



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:38 AM UTC

PDB ID : 8VR8 / pdb_00008vr8
EMDB ID : EMD-43477
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX and chloramphenicol:50S-HflX-B-Clm
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-20
Resolution : 3.25 Å (reported)
Based on initial models : 6DZI, 5O61

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:

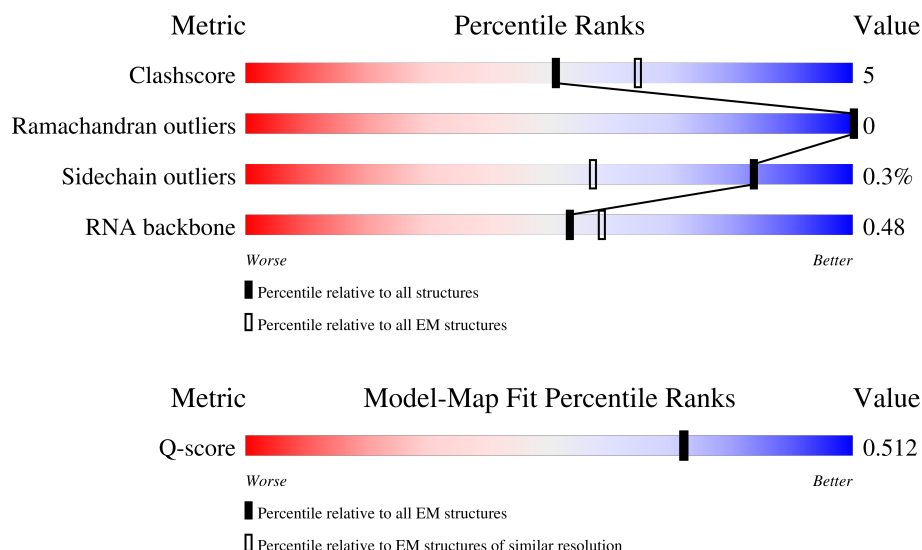
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.25 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.



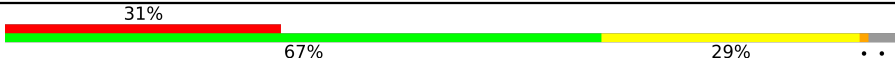
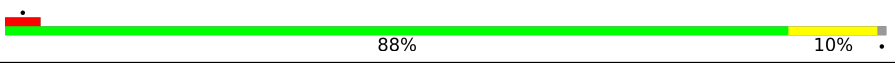
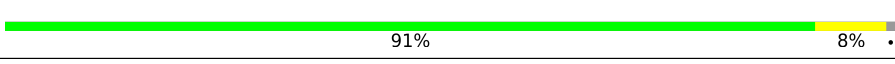
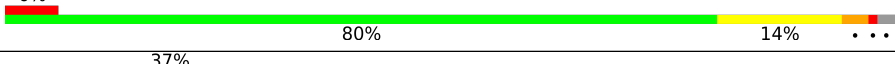
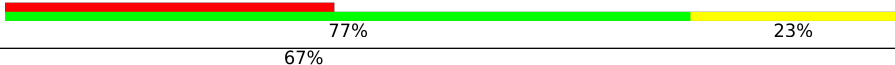
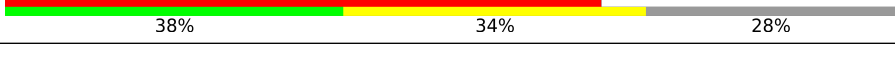
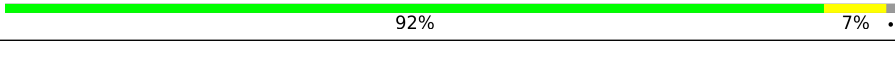
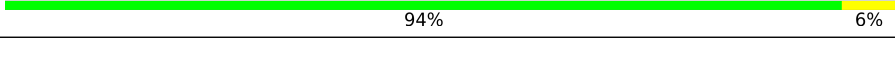
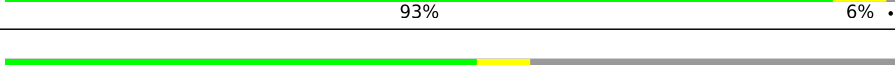
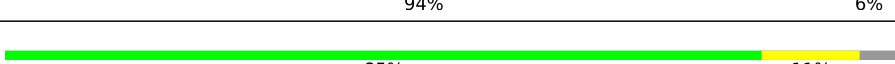
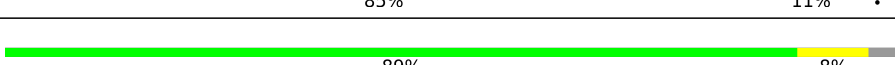
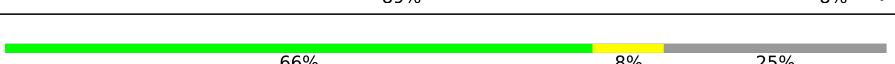
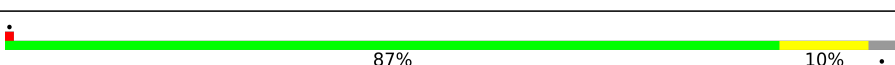
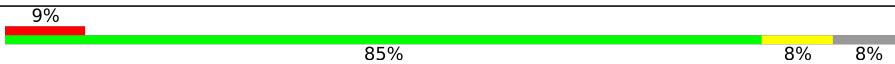
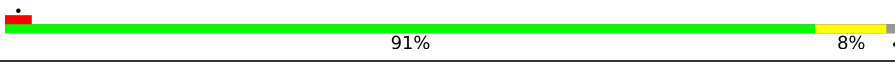
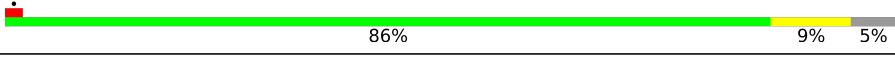
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14599 (2.75 - 3.75)

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	2	61	
2	3	24	

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Mol	Chain	Length	Quality of chain
3	4	470	
4	B	118	
5	C	278	
6	D	217	
7	E	215	
8	G	179	
9	H	151	
10	I	175	
11	K	147	
12	L	122	
13	M	147	
14	N	138	
15	O	199	
16	Q	113	
17	R	129	
18	S	103	
19	T	153	
20	U	100	
21	V	105	
22	W	215	
23	X	88	
24	Y	64	
25	Z	77	
26	b	57	
27	c	55	

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Mol	Chain	Length	Quality of chain
28	d	47	91% 6%
29	e	64	83% 16%
30	f	37	78% 22%
31	A	3120	9% 64% 24% 6% 5%

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 93099 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 protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 2 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	456	Total	C	N	O	S	0	0
			3444	2127	638	672	7		

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 7 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 11 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 17 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 18 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 19 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	114	Total	C	N	O		0	0
			873	543	171	159			

- Molecule 20 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	97	Total	C	N	O		0	0
			756	479	138	139			

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	95	Total	C	N	O		0	0
			735	452	149	134			

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	79	Total	C	N	O		0	0
			586	361	123	102			

- Molecule 24 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 27 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	63	Total	C	N	O		0	0
			502	302	115	85			

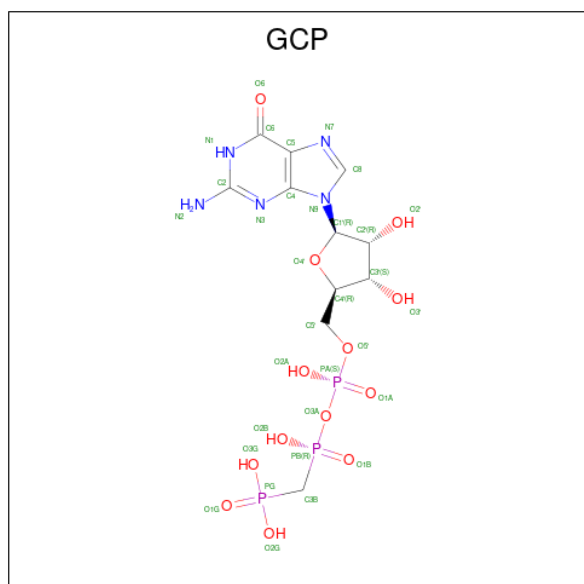
- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

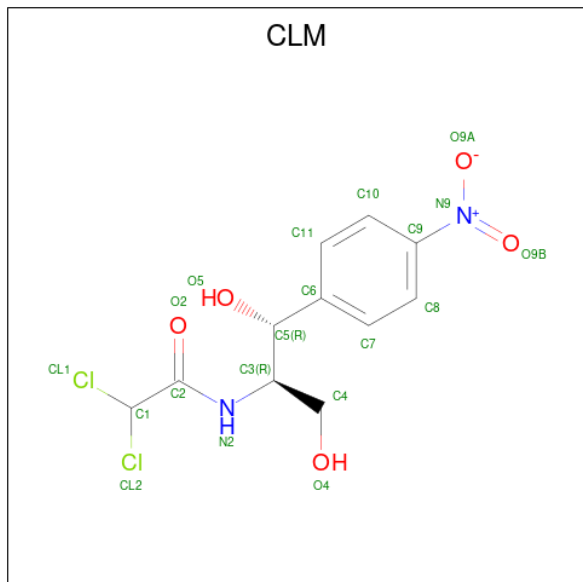
Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	2950	Total	C	N	O	P	0	0
			63364	28241	11658	20515	2950		

- Molecule 32 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
32	4	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 33 is CHLORAMPHENICOL (CCD ID: CLM) (formula: $C_{11}H_{12}Cl_2N_2O_5$) (labeled as "Ligand of Interest" by depositor).

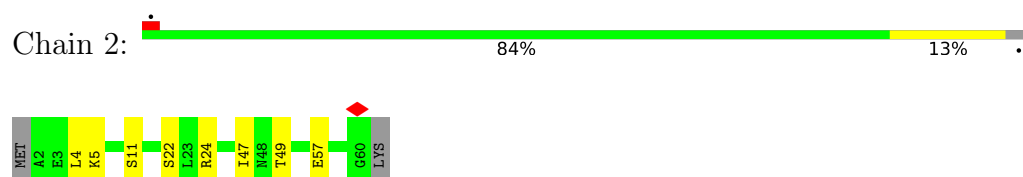


Mol	Chain	Residues	Atoms					AltConf
			Total	C	Cl	N	O	
33	A	1	20	11	2	2	5	0

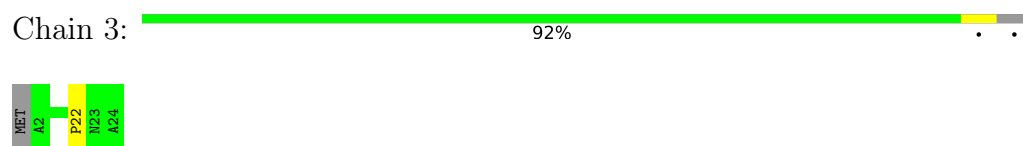
3 Residue-property plots

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

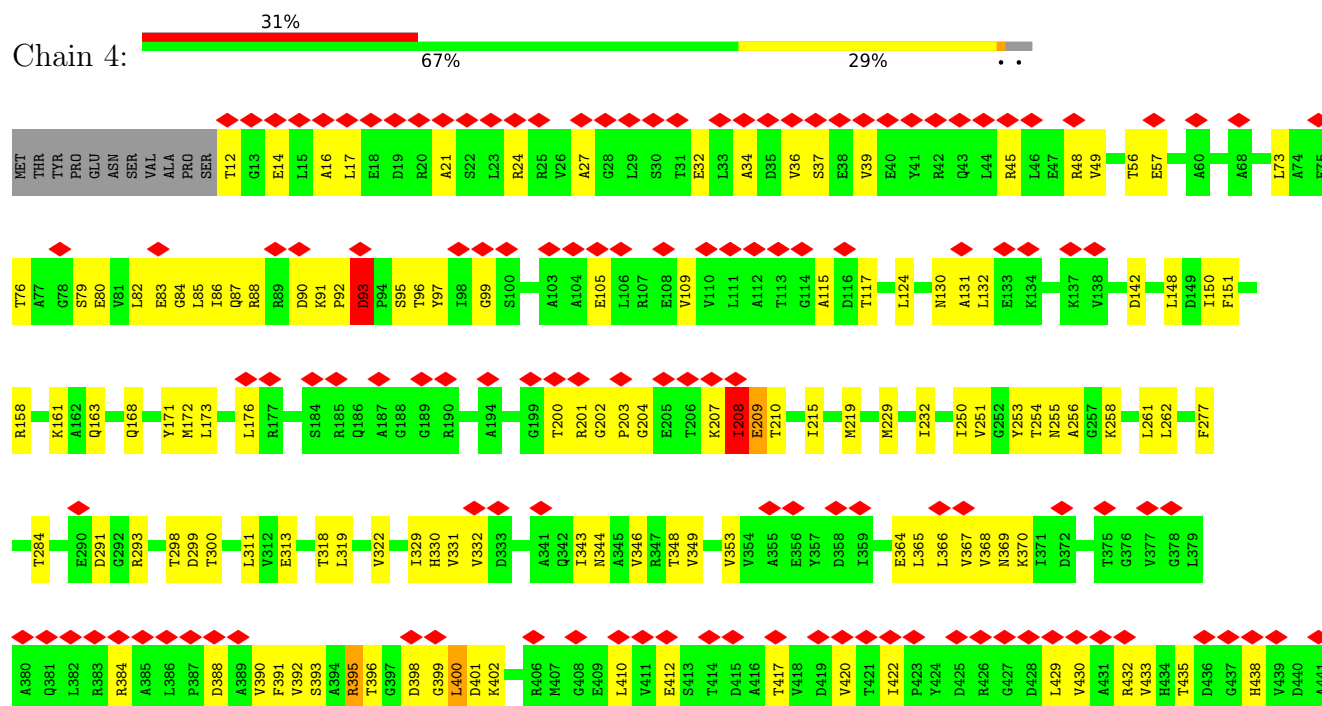
- Molecule 1: 50S ribosomal protein L30

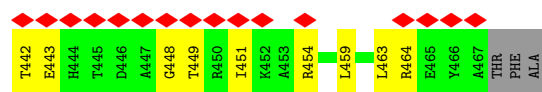


- Molecule 2: 50S Ribosomal Protein L37

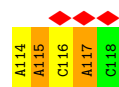
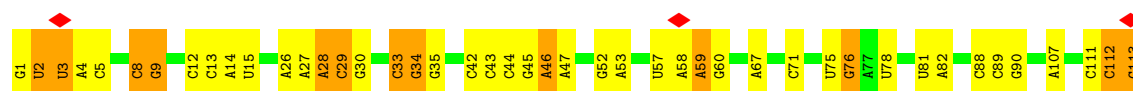


- Molecule 3: GTPase Hfx





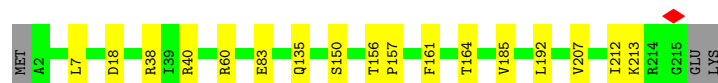
- Molecule 4: 5S ribosomal RNA



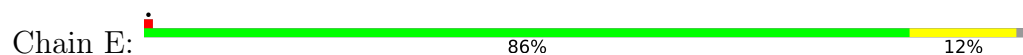
- Molecule 5: 50S ribosomal protein L2



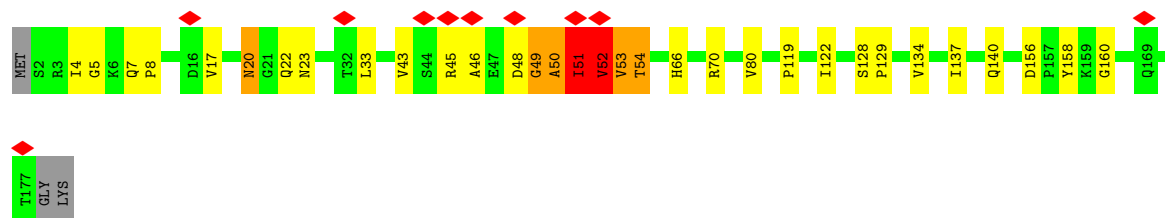
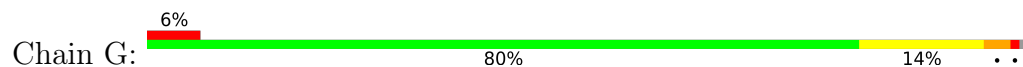
- Molecule 6: 50S ribosomal protein L3



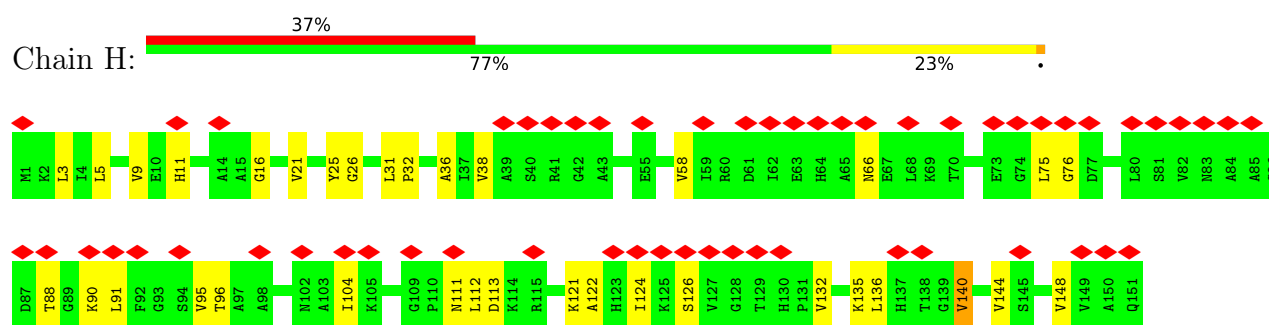
- Molecule 7: 50S Ribosomal Protein L4



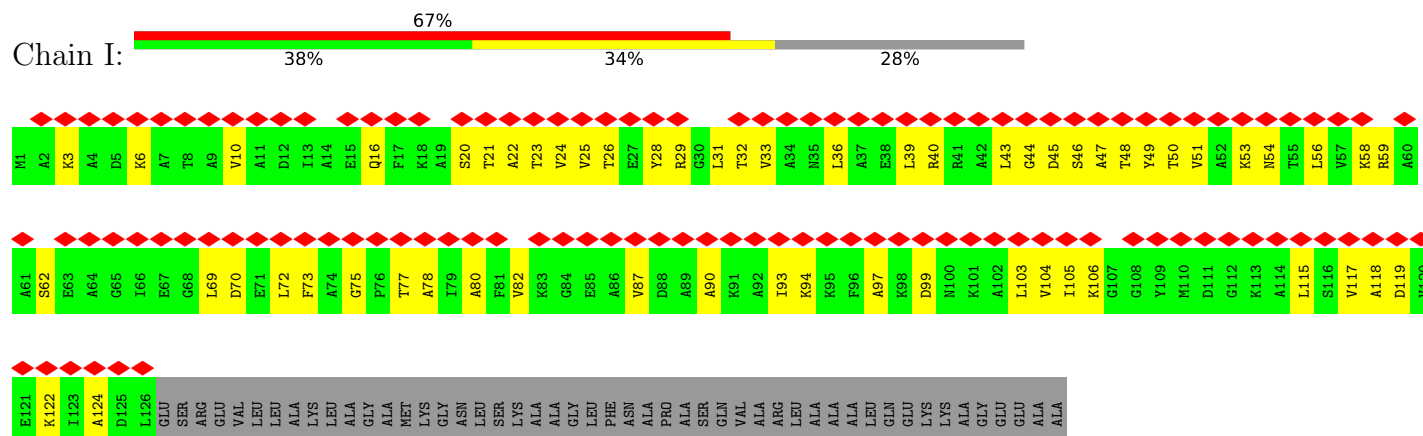
- Molecule 8: 50S ribosomal protein L6



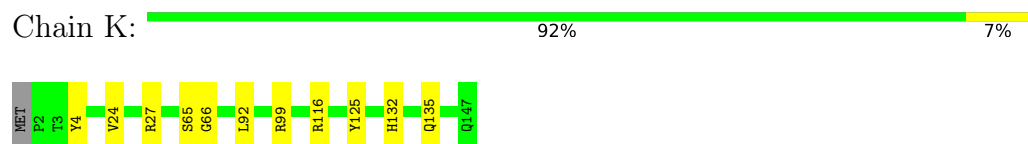
- Molecule 9: 50S ribosomal protein L9



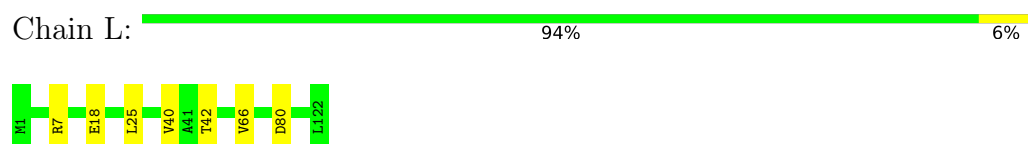
- Molecule 10: 50S ribosomal protein L10



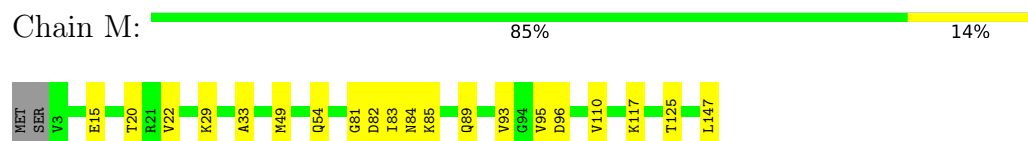
- Molecule 11: 50S Ribosomal Protein L13



- Molecule 12: 50S ribosomal protein L14

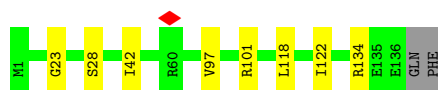


- Molecule 13: 50S ribosomal protein L15



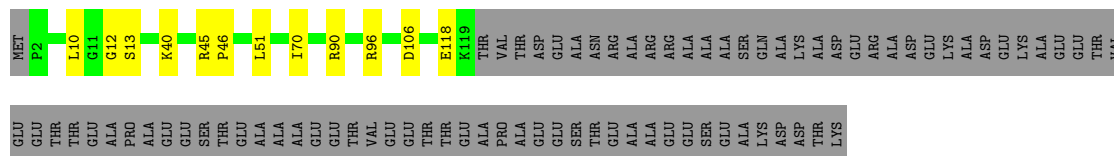
- Molecule 14: Large ribosomal subunit protein uL16





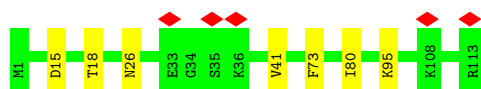
- Molecule 15: 50S ribosomal protein L17

Chain O: 53% 6% 41%



- Molecule 16: 50S ribosomal protein L19

Chain Q: 94% 6%



- Molecule 17: 50S Ribosomal Protein L20

Chain R: 85% 11% .



