



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 04:17 AM UTC

PDB ID : 8RL2 / pdb_00008rl2
EMDB ID : EMD-19330
Title : Human pre-60S - State 5
Authors : Thoms, M.; Denk, T.; Beckmann, R.
Deposited on : 2024-01-02
Resolution : 2.84 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

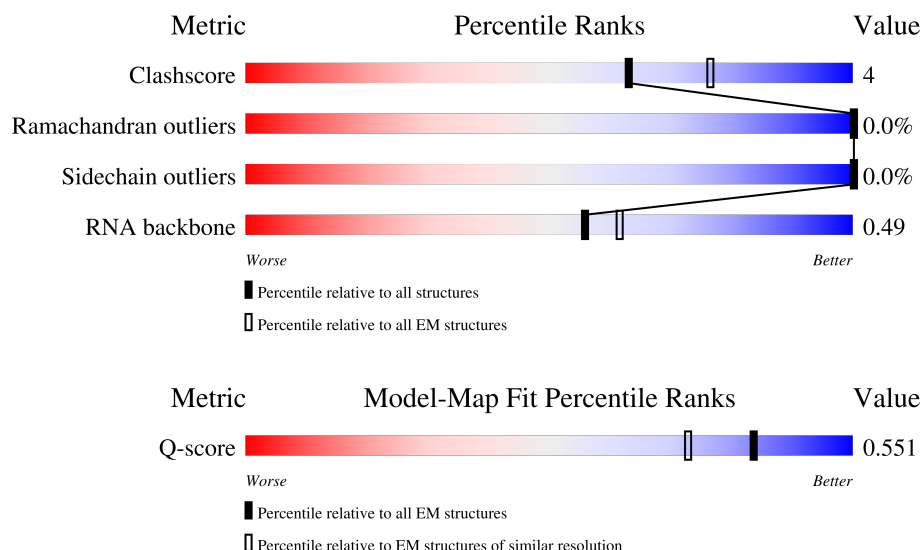
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.84 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	11884 (2.34 - 3.34)

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

Mol	Chain	Length	Quality of chain
1	L5	5070	9% 43% 21% • 33%
2	L7	121	19% 65% 30% • •
3	L8	157	6% 69% 27% • •

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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LJ	178	
13	LL	211	
14	LM	215	
15	LN	204	
16	LO	203	
17	LP	184	
18	LQ	188	
19	LR	196	
20	LS	176	
21	LT	160	
22	LU	128	
23	LV	140	
24	LX	156	
25	LY	145	
26	LZ	136	
27	La	148	
28	Lc	115	

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Mol	Chain	Length	Quality of chain
29	Ld	125	
30	Le	135	
31	Lf	110	
32	Lg	117	
33	Lh	123	
34	Li	105	
35	Lj	97	
36	Lk	70	
37	Ll	51	
38	Lp	92	
39	Lr	137	
40	Lt	165	
41	CA	245	
42	CB	731	
43	CC	549	
44	CD	634	
45	CE	129	
46	CF	239	
47	CG	485	
48	CH	260	
49	CI	163	
50	CJ	306	
51	CK	365	
52	CL	134	

2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 149669 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3382	Total	C	N	O	P	0	0
			72529	32297	13288	23563	3381		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 3 is a RNA chain called 5.8S rRNA.

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

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	204	Total	C	N	O	S	0	0
			1558	984	308	260	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	402	Total	C	N	O	S	0	0
			3224	2051	606	553	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	362	Total	C	N	O	S	0	0
			2870	1806	574	477	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	231	Total	C	N	O	S	0	0
			1886	1197	339	337	13		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	209	Total	C	N	O	S	0	0
			1680	1086	316	274	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	219	Total	C	N	O	S	0	0
			1790	1148	341	292	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	216	Total	C	N	O	S	0	0
			1744	1113	337	290	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LJ	170	Total	C	N	O	S	0	0
			1335	845	245	239	6		

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LL	193	Total	C	N	O	S	0	0
			1564	983	326	252	3		

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LM	135	Total	C	N	O	S	0	0
			1105	707	213	178	7		

- Molecule 15 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LN	203	Total	C	N	O	S	0	0
			1690	1065	357	264	4		

- Molecule 16 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LO	201	Total	C	N	O	S	0	0
			1642	1058	320	259	5		

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LP	157	Total	C	N	O	S	0	0
			1260	788	245	218	9		

- Molecule 18 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LQ	151	Total	C	N	O	S	0	0
			1223	768	247	203	5		

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LR	149	Total	C	N	O	S	0	0
			1244	775	267	193	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LS	176	Total	C	N	O	S	0	0
			1457	927	283	236	11		

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LT	127	Total	C	N	O	S	0	0
			994	630	190	172	2		

- Molecule 22 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LU	102	Total	C	N	O	S	0	0
			833	533	146	152	2		

- Molecule 23 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LV	137	Total	C	N	O	S	0	0
			1019	639	196	179	5		

- Molecule 24 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	132	Total	C	N	O	S	0	0
			1098	689	222	184	3		

- Molecule 26 is a protein called 60S ribosomal protein L27.

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

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	105	Total	C	N	O	S	0	0
			823	524	160	136	3		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lc	95	Total	C	N	O	S	0	0
			715	457	126	126	6		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ld	105	Total	C	N	O	S	0	0
			857	545	168	142	2		

- Molecule 30 is a protein called 60S ribosomal protein L32.

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

- Molecule 31 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lg	111	Total	C	N	O	S	0	0
			874	548	180	140	6		

- Molecule 33 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lh	121	Total	C	N	O	S	0	0
			1010	638	204	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Li	104	Total	C	N	O	S	0	0
			839	524	178	132	5		

- Molecule 35 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lj	85	Total	C	N	O	S	0	0
			696	428	153	110	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called 60S ribosomal protein L39.

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

- Molecule 38 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lp	90	Total	C	N	O	S	0	0
			696	439	134	116	7		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lr	123	Total	C	N	O	S	0	0
			984	611	205	164	4		

- Molecule 40 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lt	159	Total	C	N	O	S	0	0
			1186	736	223	223	4		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CA	245	Total	C	N	O	S	0	0
			1860	1153	319	375	13		

- Molecule 42 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CB	448	Total	C	N	O	S	0	0
			3600	2287	641	660	12		

- Molecule 43 is a protein called Guanine nucleotide-binding protein-like 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CC	80	Total	C	N	O	S	0	0
			594	369	126	96	3		

- Molecule 44 is a protein called GTP-binding protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CD	614	Total	C	N	O	S	0	0
			4957	3119	906	904	28		

- Molecule 45 is a protein called Protein LLP homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CE	69	Total	C	N	O	S	0	0
			569	354	125	88	2		

- Molecule 46 is a protein called mRNA turnover protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CF	219	Total	C	N	O	S	0	0
			1783	1136	313	322	12		

- Molecule 47 is a protein called Notchless protein homolog 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CG	471	Total	C	N	O	S	0	0
			3449	2149	641	648	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CG	85	ALA	GLU	engineered mutation	UNP Q9NVX2

- Molecule 48 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CH	259	Total	C	N	O	S	0	0
			2066	1315	389	353	9		

- Molecule 49 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CI	140	Total	C	N	O	S	0	0
			1188	756	230	192	10		

- Molecule 50 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CJ	281	Total	C	N	O	S	0	0
			2259	1448	400	399	12		

- Molecule 51 is a protein called Ribosome biogenesis regulatory protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CK	195	Total	C	N	O	S	0	0
			1559	976	307	275	1		

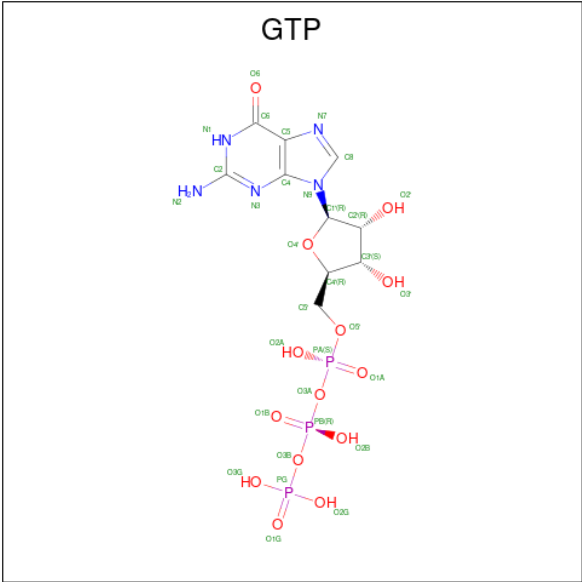
- Molecule 52 is a protein called Zinc finger protein 593.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CL	111	Total	C	N	O	S	0	0
			887	544	183	155	5		

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	Lg	1	Total	Zn	0
			1	1	
53	Lj	1	Total	Zn	0
			1	1	
53	Lp	1	Total	Zn	0
			1	1	
53	CI	1	Total	Zn	0
			1	1	
53	CL	1	Total	Zn	0
			1	1	

- Molecule 54 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

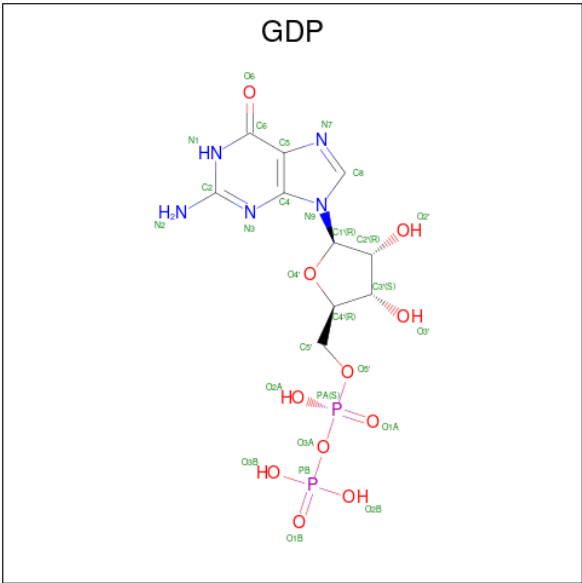


Mol	Chain	Residues	Atoms					AltConf
54	CB	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	CB	1	Total	Mg	0
			1	1	
55	CD	1	Total	Mg	0
			1	1	

- Molecule 56 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

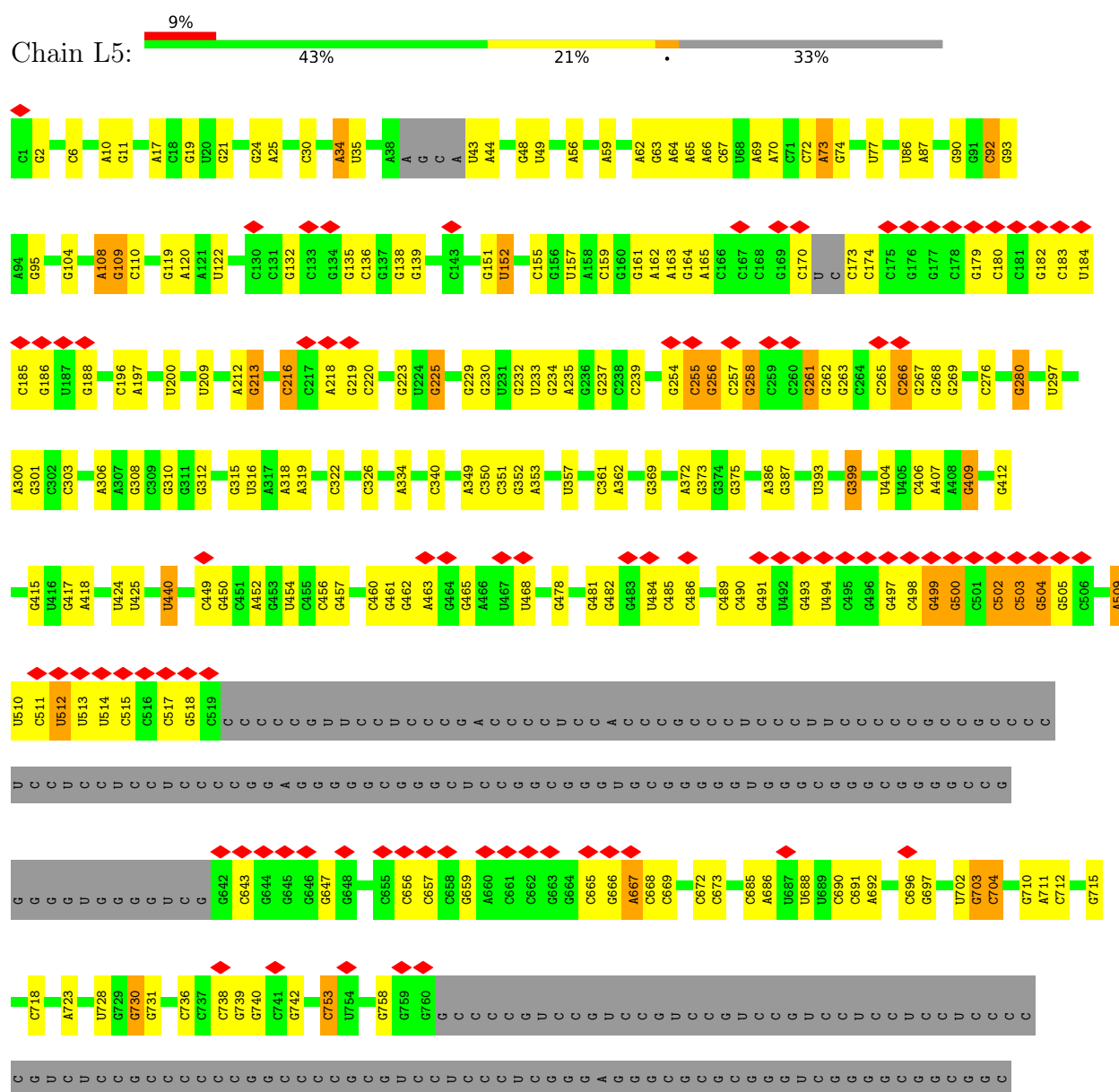


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
56	CD	1	28	10	5	11	2	0

3 Residue-property plots [i](#)

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.

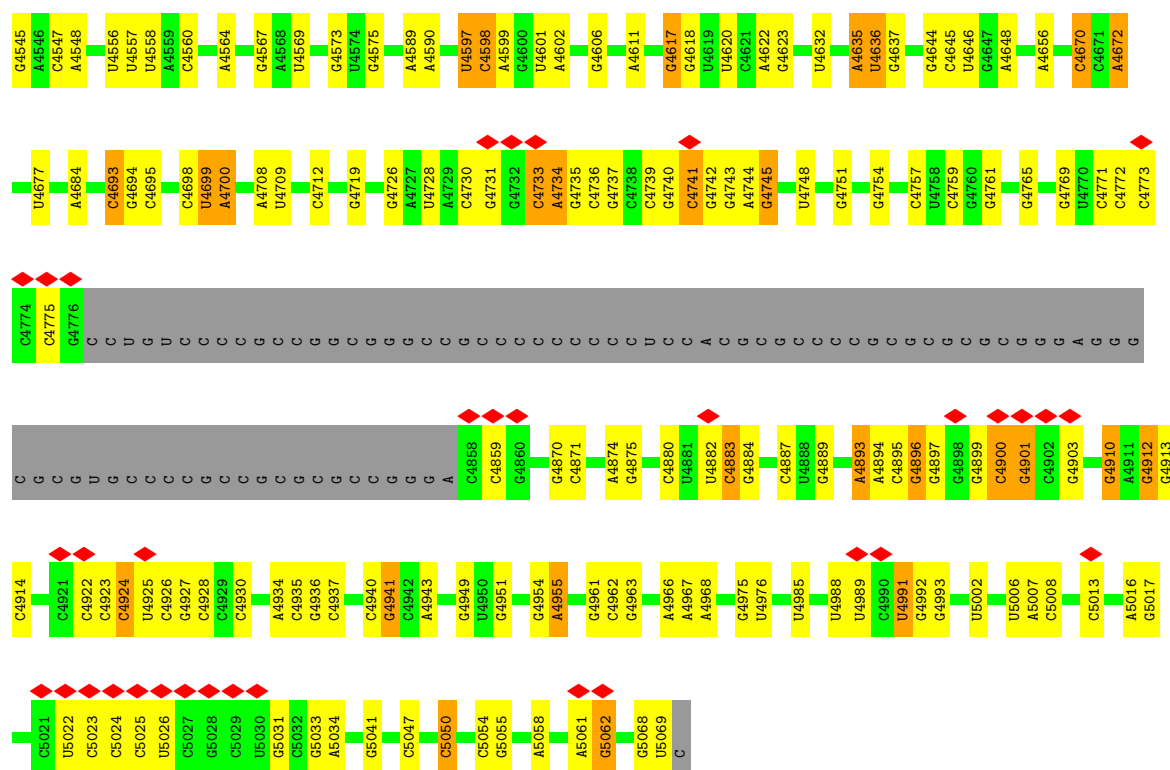
• Molecule 1: 28S rRNA



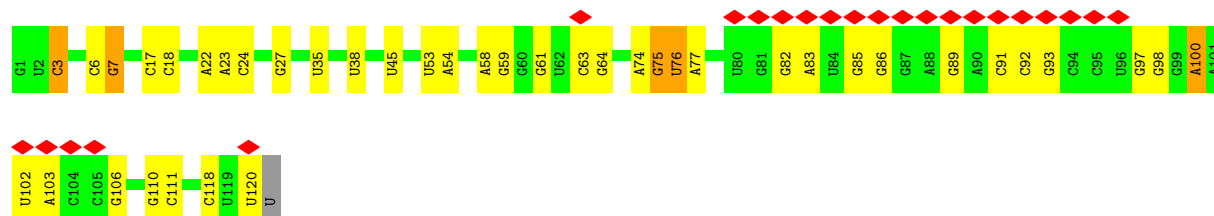




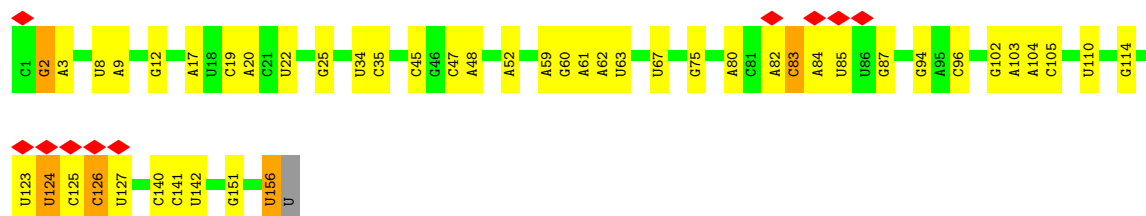




• Molecule 2: 5S rRNA

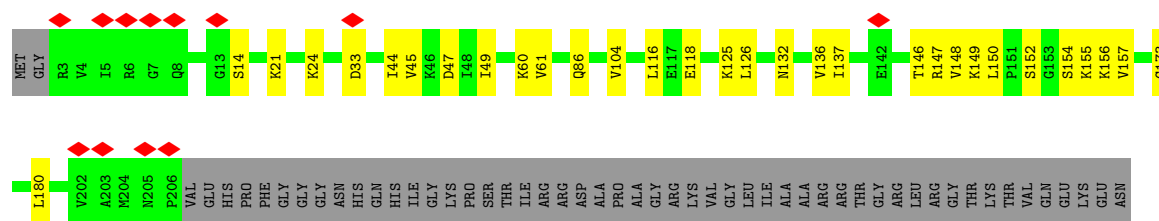


• Molecule 3: 5.8S rRNA

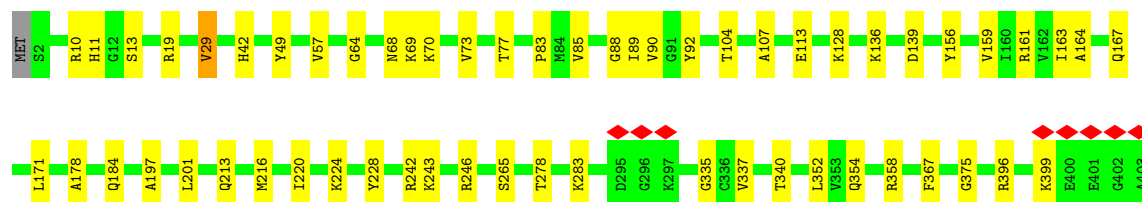
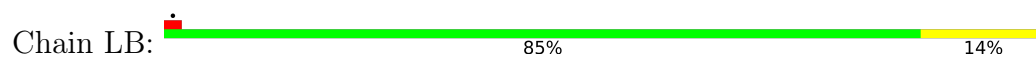


• Molecule 4: 60S ribosomal protein L8

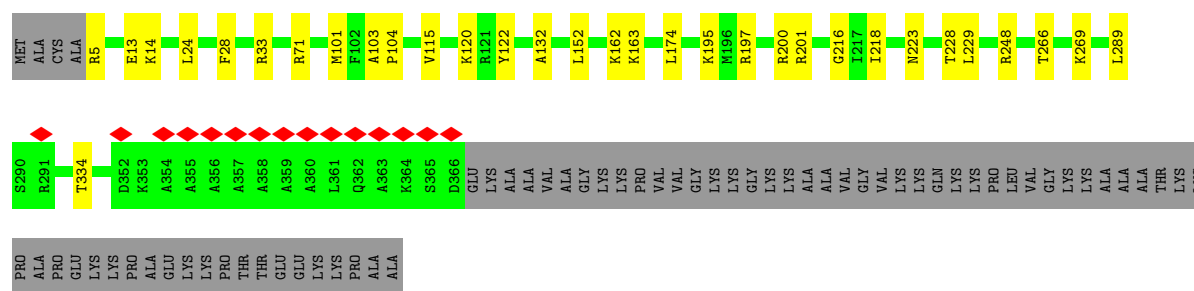
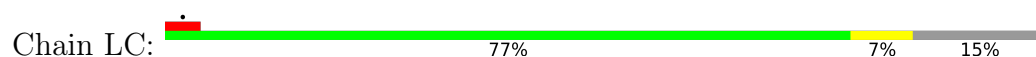




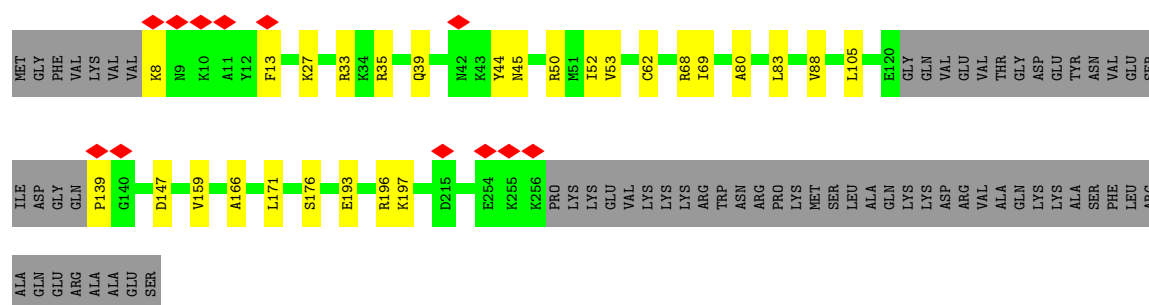
• Molecule 5: 60S ribosomal protein L3



• Molecule 6: 60S ribosomal protein L4

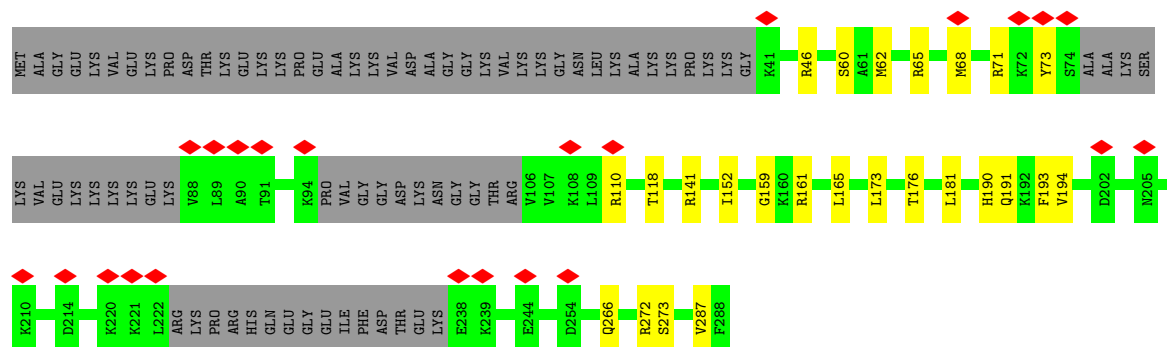


• Molecule 7: 60S ribosomal protein L5



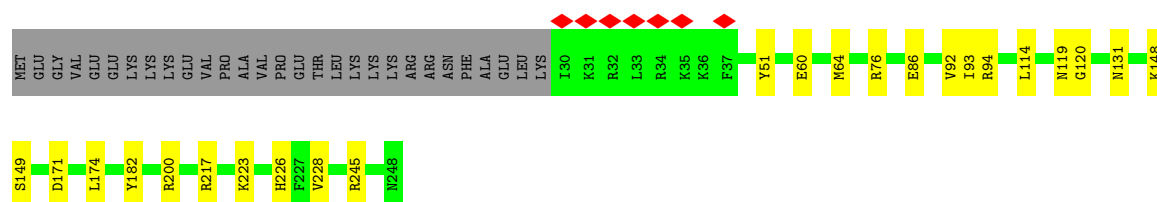
• Molecule 8: 60S ribosomal protein L6





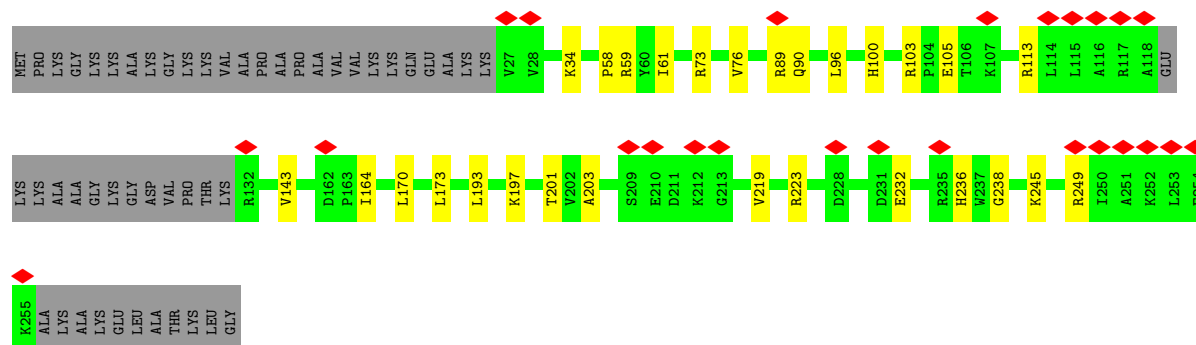
• Molecule 9: 60S ribosomal protein L7

Chain LF: 79% 9% 12%



• Molecule 10: 60S ribosomal protein L7a

Chain LG: 9% 71% 11% 19%



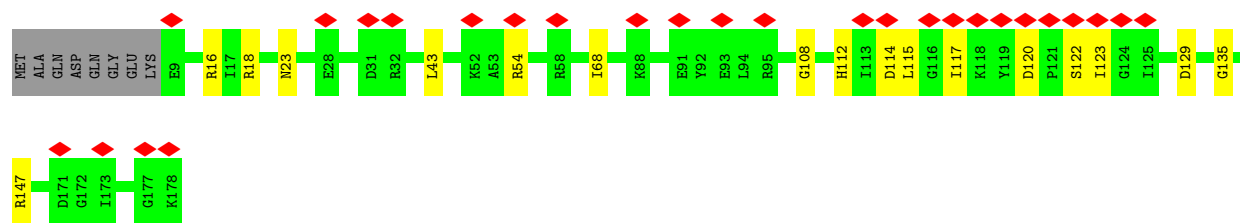
• Molecule 11: 60S ribosomal protein L9

Chain LH: 90% 9%

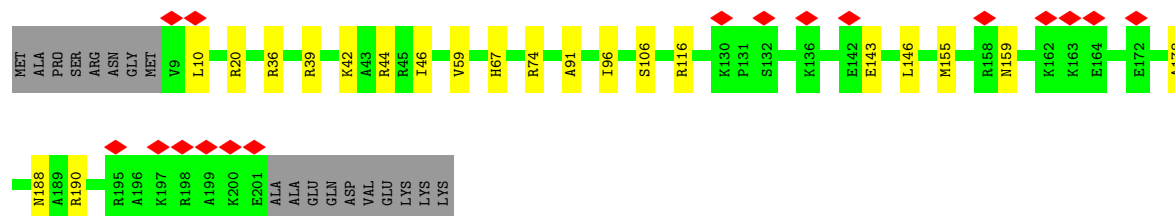
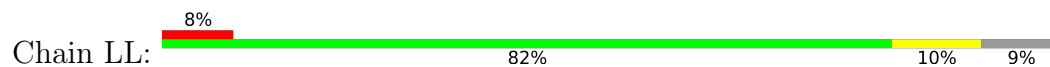


