



wwPDB EM Validation Summary Report ⓘ

Jan 22, 2025 – 06:30 am GMT

PDB ID : 8RG0
EMDB ID : EMD-19128
Title : Structure of human eIF3 core from closed 48S translation initiation complex
Authors : Petrychenko, V.; Yi, S.-H.; Liedtke, D.; Peng, B.Z.; Rodnina, M.V.; Fischer, N.
Deposited on : 2023-12-13
Resolution : 3.40 Å(reported)

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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:

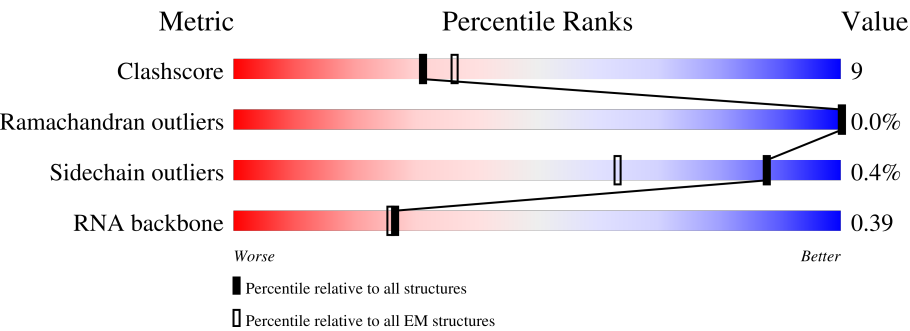
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.








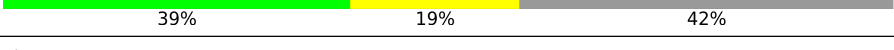
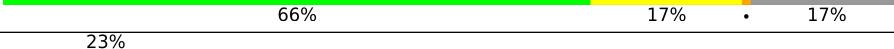
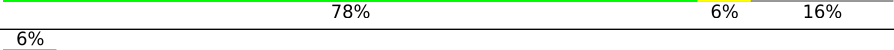
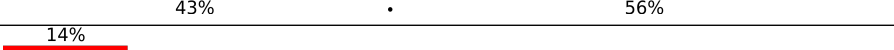
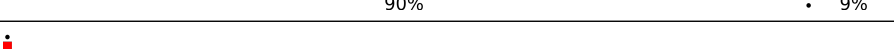

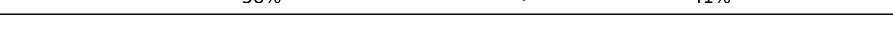
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	3	218	<div><div>71%</div><div>95%</div><div>..</div></div>
2	4	357	<div><div>17%</div><div>71%</div><div>28%</div></div>
3	5	564	<div><div>71%</div><div>79%</div><div>13%</div><div>8%</div></div>
4	6	374	<div><div>23%</div><div>87%</div><div>9%</div><div>.</div></div>
5	7	255	<div><div>11%</div><div>7%</div><div>88%</div></div>
6	8	352	<div><div>31%</div><div>89%</div><div>10%</div></div>
7	A	1869	<div><div>94%</div></div>

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Mol	Chain	Length	Quality of chain
8	H	84	
9	I	151	
10	M	135	
11	N	295	
12	O	264	
13	P	151	
14	Q	115	
15	n	69	
16	u	1382	
17	v	445	
18	x	548	
19	y	913	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 31348 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	213	Total	C	N	O	0	0
			1057	631	213	213		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	4	257	Total	C	N	O	0	0
			1272	757	257	258		

- Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	520	Total	C	N	O	S	0	0
			4347	2814	721	793	19		

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	362	Total	C	N	O	S	0	0
			2196	1348	414	427	7		

- Molecule 5 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	31	Total	C	N	O	P	0	0
			663	299	132	201	31		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	8	317	Total	C	N	O	0	0
			1574	937	318	319		

- Molecule 7 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	121	Total	C	N	O	P	0	0
			2594	1154	467	852	121		

- Molecule 8 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	71	Total	C	N	O	S	0	0
			555	347	103	98	7		

- Molecule 9 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	95	Total	C	N	O	0	0
			753	484	139	130		

- Molecule 10 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	32	Total	C	N	O	S	0	0
			257	161	43	51	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	32	Total	C	N	O	S	0	0
			255	163	43	48	1		

- Molecule 12 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	178	Total	C	N	O	S	0	0
			1455	925	260	256	14		

- Molecule 13 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	88	Total	C	N	O	S	0	0
			651	404	120	124	3		

- Molecule 14 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	96	Total	C	N	O	S	0	0
			767	476	160	126	5		

- Molecule 15 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	n	58	Total	C	N	O	S	0	0
			455	275	91	87	2		

- Molecule 16 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	u	603	Total	C	N	O	S	1	0
			4869	3071	879	896	23		

- Molecule 17 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	v	405	Total	C	N	O	S	0	0
			2740	1720	498	510	12		

- Molecule 18 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	x	63	Total	C	N	O	S	0	0
			525	331	88	104	2		

- Molecule 19 is a protein called Eukaryotic translation initiation factor 3 subunit C.

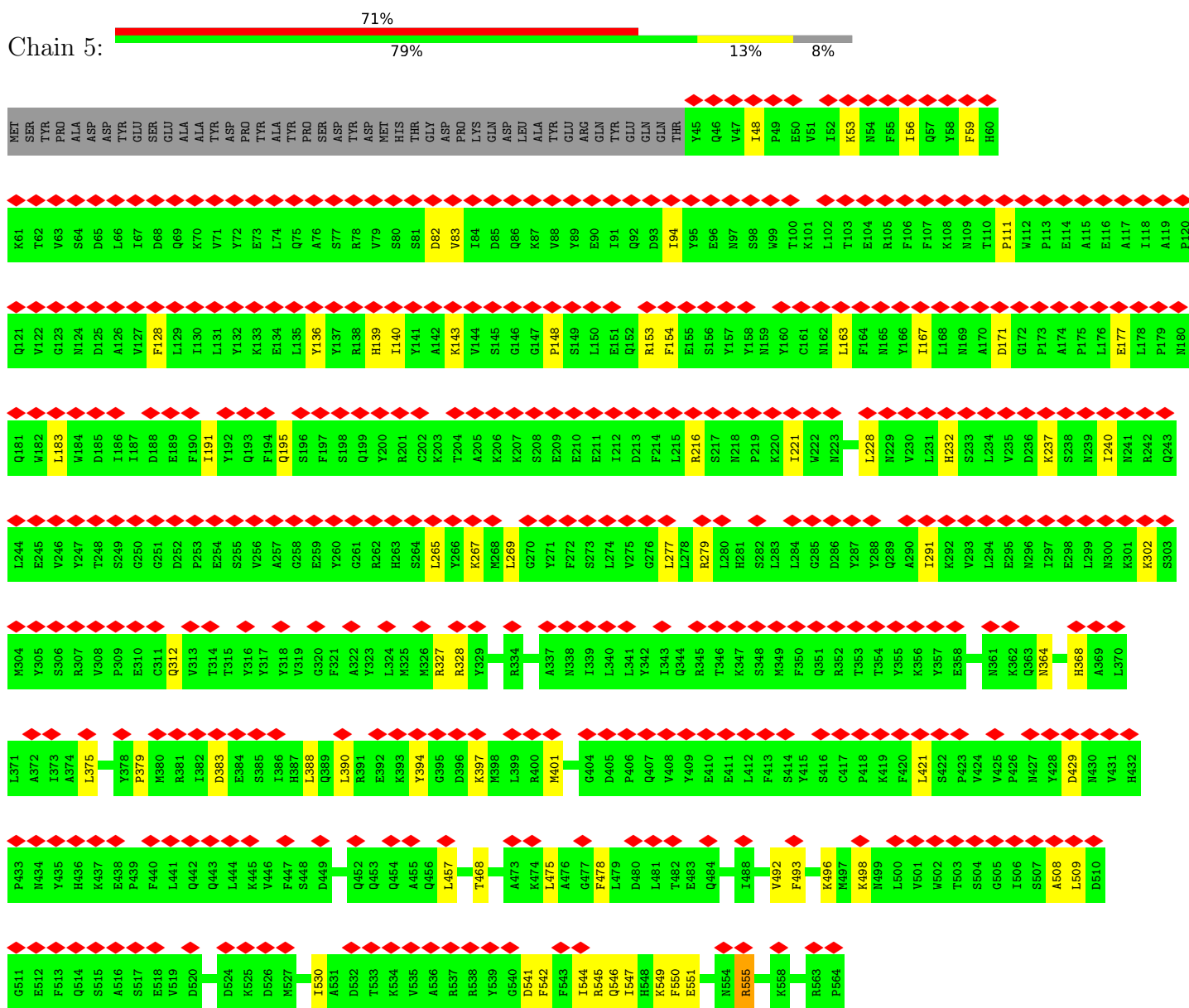
Mol	Chain	Residues	Atoms					AltConf	Trace
19	y	543	Total	C	N	O	S	0	0
			4361	2743	776	809	33		

