



## wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 05:03 PM EDT

PDB ID : 7RMG  
EMDB ID : EMD-24569  
Title : Substance P bound to active human neurokinin 1 receptor in complex with miniGs/q70  
Authors : Harris, J.A.; Faust, B.; Gondin, A.B.; Daemgen, M.A.; Suomivuori, C.M.; Veldhuis, N.A.; Cheng, Y.; Dror, R.O.; Thal, D.; Manglik, A.  
Deposited on : 2021-07-27  
Resolution : 3.00 Å (reported)  
Based on initial model : 6HLP

This is a wwPDB EM Validation Summary 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.dev113  
MolProbity : 4.02b-467  
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) : 2.39

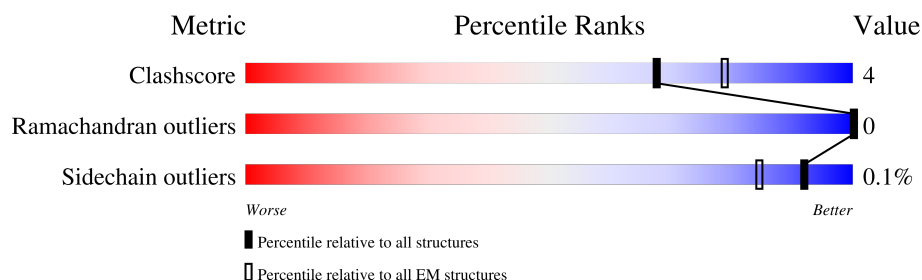
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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	229	
2	R	418	
3	S	12	
4	B	370	
5	G	68	
6	N	142	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7316 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 Guanine nucleotide-binding protein G(s) subunit alpha isoforms short, with certain residues mutated to match Guanine nucleotide-binding protein G(q) subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	193	Total	C	N	O	S	0	0
			1510	974	260	271	5		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLY	-	expression tag	UNP P63092
A	49	ASP	GLY	engineered mutation	UNP P63092
A	50	ASN	GLU	engineered mutation	UNP P63092
A	196	GLY	-	linker	UNP P63092
A	197	GLY	-	linker	UNP P63092
A	198	SER	-	linker	UNP P63092
A	199	GLY	-	linker	UNP P63092
A	200	GLY	-	linker	UNP P63092
A	201	SER	-	linker	UNP P63092
A	202	GLY	-	linker	UNP P63092
A	203	GLY	-	linker	UNP P63092
A	249	ASP	ALA	engineered mutation	UNP P63092
A	252	ASP	SER	engineered mutation	UNP P63092
A	?	-	ASN	deletion	UNP P63092
A	?	-	MET	deletion	UNP P63092
A	?	-	VAL	deletion	UNP P63092
A	?	-	ILE	deletion	UNP P63092
A	?	-	ARG	deletion	UNP P63092
A	?	-	GLU	deletion	UNP P63092
A	?	-	ASP	deletion	UNP P63092
A	?	-	ASN	deletion	UNP P63092
A	?	-	GLN	deletion	UNP P63092
A	?	-	THR	deletion	UNP P63092
A	272	ASP	LEU	engineered mutation	UNP P63092
A	372	ALA	ILE	engineered mutation	UNP P63092
A	375	ILE	VAL	engineered mutation	UNP P63092

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Chain	Residue	Modelled	Actual	Comment	Reference
A	380	LYS	ARG	engineered mutation	UNP P63092
A	384	LEU	GLN	engineered mutation	UNP P63092
A	385	GLN	ARG	engineered mutation	UNP P63092
A	387	ASN	HIS	engineered mutation	UNP P63092
A	390	GLU	GLN	engineered mutation	UNP P63092
A	392	ASN	GLU	engineered mutation	UNP P63092
A	394	VAL	LEU	engineered mutation	UNP P63092

- Molecule 2 is a protein called Substance-P receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	289	Total	C	N	O	S	0	0
			2306	1557	355	374	20		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-10	ASP	-	expression tag	UNP P25103
R	-9	TYR	-	expression tag	UNP P25103
R	-8	LYS	-	expression tag	UNP P25103
R	-7	ASP	-	expression tag	UNP P25103
R	-6	ASP	-	expression tag	UNP P25103
R	-5	ASP	-	expression tag	UNP P25103
R	-4	ASP	-	expression tag	UNP P25103
R	-3	ALA	-	expression tag	UNP P25103
R	-2	SER	-	expression tag	UNP P25103
R	-1	ILE	-	expression tag	UNP P25103
R	0	ASP	-	expression tag	UNP P25103

- Molecule 3 is a protein called Substance P.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	12	Total	C	N	O	S	0	1
			85	57	14	13	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	12	NH2	-	amidation	UNP P20366

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	322	Total	C	N	O	S	0	0
			2319	1458	409	434	18		

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-29	MET	-	initiating methionine	UNP P62873
B	-28	HIS	-	expression tag	UNP P62873
B	-27	HIS	-	expression tag	UNP P62873
B	-26	HIS	-	expression tag	UNP P62873
B	-25	HIS	-	expression tag	UNP P62873
B	-24	HIS	-	expression tag	UNP P62873
B	-23	HIS	-	expression tag	UNP P62873
B	-22	LEU	-	expression tag	UNP P62873
B	-21	GLU	-	expression tag	UNP P62873
B	-20	VAL	-	expression tag	UNP P62873
B	-19	LEU	-	expression tag	UNP P62873
B	-18	PHE	-	expression tag	UNP P62873
B	-17	GLN	-	expression tag	UNP P62873
B	-16	GLY	-	expression tag	UNP P62873
B	-15	PRO	-	expression tag	UNP P62873
B	-14	GLU	-	expression tag	UNP P62873
B	-13	ASP	-	expression tag	UNP P62873
B	-12	GLN	-	expression tag	UNP P62873
B	-11	VAL	-	expression tag	UNP P62873
B	-10	ASP	-	expression tag	UNP P62873
B	-9	PRO	-	expression tag	UNP P62873
B	-8	ARG	-	expression tag	UNP P62873
B	-7	LEU	-	expression tag	UNP P62873
B	-6	ILE	-	expression tag	UNP P62873
B	-5	ASP	-	expression tag	UNP P62873
B	-4	GLY	-	expression tag	UNP P62873
B	-3	LYS	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873

- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	38	Total	C	N	O	S	0	0
			245	154	41	47	3		

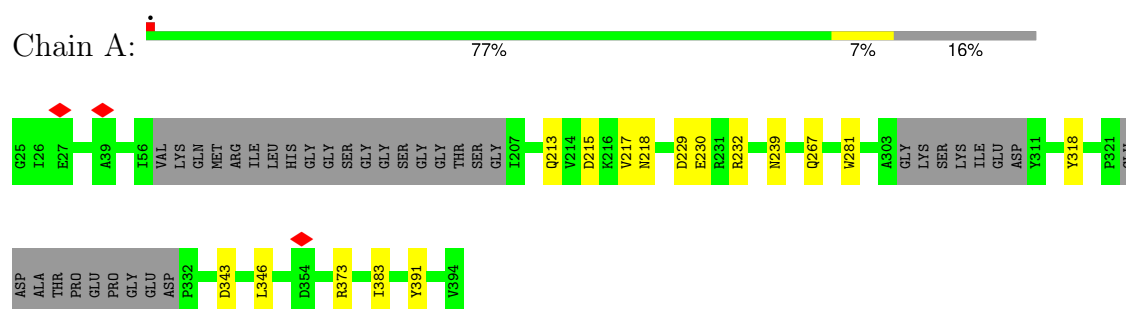
- Molecule 6 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	115	Total	C	N	O	S	0	0
			851	537	147	161	6		

