



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 05:23 PM UTC

PDB ID : 6Y57 / pdb_00006y57
EMDB ID : EMD-10690
Title : Structure of human ribosome in hybrid-PRE state
Authors : Bhaskar, V.; Schenk, A.D.; Cavadini, S.; von Loeffelholz, O.; Natchiar, S.K.; Klaholz, B.P.; Chao, J.A.
Deposited on : 2020-02-25
Resolution : 3.50 Å(reported)
Based on initial models : 6QZP, 5LKS, 3J7R, 5AJ0

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

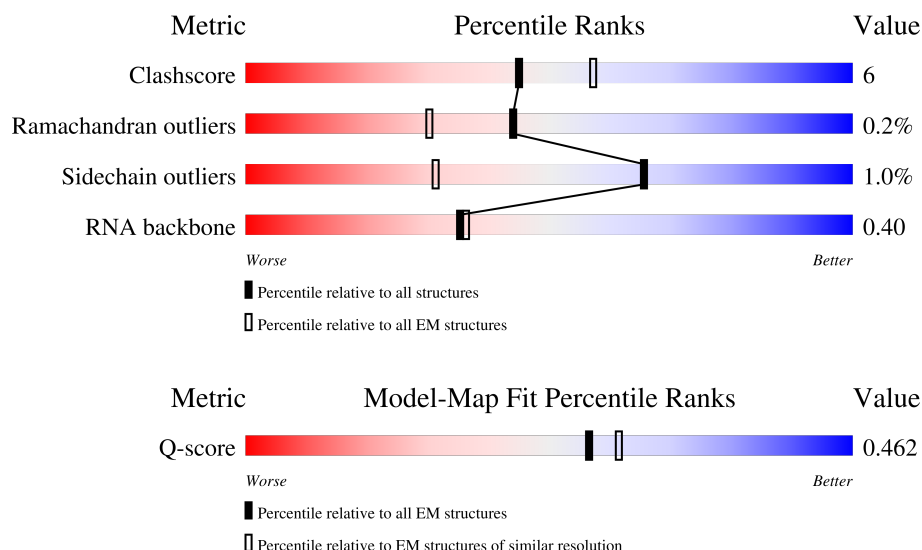
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



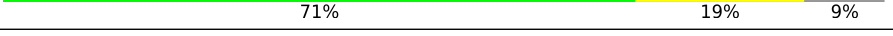
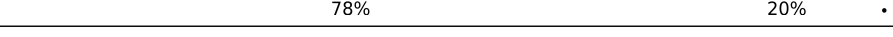
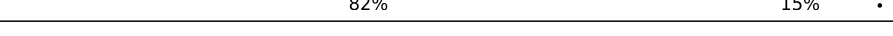
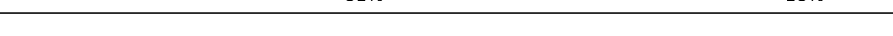
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A4	16	
2	B4	75	
3	D4	76	

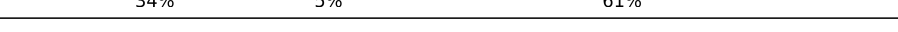
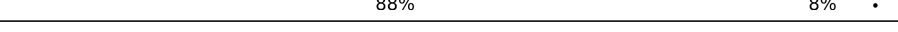
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Mol	Chain	Length	Quality of chain
4	L5	5070	
5	L7	120	
6	L8	156	
7	LA	257	
8	LB	403	
9	LC	427	
10	LD	297	
11	LE	288	
12	LF	248	
13	LG	266	
14	LH	192	
15	LI	214	
16	LJ	178	
17	LL	211	
18	LM	215	
19	LN	204	
20	LO	203	
21	LP	184	
22	LQ	188	
23	LR	196	
24	LS	176	
25	LT	160	
26	LU	128	
27	LV	140	
28	LW	157	

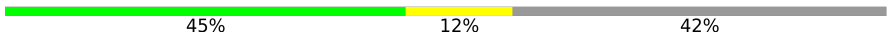
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Mol	Chain	Length	Quality of chain
29	LX	156	
30	LY	145	
31	LZ	136	
32	La	148	
33	Lb	159	
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SC	293	
53	SD	243	

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Mol	Chain	Length	Quality of chain
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	
58	SI	208	
59	SJ	194	
60	SK	165	
61	SL	158	
62	SN	151	
63	SO	151	
64	SP	145	
65	SQ	146	
66	SR	135	
67	SS	152	
68	ST	145	
69	SU	119	
70	SV	83	
71	SW	130	
72	SX	143	
73	SY	133	
74	SZ	125	
75	Sa	115	
76	Sb	84	
77	Sc	69	
78	Sd	56	

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Mol	Chain	Length	Quality of chain
79	Se	59	 78% 8% 14%
80	Sf	132	 5% 57% 41%
81	Sg	317	 64% 24% 11%
82	sh	156	 26% 74%

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 206539 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 mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A4	13	Total	C	N	O	P	0	0
			260	117	26	104	13		

- Molecule 2 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B4	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 3 is a RNA chain called A/P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D4	73	Total	C	N	O	P	0	0
			1559	696	283	508	72		

- Molecule 4 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L5	3574	Total	C	N	O	P	0	0
			76607	34114	14012	24908	3573		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB 86475748

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

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

- Molecule 6 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LA	248	Total	C	N	O	S	0	0
			1886	1183	386	311	6		

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LB	393	Total	C	N	O	S	0	0
			3101	1979	583	525	14		

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	365	Total	C	N	O	S	0	0
			2894	1819	578	482	15		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LD	293	Total	C	N	O	S	0	0
			2287	1455	426	392	14		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	220	Total	C	N	O	S	0	0
			1713	1104	326	279	4		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF	225	Total	C	N	O	S	0	0
			1844	1189	355	291	9		

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	229	Total	C	N	O	S	0	0
			1733	1106	335	288	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LH	189	Total	C	N	O	S	0	0
			1439	910	273	250	6		

- Molecule 15 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	203	Total	C	N	O	S	0	0
			1581	1007	306	254	14		

- Molecule 16 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	167	Total	C	N	O	S	0	0
			1226	780	228	212	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LL	204	Total	C	N	O	S	0	0
			1580	992	335	249	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LM	136	Total	C	N	O	S	0	0
			1097	705	211	174	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LN	203	Total	C	N	O	S	0	0
			1693	1068	359	262	4		

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	201	Total	C	N	O	S	0	0
			1613	1042	318	248	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	153	Total	C	N	O	S	0	0
			1203	754	238	202	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LQ	187	Total	C	N	O	S	0	0
			1493	931	311	246	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	175	Total	C	N	O	S	0	0
			1412	874	312	218	8		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LS	175	Total	C	N	O	S	0	0
			1436	915	281	230	10		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LT	159	Total	C	N	O	S	0	0
			1268	805	249	209	5		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LU	101	Total	C	N	O	S	0	0
			768	497	136	133	2		

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	131	Total	C	N	O	S	0	0
			954	604	180	165	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	115	Total	C	N	O	S	0	0
			784	493	154	135	2		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	120	Total	C	N	O	S	0	0
			950	611	182	156	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LY	134	Total	C	N	O	S	0	0
			1084	681	220	180	3		

- Molecule 31 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LZ	135	Total	C	N	O	S	0	0
			1082	703	207	169	3		

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	La	146	Total	C	N	O	S	0	0
			1145	726	233	183	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lb	63	Total	C	N	O	S	0	0
			499	310	107	80	2		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	93	Total	C	N	O	S	0	0
			716	456	125	129	6		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ld	107	Total	C	N	O	S	0	0
			856	546	168	140	2		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Le	127	Total	C	N	O	S	0	0
			1045	661	215	164	5		

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lf	109	Total	C	N	O	S	0	0
			864	547	173	141	3		

- Molecule 38 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	110	Total	C	N	O	S	0	0
			851	531	175	139	6		

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lh	121	Total	C	N	O	S	0	0
			975	617	200	157	1		

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	101	Total	C	N	O	S	0	0
			797	500	170	122	5		

- Molecule 41 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lj	86	Total	C	N	O	S	0	0
			701	431	154	111	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lk	69	Total	C	N	O	S	0	0
			528	339	99	89	1		

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ll	50	Total	C	N	O	S	0	0
			440	278	97	64	1		

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lm	50	Total	C	N	O	S	0	0
			393	244	82	61	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lo	98	Total	C	N	O	S	0	0
			774	488	159	121	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lp	91	Total	C	N	O	S	0	0
			689	436	132	114	7		

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			982	609	205	164	4		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1658	Total	C	N	O	P	0	0
			35397	15801	6361	11578	1657		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	582	C	U	conflict	GB 36162
S2	583	C	A	conflict	GB 36162
S2	584	G	A	conflict	GB 36162
S2	798	A	G	conflict	GB 36162
S2	1095	U	C	conflict	GB 36162

- Molecule 50 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	212	Total	C	N	O	S	0	0
			1575	1016	285	266	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	214	Total	C	N	O	S	0	0
			1627	1041	296	277	13		

- Molecule 52 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	217	Total	C	N	O	S	0	0
			1590	1039	276	266	9		

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SD	215	Total	C	N	O	S	0	0
			1475	950	267	251	7		

- Molecule 54 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	257	Total	C	N	O	S	0	0
			1891	1218	358	307	8		

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SF	180	Total	C	N	O	S	0	0
			1365	861	261	237	6		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SG	212	Total	C	N	O	S	0	0
			1544	968	312	258	6		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH	176	Total	C	N	O	S	0	0
			1342	871	249	221	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI	187	Total	C	N	O	S	0	0
			1450	910	286	249	5		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ	176	Total	C	N	O	S	0	0
			1407	899	280	226	2		

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK	95	Total	C	N	O	S	0	0
			736	482	131	119	4		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL	140	Total	C	N	O	S	0	0
			1139	725	214	194	6		

- Molecule 62 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SN	150	Total	C	N	O	S	0	0
			1199	766	229	203	1		

- Molecule 63 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SO	135	Total	C	N	O	S	0	0
			1003	615	198	184	6		

- Molecule 64 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SP	127	Total	C	N	O	S	0	0
			1001	636	188	170	7		

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ	141	Total	C	N	O	S	0	0
			1078	690	207	178	3		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR	125	Total	C	N	O	S	0	0
			879	551	166	159	3		

- Molecule 67 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS	138	Total	C	N	O	S	0	0
			1080	684	220	175	1		

- Molecule 68 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST	141	Total	C	N	O	S	0	0
			993	624	195	172	2		

- Molecule 69 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU	100	Total	C	N	O	S	0	0
			749	470	143	134	2		

- Molecule 70 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV	83	Total	C	N	O	S	0	0
			589	369	111	104	5		

- Molecule 71 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW	129	Total	C	N	O	S	0	0
			1027	655	192	174	6		

- Molecule 72 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX	141	Total	C	N	O	S	0	0
			1048	663	206	176	3		

- Molecule 73 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY	113	Total	C	N	O	S	0	0
			855	544	164	143	4		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ	70	Total	C	N	O	S	0	0
			487	311	90	85	1		

- Molecule 75 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sa	99	Total	C	N	O	S	0	0
			762	478	157	122	5		

- Molecule 76 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sb	83	Total	C	N	O	S	0	0
			617	390	114	109	4		

- Molecule 77 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sc	61	Total	C	N	O	S	0	0
			430	267	83	78	2		

- Molecule 78 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sd	52	Total	C	N	O	S	0	0
			420	264	83	69	4		

- Molecule 79 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Se	51	Total	C	N	O	S	0	0
			386	240	83	62	1		

- Molecule 80 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sf	78	Total	C	N	O	S	0	0
			483	307	90	82	4		

- Molecule 81 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sg	283	Total	C	N	O	S	0	0
			1952	1243	341	359	9		

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	sh	41	Total	C	N	O	S	0	0
			269	168	54	44	3		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	A4	1	Total	Mg	0
			1	1	
83	L5	91	Total	Mg	0
			91	91	
83	L7	2	Total	Mg	0
			2	2	
83	L8	5	Total	Mg	0
			5	5	
83	LQ	1	Total	Mg	0
			1	1	
83	LV	1	Total	Mg	0
			1	1	
83	Le	1	Total	Mg	0
			1	1	
83	Lg	1	Total	Mg	0
			1	1	
83	S2	57	Total	Mg	0
			57	57	

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	Lg	1	Total	Zn	0
			1	1	
84	Lj	1	Total	Zn	0
			1	1	
84	Lm	1	Total	Zn	0
			1	1	
84	Lo	1	Total	Zn	0
			1	1	
84	Lp	1	Total	Zn	0
			1	1	
84	Sa	1	Total	Zn	0
			1	1	
84	Sd	1	Total	Zn	0
			1	1	

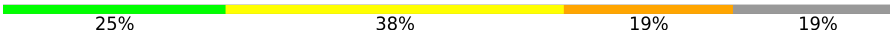
- Molecule 85 is water.

Mol	Chain	Residues	Atoms		AltConf
85	L5	10	Total 10	O 10	0
85	LH	1	Total 1	O 1	0
85	LI	1	Total 1	O 1	0
85	LP	1	Total 1	O 1	0
85	La	1	Total 1	O 1	0
85	S2	3	Total 3	O 3	0
85	SB	1	Total 1	O 1	0
85	SF	1	Total 1	O 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: mRNA

Chain A4: 

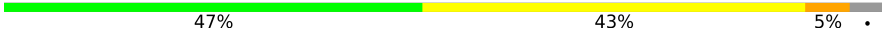


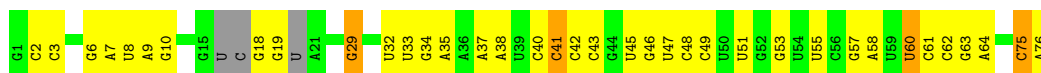
- Molecule 2: P/E tRNA

Chain B4: 



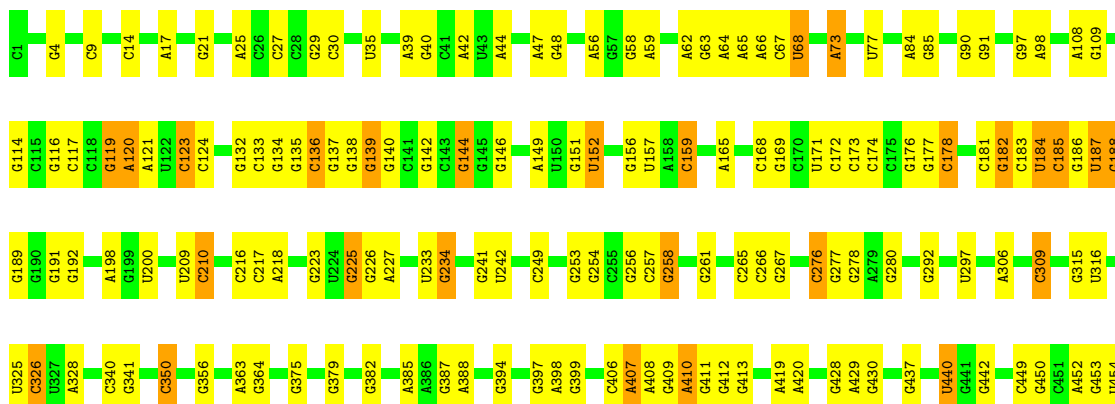
- Molecule 3: A/P tRNA

Chain D4: 



- Molecule 4: 28S ribosomal RNA

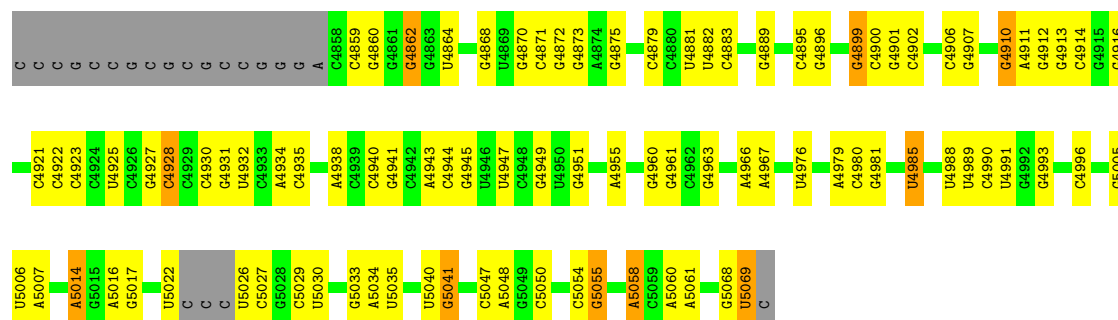
Chain L5: 





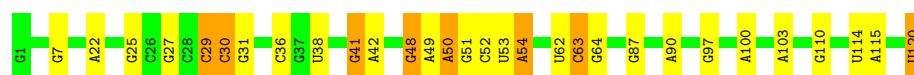






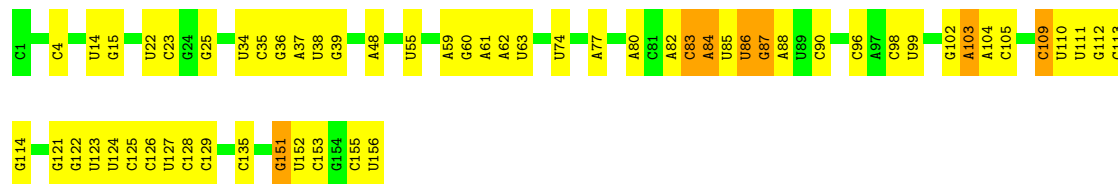
• Molecule 5: 5S ribosomal RNA

Chain L7: 75% 18% 7%



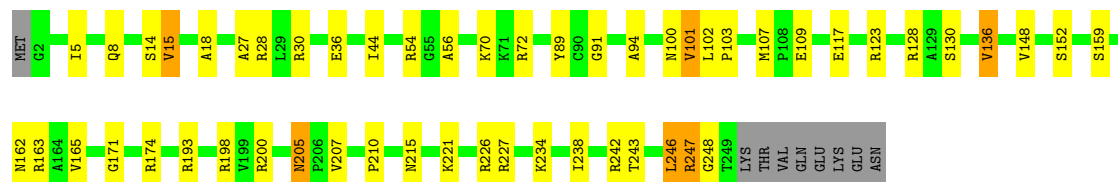
• Molecule 6: 5.8S ribosomal RNA

Chain L8: 63% 33%



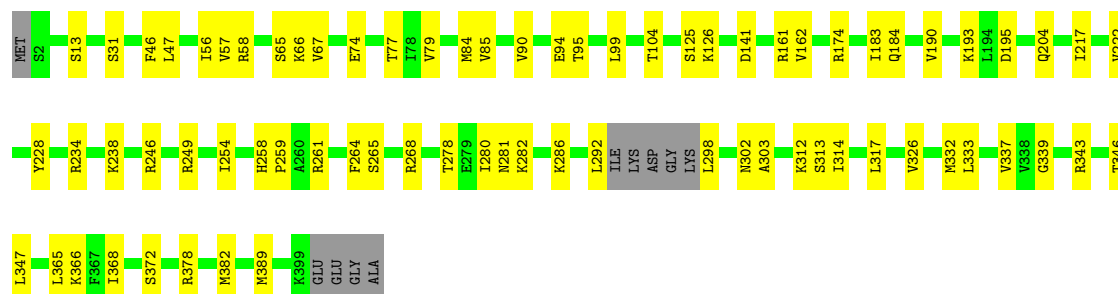
• Molecule 7: 60S ribosomal protein L8

Chain LA: 76% 18%

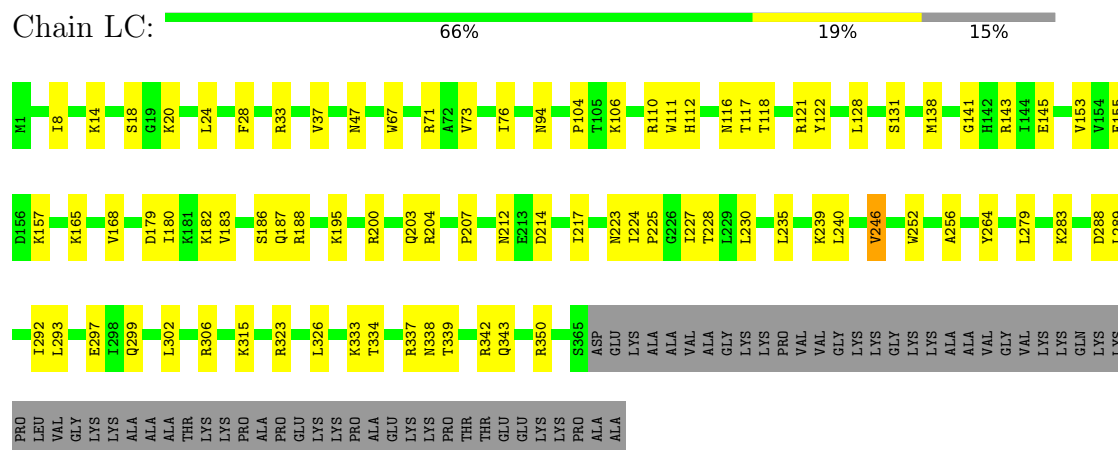


• Molecule 8: 60S ribosomal protein L3

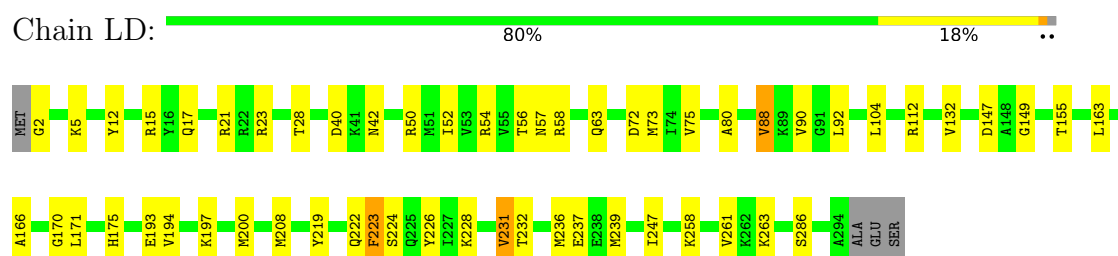
Chain LB: 79% 18%



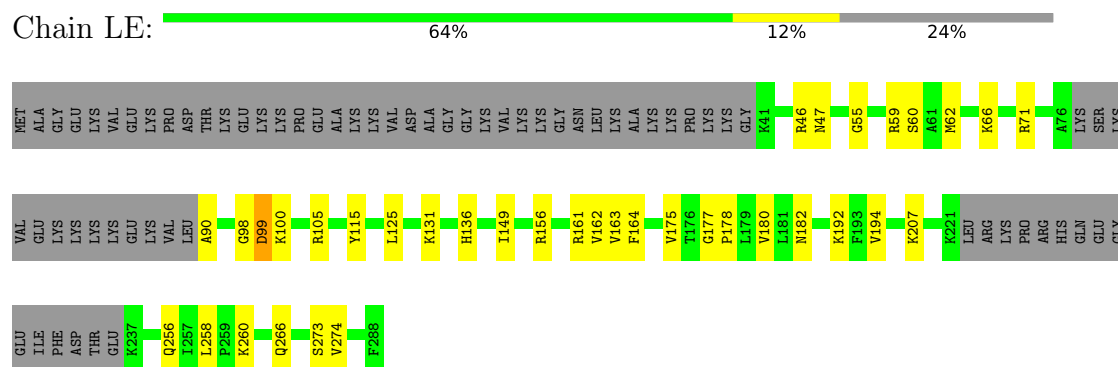
- Molecule 9: 60S ribosomal protein L4



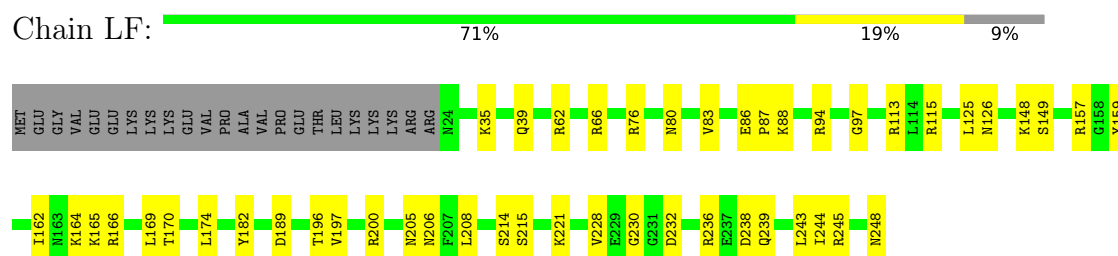
- Molecule 10: 60S ribosomal protein L5



- Molecule 11: 60S ribosomal protein L6

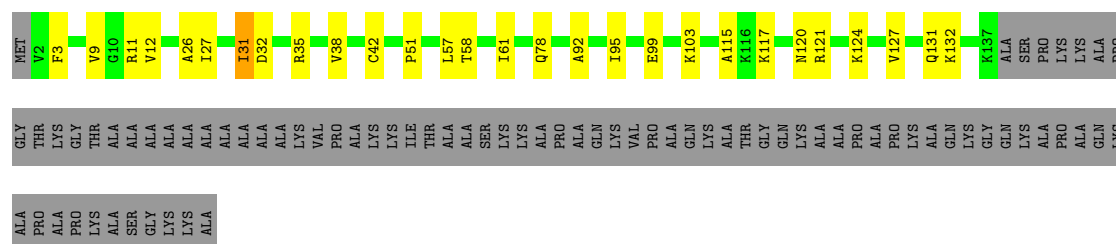


- Molecule 12: 60S ribosomal protein L7



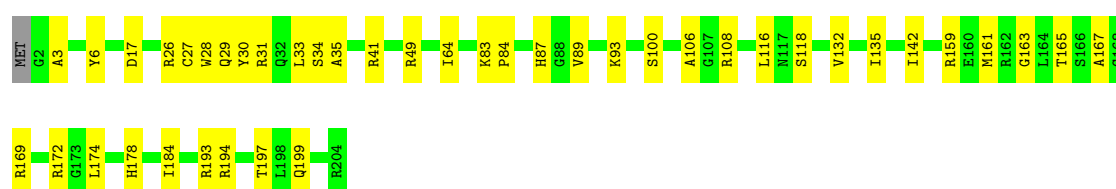
- Molecule 13: 60S ribosomal protein L7a

Chain LM:  50% 13% 37%



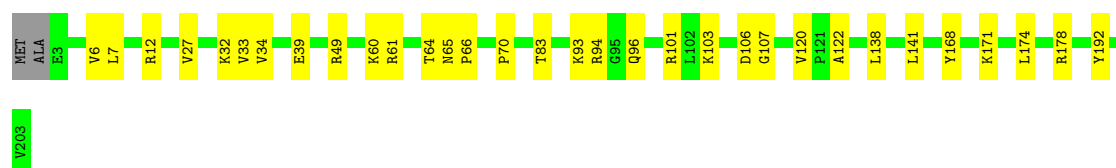
- Molecule 19: 60S ribosomal protein L15

Chain LN:  79% 21%



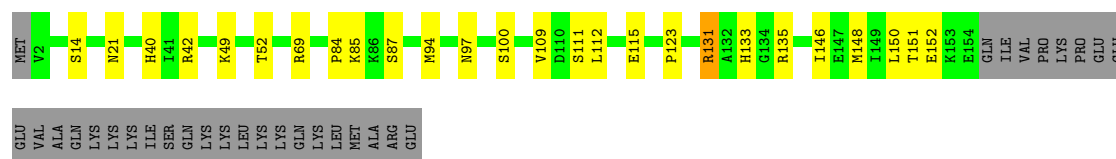
- Molecule 20: 60S ribosomal protein L13a

Chain LO:  83% 16%



- Molecule 21: 60S ribosomal protein L17

Chain LP:  69% 14% 17%



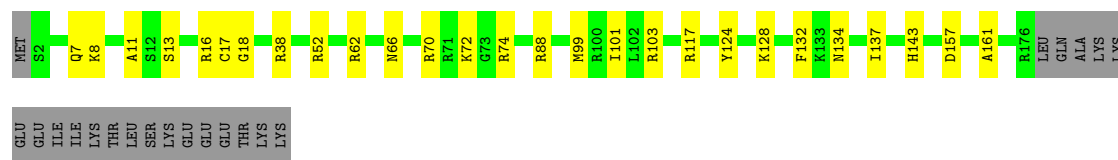
- Molecule 22: 60S ribosomal protein L18

Chain LQ:  81% 18%



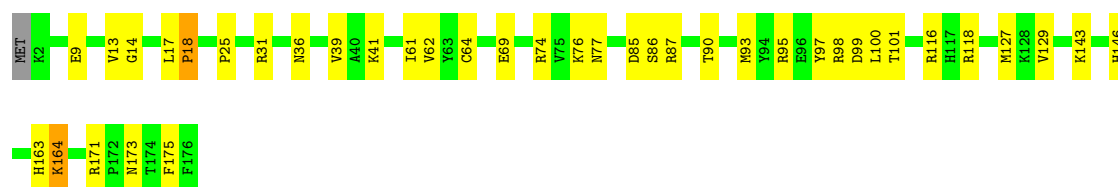
- Molecule 23: 60S ribosomal protein L19

Chain LR:  76% 14% 11%



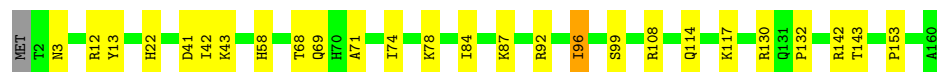
- Molecule 24: 60S ribosomal protein L18a

Chain LS:  77% 21% ..



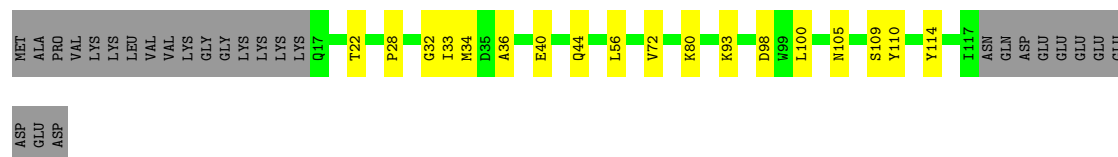
- Molecule 25: 60S ribosomal protein L21

Chain LT:  83% 16% ..



- Molecule 26: 60S ribosomal protein L22

Chain LU:  65% 14% 21%



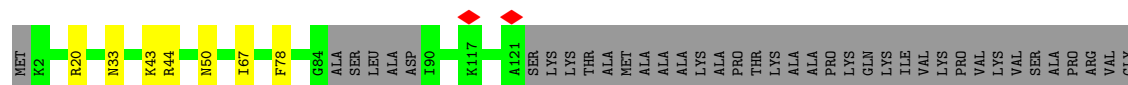
- Molecule 27: 60S ribosomal protein L23

Chain LV:  78% 16% 6%

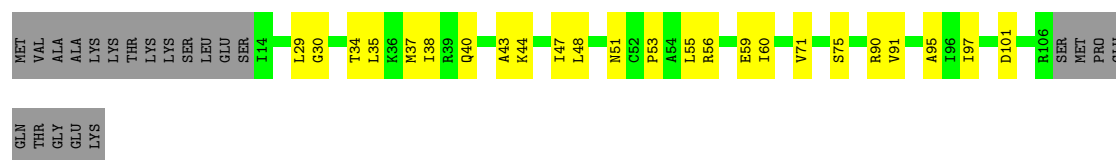


- Molecule 28: 60S ribosomal protein L24

Chain LW:  69% 27%



Chain Lc:  60% 21% 19%



- Molecule 35: 60S ribosomal protein L31

Chain Ld:  72% 14% 14%



- Molecule 36: 60S ribosomal protein L32

Chain Le:  79% 16% 6%



- Molecule 37: 60S ribosomal protein L35a

Chain Lf:  84% 15% .



- Molecule 38: 60S ribosomal protein L34

Chain Lg:  78% 16% 6%



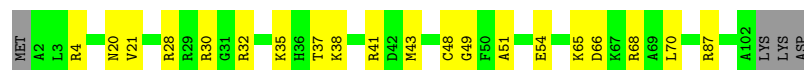
- Molecule 39: 60S ribosomal protein L35

Chain Lh:  85% 12% ..



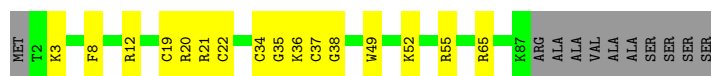
- Molecule 40: 60S ribosomal protein L36

Chain Li:  77% 19% .



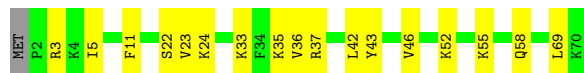
- Molecule 41: 60S ribosomal protein L37

Chain Lj:  72% 16% 11%



- Molecule 42: 60S ribosomal protein L38

Chain Lk:  74% 24% .



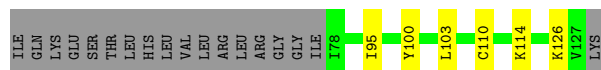
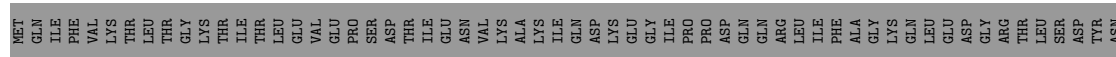
- Molecule 43: 60S ribosomal protein L39

Chain Ll:  67% 31% .



- Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:  34% 5% 61%



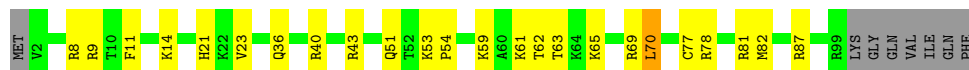
- Molecule 45: 60S ribosomal protein L41

Chain Ln:  88% 8% .



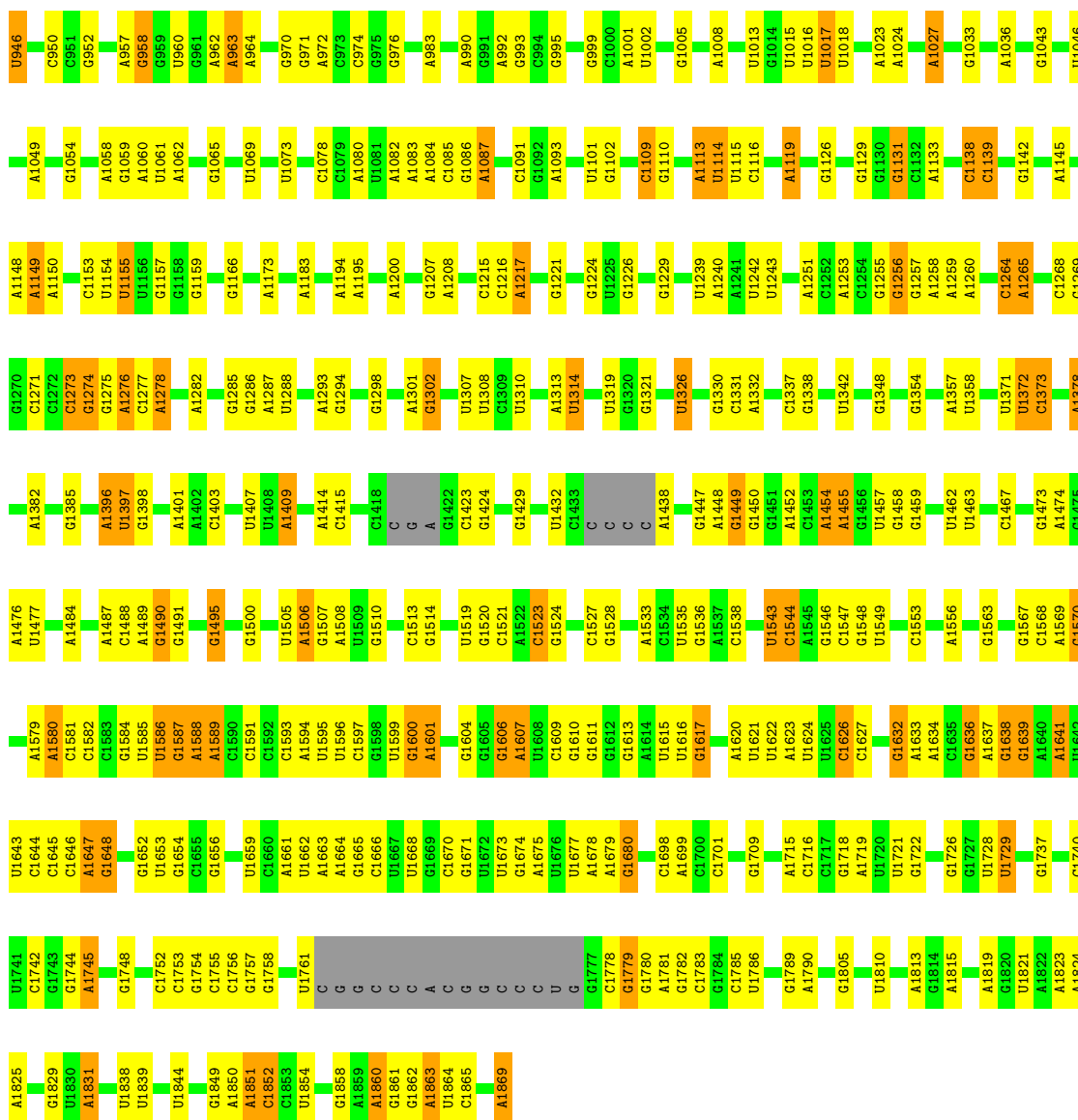
- Molecule 46: 60S ribosomal protein L36a

Chain Lo:  70% 22% 8%



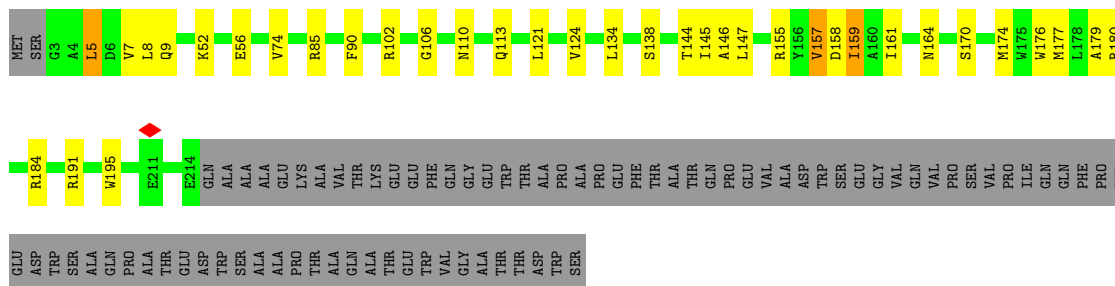
- Molecule 47: 60S ribosomal protein L37a

Chain Lp:  76% 22% ..



