



wwPDB EM Validation Summary Report ⓘ

Apr 10, 2026 – 12:46 PM UTC

PDB ID : 8YJB / pdb_00008yjb
EMDB ID : EMD-39338
Title : Cryo-EM structure of the human DSS1-INTAC complex
Authors : Zheng, H.; Xu, Y.; Cheng, J.
Deposited on : 2024-03-01
Resolution : 4.10 Å(reported)
Based on initial model : 7YCX

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

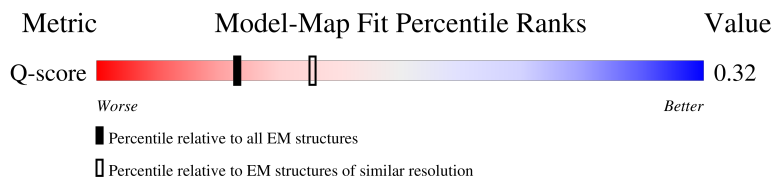
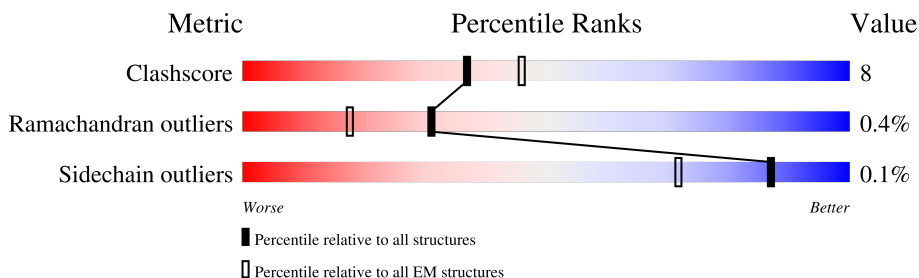
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

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

Mol	Chain	Length	Quality of chain
1	0	70	
2	I	658	
3	K	600	
4	B	1204	

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Mol	Chain	Length	Quality of chain
5	D	963	
6	G	962	
7	P	589	
8	Q	309	
9	A	2190	
10	E	1019	
11	F	887	
12	H	995	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 62555 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 26S proteasome complex subunit DSS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	32	Total	C	N	O	S	0	0
			275	169	47	58	1		

- Molecule 2 is a protein called Integrator complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	633	Total	C	N	O	S	0	0
			4985	3210	815	926	34		

- Molecule 3 is a protein called Integrator complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	590	Total	C	N	O	S	0	0
			4646	2964	806	841	35		

- Molecule 4 is a protein called Integrator complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	1061	Total	C	N	O	S	0	0
			8328	5322	1412	1530	64		

- Molecule 5 is a protein called Integrator complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	817	Total	C	N	O	S	0	0
			6108	3872	1065	1140	31		

- Molecule 6 is a protein called Integrator complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	901	Total	C	N	O	S	0	0
			6873	4348	1202	1282	41		

- Molecule 7 is a protein called Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	P	581	Total	C	N	O	S	0	0
			4527	2877	763	860	27		

- Molecule 8 is a protein called Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	293	Total	C	N	O	S	0	0
			2366	1497	405	449	15		

- Molecule 9 is a protein called Integrator complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1091	Total	C	N	O	S	0	0
			7530	4708	1373	1410	39		

- Molecule 10 is a protein called Integrator complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	798	Total	C	N	O	S	0	0
			5244	3284	988	958	14		

- Molecule 11 is a protein called Integrator complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	551	Total	C	N	O	S	0	0
			4229	2702	723	782	22		

- Molecule 12 is a protein called Integrator complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	937	Total	C	N	O	S	0	0
			7440	4761	1274	1361	44		

- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	K	2	Total	Zn	0
			2	2	

- Molecule 14 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

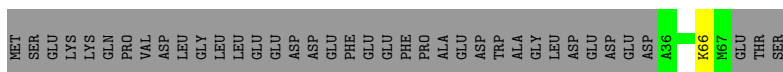
Mol	Chain	Residues	Atoms		AltConf
14	Q	2	Total 2	Mn 2	0

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.

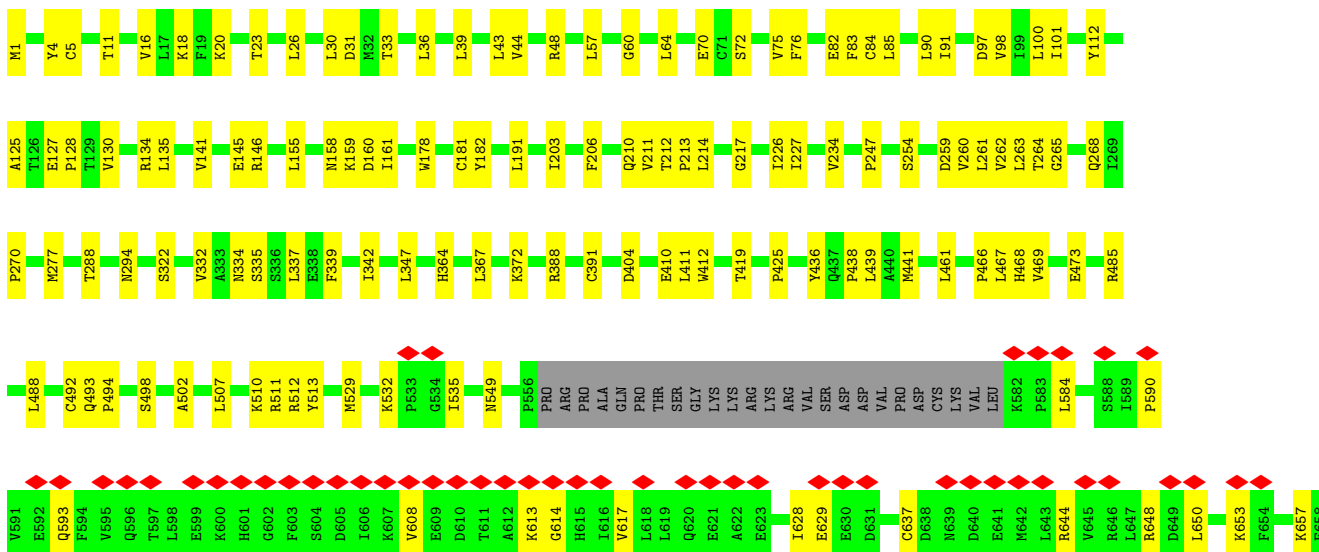
- Molecule 1: 26S proteasome complex subunit DSS1

Chain 0: 



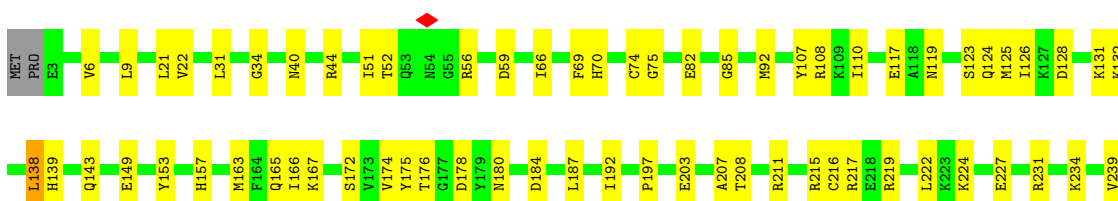
- Molecule 2: Integrator complex subunit 9

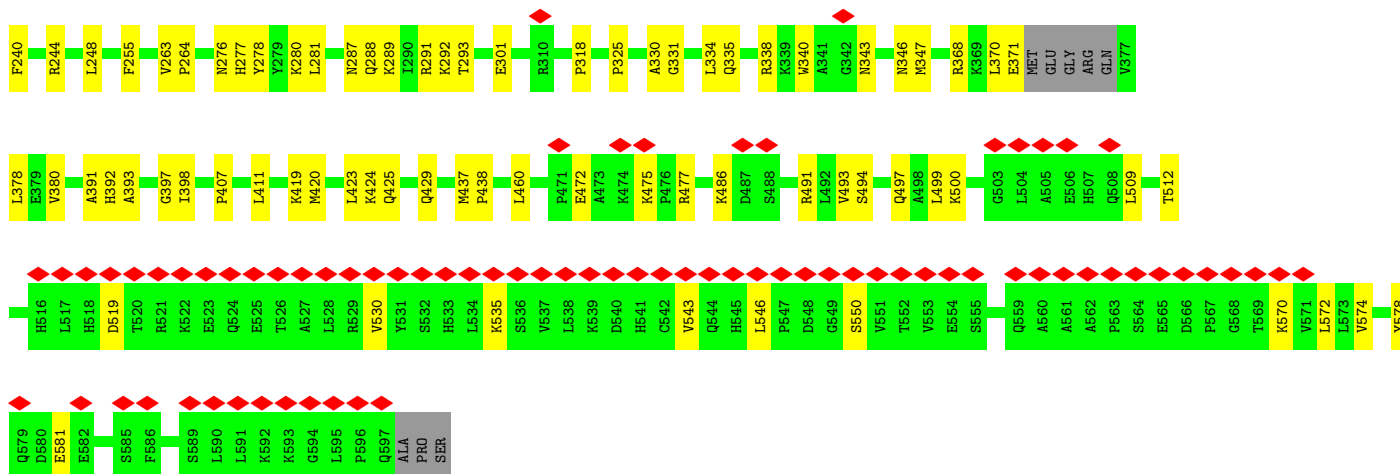
Chain I: 



