



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 04:58 AM UTC

PDB ID : 8A63 / pdb_00008a63
EMDB ID : EMD-15204
Title : Cryo-EM structure of *Listeria monocytogenes* 50S ribosomal subunit.
Authors : Koller, T.O.; Crowe-McAuliffe, C.; Wilson, D.N.
Deposited on : 2022-06-16
Resolution : 3.10 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
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

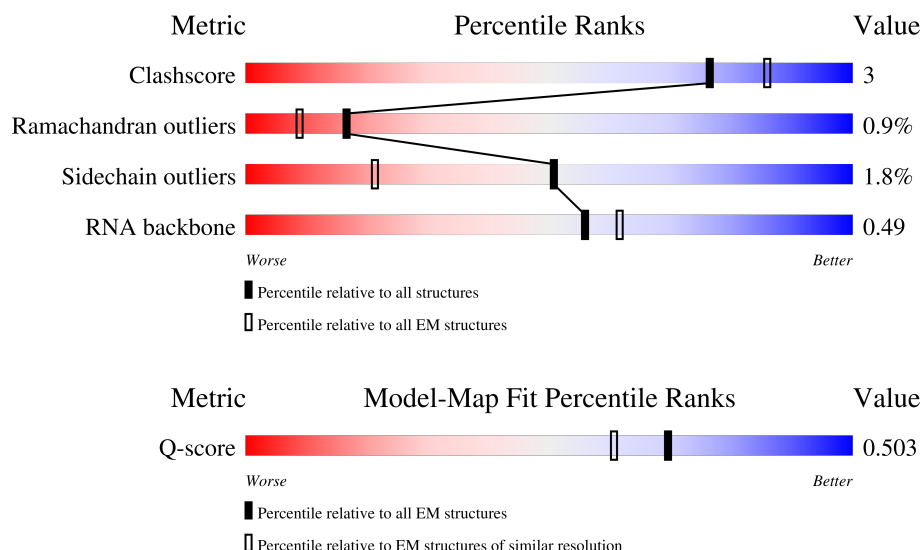
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	1	62	
2	2	63	
3	3	59	

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Mol	Chain	Length	Quality of chain
4	4	81	
5	5	57	
6	6	49	
7	7	44	
8	8	66	
9	9	37	
10	A	2931	
11	B	114	
12	G	277	
13	H	209	
14	I	207	
15	J	179	
16	K	178	
17	M	145	
18	N	122	
19	O	146	
20	P	144	
21	Q	135	
22	R	119	
23	S	114	
24	T	119	
25	U	102	
26	V	118	
27	W	94	
28	X	103	

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Mol	Chain	Length	Quality of chain
29	Z	96	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 88390 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	58	Total	C	N	O	S	0	0
			457	283	96	76	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	59	Total	C	N	O	S	0	0
			487	298	94	94	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	56	Total	C	N	O	S	0	0
			433	272	82	78	1		

- Molecule 4 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	59	Total	C	N	O	S	0	0
			477	305	75	96	1		

- Molecule 5 is a protein called 50S ribosomal protein L32-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	53	Total	C	N	O	S	0	0
			425	259	87	74	5		

- Molecule 6 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	47	Total	C	N	O	S	0	0
			400	243	81	73	3		

- Molecule 7 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	42	Total	C	N	O	S	0	0
			357	217	87	52	1		

- Molecule 8 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	63	Total	C	N	O	S	0	0
			512	317	113	78	4		

- Molecule 9 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	36	Total	C	N	O	S	0	0
			292	183	59	44	6		

- Molecule 10 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	2908	Total	C	N	O	P	0	0
			62459	27874	11544	20133	2908		

- Molecule 11 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	114	Total	C	N	O	P	0	0
			2430	1083	430	803	114		

- Molecule 12 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	273	Total	C	N	O	S	0	0
			2108	1307	415	379	7		

- Molecule 13 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	206	Total	C	N	O	S	0	0
			1582	995	291	292	4		

- Molecule 14 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	I	203	Total	C	N	O	0	0
			1563	987	286	290		

- Molecule 15 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	175	Total	C	N	O	S	0	0
			1365	865	236	258	6		

- Molecule 16 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	165	Total	C	N	O	S	0	0
			1271	801	232	237	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	142	Total	C	N	O	S	0	0
			1117	708	201	205	3		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	122	Total	C	N	O	S	0	0
			925	573	175	172	5		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	O	144	Total	C	N	O	0	0
			1094	675	214	205		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	133	Total	C	N	O	S	0	0
			1055	675	205	170	5		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	122	Total	C	N	O	S	0	0
			983	619	191	172	1		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	118	Total	C	N	O		0	0
			914	564	176	174			

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	112	Total	C	N	O		0	0
			905	570	181	154			

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	116	Total	C	N	O	S	0	0
			939	596	185	154	4		

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	101	Total	C	N	O	S	0	0
			786	507	134	144	1		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	110	Total	C	N	O		0	0
			848	534	160	154			

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	90	Total	C	N	O	S	0	0
			731	462	129	138	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	95	Total	C	N	O	S	0	0
			723	459	134	127	3		

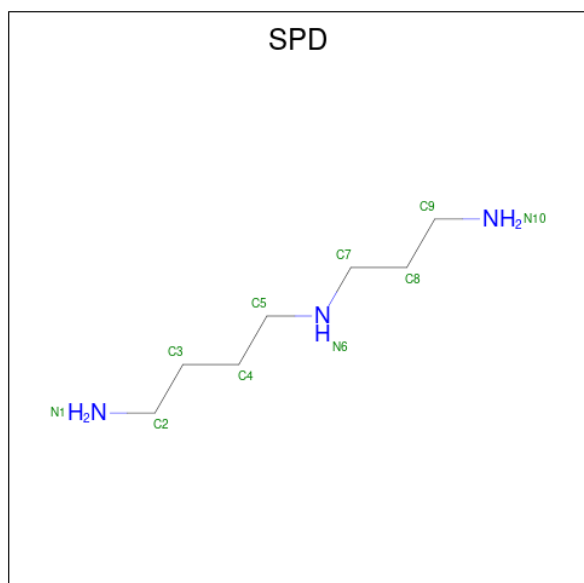
- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	73	Total	C	N	O	S	0	0
			563	345	111	106	1		

- Molecule 30 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
30	5	1	Total	Zn	0
			1	1	
30	9	1	Total	Zn	0
			1	1	

- Molecule 31 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).

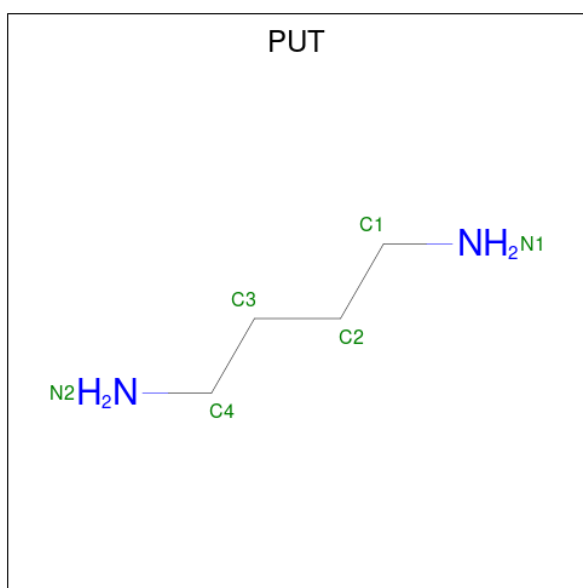


Mol	Chain	Residues	Atoms			AltConf
31	A	1	Total	C	N	0
			10	7	3	

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
32	A	161	Total	Mg	0
			161	161	
32	G	1	Total	Mg	0
			1	1	
32	H	1	Total	Mg	0
			1	1	
32	O	1	Total	Mg	0
			1	1	

- Molecule 33 is 1,4-DIAMINOBTUTANE (CCD ID: PUT) (formula: $C_4H_{12}N_2$).



Mol	Chain	Residues	Atoms			AltConf
33	A	1	Total	C	N	0
			6	4	2	
33	A	1	Total	C	N	0
			6	4	2	

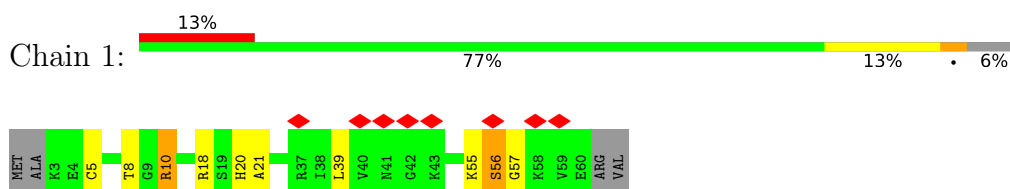
- Molecule 34 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
34	P	1	Total	K	0
			1	1	

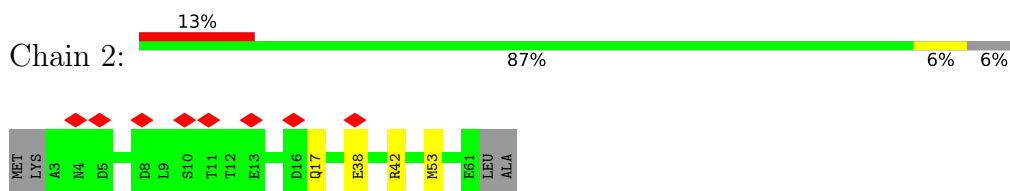
3 Residue-property plots [i](#)

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.

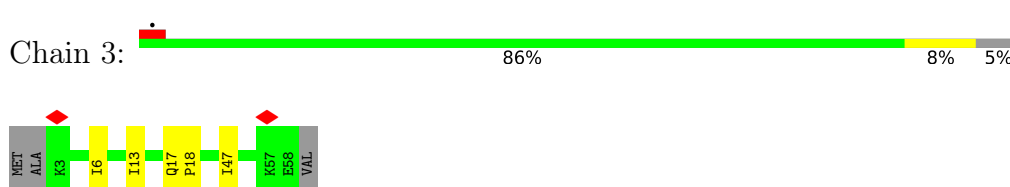
- Molecule 1: 50S ribosomal protein L28



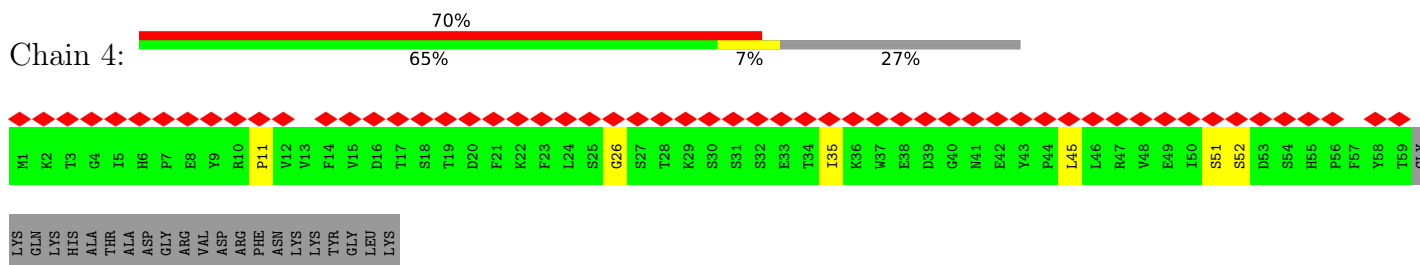
- Molecule 2: 50S ribosomal protein L29



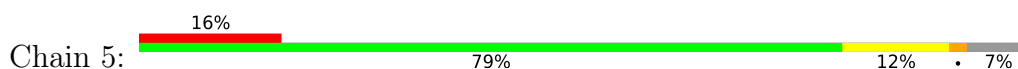
- Molecule 3: 50S ribosomal protein L30

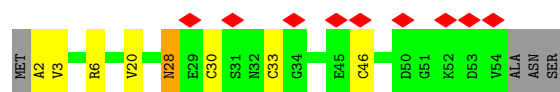


- Molecule 4: 50S ribosomal protein L31 type B

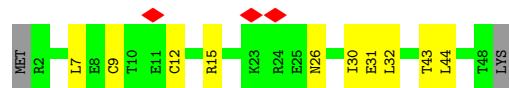
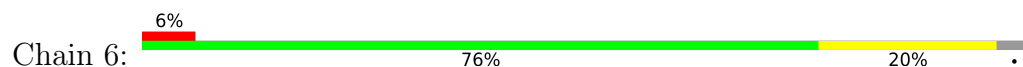


- Molecule 5: 50S ribosomal protein L32-2

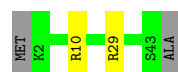
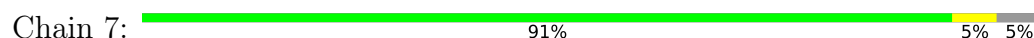




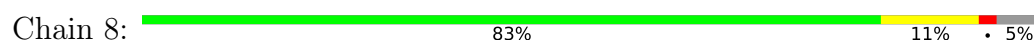
- Molecule 6: 50S ribosomal protein L33 1



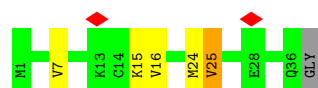
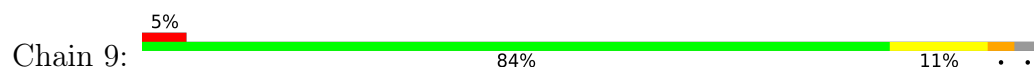
- Molecule 7: 50S ribosomal protein L34



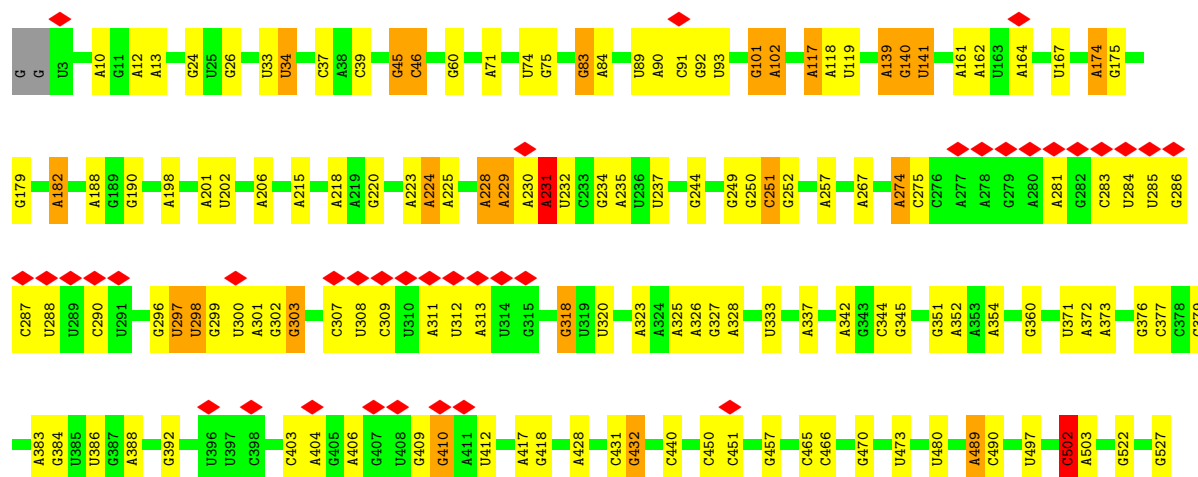
- Molecule 8: 50S ribosomal protein L35



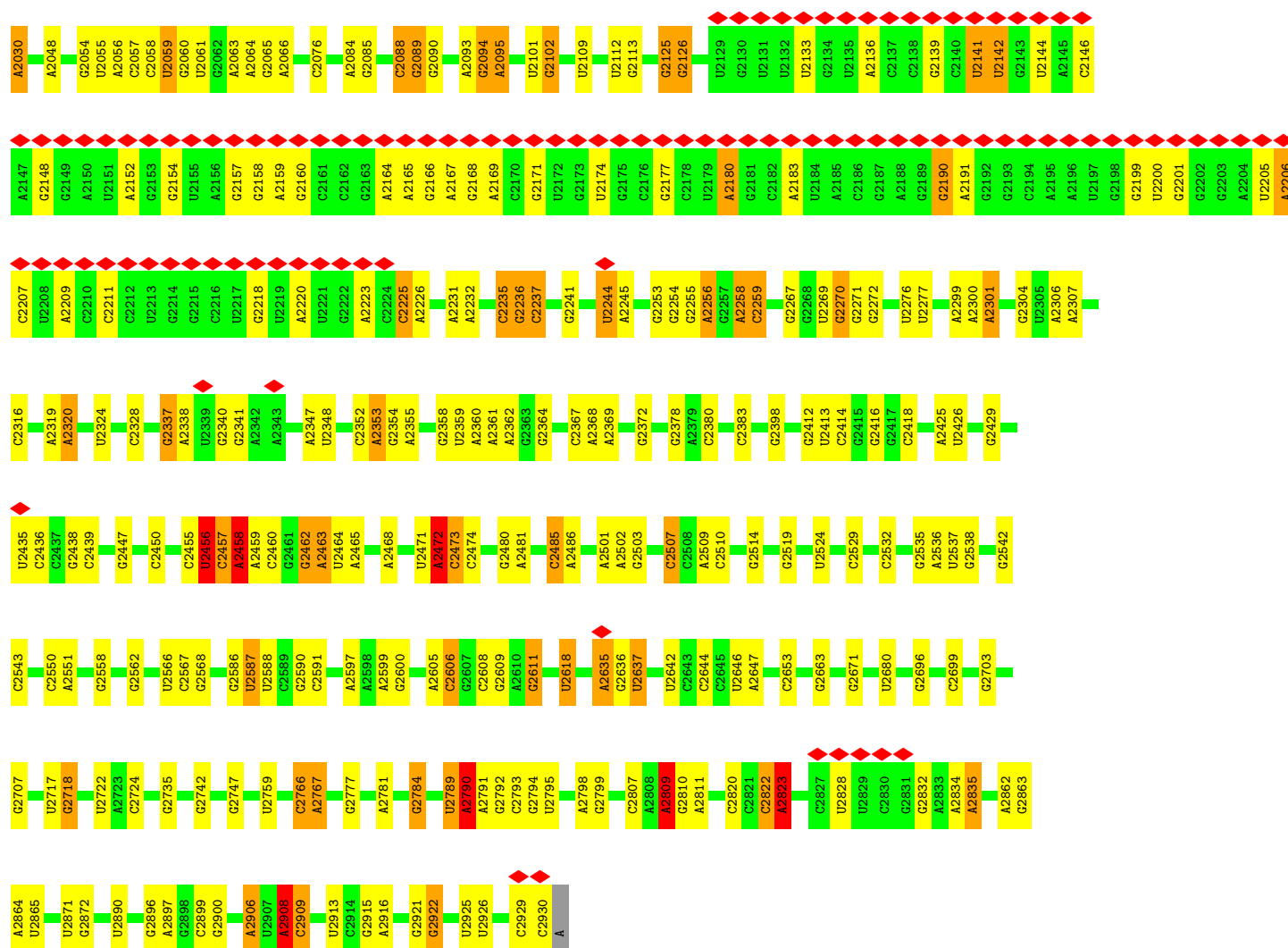
- Molecule 9: 50S ribosomal protein L36



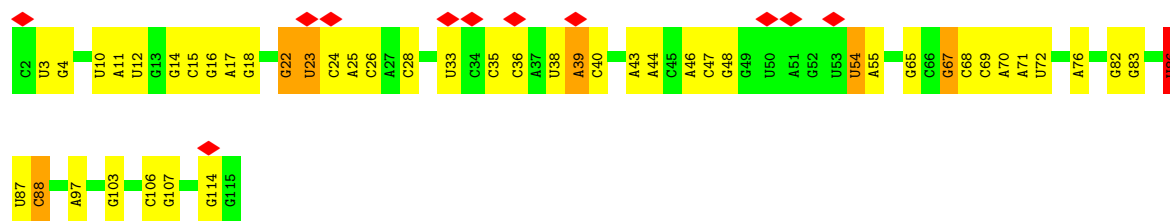
- Molecule 10: 23S ribosomal RNA



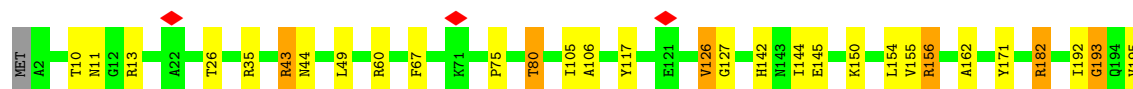
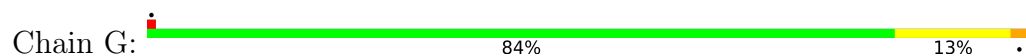




