



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:13 AM UTC

PDB ID : 8OEW / pdb_00008oew
EMDB ID : EMD-16838
Title : Structure of the mammalian Pol II-Elongin complex, lacking the ELOA latch
(composite structure, structure 2)
Authors : Chen, Y.; Kokic, G.; Dienemann, C.; Dybkov, O.; Urlaub, H.; Cramer, P.
Deposited on : 2023-03-13
Resolution : 2.80 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:

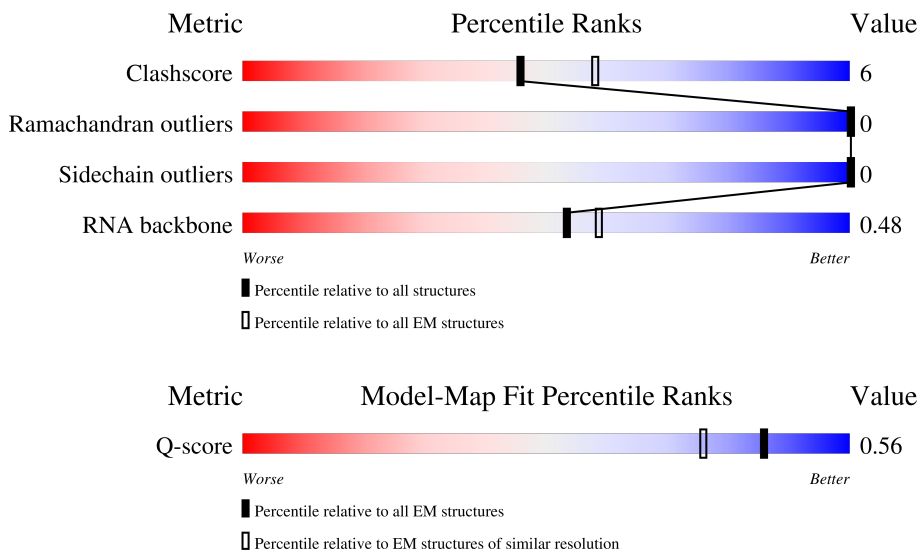
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.80 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	11806 (2.30 - 3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1970	
2	B	1251	
3	C	275	

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Mol	Chain	Length	Quality of chain
4	D	184	
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	N	48	
14	P	46	
15	T	48	
16	M	801	
17	O	112	
18	Q	118	

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 35037 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1409	11159	7024	2000	2064	71	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1131	9047	5721	1592	1670	64	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	258	2072	1300	356	410	6	0	0

- Molecule 4 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	118	967	608	167	188	4	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	209	1721	1089	300	324	8	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	78	626	401	106	114	5	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	171	1347	872	218	249	8	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	148	1186	750	194	237	5	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	116	932	577	165	179	11	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	66	524	339	88	91	6	0	0

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	115	920	593	152	173	2	0	0

- Molecule 12 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	44	367	228	69	64	6	0	0

- Molecule 13 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
13	N	26	549	255	117	151	26	0	0

- Molecule 14 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	13	Total	C	N	O	P	0	0
			280	125	54	88	13		

- Molecule 15 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	38	Total	C	N	O	P	0	0
			769	365	130	236	38		

- Molecule 16 is a protein called Elongin-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	128	Total	C	N	O	S	0	0
			1074	680	195	192	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP Q14241
M	-1	ASN	-	expression tag	UNP Q14241
M	0	ALA	-	expression tag	UNP Q14241

- Molecule 17 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	101	Total	C	N	O	S	0	0
			792	506	127	153	6		

- Molecule 18 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	88	Total	C	N	O	S	0	0
			696	437	121	135	3		

- Molecule 19 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

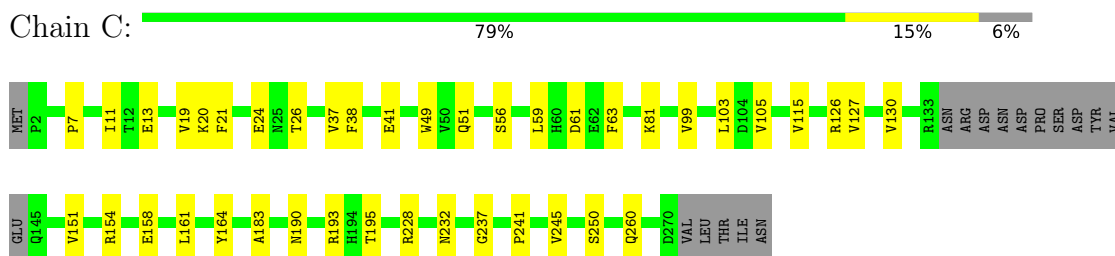
Mol	Chain	Residues	Atoms		AltConf
19	A	1	Total	Mg	0
			1	1	

- Molecule 20 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by

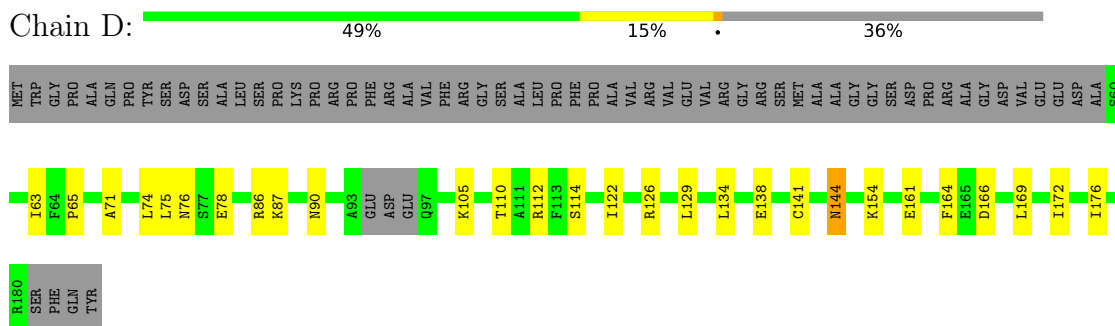
depositor).

