



Full wwPDB EM Validation Report ⓘ

Oct 14, 2024 – 06:46 PM JST

PDB ID : 7X2V
EMDB ID : EMD-32972
Title : GPR110/Gi complex
Authors : He, Y.; Zhu, X.
Deposited on : 2022-02-26
Resolution : 3.09 Å (reported)
Based on initial model : 6VMS

This is a Full wwPDB EM Validation 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.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

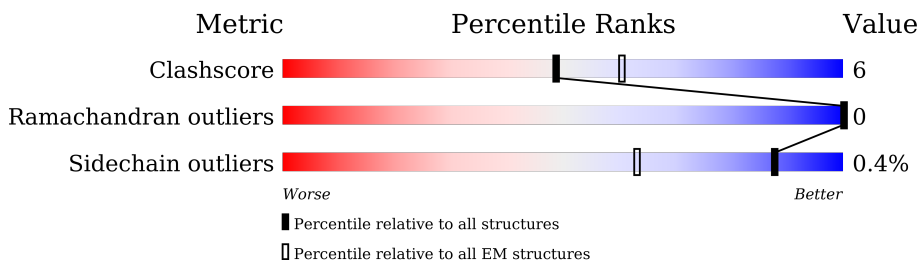
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.09 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 ≥ 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	D	71	
2	B	354	
3	E	247	
4	R	910	
5	C	345	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8755 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(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	58	Total	C	N	O	S	0	0
			444	277	79	85	3		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	220	Total	C	N	O	S	0	0
			1769	1126	295	335	13		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	203	ALA	GLY	conflict	UNP P63096
B	326	SER	ALA	conflict	UNP P63096

- 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 Adhesion G-protein coupled receptor F1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	277	Total	C	N	O	S	0	0
			2179	1472	346	347	14		

- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	337	Total	C	N	O	S	0	0
			2592	1599	466	506	21		

There are 6 discrepancies between the modelled and reference sequences:

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

Chain R:  27% 70%

[illegible]

- Molecule 5: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain C:  11% 74% 23%

V213	D83	WET
R219	T87	GLY
Q220	N88	SER
T221		LEU
H225	R96	LEU
	V100	GLN
D228		SER
C232	C103	GLU
T233	A104	L4
F234	T105	D5
		Q6
G238	Y111	L7
F241	V112	R8
A242	A113	Q9
T243	C114	E10
A248	G115	A11
R251	G116	E12
L252	L117	Q13
F253	R129	L14
D254	E130	K15
D258	A140	N16
L261	G144	Q17
T263	Y146	I18
C271	C148	R19
S279	G149	D20
L286	R150	A21
Y289	S161	K23
D290	G162	A24
N295	D163	C25
V296	T164	A26
W297	T165	D27
D303	T166	A28
R314	A167	T29
V315	L168	L30
S316	W169	S31
V320	F180	Q32
M325	H183	I33
A326	V187	T34
V327	M188	I43
A328	S189	M44
W332	L190	M45
	S191	G53
	C204	H54
	D205	L55
	A206	I58
	S207	Y59
	A208	A60
		M61
		L70
		V71
		S72
		I80
		I81
		I82



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	350000	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	2.164	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.04	Depositor
Map size (\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 (\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	D	0.30	0/450	0.44	0/608
2	B	0.36	0/1797	0.51	0/2410
3	E	0.41	0/1815	0.59	0/2461
4	R	0.40	0/2238	0.51	0/3053
5	C	0.41	0/2639	0.62	1/3577 (0.0%)
All	All	0.39	0/8939	0.56	1/12109 (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	C	205	ASP	CB-CG-OD1	6.00	123.70	118.30

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	D	444	0	454	7	0
2	B	1769	0	1773	12	0
3	E	1771	0	1709	18	0
4	R	2179	0	2306	17	0
5	C	2592	0	2499	56	0
All	All	8755	0	8741	98	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 6.