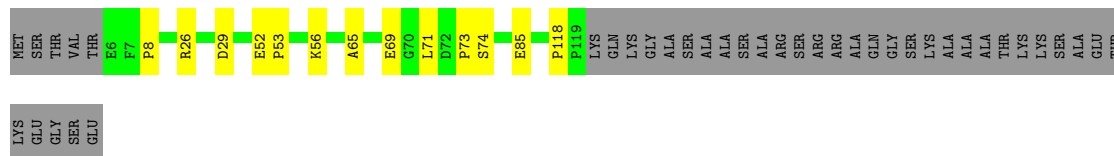
- Molecule 18: 50S Ribosomal Protein L21

Chain S: 89% 8% .



- Molecule 19: 50S Ribosomal Protein L22

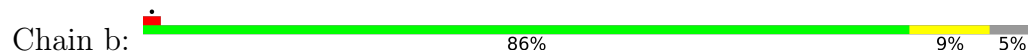
Chain T: 66% 8% 25%

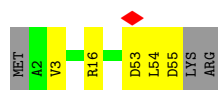


- Molecule 20: 50S Ribosomal Protein L23

Chain U: 87% 10% .







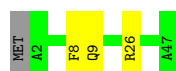
• Molecule 27: 50S Ribosomal Protein L33

Chain c: 75% 15% 11%



• Molecule 28: 50S ribosomal protein L34

Chain d: 91% 6%



• Molecule 29: 50S ribosomal protein L35

Chain e: 83% 16%



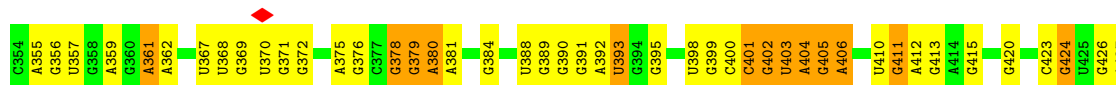
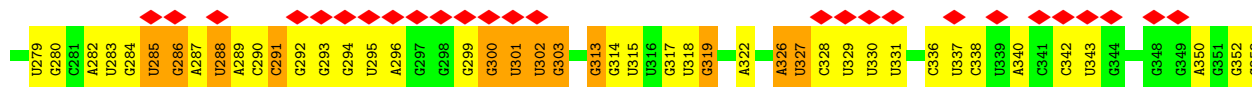
• Molecule 30: 50S ribosomal protein L36

Chain f: 78% 22%

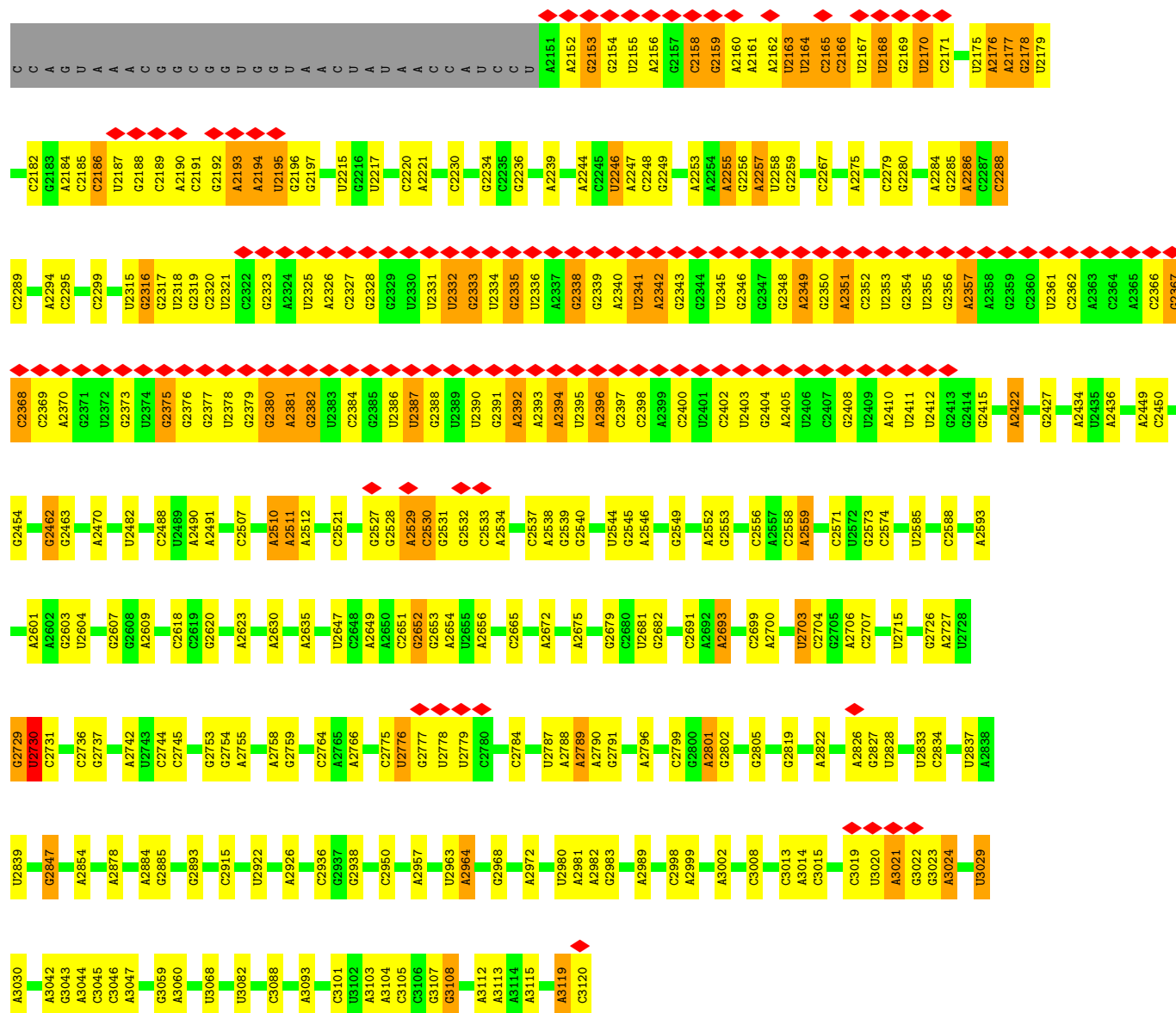


• Molecule 31: 23S ribosomal RNA

Chain A: 9% 64% 24% 6% 5%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	116149	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70.14	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.775	Depositor
Minimum map value	-1.185	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	432.2816, 432.2816, 432.2816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8443, 0.8443, 0.8443	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	2	0.16	0/477	0.37	0/640
2	3	0.12	0/191	0.31	0/247
3	4	0.26	0/3484	0.51	4/4721 (0.1%)
4	B	0.12	0/2821	0.29	0/4396
5	C	0.15	0/2153	0.38	0/2895
6	D	0.14	0/1609	0.37	0/2165
7	E	0.14	0/1592	0.32	0/2153
8	G	0.34	2/1369 (0.1%)	0.56	5/1848 (0.3%)
9	H	0.21	0/1027	0.47	0/1398
10	I	0.18	0/925	0.47	0/1246
11	K	0.15	0/1157	0.32	0/1567
12	L	0.14	0/946	0.35	0/1268
13	M	0.17	0/1091	0.40	0/1457
14	N	0.15	0/1118	0.34	0/1506
15	O	0.15	0/945	0.39	0/1267
16	Q	0.17	0/921	0.37	0/1236
17	R	0.15	0/1000	0.38	0/1341
18	S	0.13	0/764	0.37	0/1030
19	T	0.17	0/887	0.45	1/1204 (0.1%)
20	U	0.16	0/766	0.36	0/1030
21	V	0.16	0/738	0.38	0/987
22	W	0.13	0/745	0.39	0/1008
23	X	0.15	0/595	0.37	0/798
24	Y	0.14	0/478	0.34	0/641
25	Z	0.16	0/534	0.40	0/713
26	b	0.13	0/427	0.33	0/572
27	c	0.19	0/413	0.38	0/553
28	d	0.13	0/380	0.37	0/500
29	e	0.27	0/507	0.40	0/672
30	f	0.17	0/303	0.37	0/401
31	A	0.13	1/70952 (0.0%)	0.28	4/110707 (0.0%)
All	All	0.15	3/101315 (0.0%)	0.32	14/152167 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	G	50	ALA	CA-C	-5.69	1.45	1.52
31	A	2286	A	O3'-P	-5.61	1.52	1.61
8	G	51	ILE	CA-C	-5.31	1.46	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	G	51	ILE	N-CA-C	-9.51	101.08	110.30
3	4	208	ILE	N-CA-C	-8.67	98.46	109.30
31	A	2286	A	C1'-C2'-O2'	-8.48	95.68	108.40
31	A	2730	U	C1'-C2'-O2'	-7.94	96.49	108.40
8	G	49	GLY	N-CA-C	-6.68	97.34	113.18
31	A	2288	C	C1'-C2'-O2'	-5.93	99.51	108.40
31	A	2286	A	C2'-C3'-O3'	-5.75	105.07	113.70
3	4	93	ASP	CA-C-N	-5.58	112.86	119.84
3	4	93	ASP	C-N-CA	-5.58	112.86	119.84
8	G	54	THR	N-CA-C	5.34	118.16	109.24
3	4	395	ARG	N-CA-C	-5.15	100.90	108.99
19	T	118	PRO	CA-N-CD	-5.12	104.84	112.00
8	G	53	VAL	N-CA-C	-5.04	101.24	108.89
8	G	52	VAL	N-CA-C	-5.03	98.87	109.34

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	474	0	500	7	0
2	3	189	0	205	1	0
3	4	3444	0	3500	129	0
4	B	2522	0	1285	21	0
5	C	2110	0	2165	22	0
6	D	1587	0	1630	14	0
7	E	1569	0	1607	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	G	1348	0	1399	50	0
9	H	1018	0	988	30	0
10	I	918	0	959	69	0
11	K	1130	0	1167	7	0
12	L	938	0	1000	6	0
13	M	1078	0	1151	17	0
14	N	1092	0	1128	5	0
15	O	928	0	972	7	0
16	Q	907	0	938	5	0
17	R	988	0	1038	14	0
18	S	754	0	802	6	0
19	T	873	0	909	7	0
20	U	756	0	802	8	0
21	V	732	0	782	7	0
22	W	735	0	756	14	0
23	X	586	0	601	5	0
24	Y	470	0	484	3	0
25	Z	531	0	541	4	0
26	b	423	0	463	5	0
27	c	405	0	411	4	0
28	d	377	0	411	2	0
29	e	502	0	541	8	0
30	f	299	0	324	5	0
31	A	63364	0	31879	392	0
32	4	32	0	14	3	0
33	A	20	0	11	4	0
All	All	93099	0	61363	821	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 5.