- Molecule 20 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

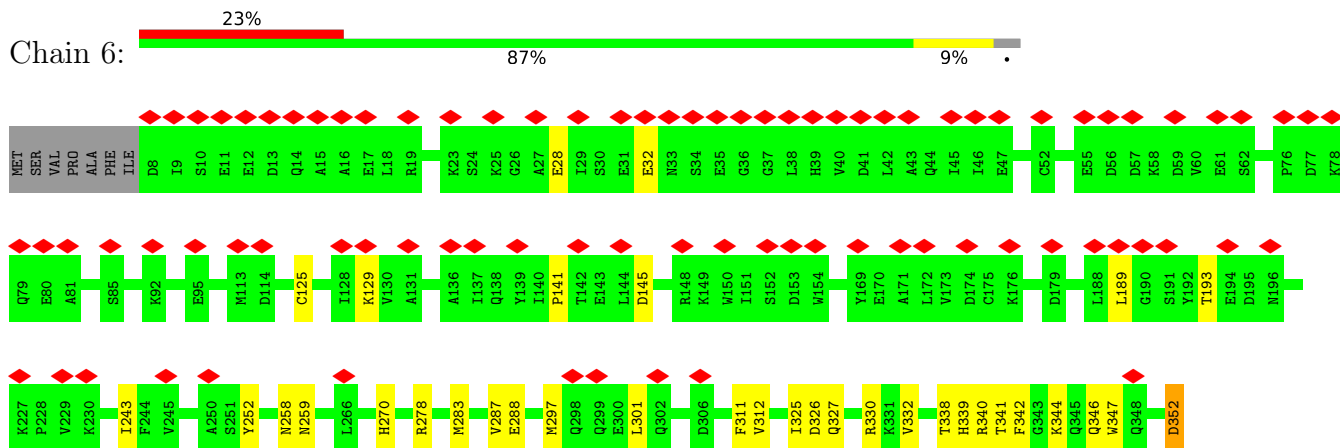
Mol	Chain	Residues	Atoms		AltConf
20	A	1	Total	Mg	0
			1	1	

- Molecule 21 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
21	Q	1	Total	Zn	0
			1	1	

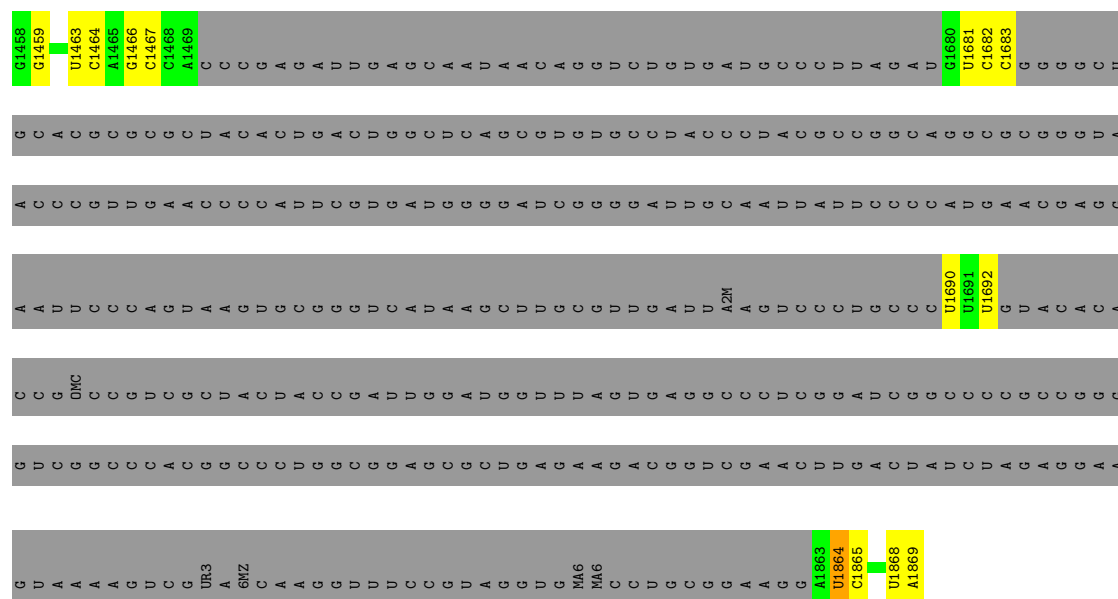


- Molecule 4: Eukaryotic translation initiation factor 3 subunit M





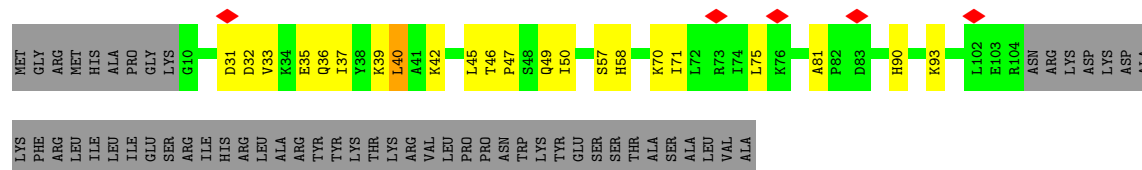




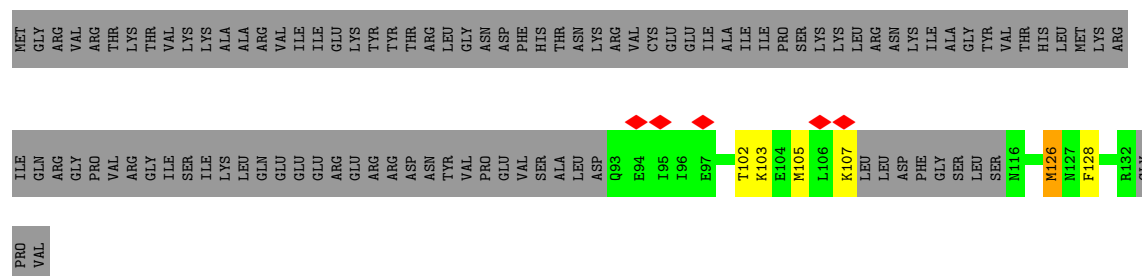
• Molecule 8: 40S ribosomal protein S27



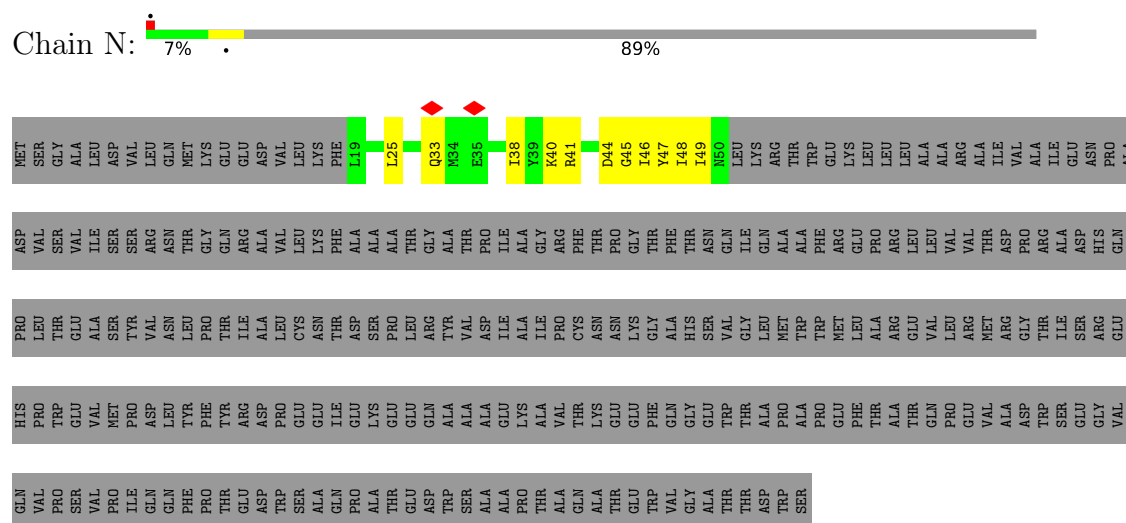
• Molecule 9: 40S ribosomal protein S13



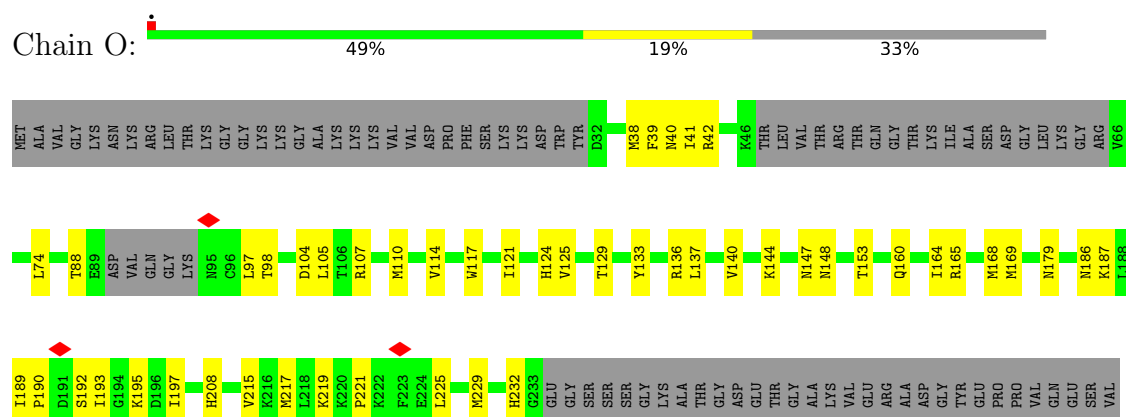
• Molecule 10: 40S ribosomal protein S17



