



Full wwPDB EM Validation Report ⓘ

Jan 30, 2025 – 02:29 PM JST

PDB ID : 8WQ2
EMDB ID : EMD-37733
Title : Structural basis of translation inhibition by a valine tRNA-derived fragment
Authors : Wang, Y.H.; Zhou, J.
Deposited on : 2023-10-10
Resolution : 4.10 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

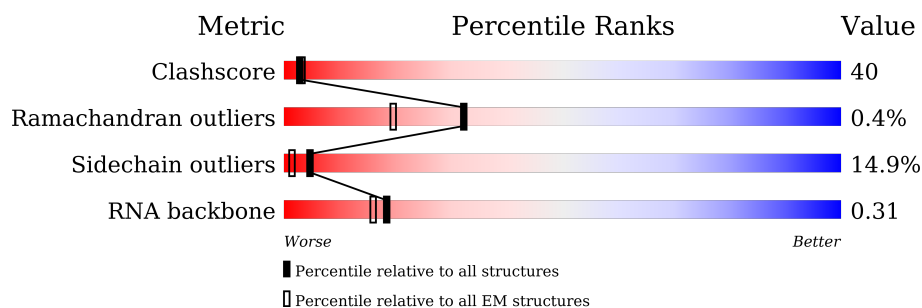
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A16S	1501	
2	VTRF	26	
3	AS2P	196	
4	AS4E	240	
5	AS4P	166	
6	AS5P	204	
7	AS6E	105	

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Mol	Chain	Length	Quality of chain
8	AS8E	126	
9	S11P	128	
10	S12P	143	
11	S15P	149	
12	S17P	111	
13	S24E	96	
14	S27E	59	
15	S3AE	189	
16	AS3P	201	
17	AS7P	193	
18	AS9P	136	
19	S10P	100	
20	S13P	147	
21	S14P	52	
22	S17E	62	
23	S19E	150	
24	S19P	115	
25	S27A	54	
26	S28E	63	
27	SL7A	123	
28	AS8P	130	

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 56872 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (1328-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A16S	1328	Total	C	N	O	P	0	0
			28525	12702	5278	9217	1328		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A16S	?	-	U	deletion	GB 2440479486
A16S	?	-	C	deletion	GB 2440479486
A16S	1450	G	-	insertion	GB 2440479486

- Molecule 2 is a RNA chain called RNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	VTRF	26	Total	C	N	O	P	0	0
			556	248	96	187	25		

- Molecule 3 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AS2P	196	Total	C	N	O	S	0	0
			1587	1022	277	286	2		

- Molecule 4 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AS4E	240	Total	C	N	O	S	0	0
			1925	1238	335	348	4		

- Molecule 5 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AS4P	166	Total	C	N	O	S	0	0
			1370	874	252	241	3		

- Molecule 6 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AS5P	204	Total	C	N	O	S	0	0
			1600	1028	277	287	8		

- Molecule 7 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AS6E	105	Total	C	N	O	S	0	0
			805	506	149	147	3		

- Molecule 8 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AS8E	126	Total	C	N	O	S	0	0
			993	619	187	187			

- Molecule 9 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S11P	128	Total	C	N	O	S	0	0
			960	595	190	173	2		

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	S12P	143	Total	C	N	O	S	0	0
			1103	701	209	189	4		

- Molecule 11 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	S15P	149	Total	C	N	O	S	0	0
			1225	778	228	214	5		

- Molecule 12 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S17P	111	Total	C	N	O	S	0	0
			885	557	165	160	3		

- Molecule 13 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	S24E	96	Total	C	N	O		
			759	479	133	147	0	0

- Molecule 14 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S27E	59	Total	C	N	O	S		
			458	294	83	76	5	0	0

- Molecule 15 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S3AE	189	Total	C	N	O	S		
			1545	1004	264	276	1	0	0

- Molecule 16 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AS3P	201	Total	C	N	O	S		
			1576	1020	274	278	4	0	0

- Molecule 17 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS7P	193	Total	C	N	O	S		
			1537	969	285	279	4	0	0

- Molecule 18 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS9P	136	Total	C	N	O	S		
			1096	692	200	197	7	0	0

- Molecule 19 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S10P	100	Total	C	N	O	S		
			824	522	154	142	6	0	0

- Molecule 20 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S13P	147	Total	C	N	O	S	0	0
			1204	753	230	217	4		

- Molecule 21 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S14P	52	Total	C	N	O	S	0	0
			432	273	85	69	5		

- Molecule 22 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S17E	62	Total	C	N	O	S	0	0
			517	326	92	99			

- Molecule 23 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S19E	150	Total	C	N	O	S	0	0
			1239	801	223	213	2		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S19P	115	Total	C	N	O	S	0	0
			969	620	181	163	5		

- Molecule 25 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S27A	54	Total	C	N	O	S	0	0
			435	274	79	76	6		

- Molecule 26 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S28E	63	Total	C	N	O	S	0	0
			498	308	99	91			

- Molecule 27 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SL7A	123	Total	C	N	O	S	0	0
			935	593	155	184	3		

- Molecule 28 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AS8P	130	Total	C	N	O	S	0	0
			1028	661	181	182	4		

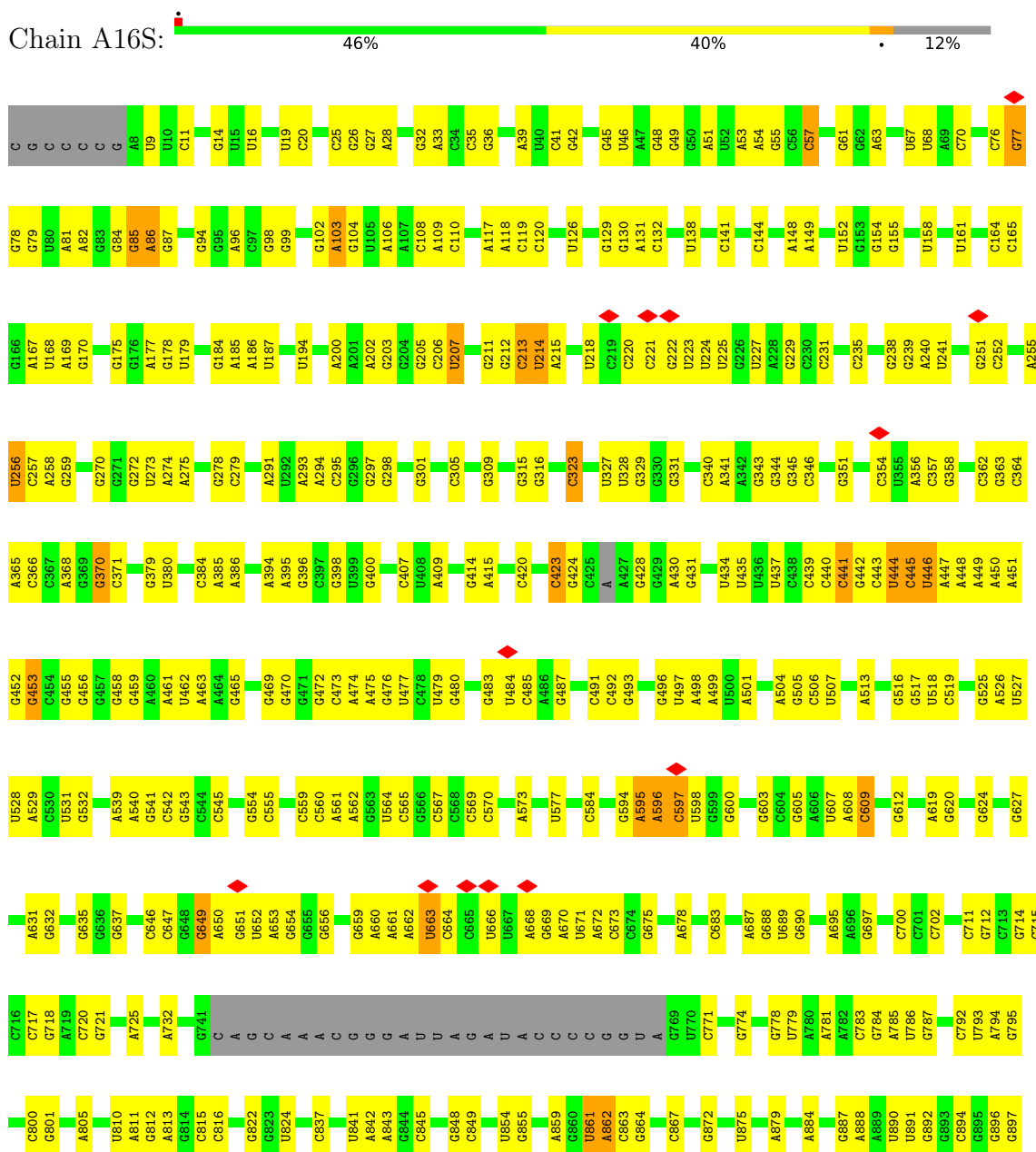
- Molecule 29 is UNKNOWN LIGAND (three-letter code: UNL) (formula:) (labeled as "Ligand of Interest" by depositor).

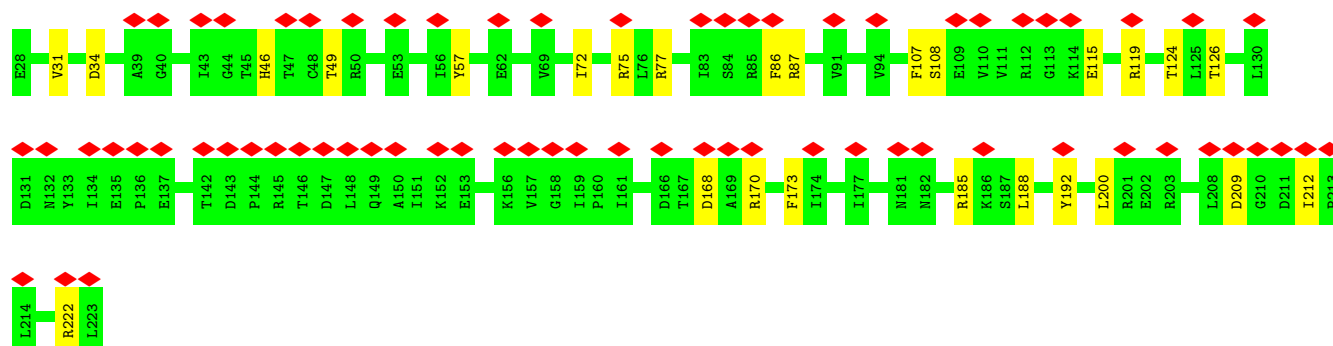
Mol	Chain	Residues	Atoms				AltConf
29	AS2P	34	Total	C	N	O	0
			171	102	34	35	
29	AS5P	17	Total	C	N	O	0
			85	51	17	17	
29	AS8P	6	Total	C	N	O	0
			30	18	6	6	

3 Residue-property plots

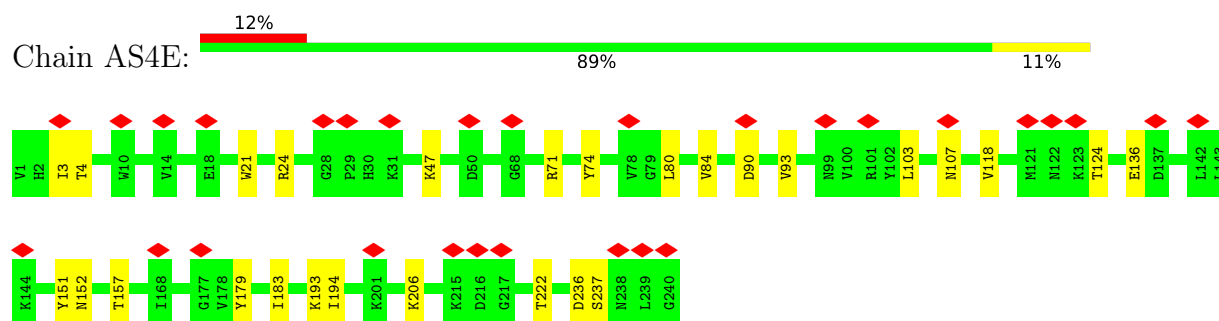
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA (1328-MER)