All (98) 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:162:LEU:HB3	3:E:180:MET:HB3	1.42	1.00
4:R:758:ASN:HB3	4:R:800:LEU:HB3	1.55	0.88
5:C:219:ARG:O	5:C:220:GLN:NE2	2.11	0.83
5:C:168:LEU:HD22	5:C:213:VAL:HB	1.59	0.82
5:C:103:CYS:O	5:C:150:ARG:NH2	2.18	0.75
3:E:94:TYR:O	3:E:114:GLY:HA2	1.86	0.75
3:E:166:LEU:HB2	3:E:176:LEU:HD11	1.71	0.73
1:D:61:PHE:HB2	5:C:340:ASN:HD21	1.55	0.72
4:R:758:ASN:ND2	4:R:800:LEU:O	2.17	0.71
4:R:619:THR:OG1	4:R:685:ARG:NE	2.26	0.69
5:C:144:GLY:N	5:C:163:ASP:OD2	2.21	0.68
1:D:54:VAL:HB	1:D:59:ASN:HB2	1.76	0.67
4:R:569:PHE:N	4:R:589:THR:OG1	2.26	0.67
3:E:24:ALA:HB1	3:E:27:PHE:CE1	2.30	0.66
1:D:49:PRO:HG2	5:C:325:MET:HA	1.79	0.64
5:C:271:CYS:HB3	5:C:290:ASP:HB2	1.80	0.64
1:D:30:VAL:HB	5:C:261:LEU:CD1	2.28	0.64
5:C:279:SER:HA	5:C:320:VAL:HG11	1.81	0.63
2:B:27:GLY:HA3	5:C:55:LEU:HG	1.79	0.63
3:E:164:TRP:HB2	3:E:177:ILE:HB	1.80	0.62
5:C:234:PHE:HE2	5:C:238:GLY:HA2	1.64	0.62
4:R:797:THR:HA	4:R:802:LEU:HD12	1.81	0.62
5:C:71:VAL:HA	5:C:80:ILE:O	2.00	0.61
5:C:251:ARG:NH1	5:C:263:THR:OG1	2.33	0.61
4:R:637:ALA:HB2	4:R:667:PHE:HB3	1.82	0.61
5:C:232:ILE:HG13	5:C:243:THR:HG22	1.82	0.61
5:C:289:TYR:OH	5:C:297:TRP:NE1	2.29	0.59
5:C:148:CYS:HB2	5:C:189:SER:HA	1.84	0.58
2:B:23:LEU:HD11	5:C:80:ILE:HD11	1.85	0.58
5:C:289:TYR:HE1	5:C:295:ASN:HB2	1.69	0.57
4:R:674:TRP:CE2	4:R:706:GLY:HA3	2.39	0.57
3:E:111:TRP:HE1	3:E:165:PHE:HE2	1.51	0.56
4:R:735:LEU:HB3	4:R:743:PRO:HG2	1.87	0.56
5:C:54:HIS:O	5:C:334:SER:HB3	2.06	0.55
4:R:597:ILE:HD11	4:R:638:ASP:HB2	1.88	0.55
5:C:289:TYR:HH	5:C:297:TRP:HE1	1.54	0.55
3:E:163:TYR:HB3	3:E:165:PHE:HE1	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:206:ALA:HB1	5:C:225:HIS:H	1.72	0.54
3:E:91:THR:OG1	3:E:119:VAL:O	2.25	0.53
5:C:43:ILE:HG22	5:C:45:MET:HB2	1.91	0.53
5:C:234:PHE:CE2	5:C:238:GLY:HA2	2.43	0.53
3:E:163:TYR:HB3	3:E:165:PHE:CE1	2.44	0.52
4:R:784:ALA:HB1	4:R:787:ILE:HB	1.90	0.52
5:C:117:LEU:HA	5:C:145:TYR:HB2	1.92	0.52
4:R:735:LEU:HB3	4:R:743:PRO:CG	2.39	0.52
2:B:23:LEU:HD21	5:C:53:GLY:O	2.09	0.51
4:R:758:ASN:CB	4:R:800:LEU:HB3	2.35	0.51
5:C:59:TYR:CE2	5:C:100:VAL:HG13	2.46	0.51
1:D:61:PHE:HB2	5:C:340:ASN:ND2	2.24	0.50
5:C:233:CYS:O	5:C:241:PHE:HB2	2.10	0.50
3:E:24:ALA:HB1	3:E:27:PHE:HE1	1.74	0.50
2:B:23:LEU:CD1	5:C:80:ILE:HD11	2.41	0.50
3:E:28:ALA:N	5:C:130:GLU:O	2.33	0.50
3:E:94:TYR:O	3:E:114:GLY:CA	2.59	0.49
5:C:70:LEU:O	5:C:81:ILE:HA	2.13	0.49
3:E:163:TYR:CB	3:E:165:PHE:HE1	2.26	0.49
5:C:164:THR:HB	5:C:183:HIS:HB2	1.95	0.48
2:B:191:PHE:HB3	2:B:196:PHE:HE2	1.79	0.48
5:C:161:SER:O	5:C:187:VAL:HB	2.13	0.47
5:C:208:ALA:O	5:C:221:THR:HA	2.13	0.47
5:C:167:ALA:HB3	5:C:169:TRP:HE1	1.78	0.47
5:C:314:ARG:HB2	5:C:332:TRP:CD2	2.50	0.47
4:R:730:LYS:NZ	4:R:731:ASP:OD2	2.36	0.47
4:R:807:GLY:O	4:R:811:ILE:HG12	2.14	0.47
2:B:223:PHE:CE1	2:B:225:VAL:HG23	2.51	0.46
5:C:82:TRP:CZ2	5:C:87:THR:HA	2.50	0.46
5:C:248:ALA:HA	5:C:271:CYS:O	2.15	0.46
2:B:223:PHE:HE1	2:B:225:VAL:HG23	1.80	0.46
2:B:223:PHE:HE1	2:B:225:VAL:CG2	2.28	0.46
5:C:106:ALA:HB3	5:C:111:TYR:H	1.80	0.46
5:C:83:ASP:N	5:C:88:ASN:O	2.39	0.46
2:B:185:VAL:HB	2:B:200:ASP:HB3	1.97	0.45
5:C:286:LEU:CD2	5:C:327:VAL:HG21	2.45	0.45
5:C:328:ALA:HA	5:C:337:LYS:O	2.17	0.45
5:C:166:CYS:HB2	5:C:180:PHE:HB2	1.99	0.45
5:C:191:SER:HB2	5:C:234:PHE:HB2	1.98	0.45
3:E:24:ALA:HB1	3:E:27:PHE:CZ	2.51	0.44
4:R:808:ILE:HD12	4:R:811:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:573:MET:HB3	4:R:811:ILE:CG2	2.48	0.43
1:D:50:LEU:HD21	5:C:327:VAL:HB	1.99	0.43
2:B:191:PHE:HB3	2:B:196:PHE:CE2	2.53	0.43
5:C:140:ALA:O	5:C:169:TRP:HH2	2.01	0.43
5:C:166:CYS:C	5:C:180:PHE:HD1	2.21	0.43
5:C:252:LEU:O	5:C:261:LEU:HB3	2.19	0.42
5:C:61:MET:HA	5:C:72:SER:HA	2.01	0.42
5:C:191:SER:CB	5:C:234:PHE:HB2	2.50	0.42
2:B:348:LEU:HD12	4:R:686:ILE:HD11	2.02	0.41
5:C:286:LEU:HD22	5:C:327:VAL:HG21	2.01	0.41
2:B:268:LEU:O	2:B:324:THR:N	2.46	0.41
3:E:34:MET:HG3	3:E:79:LEU:HD13	2.03	0.41
5:C:58:ILE:O	5:C:316:SER:OG	2.32	0.40
3:E:127:VAL:O	3:E:150:SER:N	2.54	0.40
3:E:175:LEU:HD11	3:E:178:TYR:HB3	2.03	0.40
5:C:191:SER:HG	5:C:234:PHE:HD1	1.69	0.40
5:C:204:CYS:HB3	5:C:228:ASP:OD1	2.21	0.40
5:C:104:ALA:HB3	5:C:113:ALA:HB3	2.04	0.40
1:D:47:GLU:O	1:D:49:PRO:HD3	2.21	0.40
3:E:2:VAL:HG13	5:C:129:ARG:HG3	2.02	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	D	56/71 (79%)	55 (98%)	1 (2%)	0	100	100
2	B	214/354 (60%)	207 (97%)	7 (3%)	0	100	100
3	E	226/247 (92%)	214 (95%)	12 (5%)	0	100	100
4	R	273/910 (30%)	252 (92%)	21 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	C	335/345 (97%)	315 (94%)	20 (6%)	0	100	100
All	All	1104/1927 (57%)	1043 (94%)	61 (6%)	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	D	47/58 (81%)	46 (98%)	1 (2%)	48	72
2	B	196/306 (64%)	195 (100%)	1 (0%)	86	92
3	E	195/198 (98%)	195 (100%)	0	100	100
4	R	242/809 (30%)	240 (99%)	2 (1%)	79	89
5	C	280/287 (98%)	280 (100%)	0	100	100
All	All	960/1658 (58%)	956 (100%)	4 (0%)	88	94

