



wwPDB EM Validation Summary Report ⓘ

Jul 10, 2026 – 08:18 AM JST

PDB ID : 9XAJ / pdb_00009xaj
EMDB ID : EMD-66689
Title : Cryo-EM structure of the pre-40S ribosome (Enp1-Rrp12 Mut) from *Chaetomium thermophilum*, state Rrp12-A1*
Authors : Lau, B.; Li, Y.; Zhu, J.; Fischer, P.; Hong, X.; Yuan, R.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2025-10-22
Resolution : 3.10 Å (reported)
Based on initial model : 6G18

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
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) : 2.50

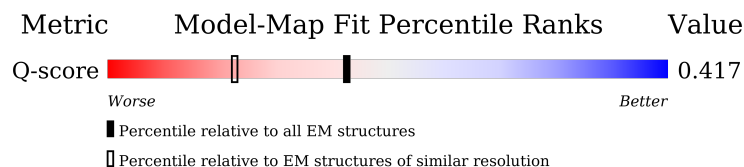
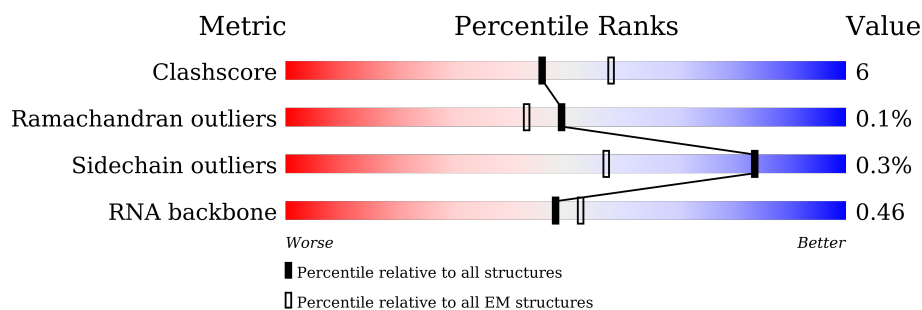
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



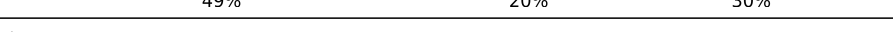
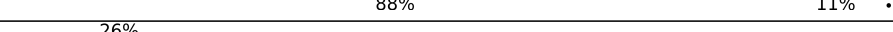
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	E	255	
2	H	264	
3	I	212	

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Mol	Chain	Length	Quality of chain
4	J	239	
5	K	203	
6	L	202	
7	M	190	
8	O	161	
9	P	144	
10	Q	151	
11	R	150	
12	S	153	
13	T	119	
14	V	156	
15	W	153	
16	Z	130	
17	a	145	
18	b	136	
19	c	99	
20	e	82	
21	f	68	
22	h	62	
23	i	154	
24	A	1797	
25	0	127	
26	1	282	
27	2	830	
28	3	259	

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Mol	Chain	Length	Quality of chain
29	4	480	48%8%44%
30	5	445	15%82%
31	6	519	7%92%
32	7	1235	81%70%11%19%
33	8	938	5%93%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 81108 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 Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	213	Total	C	N	O	S	0	0
			1723	1096	319	303	5		

- Molecule 2 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	261	Total	C	N	O	S	0	0
			2072	1314	389	362	7		

- Molecule 3 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	199	Total	C	N	O	S	0	0
			1557	971	294	285	7		

- Molecule 4 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	232	Total	C	N	O	S	0	0
			1875	1171	376	323	5		

- Molecule 5 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	K	195	Total	C	N	O	0	0
			1562	983	300	279		

- Molecule 6 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	201	Total	C	N	O	S	0	0
			1621	1009	330	281	1		

- Molecule 7 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	179	Total	C	N	O	S	0	0
			1466	933	290	241	2		

- Molecule 8 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	150	Total	C	N	O	S	0	0
			1222	780	236	201	5		

- Molecule 9 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	118	Total	C	N	O	S	0	0
			923	577	167	171	8		

- Molecule 10 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	150	Total	C	N	O	S	0	0
			1182	756	220	205	1		

- Molecule 11 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	135	Total	C	N	O	S	0	0
			1002	614	199	184	5		

- Molecule 12 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	115	Total	C	N	O	S	0	0
			917	583	172	159	3		

- Molecule 13 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	117	Total	C	N	O	S	0	0
			909	588	162	158	1		

- Molecule 14 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	122	Total	C	N	O	S	0	0
			998	629	191	177	1		

- Molecule 15 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	142	Total	C	N	O	S	0	0
			1117	694	221	201	1		

- Molecule 16 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Z	129	Total	C	N	O	S	0	0
			1037	659	195	178	5		

- Molecule 17 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	142	Total	C	N	O	S	0	0
			1099	694	215	188	2		

- Molecule 18 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	132	Total	C	N	O	S	0	0
			1061	668	209	182	2		

- Molecule 19 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	69	Total	C	N	O	S	0	0
			546	345	101	98	2		

- Molecule 20 is a protein called Ribosomal protein s27-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	e	81	Total	C	N	O	S	0	0
			611	386	111	107	7		

- Molecule 21 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	f	61	Total	C	N	O	S	0	0
			484	298	97	88	1		

- Molecule 22 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	h	21	Total	C	N	O		0	0
			181	117	38	26			

- Molecule 23 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	i	65	Total	C	N	O	S	0	0
			528	332	97	93	6		

- Molecule 24 is a RNA chain called pre-18S.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	A	1586	Total	C	N	O	P	0	0
			33827	15115	6032	11094	1586		

- Molecule 25 is a protein called Trm112.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	0	127	Total	C	N	O	S	0	0
			993	636	163	187	7		

- Molecule 26 is a protein called Methyltransferase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	267	Total	C	N	O	S	0	0
			2013	1260	355	388	10		

- Molecule 27 is a protein called Bms1-type G domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	699	Total	C	N	O	S	0	0
			5579	3506	997	1056	20		

- Molecule 28 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	184	Total	C	N	O	S	0	0
			1451	921	267	256	7		

- Molecule 29 is a protein called Bystin-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	270	Total	C	N	O	S	0	0
			2154	1401	377	366	10		

- Molecule 30 is a protein called Putative low-temperature viability protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	5	81	Total	C	N	O	S	0	0
			660	416	113	130	1		

- Molecule 31 is a protein called Serine/threonine-protein kinase RIO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	6	43	Total	C	N	O	S	0	0
			352	222	74	54	2		

- Molecule 32 is a protein called Ribosomal RNA-processing protein 12-like conserved domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	7	1004	Total	C	N	O	S	0	0
			7841	5009	1353	1441	38		

- Molecule 33 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	8	62	Total	C	N	O	S	0	0
			537	335	112	89	1		

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	Q	1	Total	Mg	0
			1	1	
34	a	1	Total	Mg	0
			1	1	

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

- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	e	1	Total	Zn	0
			1	1	

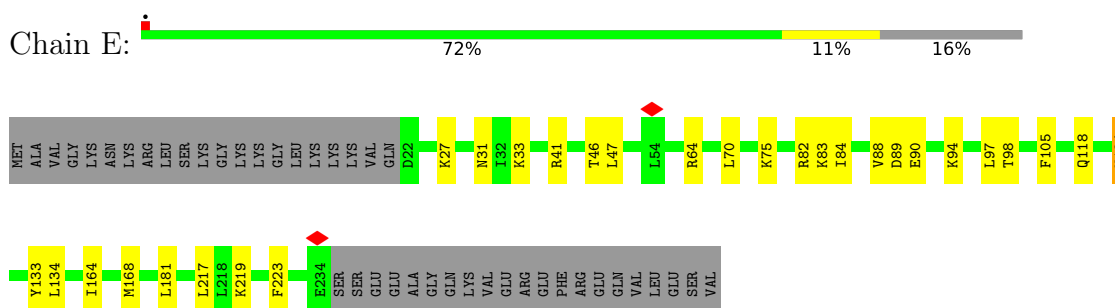
- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	Q	1	Total	O	0
			1	1	
36	A	3	Total	O	0
			3	3	

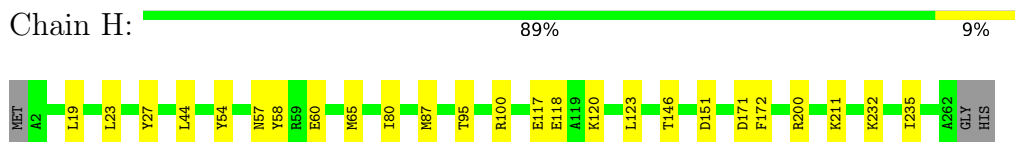
3 Residue-property plots

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.

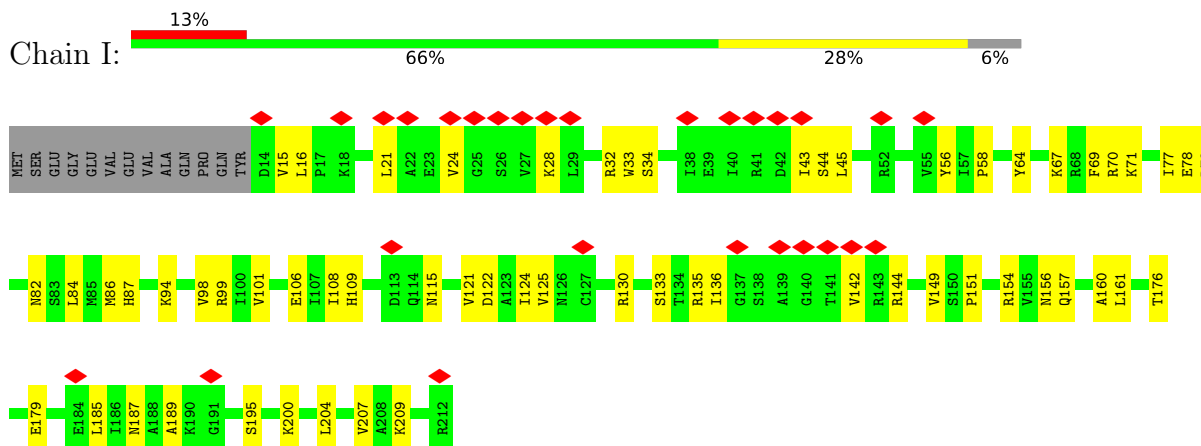
- Molecule 1: Small ribosomal subunit protein eS1



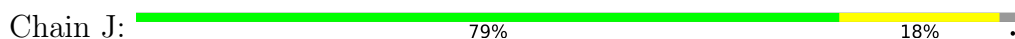
- Molecule 2: 40S ribosomal protein S4

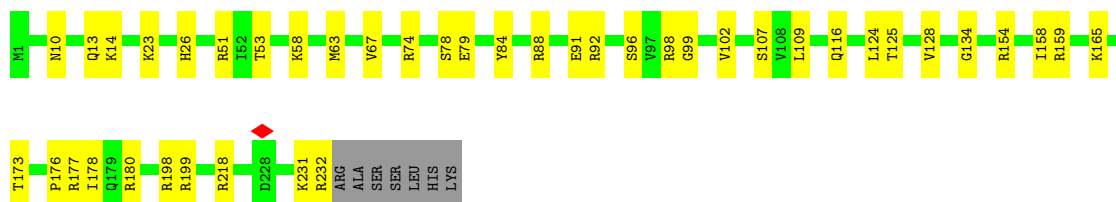


- Molecule 3: 40S ribosomal protein s5-like protein

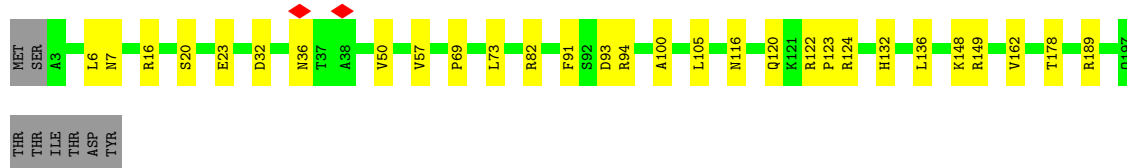
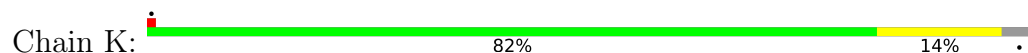


