



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 06:51 PM UTC

PDB ID : 7WTW / pdb_00007wtw
EMDB ID : EMD-32803
Title : Cryo-EM structure of a human pre-40S ribosomal subunit - State RRP12-A3
Authors : Cheng, J.; Lau, B.; Thoms, M.; Ameismeier, M.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : 2022-02-05
Resolution : 3.20 Å(reported)

This is a wwPDB EM Validation Summary 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:

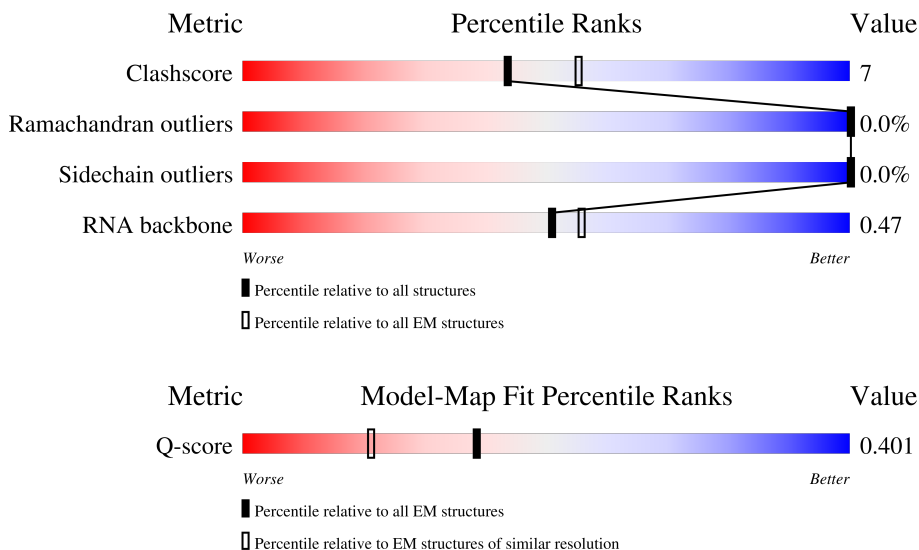
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	2	1873	51% (green), 30% (yellow), 15% (grey)
2	R	135	51% (green), 9% (yellow), 40% (grey)
3	b	84	92% (green), 6% (yellow), 2% (grey)






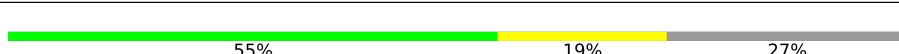
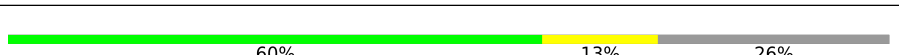
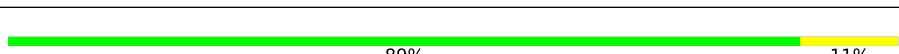
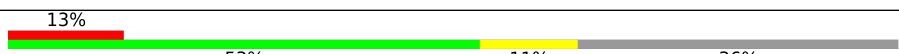
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Mol	Chain	Length	Quality of chain
4	B	264	64% 17% 19%
5	c	69	70% 19% 12%
6	E	263	85% 15%
7	e	59	31% 66%
8	F	204	75% 18% 7%
9	H	194	78% 18%
10	G	249	79% 13% 8%
11	Z	125	44% 14% 42%
12	Y	133	80% 14% 7%
13	x	252	55% 14% 31%
14	X	143	90% 9%
15	w	437	7% 66% 10% 24%
16	t	475	20% 77%
17	W	130	89% 10%
18	u	804	68% 12% 20%
19	T	145	72% 27%
20	S	152	63% 20% 16%
21	Q	146	63% 23% 14%
22	P	145	61% 23% 17%
23	O	151	70% 19% 11%
24	N	151	91% 8%
25	L	158	78% 18%
26	J	194	79% 14% 7%
27	I	208	77% 21%
28	r	125	62% 79% 14% 6%

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Mol	Chain	Length	Quality of chain
29	q	207	
30	K	1297	
31	M	132	
32	f	156	
33	z	230	
34	A	295	
35	C	293	
36	V	83	
37	y	412	

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 87147 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1586	33870	15116	6080	11088	1586	0	0

- Molecule 2 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	R	81	673	420	137	114	2	0	0

- Molecule 3 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	b	82	640	402	118	113	7	0	0

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	B	213	1729	1098	309	308	14	0	0

- Molecule 5 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	c	61	471	288	95	86	2	0	0

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	262	2076	1324	386	358	8	0	0

- Molecule 7 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	e	20	179	110	43	25	1	0	0

- Molecule 8 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	F	189	1494	934	284	269	7	0	0

- Molecule 9 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	186	1501	957	276	267	1	0	0

- Molecule 10 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	230	1862	1164	371	320	7	0	0

- Molecule 11 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	Z	72	574	368	104	101	1	0	0

- Molecule 12 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	Y	124	1014	641	198	170	5	0	0

- Molecule 13 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	x	175	1372	881	249	238	4	0	0

- Molecule 14 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	X	141	1098	693	219	183	3	0	0

- Molecule 15 is a protein called Bystin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	w	332	2617	1676	478	454	9	0	0

- Molecule 16 is a protein called Protein LTV1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	t	108	931	578	177	173	3	0	0

- Molecule 17 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	W	129	1033	659	193	175	6	0	0

- Molecule 18 is a protein called Pre-rRNA-processing protein TSR1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	u	642	5168	3315	928	901	24	0	0

- Molecule 19 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	144	1122	703	217	199	3	0	0

- Molecule 20 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	S	127	1054	669	205	179	1	0	0

- Molecule 21 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	125	Total	C	N	O	S	0	0
			998	637	185	173	3		

- Molecule 22 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	121	Total	C	N	O	S	0	0
			1006	643	186	170	7		

- Molecule 23 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	135	Total	C	N	O	S	0	0
			1009	618	198	187	6		

- Molecule 24 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 25 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 27 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 28 is a protein called Multifunctional methyltransferase subunit TRM112-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	r	118	Total	C	N	O	S	0	0
			940	601	166	166	7		

- Molecule 29 is a protein called Probable 18S rRNA (guanine-N(7))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	q	202	Total	C	N	O	S	0	0
			1571	999	264	297	11		

- Molecule 30 is a protein called RRP12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	K	993	Total	C	N	O	S	0	0
			7707	4938	1337	1387	45		

- Molecule 31 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	108	Total	C	N	O	S	0	0
			837	530	147	153	7		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	57	Total	C	N	O	S	0	0
			465	295	89	74	7		

- Molecule 33 is a protein called Ribosome biogenesis protein SLX9 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	z	52	Total	C	N	O	S	0	0
			416	255	80	79	2		

- Molecule 34 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A	216	Total	C	N	O	S	0	0
			1705	1083	299	315	8		

- Molecule 35 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	C	216	1674	1085	287	292	10	0	0

- Molecule 36 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	V	83	636	393	117	121	5	0	0

- Molecule 37 is a protein called RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	y	265	2091	1324	384	373	10	0	0

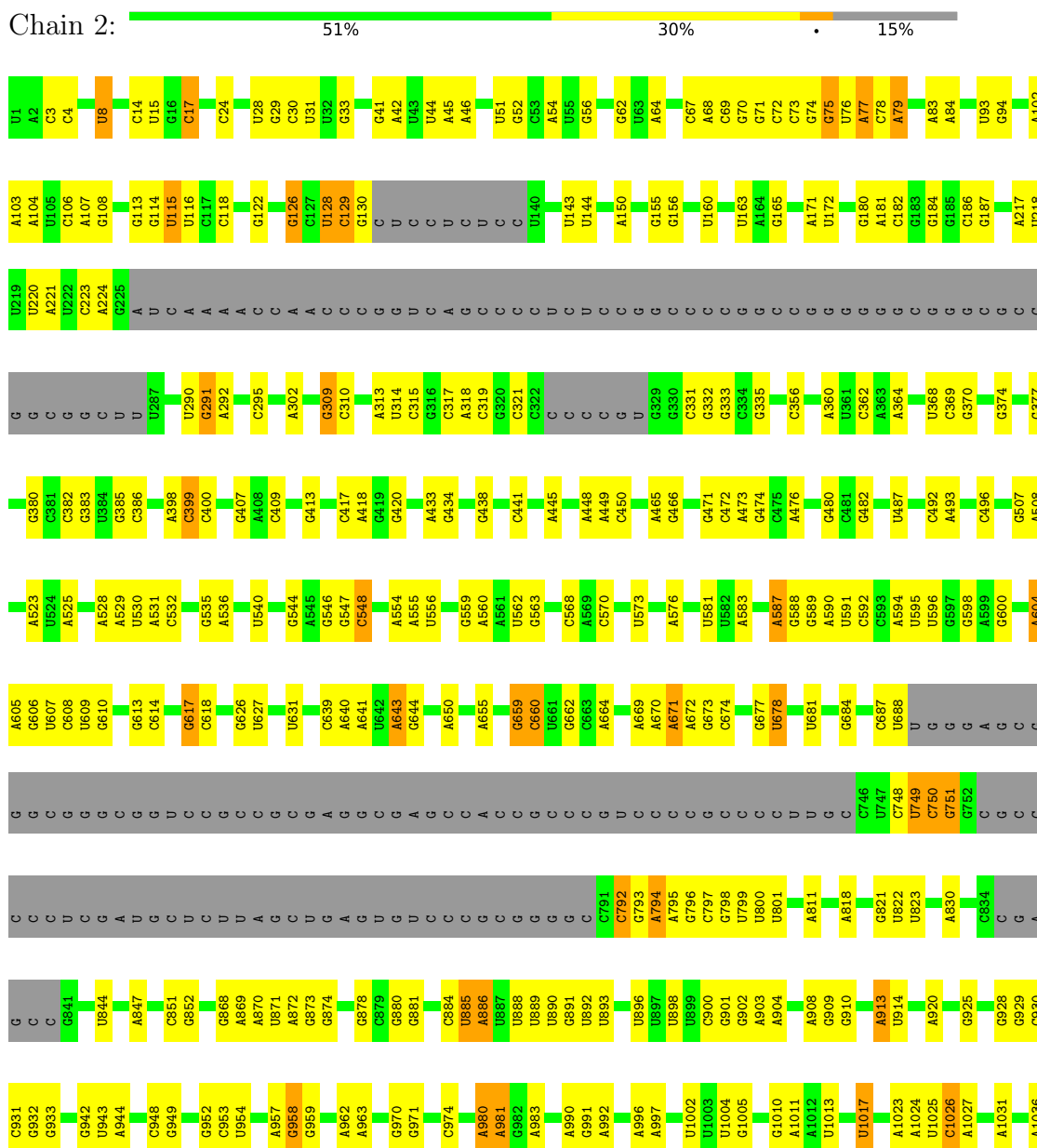
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