Mol	Chain	Residues	Atoms		AltConf
20	A	2	Total 2	Zn 2	0
20	B	1	Total 1	Zn 1	0
20	C	1	Total 1	Zn 1	0
20	I	2	Total 2	Zn 2	0
20	J	1	Total 1	Zn 1	0
20	L	1	Total 1	Zn 1	0

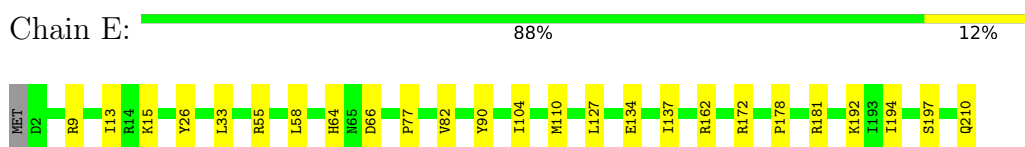
- Molecule 3: DNA-directed RNA polymerase II subunit RPB3



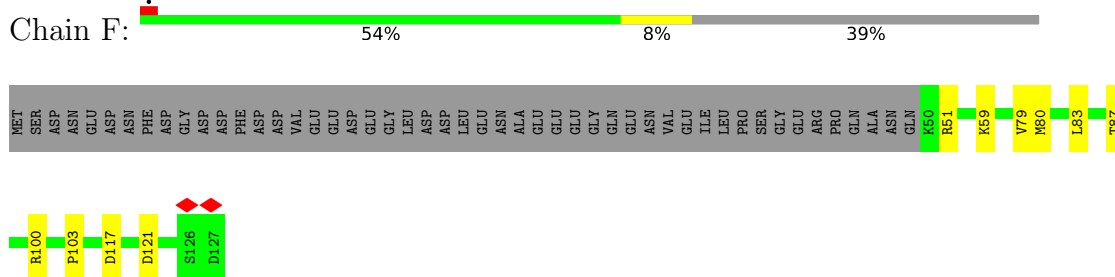
- Molecule 4: RNA polymerase II subunit D



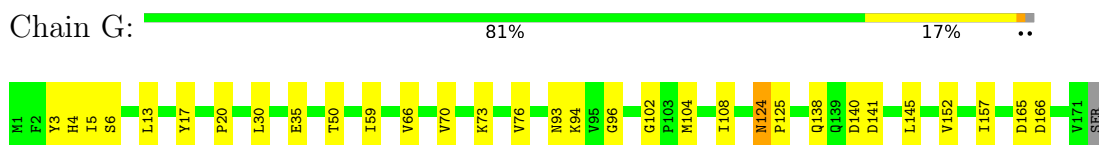
- Molecule 5: DNA-directed RNA polymerase II subunit E



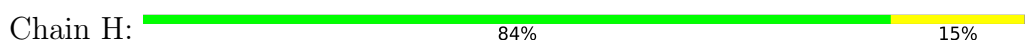
- Molecule 6: DNA-directed RNA polymerase II subunit F



- Molecule 7: DNA-directed RNA polymerase II subunit RPB7

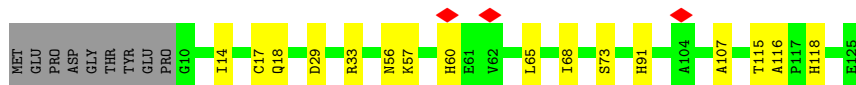
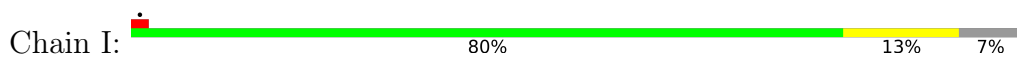


- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

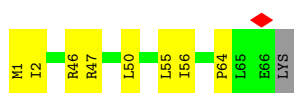
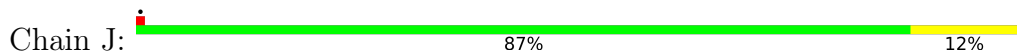




● Molecule 9: DNA-directed RNA polymerase II subunit RPB9



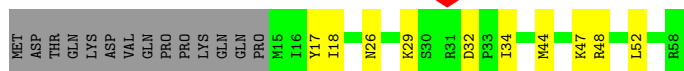
● Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



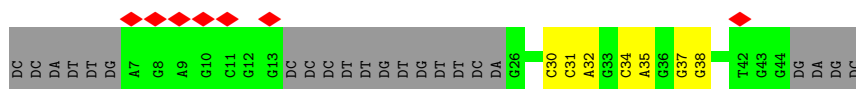
● Molecule 11: DNA-directed RNA polymerase II subunit RPB11-a



● Molecule 12: RNA polymerase II subunit K



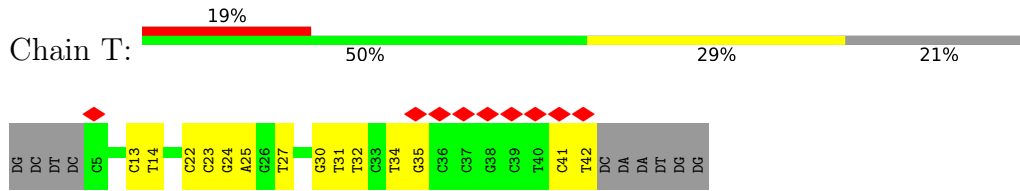
● Molecule 13: Non-template DNA



● Molecule 14: RNA



● Molecule 15: Template DNA



● Molecule 16: Elongin-A



SER	ASN	ALA	MET	HIS	GLY	ARG	SER	ARG	CYS	GLY	PRO	ARG	THR	ARG	GLY	PRO	GLU	GLY	THR	ARG	GLY	GLY	GLU	GLU	GLU	GLU	ALA	ALA	GLU	GLU	DA	DA	DT	DG	DG			
LYS	LEU	SER	THR	LEU	PRO	ILE	THR	VAL	ASP	ASP	LEU	ILE	ALA	GLU	THR	VAL	GLY	GLY	THR	VAL	ASN	GLU	ASN	GLU	GLU	GLU	ALA	ALA	GLY	PHE	GLU	DA	DA	DT	DG	DG		
SER	ASN	ARG	ARG	LYS	ARG	PRO	ARG	ASP	ASP	ARG	GLN	GLY	LYS	THR	GLY	ASP	TYR	GLY	THR	GLN	GLN	GLY	GLY	GLY	GLY	GLY	ALA	ALA	THR	TYR	TYR	SER	PRO	DA	DG	DG		
ARG	ASP	GLU	ARG	LYS	ARG	CYS	HIS	ARG	ARG	ASP	ARG	MET	LEU	PRO	THR	TYR	SER	SER	ASP	PRO	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR		
LYS	GLY	HIS	LEU	ASN	ALA	PHE	GLN	ASP	ASP	ASP	GLN	ALA	HIS	ARG	LEU	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
HIS	LYS	LEU	ALA	SER	LYS	GLU	GLU	ASN	ASP	ASP	ASP	ARG	ARG	PRO	PRO	SER	GLY	GLN	ASN	ALA	HIS	ARG	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
ASP	PRO	GLU	LYS	ALA	LYS	LEU	ASP	LYS	LYS	LYS	GLN	GLY	ASP	GLY	THR	GLY	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
GLU	THR	ASP	MET	GLY	GLY	ASP	PHE	PHE	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
GLN	LYS	LEU	PRO	VAL	ASN	GLN	THR	THR	LYS	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LYS	ALA	PHE	SER	PRO	VAL	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
R609	P612	R617	I618	E619	E620	N622	L625	E628	T629	L632	M633	D640	E647	E650	R653	E654	M655	Y656	L659	L670	K683	G684	R685	A690	F691	V692	P698	PRO	ARG	ASP	VAL	ARG	ARG	ARG	ARG	ARG		
VAL	PRO	GLY	ILE	ILE	LYS	PRO	ALA	MET	GLY	SER	HIS	SER	ALA	SER	ASN	ALA	SER	SER	ILE	PHE	ASN	PRO	SER	PRO	GLY	GLY	PRO	SER	ALA	LEU	ALA	VAL	VAL	VAL	VAL	VAL	VAL	
THR	VAL	LYS	ILE	ALA	PRO	MET	LYS	ALA	PHE	SER	LYS	ARG	SER	ALA	SER	ALA	SER	SER	ILE	PHE	ASN	PRO	SER	PRO	GLY	GLY	PRO	SER	ALA	LEU	ALA	VAL	VAL	VAL	VAL	VAL	VAL	