- Molecule 50: 40S ribosomal protein SA

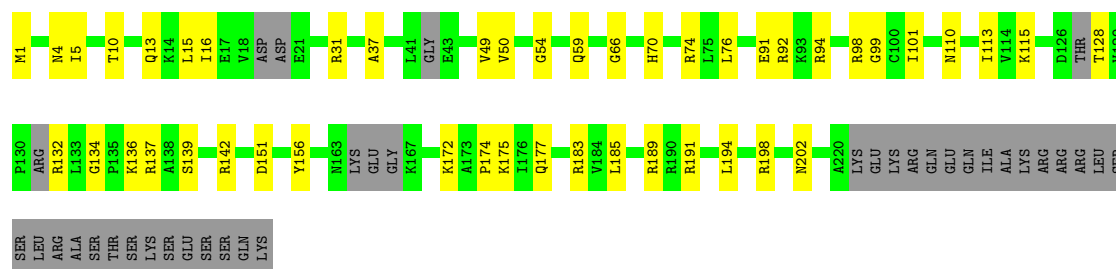
Chain SA: 60% 11% 28%



- Molecule 51: 40S ribosomal protein S3a

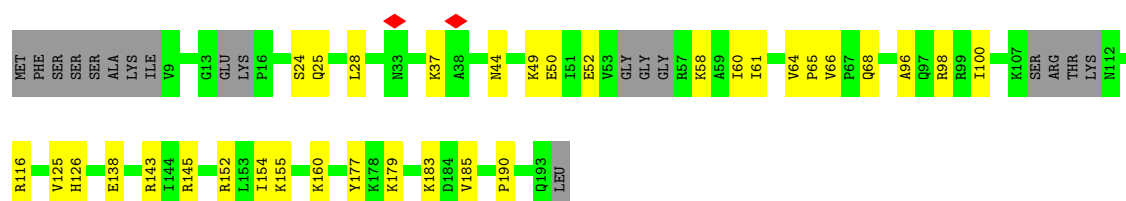
Chain SB: 63% 18% 19%

Chain SG:  67% 18% 15%



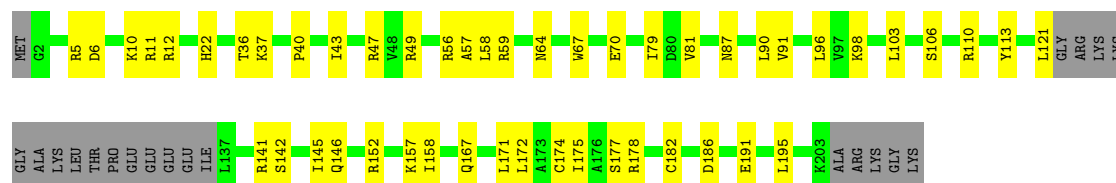
- Molecule 57: 40S ribosomal protein S7

Chain SH:  74% 17% 9%



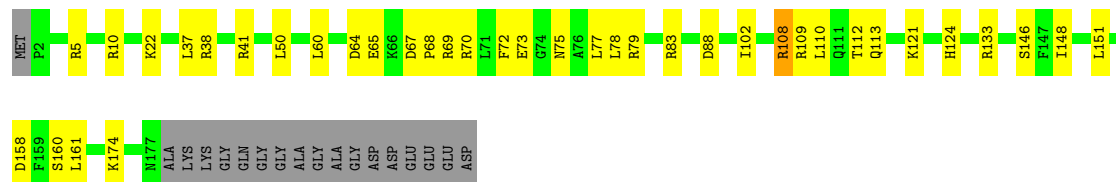
- Molecule 58: 40S ribosomal protein S8

Chain SI:  66% 24% 10%

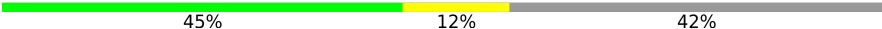


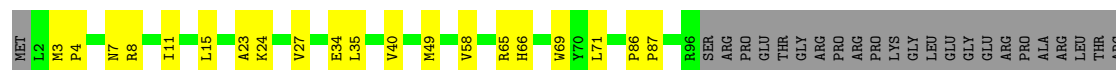
- Molecule 59: 40S ribosomal protein S9

Chain SJ:  71% 19% 9%



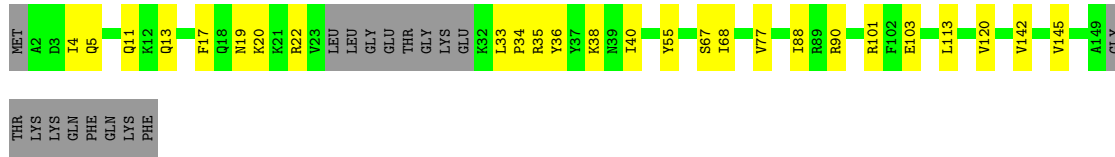
- Molecule 60: 40S ribosomal protein S10

Chain SK:  45% 12% 42%

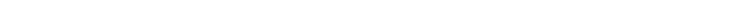


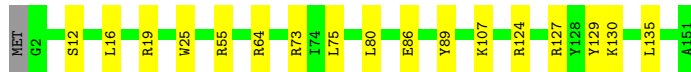
- Molecule 61: 40S ribosomal protein S11

Chain SL:

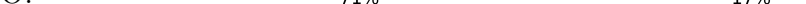


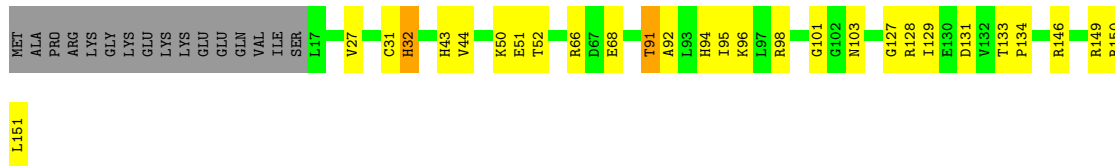
- Molecule 62: 40S ribosomal protein S13

Chain SN:  88% 11%

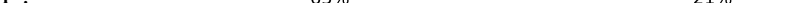


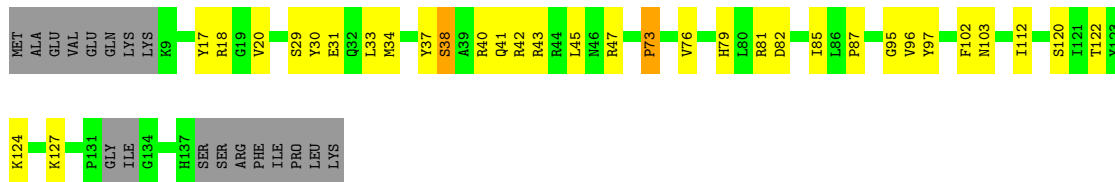
- Molecule 63: 40S ribosomal protein S14

Chain SO:  71% 17% • 11%

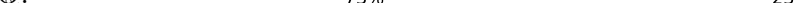


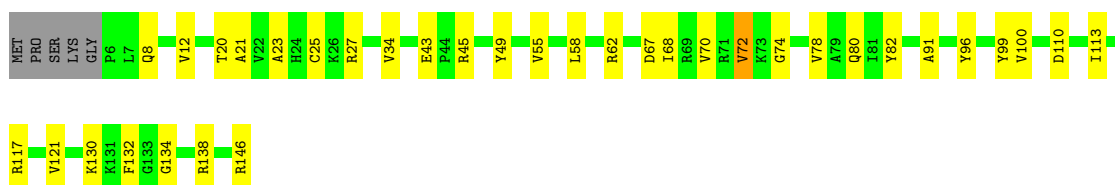
- Molecule 64: 40S ribosomal protein S15

Chain SP: 



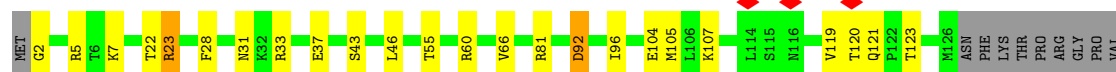
- Molecule 65: 40S ribosomal protein S16

Chain SQ:  73% 23% ..



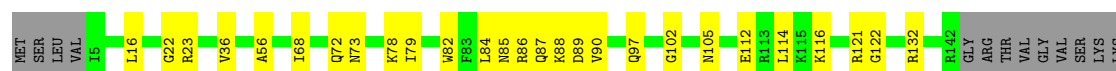
- Molecule 66: 40S ribosomal protein S17

Chain SR:  75% 16% 7%



- Molecule 67: 40S ribosomal protein S18

Chain SS:  73% 18% 9%



LYS

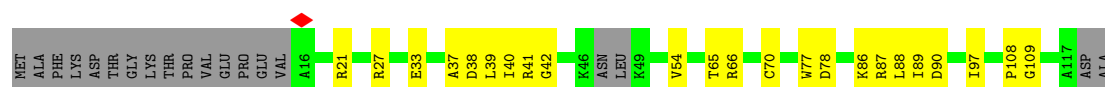
- Molecule 68: 40S ribosomal protein S19

Chain ST:  82% 15% 3%



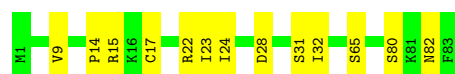
- Molecule 69: 40S ribosomal protein S20

Chain SU:  65% 19% 16%



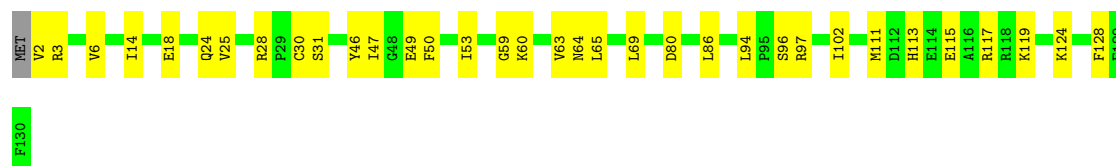
- Molecule 70: 40S ribosomal protein S21

Chain SV:  84% 16%



- Molecule 71: 40S ribosomal protein S15a

Chain SW:  73% 26% 1%



- Molecule 72: 40S ribosomal protein S23

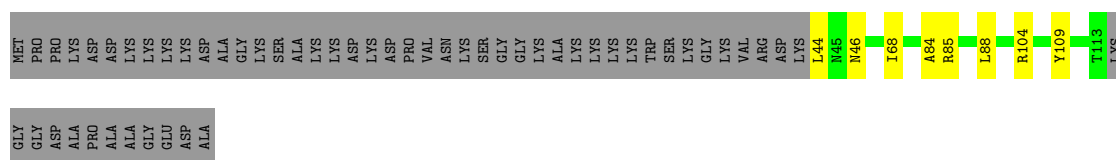
Chain SX:  79% 18% 3%



- Molecule 73: 40S ribosomal protein S24



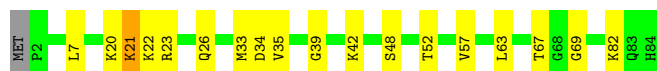
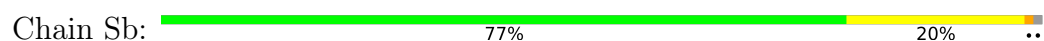
- Molecule 74: 40S ribosomal protein S25



- Molecule 75: 40S ribosomal protein S26



- Molecule 76: 40S ribosomal protein S27



- Molecule 77: 40S ribosomal protein S28

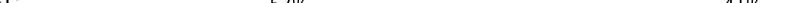


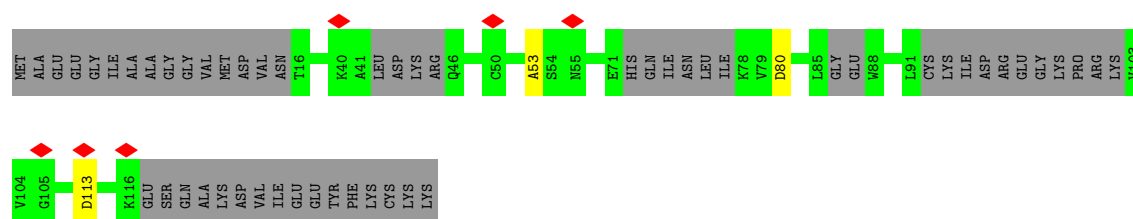
- Molecule 78: 40S ribosomal protein S29

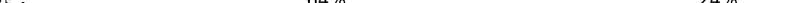


- Molecule 79: 40S ribosomal protein S30

LYS	VAL	H76	K94	K99	R107	R108	M109	Q110	P120	THR	PHE	GLY	LYS	LYS	K126	N131	SER
-----	-----	-----	-----	-----	------	------	------	------	------	-----	-----	-----	-----	-----	------	------	-----

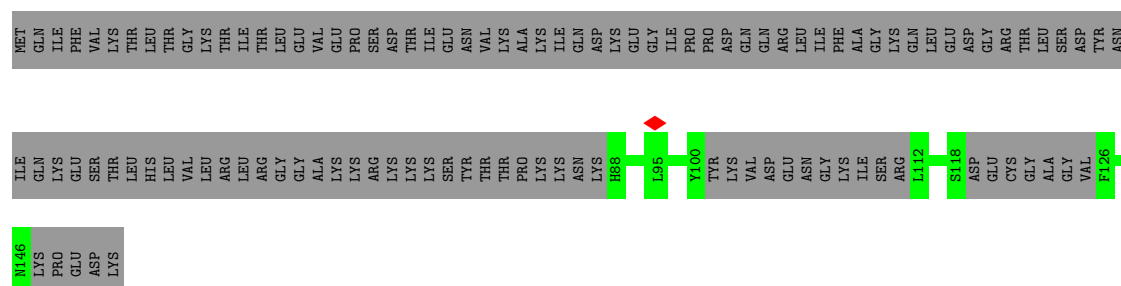
- Chain Sf: 



- Chain Sg: 



- Chain sh: 26% 74%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12694	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.098	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.009	Depositor
Map size (Å)	473.0, 473.0, 473.0	wwPDB
Map dimensions	550, 550, 550	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	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	A4	0.31	0/285	0.70	0/438
2	B4	0.22	0/1795	0.33	0/2798
3	D4	0.21	0/1741	0.46	0/2709
4	L5	0.34	0/85684	0.37	4/133644 (0.0%)
5	L7	0.33	0/2858	0.31	0/4455
6	L8	0.35	0/3701	0.38	0/5766
7	LA	0.40	0/1924	0.67	0/2581
8	LB	0.36	0/3168	0.57	0/4253
9	LC	0.37	0/2948	0.59	2/3960 (0.1%)
10	LD	0.33	0/2333	0.60	0/3139
11	LE	0.35	0/1747	0.66	2/2354 (0.1%)
12	LF	0.38	0/1879	0.66	2/2507 (0.1%)
13	LG	0.36	1/1765 (0.1%)	0.68	1/2400 (0.0%)
14	LH	0.33	0/1458	0.61	0/1973
15	LI	0.32	0/1619	0.56	0/2170
16	LJ	0.29	0/1249	0.59	0/1690
17	LL	0.35	0/1611	0.60	0/2167
18	LM	0.33	0/1119	0.58	0/1501
19	LN	0.42	0/1738	0.58	0/2328
20	LO	0.37	0/1645	0.54	0/2205
21	LP	0.37	0/1229	0.51	0/1655
22	LQ	0.38	0/1517	0.57	0/2030
23	LR	0.33	0/1428	0.54	0/1897
24	LS	0.35	0/1476	0.59	2/1983 (0.1%)
25	LT	0.35	0/1296	0.53	0/1734
26	LU	0.30	0/782	0.65	0/1057
27	LV	0.34	0/968	0.54	0/1303
28	LW	0.30	0/798	0.60	2/1081 (0.2%)
29	LX	0.34	0/967	0.60	0/1304
30	LY	0.34	0/1101	0.55	0/1469
31	LZ	0.31	0/1105	0.47	0/1475
32	La	0.37	0/1173	0.52	0/1568

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lb	0.31	0/509	0.48	0/675
34	Lc	0.34	0/726	0.56	0/977
35	Ld	0.33	0/871	0.56	0/1176
36	Le	0.35	0/1063	0.54	0/1418
37	Lf	0.39	0/883	0.67	0/1185
38	Lg	0.35	0/861	0.61	2/1153 (0.2%)
39	Lh	0.31	0/983	0.51	0/1304
40	Li	0.30	0/808	0.54	0/1074
41	Lj	0.37	0/716	0.56	0/948
42	Lk	0.34	0/534	0.62	0/712
43	Ll	0.36	0/450	0.51	0/595
44	Lm	0.31	0/399	0.51	0/532
45	Ln	0.31	0/231	0.55	0/294
46	Lo	0.35	0/787	0.54	0/1042
47	Lp	0.35	0/699	0.54	0/931
48	Lr	0.37	0/997	0.58	0/1341
49	S2	0.29	0/39578	0.38	0/61671
50	SA	0.32	0/1612	0.63	0/2203
51	SB	0.29	0/1654	0.55	0/2227
52	SC	0.31	0/1626	0.58	0/2211
53	SD	0.28	0/1499	0.62	0/2041
54	SE	0.29	0/1933	0.63	2/2623 (0.1%)
55	SF	0.28	0/1385	0.59	0/1870
56	SG	0.25	0/1562	0.63	0/2099
57	SH	0.31	0/1362	0.67	2/1831 (0.1%)
58	SI	0.27	0/1477	0.57	0/1990
59	SJ	0.28	0/1432	0.63	0/1926
60	SK	0.26	0/759	0.62	0/1036
61	SL	0.31	0/1159	0.58	1/1555 (0.1%)
62	SN	0.30	0/1223	0.65	0/1644
63	SO	0.31	0/1016	0.67	3/1363 (0.2%)
64	SP	0.31	0/1020	0.67	0/1369
65	SQ	0.30	0/1096	0.68	0/1473
66	SR	0.33	0/890	0.77	2/1207 (0.2%)
67	SS	0.32	0/1098	0.71	0/1480
68	ST	0.29	0/1012	0.61	0/1371
69	SU	0.28	0/758	0.64	0/1023
70	SV	0.28	0/596	0.52	0/800
71	SW	0.35	0/1044	0.59	0/1398
72	SX	0.32	0/1066	0.76	0/1434
73	SY	0.24	0/871	0.58	0/1169
74	SZ	0.33	0/493	0.84	0/672
75	Sa	0.32	0/775	0.54	0/1042

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sb	0.30	0/631	0.73	0/853
77	Sc	0.29	0/432	0.77	0/582
78	Sd	0.29	0/430	0.59	0/573
79	Se	0.24	0/390	0.52	0/515
80	Sf	0.25	0/485	0.70	2/661 (0.3%)
81	Sg	0.29	0/1993	0.75	3/2730 (0.1%)
82	sh	0.21	0/270	0.67	0/359
All	All	0.33	1/222251 (0.0%)	0.47	32/327952 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	LA	0	1
10	LD	0	1
11	LE	0	2
16	LJ	0	1
17	LL	0	1
18	LM	0	1
21	LP	0	1
24	LS	0	2
27	LV	0	1
29	LX	0	1
64	SP	0	2
65	SQ	0	1
66	SR	0	5
72	SX	0	2
76	Sb	0	1
77	Sc	0	1
81	Sg	0	2
All	All	0	26

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	LG	77	PRO	CA-C	-5.06	1.48	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	SL	4	ILE	N-CA-C	-8.43	105.70	113.71
12	LF	162	ILE	CA-C-N	6.69	134.32	121.54
12	LF	162	ILE	C-N-CA	6.69	134.32	121.54
28	LW	67	ILE	CA-C-N	6.46	129.25	120.54
28	LW	67	ILE	C-N-CA	6.46	129.25	120.54
4	L5	2117	G	P-O3'-C3'	6.31	129.66	120.20
54	SE	195	ILE	CA-C-N	5.79	132.61	121.54
54	SE	195	ILE	C-N-CA	5.79	132.61	121.54
11	LE	99	ASP	CA-C-N	5.75	132.52	121.54
11	LE	99	ASP	C-N-CA	5.75	132.52	121.54
80	Sf	113	ASP	CA-C-N	5.73	128.75	120.79
80	Sf	113	ASP	C-N-CA	5.73	128.75	120.79
9	LC	76	ILE	N-CA-C	-5.70	104.52	109.19
66	SR	92	ASP	CA-C-N	5.58	130.06	121.19
66	SR	92	ASP	C-N-CA	5.58	130.06	121.19
4	L5	2117	G	C2'-C3'-O3'	5.46	117.68	109.50
81	Sg	109	LEU	CA-CB-CG	5.44	135.33	116.30
24	LS	163	HIS	CA-C-N	5.38	134.93	121.80
24	LS	163	HIS	C-N-CA	5.38	134.93	121.80
57	SH	37	LYS	CA-C-N	5.36	131.78	121.54
57	SH	37	LYS	C-N-CA	5.36	131.78	121.54
13	LG	165	GLU	N-CA-C	-5.33	100.72	108.07
81	Sg	17	TRP	CA-C-N	5.28	131.20	121.70
81	Sg	17	TRP	C-N-CA	5.28	131.20	121.70
38	Lg	51	GLY	CA-C-N	5.25	131.56	121.54
38	Lg	51	GLY	C-N-CA	5.25	131.56	121.54
63	SO	92	ALA	N-CA-C	5.19	117.62	110.35
4	L5	914	U	P-O3'-C3'	5.16	127.95	120.20
9	LC	76	ILE	CB-CA-C	5.12	114.35	109.33
4	L5	2760	G	P-O3'-C3'	5.04	127.75	120.20
63	SO	91	THR	CA-C-N	5.03	128.81	121.31
63	SO	91	THR	C-N-CA	5.03	128.81	121.31

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	LA	247	ARG	Peptide
10	LD	231	VAL	Peptide
11	LE	98	GLY	Peptide
11	LE	99	ASP	Peptide
16	LJ	122	SER	Peptide
17	LL	47	ALA	Peptide