• Molecule 11: 5S ribosomal RNA

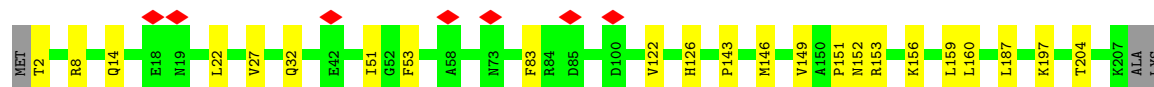
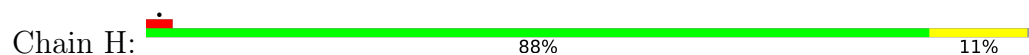


• Molecule 12: 50S ribosomal protein L2

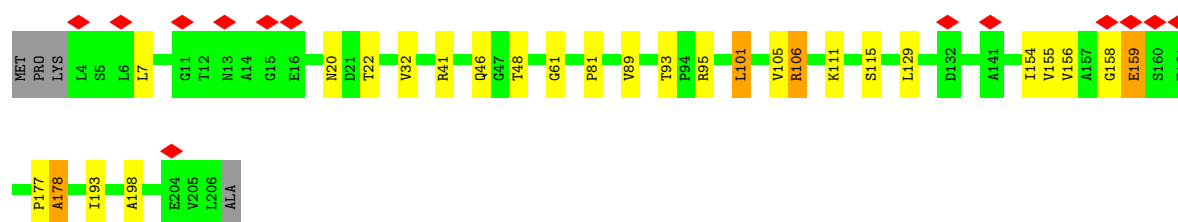
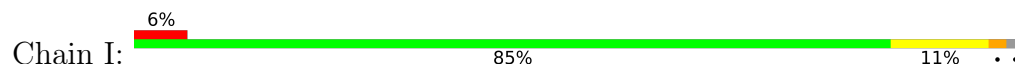




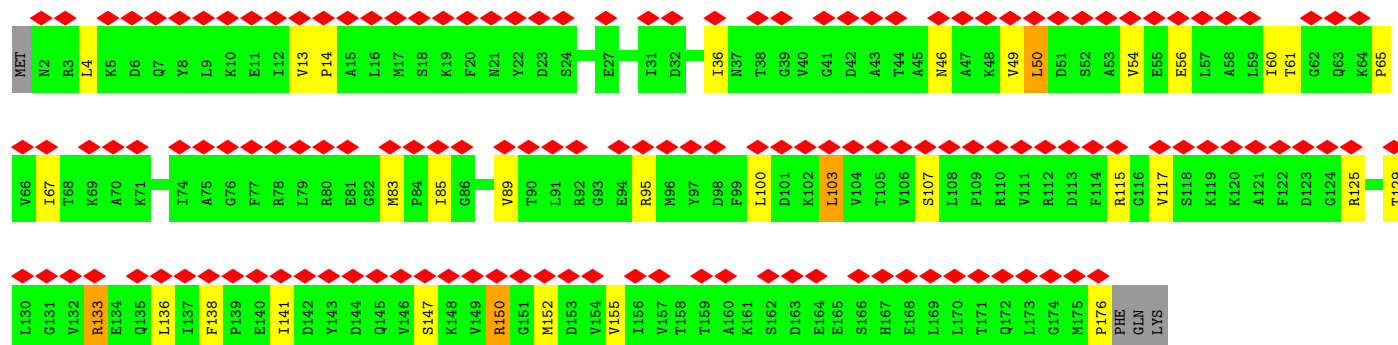
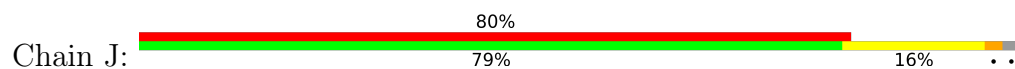
- Molecule 13: 50S ribosomal protein L3



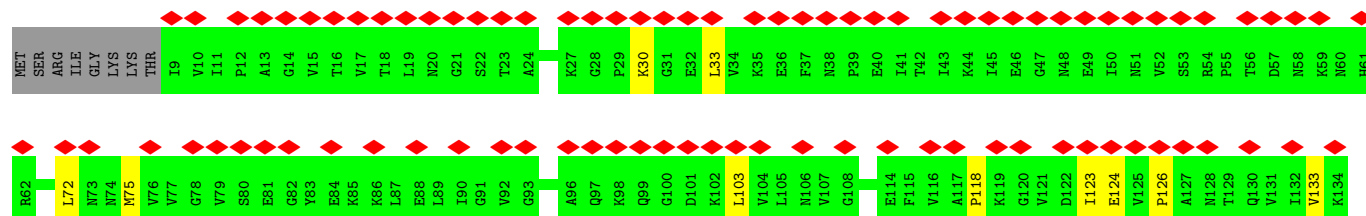
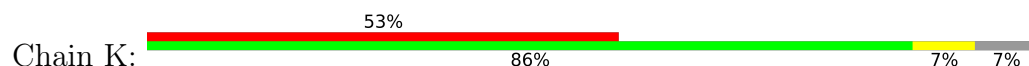
- Molecule 14: 50S ribosomal protein L4

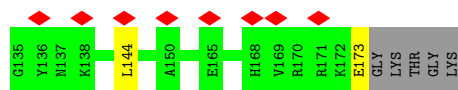


- Molecule 15: 50S ribosomal protein L5

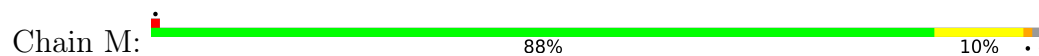


- Molecule 16: 50S ribosomal protein L6

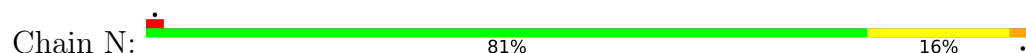




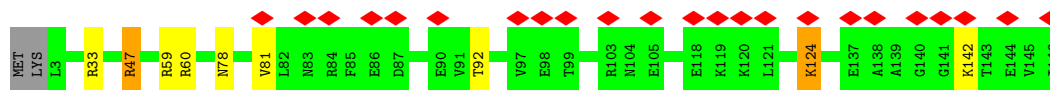
- Molecule 17: 50S ribosomal protein L13



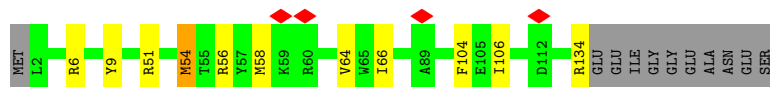
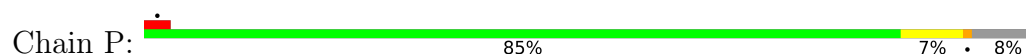
- Molecule 18: 50S ribosomal protein L14



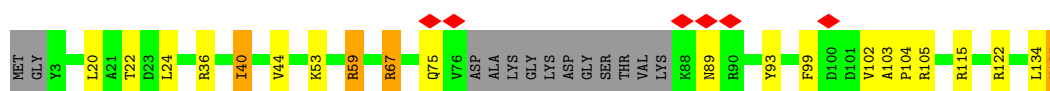
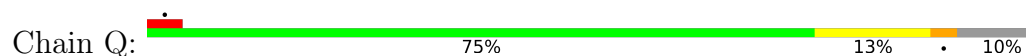
- Molecule 19: 50S ribosomal protein L15



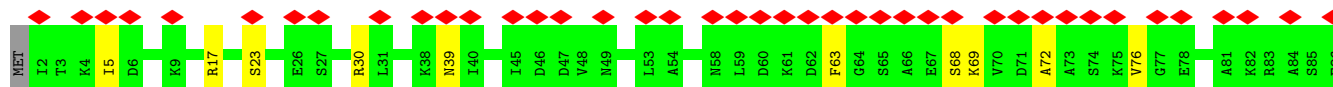
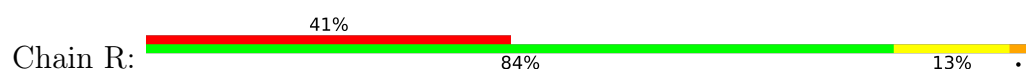
- Molecule 20: 50S ribosomal protein L16

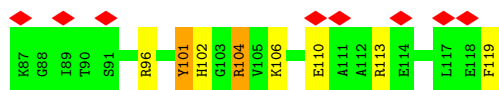


- Molecule 21: 50S ribosomal protein L17

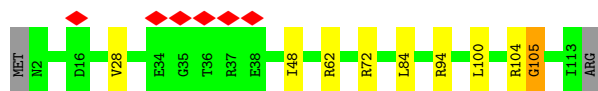


- Molecule 22: 50S ribosomal protein L18

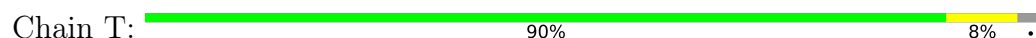




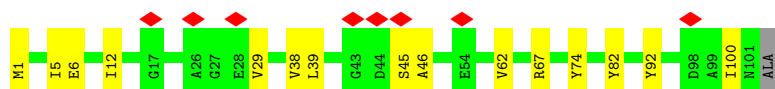
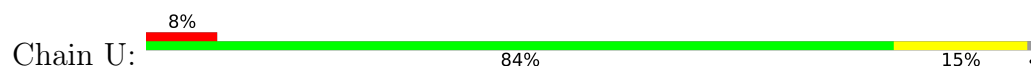
- Molecule 23: 50S ribosomal protein L19



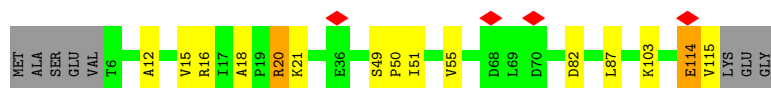
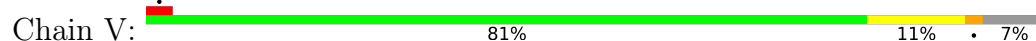
- Molecule 24: 50S ribosomal protein L20



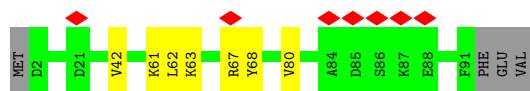
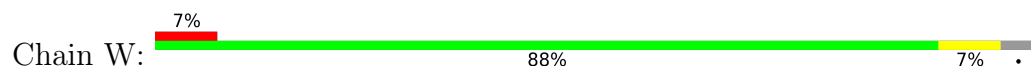
- Molecule 25: 50S ribosomal protein L21



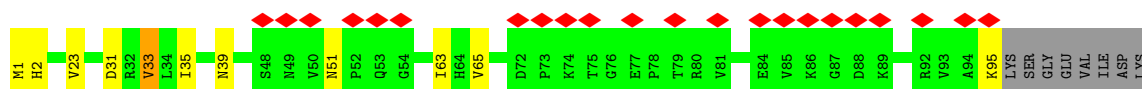
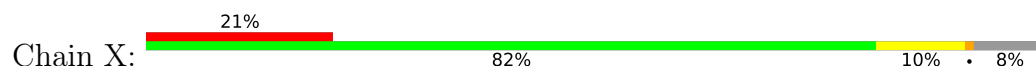
- Molecule 26: 50S ribosomal protein L22



- Molecule 27: 50S ribosomal protein L23



- Molecule 28: 50S ribosomal protein L24



- Molecule 29: 50S ribosomal protein L27



MET	LEU	LYS	PHE	ASP	ILE	GLN	HIS	PHE	ALA	HIS	LYS	LYS	GLY	GLY	GLY	SER	THR	S19	S26	R27	R28	E47	T57	G81	R82	P91	GLU	VAL	GLN	GLU	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14097	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 ($e^-/\text{\AA}^2$)	30.255	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.228	Depositor
Minimum map value	-0.092	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	344.4, 344.4, 344.4	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

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

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	1	0.48	0/462	0.79	0/612
2	2	0.38	0/488	0.82	0/651
3	3	0.47	0/436	0.75	0/585
4	4	0.50	0/491	0.82	0/666
5	5	0.57	0/433	0.80	0/577
6	6	0.43	0/404	0.75	0/541
7	7	0.52	0/360	0.85	0/469
8	8	0.53	0/519	0.77	0/675
9	9	0.50	0/295	0.81	0/387
10	A	0.62	0/69974	1.06	232/109160 (0.2%)
11	B	0.80	0/2714	1.08	18/4229 (0.4%)
12	G	0.99	0/2144	1.30	5/2875 (0.2%)
13	H	0.97	0/1604	1.28	0/2156
14	I	0.99	0/1583	1.40	0/2133
15	J	1.06	0/1383	1.55	0/1863
16	K	1.10	0/1293	1.44	0/1749
17	M	0.98	0/1140	1.29	0/1533
18	N	0.97	0/932	1.33	0/1248
19	O	1.01	0/1105	1.38	0/1470
20	P	0.97	0/1077	1.34	0/1439
21	Q	0.94	0/994	1.38	0/1329
22	R	1.04	0/923	1.56	2/1232 (0.2%)
23	S	0.97	0/917	1.25	0/1230
24	T	0.90	0/952	1.42	0/1266
25	U	0.98	0/799	1.23	0/1072
26	V	0.97	0/858	1.34	0/1160
27	W	0.94	0/739	1.33	0/990
28	X	1.08	0/733	1.36	0/980
29	Z	0.93	0/570	1.25	0/758
All	All	0.71	0/96322	1.11	257/145035 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	2
5	5	0	1
7	7	0	2
8	8	0	1
12	G	0	8
14	I	0	3
15	J	0	2
17	M	0	1
18	N	0	2
19	O	0	4
20	P	0	3
21	Q	0	4
22	R	0	4
23	S	0	2
24	T	0	2
25	U	0	1
26	V	0	1
29	Z	0	2
All	All	0	45

There are no bond length outliers.