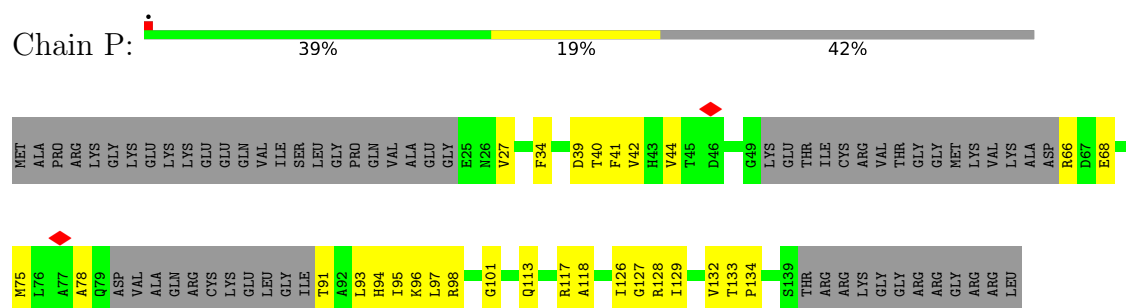
• Molecule 11: 40S ribosomal protein SA



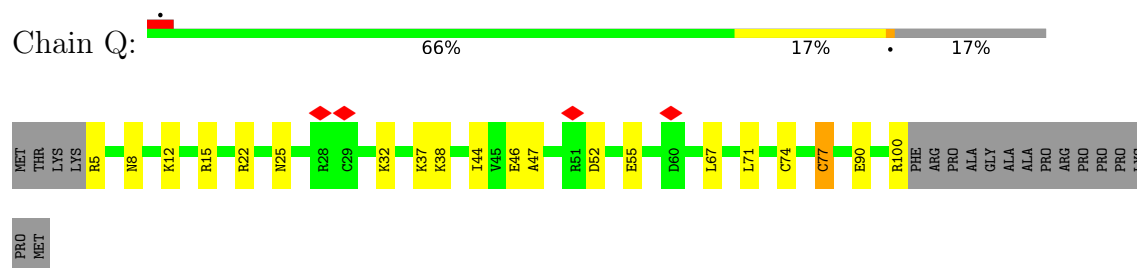
- Molecule 12: 40S ribosomal protein S3a



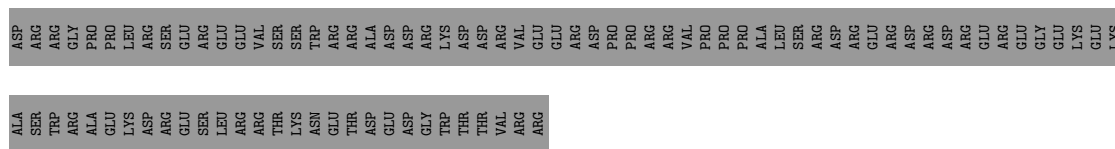
- Molecule 13: 40S ribosomal protein S14



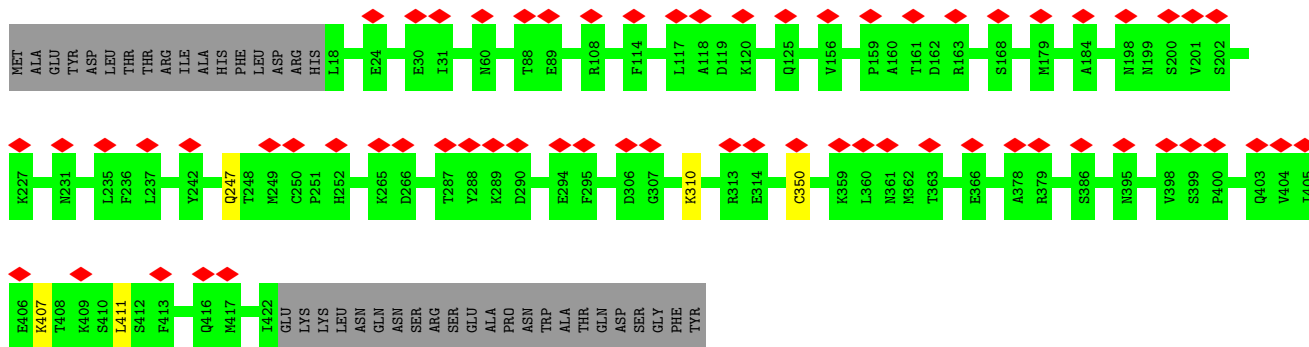
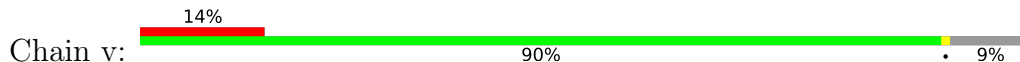
- Molecule 14: 40S ribosomal protein S26



- ASP ARG GLU ASP PHE ARG ARG PRO ASP GLY GLY TRP ARG ARG GLY PRO ALA GLU SER SER TRP ARG ASP ASP ASP ARG ARG ARG GLU ASP ARG ASP ASP ARG ARG ASP ARG LEU GLU ARG ARG ASP ARG ASP ARG ASP



- Molecule 17: Eukaryotic translation initiation factor 3 subunit E



- Molecule 18: Eukaryotic translation initiation factor 3 subunit D



- Molecule 19: Eukaryotic translation initiation factor 3 subunit C



HIS	PRO	TRP	ASP	SER	THR	MET
LYS	GLU	GLU	SER	SER	ASN	SER
GLN	GLY	GLN	GLU	ASP	LEU	ARG
THR	SER	VAL	GLU	GLU	ILE	PHE
TYR	SER	GLY	GLU	ASP	THR	ARG
GLY	SER	GLY	GLY	ASP	ILE	THR
GLY	GLU	VAL	LYS	GLU	ARG	GLY
TYR	GLN	PRO	GLN	GLU	ASN	SER
PHE	ASP	LEU	THR	GLY	MET	ASP
ARG	GLN	VAL	LEU	VAL	ASN	GLU
ASP	ALA	LYS	LEU	SER	LYS	SER
GLN	GLU	GLU	ALA	ALA	ILE	GLU
LYS	N539	LYS	SER	THR	ASN	GLY
ASP	E540	PRO	ARG	THR	ALA	SER
GLY	G541	LYS	PHE	PHE	LYS	SER
TYR	ARG	M317	LEU	LEU	ALA	LEU
ARG	D596	F318	LYS	LYS	LYS	THR
ASN	GLY	A319	ALA	LYS	THR	GLY
GLY	L625	K320	PRO	SER	LEU	LEU
GLY	L634	G321	THR	GLU	ARG	LEU
TYR	ARG	T322	THR	ALA	GLN	VAL
MET	ARG	E323	ASP	PRO	GLY	THR
ARG	G649	I324	GLU	SER	GLY	PRO
ARG	L650	T325	ASP	GLY	ARG	LYS
GLY	L651	H326	LYS	GLU	LYS	VAL
TYR	L652	ASN	LYS	SER	TYR	GLY
ARG	R653	N365	ALA	ARG	ASN	GLY
GLN	S654	E368	GLU	PHE	ARG	ASN
GLN	L655	GLY	LYS	LEU	ASP	TYR
SER	Q656	GLU	ARG	LYS	GLU	GLY
GLN	R657	G421	GLY	MET	SER	GLN
THR	R658	E422	ASP	ASP	ILE	LEU
ALA	N659	N423	LYS	ASP	THR	LEU
TYR	Q660	GLY	ALA	GLU	SER	LEU
	E661	GLY	LYS	ASP	TYR	LEU
	D704	E426	LYS	ASP	LYS	LEU
	A705	E427	LYS	GLU	GLY	GLU
	R706	S428	LYS	SER	GLN	GLU
	R707	E429	ASP	GLU	PRO	GLU
	L726	H432	LYS	SER	GLN	ASP
	M744	N433	ARG	GLU	SER	THR
	C752	A434	ARG	LEU	ALA	LYS
	L783	D435	ASP	GLY	GLU	VAL
	L831	Q436	ASP	THR	ALA	ARG
	Q837	P437	GLY	THR	GLU	SER
	P649	L438	GLU	ASP	ALA	ALA
	L857	R439	GLU	THR	LYS	LYS
	F874	V440	ASP	GLY	ASN	ASP
	D875	R441	ASN	THR	GLU	LYS
		L445	GLY	SER	ASP	PHE
		L508	GLY	ASP	SER	GLU
		R521	GLY	ASP	GLY	GLU
		Q522	GLU	ASP	GLY	LEU
		THR	PRO	SER	THR	PRO

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	356632	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	34.833	Depositor
Minimum map value	-15.718	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4	Depositor
Map size (Å)	278.4, 278.4, 278.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality

5.1 Standard geometry

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

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	3	0.24	0/1055	0.36	0/1469
2	4	0.24	0/1269	0.39	0/1762
3	5	0.29	0/4458	0.60	3/6027 (0.0%)
4	6	0.30	0/2212	0.59	2/3034 (0.1%)
5	7	0.54	4/744 (0.5%)	0.82	1/1156 (0.1%)
6	8	0.26	0/1572	0.43	0/2187
7	A	0.46	0/2889	1.09	10/4479 (0.2%)
8	H	0.39	0/565	0.82	1/755 (0.1%)
9	I	0.35	0/766	0.81	1/1032 (0.1%)
10	M	0.37	0/259	0.88	1/348 (0.3%)
11	N	0.36	0/259	0.96	1/347 (0.3%)
12	O	0.40	0/1475	0.85	3/1968 (0.2%)
13	P	0.34	0/661	0.79	1/891 (0.1%)
14	Q	0.44	1/780 (0.1%)	0.82	0/1047
15	n	0.35	0/456	1.04	4/610 (0.7%)
16	u	0.38	2/4961 (0.0%)	0.75	7/6713 (0.1%)
17	v	0.33	0/2778	0.69	3/3797 (0.1%)
18	x	0.36	0/539	0.79	1/727 (0.1%)
19	y	0.35	0/4436	0.75	11/5989 (0.2%)
All	All	0.35	7/32134 (0.0%)	0.75	50/44338 (0.1%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	7	-34	C	C1'-N1	5.99	1.57	1.48
16	u	350	GLU	C-N	5.95	1.47	1.34
5	7	-25	C	C1'-N1	5.91	1.57	1.48
5	7	-31	C	C1'-N1	5.67	1.57	1.48
14	Q	77	CYS	CB-SG	-5.66	1.72	1.81

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	u	342	LEU	N-CA-C	-9.46	85.46	111.00
19	y	726	LEU	CA-CB-CG	8.83	135.60	115.30
3	5	388	LEU	CA-CB-CG	7.85	133.34	115.30
10	M	126	MET	CA-CB-CG	7.58	126.19	113.30
9	I	40	LEU	CA-CB-CG	7.49	132.53	115.30

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	3	1057	0	475	3	0
2	4	1272	0	564	3	0
3	5	4347	0	4294	44	0
4	6	2196	0	1547	22	0
5	7	663	0	341	1	0
6	8	1574	0	687	3	0
7	A	2594	0	1317	24	0
8	H	555	0	576	6	0
9	I	753	0	814	15	0
10	M	257	0	262	3	0
11	N	255	0	250	5	0
12	O	1455	0	1519	29	0
13	P	651	0	644	18	0
14	Q	767	0	808	16	0
15	n	455	0	475	0	0
16	u	4869	0	4861	0	0
17	v	2740	0	2251	0	0
18	x	525	0	476	0	0
19	y	4361	0	4335	0	0
20	A	1	0	0	0	0
21	Q	1	0	0	0	0
All	All	31348	0	26496	179	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 9.

