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:473:C:H4'	46:S2:475:G:OP1	2.16	0.45
46:S2:750:U:O4	46:S2:795:A:O2'	2.25	0.45
48:SA:29:ASN:OD1	48:SA:151:ASP:HB3	2.16	0.45
65:SS:114:LEU:HD22	65:SS:121:ARG:HB3	1.99	0.45
75:Sc:13:ARG:NH1	75:Sc:13:ARG:HB3	2.31	0.45
78:Sg:92:LEU:HD12	78:Sg:92:LEU:HA	1.80	0.45
78:Sg:164:ILE:HD12	78:Sg:164:ILE:HA	1.82	0.45
1:L5:662:C:H2'	1:L5:663:C:O2	2.16	0.45
1:L5:1597:A:H5''	1:L5:3867:A:H61	1.82	0.45
1:L5:4589:G:C8	8:LE:180:LEU:HD21	2.51	0.45
3:L8:5:U:O2'	3:L8:6:C:OP1	2.33	0.45
10:LG:101:LYS:HG3	10:LG:102:TYR:CE1	2.51	0.45
10:LG:180:PRO:HD3	10:LG:223:ARG:NH2	2.30	0.45
20:LR:47:ASP:N	20:LR:47:ASP:OD1	2.48	0.45
24:LV:124:GLU:OE1	24:LV:124:GLU:N	2.48	0.45
46:S2:121:U:H5	46:S2:340:A:H61	1.63	0.45
46:S2:177:G:H2'	46:S2:178:C:C5	2.52	0.45
46:S2:863:A:C8	69:SW:107:SER:HA	2.51	0.45
46:S2:1260:A:N6	46:S2:1520:U:H5'	2.31	0.45
49:SB:144:LYS:HD3	49:SB:208:HIS:HB3	1.97	0.45
56:SI:107:THR:HG22	56:SI:108:PRO:HD3	1.98	0.45
65:SS:64:VAL:O	65:SS:68:ILE:HG12	2.15	0.45
1:L5:139:G:H2'	1:L5:140:G:O4'	2.16	0.45
1:L5:1147:C:H2'	1:L5:1148:A:C8	2.51	0.45
1:L5:4208:U:C6	80:Z:-1:UNK:CB	2.99	0.45
1:L5:4529:C:H2'	1:L5:4530:G:H8	1.82	0.45
7:LD:53:VAL:HG12	7:LD:62:CYS:SG	2.57	0.45
7:LD:259:ARG:HD2	7:LD:259:ARG:HA	1.74	0.45
14:LL:100:PRO:O	37:Li:25:ARG:NH2	2.36	0.45
16:LN:83:LYS:O	16:LN:85:VAL:N	2.49	0.45
37:Li:42:ASP:OD1	37:Li:42:ASP:C	2.60	0.45
46:S2:1048:C:H2'	46:S2:1049:G:O4'	2.15	0.45
48:SA:147:LEU:HD12	48:SA:161:ILE:HB	1.98	0.45
50:SC:60:TRP:CE2	50:SC:62:PRO:HG3	2.51	0.45
53:SF:146:ARG:O	53:SF:150:ALA:N	2.44	0.45
56:SI:148:LYS:HA	56:SI:151:GLU:OE1	2.17	0.45
62:SP:25:LEU:O	62:SP:28:MET:HB3	2.15	0.45
63:SQ:128:GLU:CD	63:SQ:129:SER:H	2.25	0.45
66:ST:10:ASN:HB3	66:ST:13:GLU:HG2	1.99	0.45
8:LE:78:ARG:HA	8:LE:78:ARG:HD2	1.64	0.45
20:LR:173:ARG:NH2	46:S2:910:G:OP1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Lc:53:PRO:HG2	31:Lc:56:ARG:HB3	1.98	0.45
39:Lk:67:LYS:HE2	39:Lk:67:LYS:HB3	1.73	0.45
46:S2:515:U:H2'	46:S2:516:G:O4'	2.16	0.45
46:S2:1408:U:H2'	46:S2:1409:U:C6	2.51	0.45
47:S7:44:A:H2'	47:S7:45:G:O4'	2.16	0.45
52:SE:18:TRP:CD1	52:SE:20:LEU:HG	2.52	0.45
55:SH:49:LYS:HB2	55:SH:61:ILE:CG1	2.47	0.45
57:SJ:59:GLU:H	57:SJ:59:GLU:CD	2.19	0.45
71:SY:26:ASP:HB3	71:SY:68:LYS:HZ1	1.82	0.45
4:LA:248:GLY:O	4:LA:249:THR:OG1	2.30	0.45
9:LF:61:LEU:HD23	9:LF:61:LEU:HA	1.78	0.45
9:LF:169:LEU:O	9:LF:173:ASN:ND2	2.48	0.45
11:LH:58:ASP:OD1	11:LH:58:ASP:N	2.50	0.45
14:LL:121:ARG:HH11	14:LL:121:ARG:HG2	1.81	0.45
20:LR:160:GLU:OE2	20:LR:160:GLU:HA	2.17	0.45
43:Lo:76:ASN:OD1	43:Lo:76:ASN:N	2.50	0.45
46:S2:497:C:H2'	46:S2:499:C:H6	1.82	0.45
46:S2:1644:U:H2'	46:S2:1645:C:C6	2.52	0.45
46:S2:1723:G:H1	46:S2:1813:U:H3	1.65	0.45
51:SD:63:GLY:HA2	51:SD:66:ILE:HG22	1.99	0.45
54:SG:115:LYS:HB3	54:SG:115:LYS:HE3	1.81	0.45
57:SJ:124:HIS:NE2	77:Se:109:ARG:HD3	2.31	0.45
58:SK:63:ALA:HB3	58:SK:66:HIS:HB2	1.99	0.45
63:SQ:98:LYS:HG2	63:SQ:99:TYR:CE1	2.51	0.45
75:Sc:15:THR:HG22	75:Sc:16:LYS:N	2.23	0.45
78:Sg:249:CYS:HA	78:Sg:258:ILE:HA	1.98	0.45
2:L7:60:G:O2'	2:L7:61:G:OP1	2.32	0.45
4:LA:176:ASP:C	4:LA:176:ASP:OD1	2.60	0.45
31:Lc:21:VAL:HG11	31:Lc:96:ILE:HG12	1.98	0.45
46:S2:1159:G:H5''	69:SW:76:SER:HB2	1.98	0.45
46:S2:1410:A:H2'	46:S2:1411:C:C6	2.51	0.45
46:S2:1517:G:O2'	46:S2:1518:G:OP1	2.33	0.45
48:SA:148:CYS:O	48:SA:162:PRO:HA	2.17	0.45
58:SK:5:LYS:HD3	58:SK:8:ARG:HE	1.81	0.45
59:SL:147:LYS:HE2	59:SL:147:LYS:HB2	1.71	0.45
70:SX:24:ASP:OD1	70:SX:27:TYR:HB3	2.17	0.45
70:SX:124:LYS:HA	70:SX:129:SER:HA	1.99	0.45
73:Sa:94:ASP:C	73:Sa:94:ASP:OD1	2.59	0.45
78:Sg:152:SER:HB2	78:Sg:168:CYS:HB2	1.98	0.45
1:L5:212:A:H2'	1:L5:213:G:C8	2.51	0.45
1:L5:1026:C:H2'	1:L5:1027:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1251:C:O2'	1:L5:1901:G:OP2	2.30	0.45
1:L5:3597:U:O3'	10:LG:75:LYS:NZ	2.50	0.45
7:LD:83:LEU:N	7:LD:84:PRO:HD2	2.32	0.45
11:LH:59:LYS:HD2	11:LH:59:LYS:HA	1.73	0.45
46:S2:163:U:OP1	54:SG:84:TYR:HA	2.17	0.45
46:S2:970:U:O2	46:S2:972:G:N1	2.50	0.45
46:S2:1280:C:H2'	46:S2:1281:G:C8	2.51	0.45
46:S2:1452:G:H21	46:S2:1475:A:N6	2.14	0.45
46:S2:1589:A:H2'	46:S2:1590:A:C8	2.51	0.45
54:SG:18:VAL:HG11	54:SG:24:LEU:HD21	1.99	0.45
62:SP:56:LEU:O	62:SP:57:LEU:C	2.60	0.45
64:SR:87:GLU:H	64:SR:87:GLU:CD	2.24	0.45
1:L5:1338:A:N1	1:L5:3572:U:O2'	2.48	0.45
1:L5:3518:A:H2'	1:L5:3519:A:C8	2.51	0.45
1:L5:4615:A:H2'	1:L5:4616:A:C8	2.51	0.45
17:LO:186:GLU:OE1	17:LO:186:GLU:O	2.34	0.45
19:LQ:158:THR:HG22	19:LQ:161:SER:HB3	1.99	0.45
46:S2:852:C:H5''	46:S2:853:G:H5'	1.99	0.45
48:SA:29:ASN:OD1	48:SA:29:ASN:C	2.60	0.45
50:SC:73:MET:SD	50:SC:96:PHE:HZ	2.39	0.45
51:SD:23:GLU:HG2	58:SK:64:TRP:CD1	2.52	0.45
55:SH:73:GLN:HA	55:SH:76:GLN:HB2	1.97	0.45
62:SP:51:ARG:O	62:SP:52:LYS:C	2.60	0.45
70:SX:37:LYS:HD2	70:SX:37:LYS:O	2.17	0.45
71:SY:85:ASN:O	71:SY:85:ASN:OD1	2.34	0.45
78:Sg:27:PHE:C	78:Sg:29:ASP:H	2.25	0.45
1:L5:307:G:OP2	1:L5:307:G:N2	2.32	0.45
1:L5:823:C:O2'	1:L5:824:C:OP1	2.31	0.45
1:L5:1362:G:O2'	1:L5:2566:A:N3	2.50	0.45
1:L5:1698:G:H2'	1:L5:1699:A:O4'	2.18	0.45
1:L5:4615:A:H2'	1:L5:4616:A:H8	1.82	0.45
10:LG:106:THR:HG23	10:LG:109:GLU:OE2	2.16	0.45
13:LJ:85:LYS:O	13:LJ:88:LYS:HB3	2.17	0.45
15:LM:66:HIS:O	15:LM:67:SER:OG	2.33	0.45
46:S2:310:G:H1'	56:SI:55:TYR:OH	2.17	0.45
46:S2:862:A:O2'	46:S2:863:A:OP2	2.24	0.45
49:SB:199:LYS:HD2	49:SB:199:LYS:HA	1.84	0.45
53:SF:58:ALA:HB3	53:SF:62:ARG:NE	2.30	0.45
54:SG:20:ASP:OD1	54:SG:21:GLU:N	2.50	0.45
54:SG:199:THR:O	54:SG:203:LYS:HG3	2.17	0.45
58:SK:2:LEU:CD2	58:SK:4:PRO:HD3	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SP:65:LYS:HD3	62:SP:65:LYS:HA	1.80	0.45
77:Se:79:SER:OG	77:Se:80:LEU:N	2.48	0.45
78:Sg:234:ASP:O	78:Sg:252:THR:HG23	2.17	0.45
1:L5:829:G:O2'	1:L5:830:C:H5'	2.16	0.44
1:L5:3965:U:H2'	1:L5:3966:A:C8	2.51	0.44
1:L5:4395:A:N6	1:L5:4598:U:O4'	2.51	0.44
1:L5:4652:C:H2'	1:L5:4653:G:O4'	2.16	0.44
7:LD:187:SER:OG	7:LD:189:GLU:HG2	2.17	0.44
12:LI:35:ASP:OD1	12:LI:88:ARG:HG3	2.17	0.44
17:LO:9:LEU:HD23	17:LO:118:MET:HB2	1.99	0.44
33:Le:69:MET:HE3	33:Le:69:MET:HB2	1.66	0.44
44:Lp:61:MET:HE3	44:Lp:61:MET:HB3	1.77	0.44
46:S2:1569:C:H2'	46:S2:1570:A:C8	2.52	0.44
46:S2:1668:U:H2'	46:S2:1669:U:C6	2.53	0.44
50:SC:167:ARG:HB2	50:SC:177:PRO:HB2	1.99	0.44
54:SG:57:ASP:OD1	54:SG:58:LYS:N	2.50	0.44
55:SH:160:LYS:HA	55:SH:189:PHE:HD2	1.82	0.44
57:SJ:78:LEU:HD12	57:SJ:78:LEU:HA	1.84	0.44
65:SS:114:LEU:HB3	65:SS:119:ALA:HB3	1.99	0.44
66:ST:39:LEU:H	66:ST:39:LEU:HD23	1.81	0.44
70:SX:65:ALA:HB3	70:SX:67:ARG:HH11	1.81	0.44
78:Sg:286:CYS:HB3	78:Sg:302:TYR:CE1	2.52	0.44
1:L5:212:A:H2'	1:L5:213:G:H8	1.83	0.44
1:L5:1523:C:H5''	1:L5:1524:G:N7	2.33	0.44
5:LB:257:TRP:CD1	5:LB:257:TRP:C	2.94	0.44
39:Lk:27:LYS:HA	39:Lk:32:VAL:HG12	1.98	0.44
46:S2:64:A:P	46:S2:83:A:H62	2.41	0.44
46:S2:98:C:H5'	46:S2:99:A:H5'	2.00	0.44
46:S2:447:G:OP2	56:SI:47:ARG:NH2	2.50	0.44
46:S2:887:A:C6	46:S2:888:U:H1'	2.52	0.44
46:S2:1704:C:H2'	46:S2:1705:C:O4'	2.17	0.44
49:SB:85:LYS:CB	49:SB:101:HIS:HB3	2.47	0.44
49:SB:180:ASP:OD1	49:SB:183:GLU:HG3	2.17	0.44
51:SD:107:TYR:HE1	51:SD:108:LYS:HZ3	1.66	0.44
55:SH:147:LYS:O	55:SH:149:ASP:N	2.50	0.44
55:SH:158:LEU:HD23	55:SH:158:LEU:HA	1.83	0.44
58:SK:27:VAL:O	58:SK:43:LEU:HD12	2.17	0.44
1:L5:1221:G:N2	1:L5:1227:G:H1	2.15	0.44
1:L5:3368:A:N3	46:S2:971:G:N1	2.65	0.44
22:LT:117:LYS:HD2	22:LT:117:LYS:HA	1.65	0.44
27:LY:127:GLN:OE1	27:LY:127:GLN:HA	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lk:60:LEU:HG	39:Lk:61:PRO:HD2	1.99	0.44
46:S2:555:A:O2'	46:S2:556:A:N1	2.49	0.44
46:S2:947:U:H2'	46:S2:948:G:H8	1.81	0.44
46:S2:1260:A:H3'	46:S2:1260:A:N3	2.32	0.44
53:SF:144:LEU:HD23	75:Sc:49:PRO:HG2	1.99	0.44
54:SG:50:VAL:HG11	54:SG:111:LEU:HD23	2.00	0.44
57:SJ:110:LEU:HA	57:SJ:113:GLN:HB2	1.98	0.44
58:SK:58:VAL:HG23	58:SK:70:TYR:O	2.17	0.44
1:L5:1562:G:H3'	1:L5:1563:G:H8	1.83	0.44
1:L5:3787:U:O4	1:L5:3801:G:O6	2.36	0.44
1:L5:4177:G:N3	5:LB:252:ALA:HB1	2.33	0.44
6:LC:189:MET:HE3	6:LC:189:MET:HB2	1.86	0.44
6:LC:269:LYS:HE3	6:LC:269:LYS:HB3	1.67	0.44
28:LZ:33:THR:C	28:LZ:35:ASP:H	2.25	0.44
46:S2:62:G:H2'	46:S2:62:G:N3	2.32	0.44
46:S2:480:C:H3'	46:S2:481:G:C8	2.52	0.44
46:S2:895:G:H5''	46:S2:896:G:H8	1.83	0.44
46:S2:919:U:O3'	60:SN:20:ARG:NH1	2.50	0.44
46:S2:1537:G:P	53:SF:88:MET:HE1	2.57	0.44
48:SA:183:LEU:HD22	48:SA:188:THR:HG21	1.99	0.44
48:SA:205:ARG:CZ	48:SA:205:ARG:HA	2.48	0.44
69:SW:54:ASP:C	69:SW:54:ASP:OD1	2.60	0.44
1:L5:2019:G:N2	45:Lr:98:ARG:HH12	2.15	0.44
1:L5:2478:G:O2'	1:L5:2480:G:OP2	2.34	0.44
43:Lo:66:ILE:HG13	43:Lo:88:CYS:SG	2.58	0.44
46:S2:1319:G:C2	46:S2:1320:U:C4	3.06	0.44
57:SJ:83:ARG:NE	57:SJ:150:ARG:HD3	2.32	0.44
66:ST:82:ARG:HE	66:ST:82:ARG:HB3	1.70	0.44
70:SX:107:ARG:HG3	70:SX:112:VAL:HG12	1.99	0.44
78:Sg:172:LYS:HB3	78:Sg:172:LYS:HE2	1.71	0.44
80:Z:1:UNK:O	80:Z:2:UNK:C	2.66	0.44
1:L5:3419:U:H3'	1:L5:3420:A:H8	1.83	0.44
7:LD:81:HIS:ND1	7:LD:81:HIS:C	2.76	0.44
8:LE:191:ARG:HD2	8:LE:191:ARG:HA	1.71	0.44
20:LR:95:TRP:CH2	20:LR:99:MET:HE3	2.53	0.44
22:LT:115:LYS:HE2	22:LT:115:LYS:HB2	1.64	0.44
28:LZ:97:ASN:HB3	28:LZ:99:ASP:H	1.83	0.44
36:Lh:14:LYS:H	36:Lh:14:LYS:HG2	1.61	0.44
46:S2:906:C:H2'	46:S2:907:U:C6	2.51	0.44
46:S2:1308:U:OP1	46:S2:1308:U:H4'	2.18	0.44
46:S2:1319:G:H2'	46:S2:1320:U:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SE:8:HIS:O	52:SE:30:ARG:NH2	2.44	0.44
71:SY:56:PHE:HE1	71:SY:94:HIS:NE2	2.15	0.44
1:L5:159:C:OP2	37:Li:25:ARG:HB3	2.17	0.44
1:L5:885:C:C4	1:L5:886:U:H1'	2.53	0.44
1:L5:1003:G:H3'	1:L5:1004:G:H8	1.83	0.44
1:L5:1312:G:OP1	19:LQ:150:ARG:NH1	2.49	0.44
1:L5:3417:A:O2'	1:L5:3418:C:OP2	2.35	0.44
1:L5:4000:G:O2'	1:L5:4001:A:H5'	2.18	0.44
10:LG:107:LYS:HA	10:LG:107:LYS:HD2	1.72	0.44
11:LH:180:TYR:HB2	41:Lm:85:LEU:HD11	1.99	0.44
26:LX:151:ASN:OD1	26:LX:156:ILE:HG23	2.17	0.44
46:S2:72:C:O2'	46:S2:74:G:N2	2.51	0.44
46:S2:75:G:N3	54:SG:159:ARG:NH2	2.66	0.44
46:S2:1628:C:H2'	46:S2:1629:C:H6	1.83	0.44
52:SE:133:THR:HG23	52:SE:134:LYS:HG2	2.00	0.44
55:SH:80:VAL:HG23	55:SH:92:VAL:HB	2.00	0.44
62:SP:57:LEU:C	62:SP:57:LEU:HD22	2.43	0.44
1:L5:754:A:H2'	1:L5:755:A:C8	2.53	0.44
1:L5:1027:G:H2'	1:L5:1028:G:N7	2.32	0.44
1:L5:1589:A:H2'	1:L5:1592:C:C5	2.53	0.44
1:L5:4554:G:H2'	1:L5:4558:G:N3	2.33	0.44
2:L7:4:U:H2'	2:L7:5:A:C8	2.52	0.44
46:S2:586:C:HO2'	46:S2:587:G:C5'	2.30	0.44
49:SB:37:ALA:HB2	49:SB:42:ARG:HH21	1.82	0.44
51:SD:113:LEU:HD12	51:SD:114:ALA:H	1.82	0.44
77:Se:105:ARG:HG2	77:Se:109:ARG:HH21	1.83	0.44
1:L5:140:G:H2'	1:L5:141:C:O4'	2.18	0.44
1:L5:4686:A:H2'	1:L5:4687:U:C6	2.53	0.44
5:LB:35:ASP:OD1	5:LB:36:ASP:N	2.51	0.44
9:LF:204:PHE:CD1	9:LF:222:ARG:HD2	2.53	0.44
46:S2:1278:C:H2'	46:S2:1279:A:O4'	2.18	0.44
47:S7:17:C:O2	47:S7:60:A:O2'	2.24	0.44
52:SE:36:HIS:HB2	52:SE:83:PRO:HB2	2.00	0.44
53:SF:69:VAL:O	53:SF:73:THR:HG23	2.18	0.44
55:SH:139:ILE:HG23	55:SH:156:VAL:HG13	1.98	0.44
65:SS:5:ILE:HB	72:SZ:49:LEU:O	2.17	0.44
65:SS:86:ARG:HE	65:SS:86:ARG:HB3	1.48	0.44
1:L5:1005:C:HO2'	1:L5:1006:G:N2	2.16	0.43
1:L5:1009:C:N4	1:L5:1017:A:H61	1.99	0.43
1:L5:1027:G:H2'	1:L5:1028:G:C8	2.53	0.43
1:L5:2036:A:O2'	33:Le:48:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2216:G:H2'	1:L5:2218:G:OP2	2.18	0.43
1:L5:3313:A:H2'	1:L5:3314:U:H6	1.83	0.43
3:L8:1:C:H3'	3:L8:2:G:H21	1.83	0.43
3:L8:148:A:H2'	3:L8:149:G:C8	2.53	0.43
7:LD:70:GLU:H	7:LD:70:GLU:CD	2.25	0.43
8:LE:185:GLY:O	8:LE:186:PRO:C	2.61	0.43
10:LG:160:ASP:OD1	10:LG:187:LYS:HB2	2.18	0.43
46:S2:500:G:N1	46:S2:504:C:OP1	2.29	0.43
46:S2:1441:C:H2'	46:S2:1442:U:C2	2.53	0.43
56:SI:13:LYS:H	56:SI:13:LYS:HG2	1.65	0.43
57:SJ:134:HIS:C	57:SJ:135:ILE:HD13	2.42	0.43
62:SP:18:ARG:NH1	65:SS:88:LYS:O	2.51	0.43
62:SP:38:SER:OG	62:SP:39:ALA:N	2.50	0.43
63:SQ:43:GLU:HB3	63:SQ:44:PRO:HD2	1.99	0.43
1:L5:467:U:H5	1:L5:696:U:O4	2.01	0.43
1:L5:3927:A:H2'	1:L5:3928:G:H8	1.82	0.43
1:L5:4286:G:O2'	1:L5:4288:A:OP2	2.29	0.43
1:L5:4427:C:N4	1:L5:4507:G:H21	2.17	0.43
14:LL:171:GLU:C	14:LL:171:GLU:OE1	2.61	0.43
17:LO:183:LYS:HA	17:LO:183:LYS:HD3	1.85	0.43
46:S2:864:U:O4	46:S2:865:A:N6	2.51	0.43
46:S2:1165:G:O2'	46:S2:1166:G:H5'	2.17	0.43
46:S2:1509:A:C6	46:S2:1511:G:C4	3.06	0.43
54:SG:165:GLU:C	54:SG:167:LYS:H	2.26	0.43
62:SP:34:MET:N	62:SP:34:MET:HE2	2.32	0.43
65:SS:15:VAL:HG13	65:SS:16:LEU:N	2.33	0.43
73:Sa:44:ILE:HG13	73:Sa:45:VAL:HG23	2.01	0.43
78:Sg:32:LEU:HD12	78:Sg:42:MET:HG3	2.00	0.43
1:L5:121:A:H62	1:L5:152:U:H3	1.65	0.43
1:L5:3341:G:H2'	1:L5:3342:C:C6	2.53	0.43
1:L5:4664:A:H2'	1:L5:4664:A:N3	2.34	0.43
5:LB:297:LYS:HE3	5:LB:297:LYS:HB3	1.78	0.43
14:LL:42:LYS:HG3	14:LL:45:ARG:NH1	2.33	0.43
24:LV:57:VAL:HG21	24:LV:122:ALA:HB3	2.00	0.43
46:S2:16:G:H2'	46:S2:17:C:C6	2.53	0.43
46:S2:345:U:H2'	46:S2:346:U:C6	2.52	0.43
46:S2:381:G:P	56:SI:56:ARG:HH22	2.42	0.43
46:S2:526:A:H2	46:S2:591:A:C4	2.36	0.43
46:S2:895:G:H5'	46:S2:896:G:H5''	1.98	0.43
48:SA:10:MET:HB3	64:SR:111:PHE:CE2	2.54	0.43
51:SD:100:ALA:O	51:SD:104:SER:OG	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SO:50:LYS:HB2	61:SO:50:LYS:HE2	1.75	0.43
1:L5:1294:C:O2'	1:L5:1296:G:OP2	2.35	0.43
1:L5:1765:A:C5	1:L5:1766:C:C6	3.06	0.43
12:LI:133:GLN:HG3	12:LI:134:VAL:N	2.34	0.43
13:LJ:119:TYR:HE2	13:LJ:125:ILE:HD11	1.83	0.43
20:LR:156:ALA:O	20:LR:160:GLU:HG2	2.19	0.43
24:LV:107:ASN:ND2	24:LV:111:GLU:HB3	2.34	0.43
31:Lc:99:PRO:HG3	31:Lc:104:ILE:HD13	2.00	0.43
39:Lk:8:ILE:HD13	39:Lk:45:LEU:HD21	1.99	0.43
46:S2:953:G:H2'	46:S2:954:C:C6	2.53	0.43
51:SD:97:CYS:SG	51:SD:99:ILE:HG23	2.59	0.43
52:SE:212:ASP:OD1	52:SE:212:ASP:N	2.45	0.43
57:SJ:131:ARG:HA	57:SJ:131:ARG:HD2	1.70	0.43
69:SW:55:ASP:OD1	69:SW:59:GLY:HA2	2.18	0.43
1:L5:1123:C:H2'	1:L5:1124:C:C6	2.53	0.43
1:L5:1590:A:N3	1:L5:3863:U:O2'	2.51	0.43
1:L5:1904:C:O2	1:L5:1905:G:N1	2.52	0.43
1:L5:4183:U:H2'	1:L5:4184:U:H2'	2.01	0.43
1:L5:4237:A:H2'	1:L5:4238:U:O4'	2.18	0.43
6:LC:317:ASN:HD22	6:LC:320:LYS:HD3	1.83	0.43
6:LC:352:LYS:HB3	6:LC:352:LYS:HE2	1.72	0.43
12:LI:193:ASP:OD1	12:LI:193:ASP:N	2.52	0.43
15:LM:32:ASP:OD1	15:LM:33:GLN:N	2.51	0.43
22:LT:122:LYS:HA	22:LT:122:LYS:HD3	1.80	0.43
25:LW:23:ARG:HG3	25:LW:29:PHE:HE2	1.84	0.43
31:Lc:22:MET:H	31:Lc:22:MET:HG2	1.70	0.43
46:S2:152:U:OP2	54:SG:132:ARG:NH1	2.52	0.43
46:S2:456:A:H2'	46:S2:457:C:C6	2.54	0.43
46:S2:847:G:OP2	52:SE:108:ARG:NH1	2.51	0.43
46:S2:905:A:H2'	46:S2:906:C:C5	2.53	0.43
46:S2:1498:G:H4'	46:S2:1499:A:H5'	2.01	0.43
46:S2:1752:C:N3	46:S2:1753:C:O2'	2.51	0.43
54:SG:67:VAL:HG12	54:SG:69:THR:HG22	2.00	0.43
55:SH:160:LYS:HE3	55:SH:189:PHE:HB3	2.00	0.43
62:SP:79:HIS:CD2	62:SP:79:HIS:O	2.71	0.43
64:SR:51:ALA:HA	64:SR:54:VAL:HG22	2.00	0.43
78:Sg:150:TRP:HB2	78:Sg:170:TRP:CD1	2.54	0.43
1:L5:3425:U:HO2'	1:L5:3426:C:P	2.42	0.43
1:L5:3782:G:H2'	1:L5:3783:U:C6	2.53	0.43
