



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 05:09 PM UTC

PDB ID : 6G18 / pdb_00006g18
EMDB ID : EMD-4337
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - State C
Authors : Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on : 2018-03-20
Resolution : 3.60 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:

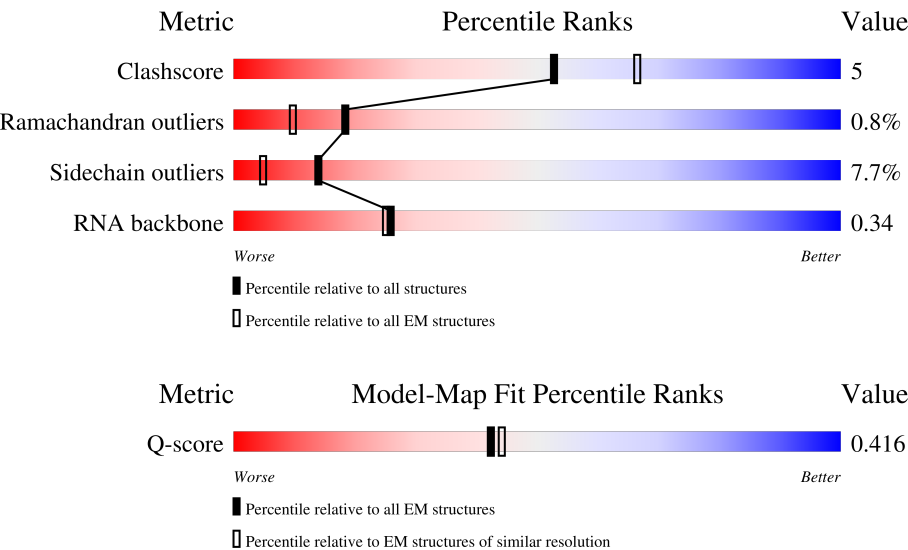
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.60 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.



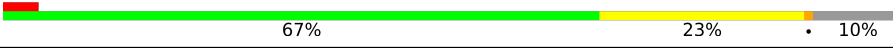
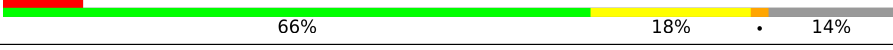
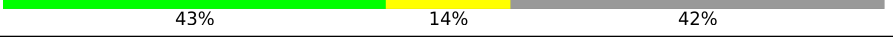
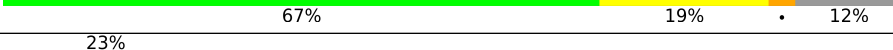
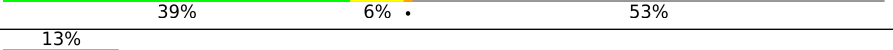
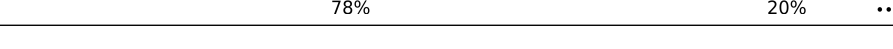
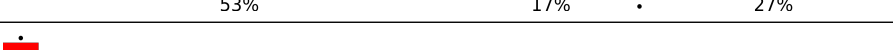
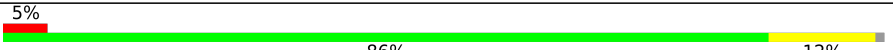
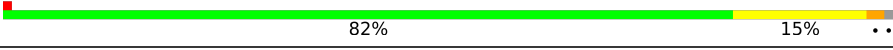
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	
2	F	204	
3	M	132	

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Mol	Chain	Length	Quality of chain
4	P	145	
5	Q	146	
6	R	135	
7	S	152	
8	T	145	
9	Z	125	
10	c	69	
11	f	156	
12	g	317	
13	A	295	
14	B	264	
15	C	293	
16	E	263	
17	G	249	
18	H	194	
19	I	208	
20	J	194	
21	L	158	
22	N	151	
23	O	151	
24	V	83	
25	W	130	
26	X	143	
27	Y	133	
28	b	84	

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Mol	Chain	Length	Quality of chain
29	e	59	
30	x	252	
31	y	412	
32	u	804	
33	w	437	
34	v	552	
35	t	475	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 83819 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 pre-18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1658	Total	C	N	O	P	0	0
			35407	15804	6362	11584	1657		

- Molecule 2 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 3 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 4 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 5 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Q	122	Total	C	N	O	S	0	0
			969	616	180	170	3		

- Molecule 6 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	122	Total	C	N	O	S	0	0
			990	621	184	182	3		

- Molecule 7 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S	130	Total	C	N	O	S	0	0
			1083	686	214	182	1		

- Molecule 8 is a protein called 40S ribosomal protein S19.

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

- Molecule 9 is a protein called 40S ribosomal protein S25.

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

- Molecule 10 is a protein called 40S ribosomal protein S28.

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

- Molecule 11 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	f	73	Total	C	N	O	S	0	0
			596	375	115	99	7		

- Molecule 12 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	g	313	Total	C	N	O	S	0	0
			2433	1533	424	464	12		

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

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

- Molecule 14 is a protein called 40S ribosomal protein S3a.

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

- Molecule 15 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 16 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 17 is a protein called 40S ribosomal protein S6.

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

- Molecule 18 is a protein called 40S ribosomal protein S7.

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

- Molecule 19 is a protein called 40S ribosomal protein S8.

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

- Molecule 20 is a protein called 40S ribosomal protein S9.

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

- Molecule 21 is a protein called 40S ribosomal protein S11.

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

- Molecule 22 is a protein called 40S ribosomal protein S13.

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

- 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 S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 25 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 26 is a protein called 40S ribosomal protein S23.

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

- Molecule 27 is a protein called 40S ribosomal protein S24.

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

- Molecule 28 is a protein called 40S ribosomal protein S27.

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

- Molecule 29 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	55	Total	C	N	O	S	0	0
			438	271	95	71	1		

- Molecule 30 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	x	178	Total	C	N	O	S	0	0
			1391	891	252	244	4		

- Molecule 31 is a protein called RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	325	Total	C	N	O	S	0	0
			2568	1622	473	463	10		

- Molecule 32 is a protein called Pre-rRNA-processing protein TSR1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	u	629	Total	C	N	O	S	0	0
			5062	3249	902	887	24		

- Molecule 33 is a protein called Bystin.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	w	249	Total	C	N	O	S	0	0
			2027	1322	354	342	9		

- Molecule 34 is a protein called Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	v	325	Total	C	N	O	S	0	0
			2593	1649	460	470	14		

- Molecule 35 is a protein called Protein LTV1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	t	127	Total	C	N	O	S	0	0
			1066	661	204	199	2		

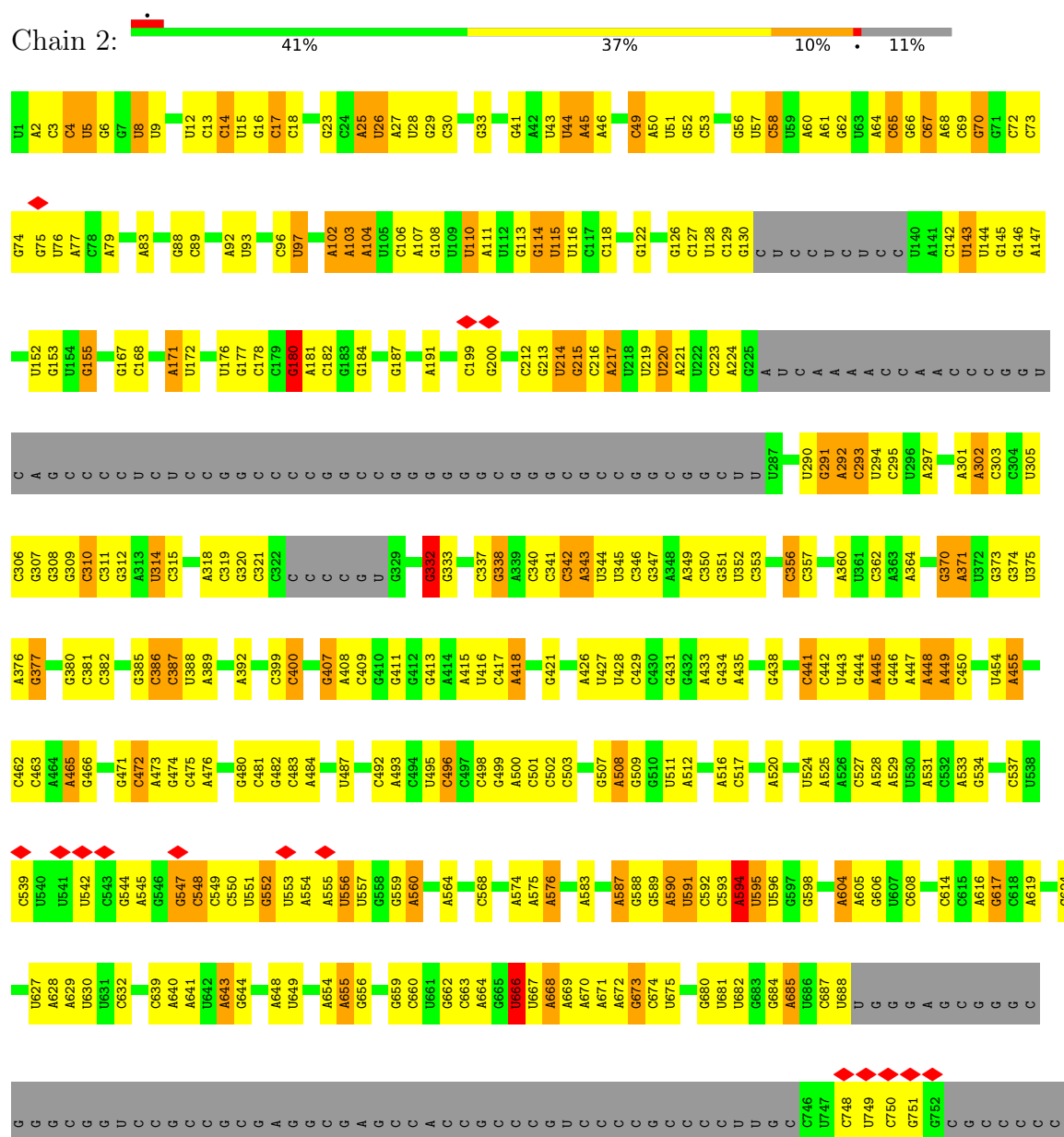
- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

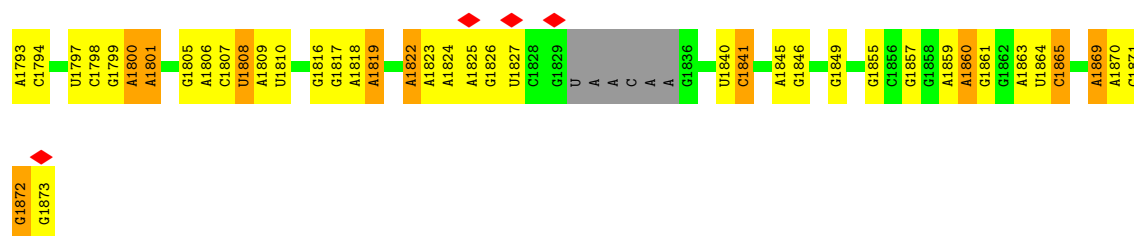
3 Residue-property plots

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.