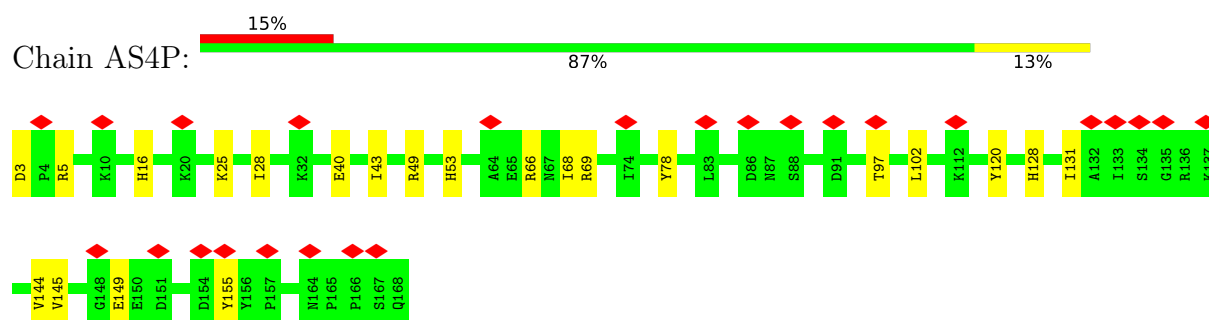




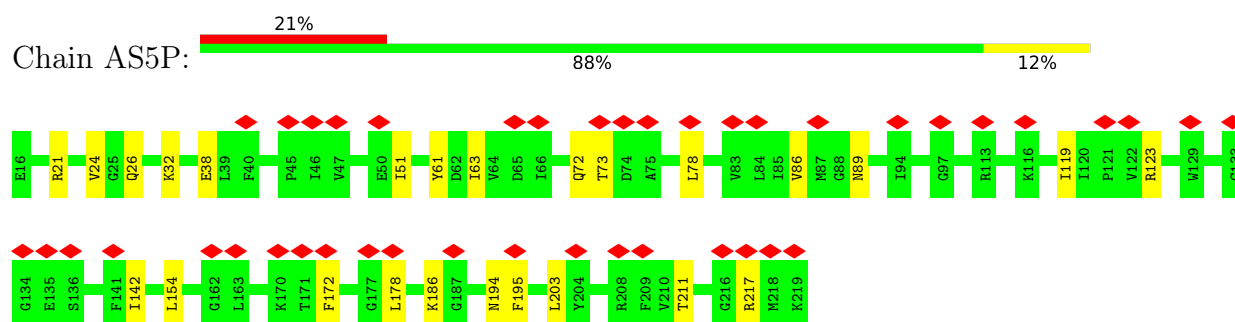
- Molecule 4: 30S ribosomal protein S4e



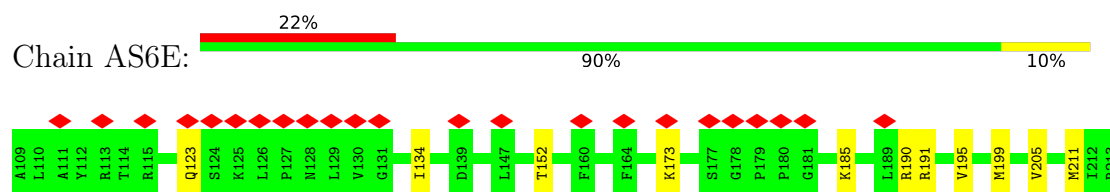
- Molecule 5: 30S ribosomal protein S4



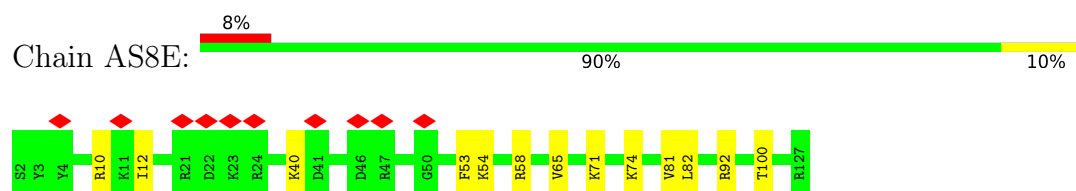
- Molecule 6: 30S ribosomal protein S5



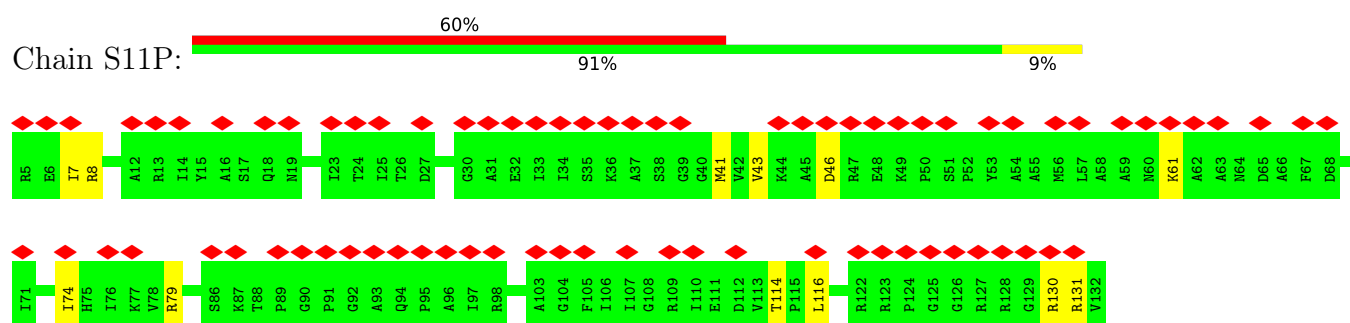
- Molecule 7: 30S ribosomal protein S6e



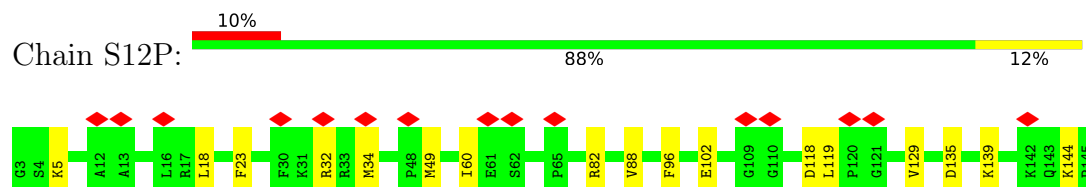
- Molecule 8: 30S ribosomal protein S8e



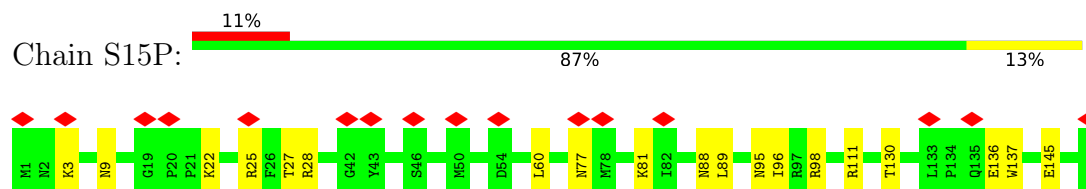
- Molecule 9: 30S ribosomal protein S11



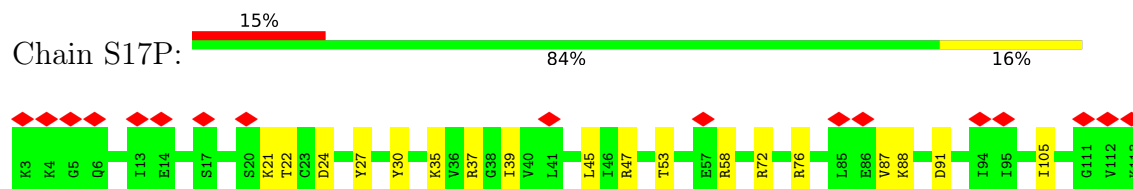
- Molecule 10: 30S ribosomal protein S12



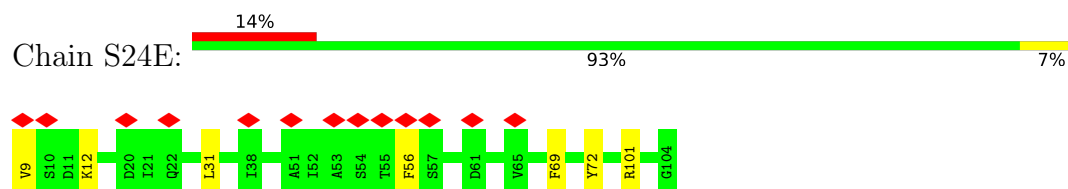
- Molecule 11: 30S ribosomal protein S15



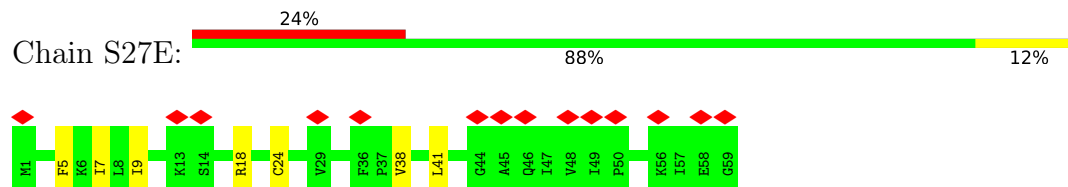
- Molecule 12: 30S ribosomal protein S17



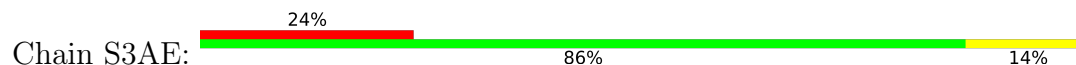
- Molecule 13: 30S ribosomal protein S24e

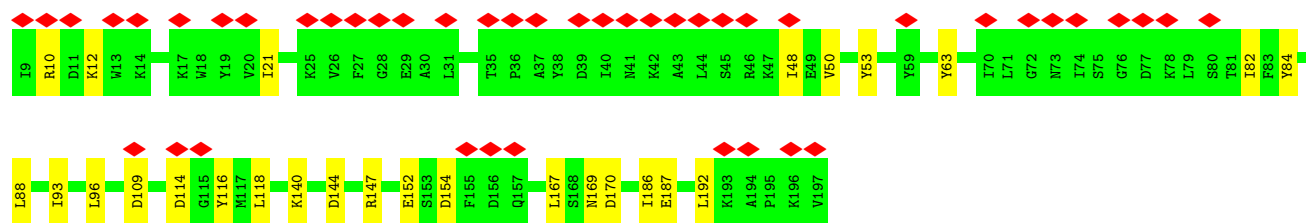


- Molecule 14: 30S ribosomal protein S27e

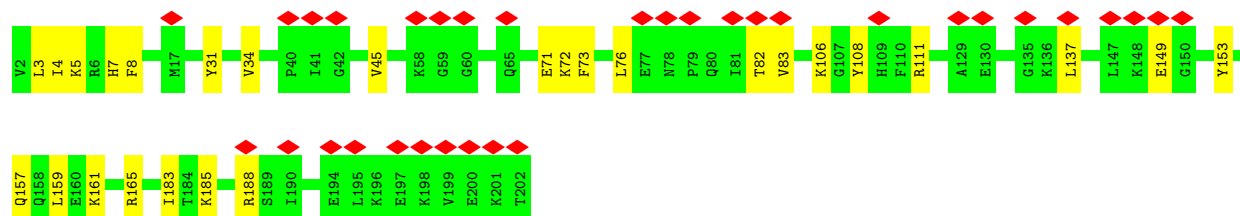
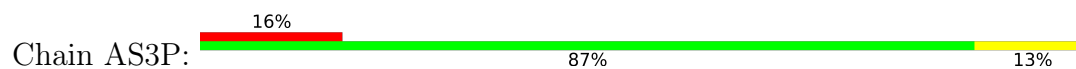


- Molecule 15: 30S ribosomal protein S3Ae

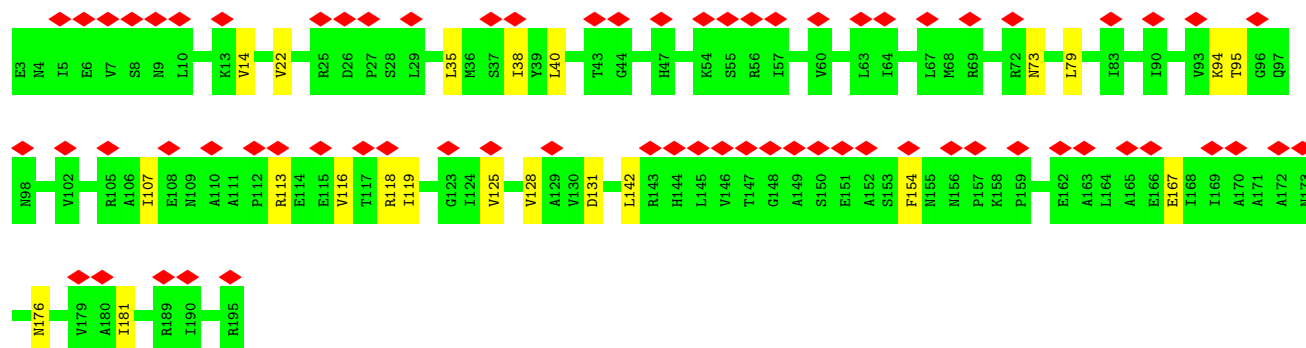
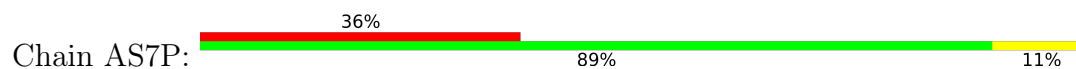




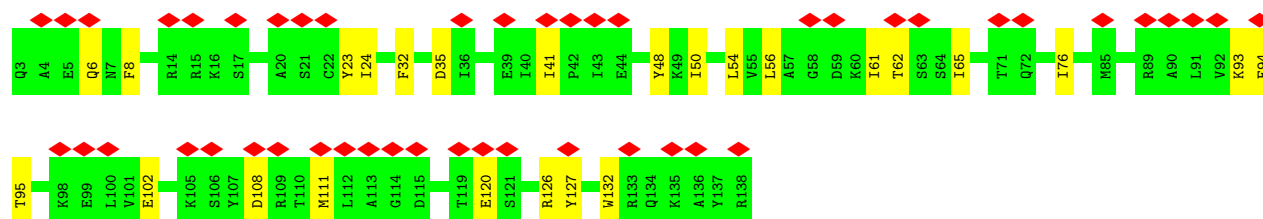
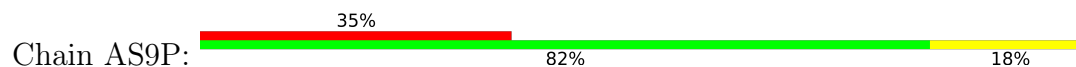
- Molecule 16: 30S ribosomal protein S3



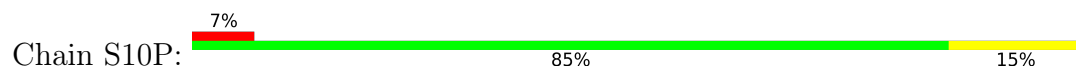
- Molecule 17: 30S ribosomal protein S7



- Molecule 18: 30S ribosomal protein S9

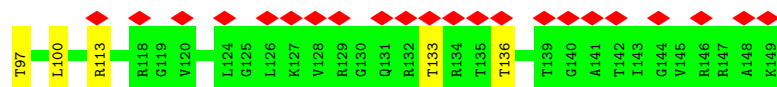
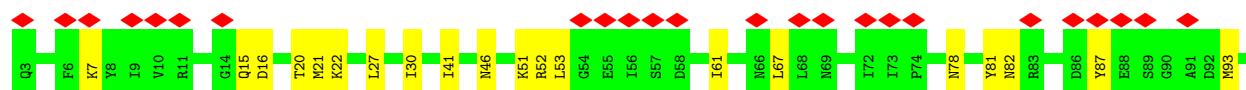
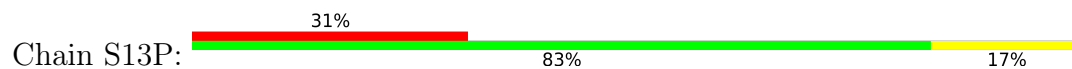


- Molecule 19: 30S ribosomal protein S10

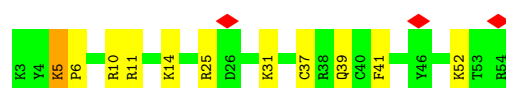
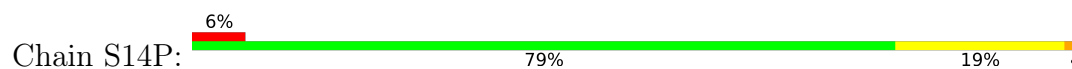




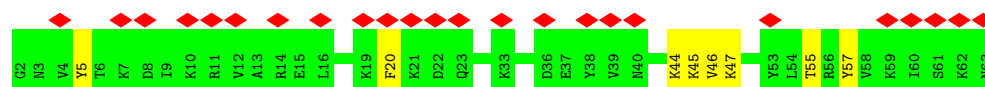
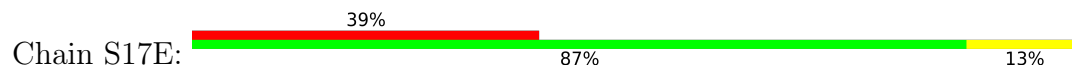
- Molecule 20: 30S ribosomal protein S13



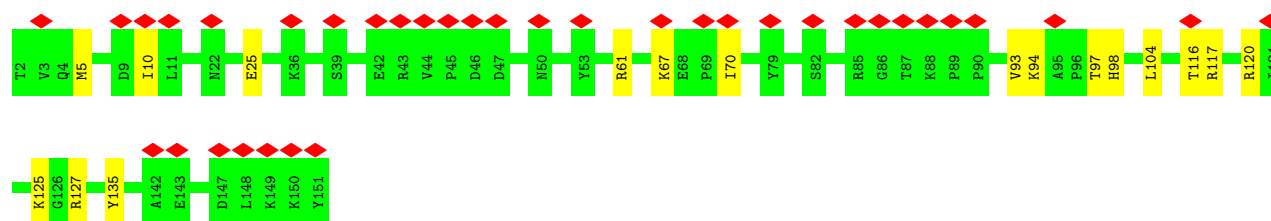
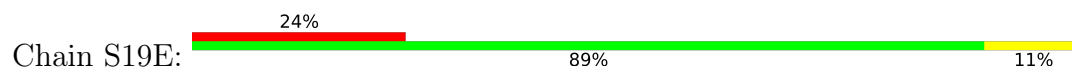
- Molecule 21: 30S ribosomal protein S14 type Z



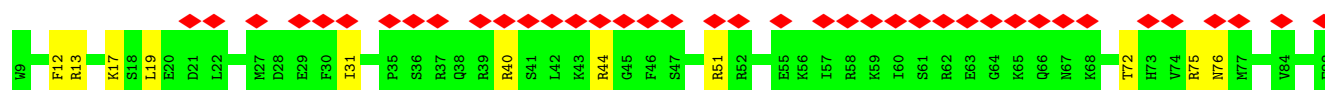
- Molecule 22: 30S ribosomal protein S17e

