



wwPDB EM Validation Summary Report ⓘ

Jun 8, 2024 – 08:17 AM EDT

PDB ID : 8E5T
EMDB ID : EMD-27919
Title : Yeast co-transcriptional Noc1-Noc2 RNP assembly checkpoint intermediate
Authors : Sanghai, Z.A.; Piwowarczyk, R.; Vanden Broeck, A.; Klinge, S.
Deposited on : 2022-08-22
Resolution : 4.00 Å(reported)
Based on initial model : 6C0F

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

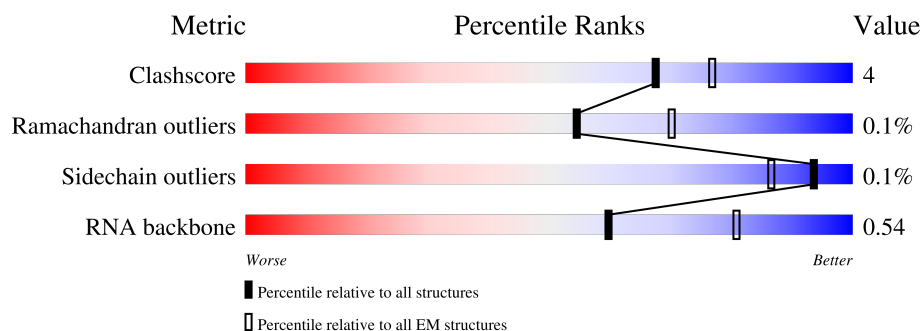
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	5	1025	
2	6	710	
3	C	362	
4	D	306	
5	E	176	
6	F	244	
7	G	256	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	K	376	
9	L	199	
10	M	138	
11	N	204	
12	Q	186	
13	S	172	
14	b	291	
15	e	130	
16	f	107	
17	i	100	
18	m	427	
19	n	605	
20	o	220	
21	p	505	
22	s	807	
23	t	322	
24	z	278	
25	O	199	
26	1	3396	
27	2	159	
28	3	232	

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 55125 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 Ribosome biogenesis protein MAK21.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	530	Total	C	N	O	S	0	0
			4332	2806	716	803	7		

- Molecule 2 is a protein called NOC2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	6	514	Total	C	N	O	S	0	0
			4156	2678	704	759	15		

- Molecule 3 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	283	Total	C	N	O	0	0
			2166	1371	404	391		

- Molecule 4 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	130	Total	C	N	O	S	0	0
			1086	685	202	191	8		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	143	Total	C	N	O	S	0	0
			1136	738	202	195	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	242	Total	C	N	O	S	0	0
			1941	1249	352	339	1		

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	187	Total	C	N	O	0	0
			926	552	187	187		

- Molecule 8 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	K	254	Total	C	N	O	0	0
			1263	755	254	254		

- Molecule 9 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	L	76	Total	C	N	O	0	0
			376	224	76	76		

- Molecule 10 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	115	Total	C	N	O	S	0	0
			892	573	169	148	2		

- Molecule 11 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	N	148	Total	C	N	O	0	0
			733	437	148	148		

- Molecule 12 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	132	Total	C	N	O	S	0	0
			1015	648	191	175	1		

- Molecule 13 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	166	Total	C	N	O	S	0	0
			1394	895	261	235	3		

- Molecule 14 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	b	217	Total	C	N	O	0	0
			1075	641	217	217		

- Molecule 15 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	e	78	Total	C	N	O	S	0
			598	382	110	105	1	0

- Molecule 16 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	f	88	Total	C	N	O	S	0
			706	454	134	117	1	0

- Molecule 17 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	i	76	Total	C	N	O		0
			376	224	76	76		0

- Molecule 18 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	m	62	Total	C	N	O	0	0
			310	186	62	62		

- Molecule 19 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	n	348	Total	C	N	O	0	0
			1728	1032	348	348		

- Molecule 20 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	o	133	Total	C	N	O	0	0
			656	390	133	133		

- Molecule 21 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	p	437	Total	C	N	O	0	0
			2158	1284	437	437		

- Molecule 22 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	s	137	Total	C	N	O	0	0
			682	408	137	137		

- Molecule 23 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	t	236	Total	C	N	O	0	0
			1168	696	236	236		

- Molecule 24 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z	243	Total	C	N	O	S	0	0
			2058	1334	353	366	5		

- Molecule 25 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	183	Total	C	N	O	S	0	0
			1440	930	264	245	1		

- Molecule 26 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	743	Total	C	N	O	P	0	0
			15943	7115	2912	5173	743		

- Molecule 27 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	138	Total	C	N	O	P	0	0
			2939	1314	522	965	138		

- Molecule 28 is a RNA chain called ITS2 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	87	Total	C	N	O	P	0	0
			1838	823	309	619	87		

- Molecule 29 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
29	C	2	Total	Mg	0
			2	2	
29	F	1	Total	Mg	0
			1	1	
29	1	30	Total	Mg	0
			30	30	

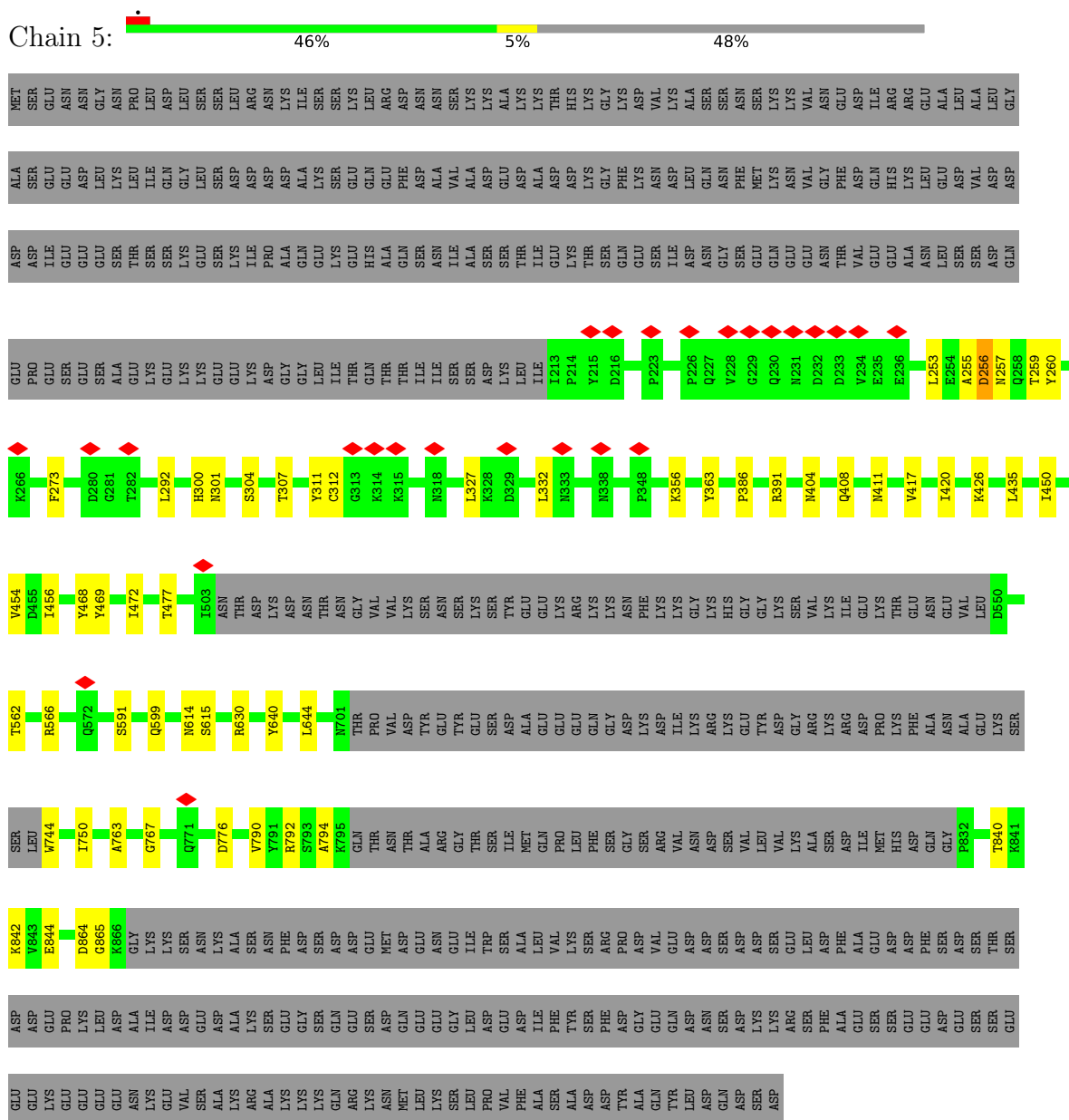
- Molecule 30 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
30	D	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: Ribosome biogenesis protein MAK21



Chain 6:



F567	D394	L198	ASP	ALA	MET
V568	I411	L199	PRO	GLY	GLY
L571		R200	GLU	GLU	LYS
	R414	I203	PHE	VAL	VAL
I582	R415		TYR	VAL	SER
V591	T416	R207	LYS	PHE	LYS
		V208	LEU	ASP	THR
Y598	K426	A209	GLU	LYS	LYS
	I427		GLU	SER	LYS
K609	N428	N213	ASN	VAL	PHE
R610		R214	ASP	GLU	GLN
	K434	E215	LYS	THR	SER
K617	I435	GLU	ASP	PHE	LYS
L618	V436	ASN	LEU	PHE	HIS
	Y437	I1E	LEU	GLU	LYS
K639	N438	ASP	ASP	LYS	LYS
		D220	PHE	GLY	HIS
	F441	Y221	ALA	ILE	THR
N647	C442		GLY	GLU	LEU
	H443	A224	THR	ILE	ASP
L656	S444	F231	ASN	PRO	GLN
M674	L445		PRO	LYS	ARG
	D446	R269	ASP	ASN	LYS
S677	F447		GLY	LYS	GLU
	V451	I273	ILE	LYS	LYS
A690		H277	ASP	LEU	ILE
K691	G463	A278	SER	LYS	GLN
L692		C279	GLN	LYS	LYS
LEU	V478	S280	ASP	THR	ARG
ASN			GLU	THR	ILE
SER	V482	I288	GLY	LYS	GLN
LEU			GLU	GLY	GLY
GLU	L494	V297	ASP	GLN	ARG
GLU	R495		GLU	GLN	ARG
SER		V301	ARG	ASP	GLY
ASP	Y516		ASN	GLU	ASN
ASP		R313	SER	ASP	LYS
ASN	I522		ASN	SER	THR
GLU	L523	I319	ASN	THR	ASP
ASP	T524		ILE	ASP	GLN
VAL	S525	I322	GLU	SER	GLU
GLU	T526		LYS	GLU	LYS
MET	A527	V325	SER	GLU	ALA
SER	F528	H326	GLU	GLU	ASP
ASP	T529		GLN	GLU	ALA
ALA		Q335	MET	ASP	ALA
	N537		GLU	GLY	GLY
	K548	L354	LEU	GLN	THR
	C549	R370	GLU	GLY	ARG
	T550	V371	LYS	SER	GLU
		I372	GLU	THR	GLN
	I558			ALA	GLN
	Y559	L379		LYS	GLN
			X176	LEU	GLN
			L178	ALA	LYS
			Q189	GLU	LYS
	L563	A388		LYS	SER
	S564				

Chain C:



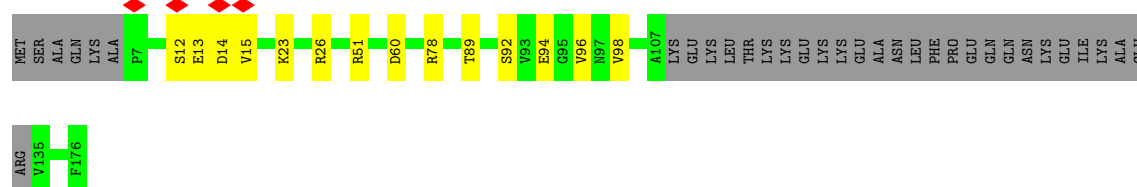
L244	G245	R246	S269	S270	V286	T287	R288	I289	I290	I295	A298	I299	R300	K346	T347	GLY	THR	LYS	PRO	ALA	ALA	VAL	PHE	THR	GLU	THR	LEU	LYS	HIS	ASP	GLY	ASN	MET	R3	V6	A19	L20	P32	V35	V42	K46	ARG	GLN	ALA	TTR	ARG	GLN	GLY	VAL	SER	GLU	LYS	LYS	ALA	GLY	HIS	GLN	THR	SER	ALA	GLU	SER	TRP	GLY	THR	GLY	ARG	ALA	VAL	ALA	ARG	ILE	PRO	PRO	ARG	VAL	GLY	GLY	GLY	GLY	THR	ARG	SER	GLN	GLY	ALA	PHE
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain D:

[illegible]

- Molecule 5: 60S ribosomal protein L6-A

Chain E:



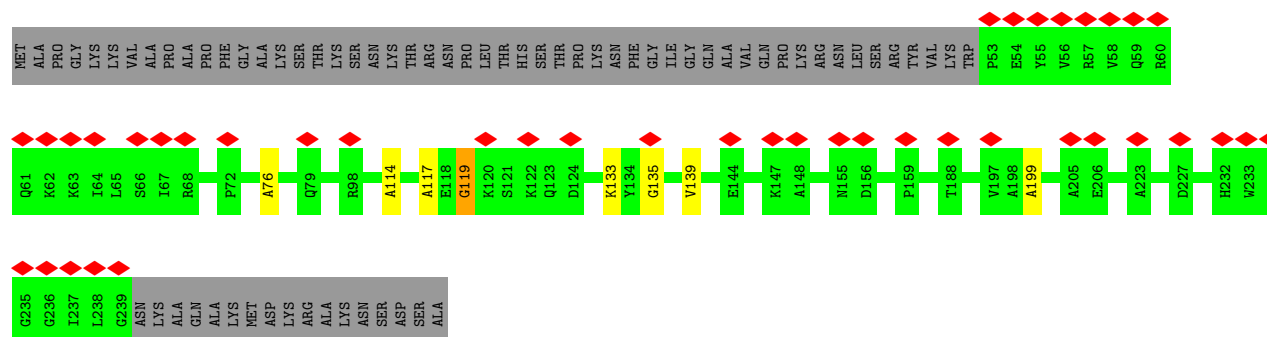
- Molecule 6: 60S ribosomal protein L7-A

Chain F:



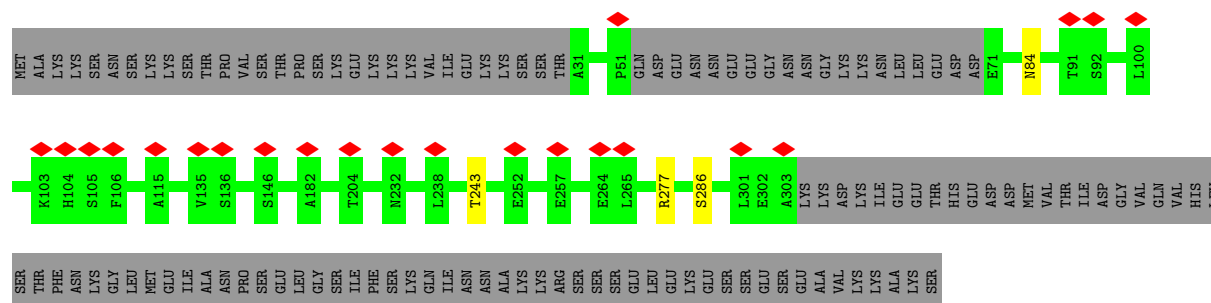
- Molecule 7: 60S ribosomal protein L8-A

Chain G:



- Molecule 8: Proteasome-interacting protein CIC1

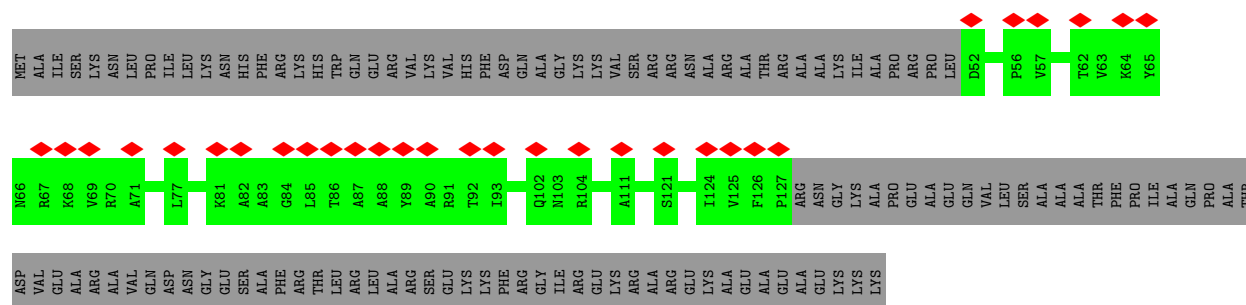
Chain K:



- Molecule 9: 60S ribosomal protein L13-A

Chain L:

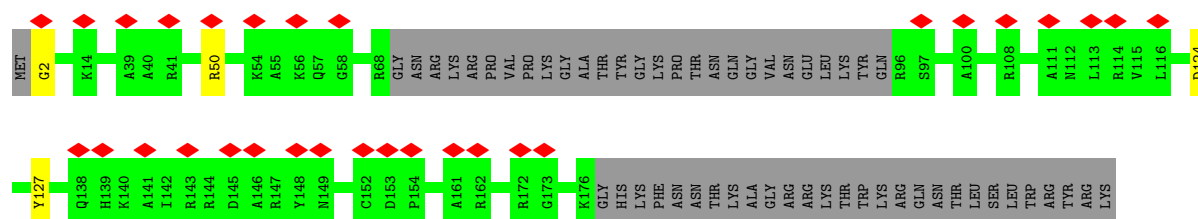




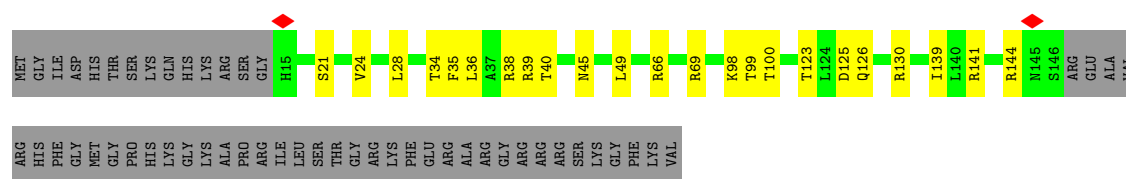
- Molecule 10: 60S ribosomal protein L14-A



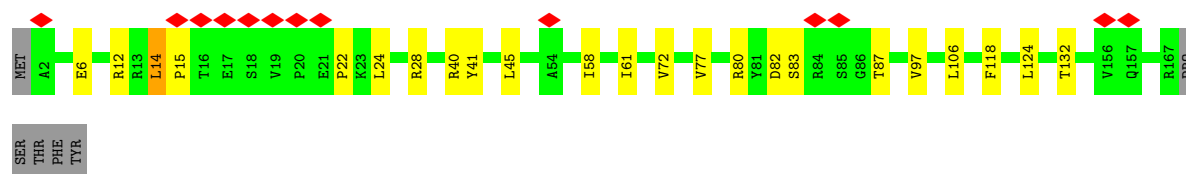
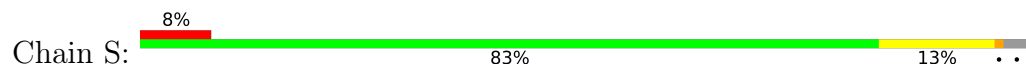
- Molecule 11: 60S ribosomal protein L15-A



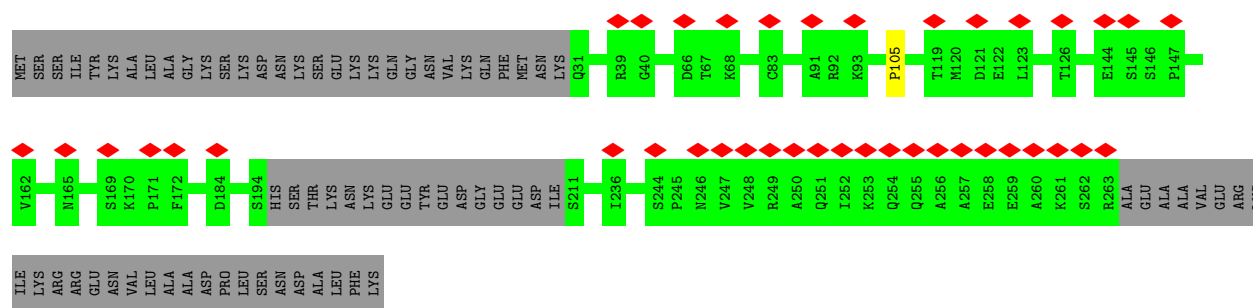
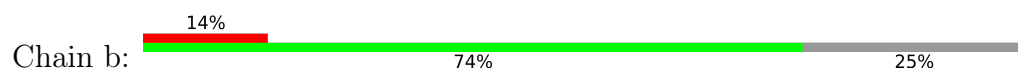
- Molecule 12: 60S ribosomal protein L18-A



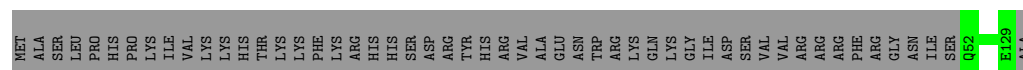
- Molecule 13: 60S ribosomal protein L20-A



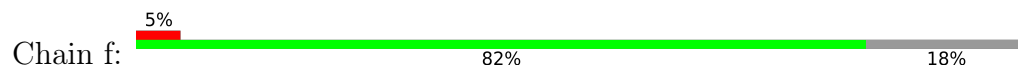
- Molecule 14: Ribosome biogenesis protein BRX1



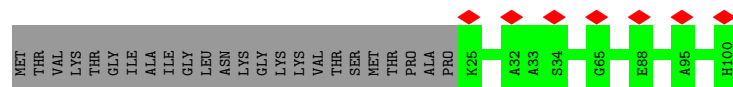
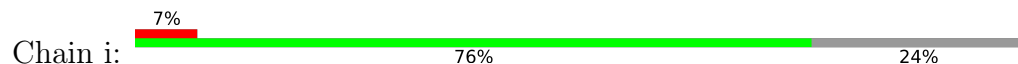
- Molecule 15: 60S ribosomal protein L32