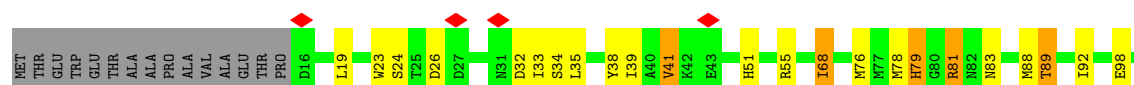
- Molecule 1: pre-18S ribosomal RNA



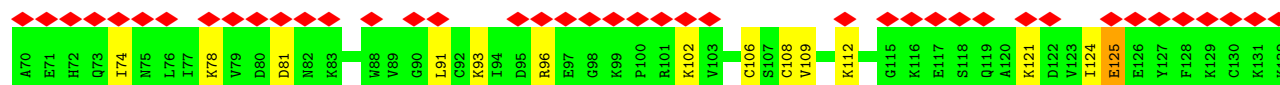
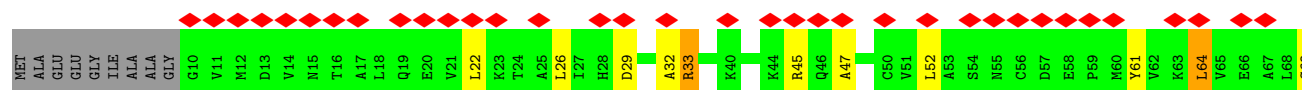
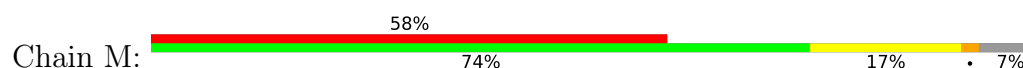




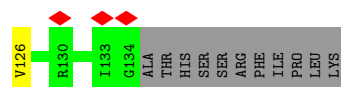
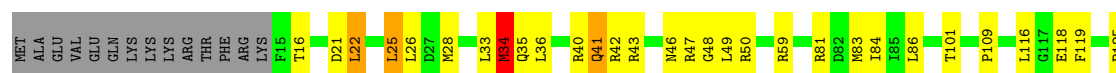
• Molecule 2: 40S ribosomal protein S5



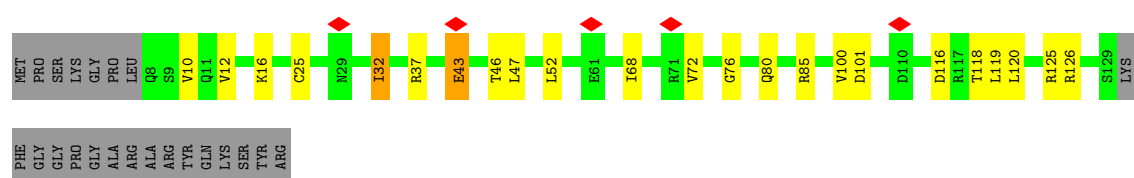
• Molecule 3: 40S ribosomal protein S12



• Molecule 4: 40S ribosomal protein S15

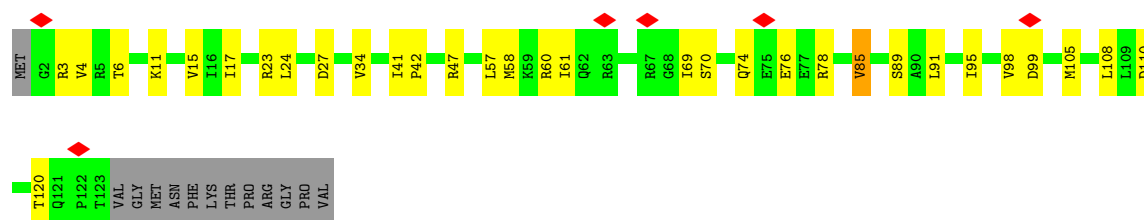


• Molecule 5: 40S ribosomal protein S16



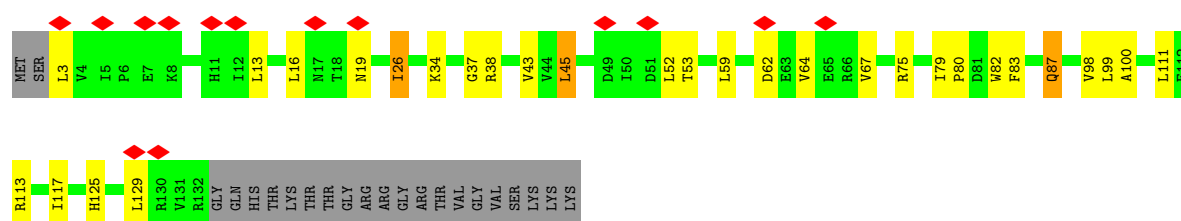
- Molecule 6: 40S ribosomal protein S17

Chain R: 



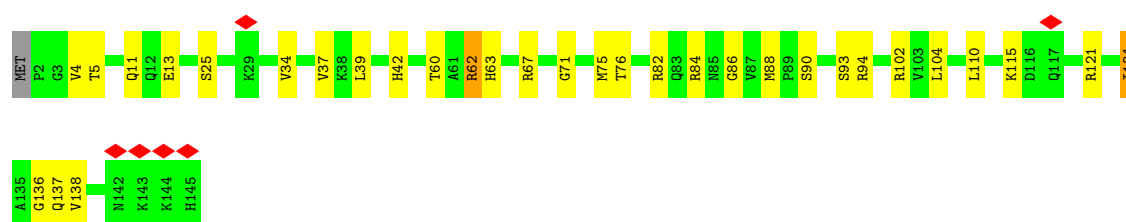
- Molecule 7: 40S ribosomal protein S18

Chain S: 

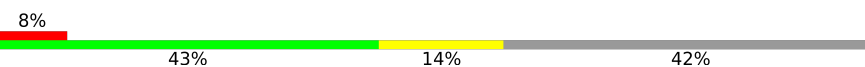


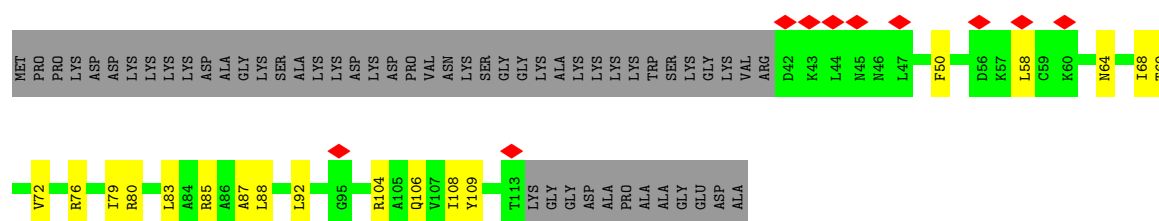
- Molecule 8: 40S ribosomal protein S19

Chain T: 



- Molecule 9: 40S ribosomal protein S25

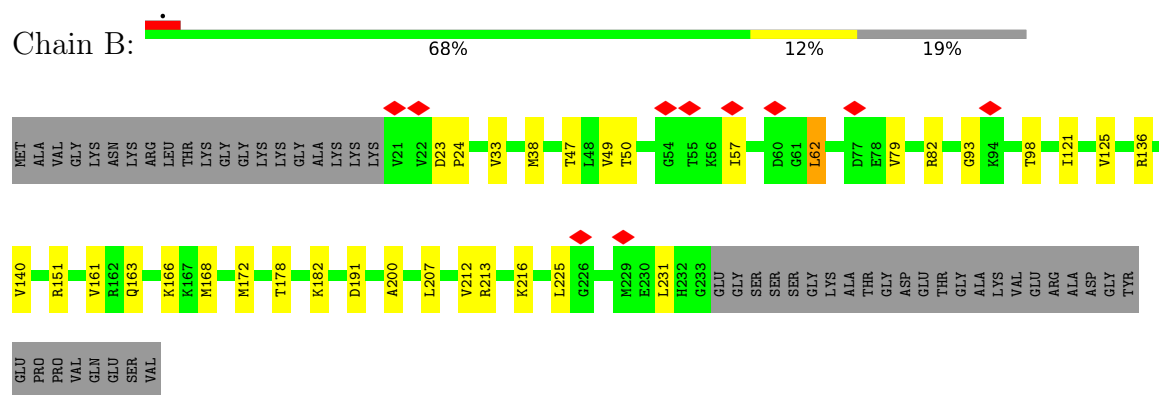
Chain Z: 



- Molecule 10: 40S ribosomal protein S28

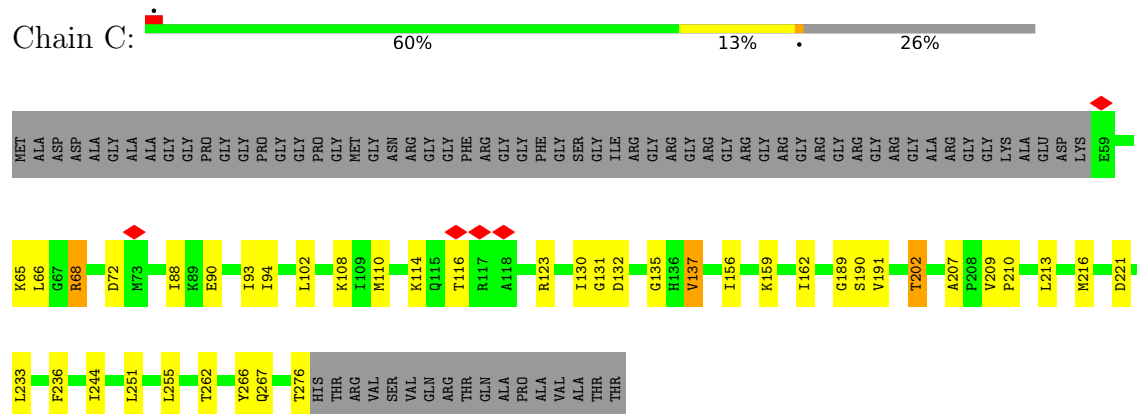
Chain c: 

Chain B:



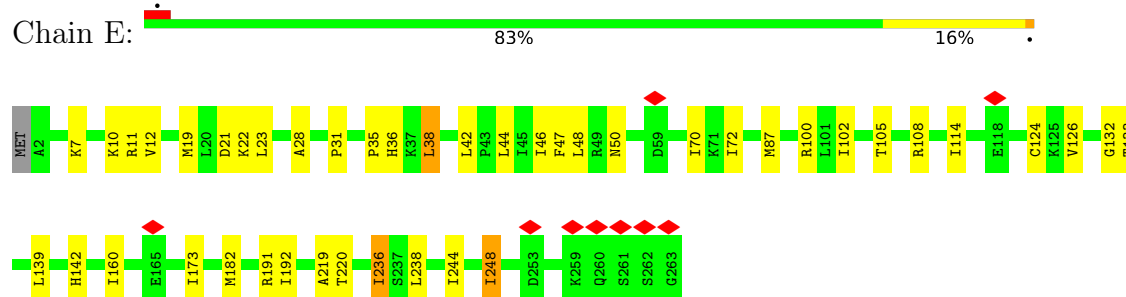
- Molecule 15: 40S ribosomal protein S2

Chain C:



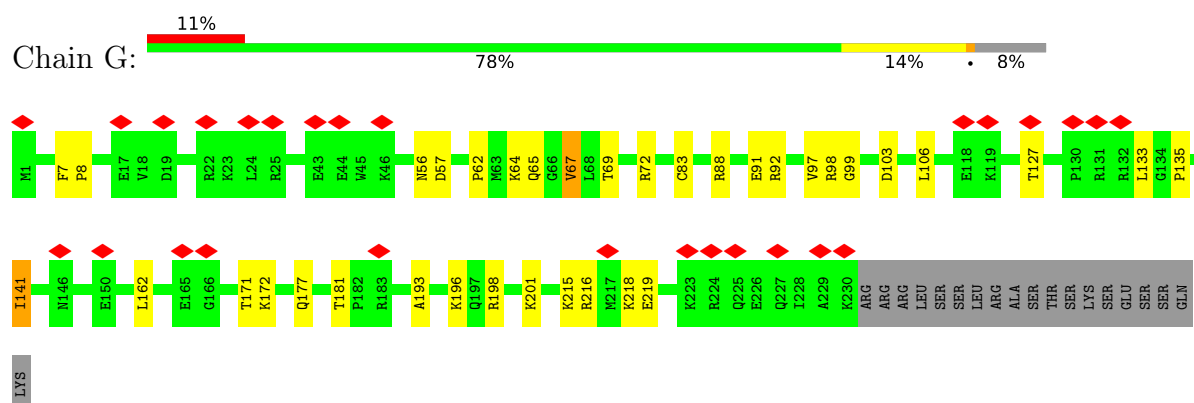
- Molecule 16: 40S ribosomal protein S4, X isoform

Chain E:

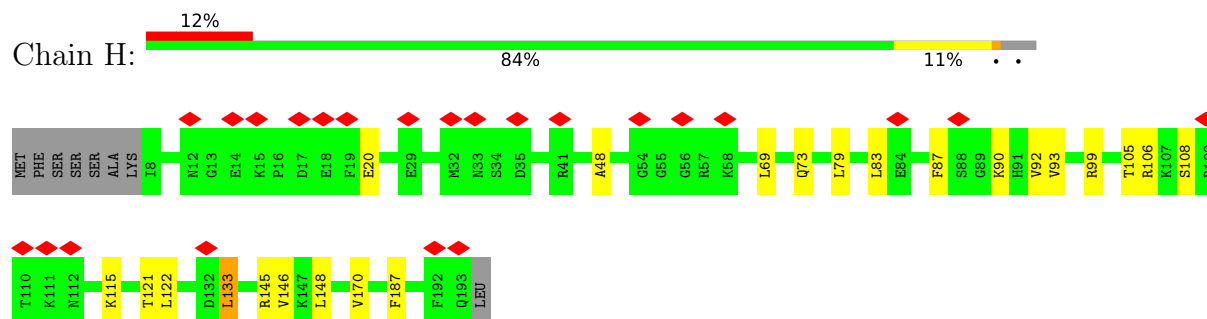


- Molecule 17: 40S ribosomal protein S6

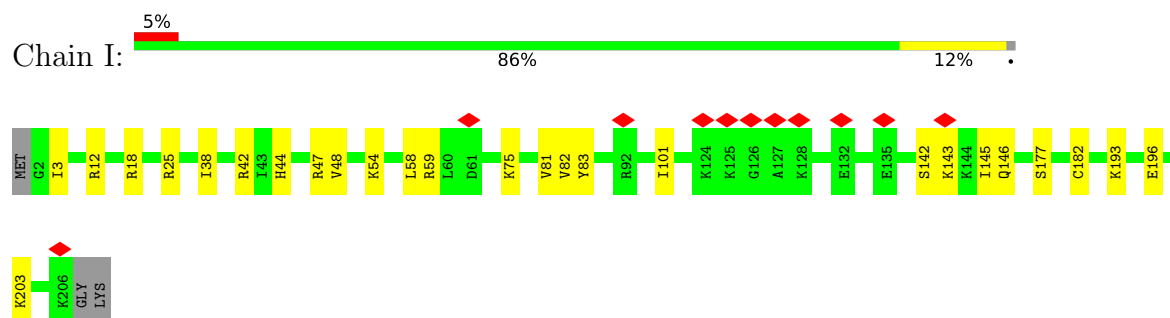
Chain G:



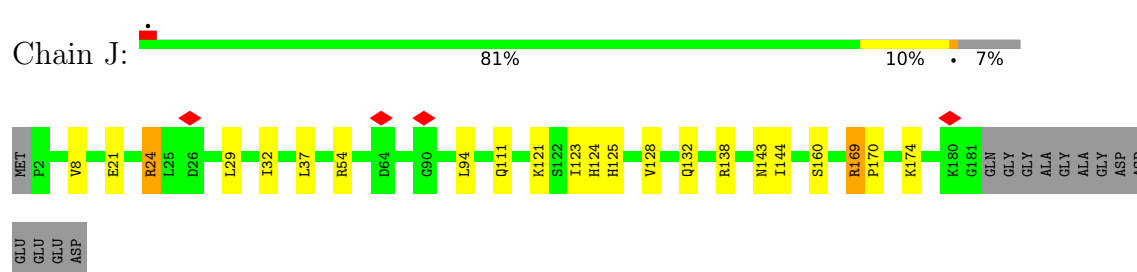
- Molecule 18: 40S ribosomal protein S7



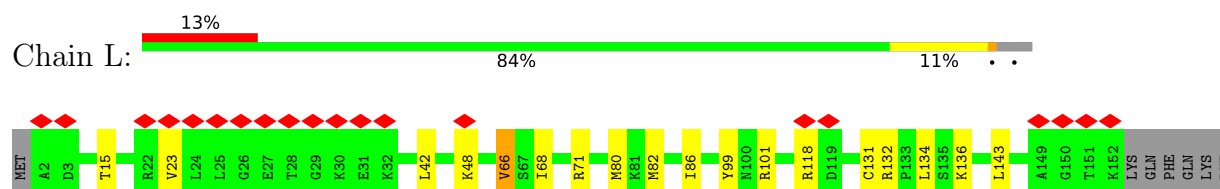
- Molecule 19: 40S ribosomal protein S8



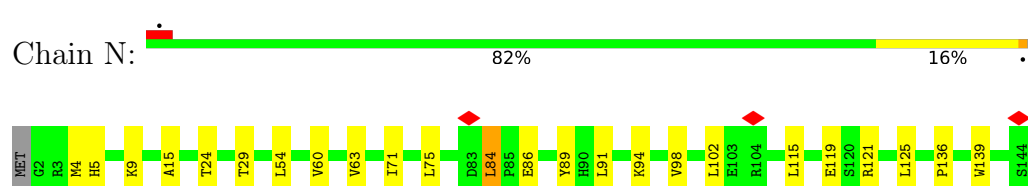
- Molecule 20: 40S ribosomal protein S9



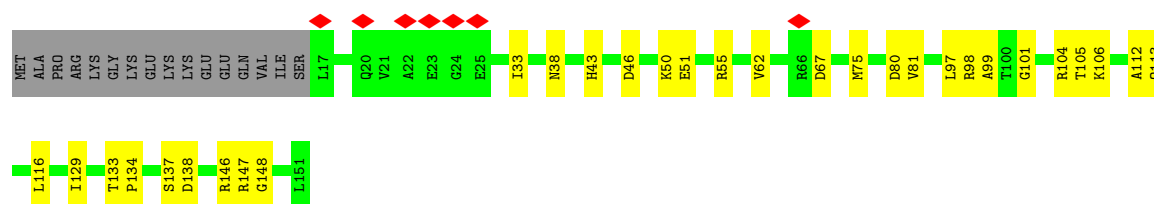
- Molecule 21: 40S ribosomal protein S11



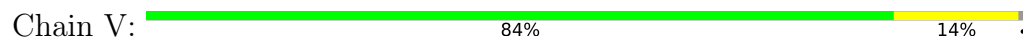
- Molecule 22: 40S ribosomal protein S13



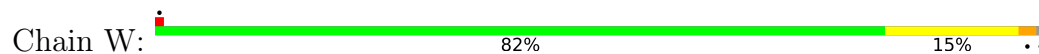
- Molecule 23: 40S ribosomal protein S14



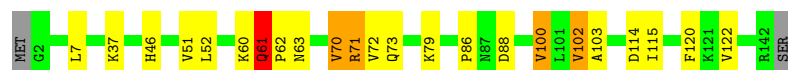
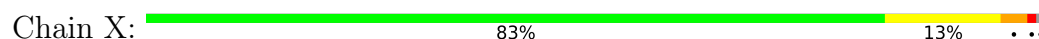
- Molecule 24: 40S ribosomal protein S21



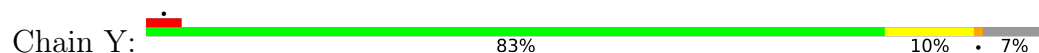
- Molecule 25: 40S ribosomal protein S15a



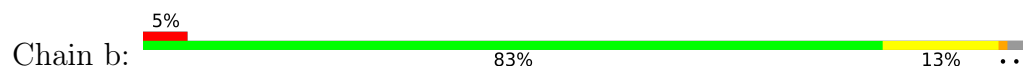
- Molecule 26: 40S ribosomal protein S23



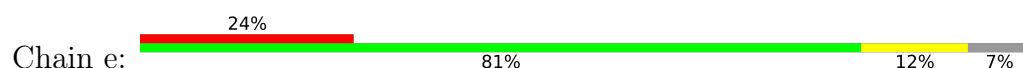
- Molecule 27: 40S ribosomal protein S24



- Molecule 28: 40S ribosomal protein S27

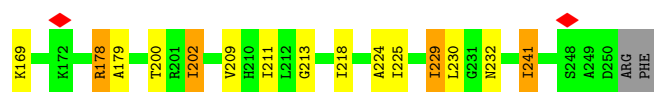
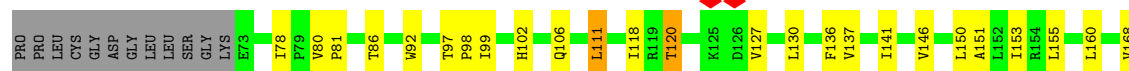


- Molecule 29: 40S ribosomal protein S30

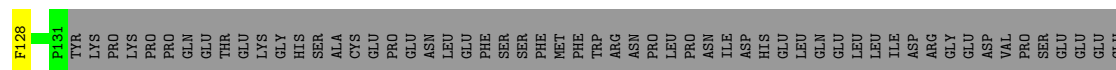
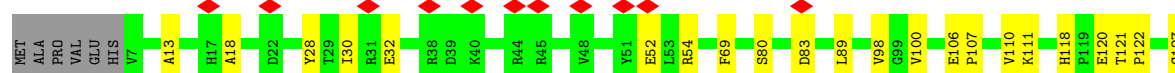




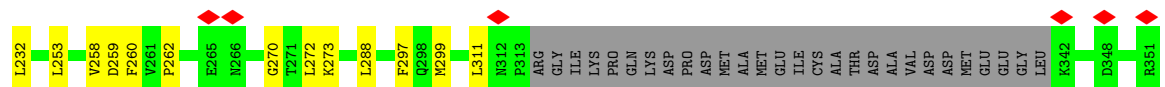
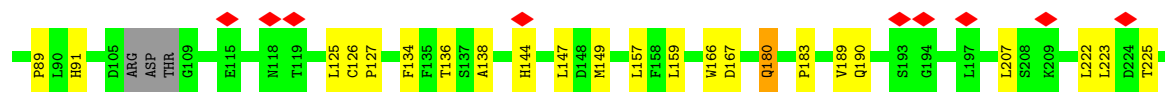
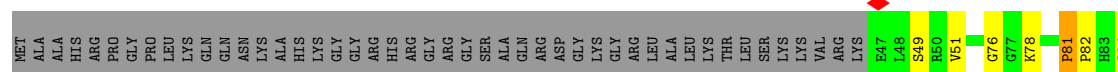
• Molecule 30: RNA-binding protein PNO1