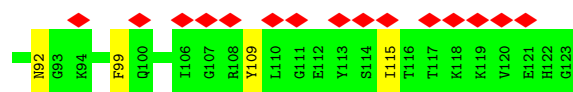


- Molecule 23: 30S ribosomal protein S19e

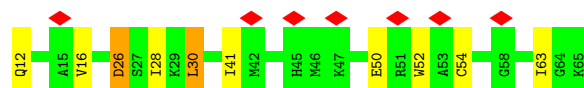
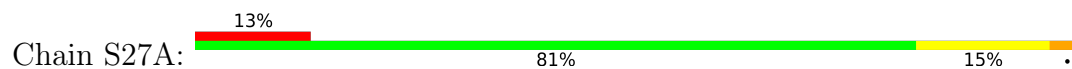


- Molecule 24: 30S ribosomal protein S19

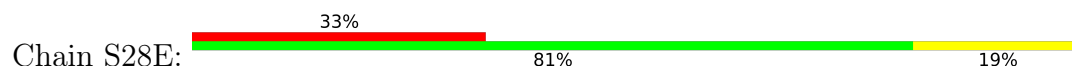




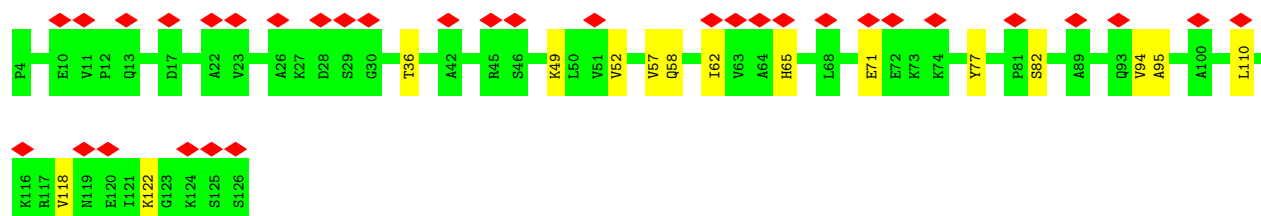
- Molecule 25: 30S ribosomal protein S27ae



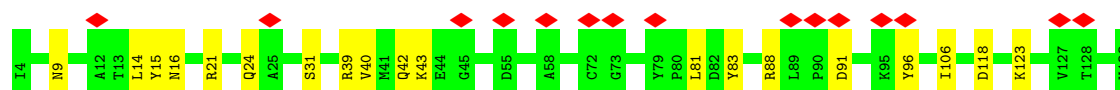
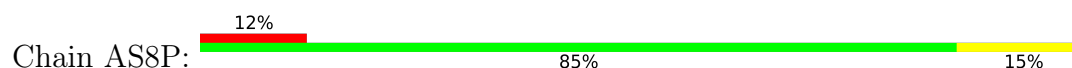
- Molecule 26: 30S ribosomal protein S28e



- Molecule 27: 50S ribosomal protein L7Ae



- Molecule 28: Small ribosomal subunit protein uS8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9742	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 ($e^-/\text{\AA}^2$)	26.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.338	Depositor
Minimum map value	-0.567	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.089	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	326.1, 326.1, 326.1	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	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: UNL

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	A16S	0.52	6/31928 (0.0%)	1.06	109/49820 (0.2%)
2	VTRF	0.39	0/621	0.95	2/968 (0.2%)
3	AS2P	0.30	0/1621	0.55	0/2202
4	AS4E	0.30	0/1956	0.54	0/2635
5	AS4P	0.28	0/1399	0.53	0/1883
6	AS5P	0.31	0/1631	0.52	0/2200
7	AS6E	0.26	0/815	0.56	0/1093
8	AS8E	0.29	0/1005	0.56	0/1342
9	S11P	0.27	0/976	0.57	0/1315
10	S12P	0.29	0/1120	0.56	0/1495
11	S15P	0.29	0/1250	0.54	0/1677
12	S17P	0.31	0/899	0.55	0/1203
13	S24E	0.29	0/769	0.50	0/1034
14	S27E	0.30	0/465	0.50	0/618
15	S3AE	0.29	0/1573	0.51	0/2115
16	AS3P	0.29	0/1599	0.52	0/2147
17	AS7P	0.28	0/1561	0.56	0/2105
18	AS9P	0.29	0/1115	0.58	0/1496
19	S10P	0.29	0/840	0.56	0/1132
20	S13P	0.28	0/1221	0.56	0/1634
21	S14P	0.32	0/441	0.58	0/583
22	S17E	0.28	0/523	0.47	0/696
23	S19E	0.30	0/1267	0.51	0/1705
24	S19P	0.29	0/986	0.59	0/1310
25	S27A	0.31	0/444	0.57	0/590
26	S28E	0.27	0/500	0.63	0/669
27	SL7A	0.27	0/946	0.47	0/1272
28	AS8P	0.32	0/1046	0.56	0/1410
All	All	0.43	6/60517 (0.0%)	0.87	111/88349 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A16S	597	C	O3'-P	7.05	1.69	1.61
1	A16S	594	G	O3'-P	6.94	1.69	1.61
1	A16S	595	A	O3'-P	6.60	1.69	1.61
1	A16S	86	A	O3'-P	6.22	1.68	1.61
1	A16S	76	C	O3'-P	6.10	1.68	1.61
1	A16S	596	A	O3'-P	5.87	1.68	1.61

All (111) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A16S	1358	C	N1-C2-O2	16.78	128.97	118.90
1	A16S	1358	C	N3-C2-O2	-14.14	112.00	121.90
1	A16S	81	A	C4'-C3'-O3'	13.08	139.16	113.00
1	A16S	1358	C	N3-C4-N4	-11.34	110.06	118.00
1	A16S	898	G	N3-C2-N2	10.65	127.36	119.90
1	A16S	1358	C	C5-C4-N4	10.62	127.64	120.20
1	A16S	898	G	C5-C6-O6	9.87	134.52	128.60
1	A16S	898	G	N1-C2-N2	-9.62	107.54	116.20
1	A16S	950	U	N1-C2-O2	8.91	129.03	122.80
1	A16S	1351	C	N1-C2-O2	8.76	124.15	118.90
1	A16S	1351	C	C2-N1-C1'	8.33	127.96	118.80
1	A16S	950	U	C2-N1-C1'	8.30	127.66	117.70
1	A16S	443	C	N1-C2-O2	8.14	123.78	118.90
1	A16S	1351	C	N3-C2-O2	-8.12	116.21	121.90
1	A16S	440	C	C2-N1-C1'	8.11	127.72	118.80
1	A16S	605	G	N3-C4-N9	-7.99	121.21	126.00
1	A16S	1042	U	N3-C2-O2	-7.84	116.71	122.20
1	A16S	1351	C	C6-N1-C2	-7.80	117.18	120.30
1	A16S	1042	U	N1-C2-O2	7.66	128.16	122.80
1	A16S	950	U	N3-C2-O2	-7.49	116.96	122.20
1	A16S	256	U	O4'-C1'-N1	-7.43	102.26	108.20
1	A16S	1129	C	C2-N1-C1'	7.25	126.78	118.80
2	VTRF	25	G	C5-C6-O6	-7.18	124.29	128.60
1	A16S	423	C	N1-C2-O2	7.18	123.21	118.90
1	A16S	85	G	C2'-C3'-O3'	7.18	125.29	109.50
1	A16S	597	C	C4'-C3'-O3'	7.07	127.15	113.00
1	A16S	1129	C	C5-C6-N1	6.87	124.43	121.00
1	A16S	81	A	N9-C1'-C2'	-6.84	104.47	112.00
1	A16S	440	C	N1-C2-O2	6.71	122.93	118.90
1	A16S	605	G	N3-C4-C5	6.66	131.93	128.60
1	A16S	440	C	C6-N1-C1'	-6.58	112.90	120.80
1	A16S	57	C	N3-C2-O2	-6.58	117.30	121.90
1	A16S	1012	G	C5-C6-O6	6.54	132.52	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A16S	1331	C	N1-C2-O2	6.40	122.74	118.90
1	A16S	1129	C	N1-C2-O2	6.38	122.73	118.90
1	A16S	957	G	C4-C5-N7	6.36	113.34	110.80
1	A16S	423	C	C2-N1-C1'	6.34	125.78	118.80
1	A16S	957	G	N9-C4-C5	-6.32	102.87	105.40
1	A16S	996	C	C2-N1-C1'	6.29	125.72	118.80
1	A16S	144	C	N3-C2-O2	-6.25	117.53	121.90
1	A16S	711	C	N3-C2-O2	-6.23	117.54	121.90
1	A16S	1180	C	N3-C2-O2	-6.22	117.55	121.90
1	A16S	771	C	N3-C2-O2	-6.21	117.55	121.90
1	A16S	898	G	N1-C6-O6	-6.16	116.20	119.90
1	A16S	1042	U	C2-N1-C1'	6.15	125.08	117.70
1	A16S	141	C	N1-C2-O2	6.15	122.59	118.90
1	A16S	154	G	N1-C6-O6	-6.06	116.27	119.90
1	A16S	663	U	C2-N1-C1'	6.00	124.90	117.70
1	A16S	81	A	C2'-C3'-O3'	-5.95	96.41	109.50
1	A16S	595	A	P-O3'-C3'	5.93	126.81	119.70
1	A16S	1362	C	N1-C2-O2	5.92	122.45	118.90
1	A16S	446	U	C2-N1-C1'	5.91	124.80	117.70
1	A16S	673	C	N1-C2-O2	5.83	122.40	118.90
1	A16S	370	G	C5-C6-O6	5.80	132.08	128.60
1	A16S	453	G	C5-C6-O6	5.78	132.07	128.60
1	A16S	154	G	C5-C6-O6	5.76	132.06	128.60
1	A16S	950	U	C6-N1-C1'	-5.76	113.14	121.20
1	A16S	938	C	N1-C2-O2	5.72	122.33	118.90
1	A16S	1362	C	N3-C2-O2	-5.72	117.90	121.90
1	A16S	25	C	N3-C2-O2	-5.71	117.90	121.90
1	A16S	967	G	C4-N9-C1'	-5.70	119.09	126.50
1	A16S	996	C	C5-C6-N1	5.70	123.85	121.00
1	A16S	77	G	C4'-C3'-O3'	5.67	124.35	113.00
1	A16S	423	C	N3-C2-O2	-5.65	117.94	121.90
1	A16S	443	C	N3-C2-O2	-5.61	117.97	121.90
1	A16S	649	G	C5-C6-O6	5.60	131.96	128.60
1	A16S	206	C	C6-N1-C2	-5.55	118.08	120.30
1	A16S	596	A	C4'-C3'-O3'	5.53	124.05	113.00
1	A16S	213	C	C2'-C3'-O3'	5.50	122.50	113.70
1	A16S	1012	G	N1-C6-O6	-5.36	116.68	119.90
2	VTRF	25	G	N1-C6-O6	5.36	123.11	119.90
1	A16S	1158	G	C2-N3-C4	-5.35	109.23	111.90
1	A16S	103	A	P-O3'-C3'	5.35	126.11	119.70
1	A16S	559	C	N1-C2-O2	5.32	122.09	118.90
1	A16S	984	C	N1-C2-O2	5.32	122.09	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A16S	1240	G	N9-C4-C5	-5.31	103.28	105.40
1	A16S	444	U	C2-N1-C1'	5.30	124.06	117.70
1	A16S	605	G	C5-C6-O6	5.30	131.78	128.60
1	A16S	1042	U	O4'-C1'-N1	5.29	112.44	108.20
1	A16S	612	G	N9-C4-C5	-5.25	103.30	105.40
1	A16S	898	G	C2-N3-C4	-5.25	109.28	111.90
1	A16S	445	C	C6-N1-C1'	5.23	127.08	120.80
1	A16S	323	C	N3-C2-O2	-5.23	118.24	121.90
1	A16S	861	U	C2-N1-C1'	5.21	123.95	117.70
1	A16S	609	C	N1-C2-O2	5.20	122.02	118.90
1	A16S	605	G	C4-N9-C1'	-5.19	119.75	126.50
1	A16S	967	G	N3-C4-C5	5.17	131.19	128.60
1	A16S	213	C	C4'-C3'-O3'	5.17	123.33	113.00
1	A16S	441	C	N1-C2-O2	5.16	121.99	118.90
1	A16S	967	G	N3-C4-N9	-5.15	122.91	126.00
1	A16S	1138	U	N3-C2-O2	-5.15	118.60	122.20
1	A16S	206	C	N3-C2-O2	-5.14	118.30	121.90
1	A16S	673	C	N3-C2-O2	-5.12	118.32	121.90
1	A16S	25	C	C6-N1-C1'	5.11	126.93	120.80
1	A16S	605	G	N1-C6-O6	-5.11	116.84	119.90
1	A16S	207	U	C2-N1-C1'	5.10	123.83	117.70
1	A16S	1001	C	C2-N1-C1'	-5.10	113.19	118.80
1	A16S	1129	C	C6-N1-C2	-5.08	118.27	120.30
1	A16S	605	G	C6-C5-N7	5.08	133.45	130.40
1	A16S	1351	C	C6-N1-C1'	-5.08	114.71	120.80
1	A16S	1012	G	N3-C4-N9	-5.06	122.96	126.00
1	A16S	950	U	C5-C6-N1	5.05	125.23	122.70
1	A16S	214	U	C1'-O4'-C4'	-5.05	105.86	109.90
1	A16S	673	C	C5-C4-N4	5.05	123.74	120.20
1	A16S	1316	G	P-O3'-C3'	5.04	125.75	119.70
1	A16S	445	C	C2-N1-C1'	-5.04	113.26	118.80
1	A16S	717	C	N3-C2-O2	-5.02	118.38	121.90
1	A16S	862	A	C4-C5-N7	5.02	113.21	110.70
1	A16S	595	A	C2'-C3'-O3'	5.02	121.73	113.70
1	A16S	1254	U	P-O3'-C3'	5.01	125.72	119.70
1	A16S	441	C	N3-C2-O2	-5.01	118.39	121.90

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	A16S	28525	0	0	0	0
2	VTRF	556	0	0	0	0
3	AS2P	1587	0	0	0	0
4	AS4E	1925	0	0	0	0
5	AS4P	1370	0	0	0	0
6	AS5P	1600	0	0	0	0
7	AS6E	805	0	0	0	0
8	AS8E	993	0	0	0	0
9	S11P	960	0	0	0	0
10	S12P	1103	0	0	0	0
11	S15P	1225	0	0	0	0
12	S17P	885	0	0	0	0
13	S24E	759	0	0	0	0
14	S27E	458	0	0	0	0
15	S3AE	1545	0	0	0	0
16	AS3P	1576	0	0	0	0
17	AS7P	1537	0	0	0	0
18	AS9P	1096	0	0	0	0
19	S10P	824	0	0	0	0
20	S13P	1204	0	0	0	0
21	S14P	432	0	0	0	0
22	S17E	517	0	0	0	0
23	S19E	1239	0	0	0	0
24	S19P	969	0	0	0	0
25	S27A	435	0	0	0	0
26	S28E	498	0	0	0	0
27	SL7A	935	0	0	0	0
28	AS8P	1028	0	0	0	0
29	AS2P	171	0	0	0	0
29	AS5P	85	0	0	0	0
29	AS8P	30	0	0	0	0
All	All	56872	0	0	0	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 40.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AS2P	194/196 (99%)	185 (95%)	9 (5%)	0	100	100
4	AS4E	238/240 (99%)	210 (88%)	28 (12%)	0	100	100
5	AS4P	164/166 (99%)	140 (85%)	24 (15%)	0	100	100
6	AS5P	202/204 (99%)	183 (91%)	19 (9%)	0	100	100
7	AS6E	103/105 (98%)	88 (85%)	15 (15%)	0	100	100
8	AS8E	124/126 (98%)	111 (90%)	13 (10%)	0	100	100
9	S11P	126/128 (98%)	114 (90%)	12 (10%)	0	100	100
10	S12P	141/143 (99%)	121 (86%)	20 (14%)	0	100	100
11	S15P	147/149 (99%)	130 (88%)	17 (12%)	0	100	100
12	S17P	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
13	S24E	94/96 (98%)	88 (94%)	6 (6%)	0	100	100
14	S27E	57/59 (97%)	49 (86%)	8 (14%)	0	100	100
15	S3AE	187/189 (99%)	159 (85%)	28 (15%)	0	100	100
16	AS3P	199/201 (99%)	173 (87%)	23 (12%)	3 (2%)	8	40
17	AS7P	191/193 (99%)	151 (79%)	39 (20%)	1 (0%)	25	62
18	AS9P	134/136 (98%)	112 (84%)	22 (16%)	0	100	100
19	S10P	98/100 (98%)	86 (88%)	12 (12%)	0	100	100
20	S13P	145/147 (99%)	132 (91%)	12 (8%)	1 (1%)	19	56
21	S14P	50/52 (96%)	38 (76%)	10 (20%)	2 (4%)	2	21
22	S17E	60/62 (97%)	53 (88%)	7 (12%)	0	100	100
23	S19E	148/150 (99%)	129 (87%)	19 (13%)	0	100	100
24	S19P	113/115 (98%)	85 (75%)	28 (25%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	S27A	52/54 (96%)	35 (67%)	14 (27%)	3 (6%)	1	17
26	S28E	61/63 (97%)	44 (72%)	15 (25%)	2 (3%)	3	25
27	SL7A	121/123 (98%)	106 (88%)	13 (11%)	2 (2%)	7	37
28	AS8P	128/130 (98%)	117 (91%)	11 (9%)	0	100	100
All	All	3386/3438 (98%)	2937 (87%)	435 (13%)	14 (0%)	32	67