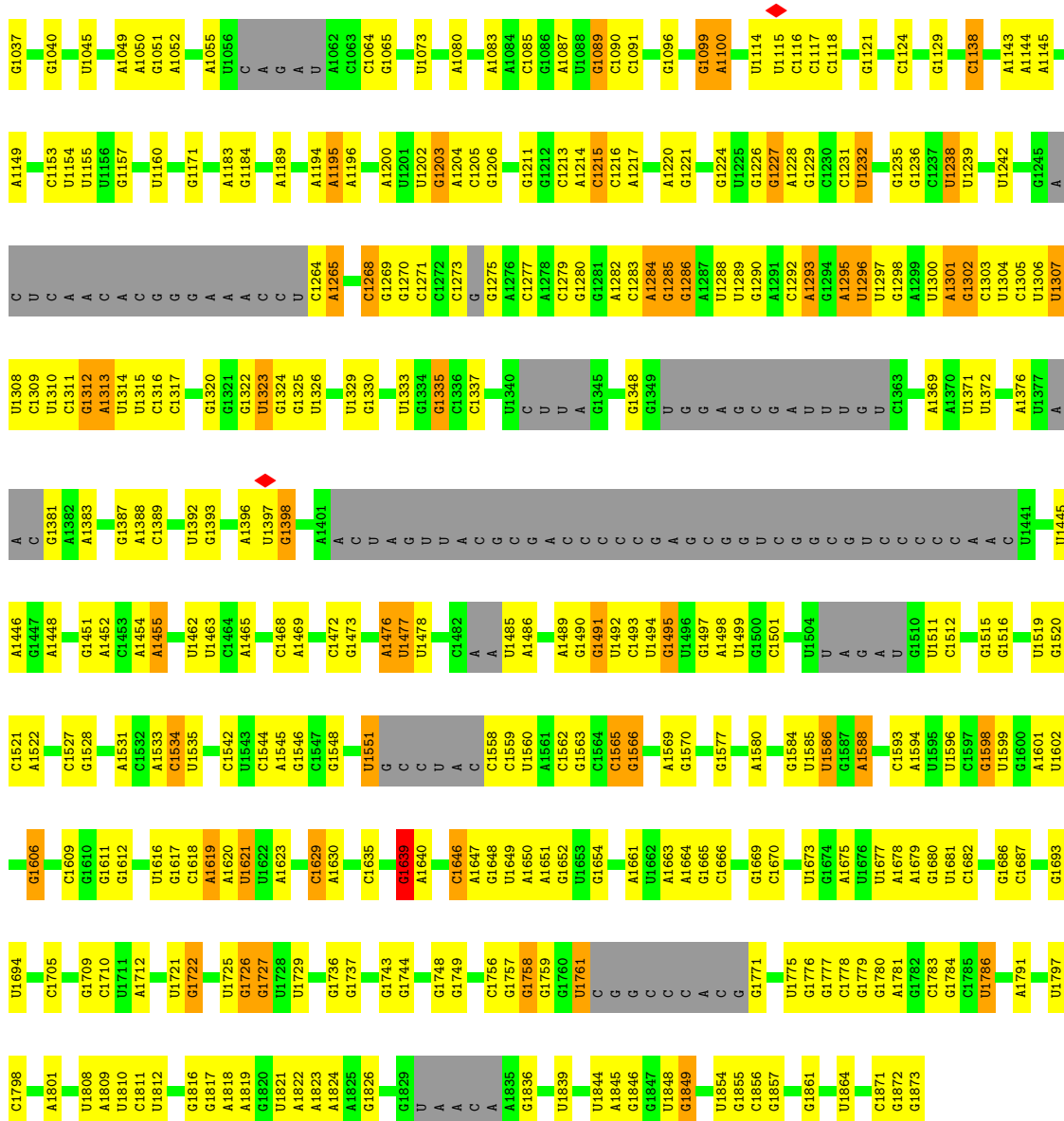
Mol	Chain	Residues	Atoms		AltConf
38	f	1	Total	Zn	0
			1	1	
38	y	1	Total	Zn	0
			1	1	

3 Residue-property plots

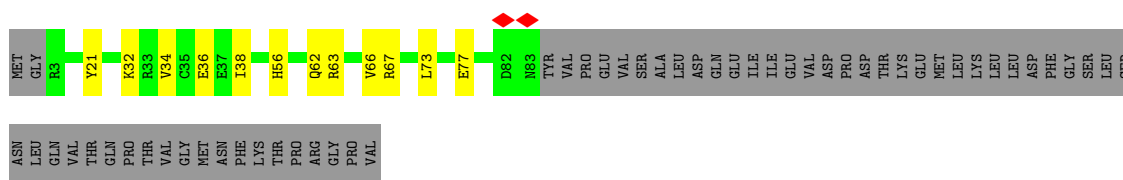
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S rRNA





• Molecule 2: 40S ribosomal protein S17

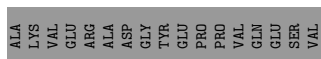


• Molecule 3: 40S ribosomal protein S27

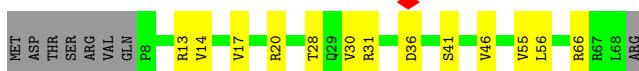




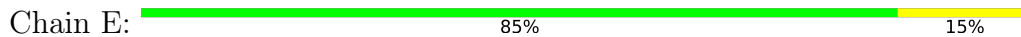
• Molecule 4: 40S ribosomal protein S3a



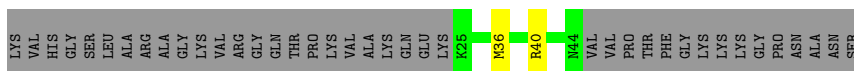
• Molecule 5: 40S ribosomal protein S28



• Molecule 6: 40S ribosomal protein S4, X isoform



• Molecule 7: 40S ribosomal protein S30

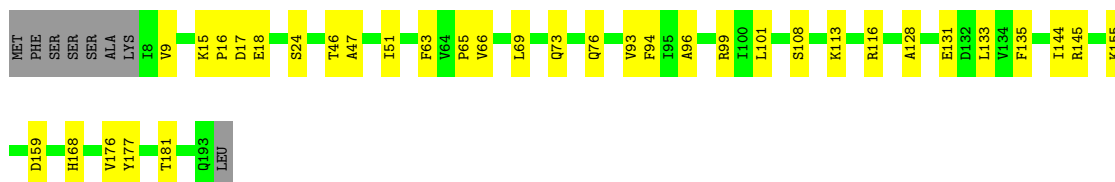
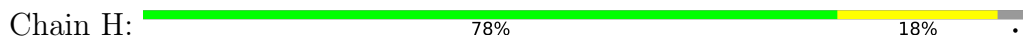


• Molecule 8: 40S ribosomal protein S5

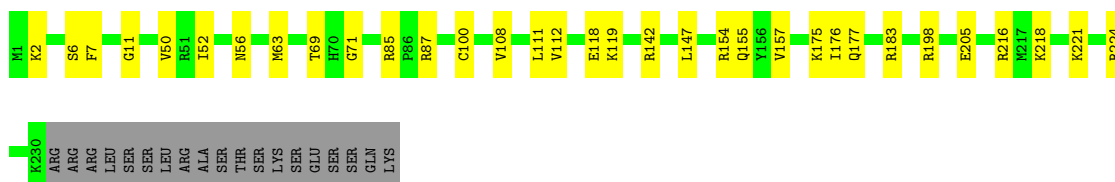
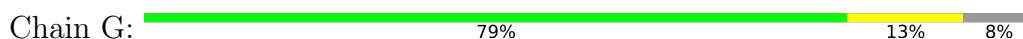