5:LB:238:LYS:HE2	5:LB:238:LYS:HB2	1.64	0.43
7:LD:51:MET:HE1	7:LD:173:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LJ:38:LYS:HZ3	13:LJ:42:GLN:HB2	1.84	0.43
17:LO:39:GLU:OE2	17:LO:39:GLU:N	2.34	0.43
17:LO:128:ARG:HE	17:LO:128:ARG:HB3	1.62	0.43
19:LQ:175:GLU:HA	29:La:51:GLY:O	2.18	0.43
21:LS:21:LYS:HE2	21:LS:21:LYS:HB2	1.73	0.43
24:LV:112:MET:HE3	24:LV:112:MET:HB2	1.73	0.43
31:Lc:101:ASP:O	31:Lc:102:SER:OG	2.28	0.43
46:S2:445:G:H8	46:S2:447:G:N7	2.16	0.43
46:S2:1223:G:H2'	46:S2:1224:A:C8	2.53	0.43
50:SC:149:THR:HA	50:SC:152:ARG:HG2	2.00	0.43
61:SO:95:ILE:HB	61:SO:129:ILE:HA	1.99	0.43
64:SR:44:LYS:HG3	64:SR:47:ARG:HH21	1.83	0.43
74:Sb:31:TYR:CD2	74:Sb:81:ARG:HD3	2.53	0.43
1:L5:37:U:H2'	1:L5:38:A:O4'	2.19	0.43
1:L5:2599:A:H61	1:L5:3500:C:N4	2.13	0.43
5:LB:222:VAL:O	5:LB:343:ARG:NH1	2.52	0.43
5:LB:317:LEU:HA	5:LB:317:LEU:HD23	1.79	0.43
17:LO:197:LYS:HB3	17:LO:197:LYS:HE3	1.55	0.43
19:LQ:93:LEU:HB2	19:LQ:94:GLU:OE1	2.19	0.43
22:LT:11:THR:HG22	22:LT:14:MET:HE2	2.01	0.43
46:S2:498:C:O5'	46:S2:499:C:H5''	2.19	0.43
48:SA:36:GLN:NE2	68:SV:67:ASP:OD1	2.51	0.43
50:SC:65:LYS:O	50:SC:69:LEU:HG	2.18	0.43
78:Sg:174:VAL:HG13	78:Sg:195:LEU:HD13	2.00	0.43
1:L5:432:A:C2	1:L5:3524:A:H4'	2.54	0.43
1:L5:1684:C:H5'	1:L5:2038:U:H1'	2.01	0.43
21:LS:30:MET:HE2	22:LT:151:LEU:HB2	2.01	0.43
46:S2:126:G:C2	46:S2:181:A:H4'	2.53	0.43
46:S2:922:G:C6	69:SW:28:ARG:HD2	2.54	0.43
46:S2:1219:C:H2'	46:S2:1220:C:C6	2.53	0.43
46:S2:1617:U:O2'	46:S2:1662:A:N3	2.43	0.43
56:SI:199:LEU:HD23	56:SI:199:LEU:HA	1.85	0.43
57:SJ:97:ILE:H	57:SJ:97:ILE:HG13	1.59	0.43
62:SP:83:MET:HB3	62:SP:116:LEU:HD13	1.99	0.43
63:SQ:97:GLN:HB2	63:SQ:105:LYS:HG3	2.00	0.43
64:SR:33:ARG:O	64:SR:36:GLU:HG2	2.19	0.43
64:SR:44:LYS:HB2	64:SR:44:LYS:HE3	1.61	0.43
66:ST:123:LEU:HA	66:ST:123:LEU:HD12	1.77	0.43
67:SU:38:ASP:CG	67:SU:41:ARG:HH21	2.27	0.43
73:Sa:52:ASP:OD1	73:Sa:52:ASP:N	2.51	0.43
1:L5:809:A:H2'	1:L5:810:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4581:C:H2'	1:L5:4582:G:C8	2.53	0.43
4:LA:245:ARG:HA	4:LA:245:ARG:HD2	1.94	0.43
6:LC:20:LYS:HB2	6:LC:20:LYS:HE3	1.80	0.43
6:LC:186:SER:O	6:LC:188:ARG:HD3	2.19	0.43
13:LJ:113:ILE:HD11	13:LJ:119:TYR:HB2	2.01	0.43
20:LR:13:SER:OG	20:LR:38:ARG:NH2	2.51	0.43
25:LW:9:SER:HB2	25:LW:11:TYR:CD1	2.53	0.43
36:Lh:82:ASP:OD1	36:Lh:82:ASP:C	2.62	0.43
41:Lm:94:MET:HG3	41:Lm:105:PRO:HA	2.01	0.43
46:S2:84:A:H5'	46:S2:149:A:O2'	2.19	0.43
46:S2:152:U:H1'	46:S2:153:G:N2	2.34	0.43
46:S2:804:C:O2'	69:SW:124:LYS:NZ	2.52	0.43
46:S2:1407:G:H2'	46:S2:1408:U:C6	2.54	0.43
46:S2:1408:U:O5'	46:S2:1408:U:H6	2.02	0.43
51:SD:137:VAL:HB	51:SD:185:LYS:HB2	2.01	0.43
53:SF:162:ALA:HB2	53:SF:172:CYS:SG	2.59	0.43
62:SP:111:MET:HA	62:SP:114:HIS:HD2	1.84	0.43
64:SR:43:SER:HB3	64:SR:46:LEU:HD13	2.00	0.43
68:SV:32:ILE:HD12	68:SV:33:GLN:H	1.83	0.43
71:SY:88:LYS:HE3	71:SY:97:TYR:CE2	2.54	0.43
1:L5:758:U:H2'	1:L5:759:G:C8	2.53	0.43
1:L5:1044:C:OP1	9:LF:92:ARG:HD3	2.19	0.43
1:L5:3909:A:HO2'	13:LJ:55:TYR:HH	1.67	0.43
1:L5:4190:C:H2'	1:L5:4191:G:C8	2.54	0.43
13:LJ:47:THR:HA	13:LJ:48:PRO:HD3	1.91	0.43
30:Lb:56:LYS:H	30:Lb:56:LYS:HG3	1.70	0.43
31:Lc:18:LEU:HD12	31:Lc:18:LEU:HA	1.83	0.43
37:Li:16:LYS:HA	37:Li:16:LYS:HD3	1.84	0.43
46:S2:28:U:H2'	46:S2:29:G:C8	2.54	0.43
46:S2:65:C:H41	54:SG:174:PRO:HD3	1.84	0.43
46:S2:838:A:H61	71:SY:26:ASP:N	2.11	0.43
46:S2:922:G:C5	69:SW:28:ARG:HD2	2.53	0.43
46:S2:1447:A:N3	67:SU:55:ARG:HD2	2.34	0.43
46:S2:1596:U:H2'	46:S2:1597:U:C6	2.54	0.43
46:S2:1786:C:O2'	46:S2:1787:U:O4'	2.37	0.43
47:S7:30:G:O2'	47:S7:31:G:H5'	2.19	0.43
52:SE:15:PRO:HD2	52:SE:18:TRP:CZ2	2.53	0.43
53:SF:68:ILE:HD12	53:SF:68:ILE:HA	1.90	0.43
56:SI:106:SER:HB3	56:SI:171:LEU:HG	2.00	0.43
63:SQ:50:LYS:HE3	63:SQ:50:LYS:HB3	1.85	0.43
1:L5:266:G:HO2'	1:L5:267:G:P	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:350:C:H2'	1:L5:351:G:O4'	2.19	0.42
1:L5:1182:U:O2'	1:L5:1184:C:OP2	2.34	0.42
1:L5:1379:A:H3'	1:L5:1380:C:O4'	2.18	0.42
1:L5:1715:G:N2	17:LO:87:MET:HE2	2.34	0.42
1:L5:3587:U:H3	1:L5:3833:G:H1	1.66	0.42
1:L5:4538:A:H2'	1:L5:4539:A:O4'	2.19	0.42
5:LB:17:LEU:HB3	5:LB:18:PRO:HD3	2.01	0.42
9:LF:62:LYS:HB3	9:LF:62:LYS:HE2	1.78	0.42
13:LJ:85:LYS:HA	13:LJ:85:LYS:HD2	1.90	0.42
13:LJ:120:ASP:OD2	13:LJ:122:SER:OG	2.23	0.42
46:S2:1601:G:H2'	46:S2:1601:G:N3	2.34	0.42
51:SD:65:ARG:HH22	58:SK:59:LYS:HD2	1.85	0.42
55:SH:51:ILE:HG21	55:SH:179:LYS:HE2	2.00	0.42
58:SK:1:MET:HG3	58:SK:3:MET:HB2	2.00	0.42
61:SO:54:CYS:SG	61:SO:81:VAL:HG22	2.59	0.42
72:SZ:44:LEU:HD12	72:SZ:44:LEU:H	1.83	0.42
78:Sg:220:ASP:HB2	78:Sg:224:GLY:N	2.29	0.42
78:Sg:236:ILE:HD11	78:Sg:239:LEU:HG	2.01	0.42
1:L5:443:G:H2'	1:L5:444:U:C6	2.54	0.42
1:L5:936:C:N4	1:L5:1054:G:O6	2.52	0.42
1:L5:1261:C:H2'	1:L5:1262:G:H8	1.84	0.42
1:L5:1480:C:O2'	1:L5:1502:G:OP1	2.33	0.42
1:L5:3264:U:H2'	1:L5:3265:A:C8	2.53	0.42
1:L5:4402:U:H2'	1:L5:4403:C:C6	2.53	0.42
7:LD:282:GLN:HE21	7:LD:282:GLN:HB3	1.69	0.42
11:LH:53:LYS:C	11:LH:54:ARG:HG3	2.44	0.42
13:LJ:112:HIS:HA	13:LJ:115:LEU:HD23	2.02	0.42
14:LL:80:GLU:OE2	14:LL:104:ASN:ND2	2.37	0.42
16:LN:73:ARG:HA	16:LN:74:PRO:HD3	1.86	0.42
44:Lp:88:GLU:C	44:Lp:88:GLU:OE1	2.62	0.42
46:S2:95:G:H1'	46:S2:475:G:H5''	2.01	0.42
46:S2:475:G:HO2'	46:S2:476:C:H2'	1.84	0.42
46:S2:1389:A:C2	51:SD:205:PRO:HG2	2.54	0.42
46:S2:1721:U:H3	46:S2:1815:G:H1	1.67	0.42
46:S2:1798:U:H2'	46:S2:1799:C:C6	2.53	0.42
46:S2:1808:C:H2'	46:S2:1809:U:O4'	2.19	0.42
58:SK:15:LEU:HD11	58:SK:71:LEU:HG	2.00	0.42
64:SR:87:GLU:OE2	64:SR:87:GLU:N	2.39	0.42
66:ST:100:ALA:O	66:ST:104:LEU:HD12	2.19	0.42
75:Sc:13:ARG:HB3	75:Sc:13:ARG:HH11	1.83	0.42
1:L5:1024:C:H2'	1:L5:1025:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1037:G:H2'	1:L5:1038:C:O4'	2.20	0.42
1:L5:2205:G:H2'	1:L5:2206:A:C8	2.53	0.42
1:L5:4392:C:H3'	1:L5:4393:G:C5'	2.48	0.42
8:LE:53:ARG:O	8:LE:72:ARG:NH1	2.52	0.42
46:S2:1629:C:H2'	46:S2:1630:C:H6	1.85	0.42
49:SB:219:LYS:HD3	49:SB:219:LYS:HA	1.56	0.42
54:SG:135:PRO:HB3	54:SG:140:ARG:HG3	2.01	0.42
78:Sg:133:ASN:OD1	78:Sg:136:GLY:N	2.51	0.42
78:Sg:152:SER:HB2	78:Sg:168:CYS:CB	2.49	0.42
1:L5:457:C:OP1	8:LE:121:PRO:HA	2.20	0.42
1:L5:672:G:C5	1:L5:673:C:H5	2.37	0.42
1:L5:741:A:H61	1:L5:829:G:H8	1.66	0.42
1:L5:1723:C:H3'	1:L5:1724:C:H5''	2.02	0.42
1:L5:1832:A:H2'	1:L5:1833:A:C8	2.54	0.42
1:L5:2386:U:H2'	1:L5:2387:U:C6	2.55	0.42
1:L5:2611:A:H8	1:L5:2611:A:O5'	2.02	0.42
1:L5:3550:C:H2'	1:L5:3551:A:C8	2.54	0.42
1:L5:3845:A:H2'	1:L5:3846:C:H6	1.83	0.42
1:L5:3967:C:H4'	22:LT:68:THR:HG21	2.00	0.42
3:L8:129:C:H2'	3:L8:130:C:C6	2.54	0.42
21:LS:150:ILE:HD12	21:LS:150:ILE:HA	1.82	0.42
46:S2:156:G:H21	54:SG:59:GLN:HB2	1.84	0.42
46:S2:840:C:H41	71:SY:23:MET:HG3	1.84	0.42
46:S2:1287:G:N2	46:S2:1313:G:N3	2.67	0.42
48:SA:18:PHE:CE1	48:SA:174:MET:HE3	2.54	0.42
66:ST:27:LYS:HE3	66:ST:27:LYS:HB3	1.82	0.42
66:ST:122:LYS:HE3	66:ST:122:LYS:HB3	1.70	0.42
73:Sa:7:ASN:ND2	73:Sa:7:ASN:O	2.52	0.42
1:L5:297:G:OP1	16:LN:179:LYS:HD3	2.18	0.42
1:L5:1012:U:HO2'	1:L5:1013:C:P	2.41	0.42
1:L5:1617:C:OP1	30:Lb:52:LYS:NZ	2.41	0.42
1:L5:3264:U:H2'	1:L5:3265:A:H8	1.85	0.42
1:L5:4664:A:O2'	1:L5:4665:G:O4'	2.31	0.42
3:L8:3:A:H2'	3:L8:4:C:H6	1.85	0.42
5:LB:300:LYS:HB2	5:LB:311:ASP:HA	2.02	0.42
9:LF:69:ARG:HD2	9:LF:69:ARG:HA	1.90	0.42
46:S2:115:U:O2'	46:S2:116:U:H6	2.02	0.42
46:S2:800:U:H2'	46:S2:801:U:O4'	2.19	0.42
46:S2:858:U:H2'	46:S2:859:A:C8	2.55	0.42
46:S2:1418:C:H6	46:S2:1418:C:H2'	1.67	0.42
46:S2:1540:U:H1'	66:ST:48:TYR:CZ	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:SB:108:ASP:OD1	49:SB:108:ASP:C	2.63	0.42
56:SI:86:SER:OG	56:SI:87:ASN:N	2.52	0.42
58:SK:80:ARG:HA	58:SK:80:ARG:HD2	1.76	0.42
62:SP:28:MET:SD	62:SP:32:GLN:HB2	2.59	0.42
66:ST:129:ARG:HA	66:ST:129:ARG:HD2	1.79	0.42
78:Sg:191:HIS:CE1	78:Sg:217:MET:HG2	2.54	0.42
1:L5:415:U:H4'	1:L5:2087:G:H4'	2.00	0.42
1:L5:2618:A:H2'	1:L5:2619:U:C6	2.54	0.42
1:L5:3719:U:O2'	1:L5:3720:U:O5'	2.38	0.42
5:LB:189:THR:HG22	5:LB:192:GLU:HG3	2.01	0.42
6:LC:240:LEU:HD12	6:LC:240:LEU:HA	1.90	0.42
14:LL:58:ILE:HG12	14:LL:157:ILE:CD1	2.48	0.42
21:LS:21:LYS:HG3	21:LS:22:CYS:N	2.34	0.42
24:LV:30:ASP:OD1	24:LV:31:ASN:N	2.50	0.42
41:Lm:99:CYS:HB2	41:Lm:114:LYS:HD2	2.01	0.42
48:SA:38:ILE:HG22	48:SA:49:ILE:HG22	2.01	0.42
50:SC:107:LEU:HB2	50:SC:127:PHE:HB2	2.01	0.42
64:SR:72:LYS:HA	64:SR:75:GLU:OE1	2.20	0.42
65:SS:6:PRO:HD3	72:SZ:49:LEU:HD22	2.00	0.42
68:SV:40:ASP:OD1	68:SV:40:ASP:C	2.62	0.42
77:Se:102:LYS:HD2	77:Se:106:ALA:HB1	2.02	0.42
1:L5:10:A:H2'	1:L5:11:G:C8	2.55	0.42
1:L5:950:G:N2	1:L5:1037:G:N3	2.68	0.42
1:L5:3379:G:H2'	1:L5:3380:A:C8	2.55	0.42
1:L5:3809:G:OP2	1:L5:3810:A:O2'	2.28	0.42
23:LU:35:ASP:OD1	23:LU:36:ALA:N	2.52	0.42
24:LV:25:VAL:HA	24:LV:37:LEU:O	2.18	0.42
26:LX:105:ASN:OD1	26:LX:107:HIS:N	2.52	0.42
46:S2:1276:G:H4'	46:S2:1277:A:C8	2.55	0.42
51:SD:107:TYR:HE1	51:SD:108:LYS:NZ	2.18	0.42
53:SF:42:LYS:H	53:SF:42:LYS:HG3	1.69	0.42
1:L5:1005:C:O2'	1:L5:1006:G:N2	2.52	0.42
1:L5:3269:C:H1'	1:L5:4664:A:H8	1.85	0.42
6:LC:143:ARG:HA	6:LC:143:ARG:HD2	1.77	0.42
6:LC:211:TYR:HE2	6:LC:229:LEU:HB3	1.85	0.42
10:LG:182:CYS:HB3	10:LG:222:ILE:HD13	2.02	0.42
12:LI:86:HIS:HB3	12:LI:139:ARG:HG2	2.00	0.42
23:LU:55:ASN:OD1	23:LU:55:ASN:C	2.62	0.42
36:Lh:96:THR:OG1	36:Lh:99:GLU:HG3	2.19	0.42
46:S2:62:G:H3'	46:S2:63:U:C5'	2.50	0.42
46:S2:126:G:OP1	54:SG:198:ARG:NH1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:822:G:H8	46:S2:825:C:H5''	1.84	0.42
46:S2:1237:G:H2'	46:S2:1238:C:C6	2.55	0.42
46:S2:1507:A:H2	46:S2:1509:A:H62	1.68	0.42
46:S2:1737:G:H2'	46:S2:1738:G:H8	1.85	0.42
49:SB:74:LEU:HD23	49:SB:74:LEU:HA	1.92	0.42
56:SI:170:LYS:HB3	56:SI:170:LYS:HE2	1.53	0.42
57:SJ:129:LEU:HD12	57:SJ:129:LEU:HA	1.85	0.42
65:SS:70:ILE:HG12	65:SS:77:TYR:CD2	2.55	0.42
66:ST:75:MET:HE2	66:ST:75:MET:HA	2.00	0.42
76:Sd:31:ILE:HD11	76:Sd:40:ARG:HA	2.01	0.42
78:Sg:135:LEU:HD23	78:Sg:135:LEU:HA	1.88	0.42
1:L5:805:C:O2'	1:L5:806:C:H5'	2.20	0.42
1:L5:3313:A:H2'	1:L5:3314:U:C6	2.54	0.42
4:LA:30:ARG:O	4:LA:163:ARG:NH2	2.47	0.42
7:LD:241:LYS:HB2	7:LD:241:LYS:HE3	1.83	0.42
14:LL:75:GLY:HA2	14:LL:97:SER:HB3	2.01	0.42
15:LM:81:ASP:O	15:LM:85:LYS:HG3	2.19	0.42
33:Le:22:ARG:HB2	33:Le:34:ASN:O	2.20	0.42
46:S2:339:G:H3'	46:S2:340:A:H4'	2.01	0.42
47:S7:11:G:H1	47:S7:25:U:H3	1.67	0.42
48:SA:80:ARG:HD3	48:SA:126:ASP:OD2	2.20	0.42
56:SI:102:VAL:HG22	56:SI:103:LEU:H	1.84	0.42
57:SJ:60:LEU:O	57:SJ:70:ARG:NH1	2.53	0.42
65:SS:12:ILE:HD11	65:SS:19:ASN:HB2	2.02	0.42
65:SS:94:LYS:HE3	65:SS:94:LYS:HB2	1.87	0.42
67:SU:88:LEU:HD12	67:SU:88:LEU:O	2.19	0.42
76:Sd:36:LEU:HD12	76:Sd:38:MET:SD	2.60	0.42
1:L5:1029:G:H3'	1:L5:1030:C:C6	2.55	0.42
1:L5:2060:C:H5''	33:Le:104:SER:HB3	2.02	0.42
1:L5:4506:G:O2'	1:L5:4507:G:H5'	2.20	0.42
2:L7:58:A:H2'	2:L7:59:G:H8	1.84	0.42
5:LB:54:THR:OG1	5:LB:55:HIS:N	2.53	0.42
6:LC:149:GLU:HG3	45:Lr:71:ARG:HD2	2.02	0.42
19:LQ:186:TYR:CD2	19:LQ:188:ASN:HB2	2.55	0.42
39:Lk:49:ASP:OD2	39:Lk:52:LYS:HE3	2.20	0.42
46:S2:63:U:H3'	46:S2:83:A:H62	1.84	0.42
46:S2:510:G:H2'	46:S2:511:G:H8	1.84	0.42
46:S2:514:G:H2'	46:S2:514:G:N3	2.35	0.42
46:S2:1011:G:H2'	46:S2:1012:A:C8	2.55	0.42
46:S2:1515:G:H2'	46:S2:1516:G:C8	2.55	0.42
49:SB:231:LEU:HD23	49:SB:231:LEU:HA	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SD:113:LEU:HD11	51:SD:117:ARG:HD3	2.01	0.42
62:SP:95:GLY:HA2	62:SP:104:GLN:HA	2.01	0.42
68:SV:58:ALA:O	68:SV:62:MET:HG3	2.19	0.42
78:Sg:155:ARG:HD2	78:Sg:155:ARG:HA	1.89	0.42
1:L5:175:C:H2'	1:L5:176:G:C8	2.55	0.41
1:L5:251:C:H2'	1:L5:252:G:C8	2.55	0.41
1:L5:828:C:H3'	1:L5:829:G:N2	2.35	0.41
1:L5:940:C:H2'	1:L5:941:C:H6	1.83	0.41
13:LJ:119:TYR:CE2	13:LJ:125:ILE:HD11	2.54	0.41
21:LS:85:ASP:HA	21:LS:90:THR:HA	2.01	0.41
26:LX:114:LYS:NZ	26:LX:120:ASP:HA	2.35	0.41
36:Lh:87:LYS:HE3	36:Lh:87:LYS:HB3	1.87	0.41
45:Lr:28:GLU:H	45:Lr:28:GLU:HG3	1.69	0.41
46:S2:91:A:H1'	52:SE:3:ARG:HB3	2.02	0.41
46:S2:554:U:H2'	46:S2:555:A:H8	1.85	0.41
46:S2:944:U:H2'	46:S2:945:A:H8	1.85	0.41
46:S2:1513:C:O2'	46:S2:1514:C:H5'	2.20	0.41
50:SC:104:ASP:OD1	50:SC:104:ASP:N	2.52	0.41
51:SD:104:SER:HA	51:SD:107:TYR:CZ	2.55	0.41
52:SE:252:ARG:HE	52:SE:252:ARG:HB3	1.55	0.41
55:SH:63:PHE:HA	55:SH:95:ILE:O	2.20	0.41
67:SU:33:GLU:OE2	67:SU:87:ARG:NH1	2.53	0.41
1:L5:829:G:C2'	1:L5:830:C:H5'	2.50	0.41
1:L5:2314:G:H3'	1:L5:2315:C:H5''	2.02	0.41
1:L5:3845:A:H2'	1:L5:3846:C:C6	2.55	0.41
1:L5:4161:C:H5''	24:LV:43:LYS:HE3	2.01	0.41
5:LB:189:THR:HG22	5:LB:192:GLU:OE2	2.19	0.41
9:LF:199:ARG:HA	9:LF:199:ARG:HD3	1.95	0.41
9:LF:243:LYS:HB3	9:LF:243:LYS:HE3	1.81	0.41
13:LJ:12:MET:HA	13:LJ:12:MET:HE3	2.01	0.41
18:LP:31:GLU:H	18:LP:31:GLU:HG2	1.70	0.41
19:LQ:172:ARG:NH1	29:La:56:VAL:O	2.46	0.41
46:S2:496:U:H5	46:S2:508:G:H1	1.67	0.41
46:S2:619:C:H41	70:SX:67:ARG:NH2	2.18	0.41
46:S2:1008:C:H2'	46:S2:1009:A:C8	2.55	0.41
46:S2:1396:C:H1'	46:S2:1475:A:C4	2.55	0.41
51:SD:141:LYS:HE3	51:SD:179:GLN:CG	2.49	0.41
54:SG:22:ARG:N	54:SG:22:ARG:HH11	2.18	0.41
75:Sc:12:ALA:HB1	75:Sc:33:GLU:O	2.20	0.41
77:Se:110:MET:SD	77:Se:114:ARG:NH2	2.93	0.41
78:Sg:32:LEU:HD23	78:Sg:69:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:953:C:H2'	1:L5:954:G:C8	2.55	0.41
1:L5:3719:U:OP2	1:L5:3719:U:H6	2.03	0.41
6:LC:152:LEU:HD12	6:LC:152:LEU:HA	1.91	0.41
24:LV:131:ARG:CZ	24:LV:131:ARG:HB2	2.51	0.41
46:S2:47:G:N2	46:S2:479:G:H22	2.18	0.41
46:S2:1218:A:H2'	46:S2:1219:C:C6	2.55	0.41
46:S2:1369:U:H2'	46:S2:1371:A:OP2	2.20	0.41
46:S2:1448:G:OP1	67:SU:85:HIS:ND1	2.46	0.41
52:SE:42:LEU:HD12	52:SE:43:PRO:HD2	2.01	0.41
53:SF:178:ILE:HD12	53:SF:178:ILE:HA	1.83	0.41
60:SN:42:LYS:HE2	60:SN:42:LYS:HB2	1.69	0.41
67:SU:99:LYS:NZ	67:SU:114:VAL:HG11	2.35	0.41
73:Sa:13:LYS:HA	73:Sa:13:LYS:HD3	1.82	0.41
78:Sg:35:SER:OG	78:Sg:36:ARG:N	2.52	0.41
1:L5:162:A:H2'	1:L5:163:A:H8	1.84	0.41
1:L5:223:G:N2	6:LC:223:ASN:O	2.52	0.41
1:L5:415:U:HO2'	1:L5:416:G:P	2.43	0.41
1:L5:765:G:H3'	1:L5:766:G:H2'	2.02	0.41
1:L5:3567:C:H2'	1:L5:3568:C:C6	2.55	0.41
1:L5:4113:U:H2'	1:L5:4114:C:H6	1.85	0.41
9:LF:238:PRO:HD3	9:LF:269:MET:HE2	2.01	0.41
12:LI:140:THR:OG1	12:LI:141:LYS:N	2.54	0.41
28:LZ:4:PHE:CE1	31:Lc:67:ALA:HB2	2.55	0.41
39:Lk:34:PHE:CE2	39:Lk:56:LEU:HD22	2.56	0.41
46:S2:415:A:OP1	46:S2:815:U:O2'	2.31	0.41
46:S2:502:C:O2	46:S2:502:C:H2'	2.20	0.41
46:S2:923:A:OP1	69:SW:28:ARG:NH2	2.53	0.41
46:S2:1399:G:H1	46:S2:1449:A:H2	1.64	0.41
46:S2:1399:G:O6	46:S2:1449:A:N1	2.54	0.41
46:S2:1537:G:H2'	46:S2:1538:A:H8	1.85	0.41
74:Sb:36:LYS:NZ	74:Sb:41:TYR:HA	2.34	0.41
1:L5:1724:C:H1'	21:LS:160:ARG:HB3	2.02	0.41
17:LO:125:LYS:HE3	17:LO:125:LYS:HB3	1.82	0.41
28:LZ:92:ASP:O	28:LZ:96:VAL:HG22	2.20	0.41
38:Lj:83:THR:HA	38:Lj:84:PRO:HD3	1.89	0.41
46:S2:41:G:N2	46:S2:481:G:N2	2.68	0.41
46:S2:155:G:OP1	54:SG:2:LYS:NZ	2.53	0.41
46:S2:885:C:H1'	46:S2:902:G:N1	2.36	0.41