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

Mol	Chain	Res	Type
1	D	27	ARG
2	B	271	LYS
4	R	668	TYR
4	R	817	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	E	159	ASN
5	C	340	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](#)

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.

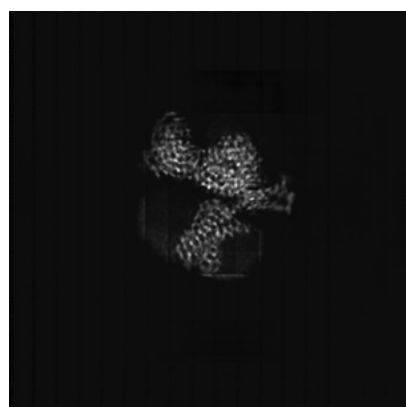
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32972. These allow visual inspection of the internal detail of the map and identification of artifacts.

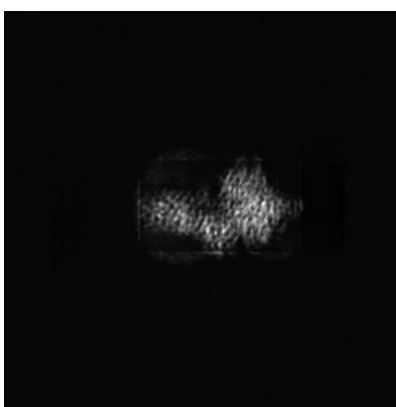
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