The worst 5 of 179 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)
7:A:925:G:H1	7:A:1017:U:H3	1.39	0.70
13:P:75:MET:HG2	13:P:118:ALA:HB2	1.73	0.70
10:M:102:THR:HA	10:M:105:MET:HG2	1.73	0.70
12:O:217:MET:SD	12:O:217:MET:N	2.68	0.66
3:5:48:ILE:HB	3:5:53:LYS:HE3	1.80	0.64

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	
1	3	209/218 (96%)	202 (97%)	7 (3%)	0	100	100
2	4	251/357 (70%)	235 (94%)	16 (6%)	0	100	100
3	5	518/564 (92%)	501 (97%)	17 (3%)	0	100	100
4	6	360/374 (96%)	339 (94%)	21 (6%)	0	100	100
6	8	313/352 (89%)	289 (92%)	24 (8%)	0	100	100
8	H	69/84 (82%)	67 (97%)	2 (3%)	0	100	100
9	I	93/151 (62%)	87 (94%)	6 (6%)	0	100	100
10	M	28/135 (21%)	27 (96%)	1 (4%)	0	100	100
11	N	30/295 (10%)	28 (93%)	2 (7%)	0	100	100
12	O	172/264 (65%)	163 (95%)	9 (5%)	0	100	100
13	P	82/151 (54%)	77 (94%)	5 (6%)	0	100	100
14	Q	94/115 (82%)	89 (95%)	5 (5%)	0	100	100
15	n	56/69 (81%)	51 (91%)	5 (9%)	0	100	100
16	u	602/1382 (44%)	552 (92%)	49 (8%)	1 (0%)	44	72

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	v	403/445 (91%)	367 (91%)	36 (9%)	0	100	100
18	x	59/548 (11%)	52 (88%)	7 (12%)	0	100	100
19	y	539/913 (59%)	513 (95%)	26 (5%)	0	100	100
All	All	3878/6417 (60%)	3639 (94%)	238 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	u	337	ASP

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	5	477/515 (93%)	477 (100%)	0	100	100
4	6	112/335 (33%)	112 (100%)	0	100	100
6	8	1/310 (0%)	1 (100%)	0	100	100
8	H	64/76 (84%)	63 (98%)	1 (2%)	58	75
9	I	83/131 (63%)	83 (100%)	0	100	100
10	M	31/122 (25%)	31 (100%)	0	100	100
11	N	26/243 (11%)	25 (96%)	1 (4%)	28	54
12	O	164/231 (71%)	164 (100%)	0	100	100
13	P	69/119 (58%)	69 (100%)	0	100	100
14	Q	83/98 (85%)	82 (99%)	1 (1%)	67	80
15	n	51/62 (82%)	51 (100%)	0	100	100
16	u	528/1259 (42%)	524 (99%)	4 (1%)	79	87
17	v	206/406 (51%)	204 (99%)	2 (1%)	73	83
18	x	55/494 (11%)	55 (100%)	0	100	100
19	y	472/811 (58%)	471 (100%)	1 (0%)	92	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2422/5212 (46%)	2412 (100%)	10 (0%)	88 93

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	v	310	LYS
17	v	407	LYS
19	y	439	ARG
16	u	169	ARG
16	u	335	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
17	v	247	GLN
17	v	377	ASN
19	y	662	GLN
17	v	416	GLN
16	u	522	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	7	30/255 (11%)	17 (56%)	2 (6%)
7	A	109/1869 (5%)	34 (31%)	1 (0%)
All	All	139/2124 (6%)	51 (36%)	3 (2%)

5 of 51 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	7	-33	A
5	7	-30	A
5	7	-28	C
5	7	-27	A
5	7	-26	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	7	-21	A

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Mol	Chain	Res	Type
5	7	-10	A
7	A	1682	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 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.

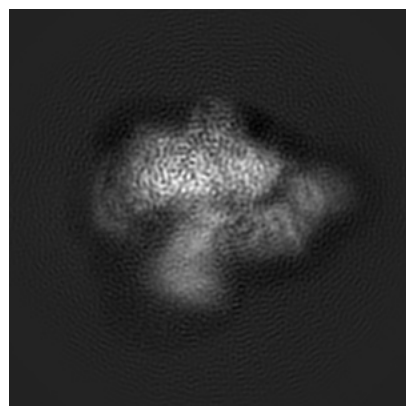
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19128. These allow visual inspection of the internal detail of the map and identification of artifacts.

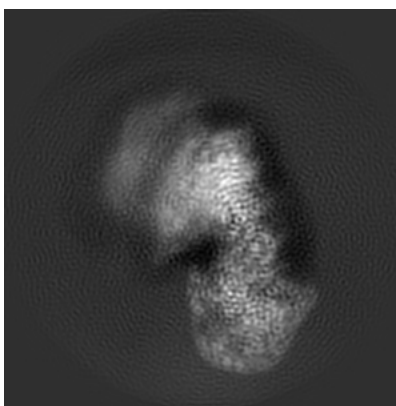
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

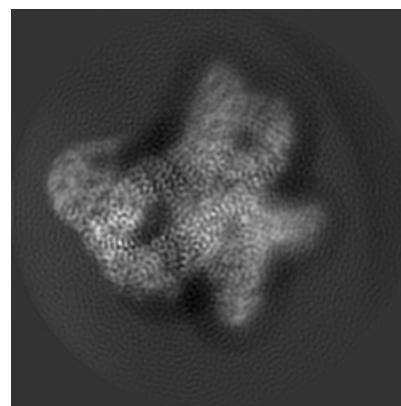
6.1.1 Primary map



X

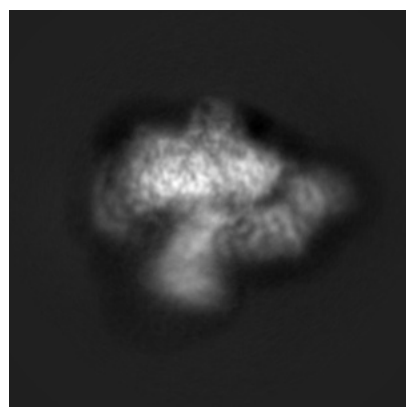


Y

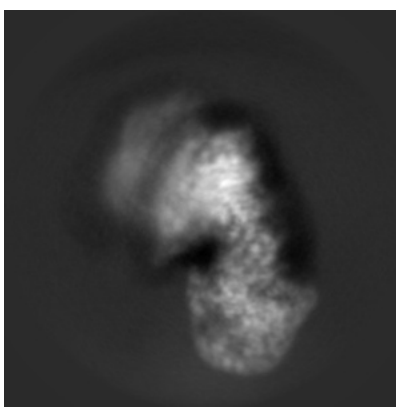


Z

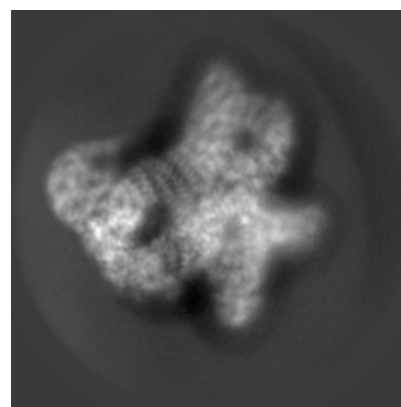
6.1.2 Raw map



X



Y

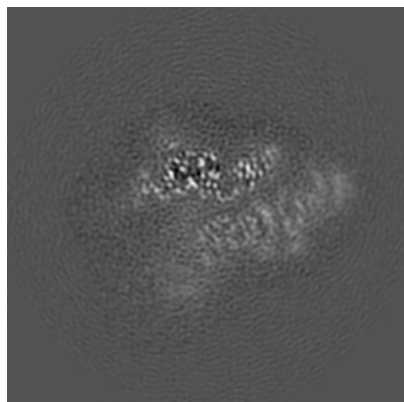


Z

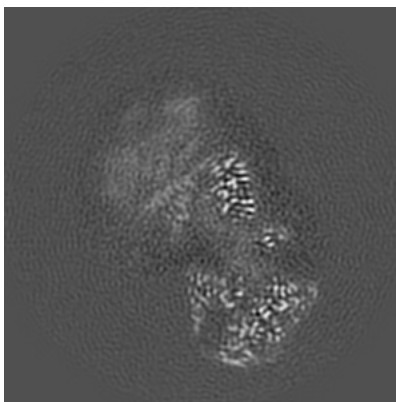
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