46:S2:1261:A:C2	46:S2:1621:A:C4	3.08	0.41
61:SO:103:ASN:HB3	61:SO:142:ARG:HD2	2.02	0.41
65:SS:40:TYR:CZ	65:SS:97:GLN:HG3	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SX:82:THR:OG1	70:SX:118:VAL:HG12	2.20	0.41
71:SY:27:VAL:HG12	71:SY:29:HIS:HD2	1.85	0.41
73:Sa:90:GLU:HA	73:Sa:90:GLU:OE2	2.20	0.41
74:Sb:24:LEU:HD12	74:Sb:24:LEU:HA	1.91	0.41
80:Z:-1:UNK:O	80:Z:0:UNK:C	2.68	0.41
1:L5:233:U:O2'	1:L5:2061:U:O4	2.35	0.41
1:L5:3428:C:H2'	1:L5:3429:U:O4'	2.20	0.41
1:L5:3891:G:H2'	1:L5:3892:A:H8	1.86	0.41
5:LB:154:LYS:HB3	5:LB:154:LYS:HE2	1.75	0.41
11:LH:36:ARG:HE	11:LH:36:ARG:HB3	1.69	0.41
36:Lh:10:ARG:NH2	36:Lh:63:GLN:OE1	2.45	0.41
43:Lo:4:VAL:HG13	43:Lo:93:LEU:HD12	2.03	0.41
46:S2:155:G:H2'	46:S2:156:G:H3'	2.03	0.41
54:SG:175:LYS:HE3	54:SG:177:GLN:HE21	1.84	0.41
55:SH:76:GLN:O	55:SH:80:VAL:HG12	2.20	0.41
56:SI:103:LEU:HD12	56:SI:172:LEU:HB3	2.01	0.41
78:Sg:31:ILE:HG23	78:Sg:43:TRP:CD1	2.56	0.41
78:Sg:42:MET:HE2	78:Sg:42:MET:HB3	1.97	0.41
1:L5:4072:U:H6	1:L5:4072:U:H2'	1.63	0.41
1:L5:4383:C:H2'	1:L5:4384:G:O4'	2.19	0.41
1:L5:4399:G:H1	1:L5:4603:A:H62	1.68	0.41
2:L7:52:C:O2'	2:L7:53:U:OP1	2.37	0.41
5:LB:19:ARG:HB2	5:LB:234:ARG:NH2	2.36	0.41
6:LC:290:SER:O	6:LC:294:LYS:HG2	2.21	0.41
7:LD:234:ASP:O	7:LD:235:MET:HB3	2.19	0.41
22:LT:5:LYS:HE2	22:LT:5:LYS:HB2	1.90	0.41
23:LU:33:ILE:HA	23:LU:33:ILE:HD12	1.86	0.41
24:LV:72:LEU:HA	24:LV:75:LYS:HE2	2.03	0.41
26:LX:64:SER:HB2	36:Lh:69:LEU:HD13	2.03	0.41
34:Lf:33:VAL:HG13	34:Lf:38:GLU:HB3	2.03	0.41
46:S2:1829:C:H2'	46:S2:1830:G:O4'	2.21	0.41
51:SD:133:GLY:HA2	51:SD:155:GLY:HA3	2.03	0.41
55:SH:18:GLU:N	55:SH:20:GLU:OE1	2.53	0.41
61:SO:57:THR:OG1	61:SO:60:MET:HG3	2.20	0.41
62:SP:15:PHE:CE2	62:SP:17:TYR:HB2	2.56	0.41
66:ST:102:ARG:HA	66:ST:102:ARG:HD3	1.71	0.41
74:Sb:79:PHE:CD1	74:Sb:79:PHE:C	2.98	0.41
1:L5:1523:C:H5''	1:L5:1524:G:C8	2.55	0.41
1:L5:3369:A:C6	1:L5:3370:U:H1'	2.55	0.41
1:L5:4529:C:H2'	1:L5:4530:G:C8	2.55	0.41
1:L5:4664:A:HO2'	1:L5:4665:G:C1'	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:103:A:C8	3:L8:104:A:C8	3.09	0.41
8:LE:289:MET:HE3	8:LE:289:MET:HB3	1.83	0.41
11:LH:93:ARG:HD2	11:LH:143:GLU:HB3	2.03	0.41
13:LJ:95:ARG:O	13:LJ:98:ASN:HB2	2.20	0.41
14:LL:123:LYS:HD2	36:Lh:122:LYS:O	2.20	0.41
20:LR:171:LYS:NZ	20:LR:172:ARG:HB2	2.36	0.41
21:LS:83:ARG:HB3	21:LS:127:MET:HE1	2.03	0.41
29:La:84:GLU:OE2	29:La:87:ARG:NH2	2.37	0.41
32:Ld:123:ASP:OD1	32:Ld:123:ASP:N	2.48	0.41
46:S2:1335:G:H2'	46:S2:1336:G:O4'	2.21	0.41
46:S2:1375:C:H2'	46:S2:1376:G:O4'	2.20	0.41
46:S2:1483:C:H2'	46:S2:1484:A:O4'	2.21	0.41
46:S2:1799:C:H2'	46:S2:1800:G:O4'	2.21	0.41
54:SG:28:TYR:O	54:SG:30:LYS:HD2	2.20	0.41
56:SI:53:LYS:HE2	56:SI:53:LYS:HB2	1.78	0.41
63:SQ:52:LEU:O	63:SQ:56:LEU:HD12	2.20	0.41
70:SX:102:VAL:CG1	70:SX:120:PHE:HB3	2.51	0.41
1:L5:82:U:H2'	1:L5:83:C:O4'	2.21	0.41
1:L5:373:G:OP2	38:Lj:56:ARG:NH2	2.50	0.41
1:L5:2314:G:H1	1:L5:2324:G:N2	2.19	0.41
1:L5:3892:A:H2'	1:L5:3893:G:C8	2.55	0.41
1:L5:4705:C:H2'	1:L5:4706:A:C8	2.56	0.41
3:L8:127:U:H2'	3:L8:128:C:O4'	2.20	0.41
4:LA:101:VAL:HG22	4:LA:165:VAL:HG22	2.03	0.41
7:LD:256:LYS:HD2	7:LD:256:LYS:HA	1.93	0.41
10:LG:112:GLN:O	10:LG:115:LEU:HG	2.21	0.41
10:LG:160:ASP:OD1	10:LG:160:ASP:N	2.54	0.41
13:LJ:51:SER:O	13:LJ:67:LYS:HA	2.21	0.41
16:LN:108:ARG:CZ	16:LN:161:MET:HE1	2.51	0.41
17:LO:198:THR:O	17:LO:198:THR:OG1	2.28	0.41
22:LT:51:GLY:HA3	22:LT:92:ARG:HG3	2.03	0.41
23:LU:36:ALA:HB3	23:LU:65:ARG:HH22	1.86	0.41
23:LU:65:ARG:NE	23:LU:67:LYS:H	2.10	0.41
29:La:89:ASN:N	29:La:89:ASN:OD1	2.53	0.41
31:Lc:17:ARG:HB3	31:Lc:103:ASP:OD1	2.21	0.41
31:Lc:20:LEU:HD23	31:Lc:101:ASP:HB3	2.03	0.41
37:Li:71:LYS:HE3	37:Li:71:LYS:HB3	1.62	0.41
46:S2:106:C:H2'	46:S2:107:A:H8	1.86	0.41
46:S2:176:U:H5'	46:S2:177:G:OP1	2.20	0.41
46:S2:514:G:H3'	46:S2:515:U:H6	1.86	0.41
46:S2:563:U:H2'	46:S2:564:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:964:A:H2'	46:S2:965:A:C8	2.56	0.41
46:S2:986:G:H4'	61:SO:138:ASP:OD2	2.20	0.41
46:S2:1350:G:H2'	46:S2:1351:U:C6	2.56	0.41
47:S7:33:C:H2'	47:S7:34:C:H2'	2.03	0.41
49:SB:166:LYS:HB3	49:SB:166:LYS:HE3	1.80	0.41
56:SI:148:LYS:O	56:SI:151:GLU:HG2	2.21	0.41
57:SJ:27:GLN:OE1	57:SJ:27:GLN:C	2.64	0.41
58:SK:75:GLY:O	58:SK:79:LEU:HB2	2.21	0.41
62:SP:76:VAL:O	62:SP:76:VAL:HG12	2.20	0.41
63:SQ:93:VAL:HG12	63:SQ:108:ILE:HD12	2.03	0.41
64:SR:62:GLN:HG3	64:SR:63:ARG:NH1	2.36	0.41
64:SR:85:VAL:HA	64:SR:86:PRO:HD3	1.83	0.41
67:SU:44:LYS:HD3	67:SU:44:LYS:HA	1.73	0.41
68:SV:71:ARG:HH22	74:Sb:4:ALA:HB2	1.86	0.41
69:SW:28:ARG:O	69:SW:60:LYS:HG2	2.20	0.41
78:Sg:207:CYS:N	78:Sg:219:TRP:O	2.47	0.41
78:Sg:237:ASN:ND2	78:Sg:286:CYS:O	2.40	0.41
1:L5:1761:A:O2'	1:L5:1764:G:N2	2.54	0.41
1:L5:2613:G:H2'	1:L5:2614:C:H6	1.86	0.41
1:L5:2657:G:N2	1:L5:2657:G:OP1	2.28	0.41
1:L5:3362:G:H2'	1:L5:3363:C:C6	2.56	0.41
1:L5:3577:U:H2'	1:L5:3578:U:C6	2.55	0.41
1:L5:4542:G:H2'	1:L5:4543:G:H8	1.84	0.41
3:L8:128:C:H2'	3:L8:129:C:C6	2.56	0.41
6:LC:235:LEU:HD23	6:LC:235:LEU:HA	1.92	0.41
7:LD:135:ILE:HG13	7:LD:135:ILE:O	2.20	0.41
10:LG:252:LYS:HE3	10:LG:252:LYS:HB2	1.90	0.41
23:LU:50:ASN:OD1	23:LU:50:ASN:N	2.53	0.41
26:LX:123:LYS:HE3	26:LX:123:LYS:HB2	1.83	0.41
44:Lp:86:LEU:HD23	44:Lp:86:LEU:HA	1.85	0.41
46:S2:603:G:OP2	46:S2:604:C:O2'	2.30	0.41
46:S2:1426:G:H2'	46:S2:1427:U:O4'	2.21	0.41
46:S2:1443:U:H3'	46:S2:1443:U:OP1	2.21	0.41
46:S2:1545:C:H4'	63:SQ:80:GLN:HE22	1.86	0.41
46:S2:1564:G:H2'	46:S2:1565:C:H6	1.86	0.41
49:SB:37:ALA:HA	49:SB:42:ARG:HE	1.86	0.41
50:SC:270:THR:HA	50:SC:273:LEU:HD23	2.03	0.41
53:SF:56:TYR:O	53:SF:62:ARG:HB3	2.22	0.41
54:SG:136:LYS:HD2	54:SG:174:PRO:HB2	2.02	0.41
55:SH:10:LYS:HA	55:SH:10:LYS:HD3	1.87	0.41
55:SH:107:LYS:HA	55:SH:107:LYS:HD3	1.71	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SK:14:LEU:HD11	58:SK:35:LEU:HD21	2.01	0.41
58:SK:57:TYR:HB3	58:SK:75:GLY:HA2	2.02	0.41
59:SL:56:ILE:HD13	59:SL:56:ILE:HA	1.89	0.41
1:L5:725:U:H2'	1:L5:726:C:C6	2.56	0.40
1:L5:1012:U:HO2'	1:L5:1015:C:H42	1.69	0.40
1:L5:2323:G:N3	1:L5:2323:G:H2'	2.36	0.40
1:L5:3261:A:H2'	1:L5:3262:C:O4'	2.21	0.40
1:L5:3716:G:H2'	1:L5:3717:U:H6	1.86	0.40
3:L8:94:G:H21	38:Lj:82:THR:HB	1.86	0.40
4:LA:28:ARG:HB2	4:LA:123:ARG:HD3	2.03	0.40
4:LA:106:THR:O	4:LA:106:THR:OG1	2.31	0.40
5:LB:36:ASP:OD1	5:LB:38:SER:OG	2.32	0.40
7:LD:232:THR:O	7:LD:234:ASP:N	2.40	0.40
7:LD:265:ARG:NE	7:LD:267:ASN:O	2.55	0.40
11:LH:101:ILE:HD11	11:LH:117:PHE:HD1	1.86	0.40
13:LJ:41:GLU:O	13:LJ:45:GLY:N	2.53	0.40
14:LL:47:ALA:HB3	14:LL:48:PRO:HD3	2.03	0.40
14:LL:200:LYS:NZ	14:LL:204:GLU:HB3	2.36	0.40
17:LO:173:GLN:C	17:LO:173:GLN:OE1	2.64	0.40
18:LP:125:MET:HE3	18:LP:125:MET:HB2	1.89	0.40
33:Le:109:LYS:HB2	33:Le:109:LYS:HE2	1.85	0.40
36:Lh:15:GLU:H	36:Lh:15:GLU:CD	2.29	0.40
36:Lh:43:LYS:HE3	36:Lh:43:LYS:HB3	1.95	0.40
37:Li:38:LYS:HE2	37:Li:38:LYS:HB3	1.58	0.40
37:Li:58:MET:HB2	37:Li:58:MET:HE2	1.77	0.40
38:Lj:64:MET:O	38:Lj:68:LYS:HG2	2.21	0.40
46:S2:1623:U:O4	62:SP:122:THR:HG23	2.21	0.40
46:S2:1649:G:H5''	63:SQ:125:ARG:HB2	2.04	0.40
46:S2:1729:U:HO2'	46:S2:1730:U:H6	1.68	0.40
51:SD:31:GLU:OE1	51:SD:31:GLU:N	2.53	0.40
62:SP:72:LYS:HA	62:SP:73:PRO:HD3	1.83	0.40
66:ST:66:LEU:HD13	66:ST:66:LEU:HA	1.95	0.40
67:SU:38:ASP:OD1	67:SU:41:ARG:NH2	2.50	0.40
67:SU:48:LEU:HD13	67:SU:93:SER:OG	2.21	0.40
68:SV:71:ARG:HG2	68:SV:71:ARG:H	1.67	0.40
71:SY:20:ARG:HG3	71:SY:74:MET:HE2	2.02	0.40
78:Sg:142:VAL:HG11	78:Sg:177:TRP:CH2	2.55	0.40
12:LI:181:PHE:O	12:LI:185:VAL:HG23	2.21	0.40
14:LL:197:LYS:O	14:LL:201:GLU:HG2	2.22	0.40
23:LU:112:LEU:HD13	23:LU:112:LEU:HA	1.89	0.40
32:Ld:26:THR:OG1	32:Ld:85:ARG:NH1	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lk:24:LYS:C	39:Lk:25:ILE:HD13	2.46	0.40
46:S2:69:C:H2'	46:S2:70:G:O4'	2.22	0.40
46:S2:477:A:O2'	46:S2:489:U:O5'	2.39	0.40
46:S2:1345:A:H8	46:S2:1345:A:OP2	2.04	0.40
46:S2:1564:G:H4'	66:ST:115:LYS:NZ	2.37	0.40
48:SA:158:ASP:O	48:SA:159:ILE:HD13	2.20	0.40
49:SB:71:LEU:HA	49:SB:71:LEU:HD23	1.88	0.40
52:SE:52:LEU:HD23	52:SE:52:LEU:HA	1.80	0.40
54:SG:113:ILE:HD12	54:SG:124:LEU:HD21	2.03	0.40
57:SJ:93:LYS:HE3	57:SJ:93:LYS:HB3	1.95	0.40
64:SR:26:ASN:HD21	64:SR:59:LYS:HE2	1.86	0.40
67:SU:56:MET:HG3	67:SU:57:PRO:HD2	2.03	0.40
78:Sg:49:GLU:H	78:Sg:49:GLU:HG2	1.68	0.40
78:Sg:174:VAL:HG23	78:Sg:188:HIS:HB2	2.02	0.40
1:L5:423:U:H2'	1:L5:424:U:H6	1.85	0.40
1:L5:735:C:O2'	1:L5:736:C:H5'	2.21	0.40
1:L5:826:G:H2'	1:L5:827:C:C6	2.56	0.40
1:L5:1542:G:H2'	1:L5:1543:C:C6	2.56	0.40
1:L5:3719:U:O2'	1:L5:3720:U:H6	2.04	0.40
1:L5:3891:G:H2'	1:L5:3892:A:C8	2.56	0.40
1:L5:4552:C:C6	1:L5:4553:G:H1'	2.56	0.40
3:L8:144:U:H2'	3:L8:145:C:C6	2.57	0.40
10:LG:264:LYS:HE2	49:SB:225:LEU:HG	2.02	0.40
12:LI:35:ASP:O	12:LI:36:LEU:HD12	2.21	0.40
21:LS:2:LYS:HG2	21:LS:3:ALA:H	1.85	0.40
28:LZ:76:ASN:OD1	28:LZ:77:TYR:N	2.55	0.40
29:La:94:LYS:H	29:La:94:LYS:HG2	1.56	0.40
46:S2:95:G:N2	46:S2:435:G:N2	2.63	0.40
46:S2:106:C:OP1	46:S2:432:G:O2'	2.36	0.40
46:S2:351:C:O2'	46:S2:384:G:N1	2.48	0.40
46:S2:570:A:H2'	46:S2:571:C:O4'	2.22	0.40
46:S2:640:C:H2'	46:S2:641:A:H8	1.85	0.40
46:S2:1118:C:H2'	46:S2:1119:C:O4'	2.20	0.40
46:S2:1445:U:O2'	46:S2:1581:A:N1	2.48	0.40
46:S2:1580:A:H4'	46:S2:1582:C:H5	1.86	0.40
46:S2:1752:C:H2'	46:S2:1753:C:H4'	2.03	0.40
46:S2:1753:C:O2'	46:S2:1783:G:N1	2.55	0.40
48:SA:174:MET:HE2	48:SA:174:MET:HB3	2.00	0.40
49:SB:65:ARG:NH2	61:SO:51:GLU:OE2	2.55	0.40
49:SB:84:PHE:HD2	49:SB:100:PHE:HE1	1.69	0.40
51:SD:66:ILE:HG23	51:SD:67:ARG:CD	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SD:132:LYS:O	51:SD:156:LEU:N	2.53	0.40
51:SD:152:PHE:N	51:SD:152:PHE:CD1	2.86	0.40
60:SN:100:LYS:HB3	60:SN:100:LYS:HE3	1.66	0.40
63:SQ:62:ARG:HH22	63:SQ:107:GLU:CD	2.29	0.40
64:SR:11:LYS:HE2	64:SR:11:LYS:HB2	1.82	0.40
65:SS:89:ASP:CG	65:SS:91:LYS:H	2.29	0.40
78:Sg:104:HIS:CE1	78:Sg:124:SER:HB3	2.56	0.40
1:L5:189:G:C2	1:L5:253:G:C2	3.10	0.40
1:L5:1183:C:H1'	27:LY:1:MET:HE2	2.03	0.40
1:L5:1322:A:OP1	6:LC:110:ARG:NH2	2.54	0.40
1:L5:2618:A:H2'	1:L5:2619:U:H6	1.86	0.40
1:L5:3326:G:N2	1:L5:3329:G:H21	2.12	0.40
9:LF:116:ARG:HD3	9:LF:138:GLN:O	2.22	0.40
11:LH:60:TRP:O	11:LH:61:TRP:HB2	2.22	0.40
30:Lb:68:ARG:NH2	30:Lb:69:ALA:HB2	2.36	0.40
41:Lm:95:ILE:HD11	41:Lm:124:LYS:HD2	2.03	0.40
43:Lo:2:VAL:N	43:Lo:90:HIS:O	2.55	0.40
46:S2:582:U:H4'	71:SY:66:GLY:HA2	2.02	0.40
46:S2:610:U:H2'	46:S2:611:G:H8	1.86	0.40
46:S2:1137:U:H2'	46:S2:1138:U:C6	2.56	0.40
46:S2:1556:U:O4	76:Sd:19:ARG:N	2.55	0.40
48:SA:97:THR:HG21	48:SA:117:ARG:HD3	2.03	0.40
52:SE:225:ILE:HD13	52:SE:225:ILE:HA	1.86	0.40
58:SK:59:LYS:O	58:SK:59:LYS:HG3	2.20	0.40
59:SL:97:ARG:HA	59:SL:97:ARG:HD2	1.92	0.40
64:SR:74:GLN:O	64:SR:78:ARG:HG3	2.22	0.40
71:SY:42:GLU:HG3	71:SY:52:PRO:HG3	2.04	0.40
78:Sg:131:LEU:H	78:Sg:131:LEU:HD23	1.86	0.40
1:L5:950:G:N1	1:L5:1037:G:C2	2.90	0.40
1:L5:3720:U:H2'	1:L5:3721:U:C6	2.56	0.40
17:LO:3:GLU:HG3	17:LO:31:ARG:HH22	1.87	0.40
39:Lk:23:VAL:HG11	39:Lk:60:LEU:HD21	2.04	0.40
46:S2:97:U:H4'	46:S2:98:C:OP2	2.18	0.40
46:S2:1011:G:H2'	46:S2:1012:A:H8	1.87	0.40
46:S2:1553:G:OP1	51:SD:9:ARG:NH2	2.48	0.40
47:S7:31:G:O2'	47:S7:32:C:O5'	2.40	0.40
57:SJ:84:ILE:HG23	57:SJ:86:VAL:H	1.86	0.40
57:SJ:124:HIS:CD2	77:Se:109:ARG:HD3	2.57	0.40
59:SL:68:ILE:HD13	59:SL:131:CYS:HB3	2.04	0.40
80:Z:-1:UNK:C	80:Z:1:UNK:N	2.83	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%)	225 (92%)	21 (8%)	0	100	100
5	LB	395/403 (98%)	371 (94%)	24 (6%)	0	100	100
6	LC	355/419 (85%)	338 (95%)	17 (5%)	0	100	100
7	LD	291/297 (98%)	266 (91%)	25 (9%)	0	100	100
8	LE	210/296 (71%)	194 (92%)	16 (8%)	0	100	100
9	LF	212/270 (78%)	201 (95%)	11 (5%)	0	100	100
10	LG	225/266 (85%)	214 (95%)	11 (5%)	0	100	100
11	LH	188/192 (98%)	176 (94%)	9 (5%)	3 (2%)	7	21
12	LI	197/214 (92%)	191 (97%)	6 (3%)	0	100	100
13	LJ	165/178 (93%)	155 (94%)	10 (6%)	0	100	100
14	LL	204/211 (97%)	189 (93%)	15 (7%)	0	100	100
15	LM	134/217 (62%)	126 (94%)	8 (6%)	0	100	100
16	LN	201/204 (98%)	191 (95%)	9 (4%)	1 (0%)	24	49
17	LO	199/203 (98%)	191 (96%)	8 (4%)	0	100	100
18	LP	152/184 (83%)	149 (98%)	3 (2%)	0	100	100
19	LQ	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
20	LR	172/196 (88%)	170 (99%)	2 (1%)	0	100	100
21	LS	173/176 (98%)	166 (96%)	7 (4%)	0	100	100
22	LT	158/160 (99%)	151 (96%)	7 (4%)	0	100	100
23	LU	98/128 (77%)	87 (89%)	11 (11%)	0	100	100
24	LV	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
25	LW	60/157 (38%)	60 (100%)	0	0	100	100
26	LX	116/156 (74%)	110 (95%)	6 (5%)	0	100	100
27	LY	130/145 (90%)	130 (100%)	0	0	100	100
28	LZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	95/160 (59%)	92 (97%)	3 (3%)	0	100	100
31	Lc	92/115 (80%)	90 (98%)	1 (1%)	1 (1%)	11	29
32	Ld	106/125 (85%)	103 (97%)	3 (3%)	0	100	100
33	Le	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
34	Lf	107/110 (97%)	103 (96%)	4 (4%)	0	100	100
35	Lg	108/117 (92%)	106 (98%)	2 (2%)	0	100	100
36	Lh	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
37	Li	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
38	Lj	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
39	Lk	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	96 (95%)	4 (4%)	1 (1%)	12	32
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Lr	122/137 (89%)	117 (96%)	5 (4%)	0	100	100
48	SA	205/295 (70%)	184 (90%)	20 (10%)	1 (0%)	24	49
49	SB	211/264 (80%)	199 (94%)	12 (6%)	0	100	100
50	SC	213/293 (73%)	204 (96%)	9 (4%)	0	100	100
51	SD	207/243 (85%)	191 (92%)	15 (7%)	1 (0%)	24	49
52	SE	256/263 (97%)	234 (91%)	21 (8%)	1 (0%)	30	53
53	SF	175/204 (86%)	161 (92%)	14 (8%)	0	100	100
54	SG	200/249 (80%)	186 (93%)	13 (6%)	1 (0%)	24	49
55	SH	176/194 (91%)	156 (89%)	20 (11%)	0	100	100
56	SI	179/208 (86%)	170 (95%)	9 (5%)	0	100	100
57	SJ	130/194 (67%)	121 (93%)	9 (7%)	0	100	100
58	SK	86/165 (52%)	73 (85%)	13 (15%)	0	100	100
59	SL	131/158 (83%)	120 (92%)	11 (8%)	0	100	100
60	SN	148/151 (98%)	148 (100%)	0	0	100	100
61	SO	132/151 (87%)	124 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	SP	116/145 (80%)	97 (84%)	16 (14%)	3 (3%)	4	12
63	SQ	137/146 (94%)	116 (85%)	21 (15%)	0	100	100
64	SR	129/135 (96%)	117 (91%)	12 (9%)	0	100	100
65	SS	138/152 (91%)	127 (92%)	11 (8%)	0	100	100
66	ST	138/145 (95%)	134 (97%)	4 (3%)	0	100	100
67	SU	93/119 (78%)	83 (89%)	10 (11%)	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%)	128 (93%)	8 (6%)	1 (1%)	18	40
71	SY	108/133 (81%)	97 (90%)	11 (10%)	0	100	100
72	SZ	70/125 (56%)	61 (87%)	9 (13%)	0	100	100
73	Sa	97/115 (84%)	90 (93%)	7 (7%)	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	17
76	Sd	52/56 (93%)	49 (94%)	3 (6%)	0	100	100
77	Se	44/133 (33%)	39 (89%)	5 (11%)	0	100	100
78	Sg	270/317 (85%)	240 (89%)	29 (11%)	1 (0%)	30	53
All	All	10626/12499 (85%)	9966 (94%)	644 (6%)	16 (0%)	44	66