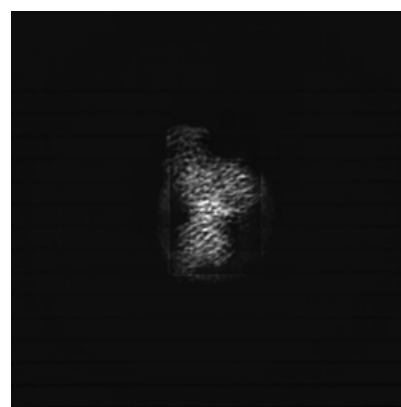
6.1.1 Primary map



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: 127



Y Index: 128



Z Index: 154

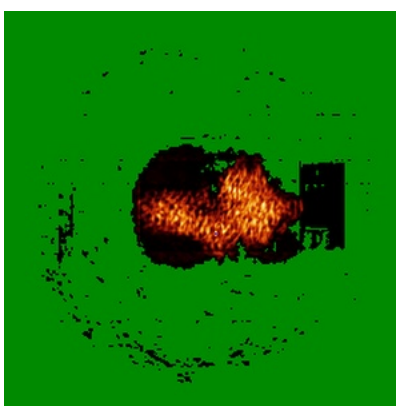
The images above show the largest variance slices of the map in three orthogonal directions.

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

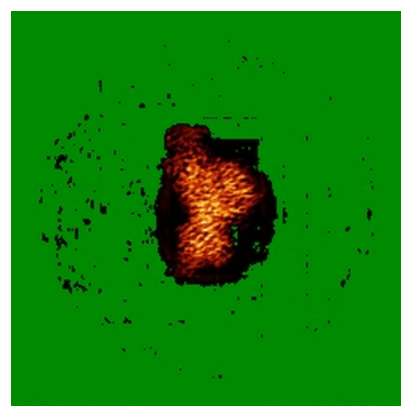
6.4.1 Primary map



X



Y

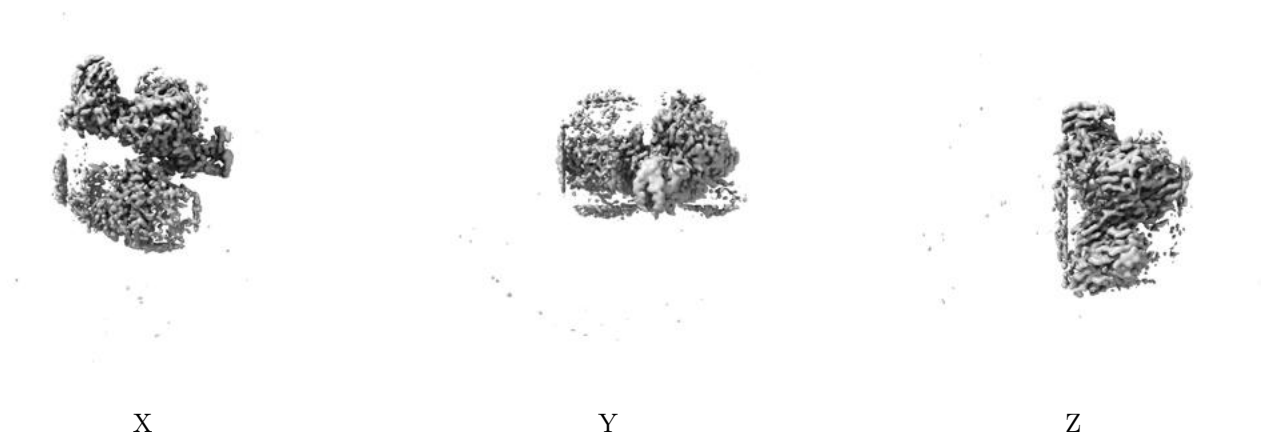


Z

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.