• Molecule 12: 60S ribosomal protein L11

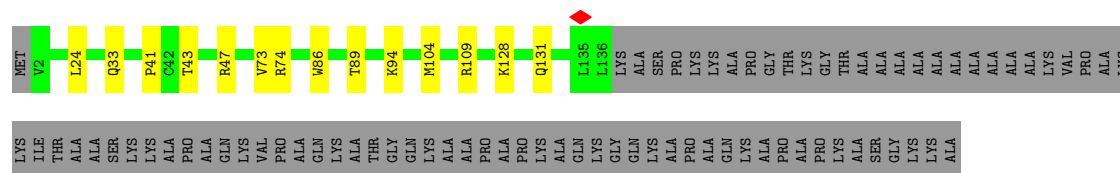
Chain LJ: 15% 86% 10%



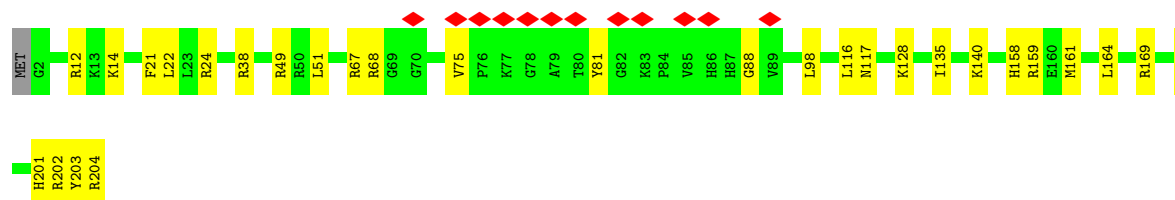
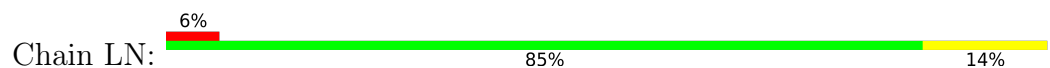
- Molecule 13: 60S ribosomal protein L13



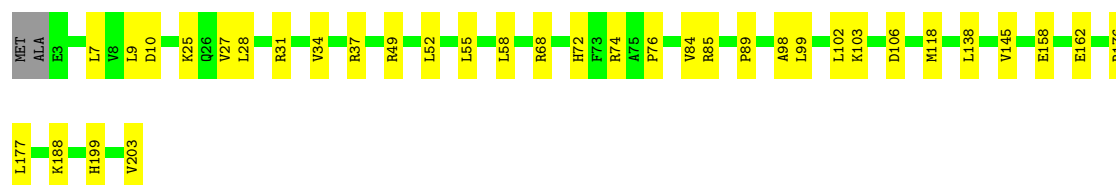
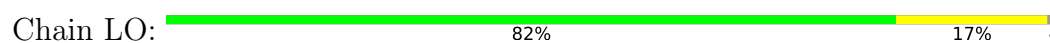
- Molecule 14: 60S ribosomal protein L14



- Molecule 15: 60S ribosomal protein L15

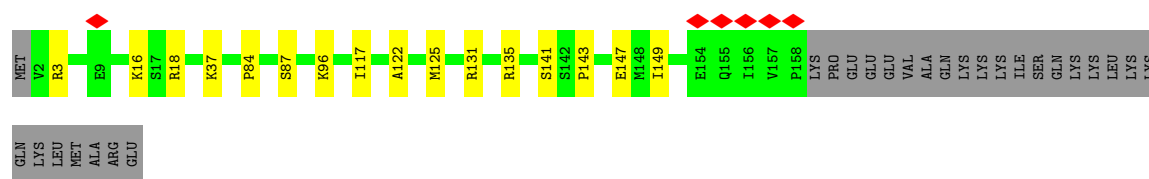


- Molecule 16: 60S ribosomal protein L13a



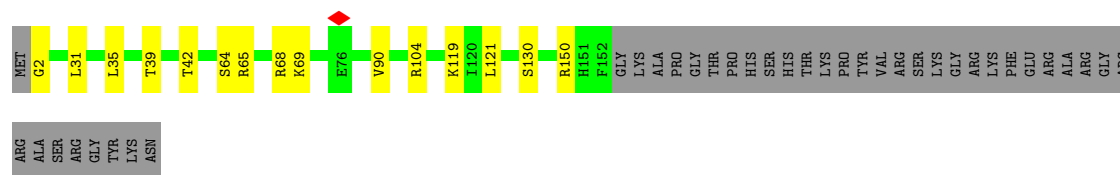
- Molecule 17: 60S ribosomal protein L17

Chain LP: 



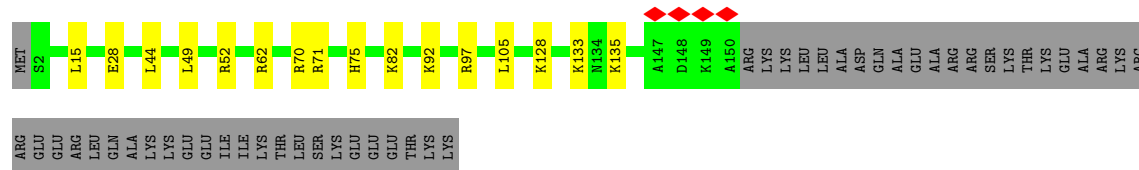
- Molecule 18: 60S ribosomal protein L18

Chain LQ: 



- Molecule 19: 60S ribosomal protein L19

Chain LR: 



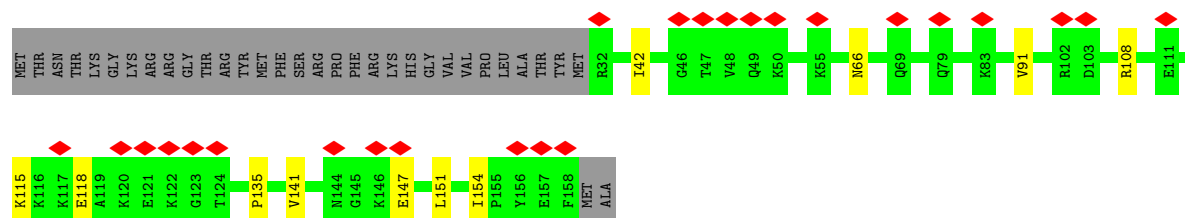
- Molecule 20: 60S ribosomal protein L18a

Chain LS: 



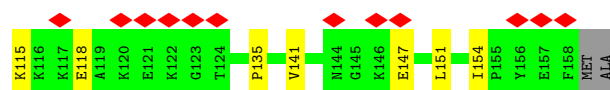
- Molecule 21: 60S ribosomal protein L21

Chain LT: 

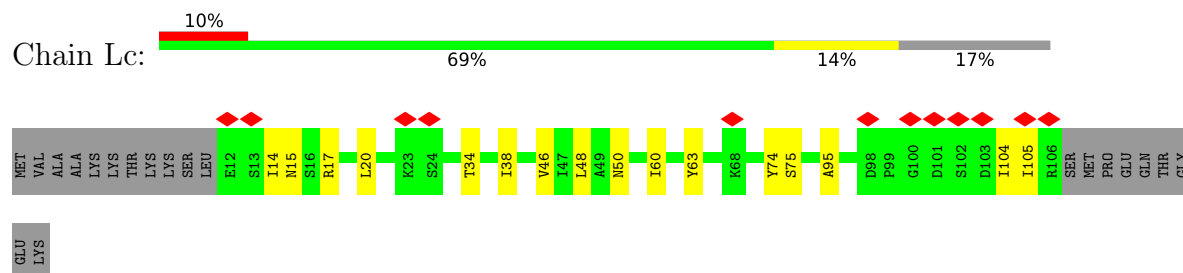


- Molecule 22: 60S ribosomal protein L22

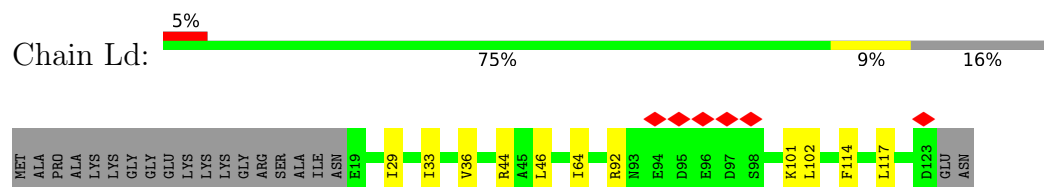
Chain LU: 



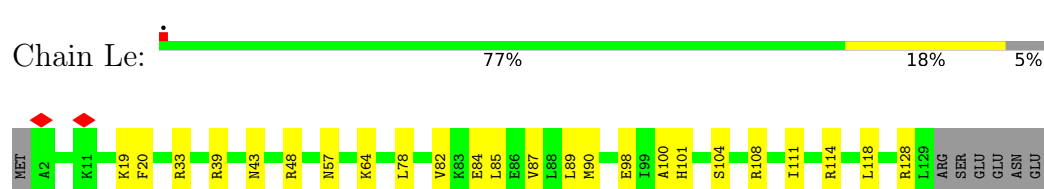
- Molecule 28: 60S ribosomal protein L30



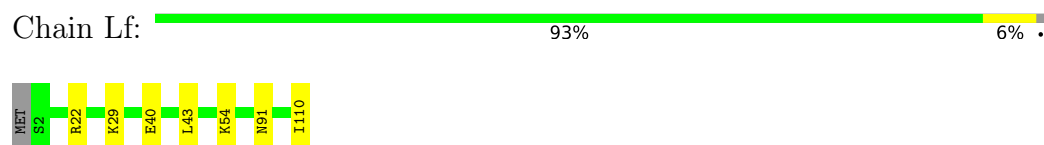
- Molecule 29: 60S ribosomal protein L31



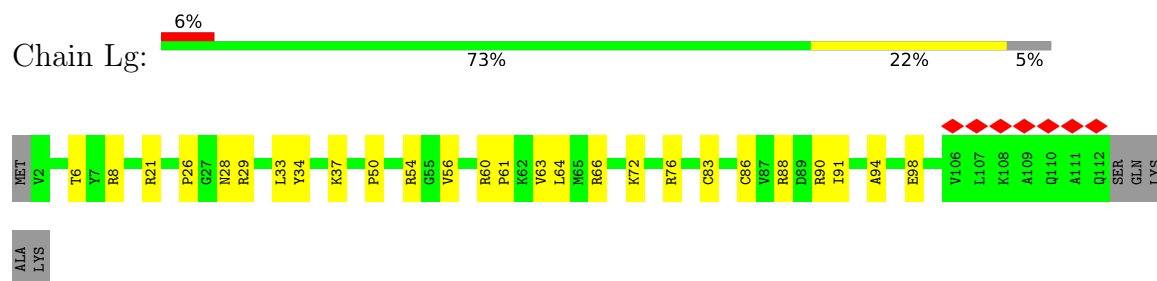
- Molecule 30: 60S ribosomal protein L32



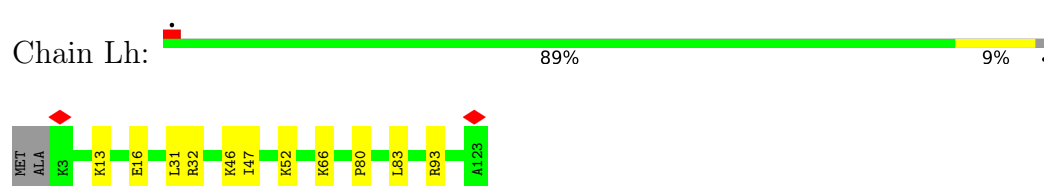
- Molecule 31: 60S ribosomal protein L35a



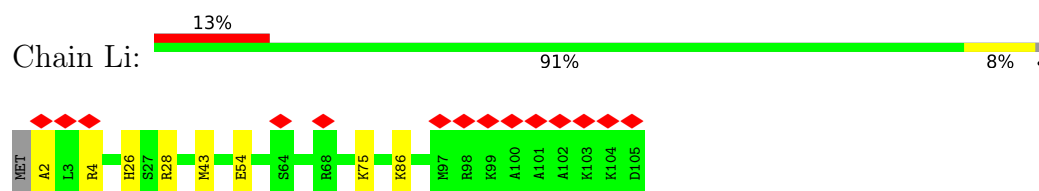
- Molecule 32: 60S ribosomal protein L34



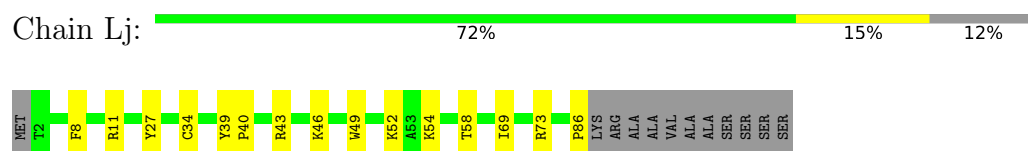
- Molecule 33: 60S ribosomal protein L35



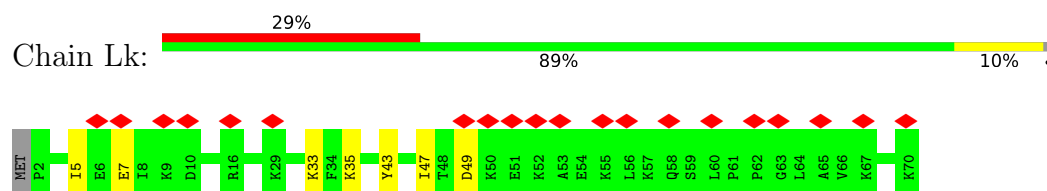
- Molecule 34: 60S ribosomal protein L36



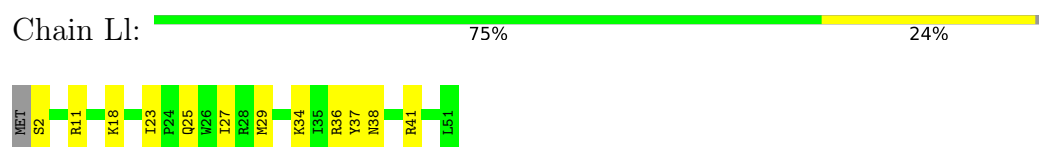
- Molecule 35: 60S ribosomal protein L37



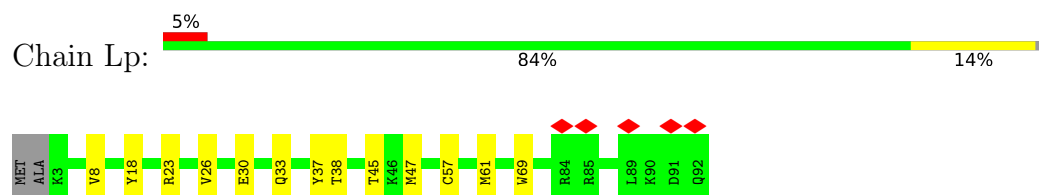
- Molecule 36: 60S ribosomal protein L38



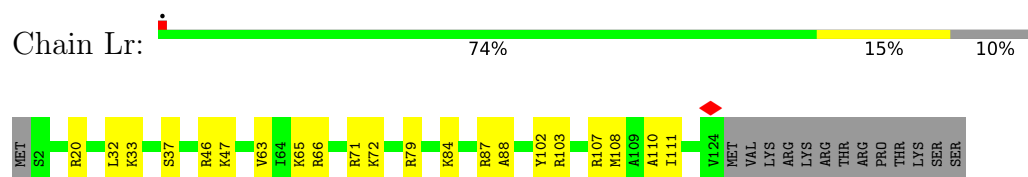
- Molecule 37: 60S ribosomal protein L39



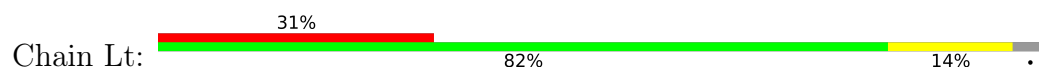
- Molecule 38: 60S ribosomal protein L37a



- Molecule 39: 60S ribosomal protein L28

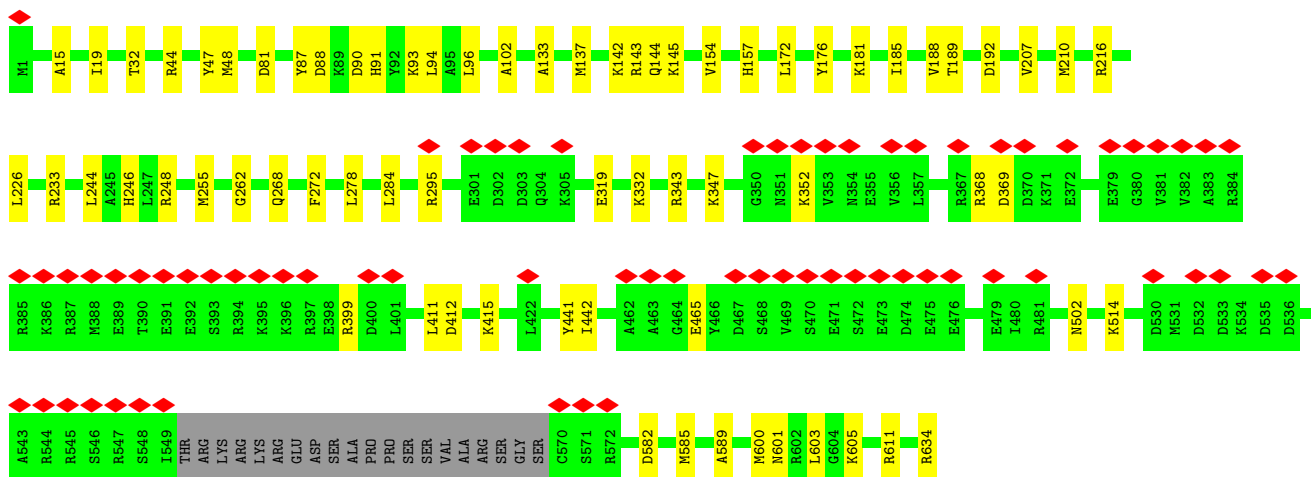
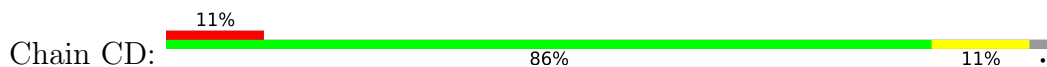


- Molecule 40: Large ribosomal subunit protein uL11

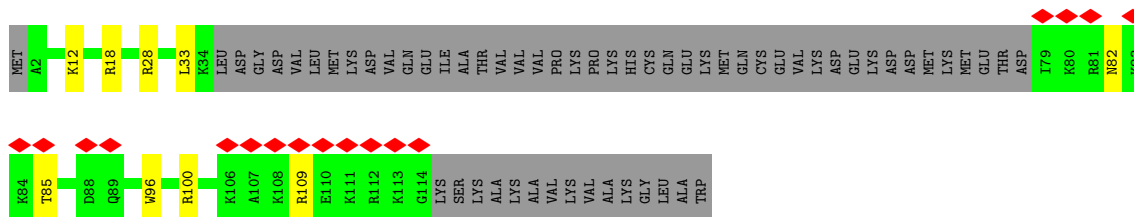


[illegible]

- Molecule 44: GTP-binding protein 4

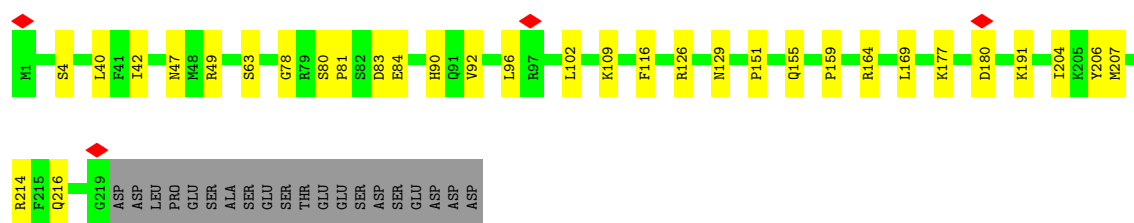


- Molecule 45: Protein LLP homolog



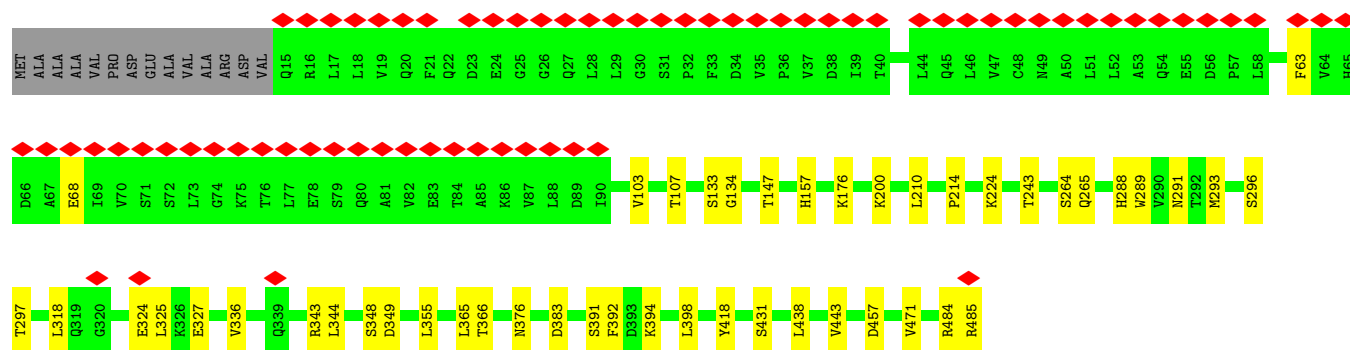
- Molecule 46: mRNA turnover protein 4 homolog

Chain CF: 



- Molecule 47: Notchless protein homolog 1

Chain CG: 



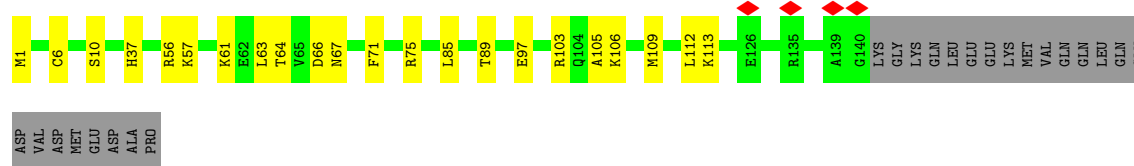
- Molecule 48: Ribosome biogenesis protein NSA2 homolog

Chain CH: 



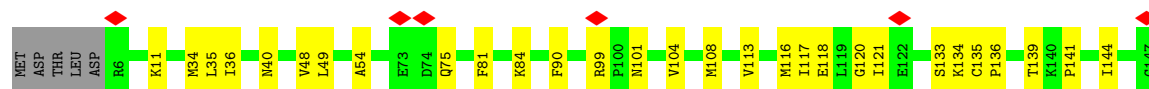
- Molecule 49: Probable ribosome biogenesis protein RLP24

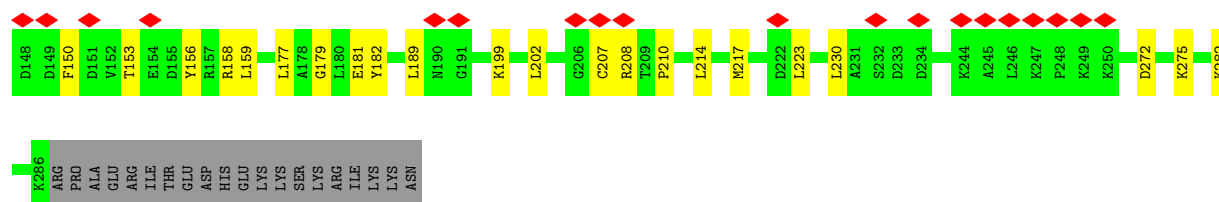
Chain CI: 



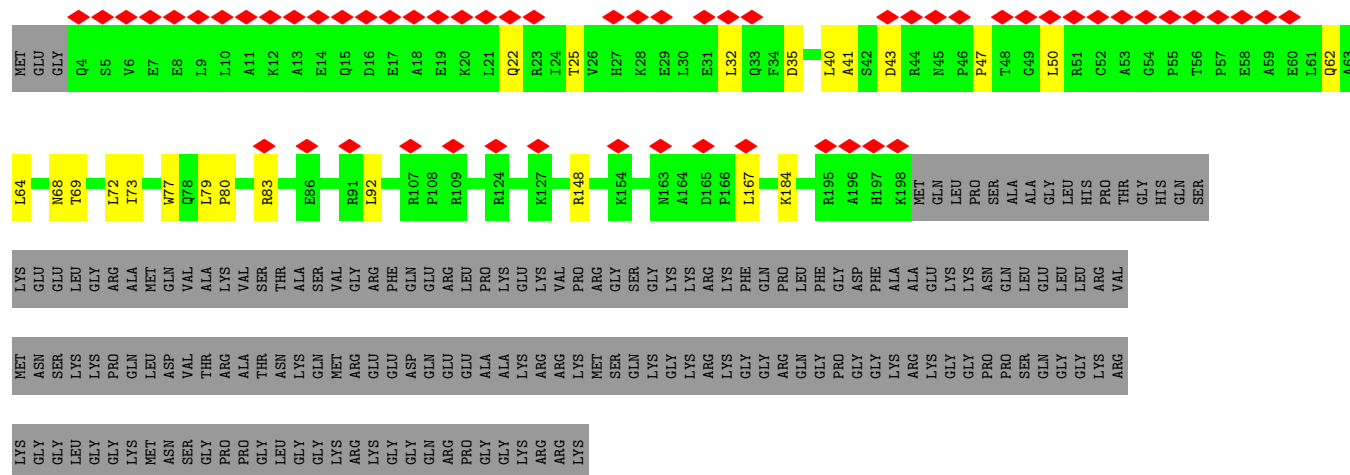
- Molecule 50: Ribosome production factor 2 homolog

Chain CJ: 

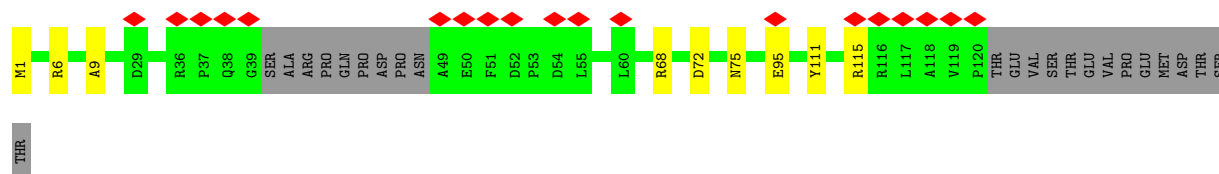
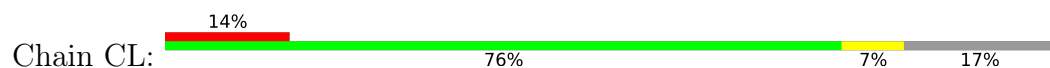




