



wwPDB EM Validation Summary Report ⓘ

Jul 29, 2026 – 07:30 pm BST

PDB ID : 32NJ / pdb_000032nj
EMDB ID : EMD-59026
Title : Cryo-EM structure of SKM-M.smegmatis 70S ribosomal complex
Authors : Cook, M.A.; Xu, M.; Morici, M.; Travin, D.T.; Wang, W.; Klepacki, D.; Nandini, N.; Rao, V.N.; Sahile, H.; Hackenberger, D.; Golas, A.J.; Nietupski, R.M.; Fitzgerald, M.; Safdari, H.A.; Berger, M.; Corazza, M.; Bond, A.; Ben-Zion, I.; Guitor, A.K.; Tertigas, D.; Wang, L.; Schaezner, A.J.; Ejim, L.; Yarlagadda, V.; Gomez, J.; Surette, M.G.; Av-Gay, Y.; Dhar, N.; Hung, D.T.; Vazquez Laslop, N.; Mankin, A.; Wilson, D.N.; Wright, G.D.
Deposited on : 2026-07-16
Resolution : 3.00 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.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)

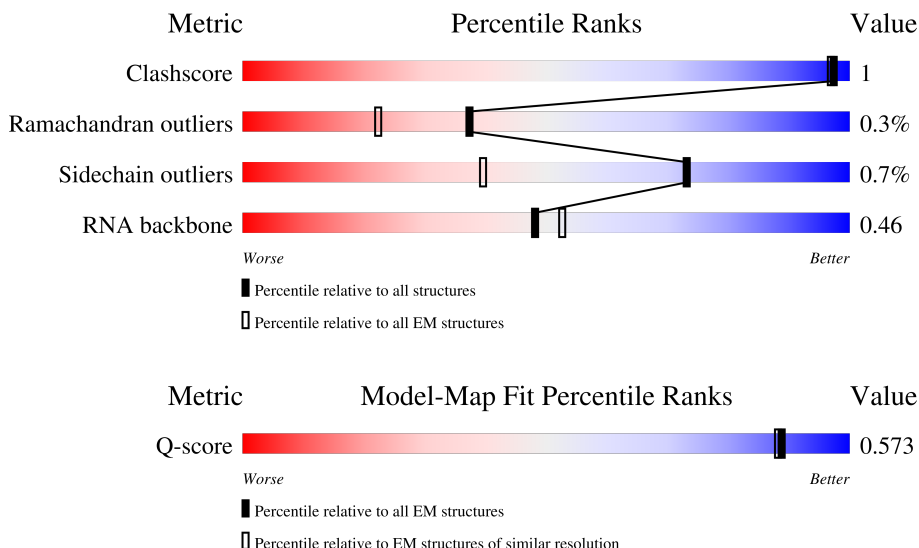
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

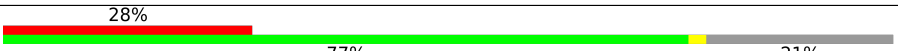
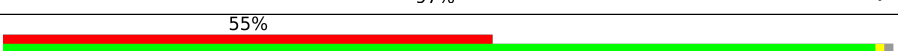
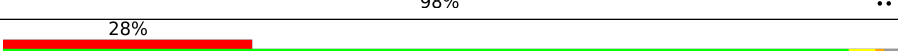
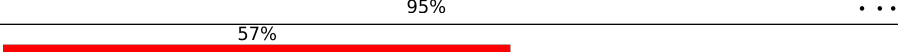
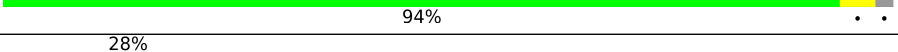
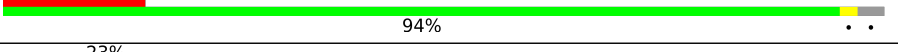
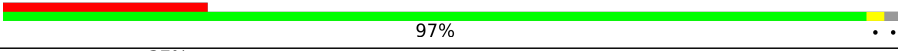
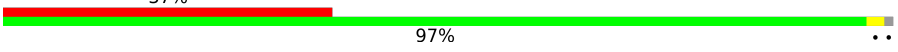
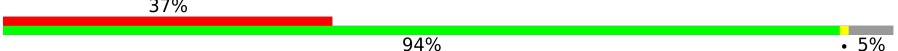
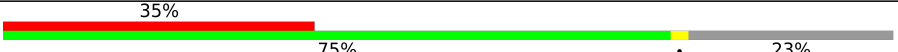
The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment 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	A	1528	

Continued on next page...

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.50

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	x	33	
3	C	275	
4	D	201	
5	E	214	
6	F	96	
7	G	156	
8	H	132	
9	I	150	
10	J	101	
11	K	138	
12	L	124	
13	N	61	
14	O	89	
15	P	156	
16	Q	98	
17	R	84	
18	T	86	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 44891 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1367	Total	C	N	O	P	0	0
			29386	13088	5411	9520	1367		

- Molecule 2 is a protein called Small ribosomal subunit protein bS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	x	30	Total	C	N	O	S	0	0
			267	164	68	34	1		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	205	Total	C	N	O	S	0	0
			1641	1023	319	295	4		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	200	Total	C	N	O	S	0	0
			1642	1028	316	296	2		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	170	Total	C	N	O	S	0	0
			1233	777	231	221	4		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	96	Total	C	N	O	S	0	0
			772	486	138	146	2		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	154	Total	C	N	O	S	0	0
			1218	757	239	220	2		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	130	Total	C	N	O	S	0	0
			1004	629	188	186	1		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	126	Total	C	N	O	0	0
			995	630	194	171		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	99	Total	C	N	O	S	0	0
			789	495	146	145	3		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	120	Total	C	N	O	S	0	0
			940	583	194	161	2		

- Molecule 13 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	60	Total	C	N	O	S	0	0
			478	302	97	74	5		

- Molecule 14 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	O	88	Total	C	N	O	0	0
			721	449	147	125		

- Molecule 15 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	P	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 16 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	93	Total	C	N	O	S	0	0
			739	464	140	133	2		

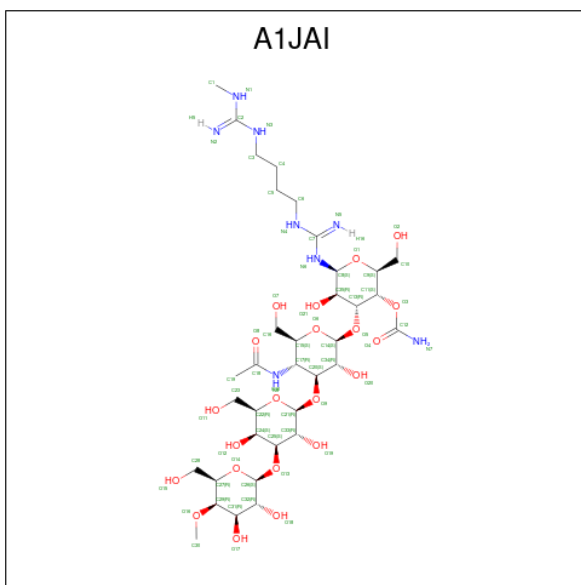
- Molecule 17 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 18 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	T	85	Total	C	N	O	0	0
			661	402	139	120		

- Molecule 19 is [(2 {S},3 {S},4 {R},5 {R},6 {S})-4-[(2 {S},3 {R},4 {S},5 {R},6 {S})-5-acetamido-6-(hydroxymethyl)-4-[(2 {R},3 {R},4 {S},5 {S},6 {R})-6-(hydroxymethyl)-4-[(2 {S},3 {R},4 {R},5 {R},6 {R})-6-(hydroxymethyl)-5-methoxy-3,4-bis(oxidanyl)oxan-2-yl]oxy-3,5-bis(oxidanyl)oxan-2-yl]oxy-3-oxidanyl-oxan-2-yl]oxy-2-(hydroxymethyl)-6-[[{N}]-4-[({N}-methylcarbamimidoyl)amino]butyl]carbamimidoyl]amino]-5-oxidanyl-oxan-3-yl] carbamate (CCD ID: A1JAI) (formula: C₃₅H₆₄N₈O₂₁) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
19	A	1	Total	C	N	O	0
			64	35	8	21	

- Molecule 20 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
20	A	75	Total	Mg	0
			75	75	
20	C	1	Total	Mg	0
			1	1	
20	R	1	Total	Mg	0
			1	1	

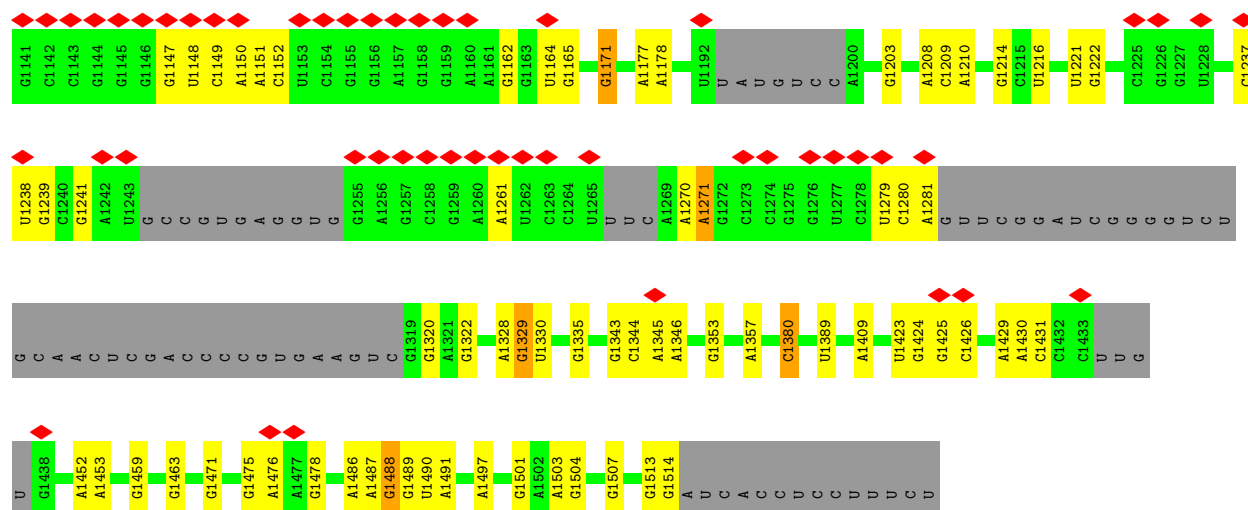
- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
21	N	1	Total	Zn	0
			1	1	
21	R	1	Total	Zn	0
			1	1	

- Molecule 22 is water.