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	AS3P	83	VAL
21	S14P	5	LYS
25	S27A	26	ASP
16	AS3P	137	LEU
16	AS3P	183	ILE
17	AS7P	128	VAL
26	S28E	44	VAL
26	S28E	24	VAL
20	S13P	22	LYS
25	S27A	30	LEU
25	S27A	41	ILE
27	SL7A	95	ALA
21	S14P	6	PRO
27	SL7A	52	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AS2P	174/174 (100%)	148 (85%)	26 (15%)	2	14
4	AS4E	210/210 (100%)	183 (87%)	27 (13%)	3	17
5	AS4P	149/149 (100%)	127 (85%)	22 (15%)	2	14
6	AS5P	174/174 (100%)	149 (86%)	25 (14%)	2	15
7	AS6E	88/88 (100%)	77 (88%)	11 (12%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	AS8E	106/106 (100%)	93 (88%)	13 (12%)	4	18
9	S11P	94/94 (100%)	82 (87%)	12 (13%)	3	17
10	S12P	116/116 (100%)	99 (85%)	17 (15%)	2	14
11	S15P	133/133 (100%)	114 (86%)	19 (14%)	2	15
12	S17P	97/97 (100%)	79 (81%)	18 (19%)	1	8
13	S24E	84/84 (100%)	77 (92%)	7 (8%)	9	30
14	S27E	51/51 (100%)	44 (86%)	7 (14%)	3	16
15	S3AE	170/170 (100%)	143 (84%)	27 (16%)	2	13
16	AS3P	165/165 (100%)	141 (86%)	24 (14%)	2	15
17	AS7P	166/166 (100%)	145 (87%)	21 (13%)	3	17
18	AS9P	113/113 (100%)	88 (78%)	25 (22%)	1	5
19	S10P	92/92 (100%)	77 (84%)	15 (16%)	2	12
20	S13P	129/129 (100%)	105 (81%)	24 (19%)	1	8
21	S14P	45/45 (100%)	35 (78%)	10 (22%)	1	5
22	S17E	57/57 (100%)	49 (86%)	8 (14%)	3	16
23	S19E	134/134 (100%)	117 (87%)	17 (13%)	3	17
24	S19P	106/106 (100%)	91 (86%)	15 (14%)	2	15
25	S27A	47/47 (100%)	38 (81%)	9 (19%)	1	8
26	S28E	54/54 (100%)	44 (82%)	10 (18%)	1	9
27	SL7A	104/104 (100%)	91 (88%)	13 (12%)	3	17
28	AS8P	111/111 (100%)	92 (83%)	19 (17%)	1	11
All	All	2969/2969 (100%)	2528 (85%)	441 (15%)	5	14

All (441) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	AS2P	31	VAL
3	AS2P	34	ASP
3	AS2P	46	HIS
3	AS2P	49	THR
3	AS2P	57	TYR
3	AS2P	72	ILE
3	AS2P	75	ARG
3	AS2P	77	ARG
3	AS2P	86	PHE

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Mol	Chain	Res	Type
3	AS2P	87	ARG
3	AS2P	107	PHE
3	AS2P	108	SER
3	AS2P	115	GLU
3	AS2P	119	ARG
3	AS2P	124	THR
3	AS2P	126	THR
3	AS2P	168	ASP
3	AS2P	170	ARG
3	AS2P	173	PHE
3	AS2P	185	ARG
3	AS2P	188	LEU
3	AS2P	192	TYR
3	AS2P	200	LEU
3	AS2P	209	ASP
3	AS2P	212	ILE
3	AS2P	222	ARG
4	AS4E	3	ILE
4	AS4E	4	THR
4	AS4E	21	TRP
4	AS4E	24	ARG
4	AS4E	47	LYS
4	AS4E	71	ARG
4	AS4E	74	TYR
4	AS4E	80	LEU
4	AS4E	84	VAL
4	AS4E	90	ASP
4	AS4E	93	VAL
4	AS4E	103	LEU
4	AS4E	107	ASN
4	AS4E	118	VAL
4	AS4E	124	THR
4	AS4E	136	GLU
4	AS4E	151	TYR
4	AS4E	152	ASN
4	AS4E	157	THR
4	AS4E	179	TYR
4	AS4E	183	ILE
4	AS4E	193	LYS
4	AS4E	194	ILE
4	AS4E	206	LYS
4	AS4E	222	THR

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Mol	Chain	Res	Type
4	AS4E	236	ASP
4	AS4E	237	SER
5	AS4P	3	ASP
5	AS4P	5	ARG
5	AS4P	16	HIS
5	AS4P	25	LYS
5	AS4P	28	ILE
5	AS4P	40	GLU
5	AS4P	43	ILE
5	AS4P	49	ARG
5	AS4P	53	HIS
5	AS4P	66	ARG
5	AS4P	68	ILE
5	AS4P	69	ARG
5	AS4P	78	TYR
5	AS4P	97	THR
5	AS4P	102	LEU
5	AS4P	120	TYR
5	AS4P	128	HIS
5	AS4P	131	ILE
5	AS4P	144	VAL
5	AS4P	145	VAL
5	AS4P	149	GLU
5	AS4P	155	TYR
6	AS5P	21	ARG
6	AS5P	24	VAL
6	AS5P	26	GLN
6	AS5P	32	LYS
6	AS5P	38	GLU
6	AS5P	51	ILE
6	AS5P	61	TYR
6	AS5P	63	ILE
6	AS5P	72	GLN
6	AS5P	73	THR
6	AS5P	78	LEU
6	AS5P	86	VAL
6	AS5P	89	ASN
6	AS5P	119	ILE
6	AS5P	123	ARG
6	AS5P	142	ILE
6	AS5P	154	LEU
6	AS5P	172	PHE

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Mol	Chain	Res	Type
6	AS5P	178	LEU
6	AS5P	186	LYS
6	AS5P	194	ASN
6	AS5P	195	PHE
6	AS5P	203	LEU
6	AS5P	211	THR
6	AS5P	217	ARG
7	AS6E	123	GLN
7	AS6E	134	ILE
7	AS6E	152	THR
7	AS6E	173	LYS
7	AS6E	185	LYS
7	AS6E	190	ARG
7	AS6E	191	ARG
7	AS6E	195	VAL
7	AS6E	199	MET
7	AS6E	205	VAL
7	AS6E	211	MET
8	AS8E	10	ARG
8	AS8E	12	ILE
8	AS8E	40	LYS
8	AS8E	53	PHE
8	AS8E	54	LYS
8	AS8E	58	ARG
8	AS8E	65	VAL
8	AS8E	71	LYS
8	AS8E	74	LYS
8	AS8E	81	VAL
8	AS8E	82	LEU
8	AS8E	92	ARG
8	AS8E	100	THR
9	S11P	7	ILE
9	S11P	8	ARG
9	S11P	41	MET
9	S11P	43	VAL
9	S11P	46	ASP
9	S11P	61	LYS
9	S11P	74	ILE
9	S11P	79	ARG
9	S11P	114	THR
9	S11P	116	LEU
9	S11P	130	ARG

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Mol	Chain	Res	Type
9	S11P	131	ARG
10	S12P	5	LYS
10	S12P	18	LEU
10	S12P	23	PHE
10	S12P	32	ARG
10	S12P	34	MET
10	S12P	49	MET
10	S12P	60	ILE
10	S12P	82	ARG
10	S12P	88	VAL
10	S12P	96	PHE
10	S12P	102	GLU
10	S12P	118	ASP
10	S12P	119	LEU
10	S12P	129	VAL
10	S12P	135	ASP
10	S12P	139	LYS
10	S12P	144	LYS
11	S15P	3	LYS
11	S15P	9	ASN
11	S15P	22	LYS
11	S15P	25	ARG
11	S15P	27	THR
11	S15P	28	ARG
11	S15P	60	LEU
11	S15P	77	ASN
11	S15P	81	LYS
11	S15P	88	ASN
11	S15P	89	LEU
11	S15P	95	ASN
11	S15P	96	ILE
11	S15P	98	ARG
11	S15P	111	ARG
11	S15P	130	THR
11	S15P	136	GLU
11	S15P	137	TRP
11	S15P	145	GLU
12	S17P	21	LYS
12	S17P	22	THR
12	S17P	24	ASP
12	S17P	27	TYR
12	S17P	30	TYR

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Mol	Chain	Res	Type
12	S17P	35	LYS
12	S17P	37	ARG
12	S17P	39	ILE
12	S17P	45	LEU
12	S17P	47	ARG
12	S17P	53	THR
12	S17P	58	ARG
12	S17P	72	ARG
12	S17P	76	ARG
12	S17P	87	VAL
12	S17P	88	LYS
12	S17P	91	ASP
12	S17P	105	ILE
13	S24E	9	VAL
13	S24E	12	LYS
13	S24E	31	LEU
13	S24E	56	PHE
13	S24E	69	PHE
13	S24E	72	TYR
13	S24E	101	ARG
14	S27E	5	PHE
14	S27E	7	ILE
14	S27E	9	ILE
14	S27E	18	ARG
14	S27E	24	CYS
14	S27E	38	VAL
14	S27E	41	LEU
15	S3AE	10	ARG
15	S3AE	12	LYS
15	S3AE	21	ILE
15	S3AE	48	ILE
15	S3AE	50	VAL
15	S3AE	53	TYR
15	S3AE	63	TYR
15	S3AE	82	ILE
15	S3AE	84	TYR
15	S3AE	88	LEU
15	S3AE	93	ILE
15	S3AE	96	LEU
15	S3AE	109	ASP
15	S3AE	114	ASP
15	S3AE	116	TYR

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Mol	Chain	Res	Type
15	S3AE	118	LEU
15	S3AE	140	LYS
15	S3AE	144	ASP
15	S3AE	147	ARG
15	S3AE	152	GLU
15	S3AE	154	ASP
15	S3AE	167	LEU
15	S3AE	169	ASN
15	S3AE	170	ASP
15	S3AE	186	ILE
15	S3AE	187	GLU
15	S3AE	192	LEU
16	AS3P	3	LEU
16	AS3P	4	ILE
16	AS3P	5	LYS
16	AS3P	7	HIS
16	AS3P	8	PHE
16	AS3P	31	TYR
16	AS3P	34	VAL
16	AS3P	45	VAL
16	AS3P	71	GLU
16	AS3P	72	LYS
16	AS3P	73	PHE
16	AS3P	76	LEU
16	AS3P	82	THR
16	AS3P	106	LYS
16	AS3P	108	TYR
16	AS3P	111	ARG
16	AS3P	149	GLU
16	AS3P	153	TYR
16	AS3P	157	GLN
16	AS3P	159	LEU
16	AS3P	161	LYS
16	AS3P	165	ARG
16	AS3P	185	LYS
16	AS3P	188	ARG
17	AS7P	14	VAL
17	AS7P	22	VAL
17	AS7P	35	LEU
17	AS7P	38	ILE
17	AS7P	40	LEU
17	AS7P	73	ASN

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Mol	Chain	Res	Type
17	AS7P	79	LEU
17	AS7P	94	LYS
17	AS7P	95	THR
17	AS7P	107	ILE
17	AS7P	113	ARG
17	AS7P	116	VAL
17	AS7P	118	ARG
17	AS7P	119	ILE
17	AS7P	125	VAL
17	AS7P	131	ASP
17	AS7P	142	LEU
17	AS7P	154	PHE
17	AS7P	167	GLU
17	AS7P	176	ASN
17	AS7P	181	ILE
18	AS9P	6	GLN
18	AS9P	8	PHE
18	AS9P	23	TYR
18	AS9P	24	ILE
18	AS9P	32	PHE
18	AS9P	35	ASP
18	AS9P	41	ILE
18	AS9P	48	TYR
18	AS9P	50	ILE
18	AS9P	54	LEU
18	AS9P	56	LEU
18	AS9P	61	ILE
18	AS9P	62	THR
18	AS9P	65	ILE
18	AS9P	76	ILE
18	AS9P	93	LYS
18	AS9P	94	PHE
18	AS9P	95	THR
18	AS9P	102	GLU
18	AS9P	108	ASP
18	AS9P	111	MET
18	AS9P	120	GLU
18	AS9P	126	ARG
18	AS9P	127	TYR
18	AS9P	132	TRP
19	S10P	4	LYS
19	S10P	7	ILE

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Mol	Chain	Res	Type
19	S10P	15	ASP
19	S10P	21	VAL
19	S10P	29	GLN
19	S10P	35	VAL
19	S10P	44	THR
19	S10P	50	VAL
19	S10P	51	MET
19	S10P	63	GLU
19	S10P	68	LYS
19	S10P	94	ASP
19	S10P	95	VAL
19	S10P	96	TYR
19	S10P	97	ILE
20	S13P	7	LYS
20	S13P	15	GLN
20	S13P	16	ASP
20	S13P	20	THR
20	S13P	21	MET
20	S13P	27	LEU
20	S13P	30	ILE
20	S13P	41	ILE
20	S13P	46	ASN
20	S13P	51	LYS
20	S13P	52	ARG
20	S13P	53	LEU
20	S13P	61	ILE
20	S13P	67	LEU
20	S13P	78	ASN
20	S13P	81	TYR
20	S13P	82	ASN
20	S13P	87	TYR
20	S13P	93	MET
20	S13P	97	THR
20	S13P	100	LEU
20	S13P	113	ARG
20	S13P	133	THR
20	S13P	136	THR
21	S14P	5	LYS
21	S14P	10	ARG
21	S14P	11	ARG
21	S14P	14	LYS
21	S14P	25	ARG