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Mol	Chain	Res	Type	Group
18	LM	31	ILE	Peptide
21	LP	131	ARG	Peptide
24	LS	164	LYS	Peptide
24	LS	17	LEU	Peptide
27	LV	109	LYS	Peptide
29	LX	39	LYS	Peptide
64	SP	37	TYR	Peptide
64	SP	73	PRO	Peptide
65	SQ	43	GLU	Peptide
66	SR	121	GLN	Peptide
66	SR	22	THR	Peptide
66	SR	23	ARG	Mainchain
66	SR	92	ASP	Peptide
66	SR	96	ILE	Peptide
72	SX	105	PHE	Peptide
72	SX	107	ARG	Peptide
76	Sb	21	LYS	Peptide
77	Sc	59	LEU	Peptide
81	Sg	109	LEU	Peptide
81	Sg	310	TRP	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A4	260	0	131	2	0
2	B4	1604	0	816	17	0
3	D4	1559	0	793	6	0
4	L5	76607	0	38728	451	0
5	L7	2558	0	1296	15	0
6	L8	3314	0	1683	25	0
7	LA	1886	0	1973	38	0
8	LB	3101	0	3177	50	0
9	LC	2894	0	3061	62	0
10	LD	2287	0	2254	38	0
11	LE	1713	0	1812	29	0
12	LF	1844	0	1961	32	0
13	LG	1733	0	1750	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	LH	1439	0	1469	23	0
15	LI	1581	0	1574	20	0
16	LJ	1226	0	1168	19	0
17	LL	1580	0	1646	23	0
18	LM	1097	0	1142	17	0
19	LN	1693	0	1741	31	0
20	LO	1613	0	1737	26	0
21	LP	1203	0	1210	17	0
22	LQ	1493	0	1587	24	0
23	LR	1412	0	1515	20	0
24	LS	1436	0	1457	29	0
25	LT	1268	0	1309	21	0
26	LU	768	0	762	9	0
27	LV	954	0	994	15	0
28	LW	784	0	662	6	0
29	LX	950	0	1010	15	0
30	LY	1084	0	1143	28	0
31	LZ	1082	0	1152	23	0
32	La	1145	0	1178	13	0
33	Lb	499	0	506	3	0
34	Lc	716	0	742	16	0
35	Ld	856	0	890	11	0
36	Le	1045	0	1133	14	0
37	Lf	864	0	888	14	0
38	Lg	851	0	909	14	0
39	Lh	975	0	1081	13	0
40	Li	797	0	859	17	0
41	Lj	701	0	726	13	0
42	Lk	528	0	554	12	0
43	Ll	440	0	472	12	0
44	Lm	393	0	410	4	0
45	Ln	230	0	276	2	0
46	Lo	774	0	819	16	0
47	Lp	689	0	731	15	0
48	Lr	982	0	1026	22	0
49	S2	35397	0	17881	296	0
50	SA	1575	0	1533	25	0
51	SB	1627	0	1616	33	0
52	SC	1590	0	1606	13	0
53	SD	1475	0	1389	15	0
54	SE	1891	0	1867	34	0
55	SF	1365	0	1367	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	SG	1544	0	1503	35	0
57	SH	1342	0	1382	19	0
58	SI	1450	0	1421	37	0
59	SJ	1407	0	1450	28	0
60	SK	736	0	691	12	0
61	SL	1139	0	1185	19	0
62	SN	1199	0	1274	16	0
63	SO	1003	0	1028	21	0
64	SP	1001	0	1011	30	0
65	SQ	1078	0	1124	24	0
66	SR	879	0	816	14	0
67	SS	1080	0	1092	18	0
68	ST	993	0	928	15	0
69	SU	749	0	762	16	0
70	SV	589	0	566	8	0
71	SW	1027	0	1067	25	0
72	SX	1048	0	1065	19	0
73	SY	855	0	831	13	0
74	SZ	487	0	453	8	0
75	Sa	762	0	800	18	0
76	Sb	617	0	602	11	0
77	Sc	430	0	425	7	0
78	Sd	420	0	400	11	0
79	Se	386	0	411	5	0
80	Sf	483	0	399	1	0
81	Sg	1952	0	1657	51	0
82	sh	269	0	221	0	0
83	A4	1	0	0	0	0
83	L5	91	0	0	0	0
83	L7	2	0	0	0	0
83	L8	5	0	0	0	0
83	LQ	1	0	0	0	0
83	LV	1	0	0	0	0
83	Le	1	0	0	0	0
83	Lg	1	0	0	0	0
83	S2	57	0	0	0	0
84	Lg	1	0	0	0	0
84	Lj	1	0	0	0	0
84	Lm	1	0	0	0	0
84	Lo	1	0	0	0	0
84	Lp	1	0	0	0	0
84	Sa	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	Sd	1	0	0	0	0
85	L5	10	0	0	0	0
85	LH	1	0	0	0	0
85	LI	1	0	0	0	0
85	LP	1	0	0	0	0
85	La	1	0	0	0	0
85	S2	3	0	0	0	0
85	SB	1	0	0	0	0
85	SF	1	0	0	0	0
All	All	206539	0	147736	1832	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (1832) 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)
49:S2:1091:C:HO2'	71:SW:2:VAL:N	1.57	1.02
49:S2:1033:G:H1	49:S2:1080:A:HO2'	1.18	0.90
64:SP:79:HIS:HB3	64:SP:97:TYR:HB3	1.64	0.78
40:Li:66:ASP:HB2	40:Li:87:ARG:HH22	1.48	0.77
81:Sg:109:LEU:HD23	81:Sg:125:ARG:HE	1.50	0.76
56:SG:10:THR:HG1	56:SG:128:THR:N	1.84	0.75
54:SE:127:ARG:HH11	54:SE:142:HIS:HB3	1.52	0.73
51:SB:52:THR:HG22	51:SB:58:ALA:H	1.53	0.72
4:L5:468:U:N3	4:L5:686:A:N1	2.38	0.72
4:L5:489:C:H42	4:L5:664:G:H1	1.38	0.72
49:S2:1278:A:H61	49:S2:1319:U:H3	1.35	0.71
49:S2:1656:G:H1	49:S2:1668:U:H3	1.39	0.69
4:L5:759:G:H22	4:L5:904:C:H2'	1.57	0.69
4:L5:2901:G:H1	4:L5:3598:C:H42	1.41	0.68
49:S2:154:U:H3	49:S2:164:A:H61	1.39	0.68
60:SK:15:LEU:HD22	60:SK:49:MET:HE1	1.75	0.67
56:SG:5:ILE:HD11	56:SG:16:ILE:HG12	1.77	0.67
4:L5:2429:A:H5''	43:Ll:43:HIS:HE2	1.59	0.67
8:LB:47:LEU:H	8:LB:84:MET:HE1	1.59	0.67
73:SY:18:LEU:HD23	73:SY:85:ASN:HB3	1.77	0.67
4:L5:178:C:H42	4:L5:258:G:H1	1.44	0.66
4:L5:2481:G:H1	4:L5:2497:C:H42	1.41	0.66
57:SH:66:VAL:HG22	57:SH:96:ALA:HB1	1.77	0.66
10:LD:200:MET:HB3	10:LD:237:GLU:HG3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1679:A:H2'	55:SF:60:ARG:HD2	1.78	0.66
4:L5:3898:G:H5'	8:LB:254:ILE:HG13	1.78	0.65
66:SR:104:GLU:HA	66:SR:107:LYS:HD3	1.78	0.65
49:S2:1544:C:N4	49:S2:1588:A:O2'	2.28	0.65
67:SS:85:ASN:H	67:SS:97:GLN:HG3	1.62	0.65
31:LZ:89:ILE:HG12	31:LZ:121:ARG:HD3	1.79	0.65
51:SB:176:VAL:HG23	51:SB:184:VAL:HG21	1.78	0.65
6:L8:96:C:H5''	39:Lh:66:LYS:HD3	1.79	0.65
61:SL:101:ARG:HB2	72:SX:10:ALA:HB2	1.78	0.65
4:L5:500:G:O6	4:L5:654:C:N4	2.30	0.64
15:LI:61:SER:HA	15:LI:126:VAL:HG12	1.79	0.64
61:SL:35:ARG:NH1	61:SL:55:TYR:O	2.29	0.64
13:LG:162:ASP:OD2	19:LN:41:ARG:NH2	2.30	0.64
49:S2:1546:G:N2	49:S2:1670:C:O2	2.29	0.64
40:Li:70:LEU:HB2	40:Li:87:ARG:HH11	1.62	0.64
44:Lm:103:LEU:HD21	44:Lm:110:CYS:HA	1.78	0.64
49:S2:928:G:H1	49:S2:1013:U:H3	1.45	0.64
59:SJ:69:ARG:HA	59:SJ:72:PHE:HB3	1.78	0.64
4:L5:3594:C:O2	4:L5:3597:G:N2	2.31	0.64
4:L5:1445:U:H3	4:L5:2100:A:H61	1.46	0.64
49:S2:1568:C:H5''	68:ST:96:SER:HB2	1.80	0.64
57:SH:25:GLN:HA	57:SH:28:LEU:HB2	1.79	0.64
49:S2:94:G:HO2'	49:S2:508:A:HO2'	1.44	0.63
49:S2:1139:C:H41	49:S2:1149:A:H62	1.44	0.63
5:L7:7:G:N7	10:LD:21:ARG:NH2	2.45	0.63
7:LA:234:LYS:HG2	7:LA:238:ILE:HD12	1.79	0.63
11:LE:177:GLY:HA3	11:LE:182:ASN:HD22	1.64	0.63
49:S2:1113:A:N6	49:S2:1119:A:N7	2.46	0.63
61:SL:103:GLU:HB3	72:SX:10:ALA:HB3	1.80	0.63
4:L5:1739:G:N3	4:L5:1742:A:N6	2.47	0.63
49:S2:65:C:N4	56:SG:134:GLY:O	2.32	0.63
4:L5:123:C:H42	4:L5:146:G:H1	1.45	0.63
54:SE:79:ASP:HB3	54:SE:82:TYR:HB2	1.79	0.63
9:LC:230:LEU:HD21	9:LC:235:LEU:HA	1.81	0.62
14:LH:89:ARG:HE	14:LH:187:VAL:HG22	1.63	0.62
49:S2:1109:C:N3	66:SR:123:THR:OG1	2.30	0.62
60:SK:7:ASN:HD22	60:SK:40:VAL:HG12	1.63	0.62
67:SS:114:LEU:HD13	67:SS:122:GLY:HA2	1.79	0.62
4:L5:1400:G:H1	4:L5:1417:C:H42	1.45	0.62
4:L5:2102:G:N2	4:L5:2103:G:O6	2.32	0.62
81:Sg:230:LEU:HB3	81:Sg:259:TRP:HH2	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1091:C:O2'	71:SW:2:VAL:N	2.31	0.62
6:L8:74:U:O4	30:LY:72:GLN:NE2	2.33	0.62
16:LJ:90:ARG:NH2	16:LJ:108:GLY:O	2.32	0.62
49:S2:1740:C:H5''	58:SI:58:LEU:HD21	1.80	0.62
4:L5:1524:A:H61	4:L5:1651:G:H22	1.48	0.62
5:L7:30:C:O2	5:L7:48:G:N2	2.30	0.62
29:LX:81:LEU:HD11	29:LX:99:ILE:HG23	1.80	0.62
40:Li:66:ASP:O	40:Li:87:ARG:NH1	2.32	0.62
4:L5:4313:A:OP1	25:LT:92:ARG:NH2	2.33	0.61
49:S2:1396:A:O2'	49:S2:1398:G:N7	2.33	0.61
22:LQ:39:THR:HG23	22:LQ:41:SER:H	1.65	0.61
65:SQ:110:ASP:HA	65:SQ:113:ILE:HD12	1.83	0.61
4:L5:4076:G:OP1	13:LG:73:ARG:NH1	2.34	0.61
27:LV:88:TYR:OH	27:LV:90:ARG:NH2	2.33	0.61
4:L5:4980:C:N3	21:LP:69:ARG:NH2	2.48	0.61
14:LH:46:SER:HB2	14:LH:56:ARG:HB3	1.83	0.61
15:LI:80:CYS:SG	15:LI:144:ASN:ND2	2.74	0.61
49:S2:54:A:OP1	73:SY:111:LYS:NZ	2.34	0.61
4:L5:2643:G:O2'	42:Lk:3:ARG:NH2	2.32	0.61
30:LY:112:ASP:H	30:LY:115:ARG:HB3	1.66	0.61
14:LH:132:VAL:HG12	14:LH:154:VAL:HG12	1.81	0.61
49:S2:43:U:OP2	49:S2:485:A:N6	2.34	0.61
4:L5:1353:G:N7	22:LQ:104:ARG:NH1	2.48	0.61
4:L5:2578:G:N7	31:LZ:17:ARG:NH1	2.48	0.61
49:S2:830:A:OP2	49:S2:846:G:N2	2.32	0.60
4:L5:375:G:OP2	41:Lj:52:LYS:NZ	2.33	0.60
34:Lc:38:ILE:HD13	34:Lc:43:ALA:HB3	1.84	0.60
4:L5:152:U:OP1	19:LN:49:ARG:NH1	2.33	0.60
4:L5:989:U:O2'	4:L5:1065:G:N2	2.35	0.60
4:L5:1932:A:OP1	20:LO:49:ARG:NH2	2.34	0.60
4:L5:3709:U:O2	4:L5:3711:A:N6	2.34	0.60
6:L8:122:G:H1	6:L8:128:C:H42	1.48	0.60
10:LD:56:THR:HG23	10:LD:58:ARG:H	1.65	0.60
13:LG:199:CYS:SG	13:LG:200:THR:N	2.75	0.60
49:S2:312:G:OP2	56:SG:191:ARG:NH2	2.34	0.60
2:B4:54:U:N3	2:B4:57:A:OP2	2.34	0.60
38:Lg:49:CYS:SG	38:Lg:85:LYS:NZ	2.73	0.60
4:L5:2793:G:H5''	4:L5:2794:C:H5''	1.82	0.60
4:L5:2262:G:OP2	48:Lr:98:ARG:NH1	2.35	0.60
4:L5:2341:A:OP2	32:La:4:ARG:NH2	2.35	0.60
4:L5:4252:C:H42	16:LJ:25:CYS:HB2	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1503:A:H4'	4:L5:1504:G:H5'	1.82	0.60
7:LA:103:PRO:HA	7:LA:163:ARG:H	1.67	0.60
20:LO:12:ARG:O	24:LS:171:ARG:NH2	2.35	0.60
69:SU:78:ASP:OD2	78:Sd:44:ARG:NH1	2.35	0.60
71:SW:24:GLN:HB2	76:Sb:7:LEU:HD13	1.83	0.60
49:S2:1636:G:OP2	49:S2:1638:G:N2	2.35	0.60
4:L5:1316:G:OP1	36:Le:43:ASN:ND2	2.35	0.59
13:LG:165:GLU:OE2	19:LN:26:ARG:NH2	2.35	0.59
31:LZ:9:LYS:HE2	31:LZ:82:PRO:HB2	1.83	0.59
49:S2:189:U:OP1	58:SI:152:ARG:NH2	2.35	0.59
24:LS:85:ASP:HB3	24:LS:90:THR:HG22	1.83	0.59
34:Lc:53:PRO:HG2	34:Lc:56:ARG:HD3	1.84	0.59
57:SH:152:ARG:HB2	57:SH:183:LYS:HD3	1.84	0.59
64:SP:38:SER:OG	64:SP:41:GLN:N	2.34	0.59
4:L5:4566:U:O2'	8:LB:234:ARG:NH1	2.33	0.59
4:L5:1865:G:N2	4:L5:1868:A:OP2	2.34	0.59
18:LM:11:ARG:HD2	18:LM:61:ILE:HG22	1.84	0.59
24:LS:143:LYS:HA	24:LS:146:HIS:HD2	1.66	0.59
32:La:11:LEU:HD21	32:La:18:GLY:H	1.65	0.59
47:Lp:38:THR:HA	47:Lp:45:THR:HA	1.85	0.59
4:L5:184:U:H4'	4:L5:254:G:H22	1.67	0.59
12:LF:80:ASN:HD21	25:LT:142:ARG:HA	1.68	0.59
49:S2:332:G:N7	56:SG:189:ARG:NH2	2.49	0.59
49:S2:589:G:H21	79:Se:99:LYS:HD3	1.66	0.59
4:L5:669:C:OP1	48:Lr:71:ARG:NH2	2.36	0.59
49:S2:534:G:O6	49:S2:548:C:N4	2.35	0.59
49:S2:926:A:H61	49:S2:1015:U:H3	1.48	0.59
59:SJ:109:ARG:HE	59:SJ:146:SER:HA	1.67	0.59
61:SL:33:LEU:HD12	61:SL:34:PRO:HD2	1.84	0.59
4:L5:666:G:H1'	4:L5:667:A:H2'	1.84	0.59
6:L8:14:U:H5''	21:LP:123:PRO:HD3	1.85	0.59
15:LI:20:SER:OG	15:LI:21:ARG:N	2.36	0.59
19:LN:135:ILE:HG23	19:LN:142:ILE:HD13	1.83	0.59
25:LT:74:ILE:HD11	25:LT:96:ILE:HD11	1.84	0.59
31:LZ:22:LYS:NZ	31:LZ:129:TRP:O	2.36	0.59
8:LB:259:PRO:O	8:LB:261:ARG:NH1	2.36	0.59
9:LC:153:VAL:HG12	9:LC:252:TRP:HB2	1.85	0.59
12:LF:94:ARG:NH2	12:LF:115:ARG:O	2.35	0.59
49:S2:1217:A:N6	49:S2:1680:G:O6	2.36	0.59
56:SG:37:ALA:HA	56:SG:49:VAL:HA	1.84	0.59
65:SQ:74:GLY:O	65:SQ:80:GLN:NE2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SW:50:PHE:HB3	71:SW:63:VAL:HG23	1.85	0.59
4:L5:4137:C:H42	4:L5:4147:G:H1	1.49	0.58
14:LH:23:ARG:NH2	14:LH:41:ILE:O	2.36	0.58
49:S2:492:C:N4	49:S2:507:G:OP2	2.36	0.58
81:Sg:67:SER:H	81:Sg:82:SER:HA	1.67	0.58
49:S2:1024:A:OP2	62:SN:124:ARG:NH2	2.37	0.58
49:S2:1589:A:N3	49:S2:1653:U:O2'	2.36	0.58
4:L5:978:G:OP1	11:LE:47:ASN:ND2	2.36	0.58
4:L5:2407:G:N7	43:Ll:5:LYS:NZ	2.50	0.58
4:L5:5005:G:N2	4:L5:5041:G:O2'	2.37	0.58
9:LC:195:LYS:HB2	9:LC:200:ARG:HD2	1.85	0.58
9:LC:293:LEU:O	9:LC:299:GLN:NE2	2.36	0.58
30:LY:73:VAL:HG12	30:LY:80:ILE:HG12	1.84	0.58
4:L5:1506:G:O2'	9:LC:116:ASN:ND2	2.35	0.58
11:LE:161:ARG:O	11:LE:182:ASN:ND2	2.36	0.58
17:LL:56:ARG:NH1	17:LL:74:ARG:O	2.37	0.58
4:L5:4674:C:O2'	8:LB:282:LYS:NZ	2.35	0.58
42:Lk:55:LYS:O	42:Lk:58:GLN:NE2	2.36	0.58
49:S2:1869:A:N6	51:SB:114:VAL:O	2.37	0.58
58:SI:37:LYS:HG3	58:SI:59:ARG:HG3	1.86	0.58
63:SO:32:HIS:HB3	63:SO:96:LYS:HB2	1.84	0.58
49:S2:1595:U:O4	74:SZ:104:ARG:NH1	2.36	0.58
50:SA:74:VAL:HG23	50:SA:121:LEU:HB3	1.86	0.58
4:L5:2400:G:H21	38:Lg:6:THR:HG22	1.68	0.58
4:L5:4162:C:O2	13:LG:73:ARG:NH2	2.33	0.58
34:Lc:35:LEU:HA	34:Lc:38:ILE:HG22	1.84	0.58
81:Sg:195:LEU:HA	81:Sg:211:GLY:HA3	1.85	0.58
12:LF:236:ARG:HB3	12:LF:239:GLN:HB2	1.86	0.58
49:S2:1302:G:H1	49:S2:1307:U:H3	1.52	0.58
67:SS:84:LEU:O	67:SS:87:GLN:NE2	2.36	0.58
49:S2:1613:G:H1	49:S2:1626:C:H42	1.52	0.58
50:SA:145:ILE:HG22	50:SA:159:ILE:HG23	1.86	0.58
2:B4:32:C:OP2	65:SQ:146:ARG:NH2	2.34	0.58
23:LR:13:SER:OG	23:LR:38:ARG:NH1	2.37	0.58
55:SF:190:ILE:HA	55:SF:193:LYS:HG2	1.86	0.58
4:L5:186:G:N2	4:L5:1365:C:O2'	2.37	0.57
4:L5:1707:C:O2'	4:L5:2118:G:N2	2.37	0.57
26:LU:98:ASP:OD1	26:LU:98:ASP:N	2.37	0.57
51:SB:149:GLN:NE2	51:SB:151:ARG:O	2.35	0.57
51:SB:175:GLU:O	51:SB:179:ASN:ND2	2.36	0.57
2:B4:20:A:N6	2:B4:45:G:O2'	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:Sb:34:ASP:HB2	76:Sb:82:LYS:HD2	1.86	0.57
81:Sg:176:VAL:HG23	81:Sg:185:LYS:HB2	1.86	0.57
4:L5:2274:C:O2	12:LF:165:LYS:NZ	2.36	0.57
4:L5:2562:G:H21	4:L5:2565:A:H8	1.51	0.57
43:Ll:38:ASN:HD22	43:Ll:41:ARG:HB2	1.68	0.57
48:Lr:39:ARG:O	48:Lr:103:ARG:NH2	2.36	0.57
4:L5:1468:C:OP1	32:La:132:ARG:NH2	2.35	0.57
22:LQ:180:ARG:NH1	32:La:50:PRO:O	2.37	0.57
31:LZ:17:ARG:NH2	31:LZ:18:TYR:OH	2.37	0.57
49:S2:925:G:H1	49:S2:1017:U:H3	1.51	0.57
4:L5:172:C:O2	39:Lh:112:ARG:NH2	2.37	0.57
4:L5:1081:C:N3	4:L5:1082:C:N4	2.53	0.57
4:L5:1420:A:H3'	22:LQ:68:ARG:HH22	1.70	0.57
31:LZ:51:ARG:HB2	31:LZ:65:ARG:HG3	1.86	0.57
32:La:75:LEU:HB2	32:La:113:GLY:HA2	1.85	0.57
49:S2:446:G:OP2	58:Sl:47:ARG:NH2	2.36	0.57
49:S2:1860:A:N7	75:Sa:34:LYS:NZ	2.53	0.57
53:SD:158:ILE:HG12	53:SD:189:MET:HE1	1.86	0.57
4:L5:4472:G:O2'	44:Lm:100:TYR:O	2.22	0.57
6:L8:121:G:H1	6:L8:129:C:H42	1.52	0.57
9:LC:143:ARG:HB2	9:LC:179:ASP:HB3	1.87	0.57
10:LD:50:ARG:NH2	10:LD:72:ASP:OD2	2.36	0.57
46:Lo:51:GLN:HE21	46:Lo:53:LYS:H	1.53	0.57
49:S2:167:G:H21	56:SG:132:ARG:HG3	1.68	0.57
49:S2:835:C:N4	73:SY:9:THR:O	2.38	0.57
57:SH:138:GLU:OE2	62:SN:19:ARG:NH2	2.37	0.57
68:ST:56:ARG:HG2	68:ST:103:VAL:HG11	1.86	0.57
69:SU:54:VAL:HB	69:SU:88:LEU:HB3	1.86	0.57
2:B4:22:C:H2'	2:B4:23:G:H8	1.70	0.57
4:L5:35:U:OP2	19:LN:83:LYS:NZ	2.38	0.57
4:L5:2406:G:N7	43:Ll:2:SER:N	2.52	0.57
49:S2:39:A:OP2	59:SJ:5:ARG:NH1	2.38	0.57
49:S2:150:A:N7	49:S2:168:C:N4	2.44	0.57
49:S2:196:C:O2'	49:S2:203:G:N2	2.37	0.57
49:S2:1597:C:OP2	74:SZ:85:ARG:NH2	2.37	0.57
49:S2:1864:U:OP2	75:Sa:5:ARG:NH2	2.37	0.57
4:L5:4305:G:N7	25:LT:87:LYS:NZ	2.52	0.57
49:S2:919:A:H5'	62:SN:16:LEU:HD21	1.86	0.57
62:SN:129:TYR:HB3	62:SN:135:LEU:HD13	1.87	0.57
4:L5:1366:G:N7	17:LL:37:LYS:NZ	2.52	0.57
4:L5:4097:G:N2	4:L5:4113:U:O4'	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1535:U:O2'	55:SF:88:MET:SD	2.63	0.57
4:L5:171:U:H5'	17:LL:135:LYS:HD3	1.87	0.57
4:L5:1172:C:O2'	4:L5:1189:G:N2	2.38	0.57
8:LB:58:ARG:NH1	8:LB:74:GLU:OE2	2.37	0.57
22:LQ:26:ARG:HA	22:LQ:29:VAL:HG12	1.86	0.57
4:L5:394:G:N2	4:L5:397:G:OP2	2.38	0.56
4:L5:2258:C:N4	4:L5:2259:G:O6	2.38	0.56
49:S2:1273:C:O2'	49:S2:1506:A:N6	2.38	0.56
78:Sd:22:ARG:NH1	78:Sd:36:LEU:O	2.38	0.56
81:Sg:126:ASP:OD1	81:Sg:126:ASP:N	2.36	0.56
4:L5:2263:A:OP1	48:Lr:107:ARG:NH1	2.38	0.56
4:L5:4618:G:H5''	27:LV:15:ARG:HB2	1.88	0.56
22:LQ:79:THR:HB	22:LQ:136:THR:HG22	1.87	0.56
49:S2:1615:U:O4	64:SP:40:ARG:NH2	2.38	0.56
58:SI:87:ASN:HB3	58:SI:90:LEU:HG	1.87	0.56
58:SI:106:SER:HB3	58:SI:171:LEU:HG	1.87	0.56
4:L5:725:G:OP2	9:LC:350:ARG:NH2	2.38	0.56
4:L5:963:G:N7	4:L5:964:A:N6	2.53	0.56
4:L5:3756:A:N6	4:L5:3757:G:O6	2.39	0.56
4:L5:4648:A:OP1	23:LR:62:ARG:NH2	2.38	0.56
18:LM:12:VAL:HA	18:LM:26:ALA:HA	1.87	0.56
35:Ld:26:THR:HB	35:Ld:85:ARG:HE	1.71	0.56
49:S2:1354:G:N2	49:S2:1357:A:OP2	2.35	0.56
49:S2:1753:C:O2	49:S2:1779:G:N2	2.33	0.56
51:SB:146:ARG:HH21	51:SB:206:PRO:HG3	1.70	0.56
55:SF:28:VAL:HG12	55:SF:110:GLN:HB2	1.86	0.56
56:SG:139:SER:OG	56:SG:142:ARG:NH1	2.38	0.56
81:Sg:12:LYS:O	81:Sg:43:TRP:NE1	2.39	0.56
4:L5:4765:G:H21	24:LS:173:ASN:HD21	1.53	0.56
10:LD:166:ALA:HB1	10:LD:171:LEU:HD12	1.87	0.56
47:Lp:33:GLN:OE1	47:Lp:49:ARG:NH2	2.38	0.56
49:S2:1495:G:H22	78:Sd:45:GLN:HE22	1.54	0.56
54:SE:112:HIS:NE2	54:SE:237:SER:O	2.38	0.56
4:L5:1759:G:O6	4:L5:1760:G:N2	2.37	0.56
4:L5:2601:A:N6	4:L5:2744:A:OP2	2.38	0.56
4:L5:2637:U:OP1	38:Lg:28:ASN:ND2	2.38	0.56
4:L5:3589:G:N2	4:L5:3590:G:N7	2.51	0.56
4:L5:3697:U:H5''	4:L5:3698:G:H5'	1.86	0.56
4:L5:3853:U:O2'	4:L5:4979:A:N3	2.37	0.56
4:L5:4077:A:N1	4:L5:4171:C:N4	2.53	0.56
49:S2:190:G:O2'	49:S2:209:A:N6	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:993:G:N7	75:Sa:15:ARG:NH2	2.54	0.56
70:SV:15:ARG:HH21	70:SV:24:ILE:HG21	1.70	0.56
4:L5:198:A:OP1	30:LY:126:ARG:NH2	2.38	0.56
4:L5:502:C:H5'	4:L5:503:C:H3'	1.88	0.56
4:L5:1508:A:OP1	9:LC:110:ARG:NH1	2.38	0.56
4:L5:2520:C:O2	4:L5:2640:G:N2	2.39	0.56
5:L7:51:G:N2	16:LJ:12:MET:SD	2.79	0.56
14:LH:128:MET:N	14:LH:128:MET:SD	2.79	0.56
53:SD:167:TYR:OH	53:SD:202:LYS:O	2.24	0.56
81:Sg:123:GLY:O	81:Sg:125:ARG:NH1	2.39	0.56
4:L5:1391:A:OP1	22:LQ:181:ARG:NH2	2.38	0.56
4:L5:3684:G:OP1	7:LA:174:ARG:NH2	2.39	0.56
6:L8:152:U:O2'	13:LG:160:ASP:OD2	2.22	0.56
11:LE:178:PRO:HB3	11:LE:258:LEU:HD11	1.87	0.56
43:Ll:28:ARG:HA	43:Ll:33:ASN:HD22	1.71	0.56
49:S2:534:G:N2	49:S2:550:C:O2	2.39	0.56
68:ST:85:ASN:ND2	68:ST:89:PRO:O	2.38	0.56
2:B4:18:G:N2	2:B4:55:C:O2'	2.39	0.56
4:L5:210:C:OP1	30:LY:59:ARG:NH1	2.39	0.56
4:L5:1755:C:H1'	10:LD:2:GLY:HA3	1.88	0.56
4:L5:3842:C:OP1	8:LB:238:LYS:NZ	2.36	0.56
6:L8:37:A:OP2	39:Lh:89:ARG:NH1	2.39	0.56
15:LI:33:ILE:HB	15:LI:69:ARG:HH22	1.71	0.56
31:LZ:88:ASP:O	31:LZ:121:ARG:NH1	2.39	0.56
31:LZ:124:THR:OG1	31:LZ:126:LYS:NZ	2.39	0.56
39:Lh:104:THR:HG22	39:Lh:106:LYS:H	1.71	0.56
49:S2:1159:G:OP2	72:SX:5:ARG:NH1	2.38	0.56
4:L5:1364:U:OP2	17:LL:36:ARG:NH2	2.39	0.56
4:L5:1599:A:OP1	4:L5:2795:A:N6	2.36	0.56
4:L5:2262:G:OP1	48:Lr:94:ARG:NH1	2.38	0.56
4:L5:4694:G:H4'	14:LH:71:ARG:HH12	1.69	0.56
4:L5:5055:G:N2	35:Ld:118:GLN:OE1	2.37	0.56
8:LB:90:VAL:HG23	8:LB:104:THR:HG22	1.87	0.56
42:Lk:52:LYS:O	42:Lk:55:LYS:NZ	2.37	0.56
49:S2:377:G:H5'	58:SI:98:LYS:HB3	1.88	0.56
49:S2:380:G:OP1	58:SI:56:ARG:NH2	2.38	0.56
49:S2:809:A:H4'	54:SE:221:ARG:HH22	1.70	0.56
49:S2:1653:U:H3	49:S2:1671:G:H1	1.54	0.56
49:S2:1858:G:OP2	63:SO:146:ARG:NH2	2.34	0.56
4:L5:2848:G:O2'	4:L5:3838:U:O4	2.24	0.56
4:L5:3717:A:OP2	4:L5:3735:G:N2	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4753:U:OP1	37:Lf:8:LYS:NZ	2.39	0.56
9:LC:326:LEU:HD13	9:LC:333:LYS:HB2	1.87	0.56
12:LF:62:ARG:HH21	12:LF:66:ARG:HH22	1.53	0.56
21:LP:42:ARG:HH12	21:LP:109:VAL:HG22	1.71	0.56
29:LX:110:LYS:NZ	29:LX:121:VAL:O	2.39	0.56
49:S2:1455:A:OP1	66:SR:5:ARG:NH1	2.39	0.56
4:L5:3653:A:N6	4:L5:3691:G:O2'	2.39	0.55
4:L5:4194:U:O2'	15:LI:116:ARG:NH1	2.39	0.55
8:LB:222:VAL:O	8:LB:343:ARG:NH1	2.38	0.55
32:La:85:GLN:O	32:La:89:ASN:ND2	2.40	0.55
49:S2:447:A:OP1	58:SI:49:ARG:NH1	2.38	0.55
57:SH:145:ARG:HB2	57:SH:155:LYS:HZ2	1.71	0.55
67:SS:23:ARG:NH2	74:SZ:46:ASN:O	2.34	0.55
73:SY:81:TYR:O	73:SY:85:ASN:ND2	2.39	0.55
4:L5:1100:U:O3'	4:L5:1167:C:N4	2.39	0.55
8:LB:313:SER:OG	8:LB:314:ILE:N	2.37	0.55
31:LZ:22:LYS:NZ	31:LZ:132:GLN:O	2.35	0.55
49:S2:104:A:OP1	58:SI:12:ARG:NH1	2.39	0.55
49:S2:482:G:N1	49:S2:485:A:OP2	2.33	0.55
67:SS:112:GLU:O	67:SS:116:LYS:NZ	2.36	0.55
81:Sg:91:ASP:OD2	81:Sg:94:THR:N	2.39	0.55
4:L5:1390:G:N2	4:L5:1393:G:OP2	2.39	0.55
40:Li:37:THR:OG1	40:Li:41:ARG:NH2	2.39	0.55
51:SB:44:ILE:HD11	51:SB:69:VAL:HG11	1.87	0.55
4:L5:1697:G:N2	4:L5:2084:C:OP1	2.39	0.55
19:LN:27:CYS:SG	19:LN:31:ARG:NH2	2.79	0.55
81:Sg:104:HIS:NE2	81:Sg:126:ASP:OD1	2.39	0.55
4:L5:3659:G:O2'	7:LA:227:ARG:NH2	2.40	0.55
8:LB:161:ARG:HG2	8:LB:184:GLN:HG2	1.87	0.55
27:LV:84:GLN:HE21	27:LV:86:LYS:HB3	1.71	0.55
38:Lg:41:ALA:O	38:Lg:52:ARG:NH2	2.39	0.55
41:Lj:34:CYS:SG	41:Lj:35:GLY:N	2.79	0.55
49:S2:1454:A:N1	49:S2:1476:A:O2'	2.40	0.55
49:S2:1854:U:H5'	63:SO:150:ARG:HH12	1.71	0.55
4:L5:3641:U:OP2	4:L5:3646:A:N6	2.40	0.55
49:S2:1239:U:H5''	64:SP:124:LYS:HE3	1.89	0.55
54:SE:11:ARG:HE	54:SE:20:LEU:HB3	1.71	0.55
4:L5:703:G:H2'	4:L5:704:C:H4'	1.88	0.55
4:L5:1368:A:H1'	30:LY:1:MET:HE2	1.87	0.55
12:LF:113:ARG:NH2	12:LF:208:LEU:O	2.39	0.55
24:LS:86:SER:OG	24:LS:87:ARG:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Lo:59:LYS:NZ	46:Lo:61:LYS:O	2.40	0.55
53:SD:168:VAL:HA	53:SD:189:MET:HA	1.89	0.55
60:SK:65:ARG:NH2	78:Sd:21:CYS:O	2.40	0.55
66:SR:60:ARG:HH22	66:SR:66:VAL:HG21	1.71	0.55
75:Sa:22:ARG:NH2	75:Sa:27:ALA:O	2.39	0.55
75:Sa:23:CYS:SG	75:Sa:24:THR:N	2.79	0.55
14:LH:18:ILE:HG22	14:LH:27:VAL:HG12	1.88	0.55
17:LL:63:THR:HG23	17:LL:65:ARG:H	1.72	0.55
64:SP:76:VAL:O	64:SP:95:GLY:N	2.40	0.55
3:D4:18:G:H22	3:D4:55:U:H1'	1.72	0.55
4:L5:2759:G:O2'	4:L5:2762:G:N2	2.40	0.55
10:LD:193:GLU:O	10:LD:197:LYS:NZ	2.39	0.55
13:LG:157:ILE:HD13	13:LG:170:LEU:HD11	1.88	0.55
46:Lo:36:GLN:OE1	46:Lo:40:ARG:NH1	2.40	0.55
49:S2:672:A:N6	49:S2:1027:A:OP1	2.40	0.55
56:SG:54:GLY:O	56:SG:110:ASN:ND2	2.39	0.55
4:L5:85:G:O2'	4:L5:97:G:O6	2.25	0.55
4:L5:1269:G:HO2'	4:L5:1440:U:HO2'	1.49	0.55
4:L5:1502:G:OP2	22:LQ:65:ARG:NH1	2.39	0.55
5:L7:120:U:O2	10:LD:258:LYS:NZ	2.37	0.55
63:SO:95:ILE:HB	63:SO:129:ILE:HG22	1.88	0.55
64:SP:18:ARG:HH11	67:SS:88:LYS:HG2	1.70	0.55
4:L5:182:G:N2	4:L5:256:G:O4'	2.40	0.54
4:L5:2000:G:O2'	4:L5:2017:A:N1	2.37	0.54
4:L5:2059:C:O2	24:LS:118:ARG:NH1	2.40	0.54
4:L5:3654:G:O2'	4:L5:3693:U:OP1	2.24	0.54
7:LA:117:GLU:OE2	7:LA:163:ARG:NH1	2.40	0.54
18:LM:3:PHE:H	24:LS:175:PHE:HZ	1.54	0.54
22:LQ:171:GLY:O	22:LQ:176:ARG:NH2	2.41	0.54
69:SU:21:ARG:HA	69:SU:90:ASP:HA	1.89	0.54
81:Sg:78:ALA:HB3	81:Sg:90:TRP:HB2	1.88	0.54
4:L5:3688:U:OP2	7:LA:198:ARG:NH1	2.37	0.54
49:S2:1745:A:N6	49:S2:1789:G:O2'	2.41	0.54
52:SC:233:LEU:HA	52:SC:236:PHE:HB3	1.88	0.54
4:L5:1270:A:H8	4:L5:2106:G:H21	1.53	0.54
4:L5:2674:A:N6	34:Lc:51:ASN:O	2.41	0.54
4:L5:4693:C:OP1	14:LH:64:ARG:NH1	2.41	0.54
4:L5:4775:C:N3	4:L5:4860:G:N2	2.54	0.54
4:L5:5068:G:N2	4:L5:5069:U:O4	2.39	0.54
7:LA:54:ARG:HG3	7:LA:56:ALA:H	1.72	0.54
8:LB:302:ASN:HB2	8:LB:313:SER:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LF:94:ARG:NH1	12:LF:97:GLY:O	2.35	0.54
24:LS:61:ILE:HD11	24:LS:64:CYS:HB2	1.89	0.54
54:SE:139:LEU:HD22	54:SE:147:ILE:HD11	1.90	0.54
58:SI:157:LYS:O	61:SL:22:ARG:NH2	2.41	0.54
75:Sa:88:SER:OG	75:Sa:89:ARG:N	2.40	0.54
6:L8:155:C:OP2	13:LG:89:ARG:NH1	2.34	0.54
18:LM:42:CYS:SG	18:LM:78:GLN:NE2	2.81	0.54
49:S2:379:C:O2	58:SI:5:ARG:NH1	2.36	0.54
51:SB:107:ARG:NH2	63:SO:133:THR:O	2.40	0.54
54:SE:152:PRO:O	54:SE:155:LYS:NZ	2.39	0.54
63:SO:131:ASP:OD1	63:SO:131:ASP:N	2.40	0.54
72:SX:63:ASN:ND2	72:SX:114:ASP:OD2	2.40	0.54
4:L5:1654:G:N2	4:L5:1678:C:OP1	2.41	0.54
4:L5:3607:U:OP1	23:LR:88:ARG:NH1	2.41	0.54
9:LC:207:PRO:HG2	9:LC:227:ILE:HG13	1.89	0.54
49:S2:125:C:OP1	56:SG:202:ASN:ND2	2.40	0.54
49:S2:1610:G:OP1	67:SS:121:ARG:NH2	2.40	0.54
54:SE:57:THR:HG23	54:SE:60:GLU:H	1.73	0.54
2:B4:14:A:H61	2:B4:20:A:H2	1.55	0.54
4:L5:309:C:O2	40:Li:32:ARG:NH1	2.38	0.54
8:LB:162:VAL:N	8:LB:183:ILE:O	2.38	0.54
56:SG:74:ARG:NH2	56:SG:94:ARG:O	2.41	0.54
4:L5:63:G:OP1	19:LN:169:ARG:NH1	2.41	0.54
4:L5:4120:U:O2'	38:Lg:93:ARG:NH1	2.41	0.54
4:L5:4163:U:H5'	4:L5:4164:C:H5''	1.90	0.54
4:L5:4910:G:H4'	8:LB:95:THR:HG22	1.89	0.54
9:LC:334:THR:O	9:LC:338:ASN:ND2	2.40	0.54
11:LE:256:GLN:O	11:LE:260:LYS:NZ	2.40	0.54
13:LG:96:LEU:O	13:LG:100:HIS:ND1	2.39	0.54
20:LO:6:VAL:HG12	20:LO:32:LYS:HB2	1.89	0.54
40:Li:70:LEU:HD12	40:Li:87:ARG:HE	1.72	0.54
49:S2:635:G:OP1	79:Se:94:LYS:NZ	2.41	0.54
49:S2:863:U:O2	71:SW:124:LYS:NZ	2.40	0.54
51:SB:134:LEU:HD22	51:SB:218:LEU:HB2	1.90	0.54
47:Lp:22:LEU:HA	47:Lp:25:MET:HG2	1.89	0.54
49:S2:41:G:H1	49:S2:481:C:H42	1.54	0.54
4:L5:3620:G:OP1	4:L5:3622:C:N4	2.41	0.54
4:L5:5006:U:OP2	28:LW:50:ASN:ND2	2.39	0.54
16:LJ:35:ARG:HB3	16:LJ:123:ILE:HG23	1.89	0.54
24:LS:77:ASN:OD1	24:LS:98:ARG:NH1	2.41	0.54
32:La:17:HIS:O	32:La:19:HIS:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:960:U:O2'	49:S2:962:A:N7	2.36	0.54
49:S2:1616:U:OP2	64:SP:43:ARG:NH1	2.37	0.54
65:SQ:58:LEU:O	65:SQ:62:ARG:NH2	2.41	0.54
66:SR:37:GLU:OE1	81:Sg:150:TRP:NE1	2.36	0.54
14:LH:37:ASP:OD1	14:LH:37:ASP:N	2.41	0.54
4:L5:40:G:N2	4:L5:4380:A:N7	2.56	0.53
4:L5:3751:G:H21	4:L5:3775:A:H8	1.56	0.53
4:L5:4084:G:O6	7:LA:70:LYS:NZ	2.40	0.53
7:LA:130:SER:HB2	7:LA:171:GLY:HA3	1.90	0.53
8:LB:317:LEU:HB2	8:LB:372:SER:HB3	1.90	0.53
49:S2:506:G:N2	49:S2:508:A:N1	2.56	0.53
65:SQ:130:LYS:NZ	65:SQ:134:GLY:O	2.42	0.53
9:LC:141:GLY:O	9:LC:204:ARG:NH1	2.41	0.53
14:LH:23:ARG:HD3	14:LH:39:ASN:HA	1.90	0.53
14:LH:137:SER:OG	14:LH:139:ALA:O	2.27	0.53
49:S2:1543:U:OP2	68:ST:62:ARG:NH2	2.40	0.53
49:S2:1863:A:N6	75:Sa:76:SER:OG	2.41	0.53
75:Sa:33:ASP:OD1	75:Sa:33:ASP:N	2.38	0.53
81:Sg:86:THR:OG1	81:Sg:101:PHE:O	2.27	0.53
3:D4:53:G:H22	3:D4:58:A:H8	1.56	0.53
4:L5:4485:C:O2'	44:Lm:114:LYS:NZ	2.41	0.53
8:LB:56:ILE:HG21	8:LB:365:LEU:HD22	1.89	0.53
13:LG:157:ILE:HG21	13:LG:170:LEU:HD11	1.90	0.53
48:Lr:28:GLU:OE2	48:Lr:31:ASN:ND2	2.41	0.53
49:S2:635:G:H5''	79:Se:94:LYS:HG3	1.90	0.53
4:L5:156:G:N2	4:L5:157:U:O4	2.41	0.53
49:S2:806:U:H3	49:S2:857:U:H3	1.56	0.53
49:S2:1326:U:O4	78:Sd:28:HIS:NE2	2.42	0.53
51:SB:159:GLN:HA	51:SB:162:ARG:HB2	1.89	0.53
4:L5:690:C:OP1	48:Lr:87:ARG:NH1	2.39	0.53
4:L5:4541:G:N2	4:L5:4544:A:OP2	2.42	0.53
5:L7:48:G:O2'	10:LD:222:GLN:O	2.27	0.53
30:LY:54:GLU:HB3	30:LY:108:ARG:HB3	1.90	0.53
40:Li:48:CYS:SG	40:Li:49:GLY:N	2.81	0.53
49:S2:696:G:H2'	49:S2:734:C:H2'	1.91	0.53
50:SA:157:VAL:O	70:SV:65:SER:OG	2.25	0.53
71:SW:96:SER:OG	71:SW:97:ARG:N	2.41	0.53
4:L5:959:G:O2'	4:L5:2263:A:N6	2.39	0.53
4:L5:2578:G:OP1	31:LZ:107:LYS:NZ	2.40	0.53
8:LB:286:LYS:H	8:LB:332:MET:HB3	1.73	0.53
11:LE:46:ARG:HB2	11:LE:62:MET:HE1	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LV:94:VAL:HG11	28:LW:20:ARG:HE	1.73	0.53
35:Ld:23:ARG:HG2	35:Ld:121:ASN:HA	1.89	0.53
35:Ld:68:LEU:HB3	35:Ld:108:TYR:HB2	1.89	0.53
51:SB:192:SER:O	51:SB:196:ASP:N	2.41	0.53
72:SX:104:GLY:HA2	72:SX:120:PHE:HA	1.89	0.53
4:L5:1373:A:OP1	9:LC:47:ASN:ND2	2.41	0.53
4:L5:3689:G:O2'	4:L5:3818:U:OP2	2.27	0.53
49:S2:1200:A:O2'	49:S2:1357:A:N1	2.37	0.53
77:Sc:13:ARG:N	77:Sc:33:GLU:O	2.42	0.53
4:L5:2583:C:OP2	38:Lg:76:ARG:NH2	2.42	0.53
4:L5:4101:C:H4'	4:L5:4109:G:H22	1.74	0.53
34:Lc:37:MET:HA	34:Lc:40:GLN:HE21	1.74	0.53
57:SH:154:ILE:HB	57:SH:185:VAL:HG22	1.90	0.53
31:LZ:93:LYS:O	31:LZ:97:ASN:ND2	2.32	0.53
49:S2:921:G:H5'	76:Sb:21:LYS:HD3	1.91	0.53
4:L5:187:U:H5''	4:L5:188:G:H5'	1.91	0.53
4:L5:1387:A:N7	32:La:74:ASN:ND2	2.55	0.53
4:L5:1394:G:OP1	17:LL:186:ARG:NH1	2.40	0.53
19:LN:163:GLY:O	19:LN:172:ARG:NH1	2.42	0.53
21:LP:111:SER:O	21:LP:111:SER:OG	2.27	0.53
49:S2:934:G:OP2	49:S2:993:G:N2	2.38	0.53
52:SC:102:LEU:HD22	52:SC:130:ILE:HG22	1.90	0.53
64:SP:33:LEU:HD21	64:SP:87:PRO:HD2	1.90	0.53
64:SP:81:ARG:NH2	64:SP:120:SER:O	2.37	0.53
71:SW:3:ARG:HD3	71:SW:6:VAL:HG12	1.90	0.53
10:LD:261:VAL:HG22	10:LD:263:LYS:H	1.74	0.52
19:LN:17:ASP:N	19:LN:17:ASP:OD1	2.42	0.52
31:LZ:121:ARG:NH2	31:LZ:127:ASN:OD1	2.43	0.52
49:S2:916:A:N3	62:SN:73:ARG:NH1	2.58	0.52
72:SX:107:ARG:NH1	72:SX:111:ALA:O	2.41	0.52
75:Sa:2:THR:OG1	75:Sa:3:LYS:N	2.41	0.52
4:L5:1577:G:OP1	47:Lp:17:ARG:NH1	2.39	0.52
12:LF:113:ARG:NH2	12:LF:205:ASN:O	2.42	0.52
20:LO:120:VAL:HG22	20:LO:122:ALA:H	1.73	0.52
49:S2:1372:U:OP1	49:S2:1385:G:N2	2.36	0.52
54:SE:247:THR:O	54:SE:251:GLU:N	2.36	0.52
65:SQ:12:VAL:HG21	65:SQ:91:ALA:HA	1.91	0.52
72:SX:24:ASP:HB3	72:SX:27:TYR:HB3	1.91	0.52
4:L5:442:G:OP1	37:Lf:68:ARG:NH1	2.43	0.52
4:L5:2049:G:HO2'	4:L5:3884:U:HO2'	1.54	0.52
49:S2:56:G:OP2	73:SY:115:LYS:NZ	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SB:33:VAL:HG22	51:SB:96:CYS:HB2	1.91	0.52
55:SF:126:THR:HB	77:Sc:47:LYS:HE2	1.92	0.52
64:SP:97:TYR:HA	64:SP:102:PHE:HA	1.90	0.52
74:SZ:84:ALA:O	74:SZ:88:LEU:N	2.38	0.52
4:L5:467:U:H3	4:L5:689:U:H3	1.57	0.52
34:Lc:55:LEU:HD13	38:Lg:92:LYS:HG2	1.91	0.52
39:Lh:104:THR:HB	39:Lh:107:GLN:HG2	1.90	0.52
48:Lr:94:ARG:HB3	48:Lr:111:ILE:HD11	1.91	0.52
49:S2:45:A:N1	49:S2:480:G:O2'	2.41	0.52
50:SA:174:MET:HA	50:SA:177:MET:HB2	1.91	0.52
4:L5:382:G:N1	4:L5:385:A:OP2	2.42	0.52
4:L5:496:G:O6	4:L5:497:G:N2	2.38	0.52
4:L5:1476:C:O2	4:L5:1489:G:N2	2.40	0.52
4:L5:4250:G:OP1	16:LJ:98:ASN:ND2	2.40	0.52
4:L5:4280:A:OP2	10:LD:23:ARG:NH1	2.42	0.52
8:LB:264:PHE:HB3	20:LO:65:ASN:HB3	1.92	0.52
17:LL:71:ARG:NH1	17:LL:72:ALA:O	2.42	0.52
49:S2:1113:A:H62	49:S2:1119:A:H62	1.56	0.52
50:SA:176:TRP:HE1	50:SA:195:TRP:HE3	1.58	0.52
56:SG:4:ASN:HA	56:SG:15:LEU:HA	1.91	0.52
75:Sa:40:VAL:HG23	75:Sa:69:VAL:HG13	1.91	0.52
2:B4:5:G:H2'	2:B4:6:A:H8	1.74	0.52
4:L5:27:C:OP1	19:LN:193:ARG:NH1	2.42	0.52
4:L5:1669:A:N3	4:L5:1852:U:O2'	2.38	0.52
4:L5:1885:G:OP1	37:Lf:20:ASN:ND2	2.42	0.52
10:LD:75:VAL:O	10:LD:112:ARG:NH1	2.43	0.52
14:LH:48:LEU:HD11	14:LH:56:ARG:HH11	1.74	0.52
49:S2:1256:G:H21	69:SU:77:TRP:HZ3	1.57	0.52
74:SZ:68:ILE:HB	74:SZ:109:TYR:HB2	1.92	0.52
4:L5:172:C:H4'	4:L5:173:C:H5'	1.92	0.52
25:LT:41:ASP:HB2	25:LT:99:SER:HB2	1.92	0.52
49:S2:821:G:N2	59:SJ:148:ILE:O	2.42	0.52
49:S2:1268:C:O2	64:SP:97:TYR:OH	2.23	0.52
49:S2:1314:U:H2'	60:SK:3:MET:HG3	1.91	0.52
50:SA:8:LEU:O	50:SA:9:GLN:NE2	2.42	0.52
50:SA:184:ARG:HD2	50:SA:191:ARG:HG3	1.92	0.52
59:SJ:50:LEU:HD22	59:SJ:102:ILE:HB	1.91	0.52
64:SP:82:ASP:OD1	64:SP:82:ASP:N	2.42	0.52
81:Sg:152:SER:OG	81:Sg:153:CYS:N	2.43	0.52
4:L5:2318:G:N2	4:L5:2321:G:OP2	2.37	0.52
47:Lp:57:CYS:SG	47:Lp:58:GLY:N	2.83	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1005:G:OP2	51:SB:162:ARG:NH1	2.42	0.52
49:S2:1264:C:H4'	49:S2:1265:A:H5'	1.92	0.52
50:SA:110:ASN:ND2	50:SA:113:GLN:OE1	2.43	0.52
63:SO:98:ARG:HA	63:SO:133:THR:HG22	1.91	0.52
8:LB:77:THR:HG21	8:LB:337:VAL:HG22	1.92	0.52
21:LP:112:LEU:HA	21:LP:152:GLU:HA	1.92	0.52
49:S2:196:C:H1'	49:S2:203:G:H1	1.75	0.52
57:SH:49:LYS:HG3	57:SH:61:ILE:HG23	1.91	0.52
58:SL:158:ILE:HA	61:SL:22:ARG:HH22	1.73	0.52
63:SO:27:VAL:HG13	63:SO:91:THR:H	1.75	0.52
68:ST:37:VAL:HG13	68:ST:39:LEU:H	1.75	0.52
4:L5:1174:G:H1	4:L5:1186:U:H3	1.57	0.52
4:L5:2611:A:H5'	4:L5:2688:G:H4'	1.91	0.52
19:LN:184:ILE:HB	19:LN:194:ARG:HH12	1.75	0.52
35:Ld:64:ILE:HG23	35:Ld:68:LEU:HD21	1.91	0.52
36:Le:114:ARG:HD2	36:Le:117:GLN:HE21	1.74	0.52
49:S2:685:A:H5''	71:SW:31:SER:HB3	1.92	0.52
49:S2:983:A:OP1	49:S2:1073:U:O2'	2.27	0.52
54:SE:106:LYS:HD2	54:SE:108:ARG:HH22	1.75	0.52
56:SG:151:ASP:OD1	56:SG:156:TYR:OH	2.27	0.52
59:SJ:158:ASP:OD1	59:SJ:158:ASP:N	2.42	0.52
65:SQ:117:ARG:HH12	65:SQ:121:VAL:HG23	1.74	0.52
4:L5:730:G:OP2	12:LF:76:ARG:NE	2.42	0.51
4:L5:1238:A:OP2	11:LE:60:SER:OG	2.29	0.51
25:LT:12:ARG:NH1	25:LT:13:TYR:OH	2.44	0.51
38:Lg:10:ARG:NH1	43:Ll:3:SER:OG	2.43	0.51
49:S2:1240:A:N6	64:SP:122:THR:O	2.43	0.51
55:SF:49:LEU:HD11	65:SQ:49:TYR:HB3	1.93	0.51
56:SG:185:LEU:HG	56:SG:189:ARG:HE	1.76	0.51
4:L5:62:A:N3	4:L5:77:U:O2'	2.39	0.51
4:L5:1444:G:H1	4:L5:2102:G:H22	1.58	0.51
4:L5:2666:U:O4	23:LR:128:LYS:NZ	2.43	0.51
17:LL:77:SER:N	17:LL:80:GLU:OE1	2.41	0.51
49:S2:1674:G:OP1	55:SF:51:HIS:NE2	2.43	0.51
50:SA:184:ARG:O	50:SA:191:ARG:NH2	2.43	0.51
4:L5:508:G:O2'	4:L5:510:U:OP2	2.24	0.51
4:L5:4265:U:OP1	10:LD:12:TYR:OH	2.28	0.51
8:LB:125:SER:OG	8:LB:126:LYS:N	2.44	0.51
9:LC:104:PRO:O	9:LC:106:LYS:NZ	2.43	0.51