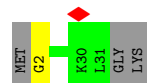
Mol	Chain	Residues	Atoms		AltConf
22	A	3	Total	O	0
			3	3	





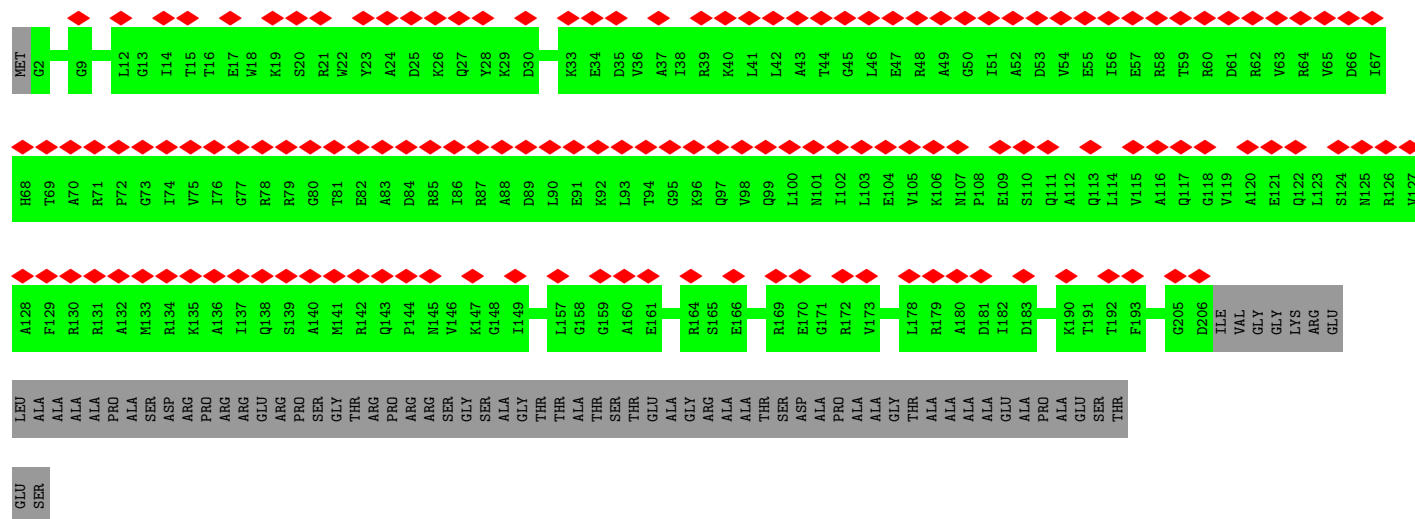
- Molecule 2: Small ribosomal subunit protein bs22

Chain x: 88% 9%



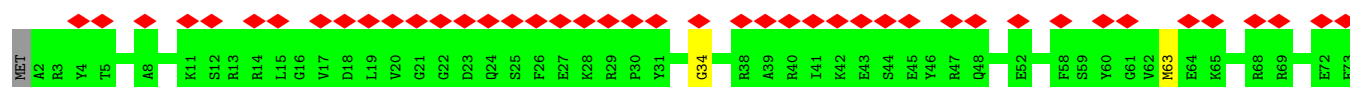
- Molecule 3: Small ribosomal subunit protein uS3

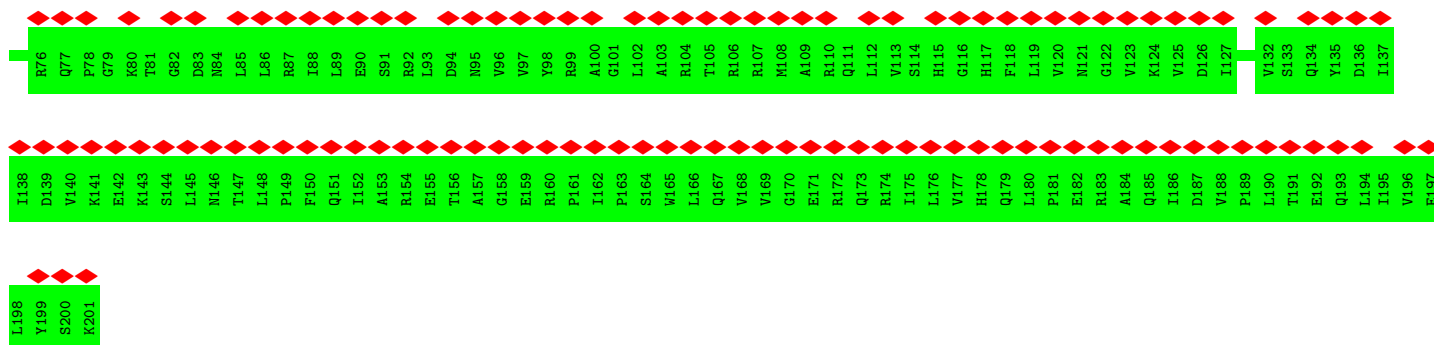
Chain C: 52% 75% 25%



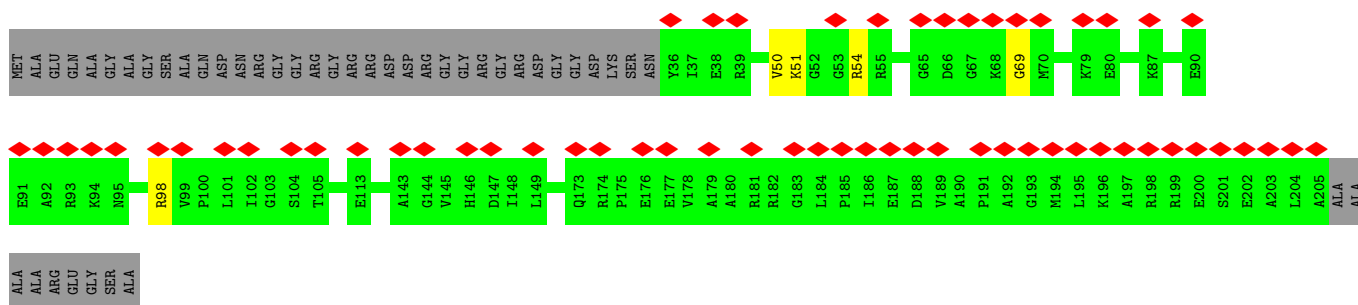
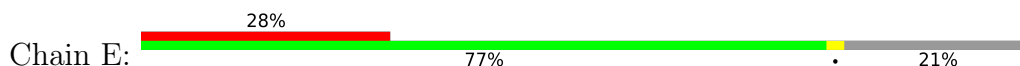
- Molecule 4: Small ribosomal subunit protein uS4

Chain D: 77% 99%

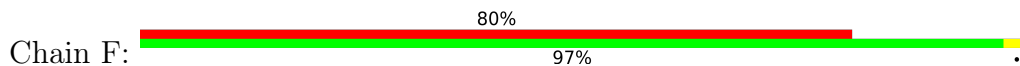




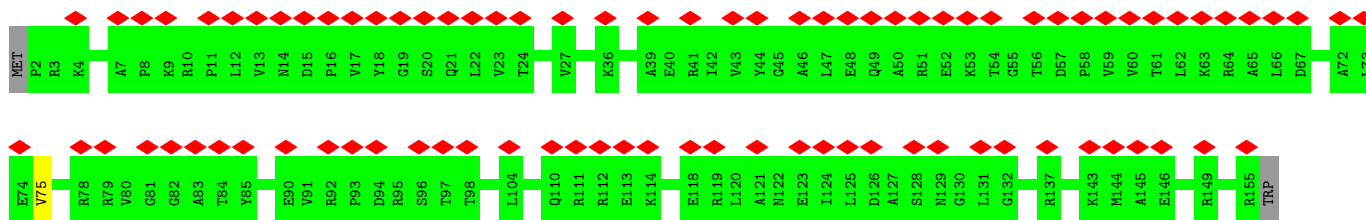
- Molecule 5: Small ribosomal subunit protein uS5



- Molecule 6: Small ribosomal subunit protein bS6

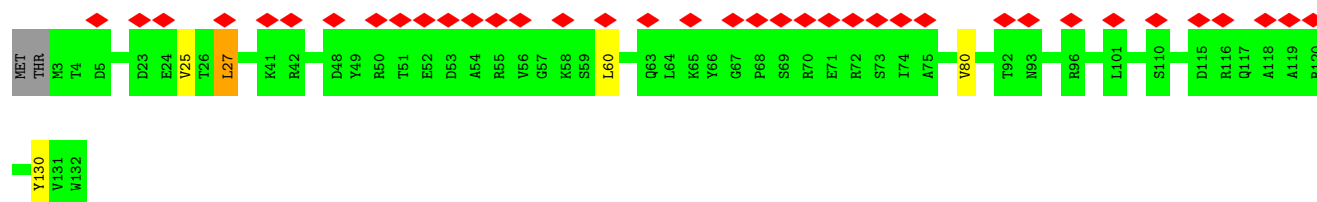


- Molecule 7: Small ribosomal subunit protein uS7

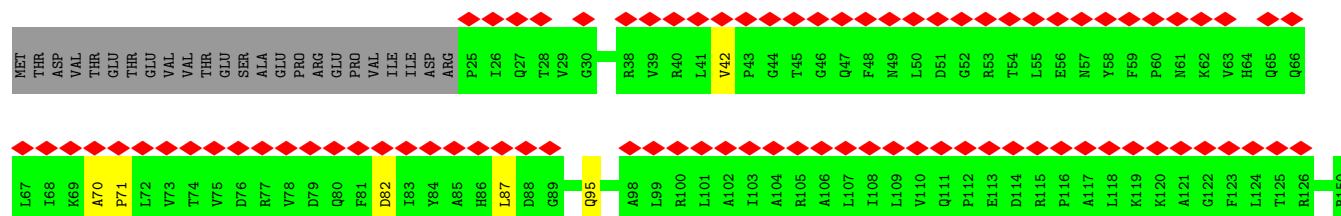
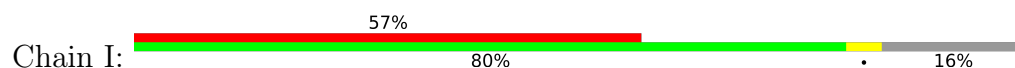


