



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:50 PM UTC

PDB ID : 7X10 / pdb_00007x10
EMDB ID : EMD-32932
Title : ADGRL3/miniG12 complex
Authors : He, Y.; Qian, Y.
Deposited on : 2022-02-22
Resolution : 2.93 Å(reported)
Based on initial model : 6VMS

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

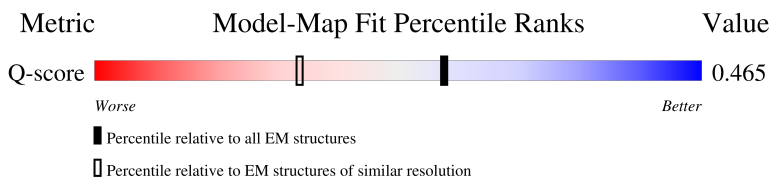
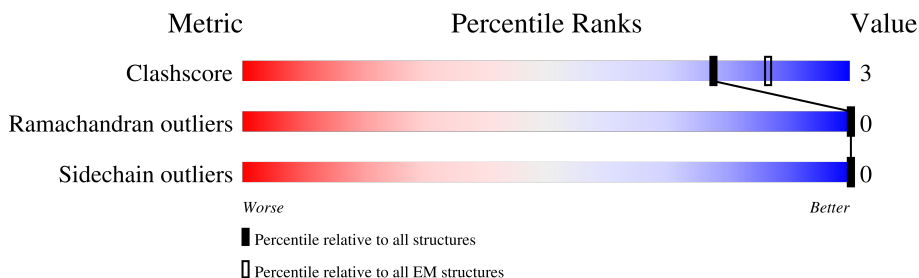
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.93 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	13037 (2.43 - 3.43)

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

Mol	Chain	Length	Quality of chain
1	A	345	
2	B	345	
3	E	247	
4	G	71	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	R	1543	15% . 83%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8674 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 engineered G alpha 12 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	211	Total	C	N	O	S	0	0
			1744	1115	315	305	9		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	338	Total	C	N	O	S	0	0
			2600	1604	467	508	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P62873
B	-3	GLY	-	expression tag	UNP P62873
B	-2	SER	-	expression tag	UNP P62873
B	-1	LEU	-	expression tag	UNP P62873
B	0	LEU	-	expression tag	UNP P62873
B	1	GLN	-	expression tag	UNP P62873

- Molecule 3 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	230	Total	C	N	O	S	0	0
			1771	1125	293	343	10		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	57	Total	C	N	O	S	0	0
			436	273	77	83	3		

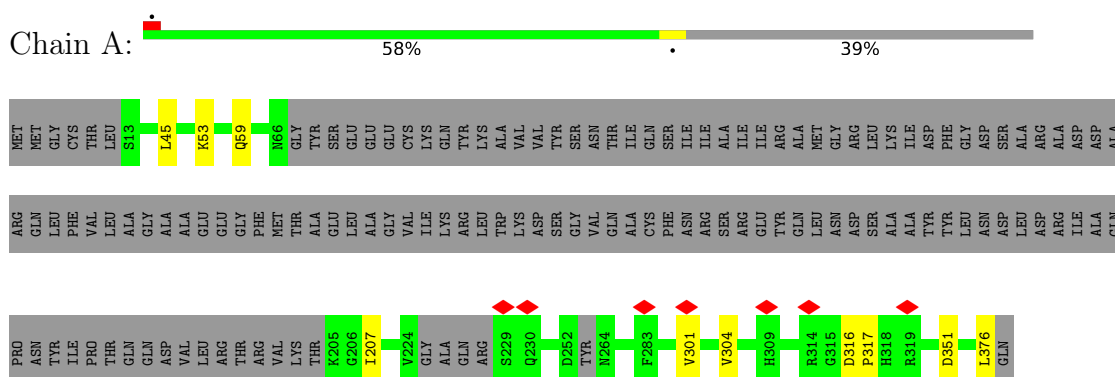
- Molecule 5 is a protein called Isoform 3 of Adhesion G protein-coupled receptor L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	R	262	2123	1429	334	342	18	0	0

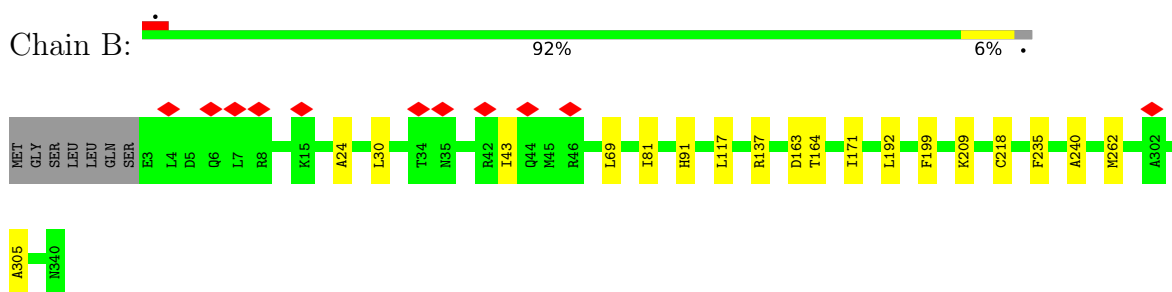
3 Residue-property plots

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.