All (821) 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)
8:G:7:GLN:C	8:G:51:ILE:HD12	1.64	1.20
8:G:7:GLN:O	8:G:51:ILE:HD12	1.03	1.19
8:G:7:GLN:O	8:G:51:ILE:CD1	1.96	1.12
8:G:8:PRO:HA	8:G:51:ILE:CD1	1.80	1.11
8:G:51:ILE:HB	8:G:53:VAL:HG22	1.35	1.08
8:G:8:PRO:HA	8:G:51:ILE:HD13	1.12	1.08
8:G:7:GLN:C	8:G:51:ILE:CD1	2.28	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:77:ASN:OD1	31:A:1270:G:O2'	1.80	1.00
8:G:8:PRO:CA	8:G:51:ILE:CD1	2.41	0.98
31:A:163:U:O2'	31:A:164:A:O4'	1.82	0.97
21:V:94:LYS:NZ	31:A:80:G:OP1	1.98	0.95
31:A:163:U:O2'	31:A:164:A:O5'	1.89	0.91
8:G:8:PRO:CA	8:G:51:ILE:HD13	1.99	0.89
3:4:255:ASN:HA	32:4:501:GCP:O1B	1.71	0.89
17:R:33:ARG:NH2	31:A:672:C:OP1	2.05	0.89
13:M:84:ASN:ND2	13:M:117:LYS:O	2.07	0.88
31:A:1710:A:N6	31:A:1716:A:OP2	2.06	0.88
21:V:94:LYS:NZ	31:A:378:G:OP1	2.07	0.87
31:A:635:G:N2	31:A:635:G:OP2	2.07	0.86
1:2:4:LEU:HD21	1:2:47:ILE:HD11	1.56	0.86
3:4:56:THR:OG1	3:4:57:GLU:OE1	1.93	0.85
3:4:392:VAL:HG23	3:4:398:ASP:HB3	1.55	0.85
31:A:1203:A:O2'	31:A:1204:A:O5'	1.91	0.85
31:A:2255:A:N3	31:A:2679:G:O2'	2.09	0.85
31:A:2257:A:O2'	31:A:2259:G:OP2	1.95	0.84
31:A:1854:U:O2'	31:A:1977:C:O2'	1.95	0.84
9:H:58:VAL:O	9:H:111:ASN:ND2	2.12	0.83
31:A:1996:U:OP2	31:A:2001:A:N6	2.11	0.82
10:I:58:LYS:O	10:I:62:SER:OG	1.96	0.82
31:A:980:C:O2'	31:A:981:U:O5'	1.96	0.81
31:A:1170:C:N4	31:A:1225:G:O6	2.11	0.81
10:I:49:TYR:OH	31:A:1203:A:N6	2.14	0.81
31:A:291:C:N4	31:A:293:G:O6	2.13	0.80
31:A:2805:G:N2	31:A:2805:G:OP2	2.14	0.80
8:G:45:ARG:O	8:G:52:VAL:HB	1.82	0.80
8:G:8:PRO:N	8:G:51:ILE:CD1	2.43	0.80
31:A:447:A:O2'	31:A:448:U:O4'	1.99	0.80
10:I:21:THR:HG22	10:I:22:ALA:H	1.46	0.79
31:A:2366:C:O2'	31:A:2368:C:N4	2.16	0.79
10:I:28:TYR:OH	31:A:1225:G:O4'	1.99	0.78
6:D:40:ARG:NH1	6:D:83:GLU:OE2	2.17	0.78
8:G:53:VAL:HG23	8:G:66:HIS:CE1	2.19	0.78
8:G:51:ILE:O	8:G:52:VAL:C	2.27	0.77
8:G:20:ASN:O	8:G:20:ASN:ND2	2.13	0.77
3:4:201:ARG:O	3:4:204:GLY:N	2.17	0.77
31:A:499:G:OP2	31:A:2630:A:O2'	2.02	0.77
10:I:93:ILE:HD12	10:I:105:ILE:HG21	1.67	0.76
31:A:218:A:N3	31:A:234:U:O2'	2.17	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1530:G:H21	31:A:1805:G:H22	1.34	0.76
31:A:103:C:HO2'	31:A:375:A:HO2'	1.33	0.76
31:A:1426:G:OP2	31:A:1426:G:N2	2.16	0.75
31:A:2482:U:O2'	31:A:2651:C:OP2	2.04	0.75
3:4:384:ARG:HD3	3:4:391:PHE:HE2	1.51	0.74
31:A:1825:C:N4	31:A:1840:G:OP2	2.19	0.74
31:A:2527:G:C6	31:A:2538:A:N6	2.56	0.74
6:D:38:ARG:NH2	31:A:3008:C:O2'	2.20	0.74
8:G:5:GLY:O	8:G:51:ILE:HG21	1.88	0.74
10:I:72:LEU:HD22	10:I:115:LEU:HD21	1.70	0.73
3:4:203:PRO:O	3:4:207:LYS:N	2.22	0.73
17:R:8:LEU:HD23	17:R:8:LEU:O	1.88	0.73
20:U:68:ARG:NH2	31:A:1449:C:OP1	2.21	0.73
31:A:1758:G:O2'	31:A:1759:A:O4'	2.06	0.73
13:M:84:ASN:OD1	13:M:85:LYS:N	2.22	0.73
22:W:9:ASN:ND2	22:W:66:ILE:O	2.21	0.73
31:A:1533:U:OP2	31:A:1536:A:N6	2.21	0.72
10:I:48:THR:HG23	10:I:49:TYR:H	1.53	0.72
31:A:285:U:O2'	31:A:287:A:OP1	2.06	0.72
7:E:128:THR:HG22	7:E:129:GLU:H	1.53	0.72
31:A:815:G:O2'	31:A:1850:A:N3	2.19	0.72
8:G:48:ASP:OD1	8:G:50:ALA:N	2.22	0.72
8:G:51:ILE:HD13	8:G:51:ILE:H	1.55	0.71
15:O:96:ARG:NH1	31:A:3103:A:OP1	2.22	0.71
10:I:10:VAL:HG22	10:I:56:LEU:HD11	1.72	0.71
31:A:2375:G:O2'	31:A:2376:G:O4'	2.04	0.71
31:A:544:U:O2	31:A:547:U:O2'	2.09	0.71
31:A:1196:C:O2'	31:A:1197:C:O5'	2.09	0.71
10:I:119:ASP:OD1	10:I:122:LYS:NZ	2.24	0.70
15:O:106:ASP:OD2	31:A:1867:G:O2'	2.10	0.70
3:4:384:ARG:HD3	3:4:391:PHE:CE2	2.25	0.70
8:G:8:PRO:N	8:G:51:ILE:HD11	2.04	0.70
3:4:331:VAL:HG22	3:4:367:VAL:HB	1.73	0.70
10:I:50:THR:HG22	10:I:50:THR:O	1.92	0.70
1:2:11:SER:OG	31:A:1107:G:OP2	2.09	0.69
31:A:2163:U:O2'	31:A:2164:U:N3	2.25	0.69
7:E:137:SER:O	7:E:168:SER:OG	2.10	0.69
31:A:392:A:O2'	31:A:393:U:OP2	2.06	0.69
31:A:1174:G:N2	31:A:1222:C:N3	2.40	0.69
31:A:378:G:O2'	31:A:424:G:N1	2.25	0.69
31:A:1545:C:N4	31:A:1623:U:O2	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:17:LEU:O	3:4:17:LEU:HD23	1.93	0.69
3:4:433:VAL:HG11	3:4:451:ILE:HD13	1.75	0.69
31:A:2754:G:OP2	31:A:2759:G:N2	2.26	0.69
3:4:208:ILE:O	3:4:209:GLU:C	2.36	0.68
31:A:1174:G:O2'	31:A:1204:A:O2'	2.04	0.68
7:E:41:GLN:NE2	7:E:184:ASN:OD1	2.26	0.68
27:c:28:ASN:ND2	27:c:31:ASN:OD1	2.27	0.68
10:I:59:ARG:NH1	31:A:1164:A:O4'	2.27	0.68
31:A:1932:U:O2'	31:A:1933:G:OP1	2.12	0.68
3:4:45:ARG:NH1	3:4:79:SER:O	2.27	0.67
5:C:209:ALA:HB2	31:A:2007:C:O2'	1.95	0.67
3:4:132:LEU:O	3:4:132:LEU:HD23	1.94	0.67
4:B:35:G:O2'	4:B:45:G:N7	2.24	0.67
31:A:2253:A:N6	31:A:2257:A:OP2	2.22	0.67
31:A:245:G:O2'	31:A:246:U:H5'	1.95	0.67
1:2:24:ARG:NH2	31:A:1044:U:O2	2.27	0.67
12:L:7:ARG:NE	12:L:18:GLU:OE2	2.27	0.67
10:I:59:ARG:NH2	31:A:1164:A:OP1	2.28	0.66
31:A:1177:G:N2	31:A:1199:U:O4	2.29	0.66
8:G:140:GLN:OE1	31:A:2983:G:N2	2.28	0.66
19:T:73:PRO:O	19:T:74:SER:OG	2.12	0.66
1:2:4:LEU:HD21	1:2:47:ILE:CD1	2.24	0.65
3:4:93:ASP:OD1	3:4:96:THR:O	2.14	0.65
31:A:283:U:O2	31:A:303:G:O6	2.13	0.65
6:D:7:LEU:HD23	6:D:207:VAL:HG22	1.77	0.65
31:A:3043:G:O2'	31:A:3045:C:OP2	2.11	0.65
31:A:103:C:O2'	31:A:375:A:O2'	2.02	0.65
10:I:40:ARG:NH2	10:I:48:THR:OG1	2.30	0.65
31:A:7:U:O2'	31:A:8:U:O4'	2.15	0.65
3:4:148:LEU:HD23	3:4:311:LEU:HD11	1.79	0.64
3:4:370:LYS:HA	32:4:501:GCP:O6	1.97	0.64
22:W:26:GLN:OE1	22:W:29:ARG:NH2	2.30	0.64
22:W:28:ARG:NH1	22:W:93:GLN:O	2.30	0.64
26:b:3:VAL:HG12	31:A:2239:A:C2	2.32	0.64
30:f:16:VAL:HG22	30:f:25:VAL:HG22	1.78	0.64
9:H:124:ILE:HG22	9:H:124:ILE:O	1.97	0.64
10:I:54:ASN:ND2	10:I:77:THR:O	2.29	0.64
10:I:31:LEU:HD12	10:I:31:LEU:O	1.97	0.63
9:H:38:VAL:HG13	9:H:38:VAL:O	1.97	0.63
10:I:51:VAL:HG23	10:I:78:ALA:HB1	1.80	0.63
31:A:2801:A:H5'	31:A:2802:G:C5'	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2529:A:O2'	31:A:2530:C:O5'	2.15	0.63
31:A:1198:C:N4	31:A:1206:A:OP1	2.31	0.63
29:e:28:ASN:O	29:e:36:LYS:NZ	2.31	0.63
8:G:51:ILE:C	8:G:53:VAL:N	2.50	0.63
17:R:77:ASN:ND2	31:A:1270:G:N3	2.47	0.63
29:e:26:LYS:HE3	29:e:48:THR:HG23	1.80	0.63
3:4:90:ASP:OD1	3:4:91:LYS:N	2.32	0.62
4:B:76:G:H21	22:W:94:HIS:CD2	2.17	0.62
8:G:51:ILE:HG12	8:G:52:VAL:H	1.63	0.62
8:G:7:GLN:C	8:G:51:ILE:HD11	2.21	0.62
13:M:82:ASP:OD1	13:M:83:ILE:N	2.32	0.62
31:A:2351:A:O2'	31:A:2352:C:O5'	2.14	0.62
31:A:287:A:OP2	31:A:299:G:N2	2.33	0.62
3:4:142:ASP:OD2	3:4:171:TYR:OH	2.17	0.62
3:4:163:GLN:NE2	3:4:313:GLU:O	2.32	0.62
31:A:1668:C:O2'	31:A:1764:A:N3	2.32	0.62
3:4:393:SER:C	3:4:395:ARG:H	2.07	0.62
8:G:20:ASN:HD22	8:G:20:ASN:C	2.04	0.61
31:A:1886:A:N3	31:A:1888:C:N4	2.47	0.61
16:Q:95:LYS:NZ	31:A:3068:U:OP1	2.29	0.61
21:V:9:VAL:HB	21:V:71:VAL:HG13	1.82	0.61
31:A:2328:G:N1	31:A:2408:G:O6	2.33	0.61
8:G:51:ILE:CB	8:G:53:VAL:HG22	2.20	0.61
10:I:21:THR:HG22	10:I:22:ALA:N	2.15	0.61
31:A:153:G:O6	31:A:171:U:O2	2.18	0.61
31:A:2538:A:H2'	31:A:2539:G:O4'	2.01	0.61
3:4:432:ARG:HA	3:4:435:THR:HG22	1.83	0.60
4:B:15:U:OP2	4:B:71:C:O2'	2.19	0.60
3:4:392:VAL:CG2	3:4:398:ASP:HB3	2.31	0.60
31:A:2332:U:O4	31:A:2394:A:O2'	2.16	0.60
5:C:158:SER:O	5:C:196:VAL:HG11	2.00	0.60
20:U:62:ARG:NH2	31:A:1455:U:OP2	2.35	0.60
31:A:2727:A:O2'	31:A:2729:G:OP2	2.19	0.60
31:A:176:G:N2	31:A:176:G:OP2	2.30	0.60
4:B:29:C:O2'	4:B:60:G:N2	2.35	0.60
10:I:117:VAL:HG13	10:I:118:ALA:H	1.65	0.60
3:4:253:TYR:O	3:4:258:LYS:NZ	2.35	0.60
20:U:36:ASP:OD1	20:U:36:ASP:O	2.20	0.60
3:4:32:GLU:HG2	3:4:80:GLU:OE2	2.02	0.59
31:A:2170:U:O2'	31:A:2185:C:O2	2.18	0.59
8:G:53:VAL:HG23	8:G:66:HIS:HE1	1.64	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:42:THR:HG21	31:A:2176:A:OP1	2.01	0.59
3:4:161:LYS:NZ	31:A:2707:C:OP1	2.34	0.59
4:B:111:C:H2'	4:B:112:C:H5'	1.84	0.59
3:4:84:GLY:O	3:4:86:ILE:HD12	2.02	0.59
31:A:1478:C:O2'	31:A:2026:A:N3	2.30	0.59
31:A:2422:A:N1	31:A:2450:C:N4	2.50	0.59
3:4:429:LEU:O	3:4:433:VAL:HG23	2.03	0.59
6:D:135:GLN:HE21	31:A:2802:G:H21	1.49	0.59
10:I:21:THR:HG21	10:I:82:VAL:HG13	1.85	0.59
20:U:26:ASP:OD1	20:U:26:ASP:O	2.21	0.59
3:4:393:SER:H	3:4:398:ASP:CB	2.16	0.59
10:I:16:GLN:O	10:I:16:GLN:NE2	2.35	0.59
8:G:80:VAL:HG12	8:G:80:VAL:O	2.03	0.59
8:G:119:PRO:O	8:G:122:ILE:HG22	2.03	0.58
9:H:135:LYS:C	9:H:136:LEU:HD12	2.28	0.58
3:4:93:ASP:O	3:4:95:SER:N	2.35	0.58
3:4:366:LEU:HD23	3:4:388:ASP:O	2.02	0.58
31:A:1076:A:O2'	31:A:1077:A:O5'	2.14	0.58
31:A:2335:G:O6	31:A:2392:A:N6	2.35	0.58
31:A:2179:U:O2'	31:A:2776:U:OP1	2.21	0.58
31:A:3014:A:H62	31:A:3113:A:H2	1.50	0.58
11:K:24:VAL:HG12	11:K:27:ARG:HD2	1.84	0.58
31:A:1294:U:HO2'	31:A:1295:U:H6	1.49	0.58
31:A:199:U:O2'	31:A:200:C:OP1	2.20	0.58
1:2:4:LEU:CD2	1:2:47:ILE:HD11	2.31	0.58
3:4:151:PHE:HE2	3:4:311:LEU:HD13	1.69	0.58
3:4:449:THR:HB	3:4:451:ILE:HG23	1.86	0.58
3:4:151:PHE:CE2	3:4:311:LEU:HD13	2.39	0.58
10:I:10:VAL:CG2	10:I:56:LEU:HD11	2.34	0.57
8:G:122:ILE:HD11	8:G:134:VAL:CG1	2.34	0.57
15:O:10:LEU:HD21	15:O:40:LYS:HG2	1.85	0.57
23:X:53:ARG:NH1	23:X:57:ASP:OD1	2.36	0.57
31:A:2819:G:N2	31:A:2822:A:OP2	2.34	0.57
14:N:23:GLY:O	14:N:101:ARG:NH2	2.37	0.57
22:W:10:LYS:H	22:W:68:THR:HG1	1.51	0.57
30:f:19:ARG:NE	31:A:2980:U:OP2	2.37	0.57
18:S:22:VAL:HG12	18:S:24:VAL:HG13	1.87	0.57
3:4:39:VAL:HG23	3:4:39:VAL:O	2.05	0.57
3:4:87:GLN:NE2	3:4:88:ARG:O	2.37	0.57
3:4:173:LEU:HD22	3:4:219:MET:HE1	1.85	0.57
5:C:271:ARG:NH2	5:C:274:THR:HG21	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1530:G:N2	31:A:1805:G:H22	2.00	0.57
10:I:69:LEU:HD11	10:I:73:PHE:CZ	2.40	0.56
3:4:329:ILE:HG23	3:4:367:VAL:HG23	1.85	0.56
4:B:78:U:OP1	22:W:28:ARG:NH2	2.38	0.56
8:G:8:PRO:CA	8:G:51:ILE:HD11	2.28	0.56
31:A:161:U:O2'	31:A:162:A:OP2	2.19	0.56
31:A:1063:G:O6	31:A:1090:G:N2	2.39	0.56
13:M:125:THR:HG23	13:M:125:THR:O	2.05	0.56
31:A:678:A:N1	31:A:924:G:O2'	2.36	0.56
31:A:1292:U:O2'	31:A:1293:G:O5'	2.23	0.56
31:A:2176:A:N3	31:A:2784:C:O2'	2.36	0.56
29:e:45:ASP:OD1	29:e:46:GLY:N	2.39	0.56
9:H:90:LYS:C	9:H:91:LEU:HD12	2.31	0.56
13:M:22:VAL:HB	13:M:33:ALA:HB1	1.88	0.56
11:K:125:TYR:OH	11:K:132:HIS:NE2	2.27	0.55
29:e:30:ARG:NH1	31:A:2618:C:OP2	2.39	0.55
3:4:83:GLU:OE2	3:4:85:LEU:HD21	2.07	0.55
9:H:11:HIS:NE2	31:A:2318:U:O3'	2.39	0.55
12:L:66:VAL:HG22	12:L:66:VAL:O	2.07	0.55
31:A:401:C:O2'	31:A:415:G:N2	2.40	0.55
31:A:2573:G:O6	31:A:2593:A:N6	2.40	0.55
31:A:2745:C:O2'	31:A:2788:A:N3	2.37	0.55
9:H:135:LYS:O	9:H:136:LEU:HD12	2.06	0.55
31:A:941:U:OP1	31:A:2652:G:H3'	2.06	0.55
31:A:1172:A:N6	31:A:1224:G:O6	2.40	0.55
31:A:402:G:N3	31:A:405:G:N1	2.55	0.55
31:A:1756:G:O5'	31:A:1758:G:N2	2.40	0.55
3:4:393:SER:H	3:4:398:ASP:HB2	1.72	0.54
3:4:32:GLU:O	3:4:82:LEU:HA	2.08	0.54
9:H:21:VAL:HG21	9:H:25:TYR:CD2	2.42	0.54
31:A:597:C:O2'	31:A:1351:G:OP1	2.21	0.54
31:A:287:A:O2'	31:A:288:U:O4'	2.24	0.54
3:4:168:GLN:HB3	3:4:208:ILE:HG13	1.89	0.54
31:A:2730:U:H3'	31:A:2730:U:O2	2.08	0.54
31:A:114:G:OP2	31:A:116:A:O2'	2.20	0.54
31:A:2333:G:OP1	31:A:2341:U:N3	2.40	0.54
17:R:4:VAL:HG22	31:A:1314:C:H1'	1.89	0.54
31:A:3020:U:O2'	31:A:3021:A:O5'	2.24	0.54
3:4:429:LEU:HD21	3:4:463:LEU:HD21	1.90	0.54
3:4:344:ASN:O	3:4:348:THR:HG23	2.07	0.54
31:A:1381:G:O2'	31:A:2236:G:O6	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:145:VAL:HG23	5:C:155:LEU:HD12	1.90	0.53
5:C:161:VAL:O	5:C:196:VAL:HG12	2.09	0.53
8:G:45:ARG:HG3	8:G:46:ALA:H	1.73	0.53
31:A:2847:G:OP1	31:A:3047:A:O2'	2.25	0.53
5:C:2:GLY:N	5:C:20:ASP:OD1	2.41	0.53
11:K:116:ARG:NH2	31:A:615:A:OP2	2.41	0.53
23:X:51:VAL:HG21	23:X:78:VAL:O	2.08	0.53
31:A:940:A:H2'	31:A:941:U:O4'	2.08	0.53
31:A:2338:G:N1	31:A:2342:A:OP1	2.42	0.53
3:4:262:LEU:HD22	3:4:299:ASP:OD2	2.09	0.53
3:4:250:ILE:O	3:4:300:THR:OG1	2.23	0.53
31:A:1291:G:H2'	31:A:1292:U:H4'	1.90	0.53
31:A:2801:A:H5'	31:A:2802:G:H5'	1.91	0.53
17:R:83:LEU:HD22	17:R:88:VAL:HG11	1.91	0.53
31:A:2357:A:H8	31:A:2380:G:H21	1.56	0.53
9:H:122:ALA:HB3	9:H:124:ILE:HD11	1.90	0.53
7:E:52:THR:HG22	7:E:53:LYS:H	1.74	0.52
8:G:17:VAL:O	8:G:17:VAL:HG23	2.08	0.52
10:I:51:VAL:HG23	10:I:78:ALA:CB	2.39	0.52
10:I:97:ALA:HB1	10:I:104:VAL:HA	1.91	0.52
22:W:40:HIS:ND1	22:W:40:HIS:O	2.43	0.52
31:A:227:A:N1	31:A:505:C:O2'	2.42	0.52
6:D:156:THR:HB	6:D:157:PRO:HD3	1.90	0.52
31:A:1188:A:H3'	31:A:1189:G:H3'	1.90	0.52
31:A:1402:A:O2'	31:A:1403:C:O5'	2.27	0.52
20:U:93:ILE:HG21	20:U:96:PHE:CE2	2.44	0.52
3:4:200:THR:O	3:4:201:ARG:HG2	2.09	0.52
10:I:26:THR:HB	10:I:103:LEU:HA	1.90	0.52
31:A:808:A:O2'	31:A:1468:A:N3	2.39	0.52
31:A:2528:G:N2	31:A:2537:C:O2	2.42	0.52
10:I:47:ALA:HB1	10:I:80:ALA:HB1	1.91	0.52
10:I:25:VAL:HB	10:I:77:THR:HB	1.91	0.52
10:I:56:LEU:HD13	31:A:1164:A:H1'	1.92	0.52
29:e:26:LYS:CE	29:e:48:THR:HG23	2.39	0.52
31:A:2799:C:H6	31:A:2799:C:O5'	1.93	0.52
31:A:1991:C:H2'	31:A:1991:C:O2	2.09	0.52
3:4:27:ALA:HA	3:4:85:LEU:HD23	1.91	0.51
3:4:365:LEU:HD12	3:4:388:ASP:HB2	1.92	0.51
10:I:117:VAL:HG13	10:I:118:ALA:N	2.25	0.51
10:I:24:VAL:HG23	10:I:82:VAL:HG12	1.92	0.51