- Molecule 8: Small ribosomal subunit protein uS8

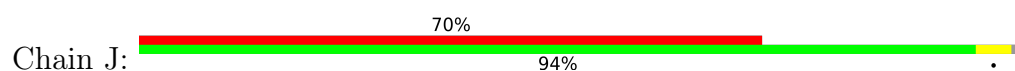




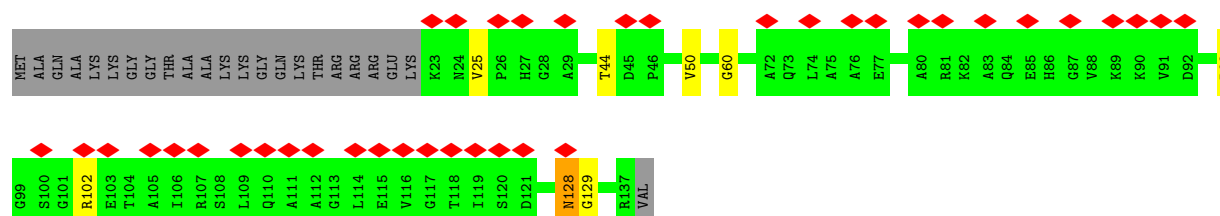
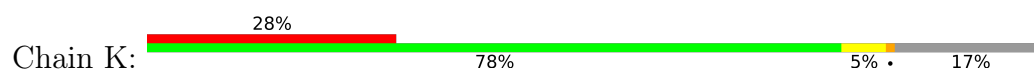
- Molecule 9: Small ribosomal subunit protein uS9



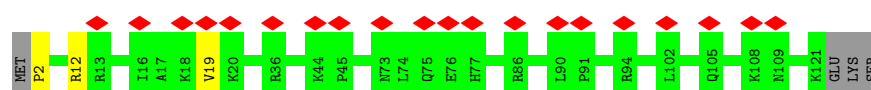
- Molecule 10: Small ribosomal subunit protein uS10



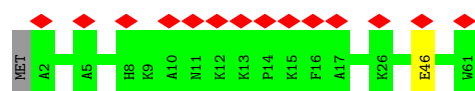
- Molecule 11: Small ribosomal subunit protein uS11



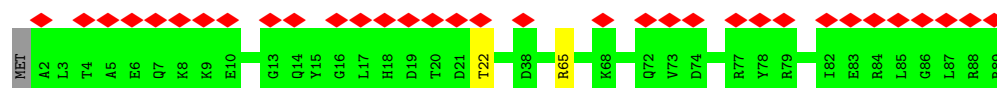
- Molecule 12: Small ribosomal subunit protein uS12



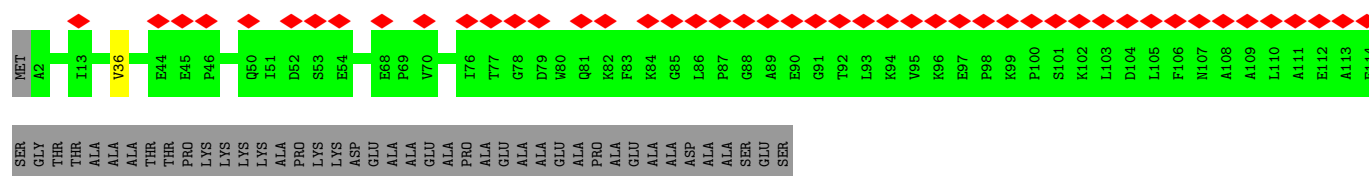
- Molecule 13: Small ribosomal subunit protein uS14B



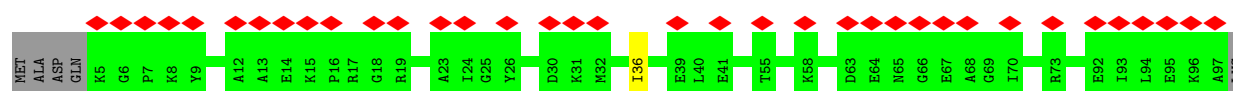
- Molecule 14: Small ribosomal subunit protein uS15



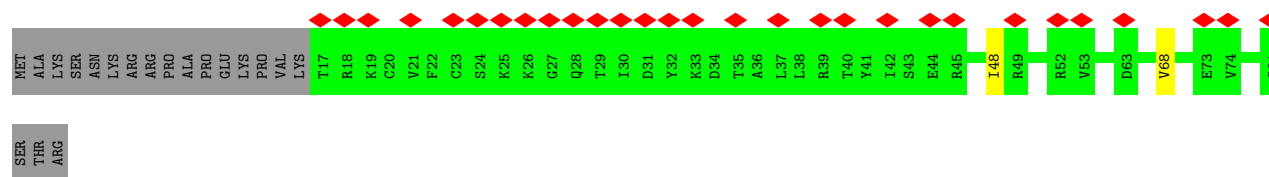
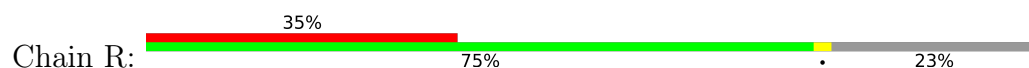
- Molecule 15: Small ribosomal subunit protein bS16



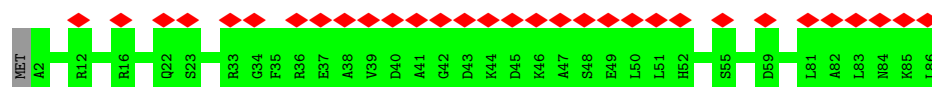
- Molecule 16: Small ribosomal subunit protein uS17



- Molecule 17: Small ribosomal subunit protein bS18B



- Molecule 18: Small ribosomal subunit protein bS20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68217	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0152	Depositor
Map size (Å)	359.424, 359.424, 359.424	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	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, MG, A1JAI

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	A	0.64	0/32895	0.79	5/51315 (0.0%)
2	x	0.65	0/267	0.90	0/343
3	C	0.64	0/1665	0.81	0/2235
4	D	0.63	0/1673	0.83	0/2251
5	E	0.68	0/1249	0.80	0/1687
6	F	0.62	0/783	0.83	0/1059
7	G	0.66	0/1236	0.88	0/1667
8	H	0.66	0/1019	0.82	0/1375
9	I	0.67	0/1013	0.83	0/1362
10	J	0.65	0/803	0.84	0/1086
11	K	0.69	0/873	0.79	0/1180
12	L	0.69	0/951	0.76	0/1271
13	N	0.64	0/489	0.79	0/650
14	O	0.63	0/730	0.92	0/977
15	P	0.63	0/908	0.80	0/1226
16	Q	0.66	0/750	0.72	0/1004
17	R	0.66	0/518	0.90	0/693
18	T	0.62	0/664	0.96	0/882
All	All	0.64	0/48486	0.80	5/72263 (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
14	O	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	756	G	O3'-P-O5'	-5.67	95.49	104.00
1	A	764	A	O3'-P-O5'	-5.51	95.73	104.00
1	A	1343	G	O3'-P-O5'	-5.29	96.07	104.00
1	A	794	A	O3'-P-O5'	-5.28	96.09	104.00
1	A	1329	G	C3'-C2'-C1'	-5.12	96.38	101.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	O	22	THR	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	A	29386	0	14787	29	0
2	x	267	0	326	1	0
3	C	1641	0	1684	0	0
4	D	1642	0	1668	1	0
5	E	1233	0	1302	3	0
6	F	772	0	797	1	0
7	G	1218	0	1272	0	0
8	H	1004	0	1039	2	0
9	I	995	0	1050	3	0
10	J	789	0	819	1	0
11	K	855	0	863	2	0
12	L	940	0	1026	1	0
13	N	478	0	499	0	0
14	O	721	0	760	0	0
15	P	891	0	935	0	0
16	Q	739	0	787	0	0
17	R	513	0	537	1	0
18	T	661	0	712	0	0
19	A	64	0	0	0	0
20	A	75	0	0	0	0
20	C	1	0	0	0	0
20	R	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	N	1	0	0	0	0
21	R	1	0	0	0	0
22	A	3	0	0	0	0
All	All	44891	0	30863	41	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 1.