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Mol	Chain	Res	Type
21	S14P	31	LYS
21	S14P	37	CYS
21	S14P	39	GLN
21	S14P	41	PHE
21	S14P	52	LYS
22	S17E	5	TYR
22	S17E	20	PHE
22	S17E	44	LYS
22	S17E	45	LYS
22	S17E	46	VAL
22	S17E	47	LYS
22	S17E	55	THR
22	S17E	57	TYR
23	S19E	5	MET
23	S19E	10	ILE
23	S19E	25	GLU
23	S19E	61	ARG
23	S19E	67	LYS
23	S19E	70	ILE
23	S19E	93	VAL
23	S19E	94	LYS
23	S19E	97	THR
23	S19E	98	HIS
23	S19E	104	LEU
23	S19E	116	THR
23	S19E	117	ARG
23	S19E	120	ARG
23	S19E	125	LYS
23	S19E	127	ARG
23	S19E	135	TYR
24	S19P	12	PHE
24	S19P	13	ARG
24	S19P	17	LYS
24	S19P	19	LEU
24	S19P	31	ILE
24	S19P	40	ARG
24	S19P	44	ARG
24	S19P	51	ARG
24	S19P	72	THR
24	S19P	75	ARG
24	S19P	76	ASN
24	S19P	92	ASN

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Mol	Chain	Res	Type
24	S19P	99	PHE
24	S19P	109	TYR
24	S19P	115	ILE
25	S27A	12	GLN
25	S27A	16	VAL
25	S27A	26	ASP
25	S27A	28	ILE
25	S27A	30	LEU
25	S27A	50	GLU
25	S27A	52	TRP
25	S27A	54	CYS
25	S27A	63	ILE
26	S28E	30	ARG
26	S28E	33	VAL
26	S28E	37	VAL
26	S28E	41	ARG
26	S28E	49	ASP
26	S28E	55	THR
26	S28E	67	ILE
26	S28E	71	ARG
26	S28E	75	ARG
26	S28E	78	ARG
27	SL7A	36	THR
27	SL7A	49	LYS
27	SL7A	57	VAL
27	SL7A	58	GLN
27	SL7A	62	ILE
27	SL7A	65	HIS
27	SL7A	71	GLU
27	SL7A	77	TYR
27	SL7A	82	SER
27	SL7A	94	VAL
27	SL7A	110	LEU
27	SL7A	118	VAL
27	SL7A	122	LYS
28	AS8P	9	ASN
28	AS8P	14	LEU
28	AS8P	15	TYR
28	AS8P	16	ASN
28	AS8P	21	ARG
28	AS8P	24	GLN
28	AS8P	31	SER

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Mol	Chain	Res	Type
28	AS8P	39	ARG
28	AS8P	40	VAL
28	AS8P	42	GLN
28	AS8P	43	LYS
28	AS8P	81	LEU
28	AS8P	83	TYR
28	AS8P	88	ARG
28	AS8P	91	ASP
28	AS8P	96	TYR
28	AS8P	106	ILE
28	AS8P	118	ASP
28	AS8P	123	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A16S	1325/1501 (88%)	604 (45%)	41 (3%)
2	VTRF	25/26 (96%)	21 (84%)	0
All	All	1350/1527 (88%)	625 (46%)	41 (3%)

All (625) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A16S	9	U
1	A16S	11	C
1	A16S	14	G
1	A16S	16	U
1	A16S	19	U
1	A16S	20	C
1	A16S	26	G
1	A16S	27	G
1	A16S	28	A
1	A16S	32	G
1	A16S	33	A
1	A16S	35	C
1	A16S	36	G
1	A16S	39	A
1	A16S	41	C

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Mol	Chain	Res	Type
1	A16S	42	G
1	A16S	45	G
1	A16S	46	U
1	A16S	48	G
1	A16S	49	G
1	A16S	51	A
1	A16S	53	A
1	A16S	54	A
1	A16S	55	G
1	A16S	57	C
1	A16S	61	G
1	A16S	63	A
1	A16S	67	U
1	A16S	68	U
1	A16S	70	C
1	A16S	77	G
1	A16S	78	G
1	A16S	79	G
1	A16S	82	A
1	A16S	84	G
1	A16S	85	G
1	A16S	86	A
1	A16S	87	G
1	A16S	94	G
1	A16S	96	A
1	A16S	98	G
1	A16S	99	G
1	A16S	103	A
1	A16S	104	G
1	A16S	106	A
1	A16S	108	C
1	A16S	109	A
1	A16S	110	C
1	A16S	117	A
1	A16S	118	A
1	A16S	119	C
1	A16S	120	C
1	A16S	126	U
1	A16S	129	G
1	A16S	130	G
1	A16S	131	A
1	A16S	132	C

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Mol	Chain	Res	Type
1	A16S	138	U
1	A16S	148	A
1	A16S	149	A
1	A16S	152	U
1	A16S	155	G
1	A16S	158	U
1	A16S	161	U
1	A16S	164	C
1	A16S	165	C
1	A16S	167	A
1	A16S	168	U
1	A16S	169	A
1	A16S	170	G
1	A16S	175	G
1	A16S	177	A
1	A16S	178	G
1	A16S	179	U
1	A16S	184	G
1	A16S	185	A
1	A16S	186	A
1	A16S	187	U
1	A16S	194	U
1	A16S	200	A
1	A16S	202	A
1	A16S	203	G
1	A16S	205	G
1	A16S	207	U
1	A16S	211	G
1	A16S	212	G
1	A16S	213	C
1	A16S	214	U
1	A16S	215	A
1	A16S	218	U
1	A16S	220	C
1	A16S	221	C
1	A16S	222	G
1	A16S	223	U
1	A16S	224	U
1	A16S	225	U
1	A16S	227	U
1	A16S	229	G
1	A16S	235	C

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Mol	Chain	Res	Type
1	A16S	238	G
1	A16S	239	G
1	A16S	240	A
1	A16S	241	U
1	A16S	251	G
1	A16S	252	C
1	A16S	255	A
1	A16S	256	U
1	A16S	257	C
1	A16S	258	A
1	A16S	259	G
1	A16S	270	G
1	A16S	272	G
1	A16S	273	U
1	A16S	274	A
1	A16S	275	A
1	A16S	278	G
1	A16S	279	C
1	A16S	291	A
1	A16S	293	A
1	A16S	294	A
1	A16S	295	C
1	A16S	297	G
1	A16S	298	G
1	A16S	301	G
1	A16S	305	C
1	A16S	309	G
1	A16S	315	G
1	A16S	316	G
1	A16S	323	C
1	A16S	327	U
1	A16S	328	U
1	A16S	329	G
1	A16S	331	G
1	A16S	340	C
1	A16S	341	A
1	A16S	343	G
1	A16S	344	G
1	A16S	345	G
1	A16S	346	C
1	A16S	351	G
1	A16S	354	C

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Mol	Chain	Res	Type
1	A16S	356	A
1	A16S	357	C
1	A16S	358	G
1	A16S	362	C
1	A16S	363	G
1	A16S	364	C
1	A16S	365	A
1	A16S	366	C
1	A16S	368	A
1	A16S	370	G
1	A16S	371	C
1	A16S	379	G
1	A16S	380	U
1	A16S	385	A
1	A16S	386	A
1	A16S	394	A
1	A16S	395	A
1	A16S	396	G
1	A16S	398	G
1	A16S	400	G
1	A16S	407	C
1	A16S	409	A
1	A16S	414	G
1	A16S	415	A
1	A16S	420	C
1	A16S	423	C
1	A16S	424	G
1	A16S	428	G
1	A16S	430	A
1	A16S	431	G
1	A16S	434	U
1	A16S	435	U
1	A16S	437	U
1	A16S	439	C
1	A16S	441	C
1	A16S	442	G
1	A16S	444	U
1	A16S	445	C
1	A16S	446	U
1	A16S	447	A
1	A16S	448	A
1	A16S	449	A

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Mol	Chain	Res	Type
1	A16S	450	A
1	A16S	451	A
1	A16S	452	G
1	A16S	453	G
1	A16S	455	G
1	A16S	456	G
1	A16S	458	G
1	A16S	459	G
1	A16S	461	A
1	A16S	462	U
1	A16S	463	A
1	A16S	465	G
1	A16S	470	G
1	A16S	472	G
1	A16S	473	C
1	A16S	474	A
1	A16S	475	A
1	A16S	476	G
1	A16S	477	U
1	A16S	479	U
1	A16S	480	G
1	A16S	483	G
1	A16S	484	U
1	A16S	485	C
1	A16S	487	G
1	A16S	491	C
1	A16S	492	C
1	A16S	493	G
1	A16S	496	G
1	A16S	497	U
1	A16S	498	A
1	A16S	499	A
1	A16S	501	A
1	A16S	504	A
1	A16S	505	G
1	A16S	506	C
1	A16S	507	U
1	A16S	513	A
1	A16S	516	G
1	A16S	517	G
1	A16S	518	U
1	A16S	519	C

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Mol	Chain	Res	Type
1	A16S	525	G
1	A16S	526	A
1	A16S	527	U
1	A16S	528	U
1	A16S	529	A
1	A16S	531	U
1	A16S	532	G
1	A16S	539	A
1	A16S	540	A
1	A16S	541	G
1	A16S	542	C
1	A16S	543	G
1	A16S	545	C
1	A16S	554	G
1	A16S	555	C
1	A16S	560	C
1	A16S	561	A
1	A16S	562	A
1	A16S	564	U
1	A16S	565	C
1	A16S	567	C
1	A16S	569	C
1	A16S	570	C
1	A16S	573	A
1	A16S	577	U
1	A16S	584	C
1	A16S	595	A
1	A16S	596	A
1	A16S	597	C
1	A16S	598	U
1	A16S	600	G
1	A16S	603	G
1	A16S	607	U
1	A16S	608	A
1	A16S	609	C
1	A16S	619	A
1	A16S	620	G
1	A16S	624	G
1	A16S	627	G
1	A16S	631	A
1	A16S	632	G
1	A16S	635	G

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Mol	Chain	Res	Type
1	A16S	637	G
1	A16S	646	C
1	A16S	647	C
1	A16S	649	G
1	A16S	650	A
1	A16S	651	G
1	A16S	652	U
1	A16S	653	A
1	A16S	654	G
1	A16S	656	G
1	A16S	659	G
1	A16S	660	A
1	A16S	661	A
1	A16S	662	A
1	A16S	663	U
1	A16S	664	C
1	A16S	666	U
1	A16S	668	A
1	A16S	669	G
1	A16S	670	A
1	A16S	671	U
1	A16S	672	A
1	A16S	675	G
1	A16S	678	A
1	A16S	683	C
1	A16S	687	A
1	A16S	688	G
1	A16S	689	U
1	A16S	690	G
1	A16S	695	A
1	A16S	697	G
1	A16S	700	C
1	A16S	702	C
1	A16S	712	G
1	A16S	714	G
1	A16S	715	C
1	A16S	718	G
1	A16S	720	C
1	A16S	721	G
1	A16S	725	A
1	A16S	732	A
1	A16S	774	G

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Mol	Chain	Res	Type
1	A16S	778	G
1	A16S	779	U
1	A16S	781	A
1	A16S	783	C
1	A16S	784	G
1	A16S	785	A
1	A16S	786	U
1	A16S	787	G
1	A16S	792	C
1	A16S	793	U
1	A16S	794	A
1	A16S	795	G
1	A16S	800	C
1	A16S	801	G
1	A16S	805	A
1	A16S	810	U
1	A16S	811	A
1	A16S	812	G
1	A16S	813	A
1	A16S	815	C
1	A16S	816	C
1	A16S	822	G
1	A16S	824	U
1	A16S	837	C
1	A16S	841	U
1	A16S	842	A
1	A16S	843	A
1	A16S	845	C
1	A16S	848	G
1	A16S	849	C
1	A16S	854	U
1	A16S	855	G
1	A16S	859	A
1	A16S	861	U
1	A16S	862	A
1	A16S	863	C
1	A16S	864	G
1	A16S	867	C
1	A16S	872	G
1	A16S	875	U
1	A16S	879	A
1	A16S	884	A

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Mol	Chain	Res	Type
1	A16S	887	G
1	A16S	888	A
1	A16S	891	U
1	A16S	892	G
1	A16S	894	C
1	A16S	896	G
1	A16S	897	G
1	A16S	898	G
1	A16S	902	C
1	A16S	905	C
1	A16S	906	A
1	A16S	911	G
1	A16S	912	G
1	A16S	915	G
1	A16S	920	C
1	A16S	922	G
1	A16S	925	G
1	A16S	926	C
1	A16S	927	U
1	A16S	928	C
1	A16S	929	A
1	A16S	930	A
1	A16S	931	U
1	A16S	932	U
1	A16S	935	A
1	A16S	937	U
1	A16S	938	C
1	A16S	939	A
1	A16S	940	A
1	A16S	942	G
1	A16S	944	C
1	A16S	945	U
1	A16S	946	G
1	A16S	948	A
1	A16S	949	A
1	A16S	952	U
1	A16S	953	U
1	A16S	954	A
1	A16S	956	C
1	A16S	957	G
1	A16S	958	G
1	A16S	960	G

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Mol	Chain	Res	Type
1	A16S	961	G
1	A16S	962	A
1	A16S	963	G
1	A16S	964	A
1	A16S	965	C
1	A16S	966	C
1	A16S	967	G
1	A16S	969	A
1	A16S	970	G
1	A16S	971	U
1	A16S	972	A
1	A16S	973	U
1	A16S	974	G
1	A16S	975	A
1	A16S	976	C
1	A16S	979	C
1	A16S	980	C
1	A16S	981	A
1	A16S	982	G
1	A16S	985	U
1	A16S	986	A
1	A16S	987	A
1	A16S	989	G
1	A16S	990	A
1	A16S	993	U
1	A16S	995	G
1	A16S	996	C
1	A16S	997	C
1	A16S	998	U
1	A16S	999	G
1	A16S	1000	A
1	A16S	1001	C
1	A16S	1004	G
1	A16S	1005	C
1	A16S	1010	A
1	A16S	1013	A
1	A16S	1014	G
1	A16S	1017	G
1	A16S	1023	C
1	A16S	1027	C
1	A16S	1028	G
1	A16S	1029	C

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Mol	Chain	Res	Type
1	A16S	1030	C
1	A16S	1031	A
1	A16S	1032	G
1	A16S	1034	U
1	A16S	1038	G
1	A16S	1041	G
1	A16S	1042	U
1	A16S	1043	G
1	A16S	1045	A
1	A16S	1047	U
1	A16S	1049	U
1	A16S	1050	C
1	A16S	1051	C
1	A16S	1056	A
1	A16S	1057	A
1	A16S	1058	G
1	A16S	1061	C
1	A16S	1063	G
1	A16S	1065	A
1	A16S	1068	G
1	A16S	1071	C
1	A16S	1072	G
1	A16S	1073	A
1	A16S	1076	C
1	A16S	1077	C
1	A16S	1078	C
1	A16S	1082	C
1	A16S	1088	G
1	A16S	1091	G
1	A16S	1092	G
1	A16S	1093	U
1	A16S	1094	A
1	A16S	1096	U
1	A16S	1097	C
1	A16S	1098	U
1	A16S	1099	G
1	A16S	1101	A
1	A16S	1102	C
1	A16S	1104	C
1	A16S	1105	C
1	A16S	1106	G
1	A16S	1107	G

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Mol	Chain	Res	Type
1	A16S	1111	A
1	A16S	1113	A
1	A16S	1114	A
1	A16S	1116	C
1	A16S	1117	A
1	A16S	1118	C
1	A16S	1120	C
1	A16S	1121	U
1	A16S	1122	A
1	A16S	1124	G
1	A16S	1126	G
1	A16S	1128	A
1	A16S	1129	C
1	A16S	1130	U
1	A16S	1134	G
1	A16S	1135	G
1	A16S	1138	U
1	A16S	1140	A
1	A16S	1148	G
1	A16S	1151	G
1	A16S	1152	G
1	A16S	1153	A
1	A16S	1154	G
1	A16S	1156	G
1	A16S	1157	G
1	A16S	1158	G
1	A16S	1159	C
1	A16S	1160	C
1	A16S	1166	A
1	A16S	1167	G
1	A16S	1170	C
1	A16S	1171	A
1	A16S	1175	U
1	A16S	1176	G
1	A16S	1181	G
1	A16S	1182	A
1	A16S	1183	A
1	A16S	1185	C
1	A16S	1188	C
1	A16S	1190	G
1	A16S	1191	G
1	A16S	1193	C