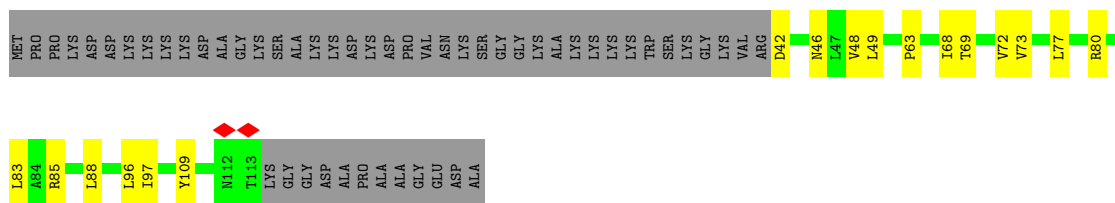
- Molecule 9: 40S ribosomal protein S7



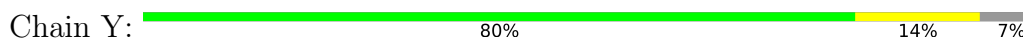
- Molecule 10: 40S ribosomal protein S6



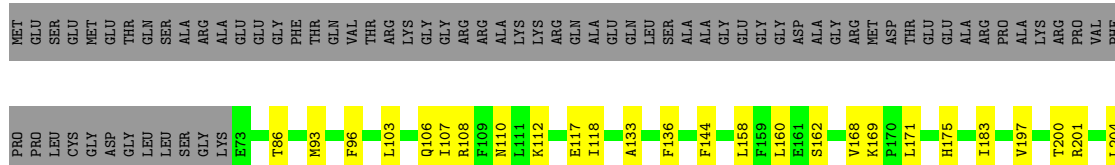
- Molecule 11: 40S ribosomal protein S25

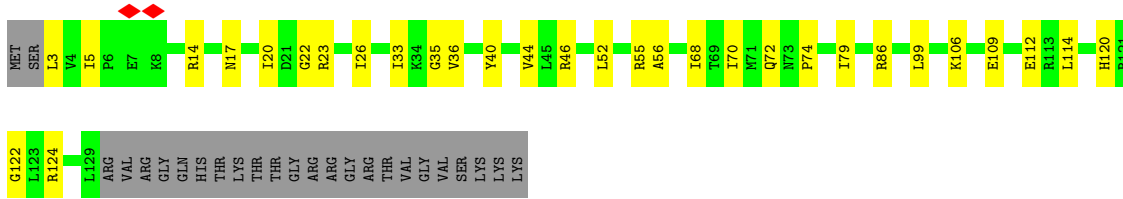


- Molecule 12: 40S ribosomal protein S24

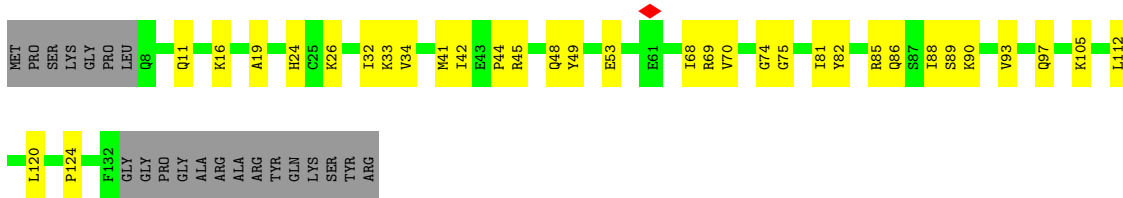


- Molecule 13: RNA-binding protein PNO1

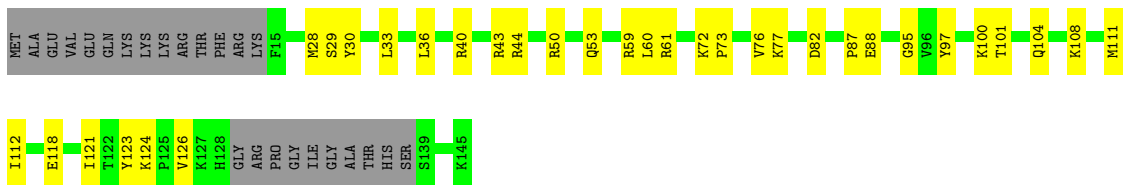




• Molecule 21: 40S ribosomal protein S16



• Molecule 22: 40S ribosomal protein S15



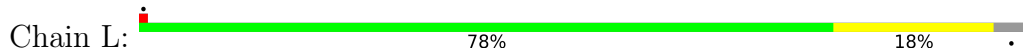
• Molecule 23: 40S ribosomal protein S14

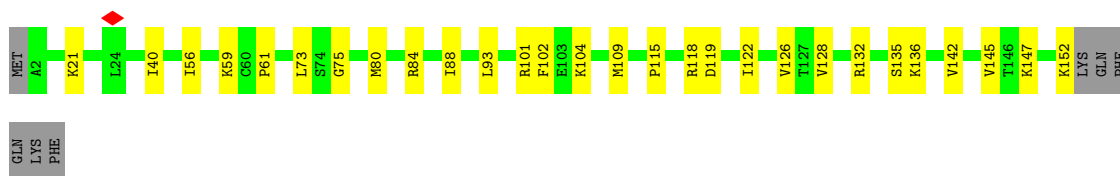


• Molecule 24: 40S ribosomal protein S13

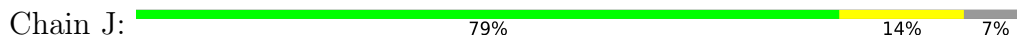


• Molecule 25: 40S ribosomal protein S11

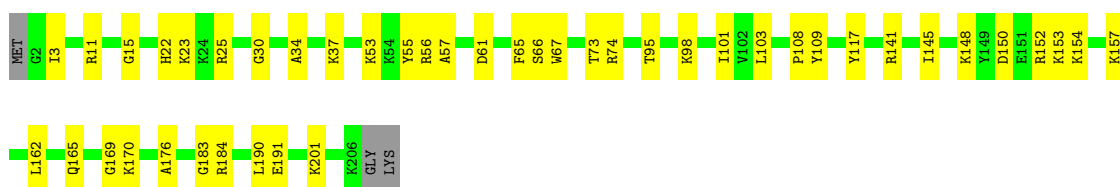




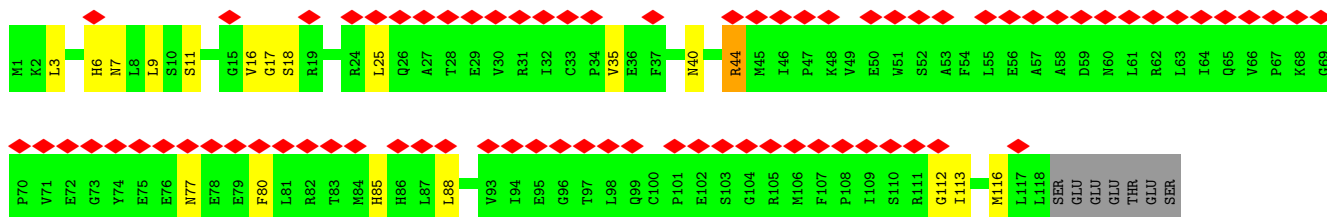
• Molecule 26: 40S ribosomal protein S9



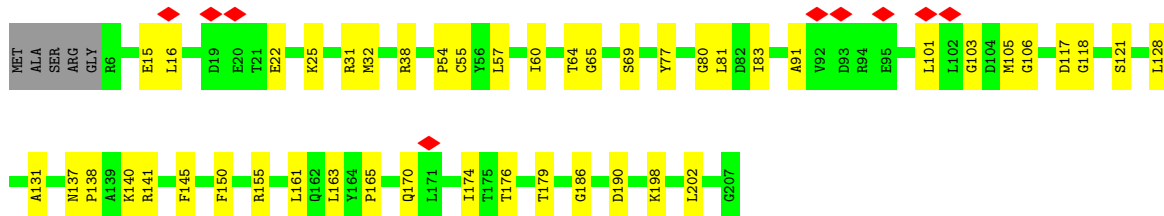
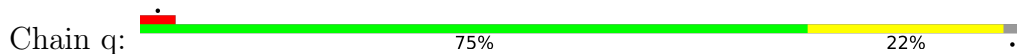
• Molecule 27: 40S ribosomal protein S8



• Molecule 28: Multifunctional methyltransferase subunit TRM112-like protein



• Molecule 29: Probable 18S rRNA (guanine-N(7))-methyltransferase



• Molecule 30: RRP12-like protein

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28656	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.479	Depositor
Minimum map value	-0.215	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	381.24, 381.24, 381.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.059, 1.059, 1.059	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: ZN, G7M