The worst 5 of 41 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:551:U:HO2'	2:x:2:GLY:N	1.95	0.65
1:A:694:G:H2'	1:A:695:A:C8	2.41	0.55
1:A:504:G:H2'	1:A:505:C:C6	2.43	0.53
1:A:749:G:H4'	1:A:1497:A:H4'	1.91	0.53
1:A:1488:G:OP1	1:A:1491:A:H4'	2.10	0.52

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	x	28/33 (85%)	27 (96%)	1 (4%)	0	100	100
3	C	203/275 (74%)	190 (94%)	13 (6%)	0	100	100
4	D	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
5	E	168/214 (78%)	153 (91%)	15 (9%)	0	100	100
6	F	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
7	G	152/156 (97%)	146 (96%)	6 (4%)	0	100	100
8	H	128/132 (97%)	122 (95%)	6 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	124/150 (83%)	113 (91%)	11 (9%)	0	100	100
10	J	97/101 (96%)	90 (93%)	6 (6%)	1 (1%)	12	45
11	K	113/138 (82%)	103 (91%)	5 (4%)	5 (4%)	2	12
12	L	118/124 (95%)	107 (91%)	11 (9%)	0	100	100
13	N	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
14	O	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
15	P	111/156 (71%)	108 (97%)	3 (3%)	0	100	100
16	Q	91/98 (93%)	84 (92%)	7 (8%)	0	100	100
17	R	63/84 (75%)	60 (95%)	3 (5%)	0	100	100
18	T	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
All	All	1915/2194 (87%)	1804 (94%)	105 (6%)	6 (0%)	37	70

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	K	102	ARG
11	K	60	GLY
11	K	128	ASN
10	J	33	GLY
11	K	98	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	x	29/31 (94%)	29 (100%)	0	100	100
3	C	168/212 (79%)	168 (100%)	0	100	100
4	D	175/176 (99%)	174 (99%)	1 (1%)	78	88
5	E	123/147 (84%)	123 (100%)	0	100	100
6	F	85/85 (100%)	84 (99%)	1 (1%)	63	82
7	G	130/132 (98%)	129 (99%)	1 (1%)	73	86

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	106/108 (98%)	104 (98%)	2 (2%)	50	76
9	I	102/125 (82%)	102 (100%)	0	100	100
10	J	89/90 (99%)	88 (99%)	1 (1%)	65	83
11	K	89/105 (85%)	88 (99%)	1 (1%)	65	83
12	L	101/105 (96%)	100 (99%)	1 (1%)	68	84
13	N	49/50 (98%)	48 (98%)	1 (2%)	48	76
14	O	76/77 (99%)	75 (99%)	1 (1%)	61	81
15	P	92/118 (78%)	91 (99%)	1 (1%)	65	83
16	Q	79/83 (95%)	78 (99%)	1 (1%)	61	81
17	R	55/72 (76%)	55 (100%)	0	100	100
18	T	69/70 (99%)	69 (100%)	0	100	100
All	All	1617/1786 (90%)	1605 (99%)	12 (1%)	73	86

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	L	19	VAL
13	N	46	GLU
16	Q	36	ILE
14	O	65	ARG
8	H	25	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	47	GLN
10	J	101	GLN
10	J	70	HIS
11	K	37	ASN
4	D	134	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1357/1528 (88%)	250 (18%)	23 (1%)

5 of 250 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	U
1	A	8	U
1	A	9	U
1	A	11	G
1	A	12	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	972	U
1	A	1149	C
1	A	1147	G
1	A	1177	A
1	A	279	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 80 ligands modelled in this entry, 79 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
19	A1JAI	A	1601	-	65,67,67	0.55	1 (1%)	87,94,94	0.70	2 (2%)

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
19	A1JAI	A	1601	-	-	4/43/125/125	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	A	1601	A1JAI	C2-N2	2.36	1.36	1.29

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	A	1601	A1JAI	O1-C8-N6	2.72	112.91	108.01
19	A	1601	A1JAI	C8-N6-C7	2.31	127.19	123.30

There are no chirality outliers.

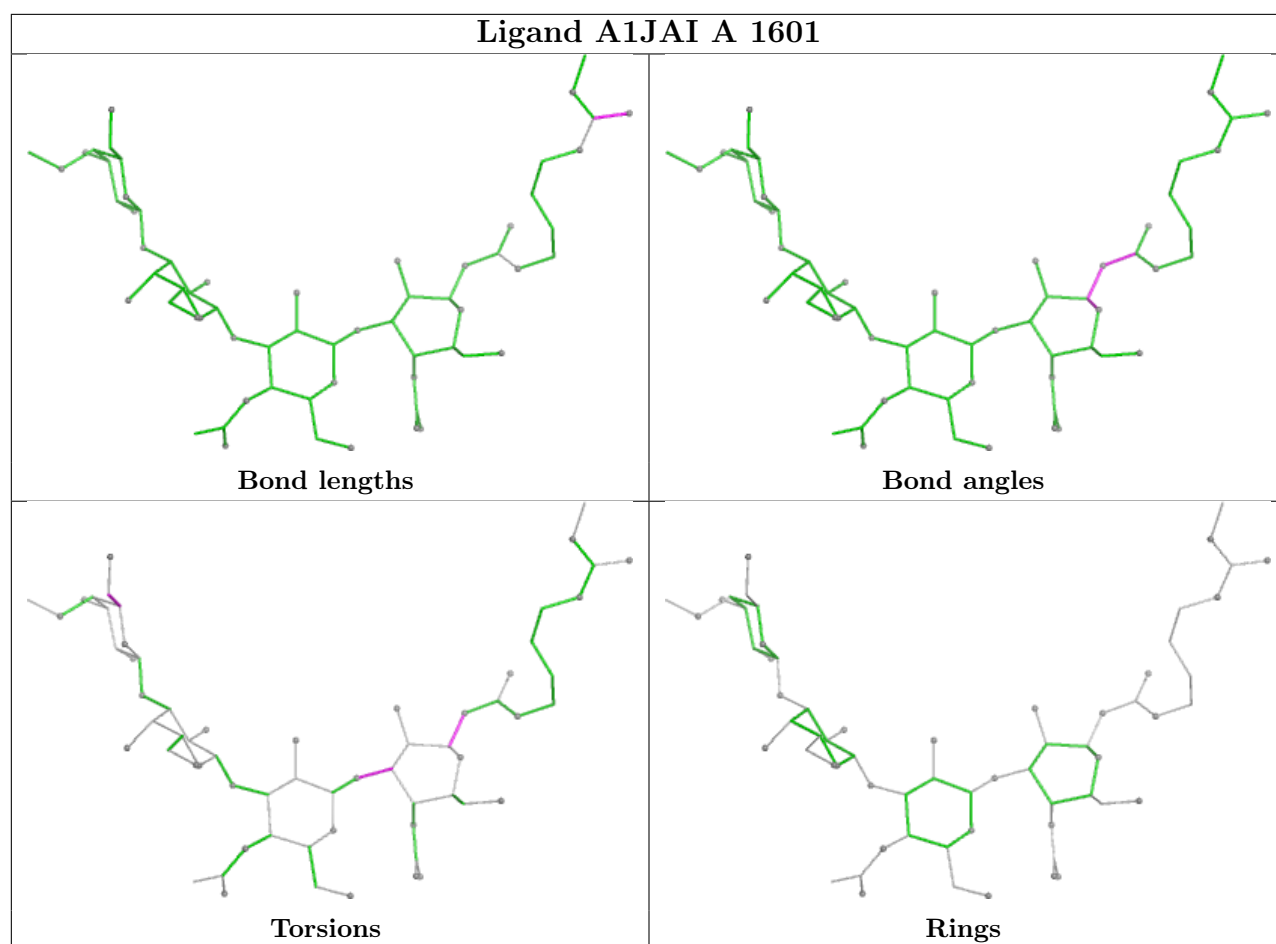
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	A	1601	A1JAI	O1-C8-N6-C7
19	A	1601	A1JAI	O14-C27-C28-O15
19	A	1601	A1JAI	C11-C13-O5-C14
19	A	1601	A1JAI	C35-C13-O5-C14

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

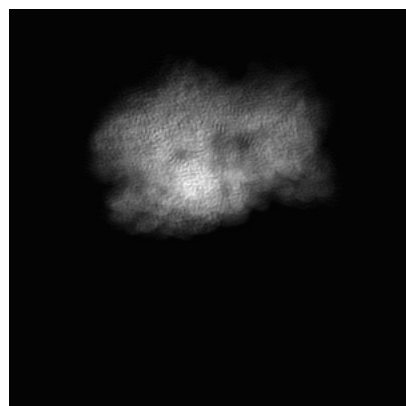
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-59026. These allow visual inspection of the internal detail of the map and identification of artifacts.

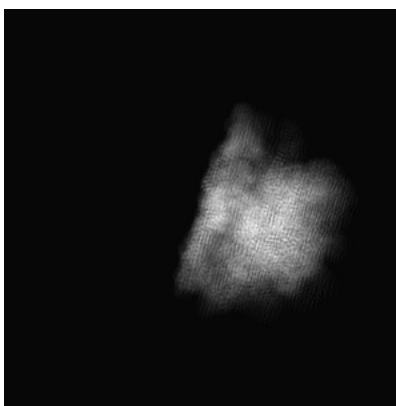
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