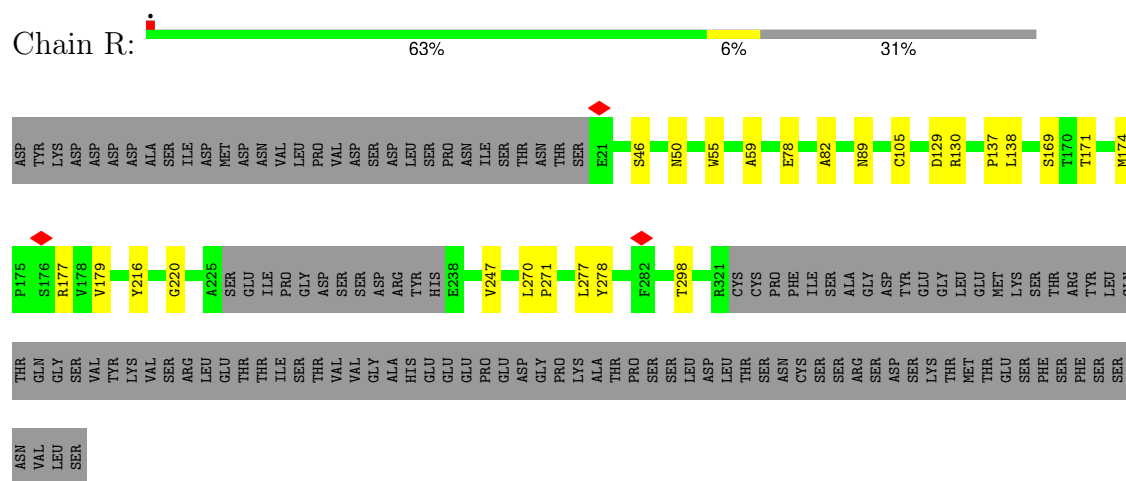
### 3 Residue-property plots [i](#)

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.

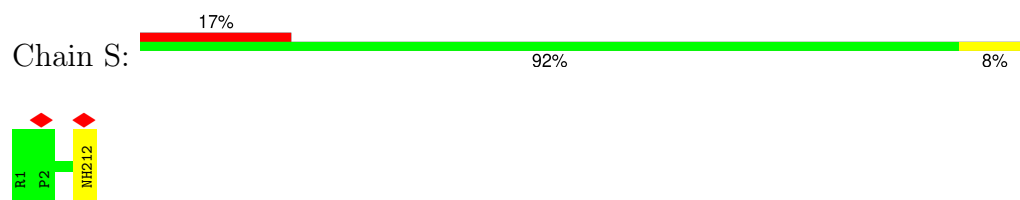
- Molecule 1: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short, with certain residues mutated to match Guanine nucleotide-binding protein G(q) subunit



- Molecule 2: Substance-P receptor



- Molecule 3: Substance P



- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

MET	HIS	HIS	HIS	HIS	HIS	LEU	GLU	VAL	LEU	PHE	GLN	GLY	PRO	GLU	ASP	ASN	VAL	ASP	PRO	ARG	LEU	ILE	ASP	GLY	LYS	GLY	SER	GLY	SER	GLU	LEU	ASP	GLN	LEU	ARG	GLN	GLU	ALA	GLU	GLU	GLU	GLN	L14	K15	A24	C25	A26	T34	N35	D38	R49	Y59
	S98	K127	THR	ARG	GLU	GLY	ASN	V133	T159	S160	G161	G162	D163	T164	T165	W169	T181	L190	S191	L192	F199	S245	D246	L252	L261	R283	Y289	D290	M295	D298	A299	L300	R314	I338	I339	R340																

- Chain G: 

MET  
 ALA  
 SER  
 ASN  
 ASN  
 THR  
 ALA  
 SER  
 ILE  
 ALA  
 GLN  
 ALA  
 R13  
 Q18  
 L19  
 E22  
 A23  
 N24  
 I25  
 D26  
 R27  
 I28  
 L50  
 LEU  
 THR  
 PRO  
 VAL  
 PRO  
 PRO  
 SER  
 SER  
 GLU  
 ASN  
 PRO  
 PHE  
 ARG  
 GLU  
 LYS  
 LYS  
 PHE  
 PHE  
 CYS

- Chain N:  69% 11% 19%

PRO	ARG	LEU	ILE	ASP	GLY	LYS	Q1	G8	GLY	LEU	VAL	GLN	PRO	GLY	GLY	SER	L18	F29	K33	A40	P41	G42	K43	D50	I51	S52	Q53	I58	T61	R72	D73	N77	T91	Y94	T104	ARG	ASP	C107	G121	V124	T125	V126	SER	SER	GLY	SER	GLU	ASP	GLN	VAL
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	122220	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 ( $e^-/\text{\AA}^2$ )	67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	13.771	Depositor
Minimum map value	-5.802	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.412	Depositor
Recommended contour level	3	Depositor
Map size ( $\text{\AA}$ )	240.48, 240.48, 240.48	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.835, 0.835, 0.835	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NH2

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	0.27	0/1542	0.49	0/2093
2	R	0.29	0/2383	0.52	0/3272
3	S	0.33	0/87	0.57	0/117
4	B	0.27	0/2365	0.59	0/3225
5	G	0.24	0/247	0.41	0/339
6	N	0.28	0/868	0.60	1/1178 (0.1%)
All	All	0.28	0/7492	0.54	1/10224 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	N	50	ASP	CB-CG-OD1	5.54	123.29	118.30

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	1510	0	1414	14	0
2	R	2306	0	2289	18	0
3	S	85	0	77	1	0
4	B	2319	0	2150	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	245	0	206	1	0
6	N	851	0	787	12	0
All	All	7316	0	6923	51	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 51 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:383:ILE:HD11	2:R:138:LEU:HD23	1.52	0.92
4:B:159:THR:HG1	4:B:169:TRP:HE1	1.44	0.66
1:A:383:ILE:CD1	2:R:138:LEU:HD23	2.26	0.65
2:R:89:ASN:HD21	3:S:12:NH2:N	1.97	0.62
6:N:94:TYR:O	6:N:121:GLY:HA2	2.04	0.57

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	185/229 (81%)	183 (99%)	2 (1%)	0	100	100
2	R	285/418 (68%)	277 (97%)	8 (3%)	0	100	100
3	S	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
4	B	318/370 (86%)	308 (97%)	10 (3%)	0	100	100
5	G	36/68 (53%)	36 (100%)	0	0	100	100
6	N	109/142 (77%)	105 (96%)	4 (4%)	0	100	100
All	All	943/1239 (76%)	918 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	A	151/201 (75%)	151 (100%)	0	100	100
2	R	242/374 (65%)	242 (100%)	0	100	100
3	S	8/10 (80%)	8 (100%)	0	100	100
4	B	224/309 (72%)	223 (100%)	1 (0%)	89	95
5	G	18/56 (32%)	18 (100%)	0	100	100
6	N	85/118 (72%)	85 (100%)	0	100	100
All	All	728/1068 (68%)	727 (100%)	1 (0%)	92	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	59	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

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.

