



## Full wwPDB EM Validation Report ⓘ

Jun 10, 2025 – 07:30 PM JST

PDB ID : 8XQ9 / pdb\_00008xq9  
EMDB ID : EMD-38570  
Title : Structure of the sea urchin spSLC9C1 in state-2 w/ cAMP dimer  
Authors : Qu, H.; Zheng, X.  
Deposited on : 2024-01-04  
Resolution : 3.77 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

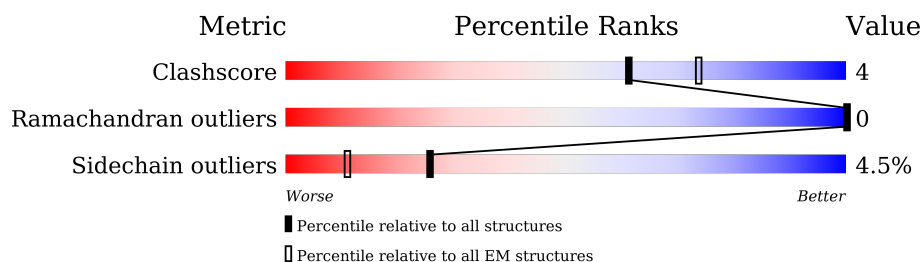
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.77 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	1308	<div> <div>5%</div> <div>45%</div> <div>7%</div> <div>48%</div> </div>
1	B	1308	<div> <div>5%</div> <div>44%</div> <div>7%</div> <div>48%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10672 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 Sperm-specific sodium proton exchanger.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	683	Total	C	N	O	S	0	0
			5336	3488	883	935	30		
1	B	683	Total	C	N	O	S	0	0
			5336	3488	883	935	30		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLY	-	expression tag	UNP A3RL54
A	29	SER	-	expression tag	UNP A3RL54
A	1326	ALA	-	expression tag	UNP A3RL54
A	1327	SER	-	expression tag	UNP A3RL54
A	1328	ASN	-	expression tag	UNP A3RL54
A	1329	SER	-	expression tag	UNP A3RL54
A	1330	LEU	-	expression tag	UNP A3RL54
A	1331	GLU	-	expression tag	UNP A3RL54
A	1332	VAL	-	expression tag	UNP A3RL54
A	1333	LEU	-	expression tag	UNP A3RL54
A	1334	PHE	-	expression tag	UNP A3RL54
A	1335	GLN	-	expression tag	UNP A3RL54
B	28	GLY	-	expression tag	UNP A3RL54
B	29	SER	-	expression tag	UNP A3RL54
B	1326	ALA	-	expression tag	UNP A3RL54
B	1327	SER	-	expression tag	UNP A3RL54
B	1328	ASN	-	expression tag	UNP A3RL54
B	1329	SER	-	expression tag	UNP A3RL54
B	1330	LEU	-	expression tag	UNP A3RL54
B	1331	GLU	-	expression tag	UNP A3RL54
B	1332	VAL	-	expression tag	UNP A3RL54
B	1333	LEU	-	expression tag	UNP A3RL54
B	1334	PHE	-	expression tag	UNP A3RL54
B	1335	GLN	-	expression tag	UNP A3RL54





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

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	111475	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.219	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.13	Depositor
Map size ( $\text{\AA}$ )	276.48, 276.48, 276.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.08, 1.08, 1.08	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	A	0.18	0/5440	0.43	0/7381
1	B	0.18	0/5440	0.42	0/7381
All	All	0.18	0/10880	0.43	0/14762

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	A	5336	0	5579	43	0
1	B	5336	0	5579	55	0
All	All	10672	0	11158	92	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.