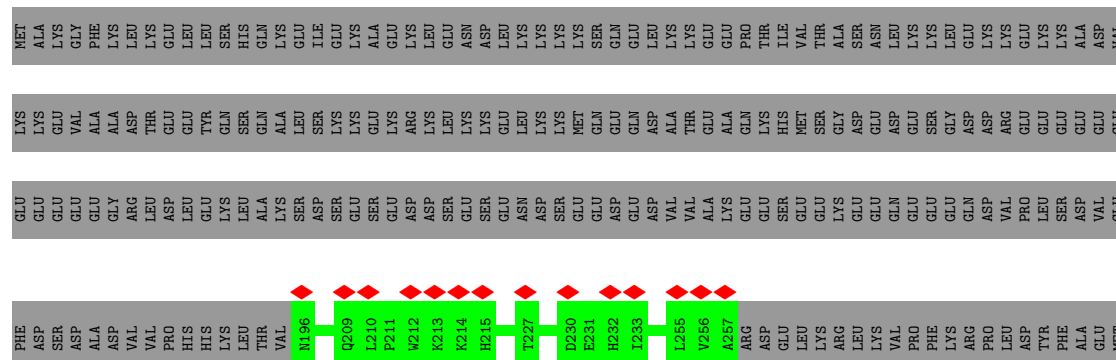
- Molecule 16: 60S ribosomal protein L33-A

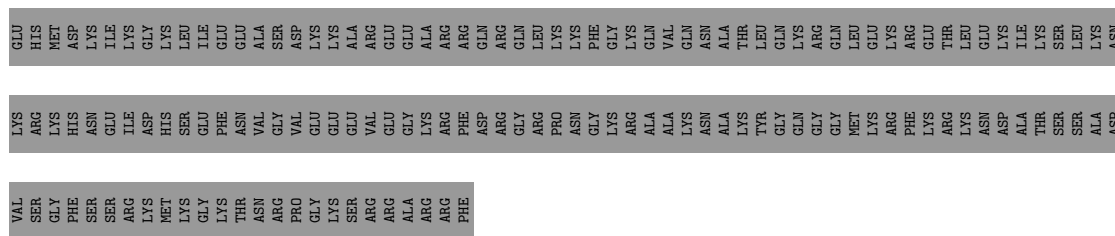


- Molecule 17: 60S ribosomal protein L36-A

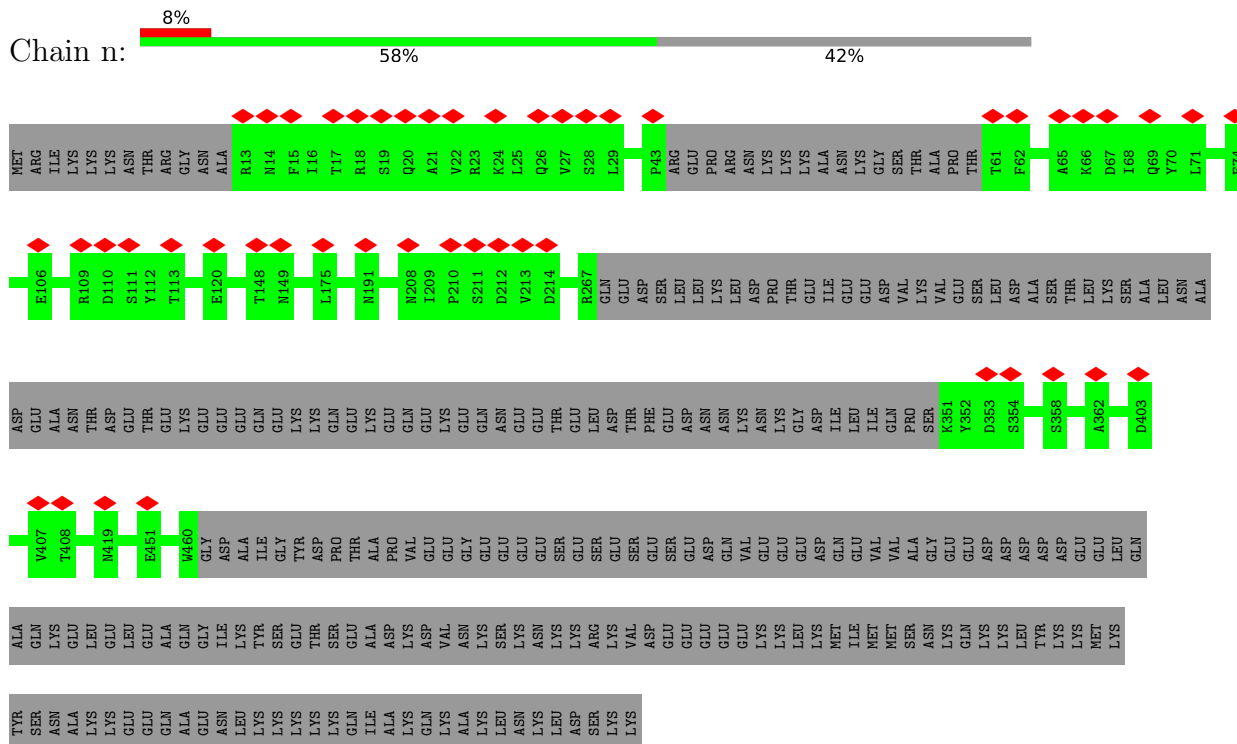


- Molecule 18: rRNA-processing protein EBP2

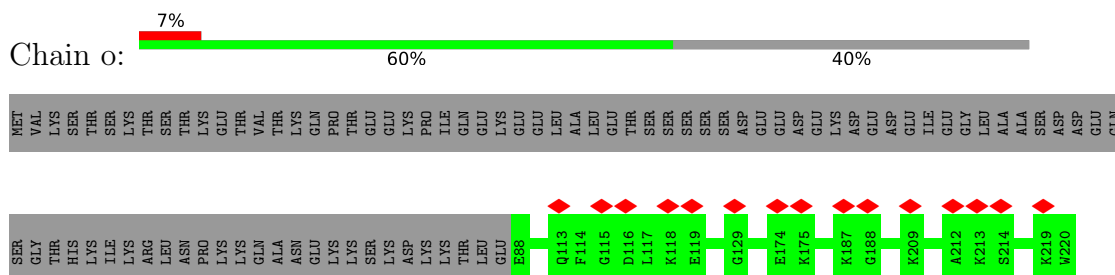




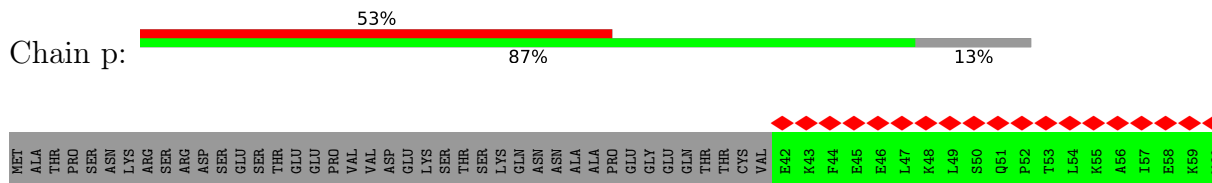
- Molecule 19: Pescadillo homolog

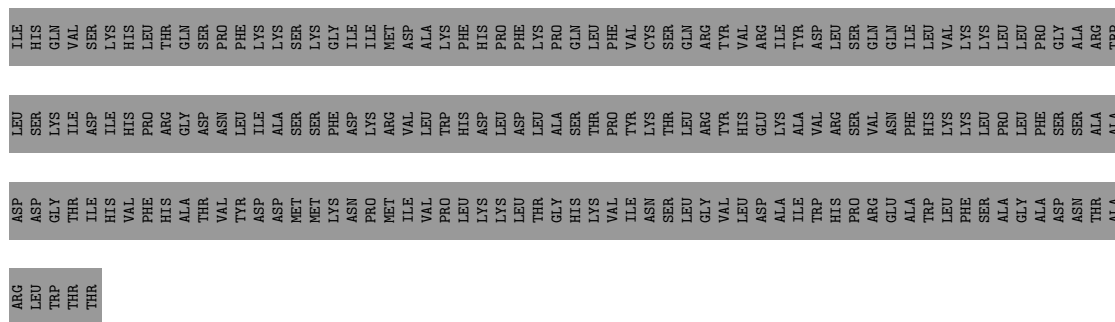


- Molecule 20: Ribosome biogenesis protein 15

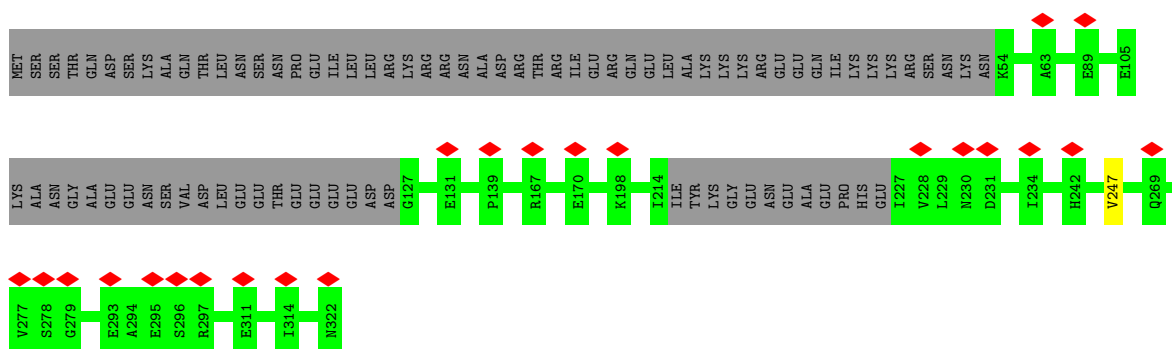


- Molecule 21: ATP-dependent RNA helicase HAS1

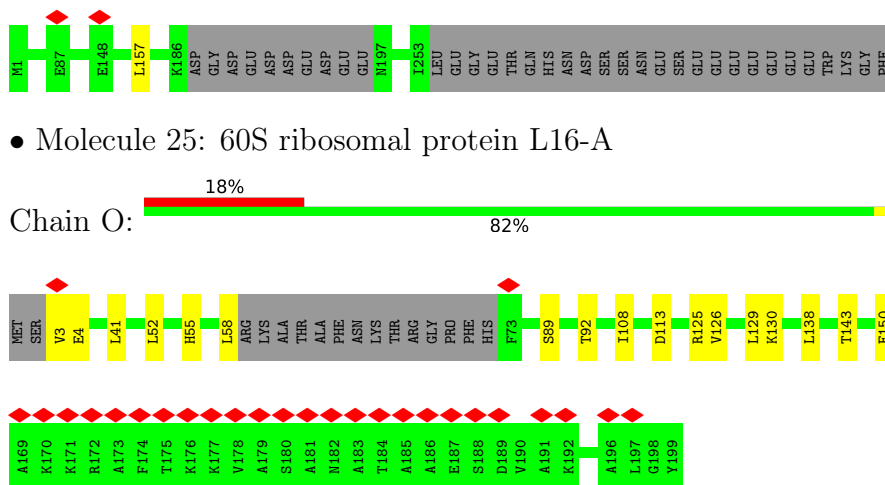
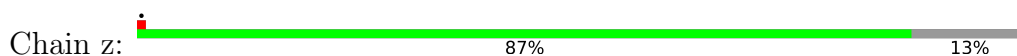