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Mol	Chain	Res	Type
1	A16S	1194	C
1	A16S	1195	G
1	A16S	1196	C
1	A16S	1197	A
1	A16S	1198	C
1	A16S	1201	G
1	A16S	1208	A
1	A16S	1210	U
1	A16S	1211	G
1	A16S	1219	C
1	A16S	1221	A
1	A16S	1226	A
1	A16S	1227	U
1	A16S	1228	G
1	A16S	1230	U
1	A16S	1232	C
1	A16S	1233	C
1	A16S	1236	G
1	A16S	1237	A
1	A16S	1238	A
1	A16S	1241	G
1	A16S	1249	A
1	A16S	1250	A
1	A16S	1251	U
1	A16S	1252	C
1	A16S	1253	C
1	A16S	1254	U
1	A16S	1255	U
1	A16S	1256	A
1	A16S	1258	A
1	A16S	1264	C
1	A16S	1266	G
1	A16S	1267	C
1	A16S	1268	A
1	A16S	1270	U
1	A16S	1271	U
1	A16S	1272	G
1	A16S	1274	G
1	A16S	1276	U
1	A16S	1280	G
1	A16S	1281	G
1	A16S	1282	G

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Mol	Chain	Res	Type
1	A16S	1284	U
1	A16S	1287	A
1	A16S	1288	A
1	A16S	1289	C
1	A16S	1291	C
1	A16S	1294	C
1	A16S	1295	C
1	A16S	1296	U
1	A16S	1298	G
1	A16S	1301	A
1	A16S	1302	A
1	A16S	1303	C
1	A16S	1304	G
1	A16S	1305	A
1	A16S	1307	G
1	A16S	1314	U
1	A16S	1315	A
1	A16S	1316	G
1	A16S	1317	U
1	A16S	1322	G
1	A16S	1324	G
1	A16S	1325	G
1	A16S	1326	G
1	A16S	1329	A
1	A16S	1330	A
1	A16S	1331	C
1	A16S	1332	A
1	A16S	1333	A
1	A16S	1334	C
1	A16S	1335	C
1	A16S	1339	G
1	A16S	1343	A
1	A16S	1344	A
1	A16S	1346	A
1	A16S	1350	C
1	A16S	1351	C
1	A16S	1352	C
1	A16S	1356	U
1	A16S	1357	C
1	A16S	1360	U
1	A16S	1362	C
1	A16S	1363	A

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Mol	Chain	Res	Type
1	A16S	1364	C
2	VTRF	2	G
2	VTRF	4	U
2	VTRF	5	U
2	VTRF	6	G
2	VTRF	7	G
2	VTRF	8	U
2	VTRF	9	G
2	VTRF	10	G
2	VTRF	11	U
2	VTRF	13	U
2	VTRF	14	A
2	VTRF	15	G
2	VTRF	16	U
2	VTRF	17	C
2	VTRF	19	G
2	VTRF	20	G
2	VTRF	21	U
2	VTRF	23	A
2	VTRF	24	U
2	VTRF	25	G
2	VTRF	26	A

All (41) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A16S	54	A
1	A16S	78	G
1	A16S	85	G
1	A16S	86	A
1	A16S	102	G
1	A16S	103	A
1	A16S	168	U
1	A16S	213	C
1	A16S	220	C
1	A16S	221	C
1	A16S	222	G
1	A16S	231	C
1	A16S	255	A
1	A16S	272	G
1	A16S	384	C
1	A16S	395	A

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Mol	Chain	Res	Type
1	A16S	444	U
1	A16S	449	A
1	A16S	469	G
1	A16S	475	A
1	A16S	484	U
1	A16S	539	A
1	A16S	541	G
1	A16S	595	A
1	A16S	596	A
1	A16S	651	G
1	A16S	662	A
1	A16S	778	G
1	A16S	890	U
1	A16S	972	A
1	A16S	973	U
1	A16S	986	A
1	A16S	996	C
1	A16S	1026	U
1	A16S	1158	G
1	A16S	1220	A
1	A16S	1237	A
1	A16S	1254	U
1	A16S	1265	C
1	A16S	1316	G
1	A16S	1350	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 57 ligands modelled in this entry, 57 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

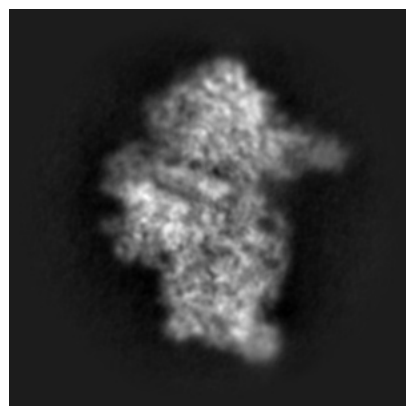
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37733. These allow visual inspection of the internal detail of the map and identification of artifacts.

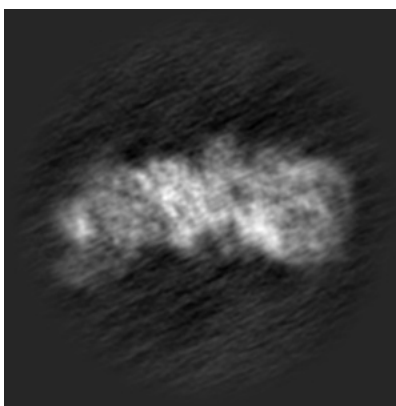
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

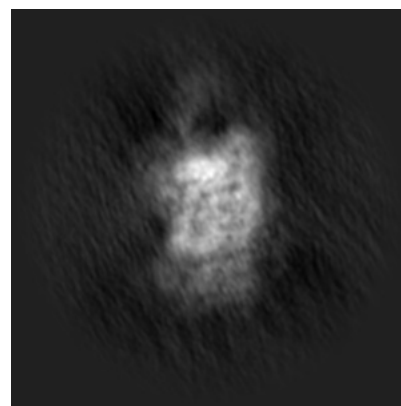
6.1.1 Primary map



X

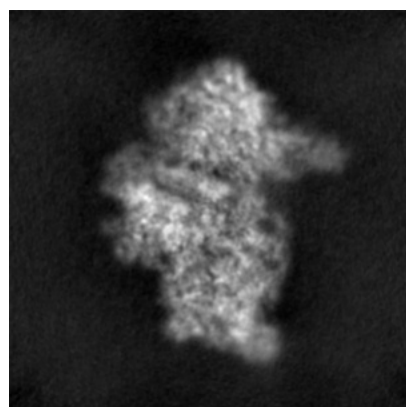


Y

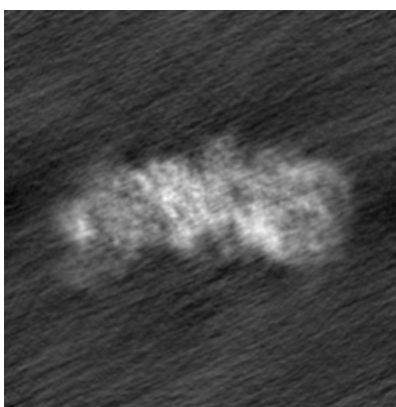


Z

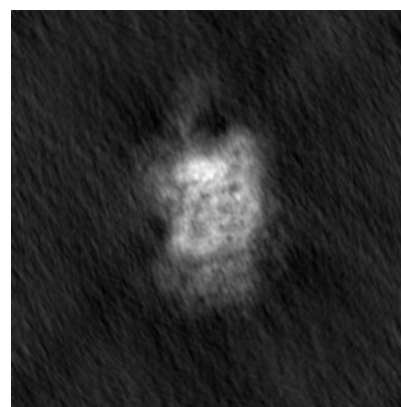
6.1.2 Raw map



X



Y

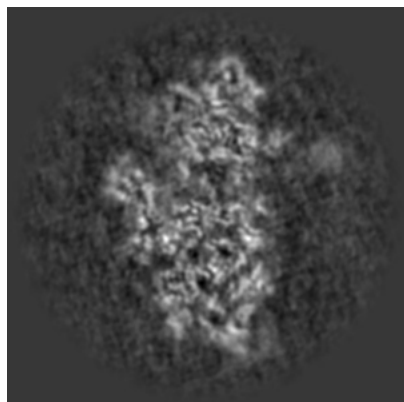


Z

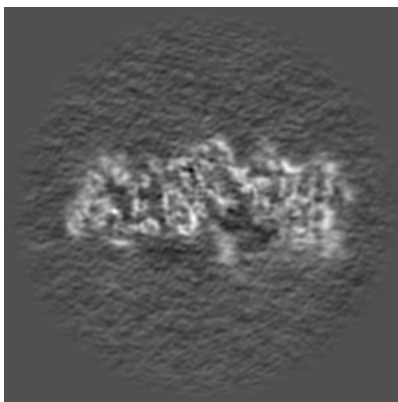
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

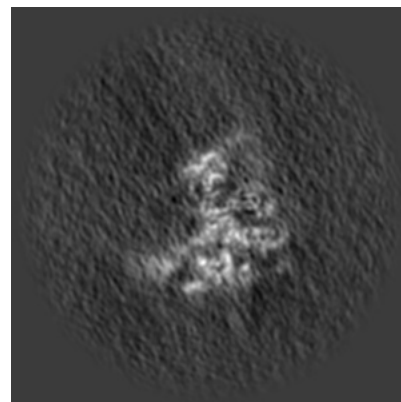
6.2.1 Primary map



X Index: 150

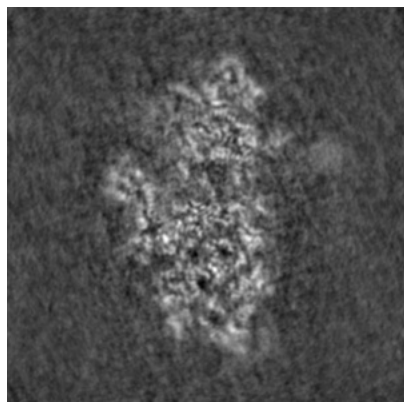


Y Index: 150

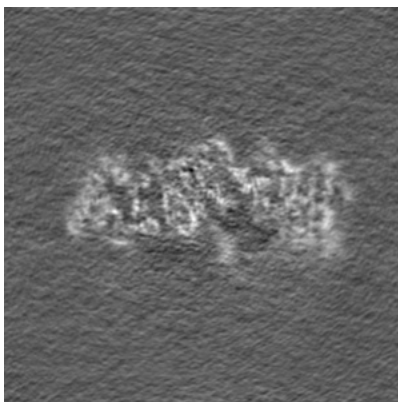


Z Index: 150

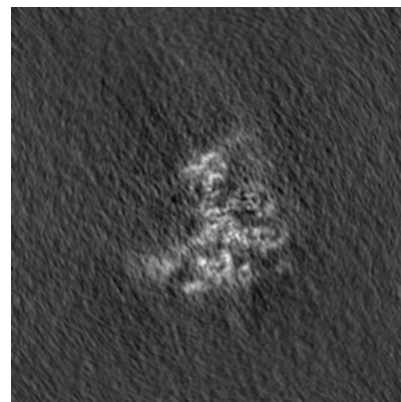
6.2.2 Raw map



X Index: 150



Y Index: 150

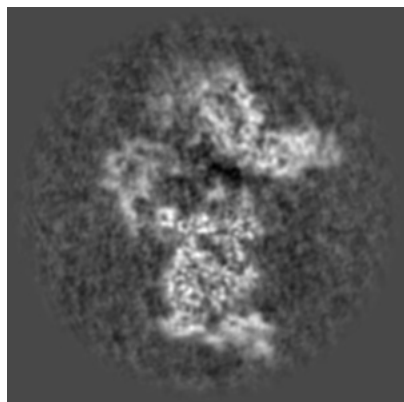


Z Index: 150

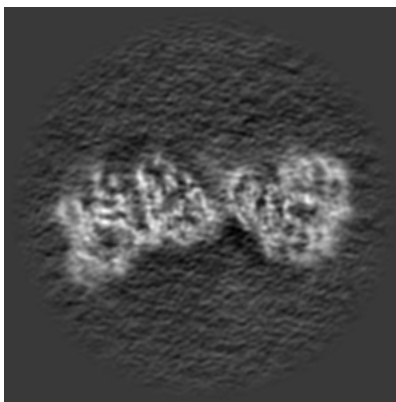
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

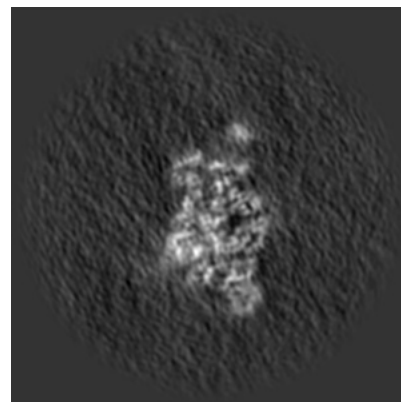
6.3.1 Primary map



X Index: 133

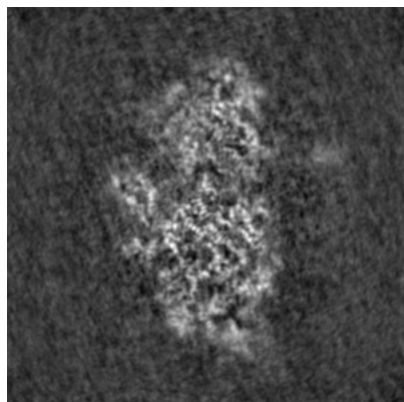


Y Index: 174

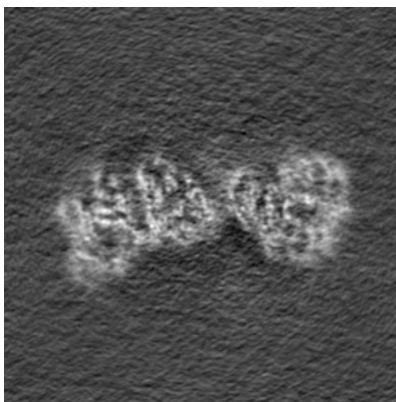


Z Index: 135

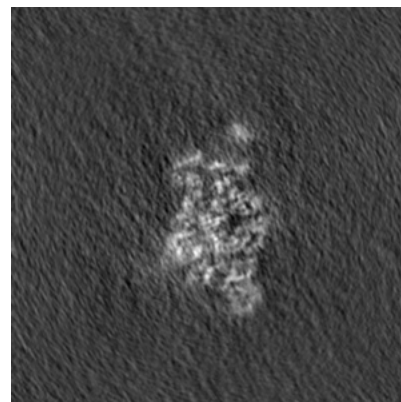
6.3.2 Raw map



X Index: 153



Y Index: 174

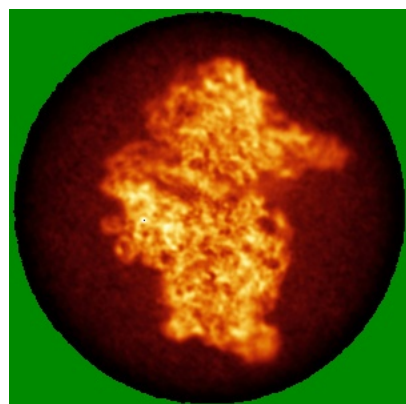


Z Index: 135

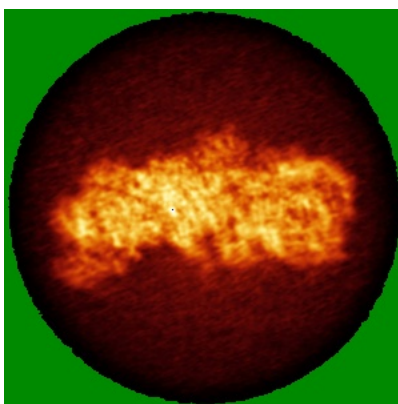
The images above show the largest variance slices of the map in three orthogonal directions.