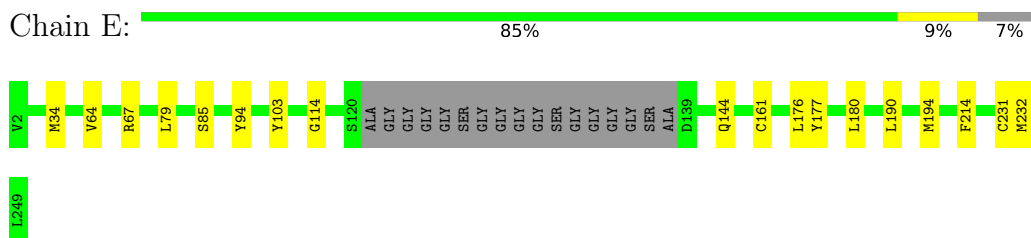
- Molecule 1: engineered G alpha 12 subunit



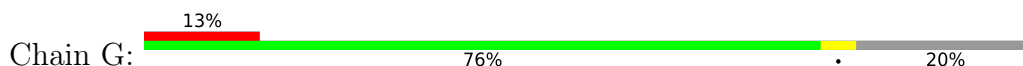
- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 3: scFv16



- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2





VAL	VAL	VAL	VAL	ASN	SER	SER	ALA
THR	THR	THR	HIS	GLU	VAL	THR	ILE
THR	THR	THR	GLU	GLU	MET	THR	LEU
THR	THR	THR	ARG	ARG	ASP	PRO	PRO
GLN	ASN	ASN	SER	SER	THR	GLY	LYS
GLN	HIS	GLU	SER	PRO	LEU	ARG	GLU
GLU	GLN	GLN	GLU	TYR	THR	SER	GLY
PRO	ASN	ASN	ASN	ASN	ASN	THR	SER
ALA	HIS	ARG	ARG	GLY	GLY	THR	CYS
ALA	ALA	ASN	ASN	ASN	SER	GLN	ASP
ALA	HIS	MET	MET	HIS	GLN	ASN	ASN
LEU	TYR	SER	GLY	GLY	SER	ILE	ASN
VAL	LYS	SER	MET	ASN	THR	ASN	ILE
THR	GLY	GLY	ASN	ASN	ARG	ASN	ASN
SER	ASP	ASP	LEU	TYR	THR	ARG	GLU
LEU	ASP	ALA	LEU	VAL	SER	ARG	ASP
	GLU	GLU	PRO	ASN	ILE	MET	ASN
	ASP	GLN	ASN	ALA	TRP	ARG	ARG
VAL	VAL	ASP	LEU	GLY	ASN	PRO	PRO
TYR	TYR	HIS	GLY	GLY	ASP	PHE	PHE
TYR	TYR	SER	SER	SER	GLU	THR	ILE
LYS	LYS	GLU	GLY	GLY	TYR	VAL	LYS
SER	SER	SER	SER	SER	LEU	ARG	SER
MET	MET	PHE	GLU	GLU	SER	LYS	91143
PRO	PRO	PHE	ASP	ASP	ASN	GLN	91143
ASN	ASN	ASN	GLU	CYS	SER	SER	T1177
LEU	LEU	LEU	ALA	VAL	GLU	SER	T1177
GLY	GLY	ILE	ILE	GLN	SER	SER	S1181
SER	SER	VAL	VAL	ILE	SER	PHE	S1181
ARG	ARG	ASP	LEU	ILE	ILE	ILE	F1188
ASN	ASN	ASP	ASP	ASP	ASP	ILE	F1188
HIS	HIS	HIS	ASP	ASN	THR	THR	C1192
VAL	THR	ALA	ALA	GLY	GLY	THR	C1192
GLU	GLU	ALA	ALA	TYR	ASP	ASP	E1201
PRO	ASP	ASP	SER	ASN	ILE	ILE	E1201
LEU	LEU	LEU	PHE	HIS	ASN	ASN	Y1202
HIS	GLN	ASN	ASN	ASN	SER	SER	Y1202
ALA	SER	HIS	GLU	GLU	SER	SER	G1203
TYR	PRO	GLU	HIS	THR	SER	SER	G1203
TYR	HIS	GLU	GLU	ALA	ALA	ALA	L1206
GLN	ARG	SER	SER	LEU	LEU	SER	L1206
GLY	SER	GLY	GLY	GLU	ASN	HIS	A1207
ARG	ARG	LEU	LEU	LYS	ARG	CYS	A1207
GLY	TYR	LEU	LEU	ILE	GLU	CYS	T1208
SER	THR	THR	LEU	LEU	PRO	SER	T1208
SER	SER	SER	LEU	TYR	THR	GLY	GLY
GLY	PHE	ALA	SER	THR	THR	GLU	THR
VAL	ILE	LEU	LEU	GLU	THR	LYS	THR
PRO	VAL	ALA	ASP	ASP	LEU	SER	SER
PRO	GLY	GLY	ALA	ASN	LEU	ILE	ILE
ASN	PRO	GLY	ALA	TYR	LEU	GLY	GLY
LYS	ASN	VAL	PRO	ILE	ASN	ASN	ASN
ASP	ASN	ALA	LEU	PRO	ASN	ALA	GLY
GLY	ASP	ALA	LEU	SER	THR	LYS	LYS
ALA	ASP	ASP	PRO	THR	ARG	ASP	THR
	GLY	ASP	PRO	LEU	THR	SER	SER
	ALA	ALA	ARG	ASN	THR	CYS	CYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	320000	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.946	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.23	0/1771	0.43	0/2369
2	B	0.23	0/2647	0.50	0/3589
3	E	0.33	0/1815	0.55	0/2461
4	G	0.15	0/442	0.38	0/597
5	R	0.25	0/2181	0.47	1/2960 (0.0%)
All	All	0.25	0/8856	0.49	1/11976 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	1009	ALA	N-CA-C	-8.97	99.88	113.51

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1744	0	1799	6	0
2	B	2600	0	2505	11	0
3	E	1771	0	1709	16	0
4	G	436	0	448	2	0
5	R	2123	0	2172	19	0
All	All	8674	0	8633	50	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 3.