- Molecule 4: 40S ribosomal protein S6

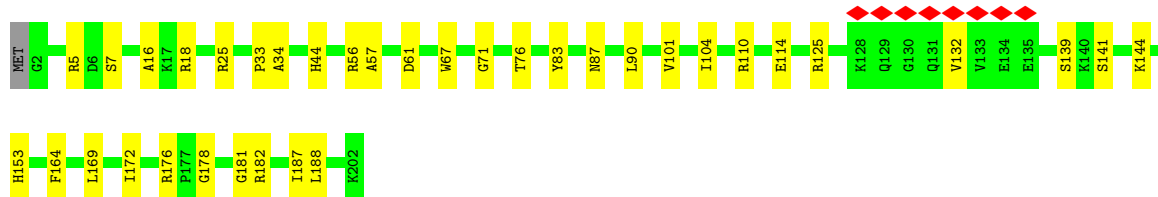
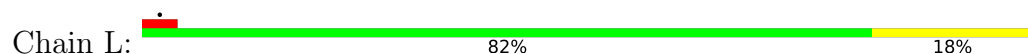




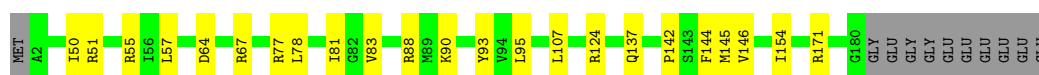
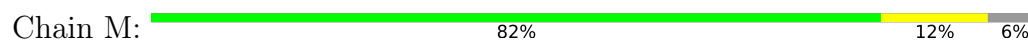
- Molecule 5: 40S ribosomal protein S7



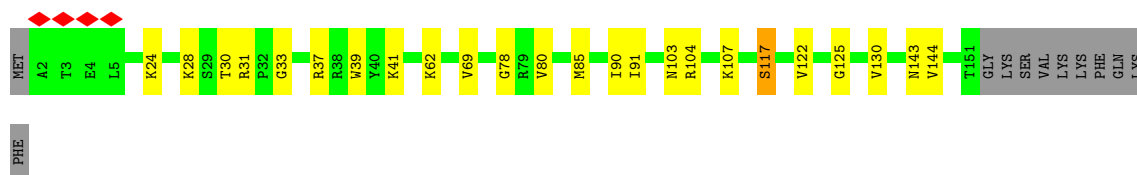
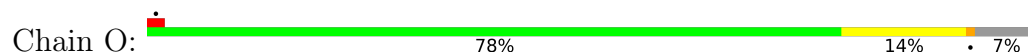
- Molecule 6: 40S ribosomal protein S8



- Molecule 7: 40S ribosomal protein s9-like protein

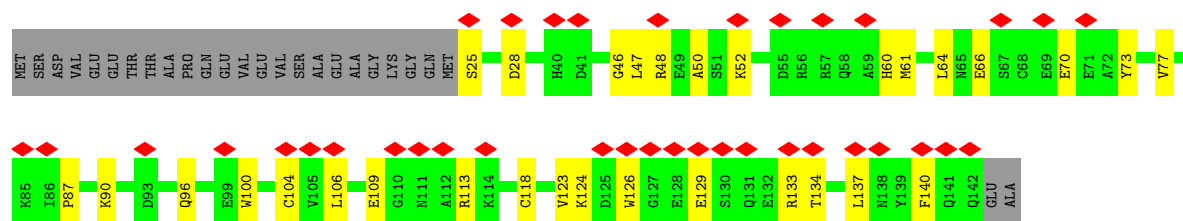


- Molecule 8: 40S ribosomal protein S11-like protein

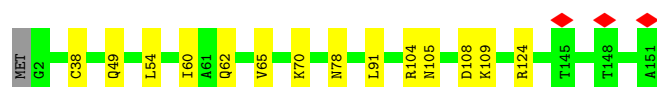
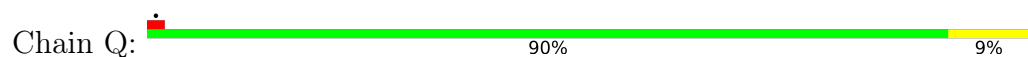


- Molecule 9: 40S ribosomal protein S12

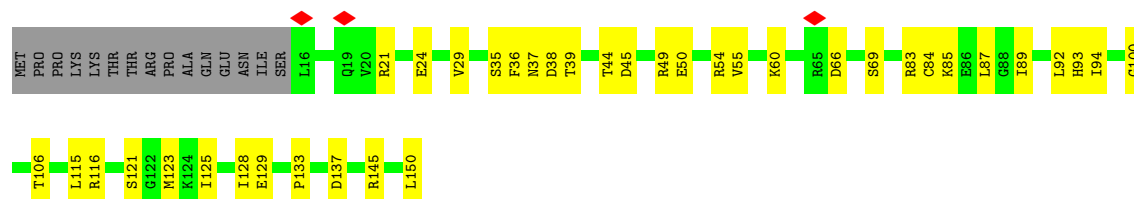




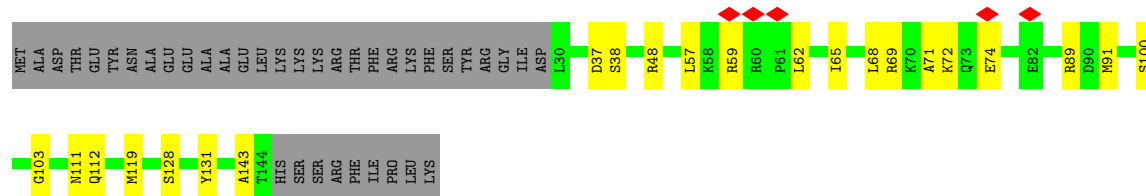
- Molecule 10: 40S ribosomal protein S13-like protein



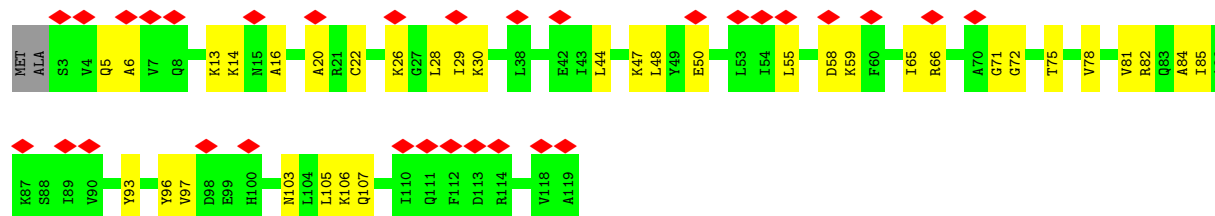
- Molecule 11: 40S ribosomal protein S14-like protein



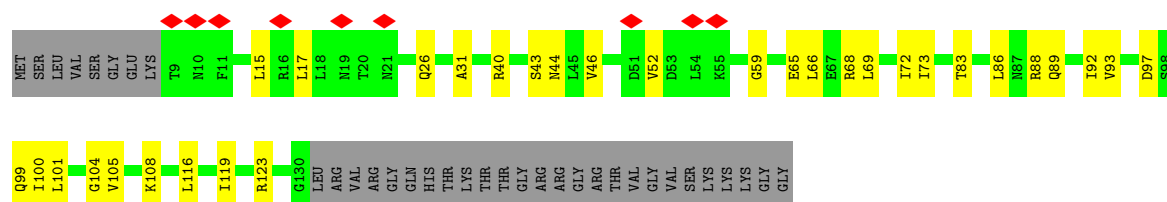
- Molecule 12: 40S ribosomal protein s15-like protein



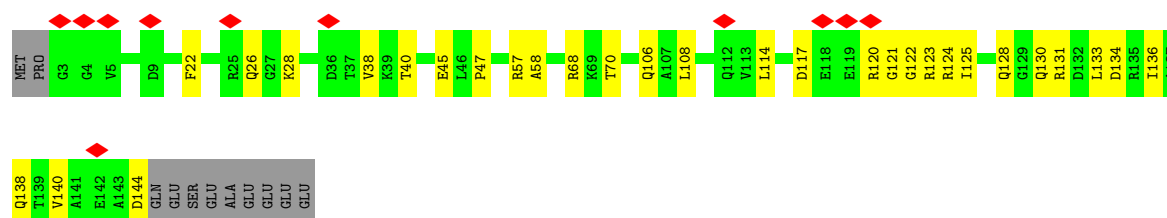
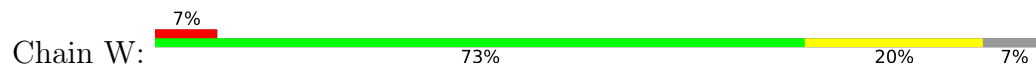
- Molecule 13: 40S ribosomal protein S16



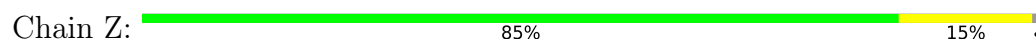
- Molecule 14: Putative ribosomal protein



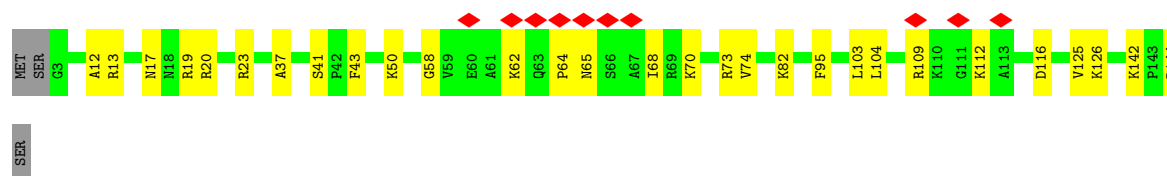
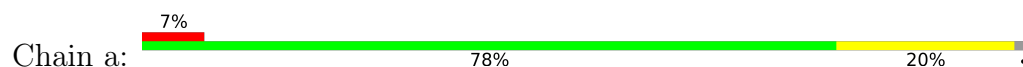
- Molecule 15: 40S ribosomal protein S19-like protein



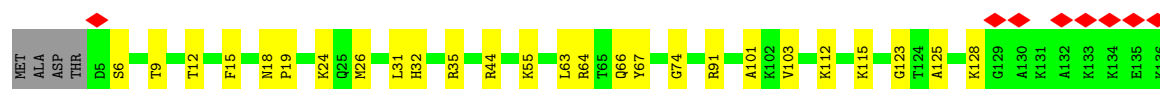
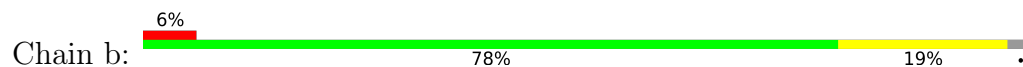
- Molecule 16: 40S ribosomal protein S22-like protein



- Molecule 17: 40S ribosomal protein s23-like protein



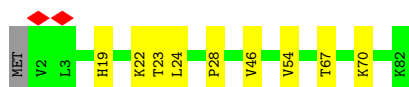
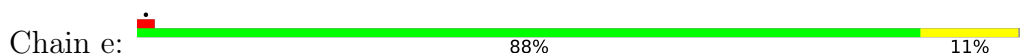
- Molecule 18: Small ribosomal subunit protein eS24



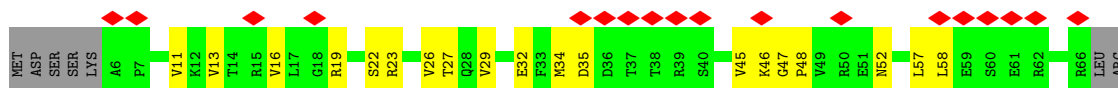
- Molecule 19: 40S ribosomal protein S25



- Molecule 20: Ribosomal protein s27-like protein



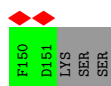
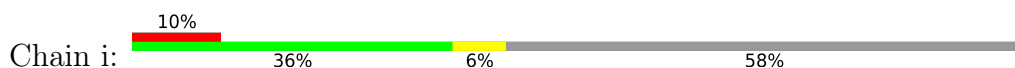
- Molecule 21: 40S ribosomal protein S28-like protein