All (92) 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)
1:A:368:VAL:HG21	1:A:436:LEU:HB3	1.73	0.70
1:B:466:THR:O	1:B:470:ASN:HB2	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:470:ASN:O	1:B:474:ILE:HB	1.99	0.62
1:B:910:ARG:NH2	1:B:938:MET:SD	2.76	0.58
1:A:505:GLN:HG2	1:B:905:ILE:HD11	1.84	0.58
1:B:388:LEU:HD11	1:B:461:GLY:HA3	1.84	0.58
1:A:156:VAL:HG11	1:A:336:ALA:HA	1.85	0.57
1:A:466:THR:O	1:A:470:ASN:HB2	2.05	0.57
1:B:610:LEU:O	1:B:614:HIS:ND1	2.38	0.56
1:B:106:LEU:HD21	1:B:362:THR:HG23	1.88	0.56
1:A:583:ARG:NH2	1:A:618:ALA:O	2.39	0.55
1:A:372:VAL:HA	1:A:376:ALA:HB3	1.87	0.55
1:A:872:GLU:OE1	1:A:875:ARG:NH2	2.39	0.55
1:A:894:VAL:HA	1:A:897:LYS:HE2	1.90	0.54
1:B:635:TRP:HD1	1:B:885:LEU:HD13	1.74	0.52
1:B:368:VAL:HG21	1:B:436:LEU:HD12	1.91	0.52
1:B:210:PRO:HB2	1:B:213:VAL:HB	1.93	0.51
1:B:139:LEU:HD13	1:B:441:VAL:HG21	1.91	0.51
1:A:96:LYS:NZ	1:B:296:ASP:OD2	2.44	0.50
1:B:498:VAL:HG21	1:B:534:ASP:HB3	1.93	0.50
1:B:233:GLU:O	1:B:237:ASN:HB2	2.12	0.50
1:B:156:VAL:HG11	1:B:336:ALA:HA	1.93	0.50
1:B:642:PRO:HA	1:B:645:LYS:HB3	1.92	0.50
1:A:462:ILE:O	1:A:466:THR:HB	2.12	0.50
1:A:899:ARG:HH22	1:A:946:SER:HA	1.76	0.50
1:A:271:VAL:HG13	1:A:322:SER:HB3	1.95	0.49
1:B:534:ASP:N	1:B:534:ASP:OD1	2.43	0.49
1:A:233:GLU:O	1:A:237:ASN:HB2	2.13	0.49
1:B:134:ASP:HB3	1:B:137:VAL:HG12	1.95	0.49
1:B:463:VAL:O	1:B:467:LEU:HB2	2.12	0.49
1:A:427:TRP:NE1	1:A:473:THR:OG1	2.44	0.48
1:A:106:LEU:HD21	1:A:362:THR:HG23	1.96	0.48
1:A:275:GLY:HA2	1:A:321:VAL:HG13	1.95	0.47
1:A:502:HIS:O	1:A:506:ASN:ND2	2.47	0.47
1:A:818:ILE:HG13	1:A:819:PRO:HD3	1.96	0.47
1:B:319:LEU:HB2	1:B:321:VAL:HG12	1.97	0.47
1:B:436:LEU:HD21	1:B:463:VAL:HG11	1.96	0.47
1:A:501:ILE:HD12	1:B:913:ILE:HD11	1.95	0.47
1:B:368:VAL:HG11	1:B:436:LEU:HG	1.97	0.47
1:A:169:LEU:HB2	1:A:410:LEU:HD21	1.97	0.47
1:B:158:THR:HA	1:B:161:ARG:HG2	1.97	0.46
1:B:585:ARG:NH1	1:B:857:MET:O	2.49	0.46
1:B:135:PRO:HG3	1:B:444:ASN:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:819:PRO:HA	1:B:822:ILE:HG22	1.98	0.46
1:B:610:LEU:HD12	1:B:613:GLN:HE21	1.80	0.45
1:A:158:THR:HB	1:A:228:THR:HG21	1.98	0.45
1:A:916:LEU:HD11	1:B:500:ARG:HD2	1.98	0.45
1:B:427:TRP:NE1	1:B:473:THR:OG1	2.47	0.45
1:A:404:SER:O	1:A:407:SER:OG	2.35	0.45
1:A:603:LEU:HD21	1:A:842:GLY:HA3	1.97	0.45
1:B:217:LEU:HD23	1:B:220:LEU:HD21	1.97	0.44
1:B:449:ASP:N	1:B:449:ASP:OD1	2.46	0.44
1:A:210:PRO:HB2	1:A:213:VAL:HB	1.99	0.44
1:B:441:VAL:O	1:B:445:LEU:HB2	2.18	0.44
1:B:488:ILE:HG23	1:B:491:ARG:HH12	1.81	0.44
1:B:938:MET:HA	1:B:941:LEU:HD23	2.00	0.44
1:A:194:ASN:OD1	1:A:196:SER:OG	2.29	0.44
1:A:214:VAL:HG21	1:A:231:GLU:HG3	1.98	0.44
1:B:572:PRO:HB2	1:B:573:ARG:H	1.70	0.44
1:A:295:ASN:HB3	1:A:936:ILE:HD11	1.99	0.43
1:A:924:GLU:HB2	1:B:595:TRP:HZ2	1.83	0.43
1:A:470:ASN:O	1:A:474:ILE:HB	2.18	0.43
1:B:270:GLN:HE22	1:B:320:GLU:HB3	1.84	0.43
1:A:76:LYS:NZ	1:A:125:GLU:OE1	2.51	0.43
1:A:338:LYS:NZ	1:A:346:GLU:OE1	2.42	0.43
1:B:878:VAL:HA	1:B:881:GLU:HG2	2.01	0.42
1:B:648:LEU:HD22	1:B:818:ILE:HG23	2.01	0.42
1:B:847:GLU:HA	1:B:850:VAL:HG12	2.02	0.42
1:B:648:LEU:HB2	1:B:822:ILE:HD13	2.01	0.42
1:A:233:GLU:OE2	1:A:399:ARG:NH2	2.39	0.42
1:A:342:SER:HB2	1:A:345:VAL:HG23	2.02	0.42
1:B:603:LEU:HD23	1:B:603:LEU:HA	1.90	0.42
1:B:234:SER:O	1:B:238:ASP:HB2	2.20	0.42
1:B:244:ILE:HA	1:B:247:VAL:HG12	2.01	0.42
1:B:223:SER:HB3	1:B:226:LEU:HB3	2.01	0.42
1:A:860:ASN:HB3	1:A:863:ILE:HG12	2.02	0.42
1:A:925:MET:HE2	1:A:925:MET:HB2	1.85	0.42
1:A:884:LEU:HA	1:A:887:ARG:HE	1.85	0.41
1:B:431:ARG:HB2	1:B:463:VAL:HG23	2.01	0.41
1:A:613:GLN:HA	1:A:616:GLU:HG2	2.02	0.41
1:B:145:VAL:HG12	1:B:353:TRP:HZ3	1.85	0.41
1:A:338:LYS:HB2	1:A:346:GLU:HG2	2.01	0.41
1:B:923:ASP:OD1	1:B:923:ASP:N	2.47	0.41
1:A:137:VAL:HG12	1:B:75:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:937:LYS:HD3	1:B:937:LYS:HA	1.86	0.41
1:B:147:ILE:HD13	1:B:324:VAL:HG13	2.01	0.41
1:A:298:LEU:HA	1:A:301:ILE:HD12	2.02	0.41
1:B:906:LEU:HD13	1:B:906:LEU:HA	1.96	0.41
1:A:147:ILE:HD13	1:A:147:ILE:HA	1.96	0.40
1:B:942:MET:HE3	1:B:942:MET:HB3	1.93	0.40
1:B:925:MET:N	1:B:925:MET:SD	2.95	0.40
1:A:143:LEU:HD13	1:A:242:ILE:HD13	2.03	0.40

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	677/1308 (52%)	659 (97%)	18 (3%)	0	100	100
1	B	677/1308 (52%)	667 (98%)	10 (2%)	0	100	100
All	All	1354/2616 (52%)	1326 (98%)	28 (2%)	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	580/1120 (52%)	554 (96%)	26 (4%)	23	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	580/1120 (52%)	554 (96%)	26 (4%)	23 49
All	All	1160/2240 (52%)	1108 (96%)	52 (4%)	26 49

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	ILE
1	A	138	LEU
1	A	155	ASP
1	A	209	ASP
1	A	211	VAL
1	A	226	LEU
1	A	240	CYS
1	A	368	VAL
1	A	372	VAL
1	A	405	LEU
1	A	413	ILE
1	A	418	THR
1	A	445	LEU
1	A	451	ILE
1	A	465	LEU
1	A	488	ILE
1	A	492	LEU
1	A	628	VAL
1	A	631	LEU
1	A	818	ILE
1	A	823	LEU
1	A	835	LEU
1	A	841	LYS
1	A	857	MET
1	A	925	MET
1	A	948	ILE
1	B	78	ILE
1	B	100	ILE
1	B	103	THR
1	B	138	LEU
1	B	155	ASP
1	B	197	GLU
1	B	211	VAL
1	B	238	ASP
1	B	296	ASP
1	B	303	ILE

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Mol	Chain	Res	Type
1	B	321	VAL
1	B	345	VAL
1	B	372	VAL
1	B	413	ILE
1	B	418	THR
1	B	436	LEU
1	B	499	ARG
1	B	583	ARG
1	B	595	TRP
1	B	610	LEU
1	B	626	ILE
1	B	823	LEU
1	B	857	MET
1	B	906	LEU
1	B	936	ILE
1	B	941	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	126	HIS
1	A	187	ASN
1	A	264	ASN
1	A	292	HIS
1	A	295	ASN
1	A	374	GLN
1	A	502	HIS
1	B	126	HIS
1	B	140	GLN
1	B	246	ASN
1	B	264	ASN
1	B	295	ASN
1	B	361	ASN
1	B	444	ASN
1	B	475	GLN
1	B	636	GLN
1	B	826	ASN
1	B	889	HIS
1	B	900	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](#)

There are no chain breaks in this entry.