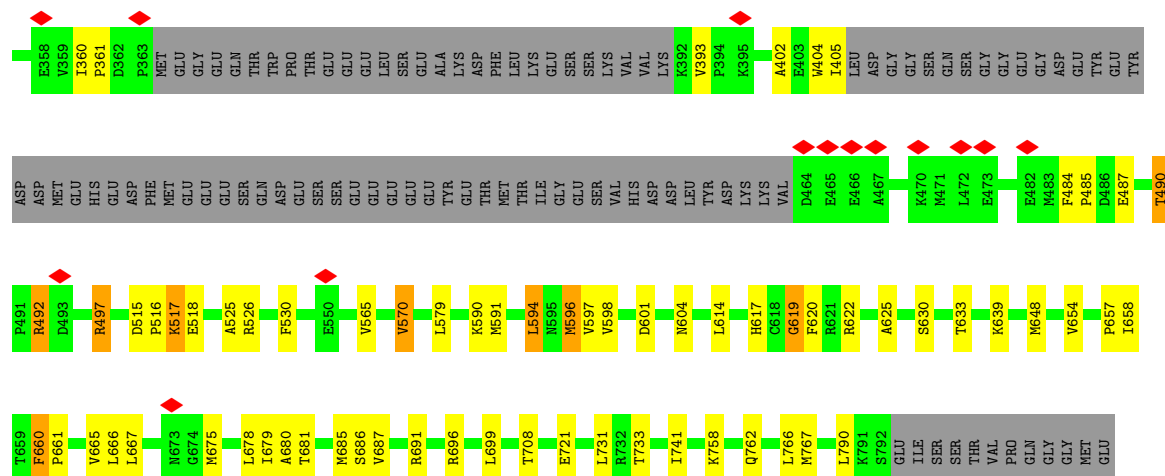


• Molecule 31: RNA-binding protein NOB1

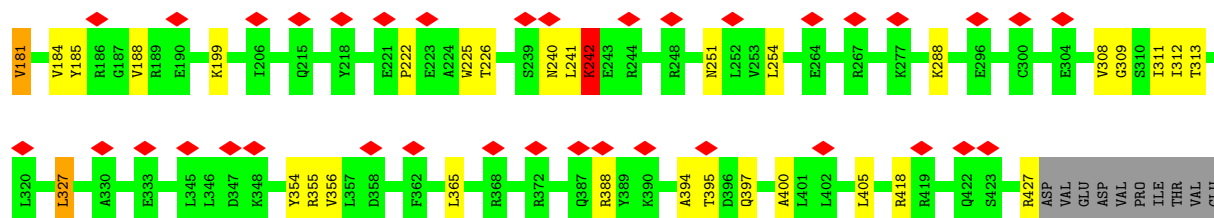
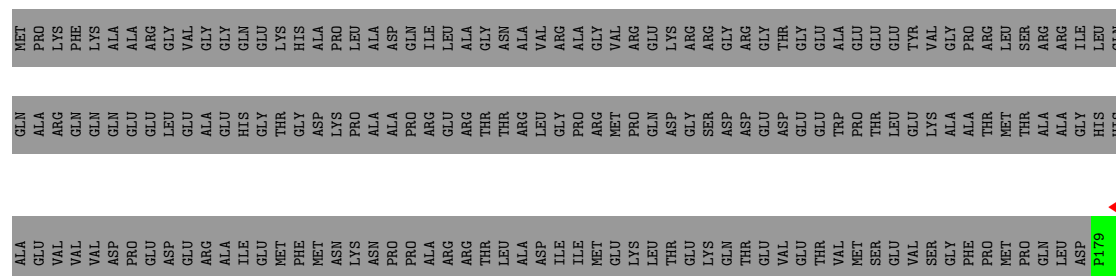


• Molecule 32: Pre-rRNA-processing protein TSR1 homolog

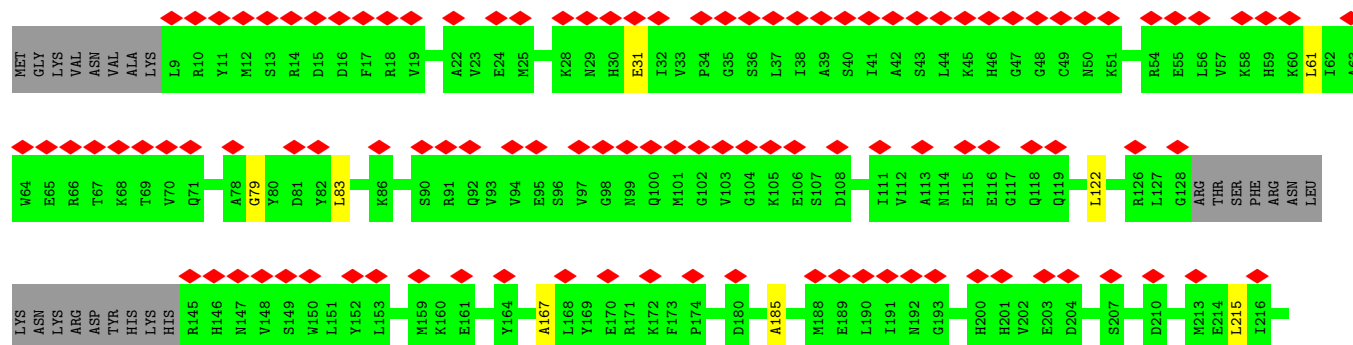




• Molecule 33: Bystin



• Molecule 34: Serine/threonine-protein kinase RIO2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	287847	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 ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.470	Depositor
Minimum map value	-0.211	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.0583	Depositor
Map size ($\text{\AA}$)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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

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	0.40	0/39590	0.78	50/61690 (0.1%)
2	F	0.51	0/1516	1.05	3/2037 (0.1%)
3	M	0.56	0/963	0.98	0/1291
4	P	0.53	0/1003	0.95	0/1341
5	Q	0.56	0/982	1.01	1/1318 (0.1%)
6	R	0.56	0/1002	1.03	0/1345
7	S	0.51	0/1100	0.99	1/1475 (0.1%)
8	T	0.58	0/1142	1.06	0/1530
9	Z	0.51	0/580	0.93	0/780
10	c	0.47	0/473	0.84	0/633
11	f	0.53	0/607	0.86	0/802
12	g	0.49	0/2490	0.79	0/3389
13	A	0.56	0/1742	1.00	2/2367 (0.1%)
14	B	0.48	0/1756	0.90	1/2350 (0.0%)
15	C	0.58	0/1726	0.92	0/2332
16	E	0.47	0/2118	0.87	0/2849
17	G	0.51	0/1885	0.92	0/2510
18	H	0.51	0/1524	0.91	0/2042
19	I	0.47	0/1711	0.90	0/2282
20	J	0.54	0/1524	1.01	0/2035
21	L	0.51	0/1250	0.83	1/1673 (0.1%)
22	N	0.57	0/1226	1.04	0/1649
23	O	0.58	0/1022	1.03	1/1372 (0.1%)
24	V	0.50	0/631	0.90	0/844
25	W	0.55	0/1051	0.94	1/1406 (0.1%)
26	X	0.55	0/1116	0.94	1/1490 (0.1%)
27	Y	0.50	0/1031	0.88	0/1370
28	b	0.47	0/653	0.82	1/876 (0.1%)
29	e	0.57	0/443	0.88	0/582
30	x	0.56	0/1413	1.01	2/1906 (0.1%)
31	y	0.50	0/2618	0.91	2/3536 (0.1%)
32	u	0.49	0/5187	0.87	2/7011 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	w	0.52	0/2074	1.01	0/2806
34	v	0.51	0/2644	0.91	0/3562
35	t	0.48	0/1075	1.10	4/1424 (0.3%)
All	All	0.47	0/88868	0.86	73/127905 (0.1%)

There are no bond length outliers.

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	t	357	TYR	N-CA-C	-14.77	83.79	108.76
1	2	1494	U	C2'-C3'-O3'	11.15	126.22	109.50
35	t	357	TYR	CB-CA-C	-11.04	89.73	109.70
1	2	1648	G	C4'-C3'-O3'	9.49	123.64	109.40
1	2	547	G	C2'-C3'-O3'	9.16	123.24	109.50

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	2	35407	0	17876	432	0
2	F	1495	0	1549	24	0
3	M	953	0	990	10	0
4	P	984	0	1028	17	0
5	Q	969	0	1030	7	0
6	R	990	0	1037	8	0
7	S	1083	0	1140	10	0
8	T	1122	0	1153	21	0
9	Z	574	0	627	6	0
10	c	471	0	499	7	0
11	f	596	0	627	4	0
12	g	2433	0	2389	16	0
13	A	1705	0	1706	29	0
14	B	1729	0	1803	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	C	1690	0	1777	19	0
16	E	2076	0	2177	19	0
17	G	1862	0	2018	20	0
18	H	1501	0	1593	14	0
19	I	1682	0	1769	15	0
20	J	1499	0	1618	12	0
21	L	1229	0	1302	6	0
22	N	1202	0	1289	10	0
23	O	1009	0	1034	16	0
24	V	625	0	628	9	0
25	W	1034	0	1080	9	0
26	X	1098	0	1167	12	0
27	Y	1014	0	1082	6	0
28	b	640	0	665	6	0
29	e	438	0	484	3	0
30	x	1391	0	1467	22	0
31	y	2568	0	2624	32	0
32	u	5062	0	5113	53	0
33	w	2027	0	2126	13	0
34	v	2593	0	2551	7	0
35	t	1066	0	1070	19	0
36	f	1	0	0	0	0
36	y	1	0	0	0	0
All	All	83819	0	68088	794	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 5.

The worst 5 of 794 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)
1:2:872:A:N6	1:2:914:U:H3	1.01	1.43
1:2:830:A:N6	1:2:844:U:H3	0.85	1.32
1:2:1144:A:H2'	1:2:1145:A:C8	1.74	1.23
32:u:525:ALA:HB2	35:t:362:ASN:ND2	1.52	1.23
1:2:872:A:N1	1:2:914:U:O4	1.82	1.11

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	F	187/204 (92%)	173 (92%)	13 (7%)	1 (0%)	24	57
3	M	121/132 (92%)	112 (93%)	9 (7%)	0	100	100
4	P	118/145 (81%)	111 (94%)	6 (5%)	1 (1%)	16	49
5	Q	120/146 (82%)	115 (96%)	5 (4%)	0	100	100
6	R	120/135 (89%)	110 (92%)	9 (8%)	1 (1%)	16	49
7	S	128/152 (84%)	118 (92%)	9 (7%)	1 (1%)	16	49
8	T	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
9	Z	70/125 (56%)	65 (93%)	5 (7%)	0	100	100
10	c	59/69 (86%)	54 (92%)	4 (7%)	1 (2%)	7	35
11	f	71/156 (46%)	58 (82%)	10 (14%)	3 (4%)	2	19
12	g	311/317 (98%)	282 (91%)	23 (7%)	6 (2%)	6	33
13	A	214/295 (72%)	201 (94%)	12 (6%)	1 (0%)	24	57
14	B	211/264 (80%)	198 (94%)	12 (6%)	1 (0%)	24	57
15	C	216/293 (74%)	203 (94%)	11 (5%)	2 (1%)	14	46
16	E	260/263 (99%)	246 (95%)	13 (5%)	1 (0%)	30	61
17	G	228/249 (92%)	218 (96%)	9 (4%)	1 (0%)	30	61
18	H	184/194 (95%)	175 (95%)	9 (5%)	0	100	100
19	I	203/208 (98%)	195 (96%)	8 (4%)	0	100	100
20	J	178/194 (92%)	164 (92%)	11 (6%)	3 (2%)	7	35
21	L	149/158 (94%)	144 (97%)	5 (3%)	0	100	100
22	N	147/151 (97%)	139 (95%)	8 (5%)	0	100	100
23	O	133/151 (88%)	123 (92%)	10 (8%)	0	100	100
24	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
25	W	127/130 (98%)	120 (94%)	6 (5%)	1 (1%)	16	49
26	X	139/143 (97%)	131 (94%)	6 (4%)	2 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Y	122/133 (92%)	115 (94%)	6 (5%)	1 (1%)	16	49
28	b	80/84 (95%)	73 (91%)	7 (9%)	0	100	100
29	e	53/59 (90%)	47 (89%)	5 (9%)	1 (2%)	6	33
30	x	176/252 (70%)	170 (97%)	6 (3%)	0	100	100
31	y	319/412 (77%)	295 (92%)	20 (6%)	4 (1%)	9	39
32	u	619/804 (77%)	573 (93%)	38 (6%)	8 (1%)	9	39
33	w	247/437 (56%)	236 (96%)	10 (4%)	1 (0%)	30	61
34	v	317/552 (57%)	297 (94%)	17 (5%)	3 (1%)	14	46
35	t	119/475 (25%)	101 (85%)	15 (13%)	3 (2%)	4	28
All	All	5968/7710 (77%)	5572 (93%)	349 (6%)	47 (1%)	18	49