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	LH	13	PRO
70	SX	61	GLN
51	SD	93	THR
75	Sc	51	ARG
78	Sg	95	GLY
11	LH	189	GLN
43	Lo	59	LYS
48	SA	11	LYS
62	SP	51	ARG
11	LH	53	LYS
52	SE	247	THR
62	SP	53	GLN
62	SP	50	ARG
31	Lc	99	PRO

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Mol	Chain	Res	Type
16	LN	84	PRO
54	SG	169	PRO

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%)	186 (98%)	4 (2%)	47	69
5	LB	344/348 (99%)	331 (96%)	13 (4%)	29	55
6	LC	301/348 (86%)	293 (97%)	8 (3%)	39	64
7	LD	246/249 (99%)	236 (96%)	10 (4%)	27	53
8	LE	194/256 (76%)	185 (95%)	9 (5%)	24	50
9	LF	185/234 (79%)	182 (98%)	3 (2%)	55	75
10	LG	197/223 (88%)	196 (100%)	1 (0%)	81	90
11	LH	169/171 (99%)	158 (94%)	11 (6%)	15	37
12	LI	170/180 (94%)	162 (95%)	8 (5%)	23	49
13	LJ	141/149 (95%)	140 (99%)	1 (1%)	76	87
14	LL	173/178 (97%)	168 (97%)	5 (3%)	37	61
15	LM	116/157 (74%)	110 (95%)	6 (5%)	21	46
16	LN	171/172 (99%)	166 (97%)	5 (3%)	37	61
17	LO	172/173 (99%)	166 (96%)	6 (4%)	32	57
18	LP	135/163 (83%)	129 (96%)	6 (4%)	25	51
19	LQ	164/165 (99%)	161 (98%)	3 (2%)	51	72
20	LR	154/175 (88%)	152 (99%)	2 (1%)	61	78
21	LS	155/156 (99%)	148 (96%)	7 (4%)	24	50
22	LT	140/140 (100%)	138 (99%)	2 (1%)	59	77
23	LU	90/114 (79%)	82 (91%)	8 (9%)	9	24
24	LV	100/107 (94%)	95 (95%)	5 (5%)	22	47
25	LW	54/126 (43%)	53 (98%)	1 (2%)	50	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	LX	106/133 (80%)	102 (96%)	4 (4%)	29	55
27	LY	123/135 (91%)	122 (99%)	1 (1%)	73	85
28	LZ	117/118 (99%)	111 (95%)	6 (5%)	21	47
29	La	120/121 (99%)	118 (98%)	2 (2%)	53	73
30	Lb	83/124 (67%)	82 (99%)	1 (1%)	63	79
31	Lc	79/97 (81%)	76 (96%)	3 (4%)	29	55
32	Ld	99/110 (90%)	94 (95%)	5 (5%)	21	47
33	Le	114/121 (94%)	112 (98%)	2 (2%)	51	72
34	Lf	88/89 (99%)	85 (97%)	3 (3%)	32	58
35	Lg	94/100 (94%)	91 (97%)	3 (3%)	34	59
36	Lh	109/110 (99%)	105 (96%)	4 (4%)	30	55
37	Li	86/89 (97%)	84 (98%)	2 (2%)	44	67
38	Lj	73/80 (91%)	72 (99%)	1 (1%)	59	77
39	Lk	64/65 (98%)	62 (97%)	2 (3%)	35	59
40	Ll	46/47 (98%)	44 (96%)	2 (4%)	26	52
41	Lm	47/116 (40%)	46 (98%)	1 (2%)	47	69
42	Ln	24/24 (100%)	24 (100%)	0	100	100
43	Lo	91/94 (97%)	89 (98%)	2 (2%)	45	69
44	Lp	74/75 (99%)	69 (93%)	5 (7%)	14	35
45	Lr	108/121 (89%)	106 (98%)	2 (2%)	50	71
48	SA	173/242 (72%)	157 (91%)	16 (9%)	8	23
49	SB	194/229 (85%)	190 (98%)	4 (2%)	47	69
50	SC	181/224 (81%)	175 (97%)	6 (3%)	33	58
51	SD	173/202 (86%)	163 (94%)	10 (6%)	18	41
52	SE	221/225 (98%)	213 (96%)	8 (4%)	31	56
53	SF	152/170 (89%)	149 (98%)	3 (2%)	48	71
54	SG	178/218 (82%)	163 (92%)	15 (8%)	10	26
55	SH	161/174 (92%)	150 (93%)	11 (7%)	14	35
56	SI	159/180 (88%)	148 (93%)	11 (7%)	14	35
57	SJ	126/168 (75%)	121 (96%)	5 (4%)	28	53
58	SK	81/136 (60%)	78 (96%)	3 (4%)	30	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	SL	123/142 (87%)	114 (93%)	9 (7%)	13	33
60	SN	130/131 (99%)	127 (98%)	3 (2%)	44	67
61	SO	104/119 (87%)	101 (97%)	3 (3%)	37	61
62	SP	107/130 (82%)	91 (85%)	16 (15%)	3	8
63	SQ	115/121 (95%)	107 (93%)	8 (7%)	14	34
64	SR	119/121 (98%)	114 (96%)	5 (4%)	26	53
65	SS	122/132 (92%)	118 (97%)	4 (3%)	33	58
66	ST	110/115 (96%)	106 (96%)	4 (4%)	31	56
67	SU	88/107 (82%)	85 (97%)	3 (3%)	32	58
68	SV	65/67 (97%)	62 (95%)	3 (5%)	24	50
69	SW	112/113 (99%)	105 (94%)	7 (6%)	16	38
70	SX	111/115 (96%)	108 (97%)	3 (3%)	39	64
71	SY	93/115 (81%)	82 (88%)	11 (12%)	5	15
72	SZ	64/103 (62%)	56 (88%)	8 (12%)	4	13
73	Sa	86/98 (88%)	82 (95%)	4 (5%)	23	49
74	Sb	75/76 (99%)	69 (92%)	6 (8%)	11	28
75	Sc	48/62 (77%)	47 (98%)	1 (2%)	47	69
76	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	69
77	Se	39/106 (37%)	38 (97%)	1 (3%)	40	65
78	Sg	237/275 (86%)	223 (94%)	14 (6%)	18	41
All	All	9301/10617 (88%)	8920 (96%)	381 (4%)	28	53