9:LC:214:ASP:OD1	9:LC:217:ILE:N	2.43	0.51
12:LF:182:TYR:HB3	12:LF:200:ARG:HG3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LH:1:MET:HE3	14:LH:3:THR:HG22	1.92	0.51
26:LU:34:MET:SD	26:LU:34:MET:N	2.84	0.51
36:Le:85:LEU:HD21	36:Le:115:ALA:HB2	1.91	0.51
45:Ln:9:ARG:NH1	49:S2:1851:A:OP1	2.43	0.51
49:S2:95:G:OP1	54:SE:10:LYS:NZ	2.43	0.51
49:S2:508:A:H3'	49:S2:509:G:H8	1.75	0.51
58:SI:142:SER:HA	58:SI:146:GLN:HB3	1.91	0.51
71:SW:14:ILE:HG22	71:SW:25:VAL:HG21	1.92	0.51
76:Sb:33:MET:HE2	76:Sb:48:SER:HA	1.91	0.51
2:B4:20:A:N6	2:B4:47:C:O4'	2.43	0.51
4:L5:114:G:N2	4:L5:276:C:O2'	2.43	0.51
4:L5:1780:A:N3	15:LI:198:LYS:NZ	2.58	0.51
4:L5:2740:U:O2'	4:L5:2742:G:N2	2.43	0.51
11:LE:194:VAL:O	37:Lf:108:SER:OG	2.27	0.51
24:LS:13:VAL:HG23	24:LS:62:VAL:HB	1.91	0.51
25:LT:43:LYS:O	25:LT:58:HIS:ND1	2.34	0.51
49:S2:74:G:H21	49:S2:75:G:H22	1.59	0.51
50:SA:144:THR:N	50:SA:158:ASP:OD2	2.42	0.51
4:L5:132:G:N2	4:L5:136:C:O2'	2.43	0.51
4:L5:1356:U:O2'	4:L5:1505:C:O2	2.25	0.51
4:L5:4996:C:OP1	35:Ld:32:ARG:NH2	2.43	0.51
6:L8:99:U:O4	41:Lj:65:ARG:NH2	2.43	0.51
8:LB:85:VAL:HG22	8:LB:204:GLN:HG3	1.91	0.51
16:LJ:129:ASP:OD1	16:LJ:129:ASP:N	2.43	0.51
47:Lp:10:ILE:HG23	47:Lp:11:VAL:HG13	1.92	0.51
55:SF:88:MET:HE2	55:SF:91:ARG:HH21	1.75	0.51
57:SH:160:LYS:NZ	57:SH:190:PRO:O	2.35	0.51
59:SJ:37:LEU:HD21	59:SJ:109:ARG:HH22	1.75	0.51
73:SY:29:HIS:HB2	73:SY:32:LYS:HG3	1.92	0.51
4:L5:1958:A:O2'	4:L5:2025:A:N1	2.42	0.51
13:LG:231:ASP:O	13:LG:234:ARG:NH1	2.44	0.51
57:SH:96:ALA:HB3	57:SH:98:ARG:HH21	1.76	0.51
81:Sg:147:HIS:HB2	81:Sg:151:VAL:HG22	1.93	0.51
2:B4:11:C:N4	2:B4:12:G:O6	2.43	0.51
4:L5:1253:G:H1'	4:L5:1257:A:H62	1.76	0.51
23:LR:8:LYS:HA	23:LR:11:ALA:HB3	1.93	0.51
27:LV:48:ARG:NH2	27:LV:49:LEU:O	2.44	0.51
49:S2:1358:U:OP2	52:SC:123:ARG:NH1	2.44	0.51
49:S2:1587:G:C6	68:ST:67:ARG:HD2	2.46	0.51
81:Sg:74:ASP:OD1	81:Sg:74:ASP:N	2.42	0.51
4:L5:1633:G:O4'	7:LA:205:ASN:ND2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4930:C:OP1	11:LE:266:GLN:NE2	2.44	0.51
7:LA:14:SER:OG	7:LA:15:VAL:N	2.42	0.51
9:LC:67:TRP:CD1	9:LC:71:ARG:HG3	2.46	0.51
13:LG:61:ILE:HA	13:LG:64:GLN:HG2	1.93	0.51
15:LI:145:GLU:HA	15:LI:148:VAL:HG12	1.92	0.51
49:S2:1255:G:OP1	49:S2:1256:G:O2'	2.28	0.51
49:S2:1488:C:O2'	49:S2:1490:G:OP2	2.26	0.51
2:B4:5:G:N2	2:B4:67:C:O2'	2.44	0.51
4:L5:97:G:OP1	17:LL:16:LYS:NZ	2.44	0.51
4:L5:430:G:H1	6:L8:4:C:H42	1.57	0.51
4:L5:1432:G:O2'	4:L5:1452:A:N6	2.44	0.51
4:L5:4070:U:O2'	4:L5:4071:U:O4'	2.24	0.51
4:L5:4546:A:N7	7:LA:215:ASN:ND2	2.58	0.51
4:L5:4985:U:O2	8:LB:174:ARG:NH2	2.44	0.51
4:L5:5006:U:H4'	4:L5:5007:A:H5'	1.92	0.51
11:LE:131:LYS:O	11:LE:136:HIS:NE2	2.44	0.51
19:LN:165:THR:O	19:LN:169:ARG:N	2.44	0.51
30:LY:62:TYR:HB3	30:LY:85:VAL:HG11	1.93	0.51
49:S2:14:C:OP1	52:SC:235:ASN:ND2	2.44	0.51
4:L5:504:G:N2	4:L5:656:C:O2'	2.42	0.51
4:L5:977:C:OP2	11:LE:59:ARG:NH1	2.43	0.51
8:LB:190:VAL:HA	8:LB:193:LYS:HG2	1.93	0.51
12:LF:189:ASP:OD1	12:LF:189:ASP:N	2.44	0.51
21:LP:97:ASN:HA	21:LP:100:SER:HB3	1.92	0.51
23:LR:72:LYS:O	23:LR:74:ARG:NH2	2.44	0.51
23:LR:99:MET:HB3	23:LR:103:ARG:HE	1.76	0.51
30:LY:32:SER:OG	30:LY:101:PRO:O	2.22	0.51
46:Lo:51:GLN:NE2	46:Lo:53:LYS:O	2.43	0.51
49:S2:1274:G:H21	60:SK:27:VAL:HB	1.76	0.51
54:SE:92:ILE:HG22	54:SE:94:LYS:H	1.75	0.51
58:SI:191:GLU:O	61:SL:19:ASN:ND2	2.42	0.51
64:SP:31:GLU:HA	64:SP:34:MET:HE3	1.93	0.51
68:ST:76:THR:HG23	68:ST:94:ARG:HH11	1.76	0.51
81:Sg:236:ILE:HD12	81:Sg:239:LEU:HD11	1.92	0.51
3:D4:29:G:N2	3:D4:42:C:O2	2.44	0.50
4:L5:500:G:O2'	4:L5:505:G:OP2	2.28	0.50
4:L5:2695:A:OP1	42:Lk:35:LYS:NZ	2.43	0.50
10:LD:236:MET:HA	10:LD:239:MET:HG3	1.92	0.50
20:LO:39:GLU:OE2	20:LO:107:GLY:N	2.43	0.50
31:LZ:52:LYS:O	31:LZ:65:ARG:NH2	2.42	0.50
4:L5:469:C:N3	11:LE:105:ARG:NH2	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LA:27:ALA:O	7:LA:128:ARG:NH1	2.44	0.50
18:LM:115:ALA:HB1	20:LO:192:TYR:HB3	1.93	0.50
20:LO:168:TYR:HA	20:LO:171:LYS:HG2	1.94	0.50
49:S2:1680:G:OP1	77:Sc:20:ARG:NH2	2.44	0.50
58:SI:40:PRO:HD2	58:SI:59:ARG:HD2	1.92	0.50
58:SI:43:ILE:HG12	58:SI:57:ALA:HA	1.93	0.50
4:L5:419:A:N3	4:L5:1332:C:O2'	2.36	0.50
4:L5:1850:A:N3	4:L5:2283:G:O2'	2.44	0.50
4:L5:4492:U:O2'	4:L5:4512:U:O2	2.25	0.50
5:L7:54:A:O2'	16:LJ:13:ARG:NH2	2.44	0.50
11:LE:149:ILE:HG22	11:LE:163:VAL:HG22	1.93	0.50
27:LV:90:ARG:NH1	27:LV:124:GLU:OE2	2.44	0.50
49:S2:1373:C:OP1	66:SR:7:LYS:N	2.45	0.50
71:SW:30:CYS:SG	71:SW:59:GLY:N	2.82	0.50
4:L5:1617:G:O3'	41:Lj:12:ARG:NH2	2.45	0.50
4:L5:2660:A:OP1	23:LR:117:ARG:NH1	2.44	0.50
4:L5:4620:U:OP2	4:L5:4670:C:N4	2.44	0.50
21:LP:94:MET:HE3	21:LP:148:MET:HE3	1.94	0.50
21:LP:133:HIS:HB2	21:LP:135:ARG:HD3	1.93	0.50
48:Lr:53:PRO:HD3	48:Lr:117:ILE:HD11	1.94	0.50
49:S2:367:U:OP1	58:SI:11:ARG:NH2	2.44	0.50
49:S2:1142:G:N2	49:S2:1145:A:OP2	2.40	0.50
4:L5:2046:G:OP1	20:LO:60:LYS:NZ	2.44	0.50
30:LY:86:GLN:HA	30:LY:96:HIS:HA	1.92	0.50
30:LY:102:SER:OG	30:LY:103:LYS:NZ	2.38	0.50
35:Ld:85:ARG:HG3	35:Ld:109:VAL:HB	1.94	0.50
36:Le:16:ARG:NH2	36:Le:19:LYS:O	2.40	0.50
41:Lj:19:CYS:SG	41:Lj:20:ARG:N	2.84	0.50
41:Lj:22:CYS:HB3	41:Lj:37:CYS:HB3	1.94	0.50
49:S2:1863:A:OP2	75:Sa:4:LYS:NZ	2.42	0.50
54:SE:100:ARG:HH22	54:SE:236:ILE:HG23	1.77	0.50
2:B4:46:U:H5'	2:B4:47:C:H5''	1.92	0.50
4:L5:4290:U:OP1	46:Lo:9:ARG:NH1	2.43	0.50
12:LF:228:VAL:HA	24:LS:39:VAL:HG22	1.93	0.50
26:LU:28:PRO:O	26:LU:32:GLY:N	2.44	0.50
48:Lr:65:LYS:O	48:Lr:102:TYR:OH	2.29	0.50
49:S2:1587:G:OP2	68:ST:67:ARG:NH1	2.40	0.50
81:Sg:300:ALA:HB3	81:Sg:308:ARG:H	1.77	0.50
4:L5:461:G:N2	4:L5:694:C:O2	2.39	0.50
4:L5:1751:A:H4'	15:LI:194:GLY:HA3	1.92	0.50
4:L5:1787:A:N3	4:L5:4210:U:O2'	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2628:U:OP1	26:LU:93:LYS:NZ	2.45	0.50
4:L5:3621:A:HO2'	4:L5:4658:G:HO2'	1.57	0.50
4:L5:3888:G:O6	20:LO:96:GLN:NE2	2.45	0.50
27:LV:30:ASP:HA	27:LV:117:ILE:HG22	1.94	0.50
49:S2:359:U:OP1	72:SX:22:TRP:NE1	2.40	0.50
52:SC:123:ARG:HB2	52:SC:145:LYS:HA	1.94	0.50
53:SD:132:LYS:HG2	53:SD:191:PRO:HA	1.92	0.50
3:D4:75:C:H3'	4:L5:4499:G:H1	1.77	0.50
4:L5:4441:A:H5'	15:LI:102:MET:HE1	1.94	0.50
14:LH:102:ASN:HB3	14:LH:115:ARG:HB2	1.93	0.50
19:LN:116:LEU:O	19:LN:159:ARG:NH1	2.41	0.50
24:LS:41:LYS:HE3	24:LS:61:ILE:HD13	1.93	0.50
49:S2:659:G:H21	72:SX:17:ARG:HH12	1.58	0.50
51:SB:37:ALA:HA	51:SB:42:ARG:HH12	1.74	0.50
66:SR:33:ARG:NH2	81:Sg:107:ASP:OD2	2.44	0.50
78:Sd:49:ASP:OD2	78:Sd:49:ASP:N	2.44	0.50
4:L5:121:A:H62	4:L5:152:U:H3	1.60	0.50
6:L8:36:G:O2'	6:L8:103:A:N1	2.44	0.50
8:LB:65:SER:OG	8:LB:66:LYS:N	2.45	0.50
13:LG:158:ALA:HB2	13:LG:190:LEU:HD12	1.94	0.50
16:LJ:29:SER:HA	16:LJ:33:LEU:HD23	1.93	0.50
32:La:103:VAL:HG22	32:La:108:TYR:HB2	1.93	0.50
43:Ll:21:ARG:NH1	43:Ll:22:PRO:O	2.44	0.50
49:S2:574:A:O2'	49:S2:575:A:O4'	2.30	0.50
59:SJ:124:HIS:CG	79:Se:108:ARG:HE	2.30	0.50
4:L5:1785:C:OP1	15:LI:133:GLN:NE2	2.44	0.49
4:L5:1802:A:H5''	4:L5:1803:G:H5'	1.94	0.49
4:L5:2778:G:N2	6:L8:113:C:OP2	2.43	0.49
19:LN:64:ILE:HD11	19:LN:106:ALA:HB2	1.94	0.49
19:LN:100:SER:OG	19:LN:167:ALA:O	2.30	0.49
48:Lr:91:SER:O	48:Lr:95:HIS:ND1	2.45	0.49
50:SA:5:LEU:O	50:SA:9:GLN:NE2	2.44	0.49
60:SK:58:VAL:HG12	60:SK:71:LEU:HG	1.92	0.49
75:Sa:24:THR:HG21	75:Sa:71:LEU:HB2	1.94	0.49
4:L5:2258:C:O2	11:LE:90:ALA:N	2.45	0.49
4:L5:4940:C:OP1	11:LE:156:ARG:NH1	2.40	0.49
7:LA:5:ILE:HG12	7:LA:8:GLN:HB2	1.94	0.49
8:LB:46:PHE:O	8:LB:347:LEU:N	2.44	0.49
12:LF:214:SER:OG	12:LF:215:SER:N	2.43	0.49
13:LG:141:ASN:HD22	19:LN:3:ALA:H	1.58	0.49
29:LX:77:ILE:HD13	29:LX:100:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1593:C:O2	68:ST:12:GLN:NE2	2.45	0.49
51:SB:49:VAL:HG12	51:SB:65:ARG:HH22	1.76	0.49
59:SJ:68:PRO:O	59:SJ:72:PHE:N	2.44	0.49
76:Sb:35:VAL:HG11	76:Sb:63:LEU:HD21	1.95	0.49
4:L5:1398:A:OP1	32:La:136:LYS:NZ	2.41	0.49
4:L5:1865:G:OP2	15:LI:98:ARG:NH1	2.36	0.49
10:LD:54:ARG:HH12	10:LD:149:GLY:HA3	1.77	0.49
48:Lr:28:GLU:HG2	48:Lr:31:ASN:HB2	1.94	0.49
49:S2:219:U:O2'	58:SI:186:ASP:OD2	2.29	0.49
49:S2:1093:A:H5''	71:SW:28:ARG:HH21	1.77	0.49
49:S2:1580:A:OP1	69:SU:86:LYS:NZ	2.40	0.49
53:SD:74:GLN:HA	53:SD:79:PHE:HB2	1.93	0.49
4:L5:1530:G:O6	4:L5:1643:A:N6	2.45	0.49
4:L5:2517:A:O2'	38:Lg:66:ARG:NH2	2.45	0.49
9:LC:110:ARG:O	9:LC:112:HIS:N	2.46	0.49
10:LD:223:PHE:HB2	10:LD:226:TYR:HB2	1.95	0.49
11:LE:192:LYS:HD3	37:Lf:107:PRO:HB3	1.95	0.49
24:LS:74:ARG:O	24:LS:76:LYS:NZ	2.37	0.49
35:Ld:46:LEU:HD13	35:Ld:72:VAL:HG11	1.94	0.49
37:Lf:4:ARG:NH2	37:Lf:6:TRP:O	2.45	0.49
49:S2:1113:A:N6	49:S2:1114:U:O4	2.44	0.49
55:SF:32:ASP:OD2	55:SF:34:SER:OG	2.31	0.49
4:L5:2479:G:H22	4:L5:2500:U:H1'	1.77	0.49
5:L7:52:C:O2'	5:L7:54:A:N7	2.46	0.49
7:LA:30:ARG:O	7:LA:163:ARG:NH2	2.38	0.49
7:LA:242:ARG:NH1	7:LA:243:THR:O	2.45	0.49
10:LD:42:ASN:ND2	25:LT:69:GLN:OE1	2.43	0.49
49:S2:1013:U:OP1	49:S2:1129:G:O2'	2.27	0.49
4:L5:4670:C:O2'	4:L5:4672:A:OP2	2.28	0.49
4:L5:4771:C:N4	4:L5:4862:G:O6	2.43	0.49
9:LC:235:LEU:HD23	9:LC:240:LEU:HD11	1.94	0.49
9:LC:264:TYR:HB3	9:LC:279:LEU:HD11	1.95	0.49
9:LC:315:LYS:HG3	12:LF:170:THR:HG22	1.94	0.49
14:LH:105:ILE:HD11	14:LH:109:GLY:HA2	1.94	0.49
15:LI:66:GLU:OE2	15:LI:69:ARG:NH1	2.46	0.49
17:LL:116:ARG:HH11	17:LL:155:MET:HB3	1.77	0.49
24:LS:95:ARG:NE	24:LS:97:TYR:OH	2.40	0.49
49:S2:145:G:N7	56:SG:137:ARG:NH2	2.60	0.49
49:S2:1677:U:OP1	55:SF:71:ARG:NH1	2.45	0.49
4:L5:3792:G:O6	4:L5:3807:A:N6	2.45	0.49
4:L5:3930:U:H3	4:L5:4180:G:H1	1.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LB:56:ILE:HD12	8:LB:368:ILE:HG13	1.95	0.49
9:LC:165:LYS:HA	9:LC:168:VAL:HG12	1.94	0.49
10:LD:208:MET:HB2	10:LD:219:TYR:HE1	1.77	0.49
38:Lg:67:LEU:O	38:Lg:72:LYS:NZ	2.46	0.49
50:SA:146:ALA:HB2	50:SA:157:VAL:HG21	1.93	0.49
71:SW:49:GLU:O	71:SW:64:ASN:ND2	2.45	0.49
72:SX:73:GLN:HA	72:SX:80:LYS:HA	1.95	0.49
4:L5:1952:G:H4'	24:LS:93:MET:HE3	1.93	0.49
4:L5:4220:A:H2'	4:L5:4222:G:H5''	1.95	0.49
17:LL:107:THR:OG1	40:Li:20:ASN:ND2	2.45	0.49
30:LY:69:LYS:H	30:LY:83:GLU:HG2	1.76	0.49
47:Lp:21:SER:HA	47:Lp:24:LYS:HG2	1.95	0.49
51:SB:30:TRP:O	51:SB:94:LYS:NZ	2.41	0.49
56:SG:136:LYS:HZ2	56:SG:174:PRO:HB2	1.78	0.49
65:SQ:21:ALA:HB2	65:SQ:72:VAL:HG13	1.95	0.49
4:L5:364:G:N7	41:Lj:55:ARG:NH1	2.61	0.49
4:L5:2575:U:H3'	31:LZ:48:ARG:HH22	1.78	0.49
24:LS:36:ASN:OD1	24:LS:36:ASN:N	2.45	0.49
53:SD:37:VAL:HG22	53:SD:50:ILE:HA	1.94	0.49
72:SX:63:ASN:HD21	72:SX:67:ARG:HH11	1.61	0.49
76:Sb:67:THR:HG23	76:Sb:69:GLY:H	1.77	0.49
81:Sg:168:CYS:SG	81:Sg:169:GLY:N	2.86	0.49
81:Sg:289:LEU:HD21	81:Sg:298:LEU:HD12	1.95	0.49
4:L5:1836:G:O2'	25:LT:108:ARG:NH2	2.46	0.49
4:L5:3661:G:N7	7:LA:152:SER:OG	2.41	0.49
4:L5:4879:C:H5''	18:LM:120:ASN:HD21	1.77	0.49
10:LD:194:VAL:HA	10:LD:197:LYS:HG2	1.94	0.49
31:LZ:16:GLY:O	31:LZ:19:SER:OG	2.31	0.49
32:La:115:GLY:O	32:La:136:LYS:NZ	2.42	0.49
49:S2:918:U:OP1	62:SN:64:ARG:NH2	2.46	0.49
79:Se:107:ARG:NH1	79:Se:110:GLN:OE1	2.46	0.49
4:L5:62:A:H5''	19:LN:174:LEU:HD21	1.94	0.48
4:L5:188:G:N2	4:L5:191:G:N7	2.60	0.48
4:L5:2265:G:OP1	48:Lr:33:LYS:NZ	2.46	0.48
51:SB:37:ALA:HB2	51:SB:42:ARG:HH22	1.77	0.48
71:SW:86:LEU:HD22	71:SW:117:ARG:HH21	1.78	0.48
4:L5:1308:C:O2'	37:Lf:94:ALA:O	2.31	0.48
4:L5:4415:A:O2'	15:LI:74:LYS:NZ	2.39	0.48
9:LC:18:SER:OG	9:LC:20:LYS:NZ	2.43	0.48
12:LF:113:ARG:NH1	12:LF:206:ASN:OD1	2.46	0.48
19:LN:108:ARG:NH2	19:LN:161:MET:SD	2.87	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Li:35:LYS:HA	40:Li:38:LYS:HE3	1.95	0.48
43:Li:16:LYS:NZ	43:Li:19:GLN:OE1	2.43	0.48
49:S2:452:G:O2'	56:SG:91:GLU:OE1	2.28	0.48
49:S2:594:A:H4'	49:S2:595:U:H5'	1.95	0.48
49:S2:692:G:N2	49:S2:739:C:O2	2.46	0.48
56:SG:70:HIS:HA	56:SG:99:GLY:HA3	1.95	0.48
59:SJ:60:LEU:HD11	59:SJ:70:ARG:HA	1.94	0.48
67:SS:72:GLN:NE2	67:SS:73:ASN:OD1	2.46	0.48
69:SU:40:ILE:HD11	69:SU:89:ILE:HD12	1.94	0.48
4:L5:4868:G:O2'	4:L5:4872:G:OP1	2.31	0.48
7:LA:94:ALA:HB3	7:LA:102:LEU:HD13	1.94	0.48
9:LC:288:ASP:OD1	9:LC:288:ASP:N	2.41	0.48
49:S2:1864:U:H5'	75:Sa:79:ILE:HD11	1.96	0.48
56:SG:70:HIS:HB2	56:SG:98:ARG:HH22	1.78	0.48
73:SY:41:ARG:NE	73:SY:55:ILE:O	2.40	0.48
4:L5:509:A:N6	32:La:102:ASP:O	2.35	0.48
4:L5:2897:G:H4'	23:LR:101:ILE:HD11	1.94	0.48
8:LB:94:GLU:HA	8:LB:99:LEU:HA	1.96	0.48
12:LF:149:SER:HB3	12:LF:244:ILE:HD11	1.95	0.48
49:S2:886:A:H2	49:S2:900:C:H41	1.61	0.48
49:S2:1600:G:OP1	74:SZ:44:LEU:N	2.47	0.48
52:SC:241:PHE:HA	52:SC:244:ILE:HG22	1.94	0.48
58:SI:177:SER:OG	58:SI:182:CYS:SG	2.71	0.48
66:SR:31:ASN:HD22	66:SR:55:THR:HG22	1.79	0.48
67:SS:86:ARG:HD2	67:SS:89:ASP:HA	1.94	0.48
4:L5:5016:A:N6	4:L5:5033:G:O2'	2.45	0.48
6:L8:151:G:O4'	13:LG:64:GLN:NE2	2.46	0.48
11:LE:66:LYS:O	11:LE:71:ARG:NH1	2.46	0.48
49:S2:828:G:N2	49:S2:830:A:O2'	2.41	0.48
49:S2:1229:G:HO2'	49:S2:1607:A:HO2'	1.59	0.48
49:S2:1611:G:N2	67:SS:87:GLN:OE1	2.46	0.48
71:SW:102:ILE:HG13	71:SW:113:HIS:HB3	1.95	0.48
2:B4:74:C:O2'	46:Lo:54:PRO:O	2.31	0.48
4:L5:4459:U:O2'	8:LB:265:SER:OG	2.32	0.48
11:LE:164:PHE:HA	11:LE:175:VAL:HG23	1.96	0.48
46:Lo:8:ARG:O	46:Lo:21:HIS:N	2.47	0.48
49:S2:363:A:N6	49:S2:400:C:O2'	2.46	0.48
71:SW:111:MET:HB2	71:SW:115:GLU:HB3	1.96	0.48
4:L5:2443:G:OP2	4:L5:2516:G:N2	2.40	0.48
23:LR:157:ASP:O	23:LR:161:ALA:N	2.46	0.48
49:S2:463:C:O2'	49:S2:466:G:O6	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SK:34:GLU:HA	60:SK:35:LEU:HA	1.65	0.48
61:SL:13:GLN:HE22	61:SL:35:ARG:HB3	1.78	0.48
75:Sa:79:ILE:HG12	75:Sa:84:VAL:HG13	1.96	0.48
81:Sg:165:ILE:HB	81:Sg:177:TRP:HB2	1.96	0.48
4:L5:159:C:O2	17:LL:88:LYS:NZ	2.43	0.48
4:L5:1481:C:O2'	4:L5:1482:G:O4'	2.32	0.48
4:L5:3641:U:H5''	4:L5:3642:A:H5''	1.96	0.48
4:L5:4122:G:N2	38:Lg:98:GLU:OE2	2.41	0.48
19:LN:28:TRP:HA	19:LN:31:ARG:HE	1.79	0.48
24:LS:127:MET:HB3	25:LT:153:PRO:HG2	1.95	0.48
57:SH:126:HIS:O	57:SH:177:TYR:OH	2.32	0.48
4:L5:2840:A:H61	4:L5:3848:U:H3	1.61	0.48
29:LX:99:ILE:HA	29:LX:135:LYS:HA	1.96	0.48
30:LY:70:VAL:HA	30:LY:82:ILE:HA	1.96	0.48
49:S2:57:U:O2'	49:S2:499:G:N3	2.45	0.48
49:S2:628:A:N6	49:S2:1500:G:O2'	2.46	0.48
49:S2:1617:G:O6	64:SP:47:ARG:NH1	2.46	0.48
81:Sg:124:SER:O	81:Sg:125:ARG:NH1	2.47	0.48
4:L5:1351:G:OP1	9:LC:33:ARG:NH2	2.41	0.48
4:L5:1554:A:OP1	47:Lp:5:THR:OG1	2.29	0.48
12:LF:148:LYS:HD3	12:LF:245:ARG:HH11	1.79	0.48
14:LH:16:VAL:HG11	14:LH:81:ILE:HD12	1.95	0.48
49:S2:616:A:H61	49:S2:629:A:H61	1.61	0.48
50:SA:164:ASN:O	50:SA:170:SER:OG	2.32	0.48
4:L5:407:A:O2'	4:L5:410:A:OP1	2.32	0.47
4:L5:2097:U:O4	12:LF:39:GLN:NE2	2.47	0.47
4:L5:4208:U:OP1	4:L5:4334:U:O2'	2.25	0.47
4:L5:4568:A:O2'	4:L5:4981:G:N7	2.47	0.47
4:L5:4881:U:OP2	18:LM:117:LYS:NZ	2.46	0.47
5:L7:49:A:N6	10:LD:57:ASN:O	2.47	0.47
49:S2:1579:A:H4'	49:S2:1581:C:H5	1.79	0.47
4:L5:3661:G:N2	4:L5:3681:G:O2'	2.45	0.47
6:L8:98:C:OP2	29:LX:67:ARG:NH1	2.45	0.47
8:LB:280:ILE:HG13	8:LB:281:ASN:HB2	1.97	0.47
16:LJ:19:LYS:HB3	16:LJ:75:ARG:HG2	1.95	0.47
20:LO:7:LEU:HG	20:LO:33:VAL:HG12	1.96	0.47
29:LX:80:PRO:HA	29:LX:98:PHE:HA	1.96	0.47
48:Lr:21:ASN:N	48:Lr:21:ASN:OD1	2.46	0.47
49:S2:1409:A:H61	49:S2:1432:U:H3	1.61	0.47
49:S2:1513:C:H2'	49:S2:1514:G:H8	1.79	0.47
50:SA:85:ARG:NH2	66:SR:81:ARG:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SA:138:SER:O	50:SA:138:SER:OG	2.31	0.47
67:SS:102:GLY:HA2	67:SS:105:ASN:HD21	1.79	0.47
4:L5:67:C:N4	4:L5:325:U:O3'	2.45	0.47
4:L5:1311:G:O3'	36:Le:50:LYS:NZ	2.47	0.47
4:L5:2303:C:OP1	36:Le:107:ASN:ND2	2.40	0.47
4:L5:3896:C:O2'	8:LB:268:ARG:NH2	2.46	0.47
9:LC:337:ARG:NH1	11:LE:55:GLY:O	2.46	0.47
43:L1:44:TRP:O	43:L1:48:LYS:NZ	2.39	0.47
49:S2:581:U:OP1	59:SJ:133:ARG:NH2	2.47	0.47
49:S2:644:G:H5'	59:SJ:41:ARG:HH22	1.78	0.47
49:S2:1138:C:OP1	50:SA:155:ARG:NH2	2.46	0.47
49:S2:1216:C:O2'	49:S2:1644:C:OP1	2.32	0.47
54:SE:13:ALA:O	54:SE:39:ARG:NH2	2.47	0.47
62:SN:25:TRP:CD1	62:SN:25:TRP:H	2.32	0.47
81:Sg:42:MET:O	81:Sg:56:GLN:N	2.42	0.47
4:L5:513:U:O2'	4:L5:647:G:N2	2.48	0.47
4:L5:1925:G:O3'	24:LS:116:ARG:NH2	2.47	0.47
4:L5:2529:A:O2'	4:L5:2531:C:OP2	2.32	0.47
4:L5:2562:G:N2	4:L5:2565:A:O5'	2.47	0.47
25:LT:3:ASN:N	25:LT:3:ASN:OD1	2.48	0.47
46:Lo:11:PHE:O	46:Lo:81:ARG:NH1	2.43	0.47
49:S2:323:C:O2	49:S2:329:G:N2	2.47	0.47
55:SF:19:LEU:HD22	55:SF:24:SER:HA	1.97	0.47
61:SL:5:GLN:HE22	61:SL:11:GLN:H	1.63	0.47
67:SS:16:LEU:HD22	67:SS:68:ILE:HD11	1.96	0.47
4:L5:1440:U:H3	4:L5:2105:A:H2	1.62	0.47
4:L5:2084:C:C4	22:LQ:14:ARG:HD2	2.50	0.47
49:S2:27:A:O2'	49:S2:483:C:O2'	2.31	0.47
49:S2:595:U:O2'	49:S2:596:U:O4'	2.32	0.47
49:S2:881:G:N1	49:S2:906:U:O2	2.42	0.47
49:S2:1568:C:O2	49:S2:1627:C:O2'	2.28	0.47
53:SD:132:LYS:HD3	53:SD:156:LEU:HD21	1.96	0.47
59:SJ:75:ASN:HA	59:SJ:78:LEU:HB2	1.96	0.47
61:SL:120:VAL:HG12	61:SL:145:VAL:HG21	1.94	0.47
74:SZ:68:ILE:HG22	74:SZ:88:LEU:HD22	1.97	0.47
81:Sg:121:VAL:HA	81:Sg:131:LEU:HA	1.95	0.47
4:L5:1516:G:O2'	17:LL:18:TRP:NE1	2.46	0.47
18:LM:11:ARG:HG2	18:LM:57:LEU:HD12	1.96	0.47
54:SE:195:ILE:HG22	54:SE:197:ASN:H	1.79	0.47
60:SK:4:PRO:HG2	60:SK:8:ARG:HD2	1.95	0.47
4:L5:1759:G:H1	4:L5:1773:U:H3	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1889:U:OP2	4:L5:1890:G:N2	2.48	0.47
4:L5:3680:U:OP1	7:LA:54:ARG:NH2	2.47	0.47
4:L5:4304:A:OP2	4:L5:4305:G:N2	2.47	0.47
6:L8:83:C:O2	6:L8:87:G:N2	2.47	0.47
12:LF:221:LYS:NZ	12:LF:230:GLY:O	2.47	0.47
13:LG:57:TRP:HB3	13:LG:61:ILE:HG23	1.97	0.47
13:LG:137:ARG:HH11	13:LG:146:LEU:HD21	1.79	0.47
15:LI:36:LEU:HD13	15:LI:87:MET:HE3	1.95	0.47
17:LL:50:PRO:HA	17:LL:150:LEU:HB3	1.96	0.47
23:LR:62:ARG:O	23:LR:66:ASN:ND2	2.47	0.47
24:LS:18:PRO:HA	24:LS:25:PRO:HG3	1.97	0.47
24:LS:99:ASP:OD1	24:LS:100:LEU:N	2.48	0.47
29:LX:153:ILE:HG13	29:LX:155:ILE:HG23	1.97	0.47
34:Lc:30:GLY:O	34:Lc:34:THR:OG1	2.30	0.47
42:Lk:37:ARG:HH11	42:Lk:42:LEU:HB2	1.80	0.47
47:Lp:2:ALA:N	47:Lp:5:THR:O	2.47	0.47
49:S2:293:C:H4'	61:SL:38:LYS:HZ2	1.79	0.47
49:S2:688:U:OP1	57:SH:116:ARG:NH2	2.45	0.47
49:S2:946:U:O2'	49:S2:1046:U:OP1	2.31	0.47
49:S2:1570:G:N7	68:ST:97:LYS:NZ	2.55	0.47
51:SB:71:LEU:HA	51:SB:74:LEU:HD12	1.97	0.47
57:SH:50:GLU:HG2	57:SH:60:ILE:HB	1.97	0.47
2:B4:30:G:HO2'	49:S2:1641:A:HO2'	1.57	0.47
4:L5:1270:A:N6	4:L5:2107:C:O3'	2.48	0.47
46:Lo:78:ARG:HD3	46:Lo:78:ARG:HA	1.69	0.47
48:Lr:46:ARG:HE	48:Lr:46:ARG:HB3	1.53	0.47
49:S2:1745:A:H8	56:SG:66:GLY:HA3	1.79	0.47
69:SU:33:GLU:OE2	69:SU:87:ARG:NE	2.39	0.47
4:L5:1279:A:O2'	4:L5:1281:G:N7	2.47	0.47
4:L5:1931:C:N4	4:L5:2040:A:O2'	2.48	0.47
11:LE:62:MET:HE3	11:LE:66:LYS:HD3	1.97	0.47
40:Li:68:ARG:NH1	40:Li:68:ARG:O	2.48	0.47
49:S2:1523:C:H2'	49:S2:1524:G:H8	1.80	0.47
50:SA:106:GLY:O	50:SA:110:ASN:N	2.47	0.47
59:SJ:67:ASP:OD2	59:SJ:70:ARG:N	2.41	0.47
70:SV:14:PRO:HG2	70:SV:23:ILE:HD11	1.96	0.47
71:SW:25:VAL:HG22	71:SW:63:VAL:HG12	1.95	0.47
78:Sd:25:SER:O	78:Sd:25:SER:OG	2.31	0.47
4:L5:2901:G:H1	4:L5:3598:C:N4	2.11	0.47
27:LV:101:ASN:OD1	27:LV:101:ASN:N	2.45	0.47
40:Li:51:ALA:N	40:Li:54:GLU:OE2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1087:A:OP1	75:Sa:3:LYS:NZ	2.42	0.47
49:S2:1610:G:OP2	67:SS:132:ARG:NH1	2.34	0.47
4:L5:73:A:H62	17:LL:103:ARG:HH22	1.64	0.46
4:L5:356:G:O2'	6:L8:25:G:N3	2.47	0.46
4:L5:679:C:H2'	4:L5:680:G:H8	1.80	0.46
18:LM:127:VAL:O	18:LM:131:GLN:N	2.48	0.46
24:LS:85:ASP:HA	24:LS:90:THR:HA	1.96	0.46
29:LX:120:ASP:N	29:LX:144:TYR:OH	2.46	0.46
37:Lf:50:VAL:HG22	37:Lf:69:VAL:HG12	1.97	0.46
49:S2:1:U:O2'	49:S2:3:C:N4	2.47	0.46
55:SF:77:MET:HG2	55:SF:89:THR:HG21	1.98	0.46
81:Sg:7:LEU:HA	81:Sg:310:TRP:CD1	2.51	0.46
81:Sg:191:HIS:NE2	81:Sg:209:SER:O	2.46	0.46
4:L5:1279:A:H1'	9:LC:323:ARG:HH12	1.81	0.46
4:L5:1480:C:O2'	4:L5:1482:G:OP2	2.31	0.46
4:L5:4715:C:H5''	8:LB:278:THR:HG21	1.97	0.46
5:L7:50:A:OP1	10:LD:224:SER:OG	2.28	0.46
10:LD:40:ASP:OD1	10:LD:40:ASP:N	2.48	0.46
10:LD:80:ALA:HB1	10:LD:92:LEU:HD22	1.96	0.46
34:Lc:55:LEU:O	34:Lc:59:GLU:N	2.47	0.46
49:S2:354:U:OP1	61:SL:90:ARG:NH1	2.48	0.46
49:S2:1549:U:OP1	78:Sd:34:TYR:OH	2.33	0.46
49:S2:1569:A:O2'	49:S2:1626:C:O2	2.33	0.46
54:SE:125:LYS:NZ	54:SE:157:ASN:O	2.46	0.46
64:SP:29:SER:OG	64:SP:30:TYR:N	2.47	0.46
65:SQ:96:TYR:HA	65:SQ:100:VAL:HG12	1.97	0.46
4:L5:440:U:O2'	37:Lf:91:ASN:O	2.34	0.46
4:L5:2298:U:O4	9:LC:188:ARG:NH2	2.48	0.46
5:L7:38:U:N3	5:L7:41:G:OP2	2.39	0.46
7:LA:210:PRO:O	7:LA:221:LYS:NZ	2.38	0.46
42:Lk:5:ILE:HD12	42:Lk:11:PHE:HD1	1.80	0.46
49:S2:429:C:H5''	54:SE:10:LYS:HG3	1.97	0.46
49:S2:1258:A:N7	49:S2:1659:U:O2'	2.42	0.46
49:S2:1314:U:O2'	60:SK:8:ARG:NH1	2.46	0.46
52:SC:206:SER:OG	52:SC:207:ALA:N	2.48	0.46
68:ST:77:LYS:HG3	68:ST:94:ARG:HH12	1.81	0.46
7:LA:101:VAL:HG12	7:LA:165:VAL:HG12	1.96	0.46
8:LB:378:ARG:NH1	28:LW:33:ASN:OD1	2.49	0.46
11:LE:162:VAL:HG22	11:LE:175:VAL:HG22	1.97	0.46
16:LJ:103:GLY:HA3	16:LJ:157:ILE:HG22	1.97	0.46
49:S2:560:A:H5'	59:SJ:174:LYS:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1378:A:OP2	50:SA:102:ARG:NH2	2.43	0.46
51:SB:136:ARG:HH11	51:SB:218:LEU:HD21	1.80	0.46
57:SH:52:GLU:HA	57:SH:58:LYS:HB2	1.98	0.46
69:SU:37:ALA:O	69:SU:41:ARG:N	2.40	0.46
81:Sg:86:THR:HG21	81:Sg:100:ARG:HH22	1.81	0.46
4:L5:1753:G:O6	4:L5:1776:A:N6	2.49	0.46
4:L5:4237:C:O3'	4:L5:4326:G:N2	2.49	0.46
4:L5:4899:G:N2	4:L5:4922:C:O2'	2.48	0.46
11:LE:62:MET:HG3	11:LE:66:LYS:HE2	1.97	0.46
16:LJ:18:ARG:H	16:LJ:134:LEU:HA	1.80	0.46
27:LV:48:ARG:HG3	27:LV:49:LEU:H	1.80	0.46
49:S2:520:A:O2'	49:S2:825:A:N3	2.45	0.46
49:S2:737:G:H8	49:S2:738:C:H4'	1.80	0.46
57:SH:100:ILE:HG12	57:SH:125:VAL:HG21	1.96	0.46
81:Sg:215:GLN:HA	81:Sg:230:LEU:HG	1.97	0.46
4:L5:457:G:H5''	11:LE:115:TYR:HB3	1.97	0.46
4:L5:2097:U:OP2	12:LF:35:LYS:NZ	2.37	0.46
4:L5:4622:A:H4'	8:LB:13:SER:HB2	1.97	0.46
4:L5:4906:C:H2'	4:L5:4907:G:C8	2.50	0.46
24:LS:143:LYS:HA	24:LS:146:HIS:CD2	2.49	0.46
34:Lc:34:THR:HG23	34:Lc:95:ALA:HB2	1.97	0.46
40:Li:65:LYS:HE2	40:Li:65:LYS:HB3	1.78	0.46
49:S2:189:U:H3	49:S2:210:U:H3	1.64	0.46
49:S2:1036:A:N3	49:S2:1844:U:O2'	2.42	0.46
49:S2:1155:U:OP2	52:SC:194:ARG:NH2	2.48	0.46
49:S2:1617:G:N1	49:S2:1620:A:OP2	2.43	0.46
49:S2:1737:G:OP1	56:SG:94:ARG:NH2	2.42	0.46
50:SA:52:LYS:NZ	70:SV:82:ASN:O	2.44	0.46
58:SI:174:CYS:SG	58:SI:175:ILE:N	2.88	0.46
81:Sg:133:ASN:HD21	81:Sg:137:VAL:HG22	1.81	0.46
4:L5:1279:A:O3'	9:LC:323:ARG:NH1	2.48	0.46
4:L5:1590:C:H4'	4:L5:2857:A:H5'	1.97	0.46
7:LA:136:VAL:HA	7:LA:148:VAL:HG12	1.97	0.46
10:LD:52:ILE:HD11	10:LD:63:GLN:HE21	1.80	0.46
49:S2:885:U:O2	49:S2:902:G:N1	2.48	0.46
49:S2:964:A:N3	49:S2:1054:G:O2'	2.43	0.46
49:S2:1459:G:H1	49:S2:1467:C:H42	1.64	0.46
49:S2:1674:G:H5'	55:SF:86:LYS:HD3	1.98	0.46
58:SI:172:LEU:HD11	58:SI:195:LEU:HD13	1.96	0.46
64:SP:38:SER:H	64:SP:42:ARG:HH21	1.62	0.46
73:SY:15:ASN:HB3	73:SY:20:ARG:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2793:G:H4'	41:Lj:8:PHE:HD2	1.80	0.46
4:L5:4081:G:H2'	4:L5:4082:G:H8	1.81	0.46
4:L5:4633:G:N2	4:L5:4664:A:N7	2.64	0.46
4:L5:5026:U:O2	58:SI:167:GLN:NE2	2.48	0.46
7:LA:89:TYR:N	7:LA:100:ASN:OD1	2.42	0.46
9:LC:118:THR:O	9:LC:122:TYR:N	2.48	0.46
22:LQ:48:LEU:HA	22:LQ:51:LEU:HD23	1.97	0.46
25:LT:114:GLN:HA	25:LT:117:LYS:HE2	1.98	0.46
49:S2:1647:A:OP1	65:SQ:138:ARG:NH2	2.42	0.46
71:SW:80:ASP:OD1	71:SW:80:ASP:N	2.49	0.46
75:Sa:23:CYS:HB3	75:Sa:28:ARG:H	1.80	0.46
77:Sc:10:LYS:HB3	77:Sc:10:LYS:HE2	1.79	0.46
4:L5:2573:A:O3'	31:LZ:115:LYS:NZ	2.47	0.46
20:LO:174:LEU:O	20:LO:178:ARG:N	2.48	0.46
30:LY:43:ASN:ND2	30:LY:127:GLN:OE1	2.48	0.46
49:S2:73:C:N4	49:S2:79:A:O4'	2.48	0.46
49:S2:809:A:HO2'	54:SE:221:ARG:HH12	1.59	0.46
49:S2:1226:G:N1	49:S2:1639:G:OP2	2.49	0.46
58:SI:110:ARG:HB2	58:SI:121:LEU:HD13	1.97	0.46
64:SP:127:LYS:HD3	64:SP:127:LYS:HA	1.73	0.46
71:SW:115:GLU:OE2	71:SW:119:LYS:NZ	2.47	0.46
4:L5:1771:U:O2'	4:L5:1772:C:O4'	2.34	0.46
4:L5:1915:C:OP2	20:LO:94:ARG:NH2	2.49	0.46
23:LR:103:ARG:NH1	23:LR:124:TYR:OH	2.48	0.46
38:Lg:60:ARG:HD2	38:Lg:60:ARG:HA	1.70	0.46
49:S2:10:G:H21	52:SC:114:LYS:HA	1.81	0.46
49:S2:527:C:H4'	59:SJ:121:LYS:HD3	1.97	0.46
49:S2:1579:A:O2'	49:S2:1582:C:N4	2.49	0.46
4:L5:119:G:C6	13:LG:132:ARG:HG3	2.51	0.45
4:L5:1309:C:H5''	20:LO:94:ARG:HB2	1.98	0.45
4:L5:2299:G:OP1	9:LC:182:LYS:NZ	2.42	0.45
9:LC:157:LYS:HE3	9:LC:157:LYS:HB2	1.77	0.45
10:LD:104:LEU:HB2	10:LD:247:ILE:HD11	1.98	0.45
13:LG:153:GLN:HE22	13:LG:206:GLN:H	1.63	0.45
47:Lp:49:ARG:HE	47:Lp:52:VAL:HA	1.82	0.45
49:S2:190:G:H3'	58:SI:145:ILE:HG13	1.98	0.45
59:SJ:75:ASN:O	59:SJ:79:ARG:N	2.44	0.45
59:SJ:88:ASP:OD1	59:SJ:88:ASP:N	2.42	0.45
62:SN:127:ARG:HA	62:SN:130:LYS:HG2	1.97	0.45
63:SO:94:HIS:ND1	63:SO:127:GLY:O	2.49	0.45
81:Sg:106:LYS:HE3	81:Sg:126:ASP:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:989:U:O2'	4:L5:990:C:O4'	2.29	0.45
4:L5:1326:A:OP2	4:L5:4445:U:O2'	2.31	0.45
4:L5:2052:G:O5'	20:LO:83:THR:OG1	2.28	0.45
7:LA:246:LEU:HB3	7:LA:247:ARG:H	1.64	0.45
9:LC:338:ASN:O	9:LC:342:ARG:NH1	2.48	0.45
22:LQ:18:PRO:O	22:LQ:26:ARG:NH1	2.48	0.45
37:Lf:28:LEU:HD22	37:Lf:101:ILE:HG21	1.98	0.45
42:Lk:33:LYS:HG2	42:Lk:46:VAL:HG12	1.98	0.45
49:S2:958:G:N2	63:SO:68:GLU:OE1	2.49	0.45
57:SH:24:SER:O	57:SH:28:LEU:N	2.48	0.45
59:SJ:108:ARG:HH11	59:SJ:113:GLN:HE22	1.64	0.45
64:SP:18:ARG:HE	67:SS:90:VAL:HG23	1.81	0.45
65:SQ:34:VAL:HG22	65:SQ:70:VAL:HB	1.98	0.45
70:SV:17:CYS:HB3	70:SV:22:ARG:H	1.81	0.45
76:Sb:21:LYS:HB3	76:Sb:26:GLN:HE22	1.81	0.45
81:Sg:110:SER:HB3	81:Sg:153:CYS:HB3	1.98	0.45
4:L5:1646:A:O2'	41:Lj:49:TRP:O	2.31	0.45
4:L5:1758:G:H2'	4:L5:1759:G:C8	2.51	0.45
4:L5:2900:U:O2	4:L5:3600:G:N2	2.50	0.45
13:LG:78:PRO:HB3	13:LG:236:HIS:H	1.81	0.45
19:LN:34:SER:OG	19:LN:35:ALA:N	2.48	0.45
49:S2:387:C:OP2	58:SI:10:LYS:NZ	2.49	0.45
50:SA:176:TRP:O	50:SA:180:ARG:N	2.45	0.45
54:SE:37:LYS:N	54:SE:40:GLU:OE2	2.48	0.45
57:SH:44:ASN:OD1	57:SH:44:ASN:N	2.48	0.45
60:SK:24:LYS:HA	60:SK:66:HIS:HA	1.97	0.45
66:SR:43:SER:HB3	66:SR:46:LEU:HB2	1.99	0.45
71:SW:86:LEU:HD21	71:SW:113:HIS:HB2	1.99	0.45
81:Sg:17:TRP:H	81:Sg:36:ARG:H	1.63	0.45
4:L5:29:G:H5''	19:LN:172:ARG:HG2	1.98	0.45
4:L5:4116:C:O2'	13:LG:43:GLN:NE2	2.45	0.45
8:LB:339:GLY:HA3	8:LB:343:ARG:HG2	1.99	0.45
13:LG:148:GLU:OE2	19:LN:6:TYR:OH	2.28	0.45
22:LQ:106:THR:O	22:LQ:110:ARG:N	2.50	0.45
27:LV:64:THR:HG22	27:LV:76:VAL:HA	1.99	0.45
46:Lo:23:VAL:HG12	46:Lo:70:LEU:HB3	1.98	0.45
49:S2:312:G:H5'	56:SG:191:ARG:HH21	1.80	0.45
49:S2:1718:G:O2'	49:S2:1815:A:N6	2.50	0.45
58:SI:36:THR:O	58:SI:96:LEU:N	2.39	0.45
64:SP:34:MET:HB3	64:SP:45:LEU:HD11	1.97	0.45
75:Sa:74:CYS:SG	75:Sa:75:VAL:N	2.90	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Sg:38:LYS:HA	81:Sg:66:VAL:H	1.81	0.45
4:L5:976:G:H4'	9:LC:326:LEU:HD11	1.98	0.45
12:LF:238:ASP:OD1	12:LF:239:GLN:NE2	2.45	0.45
16:LJ:52:LYS:HA	16:LJ:67:LYS:HA	1.99	0.45
18:LM:99:GLU:O	18:LM:103:LYS:NZ	2.42	0.45
42:Lk:24:LYS:HD2	42:Lk:69:LEU:HD11	1.99	0.45
49:S2:64:A:N6	49:S2:83:A:OP2	2.39	0.45
49:S2:414:A:OP1	49:S2:814:U:O2'	2.31	0.45
49:S2:1620:A:H5'	64:SP:40:ARG:HH11	1.82	0.45
55:SF:100:ILE:HG23	55:SF:178:ILE:HD11	1.98	0.45
59:SJ:64:ASP:OD1	59:SJ:65:GLU:N	2.50	0.45
59:SJ:83:ARG:O	59:SJ:151:LEU:N	2.45	0.45
65:SQ:25:CYS:HB3	65:SQ:68:ILE:HD12	1.97	0.45
81:Sg:24:THR:OG1	81:Sg:27:PHE:O	2.32	0.45
81:Sg:109:LEU:HG	81:Sg:125:ARG:HH21	1.81	0.45
4:L5:1267:C:OP2	4:L5:2121:C:N4	2.33	0.45
4:L5:4759:C:OP2	20:LO:171:LYS:NZ	2.41	0.45
9:LC:37:VAL:HG11	9:LC:246:VAL:HG22	1.98	0.45
16:LJ:146:ARG:HG2	16:LJ:147:ARG:HG3	1.99	0.45
17:LL:19:GLN:HA	17:LL:22:VAL:HG23	1.99	0.45
27:LV:82:ILE:HB	27:LV:121:VAL:HG23	1.98	0.45
55:SF:111:VAL:HA	55:SF:114:ASN:HD22	1.81	0.45
61:SL:77:VAL:HA	61:SL:88:ILE:HA	1.98	0.45
62:SN:12:SER:O	62:SN:12:SER:OG	2.34	0.45
63:SO:31:CYS:HB3	63:SO:95:ILE:HD13	1.97	0.45
80:Sf:53:ALA:HB1	80:Sf:80:ASP:H	1.81	0.45
4:L5:2474:G:N2	4:L5:2502:G:O2'	2.49	0.45
11:LE:273:SER:OG	11:LE:274:VAL:N	2.50	0.45
14:LH:123:ILE:HD12	14:LH:125:ARG:HH11	1.81	0.45
30:LY:23:SER:O	30:LY:23:SER:OG	2.30	0.45
34:Lc:101:ASP:OD1	34:Lc:101:ASP:N	2.46	0.45
49:S2:806:U:H2'	49:S2:807:G:H8	1.81	0.45
49:S2:816:A:OP2	59:SJ:10:ARG:NH2	2.50	0.45
51:SB:198:GLU:HB2	51:SB:210:VAL:HG21	1.98	0.45
53:SD:100:ALA:O	53:SD:104:SER:OG	2.31	0.45
53:SD:167:TYR:O	53:SD:190:LEU:N	2.47	0.45
58:SI:36:THR:OG1	58:SI:96:LEU:O	2.34	0.45
65:SQ:23:ALA:HB1	65:SQ:68:ILE:HD11	1.99	0.45
4:L5:945:U:OP1	9:LC:342:ARG:NH2	2.35	0.45
10:LD:17:GLN:NE2	25:LT:22:HIS:O	2.48	0.45
34:Lc:90:ARG:HH12	47:Lp:44:LYS:HG2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:433:A:H5''	58:SI:22:HIS:HB3	1.99	0.45
49:S2:595:U:O4	49:S2:641:A:N6	2.50	0.45
49:S2:1495:G:O2'	78:Sd:24:CYS:SG	2.73	0.45
49:S2:1617:G:N7	64:SP:47:ARG:NH2	2.53	0.45
51:SB:65:ARG:NH1	63:SO:51:GLU:OE2	2.50	0.45
54:SE:51:ARG:NH1	54:SE:109:PHE:O	2.47	0.45
12:LF:232:ASP:OD1	12:LF:232:ASP:N	2.48	0.45
13:LG:139:GLY:O	13:LG:201:THR:OG1	2.34	0.45
15:LI:150:GLU:HA	15:LI:153:ARG:HG2	1.98	0.45
21:LP:84:PRO:HB2	21:LP:87:SER:HB3	1.99	0.45
26:LU:80:LYS:HZ1	26:LU:109:SER:H	1.63	0.45
34:Lc:56:ARG:HA	34:Lc:59:GLU:HG2	1.98	0.45
48:Lr:39:ARG:HH12	48:Lr:105:ASP:HB2	1.81	0.45
50:SA:147:LEU:HD12	50:SA:161:ILE:HB	1.99	0.45
51:SB:42:ARG:HD3	51:SB:42:ARG:HA	1.81	0.45
55:SF:108:PRO:HA	55:SF:111:VAL:HG12	1.98	0.45
4:L5:742:G:H2'	4:L5:743:G:C8	2.52	0.45
14:LH:173:ARG:HE	44:Lm:126:LYS:HA	1.82	0.45
49:S2:1645:C:H4'	65:SQ:138:ARG:HB3	1.98	0.45
53:SD:136:VAL:HG23	53:SD:186:VAL:HG22	1.99	0.45
66:SR:28:PHE:HA	66:SR:55:THR:HG21	1.97	0.45
4:L5:967:C:O2'	4:L5:969:C:OP2	2.27	0.44
4:L5:2558:C:N4	4:L5:2559:G:O6	2.50	0.44
4:L5:4093:G:H2'	4:L5:4094:G:C8	2.52	0.44
4:L5:5016:A:H2	4:L5:5033:G:H21	1.64	0.44
16:LJ:143:ASP:N	16:LJ:143:ASP:OD1	2.46	0.44
49:S2:1661:A:OP2	78:Sd:19:ARG:NH1	2.42	0.44
53:SD:11:PHE:HZ	69:SU:27:ARG:HB3	1.82	0.44
71:SW:94:LEU:HD21	71:SW:102:ILE:HG23	1.98	0.44
72:SX:100:VAL:HG13	72:SX:125:VAL:HA	1.99	0.44
81:Sg:125:ARG:NH1	81:Sg:151:VAL:O	2.49	0.44
1:A4:47:U:O2'	1:A4:48:U:O2	2.31	0.44
4:L5:223:G:N2	9:LC:223:ASN:O	2.49	0.44
4:L5:326:C:OP2	40:Li:28:ARG:NH2	2.51	0.44
4:L5:2837:U:H5''	8:LB:249:ARG:HB2	1.99	0.44
4:L5:4589:A:N1	4:L5:4621:C:O2'	2.50	0.44
4:L5:4928:C:O2'	18:LM:121:ARG:NH1	2.51	0.44
20:LO:34:VAL:HG22	20:LO:103:LYS:HB2	1.99	0.44
29:LX:124:VAL:HG22	29:LX:138:VAL:HG22	2.00	0.44
49:S2:306:C:H4'	49:S2:307:G:H5''	1.98	0.44
49:S2:625:G:H22	72:SX:65:ALA:HB2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:660:C:H5'	72:SX:13:LEU:HD21	2.00	0.44
49:S2:834:C:N4	49:S2:841:G:O6	2.50	0.44
49:S2:952:G:H21	63:SO:52:THR:HG21	1.82	0.44
51:SB:140:VAL:HG13	51:SB:213:ARG:HB2	2.00	0.44