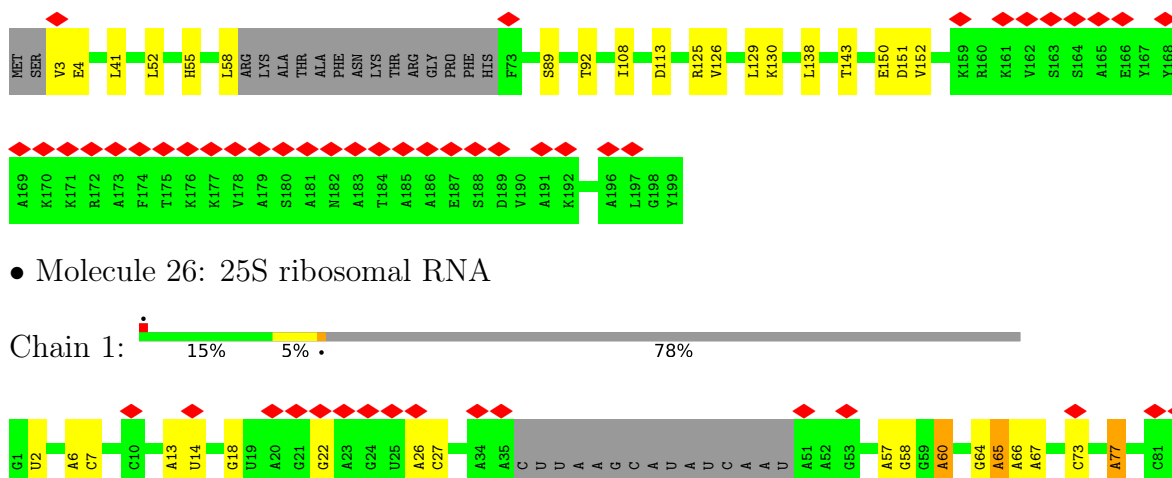
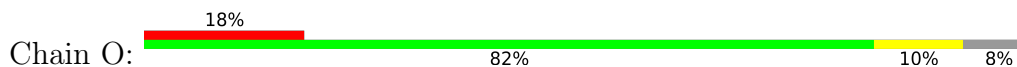
- Molecule 23: Ribosome biogenesis protein RLP7



- Molecule 24: Ribosomal RNA-processing protein 1



- Molecule 25: 60S ribosomal protein L16-A

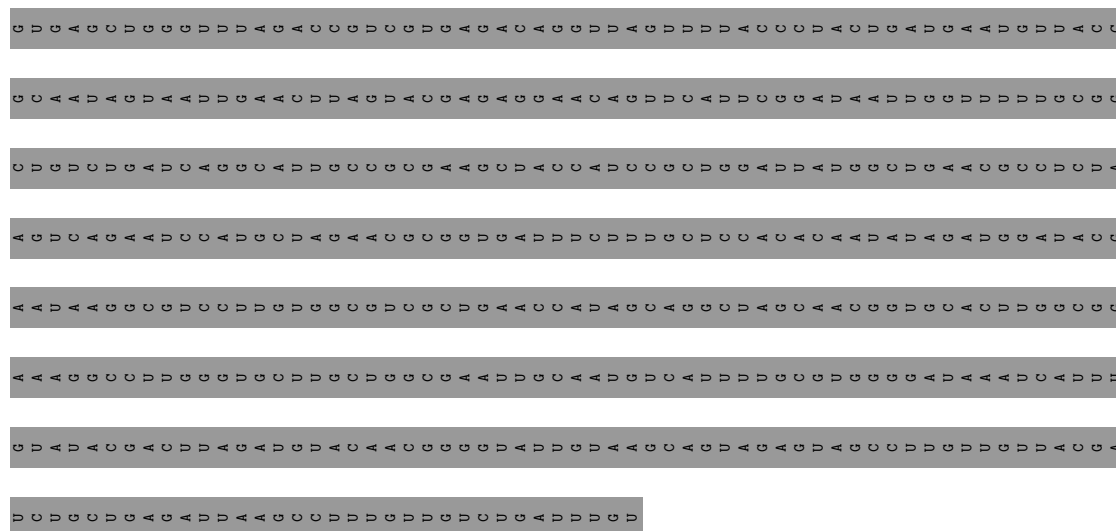


- Molecule 26: 25S ribosomal RNA

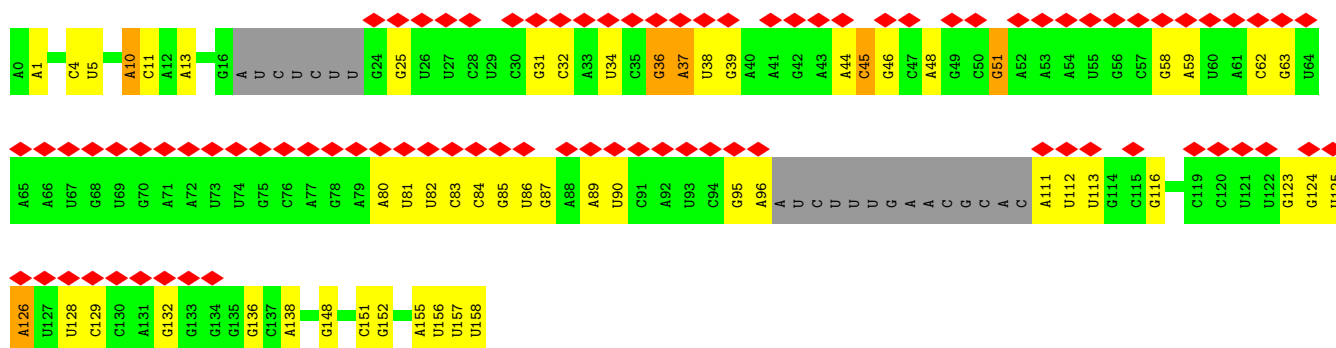




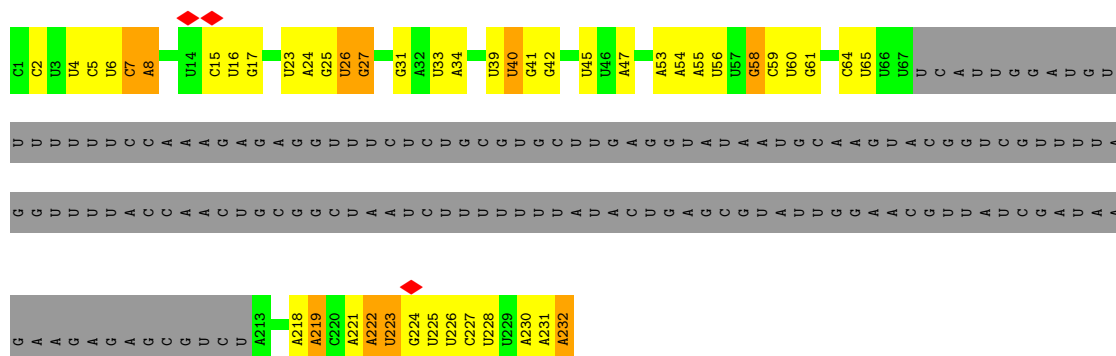




- Molecule 27: 5.8S ribosomal RNA



- Molecule 28: ITS2 ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	158915	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 ($e^-/\text{\AA}^2$)	1.184	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	50.642	Depositor
Minimum map value	-21.765	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	1.055	Depositor
Recommended contour level	6.34	Depositor
Map size (Å)	572.0, 572.0, 572.0	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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	5	0.29	0/4423	0.49	0/5985
2	6	0.30	0/4236	0.53	0/5720
3	C	0.26	0/2202	0.53	0/2985
4	D	0.33	0/1110	0.57	0/1493
5	E	0.27	0/1157	0.56	0/1558
6	F	0.28	0/1979	0.52	0/2661
7	G	0.27	0/925	0.57	1/1288 (0.1%)
8	K	0.26	0/1261	0.49	0/1758
9	L	0.24	0/375	0.49	0/521
10	M	0.26	0/906	0.56	0/1222
11	N	0.24	0/731	0.48	0/1016
12	Q	0.28	0/1030	0.61	0/1393
13	S	0.26	0/1427	0.57	0/1916
14	b	0.25	0/1073	0.52	0/1493
15	e	0.27	0/607	0.56	0/816
16	f	0.27	0/721	0.56	0/971
17	i	0.24	0/375	0.42	0/521
18	m	0.24	0/309	0.48	0/431
19	n	0.25	0/1725	0.49	0/2403
20	o	0.26	0/655	0.54	0/910
21	p	0.26	0/2156	0.50	0/2999
22	s	0.28	0/680	0.52	0/947
23	t	0.26	0/1166	0.52	0/1622
24	z	0.29	0/2104	0.52	0/2832
25	O	0.28	0/1465	0.59	0/1966
26	1	0.29	0/17844	0.83	7/27804 (0.0%)
27	2	0.23	0/3284	0.80	0/5110
28	3	0.34	0/2050	0.94	2/3186 (0.1%)
All	All	0.28	0/57976	0.68	10/83527 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	G	0	2
13	S	0	1
14	b	0	1
26	1	1	0
All	All	1	4

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	1	330	G	O4'-C1'-N9	11.78	117.62	108.20
26	1	311	C	N1-C2-O2	6.73	122.94	118.90
26	1	117	U	C2-N1-C1'	6.68	125.72	117.70
26	1	311	C	N3-C2-O2	-6.21	117.55	121.90
26	1	117	U	N3-C2-O2	-5.76	118.17	122.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
26	1	330	G	C1'

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	G	119	GLY	Peptide
7	G	76	ALA	Peptide
13	S	83	SER	Peptide
14	b	105	PRO	Peptide

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	5	4332	0	4392	40	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	6	4156	0	4302	59	0
3	C	2166	0	2291	30	0
4	D	1086	0	1088	25	0
5	E	1136	0	1218	8	0
6	F	1941	0	2037	12	0
7	G	926	0	452	3	0
8	K	1263	0	542	3	0
9	L	376	0	182	0	0
10	M	892	0	966	8	0
11	N	733	0	336	3	0
12	Q	1015	0	1096	22	0
13	S	1394	0	1438	15	0
14	b	1075	0	450	0	0
15	e	598	0	645	0	0
16	f	706	0	727	0	0
17	i	376	0	181	0	0
18	m	310	0	137	0	0
19	n	1728	0	746	0	0
20	o	656	0	289	0	0
21	p	2158	0	965	0	0
22	s	682	0	277	0	0
23	t	1168	0	519	0	0
24	z	2058	0	2096	0	0
25	O	1440	0	1541	13	0
26	1	15943	0	8013	82	0
27	2	2939	0	1485	13	0
28	3	1838	0	927	10	0
29	1	30	0	0	0	0
29	C	2	0	0	0	0
29	F	1	0	0	0	0
30	D	1	0	0	0	0
All	All	55125	0	39338	281	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 4.

