



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 02:04 PM UTC

PDB ID : 8RWV / pdb_00008rwv
EMDB ID : EMD-19566
Title : Human OCCM DNA licensing intermediate
Authors : Wells, J.N.; Leber, V.; Edwards, L.V.; Allyjaun, S.; Peach, M.; Tomkins, J.;
Kefala-Stavridi, A.; Faull, S.V.; Aramayo, R.; Pestana, C.M.; Ranjha, L.;
Speck, C.
Deposited on : 2024-02-05
Resolution : 6.68 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

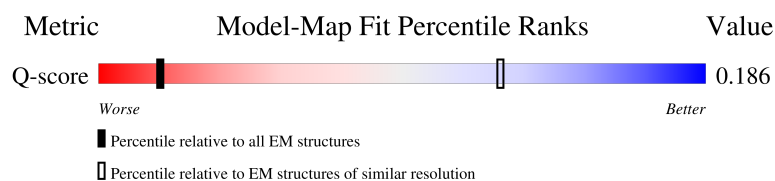
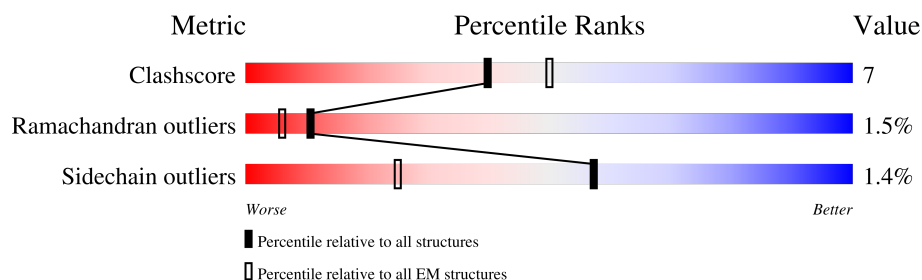
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.68 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	-
Q-score	-	25397	494 (6.18 - 7.17)

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

Mol	Chain	Length	Quality of chain
1	2	947	12% 58% 11% 31%
2	3	853	41% 67% 17% 15%
3	4	883	13% 60% 11% 28%
4	6	821	7% 63% 16% 20%

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Mol	Chain	Length	Quality of chain
5	7	719	
6	A	961	
7	B	577	
8	C	712	
9	D	436	
10	E	435	
11	F	560	
12	G	410	
13	H	39	
14	J	40	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 51862 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 replication licensing factor MCM2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	653	Total	C	N	O	S	0	0
			5131	3221	913	966	31		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	-42	MET	-	initiating methionine	UNP P49736
2	-41	SER	-	expression tag	UNP P49736
2	-40	ALA	-	expression tag	UNP P49736
2	-39	TRP	-	expression tag	UNP P49736
2	-38	SER	-	expression tag	UNP P49736
2	-37	HIS	-	expression tag	UNP P49736
2	-36	PRO	-	expression tag	UNP P49736
2	-35	GLN	-	expression tag	UNP P49736
2	-34	PHE	-	expression tag	UNP P49736
2	-33	GLU	-	expression tag	UNP P49736
2	-32	LYS	-	expression tag	UNP P49736
2	-31	GLY	-	expression tag	UNP P49736
2	-30	GLY	-	expression tag	UNP P49736
2	-29	GLY	-	expression tag	UNP P49736
2	-28	SER	-	expression tag	UNP P49736
2	-27	GLY	-	expression tag	UNP P49736
2	-26	GLY	-	expression tag	UNP P49736
2	-25	GLY	-	expression tag	UNP P49736
2	-24	SER	-	expression tag	UNP P49736
2	-23	GLY	-	expression tag	UNP P49736
2	-22	GLY	-	expression tag	UNP P49736
2	-21	SER	-	expression tag	UNP P49736
2	-20	ALA	-	expression tag	UNP P49736
2	-19	TRP	-	expression tag	UNP P49736
2	-18	SER	-	expression tag	UNP P49736
2	-17	HIS	-	expression tag	UNP P49736
2	-16	PRO	-	expression tag	UNP P49736
2	-15	GLN	-	expression tag	UNP P49736

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Chain	Residue	Modelled	Actual	Comment	Reference
2	-14	PHE	-	expression tag	UNP P49736
2	-13	GLU	-	expression tag	UNP P49736
2	-12	LYS	-	expression tag	UNP P49736
2	-11	GLU	-	expression tag	UNP P49736
2	-10	ASN	-	expression tag	UNP P49736
2	-9	LEU	-	expression tag	UNP P49736
2	-8	TYR	-	expression tag	UNP P49736
2	-7	PHE	-	expression tag	UNP P49736
2	-6	GLN	-	expression tag	UNP P49736
2	-5	GLY	-	expression tag	UNP P49736
2	-4	ALA	-	expression tag	UNP P49736
2	-3	GLY	-	expression tag	UNP P49736
2	-2	SER	-	expression tag	UNP P49736
2	-1	ALA	-	expression tag	UNP P49736
2	0	THR	-	expression tag	UNP P49736

- Molecule 2 is a protein called Isoform 2 of DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	724	Total	C	N	O	S	0	0
			5674	3541	994	1109	30		

- Molecule 3 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	632	Total	C	N	O	S	0	0
			5017	3155	883	953	26		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	-19	MET	-	initiating methionine	UNP P33991
4	-18	HIS	-	expression tag	UNP P33991
4	-17	HIS	-	expression tag	UNP P33991
4	-16	HIS	-	expression tag	UNP P33991
4	-15	HIS	-	expression tag	UNP P33991
4	-14	HIS	-	expression tag	UNP P33991
4	-13	HIS	-	expression tag	UNP P33991
4	-12	HIS	-	expression tag	UNP P33991
4	-11	HIS	-	expression tag	UNP P33991
4	-10	GLU	-	expression tag	UNP P33991
4	-9	ASN	-	expression tag	UNP P33991

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Chain	Residue	Modelled	Actual	Comment	Reference
4	-8	LEU	-	expression tag	UNP P33991
4	-7	TYR	-	expression tag	UNP P33991
4	-6	PHE	-	expression tag	UNP P33991
4	-5	GLN	-	expression tag	UNP P33991
4	-4	GLY	-	expression tag	UNP P33991
4	-3	SER	-	expression tag	UNP P33991
4	-2	SER	-	expression tag	UNP P33991
4	-1	ALA	-	expression tag	UNP P33991
4	0	THR	-	expression tag	UNP P33991

- Molecule 4 is a protein called DNA replication licensing factor MCM6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	660	Total	C	N	O	S	0	0
			5311	3342	935	1007	27		

- Molecule 5 is a protein called DNA replication licensing factor MCM7.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	719	Total	C	N	O	S	0	0
			5698	3556	1023	1085	34		

- Molecule 6 is a protein called Origin recognition complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	387	Total	C	N	O	S	0	0
			3061	1919	542	577	23		

- Molecule 7 is a protein called Origin recognition complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	313	Total	C	N	O	S	0	0
			2575	1649	437	483	6		

- Molecule 8 is a protein called Isoform 2 of Origin recognition complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	678	Total	C	N	O	S	0	0
			5509	3525	930	1021	33		

- Molecule 9 is a protein called Origin recognition complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	428	Total	C	N	O	S	0	0
			3472	2206	607	637	22		

- Molecule 10 is a protein called Origin recognition complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	431	Total	C	N	O	S	0	0
			3514	2277	588	637	12		

- Molecule 11 is a protein called Cell division control protein 6 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	395	Total	C	N	O	S	0	0
			3105	1956	557	571	21		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	441	ILE	VAL	variant	UNP Q99741

- Molecule 12 is a protein called DNA replication factor Cdt1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	270	Total	C	N	O	S	0	0
			2175	1359	406	395	15		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	137	MET	-	initiating methionine	UNP Q9H211
G	138	GLY	-	expression tag	UNP Q9H211
G	139	SER	-	expression tag	UNP Q9H211
G	140	SER	-	expression tag	UNP Q9H211
G	141	HIS	-	expression tag	UNP Q9H211
G	142	HIS	-	expression tag	UNP Q9H211
G	143	HIS	-	expression tag	UNP Q9H211
G	144	HIS	-	expression tag	UNP Q9H211
G	145	HIS	-	expression tag	UNP Q9H211
G	146	HIS	-	expression tag	UNP Q9H211
G	147	SER	-	expression tag	UNP Q9H211
G	148	SER	-	expression tag	UNP Q9H211
G	149	GLY	-	expression tag	UNP Q9H211

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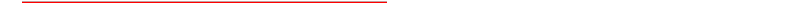
Chain	Residue	Modelled	Actual	Comment	Reference
G	150	LEU	-	expression tag	UNP Q9H211
G	151	GLU	-	expression tag	UNP Q9H211
G	152	VAL	-	expression tag	UNP Q9H211
G	153	LEU	-	expression tag	UNP Q9H211
G	154	PHE	-	expression tag	UNP Q9H211
G	155	GLN	-	expression tag	UNP Q9H211
G	156	GLY	-	expression tag	UNP Q9H211
G	157	PRO	-	expression tag	UNP Q9H211