- Molecule 3: Integrator complex subunit 11

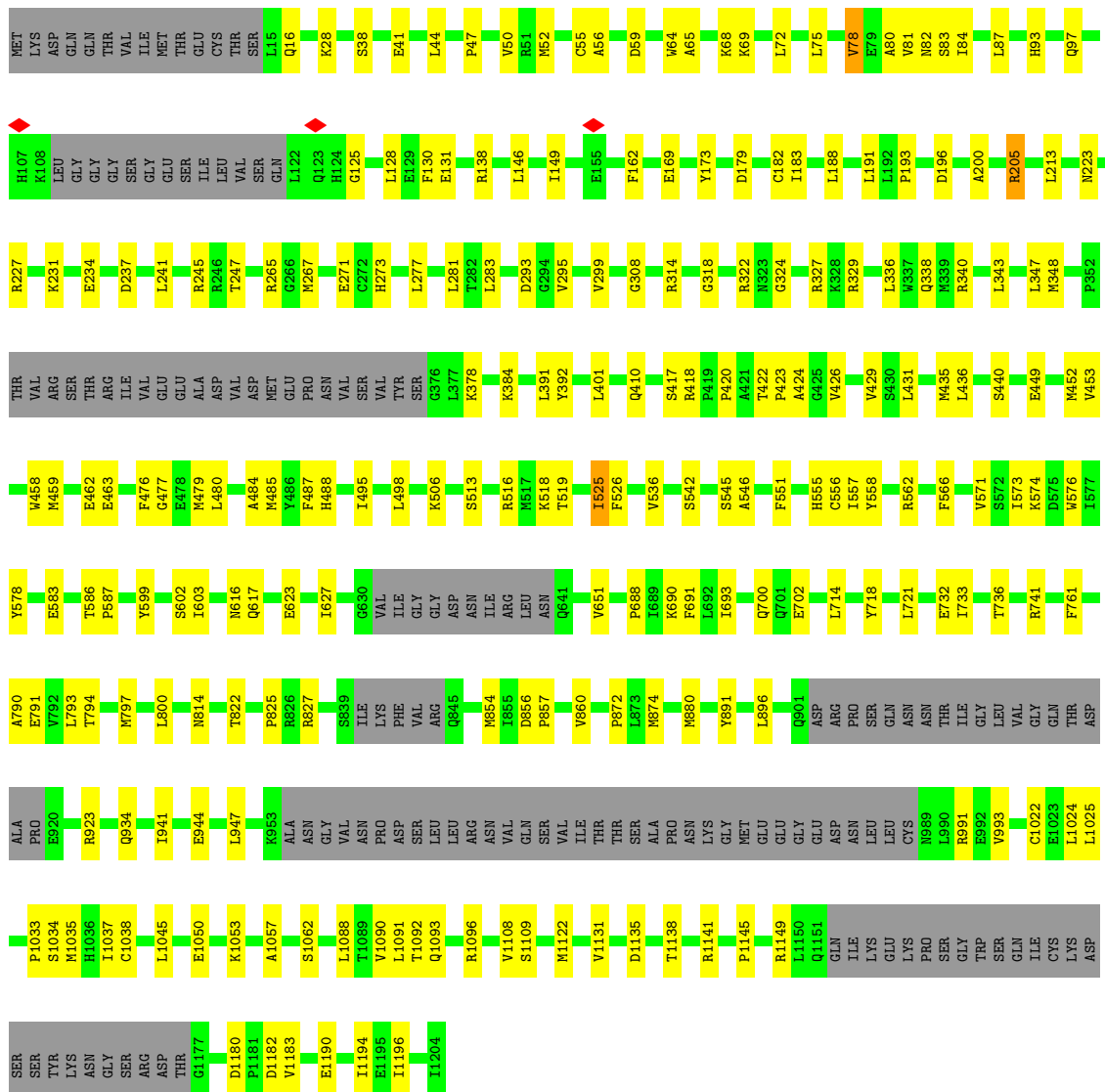
Chain K: 