All (257) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	731	A	O3'-P-O5'	-10.71	87.94	104.00
10	A	1849	C	C2'-C3'-O3'	-9.98	98.72	113.70
10	A	605	U	P-O3'-C3'	-9.65	105.72	120.20
10	A	2908	A	C2'-C3'-O3'	9.06	123.08	109.50
10	A	1958	C	P-O3'-C3'	-8.93	106.81	120.20
10	A	1946	A	P-O3'-C3'	-8.75	107.07	120.20
10	A	1832	G	P-O3'-C3'	8.57	133.06	120.20
10	A	251	C	C2'-C3'-O3'	8.55	122.32	109.50
10	A	1959	U	P-O3'-C3'	-8.51	107.44	120.20
10	A	1956	U	P-O3'-C3'	-8.48	107.48	120.20
10	A	1940	G	P-O3'-C3'	-8.45	107.52	120.20
10	A	1941	C	P-O3'-C3'	-8.41	107.59	120.20
10	A	1944	U	P-O3'-C3'	-8.26	107.81	120.20
10	A	1939	G	P-O3'-C3'	-8.17	107.95	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1957	C	P-O3'-C3'	-8.06	108.11	120.20
10	A	2809	A	C2'-C3'-O3'	7.98	121.47	109.50
10	A	1249	A	C2'-C3'-O3'	7.77	125.35	113.70
10	A	1712	U	C4'-C3'-O3'	-7.74	101.39	113.00
10	A	2337	G	P-O3'-C3'	-7.72	108.61	120.20
10	A	2809	A	P-O3'-C3'	7.58	131.57	120.20
10	A	2458	A	P-O3'-C3'	7.57	131.55	120.20
10	A	2095	A	P-O3'-C3'	-7.56	108.86	120.20
10	A	1960	A	P-O3'-C3'	-7.45	109.03	120.20
10	A	1849	C	O3'-P-O5'	-7.38	92.93	104.00
10	A	2618	U	P-O3'-C3'	-7.21	109.39	120.20
10	A	1949	A	P-O3'-C3'	-7.08	109.57	120.20
10	A	1955	G	P-O3'-C3'	-7.00	109.70	120.20
10	A	224	A	O3'-P-O5'	-6.97	93.55	104.00
10	A	1945	A	P-O3'-C3'	-6.91	109.83	120.20
11	B	86	U	P-O3'-C3'	-6.79	110.01	120.20
10	A	2532	C	P-O3'-C3'	-6.78	110.03	120.20
10	A	1748	G	O3'-P-O5'	-6.77	93.84	104.00
10	A	1953	C	P-O3'-C3'	-6.74	110.10	120.20
10	A	1178	U	P-O3'-C3'	-6.61	110.29	120.20
10	A	2057	C	P-O3'-C3'	-6.61	110.29	120.20
10	A	2606	C	O3'-P-O5'	-6.59	94.11	104.00
10	A	489	A	O3'-P-O5'	-6.55	94.18	104.00
10	A	1388	U	P-O3'-C3'	-6.54	110.40	120.20
10	A	1711	U	O3'-P-O5'	-6.54	94.20	104.00
10	A	1952	A	P-O3'-C3'	-6.52	110.42	120.20
10	A	2059	U	P-O3'-C3'	-6.44	110.53	120.20
10	A	2085	G	P-O3'-C3'	-6.39	110.62	120.20
10	A	598	G	P-O3'-C3'	-6.33	110.70	120.20
10	A	2550	C	P-O3'-C3'	-6.33	110.70	120.20
10	A	574	A	C2'-C3'-O3'	6.31	118.97	109.50
10	A	1891	G	P-O3'-C3'	-6.30	110.76	120.20
10	A	2109	U	P-O3'-C3'	-6.28	110.78	120.20
10	A	431	C	O3'-P-O5'	-6.27	94.60	104.00
10	A	1118	C	P-O3'-C3'	-6.25	110.82	120.20
10	A	2807	C	P-O3'-C3'	-6.24	110.85	120.20
10	A	298	U	P-O3'-C3'	-6.22	110.87	120.20
10	A	548	A	P-O3'-C3'	6.21	129.51	120.20
10	A	502	C	P-O3'-C3'	-6.15	110.98	120.20
11	B	47	C	P-O3'-C3'	-6.15	110.98	120.20
10	A	2609	G	P-O3'-C3'	-6.12	111.01	120.20
10	A	745	A	O3'-P-O5'	-6.12	94.82	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1004	U	P-O3'-C3'	-6.12	111.02	120.20
10	A	1362	A	P-O3'-C3'	-6.10	111.05	120.20
10	A	83	G	O3'-P-O5'	-6.08	94.88	104.00
10	A	2485	C	P-O3'-C3'	-6.08	111.08	120.20
10	A	980	A	P-O3'-C3'	-6.08	111.08	120.20
10	A	1538	U	P-O3'-C3'	-6.04	111.14	120.20
10	A	827	A	O3'-P-O5'	-6.00	94.99	104.00
10	A	2190	G	P-O3'-C3'	-5.97	111.24	120.20
10	A	2002	A	O3'-P-O5'	5.89	112.83	104.00
10	A	1706	U	P-O3'-C3'	-5.88	111.38	120.20
10	A	731	A	C4'-C3'-O3'	5.88	118.22	109.40
10	A	574	A	P-O3'-C3'	5.86	129.00	120.20
10	A	873	U	C2'-C3'-O3'	-5.86	104.91	113.70
10	A	1135	G	P-O3'-C3'	-5.86	111.41	120.20
10	A	2255	G	P-O3'-C3'	-5.86	111.41	120.20
10	A	2456	U	C2'-C3'-O3'	5.85	118.28	109.50
10	A	1602	C	P-O3'-C3'	-5.83	111.46	120.20
10	A	2463	A	P-O3'-C3'	-5.81	111.48	120.20
10	A	1795	A	P-O3'-C3'	-5.80	111.50	120.20
12	G	193	GLY	CA-C-O	-5.79	118.45	122.22
10	A	904	A	P-O3'-C3'	-5.79	111.52	120.20
10	A	2458	A	C2'-C3'-O3'	5.79	118.18	109.50
10	A	2472	A	C2'-C3'-O3'	5.78	118.17	109.50
10	A	1249	A	C4'-C3'-C2'	-5.78	96.82	102.60
10	A	2635	A	P-O3'-C3'	-5.77	111.54	120.20
10	A	1888	G	O3'-P-O5'	-5.77	95.35	104.00
10	A	699	U	P-O3'-C3'	-5.77	111.55	120.20
10	A	891	U	P-O3'-C3'	-5.76	111.57	120.20
10	A	1282	A	O3'-P-O5'	-5.75	95.37	104.00
10	A	2501	A	P-O3'-C3'	-5.75	111.58	120.20
10	A	2455	C	P-O3'-C3'	-5.74	111.60	120.20
10	A	829	A	P-O3'-C3'	-5.73	111.60	120.20
10	A	2644	C	P-O3'-C3'	-5.73	111.61	120.20
11	B	54	U	P-O3'-C3'	-5.72	111.62	120.20
10	A	1564	U	P-O3'-C3'	-5.71	111.63	120.20
10	A	89	U	P-O3'-C3'	-5.71	111.64	120.20
11	B	16	G	P-O3'-C3'	-5.70	111.64	120.20
10	A	1116	A	P-O3'-C3'	-5.69	111.66	120.20
10	A	1380	A	O3'-P-O5'	-5.69	95.46	104.00
10	A	403	C	P-O3'-C3'	-5.68	111.68	120.20
10	A	1422	A	O3'-P-O5'	-5.67	95.49	104.00
10	A	377	C	O3'-P-O5'	-5.67	95.49	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1832	G	C2'-C3'-O3'	5.67	118.01	109.50
10	A	231	A	C4'-C3'-O3'	5.66	117.89	109.40
10	A	1887	A	O3'-P-O5'	-5.65	95.53	104.00
10	A	979	U	P-O3'-C3'	-5.63	111.75	120.20
10	A	1529	U	P-O3'-C3'	-5.63	111.75	120.20
10	A	1895	G	P-O3'-C3'	-5.62	111.77	120.20
10	A	539	G	C4'-C3'-O3'	-5.62	104.58	113.00
10	A	790	C	P-O3'-C3'	-5.60	111.80	120.20
10	A	2258	A	C2'-C3'-O3'	5.60	117.90	109.50
10	A	961	C	P-O3'-C3'	-5.59	111.82	120.20
10	A	1620	G	C4'-C3'-O3'	-5.58	104.63	113.00
10	A	2793	C	P-O3'-C3'	-5.58	111.84	120.20
10	A	228	A	C4'-C3'-O3'	-5.57	104.64	113.00
10	A	580	U	P-O3'-C3'	-5.57	111.85	120.20
10	A	2225	C	P-O3'-C3'	-5.56	111.86	120.20
10	A	789	A	P-O3'-C3'	-5.56	111.86	120.20
10	A	2055	U	O3'-P-O5'	-5.56	95.66	104.00
10	A	1620	G	O3'-P-O5'	-5.55	95.67	104.00
10	A	2141	U	P-O3'-C3'	-5.54	111.89	120.20
10	A	2235	C	P-O3'-C3'	-5.54	111.89	120.20
10	A	916	G	P-O3'-C3'	-5.53	111.91	120.20
10	A	465	C	P-O3'-C3'	-5.52	111.92	120.20
10	A	2718	G	P-O3'-C3'	-5.52	111.92	120.20
10	A	2566	U	P-O3'-C3'	-5.52	111.92	120.20
10	A	1177	G	O3'-P-O5'	-5.52	95.73	104.00
10	A	33	U	P-O3'-C3'	-5.51	111.94	120.20
10	A	984	G	P-O3'-C3'	-5.50	111.95	120.20
11	B	17	A	P-O3'-C3'	-5.49	111.96	120.20
10	A	1962	G	P-O3'-C3'	-5.49	111.97	120.20
10	A	489	A	C2'-C3'-O3'	-5.48	105.48	113.70
10	A	1289	A	P-O3'-C3'	-5.47	112.00	120.20
10	A	746	G	P-O3'-C3'	-5.47	112.00	120.20
11	B	70	A	P-O3'-C3'	-5.46	112.00	120.20
10	A	1315	C	C2'-C3'-O3'	-5.46	105.52	113.70
10	A	1889	A	P-O3'-C3'	-5.46	112.02	120.20
10	A	581	A	P-O3'-C3'	-5.45	112.02	120.20
10	A	539	G	P-O3'-C3'	-5.45	112.02	120.20
10	A	1785	C	P-O5'-C5'	-5.44	112.73	120.90
10	A	2061	U	P-O3'-C3'	-5.44	112.03	120.20
10	A	1102	G	P-O3'-C3'	-5.44	112.03	120.20
10	A	34	U	P-O3'-C3'	-5.44	112.04	120.20
10	A	2820	C	P-O3'-C3'	-5.43	112.05	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	2438	G	P-O3'-C3'	-5.43	112.05	120.20
10	A	2647	A	O3'-P-O5'	-5.43	95.85	104.00
10	A	2792	G	P-O3'-C3'	-5.43	112.06	120.20
10	A	297	U	P-O3'-C3'	-5.42	112.07	120.20
10	A	2472	A	P-O3'-C3'	5.41	128.31	120.20
10	A	46	C	P-O3'-C3'	-5.38	112.13	120.20
10	A	1497	G	P-O3'-C3'	-5.38	112.13	120.20
10	A	745	A	P-O3'-C3'	-5.37	112.14	120.20
10	A	2823	A	P-O3'-C3'	-5.37	112.14	120.20
10	A	1208	G	O3'-P-O5'	-5.35	95.97	104.00
10	A	2244	U	P-O3'-C3'	-5.35	112.17	120.20
10	A	2671	G	P-O3'-C3'	-5.35	112.17	120.20
10	A	190	G	C4'-C3'-C2'	-5.35	97.25	102.60
10	A	1343	G	C2'-C3'-O3'	-5.35	105.68	113.70
10	A	1571	U	P-O3'-C3'	-5.35	112.18	120.20
10	A	1786	G	P-O5'-C5'	-5.35	112.88	120.90
10	A	2267	G	P-O3'-C3'	-5.35	112.18	120.20
10	A	1381	G	P-O3'-C3'	-5.35	112.18	120.20
10	A	1461	U	P-O3'-C3'	-5.35	112.18	120.20
10	A	1999	A	P-O3'-C3'	-5.35	112.18	120.20
10	A	480	U	P-O3'-C3'	-5.34	112.19	120.20
10	A	538	G	O3'-P-O5'	-5.34	95.99	104.00
11	B	14	G	P-O3'-C3'	-5.34	112.19	120.20
12	G	196	GLY	CA-C-O	-5.33	118.55	122.23
11	B	71	A	P-O3'-C3'	-5.33	112.21	120.20
10	A	1625	G	C4'-C3'-O3'	-5.32	105.03	113.00
10	A	1719	C	P-O3'-C3'	-5.32	112.23	120.20
10	A	1250	G	P-O3'-C3'	-5.30	112.25	120.20
10	A	2241	G	P-O3'-C3'	-5.29	112.26	120.20
10	A	2354	G	P-O3'-C3'	-5.29	112.26	120.20
10	A	337	A	P-O3'-C3'	-5.29	112.27	120.20
10	A	936	U	P-O3'-C3'	-5.29	112.27	120.20
11	B	18	G	P-O3'-C3'	-5.29	112.27	120.20
10	A	234	G	P-O3'-C3'	-5.28	112.28	120.20
11	B	15	C	P-O3'-C3'	-5.28	112.28	120.20
10	A	1299	A	C4'-C3'-O3'	-5.28	105.09	113.00
10	A	2922	G	P-O3'-C3'	-5.28	112.29	120.20
10	A	2270	G	P-O3'-C3'	-5.27	112.29	120.20
10	A	2101	U	O3'-P-O5'	-5.27	96.09	104.00
10	A	379	C	P-O3'-C3'	-5.26	112.30	120.20
10	A	410	G	P-O3'-C3'	-5.26	112.32	120.20
12	G	145	GLU	CB-CA-C	5.25	118.37	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	770	U	P-O3'-C3'	-5.24	112.34	120.20
10	A	1310	A	P-O3'-C3'	-5.24	112.35	120.20
10	A	2906	A	P-O3'-C3'	-5.23	112.35	120.20
10	A	2142	U	P-O3'-C3'	-5.22	112.37	120.20
10	A	2542	G	P-O3'-C3'	-5.22	112.37	120.20
10	A	428	A	P-O3'-C3'	-5.21	112.38	120.20
10	A	1233	G	C4'-C3'-O3'	-5.21	105.18	113.00
11	B	26	C	P-O3'-C3'	-5.20	112.40	120.20
10	A	1782	A	P-O3'-C3'	-5.20	112.40	120.20
10	A	2207	C	P-O3'-C3'	-5.20	112.41	120.20
10	A	1092	A	P-O3'-C3'	-5.19	112.42	120.20
10	A	1254	G	O3'-P-O5'	-5.19	96.22	104.00
10	A	1999	A	O3'-P-O5'	-5.19	96.21	104.00
10	A	1576	G	P-O3'-C3'	-5.18	112.42	120.20
10	A	1887	A	P-O3'-C3'	-5.18	112.43	120.20
10	A	2232	A	P-O3'-C3'	-5.18	112.44	120.20
10	A	1344	A	C2'-C3'-O3'	5.17	117.26	109.50
10	A	1288	U	O3'-P-O5'	-5.17	96.25	104.00
22	R	23	SER	CA-C-N	5.16	125.00	120.10
22	R	23	SER	C-N-CA	5.16	125.00	120.10
10	A	2425	A	P-O3'-C3'	-5.16	112.47	120.20
10	A	2372	G	P-O3'-C3'	-5.15	112.47	120.20
10	A	1065	U	P-O3'-C3'	-5.15	112.48	120.20
11	B	28	C	P-O3'-C3'	-5.15	112.48	120.20
10	A	1716	G	P-O3'-C3'	-5.14	112.48	120.20
11	B	69	C	P-O3'-C3'	-5.13	112.50	120.20
10	A	2450	C	P-O3'-C3'	-5.13	112.50	120.20
10	A	206	A	O3'-P-O5'	-5.12	96.32	104.00
10	A	2921	G	P-O3'-C3'	-5.12	112.52	120.20
10	A	952	A	P-O3'-C3'	-5.11	112.53	120.20
10	A	371	U	C4'-C3'-O3'	-5.11	105.33	113.00
11	B	88	C	P-O3'-C3'	-5.11	112.54	120.20
10	A	1655	G	C2'-C3'-O3'	-5.10	106.04	113.70
10	A	244	G	C3'-C2'-C1'	-5.10	96.40	101.50
10	A	1422	A	C2'-C3'-O3'	5.10	117.14	109.50
11	B	23	U	P-O3'-C3'	-5.09	112.56	120.20
10	A	2256	A	P-O3'-C3'	-5.09	112.56	120.20
10	A	1208	G	P-O3'-C3'	-5.09	112.57	120.20
10	A	2790	A	P-O3'-C3'	-5.09	112.56	120.20
10	A	1432	G	P-O3'-C3'	-5.09	112.57	120.20
10	A	2529	C	P-O3'-C3'	-5.09	112.57	120.20
10	A	2510	C	O3'-P-O5'	-5.08	96.37	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1954	G	P-O3'-C3'	-5.08	112.58	120.20
10	A	2767	A	P-O3'-C3'	-5.08	112.59	120.20
10	A	1993	A	P-O3'-C3'	-5.07	112.59	120.20
10	A	1938	C	P-O3'-C3'	-5.06	112.61	120.20
10	A	1713	A	P-O3'-C3'	-5.05	112.63	120.20
10	A	1818	A	C4'-C3'-O3'	-5.05	105.43	113.00
10	A	588	G	P-O3'-C3'	-5.04	112.64	120.20
10	A	1129	G	P-O3'-C3'	-5.04	112.64	120.20
10	A	1253	C	P-O3'-C3'	-5.04	112.64	120.20
11	B	4	G	P-O3'-C3'	-5.04	112.64	120.20
10	A	1504	U	O3'-P-O5'	-5.04	96.44	104.00
10	A	2543	C	P-O3'-C3'	-5.04	112.65	120.20
10	A	2209	A	P-O3'-C3'	-5.03	112.65	120.20
10	A	745	A	C4'-C3'-O3'	-5.03	105.45	113.00
10	A	2429	G	P-O3'-C3'	-5.03	112.66	120.20
10	A	1614	U	P-O3'-C3'	-5.03	112.66	120.20
10	A	2126	G	C4'-C3'-C2'	-5.03	97.57	102.60
10	A	1165	C	P-O3'-C3'	-5.03	112.66	120.20
10	A	1523	A	P-O3'-C3'	-5.03	112.66	120.20
10	A	2254	G	P-O3'-C3'	-5.02	112.67	120.20
10	A	886	C	P-O3'-C3'	-5.02	112.67	120.20
10	A	2102	G	O3'-P-O5'	-5.02	96.47	104.00
10	A	1367	G	P-O3'-C3'	-5.02	112.67	120.20
10	A	1480	C	P-O3'-C3'	-5.02	112.68	120.20
11	B	46	A	P-O3'-C3'	-5.01	112.68	120.20
10	A	386	U	P-O3'-C3'	-5.01	112.68	120.20
11	B	72	U	P-O3'-C3'	-5.01	112.68	120.20
10	A	1733	C	P-O3'-C3'	-5.01	112.68	120.20
10	A	2253	G	P-O3'-C3'	-5.01	112.68	120.20
10	A	1712	U	O3'-P-O5'	-5.01	96.49	104.00
12	G	11	ASN	CA-C-N	5.01	125.51	120.00
12	G	11	ASN	C-N-CA	5.01	125.51	120.00
10	A	2462	G	C4'-C3'-O3'	-5.00	105.49	113.00

There are no chirality outliers.

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	10	ARG	Sidechain
1	1	18	ARG	Sidechain
5	5	6	ARG	Sidechain
7	7	10	ARG	Sidechain

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Mol	Chain	Res	Type	Group
7	7	29	ARG	Sidechain
8	8	13	ARG	Sidechain
12	G	13	ARG	Sidechain
12	G	156	ARG	Sidechain
12	G	182	ARG	Sidechain
12	G	243	ARG	Sidechain
12	G	274	ARG	Sidechain
12	G	35	ARG	Sidechain
12	G	43	ARG	Sidechain
12	G	60	ARG	Sidechain
14	I	106	ARG	Sidechain
14	I	41	ARG	Sidechain
14	I	95	ARG	Sidechain
15	J	133	ARG	Sidechain
15	J	150	ARG	Sidechain
17	M	14	ARG	Sidechain
18	N	64	ARG	Sidechain
18	N	71	ARG	Sidechain
19	O	33	ARG	Sidechain
19	O	47	ARG	Sidechain
19	O	59	ARG	Sidechain
19	O	60	ARG	Sidechain
20	P	134	ARG	Sidechain
20	P	56	ARG	Sidechain
20	P	6	ARG	Sidechain
21	Q	122	ARG	Sidechain
21	Q	36	ARG	Sidechain
21	Q	59	ARG	Sidechain
21	Q	67	ARG	Sidechain
22	R	104	ARG	Sidechain
22	R	17	ARG	Sidechain
22	R	30	ARG	Sidechain
22	R	96	ARG	Sidechain
23	S	72	ARG	Sidechain
23	S	94	ARG	Sidechain
24	T	51	ARG	Sidechain
24	T	92	ARG	Sidechain
25	U	67	ARG	Sidechain
26	V	20	ARG	Sidechain
29	Z	28	ARG	Sidechain
29	Z	47	ARG	Sidechain

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	1	457	0	502	10	0
2	2	487	0	504	1	0
3	3	433	0	479	3	0
4	4	477	0	454	3	0
5	5	425	0	423	10	0
6	6	400	0	410	4	0
7	7	357	0	405	0	0
8	8	512	0	562	7	0
9	9	292	0	334	3	0
10	A	62459	0	31405	250	0
11	B	2430	0	1229	10	0
12	G	2108	0	2184	22	0
13	H	1582	0	1646	15	0
14	I	1563	0	1655	15	0
15	J	1365	0	1417	15	0
16	K	1271	0	1308	8	0
17	M	1117	0	1140	11	0
18	N	925	0	982	15	0
19	O	1094	0	1137	3	0
20	P	1055	0	1125	8	0
21	Q	983	0	1045	15	0
22	R	914	0	941	7	0
23	S	905	0	973	5	0
24	T	939	0	1011	5	0
25	U	786	0	825	7	0
26	V	848	0	905	8	0
27	W	731	0	763	6	0
28	X	723	0	794	8	0
29	Z	563	0	568	1	0
30	5	1	0	0	0	0
30	9	1	0	0	0	0
31	A	10	0	19	2	0
32	A	161	0	0	0	0
32	G	1	0	0	0	0
32	H	1	0	0	0	0
32	O	1	0	0	0	0
33	A	12	0	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	P	1	0	0	0	0
All	All	88390	0	57169	435	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 3.