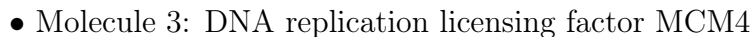
- Molecule 13 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	39	Total	C	N	O	P	0	0
			795	382	143	231	39		

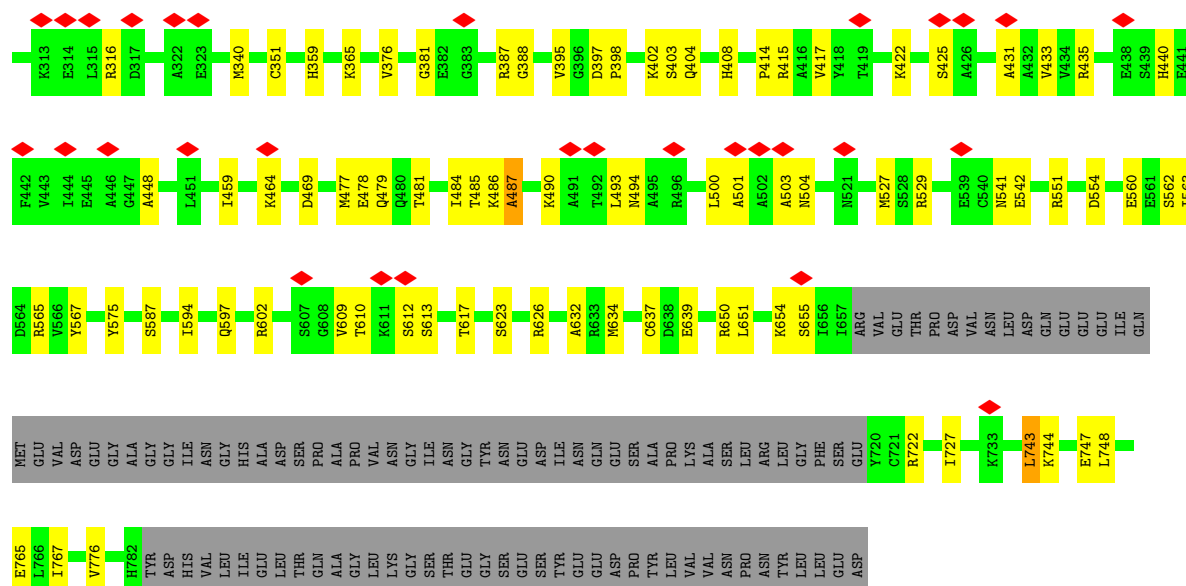
- Molecule 14 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	40	Total	C	N	O	P	0	0
			825	396	147	242	40		

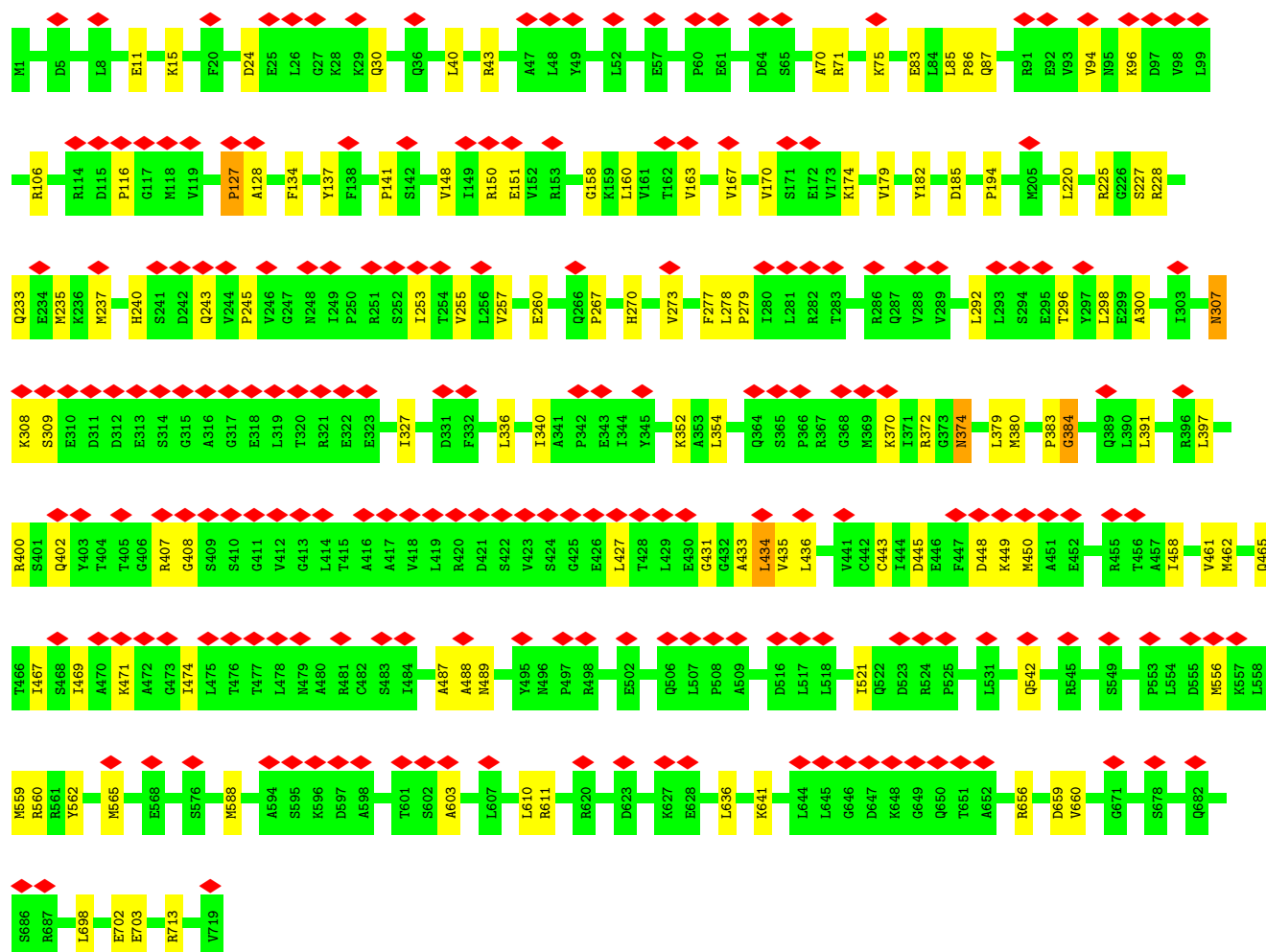
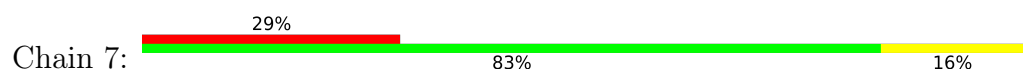
- Chain 3: 







• Molecule 5: DNA replication licensing factor MCM7

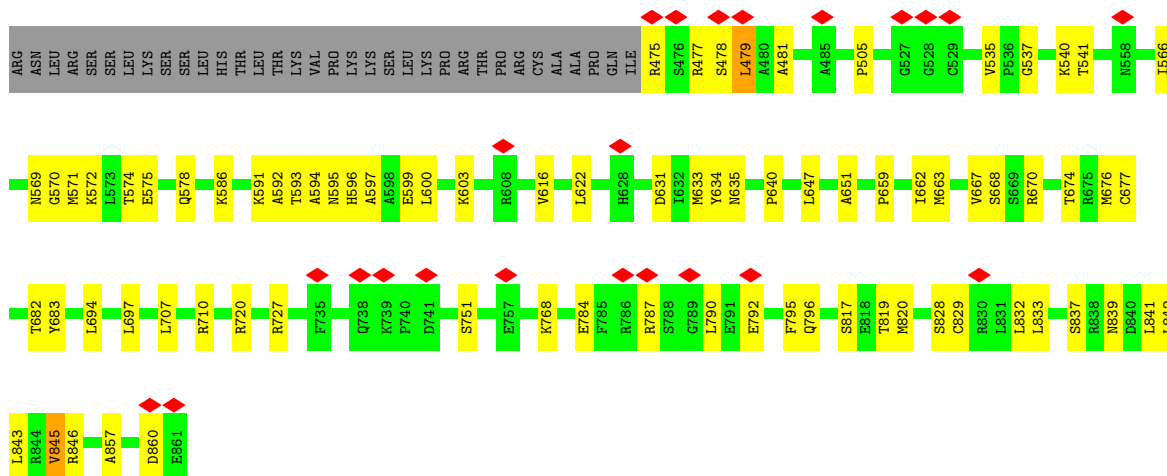


Chain A:

32%

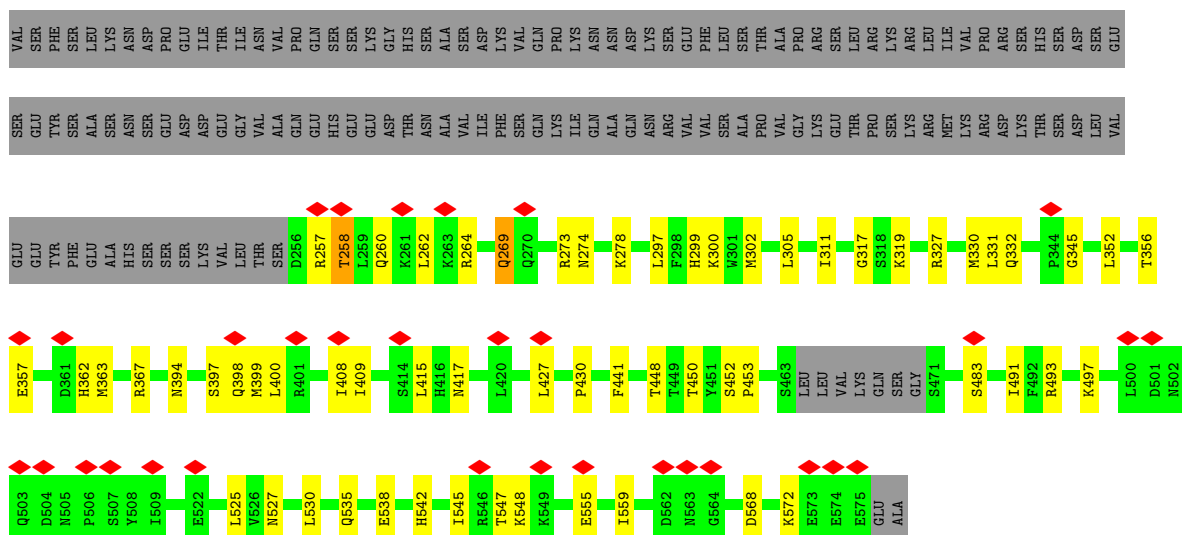
8%

60%

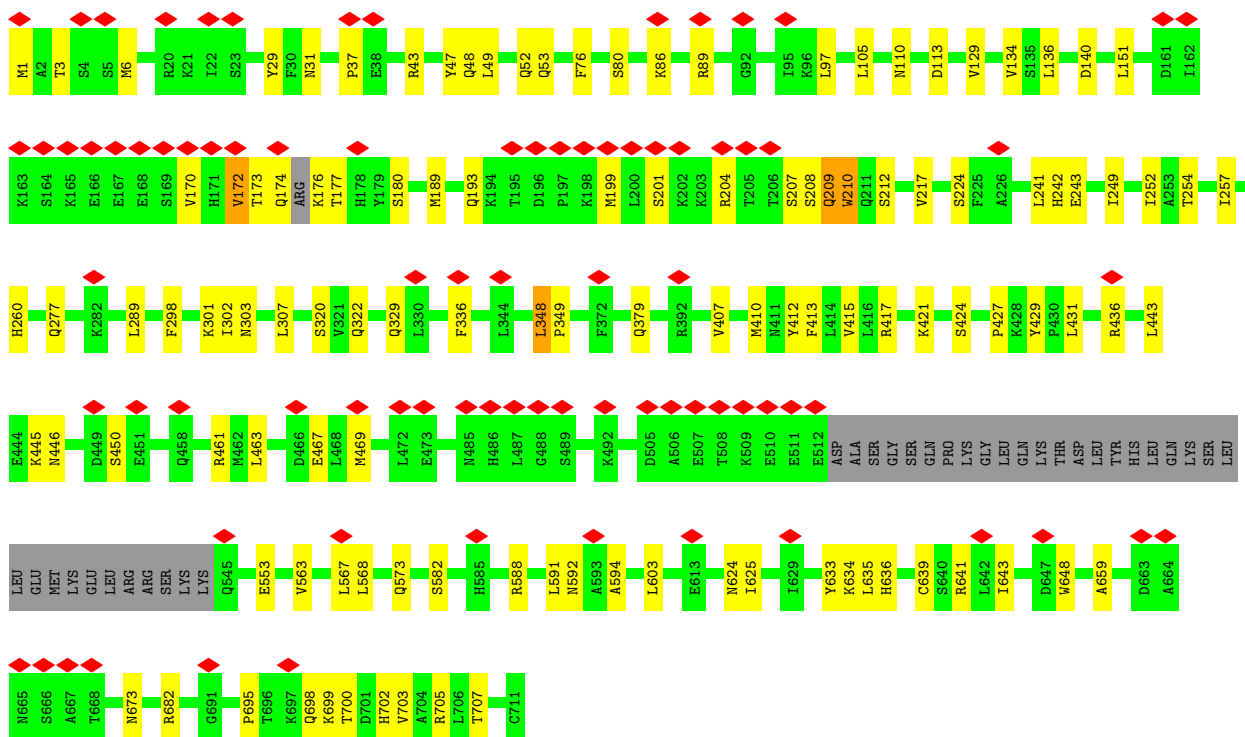
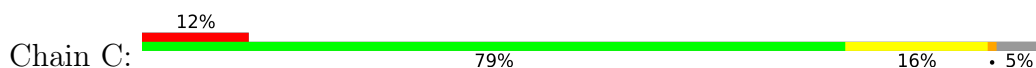


Chain B:

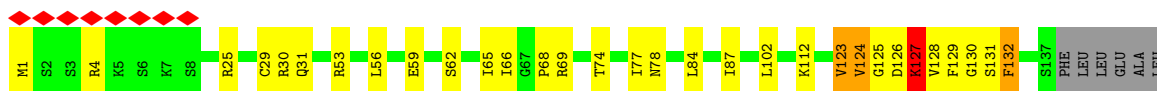
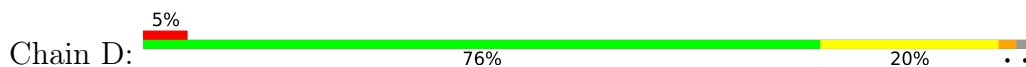
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• Molecule 8: Isoform 2 of Origin recognition complex subunit 3



• Molecule 9: Origin recognition complex subunit 4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8730	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.046	Depositor
Minimum map value	-0.437	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	330.0, 330.0, 330.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	2	0.08	0/5227	0.23	0/7064
2	3	0.08	0/5759	0.22	0/7774
3	4	0.07	0/5104	0.21	0/6902
4	6	0.39	2/5397 (0.0%)	0.30	4/7276 (0.1%)
5	7	0.08	0/5788	0.22	0/7815
6	A	0.14	0/3114	0.28	0/4214
7	B	0.08	0/2628	0.25	0/3553
8	C	0.11	0/5622	0.25	0/7597
9	D	0.19	0/3537	0.38	2/4766 (0.0%)
10	E	0.09	0/3601	0.25	0/4885
11	F	0.09	0/3140	0.26	0/4220
12	G	0.09	0/2209	0.27	0/2968
13	H	0.72	1/891 (0.1%)	1.30	21/1371 (1.5%)
14	J	0.64	0/925	1.32	25/1427 (1.8%)
All	All	0.20	3/52942 (0.0%)	0.36	52/71832 (0.1%)

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
4	6	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	6	487	ALA	C-N	-20.38	1.03	1.33
4	6	485	THR	C-N	-19.18	1.05	1.33
13	H	47	DG	O3'-P	-10.25	1.45	1.61

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	H	47	DG	O3'-P-O5'	11.02	120.53	104.00
14	J	43	DC	P-O3'-C3'	-10.59	104.31	120.20
14	J	43	DC	OP2-P-O3'	10.52	139.56	108.00
13	H	47	DG	P-O3'-C3'	9.92	135.09	120.20
13	H	49	DC	P-O3'-C3'	-9.07	106.59	120.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	6	487	ALA	Mainchain

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	2	5131	0	5126	61	0
2	3	5674	0	5688	80	0
3	4	5017	0	5038	68	0
4	6	5311	0	5334	82	0
5	7	5698	0	5726	74	0
6	A	3061	0	3076	48	0
7	B	2575	0	2572	40	0
8	C	5509	0	5564	66	0
9	D	3472	0	3511	73	0
10	E	3514	0	3529	49	0
11	F	3105	0	3272	51	0
12	G	2175	0	2232	38	0
13	H	795	0	441	85	0
14	J	825	0	456	73	0
All	All	51862	0	51565	731	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 7.