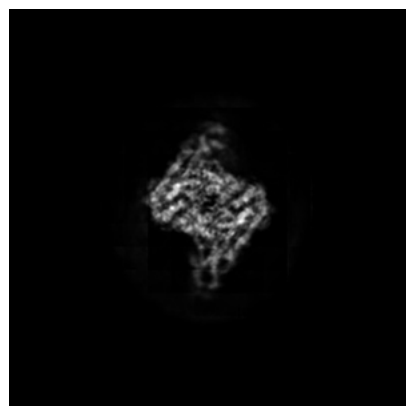
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38570. These allow visual inspection of the internal detail of the map and identification of artifacts.

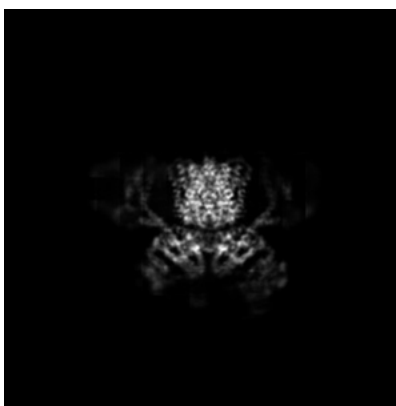
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

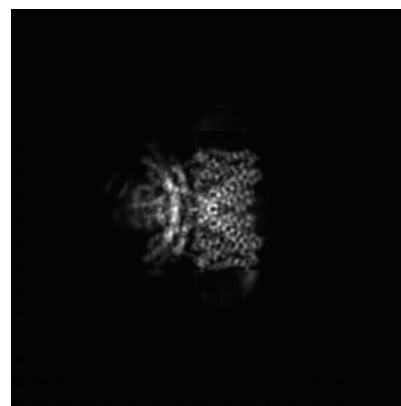
#### 6.1.1 Primary map



X

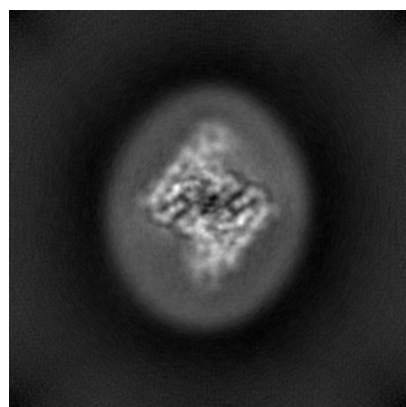


Y

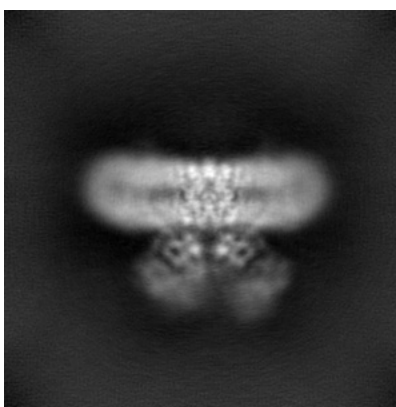


Z

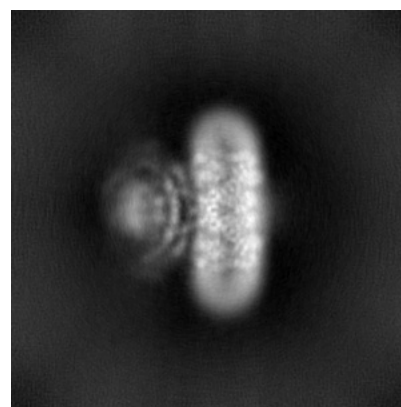
#### 6.1.2 Raw map



X



Y



Z

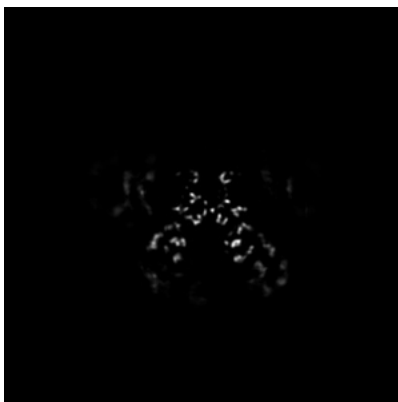
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 128

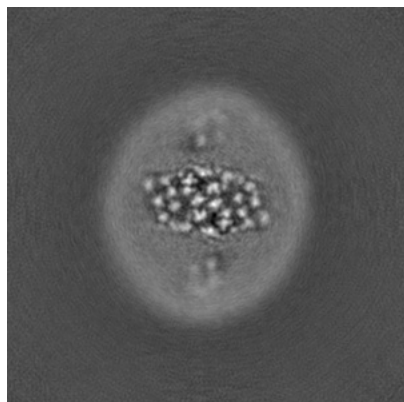


Y Index: 128

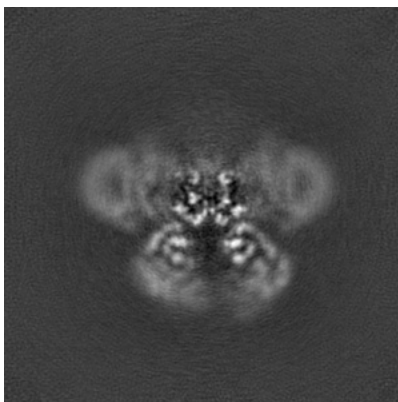


Z Index: 128

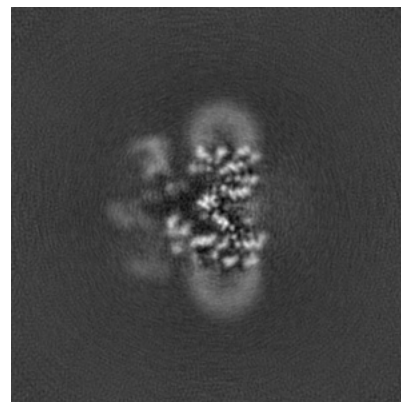
### 6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