- Molecule 22: 40S ribosomal protein S30



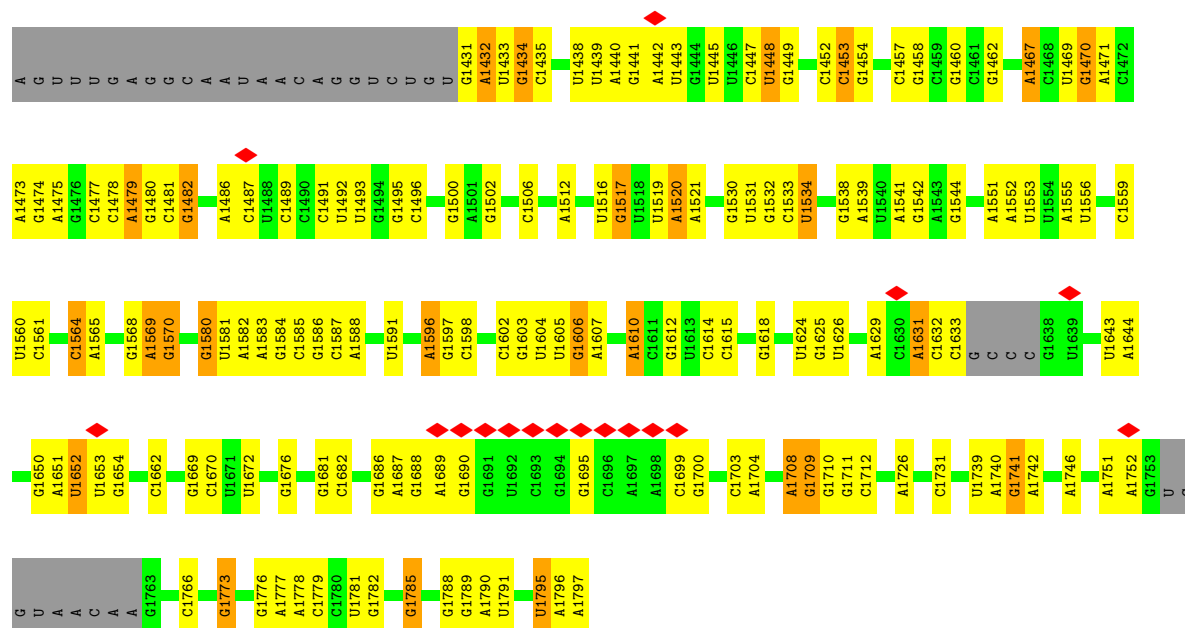
- Molecule 23: 40S ribosomal protein S27a-like protein



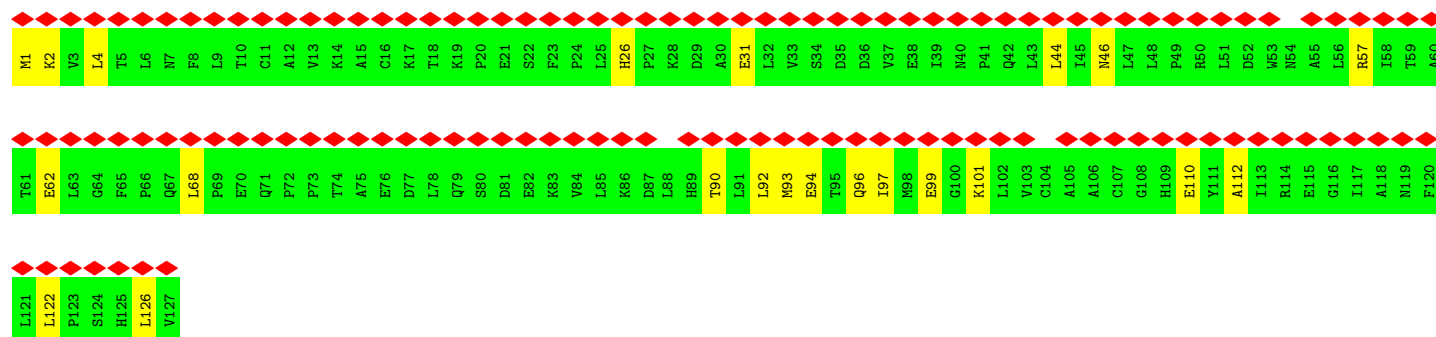
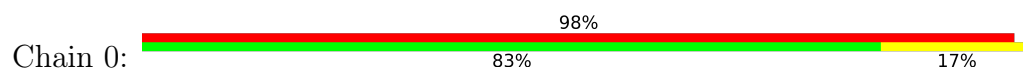
- Molecule 24: pre-18S



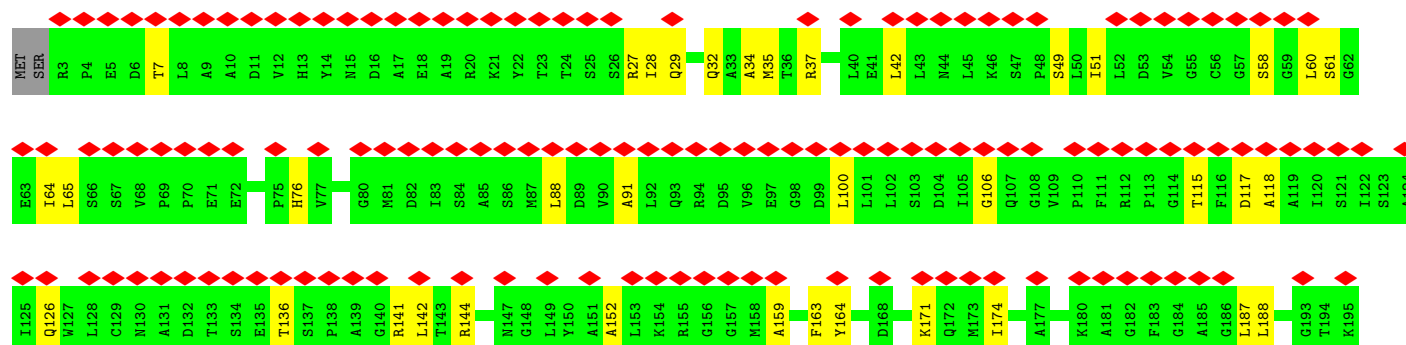
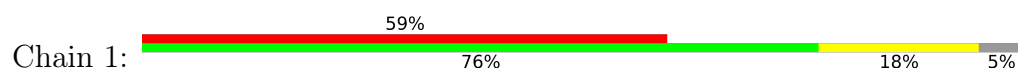


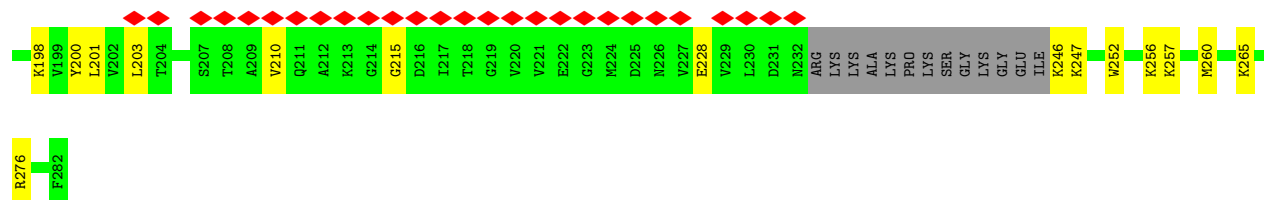


• Molecule 25: Trm112

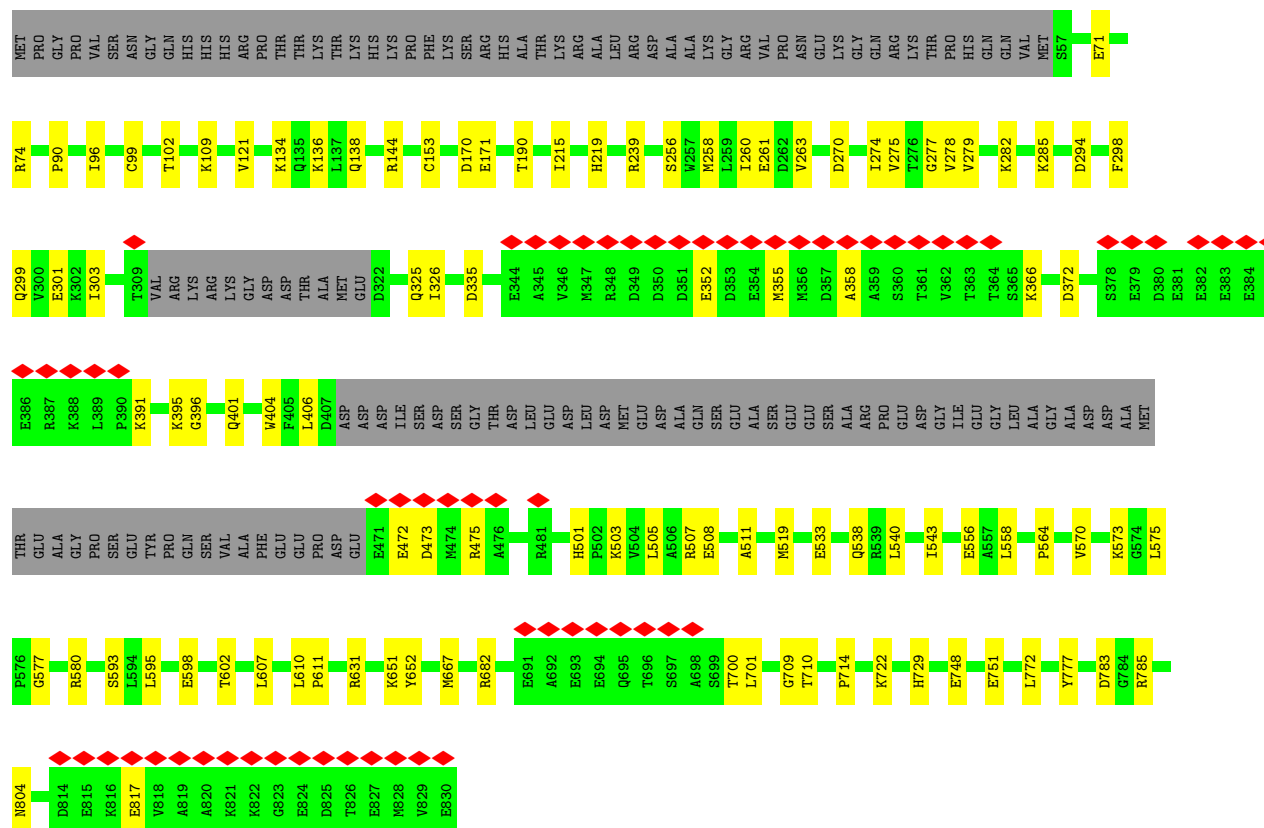


• Molecule 26: Methyltransferase-like protein

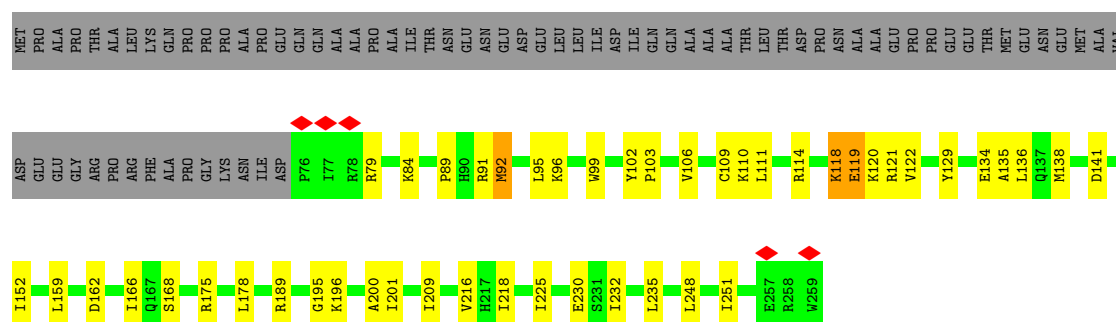




• Molecule 27: Bms1-type G domain-containing protein

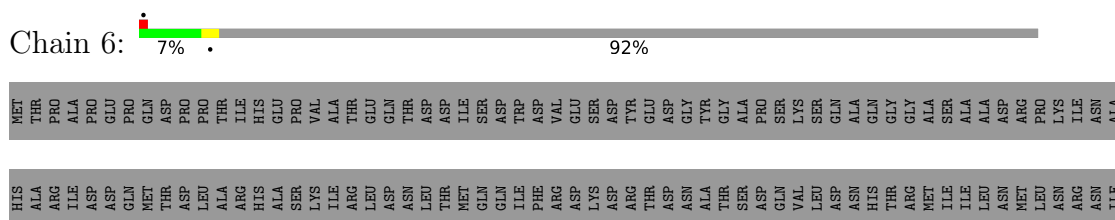


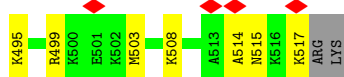
• Molecule 28: Pre-rRNA-processing protein PNO1