The worst 5 of 281 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)
26:1:251:G:O2'	26:1:252:U:OP2	1.97	0.82
26:1:439:C:OP1	26:1:440:A:O2'	1.98	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:44:PRO:O	4:D:65:LYS:NZ	2.13	0.81
26:1:518:G:OP2	26:1:518:G:N2	2.15	0.80
2:6:441:PHE:O	2:6:444:SER:OG	2.00	0.79

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	5	522/1025 (51%)	506 (97%)	15 (3%)	1 (0%)	47	79
2	6	510/710 (72%)	495 (97%)	15 (3%)	0	100	100
3	C	279/362 (77%)	268 (96%)	11 (4%)	0	100	100
4	D	128/306 (42%)	124 (97%)	4 (3%)	0	100	100
5	E	139/176 (79%)	133 (96%)	6 (4%)	0	100	100
6	F	240/244 (98%)	235 (98%)	5 (2%)	0	100	100
7	G	185/256 (72%)	173 (94%)	12 (6%)	0	100	100
8	K	250/376 (66%)	244 (98%)	6 (2%)	0	100	100
9	L	74/199 (37%)	69 (93%)	5 (7%)	0	100	100
10	M	113/138 (82%)	112 (99%)	1 (1%)	0	100	100
11	N	144/204 (71%)	137 (95%)	7 (5%)	0	100	100
12	Q	130/186 (70%)	128 (98%)	2 (2%)	0	100	100
13	S	164/172 (95%)	157 (96%)	6 (4%)	1 (1%)	25	63
14	b	213/291 (73%)	202 (95%)	11 (5%)	0	100	100
15	e	76/130 (58%)	74 (97%)	2 (3%)	0	100	100
16	f	82/107 (77%)	79 (96%)	3 (4%)	0	100	100
17	i	74/100 (74%)	71 (96%)	3 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	m	60/427 (14%)	54 (90%)	6 (10%)	0	100	100
19	n	342/605 (56%)	330 (96%)	12 (4%)	0	100	100
20	o	131/220 (60%)	126 (96%)	5 (4%)	0	100	100
21	p	433/505 (86%)	421 (97%)	12 (3%)	0	100	100
22	s	133/807 (16%)	122 (92%)	10 (8%)	1 (1%)	19	58
23	t	232/322 (72%)	210 (90%)	21 (9%)	1 (0%)	34	71
24	z	239/278 (86%)	235 (98%)	3 (1%)	1 (0%)	34	71
25	O	179/199 (90%)	175 (98%)	4 (2%)	0	100	100
All	All	5072/8345 (61%)	4880 (96%)	187 (4%)	5 (0%)	54	84

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	5	256	ASP
22	s	340	PRO
24	z	157	LEU
13	S	14	LEU
23	t	247	VAL

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	5	489/932 (52%)	488 (100%)	1 (0%)	93	96
2	6	469/647 (72%)	469 (100%)	0	100	100
3	C	234/289 (81%)	234 (100%)	0	100	100
4	D	120/274 (44%)	120 (100%)	0	100	100
5	E	124/153 (81%)	123 (99%)	1 (1%)	81	89
6	F	204/205 (100%)	203 (100%)	1 (0%)	88	93
10	M	90/109 (83%)	90 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	Q	108/151 (72%)	108 (100%)	0	100	100
13	S	150/156 (96%)	150 (100%)	0	100	100
15	e	64/111 (58%)	64 (100%)	0	100	100
16	f	75/91 (82%)	75 (100%)	0	100	100
24	z	225/257 (88%)	225 (100%)	0	100	100
25	O	149/162 (92%)	149 (100%)	0	100	100
All	All	2501/3537 (71%)	2498 (100%)	3 (0%)	93	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5	356	LYS
5	E	51	ARG
6	F	5	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	5	581	HIS
1	5	599	GLN
1	5	754	HIS
1	5	784	HIS
4	D	71	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	1	730/3396 (21%)	157 (21%)	7 (0%)
27	2	135/159 (84%)	40 (29%)	3 (2%)
28	3	85/232 (36%)	37 (43%)	4 (4%)
All	All	950/3787 (25%)	234 (24%)	14 (1%)

5 of 234 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
26	1	2	U
26	1	6	A
26	1	7	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
26	1	13	A
26	1	14	U

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	2	31	G
27	2	36	G
28	3	225	U
28	3	60	U
28	3	222	A

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 34 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 ⓘ

There are no chain breaks in this entry.

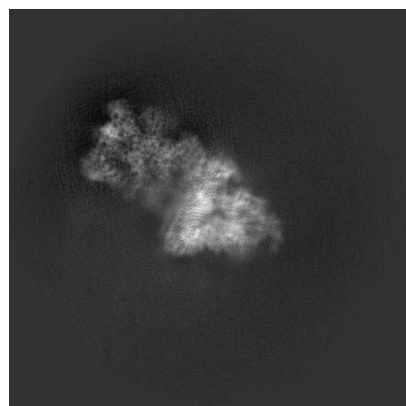
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27919. These allow visual inspection of the internal detail of the map and identification of artifacts.

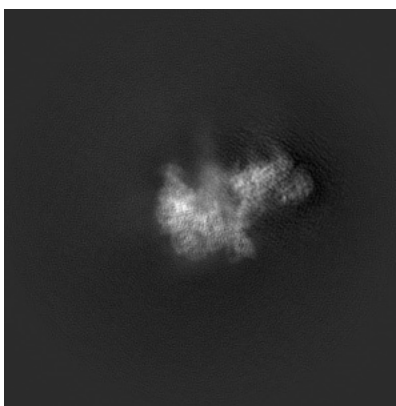
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

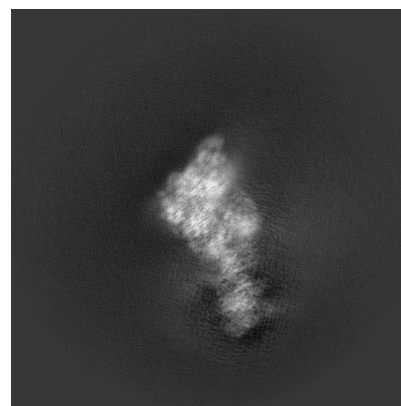
6.1.1 Primary map



X

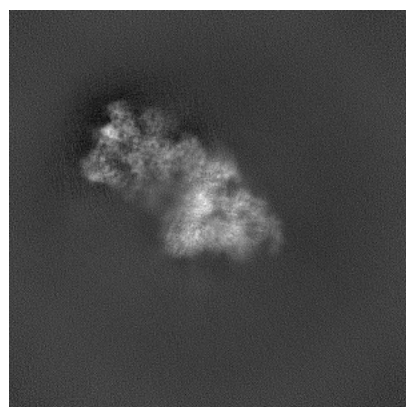


Y

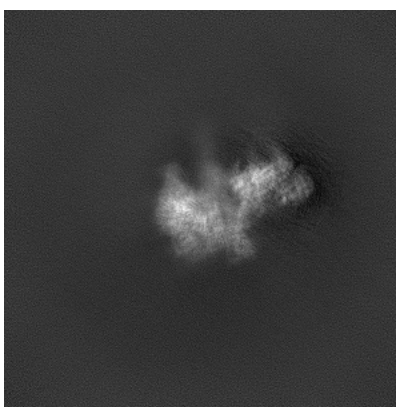


Z

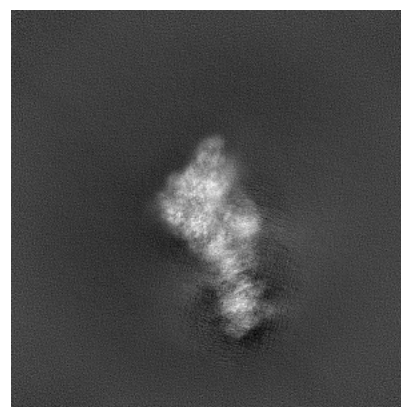
6.1.2 Raw map



X



Y

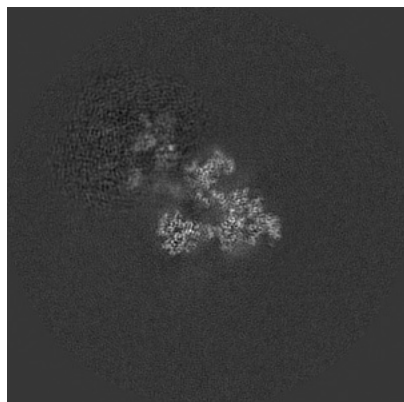


Z

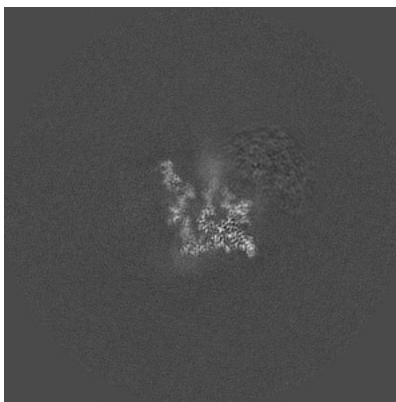
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

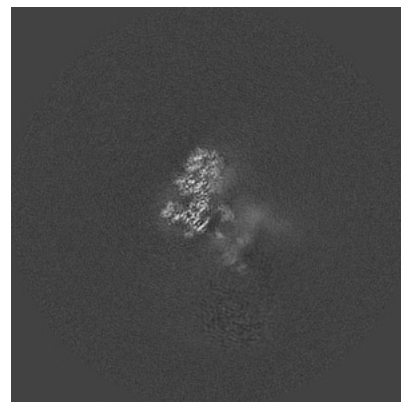
6.2.1 Primary map



X Index: 220

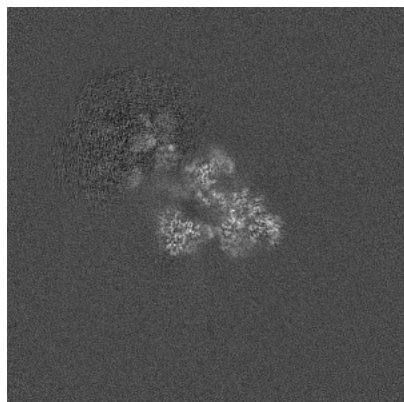


Y Index: 220

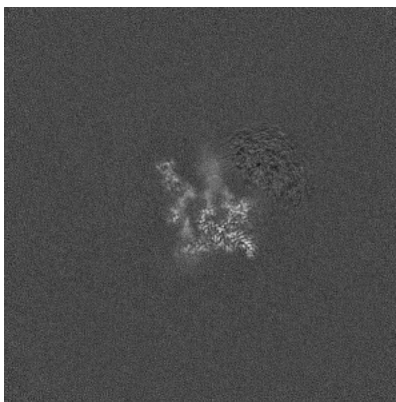


Z Index: 220

6.2.2 Raw map



X Index: 220



Y Index: 220

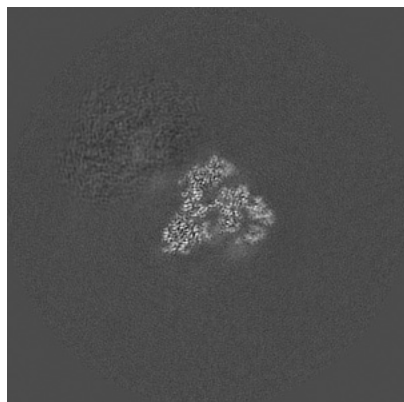


Z Index: 220

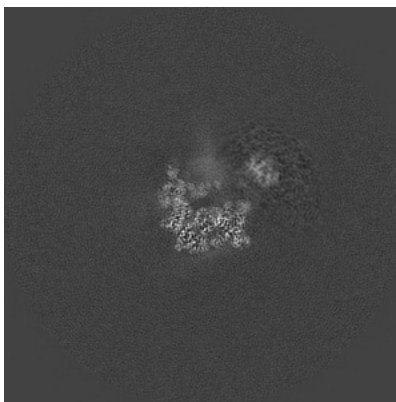
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 207