- Molecule 51: Ribosome biogenesis regulatory protein homolog



- Molecule 52: Zinc finger protein 593



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	78099	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 ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	9.113	Depositor
Minimum map value	-1.128	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.148	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.16	0/81120	0.32	0/126499
2	L7	0.13	0/2861	0.29	0/4459
3	L8	0.16	0/3701	0.30	0/5766
4	LA	0.17	0/1589	0.44	0/2133
5	LB	0.17	0/3292	0.42	0/4407
6	LC	0.17	0/2924	0.38	0/3929
7	LD	0.19	0/1924	0.45	0/2577
8	LE	0.14	0/1712	0.37	0/2300
9	LF	0.19	0/1824	0.43	0/2437
10	LG	0.18	0/1775	0.42	0/2395
11	LH	0.18	0/1529	0.39	0/2058
12	LJ	0.16	0/1358	0.40	0/1820
13	LL	0.16	0/1594	0.37	0/2135
14	LM	0.18	0/1127	0.38	0/1508
15	LN	0.18	0/1735	0.45	0/2323
16	LO	0.19	0/1674	0.39	0/2241
17	LP	0.16	0/1287	0.40	0/1729
18	LQ	0.16	0/1239	0.37	0/1658
19	LR	0.17	0/1260	0.40	0/1669
20	LS	0.16	0/1497	0.38	0/2009
21	LT	0.17	0/1015	0.39	0/1365
22	LU	0.19	0/847	0.48	0/1137
23	LV	0.16	0/1033	0.40	0/1383
24	LX	0.14	0/993	0.37	0/1334
25	LY	0.16	0/1115	0.42	0/1484
26	LZ	0.15	0/1130	0.36	0/1507
27	La	0.17	0/837	0.41	0/1118
28	Lc	0.18	0/725	0.46	0/978
29	Ld	0.18	0/872	0.40	0/1175
30	Le	0.20	0/1071	0.48	0/1429
31	Lf	0.15	0/891	0.34	0/1194
32	Lg	0.16	0/884	0.42	0/1179

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lh	0.16	0/1018	0.38	0/1344
34	Li	0.23	0/850	0.50	0/1125
35	Lj	0.18	0/711	0.46	0/941
36	Lk	0.15	0/575	0.39	0/761
37	Ll	0.20	0/454	0.45	0/599
38	Lp	0.18	0/706	0.43	0/937
39	Lr	0.17	0/999	0.40	0/1340
40	Lt	0.18	0/1202	0.43	0/1622
41	CA	0.17	0/1885	0.48	0/2564
42	CB	0.18	0/3676	0.42	0/4964
43	CC	0.14	0/602	0.34	0/800
44	CD	0.18	0/5040	0.42	0/6772
45	CE	0.15	0/575	0.37	0/755
46	CF	0.20	0/1818	0.46	0/2436
47	CG	0.17	0/3526	0.46	0/4799
48	CH	0.16	0/2106	0.39	0/2820
49	CI	0.23	0/1211	0.46	0/1605
50	CJ	0.15	0/2301	0.39	0/3081
51	CK	0.14	0/1591	0.36	0/2159
52	CL	0.15	0/905	0.38	0/1210
All	All	0.16	0/160186	0.36	0/233969

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	72529	0	36659	485	0
2	L7	2561	0	1295	19	0
3	L8	3314	0	1683	18	0
4	LA	1558	0	1633	22	0
5	LB	3224	0	3348	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	LC	2870	0	3027	21	0
7	LD	1886	0	1895	21	0
8	LE	1680	0	1812	20	0
9	LF	1790	0	1873	17	0
10	LG	1744	0	1861	19	0
11	LH	1510	0	1579	13	0
12	LJ	1335	0	1345	13	0
13	LL	1564	0	1673	19	0
14	LM	1105	0	1156	11	0
15	LN	1690	0	1725	23	0
16	LO	1642	0	1779	27	0
17	LP	1260	0	1278	12	0
18	LQ	1223	0	1330	14	0
19	LR	1244	0	1368	15	0
20	LS	1457	0	1491	20	0
21	LT	994	0	996	10	0
22	LU	833	0	856	8	0
23	LV	1019	0	1079	13	0
24	LX	976	0	1053	6	0
25	LY	1098	0	1178	23	0
26	LZ	1107	0	1182	19	0
27	La	823	0	879	14	0
28	Lc	715	0	728	9	0
29	Ld	857	0	906	7	0
30	Le	1053	0	1147	19	0
31	Lf	872	0	901	6	0
32	Lg	874	0	960	20	0
33	Lh	1010	0	1143	8	0
34	Li	839	0	910	6	0
35	Lj	696	0	724	10	0
36	Lk	569	0	637	4	0
37	Ll	444	0	483	11	0
38	Lp	696	0	743	10	0
39	Lr	984	0	1048	15	0
40	Lt	1186	0	1226	16	0
41	CA	1860	0	1835	23	0
42	CB	3600	0	3653	44	0
43	CC	594	0	584	7	0
44	CD	4957	0	5022	57	0
45	CE	569	0	615	10	0
46	CF	1783	0	1824	19	0
47	CG	3449	0	3178	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	CH	2066	0	2168	20	0
49	CI	1188	0	1251	18	0
50	CJ	2259	0	2350	38	0
51	CK	1559	0	1558	18	0
52	CL	887	0	887	6	0
53	CI	1	0	0	0	0
53	CL	1	0	0	0	0
53	Lg	1	0	0	0	0
53	Lj	1	0	0	0	0
53	Lp	1	0	0	0	0
54	CB	32	0	12	0	0
55	CB	1	0	0	0	0
55	CD	1	0	0	0	0
56	CD	28	0	12	0	0
All	All	149669	0	113538	1070	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 4.

