



## Full wwPDB EM Validation Report ⓘ

May 4, 2026 – 05:23 PM JST

PDB ID : 9KDV / pdb\_00009kdv  
EMDB ID : EMD-62287  
Title : Cryo-EM structure of 80S ribosome  
Authors : Lu, Y.; Wang, X.; Qin, Y.; Cao, Y.  
Deposited on : 2024-11-04  
Resolution : 3.33 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](mailto: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>.

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

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



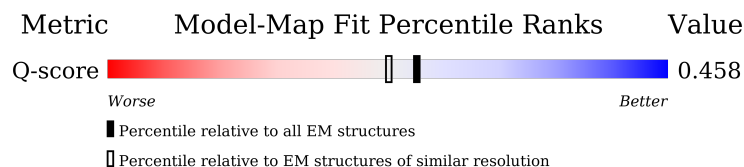
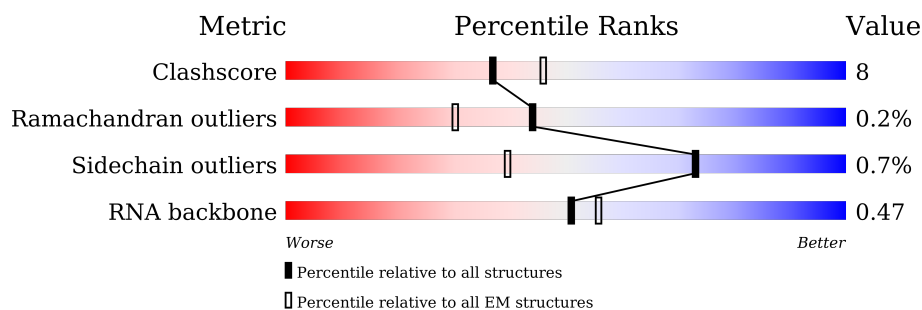
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*




The reported resolution of this entry is 3.33 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	14484 ( 2.83 - 3.83 )







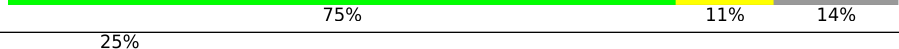
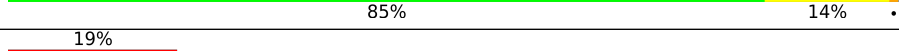
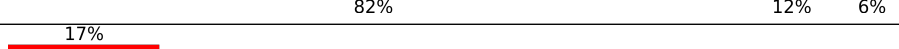
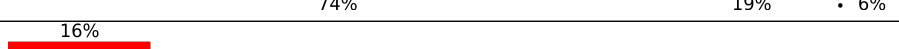


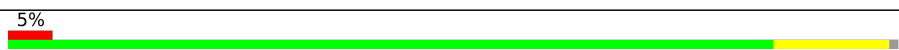

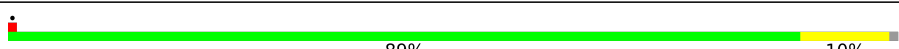






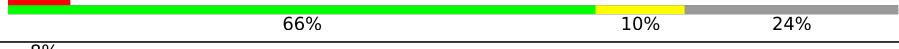



The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey 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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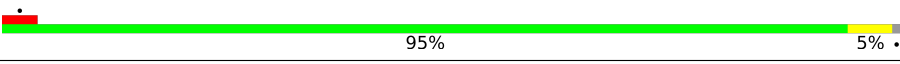






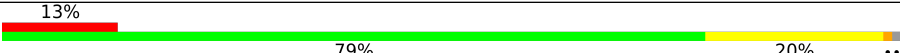
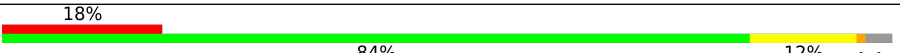
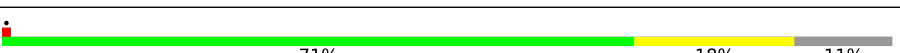

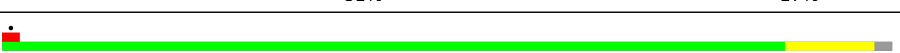

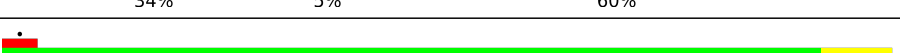
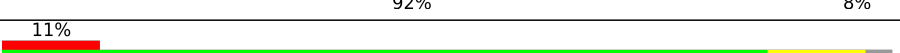

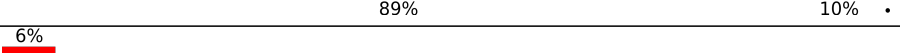
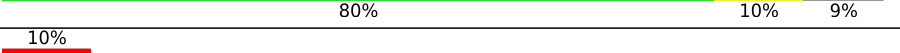





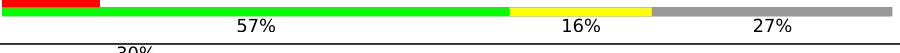
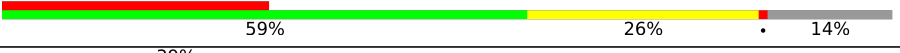
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	419	
7	LD	297	
8	LE	296	
9	LF	270	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	217	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

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

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

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Mol	Chain	Length	Quality of chain
78	Sg	317	
79	Sx	10	
80	Z	8	



## 2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 204068 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	357	Total	C	N	O	S	0	0
			2857	1797	571	474	15		



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

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

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

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

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

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

- Molecule 10 is a protein called Large ribosomal subunit protein eL8.

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

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

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

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

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

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

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

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



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

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

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL15.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	174	Total	C	N	O	S	0	0
			1457	901	316	231	9		

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



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

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

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

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

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

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

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

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

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

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

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



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

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	99	Total	C	N	O	S	0	0
			807	505	174	124	4		

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

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

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

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

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

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

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

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.



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

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

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

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

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

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

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

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

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

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

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

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



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

- Molecule 43 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL43.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	124	Total	C	N	O	S	0	0
			994	616	206	167	5		

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sb	82	Total	C	N	O	S	0	0
			644	403	120	114	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	8	Total	C	N	O	0	0
			39	23	8	8		

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

Mol	Chain	Residues	Atoms		AltConf
81	L5	93	Total	Mg	0
			93	93	
81	L7	1	Total	Mg	0
			1	1	
81	LN	1	Total	Mg	0
			1	1	
81	LP	1	Total	Mg	0
			1	1	
81	Le	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	

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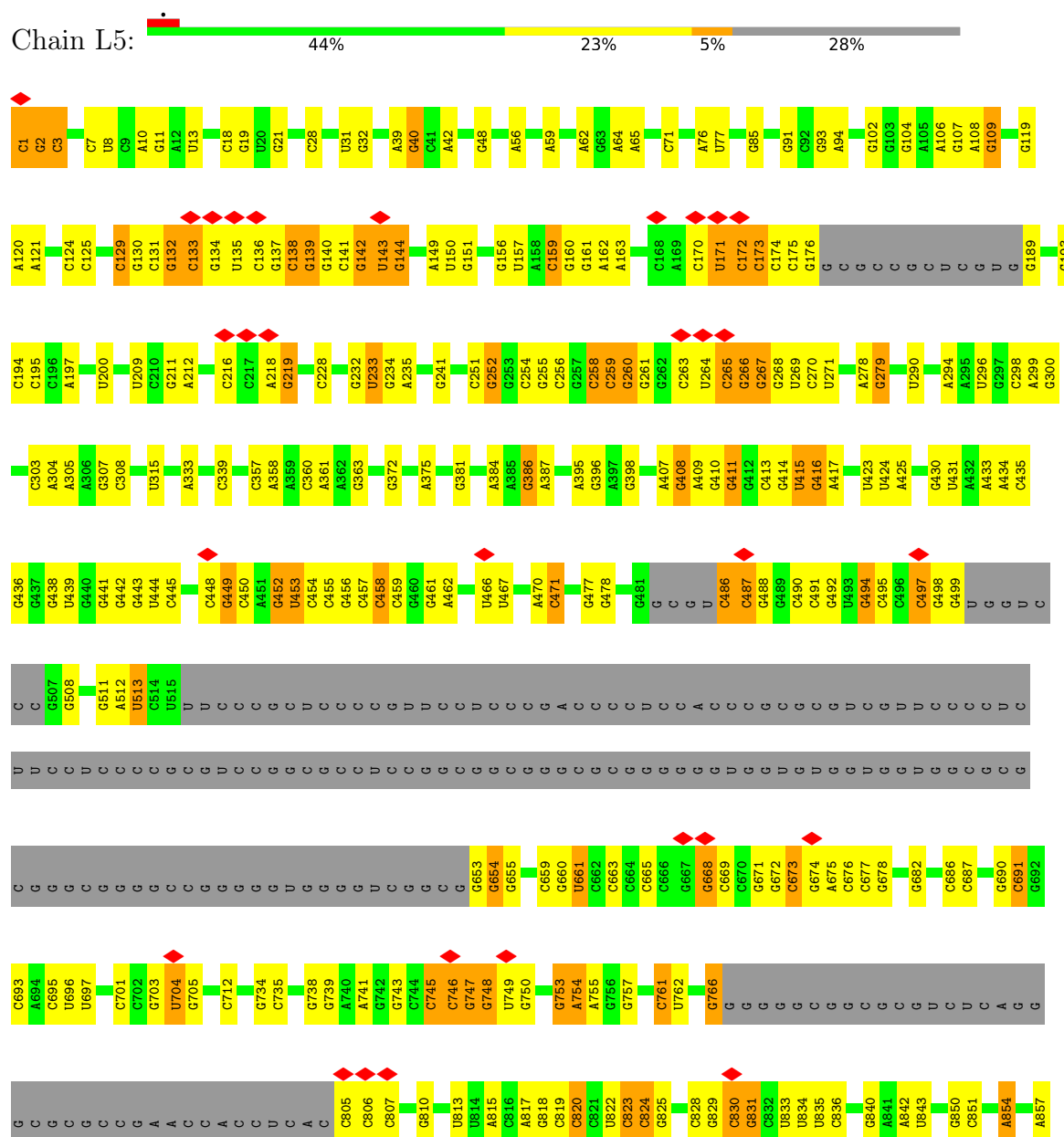
Mol	Chain	Residues	Atoms		AltConf
82	Lm	1	Total 1	Zn 1	0
82	Lp	1	Total 1	Zn 1	0



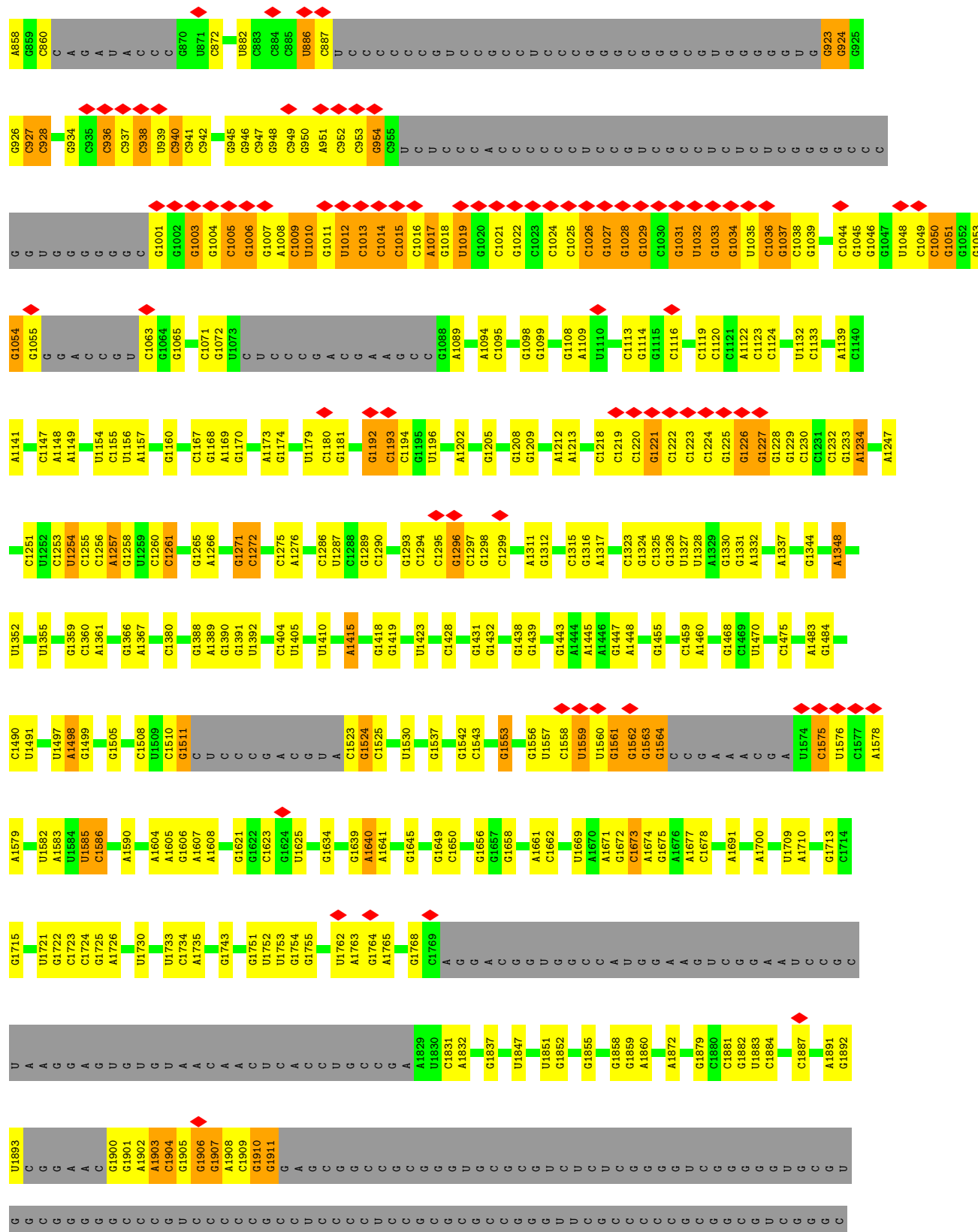
### 3 Residue-property plots

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











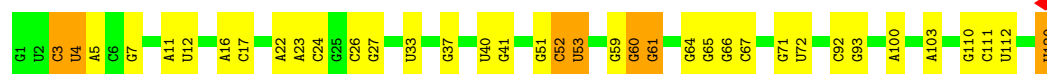


C4605	U4527	C4392	U4291	A4197	A4075	A3934	A3823	C3747	G	U	G3530	U3430
C4606	U4528	C4393	G4300	G4198	U4076	C3941	C3824	G3748	C	G	G3531	A3431
U4607	G4529	A4394	A4301	A4201	G4077	C3944	U3827	A	C	U	A3534	A3432
G4608	G4530	A4395	G4305	G4202	G4078	G3944	G3828	G	G	G	C3535	G3433
G4609	U4531	C4396	G4309	U4208	C4087	G3950	G3836	C	C	A	G3536	G3434
C4612	C4532	A4397	G4309	C4213	U4088	G3958	G3837	C	C	A	G3537	A3441
U4613	U4533	G4399	C4323	G4213	U4089	C3967	G3838	G	C	A	G3538	A3442
A4614	G4537	U4402	C4324	U4216	U4090	C3967	U3842	A	C	A	C3544	U3443
A4615	A4538	G4403	A4325	A4217	U4095	C3975	U3843	G	G	U	A3547	G3449
A4616	A4539	G4404	U4326	A4217	U4096	A3976	A3844	G	G	G	A3548	A3452
C4617	A4540	G4408	U4326	G4220	C4097	A3977	A3845	G	G	G	U3549	U3453
A4618	C4541	G4408	G4331	G4220	C4097	A3977	U3846	C	C	G	C3553	U3459
U4619	U4546	C4411	G4332	A4224	G4101	A3978	U3847	U	C	A	G3554	U3462
U4620	G4549	C4412	A4333	U4225	U4105	A3978	G3848	C	C	G	A3558	G3463
U4621	C4550	C4413	A4334	G4228	U4110	C3982	G3849	U	C	G	C3563	U3469
U4624	C4551	C4414	G4341	G4228	C4111	C3983	A3856	G	C	C	G3564	U3471
A4627	C4552	C4415	U4342	G4231	C4112	C3984	C3868	C3767	G	C	A3563	G3466
C4628	G4553	U4419	G4343	U4232	U4112	C3985	G3869	U3768	U	C	G3564	C3467
A4630	G4554	C4425	A4344	U4233	U4113	A3989	C3869	U3769	C	C	A3565	G3468
U4633	U4557	C4426	C4345	G4234	A4117	C3991	A3872	C3770	A	G	C3566	U3471
U4636	G4558	C4427	A4346	G4236	U4118	A3992	G3878	G3773	A	C	C3567	U3471
U4637	G4559	C4428	U4352	A4237	C4119	A3992	G3878	G3773	U	C	C3568	A3474
U4638	C4560	C	A4353	U4238	C4120	G4008	U3882	A3778	C	C	U3572	U3475
U4639	G4561	U	A4354	G4239	G4125	G4009	U3882	A3779	C	C	A3573	G3476
C4640	C4562	C	C4357	A4242	U4131	U4011	U3885	C3780	A	G	A3574	G3480
U4641	G4563	C	A4358	A4243	U4146	U4012	A3886	C3786	C	C	C3575	C3491
U4645	C4564	C	U4361	U4247	U4153	U4013	G3888	U3787	A	C	C3576	C3492
C4652	G4565	C	U4362	G4248	U4154	G4021	A3891	C3788	C	C	U3577	C3495
C4653	C4566	C	C4363	U4253	C4155	G4024	A3892	C3789	C	C	U3584	G3496
U4654	C4567	C	G4364	U4254	C4155	U4025	G3893	C	C	U	A3585	U3497
U4654	U4569	C	G4365	A4255	U4165	G4026	C3896	C	C	C	G3586	C3500
C4661	C4570	C	A4370	G4259	A4166	C4030	A3904	C	C	C	U3587	U3501
A4662	U4571	C	C4373	A4263	A4171	A4031	C3905	G	C	C	A3502	A3502
A4663	C4572	C	G4376	G4271	G4173	A4032	A3906	U	C	C	C3594	U3505
A4665	G4573	C	A4377	U4272	G4174	A4033	A3907	C	C	G	G3595	A3506
C4669	A4579	C	C4378	U4273	G4175	C4040	A3908	G3799	C	U	G3598	C3507
U	C4580	G	G4379	U4273	A4176	A4047	A3909	G3723	C	C	G3602	U3508
C	U4581	G	U4380	C4278	G4177	U4059	A3910	G3727	G	G	A3601	A3513
C	U4582	C	U4381	U4279	C4178	G4060	C3911	G3733	G	G	G3603	G3516
U	U4583	C	A4382	U4280	U4181	C4064	U3913	G3735	G	U	A3604	A3517
C	U4584	C	C4383	U4281	G4182	U4064	C3914	G3735	C	C	A3605	A3518
C	G4585	C	G4384	U4282	C4182	G4068	G3917	G3735	G	G	A3606	A3519
C	A4586	C	A4385	G4283	C4190	A4068	G3917	G3739	G	G	U3607	A3524
C	U4587	C	C4386	U4284	G4191	G4071	A3924	G3740	C	C	G3608	A3527
C	G4588	C	A4387	U4287	U4192	U4072	G3925	G3744	C	C	A	C3528
C	U4589	C	C4388	A4288	C4193	U4073	A3926	G3745	A	A	G	A3529
C	U4594	C	G4389	U4289	G4194	C4074	A3933	U3816	C	C	G	
C	U4595	C	C4390	G4290								
C	U4596	C	G4391									
C	U4597	C										
C	A4603	C										
C	A4604	C										

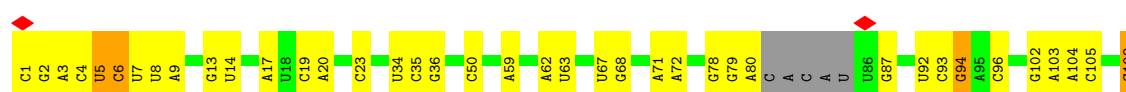




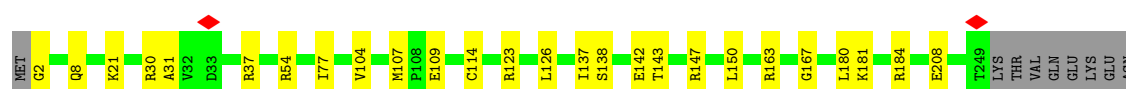
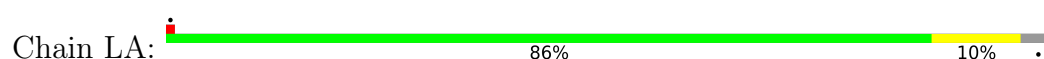
- Molecule 2: Mus musculus 5S ribosomal RNA



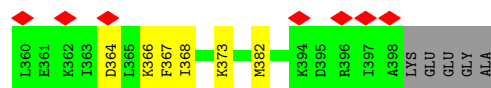
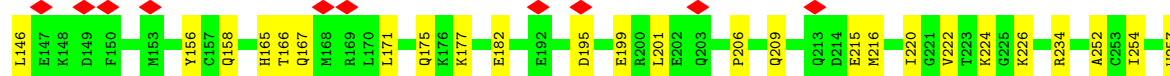
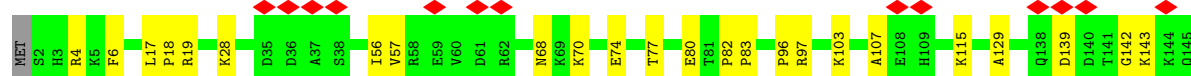
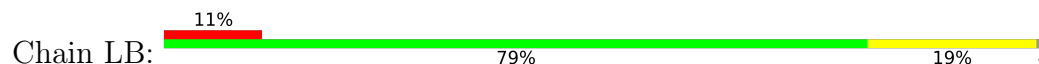
- Molecule 3: Mus musculus 5.8S ribosomal RNA



- Molecule 4: Large ribosomal subunit protein uL2



- Molecule 5: Large ribosomal subunit protein uL3



- Molecule 6: Large ribosomal subunit protein uL4



Frequency	Percentage
Daily	77%
Weekly	8%
Monthly	15%



Category	Percentage
Very bad	25%
Bad	84%
Good	14%

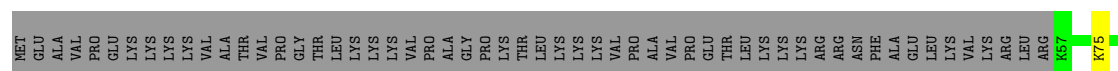


Frequency	Percentage
Daily	11%
Often	61%
Sometimes	11%
Not at all	27%

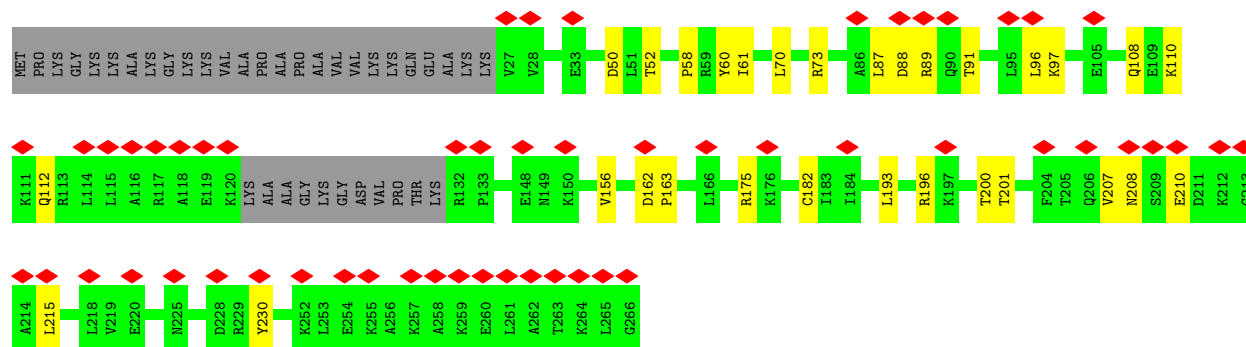
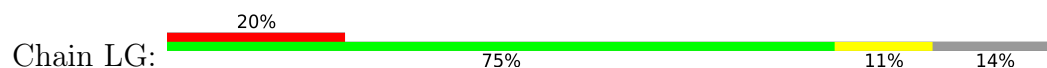


Response	Percentage
U.S. should take action to protect the environment	69%
U.S. should not take action to protect the environment	10%
U.S. should not take action to protect the environment	21%

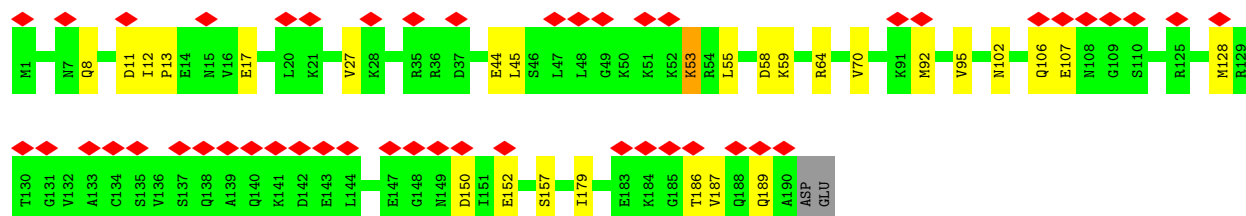
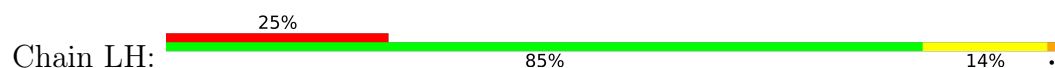




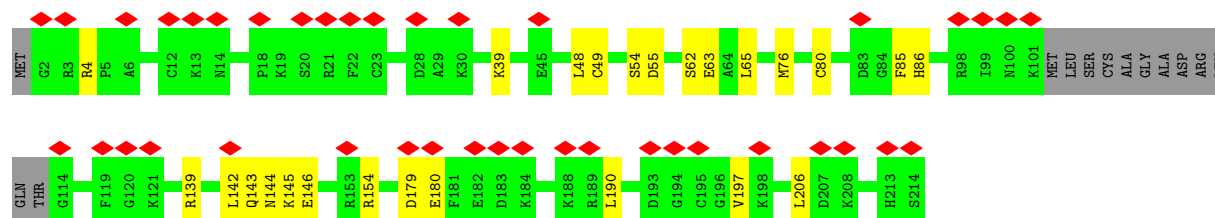
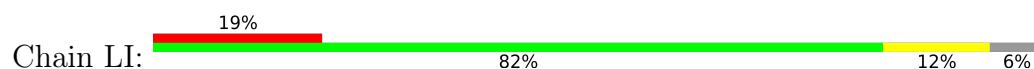
• Molecule 10: Large ribosomal subunit protein eL8



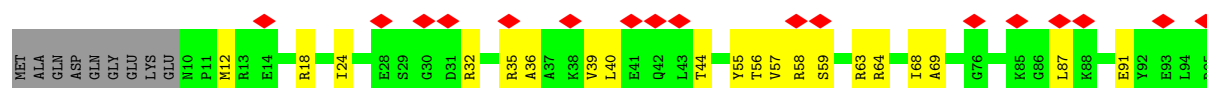
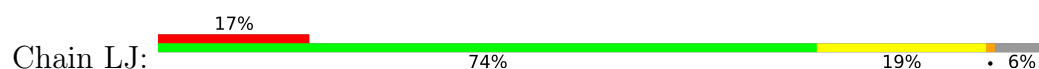
• Molecule 11: Large ribosomal subunit protein uL6



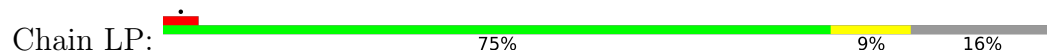
• Molecule 12: Large ribosomal subunit protein uL16-like



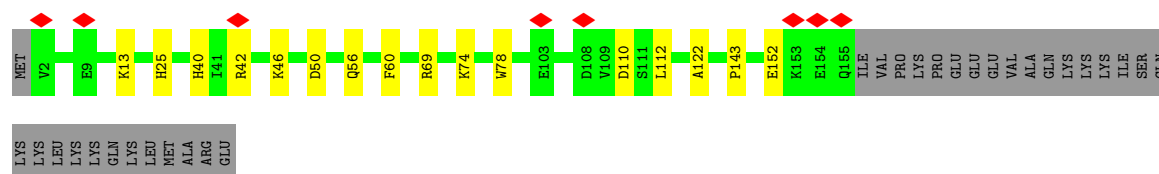
• Molecule 13: Large ribosomal subunit protein uL5



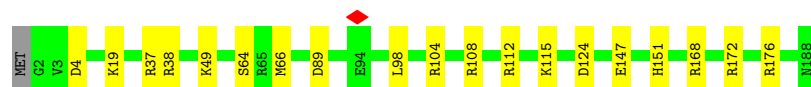




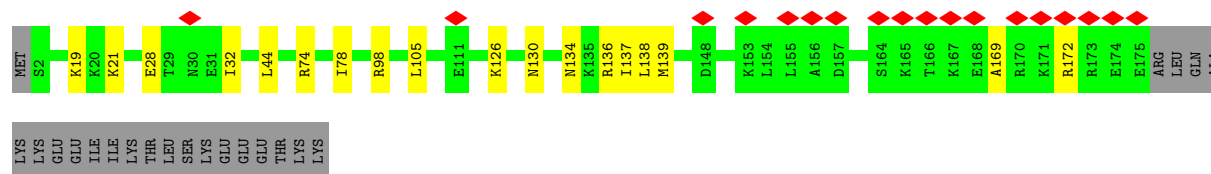
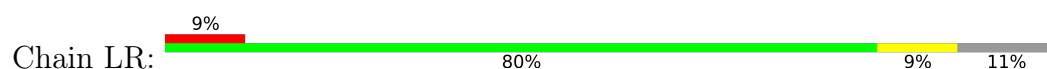




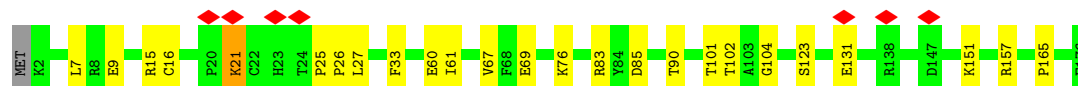
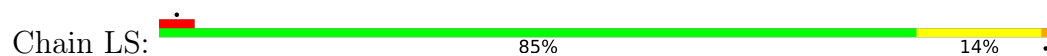
- Molecule 19: Large ribosomal subunit protein eL18



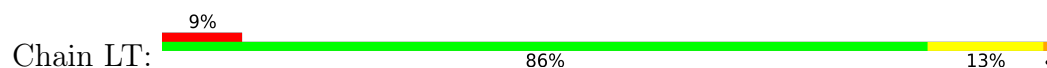
- Molecule 20: Large ribosomal subunit protein eL19



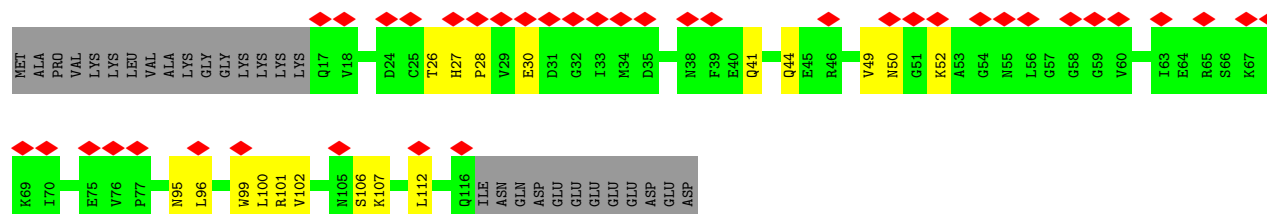
- Molecule 21: Large ribosomal subunit protein eL20



- Molecule 22: Large ribosomal subunit protein eL21




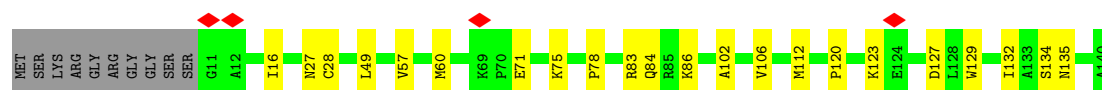
- Molecule 23: Large ribosomal subunit protein eL22





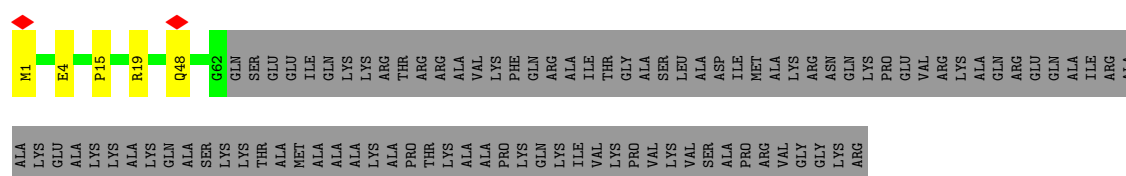
- Molecule 24: Large ribosomal subunit protein uL14

Chain LV: 



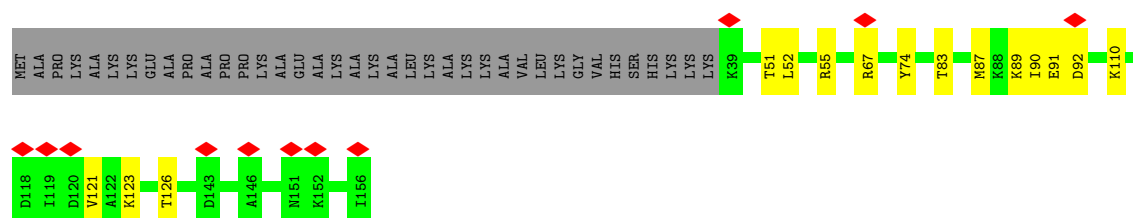
- Molecule 25: Large ribosomal subunit protein eL24

Chain LW: 




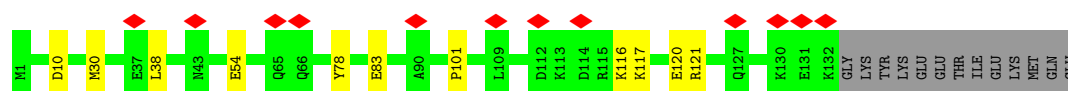
- Molecule 26: Large ribosomal subunit protein uL23

Chain LX: 




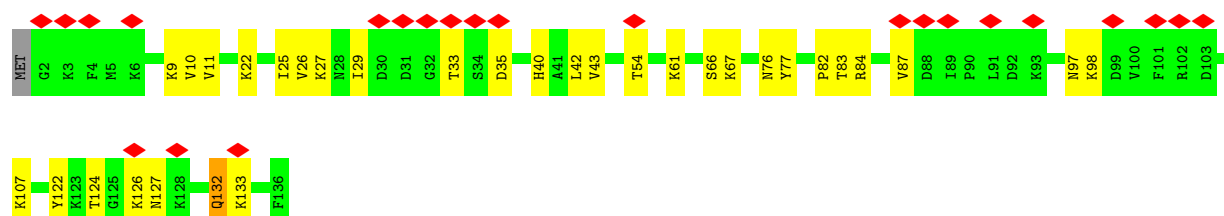
- Molecule 27: Large ribosomal subunit protein uL24

Chain LY: 



- Molecule 28: Large ribosomal subunit protein eL27

Chain LZ: 



- Molecule 29: Large ribosomal subunit protein uL15



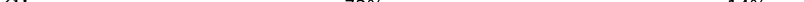
Diagram illustrating the structure of the human PTPN22 gene, showing exons (yellow) and introns (green). The gene structure includes exons MET, P2, R26, K27, D76, V82, A91, K94, T95, G96, I101, I137, G142, and A148. Red diamonds indicate the positions of specific mutations or variants, including D76, A91, K94, T95, G96, and A148.

- Chain Lb: 

Figure 1: Schematic representation of the protein structure of the human PTPN22 protein. The protein is shown as a horizontal bar with various domains and motifs labeled. The bar is divided into segments representing different regions: MET, A2, K33, D36, K51, L54, K55, K56, N60, K63, S66, A67, R68, A69, GLU, ALA, ALA, ILE, LYS, LYS, LEU, VAL, LYS, PRO, GLN, ALA, ILE, LYS, PRO, LYS, MET, K87, L91, I106, M110, C117, GLN, PRO, LYS, PRO, VAL, THR, LYS, ALA, GLY, ALA, THR. Red diamonds indicate specific sites of interest, and yellow boxes highlight certain domains.

- Chain Lc: 

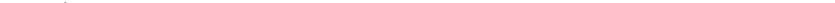
[illegible]

- Chain Ld: 

[illegible]

- Chain Le:  81% 14% 5%

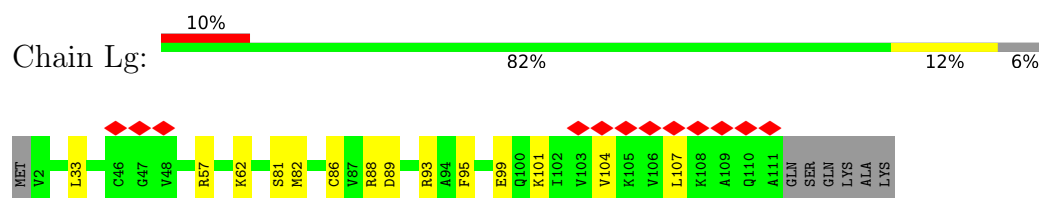
[illegible]

- Chain Lf:  85% 15%

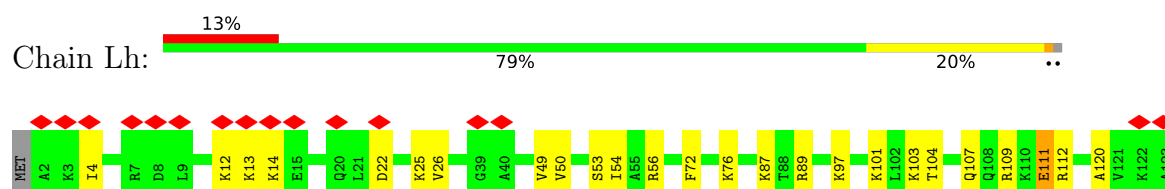
Protein	Number of amino acid mutations	Color	Marker
MET	1	Yellow	Red Diamond
S2	1	Yellow	
N20	1	Yellow	
Q21	2	Green	
R22	1	Yellow	
E23	1	Yellow	
L28	1	Yellow	
V33	1	Yellow	
E38	1	Yellow	
T39	2	Green	
E40	1	Green	
L43	1	Yellow	
K63	1	Yellow	Red Diamond
P64	1	Yellow	
V84	1	Yellow	
Y106	1	Yellow	
P107	1	Yellow	
S108	1	Yellow	
R109	1	Yellow	
I110	1	Yellow	Red Diamond



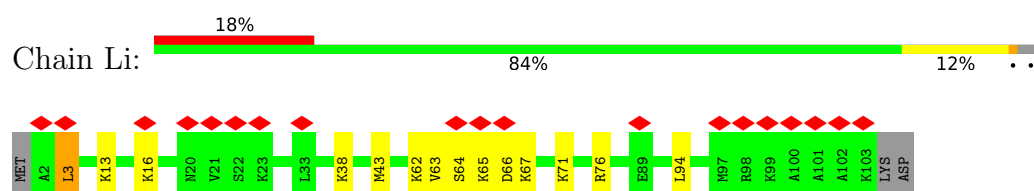
- Molecule 35: Large ribosomal subunit protein eL34



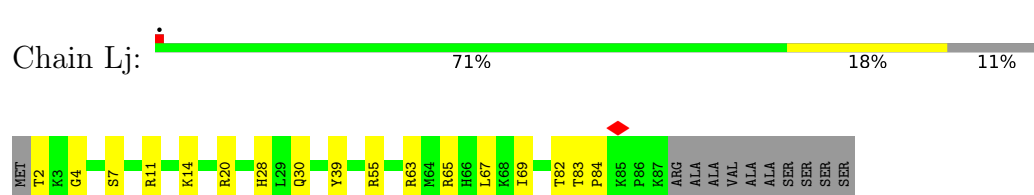
- Molecule 36: Large ribosomal subunit protein uL29



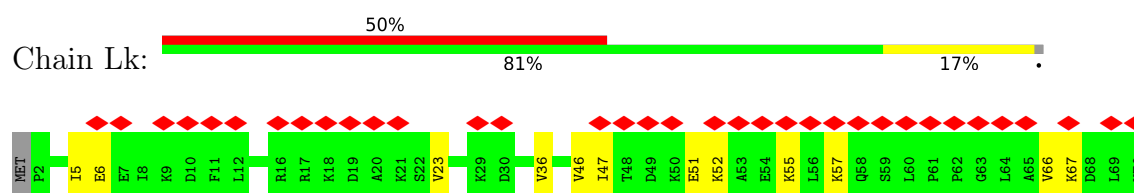
- Molecule 37: Large ribosomal subunit protein eL36



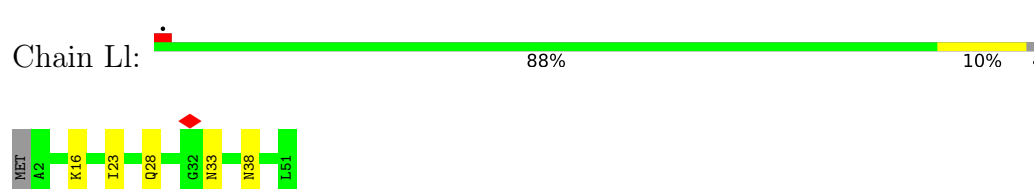
- Molecule 38: Large ribosomal subunit protein eL37



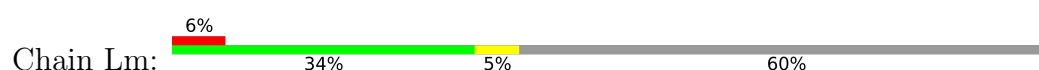
- Molecule 39: Large ribosomal subunit protein eL38



- Molecule 40: Large ribosomal subunit protein eL39-like

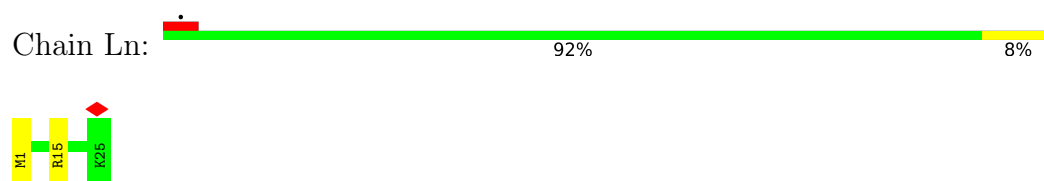


- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein

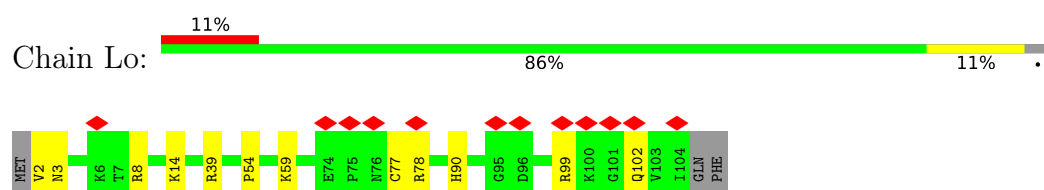




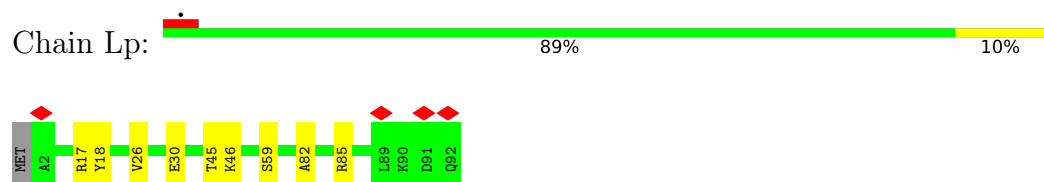
- Molecule 42: Small ribosomal subunit protein eS32



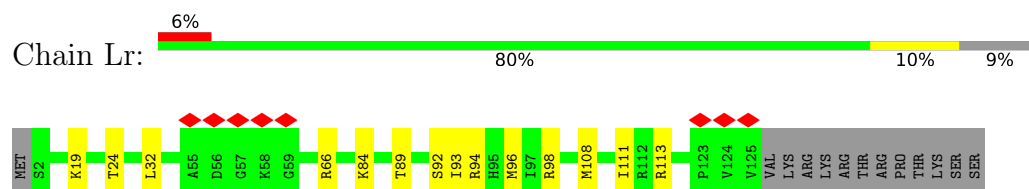
- Molecule 43: Large ribosomal subunit protein eL42



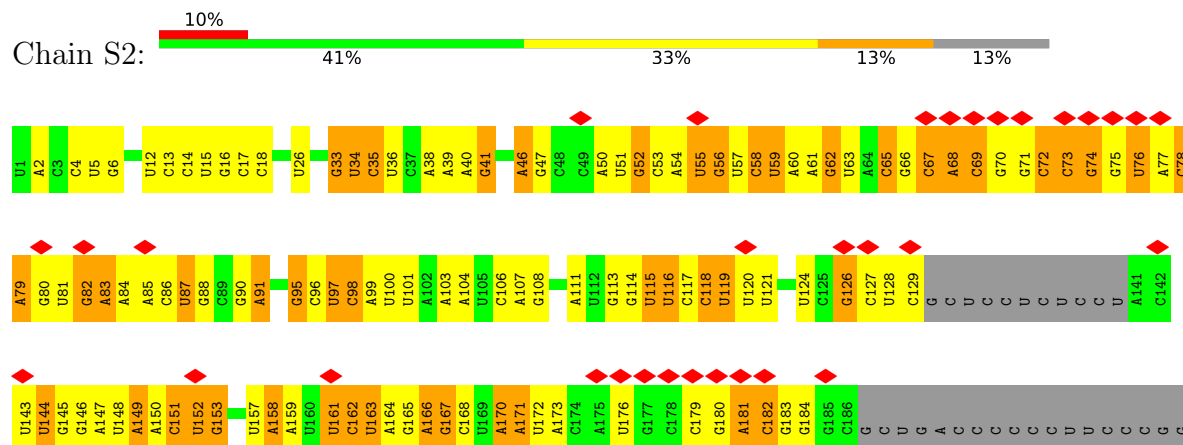
- Molecule 44: Large ribosomal subunit protein eL43



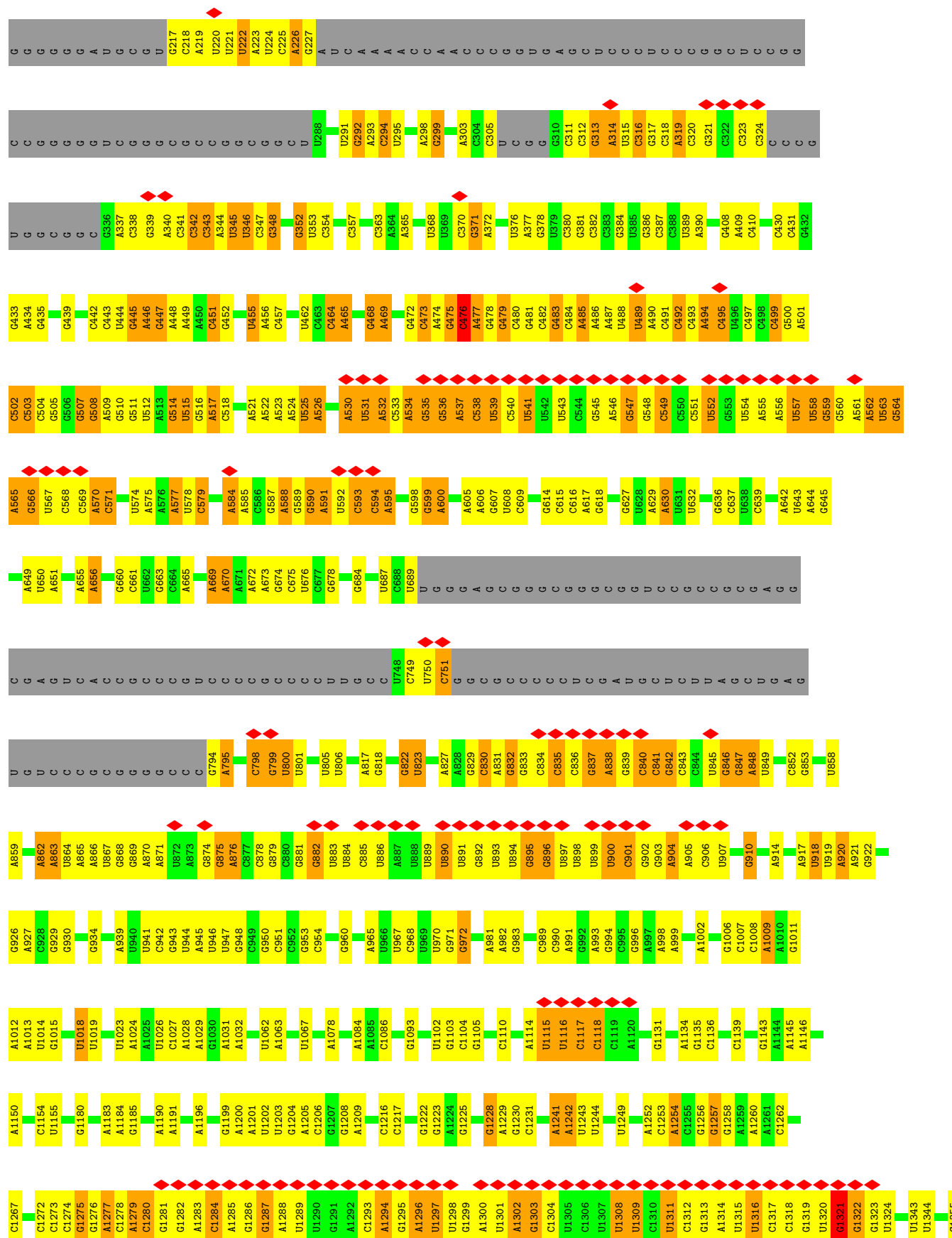
- Molecule 45: Large ribosomal subunit protein eL28