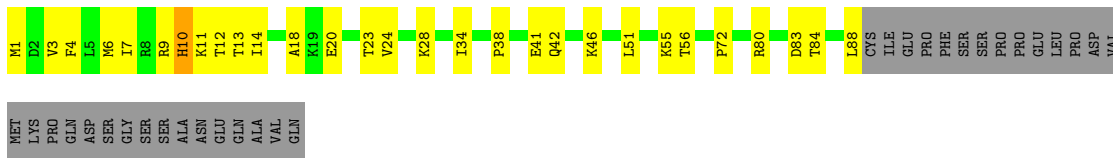
● Molecule 17: Elongin-C



MET	ASP	GLY	GLY	GLY	LYS	THR	TYR	GLY	CYS	E12	Y18	S23	I30	H35	S39	C40	T41	I42	L46	F52	N55	I65	C74	F77	T78	Y79	R80	V81	S86	S87	E92	A96	I99	A100	L103	L104	M105	A106	A107	M108	D111
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• Molecule 18: Elongin-B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136189	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 ($e^-/\text{\AA}^2$)	40.09	Depositor
Minimum defocus (nm)	350	Depositor
Maximum defocus (nm)	7500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	46.270	Depositor
Minimum map value	-25.666	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.056	Depositor
Recommended contour level	3.5	Depositor
Map size (\AA)	461.99997, 461.99997, 461.99997	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.20	0/11360	0.45	2/15328 (0.0%)
2	B	0.22	0/9227	0.44	0/12454
3	C	0.21	0/2115	0.39	0/2873
4	D	0.26	0/979	0.63	0/1312
5	E	0.19	0/1752	0.44	0/2366
6	F	0.18	0/636	0.45	0/859
7	G	0.23	0/1378	0.57	0/1870
8	H	0.18	0/1207	0.40	0/1628
9	I	0.17	0/954	0.43	0/1293
10	J	0.20	0/533	0.41	0/719
11	K	0.22	0/939	0.41	0/1271
12	L	0.21	0/372	0.48	0/493
13	N	0.18	0/619	0.31	0/954
14	P	0.13	0/313	0.21	0/486
15	T	0.23	0/857	0.43	0/1319
16	M	0.24	0/1098	0.58	0/1481
17	O	0.24	0/810	0.68	2/1097 (0.2%)
18	Q	0.26	0/707	0.73	2/952 (0.2%)
All	All	0.21	0/35856	0.46	6/48755 (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
1	A	0	1
4	D	0	1
7	G	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	538	VAL	CA-C-N	6.42	133.79	121.54
1	A	538	VAL	C-N-CA	6.42	133.79	121.54
18	Q	10	HIS	CA-C-N	5.93	136.64	126.32
18	Q	10	HIS	C-N-CA	5.93	136.64	126.32
17	O	52	PHE	CA-C-N	5.23	131.53	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	539	GLN	Mainchain
4	D	144	ASN	Peptide
7	G	124	ASN	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11159	0	11304	148	0
2	B	9047	0	9080	124	0
3	C	2072	0	2019	28	0
4	D	967	0	973	19	0
5	E	1721	0	1737	16	0
6	F	626	0	657	7	0
7	G	1347	0	1347	20	0
8	H	1186	0	1147	15	0
9	I	932	0	856	13	0
10	J	524	0	540	5	0
11	K	920	0	942	9	0
12	L	367	0	367	9	0
13	N	549	0	289	4	0
14	P	280	0	142	2	0
15	T	769	0	429	12	0
16	M	1074	0	1070	29	0
17	O	792	0	774	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Q	696	0	694	16	0
19	A	1	0	0	0	0
20	A	2	0	0	0	0
20	B	1	0	0	0	0
20	C	1	0	0	0	0
20	I	2	0	0	0	0
20	J	1	0	0	0	0
20	L	1	0	0	0	0
All	All	35037	0	34367	429	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 429 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)
16:M:585:LEU:HG	16:M:606:VAL:HG21	1.74	0.70
17:O:104:LEU:O	17:O:107:ALA:HB3	1.92	0.69
18:Q:7:ILE:HB	18:Q:14:ILE:HB	1.73	0.69
2:B:825:ALA:HB3	2:B:888:TYR:HB2	1.75	0.69
18:Q:9:ARG:HD3	18:Q:12:THR:OG1	1.93	0.68