The worst 5 of 50 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)
3:E:144:GLN:HG3	3:E:244:GLY:H	1.38	0.89
3:E:144:GLN:NE2	3:E:231:CYS:SG	2.51	0.83
5:R:966:THR:HG23	5:R:1202:TYR:HE2	1.53	0.72
2:B:137:ARG:NH1	2:B:171:ILE:O	2.27	0.68
5:R:966:THR:HG23	5:R:1202:TYR:CE2	2.28	0.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	203/345 (59%)	179 (88%)	24 (12%)	0	100	100
2	B	336/345 (97%)	317 (94%)	19 (6%)	0	100	100
3	E	226/247 (92%)	211 (93%)	15 (7%)	0	100	100
4	G	55/71 (78%)	55 (100%)	0	0	100	100
5	R	258/1543 (17%)	235 (91%)	23 (9%)	0	100	100
All	All	1078/2551 (42%)	997 (92%)	81 (8%)	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	197/306 (64%)	197 (100%)	0	100	100
2	B	281/287 (98%)	281 (100%)	0	100	100
3	E	195/198 (98%)	195 (100%)	0	100	100
4	G	46/58 (79%)	46 (100%)	0	100	100
5	R	228/1331 (17%)	228 (100%)	0	100	100
All	All	947/2180 (43%)	947 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	354	ASN
2	B	259	GLN
3	E	39	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 ⓘ

There are no chain breaks in this entry.

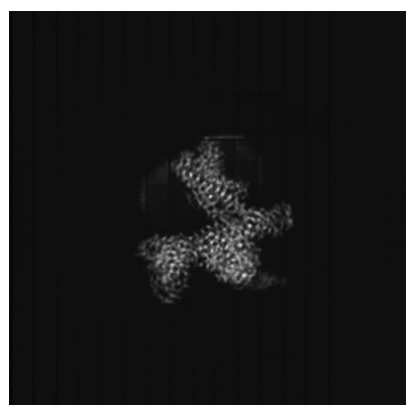
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32932. These allow visual inspection of the internal detail of the map and identification of artifacts.

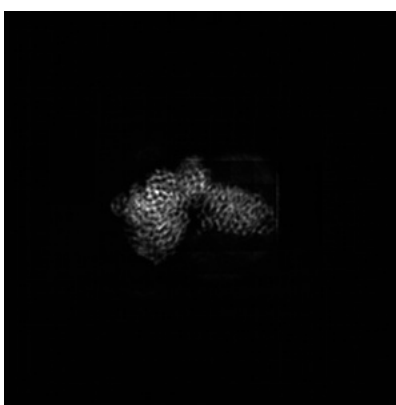
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

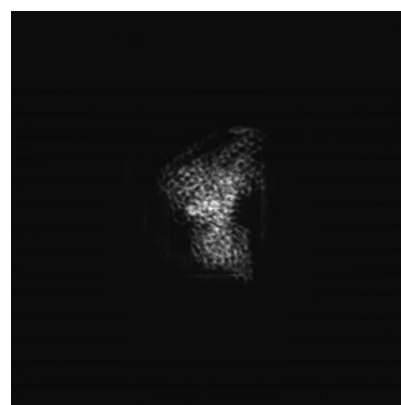
6.1.1 Primary map



X



Y

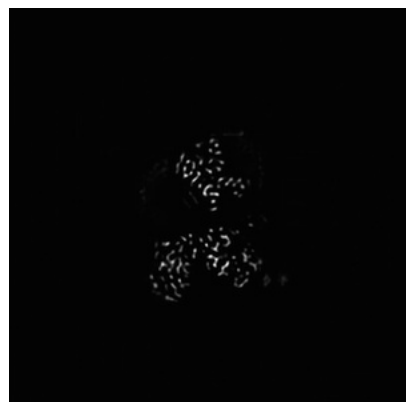


Z

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

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: 139



Y Index: 129

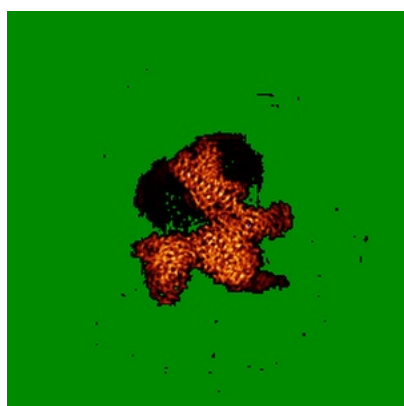


Z Index: 97

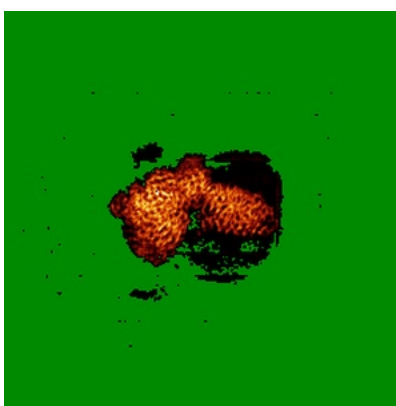
The images above show the largest variance slices of the map in three orthogonal directions.