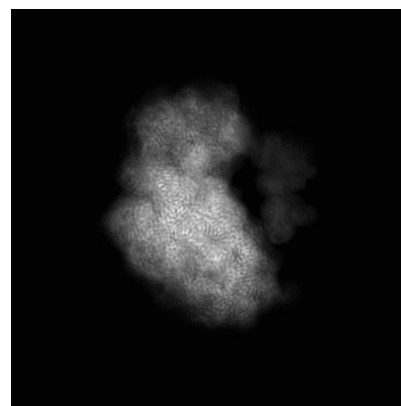
6.1.1 Primary map



X

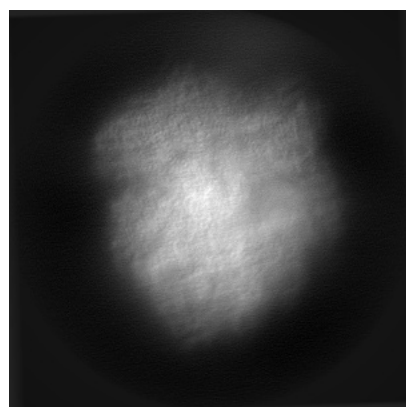


Y

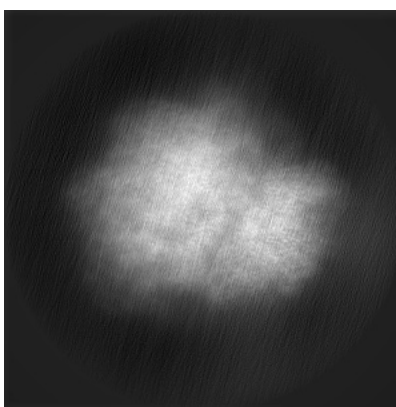


Z

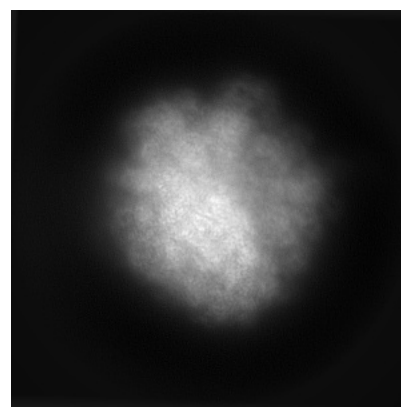
6.1.2 Raw map



X



Y

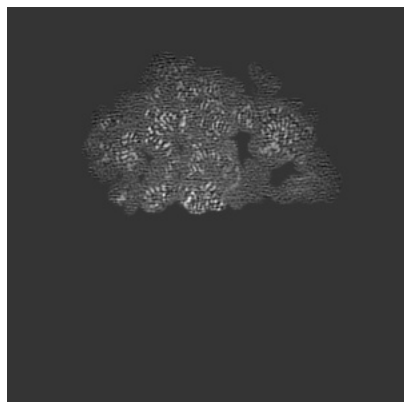


Z

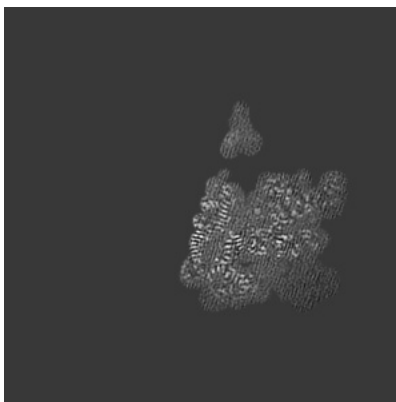
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

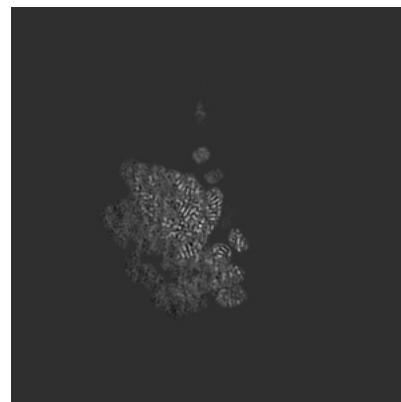
6.2.1 Primary map



X Index: 216

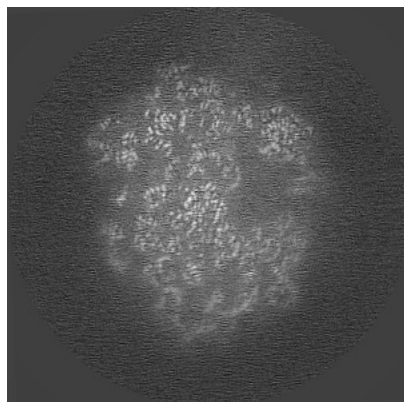


Y Index: 216

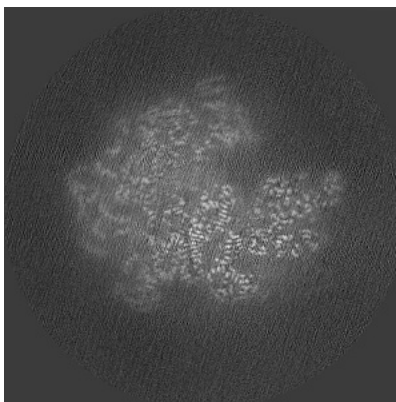


Z Index: 216

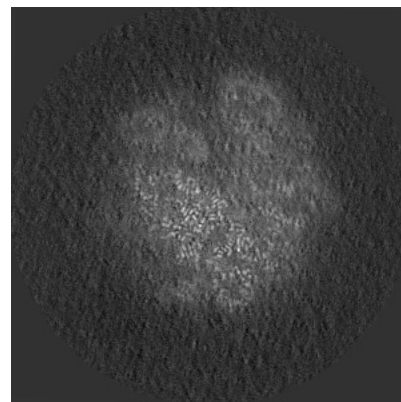
6.2.2 Raw map



X Index: 216



Y Index: 216

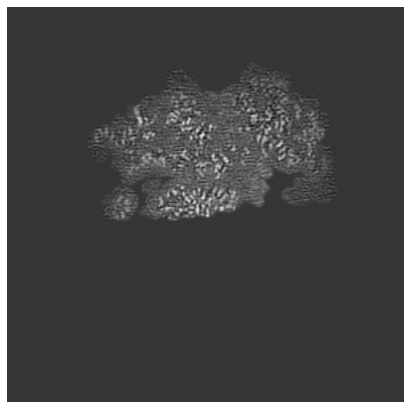


Z Index: 216

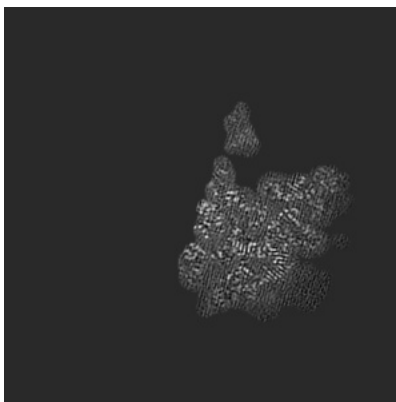
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

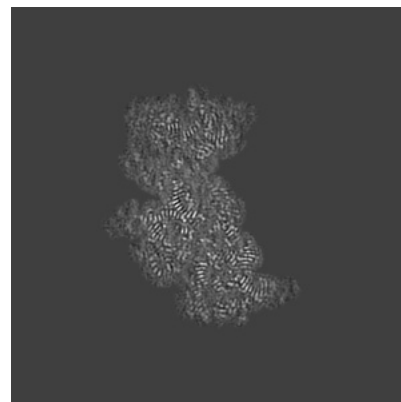
6.3.1 Primary map



X Index: 196

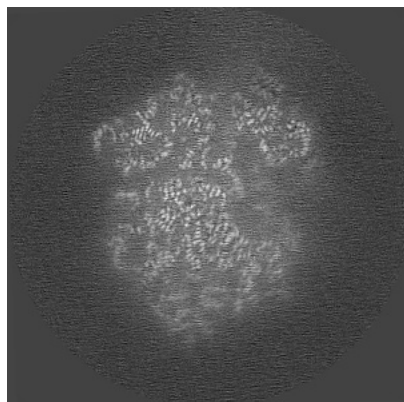


Y Index: 203

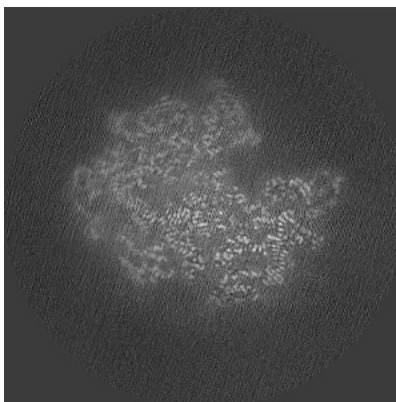


Z Index: 298

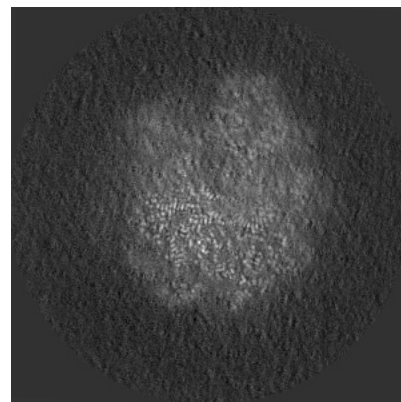
6.3.2 Raw map



X Index: 206



Y Index: 206

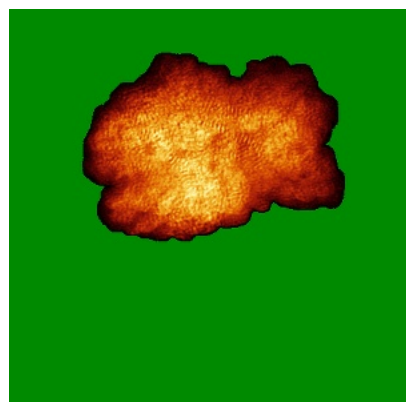


Z Index: 206

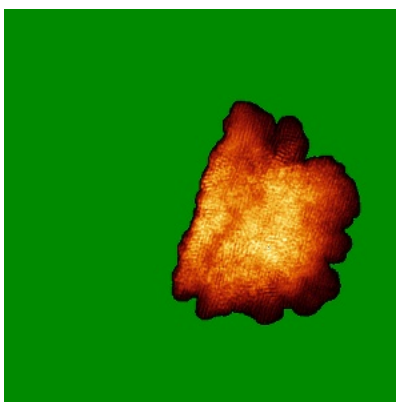
The images above show the largest variance slices of the map in three orthogonal directions.