The worst 5 of 731 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)
13:H:78:DA:N1	14:J:12:DT:N3	1.72	1.38
13:H:75:DA:N1	14:J:15:DT:N3	1.68	1.34
9:D:390:ARG:NH1	13:H:67:DA:H2''	1.45	1.31
3:4:549:LYS:HE3	14:J:45:DT:C5'	1.64	1.25
10:E:337:LYS:HE2	13:H:57:DT:OP2	1.30	1.25

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	2	647/947 (68%)	547 (84%)	92 (14%)	8 (1%)	10	44
2	3	720/853 (84%)	602 (84%)	99 (14%)	19 (3%)	4	25
3	4	628/883 (71%)	573 (91%)	49 (8%)	6 (1%)	12	48
4	6	654/821 (80%)	562 (86%)	87 (13%)	5 (1%)	16	54
5	7	717/719 (100%)	612 (85%)	97 (14%)	8 (1%)	11	46
6	A	385/961 (40%)	343 (89%)	38 (10%)	4 (1%)	12	48
7	B	309/577 (54%)	272 (88%)	33 (11%)	4 (1%)	9	42
8	C	672/712 (94%)	608 (90%)	55 (8%)	9 (1%)	9	42
9	D	424/436 (97%)	359 (85%)	56 (13%)	9 (2%)	5	30
10	E	427/435 (98%)	379 (89%)	44 (10%)	4 (1%)	14	51
11	F	391/560 (70%)	333 (85%)	51 (13%)	7 (2%)	6	34
12	G	266/410 (65%)	223 (84%)	32 (12%)	11 (4%)	2	18
All	All	6240/8314 (75%)	5413 (87%)	733 (12%)	94 (2%)	11	40

5 of 94 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	F	458	PRO

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Mol	Chain	Res	Type
12	G	256	PRO
1	2	401	ASP
1	2	704	PRO
1	2	716	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	2	565/810 (70%)	556 (98%)	9 (2%)	55	70
2	3	626/742 (84%)	615 (98%)	11 (2%)	51	68
3	4	556/771 (72%)	551 (99%)	5 (1%)	70	79
4	6	594/724 (82%)	584 (98%)	10 (2%)	53	69
5	7	619/619 (100%)	617 (100%)	2 (0%)	86	86
6	A	340/854 (40%)	334 (98%)	6 (2%)	51	68
7	B	292/529 (55%)	288 (99%)	4 (1%)	59	72
8	C	628/659 (95%)	621 (99%)	7 (1%)	65	76
9	D	396/403 (98%)	385 (97%)	11 (3%)	38	60
10	E	394/399 (99%)	391 (99%)	3 (1%)	73	80
11	F	346/499 (69%)	341 (99%)	5 (1%)	59	72
12	G	237/351 (68%)	231 (98%)	6 (2%)	42	63
All	All	5593/7360 (76%)	5514 (99%)	79 (1%)	57	72

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	D	131	SER
11	F	485	LEU
9	D	185	THR
10	E	69	LEU
12	G	418	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 154 such sidechains are listed below:

Mol	Chain	Res	Type
8	C	360	ASN
11	F	349	ASN
8	C	420	HIS
9	D	252	ASN
12	G	300	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	6	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	6	485:THR	C	486:LYS	N	1.06
1	6	487:ALA	C	488:GLY	N	1.03

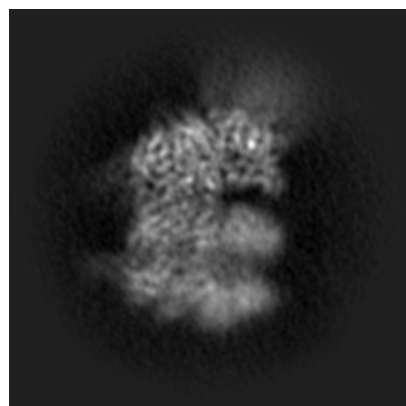
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19566. These allow visual inspection of the internal detail of the map and identification of artifacts.

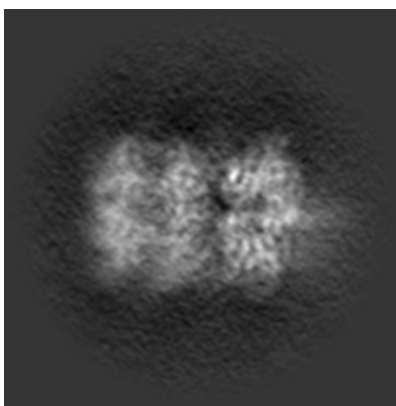
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

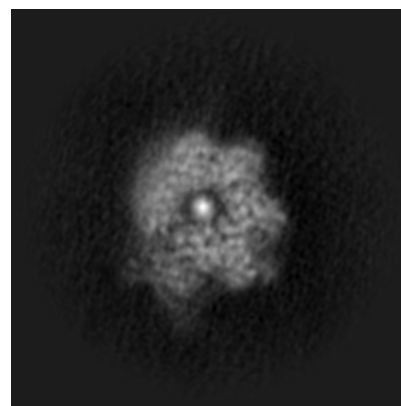
6.1.1 Primary map



X

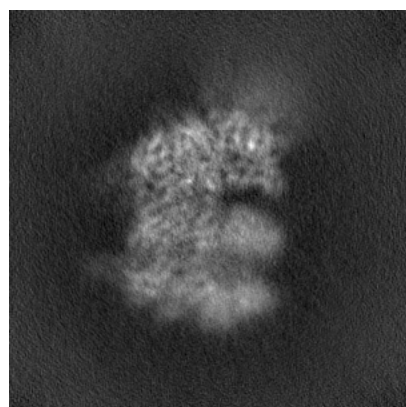


Y

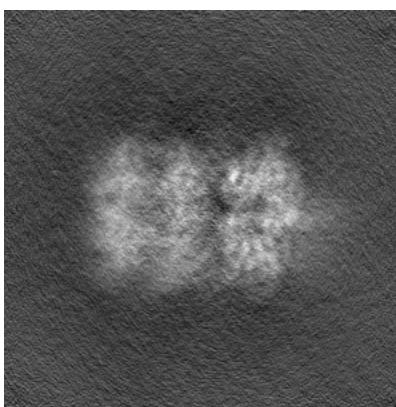


Z

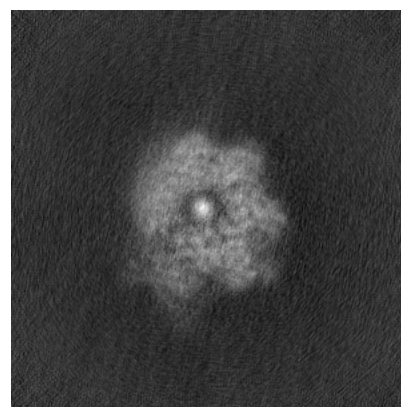
6.1.2 Raw map



X



Y

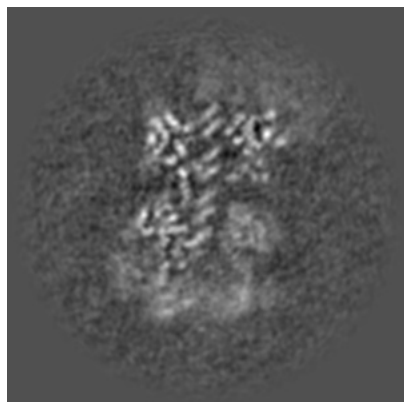


Z

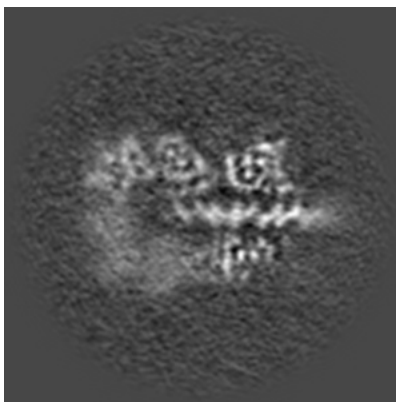
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

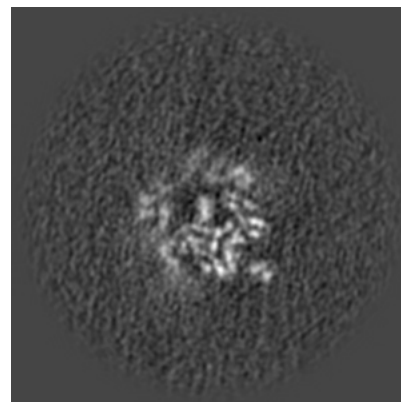
6.2.1 Primary map



X Index: 150

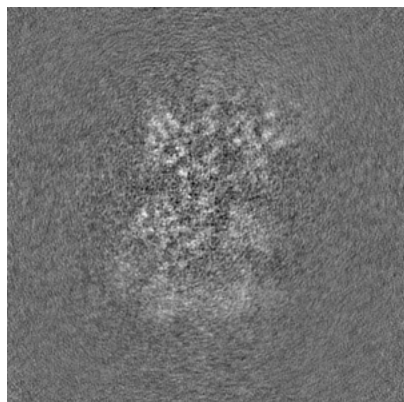


Y Index: 150

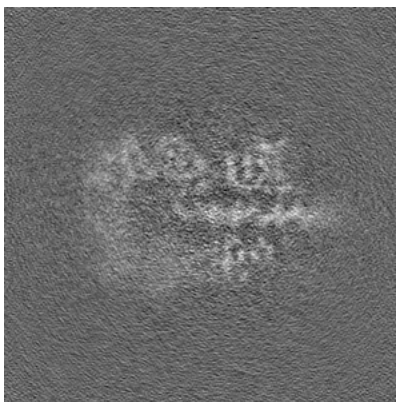


Z Index: 150

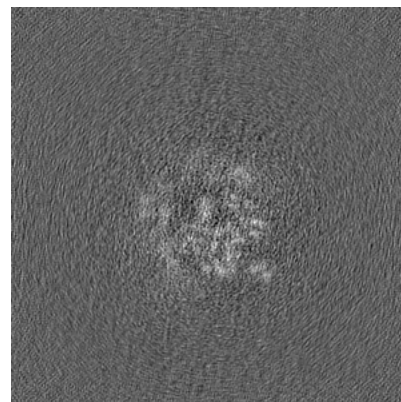
6.2.2 Raw map



X Index: 150



Y Index: 150

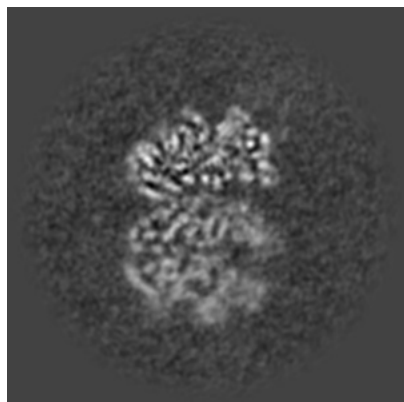


Z Index: 150

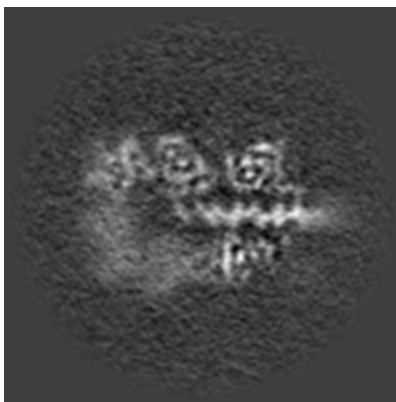
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