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

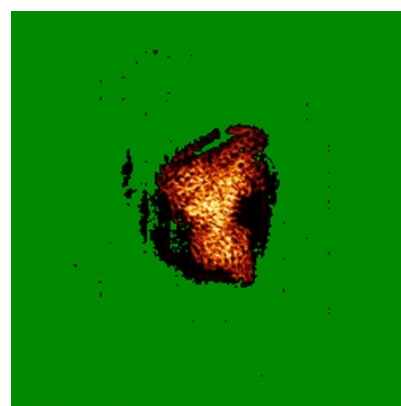
6.4.1 Primary map



X



Y

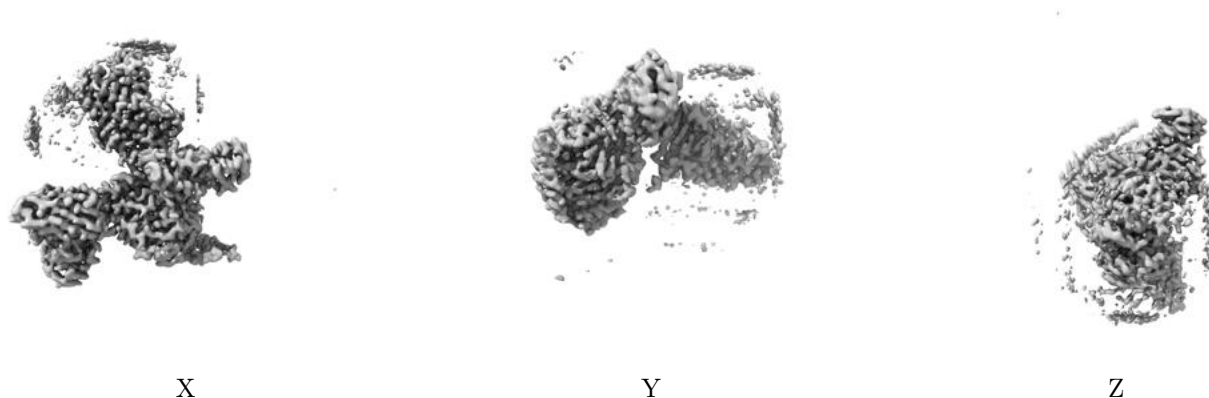


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

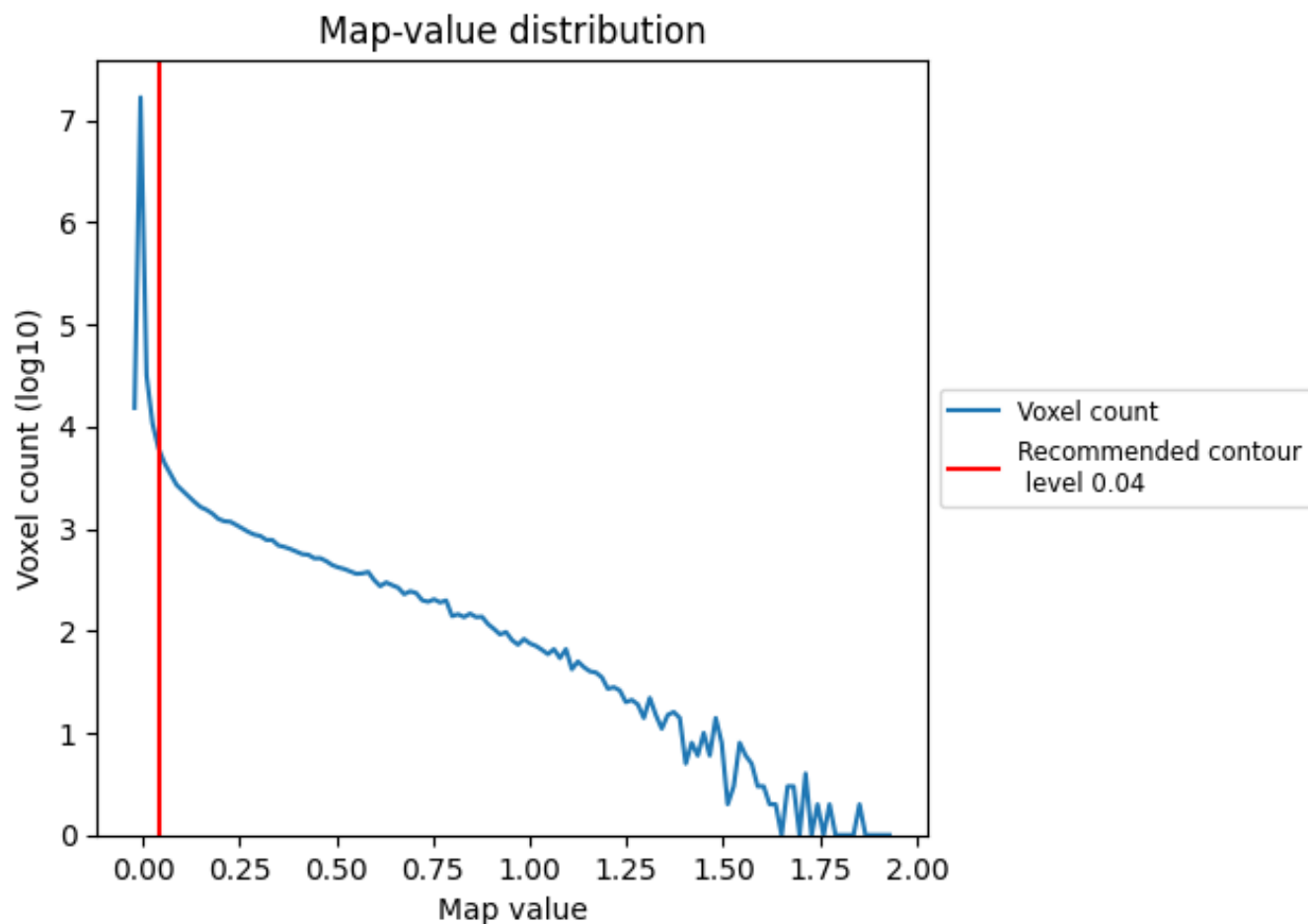
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