All (1070) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4496:A:H61	1:L5:4504:C:N4	1.45	1.14
1:L5:4496:A:N6	1:L5:4504:C:H42	1.48	1.08
1:L5:3701:C:N4	1:L5:3748:A:H62	1.61	0.98
1:L5:2483:G:H1	1:L5:2495:U:H3	0.99	0.97
1:L5:4745:G:H1	1:L5:4955:A:H61	1.09	0.94
1:L5:3701:C:H42	1:L5:3748:A:N6	1.67	0.92
1:L5:3701:C:H42	1:L5:3748:A:H62	0.97	0.92
1:L5:3759:A:N6	1:L5:3764:U:H3	1.67	0.91
1:L5:3930:U:H3	1:L5:4180:G:H1	1.13	0.90
44:CD:248:ARG:HH12	44:CD:343:ARG:HE	1.25	0.85
1:L5:512:U:H3	1:L5:647:G:H1	1.24	0.85
1:L5:3759:A:H62	1:L5:3764:U:H3	0.87	0.84
1:L5:4295:U:H3	1:L5:4316:G:H1	1.31	0.79
1:L5:1541:C:H5''	4:LA:21:LYS:HD2	1.67	0.76
1:L5:4745:G:H1	1:L5:4955:A:N6	1.82	0.73
46:CF:42:ILE:HB	46:CF:206:TYR:HB2	1.70	0.73
5:LB:396:ARG:HD3	49:CI:112:LEU:HB3	1.69	0.73
1:L5:4769:G:H5''	16:LO:176:ARG:HD3	1.71	0.72
10:LG:232:GLU:O	10:LG:236:HIS:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:92:MET:HB2	11:LH:144:LEU:HB2	1.72	0.72
1:L5:35:U:O2'	1:L5:1651:G:N3	2.24	0.70
5:LB:224:LYS:HG3	5:LB:340:THR:HG22	1.72	0.70
14:LM:24:LEU:HB2	14:LM:43:THR:HG21	1.74	0.69
25:LY:31:SER:HA	25:LY:48:PRO:HA	1.75	0.69
3:L8:83:C:H41	25:LY:50:ARG:HH21	1.39	0.68
1:L5:4093:G:C2	1:L5:4114:C:N3	2.61	0.68
1:L5:2845:A:H61	1:L5:3843:C:H42	1.42	0.68
50:CJ:117:ILE:HD13	50:CJ:159:LEU:HD22	1.76	0.68
1:L5:2049:G:HO2'	1:L5:3884:U:HO2'	1.42	0.67
28:Lc:104:ILE:HG23	28:Lc:105:ILE:HD12	1.75	0.67
1:L5:2573:A:H62	1:L5:2761:U:H3	1.39	0.67
11:LH:64:ARG:HH12	46:CF:4:SER:HB2	1.60	0.67
9:LF:93:ILE:HA	9:LF:119:ASN:O	1.95	0.67
1:L5:2458:C:H5''	15:LN:67:ARG:HD2	1.78	0.66
24:LX:55:ARG:HE	24:LX:56:ARG:H	1.44	0.66
41:CA:242:ASP:OD1	44:CD:343:ARG:NH1	2.29	0.65
7:LD:39:GLN:NE2	7:LD:44:TYR:O	2.29	0.65
5:LB:213:GLN:O	45:CE:28:ARG:NH2	2.28	0.65
1:L5:3944:G:H1	1:L5:4069:U:H3	1.45	0.64
44:CD:188:VAL:HG13	44:CD:189:THR:HG23	1.79	0.64
1:L5:4199:C:OP2	51:CK:148:ARG:NH2	2.30	0.64
1:L5:2562:G:N2	1:L5:2565:A:OP2	2.30	0.64
1:L5:2611:A:H5'	1:L5:2688:G:H4'	1.79	0.64
4:LA:116:LEU:HB3	4:LA:126:LEU:HB2	1.79	0.64
34:Li:2:ALA:HB3	34:Li:4:ARG:HH22	1.63	0.63
1:L5:4496:A:N1	1:L5:4504:C:N3	2.45	0.63
24:LX:78:LYS:O	33:Lh:32:ARG:NH1	2.31	0.63
22:LU:65:ARG:HG3	22:LU:70:ILE:HG12	1.79	0.63
37:Ll:41:ARG:O	44:CD:611:ARG:NH2	2.32	0.63
46:CF:42:ILE:HD11	46:CF:92:VAL:HG13	1.81	0.63
38:Lp:30:GLU:HA	38:Lp:33:GLN:HG2	1.81	0.62
44:CD:248:ARG:HH22	44:CD:343:ARG:HH21	1.45	0.62
1:L5:2583:C:OP2	32:Lg:76:ARG:NH2	2.33	0.62
42:CB:233:ARG:NH1	42:CB:275:ASP:OD2	2.32	0.62
1:L5:152:U:OP1	15:LN:49:ARG:NH1	2.28	0.62
16:LO:85:ARG:HG3	16:LO:99:LEU:HD11	1.81	0.62
1:L5:2669:C:OP2	19:LR:128:LYS:NZ	2.32	0.62
44:CD:81:ASP:OD2	44:CD:246:HIS:NE2	2.33	0.62
1:L5:2457:G:O2'	1:L5:3672:G:O2'	2.17	0.62
40:Lt:20:GLY:HA2	40:Lt:51:GLY:HA2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1363:C:H3'	13:LL:36:ARG:HH12	1.65	0.61
1:L5:4496:A:H61	1:L5:4504:C:H42	0.70	0.61
42:CB:215:ASP:HA	42:CB:248:LYS:HZ3	1.63	0.61
1:L5:1498:G:H5''	18:LQ:150:ARG:HH22	1.64	0.61
1:L5:1946:G:HO2'	48:CH:36:SER:HG	1.49	0.61
1:L5:4617:G:OP2	5:LB:358:ARG:NH2	2.32	0.61
25:LY:22:PRO:HD2	25:LY:25:ILE:HD12	1.82	0.61
1:L5:109:G:OP2	13:LL:74:ARG:NH2	2.33	0.61
44:CD:88:ASP:HB3	44:CD:91:HIS:HB2	1.81	0.61
23:LV:58:GLY:N	23:LV:81:VAL:O	2.32	0.61
44:CD:207:VAL:O	48:CH:3:GLN:NE2	2.33	0.61
1:L5:1501:C:HO2'	18:LQ:64:SER:HG	1.46	0.61
1:L5:4748:U:H5''	31:Lf:54:LYS:HE2	1.83	0.60
30:Le:19:LYS:HD3	30:Le:33:ARG:HH21	1.66	0.60
40:Lt:13:VAL:HB	40:Lt:62:LEU:HB2	1.82	0.60
1:L5:730:G:OP2	9:LF:76:ARG:NH1	2.35	0.60
4:LA:150:LEU:HB2	4:LA:154:SER:HB2	1.83	0.60
41:CA:200:ASN:ND2	41:CA:203:CYS:SG	2.73	0.60
1:L5:2335:C:H2'	1:L5:2336:G:H8	1.66	0.60
28:Lc:34:THR:HG23	28:Lc:95:ALA:HB2	1.83	0.60
1:L5:2520:C:O2	1:L5:2640:G:N2	2.35	0.60
1:L5:3672:G:N2	1:L5:3672:G:OP2	2.32	0.60
1:L5:4077:A:N1	1:L5:4171:C:N4	2.50	0.60
35:Lj:54:LYS:O	35:Lj:58:THR:HB	2.01	0.60
41:CA:95:ARG:HG3	41:CA:132:VAL:HG21	1.82	0.60
30:Le:82:VAL:HG13	30:Le:114:ARG:HG2	1.84	0.59
1:L5:1951:G:O2'	20:LS:95:ARG:NH2	2.35	0.59
3:L8:156:U:OP2	10:LG:89:ARG:NH2	2.35	0.59
15:LN:51:LEU:O	15:LN:117:ASN:ND2	2.35	0.59
5:LB:57:VAL:HG22	5:LB:73:VAL:HG22	1.84	0.59
1:L5:67:C:OP2	1:L5:312:G:N2	2.34	0.59
1:L5:2898:G:OP2	19:LR:135:LYS:NZ	2.35	0.59
1:L5:34:A:H1'	1:L5:1526:G:H21	1.67	0.59
1:L5:1378:C:N4	13:LL:159:ASN:O	2.27	0.59
4:LA:137:ILE:HD11	4:LA:149:LYS:HB2	1.85	0.59
21:LT:66:ASN:HD21	51:CK:167:LEU:HD13	1.67	0.59
42:CB:432:LEU:HD13	42:CB:436:GLY:HA2	1.85	0.59
29:Ld:46:LEU:HD11	29:Ld:64:ILE:HG21	1.85	0.59
49:CI:109:MET:HE3	49:CI:113:LYS:HE3	1.85	0.59
1:L5:4539:U:H5''	42:CB:352:THR:HG23	1.84	0.59
44:CD:102:ALA:HB2	44:CD:144:GLN:HG3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:417:G:OP1	1:L5:2329:U:O2'	2.21	0.59
1:L5:1525:A:H2'	1:L5:1526:G:C8	2.37	0.59
30:Le:84:GLU:HA	30:Le:87:VAL:HG12	1.84	0.59
47:CG:457:ASP:OD2	48:CH:98:ARG:NH2	2.36	0.59
11:LH:91:LYS:HB2	11:LH:183:GLU:HB3	1.85	0.59
42:CB:282:HIS:HB3	42:CB:289:PHE:HB3	1.84	0.59
8:LE:118:THR:HG23	30:Le:90:MET:HE3	1.84	0.58
26:LZ:21:ARG:NH1	26:LZ:47:ASP:O	2.36	0.58
1:L5:1861:U:H3	1:L5:1873:A:H62	1.50	0.58
1:L5:1931:C:H1'	43:CC:7:LYS:HA	1.84	0.58
28:Lc:48:LEU:HD21	28:Lc:60:ILE:HG21	1.84	0.58
34:Li:54:GLU:OE2	34:Li:86:LYS:NZ	2.37	0.58
37:Ll:25:GLN:HB3	44:CD:589:ALA:HB1	1.85	0.58
44:CD:210:MET:HE1	44:CD:332:LYS:HG3	1.86	0.58
46:CF:214:ARG:NH1	46:CF:216:GLN:OE1	2.36	0.58
1:L5:4884:G:O6	8:LE:272:ARG:NH2	2.36	0.58
46:CF:116:PHE:HB2	46:CF:204:ILE:HD11	1.86	0.58
1:L5:2758:G:O2'	1:L5:2765:A:N3	2.36	0.58
4:LA:47:ASP:HB3	4:LA:60:LYS:HB2	1.85	0.58
1:L5:3773:U:N3	42:CB:274:GLN:OE1	2.37	0.57
1:L5:4726:G:N7	45:CE:100:ARG:NH2	2.47	0.57
1:L5:4741:C:OP1	1:L5:4900:C:N4	2.37	0.57
20:LS:77:ASN:HB2	20:LS:132:ILE:HG13	1.86	0.57
26:LZ:53:VAL:HG13	26:LZ:62:ILE:HD12	1.85	0.57
44:CD:295:ARG:NH1	44:CD:319:GLU:OE1	2.37	0.57
1:L5:4093:G:N1	1:L5:4114:C:N3	2.52	0.57
2:L7:23:A:N3	2:L7:118:C:O2'	2.33	0.57
30:Le:78:LEU:O	39:Lr:20:ARG:NH1	2.36	0.57
1:L5:1070:G:OP2	8:LE:65:ARG:NH1	2.38	0.57
1:L5:4645:C:H3'	19:LR:62:ARG:HH22	1.67	0.57
1:L5:4648:A:OP1	19:LR:62:ARG:NH1	2.36	0.57
44:CD:442:ILE:HD13	49:CI:89:THR:HG21	1.86	0.57
1:L5:3759:A:N7	1:L5:3764:U:O4	2.36	0.57
22:LU:96:LEU:HB3	22:LU:100:LEU:HD12	1.86	0.57
1:L5:1727:U:OP1	9:LF:131:ASN:ND2	2.38	0.57
46:CF:47:ASN:ND2	46:CF:129:ASN:OD1	2.38	0.57
8:LE:141:ARG:NH1	8:LE:191:GLN:O	2.37	0.57
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.70	0.57
7:LD:53:VAL:HB	7:LD:159:VAL:HG13	1.87	0.56
1:L5:308:G:OP2	1:L5:308:G:N2	2.30	0.56
1:L5:2486:G:O6	1:L5:2493:G:O6	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LA:180:LEU:HD11	38:Lp:26:VAL:HG21	1.87	0.56
41:CA:176:LEU:O	44:CD:368:ARG:NH2	2.38	0.56
47:CG:431:SER:O	47:CG:438:LEU:HA	2.05	0.56
1:L5:3641:U:OP2	1:L5:3646:A:N6	2.35	0.56
42:CB:291:LYS:NZ	42:CB:332:SER:OG	2.32	0.56
1:L5:24:G:N7	35:Lj:46:LYS:NZ	2.53	0.56
1:L5:1368:A:H1'	25:LY:1:MET:HE2	1.88	0.56
1:L5:1743:A:N1	1:L5:1789:C:O2'	2.38	0.56
1:L5:4618:G:H5''	23:LV:15:ARG:HB2	1.88	0.56
1:L5:4693:C:OP1	11:LH:64:ARG:NH2	2.38	0.56
1:L5:509:A:N6	27:La:106:SER:OG	2.38	0.56
1:L5:3938:G:OP2	15:LN:24:ARG:NH1	2.39	0.56
5:LB:10:ARG:NH2	5:LB:265:SER:O	2.36	0.56
29:Ld:36:VAL:HG21	29:Ld:44:ARG:HG2	1.87	0.56
32:Lg:61:PRO:HA	32:Lg:64:LEU:HD12	1.88	0.56
48:CH:103:SER:HB2	48:CH:109:LYS:HZ3	1.71	0.56
1:L5:1594:C:N3	44:CD:634:ARG:NH2	2.54	0.56
11:LH:113:GLU:HG2	11:LH:125:ARG:HG2	1.88	0.56
47:CG:107:THR:HG21	47:CG:484:ARG:HD3	1.88	0.56
1:L5:1671:U:O4	1:L5:1685:G:N2	2.39	0.56
8:LE:46:ARG:O	8:LE:65:ARG:NH2	2.35	0.56
14:LM:41:PRO:HG3	14:LM:73:VAL:HG12	1.89	0.56
14:LM:104:MET:HE2	16:LO:199:HIS:HB3	1.88	0.56
1:L5:690:C:OP1	39:Lr:87:ARG:NH1	2.39	0.55
1:L5:1362:G:OP1	13:LL:39:ARG:NH2	2.39	0.55
1:L5:4930:C:OP1	8:LE:266:GLN:NE2	2.40	0.55
37:Ll:23:ILE:HB	37:Ll:27:ILE:HD11	1.88	0.55
1:L5:2601:A:N6	1:L5:2744:A:OP2	2.36	0.55
40:Lt:59:THR:HB	40:Lt:74:VAL:HB	1.87	0.55
1:L5:386:A:OP2	25:LY:89:LYS:NZ	2.38	0.55
1:L5:4910:G:N2	16:LO:106:ASP:O	2.40	0.55
7:LD:62:CYS:HB3	7:LD:105:LEU:HD22	1.87	0.55
23:LV:134:SER:HA	41:CA:61:ARG:HD3	1.88	0.55
28:Lc:38:ILE:HD11	28:Lc:46:VAL:HG21	1.87	0.55
1:L5:2483:G:O6	1:L5:2495:U:O4	2.24	0.55
1:L5:2875:C:OP1	38:Lp:23:ARG:NH1	2.37	0.55
1:L5:3774:A:O2'	42:CB:266:LYS:NZ	2.39	0.55
1:L5:4407:G:H2'	1:L5:4408:G:C8	2.42	0.55
15:LN:159:ARG:HB3	15:LN:164:LEU:HB2	1.89	0.55
25:LY:26:ARG:HG2	25:LY:78:TYR:HE1	1.71	0.55
41:CA:242:ASP:OD1	44:CD:347:LYS:NZ	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:CB:119:SER:O	47:CG:394:LYS:NZ	2.39	0.55
42:CB:396:ALA:HA	42:CB:399:GLU:HG2	1.89	0.55
1:L5:2641:A:OP1	32:Lg:21:ARG:NH2	2.39	0.55
26:LZ:92:ASP:HB3	26:LZ:95:VAL:HG12	1.87	0.55
17:LP:131:ARG:HB2	17:LP:135:ARG:HB3	1.89	0.55
42:CB:75:GLU:OE2	48:CH:201:LYS:NZ	2.39	0.55
1:L5:2845:A:H61	1:L5:3843:C:N4	2.05	0.55
1:L5:4670:C:O2'	23:LV:15:ARG:NH2	2.40	0.55
5:LB:352:LEU:HD13	45:CE:18:ARG:HH21	1.72	0.55
8:LE:152:ILE:O	8:LE:159:GLY:N	2.40	0.55
44:CD:465:GLU:HG3	49:CI:106:LYS:HE3	1.87	0.55
49:CI:57:LYS:NZ	49:CI:63:LEU:O	2.40	0.55
1:L5:3707:U:H3	1:L5:3743:G:H1	1.54	0.55
1:L5:4541:G:N2	1:L5:4544:A:OP2	2.34	0.55
5:LB:113:GLU:HB2	5:LB:178:ALA:HB2	1.89	0.55
20:LS:80:ILE:HG12	20:LS:129:VAL:HG22	1.88	0.55
1:L5:1921:C:O2'	20:LS:160:ARG:NH2	2.37	0.55
1:L5:1943:A:N1	1:L5:4414:A:O2'	2.34	0.55
1:L5:2495:U:H2'	1:L5:2496:G:H8	1.71	0.55
44:CD:192:ASP:OD2	46:CF:164:ARG:NH2	2.41	0.55
48:CH:98:ARG:HD2	48:CH:188:LEU:HA	1.89	0.55
1:L5:4464:A:N7	44:CD:32:THR:OG1	2.38	0.54
1:L5:4620:U:OP2	1:L5:4670:C:N4	2.40	0.54
13:LL:91:ALA:HB1	13:LL:96:ILE:HB	1.88	0.54
32:Lg:50:PRO:HG3	38:Lp:61:MET:HE3	1.89	0.54
42:CB:422:LEU:HD22	42:CB:443:VAL:HG23	1.89	0.54
1:L5:2345:G:N7	27:La:9:ARG:NH2	2.55	0.54
25:LY:54:GLU:HB2	25:LY:108:ARG:HB3	1.90	0.54
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.90	0.54
33:Lh:31:LEU:HD21	33:Lh:46:LYS:HE2	1.89	0.54
42:CB:164:ILE:HD11	44:CD:278:LEU:HD23	1.90	0.54
1:L5:4454:G:H1	1:L5:4526:U:H3	1.56	0.54
7:LD:68:ARG:NH2	50:CJ:134:LYS:O	2.39	0.54
39:Lr:65:LYS:O	39:Lr:102:TYR:OH	2.25	0.54
1:L5:1406:G:H2'	1:L5:1409:C:H41	1.73	0.54
1:L5:4093:G:N1	1:L5:4114:C:C2	2.76	0.54
22:LU:46:ARG:HH21	22:LU:89:LYS:HE2	1.72	0.54
25:LY:74:TYR:HE2	25:LY:77:LYS:HG3	1.73	0.54
1:L5:72:C:H5	13:LL:67:HIS:HD2	1.54	0.54
1:L5:2572:C:O2'	26:LZ:112:ARG:NH2	2.40	0.54
1:L5:4163:U:H5'	1:L5:4164:C:H5''	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LO:34:VAL:HG22	16:LO:103:LYS:HB2	1.89	0.54
25:LY:18:HIS:O	25:LY:78:TYR:OH	2.26	0.54
1:L5:308:G:O6	15:LN:12:ARG:NH1	2.40	0.54
19:LR:28:GLU:HG3	19:LR:49:LEU:HD22	1.89	0.54
1:L5:1332:C:H2'	1:L5:1333:A:H8	1.72	0.54
7:LD:68:ARG:HH22	50:CJ:133:SER:HB2	1.72	0.54
8:LE:287:VAL:O	14:LM:109:ARG:NH2	2.40	0.54
17:LP:125:MET:HB2	17:LP:141:SER:HB3	1.90	0.54
1:L5:1919:G:O6	31:Lf:29:LYS:NZ	2.37	0.53
1:L5:1628:C:OP1	4:LA:14:SER:OG	2.26	0.53
1:L5:1596:U:H1'	17:LP:135:ARG:HH21	1.73	0.53
1:L5:2885:A:OP1	52:CL:68:ARG:NH2	2.41	0.53
1:L5:2406:G:N7	37:Ll:2:SER:N	2.57	0.53
5:LB:161:ARG:HG2	5:LB:184:GLN:HA	1.90	0.53
11:LH:44:GLU:HB3	11:LH:58:ASP:HB2	1.91	0.53
21:LT:115:LYS:HA	21:LT:118:GLU:HG3	1.90	0.53
23:LV:23:GLY:N	23:LV:39:ILE:O	2.39	0.53
44:CD:226:LEU:O	44:CD:233:ARG:NH2	2.41	0.53
51:CK:79:LEU:HD21	51:CK:92:LEU:HA	1.90	0.53
1:L5:229:G:H5''	25:LY:11:ARG:HG3	1.90	0.53
1:L5:3683:C:OP1	4:LA:132:ASN:ND2	2.41	0.53
1:L5:2016:C:H2'	1:L5:2017:A:H8	1.74	0.53
1:L5:2651:C:O2	32:Lg:54:ARG:NH2	2.42	0.53
18:LQ:35:LEU:O	18:LQ:39:THR:HB	2.09	0.53
19:LR:44:LEU:HD22	19:LR:49:LEU:HD12	1.90	0.53
42:CB:222:GLN:NE2	42:CB:233:ARG:O	2.42	0.53
10:LG:219:VAL:O	10:LG:223:ARG:HB2	2.09	0.53
28:Lc:50:ASN:ND2	28:Lc:75:SER:O	2.39	0.53
51:CK:35:ASP:HB3	51:CK:40:LEU:HB3	1.90	0.53
42:CB:308:LYS:O	42:CB:356:ARG:NH2	2.40	0.53
44:CD:172:LEU:HD13	44:CD:244:LEU:HD23	1.90	0.53
19:LR:70:ARG:NH1	19:LR:75:HIS:O	2.42	0.52
39:Lr:107:ARG:HE	39:Lr:108:MET:HG2	1.75	0.52
41:CA:79:GLN:OE1	49:CI:1:MET:N	2.40	0.52
1:L5:261:G:H2'	1:L5:262:G:C8	2.44	0.52
1:L5:300:A:H2'	1:L5:301:G:H8	1.74	0.52
1:L5:2070:U:OP1	31:Lf:22:ARG:NH2	2.38	0.52
1:L5:2798:A:N6	52:CL:1:MET:SD	2.82	0.52
6:LC:195:LYS:HG2	6:LC:200:ARG:HG3	1.89	0.52
23:LV:97:TYR:OH	49:CI:37:HIS:NE2	2.35	0.52
1:L5:3927:U:H2'	1:L5:3928:A:H8	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:CE:82:ASN:HD22	45:CE:85:THR:HG22	1.74	0.52
51:CK:41:ALA:HB2	51:CK:72:LEU:HD13	1.91	0.52
1:L5:2349:A:H5''	1:L5:2350:U:H5''	1.90	0.52
4:LA:147:ARG:HG2	4:LA:157:VAL:HG22	1.90	0.52
18:LQ:119:LYS:HE3	18:LQ:121:LEU:HD21	1.91	0.52
22:LU:67:LYS:HG3	22:LU:68:SER:H	1.73	0.52
47:CG:355:LEU:O	47:CG:365:LEU:N	2.42	0.52
50:CJ:214:LEU:O	51:CK:62:GLN:NE2	2.42	0.52
2:L7:3:C:OP1	2:L7:58:A:O2'	2.24	0.52
26:LZ:29:ILE:HG22	26:LZ:32:GLY:H	1.74	0.52
26:LZ:100:VAL:HG12	26:LZ:106:LEU:HB3	1.92	0.52
1:L5:4924:C:O2'	1:L5:4926:C:O2	2.26	0.52
44:CD:441:TYR:OH	49:CI:97:GLU:OE2	2.22	0.52
1:L5:1684:A:H62	1:L5:1853:G:H8	1.56	0.52
1:L5:4210:U:O2	1:L5:4222:G:O6	2.28	0.52
1:L5:4698:C:OP2	48:CH:26:LYS:NZ	2.42	0.52
1:L5:4733:C:H1'	1:L5:4734:A:H2'	1.92	0.52
8:LE:68:MET:HA	8:LE:71:ARG:HG2	1.92	0.52
40:Lt:10:ILE:HA	40:Lt:64:ILE:O	2.08	0.52
1:L5:276:C:O2	34:Li:26:HIS:NE2	2.39	0.52
1:L5:1468:C:OP1	27:La:132:ARG:NH2	2.43	0.52
12:LJ:23:ASN:HB3	12:LJ:129:ASP:HB2	1.91	0.52
17:LP:16:LYS:HG2	17:LP:149:ILE:HG12	1.91	0.52
44:CD:368:ARG:NH1	44:CD:369:ASP:OD2	2.42	0.52
50:CJ:104:VAL:HG22	50:CJ:118:GLU:HG2	1.92	0.52
1:L5:1538:U:H2'	1:L5:1539:G:H8	1.75	0.52
1:L5:3711:A:H2'	1:L5:3712:A:H8	1.75	0.52
4:LA:173:GLY:O	38:Lp:69:TRP:NE1	2.39	0.52
42:CB:303:LYS:O	42:CB:306:THR:OG1	2.27	0.52
1:L5:1393:G:O2'	13:LL:190:ARG:NH2	2.36	0.52
22:LU:47:ILE:HD12	22:LU:63:ILE:HD11	1.92	0.52
41:CA:88:LEU:HD12	41:CA:94:ILE:HD11	1.92	0.52
1:L5:942:G:H3'	9:LF:148:LYS:HD2	1.92	0.51
1:L5:989:U:O2	1:L5:1064:G:O6	2.28	0.51
1:L5:1480:C:O2'	1:L5:1482:G:OP2	2.28	0.51
1:L5:3605:C:OP1	19:LR:71:ARG:NH2	2.41	0.51
1:L5:3620:G:OP1	1:L5:3622:C:N4	2.43	0.51
1:L5:1502:G:OP1	18:LQ:65:ARG:NH1	2.44	0.51
1:L5:4337:C:OP2	51:CK:184:LYS:NZ	2.42	0.51
6:LC:13:GLU:HG3	6:LC:14:LYS:HD3	1.93	0.51
25:LY:108:ARG:HE	25:LY:109:LEU:H	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:62:A:N3	1:L5:77:U:O2'	2.37	0.51
1:L5:4510:A:OP2	23:LV:4:ARG:NH2	2.43	0.51
26:LZ:5:MET:O	26:LZ:28:ASN:ND2	2.43	0.51
48:CH:185:HIS:CE1	48:CH:187:GLU:HB2	2.45	0.51
1:L5:703:G:H2'	1:L5:704:C:H4'	1.93	0.51
1:L5:4295:U:O2'	42:CB:84:THR:O	2.28	0.51
5:LB:69:LYS:HE3	44:CD:411:LEU:HB3	1.92	0.51
5:LB:136:LYS:HB2	45:CE:96:TRP:HB2	1.91	0.51
7:LD:139:PRO:O	47:CG:485:ARG:NH2	2.42	0.51
37:Ll:34:LYS:O	37:Ll:36:ARG:NH1	2.44	0.51
44:CD:176:TYR:O	44:CD:181:LYS:NZ	2.43	0.51
1:L5:170:C:H42	1:L5:266:C:H42	1.58	0.51
1:L5:1306:C:H2'	1:L5:1307:A:H8	1.75	0.51
7:LD:45:ASN:ND2	50:CJ:179:GLY:O	2.43	0.51
7:LD:50:ARG:NH1	7:LD:147:ASP:OD2	2.43	0.51
50:CJ:35:LEU:HB3	50:CJ:49:LEU:HD22	1.93	0.51
1:L5:1907:A:H4'	9:LF:223:LYS:HE3	1.93	0.51
1:L5:1933:G:H2'	1:L5:1934:A:C8	2.46	0.51
1:L5:4927:G:OP2	1:L5:4927:G:N2	2.42	0.51
5:LB:92:TYR:HB2	5:LB:159:VAL:HB	1.91	0.51
12:LJ:112:HIS:HB2	12:LJ:117:ILE:HD13	1.92	0.51
42:CB:429:THR:O	42:CB:431:LYS:NZ	2.44	0.51
47:CG:398:LEU:HD13	47:CG:443:VAL:HG13	1.93	0.51
1:L5:151:G:OP1	15:LN:49:ARG:NH2	2.44	0.51
1:L5:2539:C:H5''	32:Lg:66:ARG:HD3	1.93	0.51
1:L5:4606:G:O3'	44:CD:216:ARG:NH1	2.43	0.51
4:LA:118:GLU:OE2	4:LA:156:LYS:NZ	2.44	0.51
6:LC:228:THR:OG1	6:LC:248:ARG:NH2	2.44	0.51
38:Lp:38:THR:HA	38:Lp:45:THR:HA	1.92	0.51
40:Lt:32:ILE:HG12	40:Lt:42:VAL:HG21	1.92	0.51
44:CD:15:ALA:HB2	44:CD:145:LYS:HA	1.92	0.51
50:CJ:207:CYS:SG	50:CJ:208:ARG:N	2.83	0.51
1:L5:3908:A:H61	1:L5:4394:A:H61	1.58	0.51
1:L5:2573:A:N7	1:L5:2761:U:O4	2.44	0.51
2:L7:85:G:H2'	2:L7:86:G:H8	1.76	0.51
4:LA:136:VAL:HA	4:LA:148:VAL:HG12	1.92	0.51
27:La:2:PRO:HG2	27:La:5:LEU:HD12	1.93	0.51
41:CA:93:GLN:HG3	41:CA:132:VAL:HG13	1.91	0.51
1:L5:1364:U:OP2	13:LL:36:ARG:NH2	2.44	0.51
1:L5:1503:A:H4'	1:L5:1504:G:H5'	1.93	0.51
9:LF:149:SER:HA	9:LF:245:ARG:HH12	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:460:C:H2'	1:L5:461:G:H8	1.75	0.50
1:L5:4670:C:O2'	1:L5:4672:A:OP2	2.27	0.50
50:CJ:90:PHE:HZ	50:CJ:116:MET:HG2	1.76	0.50
1:L5:230:G:OP1	25:LY:15:ARG:NH1	2.42	0.50
1:L5:1739:G:N3	1:L5:1742:A:N6	2.59	0.50
1:L5:1914:C:H4'	16:LO:89:PRO:HD3	1.92	0.50
1:L5:5002:U:H4'	5:LB:375:GLY:HA3	1.93	0.50
46:CF:78:GLY:HA3	46:CF:84:GLU:HA	1.92	0.50
50:CJ:136:PRO:HD2	50:CJ:181:GLU:HG3	1.92	0.50
1:L5:4437:U:O4	44:CD:144:GLN:NE2	2.44	0.50
2:L7:7:G:OP1	7:LD:33:ARG:NE	2.38	0.50
5:LB:57:VAL:HB	5:LB:367:PHE:HB3	1.93	0.50
36:Lk:47:ILE:HG22	36:Lk:49:ASP:H	1.76	0.50
44:CD:90:ASP:O	44:CD:94:LEU:HB2	2.10	0.50
49:CI:6:CYS:O	49:CI:10:SER:HA	2.11	0.50
1:L5:1918:U:O2'	1:L5:1920:C:OP2	2.29	0.50
6:LC:289:LEU:HD11	18:LQ:31:LEU:HB2	1.94	0.50
7:LD:80:ALA:HA	7:LD:83:LEU:HD23	1.92	0.50
20:LS:15:ARG:HB3	20:LS:27:LEU:HD23	1.94	0.50
1:L5:3661:G:N7	4:LA:152:SER:OG	2.45	0.50
27:La:79:TRP:HA	27:La:82:VAL:HG12	1.93	0.50
50:CJ:34:MET:HE1	50:CJ:81:PHE:HB3	1.93	0.50
50:CJ:34:MET:HE2	50:CJ:36:ILE:HD11	1.94	0.50
1:L5:1925:G:OP1	14:LM:33:GLN:NE2	2.45	0.50
1:L5:2521:G:H4'	32:Lg:26:PRO:HD2	1.94	0.50
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.47	0.50
4:LA:24:LYS:HG3	4:LA:49:ILE:HD12	1.94	0.50
38:Lp:37:TYR:HB2	38:Lp:47:MET:HB2	1.93	0.50
42:CB:384:VAL:HG11	42:CB:448:LEU:HB3	1.93	0.50
1:L5:478:G:OP1	39:Lr:66:ARG:NH1	2.45	0.50
1:L5:4093:G:N7	1:L5:4095:G:C2	2.79	0.50
8:LE:191:GLN:HA	8:LE:194:VAL:HG22	1.94	0.50
41:CA:232:ILE:HA	41:CA:236:MET:HB3	1.94	0.50
1:L5:1372:A:OP1	15:LN:202:ARG:NH2	2.36	0.50
1:L5:1574:G:OP2	19:LR:92:LYS:NZ	2.45	0.50
1:L5:4897:G:OP1	14:LM:128:LYS:NZ	2.44	0.50
17:LP:18:ARG:NH1	17:LP:147:GLU:OE1	2.44	0.50
30:Le:101:HIS:O	30:Le:128:ARG:NH2	2.44	0.50
1:L5:2845:A:N6	1:L5:3843:C:H42	2.10	0.49
1:L5:3932:U:H2'	1:L5:3933:G:H8	1.77	0.49
16:LO:52:LEU:HD13	43:CC:5:LYS:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:165:LEU:HD11	8:LE:176:THR:HB	1.94	0.49
1:L5:2072:C:OP1	18:LQ:2:GLY:N	2.45	0.49
1:L5:4093:G:C6	1:L5:4114:C:C2	3.00	0.49
1:L5:4564:A:OP1	16:LO:68:ARG:NH2	2.44	0.49
7:LD:139:PRO:O	51:CK:83:ARG:NH1	2.45	0.49
20:LS:112:ASP:OD1	20:LS:116:ARG:NH1	2.44	0.49
25:LY:101:PRO:HA	25:LY:104:VAL:HG22	1.94	0.49
35:Lj:27:TYR:HA	35:Lj:34:CYS:HA	1.94	0.49
16:LO:76:PRO:HB3	16:LO:138:LEU:HG	1.94	0.49
1:L5:2287:G:N7	27:La:10:LYS:NZ	2.53	0.49
1:L5:2520:C:H2'	1:L5:2521:G:C8	2.47	0.49
3:L8:67:U:H5''	35:Lj:86:PRO:HA	1.94	0.49
10:LG:164:ILE:HG22	15:LN:22:LEU:HD21	1.94	0.49
1:L5:74:G:H5''	13:LL:59:VAL:HB	1.94	0.49
1:L5:182:G:H1	1:L5:254:G:H1	1.59	0.49
1:L5:499:G:H2'	1:L5:504:G:H22	1.78	0.49
1:L5:1516:G:H2'	1:L5:1518:A:H62	1.77	0.49
44:CD:44:ARG:O	44:CD:48:MET:HG3	2.11	0.49
1:L5:982:U:OP1	8:LE:73:TYR:OH	2.30	0.49
1:L5:2436:U:OP2	24:LX:135:LYS:NZ	2.45	0.49
1:L5:2809:G:O2'	1:L5:4644:G:OP1	2.29	0.49
1:L5:4187:G:N3	15:LN:81:TYR:OH	2.45	0.49
1:L5:4623:G:OP1	5:LB:19:ARG:NH2	2.37	0.49
1:L5:4735:G:O2'	1:L5:5068:G:N7	2.45	0.49
2:L7:100:A:OP1	50:CJ:40:ASN:ND2	2.45	0.49
39:Lr:63:VAL:HG22	39:Lr:79:ARG:HG2	1.94	0.49
46:CF:177:LYS:HB2	46:CF:180:ASP:HB2	1.94	0.49
1:L5:1720:C:OP1	1:L5:1835:G:O2'	2.30	0.49
1:L5:2637:U:OP1	32:Lg:28:ASN:ND2	2.45	0.49
7:LD:166:ALA:HB1	7:LD:171:LEU:HD12	1.95	0.49
47:CG:157:HIS:CE1	47:CG:176:LYS:HD3	2.48	0.49
47:CG:318:LEU:HD23	47:CG:325:LEU:HD22	1.95	0.49
50:CJ:214:LEU:HD21	51:CK:69:THR:HG21	1.94	0.49
1:L5:2267:U:OP1	39:Lr:37:SER:OG	2.31	0.49
1:L5:3887:C:OP2	16:LO:85:ARG:NH2	2.42	0.49
1:L5:4436:U:H6	44:CD:143:ARG:HH11	1.60	0.49
1:L5:4509:U:H3'	23:LV:4:ARG:HH21	1.77	0.49
1:L5:4739:C:OP1	45:CE:109:ARG:NH2	2.45	0.49
27:La:100:ILE:HG12	27:La:123:ILE:HB	1.95	0.49
41:CA:109:THR:HB	41:CA:149:GLY:HA2	1.94	0.49
50:CJ:153:THR:HG23	50:CJ:156:TYR:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1461:C:H2'	1:L5:1462:A:H8	1.78	0.49
1:L5:2543:A:H2	1:L5:2773:G:H22	1.59	0.49
1:L5:4122:G:H4'	32:Lg:90:ARG:HD2	1.93	0.49
26:LZ:128:LYS:O	26:LZ:132:GLN:HG2	2.13	0.49
41:CA:18:LYS:HE2	41:CA:60:GLY:HA2	1.95	0.49
42:CB:23:ARG:NH2	42:CB:33:ARG:O	2.46	0.49
1:L5:1517:G:H22	6:LC:103:ALA:HA	1.77	0.48
1:L5:4438:U:C4	44:CD:94:LEU:HD11	2.48	0.48
9:LF:182:TYR:HB3	9:LF:200:ARG:HG3	1.94	0.48
20:LS:142:VAL:HG12	20:LS:146:HIS:CE1	2.48	0.48
23:LV:82:ILE:HD12	23:LV:121:VAL:HG22	1.95	0.48
42:CB:80:TRP:HB3	48:CH:259:LEU:HD13	1.94	0.48
44:CD:272:PHE:HE1	44:CD:284:LEU:HD21	1.76	0.48
46:CF:151:PRO:O	46:CF:155:GLN:OE1	2.30	0.48
32:Lg:8:ARG:HB2	32:Lg:34:TYR:HE1	1.77	0.48
1:L5:49:U:O2'	13:LL:20:ARG:NH2	2.45	0.48
1:L5:1779:U:H2'	1:L5:1780:A:C8	2.48	0.48
7:LD:83:LEU:HB3	7:LD:88:VAL:HG23	1.95	0.48
33:Lh:31:LEU:HB3	33:Lh:47:ILE:HG12	1.96	0.48
38:Lp:47:MET:SD	38:Lp:57:CYS:HB2	2.53	0.48
1:L5:2079:G:OP2	30:Le:64:LYS:NZ	2.39	0.48
1:L5:2279:A:O2'	30:Le:48:ARG:NH2	2.45	0.48
1:L5:4088:C:H2'	1:L5:4089:G:H8	1.78	0.48
2:L7:92:C:H2'	2:L7:93:G:H8	1.78	0.48
4:LA:45:VAL:HG22	4:LA:61:VAL:HG22	1.96	0.48
6:LC:218:ILE:HA	6:LC:229:LEU:HD13	1.95	0.48
47:CG:296:SER:HB2	47:CG:343:ARG:HH21	1.78	0.48
1:L5:409:G:O2'	1:L5:2330:G:OP1	2.31	0.48
1:L5:736:C:OP1	14:LM:74:ARG:NH2	2.45	0.48
1:L5:1525:A:H2'	1:L5:1526:G:H8	1.78	0.48
1:L5:2844:A:N6	1:L5:3839:G:O2'	2.46	0.48
2:L7:75:G:H4'	2:L7:76:U:H5'	1.95	0.48
16:LO:10:ASP:OD2	16:LO:37:ARG:NH2	2.46	0.48
42:CB:229:PRO:HB3	42:CB:254:LEU:HD21	1.95	0.48
1:L5:352:G:O2'	3:L8:22:U:O4	2.31	0.48
1:L5:1353:G:N7	18:LQ:104:ARG:NH2	2.55	0.48
1:L5:4991:U:H2'	1:L5:4992:G:H8	1.78	0.48
2:L7:98:G:OP1	50:CJ:99:ARG:NH1	2.37	0.48
5:LB:29:VAL:HG22	5:LB:220:ILE:HD12	1.94	0.48
10:LG:173:LEU:HA	34:Li:43:MET:HE1	1.94	0.48
10:LG:232:GLU:O	10:LG:236:HIS:CB	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LU:23:LEU:HD23	22:LU:110:TYR:HB2	1.95	0.48
2:L7:35:U:O2	2:L7:45:U:O2'	2.30	0.48
4:LA:104:VAL:HG12	4:LA:146:THR:HG21	1.95	0.48
5:LB:42:HIS:HB3	45:CE:33:LEU:HD11	1.94	0.48
17:LP:122:ALA:HB3	17:LP:143:PRO:HG2	1.96	0.48
30:Le:100:ALA:O	30:Le:108:ARG:NH1	2.47	0.48
1:L5:512:U:O4	1:L5:647:G:O6	2.31	0.48
1:L5:723:A:OP1	1:L5:934:C:N4	2.46	0.48
3:L8:12:G:OP1	17:LP:3:ARG:NE	2.42	0.48
5:LB:220:ILE:HG12	5:LB:278:THR:HG23	1.94	0.48
8:LE:141:ARG:NH2	31:Lf:110:ILE:O	2.46	0.48
35:Lj:39:TYR:CD1	35:Lj:40:PRO:HA	2.49	0.48
1:L5:1523:A:N3	1:L5:4389:C:O2'	2.46	0.48
1:L5:1552:G:O2'	1:L5:1574:G:N2	2.35	0.48
1:L5:2835:A:O2'	5:LB:228:TYR:O	2.30	0.48
24:LX:100:VAL:O	24:LX:134:LYS:HB3	2.13	0.48
40:Lt:25:THR:OG1	44:CD:262:GLY:O	2.26	0.48
42:CB:243:LYS:HE3	42:CB:244:GLU:HG2	1.95	0.48
46:CF:49:ARG:HH12	46:CF:191:LYS:HD2	1.78	0.48
47:CG:348:SER:OG	47:CG:349:ASP:N	2.45	0.48
1:L5:4251:A:H5''	12:LJ:108:GLY:HA3	1.96	0.48
8:LE:190:HIS:HB3	8:LE:193:PHE:HD2	1.79	0.48
20:LS:98:ARG:HG3	20:LS:142:VAL:HG13	1.94	0.48
51:CK:32:LEU:HG	51:CK:43:ASP:HB3	1.96	0.48
1:L5:43:U:H3'	1:L5:44:A:H8	1.79	0.47
1:L5:239:C:H5'	25:LY:33:PRO:HD3	1.96	0.47
1:L5:2265:G:OP2	39:Lr:33:LYS:NZ	2.47	0.47
1:L5:4101:C:N4	1:L5:4107:G:O6	2.47	0.47
1:L5:4271:A:H5''	50:CJ:11:LYS:HB2	1.96	0.47
1:L5:4899:G:O2'	1:L5:4901:G:O4'	2.29	0.47
1:L5:4903:G:OP1	45:CE:82:ASN:ND2	2.47	0.47
16:LO:72:HIS:O	16:LO:74:ARG:NH1	2.45	0.47
20:LS:1:MET:HE3	20:LS:34:ALA:HA	1.96	0.47
28:Lc:14:ILE:HA	28:Lc:17:ARG:HG2	1.96	0.47
42:CB:251:ILE:HG22	42:CB:277:PRO:HB2	1.96	0.47
1:L5:4611:A:H2	11:LH:120:GLU:HG2	1.78	0.47
46:CF:40:LEU:HD21	46:CF:102:LEU:HD22	1.96	0.47
49:CI:56:ARG:HB3	49:CI:61:LYS:HB2	1.95	0.47
1:L5:2324:C:O2'	30:Le:98:GLU:OE1	2.33	0.47
1:L5:3654:G:O2'	1:L5:3693:U:OP1	2.31	0.47
4:LA:33:ASP:OD2	4:LA:33:ASP:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LA:147:ARG:HH22	4:LA:155:LYS:HD2	1.78	0.47
37:L1:23:ILE:HG23	37:L1:38:ASN:HB2	1.96	0.47
42:CB:175:ASP:HB3	42:CB:178:LYS:HG3	1.96	0.47
1:L5:1974:U:OP2	40:Lt:119:ARG:NH2	2.48	0.47
1:L5:2425:U:H5''	1:L5:2426:U:H5	1.80	0.47
1:L5:2485:U:O2'	1:L5:2486:G:N1	2.48	0.47
1:L5:4967:A:H2'	1:L5:4968:A:C8	2.50	0.47
18:LQ:65:ARG:HG3	18:LQ:68:ARG:HH21	1.79	0.47
26:LZ:51:ARG:HB2	26:LZ:65:ARG:HB3	1.96	0.47
1:L5:1895:G:O2'	1:L5:1907:A:N3	2.45	0.47
3:L8:47:C:H1'	3:L8:61:A:H2'	1.96	0.47
4:LA:180:LEU:HD22	38:Lp:18:TYR:HB3	1.96	0.47
20:LS:29:ARG:NE	21:LT:147:GLU:OE2	2.48	0.47
1:L5:461:G:H2'	1:L5:462:G:H8	1.80	0.47
1:L5:1332:C:H2'	1:L5:1333:A:C8	2.50	0.47
1:L5:1646:A:O2'	35:Lj:49:TRP:O	2.29	0.47
1:L5:1654:G:H5''	1:L5:1655:C:H5	1.80	0.47
1:L5:2523:G:OP2	32:Lg:29:ARG:NH2	2.46	0.47
1:L5:2754:G:OP2	26:LZ:133:LYS:NZ	2.39	0.47
1:L5:3732:A:H2'	1:L5:3733:A:H8	1.79	0.47
2:L7:85:G:H2'	2:L7:86:G:C8	2.50	0.47
7:LD:196:ARG:HB2	47:CG:147:THR:HG21	1.96	0.47
12:LJ:18:ARG:HG3	12:LJ:135:GLY:HA3	1.97	0.47
19:LR:105:LEU:HD12	19:LR:135:LYS:HE3	1.95	0.47
25:LY:72:GLN:HB3	25:LY:81:TYR:HB2	1.97	0.47
44:CD:412:ASP:HB3	44:CD:415:LYS:HD2	1.97	0.47
47:CG:133:SER:OG	47:CG:134:GLY:N	2.47	0.47
50:CJ:150:PHE:HA	50:CJ:156:TYR:HB3	1.94	0.47
1:L5:62:A:OP1	15:LN:172:ARG:NH1	2.40	0.47
1:L5:63:G:OP2	15:LN:169:ARG:NH2	2.33	0.47
1:L5:2471:G:H5''	10:LG:59:ARG:HD2	1.97	0.47
1:L5:4537:C:H2'	1:L5:4538:G:H8	1.80	0.47
5:LB:85:VAL:O	5:LB:164:ALA:HA	2.15	0.47
6:LC:334:THR:HG1	9:LF:51:TYR:HH	1.58	0.47
40:Lt:55:GLY:O	40:Lt:92:ARG:NH1	2.47	0.47
16:LO:9:LEU:HD23	16:LO:118:MET:HB2	1.96	0.47
44:CD:93:LYS:HB3	44:CD:93:LYS:HE3	1.73	0.47
1:L5:280:G:H5''	15:LN:14:LYS:HE2	1.96	0.47
1:L5:1725:U:H2'	1:L5:1726:U:C6	2.50	0.47
1:L5:4597:U:O2'	44:CD:399:ARG:NH2	2.48	0.47
1:L5:4940:C:H5'	1:L5:4941:G:H5''	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:5006:U:H4'	1:L5:5007:A:H5'	1.96	0.47
2:L7:82:G:H2'	2:L7:83:A:C8	2.50	0.47
5:LB:77:THR:HG21	5:LB:337:VAL:HG22	1.98	0.47
5:LB:88:GLY:HA3	5:LB:163:ILE:HD12	1.97	0.47
20:LS:48:VAL:HG11	20:LS:54:MET:HG2	1.96	0.47
30:Le:89:LEU:HD13	30:Le:118:LEU:HD22	1.97	0.47
51:CK:79:LEU:HD12	51:CK:80:PRO:HD2	1.96	0.47
1:L5:1308:C:H2'	1:L5:1309:C:C6	2.51	0.46
1:L5:1932:A:OP2	16:LO:49:ARG:NH2	2.48	0.46
1:L5:3607:U:H2'	1:L5:3608:A:C8	2.51	0.46
5:LB:399:LYS:HD3	49:CI:109:MET:HE2	1.96	0.46
1:L5:86:U:H2'	1:L5:87:A:H8	1.79	0.46
1:L5:753:C:H41	1:L5:910:G:H1	1.63	0.46
1:L5:1243:C:H2'	1:L5:1244:G:C8	2.50	0.46
1:L5:1344:C:H1'	13:LL:10:LEU:HD21	1.97	0.46
1:L5:2394:G:O2'	1:L5:2819:U:O4	2.27	0.46
1:L5:4062:A:H2'	1:L5:4063:U:C6	2.50	0.46
1:L5:4622:A:H4'	5:LB:13:SER:HB2	1.96	0.46
1:L5:4962:C:H2'	1:L5:4963:G:H8	1.80	0.46
5:LB:10:ARG:NH1	5:LB:11:HIS:O	2.48	0.46
17:LP:37:LYS:HG3	17:LP:117:ILE:HG22	1.96	0.46
18:LQ:90:VAL:HB	27:La:80:THR:HG21	1.97	0.46
27:La:77:LYS:O	27:La:80:THR:OG1	2.33	0.46
33:Lh:80:PRO:HD2	33:Lh:83:LEU:HD12	1.98	0.46
46:CF:80:SER:OG	46:CF:83:ASP:OD2	2.29	0.46
1:L5:1899:G:O2'	30:Le:57:ASN:OD1	2.33	0.46
1:L5:3619:G:H22	1:L5:3624:A:H1'	1.81	0.46
1:L5:3871:A:H2'	1:L5:3872:A:C8	2.50	0.46
1:L5:4896:G:H2'	1:L5:4897:G:C8	2.50	0.46
30:Le:20:PHE:O	30:Le:33:ARG:NH1	2.35	0.46
42:CB:34:ASP:OD1	42:CB:34:ASP:N	2.48	0.46
42:CB:44:TYR:OH	48:CH:166:LYS:O	2.28	0.46
1:L5:2658:G:N2	1:L5:2676:A:OP2	2.42	0.46
1:L5:4893:A:OP1	16:LO:188:LYS:NZ	2.48	0.46
15:LN:158:HIS:HB3	15:LN:161:MET:HB2	1.97	0.46