All (435) 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)
10:A:1416:U:HO2'	10:A:2245:A:H8	1.16	0.91
13:H:151:PRO:O	13:H:153:ARG:N	2.08	0.87
14:I:156:VAL:O	14:I:177:PRO:O	1.93	0.87
10:A:566:U:O2'	10:A:567:G:C8	2.28	0.85
10:A:2653:C:OP1	13:H:156:LYS:O	1.97	0.83
10:A:1812:U:H5	10:A:1817:A:N7	1.76	0.82
10:A:1713:A:H61	10:A:2029:C:H5	1.25	0.82
10:A:830:U:H5	10:A:839:A:N1	1.78	0.81
10:A:1489:A:H2	10:A:1604:G:H21	1.26	0.80
10:A:2471:U:O3'	10:A:2472:A:H3'	1.82	0.79
18:N:102:VAL:HG13	18:N:106:LEU:HD12	1.62	0.79
10:A:1952:A:H5''	10:A:1953:C:H5	1.50	0.77
15:J:61:THR:HG21	15:J:89:VAL:HG11	1.67	0.77
10:A:1891:G:O2'	10:A:1916:G:N2	2.17	0.77
10:A:890:G:H1	10:A:980:A:H61	1.29	0.76
10:A:1519:A:H62	10:A:1573:A:H2	1.31	0.76
10:A:1501:G:H21	10:A:1509:A:H62	1.33	0.76
10:A:1833:C:OP2	12:G:182:ARG:NH1	2.17	0.76
15:J:46:ASN:HD22	15:J:49:VAL:HG23	1.51	0.75
10:A:1960:A:H2'	10:A:1961:A:C8	2.24	0.73
18:N:65:THR:OG1	18:N:67:SER:O	2.05	0.72
10:A:1311:G:H5''	26:V:20:ARG:HH22	1.55	0.71
10:A:1501:G:N2	10:A:1509:A:H62	1.88	0.71
15:J:129:THR:HG22	15:J:155:VAL:HG22	1.72	0.71
10:A:1850:G:OP2	12:G:156:ARG:NH2	2.24	0.70
10:A:1416:U:O2'	10:A:2245:A:H8	1.75	0.70
13:H:32:GLN:O	13:H:53:PHE:O	2.10	0.69
16:K:103:LEU:HD22	16:K:123:ILE:HG21	1.74	0.69
10:A:1890:G:H8	10:A:1918:A:H62	1.41	0.69
21:Q:103:ALA:HB3	21:Q:104:PRO:HD3	1.74	0.68
21:Q:24:LEU:HD23	21:Q:44:VAL:HG21	1.74	0.68
10:A:1852:A:OP2	12:G:154:LEU:O	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:20:HIS:O	1:1:21:ALA:HB3	1.93	0.67
18:N:68:GLY:HA3	18:N:77:ILE:O	1.95	0.67
10:A:1956:U:H2'	10:A:1957:C:C6	2.30	0.67
21:Q:115:ARG:NH1	21:Q:135:VAL:HG21	2.10	0.66
10:A:1957:C:H2'	10:A:1958:C:C6	2.31	0.66
10:A:2789:U:H5	10:A:2791:A:N7	1.94	0.66
12:G:106:ALA:O	12:G:195:VAL:O	2.14	0.66
5:5:28:ASN:HD22	5:5:28:ASN:N	1.93	0.66
10:A:45:G:H21	10:A:182:A:H62	1.42	0.66
12:G:142:HIS:ND1	12:G:193:GLY:O	2.29	0.65
10:A:655:G:H21	10:A:661:A:H62	1.43	0.65
10:A:566:U:O2'	10:A:567:G:N7	2.26	0.65
18:N:35:ILE:HG21	18:N:103:ALA:HB3	1.79	0.65
25:U:29:VAL:O	25:U:62:VAL:O	2.16	0.64
15:J:60:ILE:HD13	15:J:152:MET:HE1	1.79	0.64
10:A:2235:C:O2'	10:A:2237:C:OP1	2.10	0.64
10:A:579:U:O2'	24:T:49:ASP:OD2	2.13	0.64
20:P:64:VAL:HG22	20:P:106:ILE:HG22	1.81	0.63
10:A:1332:U:H5	10:A:1370:U:O2	1.81	0.63
21:Q:134:LEU:O	21:Q:135:VAL:HG13	1.99	0.63
1:1:20:HIS:O	10:A:2113:G:OP1	2.17	0.62
14:I:154:ILE:HD13	14:I:193:ILE:HB	1.81	0.62
10:A:333:U:H3	10:A:392:G:H1	1.48	0.62
10:A:2177:G:H21	10:A:2180:A:H61	1.48	0.61
13:H:122:VAL:HG21	13:H:143:PRO:HA	1.83	0.60
10:A:655:G:N2	10:A:661:A:H62	1.98	0.60
5:5:20:VAL:HG23	5:5:20:VAL:O	2.00	0.60
10:A:2908:A:O2'	10:A:2909:C:OP2	2.16	0.60
11:B:86:U:H2'	11:B:86:U:O2	2.02	0.59
28:X:1:MET:SD	28:X:65:VAL:HG21	2.42	0.59
10:A:2456:U:O2'	10:A:2457:C:OP2	2.14	0.59
21:Q:134:LEU:O	21:Q:135:VAL:HG22	2.02	0.59
28:X:2:HIS:CE1	28:X:65:VAL:HG12	2.38	0.59
10:A:1233:G:H5''	25:U:82:TYR:CE1	2.38	0.59
10:A:2125:G:N2	10:A:2259:C:OP2	2.35	0.59
18:N:24:VAL:HG13	18:N:33:ALA:HB2	1.84	0.58
15:J:54:VAL:HG13	15:J:65:PRO:HG2	1.84	0.58
10:A:1939:G:H2'	10:A:1940:G:O4'	2.04	0.58
10:A:890:G:N2	10:A:980:A:N1	2.35	0.58
10:A:2029:C:O2	10:A:2029:C:O5'	2.21	0.58
10:A:1952:A:C5'	10:A:1953:C:H5	2.16	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:12:U:OP2	11:B:68:C:O2'	2.22	0.57
16:K:123:ILE:HD11	16:K:144:LEU:CD2	2.35	0.57
22:R:113:ARG:NH1	22:R:119:PHE:OXT	2.31	0.57
17:M:29:LEU:HD23	17:M:143:LEU:HD11	1.87	0.57
18:N:63:VAL:HG12	18:N:106:LEU:HD11	1.87	0.57
10:A:2485:C:H2'	10:A:2486:A:C8	2.40	0.56
8:8:30:SER:O	8:8:31:HIS:O	2.24	0.56
10:A:1785:C:H5''	10:A:1785:C:H6	1.69	0.56
18:N:102:VAL:CG1	18:N:106:LEU:HD12	2.32	0.56
20:P:54:MET:HE1	20:P:104:PHE:HB3	1.87	0.56
8:8:31:HIS:CD2	8:8:32:MET:HG2	2.41	0.56
10:A:1944:U:H2'	10:A:1944:U:O2	2.04	0.56
18:N:81:GLU:N	18:N:81:GLU:OE1	2.38	0.56
23:S:48:ILE:CD1	23:S:100:LEU:HD12	2.35	0.56
26:V:15:VAL:HG11	26:V:51:ILE:HG21	1.86	0.56
10:A:1501:G:H21	10:A:1509:A:N6	2.01	0.56
10:A:1945:A:H2'	10:A:1946:A:H5''	1.87	0.56
24:T:76:TYR:CZ	24:T:80:MET:HG3	2.41	0.56
1:1:20:HIS:O	1:1:21:ALA:CB	2.52	0.56
10:A:829:A:H2'	10:A:830:U:H4'	1.88	0.56
28:X:23:VAL:HG13	28:X:33:VAL:HG13	1.88	0.55
10:A:1028:C:O2	10:A:1028:C:O5'	2.24	0.55
13:H:8:ARG:NH1	13:H:197:LYS:O	2.40	0.55
26:V:87:LEU:HB2	26:V:103:LYS:HB2	1.89	0.55
8:8:27:GLY:O	10:A:2426:U:OP1	2.25	0.54
10:A:1503:A:C2	21:Q:93:TYR:CD1	2.96	0.54
11:B:86:U:O2	11:B:86:U:C2'	2.55	0.54
10:A:1939:G:H5''	10:A:1962:G:C8	2.41	0.54
11:B:44:A:H4'	22:R:5:ILE:HD11	1.90	0.54
23:S:48:ILE:HG13	23:S:62:ARG:HB2	1.89	0.54
10:A:1811:U:H2'	10:A:1817:A:N6	2.23	0.54
10:A:1899:A:H2'	10:A:1900:G:O4'	2.07	0.54
10:A:2611:G:H4'	10:A:2611:G:OP2	2.08	0.54
10:A:2699:C:O2	10:A:2699:C:O5'	2.26	0.54
21:Q:75:GLN:HA	21:Q:89:ASN:HA	1.90	0.54
17:M:54:PHE:CE2	17:M:122:LYS:HG2	2.43	0.54
10:A:2834:A:O2'	10:A:2835:A:O5'	2.24	0.54
10:A:1951:A:O2'	10:A:1952:A:N3	2.40	0.53
10:A:2809:A:H3'	10:A:2809:A:OP1	2.08	0.53
10:A:1786:G:H8	10:A:1786:G:H5''	1.72	0.53
13:H:2:THR:HG23	13:H:204:THR:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:16:VAL:HG22	9:9:25:VAL:HG12	1.90	0.53
10:A:2094:G:H5'	10:A:2536:A:C2	2.43	0.53
17:M:49:ILE:O	17:M:50:ASP:HB3	2.09	0.53
19:O:92:THR:HG22	19:O:124:LYS:HG3	1.89	0.53
10:A:698:A:H5''	10:A:699:U:H5''	1.91	0.53
10:A:1058:U:O4	17:M:28:ARG:HA	2.08	0.53
11:B:22:G:H21	11:B:25:A:H62	1.56	0.53
10:A:1533:A:O2'	10:A:1534:G:OP1	2.26	0.53
28:X:39:ASN:HB2	28:X:63:ILE:HD11	1.91	0.53
27:W:62:LEU:HD13	27:W:62:LEU:C	2.34	0.52
10:A:2361:A:H2'	10:A:2362:A:C8	2.43	0.52
9:9:7:VAL:HG13	9:9:25:VAL:HG13	1.92	0.52
10:A:2472:A:H4'	10:A:2473:C:O5'	2.09	0.52
10:A:1949:A:H3'	10:A:1950:U:H6	1.74	0.52
10:A:1972:U:OP1	10:A:2637:U:O2'	2.22	0.52
10:A:1706:U:H2'	10:A:1707:C:C6	2.45	0.52
10:A:1945:A:C2'	10:A:1946:A:H5''	2.38	0.52
10:A:842:U:H2'	10:A:843:U:C6	2.45	0.52
10:A:2299:A:H4'	10:A:2300:A:O5'	2.10	0.52
8:8:27:GLY:O	8:8:29:THR:N	2.42	0.52
10:A:318:G:H8	10:A:318:G:H5''	1.74	0.51
10:A:1943:G:H1'	10:A:1954:G:N2	2.25	0.51
4:4:35:ILE:HG22	4:4:45:LEU:HD13	1.92	0.51
18:N:63:VAL:HB	18:N:102:VAL:HG22	1.92	0.51
10:A:548:A:H4'	10:A:549:C:O5'	2.10	0.51
10:A:908:A:C2	10:A:964:A:C4	2.98	0.51
10:A:1941:C:H2'	10:A:1942:C:C6	2.45	0.51
10:A:220:G:N2	10:A:237:U:H4'	2.25	0.51
10:A:1249:A:C8	10:A:1249:A:H3'	2.45	0.51
21:Q:115:ARG:NH1	21:Q:135:VAL:CG2	2.72	0.51
10:A:344:C:O2	10:A:344:C:O4'	2.28	0.51
17:M:25:SER:O	17:M:27:GLY:O	2.29	0.51
15:J:56:GLU:HB2	15:J:141:ILE:HD11	1.93	0.51
10:A:1319:A:H4'	10:A:1320:G:OP1	2.11	0.51
20:P:58:MET:HE1	20:P:106:ILE:HB	1.93	0.51
25:U:1:MET:HE3	25:U:100:ILE:HB	1.93	0.50
10:A:1947:C:C5	10:A:1948:U:H1'	2.46	0.50
10:A:2088:C:H2'	10:A:2537:U:H4'	1.93	0.50
6:6:31:GLU:HB3	6:6:44:LEU:HD11	1.92	0.50
16:K:123:ILE:HD11	16:K:144:LEU:HD21	1.91	0.50
10:A:2502:A:N6	10:A:2514:G:O2'	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:575:G:N3	10:A:575:G:H2'	2.27	0.50
12:G:268:LYS:HE2	12:G:269:PHE:CE2	2.46	0.50
10:A:1944:U:H3	10:A:1953:C:H42	1.57	0.50
28:X:31:ASP:O	28:X:65:VAL:HG23	2.11	0.50
10:A:2507:C:O2	10:A:2507:C:O4'	2.28	0.50
15:J:54:VAL:HG13	15:J:65:PRO:CG	2.41	0.50
21:Q:102:VAL:O	21:Q:105:ARG:HG2	2.12	0.50
28:X:2:HIS:HE1	28:X:65:VAL:HG12	1.76	0.50
17:M:27:GLY:O	17:M:28:ARG:HB2	2.12	0.50
13:H:146:MET:HE1	13:H:160:LEU:HD11	1.93	0.49
10:A:661:A:OP1	14:I:106:ARG:HD2	2.11	0.49
28:X:33:VAL:CG1	28:X:35:ILE:HD11	2.42	0.49
5:5:2:ALA:HB3	10:A:2089:G:N2	2.27	0.49
21:Q:20:LEU:HB2	21:Q:40:ILE:HD11	1.93	0.49
10:A:2458:A:H5''	10:A:2460:C:O4'	2.12	0.49
15:J:117:VAL:HG23	15:J:176:PRO:C	2.38	0.49
10:A:1503:A:N6	10:A:2735:G:OP2	2.45	0.49
10:A:1489:A:H2	10:A:1604:G:N2	2.04	0.49
18:N:97:ARG:C	18:N:98:ILE:HD12	2.38	0.49
10:A:566:U:O2'	10:A:567:G:H8	1.88	0.49
10:A:631:U:H2'	10:A:632:U:C6	2.48	0.49
10:A:1951:A:N3	10:A:1952:A:H2	2.11	0.48
12:G:142:HIS:HB2	12:G:155:VAL:O	2.14	0.48
15:J:13:VAL:HB	15:J:14:PRO:HD3	1.95	0.48
10:A:1949:A:H3'	10:A:1950:U:C6	2.48	0.48
15:J:60:ILE:HG23	15:J:138:PHE:CE1	2.49	0.48
10:A:26:G:H1'	10:A:559:A:N6	2.29	0.48
18:N:91:LYS:HB3	18:N:111:PHE:CD2	2.48	0.48
10:A:2347:A:H2'	10:A:2348:U:C6	2.48	0.48
23:S:104:ARG:O	23:S:105:GLY:O	2.32	0.48
6:6:7:LEU:HD11	6:6:32:LEU:HD12	1.96	0.48
10:A:828:A:H5'	10:A:829:A:C2	2.48	0.48
26:V:114:GLU:O	26:V:115:VAL:HB	2.14	0.48
16:K:33:LEU:HD13	16:K:75:MET:HG2	1.95	0.48
10:A:1997:G:H4'	10:A:1998:C:OP2	2.13	0.47
11:B:39:A:N6	15:J:67:ILE:O	2.46	0.47
15:J:36:ILE:HD13	15:J:61:THR:HG22	1.95	0.47
17:M:5:TYR:CG	24:T:100:VAL:HG11	2.48	0.47
27:W:42:VAL:HG11	27:W:80:VAL:HG11	1.96	0.47
19:O:78:ASN:O	19:O:81:VAL:HG22	2.14	0.47
28:X:31:ASP:C	28:X:65:VAL:HG23	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1832:G:H4'	10:A:1833:C:O5'	2.14	0.47
5:5:33:CYS:N	5:5:46:CYS:SG	2.88	0.47
10:A:1954:G:H2'	10:A:1954:G:N3	2.29	0.47
3:3:13:ILE:HD11	10:A:1035:G:C8	2.50	0.47
5:5:20:VAL:O	5:5:20:VAL:CG2	2.63	0.47
10:A:1785:C:H6	10:A:1785:C:C5'	2.28	0.47
23:S:48:ILE:HD13	23:S:100:LEU:HD12	1.97	0.47
24:T:43:TYR:HB3	25:U:74:TYR:HB3	1.95	0.47
5:5:28:ASN:N	5:5:28:ASN:ND2	2.62	0.47
10:A:1245:U:H1'	24:T:4:VAL:HG22	1.95	0.47
13:H:126:HIS:ND1	13:H:159:LEU:HD13	2.29	0.47
8:8:30:SER:O	8:8:31:HIS:HD2	1.97	0.47
10:A:1784:C:H2'	10:A:1785:C:H5''	1.96	0.47
10:A:2059:U:H2'	10:A:2060:G:O4'	2.14	0.46
10:A:2899:C:H2'	10:A:2900:G:O4'	2.16	0.46
27:W:42:VAL:HG21	27:W:80:VAL:HG21	1.97	0.46
10:A:2537:U:O5'	10:A:2537:U:H6	1.99	0.46
23:S:28:VAL:HG22	23:S:84:LEU:CD1	2.46	0.46
10:A:2276:U:H2'	10:A:2277:U:C6	2.51	0.46
15:J:136:LEU:HA	15:J:141:ILE:HG21	1.97	0.46
21:Q:134:LEU:C	21:Q:135:VAL:HG22	2.40	0.46
10:A:220:G:H22	10:A:237:U:H4'	1.81	0.46
10:A:762:A:C2	10:A:763:U:H1'	2.50	0.46
10:A:1952:A:H3'	10:A:1953:C:H6	1.81	0.46
12:G:43:ARG:NH1	12:G:49:LEU:HD13	2.31	0.46
1:1:8:THR:HG21	1:1:10:ARG:NH1	2.31	0.46
10:A:579:U:H2'	10:A:580:U:C6	2.50	0.46
14:I:177:PRO:O	14:I:178:ALA:HB2	2.16	0.46
10:A:141:U:H5''	10:A:141:U:H6	1.81	0.46
10:A:2157:G:N2	10:A:2206:A:H62	2.13	0.46
10:A:1074:A:N6	10:A:1171:G:H2'	2.31	0.46
10:A:1533:A:O2'	10:A:1534:G:P	2.74	0.46
10:A:2789:U:C5	10:A:2791:A:N7	2.79	0.46
16:K:123:ILE:CD1	16:K:133:VAL:HG13	2.46	0.46
21:Q:22:THR:HG21	21:Q:67:ARG:HB2	1.98	0.46
5:5:33:CYS:SG	5:5:46:CYS:N	2.89	0.46
22:R:69:LYS:HB3	22:R:104:ARG:HD3	1.98	0.46
4:4:11:PRO:HA	4:4:26:GLY:HA2	1.98	0.46
10:A:1940:G:H1	10:A:1956:U:H3	1.64	0.46
10:A:1635:A:H1'	10:A:1636:G:O4'	2.16	0.45
10:A:1939:G:C6	10:A:1940:G:C5	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:21:ALA:HA	10:A:2465:A:N1	2.31	0.45
10:A:831:U:H2'	10:A:832:C:C6	2.51	0.45
10:A:1049:G:O2'	10:A:1056:A:N1	2.46	0.45
20:P:54:MET:HE2	20:P:64:VAL:HG13	1.97	0.45
10:A:1944:U:H3	10:A:1951:A:H2'	1.81	0.45
10:A:1249:A:C2'	10:A:1250:G:O5'	2.63	0.45
10:A:2090:G:P	31:A:3001:SPD:H102	2.39	0.45
25:U:6:GLU:HG3	25:U:39:LEU:HD21	1.97	0.45
10:A:859:U:H2'	10:A:860:C:C6	2.52	0.45
10:A:1952:A:H5''	10:A:1953:C:C5	2.41	0.45
14:I:81:PRO:HB3	14:I:89:VAL:HG23	1.99	0.45
22:R:102:HIS:O	22:R:106:LYS:HB3	2.17	0.45
10:A:2058:C:H2'	10:A:2059:U:C6	2.50	0.45
10:A:2256:A:OP1	12:G:171:TYR:OH	2.33	0.45
11:B:11:A:N1	11:B:67:G:O2'	2.45	0.45
14:I:46:GLN:HG2	14:I:48:THR:HG23	1.99	0.45
16:K:123:ILE:O	16:K:123:ILE:HG22	2.17	0.45
20:P:54:MET:HE3	20:P:106:ILE:HG23	1.99	0.45
10:A:1074:A:N3	10:A:2519:G:O2'	2.39	0.45
10:A:1812:U:C5	10:A:1817:A:N7	2.68	0.45
10:A:1889:A:C8	10:A:1889:A:H5''	2.52	0.45
14:I:177:PRO:O	14:I:178:ALA:CB	2.64	0.45
1:1:55:LYS:O	1:1:56:SER:OG	2.31	0.45
20:P:51:ARG:HD3	20:P:66:ILE:HD11	1.99	0.45
10:A:1187:U:H4'	10:A:1188:A:O4'	2.17	0.45
10:A:83:G:N2	10:A:101:G:O2'	2.51	0.44
10:A:1957:C:H2'	10:A:1958:C:H6	1.82	0.44
12:G:126:VAL:HA	12:G:192:ILE:HG22	1.99	0.44
14:I:155:VAL:HG12	14:I:198:ALA:HB1	1.99	0.44
10:A:1066:A:C2	10:A:1187:U:C2	3.05	0.44
10:A:2789:U:H1'	10:A:2790:A:H5''	1.99	0.44
13:H:14:GLN:HB2	13:H:22:LEU:HD11	2.00	0.44
10:A:2319:A:H4'	10:A:2320:A:O4'	2.18	0.44
10:A:2925:U:H2'	10:A:2926:U:C6	2.52	0.44
10:A:351:G:H2'	10:A:352:A:C8	2.52	0.44
10:A:1939:G:C5	10:A:1940:G:C8	3.05	0.44
12:G:205:ILE:O	12:G:210:ARG:HD3	2.17	0.44
13:H:53:PHE:CD1	13:H:53:PHE:C	2.96	0.44
18:N:64:ARG:HB2	18:N:79:PHE:CG	2.53	0.44
25:U:5:ILE:HG22	25:U:38:VAL:HG22	2.00	0.44
10:A:804:G:N3	10:A:2014:A:H2	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:17:GLN:HB3	2:2:53:MET:HE3	1.99	0.44
10:A:274:A:H61	10:A:296:G:H1'	1.83	0.44
10:A:1027:A:N1	10:A:2060:G:O2'	2.46	0.44
10:A:1177:G:O2'	10:A:2059:U:H5'	2.17	0.44
10:A:2699:C:O2	10:A:2699:C:O4'	2.33	0.44
17:M:38:ARG:HD2	17:M:119:LEU:HD11	2.00	0.44
26:V:12:ALA:HB2	26:V:55:VAL:HG22	2.00	0.44
10:A:37:C:H4'	10:A:497:U:OP1	2.18	0.43
10:A:174:A:H8	10:A:174:A:H5''	1.83	0.43
10:A:613:G:H2'	10:A:2063:A:N7	2.32	0.43
10:A:655:G:C6	10:A:656:G:C6	3.05	0.43
10:A:1985:A:C2	18:N:22:ILE:HG23	2.53	0.43
10:A:1340:A:OP1	10:A:2742:G:O2'	2.31	0.43
10:A:1834:A:H4'	10:A:2236:G:C2	2.53	0.43
5:5:30:CYS:HB3	5:5:33:CYS:HB2	2.00	0.43
10:A:746:G:O2'	10:A:1681:A:N3	2.39	0.43
10:A:1176:U:N3	13:H:151:PRO:HB3	2.33	0.43
17:M:27:GLY:O	17:M:28:ARG:CB	2.67	0.43
10:A:617:A:OP2	31:A:3001:SPD:H22	2.18	0.43
12:G:126:VAL:O	12:G:192:ILE:O	2.37	0.43
10:A:646:A:N1	10:A:670:G:O2'	2.46	0.43
10:A:865:A:C4	10:A:1235:A:C2	3.06	0.43
14:I:193:ILE:HD12	14:I:193:ILE:N	2.34	0.43
16:K:123:ILE:HD13	16:K:133:VAL:HG13	1.99	0.43
27:W:62:LEU:HD13	27:W:63:LYS:N	2.33	0.43
14:I:158:GLY:O	14:I:159:GLU:C	2.61	0.43
26:V:49:SER:HB2	26:V:50:PRO:HD3	2.01	0.43
10:A:1950:U:H2'	10:A:1951:A:C8	2.53	0.43
10:A:1951:A:H2'	10:A:1953:C:N4	2.34	0.43
10:A:2353:A:H2'	10:A:2353:A:N3	2.33	0.43
10:A:2707:G:H4'	18:N:30:ARG:HD2	2.00	0.43
12:G:67:PHE:HE1	12:G:105:ILE:HD11	1.84	0.43
10:A:522:G:H4'	10:A:547:A:N1	2.34	0.43
10:A:2306:A:H2'	10:A:2307:A:C8	2.54	0.43
10:A:2605:A:N7	13:H:149:VAL:HG11	2.34	0.43
12:G:26:THR:HG22	12:G:80:THR:OG1	2.18	0.43
21:Q:59:ARG:HA	21:Q:99:PHE:CZ	2.54	0.43
10:A:1015:G:H2'	10:A:1016:U:C6	2.54	0.42
10:A:2112:U:H2'	10:A:2113:G:O4'	2.19	0.42
10:A:2608:C:H5'	13:H:149:VAL:HG23	2.01	0.42
10:A:2766:C:H2'	10:A:2767:A:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:101:LEU:N	14:I:101:LEU:HD23	2.34	0.42
21:Q:40:ILE:HD13	21:Q:40:ILE:HA	1.84	0.42
1:1:5:CYS:O	1:1:8:THR:O	2.37	0.42
1:1:55:LYS:O	1:1:56:SER:CB	2.67	0.42
10:A:2324:U:OP1	10:A:2413:U:O2'	2.35	0.42
5:5:3:VAL:HG12	10:A:2048:A:C2	2.54	0.42
10:A:874:U:H4'	10:A:877:G:N1	2.34	0.42
10:A:1951:A:H4'	10:A:1952:A:OP1	2.11	0.42
14:I:32:VAL:HG13	14:I:105:VAL:HG13	2.01	0.42
6:6:9:CYS:SG	6:6:43:THR:HG21	2.60	0.42
10:A:2304:G:OP1	29:Z:26:SER:HB3	2.19	0.42
10:A:1332:U:C5	10:A:1370:U:O2	2.69	0.42
10:A:1889:A:H5''	10:A:1889:A:H8	1.84	0.42
10:A:2269:U:H2'	10:A:2270:G:O4'	2.19	0.42
10:A:2863:G:H2'	10:A:2908:A:N6	2.34	0.42
10:A:267:A:N1	10:A:473:U:O2'	2.48	0.42
10:A:1947:C:H3'	10:A:1948:U:O2	2.20	0.42
17:M:2:ARG:HG3	17:M:3:THR:HG23	2.02	0.42
20:P:54:MET:HE3	20:P:106:ILE:CG2	2.50	0.42
6:6:26:ASN:HB3	6:6:30:ILE:HD11	2.01	0.42
11:B:48:G:OP1	22:R:68:SER:OG	2.38	0.42
11:B:76:A:C2	11:B:97:A:C4	3.07	0.42
10:A:24:G:O2'	26:V:82:ASP:HB3	2.20	0.42
10:A:83:G:N2	10:A:102:A:OP2	2.47	0.42
10:A:117:A:N3	10:A:179:G:H1'	2.35	0.42
10:A:249:G:H4'	10:A:432:G:C5	2.55	0.42
10:A:1597:A:N7	10:A:1598:G:C6	2.88	0.42
10:A:1706:U:H2'	10:A:1707:C:H6	1.84	0.42
10:A:1834:A:OP2	12:G:150:LYS:NZ	2.53	0.42
10:A:2456:U:HO2'	10:A:2457:C:P	2.37	0.42
26:V:18:ALA:HB3	26:V:21:LYS:HD2	2.00	0.42
10:A:1530:G:C2	10:A:1563:A:C2	3.08	0.42
3:3:6:ILE:HD11	3:3:47:ILE:HD11	2.01	0.41
10:A:342:A:N1	10:A:376:G:O2'	2.50	0.41
10:A:1779:G:H3'	10:A:1780:A:H5''	2.02	0.41
10:A:1819:A:H1'	10:A:1971:A:N6	2.35	0.41
10:A:2054:G:H2'	10:A:2054:G:N3	2.35	0.41
12:G:248:SER:OG	12:G:251:GLY:O	2.25	0.41
14:I:111:LYS:O	14:I:115:SER:OG	2.37	0.41
9:9:15:LYS:HE2	9:9:15:LYS:HA	2.02	0.41
10:A:909:G:H2'	10:A:910:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1357:U:O2	10:A:1357:U:H2'	2.19	0.41
10:A:1469:A:H2'	10:A:1471:G:N7	2.35	0.41
10:A:1482:G:H2'	10:A:1483:A:C8	2.55	0.41
10:A:2300:A:H5''	10:A:2301:A:H5'	2.02	0.41
12:G:126:VAL:HG12	12:G:127:GLY:N	2.34	0.41
19:O:92:THR:HG22	19:O:124:LYS:CG	2.50	0.41
25:U:92:TYR:CD1	25:U:92:TYR:C	2.97	0.41
10:A:139:A:H4'	10:A:140:G:OP1	2.20	0.41
10:A:1066:A:H4'	10:A:1067:A:O5'	2.20	0.41
10:A:1965:A:H2'	10:A:1966:G:O4'	2.19	0.41
10:A:1977:U:C5	10:A:1988:U:C2	3.08	0.41
16:K:103:LEU:HD22	16:K:123:ILE:CG2	2.46	0.41
22:R:72:ALA:O	22:R:76:VAL:HG23	2.20	0.41
10:A:489:A:H1'	10:A:1247:U:O4'	2.21	0.41
10:A:2586:G:H2'	10:A:2587:U:O4'	2.20	0.41
13:H:51:ILE:HD12	13:H:83:PHE:CE1	2.55	0.41
15:J:103:LEU:HA	15:J:107:SER:HB3	2.03	0.41
1:1:56:SER:OG	1:1:57:GLY:N	2.54	0.41
10:A:1372:G:H2'	10:A:1374:C:C5	2.56	0.41
10:A:2029:C:H4'	10:A:2030:A:OP1	2.20	0.41
10:A:684:U:H2'	10:A:685:C:C6	2.54	0.41
10:A:1832:G:N2	12:G:154:LEU:O	2.54	0.41
18:N:35:ILE:HG21	18:N:103:ALA:CB	2.46	0.41
10:A:39:C:O2'	10:A:658:A:N1	2.52	0.41
10:A:228:A:C2'	10:A:231:A:H61	2.33	0.41
10:A:229:A:O4'	10:A:231:A:N6	2.54	0.41
10:A:789:A:O2'	10:A:1708:U:OP1	2.33	0.41
10:A:1308:U:C4	10:A:1309:G:C6	3.08	0.41
10:A:1357:U:O2	10:A:1357:U:C2'	2.68	0.41
10:A:383:A:H2'	10:A:384:G:O4'	2.21	0.41
10:A:1845:G:N3	12:G:44:ASN:OD1	2.54	0.41
10:A:2364:G:O2'	10:A:2369:A:N1	2.48	0.41
11:B:35:C:C5	11:B:36:C:C5	3.08	0.41
14:I:20:ASN:OD1	14:I:22:THR:OG1	2.37	0.41
21:Q:103:ALA:HB3	21:Q:104:PRO:CD	2.46	0.41
4:4:51:SER:OG	4:4:52:SER:N	2.53	0.41
8:8:23:LYS:NZ	10:A:675:G:OP1	2.48	0.41
10:A:1344:A:C2	10:A:1675:G:C6	3.09	0.41
10:A:1398:A:H2'	10:A:1399:G:O4'	2.21	0.41
10:A:1829:U:H2'	10:A:1830:C:C6	2.56	0.41
10:A:1955:G:N3	10:A:1955:G:H2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:2590:G:H2'	10:A:2591:C:C6	2.56	0.41
10:A:2822:C:O2'	10:A:2823:A:O4'	2.38	0.41
12:G:144:ILE:HD11	12:G:162:ALA:HB3	2.03	0.41
13:H:27:VAL:HG22	13:H:187:LEU:HD22	2.02	0.41
15:J:50:LEU:HD22	15:J:54:VAL:HG23	2.03	0.41
17:M:25:SER:C	17:M:27:GLY:O	2.63	0.41
22:R:101:TYR:OH	22:R:113:ARG:NH2	2.54	0.41
10:A:958:A:H2'	20:P:9:TYR:OH	2.21	0.41
10:A:1943:G:H2'	10:A:1943:G:N3	2.35	0.41
10:A:1952:A:H3'	10:A:1953:C:C6	2.56	0.41
10:A:2353:A:N3	10:A:2353:A:C2'	2.84	0.41
12:G:75:PRO:HB3	12:G:117:TYR:CE2	2.56	0.41
10:A:759:G:H21	10:A:764:A:H2	1.68	0.40
10:A:1827:U:H2'	10:A:1828:C:C6	2.56	0.40
1:1:8:THR:HG21	1:1:10:ARG:HH12	1.87	0.40
8:8:39:LYS:NZ	10:A:2398:G:N7	2.50	0.40
10:A:1096:A:C2	10:A:2784:G:C4	3.09	0.40
10:A:1940:G:C6	10:A:1941:C:C4	3.09	0.40
3:3:17:GLN:N	3:3:18:PRO:CD	2.84	0.40
10:A:502:C:C2	27:W:68:TYR:CE1	3.09	0.40
10:A:719:C:H5''	14:I:81:PRO:HD2	2.03	0.40
10:A:903:G:H2'	10:A:904:A:C8	2.56	0.40
10:A:1943:G:H1	10:A:1953:C:N4	2.19	0.40
10:A:2378:G:N3	10:A:2414:C:H2'	2.36	0.40
10:A:2587:U:H2'	10:A:2588:U:C6	2.56	0.40
10:A:775:G:OP1	12:G:10:THR:OG1	2.33	0.40
10:A:1486:G:O2'	10:A:1527:A:H1'	2.21	0.40
10:A:2597:A:C2	10:A:2680:U:H4'	2.56	0.40
10:A:2717:U:C4	10:A:2718:G:N7	2.89	0.40
5:5:28:ASN:HD22	5:5:28:ASN:H	1.68	0.40
10:A:302:G:H2'	10:A:303:G:O4'	2.22	0.40
10:A:1382:G:N7	27:W:61:LYS:NZ	2.69	0.40
10:A:1438:G:H4'	10:A:1652:A:H4'	2.04	0.40
10:A:1690:A:H2'	10:A:1691:G:O4'	2.22	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	1	56/62 (90%)	50 (89%)	5 (9%)	1 (2%)	6	28
2	2	57/63 (90%)	56 (98%)	0	1 (2%)	6	28
3	3	54/59 (92%)	54 (100%)	0	0	100	100
4	4	57/81 (70%)	52 (91%)	5 (9%)	0	100	100
5	5	51/57 (90%)	49 (96%)	2 (4%)	0	100	100
6	6	45/49 (92%)	45 (100%)	0	0	100	100
7	7	40/44 (91%)	39 (98%)	1 (2%)	0	100	100
8	8	61/66 (92%)	58 (95%)	2 (3%)	1 (2%)	7	30
9	9	34/37 (92%)	34 (100%)	0	0	100	100
12	G	271/277 (98%)	260 (96%)	8 (3%)	3 (1%)	11	39
13	H	204/209 (98%)	191 (94%)	12 (6%)	1 (0%)	24	57
14	I	201/207 (97%)	186 (92%)	11 (6%)	4 (2%)	6	25
15	J	173/179 (97%)	159 (92%)	11 (6%)	3 (2%)	7	30
16	K	163/178 (92%)	154 (94%)	7 (4%)	2 (1%)	10	37
17	M	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
18	N	120/122 (98%)	111 (92%)	7 (6%)	2 (2%)	7	30
19	O	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
20	P	131/144 (91%)	127 (97%)	4 (3%)	0	100	100
21	Q	118/135 (87%)	111 (94%)	7 (6%)	0	100	100
22	R	116/119 (98%)	103 (89%)	11 (10%)	2 (2%)	7	30
23	S	110/114 (96%)	106 (96%)	3 (3%)	1 (1%)	14	44
24	T	114/119 (96%)	111 (97%)	3 (3%)	0	100	100
25	U	99/102 (97%)	92 (93%)	5 (5%)	2 (2%)	6	25
26	V	108/118 (92%)	106 (98%)	1 (1%)	1 (1%)	14	44
27	W	88/94 (94%)	84 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	X	93/103 (90%)	89 (96%)	3 (3%)	1 (1%)	11	39
29	Z	71/96 (74%)	65 (92%)	5 (7%)	1 (1%)	9	34
All	All	2917/3125 (93%)	2760 (95%)	131 (4%)	26 (1%)	16	44