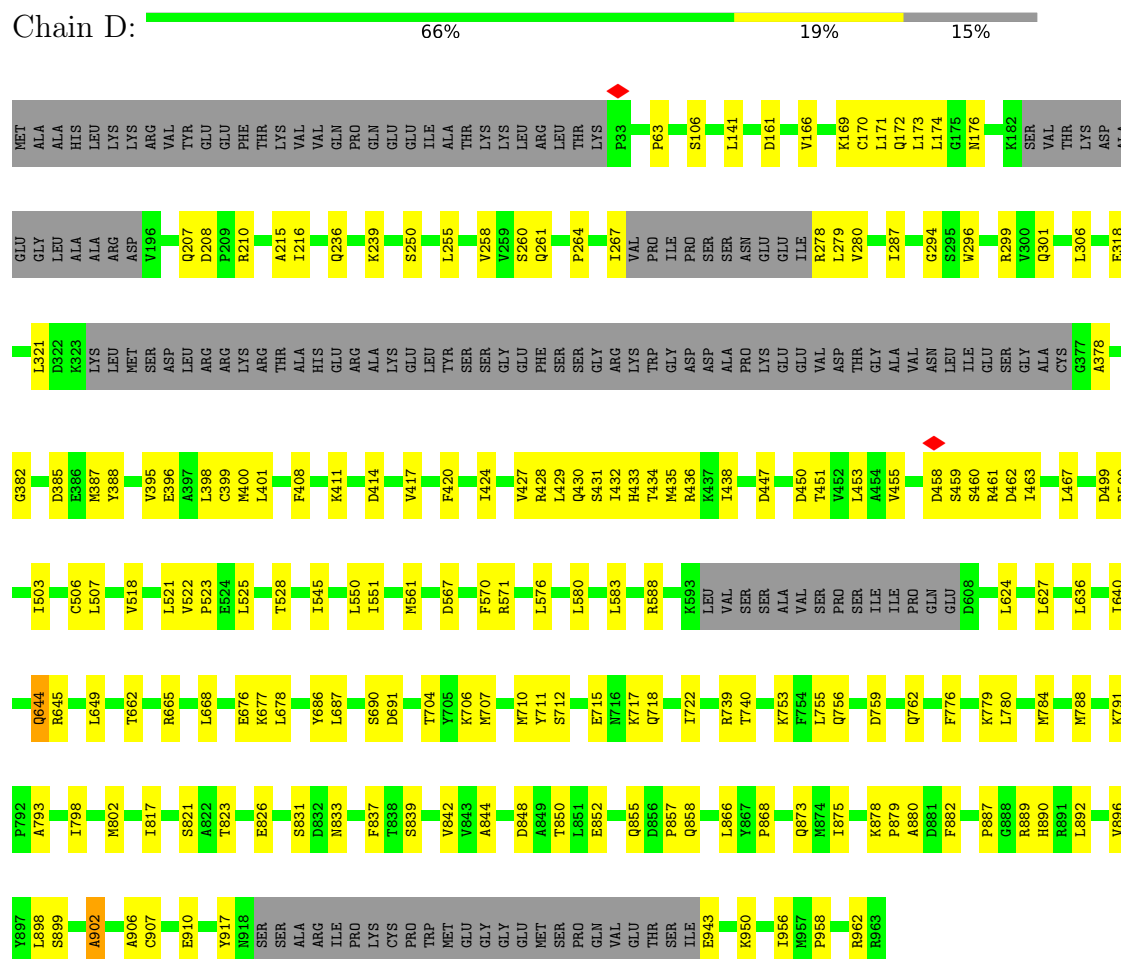


• Molecule 4: Integrator complex subunit 2

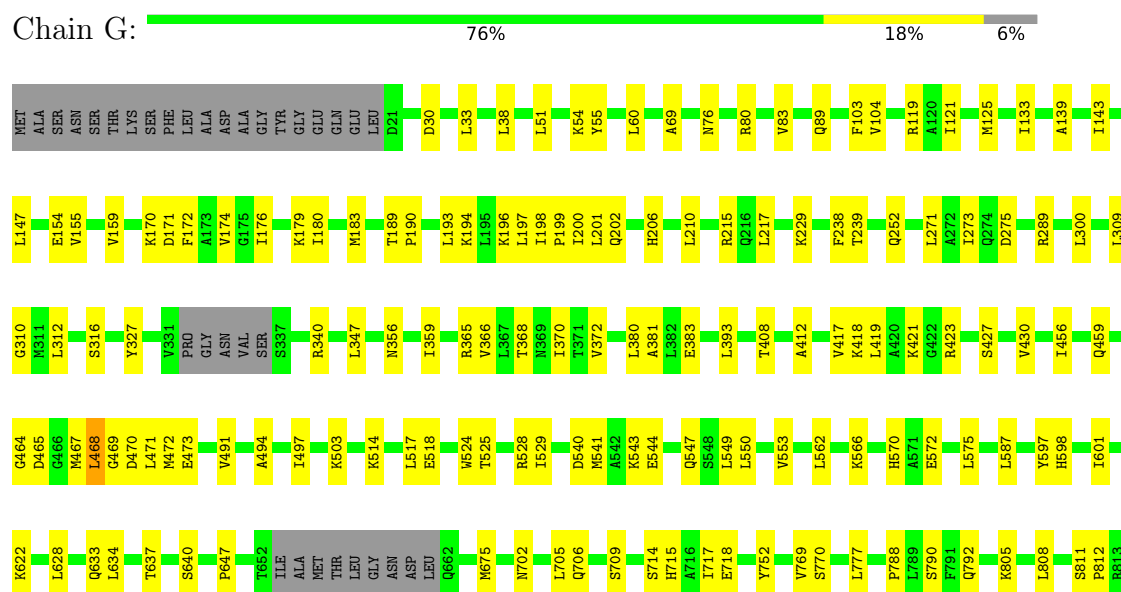
Chain B: 70% 18% 12%

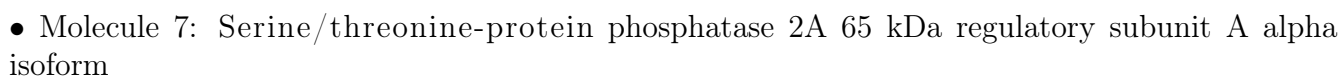


- Molecule 5: Integrator complex subunit 4



- Molecule 6: Integrator complex subunit 7



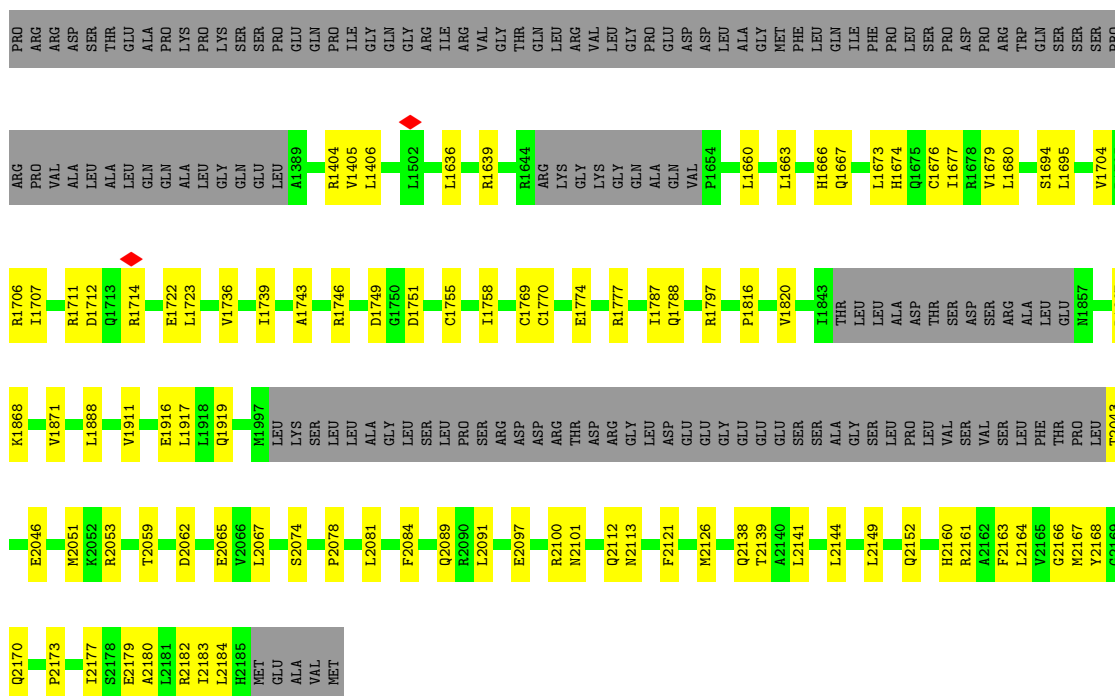


- Molecule 8: Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform

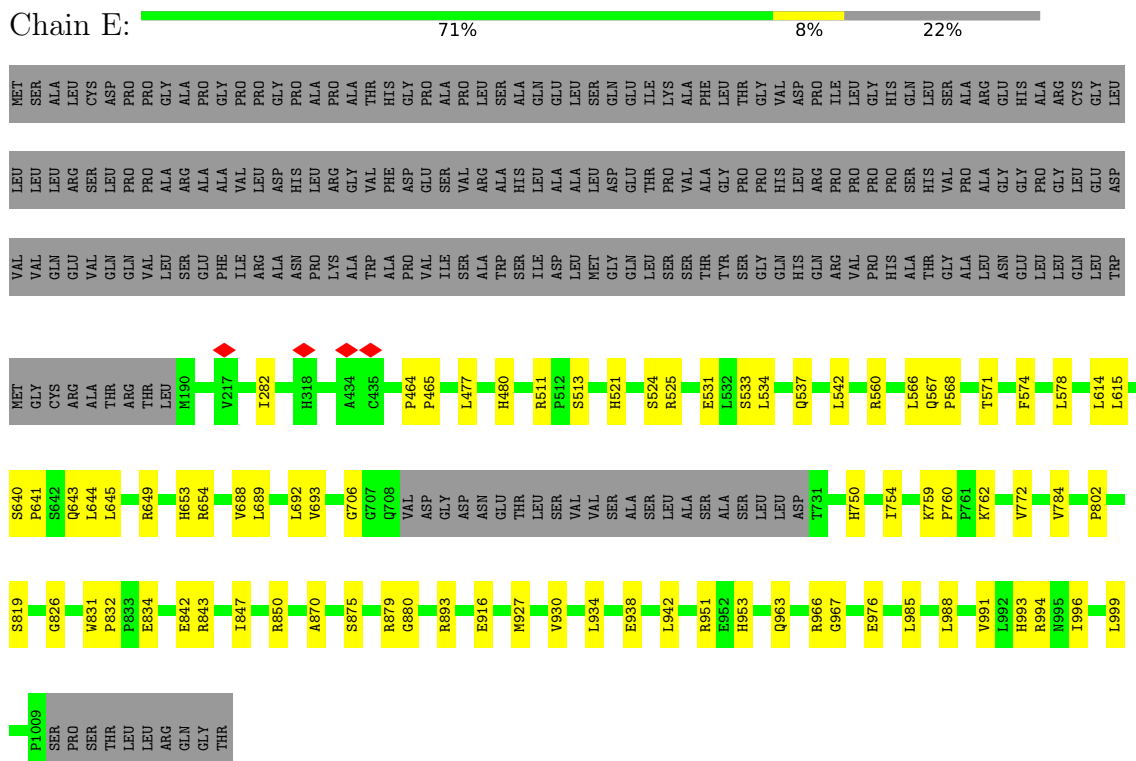
- Molecule 9: Integrator complex subunit 1

ILE	VAL	ALA	MET
GLU	LEU	ALA	ASN
ALA	LEU	ALA	ARG
LEU	ASP	ALA	ALA
CYS	GLU	LEU	LYS
SER	ILE	SER	PRO
LEU	GLU	SER	THR
LEU	ALA	ALA	THR
ARG	ALA	SER	VAL
ARG	GLU	ALA	ARG
ASP	LEU	ALA	ARG
ALA	GLU	THR	PRO
SER	GLY	GLY	SER
ILE	ASN	LEU	ALA
PHE	ASP	THR	ALA
LYS	ASP	ARG	LYS
ALA	ILE	PRO	PRO
LYS	GLU	LYS	SER
GLY	GLY	LEU	GLY
ASN	VAL	SER	HIS
LEU	LEU	SER	PRO
LEU	CYS	THR	PRO
VAL	GLY	PRO	PRO
SER	ALA	PRO	GLY
VAL	VAL	LEU	ASP
LEU	LYS	SER	PHE
LEU	GLN	ALA	ILE
CYS	ALA	LEU	ALA
ASN	LYS	GLY	LEU
LEU	VAL	ARG	GLY
LEU	THR	LEU	SER
MET	ARG	ALA	LYS
ALA	ALA	GLU	GLY
ALA	LYS	ALA	GLN
TYR	PRO	ALA	ALA
GLU	ASP	VAL	ASN
GLU	SER	ALA	GLU
ASP	THR	GLU	SER
GLU	LEU	LYS	LYS
ASN	TYR	ARG	THR
TRP	LEU	ALA	ALA
PRO	SER	ILE	SER
GLU	LEU	SER	THR
ILE	MET	PRO	LEU
PHE	TYR	SER	LEU
VAL	LEU	ILE	LYS
LYS	ALA	LYS	PRO
VAL	LYS	GLU	ALA
TYR	ILE	PRO	PRO
ILE	LYS	SER	GLY
GLU	PRO	VAL	SER
GLU	ASP	VAL	SER
ARG	ASN	VAL	GLU
GLY	ILE	PRO	GLY
ILE	VAL	ILE	ARG
TRP	VAL	THR	LYS
		GLY	LEU
		PRO	ARG
		THR	ASP