- Molecule 46: *Mus musculus* 18S ribosomal RNA



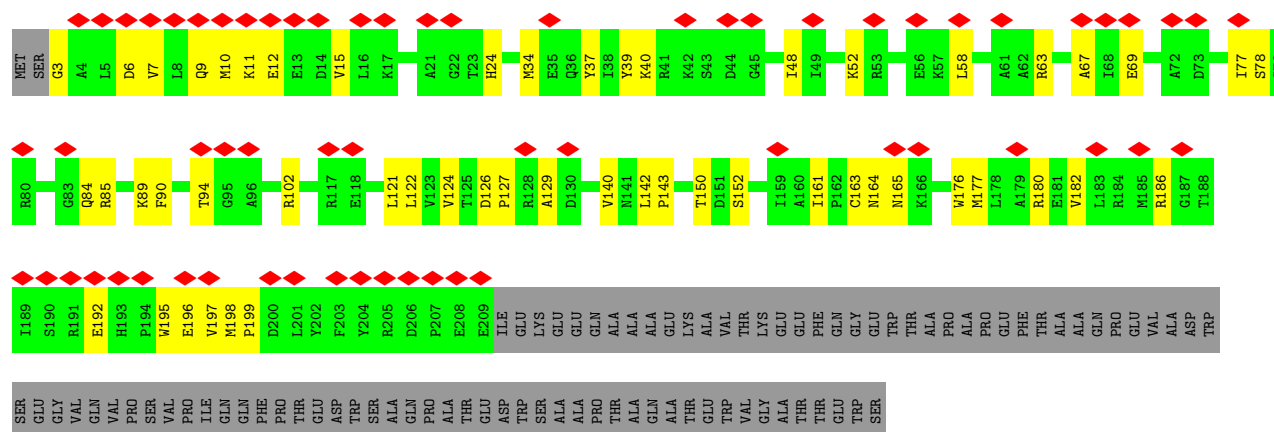




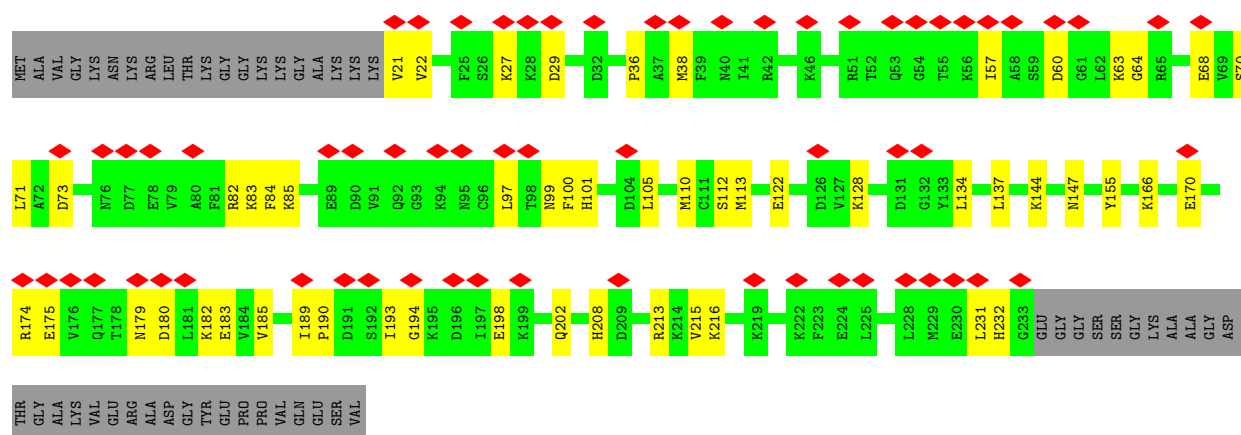




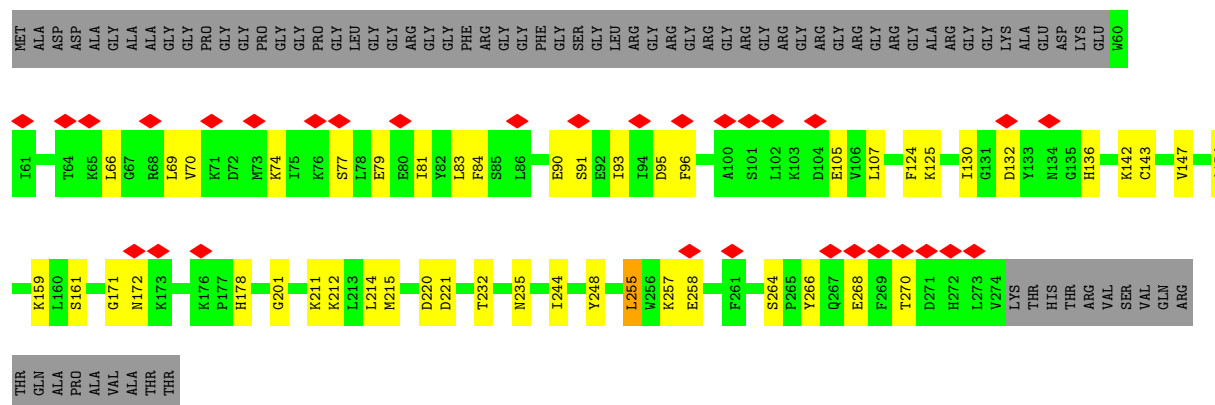




• Molecule 49: Small ribosomal subunit protein eS1



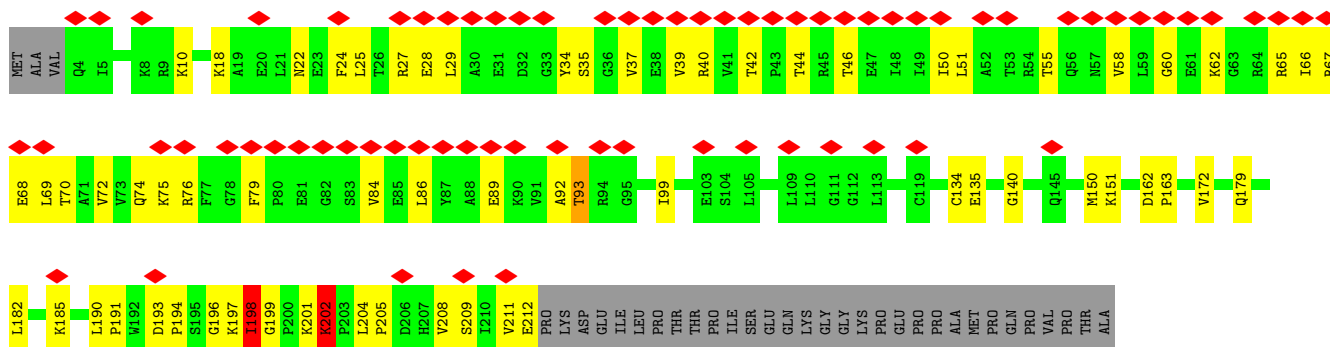
• Molecule 50: Small ribosomal subunit protein uS5



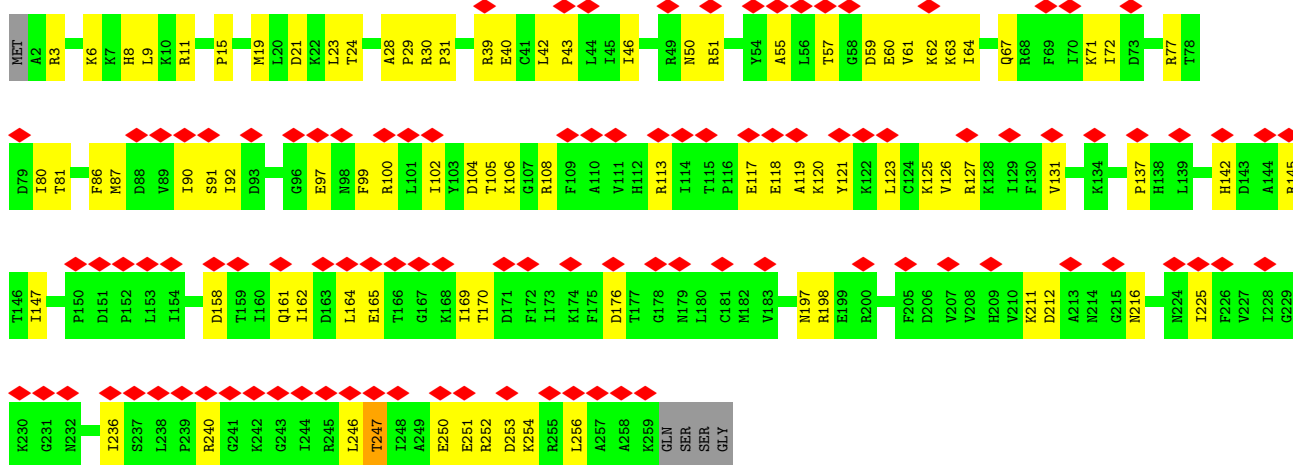
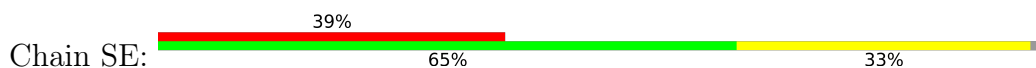
• Molecule 51: Small ribosomal subunit protein uS3



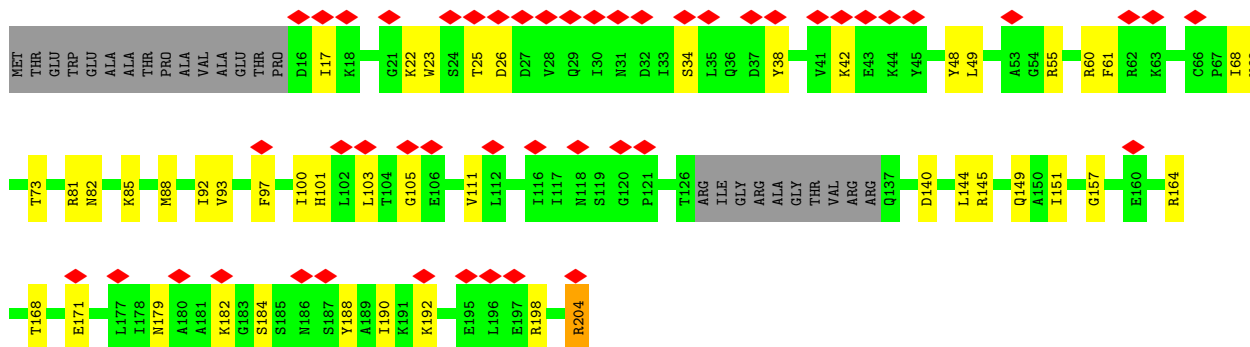




• Molecule 52: Small ribosomal subunit protein eS4



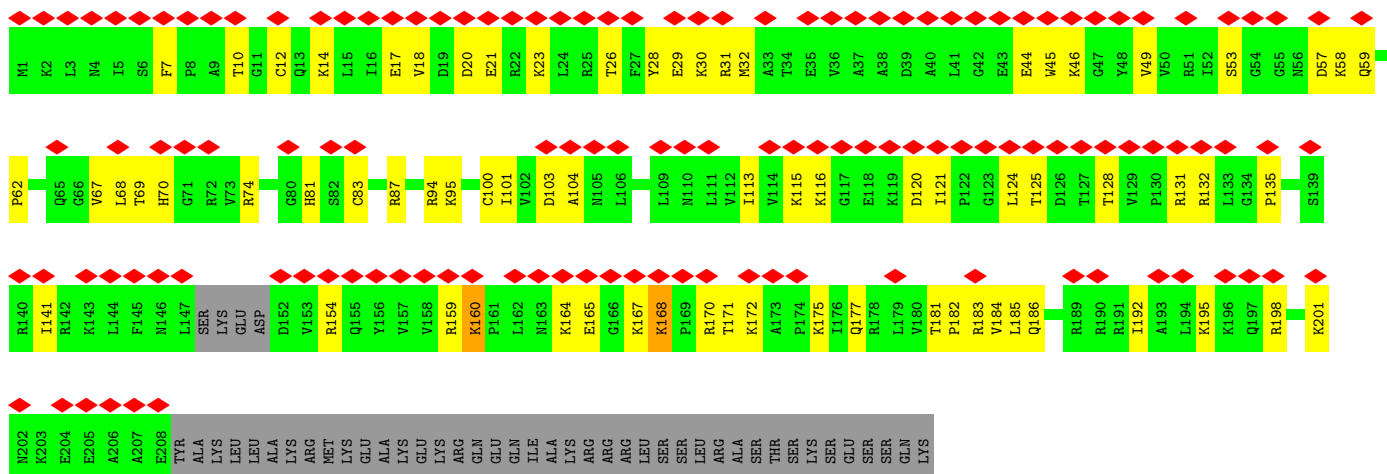
• Molecule 53: Small ribosomal subunit protein uS7



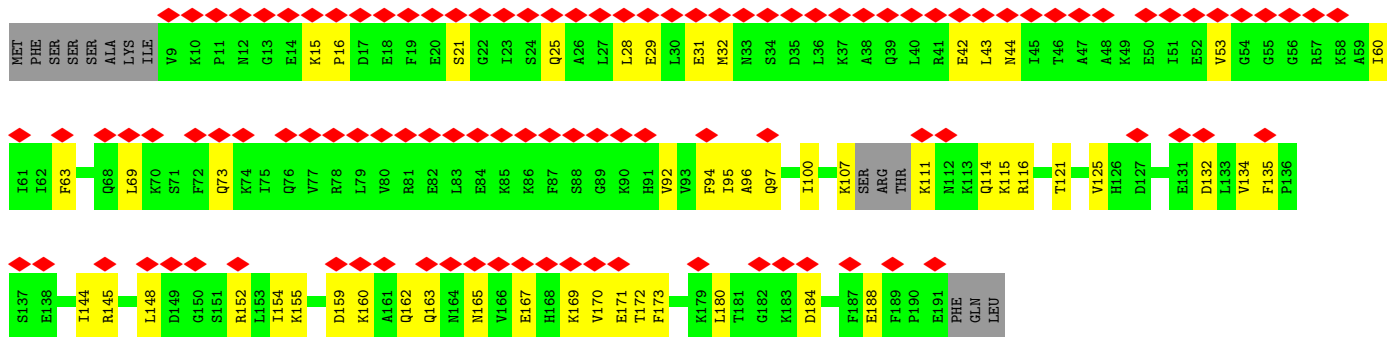
• Molecule 54: Small ribosomal subunit protein eS6



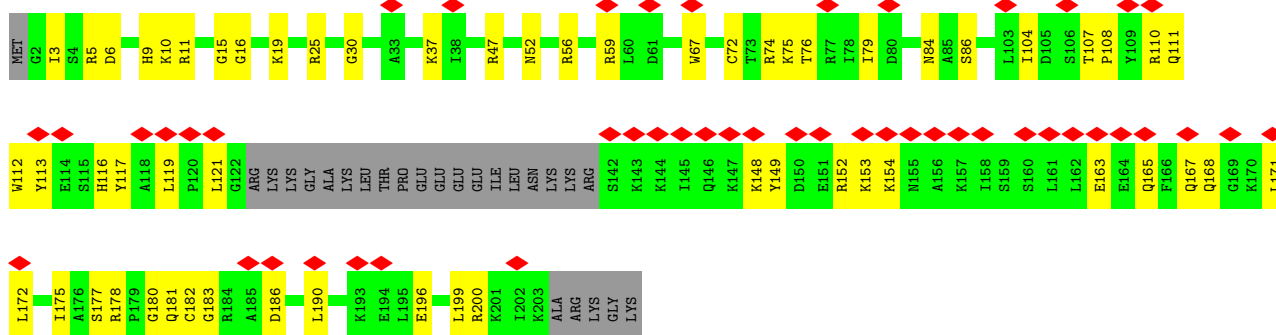




• Molecule 55: Small ribosomal subunit protein eS7



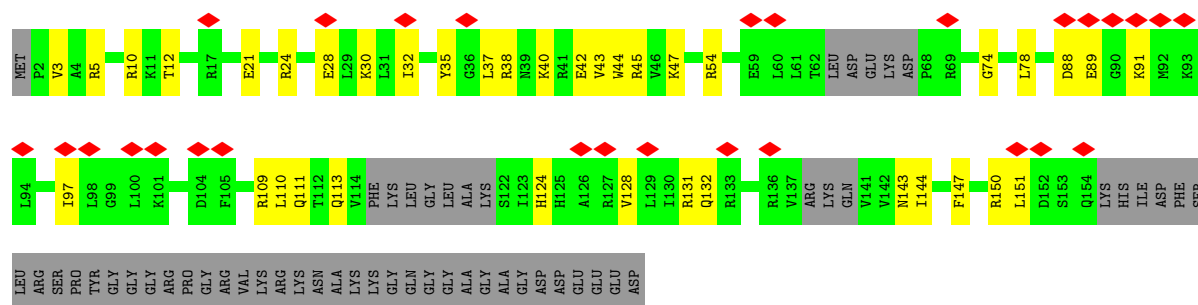
• Molecule 56: Small ribosomal subunit protein eS8



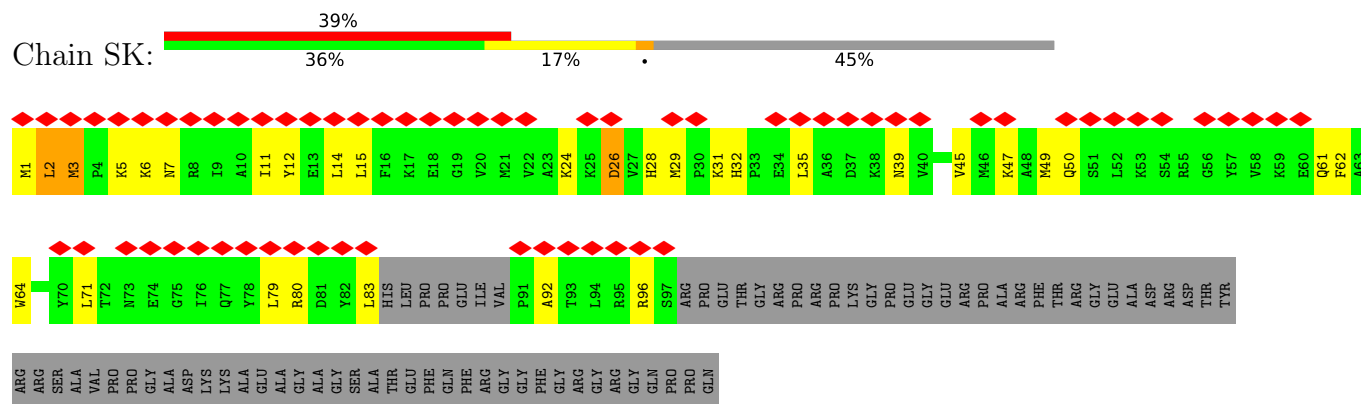
• Molecule 57: Small ribosomal subunit protein uS4



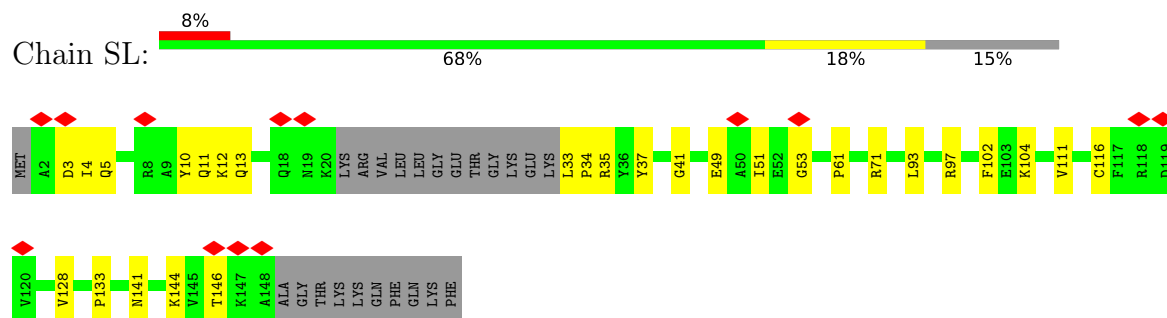




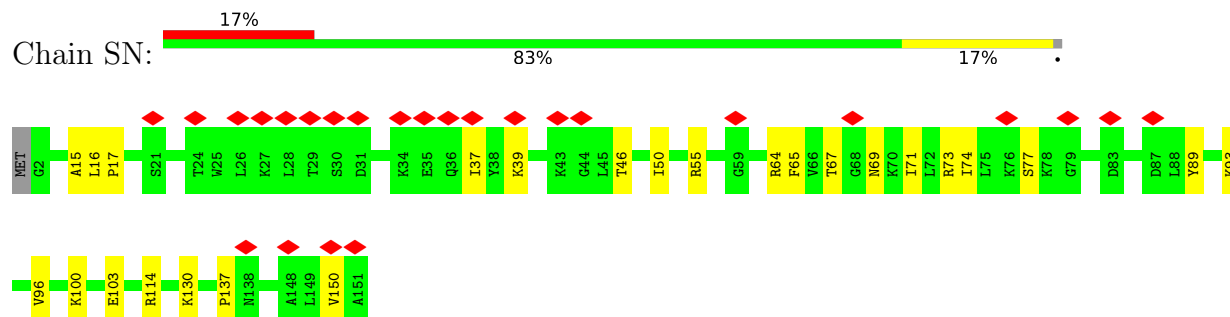
- Molecule 58: Small ribosomal subunit protein eS10



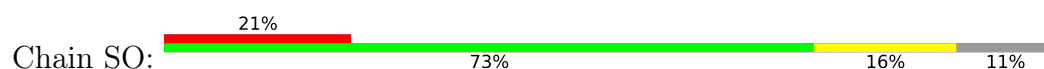
- Molecule 59: Small ribosomal subunit protein uS17



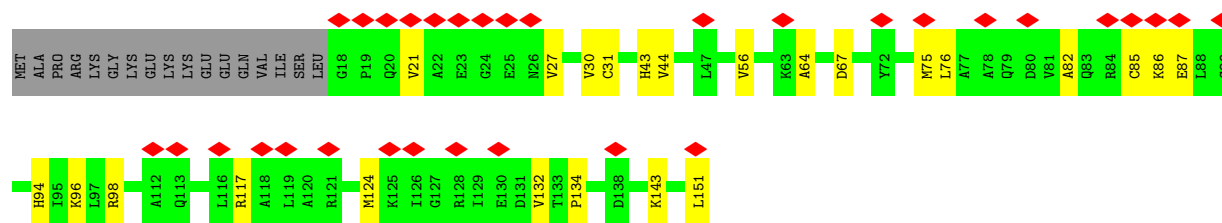
- Molecule 60: Small ribosomal subunit protein uS15



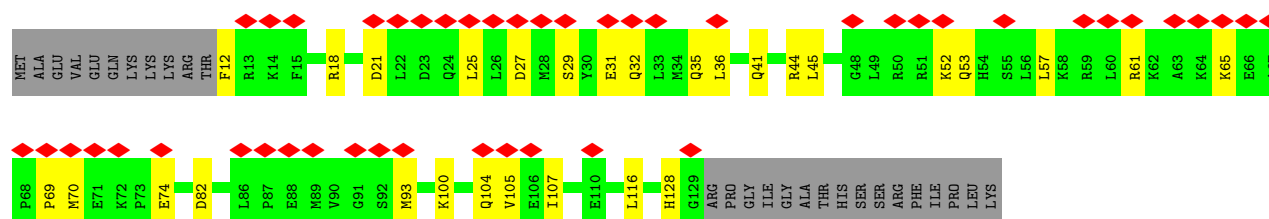
- Molecule 61: Small ribosomal subunit protein uS11



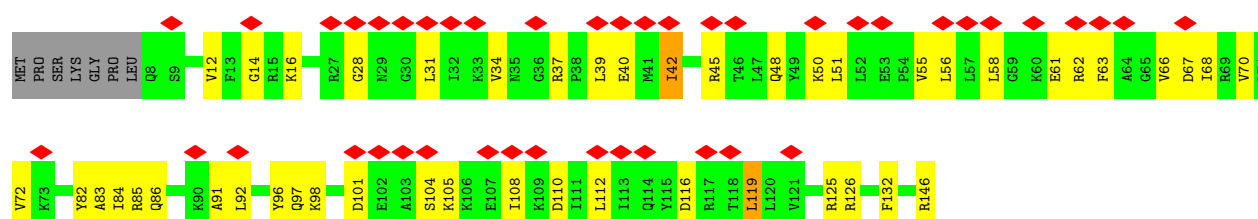




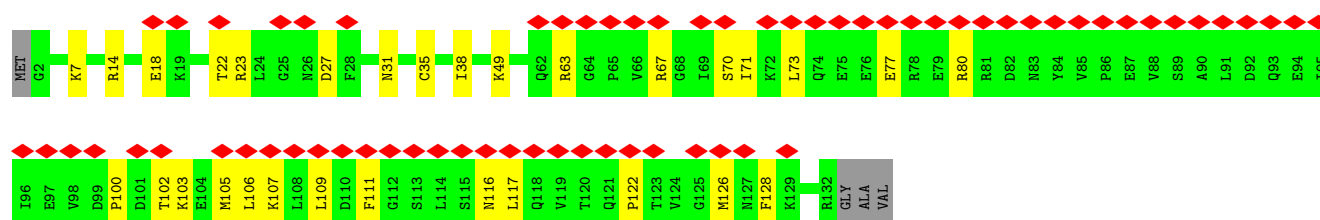
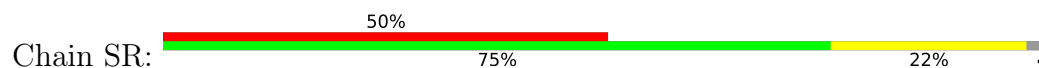
- Molecule 62: Small ribosomal subunit protein uS19



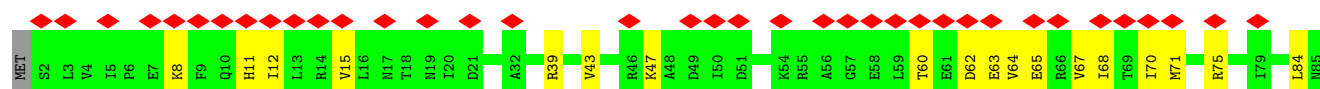
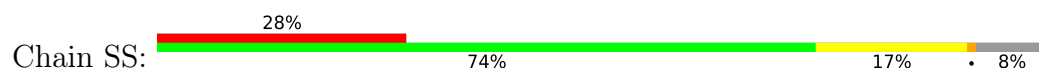
- Molecule 63: Small ribosomal subunit protein uS9



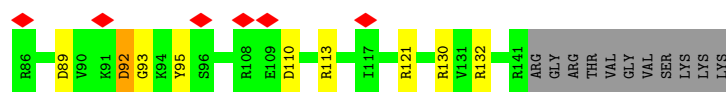
- Molecule 64: Small ribosomal subunit protein eS17



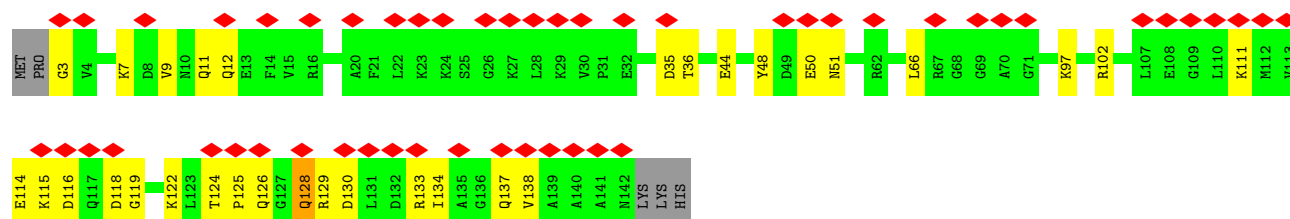
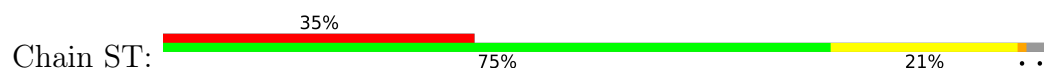
- Molecule 65: Small ribosomal subunit protein uS13



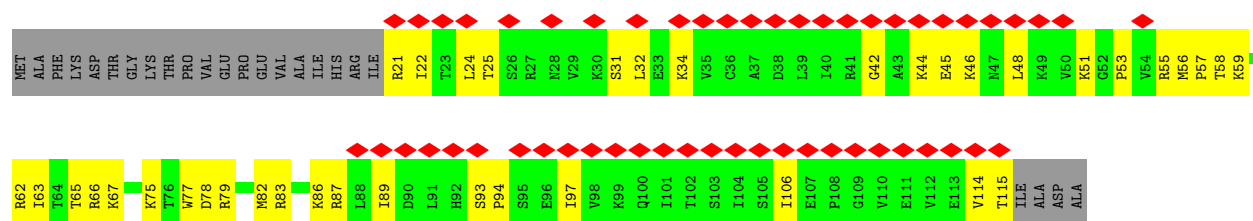




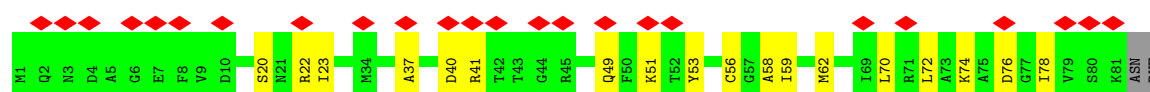
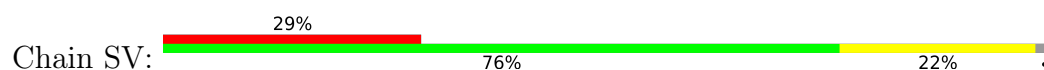
- Molecule 66: Small ribosomal subunit protein eS19



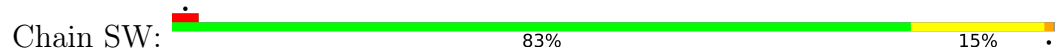
- Molecule 67: Small ribosomal subunit protein uS10



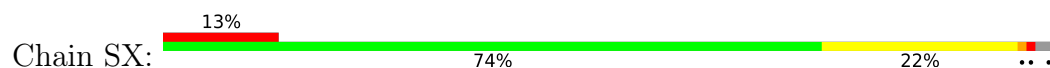
- Molecule 68: Small ribosomal subunit protein eS21



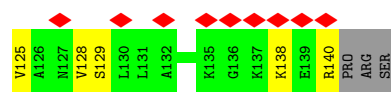
- Molecule 69: Small ribosomal subunit protein uS8



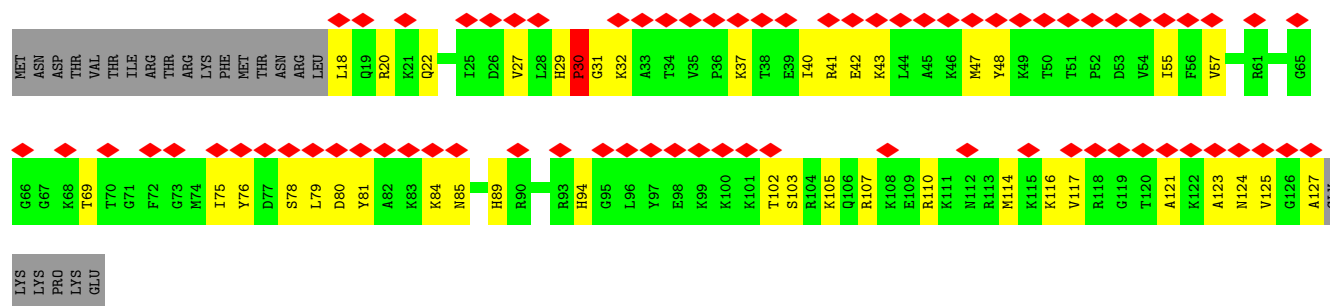
- Molecule 70: Small ribosomal subunit protein uS12



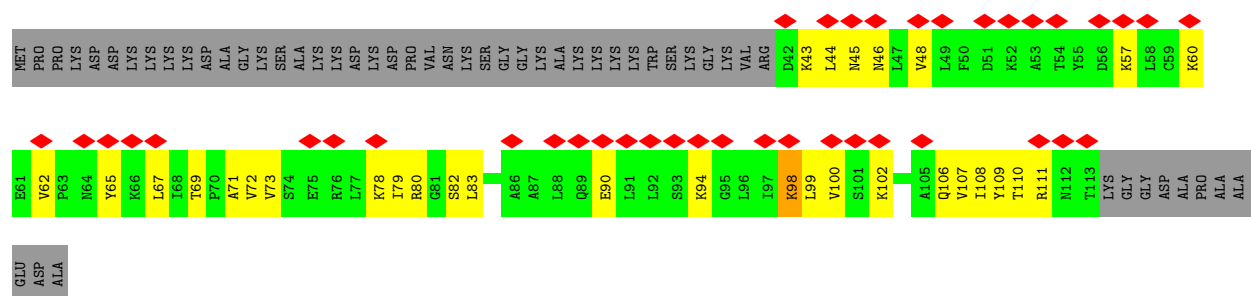
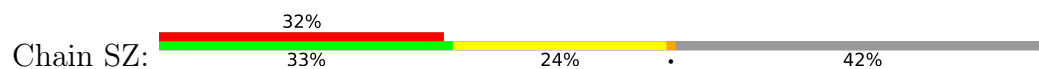




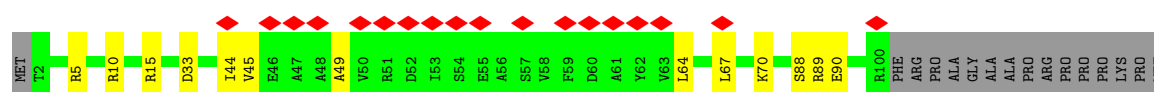
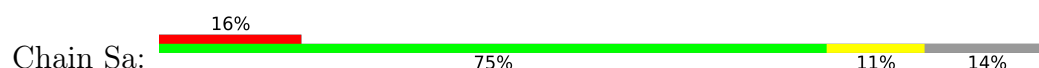
- Molecule 71: Small ribosomal subunit protein eS24



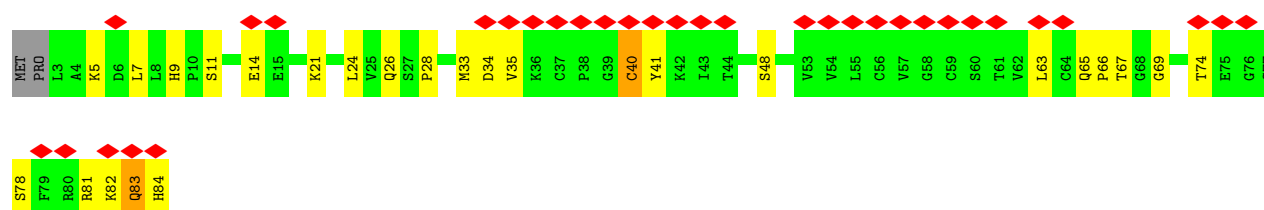
- Molecule 72: Small ribosomal subunit protein eS25



- Molecule 73: Small ribosomal subunit protein eS26

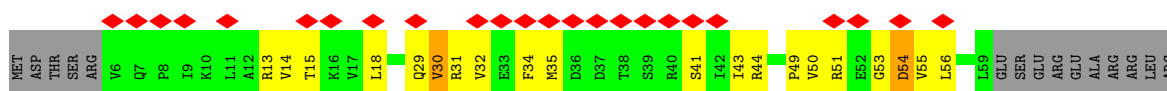


- Molecule 74: Small ribosomal subunit protein eS27

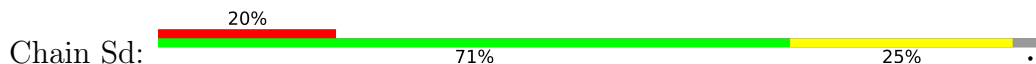


- Molecule 75: Small ribosomal subunit protein eS28

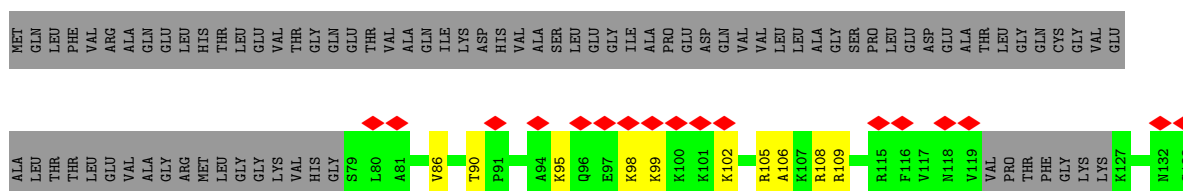




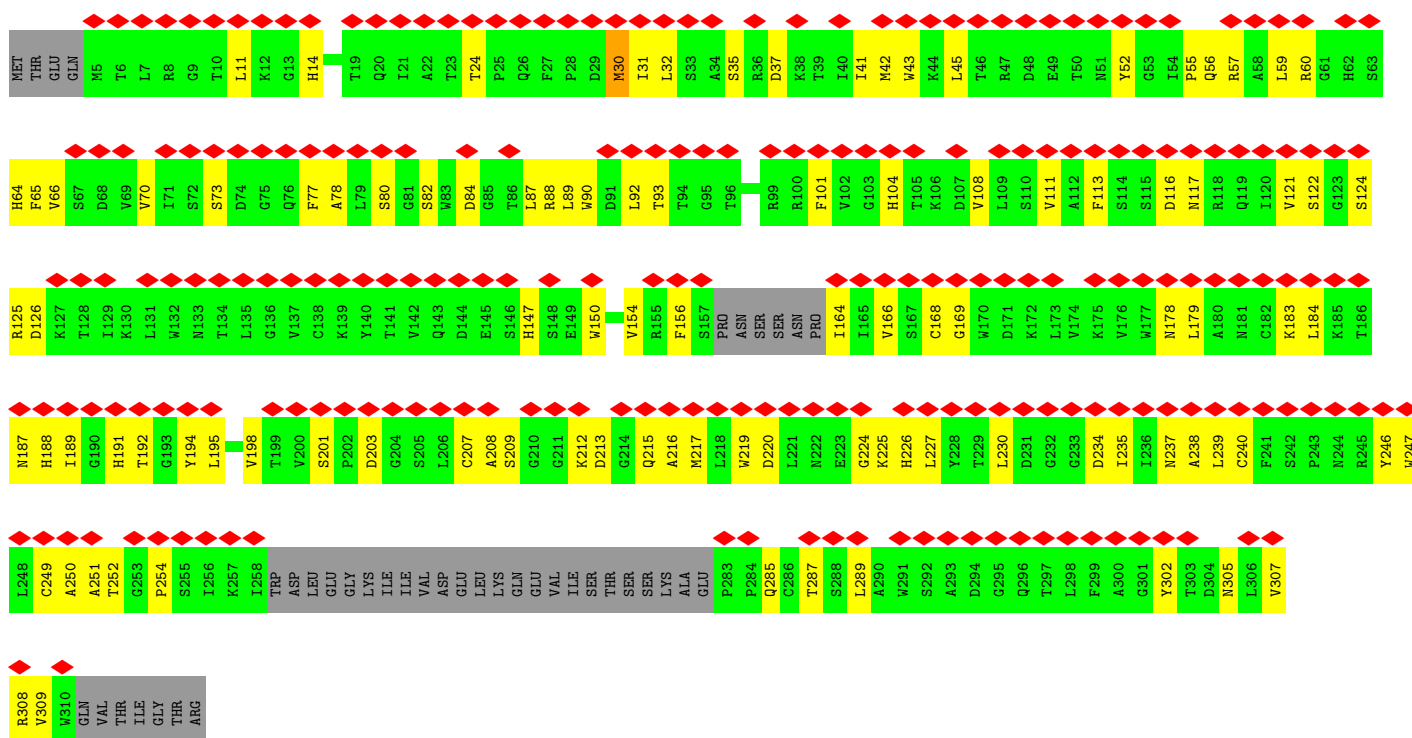
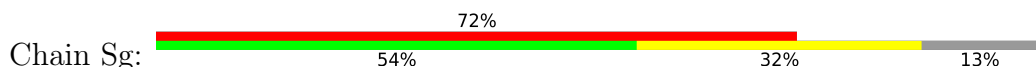
- Molecule 76: Small ribosomal subunit protein uS14



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



- Molecule 78: Small ribosomal subunit protein RACK1

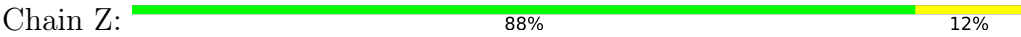


- Molecule 79: RNA (5'-R(P\*AP\*UP\*CP\*AP\*UP\*GP\*AP\*AP\*GP\*U)-3')





● 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	7458	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	1.513	Depositor
Minimum map value	-0.466	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.38	Depositor
Map size ( $\text{\AA}$ )	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 ( $\text{\AA}$ )	1.1, 1.1, 1.1	Depositor



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.17	0/81527	0.31	8/127149 (0.0%)
2	L7	0.15	0/2858	0.29	0/4455
3	L8	0.15	0/3584	0.29	0/5582
4	LA	0.17	0/1936	0.36	0/2596
5	LB	0.16	0/3269	0.35	0/4375
6	LC	0.16	0/2911	0.36	0/3907
7	LD	0.16	0/2435	0.39	0/3260
8	LE	0.15	0/1775	0.39	0/2381
9	LF	0.18	0/1805	0.37	0/2408
10	LG	0.14	0/1880	0.34	0/2531
11	LH	0.17	0/1537	0.43	0/2065
12	LI	0.15	0/1669	0.38	0/2227
13	LJ	0.14	0/1363	0.33	0/1824
14	LL	0.15	0/1698	0.32	0/2274
15	LM	0.14	0/1146	0.34	0/1531
16	LN	0.16	0/1746	0.31	0/2338
17	LO	0.16	0/1670	0.33	0/2232
18	LP	0.15	0/1277	0.34	0/1712
19	LQ	0.17	0/1539	0.34	0/2053
20	LR	0.13	0/1473	0.30	0/1947
21	LS	0.25	0/1491	0.41	0/2000
22	LT	0.15	0/1335	0.34	1/1781 (0.1%)
23	LU	0.18	0/831	0.49	0/1115
24	LV	0.15	0/987	0.35	0/1324
25	LW	0.14	0/532	0.32	0/708
26	LX	0.16	0/984	0.35	0/1323
27	LY	0.14	0/1119	0.33	0/1488
28	LZ	0.15	0/1130	0.35	0/1507
29	La	0.15	0/1193	0.32	0/1593
30	Lb	0.13	0/821	0.30	0/1082
31	Lc	0.16	0/742	0.38	0/996
32	Ld	0.15	0/911	0.32	0/1227



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Le	0.16	0/1071	0.32	0/1429
34	Lf	0.17	0/895	0.41	0/1198
35	Lg	0.14	0/883	0.34	0/1178
36	Lh	0.17	0/1023	0.34	0/1350
37	Li	0.13	0/843	0.36	0/1115
38	Lj	0.16	0/720	0.32	0/952
39	Lk	0.18	0/574	0.45	0/760
40	Ll	0.16	0/448	0.30	0/592
41	Lm	0.14	0/425	0.38	0/564
42	Ln	0.13	0/240	0.26	0/305
43	Lo	0.16	0/855	0.36	0/1128
44	Lp	0.15	0/718	0.27	0/953
45	Lr	0.15	0/1009	0.31	0/1353
46	S2	0.17	0/38859	0.33	5/60556 (0.0%)
47	S6	0.12	0/1795	0.27	0/2798
47	S7	0.17	0/1795	0.38	0/2798
48	SA	0.15	0/1673	0.45	2/2275 (0.1%)
49	SB	0.15	0/1756	0.41	0/2350
50	SC	0.26	0/1701	0.48	0/2300
51	SD	0.37	0/1651	0.60	0/2219
52	SE	0.15	0/2092	0.44	0/2816
53	SF	0.15	0/1436	0.38	0/1930
54	SG	0.28	0/1666	0.53	0/2222
55	SH	0.16	0/1470	0.43	0/1968
56	SI	0.13	0/1526	0.36	0/2038
57	SJ	0.12	0/1178	0.33	0/1574
58	SK	0.30	0/780	0.50	0/1046
59	SL	0.14	0/1130	0.37	0/1514
60	SN	0.13	0/1232	0.30	0/1656
61	SO	0.16	0/1015	0.40	0/1361
62	SP	0.16	0/1000	0.43	0/1335
63	SQ	0.22	0/1126	0.47	1/1506 (0.1%)
64	SR	0.27	0/1078	0.45	0/1447
65	SS	0.14	0/1175	0.37	0/1575
66	ST	0.15	0/1108	0.36	0/1486
67	SU	0.16	0/762	0.48	0/1023
68	SV	0.17	0/625	0.50	1/836 (0.1%)
69	SW	0.15	0/1051	0.34	0/1406
70	SX	0.20	0/1097	0.52	3/1464 (0.2%)
71	SY	0.20	0/907	0.54	1/1204 (0.1%)
72	SZ	0.16	0/580	0.46	0/780
73	Sa	0.14	0/805	0.35	0/1079
74	Sb	0.35	0/657	0.61	0/880



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
75	Sc	0.15	0/418	0.42	0/562
76	Sd	0.27	1/466 (0.2%)	0.33	0/618
77	Se	0.15	0/386	0.38	0/504
78	Sg	0.22	0/2199	0.49	0/2989
79	Sx	0.13	0/239	0.33	0/370
All	All	0.17	1/219312 (0.0%)	0.35	22/322353 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	Sd	8	TRP	CA-CB	5.01	1.58	1.52

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	476	C	C4'-C3'-O3'	12.17	131.25	113.00
46	S2	477	A	C2'-C3'-O3'	-9.21	99.88	113.70
1	L5	458	C	C2'-C3'-O3'	8.85	126.97	113.70
1	L5	4549	G	C3'-C2'-C1'	-8.63	92.87	101.50
48	SA	197	VAL	CA-C-N	8.54	133.66	120.68
48	SA	197	VAL	C-N-CA	8.54	133.66	120.68
46	S2	1321	G	C3'-C2'-C1'	-7.13	94.37	101.50
1	L5	3904	A	C2'-C3'-O3'	6.84	119.77	109.50
1	L5	4549	G	C2'-C3'-O3'	-6.76	99.36	109.50
68	SV	78	ILE	N-CA-C	-6.55	106.74	113.10
46	S2	476	C	O4'-C1'-C2'	-6.28	101.32	107.60
63	SQ	42	ILE	N-CA-C	-6.25	107.77	113.71
1	L5	3904	A	C4'-C3'-O3'	6.07	118.51	109.40
70	SX	61	GLN	CB-CG-CD	5.96	122.73	112.60
1	L5	453	U	P-O3'-C3'	5.87	129.00	120.20
1	L5	4676	G	C3'-C2'-C1'	-5.81	95.69	101.50
70	SX	60	LYS	CA-C-N	5.70	135.70	121.80
70	SX	60	LYS	C-N-CA	5.70	135.70	121.80
71	SY	30	PRO	CA-N-CD	-5.60	104.16	112.00
46	S2	476	C	C4'-C3'-C2'	-5.07	97.53	102.60
1	L5	4552	C	C4'-C3'-O3'	5.05	120.58	113.00
22	LT	122	LYS	N-CA-C	-5.05	108.15	114.56

There are no chirality outliers.

There are no planarity outliers.



## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	72884	0	36802	685	0
2	L7	2558	0	1296	26	0
3	L8	3210	0	1630	38	0
4	LA	1898	0	1993	19	0
5	LB	3202	0	3347	53	0
6	LC	2857	0	3030	23	0
7	LD	2389	0	2420	32	0
8	LE	1743	0	1880	25	0
9	LF	1771	0	1886	23	0
10	LG	1848	0	1981	22	0
11	LH	1519	0	1603	18	0
12	LI	1631	0	1682	17	0
13	LJ	1340	0	1377	24	0
14	LL	1667	0	1771	18	0
15	LM	1125	0	1202	22	0
16	LN	1701	0	1749	18	0
17	LO	1640	0	1792	20	0
18	LP	1251	0	1282	11	0
19	LQ	1515	0	1639	16	0
20	LR	1457	0	1601	15	0
21	LS	1451	0	1488	15	0
22	LT	1307	0	1380	17	0
23	LU	817	0	839	12	0
24	LV	973	0	1034	13	0
25	LW	519	0	533	4	0
26	LX	967	0	1040	10	0
27	LY	1102	0	1189	9	0
28	LZ	1107	0	1182	21	0
29	La	1164	0	1213	5	0
30	Lb	807	0	875	6	0
31	Lc	732	0	769	13	0
32	Ld	896	0	941	13	0
33	Le	1053	0	1147	11	0
34	Lf	876	0	912	12	0
35	Lg	873	0	961	11	0
36	Lh	1015	0	1156	21	0
37	Li	832	0	917	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	705	0	737	15	0
39	Lk	568	0	635	9	0
40	Ll	438	0	474	3	0
41	Lm	419	0	452	6	0
42	Ln	239	0	289	1	0
43	Lo	842	0	916	9	0
44	Lp	708	0	756	6	0
45	Lr	994	0	1057	10	0
46	S2	34749	0	17548	611	0
47	S6	1604	0	816	20	0
47	S7	1604	0	816	35	0
48	SA	1636	0	1641	35	0
49	SB	1729	0	1803	39	0
50	SC	1665	0	1753	32	0
51	SD	1626	0	1714	38	0
52	SE	2050	0	2156	66	0
53	SF	1416	0	1458	39	0
54	SG	1645	0	1780	57	0
55	SH	1449	0	1539	35	0
56	SI	1499	0	1561	44	0
57	SJ	1162	0	1252	33	0
58	SK	760	0	783	22	0
59	SL	1110	0	1165	19	0
60	SN	1208	0	1294	18	0
61	SO	1002	0	1023	17	0
62	SP	981	0	1026	24	0
63	SQ	1109	0	1174	39	0
64	SR	1064	0	1118	20	0
65	SS	1157	0	1213	21	0
66	ST	1090	0	1116	29	0
67	SU	753	0	815	30	0
68	SV	619	0	620	12	0
69	SW	1034	0	1080	19	0
70	SX	1080	0	1147	26	0
71	SY	891	0	948	38	0
72	SZ	574	0	627	24	0
73	Sa	792	0	845	13	0
74	Sb	644	0	664	17	0
75	Sc	416	0	445	18	0
76	Sd	455	0	449	15	0
77	Se	384	0	422	13	0
78	Sg	2148	0	2108	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	Sx	214	0	108	3	0
80	Z	39	0	13	1	0
81	L5	93	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
81	Le	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	204068	0	150895	2646	0