10:I:47:ALA:CB	10:I:80:ALA:HB1	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:300:G:H22	31:A:303:G:H5'	1.76	0.51
31:A:1206:A:O2'	31:A:1207:G:OP1	2.22	0.51
8:G:158:TYR:O	8:G:160:GLY:N	2.43	0.51
9:H:88:THR:O	9:H:88:THR:HG22	2.11	0.51
10:I:46:SER:HB2	10:I:82:VAL:HG23	1.92	0.51
31:A:301:U:O2'	31:A:302:U:OP1	2.23	0.51
31:A:2230:C:O2'	31:A:3044:A:N3	2.43	0.51
10:I:90:ALA:O	10:I:94:LYS:HG2	2.11	0.51
31:A:2544:U:O2	31:A:2545:G:N1	2.42	0.51
3:4:390:VAL:HG22	3:4:391:PHE:N	2.26	0.51
5:C:160:GLY:H	5:C:196:VAL:HG13	1.76	0.51
3:4:105:GLU:O	3:4:109:VAL:HG23	2.10	0.51
3:4:251:VAL:O	3:4:330:HIS:HA	2.10	0.51
8:G:20:ASN:ND2	8:G:20:ASN:C	2.64	0.51
31:A:2510:A:H4'	31:A:2511:A:O4'	2.11	0.51
3:4:251:VAL:HG23	3:4:330:HIS:CB	2.40	0.51
31:A:920:G:N2	31:A:944:A:OP1	2.44	0.51
31:A:2963:U:H2'	31:A:2964:A:H5'	1.92	0.51
31:A:718:C:O2'	31:A:772:U:OP1	2.28	0.50
31:A:2006:A:H2'	31:A:2007:C:O4'	2.11	0.50
13:M:15:GLU:O	31:A:690:G:N2	2.43	0.50
23:X:56:ASP:O	23:X:57:ASP:HB2	2.11	0.50
31:A:327:U:O2	31:A:328:C:N4	2.43	0.50
22:W:71:ILE:HG22	22:W:72:GLU:H	1.76	0.50
31:A:1532:G:N2	31:A:1804:G:C4	2.79	0.50
31:A:2161:A:H61	31:A:2193:A:H61	1.59	0.50
3:4:433:VAL:HG22	3:4:459:LEU:HD21	1.94	0.50
30:f:8:LYS:NZ	31:A:2691:C:OP1	2.44	0.50
8:G:51:ILE:O	8:G:53:VAL:HG13	2.11	0.50
22:W:71:ILE:HG22	22:W:72:GLU:N	2.27	0.50
31:A:389:G:N1	31:A:392:A:OP2	2.36	0.50
31:A:637:G:O2'	31:A:638:U:OP2	2.20	0.50
31:A:2244:A:O2'	31:A:2246:U:OP2	2.13	0.50
3:4:124:LEU:HD12	3:4:142:ASP:OD1	2.12	0.50
3:4:300:THR:HG22	3:4:318:THR:HG23	1.93	0.50
3:4:364:GLU:O	3:4:365:LEU:C	2.54	0.50
5:C:158:SER:OG	5:C:159:ALA:N	2.45	0.50
10:I:47:ALA:HA	10:I:80:ALA:HB1	1.93	0.50
31:A:935:A:H4'	31:A:951:G:H22	1.77	0.50
31:A:996:G:H2'	31:A:997:G:C8	2.47	0.50
3:4:319:LEU:HD22	3:4:353:VAL:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:92:LEU:HD11	11:K:99:ARG:HD2	1.94	0.49
31:A:302:U:HO2'	31:A:303:G:H8	1.58	0.49
31:A:1221:A:OP2	31:A:1222:C:N4	2.45	0.49
16:Q:73:PHE:HB3	16:Q:80:ILE:HD11	1.93	0.49
30:f:2:LYS:NZ	30:f:31:ARG:O	2.45	0.49
31:A:2054:C:O2	31:A:2153:G:O2'	2.21	0.49
3:4:331:VAL:HG22	3:4:367:VAL:CB	2.40	0.49
3:4:442:THR:OG1	3:4:443:GLU:N	2.44	0.49
31:A:380:A:N6	31:A:404:A:O2'	2.40	0.49
31:A:1025:A:N3	31:A:2488:C:O2'	2.39	0.49
31:A:2050:C:H4'	31:A:2051:U:OP1	2.11	0.49
8:G:46:ALA:HA	8:G:52:VAL:HG21	1.93	0.49
9:H:66:ASN:O	9:H:136:LEU:HD23	2.12	0.49
23:X:38:VAL:HG12	23:X:40:GLN:OE1	2.13	0.49
31:A:940:A:H3'	31:A:940:A:C8	2.48	0.49
31:A:1630:U:O4	31:A:1631:A:N6	2.46	0.49
31:A:3107:G:O2'	31:A:3108:G:OP2	2.26	0.49
12:L:25:LEU:HD13	12:L:40:VAL:HG23	1.94	0.49
12:L:80:ASP:OD1	12:L:80:ASP:O	2.29	0.49
18:S:25:GLU:OE2	31:A:1111:G:N2	2.39	0.49
31:A:1402:A:C2'	31:A:1403:C:O5'	2.61	0.49
4:B:30:G:O2'	4:B:59:A:N1	2.44	0.49
3:4:34:ALA:HB3	3:4:48:ARG:NH1	2.28	0.49
3:4:332:VAL:HG21	3:4:343:ILE:CD1	2.42	0.49
9:H:26:GLY:O	9:H:31:LEU:HD13	2.13	0.49
31:A:1403:C:H2'	31:A:1403:C:O2	2.13	0.49
31:A:1530:G:H22	31:A:1805:G:H1	1.59	0.49
31:A:2727:A:C8	33:A:3201:CLM:CL1	3.03	0.49
3:4:49:VAL:HG12	3:4:117:THR:CG2	2.43	0.49
4:B:33:C:O2'	4:B:34:G:OP1	2.29	0.49
6:D:185:VAL:HG13	6:D:185:VAL:O	2.13	0.49
23:X:56:ASP:OD2	31:A:2588:C:H5'	2.13	0.49
31:A:2351:A:H2'	31:A:2352:C:H6	1.78	0.49
10:I:48:THR:HG23	10:I:49:TYR:N	2.24	0.49
29:e:5:LYS:NZ	31:A:253:C:OP2	2.39	0.49
31:A:388:U:H2'	31:A:389:G:O4'	2.13	0.49
13:M:20:THR:O	13:M:20:THR:HG23	2.11	0.48
4:B:116:C:H2'	4:B:117:A:O4'	2.12	0.48
5:C:99:ASP:O	31:A:1720:G:N2	2.45	0.48
31:A:1189:G:O2'	31:A:1190:C:O4'	2.24	0.48
31:A:2010:G:H2'	31:A:2011:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2387:U:O4	31:A:2394:A:N6	2.46	0.48
3:4:12:THR:O	3:4:12:THR:HG23	2.13	0.48
31:A:1179:U:O4'	31:A:1188:A:O4'	2.31	0.48
31:A:2630:A:OP2	31:A:2635:A:N6	2.39	0.48
9:H:124:ILE:O	9:H:126:SER:N	2.45	0.48
16:Q:15:ASP:C	16:Q:15:ASP:OD2	2.56	0.48
16:Q:18:THR:HG23	16:Q:18:THR:O	2.13	0.48
4:B:28:A:HO2'	4:B:29:C:P	2.35	0.48
31:A:2529:A:H2'	31:A:2530:C:C6	2.49	0.48
5:C:244:ARG:O	5:C:245:HIS:CG	2.67	0.48
31:A:378:G:H2'	31:A:379:G:C8	2.49	0.48
31:A:2351:A:O4'	31:A:2396:A:O2'	2.30	0.48
3:4:429:LEU:HD21	3:4:463:LEU:HD11	1.96	0.48
31:A:245:G:H2'	31:A:246:U:C6	2.48	0.48
31:A:3029:U:O2	31:A:3030:A:C8	2.67	0.47
3:4:251:VAL:HG11	3:4:322:VAL:HG22	1.96	0.47
5:C:235:GLY:HA2	5:C:240:THR:HB	1.96	0.47
8:G:48:ASP:OD1	8:G:49:GLY:N	2.47	0.47
15:O:90:ARG:NH2	15:O:118:GLU:O	2.46	0.47
21:V:81:THR:HG21	21:V:98:ALA:HB1	1.95	0.47
31:A:2043:C:H6	31:A:2043:C:O5'	1.96	0.47
3:4:97:TYR:CD2	3:4:124:LEU:HD21	2.49	0.47
3:4:400:LEU:C	3:4:402:LYS:N	2.70	0.47
4:B:115:A:H2'	4:B:116:C:O4'	2.14	0.47
31:A:326:A:N6	31:A:450:G:C6	2.83	0.47
31:A:2025:C:O2	31:A:2025:C:O4'	2.32	0.47
3:4:208:ILE:HD13	3:4:208:ILE:HA	1.75	0.47
3:4:399:GLY:O	3:4:402:LYS:HB2	2.14	0.47
9:H:95:VAL:HG12	9:H:96:THR:N	2.29	0.47
3:4:433:VAL:HG11	3:4:451:ILE:CD1	2.44	0.47
31:A:1804:G:H2'	31:A:1805:G:O4'	2.14	0.47
7:E:151:ASN:ND2	7:E:193:ASP:OD1	2.43	0.47
10:I:25:VAL:O	10:I:106:LYS:N	2.48	0.47
13:M:84:ASN:OD1	13:M:84:ASN:C	2.57	0.47
22:W:42:THR:HG22	22:W:42:THR:O	2.15	0.47
31:A:162:A:O2'	31:A:163:U:O5'	2.33	0.47
31:A:844:G:O2'	31:A:878:G:H4'	2.15	0.47
31:A:1069:G:C6	31:A:1083:G:C6	3.03	0.47
31:A:1163:A:H4'	31:A:1164:A:O5'	2.13	0.47
3:4:330:HIS:O	3:4:367:VAL:N	2.38	0.47
3:4:330:HIS:CG	3:4:346:VAL:HG11	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:99:ASP:OD1	10:I:99:ASP:N	2.42	0.47
31:A:163:U:HO2'	31:A:164:A:P	2.30	0.47
31:A:273:A:H62	31:A:313:G:H21	1.63	0.47
31:A:318:U:O2'	31:A:319:G:O5'	2.19	0.47
31:A:1289:A:H2'	31:A:1290:C:O4'	2.15	0.47
3:4:172:MET:HE2	3:4:210:THR:HG23	1.96	0.47
8:G:23:ASN:CG	8:G:23:ASN:O	2.57	0.47
31:A:979:G:H2'	31:A:980:C:C6	2.50	0.47
3:4:364:GLU:O	3:4:364:GLU:CD	2.58	0.47
9:H:5:LEU:O	9:H:16:GLY:N	2.44	0.47
17:R:89:GLU:HG3	17:R:89:GLU:O	2.15	0.47
3:4:258:LYS:HB2	32:4:501:GCP:O2B	2.15	0.46
6:D:161:PHE:O	6:D:164:THR:OG1	2.32	0.46
9:H:38:VAL:O	9:H:38:VAL:CG1	2.63	0.46
31:A:1350:G:O2'	31:A:1351:G:C8	2.66	0.46
31:A:1473:G:N1	31:A:1487:U:OP2	2.35	0.46
3:4:293:ARG:NH2	3:4:412:GLU:O	2.49	0.46
4:B:46:A:C4	4:B:47:A:C8	3.02	0.46
7:E:119:ALA:HB2	7:E:124:ILE:HD12	1.97	0.46
13:M:96:ASP:N	13:M:96:ASP:OD1	2.46	0.46
31:A:1203:A:O2'	31:A:1204:A:P	2.73	0.46
1:2:5:LYS:HB3	1:2:57:GLU:O	2.16	0.46
3:4:253:TYR:CD2	3:4:254:THR:HG22	2.50	0.46
31:A:243:U:O2	31:A:243:U:H2'	2.15	0.46
31:A:899:G:H5'	31:A:900:G:OP1	2.16	0.46
10:I:45:ASP:N	10:I:45:ASP:OD1	2.48	0.46
31:A:2573:G:C6	31:A:2593:A:C6	3.03	0.46
5:C:80:ALA:HB2	5:C:96:HIS:NE2	2.30	0.46
9:H:9:VAL:O	9:H:9:VAL:HG13	2.14	0.46
10:I:24:VAL:HG12	10:I:80:ALA:HB3	1.97	0.46
22:W:39:GLY:HA3	22:W:98:LEU:HD12	1.98	0.46
31:A:1167:C:N3	31:A:1168:A:N6	2.63	0.46
31:A:1856:C:O2	31:A:2922:U:O2'	2.33	0.46
31:A:2007:C:H2'	31:A:2008:A:C8	2.51	0.46
3:4:261:LEU:CD1	3:4:367:VAL:HG11	2.46	0.46
9:H:121:LYS:NZ	31:A:158:G:OP2	2.45	0.46
31:A:244:A:C2	31:A:255:A:C2	3.04	0.46
31:A:617:U:O2	31:A:617:U:C2'	2.64	0.46
3:4:254:THR:O	3:4:255:ASN:C	2.58	0.46
3:4:420:VAL:HG13	3:4:422:ILE:HG23	1.97	0.46
8:G:45:ARG:O	8:G:52:VAL:CB	2.61	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:124:ILE:CG2	9:H:148:VAL:HG21	2.45	0.46
15:O:45:ARG:HB3	15:O:46:PRO:HD3	1.98	0.46
31:A:1822:C:O2'	31:A:1828:A:N1	2.49	0.46
31:A:2328:G:C6	31:A:2408:G:O6	2.68	0.46
31:A:3019:C:N4	31:A:3024:A:C2	2.84	0.46
3:4:93:ASP:C	3:4:95:SER:N	2.73	0.46
10:I:31:LEU:O	10:I:32:THR:C	2.59	0.46
24:Y:36:VAL:HG11	24:Y:61:VAL:HG11	1.97	0.46
31:A:2411:U:H2'	31:A:2412:U:O4'	2.16	0.46
31:A:2827:G:C2	31:A:2828:U:C5	3.04	0.46
5:C:273:ARG:O	5:C:274:THR:OG1	2.18	0.46
10:I:50:THR:O	10:I:50:THR:CG2	2.62	0.46
31:A:1159:C:H2'	31:A:1160:G:H5'	1.97	0.46
31:A:1178:U:H4'	31:A:1179:U:H5'	1.97	0.46
31:A:2334:U:O2'	31:A:2342:A:OP1	2.34	0.46
3:4:158:ARG:NE	3:4:229:MET:HE2	2.31	0.46
9:H:3:LEU:HD13	9:H:36:ALA:HB1	1.98	0.46
10:I:51:VAL:O	10:I:51:VAL:HG13	2.16	0.46
19:T:8:PRO:HB2	19:T:71:LEU:HD21	1.98	0.46
31:A:1213:A:O2'	31:A:1214:A:C5'	2.64	0.46
4:B:81:U:H2'	4:B:82:A:C8	2.51	0.45
8:G:156:ASP:OD2	8:G:158:TYR:O	2.33	0.45
15:O:12:GLY:O	15:O:13:SER:OG	2.31	0.45
20:U:4:ILE:HD12	25:Z:22:LEU:HD22	1.98	0.45
10:I:43:LEU:HD13	10:I:46:SER:O	2.16	0.45
31:A:485:U:O2'	31:A:2454:G:N2	2.49	0.45
6:D:60:ARG:O	6:D:60:ARG:HG2	2.16	0.45
10:I:26:THR:HA	10:I:104:VAL:O	2.16	0.45
31:A:1202:A:N3	31:A:1223:U:H2'	2.31	0.45
31:A:2008:A:C2	31:A:2046:A:H4'	2.50	0.45
3:4:464:ARG:HD3	3:4:464:ARG:C	2.40	0.45
5:C:257:THR:O	5:C:257:THR:HG22	2.16	0.45
10:I:39:LEU:HD22	10:I:103:LEU:HB2	1.99	0.45
14:N:28:SER:O	14:N:134:ARG:NH2	2.49	0.45
22:W:11:LEU:HD11	22:W:57:VAL:HG11	1.98	0.45
31:A:2164:U:O2'	31:A:2165:C:OP2	2.27	0.45
2:3:22:PRO:HB3	31:A:1102:G:H2'	1.98	0.45
8:G:50:ALA:HB3	8:G:52:VAL:CG2	2.46	0.45
13:M:54:GLN:OE1	31:A:940:A:H1'	2.17	0.45
21:V:45:THR:O	31:A:571:A:O2'	2.32	0.45
31:A:399:G:H2'	31:A:400:C:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:765:G:C6	31:A:766:G:N7	2.85	0.45
3:4:201:ARG:O	3:4:202:GLY:C	2.58	0.45
3:4:293:ARG:HG3	3:4:438:HIS:CG	2.51	0.45
13:M:89:GLN:N	13:M:89:GLN:OE1	2.49	0.45
3:4:365:LEU:HD22	3:4:410:LEU:HD12	1.99	0.45
7:E:141:ALA:HB1	7:E:169:VAL:HG12	1.98	0.45
26:b:54:LEU:O	26:b:55:ASP:C	2.60	0.45
31:A:2158:C:H1'	31:A:2159:G:H2'	1.98	0.45
31:A:2178:G:O2'	31:A:2179:U:OP2	2.33	0.45
3:4:130:ASN:OD1	3:4:131:ALA:N	2.49	0.45
10:I:47:ALA:CA	10:I:80:ALA:HB1	2.46	0.45
31:A:107:G:C2	31:A:108:A:C8	3.05	0.45
3:4:329:ILE:HA	3:4:365:LEU:O	2.17	0.45
5:C:99:ASP:OD1	5:C:99:ASP:N	2.50	0.45
8:G:48:ASP:OD1	8:G:50:ALA:HB2	2.17	0.45
8:G:122:ILE:HD11	8:G:134:VAL:HG11	1.99	0.45
31:A:2366:C:H3'	31:A:2367:G:C5'	2.46	0.45
3:4:93:ASP:C	3:4:95:SER:H	2.21	0.45
9:H:136:LEU:HB2	9:H:140:VAL:HG13	1.98	0.45
31:A:1531:C:N4	31:A:1532:G:O6	2.50	0.45
31:A:1688:G:C6	31:A:1748:A:C2	3.05	0.45
7:E:144:PHE:O	7:E:147:THR:HG22	2.18	0.44
9:H:136:LEU:HD22	9:H:140:VAL:CG2	2.47	0.44
17:R:73:ASP:O	17:R:73:ASP:OD2	2.35	0.44
31:A:41:A:H2'	31:A:42:G:O4'	2.17	0.44
31:A:2031:G:OP2	31:A:2032:A:O2'	2.20	0.44
31:A:2378:U:O2'	31:A:2379:G:O4'	2.35	0.44
31:A:2998:C:H2'	31:A:2999:A:O4'	2.17	0.44
3:4:284:THR:HG22	3:4:298:THR:HG22	1.99	0.44
3:4:332:VAL:HG21	3:4:343:ILE:HD11	1.99	0.44
31:A:317:G:O2'	31:A:509:U:OP2	2.27	0.44
31:A:1640:A:H2'	31:A:1642:G:N7	2.32	0.44
31:A:2675:A:C2	33:A:3201:CLM:H8	2.53	0.44
7:E:167:LYS:O	31:A:403:U:H1'	2.17	0.44
31:A:551:G:N2	31:A:554:A:OP2	2.46	0.44
31:A:1437:A:N1	31:A:1448:C:O2'	2.46	0.44
31:A:2288:C:H2'	31:A:2289:C:H6	1.82	0.44
8:G:51:ILE:C	8:G:53:VAL:HG13	2.42	0.44
11:K:65:SER:OG	11:K:66:GLY:N	2.49	0.44
18:S:14:TYR:CE2	18:S:24:VAL:HG12	2.52	0.44
31:A:950:A:C4	31:A:951:G:C8	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:3014:A:N6	31:A:3113:A:OP2	2.51	0.44
9:H:124:ILE:O	9:H:124:ILE:CG2	2.64	0.44
9:H:132:VAL:CG1	9:H:144:VAL:HG23	2.46	0.44
13:M:147:LEU:C	13:M:147:LEU:HD12	2.43	0.44
18:S:64:VAL:HG22	18:S:97:LEU:HD23	1.99	0.44
31:A:2727:A:H8	33:A:3201:CLM:CL1	2.38	0.44
8:G:51:ILE:CD1	8:G:51:ILE:H	2.21	0.44
31:A:940:A:C2'	31:A:941:U:O5'	2.66	0.44
31:A:2153:G:H2'	31:A:2153:G:N3	2.32	0.44
31:A:2351:A:H2'	31:A:2352:C:C6	2.52	0.44
3:4:48:ARG:HB3	3:4:82:LEU:HD23	1.99	0.44
3:4:92:PRO:O	3:4:93:ASP:C	2.61	0.44
5:C:145:VAL:HG12	5:C:191:ALA:CB	2.48	0.44
31:A:1334:C:H2'	31:A:1335:G:O4'	2.18	0.44
31:A:2244:A:C2	31:A:2246:U:O4'	2.70	0.44
3:4:209:GLU:O	3:4:215:ILE:HD11	2.18	0.44
3:4:393:SER:C	3:4:395:ARG:N	2.72	0.44
12:L:25:LEU:CD1	12:L:40:VAL:HG23	2.48	0.44
14:N:42:ILE:CD1	14:N:97:VAL:HG11	2.48	0.44
31:A:9:U:H2'	31:A:9:U:O2	2.18	0.44
4:B:1:G:C2	4:B:2:U:C4	3.06	0.43
9:H:11:HIS:HE2	31:A:2319:G:P	2.41	0.43
30:f:5:PRO:O	30:f:36:GLN:NE2	2.51	0.43
31:A:137:G:H4'	31:A:138:A:OP1	2.17	0.43
31:A:1196:C:H4'	31:A:1197:C:OP1	2.18	0.43
31:A:1536:A:H2'	31:A:1537:U:O4'	2.18	0.43
3:4:291:ASP:OD1	3:4:291:ASP:N	2.46	0.43
5:C:186:ASP:OD2	5:C:188:ARG:NH2	2.51	0.43
6:D:185:VAL:HG23	6:D:192:LEU:HD23	2.00	0.43
8:G:51:ILE:CA	8:G:53:VAL:HG13	2.48	0.43
10:I:33:VAL:CG2	31:A:1173:G:O2'	2.66	0.43
29:e:32:LEU:O	29:e:36:LYS:HE3	2.18	0.43
31:A:284:G:N3	31:A:286:G:O2'	2.47	0.43
31:A:1001:C:C5	31:A:1002:C:H1'	2.53	0.43
31:A:1758:G:H2'	31:A:1759:A:C8	2.53	0.43
5:C:75:VAL:O	5:C:75:VAL:HG23	2.18	0.43
6:D:18:ASP:OD1	6:D:18:ASP:C	2.61	0.43
16:Q:26:ASN:OD1	16:Q:41:VAL:CG1	2.66	0.43
21:V:15:LYS:NZ	31:A:390:G:O2'	2.30	0.43
28:d:8:PHE:O	28:d:9:GLN:NE2	2.51	0.43
31:A:681:C:H2'	31:A:682:A:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2730:U:O2	31:A:2730:U:C2'	2.66	0.43
3:4:14:GLU:O	3:4:16:ALA:N	2.51	0.43
7:E:52:THR:HG22	7:E:53:LYS:N	2.33	0.43
26:b:16:ARG:NH2	31:A:1379:G:OP1	2.31	0.43
31:A:899:G:H4'	31:A:900:G:O5'	2.17	0.43
31:A:940:A:H2'	31:A:941:U:O5'	2.18	0.43
3:4:97:TYR:CG	3:4:124:LEU:HD21	2.53	0.43
3:4:392:VAL:HG22	3:4:393:SER:N	2.33	0.43
7:E:128:THR:HG22	7:E:129:GLU:N	2.28	0.43