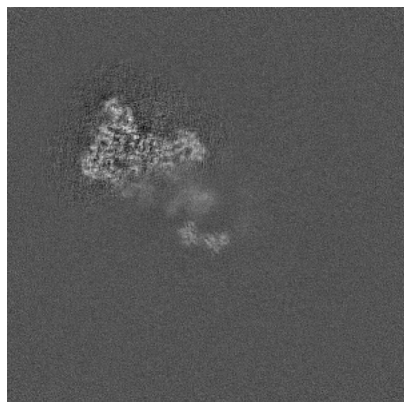


Y Index: 206

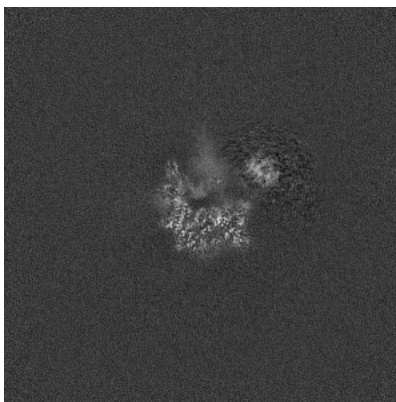


Z Index: 191

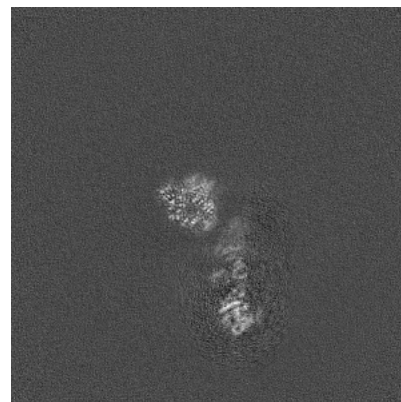
6.3.2 Raw map



X Index: 255



Y Index: 206

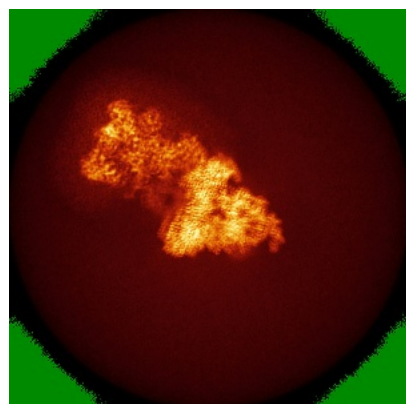


Z Index: 259

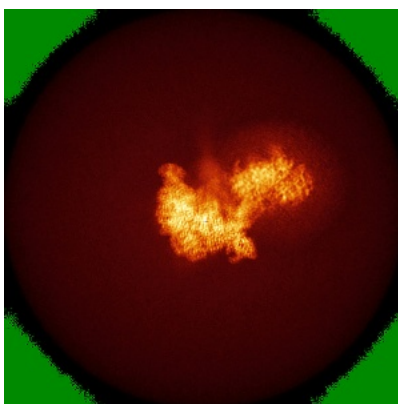
The images above show the largest variance slices of the map in three orthogonal directions.

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

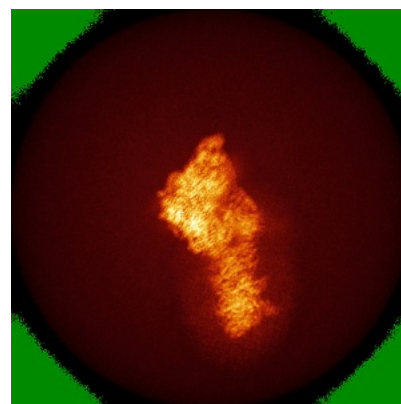
6.4.1 Primary map



X

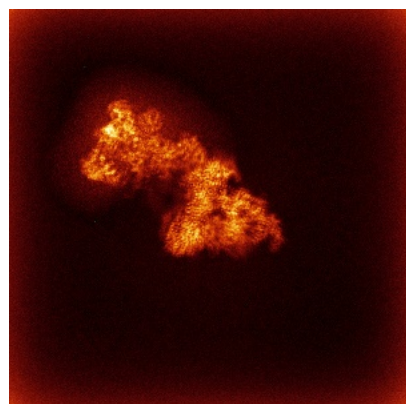


Y

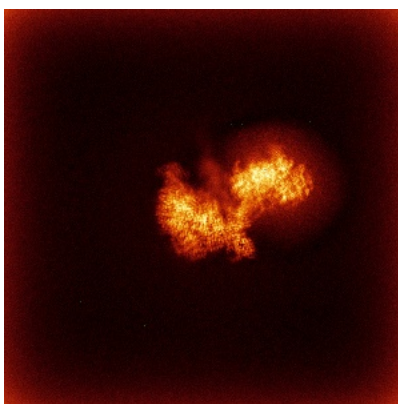


Z

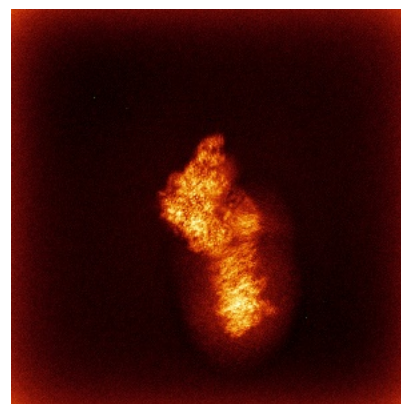
6.4.2 Raw map



X



Y

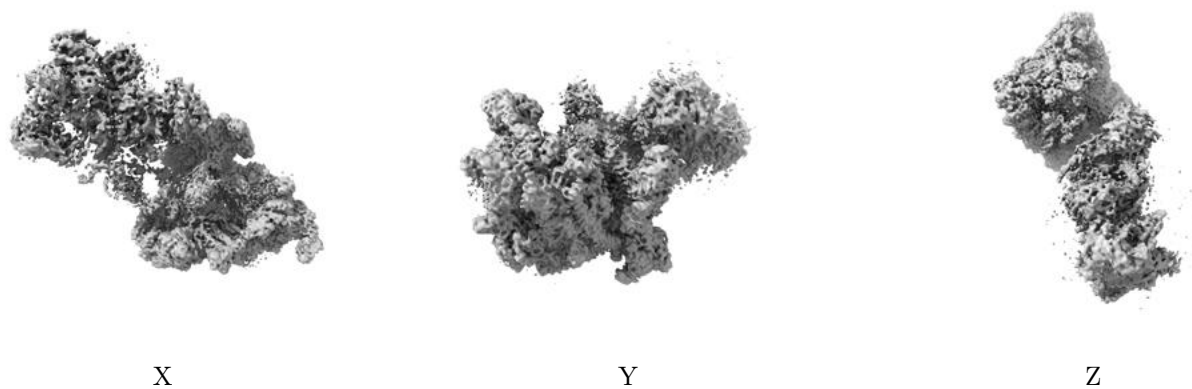


Z

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.

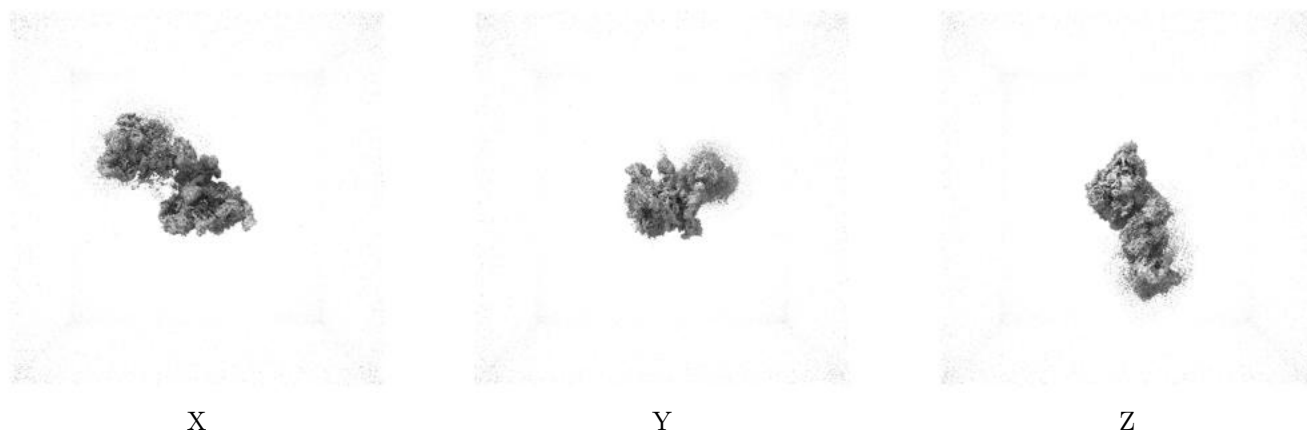
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 6.34. 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.

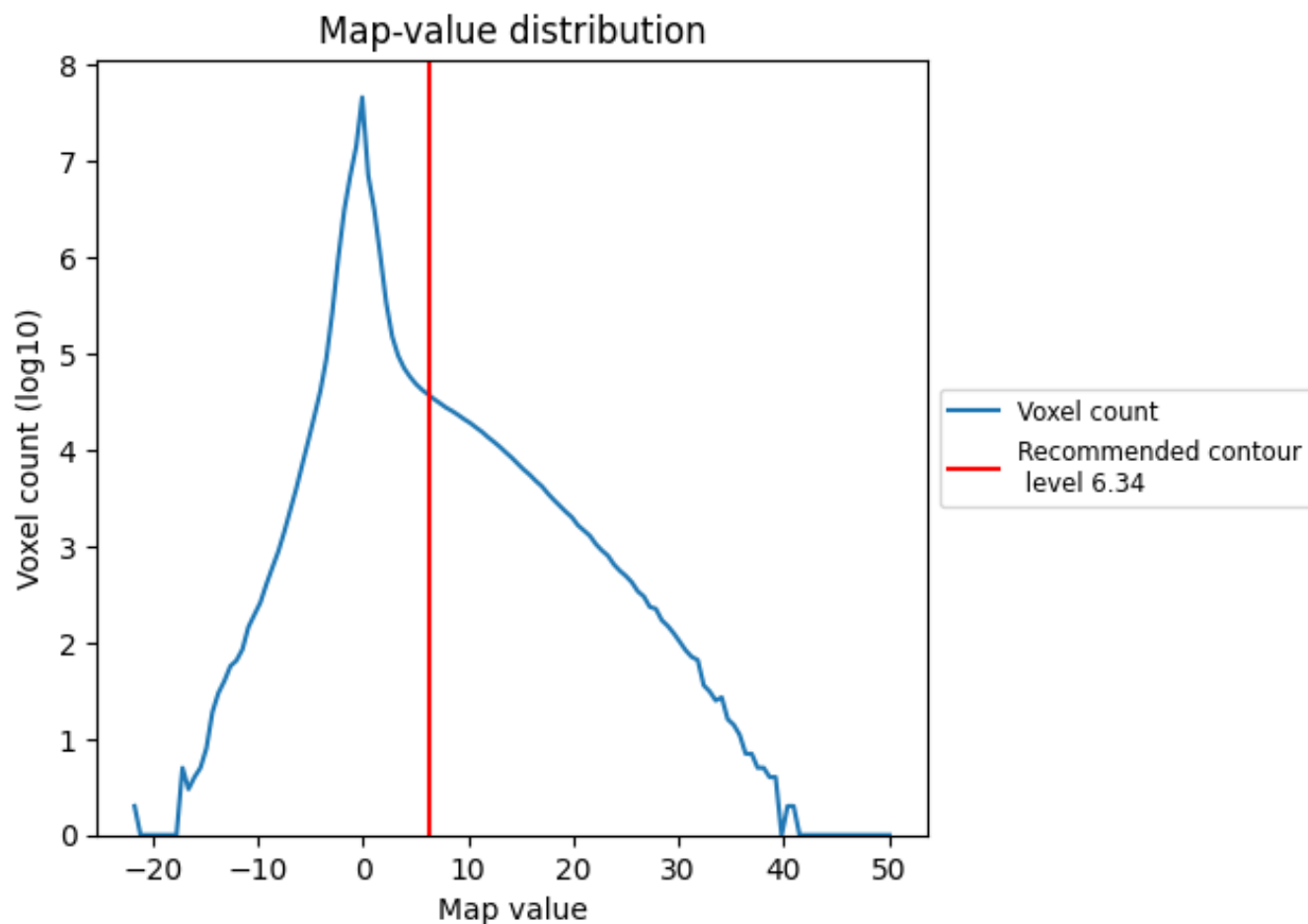
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