27:La:72:THR:HG22	27:La:110:LYS:HB3	1.96	0.46
1:L5:326:C:OP2	34:Li:28:ARG:NH2	2.40	0.46
42:CB:413:ASP:OD1	42:CB:414:SER:N	2.48	0.46
48:CH:195:PRO:HD2	48:CH:223:ASN:HB3	1.97	0.46
50:CJ:120:GLY:O	50:CJ:223:LEU:HA	2.16	0.46
1:L5:1498:G:H5''	18:LQ:150:ARG:HH12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4712:C:OP1	16:LO:74:ARG:NH2	2.48	0.46
32:Lg:83:CYS:SG	32:Lg:86:CYS:HB2	2.54	0.46
1:L5:728:U:OP1	9:LF:76:ARG:NH2	2.48	0.46
1:L5:1725:U:H2'	1:L5:1726:U:H6	1.80	0.46
1:L5:1849:U:H2'	1:L5:1850:A:C8	2.51	0.46
1:L5:2020:U:H2'	1:L5:2021:G:H8	1.81	0.46
1:L5:2666:U:O4	19:LR:128:LYS:NZ	2.41	0.46
5:LB:68:ASN:O	5:LB:70:LYS:NZ	2.45	0.46
5:LB:77:THR:OG1	5:LB:335:GLY:O	2.32	0.46
50:CJ:144:ILE:HG12	51:CK:41:ALA:HB3	1.98	0.46
1:L5:351:C:OP2	6:LC:197:ARG:NH1	2.38	0.46
3:L8:8:U:H2'	3:L8:9:A:C8	2.51	0.46
44:CD:87:TYR:CE1	44:CD:154:VAL:HG22	2.51	0.46
1:L5:2362:U:H2'	1:L5:2363:A:H8	1.81	0.46
1:L5:3700:C:H2'	1:L5:3746:A:H62	1.81	0.46
1:L5:4453:C:OP2	1:L5:4519:C:N4	2.45	0.46
20:LS:83:ARG:NH2	43:CC:47:ASP:OD1	2.48	0.46
1:L5:1939:A:H2'	1:L5:1940:G:C8	2.51	0.45
1:L5:4074:C:O3'	10:LG:249:ARG:NH2	2.49	0.45
1:L5:4601:U:H2'	1:L5:4602:A:H8	1.81	0.45
2:L7:76:U:H2'	2:L7:77:A:C8	2.51	0.45
3:L8:2:G:H3'	3:L8:3:A:H8	1.82	0.45
8:LE:161:ARG:NH1	8:LE:273:SER:OG	2.49	0.45
9:LF:92:VAL:O	9:LF:120:GLY:HA2	2.15	0.45
12:LJ:120:ASP:HB3	12:LJ:123:ILE:HG12	1.98	0.45
41:CA:78:ASP:OD1	41:CA:78:ASP:N	2.48	0.45
47:CG:293:MET:HB2	47:CG:344:LEU:HD11	1.98	0.45
1:L5:186:G:OP2	13:LL:44:ARG:NH1	2.49	0.45
1:L5:223:G:N3	6:LC:223:ASN:ND2	2.63	0.45
1:L5:502:C:H3'	1:L5:503:C:H3'	1.97	0.45
1:L5:4122:G:O2'	26:LZ:136:PHE:OXT	2.33	0.45
1:L5:4699:U:H1'	1:L5:4700:A:H5''	1.97	0.45
23:LV:21:PRO:HA	23:LV:54:ALA:HA	1.99	0.45
39:Lr:84:LYS:HE3	39:Lr:88:ALA:HB1	1.99	0.45
42:CB:402:LYS:HE2	42:CB:404:GLU:HB3	1.98	0.45
44:CD:87:TYR:OH	44:CD:157:HIS:HB3	2.16	0.45
1:L5:268:G:H2'	1:L5:269:G:H8	1.80	0.45
50:CJ:135:CYS:HB3	50:CJ:217:MET:HE1	1.98	0.45
1:L5:108:A:O2'	1:L5:334:A:N6	2.49	0.45
1:L5:1596:U:H2'	17:LP:131:ARG:HH21	1.80	0.45
1:L5:4646:U:O2'	44:CD:502:ASN:OD1	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB:107:ALA:HB2	5:LB:201:LEU:HD22	1.99	0.45
26:LZ:121:ARG:HA	26:LZ:124:THR:HG22	1.98	0.45
49:CI:66:ASP:OD1	49:CI:67:ASN:N	2.49	0.45
51:CK:73:ILE:HG23	51:CK:77:TRP:CZ3	2.52	0.45
52:CL:72:ASP:HB2	52:CL:75:ASN:HD22	1.81	0.45
1:L5:318:A:H2'	1:L5:319:A:C8	2.52	0.45
1:L5:3732:A:H2'	1:L5:3733:A:C8	2.51	0.45
1:L5:4260:U:H2'	1:L5:4261:C:C6	2.51	0.45
11:LH:18:ILE:HG12	11:LH:27:VAL:HG22	1.98	0.45
12:LJ:120:ASP:OD2	12:LJ:122:SER:OG	2.27	0.45
23:LV:57:VAL:HG23	23:LV:84:GLN:HG2	1.98	0.45
32:Lg:88:ARG:HA	32:Lg:91:ILE:HD12	1.98	0.45
49:CI:109:MET:O	49:CI:113:LYS:HG2	2.17	0.45
50:CJ:75:GLN:HG2	50:CJ:113:VAL:HG21	1.99	0.45
1:L5:162:A:H2'	1:L5:163:A:H8	1.81	0.45
1:L5:362:A:N6	37:Ll:37:TYR:O	2.44	0.45
1:L5:2749:C:H2'	1:L5:2750:G:C8	2.52	0.45
1:L5:4935:C:H2'	1:L5:4936:G:C8	2.52	0.45
3:L8:142:U:OP1	15:LN:38:ARG:NH2	2.43	0.45
5:LB:69:LYS:HA	5:LB:69:LYS:HD3	1.82	0.45
1:L5:1399:G:H2'	1:L5:1400:G:H8	1.82	0.45
1:L5:2275:G:H2'	1:L5:2276:A:C8	2.51	0.45
1:L5:2578:G:N7	26:LZ:17:ARG:NH2	2.63	0.45
1:L5:4728:U:OP1	5:LB:128:LYS:NZ	2.47	0.45
10:LG:96:LEU:HD22	10:LG:193:LEU:HD11	1.98	0.45
16:LO:7:LEU:HB2	16:LO:31:ARG:HD3	1.98	0.45
28:Lc:15:ASN:OD1	28:Lc:74:TYR:OH	2.26	0.45
40:Lt:20:GLY:HA3	40:Lt:54:LYS:HD2	1.99	0.45
41:CA:39:GLU:O	41:CA:43:SER:CB	2.65	0.45
44:CD:185:ILE:HA	44:CD:188:VAL:HG12	1.98	0.45
37:Ll:29:MET:HE1	44:CD:585:MET:HG2	1.98	0.45
47:CG:200:LYS:HB2	47:CG:224:LYS:HB3	1.99	0.45
47:CG:291:ASN:ND2	47:CG:349:ASP:OD1	2.50	0.45
1:L5:2843:U:O2'	1:L5:4632:U:OP1	2.34	0.45
1:L5:4322:G:N2	1:L5:4325:A:OP2	2.43	0.45
26:LZ:121:ARG:NH2	26:LZ:127:ASN:OD1	2.50	0.45
29:Ld:114:PHE:HA	29:Ld:117:LEU:HD12	1.98	0.45
1:L5:1662:C:OP2	30:Le:39:ARG:NH2	2.50	0.45
20:LS:27:LEU:HD21	21:LT:141:VAL:HG11	1.98	0.45
42:CB:384:VAL:HA	42:CB:387:ILE:HG12	1.99	0.45
44:CD:19:ILE:HD13	44:CD:142:LYS:HE3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:CG:355:LEU:HB3	47:CG:366:THR:HG22	1.99	0.45
1:L5:1243:C:H2'	1:L5:1244:G:H8	1.82	0.44
5:LB:90:VAL:HG22	5:LB:104:THR:HG23	1.99	0.44
49:CI:71:PHE:O	49:CI:75:ARG:NH2	2.51	0.44
1:L5:66:A:O2'	1:L5:326:C:O2	2.33	0.44
1:L5:1346:C:H2'	1:L5:1347:G:H8	1.83	0.44
1:L5:4259:C:OP2	12:LJ:54:ARG:NH1	2.50	0.44
28:Lc:38:ILE:HG21	28:Lc:63:TYR:HB3	2.00	0.44
1:L5:1359:G:H4'	15:LN:203:TYR:HB2	1.99	0.44
1:L5:1724:G:N2	1:L5:1876:U:OP1	2.40	0.44
1:L5:1845:U:H2'	1:L5:1846:G:H8	1.83	0.44
1:L5:2856:C:O2	5:LB:242:ARG:NH2	2.48	0.44
1:L5:3753:G:H5'	42:CB:303:LYS:HD2	1.99	0.44
1:L5:3903:A:OP1	6:LC:71:ARG:NH2	2.50	0.44
11:LH:12:ILE:HG12	11:LH:18:ILE:HD12	1.99	0.44
15:LN:98:LEU:HD12	15:LN:128:LYS:HD2	1.99	0.44
1:L5:197:A:N1	1:L5:225:G:O2'	2.46	0.44
1:L5:1306:C:H2'	1:L5:1307:A:C8	2.51	0.44
1:L5:4319:C:H2'	1:L5:4320:G:H8	1.82	0.44
1:L5:4404:U:OP1	44:CD:47:TYR:OH	2.32	0.44
1:L5:5016:A:C2	1:L5:5033:G:N2	2.73	0.44
10:LG:170:LEU:HD23	10:LG:201:THR:HG21	1.99	0.44
15:LN:21:PHE:HD2	15:LN:22:LEU:HD12	1.82	0.44
1:L5:73:A:OP1	13:LL:106:SER:OG	2.32	0.44
1:L5:2375:A:H2'	1:L5:2376:A:H8	1.83	0.44
12:LJ:114:ASP:OD1	12:LJ:114:ASP:N	2.50	0.44
30:Le:85:LEU:HD11	30:Le:111:ILE:HG23	1.99	0.44
46:CF:92:VAL:O	46:CF:96:LEU:HB2	2.17	0.44
1:L5:161:G:H2'	1:L5:162:A:H8	1.82	0.44
1:L5:418:A:C2	3:L8:17:A:H1'	2.53	0.44
1:L5:1067:G:H2'	1:L5:1068:G:C8	2.52	0.44
1:L5:2495:U:H2'	1:L5:2496:G:C8	2.50	0.44
1:L5:2725:A:OP2	19:LR:97:ARG:NH2	2.51	0.44
16:LO:84:VAL:HG11	16:LO:102:LEU:HD22	2.00	0.44
24:LX:131:ASP:O	37:LI:18:LYS:NZ	2.42	0.44
47:CG:376:ASN:ND2	47:CG:418:TYR:O	2.46	0.44
48:CH:185:HIS:HE1	48:CH:187:GLU:HB2	1.82	0.44
49:CI:105:ALA:O	49:CI:109:MET:HB2	2.17	0.44
50:CJ:202:LEU:HD11	50:CJ:210:PRO:HG2	1.99	0.44
1:L5:2693:G:OP2	36:Lk:33:LYS:NZ	2.42	0.44
6:LC:152:LEU:HD21	6:LC:174:LEU:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:CD:133:ALA:O	44:CD:137:MET:HG3	2.17	0.44
46:CF:81:PRO:HG3	46:CF:90:HIS:CD2	2.53	0.44
1:L5:462:G:H2'	1:L5:463:A:C8	2.53	0.44
1:L5:710:G:H2'	1:L5:711:A:H8	1.82	0.44
1:L5:1478:C:H2'	1:L5:1479:G:H8	1.82	0.44
1:L5:4128:A:H2	10:LG:34:LYS:HG3	1.82	0.44
1:L5:4238:G:OP1	7:LD:35:ARG:NH1	2.46	0.44
5:LB:216:MET:HG3	5:LB:283:LYS:HD2	1.98	0.44
17:LP:84:PRO:HB2	17:LP:87:SER:HB2	2.00	0.44
29:Ld:29:ILE:O	29:Ld:33:ILE:HG12	2.18	0.44
42:CB:126:ARG:HB3	42:CB:129:ASN:HB2	2.00	0.44
1:L5:2521:G:H5'	1:L5:2640:G:H1'	2.00	0.44
1:L5:4598:C:OP1	44:CD:399:ARG:NH2	2.51	0.44
6:LC:5:ARG:NE	6:LC:24:LEU:O	2.49	0.44
6:LC:28:PHE:CD1	6:LC:132:ALA:HB2	2.52	0.44
30:Le:90:MET:HG2	39:Lr:33:LYS:HA	1.99	0.44
42:CB:224:LEU:HB2	42:CB:254:LEU:HD23	2.00	0.44
50:CJ:113:VAL:HG11	50:CJ:116:MET:HE2	1.98	0.44
1:L5:1428:U:H5''	18:LQ:42:THR:HB	2.00	0.43
1:L5:1802:A:O2'	21:LT:108:ARG:NH2	2.50	0.43
1:L5:2875:C:H5'	38:Lp:8:VAL:HG13	2.00	0.43
1:L5:4323:A:H4'	7:LD:176:SER:HB3	2.00	0.43
2:L7:76:U:H2'	2:L7:77:A:H8	1.83	0.43
4:LA:44:ILE:HA	4:LA:86:GLN:O	2.18	0.43
5:LB:246:ARG:HA	5:LB:246:ARG:HD2	1.77	0.43
13:LL:143:GLU:HA	13:LL:146:LEU:HG	2.00	0.43
16:LO:58:LEU:HD11	16:LO:145:VAL:HG13	1.99	0.43
22:LU:116:GLN:OE1	44:CD:514:LYS:NZ	2.44	0.43
51:CK:64:LEU:O	51:CK:68:ASN:ND2	2.51	0.43
1:L5:404:U:O3'	25:LY:87:ARG:NH2	2.47	0.43
1:L5:481:G:H2'	1:L5:482:G:C8	2.53	0.43
1:L5:2400:G:H21	32:Lg:6:THR:HG22	1.83	0.43
1:L5:4258:C:H5'	12:LJ:68:ILE:HD11	1.98	0.43
3:L8:8:U:H2'	3:L8:9:A:H8	1.83	0.43
10:LG:76:VAL:N	10:LG:238:GLY:O	2.52	0.43
11:LH:163:GLN:HA	11:LH:166:THR:HG23	2.00	0.43
1:L5:1538:U:H2'	1:L5:1539:G:C8	2.52	0.43
1:L5:2399:G:O2'	1:L5:2822:G:O2'	2.35	0.43
1:L5:2520:C:H2'	1:L5:2521:G:H8	1.83	0.43
1:L5:4274:A:O5'	50:CJ:84:LYS:NZ	2.49	0.43
20:LS:99:ASP:OD2	20:LS:100:LEU:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:CB:305:HIS:O	42:CB:356:ARG:NH2	2.48	0.43
1:L5:908:G:H2'	1:L5:909:A:H8	1.83	0.43
1:L5:1968:G:H4'	46:CF:126:ARG:HE	1.83	0.43
1:L5:4635:A:OP1	1:L5:4636:U:O2'	2.30	0.43
2:L7:102:U:H3'	2:L7:103:A:H8	1.83	0.43
20:LS:154:LEU:HB3	20:LS:157:ARG:HD3	2.00	0.43
32:Lg:33:LEU:HD23	32:Lg:33:LEU:HA	1.92	0.43
48:CH:185:HIS:HB3	48:CH:188:LEU:HB2	2.01	0.43
50:CJ:139:THR:HG21	50:CJ:181:GLU:HB2	1.99	0.43
1:L5:138:G:H2'	1:L5:139:G:H8	1.82	0.43
1:L5:399:G:H4'	17:LP:18:ARG:HB3	2.00	0.43
1:L5:440:U:O2'	31:Lf:91:ASN:O	2.33	0.43
1:L5:1779:U:H2'	1:L5:1780:A:H8	1.84	0.43
1:L5:1859:C:OP1	43:CC:30:ARG:NH2	2.43	0.43
2:L7:17:C:H2'	2:L7:18:C:H6	1.83	0.43
40:Lt:99:LYS:HB2	47:CG:243:THR:HG21	2.00	0.43
40:Lt:123:ARG:NH2	46:CF:63:SER:O	2.51	0.43
1:L5:1239:C:H5	8:LE:60:SER:HB2	1.83	0.43
1:L5:1316:G:OP1	30:Le:43:ASN:ND2	2.40	0.43
1:L5:2378:G:N2	1:L5:2381:A:OP2	2.50	0.43
8:LE:110:ARG:HD2	8:LE:110:ARG:HA	1.84	0.43
10:LG:105:GLU:OE2	10:LG:113:ARG:NH1	2.52	0.43
41:CA:2:ALA:HA	41:CA:204:ALA:O	2.19	0.43
1:L5:1913:C:H5''	16:LO:25:LYS:HD3	2.00	0.43
1:L5:4260:U:H2'	1:L5:4261:C:H6	1.83	0.43
3:L8:124:U:OP1	3:L8:126:C:N4	2.51	0.43
9:LF:171:ASP:HB3	9:LF:174:LEU:HG	2.01	0.43
23:LV:82:ILE:HG13	23:LV:83:ARG:HG3	2.01	0.43
34:Li:75:LYS:HB2	34:Li:75:LYS:HE3	1.91	0.43
44:CD:255:MET:HG2	44:CD:268:GLN:HB3	2.01	0.43
47:CG:297:THR:HG22	47:CG:336:VAL:HG13	2.01	0.43
52:CL:95:GLU:HG2	52:CL:115:ARG:HD3	2.01	0.43
1:L5:90:G:OP2	1:L5:92:C:N4	2.51	0.43
1:L5:2340:C:OP2	27:La:4:ARG:NH2	2.52	0.43
3:L8:96:C:H5''	33:Lh:66:LYS:HD3	2.00	0.43
7:LD:27:LYS:HE2	12:LJ:147:ARG:HH11	1.84	0.43
14:LM:86:TRP:O	14:LM:89:THR:OG1	2.36	0.43
42:CB:431:LYS:HD3	42:CB:431:LYS:HA	1.80	0.43
43:CC:39:ARG:HD2	43:CC:39:ARG:HA	1.83	0.43
48:CH:113:LYS:HD2	48:CH:117:TRP:HA	2.01	0.43
1:L5:10:A:H2'	1:L5:11:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:19:G:P	33:Lh:93:ARG:HE	2.42	0.43
1:L5:456:C:H2'	1:L5:457:G:H8	1.84	0.43
1:L5:3893:C:H2'	1:L5:3894:A:C8	2.54	0.43
1:L5:4304:A:O2'	42:CB:309:LYS:NZ	2.51	0.43
3:L8:141:C:H2'	3:L8:142:U:C6	2.54	0.43
5:LB:139:ASP:OD2	45:CE:96:TRP:NE1	2.52	0.43
20:LS:51:LEU:HD13	21:LT:151:LEU:HD12	2.00	0.43
47:CG:383:ASP:OD1	47:CG:383:ASP:N	2.49	0.43
1:L5:216:C:OP2	1:L5:219:G:O2'	2.34	0.43
1:L5:4477:A:OP1	48:CH:6:TYR:OH	2.32	0.43
7:LD:193:GLU:O	7:LD:197:LYS:HG2	2.19	0.43
10:LG:100:HIS:HA	10:LG:103:ARG:HG3	2.01	0.43
12:LJ:112:HIS:HA	12:LJ:115:LEU:HD12	2.01	0.43
29:Ld:117:LEU:HD23	29:Ld:117:LEU:HA	1.93	0.43
48:CH:86:VAL:HG22	48:CH:90:LEU:HB2	2.01	0.43
1:L5:86:U:H2'	1:L5:87:A:C8	2.54	0.42
1:L5:2521:G:H2'	1:L5:2522:G:C8	2.54	0.42
1:L5:2744:A:H2'	1:L5:2745:A:C8	2.53	0.42
1:L5:4239:A:H2'	1:L5:4240:G:C8	2.54	0.42
6:LC:266:THR:HG1	6:LC:269:LYS:H	1.67	0.42
12:LJ:43:LEU:HD13	12:LJ:117:ILE:HD11	2.01	0.42
21:LT:154:ILE:HD13	43:CC:60:LEU:HD21	2.00	0.42
26:LZ:87:VAL:HG22	26:LZ:89:ILE:HG13	2.00	0.42
1:L5:1346:C:H2'	1:L5:1347:G:C8	2.54	0.42
1:L5:2417:A:N3	44:CD:601:ASN:ND2	2.67	0.42
1:L5:3938:G:N2	1:L5:4171:C:OP2	2.50	0.42
1:L5:4912:G:N2	5:LB:156:TYR:OH	2.52	0.42
35:Lj:69:ILE:HG22	35:Lj:73:ARG:HD3	2.01	0.42
46:CF:109:LYS:HD2	46:CF:207:MET:HE1	2.01	0.42
1:L5:70:A:OP2	27:La:64:LYS:NZ	2.38	0.42
1:L5:1591:U:H5'	5:LB:243:LYS:HB3	2.01	0.42
1:L5:4934:A:H2'	1:L5:4935:C:C6	2.54	0.42
1:L5:4954:G:H2'	1:L5:4955:A:C8	2.53	0.42
25:LY:52:ASP:HB2	25:LY:110:LYS:HD2	2.01	0.42
42:CB:333:LYS:HG3	42:CB:335:VAL:HG13	2.00	0.42
47:CG:264:SER:OG	47:CG:265:GLN:N	2.52	0.42
50:CJ:108:MET:HE3	50:CJ:108:MET:HB3	1.90	0.42
1:L5:1482:G:N7	13:LL:188:ASN:ND2	2.67	0.42
1:L5:1984:A:N7	1:L5:2010:A:O2'	2.52	0.42
1:L5:2303:C:H5''	30:Le:104:SER:HB3	2.01	0.42
1:L5:2749:C:H2'	1:L5:2750:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3681:G:C6	4:LA:125:LYS:HB3	2.54	0.42
1:L5:3927:U:H2'	1:L5:3928:A:C8	2.54	0.42
1:L5:4991:U:H2'	1:L5:4992:G:C8	2.55	0.42
13:LL:42:LYS:HE2	13:LL:46:ILE:HD13	2.01	0.42
33:Lh:13:LYS:HB2	33:Lh:16:GLU:HG3	2.01	0.42
41:CA:4:ARG:HB3	41:CA:208:LEU:HD23	2.01	0.42
41:CA:42:LEU:HD22	41:CA:46:ILE:HD11	2.02	0.42
44:CD:600:MET:HB2	44:CD:605:LYS:HB2	2.01	0.42
1:L5:4178:A:H2'	1:L5:4179:G:H8	1.84	0.42
1:L5:4440:G:C2	44:CD:96:LEU:HD13	2.54	0.42
26:LZ:103:ASP:HB2	26:LZ:106:LEU:HB2	2.01	0.42
32:Lg:56:VAL:HG13	32:Lg:72:LYS:HA	2.01	0.42
33:Lh:52:LYS:HD3	33:Lh:52:LYS:HA	1.79	0.42
48:CH:89:TYR:O	48:CH:93:ARG:NH1	2.52	0.42
1:L5:711:A:H2'	1:L5:712:C:C6	2.55	0.42
1:L5:1458:C:H5''	18:LQ:69:LYS:HD2	2.00	0.42
1:L5:2029:A:H2'	1:L5:2030:A:C8	2.54	0.42
1:L5:3598:C:H2'	1:L5:3599:A:H8	1.84	0.42
1:L5:4088:C:H2'	1:L5:4089:G:C8	2.53	0.42
2:L7:110:G:H2'	2:L7:111:C:C6	2.54	0.42
3:L8:19:C:H2'	3:L8:20:A:C8	2.55	0.42
7:LD:69:ILE:HG23	50:CJ:54:ALA:HB1	2.02	0.42
11:LH:92:MET:HE1	11:LH:181:VAL:HG22	2.01	0.42
14:LM:131:GLN:HG2	16:LO:177:LEU:HD13	2.01	0.42
18:LQ:130:SER:O	18:LQ:130:SER:OG	2.36	0.42
21:LT:42:ILE:HG23	21:LT:91:VAL:HG11	2.02	0.42
25:LY:10:ASP:HB3	25:LY:13:LYS:HB2	2.01	0.42
26:LZ:25:ILE:HA	26:LZ:43:VAL:HG12	2.01	0.42
36:Lk:5:ILE:HG22	36:Lk:7:GLU:H	1.84	0.42
48:CH:110:ARG:HG2	48:CH:117:TRP:HZ2	1.85	0.42
1:L5:212:A:H2'	1:L5:213:G:H8	1.85	0.42
1:L5:393:U:O2'	17:LP:96:LYS:NZ	2.46	0.42
1:L5:1248:C:H2'	1:L5:1249:C:C6	2.55	0.42
1:L5:1633:G:H1	1:L5:4386:C:H4'	1.83	0.42
5:LB:49:TYR:CD1	5:LB:171:LEU:HD21	2.54	0.42
16:LO:27:VAL:HG23	16:LO:98:ALA:HB1	2.01	0.42
44:CD:582:ASP:N	44:CD:582:ASP:OD1	2.51	0.42
47:CG:63:PHE:HA	47:CG:68:GLU:HA	2.00	0.42
1:L5:21:G:H5''	35:Lj:43:ARG:HG2	2.01	0.42
1:L5:196:C:H4'	25:LY:126:ARG:HG3	2.02	0.42
1:L5:691:C:H2'	1:L5:692:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:926:G:H2'	1:L5:927:G:H8	1.84	0.42
1:L5:1979:A:H5'	40:Lt:96:LYS:HD2	2.01	0.42
1:L5:3607:U:H2'	1:L5:3608:A:H8	1.85	0.42
3:L8:102:G:OP2	3:L8:104:A:O2'	2.29	0.42
5:LB:83:PRO:O	5:LB:167:GLN:NE2	2.53	0.42
25:LY:103:LYS:HD3	25:LY:103:LYS:HA	1.79	0.42
28:Lc:17:ARG:HA	28:Lc:20:LEU:HG	2.00	0.42
41:CA:76:THR:O	41:CA:96:ARG:NH1	2.44	0.42
44:CD:181:LYS:HE2	44:CD:181:LYS:HB2	1.81	0.42
44:CD:600:MET:O	44:CD:603:LEU:C	2.63	0.42
49:CI:64:THR:HB	52:CL:111:TYR:HB3	2.02	0.42
1:L5:1972:G:N2	40:Lt:131:GLU:OE2	2.39	0.42
1:L5:2570:U:H2'	1:L5:2571:C:C6	2.54	0.42
1:L5:3782:C:H2'	1:L5:3783:A:H8	1.85	0.42
1:L5:4440:G:N7	44:CD:93:LYS:NZ	2.53	0.42
1:L5:4769:G:OP1	16:LO:176:ARG:NH1	2.52	0.42
14:LM:94:LYS:HG2	16:LO:203:VAL:HG21	2.02	0.42
16:LO:55:LEU:HD23	16:LO:58:LEU:HD12	2.01	0.42
22:LU:61:VAL:HG22	22:LU:74:SER:HB3	2.01	0.42
1:L5:179:G:H2'	1:L5:180:C:C6	2.55	0.42
1:L5:1490:G:H2'	1:L5:1491:A:H8	1.83	0.42
1:L5:3670:C:H2'	1:L5:3671:G:C8	2.55	0.42
1:L5:4543:G:O6	42:CB:33:ARG:NH2	2.53	0.42
6:LC:200:ARG:HG2	6:LC:201:ARG:HD3	2.02	0.42
10:LG:143:VAL:HG22	10:LG:203:ALA:HB2	2.02	0.42
11:LH:7:ASN:HA	11:LH:57:VAL:O	2.20	0.42
19:LR:15:LEU:O	19:LR:52:ARG:NH1	2.52	0.42
32:Lg:60:ARG:HB2	32:Lg:63:VAL:HG23	2.01	0.42
1:L5:318:A:H2'	1:L5:319:A:H8	1.84	0.41
1:L5:1273:G:H2'	1:L5:1274:A:C8	2.55	0.41
1:L5:1333:A:H2'	1:L5:1334:A:C8	2.55	0.41
1:L5:2706:G:N2	1:L5:2710:C:H41	2.18	0.41
1:L5:3667:C:H2'	1:L5:3668:C:C6	2.54	0.41
1:L5:4223:C:H2'	1:L5:4224:A:H8	1.85	0.41
1:L5:4437:U:H5'	42:CB:128:HIS:HA	2.01	0.41
2:L7:6:C:H4'	7:LD:52:ILE:HD13	2.02	0.41
6:LC:162:LYS:HD3	6:LC:216:GLY:HA3	2.02	0.41
8:LE:62:MET:HE3	8:LE:62:MET:HB3	1.87	0.41
23:LV:32:THR:HG23	23:LV:34:ALA:H	1.85	0.41
42:CB:194:GLN:NE2	42:CB:195:GLU:O	2.53	0.41
50:CJ:141:PRO:HB3	50:CJ:182:TYR:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:490:C:H2'	1:L5:491:G:C8	2.55	0.41
1:L5:4076:G:OP1	10:LG:73:ARG:NE	2.40	0.41
1:L5:4238:G:H2'	1:L5:4239:A:C8	2.55	0.41
1:L5:4538:G:O2'	42:CB:350:TYR:O	2.39	0.41
1:L5:4736:C:H2'	1:L5:4737:G:H8	1.84	0.41
40:Lt:25:THR:HG22	40:Lt:28:LEU:HD12	2.01	0.41
40:Lt:61:LYS:HB3	40:Lt:72:GLU:HG2	2.02	0.41
41:CA:245:THR:HG21	44:CD:352:LYS:HB2	2.02	0.41
50:CJ:199:LYS:HB2	50:CJ:217:MET:HE3	2.02	0.41
51:CK:47:PRO:HB2	51:CK:50:LEU:HB3	2.03	0.41
1:L5:3746:A:H1'	1:L5:3749:C:H41	1.85	0.41
1:L5:4743:G:H2'	1:L5:4744:A:C8	2.56	0.41
6:LC:163:LYS:HB3	6:LC:163:LYS:HE3	1.78	0.41
20:LS:113:MET:HE3	20:LS:113:MET:HB3	1.93	0.41
20:LS:128:LYS:HB2	21:LT:154:ILE:HD11	2.02	0.41
25:LY:23:SER:OG	25:LY:75:ARG:NH1	2.47	0.41
26:LZ:13:VAL:O	26:LZ:20:GLY:N	2.53	0.41
41:CA:116:LEU:HD13	41:CA:177:LEU:HD21	2.01	0.41
47:CG:210:LEU:HD12	47:CG:214:PRO:HA	2.01	0.41
50:CJ:158:ARG:HG3	50:CJ:230:LEU:HD13	2.02	0.41
50:CJ:272:ASP:OD2	50:CJ:275:LYS:NZ	2.44	0.41
1:L5:4967:A:H2'	1:L5:4968:A:H8	1.86	0.41
2:L7:83:A:H61	2:L7:93:G:H1	1.69	0.41
12:LJ:16:ARG:O	12:LJ:135:GLY:N	2.51	0.41
16:LO:158:GLU:O	16:LO:162:GLU:HG3	2.20	0.41
1:L5:909:A:H2'	1:L5:910:G:H8	1.85	0.41
1:L5:2374:A:H2'	1:L5:2375:A:C8	2.56	0.41
25:LY:111:LEU:HB3	25:LY:116:LYS:HE3	2.03	0.41
26:LZ:11:VAL:HG12	26:LZ:82:PRO:HA	2.03	0.41
32:Lg:86:CYS:O	32:Lg:90:ARG:HG2	2.20	0.41
36:Lk:35:LYS:HA	36:Lk:43:TYR:O	2.21	0.41
39:Lr:107:ARG:HD2	39:Lr:111:ILE:HD12	2.02	0.41
1:L5:162:A:H2'	1:L5:163:A:C8	2.55	0.41
1:L5:1734:G:N2	1:L5:1735:U:O4	2.53	0.41
1:L5:1901:C:H2'	1:L5:1902:G:H8	1.84	0.41
1:L5:3598:C:H2'	1:L5:3599:A:C8	2.56	0.41
1:L5:3948:C:H3'	1:L5:3949:A:H8	1.85	0.41
1:L5:4883:C:N4	8:LE:181:LEU:O	2.40	0.41
2:L7:58:A:H2'	2:L7:59:G:C8	2.55	0.41
5:LB:64:GLY:HA2	41:CA:30:GLY:HA2	2.02	0.41
5:LB:89:ILE:HG12	5:LB:197:ALA:HB1	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:CH:164:PRO:HA	48:CH:165:PRO:HD3	1.93	0.41
1:L5:375:G:OP2	35:Lj:52:LYS:NZ	2.41	0.41
1:L5:2745:A:H2'	1:L5:2746:A:H8	1.86	0.41
1:L5:5061:A:H5''	1:L5:5062:G:H5''	2.03	0.41
4:LA:49:ILE:HD13	4:LA:60:LYS:HE3	2.02	0.41
41:CA:155:SER:OG	41:CA:156:ASN:N	2.53	0.41
50:CJ:189:LEU:HD21	51:CK:47:PRO:HG2	2.03	0.41
1:L5:6:C:H5''	10:LG:197:LYS:HB3	2.02	0.41
1:L5:1461:C:H2'	1:L5:1462:A:C8	2.56	0.41
1:L5:2469:C:H5	1:L5:2471:G:H1	1.69	0.41
1:L5:2863:G:O2'	19:LR:82:LYS:O	2.38	0.41
1:L5:3759:A:N6	1:L5:3764:U:N3	2.43	0.41
31:Lf:40:GLU:HA	31:Lf:43:LEU:HD13	2.03	0.41
45:CE:12:LYS:HE3	45:CE:12:LYS:HB2	1.89	0.41
47:CG:391:SER:OG	47:CG:392:PHE:N	2.54	0.41
1:L5:710:G:H2'	1:L5:711:A:C8	2.55	0.41
1:L5:1577:G:H5'	1:L5:1578:U:H5''	2.02	0.41
1:L5:1849:U:H2'	1:L5:1850:A:H8	1.85	0.41
1:L5:2870:A:H2'	1:L5:2871:A:C8	2.55	0.41
1:L5:4476:C:O2'	1:L5:4478:G:OP2	2.38	0.41
1:L5:4962:C:H2'	1:L5:4963:G:C8	2.55	0.41
6:LC:334:THR:OG1	9:LF:51:TYR:OH	2.27	0.41
7:LD:8:LYS:HB3	7:LD:13:PHE:HE1	1.84	0.41
8:LE:173:LEU:HD11	8:LE:191:GLN:HB3	2.03	0.41
9:LF:86:GLU:HB3	21:LT:135:PRO:HB2	2.02	0.41
15:LN:116:LEU:HD22	15:LN:135:ILE:HD11	2.02	0.41
15:LN:201:HIS:O	15:LN:204:ARG:NH1	2.54	0.41
29:Ld:92:ARG:HA	29:Ld:102:LEU:HD23	2.03	0.41
39:Lr:47:LYS:O	39:Lr:103:ARG:NH1	2.52	0.41
42:CB:349:GLN:O	42:CB:360:ILE:HA	2.20	0.41
50:CJ:48:VAL:HG21	50:CJ:121:ILE:HD13	2.03	0.41
52:CL:6:ARG:NH1	52:CL:9:ALA:O	2.54	0.41
1:L5:257:C:H2'	1:L5:258:G:C8	2.56	0.41
14:LM:47:ARG:HG2	20:LS:73:LEU:HD22	2.02	0.41
24:LX:102:VAL:HA	24:LX:134:LYS:HE3	2.03	0.41
35:Lj:8:PHE:HA	35:Lj:11:ARG:HD2	2.03	0.41
49:CI:85:LEU:O	49:CI:89:THR:OG1	2.30	0.41
50:CJ:177:LEU:HB3	51:CK:77:TRP:CZ2	2.56	0.41
1:L5:173:C:H2'	1:L5:174:C:C6	2.56	0.40
1:L5:300:A:H2'	1:L5:301:G:C8	2.54	0.40
1:L5:424:U:H2'	1:L5:425:U:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:667:A:N3	39:Lr:46:ARG:NH2	2.65	0.40
1:L5:1339:U:H2'	1:L5:1340:C:C6	2.56	0.40
6:LC:101:MET:SD	6:LC:104:PRO:HA	2.62	0.40
9:LF:60:GLU:O	9:LF:64:MET:HG3	2.20	0.40
9:LF:226:HIS:ND1	9:LF:228:VAL:HG22	2.36	0.40
15:LN:75:VAL:HG23	15:LN:88:GLY:HA2	2.02	0.40
19:LR:133:LYS:HD3	19:LR:133:LYS:HA	1.74	0.40
25:LY:118:ILE:HG12	25:LY:121:ARG:HH21	1.86	0.40
30:Le:19:LYS:HB3	30:Le:33:ARG:NH2	2.36	0.40
42:CB:309:LYS:HE3	42:CB:309:LYS:HB2	1.92	0.40
47:CG:288:HIS:HD1	47:CG:289:TRP:H	1.69	0.40
47:CG:324:GLU:HA	47:CG:327:GLU:HG3	2.03	0.40
50:CJ:199:LYS:HE2	50:CJ:199:LYS:HB3	1.77	0.40
1:L5:72:C:C5	13:LL:67:HIS:HD2	2.37	0.40
1:L5:255:C:N4	1:L5:256:G:O6	2.55	0.40
1:L5:718:C:OP1	9:LF:217:ARG:NH1	2.53	0.40
1:L5:2515:G:OP1	32:Lg:37:LYS:NZ	2.47	0.40
1:L5:2745:A:H2'	1:L5:2746:A:C8	2.57	0.40
1:L5:4317:A:H4'	48:CH:235:LYS:HE2	2.03	0.40
16:LO:28:LEU:HD23	16:LO:28:LEU:HA	1.90	0.40
29:Ld:101:LYS:HD2	29:Ld:102:LEU:HG	2.03	0.40
32:Lg:94:ALA:O	32:Lg:98:GLU:HG2	2.21	0.40
40:Lt:62:LEU:HD12	40:Lt:69:ALA:HB1	2.03	0.40
1:L5:86:U:O2'	27:La:65:ARG:NH2	2.54	0.40
1:L5:369:G:N2	1:L5:372:A:OP2	2.37	0.40
1:L5:500:G:O5'	1:L5:504:G:N2	2.53	0.40
1:L5:1390:G:N2	1:L5:1393:G:OP2	2.51	0.40
1:L5:1750:G:H22	1:L5:1780:A:H2	1.70	0.40
1:L5:1876:U:H2'	1:L5:1877:G:C8	2.56	0.40
1:L5:2404:A:OP2	37:Ll:2:SER:OG	2.34	0.40
1:L5:2539:C:H2'	1:L5:2540:C:C6	2.56	0.40
1:L5:2568:C:N4	1:L5:2569:G:O6	2.54	0.40
1:L5:2872:C:OP1	50:CJ:282:LYS:NZ	2.53	0.40
1:L5:4449:A:N6	1:L5:4502:C:O2'	2.54	0.40
3:L8:140:C:H2'	3:L8:141:C:C6	2.56	0.40
6:LC:115:VAL:HB	6:LC:120:LYS:HE3	2.02	0.40
9:LF:94:ARG:HB2	9:LF:114:LEU:HB3	2.02	0.40
13:LL:116:ARG:NH2	13:LL:155:MET:O	2.44	0.40
13:LL:178:ALA:N	27:La:134:GLU:OE1	2.46	0.40
20:LS:24:THR:O	20:LS:24:THR:OG1	2.35	0.40
39:Lr:71:ARG:HH12	39:Lr:72:LYS:NZ	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:303:C:OP2	15:LN:68:ARG:NH2	2.54	0.40
1:L5:1067:G:H2'	1:L5:1068:G:H8	1.87	0.40
1:L5:1850:A:H2'	1:L5:1851:G:C8	2.56	0.40
1:L5:2375:A:H2'	1:L5:2376:A:C8	2.56	0.40
1:L5:3610:A:H2'	1:L5:3611:A:C8	2.56	0.40
3:L8:45:C:H4'	37:L1:11:ARG:HD2	2.03	0.40
15:LN:140:LYS:HD3	15:LN:140:LYS:HA	1.90	0.40
39:Lr:32:LEU:HD22	39:Lr:110:ALA:HA	2.03	0.40
41:CA:126:GLU:OE1	41:CA:139:ARG:NH2	2.55	0.40
50:CJ:101:ASN:HB3	50:CJ:121:ILE:HB	2.04	0.40
51:CK:22:GLN:HA	51:CK:25:THR:HG22	2.03	0.40
1:L5:262:G:H2'	1:L5:263:G:C8	2.57	0.40
1:L5:1068:G:H2'	1:L5:1069:G:C8	2.57	0.40
1:L5:1738:A:H2'	1:L5:1739:G:C8	2.56	0.40
1:L5:1949:U:OP1	11:LH:64:ARG:NH1	2.55	0.40
1:L5:3855:C:H2'	1:L5:3856:A:H8	1.87	0.40
1:L5:3893:C:H2'	1:L5:3894:A:H8	1.86	0.40
1:L5:5047:C:O2'	1:L5:5050:C:OP2	2.30	0.40
5:LB:201:LEU:HD23	5:LB:201:LEU:HA	1.96	0.40
6:LC:33:ARG:HG3	6:LC:122:TYR:HE2	1.86	0.40
10:LG:245:LYS:HB2	10:LG:245:LYS:HE2	1.87	0.40
42:CB:210:LEU:HD22	42:CB:365:VAL:HG21	2.03	0.40
43:CC:50:VAL:HG21	43:CC:60:LEU:HD23	2.03	0.40
46:CF:159:PRO:HD2	46:CF:169:LEU:HD11	2.03	0.40
47:CG:103:VAL:HG11	47:CG:471:VAL:HG23	2.03	0.40
49:CI:66:ASP:OD1	49:CI:103:ARG:NH1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	202/257 (79%)	194 (96%)	8 (4%)	0	100	100
5	LB	400/403 (99%)	390 (98%)	9 (2%)	1 (0%)	36	55
6	LC	360/427 (84%)	351 (98%)	9 (2%)	0	100	100
7	LD	227/297 (76%)	221 (97%)	6 (3%)	0	100	100
8	LE	201/288 (70%)	191 (95%)	10 (5%)	0	100	100
9	LF	217/248 (88%)	211 (97%)	6 (3%)	0	100	100
10	LG	212/266 (80%)	205 (97%)	7 (3%)	0	100	100
11	LH	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
12	LJ	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
13	LL	191/211 (90%)	188 (98%)	3 (2%)	0	100	100
14	LM	133/215 (62%)	126 (95%)	7 (5%)	0	100	100
15	LN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
16	LO	199/203 (98%)	198 (100%)	1 (0%)	0	100	100
17	LP	155/184 (84%)	153 (99%)	2 (1%)	0	100	100
18	LQ	149/188 (79%)	147 (99%)	2 (1%)	0	100	100
19	LR	147/196 (75%)	146 (99%)	1 (1%)	0	100	100
20	LS	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
21	LT	125/160 (78%)	123 (98%)	2 (2%)	0	100	100
22	LU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
23	LV	135/140 (96%)	130 (96%)	5 (4%)	0	100	100
24	LX	117/156 (75%)	116 (99%)	1 (1%)	0	100	100
25	LY	130/145 (90%)	124 (95%)	6 (5%)	0	100	100
26	LZ	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
27	La	101/148 (68%)	98 (97%)	3 (3%)	0	100	100
28	Lc	93/115 (81%)	91 (98%)	2 (2%)	0	100	100
29	Ld	103/125 (82%)	103 (100%)	0	0	100	100
30	Le	126/135 (93%)	126 (100%)	0	0	100	100
31	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
32	Lg	109/117 (93%)	108 (99%)	1 (1%)	0	100	100
33	Lh	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
34	Li	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
35	Lj	83/97 (86%)	78 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	Ll	48/51 (94%)	48 (100%)	0	0	100	100
38	Lp	88/92 (96%)	84 (96%)	4 (4%)	0	100	100
39	Lr	121/137 (88%)	117 (97%)	4 (3%)	0	100	100
40	Lt	157/165 (95%)	155 (99%)	2 (1%)	0	100	100
41	CA	243/245 (99%)	233 (96%)	10 (4%)	0	100	100
42	CB	444/731 (61%)	434 (98%)	10 (2%)	0	100	100
43	CC	78/549 (14%)	78 (100%)	0	0	100	100
44	CD	610/634 (96%)	599 (98%)	11 (2%)	0	100	100
45	CE	65/129 (50%)	64 (98%)	1 (2%)	0	100	100
46	CF	217/239 (91%)	209 (96%)	8 (4%)	0	100	100
47	CG	469/485 (97%)	458 (98%)	11 (2%)	0	100	100
48	CH	257/260 (99%)	250 (97%)	7 (3%)	0	100	100
49	CI	138/163 (85%)	137 (99%)	1 (1%)	0	100	100
50	CJ	279/306 (91%)	274 (98%)	5 (2%)	0	100	100
51	CK	193/365 (53%)	189 (98%)	4 (2%)	0	100	100
52	CL	107/134 (80%)	104 (97%)	3 (3%)	0	100	100
All	All	8788/10828 (81%)	8579 (98%)	208 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	LB	29	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	
4	LA	157/199 (79%)	157 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	LB	344/349 (99%)	343 (100%)	1 (0%)	86	94
6	LC	297/348 (85%)	297 (100%)	0	100	100
7	LD	194/250 (78%)	194 (100%)	0	100	100
8	LE	184/252 (73%)	184 (100%)	0	100	100
9	LF	182/215 (85%)	182 (100%)	0	100	100
10	LG	186/223 (83%)	185 (100%)	1 (0%)	81	90
11	LH	167/171 (98%)	167 (100%)	0	100	100
12	LJ	137/149 (92%)	137 (100%)	0	100	100
13	LL	161/177 (91%)	161 (100%)	0	100	100
14	LM	113/161 (70%)	113 (100%)	0	100	100
15	LN	167/172 (97%)	167 (100%)	0	100	100
16	LO	171/174 (98%)	171 (100%)	0	100	100
17	LP	134/163 (82%)	134 (100%)	0	100	100
18	LQ	136/165 (82%)	136 (100%)	0	100	100
19	LR	133/175 (76%)	133 (100%)	0	100	100
20	LS	156/157 (99%)	156 (100%)	0	100	100
21	LT	101/140 (72%)	101 (100%)	0	100	100
22	LU	92/115 (80%)	92 (100%)	0	100	100
23	LV	104/107 (97%)	104 (100%)	0	100	100
24	LX	107/133 (80%)	107 (100%)	0	100	100
25	LY	122/135 (90%)	122 (100%)	0	100	100
26	LZ	117/118 (99%)	117 (100%)	0	100	100
27	La	87/121 (72%)	87 (100%)	0	100	100
28	Lc	72/97 (74%)	72 (100%)	0	100	100
29	Ld	92/110 (84%)	92 (100%)	0	100	100
30	Le	114/121 (94%)	114 (100%)	0	100	100
31	Lf	87/89 (98%)	87 (100%)	0	100	100
32	Lg	93/100 (93%)	93 (100%)	0	100	100
33	Lh	109/110 (99%)	109 (100%)	0	100	100
34	Li	85/89 (96%)	85 (100%)	0	100	100
35	Lj	72/80 (90%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lk	64/65 (98%)	64 (100%)	0	100	100
37	Ll	47/48 (98%)	47 (100%)	0	100	100
38	Lp	72/75 (96%)	72 (100%)	0	100	100
39	Lr	106/121 (88%)	106 (100%)	0	100	100
40	Lt	127/137 (93%)	127 (100%)	0	100	100
41	CA	213/213 (100%)	213 (100%)	0	100	100
42	CB	398/654 (61%)	398 (100%)	0	100	100
43	CC	51/485 (10%)	51 (100%)	0	100	100
44	CD	533/574 (93%)	533 (100%)	0	100	100
45	CE	56/115 (49%)	56 (100%)	0	100	100
46	CF	195/214 (91%)	195 (100%)	0	100	100
47	CG	327/403 (81%)	327 (100%)	0	100	100
48	CH	217/228 (95%)	217 (100%)	0	100	100
49	CI	128/149 (86%)	128 (100%)	0	100	100
50	CJ	248/279 (89%)	248 (100%)	0	100	100
51	CK	156/300 (52%)	156 (100%)	0	100	100
52	CL	91/114 (80%)	91 (100%)	0	100	100
All	All	7502/9339 (80%)	7500 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	LB	354	GLN
10	LG	90	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (85) such sidechains are listed below:

Mol	Chain	Res	Type
6	LC	21	ASN
6	LC	38	ASN
6	LC	50	GLN
6	LC	203	GLN
6	LC	212	ASN
6	LC	299	GLN
7	LD	17	GLN

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Mol	Chain	Res	Type
7	LD	198	HIS
8	LE	191	GLN
9	LF	58	HIS
9	LF	126	ASN
10	LG	153	GLN
10	LG	195	HIS
10	LG	227	ASN
11	LH	98	HIS
12	LJ	71	HIS
13	LL	67	HIS
13	LL	111	GLN
13	LL	149	GLN
13	LL	175	ASN
14	LM	20	HIS
14	LM	48	GLN
15	LN	139	HIS
15	LN	199	GLN
16	LO	26	GLN
16	LO	42	ASN
16	LO	173	GLN
16	LO	180	GLN
17	LP	28	ASN
17	LP	75	GLN
17	LP	97	ASN
17	LP	133	HIS
18	LQ	7	HIS
18	LQ	125	GLN
19	LR	40	GLN
20	LS	66	GLN
20	LS	122	HIS
21	LT	54	HIS
21	LT	131	GLN
22	LU	38	ASN
22	LU	94	ASN
22	LU	119	GLN
23	LV	36	ASN
23	LV	135	ASN
24	LX	73	HIS
24	LX	151	ASN
25	LY	61	HIS
25	LY	127	GLN
26	LZ	78	ASN

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Mol	Chain	Res	Type
27	La	60	HIS
28	Lc	33	GLN
28	Lc	40	GLN
31	Lf	20	ASN
31	Lf	21	GLN
31	Lf	56	ASN
33	Lh	98	HIS
34	Li	36	HIS
38	Lp	33	GLN
39	Lr	36	ASN
40	Lt	65	GLN
40	Lt	97	ASN
40	Lt	103	ASN
40	Lt	115	GLN
41	CA	10	ASN
41	CA	68	HIS
41	CA	145	GLN
42	CB	113	GLN
42	CB	129	ASN
42	CB	149	GLN
44	CD	178	ASN
44	CD	274	ASN
45	CE	92	GLN
46	CF	47	ASN
46	CF	129	ASN
47	CG	213	ASN
47	CG	323	GLN
48	CH	96	GLN
48	CH	108	GLN
48	CH	185	HIS
48	CH	202	ASN
49	CI	82	GLN
49	CI	110	ASN
49	CI	130	ASN
50	CJ	229	HIS
51	CK	197	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3351/5070 (66%)	727 (21%)	22 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	L7	119/121 (98%)	20 (16%)	1 (0%)
3	L8	155/157 (98%)	29 (18%)	0
All	All	3625/5348 (67%)	776 (21%)	23 (0%)

All (776) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	17	A
1	L5	25	A
1	L5	30	C
1	L5	34	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	69	A
1	L5	73	A
1	L5	92	C
1	L5	93	G
1	L5	95	G
1	L5	104	G
1	L5	108	A
1	L5	109	G
1	L5	110	C
1	L5	119	G
1	L5	120	A
1	L5	122	U
1	L5	132	G
1	L5	135	G
1	L5	136	C
1	L5	152	U
1	L5	155	C
1	L5	157	U
1	L5	159	C
1	L5	164	G
1	L5	165	A
1	L5	183	C
1	L5	184	U
1	L5	185	C
1	L5	188	G

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Mol	Chain	Res	Type
1	L5	200	U
1	L5	209	U
1	L5	213	G
1	L5	216	C
1	L5	218	A
1	L5	220	C
1	L5	225	G
1	L5	232	G
1	L5	233	U
1	L5	234	G
1	L5	235	A
1	L5	237	G
1	L5	255	C
1	L5	256	G
1	L5	258	G
1	L5	261	G
1	L5	265	C
1	L5	266	C
1	L5	267	G
1	L5	280	G
1	L5	297	U
1	L5	306	A
1	L5	310	G
1	L5	315	G
1	L5	316	U
1	L5	322	C
1	L5	340	C
1	L5	349	A
1	L5	350	C
1	L5	353	A
1	L5	357	U
1	L5	361	C
1	L5	373	G
1	L5	387	G
1	L5	399	G
1	L5	407	A
1	L5	409	G
1	L5	412	G
1	L5	415	G
1	L5	440	U
1	L5	449	C
1	L5	450	G

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Mol	Chain	Res	Type
1	L5	452	A
1	L5	454	U
1	L5	465	G
1	L5	468	U
1	L5	484	U
1	L5	485	C
1	L5	486	C
1	L5	489	C
1	L5	493	G
1	L5	494	U
1	L5	497	G
1	L5	498	C
1	L5	499	G
1	L5	500	G
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	505	G
1	L5	509	A
1	L5	510	U
1	L5	511	C
1	L5	512	U
1	L5	513	U
1	L5	514	U
1	L5	515	C
1	L5	517	C
1	L5	518	G
1	L5	643	C
1	L5	656	C
1	L5	657	C
1	L5	659	G
1	L5	665	C
1	L5	666	G
1	L5	667	A
1	L5	668	C
1	L5	669	C
1	L5	672	C
1	L5	673	C
1	L5	685	C
1	L5	686	A
1	L5	688	U
1	L5	696	C