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

All (2646) 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)
1:L5:1910:G:C3'	1:L5:1911:G:H5'	1.61	1.28
1:L5:1910:G:H3'	1:L5:1911:G:C5'	1.64	1.26
1:L5:1910:G:N3	1:L5:1911:G:H5''	1.76	1.00
49:SB:189:ILE:HG23	49:SB:190:PRO:HD3	1.56	0.87
12:LI:80:CYS:SG	12:LI:144:ASN:ND2	2.47	0.87
46:S2:176:U:H3	46:S2:314:A:H62	1.18	0.87
1:L5:2599:A:H61	1:L5:3500:C:H42	1.20	0.85
2:L7:51:G:H21	13:LJ:12:MET:HE1	1.42	0.85
46:S2:41:G:H22	46:S2:481:G:H1	1.21	0.85
46:S2:53:C:H42	46:S2:473:C:H42	1.24	0.84
52:SE:71:LYS:HB2	52:SE:91:SER:HB2	1.60	0.83
46:S2:176:U:H3	46:S2:314:A:N6	1.75	0.83
1:L5:2277:C:O2	1:L5:2394:G:N2	2.11	0.82
1:L5:265:C:H1'	36:Lh:109:ARG:HH12	1.43	0.82
46:S2:66:G:H22	71:SY:121:ALA:HB2	1.45	0.82
1:L5:497:C:H42	1:L5:665:C:H42	1.28	0.81
47:S6:13:G:H1	47:S6:23:C:H42	1.27	0.81
52:SE:9:LEU:HB3	52:SE:28:ALA:HB3	1.63	0.81
46:S2:1145:A:H5'	46:S2:1356:C:H41	1.46	0.80
54:SG:70:HIS:HB2	54:SG:101:ILE:HD11	1.65	0.79
46:S2:482:C:O2'	46:S2:485:A:OP1	2.01	0.79
1:L5:494:G:H1	1:L5:668:G:H1	1.28	0.78
1:L5:766:G:H22	1:L5:805:C:H42	1.30	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SE:145:ARG:HH22	52:SE:162:ILE:HG21	1.48	0.78
46:S2:483:G:N2	46:S2:485:A:OP2	2.16	0.78
46:S2:889:U:H4'	46:S2:890:U:H5'	1.66	0.78
46:S2:389:U:H2'	46:S2:390:A:H8	1.49	0.77
1:L5:171:U:OP2	1:L5:172:C:N4	2.16	0.77
1:L5:3298:U:OP2	1:L5:3303:A:N6	2.17	0.77
43:Lo:14:LYS:HD2	43:Lo:77:CYS:HB2	1.67	0.77
46:S2:116:U:H3	46:S2:348:G:H1	1.33	0.77
71:SY:37:LYS:NZ	71:SY:57:VAL:O	2.18	0.76
46:S2:1355:G:N2	46:S2:1358:A:OP2	2.18	0.76
74:Sb:83:GLN:O	74:Sb:83:GLN:NE2	2.17	0.76
46:S2:1279:A:H2	46:S2:1321:G:H22	1.31	0.76
46:S2:462:U:H3	46:S2:469:A:H61	1.33	0.76
77:Se:98:LYS:HE2	77:Se:99:LYS:HB2	1.67	0.76
1:L5:1910:G:C3'	1:L5:1911:G:C5'	2.39	0.76
48:SA:163:CYS:SG	48:SA:164:ASN:N	2.58	0.76
46:S2:516:G:H5''	46:S2:517:A:H5'	1.68	0.76
49:SB:57:ILE:HB	49:SB:60:ASP:HB2	1.67	0.76
1:L5:1910:G:N3	1:L5:1910:G:H2'	2.01	0.75
1:L5:2513:G:H21	1:L5:2518:A:H62	1.34	0.75
53:SF:88:MET:HE3	53:SF:92:ILE:HD12	1.67	0.75
71:SY:123:ALA:HA	71:SY:127:ALA:HB2	1.65	0.75
1:L5:4425:U:H3	1:L5:4509:G:H1	1.33	0.75
13:LJ:24:ILE:HD13	13:LJ:40:LEU:HD11	1.69	0.75
36:Lh:72:PHE:O	36:Lh:76:LYS:NZ	2.17	0.75
1:L5:2019:G:OP2	45:Lr:98:ARG:NH2	2.20	0.75
1:L5:761:C:H5	1:L5:810:G:H1	1.34	0.74
1:L5:4273:U:OP2	1:L5:4323:C:N4	2.17	0.74
78:Sg:87:LEU:HB2	78:Sg:101:PHE:HB2	1.70	0.74
78:Sg:31:ILE:HG12	78:Sg:45:LEU:HD21	1.70	0.74
1:L5:2656:G:N2	1:L5:3255:C:N3	2.34	0.74
67:SU:56:MET:HB2	67:SU:86:LYS:HB3	1.68	0.74
1:L5:3975:G:N2	1:L5:3978:A:OP2	2.19	0.73
1:L5:2599:A:H61	1:L5:3500:C:N4	1.87	0.73
52:SE:60:GLU:OE2	52:SE:60:GLU:N	2.21	0.73
56:SI:76:THR:HG22	56:SI:108:PRO:HG2	1.70	0.73
1:L5:4664:A:H2	1:L5:4681:G:H21	1.34	0.73
51:SD:42:THR:HG22	51:SD:44:THR:H	1.53	0.72
52:SE:253:ASP:HA	52:SE:256:LEU:HG	1.70	0.72
46:S2:321:G:O6	54:SG:186:GLN:NE2	2.22	0.72
46:S2:650:U:H2'	46:S2:651:A:H8	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S7:10:G:O2'	47:S7:11:G:N7	2.19	0.72
54:SG:120:ASP:HB3	54:SG:125:THR:HG21	1.71	0.72
57:SJ:40:LYS:H	57:SJ:40:LYS:HZ3	1.36	0.72
56:SI:110:ARG:NH1	56:SI:121:LEU:O	2.22	0.72
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.72	0.72
10:LG:162:ASP:HB2	10:LG:163:PRO:HD3	1.71	0.72
1:L5:4068:A:OP1	12:LI:154:ARG:NH1	2.22	0.71
52:SE:117:GLU:OE2	52:SE:118:GLU:N	2.23	0.71
70:SX:107:ARG:HE	70:SX:112:VAL:HG12	1.54	0.71
72:SZ:98:LYS:NZ	72:SZ:111:ARG:O	2.22	0.71
1:L5:3374:A:OP2	1:L5:3392:G:N2	2.23	0.71
46:S2:534:A:H2'	46:S2:535:G:C8	2.25	0.71
46:S2:1418:C:N4	46:S2:1422:A:C6	2.58	0.71
1:L5:950:G:H22	1:L5:1035:U:H3	1.36	0.71
46:S2:54:A:OP2	46:S2:452:G:N2	2.22	0.71
46:S2:176:U:O4	46:S2:314:A:N7	2.22	0.71
46:S2:1514:C:H2'	46:S2:1515:G:H8	1.54	0.71
1:L5:3480:G:OP2	1:L5:3480:G:N2	2.22	0.71
52:SE:162:ILE:HG22	52:SE:169:ILE:HA	1.72	0.71
56:SI:119:LEU:HD21	56:SI:153:LYS:HE2	1.73	0.71
6:LC:281:MET:HE3	6:LC:282:HIS:H	1.54	0.71
36:Lh:111:GLU:N	36:Lh:111:GLU:OE1	2.20	0.71
46:S2:1425:G:H2'	46:S2:1426:G:H8	1.56	0.71
1:L5:1147:C:H2'	1:L5:1148:A:H8	1.56	0.71
18:LP:112:LEU:HD23	18:LP:152:GLU:HB3	1.73	0.71
46:S2:117:C:OP1	56:SI:52:ASN:ND2	2.23	0.71
1:L5:1205:G:N2	1:L5:1208:G:OP2	2.23	0.70
1:L5:2656:G:H3'	1:L5:2657:G:H21	1.56	0.70
46:S2:554:U:H2'	46:S2:555:A:H2'	1.72	0.70
74:Sb:81:ARG:NH2	74:Sb:84:HIS:OXT	2.24	0.70
53:SF:38:TYR:OH	75:Sc:54:ASP:OD2	2.09	0.70
68:SV:53:TYR:HD2	68:SV:72:LEU:HD23	1.56	0.70
73:Sa:45:VAL:HG11	73:Sa:64:LEU:HD23	1.73	0.70
46:S2:1537:G:H2'	46:S2:1538:A:H8	1.56	0.70
46:S2:1659:G:OP2	46:S2:1661:C:N4	2.24	0.70
1:L5:936:C:N4	1:L5:1054:G:O6	2.25	0.70
17:LO:198:THR:O	17:LO:199:ASN:ND2	2.25	0.70
67:SU:21:ARG:N	67:SU:115:THR:O	2.24	0.70
1:L5:1634:G:H5'	30:Lb:68:ARG:HH12	1.57	0.70
59:SL:104:LYS:O	70:SX:11:ARG:NH2	2.24	0.70
76:Sd:22:ARG:NH2	76:Sd:36:LEU:O	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SE:29:PRO:HG2	52:SE:46:ILE:HD11	1.73	0.70
1:L5:3739:C:OP1	4:LA:37:ARG:NH1	2.24	0.70
1:L5:294:A:OP2	43:Lo:39:ARG:NH1	2.23	0.69
52:SE:100:ARG:NH1	52:SE:118:GLU:OE2	2.25	0.69
62:SP:104:GLN:OE1	62:SP:105:VAL:N	2.25	0.69
1:L5:2314:G:H22	1:L5:2324:G:H22	1.40	0.69
46:S2:1489:C:O2'	46:S2:1491:G:OP2	2.09	0.69
72:SZ:69:THR:HG22	72:SZ:72:VAL:HG12	1.72	0.69
1:L5:1258:G:H1	1:L5:1904:C:H42	1.40	0.69
78:Sg:164:ILE:HD12	78:Sg:178:ASN:HA	1.75	0.69
46:S2:126:G:OP1	54:SG:198:ARG:NH1	2.26	0.69
1:L5:4516:G:OP2	15:LM:5:ARG:NH2	2.22	0.69
1:L5:2237:G:N2	1:L5:2238:G:O6	2.23	0.69
51:SD:28:GLU:OE1	58:SK:61:GLN:NE2	2.24	0.69
51:SD:76:ARG:NH1	51:SD:76:ARG:O	2.25	0.69
63:SQ:37:ARG:HG3	66:ST:7:LYS:HE2	1.74	0.69
67:SU:56:MET:HE3	67:SU:57:PRO:HD2	1.75	0.69
1:L5:1733:U:OP2	17:LO:49:ARG:NH1	2.24	0.69
60:SN:16:LEU:HD12	60:SN:17:PRO:HD2	1.73	0.69
26:LX:91:GLU:N	26:LX:91:GLU:OE2	2.26	0.68
46:S2:574:U:N3	46:S2:577:A:OP2	2.25	0.68
71:SY:114:MET:HG3	71:SY:124:ASN:HA	1.74	0.68
1:L5:1012:U:HO2'	1:L5:1015:C:N4	1.89	0.68
1:L5:4560:C:H2'	1:L5:4561:G:C8	2.28	0.68
46:S2:569:C:H1'	46:S2:584:A:H61	1.58	0.68
49:SB:112:SER:OG	49:SB:113:MET:SD	2.51	0.68
54:SG:68:LEU:N	54:SG:100:CYS:SG	2.62	0.68
49:SB:83:LYS:NZ	49:SB:105:LEU:O	2.27	0.68
51:SD:29:LEU:HB2	51:SD:34:TYR:HB2	1.75	0.68
34:Lf:40:GLU:O	34:Lf:109:ARG:NH2	2.27	0.68
46:S2:558:U:H2'	46:S2:559:G:C8	2.29	0.68
50:SC:266:TYR:O	50:SC:270:THR:OG1	2.11	0.68
1:L5:3433:G:OP2	1:L5:3433:G:N2	2.25	0.68
69:SW:2:VAL:HG13	69:SW:3:ARG:H	1.59	0.68
46:S2:91:A:H61	46:S2:445:G:H8	1.42	0.68
53:SF:145:ARG:HE	53:SF:149:GLN:HE21	1.42	0.68
27:LY:54:GLU:OE1	27:LY:54:GLU:N	2.27	0.68
46:S2:53:C:N4	46:S2:473:C:H42	1.92	0.68
46:S2:1294:A:H62	46:S2:1303:G:H1	1.40	0.68
54:SG:32:MET:N	54:SG:32:MET:SD	2.67	0.68
55:SH:21:SER:HA	55:SH:25:GLN:HE22	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1709:U:H2'	1:L5:1710:A:H8	1.59	0.67
1:L5:4630:A:OP1	18:LP:74:LYS:NZ	2.27	0.67
27:LY:83:GLU:OE1	27:LY:83:GLU:N	2.24	0.67
52:SE:31:PRO:HG3	52:SE:43:PRO:HG3	1.76	0.67
78:Sg:191:HIS:HE2	78:Sg:209:SER:HG	1.41	0.67
46:S2:1276:G:H5'	46:S2:1277:A:H5'	1.75	0.67
48:SA:52:LYS:HB2	64:SR:109:LEU:HD21	1.76	0.67
55:SH:53:VAL:HG21	55:SH:172:THR:HA	1.77	0.67
1:L5:2205:G:O2'	4:LA:21:LYS:NZ	2.26	0.67
46:S2:838:A:H2'	71:SY:47:MET:HE1	1.77	0.67
46:S2:852:C:H5''	46:S2:853:G:H5'	1.76	0.67
46:S2:66:G:H3'	46:S2:68:A:H62	1.60	0.67
50:SC:79:GLU:N	50:SC:79:GLU:OE1	2.27	0.67
1:L5:1470:U:OP2	29:La:26:ARG:NH2	2.28	0.67
16:LN:116:LEU:HD22	16:LN:135:ILE:HD11	1.76	0.67
46:S2:59:U:N3	46:S2:62:G:OP2	2.28	0.67
1:L5:934:G:H1	1:L5:1063:C:H42	1.41	0.67
61:SO:30:VAL:HG12	61:SO:94:HIS:HB2	1.75	0.67
9:LF:93:MET:HA	9:LF:93:MET:HE3	1.77	0.67
1:L5:2075:G:N2	1:L5:2078:G:OP2	2.26	0.67
46:S2:526:A:H2	46:S2:591:A:C5	2.13	0.66
1:L5:1094:A:OP1	8:LE:139:LYS:NZ	2.28	0.66
1:L5:4378:C:OP1	5:LB:103:LYS:NZ	2.28	0.66
46:S2:1680:A:H2'	53:SF:60:ARG:HD2	1.77	0.66
1:L5:3346:G:O2'	1:L5:3475:U:OP2	2.14	0.66
25:LW:1:MET:HE2	25:LW:15:PRO:HB3	1.76	0.66
46:S2:52:G:N2	46:S2:489:U:O2'	2.29	0.66
46:S2:522:A:OP1	57:SJ:45:ARG:NH1	2.27	0.66
62:SP:29:SER:OG	62:SP:31:GLU:OE2	2.12	0.66
1:L5:1669:U:OP1	12:LI:4:ARG:NH2	2.27	0.66
16:LN:46:ASP:OD1	16:LN:47:LYS:N	2.29	0.66
47:S7:11:G:O6	47:S7:45:G:N2	2.26	0.66
58:SK:92:ALA:HB1	58:SK:96:ARG:HH21	1.61	0.66
78:Sg:82:SER:OG	78:Sg:84:ASP:OD1	2.13	0.66
46:S2:875:G:H2'	46:S2:876:A:H8	1.61	0.66
52:SE:63:LYS:O	52:SE:67:GLN:NE2	2.29	0.66
52:SE:251:GLU:OE1	52:SE:251:GLU:N	2.27	0.66
46:S2:530:A:N6	46:S2:531:U:O2	2.28	0.66
52:SE:40:GLU:N	52:SE:40:GLU:OE1	2.27	0.66
52:SE:104:ASP:OD1	52:SE:105:THR:N	2.29	0.66
1:L5:828:C:H3'	1:L5:829:G:H21	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1605:A:H5''	1:L5:1606:G:H5'	1.77	0.66
1:L5:2599:A:N6	1:L5:3500:C:H42	1.93	0.66
5:LB:224:LYS:HG3	5:LB:340:THR:HG22	1.77	0.66
13:LJ:35:ARG:NH1	13:LJ:122:SER:O	2.28	0.65
46:S2:1537:G:H2'	46:S2:1538:A:C8	2.30	0.65
46:S2:1611:G:OP1	65:SS:121:ARG:NH1	2.29	0.65
1:L5:2301:G:H5''	1:L5:2303:G:H5''	1.77	0.65
11:LH:44:GLU:HB3	11:LH:58:ASP:HB2	1.79	0.65
46:S2:47:G:H22	46:S2:479:G:H22	1.44	0.65
78:Sg:73:SER:HB3	78:Sg:117:ASN:HD21	1.60	0.65
78:Sg:216:ALA:N	78:Sg:230:LEU:O	2.29	0.65
3:L8:8:U:H2'	3:L8:9:A:H8	1.60	0.65
3:L8:155:C:OP2	10:LG:89:ARG:NH1	2.29	0.65
48:SA:34:MET:HG3	48:SA:37:TYR:HD2	1.61	0.65
16:LN:68:ARG:NH1	16:LN:124:ASP:O	2.26	0.65
46:S2:1262:C:O2	76:Sd:10:HIS:NE2	2.28	0.65
47:S7:25:U:H3	47:S7:45:G:H1	1.44	0.65
65:SS:60:THR:OG1	65:SS:62:ASP:OD1	2.13	0.65
13:LJ:163:MET:O	13:LJ:167:GLN:NE2	2.29	0.65
50:SC:268:GLU:OE2	50:SC:268:GLU:N	2.25	0.65
63:SQ:58:LEU:HD11	63:SQ:112:LEU:HD21	1.78	0.65
46:S2:381:G:OP1	56:SI:56:ARG:NH2	2.30	0.65
66:ST:134:ILE:H	66:ST:134:ILE:HD12	1.62	0.65
75:Sc:15:THR:OG1	75:Sc:31:ARG:O	2.13	0.65
39:Lk:23:VAL:HG22	39:Lk:36:VAL:HG22	1.79	0.65
46:S2:1277:A:O2'	58:SK:50:GLN:NE2	2.29	0.65
63:SQ:116:ASP:HB3	63:SQ:119:LEU:HD23	1.79	0.65
1:L5:3422:G:O2'	1:L5:3424:C:N4	2.30	0.64
46:S2:152:U:N3	46:S2:167:G:N1	2.45	0.64
54:SG:7:PHE:HB2	54:SG:113:ILE:HD12	1.77	0.64
1:L5:4395:A:O2'	1:L5:4397:G:OP1	2.14	0.64
5:LB:224:LYS:O	5:LB:274:TYR:N	2.28	0.64
1:L5:1179:U:OP2	14:LL:36:ARG:NH2	2.28	0.64
5:LB:300:LYS:HG2	5:LB:311:ASP:HA	1.78	0.64
46:S2:171:A:O2'	46:S2:173:A:N7	2.28	0.64
60:SN:15:ALA:HA	74:Sb:26:GLN:HE21	1.61	0.64
78:Sg:192:THR:OG1	78:Sg:213:ASP:OD2	2.15	0.64
11:LH:95:VAL:HG22	41:Lm:82:LEU:HD22	1.79	0.64
1:L5:2602:G:O2'	1:L5:3495:U:O4	2.15	0.64
8:LE:149:ARG:NH2	8:LE:199:GLN:O	2.31	0.64
34:Lf:63:LYS:NZ	34:Lf:64:PRO:O	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2586:A:H2'	1:L5:2587:A:C8	2.32	0.64
71:SY:102:THR:HG22	71:SY:103:SER:H	1.62	0.64
1:L5:3885:U:O4	43:Lo:8:ARG:NH2	2.31	0.64
1:L5:4323:C:O2'	1:L5:4325:A:OP2	2.14	0.64
37:Li:66:ASP:OD1	37:Li:67:LYS:N	2.30	0.64
65:SS:67:VAL:HA	65:SS:70:ILE:HD12	1.80	0.64
72:SZ:99:LEU:HD21	72:SZ:102:LYS:HB2	1.80	0.64
46:S2:225:C:HO2'	46:S2:226:A:H8	1.44	0.64
49:SB:38:MET:SD	49:SB:38:MET:N	2.69	0.64
1:L5:494:G:H22	1:L5:668:G:H22	1.45	0.63
57:SJ:110:LEU:HD22	57:SJ:147:PHE:HB3	1.79	0.63
46:S2:182:C:H5'	46:S2:183:G:C2	2.33	0.63
63:SQ:98:LYS:HZ1	78:Sg:59:LEU:HD13	1.62	0.63
46:S2:53:C:N4	46:S2:473:C:N4	2.45	0.63
46:S2:1093:G:H4'	69:SW:2:VAL:HG23	1.79	0.63
46:S2:1316:U:H2'	46:S2:1317:C:C6	2.33	0.63
5:LB:115:LYS:NZ	5:LB:129:ALA:O	2.32	0.63
32:Ld:84:ILE:HD11	32:Ld:108:TYR:HE1	1.63	0.63
1:L5:1213:A:N1	1:L5:1233:G:O2'	2.32	0.63
1:L5:3466:G:OP2	1:L5:3466:G:N2	2.29	0.63
8:LE:252:GLU:OE1	8:LE:252:GLU:N	2.24	0.63
46:S2:106:C:H2'	46:S2:107:A:H8	1.63	0.63
46:S2:636:G:OP1	77:Se:95:LYS:NZ	2.27	0.63
53:SF:68:ILE:HD11	53:SF:151:ILE:HD11	1.80	0.63
3:L8:1:C:O5'	3:L8:2:G:N2	2.31	0.63
39:Lk:51:GLU:N	39:Lk:51:GLU:OE1	2.32	0.63
54:SG:57:ASP:OD1	54:SG:58:LYS:N	2.30	0.63
1:L5:1355:U:H3	1:L5:1432:G:H1	1.46	0.63
33:Le:89:LEU:HD13	33:Le:118:LEU:HD22	1.80	0.63
46:S2:800:U:OP2	46:S2:868:G:N2	2.32	0.63
1:L5:1003:G:O6	1:L5:1024:C:N4	2.31	0.63
1:L5:1562:G:H22	1:L5:1576:U:H3	1.45	0.63
47:S6:25:U:H2'	47:S6:26:G:H8	1.64	0.63
71:SY:30:PRO:HD2	71:SY:31:GLY:H	1.64	0.63
12:LI:180:GLU:OE1	12:LI:180:GLU:N	2.32	0.63
46:S2:126:G:H8	54:SG:195:LYS:HB2	1.64	0.63
46:S2:588:A:O2'	46:S2:589:G:N2	2.31	0.63
46:S2:832:G:H2'	46:S2:833:G:H8	1.64	0.62
1:L5:508:G:H1	1:L5:661:U:H3	1.46	0.62
1:L5:1582:U:H2'	1:L5:1583:A:H8	1.64	0.62
1:L5:1891:A:OP2	19:LQ:37:ARG:NH2	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:451:C:OP1	52:SE:3:ARG:NH1	2.32	0.62
52:SE:92:ILE:HD13	52:SE:97:GLU:HB2	1.81	0.62
63:SQ:55:VAL:HA	63:SQ:63:PHE:HE2	1.64	0.62
1:L5:1564:G:H1	1:L5:1575:C:H1'	1.64	0.62
13:LJ:144:LYS:O	13:LJ:148:THR:OG1	2.17	0.62
46:S2:536:G:H2'	46:S2:538:C:H1'	1.81	0.62
46:S2:157:U:O2'	46:S2:158:A:N7	2.30	0.62
68:SV:53:TYR:CD2	68:SV:72:LEU:HD23	2.34	0.62
1:L5:4247:U:H2'	1:L5:4248:G:H8	1.64	0.62
13:LJ:91:GLU:OE1	62:SP:12:PHE:N	2.33	0.62
47:S7:54:A:N6	47:S7:58:A:C2	2.68	0.62
59:SL:10:TYR:HD2	59:SL:12:LYS:HD3	1.65	0.62
1:L5:1013:C:OP1	1:L5:1015:C:N4	2.33	0.62
46:S2:40:A:H3'	46:S2:487:A:H62	1.64	0.62
22:LT:115:LYS:HD2	22:LT:126:VAL:HG21	1.81	0.62
24:LV:27:ASN:OD1	24:LV:28:CYS:N	2.33	0.62
46:S2:869:G:N2	46:S2:869:G:OP2	2.33	0.62
46:S2:1855:U:H2'	46:S2:1856:G:H8	1.64	0.62
48:SA:7:VAL:O	48:SA:11:LYS:NZ	2.28	0.62
1:L5:498:G:H2'	1:L5:499:G:H8	1.65	0.62
13:LJ:32:ARG:NH1	13:LJ:126:TYR:OH	2.32	0.62
51:SD:62:LYS:O	51:SD:67:ARG:NH2	2.33	0.62
1:L5:1910:G:C2	1:L5:1911:G:H5''	2.34	0.62
4:LA:147:ARG:HH22	46:S2:950:G:H4'	1.65	0.62
1:L5:3815:C:H5	10:LG:73:ARG:HH12	1.48	0.61
1:L5:4553:G:H2'	1:L5:4554:G:C8	2.35	0.61
51:SD:51:LEU:HD23	51:SD:89:GLU:HB3	1.81	0.61
64:SR:126:MET:HB3	64:SR:128:PHE:HE1	1.65	0.61
1:L5:687:C:OP1	45:Lr:84:LYS:NZ	2.29	0.61
1:L5:4581:C:H2'	1:L5:4582:G:C8	2.36	0.61
15:LM:124:LYS:O	15:LM:128:LYS:NZ	2.32	0.61
46:S2:840:C:H2'	46:S2:841:C:C5	2.36	0.61
57:SJ:109:ARG:NH2	57:SJ:111:GLN:OE1	2.29	0.61
62:SP:29:SER:OG	62:SP:32:GLN:NE2	2.33	0.61
1:L5:1218:C:H2'	1:L5:1219:C:C6	2.35	0.61
46:S2:1425:G:H2'	46:S2:1426:G:C8	2.35	0.61
63:SQ:40:GLU:O	63:SQ:48:GLN:NE2	2.26	0.61
1:L5:1730:U:OP1	1:L5:1752:U:O2'	2.18	0.61
1:L5:4640:G:H2'	1:L5:4641:G:C8	2.35	0.61
46:S2:176:U:N3	46:S2:314:A:N6	2.41	0.61
67:SU:82:MET:HE2	67:SU:82:MET:HA	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:290:U:O2'	16:LN:182:HIS:NE2	2.33	0.61
1:L5:3516:G:OP2	18:LP:25:HIS:NE2	2.29	0.61
46:S2:539:U:O2	46:S2:547:G:N2	2.33	0.61
52:SE:11:ARG:NH1	52:SE:24:THR:OG1	2.34	0.61
53:SF:168:THR:HG23	53:SF:171:GLU:H	1.66	0.61
71:SY:41:ARG:HH12	71:SY:57:VAL:H	1.47	0.61
1:L5:267:G:H2'	1:L5:268:G:H8	1.64	0.61
1:L5:840:G:OP1	9:LF:267:ARG:NH2	2.34	0.61
24:LV:83:ARG:NH1	24:LV:120:PRO:O	2.32	0.61
49:SB:110:MET:HE1	49:SB:213:ARG:HD2	1.83	0.61
50:SC:70:VAL:HG21	50:SC:93:ILE:HG23	1.83	0.61
55:SH:171:GLU:OE1	55:SH:171:GLU:N	2.29	0.61
58:SK:49:MET:N	58:SK:49:MET:SD	2.73	0.61
63:SQ:110:ASP:N	63:SQ:110:ASP:OD1	2.33	0.61
1:L5:121:A:OP1	10:LG:110:LYS:NZ	2.28	0.61
5:LB:156:TYR:O	5:LB:158:GLN:NE2	2.34	0.61
11:LH:8:GLN:HE22	11:LH:70:VAL:HG23	1.66	0.61
46:S2:317:G:H2'	46:S2:318:C:C6	2.36	0.61
46:S2:1067:U:OP2	61:SO:143:LYS:NZ	2.31	0.61
47:S7:58:A:H5'	47:S7:60:A:N7	2.15	0.61
12:LI:48:LEU:HD21	12:LI:145:LYS:HG3	1.83	0.61
46:S2:830:C:O2'	46:S2:846:G:N3	2.34	0.61
67:SU:24:LEU:HB3	67:SU:32:LEU:HD11	1.83	0.61
1:L5:407:A:O2'	1:L5:410:G:OP2	2.13	0.60
5:LB:83:PRO:O	5:LB:167:GLN:NE2	2.28	0.60
11:LH:17:GLU:HG2	11:LH:27:VAL:HG22	1.82	0.60
1:L5:3366:U:H3	1:L5:3368:A:H62	1.49	0.60
17:LO:27:VAL:O	17:LO:101:ARG:NH1	2.34	0.60
2:L7:3:C:H2'	2:L7:4:U:C6	2.35	0.60
13:LJ:18:ARG:HB2	13:LJ:133:VAL:HG23	1.82	0.60
46:S2:66:G:O4'	46:S2:83:A:N6	2.35	0.60
46:S2:1417:C:O3'	66:ST:3:GLY:N	2.33	0.60
50:SC:77:SER:OG	50:SC:79:GLU:OE1	2.14	0.60
62:SP:74:GLU:N	62:SP:74:GLU:OE1	2.33	0.60
1:L5:102:G:HO2'	1:L5:1196:U:HO2'	1.50	0.60
1:L5:1012:U:O2'	1:L5:1015:C:N4	2.34	0.60
4:LA:30:ARG:O	4:LA:163:ARG:NH2	2.29	0.60
46:S2:1392:C:H4'	76:Sd:55:LEU:HD21	1.83	0.60
59:SL:33:LEU:HD12	59:SL:34:PRO:HD2	1.81	0.60
72:SZ:102:LYS:HA	72:SZ:107:VAL:HG12	1.83	0.60
22:LT:94:GLU:N	22:LT:94:GLU:OE1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1798:U:H2'	46:S2:1799:C:C6	2.36	0.60
58:SK:31:LYS:HD3	58:SK:39:ASN:HA	1.84	0.60
63:SQ:62:ARG:O	63:SQ:96:TYR:OH	2.20	0.60
78:Sg:212:LYS:HA	78:Sg:235:ILE:HG23	1.82	0.60
46:S2:499:C:H2'	46:S2:500:G:C8	2.35	0.60
46:S2:863:A:C8	69:SW:107:SER:HA	2.37	0.60
46:S2:929:G:H2'	46:S2:930:G:C8	2.36	0.60
46:S2:1280:C:H2'	46:S2:1281:G:C8	2.36	0.60
47:S6:33:C:OP2	63:SQ:146:ARG:NH2	2.30	0.60
46:S2:499:C:H2'	46:S2:500:G:H8	1.66	0.60
46:S2:1131:G:OP2	46:S2:1131:G:N2	2.35	0.60
55:SH:144:ILE:HG23	55:SH:154:ILE:HG22	1.82	0.60
1:L5:307:G:OP2	1:L5:307:G:N2	2.24	0.60
1:L5:4280:U:H4'	5:LB:373:LYS:HE2	1.83	0.60
56:SI:37:LYS:HB2	56:SI:59:ARG:HG2	1.84	0.60
58:SK:32:HIS:HB3	58:SK:35:LEU:HD23	1.84	0.60
74:Sb:33:MET:HE2	74:Sb:48:SER:HA	1.83	0.60
1:L5:3574:A:H2'	1:L5:3575:G:H8	1.67	0.60
46:S2:918:U:H2'	46:S2:919:U:C6	2.37	0.60
46:S2:1308:U:O2'	46:S2:1309:U:O4'	2.20	0.60
51:SD:74:GLN:NE2	51:SD:79:PHE:O	2.34	0.60
56:SI:116:HIS:O	56:SI:152:ARG:NH1	2.34	0.60
43:Lo:2:VAL:N	43:Lo:90:HIS:O	2.35	0.60
46:S2:1411:C:O2'	46:S2:1412:G:O5'	2.18	0.60
64:SR:22:THR:HG23	64:SR:23:ARG:HG3	1.84	0.60
67:SU:65:THR:HG22	67:SU:66:ARG:H	1.66	0.60
1:L5:386:G:O2'	1:L5:411:G:O6	2.15	0.59
46:S2:47:G:H22	46:S2:479:G:N2	1.99	0.59
46:S2:1777:G:H5'	46:S2:1778:G:N7	2.17	0.59
1:L5:109:G:OP2	14:LL:74:ARG:NH2	2.35	0.59
1:L5:4392:C:OP1	1:L5:4394:A:N6	2.36	0.59
5:LB:206:PRO:HG2	5:LB:209:GLN:HG3	1.84	0.59
13:LJ:158:SER:OG	13:LJ:161:GLU:OE1	2.18	0.59
46:S2:751:C:H42	46:S2:795:A:H1'	1.67	0.59
1:L5:176:G:OP1	36:Lh:101:LYS:NZ	2.35	0.59
1:L5:1910:G:H3'	1:L5:1911:G:H5'	0.74	0.59
7:LD:82:GLU:OE1	7:LD:82:GLU:N	2.36	0.59
13:LJ:56:THR:HG22	13:LJ:63:ARG:HA	1.83	0.59
46:S2:1553:G:N2	76:Sd:32:ARG:O	2.35	0.59
1:L5:1553:G:OP1	12:LI:39:LYS:NZ	2.29	0.59
1:L5:2586:A:H2'	1:L5:2587:A:H8	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:8:U:H2'	3:L8:9:A:C8	2.37	0.59
9:LF:120:ILE:O	9:LF:120:ILE:HD12	2.03	0.59
7:LD:226:TYR:O	7:LD:228:LYS:N	2.36	0.59
19:LQ:147:GLU:OE1	19:LQ:151:HIS:NE2	2.35	0.59
46:S2:158:A:H5'	46:S2:465:A:C6	2.37	0.59
46:S2:353:U:O2	59:SL:71:ARG:NH1	2.36	0.59
46:S2:564:G:H2'	46:S2:565:A:C8	2.37	0.59
1:L5:270:C:H2'	1:L5:271:U:O2	2.03	0.59
1:L5:477:G:OP1	45:Lr:66:ARG:NH2	2.35	0.59
33:Le:78:LEU:HD23	33:Le:98:GLU:HB3	1.85	0.59
56:SI:3:ILE:O	56:SI:30:GLY:N	2.35	0.59
33:Le:69:MET:SD	33:Le:75:ARG:NH1	2.75	0.59
46:S2:1680:A:OP1	53:SF:60:ARG:NH2	2.35	0.59
24:LV:134:SER:OG	24:LV:135:ASN:OD1	2.21	0.59
68:SV:51:LYS:HA	68:SV:51:LYS:HE3	1.84	0.59
6:LC:150:LEU:HB3	6:LC:151:PRO:HD3	1.84	0.59
39:Lk:6:GLU:OE1	39:Lk:6:GLU:N	2.35	0.59
47:S7:11:G:C6	47:S7:45:G:N2	2.71	0.59
46:S2:660:G:HO2'	46:S2:663:G:HO2'	1.47	0.59
52:SE:126:VAL:HG22	52:SE:158:ASP:H	1.67	0.59
1:L5:260:G:H2'	1:L5:261:G:H8	1.68	0.58
46:S2:442:C:H2'	46:S2:443:C:C6	2.38	0.58
46:S2:575:A:H4'	71:SY:89:HIS:HB2	1.85	0.58
46:S2:1600:U:H3'	72:SZ:44:LEU:HD23	1.84	0.58
49:SB:85:LYS:HB2	49:SB:101:HIS:HB3	1.83	0.58
1:L5:4194:G:N2	1:L5:4197:A:OP2	2.31	0.58
1:L5:4639:U:H2'	1:L5:4640:G:C8	2.39	0.58
46:S2:144:U:H2'	46:S2:145:G:C8	2.38	0.58
48:SA:10:MET:HB3	64:SR:111:PHE:HE2	1.67	0.58
78:Sg:70:VAL:HG12	78:Sg:113:PHE:HD2	1.66	0.58
5:LB:4:ARG:NH2	5:LB:6:PHE:O	2.35	0.58
23:LU:44:GLN:OE1	23:LU:44:GLN:N	2.32	0.58
46:S2:339:G:H2'	46:S2:340:A:O4'	2.03	0.58
46:S2:1629:C:H2'	46:S2:1630:C:H6	1.69	0.58
52:SE:80:ILE:HG23	52:SE:81:THR:HG23	1.84	0.58
67:SU:22:ILE:HG22	67:SU:114:VAL:HG12	1.85	0.58
1:L5:4283:G:OP1	25:LW:19:ARG:NH1	2.36	0.58
8:LE:257:ASP:N	8:LE:257:ASP:OD1	2.35	0.58
40:Ll:23:ILE:HG23	40:Ll:38:ASN:HB2	1.86	0.58
1:L5:4233:U:O2'	5:LB:182:GLU:OE2	2.15	0.58
2:L7:27:G:N7	7:LD:58:ARG:NH2	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB:80:GLU:OE1	5:LB:323:TYR:OH	2.19	0.58
29:La:137:ILE:HG22	29:La:142:GLY:HA3	1.85	0.58
46:S2:52:G:H2'	46:S2:53:C:C6	2.38	0.58
46:S2:434:A:H2'	46:S2:435:G:C8	2.38	0.58
46:S2:1115:U:O2'	46:S2:1116:U:O5'	2.21	0.58
51:SD:150:MET:SD	51:SD:151:LYS:N	2.76	0.58
1:L5:1418:G:H2'	1:L5:1419:G:C8	2.38	0.58
46:S2:67:C:OP2	46:S2:68:A:N6	2.33	0.58
46:S2:1418:C:C4	46:S2:1422:A:C6	2.91	0.58
1:L5:2314:G:H1	1:L5:2324:G:H1	1.52	0.58
1:L5:4639:U:H2'	1:L5:4640:G:H8	1.69	0.58
16:LN:44:ARG:NH1	16:LN:120:TRP:O	2.35	0.58
46:S2:1275:G:H5''	46:S2:1277:A:H5''	1.84	0.58
46:S2:1417:C:O5'	66:ST:129:ARG:NH1	2.36	0.58
46:S2:1556:U:N3	76:Sd:19:ARG:HA	2.19	0.58
58:SK:28:HIS:ND1	58:SK:28:HIS:O	2.33	0.58
1:L5:1562:G:H1	1:L5:1576:U:H3	1.50	0.58
46:S2:847:G:H2'	52:SE:108:ARG:HD3	1.86	0.58
46:S2:1428:C:O2'	46:S2:1430:G:OP1	2.21	0.58
1:L5:1510:C:H2'	1:L5:1511:G:C8	2.38	0.58
1:L5:3806:C:H2'	1:L5:3807:G:H8	1.67	0.58
2:L7:52:C:O2'	2:L7:53:U:OP1	2.21	0.58
37:Li:63:VAL:HG12	37:Li:65:LYS:HG3	1.85	0.58
1:L5:4399:G:H1	1:L5:4603:A:H62	1.50	0.58
1:L5:4594:U:HO2'	34:Lf:2:SER:N	2.02	0.58
12:LI:146:GLU:OE2	12:LI:146:GLU:N	2.35	0.58
46:S2:67:C:H41	54:SG:164:LYS:HG3	1.68	0.58
46:S2:1746:A:O3'	54:SG:31:ARG:NH1	2.37	0.58
51:SD:37:VAL:HG23	51:SD:50:ILE:HG22	1.86	0.58
46:S2:535:G:H2'	46:S2:536:G:C8	2.38	0.57
54:SG:67:VAL:HG12	54:SG:69:THR:HG22	1.85	0.57
55:SH:148:LEU:HA	69:SW:42:MET:HE1	1.85	0.57
74:Sb:67:THR:HG22	74:Sb:69:GLY:H	1.68	0.57
1:L5:3536:G:O2'	1:L5:3538:G:OP2	2.20	0.57
46:S2:876:A:H1'	55:SH:114:GLN:HE21	1.69	0.57
1:L5:4552:C:H2'	1:L5:4553:G:H4'	1.85	0.57
49:SB:174:ARG:NH1	49:SB:175:GLU:OE1	2.36	0.57
67:SU:94:PRO:HD2	67:SU:97:ILE:HD13	1.85	0.57
1:L5:1009:C:H42	1:L5:1017:A:N6	2.03	0.57
10:LG:156:VAL:O	10:LG:201:THR:OG1	2.21	0.57
46:S2:1555:C:H2'	46:S2:1556:U:C5	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1781:G:H3'	46:S2:1782:A:H4'	1.87	0.57
1:L5:2163:G:OP1	38:Lj:14:LYS:NZ	2.35	0.57
1:L5:3933:A:N6	7:LD:28:THR:O	2.36	0.57
50:SC:161:SER:O	50:SC:161:SER:OG	2.20	0.57
52:SE:246:LEU:HD21	52:SE:254:LYS:HG3	1.87	0.57
58:SK:14:LEU:HD11	58:SK:35:LEU:HD11	1.86	0.57
78:Sg:88:ARG:HB2	78:Sg:90:TRP:HE1	1.69	0.57
78:Sg:111:VAL:HG12	78:Sg:122:SER:HA	1.85	0.57
1:L5:1010:U:H3	1:L5:1013:C:HO2'	1.52	0.57
46:S2:47:G:H1	46:S2:479:G:H22	1.53	0.57
22:LT:88:ARG:NH1	30:Lb:33:LYS:O	2.37	0.57
66:ST:50:GLU:OE1	66:ST:50:GLU:N	2.38	0.57
46:S2:594:C:H3'	46:S2:595:A:H4'	1.87	0.57
6:LC:303:ARG:O	19:LQ:38:ARG:NH2	2.28	0.57
15:LM:39:ASP:O	15:LM:41:PRO:HD3	2.05	0.57
46:S2:1745:G:O2'	46:S2:1791:A:N6	2.37	0.57
1:L5:1391:G:OP1	44:Lp:17:ARG:NH2	2.27	0.57
2:L7:12:U:OP2	2:L7:67:C:O2'	2.23	0.57
57:SJ:128:VAL:O	57:SJ:132:GLN:NE2	2.38	0.57
60:SN:89:TYR:HE1	60:SN:150:VAL:HG23	1.69	0.57
1:L5:2194:C:H42	26:LX:89:LYS:HE3	1.69	0.56
46:S2:66:G:OP1	46:S2:82:G:N2	2.34	0.56
46:S2:106:C:H2'	46:S2:107:A:C8	2.39	0.56
70:SX:71:ARG:HH21	70:SX:80:LYS:HZ3	1.53	0.56
2:L7:92:C:H2'	2:L7:93:G:H8	1.69	0.56
46:S2:313:G:H22	46:S2:337:A:H61	1.53	0.56
56:SI:56:ARG:NH1	56:SI:180:GLY:O	2.38	0.56
63:SQ:83:ALA:HA	63:SQ:86:GLN:HE21	1.69	0.56
64:SR:126:MET:HB3	64:SR:128:PHE:CE1	2.39	0.56
1:L5:299:A:H2'	1:L5:300:G:H8	1.68	0.56
1:L5:3326:G:N2	1:L5:3329:G:OP2	2.39	0.56
3:L8:102:G:OP2	3:L8:104:A:O2'	2.19	0.56
24:LV:84:GLN:NE2	24:LV:86:LYS:O	2.35	0.56
46:S2:147:A:H2'	46:S2:148:U:C6	2.40	0.56
46:S2:942:C:H2'	46:S2:943:G:H8	1.71	0.56
46:S2:1715:U:H2'	46:S2:1716:A:H8	1.70	0.56
48:SA:90:PHE:O	48:SA:94:THR:OG1	2.20	0.56
49:SB:179:ASN:HD22	49:SB:183:GLU:HB3	1.71	0.56
51:SD:70:THR:HB	51:SD:86:LEU:HD23	1.86	0.56
61:SO:87:GLU:H	61:SO:87:GLU:CD	2.14	0.56
63:SQ:83:ALA:O	63:SQ:86:GLN:NE2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SU:25:THR:HG22	67:SU:86:LYS:HG3	1.87	0.56
1:L5:4247:U:H2'	1:L5:4248:G:C8	2.40	0.56
20:LR:105:LEU:HD23	20:LR:138:LEU:HD23	1.87	0.56
46:S2:223:A:H2'	46:S2:224:U:H6	1.70	0.56
46:S2:1446:U:O4	46:S2:1447:A:N6	2.39	0.56
78:Sg:238:ALA:H	78:Sg:251:ALA:HB3	1.71	0.56
1:L5:672:G:N7	1:L5:673:C:N4	2.53	0.56
1:L5:3788:C:H1'	1:L5:3789:C:H5''	1.87	0.56
5:LB:261:ARG:HB2	17:LO:64:THR:HG21	1.86	0.56
22:LT:107:LYS:HA	22:LT:110:LYS:HE3	1.88	0.56
46:S2:72:C:O2'	46:S2:74:G:N2	2.23	0.56
46:S2:152:U:O2	46:S2:153:G:N2	2.39	0.56
46:S2:475:G:H8	46:S2:476:C:H5''	1.70	0.56
46:S2:540:C:H2'	46:S2:541:U:H5	1.71	0.56
46:S2:589:G:H4'	46:S2:590:G:H5'	1.87	0.56
65:SS:89:ASP:HB2	65:SS:93:GLY:H	1.70	0.56
1:L5:3412:G:H2'	1:L5:3413:A:H8	1.71	0.56
5:LB:224:LYS:HB3	5:LB:226:LYS:HE3	1.88	0.56
8:LE:161:LEU:HD11	8:LE:203:ILE:HG13	1.87	0.56
9:LF:197:ILE:HD12	9:LF:209:MET:HB2	1.87	0.56
21:LS:9:GLU:HB3	21:LS:67:VAL:HB	1.87	0.56
46:S2:446:A:H5''	56:SI:47:ARG:HH21	1.69	0.56
1:L5:1332:A:OP1	29:La:27:LYS:NZ	2.29	0.56
1:L5:3806:C:H2'	1:L5:3807:G:C8	2.41	0.56
7:LD:152:ARG:O	7:LD:157:ASN:ND2	2.38	0.56
46:S2:58:C:N4	46:S2:62:G:N7	2.53	0.56
53:SF:49:LEU:HD12	63:SQ:50:LYS:HG3	1.88	0.56
55:SH:25:GLN:O	55:SH:29:GLU:N	2.34	0.56
57:SJ:88:ASP:HB3	57:SJ:91:LYS:HD2	1.88	0.56
1:L5:753:G:O2'	1:L5:754:A:OP1	2.24	0.56
1:L5:4561:G:H2'	1:L5:4562:G:C8	2.41	0.56
6:LC:92:PHE:O	6:LC:100:ARG:NH2	2.39	0.56
9:LF:120:ILE:HG21	19:LQ:4:ASP:HB2	1.87	0.56
46:S2:589:G:N2	46:S2:589:G:OP2	2.35	0.56
46:S2:943:G:H2'	46:S2:944:U:C6	2.40	0.56
46:S2:1406:A:H61	46:S2:1441:C:H42	1.53	0.56
64:SR:116:ASN:OD1	64:SR:117:LEU:N	2.38	0.56
78:Sg:11:LEU:HB2	78:Sg:307:VAL:HB	1.88	0.56
1:L5:1008:A:H3'	1:L5:1009:C:H5''	1.87	0.56
46:S2:104:A:H62	46:S2:357:C:H5	1.54	0.56
51:SD:27:ARG:NH1	58:SK:62:PHE:O	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:477:G:H2'	1:L5:478:G:H8	1.70	0.55
1:L5:3891:G:H2'	1:L5:3892:A:H8	1.71	0.55
1:L5:4239:G:O6	1:L5:4370:A:N6	2.39	0.55
14:LL:87:HIS:HB3	14:LL:90:VAL:HG23	1.88	0.55
46:S2:1736:A:H2	46:S2:1800:G:H21	1.52	0.55
63:SQ:31:LEU:HB3	63:SQ:67:ASP:OD1	2.06	0.55
63:SQ:101:ASP:O	63:SQ:104:SER:OG	2.22	0.55
70:SX:68:LYS:HB3	70:SX:91:LEU:HD22	1.87	0.55
1:L5:2314:G:H22	1:L5:2324:G:N2	2.01	0.55
1:L5:4333:G:H2'	1:L5:4334:A:C8	2.41	0.55
11:LH:8:GLN:N	11:LH:8:GLN:OE1	2.39	0.55
46:S2:848:A:OP1	52:SE:108:ARG:NH1	2.39	0.55
46:S2:1276:G:O4'	46:S2:1507:A:N6	2.38	0.55
63:SQ:14:GLY:HA3	63:SQ:86:GLN:HE22	1.71	0.55
1:L5:417:A:C2	3:L8:17:A:H1'	2.41	0.55
1:L5:2333:G:N2	1:L5:2336:A:OP2	2.29	0.55
46:S2:318:C:H2'	46:S2:319:A:C4	2.40	0.55
46:S2:1589:A:H2'	46:S2:1590:A:C8	2.40	0.55
1:L5:953:C:H2'	1:L5:954:G:C8	2.41	0.55
1:L5:4171:A:OP2	5:LB:258:HIS:HB2	2.07	0.55
40:L1:28:GLN:HA	40:L1:33:ASN:HD22	1.71	0.55
47:S6:53:G:O2'	47:S6:54:A:OP1	2.23	0.55
1:L5:2168:C:H2'	1:L5:2169:A:H8	1.71	0.55
1:L5:4512:C:H2'	1:L5:4513:G:H8	1.71	0.55
38:Lj:2:THR:O	38:Lj:7:SER:OG	2.23	0.55
46:S2:54:A:H1'	46:S2:476:C:C5	2.40	0.55
46:S2:569:C:H1'	46:S2:584:A:N6	2.22	0.55
46:S2:642:A:OP2	77:Se:108:ARG:NH2	2.39	0.55
46:S2:982:A:H2'	46:S2:983:G:C8	2.41	0.55
51:SD:29:LEU:HD12	51:SD:34:TYR:HD2	1.72	0.55
70:SX:128:VAL:HG13	70:SX:129:SER:H	1.71	0.55
1:L5:2221:C:HO2'	1:L5:2222:C:H6	1.51	0.55
7:LD:232:THR:O	7:LD:234:ASP:N	2.32	0.55
15:LM:12:VAL:O	15:LM:58:THR:OG1	2.25	0.55
46:S2:34:U:H2'	46:S2:35:C:C6	2.41	0.55
46:S2:305:C:OP1	56:SI:75:LYS:NZ	2.38	0.55
46:S2:1011:G:H2'	46:S2:1012:A:H8	1.72	0.55
46:S2:1241:A:N1	62:SP:100:LYS:HB2	2.22	0.55
46:S2:1735:G:H21	46:S2:1801:A:H62	1.55	0.55
58:SK:12:TYR:HB3	58:SK:83:LEU:HD11	1.89	0.55
71:SY:121:ALA:O	71:SY:125:VAL:N	2.29	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:62:A:N3	1:L5:77:U:O2'	2.33	0.55
15:LM:40:GLY:HA3	15:LM:45:VAL:HB	1.88	0.55
52:SE:197:ASN:OD1	52:SE:198:ARG:N	2.39	0.55
1:L5:2378:G:H2'	1:L5:2379:U:C6	2.42	0.55
1:L5:4654:U:O2'	1:L5:4688:U:O2	2.25	0.55
20:LR:136:ARG:HA	20:LR:139:MET:HE2	1.89	0.55
46:S2:1229:A:H2'	46:S2:1230:G:C8	2.42	0.55
49:SB:36:PRO:HB2	49:SB:38:MET:SD	2.46	0.55
52:SE:106:LYS:HE3	52:SE:108:ARG:HH22	1.71	0.55
71:SY:27:VAL:HB	71:SY:69:THR:HB	1.89	0.55
72:SZ:90:GLU:OE1	72:SZ:94:LYS:NZ	2.40	0.55
1:L5:102:G:O2'	1:L5:1196:U:O2'	2.23	0.55
10:LG:208:ASN:HB3	10:LG:210:GLU:OE2	2.07	0.55
63:SQ:34:VAL:HG12	63:SQ:70:VAL:HB	1.88	0.55
1:L5:4125:G:O2'	41:Lm:100:TYR:O	2.24	0.54
2:L7:3:C:H2'	2:L7:4:U:H6	1.72	0.54
8:LE:186:PRO:HB2	8:LE:189:ILE:HG13	1.90	0.54
9:LF:116:ARG:NH1	9:LF:136:LEU:O	2.39	0.54
17:LO:105:LEU:HD13	17:LO:109:PRO:HG2	1.89	0.54
46:S2:570:A:H2'	46:S2:571:C:C6	2.41	0.54
1:L5:1024:C:H2'	1:L5:1025:C:C6	2.41	0.54
1:L5:1530:U:OP1	9:LF:153:ASN:ND2	2.40	0.54
1:L5:4573:G:N2	1:L5:4573:G:OP2	2.40	0.54
9:LF:176:ILE:HG22	9:LF:209:MET:HE3	1.89	0.54
46:S2:614:G:N1	46:S2:630:A:OP2	2.27	0.54
46:S2:678:G:H21	46:S2:1029:A:H62	1.56	0.54
46:S2:1276:G:N2	46:S2:1507:A:OP2	2.33	0.54
46:S2:1830:G:H1'	46:S2:1851:A:H2	1.72	0.54
50:SC:66:LEU:HD21	50:SC:81:ILE:HG12	1.89	0.54
1:L5:2342:C:OP1	1:L5:2522:C:O2'	2.24	0.54
2:L7:51:G:H21	13:LJ:12:MET:CE	2.16	0.54
46:S2:551:C:H2'	46:S2:552:U:C6	2.42	0.54
54:SG:67:VAL:N	54:SG:100:CYS:SG	2.80	0.54
71:SY:114:MET:H	71:SY:114:MET:HE2	1.71	0.54
1:L5:1331:G:H22	6:LC:103:ALA:HA	1.72	0.54
1:L5:3501:U:H2'	1:L5:3502:A:H8	1.71	0.54
46:S2:389:U:H2'	46:S2:390:A:C8	2.37	0.54
46:S2:455:U:O3'	54:SG:94:ARG:NH1	2.40	0.54
46:S2:1506:U:H4'	46:S2:1509:A:H1'	1.89	0.54
48:SA:126:ASP:HB3	48:SA:129:ALA:HB3	1.90	0.54
1:L5:823:C:O2'	1:L5:824:C:OP1	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1562:G:H3'	1:L5:1563:G:C8	2.43	0.54
1:L5:3325:C:OP1	4:LA:8:GLN:NE2	2.40	0.54
43:Lo:99:ARG:HD3	43:Lo:102:GLN:HB3	1.90	0.54
46:S2:487:A:H1'	46:S2:514:G:C6	2.43	0.54
47:S7:18:G:O2'	47:S7:57:G:N2	2.40	0.54
47:S7:58:A:H4'	47:S7:59:A:H5'	1.89	0.54
1:L5:738:G:OP2	9:LF:98:ARG:NE	2.40	0.54
1:L5:3989:A:H5''	1:L5:3990:C:H5'	1.89	0.54
2:L7:60:G:O2'	2:L7:61:G:OP1	2.25	0.54
46:S2:1415:A:H2'	46:S2:1416:C:H5'	1.90	0.54
57:SJ:124:HIS:HA	77:Se:109:ARG:HH22	1.71	0.54
72:SZ:46:ASN:HA	72:SZ:78:LYS:HG3	1.89	0.54
1:L5:3326:G:H21	1:L5:3329:G:N2	2.06	0.54
1:L5:3595:G:N2	1:L5:3824:C:OP2	2.41	0.54
1:L5:4190:C:H2'	1:L5:4191:G:H8	1.73	0.54
1:L5:4686:A:O2'	1:L5:4687:U:OP1	2.26	0.54
46:S2:80:G:H2'	46:S2:81:U:C6	2.43	0.54
46:S2:1569:C:H2'	46:S2:1570:A:C8	2.43	0.54
78:Sg:213:ASP:HB3	78:Sg:215:GLN:HG2	1.89	0.54
78:Sg:216:ALA:HB3	78:Sg:230:LEU:HB3	1.90	0.54
1:L5:10:A:H2'	1:L5:11:G:C8	2.43	0.54
1:L5:28:C:OP2	16:LN:189:ARG:NH1	2.41	0.54
1:L5:1582:U:H2'	1:L5:1583:A:C8	2.42	0.54
1:L5:3848:G:O2'	1:L5:4095:U:OP1	2.22	0.54
46:S2:1866:C:OP2	73:Sa:5:ARG:NH2	2.33	0.54
48:SA:164:ASN:O	48:SA:165:ASN:ND2	2.41	0.54
11:LH:186:THR:OG1	11:LH:187:VAL:N	2.41	0.54
12:LI:179:ASP:OD1	12:LI:179:ASP:N	2.38	0.54
42:Ln:15:ARG:NH2	46:S2:1184:A:OP1	2.41	0.54
46:S2:81:U:H2'	46:S2:82:G:C8	2.43	0.54
46:S2:1311:U:H2'	46:S2:1312:C:C6	2.42	0.54
48:SA:77:ILE:HG22	48:SA:124:VAL:HA	1.90	0.54
54:SG:28:TYR:O	54:SG:29:GLU:HG3	2.07	0.54
73:Sa:88:SER:OG	73:Sa:89:ARG:N	2.40	0.54
1:L5:3359:A:N3	1:L5:3430:U:O2'	2.40	0.54
1:L5:4216:U:H2'	1:L5:4217:A:H8	1.73	0.54
46:S2:87:U:H3	46:S2:501:A:H2	1.55	0.54
46:S2:1778:G:H2'	46:S2:1779:C:O4'	2.08	0.54
48:SA:140:VAL:HG13	48:SA:142:LEU:HB2	1.89	0.54
51:SD:194:PRO:HG2	51:SD:199:GLY:H	1.73	0.54
59:SL:49:GLU:HG3	59:SL:116:CYS:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sg:59:LEU:HB3	78:Sg:90:TRP:HZ3	1.73	0.54
1:L5:1009:C:H42	1:L5:1017:A:H61	1.55	0.53
1:L5:1221:G:H21	1:L5:1227:G:H1	1.55	0.53
2:L7:4:U:H2'	2:L7:5:A:H8	1.73	0.53
4:LA:181:LYS:HB2	4:LA:184:ARG:HG3	1.90	0.53
24:LV:16:ILE:HD13	24:LV:57:VAL:HG12	1.91	0.53
46:S2:1418:C:C4	46:S2:1422:A:N6	2.76	0.53
67:SU:44:LYS:NZ	67:SU:48:LEU:O	2.40	0.53
1:L5:10:A:H2'	1:L5:11:G:H8	1.73	0.53
1:L5:1260:C:H2'	1:L5:1261:C:C6	2.44	0.53
19:LQ:172:ARG:HA	19:LQ:176:ARG:HD2	1.91	0.53
46:S2:1629:C:H2'	46:S2:1630:C:C6	2.43	0.53
48:SA:6:ASP:HA	48:SA:9:GLN:HG2	1.89	0.53
65:SS:47:LYS:NZ	66:ST:35:ASP:OD2	2.34	0.53
34:Lf:20:ASN:HD22	34:Lf:22:ARG:HH21	1.56	0.53
46:S2:223:A:H2'	46:S2:224:U:C6	2.44	0.53
46:S2:970:U:O2	46:S2:972:G:N1	2.42	0.53
78:Sg:124:SER:OG	78:Sg:126:ASP:OD1	2.22	0.53
1:L5:486:C:O2'	1:L5:487:C:OP1	2.27	0.53
12:LI:143:GLN:OE1	12:LI:143:GLN:N	2.36	0.53
15:LM:70:GLN:HE22	15:LM:74:ARG:HH11	1.56	0.53
46:S2:384:G:H21	59:SL:133:PRO:HG2	1.74	0.53
46:S2:1741:C:H2'	46:S2:1742:U:C6	2.43	0.53
52:SE:87:MET:HE2	52:SE:123:LEU:HB2	1.91	0.53
78:Sg:92:LEU:HD12	78:Sg:93:THR:H	1.74	0.53
1:L5:831:G:N2	1:L5:836:C:H2'	2.23	0.53
1:L5:4506:G:O2'	1:L5:4507:G:H8	1.91	0.53
11:LH:11:ASP:OD1	11:LH:12:ILE:N	2.42	0.53
46:S2:181:A:H2'	46:S2:182:C:C5	2.44	0.53
46:S2:1273:C:H2'	46:S2:1274:C:C6	2.44	0.53
46:S2:1409:U:O4	46:S2:1410:A:N6	2.42	0.53
62:SP:18:ARG:NH1	62:SP:36:LEU:O	2.42	0.53
66:ST:50:GLU:HG2	66:ST:51:ASN:OD1	2.09	0.53
1:L5:1123:C:H2'	1:L5:1124:C:C6	2.43	0.53
28:LZ:76:ASN:OD1	28:LZ:77:TYR:N	2.42	0.53
46:S2:434:A:OP1	56:SI:25:ARG:NH2	2.42	0.53
46:S2:1294:A:N6	46:S2:1303:G:H22	2.06	0.53
46:S2:1728:G:H2'	46:S2:1729:U:C6	2.43	0.53
47:S6:4:C:H2'	47:S6:5:A:C8	2.43	0.53
49:SB:137:LEU:HG	49:SB:215:VAL:HG22	1.90	0.53
52:SE:125:LYS:O	52:SE:142:HIS:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70: SX:61: GLN: HB3	70: SX:62: PRO: HD3	1.90	0.53
1: L5:4532: C: H42	1: L5:4579: C: H42	1.57	0.53
3: L8:141: C: H2'	3: L8:142: U: C6	2.44	0.53
18: LP:40: HIS: NE2	18: LP:110: ASP: O	2.40	0.53
22: LT:143: THR: HG23	22: LT:145: GLY: H	1.74	0.53
46: S2:446: A: H2'	46: S2:447: G: O4'	2.09	0.53
46: S2:494: A: O2'	46: S2:495: C: H5'	2.09	0.53
53: SF:100: ILE: HD11	53: SF:111: VAL: HG11	1.90	0.53
1: L5:1028: G: O2'	1: L5:1029: G: N2	2.42	0.53
46: S2:669: A: H5'	46: S2:670: A: OP2	2.09	0.53
46: S2:922: G: C6	69: SW:28: ARG: HD2	2.44	0.53
46: S2:1421: G: H1'	46: S2:1422: A: H4'	1.91	0.53
54: SG:10: THR: OG1	54: SG:12: CYS: SG	2.66	0.53
55: SH:69: LEU: HD22	55: SH:96: ALA: HB2	1.90	0.53
1: L5:438: G: O2'	34: Lf:23: GLU: HG2	2.08	0.53
1: L5:2169: A: H2'	1: L5:2170: U: C6	2.44	0.53
5: LB:215: GLU: OE2	5: LB:349: LYS: NZ	2.41	0.53
9: LF:127: VAL: HG13	9: LF:158: VAL: HG12	1.91	0.53
46: S2:316: C: H4'	46: S2:317: G: C8	2.43	0.53
46: S2:1104: C: H2'	46: S2:1105: G: H8	1.73	0.53
48: SA:78: SER: O	48: SA:84: GLN: NE2	2.42	0.53
1: L5:1561: G: C8	1: L5:1578: A: H1'	2.44	0.53
1: L5:3389: A: H2'	1: L5:3390: A: C8	2.44	0.53
6: LC:101: MET: SD	6: LC:104: PRO: HA	2.49	0.53
12: LI:62: SER: HA	12: LI:65: LEU: HD12	1.91	0.53
22: LT:137: GLU: OE2	22: LT:137: GLU: N	2.30	0.53
44: Lp:82: ALA: HA	44: Lp:85: ARG: HD3	1.91	0.53
46: S2:660: G: H21	70: SX:17: ARG: NH2	2.07	0.53
46: S2:1256: G: OP1	46: S2:1257: G: O2'	2.18	0.53
46: S2:1407: G: H22	46: S2:1440: A: H2	1.55	0.53
52: SE:6: LYS: HE3	52: SE:30: ARG: HH12	1.73	0.53
63: SQ:28: GLY: HA3	63: SQ:67: ASP: OD2	2.09	0.53
64: SR:27: ASP: O	64: SR:31: ASN: ND2	2.42	0.53
74: Sb:65: GLN: HG3	74: Sb:66: PRO: HD2	1.91	0.53
1: L5:1122: A: H2'	1: L5:1123: C: H6	1.73	0.52
1: L5:4111: C: H2'	1: L5:4112: U: C6	2.44	0.52
15: LM:100: ARG: NH2	17: LO:197: LYS: O	2.38	0.52
35: Lg:82: MET: HE2	35: Lg:86: CYS: HB3	1.91	0.52
36: Lh:104: THR: HG23	36: Lh:107: GLN: H	1.74	0.52
46: S2:126: G: C8	54: SG:195: LYS: HB2	2.44	0.52
46: S2:536: G: N2	46: S2:549: C: O2'	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1662:A:OP1	76:Sd:19:ARG:NH1	2.37	0.52
1:L5:151:G:OP2	16:LN:4:TYR:OH	2.25	0.52
1:L5:2118:G:N2	1:L5:3517:A:OP2	2.40	0.52
1:L5:3913:U:H2'	1:L5:3914:C:C6	2.45	0.52
46:S2:170:A:O2'	46:S2:171:A:H5'	2.09	0.52
46:S2:538:C:H5'	46:S2:539:U:H5	1.73	0.52
46:S2:817:A:OP1	57:SJ:10:ARG:NH2	2.39	0.52
46:S2:1534:A:OP2	53:SF:164:ARG:NH1	2.42	0.52
47:S7:36:U:H2'	47:S7:37:A:H8	1.75	0.52
74:Sb:11:SER:HB3	74:Sb:14:GLU:HG3	1.91	0.52
78:Sg:121:VAL:HG21	78:Sg:154:VAL:HG11	1.91	0.52
1:L5:1005:C:O2'	1:L5:1006:G:O5'	2.25	0.52
1:L5:1275:C:H2'	1:L5:1276:A:H8	1.75	0.52
1:L5:4561:G:H2'	1:L5:4562:G:H8	1.73	0.52
1:L5:4585:G:O2'	1:L5:4587:A:N7	2.36	0.52
46:S2:57:U:H3	46:S2:88:G:H1	1.58	0.52
46:S2:798:C:H3'	46:S2:800:U:H5'	1.91	0.52
46:S2:1846:A:H2'	46:S2:1847:G:C8	2.44	0.52
49:SB:63:LYS:HD3	49:SB:64:GLY:N	2.24	0.52
63:SQ:85:ARG:NH2	63:SQ:116:ASP:OD2	2.42	0.52
1:L5:1113:C:H2'	1:L5:1114:G:H8	1.74	0.52
3:L8:125:C:OP2	3:L8:126:C:N4	2.43	0.52
32:Ld:95:ASP:N	32:Ld:95:ASP:OD1	2.42	0.52
51:SD:92:ALA:O	51:SD:93:THR:OG1	2.22	0.52
64:SR:35:CYS:HA	64:SR:38:ILE:HG22	1.92	0.52
69:SW:24:GLN:HB3	74:Sb:7:LEU:HD12	1.92	0.52
71:SY:114:MET:HE2	71:SY:114:MET:N	2.24	0.52
19:LQ:124:ASP:N	19:LQ:124:ASP:OD1	2.41	0.52
49:SB:21:VAL:HG12	49:SB:22:VAL:HG23	1.91	0.52
70:SX:41:PHE:HZ	70:SX:102:VAL:HG12	1.73	0.52
72:SZ:48:VAL:HA	72:SZ:83:LEU:HD22	1.91	0.52
1:L5:654:G:H2'	1:L5:655:G:O4'	2.10	0.52
1:L5:4352:U:H1'	1:L5:4353:A:H5''	1.90	0.52
13:LJ:55:TYR:HA	13:LJ:64:ARG:HG2	1.91	0.52
14:LL:47:ALA:HB3	14:LL:48:PRO:HD3	1.91	0.52
46:S2:157:U:O2	46:S2:159:A:N6	2.43	0.52
67:SU:53:PRO:HA	67:SU:89:ILE:HG22	1.91	0.52
1:L5:2:G:H2'	1:L5:3:C:C6	2.45	0.52
1:L5:1275:C:H2'	1:L5:1276:A:C8	2.45	0.52
1:L5:3462:U:H2'	1:L5:3463:G:H8	1.75	0.52
9:LF:197:ILE:CD1	9:LF:209:MET:HB2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LT:52:MET:HG3	22:LT:95:HIS:CE1	2.45	0.52
46:S2:168:C:H4'	54:SG:131:ARG:HG2	1.91	0.52
46:S2:218:C:H2'	46:S2:219:A:H8	1.73	0.52
46:S2:847:G:C5	52:SE:19:MET:HE2	2.45	0.52
47:S7:2:A:H2'	47:S7:3:G:C8	2.45	0.52
47:S7:35:A:N7	79:Sx:40:G:N2	2.57	0.52
1:L5:950:G:N2	1:L5:1035:U:H3	2.07	0.52
1:L5:3505:U:H2'	1:L5:3506:A:H8	1.75	0.52
1:L5:4612:C:H2'	1:L5:4613:U:C6	2.45	0.52
2:L7:26:C:O2'	13:LJ:147:ARG:NH1	2.40	0.52
5:LB:322:HIS:O	5:LB:342:LYS:NZ	2.40	0.52
23:LU:50:ASN:OD1	23:LU:52:LYS:NZ	2.38	0.52
31:Lc:51:ASN:ND2	31:Lc:78:ASN:OD1	2.31	0.52
32:Ld:26:THR:OG1	32:Ld:85:ARG:NH1	2.42	0.52
46:S2:161:U:H5''	71:SY:116:LYS:HD2	1.92	0.52
46:S2:981:A:H2'	46:S2:982:A:C8	2.45	0.52
57:SJ:21:GLU:HG3	57:SJ:24:ARG:H	1.74	0.52
1:L5:139:G:H2'	1:L5:140:G:C8	2.45	0.52
1:L5:438:G:OP2	33:Lc:18:LYS:NZ	2.36	0.52
1:L5:1649:G:H2'	1:L5:1650:C:C6	2.44	0.52
1:L5:3892:A:H2'	1:L5:3893:G:H8	1.75	0.52
1:L5:4344:A:H2'	1:L5:4345:A:O4'	2.10	0.52
1:L5:4392:C:H1'	1:L5:4609:G:C2	2.45	0.52
46:S2:1407:G:H2'	46:S2:1408:U:C6	2.45	0.52
46:S2:1415:A:N6	46:S2:1416:C:N3	2.57	0.52
55:SH:94:PHE:O	55:SH:95:ILE:HD13	2.09	0.52
55:SH:100:ILE:HG12	55:SH:125:VAL:HG21	1.91	0.52
1:L5:415:U:O2'	1:L5:416:G:OP1	2.24	0.52
46:S2:41:G:N2	46:S2:481:G:H1	2.00	0.52
46:S2:1441:C:O2'	46:S2:1443:U:OP1	2.27	0.52
46:S2:1715:U:H2'	46:S2:1716:A:C8	2.44	0.52
47:S6:51:U:H2'	47:S6:52:G:C8	2.45	0.52
51:SD:191:PRO:O	51:SD:199:GLY:HA3	2.10	0.52
54:SG:181:THR:HG22	54:SG:183:ARG:H	1.75	0.52
56:SI:104:ILE:O	56:SI:171:LEU:N	2.41	0.52
59:SL:35:ARG:NE	59:SL:53:GLY:O	2.43	0.52
1:L5:415:U:HO2'	1:L5:416:G:P	2.33	0.51
1:L5:3827:U:H2'	1:L5:3828:G:H8	1.75	0.51
14:LL:144:LEU:O	14:LL:145:LYS:HD2	2.10	0.51
31:Lc:53:PRO:HG2	31:Lc:56:ARG:HB2	1.92	0.51
46:S2:83:A:H2'	46:S2:84:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S6:29:G:H22	47:S6:41:C:H5	1.56	0.51
47:S7:28:U:O2'	47:S7:29:G:H8	1.92	0.51
49:SB:180:ASP:OD1	49:SB:182:LYS:N	2.42	0.51
55:SH:134:VAL:HG12	55:SH:173:PHE:CE2	2.46	0.51
67:SU:56:MET:HG3	67:SU:86:LYS:HD3	1.91	0.51
78:Sg:14:HIS:CD2	78:Sg:35:SER:HB2	2.45	0.51
78:Sg:80:SER:OG	78:Sg:88:ARG:O	2.25	0.51
46:S2:1117:C:H2'	46:S2:1118:C:H5''	1.91	0.51
46:S2:1254:A:OP2	46:S2:1527:G:N2	2.37	0.51
52:SE:118:GLU:HA	52:SE:121:TYR:CD2	2.46	0.51
63:SQ:66:VAL:HG12	63:SQ:68:ILE:HG13	1.92	0.51
75:Sc:32:VAL:HG11	75:Sc:56:LEU:HD12	1.92	0.51
8:LE:103:THR:OG1	8:LE:104:VAL:N	2.43	0.51
20:LR:32:ILE:HD13	20:LR:44:LEU:HD13	1.92	0.51
46:S2:218:C:C2	46:S2:219:A:C8	2.99	0.51
46:S2:1296:A:C2	46:S2:1297:U:H1'	2.45	0.51
49:SB:193:ILE:HD12	49:SB:193:ILE:H	1.75	0.51
56:SI:74:ARG:HH22	56:SI:112:TRP:HD1	1.58	0.51
1:L5:415:U:H4'	1:L5:2087:G:H4'	1.93	0.51
1:L5:498:G:H2'	1:L5:499:G:C8	2.46	0.51
1:L5:1148:A:H2'	1:L5:1149:A:C8	2.46	0.51
6:LC:325:MET:HE1	9:LF:177:TYR:CZ	2.45	0.51
46:S2:1229:A:H2'	46:S2:1230:G:H8	1.75	0.51
46:S2:1596:U:H2'	46:S2:1597:U:C6	2.45	0.51
50:SC:201:GLY:N	50:SC:221:ASP:OD2	2.44	0.51
54:SG:44:GLU:H	54:SG:44:GLU:CD	2.18	0.51
60:SN:16:LEU:HD11	60:SN:65:PHE:HE2	1.76	0.51
1:L5:1013:C:O2'	1:L5:1016:C:N4	2.34	0.51
5:LB:175:GLN:HG2	5:LB:177:LYS:H	1.75	0.51
17:LO:144:GLU:OE1	17:LO:144:GLU:N	2.38	0.51
43:Lo:54:PRO:O	47:S6:75:C:O2'	2.22	0.51
46:S2:83:A:H2'	46:S2:84:A:H8	1.76	0.51
46:S2:845:U:H2'	46:S2:846:G:C8	2.45	0.51
66:ST:116:ASP:OD1	66:ST:118:ASP:N	2.44	0.51
1:L5:7:C:H2'	1:L5:8:U:C6	2.45	0.51
11:LH:12:ILE:HD11	11:LH:53:LYS:HB2	1.93	0.51
23:LU:100:LEU:HD13	23:LU:112:LEU:HD23	1.92	0.51
25:LW:4:GLU:OE1	25:LW:4:GLU:N	2.44	0.51
32:Ld:123:ASP:OD1	32:Ld:123:ASP:N	2.44	0.51
46:S2:830:C:O3'	46:S2:846:G:N2	2.44	0.51
48:SA:40:LYS:O	48:SA:48:ILE:HG12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SI:6:ASP:OD1	56:SI:9:HIS:ND1	2.35	0.51
59:SL:111:VAL:HG11	59:SL:128:VAL:HG11	1.93	0.51
67:SU:46:LYS:HE2	67:SU:97:ILE:HG21	1.93	0.51
1:L5:172:C:H4'	1:L5:173:C:H5'	1.93	0.51
1:L5:2656:G:H3'	1:L5:2657:G:N2	2.25	0.51
1:L5:3780:G:P	28:LZ:54:THR:HG1	2.34	0.51
8:LE:138:LYS:HD3	8:LE:138:LYS:N	2.25	0.51
16:LN:163:GLY:O	16:LN:172:ARG:NH1	2.44	0.51
28:LZ:11:VAL:HG12	28:LZ:82:PRO:HA	1.93	0.51
37:Li:63:VAL:O	37:Li:64:SER:OG	2.27	0.51
46:S2:62:G:H2'	46:S2:62:G:N3	2.26	0.51
46:S2:847:G:C4	52:SE:19:MET:HE2	2.45	0.51
46:S2:1242:A:O2'	46:S2:1267:C:O2'	2.24	0.51
46:S2:1458:U:H2'	46:S2:1459:G:H8	1.76	0.51
46:S2:1561:U:H2'	46:S2:1562:G:H8	1.76	0.51
60:SN:74:ILE:O	60:SN:77:SER:OG	2.27	0.51
5:LB:68:ASN:O	5:LB:70:LYS:HG2	2.11	0.51
21:LS:60:GLU:OE2	21:LS:61:ILE:N	2.43	0.51
46:S2:858:U:H2'	46:S2:859:A:C8	2.45	0.51