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

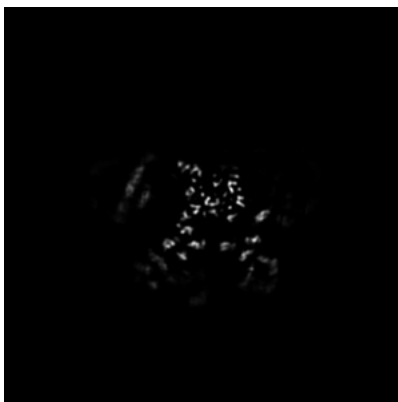


## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 131

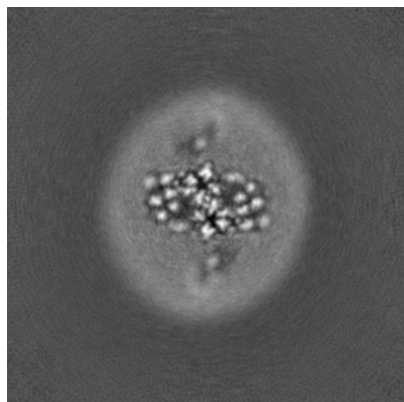


Y Index: 121

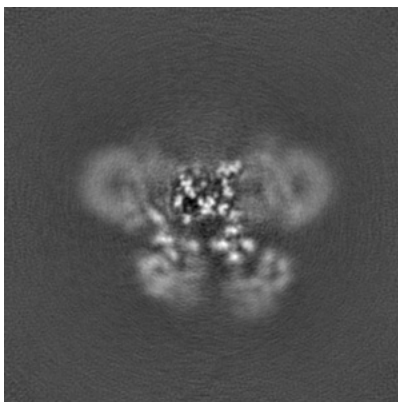


Z Index: 124

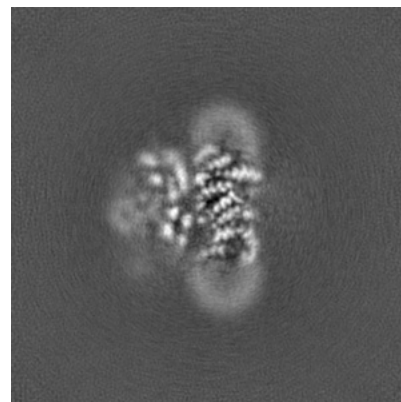
### 6.3.2 Raw map



X Index: 126



Y Index: 133

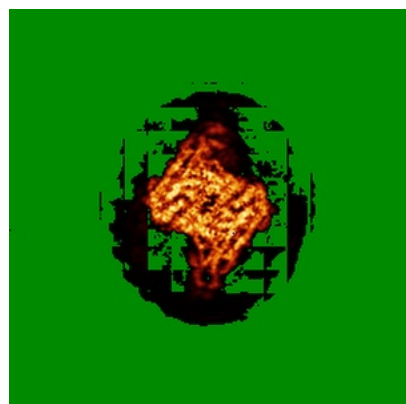


Z Index: 119

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

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

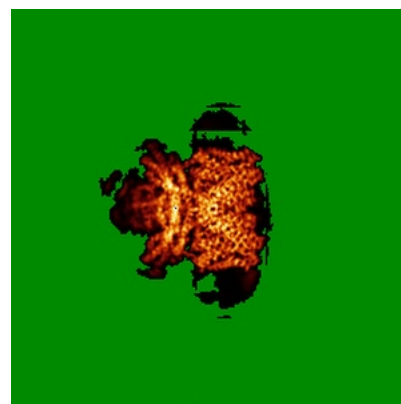
### 6.4.1 Primary map



X

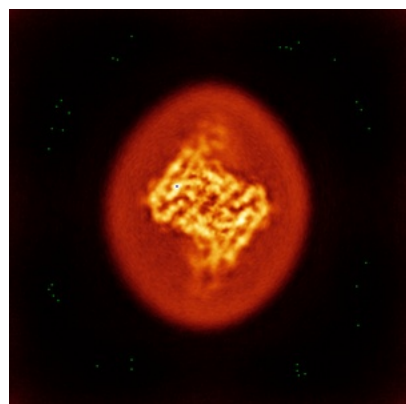


Y

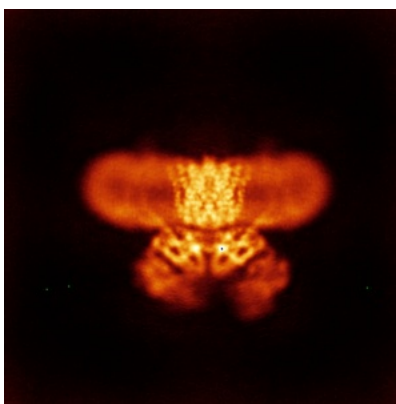


Z

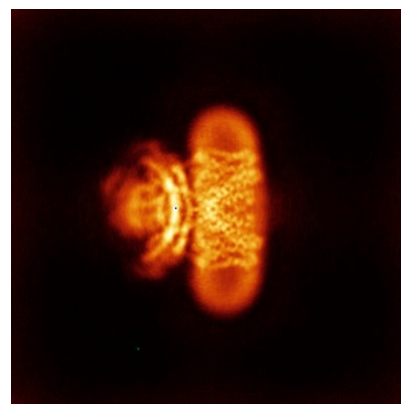
### 6.4.2 Raw map



X



Y

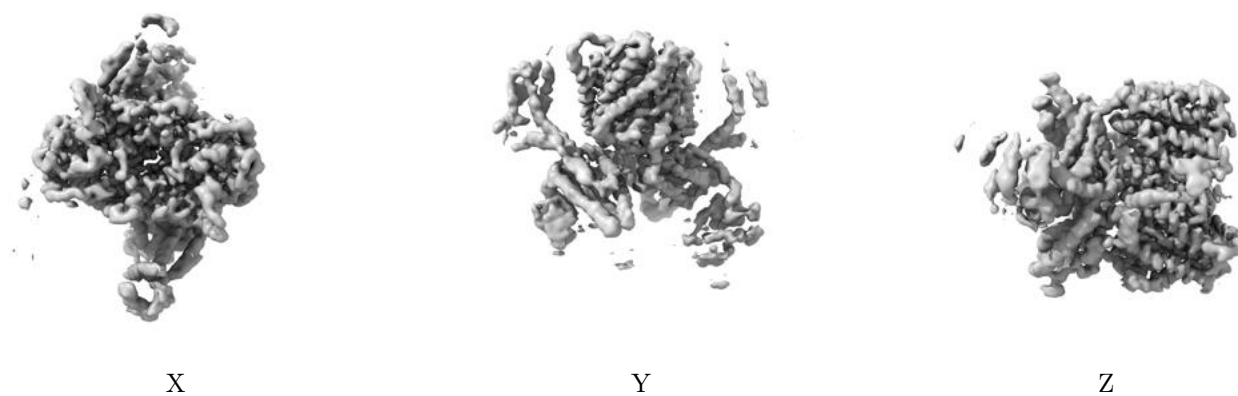


Z

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 0.13. 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.