• Molecule 29: Bystin-like protein







Chain 7: 81% 70% 11% 19%



LYS	THR	GLY	ILE	ASN	R961	F901	D841	I781	F721	K661	A601	L541	Y481	T421
GLY	THR	GLY	THR	GLU	M962	L902	A842	P782	Q722	L662	Q602	T542	T482	I422
ILE	THR	ALA	THR	TYR	I963	T903	P943	N783	I723	A663	K603	E543	T483	G423
ALA	ARG	ALA	PRO	GLN	R964	S904	K844	T784	Q724	Q664	N604	A544	N484	E424
GLY	ARG	ALA	ILE	LEU	R965	N905	A845	S785	K725	L665	L605	D546	T485	E425
VAL	GLN	VAL	LYS	ASN	F966	N906	T846	L786	K726	L666	E906	T547	L487	R426
GLY	ARG	GLY	PRO	SER	G967	R907	A847	H787	A727	Q667	Y607	T548	L488	T427
ARG	LYS	ARG	LYS	SER	V968	E908	S848	F788	Y728	E668	L608	A548	N488	N428
GLY	LYS	GLY	LYS	SER	E969	I909	L849	I789	Y729	P669	G609	F549	D429	D429
LEU	ASP	LEU	ASP	GLU	T970	V910	E950	P790	K730	V670	E610	A550	F430	F430
TRP	ASP	TRP	ASP	SER	V971	K911	E951	S791	I731	Q671	R611	E551	K491	F431
ASP	LYS	ASP	LYS	GLU	Q972	S912	Y652	I792	P732	K672	F612	M552	T492	T432
GLU	LYS	GLU	LYS	ALA	K973	N913	M653	L793	R733	P673	A613	L553	E493	G433
SER	SER	SER	SER	ASP	H974	L914	T654	S794	L734	K674	A614	T554	L494	K434
PRO	LYS	PRO	LYS	SER	T975	G915	M655	E795	A735	N675	D615	T555	V495	Q435
GLY	GLY	GLY	LYS	ASP	P976	F916	V656	V796	E736	P676	I616	V556	P496	E436
ILE	ASP	ILE	ASP	ASP	E977	N917	S857	V797	S737	N677	L617	L557	L497	A437
ASN	ASN	ASN	ASN	ASP	A978	K918	A858	I798	E738	Q678	A618	Y558	S498	D438
ASP	ALA	ASP	ALA	ASP	D979	V919	G859	G799	V739	E579	V619	E559	A499	V439
GLY	GLY	GLY	GLY	GLU	R980	C920	L860	C900	G740	Q680	L620	Q560	A500	V440
MET	LYS	MET	LYS	MET	K981	I921	A861	K601	R741	V681	F621	P561	M501	L441
THR	THR	THR	THR	THR	L982	I922	G662	E902	A742	P682	N622	E562	Y502	G442
GLY	GLY	GLY	GLY	GLY	I983	S923	S963	H603	A743	S983	V623	L563	Q503	K443
ARG	ARG	ARG	ARG	ARG	L924	L924	T964	N804	L744	T684	Y624	R564	R504	A444
GLN	GLN	GLN	GLN	GLN	P925	P925	P965	E805	E745	A885	S625	L565	V505	I445
LYS	LYS	LYS	LYS	LYS	T926	T926	H866	K806	E746	H886	T626	D566	L506	R446
ASP	ASP	ASP	ASP	ASP	D927	D927	G867	A807	R747	T687	T627	V567	E507	A447
GLU	GLU	GLU	GLU	GLU	L928	L928	I668	B608	H748	L688	T628	C568	H508	M448
THR	THR	THR	THR	THR	N929	N929	S869	T609	E749	M689	P629	R569	G509	G449
GLY	GLY	GLY	GLY	GLY	L930	L930	A870	T610	E750	D690	Q630	A570	N510	P450
ASN	ASN	ASN	ASN	ASN	P931	P931	T671	A611	V751	L691	K631	L571	A511	E451
ASP	ASP	ASP	ASP	ASP	R932	R932	L672	F612	Q752	V692	R632	R572	P512	A452
ILE	ILE	ILE	ILE	ILE	L933	L933	L873	D613	Q753	V693	G633	A573	K513	V453
LYS	LYS	LYS	LYS	LYS	P934	P934	A874	L614	L754	T694	P634	L574	T514	L454
ALA	ALA	ALA	ALA	ALA	T935	T935	L675	L615	L755	M695	V635	V575	M515	N455
MET	MET	MET	MET	MET	L936	L936	T676	V616	L756	S696	L636	E576	E516	V456
ASP	ASP	ASP	ASP	ASP	I937	I937	R677	L617	S757	I697	Q637	S577	V517	L457
ASN	ASN	ASN	ASN	ASN	P938	P938	V678	M618	A758	Y698	T638	N578	K518	P458
PRO	PRO	PRO	PRO	PRO	N939	N939	L879	M619	A759	L699	I639	Q579	I519	L459
LEU	LEU	LEU	LEU	LEU	V940	V940	Y880	H620	D760	P700	N640	A580	F520	N460
ASP	ASP	ASP	ASP	ASP	N1002	N1002	E881	K621	K761	R701	S641	I581	E521	L461
GLY	GLY	GLY	GLY	GLY	G1003	G1003	F882	M622	V762	E702	F642	V582	T522	I462
ASN	ASN	ASN	ASN	ASN	A1004	A1004	R883	V623	S763	S703	L643	S583	V523	K463
ARG	ARG	ARG	ARG	ARG	Y943	Y943	E884	E824	S764	F704	S644	A584	V524	P464
ASN	ASN	ASN	ASN	ASN	H945	H945	A885	A825	P765	E705	I645	G585	Q525	A465
ALA	ALA	ALA	ALA	ALA	E946	E946	L886	N626	A766	A706	I646	D586	Q526	R466
ALA	ALA	ALA	ALA	ALA	H947	H947	L887	N627	R767	L707	P647	V587	I527	D467
VAL	VAL	VAL	VAL	VAL	K948	K948	K888	G627	R768	F708	K648	E588	W528	Q468
ALA	ALA	ALA	ALA	ALA	G949	G949	E889	S828	E769	K709	T649	D589	S529	P469
GLY	GLY	GLY	GLY	GLY	H950	H950	T690	L830	R770	I710	R650	P590	I530	G470
LYS	LYS	LYS	LYS	LYS	F951	F951	L891	D631	L771	A711	L651	V591	L531	R471
ARG	ARG	ARG	ARG	ARG	R952	R952	T692	N832	A772	A712	M652	I592	P532	A472
LYS	LYS	LYS	LYS	LYS	A953	A953	D893	S833	A773	L713	E853	L593	G533	W473
SER	SER	SER	SER	SER	K954	K954	L894	K634	I774	V714	T654	C594	Y534	M474
ARG	ARG	ARG	ARG	ARG	V955	V955	V895	V635	A775	V715	F655	R595	C535	L475
PHE	PHE	PHE	PHE	PHE	K956	K956	Q896	P836	A776	F716	D656	V596	D536	P476
ASP	ASP	ASP	ASP	ASP	H957	H957	T697	H637	L777	L717	L657	S597	L537	L477
					T958	T958	T697	H638	L778	D718	V658	K598	P538	L478
					F959	F959	D699	P639	P779	D719	C659	Q599	L539	R479
					E960	E960	L900	K840	I780	D720	E960	T600	D540	D480

• Molecule 33: Utp14

Chain 8: 5% .

93%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	211537	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; Relion	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.485	Depositor
Minimum map value	-0.247	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	376.19998, 376.19998, 376.19998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.045, 1.045, 1.045	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

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	E	0.31	0/1752	0.57	0/2361
2	H	0.30	0/2112	0.53	1/2842 (0.0%)
3	I	0.21	0/1578	0.55	0/2130
4	J	0.33	0/1906	0.57	0/2547
5	K	0.23	0/1587	0.54	0/2140
6	L	0.28	0/1654	0.48	0/2213
7	M	0.27	0/1489	0.45	0/1993
8	O	0.52	1/1249 (0.1%)	0.71	0/1678
9	P	0.17	0/934	0.53	0/1255
10	Q	0.35	0/1205	0.54	0/1627
11	R	0.32	0/1014	0.65	0/1361
12	S	0.20	0/932	0.54	0/1248
13	T	0.19	0/922	0.56	0/1241
14	V	0.18	0/1012	0.50	0/1360
15	W	0.19	0/1137	0.55	0/1533
16	Z	0.39	0/1055	0.58	0/1416
17	a	0.28	0/1116	0.47	0/1489
18	b	0.27	0/1075	0.46	0/1431
19	c	0.19	0/550	0.53	0/736
20	e	0.30	0/623	0.64	0/843
21	f	0.22	0/487	0.64	0/653
22	h	0.61	0/184	0.98	0/242
23	i	0.19	0/535	0.54	0/710
24	A	0.28	0/37830	0.41	1/58939 (0.0%)
25	0	0.17	0/1013	0.48	0/1378
26	1	0.16	0/2043	0.46	0/2753
27	2	0.19	0/5694	0.43	0/7705
28	3	0.50	0/1475	0.79	2/1982 (0.1%)
29	4	0.19	0/2205	0.49	0/2990
30	5	0.22	0/670	0.66	0/896
31	6	0.20	0/356	0.43	0/462
32	7	0.18	0/7995	0.43	0/10857

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	8	0.82	0/544	1.33	4/717 (0.6%)
All	All	0.28	1/85933 (0.0%)	0.48	8/123728 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	O	117	SER	CA-CB	-5.69	1.44	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1073	A	C4'-C3'-O3'	5.88	121.81	113.00
2	H	232	LYS	CA-CB-CG	5.77	125.64	114.10
33	8	404	LYS	N-CA-C	-5.71	105.57	112.54
28	3	118	LYS	CA-C-N	-5.38	111.62	122.55
28	3	118	LYS	C-N-CA	-5.38	111.62	122.55

There are no chirality outliers.

There are no planarity outliers.

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	E	1723	0	1804	17	0
2	H	2072	0	2155	21	0
3	I	1557	0	1608	37	0
4	J	1875	0	1983	31	0
5	K	1562	0	1641	20	0
6	L	1621	0	1645	26	0
7	M	1466	0	1582	17	0
8	O	1222	0	1289	13	0
9	P	923	0	946	19	0
10	Q	1182	0	1264	10	0
11	R	1002	0	1034	27	0
12	S	917	0	978	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	T	909	0	973	24	0
14	V	998	0	1042	22	0
15	W	1117	0	1133	21	0
16	Z	1037	0	1076	11	0
17	a	1099	0	1169	20	0
18	b	1061	0	1150	18	0
19	c	546	0	591	12	0
20	e	611	0	635	5	0
21	f	484	0	513	15	0
22	h	181	0	207	7	0
23	i	528	0	541	6	0
24	A	33827	0	17047	303	0
25	0	993	0	1018	13	0
26	1	2013	0	2043	35	0
27	2	5579	0	5570	65	0
28	3	1451	0	1524	48	0
29	4	2154	0	2242	26	0
30	5	660	0	648	12	0
31	6	352	0	402	7	0
32	7	7841	0	8114	82	0
33	8	537	0	573	12	0
34	A	1	0	0	0	0
34	Q	1	0	0	0	0
34	a	1	0	0	0	0
35	e	1	0	0	0	0
36	A	3	0	0	0	0
36	Q	1	0	0	0	0
All	All	81108	0	66140	896	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 6.