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	c	66	ARG
26	X	61	GLN
26	X	86	PRO
31	y	370	VAL
12	g	190	GLY

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	F	159/170 (94%)	135 (85%)	24 (15%)	3	17
3	M	104/108 (96%)	92 (88%)	12 (12%)	5	25
4	P	107/130 (82%)	94 (88%)	13 (12%)	5	23
5	Q	103/121 (85%)	87 (84%)	16 (16%)	2	16
6	R	110/122 (90%)	90 (82%)	20 (18%)	2	11
7	S	114/132 (86%)	95 (83%)	19 (17%)	2	14
8	T	114/115 (99%)	100 (88%)	14 (12%)	4	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Z	64/103 (62%)	56 (88%)	8 (12%)	4	22
10	c	52/62 (84%)	45 (86%)	7 (14%)	4	21
11	f	65/140 (46%)	58 (89%)	7 (11%)	6	28
12	g	271/275 (98%)	237 (88%)	34 (12%)	4	22
13	A	180/243 (74%)	155 (86%)	25 (14%)	3	19
14	B	194/231 (84%)	179 (92%)	15 (8%)	12	38
15	C	184/225 (82%)	172 (94%)	12 (6%)	15	43
16	E	224/225 (100%)	208 (93%)	16 (7%)	13	40
17	G	200/218 (92%)	191 (96%)	9 (4%)	24	51
18	H	167/174 (96%)	163 (98%)	4 (2%)	43	63
19	I	178/180 (99%)	175 (98%)	3 (2%)	53	69
20	J	160/168 (95%)	155 (97%)	5 (3%)	35	59
21	L	135/142 (95%)	127 (94%)	8 (6%)	18	45
22	N	130/131 (99%)	122 (94%)	8 (6%)	16	44
23	O	105/119 (88%)	97 (92%)	8 (8%)	12	39
24	V	66/67 (98%)	63 (96%)	3 (4%)	24	51
25	W	112/113 (99%)	103 (92%)	9 (8%)	11	37
26	X	113/115 (98%)	104 (92%)	9 (8%)	11	37
27	Y	108/115 (94%)	103 (95%)	5 (5%)	24	51
28	b	74/76 (97%)	70 (95%)	4 (5%)	20	47
29	e	45/48 (94%)	42 (93%)	3 (7%)	15	42
30	x	150/208 (72%)	136 (91%)	14 (9%)	8	32
31	y	285/367 (78%)	273 (96%)	12 (4%)	26	53
32	u	550/705 (78%)	522 (95%)	28 (5%)	21	49
33	w	217/370 (59%)	203 (94%)	14 (6%)	15	43
34	v	274/489 (56%)	272 (99%)	2 (1%)	76	78
35	t	113/434 (26%)	102 (90%)	11 (10%)	8	31
All	All	5227/6641 (79%)	4826 (92%)	401 (8%)	14	38

5 of 401 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	E	48	LEU

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Mol	Chain	Res	Type
23	O	147	ARG
35	t	473	LEU
16	E	236	ILE
20	J	29	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
20	J	156	HIS
35	t	269	GLN
26	X	16	HIS
34	v	503	GLN
33	w	240	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1646/1873 (87%)	542 (32%)	61 (3%)

5 of 542 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	5	U
1	2	9	U

5 of 61 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	918	U
1	2	1603	G
1	2	1308	U
1	2	1601	A
1	2	1785	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.

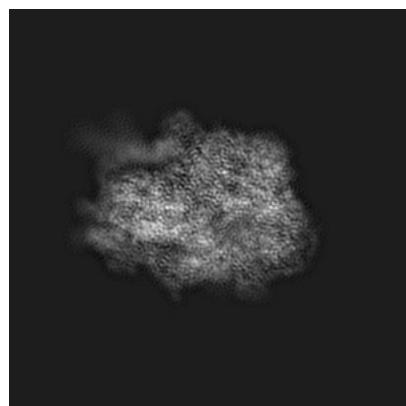
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4337. These allow visual inspection of the internal detail of the map and identification of artifacts.

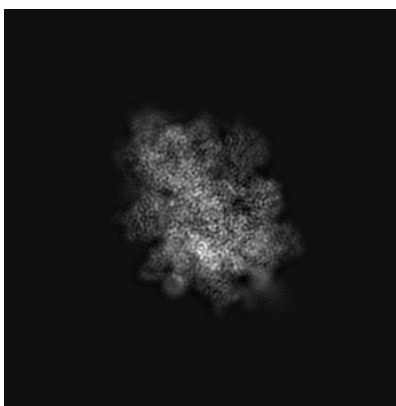
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

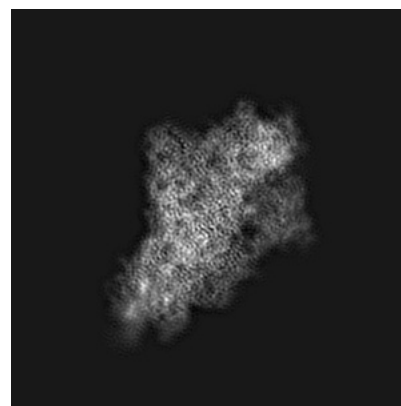
6.1.1 Primary map



X

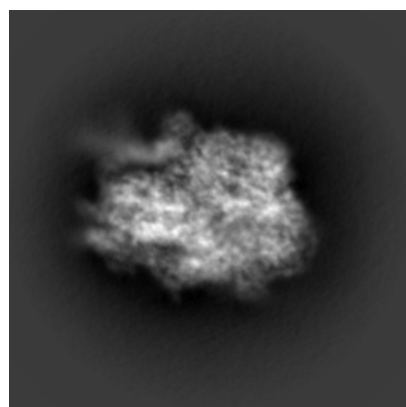


Y

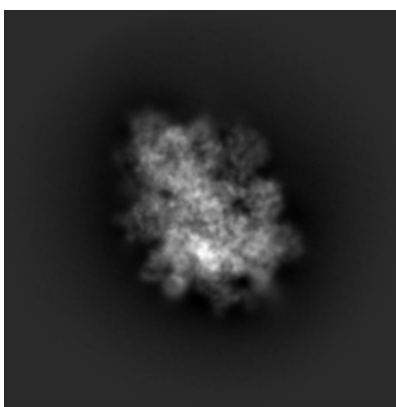


Z

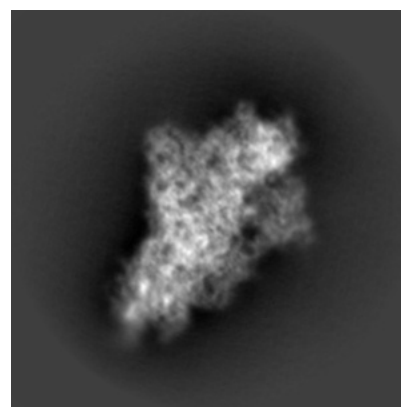
6.1.2 Raw map



X



Y

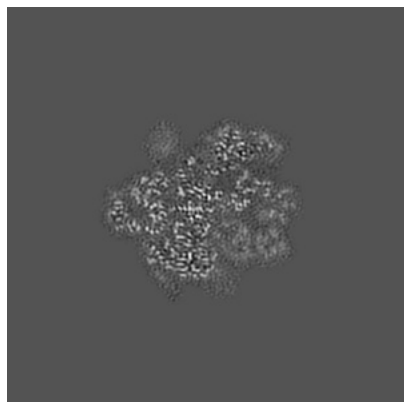


Z

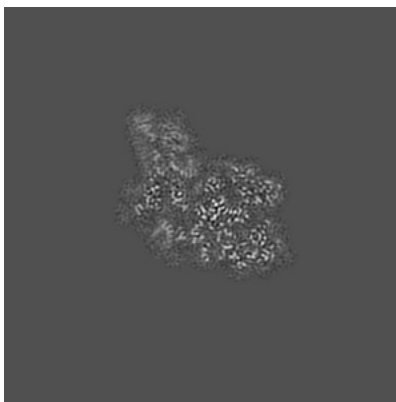
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

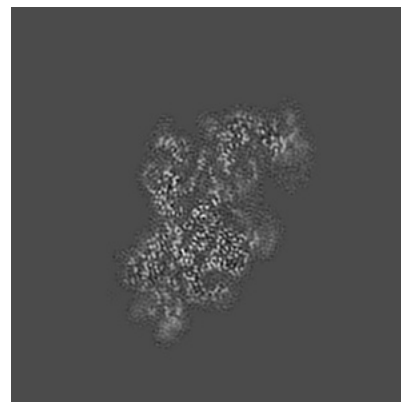
6.2.1 Primary map



X Index: 180

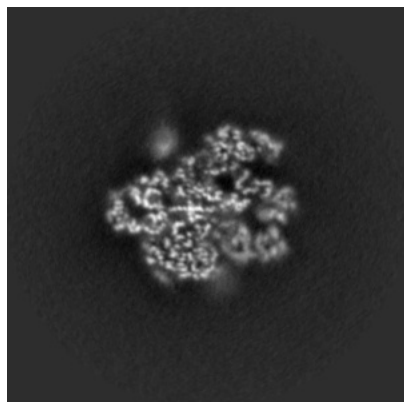


Y Index: 180

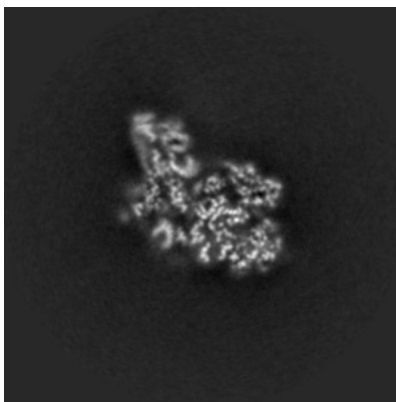


Z Index: 180

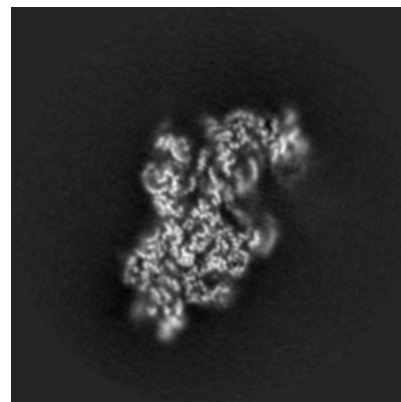
6.2.2 Raw map



X Index: 180



Y Index: 180

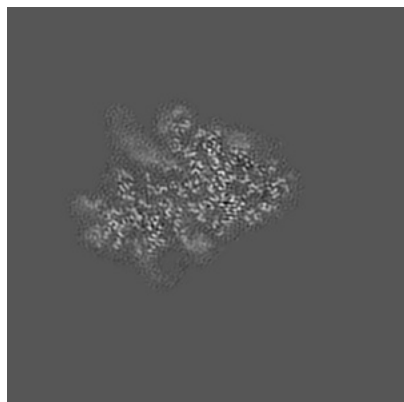


Z Index: 180

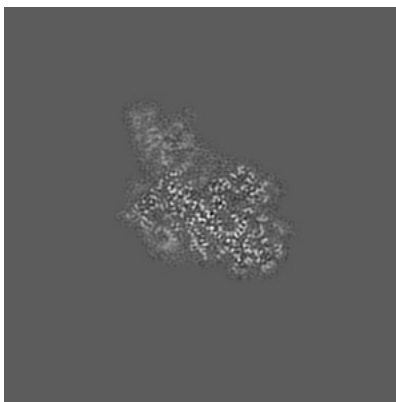
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