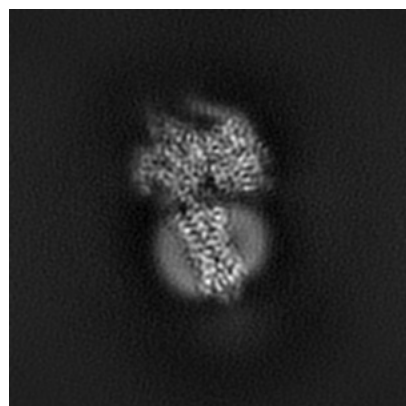
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24569. These allow visual inspection of the internal detail of the map and identification of artifacts.

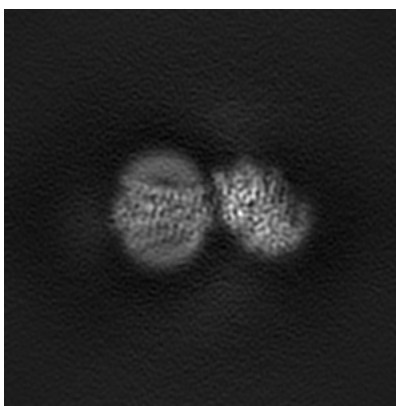
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

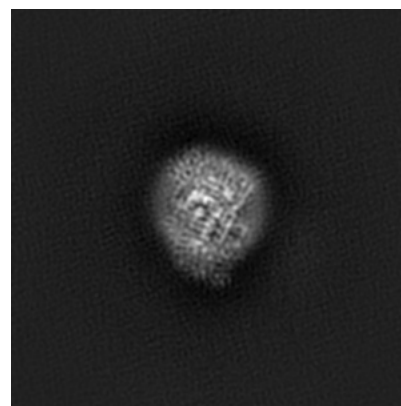
#### 6.1.1 Primary map



X

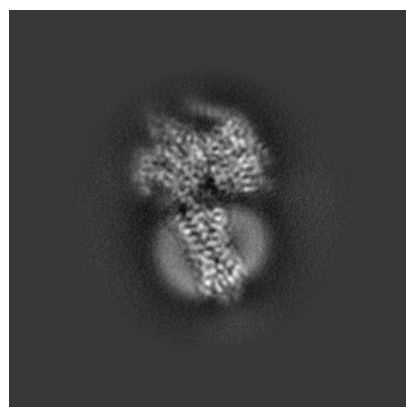


Y

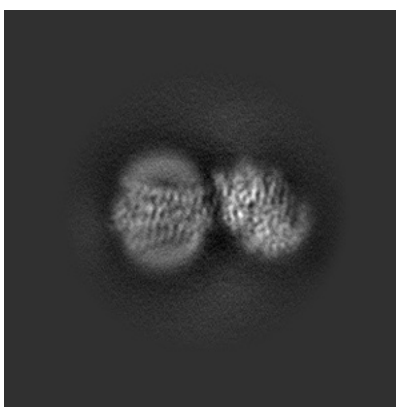


Z

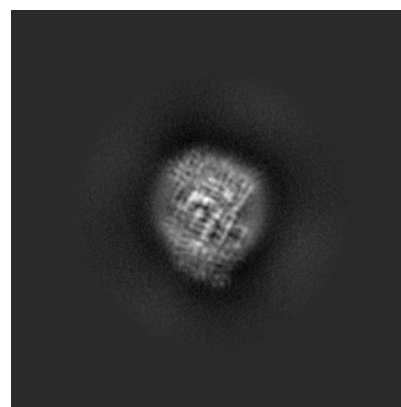
#### 6.1.2 Raw map



X



Y

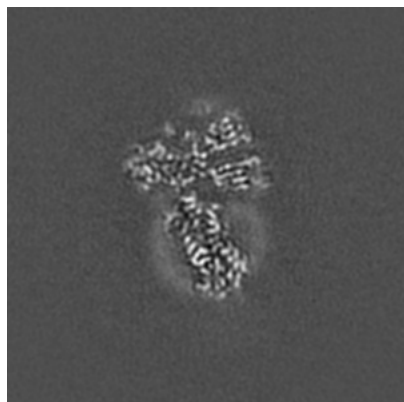


Z

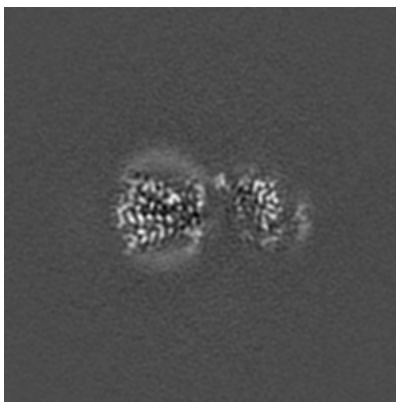
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