The worst 5 of 896 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)
28:3:119:GLU:N	28:3:119:GLU:OE2	1.62	1.28
27:2:263:VAL:HA	27:2:274:ILE:O	1.34	1.23
28:3:119:GLU:HG3	28:3:121:ARG:HH11	1.07	1.08
4:J:198:ARG:HG2	24:A:175:G:H22	1.21	1.05
28:3:119:GLU:CD	28:3:119:GLU:H	1.67	1.02

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	E	211/255 (83%)	197 (93%)	14 (7%)	0	100	100
2	H	259/264 (98%)	250 (96%)	9 (4%)	0	100	100
3	I	197/212 (93%)	183 (93%)	14 (7%)	0	100	100
4	J	230/239 (96%)	223 (97%)	7 (3%)	0	100	100
5	K	193/203 (95%)	186 (96%)	7 (4%)	0	100	100
6	L	199/202 (98%)	188 (94%)	11 (6%)	0	100	100
7	M	177/190 (93%)	169 (96%)	8 (4%)	0	100	100
8	O	148/161 (92%)	139 (94%)	9 (6%)	0	100	100
9	P	116/144 (81%)	101 (87%)	15 (13%)	0	100	100
10	Q	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
11	R	133/150 (89%)	119 (90%)	13 (10%)	1 (1%)	16	47
12	S	113/153 (74%)	105 (93%)	8 (7%)	0	100	100
13	T	115/119 (97%)	106 (92%)	9 (8%)	0	100	100
14	V	120/156 (77%)	112 (93%)	8 (7%)	0	100	100
15	W	140/153 (92%)	133 (95%)	7 (5%)	0	100	100
16	Z	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
17	a	140/145 (97%)	132 (94%)	8 (6%)	0	100	100
18	b	130/136 (96%)	125 (96%)	5 (4%)	0	100	100
19	c	67/99 (68%)	65 (97%)	2 (3%)	0	100	100
20	e	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
21	f	59/68 (87%)	53 (90%)	6 (10%)	0	100	100
22	h	19/62 (31%)	15 (79%)	3 (16%)	1 (5%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	i	61/154 (40%)	55 (90%)	6 (10%)	0	100	100
25	0	125/127 (98%)	125 (100%)	0	0	100	100
26	1	263/282 (93%)	255 (97%)	8 (3%)	0	100	100
27	2	693/830 (84%)	673 (97%)	19 (3%)	1 (0%)	48	78
28	3	182/259 (70%)	172 (94%)	9 (5%)	1 (0%)	24	57
29	4	268/480 (56%)	258 (96%)	10 (4%)	0	100	100
30	5	77/445 (17%)	72 (94%)	5 (6%)	0	100	100
31	6	41/519 (8%)	40 (98%)	1 (2%)	0	100	100
32	7	1002/1235 (81%)	988 (99%)	14 (1%)	0	100	100
33	8	58/938 (6%)	47 (81%)	9 (16%)	2 (3%)	3	16
All	All	5890/8743 (67%)	5627 (96%)	257 (4%)	6 (0%)	49	78

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	R	137	ASP
27	2	372	ASP
33	8	432	LYS
33	8	827	PRO
22	h	27	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	
1	E	187/223 (84%)	184 (98%)	3 (2%)	55	75
2	H	219/221 (99%)	219 (100%)	0	100	100
3	I	167/178 (94%)	167 (100%)	0	100	100
4	J	198/204 (97%)	198 (100%)	0	100	100
5	K	169/177 (96%)	169 (100%)	0	100	100
6	L	163/164 (99%)	163 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	M	154/162 (95%)	154 (100%)	0	100	100
8	O	133/143 (93%)	129 (97%)	4 (3%)	36	65
9	P	101/121 (84%)	101 (100%)	0	100	100
10	Q	129/130 (99%)	128 (99%)	1 (1%)	73	81
11	R	102/117 (87%)	102 (100%)	0	100	100
12	S	99/132 (75%)	99 (100%)	0	100	100
13	T	95/96 (99%)	95 (100%)	0	100	100
14	V	108/135 (80%)	108 (100%)	0	100	100
15	W	114/124 (92%)	114 (100%)	0	100	100
16	Z	112/113 (99%)	110 (98%)	2 (2%)	51	73
17	a	113/116 (97%)	113 (100%)	0	100	100
18	b	112/115 (97%)	112 (100%)	0	100	100
19	c	60/80 (75%)	60 (100%)	0	100	100
20	e	70/71 (99%)	70 (100%)	0	100	100
21	f	54/61 (88%)	54 (100%)	0	100	100
22	h	19/52 (36%)	16 (84%)	3 (16%)	2	12
23	i	57/139 (41%)	57 (100%)	0	100	100
25	0	113/113 (100%)	113 (100%)	0	100	100
26	1	215/227 (95%)	215 (100%)	0	100	100
27	2	606/714 (85%)	606 (100%)	0	100	100
28	3	155/215 (72%)	153 (99%)	2 (1%)	61	77
29	4	229/411 (56%)	229 (100%)	0	100	100
30	5	70/373 (19%)	70 (100%)	0	100	100
31	6	36/447 (8%)	36 (100%)	0	100	100
32	7	864/1049 (82%)	864 (100%)	0	100	100
33	8	57/765 (8%)	56 (98%)	1 (2%)	51	73
All	All	5080/7388 (69%)	5064 (100%)	16 (0%)	84	87

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	3	119	GLU
28	3	92	MET

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Mol	Chain	Res	Type
16	Z	19	LYS
22	h	39	LEU
10	Q	49	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
23	i	139	GLN
27	2	597	HIS
25	0	67	GLN
27	2	193	GLN
31	6	515	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	A	1576/1797 (87%)	378 (23%)	22 (1%)

5 of 378 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	A	2	A
24	A	3	C
24	A	4	C
24	A	5	U
24	A	6	G

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	A	1224	A
24	A	1531	U
24	A	1477	C
24	A	1564	C
24	A	522	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 4 ligands modelled in this entry, 4 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.

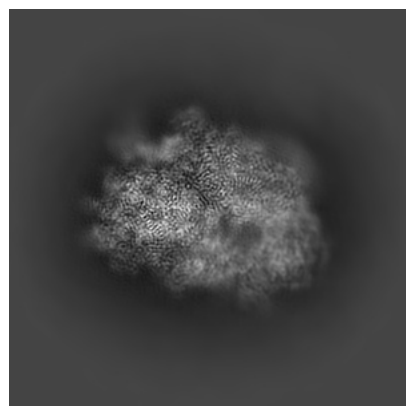
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66689. These allow visual inspection of the internal detail of the map and identification of artifacts.

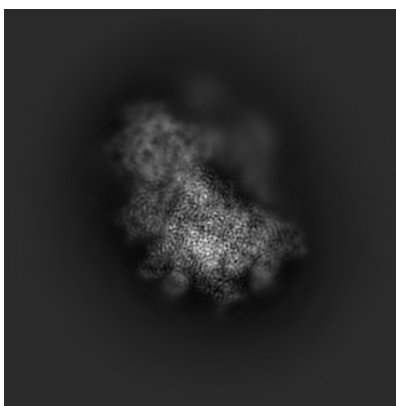
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

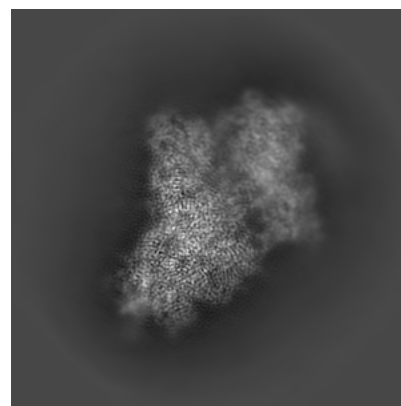
6.1.1 Primary map



X

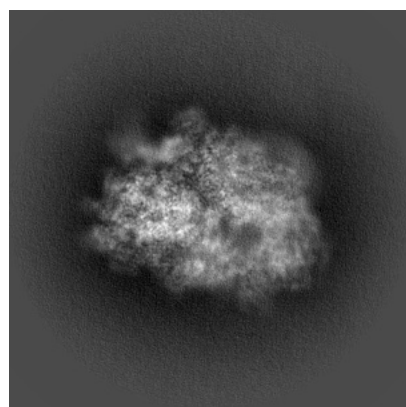


Y

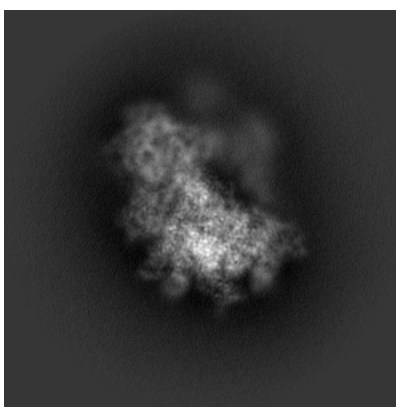


Z

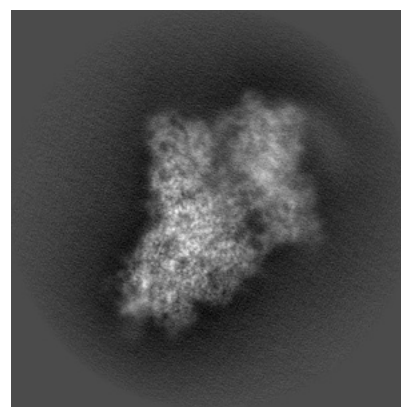
6.1.2 Raw map



X



Y

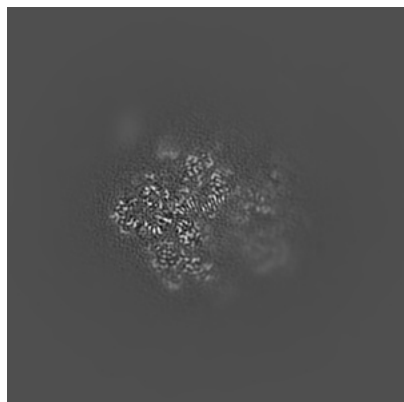


Z

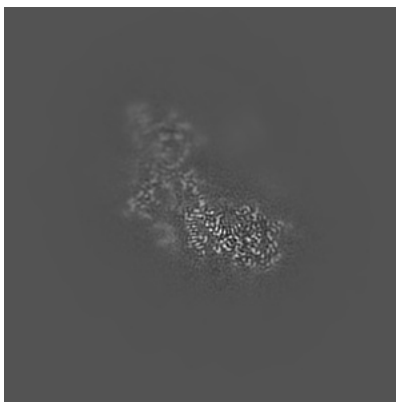
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