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.19	1/37837 (0.0%)	0.36	0/58946
2	R	0.17	0/680	0.44	0/905
3	b	0.17	0/653	0.44	0/876
4	B	0.21	0/1756	0.52	0/2350
5	c	0.20	0/473	0.50	0/633
6	E	0.22	0/2118	0.44	0/2849
7	e	0.18	0/180	0.37	0/232
8	F	0.15	0/1515	0.44	0/2037
9	H	0.20	0/1524	0.50	0/2042
10	G	0.18	0/1885	0.42	0/2510
11	Z	0.22	0/580	0.62	0/780
12	Y	0.19	0/1031	0.39	0/1370
13	x	0.26	0/1394	0.58	0/1880
14	X	0.23	0/1116	0.52	0/1490
15	w	0.16	0/2664	0.41	0/3597
16	t	0.19	0/942	0.53	0/1246
17	W	0.23	0/1050	0.50	0/1406
18	u	0.22	1/5296 (0.0%)	0.45	0/7154
19	T	0.18	0/1142	0.49	0/1530
20	S	0.21	0/1071	0.55	0/1437
21	Q	0.18	0/1012	0.45	0/1356
22	P	0.18	0/1025	0.48	0/1369
23	O	0.21	0/1022	0.58	0/1372
24	N	0.18	0/1226	0.40	0/1649
25	L	0.21	0/1250	0.40	0/1673
26	J	0.23	0/1524	0.50	2/2035 (0.1%)
27	I	0.23	0/1711	0.49	0/2282
28	r	0.17	0/961	0.47	0/1301
29	q	0.15	0/1606	0.39	0/2170
30	K	0.17	0/7851	0.44	0/10624
31	M	0.16	0/845	0.40	0/1134
32	f	0.15	0/474	0.49	0/626

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	z	0.21	0/420	0.54	1/564 (0.2%)
34	A	0.20	0/1742	0.46	0/2367
35	C	0.22	0/1710	0.49	0/2310
36	V	0.16	0/643	0.38	0/860
37	y	0.19	0/2130	0.51	3/2874 (0.1%)
All	All	0.20	2/92059 (0.0%)	0.42	6/131836 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
18	u	0	1
27	I	0	1
28	r	0	1
33	z	0	1
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	u	564	GLU	CA-CB	5.94	1.61	1.52
1	2	1639	G7M	O3'-P	5.04	1.61	1.56

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	J	137	VAL	CA-C-N	5.57	132.18	121.54
26	J	137	VAL	C-N-CA	5.57	132.18	121.54
37	y	68	GLU	CA-C-N	-5.50	110.86	121.58
37	y	68	GLU	C-N-CA	-5.50	110.86	121.58
33	z	199	GLU	N-CA-CB	5.22	117.98	110.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
27	I	66	SER	Peptide
28	r	44	ARG	Peptide
18	u	348	ASP	Peptide

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Mol	Chain	Res	Type	Group
33	z	222	MET	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	33870	0	17108	360	0
2	R	673	0	722	12	0
3	b	640	0	665	4	0
4	B	1729	0	1803	29	0
5	c	471	0	499	9	0
6	E	2076	0	2177	28	0
7	e	179	0	200	1	0
8	F	1494	0	1549	24	0
9	H	1501	0	1593	23	0
10	G	1862	0	2018	23	0
11	Z	574	0	627	14	0
12	Y	1014	0	1082	13	0
13	x	1372	0	1453	31	0
14	X	1098	0	1167	11	0
15	w	2617	0	2652	34	0
16	t	931	0	949	9	0
17	W	1033	0	1080	9	0
18	u	5168	0	5230	60	0
19	T	1122	0	1153	28	0
20	S	1054	0	1105	21	0
21	Q	998	0	1065	26	0
22	P	1006	0	1056	26	0
23	O	1009	0	1034	28	0
24	N	1202	0	1289	9	0
25	L	1229	0	1302	17	0
26	J	1499	0	1618	18	0
27	I	1682	0	1769	28	0
28	r	940	0	958	13	0
29	q	1571	0	1545	27	0
30	K	7707	0	7986	110	0
31	M	837	0	870	14	0
32	f	465	0	485	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	z	416	0	424	11	0
34	A	1705	0	1706	42	0
35	C	1674	0	1764	25	0
36	V	636	0	637	9	0
37	y	2091	0	2147	28	0
38	f	1	0	0	0	0
38	y	1	0	0	0	0
All	All	87147	0	72487	1004	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 7.

The worst 5 of 1004 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)
17:W:101:PHE:O	17:W:128:PHE:HA	1.37	1.24
1:2:748:C:H42	1:2:794:A:N6	1.46	1.12
1:2:748:C:N4	1:2:794:A:H61	1.46	1.12
1:2:1609:C:N4	1:2:1630:A:H61	1.49	1.10
1:2:1609:C:H42	1:2:1630:A:N6	1.49	1.10

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	
2	R	79/135 (58%)	75 (95%)	4 (5%)	0	100	100
3	b	80/84 (95%)	76 (95%)	4 (5%)	0	100	100
4	B	211/264 (80%)	199 (94%)	12 (6%)	0	100	100
5	c	59/69 (86%)	56 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	E	260/263 (99%)	252 (97%)	8 (3%)	0	100	100
7	e	18/59 (30%)	18 (100%)	0	0	100	100
8	F	187/204 (92%)	175 (94%)	12 (6%)	0	100	100
9	H	184/194 (95%)	175 (95%)	9 (5%)	0	100	100
10	G	228/249 (92%)	224 (98%)	4 (2%)	0	100	100
11	Z	70/125 (56%)	68 (97%)	2 (3%)	0	100	100
12	Y	122/133 (92%)	119 (98%)	3 (2%)	0	100	100
13	x	173/252 (69%)	165 (95%)	8 (5%)	0	100	100
14	X	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
15	w	322/437 (74%)	312 (97%)	10 (3%)	0	100	100
16	t	102/475 (22%)	92 (90%)	9 (9%)	1 (1%)	12	45
17	W	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
18	u	630/804 (78%)	606 (96%)	23 (4%)	1 (0%)	43	73
19	T	142/145 (98%)	139 (98%)	3 (2%)	0	100	100
20	S	125/152 (82%)	121 (97%)	4 (3%)	0	100	100
21	Q	123/146 (84%)	118 (96%)	5 (4%)	0	100	100
22	P	117/145 (81%)	112 (96%)	5 (4%)	0	100	100
23	O	133/151 (88%)	119 (90%)	13 (10%)	1 (1%)	16	50
24	N	147/151 (97%)	144 (98%)	3 (2%)	0	100	100
25	L	149/158 (94%)	142 (95%)	7 (5%)	0	100	100
26	J	178/194 (92%)	166 (93%)	12 (7%)	0	100	100
27	I	203/208 (98%)	196 (97%)	7 (3%)	0	100	100
28	r	116/125 (93%)	109 (94%)	7 (6%)	0	100	100
29	q	200/207 (97%)	196 (98%)	4 (2%)	0	100	100
30	K	973/1297 (75%)	930 (96%)	43 (4%)	0	100	100
31	M	102/132 (77%)	101 (99%)	1 (1%)	0	100	100
32	f	53/156 (34%)	48 (91%)	5 (9%)	0	100	100
33	z	50/230 (22%)	47 (94%)	3 (6%)	0	100	100
34	A	214/295 (72%)	205 (96%)	9 (4%)	0	100	100
35	C	214/293 (73%)	205 (96%)	9 (4%)	0	100	100
36	V	81/83 (98%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	y	257/412 (62%)	249 (97%)	8 (3%)	0	100	100
All	All	6568/8700 (76%)	6294 (96%)	271 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	u	509	PHE
23	O	22	ALA
16	t	261	GLU

5.3.2 Protein sidechains [i](#)

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	
2	R	72/122 (59%)	72 (100%)	0	100	100
3	b	74/76 (97%)	74 (100%)	0	100	100
4	B	194/231 (84%)	194 (100%)	0	100	100
5	c	52/62 (84%)	52 (100%)	0	100	100
6	E	224/225 (100%)	224 (100%)	0	100	100
7	e	18/48 (38%)	18 (100%)	0	100	100
8	F	159/170 (94%)	159 (100%)	0	100	100
9	H	167/174 (96%)	167 (100%)	0	100	100
10	G	200/218 (92%)	200 (100%)	0	100	100
11	Z	64/103 (62%)	64 (100%)	0	100	100
12	Y	108/115 (94%)	108 (100%)	0	100	100
13	x	148/208 (71%)	148 (100%)	0	100	100
14	X	113/115 (98%)	113 (100%)	0	100	100
15	w	263/370 (71%)	263 (100%)	0	100	100
16	t	103/434 (24%)	103 (100%)	0	100	100
17	W	112/113 (99%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	u	561/705 (80%)	561 (100%)	0	100	100
19	T	114/115 (99%)	114 (100%)	0	100	100
20	S	111/132 (84%)	111 (100%)	0	100	100
21	Q	106/121 (88%)	106 (100%)	0	100	100
22	P	111/130 (85%)	111 (100%)	0	100	100
23	O	105/119 (88%)	104 (99%)	1 (1%)	68	80
24	N	130/131 (99%)	130 (100%)	0	100	100
25	L	135/142 (95%)	135 (100%)	0	100	100
26	J	160/168 (95%)	160 (100%)	0	100	100
27	I	178/180 (99%)	178 (100%)	0	100	100
28	r	105/112 (94%)	105 (100%)	0	100	100
29	q	168/171 (98%)	168 (100%)	0	100	100
30	K	846/1094 (77%)	846 (100%)	0	100	100
31	M	91/108 (84%)	91 (100%)	0	100	100
32	f	51/140 (36%)	51 (100%)	0	100	100
33	z	44/185 (24%)	44 (100%)	0	100	100
34	A	180/243 (74%)	180 (100%)	0	100	100
35	C	182/225 (81%)	182 (100%)	0	100	100
36	V	67/67 (100%)	67 (100%)	0	100	100
37	y	233/367 (64%)	233 (100%)	0	100	100
All	All	5749/7439 (77%)	5748 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	O	26	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
27	I	64	ASN
30	K	688	ASN
27	I	155	ASN
30	K	428	HIS