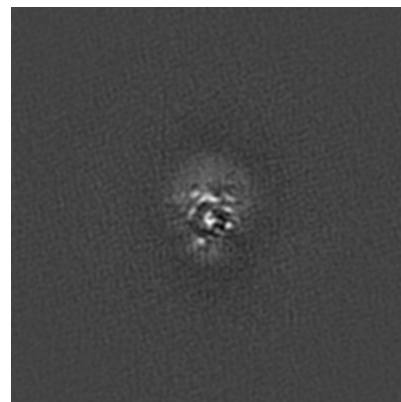
### 6.2.1 Primary map



X Index: 144

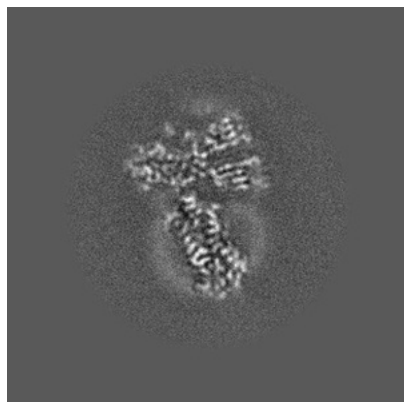


Y Index: 144

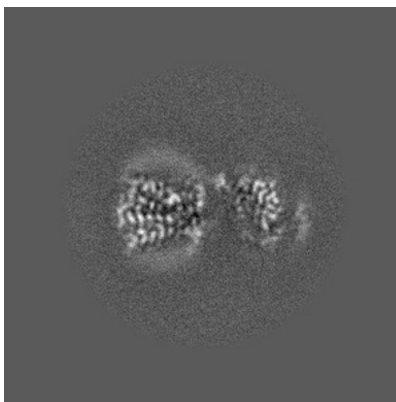


Z Index: 144

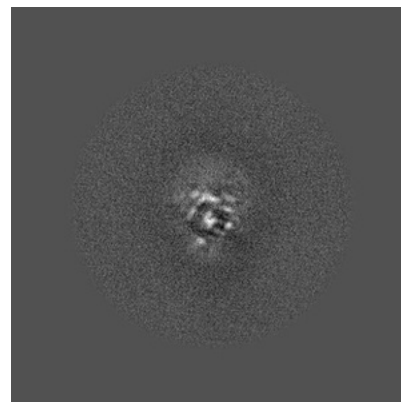
### 6.2.2 Raw map



X Index: 144



Y Index: 144

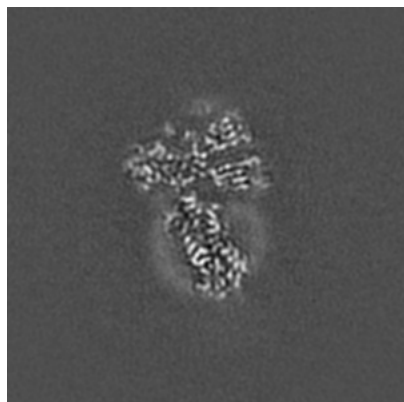


Z Index: 144

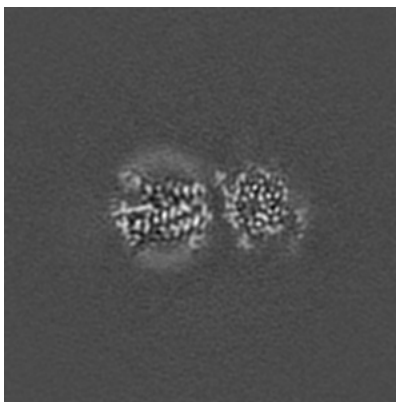
The images above show central slices of the map in three orthogonal directions.