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Mol	Chain	Res	Type
1	L5	697	G
1	L5	702	U
1	L5	703	G
1	L5	704	C
1	L5	715	G
1	L5	730	G
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	740	G
1	L5	742	G
1	L5	753	C
1	L5	758	G
1	L5	905	C
1	L5	907	C
1	L5	910	G
1	L5	913	U
1	L5	914	U
1	L5	915	A
1	L5	917	A
1	L5	925	C
1	L5	926	G
1	L5	932	A
1	L5	933	G
1	L5	943	A
1	L5	944	A
1	L5	945	U
1	L5	946	C
1	L5	956	A
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	972	C
1	L5	982	U
1	L5	984	C
1	L5	985	C
1	L5	989	U
1	L5	990	C
1	L5	992	C
1	L5	993	G
1	L5	995	C
1	L5	1048	G

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Mol	Chain	Res	Type
1	L5	1049	C
1	L5	1050	C
1	L5	1051	G
1	L5	1070	G
1	L5	1071	C
1	L5	1072	C
1	L5	1075	G
1	L5	1082	C
1	L5	1083	U
1	L5	1218	G
1	L5	1219	G
1	L5	1222	A
1	L5	1241	C
1	L5	1242	G
1	L5	1246	G
1	L5	1266	G
1	L5	1267	C
1	L5	1269	G
1	L5	1270	A
1	L5	1271	G
1	L5	1272	C
1	L5	1273	G
1	L5	1275	G
1	L5	1280	C
1	L5	1284	G
1	L5	1285	U
1	L5	1287	G
1	L5	1294	A
1	L5	1295	C
1	L5	1296	G
1	L5	1301	C
1	L5	1313	C
1	L5	1314	C
1	L5	1315	C
1	L5	1337	A
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G
1	L5	1364	U
1	L5	1365	C
1	L5	1366	G
1	L5	1367	C

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Mol	Chain	Res	Type
1	L5	1378	C
1	L5	1379	C
1	L5	1387	A
1	L5	1394	G
1	L5	1397	A
1	L5	1398	A
1	L5	1399	G
1	L5	1403	G
1	L5	1405	C
1	L5	1408	G
1	L5	1410	U
1	L5	1414	C
1	L5	1420	A
1	L5	1421	G
1	L5	1435	G
1	L5	1437	C
1	L5	1447	C
1	L5	1472	C
1	L5	1482	G
1	L5	1483	C
1	L5	1495	G
1	L5	1497	A
1	L5	1498	G
1	L5	1502	G
1	L5	1517	G
1	L5	1523	A
1	L5	1524	A
1	L5	1534	A
1	L5	1543	G
1	L5	1547	A
1	L5	1562	G
1	L5	1564	A
1	L5	1566	C
1	L5	1578	U
1	L5	1591	U
1	L5	1592	G
1	L5	1601	A
1	L5	1613	A
1	L5	1624	G
1	L5	1625	G
1	L5	1626	G
1	L5	1631	A

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Mol	Chain	Res	Type
1	L5	1632	A
1	L5	1633	G
1	L5	1634	A
1	L5	1638	A
1	L5	1640	C
1	L5	1641	G
1	L5	1653	A
1	L5	1654	G
1	L5	1655	C
1	L5	1661	C
1	L5	1671	U
1	L5	1672	U
1	L5	1684	A
1	L5	1691	G
1	L5	1733	G
1	L5	1735	U
1	L5	1742	A
1	L5	1781	U
1	L5	1785	C
1	L5	1787	A
1	L5	1788	A
1	L5	1796	U
1	L5	1799	G
1	L5	1803	G
1	L5	1804	A
1	L5	1806	G
1	L5	1810	G
1	L5	1815	G
1	L5	1818	G
1	L5	1821	G
1	L5	1822	U
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1843	A
1	L5	1854	G
1	L5	1855	G
1	L5	1870	C
1	L5	1872	G
1	L5	1873	A
1	L5	1881	C
1	L5	1882	U

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Mol	Chain	Res	Type
1	L5	1883	G
1	L5	1891	A
1	L5	1892	A
1	L5	1897	A
1	L5	1916	G
1	L5	1918	U
1	L5	1919	G
1	L5	1920	C
1	L5	1921	C
1	L5	1922	G
1	L5	1925	G
1	L5	1931	C
1	L5	1938	C
1	L5	1939	A
1	L5	1940	G
1	L5	1941	A
1	L5	1942	A
1	L5	1944	A
1	L5	1949	U
1	L5	1961	G
1	L5	1968	G
1	L5	1969	G
1	L5	1970	A
1	L5	1975	G
1	L5	1978	C
1	L5	1980	U
1	L5	1982	G
1	L5	1983	A
1	L5	1984	A
1	L5	1985	G
1	L5	1990	A
1	L5	1991	A
1	L5	1997	U
1	L5	2002	A
1	L5	2005	G
1	L5	2026	A
1	L5	2039	G
1	L5	2040	A
1	L5	2041	A
1	L5	2042	A
1	L5	2043	A
1	L5	2044	U

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Mol	Chain	Res	Type
1	L5	2046	G
1	L5	2048	U
1	L5	2055	G
1	L5	2056	G
1	L5	2069	A
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2091	C
1	L5	2270	G
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2313	A
1	L5	2316	G
1	L5	2331	G
1	L5	2332	A
1	L5	2333	G
1	L5	2344	U
1	L5	2348	G
1	L5	2351	C
1	L5	2369	U
1	L5	2389	A
1	L5	2395	A
1	L5	2397	G
1	L5	2402	G
1	L5	2408	U
1	L5	2411	C
1	L5	2414	G
1	L5	2416	G
1	L5	2421	G
1	L5	2423	A
1	L5	2425	U
1	L5	2441	C
1	L5	2450	G
1	L5	2453	A
1	L5	2469	C
1	L5	2471	G
1	L5	2474	G
1	L5	2475	G
1	L5	2484	A
1	L5	2485	U

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Mol	Chain	Res	Type
1	L5	2486	G
1	L5	2487	G
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2491	C
1	L5	2495	U
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2507	A
1	L5	2511	A
1	L5	2513	A
1	L5	2519	U
1	L5	2529	A
1	L5	2537	A
1	L5	2554	U
1	L5	2555	G
1	L5	2556	G
1	L5	2559	G
1	L5	2560	C
1	L5	2563	C
1	L5	2573	A
1	L5	2583	C
1	L5	2586	G
1	L5	2587	A
1	L5	2589	C
1	L5	2601	A
1	L5	2627	C
1	L5	2638	G
1	L5	2653	C
1	L5	2662	G
1	L5	2669	C
1	L5	2670	C
1	L5	2675	G
1	L5	2676	A
1	L5	2687	U
1	L5	2695	A
1	L5	2696	A
1	L5	2707	U
1	L5	2708	U
1	L5	2710	C

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Mol	Chain	Res	Type
1	L5	2711	G
1	L5	2719	C
1	L5	2721	G
1	L5	2724	G
1	L5	2726	G
1	L5	2739	C
1	L5	2742	G
1	L5	2743	A
1	L5	2760	G
1	L5	2761	U
1	L5	2763	U
1	L5	2764	A
1	L5	2770	C
1	L5	2787	A
1	L5	2788	U
1	L5	2790	U
1	L5	2791	C
1	L5	2794	C
1	L5	2826	U
1	L5	2827	G
1	L5	2835	A
1	L5	2840	A
1	L5	2848	G
1	L5	2852	U
1	L5	2853	C
1	L5	2855	G
1	L5	2867	C
1	L5	2875	C
1	L5	2877	G
1	L5	2886	U
1	L5	2900	U
1	L5	3604	A
1	L5	3605	C
1	L5	3616	U
1	L5	3617	G
1	L5	3618	C
1	L5	3619	G
1	L5	3626	G
1	L5	3635	A
1	L5	3644	U
1	L5	3646	A
1	L5	3648	A

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Mol	Chain	Res	Type
1	L5	3651	A
1	L5	3662	A
1	L5	3664	G
1	L5	3673	C
1	L5	3674	G
1	L5	3680	U
1	L5	3690	U
1	L5	3691	G
1	L5	3698	G
1	L5	3702	A
1	L5	3714	G
1	L5	3727	A
1	L5	3735	G
1	L5	3747	A
1	L5	3748	A
1	L5	3750	G
1	L5	3753	G
1	L5	3757	G
1	L5	3758	U
1	L5	3760	A
1	L5	3762	U
1	L5	3765	G
1	L5	3771	C
1	L5	3772	U
1	L5	3773	U
1	L5	3775	A
1	L5	3780	G
1	L5	3821	A
1	L5	3822	U
1	L5	3823	G
1	L5	3824	A
1	L5	3838	U
1	L5	3839	G
1	L5	3840	U
1	L5	3851	U
1	L5	3869	C
1	L5	3872	A
1	L5	3875	G
1	L5	3878	C
1	L5	3879	G
1	L5	3885	G
1	L5	3887	C

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Mol	Chain	Res	Type
1	L5	3892	U
1	L5	3897	G
1	L5	3903	A
1	L5	3905	A
1	L5	3906	A
1	L5	3907	G
1	L5	3922	G
1	L5	3923	A
1	L5	3942	A
1	L5	3943	A
1	L5	3944	G
1	L5	3951	G
1	L5	3952	A
1	L5	4061	G
1	L5	4062	A
1	L5	4065	G
1	L5	4066	U
1	L5	4077	A
1	L5	4085	A
1	L5	4086	G
1	L5	4088	C
1	L5	4092	G
1	L5	4093	G
1	L5	4095	G
1	L5	4097	G
1	L5	4099	G
1	L5	4101	C
1	L5	4102	C
1	L5	4104	G
1	L5	4107	G
1	L5	4108	G
1	L5	4111	U
1	L5	4113	U
1	L5	4114	C
1	L5	4115	G
1	L5	4116	C
1	L5	4117	U
1	L5	4119	C
1	L5	4121	G
1	L5	4122	G
1	L5	4127	A
1	L5	4140	C

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Mol	Chain	Res	Type
1	L5	4141	G
1	L5	4142	C
1	L5	4143	G
1	L5	4144	C
1	L5	4146	G
1	L5	4149	C
1	L5	4150	G
1	L5	4157	A
1	L5	4160	C
1	L5	4162	C
1	L5	4168	G
1	L5	4170	A
1	L5	4183	G
1	L5	4200	G
1	L5	4203	A
1	L5	4228	G
1	L5	4229	U
1	L5	4231	C
1	L5	4232	U
1	L5	4233	A
1	L5	4237	C
1	L5	4243	C
1	L5	4251	A
1	L5	4254	G
1	L5	4257	A
1	L5	4268	A
1	L5	4272	G
1	L5	4273	A
1	L5	4274	A
1	L5	4275	G
1	L5	4282	A
1	L5	4290	U
1	L5	4291	G
1	L5	4293	U
1	L5	4294	C
1	L5	4295	U
1	L5	4298	A
1	L5	4305	G
1	L5	4306	U
1	L5	4307	A
1	L5	4308	C
1	L5	4309	G

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Mol	Chain	Res	Type
1	L5	4314	C
1	L5	4331	G
1	L5	4335	C
1	L5	4343	U
1	L5	4344	U
1	L5	4347	G
1	L5	4348	A
1	L5	4349	C
1	L5	4350	C
1	L5	4354	U
1	L5	4368	G
1	L5	4371	G
1	L5	4381	A
1	L5	4385	A
1	L5	4386	C
1	L5	4388	A
1	L5	4394	A
1	L5	4401	G
1	L5	4404	U
1	L5	4428	A
1	L5	4431	U
1	L5	4432	C
1	L5	4437	U
1	L5	4440	G
1	L5	4446	U
1	L5	4464	A
1	L5	4465	U
1	L5	4471	U
1	L5	4475	G
1	L5	4476	C
1	L5	4488	A
1	L5	4500	U
1	L5	4501	U
1	L5	4503	A
1	L5	4510	A
1	L5	4512	U
1	L5	4513	A
1	L5	4518	A
1	L5	4519	C
1	L5	4524	G
1	L5	4528	G
1	L5	4534	G

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Mol	Chain	Res	Type
1	L5	4545	G
1	L5	4547	C
1	L5	4548	A
1	L5	4556	U
1	L5	4557	U
1	L5	4558	U
1	L5	4560	C
1	L5	4567	G
1	L5	4569	U
1	L5	4573	G
1	L5	4575	G
1	L5	4589	A
1	L5	4590	A
1	L5	4598	C
1	L5	4599	A
1	L5	4617	G
1	L5	4635	A
1	L5	4636	U
1	L5	4637	G
1	L5	4656	A
1	L5	4670	C
1	L5	4672	A
1	L5	4677	U
1	L5	4684	A
1	L5	4693	C
1	L5	4694	G
1	L5	4695	C
1	L5	4700	A
1	L5	4708	A
1	L5	4709	U
1	L5	4719	G
1	L5	4730	C
1	L5	4731	G
1	L5	4733	C
1	L5	4734	A
1	L5	4740	G
1	L5	4741	C
1	L5	4742	G
1	L5	4745	G
1	L5	4751	G
1	L5	4754	G
1	L5	4757	C

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Mol	Chain	Res	Type
1	L5	4759	C
1	L5	4761	G
1	L5	4765	G
1	L5	4771	C
1	L5	4772	C
1	L5	4773	C
1	L5	4775	C
1	L5	4859	C
1	L5	4870	G
1	L5	4871	C
1	L5	4874	A
1	L5	4875	G
1	L5	4880	C
1	L5	4882	U
1	L5	4883	C
1	L5	4887	C
1	L5	4889	G
1	L5	4893	A
1	L5	4894	A
1	L5	4895	C
1	L5	4896	G
1	L5	4900	C
1	L5	4901	G
1	L5	4910	G
1	L5	4912	G
1	L5	4914	C
1	L5	4922	C
1	L5	4923	C
1	L5	4924	C
1	L5	4925	U
1	L5	4928	C
1	L5	4937	C
1	L5	4941	G
1	L5	4943	A
1	L5	4949	G
1	L5	4951	G
1	L5	4955	A
1	L5	4961	G
1	L5	4966	A
1	L5	4975	G
1	L5	4976	U
1	L5	4985	U

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Mol	Chain	Res	Type
1	L5	4988	U
1	L5	4989	U
1	L5	4991	U
1	L5	5008	C
1	L5	5013	C
1	L5	5017	G
1	L5	5022	U
1	L5	5023	C
1	L5	5024	C
1	L5	5025	C
1	L5	5026	U
1	L5	5031	G
1	L5	5034	A
1	L5	5041	G
1	L5	5050	C
1	L5	5054	C
1	L5	5055	G
1	L5	5058	A
1	L5	5062	G
1	L5	5069	U
2	L7	3	C
2	L7	7	G
2	L7	22	A
2	L7	24	C
2	L7	27	G
2	L7	38	U
2	L7	53	U
2	L7	54	A
2	L7	61	G
2	L7	63	C
2	L7	64	G
2	L7	74	A
2	L7	75	G
2	L7	76	U
2	L7	89	G
2	L7	91	C
2	L7	97	G
2	L7	100	A
2	L7	106	G
2	L7	120	U
3	L8	2	G
3	L8	25	G

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Mol	Chain	Res	Type
3	L8	34	U
3	L8	35	C
3	L8	48	A
3	L8	52	A
3	L8	59	A
3	L8	60	G
3	L8	62	A
3	L8	63	U
3	L8	75	G
3	L8	80	A
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	85	U
3	L8	87	G
3	L8	94	G
3	L8	103	A
3	L8	105	C
3	L8	110	U
3	L8	114	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	126	C
3	L8	127	U
3	L8	151	G
3	L8	156	U

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	135	G
1	L5	406	C
1	L5	493	G
1	L5	914	U
1	L5	924	C
1	L5	1082	C
1	L5	1937	C
1	L5	1977	C
1	L5	2675	G
1	L5	2760	G
1	L5	2786	C

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Mol	Chain	Res	Type
1	L5	3821	A
1	L5	3822	U
1	L5	4061	G
1	L5	4065	G
1	L5	4087	G
1	L5	4297	G
1	L5	4305	G
1	L5	4347	G
1	L5	4597	U
1	L5	4699	U
1	L5	4913	G
2	L7	74	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 7 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
54	GTP	CB	1001	55	33,34,34	0.95	1 (3%)	50,54,54	1.59	8 (16%)
56	GDP	CD	801	55	29,30,30	1.17	3 (10%)	45,47,47	1.76	7 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	GTP	CB	1001	55	-	5/22/38/38	0/3/3/3
56	GDP	CD	801	55	-	5/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	CD	801	GDP	C5-C4	3.10	1.47	1.38
56	CD	801	GDP	C6-N1	-2.44	1.34	1.38
54	CB	1001	GTP	C2-N3	2.13	1.38	1.33
56	CD	801	GDP	C5-N7	-2.05	1.35	1.39

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	CD	801	GDP	C5-C4-N3	-6.07	118.72	128.39
56	CD	801	GDP	C2-N3-C4	5.02	120.94	112.30
54	CB	1001	GTP	C5-C4-N3	-4.95	120.51	128.39
54	CB	1001	GTP	C2-N3-C4	4.59	120.20	112.30
56	CD	801	GDP	N9-C4-N3	4.45	134.85	125.95
56	CD	801	GDP	C6-C5-N7	3.33	136.36	130.29
54	CB	1001	GTP	N9-C4-N3	3.21	132.38	125.95
54	CB	1001	GTP	C2-N1-C6	-2.89	119.87	125.11
54	CB	1001	GTP	N9-C8-N7	-2.77	108.27	113.40
56	CD	801	GDP	C4-C5-N7	-2.64	106.49	110.67
54	CB	1001	GTP	C8-N7-C5	2.56	108.82	104.26
54	CB	1001	GTP	C5-C6-N1	2.52	119.67	113.25
54	CB	1001	GTP	O6-C6-C5	-2.42	120.14	126.53
56	CD	801	GDP	O6-C6-C5	-2.07	121.08	126.53
56	CD	801	GDP	C3'-C2'-C1'	2.04	105.31	101.46

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	CB	1001	GTP	C5'-O5'-PA-O3A
54	CB	1001	GTP	C5'-O5'-PA-O1A
54	CB	1001	GTP	C5'-O5'-PA-O2A
56	CD	801	GDP	C5'-O5'-PA-O3A
56	CD	801	GDP	C5'-O5'-PA-O1A
56	CD	801	GDP	C5'-O5'-PA-O2A

Continued on next page...

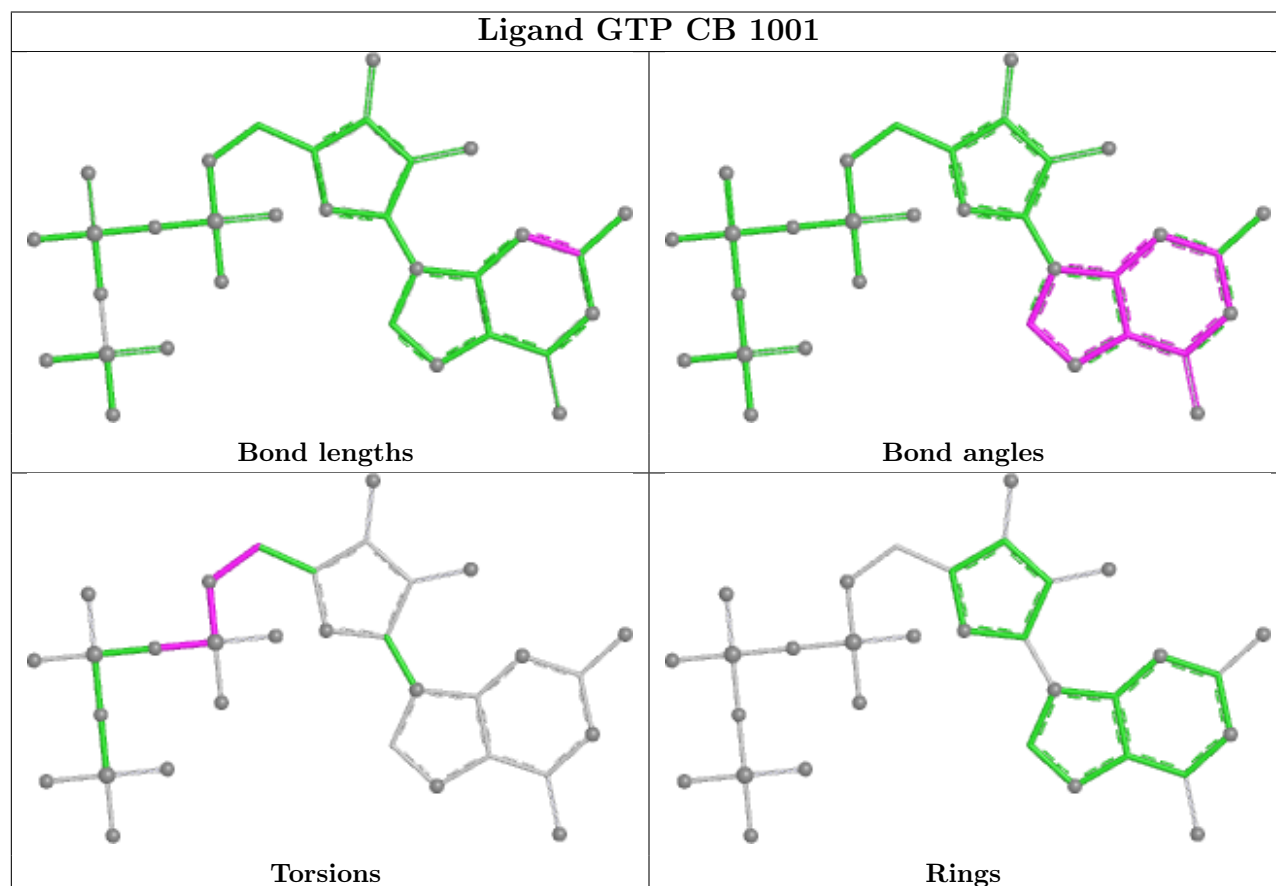
Continued from previous page...

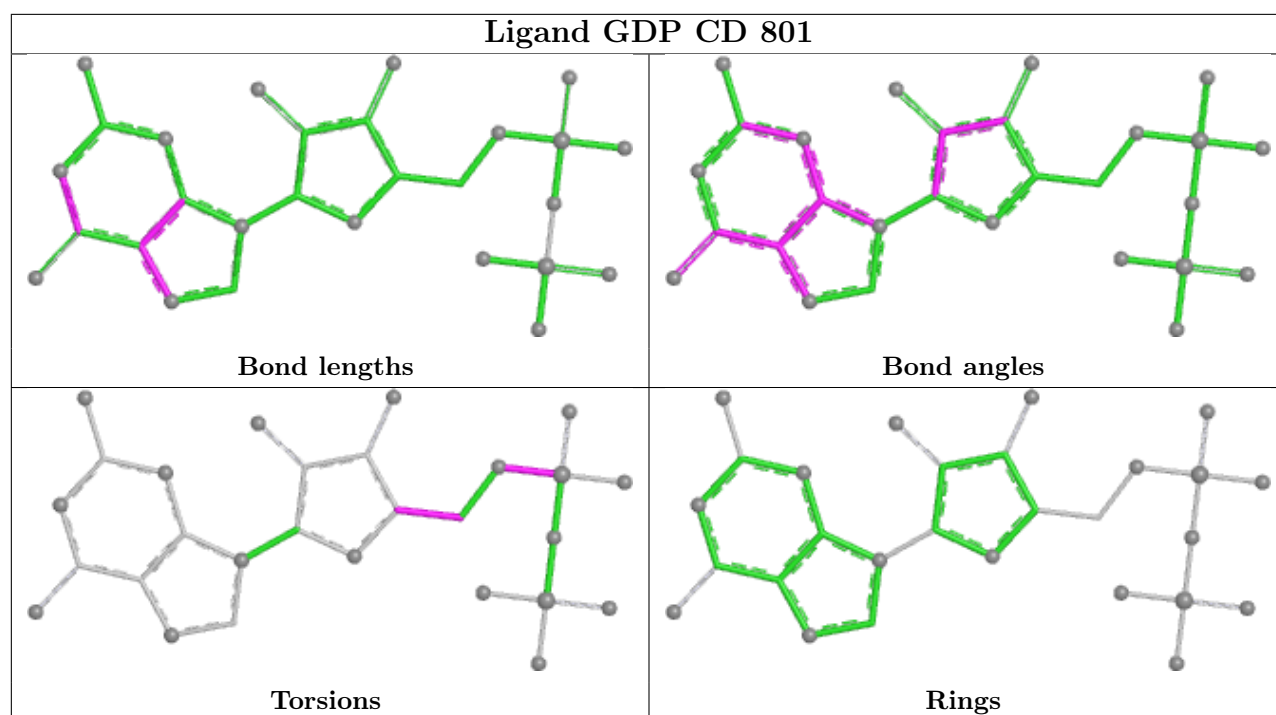
Mol	Chain	Res	Type	Atoms
56	CD	801	GDP	O4'-C4'-C5'-O5'
56	CD	801	GDP	C3'-C4'-C5'-O5'
54	CB	1001	GTP	C4'-C5'-O5'-PA
54	CB	1001	GTP	PB-O3A-PA-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

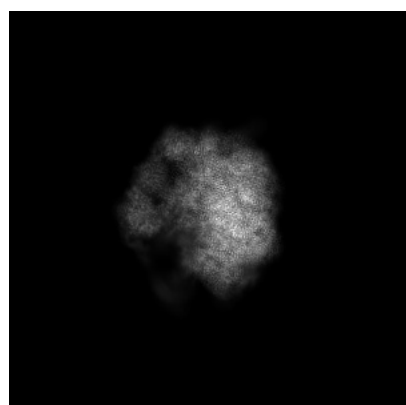
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19330. These allow visual inspection of the internal detail of the map and identification of artifacts.