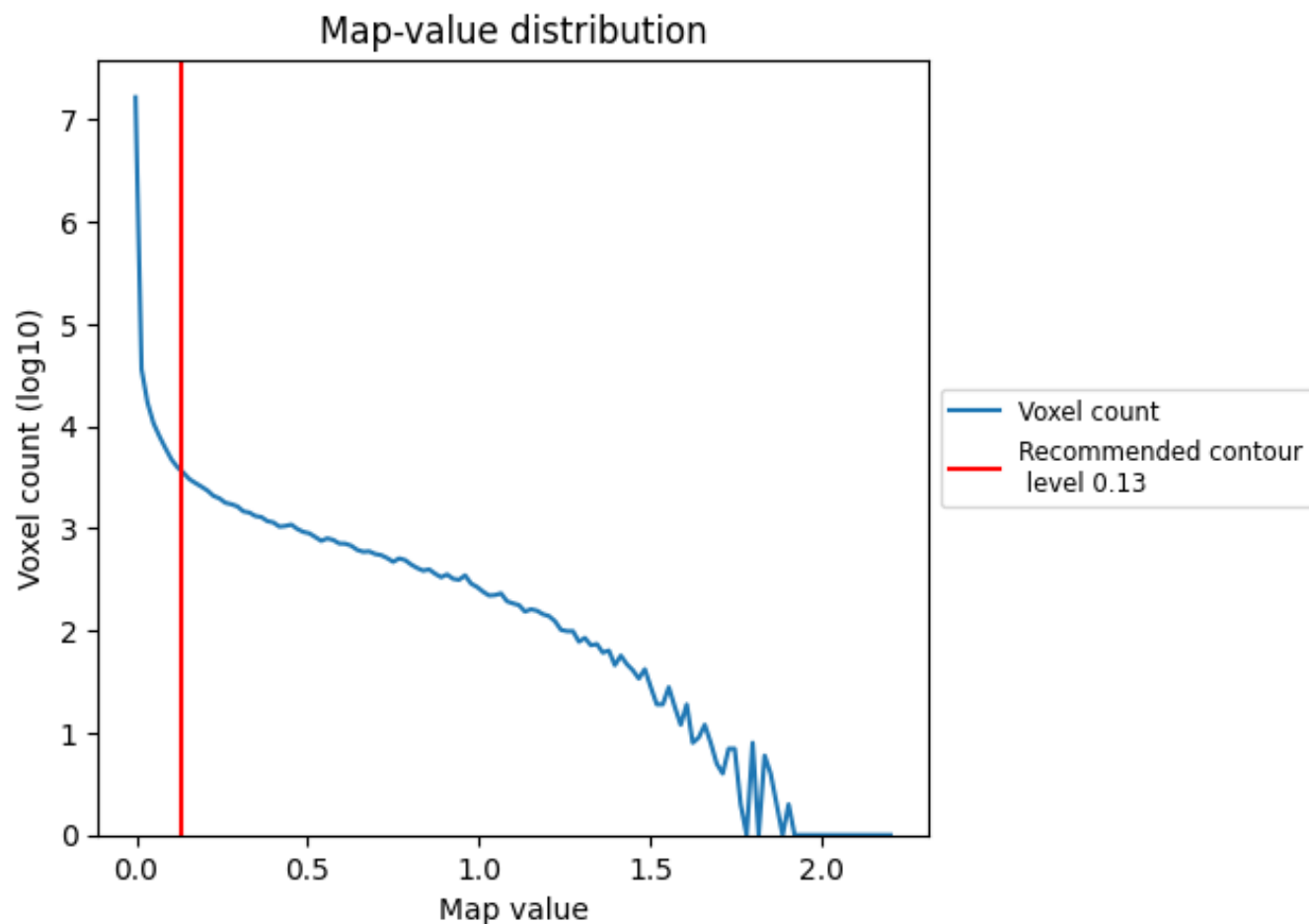
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