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

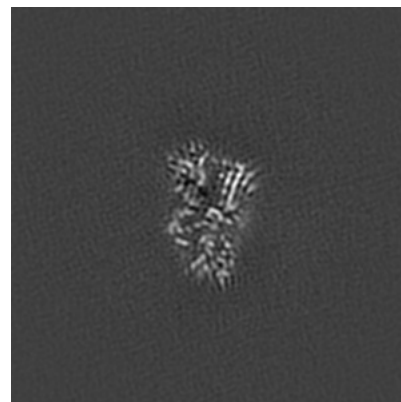
### 6.3.1 Primary map



X Index: 144

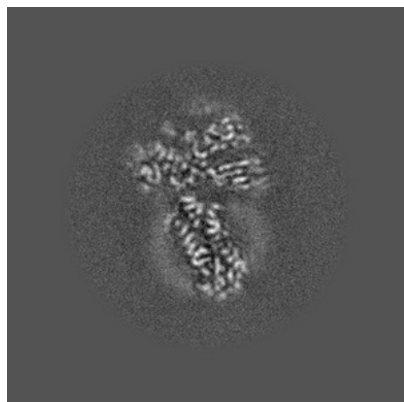


Y Index: 151

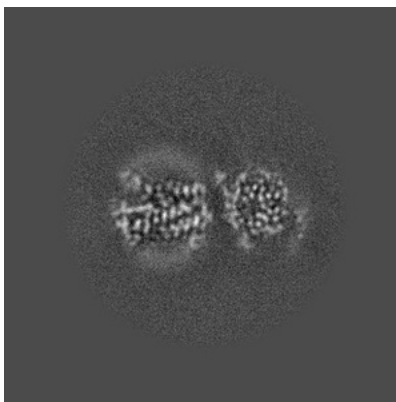


Z Index: 180

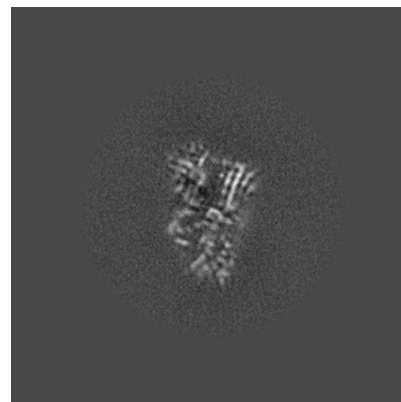
### 6.3.2 Raw map



X Index: 143



Y Index: 151



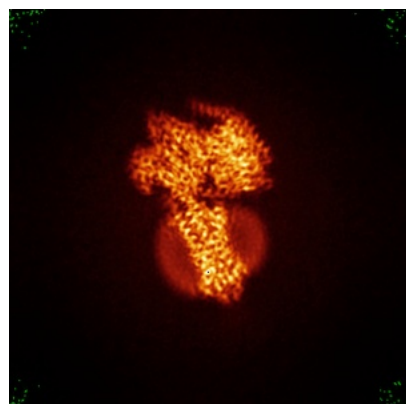
Z Index: 180

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

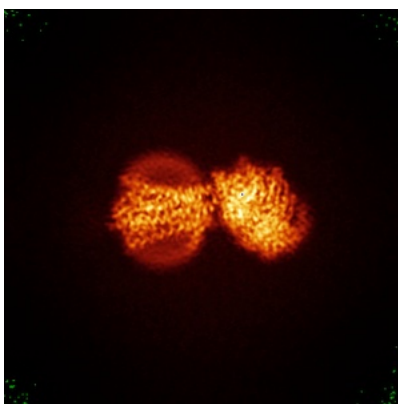


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

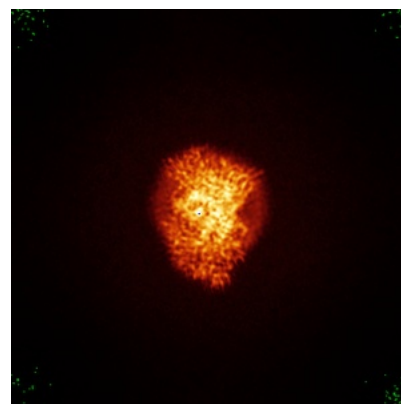
### 6.4.1 Primary map



X

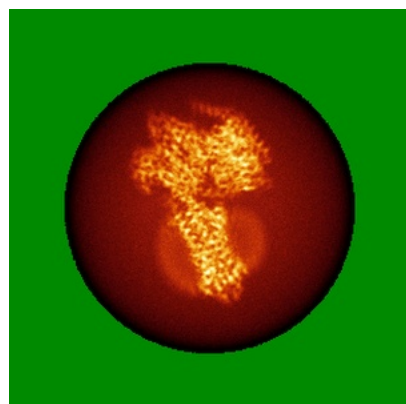


Y

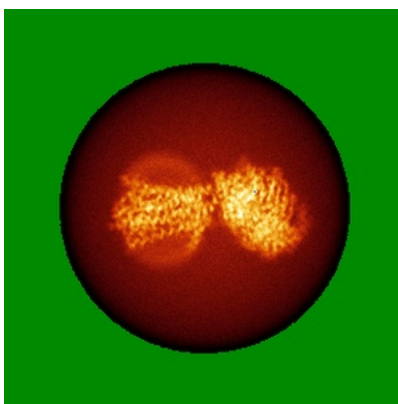


Z

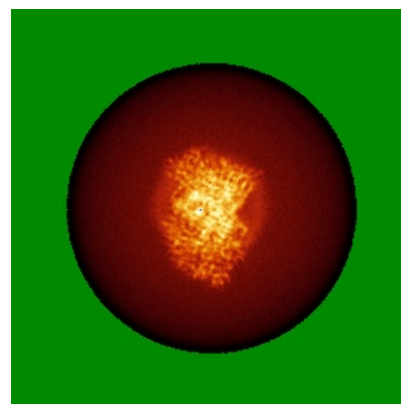
### 6.4.2 Raw map



X



Y

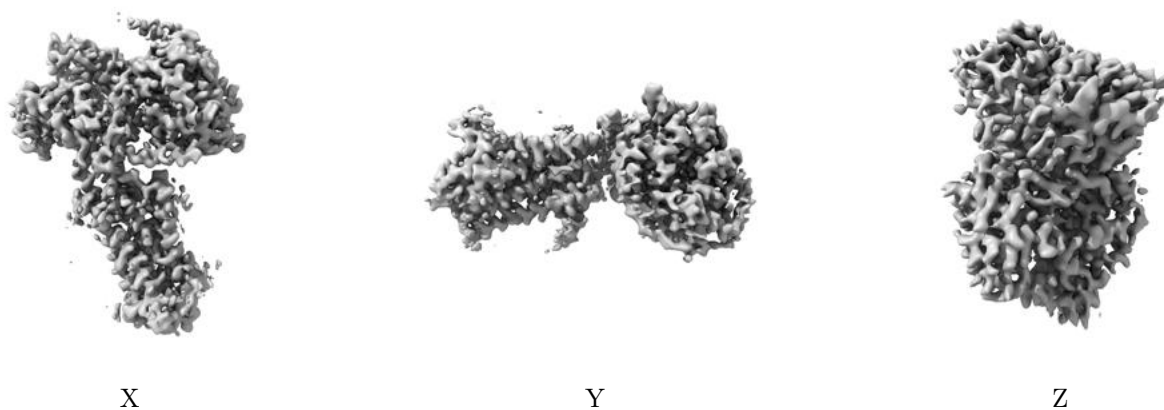


Z

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.

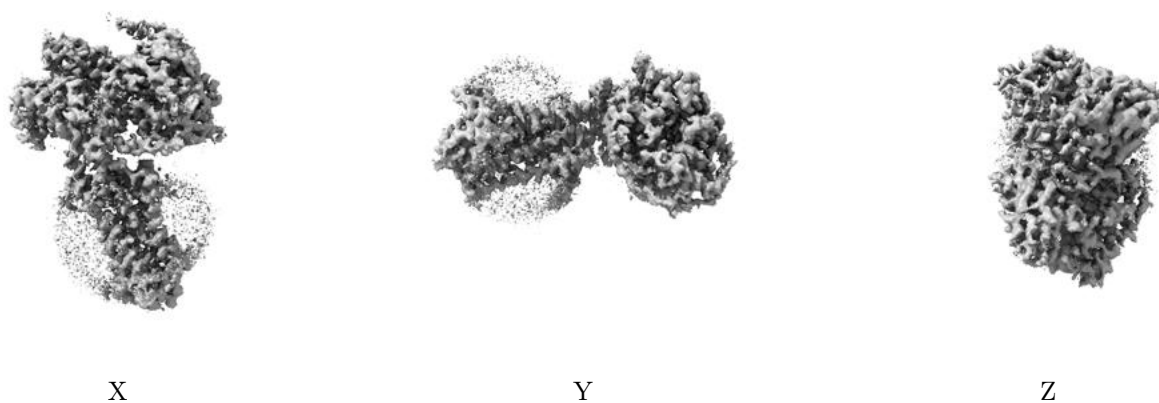
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

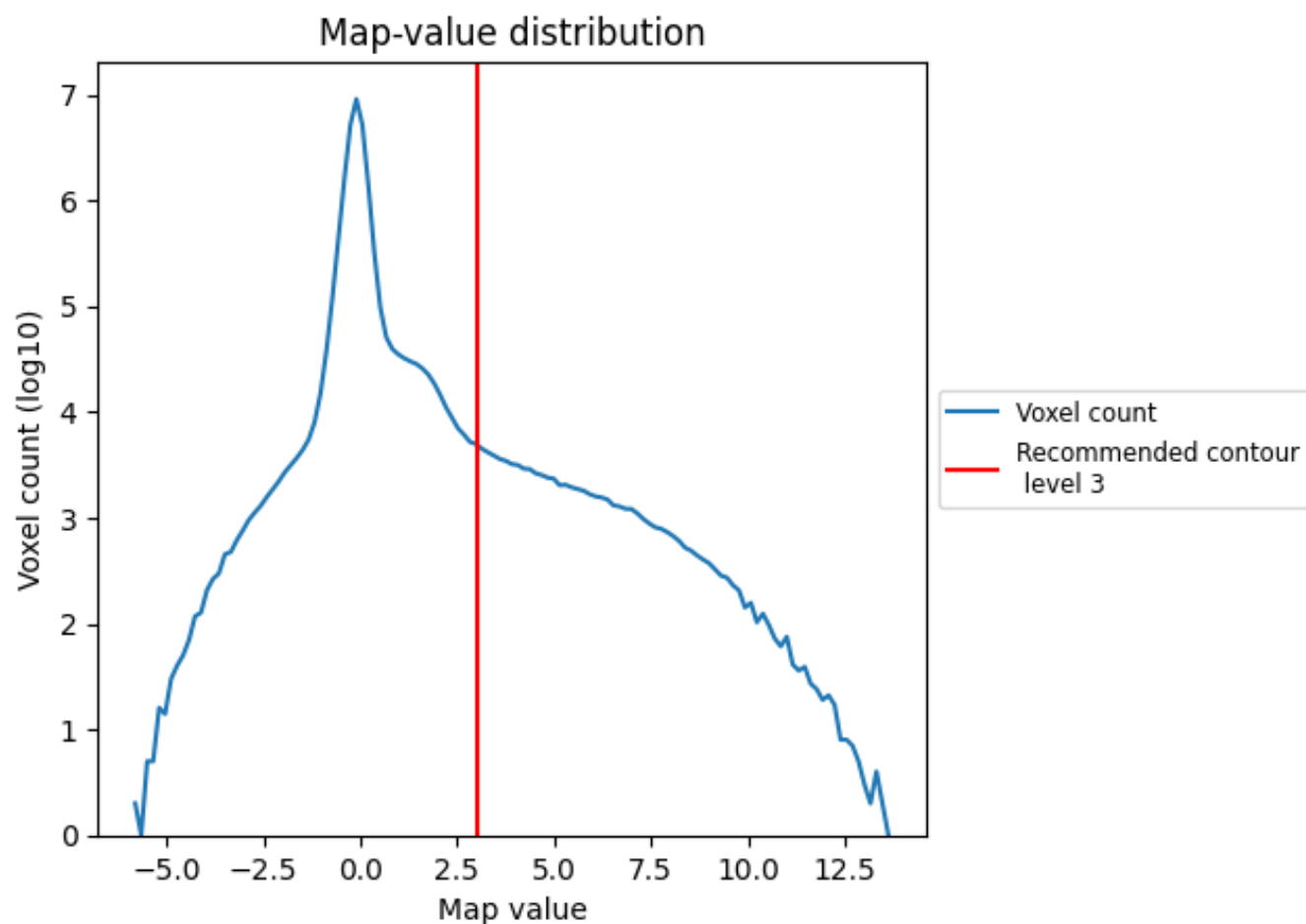
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