46:S2:1536:U:O2	53:SF:82:ASN:ND2	2.43	0.51
46:S2:1736:A:H3'	46:S2:1737:G:H8	1.76	0.51
47:S7:61:C:H2'	47:S7:62:C:C6	2.46	0.51
53:SF:48:TYR:HE2	63:SQ:56:LEU:HD12	1.74	0.51
11:LH:150:ASP:OD1	11:LH:152:GLU:N	2.43	0.51
35:Lg:89:ASP:OD2	35:Lg:93:ARG:NH2	2.43	0.51
46:S2:118:C:O2'	46:S2:119:U:OP1	2.24	0.51
46:S2:537:A:H3'	46:S2:538:C:H4'	1.92	0.51
46:S2:655:A:OP2	46:S2:656:A:O2'	2.24	0.51
46:S2:1202:U:H2'	46:S2:1203:U:C6	2.46	0.51
46:S2:1464:U:H5''	46:S2:1465:C:C5	2.45	0.51
47:S6:28:U:H2'	47:S6:29:G:C8	2.45	0.51
52:SE:55:ALA:HB3	52:SE:61:VAL:HG22	1.91	0.51
1:L5:260:G:H2'	1:L5:261:G:C8	2.46	0.51
1:L5:4376:A:H2'	1:L5:4377:A:C8	2.46	0.51
46:S2:376:U:H2'	46:S2:377:A:H8	1.76	0.51
46:S2:1542:G:N2	66:ST:12:GLN:OE1	2.40	0.51
46:S2:1784:C:H4'	46:S2:1785:G:O5'	2.11	0.51
67:SU:82:MET:SD	67:SU:83:ARG:N	2.82	0.51
1:L5:443:G:H2'	1:L5:444:U:C6	2.46	0.50
1:L5:926:G:O2'	1:L5:927:C:O5'	2.24	0.50
1:L5:4011:U:H2'	1:L5:4012:U:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:41:G:O6	46:S2:482:C:N4	2.45	0.50
46:S2:456:A:O2'	46:S2:1736:A:H8	1.94	0.50
53:SF:97:PHE:HA	53:SF:100:ILE:HG22	1.94	0.50
53:SF:103:LEU:HD21	72:SZ:67:LEU:HD22	1.94	0.50
78:Sg:156:PHE:HE1	78:Sg:179:LEU:HD11	1.75	0.50
1:L5:2168:C:H2'	1:L5:2169:A:C8	2.46	0.50
1:L5:2277:C:H2'	1:L5:2278:G:H8	1.75	0.50
1:L5:3567:C:H2'	1:L5:3568:C:H6	1.76	0.50
46:S2:455:U:O4	46:S2:456:A:N6	2.44	0.50
46:S2:595:A:H61	46:S2:643:U:H2'	1.76	0.50
46:S2:1553:G:H21	76:Sd:35:GLY:HA2	1.76	0.50
1:L5:830:C:H4'	1:L5:831:G:O5'	2.11	0.50
1:L5:3845:A:H2'	1:L5:3846:C:H6	1.76	0.50
6:LC:319:LEU:HD21	9:LF:177:TYR:CD2	2.46	0.50
26:LX:51:THR:OG1	26:LX:52:LEU:N	2.44	0.50
28:LZ:87:VAL:HG22	28:LZ:127:ASN:HD22	1.76	0.50
31:Lc:37:MET:HA	31:Lc:37:MET:HE2	1.92	0.50
35:Lg:81:SER:O	35:Lg:81:SER:OG	2.29	0.50
46:S2:881:G:H3'	46:S2:882:G:H8	1.75	0.50
53:SF:198:ARG:NE	53:SF:198:ARG:O	2.44	0.50
61:SO:85:CYS:SG	61:SO:124:MET:HE1	2.51	0.50
71:SY:121:ALA:HA	71:SY:124:ASN:HB2	1.93	0.50
1:L5:2156:G:HO2'	1:L5:2576:G:HO2'	1.59	0.50
1:L5:2314:G:H1	1:L5:2324:G:H22	1.59	0.50
1:L5:4376:A:H2'	1:L5:4377:A:H8	1.76	0.50
3:L8:148:A:N3	10:LG:60:TYR:OH	2.38	0.50
5:LB:4:ARG:HD2	24:LV:49:LEU:HD11	1.93	0.50
25:LW:48:GLN:OE1	25:LW:48:GLN:N	2.45	0.50
46:S2:1018:U:H5'	60:SN:55:ARG:HD3	1.93	0.50
46:S2:1294:A:N6	46:S2:1303:G:H1	2.09	0.50
46:S2:1534:A:H2	46:S2:1537:G:N3	2.10	0.50
58:SK:24:LYS:HG2	58:SK:26:ASP:OD1	2.12	0.50
78:Sg:207:CYS:SG	78:Sg:208:ALA:N	2.84	0.50
4:LA:104:VAL:HA	4:LA:107:MET:SD	2.52	0.50
21:LS:15:ARG:HB3	21:LS:27:LEU:HD23	1.93	0.50
27:LY:30:MET:HB3	27:LY:101:PRO:HG3	1.94	0.50
36:Lh:22:ASP:O	36:Lh:26:VAL:HG23	2.12	0.50
46:S2:1280:C:H2'	46:S2:1281:G:H8	1.76	0.50
46:S2:1514:C:H2'	46:S2:1515:G:C8	2.41	0.50
74:Sb:34:ASP:CG	74:Sb:82:LYS:HD2	2.37	0.50
78:Sg:52:TYR:HE2	78:Sg:309:VAL:HG21	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:150:U:OP2	10:LG:200:THR:OG1	2.26	0.50
1:L5:939:U:H3	1:L5:1050:C:H41	1.58	0.50
1:L5:3341:G:H2'	1:L5:3342:C:C6	2.47	0.50
1:L5:3364:U:H2'	1:L5:3365:C:C6	2.45	0.50
1:L5:4572:C:H2'	1:L5:4573:G:C4	2.47	0.50
46:S2:599:G:O2'	46:S2:600:A:OP1	2.26	0.50
46:S2:878:C:H2'	46:S2:879:G:C8	2.47	0.50
46:S2:1620:A:O2'	62:SP:82:ASP:OD2	2.29	0.50
64:SR:77:GLU:HA	64:SR:80:ARG:HD3	1.94	0.50
1:L5:461:G:H2'	1:L5:462:A:C8	2.46	0.50
1:L5:747:G:O2'	1:L5:748:G:H8	1.95	0.50
1:L5:4628:C:N3	18:LP:69:ARG:NH2	2.59	0.50
3:L8:109:C:O2'	38:Lj:20:ARG:NH2	2.44	0.50
7:LD:118:ILE:H	7:LD:118:ILE:HD12	1.77	0.50
45:Lr:94:ARG:HB2	45:Lr:111:ILE:HD11	1.94	0.50
46:S2:1114:A:H2'	46:S2:1115:U:C6	2.47	0.50
46:S2:1395:G:H5''	63:SQ:126:ARG:HH11	1.76	0.50
47:S7:40:C:H2'	47:S7:41:C:C6	2.46	0.50
47:S7:52:G:C6	47:S7:63:A:C6	2.99	0.50
49:SB:113:MET:SD	49:SB:113:MET:N	2.85	0.50
71:SY:30:PRO:HD2	71:SY:31:GLY:N	2.26	0.50
72:SZ:43:LYS:O	72:SZ:45:ASN:ND2	2.44	0.50
1:L5:1621:G:O2'	1:L5:1623:C:OP2	2.27	0.50
1:L5:1882:G:H2'	1:L5:1883:U:C6	2.47	0.50
1:L5:2394:G:H2'	1:L5:2395:A:C8	2.47	0.50
1:L5:3967:C:O2'	30:Lb:36:ASP:OD1	2.29	0.50
2:L7:92:C:H2'	2:L7:93:G:C8	2.46	0.50
14:LL:144:LEU:HD12	14:LL:145:LYS:HB2	1.93	0.50
46:S2:837:G:H2'	46:S2:838:A:H4'	1.94	0.50
46:S2:942:C:H2'	46:S2:943:G:C8	2.46	0.50
46:S2:1281:G:H2'	46:S2:1282:G:C8	2.47	0.50
52:SE:72:ILE:HD13	52:SE:77:ARG:HG3	1.94	0.50
72:SZ:69:THR:HG23	72:SZ:71:ALA:H	1.76	0.50
78:Sg:66:VAL:HA	78:Sg:82:SER:HA	1.93	0.50
1:L5:363:G:O6	38:Lj:55:ARG:NH1	2.45	0.50
1:L5:2274:A:O4'	35:Lg:62:LYS:HD2	2.12	0.50
1:L5:3432:A:H2'	1:L5:3433:G:O4'	2.12	0.50
46:S2:14:C:H2'	46:S2:15:U:C6	2.47	0.50
52:SE:15:PRO:HG3	52:SE:39:ARG:HE	1.77	0.50
54:SG:113:ILE:HD11	54:SG:124:LEU:HD21	1.93	0.50
1:L5:441:G:H2'	1:L5:442:G:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:854:A:N6	1:L5:1098:G:H1'	2.27	0.49
1:L5:4507:G:HO2'	1:L5:4508:G:H8	1.59	0.49
8:LE:278:TYR:OH	15:LM:106:ASP:OD2	2.20	0.49
26:LX:90:ILE:HG23	26:LX:91:GLU:OE2	2.12	0.49
46:S2:494:A:N6	46:S2:510:G:H8	2.09	0.49
46:S2:944:U:C2	46:S2:945:A:C8	3.00	0.49
50:SC:125:LYS:HG3	50:SC:143:CYS:HB2	1.94	0.49
51:SD:25:LEU:HB3	51:SD:34:TYR:CE2	2.47	0.49
52:SE:51:ARG:HH11	52:SE:51:ARG:HG3	1.77	0.49
53:SF:140:ASP:HB2	75:Sc:44:ARG:HH21	1.76	0.49
56:SI:172:LEU:HD13	56:SI:190:LEU:HD12	1.93	0.49
71:SY:102:THR:O	71:SY:107:ARG:NH2	2.45	0.49
1:L5:819:C:H2'	1:L5:820:C:C6	2.47	0.49
1:L5:4559:G:O2'	1:L5:4560:C:OP2	2.29	0.49
2:L7:37:G:N2	2:L7:41:G:N3	2.60	0.49
46:S2:895:G:H5'	46:S2:896:G:C8	2.46	0.49
54:SG:62:PRO:HG2	54:SG:83:CYS:SG	2.52	0.49
58:SK:32:HIS:CD2	58:SK:45:VAL:HG21	2.46	0.49
1:L5:1:C:H4'	1:L5:2:G:OP1	2.12	0.49
1:L5:1132:U:H2'	1:L5:1133:C:C6	2.47	0.49
1:L5:3367:G:H1'	1:L5:3368:A:C8	2.47	0.49
3:L8:19:C:H2'	3:L8:20:A:H8	1.76	0.49
13:LJ:120:ASP:OD2	13:LJ:122:SER:OG	2.30	0.49
22:LT:69:GLN:OE1	22:LT:69:GLN:N	2.44	0.49
28:LZ:10:VAL:O	28:LZ:83:THR:OG1	2.26	0.49
46:S2:525:U:H5''	46:S2:526:A:O5'	2.11	0.49
46:S2:564:G:H1	46:S2:593:C:N4	2.09	0.49
46:S2:904:A:O2'	46:S2:905:A:O4'	2.28	0.49
46:S2:1412:G:H1	46:S2:1431:C:H42	1.59	0.49
46:S2:1745:G:HO2'	46:S2:1791:A:N6	2.11	0.49
53:SF:69:VAL:O	53:SF:73:THR:HG23	2.13	0.49
55:SH:60:ILE:HB	55:SH:92:VAL:HG22	1.94	0.49
59:SL:13:GLN:HE22	59:SL:35:ARG:HD2	1.77	0.49
68:SV:70:LEU:O	68:SV:74:LYS:N	2.35	0.49
73:Sa:10:ARG:HB2	73:Sa:33:ASP:OD1	2.12	0.49
1:L5:490:C:H2'	1:L5:491:C:H6	1.77	0.49
1:L5:704:U:H3	8:LE:230:LEU:HD13	1.78	0.49
1:L5:1122:A:H2'	1:L5:1123:C:C6	2.47	0.49
1:L5:1192:G:H5''	1:L5:1193:C:OP2	2.12	0.49
1:L5:1257:A:H2'	1:L5:1258:G:H8	1.76	0.49
1:L5:1901:G:H2'	1:L5:1902:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:636:G:H2'	46:S2:637:C:C6	2.46	0.49
46:S2:1504:C:H2'	46:S2:1505:U:C6	2.47	0.49
65:SS:8:LYS:HG3	65:SS:8:LYS:O	2.11	0.49
65:SS:15:VAL:HG22	65:SS:68:ILE:HD11	1.95	0.49
1:L5:686:C:H2'	1:L5:687:C:C6	2.48	0.49
1:L5:1219:C:H2'	1:L5:1220:C:C6	2.48	0.49
1:L5:3267:A:H2'	1:L5:3268:A:H8	1.77	0.49
1:L5:3326:G:H21	1:L5:3329:G:H21	1.60	0.49
20:LR:172:ARG:NE	46:S2:910:G:OP1	2.45	0.49
41:Lm:79:GLU:OE1	41:Lm:82:LEU:N	2.40	0.49
52:SE:42:LEU:HD12	52:SE:43:PRO:HD2	1.95	0.49
62:SP:107:ILE:H	62:SP:107:ILE:HD12	1.77	0.49
70:SX:6:GLY:O	70:SX:9:THR:OG1	2.27	0.49
73:Sa:90:GLU:N	73:Sa:90:GLU:OE2	2.45	0.49
1:L5:1443:G:N1	4:LA:208:GLU:OE1	2.43	0.49
1:L5:2314:G:N2	1:L5:2324:G:H22	2.10	0.49
1:L5:3904:A:H5''	13:LJ:108:GLY:HA3	1.94	0.49
1:L5:4071:G:O6	1:L5:4074:C:H2'	2.12	0.49
8:LE:181:LEU:HD21	8:LE:199:GLN:HG2	1.94	0.49
28:LZ:25:ILE:HA	28:LZ:43:VAL:HG12	1.94	0.49
45:Lr:19:LYS:HG2	45:Lr:24:THR:HG23	1.94	0.49
45:Lr:92:SER:O	45:Lr:96:MET:HG2	2.13	0.49
46:S2:1403:A:O2'	46:S2:1404:C:OP2	2.29	0.49
46:S2:1496:G:N2	76:Sd:42:CYS:SG	2.74	0.49
49:SB:71:LEU:HD12	49:SB:82:ARG:HB2	1.95	0.49
56:SI:196:GLU:HG2	56:SI:200:ARG:HH22	1.76	0.49
65:SS:84:LEU:HD12	65:SS:95:TYR:HB3	1.94	0.49
78:Sg:191:HIS:CG	78:Sg:195:LEU:HD21	2.47	0.49
1:L5:1148:A:H2'	1:L5:1149:A:H8	1.78	0.49
1:L5:1154:U:H2'	1:L5:1155:C:C6	2.48	0.49
1:L5:3553:C:O2'	5:LB:268:ARG:NH1	2.40	0.49
1:L5:3745:G:H2'	1:L5:3746:G:C8	2.47	0.49
28:LZ:26:VAL:HB	28:LZ:42:LEU:HD23	1.93	0.49
46:S2:115:U:H4'	46:S2:116:U:OP1	2.11	0.49
46:S2:1281:G:H2'	46:S2:1282:G:H8	1.77	0.49
46:S2:1285:A:OP1	46:S2:1286:G:O2'	2.27	0.49
52:SE:164:LEU:HB2	52:SE:165:GLU:OE2	2.12	0.49
55:SH:31:GLU:O	55:SH:32:MET:HG2	2.13	0.49
57:SJ:32:ILE:HD13	77:Se:108:ARG:HG2	1.94	0.49
57:SJ:113:GLN:O	57:SJ:113:GLN:HG3	2.13	0.49
62:SP:69:PRO:O	62:SP:70:MET:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Se:86:VAL:O	77:Se:90:THR:OG1	2.31	0.49
1:L5:761:C:H2'	1:L5:762:U:C6	2.48	0.49
1:L5:831:G:H8	1:L5:831:G:OP1	1.96	0.49
1:L5:1323:C:H5''	29:La:2:PRO:HD2	1.95	0.49
1:L5:3845:A:H2'	1:L5:3846:C:C6	2.48	0.49
1:L5:4060:G:N2	1:L5:4090:U:O4	2.46	0.49
1:L5:4618:C:C2	1:L5:4619:A:C8	3.01	0.49
3:L8:128:C:H2'	3:L8:129:C:C6	2.47	0.49
8:LE:138:LYS:HD3	8:LE:138:LYS:H	1.76	0.49
9:LF:241:GLY:O	9:LF:268:ARG:NH2	2.46	0.49
34:Lf:28:LEU:HB2	34:Lf:84:VAL:HG23	1.93	0.49
46:S2:36:U:OP1	46:S2:579:C:O2'	2.29	0.49
54:SG:135:PRO:HG2	54:SG:141:ILE:HG13	1.95	0.49
55:SH:25:GLN:HA	55:SH:28:LEU:HB3	1.95	0.49
63:SQ:16:LYS:HG3	63:SQ:82:TYR:HB3	1.95	0.49
71:SY:114:MET:HE1	71:SY:127:ALA:HB3	1.95	0.49
78:Sg:201:SER:OG	78:Sg:203:ASP:O	2.30	0.49
1:L5:159:C:O2	14:LL:88:LYS:NZ	2.37	0.49
1:L5:254:C:H2'	1:L5:255:G:C8	2.48	0.49
1:L5:395:A:H2'	1:L5:396:G:C8	2.48	0.49
1:L5:1113:C:H2'	1:L5:1114:G:C8	2.47	0.49
1:L5:3567:C:H2'	1:L5:3568:C:C6	2.48	0.49
1:L5:4182:G:H21	47:S7:76:A:H62	1.61	0.49
32:Ld:91:LYS:HD2	32:Ld:105:LEU:HD23	1.94	0.49
46:S2:58:C:O2'	46:S2:59:U:O5'	2.27	0.49
46:S2:1422:A:H2'	46:S2:1423:G:H8	1.76	0.49
46:S2:1455:A:OP1	64:SR:49:LYS:NZ	2.37	0.49
46:S2:1799:C:H2'	46:S2:1800:G:O4'	2.12	0.49
48:SA:58:LEU:HD12	48:SA:161:ILE:HD13	1.95	0.49
55:SH:180:LEU:O	55:SH:180:LEU:HD23	2.13	0.49
68:SV:49:GLN:OE1	68:SV:49:GLN:N	2.45	0.49
1:L5:490:C:H2'	1:L5:491:C:C6	2.48	0.49
1:L5:941:C:H2'	1:L5:942:C:C6	2.48	0.49
1:L5:1881:C:H2'	1:L5:1882:G:H8	1.77	0.49
1:L5:4557:A:P	5:LB:97:ARG:HH22	2.35	0.49
3:L8:67:U:H2'	3:L8:68:G:H8	1.77	0.49
46:S2:47:G:N2	46:S2:479:G:H22	2.08	0.49
46:S2:947:U:H2'	46:S2:948:G:H8	1.78	0.49
46:S2:990:C:OP2	49:SB:155:TYR:OH	2.25	0.49
49:SB:68:GLU:OE1	49:SB:83:LYS:HD2	2.13	0.49
50:SC:90:GLU:HB2	50:SC:93:ILE:HG13	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3518:A:H2'	1:L5:3519:A:C8	2.48	0.48
5:LB:165:HIS:ND1	5:LB:166:THR:O	2.40	0.48
46:S2:96:C:H42	46:S2:434:A:H61	1.60	0.48
46:S2:853:G:O2'	59:SL:97:ARG:NH1	2.46	0.48
46:S2:1417:C:H1'	46:S2:1418:C:C5	2.48	0.48
78:Sg:35:SER:OG	78:Sg:37:ASP:OD1	2.17	0.48
1:L5:4538:A:H2'	1:L5:4539:A:O4'	2.14	0.48
2:L7:11:A:N1	2:L7:66:G:O2'	2.40	0.48
7:LD:56:THR:OG1	7:LD:57:ASN:N	2.46	0.48
7:LD:254:GLU:N	7:LD:254:GLU:OE2	2.46	0.48
46:S2:830:C:H5''	52:SE:21:ASP:HB2	1.96	0.48
50:SC:69:LEU:HD12	50:SC:74:LYS:HB2	1.94	0.48
60:SN:17:PRO:HD3	74:Sb:28:PRO:HG3	1.94	0.48
61:SO:117:ARG:HH12	73:Sa:49:ALA:HB1	1.78	0.48
65:SS:60:THR:OG1	65:SS:63:GLU:OE2	2.31	0.48
65:SS:67:VAL:O	65:SS:71:MET:HG2	2.12	0.48
69:SW:8:ALA:HA	69:SW:74:VAL:HG11	1.94	0.48
1:L5:477:G:H2'	1:L5:478:G:C8	2.47	0.48
1:L5:3318:G:H4'	1:L5:3319:A:H5'	1.95	0.48
1:L5:3367:G:N2	1:L5:3369:A:H62	2.11	0.48
45:Lr:32:LEU:O	45:Lr:113:ARG:NH1	2.47	0.48
68:SV:56:CYS:SG	68:SV:59:ILE:HG12	2.52	0.48
1:L5:1324:G:H2'	1:L5:1325:C:H6	1.79	0.48
1:L5:1743:G:N2	1:L5:4087:C:OP1	2.44	0.48
1:L5:4341:C:H2'	1:L5:4342:U:C6	2.49	0.48
2:L7:27:G:OP2	7:LD:56:THR:OG1	2.29	0.48
9:LF:114:VAL:O	9:LF:142:GLY:HA2	2.13	0.48
29:La:82:VAL:HG11	29:La:101:ILE:HD12	1.95	0.48
46:S2:72:C:H5''	46:S2:73:C:C5	2.48	0.48
46:S2:157:U:H2'	46:S2:159:A:N7	2.29	0.48
46:S2:538:C:H42	46:S2:547:G:H22	1.60	0.48
46:S2:1204:G:H2'	46:S2:1205:A:C8	2.49	0.48
46:S2:1400:C:O2'	46:S2:1401:U:H5'	2.14	0.48
46:S2:1630:C:C2	46:S2:1631:A:C8	3.01	0.48
46:S2:1682:U:H2'	46:S2:1683:C:C6	2.48	0.48
49:SB:194:GLY:O	49:SB:198:GLU:HG3	2.14	0.48
1:L5:745:C:H5''	1:L5:746:C:O5'	2.13	0.48
1:L5:1028:G:H1'	1:L5:1029:G:C2	2.48	0.48
1:L5:1542:G:H2'	1:L5:1543:C:C6	2.48	0.48
1:L5:2513:G:H2'	1:L5:2514:G:C4	2.48	0.48
1:L5:2540:C:O2'	1:L5:2541:A:OP2	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3391:U:H2'	1:L5:3392:G:O4'	2.13	0.48
1:L5:3412:G:H2'	1:L5:3413:A:C8	2.47	0.48
1:L5:4105:U:O4'	80:Z:5:UNK:O	2.31	0.48
1:L5:4570:C:H1'	1:L5:4572:C:N4	2.29	0.48
12:LI:190:LEU:HD23	12:LI:197:VAL:HG11	1.96	0.48
14:LL:63:THR:O	14:LL:67:HIS:N	2.46	0.48
15:LM:105:THR:OG1	15:LM:108:ASP:OD1	2.30	0.48
20:LR:98:ARG:NH2	20:LR:130:ASN:OD1	2.47	0.48
33:Le:85:LEU:HD12	33:Le:111:ILE:HG23	1.96	0.48
44:Lp:46:LYS:HD3	44:Lp:59:SER:HB2	1.95	0.48
46:S2:1114:A:H2'	46:S2:1115:U:C5	2.48	0.48
46:S2:1379:A:OP2	48:SA:102:ARG:NH2	2.46	0.48
46:S2:1471:C:H2'	46:S2:1472:C:H6	1.78	0.48
52:SE:161:GLN:OE1	52:SE:170:THR:OG1	2.27	0.48
56:SI:163:GLU:O	56:SI:167:GLN:HG2	2.14	0.48
64:SR:14:ARG:O	64:SR:18:GLU:HG2	2.14	0.48
1:L5:129:C:N4	1:L5:130:G:O6	2.46	0.48
1:L5:761:C:H2'	1:L5:762:U:H6	1.77	0.48
1:L5:2201:U:HO2'	3:L8:112:G:HO2'	1.62	0.48
1:L5:2377:A:OP1	23:LU:101:ARG:NH1	2.44	0.48
1:L5:3925:G:OP2	1:L5:3925:G:N2	2.34	0.48
5:LB:107:ALA:HB2	5:LB:201:LEU:HG	1.94	0.48
33:Le:80:HIS:HB2	33:Le:84:GLU:OE1	2.13	0.48
46:S2:54:A:H1'	46:S2:476:C:H5	1.78	0.48
46:S2:371:G:O2'	56:SI:10:LYS:NZ	2.46	0.48
46:S2:1421:G:O2'	46:S2:1422:A:O4'	2.26	0.48
72:SZ:62:VAL:HA	72:SZ:65:TYR:CE1	2.49	0.48
75:Sc:14:VAL:HG13	75:Sc:30:VAL:HB	1.95	0.48
78:Sg:187:ASN:O	78:Sg:189:ILE:HG12	2.14	0.48
1:L5:263:C:O2'	36:Lh:112:ARG:NH1	2.46	0.48
1:L5:1010:U:N3	1:L5:1013:C:O2'	2.45	0.48
1:L5:1147:C:H2'	1:L5:1148:A:C8	2.42	0.48
1:L5:3594:C:H1'	16:LN:125:SER:HB3	1.95	0.48
18:LP:40:HIS:HE1	18:LP:42:ARG:HG3	1.79	0.48
20:LR:28:GLU:OE1	20:LR:28:GLU:N	2.47	0.48
36:Lh:4:ILE:O	36:Lh:56:ARG:NH1	2.44	0.48
46:S2:91:A:N6	46:S2:445:G:H8	2.09	0.48
46:S2:221:U:H2'	46:S2:222:U:O4'	2.13	0.48
46:S2:881:G:H3'	46:S2:882:G:C8	2.49	0.48
48:SA:180:ARG:HG3	48:SA:195:TRP:CE3	2.48	0.48
54:SG:181:THR:HB	54:SG:184:VAL:HG23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:950:G:C2	1:L5:1037:G:C2	3.02	0.48
1:L5:1882:G:H2'	1:L5:1883:U:H6	1.79	0.48
1:L5:4216:U:C2	1:L5:4217:A:C8	3.02	0.48
1:L5:4569:U:H2'	1:L5:4570:C:C6	2.49	0.48
13:LJ:36:ALA:O	13:LJ:39:VAL:HG12	2.14	0.48
24:LV:129:TRP:HB3	24:LV:132:ILE:HD13	1.95	0.48
46:S2:535:G:H2'	46:S2:536:G:H8	1.78	0.48
46:S2:1749:G:H1	46:S2:1787:U:H3	1.62	0.48
49:SB:198:GLU:O	49:SB:202:GLN:HG2	2.14	0.48
51:SD:55:THR:HA	51:SD:58:VAL:HG12	1.95	0.48
77:Se:98:LYS:O	77:Se:99:LYS:HG2	2.14	0.48
78:Sg:234:ASP:O	78:Sg:252:THR:OG1	2.31	0.48
1:L5:138:C:H2'	1:L5:139:G:C8	2.49	0.48
1:L5:279:G:H5''	16:LN:14:LYS:NZ	2.29	0.48
1:L5:1018:G:O2'	1:L5:1019:U:H6	1.97	0.48
1:L5:2345:A:H2'	1:L5:2346:U:C6	2.48	0.48
1:L5:3267:A:H2'	1:L5:3268:A:C8	2.49	0.48
1:L5:3501:U:H2'	1:L5:3502:A:C8	2.49	0.48
46:S2:946:U:H2'	46:S2:947:U:C6	2.49	0.48
46:S2:1791:A:H4'	54:SG:81:HIS:NE2	2.29	0.48
46:S2:1846:A:H2'	46:S2:1847:G:H8	1.79	0.48
47:S7:40:C:H2'	47:S7:41:C:H6	1.78	0.48
47:S7:54:A:N6	47:S7:58:A:N1	2.62	0.48
50:SC:124:PHE:CG	50:SC:147:VAL:HG22	2.48	0.48
54:SG:26:THR:O	54:SG:30:LYS:NZ	2.36	0.48
55:SH:97:GLN:CD	55:SH:97:GLN:H	2.22	0.48
1:L5:766:G:N2	1:L5:805:C:H42	2.07	0.48
1:L5:1902:A:H2'	1:L5:1903:A:C8	2.49	0.48
1:L5:1910:G:N3	1:L5:1910:G:C2'	2.73	0.48
21:LS:83:ARG:NH1	22:LT:154:ILE:O	2.46	0.48
31:Lc:77:ASN:OD1	31:Lc:79:ILE:HG22	2.14	0.48
66:ST:134:ILE:HA	66:ST:137:GLN:HG2	1.96	0.48
78:Sg:188:HIS:HB3	78:Sg:219:TRP:CZ2	2.48	0.48
1:L5:1352:U:O2'	1:L5:1443:G:OP1	2.32	0.47
22:LT:122:LYS:HE2	22:LT:122:LYS:HB2	1.54	0.47
46:S2:107:A:H2'	46:S2:108:G:C8	2.49	0.47
46:S2:1661:C:OP1	76:Sd:19:ARG:NH2	2.47	0.47
53:SF:204:ARG:HH22	75:Sc:44:ARG:HH12	1.62	0.47
1:L5:499:G:H1	1:L5:663:C:H5	1.62	0.47
1:L5:1315:C:O2'	19:LQ:64:SER:OG	2.27	0.47
1:L5:1497:U:H2'	1:L5:1498:A:H8	1.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3838:G:OP1	4:LA:2:GLY:N	2.47	0.47
1:L5:3885:U:H1'	1:L5:3886:A:C2	2.49	0.47
1:L5:4175:G:O2'	1:L5:4178:C:OP2	2.28	0.47
1:L5:4645:G:O2'	32:Ld:118:GLN:NE2	2.48	0.47
14:LL:200:LYS:HD3	14:LL:200:LYS:N	2.28	0.47
18:LP:122:ALA:HB3	18:LP:143:PRO:HB2	1.96	0.47
46:S2:539:U:H2'	46:S2:540:C:O4'	2.13	0.47
46:S2:920:A:OP2	60:SN:64:ARG:NH2	2.45	0.47
46:S2:1011:G:H2'	46:S2:1012:A:C8	2.49	0.47
46:S2:1190:A:H2'	46:S2:1191:A:H8	1.79	0.47
57:SJ:124:HIS:HB3	77:Se:109:ARG:HH12	1.79	0.47
1:L5:1671:A:N6	1:L5:1673:C:O2	2.47	0.47
1:L5:1726:A:OP1	15:LM:53:LYS:NZ	2.40	0.47
1:L5:2019:G:H22	45:Lr:98:ARG:HH12	1.60	0.47
1:L5:2020:A:H5''	45:Lr:108:MET:HG3	1.96	0.47
1:L5:2565:G:N1	1:L5:2568:C:OP2	2.31	0.47
1:L5:2598:A:O2'	1:L5:4284:G:H4'	2.14	0.47
1:L5:4413:C:H2'	1:L5:4414:G:C8	2.50	0.47
6:LC:152:LEU:HD23	6:LC:251:ILE:HG12	1.96	0.47
6:LC:293:LEU:O	6:LC:299:GLN:NE2	2.47	0.47
28:LZ:66:SER:HB3	28:LZ:122:TYR:HE2	1.79	0.47
46:S2:56:G:C6	46:S2:90:G:H1'	2.49	0.47
46:S2:97:U:H3	46:S2:433:G:H22	1.62	0.47
46:S2:1312:C:H2'	46:S2:1313:G:O4'	2.15	0.47
46:S2:1403:A:O2'	46:S2:1406:A:N6	2.47	0.47
46:S2:1630:C:OP1	65:SS:39:ARG:HD3	2.14	0.47
47:S7:60:A:H2'	47:S7:60:A:N3	2.30	0.47
75:Sc:18:LEU:HB2	75:Sc:29:GLN:HB2	1.95	0.47
3:L8:128:C:H2'	3:L8:129:C:H6	1.79	0.47
11:LH:128:MET:CE	11:LH:157:SER:HB3	2.44	0.47
19:LQ:66:MET:HE2	19:LQ:98:LEU:HD13	1.96	0.47
46:S2:17:C:H2'	46:S2:18:C:C6	2.50	0.47
46:S2:90:G:H8	46:S2:90:G:OP2	1.98	0.47
46:S2:996:G:N2	46:S2:999:A:OP2	2.40	0.47
46:S2:1580:A:H4'	46:S2:1582:C:H5	1.80	0.47
55:SH:159:ASP:OD2	55:SH:162:GLN:NE2	2.45	0.47
63:SQ:55:VAL:HA	63:SQ:63:PHE:CE2	2.48	0.47
78:Sg:220:ASP:HB3	78:Sg:224:GLY:H	1.79	0.47
1:L5:690:G:H2'	1:L5:691:C:C6	2.49	0.47
1:L5:747:G:O2'	1:L5:748:G:O5'	2.32	0.47
1:L5:1012:U:O2'	1:L5:1013:C:OP1	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1324:G:H2'	1:L5:1325:C:C6	2.49	0.47
1:L5:2499:A:H2'	1:L5:2500:A:H8	1.80	0.47
12:LI:48:LEU:HD12	12:LI:49:CYS:H	1.78	0.47
22:LT:11:THR:HG22	22:LT:14:MET:HE2	1.96	0.47
38:Lj:28:HIS:HE1	38:Lj:30:GLN:HB2	1.79	0.47
46:S2:66:G:H3'	46:S2:68:A:N6	2.27	0.47
46:S2:1231:C:OP1	65:SS:130:ARG:NH2	2.47	0.47
46:S2:1563:C:H2'	46:S2:1564:G:H8	1.80	0.47
54:SG:74:ARG:HH21	54:SG:95:LYS:HA	1.80	0.47
66:ST:44:GLU:N	66:ST:44:GLU:OE1	2.47	0.47
1:L5:1524:G:H2'	1:L5:1525:C:H6	1.80	0.47
1:L5:1559:U:O2'	1:L5:1561:G:N2	2.47	0.47
1:L5:4059:U:C2	1:L5:4060:G:C8	3.02	0.47
1:L5:4402:U:H2'	1:L5:4403:C:C6	2.49	0.47
26:LX:83:THR:O	26:LX:87:MET:HG2	2.14	0.47
28:LZ:84:ARG:NH1	35:Lg:99:GLU:OE1	2.47	0.47
39:Lk:46:VAL:O	39:Lk:47:ILE:HD13	2.14	0.47
46:S2:78:C:O2'	46:S2:79:A:H5''	2.15	0.47
46:S2:538:C:H3'	46:S2:539:U:C6	2.50	0.47
46:S2:846:G:H2'	46:S2:847:G:C4	2.49	0.47
46:S2:1008:C:H2'	46:S2:1009:A:C8	2.48	0.47
57:SJ:35:TYR:HB2	57:SJ:37:LEU:HD11	1.96	0.47
58:SK:31:LYS:HZ1	58:SK:35:LEU:HB3	1.79	0.47
61:SO:151:LEU:HD23	61:SO:151:LEU:H	1.80	0.47
1:L5:1012:U:H3'	1:L5:1013:C:O4'	2.14	0.47
1:L5:1431:G:H1'	1:L5:2270:A:N6	2.30	0.47
1:L5:1604:A:H4'	22:LT:102:ARG:HH21	1.79	0.47
1:L5:2344:G:H22	1:L5:2508:G:H1'	1.79	0.47
1:L5:2361:C:H2'	1:L5:2362:G:H8	1.79	0.47
1:L5:3891:G:H2'	1:L5:3892:A:C8	2.49	0.47
1:L5:4380:A:H2'	1:L5:4381:U:O4'	2.14	0.47
1:L5:4516:G:O6	21:LS:157:ARG:NH1	2.45	0.47
2:L7:59:G:O2'	7:LD:267:ASN:HB2	2.15	0.47
3:L8:141:C:H2'	3:L8:142:U:H6	1.79	0.47
4:LA:142:GLU:O	4:LA:143:THR:OG1	2.28	0.47
8:LE:252:GLU:HA	8:LE:255:LYS:HG3	1.97	0.47
12:LI:86:HIS:HB3	12:LI:139:ARG:HG2	1.96	0.47
17:LO:16:LEU:HD22	17:LO:43:ILE:HD11	1.97	0.47
39:Lk:57:LYS:NZ	39:Lk:66:VAL:HG21	2.29	0.47
41:Lm:87:GLN:HE21	41:Lm:91:CYS:HB2	1.78	0.47
46:S2:69:C:H2'	46:S2:70:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:164:A:H5'	54:SG:62:PRO:HB3	1.96	0.47
46:S2:858:U:H2'	46:S2:859:A:H8	1.80	0.47
46:S2:1283:A:H2'	46:S2:1284:C:O4'	2.15	0.47
46:S2:1535:C:O2	46:S2:1599:G:N2	2.48	0.47
46:S2:1712:U:H2'	46:S2:1713:A:H8	1.79	0.47
50:SC:105:GLU:HG3	50:SC:107:LEU:HD22	1.96	0.47
52:SE:106:LYS:HE3	52:SE:108:ARG:NH2	2.30	0.47
53:SF:179:ASN:HA	53:SF:182:LYS:HG2	1.95	0.47
55:SH:170:VAL:HA	55:SH:173:PHE:HB2	1.97	0.47
57:SJ:43:VAL:HG22	57:SJ:47:LYS:HE2	1.96	0.47
62:SP:44:ARG:HH21	62:SP:53:GLN:HE21	1.63	0.47
71:SY:114:MET:HA	71:SY:123:ALA:O	2.14	0.47
78:Sg:108:VAL:HA	78:Sg:124:SER:HA	1.96	0.47
1:L5:423:U:H2'	1:L5:424:U:C6	2.50	0.47
1:L5:2656:G:H1	1:L5:3254:G:H1	1.63	0.47
6:LC:138:MET:HE1	6:LC:144:ILE:HG13	1.97	0.47
8:LE:169:ARG:NH1	8:LE:281:SER:OG	2.48	0.47
10:LG:87:LEU:HD22	10:LG:91:THR:HG21	1.96	0.47
17:LO:109:PRO:HB2	17:LO:111:PRO:HD2	1.96	0.47
17:LO:126:VAL:HG13	17:LO:127:VAL:HG23	1.95	0.47
46:S2:1458:U:H2'	46:S2:1459:G:C8	2.50	0.47
47:S7:15:A:C5	47:S7:16:G:H1'	2.50	0.47
47:S7:52:G:H2'	47:S7:53:G:C8	2.50	0.47
52:SE:8:HIS:O	52:SE:30:ARG:NH1	2.47	0.47
55:SH:73:GLN:HB3	55:SH:135:PHE:CE1	2.50	0.47
56:SI:148:LYS:HE3	56:SI:149:TYR:HE1	1.79	0.47
1:L5:1026:C:H2'	1:L5:1027:G:C8	2.50	0.47
1:L5:3452:A:H2'	1:L5:3453:U:C6	2.50	0.47
1:L5:4011:U:H2'	1:L5:4012:U:H6	1.79	0.47
1:L5:4652:C:H2'	1:L5:4653:G:O4'	2.14	0.47
8:LE:184:THR:HB	8:LE:194:LEU:HD23	1.96	0.47
28:LZ:22:LYS:NZ	28:LZ:132:GLN:O	2.37	0.47
38:Lj:69:ILE:H	38:Lj:69:ILE:HD12	1.80	0.47
46:S2:34:U:H2'	46:S2:35:C:H6	1.80	0.47
46:S2:151:C:O2'	54:SG:132:ARG:NH1	2.48	0.47
46:S2:161:U:H1'	54:SG:87:ARG:NH2	2.30	0.47
46:S2:532:A:H2'	46:S2:532:A:N3	2.30	0.47
46:S2:687:U:OP1	69:SW:32:LYS:HG2	2.15	0.47
50:SC:83:LEU:HD23	50:SC:84:PHE:CE1	2.50	0.47
51:SD:40:ARG:HE	67:SU:106:ILE:HG21	1.79	0.47
74:Sb:40:CYS:SG	74:Sb:41:TYR:N	2.88	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1483:A:H4'	1:L5:1499:G:N2	2.29	0.47
1:L5:2328:G:OP2	28:LZ:67:LYS:NZ	2.48	0.47
1:L5:4384:G:OP2	1:L5:4384:G:H8	1.96	0.47
1:L5:4686:A:H2'	1:L5:4687:U:C6	2.50	0.47
26:LX:110:LYS:HG3	26:LX:121:VAL:HG21	1.97	0.47
46:S2:55:U:H3'	46:S2:452:G:C5	2.50	0.47
46:S2:368:U:H4'	46:S2:372:A:C8	2.49	0.47
46:S2:1857:C:H2'	46:S2:1858:G:H8	1.79	0.47
52:SE:118:GLU:HA	52:SE:121:TYR:CE2	2.50	0.47
54:SG:17:GLU:N	54:SG:17:GLU:OE2	2.48	0.47
55:SH:63:PHE:HA	55:SH:95:ILE:O	2.15	0.47
56:SI:56:ARG:HA	56:SI:180:GLY:HA2	1.97	0.47
56:SI:177:SER:OG	56:SI:178:ARG:N	2.48	0.47
1:L5:132:G:H3'	1:L5:133:C:H4'	1.97	0.46
1:L5:423:U:H2'	1:L5:424:U:H6	1.79	0.46
1:L5:686:C:H2'	1:L5:687:C:H6	1.79	0.46
5:LB:222:VAL:O	5:LB:343:ARG:NH1	2.48	0.46
21:LS:69:GLU:OE1	21:LS:102:THR:OG1	2.26	0.46
46:S2:507:G:H4'	46:S2:508:G:OP2	2.15	0.46
46:S2:515:U:H2'	46:S2:516:G:O4'	2.15	0.46
46:S2:920:A:P	60:SN:64:ARG:HH22	2.38	0.46
46:S2:1581:A:H8	67:SU:56:MET:HE1	1.80	0.46
46:S2:1802:A:H2'	46:S2:1803:C:H6	1.81	0.46
51:SD:140:GLY:HA3	51:SD:182:LEU:HD23	1.96	0.46
53:SF:34:SER:HB3	75:Sc:55:VAL:HG12	1.97	0.46
56:SI:84:ASN:OD1	56:SI:86:SER:N	2.48	0.46
61:SO:67:ASP:OD1	61:SO:67:ASP:N	2.46	0.46
66:ST:115:LYS:HD3	66:ST:116:ASP:O	2.14	0.46
71:SY:78:SER:OG	71:SY:79:LEU:N	2.47	0.46
1:L5:3739:C:H2'	1:L5:3740:G:H8	1.80	0.46
23:LU:26:THR:O	23:LU:30:GLU:HG2	2.14	0.46
24:LV:106:VAL:HG12	24:LV:112:MET:HA	1.97	0.46
46:S2:76:U:O2'	46:S2:78:C:OP2	2.32	0.46
46:S2:1441:C:H2'	46:S2:1442:U:C6	2.49	0.46
49:SB:71:LEU:HG	49:SB:84:PHE:HE1	1.80	0.46
53:SF:17:ILE:HA	53:SF:48:TYR:CE1	2.50	0.46
59:SL:10:TYR:CD2	59:SL:12:LYS:HD3	2.48	0.46
73:Sa:44:ILE:HG22	73:Sa:67:LEU:HG	1.97	0.46
1:L5:754:A:H2'	1:L5:755:A:C8	2.50	0.46
1:L5:1562:G:N2	1:L5:1576:U:H3	2.13	0.46
1:L5:4290:G:H2'	1:L5:4291:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4397:G:H2'	1:L5:4398:A:C8	2.51	0.46
4:LA:137:ILE:HD11	4:LA:147:ARG:HB3	1.96	0.46
11:LH:92:MET:HE2	11:LH:179:ILE:HG22	1.95	0.46
21:LS:85:ASP:OD1	21:LS:123:SER:HB2	2.15	0.46
23:LU:95:ASN:O	23:LU:96:LEU:HD23	2.15	0.46
46:S2:88:G:H21	46:S2:501:A:H5'	1.79	0.46
46:S2:922:G:O4'	74:Sb:21:LYS:NZ	2.32	0.46
46:S2:947:U:H2'	46:S2:948:G:C8	2.50	0.46
46:S2:1228:G:C2	46:S2:1229:A:C8	3.03	0.46
68:SV:20:SER:HB3	68:SV:22:ARG:HD3	1.97	0.46
78:Sg:73:SER:HB3	78:Sg:117:ASN:ND2	2.27	0.46
78:Sg:147:HIS:NE2	78:Sg:168:CYS:O	2.48	0.46
1:L5:357:C:H2'	1:L5:358:A:C8	2.51	0.46
1:L5:840:G:H3'	9:LF:170:LYS:HD2	1.97	0.46
1:L5:941:C:H2'	1:L5:942:C:H6	1.80	0.46
1:L5:945:G:H2'	1:L5:946:G:H8	1.79	0.46
1:L5:1881:C:H2'	1:L5:1882:G:C8	2.50	0.46
1:L5:2499:A:H2'	1:L5:2500:A:C8	2.51	0.46
1:L5:3261:A:H2'	1:L5:3262:C:O4'	2.14	0.46
1:L5:3264:U:H2'	1:L5:3265:A:C8	2.50	0.46
1:L5:4231:G:H2'	1:L5:4232:U:C6	2.50	0.46
5:LB:17:LEU:HB3	5:LB:18:PRO:HD3	1.97	0.46
6:LC:211:TYR:HE1	6:LC:229:LEU:HB3	1.80	0.46
8:LE:262:ASP:OD1	8:LE:266:LEU:HD13	2.16	0.46
14:LL:11:LYS:HG3	19:LQ:168:ARG:HH22	1.80	0.46
23:LU:102:VAL:O	23:LU:102:VAL:HG12	2.15	0.46
46:S2:41:G:N2	46:S2:481:G:H22	2.13	0.46
46:S2:848:A:H3'	46:S2:849:U:H6	1.80	0.46
46:S2:1385:C:C2	46:S2:1386:G:C8	3.04	0.46
46:S2:1502:C:H2'	46:S2:1503:C:H6	1.79	0.46
51:SD:24:PHE:CD1	51:SD:24:PHE:C	2.93	0.46
57:SJ:38:ARG:N	57:SJ:42:GLU:OE2	2.41	0.46
71:SY:80:ASP:OD1	71:SY:81:TYR:N	2.49	0.46
79:Sx:36:U:H2'	79:Sx:37:G:C8	2.51	0.46
1:L5:1156:U:H2'	1:L5:1157:A:H8	1.81	0.46
1:L5:1286:C:H2'	1:L5:1287:U:C6	2.51	0.46
1:L5:3377:G:H22	1:L5:3390:A:H2	1.64	0.46
1:L5:3885:U:H5'	43:Lo:3:ASN:HB3	1.96	0.46
3:L8:36:G:C5	36:Lh:89:ARG:HD3	2.50	0.46
3:L8:92:U:H2'	3:L8:93:C:O4'	2.15	0.46
34:Lf:33:VAL:HG13	34:Lf:38:GLU:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:38:A:N1	46:S2:516:G:H2'	2.31	0.46
46:S2:39:A:N6	46:S2:516:G:H1'	2.31	0.46
46:S2:152:U:C2	46:S2:153:G:N2	2.84	0.46
46:S2:1657:G:C2	46:S2:1658:G:C8	3.03	0.46
65:SS:110:ASP:OD1	65:SS:113:ARG:NH1	2.48	0.46
70:SX:94:ILE:HD12	70:SX:125:VAL:HG21	1.97	0.46
72:SZ:60:LYS:HB3	72:SZ:60:LYS:HE2	1.67	0.46
1:L5:435:C:H2'	1:L5:436:G:H8	1.80	0.46
1:L5:1226:G:H2'	1:L5:1227:G:C8	2.51	0.46
1:L5:1251:C:H1'	1:L5:1900:G:H3'	1.96	0.46
1:L5:1564:G:N2	1:L5:1575:C:O2'	2.49	0.46
1:L5:3577:U:H2'	1:L5:3578:U:C6	2.49	0.46
11:LH:59:LYS:HA	11:LH:59:LYS:HD2	1.56	0.46
46:S2:52:G:O2'	46:S2:53:C:O4'	2.18	0.46
47:S6:7:A:H62	47:S6:67:U:H3	1.64	0.46
47:S6:29:G:H1	47:S6:41:C:H5	1.63	0.46
51:SD:60:GLY:HA3	51:SD:65:ARG:H	1.81	0.46
2:L7:120:U:H5'	7:LD:262:LYS:HE3	1.98	0.46
46:S2:171:A:H8	46:S2:171:A:OP2	1.99	0.46
46:S2:176:U:C2	46:S2:314:A:N6	2.83	0.46
46:S2:864:U:C2	46:S2:865:A:C8	3.04	0.46
46:S2:1199:G:H2'	46:S2:1200:A:C8	2.51	0.46
46:S2:1427:U:H2'	46:S2:1428:C:C6	2.50	0.46
49:SB:183:GLU:OE1	49:SB:183:GLU:N	2.48	0.46
63:SQ:132:PHE:CD2	67:SU:77:TRP:HB2	2.51	0.46
64:SR:102:THR:O	64:SR:106:LEU:HD12	2.15	0.46
65:SS:11:HIS:O	65:SS:12:ILE:HD13	2.16	0.46
71:SY:40:ILE:HG21	71:SY:57:VAL:HG21	1.98	0.46
1:L5:139:G:H2'	1:L5:140:G:H8	1.80	0.46
1:L5:2332:G:OP1	28:LZ:107:LYS:NZ	2.38	0.46
1:L5:3256:A:H2'	1:L5:3257:G:H8	1.81	0.46
1:L5:3892:A:H2'	1:L5:3893:G:C8	2.51	0.46
27:LY:116:LYS:O	27:LY:120:GLU:HG2	2.16	0.46
36:Lh:14:LYS:HB2	36:Lh:14:LYS:HE2	1.69	0.46
46:S2:65:C:OP1	54:SG:175:LYS:HE2	2.16	0.46
46:S2:636:G:H2'	46:S2:637:C:H6	1.81	0.46
49:SB:166:LYS:O	49:SB:170:GLU:HG2	2.16	0.46
52:SE:19:MET:HB2	52:SE:51:ARG:HH12	1.79	0.46
72:SZ:57:LYS:O	72:SZ:57:LYS:HD3	2.15	0.46
78:Sg:59:LEU:HG	78:Sg:60:ARG:N	2.29	0.46
1:L5:822:U:H2'	1:L5:823:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:951:A:H2	1:L5:1034:G:H22	1.63	0.46
1:L5:1271:G:H4'	1:L5:1272:C:OP1	2.16	0.46
1:L5:3604:A:H3'	1:L5:3605:C:H5''	1.97	0.46
3:L8:127:U:H3'	3:L8:128:C:H6	1.81	0.46
7:LD:280:VAL:HG13	12:LI:206:LEU:HD11	1.98	0.46
16:LN:43:THR:HG22	16:LN:131:GLU:OE1	2.16	0.46
21:LS:101:THR:HG22	21:LS:104:GLY:H	1.81	0.46
48:SA:182:VAL:O	48:SA:186:ARG:HG2	2.16	0.46
61:SO:31:CYS:HA	61:SO:44:VAL:HA	1.98	0.46
72:SZ:99:LEU:HD13	72:SZ:109:TYR:CE1	2.51	0.46
78:Sg:246:TYR:CG	78:Sg:247:TRP:N	2.83	0.46
1:L5:1661:A:H2'	1:L5:1662:C:H6	1.80	0.46
1:L5:2439:C:H2'	1:L5:2440:G:O4'	2.15	0.46
3:L8:78:G:H2'	3:L8:79:G:C8	2.51	0.46
9:LF:136:LEU:HD21	9:LF:143:THR:HG22	1.99	0.46
17:LO:39:GLU:HG2	17:LO:139:GLY:HA3	1.97	0.46
18:LP:50:ASP:OD2	18:LP:56:GLN:NE2	2.47	0.46
19:LQ:89:ASP:O	19:LQ:112:ARG:NH1	2.49	0.46
21:LS:7:LEU:HD12	21:LS:33:PHE:HB3	1.97	0.46
38:Lj:63:ARG:NE	38:Lj:65:ARG:HG3	2.31	0.46
46:S2:35:C:H2'	46:S2:36:U:C6	2.51	0.46
46:S2:52:G:H8	46:S2:52:G:OP2	1.99	0.46
46:S2:84:A:H2'	46:S2:85:A:C8	2.51	0.46
46:S2:162:C:O5'	54:SG:87:ARG:NH1	2.48	0.46
46:S2:1241:A:H2'	46:S2:1242:A:C8	2.51	0.46
46:S2:1390:C:O2'	51:SD:162:ASP:HB3	2.16	0.46
46:S2:1744:G:H5''	46:S2:1745:G:OP2	2.15	0.46
47:S7:63:A:H2'	47:S7:64:U:C6	2.51	0.46
48:SA:39:TYR:CE2	64:SR:105:MET:HB2	2.51	0.46
55:SH:160:LYS:HA	55:SH:160:LYS:HD2	1.88	0.46
56:SI:11:ARG:NH1	56:SI:15:GLY:O	2.45	0.46
65:SS:43:VAL:HG21	66:ST:36:THR:HG23	1.98	0.46
66:ST:114:GLU:O	66:ST:122:LYS:N	2.40	0.46
1:L5:193:G:H2'	1:L5:194:C:C6	2.52	0.45
1:L5:1359:G:H2'	1:L5:1360:C:C6	2.51	0.45
1:L5:4131:G:O2'	1:L5:4255:A:N1	2.47	0.45
3:L8:94:G:C5	38:Lj:84:PRO:HG3	2.51	0.45
4:LA:31:ALA:HB2	4:LA:123:ARG:HH21	1.81	0.45
6:LC:31:PRO:O	6:LC:126:SER:OG	2.31	0.45
13:LJ:58:ARG:HG2	13:LJ:58:ARG:O	2.14	0.45
28:LZ:9:LYS:O	28:LZ:25:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LZ:61:LYS:HE2	28:LZ:61:LYS:HB2	1.85	0.45
46:S2:39:A:H2'	46:S2:40:A:O4'	2.16	0.45
61:SO:64:ALA:HB3	61:SO:67:ASP:OD1	2.16	0.45
67:SU:31:SER:HA	67:SU:34:LYS:HE2	1.97	0.45
67:SU:79:ARG:NH1	76:Sd:56:ASP:OXT	2.49	0.45
78:Sg:183:LYS:HE2	78:Sg:183:LYS:HB2	1.71	0.45
1:L5:124:C:OP1	16:LN:144:ARG:NH1	2.49	0.45
1:L5:1031:G:H2'	1:L5:1033:G:C8	2.51	0.45
1:L5:1523:C:H2'	1:L5:1524:G:C8	2.51	0.45
1:L5:3298:U:H5''	1:L5:3299:A:H5''	1.98	0.45
3:L8:144:U:H2'	3:L8:145:C:C6	2.52	0.45
12:LI:63:GLU:OE1	12:LI:63:GLU:N	2.49	0.45
27:LY:30:MET:HE3	27:LY:78:TYR:HA	1.99	0.45
36:Lh:12:LYS:HB3	36:Lh:12:LYS:HE3	1.85	0.45
37:Li:38:LYS:HB3	37:Li:38:LYS:HE2	1.71	0.45
46:S2:124:U:OP1	54:SG:201:LYS:NZ	2.50	0.45
46:S2:989:C:OP1	73:Sa:70:LYS:NZ	2.50	0.45
46:S2:1446:U:H1'	46:S2:1581:A:N6	2.31	0.45
46:S2:1471:C:H2'	46:S2:1472:C:C6	2.52	0.45
46:S2:1737:G:H2'	46:S2:1738:G:C8	2.50	0.45
48:SA:12:GLU:O	48:SA:15:VAL:HG12	2.16	0.45
49:SB:29:ASP:OD1	49:SB:29:ASP:N	2.46	0.45
51:SD:202:LYS:HB2	51:SD:202:LYS:HE3	1.48	0.45
52:SE:117:GLU:O	52:SE:118:GLU:HB3	2.16	0.45
63:SQ:50:LYS:HE3	63:SQ:50:LYS:HB3	1.76	0.45
65:SS:64:VAL:O	65:SS:68:ILE:HG12	2.16	0.45
1:L5:40:G:N2	1:L5:4033:A:H62	2.15	0.45
1:L5:4235:C:OP2	5:LB:28:LYS:NZ	2.36	0.45
1:L5:4237:A:H2'	1:L5:4238:U:O4'	2.15	0.45
15:LM:39:ASP:OD2	15:LM:47:ARG:HB2	2.17	0.45
16:LN:83:LYS:O	16:LN:85:VAL:N	2.50	0.45
20:LR:19:LYS:HB2	20:LR:19:LYS:HE3	1.79	0.45
23:LU:27:HIS:HB2	23:LU:28:PRO:HD2	1.98	0.45
46:S2:101:U:H5''	56:SI:19:LYS:HD2	1.98	0.45
46:S2:376:U:H2'	46:S2:377:A:C8	2.51	0.45
46:S2:433:G:H2'	46:S2:434:A:C8	2.51	0.45
46:S2:516:G:H5''	46:S2:517:A:H3'	1.98	0.45
46:S2:1253:C:OP1	67:SU:75:LYS:NZ	2.44	0.45
58:SK:64:TRP:CG	76:Sd:23:VAL:HG13	2.51	0.45
59:SL:144:LYS:HZ3	59:SL:146:THR:HG22	1.81	0.45
67:SU:42:GLY:HA2	67:SU:45:GLU:HG3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SW:76:SER:HB3	69:SW:77:PRO:HD3	1.99	0.45
1:L5:1561:G:C5	1:L5:1562:G:N7	2.84	0.45
1:L5:2301:G:O6	3:L8:123:U:H2'	2.16	0.45
1:L5:2345:A:H2'	1:L5:2346:U:H6	1.80	0.45
1:L5:2385:U:H5''	1:L5:2386:U:H5'	1.98	0.45
1:L5:4615:A:H2'	1:L5:4616:A:H8	1.82	0.45
4:LA:126:LEU:HD13	4:LA:150:LEU:HD21	1.98	0.45
9:LF:225:GLU:OE2	9:LF:225:GLU:N	2.49	0.45
12:LI:54:SER:OG	12:LI:55:ASP:N	2.49	0.45
13:LJ:40:LEU:O	13:LJ:44:THR:OG1	2.31	0.45
33:Le:114:ARG:NH1	33:Le:117:GLN:OE1	2.49	0.45
46:S2:35:C:H2'	46:S2:36:U:H6	1.81	0.45
46:S2:66:G:O6	46:S2:82:G:O2'	2.22	0.45
46:S2:68:A:H2'	46:S2:69:C:O4'	2.16	0.45
46:S2:799:G:N3	46:S2:799:G:H2'	2.30	0.45
50:SC:178:HIS:HB2	50:SC:220:ASP:HB3	1.98	0.45
59:SL:3:ASP:OD1	59:SL:4:ILE:HG12	2.17	0.45
1:L5:850:G:H2'	1:L5:851:C:C6	2.52	0.45
1:L5:1168:G:N7	19:LQ:104:ARG:NH2	2.64	0.45
1:L5:3431:A:H2'	1:L5:3432:A:N3	2.30	0.45
46:S2:5:U:H2'	46:S2:6:G:C8	2.52	0.45
46:S2:157:U:C2	54:SG:59:GLN:NE2	2.85	0.45
46:S2:180:G:H2'	46:S2:180:G:N3	2.32	0.45
46:S2:491:C:N3	46:S2:492:C:N4	2.64	0.45
46:S2:606:A:HO2'	46:S2:639:C:HO2'	1.63	0.45
46:S2:1555:C:H2'	46:S2:1556:U:C4	2.51	0.45
48:SA:176:TRP:CD2	48:SA:199:PRO:HB3	2.52	0.45
62:SP:41:GLN:N	62:SP:41:GLN:OE1	2.49	0.45
1:L5:754:A:H2	1:L5:818:G:H22	1.64	0.45
1:L5:886:U:H2'	1:L5:923:G:O6	2.16	0.45
1:L5:1524:G:H2'	1:L5:1525:C:C6	2.52	0.45
34:Lf:38:GLU:OE2	34:Lf:38:GLU:N	2.46	0.45
34:Lf:40:GLU:OE2	34:Lf:40:GLU:N	2.34	0.45
46:S2:83:A:H2	46:S2:150:A:HO2'	1.61	0.45
46:S2:443:C:H2'	46:S2:444:U:C6	2.51	0.45
46:S2:523:A:H4'	57:SJ:131:ARG:NH1	2.32	0.45
46:S2:1408:U:O2'	46:S2:1409:U:OP1	2.29	0.45
46:S2:1865:U:H3'	73:Sa:5:ARG:NH2	2.32	0.45
49:SB:38:MET:HE2	49:SB:182:LYS:HG3	1.98	0.45
49:SB:147:ASN:N	49:SB:147:ASN:OD1	2.43	0.45
52:SE:63:LYS:HA	52:SE:63:LYS:HD2	1.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SI:182:CYS:SG	56:SI:183:GLY:N	2.90	0.45
68:SV:53:TYR:OH	68:SV:76:ASP:OD2	2.34	0.45
70:SX:33:GLY:O	70:SX:37:LYS:HG2	2.17	0.45
1:L5:381:G:N1	1:L5:384:A:OP2	2.39	0.45
1:L5:828:C:C2	1:L5:829:G:C2	3.05	0.45
1:L5:2052:C:H2'	1:L5:2053:G:H8	1.81	0.45
7:LD:83:LEU:N	7:LD:84:PRO:HD2	2.31	0.45
11:LH:106:GLN:HB3	11:LH:107:GLU:OE1	2.17	0.45
19:LQ:49:LYS:HE2	19:LQ:49:LYS:HB3	1.81	0.45
21:LS:85:ASP:HA	21:LS:90:THR:HA	1.98	0.45
39:Lk:5:ILE:HD13	39:Lk:5:ILE:HA	1.86	0.45
46:S2:33:G:C4	46:S2:524:A:N6	2.84	0.45
54:SG:49:VAL:HB	54:SG:115:LYS:HB3	1.97	0.45
55:SH:163:GLN:O	55:SH:167:GLU:HB3	2.17	0.45
56:SI:168:GLN:N	56:SI:168:GLN:OE1	2.49	0.45
70:SX:138:LYS:HZ2	70:SX:140:ARG:H	1.62	0.45
75:Sc:31:ARG:HA	75:Sc:43:ILE:HA	1.98	0.45
1:L5:106:A:H2'	1:L5:107:G:O4'	2.16	0.45
1:L5:1906:G:H2'	1:L5:1907:G:C8	2.52	0.45
1:L5:4570:C:O2	1:L5:4572:C:N4	2.39	0.45
3:L8:1:C:H3'	3:L8:2:G:H21	1.82	0.45
38:Lj:20:ARG:HD2	38:Lj:39:TYR:CZ	2.51	0.45
46:S2:1790:G:H5'	46:S2:1791:A:OP1	2.17	0.45
47:S7:34:C:H42	79:Sx:40:G:H1	1.65	0.45
47:S7:69:U:H2'	47:S7:70:G:O4'	2.16	0.45
50:SC:142:LYS:HB3	50:SC:154:ALA:HB2	1.97	0.45
53:SF:61:PHE:CE1	75:Sc:49:PRO:HB2	2.52	0.45
53:SF:192:LYS:HD3	53:SF:192:LYS:HA	1.71	0.45
55:SH:148:LEU:HD23	69:SW:42:MET:HE1	1.98	0.45
63:SQ:62:ARG:HE	63:SQ:108:ILE:HG21	1.82	0.45
70:SX:138:LYS:NZ	70:SX:140:ARG:H	2.14	0.45
71:SY:37:LYS:HE3	71:SY:37:LYS:HB3	1.60	0.45
1:L5:1155:C:H2'	1:L5:1156:U:H6	1.82	0.45
1:L5:3723:C:C2	1:L5:3724:A:C8	3.05	0.45
1:L5:4073:U:H5''	1:L5:4074:C:H5	1.81	0.45
1:L5:4087:C:H2'	1:L5:4088:U:C6	2.52	0.45
9:LF:174:GLU:HG3	9:LF:270:ASN:ND2	2.32	0.45
14:LL:49:ARG:O	14:LL:149:GLN:HG3	2.17	0.45
46:S2:53:C:H42	46:S2:473:C:N4	1.97	0.45
46:S2:1549:G:H2'	46:S2:1550:U:C6	2.52	0.45
46:S2:1588:G:OP1	46:S2:1588:G:N2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S7:9:U:O2'	47:S7:48:C:H1'	2.17	0.45
52:SE:23:LEU:HD23	52:SE:23:LEU:O	2.17	0.45
53:SF:101:HIS:O	53:SF:105:GLY:N	2.49	0.45
54:SG:18:VAL:HG13	54:SG:23:LYS:HD3	1.98	0.45
56:SI:107:THR:OG1	56:SI:108:PRO:HD3	2.17	0.45
62:SP:53:GLN:N	62:SP:53:GLN:OE1	2.50	0.45
68:SV:40:ASP:OD1	68:SV:41:ARG:N	2.49	0.45
1:L5:266:G:H2'	1:L5:267:G:C8	2.52	0.45
1:L5:4190:C:H2'	1:L5:4191:G:C8	2.50	0.45
3:L8:94:G:O2'	38:Lj:82:THR:O	2.27	0.45
7:LD:220:LYS:HB3	7:LD:220:LYS:HE2	1.63	0.45
14:LL:172:GLU:OE2	14:LL:172:GLU:N	2.45	0.45
24:LV:83:ARG:HB2	24:LV:102:ALA:HB3	1.99	0.45
33:Le:76:LYS:HE2	33:Le:98:GLU:OE2	2.16	0.45
46:S2:47:G:H1	46:S2:479:G:H1	1.64	0.45
46:S2:1104:C:H2'	46:S2:1105:G:C8	2.50	0.45
46:S2:1568:G:H2'	46:S2:1569:C:C6	2.52	0.45
49:SB:99:ASN:OD1	49:SB:100:PHE:N	2.49	0.45
57:SJ:3:VAL:HG23	57:SJ:5:ARG:HB2	1.98	0.45
59:SL:5:GLN:HE22	59:SL:11:GLN:HB2	1.81	0.45
67:SU:67:LYS:HA	76:Sd:44:ARG:HD2	1.98	0.45
72:SZ:79:ILE:HG23	72:SZ:83:LEU:HB3	1.99	0.45
75:Sc:50:VAL:HG23	75:Sc:51:ARG:H	1.82	0.45
78:Sg:11:LEU:HB3	78:Sg:43:TRP:CH2	2.52	0.45
1:L5:940:C:H2'	1:L5:941:C:C6	2.53	0.44
1:L5:2221:C:O2'	1:L5:2222:C:H6	1.99	0.44
1:L5:4387:A:H1'	1:L5:4388:G:C8	2.51	0.44
3:L8:19:C:H2'	3:L8:20:A:C8	2.51	0.44
10:LG:88:ASP:OD1	10:LG:91:THR:HG22	2.17	0.44
24:LV:127:ASP:OD1	24:LV:127:ASP:N	2.33	0.44
32:Ld:24:GLU:OE2	32:Ld:87:ARG:NH2	2.47	0.44
34:Lf:43:LEU:HD23	34:Lf:43:LEU:HA	1.82	0.44
39:Lk:52:LYS:HA	39:Lk:55:LYS:HG2	1.97	0.44
46:S2:595:A:N6	46:S2:643:U:H2'	2.31	0.44
46:S2:960:G:H1'	46:S2:965:A:N6	2.32	0.44
46:S2:1619:C:H3'	46:S2:1620:A:H8	1.82	0.44
48:SA:34:MET:SD	48:SA:150:THR:HA	2.57	0.44
53:SF:157:GLY:HA2	53:SF:188:TYR:HD2	1.82	0.44
54:SG:120:ASP:OD1	54:SG:120:ASP:N	2.49	0.44
57:SJ:143:ASN:N	57:SJ:143:ASN:OD1	2.50	0.44
59:SL:61:PRO:HD3	59:SL:141:ASN:ND2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SQ:12:VAL:HG21	63:SQ:91:ALA:HA	1.99	0.44
63:SQ:98:LYS:NZ	78:Sg:59:LEU:HD13	2.29	0.44
64:SR:70:SER:HB2	64:SR:73:LEU:HD23	2.00	0.44
1:L5:156:G:N2	1:L5:157:U:O4	2.49	0.44
1:L5:162:A:H2'	1:L5:163:A:H8	1.82	0.44
1:L5:1034:G:H2'	1:L5:1035:U:C6	2.52	0.44
1:L5:2584:G:O6	1:L5:3513:A:N6	2.49	0.44
1:L5:4510:U:H2'	1:L5:4511:C:C6	2.52	0.44
1:L5:4549:G:O6	1:L5:4565:G:H1'	2.17	0.44
8:LE:178:SER:O	8:LE:178:SER:OG	2.29	0.44
20:LR:134:ASN:HB2	20:LR:137:ILE:HG12	1.99	0.44
36:Lh:13:LYS:HD3	36:Lh:13:LYS:HA	1.74	0.44
46:S2:456:A:H2'	46:S2:457:C:H6	1.81	0.44
46:S2:1568:G:H8	46:S2:1568:G:OP1	2.01	0.44
60:SN:93:LYS:HG3	60:SN:150:VAL:HG21	1.98	0.44
66:ST:129:ARG:HD2	66:ST:129:ARG:HA	1.83	0.44
66:ST:130:ASP:HA	66:ST:133:ARG:HD2	1.98	0.44
1:L5:1675:G:O2'	1:L5:3872:A:N3	2.45	0.44
1:L5:3553:C:HO2'	5:LB:268:ARG:HH12	1.62	0.44
1:L5:3868:C:C2	1:L5:3869:G:C8	3.06	0.44
1:L5:4059:U:H2'	1:L5:4060:G:H8	1.82	0.44
2:L7:4:U:H2'	2:L7:5:A:C8	2.51	0.44
3:L8:13:G:C4	3:L8:14:U:C5	3.05	0.44
3:L8:133:G:H2'	3:L8:134:G:H8	1.82	0.44
35:Lg:101:LYS:HA	35:Lg:104:VAL:HG12	1.99	0.44
46:S2:292:G:N3	59:SL:41:GLY:HA3	2.32	0.44
46:S2:836:C:H4'	46:S2:837:G:N7	2.32	0.44
46:S2:1014:U:C2	46:S2:1015:G:C8	3.05	0.44
47:S7:34:C:H2'	47:S7:35:A:N3	2.32	0.44
50:SC:91:SER:HB2	50:SC:159:LYS:HB2	1.98	0.44
64:SR:71:ILE:HD13	64:SR:71:ILE:HA	1.88	0.44
66:ST:116:ASP:HB3	66:ST:122:LYS:HB2	1.99	0.44
78:Sg:32:LEU:HA	78:Sg:42:MET:HA	1.99	0.44
78:Sg:42:MET:SD	78:Sg:56:GLN:HG3	2.58	0.44
1:L5:7:C:H2'	1:L5:8:U:H6	1.83	0.44
1:L5:952:C:H2'	1:L5:953:C:C6	2.52	0.44
1:L5:1036:C:OP2	1:L5:1037:G:H5''	2.17	0.44
1:L5:1715:G:N2	17:LO:87:MET:HE2	2.33	0.44
1:L5:4581:C:H2'	1:L5:4582:G:H8	1.82	0.44
28:LZ:27:LYS:HE3	28:LZ:27:LYS:HB3	1.81	0.44
28:LZ:97:ASN:OD1	28:LZ:98:LYS:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Lc:22:MET:HE3	31:Lc:22:MET:HA	1.98	0.44
32:Ld:65:ASP:OD1	32:Ld:67:ARG:N	2.37	0.44
41:Lm:79:GLU:CD	41:Lm:81:SER:HG	2.21	0.44
46:S2:1278:C:H42	46:S2:1322:G:H22	1.66	0.44
46:S2:1379:A:H4'	46:S2:1380:A:O5'	2.18	0.44
48:SA:176:TRP:CE3	48:SA:177:MET:HG2	2.53	0.44
55:SH:116:ARG:CZ	55:SH:121:THR:HG22	2.47	0.44
64:SR:7:LYS:HE2	64:SR:7:LYS:HB2	1.81	0.44
1:L5:31:U:H2'	1:L5:32:G:O4'	2.18	0.44
1:L5:433:A:H3'	1:L5:434:A:H8	1.82	0.44
1:L5:1157:A:OP1	16:LN:204:ARG:HD2	2.18	0.44
1:L5:1366:G:O2'	1:L5:1388:G:N2	2.43	0.44
1:L5:2276:U:H1'	1:L5:2277:C:C6	2.52	0.44
2:L7:60:G:HO2'	2:L7:61:G:P	2.39	0.44
5:LB:364:ASP:OD1	5:LB:364:ASP:N	2.51	0.44
46:S2:381:G:OP2	56:SI:181:GLN:NE2	2.48	0.44
46:S2:1006:G:H2'	46:S2:1007:C:H6	1.82	0.44
46:S2:1615:A:H2'	46:S2:1616:U:C6	2.53	0.44
47:S7:3:G:H1	47:S7:72:U:H3	1.65	0.44
50:SC:211:LYS:HA	50:SC:214:LEU:HB2	1.99	0.44
63:SQ:72:VAL:HB	63:SQ:84:ILE:HD11	1.99	0.44
71:SY:55:ILE:HD11	71:SY:75:ILE:HG23	1.99	0.44
1:L5:174:C:H2'	1:L5:175:C:C6	2.51	0.44
7:LD:41:LYS:HE3	22:LT:93:ILE:HD13	2.00	0.44
15:LM:101:LYS:HB2	17:LO:200:GLY:HA3	1.99	0.44
46:S2:116:U:H5'	46:S2:382:C:O2	2.16	0.44
50:SC:130:ILE:HD13	50:SC:159:LYS:HG2	1.99	0.44
57:SJ:88:ASP:OD1	57:SJ:89:GLU:N	2.51	0.44
63:SQ:97:GLN:HB2	63:SQ:105:LYS:HD2	2.00	0.44
66:ST:111:LYS:HD2	66:ST:111:LYS:HA	1.90	0.44
72:SZ:98:LYS:HZ3	72:SZ:110:THR:HG1	1.56	0.44
75:Sc:13:ARG:NH1	75:Sc:53:GLY:O	2.51	0.44
78:Sg:42:MET:HG3	78:Sg:57:ARG:O	2.17	0.44
78:Sg:226:HIS:O	78:Sg:227:LEU:HD22	2.17	0.44
1:L5:854:A:H1'	1:L5:1879:G:H5''	1.99	0.44
1:L5:4008:G:C2	1:L5:4009:G:C8	3.06	0.44
7:LD:90:VAL:HG21	7:LD:231:VAL:HG21	2.00	0.44
10:LG:108:GLN:O	10:LG:112:GLN:HG2	2.17	0.44
14:LL:119:GLU:OE1	14:LL:155:MET:HE1	2.18	0.44
31:Lc:47:ILE:HB	31:Lc:94:LEU:HB3	2.00	0.44
37:Li:3:LEU:HA	37:Li:3:LEU:HD12	1.73	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:564:G:H22	46:S2:593:C:H41	1.66	0.44
46:S2:865:A:H2'	46:S2:866:A:H8	1.82	0.44
46:S2:1200:A:H2'	46:S2:1201:A:C8	2.53	0.44
46:S2:1563:C:H4'	66:ST:119:GLY:HA3	2.00	0.44
48:SA:127:PRO:HG2	48:SA:152:SER:HB3	2.00	0.44
52:SE:131:VAL:HA	52:SE:137:PRO:HA	2.00	0.44
54:SG:10:THR:HB	54:SG:128:THR:HG22	1.99	0.44
54:SG:45:TRP:NE1	54:SG:121:ILE:HG12	2.33	0.44
54:SG:192:ILE:HG13	54:SG:195:LYS:HE2	1.99	0.44
59:SL:5:GLN:NE2	59:SL:11:GLN:HB2	2.33	0.44
61:SO:96:LYS:HD2	61:SO:132:VAL:HG21	2.00	0.44
64:SR:103:LYS:O	64:SR:107:LYS:HG2	2.18	0.44
1:L5:189:G:H22	1:L5:252:G:H1	1.64	0.44
1:L5:2460:G:O2'	1:L5:2462:U:O4'	2.33	0.44
1:L5:3530:G:H2'	1:L5:3531:G:C8	2.53	0.44
5:LB:19:ARG:HB2	5:LB:234:ARG:HH21	1.82	0.44
5:LB:292:LEU:O	5:LB:298:LEU:N	2.41	0.44
37:Li:16:LYS:HA	37:Li:16:LYS:HD3	1.84	0.44
46:S2:967:U:H2'	46:S2:968:C:C6	2.53	0.44
46:S2:1026:U:H2'	46:S2:1027:C:O4'	2.18	0.44
46:S2:1184:A:H2'	46:S2:1185:G:H8	1.81	0.44
46:S2:1274:C:O3'	46:S2:1275:G:H8	2.00	0.44
46:S2:1416:C:H4'	46:S2:1417:C:OP2	2.14	0.44
46:S2:1523:A:C5	62:SP:128:HIS:HB3	2.53	0.44
48:SA:121:LEU:HD12	48:SA:122:LEU:H	1.82	0.44
48:SA:192:GLU:H	48:SA:192:GLU:CD	2.26	0.44
50:SC:201:GLY:O	57:SJ:54:ARG:NH2	2.51	0.44
62:SP:57:LEU:HD22	62:SP:61:ARG:NH2	2.32	0.44
77:Se:102:LYS:HE2	77:Se:106:ALA:HB3	2.00	0.44
1:L5:124:C:H2'	1:L5:125:C:H6	1.83	0.44
1:L5:653:G:O2'	1:L5:654:G:H5''	2.18	0.44