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

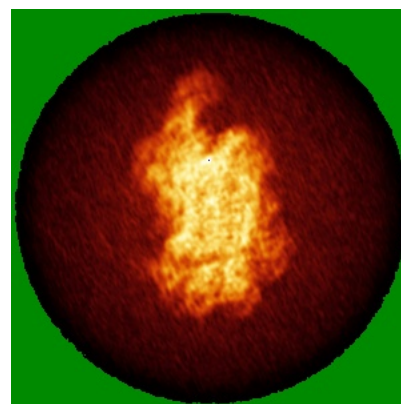
6.4.1 Primary map



X

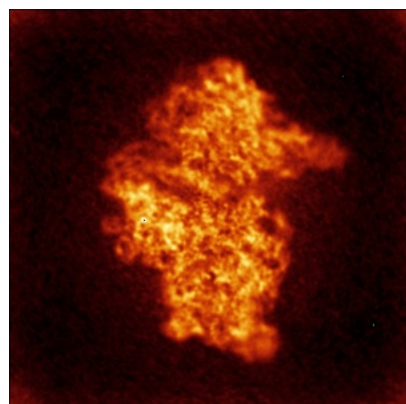


Y

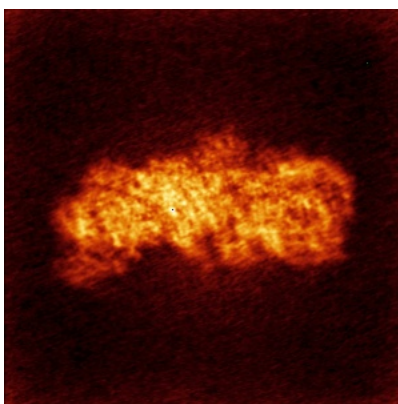


Z

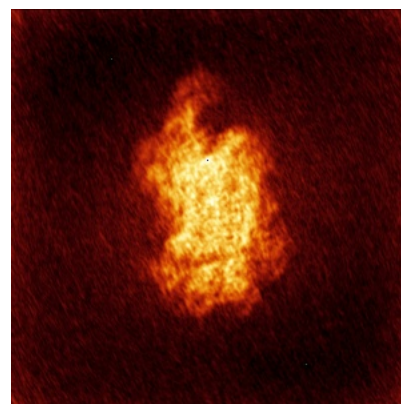
6.4.2 Raw map



X



Y

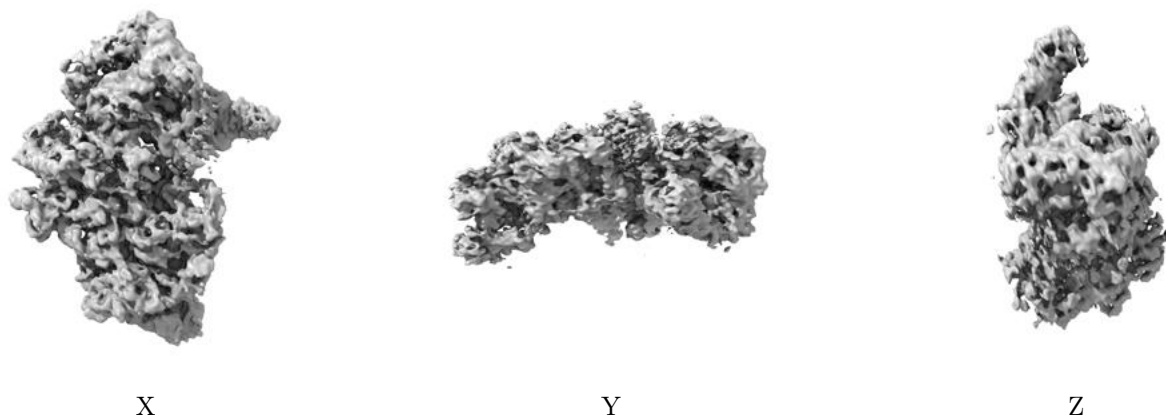


Z

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.

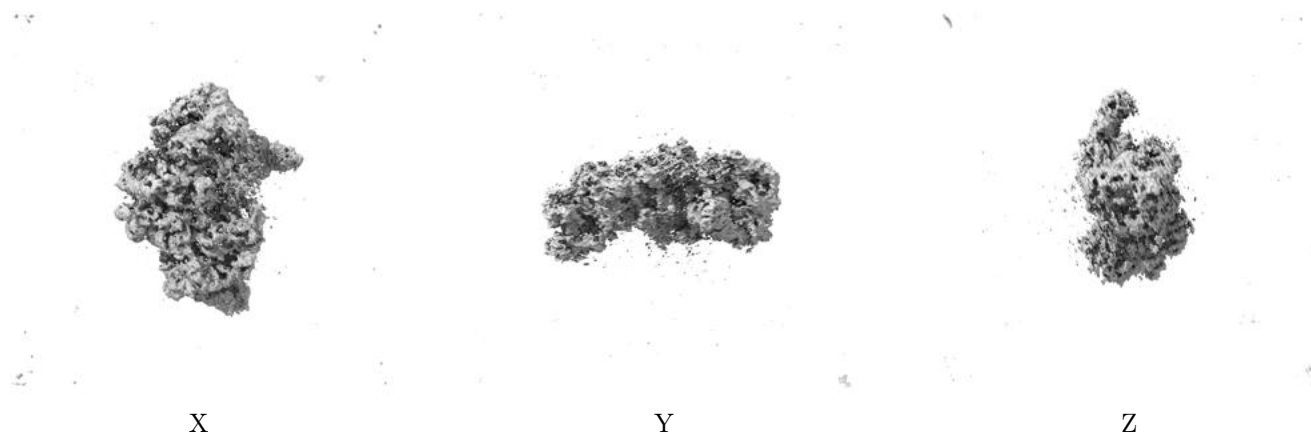
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. 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.

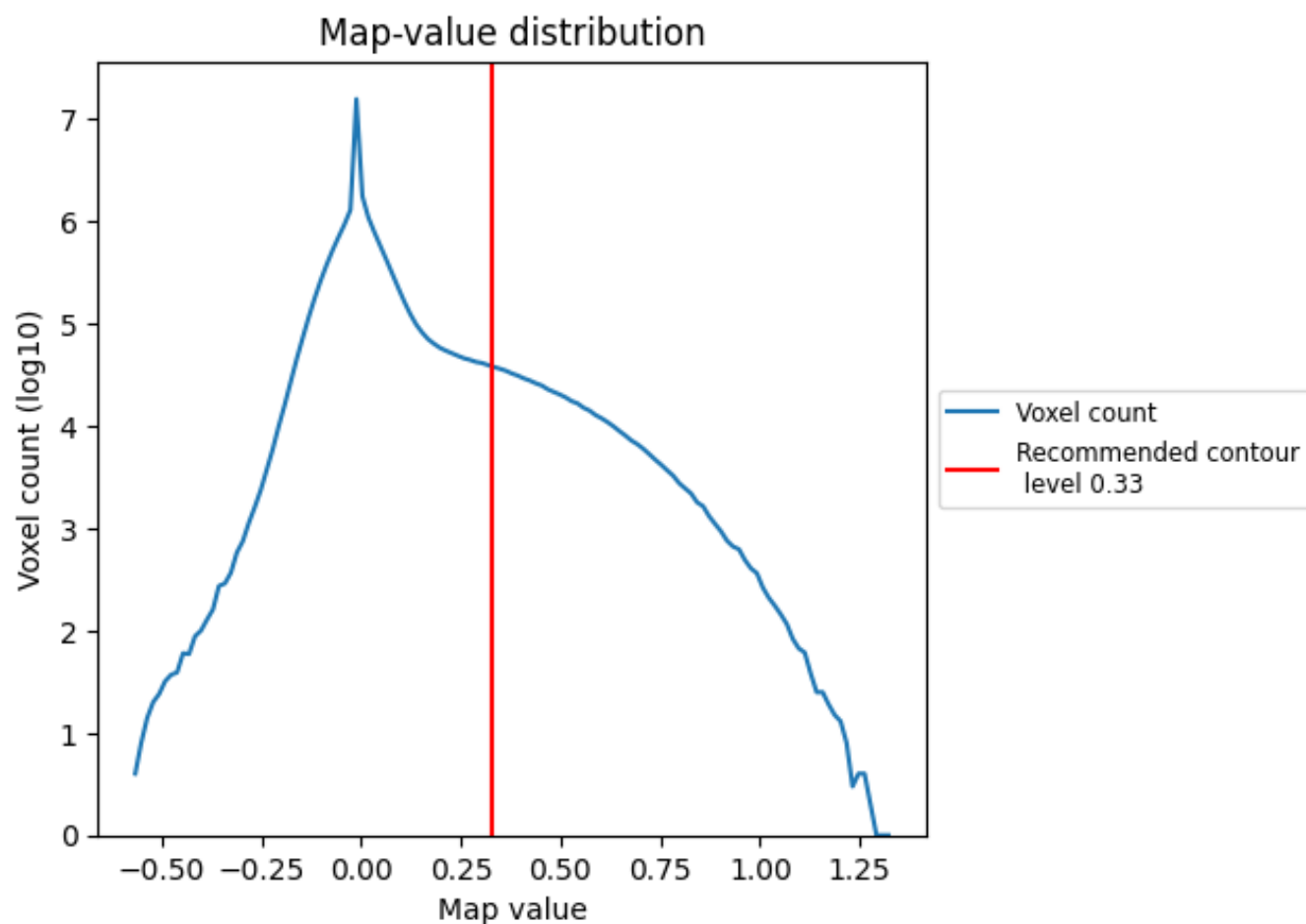
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

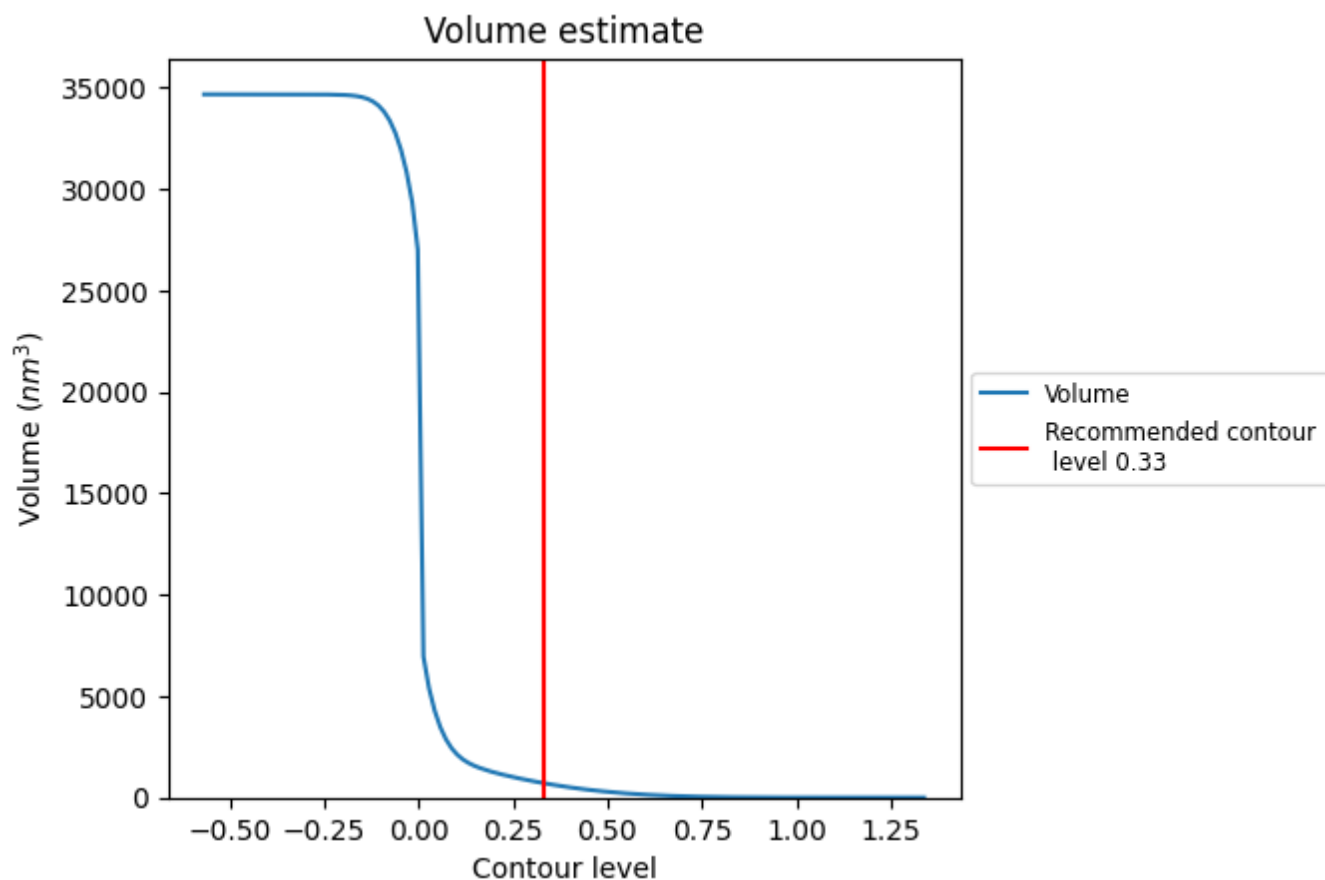
This section contains the results of statistical analysis of the map.

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.