All (381) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	15	VAL
4	LA	106	THR
4	LA	111	THR
4	LA	199	VAL
5	LB	17	LEU
5	LB	31	SER
5	LB	44	THR
5	LB	162	ILE
5	LB	213	GLN
5	LB	262	VAL

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Mol	Chain	Res	Type
5	LB	265	SER
5	LB	293	ILE
5	LB	300	LYS
5	LB	336	CYS
5	LB	340	THR
5	LB	344	VAL
5	LB	355	THR
6	LC	22	VAL
6	LC	42	THR
6	LC	84	THR
6	LC	117	THR
6	LC	124	ILE
6	LC	138	MET
6	LC	188	ARG
6	LC	351	VAL
7	LD	38	ILE
7	LD	44	TYR
7	LD	63	GLN
7	LD	81	HIS
7	LD	134	SER
7	LD	167	VAL
7	LD	232	THR
7	LD	235	MET
7	LD	261	VAL
7	LD	267	ASN
8	LE	100	VAL
8	LE	103	THR
8	LE	128	ASP
8	LE	183	VAL
8	LE	202	VAL
8	LE	207	THR
8	LE	215	LYS
8	LE	272	VAL
8	LE	289	MET
9	LF	61	LEU
9	LF	124	SER
9	LF	141	ASN
10	LG	106	THR
11	LH	9	THR
11	LH	10	VAL
11	LH	37	ASP
11	LH	41	ILE

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Mol	Chain	Res	Type
11	LH	58	ASP
11	LH	80	MET
11	LH	95	VAL
11	LH	110	SER
11	LH	120	GLU
11	LH	130	THR
11	LH	186	THR
12	LI	26	VAL
12	LI	28	ASP
12	LI	51	HIS
12	LI	91	LEU
12	LI	99	ILE
12	LI	125	THR
12	LI	191	ILE
12	LI	195	CYS
13	LJ	148	THR
14	LL	64	VAL
14	LL	80	GLU
14	LL	86	ILE
14	LL	107	THR
14	LL	170	THR
15	LM	31	ILE
15	LM	59	ASP
15	LM	104	MET
15	LM	112	VAL
15	LM	113	MET
15	LM	125	THR
16	LN	10	LEU
16	LN	43	THR
16	LN	80	THR
16	LN	124	ASP
16	LN	171	SER
17	LO	46	ASN
17	LO	132	THR
17	LO	159	LYS
17	LO	190	CYS
17	LO	197	LYS
17	LO	198	THR
18	LP	6	LEU
18	LP	29	THR
18	LP	57	CYS
18	LP	87	SER

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Mol	Chain	Res	Type
18	LP	147	GLU
18	LP	151	THR
19	LQ	42	THR
19	LQ	128	LEU
19	LQ	158	THR
20	LR	47	ASP
20	LR	164	SER
21	LS	48	VAL
21	LS	58	SER
21	LS	90	THR
21	LS	102	THR
21	LS	160	ARG
21	LS	164	LYS
21	LS	170	LYS
22	LT	68	THR
22	LT	106	LEU
23	LU	22	THR
23	LU	26	THR
23	LU	29	VAL
23	LU	69	LYS
23	LU	74	SER
23	LU	103	VAL
23	LU	109	SER
23	LU	115	PHE
24	LV	18	LEU
24	LV	28	CYS
24	LV	64	THR
24	LV	67	LYS
24	LV	72	LEU
25	LW	50	ASN
26	LX	119	ILE
26	LX	131	ASP
26	LX	138	VAL
26	LX	153	ILE
27	LY	91	ASN
28	LZ	31	ASP
28	LZ	33	THR
28	LZ	39	SER
28	LZ	53	VAL
28	LZ	89	ILE
28	LZ	95	VAL
29	La	16	SER

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Mol	Chain	Res	Type
29	La	56	VAL
30	Lb	40	LEU
31	Lc	28	VAL
31	Lc	78	ASN
31	Lc	91	VAL
32	Ld	21	VAL
32	Ld	54	MET
32	Ld	84	ILE
32	Ld	104	THR
32	Ld	107	THR
33	Le	66	THR
33	Le	126	ASN
34	Lf	20	ASN
34	Lf	43	LEU
34	Lf	58	VAL
35	Lg	2	VAL
35	Lg	48	VAL
35	Lg	104	VAL
36	Lh	22	ASP
36	Lh	23	ASP
36	Lh	29	SER
36	Lh	104	THR
37	Li	12	ASN
37	Li	27	SER
38	Lj	12	ARG
39	Lk	32	VAL
39	Lk	59	SER
40	Ll	27	ILE
40	Ll	29	MET
41	Lm	127	VAL
43	Lo	55	ILE
43	Lo	103	VAL
44	Lp	21	SER
44	Lp	26	VAL
44	Lp	45	THR
44	Lp	74	THR
44	Lp	75	SER
45	Lr	27	THR
45	Lr	52	GLU
48	SA	16	LEU
48	SA	18	PHE
48	SA	40	LYS

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Mol	Chain	Res	Type
48	SA	49	ILE
48	SA	77	ILE
48	SA	81	ASN
48	SA	94	THR
48	SA	99	ILE
48	SA	113	GLN
48	SA	121	LEU
48	SA	141	ASN
48	SA	151	ASP
48	SA	177	MET
48	SA	188	THR
48	SA	195	TRP
48	SA	198	MET
49	SB	27	LYS
49	SB	88	THR
49	SB	119	THR
49	SB	224	GLU
50	SC	61	ILE
50	SC	75	ILE
50	SC	88	ILE
50	SC	160	LEU
50	SC	244	ILE
50	SC	254	ASP
51	SD	35	SER
51	SD	48	ILE
51	SD	68	GLU
51	SD	99	ILE
51	SD	129	SER
51	SD	162	ASP
51	SD	170	THR
51	SD	174	HIS
51	SD	175	VAL
51	SD	198	ILE
52	SE	56	LEU
52	SE	91	SER
52	SE	102	ILE
52	SE	105	THR
52	SE	129	ILE
52	SE	157	ASN
52	SE	198	ARG
52	SE	210	VAL
53	SF	34	SER

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Mol	Chain	Res	Type
53	SF	39	ILE
53	SF	52	SER
54	SG	13	GLN
54	SG	15	LEU
54	SG	26	THR
54	SG	49	VAL
54	SG	50	VAL
54	SG	75	LEU
54	SG	98	ARG
54	SG	108	VAL
54	SG	129	VAL
54	SG	144	LEU
54	SG	157	VAL
54	SG	158	VAL
54	SG	168	LYS
54	SG	184	VAL
54	SG	197	GLN
55	SH	20	GLU
55	SH	23	ILE
55	SH	36	LEU
55	SH	40	LEU
55	SH	53	VAL
55	SH	61	ILE
55	SH	64	VAL
55	SH	66	VAL
55	SH	119	SER
55	SH	132	ASP
55	SH	181	THR
56	SI	7	ASN
56	SI	46	VAL
56	SI	61	ASP
56	SI	62	VAL
56	SI	66	SER
56	SI	86	SER
56	SI	95	THR
56	SI	103	LEU
56	SI	107	THR
56	SI	115	SER
56	SI	151	GLU
57	SJ	23	SER
57	SJ	103	GLU
57	SJ	110	LEU

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Mol	Chain	Res	Type
57	SJ	148	ILE
57	SJ	149	VAL
58	SK	7	ASN
58	SK	21	MET
58	SK	50	GLN
59	SL	3	ASP
59	SL	4	ILE
59	SL	38	LYS
59	SL	46	THR
59	SL	66	VAL
59	SL	77	VAL
59	SL	78	THR
59	SL	82	MET
59	SL	146	THR
60	SN	67	THR
60	SN	69	ASN
60	SN	87	ASP
61	SO	42	VAL
61	SO	88	LEU
61	SO	97	LEU
62	SP	49	LEU
62	SP	50	ARG
62	SP	51	ARG
62	SP	52	LYS
62	SP	55	SER
62	SP	57	LEU
62	SP	58	LYS
62	SP	59	ARG
62	SP	60	LEU
62	SP	61	ARG
62	SP	64	LYS
62	SP	66	GLU
62	SP	74	GLU
62	SP	77	LYS
62	SP	96	VAL
62	SP	116	LEU
63	SQ	10	VAL
63	SQ	25	CYS
63	SQ	26	LYS
63	SQ	27	ARG
63	SQ	39	LEU
63	SQ	41	MET

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Mol	Chain	Res	Type
63	SQ	42	ILE
63	SQ	113	ILE
64	SR	8	THR
64	SR	19	LYS
64	SR	102	THR
64	SR	127	ASN
64	SR	130	THR
65	SS	36	VAL
65	SS	49	ASP
65	SS	60	THR
65	SS	85	ASN
66	ST	30	VAL
66	ST	64	LEU
66	ST	104	LEU
66	ST	131	LEU
67	SU	22	ILE
67	SU	58	THR
67	SU	82	MET
68	SV	9	VAL
68	SV	23	ILE
68	SV	35	ASN
69	SW	3	ARG
69	SW	30	CYS
69	SW	53	ILE
69	SW	80	ASP
69	SW	103	VAL
69	SW	112	ASP
69	SW	124	LYS
70	SX	105	PHE
70	SX	115	ILE
70	SX	130	LEU
71	SY	22	GLN
71	SY	24	VAL
71	SY	43	LYS
71	SY	47	MET
71	SY	62	THR
71	SY	68	LYS
71	SY	102	THR
71	SY	109	GLU
71	SY	114	MET
71	SY	124	ASN
71	SY	125	VAL

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Mol	Chain	Res	Type
72	SZ	46	ASN
72	SZ	47	LEU
72	SZ	67	LEU
72	SZ	68	ILE
72	SZ	69	THR
72	SZ	72	VAL
72	SZ	82	SER
72	SZ	107	VAL
73	Sa	40	VAL
73	Sa	53	ILE
73	Sa	58	VAL
73	Sa	69	VAL
74	Sb	13	GLU
74	Sb	25	VAL
74	Sb	27	SER
74	Sb	30	SER
74	Sb	44	THR
74	Sb	57	VAL
75	Sc	17	VAL
76	Sd	36	LEU
77	Se	117	VAL
78	Sg	6	THR
78	Sg	35	SER
78	Sg	66	VAL
78	Sg	89	LEU
78	Sg	92	LEU
78	Sg	94	THR
78	Sg	96	THR
78	Sg	97	THR
78	Sg	98	THR
78	Sg	113	PHE
78	Sg	128	THR
78	Sg	150	TRP
78	Sg	152	SER
78	Sg	297	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	8	GLN
4	LA	140	ASN
5	LB	11	HIS

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Mol	Chain	Res	Type
5	LB	123	HIS
5	LB	275	HIS
5	LB	276	HIS
5	LB	328	ASN
6	LC	61	GLN
6	LC	142	HIS
6	LC	231	ASN
7	LD	63	GLN
7	LD	229	ASN
7	LD	244	HIS
7	LD	282	GLN
9	LF	102	ASN
9	LF	121	ASN
9	LF	141	ASN
9	LF	228	ASN
9	LF	261	GLN
10	LG	43	GLN
10	LG	149	ASN
12	LI	144	ASN
13	LJ	65	ASN
14	LL	67	HIS
16	LN	91	GLN
17	LO	26	GLN
18	LP	133	HIS
20	LR	40	GLN
21	LS	36	ASN
21	LS	108	GLN
23	LU	94	ASN
23	LU	105	ASN
24	LV	135	ASN
27	LY	20	ASN
27	LY	65	GLN
29	La	34	ASN
30	Lb	12	GLN
32	Ld	118	GLN
34	Lf	80	ASN
40	Ll	28	GLN
40	Ll	33	ASN
41	Lm	109	ASN
43	Lo	45	GLN
45	Lr	31	ASN
45	Lr	36	ASN

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Mol	Chain	Res	Type
48	SA	70	ASN
49	SB	149	GLN
50	SC	115	GLN
51	SD	179	GLN
52	SE	50	ASN
52	SE	214	ASN
53	SF	95	HIS
53	SF	186	ASN
54	SG	13	GLN
54	SG	146	ASN
54	SG	177	GLN
54	SG	187	HIS
54	SG	202	ASN
57	SJ	75	ASN
58	SK	28	HIS
60	SN	69	ASN
65	SS	73	ASN
66	ST	42	HIS
66	ST	51	ASN
66	ST	137	GLN
69	SW	113	HIS
72	SZ	106	GLN
73	Sa	7	ASN
74	Sb	9	HIS
74	Sb	49	HIS
76	Sd	4	GLN
78	Sg	56	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3371/4731 (71%)	739 (21%)	31 (0%)
2	L7	119/120 (99%)	17 (14%)	3 (2%)
3	L8	149/158 (94%)	26 (17%)	1 (0%)
46	S2	1603/1870 (85%)	505 (31%)	24 (1%)
47	S7	74/75 (98%)	30 (40%)	0
79	Sx	9/10 (90%)	1 (11%)	0
All	All	5325/6964 (76%)	1318 (24%)	59 (1%)

All (1318) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	13	U
1	L5	15	A
1	L5	21	G
1	L5	25	A
1	L5	30	C
1	L5	39	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	75	G
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	130	G
1	L5	131	C
1	L5	133	C
1	L5	134	G
1	L5	135	U
1	L5	136	C
1	L5	137	G
1	L5	139	G
1	L5	141	C
1	L5	142	G
1	L5	143	U
1	L5	144	G
1	L5	150	U
1	L5	151	G
1	L5	159	C
1	L5	160	G
1	L5	169	A
1	L5	170	C

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Mol	Chain	Res	Type
1	L5	171	U
1	L5	172	C
1	L5	173	C
1	L5	197	A
1	L5	200	U
1	L5	209	U
1	L5	216	C
1	L5	217	C
1	L5	218	A
1	L5	219	G
1	L5	232	G
1	L5	233	U
1	L5	234	G
1	L5	235	A
1	L5	241	G
1	L5	252	G
1	L5	256	C
1	L5	257	G
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	267	G
1	L5	269	U
1	L5	279	G
1	L5	296	U
1	L5	304	A
1	L5	305	A
1	L5	315	U
1	L5	333	A
1	L5	339	C
1	L5	349	C
1	L5	356	U
1	L5	360	C
1	L5	361	A
1	L5	372	G
1	L5	386	G
1	L5	387	A
1	L5	398	G
1	L5	408	G

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Mol	Chain	Res	Type
1	L5	409	A
1	L5	411	G
1	L5	414	G
1	L5	416	G
1	L5	430	G
1	L5	431	U
1	L5	448	C
1	L5	449	G
1	L5	452	G
1	L5	453	U
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	476	C
1	L5	480	G
1	L5	487	C
1	L5	488	G
1	L5	492	G
1	L5	494	G
1	L5	495	C
1	L5	496	C
1	L5	497	C
1	L5	498	G
1	L5	512	A
1	L5	513	U
1	L5	654	G
1	L5	655	G
1	L5	660	G
1	L5	661	U
1	L5	667	G
1	L5	668	G
1	L5	669	C
1	L5	670	C
1	L5	673	C
1	L5	674	G
1	L5	675	A

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Mol	Chain	Res	Type
1	L5	676	C
1	L5	677	C
1	L5	678	G
1	L5	680	C
1	L5	693	C
1	L5	695	C
1	L5	696	U
1	L5	697	U
1	L5	700	A
1	L5	701	C
1	L5	704	U
1	L5	705	G
1	L5	712	C
1	L5	713	G
1	L5	714	C
1	L5	728	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	766	G
1	L5	806	C
1	L5	807	C
1	L5	810	G
1	L5	813	U
1	L5	815	A
1	L5	817	A
1	L5	824	C
1	L5	825	G
1	L5	827	C
1	L5	830	C
1	L5	831	G
1	L5	833	U
1	L5	834	U
1	L5	839	C
1	L5	841	A

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Mol	Chain	Res	Type
1	L5	842	A
1	L5	843	U
1	L5	857	A
1	L5	858	A
1	L5	860	C
1	L5	882	U
1	L5	886	U
1	L5	924	G
1	L5	926	G
1	L5	927	C
1	L5	928	C
1	L5	938	C
1	L5	940	C
1	L5	953	C
1	L5	954	G
1	L5	1003	G
1	L5	1006	G
1	L5	1007	G
1	L5	1009	C
1	L5	1010	U
1	L5	1011	G
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	1020	G
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
1	L5	1034	G
1	L5	1036	C
1	L5	1037	G
1	L5	1038	C
1	L5	1039	G

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Mol	Chain	Res	Type
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	1055	G
1	L5	1065	G
1	L5	1089	A
1	L5	1095	C
1	L5	1099	G
1	L5	1109	A
1	L5	1116	C
1	L5	1117	U
1	L5	1139	A
1	L5	1141	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	1196	U
1	L5	1197	G
1	L5	1202	A
1	L5	1209	G
1	L5	1212	A
1	L5	1221	G
1	L5	1222	C
1	L5	1223	C
1	L5	1224	C
1	L5	1225	G
1	L5	1226	G
1	L5	1227	G
1	L5	1228	G
1	L5	1230	C
1	L5	1232	C
1	L5	1234	A
1	L5	1239	G

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Mol	Chain	Res	Type
1	L5	1253	C
1	L5	1257	A
1	L5	1262	G
1	L5	1263	C
1	L5	1265	G
1	L5	1266	A
1	L5	1268	G
1	L5	1272	C
1	L5	1288	C
1	L5	1289	G
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	1300	C
1	L5	1311	A
1	L5	1312	G
1	L5	1316	G
1	L5	1317	A
1	L5	1327	U
1	L5	1328	U
1	L5	1344	G
1	L5	1348	A
1	L5	1361	A
1	L5	1380	C
1	L5	1388	G
1	L5	1389	A
1	L5	1392	U
1	L5	1405	U
1	L5	1410	U
1	L5	1415	A
1	L5	1423	U
1	L5	1428	C
1	L5	1438	G
1	L5	1439	G
1	L5	1440	G
1	L5	1445	A
1	L5	1447	G
1	L5	1448	A
1	L5	1452	A

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Mol	Chain	Res	Type
1	L5	1456	A
1	L5	1465	G
1	L5	1468	G
1	L5	1475	C
1	L5	1490	C
1	L5	1491	U
1	L5	1505	G
1	L5	1508	C
1	L5	1511	G
1	L5	1524	G
1	L5	1538	U
1	L5	1553	G
1	L5	1556	G
1	L5	1558	C
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	1586	C
1	L5	1590	A
1	L5	1607	A
1	L5	1639	G
1	L5	1640	A
1	L5	1645	G
1	L5	1658	G
1	L5	1672	G
1	L5	1673	C
1	L5	1685	U
1	L5	1692	U
1	L5	1695	A
1	L5	1700	A
1	L5	1713	G
1	L5	1719	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	1734	C