1:L5:950:G:H2'	1:L5:951:A:C4	2.53	0.44
1:L5:1497:U:H2'	1:L5:1498:A:C8	2.53	0.44
1:L5:1640:A:H2'	1:L5:1641:A:H8	1.83	0.44
1:L5:2401:A:H62	1:L5:2440:G:H21	1.66	0.44
32:Ld:65:ASP:OD1	32:Ld:66:THR:N	2.50	0.44
46:S2:152:U:N3	46:S2:167:G:C6	2.85	0.44
46:S2:380:C:H2'	46:S2:381:G:C8	2.53	0.44
46:S2:994:G:N7	73:Sa:15:ARG:NH1	2.65	0.44
52:SE:86:PHE:HE1	52:SE:102:ILE:HG13	1.83	0.44
52:SE:125:LYS:HG2	52:SE:127:ARG:HH11	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SI:154:LYS:HD3	56:SI:154:LYS:H	1.83	0.44
61:SO:82:ALA:O	61:SO:86:LYS:HG3	2.16	0.44
1:L5:1167:C:H2'	1:L5:1168:G:O4'	2.17	0.43
1:L5:1181:G:C2	14:LL:33:ILE:HD13	2.53	0.43
2:L7:60:G:HO2'	7:LD:268:ARG:HH21	1.61	0.43
7:LD:157:ASN:HB3	7:LD:159:VAL:HG22	1.99	0.43
10:LG:96:LEU:HD23	10:LG:96:LEU:HA	1.84	0.43
13:LJ:68:ILE:HG13	13:LJ:69:ALA:N	2.32	0.43
21:LS:25:PRO:HA	21:LS:26:PRO:HD3	1.90	0.43
31:Lc:94:LEU:HD12	31:Lc:95:ALA:H	1.83	0.43
36:Lh:97:LYS:H	36:Lh:97:LYS:HG2	1.63	0.43
39:Lk:57:LYS:HZ3	39:Lk:66:VAL:HG21	1.83	0.43
46:S2:867:U:H2'	46:S2:868:G:C8	2.53	0.43
46:S2:943:G:OP1	49:SB:216:LYS:NZ	2.39	0.43
51:SD:68:GLU:O	51:SD:72:VAL:HG12	2.19	0.43
53:SF:17:ILE:HA	53:SF:48:TYR:HE1	1.83	0.43
78:Sg:289:LEU:HD23	78:Sg:289:LEU:HA	1.79	0.43
1:L5:93:G:H2'	1:L5:94:A:C8	2.53	0.43
1:L5:143:U:H2'	1:L5:144:G:H5''	1.99	0.43
1:L5:923:G:O2'	1:L5:924:G:OP1	2.34	0.43
1:L5:1218:C:C4	1:L5:1219:C:N4	2.86	0.43
1:L5:3491:C:H2'	1:L5:3492:C:H6	1.82	0.43
1:L5:3886:A:N7	1:L5:3888:G:C8	2.86	0.43
1:L5:4012:U:H2'	1:L5:4013:U:O2	2.18	0.43
1:L5:4331:G:N2	1:L5:4366:G:H1'	2.33	0.43
20:LR:78:ILE:HD12	20:LR:78:ILE:H	1.81	0.43
32:Ld:85:ARG:CZ	32:Ld:117:LEU:HD12	2.47	0.43
46:S2:34:U:O2'	46:S2:35:C:OP1	2.31	0.43
46:S2:502:C:H2'	46:S2:503:C:H5''	1.99	0.43
46:S2:1014:U:N3	46:S2:1015:G:N7	2.66	0.43
46:S2:1205:A:H2'	46:S2:1206:C:C6	2.53	0.43
46:S2:1403:A:H5''	67:SU:51:LYS:HG3	2.00	0.43
48:SA:67:ALA:HB2	68:SV:37:ALA:HB2	2.01	0.43
48:SA:85:ARG:O	48:SA:89:LYS:HG2	2.17	0.43
50:SC:215:MET:HE3	50:SC:215:MET:HB2	1.78	0.43
53:SF:140:ASP:HB2	75:Sc:44:ARG:NH2	2.33	0.43
59:SL:93:LEU:HD12	59:SL:102:PHE:HB3	1.99	0.43
60:SN:96:VAL:HG12	60:SN:100:LYS:HE2	1.99	0.43
63:SQ:37:ARG:HH21	66:ST:11:GLN:HE21	1.66	0.43
67:SU:62:ARG:O	67:SU:63:ILE:HG13	2.18	0.43
70:SX:7:LEU:HD23	70:SX:7:LEU:HA	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sg:147:HIS:CD2	78:Sg:169:GLY:HA3	2.53	0.43
1:L5:138:C:H2'	1:L5:139:G:H8	1.82	0.43
1:L5:441:G:H2'	1:L5:442:G:C8	2.52	0.43
1:L5:745:C:H4'	1:L5:746:C:OP2	2.18	0.43
1:L5:937:C:C2'	1:L5:938:C:H5'	2.48	0.43
1:L5:1415:A:OP2	38:Lj:4:GLY:HA3	2.19	0.43
1:L5:2505:G:C2	1:L5:2506:G:N7	2.86	0.43
1:L5:2645:U:P	20:LR:74:ARG:HH21	2.41	0.43
5:LB:139:ASP:O	5:LB:143:LYS:HG3	2.17	0.43
45:Lr:89:THR:O	45:Lr:93:ILE:HG12	2.18	0.43
46:S2:116:U:C5'	46:S2:382:C:H1'	2.48	0.43
46:S2:523:A:H3'	57:SJ:38:ARG:NH1	2.33	0.43
46:S2:805:U:H2'	46:S2:806:U:C6	2.53	0.43
47:S6:28:U:H2'	47:S6:29:G:H8	1.82	0.43
47:S6:71:C:H2'	47:S6:72:U:C6	2.52	0.43
51:SD:10:LYS:HB2	51:SD:10:LYS:HE3	1.54	0.43
52:SE:46:ILE:O	52:SE:50:ASN:HB2	2.18	0.43
54:SG:20:ASP:HB3	54:SG:23:LYS:NZ	2.33	0.43
56:SI:11:ARG:HG3	56:SI:16:GLY:O	2.18	0.43
56:SI:79:ILE:HD12	56:SI:104:ILE:HA	1.99	0.43
57:SJ:28:GLU:O	57:SJ:32:ILE:HG22	2.18	0.43
66:ST:130:ASP:O	66:ST:134:ILE:HD12	2.17	0.43
70:SX:99:GLU:HA	70:SX:99:GLU:OE2	2.18	0.43
70:SX:100:VAL:HG12	70:SX:125:VAL:HG23	2.00	0.43
1:L5:4507:G:C2	1:L5:4508:G:C6	3.06	0.43
3:L8:6:C:C2	3:L8:7:U:C5	3.07	0.43
5:LB:19:ARG:HB2	5:LB:234:ARG:NH2	2.33	0.43
5:LB:142:GLY:O	5:LB:146:LEU:HG	2.18	0.43
31:Lc:44:LYS:NZ	31:Lc:97:ILE:O	2.42	0.43
46:S2:342:C:H2'	46:S2:343:C:C6	2.53	0.43
46:S2:556:A:H2'	46:S2:557:U:O4'	2.19	0.43
46:S2:562:A:H2'	46:S2:563:U:C6	2.53	0.43
46:S2:944:U:H2'	46:S2:945:A:H8	1.84	0.43
46:S2:1380:A:H2'	46:S2:1381:C:C6	2.54	0.43
46:S2:1396:C:H2'	46:S2:1397:A:O4'	2.19	0.43
46:S2:1422:A:H3'	46:S2:1423:G:H5''	2.00	0.43
46:S2:1539:C:H2'	46:S2:1540:U:C6	2.53	0.43
51:SD:179:GLN:OE1	51:SD:179:GLN:N	2.50	0.43
52:SE:119:ALA:O	52:SE:164:LEU:HD11	2.18	0.43
53:SF:22:LYS:HE2	53:SF:23:TRP:CE2	2.54	0.43
74:Sb:63:LEU:O	74:Sb:74:THR:OG1	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sg:302:TYR:HE2	78:Sg:308:ARG:HE	1.64	0.43
1:L5:162:A:H2'	1:L5:163:A:C8	2.53	0.43
1:L5:299:A:H2'	1:L5:300:G:C8	2.52	0.43
1:L5:4527:U:C4	15:LM:113:MET:HG2	2.53	0.43
6:LC:84:THR:HG22	6:LC:85:HIS:H	1.84	0.43
19:LQ:98:LEU:HD23	19:LQ:98:LEU:HA	1.75	0.43
31:Lc:77:ASN:ND2	31:Lc:77:ASN:H	2.16	0.43
34:Lf:106:TYR:HB2	34:Lf:107:PRO:HD3	2.01	0.43
46:S2:649:A:H4'	70:SX:104:GLY:O	2.18	0.43
46:S2:864:U:H2'	46:S2:865:A:H8	1.83	0.43
55:SH:184:ASP:OD1	55:SH:184:ASP:N	2.35	0.43
58:SK:15:LEU:HG	58:SK:71:LEU:HD21	2.00	0.43
64:SR:109:LEU:HD23	64:SR:109:LEU:HA	1.77	0.43
70:SX:128:VAL:HG13	70:SX:129:SER:N	2.33	0.43
71:SY:76:TYR:OH	71:SY:85:ASN:O	2.35	0.43
71:SY:110:ARG:HG3	71:SY:114:MET:HE3	2.00	0.43
1:L5:172:C:OP2	14:LL:135:LYS:HE2	2.18	0.43
1:L5:511:G:O2'	1:L5:513:U:OP2	2.30	0.43
1:L5:1257:A:H2'	1:L5:1258:G:C8	2.54	0.43
1:L5:2386:U:H2'	1:L5:2387:U:C6	2.54	0.43
1:L5:3417:A:H4'	1:L5:3418:C:O5'	2.17	0.43
1:L5:3587:U:H2'	1:L5:3588:C:C6	2.53	0.43
1:L5:4685:U:H2'	1:L5:4686:A:C8	2.53	0.43
8:LE:127:GLU:OE1	8:LE:128:ASP:N	2.44	0.43
21:LS:16:CYS:HB2	21:LS:25:PRO:HB3	2.00	0.43
35:Lg:33:LEU:HD23	35:Lg:33:LEU:HA	1.89	0.43
46:S2:16:G:H2'	46:S2:17:C:C6	2.54	0.43
46:S2:152:U:C2	46:S2:167:G:N1	2.87	0.43
46:S2:225:C:O2'	46:S2:226:A:H8	2.00	0.43
46:S2:616:C:H2'	46:S2:617:A:O4'	2.18	0.43
46:S2:1376:G:H2'	46:S2:1377:A:C8	2.54	0.43
46:S2:1553:G:H22	76:Sd:32:ARG:HB3	1.84	0.43
48:SA:198:MET:H	48:SA:198:MET:HE3	1.83	0.43
51:SD:35:SER:HA	51:SD:99:ILE:HG23	1.99	0.43
53:SF:184:SER:O	53:SF:190:ILE:HG21	2.19	0.43
58:SK:35:LEU:HD13	58:SK:35:LEU:HA	1.91	0.43
58:SK:47:LYS:HA	58:SK:47:LYS:HD2	1.72	0.43
61:SO:117:ARG:NH2	73:Sa:49:ALA:O	2.41	0.43
62:SP:61:ARG:O	62:SP:65:LYS:HG2	2.17	0.43
78:Sg:116:ASP:OD1	78:Sg:116:ASP:N	2.42	0.43
1:L5:2378:G:H2'	1:L5:2379:U:H6	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L7:27:G:P	7:LD:56:THR:HG1	2.41	0.43
2:L7:111:C:H2'	2:L7:112:U:O4'	2.19	0.43
4:LA:109:GLU:HG2	4:LA:138:SER:HA	2.00	0.43
5:LB:82:PRO:HG3	5:LB:171:LEU:HD21	2.01	0.43
6:LC:198:ASN:ND2	27:LY:10:ASP:OD1	2.44	0.43
17:LO:144:GLU:H	17:LO:144:GLU:CD	2.26	0.43
30:Lb:106:ILE:O	30:Lb:110:MET:HG3	2.19	0.43
35:Lg:57:ARG:HE	35:Lg:57:ARG:HB3	1.68	0.43
36:Lh:50:VAL:O	36:Lh:54:ILE:HG13	2.18	0.43
46:S2:12:U:H2'	46:S2:13:C:C6	2.54	0.43
46:S2:12:U:H2'	46:S2:13:C:H6	1.83	0.43
46:S2:430:C:H2'	46:S2:431:C:C6	2.54	0.43
46:S2:1031:A:H2'	46:S2:1032:A:H8	1.83	0.43
50:SC:212:LYS:HA	50:SC:212:LYS:HD3	1.82	0.43
52:SE:240:ARG:CZ	52:SE:240:ARG:HB3	2.48	0.43
53:SF:81:ARG:O	53:SF:85:LYS:NZ	2.51	0.43
55:SH:111:LYS:HD3	55:SH:111:LYS:N	2.34	0.43
57:SJ:97:ILE:HD12	57:SJ:97:ILE:H	1.84	0.43
71:SY:43:LYS:HE3	71:SY:43:LYS:HB2	1.79	0.43
72:SZ:99:LEU:HD12	72:SZ:100:VAL:H	1.84	0.43
1:L5:219:G:OP1	6:LC:172:LYS:NZ	2.52	0.43
1:L5:1012:U:HO2'	1:L5:1013:C:P	2.39	0.43
1:L5:3527:C:H2'	1:L5:3528:A:H8	1.84	0.43
1:L5:3976:A:H2	7:LD:146:LEU:HD23	1.84	0.43
1:L5:4512:C:H2'	1:L5:4513:G:C8	2.53	0.43
3:L8:127:U:H3'	3:L8:128:C:C6	2.54	0.43
5:LB:305:THR:C	5:LB:307:TYR:H	2.27	0.43
14:LL:18:TRP:CD1	14:LL:18:TRP:H	2.37	0.43
15:LM:6:TYR:CD2	21:LS:151:LYS:HD3	2.54	0.43
46:S2:97:U:H3	46:S2:433:G:H1	1.66	0.43
46:S2:97:U:H4'	46:S2:98:C:OP2	2.18	0.43
46:S2:163:U:O2'	54:SG:62:PRO:HG3	2.19	0.43
46:S2:345:U:H2'	46:S2:346:U:H6	1.83	0.43
46:S2:353:U:H2'	46:S2:354:C:C6	2.54	0.43
46:S2:381:G:H1'	56:SI:5:ARG:HD3	2.01	0.43
46:S2:569:C:O2'	46:S2:584:A:N1	2.44	0.43
46:S2:675:C:H2'	46:S2:676:U:C6	2.54	0.43
55:SH:165:ASN:C	55:SH:165:ASN:OD1	2.61	0.43
57:SJ:143:ASN:O	57:SJ:144:ILE:HG12	2.19	0.43
67:SU:78:ASP:OD1	76:Sd:54:LYS:HD2	2.18	0.43
69:SW:11:LEU:HD12	69:SW:74:VAL:HB	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:854:A:H62	1:L5:1098:G:H1'	1.83	0.43
1:L5:2016:G:H5''	8:LE:99:THR:HG21	2.01	0.43
1:L5:2033:A:H2'	1:L5:2034:C:O4'	2.19	0.43
1:L5:2296:C:H2'	1:L5:2297:C:C6	2.53	0.43
1:L5:3518:A:H2'	1:L5:3519:A:H8	1.84	0.43
1:L5:3568:C:H2'	1:L5:3569:U:H6	1.83	0.43
22:LT:103:ASP:HA	22:LT:106:LEU:HD12	2.00	0.43
46:S2:164:A:H2'	46:S2:165:G:C4	2.53	0.43
46:S2:521:A:OP1	57:SJ:12:THR:HG22	2.19	0.43
46:S2:1102:U:H2'	46:S2:1103:G:C8	2.54	0.43
46:S2:1287:G:N2	46:S2:1313:G:O2'	2.51	0.43
46:S2:1713:A:H2'	46:S2:1714:C:C6	2.54	0.43
47:S6:35:A:OP1	63:SQ:146:ARG:NH1	2.52	0.43
48:SA:24:HIS:CD2	64:SR:102:THR:HG21	2.53	0.43
48:SA:69:GLU:OE2	50:SC:270:THR:HB	2.19	0.43
50:SC:95:ASP:OD1	50:SC:96:PHE:N	2.51	0.43
54:SG:46:LYS:HD3	54:SG:46:LYS:HA	1.79	0.43
68:SV:58:ALA:O	68:SV:62:MET:HG3	2.19	0.43
74:Sb:35:VAL:HG13	74:Sb:78:SER:O	2.19	0.43
78:Sg:78:ALA:N	78:Sg:90:TRP:O	2.52	0.43
1:L5:1222:C:O2'	1:L5:1226:G:N3	2.47	0.43
1:L5:1459:C:H2'	1:L5:1460:A:C8	2.54	0.43
1:L5:3337:U:OP1	4:LA:54:ARG:NH2	2.34	0.43
1:L5:4398:A:H2'	1:L5:4399:G:O4'	2.18	0.43
3:L8:6:C:H2'	3:L8:7:U:H6	1.83	0.43
4:LA:114:CYS:HB3	4:LA:167:GLY:O	2.19	0.43
7:LD:208:MET:HB3	7:LD:233:PRO:HG3	1.99	0.43
19:LQ:115:LYS:HE3	19:LQ:115:LYS:HB2	1.84	0.43
37:Li:67:LYS:O	37:Li:71:LYS:HG3	2.18	0.43
46:S2:615:C:H2'	46:S2:627:G:C8	2.54	0.43
46:S2:1200:A:H2'	46:S2:1201:A:H8	1.84	0.43
46:S2:1523:A:N7	62:SP:128:HIS:HB3	2.33	0.43
51:SD:172:VAL:HG22	51:SD:185:LYS:HD2	2.00	0.43
53:SF:168:THR:HG21	72:SZ:106:GLN:HE22	1.84	0.43
60:SN:100:LYS:O	60:SN:103:GLU:HG3	2.18	0.43
63:SQ:92:LEU:HD12	63:SQ:96:TYR:CE2	2.53	0.43
66:ST:125:PRO:HD2	66:ST:126:GLN:OE1	2.19	0.43
78:Sg:64:HIS:CG	78:Sg:65:PHE:H	2.36	0.43
78:Sg:237:ASN:HD22	78:Sg:287:THR:HG22	1.84	0.43
1:L5:18:C:H2'	1:L5:19:G:H8	1.84	0.42
1:L5:161:G:H2'	1:L5:162:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:734:G:H2'	1:L5:735:C:C6	2.54	0.42
1:L5:1254:U:H5	1:L5:1255:C:C4	2.37	0.42
1:L5:1673:C:H2'	1:L5:1674:A:H8	1.84	0.42
1:L5:2443:C:H2'	1:L5:2444:C:C6	2.53	0.42
1:L5:3374:A:H2'	1:L5:3375:A:H8	1.84	0.42
1:L5:3733:G:H2'	1:L5:3734:U:C6	2.54	0.42
1:L5:4073:U:O2	1:L5:4073:U:H2'	2.18	0.42
3:L8:5:U:H2'	3:L8:6:C:H6	1.84	0.42
5:LB:195:ASP:O	5:LB:199:GLU:HG2	2.18	0.42
15:LM:137:LYS:HB2	15:LM:137:LYS:HE2	1.79	0.42
18:LP:13:LYS:HG2	18:LP:152:GLU:OE2	2.18	0.42
36:Lh:103:LYS:HE2	36:Lh:103:LYS:HB2	1.89	0.42
46:S2:538:C:O2	46:S2:538:C:H2'	2.19	0.42
47:S6:19:G:O4'	47:S6:57:G:N2	2.42	0.42
48:SA:3:GLY:HA2	48:SA:63:ARG:HH21	1.84	0.42
48:SA:195:TRP:CD1	48:SA:196:GLU:H	2.37	0.42
49:SB:71:LEU:HD21	49:SB:189:ILE:HD12	2.01	0.42
51:SD:18:LYS:HD3	51:SD:39:VAL:HG21	2.01	0.42
53:SF:38:TYR:CD1	53:SF:144:LEU:HD13	2.54	0.42
55:SH:42:GLU:HB2	55:SH:43:LEU:HD22	2.01	0.42
56:SI:67:TRP:N	56:SI:72:CYS:O	2.47	0.42
56:SI:165:GLN:HB3	56:SI:171:LEU:HD23	2.01	0.42
57:SJ:30:LYS:HB2	57:SJ:30:LYS:HE2	1.78	0.42
63:SQ:39:LEU:HA	63:SQ:42:ILE:HD11	2.01	0.42
72:SZ:83:LEU:HD12	72:SZ:83:LEU:HA	1.88	0.42
72:SZ:100:VAL:HB	72:SZ:108:ILE:HG13	2.00	0.42
1:L5:1883:U:H2'	1:L5:1884:C:C6	2.54	0.42
1:L5:2484:U:H2'	1:L5:2485:C:C6	2.54	0.42
1:L5:2503:C:H2'	1:L5:2504:G:H8	1.83	0.42
1:L5:4560:C:H2'	1:L5:4561:G:H8	1.78	0.42
8:LE:247:LYS:HE2	8:LE:247:LYS:HB3	1.80	0.42
11:LH:45:LEU:HB3	11:LH:55:LEU:HD11	2.01	0.42
20:LR:169:ALA:HA	20:LR:172:ARG:HD2	2.01	0.42
44:Lp:26:VAL:HG12	44:Lp:30:GLU:HG3	2.00	0.42
46:S2:225:C:O2'	46:S2:226:A:H5'	2.19	0.42
46:S2:906:C:H2'	46:S2:907:U:C6	2.54	0.42
46:S2:1729:U:O2'	46:S2:1730:U:H6	2.02	0.42
51:SD:46:THR:HG23	51:SD:84:VAL:HA	2.01	0.42
55:SH:145:ARG:O	55:SH:152:ARG:HA	2.20	0.42
56:SI:199:LEU:HD12	56:SI:200:ARG:N	2.35	0.42
70:SX:33:GLY:O	70:SX:37:LYS:NZ	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SX:87:ASN:HB2	70:SX:90:CYS:HB2	2.01	0.42
74:Sb:24:LEU:HD12	74:Sb:24:LEU:HA	1.77	0.42
78:Sg:184:LEU:HD21	78:Sg:187:ASN:OD1	2.20	0.42
1:L5:1001:G:C6	1:L5:1026:C:C4	3.07	0.42
1:L5:2618:A:H2'	1:L5:2619:U:C6	2.54	0.42
1:L5:3360:G:H2'	1:L5:3361:U:C6	2.54	0.42
1:L5:3577:U:H2'	1:L5:3578:U:H6	1.85	0.42
1:L5:4110:U:H1'	5:LB:252:ALA:HB3	2.01	0.42
5:LB:220:ILE:HG12	5:LB:278:THR:HG23	2.00	0.42
8:LE:288:GLY:C	8:LE:289:MET:HE2	2.44	0.42
30:Lb:56:LYS:H	30:Lb:56:LYS:HG3	1.62	0.42
37:Li:13:LYS:HB3	37:Li:13:LYS:HE3	1.78	0.42
37:Li:94:LEU:HD23	37:Li:94:LEU:HA	1.87	0.42
46:S2:1296:A:N3	46:S2:1297:U:H1'	2.34	0.42
46:S2:1618:G:N1	46:S2:1621:A:OP2	2.52	0.42
70:SX:80:LYS:HB3	70:SX:80:LYS:HE2	1.84	0.42
70:SX:114:ASP:OD1	70:SX:114:ASP:N	2.51	0.42
1:L5:258:C:O2'	1:L5:259:C:O4'	2.30	0.42
1:L5:407:A:H5''	1:L5:408:G:OP1	2.20	0.42
1:L5:829:G:O2'	1:L5:830:C:H5'	2.19	0.42
1:L5:1484:G:O2'	1:L5:1656:G:H4'	2.20	0.42
1:L5:1561:G:H8	1:L5:1578:A:H1'	1.85	0.42
1:L5:2510:G:C2	1:L5:2511:A:C5	3.07	0.42
1:L5:3574:A:H2'	1:L5:3575:G:C8	2.51	0.42
1:L5:4112:U:H2'	1:L5:4113:U:C6	2.54	0.42
1:L5:4231:G:H2'	1:L5:4232:U:H6	1.84	0.42
1:L5:4363:C:H2'	1:L5:4364:C:C6	2.55	0.42
5:LB:307:TYR:HD2	5:LB:366:LYS:HG2	1.84	0.42
20:LR:139:MET:H	20:LR:139:MET:HG2	1.71	0.42
33:Le:109:LYS:O	33:Le:113:GLU:HG2	2.19	0.42
46:S2:46:A:N7	46:S2:96:C:O2'	2.41	0.42
46:S2:66:G:N2	71:SY:121:ALA:HB2	2.24	0.42
46:S2:832:G:H2'	46:S2:833:G:C8	2.49	0.42
46:S2:1567:G:O6	66:ST:97:LYS:HB2	2.20	0.42
46:S2:1624:A:C6	65:SS:132:ARG:HG2	2.54	0.42
47:S6:74:C:H5'	47:S6:75:C:OP2	2.20	0.42
51:SD:134:CYS:SG	51:SD:135:GLU:N	2.92	0.42
54:SG:20:ASP:OD1	54:SG:21:GLU:N	2.53	0.42
55:SH:169:LYS:O	55:SH:173:PHE:N	2.45	0.42
57:SJ:74:GLY:O	57:SJ:78:LEU:HB2	2.19	0.42
62:SP:31:GLU:O	62:SP:35:GLN:NE2	2.24	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:ST:9:VAL:HG21	66:ST:138:VAL:HG13	2.00	0.42
71:SY:117:VAL:HG11	71:SY:123:ALA:HB3	2.01	0.42
75:Sc:54:ASP:N	75:Sc:54:ASP:OD1	2.51	0.42
1:L5:424:U:H2'	1:L5:425:A:H8	1.85	0.42
1:L5:424:U:C2	1:L5:425:A:C8	3.07	0.42
1:L5:2644:C:H2'	1:L5:2645:U:C6	2.55	0.42
1:L5:3396:C:C2	1:L5:3397:G:C8	3.07	0.42
6:LC:269:LYS:HE3	6:LC:269:LYS:HB3	1.76	0.42
7:LD:128:GLY:O	7:LD:164:LYS:NZ	2.51	0.42
16:LN:45:PRO:O	16:LN:49:ARG:HG3	2.19	0.42
19:LQ:19:LYS:HE2	19:LQ:19:LYS:HB2	1.91	0.42
20:LR:21:LYS:HD3	20:LR:21:LYS:HA	1.74	0.42
21:LS:76:LYS:HB3	21:LS:131:GLU:OE1	2.20	0.42
40:LI:16:LYS:HA	40:LI:16:LYS:HD3	1.91	0.42
46:S2:75:G:H1	54:SG:170:ARG:HE	1.67	0.42
46:S2:146:G:H2'	46:S2:147:A:C8	2.54	0.42
46:S2:226:A:O2'	46:S2:227:G:O5'	2.37	0.42
46:S2:475:G:C8	46:S2:476:C:H5''	2.54	0.42
46:S2:538:C:H42	46:S2:547:G:H1	1.66	0.42
46:S2:817:A:H2'	46:S2:818:G:O4'	2.20	0.42
46:S2:1534:A:N3	46:S2:1534:A:H2'	2.34	0.42
47:S7:25:U:C2	47:S7:26:G:C8	3.07	0.42
50:SC:232:THR:HG22	50:SC:235:ASN:H	1.83	0.42
50:SC:255:LEU:HD13	68:SV:23:ILE:HD11	2.01	0.42
66:ST:124:THR:O	66:ST:128:GLN:HG2	2.18	0.42
66:ST:130:ASP:O	66:ST:133:ARG:HB2	2.19	0.42
70:SX:138:LYS:HD2	70:SX:138:LYS:HA	1.67	0.42
76:Sd:30:LEU:HD12	76:Sd:30:LEU:HA	1.79	0.42
78:Sg:217:MET:SD	78:Sg:217:MET:C	3.03	0.42
1:L5:267:G:H2'	1:L5:268:G:C8	2.51	0.42
1:L5:927:C:O2	8:LE:77:LYS:NZ	2.42	0.42
1:L5:1391:G:C2	1:L5:3294:U:H1'	2.54	0.42
1:L5:1578:A:C4	1:L5:1579:A:C8	3.07	0.42
1:L5:1677:A:H2'	1:L5:1678:C:C6	2.55	0.42
1:L5:2481:C:H2'	1:L5:2482:U:C6	2.55	0.42
1:L5:4537:G:N2	15:LM:118:MET:HE1	2.34	0.42
3:L8:5:U:O2'	3:L8:6:C:OP1	2.36	0.42
10:LG:97:LYS:HE3	10:LG:97:LYS:HB2	1.63	0.42
13:LJ:141:ILE:HA	13:LJ:144:LYS:HG3	2.01	0.42
41:Lm:78:ILE:H	41:Lm:78:ILE:HD12	1.85	0.42
43:Lo:14:LYS:HB2	43:Lo:14:LYS:HE3	1.74	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:823:U:H3	46:S2:827:A:H62	1.67	0.42
46:S2:869:G:C2	55:SH:115:LYS:HE2	2.54	0.42
46:S2:1693:U:H2'	46:S2:1694:G:C8	2.55	0.42
46:S2:1781:G:H2'	46:S2:1783:G:OP1	2.19	0.42
48:SA:77:ILE:HD12	48:SA:77:ILE:HA	1.89	0.42
49:SB:144:LYS:HD3	49:SB:208:HIS:HB3	2.01	0.42
52:SE:100:ARG:HH11	52:SE:236:ILE:HD13	1.84	0.42
55:SH:15:LYS:HD2	55:SH:16:PRO:HA	2.02	0.42
56:SI:117:TYR:CD1	56:SI:152:ARG:HD3	2.55	0.42
60:SN:46:THR:O	60:SN:50:ILE:HG12	2.19	0.42
72:SZ:80:ARG:O	72:SZ:82:SER:N	2.48	0.42
77:Se:105:ARG:HH12	77:Se:109:ARG:CZ	2.33	0.42
1:L5:1156:U:H2'	1:L5:1157:A:C8	2.55	0.42
1:L5:1293:G:H2'	1:L5:1294:C:C6	2.55	0.42
1:L5:2447:G:H2'	1:L5:2448:G:N2	2.34	0.42
1:L5:3739:C:H2'	1:L5:3740:G:C8	2.54	0.42
1:L5:4353:A:C2	1:L5:4354:A:C8	3.07	0.42
2:L7:16:A:H2'	2:L7:17:C:C6	2.54	0.42
15:LM:121:ARG:O	15:LM:125:THR:HG23	2.19	0.42
16:LN:104:GLU:HG3	16:LN:161:MET:SD	2.59	0.42
46:S2:72:C:OP1	46:S2:73:C:N4	2.51	0.42
46:S2:833:G:H22	46:S2:842:G:N2	2.16	0.42
46:S2:834:C:C4	46:S2:835:C:H1'	2.55	0.42
46:S2:900:U:OP2	46:S2:901:C:H5''	2.20	0.42
46:S2:1713:A:H2'	46:S2:1714:C:H6	1.84	0.42
47:S7:12:C:H2'	47:S7:13:G:C8	2.55	0.42
49:SB:231:LEU:HD12	49:SB:231:LEU:HA	1.91	0.42
50:SC:171:GLY:HA2	69:SW:98:GLN:HE22	1.84	0.42
54:SG:177:GLN:HE21	54:SG:177:GLN:HB3	1.58	0.42
78:Sg:14:HIS:O	78:Sg:305:ASN:HB3	2.19	0.42
1:L5:2:G:H2'	1:L5:3:C:H6	1.84	0.42
1:L5:142:G:H4'	1:L5:143:U:C5	2.55	0.42
1:L5:233:U:O2'	1:L5:2061:U:O4	2.29	0.42
1:L5:452:G:H2'	1:L5:452:G:N3	2.33	0.42
1:L5:2049:C:H2'	1:L5:2050:U:C6	2.55	0.42
1:L5:3786:G:H5'	1:L5:3787:U:OP2	2.20	0.42
1:L5:4271:G:C2	1:L5:4272:U:C5	3.08	0.42
5:LB:56:ILE:HG22	5:LB:368:ILE:HA	2.01	0.42
16:LN:73:ARG:HA	16:LN:74:PRO:HD3	1.85	0.42
31:Lc:102:SER:HB3	31:Lc:105:ILE:HD11	2.02	0.42
33:Le:83:LYS:O	33:Le:86:GLU:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Lg:88:ARG:HE	35:Lg:88:ARG:HB3	1.71	0.42
46:S2:217:G:H2'	46:S2:218:C:O4'	2.20	0.42
46:S2:1378:U:H3'	48:SA:102:ARG:HH22	1.84	0.42
46:S2:1403:A:N6	46:S2:1442:U:O4	2.52	0.42
46:S2:1829:C:H2'	46:S2:1830:G:C8	2.55	0.42
47:S7:17:C:C1'	47:S7:60:A:H4'	2.50	0.42
51:SD:68:GLU:OE2	51:SD:69:LEU:HD12	2.20	0.42
51:SD:75:LYS:H	51:SD:75:LYS:HD2	1.85	0.42
53:SF:93:VAL:HG22	53:SF:97:PHE:CZ	2.55	0.42
69:SW:42:MET:HE3	69:SW:42:MET:HB3	1.78	0.42
71:SY:94:HIS:O	71:SY:94:HIS:ND1	2.52	0.42
1:L5:1031:G:H4'	1:L5:1032:U:C5	2.55	0.42
1:L5:3364:U:H2'	1:L5:3365:C:H6	1.85	0.42
1:L5:4507:G:O2'	1:L5:4508:G:H8	2.01	0.42
5:LB:96:PRO:HD3	17:LO:156:LEU:HD11	2.02	0.42
26:LX:123:LYS:HB2	26:LX:123:LYS:HE3	1.93	0.42
46:S2:95:G:H22	46:S2:435:G:N2	2.18	0.42
46:S2:149:A:N7	46:S2:150:A:N6	2.68	0.42
46:S2:152:U:O2	46:S2:167:G:C2	2.73	0.42
46:S2:960:G:H1'	46:S2:965:A:H61	1.85	0.42
46:S2:1388:G:H2'	46:S2:1389:A:O4'	2.19	0.42
47:S7:33:C:N4	47:S7:36:U:OP2	2.40	0.42
53:SF:25:THR:OG1	53:SF:26:ASP:OD1	2.38	0.42
60:SN:69:ASN:OD1	60:SN:73:ARG:NH1	2.49	0.42
66:ST:102:ARG:HD3	66:ST:102:ARG:HA	1.69	0.42
70:SX:60:LYS:O	70:SX:62:PRO:HD2	2.19	0.42
1:L5:375:A:H1'	6:LC:84:THR:CG2	2.50	0.42
1:L5:2345:A:O2'	1:L5:2346:U:OP1	2.33	0.42
1:L5:3389:A:H2'	1:L5:3390:A:H8	1.83	0.42
1:L5:3811:C:H2'	1:L5:3812:C:C6	2.55	0.42
1:L5:4300:G:C2	1:L5:4301:A:C8	3.08	0.42
5:LB:57:VAL:HB	5:LB:367:PHE:HB3	2.01	0.42
7:LD:289:ARG:HB2	7:LD:293:ARG:HH12	1.84	0.42
8:LE:129:VAL:HG13	33:Le:7:LEU:HD21	2.02	0.42
9:LF:243:LYS:HE3	9:LF:243:LYS:HB3	1.89	0.42
24:LV:60:MET:HE3	24:LV:78:PRO:HB3	2.02	0.42
36:Lh:107:GLN:NE2	36:Lh:111:GLU:OE2	2.52	0.42
38:Lj:67:LEU:HD12	38:Lj:67:LEU:HA	1.87	0.42
46:S2:352:G:C2	46:S2:353:U:C6	3.07	0.42
46:S2:446:A:H5''	56:SI:47:ARG:NH2	2.33	0.42
46:S2:523:A:H3'	57:SJ:38:ARG:HH12	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:538:C:N4	46:S2:547:G:H22	2.17	0.42
46:S2:1583:C:H2'	46:S2:1584:C:C6	2.55	0.42
46:S2:1830:G:H1'	46:S2:1851:A:C2	2.54	0.42
46:S2:1857:C:H2'	46:S2:1858:G:C8	2.55	0.42
62:SP:45:LEU:HD23	62:SP:45:LEU:HA	1.94	0.42
63:SQ:61:GLU:OE1	63:SQ:61:GLU:N	2.53	0.42
71:SY:116:LYS:HD3	71:SY:116:LYS:HA	1.75	0.42
78:Sg:77:PHE:HB3	78:Sg:89:LEU:HD11	2.01	0.42
1:L5:304:A:OP1	37:Li:76:ARG:NH1	2.52	0.41
1:L5:444:U:H2'	1:L5:445:C:O4'	2.20	0.41
1:L5:1247:A:N6	1:L5:1265:G:O2'	2.43	0.41
1:L5:1271:G:O2'	1:L5:1272:C:O5'	2.32	0.41
1:L5:1294:C:O2'	1:L5:1296:G:OP2	2.37	0.41
1:L5:1621:G:OP2	1:L5:1621:G:N2	2.37	0.41
1:L5:2327:A:H2'	1:L5:2328:G:O4'	2.20	0.41
1:L5:3268:A:C2	1:L5:4664:A:H8	2.37	0.41
1:L5:3366:U:H3	1:L5:3368:A:N6	2.14	0.41
5:LB:257:TRP:CD1	5:LB:257:TRP:C	2.98	0.41
26:LX:67:ARG:HE	26:LX:67:ARG:HB3	1.75	0.41
38:Lj:28:HIS:CE1	38:Lj:30:GLN:HB2	2.54	0.41
46:S2:222:U:O4	46:S2:223:A:N6	2.53	0.41
46:S2:1686:U:C4	46:S2:1687:G:N7	2.88	0.41
51:SD:162:ASP:N	51:SD:163:PRO:HD2	2.35	0.41
52:SE:120:LYS:O	52:SE:164:LEU:HG	2.19	0.41
54:SG:103:ASP:CG	54:SG:104:ALA:H	2.28	0.41
58:SK:28:HIS:O	58:SK:29:MET:HE2	2.19	0.41
69:SW:39:THR:HA	69:SW:42:MET:HB2	2.00	0.41
74:Sb:82:LYS:HB3	74:Sb:82:LYS:HE3	1.92	0.41
1:L5:303:C:H2'	1:L5:304:A:O4'	2.20	0.41
1:L5:951:A:C4	1:L5:952:C:H5	2.38	0.41
1:L5:1325:C:C2	1:L5:1326:G:C8	3.08	0.41
1:L5:2645:U:OP2	20:LR:74:ARG:NH2	2.39	0.41
1:L5:3584:U:H2'	1:L5:3585:A:C8	2.55	0.41
1:L5:4278:C:O2'	1:L5:4279:A:H5'	2.19	0.41
2:L7:52:C:HO2'	2:L7:53:U:P	2.41	0.41
3:L8:128:C:C2	3:L8:129:C:C5	3.08	0.41
5:LB:382:MET:HE3	5:LB:382:MET:HB2	1.89	0.41
7:LD:41:LYS:HB2	22:LT:68:THR:O	2.19	0.41
8:LE:207:THR:HG21	15:LM:107:PHE:HB2	2.02	0.41
15:LM:124:LYS:HG3	15:LM:128:LYS:HZ3	1.84	0.41
28:LZ:29:ILE:HG13	28:LZ:40:HIS:NE2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:456:A:H2'	46:S2:457:C:C6	2.54	0.41
46:S2:876:A:H1'	55:SH:114:GLN:NE2	2.35	0.41
46:S2:1394:G:H2'	46:S2:1395:G:C8	2.55	0.41
50:SC:214:LEU:HD23	50:SC:244:ILE:HD11	2.02	0.41
52:SE:176:ASP:OD1	52:SE:176:ASP:C	2.63	0.41
57:SJ:151:LEU:HD12	57:SJ:151:LEU:HA	1.92	0.41
64:SR:100:PRO:HA	64:SR:103:LYS:HG2	2.01	0.41
65:SS:92:ASP:OD1	65:SS:92:ASP:C	2.63	0.41
1:L5:1119:C:H2'	1:L5:1120:C:C6	2.55	0.41
1:L5:1901:G:H2'	1:L5:1902:A:H8	1.84	0.41
1:L5:4333:G:H2'	1:L5:4334:A:H8	1.83	0.41
1:L5:4529:C:H2'	1:L5:4530:G:H8	1.84	0.41
6:LC:183:VAL:HG22	6:LC:204:ARG:HG3	2.01	0.41
7:LD:60:ILE:HB	7:LD:80:ALA:HB2	2.01	0.41
13:LJ:118:LYS:HD3	13:LJ:118:LYS:HA	1.93	0.41
30:Lb:51:LYS:O	30:Lb:54:LEU:HG	2.21	0.41
46:S2:74:G:H4'	46:S2:75:G:H5'	2.01	0.41
46:S2:800:U:H2'	46:S2:801:U:C6	2.56	0.41
46:S2:917:A:O2'	60:SN:73:ARG:NH2	2.54	0.41
46:S2:953:G:H2'	46:S2:954:C:C6	2.56	0.41
46:S2:1135:G:H2'	46:S2:1136:C:C6	2.55	0.41
46:S2:1180:G:N2	46:S2:1183:A:OP2	2.49	0.41
46:S2:1241:A:C6	62:SP:100:LYS:HB2	2.55	0.41
52:SE:99:PHE:CE1	52:SE:113:ARG:HG3	2.55	0.41
54:SG:57:ASP:C	54:SG:59:GLN:H	2.29	0.41
58:SK:7:ASN:O	58:SK:11:ILE:HG12	2.20	0.41
61:SO:21:VAL:HG11	61:SO:27:VAL:HG22	2.01	0.41
73:Sa:67:LEU:HD23	73:Sa:67:LEU:HA	1.91	0.41
78:Sg:194:TYR:CE2	78:Sg:212:LYS:HD2	2.55	0.41
78:Sg:240:CYS:SG	78:Sg:249:CYS:HB2	2.60	0.41
1:L5:298:C:H2'	1:L5:299:A:H8	1.85	0.41
1:L5:1459:C:H2'	1:L5:1460:A:H8	1.86	0.41
1:L5:1649:G:H2'	1:L5:1650:C:H6	1.85	0.41
1:L5:1903:A:H8	1:L5:1903:A:OP2	2.03	0.41
1:L5:2115:G:H2'	1:L5:2116:U:O4'	2.20	0.41
1:L5:2297:C:H2'	1:L5:2298:G:H8	1.86	0.41
1:L5:4569:U:H2'	1:L5:4570:C:H6	1.86	0.41
5:LB:220:ILE:HB	5:LB:346:THR:HB	2.02	0.41
6:LC:189:MET:HE2	6:LC:195:LYS:HD2	2.01	0.41
22:LT:5:LYS:HE2	22:LT:5:LYS:HB2	1.77	0.41
36:Lh:76:LYS:HB2	36:Lh:76:LYS:HE2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:565:A:H1'	46:S2:566:G:O4'	2.21	0.41
46:S2:1416:C:H1'	46:S2:1417:C:C5	2.55	0.41
47:S6:43:G:H2'	47:S6:44:A:C8	2.56	0.41
63:SQ:39:LEU:HA	63:SQ:39:LEU:HD12	1.91	0.41
1:L5:1014:C:H5''	1:L5:1015:C:C5	2.56	0.41
1:L5:2056:G:C2	1:L5:2093:G:C5	3.09	0.41
1:L5:3264:U:H2'	1:L5:3265:A:H8	1.84	0.41
1:L5:4633:U:H4'	5:LB:175:GLN:HG3	2.02	0.41
5:LB:74:GLU:OE1	5:LB:285:TYR:OH	2.24	0.41
10:LG:70:LEU:HD23	10:LG:70:LEU:HA	1.91	0.41
23:LU:106:SER:OG	23:LU:107:LYS:N	2.54	0.41
32:Ld:23:ARG:NH2	32:Ld:57:MET:HE1	2.36	0.41
46:S2:56:G:O6	46:S2:90:G:H1'	2.20	0.41
46:S2:82:G:OP2	46:S2:82:G:H8	2.04	0.41
46:S2:846:G:H3'	46:S2:847:G:N7	2.35	0.41
46:S2:1013:A:H2'	46:S2:1014:U:H6	1.85	0.41
46:S2:1584:C:OP2	46:S2:1585:G:O2'	2.34	0.41
47:S7:49:G:H2'	47:S7:50:A:H8	1.85	0.41
50:SC:79:GLU:N	50:SC:79:GLU:CD	2.79	0.41
51:SD:198:ILE:H	51:SD:198:ILE:HG13	1.65	0.41
56:SI:177:SER:N	56:SI:186:ASP:OD1	2.53	0.41
69:SW:42:MET:HG3	69:SW:50:PHE:HE1	1.85	0.41
77:Se:105:ARG:HH22	77:Se:109:ARG:NH2	2.19	0.41
78:Sg:191:HIS:CD2	78:Sg:195:LEU:HD21	2.56	0.41
78:Sg:239:LEU:HD23	78:Sg:250:ALA:HA	2.01	0.41
1:L5:266:G:H2'	1:L5:267:G:H8	1.85	0.41
1:L5:1026:C:H2'	1:L5:1027:G:H8	1.85	0.41
1:L5:1222:C:H41	1:L5:1227:G:H21	1.68	0.41
1:L5:3393:A:H2'	1:L5:3394:A:C8	2.56	0.41
1:L5:4171:A:OP1	1:L5:4173:G:H4'	2.19	0.41
1:L5:4224:A:H2'	1:L5:4225:U:H6	1.85	0.41
4:LA:77:ILE:HD12	4:LA:77:ILE:HA	1.95	0.41
6:LC:173:LYS:HD3	6:LC:173:LYS:HA	1.73	0.41
9:LF:138:GLN:O	9:LF:141:ASN:HB2	2.20	0.41
10:LG:50:ASP:OD1	10:LG:52:THR:HG22	2.21	0.41
10:LG:87:LEU:HD23	10:LG:87:LEU:HA	1.86	0.41
10:LG:207:VAL:HG21	10:LG:215:LEU:HD13	2.02	0.41
11:LH:128:MET:HA	11:LH:128:MET:HE3	2.02	0.41
23:LU:49:VAL:HG12	23:LU:50:ASN:H	1.85	0.41
46:S2:158:A:N6	46:S2:464:C:H1'	2.35	0.41
46:S2:822:G:O6	57:SJ:150:ARG:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1411:C:O2'	46:S2:1412:G:H8	2.03	0.41
46:S2:1414:G:H3'	46:S2:1415:A:H8	1.85	0.41
46:S2:1736:A:H3'	46:S2:1737:G:C8	2.55	0.41
49:SB:122:GLU:N	49:SB:122:GLU:OE2	2.53	0.41
52:SE:211:LYS:HE2	52:SE:211:LYS:HB2	1.92	0.41
54:SG:160:LYS:HB3	54:SG:160:LYS:HE3	1.60	0.41
58:SK:80:ARG:NE	58:SK:80:ARG:HA	2.36	0.41
61:SO:117:ARG:HH12	73:Sa:49:ALA:CB	2.33	0.41
62:SP:25:LEU:HD23	62:SP:25:LEU:HA	1.87	0.41
67:SU:21:ARG:HA	67:SU:21:ARG:NE	2.35	0.41
78:Sg:30:MET:HE2	78:Sg:30:MET:HB2	1.88	0.41
78:Sg:166:VAL:HG22	78:Sg:198:VAL:HG21	2.03	0.41
78:Sg:225:LYS:HD2	78:Sg:225:LYS:HA	1.91	0.41
1:L5:743:G:N1	1:L5:828:C:C4	2.89	0.41
1:L5:1170:G:OP1	19:LQ:108:ARG:NH2	2.33	0.41
1:L5:1234:A:N3	1:L5:1234:A:H2'	2.36	0.41
1:L5:2222:C:H2'	1:L5:2223:G:O4'	2.20	0.41
1:L5:2401:A:H2'	1:L5:2402:G:O4'	2.20	0.41
1:L5:2512:G:H2'	1:L5:2513:G:C8	2.56	0.41
2:L7:71:G:H2'	2:L7:72:U:C6	2.55	0.41
8:LE:250:ILE:HG13	8:LE:255:LYS:NZ	2.36	0.41
28:LZ:124:THR:HG21	28:LZ:126:LYS:HE2	2.01	0.41
31:Lc:98:ASP:HA	31:Lc:99:PRO:HD3	1.93	0.41
36:Lh:87:LYS:HE3	36:Lh:87:LYS:HB3	1.81	0.41
37:Li:43:MET:HE2	37:Li:43:MET:HB2	1.89	0.41
43:Lo:78:ARG:HD3	43:Lo:78:ARG:HA	1.66	0.41
46:S2:1707:G:H2'	46:S2:1708:U:C6	2.55	0.41
47:S7:3:G:C5	47:S7:4:C:H1'	2.56	0.41
49:SB:70:SER:OG	49:SB:73:ASP:OD1	2.37	0.41
49:SB:97:LEU:HD23	49:SB:232:HIS:CG	2.55	0.41
52:SE:59:ASP:O	52:SE:62:LYS:HG2	2.20	0.41
65:SS:75:ARG:CZ	65:SS:75:ARG:HB3	2.50	0.41
1:L5:211:G:C2	1:L5:212:A:C8	3.09	0.41
1:L5:948:G:H2'	1:L5:949:C:C6	2.55	0.41
1:L5:1226:G:O2'	1:L5:1227:G:O4'	2.31	0.41
1:L5:1348:A:N3	38:Lj:11:ARG:HB3	2.36	0.41
1:L5:2301:G:N2	3:L8:126:C:OP1	2.33	0.41
1:L5:2655:G:N2	1:L5:3256:A:N3	2.69	0.41
1:L5:3547:A:N6	1:L5:4224:A:O4'	2.54	0.41
4:LA:180:LEU:HD22	44:Lp:18:TYR:HB3	2.03	0.41
6:LC:13:GLU:OE1	6:LC:161:TYR:OH	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:102:ASN:OD1	11:LH:102:ASN:N	2.54	0.41
17:LO:159:LYS:O	17:LO:162:GLU:HG2	2.21	0.41
18:LP:60:PHE:O	18:LP:78:TRP:NE1	2.52	0.41
32:Ld:48:GLU:OE1	32:Ld:48:GLU:HA	2.21	0.41
36:Lh:49:VAL:O	36:Lh:53:SER:OG	2.34	0.41
46:S2:599:G:H2'	46:S2:600:A:C8	2.55	0.41
46:S2:862:A:O2'	46:S2:863:A:OP2	2.36	0.41
46:S2:950:G:H2'	46:S2:951:C:C6	2.56	0.41
46:S2:1115:U:HO2'	46:S2:1116:U:P	2.43	0.41
46:S2:1145:A:H2'	46:S2:1146:A:C8	2.56	0.41
46:S2:1390:C:H4'	51:SD:205:PRO:HG3	2.03	0.41
46:S2:1540:U:H1'	66:ST:48:TYR:CZ	2.56	0.41
46:S2:1689:C:H2'	46:S2:1690:C:H6	1.86	0.41
49:SB:185:VAL:O	49:SB:189:ILE:HG22	2.19	0.41
52:SE:225:ILE:HD13	52:SE:225:ILE:HA	1.87	0.41
53:SF:144:LEU:HD23	75:Sc:49:PRO:HG2	2.02	0.41
53:SF:204:ARG:HH12	75:Sc:44:ARG:HH12	1.67	0.41
61:SO:43:HIS:HD2	61:SO:44:VAL:N	2.18	0.41
71:SY:20:ARG:NH2	71:SY:22:GLN:OE1	2.53	0.41
71:SY:29:HIS:O	71:SY:29:HIS:CG	2.73	0.41
78:Sg:179:LEU:HD12	78:Sg:179:LEU:HA	1.85	0.41
1:L5:194:C:O2	27:LY:121:ARG:NH2	2.54	0.41
1:L5:761:C:H5	1:L5:810:G:N1	2.11	0.41
1:L5:937:C:H2'	1:L5:938:C:H5'	2.02	0.41
1:L5:1181:G:N2	14:LL:33:ILE:HD13	2.36	0.41
1:L5:1366:G:O2'	1:L5:1367:A:OP2	2.36	0.41
1:L5:1585:U:H2'	1:L5:1586:C:O2	2.21	0.41
1:L5:2174:A:C2	1:L5:2175:A:C8	3.09	0.41
1:L5:2236:G:H2'	1:L5:2236:G:N3	2.36	0.41
1:L5:2361:C:H2'	1:L5:2362:G:C8	2.55	0.41
1:L5:2511:A:H2'	1:L5:2512:G:C8	2.56	0.41
1:L5:3537:G:H2'	1:L5:3538:G:C8	2.56	0.41
1:L5:4024:G:H5'	47:S6:76:A:H62	1.85	0.41
1:L5:4279:A:OP2	5:LB:224:LYS:NZ	2.39	0.41
1:L5:4282:U:C2	1:L5:4283:G:C8	3.09	0.41
1:L5:4352:U:H4'	1:L5:4353:A:OP1	2.20	0.41
1:L5:4508:G:C6	1:L5:4509:G:C5	3.09	0.41
3:L8:2:G:C5	3:L8:3:A:C8	3.09	0.41
7:LD:260:GLU:HB2	7:LD:262:LYS:HE2	2.03	0.41
9:LF:75:LYS:NZ	9:LF:211:ASP:OD2	2.48	0.41
10:LG:175:ARG:HG3	10:LG:230:TYR:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LG:193:LEU:HD23	10:LG:193:LEU:HA	1.91	0.41
12:LI:76:MET:HG3	12:LI:85:PHE:CD2	2.56	0.41
13:LJ:57:VAL:C	13:LJ:59:SER:H	2.29	0.41
13:LJ:167:GLN:HA	13:LJ:171:ASP:O	2.21	0.41
17:LO:144:GLU:N	17:LO:144:GLU:CD	2.79	0.41
21:LS:21:LYS:HB2	21:LS:21:LYS:HE2	1.78	0.41
22:LT:103:ASP:O	22:LT:107:LYS:HG3	2.21	0.41
24:LV:71:GLU:O	24:LV:75:LYS:NZ	2.38	0.41
24:LV:123:LYS:HE2	24:LV:123:LYS:HB2	1.81	0.41
28:LZ:33:THR:C	28:LZ:35:ASP:H	2.29	0.41
28:LZ:83:THR:HG22	35:Lg:95:PHE:CZ	2.56	0.41
38:Lj:83:THR:HA	38:Lj:84:PRO:HD3	1.91	0.41
46:S2:38:A:H5''	57:SJ:5:ARG:HG3	2.02	0.41
46:S2:294:C:O2'	46:S2:295:U:H3'	2.20	0.41
46:S2:444:U:H2'	46:S2:445:G:O4'	2.21	0.41
46:S2:499:C:OP1	52:SE:30:ARG:HB3	2.21	0.41
46:S2:538:C:H3'	46:S2:539:U:H6	1.85	0.41
46:S2:941:U:H2'	46:S2:942:C:C6	2.56	0.41
46:S2:1117:C:C2'	46:S2:1118:C:H5''	2.51	0.41
46:S2:1143:G:N2	46:S2:1146:A:OP2	2.54	0.41
46:S2:1300:A:C2	46:S2:1302:A:H5''	2.56	0.41
46:S2:1398:U:H4'	46:S2:1399:G:H5''	2.03	0.41
46:S2:1589:A:H2'	46:S2:1590:A:H8	1.83	0.41
46:S2:1684:C:H2'	46:S2:1685:C:H6	1.85	0.41
47:S6:18:G:O2'	47:S6:57:G:N2	2.52	0.41
48:SA:121:LEU:HD13	48:SA:143:PRO:HB2	2.03	0.41
49:SB:27:LYS:HB2	49:SB:27:LYS:HE2	1.84	0.41
49:SB:189:ILE:CG2	49:SB:190:PRO:HD3	2.40	0.41
50:SC:84:PHE:CE2	50:SC:264:SER:HA	2.56	0.41
50:SC:211:LYS:HB2	50:SC:211:LYS:HE3	1.85	0.41
52:SE:57:THR:HB	52:SE:60:GLU:OE2	2.21	0.41
53:SF:55:ARG:NH1	63:SQ:125:ARG:HD3	2.36	0.41
53:SF:188:TYR:CE1	53:SF:192:LYS:HG2	2.56	0.41
55:SH:107:LYS:HD3	55:SH:107:LYS:HA	1.65	0.41
56:SI:108:PRO:HA	56:SI:111:GLN:OE1	2.20	0.41
57:SJ:32:ILE:HA	57:SJ:37:LEU:HD13	2.02	0.41
58:SK:2:LEU:O	58:SK:3:MET:C	2.64	0.41
59:SL:37:TYR:CE2	59:SL:51:ILE:HG23	2.55	0.41
62:SP:116:LEU:HA	62:SP:116:LEU:HD23	1.76	0.41
63:SQ:45:ARG:HH11	63:SQ:45:ARG:HG3	1.86	0.41
66:ST:66:LEU:HD23	66:ST:66:LEU:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SU:32:LEU:HD12	67:SU:32:LEU:HA	1.96	0.41
69:SW:30:CYS:SG	69:SW:31:SER:N	2.93	0.41
69:SW:84:LYS:HE2	69:SW:84:LYS:HB3	1.83	0.41
75:Sc:31:ARG:NH1	75:Sc:41:SER:OG	2.53	0.41
1:L5:486:C:O2'	1:L5:487:C:P	2.79	0.41
1:L5:747:G:H3'	1:L5:747:G:OP2	2.21	0.41
1:L5:1009:C:N4	1:L5:1017:A:H61	2.18	0.41
1:L5:1855:G:O2'	1:L5:1860:A:N1	2.51	0.41
1:L5:3584:U:H2'	1:L5:3585:A:H8	1.85	0.41
1:L5:3896:C:OP2	1:L5:3917:G:N1	2.47	0.41
1:L5:4524:C:H2'	1:L5:4525:C:H6	1.86	0.41
1:L5:4716:G:N2	1:L5:4717:U:O4	2.44	0.41
11:LH:44:GLU:OE2	15:LM:2:VAL:HB	2.21	0.41
13:LJ:87:LEU:HD23	13:LJ:87:LEU:HA	1.92	0.41
14:LL:48:PRO:HB2	36:Lh:120:ALA:HB2	2.02	0.41
27:LY:38:LEU:HD23	27:LY:38:LEU:HA	1.96	0.41
46:S2:153:G:C2	46:S2:166:A:N1	2.89	0.41
46:S2:298:A:C2	46:S2:299:G:H1'	2.56	0.41
46:S2:492:C:OP2	71:SY:105:LYS:NZ	2.48	0.41
46:S2:599:G:H2'	46:S2:600:A:H8	1.86	0.41
46:S2:1629:C:C2	46:S2:1630:C:C5	3.09	0.41
46:S2:1737:G:H2'	46:S2:1738:G:H8	1.85	0.41
46:S2:1744:G:H21	46:S2:1792:A:H62	1.68	0.41
47:S7:24:G:H2'	47:S7:25:U:O4'	2.21	0.41
52:SE:64:ILE:HG12	71:SY:18:LEU:HD13	2.03	0.41
52:SE:147:ILE:HD13	52:SE:147:ILE:HA	1.92	0.41
60:SN:130:LYS:HD3	60:SN:137:PRO:O	2.21	0.41
65:SS:63:GLU:H	65:SS:63:GLU:HG2	1.67	0.41
67:SU:48:LEU:HD11	67:SU:93:SER:OG	2.21	0.41
67:SU:55:ARG:HG2	67:SU:87:ARG:CZ	2.51	0.41
69:SW:57:ARG:NH1	74:Sb:26:GLN:OE1	2.54	0.41
71:SY:30:PRO:HD3	71:SY:32:LYS:HE3	2.02	0.41
78:Sg:168:CYS:SG	78:Sg:198:VAL:HG22	2.60	0.41
1:L5:950:G:H2'	1:L5:951:A:N9	2.36	0.40
1:L5:951:A:H2'	1:L5:952:C:H6	1.86	0.40
1:L5:2215:C:OP1	16:LN:67:ARG:HD3	2.21	0.40
1:L5:2508:G:OP2	28:LZ:133:LYS:NZ	2.53	0.40
1:L5:3809:G:OP2	1:L5:3810:A:O2'	2.29	0.40
1:L5:3811:C:H2'	1:L5:3812:C:H6	1.87	0.40
1:L5:4077:A:C4	1:L5:4078:G:C8	3.09	0.40
4:LA:142:GLU:N	4:LA:142:GLU:OE1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LG:156:VAL:HG22	10:LG:182:CYS:SG	2.60	0.40
15:LM:79:LYS:HE3	15:LM:79:LYS:HB2	1.81	0.40
17:LO:110:PRO:HA	17:LO:113:ASP:OD2	2.21	0.40
23:LU:99:TRP:O	23:LU:100:LEU:HD23	2.21	0.40
46:S2:111:A:C6	46:S2:352:G:C6	3.09	0.40
46:S2:830:C:C3'	46:S2:846:G:H21	2.34	0.40
46:S2:926:G:C2	46:S2:927:A:C8	3.09	0.40
46:S2:1222:G:H2'	46:S2:1223:G:C8	2.56	0.40
46:S2:1734:U:H2'	46:S2:1735:G:O4'	2.21	0.40
47:S6:18:G:H4'	47:S6:60:A:C2	2.56	0.40
49:SB:128:LYS:HG3	49:SB:134:LEU:HD13	2.02	0.40
54:SG:14:LYS:HD3	54:SG:14:LYS:HA	1.94	0.40
56:SI:113:TYR:HD2	56:SI:121:LEU:HD22	1.86	0.40
60:SN:37:ILE:HD11	60:SN:71:ILE:HD13	2.03	0.40
61:SO:98:ARG:HH21	61:SO:134:PRO:HG2	1.85	0.40
65:SS:64:VAL:HG23	65:SS:65:GLU:OE2	2.21	0.40
69:SW:15:ASN:O	69:SW:19:LYS:HG2	2.21	0.40
70:SX:53:GLU:HG2	70:SX:71:ARG:HG3	2.04	0.40
71:SY:84:LYS:HE2	71:SY:84:LYS:HB3	1.93	0.40
1:L5:149:A:C2	10:LG:196:ARG:HD3	2.56	0.40
1:L5:927:C:O2'	1:L5:928:C:OP1	2.30	0.40
1:L5:946:G:H2'	1:L5:947:C:C6	2.56	0.40
1:L5:1050:C:O2'	1:L5:1051:G:O4'	2.31	0.40
1:L5:1691:A:N7	1:L5:1852:G:H5'	2.36	0.40
1:L5:3359:A:C6	1:L5:3360:G:C8	3.09	0.40
1:L5:4191:G:H2'	1:L5:4192:U:H6	1.86	0.40
1:L5:4216:U:H2'	1:L5:4217:A:C8	2.55	0.40
15:LM:126:GLU:HG3	17:LO:181:ALA:HB1	2.01	0.40
31:Lc:78:ASN:ND2	31:Lc:90:ARG:HD2	2.36	0.40
34:Lf:106:TYR:O	34:Lf:108:SER:N	2.46	0.40
35:Lg:107:LEU:HD12	35:Lg:107:LEU:HA	1.91	0.40
37:Li:62:LYS:HE3	37:Li:62:LYS:HB3	1.88	0.40
46:S2:69:C:C4	46:S2:70:G:C5	3.10	0.40
46:S2:606:A:O2'	46:S2:639:C:O2'	2.34	0.40
51:SD:18:LYS:HZ3	51:SD:22:ASN:HB2	1.86	0.40
52:SE:252:ARG:HG3	52:SE:253:ASP:OD1	2.21	0.40
54:SG:116:LYS:HE3	54:SG:116:LYS:HB3	1.88	0.40
54:SG:182:PRO:HA	54:SG:185:LEU:HD12	2.03	0.40
60:SN:114:ARG:HD3	60:SN:114:ARG:HA	1.81	0.40
62:SP:93:MET:HA	62:SP:93:MET:HE3	2.04	0.40
72:SZ:43:LYS:HD3	72:SZ:43:LYS:HA	1.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SZ:69:THR:O	72:SZ:73:VAL:HG12	2.20	0.40
1:L5:449:G:H2'	1:L5:450:C:C6	2.56	0.40
1:L5:703:G:H3'	1:L5:704:U:H4'	2.04	0.40
1:L5:951:A:H2'	1:L5:952:C:C6	2.56	0.40
1:L5:1046:G:OP1	9:LF:85:GLN:NE2	2.47	0.40
1:L5:1752:U:H2'	1:L5:1753:U:C6	2.56	0.40
1:L5:2624:A:H2'	1:L5:2625:A:H8	1.86	0.40
5:LB:77:THR:OG1	5:LB:335:GLY:O	2.39	0.40
5:LB:216:MET:HE3	5:LB:283:LYS:HB2	2.03	0.40
5:LB:254:ILE:HG22	5:LB:266:VAL:HG11	2.04	0.40
7:LD:156:GLY:HA2	7:LD:181:PRO:HG3	2.04	0.40
18:LP:46:LYS:HE3	18:LP:46:LYS:HB3	1.79	0.40
27:LY:117:LYS:HE2	27:LY:117:LYS:HB3	1.97	0.40
32:Ld:84:ILE:HD12	32:Ld:84:ILE:HA	1.81	0.40
44:Lp:45:THR:O	44:Lp:45:THR:OG1	2.36	0.40
46:S2:165:G:H4'	54:SG:53:SER:HB2	2.03	0.40
46:S2:526:A:H5'	77:Se:102:LYS:HD3	2.02	0.40
46:S2:564:G:C5	46:S2:588:A:C6	3.09	0.40
46:S2:846:G:H3'	46:S2:847:G:C5	2.55	0.40
46:S2:864:U:N3	46:S2:865:A:N7	2.69	0.40
46:S2:866:A:C6	46:S2:867:U:C4	3.09	0.40
47:S7:46:G:O2'	47:S7:47:U:OP2	2.39	0.40
53:SF:42:LYS:HD3	53:SF:42:LYS:HA	1.69	0.40
54:SG:20:ASP:HB3	54:SG:23:LYS:HZ2	1.85	0.40
54:SG:168:LYS:HE2	54:SG:168:LYS:HB3	1.83	0.40
61:SO:75:MET:HG2	61:SO:76:LEU:HD23	2.03	0.40
70:SX:46:HIS:CD2	70:SX:103:ALA:HB2	2.56	0.40
77:Se:106:ALA:HB1	77:Se:109:ARG:HD2	2.02	0.40
78:Sg:41:ILE:HD11	78:Sg:55:PRO:HG3	2.02	0.40
78:Sg:254:PRO:HA	78:Sg:285:GLN:HA	2.02	0.40
1:L5:266:G:O2'	1:L5:267:G:OP1	2.36	0.40
1:L5:2618:A:H2'	1:L5:2619:U:H6	1.86	0.40
2:L7:61:G:O3'	7:LD:279:ARG:NH2	2.54	0.40
7:LD:272:SER:HB2	7:LD:275:GLN:HG3	2.03	0.40
17:LO:128:ARG:HE	17:LO:128:ARG:HB3	1.61	0.40
26:LX:55:ARG:HA	26:LX:55:ARG:HD3	1.88	0.40
46:S2:435:G:P	56:SI:25:ARG:HH12	2.45	0.40
46:S2:468:G:H2'	46:S2:469:A:O4'	2.21	0.40
46:S2:834:C:H3'	46:S2:835:C:H4'	2.04	0.40
46:S2:1289:U:H3	46:S2:1312:C:H42	1.70	0.40
46:S2:1396:C:H1'	46:S2:1475:A:C5	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1622:U:O2'	46:S2:1623:U:H2'	2.21	0.40
51:SD:18:LYS:HA	51:SD:18:LYS:HD2	1.90	0.40
52:SE:212:ASP:OD2	52:SE:216:ASN:HB2	2.20	0.40
55:SH:155:LYS:HB3	55:SH:188:GLU:OE1	2.21	0.40
56:SI:104:ILE:N	56:SI:171:LEU:O	2.36	0.40
62:SP:52:LYS:HD3	62:SP:52:LYS:HA	1.95	0.40
63:SQ:86:GLN:H	63:SQ:86:GLN:HG3	1.74	0.40
78:Sg:125:ARG:HG3	78:Sg:150:TRP:CE3	2.57	0.40
1:L5:470:A:H2'	1:L5:471:C:H6	1.86	0.40
1:L5:1003:G:H3'	1:L5:1004:G:H8	1.85	0.40
1:L5:1404:C:H4'	1:L5:2611:A:H5'	2.02	0.40
1:L5:2289:C:C2	1:L5:2290:C:C5	3.10	0.40
1:L5:2482:U:H2'	1:L5:2483:C:C6	2.56	0.40
1:L5:4346:C:OP1	11:LH:64:ARG:NH2	2.55	0.40
1:L5:4357:C:H2'	1:L5:4358:A:C8	2.57	0.40
1:L5:4529:C:H2'	1:L5:4530:G:C8	2.57	0.40
3:L8:4:C:C2	3:L8:5:U:C5	3.10	0.40
3:L8:154:G:H2'	3:L8:155:C:C6	2.57	0.40
5:LB:17:LEU:HD21	5:LB:264:PHE:HD2	1.86	0.40
6:LC:5:ARG:HD2	6:LC:24:LEU:O	2.21	0.40
7:LD:21:ARG:HA	7:LD:24:ARG:NH2	2.36	0.40
7:LD:286:SER:O	7:LD:289:ARG:HG3	2.22	0.40
20:LR:126:LYS:HE2	20:LR:126:LYS:HB3	1.76	0.40
23:LU:41:GLN:HA	23:LU:44:GLN:NE2	2.37	0.40
26:LX:74:TYR:CD2	36:Lh:25:LYS:HD3	2.56	0.40
31:Lc:13:SER:O	31:Lc:17:ARG:HG2	2.20	0.40
39:Lk:67:LYS:HE2	39:Lk:67:LYS:HB3	1.73	0.40
46:S2:77:A:H5'	54:SG:154:ARG:HG2	2.03	0.40
46:S2:95:G:H1	46:S2:435:G:H1	1.69	0.40
50:SC:132:ASP:OD1	50:SC:136:HIS:HB2	2.21	0.40
52:SE:90:ILE:HB	52:SE:99:PHE:HB2	2.03	0.40
52:SE:247:THR:HB	52:SE:250:GLU:OE1	2.22	0.40
56:SI:175:ILE:HA	56:SI:186:ASP:O	2.21	0.40
57:SJ:44:TRP:HA	57:SJ:47:LYS:HD2	2.02	0.40
58:SK:79:LEU:HA	58:SK:79:LEU:HD12	1.82	0.40
67:SU:58:THR:O	67:SU:59:LYS:HE2	2.21	0.40
71:SY:121:ALA:C	71:SY:124:ASN:H	2.30	0.40
75:Sc:34:PHE:O	75:Sc:35:MET:HG2	2.21	0.40
78:Sg:84:ASP:OD1	78:Sg:84:ASP:N	2.53	0.40
78:Sg:104:HIS:CE1	78:Sg:124:SER:HB3	2.57	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%)	230 (94%)	16 (6%)	0	100	100
5	LB	395/403 (98%)	367 (93%)	28 (7%)	0	100	100
6	LC	355/419 (85%)	331 (93%)	24 (7%)	0	100	100
7	LD	291/297 (98%)	269 (92%)	21 (7%)	1 (0%)	36	65
8	LE	210/296 (71%)	196 (93%)	14 (7%)	0	100	100
9	LF	212/270 (78%)	201 (95%)	11 (5%)	0	100	100
10	LG	225/266 (85%)	215 (96%)	10 (4%)	0	100	100
11	LH	188/192 (98%)	178 (95%)	7 (4%)	3 (2%)	7	32
12	LI	197/214 (92%)	187 (95%)	10 (5%)	0	100	100
13	LJ	165/178 (93%)	159 (96%)	6 (4%)	0	100	100
14	LL	204/211 (97%)	195 (96%)	9 (4%)	0	100	100
15	LM	134/217 (62%)	126 (94%)	8 (6%)	0	100	100
16	LN	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
17	LO	199/203 (98%)	191 (96%)	8 (4%)	0	100	100
18	LP	152/184 (83%)	150 (99%)	2 (1%)	0	100	100
19	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
20	LR	172/196 (88%)	169 (98%)	3 (2%)	0	100	100
21	LS	173/176 (98%)	162 (94%)	10 (6%)	1 (1%)	21	51
22	LT	158/160 (99%)	155 (98%)	3 (2%)	0	100	100
23	LU	98/128 (77%)	89 (91%)	9 (9%)	0	100	100
24	LV	128/140 (91%)	125 (98%)	3 (2%)	0	100	100
25	LW	60/157 (38%)	60 (100%)	0	0	100	100
26	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
27	LY	130/145 (90%)	129 (99%)	1 (1%)	0	100	100
28	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
30	Lb	95/160 (59%)	93 (98%)	2 (2%)	0	100	100
31	Lc	92/115 (80%)	91 (99%)	0	1 (1%)	11	40
32	Ld	106/125 (85%)	104 (98%)	2 (2%)	0	100	100
33	Le	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
35	Lg	108/117 (92%)	105 (97%)	3 (3%)	0	100	100
36	Lh	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
37	Li	100/105 (95%)	92 (92%)	8 (8%)	0	100	100
38	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
39	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
40	Ll	48/51 (94%)	48 (100%)	0	0	100	100
41	Lm	49/128 (38%)	49 (100%)	0	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	95 (94%)	5 (5%)	1 (1%)	12	41
44	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	Lr	122/137 (89%)	117 (96%)	5 (4%)	0	100	100
48	SA	205/295 (70%)	189 (92%)	16 (8%)	0	100	100
49	SB	211/264 (80%)	202 (96%)	9 (4%)	0	100	100
50	SC	213/293 (73%)	206 (97%)	6 (3%)	1 (0%)	24	55
51	SD	207/243 (85%)	192 (93%)	10 (5%)	5 (2%)	4	24
52	SE	256/263 (97%)	240 (94%)	15 (6%)	1 (0%)	30	59
53	SF	175/204 (86%)	165 (94%)	10 (6%)	0	100	100
54	SG	200/249 (80%)	185 (92%)	14 (7%)	1 (0%)	24	55
55	SH	176/194 (91%)	160 (91%)	16 (9%)	0	100	100
56	SI	179/208 (86%)	168 (94%)	11 (6%)	0	100	100
57	SJ	130/194 (67%)	119 (92%)	11 (8%)	0	100	100
58	SK	86/165 (52%)	75 (87%)	11 (13%)	0	100	100
59	SL	131/158 (83%)	127 (97%)	4 (3%)	0	100	100
60	SN	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
61	SO	132/151 (87%)	121 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	SP	116/145 (80%)	112 (97%)	4 (3%)	0	100	100
63	SQ	137/146 (94%)	123 (90%)	14 (10%)	0	100	100
64	SR	129/135 (96%)	116 (90%)	11 (8%)	2 (2%)	7	32
65	SS	138/152 (91%)	131 (95%)	7 (5%)	0	100	100
66	ST	138/145 (95%)	134 (97%)	4 (3%)	0	100	100
67	SU	93/119 (78%)	90 (97%)	3 (3%)	0	100	100
68	SV	79/83 (95%)	74 (94%)	5 (6%)	0	100	100
69	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
70	SX	137/143 (96%)	126 (92%)	10 (7%)	1 (1%)	18	49
71	SY	108/133 (81%)	99 (92%)	8 (7%)	1 (1%)	14	43
72	SZ	70/125 (56%)	62 (89%)	8 (11%)	0	100	100
73	Sa	97/115 (84%)	89 (92%)	8 (8%)	0	100	100
74	Sb	80/84 (95%)	74 (92%)	5 (6%)	1 (1%)	9	35
75	Sc	52/69 (75%)	43 (83%)	9 (17%)	0	100	100
76	Sd	52/56 (93%)	52 (100%)	0	0	100	100
77	Se	44/133 (33%)	38 (86%)	6 (14%)	0	100	100
78	Sg	270/317 (85%)	233 (86%)	37 (14%)	0	100	100
All	All	10625/12499 (85%)	10037 (94%)	568 (5%)	20 (0%)	44	71