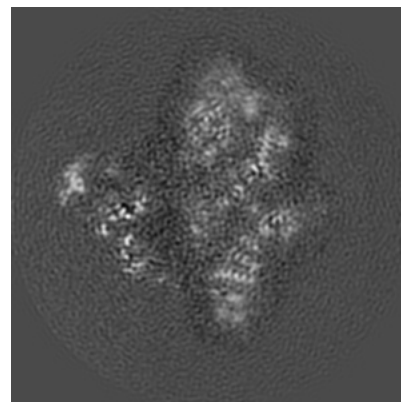
6.2.1 Primary map



X Index: 120

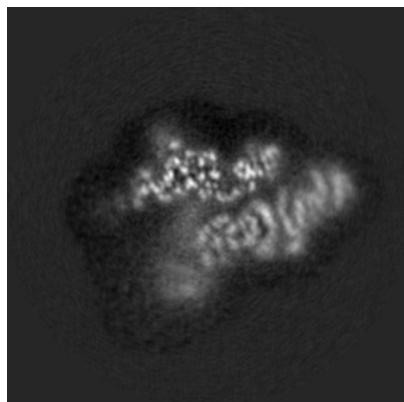


Y Index: 120

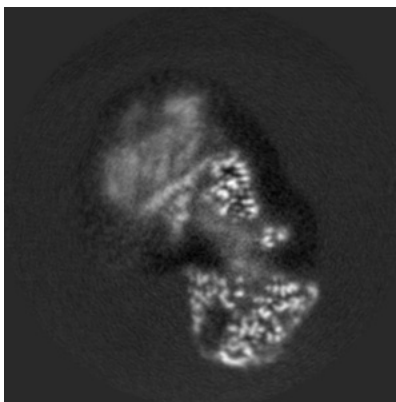


Z Index: 120

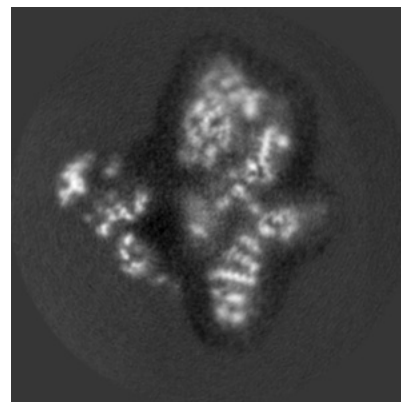
6.2.2 Raw map



X Index: 120



Y Index: 120

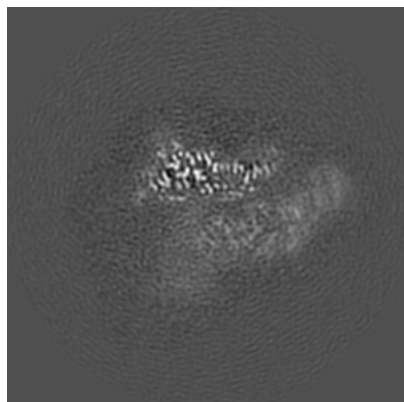


Z Index: 120

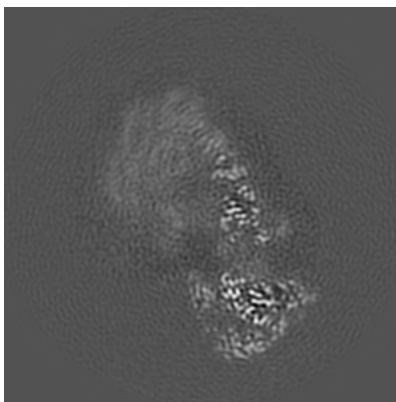
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

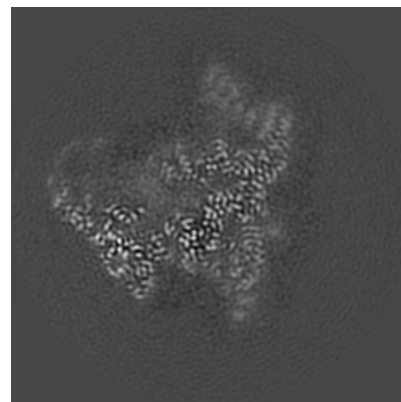
6.3.1 Primary map



X Index: 118

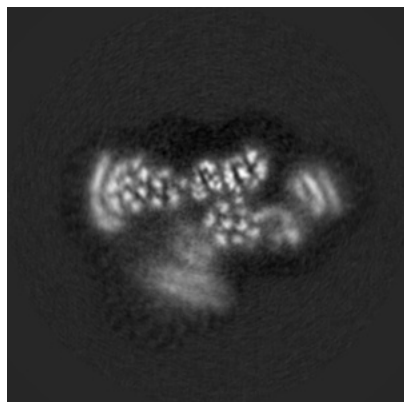


Y Index: 114

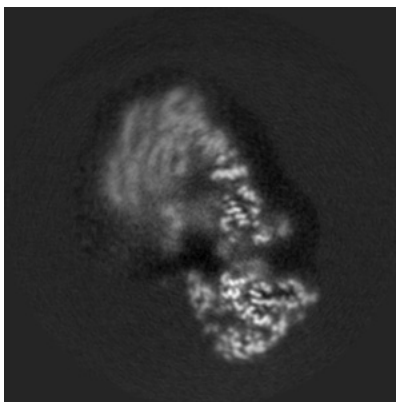


Z Index: 137

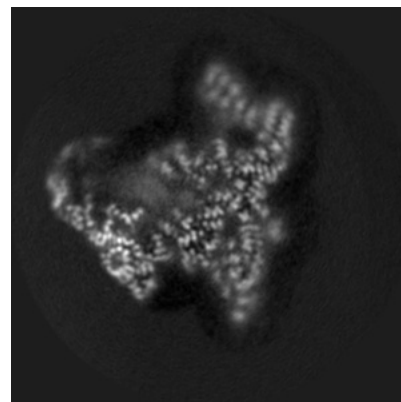
6.3.2 Raw map



X Index: 137



Y Index: 114

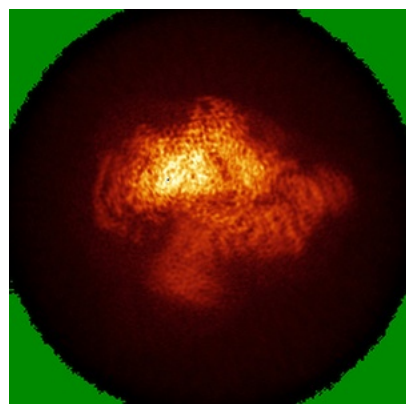


Z Index: 136

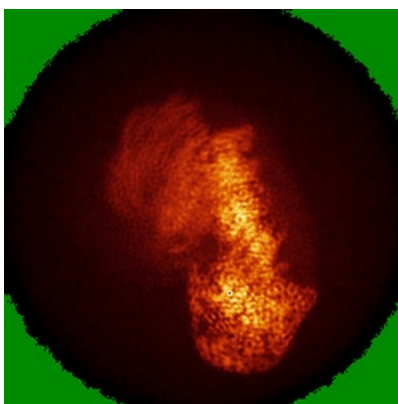
The images above show the largest variance slices of the map in three orthogonal directions.