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Mol	Chain	Res	Type
1	L5	1735	A
1	L5	1742	A
1	L5	1743	G
1	L5	1748	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	1837	G
1	L5	1851	U
1	L5	1858	G
1	L5	1859	G
1	L5	1872	A
1	L5	1887	C
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	1911	G
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	2102	G
1	L5	2105	G
1	L5	2107	U
1	L5	2108	C
1	L5	2121	G

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Mol	Chain	Res	Type
1	L5	2141	U
1	L5	2152	A
1	L5	2153	A
1	L5	2154	G
1	L5	2155	U
1	L5	2178	G
1	L5	2179	C
1	L5	2182	U
1	L5	2183	U
1	L5	2194	C
1	L5	2202	C
1	L5	2210	A
1	L5	2222	C
1	L5	2226	C
1	L5	2227	C
1	L5	2228	G
1	L5	2230	A
1	L5	2231	G
1	L5	2232	G
1	L5	2235	C
1	L5	2236	G
1	L5	2237	G
1	L5	2242	U
1	L5	2243	G
1	L5	2254	C
1	L5	2255	C
1	L5	2257	U
1	L5	2260	G
1	L5	2261	C
1	L5	2263	G
1	L5	2264	A
1	L5	2269	A
1	L5	2270	A
1	L5	2285	G
1	L5	2286	A
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

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Mol	Chain	Res	Type
1	L5	2315	C
1	L5	2324	G
1	L5	2337	C
1	L5	2340	G
1	L5	2341	A
1	L5	2343	C
1	L5	2346	U
1	L5	2381	C
1	L5	2392	G
1	L5	2406	G
1	L5	2407	C
1	L5	2414	A
1	L5	2416	G
1	L5	2417	G
1	L5	2423	C
1	L5	2435	G
1	L5	2441	U
1	L5	2448	G
1	L5	2449	A
1	L5	2450	A
1	L5	2457	G
1	L5	2460	G
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	2498	A
1	L5	2510	G
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	2523	U
1	L5	2524	C

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Mol	Chain	Res	Type
1	L5	2532	G
1	L5	2541	A
1	L5	2542	U
1	L5	2544	U
1	L5	2552	A
1	L5	2560	A
1	L5	2576	G
1	L5	2579	A
1	L5	2581	G
1	L5	2582	U
1	L5	2583	U
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	3301	U
1	L5	3319	A
1	L5	3321	G
1	L5	3330	C
1	L5	3349	A
1	L5	3353	C
1	L5	3367	G
1	L5	3368	A
1	L5	3375	A
1	L5	3405	A
1	L5	3407	G
1	L5	3410	G
1	L5	3417	A
1	L5	3418	C
1	L5	3420	A
1	L5	3421	U
1	L5	3423	A
1	L5	3426	C
1	L5	3427	U

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Mol	Chain	Res	Type
1	L5	3428	C
1	L5	3430	U
1	L5	3433	G
1	L5	3434	G
1	L5	3440	A
1	L5	3441	A
1	L5	3443	U
1	L5	3446	C
1	L5	3448	C
1	L5	3449	G
1	L5	3459	U
1	L5	3468	G
1	L5	3471	U
1	L5	3474	A
1	L5	3475	U
1	L5	3476	G
1	L5	3495	U
1	L5	3497	U
1	L5	3524	A
1	L5	3533	A
1	L5	3534	A
1	L5	3535	C
1	L5	3536	G
1	L5	3544	C
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	3599	A
1	L5	3602	A
1	L5	3603	G
1	L5	3604	A
1	L5	3605	C
1	L5	3719	U
1	L5	3720	U
1	L5	3721	U

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Mol	Chain	Res	Type
1	L5	3724	A
1	L5	3727	G
1	L5	3735	G
1	L5	3744	G
1	L5	3745	G
1	L5	3747	C
1	L5	3768	U
1	L5	3770	C
1	L5	3773	G
1	L5	3778	A
1	L5	3780	G
1	L5	3786	G
1	L5	3787	U
1	L5	3788	C
1	L5	3789	C
1	L5	3805	G
1	L5	3807	G
1	L5	3815	C
1	L5	3816	U
1	L5	3821	G
1	L5	3823	A
1	L5	3836	G
1	L5	3837	G
1	L5	3842	U
1	L5	3844	G
1	L5	3849	G
1	L5	3856	A
1	L5	3878	G
1	L5	3882	U
1	L5	3886	A
1	L5	3887	A
1	L5	3903	G
1	L5	3904	A
1	L5	3905	C
1	L5	3906	A
1	L5	3907	G
1	L5	3910	A
1	L5	3911	C
1	L5	3921	A
1	L5	3924	A
1	L5	3926	A
1	L5	3933	A

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Mol	Chain	Res	Type
1	L5	3934	A
1	L5	3942	U
1	L5	3944	G
1	L5	3958	G
1	L5	3959	U
1	L5	3977	A
1	L5	3982	G
1	L5	3983	G
1	L5	3985	C
1	L5	3992	A
1	L5	4001	A
1	L5	4002	C
1	L5	4026	G
1	L5	4029	A
1	L5	4030	G
1	L5	4031	A
1	L5	4032	A
1	L5	4040	C
1	L5	4044	G
1	L5	4047	A
1	L5	4075	A
1	L5	4077	A
1	L5	4086	G
1	L5	4088	U
1	L5	4097	C
1	L5	4101	G
1	L5	4103	U
1	L5	4105	U
1	L5	4106	C
1	L5	4117	A
1	L5	4118	U
1	L5	4128	G
1	L5	4146	U
1	L5	4153	U
1	L5	4155	C
1	L5	4163	A
1	L5	4165	U
1	L5	4166	A
1	L5	4171	A
1	L5	4172	C
1	L5	4177	G
1	L5	4181	G

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Mol	Chain	Res	Type
1	L5	4198	G
1	L5	4201	A
1	L5	4208	U
1	L5	4213	C
1	L5	4220	G
1	L5	4223	G
1	L5	4227	U
1	L5	4228	G
1	L5	4242	A
1	L5	4243	A
1	L5	4253	G
1	L5	4263	A
1	L5	4287	U
1	L5	4289	U
1	L5	4290	G
1	L5	4309	A
1	L5	4323	C
1	L5	4325	A
1	L5	4330	U
1	L5	4344	A
1	L5	4353	A
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	4385	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	4408	G
1	L5	4411	C
1	L5	4413	C
1	L5	4415	G

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Mol	Chain	Res	Type
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	4520	A
1	L5	4526	G
1	L5	4528	U
1	L5	4529	C
1	L5	4530	G
1	L5	4532	C
1	L5	4546	U
1	L5	4548	C
1	L5	4549	G
1	L5	4550	G
1	L5	4551	C
1	L5	4552	C
1	L5	4553	G
1	L5	4555	A
1	L5	4556	A
1	L5	4558	G
1	L5	4559	G
1	L5	4560	C
1	L5	4561	G
1	L5	4563	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	4588	C
1	L5	4589	G
1	L5	4591	A
1	L5	4597	G
1	L5	4603	A
1	L5	4604	A
1	L5	4605	C
1	L5	4611	G

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Mol	Chain	Res	Type
1	L5	4613	U
1	L5	4621	U
1	L5	4623	G
1	L5	4624	U
1	L5	4636	U
1	L5	4638	C
1	L5	4641	G
1	L5	4654	U
1	L5	4662	A
1	L5	4664	A
1	L5	4665	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
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	21	G
2	L7	22	A
2	L7	53	U
2	L7	54	A
2	L7	56	G
2	L7	60	G
2	L7	61	G
2	L7	64	G
2	L7	65	G
2	L7	74	A
2	L7	89	G
2	L7	100	A
2	L7	103	A
2	L7	106	G
2	L7	110	G
2	L7	120	U
3	L8	6	C

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Mol	Chain	Res	Type
3	L8	13	G
3	L8	34	U
3	L8	35	C
3	L8	59	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	104	A
3	L8	105	C
3	L8	107	C
3	L8	109	C
3	L8	110	U
3	L8	111	U
3	L8	114	G
3	L8	121	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	126	C
3	L8	150	C
3	L8	151	G
46	S2	2	A
46	S2	17	C
46	S2	20	G
46	S2	26	U
46	S2	31	U
46	S2	33	G
46	S2	41	G
46	S2	44	U
46	S2	45	A
46	S2	46	A
46	S2	49	C
46	S2	55	U
46	S2	56	G
46	S2	57	U
46	S2	58	C
46	S2	59	U
46	S2	60	A

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Mol	Chain	Res	Type
46	S2	61	A
46	S2	62	G
46	S2	63	U
46	S2	64	A
46	S2	65	C
46	S2	67	C
46	S2	68	A
46	S2	69	C
46	S2	72	C
46	S2	73	C
46	S2	74	G
46	S2	76	U
46	S2	77	A
46	S2	78	C
46	S2	79	A
46	S2	80	G
46	S2	82	G
46	S2	83	A
46	S2	84	A
46	S2	85	A
46	S2	86	C
46	S2	90	G
46	S2	91	A
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	126	G
46	S2	127	C
46	S2	128	U
46	S2	129	C
46	S2	142	C
46	S2	143	U
46	S2	144	U
46	S2	146	G
46	S2	147	A
46	S2	149	A

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Mol	Chain	Res	Type
46	S2	150	A
46	S2	151	C
46	S2	152	U
46	S2	153	G
46	S2	154	U
46	S2	156	G
46	S2	157	U
46	S2	158	A
46	S2	159	A
46	S2	162	C
46	S2	163	U
46	S2	165	G
46	S2	168	C
46	S2	170	A
46	S2	172	U
46	S2	176	U
46	S2	177	G
46	S2	178	C
46	S2	179	C
46	S2	180	G
46	S2	181	A
46	S2	182	C
46	S2	183	G
46	S2	184	G
46	S2	218	C
46	S2	220	U
46	S2	221	U
46	S2	226	A
46	S2	311	C
46	S2	312	C
46	S2	313	G
46	S2	314	A
46	S2	315	U
46	S2	316	C
46	S2	317	G
46	S2	318	C
46	S2	320	C
46	S2	321	G
46	S2	324	C
46	S2	337	A
46	S2	340	A
46	S2	341	C

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Mol	Chain	Res	Type
46	S2	342	C
46	S2	348	G
46	S2	363	C
46	S2	365	A
46	S2	366	C
46	S2	371	G
46	S2	378	G
46	S2	384	G
46	S2	386	G
46	S2	387	C
46	S2	388	C
46	S2	408	G
46	S2	409	A
46	S2	410	C
46	S2	419	A
46	S2	422	G
46	S2	448	A
46	S2	449	A
46	S2	450	A
46	S2	451	C
46	S2	452	G
46	S2	465	A
46	S2	467	G
46	S2	468	G
46	S2	472	G
46	S2	473	C
46	S2	476	C
46	S2	477	A
46	S2	478	G
46	S2	479	G
46	S2	480	C
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	492	C
46	S2	493	C
46	S2	494	A

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Mol	Chain	Res	Type
46	S2	496	U
46	S2	498	C
46	S2	499	C
46	S2	501	A
46	S2	502	C
46	S2	503	C
46	S2	504	C
46	S2	505	G
46	S2	510	G
46	S2	511	G
46	S2	514	G
46	S2	517	A
46	S2	518	C
46	S2	524	A
46	S2	525	U
46	S2	526	A
46	S2	530	A
46	S2	532	A
46	S2	533	C
46	S2	535	G
46	S2	537	A
46	S2	539	U
46	S2	540	C
46	S2	541	U
46	S2	543	U
46	S2	545	G
46	S2	546	A
46	S2	547	G
46	S2	548	G
46	S2	551	C
46	S2	554	U
46	S2	555	A
46	S2	558	U
46	S2	559	G
46	S2	560	G
46	S2	561	A
46	S2	564	G
46	S2	565	A
46	S2	566	G
46	S2	568	C
46	S2	569	C
46	S2	571	C

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Mol	Chain	Res	Type
46	S2	577	A
46	S2	580	C
46	S2	584	A
46	S2	585	A
46	S2	586	C
46	S2	587	G
46	S2	589	G
46	S2	590	G
46	S2	591	A
46	S2	592	U
46	S2	593	C
46	S2	594	C
46	S2	595	A
46	S2	596	U
46	S2	599	G
46	S2	607	G
46	S2	609	C
46	S2	615	C
46	S2	627	G
46	S2	630	A
46	S2	632	U
46	S2	635	A
46	S2	637	C
46	S2	644	A
46	S2	645	G
46	S2	647	G
46	S2	656	A
46	S2	658	U
46	S2	660	G
46	S2	661	C
46	S2	669	A
46	S2	670	A
46	S2	672	A
46	S2	673	A
46	S2	674	G
46	S2	689	U
46	S2	749	C
46	S2	750	U
46	S2	795	A
46	S2	798	C
46	S2	800	U
46	S2	801	U

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Mol	Chain	Res	Type
46	S2	810	A
46	S2	812	A
46	S2	822	G
46	S2	823	U
46	S2	831	A
46	S2	835	C
46	S2	836	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	846	G
46	S2	847	G
46	S2	848	A
46	S2	863	A
46	S2	868	G
46	S2	871	A
46	S2	872	U
46	S2	874	G
46	S2	876	A
46	S2	882	G
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	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

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Mol	Chain	Res	Type
46	S2	908	G
46	S2	909	A
46	S2	914	A
46	S2	915	U
46	S2	918	U
46	S2	920	A
46	S2	921	A
46	S2	931	C
46	S2	934	G
46	S2	939	A
46	S2	956	A
46	S2	971	G
46	S2	972	G
46	S2	987	G
46	S2	989	C
46	S2	991	A
46	S2	993	A
46	S2	1000	G
46	S2	1018	U
46	S2	1024	A
46	S2	1028	A
46	S2	1029	A
46	S2	1062	U
46	S2	1063	A
46	S2	1077	G
46	S2	1084	A
46	S2	1086	C
46	S2	1088	A
46	S2	1089	U
46	S2	1090	G
46	S2	1110	C
46	S2	1116	U
46	S2	1117	C
46	S2	1118	C
46	S2	1134	A
46	S2	1139	C
46	S2	1149	A
46	S2	1150	A
46	S2	1155	U
46	S2	1158	G
46	S2	1191	A
46	S2	1196	A

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Mol	Chain	Res	Type
46	S2	1200	A
46	S2	1208	G
46	S2	1210	A
46	S2	1216	C
46	S2	1217	C
46	S2	1225	G
46	S2	1228	G
46	S2	1230	G
46	S2	1236	G
46	S2	1241	A
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	1263	C
46	S2	1264	U
46	S2	1265	C
46	S2	1267	C
46	S2	1274	C
46	S2	1275	G
46	S2	1276	G
46	S2	1277	A
46	S2	1279	A
46	S2	1281	G
46	S2	1282	G
46	S2	1284	C
46	S2	1285	A
46	S2	1286	G
46	S2	1288	A
46	S2	1289	U
46	S2	1290	U
46	S2	1294	A
46	S2	1308	U
46	S2	1309	U
46	S2	1310	C
46	S2	1311	U

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Mol	Chain	Res	Type
46	S2	1312	C
46	S2	1313	G
46	S2	1314	A
46	S2	1315	U
46	S2	1316	U
46	S2	1317	C
46	S2	1319	G
46	S2	1322	G
46	S2	1323	G
46	S2	1324	U
46	S2	1331	G
46	S2	1343	U
46	S2	1344	U
46	S2	1345	A
46	S2	1372	U
46	S2	1373	U
46	S2	1378	U
46	S2	1379	A
46	S2	1394	G
46	S2	1396	C
46	S2	1399	G
46	S2	1402	A
46	S2	1404	C
46	S2	1406	A
46	S2	1407	G
46	S2	1411	C
46	S2	1412	G
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	1424	C
46	S2	1426	G
46	S2	1428	C
46	S2	1429	G
46	S2	1430	G
46	S2	1432	G

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Mol	Chain	Res	Type
46	S2	1433	U
46	S2	1442	U
46	S2	1443	U
46	S2	1444	C
46	S2	1445	U
46	S2	1450	G
46	S2	1455	A
46	S2	1464	U
46	S2	1467	G
46	S2	1478	U
46	S2	1479	U
46	S2	1485	A
46	S2	1490	A
46	S2	1491	G
46	S2	1494	C
46	S2	1495	U
46	S2	1496	G
46	S2	1498	G
46	S2	1507	A
46	S2	1508	G
46	S2	1510	U
46	S2	1511	G
46	S2	1518	G
46	S2	1520	U
46	S2	1521	G
46	S2	1522	C
46	S2	1523	A
46	S2	1534	A
46	S2	1536	U
46	S2	1537	G
46	S2	1550	U
46	S2	1553	G
46	S2	1554	C
46	S2	1555	C
46	S2	1556	U
46	S2	1557	A
46	S2	1558	C
46	S2	1559	C
46	S2	1567	G
46	S2	1570	A
46	S2	1571	G
46	S2	1581	A

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Mol	Chain	Res	Type
46	S2	1583	C
46	S2	1588	G
46	S2	1589	A
46	S2	1600	U
46	S2	1601	G
46	S2	1602	A
46	S2	1603	U
46	S2	1604	G
46	S2	1622	U
46	S2	1623	U
46	S2	1624	A
46	S2	1633	G
46	S2	1636	C
46	S2	1638	A
46	S2	1647	C
46	S2	1649	G
46	S2	1653	G
46	S2	1655	G
46	S2	1656	C
46	S2	1661	C
46	S2	1664	A
46	S2	1666	G
46	S2	1672	G
46	S2	1681	G
46	S2	1700	A
46	S2	1703	G
46	S2	1720	A
46	S2	1721	U
46	S2	1727	G
46	S2	1728	G
46	S2	1729	U
46	S2	1744	G
46	S2	1747	U
46	S2	1748	C
46	S2	1753	C
46	S2	1755	G
46	S2	1780	G
46	S2	1781	G
46	S2	1782	A
46	S2	1783	G
46	S2	1784	C
46	S2	1785	G

Continued on next page...

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Mol	Chain	Res	Type
46	S2	1787	U
46	S2	1788	G
46	S2	1791	A
46	S2	1798	U
46	S2	1809	U
46	S2	1810	A
46	S2	1811	U
46	S2	1814	A
46	S2	1816	A
46	S2	1817	G
46	S2	1818	G
46	S2	1819	A
46	S2	1823	A
46	S2	1825	A
46	S2	1826	A
46	S2	1830	G
46	S2	1836	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
47	S7	5	A
47	S7	9	U
47	S7	12	C
47	S7	14	C
47	S7	17	C
47	S7	18	G
47	S7	19	G
47	S7	20	A
47	S7	21	A
47	S7	27	C
47	S7	28	U
47	S7	32	C
47	S7	34	C
47	S7	35	A
47	S7	42	A
47	S7	45	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
47	S7	46	G
47	S7	48	C
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	68	C
47	S7	69	U
47	S7	73	A
79	Sx	39	A

All (59) 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	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
1	L5	1265	G
1	L5	1271	G
1	L5	1447	G
1	L5	1563	G
1	L5	1585	U
1	L5	2227	C
1	L5	2345	A
1	L5	2519	A
1	L5	2540	C

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Continued from previous page...

Mol	Chain	Res	Type
1	L5	2649	A
1	L5	3425	U
1	L5	3904	A
1	L5	4352	U
1	L5	4549	G
1	L5	4553	G
1	L5	4612	C
1	L5	4686	A
2	L7	3	C
2	L7	52	C
2	L7	60	G
3	L8	5	U
46	S2	77	A
46	S2	78	C
46	S2	97	U
46	S2	156	G
46	S2	164	A
46	S2	315	U
46	S2	482	C
46	S2	497	C
46	S2	504	C
46	S2	565	A
46	S2	629	A
46	S2	845	U
46	S2	862	A
46	S2	893	U
46	S2	1241	A
46	S2	1263	C
46	S2	1315	U
46	S2	1418	C
46	S2	1429	G
46	S2	1442	U
46	S2	1517	G
46	S2	1780	G
46	S2	1781	G
46	S2	1817	G

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

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

5.5 Carbohydrates [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.

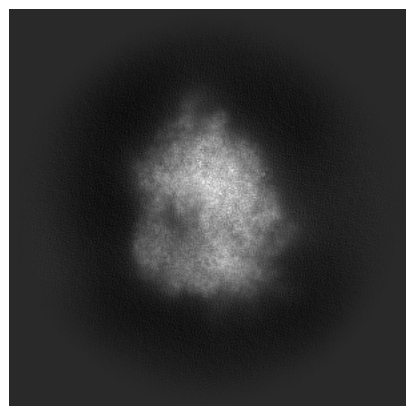
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62286. These allow visual inspection of the internal detail of the map and identification of artifacts.