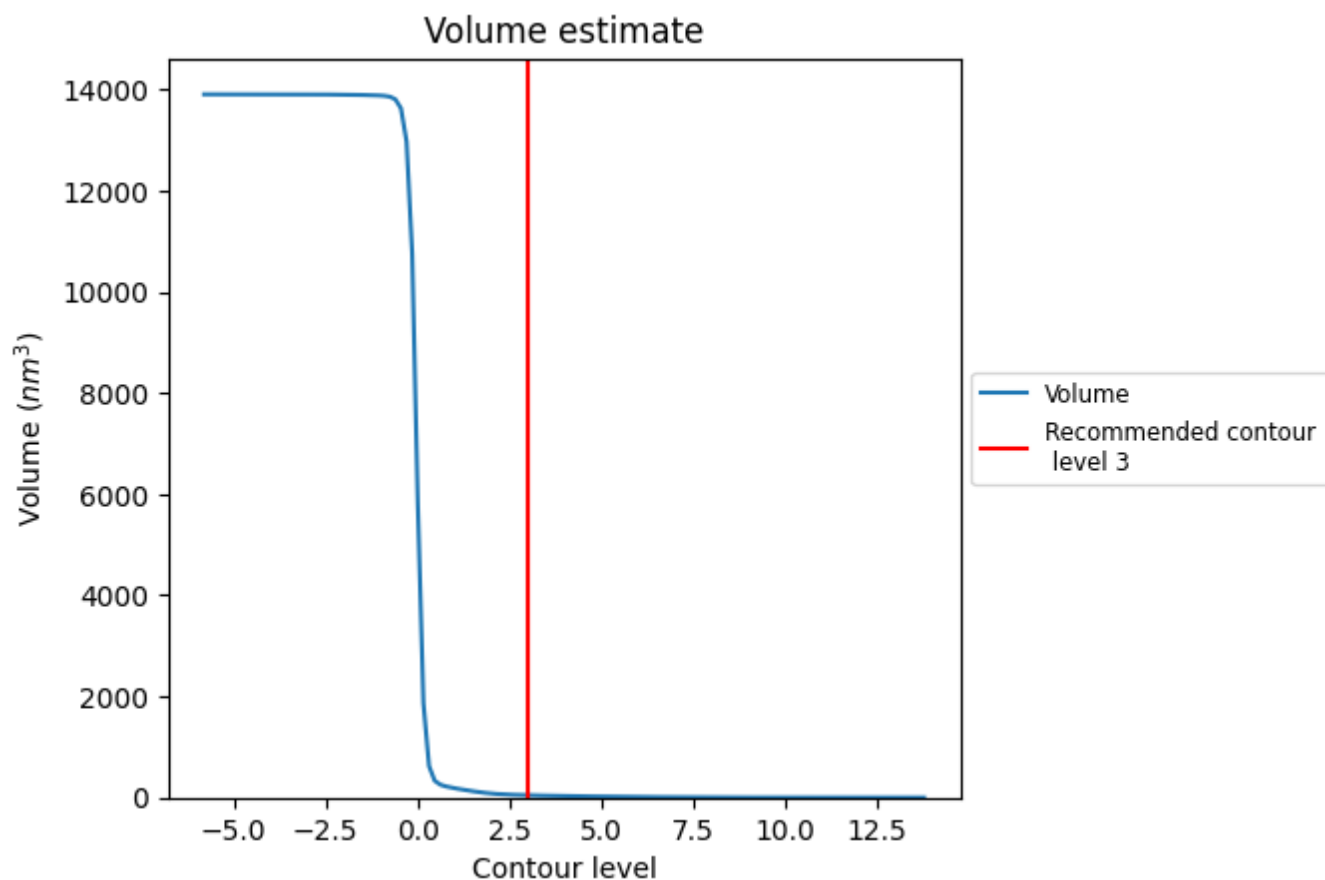
This section contains the results of statistical analysis of the map.

### 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.

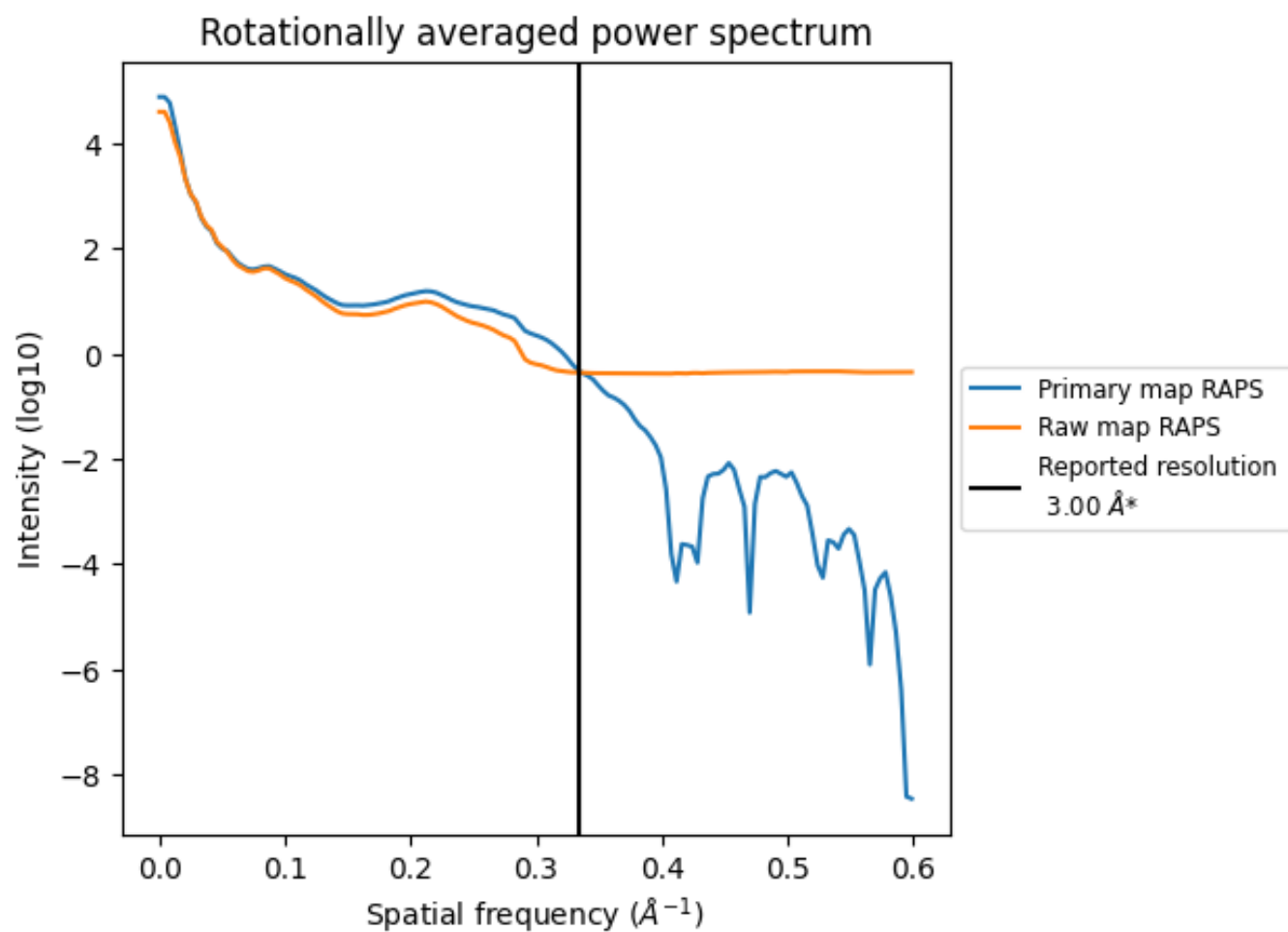
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 46  $\text{nm}^3$ ; this corresponds to an approximate mass of 41 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 ⓘ