62:SN:25:TRP:CE2	76:Sb:82:LYS:HE3	2.52	0.44
64:SP:85:ILE:HG22	64:SP:112:ILE:HG22	1.99	0.44
76:Sb:42:LYS:HE3	76:Sb:57:VAL:HB	1.99	0.44
81:Sg:286:CYS:HA	81:Sg:302:TYR:HB3	1.99	0.44
4:L5:2705:G:H22	4:L5:2710:C:H5	1.65	0.44
4:L5:3596:A:H4'	23:LR:143:HIS:HB3	1.99	0.44
8:LB:303:ALA:HB3	8:LB:312:LYS:HB3	2.00	0.44
21:LP:115:GLU:HB2	21:LP:151:THR:HG22	1.99	0.44
23:LR:16:ARG:O	23:LR:52:ARG:NH2	2.51	0.44
49:S2:941:C:H2'	49:S2:942:G:H8	1.82	0.44
49:S2:1129:G:OP1	76:Sb:22:LYS:NZ	2.39	0.44
51:SB:30:TRP:CD1	51:SB:48:LEU:HD13	2.52	0.44
4:L5:4930:C:H5''	11:LE:266:GLN:HE21	1.83	0.44
9:LC:289:LEU:HA	9:LC:292:ILE:HG12	2.00	0.44
24:LS:116:ARG:HE	24:LS:116:ARG:HB3	1.67	0.44
27:LV:13:LYS:HB2	27:LV:128:LEU:HD11	1.99	0.44
32:La:71:PRO:HG2	32:La:108:TYR:HA	2.00	0.44
49:S2:1337:C:H2'	49:S2:1338:G:C8	2.52	0.44
54:SE:6:LYS:O	54:SE:30:ARG:NH2	2.51	0.44
56:SG:31:ARG:HG2	56:SG:101:ILE:HG12	1.99	0.44
58:SI:177:SER:OG	58:SI:178:ARG:N	2.51	0.44
4:L5:690:C:H2'	4:L5:691:C:H6	1.82	0.44
4:L5:1930:U:OP2	20:LO:49:ARG:NH1	2.43	0.44
4:L5:3848:U:H2'	4:L5:3849:A:H8	1.83	0.44
7:LA:36:GLU:HA	7:LA:91:GLY:HA2	1.99	0.44
8:LB:264:PHE:N	20:LO:64:THR:O	2.46	0.44
9:LC:293:LEU:HD23	9:LC:293:LEU:HA	1.84	0.44
17:LL:81:LEU:HD23	17:LL:88:LYS:HA	1.98	0.44
36:Le:76:LYS:HB2	36:Le:98:GLU:HG3	1.98	0.44
40:Li:43:MET:HE3	40:Li:43:MET:HB3	1.93	0.44
49:S2:1601:A:N6	49:S2:1636:G:OP1	2.44	0.44
49:S2:1729:U:H3	49:S2:1805:G:H1	1.66	0.44
56:SG:50:VAL:HG23	56:SG:113:ILE:HA	1.99	0.44
77:Sc:60:GLU:HG2	77:Sc:61:SER:H	1.82	0.44
49:S2:429:C:OP1	54:SE:10:LYS:NZ	2.46	0.44
49:S2:563:G:H2'	49:S2:564:A:H8	1.83	0.44
52:SC:227:ARG:HA	52:SC:227:ARG:HD2	1.72	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SE:104:ASP:OD1	54:SE:108:ARG:N	2.51	0.44
57:SH:65:PRO:HB2	57:SH:68:GLN:HB2	1.99	0.44
72:SX:9:THR:OG1	72:SX:10:ALA:N	2.36	0.44
4:L5:499:G:H21	4:L5:504:G:H21	1.64	0.44
4:L5:1332:C:H2'	4:L5:1333:A:H8	1.82	0.44
4:L5:3615:G:H21	28:LW:44:ARG:HH11	1.64	0.44
7:LA:70:LYS:HD2	7:LA:72:ARG:HE	1.82	0.44
15:LI:36:LEU:HD11	15:LI:69:ARG:HD3	2.00	0.44
18:LM:27:ILE:HA	18:LM:38:VAL:HG23	2.00	0.44
18:LM:92:ALA:HA	18:LM:95:ILE:HG12	1.99	0.44
49:S2:65:C:H4'	56:SG:172:LYS:HE2	2.00	0.44
49:S2:99:A:H61	49:S2:433:A:H1'	1.82	0.44
49:S2:114:G:N2	49:S2:350:C:O2'	2.41	0.44
49:S2:957:A:O2'	49:S2:958:G:N3	2.37	0.44
49:S2:1675:A:O2'	55:SF:74:ASN:O	2.36	0.44
4:L5:192:G:H1	4:L5:249:C:H42	1.66	0.44
4:L5:1633:G:C5	7:LA:207:VAL:HG21	2.53	0.44
4:L5:4258:C:H1'	16:LJ:25:CYS:SG	2.57	0.44
12:LF:157:ARG:NH2	12:LF:248:ASN:O	2.39	0.44
16:LJ:12:MET:HE3	16:LJ:12:MET:HB3	1.83	0.44
17:LL:87:HIS:HB3	17:LL:90:VAL:HG22	1.99	0.44
19:LN:49:ARG:HD2	19:LN:49:ARG:HA	1.79	0.44
25:LT:84:ILE:HD11	33:Lb:23:LYS:HA	2.00	0.44
30:LY:50:ARG:HG3	30:LY:115:ARG:NH2	2.33	0.44
49:S2:42:A:O2'	49:S2:98:C:OP1	2.27	0.44
56:SG:136:LYS:NZ	56:SG:175:LYS:O	2.41	0.44
62:SN:64:ARG:HE	62:SN:64:ARG:HB3	1.53	0.44
4:L5:137:G:H2'	4:L5:138:G:C8	2.53	0.44
4:L5:3879:G:O2'	4:L5:3881:G:OP2	2.34	0.44
4:L5:4558:U:OP2	8:LB:246:ARG:NH2	2.43	0.44
7:LA:28:ARG:HB2	7:LA:123:ARG:HB3	2.00	0.44
9:LC:212:ASN:HB2	9:LC:256:ALA:HB2	2.00	0.44
9:LC:217:ILE:H	9:LC:217:ILE:HG13	1.64	0.44
12:LF:125:LEU:HD23	12:LF:125:LEU:HA	1.74	0.44
39:Lh:23:ASP:HA	39:Lh:26:VAL:HB	2.00	0.44
42:Lk:5:ILE:HD11	42:Lk:43:TYR:HB3	1.99	0.44
49:S2:165:G:OP2	49:S2:165:G:N2	2.38	0.44
50:SA:7:VAL:HG22	50:SA:191:ARG:HD2	1.99	0.44
63:SO:101:GLY:HA3	63:SO:134:PRO:HG2	1.99	0.44
4:L5:4177:C:OP1	19:LN:93:LYS:NZ	2.49	0.43
49:S2:920:A:O2'	49:S2:922:A:O5'	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1101:U:H2'	49:S2:1102:G:C8	2.53	0.43
2:B4:37:A:O2'	49:S2:1058:A:OP1	2.32	0.43
21:LP:21:ASN:N	21:LP:21:ASN:OD1	2.50	0.43
25:LT:71:ALA:HA	25:LT:92:ARG:HA	2.00	0.43
29:LX:89:LYS:HB3	29:LX:95:THR:HG23	2.00	0.43
49:S2:643:A:OP1	59:SJ:38:ARG:NH2	2.43	0.43
49:S2:1538:C:H42	74:SZ:104:ARG:HH12	1.66	0.43
73:SY:80:ASP:N	73:SY:80:ASP:OD1	2.50	0.43
81:Sg:196:ASN:OD1	81:Sg:196:ASN:N	2.52	0.43
4:L5:4691:A:O2'	14:LH:68:ALA:O	2.35	0.43
10:LD:90:VAL:HG11	10:LD:226:TYR:HA	1.99	0.43
19:LN:30:TYR:HA	19:LN:33:LEU:HD12	2.00	0.43
49:S2:1606:G:N1	49:S2:1632:G:O2'	2.39	0.43
49:S2:1831:A:H1'	49:S2:1852:C:H5'	2.01	0.43
54:SE:141:THR:OG1	54:SE:143:ASP:O	2.28	0.43
58:SI:141:ARG:HB2	58:SI:145:ILE:HB	2.00	0.43
61:SL:40:ILE:HD13	61:SL:68:ILE:HD12	2.00	0.43
61:SL:113:LEU:HD12	61:SL:142:VAL:HG11	2.00	0.43
63:SO:103:ASN:OD1	63:SO:103:ASN:N	2.51	0.43
68:ST:18:LEU:HD22	68:ST:58:ALA:HA	2.00	0.43
4:L5:1086:C:H2'	4:L5:1087:A:H8	1.83	0.43
4:L5:2533:C:OP1	29:LX:139:ARG:NH2	2.51	0.43
4:L5:2835:A:O2'	8:LB:228:TYR:O	2.31	0.43
4:L5:4672:A:OP1	27:LV:15:ARG:NH1	2.36	0.43
12:LF:169:LEU:HA	12:LF:174:LEU:HD11	2.00	0.43
46:Lo:65:LYS:HB2	46:Lo:87:ARG:HB3	2.01	0.43
49:S2:609:U:H2'	49:S2:610:G:H8	1.83	0.43
49:S2:696:G:N2	49:S2:735:C:OP2	2.41	0.43
49:S2:811:A:H2'	49:S2:812:A:C8	2.54	0.43
54:SE:192:ILE:HG12	54:SE:243:GLY:HA3	1.98	0.43
58:SI:6:ASP:N	58:SI:6:ASP:OD1	2.42	0.43
65:SQ:8:GLN:HE21	65:SQ:27:ARG:HH21	1.66	0.43
69:SU:108:PRO:HA	69:SU:109:GLY:HA2	1.66	0.43
73:SY:54:VAL:HB	73:SY:76:TYR:HB2	2.00	0.43
81:Sg:65:PHE:HB2	81:Sg:83:TRP:HB2	2.01	0.43
81:Sg:89:LEU:HB3	81:Sg:98:THR:HG23	2.00	0.43
4:L5:120:A:H2'	4:L5:149:A:H61	1.82	0.43
4:L5:420:A:H61	6:L8:15:G:H1'	1.81	0.43
4:L5:1352:C:O2'	4:L5:1356:U:OP1	2.33	0.43
4:L5:4635:A:H8	4:L5:5048:A:H61	1.64	0.43
10:LD:228:LYS:HE3	10:LD:228:LYS:HB2	1.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LE:207:LYS:H	11:LE:256:GLN:HE22	1.67	0.43
21:LP:94:MET:HE2	21:LP:146:ILE:HG12	2.00	0.43
29:LX:55:ARG:O	29:LX:57:GLN:NE2	2.52	0.43
47:Lp:8:VAL:HG22	47:Lp:11:VAL:HG23	2.00	0.43
49:S2:17:C:O2'	49:S2:1194:A:N1	2.51	0.43
56:SG:115:LYS:HD3	56:SG:115:LYS:HA	1.78	0.43
59:SJ:22:LYS:HD2	59:SJ:22:LYS:HA	1.76	0.43
7:LA:18:ALA:HA	7:LA:193:ARG:HB3	2.01	0.43
9:LC:339:THR:HG22	9:LC:342:ARG:HH22	1.83	0.43
10:LD:52:ILE:HA	10:LD:147:ASP:HB3	2.00	0.43
12:LF:126:ASN:ND2	25:LT:132:PRO:HG2	2.34	0.43
12:LF:159:TYR:HD2	12:LF:166:ARG:HG2	1.82	0.43
14:LH:182:SER:OG	14:LH:183:GLU:N	2.50	0.43
25:LT:68:THR:OG1	25:LT:69:GLN:N	2.48	0.43
35:Ld:115:LYS:HB3	35:Ld:116:ASN:HD22	1.83	0.43
39:Lh:80:PRO:HD2	39:Lh:83:LEU:HD12	2.01	0.43
49:S2:64:A:OP1	56:SG:177:GLN:NE2	2.45	0.43
49:S2:114:G:O2'	49:S2:383:G:O4'	2.35	0.43
51:SB:73:ASP:OD1	63:SO:128:ARG:NH2	2.49	0.43
59:SJ:160:SER:OG	59:SJ:161:LEU:N	2.51	0.43
4:L5:1919:G:O6	37:Lf:29:LYS:NZ	2.43	0.43
4:L5:2902:G:H21	4:L5:3598:C:H42	1.67	0.43
4:L5:4305:G:O6	25:LT:78:LYS:NZ	2.46	0.43
8:LB:84:MET:HE3	8:LB:84:MET:HB2	1.85	0.43
13:LG:180:PRO:HG3	13:LG:223:ARG:HH11	1.82	0.43
43:Ll:23:ILE:HD11	43:Ll:38:ASN:HA	2.00	0.43
48:Lr:66:ARG:O	48:Lr:70:GLN:NE2	2.50	0.43
49:S2:903:A:H2'	49:S2:904:A:C8	2.54	0.43
49:S2:974:C:O2	63:SO:43:HIS:NE2	2.52	0.43
51:SB:57:ILE:HG13	51:SB:60:ASP:H	1.84	0.43
51:SB:70:SER:HA	51:SB:83:LYS:HA	2.00	0.43
59:SJ:73:GLU:O	59:SJ:77:LEU:N	2.41	0.43
4:L5:428:G:HO2'	4:L5:1305:C:HO2'	1.65	0.43
4:L5:1802:A:N3	25:LT:130:ARG:NH1	2.67	0.43
4:L5:3786:U:OP1	4:L5:4550:G:O2'	2.26	0.43
4:L5:4139:G:O2'	4:L5:4146:G:N2	2.52	0.43
4:L5:4945:G:H1	37:Lf:5:LEU:HD23	1.82	0.43
16:LJ:87:LEU:HD21	16:LJ:166:PHE:HE1	1.84	0.43
30:LY:63:LYS:HB2	30:LY:63:LYS:HE3	1.84	0.43
38:Lg:46:CYS:SG	38:Lg:47:GLY:N	2.91	0.43
49:S2:64:A:H2	49:S2:83:A:H62	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SA:56:GLU:OE2	70:SV:80:SER:OG	2.36	0.43
52:SC:165:VAL:HG11	52:SC:217:ALA:HB1	2.00	0.43
61:SL:36:TYR:OH	61:SL:38:LYS:NZ	2.42	0.43
64:SP:17:TYR:N	64:SP:20:VAL:O	2.49	0.43
2:B4:19:A:H2'	2:B4:20:A:H4'	2.00	0.43
4:L5:142:G:H2'	4:L5:144:G:H8	1.83	0.43
21:LP:14:SER:OG	21:LP:150:LEU:O	2.33	0.43
31:LZ:76:ASN:HB3	31:LZ:79:HIS:ND1	2.34	0.43
42:Lk:23:VAL:HA	42:Lk:36:VAL:HA	2.00	0.43
45:Ln:13:LEU:HD21	49:S2:1819:A:H4'	2.01	0.43
49:S2:1017:U:O5'	62:SN:55:ARG:NH1	2.52	0.43
55:SF:75:SER:O	55:SF:159:ARG:NH2	2.52	0.43
58:SI:81:VAL:HG13	58:SI:91:VAL:HG23	1.99	0.43
59:SJ:37:LEU:HD13	59:SJ:37:LEU:HA	1.91	0.43
70:SV:28:ASP:O	70:SV:31:SER:OG	2.36	0.43
81:Sg:165:ILE:N	81:Sg:177:TRP:O	2.41	0.43
3:D4:58:A:H1'	3:D4:60:U:H2'	2.01	0.43
4:L5:1332:C:H2'	4:L5:1333:A:C8	2.54	0.43
4:L5:1699:A:O3'	9:LC:306:ARG:NH2	2.52	0.43
4:L5:4081:G:H2'	4:L5:4082:G:C8	2.54	0.43
4:L5:4587:G:OP1	20:LO:61:ARG:NH1	2.46	0.43
8:LB:292:LEU:O	8:LB:298:LEU:N	2.52	0.43
14:LH:124:ARG:NH1	14:LH:164:ALA:O	2.52	0.43
25:LT:142:ARG:NH1	25:LT:143:THR:O	2.51	0.43
34:Lc:44:LYS:NZ	34:Lc:97:ILE:O	2.42	0.43
47:Lp:47:MET:HA	47:Lp:57:CYS:HA	2.00	0.43
50:SA:124:VAL:HG21	50:SA:134:LEU:HD21	2.00	0.43
51:SB:161:VAL:HA	51:SB:164:ILE:HG22	2.01	0.43
59:SJ:108:ARG:O	59:SJ:112:THR:OG1	2.37	0.43
68:ST:84:ARG:HG2	68:ST:86:GLY:H	1.83	0.43
69:SU:38:ASP:O	69:SU:42:GLY:N	2.51	0.43
4:L5:1460:C:H5''	22:LQ:144:LYS:HB2	2.00	0.42
4:L5:1478:C:H2'	4:L5:1479:G:H8	1.84	0.42
4:L5:4736:C:H2'	4:L5:4737:G:H8	1.84	0.42
6:L8:96:C:OP1	39:Lh:70:ARG:NH1	2.48	0.42
20:LO:61:ARG:HA	20:LO:70:PRO:HD2	2.00	0.42
30:LY:35:SER:O	30:LY:39:ARG:N	2.48	0.42
49:S2:166:A:H1'	56:SG:13:GLN:HE22	1.84	0.42
60:SK:23:ALA:HB3	60:SK:69:TRP:HZ3	1.83	0.42
77:Sc:13:ARG:HB2	77:Sc:35:MET:HG2	2.01	0.42
4:L5:73:A:N6	17:LL:103:ARG:HH22	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:498:C:H42	4:L5:656:C:H42	1.67	0.42
4:L5:1358:G:OP1	9:LC:117:THR:OG1	2.34	0.42
8:LB:317:LEU:HD22	8:LB:382:MET:HG3	2.02	0.42
12:LF:236:ARG:HH12	12:LF:243:LEU:HD13	1.84	0.42
17:LL:25:TRP:HE1	19:LN:199:GLN:HE21	1.65	0.42
19:LN:118:SER:HB2	19:LN:132:VAL:HG12	2.01	0.42
19:LN:193:ARG:O	19:LN:197:THR:N	2.52	0.42
21:LP:49:LYS:O	21:LP:52:THR:OG1	2.35	0.42
24:LS:9:GLU:OE2	24:LS:31:ARG:NH2	2.52	0.42
28:LW:43:LYS:HE2	28:LW:43:LYS:HB2	1.90	0.42
46:Lo:14:LYS:HD3	46:Lo:77:CYS:HB2	2.00	0.42
49:S2:1593:C:H4'	65:SQ:45:ARG:HH11	1.84	0.42
49:S2:1673:U:H5''	65:SQ:78:VAL:HG22	2.01	0.42
51:SB:175:GLU:HG3	51:SB:193:ILE:HD11	2.00	0.42
56:SG:194:LEU:HB3	56:SG:198:ARG:HH12	1.83	0.42
77:Sc:8:PRO:HB2	77:Sc:9:ILE:H	1.61	0.42
4:L5:253:G:H2'	4:L5:254:G:H8	1.83	0.42
4:L5:277:G:C6	40:Li:30:ARG:HD2	2.54	0.42
4:L5:1811:G:O2'	33:Lb:60:ASN:ND2	2.50	0.42
4:L5:3941:G:N2	4:L5:4073:A:N3	2.67	0.42
4:L5:5014:A:H2	4:L5:5035:U:H3	1.68	0.42
6:L8:60:G:C8	39:Lh:58:LEU:HD22	2.55	0.42
9:LC:179:ASP:OD1	9:LC:179:ASP:N	2.50	0.42
18:LM:35:ARG:HA	18:LM:51:PRO:HA	2.01	0.42
24:LS:69:GLU:H	24:LS:69:GLU:HG3	1.57	0.42
30:LY:30:MET:HG2	30:LY:101:PRO:HG2	2.01	0.42
31:LZ:14:LEU:HD12	38:Lg:88:ARG:HG3	2.00	0.42
35:Ld:24:GLU:OE2	35:Ld:87:ARG:NH2	2.52	0.42
36:Le:87:VAL:HG23	36:Le:88:LEU:HD22	2.02	0.42
49:S2:806:U:H2'	49:S2:807:G:C8	2.54	0.42
49:S2:1467:C:OP1	66:SR:2:GLY:N	2.52	0.42
55:SF:168:THR:HG23	55:SF:170:ALA:H	1.85	0.42
64:SP:38:SER:HG	64:SP:41:GLN:N	2.16	0.42
68:ST:123:LEU:HD23	68:ST:128:GLN:HG2	2.01	0.42
71:SW:60:LYS:NZ	76:Sb:23:ARG:O	2.51	0.42
81:Sg:191:HIS:HE1	81:Sg:219:TRP:HZ2	1.66	0.42
4:L5:168:C:H2'	4:L5:169:G:C8	2.54	0.42
4:L5:350:C:OP1	4:L5:2294:G:O2'	2.37	0.42
4:L5:512:U:H2'	4:L5:513:U:H4'	2.01	0.42
5:L7:87:G:N2	5:L7:90:A:OP2	2.52	0.42
13:LG:50:ASP:OD1	13:LG:52:THR:OG1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Le:78:LEU:HD12	36:Le:78:LEU:HA	1.87	0.42
43:Ll:48:LYS:HA	43:Ll:48:LYS:HD3	1.77	0.42
71:SW:46:TYR:HB3	71:SW:69:LEU:HD13	2.01	0.42
4:L5:139:G:H2'	4:L5:140:G:H8	1.84	0.42
4:L5:4452:U:OP2	4:L5:4522:G:N1	2.34	0.42
4:L5:5026:U:H4'	4:L5:5027:C:H5'	2.00	0.42
7:LA:109:GLU:H	7:LA:109:GLU:HG2	1.61	0.42
13:LG:67:ARG:HD3	19:LN:29:GLN:HG3	2.02	0.42
20:LO:27:VAL:O	20:LO:101:ARG:NH1	2.50	0.42
23:LR:17:CYS:HB3	23:LR:52:ARG:HH21	1.84	0.42
46:Lo:63:THR:HG23	46:Lo:87:ARG:HB2	2.02	0.42
46:Lo:69:ARG:HG3	46:Lo:82:MET:HE1	2.02	0.42
48:Lr:47:LYS:HB2	48:Lr:102:TYR:CZ	2.54	0.42
67:SS:82:TRP:O	67:SS:87:GLN:NE2	2.52	0.42
9:LC:183:VAL:O	9:LC:186:SER:OG	2.27	0.42
10:LD:5:LYS:HE3	10:LD:5:LYS:HB2	1.90	0.42
22:LQ:4:ASP:OD1	22:LQ:4:ASP:N	2.43	0.42
30:LY:8:THR:OG1	30:LY:14:ASN:ND2	2.49	0.42
31:LZ:118:PHE:O	31:LZ:122:TYR:N	2.48	0.42
48:Lr:17:LEU:HD12	48:Lr:17:LEU:HA	1.82	0.42
49:S2:1457:U:H2'	49:S2:1458:G:H8	1.85	0.42
49:S2:1584:G:C4	49:S2:1586:U:H1'	2.55	0.42
51:SB:192:SER:O	51:SB:192:SER:OG	2.37	0.42
54:SE:102:ILE:HG12	54:SE:239:PRO:HD3	2.02	0.42
57:SH:179:LYS:HA	57:SH:179:LYS:HD2	1.83	0.42
65:SQ:132:PHE:CD1	69:SU:77:TRP:HB2	2.55	0.42
78:Sd:54:LYS:HB2	78:Sd:54:LYS:HE3	1.79	0.42
4:L5:724:C:H1'	9:LC:343:GLN:HG2	2.01	0.42
8:LB:57:VAL:HG23	8:LB:366:LYS:HB2	2.02	0.42
9:LC:228:THR:OG1	9:LC:239:LYS:NZ	2.42	0.42
10:LD:88:VAL:HG23	10:LD:239:MET:HE1	2.01	0.42
10:LD:132:VAL:HG11	10:LD:170:GLY:HA2	2.02	0.42
25:LT:84:ILE:HG13	33:Lb:24:PRO:HD3	2.02	0.42
49:S2:941:C:H2'	49:S2:942:G:C8	2.54	0.42
49:S2:1616:U:O4	64:SP:40:ARG:NH2	2.49	0.42
49:S2:1860:A:H3'	75:Sa:8:ASN:HB3	2.01	0.42
51:SB:146:ARG:HA	51:SB:146:ARG:HD3	1.84	0.42
56:SG:185:LEU:O	56:SG:189:ARG:N	2.45	0.42
62:SN:107:LYS:HE3	62:SN:107:LYS:HB2	1.94	0.42
4:L5:2579:G:N2	4:L5:2582:A:OP2	2.40	0.42
7:LA:30:ARG:NH1	7:LA:36:GLU:OE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LD:73:MET:HE2	10:LD:73:MET:HB3	1.78	0.42
12:LF:196:THR:O	12:LF:196:THR:OG1	2.38	0.42
26:LU:44:GLN:HA	26:LU:56:LEU:HD21	2.01	0.42
29:LX:79:PHE:CZ	29:LX:99:ILE:HD11	2.54	0.42
30:LY:80:ILE:HG13	30:LY:101:PRO:HG3	2.00	0.42
31:LZ:70:SER:OG	31:LZ:111:ARG:O	2.37	0.42
49:S2:493:A:H61	49:S2:510:G:H1'	1.84	0.42
49:S2:963:A:H2'	49:S2:964:A:C8	2.55	0.42
49:S2:1491:G:N2	69:SU:70:CYS:SG	2.89	0.42
54:SE:229:GLY:HA2	54:SE:235:TRP:CE2	2.55	0.42
81:Sg:229:THR:OG1	81:Sg:230:LEU:N	2.50	0.42
4:L5:68:U:OP1	19:LN:178:HIS:ND1	2.32	0.42
4:L5:227:A:N6	4:L5:241:G:O2'	2.53	0.42
4:L5:1362:G:OP1	17:LL:39:ARG:NH2	2.35	0.42
4:L5:1481:C:H5'	40:Li:4:ARG:HH22	1.85	0.42
4:L5:2474:G:H21	4:L5:2503:G:H5''	1.85	0.42
6:L8:90:C:H4'	30:LY:23:SER:HB3	2.02	0.42
6:L8:109:C:N3	41:Lj:20:ARG:NH1	2.62	0.42
8:LB:141:ASP:OD1	8:LB:141:ASP:N	2.53	0.42
9:LC:283:LYS:O	22:LQ:122:THR:OG1	2.34	0.42
26:LU:100:LEU:HA	26:LU:114:TYR:HA	2.00	0.42
30:LY:55:VAL:HG23	30:LY:106:ILE:HA	2.02	0.42
37:Lf:45:LYS:HA	37:Lf:107:PRO:HD2	2.01	0.42
49:S2:380:G:N1	49:S2:383:G:OP2	2.38	0.42
49:S2:441:C:H42	49:S2:452:G:H1	1.67	0.42
52:SC:208:PRO:HA	52:SC:211:LYS:HG2	2.02	0.42
54:SE:37:LYS:HE2	54:SE:40:GLU:HG2	2.01	0.42
54:SE:161:GLN:O	54:SE:170:THR:OG1	2.31	0.42
56:SG:1:MET:HE3	56:SG:1:MET:HB2	1.83	0.42
72:SX:68:LYS:HD3	72:SX:91:LEU:HD13	2.01	0.42
4:L5:956:A:H1'	4:L5:2076:G:H5''	2.01	0.42
4:L5:1633:G:C6	7:LA:207:VAL:HG21	2.55	0.42
4:L5:3661:G:H4'	4:L5:3662:A:H5'	2.01	0.42
4:L5:4635:A:H2	4:L5:4663:G:H21	1.68	0.42
6:L8:102:G:OP2	6:L8:104:A:O2'	2.33	0.42
23:LR:132:PHE:HD1	23:LR:137:ILE:HG22	1.85	0.42
29:LX:93:ASN:HB3	29:LX:95:THR:HG22	2.02	0.42
36:Le:102:ASN:OD1	36:Le:102:ASN:N	2.45	0.42
49:S2:1173:A:HO2'	49:S2:1716:C:HO2'	1.65	0.42
53:SD:70:THR:HB	53:SD:86:LEU:HG	2.02	0.42
54:SE:19:MET:HE3	54:SE:19:MET:HB2	1.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SH:143:ARG:HE	71:SW:53:ILE:HD12	1.85	0.42
4:L5:2758:G:O2'	4:L5:2765:A:N3	2.44	0.41
4:L5:4548:A:H5'	4:L5:4549:G:H5''	2.01	0.41
7:LA:107:MET:HE2	7:LA:107:MET:HB3	1.89	0.41
9:LC:138:MET:HE1	9:LC:145:GLU:HG3	2.01	0.41
10:LD:155:THR:O	10:LD:155:THR:OG1	2.36	0.41
28:LW:78:PHE:HD1	28:LW:78:PHE:HA	1.76	0.41
41:Lj:21:ARG:NH2	41:Lj:38:GLY:O	2.53	0.41
49:S2:224:A:OP2	61:SL:20:LYS:NZ	2.46	0.41
49:S2:1276:A:C5	49:S2:1277:C:H1'	2.55	0.41
51:SB:31:TYR:N	51:SB:47:THR:O	2.52	0.41
55:SF:51:HIS:O	65:SQ:82:TYR:OH	2.38	0.41
64:SP:34:MET:HB2	64:SP:42:ARG:HB2	2.02	0.41
64:SP:96:VAL:O	64:SP:103:ASN:N	2.49	0.41
73:SY:19:GLN:NE2	73:SY:77:ASP:OD2	2.45	0.41
4:L5:226:G:OP2	30:LY:1:MET:N	2.37	0.41
4:L5:1353:G:H3'	22:LQ:106:THR:HG21	2.01	0.41
4:L5:1354:A:OP2	22:LQ:87:THR:OG1	2.28	0.41
8:LB:217:ILE:HD11	8:LB:333:LEU:HD21	2.01	0.41
9:LC:187:GLN:HE21	9:LC:203:GLN:HE21	1.68	0.41
14:LH:93:ARG:HA	14:LH:143:GLU:HA	2.02	0.41
15:LI:48:LEU:HD21	15:LI:145:GLU:HB3	2.02	0.41
21:LP:40:HIS:HD2	21:LP:42:ARG:H	1.67	0.41
30:LY:9:SER:O	30:LY:9:SER:OG	2.37	0.41
49:S2:368:U:H2'	49:S2:369:C:H2'	2.02	0.41
50:SA:90:PHE:HD2	50:SA:179:ALA:HB2	1.85	0.41
51:SB:179:ASN:HB3	51:SB:183:GLU:HB2	2.02	0.41
71:SW:18:GLU:HB2	71:SW:65:LEU:HD13	2.01	0.41
72:SX:16:HIS:CE1	72:SX:20:GLN:HG3	2.55	0.41
4:L5:512:U:O2'	4:L5:648:G:N2	2.53	0.41
4:L5:960:A:N6	11:LE:125:LEU:O	2.53	0.41
4:L5:1350:C:H2'	4:L5:1351:G:H8	1.85	0.41
4:L5:1500:A:H5''	4:L5:1501:C:H5''	2.03	0.41
4:L5:1597:G:OP1	21:LP:131:ARG:NH2	2.53	0.41
4:L5:2262:G:N7	48:Lr:98:ARG:NH2	2.68	0.41
4:L5:2896:G:H5'	23:LR:134:ASN:HD22	1.85	0.41
7:LA:159:SER:O	7:LA:162:ASN:ND2	2.53	0.41
8:LB:195:ASP:OD1	8:LB:195:ASP:N	2.53	0.41
9:LC:94:ASN:OD1	9:LC:94:ASN:N	2.54	0.41
22:LQ:41:SER:OG	22:LQ:132:LYS:O	2.37	0.41
35:Ld:85:ARG:HH22	35:Ld:117:LEU:HG	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lh:46:LYS:HA	39:Lh:46:LYS:HD3	1.85	0.41
49:S2:618:C:H1'	49:S2:632:C:H5''	2.01	0.41
63:SO:149:ARG:HH12	63:SO:151:LEU:HD22	1.85	0.41
65:SQ:58:LEU:HD23	65:SQ:62:ARG:HH21	1.85	0.41
67:SS:22:GLY:HA2	67:SS:56:ALA:HB3	2.01	0.41
81:Sg:86:THR:OG1	81:Sg:87:LEU:N	2.54	0.41
4:L5:173:C:H2'	4:L5:174:C:C6	2.56	0.41
4:L5:1086:C:H2'	4:L5:1087:A:C8	2.55	0.41
4:L5:1375:C:OP1	9:LC:121:ARG:NH2	2.54	0.41
4:L5:1415:G:H2'	4:L5:1416:G:C8	2.55	0.41
16:LJ:109:ILE:HD11	16:LJ:130:PHE:CE1	2.54	0.41
18:LM:12:VAL:O	18:LM:58:THR:OG1	2.36	0.41
22:LQ:69:LYS:HA	22:LQ:72:LEU:HD13	2.02	0.41
49:S2:157:U:H4'	56:SG:59:GLN:HA	2.02	0.41
49:S2:1059:G:N2	49:S2:1829:G:O3'	2.54	0.41
49:S2:1589:A:O2'	49:S2:1653:U:O3'	2.35	0.41
55:SF:22:LYS:HD2	55:SF:22:LYS:HA	1.67	0.41
55:SF:152:TRP:HE3	55:SF:153:LEU:HD12	1.84	0.41
81:Sg:197:THR:HG21	81:Sg:238:ALA:HA	2.02	0.41
4:L5:328:A:OP2	40:Li:30:ARG:NH1	2.42	0.41
4:L5:742:G:H2'	4:L5:743:G:H8	1.86	0.41
4:L5:1516:G:O6	4:L5:1518:A:O2'	2.33	0.41
4:L5:2060:G:H4'	24:LS:118:ARG:HG3	2.02	0.41
4:L5:2550:G:O2'	4:L5:2587:A:N1	2.43	0.41
4:L5:3650:C:OP1	7:LA:200:ARG:NH2	2.45	0.41
4:L5:4773:C:N3	4:L5:4774:C:N4	2.68	0.41
6:L8:90:C:H1'	30:LY:24:HIS:HB3	2.02	0.41
9:LC:71:ARG:HB2	9:LC:73:VAL:HG22	2.03	0.41
9:LC:297:GLU:H	9:LC:297:GLU:HG3	1.75	0.41
20:LO:61:ARG:HB2	20:LO:66:PRO:HB3	2.03	0.41
22:LQ:28:LEU:HD23	22:LQ:28:LEU:HA	1.84	0.41
23:LR:7:GLN:O	23:LR:11:ALA:N	2.50	0.41
27:LV:65:VAL:HG23	27:LV:73:ARG:HA	2.03	0.41
36:Le:23:HIS:HA	36:Le:53:ILE:HD12	2.02	0.41
49:S2:993:G:OP1	49:S2:1131:G:N2	2.47	0.41
53:SD:75:LYS:HE3	53:SD:75:LYS:HB3	1.90	0.41
73:SY:20:ARG:NE	73:SY:74:MET:SD	2.87	0.41
4:L5:364:G:O2'	4:L5:375:G:O6	2.36	0.41
4:L5:1377:G:H4'	4:L5:1378:C:H3'	2.01	0.41
4:L5:3937:C:H3'	4:L5:3938:G:H2'	2.02	0.41
4:L5:4714:C:OP1	8:LB:31:SER:OG	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L7:63:C:H5''	15:LI:205:PRO:HA	2.03	0.41
10:LD:15:ARG:HA	10:LD:15:ARG:HD3	1.83	0.41
17:LL:165:LYS:HD2	17:LL:165:LYS:HA	1.95	0.41
24:LS:77:ASN:HD21	24:LS:146:HIS:CE1	2.39	0.41
30:LY:125:SER:O	30:LY:125:SER:OG	2.33	0.41
31:LZ:54:THR:OG1	31:LZ:55:ALA:N	2.53	0.41
34:Lc:75:SER:O	34:Lc:75:SER:OG	2.35	0.41
49:S2:114:G:OP2	61:SL:67:SER:OG	2.38	0.41
58:SI:79:ILE:HD11	58:SI:103:LEU:HD22	2.02	0.41
64:SP:38:SER:OG	64:SP:40:ARG:N	2.54	0.41
4:L5:234:G:N2	4:L5:2303:C:O2	2.49	0.41
4:L5:1741:G:O6	5:L7:103:A:O2'	2.26	0.41
4:L5:3710:G:H4'	4:L5:3711:A:H5'	2.03	0.41
4:L5:4363:A:H5''	46:Lo:36:GLN:HG2	2.02	0.41
8:LB:161:ARG:HA	8:LB:184:GLN:HA	2.02	0.41
9:LC:8:ILE:HD11	9:LC:24:LEU:HD12	2.02	0.41
11:LE:125:LEU:HD12	11:LE:125:LEU:HA	1.94	0.41
23:LR:66:ASN:O	23:LR:70:ARG:N	2.47	0.41
24:LS:14:GLY:HA2	24:LS:62:VAL:HG23	2.03	0.41
43:Ll:20:ASN:HD22	43:Ll:41:ARG:HG3	1.86	0.41
49:S2:302:A:N3	58:SI:64:ASN:ND2	2.68	0.41
49:S2:864:A:H2'	49:S2:865:A:C8	2.55	0.41
54:SE:42:LEU:O	54:SE:84:ALA:N	2.48	0.41
54:SE:57:THR:OG1	54:SE:58:GLY:N	2.54	0.41
54:SE:100:ARG:NH2	54:SE:236:ILE:HD12	2.36	0.41
65:SQ:67:ASP:OD1	65:SQ:67:ASP:N	2.46	0.41
72:SX:9:THR:HG1	72:SX:10:ALA:H	1.68	0.41
4:L5:2361:G:O2'	4:L5:3859:G:O6	2.30	0.41
4:L5:3642:A:H2'	41:Lj:3:LYS:HE2	2.02	0.41
6:L8:87:G:OP2	39:Lh:5:LYS:NZ	2.54	0.41
9:LC:180:ILE:HD11	9:LC:207:PRO:HG3	2.03	0.41
15:LI:38:ARG:HD3	15:LI:41:ALA:HB2	2.02	0.41
49:S2:1579:A:O2'	49:S2:1581:C:OP2	2.24	0.41
49:S2:1752:C:O2	49:S2:1780:G:N1	2.42	0.41
55:SF:153:LEU:HD23	55:SF:189:ALA:HA	2.03	0.41
2:B4:47:C:C2	2:B4:58:A:H1'	2.55	0.41
4:L5:253:G:H2'	4:L5:254:G:C8	2.56	0.41
4:L5:495:C:H1'	4:L5:659:G:H22	1.86	0.41
4:L5:734:G:H2'	4:L5:735:G:H8	1.86	0.41
4:L5:1178:G:N2	10:LD:286:SER:O	2.54	0.41
4:L5:1845:U:H2'	4:L5:1846:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:3848:U:H2'	4:L5:3849:A:C8	2.56	0.41
4:L5:4084:G:N7	7:LA:72:ARG:NH2	2.64	0.41
4:L5:4549:G:H2'	4:L5:4550:G:H8	1.86	0.41
4:L5:4699:U:H1'	4:L5:4700:A:H5''	2.02	0.41
4:L5:4935:C:N4	11:LE:180:VAL:O	2.43	0.41
6:L8:84:A:OP2	6:L8:86:U:N3	2.38	0.41
8:LB:389:MET:HE3	8:LB:389:MET:HB2	1.99	0.41
14:LH:12:ILE:HD13	14:LH:18:ILE:HG12	2.03	0.41
15:LI:168:SER:OG	15:LI:169:LYS:N	2.53	0.41
16:LJ:113:ILE:HD13	16:LJ:119:TYR:HB2	2.02	0.41
20:LO:138:LEU:HA	20:LO:141:LEU:HB3	2.03	0.41
26:LU:105:ASN:ND2	26:LU:110:TYR:O	2.49	0.41
36:Le:16:ARG:NE	36:Le:18:LYS:O	2.53	0.41
39:Lh:77:LYS:HD3	39:Lh:77:LYS:HA	1.86	0.41
42:Lk:24:LYS:HB3	42:Lk:69:LEU:HD11	2.02	0.41
49:S2:106:C:OP1	49:S2:431:G:O2'	2.33	0.41
49:S2:924:G:H1	49:S2:1018:U:H3	1.68	0.41
49:S2:1397:U:H3	65:SQ:12:VAL:HA	1.86	0.41
49:S2:1407:U:O4	49:S2:1438:A:N6	2.53	0.41
49:S2:1448:A:O2'	49:S2:1449:G:O4'	2.38	0.41
55:SF:119:SER:HA	55:SF:193:LYS:HD2	2.03	0.41
56:SG:76:LEU:HD13	56:SG:92:ARG:HH11	1.86	0.41
66:SR:119:VAL:HA	66:SR:120:THR:HA	1.66	0.41
70:SV:32:ILE:HD13	70:SV:32:ILE:HA	1.83	0.41
4:L5:1872:G:O2'	4:L5:4219:A:N3	2.50	0.41
4:L5:3893:C:O2'	4:L5:4979:A:N1	2.53	0.41
4:L5:4260:U:H2'	4:L5:4261:C:C6	2.55	0.41
4:L5:4307:A:H4'	22:LQ:186:TYR:CG	2.56	0.41
9:LC:24:LEU:HD21	9:LC:28:PHE:HB2	2.02	0.41
12:LF:88:LYS:HD3	12:LF:197:VAL:HB	2.03	0.41
12:LF:245:ARG:HD3	12:LF:245:ARG:HA	1.84	0.41
19:LN:84:PRO:HA	19:LN:87:HIS:ND1	2.36	0.41
34:Lc:29:LEU:HD22	34:Lc:91:VAL:HG21	2.03	0.41
47:Lp:25:MET:HE3	47:Lp:25:MET:HB2	1.98	0.41
49:S2:51:U:H2'	49:S2:52:G:H8	1.85	0.41
62:SN:86:GLU:HA	62:SN:89:TYR:HB3	2.03	0.41
64:SP:18:ARG:NH1	67:SS:88:LYS:HG2	2.35	0.41
68:ST:21:PHE:O	68:ST:25:SER:OG	2.28	0.41
69:SU:39:LEU:HD11	69:SU:89:ILE:HG13	2.03	0.41
4:L5:185:C:H2'	4:L5:186:G:H8	1.86	0.40
4:L5:225:G:N2	4:L5:242:U:O4	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2504:C:H42	4:L5:2746:A:H5'	1.86	0.40
5:L7:29:C:O2'	5:L7:50:A:N1	2.42	0.40
9:LC:224:ILE:HA	9:LC:225:PRO:HD3	1.97	0.40
24:LS:69:GLU:HG2	24:LS:101:THR:HB	2.04	0.40
31:LZ:50:PRO:HD3	31:LZ:68:ILE:HG13	2.03	0.40
49:S2:222:U:H5''	61:SL:17:PHE:CG	2.56	0.40
58:SI:113:TYR:HB3	58:SI:121:LEU:HD11	2.03	0.40
66:SR:105:MET:HE2	66:SR:105:MET:HB3	1.85	0.40
81:Sg:149:GLU:OE2	81:Sg:171:ASP:N	2.54	0.40
4:L5:496:G:H2'	4:L5:498:C:H5''	2.04	0.40
4:L5:1699:A:H2'	4:L5:1700:G:N3	2.36	0.40
4:L5:2705:G:N1	4:L5:2706:G:N7	2.69	0.40
9:LC:14:LYS:HE2	9:LC:14:LYS:HB2	1.94	0.40
9:LC:128:LEU:O	9:LC:131:SER:OG	2.40	0.40
9:LC:155:GLU:HG3	9:LC:157:LYS:H	1.86	0.40
21:LP:52:THR:O	21:LP:85:LYS:NZ	2.53	0.40
22:LQ:105:VAL:HG11	22:LQ:120:ILE:HD13	2.03	0.40
26:LU:36:ALA:O	26:LU:40:GLU:N	2.46	0.40
29:LX:83:THR:HG22	29:LX:85:SER:H	1.86	0.40
36:Le:90:MET:HG2	48:Lr:33:LYS:HG2	2.03	0.40
36:Le:100:ALA:HB3	36:Le:103:VAL:HG23	2.03	0.40
47:Lp:39:CYS:SG	47:Lp:40:SER:N	2.94	0.40
49:S2:209:A:C5	49:S2:210:U:H1'	2.56	0.40
49:S2:835:C:O2'	49:S2:839:C:OP1	2.34	0.40
49:S2:1473:G:N2	49:S2:1476:A:OP2	2.41	0.40
52:SC:210:PRO:HB3	52:SC:240:THR:HG21	2.02	0.40
55:SF:71:ARG:NH1	55:SF:148:ASN:OD1	2.55	0.40
81:Sg:94:THR:HG23	81:Sg:96:THR:HG23	2.02	0.40
1:A4:50:U:H1'	1:A4:51:U:C2	2.56	0.40
4:L5:90:G:OP1	46:Lo:43:ARG:NH2	2.55	0.40
4:L5:2493:G:H2'	4:L5:2494:U:C2	2.57	0.40
4:L5:3706:C:H5''	7:LA:226:ARG:HB3	2.04	0.40
4:L5:4599:A:N6	4:L5:4611:A:OP2	2.54	0.40
4:L5:4910:G:N2	20:LO:106:ASP:O	2.54	0.40
9:LC:302:LEU:HB3	22:LQ:38:ARG:HG2	2.02	0.40
10:LD:163:LEU:HD21	10:LD:175:HIS:CG	2.56	0.40
27:LV:40:ILE:HD13	27:LV:40:ILE:HA	1.92	0.40
30:LY:103:LYS:HA	30:LY:103:LYS:HD3	1.89	0.40
39:Lh:26:VAL:O	39:Lh:29:SER:OG	2.35	0.40
49:S2:316:G:H5''	56:SG:183:ARG:HH22	1.86	0.40
49:S2:962:A:H5''	63:SO:66:ARG:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1648:G:O2'	49:S2:1674:G:O6	2.32	0.40
53:SD:53:THR:HG21	53:SD:94:ARG:HG3	2.03	0.40
53:SD:126:ILE:HD12	53:SD:188:ILE:HG12	2.04	0.40
60:SK:86:PRO:HA	60:SK:87:PRO:HD3	1.89	0.40
62:SN:80:LEU:HD12	62:SN:80:LEU:HA	1.94	0.40
67:SS:78:LYS:HD3	67:SS:78:LYS:HA	1.77	0.40
69:SU:65:THR:HG22	69:SU:66:ARG:H	1.87	0.40
71:SW:102:ILE:HG22	71:SW:128:PHE:HB3	2.02	0.40
72:SX:50:ILE:O	72:SX:73:GLN:N	2.52	0.40
81:Sg:106:LYS:HG2	81:Sg:107:ASP:H	1.87	0.40
81:Sg:111:VAL:HG22	81:Sg:123:GLY:HA3	2.03	0.40
4:L5:746:A:H2'	4:L5:747:A:C8	2.57	0.40
4:L5:2822:G:H5''	23:LR:18:GLY:HA3	2.04	0.40
4:L5:4280:A:N6	10:LD:28:THR:O	2.36	0.40
4:L5:4564:A:O2'	8:LB:261:ARG:HB2	2.21	0.40
18:LM:124:LYS:HE2	18:LM:124:LYS:HB2	1.91	0.40
18:LM:132:LYS:HB3	18:LM:132:LYS:HE2	1.85	0.40
37:Lf:87:LYS:HE2	37:Lf:87:LYS:HB3	1.87	0.40
41:Lj:34:CYS:SG	41:Lj:36:LYS:N	2.92	0.40
49:S2:976:G:N3	63:SO:50:LYS:NZ	2.69	0.40
49:S2:1033:G:N1	49:S2:1080:A:O2'	2.36	0.40
63:SO:31:CYS:HA	63:SO:44:VAL:HA	2.02	0.40
69:SU:97:ILE:HD12	69:SU:97:ILE:HA	1.93	0.40
81:Sg:217:MET:HE3	81:Sg:227:LEU:HB2	2.04	0.40
2:B4:29:G:H1	2:B4:39:C:H42	1.70	0.40
3:D4:40:C:H2'	3:D4:41:C:C6	2.57	0.40
4:L5:678:C:H4'	48:Lr:96:MET:HE2	2.02	0.40
4:L5:2377:C:H42	4:L5:2381:A:H62	1.69	0.40
4:L5:3890:A:N6	4:L5:4570:G:O2'	2.55	0.40
4:L5:4993:G:H1	4:L5:5058:A:H61	1.68	0.40
5:L7:114:U:O4	5:L7:115:A:N6	2.55	0.40
7:LA:248:GLY:HA3	49:S2:1069:U:H5''	2.02	0.40
12:LF:86:GLU:HA	12:LF:87:PRO:HD3	1.93	0.40
17:LL:130:LYS:HE2	17:LL:130:LYS:HB2	1.92	0.40
20:LO:93:LYS:HE3	20:LO:93:LYS:HB3	1.86	0.40
31:LZ:121:ARG:HE	31:LZ:121:ARG:HB3	1.63	0.40
34:Lc:34:THR:HG21	34:Lc:60:ILE:HD11	2.03	0.40
42:Lk:22:SER:O	42:Lk:37:ARG:N	2.48	0.40
49:S2:579:C:N3	73:SY:61:ARG:NH1	2.69	0.40
49:S2:1679:A:OP1	55:SF:60:ARG:NH2	2.55	0.40
54:SE:127:ARG:HB3	54:SE:140:VAL:HG23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SF:156:THR:HA	55:SF:159:ARG:HG3	2.02	0.40
58:SI:67:TRP:CD1	58:SI:70:GLU:H	2.40	0.40
62:SN:75:LEU:HD23	62:SN:75:LEU:HA	1.92	0.40
65:SQ:8:GLN:HB3	65:SQ:99:TYR:CZ	2.56	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	
7	LA	246/257 (96%)	212 (86%)	32 (13%)	2 (1%)	16	49
8	LB	389/403 (96%)	360 (92%)	29 (8%)	0	100	100
9	LC	363/427 (85%)	337 (93%)	25 (7%)	1 (0%)	36	67
10	LD	291/297 (98%)	271 (93%)	18 (6%)	2 (1%)	18	51
11	LE	214/288 (74%)	188 (88%)	25 (12%)	1 (0%)	24	57
12	LF	223/248 (90%)	208 (93%)	15 (7%)	0	100	100
13	LG	225/266 (85%)	201 (89%)	24 (11%)	0	100	100
14	LH	187/192 (97%)	171 (91%)	16 (9%)	0	100	100
15	LI	199/214 (93%)	179 (90%)	20 (10%)	0	100	100
16	LJ	165/178 (93%)	153 (93%)	11 (7%)	1 (1%)	21	54
17	LL	202/211 (96%)	181 (90%)	21 (10%)	0	100	100
18	LM	134/215 (62%)	121 (90%)	12 (9%)	1 (1%)	18	51
19	LN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
20	LO	199/203 (98%)	194 (98%)	5 (2%)	0	100	100
21	LP	151/184 (82%)	138 (91%)	13 (9%)	0	100	100
22	LQ	185/188 (98%)	174 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	LR	173/196 (88%)	168 (97%)	5 (3%)	0	100	100
24	LS	173/176 (98%)	154 (89%)	17 (10%)	2 (1%)	10	41
25	LT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
26	LU	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
27	LV	129/140 (92%)	118 (92%)	11 (8%)	0	100	100
28	LW	111/157 (71%)	103 (93%)	8 (7%)	0	100	100
29	LX	118/156 (76%)	105 (89%)	13 (11%)	0	100	100
30	LY	132/145 (91%)	119 (90%)	13 (10%)	0	100	100
31	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
32	La	142/148 (96%)	131 (92%)	11 (8%)	0	100	100
33	Lb	61/159 (38%)	57 (93%)	4 (7%)	0	100	100
34	Lc	91/115 (79%)	86 (94%)	5 (6%)	0	100	100
35	Ld	105/125 (84%)	96 (91%)	9 (9%)	0	100	100
36	Le	125/135 (93%)	119 (95%)	6 (5%)	0	100	100
37	Lf	107/110 (97%)	95 (89%)	12 (11%)	0	100	100
38	Lg	108/117 (92%)	97 (90%)	11 (10%)	0	100	100
39	Lh	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
40	Li	99/105 (94%)	97 (98%)	2 (2%)	0	100	100
41	Lj	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
42	Lk	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
43	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
44	Lm	48/128 (38%)	45 (94%)	3 (6%)	0	100	100
45	Ln	22/25 (88%)	22 (100%)	0	0	100	100
46	Lo	96/106 (91%)	87 (91%)	9 (9%)	0	100	100
47	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
48	Lr	123/137 (90%)	113 (92%)	10 (8%)	0	100	100
50	SA	210/295 (71%)	191 (91%)	19 (9%)	0	100	100
51	SB	212/264 (80%)	199 (94%)	13 (6%)	0	100	100
52	SC	215/293 (73%)	206 (96%)	9 (4%)	0	100	100
53	SD	207/243 (85%)	188 (91%)	18 (9%)	1 (0%)	24	57
54	SE	255/263 (97%)	225 (88%)	30 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	SF	176/204 (86%)	167 (95%)	9 (5%)	0	100	100
56	SG	200/249 (80%)	186 (93%)	14 (7%)	0	100	100
57	SH	168/194 (87%)	149 (89%)	19 (11%)	0	100	100
58	SI	183/208 (88%)	165 (90%)	18 (10%)	0	100	100
59	SJ	174/194 (90%)	163 (94%)	9 (5%)	2 (1%)	11	43
60	SK	93/165 (56%)	83 (89%)	10 (11%)	0	100	100
61	SL	136/158 (86%)	123 (90%)	13 (10%)	0	100	100
62	SN	148/151 (98%)	135 (91%)	13 (9%)	0	100	100
63	SO	133/151 (88%)	118 (89%)	15 (11%)	0	100	100
64	SP	123/145 (85%)	109 (89%)	12 (10%)	2 (2%)	7	36
65	SQ	139/146 (95%)	133 (96%)	6 (4%)	0	100	100
66	SR	123/135 (91%)	102 (83%)	20 (16%)	1 (1%)	16	49
67	SS	136/152 (90%)	118 (87%)	18 (13%)	0	100	100
68	ST	139/145 (96%)	130 (94%)	9 (6%)	0	100	100
69	SU	96/119 (81%)	87 (91%)	9 (9%)	0	100	100
70	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
71	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
72	SX	139/143 (97%)	120 (86%)	18 (13%)	1 (1%)	18	51
73	SY	111/133 (84%)	104 (94%)	7 (6%)	0	100	100
74	SZ	68/125 (54%)	61 (90%)	7 (10%)	0	100	100
75	Sa	97/115 (84%)	83 (86%)	14 (14%)	0	100	100
76	Sb	81/84 (96%)	67 (83%)	12 (15%)	2 (2%)	4	28
77	Sc	59/69 (86%)	49 (83%)	10 (17%)	0	100	100
78	Sd	50/56 (89%)	46 (92%)	4 (8%)	0	100	100
79	Se	47/59 (80%)	41 (87%)	6 (13%)	0	100	100
80	Sf	68/132 (52%)	59 (87%)	9 (13%)	0	100	100
81	Sg	259/317 (82%)	216 (83%)	43 (17%)	0	100	100
82	sh	35/156 (22%)	30 (86%)	5 (14%)	0	100	100
All	All	10821/12688 (85%)	9894 (91%)	908 (8%)	19 (0%)	44	74