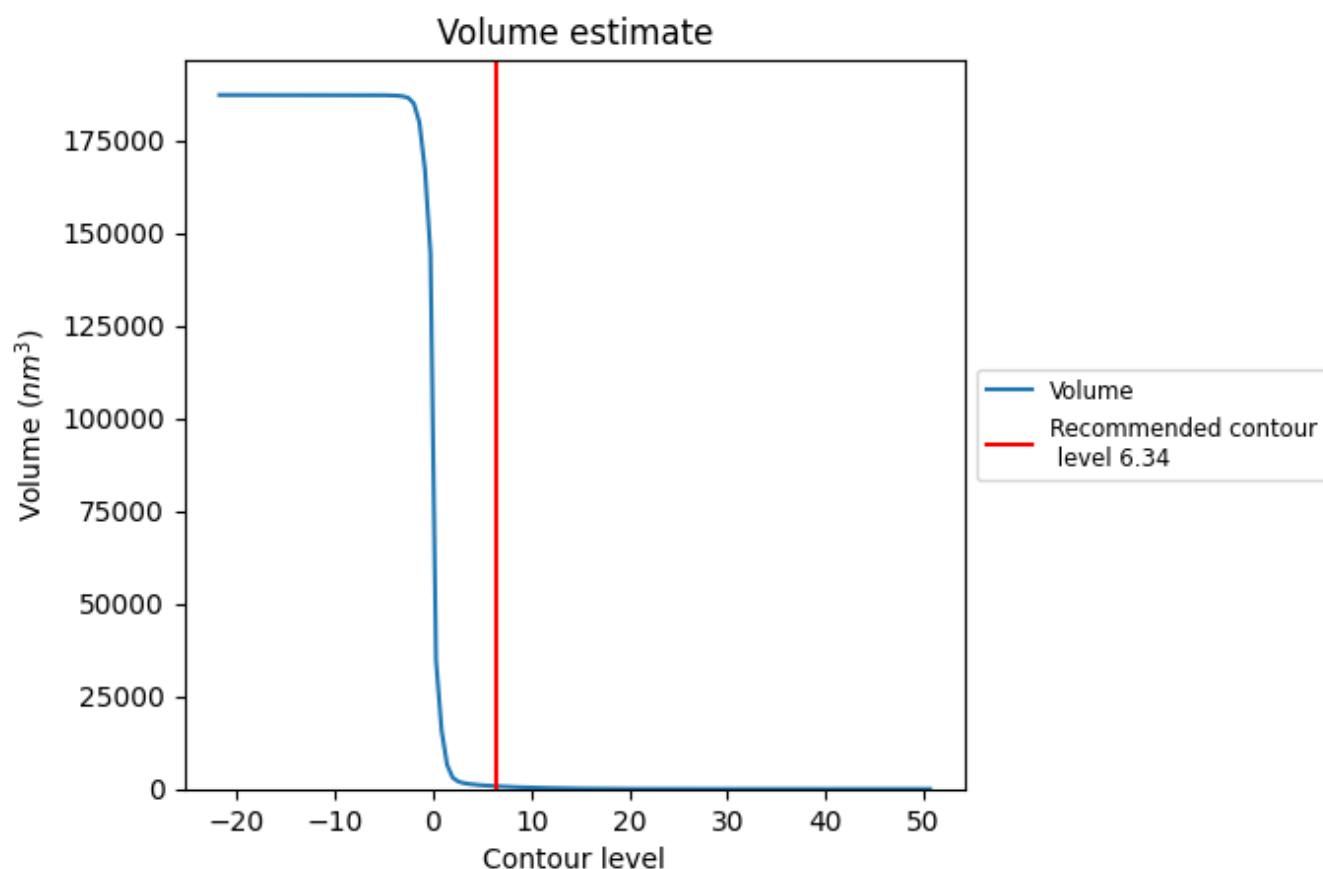
This section contains the results of statistical analysis of the map.

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.

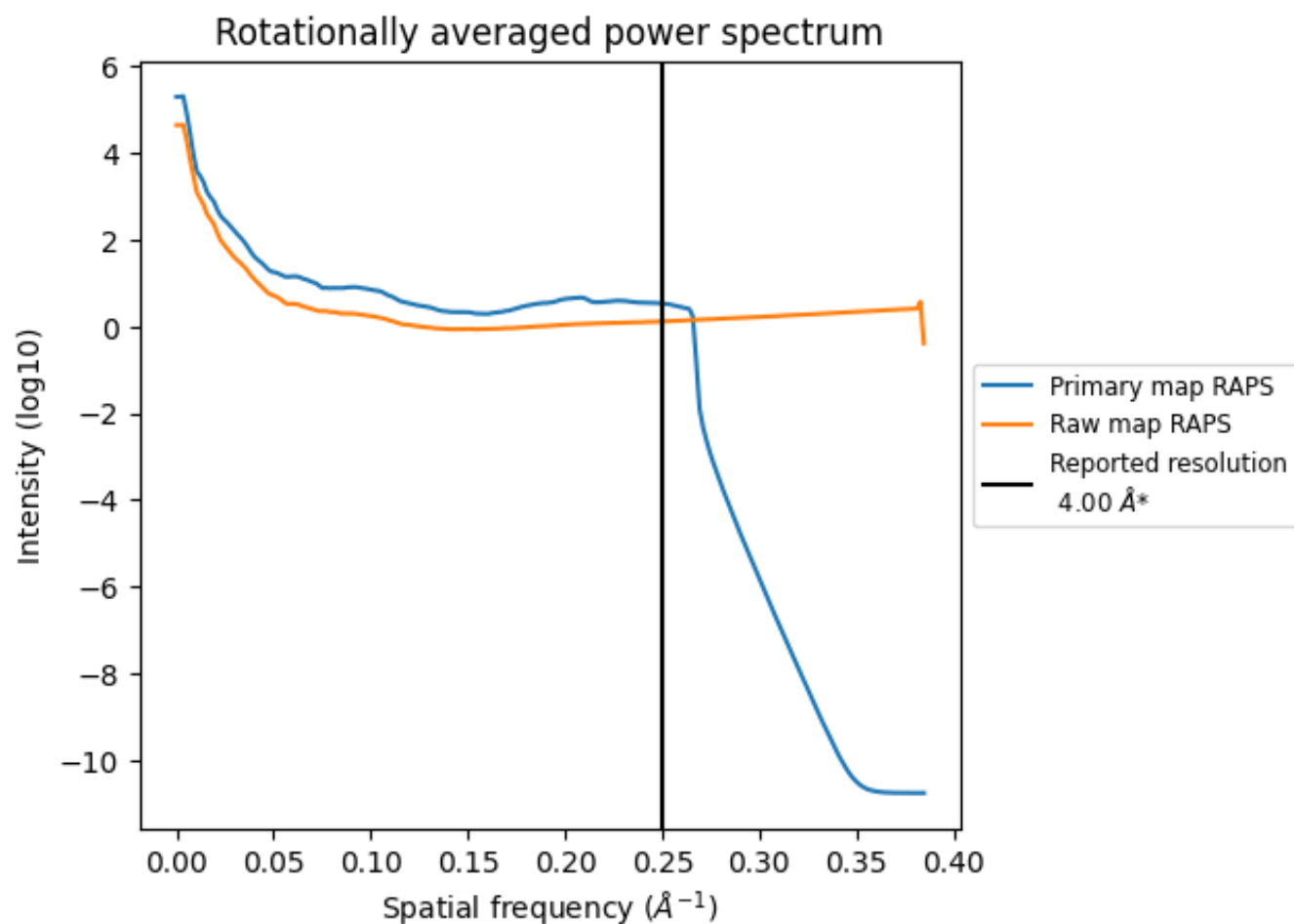
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 764 nm^3 ; this corresponds to an approximate mass of 690 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 ⓘ