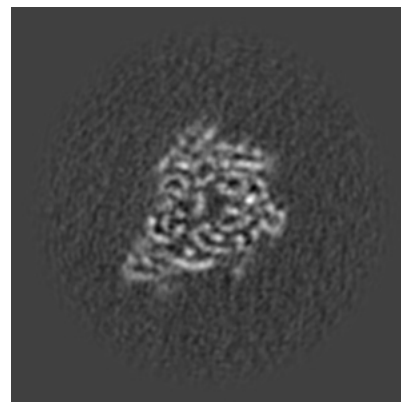
6.3.1 Primary map



X Index: 172

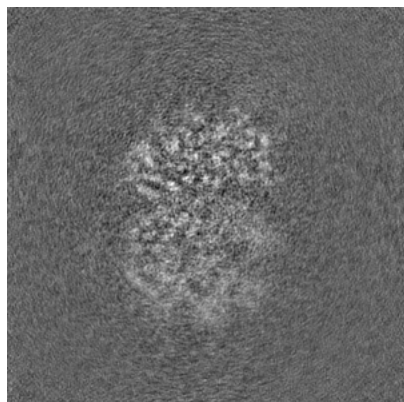


Y Index: 151

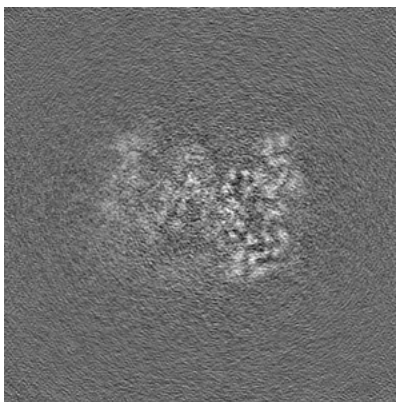


Z Index: 198

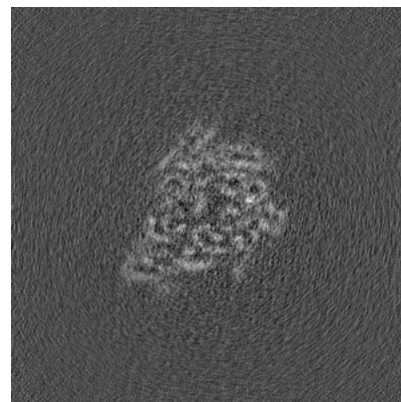
6.3.2 Raw map



X Index: 171



Y Index: 133

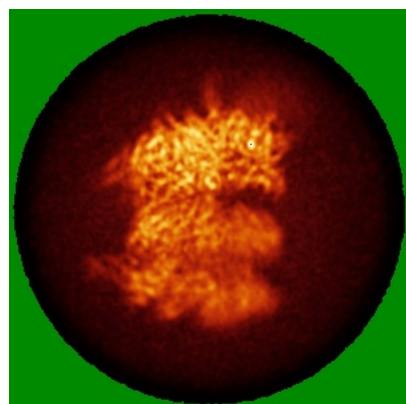


Z Index: 197

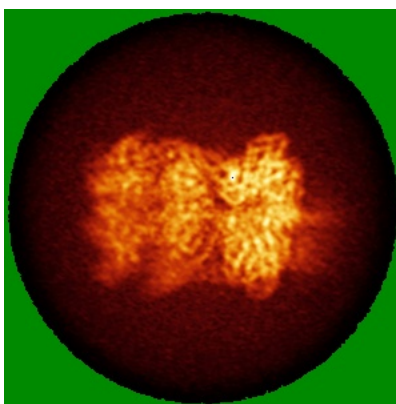
The images above show the largest variance slices of the map in three orthogonal directions.

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

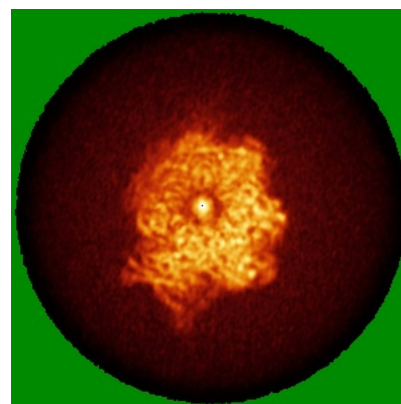
6.4.1 Primary map



X

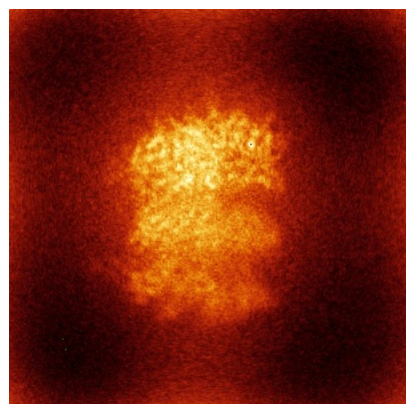


Y

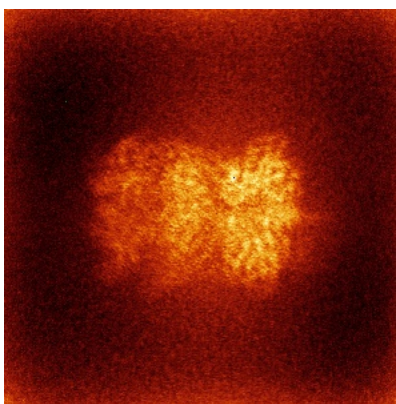


Z

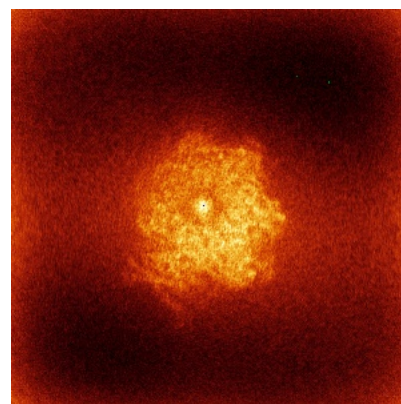
6.4.2 Raw map



X



Y



Z

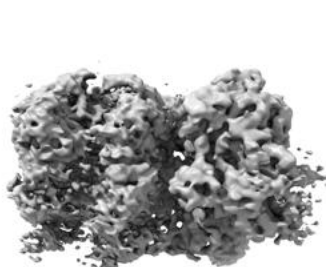
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

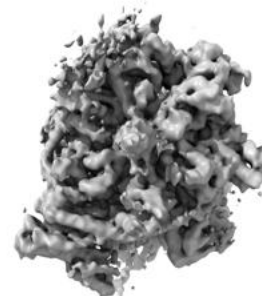
6.5.1 Primary map



X



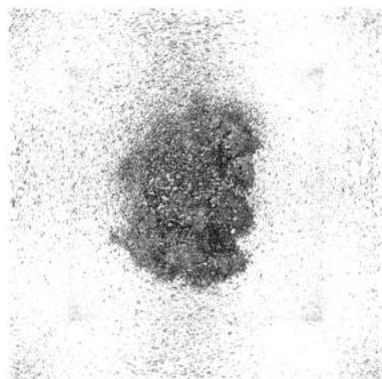
Y



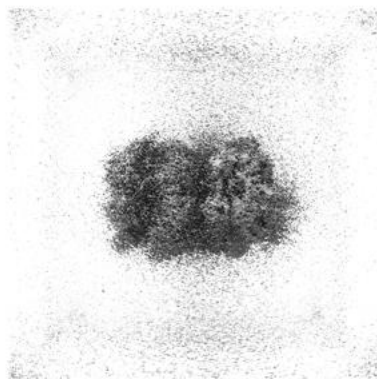
Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

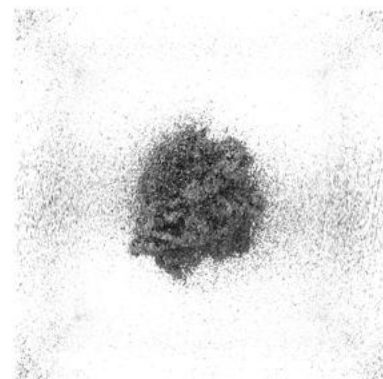
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