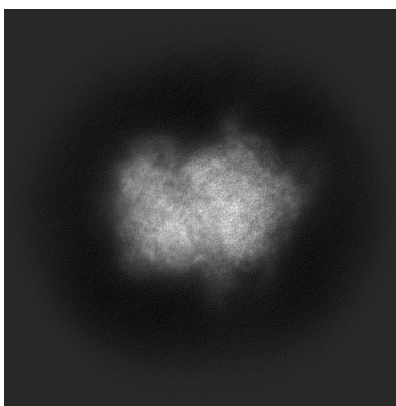
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

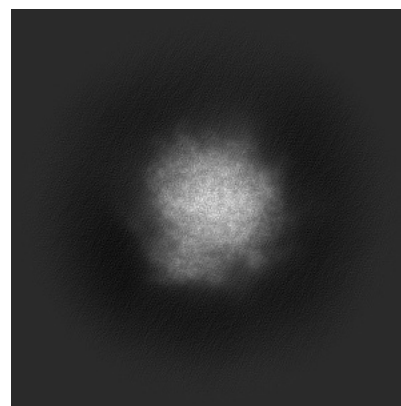
6.1.1 Primary map



X

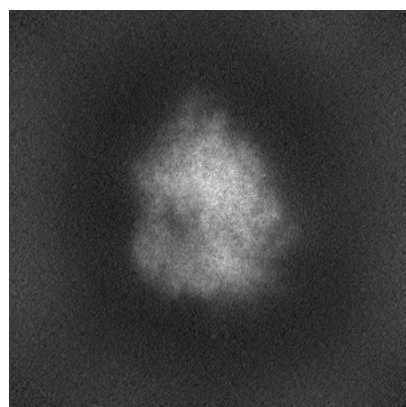


Y

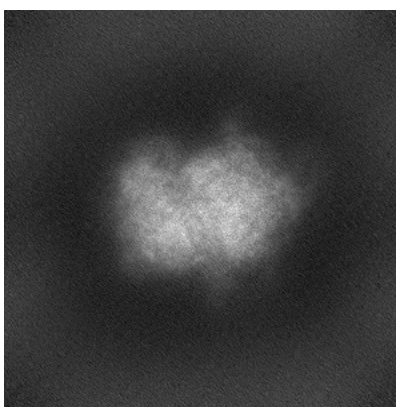


Z

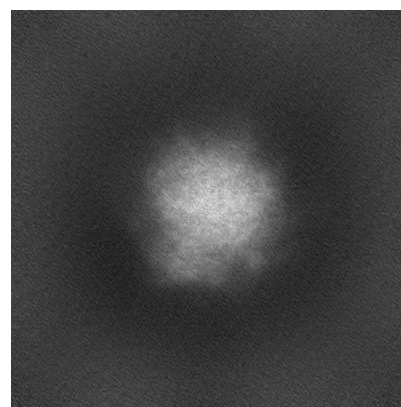
6.1.2 Raw map



X



Y

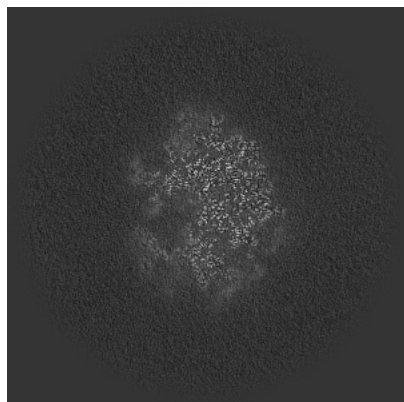


Z

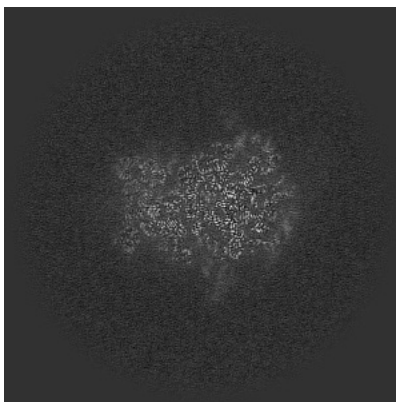
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

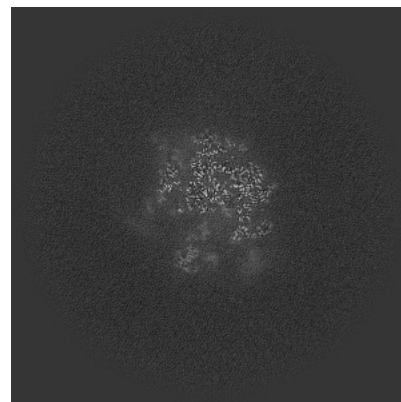
6.2.1 Primary map



X Index: 280

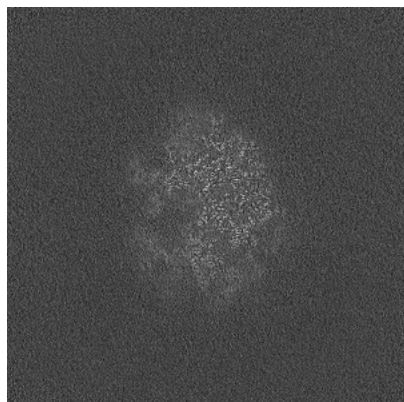


Y Index: 280

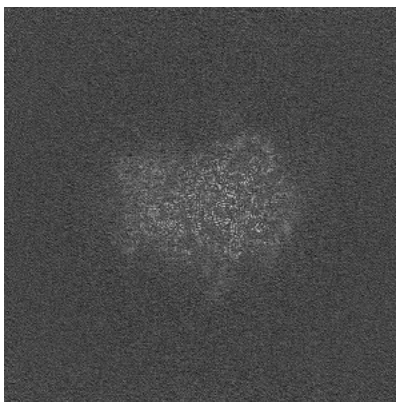


Z Index: 280

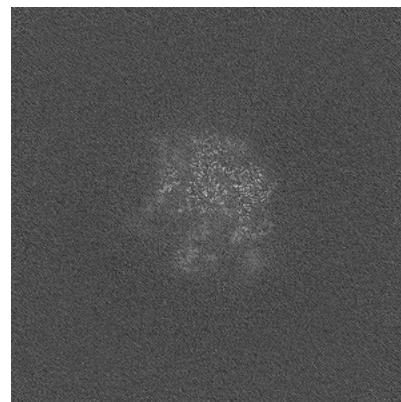
6.2.2 Raw map



X Index: 280



Y Index: 280

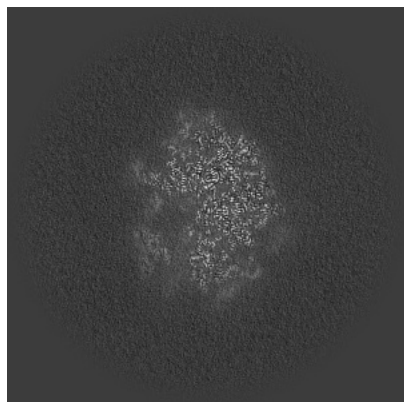


Z Index: 280

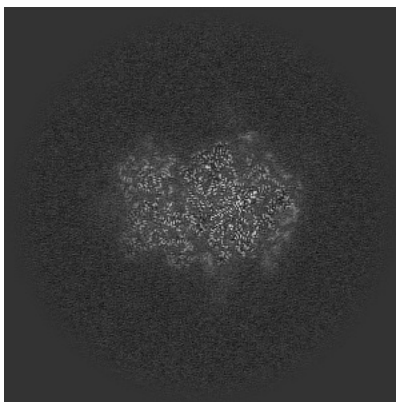
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

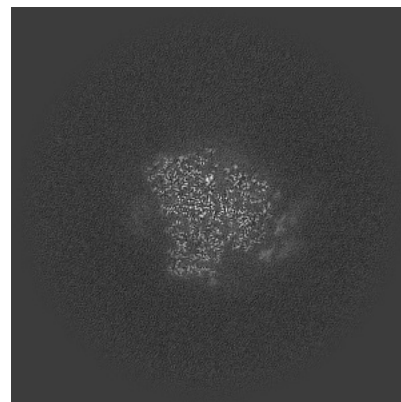
6.3.1 Primary map



X Index: 277

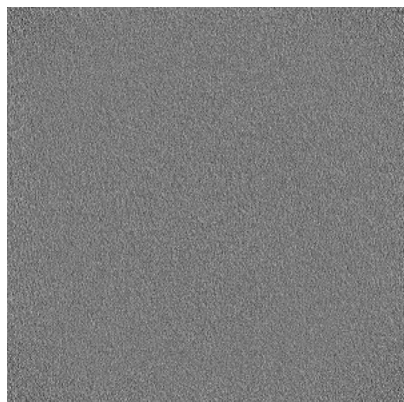


Y Index: 288

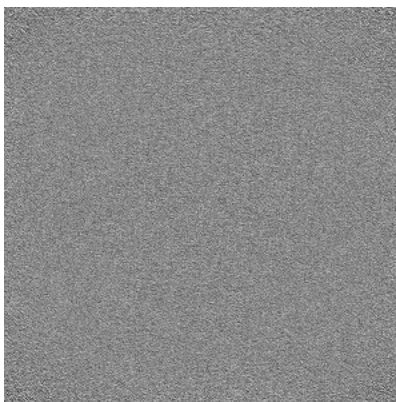


Z Index: 318

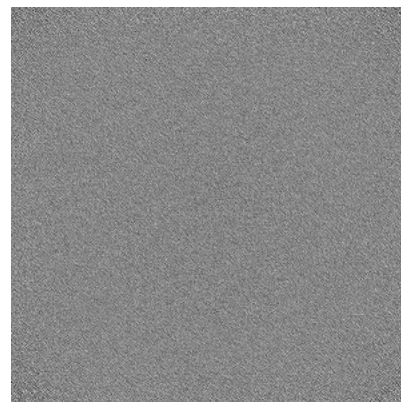
6.3.2 Raw map



X Index: 0



Y Index: 0

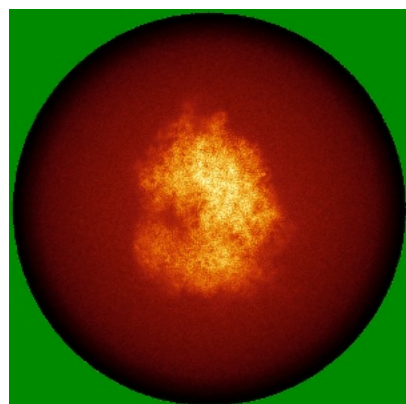


Z Index: 559

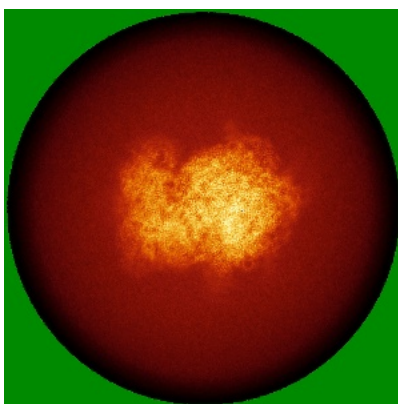
The images above show the largest variance slices of the map in three orthogonal directions.

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

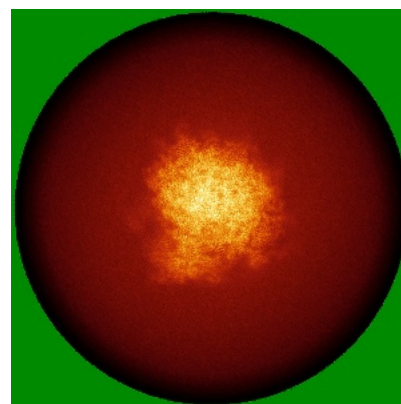
6.4.1 Primary map



X

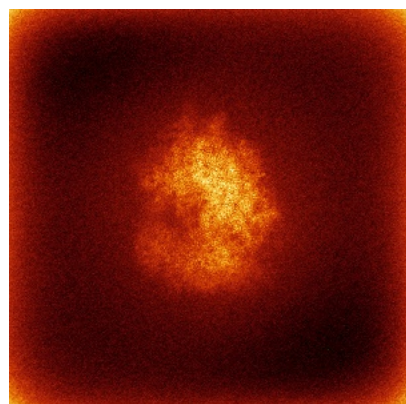


Y

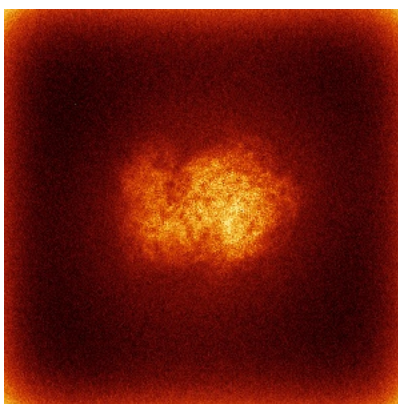


Z

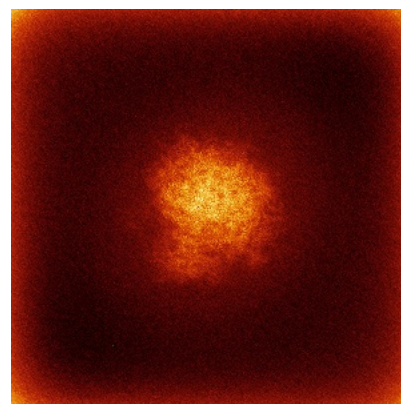
6.4.2 Raw map



X



Y

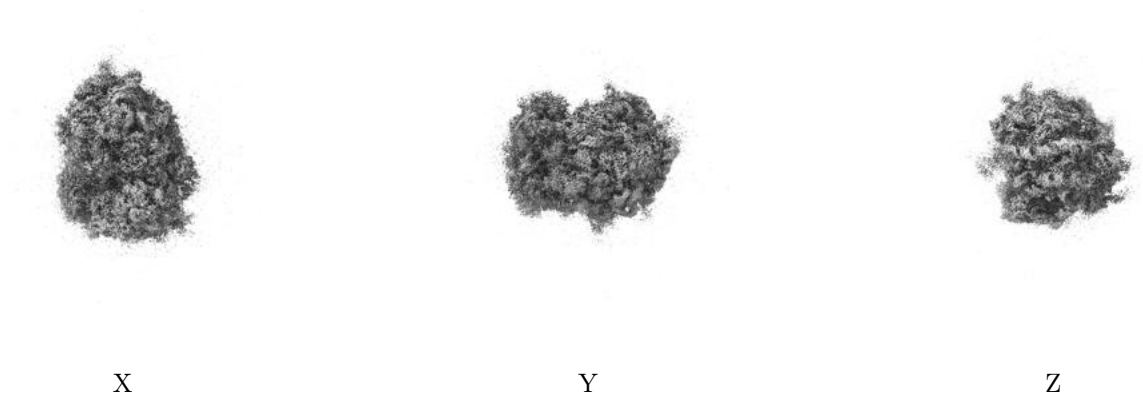


Z

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.

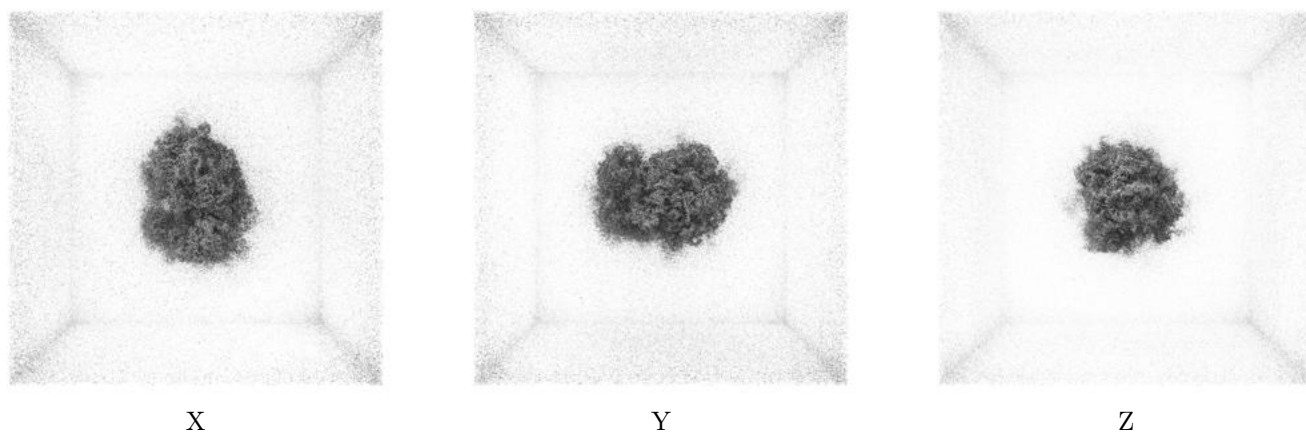
6.5 Orthogonal surface views [i](#)

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.

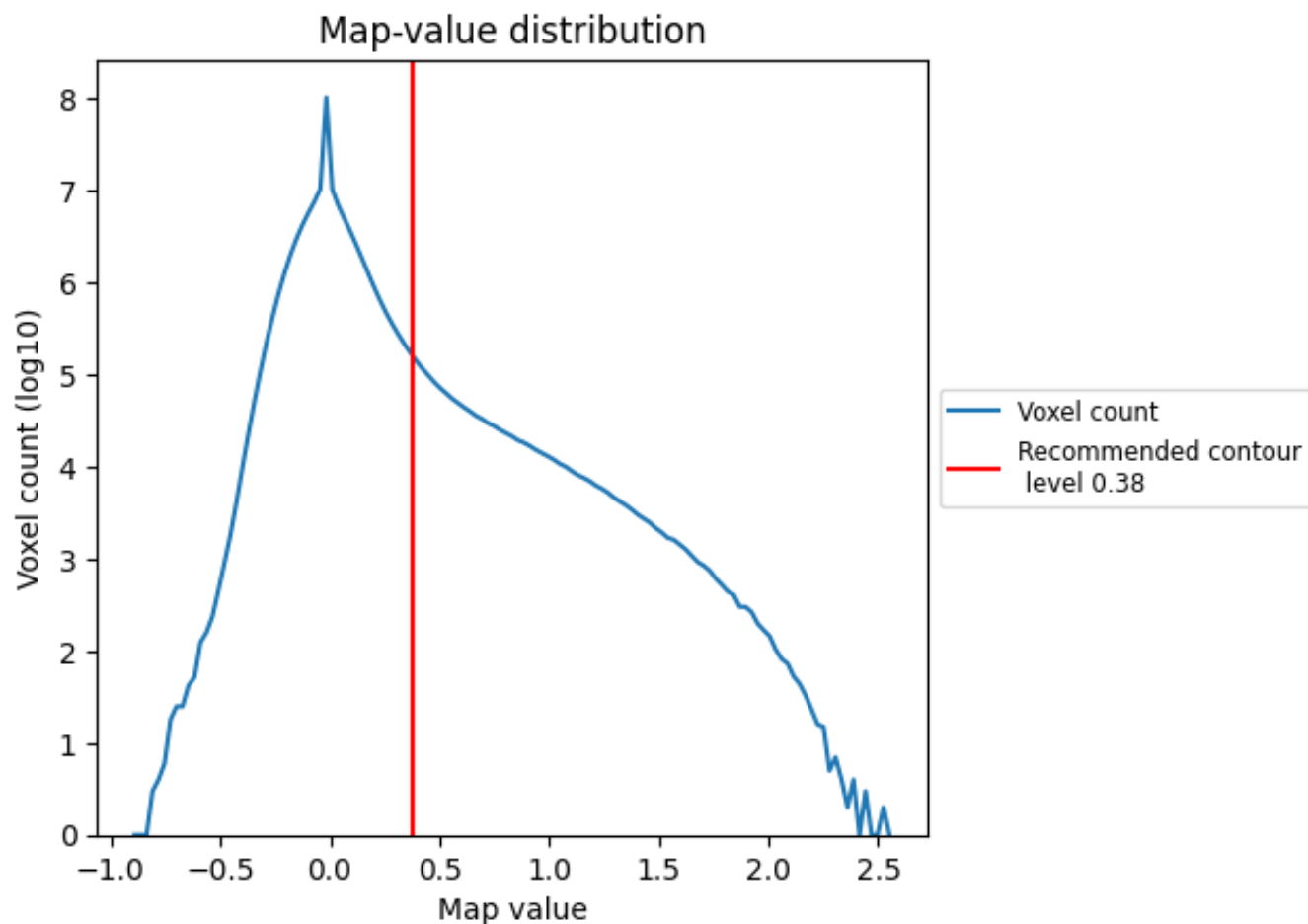
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

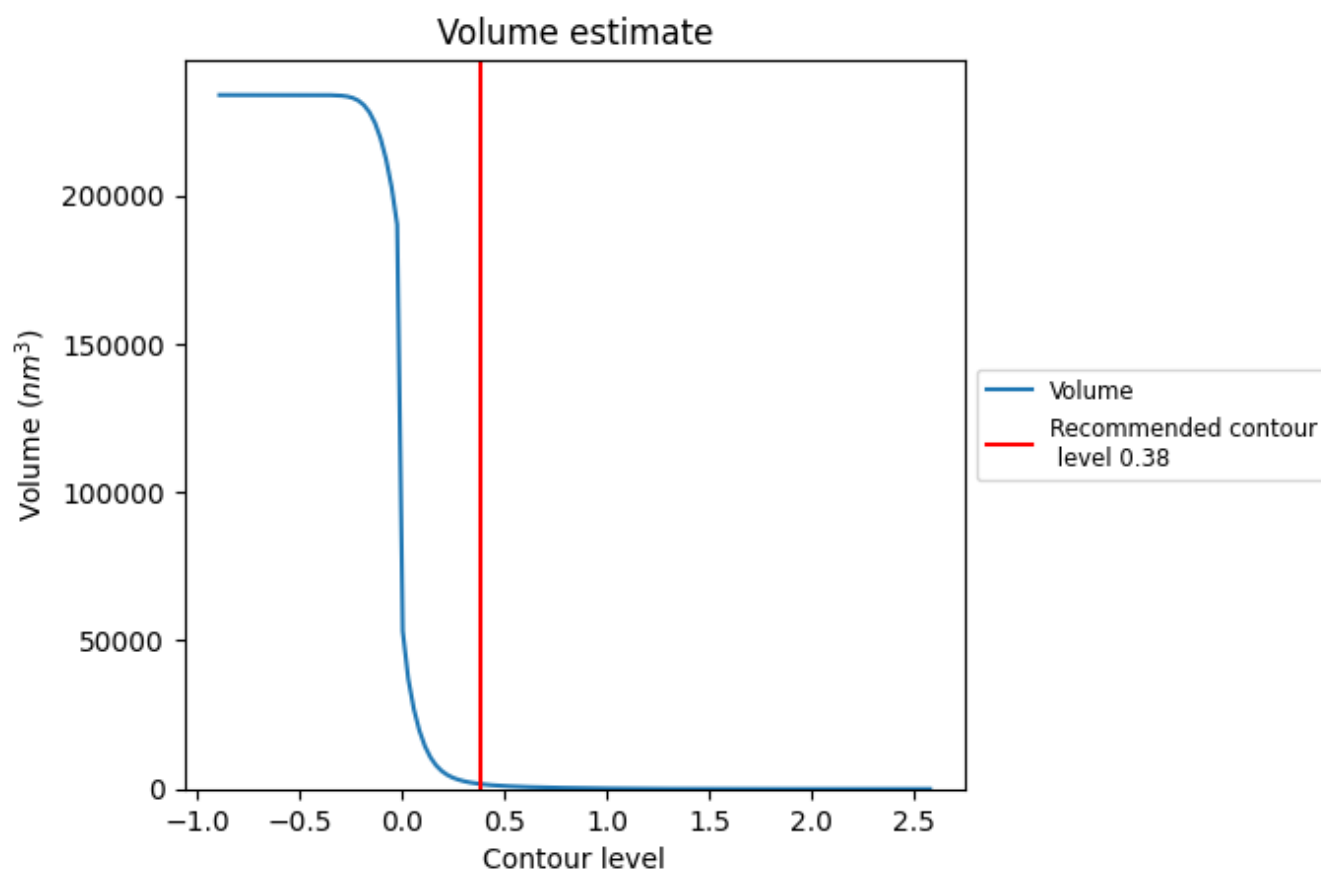
This section contains the results of statistical analysis of the map.