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

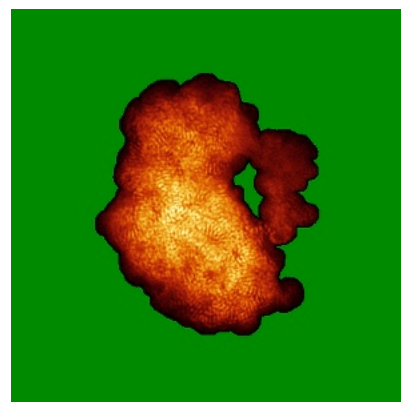
6.4.1 Primary map



X

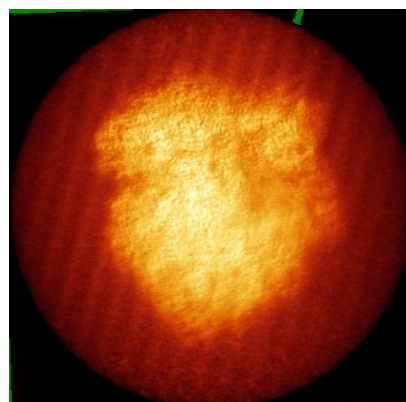


Y

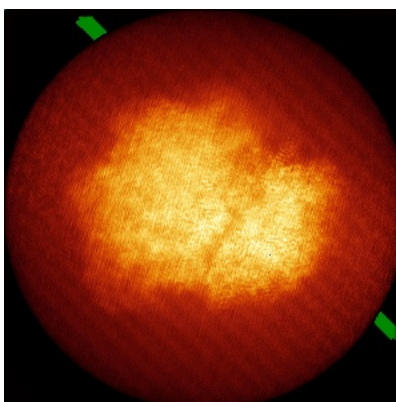


Z

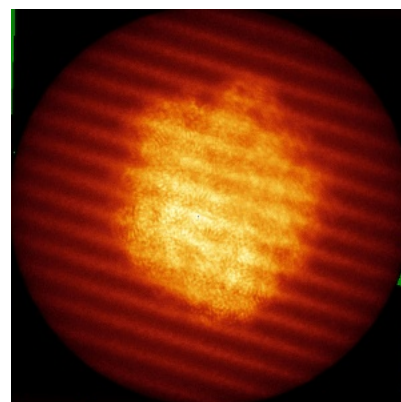
6.4.2 Raw map



X



Y

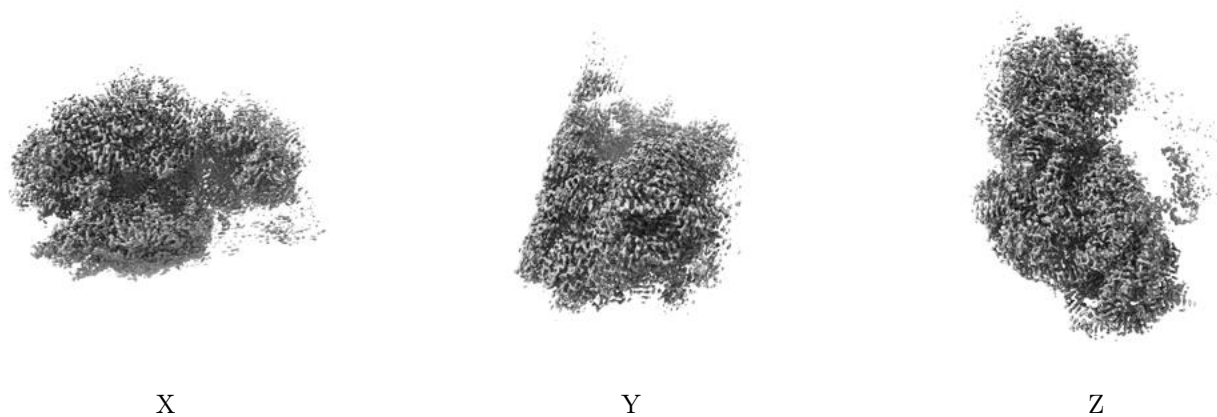


Z

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.

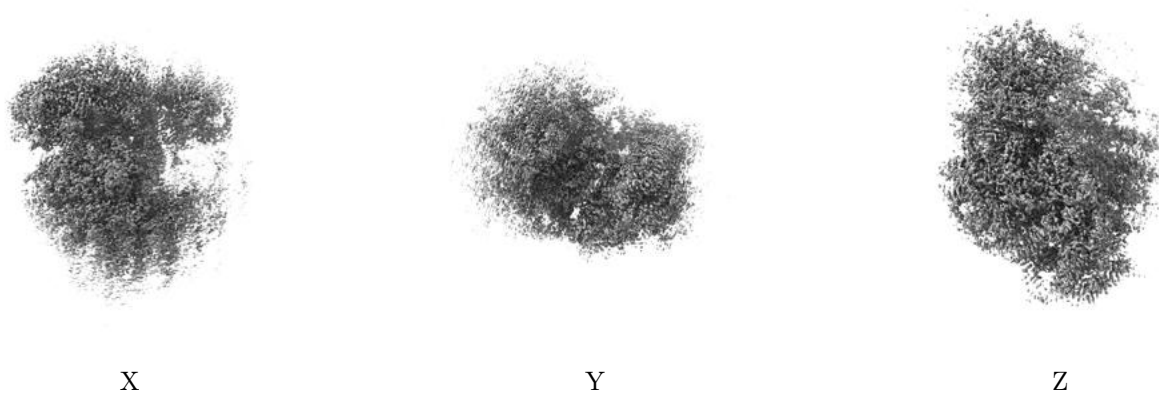
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0152. 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.

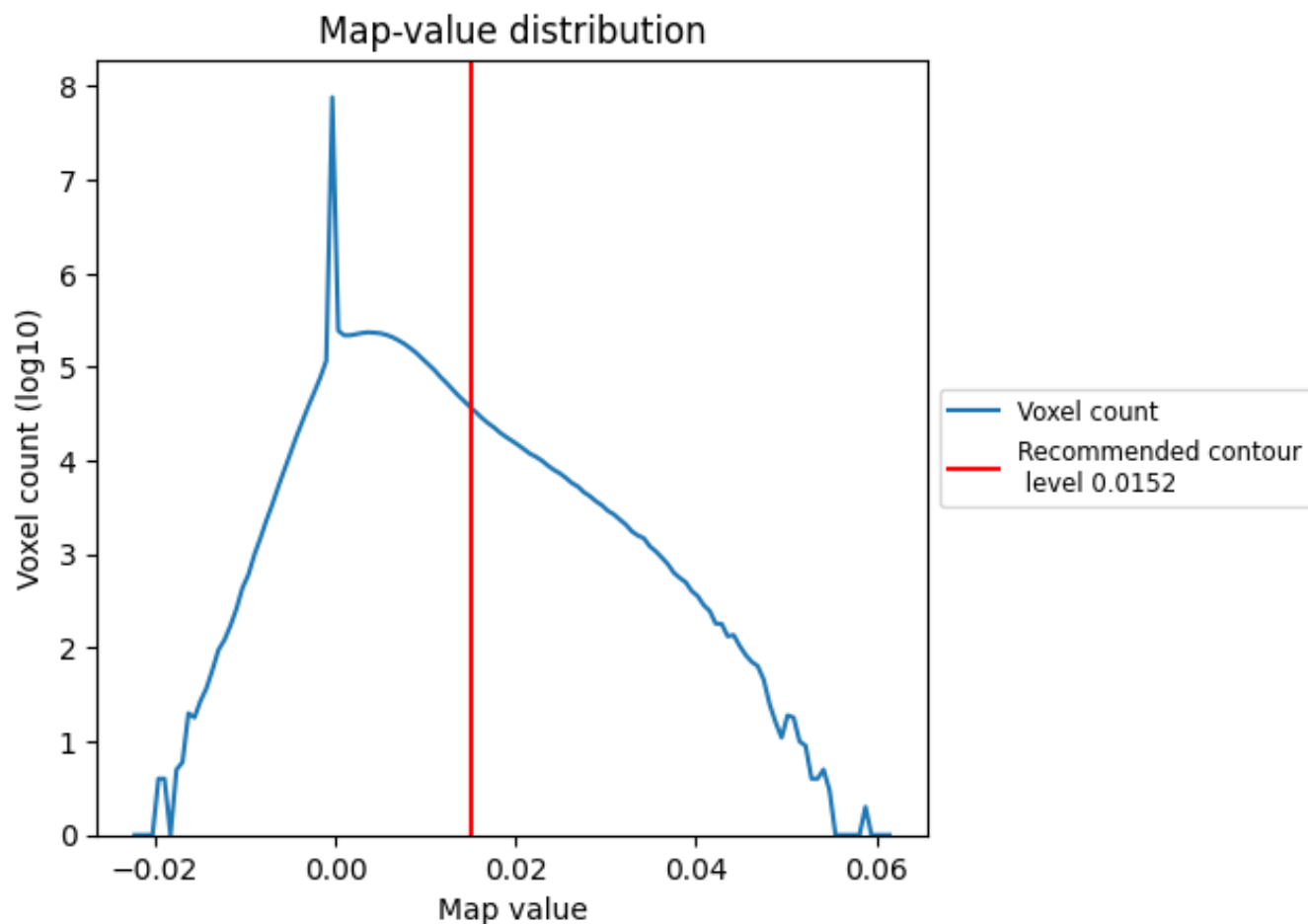
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