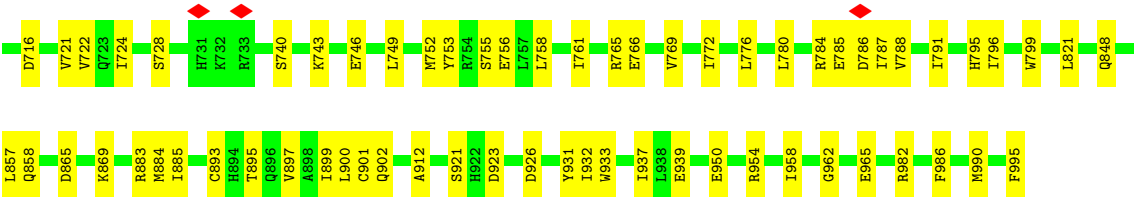


- Molecule 10: Integrator complex subunit 5



- Molecule 11: Integrator complex subunit 6





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43790	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	443.09998, 443.09998, 443.09998	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.19	0/282	0.51	0/381
2	I	0.24	0/5110	0.63	1/6959 (0.0%)
3	K	0.25	0/4747	0.66	0/6412
4	B	0.24	0/8474	0.59	0/11498
5	D	0.23	0/6217	0.61	0/8454
6	G	0.24	0/6981	0.64	0/9452
7	P	0.24	0/4601	0.64	2/6246 (0.0%)
8	Q	0.24	0/2423	0.58	1/3285 (0.0%)
9	A	0.17	0/7635	0.46	0/10415
10	E	0.20	0/5344	0.52	0/7312
11	F	0.22	0/4337	0.55	1/5907 (0.0%)
12	H	0.22	0/7583	0.59	2/10280 (0.0%)
All	All	0.23	0/63734	0.59	7/86601 (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
2	I	0	1
4	B	0	4
6	G	0	1
8	Q	0	1
10	E	0	1
12	H	0	1
All	All	0	9

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	Q	283	LYS	CA-CB-CG	6.95	128.00	114.10
12	H	44	ASP	N-CA-C	-5.69	101.71	110.58
2	I	277	MET	CB-CG-SD	-5.57	96.01	112.70
7	P	426	TYR	CA-C-N	5.24	126.64	120.09
7	P	426	TYR	C-N-CA	5.24	126.64	120.09

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B	169	GLU	Peptide
4	B	205	ARG	Peptide
4	B	573	ILE	Peptide
4	B	586	THR	Peptide
2	I	493	GLN	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	0	275	0	231	1	0
2	I	4985	0	5012	84	0
3	K	4646	0	4662	90	0
4	B	8328	0	8566	133	0
5	D	6108	0	5810	123	0
6	G	6873	0	6877	105	0
7	P	4527	0	4633	84	0
8	Q	2366	0	2269	41	0
9	A	7530	0	6625	95	0
10	E	5244	0	4501	47	0
11	F	4229	0	4121	66	0
12	H	7440	0	7530	124	0
13	K	2	0	0	0	0
14	Q	2	0	0	0	0
All	All	62555	0	60837	936	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 8.

The worst 5 of 936 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)
7:P:188:LYS:O	7:P:192:PHE:HB2	1.65	0.95
3:K:82:GLU:HG2	3:K:125:MET:HB2	1.71	0.72
3:K:108:ARG:HH22	3:K:123:SER:HB3	1.53	0.72
8:Q:196:CYS:O	8:Q:200:TRP:HB2	1.90	0.72
12:H:249:GLN:O	12:H:252:VAL:HB	1.90	0.71

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	0	30/70 (43%)	28 (93%)	2 (7%)	0	100	100
2	I	629/658 (96%)	585 (93%)	43 (7%)	1 (0%)	43	76
3	K	586/600 (98%)	528 (90%)	57 (10%)	1 (0%)	43	76
4	B	1045/1204 (87%)	977 (94%)	64 (6%)	4 (0%)	30	65
5	D	805/963 (84%)	749 (93%)	51 (6%)	5 (1%)	21	58
6	G	893/962 (93%)	819 (92%)	65 (7%)	9 (1%)	12	46
7	P	579/589 (98%)	564 (97%)	14 (2%)	1 (0%)	43	76
8	Q	291/309 (94%)	274 (94%)	17 (6%)	0	100	100
9	A	1073/2190 (49%)	1010 (94%)	60 (6%)	3 (0%)	36	70
10	E	794/1019 (78%)	740 (93%)	47 (6%)	7 (1%)	14	49
11	F	547/887 (62%)	523 (96%)	23 (4%)	1 (0%)	43	76
12	H	933/995 (94%)	880 (94%)	53 (6%)	0	100	100
All	All	8205/10446 (78%)	7677 (94%)	496 (6%)	32 (0%)	31	65

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	78	VAL
5	D	63	PRO
5	D	106	SER
5	D	561	MET
6	G	647	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	0	29/63 (46%)	29 (100%)	0	100	100
2	I	575/600 (96%)	575 (100%)	0	100	100
3	K	505/520 (97%)	505 (100%)	0	100	100
4	B	946/1072 (88%)	945 (100%)	1 (0%)	88	89
5	D	607/845 (72%)	605 (100%)	2 (0%)	86	85
6	G	742/840 (88%)	741 (100%)	1 (0%)	88	89
7	P	508/512 (99%)	508 (100%)	0	100	100
8	Q	259/274 (94%)	259 (100%)	0	100	100
9	A	636/1907 (33%)	636 (100%)	0	100	100
10	E	395/812 (49%)	395 (100%)	0	100	100
11	F	454/796 (57%)	454 (100%)	0	100	100
12	H	822/896 (92%)	822 (100%)	0	100	100
All	All	6478/9137 (71%)	6474 (100%)	4 (0%)	87	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	488	HIS
5	D	261	GLN
5	D	644	GLN
6	G	933	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76

such sidechains are listed below:

Mol	Chain	Res	Type
10	E	537	GLN
12	H	186	ASN
10	E	690	GLN
10	E	953	HIS
12	H	782	ASN

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

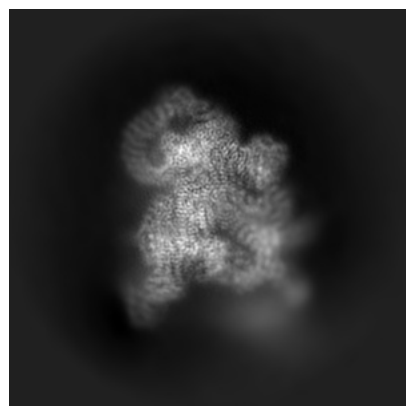
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39338. These allow visual inspection of the internal detail of the map and identification of artifacts.

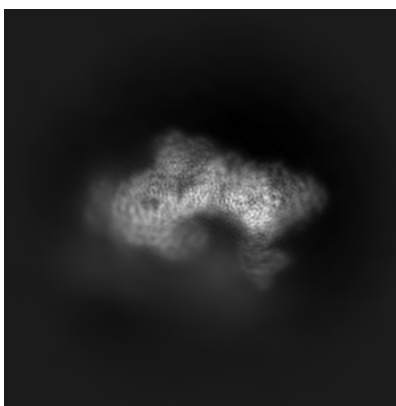
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

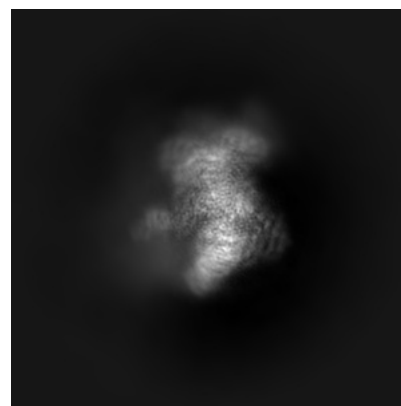
6.1.1 Primary map



X

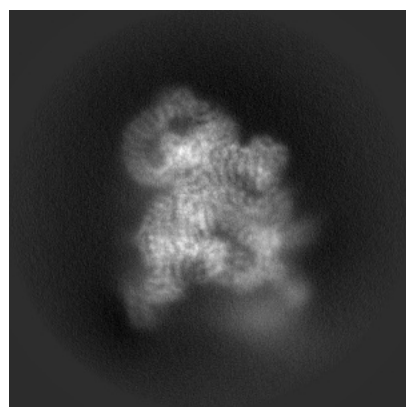


Y

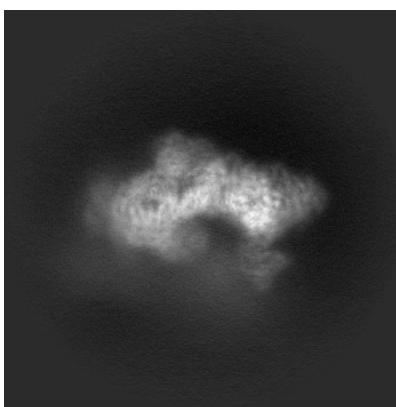


Z

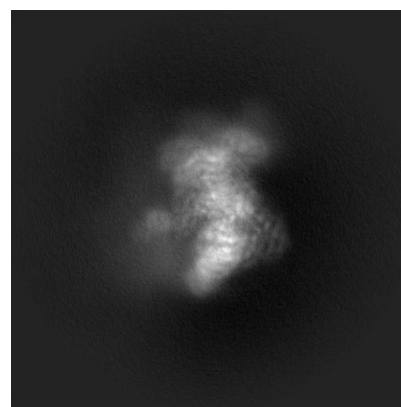
6.1.2 Raw map



X



Y

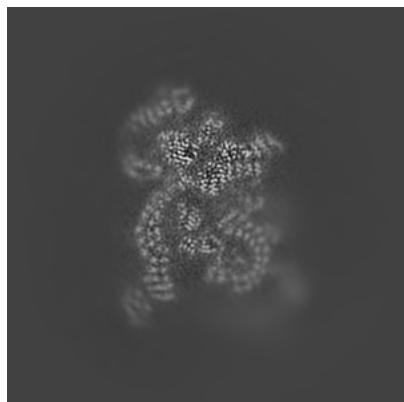


Z

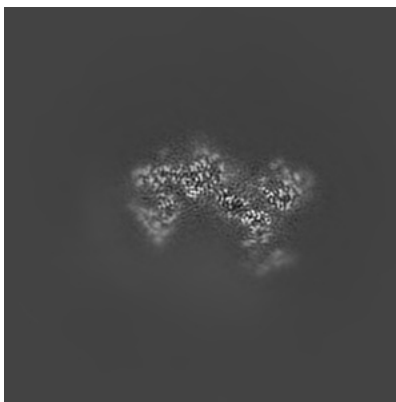
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