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

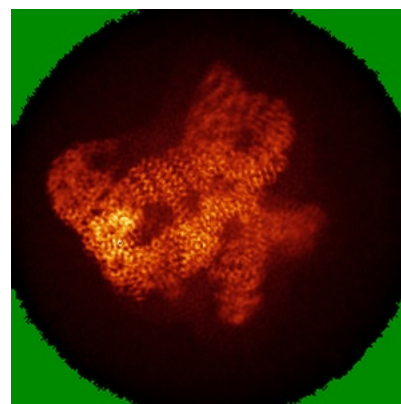
6.4.1 Primary map



X

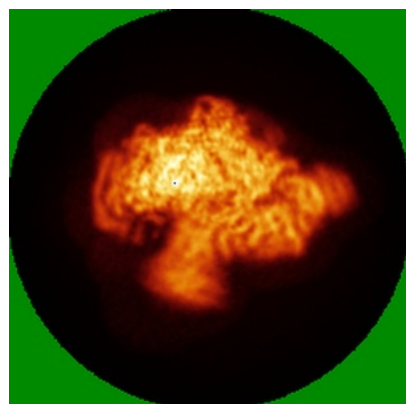


Y

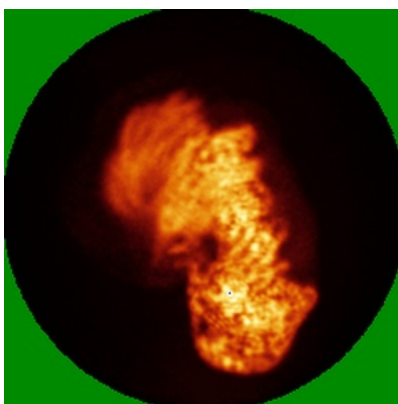


Z

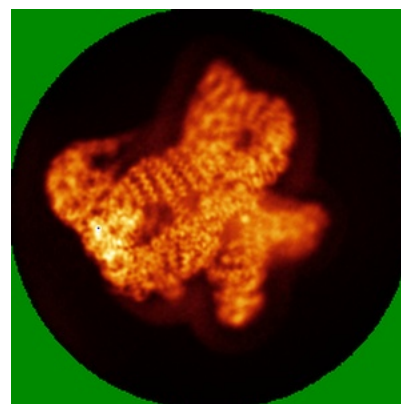
6.4.2 Raw map



X



Y

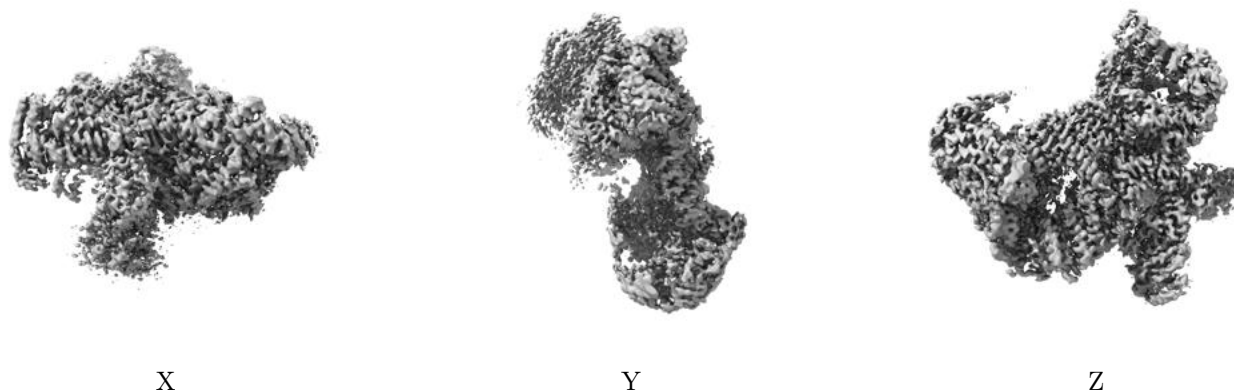


Z

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.

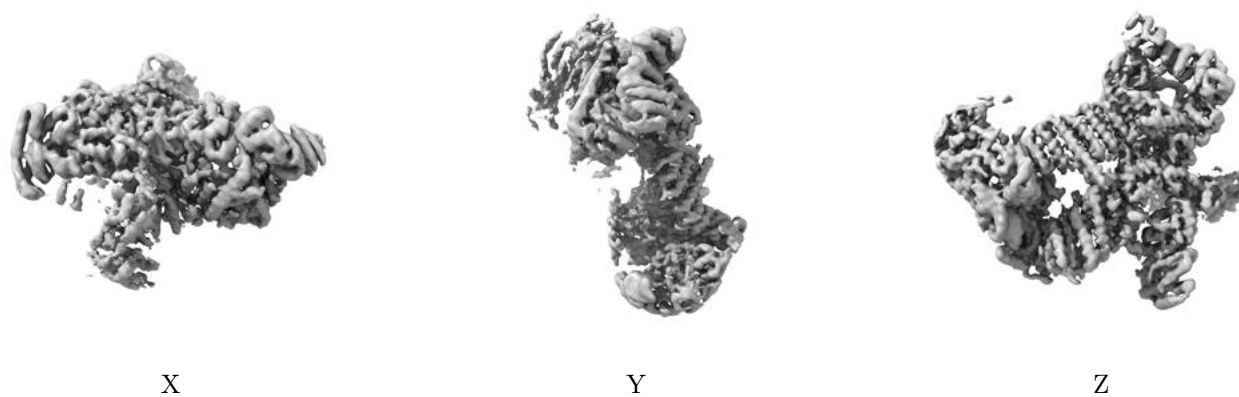
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

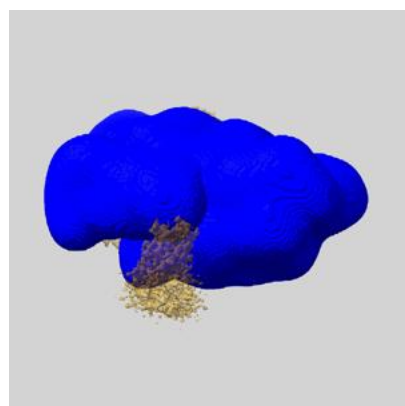
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

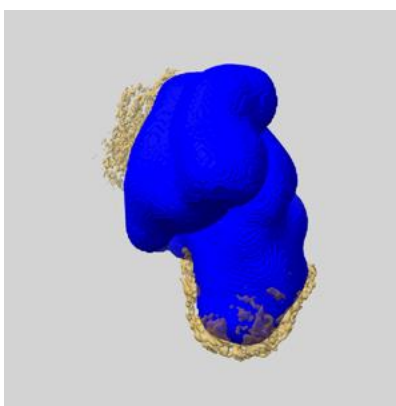
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

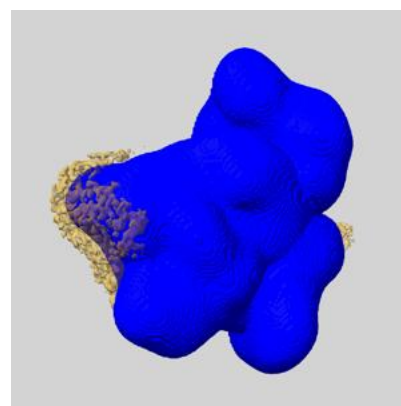
6.6.1 emd_19128_msk_1.map [i](#)