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	A	1395/1970 (71%)	1364 (98%)	31 (2%)	0	100 100
2	B	1123/1251 (90%)	1088 (97%)	35 (3%)	0	100 100
3	C	254/275 (92%)	247 (97%)	7 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	114/184 (62%)	107 (94%)	7 (6%)	0	100	100
5	E	207/210 (99%)	202 (98%)	5 (2%)	0	100	100
6	F	76/127 (60%)	76 (100%)	0	0	100	100
7	G	169/172 (98%)	158 (94%)	11 (6%)	0	100	100
8	H	146/150 (97%)	142 (97%)	4 (3%)	0	100	100
9	I	114/125 (91%)	111 (97%)	3 (3%)	0	100	100
10	J	64/67 (96%)	63 (98%)	1 (2%)	0	100	100
11	K	113/117 (97%)	111 (98%)	2 (2%)	0	100	100
12	L	42/58 (72%)	39 (93%)	3 (7%)	0	100	100
16	M	126/801 (16%)	119 (94%)	7 (6%)	0	100	100
17	O	99/112 (88%)	90 (91%)	9 (9%)	0	100	100
18	Q	86/118 (73%)	73 (85%)	13 (15%)	0	100	100
All	All	4128/5737 (72%)	3990 (97%)	138 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	A	1239/1749 (71%)	1239 (100%)	0	100	100
2	B	991/1084 (91%)	991 (100%)	0	100	100
3	C	235/252 (93%)	235 (100%)	0	100	100
4	D	109/160 (68%)	109 (100%)	0	100	100
5	E	191/192 (100%)	191 (100%)	0	100	100
6	F	68/111 (61%)	68 (100%)	0	100	100
7	G	151/153 (99%)	151 (100%)	0	100	100
8	H	129/131 (98%)	129 (100%)	0	100	100
9	I	102/112 (91%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	55/56 (98%)	55 (100%)	0	100	100
11	K	104/106 (98%)	104 (100%)	0	100	100
12	L	40/55 (73%)	40 (100%)	0	100	100
16	M	118/706 (17%)	118 (100%)	0	100	100
17	O	88/96 (92%)	88 (100%)	0	100	100
18	Q	75/103 (73%)	75 (100%)	0	100	100
All	All	3695/5066 (73%)	3695 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
11	K	69	HIS
12	L	26	ASN
2	B	265	ASN
2	B	175	HIS
16	M	638	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	12/46 (26%)	3 (25%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	35	A
14	P	36	G
14	P	37	G

There are no RNA pucker outliers to report.

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 9 ligands modelled in this entry, 9 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.

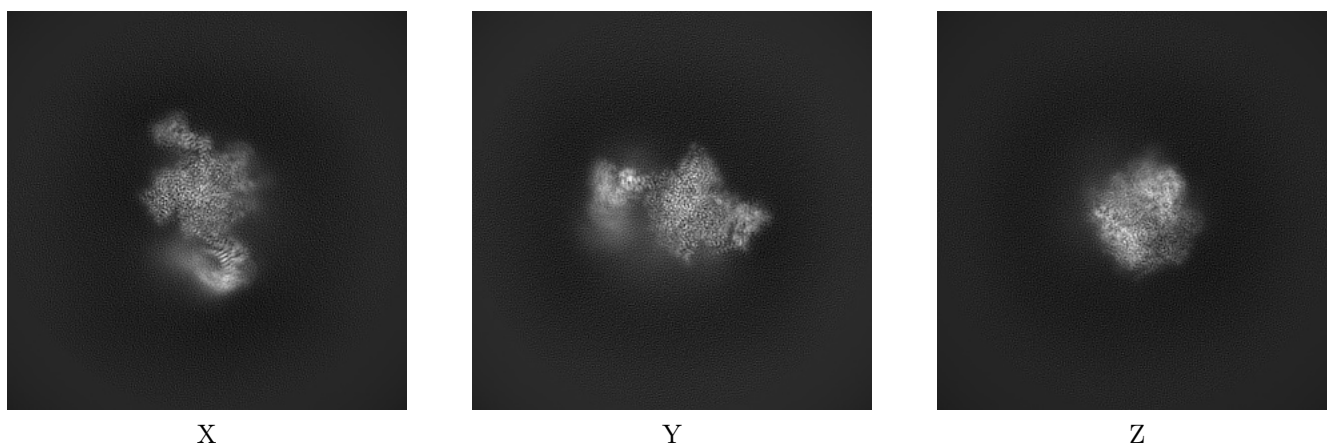
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16838. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

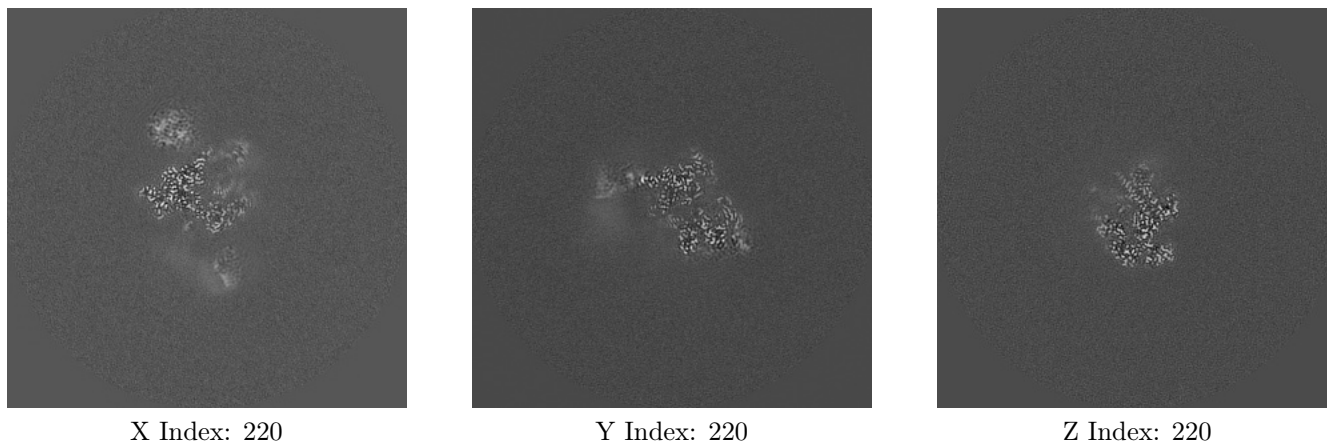
6.1.1 Primary map



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

6.2 Central slices [i](#)

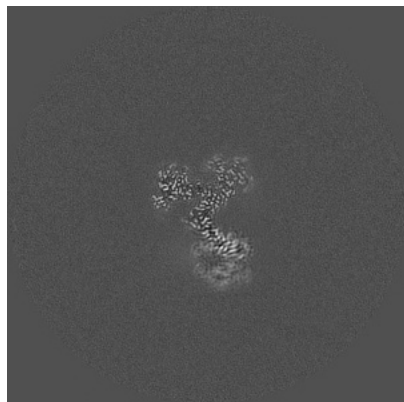
6.2.1 Primary map



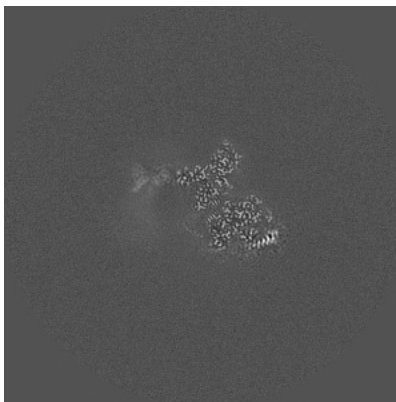
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