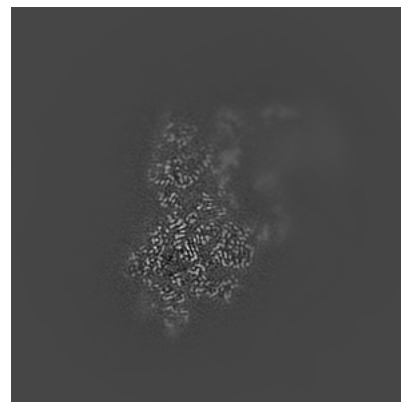
6.2.1 Primary map



X Index: 180

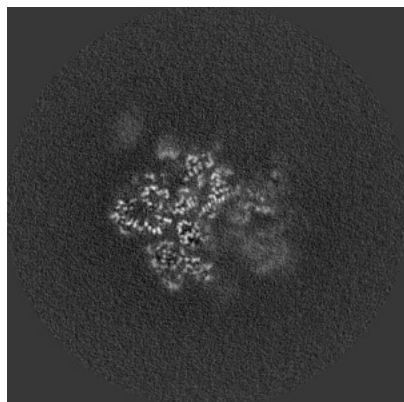


Y Index: 180

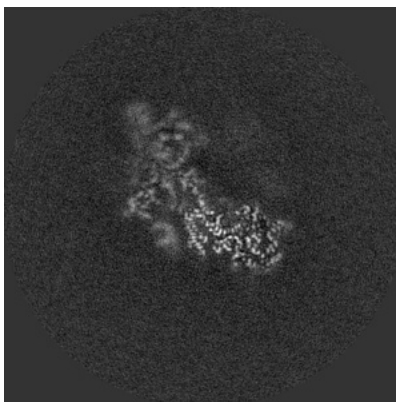


Z Index: 180

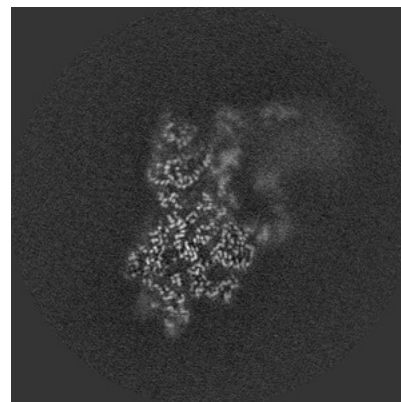
6.2.2 Raw map



X Index: 180



Y Index: 180

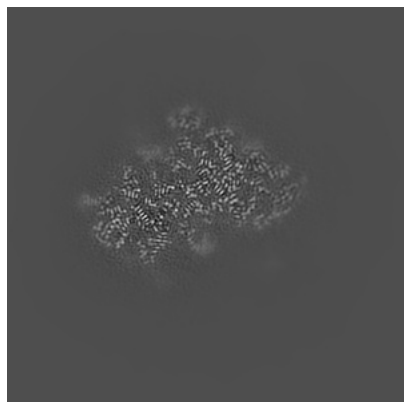


Z Index: 180

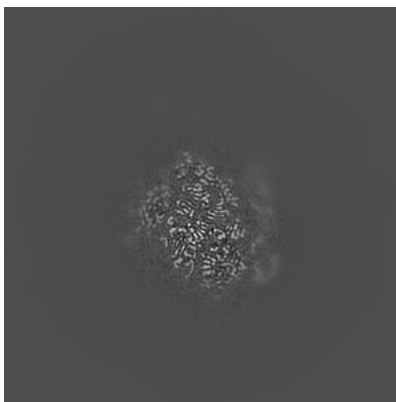
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

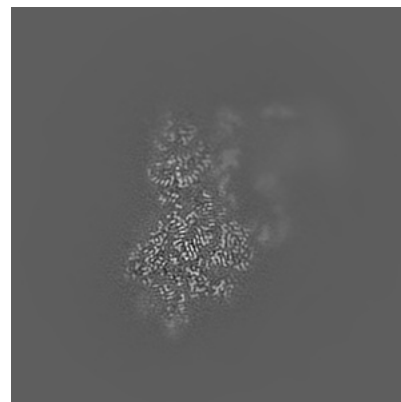
6.3.1 Primary map



X Index: 147

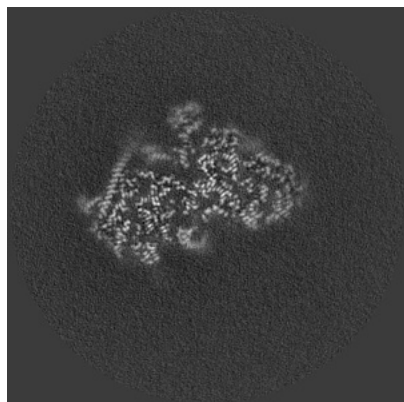


Y Index: 139

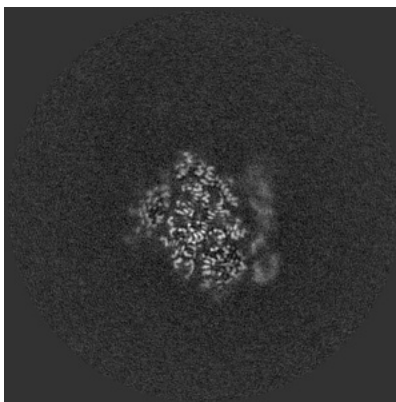


Z Index: 181

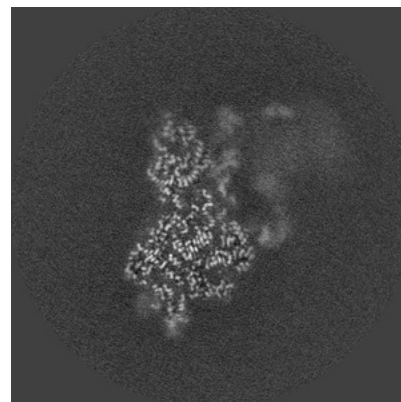
6.3.2 Raw map



X Index: 143



Y Index: 139

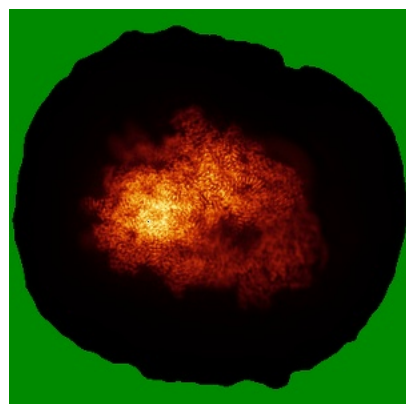


Z Index: 182

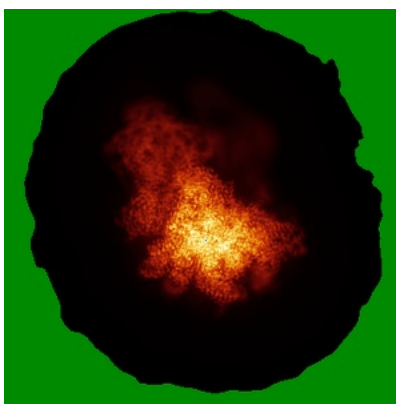
The images above show the largest variance slices of the map in three orthogonal directions.

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

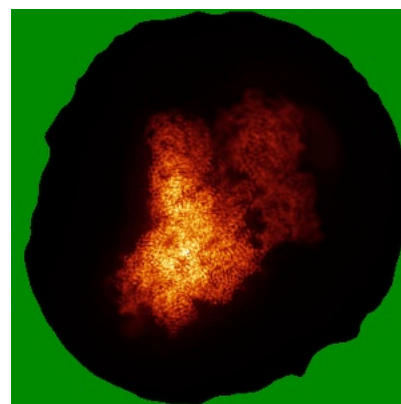
6.4.1 Primary map



X

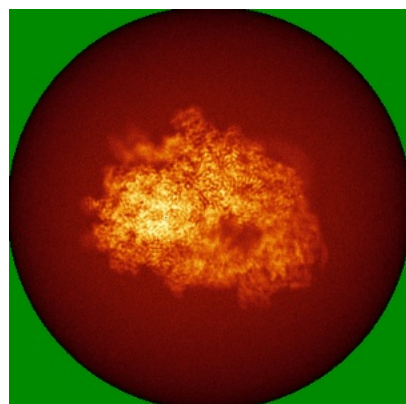


Y

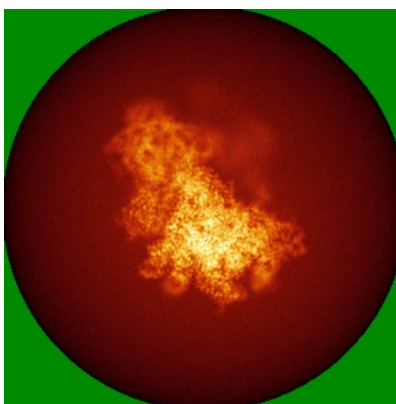


Z

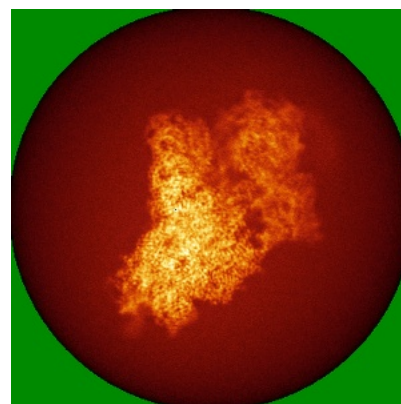
6.4.2 Raw map



X



Y

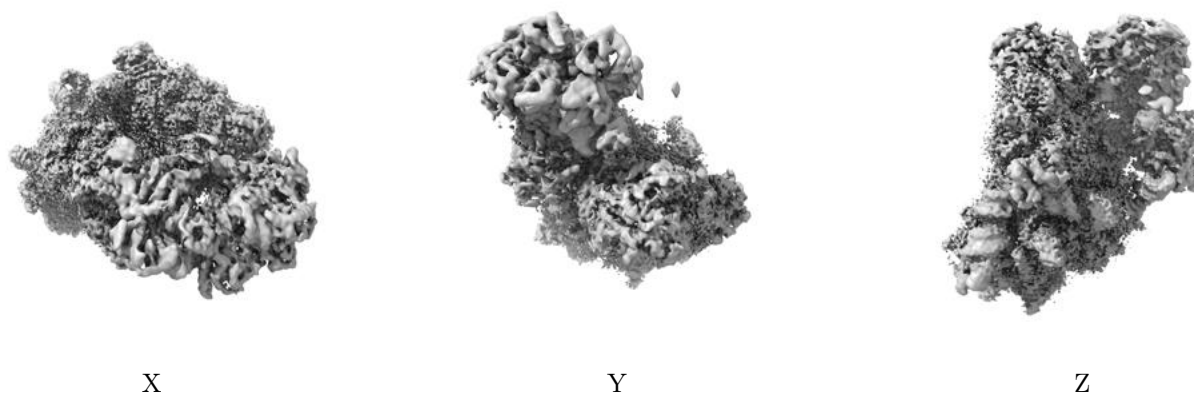


Z

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.

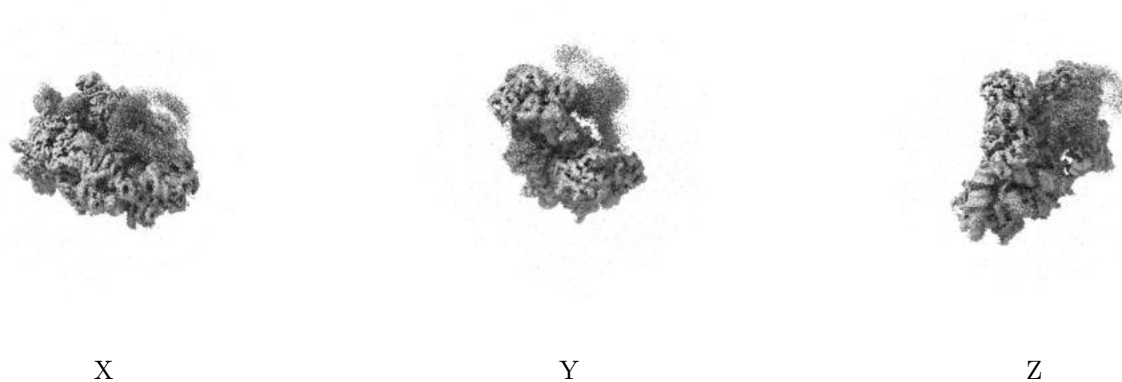
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