X



Y

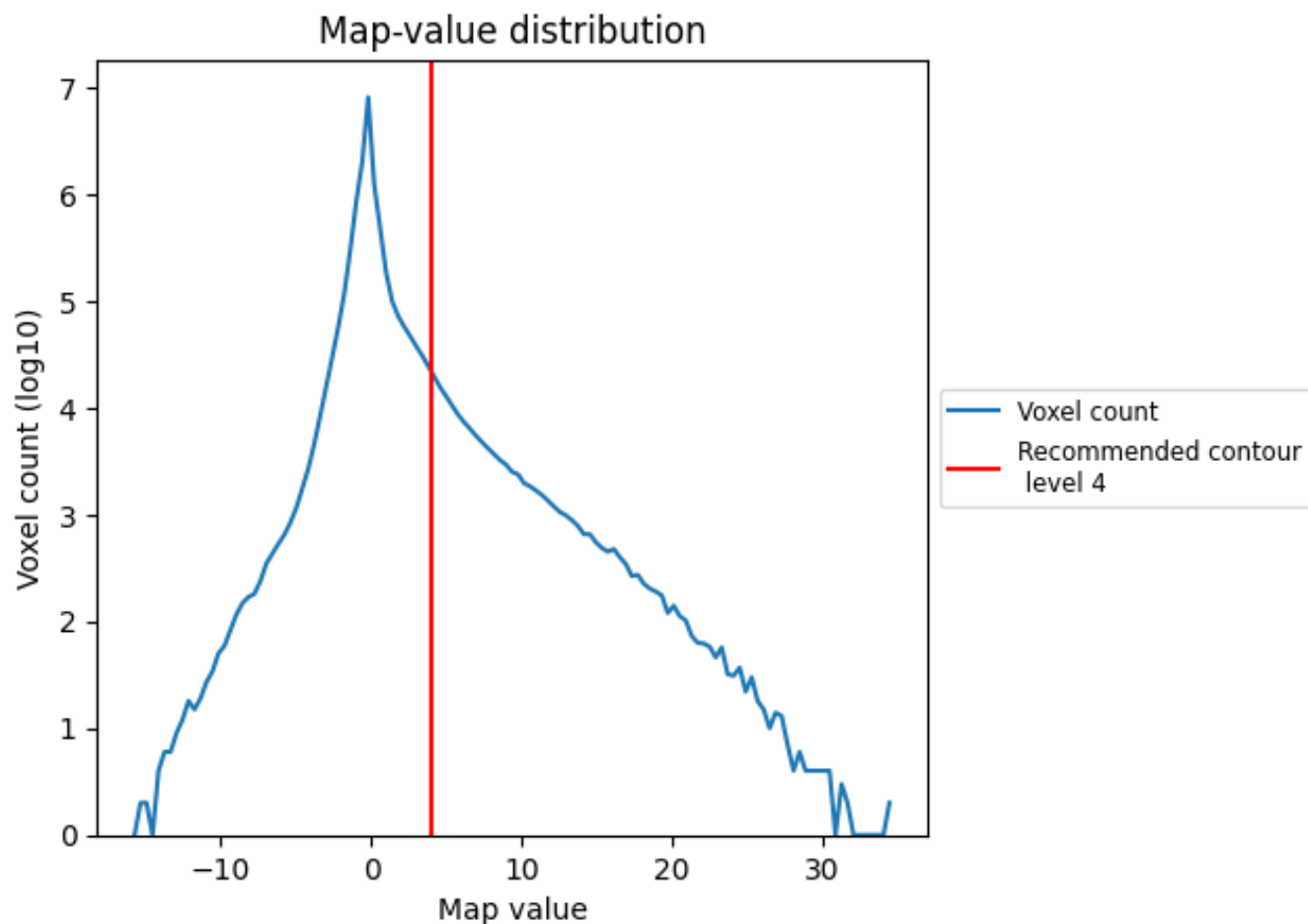


Z

7 Map analysis [i](#)

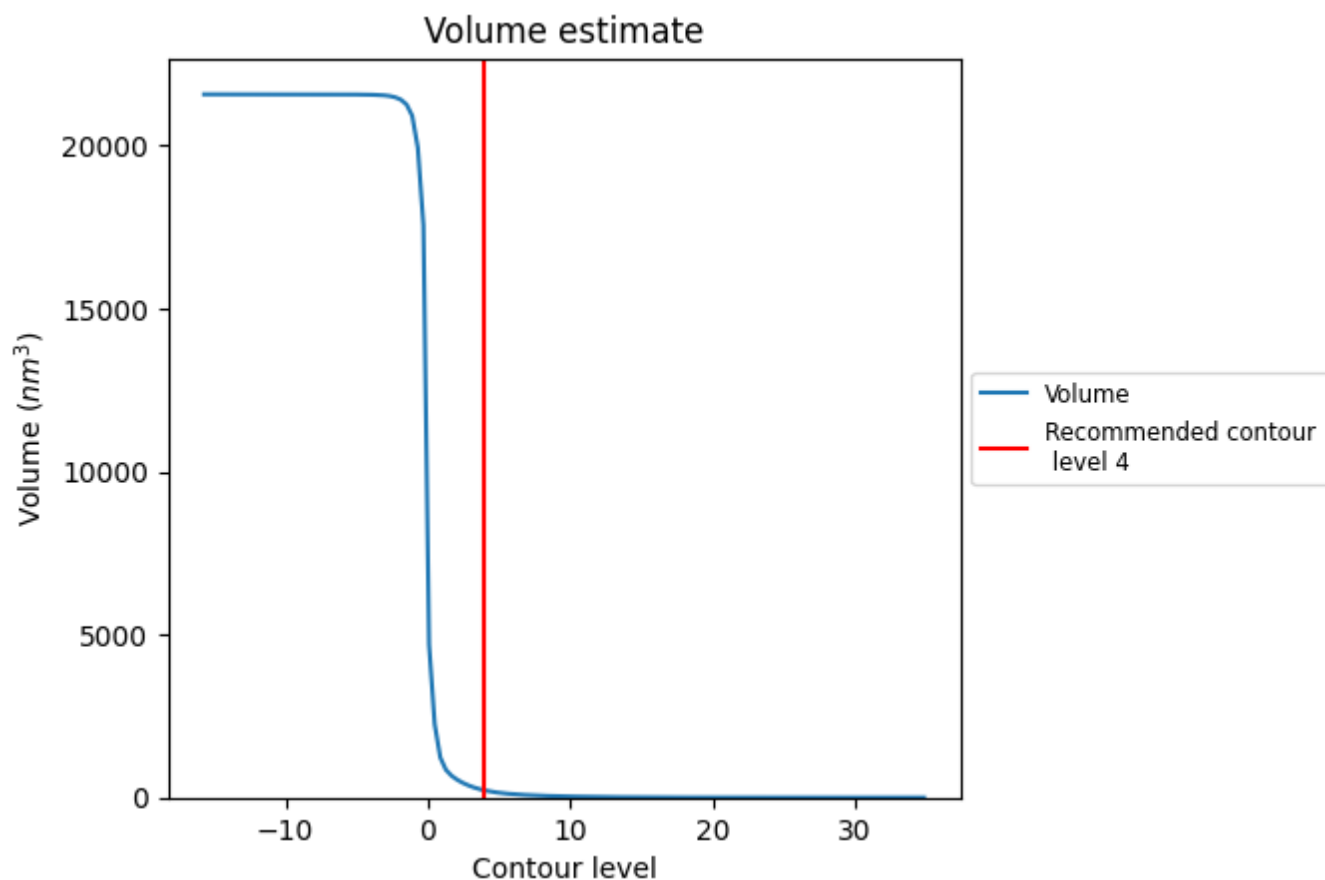
This section contains the results of statistical analysis of the map.

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.

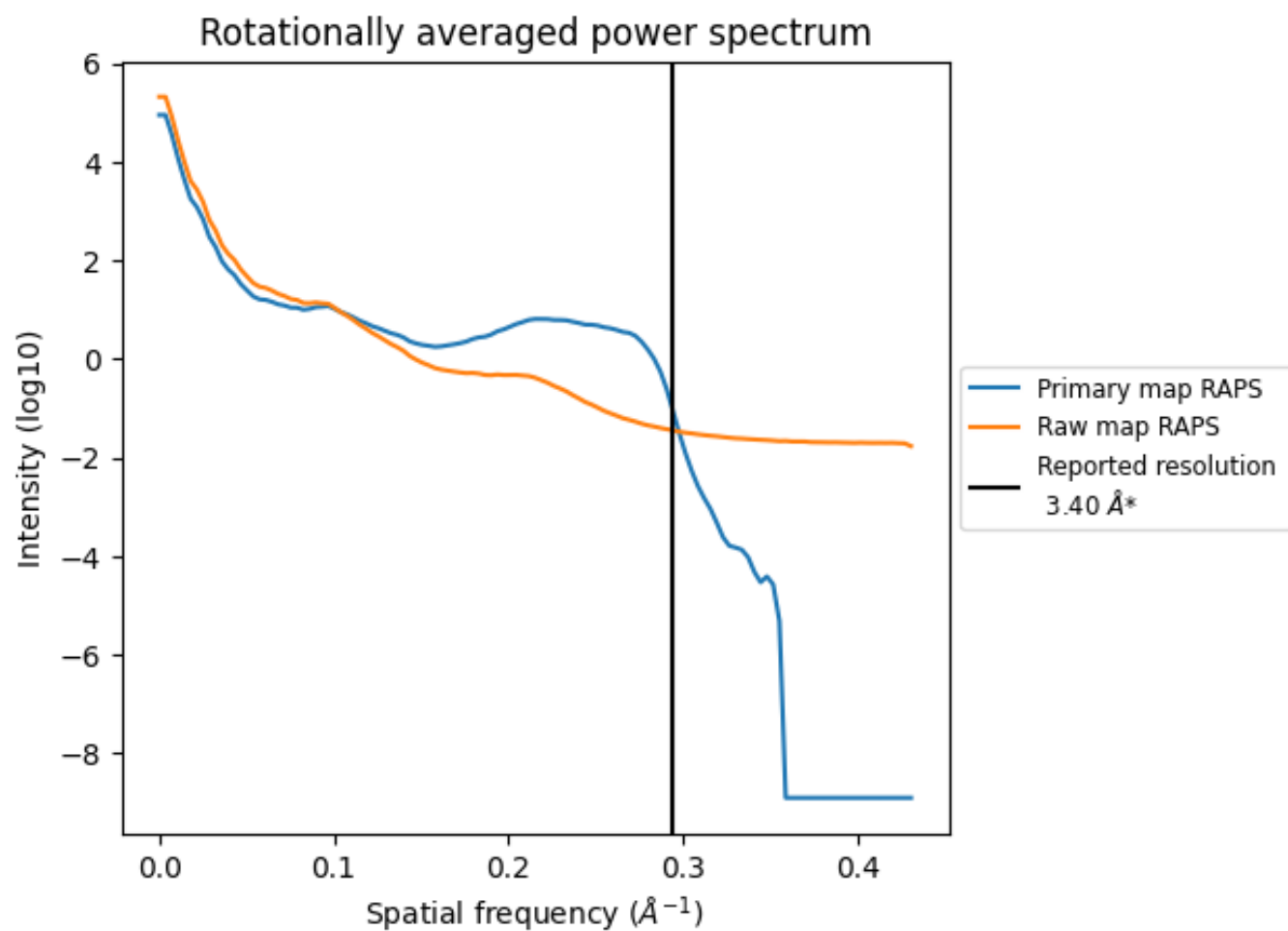
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 219 nm^3 ; this corresponds to an approximate mass of 198 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 ⓘ