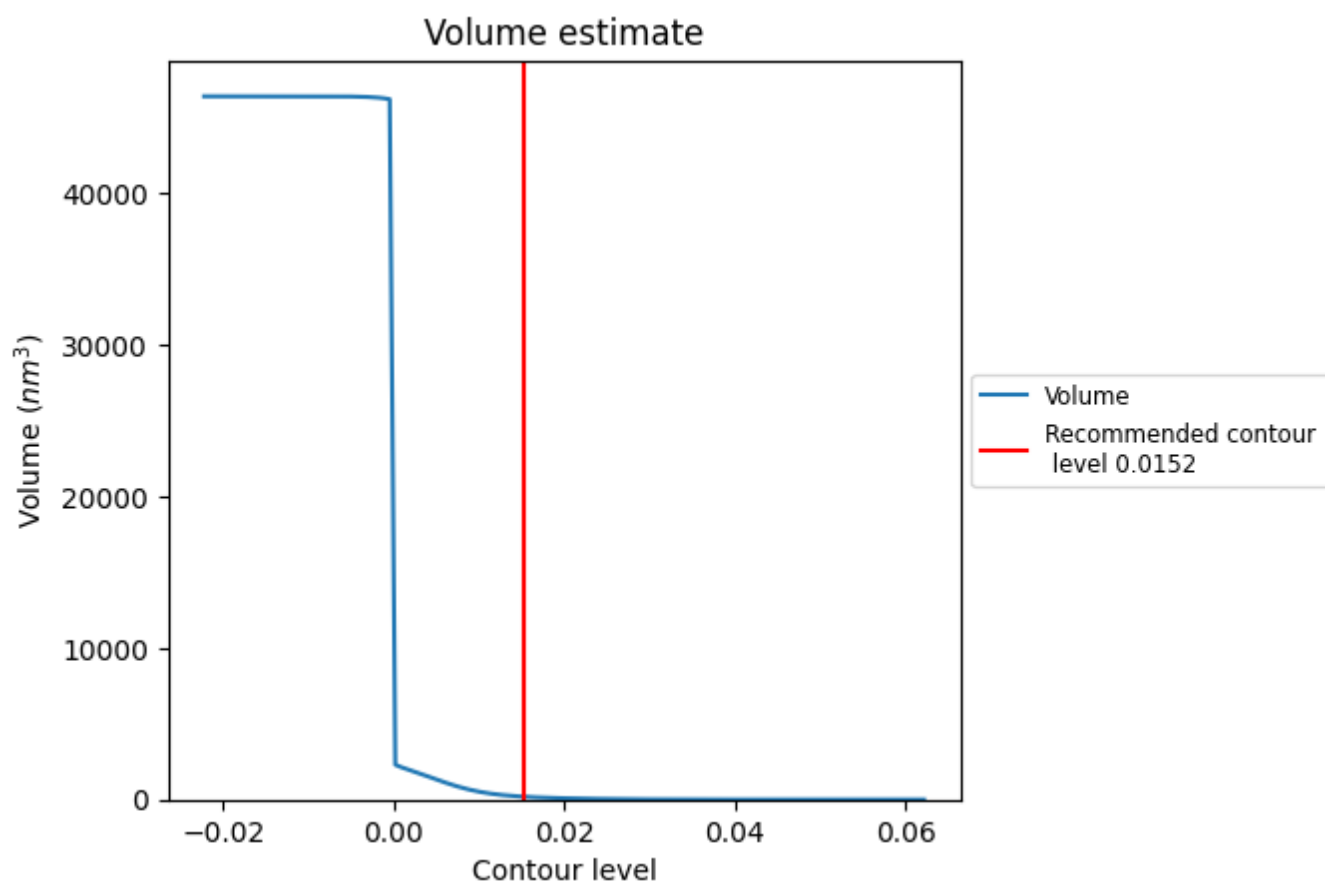
This section contains the results of statistical analysis of the map.

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.

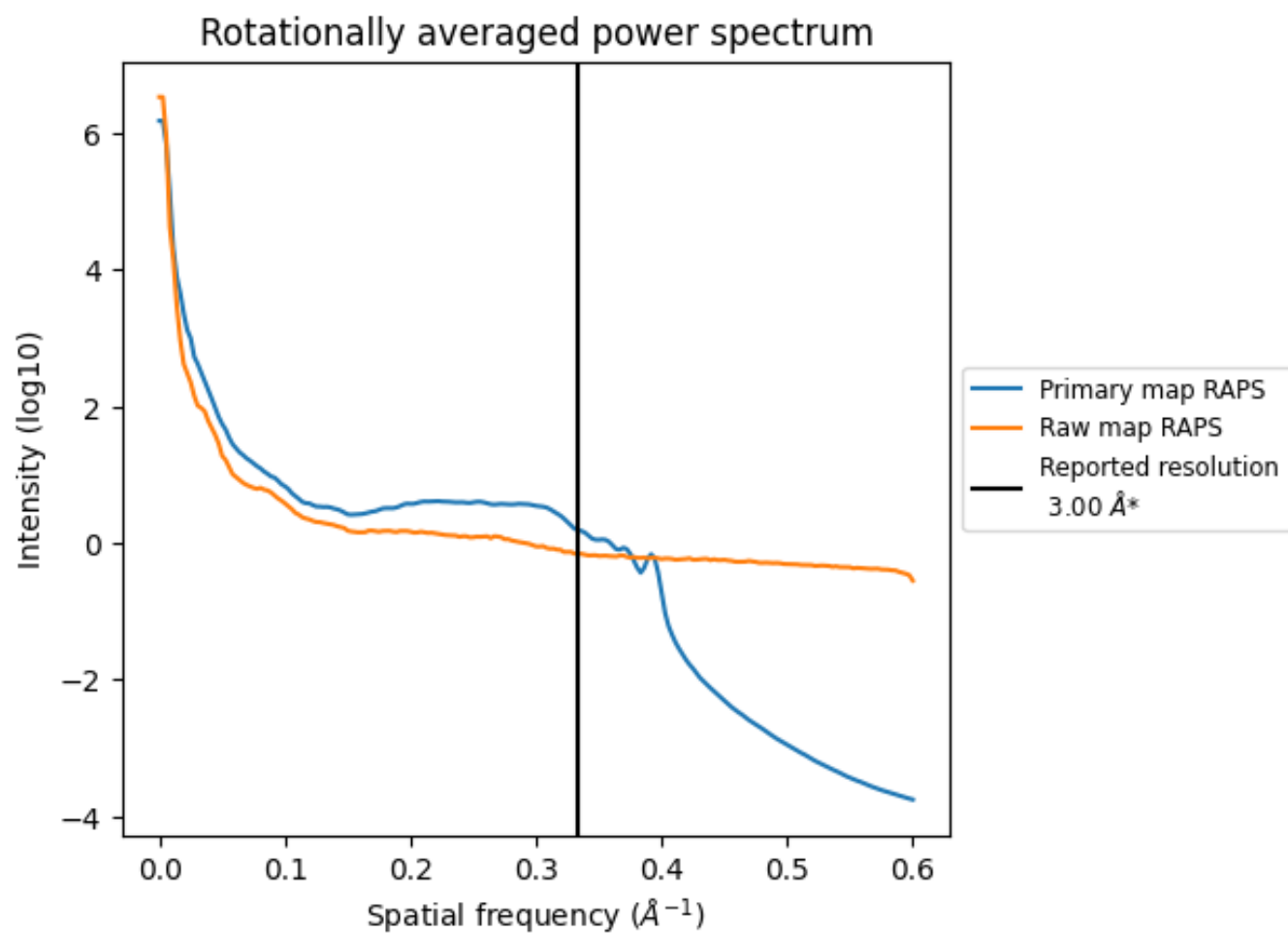
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 190 nm³; this corresponds to an approximate mass of 171 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 ⓘ