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	56	SER
8	8	31	HIS
12	G	126	VAL
13	H	152	ASN
18	N	110	ASN
23	S	105	GLY
28	X	51	ASN
14	I	61	GLY
14	I	178	ALA
26	V	114	GLU
14	I	129	LEU
15	J	83	MET
22	R	101	TYR
2	2	38	GLU
12	G	252	LYS
15	J	147	SER
15	J	150	ARG
25	U	45	SER
14	I	159	GLU
16	K	126	PRO
18	N	91	LYS
22	R	63	PHE
25	U	46	ALA
29	Z	82	ARG
12	G	241	ILE
16	K	118	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	50/53 (94%)	49 (98%)	1 (2%)	48	72
2	2	52/55 (94%)	51 (98%)	1 (2%)	50	73
3	3	50/52 (96%)	50 (100%)	0	100	100
4	4	56/73 (77%)	56 (100%)	0	100	100
5	5	47/50 (94%)	46 (98%)	1 (2%)	47	71
6	6	46/48 (96%)	44 (96%)	2 (4%)	26	57
7	7	38/39 (97%)	38 (100%)	0	100	100
8	8	53/56 (95%)	52 (98%)	1 (2%)	50	73
9	9	35/35 (100%)	33 (94%)	2 (6%)	18	49
12	G	221/225 (98%)	220 (100%)	1 (0%)	81	85
13	H	169/171 (99%)	169 (100%)	0	100	100
14	I	171/174 (98%)	168 (98%)	3 (2%)	51	73
15	J	151/155 (97%)	142 (94%)	9 (6%)	17	47
16	K	137/147 (93%)	133 (97%)	4 (3%)	37	66
17	M	119/121 (98%)	118 (99%)	1 (1%)	73	81
18	N	101/101 (100%)	98 (97%)	3 (3%)	36	65
19	O	113/115 (98%)	110 (97%)	3 (3%)	39	67
20	P	105/113 (93%)	104 (99%)	1 (1%)	68	79
21	Q	102/111 (92%)	99 (97%)	3 (3%)	37	66
22	R	96/97 (99%)	94 (98%)	2 (2%)	47	71
23	S	98/100 (98%)	98 (100%)	0	100	100
24	T	95/97 (98%)	94 (99%)	1 (1%)	65	78
25	U	82/82 (100%)	81 (99%)	1 (1%)	63	78
26	V	91/97 (94%)	90 (99%)	1 (1%)	65	78
27	W	80/84 (95%)	79 (99%)	1 (1%)	61	77
28	X	81/88 (92%)	79 (98%)	2 (2%)	42	69
29	Z	58/76 (76%)	57 (98%)	1 (2%)	53	74
All	All	2497/2615 (96%)	2452 (98%)	45 (2%)	51	73