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Mol	Chain	Res	Type
30	K	977	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1568/1873 (83%)	354 (22%)	23 (1%)

5 of 354 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	C
1	2	8	U
1	2	14	C
1	2	17	C
1	2	33	G

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1264	C
1	2	1511	U
1	2	1304	U
1	2	1534	C
1	2	332	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	G7M	2	1639	1	23,26,27	2.85	9 (39%)	34,39,42	1.83	10 (29%)

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
1	G7M	2	1639	1	-	3/7/25/26	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1639	G7M	C4-N3	6.77	1.49	1.34
1	2	1639	G7M	C2-N2	6.69	1.49	1.34
1	2	1639	G7M	C2-N3	5.72	1.47	1.33
1	2	1639	G7M	C5-C6	4.17	1.54	1.43
1	2	1639	G7M	C5-N7	-3.74	1.34	1.39

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1639	G7M	C2-N3-C4	4.89	120.73	112.30
1	2	1639	G7M	C5-C4-N3	-4.09	120.41	128.15
1	2	1639	G7M	C5-C6-N1	4.07	120.25	111.84
1	2	1639	G7M	O6-C6-C5	-2.99	121.34	128.01
1	2	1639	G7M	C2-N1-C6	-2.97	119.73	125.11

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	1639	G7M	O4'-C4'-C5'-O5'
1	2	1639	G7M	C3'-C4'-C5'-O5'
1	2	1639	G7M	C2'-C1'-N9-C8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	1639	G7M	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

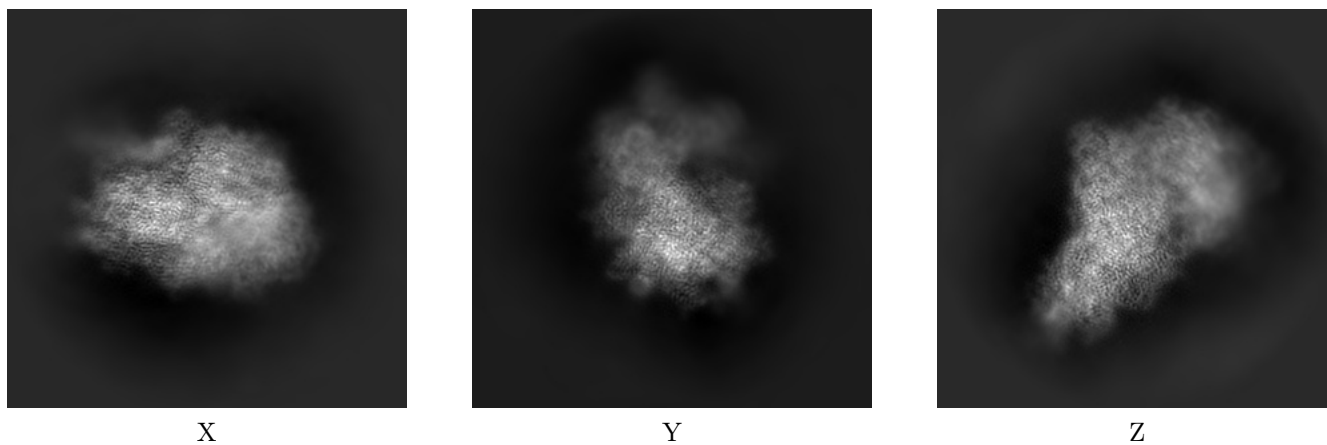
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32803. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

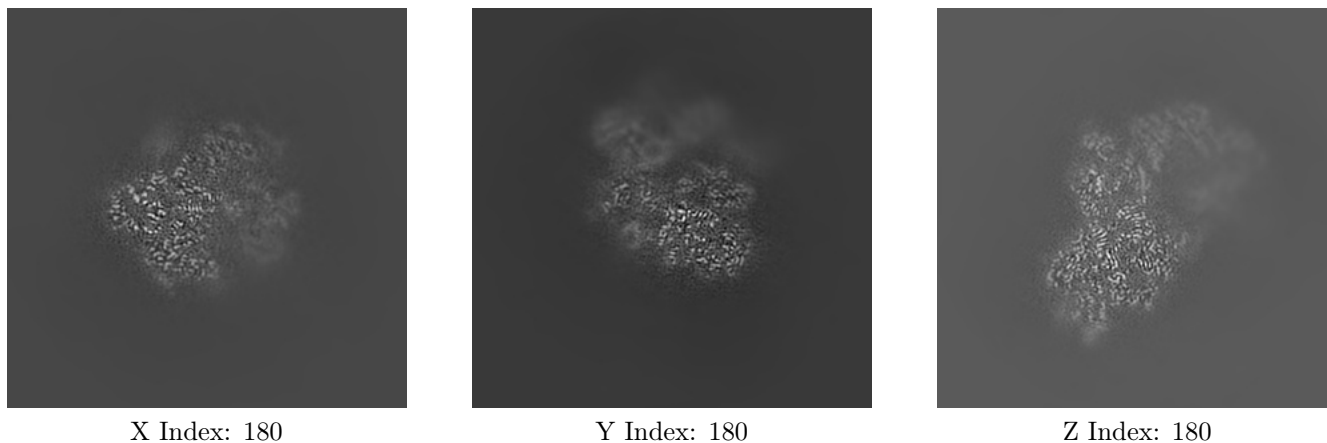
6.1.1 Primary map



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

6.2 Central slices [i](#)

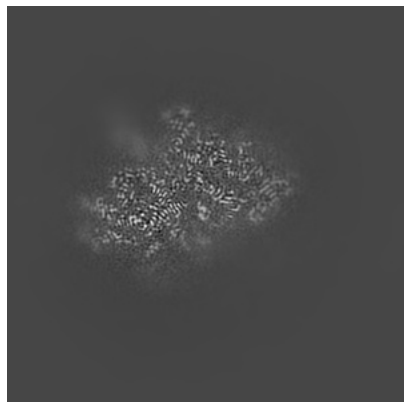
6.2.1 Primary map



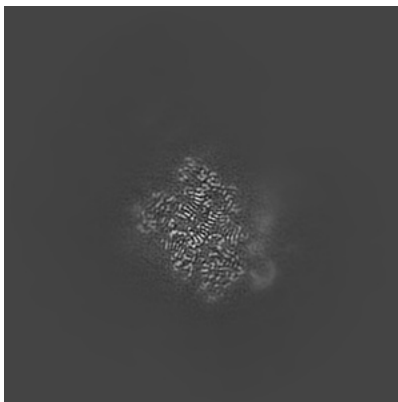
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

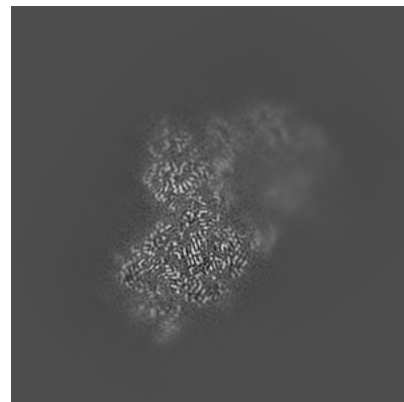
6.3.1 Primary map



X Index: 148



Y Index: 133

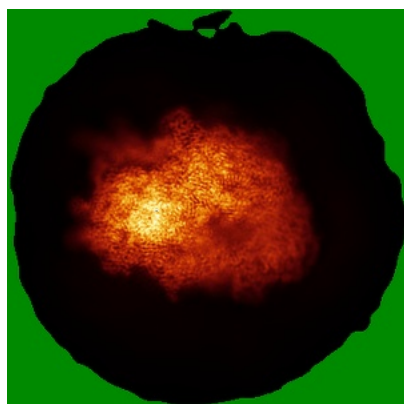


Z Index: 184

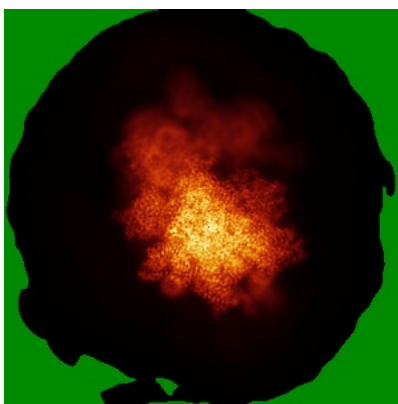
The images above show the largest variance slices of the map in three orthogonal directions.