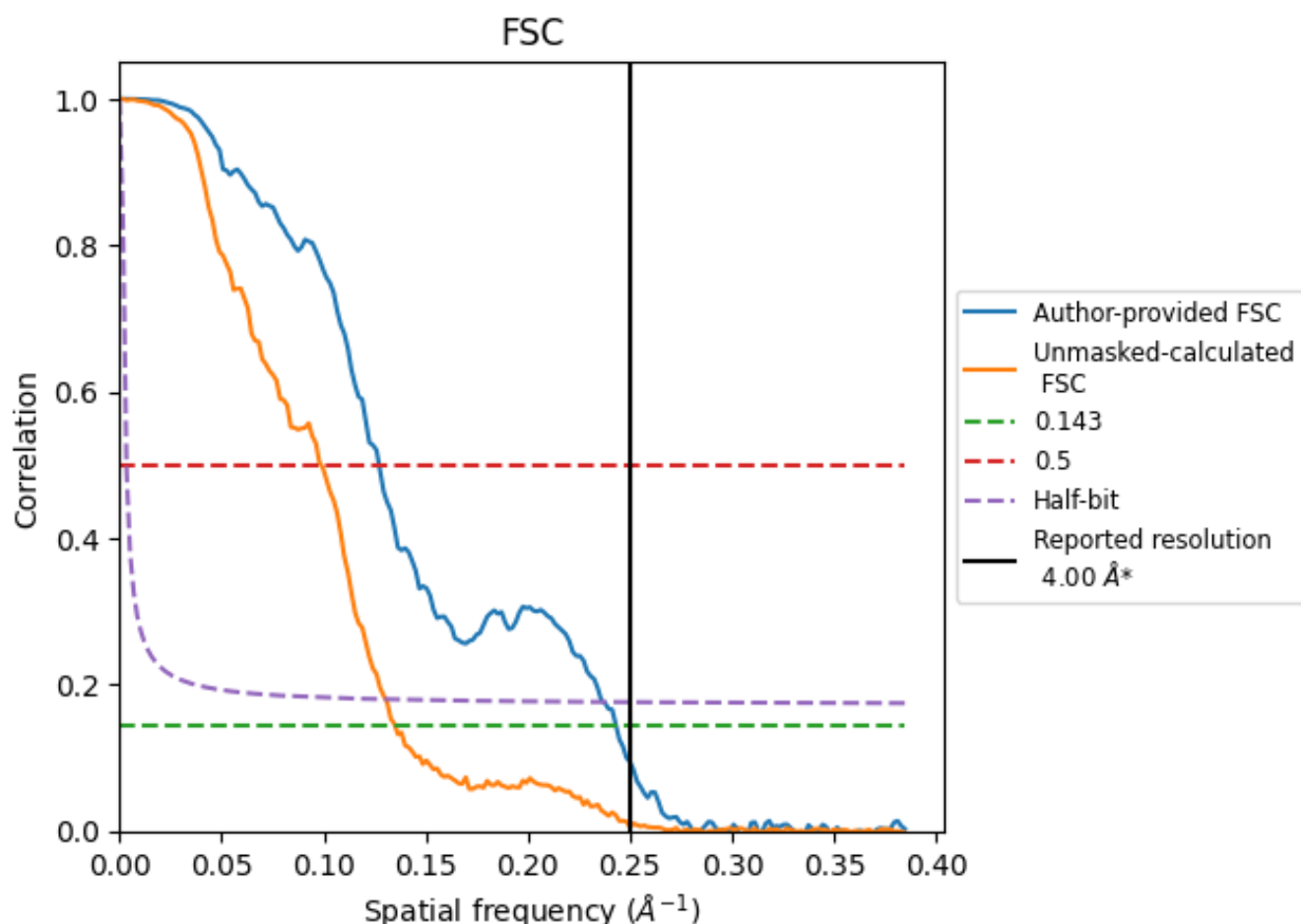


*Reported resolution corresponds to spatial frequency of 0.250 \AA^{-1}

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

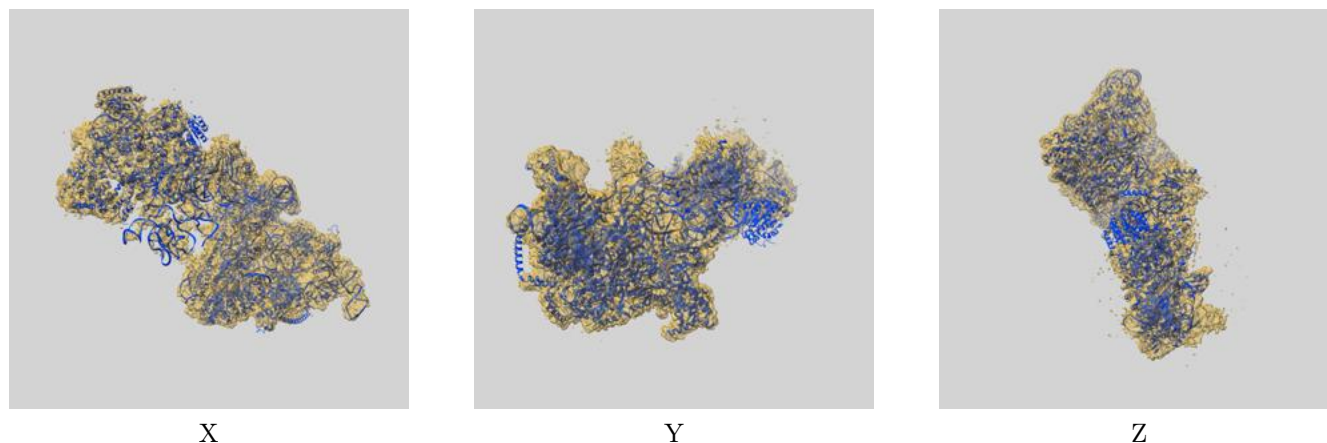
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.11	7.87	4.22
Unmasked-calculated*	7.41	10.14	7.67

*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 7.41 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

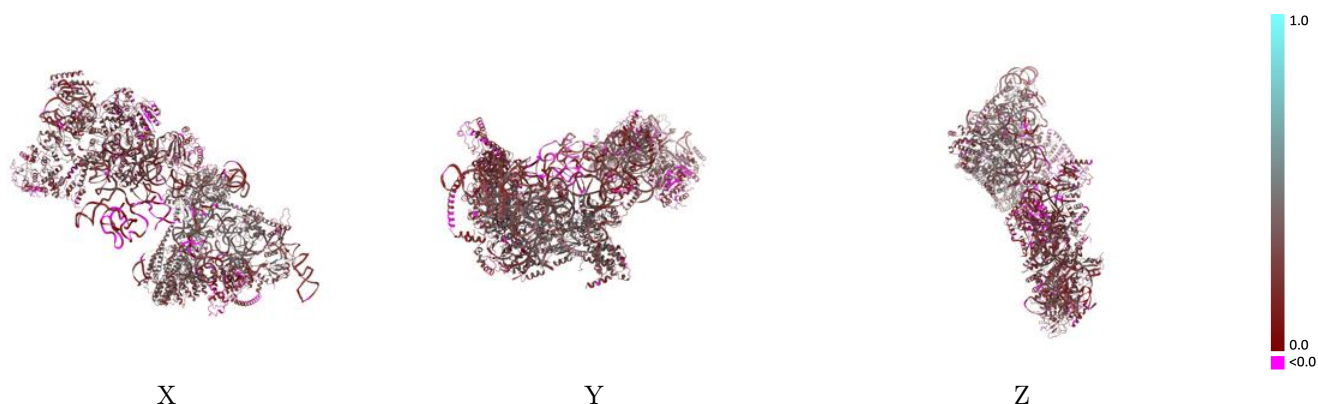
This section contains information regarding the fit between EMDB map EMD-27919 and PDB model 8E5T. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



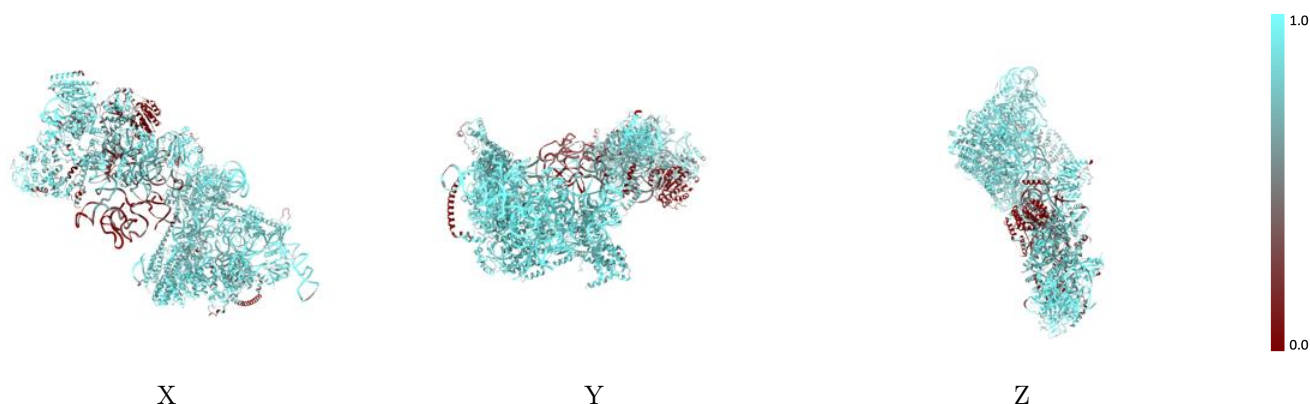
The images above show the 3D surface view of the map at the recommended contour level 6.34 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



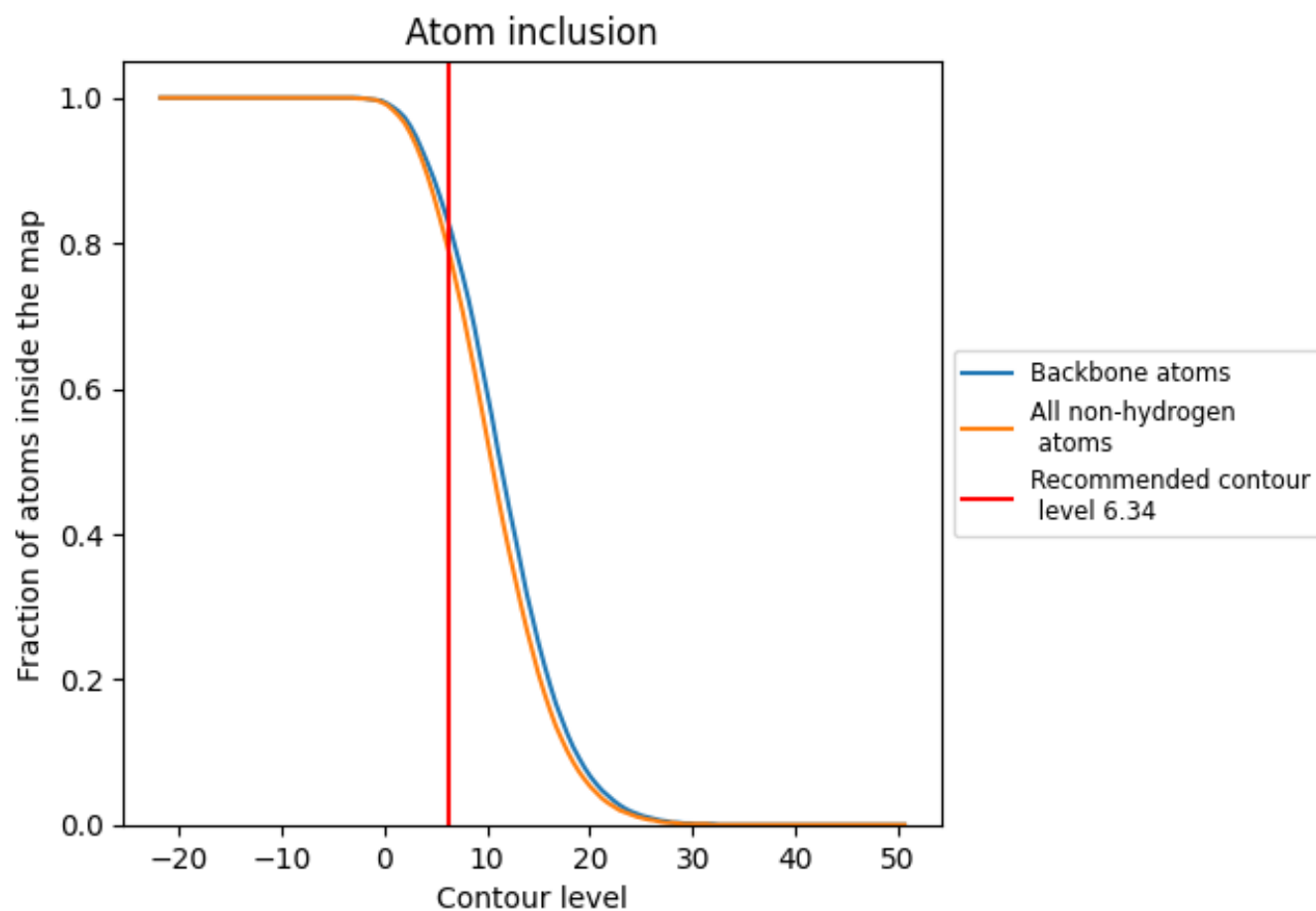
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6.34).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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 (6.34) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7850	 0.2670
1	 0.8350	 0.2670
2	 0.3530	 0.1130
3	 0.8430	 0.2310
5	 0.8230	 0.2610
6	 0.8580	 0.3340
C	 0.8590	 0.3460
D	 0.9010	 0.3880
E	 0.8500	 0.2630
F	 0.9140	 0.3380
G	 0.6770	 0.2710
K	 0.8350	 0.2730
L	 0.5690	 0.2130
M	 0.8810	 0.2670
N	 0.7070	 0.2730
O	 0.6850	 0.1870
Q	 0.8870	 0.3420
S	 0.8020	 0.2310
b	 0.7880	 0.2120
e	 0.8610	 0.3920
f	 0.8440	 0.3170
i	 0.8380	 0.2920
m	 0.7580	 0.1740
n	 0.8000	 0.2450
o	 0.8340	 0.2700
p	 0.3710	 0.1810
s	 0.7020	 0.2310
t	 0.8250	 0.2760
z	 0.8730	 0.3180