10:I:23:THR:O	10:I:24:VAL:HG23	2.18	0.43
10:I:51:VAL:HG13	31:A:1202:A:C8	2.54	0.43
10:I:93:ILE:HD12	10:I:105:ILE:CG2	2.43	0.43
13:M:95:VAL:HG23	13:M:110:VAL:HG21	2.00	0.43
26:b:3:VAL:HG12	31:A:2239:A:N3	2.33	0.43
29:e:12:LYS:NZ	31:A:247:G:O6	2.39	0.43
31:A:709:U:O2	31:A:709:U:O4'	2.35	0.43
4:B:33:C:C2	4:B:52:G:N2	2.86	0.43
31:A:193:G:H2'	31:A:194:A:O4'	2.19	0.43
31:A:451:U:H2'	31:A:452:G:C8	2.54	0.43
31:A:1010:U:H3'	31:A:1012:C:H41	1.83	0.43
31:A:1083:G:O2'	31:A:1084:U:H5'	2.19	0.43
31:A:2288:C:H2'	31:A:2289:C:C6	2.53	0.43
31:A:2731:C:O2	31:A:2731:C:H2'	2.18	0.43
31:A:2787:U:C2	31:A:2789:A:OP2	2.71	0.43
3:4:36:VAL:O	3:4:37:SER:HB2	2.19	0.43
3:4:49:VAL:HG12	3:4:117:THR:HG21	2.00	0.43
17:R:83:LEU:HD22	17:R:88:VAL:CG1	2.49	0.43
27:c:9:PRO:HD2	27:c:27:LYS:O	2.19	0.43
31:A:663:A:N3	31:A:663:A:H2'	2.33	0.43
3:4:390:VAL:CG2	3:4:391:PHE:N	2.81	0.43
10:I:24:VAL:CG1	10:I:105:ILE:HG22	2.48	0.43
10:I:47:ALA:H	10:I:82:VAL:HA	1.84	0.43
31:A:2294:A:H2'	31:A:2295:C:C6	2.54	0.43
31:A:2963:U:C2'	31:A:2964:A:H5'	2.49	0.43
7:E:138:THR:OG1	31:A:403:U:O4'	2.36	0.43
10:I:31:LEU:O	10:I:36:LEU:HD23	2.19	0.43
10:I:56:LEU:HB2	31:A:1165:G:OP2	2.18	0.43
31:A:1173:G:H2'	31:A:1174:G:C8	2.54	0.43
31:A:2349:A:N6	31:A:2386:U:O4'	2.52	0.43
3:4:422:ILE:O	3:4:448:GLY:HA2	2.19	0.43
7:E:101:ARG:O	7:E:101:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:49:ASP:OD1	31:A:651:G:N2	2.52	0.43
18:S:64:VAL:HG22	18:S:97:LEU:CD2	2.49	0.43
31:A:241:A:H5'	31:A:243:U:H1'	2.00	0.43
31:A:243:U:C5	31:A:254:G:N2	2.87	0.43
31:A:714:U:O2	31:A:714:U:C2'	2.67	0.43
20:U:69:THR:OG1	20:U:72:GLY:O	2.34	0.42
31:A:1529:U:H2'	31:A:1530:G:O4'	2.19	0.42
31:A:2378:U:HO2'	31:A:2379:G:C1'	2.32	0.42
31:A:2706:A:C5	31:A:2707:C:C5	3.07	0.42
3:4:168:GLN:HB3	3:4:208:ILE:CG1	2.49	0.42
3:4:262:LEU:HD22	3:4:299:ASP:CG	2.44	0.42
10:I:75:GLY:C	10:I:77:THR:H	2.27	0.42
31:A:2351:A:O2'	31:A:2352:C:O4'	2.37	0.42
3:4:254:THR:OG1	3:4:255:ASN:N	2.52	0.42
3:4:395:ARG:O	3:4:396:THR:CB	2.67	0.42
5:C:20:ASP:OD1	5:C:20:ASP:N	2.52	0.42
7:E:150:GLU:OE2	7:E:150:GLU:C	2.62	0.42
8:G:22:GLN:OE1	8:G:43:VAL:HG22	2.19	0.42
31:A:1937:U:H2'	31:A:1938:G:O4'	2.20	0.42
31:A:2351:A:HO2'	31:A:2352:C:C5'	2.25	0.42
3:4:393:SER:O	3:4:395:ARG:N	2.52	0.42
4:B:113:G:H2'	4:B:114:A:C8	2.54	0.42
9:H:32:PRO:HB3	24:Y:64:ALA:HB3	2.00	0.42
20:U:14:PRO:HB3	20:U:96:PHE:HD1	1.84	0.42
31:A:7:U:H2'	31:A:8:U:C6	2.54	0.42
31:A:2186:C:H2'	31:A:2187:U:O4'	2.19	0.42
3:4:329:ILE:CG2	3:4:367:VAL:HG23	2.48	0.42
3:4:392:VAL:HA	3:4:398:ASP:CG	2.44	0.42
3:4:422:ILE:CD1	3:4:430:VAL:HG23	2.49	0.42
10:I:53:LYS:HE3	31:A:1224:G:OP2	2.18	0.42
10:I:58:LYS:HG3	10:I:70:ASP:HA	2.01	0.42
31:A:270:U:O2	31:A:270:U:H2'	2.19	0.42
31:A:2552:A:H2'	31:A:2553:G:C8	2.55	0.42
10:I:75:GLY:O	31:A:1225:G:O3'	2.37	0.42
17:R:47:TYR:OH	31:A:1110:C:OP1	2.36	0.42
18:S:71:PRO:O	18:S:73:ILE:HD12	2.20	0.42
31:A:783:G:H2'	31:A:785:A:H62	1.85	0.42
31:A:986:G:H2'	31:A:987:A:O4'	2.19	0.42
31:A:2299:C:OP2	31:A:2462:G:N2	2.47	0.42
3:4:132:LEU:HD23	3:4:132:LEU:C	2.45	0.42
5:C:256:ARG:HE	5:C:271:ARG:NH1	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:21:THR:CG2	10:I:22:ALA:H	2.23	0.42
17:R:26:GLY:O	17:R:30:ARG:NH1	2.52	0.42
25:Z:18:LEU:O	25:Z:22:LEU:HD13	2.20	0.42
31:A:273:A:C2	31:A:322:A:O4'	2.72	0.42
31:A:3059:G:C4	31:A:3060:A:C8	3.08	0.42
3:4:332:VAL:HG22	3:4:368:VAL:HG12	2.01	0.42
4:B:2:U:H2'	4:B:3:U:O5'	2.20	0.42
9:H:112:LEU:HD12	9:H:113:ASP:O	2.20	0.42
13:M:81:GLY:O	13:M:84:ASN:OD1	2.38	0.42
19:T:26:ARG:O	19:T:29:ASP:OD1	2.38	0.42
19:T:56:LYS:NZ	31:A:576:G:O2'	2.45	0.42
31:A:1158:U:H2'	31:A:1159:C:O4'	2.19	0.42
31:A:1172:A:C6	31:A:1224:G:C6	3.08	0.42
31:A:1382:U:O2	31:A:1382:U:H2'	2.20	0.42
31:A:1535:C:O2	31:A:1535:C:O4'	2.35	0.42
31:A:1932:U:HO2'	31:A:1933:G:P	2.40	0.42
11:K:135:GLN:NE2	31:A:3:A:N3	2.67	0.42
27:c:37:GLU:O	27:c:38:ILE:HG23	2.20	0.42
31:A:781:C:C4	31:A:782:U:O4	2.73	0.42
31:A:1002:C:C2'	31:A:1003:A:OP1	2.67	0.42
31:A:1198:C:HO2'	31:A:1199:U:H6	1.67	0.42
31:A:1762:C:H2'	31:A:1763:G:O4'	2.19	0.42
31:A:3046:C:O2	31:A:3046:C:O5'	2.38	0.42
5:C:130:ASN:OD1	5:C:131:LEU:N	2.53	0.42
10:I:28:TYR:OH	31:A:1225:G:C1'	2.67	0.42
14:N:42:ILE:HD12	14:N:97:VAL:HG11	2.01	0.42
31:A:447:A:H2'	31:A:448:U:C6	2.54	0.42
31:A:735:U:H2'	31:A:736:G:O4'	2.20	0.42
31:A:980:C:O2'	31:A:981:U:P	2.77	0.42
31:A:1122:C:H2'	31:A:1129:G:H2'	2.01	0.42
31:A:1758:G:O2'	31:A:1759:A:O5'	2.36	0.42
31:A:2490:A:H4'	31:A:2491:A:O5'	2.20	0.42
31:A:2521:C:O2	31:A:2521:C:H2'	2.19	0.42
3:4:251:VAL:HG23	3:4:330:HIS:HB2	2.02	0.41
6:D:150:SER:OG	31:A:2736:C:O2	2.38	0.41
9:H:75:LEU:HD21	9:H:104:ILE:HD12	2.02	0.41
10:I:28:TYR:OH	31:A:1224:G:N3	2.53	0.41
31:A:472:C:O2	31:A:472:C:H2'	2.20	0.41
31:A:1216:A:C5	31:A:1217:G:C8	3.08	0.41
31:A:2194:A:H4'	31:A:2195:U:O4'	2.20	0.41
31:A:2327:C:N4	31:A:2328:G:O6	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1087:G:H2'	31:A:1088:U:C6	2.55	0.41
31:A:1183:U:H3	31:A:1187:A:HO2'	1.68	0.41
31:A:1675:U:O2'	31:A:1676:G:N7	2.53	0.41
31:A:2346:G:O6	31:A:2397:C:N4	2.53	0.41
31:A:2801:A:H5'	31:A:2802:G:H5''	2.02	0.41
6:D:185:VAL:HG23	6:D:192:LEU:CD2	2.50	0.41
10:I:28:TYR:O	10:I:29:ARG:HB2	2.20	0.41
27:c:15:CYS:SG	27:c:16:GLU:N	2.93	0.41
31:A:2:A:C2	31:A:3119:A:C2	3.08	0.41
31:A:1444:U:OP2	31:A:1445:C:N4	2.53	0.41
31:A:2177:A:H3'	31:A:2178:G:C5'	2.51	0.41
4:B:112:C:O5'	4:B:113:G:OP2	2.37	0.41
7:E:9:THR:HG23	7:E:10:PRO:HD2	2.01	0.41
10:I:3:LYS:O	10:I:6:LYS:HG3	2.20	0.41
10:I:20:SER:O	10:I:21:THR:OG1	2.37	0.41
21:V:43:LYS:NZ	31:A:568:A:OP2	2.49	0.41
25:Z:16:ASP:OD1	25:Z:17:GLU:N	2.53	0.41
31:A:621:U:H2'	31:A:622:C:C6	2.55	0.41
31:A:729:C:O2'	31:A:733:U:OP1	2.36	0.41
31:A:940:A:C8	31:A:940:A:C3'	3.03	0.41
31:A:1009:U:O3'	31:A:1010:U:O4'	2.38	0.41
31:A:1083:G:O4'	31:A:2491:A:N6	2.53	0.41
3:4:150:ILE:HG21	3:4:277:PHE:HD2	1.84	0.41
3:4:204:GLY:C	3:4:207:LYS:H	2.29	0.41
3:4:369:ASN:O	3:4:370:LYS:CG	2.69	0.41
19:T:85:GLU:O	31:A:21:G:O2'	2.39	0.41
31:A:2729:G:O4'	33:A:3201:CLM:CL2	2.75	0.41
8:G:33:LEU:HD21	8:G:137:ILE:HD12	2.03	0.41
10:I:59:ARG:HD3	31:A:1164:A:H5'	2.03	0.41
17:R:109:LEU:O	17:R:112:VAL:HG22	2.21	0.41
25:Z:66:LEU:O	25:Z:66:LEU:HD23	2.21	0.41
31:A:361:A:H2'	31:A:362:A:O5'	2.20	0.41
31:A:997:G:O6	31:A:1010:U:H2'	2.20	0.41
3:4:417:THR:HG22	3:4:454:ARG:HG2	2.02	0.41
10:I:54:ASN:OD1	31:A:1225:G:H5''	2.21	0.41
19:T:65:ALA:O	19:T:69:GLU:O	2.39	0.41
22:W:71:ILE:O	22:W:72:GLU:C	2.63	0.41
31:A:93:A:H2'	31:A:94:G:O4'	2.21	0.41
31:A:244:A:C2	31:A:255:A:C4	3.09	0.41
31:A:2166:C:H4'	31:A:2168:U:OP1	2.20	0.41
5:C:222:ARG:NH1	31:A:2006:A:OP2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:69:LEU:HB2	10:I:72:LEU:HB2	2.03	0.41
31:A:239:U:C2'	31:A:240:G:H5'	2.50	0.41
31:A:619:C:O2	31:A:619:C:H2'	2.20	0.41
31:A:905:U:O2	31:A:905:U:H2'	2.21	0.41
31:A:1441:C:O2'	31:A:2234:G:O2'	2.37	0.41
31:A:2681:U:O2'	31:A:2682:G:H5'	2.21	0.41
1:2:22:SER:OG	1:2:49:THR:HG21	2.20	0.41
3:4:346:VAL:O	3:4:349:VAL:HG12	2.20	0.41
4:B:114:A:O5'	4:B:114:A:H8	2.04	0.41
7:E:198:VAL:HG13	7:E:199:GLU:N	2.36	0.41
9:H:75:LEU:HD12	9:H:76:GLY:N	2.36	0.41
26:b:53:ASP:OD1	26:b:53:ASP:N	2.54	0.41
31:A:215:A:C4	31:A:216:A:C8	3.09	0.41
31:A:1807:C:C2	31:A:1808:A:C8	3.09	0.41
31:A:2175:U:HO2'	31:A:2176:A:P	2.44	0.41
31:A:2603:G:H2'	31:A:2604:U:C6	2.56	0.41
31:A:2980:U:H4'	31:A:2981:A:OP1	2.21	0.41
8:G:4:ILE:O	8:G:70:ARG:HD3	2.21	0.41
17:R:77:ASN:OD1	31:A:1270:G:C2'	2.66	0.41
22:W:74:THR:HG22	22:W:75:GLU:N	2.35	0.41
31:A:125:C:O2'	31:A:126:C:OP2	2.27	0.41
31:A:401:C:H2'	31:A:402:G:H5'	2.03	0.41
31:A:658:U:C2'	31:A:659:U:O5'	2.70	0.41
31:A:1076:A:C2'	31:A:1077:A:O5'	2.69	0.41
31:A:1380:A:O4'	31:A:1382:U:C6	2.74	0.41
31:A:2248:C:H2'	31:A:2249:G:H8	1.85	0.41
31:A:2693:A:C6	31:A:2706:A:C8	3.09	0.41
31:A:3046:C:O2	31:A:3046:C:O4'	2.39	0.41
3:4:48:ARG:HB2	3:4:115:ALA:CB	2.51	0.40
6:D:212:ILE:HG23	6:D:213:LYS:N	2.35	0.40
7:E:171:ASN:ND2	31:A:406:A:OP1	2.55	0.40
9:H:112:LEU:HD12	9:H:112:LEU:C	2.46	0.40
13:M:49:MET:O	13:M:49:MET:HG2	2.20	0.40
31:A:294:G:N3	31:A:294:G:H2'	2.36	0.40
31:A:752:C:C2	31:A:753:A:C8	3.09	0.40
31:A:1203:A:HO2'	31:A:1204:A:P	2.35	0.40
3:4:21:ALA:HA	3:4:24:ARG:HD2	2.03	0.40
3:4:176:LEU:HG	3:4:176:LEU:O	2.21	0.40
3:4:256:ALA:HB1	3:4:331:VAL:HG12	2.03	0.40
8:G:128:SER:OG	8:G:129:PRO:HD2	2.21	0.40
10:I:43:LEU:HD12	10:I:44:GLY:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:118:LEU:O	14:N:122:ILE:HG13	2.22	0.40
31:A:1434:G:H2'	31:A:1435:C:C6	2.55	0.40
3:4:73:LEU:O	3:4:76:THR:HG22	2.21	0.40
3:4:93:ASP:OD2	3:4:99:GLY:HA2	2.21	0.40
3:4:232:ILE:HG23	31:A:2703:U:O2'	2.22	0.40
3:4:393:SER:OG	3:4:398:ASP:HB2	2.20	0.40
4:B:8:C:H2'	4:B:9:G:O4'	2.22	0.40
8:G:7:GLN:O	8:G:51:ILE:HG23	2.22	0.40
11:K:4:TYR:CD1	11:K:4:TYR:C	2.99	0.40
13:M:93:VAL:HG13	13:M:93:VAL:O	2.20	0.40
15:O:51:LEU:HD13	15:O:70:ILE:HD11	2.04	0.40
19:T:52:GLU:HB3	19:T:53:PRO:HD3	2.01	0.40
24:Y:18:VAL:HG22	24:Y:24:ARG:HG2	2.04	0.40
31:A:279:U:H2'	31:A:280:G:H8	1.86	0.40
31:A:410:U:C2'	31:A:411:G:OP1	2.69	0.40
3:4:400:LEU:O	3:4:401:ASP:C	2.62	0.40
3:4:449:THR:O	3:4:449:THR:HG22	2.21	0.40
10:I:87:VAL:HG11	10:I:124:ALA:O	2.21	0.40
31:A:81:A:C2	31:A:100:A:C5	3.09	0.40
31:A:598:U:H2'	31:A:599:G:C5'	2.50	0.40
31:A:783:G:C5'	31:A:784:G:OP2	2.70	0.40
31:A:1005:A:H2'	31:A:1006:G:H5'	2.04	0.40
31:A:1121:G:O2'	31:A:1128:A:N1	2.44	0.40
31:A:1212:U:H2'	31:A:1213:A:C8	2.56	0.40
31:A:2381:A:C4'	31:A:2382:G:OP2	2.69	0.40
31:A:2556:C:O2'	31:A:2559:A:O2'	2.37	0.40
31:A:2764:C:O2'	31:A:2964:A:N3	2.47	0.40
4:B:59:A:H2'	4:B:59:A:N3	2.37	0.40
6:D:156:THR:HB	6:D:157:PRO:CD	2.52	0.40
13:M:22:VAL:HG12	13:M:29:LYS:HD2	2.03	0.40
28:d:26:ARG:O	28:d:26:ARG:HG2	2.21	0.40
31:A:248:G:O2'	31:A:2656:A:OP1	2.30	0.40
31:A:502:C:N4	31:A:503:A:H62	2.19	0.40
31:A:1500:A:C4	31:A:1501:C:C5	3.10	0.40
31:A:2316:G:C2	31:A:2317:G:C8	3.09	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	57/61 (93%)	53 (93%)	4 (7%)	0	100	100
2	3	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
3	4	454/470 (97%)	389 (86%)	65 (14%)	0	100	100
5	C	273/278 (98%)	254 (93%)	19 (7%)	0	100	100
6	D	212/217 (98%)	202 (95%)	10 (5%)	0	100	100
7	E	207/215 (96%)	194 (94%)	13 (6%)	0	100	100
8	G	174/179 (97%)	156 (90%)	18 (10%)	0	100	100
9	H	149/151 (99%)	136 (91%)	13 (9%)	0	100	100
10	I	124/175 (71%)	85 (68%)	39 (32%)	0	100	100
11	K	144/147 (98%)	142 (99%)	2 (1%)	0	100	100
12	L	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
13	M	143/147 (97%)	130 (91%)	13 (9%)	0	100	100
14	N	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
15	O	116/199 (58%)	109 (94%)	7 (6%)	0	100	100
16	Q	111/113 (98%)	109 (98%)	2 (2%)	0	100	100
17	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
18	S	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
19	T	112/153 (73%)	106 (95%)	6 (5%)	0	100	100
20	U	95/100 (95%)	89 (94%)	6 (6%)	0	100	100
21	V	93/105 (89%)	83 (89%)	10 (11%)	0	100	100
22	W	93/215 (43%)	83 (89%)	10 (11%)	0	100	100
23	X	77/88 (88%)	76 (99%)	1 (1%)	0	100	100
24	Y	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
25	Z	62/77 (80%)	62 (100%)	0	0	100	100
26	b	52/57 (91%)	52 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	c	47/55 (86%)	47 (100%)	0	0	100	100
28	d	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
29	e	61/64 (95%)	61 (100%)	0	0	100	100
30	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
All	All	3491/3930 (89%)	3232 (93%)	259 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	2	52/54 (96%)	52 (100%)	0	100	100
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	359/372 (96%)	355 (99%)	4 (1%)	65	75
5	C	215/218 (99%)	215 (100%)	0	100	100
6	D	160/163 (98%)	160 (100%)	0	100	100
7	E	169/173 (98%)	169 (100%)	0	100	100
8	G	148/150 (99%)	144 (97%)	4 (3%)	39	61
9	H	90/116 (78%)	89 (99%)	1 (1%)	65	75
10	I	89/120 (74%)	89 (100%)	0	100	100
11	K	119/120 (99%)	119 (100%)	0	100	100
12	L	100/100 (100%)	100 (100%)	0	100	100
13	M	112/114 (98%)	112 (100%)	0	100	100
14	N	114/116 (98%)	114 (100%)	0	100	100
15	O	97/158 (61%)	97 (100%)	0	100	100
16	Q	100/100 (100%)	100 (100%)	0	100	100
17	R	97/99 (98%)	97 (100%)	0	100	100
18	S	81/83 (98%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	T	90/117 (77%)	90 (100%)	0	100	100
20	U	83/85 (98%)	83 (100%)	0	100	100
21	V	81/86 (94%)	81 (100%)	0	100	100
22	W	77/168 (46%)	77 (100%)	0	100	100
23	X	58/63 (92%)	58 (100%)	0	100	100
24	Y	50/51 (98%)	50 (100%)	0	100	100
25	Z	58/66 (88%)	58 (100%)	0	100	100
26	b	43/46 (94%)	43 (100%)	0	100	100
27	c	47/52 (90%)	47 (100%)	0	100	100
28	d	35/36 (97%)	35 (100%)	0	100	100
29	e	53/54 (98%)	53 (100%)	0	100	100
30	f	35/35 (100%)	35 (100%)	0	100	100
All	All	2830/3134 (90%)	2821 (100%)	9 (0%)	84	86