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	LC	111	TRP
24	LS	164	LYS
64	SP	38	SER
66	SR	23	ARG
72	SX	10	ALA
59	SJ	110	LEU
64	SP	73	PRO
76	Sb	20	LYS
7	LA	246	LEU
10	LD	231	VAL
24	LS	18	PRO
53	SD	191	PRO
76	Sb	39	GLY
11	LE	100	LYS
18	LM	32	ASP
10	LD	232	THR
16	LJ	123	ILE
59	SJ	108	ARG
7	LA	15	VAL

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	
7	LA	187/199 (94%)	183 (98%)	4 (2%)	47	66
8	LB	324/349 (93%)	319 (98%)	5 (2%)	57	71
9	LC	301/348 (86%)	300 (100%)	1 (0%)	86	83
10	LD	218/250 (87%)	216 (99%)	2 (1%)	70	76
11	LE	179/252 (71%)	179 (100%)	0	100	100
12	LF	187/215 (87%)	185 (99%)	2 (1%)	65	74
13	LG	167/223 (75%)	165 (99%)	2 (1%)	63	73
14	LH	150/171 (88%)	148 (99%)	2 (1%)	61	72
15	LI	156/181 (86%)	153 (98%)	3 (2%)	50	68
16	LJ	113/149 (76%)	110 (97%)	3 (3%)	39	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	LL	152/177 (86%)	151 (99%)	1 (1%)	76	78
18	LM	110/161 (68%)	108 (98%)	2 (2%)	51	69
19	LN	169/172 (98%)	168 (99%)	1 (1%)	78	79
20	LO	163/174 (94%)	163 (100%)	0	100	100
21	LP	124/163 (76%)	124 (100%)	0	100	100
22	LQ	159/165 (96%)	155 (98%)	4 (2%)	42	63
23	LR	141/175 (81%)	141 (100%)	0	100	100
24	LS	151/157 (96%)	150 (99%)	1 (1%)	76	78
25	LT	130/140 (93%)	128 (98%)	2 (2%)	57	71
26	LU	77/115 (67%)	74 (96%)	3 (4%)	28	54
27	LV	94/107 (88%)	94 (100%)	0	100	100
28	LW	54/126 (43%)	54 (100%)	0	100	100
29	LX	98/133 (74%)	97 (99%)	1 (1%)	68	75
30	LY	116/135 (86%)	114 (98%)	2 (2%)	53	70
31	LZ	109/118 (92%)	108 (99%)	1 (1%)	70	76
32	La	116/121 (96%)	115 (99%)	1 (1%)	70	76
33	Lb	49/126 (39%)	49 (100%)	0	100	100
34	Lc	76/97 (78%)	73 (96%)	3 (4%)	28	54
35	Ld	88/110 (80%)	88 (100%)	0	100	100
36	Le	113/121 (93%)	113 (100%)	0	100	100
37	Lf	85/89 (96%)	85 (100%)	0	100	100
38	Lg	88/100 (88%)	88 (100%)	0	100	100
39	Lh	100/110 (91%)	99 (99%)	1 (1%)	68	75
40	Li	79/89 (89%)	78 (99%)	1 (1%)	61	72
41	Lj	72/80 (90%)	72 (100%)	0	100	100
42	Lk	52/65 (80%)	52 (100%)	0	100	100
43	Ll	46/48 (96%)	46 (100%)	0	100	100
44	Lm	42/116 (36%)	41 (98%)	1 (2%)	43	64
45	Ln	23/24 (96%)	23 (100%)	0	100	100
46	Lo	79/94 (84%)	77 (98%)	2 (2%)	42	63
47	Lp	70/75 (93%)	69 (99%)	1 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	Lr	103/121 (85%)	103 (100%)	0	100	100
50	SA	147/243 (60%)	144 (98%)	3 (2%)	48	67
51	SB	162/231 (70%)	162 (100%)	0	100	100
52	SC	155/225 (69%)	152 (98%)	3 (2%)	50	68
53	SD	126/202 (62%)	125 (99%)	1 (1%)	73	77
54	SE	176/225 (78%)	169 (96%)	7 (4%)	28	54
55	SF	133/170 (78%)	133 (100%)	0	100	100
56	SG	136/218 (62%)	136 (100%)	0	100	100
57	SH	134/174 (77%)	133 (99%)	1 (1%)	76	78
58	SI	141/180 (78%)	141 (100%)	0	100	100
59	SJ	140/168 (83%)	140 (100%)	0	100	100
60	SK	68/136 (50%)	67 (98%)	1 (2%)	57	71
61	SL	124/142 (87%)	124 (100%)	0	100	100
62	SN	127/131 (97%)	127 (100%)	0	100	100
63	SO	103/119 (87%)	102 (99%)	1 (1%)	68	75
64	SP	103/130 (79%)	103 (100%)	0	100	100
65	SQ	105/121 (87%)	102 (97%)	3 (3%)	37	60
66	SR	77/122 (63%)	77 (100%)	0	100	100
67	SS	103/132 (78%)	101 (98%)	2 (2%)	50	68
68	ST	82/115 (71%)	82 (100%)	0	100	100
69	SU	78/107 (73%)	78 (100%)	0	100	100
70	SV	53/67 (79%)	52 (98%)	1 (2%)	50	68
71	SW	110/113 (97%)	109 (99%)	1 (1%)	70	76
72	SX	101/115 (88%)	99 (98%)	2 (2%)	48	67
73	SY	79/115 (69%)	79 (100%)	0	100	100
74	SZ	40/103 (39%)	40 (100%)	0	100	100
75	Sa	79/98 (81%)	77 (98%)	2 (2%)	42	63
76	Sb	64/76 (84%)	63 (98%)	1 (2%)	55	70
77	Sc	41/62 (66%)	41 (100%)	0	100	100
78	Sd	42/49 (86%)	40 (95%)	2 (5%)	23	49
79	Se	37/48 (77%)	37 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	Sf	30/108 (28%)	30 (100%)	0	100	100
81	Sg	167/275 (61%)	163 (98%)	4 (2%)	43	64
82	sh	17/140 (12%)	17 (100%)	0	100	100
All	All	8390/10801 (78%)	8303 (99%)	87 (1%)	65	75