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	Lc	99	PRO
70	SX	61	GLN
21	LS	165	PRO
50	SC	172	ASN
64	SR	67	ARG
64	SR	122	PRO
43	Lo	59	LYS
51	SD	93	THR
54	SG	165	GLU
11	LH	13	PRO
11	LH	53	LYS
52	SE	247	THR
74	Sb	5	LYS
11	LH	189	GLN

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Mol	Chain	Res	Type
51	SD	202	LYS
51	SD	193	ASP
51	SD	198	ILE
51	SD	196	GLY
71	SY	30	PRO
7	LD	227	ILE

### 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%)	190 (100%)	0	100	100
5	LB	344/348 (99%)	344 (100%)	0	100	100
6	LC	301/348 (86%)	300 (100%)	1 (0%)	86	85
7	LD	246/249 (99%)	246 (100%)	0	100	100
8	LE	194/256 (76%)	193 (100%)	1 (0%)	81	82
9	LF	185/234 (79%)	185 (100%)	0	100	100
10	LG	197/223 (88%)	197 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	170/180 (94%)	169 (99%)	1 (1%)	78	81
13	LJ	141/149 (95%)	140 (99%)	1 (1%)	76	79
14	LL	173/178 (97%)	171 (99%)	2 (1%)	63	74
15	LM	116/157 (74%)	116 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	172/173 (99%)	171 (99%)	1 (1%)	78	81
18	LP	135/163 (83%)	135 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	154/175 (88%)	154 (100%)	0	100	100
21	LS	155/156 (99%)	154 (99%)	1 (1%)	78	81
22	LT	140/140 (100%)	140 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	LU	90/114 (79%)	90 (100%)	0	100	100
24	LV	100/107 (94%)	100 (100%)	0	100	100
25	LW	54/126 (43%)	54 (100%)	0	100	100
26	LX	106/133 (80%)	104 (98%)	2 (2%)	50	68
27	LY	123/135 (91%)	123 (100%)	0	100	100
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	77
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	83/124 (67%)	83 (100%)	0	100	100
31	Lc	79/97 (81%)	79 (100%)	0	100	100
32	Ld	99/110 (90%)	99 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	94/100 (94%)	94 (100%)	0	100	100
36	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	77
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	74
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	46/47 (98%)	46 (100%)	0	100	100
41	Lm	47/116 (40%)	47 (100%)	0	100	100
42	Ln	24/24 (100%)	23 (96%)	1 (4%)	26	55
43	Lo	91/94 (97%)	91 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	108/121 (89%)	108 (100%)	0	100	100
48	SA	173/242 (72%)	173 (100%)	0	100	100
49	SB	194/229 (85%)	194 (100%)	0	100	100
50	SC	181/224 (81%)	177 (98%)	4 (2%)	45	65
51	SD	173/202 (86%)	162 (94%)	11 (6%)	16	44
52	SE	221/225 (98%)	221 (100%)	0	100	100
53	SF	152/170 (89%)	151 (99%)	1 (1%)	76	79
54	SG	178/218 (82%)	172 (97%)	6 (3%)	32	59
55	SH	161/174 (92%)	159 (99%)	2 (1%)	63	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	SI	159/180 (88%)	159 (100%)	0	100	100
57	SJ	126/168 (75%)	126 (100%)	0	100	100
58	SK	81/136 (60%)	75 (93%)	6 (7%)	13	39
59	SL	123/142 (87%)	123 (100%)	0	100	100
60	SN	130/131 (99%)	128 (98%)	2 (2%)	57	71
61	SO	104/119 (87%)	103 (99%)	1 (1%)	68	75
62	SP	107/130 (82%)	105 (98%)	2 (2%)	50	68
63	SQ	115/121 (95%)	113 (98%)	2 (2%)	53	70
64	SR	119/121 (98%)	118 (99%)	1 (1%)	73	78
65	SS	122/132 (92%)	121 (99%)	1 (1%)	73	78
66	ST	110/115 (96%)	109 (99%)	1 (1%)	70	77
67	SU	88/107 (82%)	88 (100%)	0	100	100
68	SV	65/67 (97%)	65 (100%)	0	100	100
69	SW	112/113 (99%)	111 (99%)	1 (1%)	70	77
70	SX	111/115 (96%)	111 (100%)	0	100	100
71	SY	93/115 (81%)	91 (98%)	2 (2%)	45	65
72	SZ	64/103 (62%)	63 (98%)	1 (2%)	55	71
73	Sa	86/98 (88%)	86 (100%)	0	100	100
74	Sb	74/76 (97%)	71 (96%)	3 (4%)	27	55
75	Sc	48/62 (77%)	46 (96%)	2 (4%)	26	55
76	Sd	48/49 (98%)	48 (100%)	0	100	100
77	Se	39/106 (37%)	39 (100%)	0	100	100
78	Sg	237/275 (86%)	235 (99%)	2 (1%)	73	78
All	All	9300/10617 (88%)	9235 (99%)	65 (1%)	73	79

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	LC	100	ARG
8	LE	276	GLN
12	LI	142	LEU
13	LJ	158	SER
14	LL	90	VAL
14	LL	184	MET

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Mol	Chain	Res	Type
17	LO	152	VAL
21	LS	21	LYS
26	LX	92	ASP
26	LX	126	THR
28	LZ	132	GLN
36	Lh	111	GLU
37	Li	3	LEU
42	Ln	1	MET
50	SC	248	TYR
50	SC	255	LEU
50	SC	257	LYS
50	SC	258	GLU
51	SD	66	ILE
51	SD	190	LEU
51	SD	197	LYS
51	SD	198	ILE
51	SD	201	LYS
51	SD	202	LYS
51	SD	204	LEU
51	SD	208	VAL
51	SD	209	SER
51	SD	211	VAL
51	SD	212	GLU
53	SF	204	ARG
54	SG	159	ARG
54	SG	160	LYS
54	SG	167	LYS
54	SG	168	LYS
54	SG	171	THR
54	SG	172	LYS
55	SH	44	ASN
55	SH	132	ASP
58	SK	1	MET
58	SK	2	LEU
58	SK	3	MET
58	SK	5	LYS
58	SK	6	LYS
58	SK	26	ASP
60	SN	39	LYS
60	SN	67	THR
61	SO	56	VAL
62	SP	21	ASP

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Mol	Chain	Res	Type
62	SP	27	ASP
63	SQ	51	LEU
63	SQ	119	LEU
64	SR	63	ARG
65	SS	92	ASP
66	ST	128	GLN
69	SW	2	VAL
71	SY	42	GLU
71	SY	48	TYR
72	SZ	98	LYS
74	Sb	9	HIS
74	Sb	40	CYS
74	Sb	83	GLN
75	Sc	30	VAL
75	Sc	54	ASP
78	Sg	24	THR
78	Sg	30	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	140	ASN
4	LA	205	ASN
6	LC	60	HIS
6	LC	61	GLN
6	LC	329	ASN
7	LD	244	HIS
8	LE	165	HIS
8	LE	199	GLN
10	LG	81	ASN
10	LG	141	ASN
10	LG	153	GLN
10	LG	227	ASN
12	LI	92	HIS
12	LI	144	ASN
13	LJ	23	ASN
14	LL	188	ASN
15	LM	70	GLN
16	LN	91	GLN
16	LN	201	HIS
17	LO	26	GLN
17	LO	50	ASN

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Mol	Chain	Res	Type
17	LO	63	ASN
17	LO	143	HIS
17	LO	184	ASN
18	LP	21	ASN
20	LR	39	GLN
21	LS	91	HIS
22	LT	139	HIS
25	LW	50	ASN
25	LW	59	HIS
27	LY	56	GLN
27	LY	127	GLN
29	La	17	HIS
30	Lb	7	HIS
30	Lb	19	ASN
30	Lb	58	GLN
31	Lc	33	GLN
31	Lc	77	ASN
32	Ld	116	ASN
32	Ld	121	ASN
34	Lf	20	ASN
34	Lf	78	HIS
34	Lf	80	ASN
36	Lh	108	GLN
40	Li	33	ASN
40	Li	43	HIS
43	Lo	45	GLN
45	Lr	4	HIS
45	Lr	21	ASN
45	Lr	95	HIS
48	SA	165	ASN
48	SA	169	HIS
48	SA	193	HIS
49	SB	202	GLN
50	SC	113	GLN
50	SC	115	GLN
51	SD	4	GLN
51	SD	159	HIS
52	SE	179	ASN
52	SE	209	HIS
52	SE	216	ASN
52	SE	232	ASN
53	SF	149	GLN

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Mol	Chain	Res	Type
54	SG	13	GLN
55	SH	33	ASN
55	SH	97	GLN
55	SH	163	GLN
58	SK	44	HIS
58	SK	50	GLN
58	SK	61	GLN
61	SO	26	ASN
63	SQ	86	GLN
63	SQ	97	GLN
64	SR	121	GLN
65	SS	42	HIS
66	ST	42	HIS
69	SW	24	GLN
70	SX	92	ASN
71	SY	112	ASN
75	Sc	24	GLN
76	Sd	4	GLN
78	Sg	62	HIS
78	Sg	117	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3378/4731 (71%)	710 (21%)	34 (1%)
2	L7	119/120 (99%)	16 (13%)	3 (2%)
3	L8	149/158 (94%)	27 (18%)	1 (0%)
46	S2	1619/1870 (86%)	472 (29%)	25 (1%)
47	S6	74/75 (98%)	22 (29%)	2 (2%)
47	S7	74/75 (98%)	40 (54%)	2 (2%)
79	Sx	9/10 (90%)	1 (11%)	0
All	All	5422/7039 (77%)	1288 (23%)	67 (1%)

All (1288) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	13	U
1	L5	21	G
1	L5	39	A

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Mol	Chain	Res	Type
1	L5	40	G
1	L5	42	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	71	C
1	L5	76	A
1	L5	85	G
1	L5	91	G
1	L5	104	G
1	L5	108	A
1	L5	109	G
1	L5	119	G
1	L5	120	A
1	L5	129	C
1	L5	131	C
1	L5	132	G
1	L5	133	C
1	L5	134	G
1	L5	135	U
1	L5	136	C
1	L5	137	G
1	L5	138	C
1	L5	139	G
1	L5	141	C
1	L5	142	G
1	L5	143	U
1	L5	144	G
1	L5	159	C
1	L5	160	G
1	L5	170	C
1	L5	171	U
1	L5	172	C
1	L5	173	C
1	L5	195	C
1	L5	197	A
1	L5	200	U
1	L5	209	U
1	L5	216	C
1	L5	218	A

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Mol	Chain	Res	Type
1	L5	219	G
1	L5	228	C
1	L5	232	G
1	L5	233	U
1	L5	234	G
1	L5	235	A
1	L5	241	G
1	L5	251	C
1	L5	252	G
1	L5	256	C
1	L5	258	C
1	L5	259	C
1	L5	260	G
1	L5	264	U
1	L5	265	C
1	L5	267	G
1	L5	269	U
1	L5	278	A
1	L5	279	G
1	L5	296	U
1	L5	305	A
1	L5	308	C
1	L5	315	U
1	L5	333	A
1	L5	339	C
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
1	L5	409	A
1	L5	411	G
1	L5	413	C
1	L5	414	G
1	L5	416	G
1	L5	430	G
1	L5	431	U
1	L5	439	U
1	L5	448	C
1	L5	449	G

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Mol	Chain	Res	Type
1	L5	452	G
1	L5	454	C
1	L5	455	C
1	L5	456	G
1	L5	457	C
1	L5	458	C
1	L5	459	C
1	L5	466	U
1	L5	467	U
1	L5	471	C
1	L5	487	C
1	L5	488	G
1	L5	492	G
1	L5	494	G
1	L5	495	C
1	L5	497	C
1	L5	512	A
1	L5	513	U
1	L5	654	G
1	L5	659	C
1	L5	660	G
1	L5	661	U
1	L5	668	G
1	L5	669	C
1	L5	671	G
1	L5	673	C
1	L5	674	G
1	L5	675	A
1	L5	676	C
1	L5	677	C
1	L5	678	G
1	L5	682	G
1	L5	691	C
1	L5	693	C
1	L5	695	C
1	L5	696	U
1	L5	697	U
1	L5	701	C
1	L5	704	U
1	L5	705	G
1	L5	712	C
1	L5	739	G

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Mol	Chain	Res	Type
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	813	U
1	L5	815	A
1	L5	817	A
1	L5	820	C
1	L5	824	C
1	L5	825	G
1	L5	830	C
1	L5	831	G
1	L5	833	U
1	L5	834	U
1	L5	835	U
1	L5	842	A
1	L5	843	U
1	L5	854	A
1	L5	857	A
1	L5	858	A
1	L5	860	C
1	L5	872	C
1	L5	882	U
1	L5	886	U
1	L5	887	C
1	L5	924	G
1	L5	927	C
1	L5	928	C
1	L5	936	C
1	L5	938	C
1	L5	940	C
1	L5	954	G
1	L5	1003	G
1	L5	1005	C

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Mol	Chain	Res	Type
1	L5	1006	G
1	L5	1007	G
1	L5	1009	C
1	L5	1010	U
1	L5	1011	G
1	L5	1012	U
1	L5	1013	C
1	L5	1014	C
1	L5	1015	C
1	L5	1017	A
1	L5	1019	U
1	L5	1021	C
1	L5	1022	G
1	L5	1026	C
1	L5	1027	G
1	L5	1028	G
1	L5	1029	G
1	L5	1031	G
1	L5	1032	U
1	L5	1033	G
1	L5	1034	G
1	L5	1036	C
1	L5	1037	G
1	L5	1038	C
1	L5	1039	G
1	L5	1044	C
1	L5	1045	G
1	L5	1048	U
1	L5	1049	C
1	L5	1050	C
1	L5	1051	G
1	L5	1053	G
1	L5	1054	G
1	L5	1055	G
1	L5	1065	G
1	L5	1071	C
1	L5	1072	G
1	L5	1089	A
1	L5	1095	C
1	L5	1099	G
1	L5	1108	G
1	L5	1109	A

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Mol	Chain	Res	Type
1	L5	1116	C
1	L5	1139	A
1	L5	1141	A
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	1202	A
1	L5	1209	G
1	L5	1212	A
1	L5	1221	G
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	1229	G
1	L5	1230	C
1	L5	1232	C
1	L5	1234	A
1	L5	1253	C
1	L5	1254	U
1	L5	1256	C
1	L5	1257	A
1	L5	1261	C
1	L5	1266	A
1	L5	1272	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	1311	A
1	L5	1312	G
1	L5	1316	G
1	L5	1317	A

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Mol	Chain	Res	Type
1	L5	1327	U
1	L5	1328	U
1	L5	1330	G
1	L5	1337	A
1	L5	1344	G
1	L5	1348	A
1	L5	1361	A
1	L5	1380	C
1	L5	1389	A
1	L5	1390	G
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	1445	A
1	L5	1447	G
1	L5	1448	A
1	L5	1455	G
1	L5	1468	G
1	L5	1475	C
1	L5	1490	C
1	L5	1491	U
1	L5	1498	A
1	L5	1505	G
1	L5	1508	C
1	L5	1511	G
1	L5	1524	G
1	L5	1537	G
1	L5	1553	G
1	L5	1556	G
1	L5	1557	U
1	L5	1558	C
1	L5	1559	U
1	L5	1560	U
1	L5	1561	G
1	L5	1563	G
1	L5	1564	G
1	L5	1575	C

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Mol	Chain	Res	Type
1	L5	1586	C
1	L5	1590	A
1	L5	1607	A
1	L5	1608	A
1	L5	1625	U
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	1700	A
1	L5	1713	G
1	L5	1721	U
1	L5	1722	G
1	L5	1723	C
1	L5	1724	C
1	L5	1725	G
1	L5	1734	C
1	L5	1735	A
1	L5	1751	G
1	L5	1754	G
1	L5	1755	G
1	L5	1762	U
1	L5	1763	A
1	L5	1764	G
1	L5	1765	A
1	L5	1768	G
1	L5	1831	C
1	L5	1832	A
1	L5	1837	G
1	L5	1847	U
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	1893	U
1	L5	1903	A
1	L5	1904	C
1	L5	1905	G

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Mol	Chain	Res	Type
1	L5	1906	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	2105	G
1	L5	2108	C
1	L5	2121	G
1	L5	2141	U
1	L5	2146	A
1	L5	2152	A
1	L5	2153	A
1	L5	2154	G
1	L5	2174	A
1	L5	2178	G
1	L5	2179	C
1	L5	2182	U
1	L5	2194	C
1	L5	2207	G
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	2238	G
1	L5	2242	U
1	L5	2243	G
1	L5	2254	C

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Mol	Chain	Res	Type
1	L5	2255	C
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	2277	C
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
1	L5	2315	C
1	L5	2316	G
1	L5	2324	G
1	L5	2326	C
1	L5	2337	C
1	L5	2341	A
1	L5	2346	U
1	L5	2355	A
1	L5	2356	G
1	L5	2365	A
1	L5	2381	C
1	L5	2406	G
1	L5	2407	C
1	L5	2414	A
1	L5	2415	U
1	L5	2416	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	2451	A
1	L5	2457	G
1	L5	2459	G

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Mol	Chain	Res	Type
1	L5	2460	G
1	L5	2461	U
1	L5	2462	U
1	L5	2463	C
1	L5	2464	C
1	L5	2465	G
1	L5	2466	G
1	L5	2479	A
1	L5	2480	G
1	L5	2483	C
1	L5	2493	C
1	L5	2497	A
1	L5	2498	A
1	L5	2513	G
1	L5	2514	G
1	L5	2515	U
1	L5	2516	G
1	L5	2517	U
1	L5	2518	A
1	L5	2520	A
1	L5	2523	U
1	L5	2524	C
1	L5	2530	G
1	L5	2532	G
1	L5	2541	A
1	L5	2542	U
1	L5	2544	U
1	L5	2552	A
1	L5	2568	C
1	L5	2576	G
1	L5	2580	U
1	L5	2581	G
1	L5	2587	A
1	L5	2609	G
1	L5	2646	C
1	L5	2650	G
1	L5	2651	G
1	L5	2653	C
1	L5	3272	G
1	L5	3275	C
1	L5	3283	G
1	L5	3292	A

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Mol	Chain	Res	Type
1	L5	3303	A
1	L5	3319	A
1	L5	3321	G
1	L5	3330	C
1	L5	3353	C
1	L5	3367	G
1	L5	3368	A
1	L5	3387	U
1	L5	3407	G
1	L5	3411	G
1	L5	3418	C
1	L5	3431	A
1	L5	3434	G
1	L5	3441	A
1	L5	3443	U
1	L5	3449	G
1	L5	3459	U
1	L5	3468	G
1	L5	3471	U
1	L5	3474	A
1	L5	3476	G
1	L5	3495	U
1	L5	3497	U
1	L5	3508	U
1	L5	3524	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	3595	G
1	L5	3598	G
1	L5	3601	G
1	L5	3602	A
1	L5	3603	G

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Mol	Chain	Res	Type
1	L5	3604	A
1	L5	3605	C
1	L5	3606	A
1	L5	3608	G
1	L5	3712	C
1	L5	3713	A
1	L5	3714	U
1	L5	3715	C
1	L5	3716	G
1	L5	3717	U
1	L5	3727	G
1	L5	3735	G
1	L5	3744	G
1	L5	3745	G
1	L5	3747	C
1	L5	3748	G
1	L5	3768	U
1	L5	3770	C
1	L5	3773	G
1	L5	3778	A
1	L5	3780	G
1	L5	3786	G
1	L5	3787	U
1	L5	3788	C
1	L5	3789	C
1	L5	3803	G
1	L5	3804	G
1	L5	3805	G
1	L5	3815	C
1	L5	3816	U
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	3904	A

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Mol	Chain	Res	Type
1	L5	3905	C
1	L5	3907	G
1	L5	3909	A
1	L5	3910	A
1	L5	3911	C
1	L5	3924	A
1	L5	3926	A
1	L5	3933	A
1	L5	3934	A
1	L5	3941	C
1	L5	3944	G
1	L5	3950	G
1	L5	3958	G
1	L5	3967	C
1	L5	3982	G
1	L5	3983	G
1	L5	3984	G
1	L5	3985	C
1	L5	3992	A
1	L5	4021	G
1	L5	4026	G
1	L5	4030	G
1	L5	4031	A
1	L5	4040	C
1	L5	4047	A
1	L5	4064	G
1	L5	4068	A
1	L5	4073	U
1	L5	4074	C
1	L5	4075	A
1	L5	4086	G
1	L5	4088	U
1	L5	4097	C
1	L5	4101	G
1	L5	4105	U
1	L5	4117	A
1	L5	4119	C
1	L5	4124	U
1	L5	4146	U
1	L5	4153	U
1	L5	4155	C
1	L5	4165	U

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Mol	Chain	Res	Type
1	L5	4166	A
1	L5	4171	A
1	L5	4177	G
1	L5	4181	G
1	L5	4198	G
1	L5	4201	A
1	L5	4202	G
1	L5	4208	U
1	L5	4213	C
1	L5	4220	G
1	L5	4228	G
1	L5	4242	A
1	L5	4243	A
1	L5	4253	G
1	L5	4259	G
1	L5	4263	A
1	L5	4287	U
1	L5	4288	A
1	L5	4289	U
1	L5	4290	G
1	L5	4305	G
1	L5	4309	A
1	L5	4323	C
1	L5	4325	A
1	L5	4326	U
1	L5	4344	A
1	L5	4353	A
1	L5	4361	A
1	L5	4362	U
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	4390	G
1	L5	4393	G
1	L5	4394	A
1	L5	4395	A
1	L5	4396	G
1	L5	4397	G

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Mol	Chain	Res	Type
1	L5	4398	A
1	L5	4399	G
1	L5	4404	G
1	L5	4408	G
1	L5	4411	C
1	L5	4413	C
1	L5	4415	G
1	L5	4419	G
1	L5	4425	U
1	L5	4428	C
1	L5	4507	G
1	L5	4516	G
1	L5	4517	C
1	L5	4523	G
1	L5	4526	G
1	L5	4528	U
1	L5	4529	C
1	L5	4530	G
1	L5	4531	U
1	L5	4532	C
1	L5	4546	U
1	L5	4549	G
1	L5	4550	G
1	L5	4551	C
1	L5	4552	C
1	L5	4553	G
1	L5	4554	G
1	L5	4557	A
1	L5	4558	G
1	L5	4559	G
1	L5	4563	C
1	L5	4565	G
1	L5	4567	C
1	L5	4568	C
1	L5	4569	U
1	L5	4571	U
1	L5	4572	C
1	L5	4580	A
1	L5	4583	U
1	L5	4584	U
1	L5	4585	G
1	L5	4588	C

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Mol	Chain	Res	Type
1	L5	4589	G
1	L5	4596	C
1	L5	4597	G
1	L5	4603	A
1	L5	4604	A
1	L5	4607	U
1	L5	4612	C
1	L5	4613	U
1	L5	4621	U
1	L5	4624	U
1	L5	4627	A
1	L5	4636	U
1	L5	4638	C
1	L5	4639	U
1	L5	4654	U
1	L5	4662	A
1	L5	4664	A
1	L5	4665	G
1	L5	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	4696	A
1	L5	4698	C
1	L5	4702	C
1	L5	4703	G
1	L5	4706	A
1	L5	4709	A
1	L5	4710	G
1	L5	4717	U
2	L7	4	U
2	L7	7	G
2	L7	22	A
2	L7	23	A
2	L7	24	C
2	L7	33	U
2	L7	40	U
2	L7	53	U
2	L7	60	G

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Mol	Chain	Res	Type
2	L7	61	G
2	L7	64	G
2	L7	65	G
2	L7	100	A
2	L7	103	A
2	L7	110	G
2	L7	120	U
3	L8	6	C
3	L8	23	C
3	L8	34	U
3	L8	35	C
3	L8	50	C
3	L8	59	A
3	L8	62	A
3	L8	63	U
3	L8	71	A
3	L8	72	A
3	L8	80	A
3	L8	87	G
3	L8	94	G
3	L8	96	C
3	L8	103	A
3	L8	105	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	125	C
3	L8	126	C
3	L8	150	C
3	L8	151	G
3	L8	153	C
46	S2	2	A
46	S2	4	C
46	S2	26	U
46	S2	33	G
46	S2	35	C
46	S2	41	G
46	S2	46	A
46	S2	50	A

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Mol	Chain	Res	Type
46	S2	51	U
46	S2	52	G
46	S2	56	G
46	S2	58	C
46	S2	59	U
46	S2	60	A
46	S2	61	A
46	S2	62	G
46	S2	63	U
46	S2	65	C
46	S2	67	C
46	S2	68	A
46	S2	69	C
46	S2	71	G
46	S2	72	C
46	S2	73	C
46	S2	74	G
46	S2	76	U
46	S2	78	C
46	S2	79	A
46	S2	82	G
46	S2	83	A
46	S2	86	C
46	S2	87	U
46	S2	91	A
46	S2	95	G
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	114	G
46	S2	115	U
46	S2	116	U
46	S2	118	C
46	S2	119	U
46	S2	120	U
46	S2	121	U
46	S2	126	G
46	S2	127	C
46	S2	128	U

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Mol	Chain	Res	Type
46	S2	129	C
46	S2	143	U
46	S2	144	U
46	S2	149	A
46	S2	151	C
46	S2	152	U
46	S2	153	G
46	S2	158	A
46	S2	161	U
46	S2	162	C
46	S2	163	U
46	S2	166	A
46	S2	167	G
46	S2	170	A
46	S2	171	A
46	S2	172	U
46	S2	179	C
46	S2	181	A
46	S2	182	C
46	S2	184	G
46	S2	220	U
46	S2	222	U
46	S2	226	A
46	S2	291	U
46	S2	292	G
46	S2	293	A
46	S2	294	C
46	S2	299	G
46	S2	303	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	319	A
46	S2	320	C
46	S2	323	C
46	S2	324	C
46	S2	338	C
46	S2	341	C
46	S2	342	C

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Mol	Chain	Res	Type
46	S2	343	C
46	S2	344	A
46	S2	345	U
46	S2	346	U
46	S2	347	C
46	S2	348	G
46	S2	352	G
46	S2	363	C
46	S2	365	A
46	S2	370	C
46	S2	371	G
46	S2	378	G
46	S2	386	G
46	S2	387	C
46	S2	408	G
46	S2	409	A
46	S2	410	C
46	S2	439	G
46	S2	445	G
46	S2	447	G
46	S2	448	A
46	S2	449	A
46	S2	451	C
46	S2	455	U
46	S2	464	C
46	S2	465	A
46	S2	468	G
46	S2	469	A
46	S2	472	G
46	S2	473	C
46	S2	474	A
46	S2	475	G
46	S2	476	C
46	S2	477	A
46	S2	478	G
46	S2	479	G
46	S2	480	C
46	S2	483	G
46	S2	484	C
46	S2	485	A
46	S2	486	A
46	S2	488	U

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Mol	Chain	Res	Type
46	S2	489	U
46	S2	490	A
46	S2	492	C
46	S2	493	C
46	S2	494	A
46	S2	495	C
46	S2	497	C
46	S2	499	C
46	S2	502	C
46	S2	503	C
46	S2	504	C
46	S2	505	G
46	S2	507	G
46	S2	508	G
46	S2	509	A
46	S2	511	G
46	S2	512	U
46	S2	514	G
46	S2	515	U
46	S2	517	A
46	S2	518	C
46	S2	525	U
46	S2	526	A
46	S2	530	A
46	S2	531	U
46	S2	532	A
46	S2	533	C
46	S2	534	A
46	S2	535	G
46	S2	536	G
46	S2	537	A
46	S2	538	C
46	S2	539	U
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	549	C
46	S2	552	U
46	S2	557	U

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Mol	Chain	Res	Type
46	S2	558	U
46	S2	559	G
46	S2	560	G
46	S2	561	A
46	S2	562	A
46	S2	563	U
46	S2	564	G
46	S2	565	A
46	S2	566	G
46	S2	567	U
46	S2	568	C
46	S2	570	A
46	S2	571	C
46	S2	577	A
46	S2	578	U
46	S2	579	C
46	S2	584	A
46	S2	585	A
46	S2	587	G
46	S2	588	A
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	598	G
46	S2	600	A
46	S2	605	A
46	S2	607	G
46	S2	608	U
46	S2	609	C
46	S2	618	G
46	S2	629	A
46	S2	630	A
46	S2	632	U
46	S2	644	A
46	S2	645	G
46	S2	656	A
46	S2	661	C
46	S2	665	A
46	S2	669	A

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Mol	Chain	Res	Type
46	S2	670	A
46	S2	672	A
46	S2	673	A
46	S2	674	G
46	S2	684	G
46	S2	689	U
46	S2	749	C
46	S2	750	U
46	S2	751	C
46	S2	795	A
46	S2	798	C
46	S2	799	G
46	S2	800	U
46	S2	822	G
46	S2	823	U
46	S2	829	G
46	S2	830	C
46	S2	831	A
46	S2	832	G
46	S2	835	C
46	S2	837	G
46	S2	838	A
46	S2	839	G
46	S2	840	C
46	S2	841	C
46	S2	843	C
46	S2	846	G
46	S2	847	G
46	S2	848	A
46	S2	863	A
46	S2	870	A
46	S2	871	A
46	S2	874	G
46	S2	875	G
46	S2	876	A
46	S2	882	G
46	S2	883	U
46	S2	884	U
46	S2	885	C
46	S2	886	U
46	S2	890	U
46	S2	891	U