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	4	93	ASP
3	4	208	ILE
3	4	209	GLU
3	4	400	LEU
8	G	20	ASN
8	G	51	ILE
8	G	52	VAL
8	G	54	THR
9	H	140	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
2	3	23	ASN
3	4	338	ASN
3	4	444	HIS
5	C	53	HIS
5	C	81	HIS
5	C	201	GLN
6	D	130	HIS

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Mol	Chain	Res	Type
7	E	121	ASN
7	E	176	HIS
9	H	118	GLN
11	K	117	GLN
15	O	62	ASN
22	W	93	GLN
22	W	94	HIS
26	b	12	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	A	2947/3120 (94%)	623 (21%)	19 (0%)
4	B	117/118 (99%)	34 (29%)	3 (2%)
All	All	3064/3238 (94%)	657 (21%)	22 (0%)

All (657) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	B	2	U
4	B	3	U
4	B	4	A
4	B	5	C
4	B	8	C
4	B	9	G
4	B	12	C
4	B	13	C
4	B	14	A
4	B	26	A
4	B	27	A
4	B	28	A
4	B	29	C
4	B	33	C
4	B	34	G
4	B	42	C
4	B	43	C
4	B	44	C
4	B	46	A
4	B	53	A
4	B	57	U
4	B	58	A

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Mol	Chain	Res	Type
4	B	59	A
4	B	67	A
4	B	75	U
4	B	76	G
4	B	88	C
4	B	89	C
4	B	90	G
4	B	107	A
4	B	112	C
4	B	113	G
4	B	115	A
4	B	117	A
31	A	7	U
31	A	9	U
31	A	31	U
31	A	41	A
31	A	42	G
31	A	52	G
31	A	57	A
31	A	60	A
31	A	68	A
31	A	71	A
31	A	72	G
31	A	85	G
31	A	86	U
31	A	91	C
31	A	94	G
31	A	99	G
31	A	115	A
31	A	117	U
31	A	125	C
31	A	138	A
31	A	148	A
31	A	153	G
31	A	158	G
31	A	161	U
31	A	162	A
31	A	163	U
31	A	164	A
31	A	180	A
31	A	195	A
31	A	198	A

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Mol	Chain	Res	Type
31	A	199	U
31	A	200	C
31	A	214	G
31	A	215	A
31	A	221	A
31	A	222	A
31	A	227	A
31	A	229	U
31	A	230	G
31	A	233	A
31	A	243	U
31	A	244	A
31	A	248	G
31	A	265	A
31	A	270	U
31	A	271	A
31	A	274	C
31	A	282	A
31	A	285	U
31	A	286	G
31	A	288	U
31	A	289	A
31	A	290	C
31	A	291	C
31	A	292	G
31	A	295	U
31	A	296	A
31	A	300	G
31	A	301	U
31	A	302	U
31	A	303	G
31	A	313	G
31	A	314	G
31	A	315	U
31	A	319	G
31	A	326	A
31	A	327	U
31	A	329	U
31	A	330	U
31	A	331	U
31	A	336	C
31	A	337	U

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Mol	Chain	Res	Type
31	A	338	C
31	A	340	A
31	A	342	C
31	A	343	U
31	A	350	A
31	A	352	G
31	A	353	G
31	A	355	A
31	A	356	G
31	A	357	U
31	A	359	A
31	A	361	A
31	A	367	U
31	A	368	U
31	A	369	G
31	A	370	U
31	A	371	G
31	A	372	G
31	A	376	G
31	A	378	G
31	A	379	G
31	A	380	A
31	A	381	A
31	A	384	G
31	A	391	G
31	A	393	U
31	A	395	G
31	A	398	U
31	A	401	C
31	A	402	G
31	A	403	U
31	A	404	A
31	A	405	G
31	A	406	A
31	A	411	G
31	A	412	A
31	A	413	G
31	A	420	G
31	A	423	C
31	A	424	G
31	A	426	G
31	A	427	A

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Mol	Chain	Res	Type
31	A	434	G
31	A	437	G
31	A	438	U
31	A	445	U
31	A	446	G
31	A	447	A
31	A	449	G
31	A	452	G
31	A	453	U
31	A	454	U
31	A	459	A
31	A	460	G
31	A	471	C
31	A	474	G
31	A	482	U
31	A	493	U
31	A	494	G
31	A	499	G
31	A	500	A
31	A	503	A
31	A	505	C
31	A	509	U
31	A	512	G
31	A	543	U
31	A	544	U
31	A	553	G
31	A	561	G
31	A	569	G
31	A	572	C
31	A	578	G
31	A	591	G
31	A	592	A
31	A	594	U
31	A	595	A
31	A	596	C
31	A	597	C
31	A	599	G
31	A	614	C
31	A	617	U
31	A	618	C
31	A	619	C
31	A	620	G

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Mol	Chain	Res	Type
31	A	636	U
31	A	637	G
31	A	638	U
31	A	639	C
31	A	640	G
31	A	642	G
31	A	655	G
31	A	659	U
31	A	660	U
31	A	662	G
31	A	665	G
31	A	667	A
31	A	678	A
31	A	679	G
31	A	684	G
31	A	696	A
31	A	706	G
31	A	707	G
31	A	708	G
31	A	715	A
31	A	721	A
31	A	731	A
31	A	739	U
31	A	740	A
31	A	747	A
31	A	755	A
31	A	757	G
31	A	758	A
31	A	759	G
31	A	760	U
31	A	766	G
31	A	784	G
31	A	801	U
31	A	829	U
31	A	845	C
31	A	862	U
31	A	879	A
31	A	880	G
31	A	890	G
31	A	891	G
31	A	897	A
31	A	899	G

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Mol	Chain	Res	Type
31	A	900	G
31	A	907	A
31	A	920	G
31	A	921	C
31	A	927	C
31	A	928	U
31	A	940	A
31	A	941	U
31	A	942	U
31	A	974	G
31	A	981	U
31	A	982	A
31	A	987	A
31	A	994	A
31	A	995	U
31	A	996	G
31	A	1002	C
31	A	1003	A
31	A	1005	A
31	A	1008	G
31	A	1010	U
31	A	1011	A
31	A	1025	A
31	A	1030	C
31	A	1034	U
31	A	1042	A
31	A	1046	C
31	A	1047	A
31	A	1048	A
31	A	1049	G
31	A	1058	A
31	A	1063	G
31	A	1075	U
31	A	1076	A
31	A	1077	A
31	A	1078	G
31	A	1085	G
31	A	1090	G
31	A	1091	A
31	A	1092	G
31	A	1097	A
31	A	1101	A

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Mol	Chain	Res	Type
31	A	1110	C
31	A	1114	G
31	A	1131	G
31	A	1144	A
31	A	1151	U
31	A	1159	C
31	A	1160	G
31	A	1161	C
31	A	1162	G
31	A	1164	A
31	A	1165	G
31	A	1170	C
31	A	1172	A
31	A	1173	G
31	A	1175	A
31	A	1176	G
31	A	1177	G
31	A	1178	U
31	A	1179	U
31	A	1180	G
31	A	1181	G
31	A	1182	C
31	A	1184	U
31	A	1188	A
31	A	1189	G
31	A	1191	A
31	A	1192	G
31	A	1194	C
31	A	1197	C
31	A	1201	G
31	A	1202	A
31	A	1203	A
31	A	1204	A
31	A	1205	G
31	A	1206	A
31	A	1207	G
31	A	1208	U
31	A	1212	U
31	A	1213	A
31	A	1214	A
31	A	1215	U
31	A	1216	A

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Mol	Chain	Res	Type
31	A	1217	G
31	A	1222	C
31	A	1223	U
31	A	1224	G
31	A	1240	G
31	A	1245	U
31	A	1247	A
31	A	1248	U
31	A	1250	U
31	A	1253	C
31	A	1254	G
31	A	1260	C
31	A	1262	A
31	A	1277	C
31	A	1292	U
31	A	1293	G
31	A	1294	U
31	A	1295	U
31	A	1307	G
31	A	1316	U
31	A	1335	G
31	A	1343	G
31	A	1344	A
31	A	1351	G
31	A	1365	G
31	A	1368	A
31	A	1371	G
31	A	1377	A
31	A	1386	G
31	A	1387	A
31	A	1400	G
31	A	1403	C
31	A	1408	C
31	A	1415	A
31	A	1416	A
31	A	1436	C
31	A	1465	C
31	A	1466	C
31	A	1467	U
31	A	1480	A
31	A	1494	U
31	A	1499	A

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Mol	Chain	Res	Type
31	A	1501	C
31	A	1502	G
31	A	1510	A
31	A	1511	U
31	A	1527	U
31	A	1532	G
31	A	1534	C
31	A	1536	A
31	A	1538	G
31	A	1541	G
31	A	1542	A
31	A	1543	A
31	A	1544	U
31	A	1624	U
31	A	1629	G
31	A	1631	A
31	A	1632	G
31	A	1640	A
31	A	1648	A
31	A	1649	C
31	A	1679	A
31	A	1680	A
31	A	1681	U
31	A	1703	G
31	A	1710	A
31	A	1711	G
31	A	1712	G
31	A	1713	U
31	A	1714	A
31	A	1717	U
31	A	1729	A
31	A	1730	U
31	A	1737	A
31	A	1738	G
31	A	1753	C
31	A	1754	G
31	A	1755	A
31	A	1756	G
31	A	1769	G
31	A	1780	G
31	A	1786	G
31	A	1788	G

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Mol	Chain	Res	Type
31	A	1789	A
31	A	1798	U
31	A	1803	A
31	A	1811	C
31	A	1825	C
31	A	1826	A
31	A	1828	A
31	A	1831	A
31	A	1852	A
31	A	1864	U
31	A	1866	C
31	A	1869	G
31	A	1870	U
31	A	1871	G
31	A	1872	A
31	A	1884	G
31	A	1887	A
31	A	1891	G
31	A	1892	G
31	A	1911	U
31	A	1933	G
31	A	1945	U
31	A	1946	U
31	A	1947	U
31	A	1949	C
31	A	1950	G
31	A	1955	A
31	A	1967	G
31	A	1974	A
31	A	1975	A
31	A	1981	U
31	A	1990	A
31	A	2001	A
31	A	2017	C
31	A	2018	G
31	A	2025	C
31	A	2033	U
31	A	2046	A
31	A	2049	C
31	A	2051	U
31	A	2052	G
31	A	2053	C

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Mol	Chain	Res	Type
31	A	2055	C
31	A	2152	A
31	A	2153	G
31	A	2154	G
31	A	2155	U
31	A	2156	A
31	A	2158	C
31	A	2159	G
31	A	2160	A
31	A	2162	A
31	A	2163	U
31	A	2164	U
31	A	2165	C
31	A	2166	C
31	A	2167	U
31	A	2168	U
31	A	2169	G
31	A	2170	U
31	A	2171	C
31	A	2176	A
31	A	2177	A
31	A	2178	G
31	A	2182	C
31	A	2184	A
31	A	2186	C
31	A	2188	G
31	A	2189	C
31	A	2190	A
31	A	2191	C
31	A	2192	G
31	A	2193	A
31	A	2194	A
31	A	2195	U
31	A	2196	G
31	A	2197	G
31	A	2215	U
31	A	2217	U
31	A	2220	C
31	A	2221	A
31	A	2246	U
31	A	2247	A
31	A	2255	A

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Mol	Chain	Res	Type
31	A	2256	G
31	A	2257	A
31	A	2258	U
31	A	2267	C
31	A	2275	A
31	A	2279	C
31	A	2280	G
31	A	2284	A
31	A	2285	G
31	A	2286	A
31	A	2315	U
31	A	2316	G
31	A	2320	C
31	A	2321	U
31	A	2323	G
31	A	2325	U
31	A	2326	A
31	A	2331	U
31	A	2332	U
31	A	2333	G
31	A	2335	G
31	A	2336	U
31	A	2338	G
31	A	2339	G
31	A	2340	A
31	A	2341	U
31	A	2342	A
31	A	2343	G
31	A	2345	U
31	A	2348	G
31	A	2349	A
31	A	2350	G
31	A	2351	A
31	A	2353	U
31	A	2354	G
31	A	2355	U
31	A	2356	G
31	A	2357	A
31	A	2361	U
31	A	2362	C
31	A	2367	G
31	A	2368	C

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Mol	Chain	Res	Type
31	A	2369	C
31	A	2370	A
31	A	2373	G
31	A	2375	G
31	A	2377	G
31	A	2380	G
31	A	2382	G
31	A	2384	C
31	A	2387	U
31	A	2388	G
31	A	2390	U
31	A	2391	G
31	A	2392	A
31	A	2393	A
31	A	2394	A
31	A	2395	U
31	A	2396	A
31	A	2398	C
31	A	2400	C
31	A	2402	C
31	A	2403	U
31	A	2404	G
31	A	2405	A
31	A	2410	A
31	A	2415	G
31	A	2422	A
31	A	2427	G
31	A	2434	A
31	A	2436	A
31	A	2449	A
31	A	2462	G
31	A	2463	G
31	A	2470	A
31	A	2507	C
31	A	2510	A
31	A	2511	A
31	A	2512	A
31	A	2529	A
31	A	2530	C
31	A	2531	G
31	A	2532	G
31	A	2533	C

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Mol	Chain	Res	Type
31	A	2534	A
31	A	2540	G
31	A	2546	A
31	A	2549	G
31	A	2558	C
31	A	2559	A
31	A	2571	C
31	A	2574	C
31	A	2585	U
31	A	2601	A
31	A	2607	G
31	A	2609	A
31	A	2620	G
31	A	2623	A
31	A	2647	U
31	A	2649	A
31	A	2652	G
31	A	2653	G
31	A	2654	A
31	A	2665	C
31	A	2672	A
31	A	2693	A
31	A	2699	C
31	A	2700	A
31	A	2703	U
31	A	2704	C
31	A	2715	U
31	A	2726	G
31	A	2729	G
31	A	2730	U
31	A	2737	G
31	A	2742	A
31	A	2744	C
31	A	2753	G
31	A	2755	A
31	A	2758	A
31	A	2766	A
31	A	2775	C
31	A	2776	U
31	A	2777	G
31	A	2778	U
31	A	2779	U

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Mol	Chain	Res	Type
31	A	2789	A
31	A	2790	A
31	A	2791	G
31	A	2796	A
31	A	2801	A
31	A	2826	A
31	A	2833	U
31	A	2834	C
31	A	2837	U
31	A	2839	U
31	A	2847	G
31	A	2854	A
31	A	2878	A
31	A	2884	A
31	A	2885	G
31	A	2893	G
31	A	2915	C
31	A	2926	A
31	A	2936	C
31	A	2938	G
31	A	2950	C
31	A	2957	A
31	A	2964	A
31	A	2968	G
31	A	2972	A
31	A	2982	A
31	A	2989	A
31	A	3002	A
31	A	3013	C
31	A	3015	C
31	A	3021	A
31	A	3022	G
31	A	3023	G
31	A	3024	A
31	A	3029	U
31	A	3042	A
31	A	3082	U
31	A	3088	C
31	A	3093	A
31	A	3101	C
31	A	3104	A
31	A	3105	C

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Mol	Chain	Res	Type
31	A	3108	G
31	A	3112	A
31	A	3115	A
31	A	3119	A
31	A	3120	C

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	B	2	U
4	B	28	A
4	B	33	C
31	A	137	G
31	A	199	U
31	A	228	A
31	A	326	A
31	A	448	U
31	A	571	A
31	A	879	A
31	A	899	G
31	A	940	A
31	A	942	U
31	A	980	C
31	A	981	U
31	A	1163	A
31	A	1196	C
31	A	1204	A
31	A	2050	C
31	A	2339	G
31	A	2356	G
31	A	2381	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

2 ligands are modelled in this entry.

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
33	CLM	A	3201	-	20,20,20	0.76	1 (5%)	23,27,27	1.57	4 (17%)
32	GCP	4	501	-	32,34,34	1.37	7 (21%)	49,54,54	1.81	8 (16%)

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
33	CLM	A	3201	-	-	3/20/22/22	0/1/1/1
32	GCP	4	501	-	-	2/19/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	4	501	GCP	C6-N1	-2.78	1.33	1.38
32	4	501	GCP	C5-C4	2.73	1.46	1.38
32	4	501	GCP	PG-O3G	2.62	1.60	1.55
32	4	501	GCP	PG-O2G	2.36	1.60	1.55
32	4	501	GCP	C5-N7	-2.29	1.34	1.39
33	A	3201	CLM	O9A-N9	-2.13	1.21	1.35
32	4	501	GCP	C4-N9	-2.03	1.32	1.38
32	4	501	GCP	PB-O1B	-2.01	1.46	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	4	501	GCP	C5-C4-N3	-5.87	119.04	128.39
32	4	501	GCP	PB-O3A-PA	-4.93	116.28	132.37
32	4	501	GCP	C2-N3-C4	4.92	120.78	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	4	501	GCP	N9-C4-N3	4.44	134.84	125.95
33	A	3201	CLM	C3-N2-C2	-4.20	115.94	123.25
33	A	3201	CLM	C5-C3-N2	3.66	116.64	110.03
32	4	501	GCP	C6-C5-N7	3.36	136.41	130.29
33	A	3201	CLM	C6-C5-C3	3.35	117.73	111.72
33	A	3201	CLM	O5-C5-C3	2.53	114.62	107.90
32	4	501	GCP	C4-C5-N7	-2.36	106.93	110.67
32	4	501	GCP	O6-C6-C5	-2.31	120.44	126.53
32	4	501	GCP	C5-C6-N1	2.13	118.67	113.25

There are no chirality outliers.

All (5) torsion outliers are listed below:

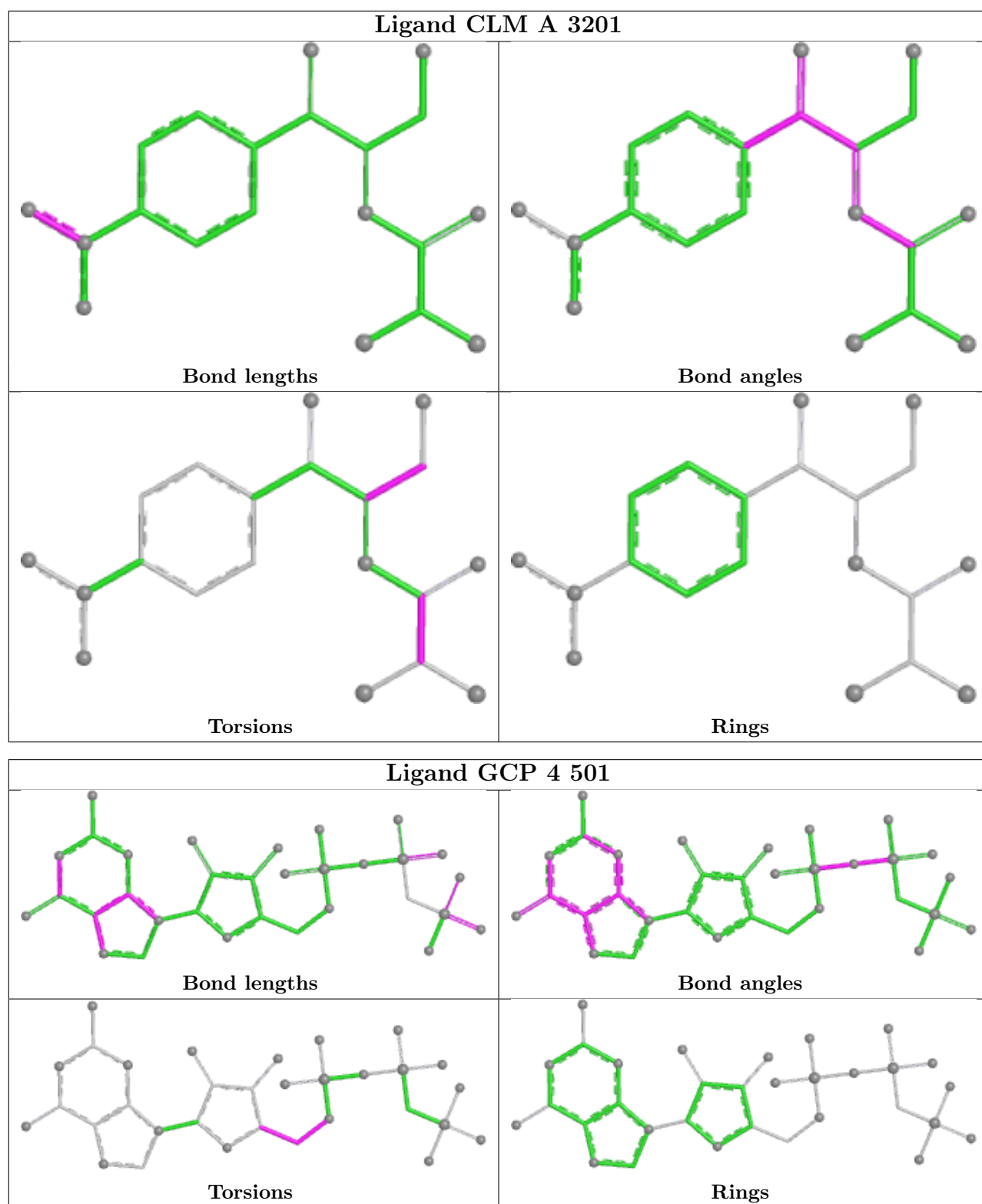
Mol	Chain	Res	Type	Atoms
33	A	3201	CLM	CL2-C1-C2-N2
32	4	501	GCP	C4'-C5'-O5'-PA
33	A	3201	CLM	N2-C3-C4-O4
32	4	501	GCP	O4'-C4'-C5'-O5'
33	A	3201	CLM	CL2-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	A	3201	CLM	4	0
32	4	501	GCP	3	0

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

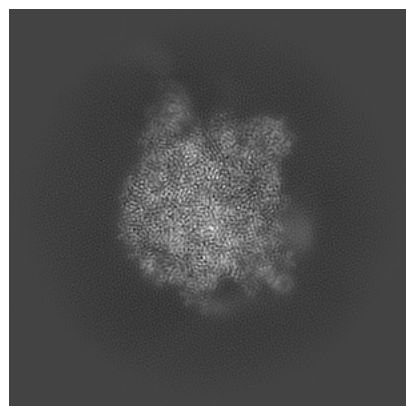
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43477. These allow visual inspection of the internal detail of the map and identification of artifacts.