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	39	LEU

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Mol	Chain	Res	Type
2	2	42	ARG
5	5	28	ASN
6	6	12	CYS
6	6	15	ARG
8	8	31	HIS
9	9	24	MET
9	9	25	VAL
12	G	80	THR
14	I	7	LEU
14	I	93	THR
14	I	101	LEU
15	J	4	LEU
15	J	50	LEU
15	J	85	ILE
15	J	95	ARG
15	J	100	LEU
15	J	103	LEU
15	J	115	ARG
15	J	125	ARG
15	J	133	ARG
16	K	30	LYS
16	K	72	LEU
16	K	124	GLU
16	K	173	GLU
17	M	29	LEU
18	N	81	GLU
18	N	102	VAL
18	N	122	LEU
19	O	47	ARG
19	O	124	LYS
19	O	142	LYS
20	P	54	MET
21	Q	40	ILE
21	Q	53	LYS
21	Q	135	VAL
22	R	39	ASN
22	R	110	GLU
24	T	78	LYS
25	U	12	ILE
26	V	16	ARG
27	W	67	ARG
28	X	33	VAL

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Mol	Chain	Res	Type
28	X	95	LYS
29	Z	57	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	20	HIS
1	1	41	ASN
2	2	17	GLN
2	2	31	GLN
2	2	39	ASN
3	3	17	GLN
5	5	28	ASN
5	5	48	GLN
12	G	44	ASN
12	G	86	ASN
12	G	194	GLN
12	G	226	ASN
13	H	128	GLN
15	J	37	ASN
15	J	46	ASN
15	J	172	GLN
16	K	38	ASN
16	K	140	HIS
18	N	109	ASN
19	O	4	HIS
21	Q	110	GLN
22	R	32	ASN
22	R	58	ASN
23	S	14	ASN
24	T	36	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	2905/2931 (99%)	524 (18%)	76 (2%)
11	B	113/114 (99%)	21 (18%)	3 (2%)
All	All	3018/3045 (99%)	545 (18%)	79 (2%)

All (545) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	A	10	A
10	A	12	A
10	A	13	A
10	A	34	U
10	A	45	G
10	A	46	C
10	A	60	G
10	A	71	A
10	A	74	U
10	A	75	G
10	A	84	A
10	A	90	A
10	A	91	C
10	A	93	U
10	A	101	G
10	A	102	A
10	A	117	A
10	A	118	A
10	A	119	U
10	A	140	G
10	A	141	U
10	A	161	A
10	A	162	A
10	A	164	A
10	A	167	U
10	A	174	A
10	A	175	G
10	A	182	A
10	A	188	A
10	A	198	A
10	A	201	A
10	A	202	U
10	A	215	A
10	A	218	A
10	A	223	A
10	A	224	A
10	A	225	A
10	A	229	A
10	A	230	A
10	A	232	U
10	A	235	A
10	A	250	G
10	A	251	C

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Mol	Chain	Res	Type
10	A	252	G
10	A	257	A
10	A	274	A
10	A	275	C
10	A	281	A
10	A	283	C
10	A	284	U
10	A	285	U
10	A	286	G
10	A	287	C
10	A	288	U
10	A	290	C
10	A	297	U
10	A	298	U
10	A	299	G
10	A	300	U
10	A	301	A
10	A	303	G
10	A	307	C
10	A	309	C
10	A	311	A
10	A	312	U
10	A	313	A
10	A	318	G
10	A	320	U
10	A	323	A
10	A	325	A
10	A	326	A
10	A	327	G
10	A	328	A
10	A	345	G
10	A	354	A
10	A	360	G
10	A	372	A
10	A	373	A
10	A	404	A
10	A	406	A
10	A	409	G
10	A	410	G
10	A	412	U
10	A	417	A
10	A	418	G

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Mol	Chain	Res	Type
10	A	432	G
10	A	440	C
10	A	450	C
10	A	451	C
10	A	457	G
10	A	466	C
10	A	470	G
10	A	490	C
10	A	503	A
10	A	527	G
10	A	549	C
10	A	550	A
10	A	552	U
10	A	566	U
10	A	567	G
10	A	575	G
10	A	576	U
10	A	577	A
10	A	578	G
10	A	583	A
10	A	591	A
10	A	592	A
10	A	594	G
10	A	599	A
10	A	606	G
10	A	616	G
10	A	618	A
10	A	629	A
10	A	630	G
10	A	646	A
10	A	656	G
10	A	657	A
10	A	658	A
10	A	659	A
10	A	672	A
10	A	679	G
10	A	682	A
10	A	690	U
10	A	699	U
10	A	700	A
10	A	731	A
10	A	732	U

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Mol	Chain	Res	Type
10	A	757	A
10	A	758	G
10	A	763	U
10	A	776	U
10	A	793	U
10	A	803	G
10	A	810	A
10	A	811	G
10	A	821	G
10	A	828	A
10	A	830	U
10	A	836	U
10	A	837	C
10	A	851	G
10	A	858	C
10	A	865	A
10	A	873	U
10	A	874	U
10	A	889	G
10	A	891	U
10	A	892	A
10	A	893	A
10	A	894	A
10	A	906	G
10	A	913	A
10	A	926	G
10	A	931	C
10	A	933	U
10	A	934	U
10	A	935	C
10	A	936	U
10	A	937	C
10	A	940	G
10	A	942	U
10	A	943	A
10	A	950	U
10	A	954	A
10	A	957	A
10	A	959	C
10	A	964	A
10	A	970	A
10	A	973	U

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Mol	Chain	Res	Type
10	A	974	A
10	A	976	U
10	A	979	U
10	A	987	A
10	A	990	C
10	A	991	A
10	A	992	G
10	A	1007	G
10	A	1020	A
10	A	1029	A
10	A	1035	G
10	A	1036	A
10	A	1042	A
10	A	1058	U
10	A	1059	A
10	A	1067	A
10	A	1068	G
10	A	1072	A
10	A	1079	U
10	A	1084	G
10	A	1092	A
10	A	1093	G
10	A	1100	A
10	A	1101	G
10	A	1102	G
10	A	1103	A
10	A	1111	U
10	A	1115	A
10	A	1116	A
10	A	1119	A
10	A	1120	G
10	A	1128	U
10	A	1129	G
10	A	1130	A
10	A	1131	A
10	A	1132	A
10	A	1133	G
10	A	1134	A
10	A	1136	U
10	A	1138	C
10	A	1139	G
10	A	1142	A

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Mol	Chain	Res	Type
10	A	1146	C
10	A	1147	U
10	A	1148	C
10	A	1149	A
10	A	1151	U
10	A	1152	G
10	A	1153	G
10	A	1154	U
10	A	1155	C
10	A	1156	G
10	A	1157	A
10	A	1158	G
10	A	1174	A
10	A	1178	U
10	A	1179	A
10	A	1180	C
10	A	1181	C
10	A	1182	G
10	A	1188	A
10	A	1189	A
10	A	1203	A
10	A	1204	C
10	A	1209	G
10	A	1241	G
10	A	1249	A
10	A	1250	G
10	A	1254	G
10	A	1265	A
10	A	1283	G
10	A	1289	A
10	A	1298	A
10	A	1301	G
10	A	1311	G
10	A	1312	U
10	A	1316	G
10	A	1317	A
10	A	1319	A
10	A	1320	G
10	A	1344	A
10	A	1345	A
10	A	1347	A
10	A	1381	G

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Mol	Chain	Res	Type
10	A	1382	G
10	A	1393	A
10	A	1394	C
10	A	1396	U
10	A	1409	A
10	A	1419	G
10	A	1423	U
10	A	1429	A
10	A	1451	G
10	A	1457	A
10	A	1462	U
10	A	1463	U
10	A	1464	A
10	A	1465	A
10	A	1469	A
10	A	1470	U
10	A	1478	C
10	A	1505	G
10	A	1509	A
10	A	1516	U
10	A	1517	C
10	A	1524	G
10	A	1528	G
10	A	1529	U
10	A	1530	G
10	A	1531	U
10	A	1532	G
10	A	1533	A
10	A	1534	G
10	A	1536	A
10	A	1539	A
10	A	1542	C
10	A	1543	A
10	A	1558	G
10	A	1561	G
10	A	1564	U
10	A	1566	A
10	A	1575	G
10	A	1594	G
10	A	1606	U
10	A	1607	U
10	A	1611	C

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Mol	Chain	Res	Type
10	A	1612	G
10	A	1618	A
10	A	1621	A
10	A	1626	C
10	A	1630	U
10	A	1634	A
10	A	1635	A
10	A	1638	G
10	A	1642	U
10	A	1657	A
10	A	1658	A
10	A	1659	A
10	A	1695	A
10	A	1696	G
10	A	1697	C
10	A	1712	U
10	A	1723	G
10	A	1749	A
10	A	1762	U
10	A	1763	U
10	A	1773	G
10	A	1779	G
10	A	1780	A
10	A	1782	A
10	A	1783	G
10	A	1785	C
10	A	1786	G
10	A	1795	A
10	A	1796	G
10	A	1797	G
10	A	1806	A
10	A	1815	C
10	A	1833	C
10	A	1834	A
10	A	1849	C
10	A	1850	G
10	A	1862	A
10	A	1880	A
10	A	1881	A
10	A	1888	G
10	A	1889	A
10	A	1891	G

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Mol	Chain	Res	Type
10	A	1892	A
10	A	1899	A
10	A	1903	U
10	A	1906	G
10	A	1939	G
10	A	1944	U
10	A	1945	A
10	A	1946	A
10	A	1947	C
10	A	1948	U
10	A	1949	A
10	A	1951	A
10	A	1952	A
10	A	1953	C
10	A	1954	G
10	A	1955	G
10	A	1956	U
10	A	1962	G
10	A	1963	G
10	A	1964	U
10	A	1970	A
10	A	1971	A
10	A	1988	U
10	A	1996	C
10	A	1998	C
10	A	2000	C
10	A	2003	A
10	A	2004	A
10	A	2005	G
10	A	2024	U
10	A	2026	U
10	A	2029	C
10	A	2030	A
10	A	2056	A
10	A	2064	A
10	A	2065	G
10	A	2066	A
10	A	2076	C
10	A	2088	C
10	A	2089	G
10	A	2093	A
10	A	2094	G

Continued on next page...

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Mol	Chain	Res	Type
10	A	2095	A
10	A	2102	G
10	A	2125	G
10	A	2126	G
10	A	2133	U
10	A	2136	A
10	A	2139	G
10	A	2141	U
10	A	2142	U
10	A	2144	U
10	A	2146	C
10	A	2148	G
10	A	2152	A
10	A	2154	G
10	A	2158	G
10	A	2159	A
10	A	2160	G
10	A	2164	A
10	A	2165	A
10	A	2166	G
10	A	2167	A
10	A	2168	G
10	A	2169	A
10	A	2171	G
10	A	2174	U
10	A	2180	A
10	A	2183	A
10	A	2190	G
10	A	2191	A
10	A	2199	G
10	A	2200	U
10	A	2201	G
10	A	2205	U
10	A	2206	A
10	A	2211	C
10	A	2218	G
10	A	2220	A
10	A	2223	A
10	A	2225	C
10	A	2226	A
10	A	2231	A
10	A	2236	G

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Mol	Chain	Res	Type
10	A	2237	C
10	A	2244	U
10	A	2258	A
10	A	2259	C
10	A	2271	G
10	A	2272	G
10	A	2301	A
10	A	2316	C
10	A	2320	A
10	A	2328	C
10	A	2337	G
10	A	2338	A
10	A	2340	G
10	A	2341	G
10	A	2352	C
10	A	2353	A
10	A	2355	A
10	A	2358	G
10	A	2360	A
10	A	2367	C
10	A	2368	A
10	A	2380	C
10	A	2383	C
10	A	2412	G
10	A	2416	G
10	A	2418	C
10	A	2435	U
10	A	2436	C
10	A	2439	C
10	A	2447	G
10	A	2456	U
10	A	2457	C
10	A	2458	A
10	A	2459	A
10	A	2462	G
10	A	2463	A
10	A	2464	U
10	A	2468	A
10	A	2472	A
10	A	2473	C
10	A	2474	C
10	A	2481	A

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Mol	Chain	Res	Type
10	A	2503	G
10	A	2507	C
10	A	2509	A
10	A	2524	U
10	A	2535	G
10	A	2538	G
10	A	2551	A
10	A	2558	G
10	A	2562	G
10	A	2567	C
10	A	2568	G
10	A	2587	U
10	A	2599	A
10	A	2600	G
10	A	2606	C
10	A	2611	G
10	A	2618	U
10	A	2635	A
10	A	2636	G
10	A	2637	U
10	A	2642	U
10	A	2646	U
10	A	2663	G
10	A	2696	G
10	A	2703	G
10	A	2722	U
10	A	2724	C
10	A	2747	G
10	A	2759	U
10	A	2766	C
10	A	2777	G
10	A	2781	A
10	A	2784	G
10	A	2790	A
10	A	2794	G
10	A	2795	U
10	A	2798	A
10	A	2799	G
10	A	2810	G
10	A	2811	A
10	A	2822	C
10	A	2828	U

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Mol	Chain	Res	Type
10	A	2832	G
10	A	2835	A
10	A	2862	A
10	A	2864	A
10	A	2865	U
10	A	2871	U
10	A	2872	G
10	A	2890	U
10	A	2896	G
10	A	2897	A
10	A	2906	A
10	A	2908	A
10	A	2909	C
10	A	2913	U
10	A	2915	G
10	A	2916	A
10	A	2922	G
10	A	2929	C
10	A	2930	C
11	B	3	U
11	B	10	U
11	B	23	U
11	B	24	C
11	B	33	U
11	B	38	U
11	B	39	A
11	B	40	C
11	B	43	A
11	B	54	U
11	B	55	A
11	B	65	G
11	B	67	G
11	B	82	G
11	B	83	G
11	B	86	U
11	B	87	U
11	B	88	C
11	B	103	G
11	B	107	G
11	B	114	G

All (79) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	12	A
10	A	45	G
10	A	90	A
10	A	92	G
10	A	101	G
10	A	139	A
10	A	174	A
10	A	201	A
10	A	231	A
10	A	251	C
10	A	274	A
10	A	297	U
10	A	308	U
10	A	388	A
10	A	409	G
10	A	502	C
10	A	548	A
10	A	566	U
10	A	574	A
10	A	591	A
10	A	614	U
10	A	630	G
10	A	794	G
10	A	810	A
10	A	836	U
10	A	851	G
10	A	873	U
10	A	913	A
10	A	990	C
10	A	1030	G
10	A	1035	G
10	A	1066	A
10	A	1148	C
10	A	1179	A
10	A	1188	A
10	A	1203	A
10	A	1249	A
10	A	1311	G
10	A	1344	A
10	A	1376	G
10	A	1462	U
10	A	1528	G
10	A	1532	G

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Mol	Chain	Res	Type
10	A	1533	A
10	A	1606	U
10	A	1611	C
10	A	1634	A
10	A	1657	A
10	A	1832	G
10	A	1849	C
10	A	1880	A
10	A	1891	G
10	A	1946	A
10	A	1950	U
10	A	1951	A
10	A	1954	G
10	A	1955	G
10	A	2030	A
10	A	2084	A
10	A	2152	A
10	A	2159	A
10	A	2166	G
10	A	2258	A
10	A	2320	A
10	A	2359	U
10	A	2456	U
10	A	2458	A
10	A	2463	A
10	A	2472	A
10	A	2480	G
10	A	2551	A
10	A	2789	U
10	A	2809	A
10	A	2823	A
10	A	2896	G
10	A	2908	A
11	B	22	G
11	B	38	U
11	B	106	C

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 170 ligands modelled in this entry, 167 are monoatomic - leaving 3 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	$\# Z > 2$
33	PUT	A	3151	-	5,5,5	0.17	0	4,4,4	0.21	0
31	SPD	A	3001	-	9,9,9	0.18	0	8,8,8	0.31	0
33	PUT	A	3152	-	5,5,5	0.21	0	4,4,4	0.21	0

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	PUT	A	3151	-	-	0/3/3/3	-
31	SPD	A	3001	-	-	1/7/7/7	-
33	PUT	A	3152	-	-	1/3/3/3	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
33	A	3152	PUT	C1-C2-C3-C4
31	A	3001	SPD	N1-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	A	3001	SPD	2	0

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.

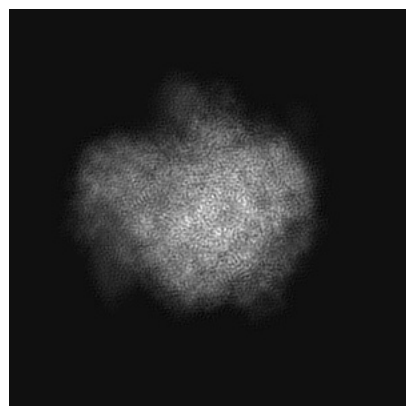
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15204. These allow visual inspection of the internal detail of the map and identification of artifacts.

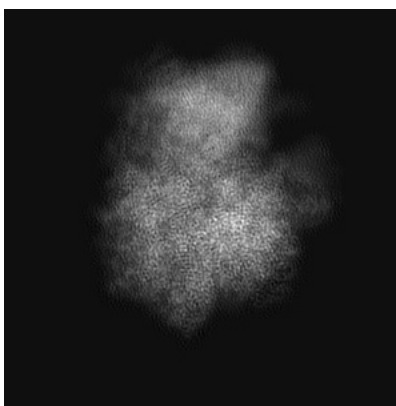
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

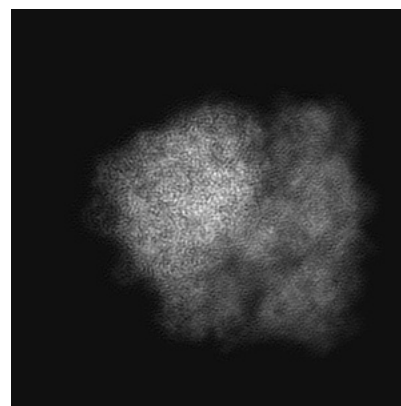
6.1.1 Primary map



X

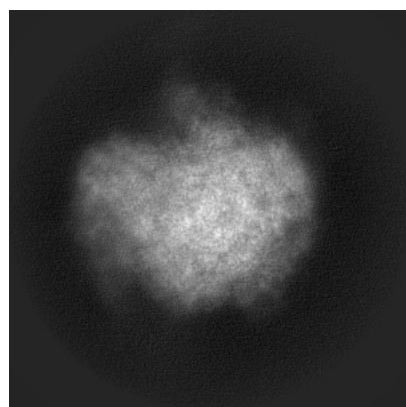


Y

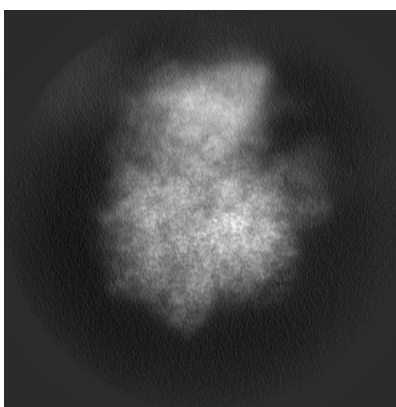


Z

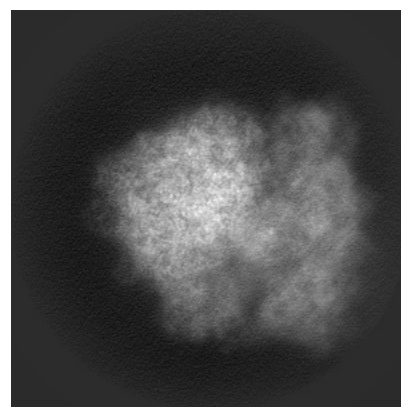
6.1.2 Raw map



X



Y

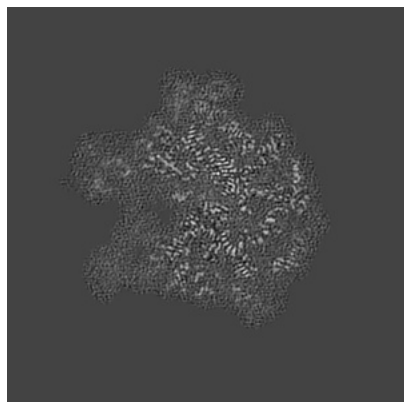


Z

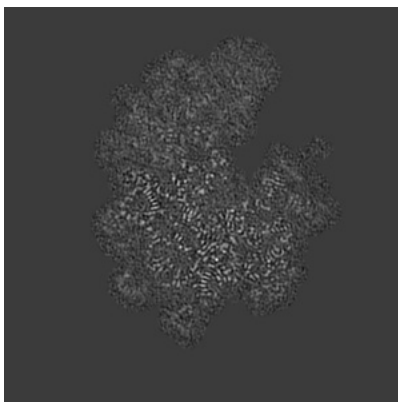
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