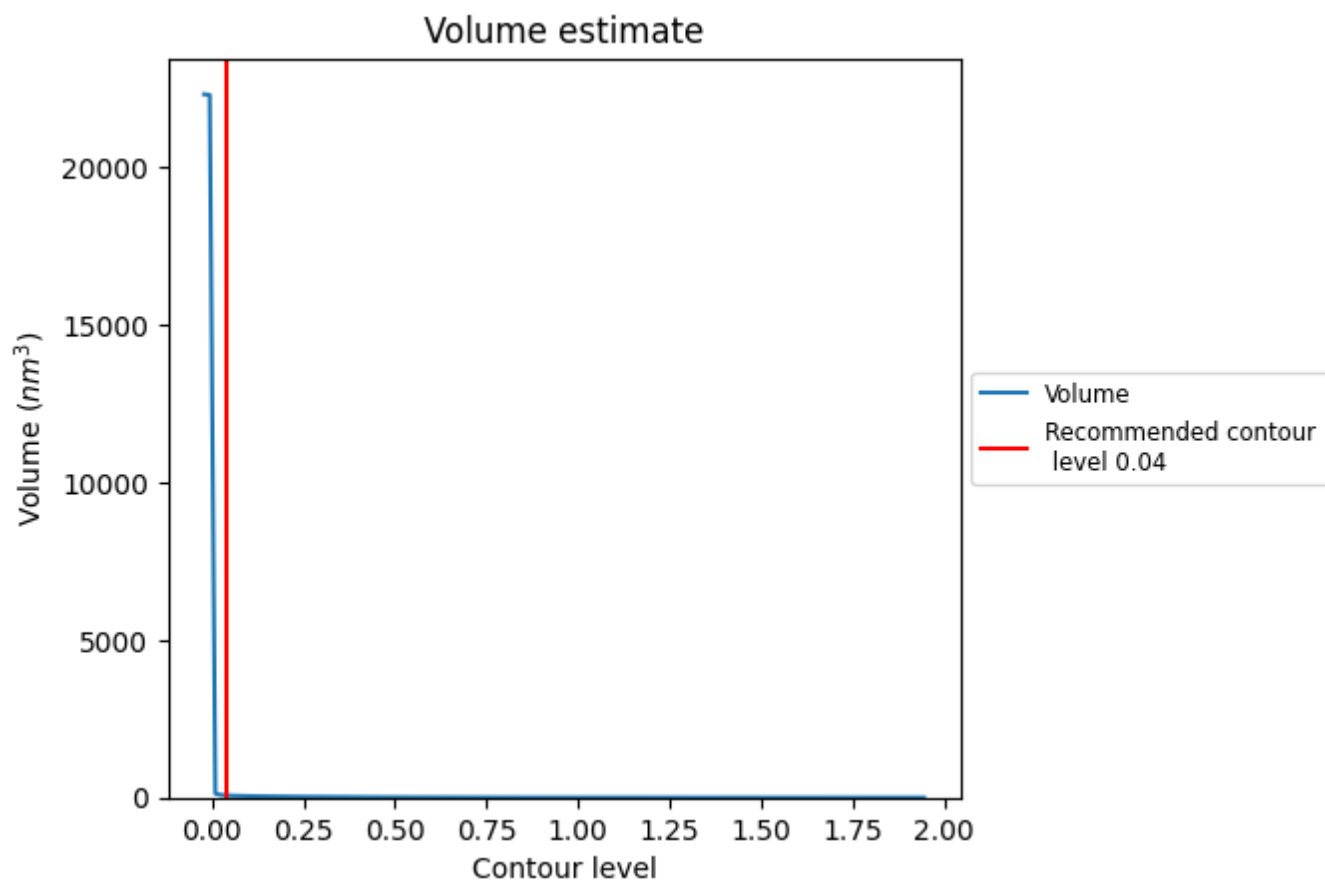
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