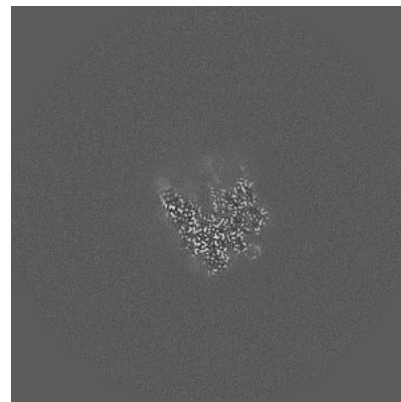
6.3.1 Primary map



X Index: 253



Y Index: 213

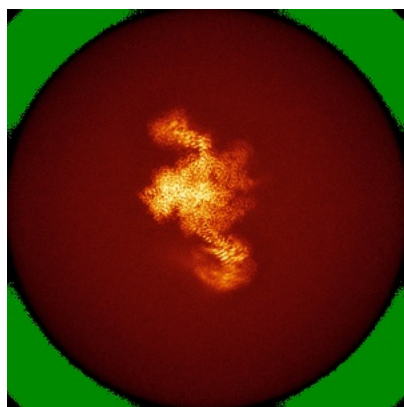


Z Index: 235

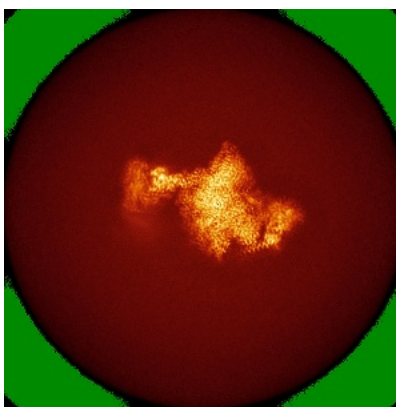
The images above show the largest variance slices of the map in three orthogonal directions.

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

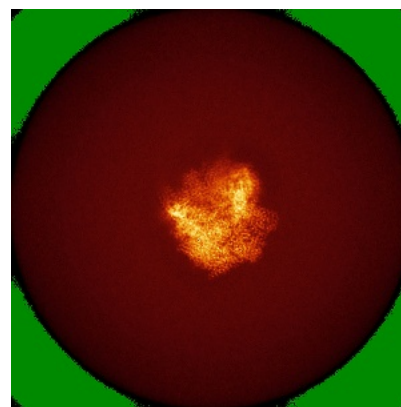
6.4.1 Primary map



X



Y

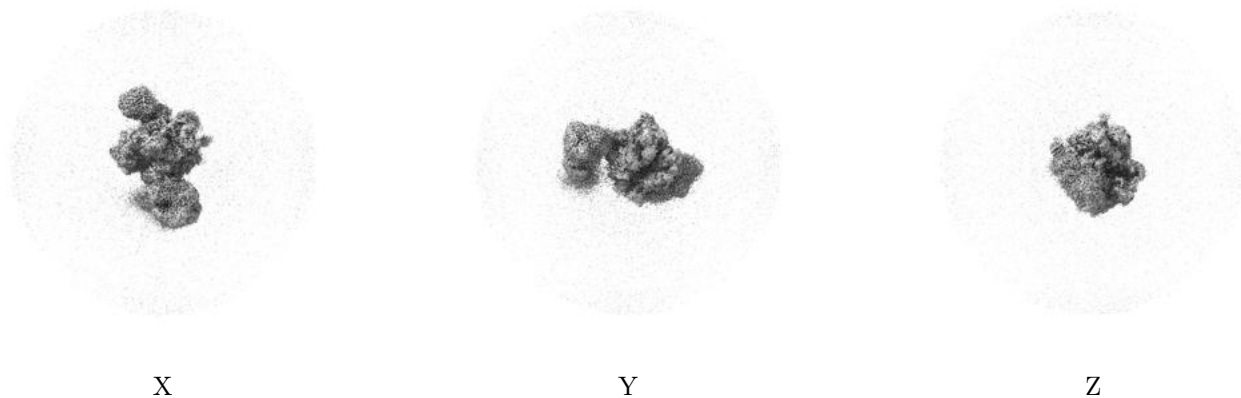


Z

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 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

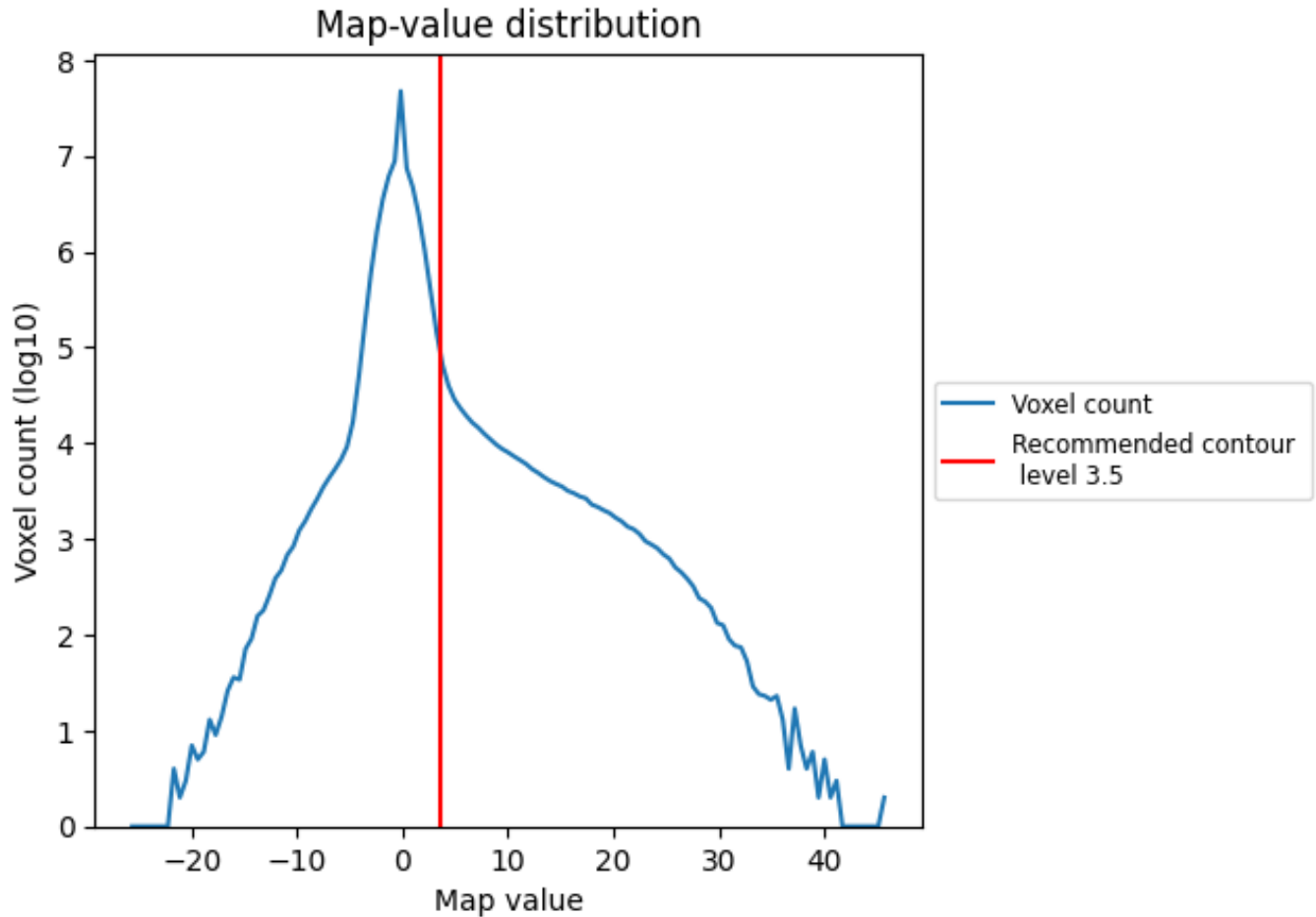
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