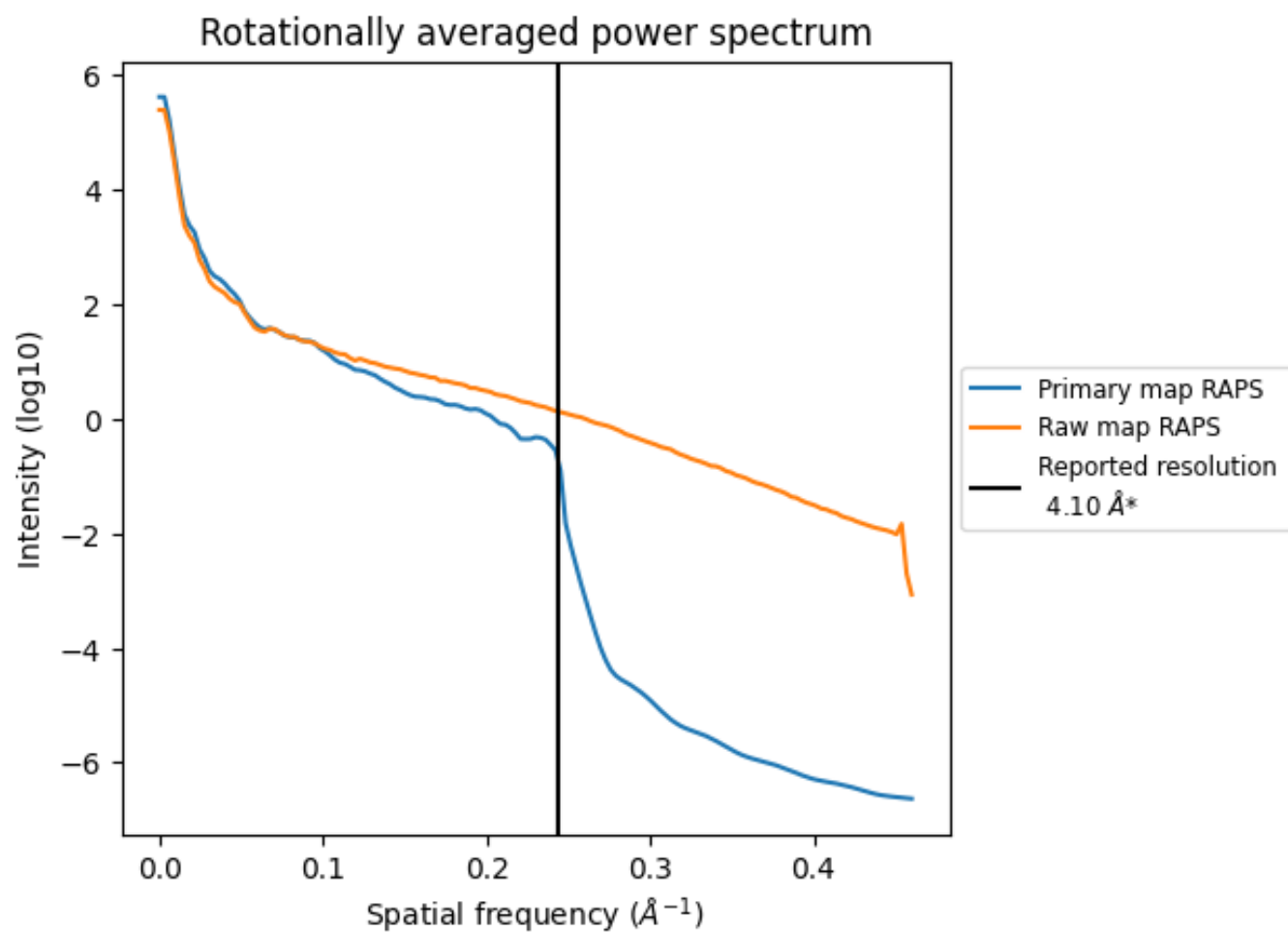
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 715 nm³; this corresponds to an approximate mass of 646 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 ⓘ

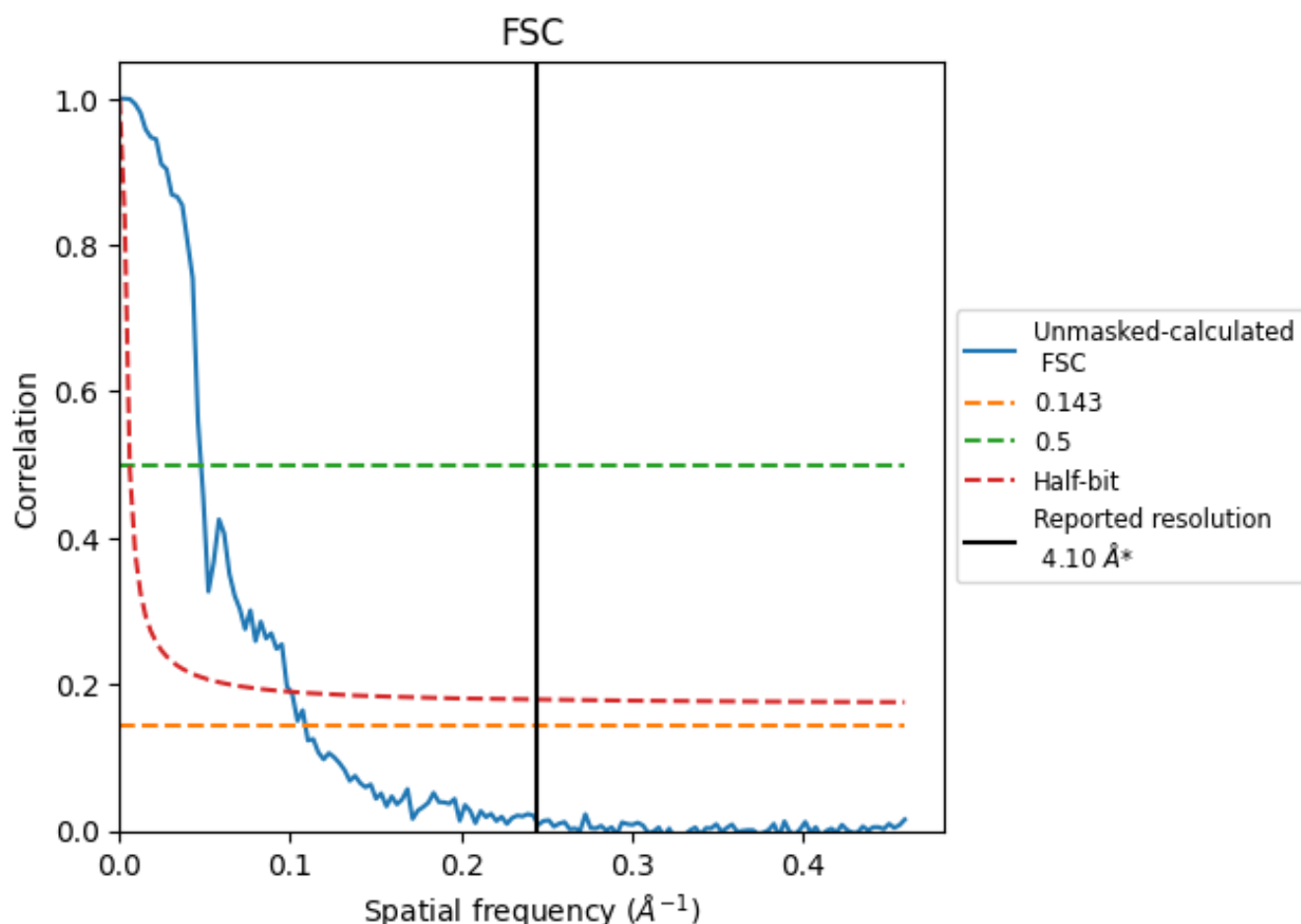


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 \AA^{-1}

8.2 Resolution estimates [i](#)

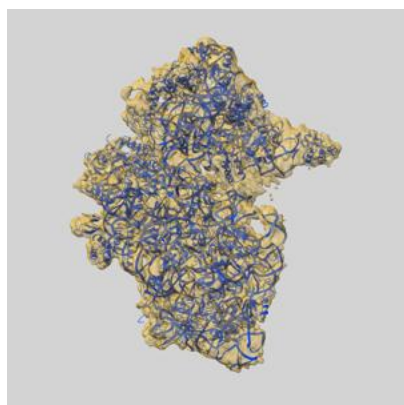
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.18	20.96	9.96

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.18 differs from the reported value 4.1 by more than 10 %

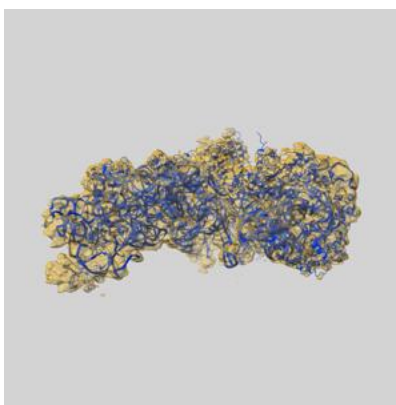
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37733 and PDB model 8WQ2. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

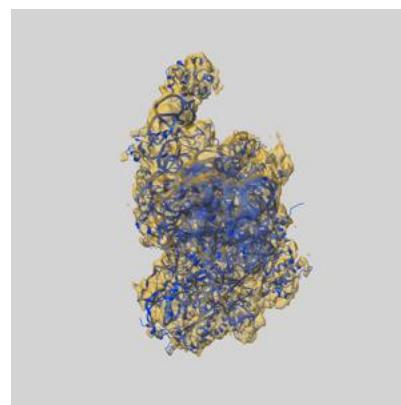
9.1 Map-model overlay [i](#)



X



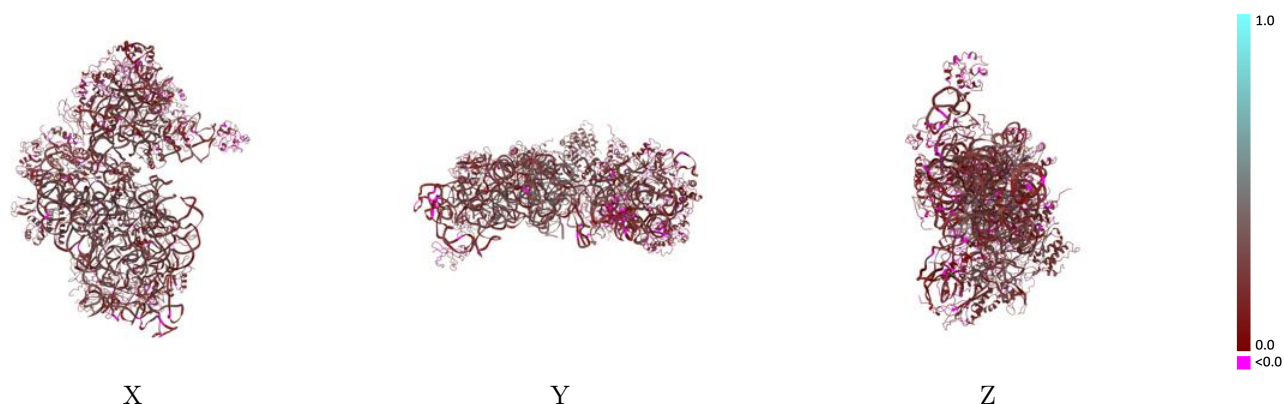
Y



Z

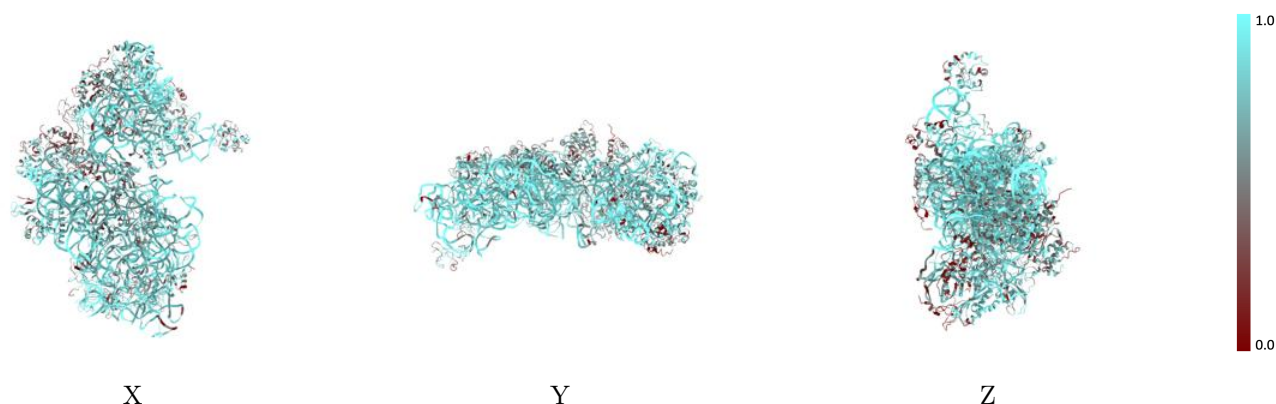
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



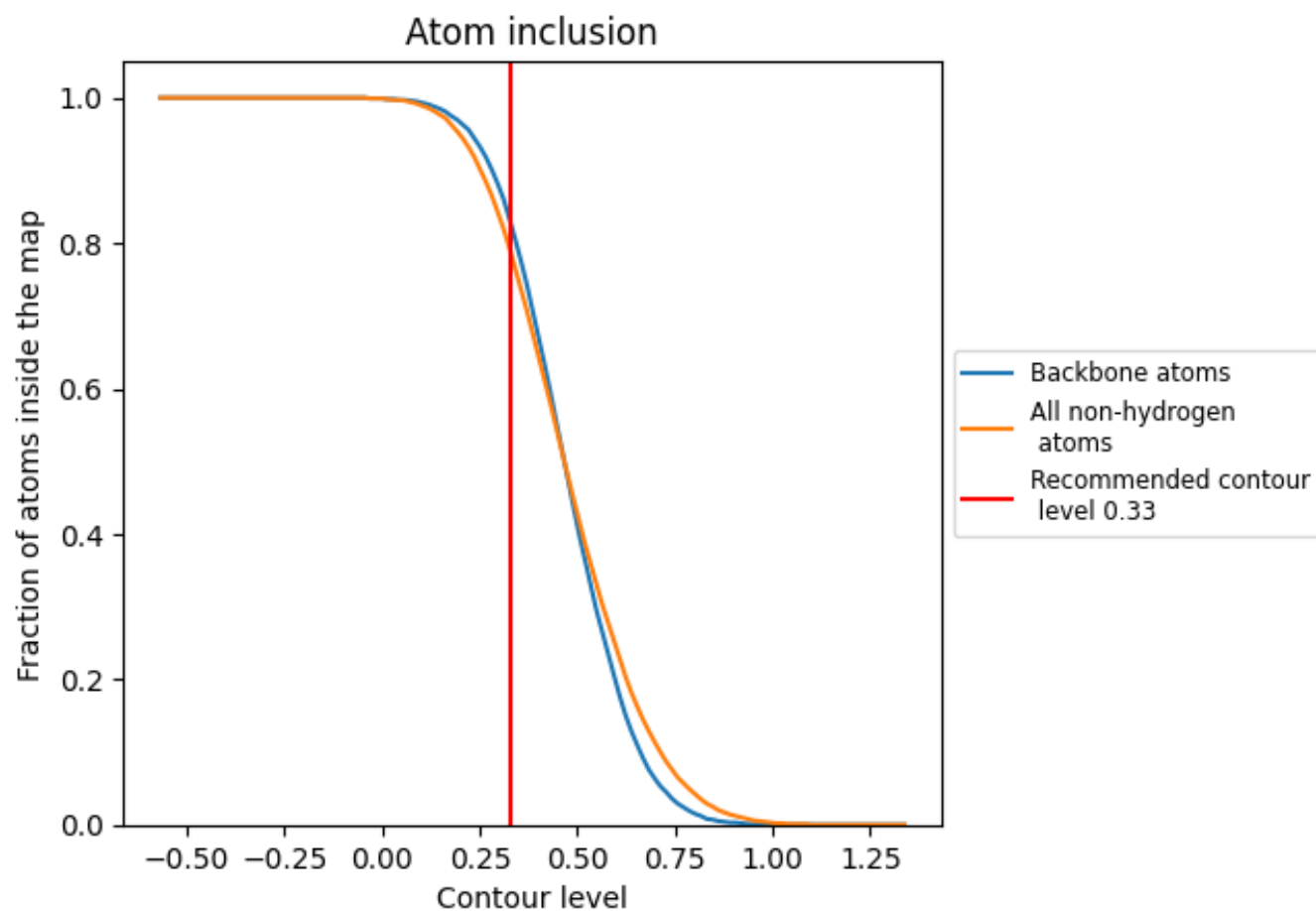
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.33).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 79% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7860	 0.2190
A16S	 0.9160	 0.2430
AS2P	 0.5420	 0.2390
AS3P	 0.7060	 0.2070
AS4E	 0.7210	 0.2230
AS4P	 0.6720	 0.2320
AS5P	 0.6250	 0.2760
AS6E	 0.6100	 0.1280
AS7P	 0.5300	 0.1370
AS8E	 0.8140	 0.2170
AS8P	 0.6880	 0.2850
AS9P	 0.5590	 0.1580
S10P	 0.8530	 0.1950
S11P	 0.3580	 0.1050
S12P	 0.7760	 0.2660
S13P	 0.5960	 0.1370
S14P	 0.8450	 0.2400
S15P	 0.7360	 0.2250
S17E	 0.5110	 0.1520
S17P	 0.7180	 0.2750
S19E	 0.6550	 0.1610
S19P	 0.4980	 0.1010
S24E	 0.7140	 0.2070
S27A	 0.8140	 0.1150
S27E	 0.6840	 0.2240
S28E	 0.5560	 0.1750
S3AE	 0.6540	 0.1820
SL7A	 0.6320	 0.1060
VTRF	 0.7550	 0.1580