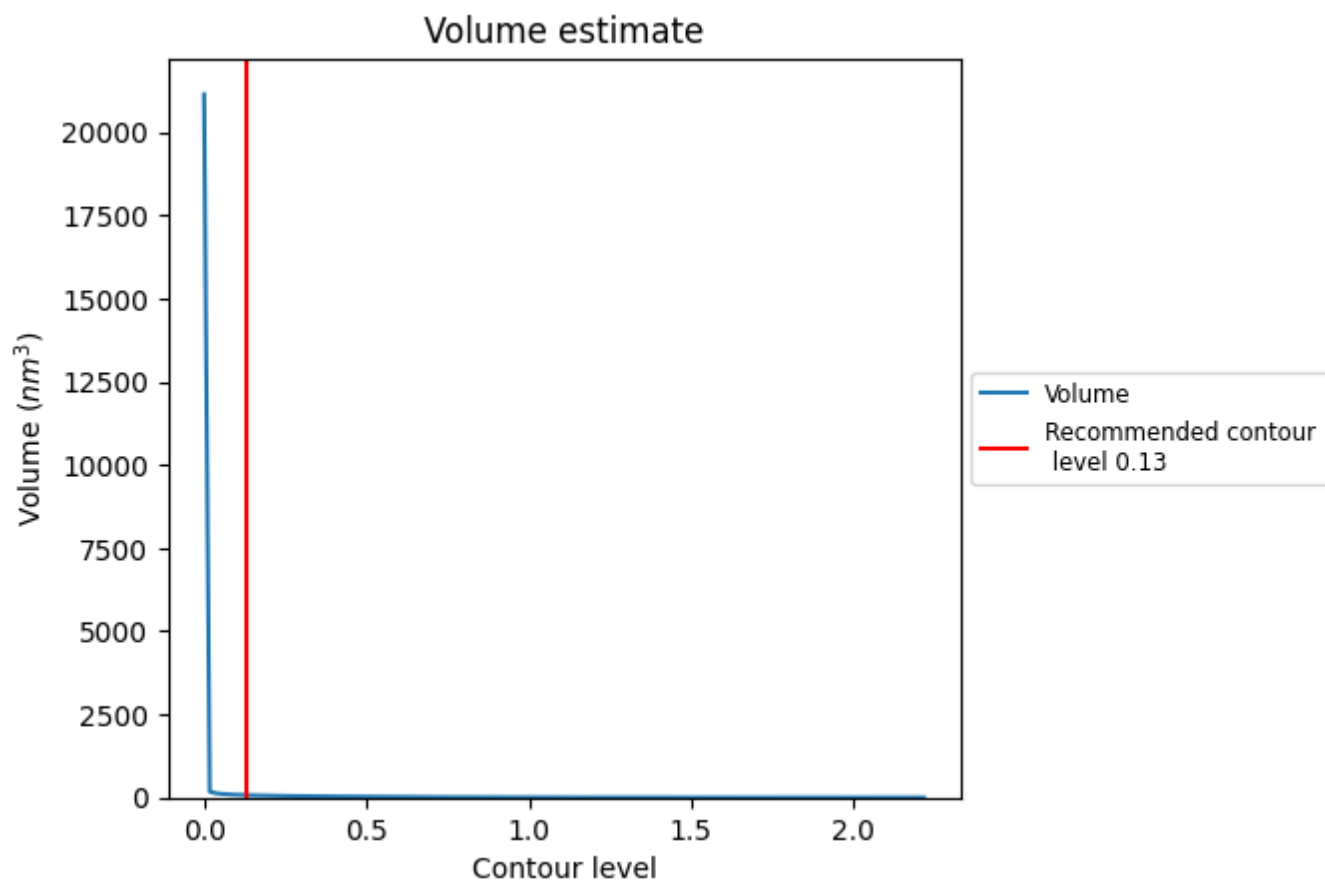
This section contains the results of statistical analysis of the map.

### 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.

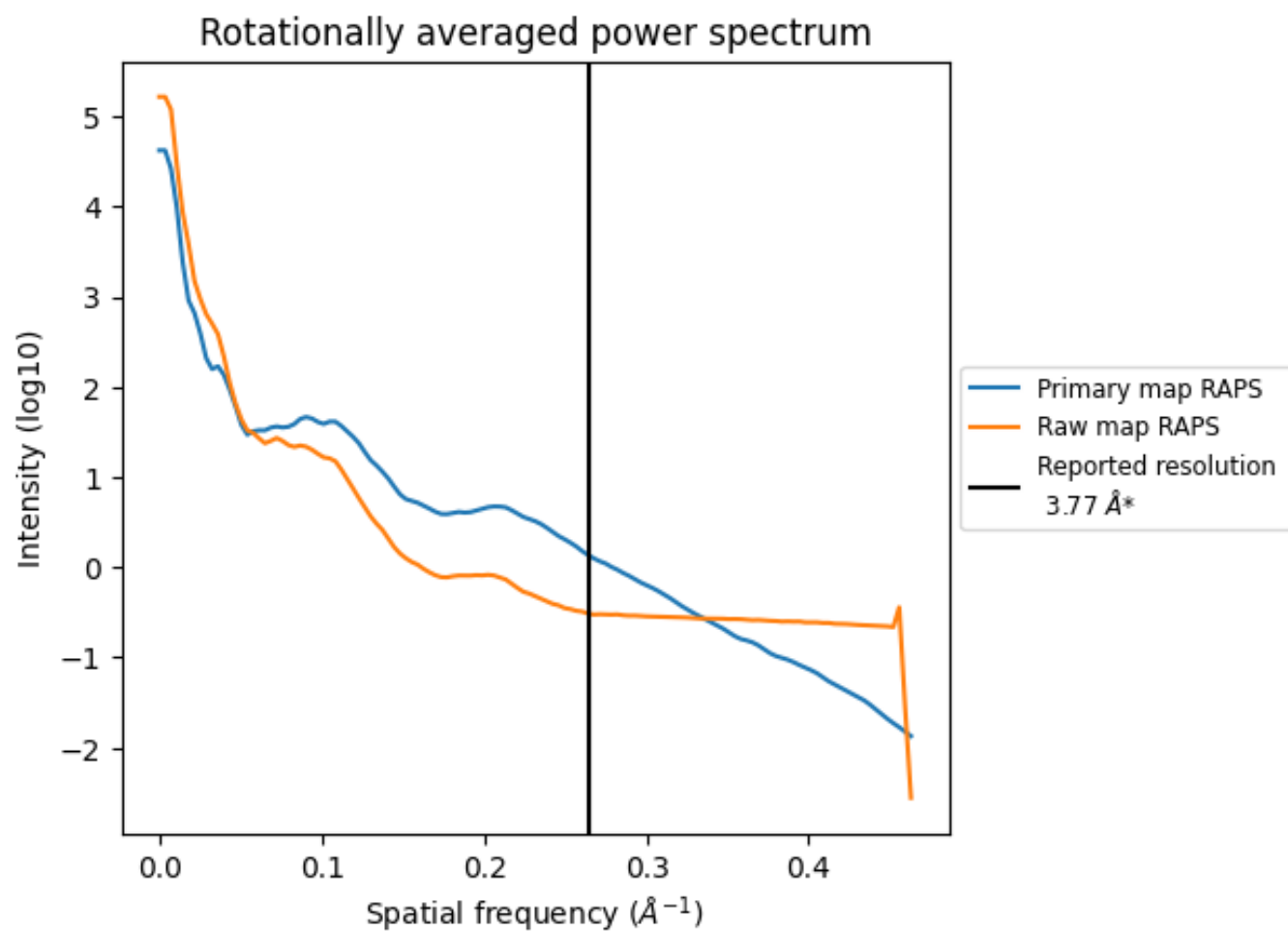
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 72  $\text{nm}^3$ ; this corresponds to an approximate mass of 65 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 ⓘ