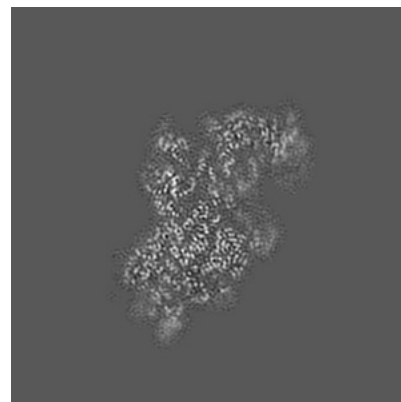
6.3.1 Primary map



X Index: 145

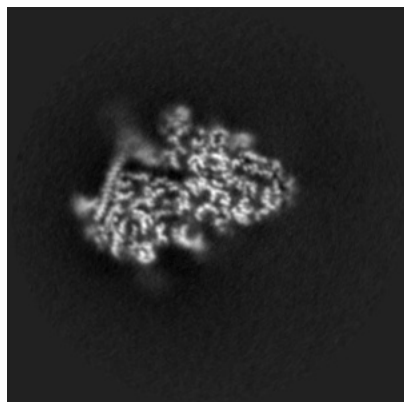


Y Index: 174

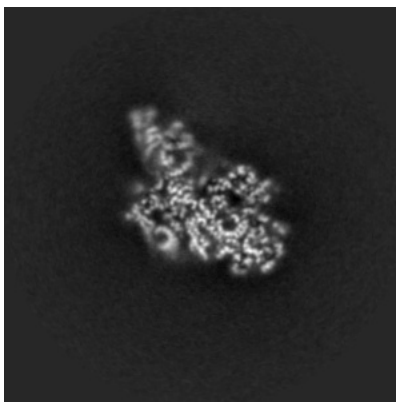


Z Index: 181

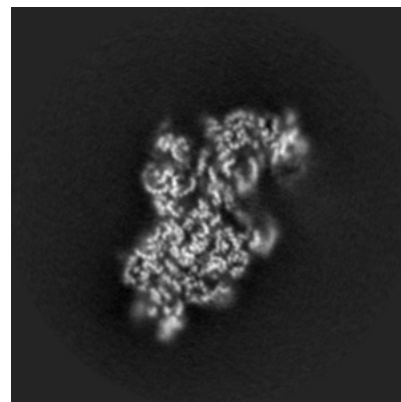
6.3.2 Raw map



X Index: 141



Y Index: 174

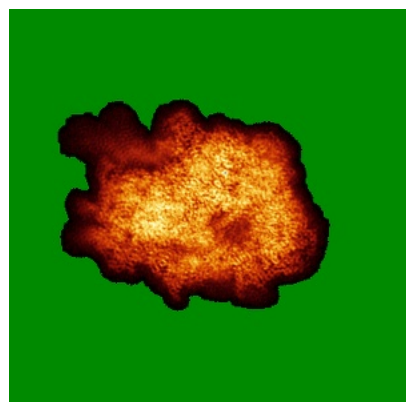


Z Index: 181

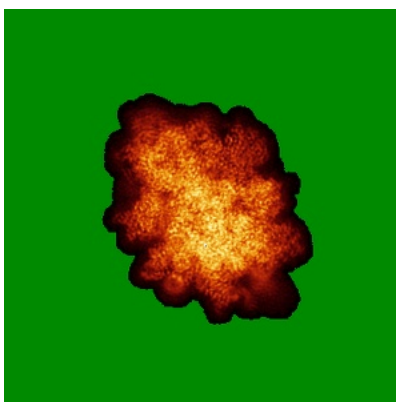
The images above show the largest variance slices of the map in three orthogonal directions.

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

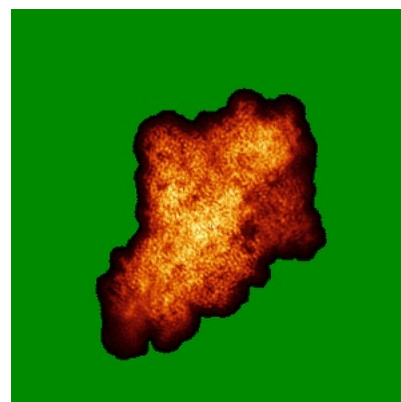
6.4.1 Primary map



X



Y

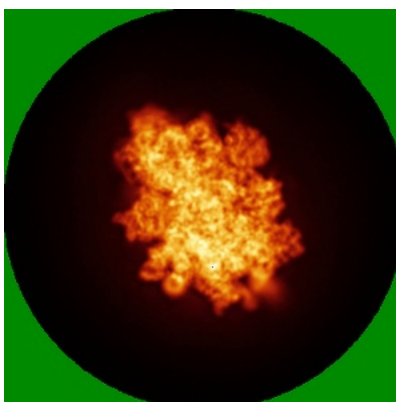


Z

6.4.2 Raw map



X



Y

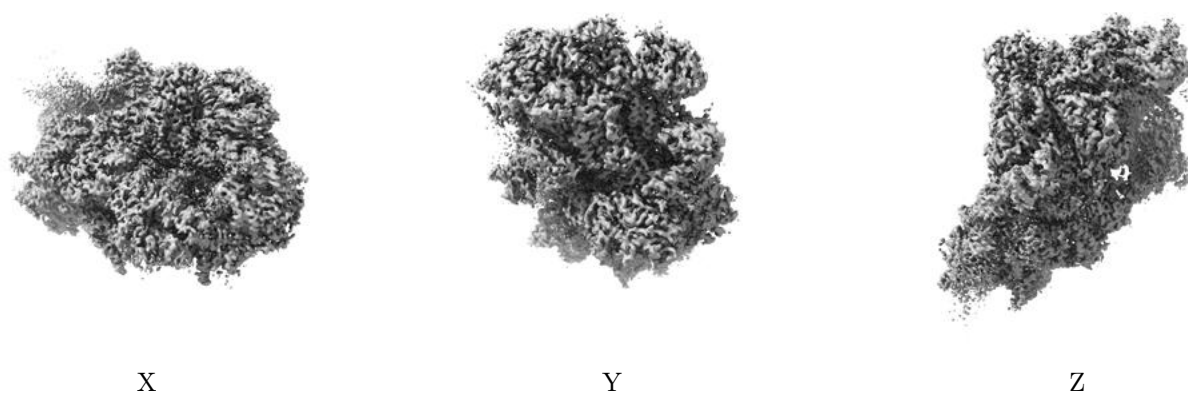


Z

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.

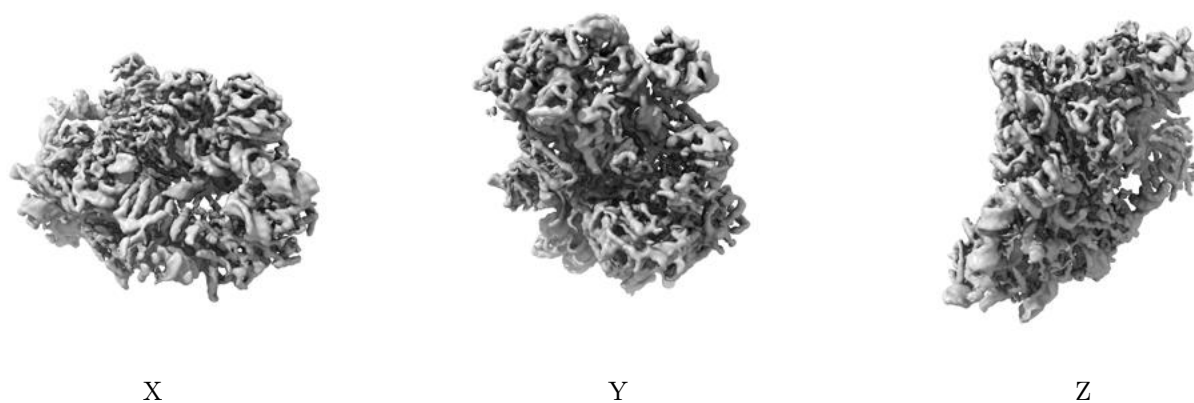
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0583. 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.

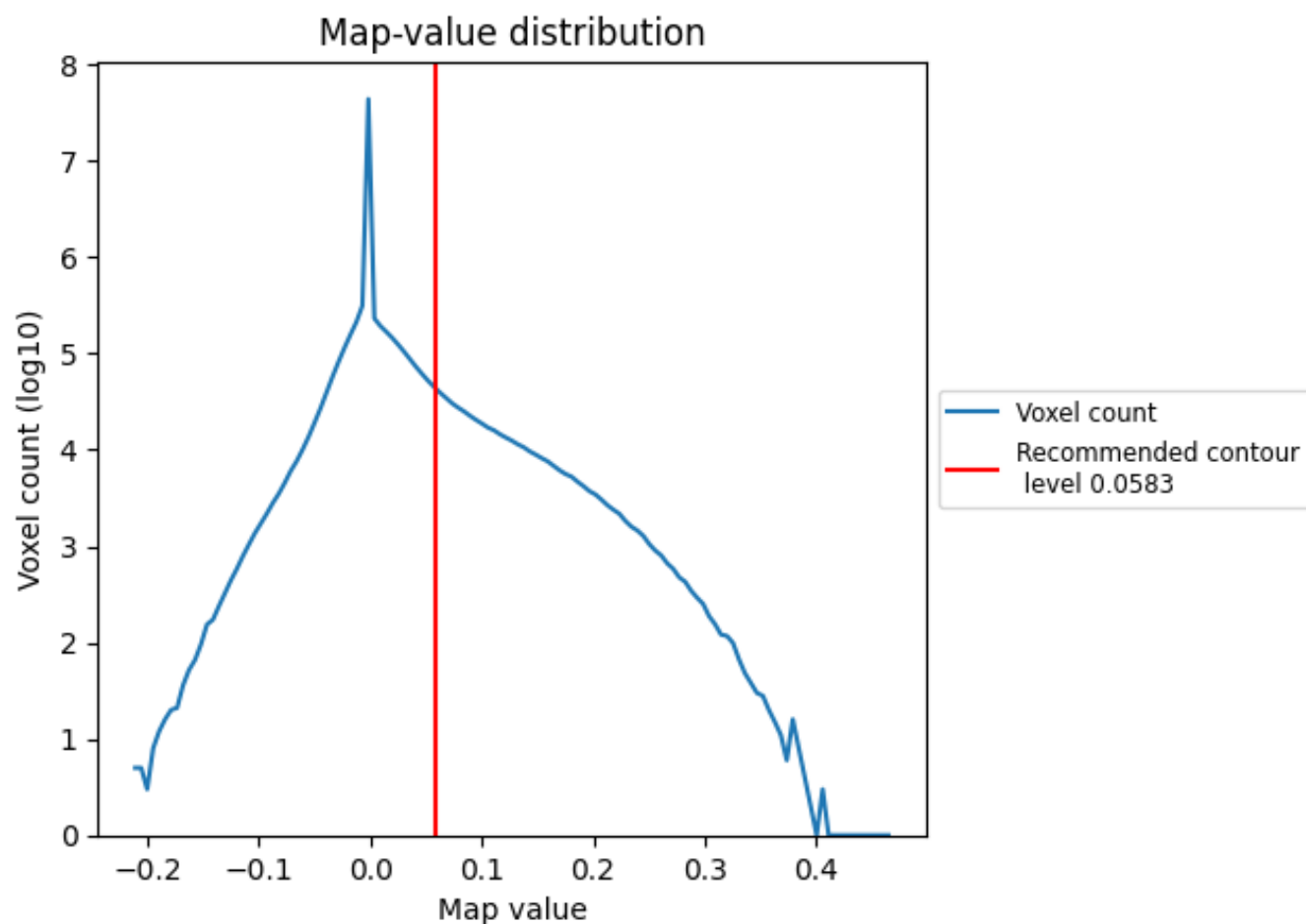
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