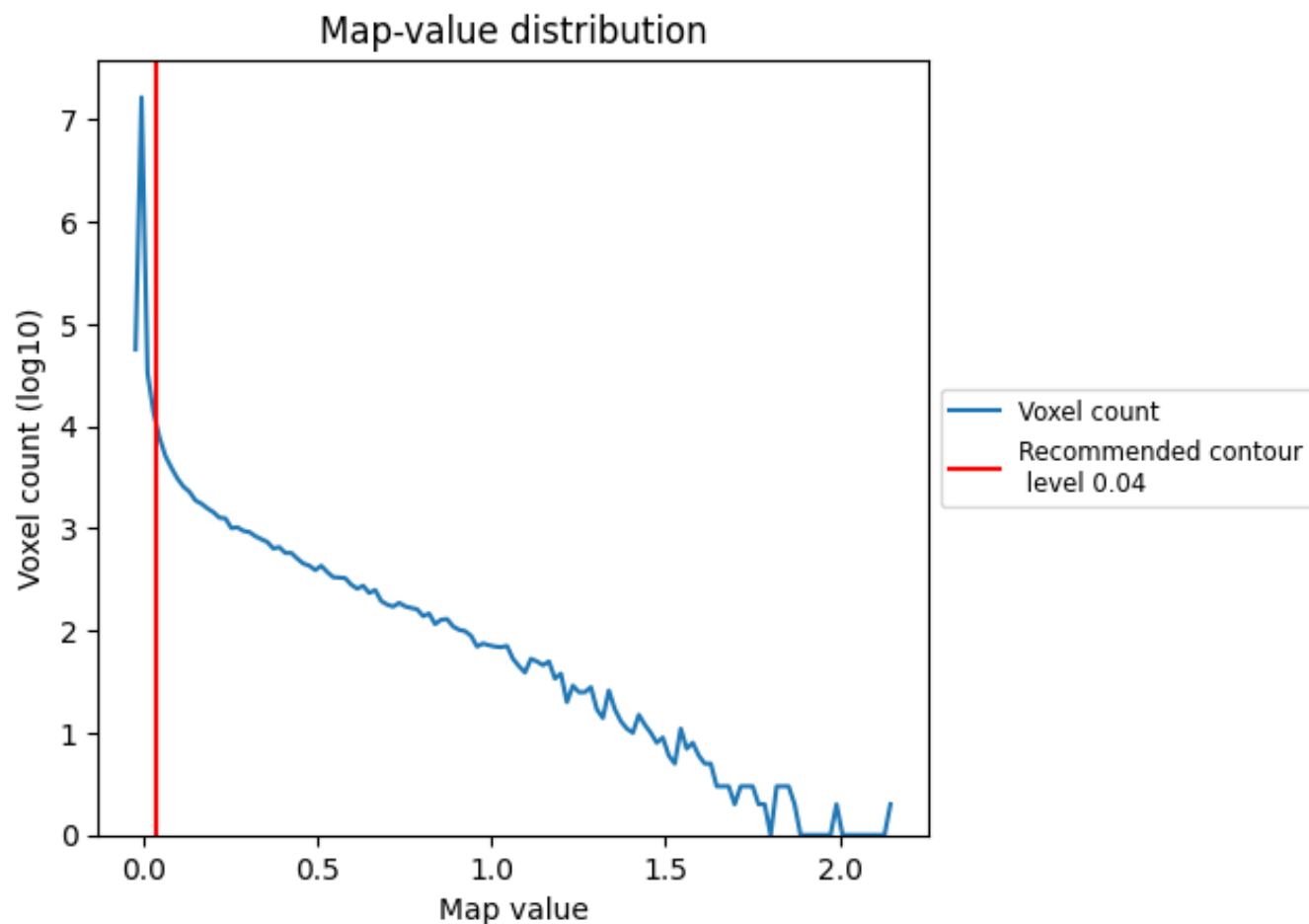
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

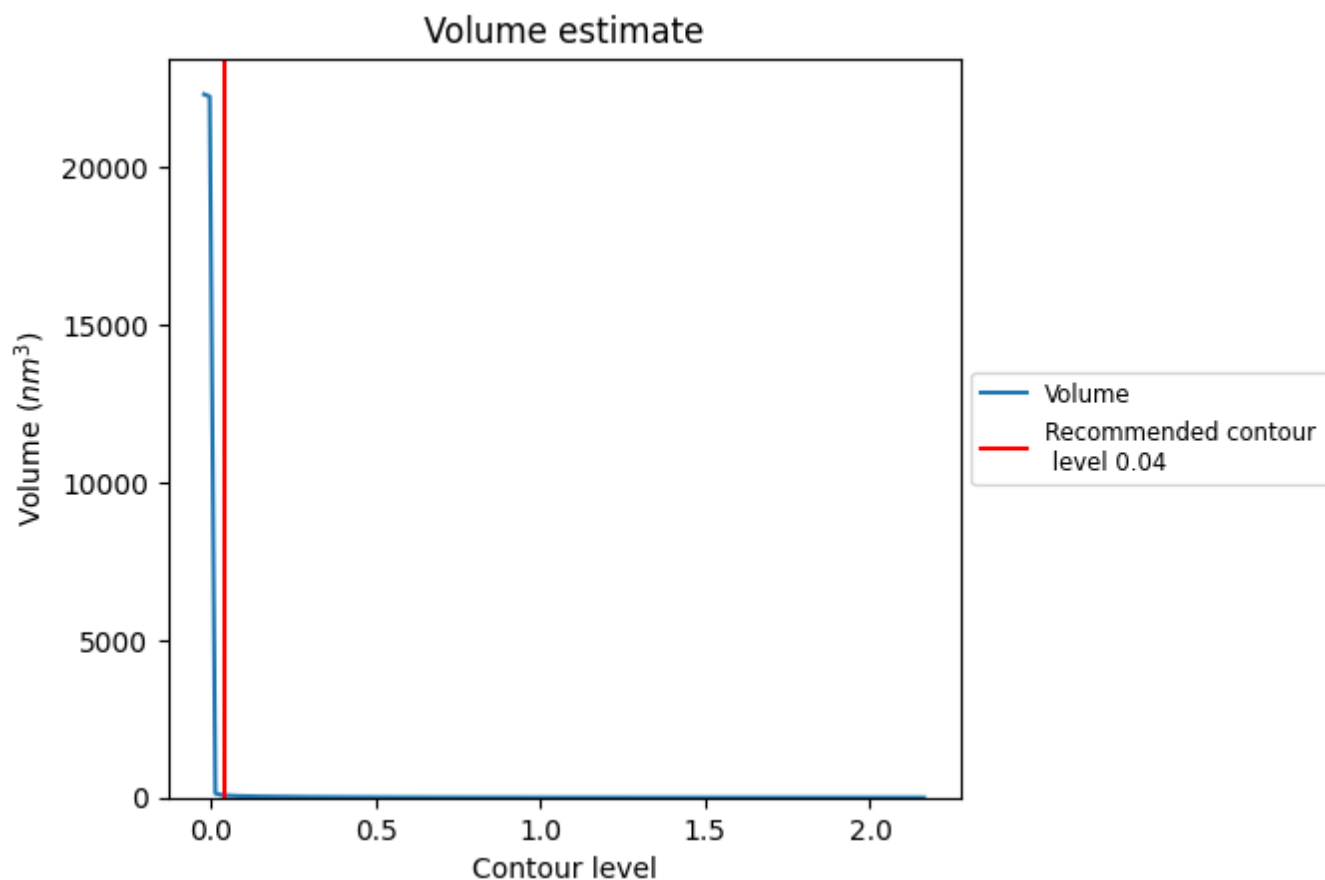
This section contains the results of statistical analysis of the map.