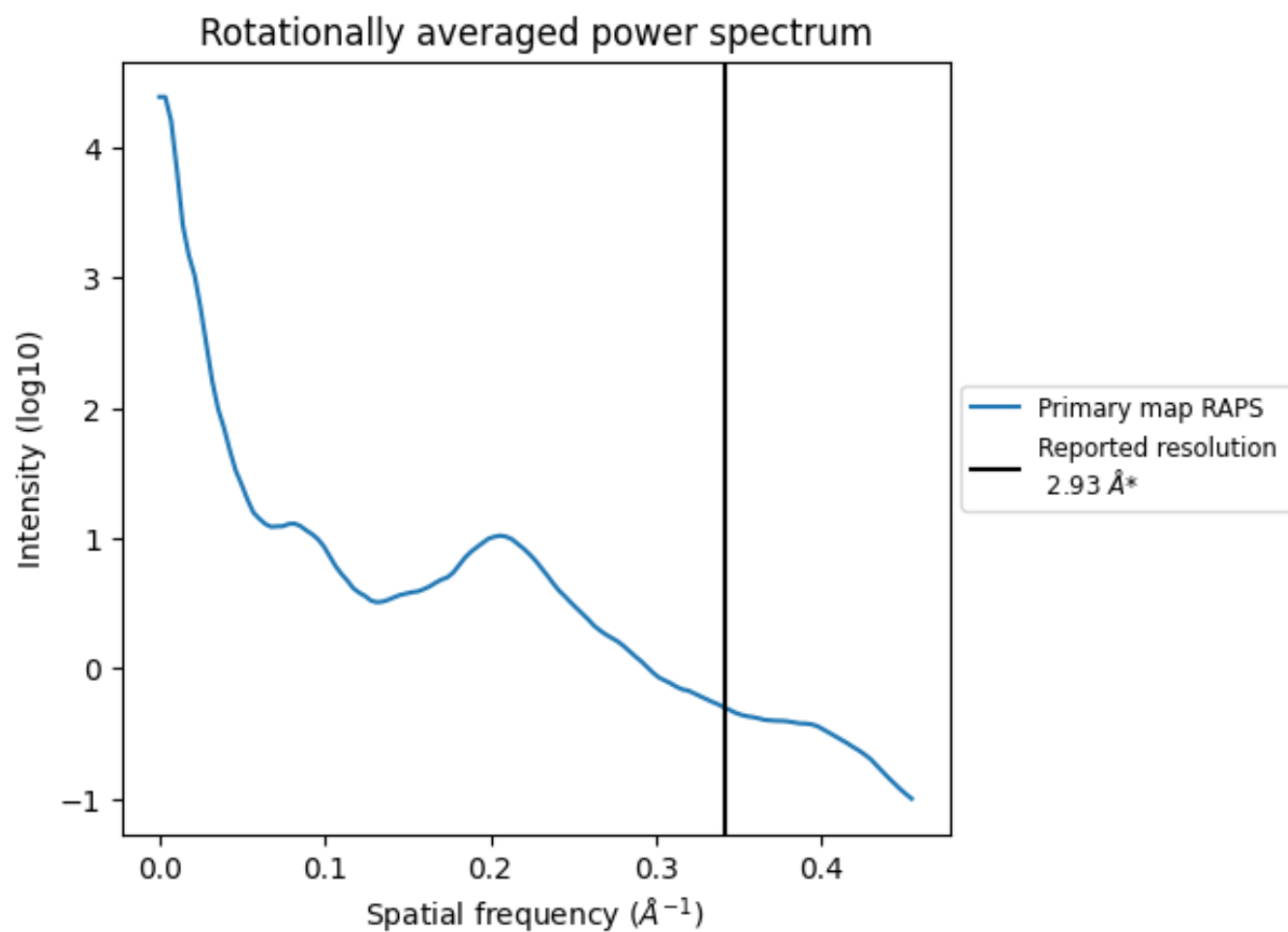
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 68 nm^3 ; this corresponds to an approximate mass of 61 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 ⓘ