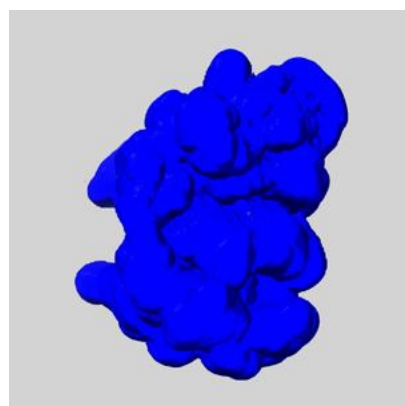
6.6 Mask visualisation [i](#)

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

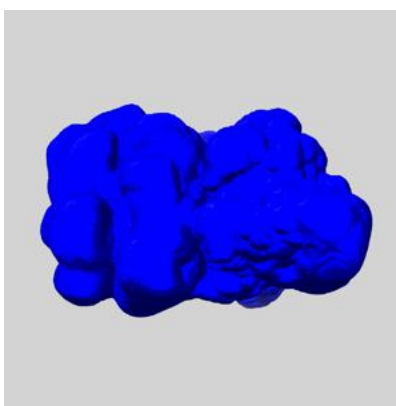
A mask typically either:

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

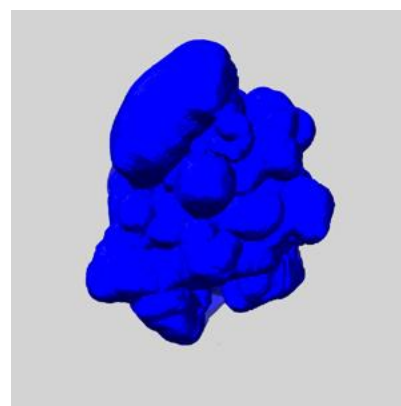
6.6.1 emd_19566_msk_1.map [i](#)



X



Y

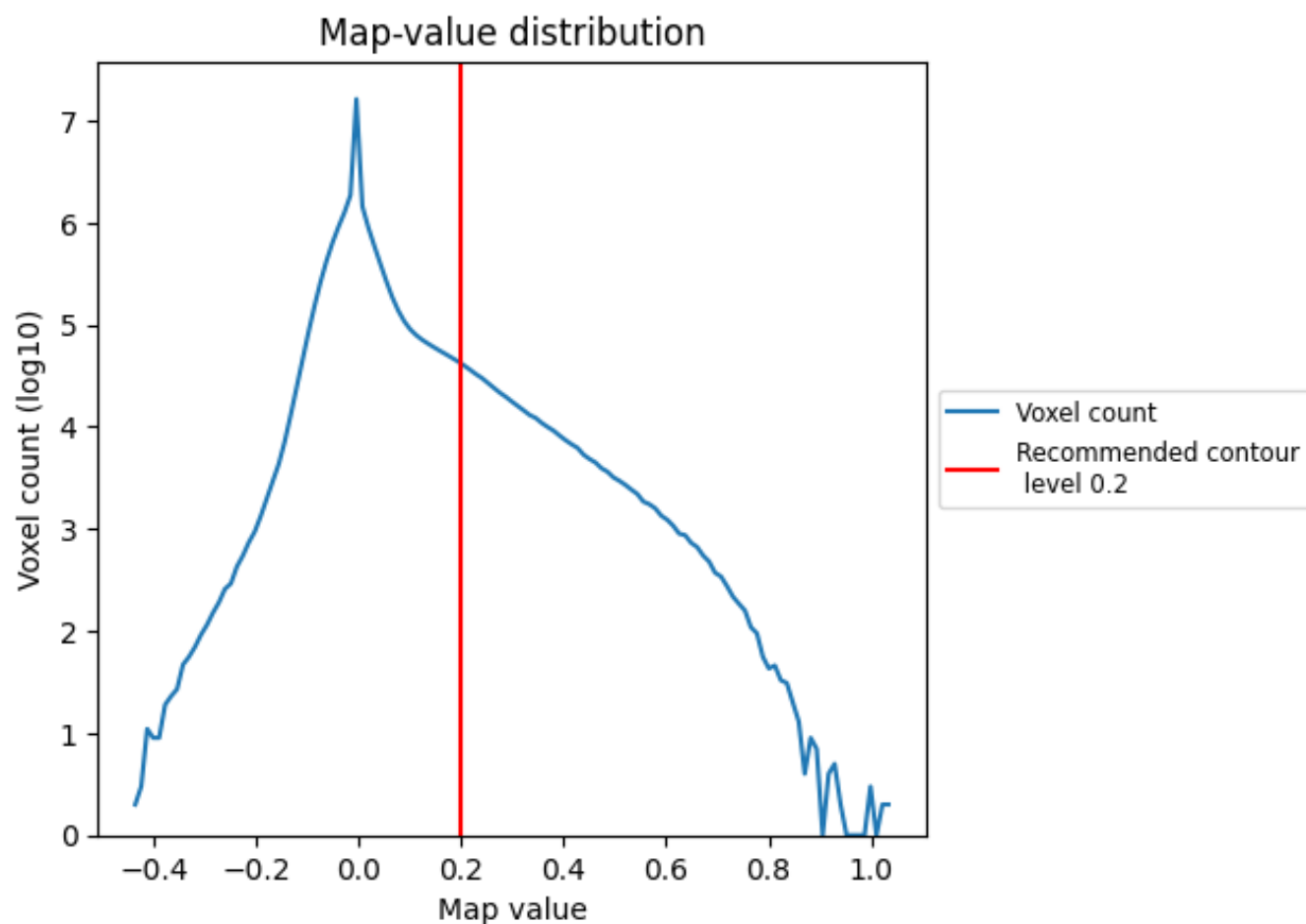


Z

7 Map analysis [i](#)

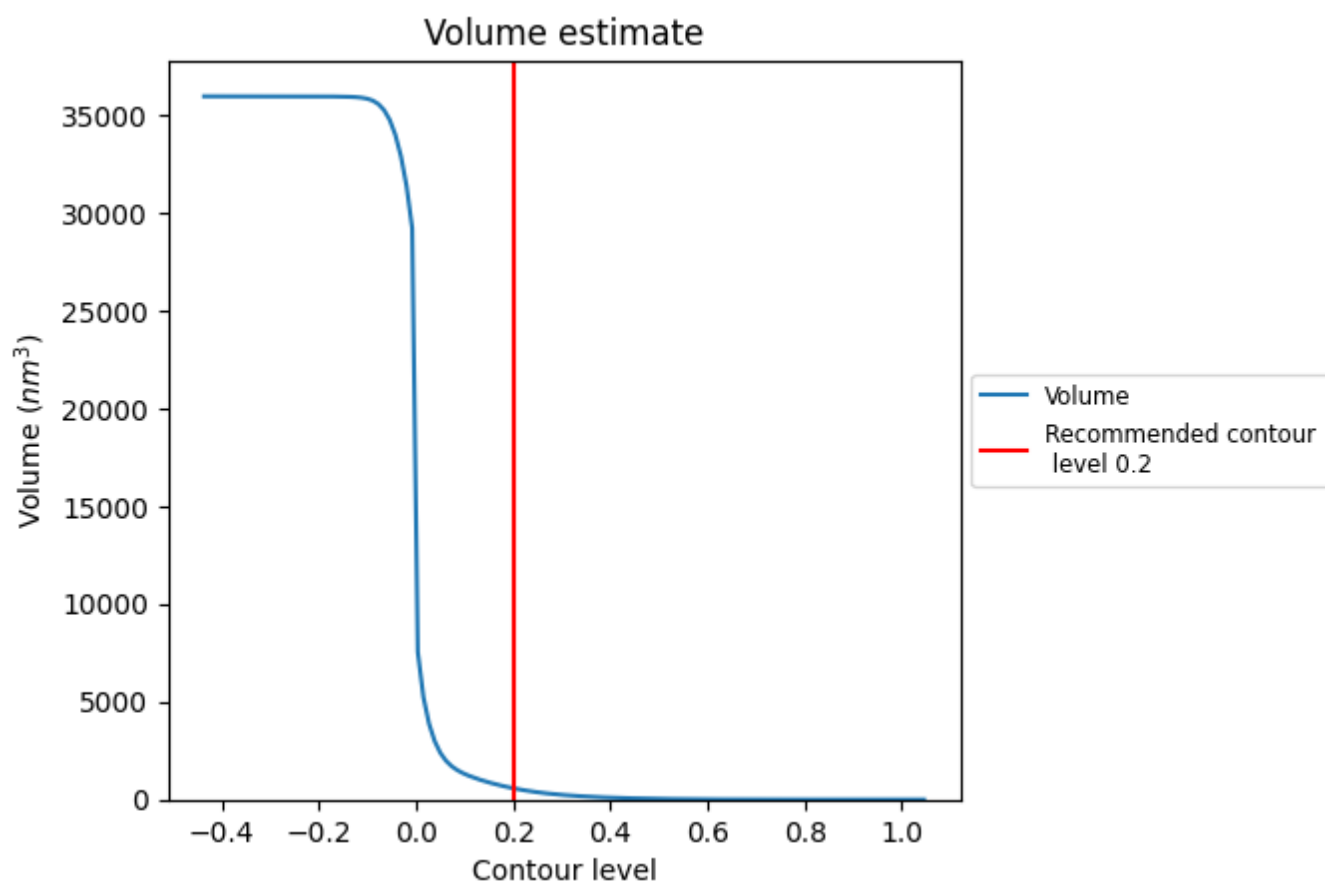
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