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.

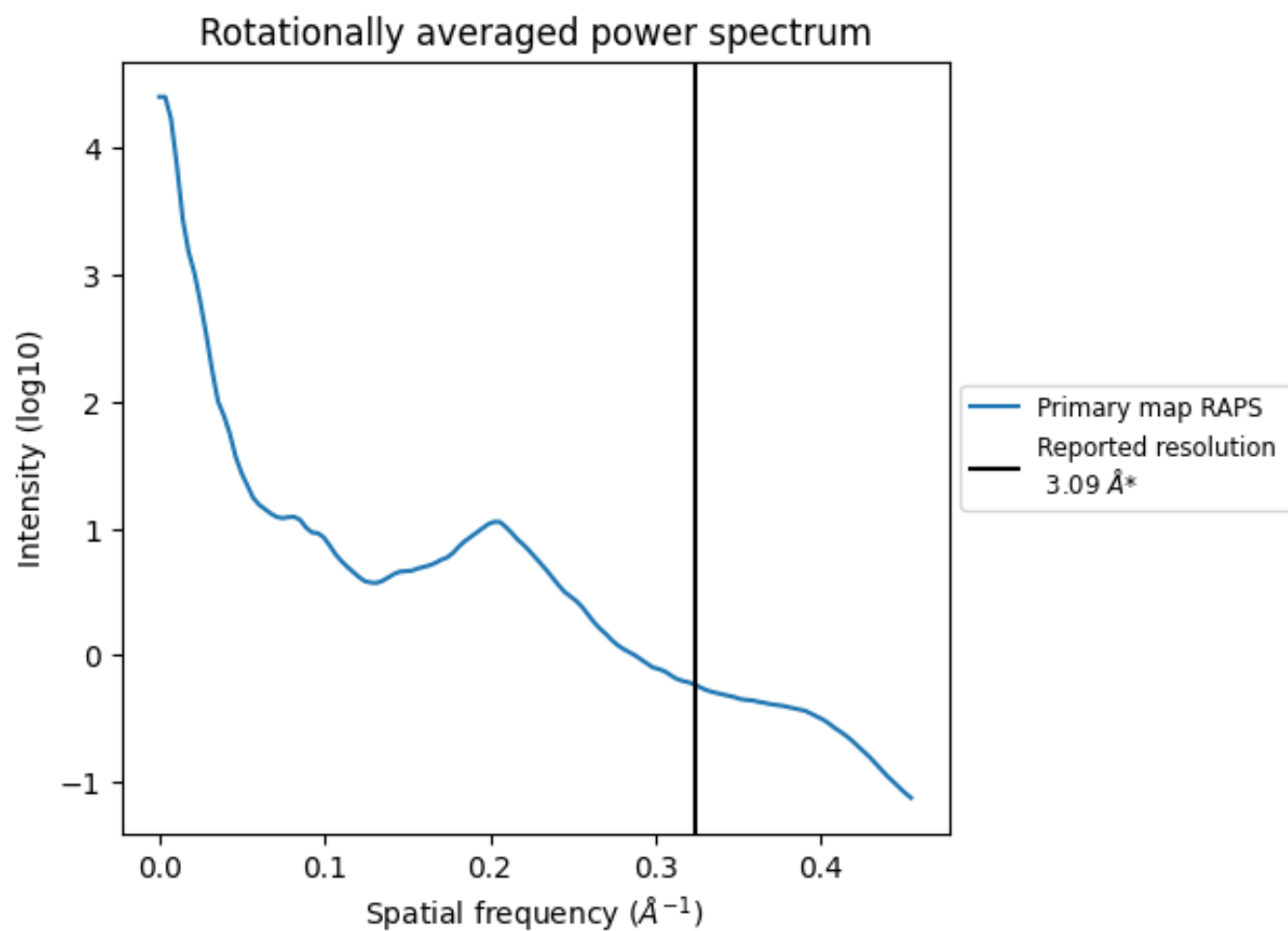
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 77 nm^3 ; this corresponds to an approximate mass of 69 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 ⓘ