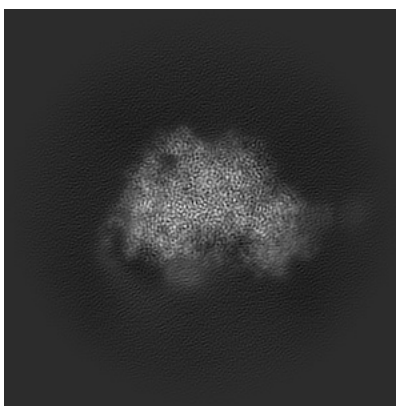
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

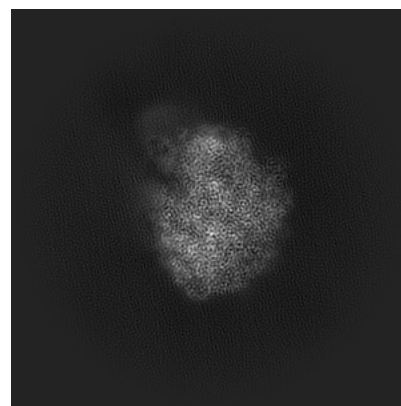
6.1.1 Primary map



X

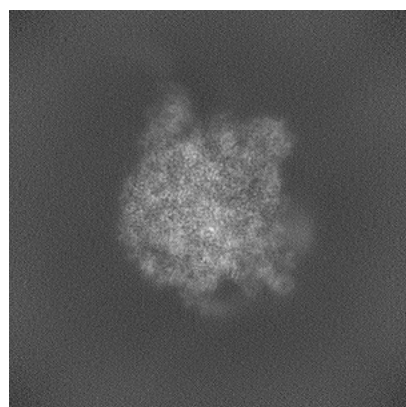


Y

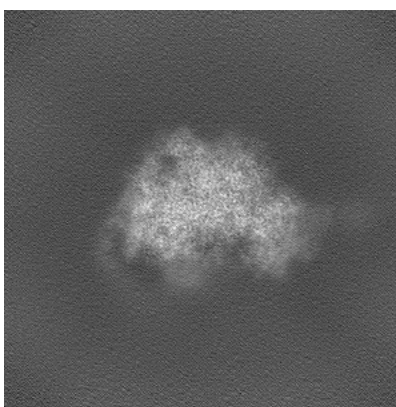


Z

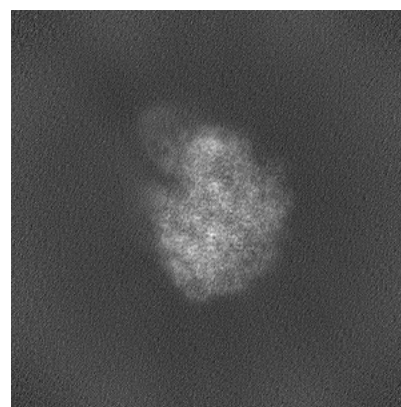
6.1.2 Raw map



X



Y

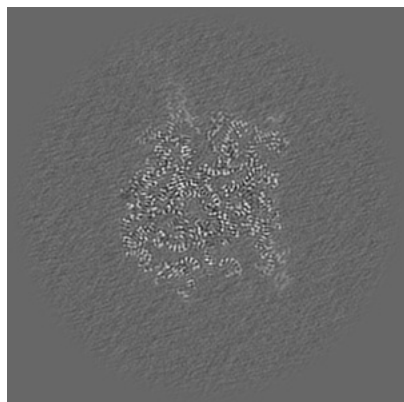


Z

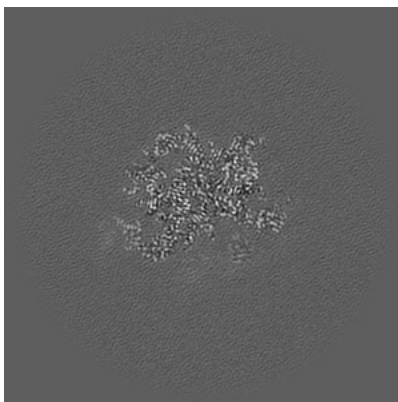
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

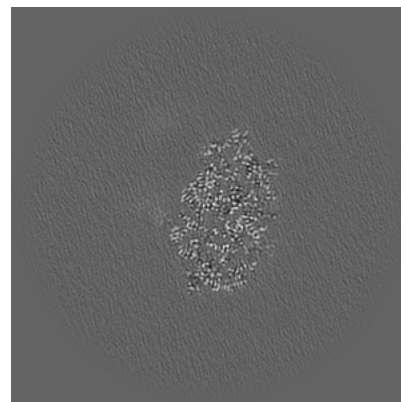
6.2.1 Primary map



X Index: 256

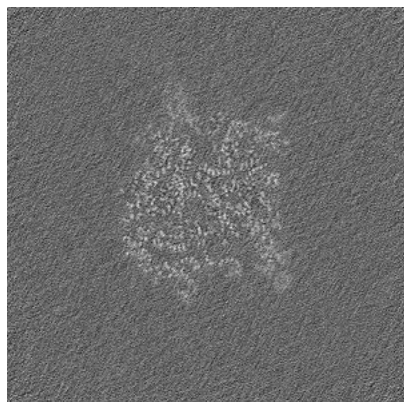


Y Index: 256

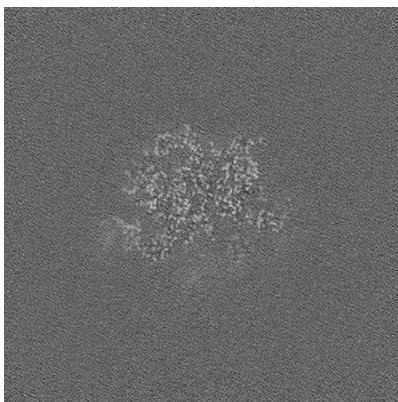


Z Index: 256

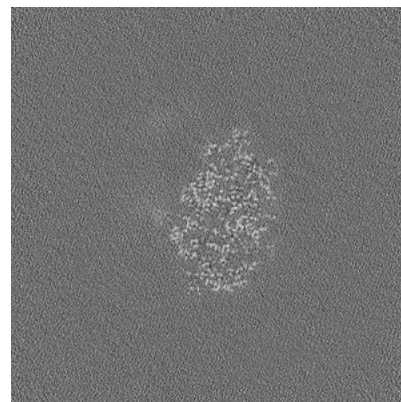
6.2.2 Raw map



X Index: 256



Y Index: 256

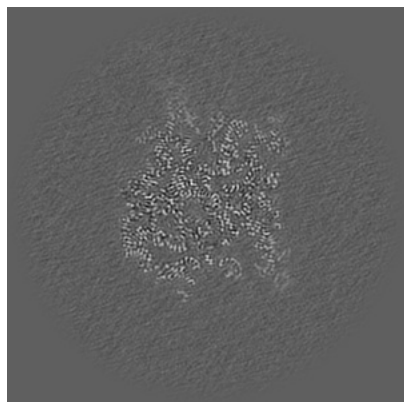


Z Index: 256

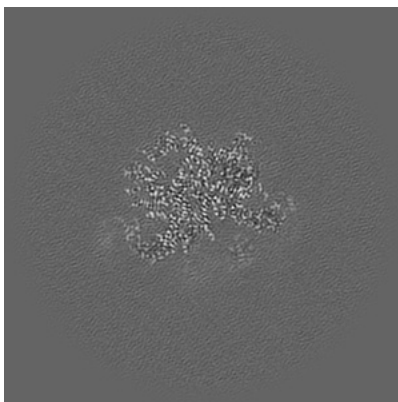
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

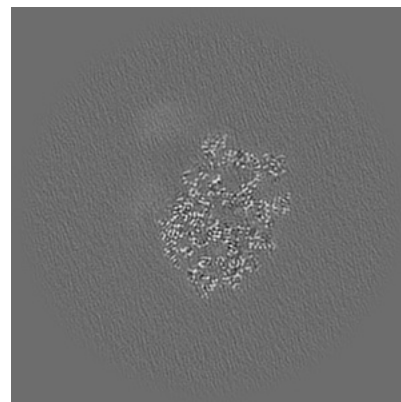
6.3.1 Primary map



X Index: 255

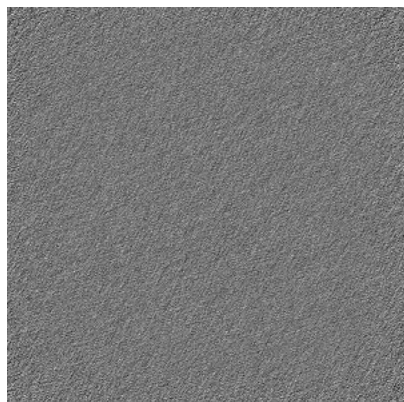


Y Index: 258

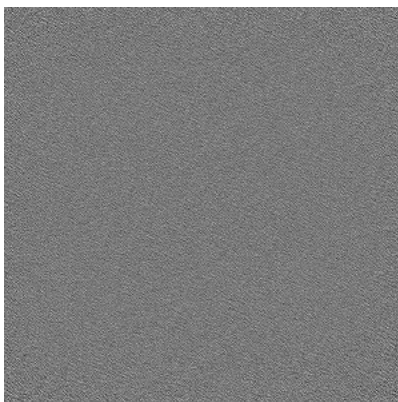


Z Index: 238

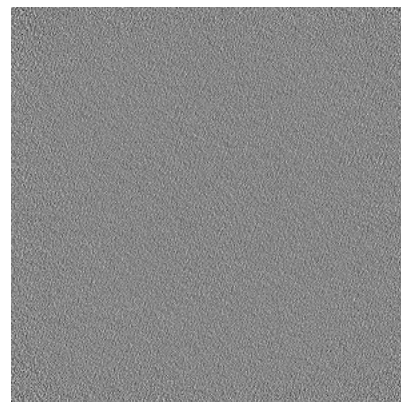
6.3.2 Raw map



X Index: 0



Y Index: 0

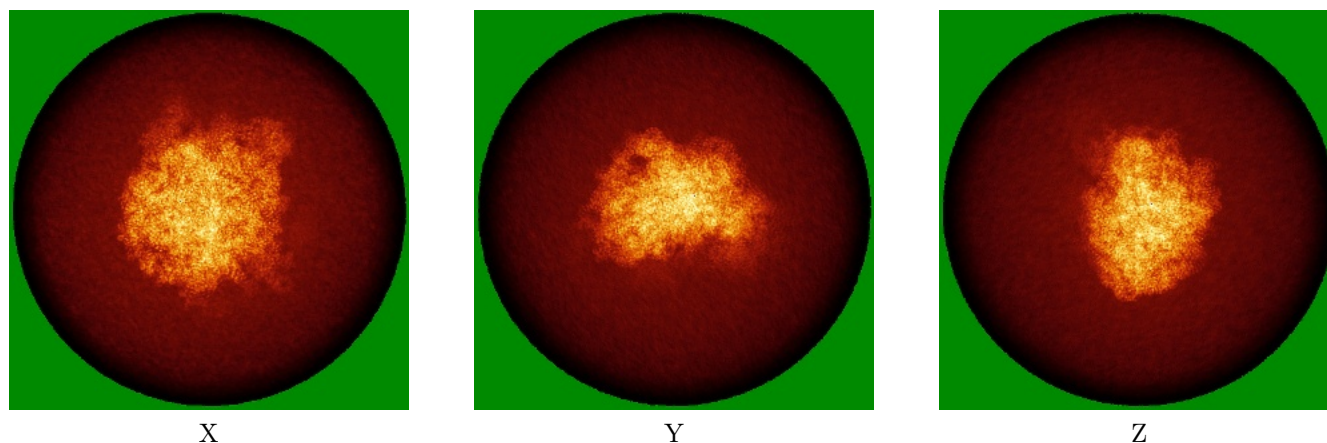


Z Index: 0

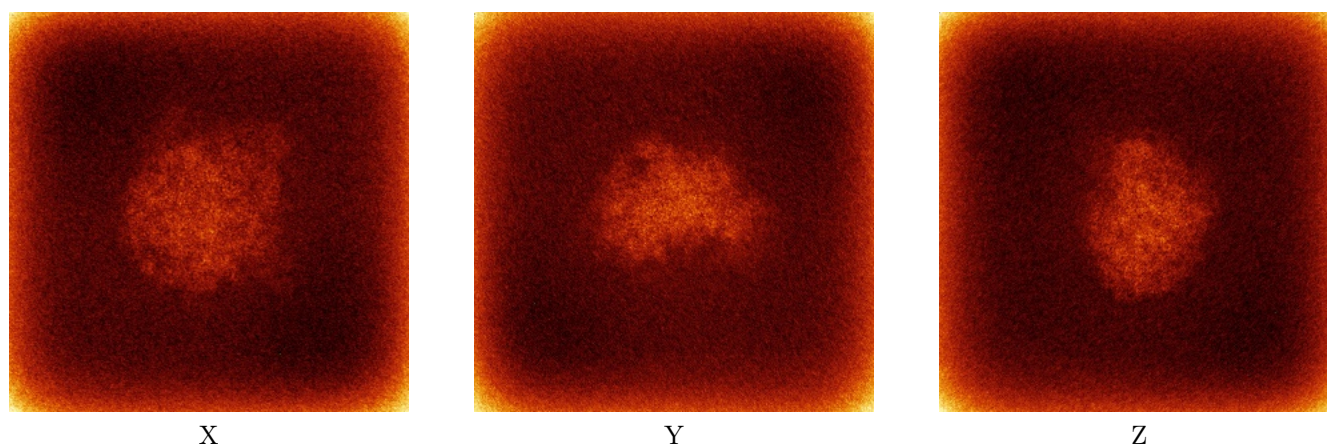
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

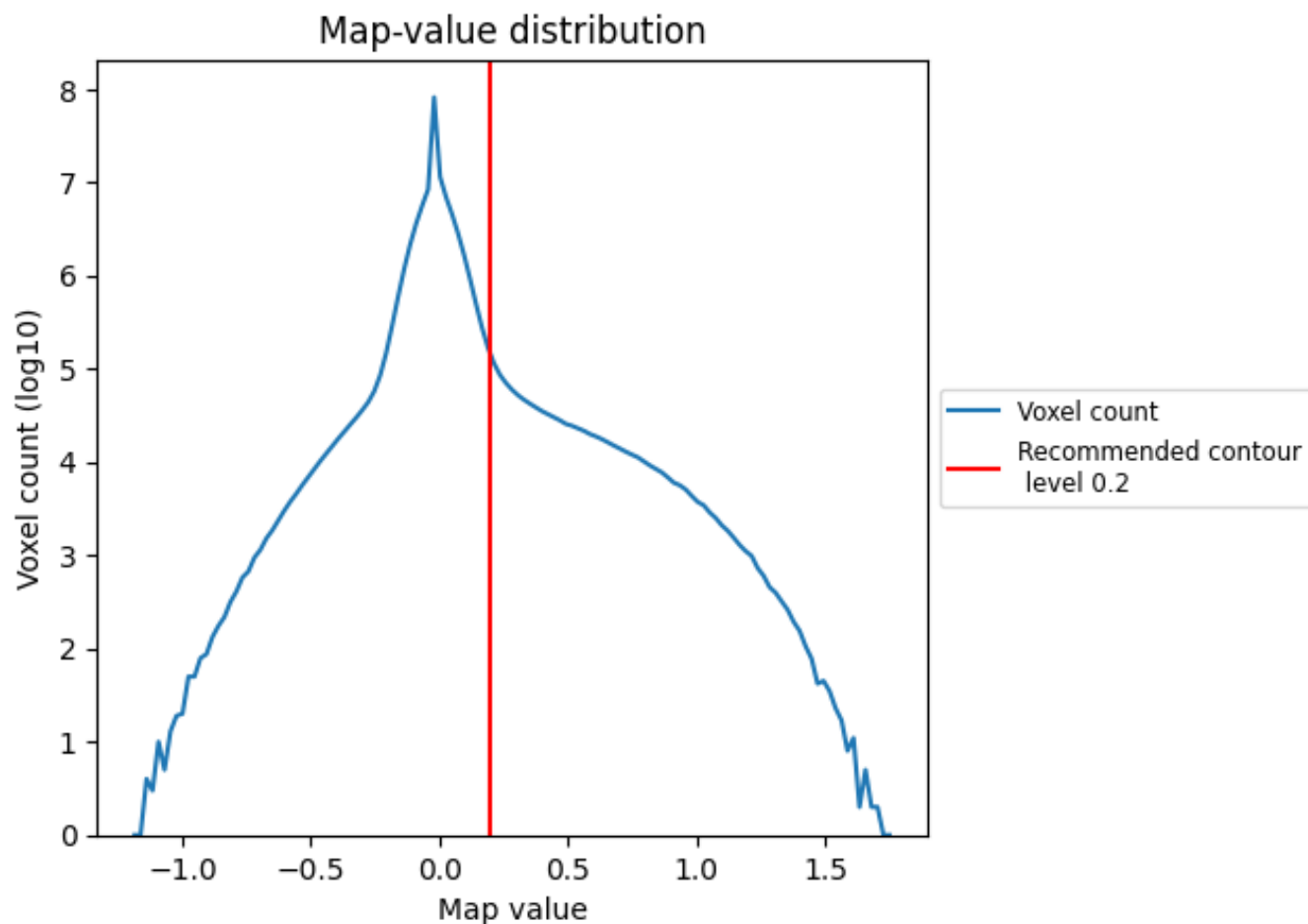
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

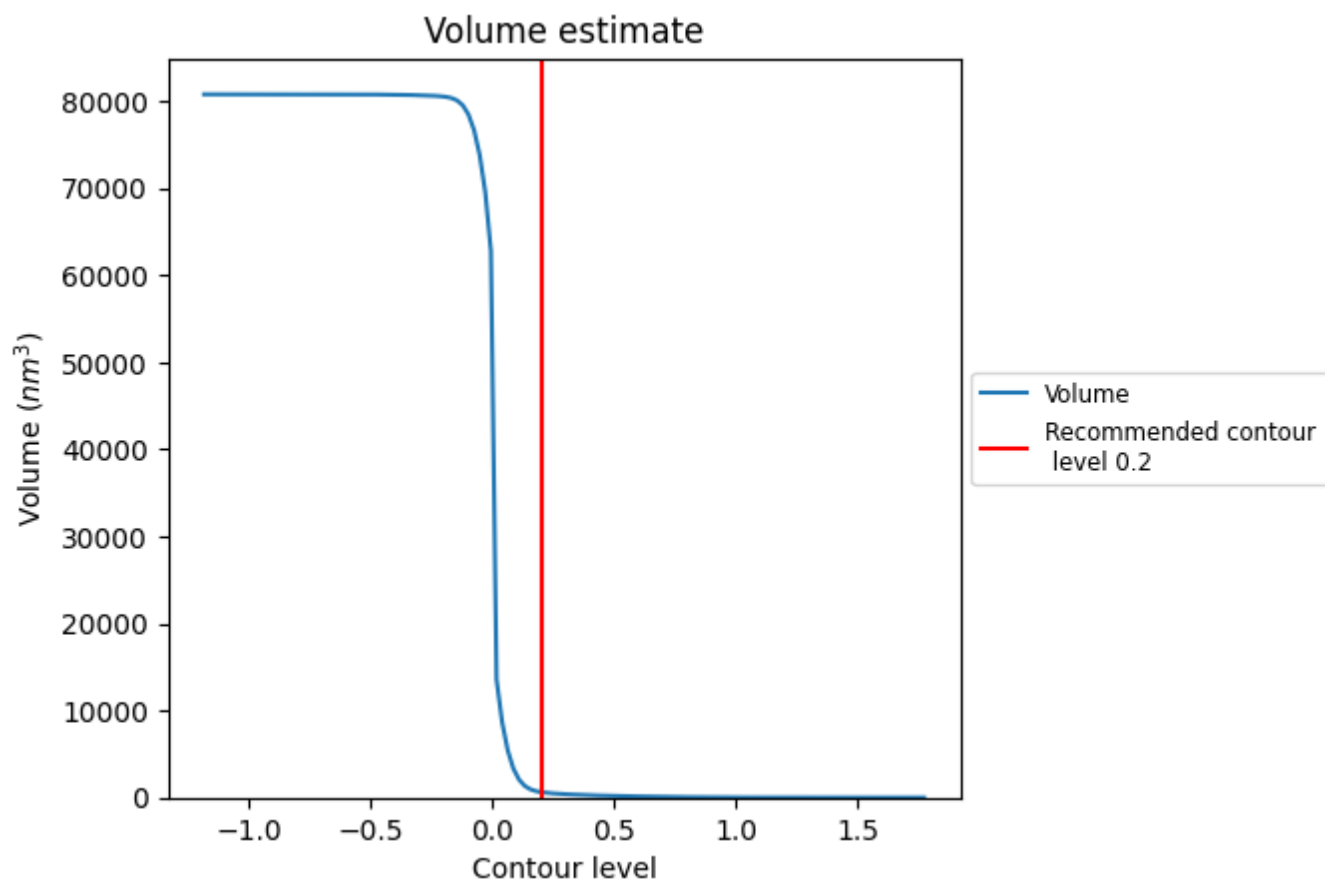
This section contains the results of statistical analysis of the map.