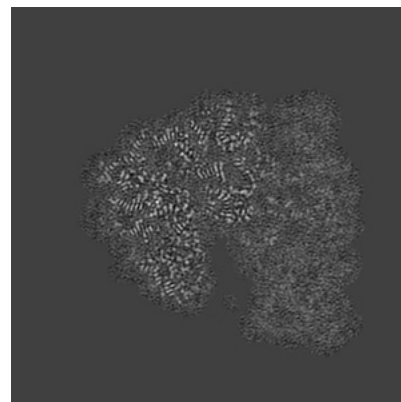
6.2.1 Primary map



X Index: 210

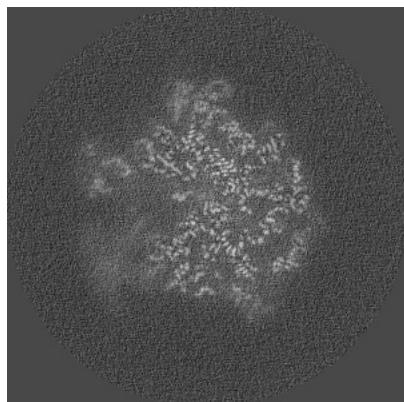


Y Index: 210

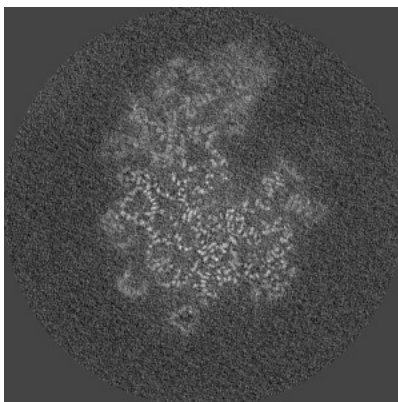


Z Index: 210

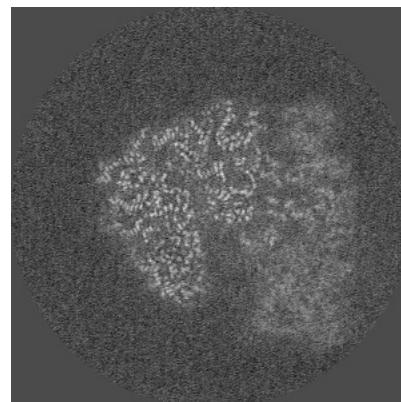
6.2.2 Raw map



X Index: 210



Y Index: 210

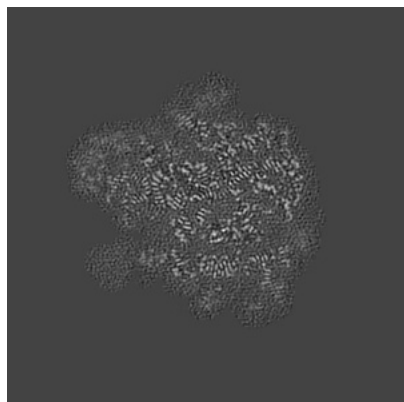


Z Index: 210

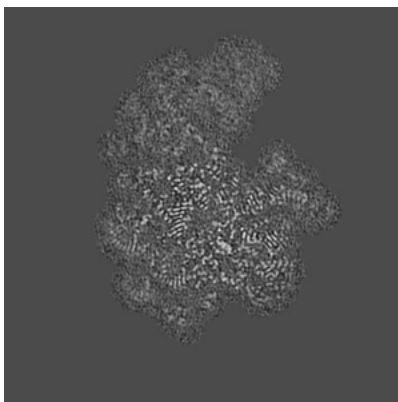
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

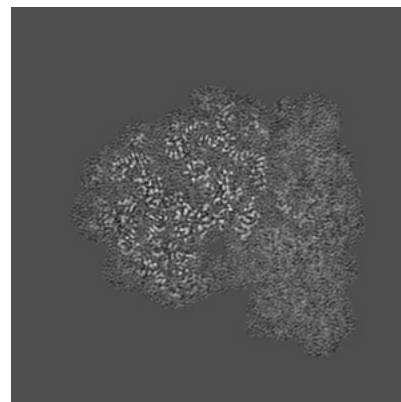
6.3.1 Primary map



X Index: 194

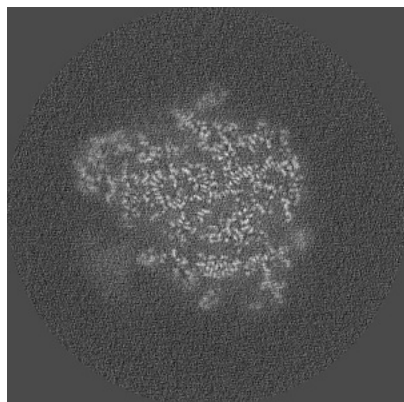


Y Index: 219

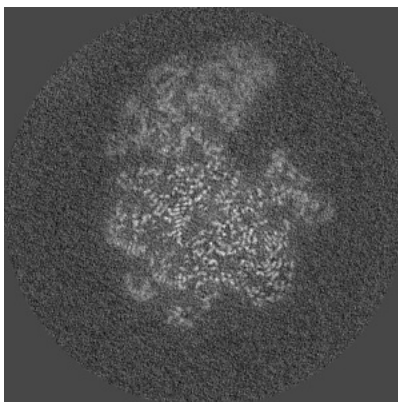


Z Index: 201

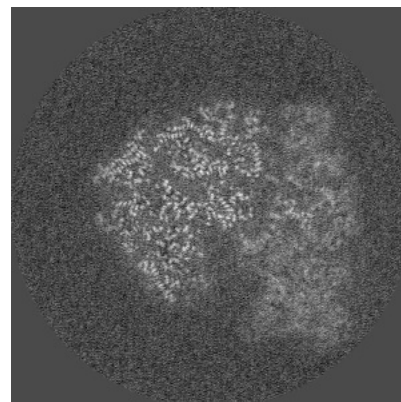
6.3.2 Raw map



X Index: 193



Y Index: 218

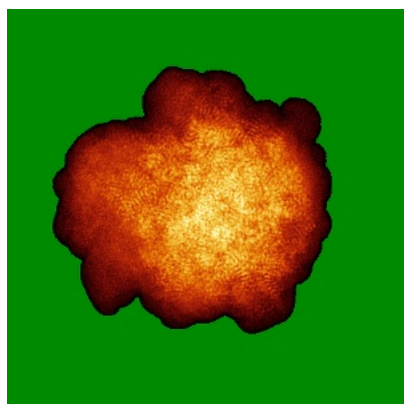


Z Index: 207

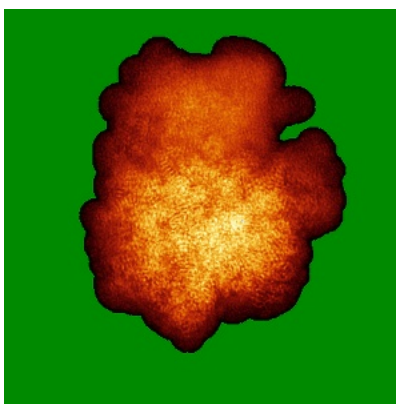
The images above show the largest variance slices of the map in three orthogonal directions.

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

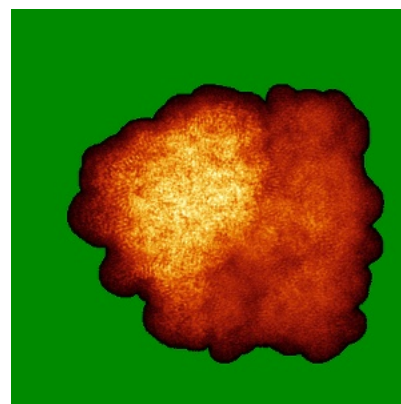
6.4.1 Primary map



X

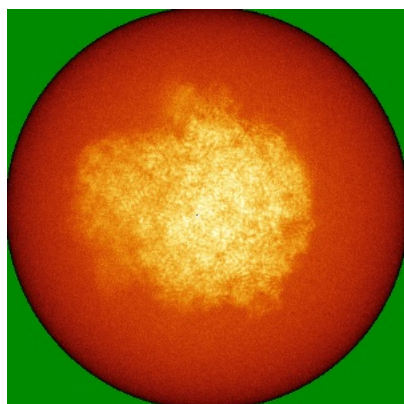


Y

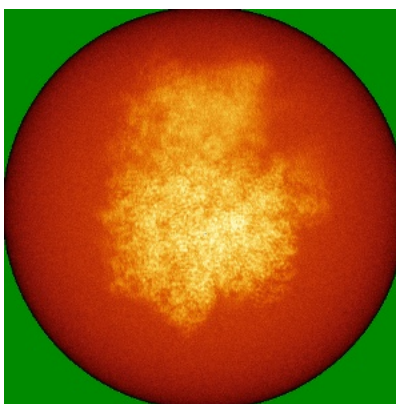


Z

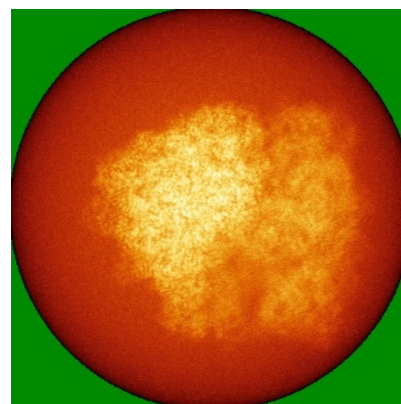
6.4.2 Raw map



X



Y

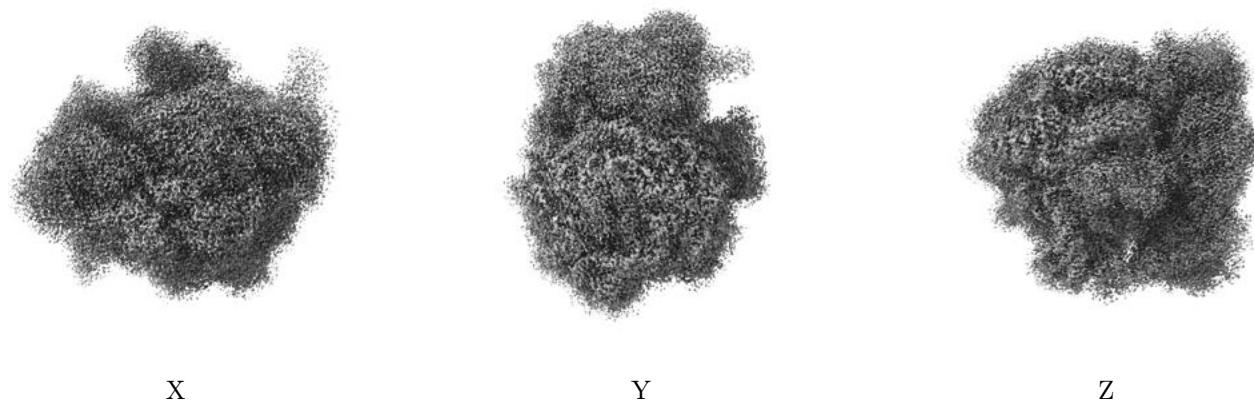


Z

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

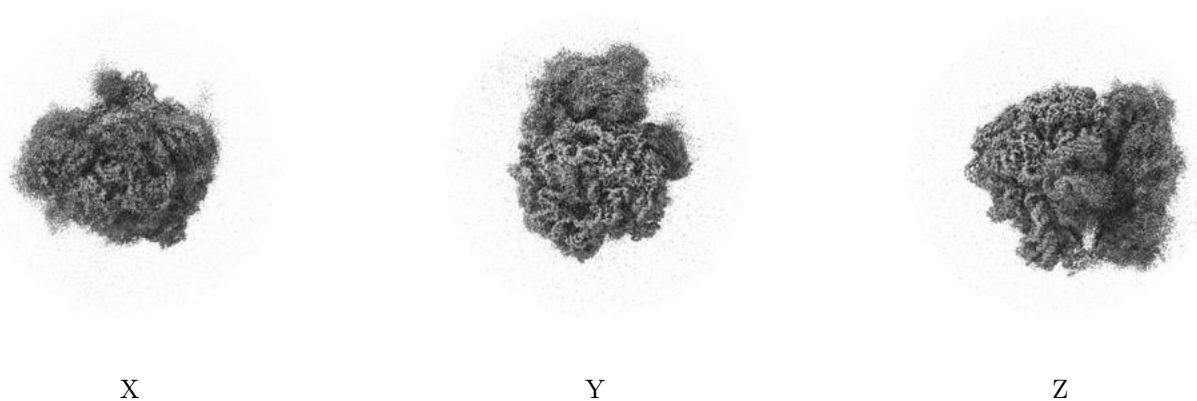
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

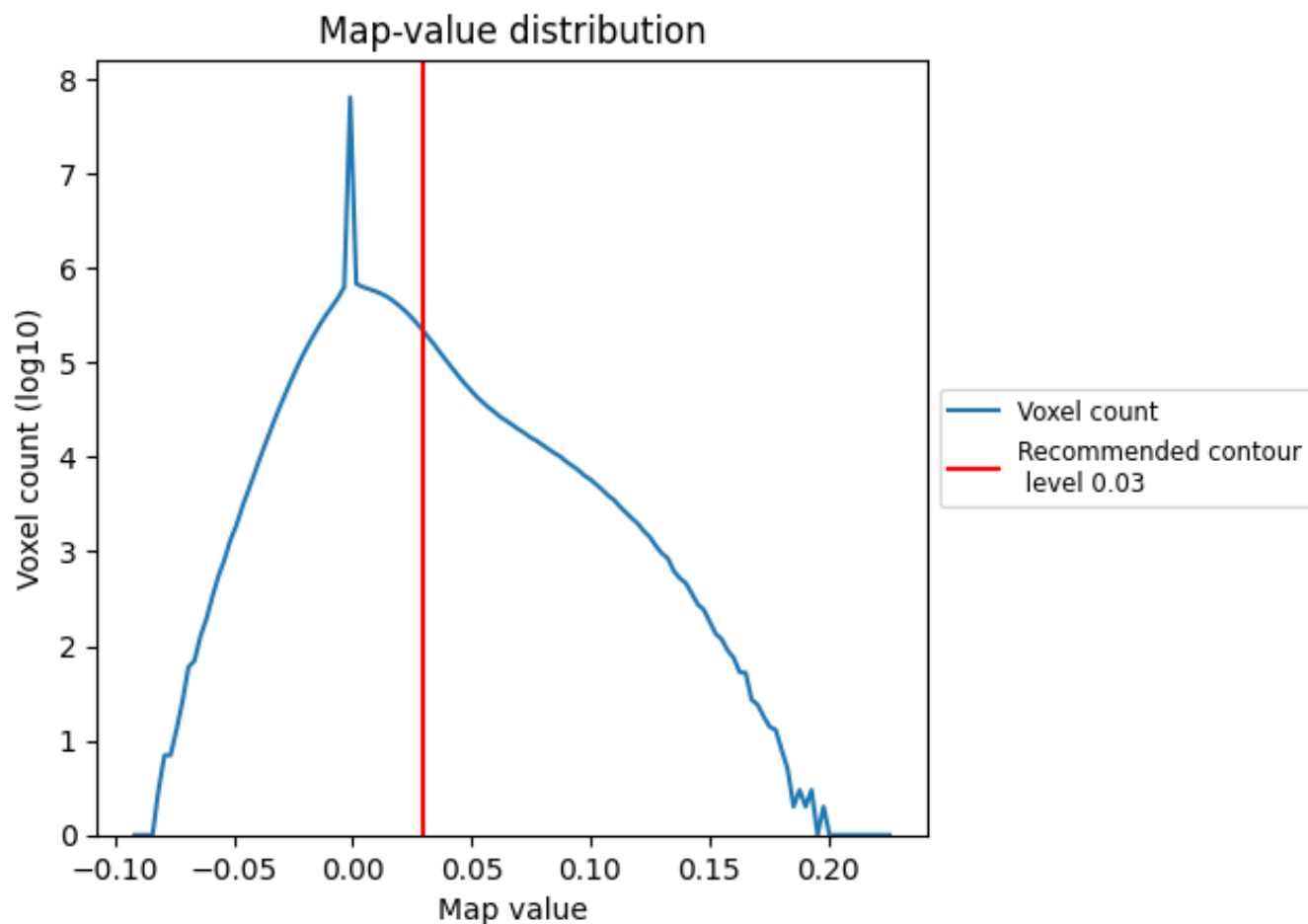
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

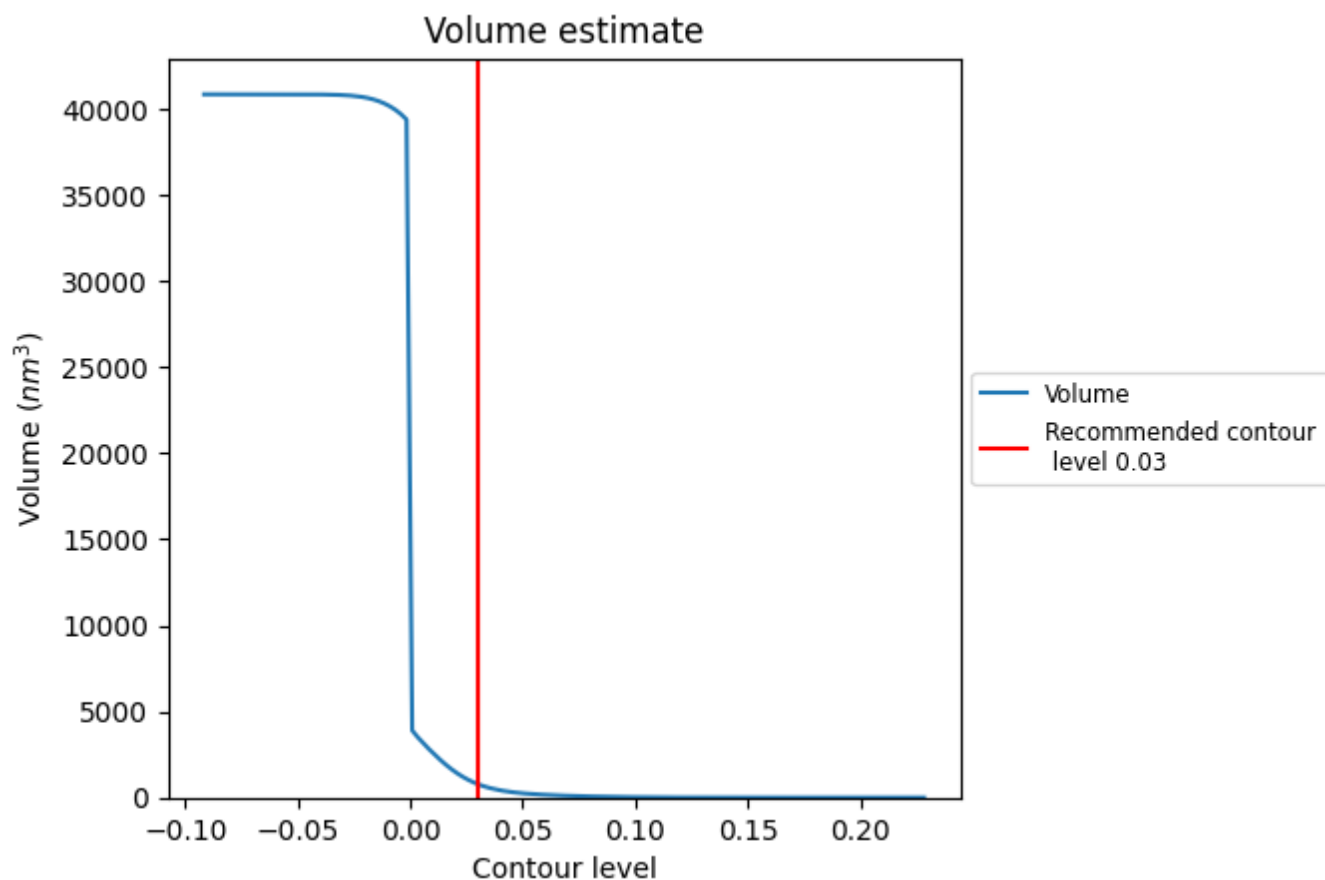
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