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	LA	44	ILE
7	LA	101	VAL
7	LA	136	VAL
7	LA	205	ASN
8	LB	67	VAL
8	LB	79	VAL
8	LB	258	HIS
8	LB	326	VAL
8	LB	346	THR
9	LC	246	VAL
10	LD	88	VAL
10	LD	223	PHE
12	LF	83	VAL
12	LF	164	LYS
13	LG	155	VAL
13	LG	156	VAL
14	LH	103	VAL
14	LH	104	VAL
15	LI	89	VAL
15	LI	197	VAL
15	LI	200	VAL
16	LJ	26	VAL
16	LJ	109	ILE
16	LJ	132	VAL
17	LL	64	VAL
18	LM	9	VAL
18	LM	31	ILE
19	LN	89	VAL
22	LQ	13	VAL
22	LQ	48	LEU
22	LQ	82	VAL
22	LQ	83	VAL
24	LS	129	VAL

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Mol	Chain	Res	Type
25	LT	42	ILE
25	LT	96	ILE
26	LU	22	THR
26	LU	33	ILE
26	LU	72	VAL
29	LX	97	VAL
30	LY	79	VAL
30	LY	96	HIS
31	LZ	53	VAL
32	La	144	CYS
34	Lc	47	ILE
34	Lc	48	LEU
34	Lc	71	VAL
39	Lh	58	LEU
40	Li	21	VAL
44	Lm	95	ILE
46	Lo	62	THR
46	Lo	70	LEU
47	Lp	52	VAL
50	SA	5	LEU
50	SA	157	VAL
50	SA	159	ILE
52	SC	106	VAL
52	SC	209	VAL
52	SC	248	TYR
53	SD	99	ILE
54	SE	72	ILE
54	SE	126	VAL
54	SE	183	VAL
54	SE	196	THR
54	SE	208	VAL
54	SE	210	VAL
54	SE	220	THR
57	SH	64	VAL
60	SK	11	ILE
63	SO	32	HIS
65	SQ	20	THR
65	SQ	55	VAL
65	SQ	72	VAL
67	SS	36	VAL
67	SS	79	ILE
70	SV	9	VAL

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Mol	Chain	Res	Type
71	SW	47	ILE
72	SX	70	VAL
72	SX	72	VAL
75	Sa	40	VAL
75	Sa	69	VAL
76	Sb	52	THR
78	Sd	23	VAL
78	Sd	49	ASP
81	Sg	108	VAL
81	Sg	176	VAL
81	Sg	192	THR
81	Sg	305	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (161) such sidechains are listed below:

Mol	Chain	Res	Type
7	LA	50	HIS
7	LA	132	ASN
7	LA	140	ASN
7	LA	217	GLN
7	LA	218	HIS
8	LB	109	HIS
8	LB	167	GLN
8	LB	236	HIS
8	LB	245	HIS
9	LC	50	GLN
9	LC	116	ASN
9	LC	119	GLN
9	LC	187	GLN
9	LC	212	ASN
9	LC	215	ASN
9	LC	317	ASN
9	LC	329	ASN
10	LD	63	GLN
10	LD	131	ASN
10	LD	175	HIS
10	LD	282	GLN
11	LE	182	ASN
11	LE	191	GLN
11	LE	256	GLN
11	LE	266	GLN
12	LF	56	HIS

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Mol	Chain	Res	Type
12	LF	58	HIS
12	LF	119	ASN
12	LF	192	HIS
13	LG	29	ASN
13	LG	64	GLN
13	LG	141	ASN
13	LG	149	ASN
14	LH	7	ASN
14	LH	8	GLN
14	LH	39	ASN
14	LH	79	ASN
14	LH	102	ASN
14	LH	149	ASN
15	LI	144	ASN
16	LJ	23	ASN
16	LJ	71	HIS
16	LJ	97	ASN
16	LJ	110	GLN
16	LJ	112	HIS
17	LL	104	ASN
17	LL	113	ASN
18	LM	34	ASN
18	LM	69	HIS
18	LM	78	GLN
19	LN	109	HIS
19	LN	199	GLN
20	LO	5	GLN
20	LO	14	HIS
20	LO	42	ASN
20	LO	50	ASN
20	LO	180	GLN
20	LO	199	HIS
21	LP	40	HIS
21	LP	56	GLN
21	LP	75	GLN
21	LP	80	GLN
21	LP	101	ASN
22	LQ	8	ASN
22	LQ	151	HIS
22	LQ	160	HIS
23	LR	30	ASN
23	LR	66	ASN

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Mol	Chain	Res	Type
23	LR	118	HIS
23	LR	141	HIS
24	LS	146	HIS
26	LU	95	ASN
27	LV	77	HIS
27	LV	84	GLN
27	LV	135	ASN
28	LW	59	HIS
29	LX	94	ASN
30	LY	14	ASN
30	LY	20	ASN
30	LY	72	GLN
31	LZ	40	HIS
32	La	14	HIS
33	Lb	60	ASN
34	Lc	40	GLN
34	Lc	72	HIS
35	Ld	116	ASN
35	Ld	121	ASN
36	Le	107	ASN
36	Le	117	GLN
37	Lf	21	GLN
37	Lf	78	HIS
37	Lf	99	HIS
39	Lh	63	GLN
39	Lh	101	ASN
40	Li	20	ASN
40	Li	26	HIS
41	Lj	13	ASN
41	Lj	48	ASN
41	Lj	66	HIS
42	Lk	28	ASN
43	Ll	17	GLN
43	Ll	20	ASN
43	Ll	33	ASN
43	Ll	38	ASN
44	Lm	104	HIS
44	Lm	120	ASN
48	Lr	4	HIS
48	Lr	30	ASN
48	Lr	45	HIS
50	SA	36	GLN

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Mol	Chain	Res	Type
50	SA	110	ASN
50	SA	113	GLN
50	SA	132	GLN
50	SA	193	HIS
51	SB	179	ASN
52	SC	136	HIS
52	SC	267	GLN
53	SD	101	GLN
53	SD	145	GLN
54	SE	142	HIS
54	SE	179	ASN
54	SE	197	ASN
55	SF	114	ASN
55	SF	149	GLN
55	SF	186	ASN
56	SG	59	GLN
56	SG	155	GLN
57	SH	39	GLN
57	SH	126	HIS
57	SH	157	HIS
57	SH	193	GLN
58	SI	146	GLN
58	SI	167	GLN
58	SI	181	GLN
59	SJ	113	GLN
59	SJ	124	HIS
59	SJ	125	HIS
61	SL	5	GLN
61	SL	141	ASN
62	SN	58	HIS
62	SN	101	HIS
62	SN	105	ASN
64	SP	35	GLN
64	SP	54	HIS
65	SQ	8	GLN
65	SQ	24	HIS
65	SQ	77	HIS
65	SQ	142	GLN
66	SR	31	ASN
66	SR	48	ASN
67	SS	72	GLN
68	ST	83	GLN

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Mol	Chain	Res	Type
72	SX	16	HIS
72	SX	20	GLN
72	SX	23	HIS
73	SY	85	ASN
76	Sb	26	GLN
77	Sc	29	GLN
80	Sf	19	GLN
80	Sf	82	ASN
81	Sg	237	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A4	12/16 (75%)	8 (66%)	1 (8%)
2	B4	74/75 (98%)	17 (22%)	0
3	D4	70/76 (92%)	29 (41%)	2 (2%)
4	L5	3555/5070 (70%)	895 (25%)	13 (0%)
49	S2	1644/1869 (87%)	505 (30%)	10 (0%)
5	L7	119/120 (99%)	20 (16%)	0
6	L8	155/156 (99%)	37 (23%)	2 (1%)
All	All	5629/7382 (76%)	1511 (26%)	28 (0%)

All (1511) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A4	43	U
1	A4	46	U
1	A4	48	U
1	A4	50	U
1	A4	51	U
1	A4	52	U
1	A4	53	U
1	A4	54	U
2	B4	2	G
2	B4	4	A
2	B4	8	U
2	B4	10	G
2	B4	12	G
2	B4	17	G
2	B4	18	G
2	B4	19	A

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Mol	Chain	Res	Type
2	B4	20	A
2	B4	21	G
2	B4	25	G
2	B4	48	G
2	B4	52	G
2	B4	54	U
2	B4	58	A
2	B4	69	G
2	B4	75	A
3	D4	2	C
3	D4	3	C
3	D4	6	G
3	D4	7	A
3	D4	8	U
3	D4	9	A
3	D4	10	G
3	D4	19	G
3	D4	29	G
3	D4	32	U
3	D4	33	U
3	D4	35	A
3	D4	37	A
3	D4	38	A
3	D4	41	C
3	D4	43	C
3	D4	45	U
3	D4	46	G
3	D4	47	U
3	D4	48	C
3	D4	49	C
3	D4	51	U
3	D4	57	G
3	D4	61	C
3	D4	62	C
3	D4	63	G
3	D4	64	A
3	D4	75	C
3	D4	76	A
4	L5	4	G
4	L5	9	C
4	L5	14	C
4	L5	17	A

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Mol	Chain	Res	Type
4	L5	21	G
4	L5	25	A
4	L5	30	C
4	L5	39	A
4	L5	42	A
4	L5	44	A
4	L5	47	A
4	L5	48	G
4	L5	56	A
4	L5	58	G
4	L5	59	A
4	L5	64	A
4	L5	65	A
4	L5	66	A
4	L5	68	U
4	L5	73	A
4	L5	84	A
4	L5	91	G
4	L5	98	A
4	L5	108	A
4	L5	109	G
4	L5	116	G
4	L5	117	C
4	L5	119	G
4	L5	120	A
4	L5	123	C
4	L5	124	C
4	L5	133	C
4	L5	134	G
4	L5	135	G
4	L5	136	C
4	L5	139	G
4	L5	144	G
4	L5	151	G
4	L5	152	U
4	L5	159	C
4	L5	165	A
4	L5	176	G
4	L5	177	G
4	L5	178	C
4	L5	181	C
4	L5	182	G

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Mol	Chain	Res	Type
4	L5	183	C
4	L5	184	U
4	L5	185	C
4	L5	187	U
4	L5	188	G
4	L5	189	G
4	L5	200	U
4	L5	209	U
4	L5	210	C
4	L5	216	C
4	L5	217	C
4	L5	218	A
4	L5	225	G
4	L5	233	U
4	L5	234	G
4	L5	257	C
4	L5	258	G
4	L5	261	G
4	L5	265	C
4	L5	266	C
4	L5	267	G
4	L5	276	C
4	L5	278	G
4	L5	280	G
4	L5	292	G
4	L5	297	U
4	L5	306	A
4	L5	309	C
4	L5	315	G
4	L5	316	U
4	L5	326	C
4	L5	340	C
4	L5	341	G
4	L5	350	C
4	L5	363	A
4	L5	379	G
4	L5	387	G
4	L5	388	A
4	L5	398	A
4	L5	399	G
4	L5	406	C
4	L5	407	A

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Mol	Chain	Res	Type
4	L5	408	A
4	L5	409	G
4	L5	410	A
4	L5	411	G
4	L5	412	G
4	L5	413	G
4	L5	429	A
4	L5	437	G
4	L5	440	U
4	L5	449	C
4	L5	450	G
4	L5	452	A
4	L5	453	G
4	L5	454	U
4	L5	456	C
4	L5	457	G
4	L5	464	G
4	L5	465	G
4	L5	467	U
4	L5	484	U
4	L5	485	C
4	L5	486	C
4	L5	494	U
4	L5	496	G
4	L5	497	G
4	L5	498	C
4	L5	500	G
4	L5	501	C
4	L5	502	C
4	L5	503	C
4	L5	504	G
4	L5	505	G
4	L5	509	A
4	L5	510	U
4	L5	511	C
4	L5	512	U
4	L5	513	U
4	L5	514	U
4	L5	515	C
4	L5	517	C
4	L5	518	G
4	L5	519	C

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Mol	Chain	Res	Type
4	L5	643	C
4	L5	644	G
4	L5	646	G
4	L5	654	C
4	L5	656	C
4	L5	657	C
4	L5	659	G
4	L5	663	G
4	L5	665	C
4	L5	666	G
4	L5	667	A
4	L5	668	C
4	L5	669	C
4	L5	673	C
4	L5	674	G
4	L5	685	C
4	L5	686	A
4	L5	687	U
4	L5	688	U
4	L5	696	C
4	L5	703	G
4	L5	704	C
4	L5	708	G
4	L5	719	C
4	L5	731	G
4	L5	738	C
4	L5	739	G
4	L5	742	G
4	L5	744	G
4	L5	746	A
4	L5	747	A
4	L5	753	C
4	L5	754	U
4	L5	755	C
4	L5	757	G
4	L5	758	G
4	L5	760	G
4	L5	904	C
4	L5	905	C
4	L5	912	G
4	L5	913	U
4	L5	914	U

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Mol	Chain	Res	Type
4	L5	915	A
4	L5	916	C
4	L5	917	A
4	L5	918	G
4	L5	923	C
4	L5	924	C
4	L5	926	G
4	L5	932	A
4	L5	933	G
4	L5	934	C
4	L5	935	A
4	L5	941	C
4	L5	943	A
4	L5	944	A
4	L5	945	U
4	L5	959	G
4	L5	960	A
4	L5	961	G
4	L5	962	C
4	L5	963	G
4	L5	965	G
4	L5	966	A
4	L5	970	G
4	L5	971	U
4	L5	977	C
4	L5	982	U
4	L5	984	C
4	L5	985	C
4	L5	988	C
4	L5	989	U
4	L5	990	C
4	L5	991	C
4	L5	992	C
4	L5	1066	G
4	L5	1069	G
4	L5	1070	G
4	L5	1073	G
4	L5	1074	G
4	L5	1082	C
4	L5	1083	U
4	L5	1095	A
4	L5	1168	G

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Mol	Chain	Res	Type
4	L5	1171	G
4	L5	1173	G
4	L5	1178	G
4	L5	1179	U
4	L5	1180	C
4	L5	1181	C
4	L5	1182	C
4	L5	1183	C
4	L5	1184	A
4	L5	1191	C
4	L5	1193	C
4	L5	1196	G
4	L5	1198	G
4	L5	1200	G
4	L5	1202	C
4	L5	1203	G
4	L5	1211	G
4	L5	1214	C
4	L5	1215	C
4	L5	1216	C
4	L5	1217	G
4	L5	1218	G
4	L5	1219	G
4	L5	1220	G
4	L5	1222	A
4	L5	1235	G
4	L5	1240	G
4	L5	1241	C
4	L5	1243	C
4	L5	1253	G
4	L5	1261	G
4	L5	1262	G
4	L5	1265	G
4	L5	1269	G
4	L5	1271	G
4	L5	1272	C
4	L5	1273	G
4	L5	1274	A
4	L5	1275	G
4	L5	1277	G
4	L5	1280	C
4	L5	1284	G

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Mol	Chain	Res	Type
4	L5	1293	G
4	L5	1294	A
4	L5	1295	C
4	L5	1296	G
4	L5	1298	C
4	L5	1301	C
4	L5	1324	A
4	L5	1326	A
4	L5	1337	A
4	L5	1354	A
4	L5	1358	G
4	L5	1359	G
4	L5	1364	U
4	L5	1365	C
4	L5	1366	G
4	L5	1370	G
4	L5	1379	C
4	L5	1382	G
4	L5	1387	A
4	L5	1394	G
4	L5	1398	A
4	L5	1399	G
4	L5	1402	C
4	L5	1404	G
4	L5	1405	C
4	L5	1407	C
4	L5	1409	C
4	L5	1410	U
4	L5	1411	C
4	L5	1415	G
4	L5	1420	A
4	L5	1425	G
4	L5	1435	G
4	L5	1439	C
4	L5	1443	A
4	L5	1444	G
4	L5	1447	C
4	L5	1453	G
4	L5	1476	C
4	L5	1481	C
4	L5	1482	G
4	L5	1483	C

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Mol	Chain	Res	Type
4	L5	1486	C
4	L5	1493	G
4	L5	1497	A
4	L5	1498	G
4	L5	1502	G
4	L5	1513	U
4	L5	1518	A
4	L5	1523	A
4	L5	1525	A
4	L5	1534	A
4	L5	1543	G
4	L5	1547	A
4	L5	1549	G
4	L5	1566	C
4	L5	1578	U
4	L5	1586	G
4	L5	1591	U
4	L5	1596	U
4	L5	1597	G
4	L5	1624	G
4	L5	1625	G
4	L5	1631	A
4	L5	1633	G
4	L5	1634	A
4	L5	1638	A
4	L5	1641	G
4	L5	1649	U
4	L5	1650	A
4	L5	1654	G
4	L5	1656	U
4	L5	1661	C
4	L5	1670	G
4	L5	1676	C
4	L5	1677	U
4	L5	1679	A
4	L5	1681	G
4	L5	1685	G
4	L5	1691	G
4	L5	1697	G
4	L5	1698	C
4	L5	1699	A
4	L5	1701	A

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Mol	Chain	Res	Type
4	L5	1703	C
4	L5	1704	C
4	L5	1705	G
4	L5	1707	C
4	L5	1716	G
4	L5	1717	C
4	L5	1719	A
4	L5	1726	U
4	L5	1729	A
4	L5	1734	G
4	L5	1742	A
4	L5	1745	G
4	L5	1750	G
4	L5	1754	U
4	L5	1758	G
4	L5	1759	G
4	L5	1760	G
4	L5	1761	G
4	L5	1762	C
4	L5	1772	C
4	L5	1775	A
4	L5	1785	C
4	L5	1787	A
4	L5	1804	A
4	L5	1810	G
4	L5	1815	G
4	L5	1820	C
4	L5	1821	G
4	L5	1822	U
4	L5	1829	G
4	L5	1834	U
4	L5	1836	G
4	L5	1837	A
4	L5	1842	G
4	L5	1855	G
4	L5	1867	A
4	L5	1869	G
4	L5	1881	C
4	L5	1882	U
4	L5	1889	U
4	L5	1890	G
4	L5	1897	A

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Mol	Chain	Res	Type
4	L5	1915	C
4	L5	1916	G
4	L5	1918	U
4	L5	1919	G
4	L5	1920	C
4	L5	1921	C
4	L5	1922	G
4	L5	1931	C
4	L5	1932	A
4	L5	1935	C
4	L5	1936	C
4	L5	1940	G
4	L5	1941	A
4	L5	1945	G
4	L5	1947	U
4	L5	1948	G
4	L5	1953	U
4	L5	1959	U
4	L5	1960	A
4	L5	1961	G
4	L5	1962	A
4	L5	1966	C
4	L5	1967	A
4	L5	1968	G
4	L5	1969	G
4	L5	1970	A
4	L5	1971	C
4	L5	1995	G
4	L5	1996	C
4	L5	1997	U
4	L5	1999	A
4	L5	2018	C
4	L5	2020	U
4	L5	2021	G
4	L5	2024	G
4	L5	2025	A
4	L5	2026	A
4	L5	2028	C
4	L5	2040	A
4	L5	2046	G
4	L5	2048	U
4	L5	2055	G

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Mol	Chain	Res	Type
4	L5	2056	G
4	L5	2069	A
4	L5	2084	C
4	L5	2085	G
4	L5	2089	G
4	L5	2092	G
4	L5	2093	A
4	L5	2094	G
4	L5	2095	A
4	L5	2096	G
4	L5	2097	U
4	L5	2098	G
4	L5	2101	C
4	L5	2102	G
4	L5	2103	G
4	L5	2106	G
4	L5	2107	C
4	L5	2116	C
4	L5	2117	G
4	L5	2118	G
4	L5	2119	C
4	L5	2120	G
4	L5	2121	C
4	L5	2122	G
4	L5	2123	C
4	L5	2255	C
4	L5	2256	C
4	L5	2258	C
4	L5	2269	C
4	L5	2289	C
4	L5	2294	G
4	L5	2299	G
4	L5	2300	A
4	L5	2301	G
4	L5	2313	A
4	L5	2331	G
4	L5	2332	A
4	L5	2333	G
4	L5	2342	G
4	L5	2346	C
4	L5	2348	G
4	L5	2351	C

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Mol	Chain	Res	Type
4	L5	2357	G
4	L5	2360	A
4	L5	2395	A
4	L5	2396	A
4	L5	2397	G
4	L5	2398	U
4	L5	2402	G
4	L5	2408	U
4	L5	2417	A
4	L5	2421	G
4	L5	2422	C
4	L5	2425	U
4	L5	2437	C
4	L5	2441	C
4	L5	2450	G
4	L5	2456	G
4	L5	2464	C
4	L5	2465	C
4	L5	2474	G
4	L5	2475	G
4	L5	2478	C
4	L5	2483	G
4	L5	2484	A
4	L5	2492	C
4	L5	2493	G
4	L5	2494	U
4	L5	2503	G
4	L5	2504	C
4	L5	2505	C
4	L5	2506	G
4	L5	2511	A
4	L5	2513	A
4	L5	2519	U
4	L5	2520	C
4	L5	2529	A
4	L5	2537	A
4	L5	2544	G
4	L5	2546	G
4	L5	2547	G
4	L5	2554	U
4	L5	2559	G
4	L5	2565	A

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Mol	Chain	Res	Type
4	L5	2573	A
4	L5	2583	C
4	L5	2586	G
4	L5	2587	A
4	L5	2588	C
4	L5	2600	A
4	L5	2602	G
4	L5	2611	A
4	L5	2618	G
4	L5	2627	C
4	L5	2638	G
4	L5	2643	G
4	L5	2653	C
4	L5	2658	G
4	L5	2661	U
4	L5	2662	G
4	L5	2664	G
4	L5	2669	C
4	L5	2670	C
4	L5	2673	G
4	L5	2675	G
4	L5	2676	A
4	L5	2679	G
4	L5	2687	U
4	L5	2694	G
4	L5	2695	A
4	L5	2696	A
4	L5	2703	G
4	L5	2707	U
4	L5	2708	U
4	L5	2711	G
4	L5	2714	G
4	L5	2721	G
4	L5	2724	G
4	L5	2726	G
4	L5	2727	C
4	L5	2732	G
4	L5	2739	C
4	L5	2742	G
4	L5	2743	A
4	L5	2754	G
4	L5	2756	G

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Mol	Chain	Res	Type
4	L5	2761	U
4	L5	2763	U
4	L5	2770	C
4	L5	2788	U
4	L5	2790	U
4	L5	2793	G
4	L5	2794	C
4	L5	2796	G
4	L5	2814	C
4	L5	2815	A
4	L5	2826	U
4	L5	2827	G
4	L5	2830	G
4	L5	2840	A
4	L5	2855	G
4	L5	2856	C
4	L5	2867	C
4	L5	2877	G
4	L5	2892	C
4	L5	2894	A
4	L5	2900	U
4	L5	2902	G
4	L5	2903	G
4	L5	2905	C
4	L5	3585	G
4	L5	3587	C
4	L5	3588	C
4	L5	3590	G
4	L5	3591	C
4	L5	3593	C
4	L5	3594	C
4	L5	3595	U
4	L5	3596	A
4	L5	3597	G
4	L5	3599	A
4	L5	3604	A
4	L5	3605	C
4	L5	3606	U
4	L5	3615	G
4	L5	3616	U
4	L5	3618	C
4	L5	3626	G

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Mol	Chain	Res	Type
4	L5	3630	A
4	L5	3635	A
4	L5	3643	A
4	L5	3644	U
4	L5	3646	A
4	L5	3648	A
4	L5	3649	A
4	L5	3662	A
4	L5	3663	A
4	L5	3672	G
4	L5	3673	C
4	L5	3674	G
4	L5	3680	U
4	L5	3683	C
4	L5	3685	C
4	L5	3691	G
4	L5	3692	A
4	L5	3696	C
4	L5	3710	G
4	L5	3711	A
4	L5	3713	U
4	L5	3714	G
4	L5	3729	U
4	L5	3732	A
4	L5	3735	G
4	L5	3736	A
4	L5	3750	G
4	L5	3753	G
4	L5	3754	G
4	L5	3756	A
4	L5	3757	G
4	L5	3758	U
4	L5	3760	A
4	L5	3769	C
4	L5	3771	C
4	L5	3773	U
4	L5	3774	A
4	L5	3775	A
4	L5	3776	G
4	L5	3777	G
4	L5	3783	A
4	L5	3784	A

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Mol	Chain	Res	Type
4	L5	3786	U
4	L5	3791	C
4	L5	3802	U
4	L5	3810	C
4	L5	3811	G
4	L5	3812	C
4	L5	3813	A
4	L5	3814	U
4	L5	3817	A
4	L5	3818	U
4	L5	3819	G
4	L5	3838	U
4	L5	3839	G
4	L5	3840	U
4	L5	3876	A
4	L5	3877	A
4	L5	3878	C
4	L5	3879	G
4	L5	3885	G
4	L5	3890	A
4	L5	3892	U
4	L5	3897	G
4	L5	3898	G
4	L5	3901	A
4	L5	3906	A
4	L5	3907	G
4	L5	3908	A
4	L5	3915	U
4	L5	3916	G
4	L5	3926	C
4	L5	3939	G
4	L5	3941	G
4	L5	3942	A
4	L5	3943	A
4	L5	3945	A
4	L5	3946	G
4	L5	3947	A
4	L5	4069	U
4	L5	4070	U
4	L5	4071	U
4	L5	4075	U
4	L5	4076	G

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Mol	Chain	Res	Type
4	L5	4084	G
4	L5	4085	A
4	L5	4086	G
4	L5	4091	G
4	L5	4094	G
4	L5	4095	G
4	L5	4099	G
4	L5	4101	C
4	L5	4110	C
4	L5	4112	C
4	L5	4113	U
4	L5	4114	C
4	L5	4115	G
4	L5	4116	C
4	L5	4117	U
4	L5	4119	C
4	L5	4127	A
4	L5	4132	C
4	L5	4133	C
4	L5	4135	G
4	L5	4137	C
4	L5	4139	G
4	L5	4140	C
4	L5	4141	G
4	L5	4142	C
4	L5	4143	G
4	L5	4144	C
4	L5	4145	C
4	L5	4147	G
4	L5	4150	G
4	L5	4157	A
4	L5	4162	C
4	L5	4163	U
4	L5	4170	A
4	L5	4183	G
4	L5	4184	G
4	L5	4191	G
4	L5	4201	G
4	L5	4212	A
4	L5	4215	C
4	L5	4220	A
4	L5	4222	G

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Mol	Chain	Res	Type
4	L5	4225	G
4	L5	4229	U
4	L5	4233	A
4	L5	4251	A
4	L5	4254	G
4	L5	4255	A
4	L5	4256	A
4	L5	4257	A
4	L5	4258	C
4	L5	4265	U
4	L5	4268	A
4	L5	4273	A
4	L5	4281	A
4	L5	4291	G
4	L5	4297	G
4	L5	4304	A
4	L5	4305	G
4	L5	4306	U
4	L5	4314	C
4	L5	4319	C
4	L5	4326	G
4	L5	4329	G
4	L5	4330	G
4	L5	4332	C
4	L5	4339	A
4	L5	4349	C
4	L5	4354	U
4	L5	4373	G
4	L5	4377	G
4	L5	4378	A
4	L5	4380	A
4	L5	4381	A
4	L5	4386	C
4	L5	4387	C
4	L5	4391	G
4	L5	4394	A
4	L5	4415	A
4	L5	4420	U
4	L5	4422	A
4	L5	4426	C
4	L5	4444	C
4	L5	4448	G

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Mol	Chain	Res	Type
4	L5	4449	A
4	L5	4452	U
4	L5	4453	C
4	L5	4464	A
4	L5	4466	C
4	L5	4481	U
4	L5	4488	A
4	L5	4500	U
4	L5	4510	A
4	L5	4512	U
4	L5	4513	A
4	L5	4519	C
4	L5	4524	G
4	L5	4528	G
4	L5	4531	U
4	L5	4545	G
4	L5	4548	A
4	L5	4549	G
4	L5	4554	G
4	L5	4560	C
4	L5	4567	G
4	L5	4572	U
4	L5	4573	G
4	L5	4575	G
4	L5	4589	A
4	L5	4590	A
4	L5	4599	A
4	L5	4600	G
4	L5	4601	U
4	L5	4617	G
4	L5	4624	A
4	L5	4627	U
4	L5	4635	A
4	L5	4636	U
4	L5	4637	G
4	L5	4652	G
4	L5	4656	A
4	L5	4658	G
4	L5	4670	C
4	L5	4671	C
4	L5	4672	A
4	L5	4678	G

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Mol	Chain	Res	Type
4	L5	4679	G
4	L5	4687	A
4	L5	4695	C
4	L5	4700	A
4	L5	4702	G
4	L5	4708	A
4	L5	4709	U
4	L5	4719	G
4	L5	4722	G
4	L5	4730	C
4	L5	4731	G
4	L5	4732	G
4	L5	4733	C
4	L5	4734	A
4	L5	4740	G
4	L5	4741	C
4	L5	4742	G
4	L5	4745	G
4	L5	4747	C
4	L5	4757	C
4	L5	4759	C
4	L5	4761	G
4	L5	4765	G
4	L5	4766	C
4	L5	4773	C
4	L5	4774	C
4	L5	4775	C
4	L5	4776	G
4	L5	4859	C
4	L5	4862	G
4	L5	4864	U
4	L5	4870	G
4	L5	4871	C
4	L5	4873	G
4	L5	4875	G
4	L5	4882	U
4	L5	4883	C
4	L5	4889	G
4	L5	4895	C
4	L5	4896	G
4	L5	4899	G
4	L5	4900	C

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Mol	Chain	Res	Type
4	L5	4901	G
4	L5	4902	C
4	L5	4910	G
4	L5	4911	A
4	L5	4912	G
4	L5	4913	G
4	L5	4914	C
4	L5	4916	G
4	L5	4921	C
4	L5	4923	C
4	L5	4925	U
4	L5	4927	G
4	L5	4928	C
4	L5	4931	G
4	L5	4932	U
4	L5	4934	A
4	L5	4938	A
4	L5	4941	G
4	L5	4943	A
4	L5	4944	C
4	L5	4947	U
4	L5	4949	G
4	L5	4951	G
4	L5	4955	A
4	L5	4960	G
4	L5	4961	G
4	L5	4963	G
4	L5	4966	A
4	L5	4967	A
4	L5	4976	U
4	L5	4985	U
4	L5	4988	U
4	L5	4989	U
4	L5	4990	C
4	L5	4991	U
4	L5	5014	A
4	L5	5017	G
4	L5	5022	U
4	L5	5029	C
4	L5	5030	U
4	L5	5034	A
4	L5	5040	U

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Mol	Chain	Res	Type
4	L5	5041	G
4	L5	5047	C
4	L5	5050	C
4	L5	5054	C
4	L5	5055	G
4	L5	5058	A
4	L5	5060	A
4	L5	5061	A
4	L5	5069	U
5	L7	22	A
5	L7	25	G
5	L7	27	G
5	L7	29	C
5	L7	30	C
5	L7	31	G
5	L7	36	C
5	L7	41	G
5	L7	42	A
5	L7	48	G
5	L7	50	A
5	L7	53	U
5	L7	54	A
5	L7	62	U
5	L7	63	C
5	L7	64	G
5	L7	97	G
5	L7	100	A
5	L7	110	G
5	L7	120	U
6	L8	22	U
6	L8	23	C
6	L8	34	U
6	L8	35	C
6	L8	38	U
6	L8	39	G
6	L8	48	A
6	L8	55	U
6	L8	59	A
6	L8	61	A
6	L8	62	A
6	L8	63	U
6	L8	77	A

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Mol	Chain	Res	Type
6	L8	80	A
6	L8	82	A
6	L8	83	C
6	L8	84	A
6	L8	85	U
6	L8	86	U
6	L8	87	G
6	L8	88	A
6	L8	103	A
6	L8	105	C
6	L8	109	C
6	L8	110	U
6	L8	111	U
6	L8	112	G
6	L8	114	G
6	L8	123	U
6	L8	124	U
6	L8	125	C
6	L8	126	C
6	L8	127	U
6	L8	135	C
6	L8	151	G
6	L8	153	C
6	L8	156	U
49	S2	2	A
49	S2	3	C
49	S2	9	U
49	S2	17	C
49	S2	25	A
49	S2	31	U
49	S2	33	G
49	S2	41	G
49	S2	42	A
49	S2	45	A
49	S2	46	A
49	S2	49	C
49	S2	54	A
49	S2	56	G
49	S2	58	C
49	S2	60	A
49	S2	64	A
49	S2	65	C

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Mol	Chain	Res	Type
49	S2	66	G
49	S2	67	C
49	S2	68	A
49	S2	70	G
49	S2	72	C
49	S2	73	C
49	S2	74	G
49	S2	75	G
49	S2	76	U
49	S2	77	A
49	S2	79	A
49	S2	93	U
49	S2	99	A
49	S2	101	U
49	S2	104	A
49	S2	108	G
49	S2	113	G
49	S2	114	G
49	S2	119	U
49	S2	125	C
49	S2	126	G
49	S2	127	C
49	S2	129	C
49	S2	130	G
49	S2	142	C
49	S2	143	U
49	S2	144	U
49	S2	148	U
49	S2	157	U
49	S2	160	U
49	S2	161	U
49	S2	162	C
49	S2	163	U
49	S2	168	C
49	S2	169	U
49	S2	170	A
49	S2	171	A
49	S2	172	U
49	S2	173	A
49	S2	175	A
49	S2	187	G
49	S2	191	A

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Mol	Chain	Res	Type
49	S2	194	C
49	S2	197	U
49	S2	198	U
49	S2	203	G
49	S2	210	U
49	S2	211	G
49	S2	214	U
49	S2	215	G
49	S2	220	U
49	S2	223	C
49	S2	224	A
49	S2	290	U
49	S2	293	C
49	S2	294	U
49	S2	295	C
49	S2	297	A
49	S2	302	A
49	S2	306	C
49	S2	307	G
49	S2	308	G
49	S2	309	G
49	S2	310	C
49	S2	311	C
49	S2	312	G
49	S2	318	A
49	S2	319	C
49	S2	322	C
49	S2	323	C
49	S2	328	U
49	S2	329	G
49	S2	331	C
49	S2	335	G
49	S2	339	A
49	S2	340	C
49	S2	347	G
49	S2	362	C
49	S2	364	A
49	S2	369	C
49	S2	370	G
49	S2	380	G
49	S2	381	C
49	S2	382	C

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Mol	Chain	Res	Type
49	S2	385	G
49	S2	386	C
49	S2	398	A
49	S2	400	C
49	S2	407	G
49	S2	408	A
49	S2	409	C
49	S2	413	G
49	S2	418	A
49	S2	428	U
49	S2	435	A
49	S2	438	G
49	S2	441	C
49	S2	448	A
49	S2	449	A
49	S2	450	C
49	S2	452	G
49	S2	453	C
49	S2	464	A
49	S2	465	A
49	S2	471	G
49	S2	472	C
49	S2	473	A
49	S2	482	G
49	S2	487	U
49	S2	488	U
49	S2	489	A
49	S2	492	C
49	S2	493	A
49	S2	496	C
49	S2	502	C
49	S2	503	C
49	S2	507	G
49	S2	513	G
49	S2	516	A
49	S2	517	C
49	S2	523	A
49	S2	525	A
49	S2	530	U
49	S2	531	A
49	S2	532	C
49	S2	533	A

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Mol	Chain	Res	Type
49	S2	534	G
49	S2	535	G
49	S2	536	A
49	S2	548	C
49	S2	551	U
49	S2	554	A
49	S2	556	U
49	S2	557	U
49	S2	558	G
49	S2	559	G
49	S2	562	U
49	S2	563	G
49	S2	573	U
49	S2	574	A
49	S2	575	A
49	S2	576	A
49	S2	581	U
49	S2	583	C
49	S2	585	C
49	S2	587	A
49	S2	588	G
49	S2	589	G
49	S2	590	A
49	S2	591	U
49	S2	592	C
49	S2	593	C
49	S2	594	A
49	S2	596	U
49	S2	598	G
49	S2	600	G
49	S2	604	A
49	S2	605	A
49	S2	606	G
49	S2	607	U
49	S2	608	C
49	S2	612	U
49	S2	613	G
49	S2	614	C
49	S2	617	G
49	S2	618	C
49	S2	621	C
49	S2	623	G

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Mol	Chain	Res	Type
49	S2	624	C
49	S2	628	A
49	S2	629	A
49	S2	632	C
49	S2	638	C
49	S2	643	A
49	S2	644	G
49	S2	650	A
49	S2	656	G
49	S2	660	C
49	S2	668	A
49	S2	669	A
49	S2	671	A
49	S2	672	A
49	S2	673	G
49	S2	683	G
49	S2	688	U
49	S2	689	U
49	S2	690	G
49	S2	691	G
49	S2	692	G
49	S2	693	A
49	S2	694	G
49	S2	696	G
49	S2	735	C
49	S2	736	C
49	S2	737	G
49	S2	738	C
49	S2	739	C
49	S2	797	C
49	S2	798	A
49	S2	799	U
49	S2	800	U
49	S2	801	U
49	S2	809	A
49	S2	810	A
49	S2	818	A
49	S2	821	G
49	S2	822	U
49	S2	824	C
49	S2	827	A
49	S2	830	A