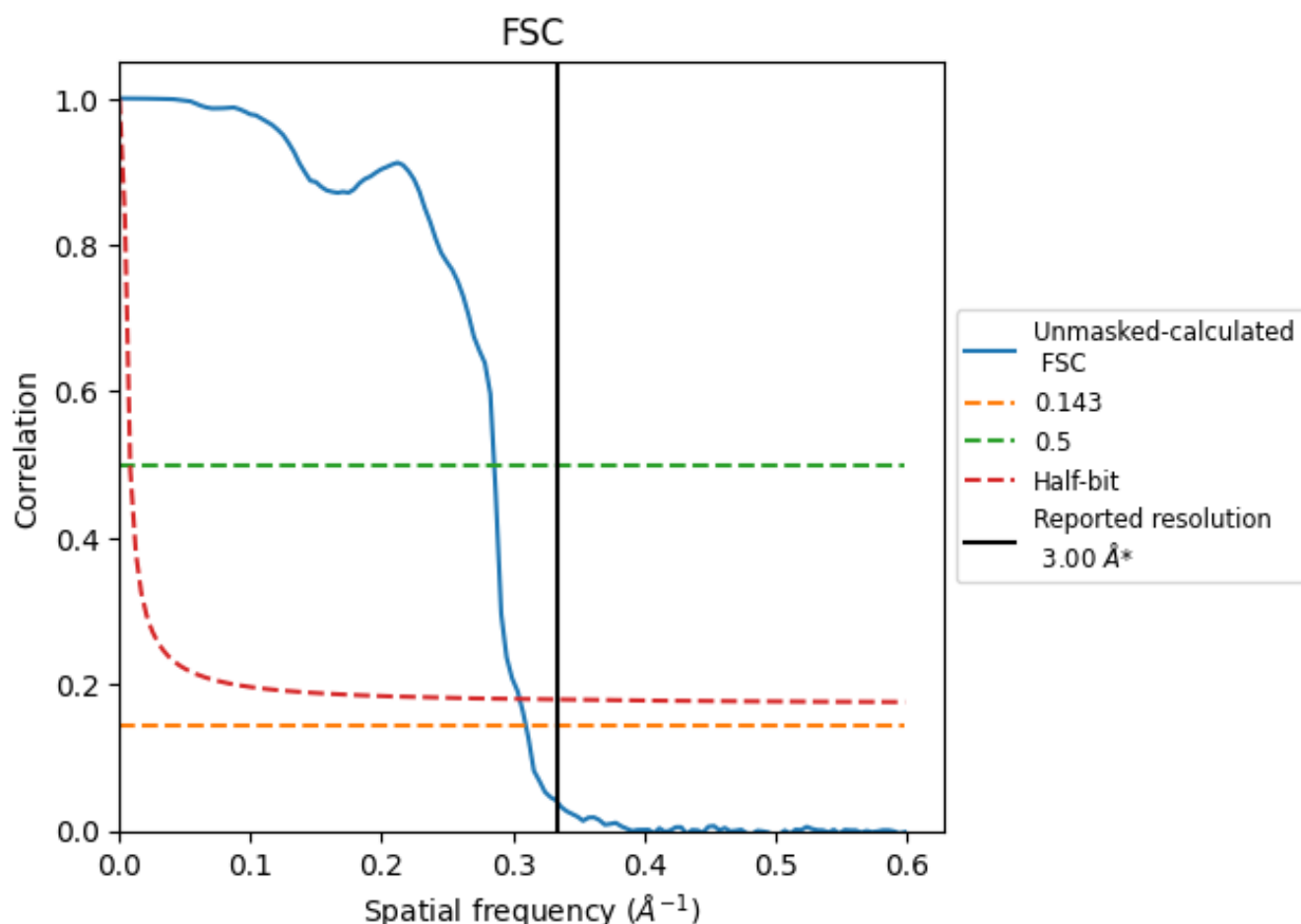


\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>

## 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 0.333 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

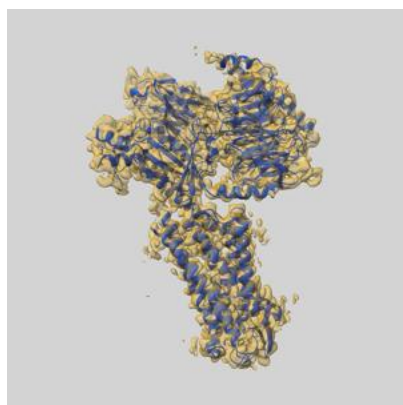
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.23	3.50	3.28

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

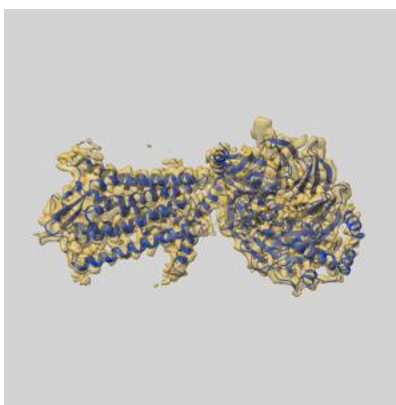
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24569 and PDB model 7RMG. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

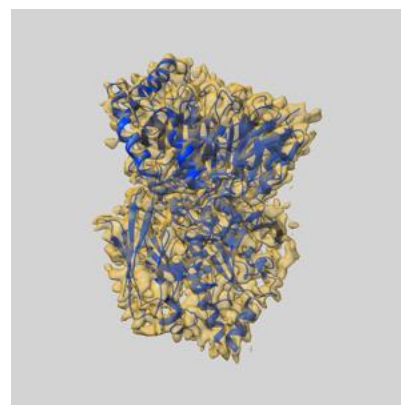
### 9.1 Map-model overlay [i](#)



X



Y

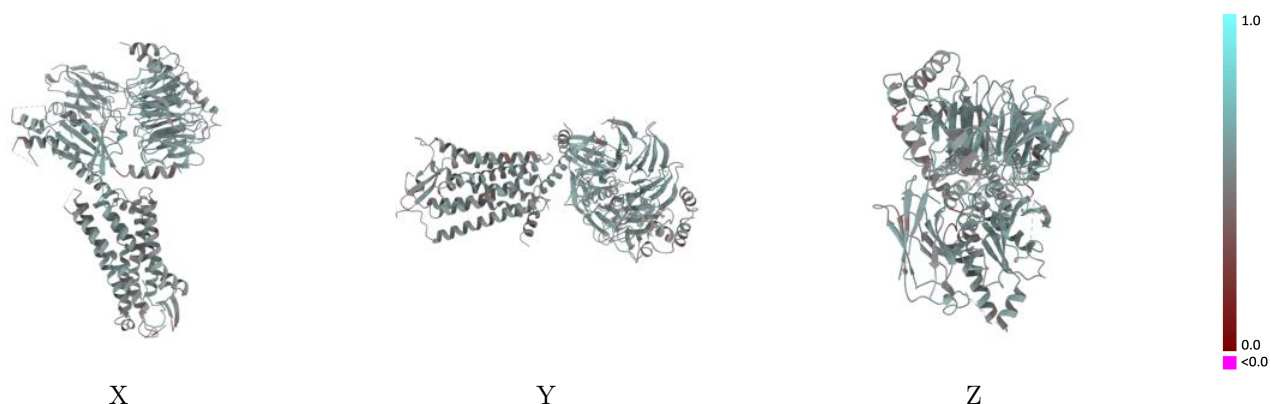


Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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.