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

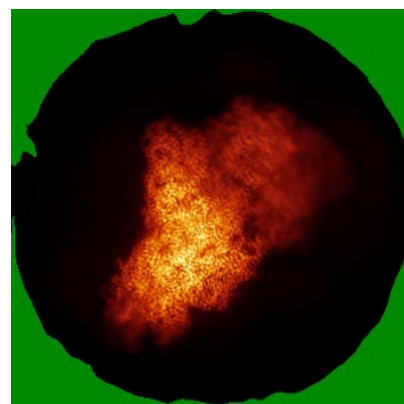
6.4.1 Primary map



X



Y

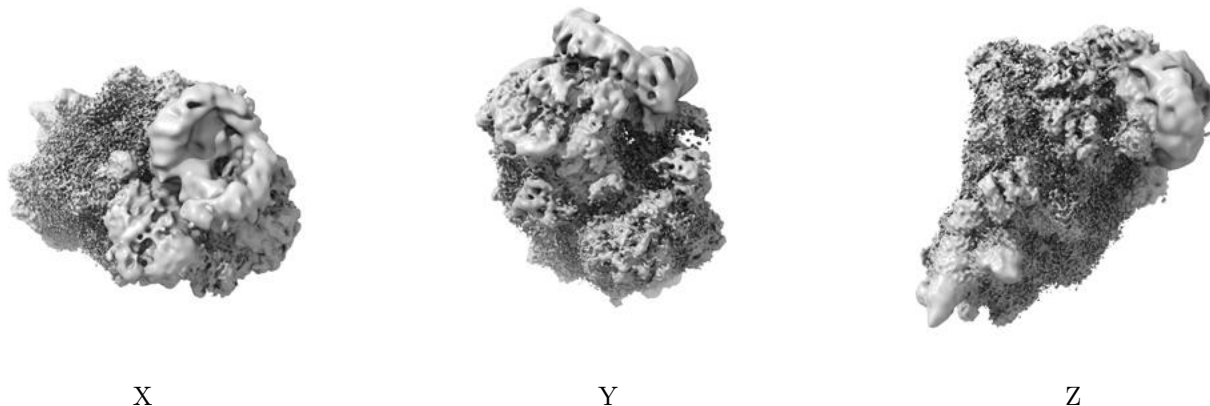


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

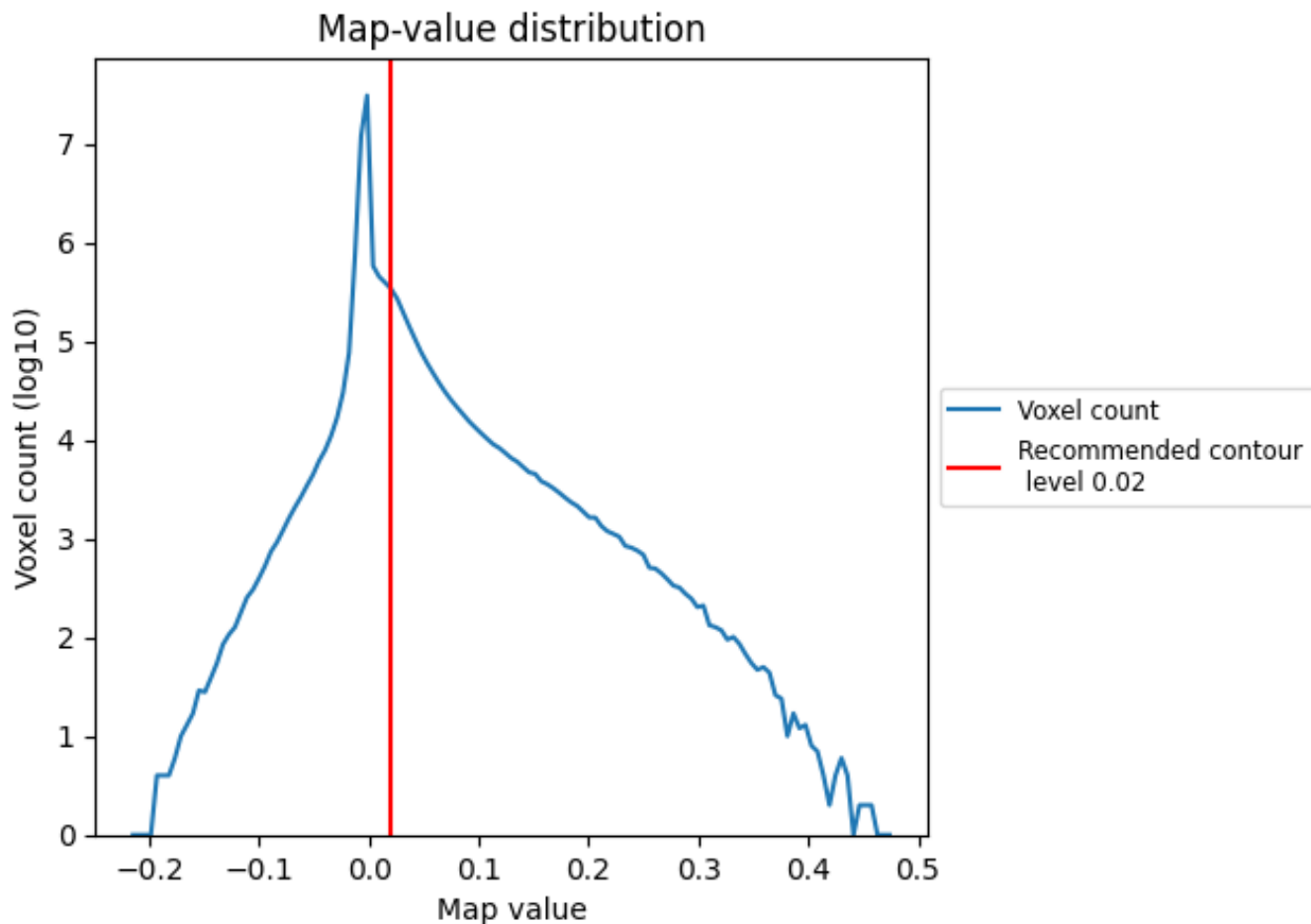
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

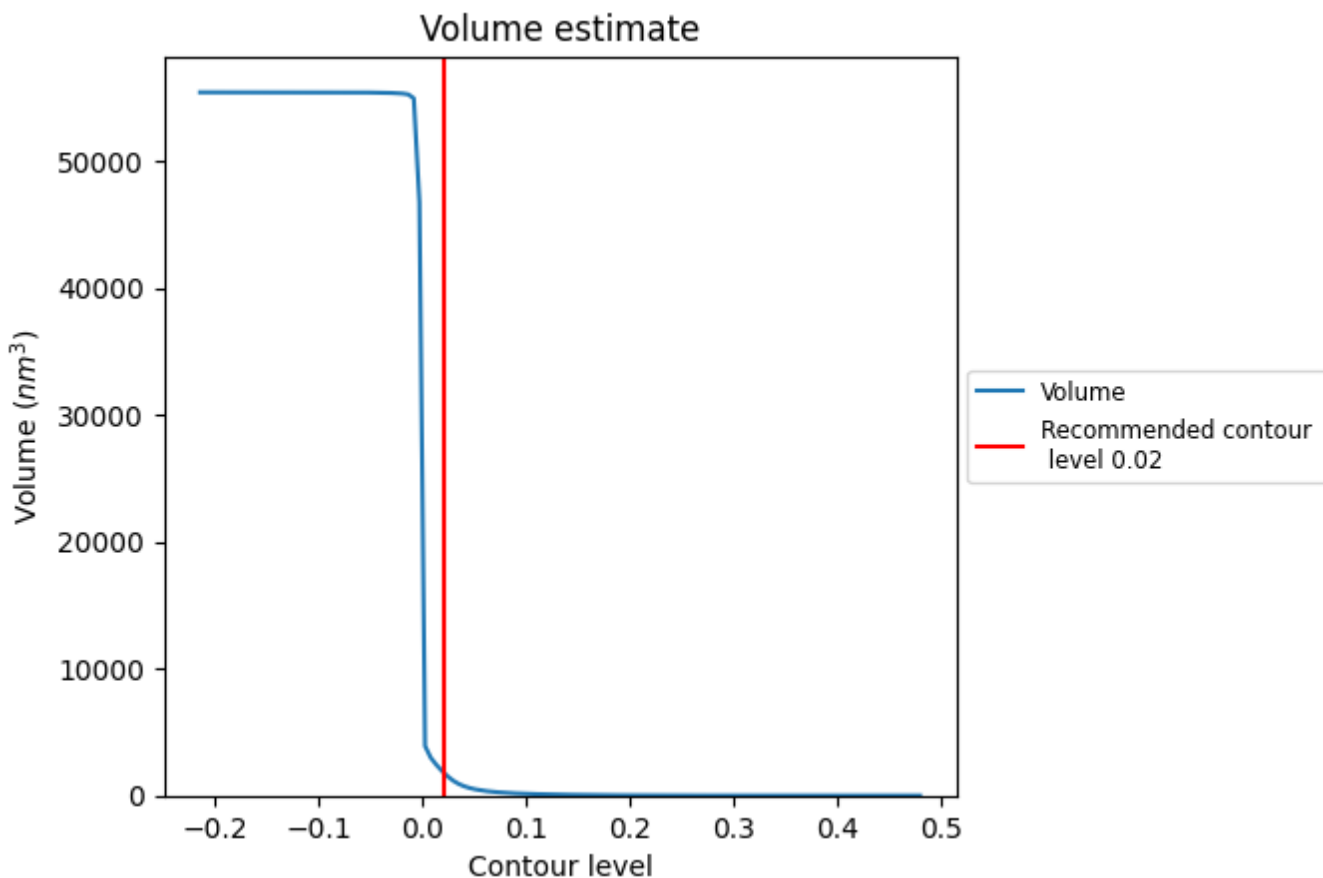
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