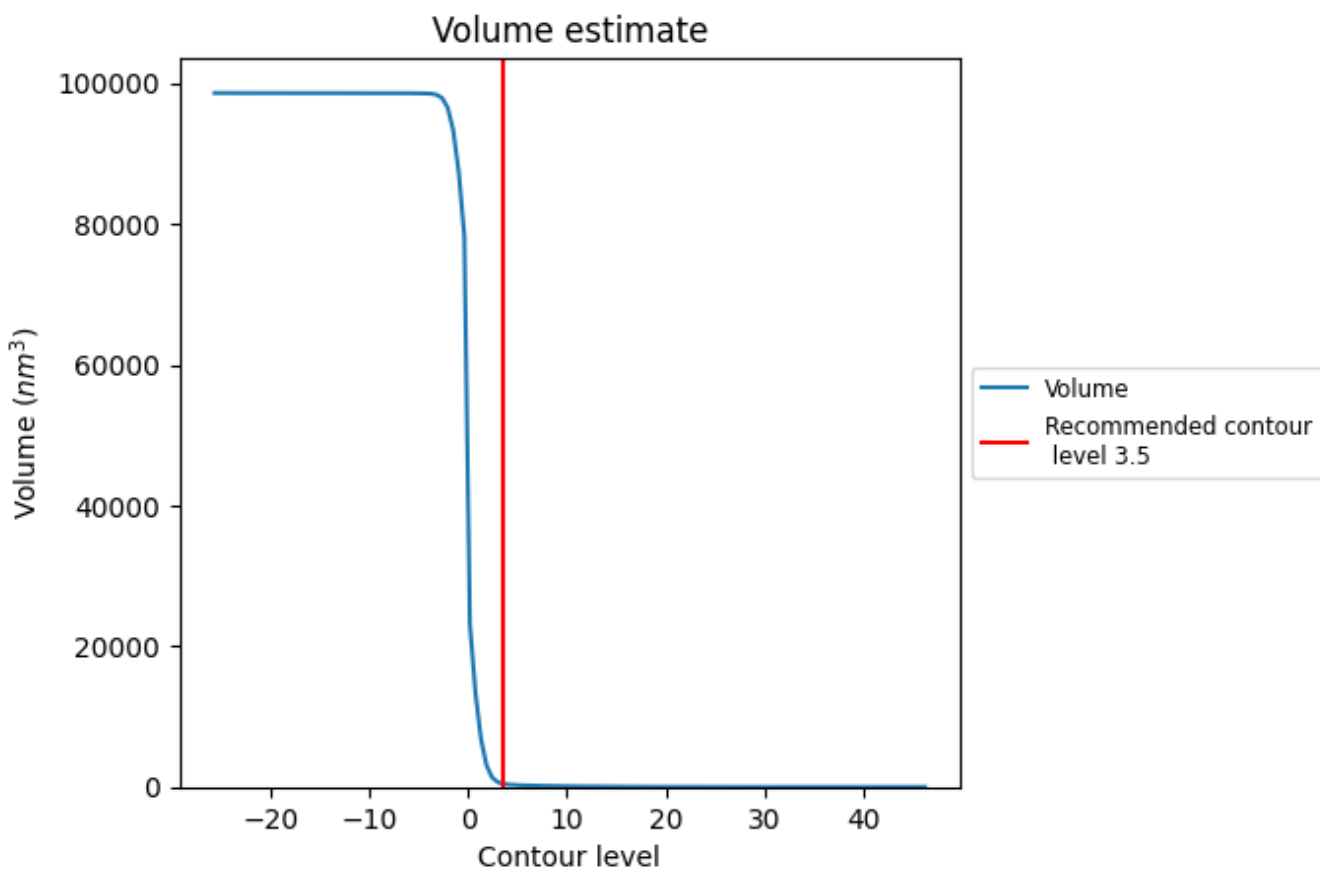
This section contains the results of statistical analysis of the map.

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.