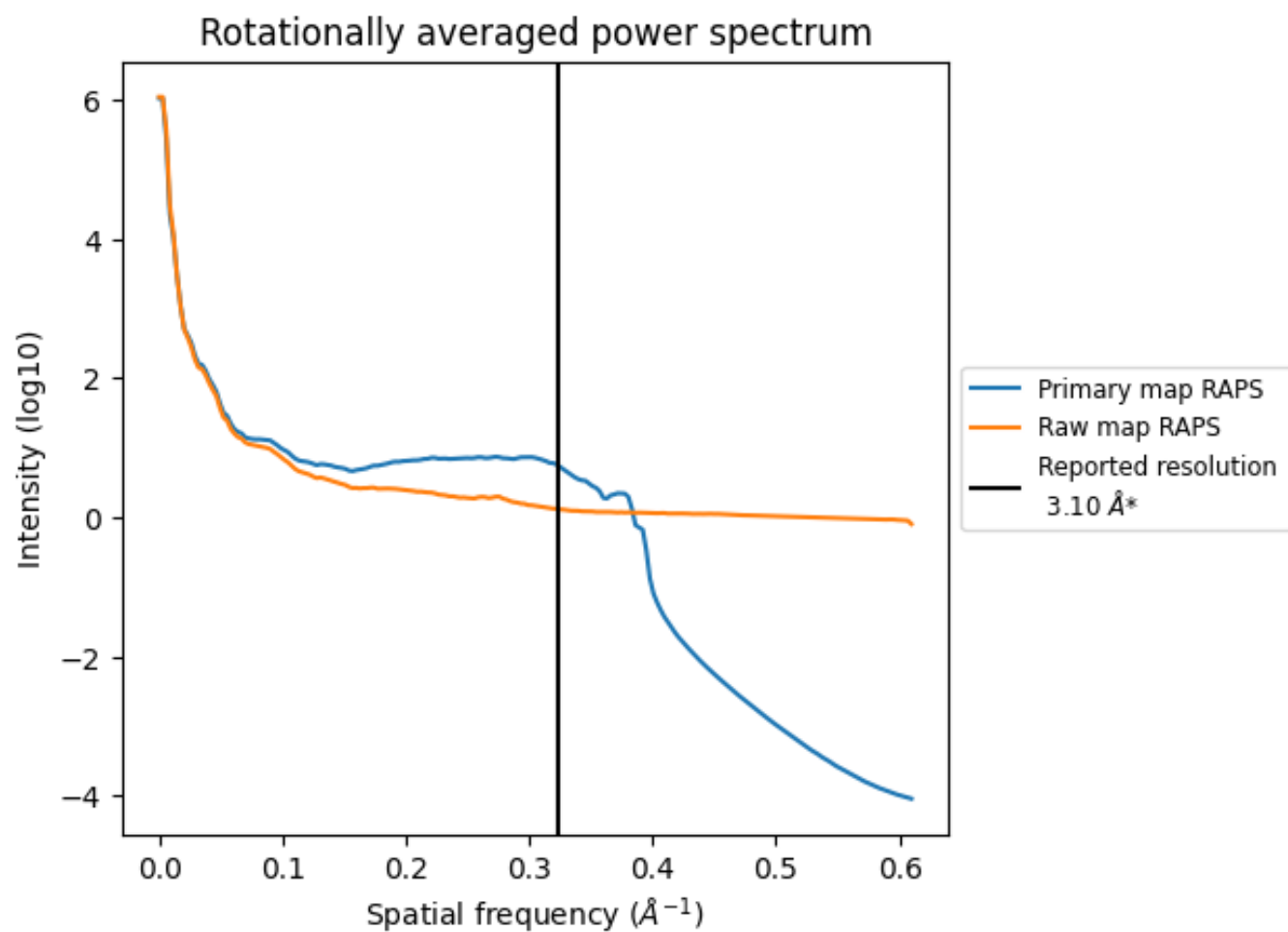
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 783 nm^3 ; this corresponds to an approximate mass of 707 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 ⓘ

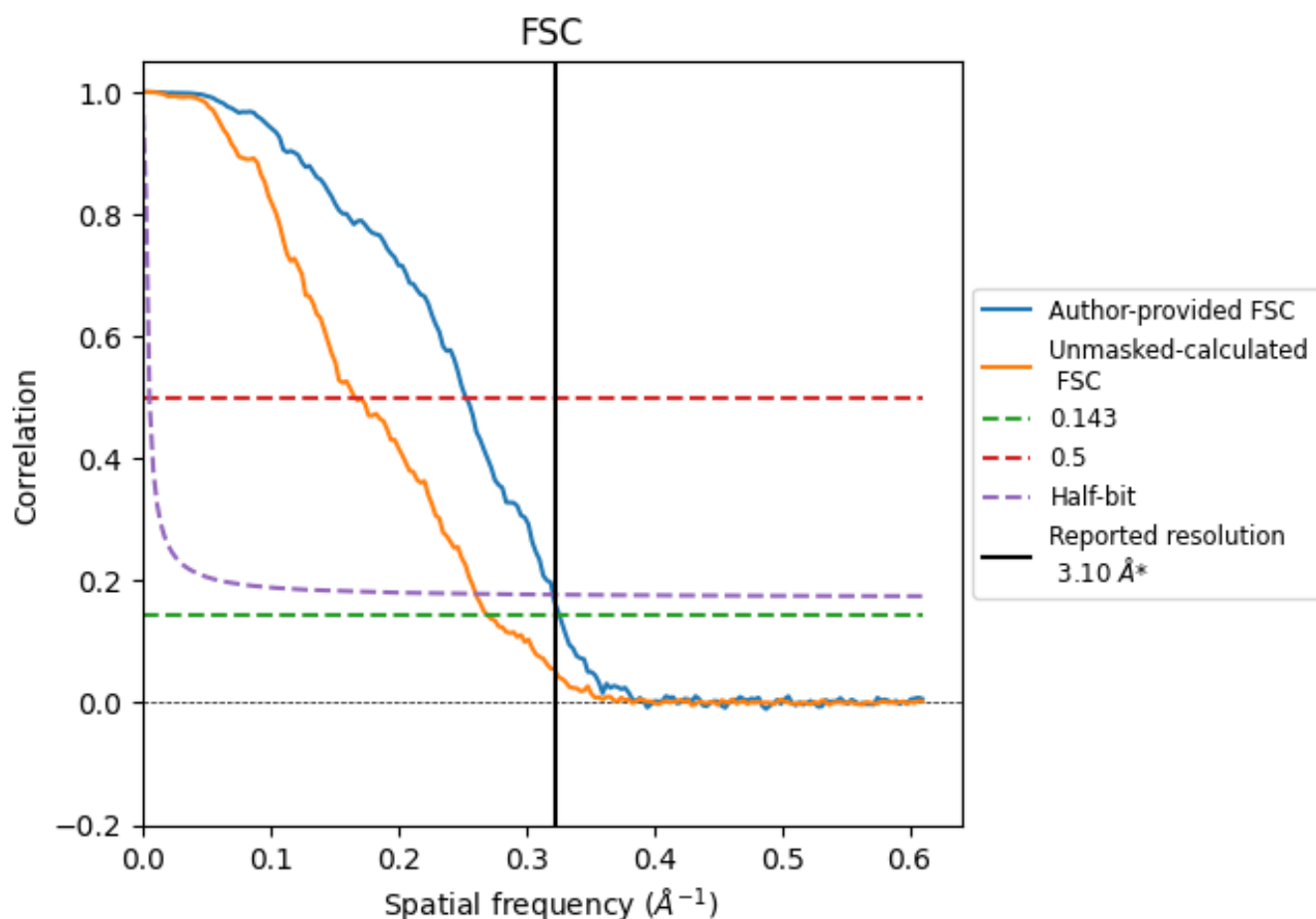


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

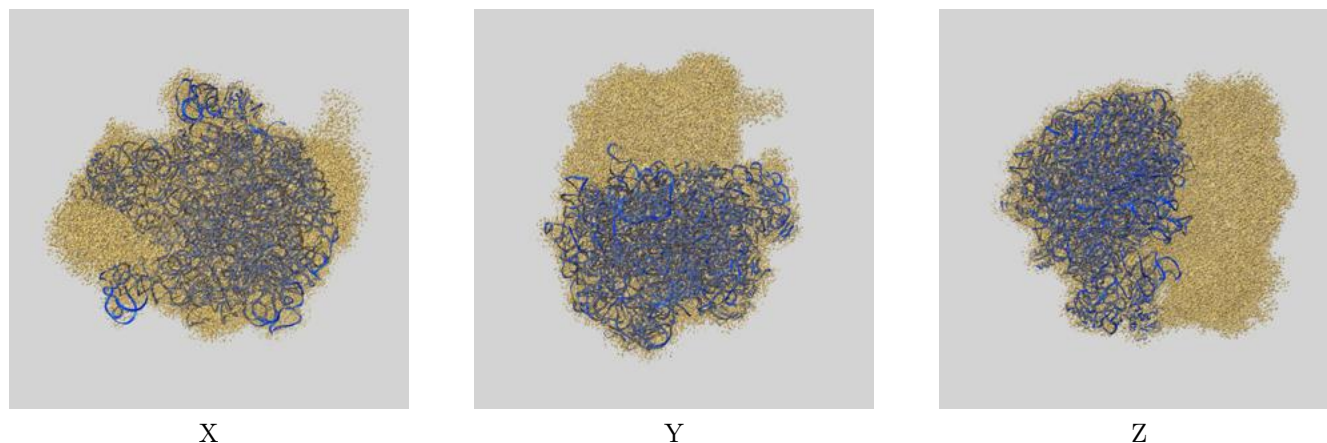
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.07	3.95	3.11
Unmasked-calculated*	3.70	6.01	3.84

*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 3.70 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

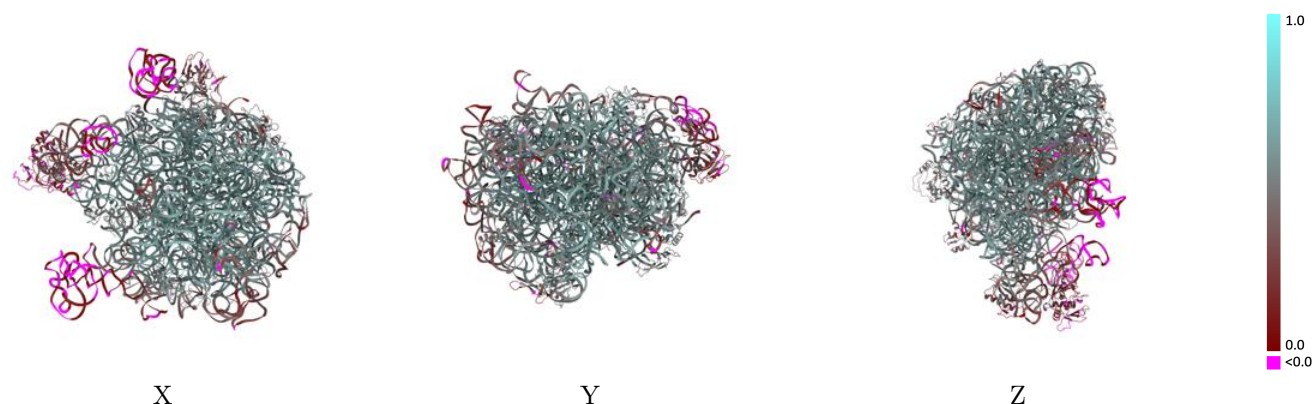
This section contains information regarding the fit between EMDB map EMD-15204 and PDB model 8A63. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



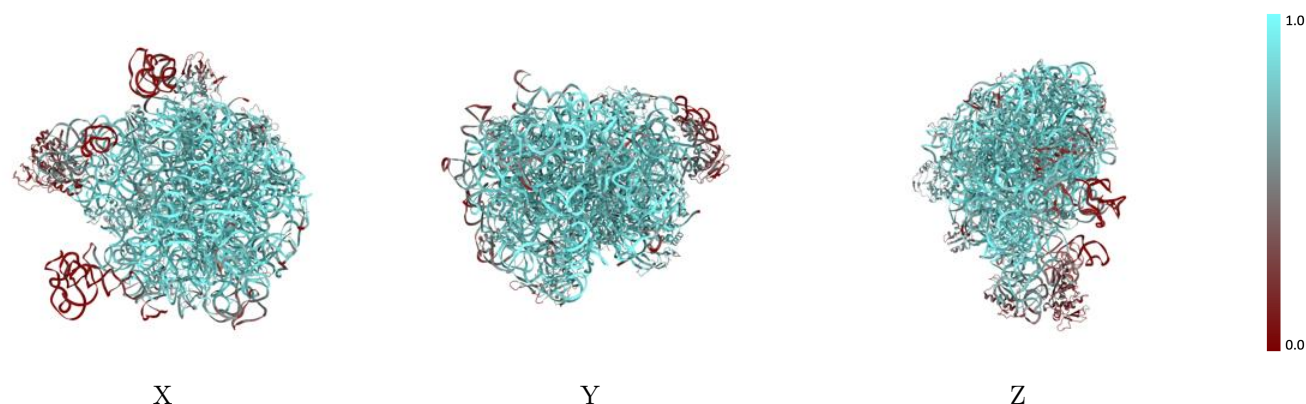
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



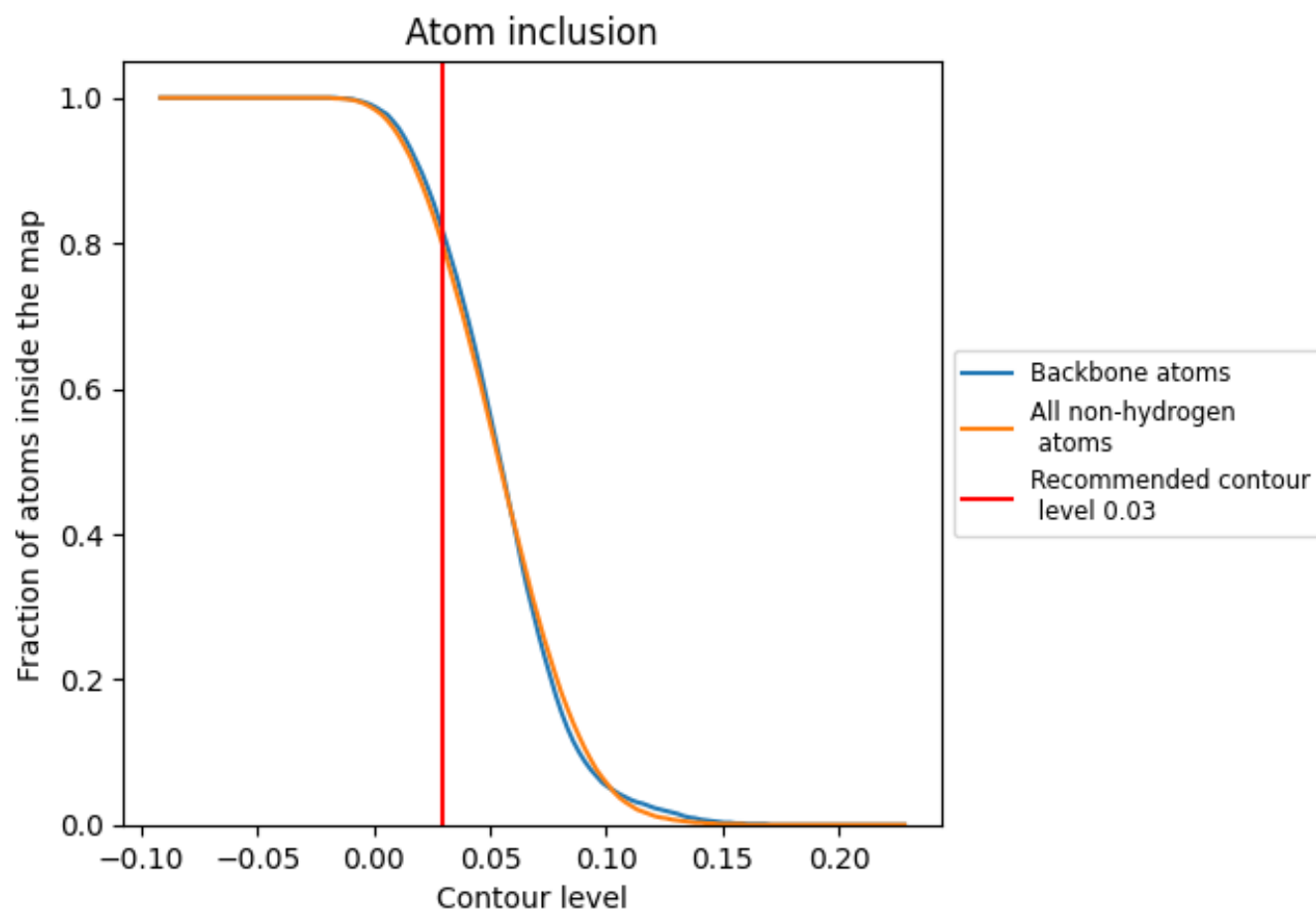
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 80% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7950	 0.5030
1	 0.7520	 0.4890
2	 0.6580	 0.4550
3	 0.7810	 0.5400
4	 0.1560	 0.1120
5	 0.7380	 0.4620
6	 0.6940	 0.4600
7	 0.9460	 0.6240
8	 0.9050	 0.5930
9	 0.8120	 0.5210
A	 0.8310	 0.5170
B	 0.6760	 0.4070
G	 0.8530	 0.5630
H	 0.8180	 0.5420
I	 0.7500	 0.5070
J	 0.2600	 0.1880
K	 0.3870	 0.2700
M	 0.8220	 0.5510
N	 0.7860	 0.5280
O	 0.7100	 0.4730
P	 0.7930	 0.5250
Q	 0.8040	 0.5390
R	 0.4490	 0.3360
S	 0.7630	 0.5030
T	 0.8620	 0.5820
U	 0.7490	 0.5230
V	 0.8270	 0.5640
W	 0.7560	 0.5020
X	 0.5670	 0.3910
Z	 0.8710	 0.5680