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Mol	Chain	Res	Type
49	S2	835	C
49	S2	840	C
49	S2	842	C
49	S2	847	A
49	S2	851	C
49	S2	852	G
49	S2	856	C
49	S2	857	U
49	S2	859	G
49	S2	860	G
49	S2	865	A
49	S2	869	A
49	S2	870	A
49	S2	871	U
49	S2	872	A
49	S2	874	G
49	S2	877	C
49	S2	878	G
49	S2	879	C
49	S2	880	G
49	S2	881	G
49	S2	882	U
49	S2	889	U
49	S2	890	U
49	S2	898	U
49	S2	899	U
49	S2	900	C
49	S2	901	G
49	S2	904	A
49	S2	905	C
49	S2	907	G
49	S2	909	G
49	S2	913	A
49	S2	919	A
49	S2	920	A
49	S2	930	C
49	S2	933	G
49	S2	946	U
49	S2	950	C
49	S2	958	G
49	S2	963	A
49	S2	970	G

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Mol	Chain	Res	Type
49	S2	971	G
49	S2	972	A
49	S2	990	A
49	S2	992	A
49	S2	995	G
49	S2	999	G
49	S2	1001	A
49	S2	1002	U
49	S2	1008	A
49	S2	1016	U
49	S2	1017	U
49	S2	1023	A
49	S2	1027	A
49	S2	1043	G
49	S2	1049	A
49	S2	1060	A
49	S2	1061	U
49	S2	1062	A
49	S2	1065	G
49	S2	1078	C
49	S2	1082	A
49	S2	1083	A
49	S2	1084	A
49	S2	1085	C
49	S2	1086	G
49	S2	1087	A
49	S2	1109	C
49	S2	1110	G
49	S2	1113	A
49	S2	1114	U
49	S2	1115	U
49	S2	1116	C
49	S2	1119	A
49	S2	1126	G
49	S2	1131	G
49	S2	1133	A
49	S2	1138	C
49	S2	1139	C
49	S2	1148	A
49	S2	1149	A
49	S2	1150	A
49	S2	1153	C

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Mol	Chain	Res	Type
49	S2	1154	U
49	S2	1155	U
49	S2	1157	G
49	S2	1166	G
49	S2	1183	A
49	S2	1195	A
49	S2	1207	G
49	S2	1208	A
49	S2	1215	C
49	S2	1217	A
49	S2	1221	G
49	S2	1224	G
49	S2	1242	U
49	S2	1243	U
49	S2	1251	A
49	S2	1253	A
49	S2	1256	G
49	S2	1257	G
49	S2	1259	A
49	S2	1260	A
49	S2	1264	C
49	S2	1265	A
49	S2	1269	G
49	S2	1271	C
49	S2	1273	C
49	S2	1274	G
49	S2	1275	G
49	S2	1276	A
49	S2	1278	A
49	S2	1282	A
49	S2	1285	G
49	S2	1286	G
49	S2	1287	A
49	S2	1288	U
49	S2	1293	A
49	S2	1294	G
49	S2	1298	G
49	S2	1301	A
49	S2	1302	G
49	S2	1308	U
49	S2	1310	U
49	S2	1313	A

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Mol	Chain	Res	Type
49	S2	1314	U
49	S2	1321	G
49	S2	1326	U
49	S2	1330	G
49	S2	1331	C
49	S2	1332	A
49	S2	1342	U
49	S2	1348	G
49	S2	1371	U
49	S2	1372	U
49	S2	1373	C
49	S2	1378	A
49	S2	1382	A
49	S2	1396	A
49	S2	1397	U
49	S2	1401	A
49	S2	1403	C
49	S2	1409	A
49	S2	1414	A
49	S2	1415	C
49	S2	1423	C
49	S2	1424	G
49	S2	1429	G
49	S2	1447	G
49	S2	1449	G
49	S2	1450	G
49	S2	1452	A
49	S2	1454	A
49	S2	1455	A
49	S2	1462	U
49	S2	1463	U
49	S2	1474	A
49	S2	1477	U
49	S2	1484	A
49	S2	1487	A
49	S2	1489	A
49	S2	1490	G
49	S2	1495	G
49	S2	1505	U
49	S2	1506	A
49	S2	1507	G
49	S2	1508	A

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Mol	Chain	Res	Type
49	S2	1510	G
49	S2	1519	U
49	S2	1520	G
49	S2	1521	C
49	S2	1523	C
49	S2	1527	C
49	S2	1528	G
49	S2	1533	A
49	S2	1536	G
49	S2	1543	U
49	S2	1544	C
49	S2	1547	C
49	S2	1548	G
49	S2	1553	C
49	S2	1556	A
49	S2	1563	G
49	S2	1567	G
49	S2	1570	G
49	S2	1580	A
49	S2	1585	U
49	S2	1586	U
49	S2	1587	G
49	S2	1588	A
49	S2	1589	A
49	S2	1591	C
49	S2	1594	A
49	S2	1596	U
49	S2	1599	U
49	S2	1600	G
49	S2	1601	A
49	S2	1604	G
49	S2	1606	G
49	S2	1607	A
49	S2	1609	C
49	S2	1617	G
49	S2	1621	U
49	S2	1622	U
49	S2	1623	A
49	S2	1624	U
49	S2	1626	C
49	S2	1632	G
49	S2	1633	A

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Mol	Chain	Res	Type
49	S2	1634	A
49	S2	1636	G
49	S2	1637	A
49	S2	1638	G
49	S2	1639	G
49	S2	1641	A
49	S2	1643	U
49	S2	1646	C
49	S2	1647	A
49	S2	1648	G
49	S2	1652	G
49	S2	1654	G
49	S2	1662	U
49	S2	1663	A
49	S2	1664	A
49	S2	1665	G
49	S2	1666	C
49	S2	1678	A
49	S2	1680	G
49	S2	1698	C
49	S2	1699	A
49	S2	1701	C
49	S2	1709	G
49	S2	1715	A
49	S2	1719	A
49	S2	1721	U
49	S2	1722	G
49	S2	1726	G
49	S2	1728	U
49	S2	1729	U
49	S2	1742	C
49	S2	1744	G
49	S2	1745	A
49	S2	1748	G
49	S2	1754	G
49	S2	1755	C
49	S2	1756	C
49	S2	1757	G
49	S2	1758	G
49	S2	1761	U
49	S2	1778	C
49	S2	1779	G

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Mol	Chain	Res	Type
49	S2	1781	A
49	S2	1782	G
49	S2	1783	C
49	S2	1785	C
49	S2	1786	U
49	S2	1790	A
49	S2	1810	U
49	S2	1813	A
49	S2	1821	U
49	S2	1823	A
49	S2	1824	A
49	S2	1825	A
49	S2	1831	A
49	S2	1838	U
49	S2	1839	U
49	S2	1849	G
49	S2	1850	A
49	S2	1851	A
49	S2	1852	C
49	S2	1860	A
49	S2	1861	G
49	S2	1862	G
49	S2	1863	A
49	S2	1865	C
49	S2	1869	A

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A4	50	U
3	D4	34	G
3	D4	60	U
4	L5	406	C
4	L5	667	A
4	L5	914	U
4	L5	1082	C
4	L5	2019	C
4	L5	2117	G
4	L5	2416	G
4	L5	2675	G
4	L5	2760	G
4	L5	3614	G

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Mol	Chain	Res	Type
4	L5	3673	C
4	L5	4699	U
4	L5	4913	G
6	L8	86	U
6	L8	87	G
49	S2	532	C
49	S2	604	A
49	S2	688	U
49	S2	1207	G
49	S2	1273	C
49	S2	1519	U
49	S2	1585	U
49	S2	1664	A
49	S2	1824	A
49	S2	1860	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 167 ligands modelled in this entry, 167 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	LA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	LA	118:GLU	C	119:LYS	N	1.20

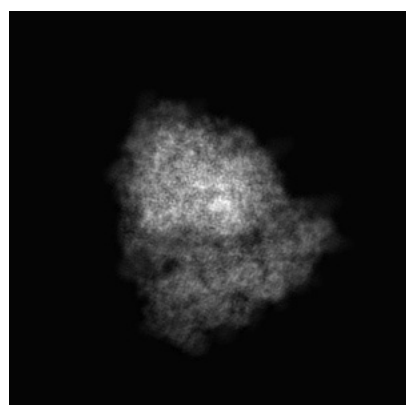
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10690. These allow visual inspection of the internal detail of the map and identification of artifacts.

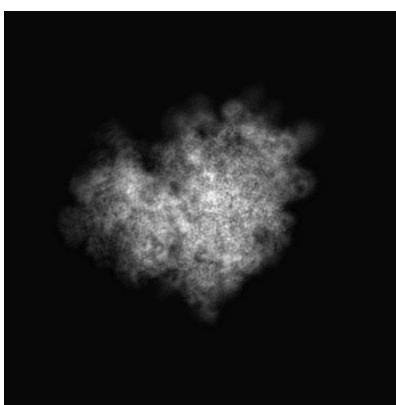
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

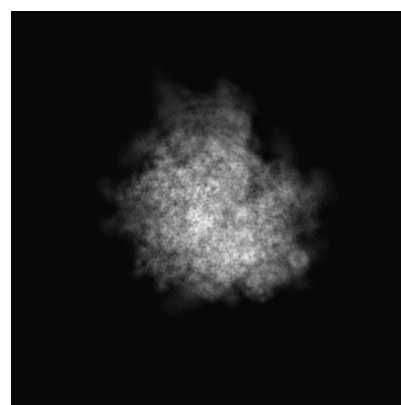
6.1.1 Primary map



X



Y

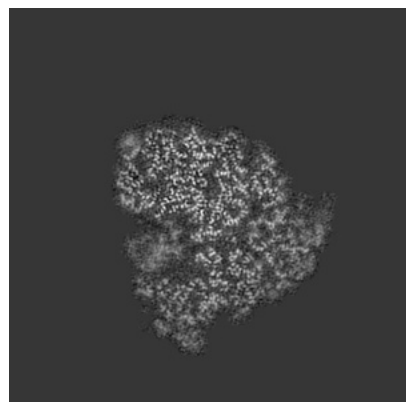


Z

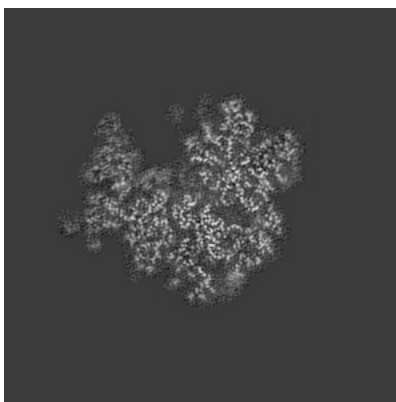
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

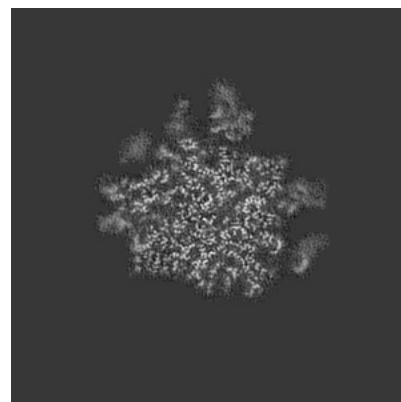
6.2.1 Primary map



X Index: 275



Y Index: 275

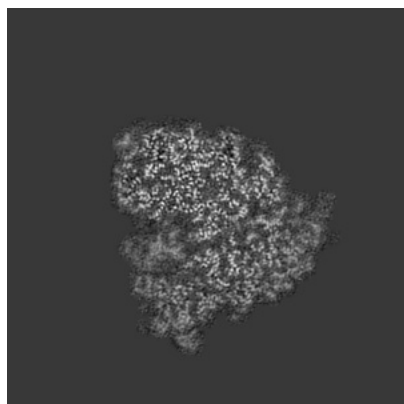


Z Index: 275

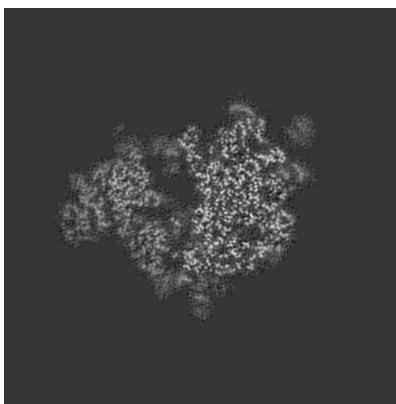
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

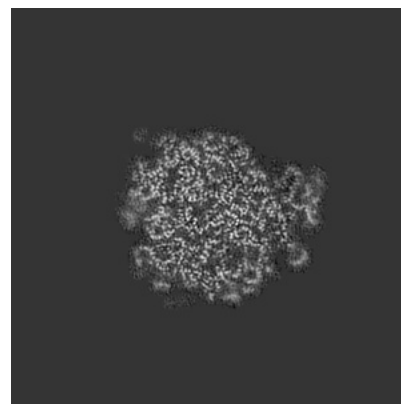
6.3.1 Primary map



X Index: 277



Y Index: 244

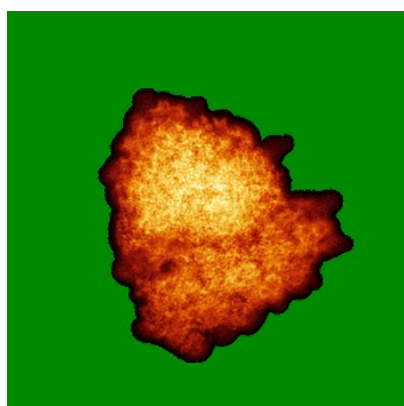


Z Index: 308

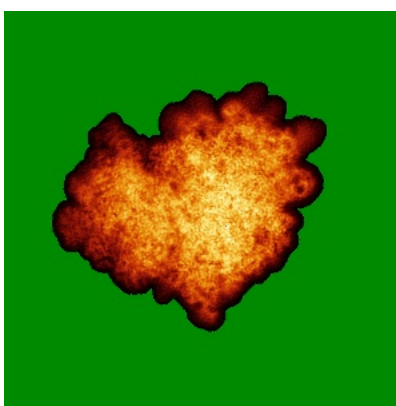
The images above show the largest variance slices of the map in three orthogonal directions.

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

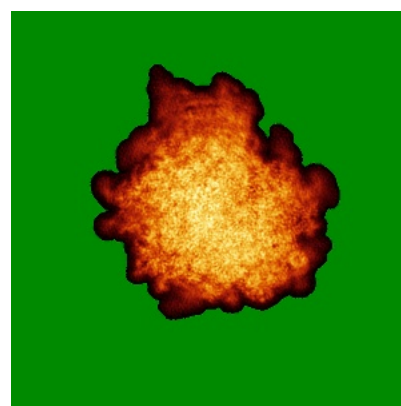
6.4.1 Primary map



X



Y



Z

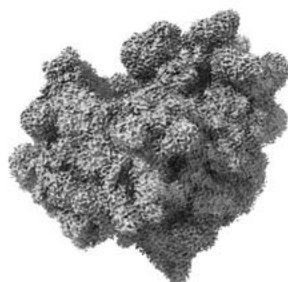
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

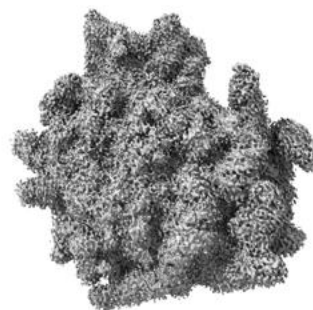
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

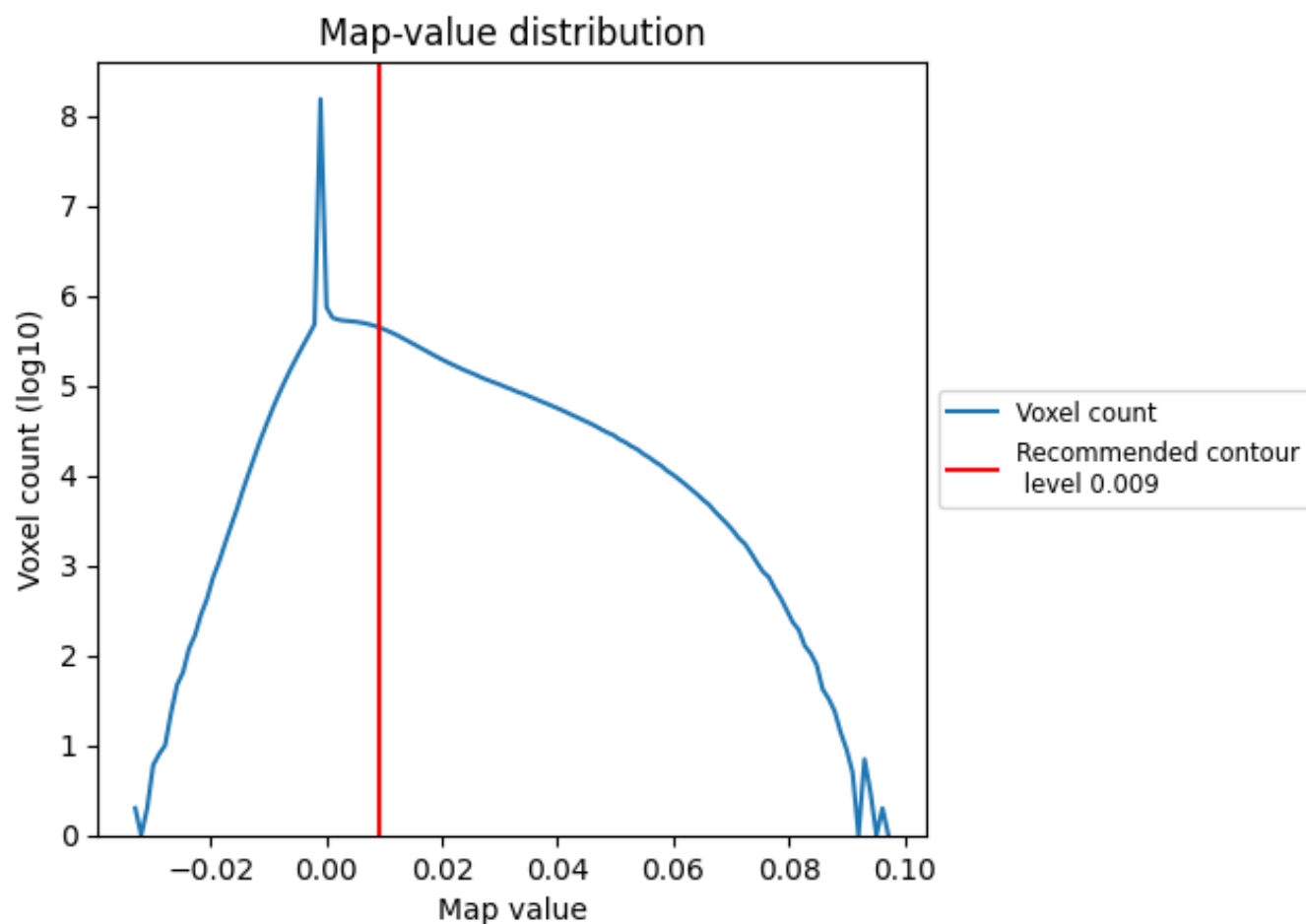
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

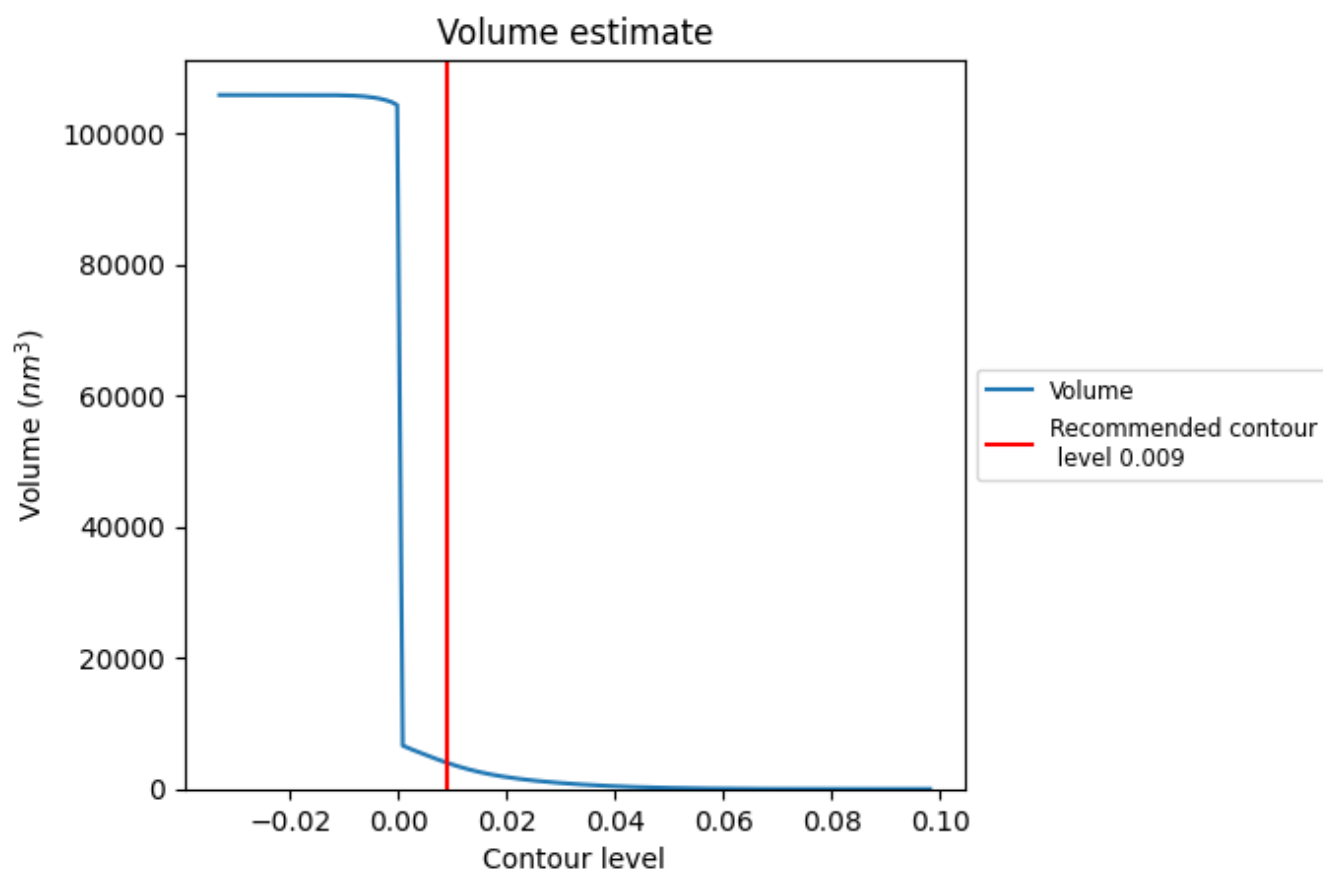
This section contains the results of statistical analysis of the map.

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.

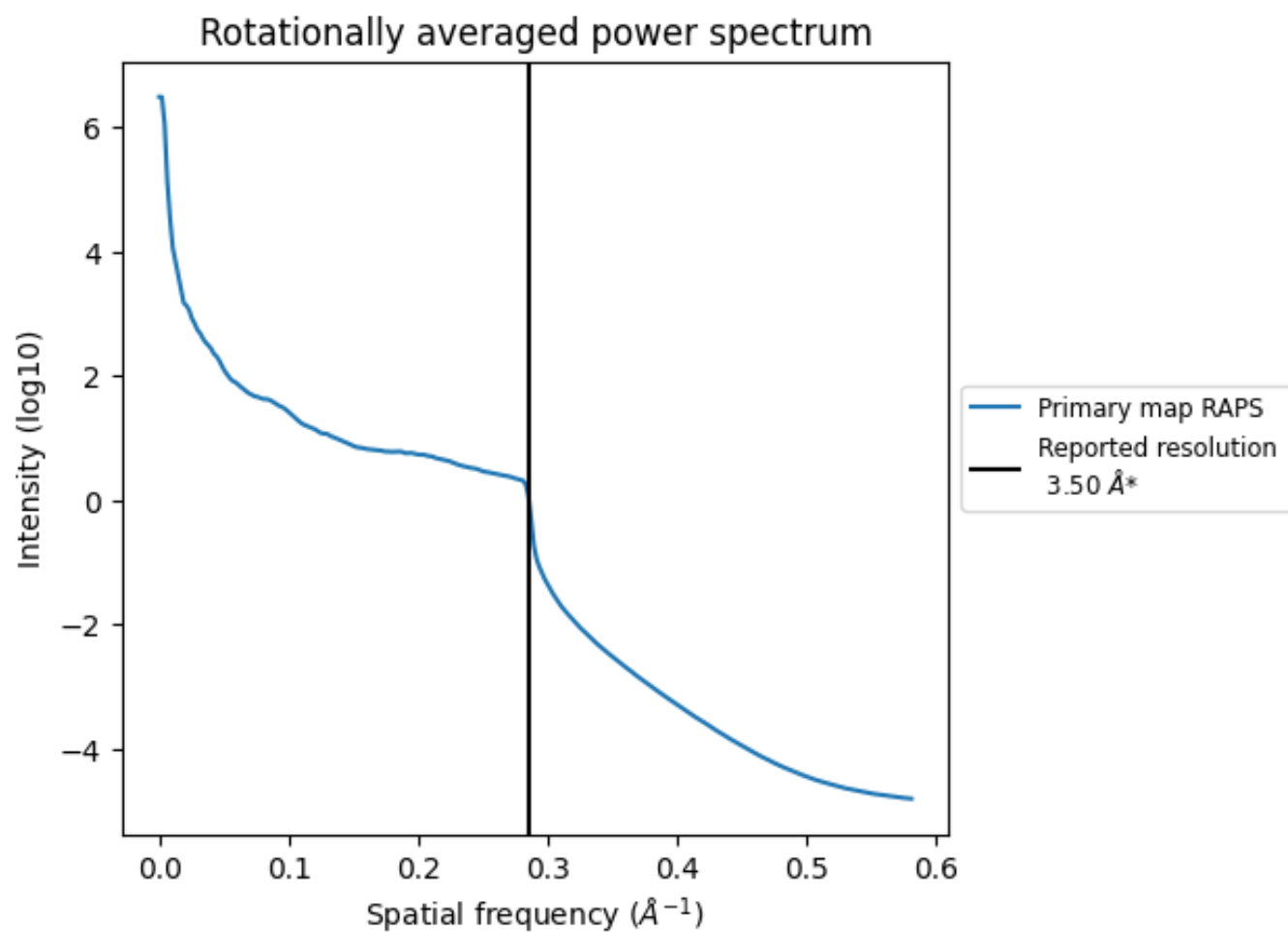
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4003 nm^3 ; this corresponds to an approximate mass of 3616 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 0.286 Å⁻¹

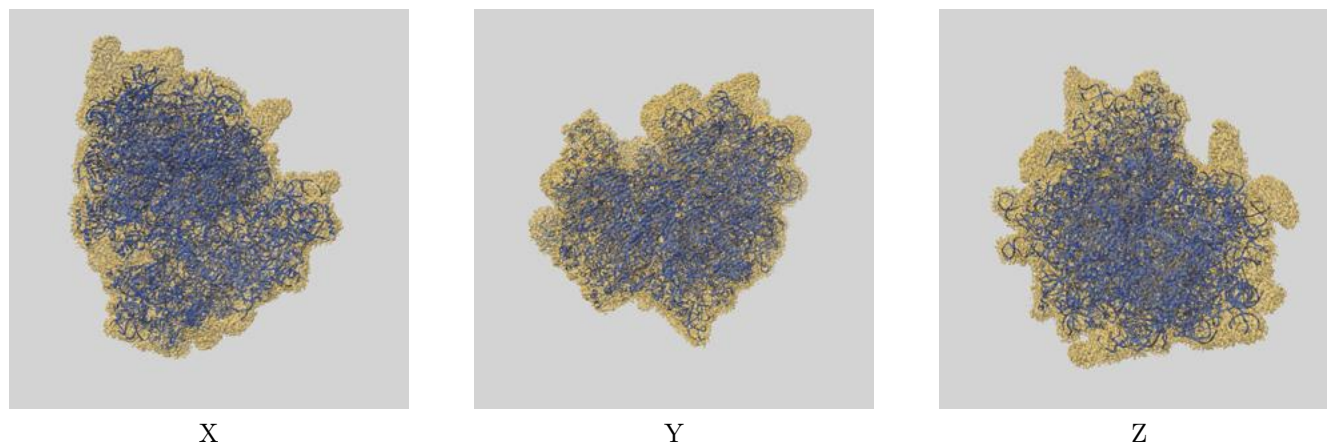
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

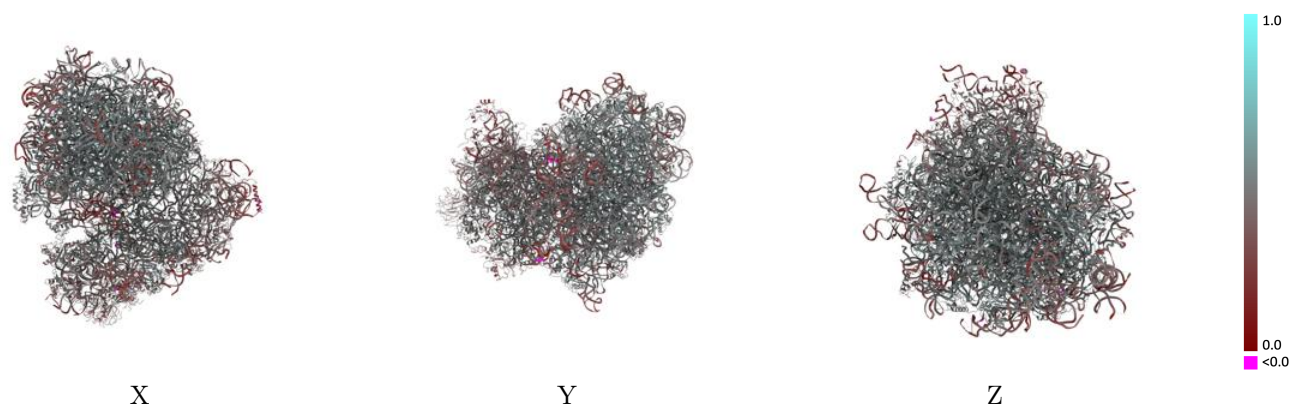
This section contains information regarding the fit between EMDB map EMD-10690 and PDB model 6Y57. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



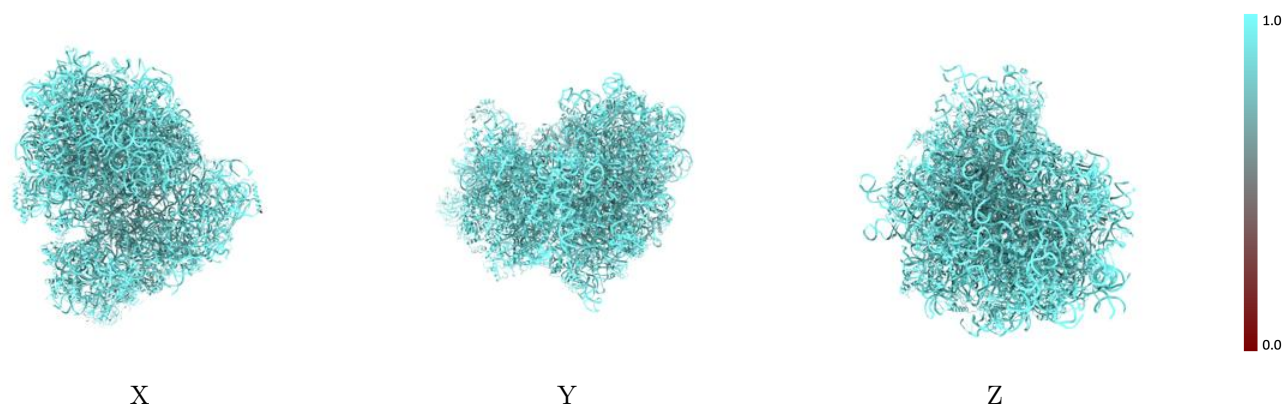
The images above show the 3D surface view of the map at the recommended contour level 0.009 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



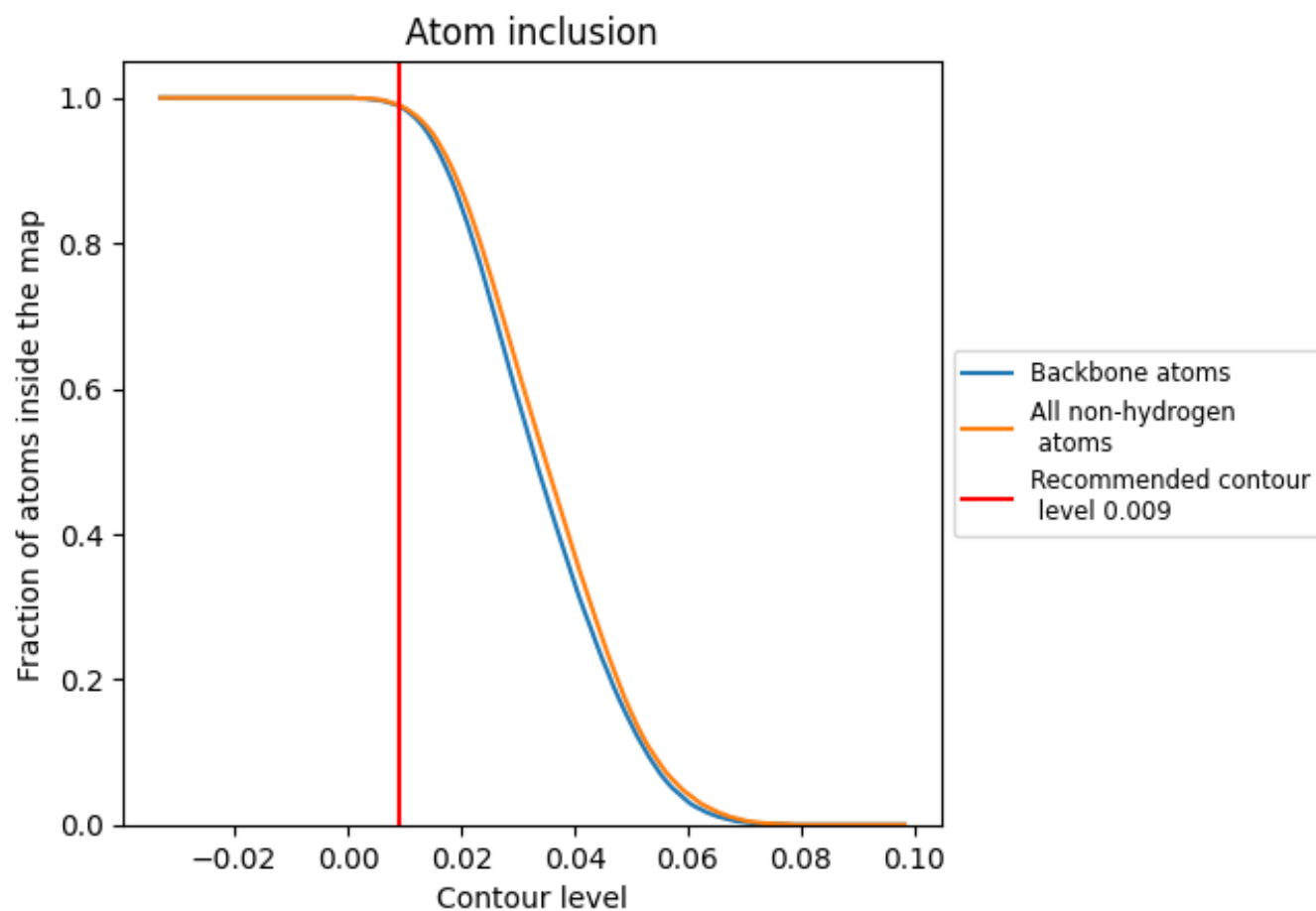
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.009).

9.4 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9900	 0.4620
A4	 0.9810	 0.4280
B4	 0.9960	 0.3380
D4	 0.8410	 0.2300
L5	 0.9960	 0.4640
L7	 0.9990	 0.4870
L8	 0.9940	 0.4760
LA	 0.9950	 0.5260
LB	 0.9900	 0.5090
LC	 0.9950	 0.5220
LD	 0.9930	 0.4790
LE	 0.9950	 0.4900
LF	 0.9920	 0.5110
LG	 0.9890	 0.4780
LH	 0.9880	 0.4890
LI	 0.9900	 0.5120
LJ	 0.9960	 0.4710
LL	 0.9950	 0.5110
LM	 0.9980	 0.4990
LN	 0.9960	 0.5370
LO	 0.9940	 0.5100
LP	 0.9970	 0.5280
LQ	 0.9970	 0.5240
LR	 0.9930	 0.4950
LS	 0.9950	 0.5140
LT	 0.9900	 0.5010
LU	 0.9960	 0.4520
LV	 0.9940	 0.5170
LW	 0.9620	 0.4180
LX	 0.9910	 0.5020
LY	 0.9920	 0.5110
LZ	 0.9920	 0.5090
La	 0.9930	 0.5370
Lb	 1.0000	 0.5000
Lc	 0.9860	 0.4910



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Chain	Atom inclusion	Q-score
Ld	 0.9950	 0.5080
Le	 0.9990	 0.5320
Lf	 0.9960	 0.5320
Lg	 0.9850	 0.5060
Lh	 0.9930	 0.5060
Li	 0.9900	 0.4900
Lj	 0.9990	 0.5350
Lk	 0.9850	 0.4720
Ll	 0.9980	 0.5300
Lm	 0.9970	 0.5140
Ln	 0.9810	 0.5040
Lo	 1.0000	 0.5270
Lp	 0.9960	 0.5200
Lr	 0.9990	 0.5220
S2	 0.9960	 0.4310
SA	 0.9680	 0.4580
SB	 0.9890	 0.4730
SC	 0.9870	 0.4790
SD	 0.9720	 0.4260
SE	 0.9910	 0.4220
SF	 0.9820	 0.4580
SG	 0.9920	 0.4130
SH	 0.9420	 0.4160
SI	 0.9930	 0.4310
SJ	 0.9920	 0.4060
SK	 0.9800	 0.4150
SL	 0.9830	 0.4660
SN	 0.9860	 0.4720
SO	 0.9820	 0.4650
SP	 0.9870	 0.4430
SQ	 0.9750	 0.4270
SR	 0.9260	 0.4140
SS	 0.9820	 0.4440
ST	 0.9890	 0.4450
SU	 0.9730	 0.4130
SV	 0.9840	 0.4640
SW	 0.9870	 0.4950
SX	 0.9810	 0.4580
SY	 0.9920	 0.4010
SZ	 0.9560	 0.3770
Sa	 0.9910	 0.4960
Sb	 0.9750	 0.4490

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Chain	Atom inclusion	Q-score
Sc	 0.9790	 0.4400
Sd	 0.9880	 0.4710
Se	 0.9950	 0.4200
Sf	 0.8140	 0.3190
Sg	 0.9640	 0.3780
sh	 0.9010	 0.3040