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Mol	Chain	Res	Type
46	S2	892	G
46	S2	893	U
46	S2	894	U
46	S2	895	G
46	S2	896	G
46	S2	897	U
46	S2	898	U
46	S2	899	U
46	S2	900	U
46	S2	901	C
46	S2	902	G
46	S2	903	G
46	S2	904	A
46	S2	910	G
46	S2	914	A
46	S2	918	U
46	S2	920	A
46	S2	921	A
46	S2	934	G
46	S2	939	A
46	S2	971	G
46	S2	972	G
46	S2	991	A
46	S2	993	A
46	S2	998	A
46	S2	1002	A
46	S2	1009	A
46	S2	1018	U
46	S2	1019	U
46	S2	1023	U
46	S2	1024	A
46	S2	1028	A
46	S2	1062	U
46	S2	1063	A
46	S2	1078	A
46	S2	1084	A
46	S2	1086	C
46	S2	1110	C
46	S2	1115	U
46	S2	1116	U
46	S2	1117	C
46	S2	1118	C

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Mol	Chain	Res	Type
46	S2	1134	A
46	S2	1139	C
46	S2	1150	A
46	S2	1154	C
46	S2	1155	U
46	S2	1196	A
46	S2	1208	G
46	S2	1209	A
46	S2	1216	C
46	S2	1217	C
46	S2	1225	G
46	S2	1228	G
46	S2	1241	A
46	S2	1242	A
46	S2	1243	U
46	S2	1244	U
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	1272	C
46	S2	1275	G
46	S2	1277	A
46	S2	1279	A
46	S2	1280	C
46	S2	1284	C
46	S2	1287	G
46	S2	1288	A
46	S2	1293	C
46	S2	1294	A
46	S2	1295	G
46	S2	1296	A
46	S2	1297	U
46	S2	1298	U
46	S2	1299	G
46	S2	1301	U
46	S2	1302	A
46	S2	1303	G
46	S2	1304	C
46	S2	1308	U

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Mol	Chain	Res	Type
46	S2	1309	U
46	S2	1311	U
46	S2	1314	A
46	S2	1315	U
46	S2	1316	U
46	S2	1318	C
46	S2	1319	G
46	S2	1320	U
46	S2	1321	G
46	S2	1322	G
46	S2	1323	G
46	S2	1324	U
46	S2	1343	U
46	S2	1344	U
46	S2	1372	U
46	S2	1373	U
46	S2	1379	A
46	S2	1391	U
46	S2	1398	U
46	S2	1399	G
46	S2	1401	U
46	S2	1403	A
46	S2	1404	C
46	S2	1405	U
46	S2	1407	G
46	S2	1409	U
46	S2	1411	C
46	S2	1412	G
46	S2	1413	C
46	S2	1414	G
46	S2	1416	C
46	S2	1417	C
46	S2	1418	C
46	S2	1419	C
46	S2	1420	C
46	S2	1421	G
46	S2	1422	A
46	S2	1423	G
46	S2	1424	C
46	S2	1426	G
46	S2	1428	C
46	S2	1430	G

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Mol	Chain	Res	Type
46	S2	1442	U
46	S2	1443	U
46	S2	1448	G
46	S2	1455	A
46	S2	1456	A
46	S2	1463	U
46	S2	1465	C
46	S2	1477	A
46	S2	1479	U
46	S2	1488	A
46	S2	1490	A
46	S2	1491	G
46	S2	1498	G
46	S2	1499	A
46	S2	1507	A
46	S2	1508	G
46	S2	1509	A
46	S2	1521	G
46	S2	1522	C
46	S2	1523	A
46	S2	1534	A
46	S2	1545	C
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	1569	C
46	S2	1580	A
46	S2	1581	A
46	S2	1582	C
46	S2	1588	G
46	S2	1589	A
46	S2	1600	U
46	S2	1601	G
46	S2	1619	C
46	S2	1622	U
46	S2	1624	A
46	S2	1635	A
46	S2	1647	C

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Mol	Chain	Res	Type
46	S2	1649	G
46	S2	1657	G
46	S2	1662	A
46	S2	1664	A
46	S2	1666	G
46	S2	1681	G
46	S2	1700	A
46	S2	1722	U
46	S2	1723	G
46	S2	1730	U
46	S2	1736	A
46	S2	1743	C
46	S2	1744	G
46	S2	1745	G
46	S2	1748	C
46	S2	1749	G
46	S2	1753	C
46	S2	1754	C
46	S2	1755	G
46	S2	1778	G
46	S2	1779	C
46	S2	1782	A
46	S2	1784	C
46	S2	1785	G
46	S2	1786	C
46	S2	1787	U
46	S2	1790	G
46	S2	1791	A
46	S2	1806	G
46	S2	1808	C
46	S2	1817	G
46	S2	1825	A
46	S2	1830	G
46	S2	1839	U
46	S2	1840	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

*Continued on next page...*



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Mol	Chain	Res	Type
46	S2	1866	C
46	S2	1870	A
47	S6	4	C
47	S6	10	G
47	S6	17	C
47	S6	18	G
47	S6	20	A
47	S6	21	A
47	S6	45	G
47	S6	46	G
47	S6	48	C
47	S6	52	G
47	S6	53	G
47	S6	54	A
47	S6	55	U
47	S6	58	A
47	S6	59	A
47	S6	61	C
47	S6	62	C
47	S6	67	U
47	S6	69	U
47	S6	74	C
47	S6	75	C
47	S6	76	A
47	S7	3	G
47	S7	4	C
47	S7	5	A
47	S7	8	G
47	S7	9	U
47	S7	10	G
47	S7	11	G
47	S7	12	C
47	S7	14	C
47	S7	16	G
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	29	G
47	S7	30	G

*Continued on next page...*



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Mol	Chain	Res	Type
47	S7	31	G
47	S7	32	C
47	S7	33	C
47	S7	38	A
47	S7	45	G
47	S7	46	G
47	S7	47	U
47	S7	48	C
47	S7	53	G
47	S7	54	A
47	S7	56	C
47	S7	57	G
47	S7	58	A
47	S7	61	C
47	S7	67	U
47	S7	69	U
47	S7	70	G
47	S7	72	U
47	S7	73	A
47	S7	74	C
47	S7	75	C
47	S7	76	A
79	Sx	33	U

All (67) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	1	C
1	L5	266	G
1	L5	415	U
1	L5	453	U
1	L5	458	C
1	L5	486	C
1	L5	745	C
1	L5	753	G
1	L5	823	C
1	L5	830	C
1	L5	923	G
1	L5	1054	G
1	L5	1192	G
1	L5	1227	G
1	L5	1271	G

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	L5	1447	G
1	L5	1562	G
1	L5	1563	G
1	L5	1585	U
1	L5	2345	A
1	L5	2519	A
1	L5	2540	C
1	L5	2649	A
1	L5	3417	A
1	L5	3715	C
1	L5	3788	C
1	L5	3904	A
1	L5	4201	A
1	L5	4352	U
1	L5	4549	G
1	L5	4552	C
1	L5	4612	C
1	L5	4676	G
1	L5	4686	A
2	L7	3	C
2	L7	52	C
2	L7	60	G
3	L8	5	U
46	S2	34	U
46	S2	55	U
46	S2	115	U
46	S2	118	C
46	S2	126	G
46	S2	293	A
46	S2	446	A
46	S2	492	C
46	S2	507	G
46	S2	565	A
46	S2	592	U
46	S2	599	G
46	S2	794	G
46	S2	842	G
46	S2	846	G
46	S2	862	A
46	S2	1241	A
46	S2	1321	G
46	S2	1323	G

*Continued on next page...*



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Mol	Chain	Res	Type
46	S2	1343	U
46	S2	1408	U
46	S2	1416	C
46	S2	1442	U
46	S2	1476	G
46	S2	1784	C
47	S6	53	G
47	S6	54	A
47	S7	29	G
47	S7	75	C

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 100 ligands modelled in this entry, 100 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



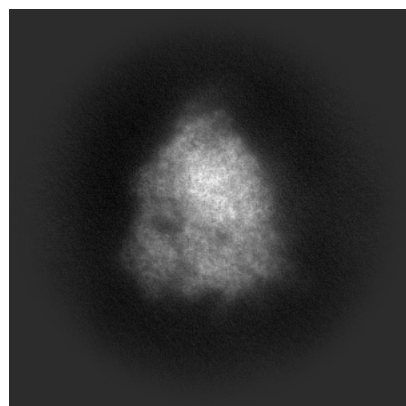
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62287. These allow visual inspection of the internal detail of the map and identification of artifacts.

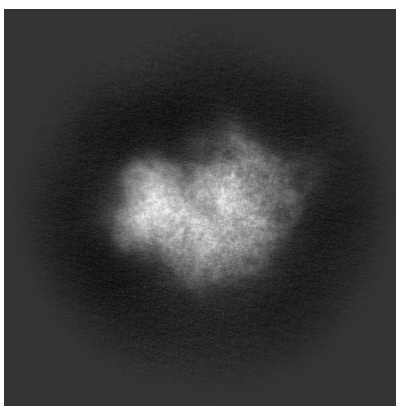
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

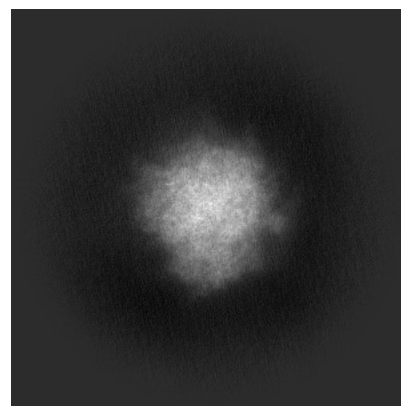
#### 6.1.1 Primary map



X

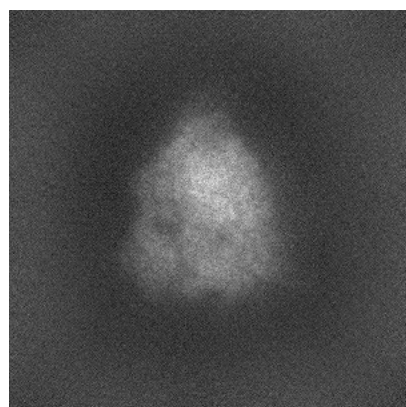


Y

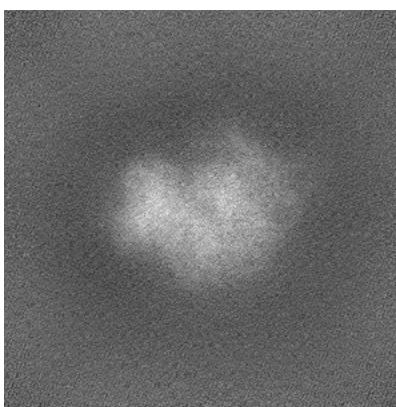


Z

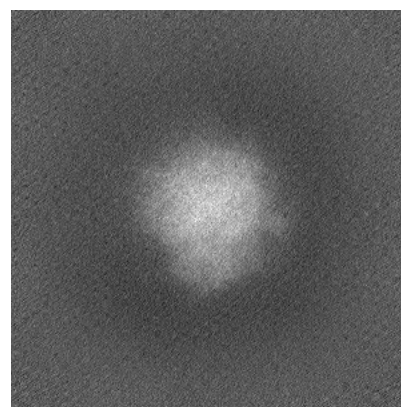
#### 6.1.2 Raw map



X



Y



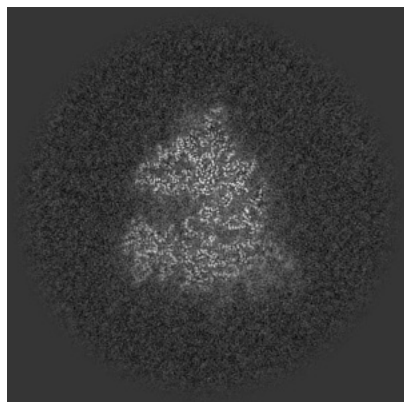
Z

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

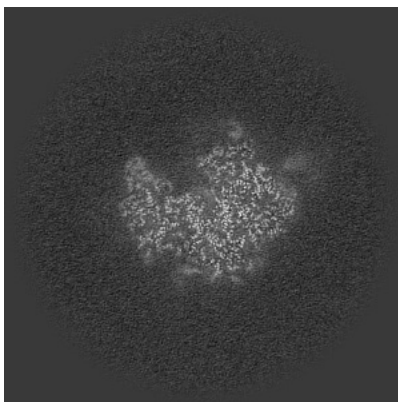


## 6.2 Central slices [i](#)

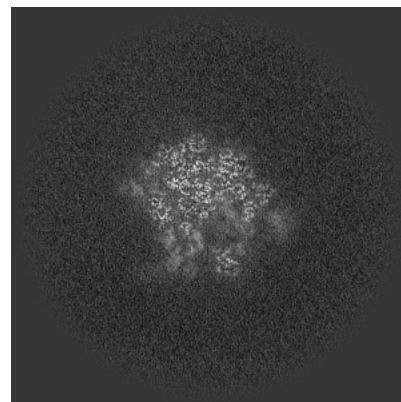
### 6.2.1 Primary map



X Index: 280

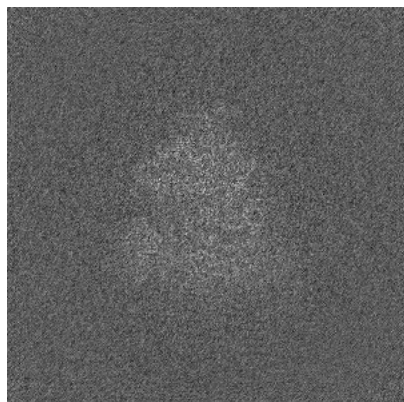


Y Index: 280

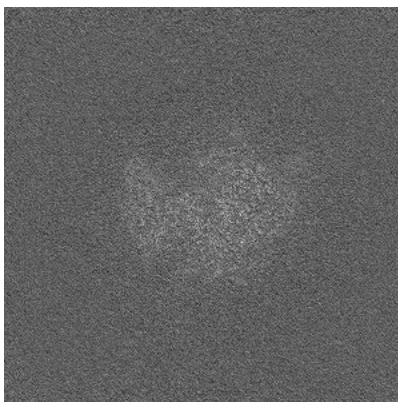


Z Index: 280

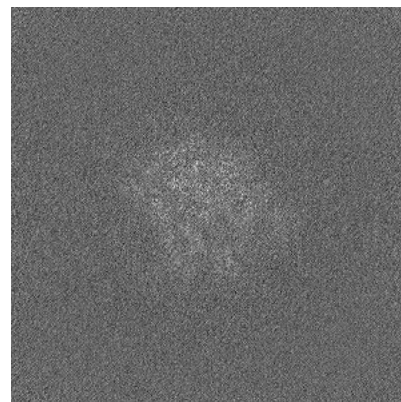
### 6.2.2 Raw map



X Index: 280



Y Index: 280



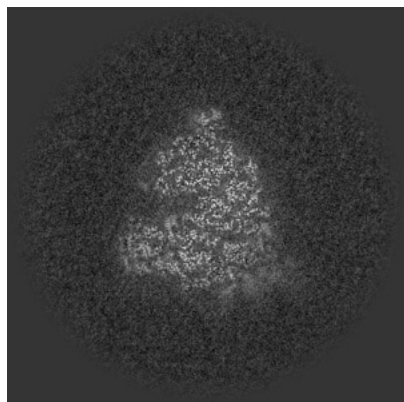
Z Index: 280

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

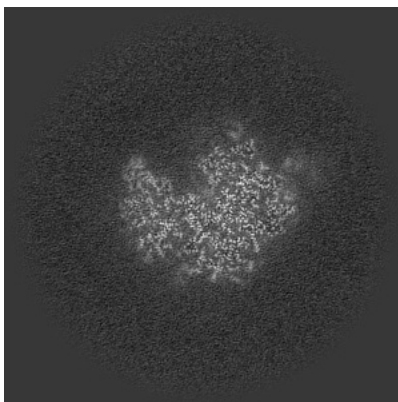


## 6.3 Largest variance slices [i](#)

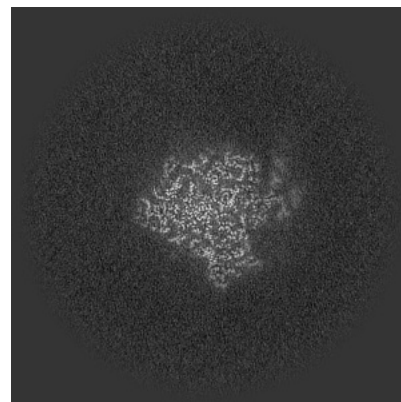
### 6.3.1 Primary map



X Index: 272

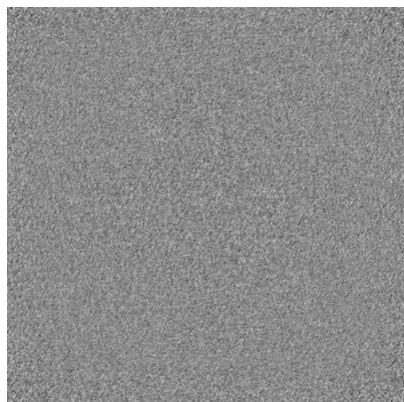


Y Index: 278

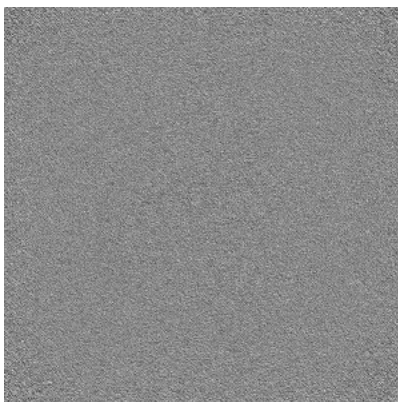


Z Index: 317

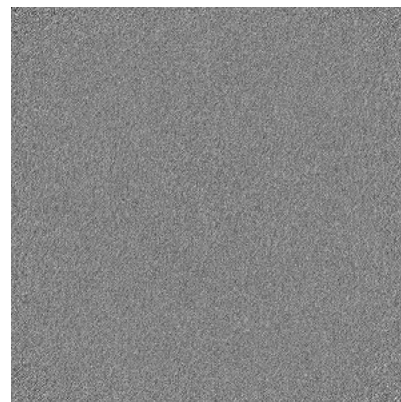
### 6.3.2 Raw map



X Index: 0



Y Index: 0



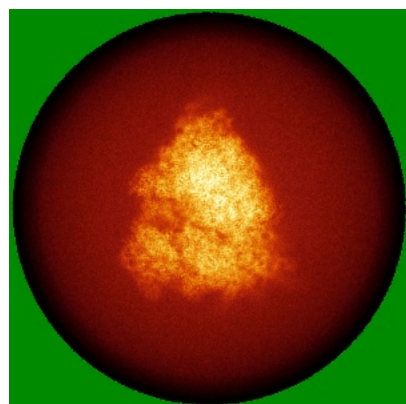
Z Index: 0

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

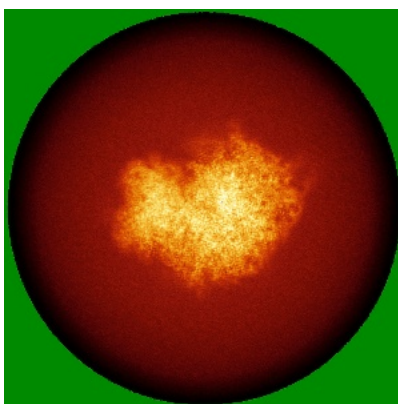


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

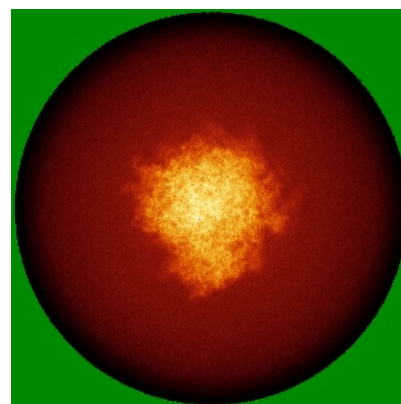
### 6.4.1 Primary map



X

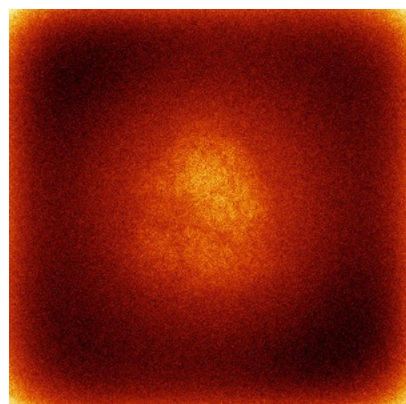


Y

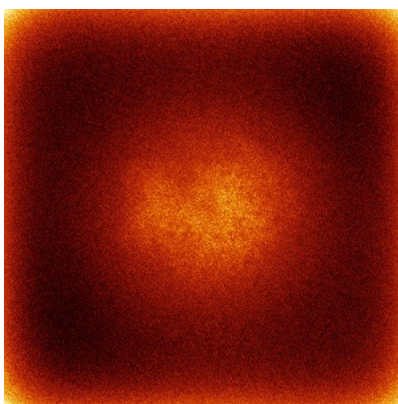


Z

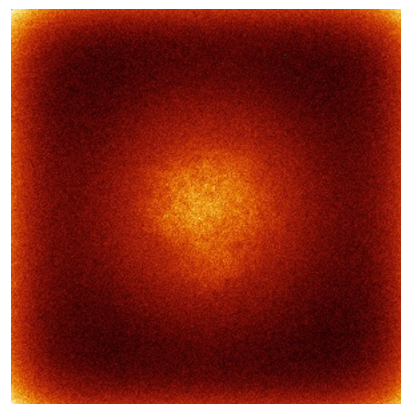
### 6.4.2 Raw map



X



Y



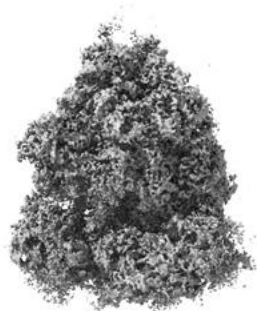
Z

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



## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



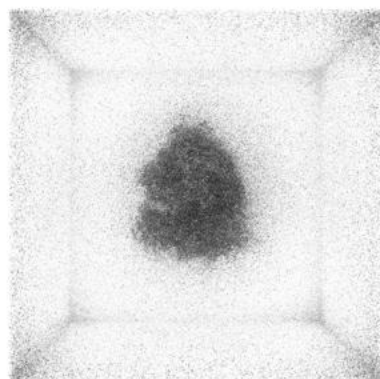
Y



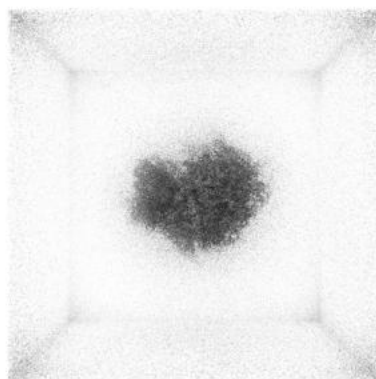
Z

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

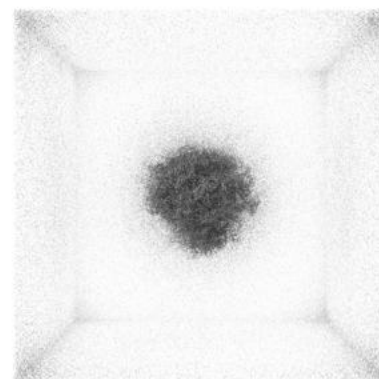
### 6.5.2 Raw map



X



Y



Z

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

## 6.6 Mask visualisation [i](#)

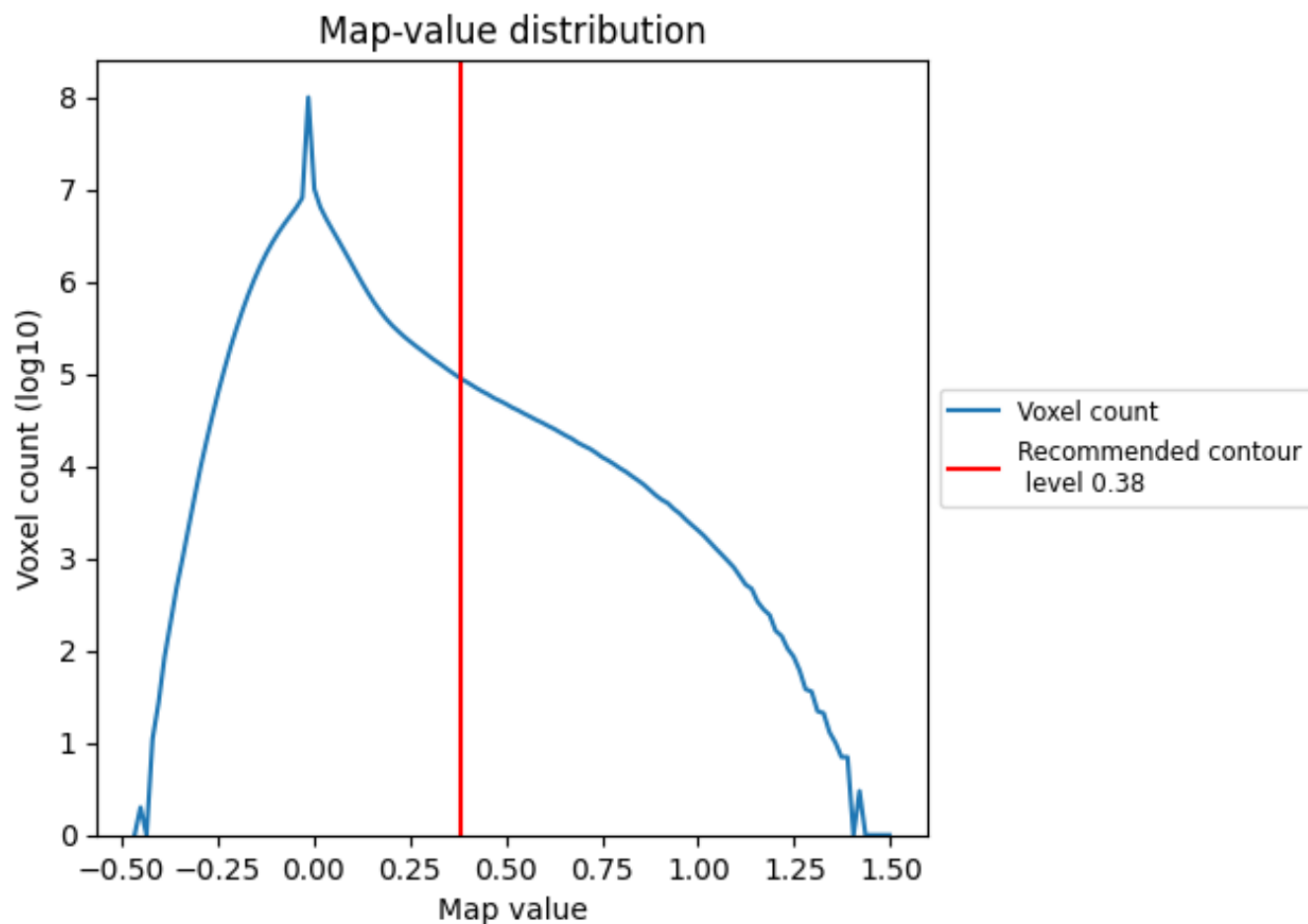
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

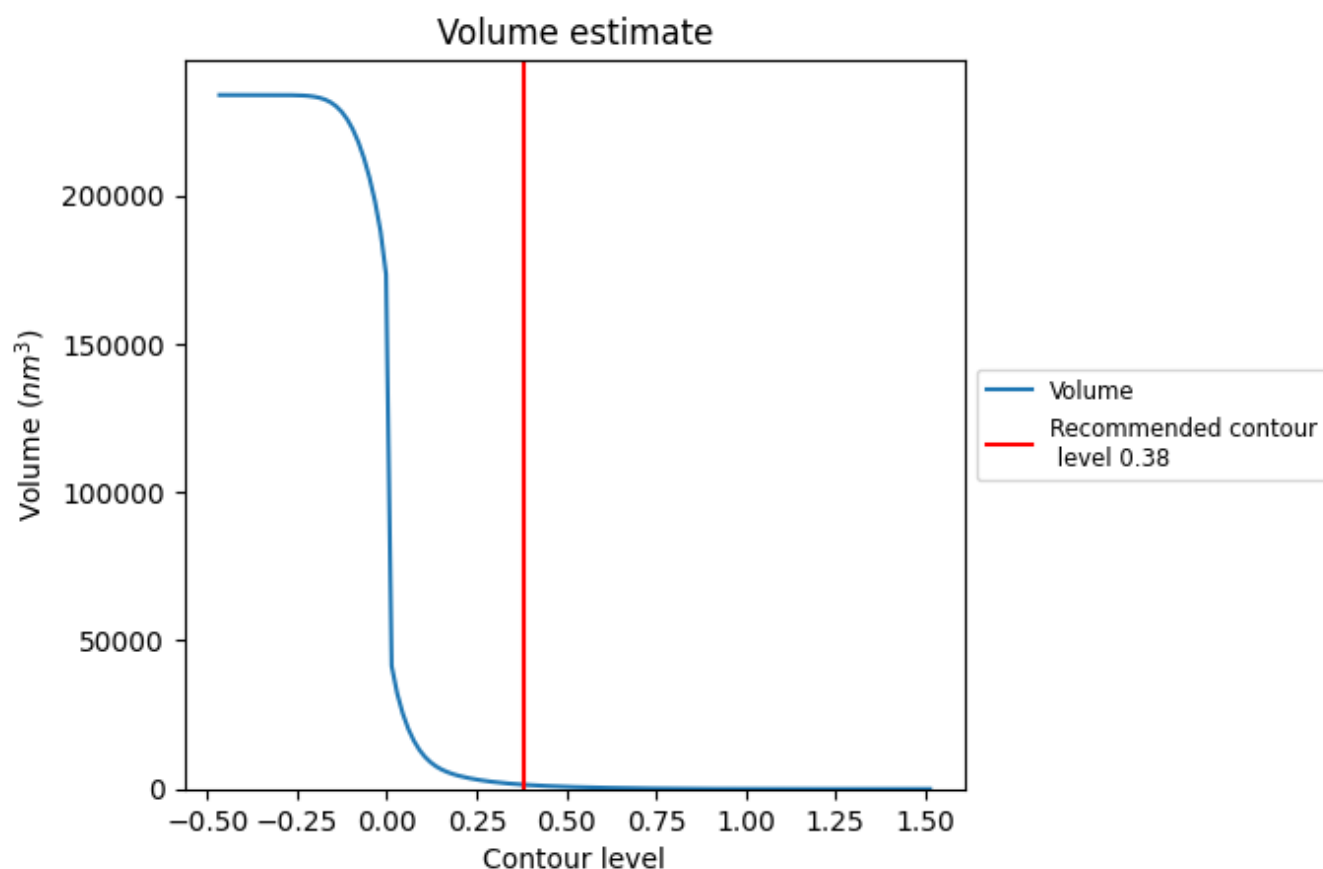
### 7.1 Map-value distribution [i](#)



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



## 7.2 Volume estimate [i](#)

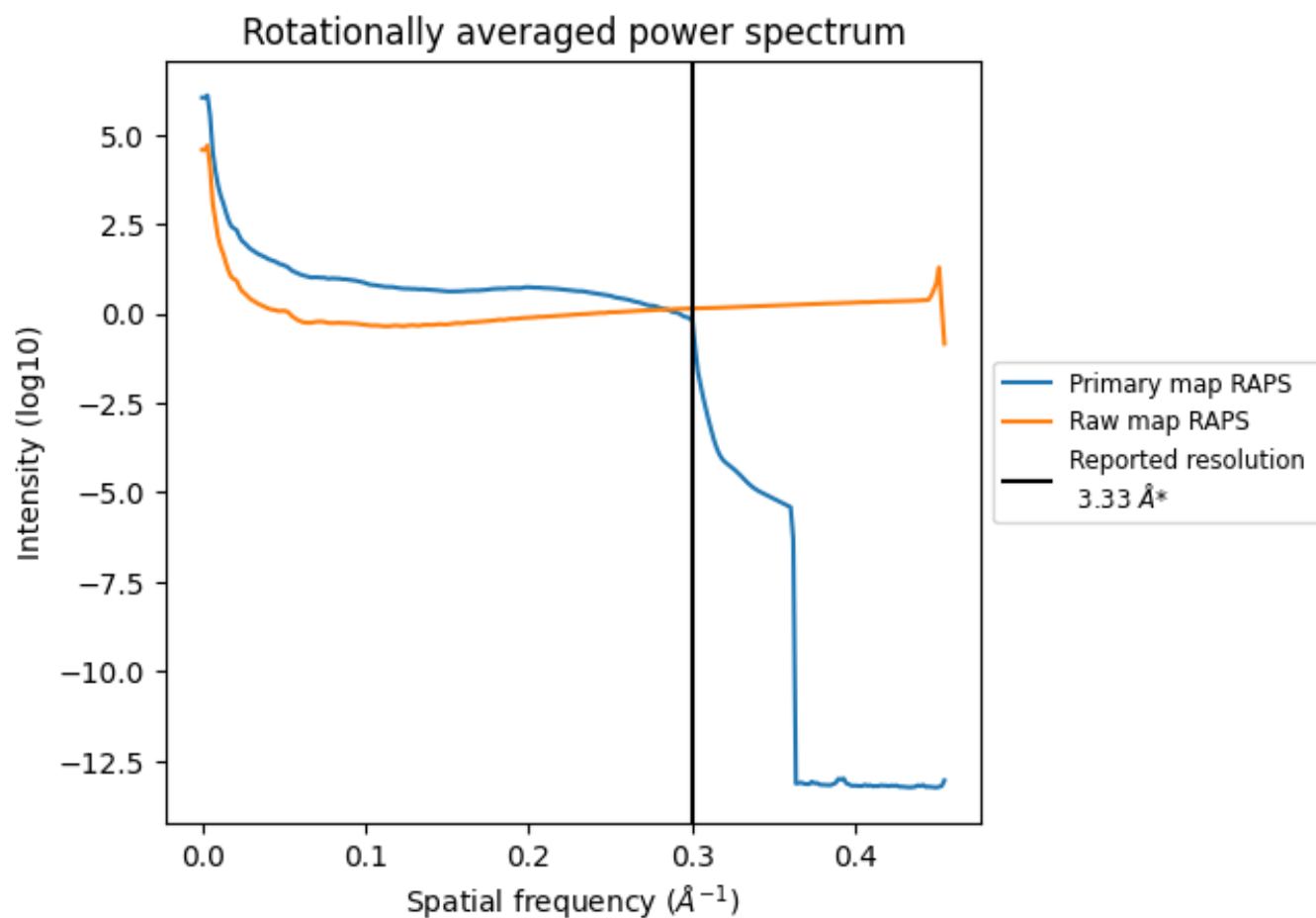


The volume at the recommended contour level is 1455 nm<sup>3</sup>; this corresponds to an approximate mass of 1314 kDa.

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 ⓘ



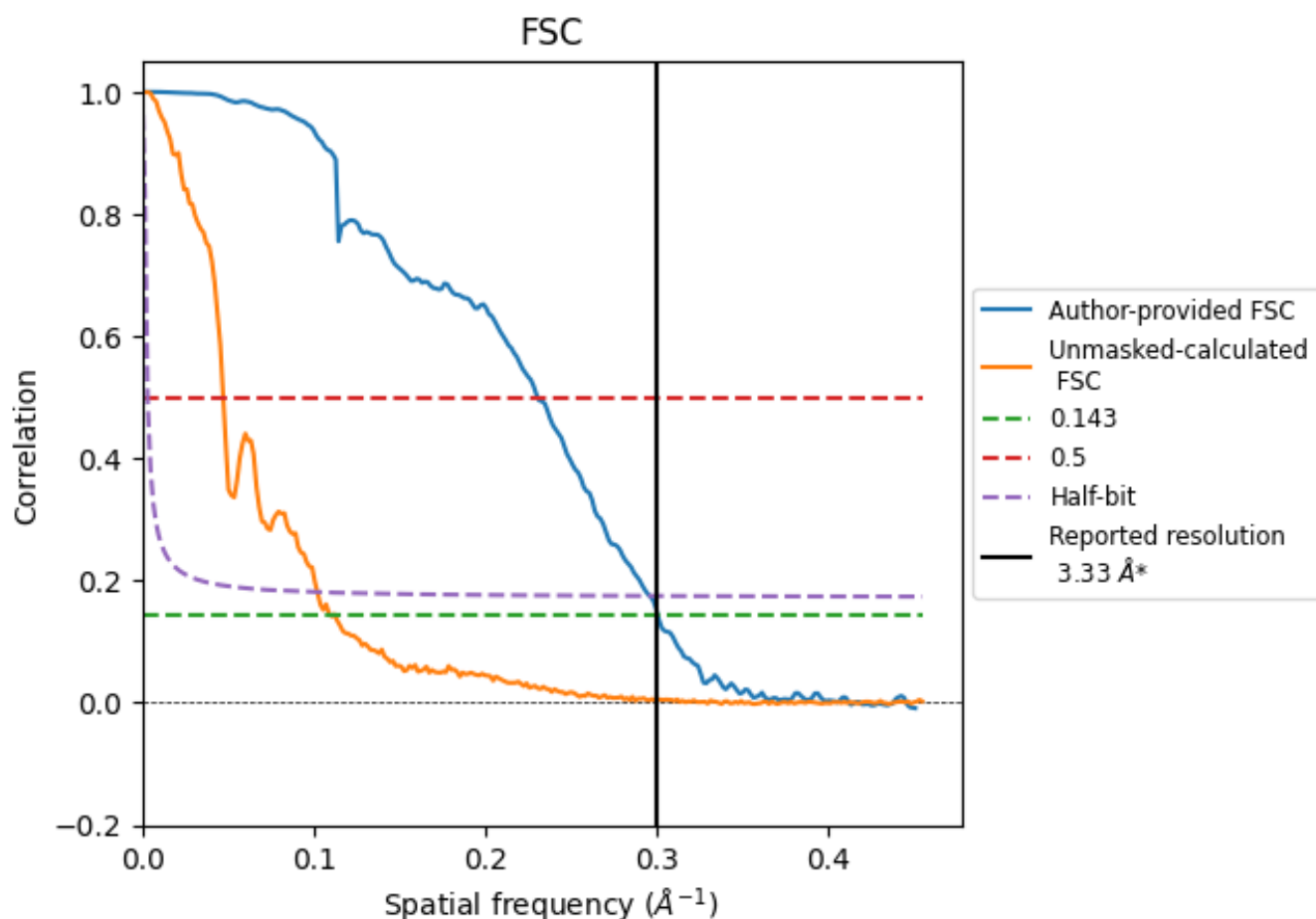
\*Reported resolution corresponds to spatial frequency of 0.300  $\text{\AA}^{-1}$



## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.300 \text{ \AA}^{-1}$



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.33	-	-
Author-provided FSC curve	3.33	4.34	3.38
Unmasked-calculated*	9.10	21.19	9.79

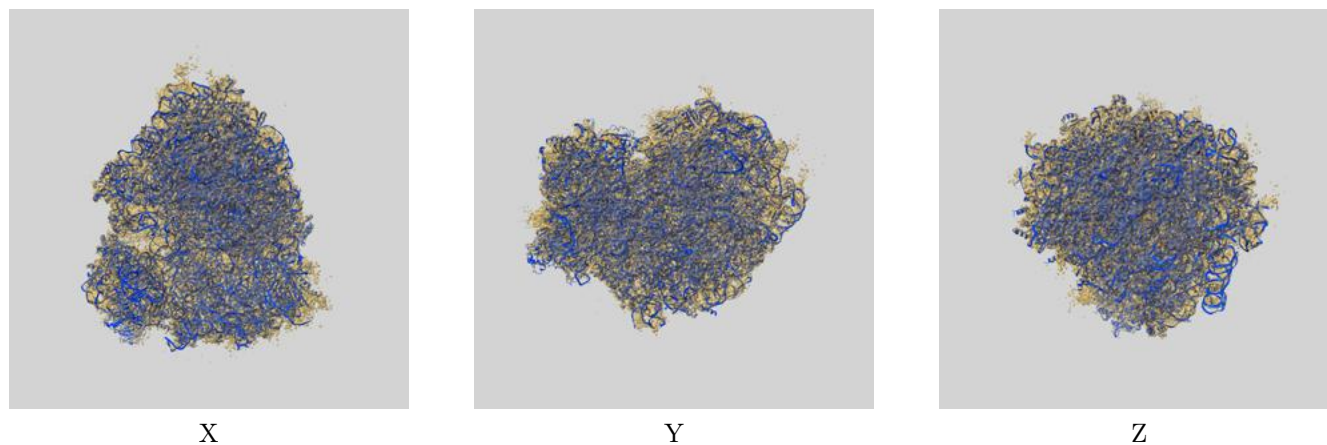
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.10 differs from the reported value 3.33 by more than 10 %



## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-62287 and PDB model 9KDV. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

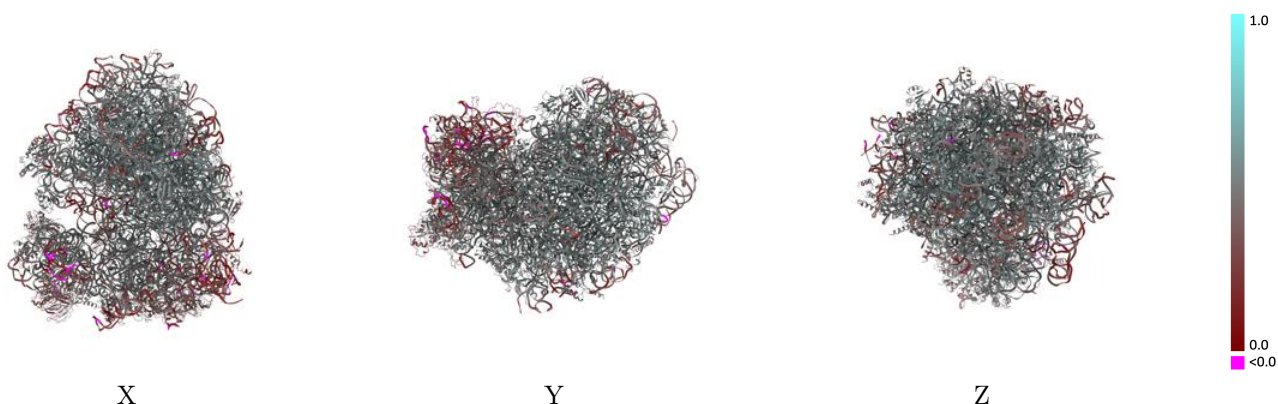
### 9.1 Map-model overlay [i](#)



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.

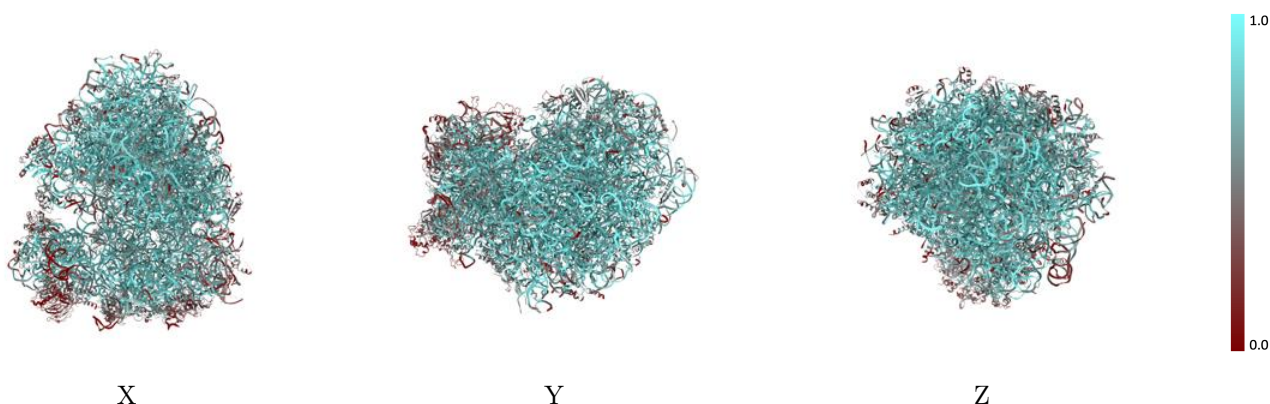


## 9.2 Q-score mapped to coordinate model [i](#)



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.

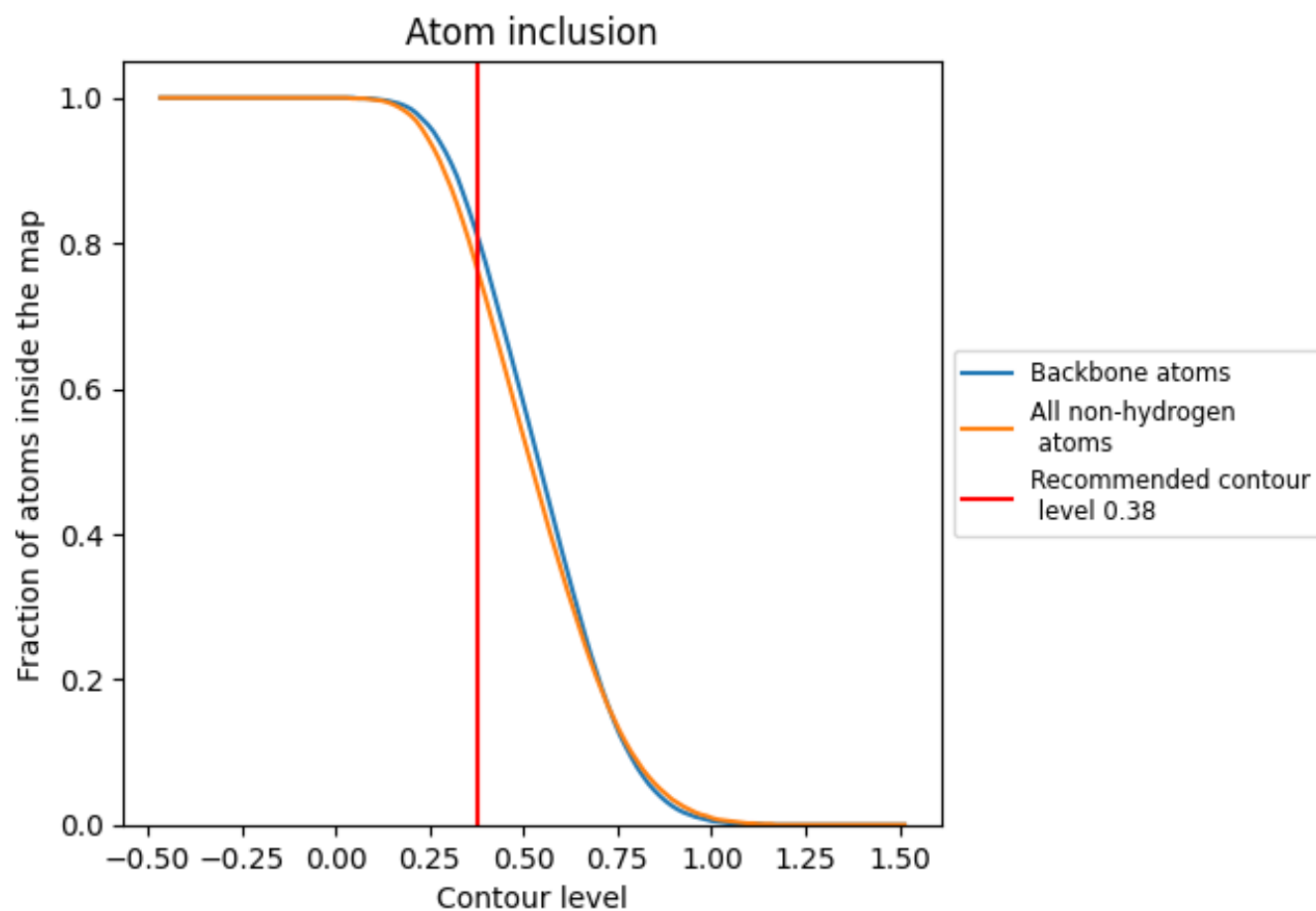
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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, 80% of all backbone atoms, 76% 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	 0.7590	 0.4580
L5	 0.8780	 0.4720
L7	 0.9200	 0.4970
L8	 0.9040	 0.4820
LA	 0.8490	 0.5370
LB	 0.7010	 0.5050
LC	 0.8040	 0.5240
LD	 0.5970	 0.4740
LE	 0.6360	 0.4770
LF	 0.8460	 0.5240
LG	 0.5780	 0.4800
LH	 0.5500	 0.4850
LI	 0.6020	 0.4680
LJ	 0.6030	 0.4740
LL	 0.6880	 0.4880
LM	 0.7090	 0.5060
LN	 0.8800	 0.5400
LO	 0.7520	 0.5180
LP	 0.7960	 0.5200
LQ	 0.8280	 0.5340
LR	 0.7390	 0.4920
LS	 0.7710	 0.5220
LT	 0.7550	 0.5010
LU	 0.4740	 0.4290
LV	 0.7780	 0.5260
LW	 0.7840	 0.5070
LX	 0.6840	 0.4980
LY	 0.7160	 0.5120
LZ	 0.6270	 0.4920
La	 0.8360	 0.5380
Lb	 0.7420	 0.4930
Lc	 0.6660	 0.4830
Ld	 0.6880	 0.4900
Le	 0.8380	 0.5300
Lf	 0.8410	 0.5260



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Chain	Atom inclusion	Q-score
Lg	 0.7550	 0.5050
Lh	 0.6900	 0.4910
Li	 0.6140	 0.4840
Lj	 0.9020	 0.5320
Lk	 0.4440	 0.4500
Ll	 0.8670	 0.5170
Lm	 0.7170	 0.4970
Ln	 0.8300	 0.5180
Lo	 0.7340	 0.5070
Lp	 0.8100	 0.5100
Lr	 0.7520	 0.5210
S2	 0.8040	 0.4070
S6	 0.7970	 0.3570
S7	 0.5660	 0.2480
SA	 0.5220	 0.4670
SB	 0.5310	 0.4640
SC	 0.6500	 0.4690
SD	 0.4620	 0.4030
SE	 0.4940	 0.3820
SF	 0.5420	 0.4400
SG	 0.3070	 0.3360
SH	 0.3330	 0.3900
SI	 0.5840	 0.4140
SJ	 0.5890	 0.4100
SK	 0.2780	 0.3630
SL	 0.6820	 0.4750
SN	 0.6300	 0.4810
SO	 0.6070	 0.4660
SP	 0.4950	 0.4480
SQ	 0.5430	 0.4350
SR	 0.3900	 0.4060
SS	 0.5390	 0.4460
ST	 0.5080	 0.4270
SU	 0.3800	 0.3840
SV	 0.5270	 0.4720
SW	 0.7110	 0.4960
SX	 0.6710	 0.4630
SY	 0.3020	 0.3230
SZ	 0.4050	 0.4260
Sa	 0.6870	 0.4830
Sb	 0.4510	 0.4370
Sc	 0.4180	 0.4230

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Chain	Atom inclusion	Q-score
Sd	 0.6410	 0.4160
Se	 0.4820	 0.3890
Sg	 0.2090	 0.3480
Sx	 0.8650	 0.4210
Z	 0.9490	 0.4250