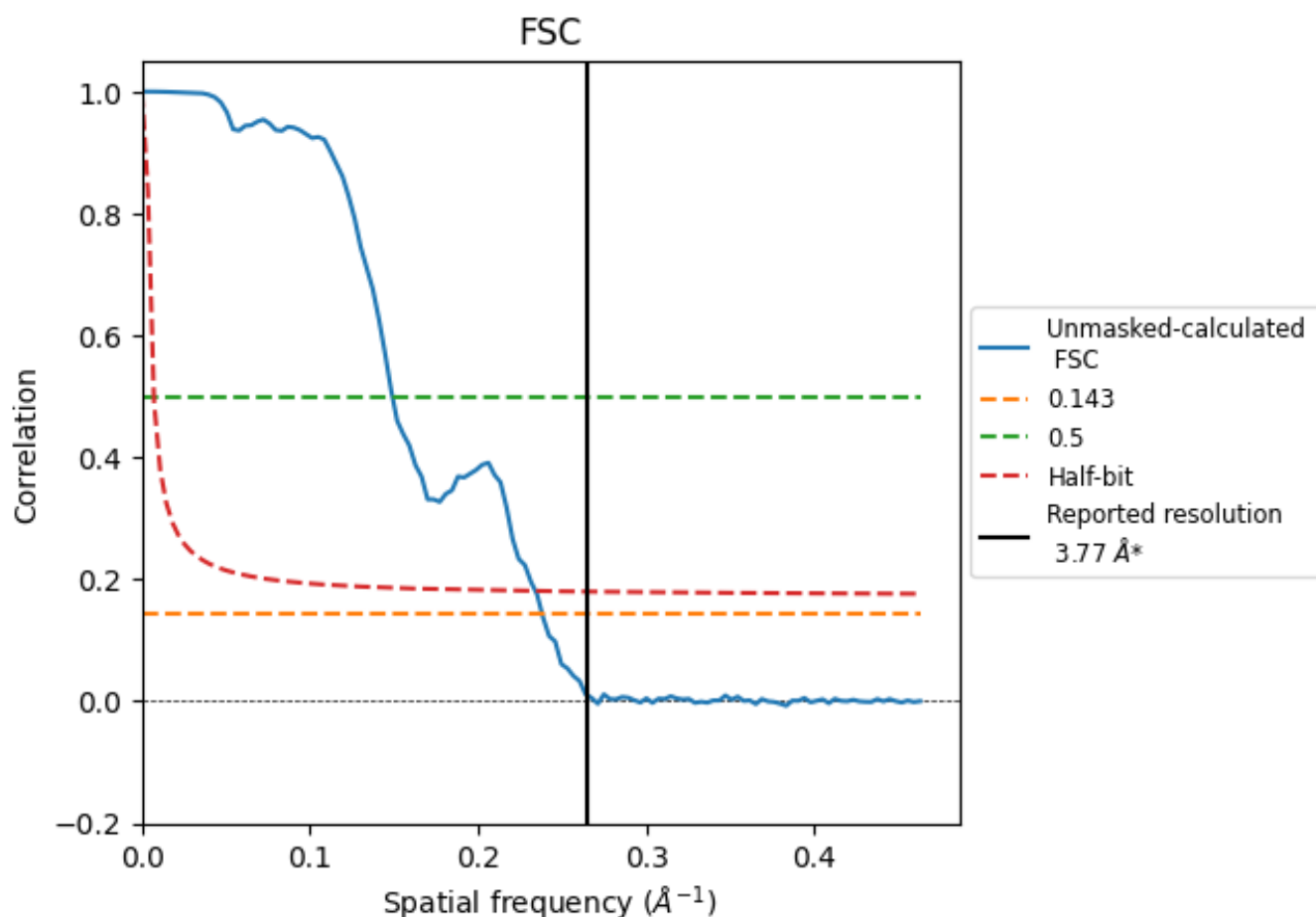


\*Reported resolution corresponds to spatial frequency of 0.265 Å<sup>-1</sup>

## 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 0.265  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.77	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.20	6.71	4.27

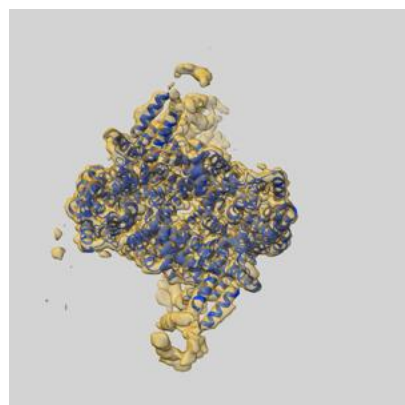
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.20 differs from the reported value 3.77 by more than 10 %



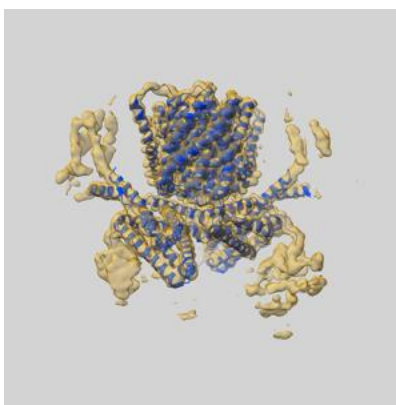
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38570 and PDB model 8XQ9. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

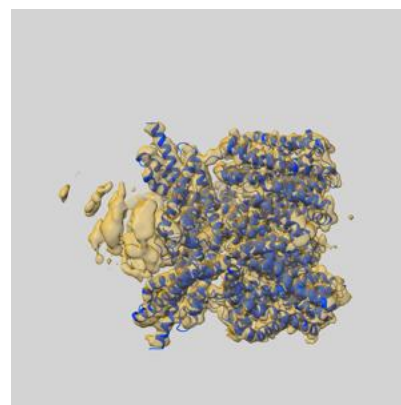
### 9.1 Map-model overlay [i](#)