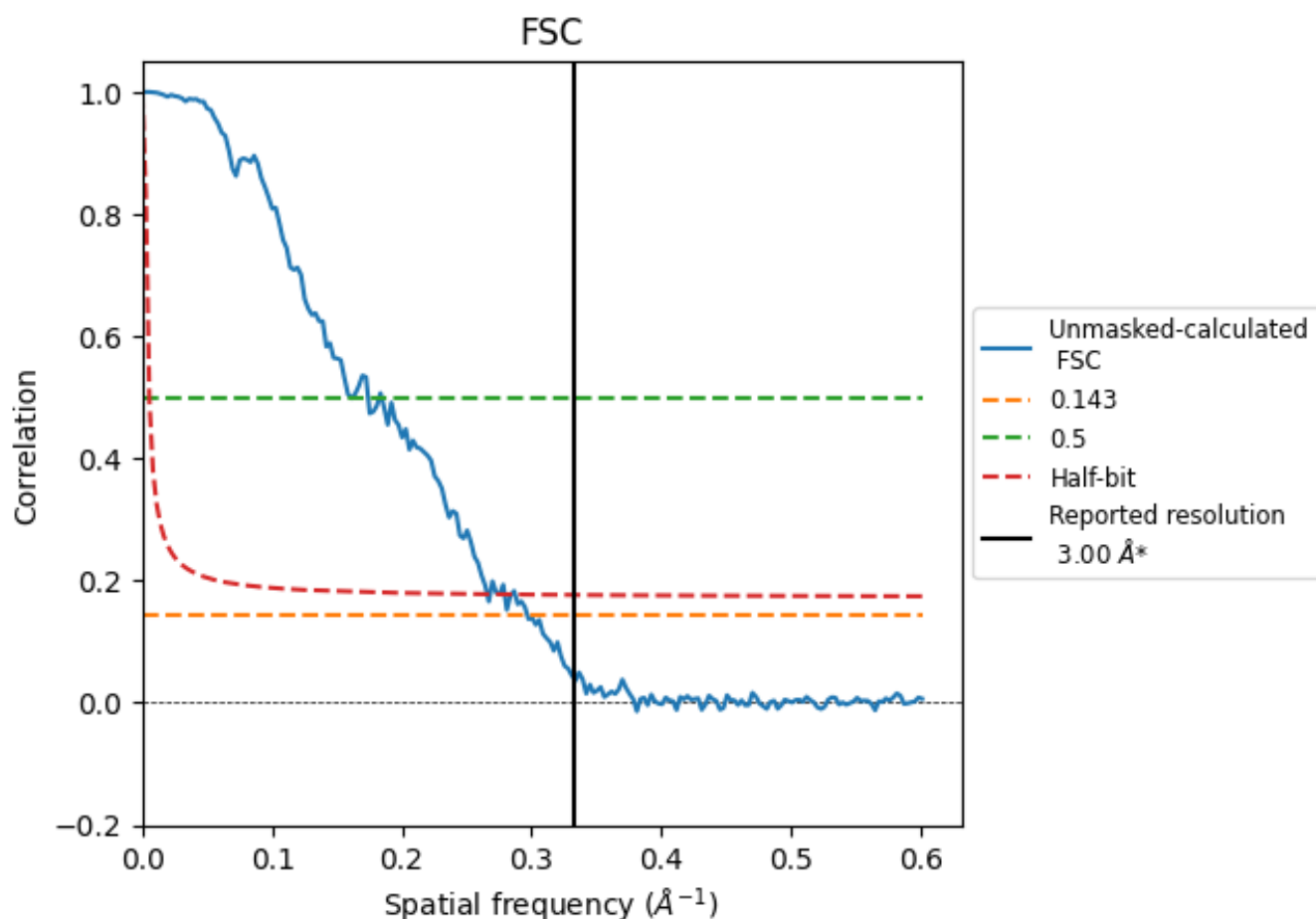


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

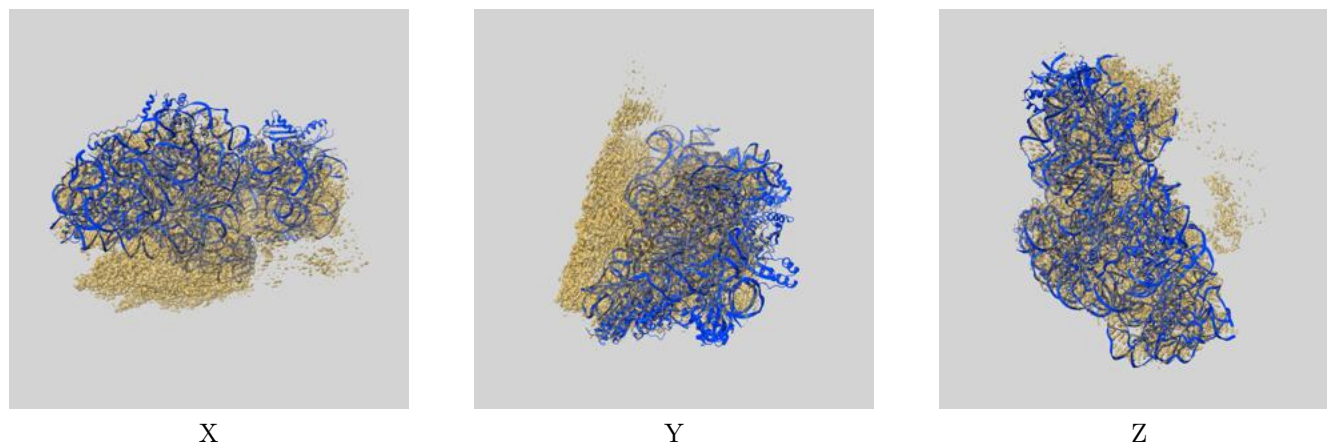
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.37	6.22	3.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.37 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

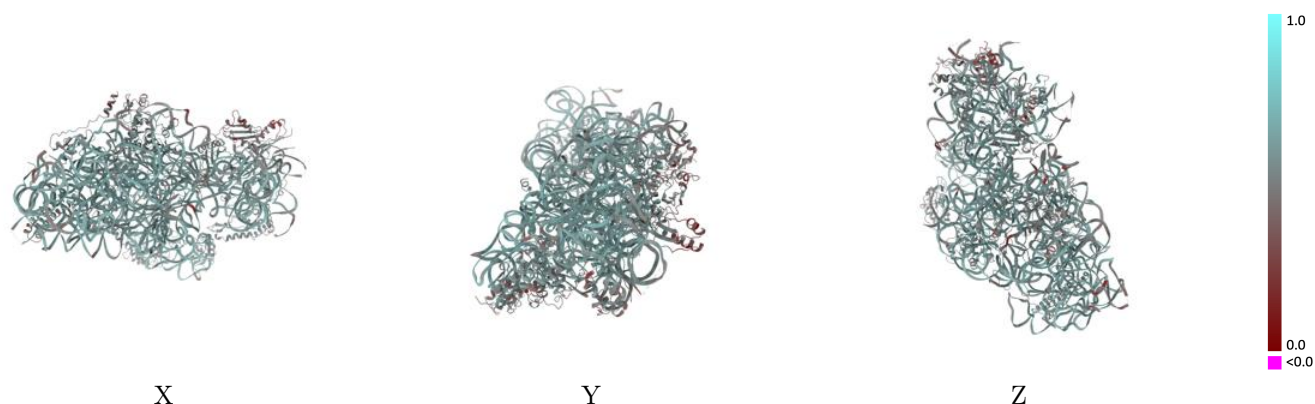
This section contains information regarding the fit between EMDB map EMD-59026 and PDB model 32NJ. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



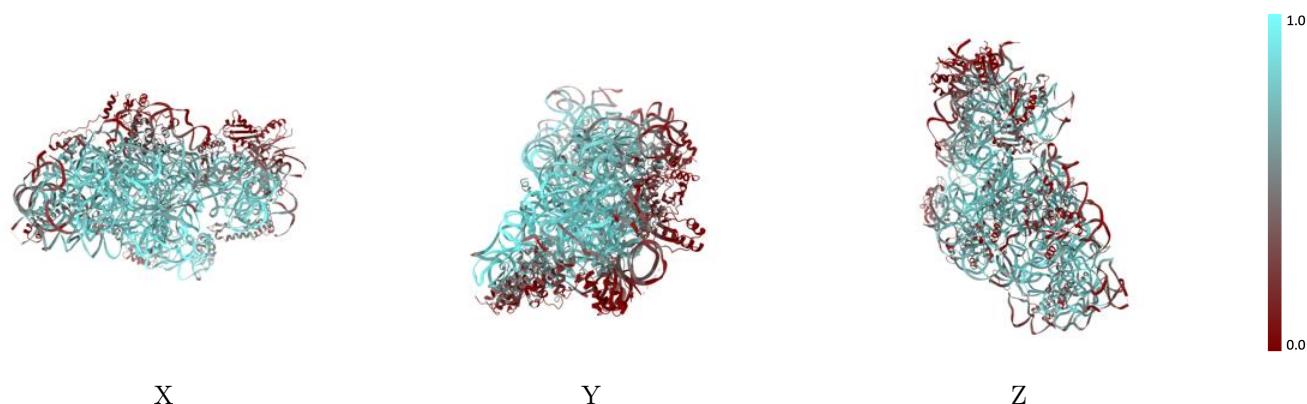
The images above show the 3D surface view of the map at the recommended contour level 0.0152 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



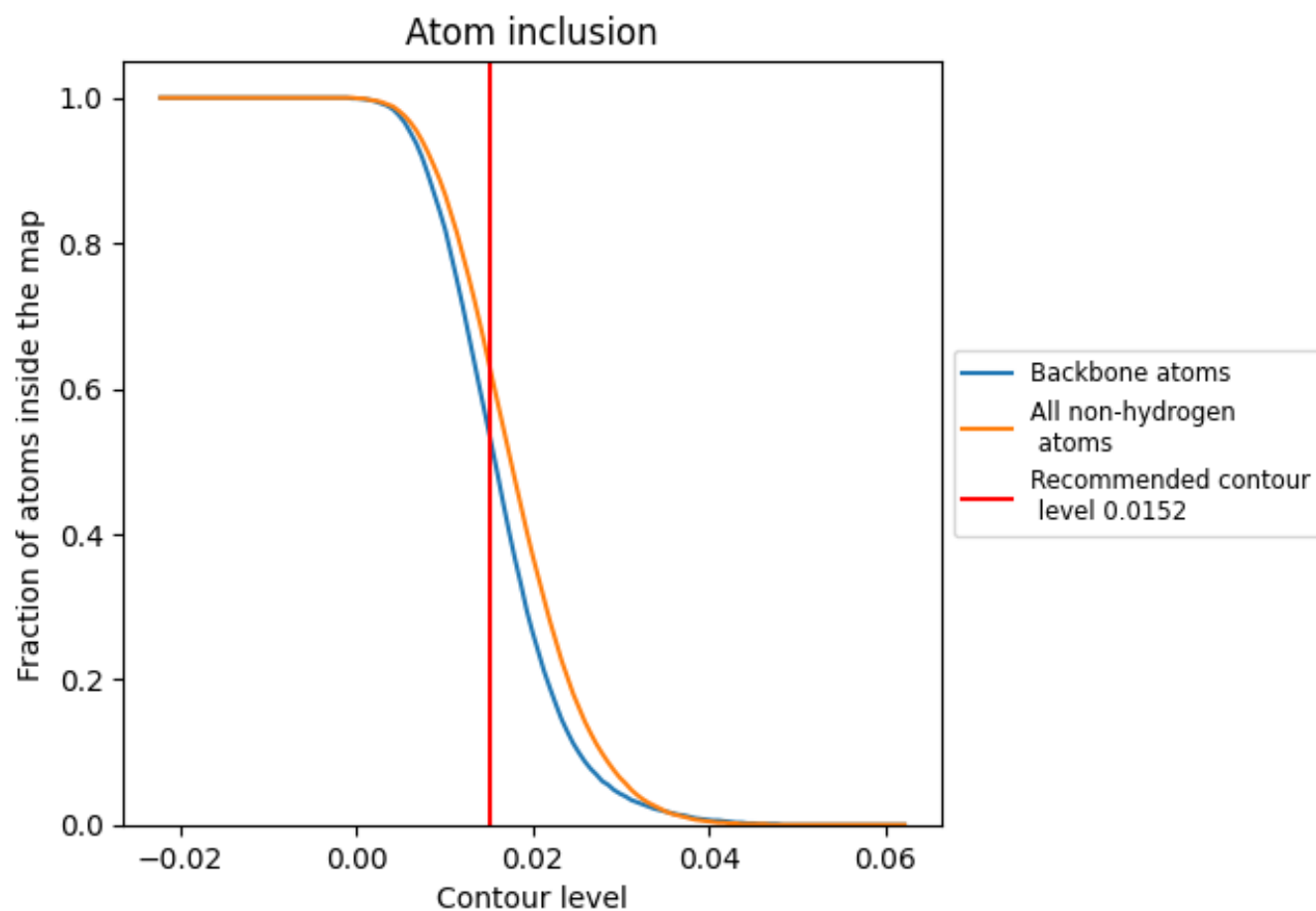
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0152).

9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 62% 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 (0.0152) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6250	 0.5730
A	 0.7390	 0.5960
C	 0.2790	 0.4980
D	 0.2250	 0.4960
E	 0.5140	 0.5550
F	 0.2360	 0.4760
G	 0.3630	 0.5170
H	 0.5560	 0.5840
I	 0.2690	 0.5230
J	 0.2630	 0.4490
K	 0.5240	 0.5400
L	 0.6360	 0.5620
N	 0.5600	 0.5860
O	 0.5300	 0.5650
P	 0.4540	 0.5580
Q	 0.5050	 0.5400
R	 0.4530	 0.5240
T	 0.5150	 0.5630
x	 0.7790	 0.5680