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.

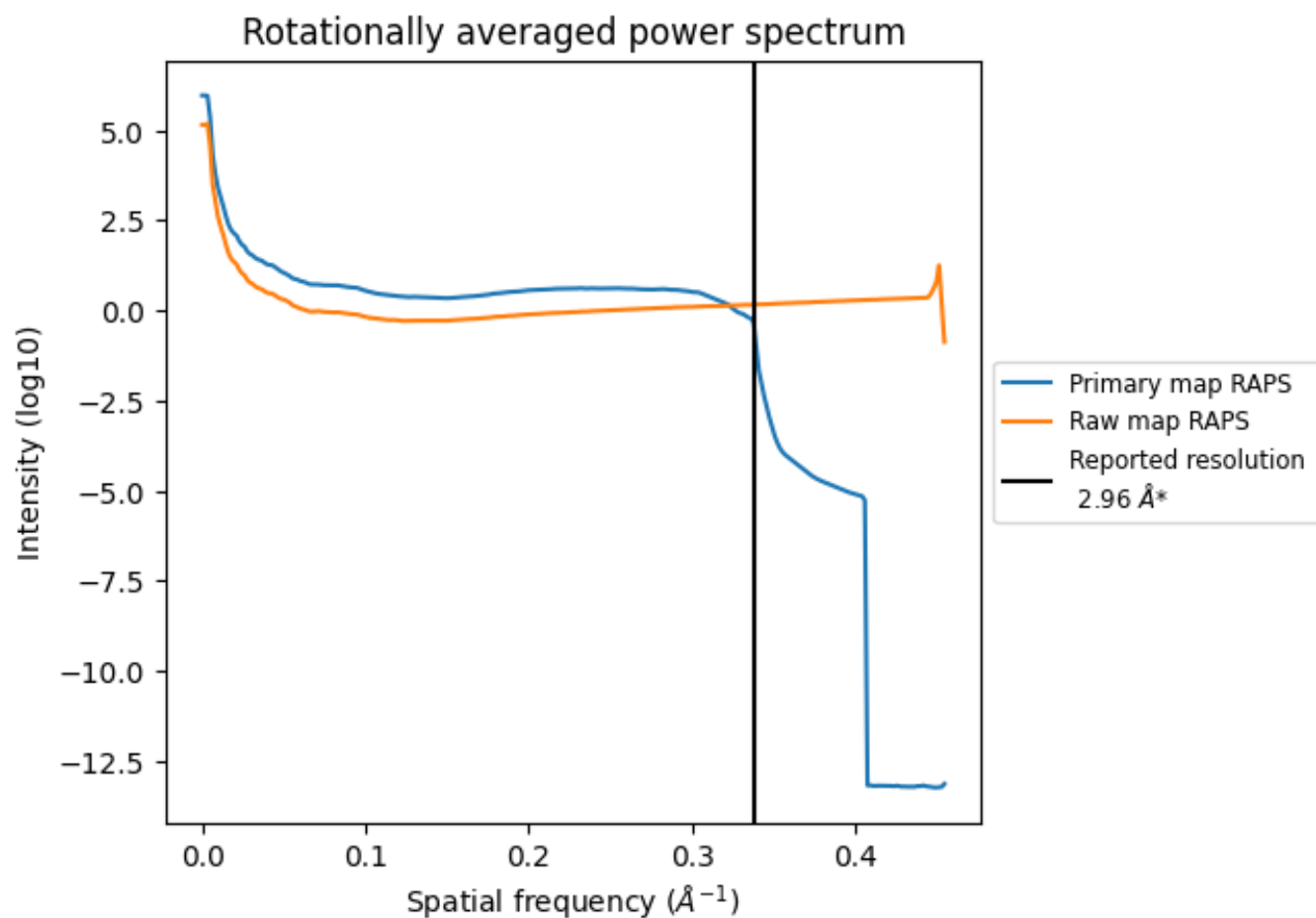
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1690 nm³; this corresponds to an approximate mass of 1527 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 ⓘ

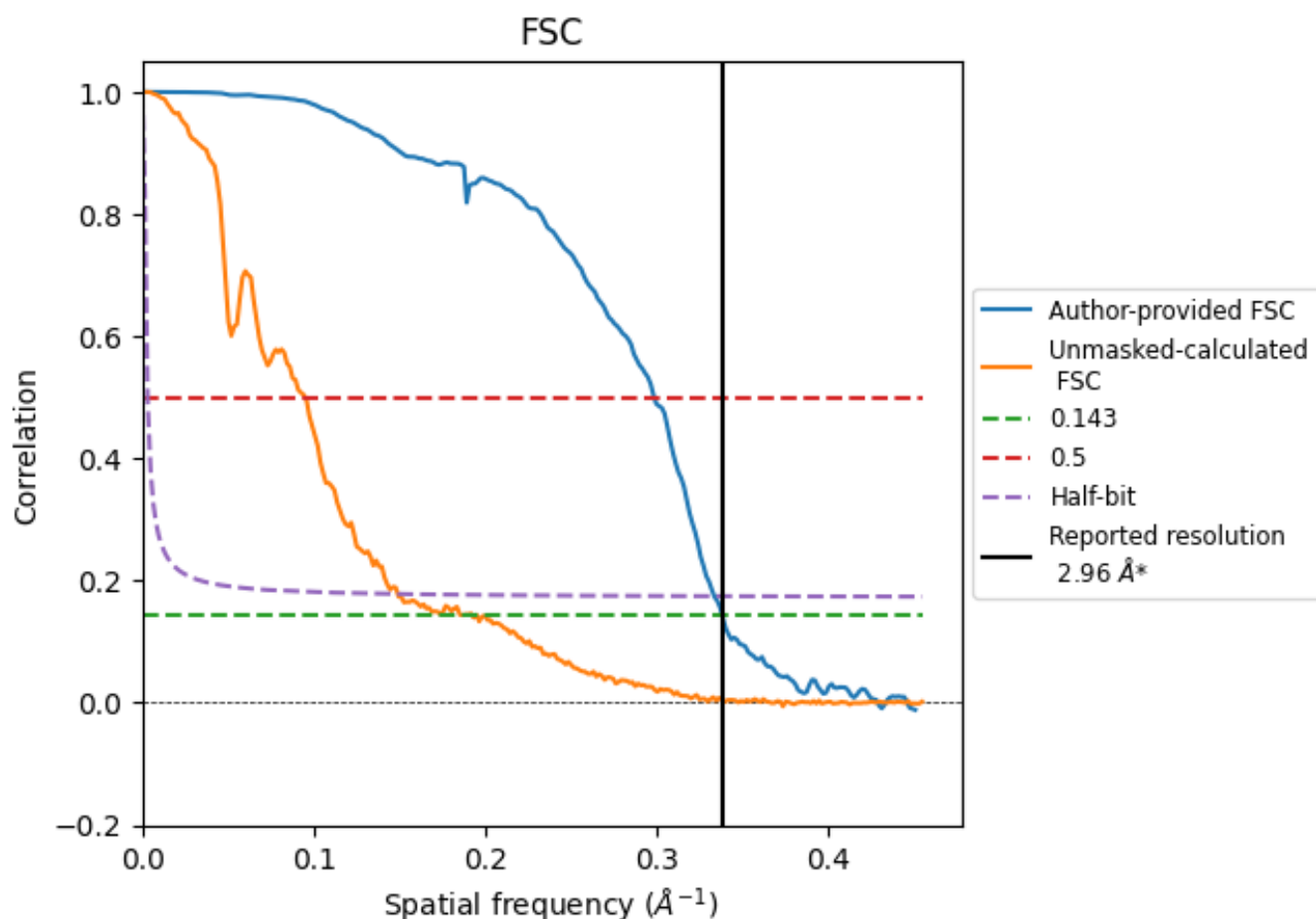


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 0.338 \AA^{-1}

8.2 Resolution estimates [i](#)

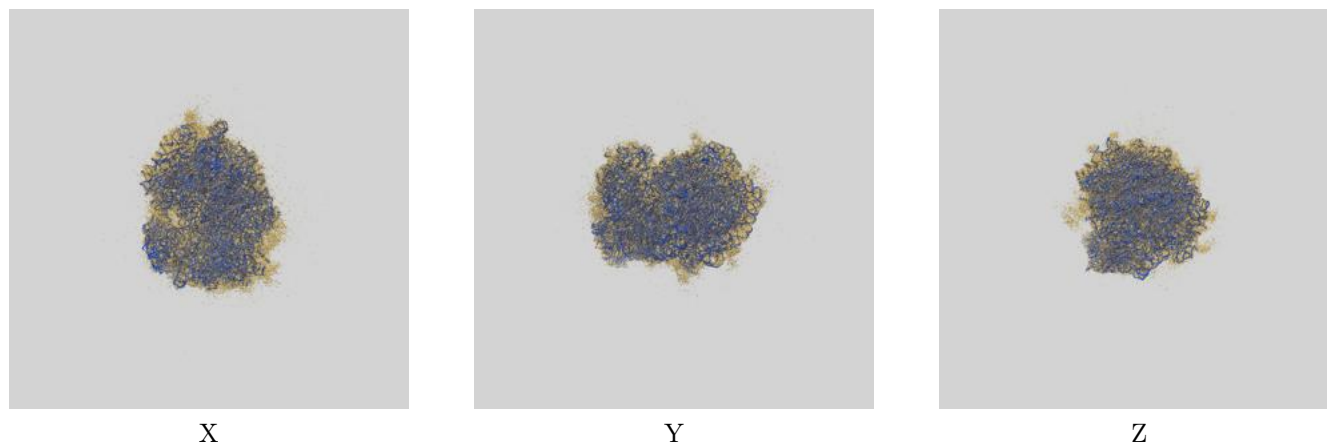
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.96	3.35	3.00
Unmasked-calculated*	5.20	10.55	6.72

*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 5.20 differs from the reported value 2.96 by more than 10 %

9 Map-model fit [i](#)

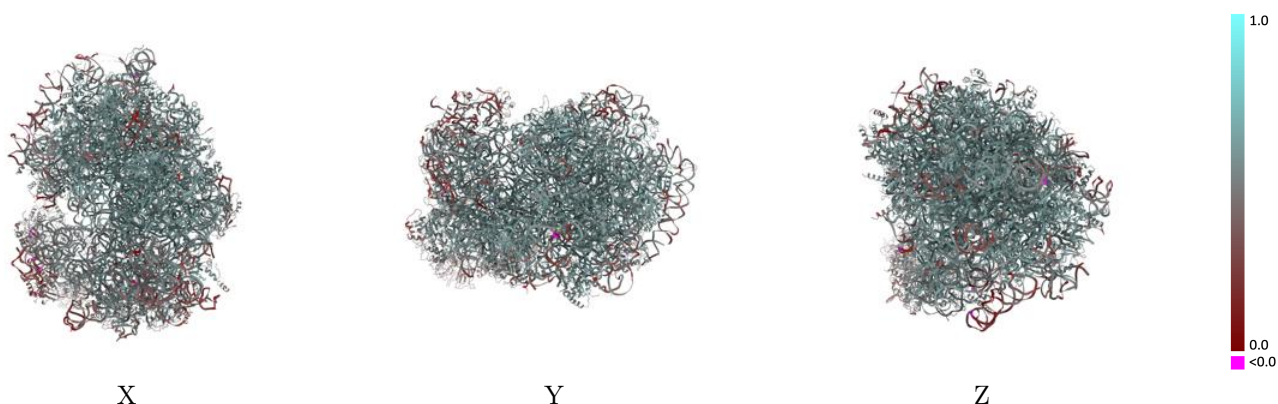
This section contains information regarding the fit between EMDB map EMD-62286 and PDB model 9KDU. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



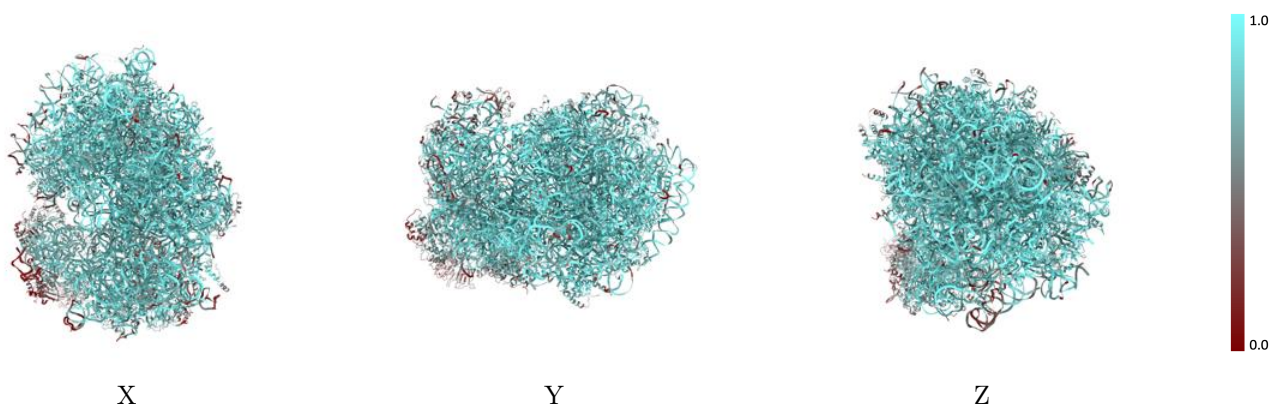
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



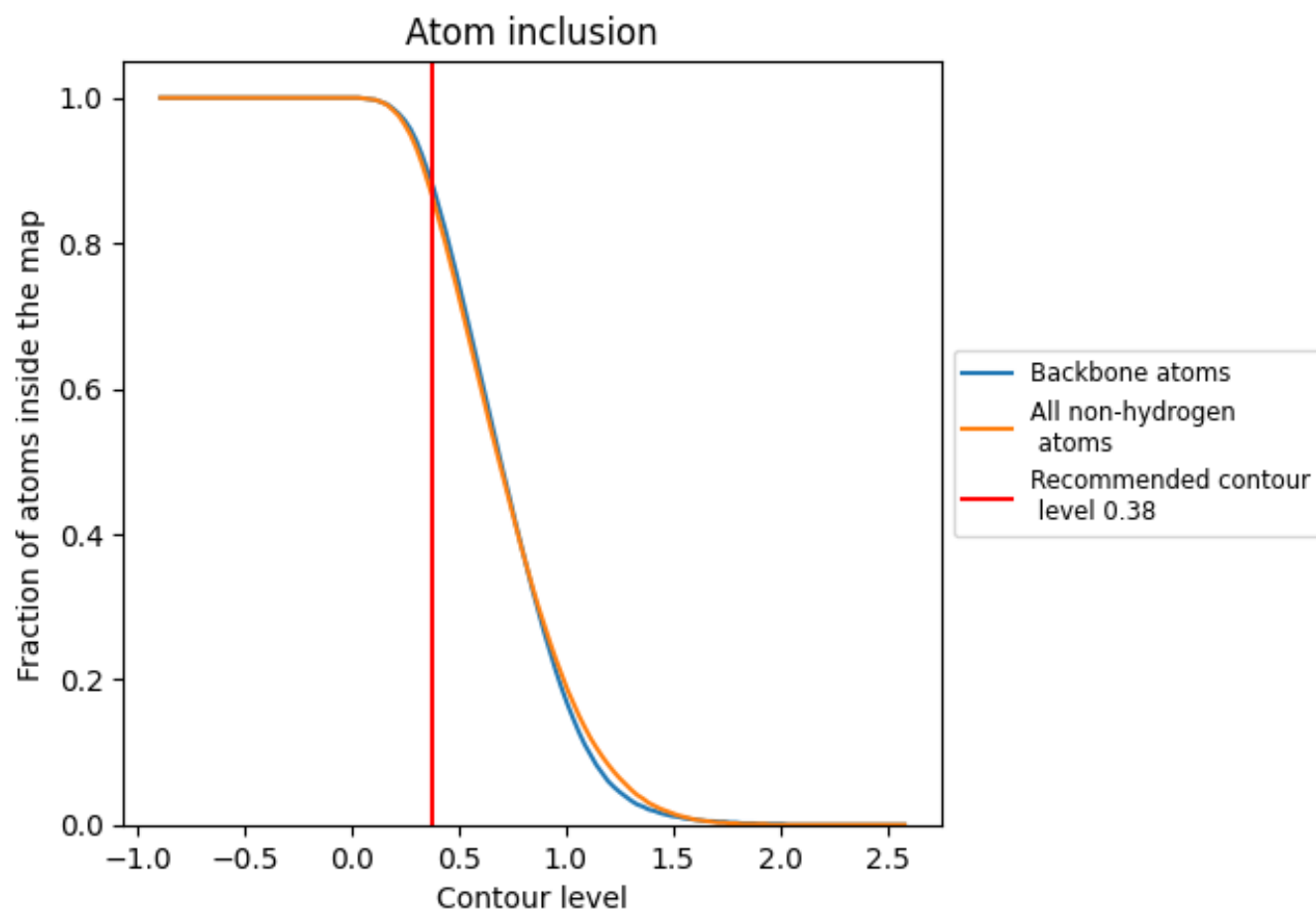
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 88% 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	 0.8610	 0.5360
L5	 0.9310	 0.5580
L7	 0.9670	 0.5720
L8	 0.9580	 0.5680
LA	 0.9540	 0.6020
LB	 0.8750	 0.5820
LC	 0.9310	 0.5880
LD	 0.7730	 0.5290
LE	 0.8490	 0.5600
LF	 0.9470	 0.6000
LG	 0.7710	 0.5250
LH	 0.7910	 0.5430
LI	 0.8330	 0.5320
LJ	 0.7320	 0.5040
LL	 0.8550	 0.5590
LM	 0.8860	 0.5720
LN	 0.9750	 0.6100
LO	 0.9250	 0.5920
LP	 0.9320	 0.5960
LQ	 0.9570	 0.6030
LR	 0.8970	 0.5760
LS	 0.9200	 0.5850
LT	 0.8990	 0.5760
LU	 0.7420	 0.4990
LV	 0.9130	 0.5830
LW	 0.9300	 0.5990
LX	 0.8670	 0.5660
LY	 0.8840	 0.5720
LZ	 0.8700	 0.5640
La	 0.9360	 0.6010
Lb	 0.8630	 0.5450
Lc	 0.9050	 0.5860
Ld	 0.8620	 0.5780
Le	 0.9550	 0.6010
Lf	 0.9660	 0.6120











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Chain	Atom inclusion	Q-score
Lg	 0.9160	 0.5820
Lh	 0.8690	 0.5600
Li	 0.8470	 0.5610
Lj	 0.9760	 0.6040
Lk	 0.7250	 0.5220
Ll	 0.9690	 0.5970
Lm	 0.8770	 0.5670
Ln	 0.9540	 0.5940
Lo	 0.8770	 0.5760
Lp	 0.9330	 0.5910
Lr	 0.9330	 0.5920
S2	 0.8620	 0.4940
S7	 0.8090	 0.4720
SA	 0.7030	 0.5180
SB	 0.7420	 0.5350
SC	 0.7990	 0.5230
SD	 0.5560	 0.4260
SE	 0.8070	 0.5130
SF	 0.6680	 0.4810
SG	 0.5690	 0.4270
SH	 0.5320	 0.4680
SI	 0.8710	 0.5520
SJ	 0.8080	 0.5090
SK	 0.3040	 0.3130
SL	 0.9290	 0.5840
SN	 0.8780	 0.5670
SO	 0.8050	 0.5440
SP	 0.4510	 0.3800
SQ	 0.6470	 0.4550
SR	 0.5290	 0.4330
SS	 0.5710	 0.4510
ST	 0.6070	 0.4430
SU	 0.4700	 0.3980
SV	 0.7000	 0.5050
SW	 0.8830	 0.5550
SX	 0.8690	 0.5440
SY	 0.6420	 0.4400
SZ	 0.4490	 0.4280
Sa	 0.8440	 0.5400
Sb	 0.6530	 0.4920
Sc	 0.6190	 0.4540
Sd	 0.6410	 0.3970

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Chain	Atom inclusion	Q-score
Se	 0.7720	 0.4790
Sg	 0.3010	 0.3580
Sx	 0.6080	 0.3170
Z	 0.8820	 0.4930