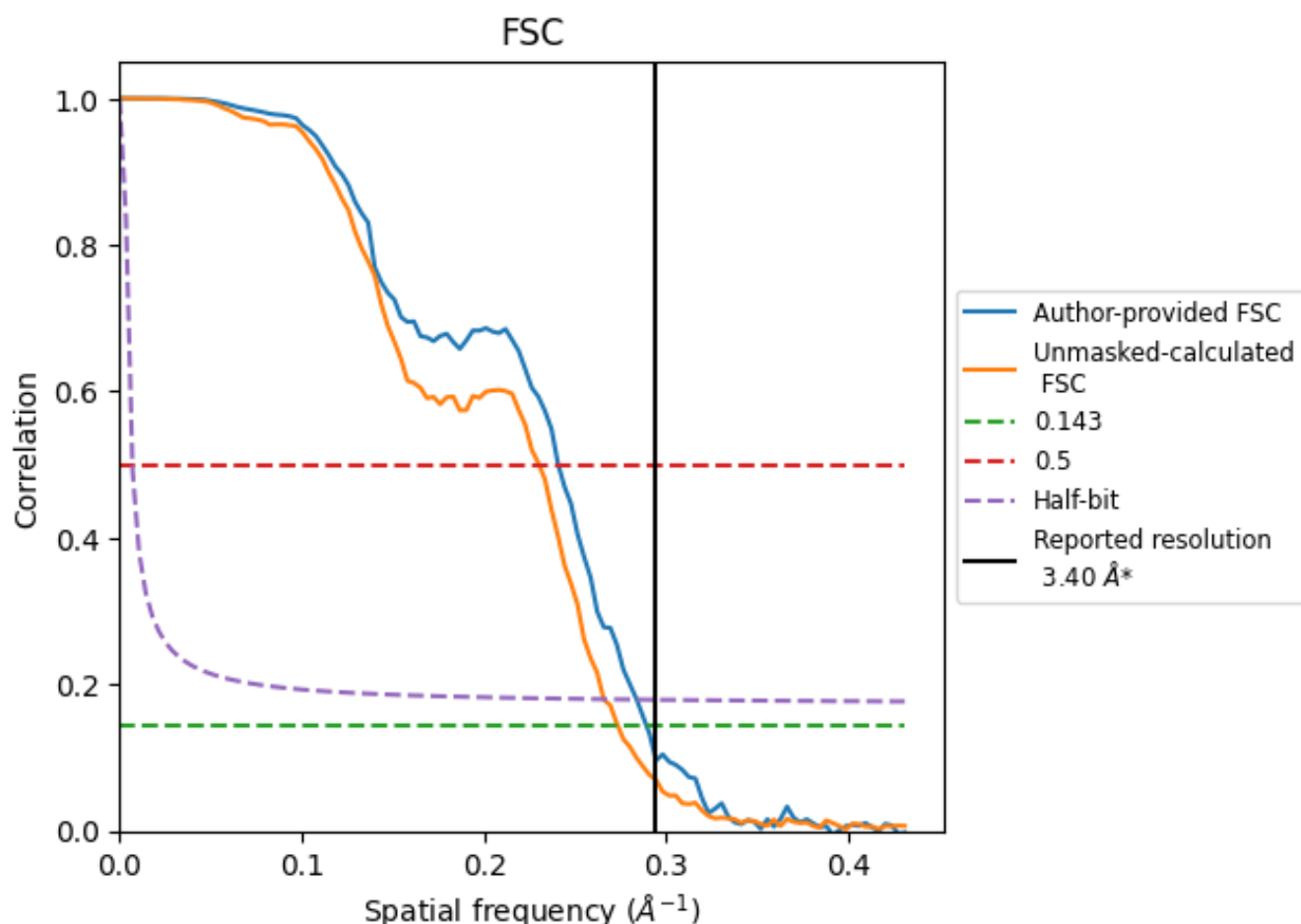


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 \AA^{-1}

8.2 Resolution estimates [i](#)

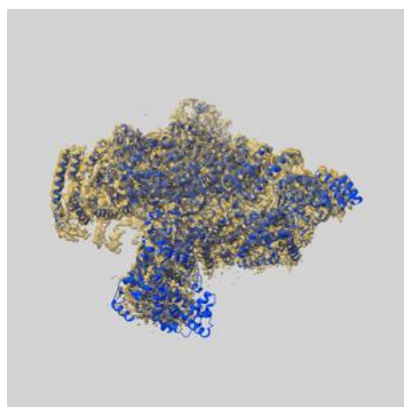
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.46	4.15	3.52
Unmasked-calculated*	3.66	4.34	3.76

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

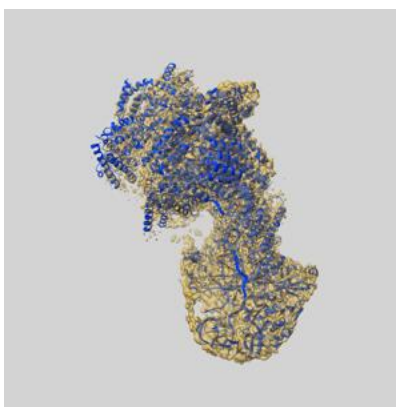
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19128 and PDB model 8RG0. Per-residue inclusion information can be found in section [3](#) on page [8](#).

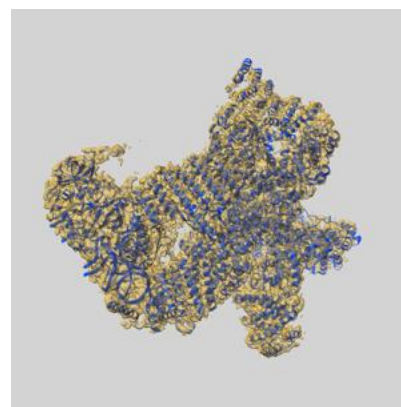
9.1 Map-model overlay [i](#)



X



Y



Z

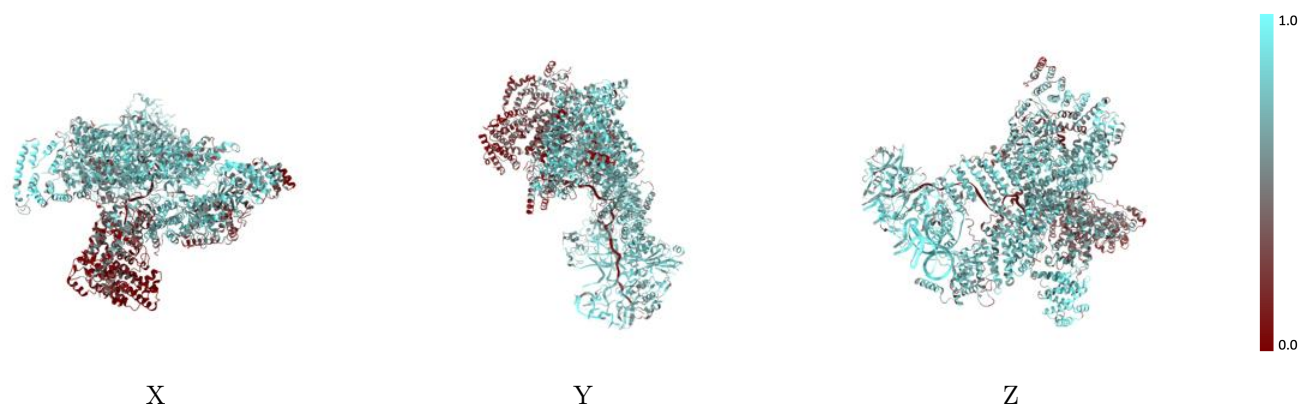
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



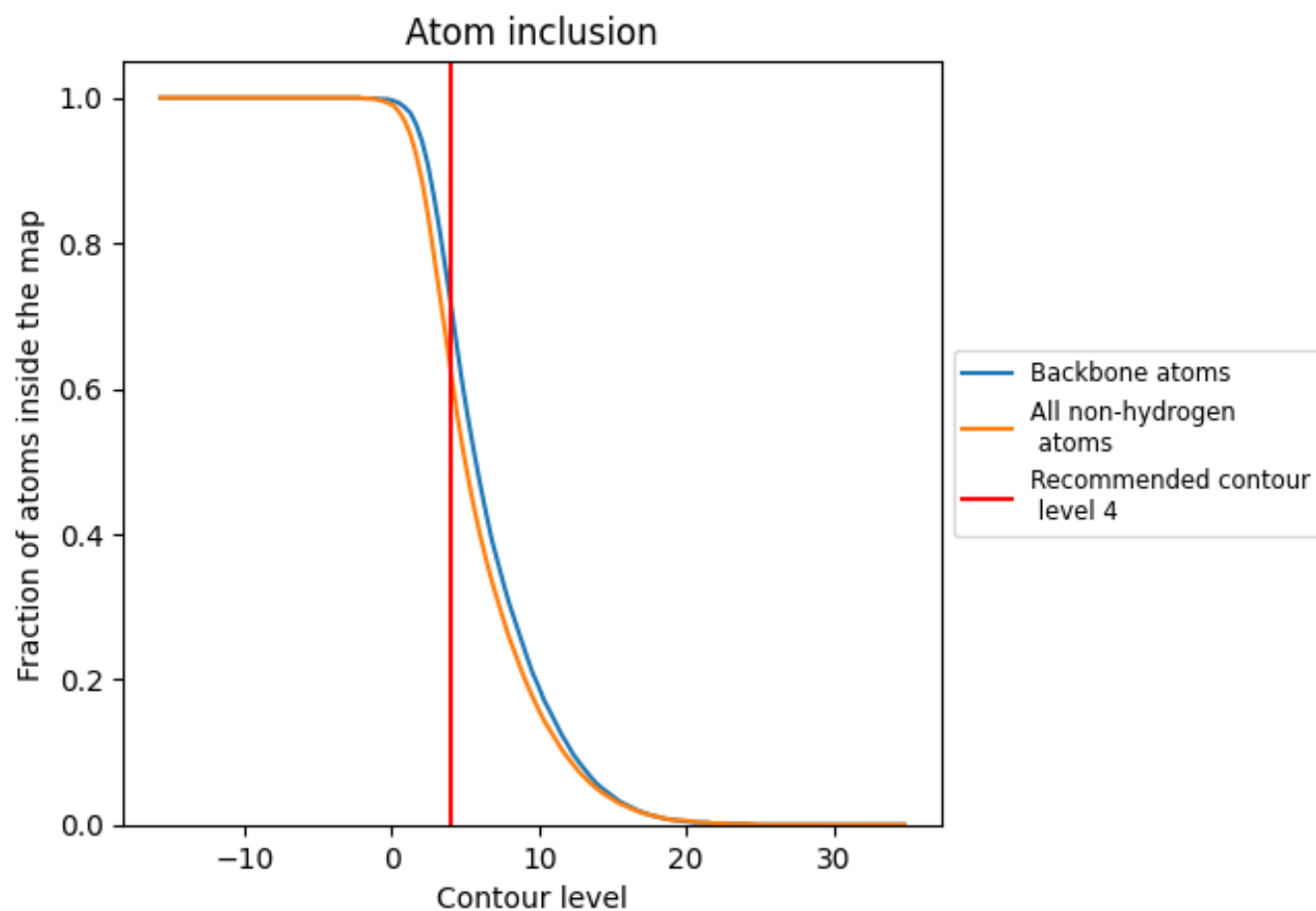
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).









































9.4 Atom inclusion [i](#)



At the recommended contour level, 72% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6240	 0.3030
3	 0.3170	 0.1290
4	 0.6930	 0.2850
5	 0.2280	 0.0850
6	 0.6530	 0.2700
7	 0.1820	 0.1020
8	 0.5900	 0.2470
A	 0.9080	 0.4280
H	 0.7840	 0.4270
I	 0.7550	 0.3900
M	 0.6590	 0.3480
N	 0.6880	 0.3580
O	 0.8010	 0.4400
P	 0.7480	 0.3970
Q	 0.7690	 0.4170
n	 0.5450	 0.3240
u	 0.6820	 0.3490
v	 0.6730	 0.2950
x	 0.6530	 0.3260
y	 0.7270	 0.3920