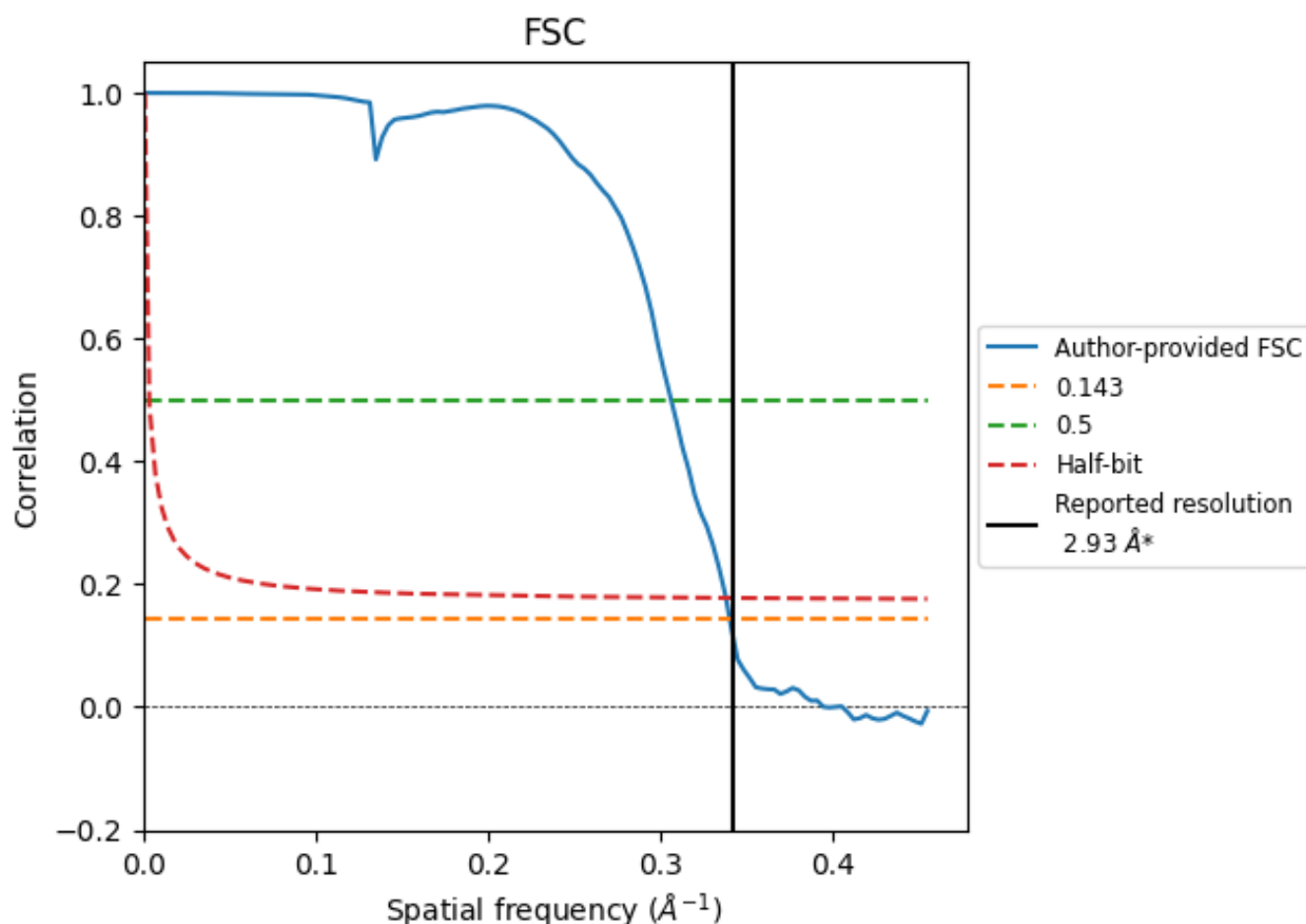


*Reported resolution corresponds to spatial frequency of 0.341 Å⁻¹

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 0.341 Å⁻¹

8.2 Resolution estimates [i](#)

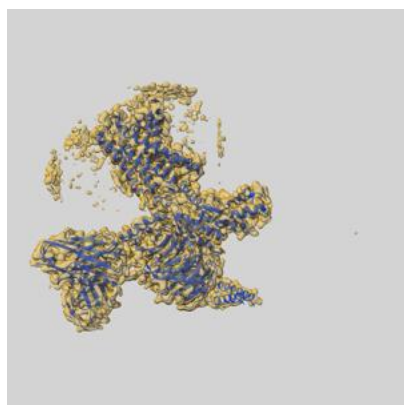
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.93	-	-
Author-provided FSC curve	2.94	3.27	2.96
Unmasked-calculated*	-	-	-

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

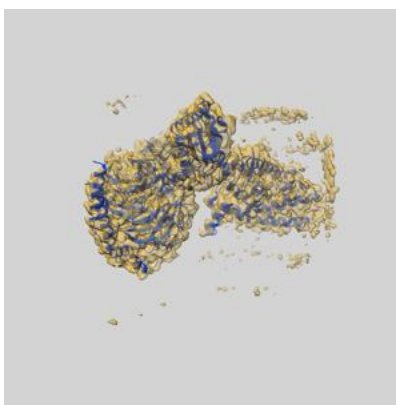
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32932 and PDB model 7X10. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

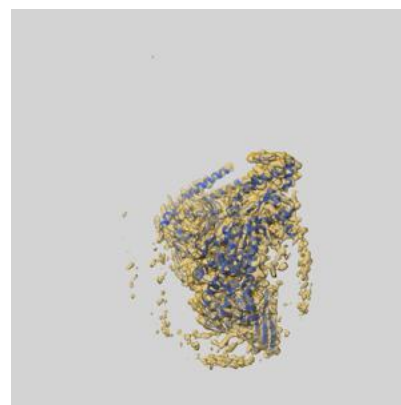
9.1 Map-model overlay [i](#)