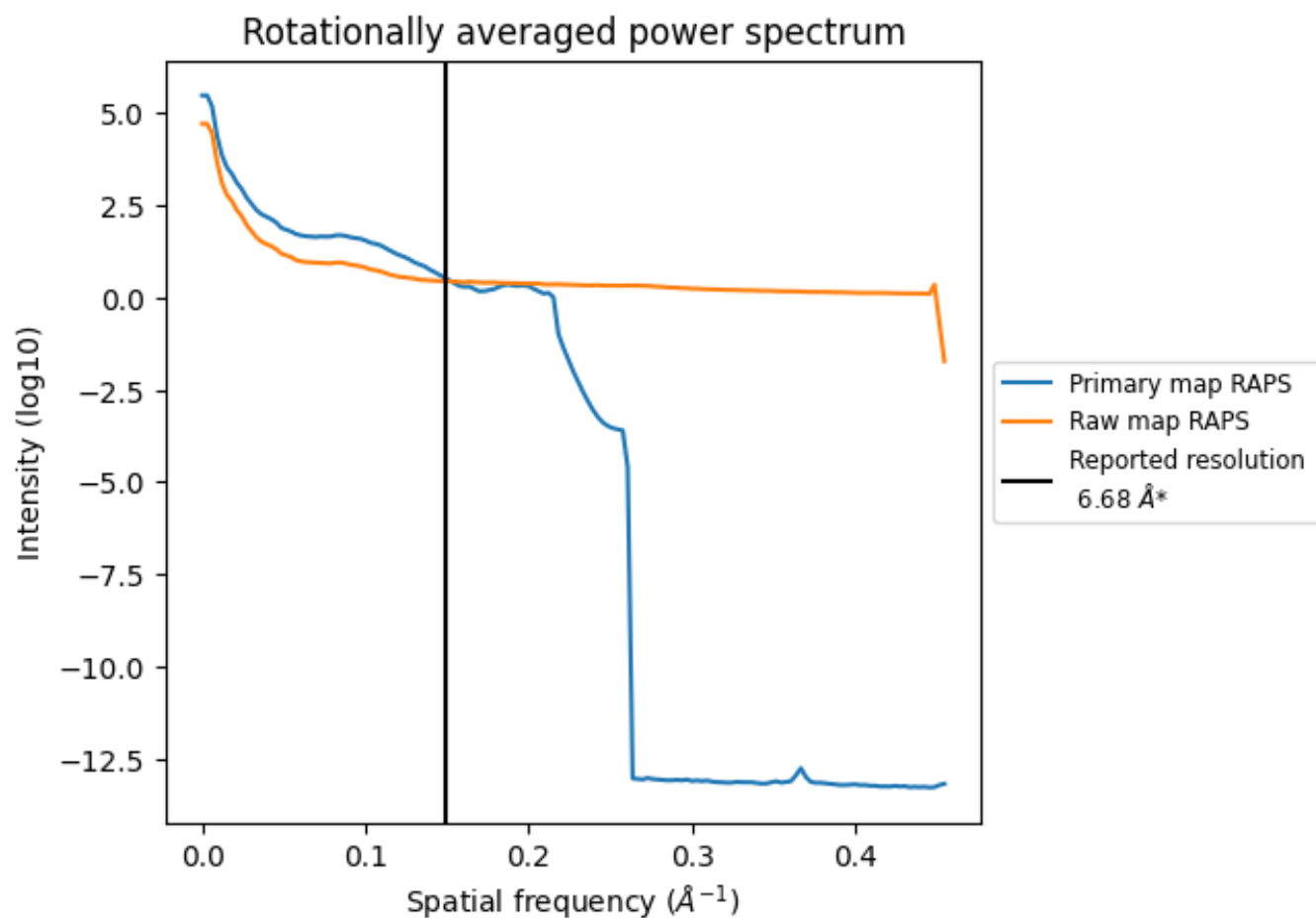
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 578 nm³; this corresponds to an approximate mass of 522 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 ⓘ

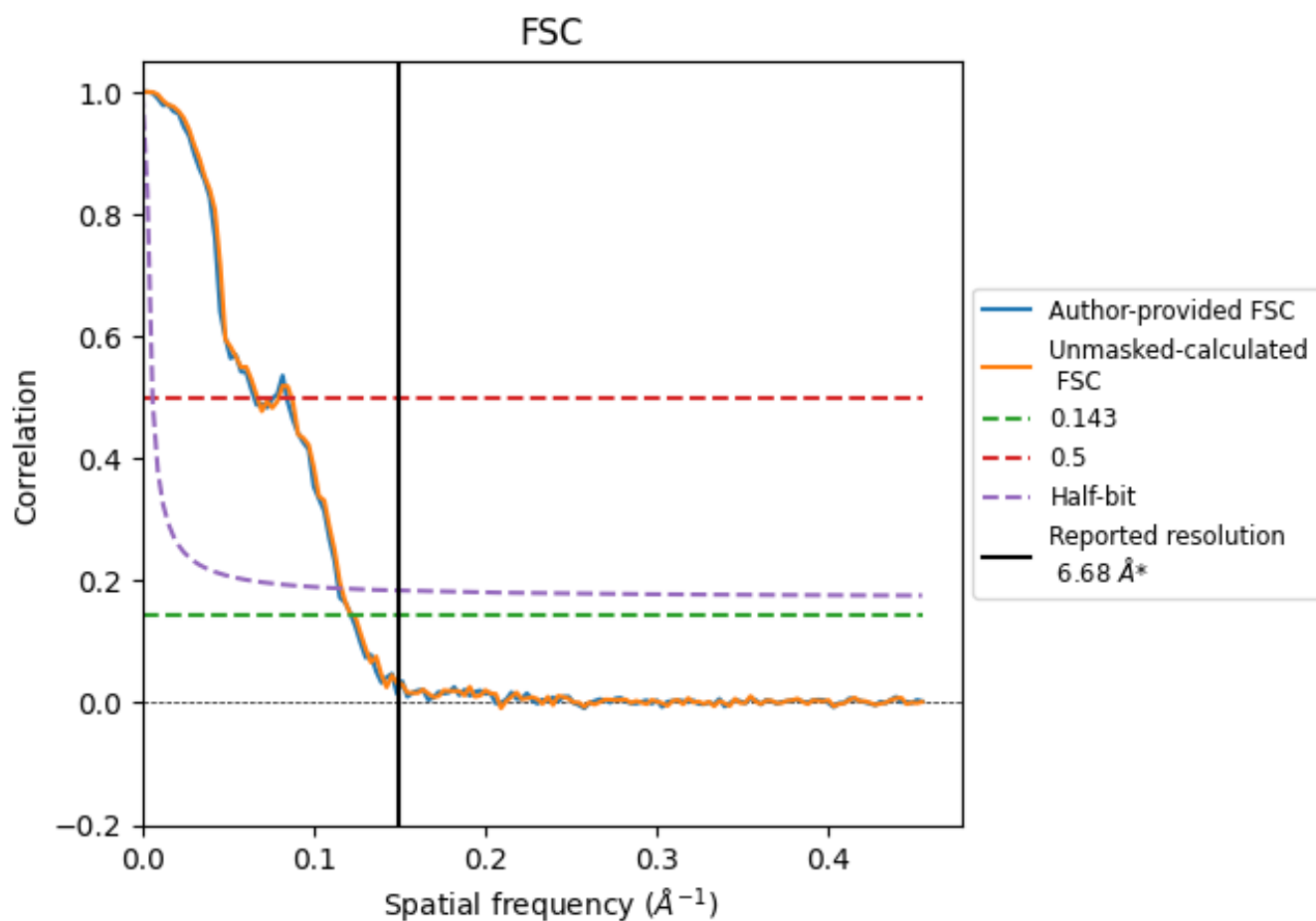


*Reported resolution corresponds to spatial frequency of 0.150 Å⁻¹

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 0.150 $\text{\AA}^{-1}$

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.68	-	-
Author-provided FSC curve	8.22	15.34	8.74
Unmasked-calculated*	8.14	14.95	8.61

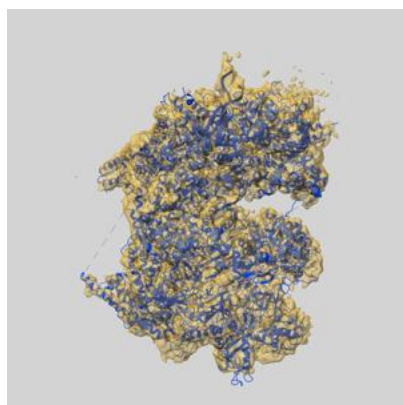
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 8.22 differs from the reported value 6.68 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.14 differs from the reported value 6.68 by more than 10 %

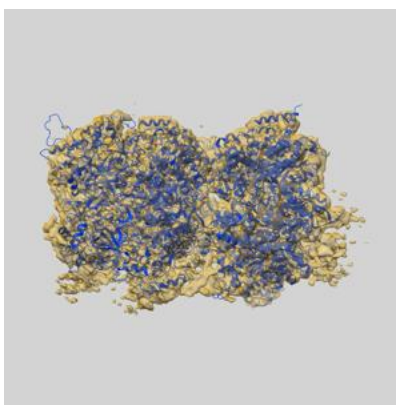
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19566 and PDB model 8RWV. Per-residue inclusion information can be found in section [3](#) on page [9](#).