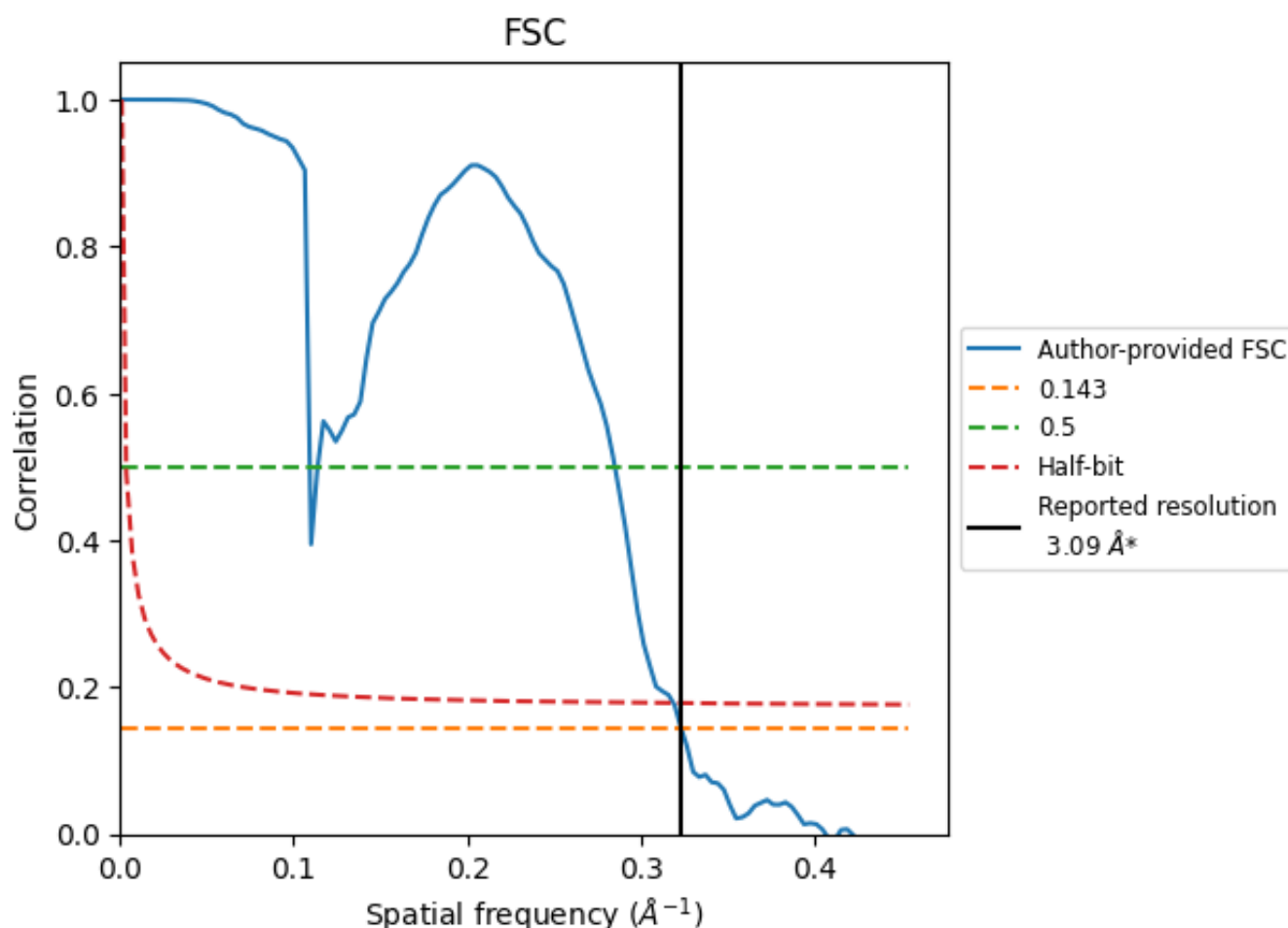


*Reported resolution corresponds to spatial frequency of 0.324 Å⁻¹

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 0.324 \AA^{-1}

8.2 Resolution estimates [i](#)

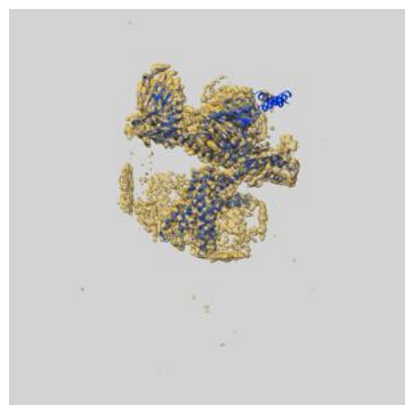
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	3.09	9.15	3.14
Unmasked-calculated*	-	-	-