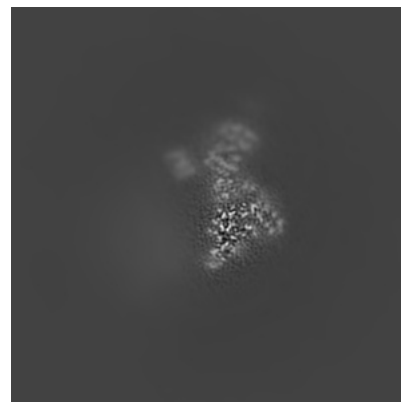
6.2.1 Primary map



X Index: 210

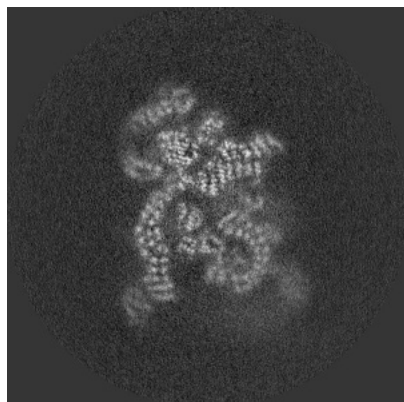


Y Index: 210

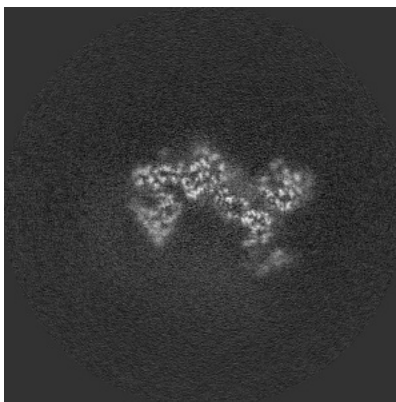


Z Index: 210

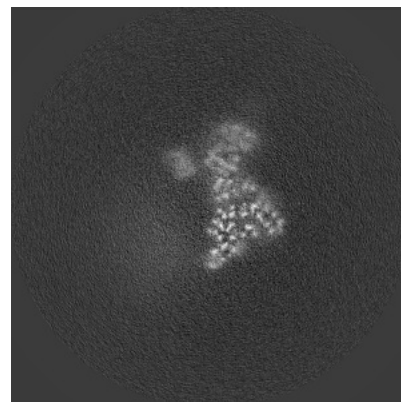
6.2.2 Raw map



X Index: 210



Y Index: 210

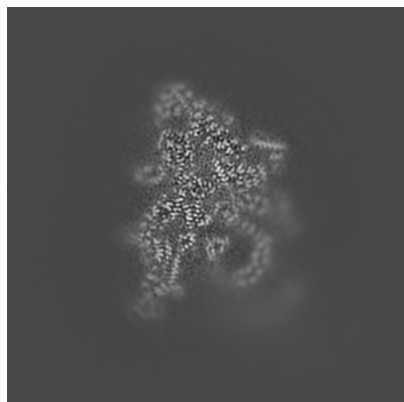


Z Index: 210

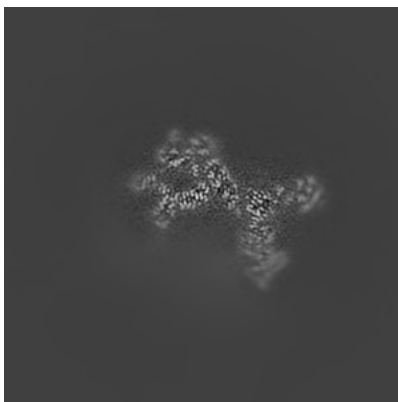
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

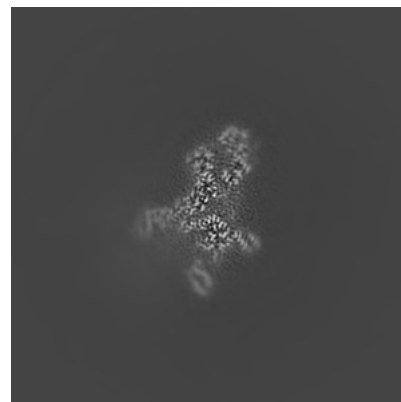
6.3.1 Primary map



X Index: 222

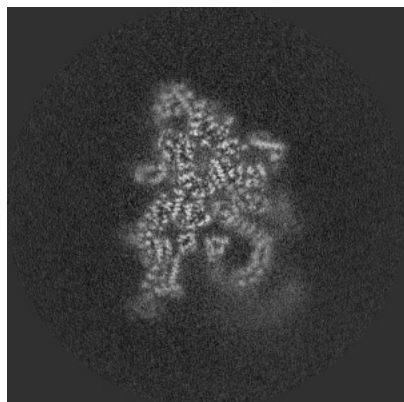


Y Index: 191

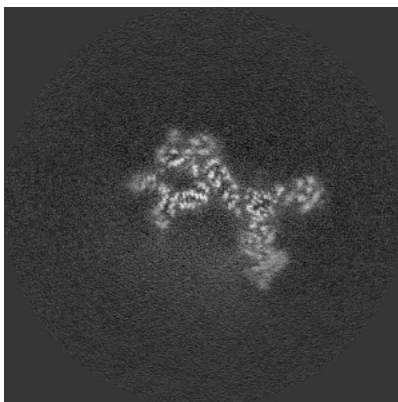


Z Index: 263

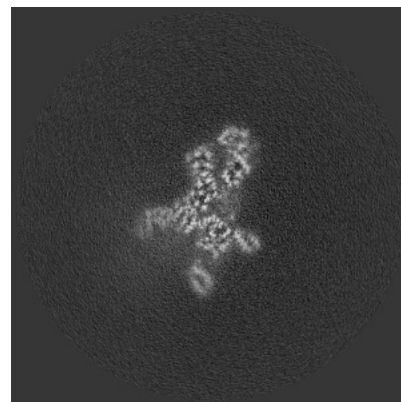
6.3.2 Raw map



X Index: 221



Y Index: 191



Z Index: 262

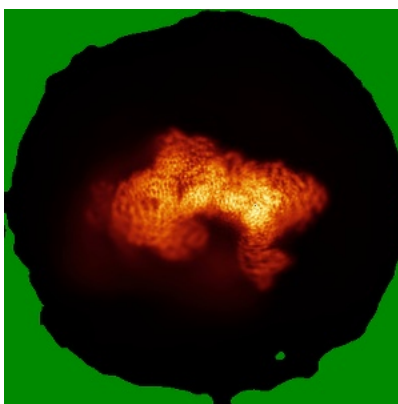
The images above show the largest variance slices of the map in three orthogonal directions.