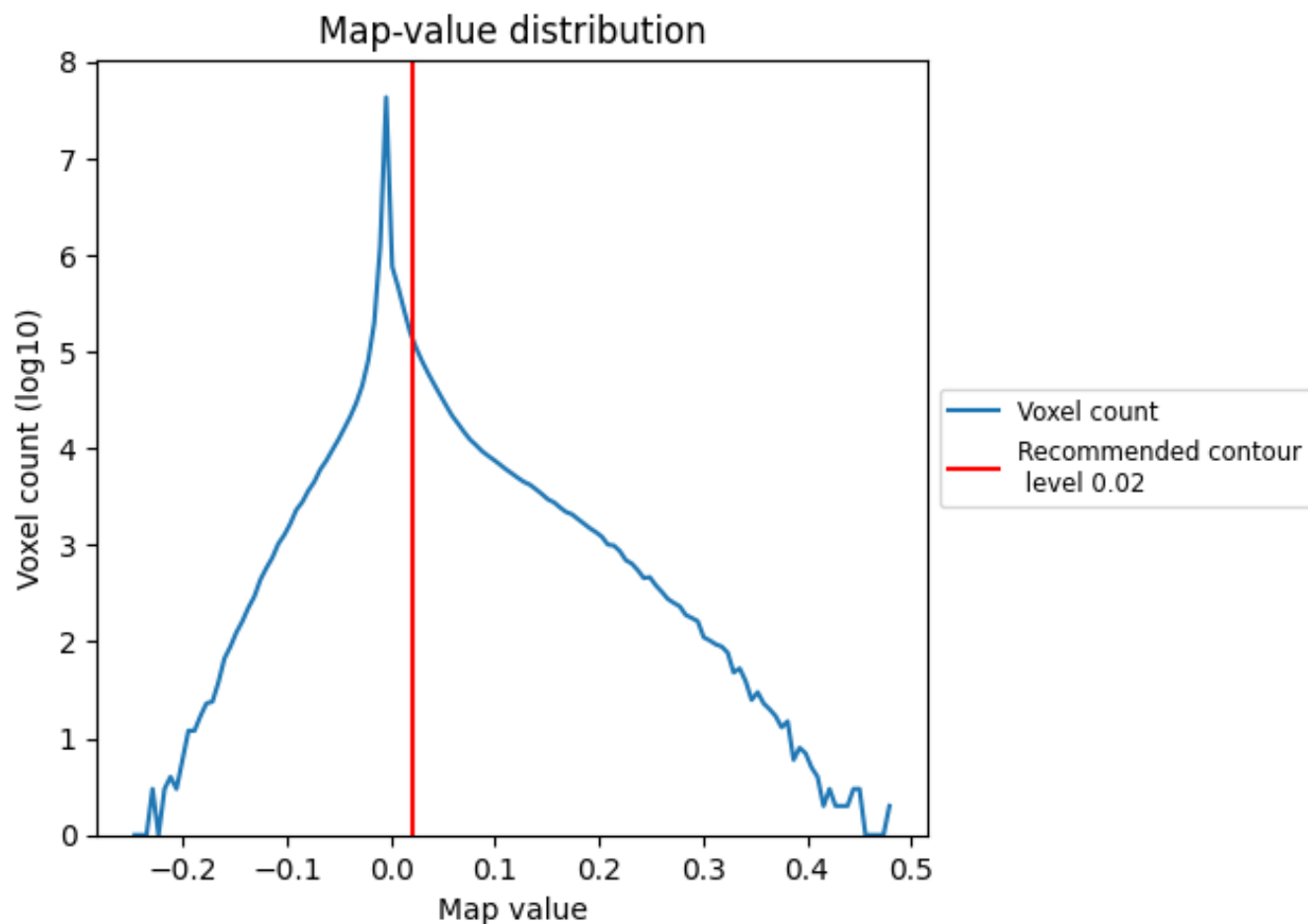
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

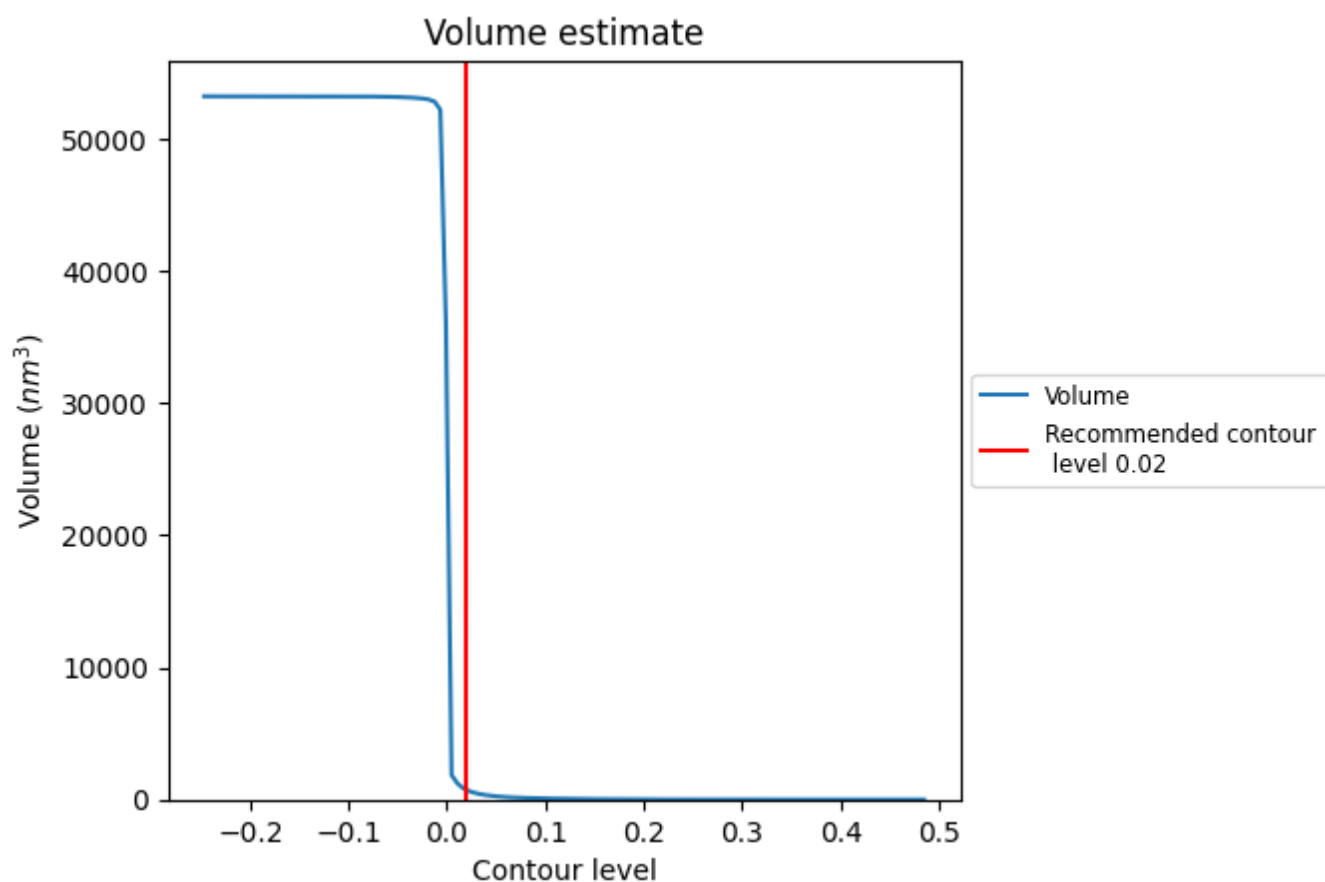
This section contains the results of statistical analysis of the map.

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.

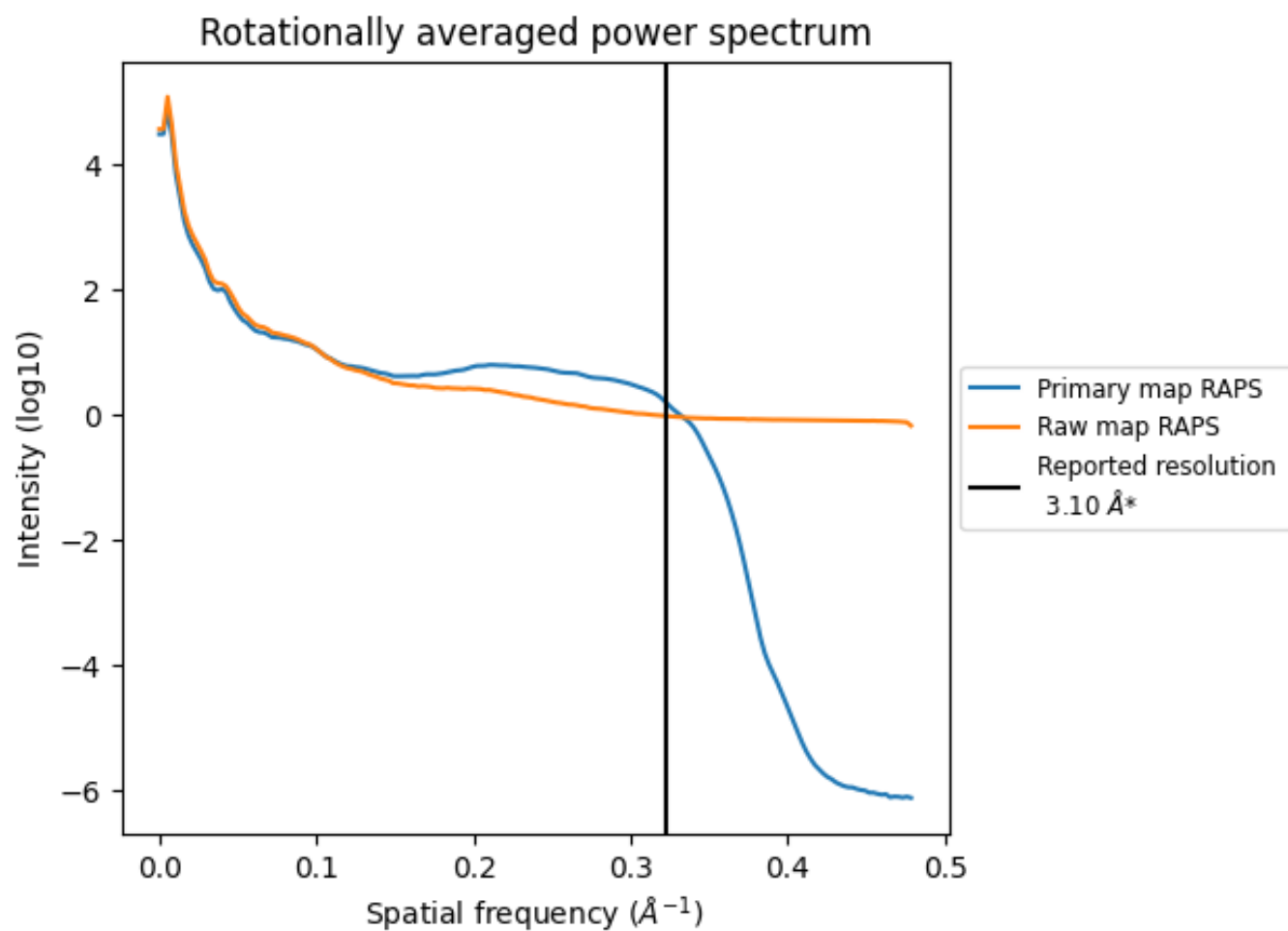
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 732 nm^3 ; this corresponds to an approximate mass of 661 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 ⓘ