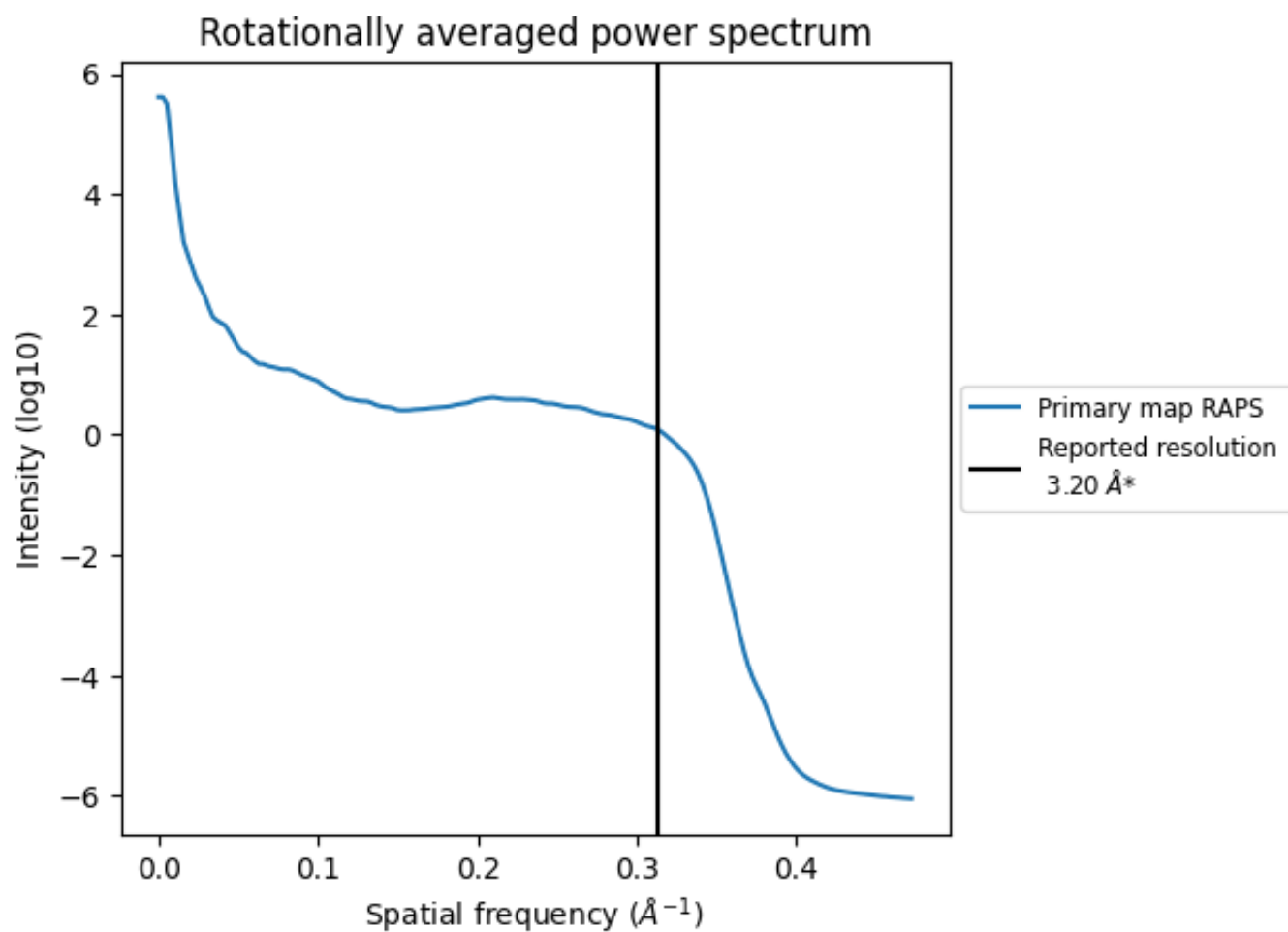
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1837 nm^3 ; this corresponds to an approximate mass of 1660 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 [i](#)

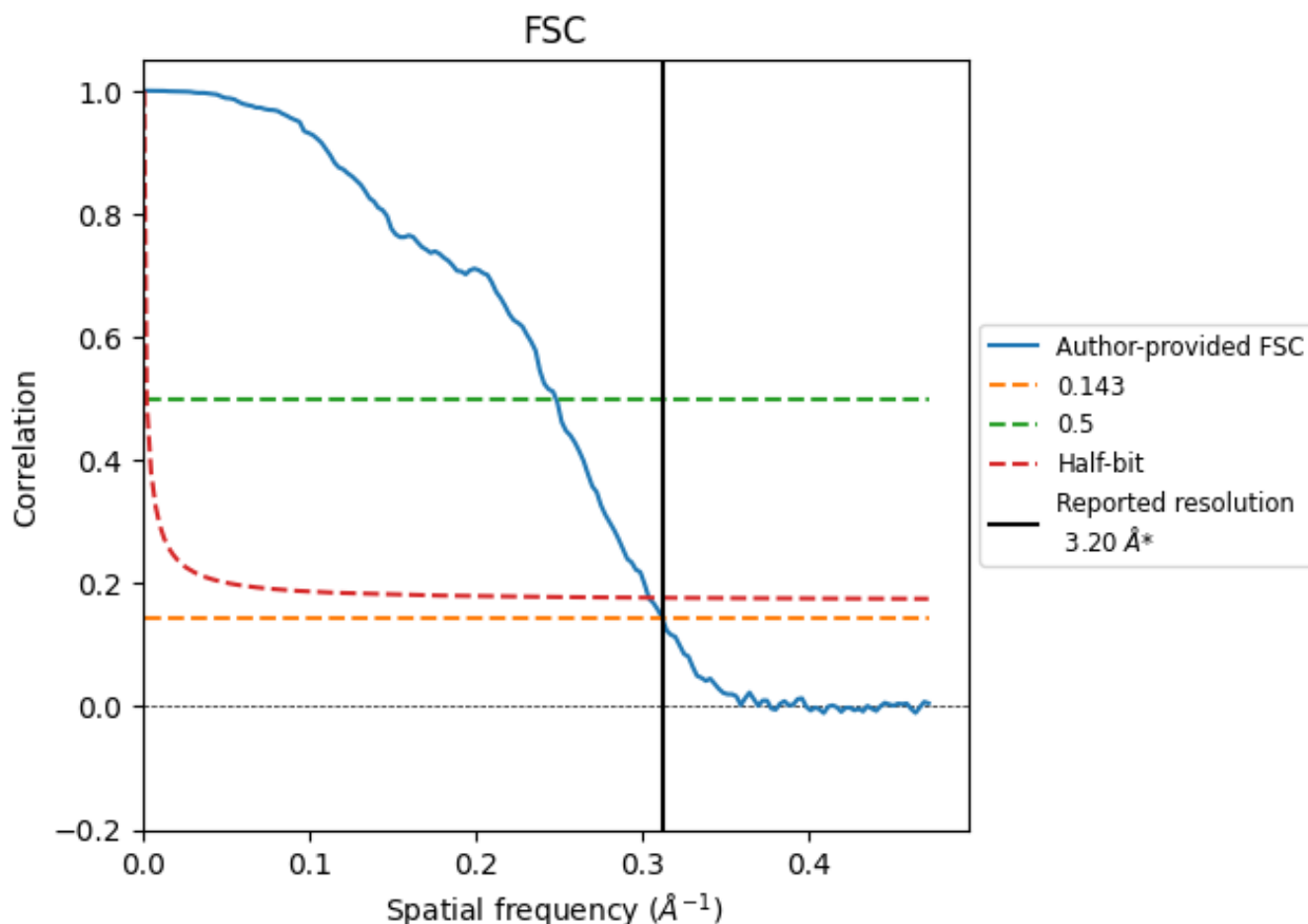


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

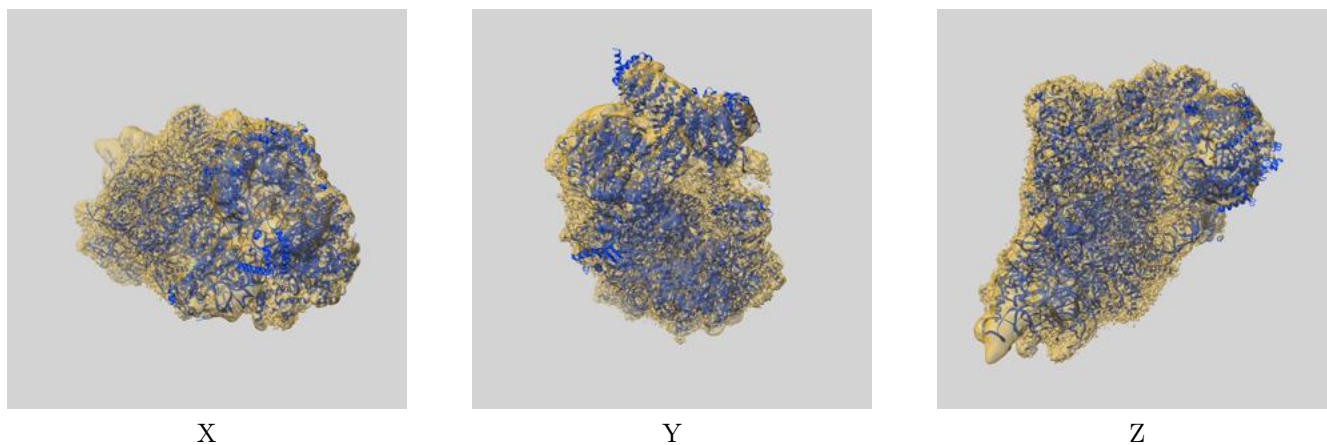
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.20	4.03	3.29
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