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

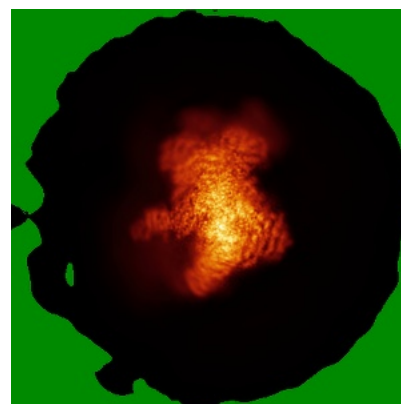
6.4.1 Primary map



X

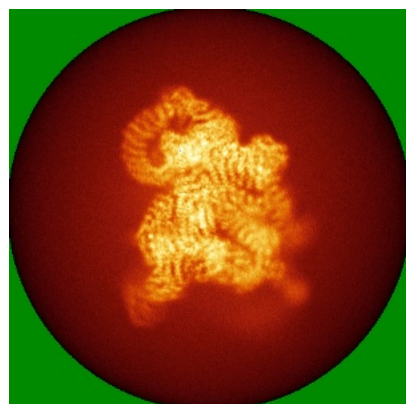


Y

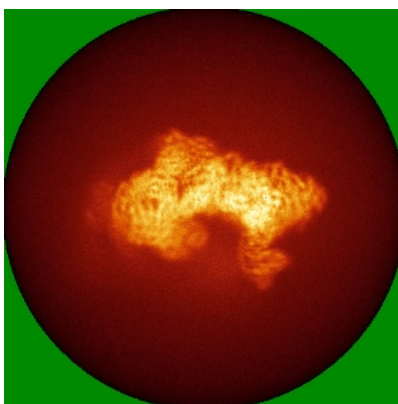


Z

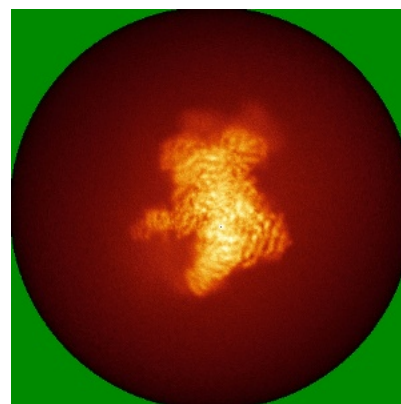
6.4.2 Raw map



X



Y

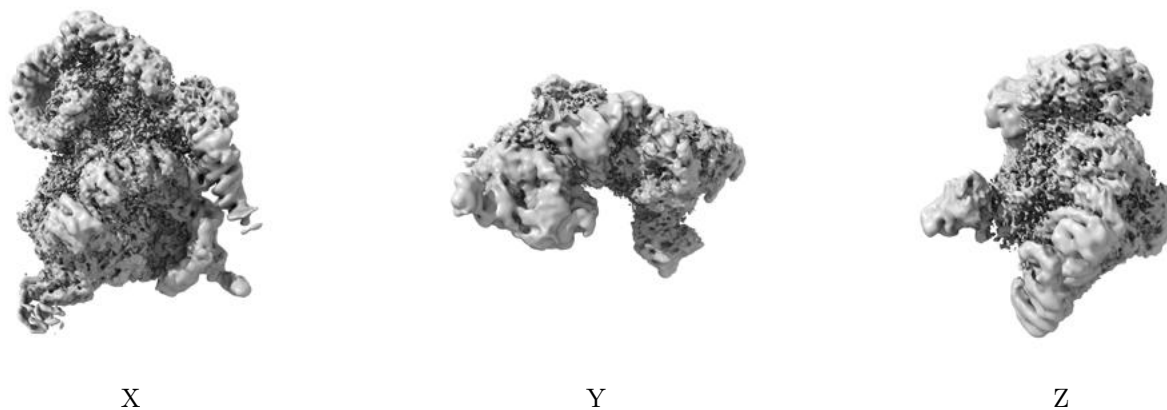


Z

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

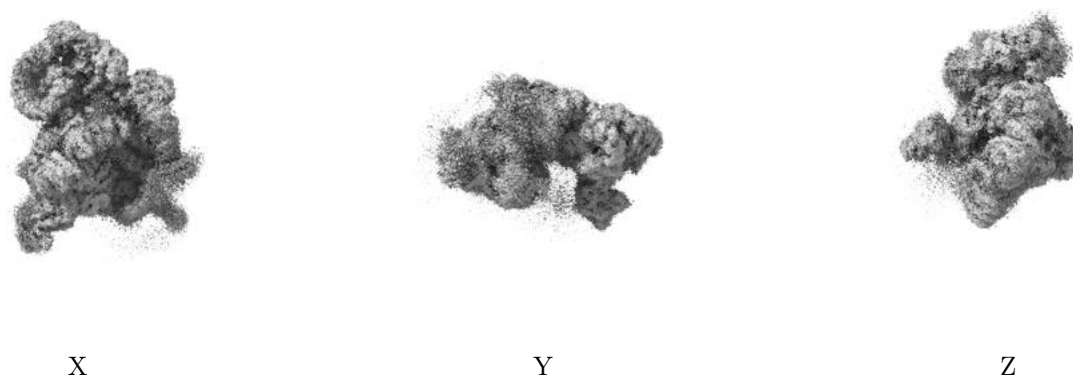
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

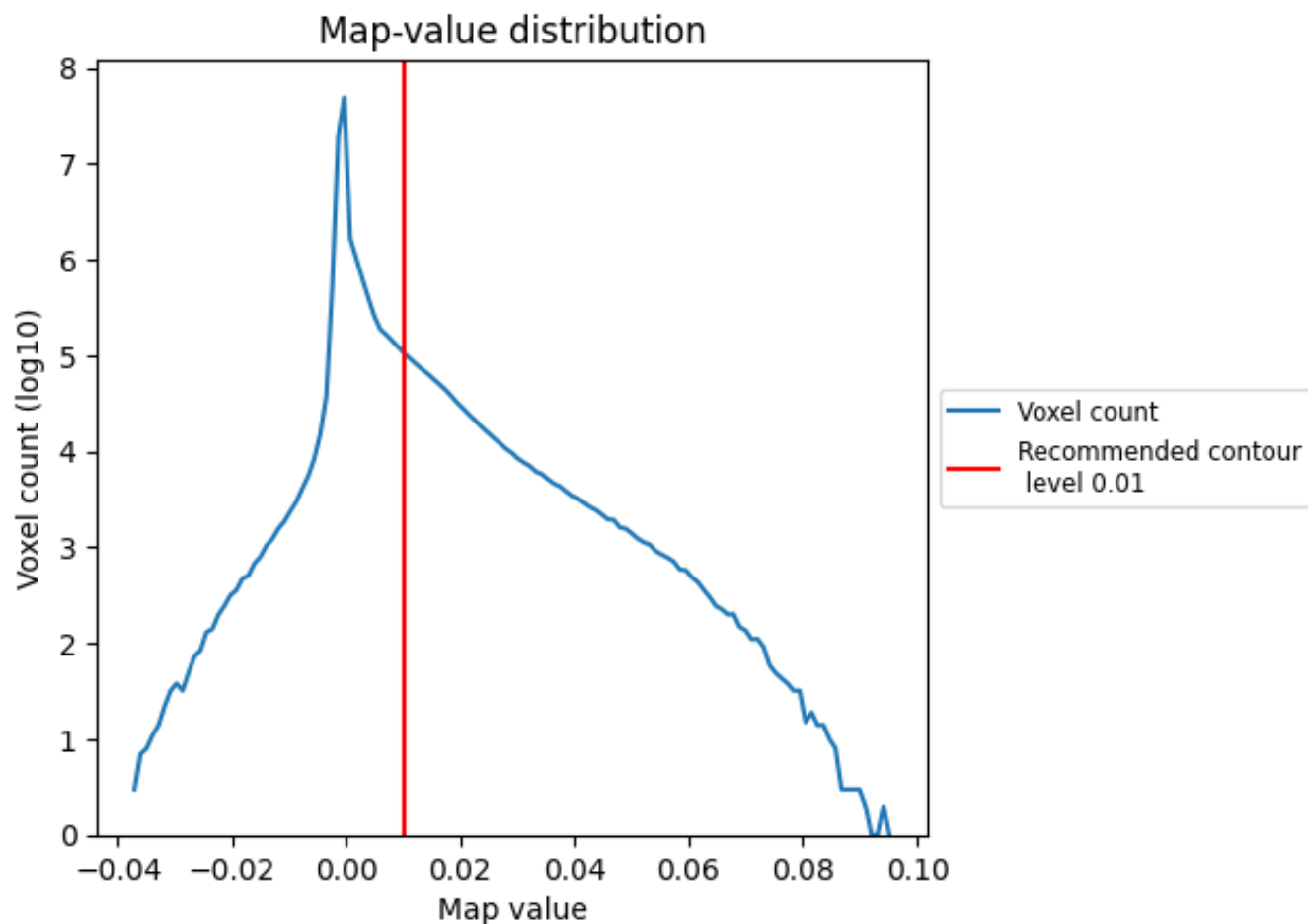
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

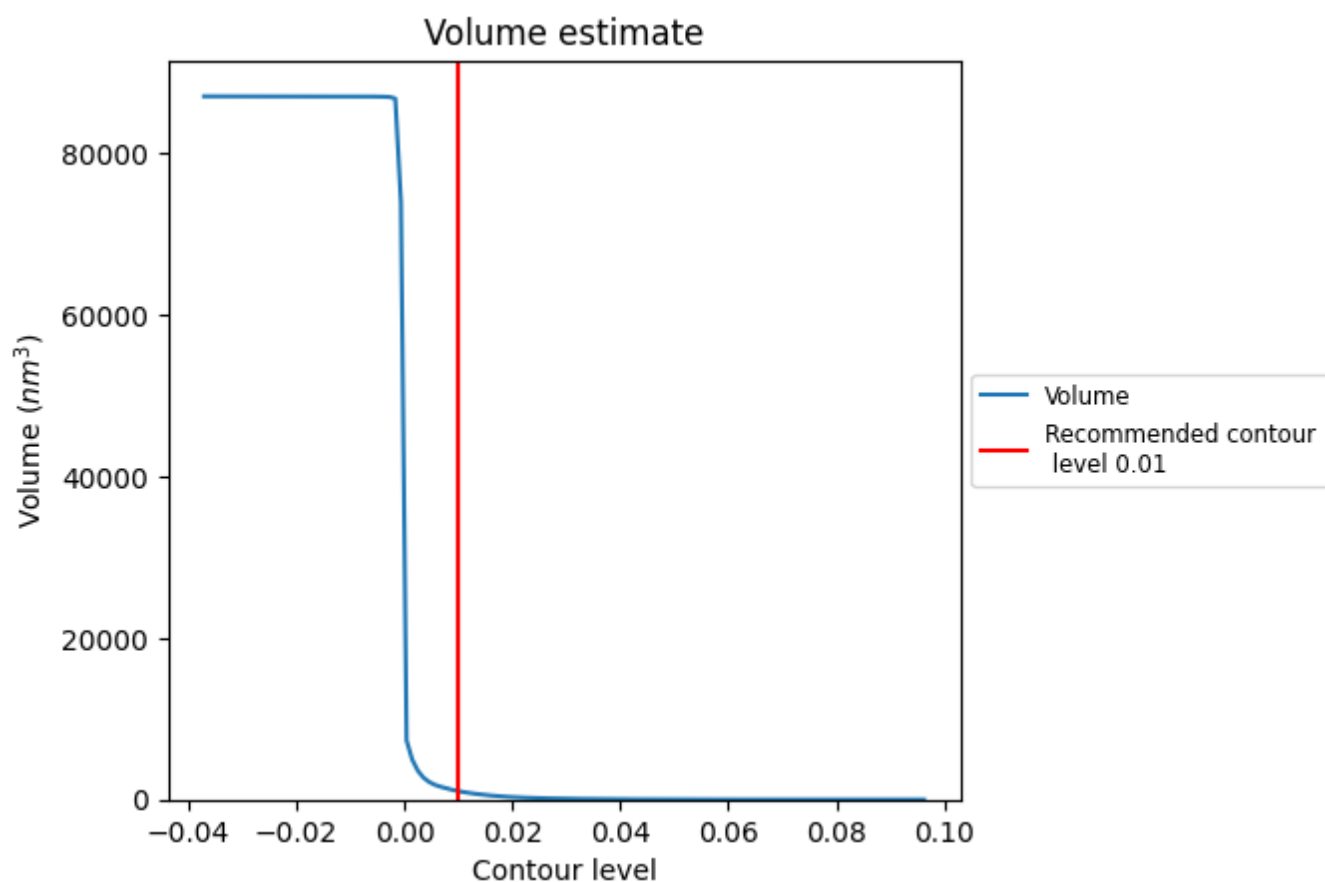
This section contains the results of statistical analysis of the map.