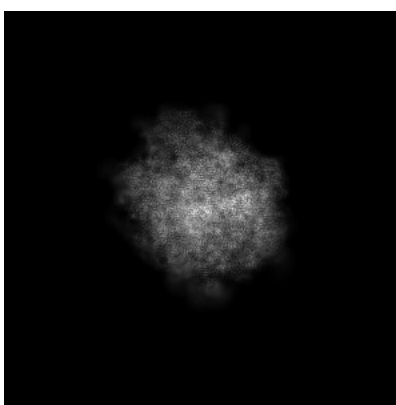
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

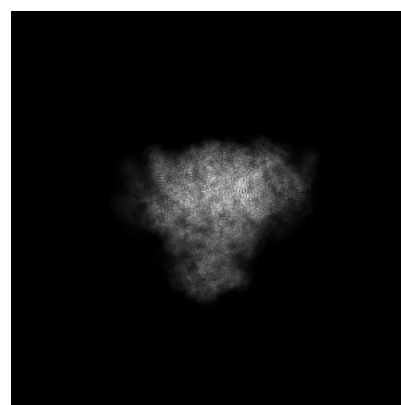
6.1.1 Primary map



X



Y

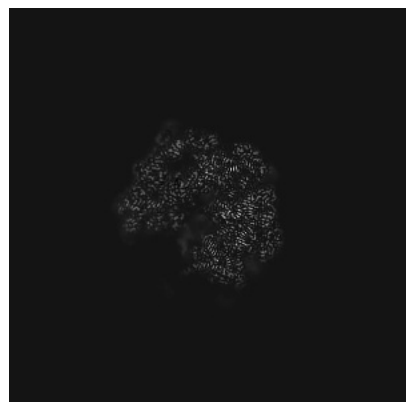


Z

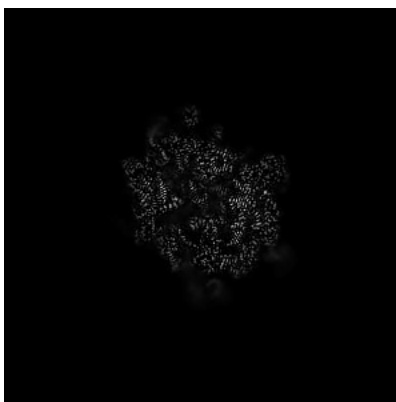
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 250



Y Index: 250

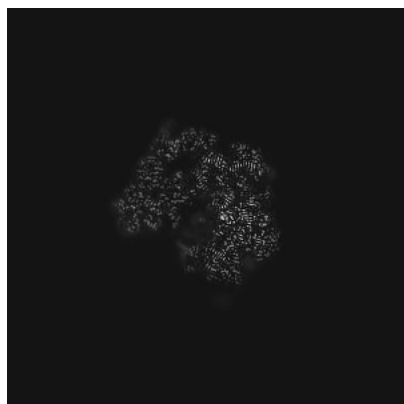


Z Index: 250

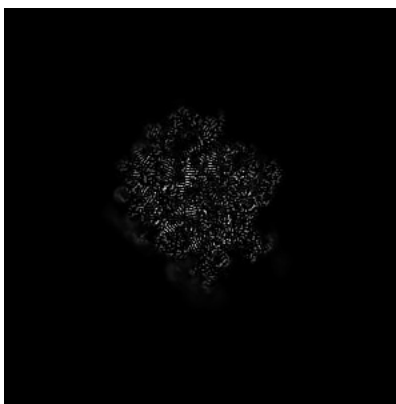
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

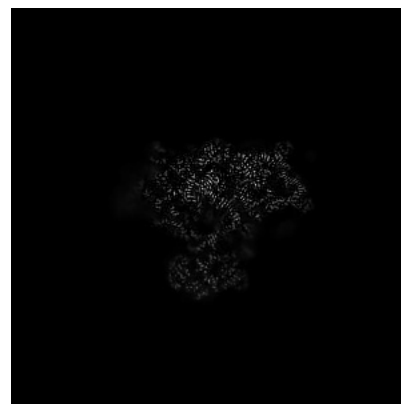
6.3.1 Primary map



X Index: 246



Y Index: 269

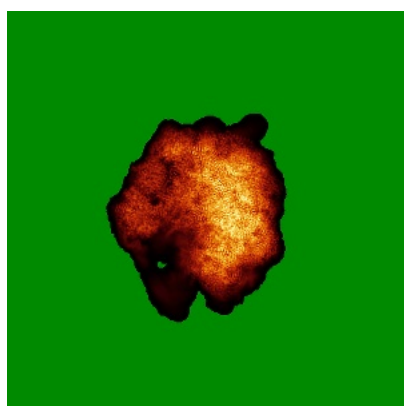


Z Index: 238

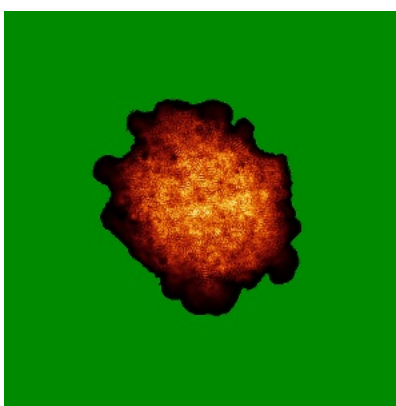
The images above show the largest variance slices of the map in three orthogonal directions.

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

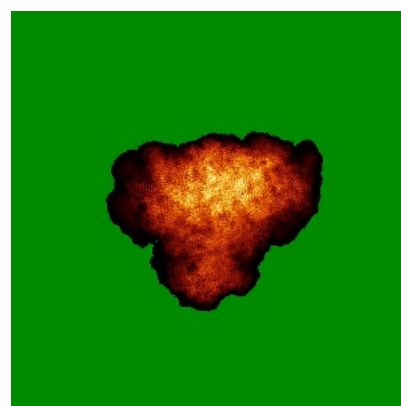
6.4.1 Primary map



X



Y

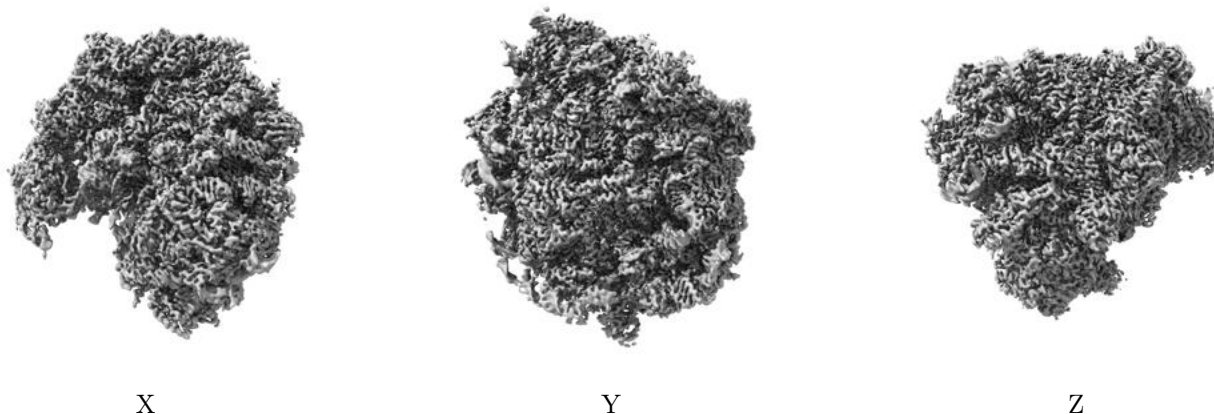


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

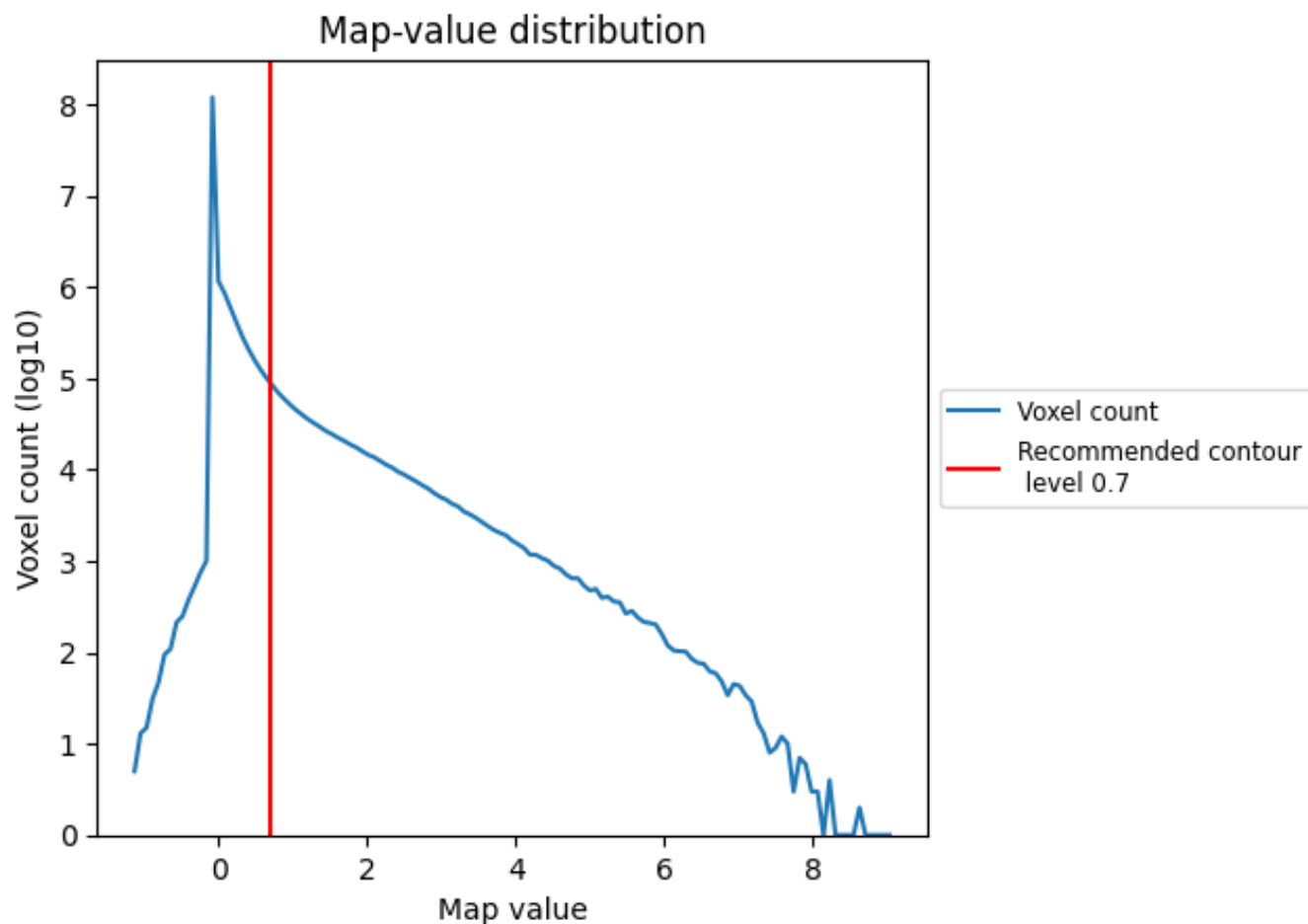
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

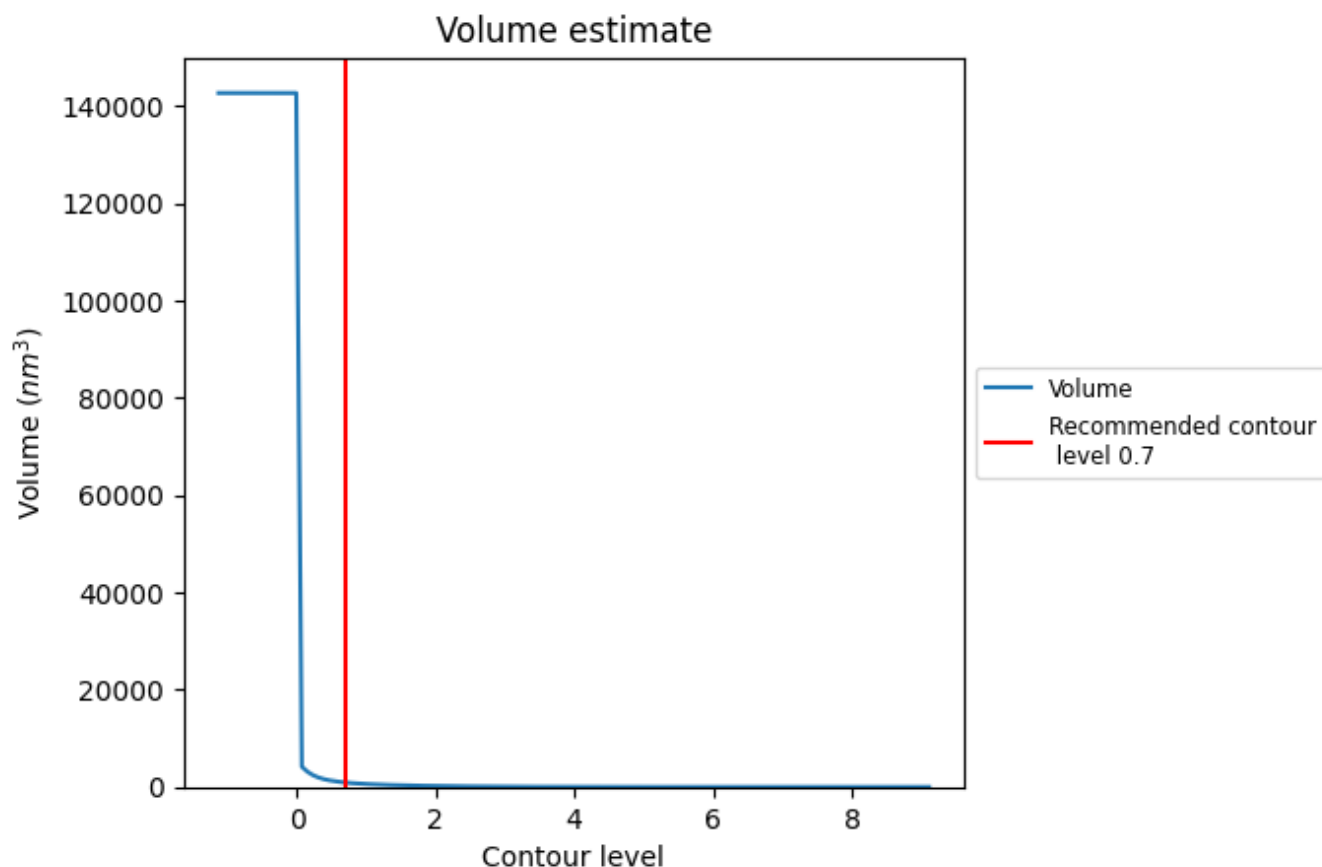
This section contains the results of statistical analysis of the map.

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.

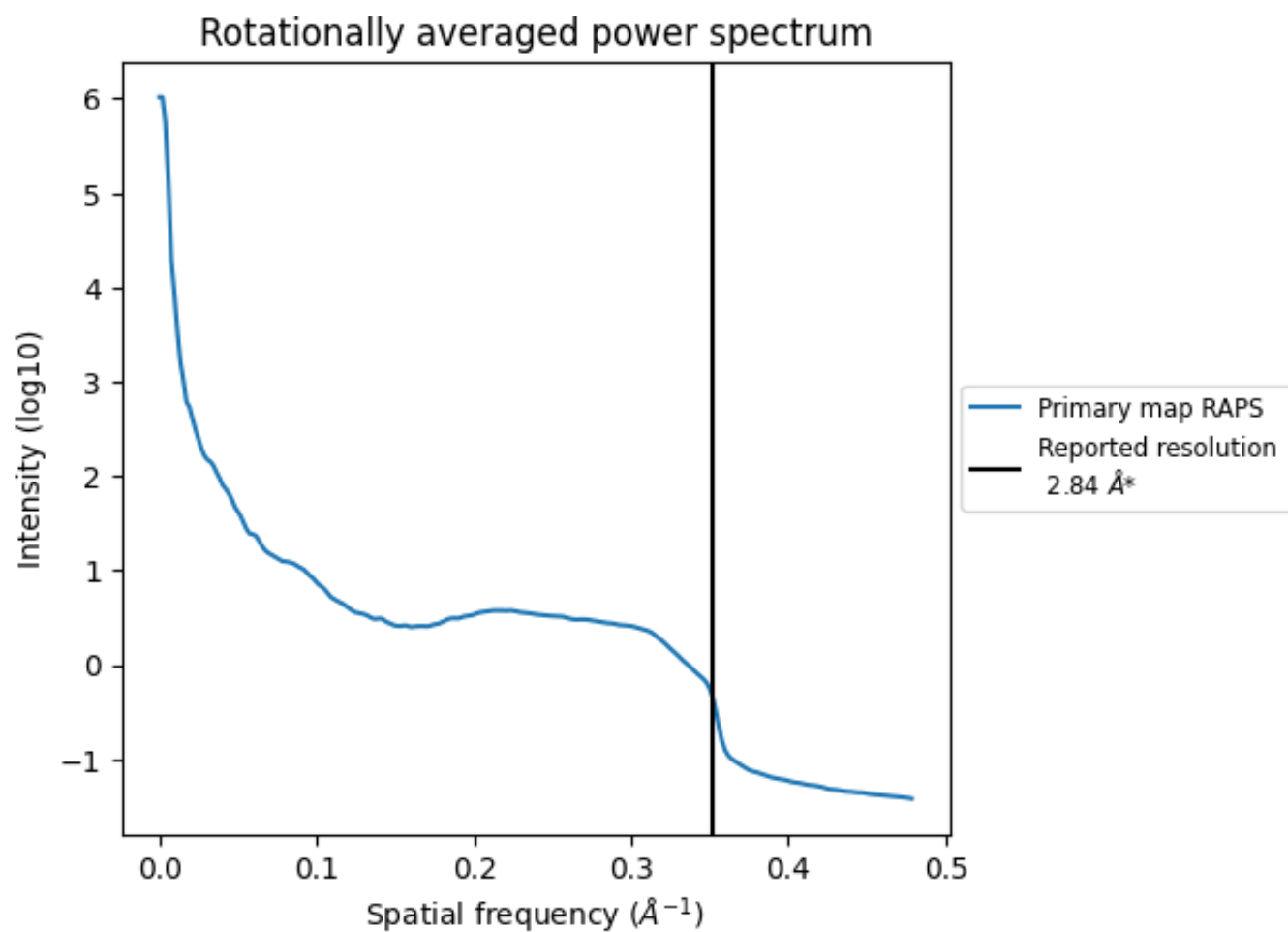
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 912 nm^3 ; this corresponds to an approximate mass of 824 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 0.352 Å⁻¹

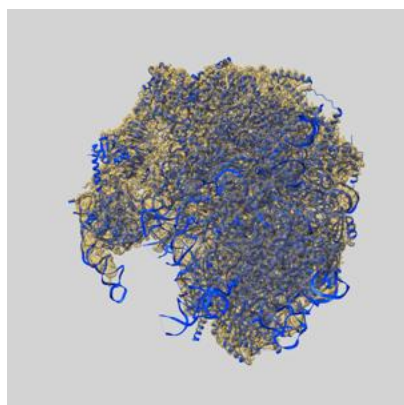
8 Fourier-Shell correlation ⓘ

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

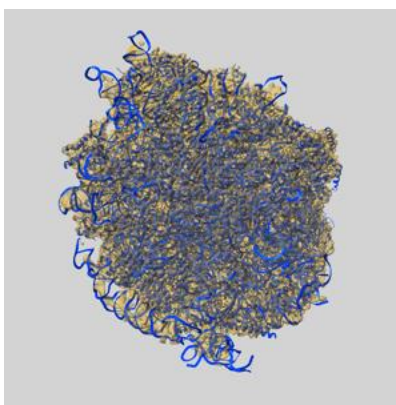
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19330 and PDB model 8RL2. Per-residue inclusion information can be found in section 3 on page 15.

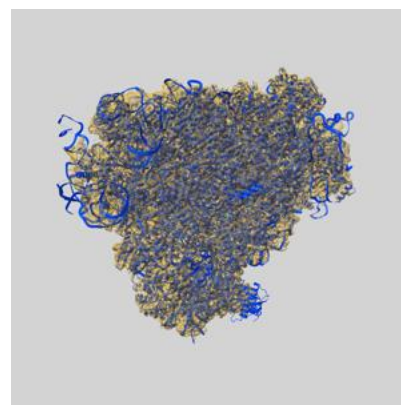
9.1 Map-model overlay [i](#)



X



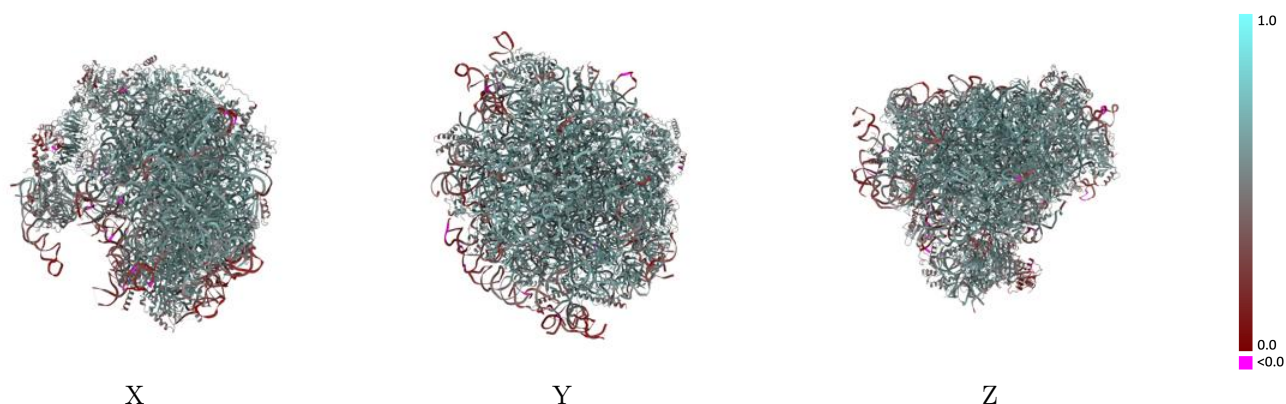
Y



Z

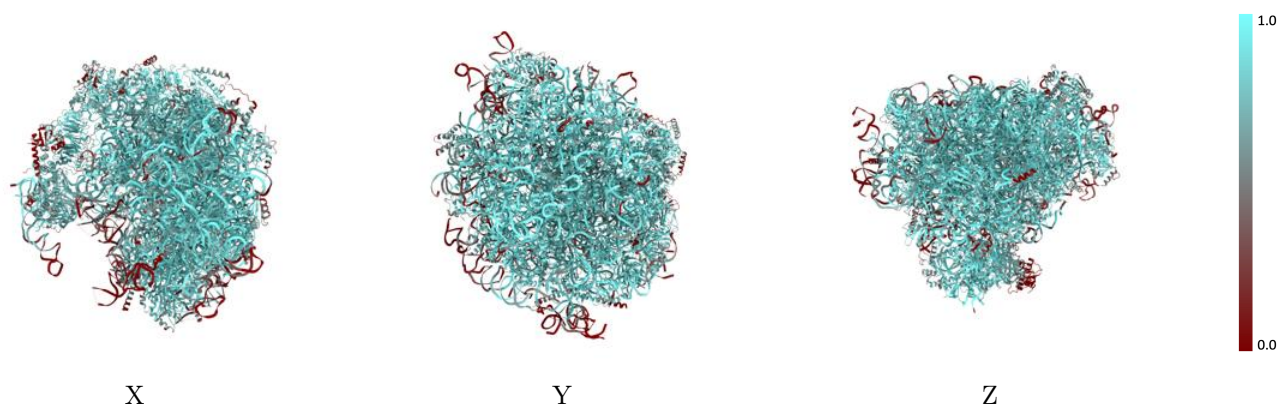
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



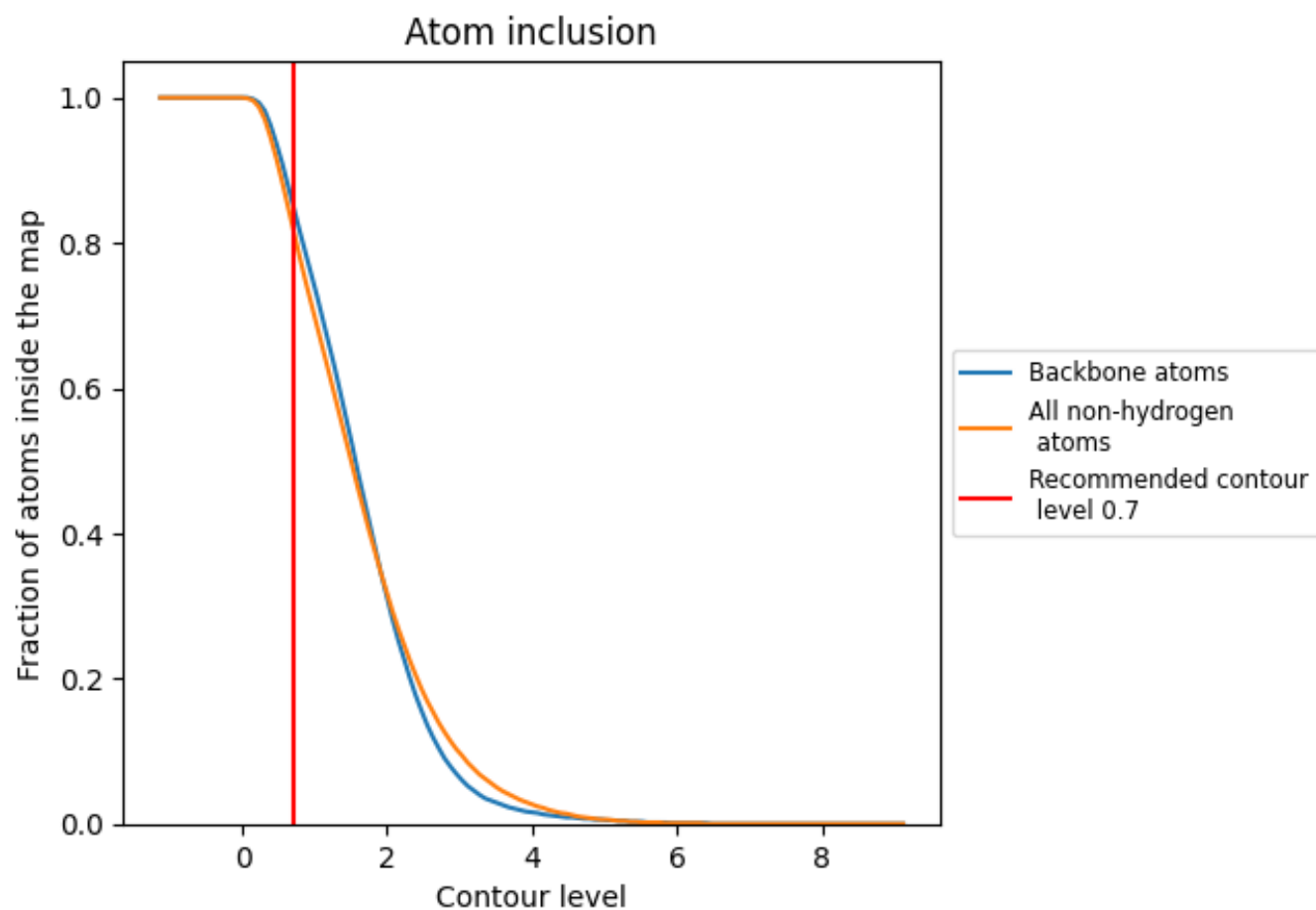
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 82% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8200	 0.5510
CA	 0.8310	 0.5710
CB	 0.8730	 0.5860
CC	 0.5980	 0.4930
CD	 0.7880	 0.5550
CE	 0.6680	 0.5230
CF	 0.7930	 0.5280
CG	 0.8080	 0.5310
CH	 0.9000	 0.6070
CI	 0.8500	 0.5900
CJ	 0.7330	 0.5080
CK	 0.5820	 0.4490
CL	 0.6810	 0.5460
L5	 0.8130	 0.5330
L7	 0.7500	 0.4520
L8	 0.9080	 0.5950
LA	 0.8430	 0.5960
LB	 0.9150	 0.6280
LC	 0.8990	 0.6090
LD	 0.8270	 0.5400
LE	 0.7950	 0.5670
LF	 0.8920	 0.6060
LG	 0.7380	 0.5320
LH	 0.8990	 0.5950
LJ	 0.6660	 0.4750
LL	 0.8000	 0.5530
LM	 0.8920	 0.6000
LN	 0.8970	 0.6150
LO	 0.9340	 0.6320
LP	 0.9180	 0.6390
LQ	 0.8890	 0.6000
LR	 0.8620	 0.5920
LS	 0.9020	 0.6030
LT	 0.6420	 0.4960
LU	 0.7730	 0.5500



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Chain	Atom inclusion	Q-score
LV	 0.9380	 0.6270
LX	 0.8530	 0.5960
LY	 0.8720	 0.5910
LZ	 0.7700	 0.5360
La	 0.8590	 0.5680
Lc	 0.7400	 0.5330
Ld	 0.8890	 0.6080
Le	 0.9150	 0.6180
Lf	 0.9680	 0.6620
Lg	 0.8700	 0.6040
Lh	 0.8360	 0.5750
Li	 0.7110	 0.5170
Lj	 0.9610	 0.6310
Lk	 0.6100	 0.4890
Ll	 0.9550	 0.6360
Lp	 0.8330	 0.5840
Lr	 0.9110	 0.6000
Lt	 0.5660	 0.4410