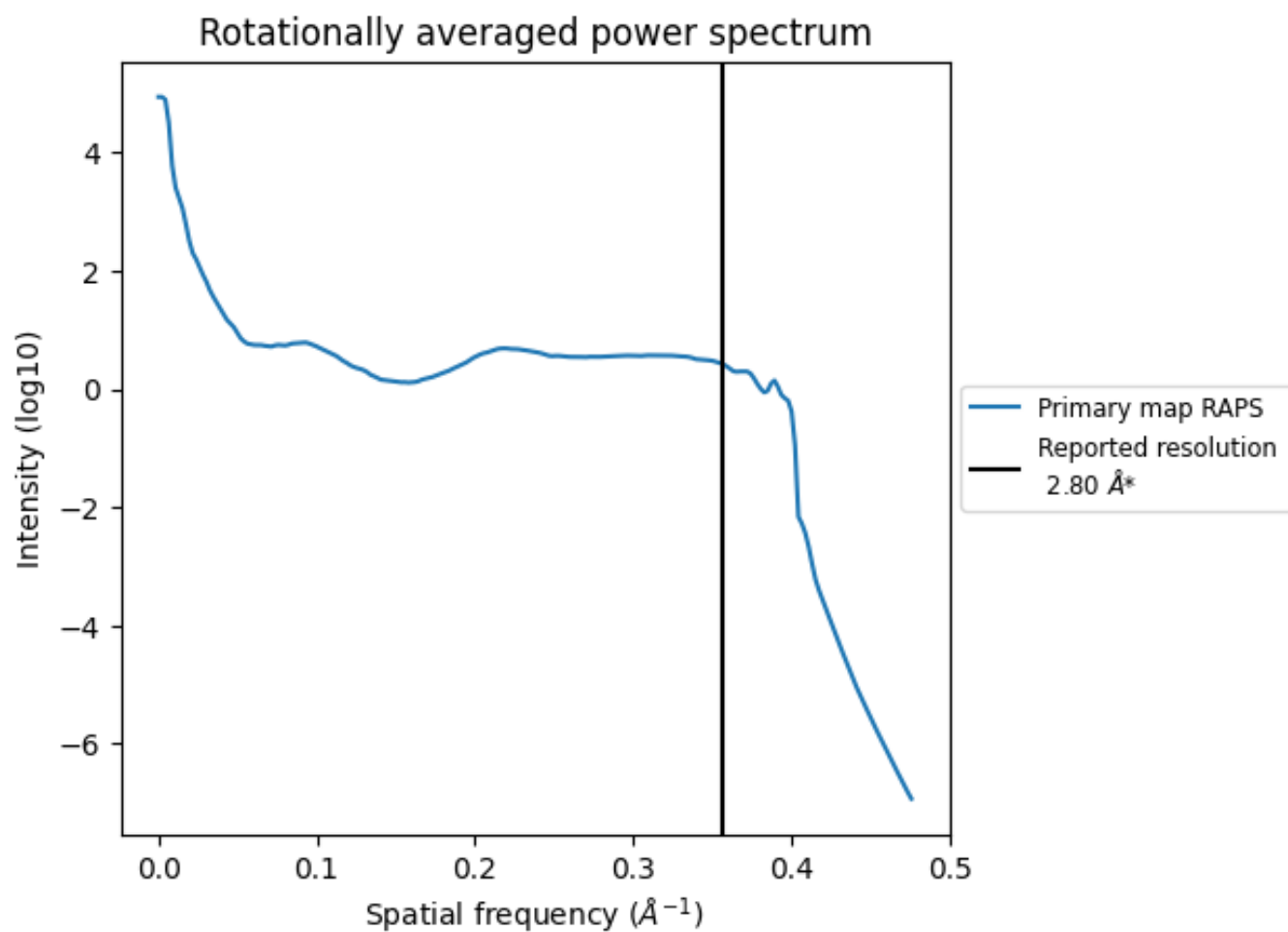
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 467 nm^3 ; this corresponds to an approximate mass of 422 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 i



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

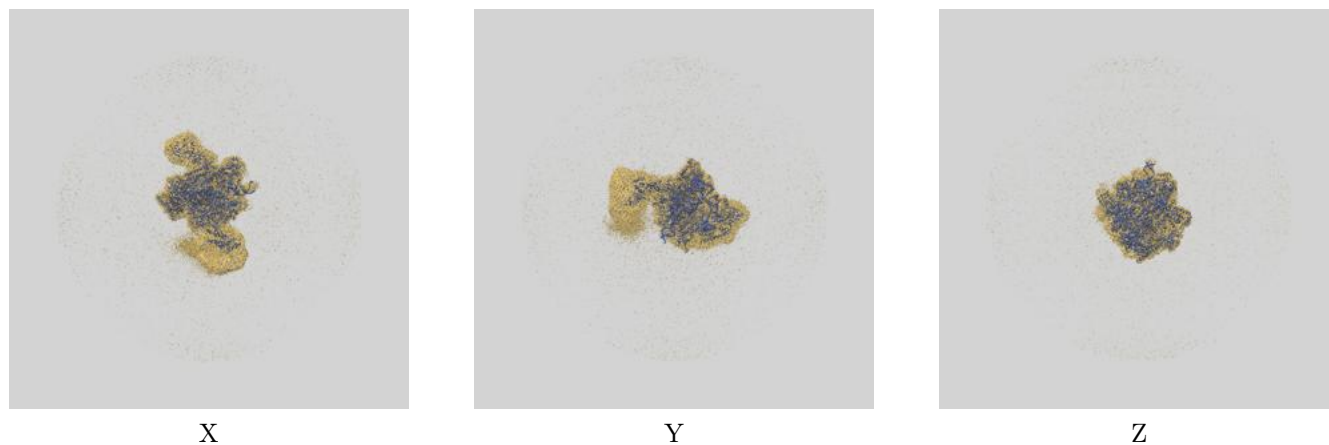
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

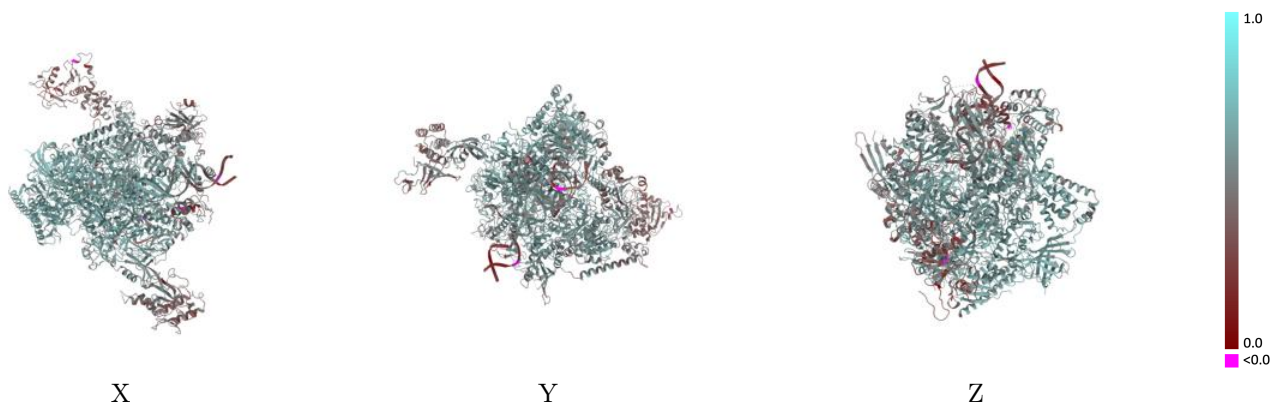
This section contains information regarding the fit between EMDB map EMD-16838 and PDB model 8OEW. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