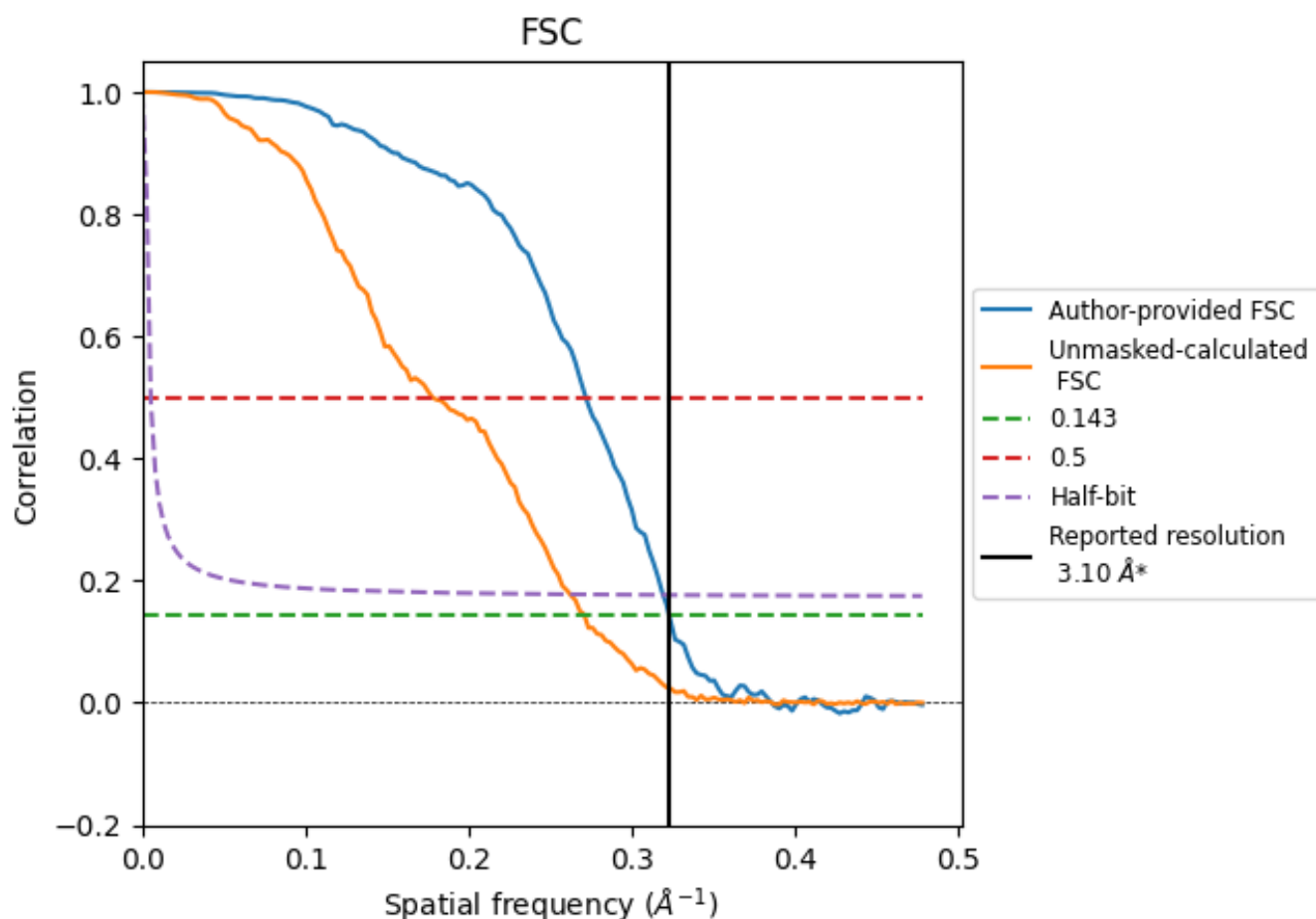


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

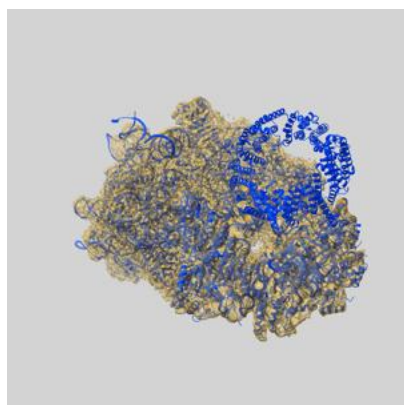
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.67	3.13
Unmasked-calculated*	3.69	5.62	3.81

*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 3.69 differs from the reported value 3.1 by more than 10 %

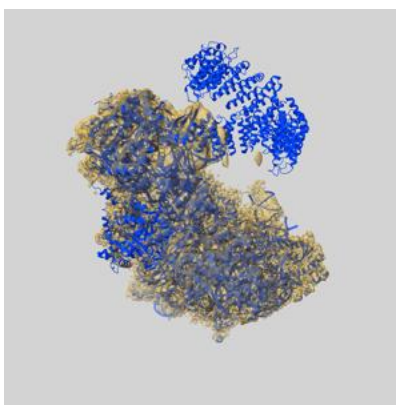
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-66689 and PDB model 9XAJ. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

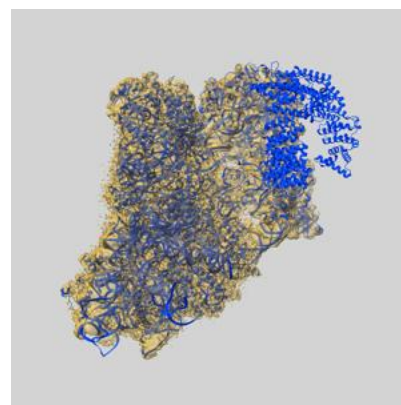
9.1 Map-model overlay [i](#)



X



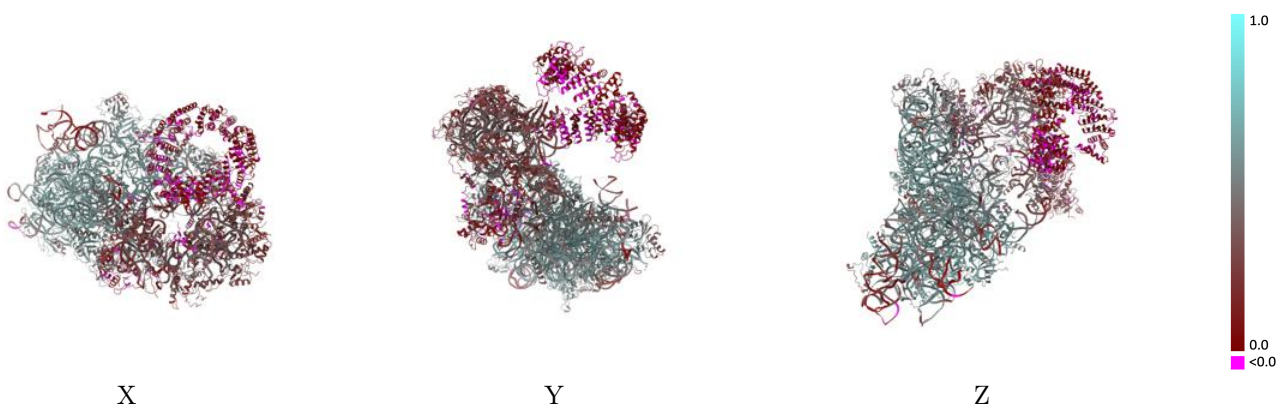
Y



Z

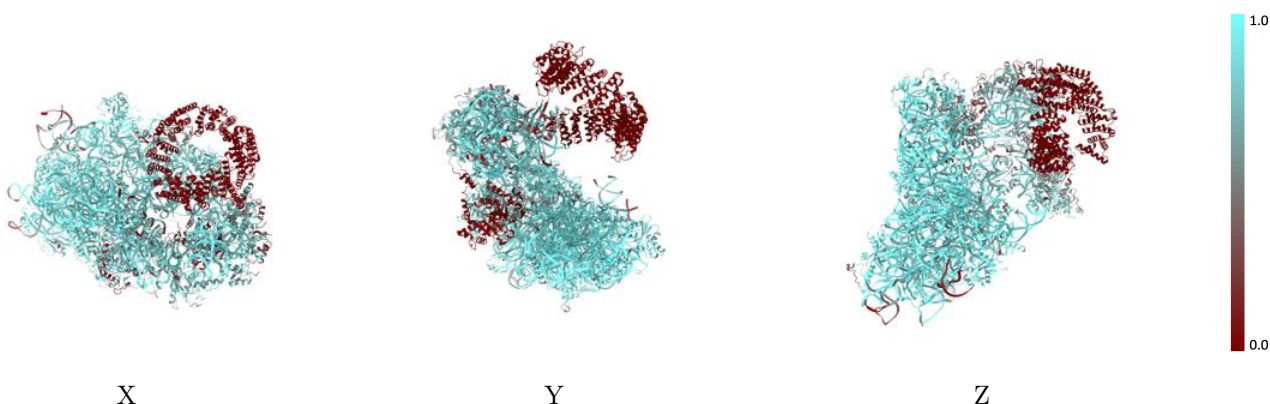
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



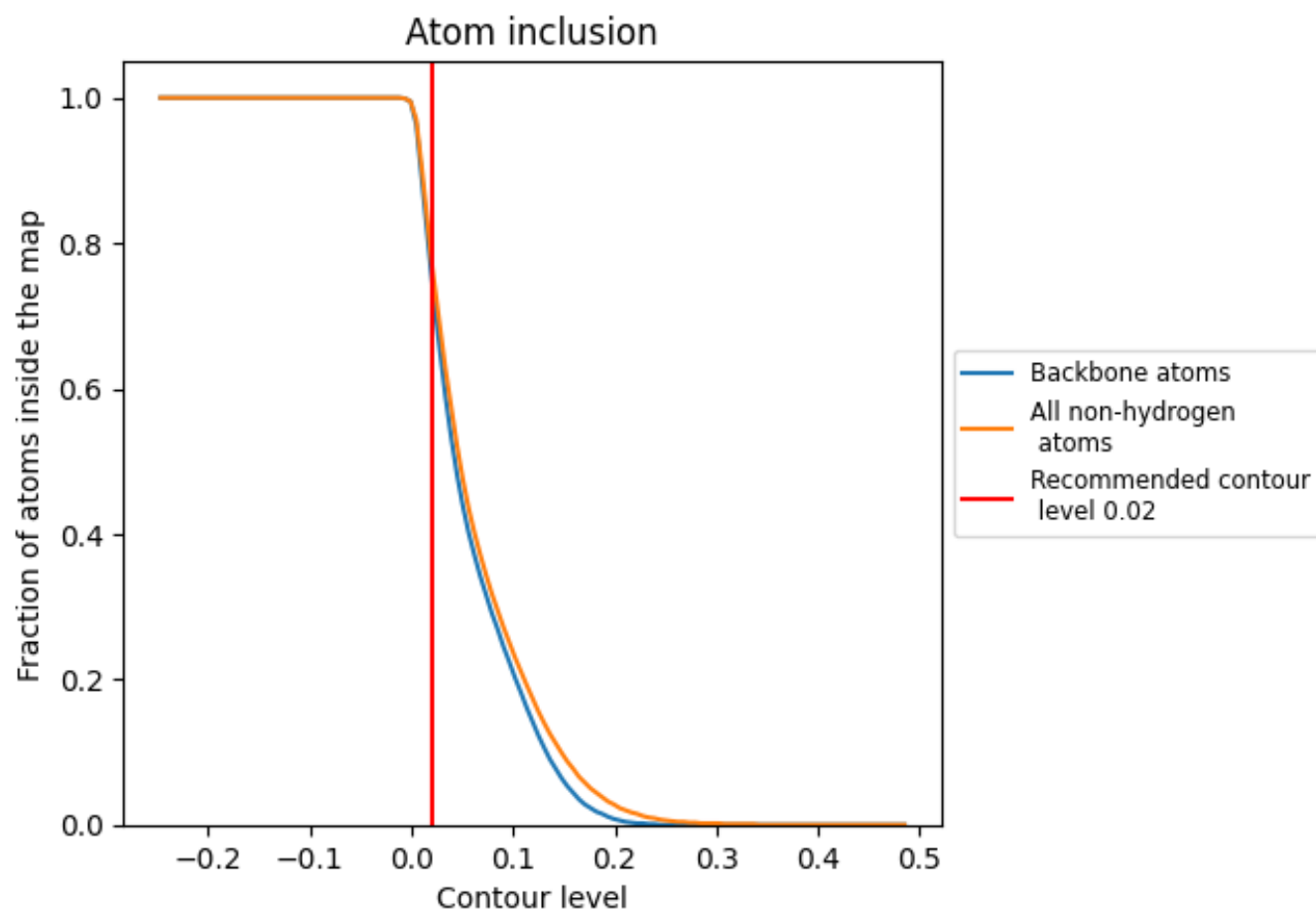
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion ⓘ



At the recommended contour level, 75% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7720	 0.4170
0	 0.0350	 0.1250
1	 0.3280	 0.2030
2	 0.8330	 0.4690
3	 0.8790	 0.4770
4	 0.7390	 0.3240
5	 0.6520	 0.2770
6	 0.7530	 0.4070
7	 0.0070	 0.0570
8	 0.7200	 0.3660
A	 0.9330	 0.4800
E	 0.9230	 0.5220
H	 0.9810	 0.6160
I	 0.6500	 0.2670
J	 0.9360	 0.5410
K	 0.9220	 0.4940
L	 0.9230	 0.5690
M	 0.9720	 0.5810
O	 0.9550	 0.6100
P	 0.5340	 0.1920
Q	 0.9590	 0.5810
R	 0.8820	 0.4880
S	 0.7830	 0.3750
T	 0.5840	 0.2630
V	 0.7450	 0.3350
W	 0.7300	 0.3190
Z	 0.9770	 0.6000
a	 0.8810	 0.5430
b	 0.9180	 0.5610
c	 0.4110	 0.2080
e	 0.9450	 0.5420
f	 0.5430	 0.2470
h	 0.9710	 0.5500
i	 0.6380	 0.2260