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.

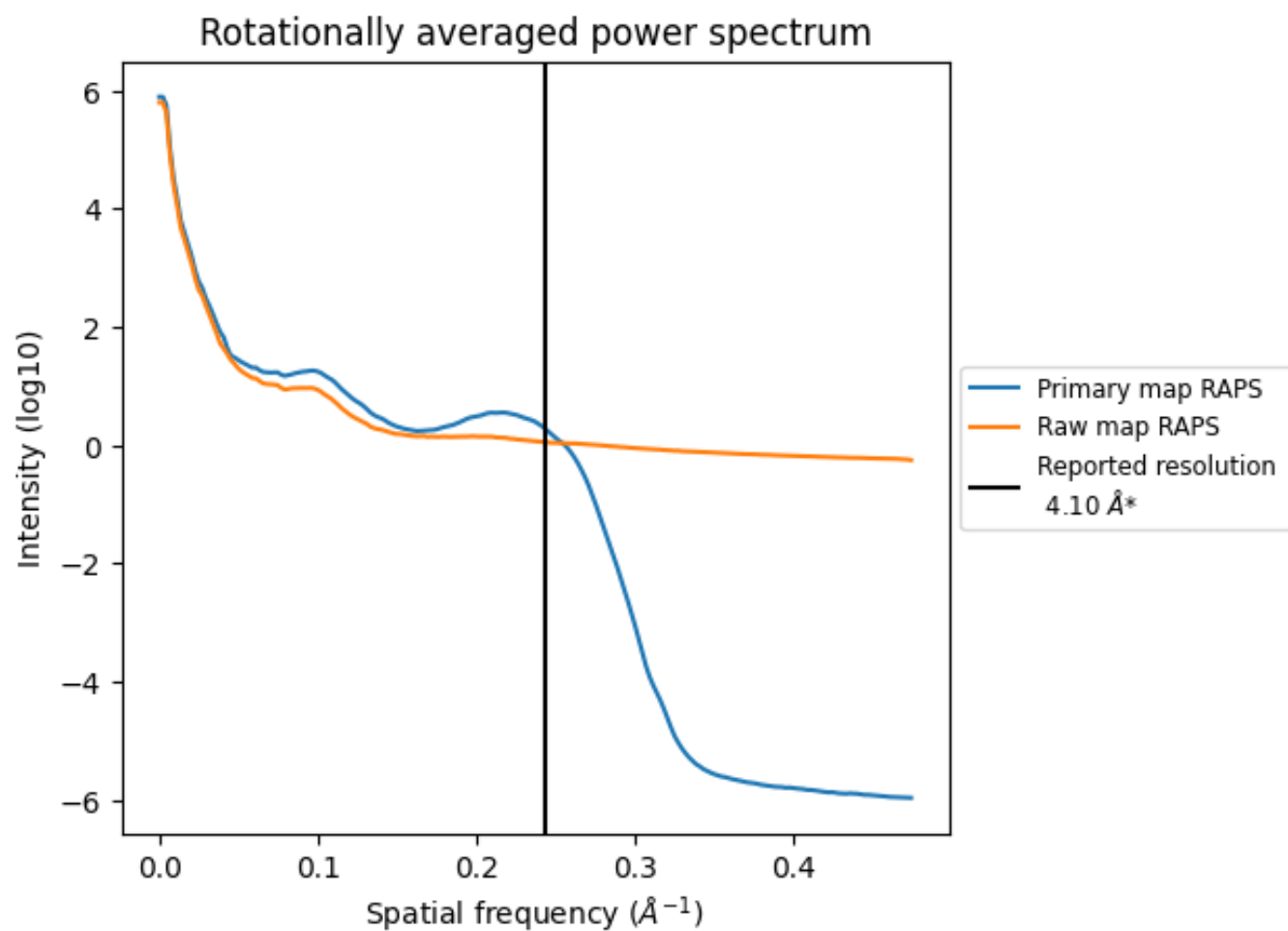
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1048 nm^3 ; this corresponds to an approximate mass of 946 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 ⓘ

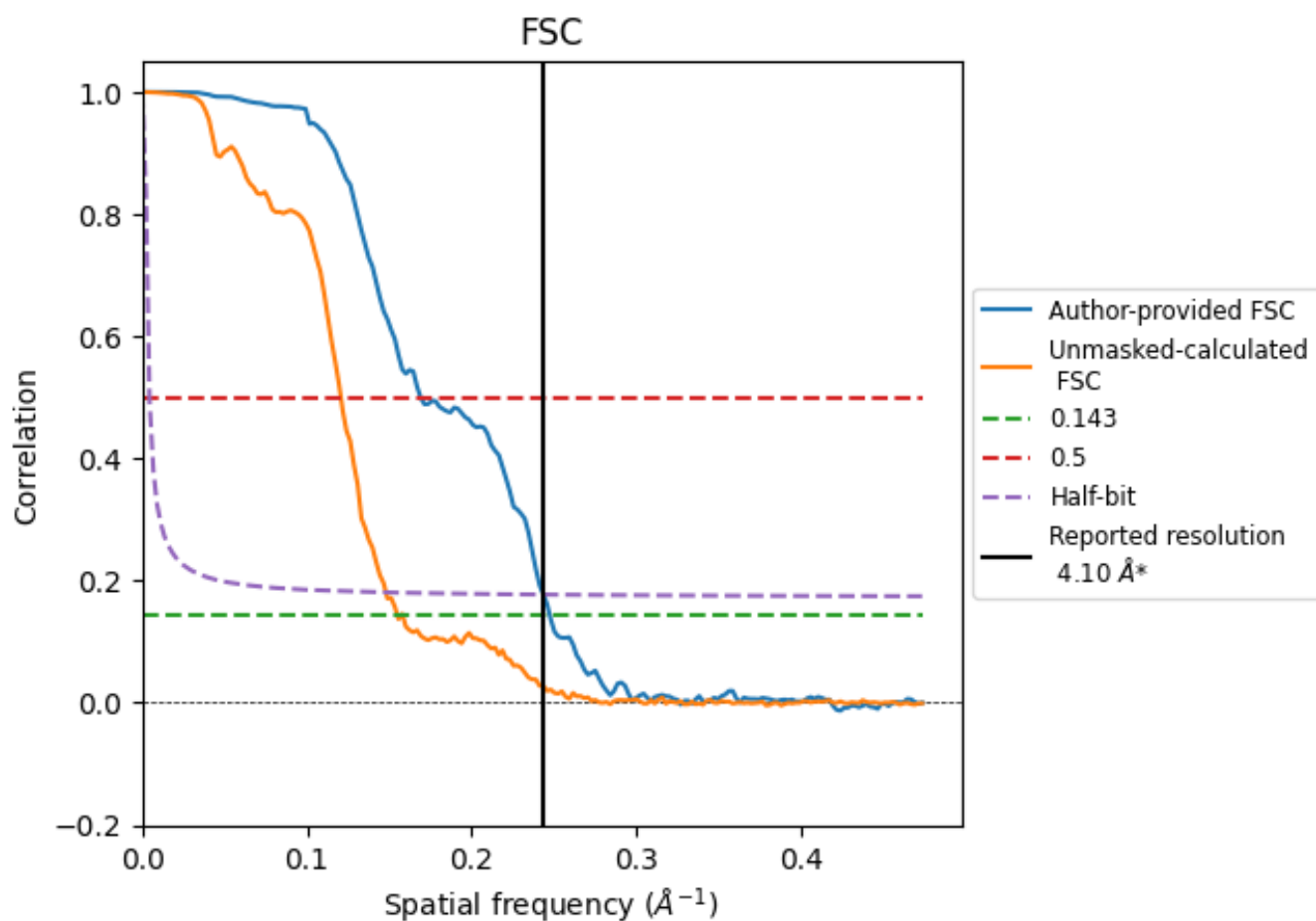


*Reported resolution corresponds to spatial frequency of $0.244 \text{ \AA}^{-1}$

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 0.244 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