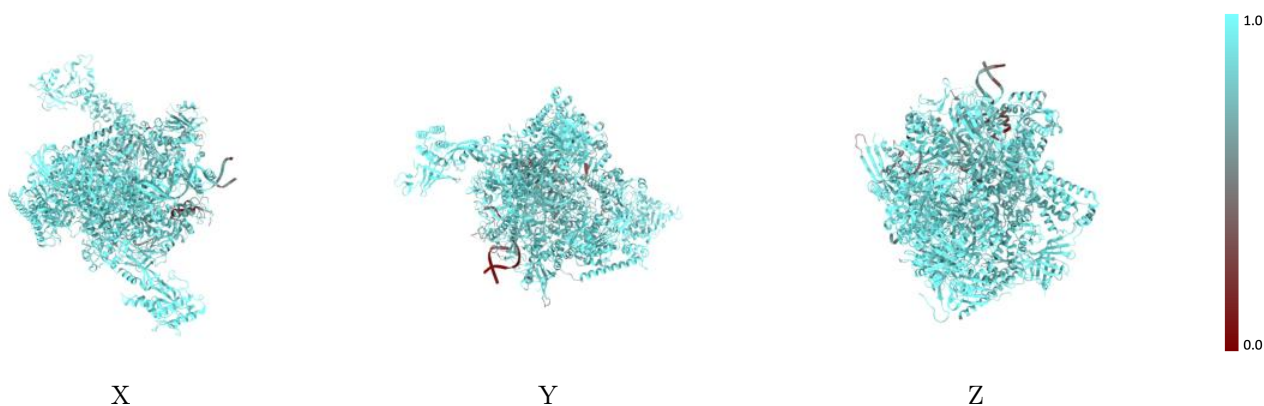
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



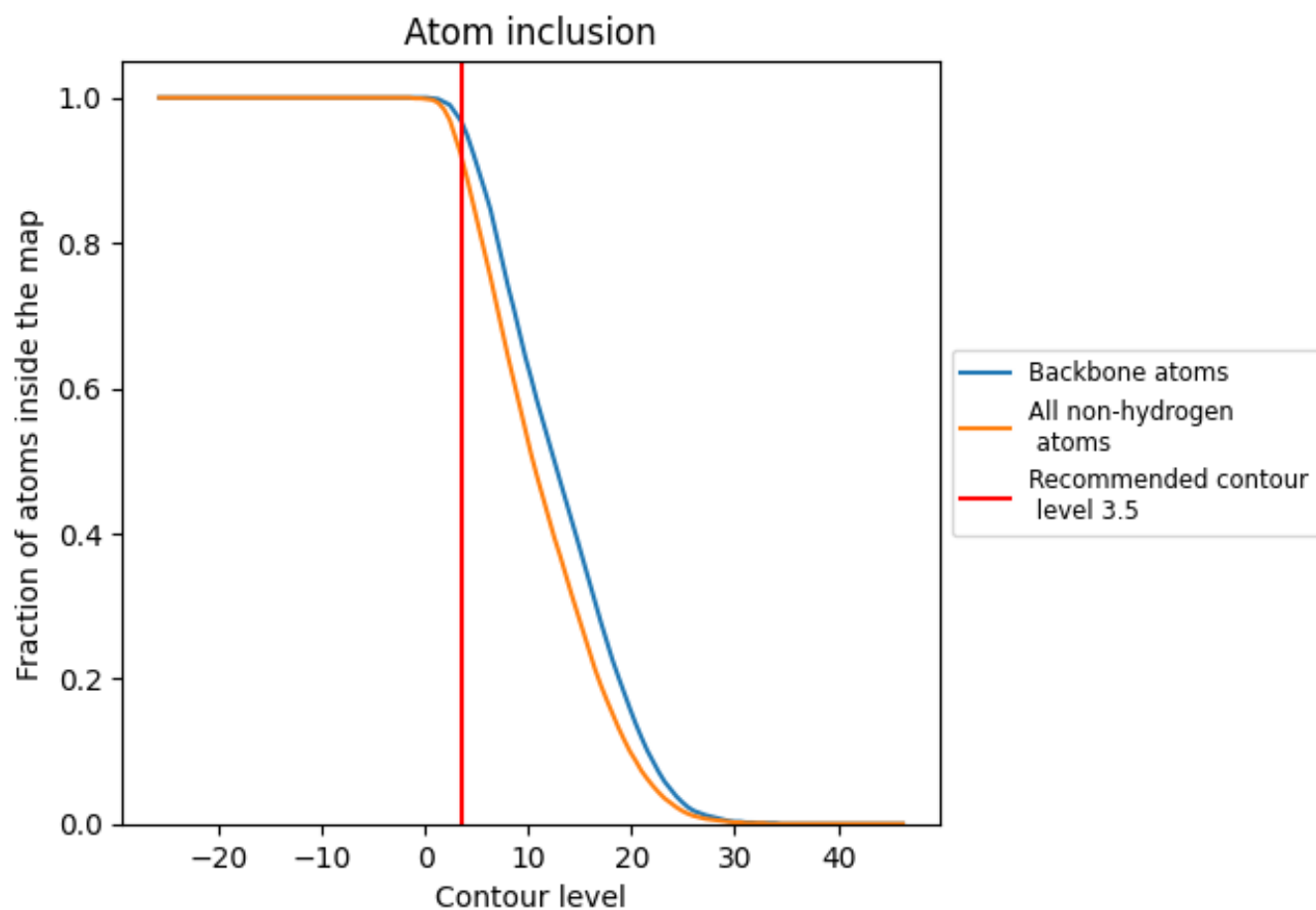
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 92% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9220	 0.5600
A	 0.9230	 0.5890
B	 0.9330	 0.6010
C	 0.9620	 0.6350
D	 0.9750	 0.4080
E	 0.9150	 0.5600
F	 0.9470	 0.6110
G	 0.9590	 0.4760
H	 0.9460	 0.6110
I	 0.8900	 0.5150
J	 0.9510	 0.6350
K	 0.9550	 0.6310
L	 0.8890	 0.5470
M	 0.9420	 0.4230
N	 0.6230	 0.3170
O	 0.9490	 0.3410
P	 0.8070	 0.5460
Q	 0.9210	 0.3240
T	 0.6980	 0.4070