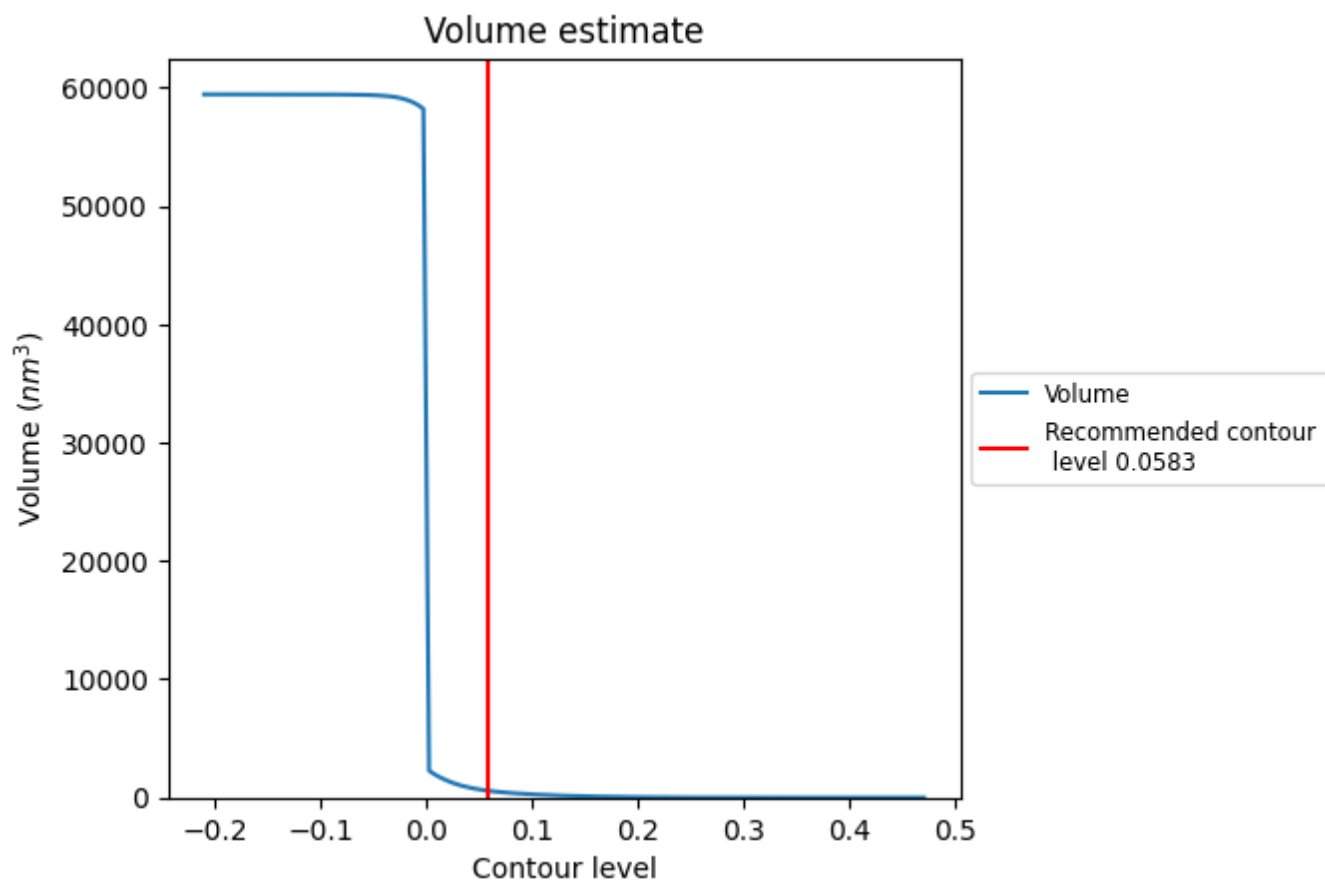
This section contains the results of statistical analysis of the map.

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.

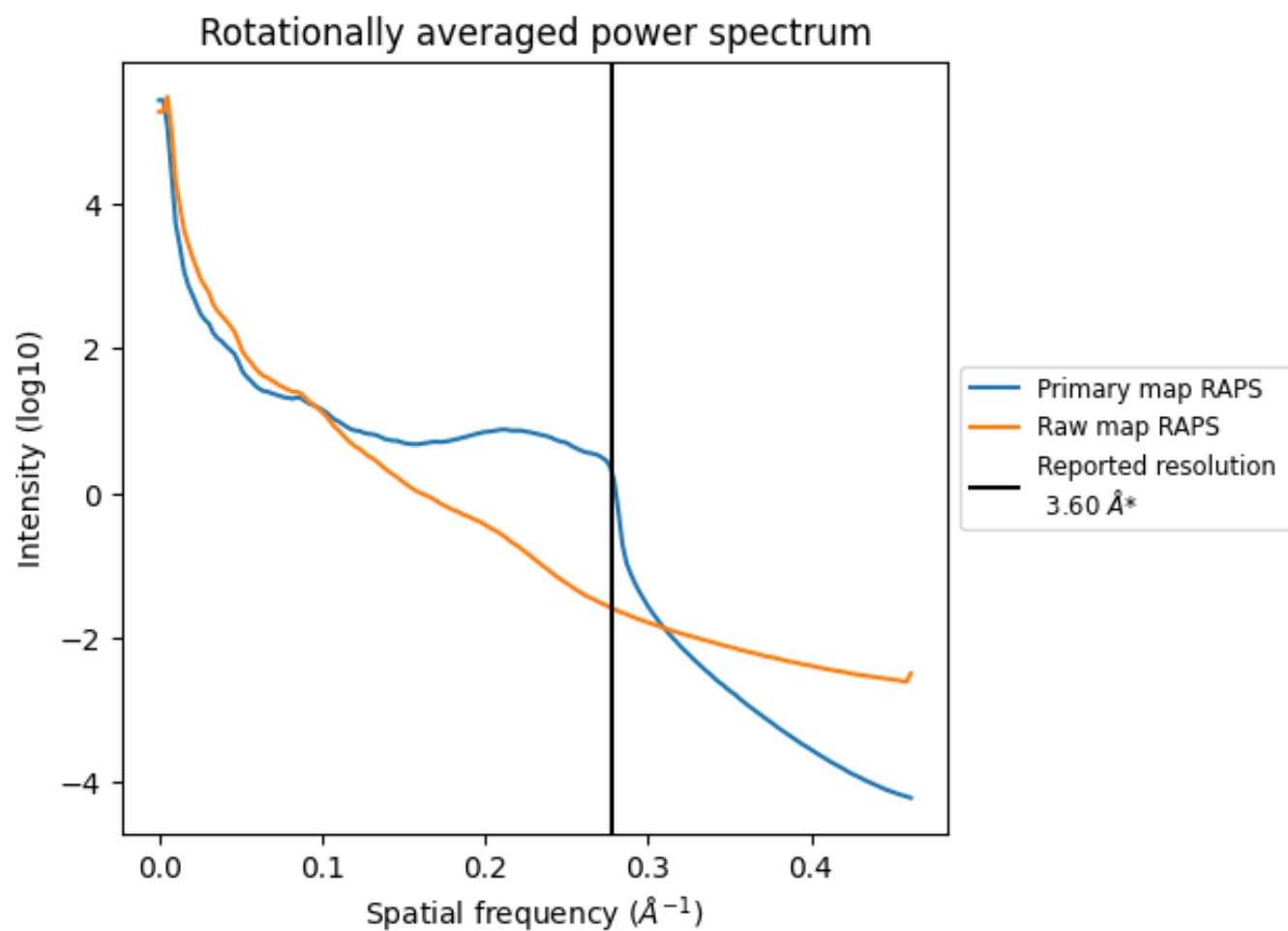
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 573 nm³; this corresponds to an approximate mass of 518 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 ⓘ

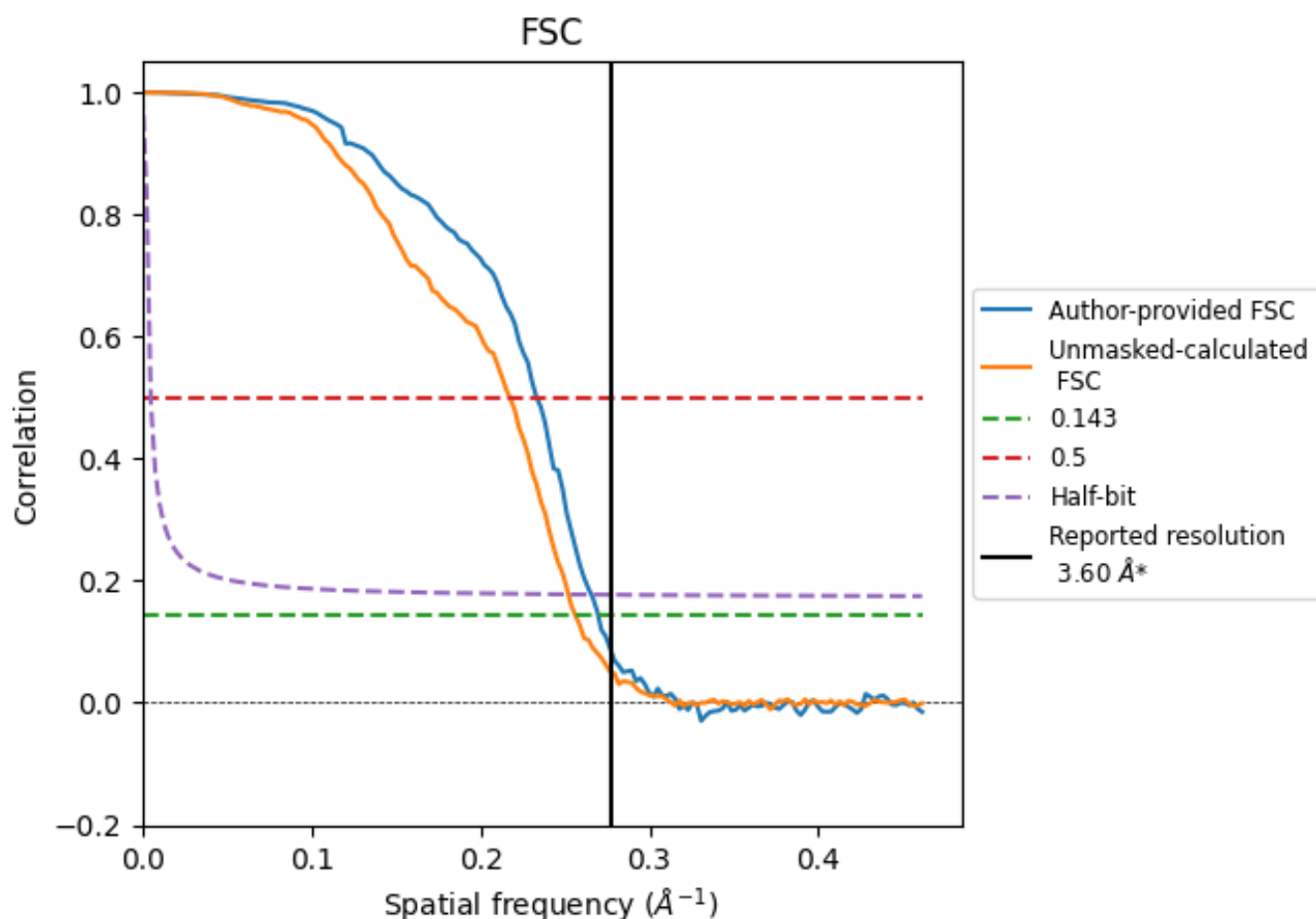


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates

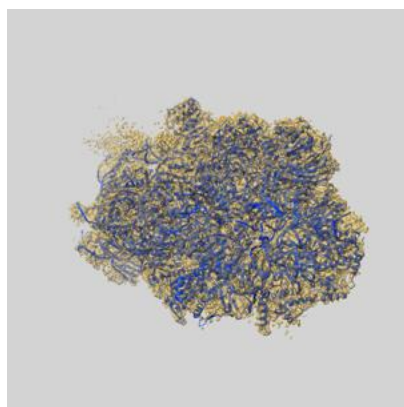
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.71	4.29	3.76
Unmasked-calculated*	3.90	4.60	3.97