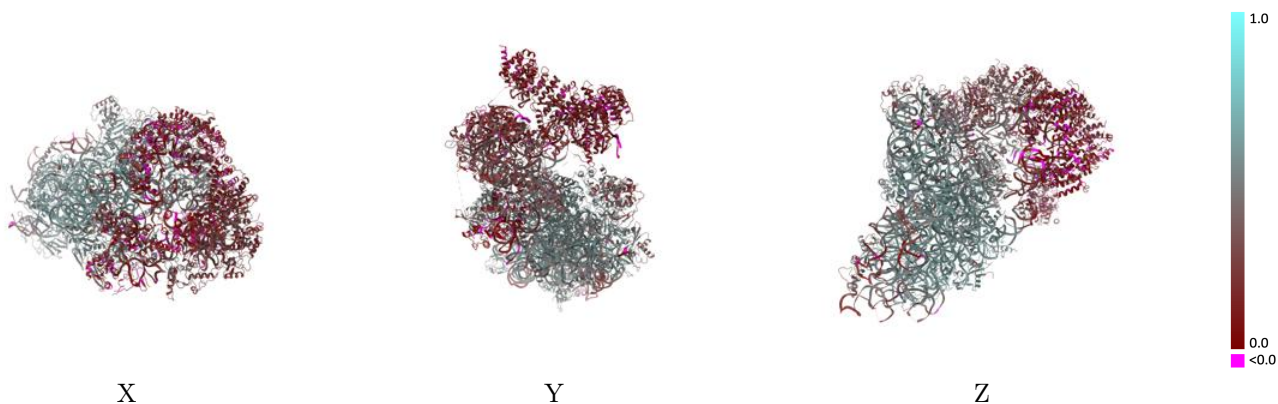
This section contains information regarding the fit between EMDB map EMD-32803 and PDB model 7WTW. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



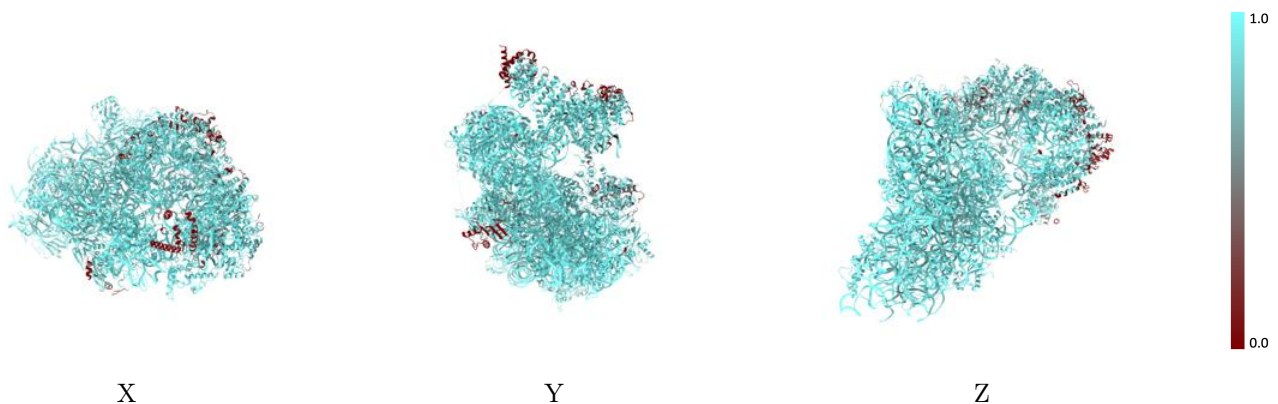
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



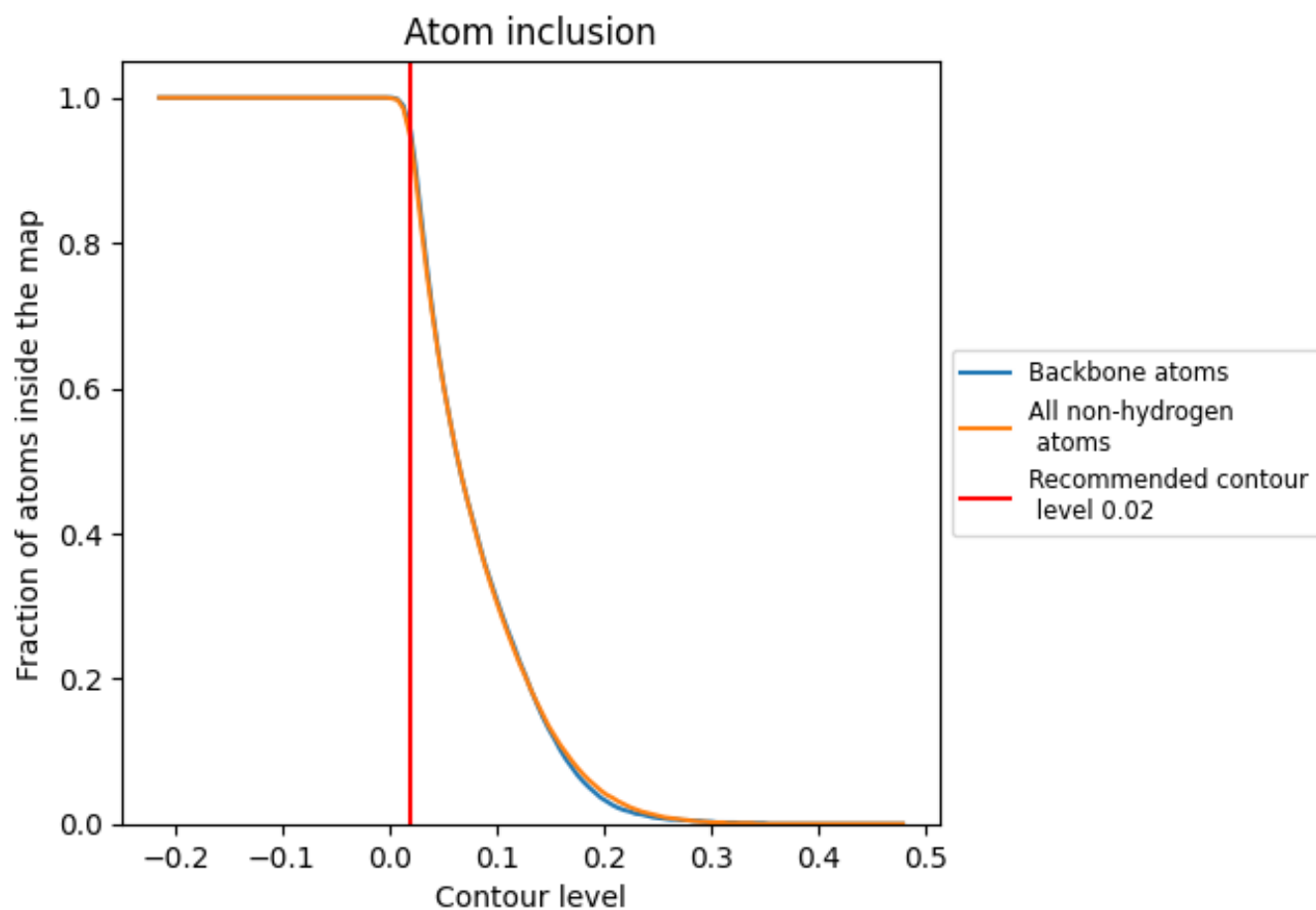
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4010
2	 0.9940	 0.4510
A	 0.9600	 0.4620
B	 0.9550	 0.4550
C	 0.9840	 0.5100
E	 0.9960	 0.5850
F	 0.9620	 0.2950
G	 0.9830	 0.5020
H	 0.9700	 0.4570
I	 0.9780	 0.5120
J	 0.9910	 0.5740
K	 0.8010	 0.1280
L	 0.9820	 0.5500
M	 0.6760	 0.1160
N	 0.9940	 0.5510
O	 0.9780	 0.4750
P	 0.9740	 0.3230
Q	 0.9370	 0.2540
R	 0.9350	 0.1270
S	 0.9260	 0.2580
T	 0.9240	 0.2660
V	 0.9860	 0.5130
W	 0.9980	 0.5840
X	 0.9870	 0.5690
Y	 0.9970	 0.5740
Z	 0.8340	 0.2240
b	 0.9920	 0.5460
c	 0.9400	 0.3180
e	 1.0000	 0.5830
f	 0.8540	 0.0900
q	 0.8710	 0.1730
r	 0.2800	 0.1070
t	 0.9610	 0.3690
u	 0.9890	 0.4990
w	 0.8990	 0.1920



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Chain	Atom inclusion	Q-score
x	 0.9940	 0.4960
y	 0.7170	 0.3450
z	 0.5690	 0.0640