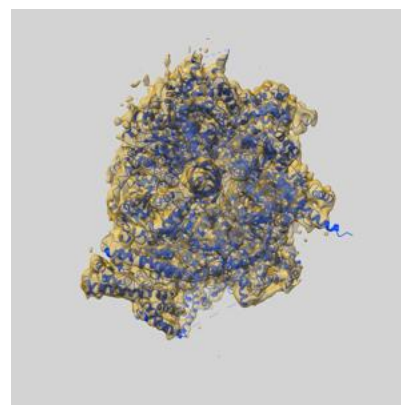
9.1 Map-model overlay [i](#)



X



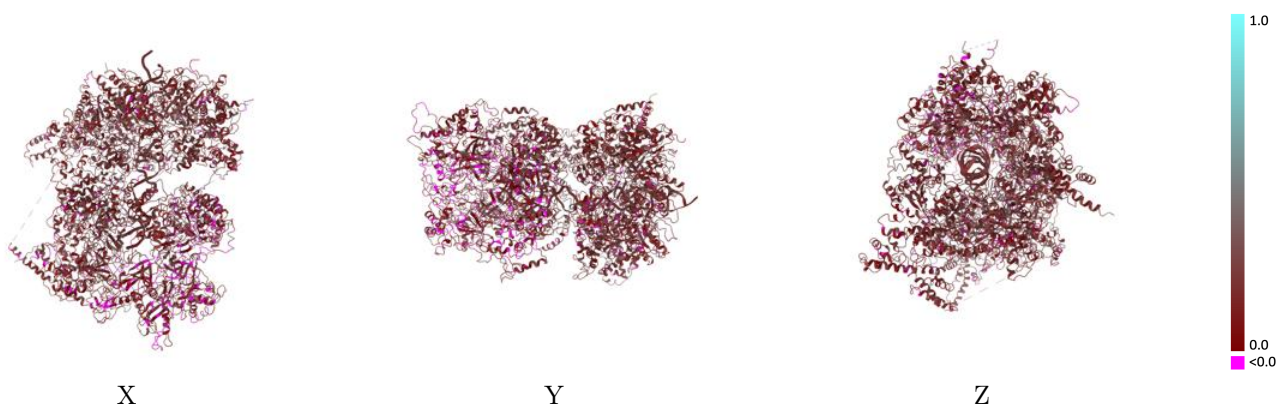
Y



Z

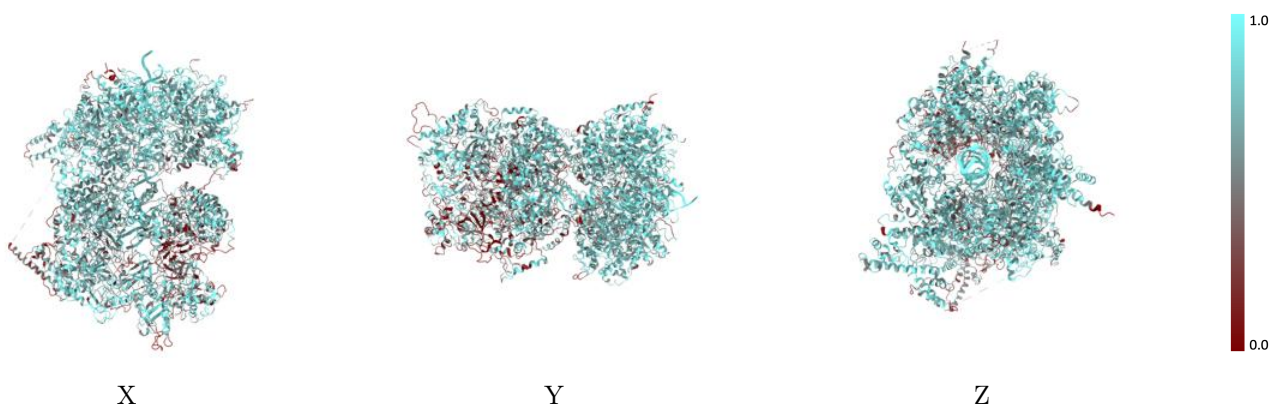
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



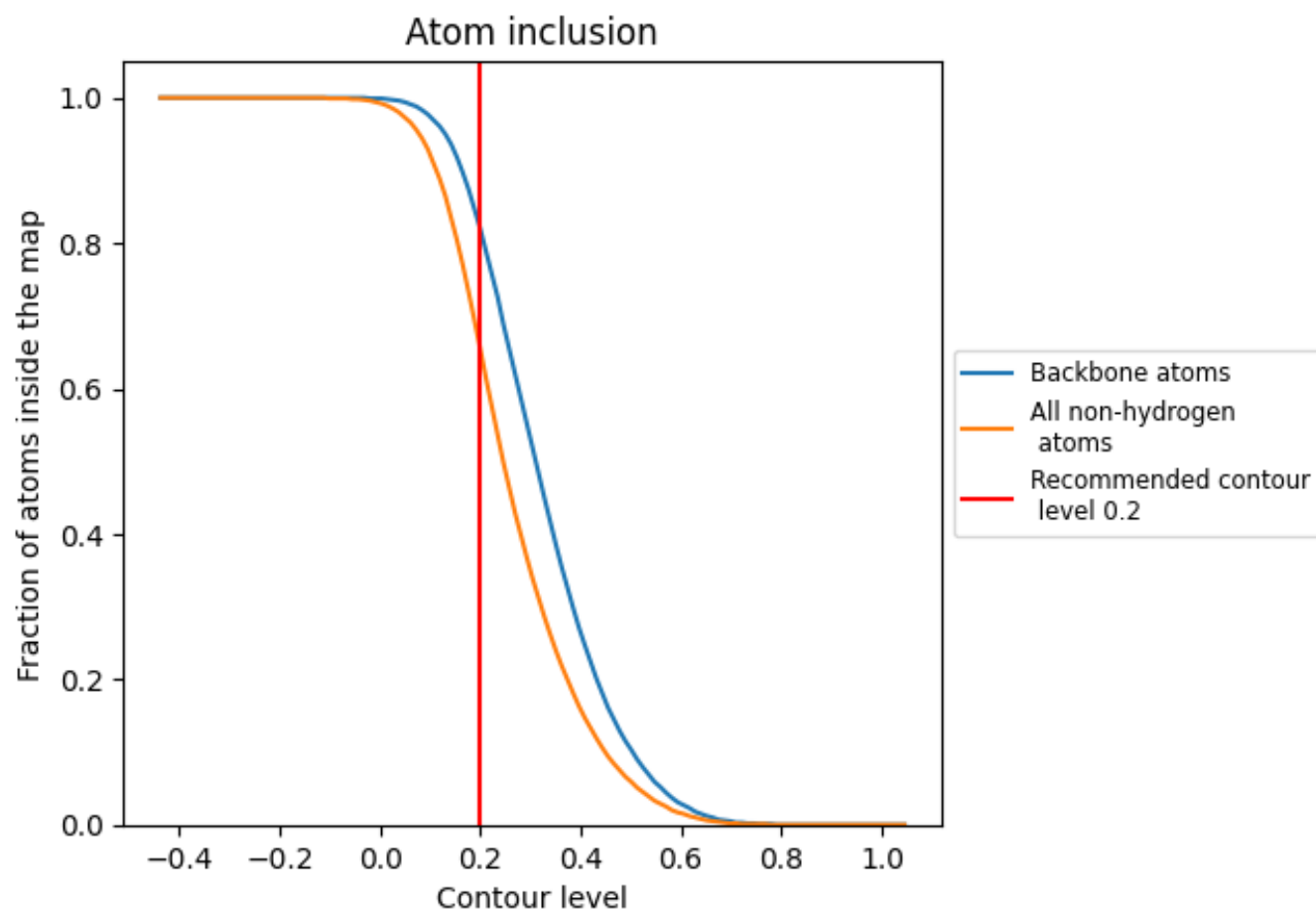
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 66% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6560	 0.1860
2	 0.6490	 0.1960
3	 0.4400	 0.1290
4	 0.6450	 0.1730
6	 0.7150	 0.2000
7	 0.5950	 0.1530
A	 0.7480	 0.2060
B	 0.6900	 0.1970
C	 0.6910	 0.1920
D	 0.7530	 0.2180
E	 0.7170	 0.2150
F	 0.6910	 0.1980
G	 0.5000	 0.1710
H	 0.9120	 0.2440
J	 0.9390	 0.2400