X



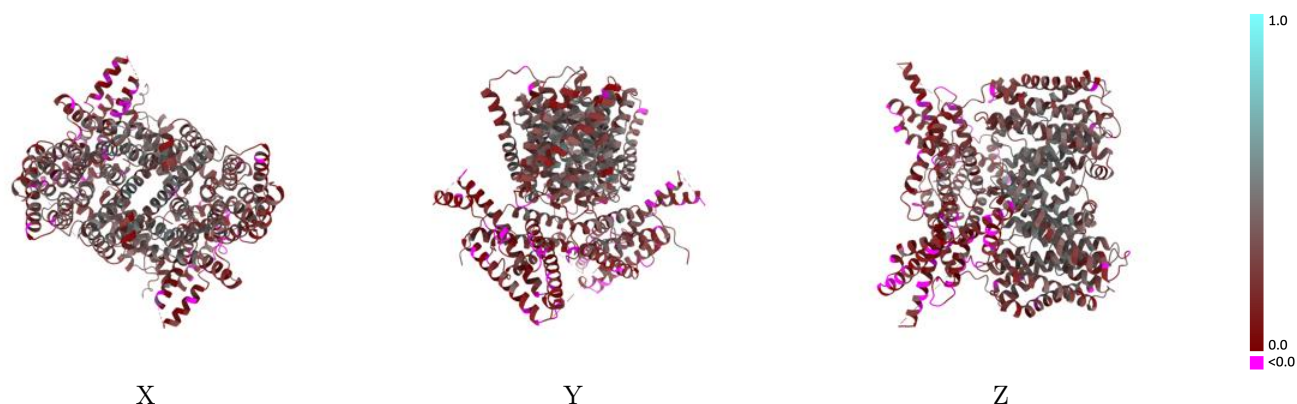
Y



Z

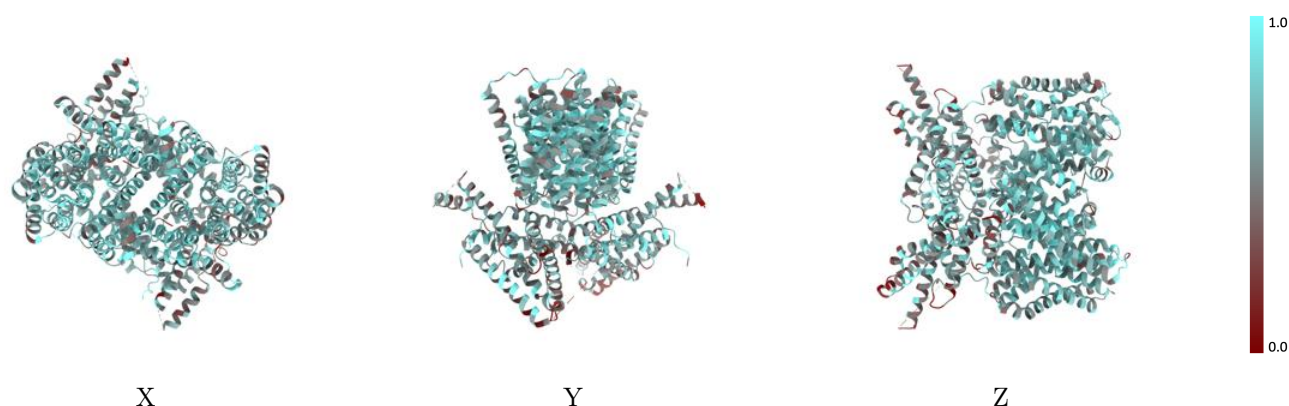
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



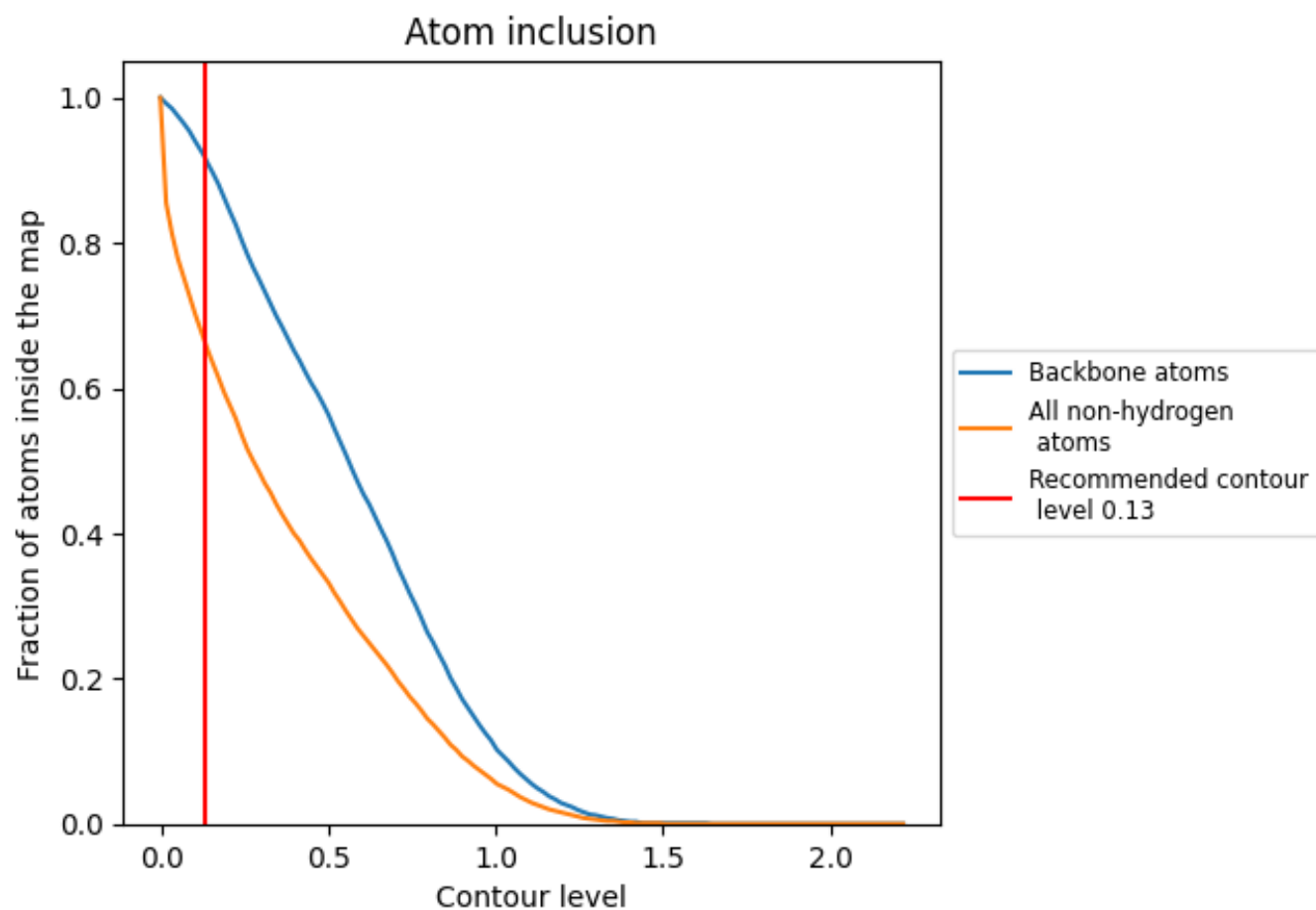
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6650	<div></div> 0.2610
A	<div></div> 0.6710	<div></div> 0.2670
B	<div></div> 0.6590	<div></div> 0.2560