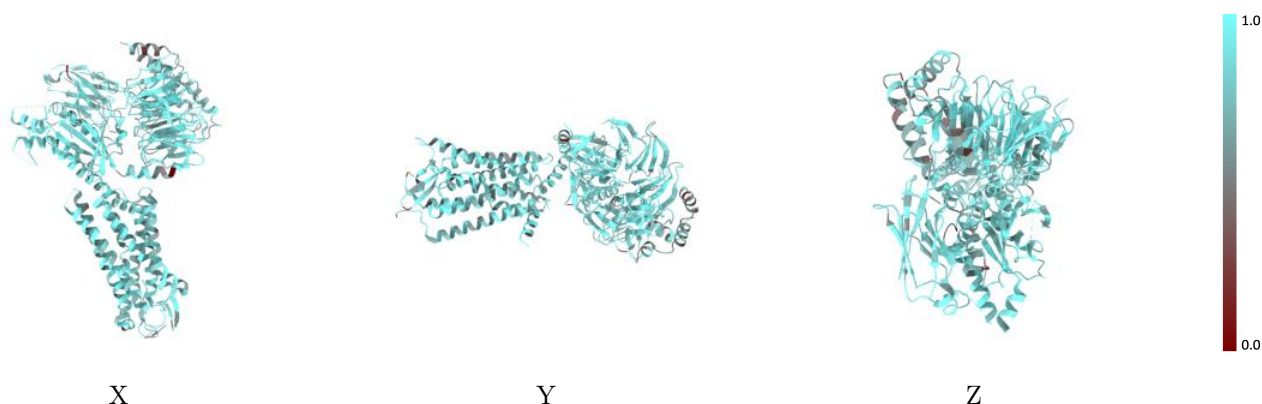


## 9.2 Q-score mapped to coordinate model [i](#)



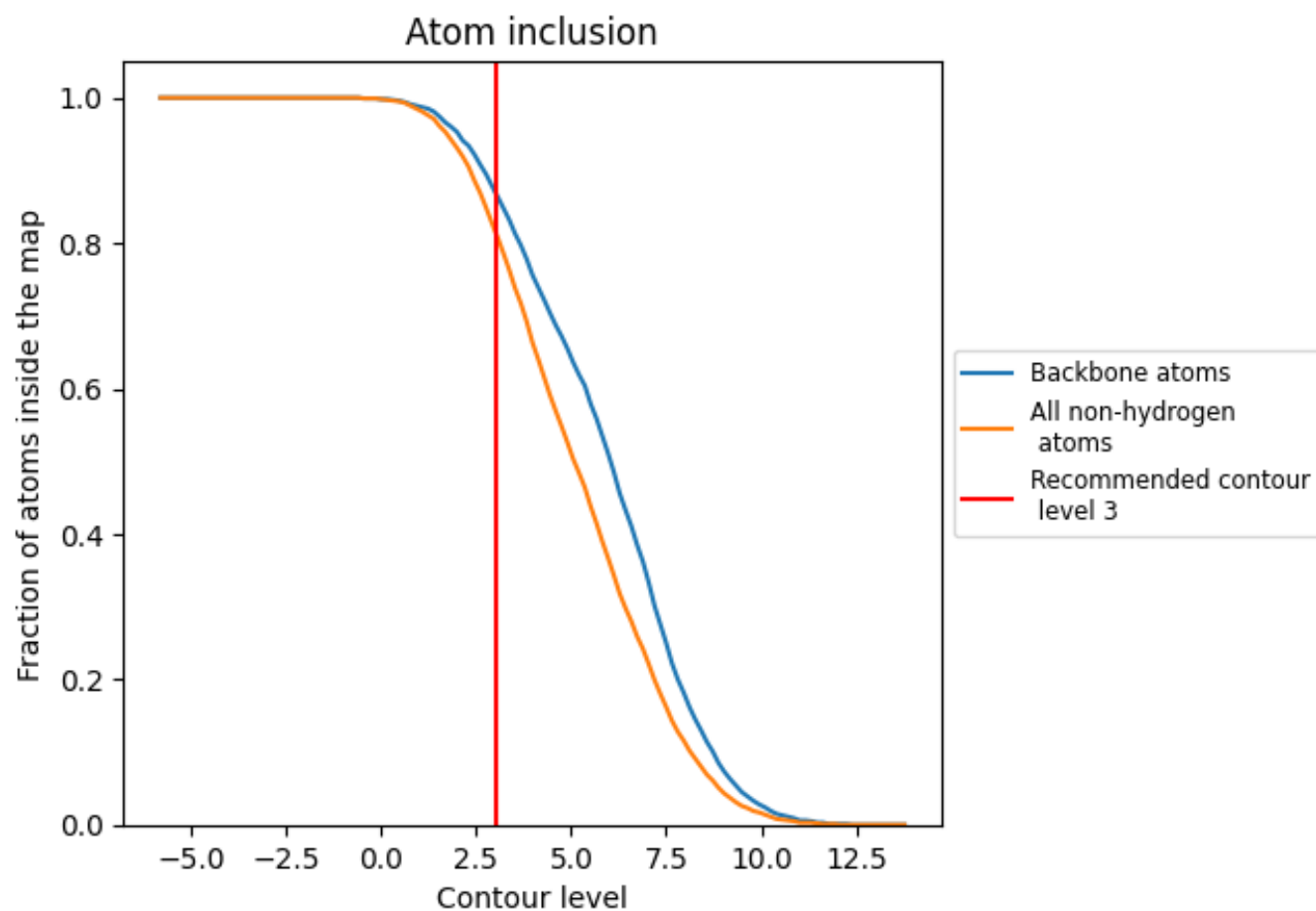
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 82% 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) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8160	<div><div></div></div> 0.5320
A	<div><div></div></div> 0.8270	<div><div></div></div> 0.5430
B	<div><div></div></div> 0.8290	<div><div></div></div> 0.5500
G	<div><div></div></div> 0.6310	<div><div></div></div> 0.4920
N	<div><div></div></div> 0.8160	<div><div></div></div> 0.5300
R	<div><div></div></div> 0.8180	<div><div></div></div> 0.5120
S	<div><div></div></div> 0.7650	<div><div></div></div> 0.5240

1.0

0.0

<0.0