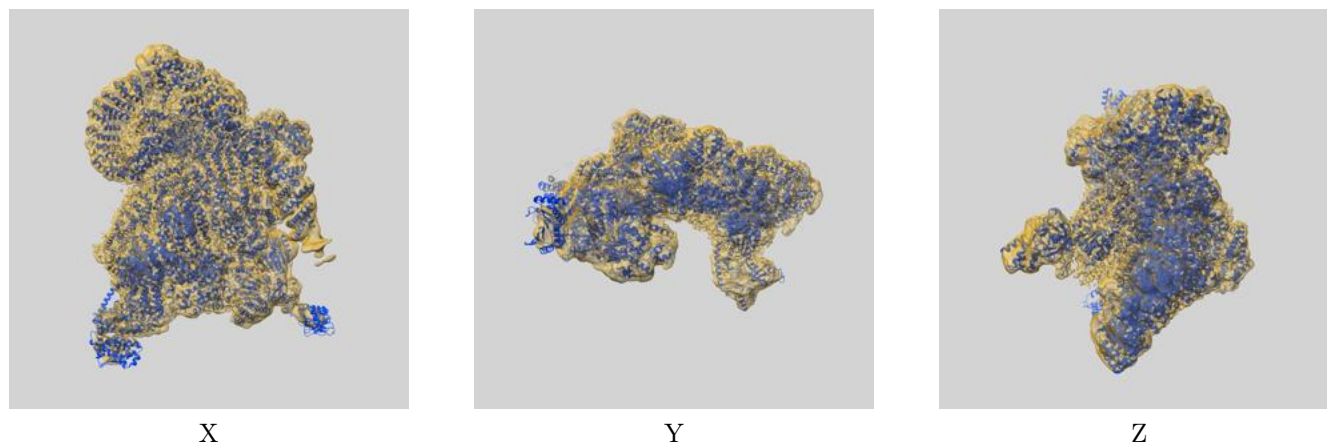
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.04	5.91	4.10
Unmasked-calculated*	6.45	8.29	6.75

*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 6.45 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

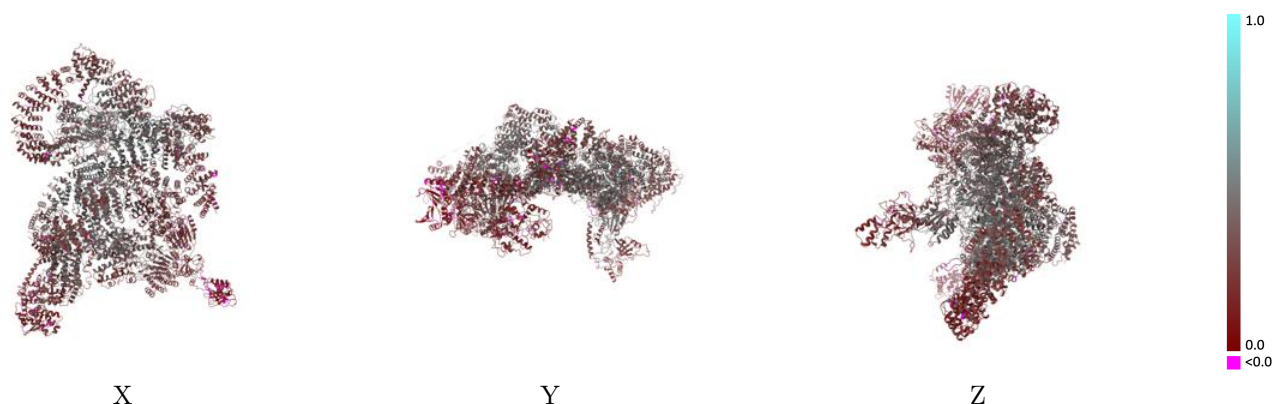
This section contains information regarding the fit between EMDB map EMD-39338 and PDB model 8YJB. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



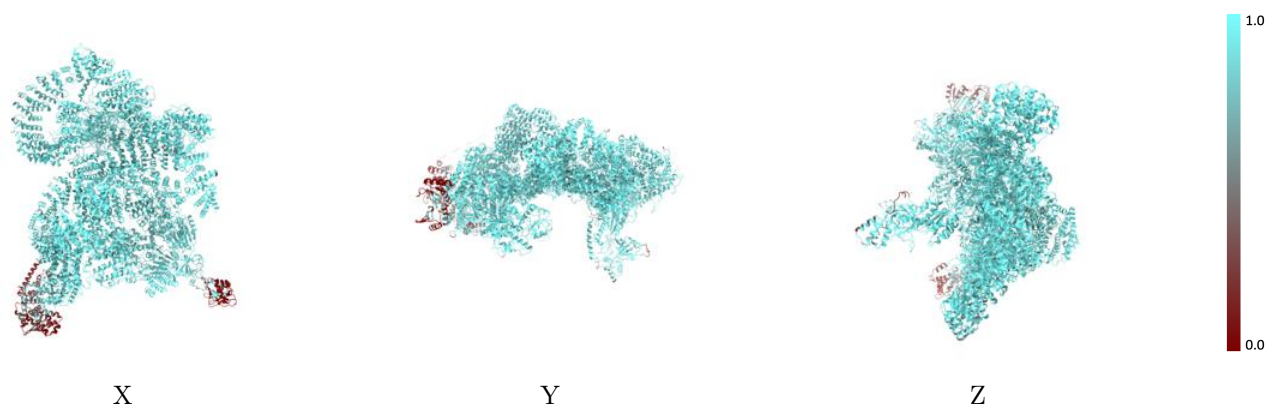
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



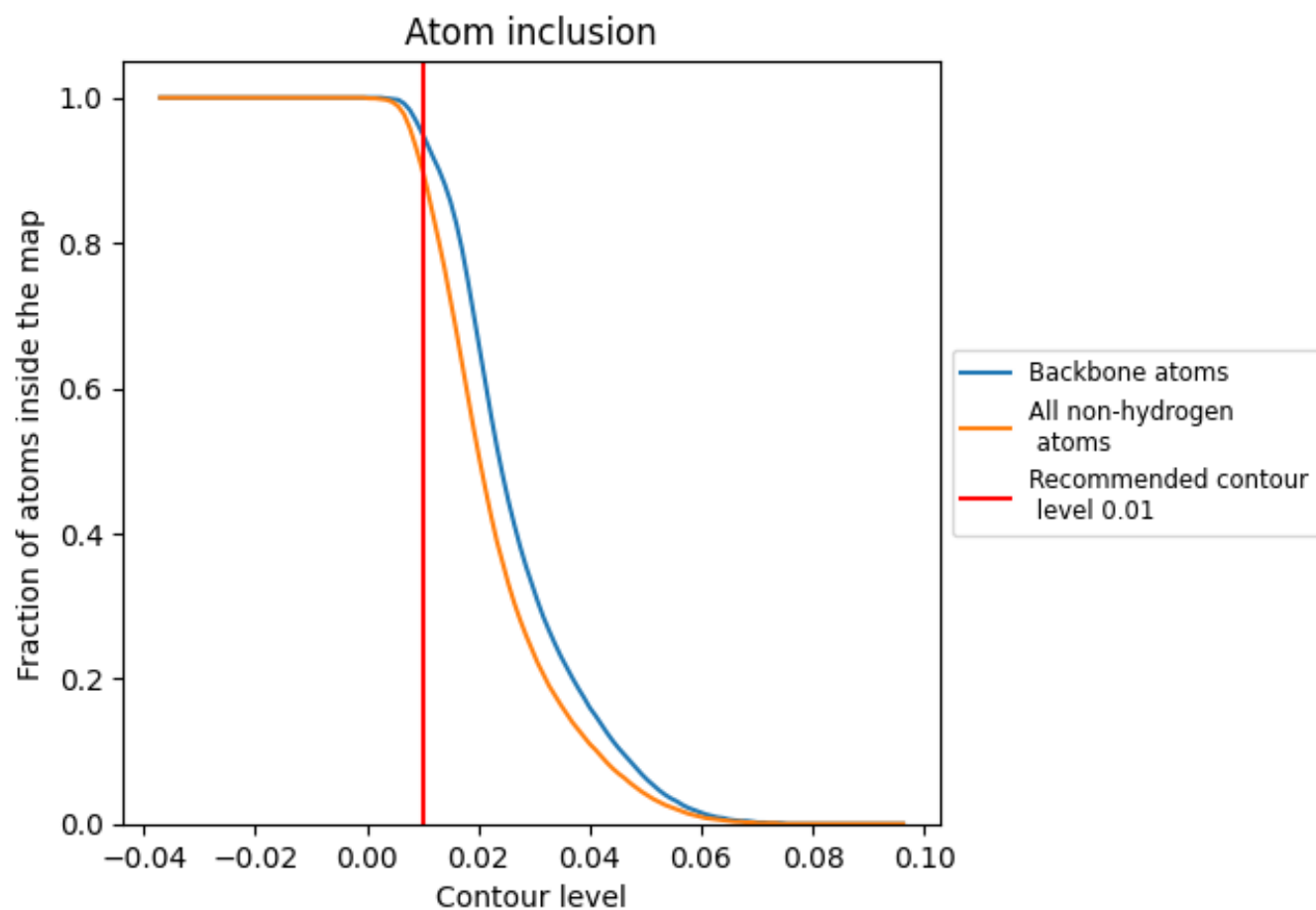
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 90% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.3200
O	 0.9040	 0.3850
A	 0.6930	 0.2640
B	 0.9380	 0.3700
D	 0.9560	 0.3080
E	 0.9740	 0.3830
F	 0.9140	 0.3110
G	 0.9580	 0.4090
H	 0.9380	 0.3360
I	 0.8730	 0.2580
K	 0.8290	 0.1690
P	 0.9140	 0.2540
Q	 0.9620	 0.4610