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.

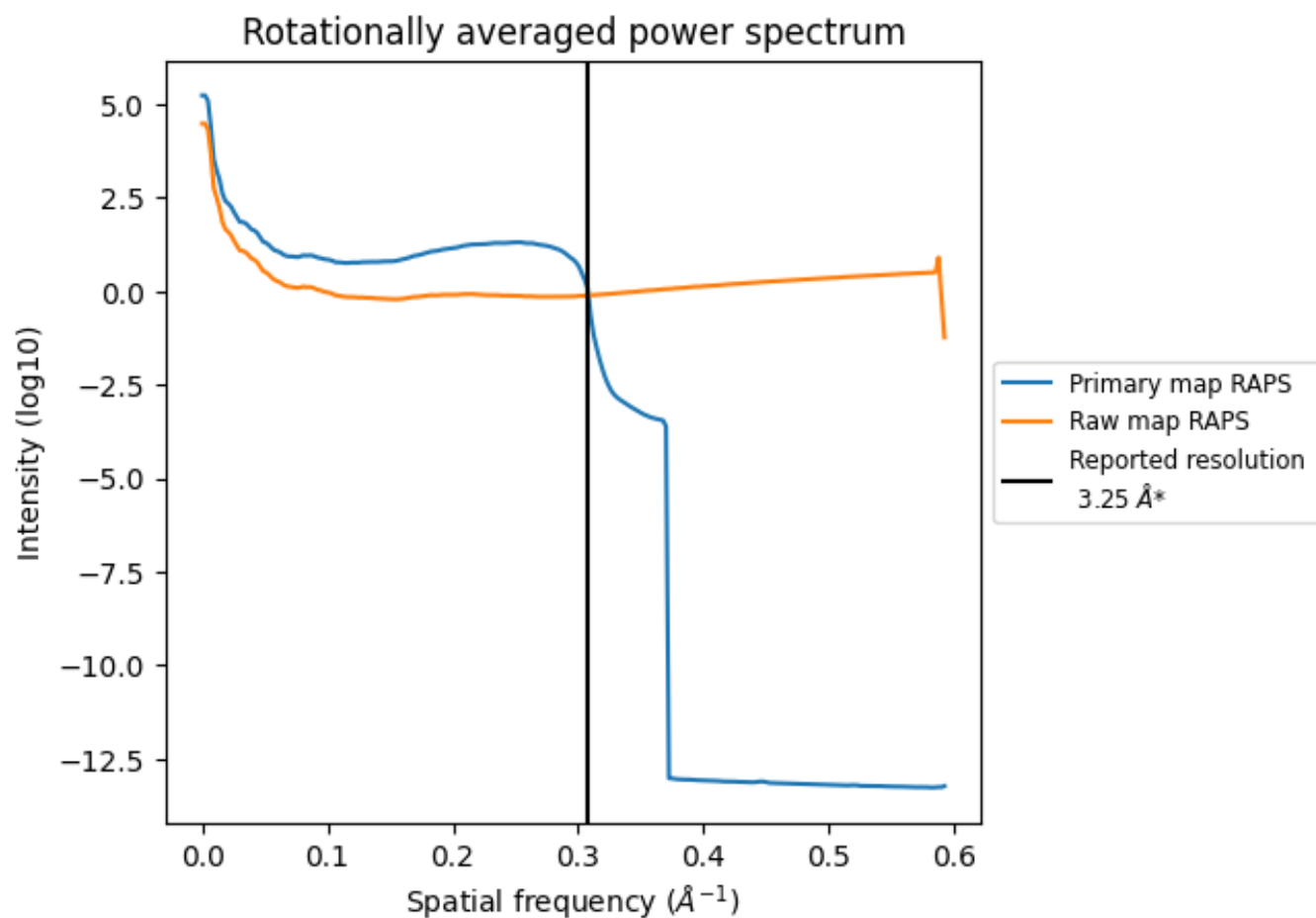
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 633 nm³; this corresponds to an approximate mass of 571 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 ⓘ

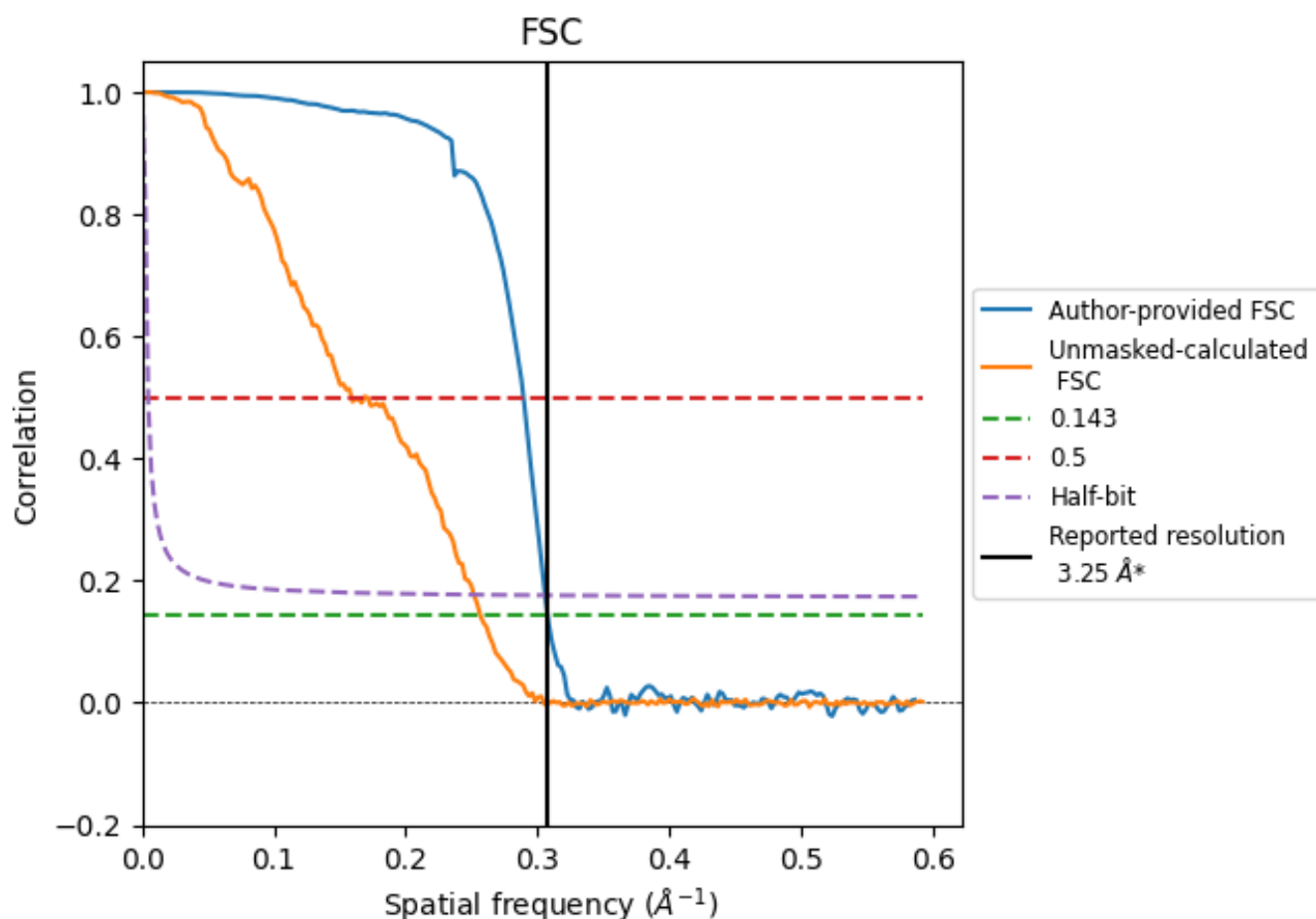


*Reported resolution corresponds to spatial frequency of 0.308 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.308 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

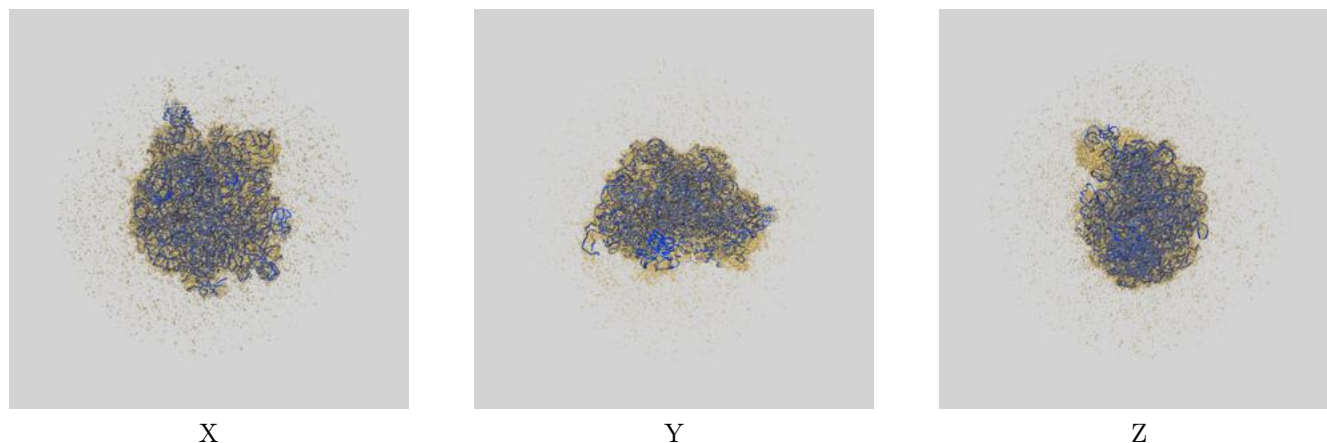
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	3.25	3.45	3.27
Unmasked-calculated*	3.90	6.29	3.97

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.90 differs from the reported value 3.25 by more than 10 %

9 Map-model fit [i](#)

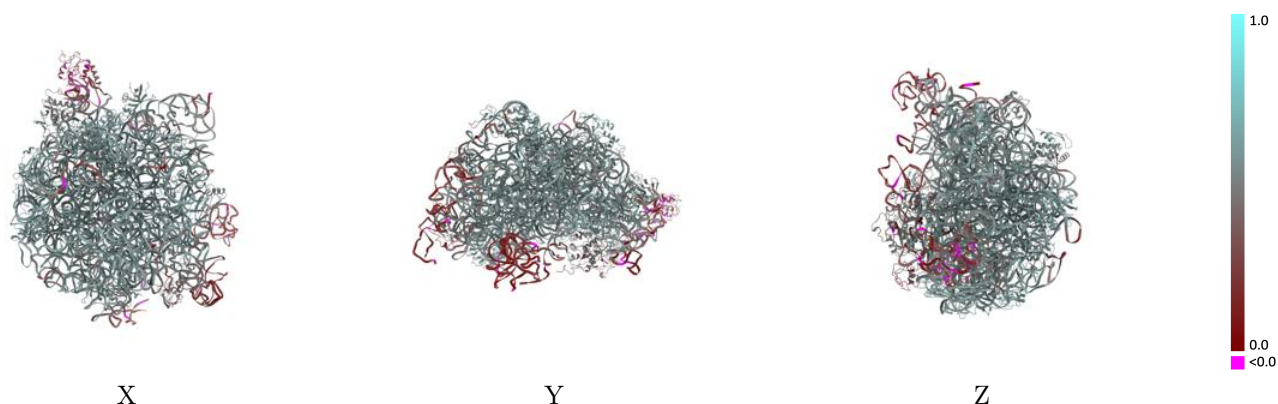
This section contains information regarding the fit between EMDB map EMD-43477 and PDB model 8VR8. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



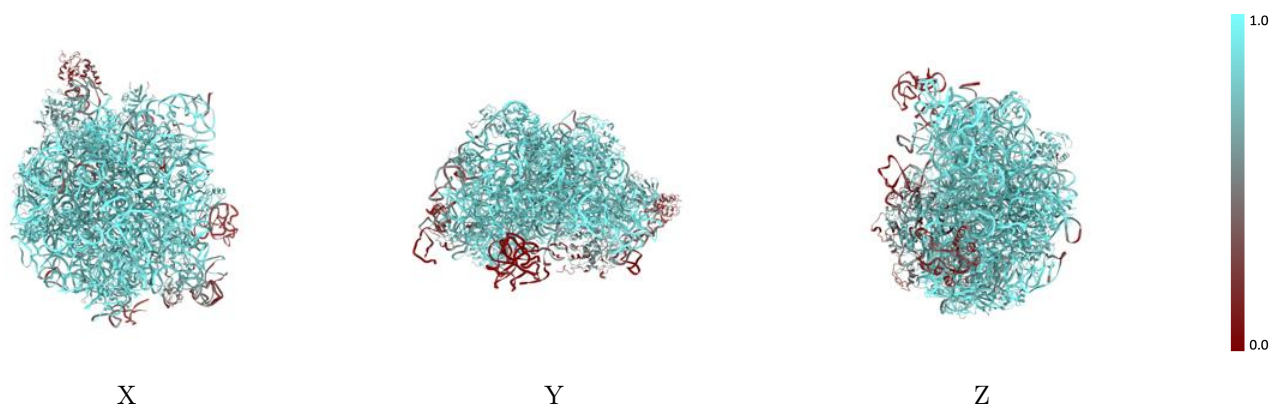
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



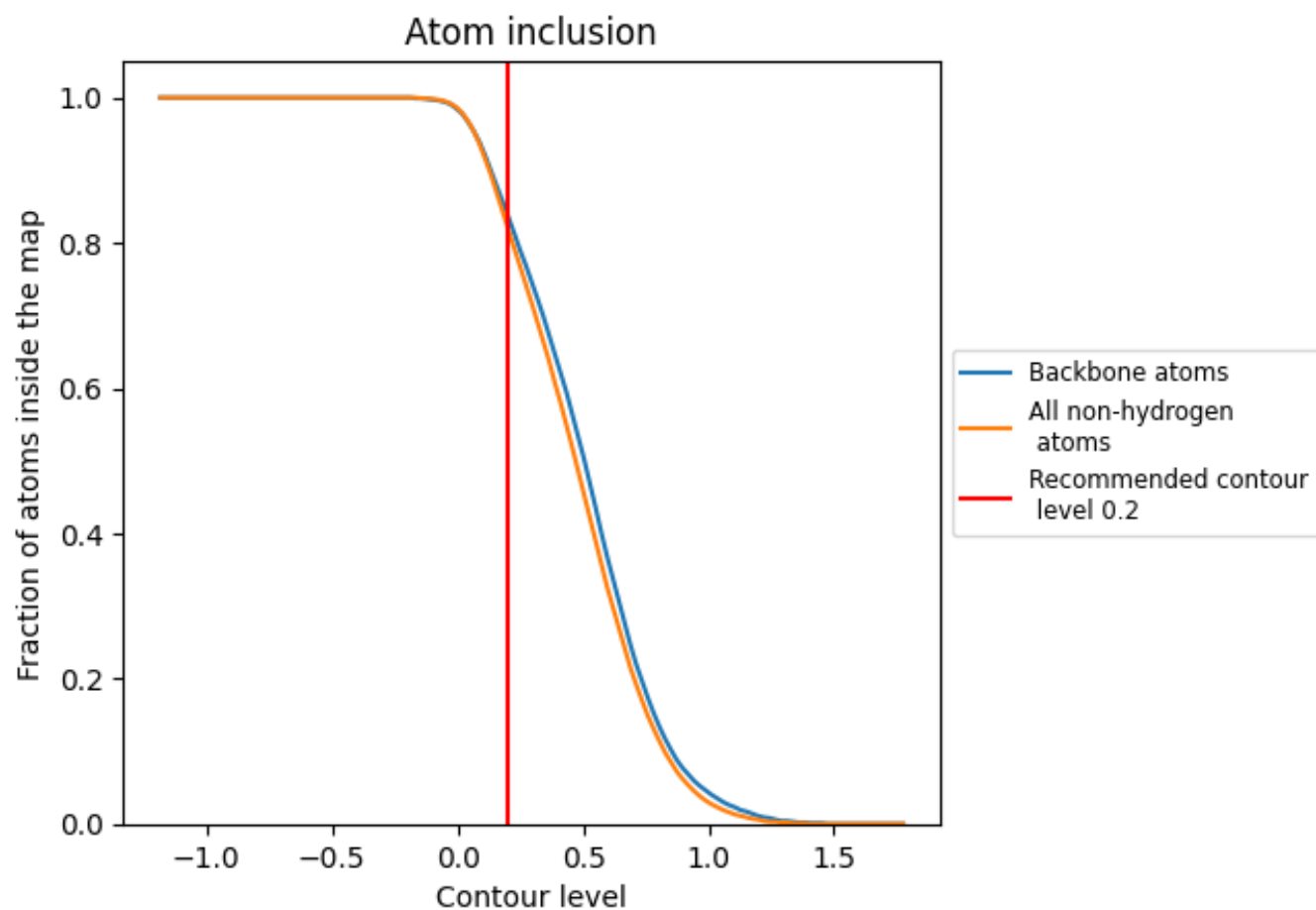
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8220	 0.5120
2	 0.8740	 0.5680
3	 0.8990	 0.5840
4	 0.5370	 0.4270
A	 0.8400	 0.5070
B	 0.8350	 0.4910
C	 0.8570	 0.5670
D	 0.8880	 0.5820
E	 0.8560	 0.5630
G	 0.7300	 0.5010
H	 0.4990	 0.4260
I	 0.1200	 0.1720
K	 0.8960	 0.5790
L	 0.8780	 0.5730
M	 0.8680	 0.5670
N	 0.8790	 0.5710
O	 0.8980	 0.5730
Q	 0.8100	 0.5570
R	 0.9010	 0.5740
S	 0.8870	 0.5830
T	 0.8730	 0.5700
U	 0.8310	 0.5620
V	 0.7680	 0.5150
W	 0.7550	 0.5310
X	 0.8590	 0.5690
Y	 0.8740	 0.5630
Z	 0.8220	 0.5260
b	 0.8710	 0.5720
c	 0.8730	 0.5580
d	 0.9170	 0.5810
e	 0.9080	 0.5780
f	 0.8950	 0.5810