X



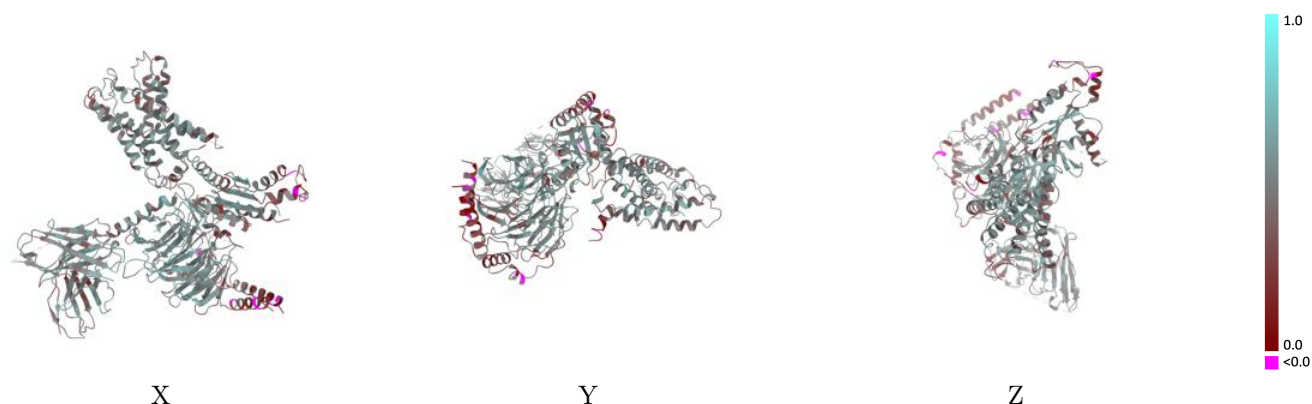
Y



Z

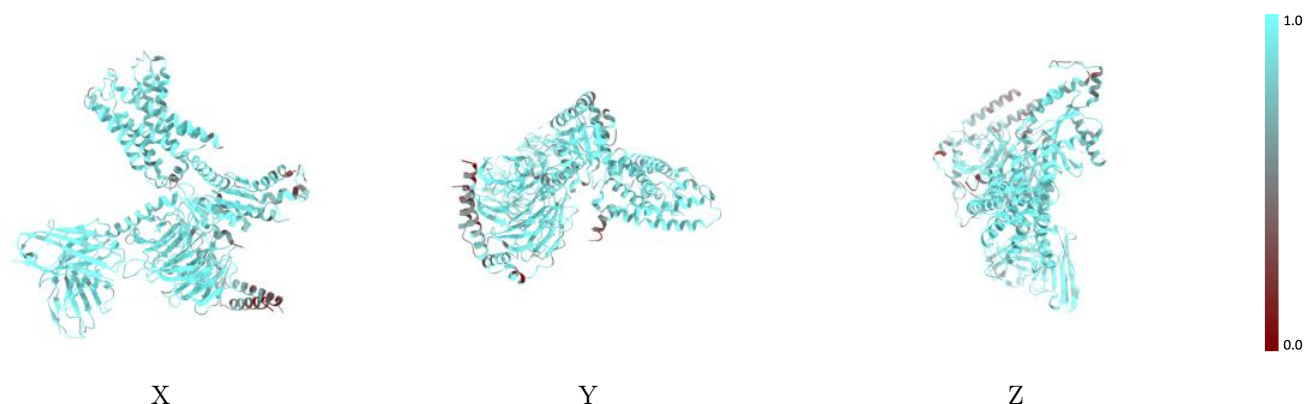
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



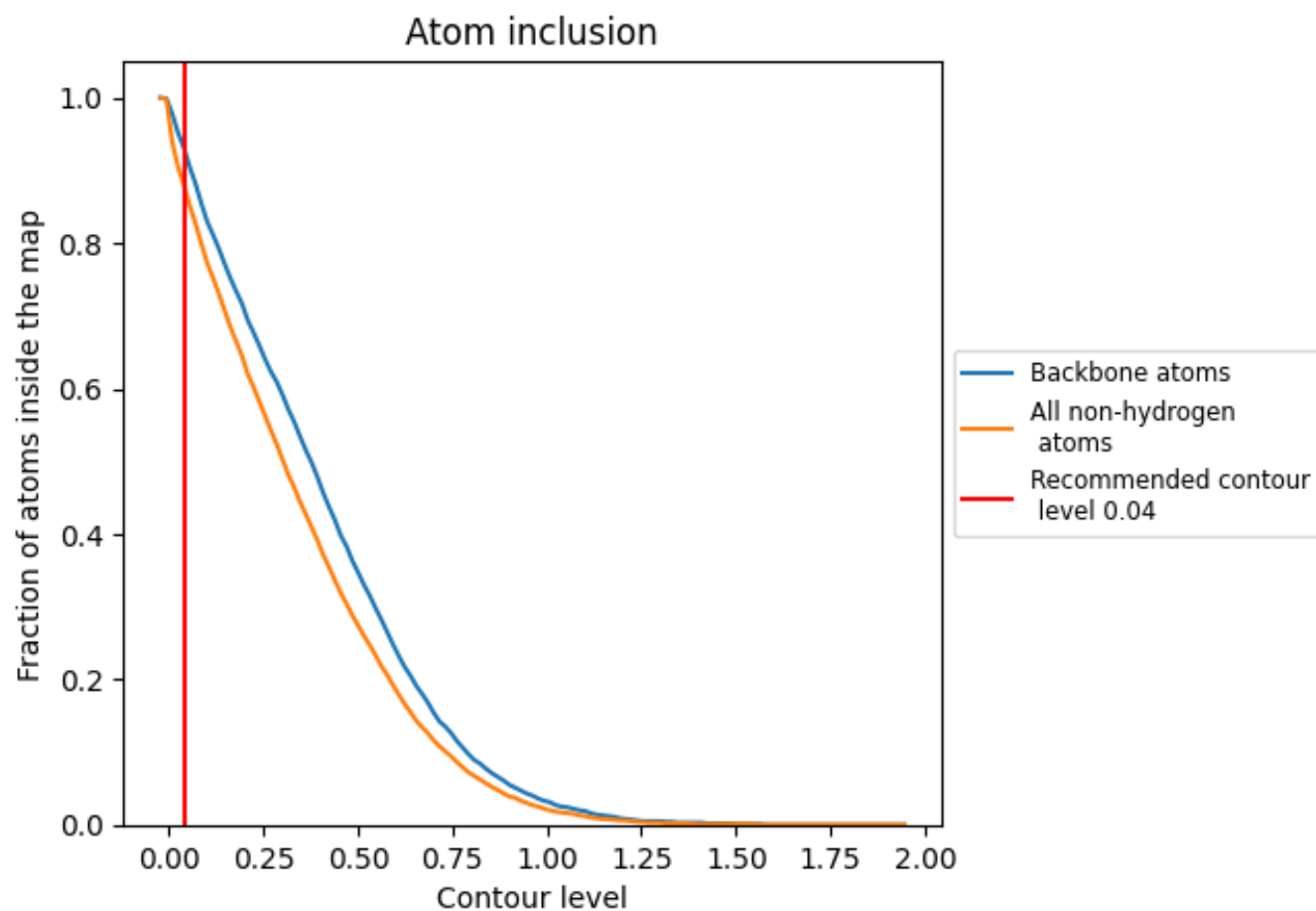
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8800	0.4650
A	0.8530	0.4490
B	0.9030	0.4860
E	0.9200	0.4880
G	0.6550	0.2850
R	0.8880	0.4700