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

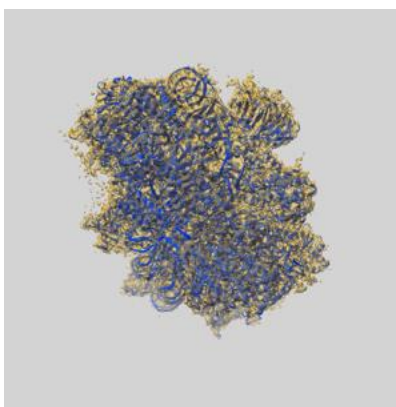
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4337 and PDB model 6G18. Per-residue inclusion information can be found in section [3](#) on page [11](#).

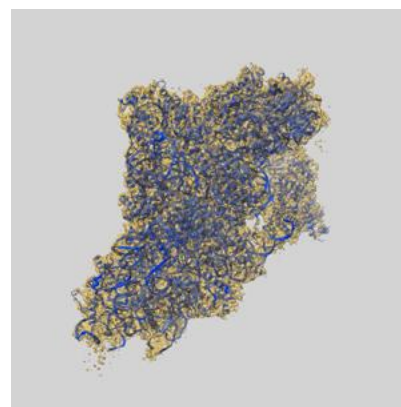
9.1 Map-model overlay [i](#)



X



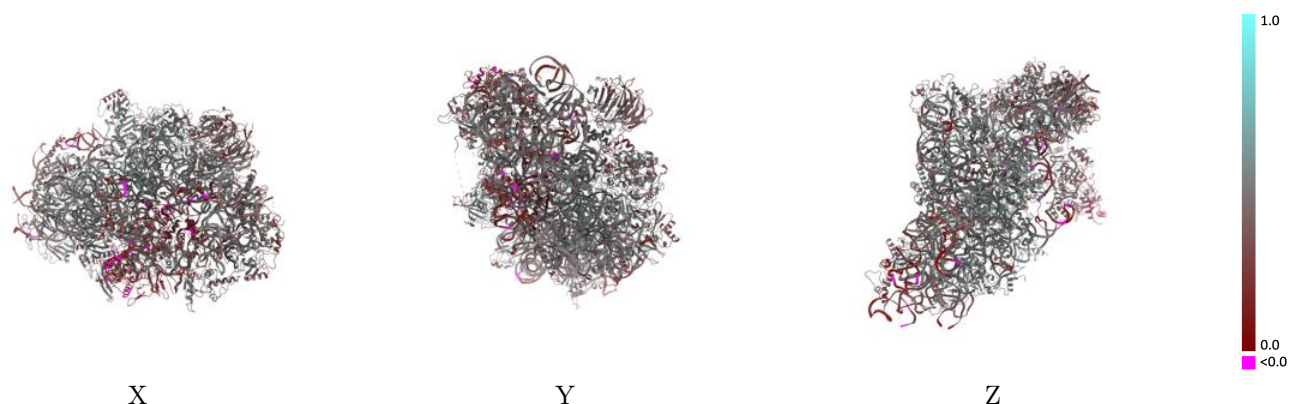
Y



Z

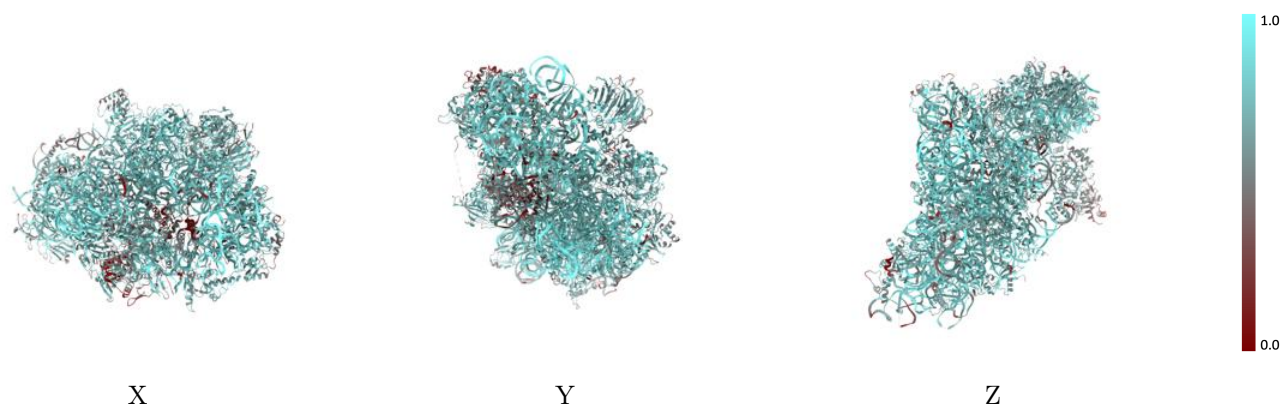
The images above show the 3D surface view of the map at the recommended contour level 0.0583 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



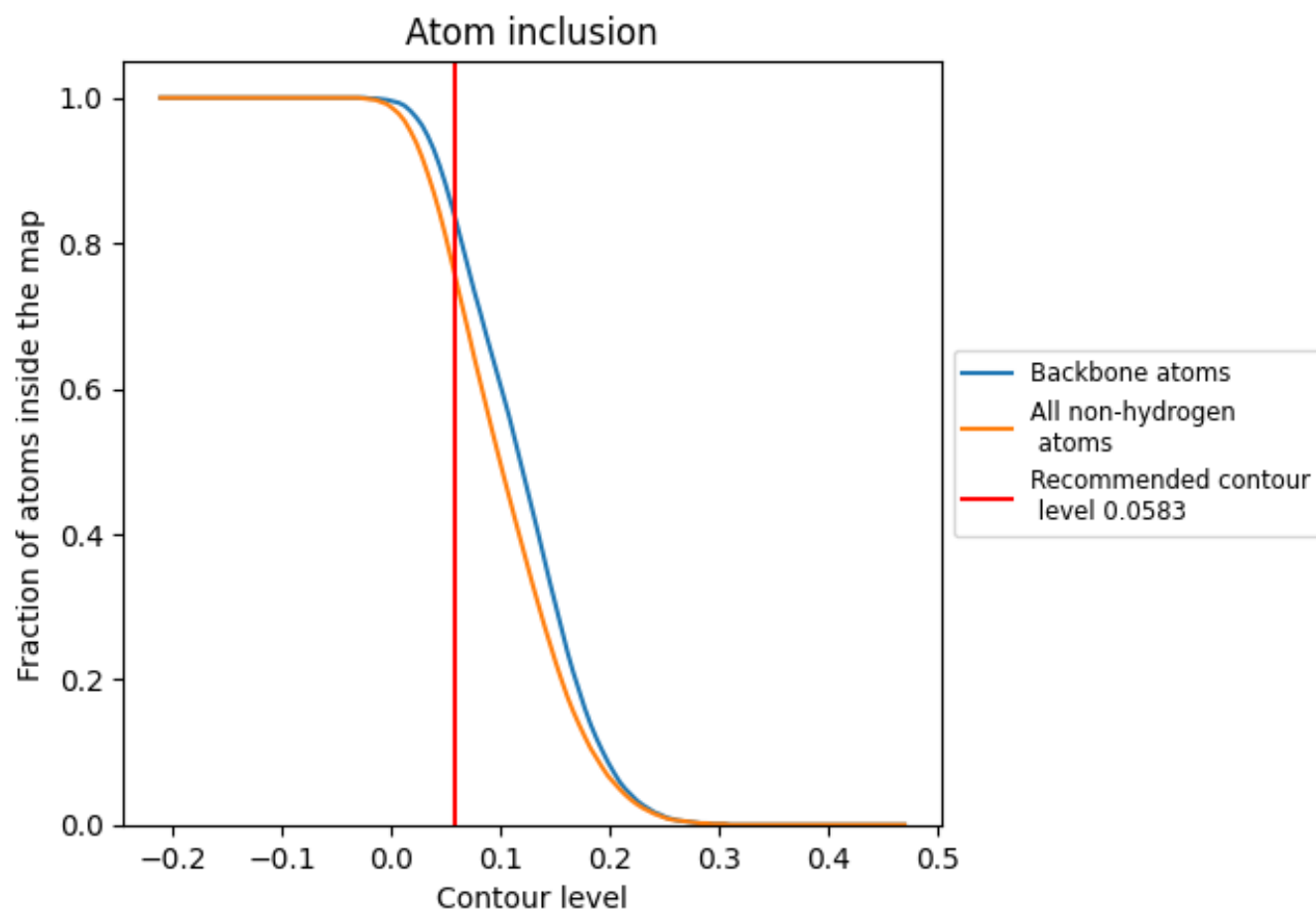
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0583).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 76% 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 (0.0583) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7590	 0.4160
2	 0.8440	 0.4090
A	 0.8090	 0.4940
B	 0.7510	 0.4600
C	 0.7660	 0.4910
E	 0.7450	 0.4680
F	 0.7270	 0.4420
G	 0.6930	 0.3970
H	 0.6580	 0.3950
I	 0.7410	 0.4350
J	 0.7880	 0.4820
L	 0.7270	 0.4580
M	 0.3300	 0.1480
N	 0.7830	 0.4590
O	 0.7350	 0.4600
P	 0.7470	 0.4540
Q	 0.7300	 0.4380
R	 0.6800	 0.4020
S	 0.6820	 0.4030
T	 0.7450	 0.4290
V	 0.7760	 0.4800
W	 0.7920	 0.4960
X	 0.7980	 0.5010
Y	 0.7570	 0.4650
Z	 0.6060	 0.3680
b	 0.7550	 0.4570
c	 0.7090	 0.4600
e	 0.6080	 0.4170
f	 0.4150	 0.2360
g	 0.6580	 0.3690
t	 0.6270	 0.3700
u	 0.7430	 0.4570
v	 0.3770	 0.2450
w	 0.6250	 0.3510
x	 0.7720	 0.4910
y	 0.7170	 0.4240