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

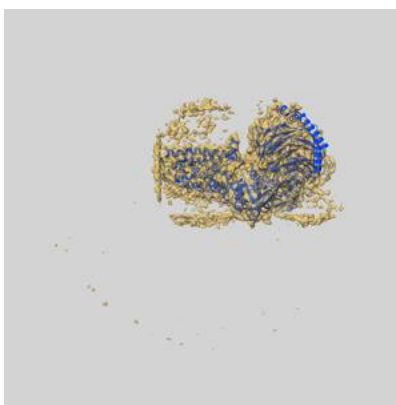
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32972 and PDB model 7X2V. Per-residue inclusion information can be found in section [3](#) on page [5](#).

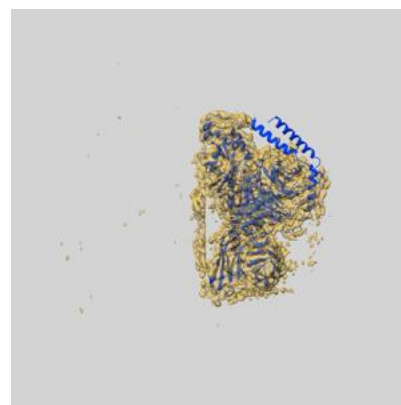
9.1 Map-model overlay [i](#)



X



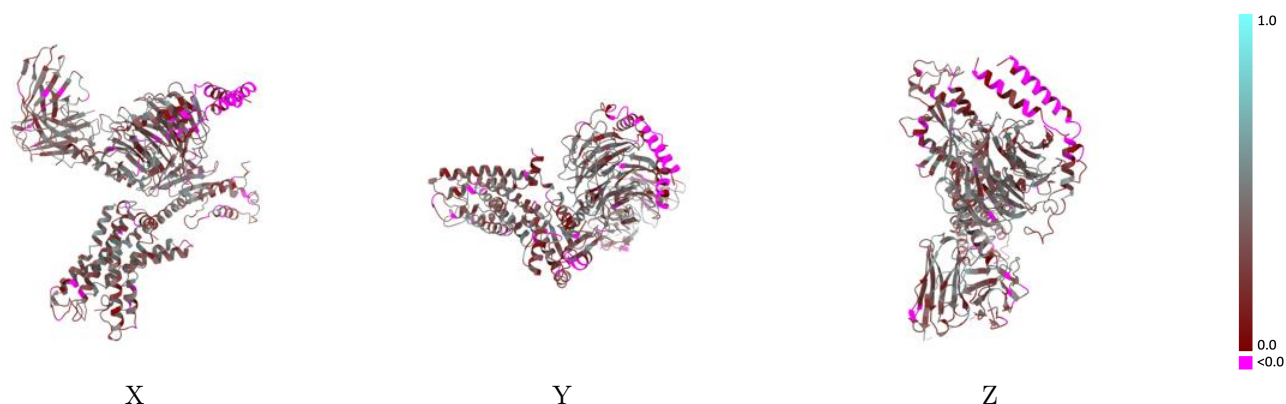
Y



Z

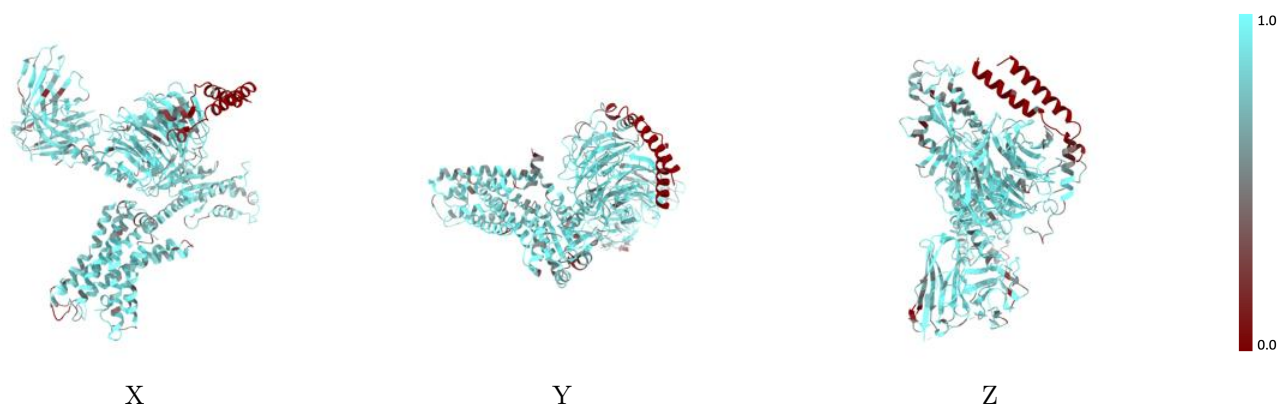
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



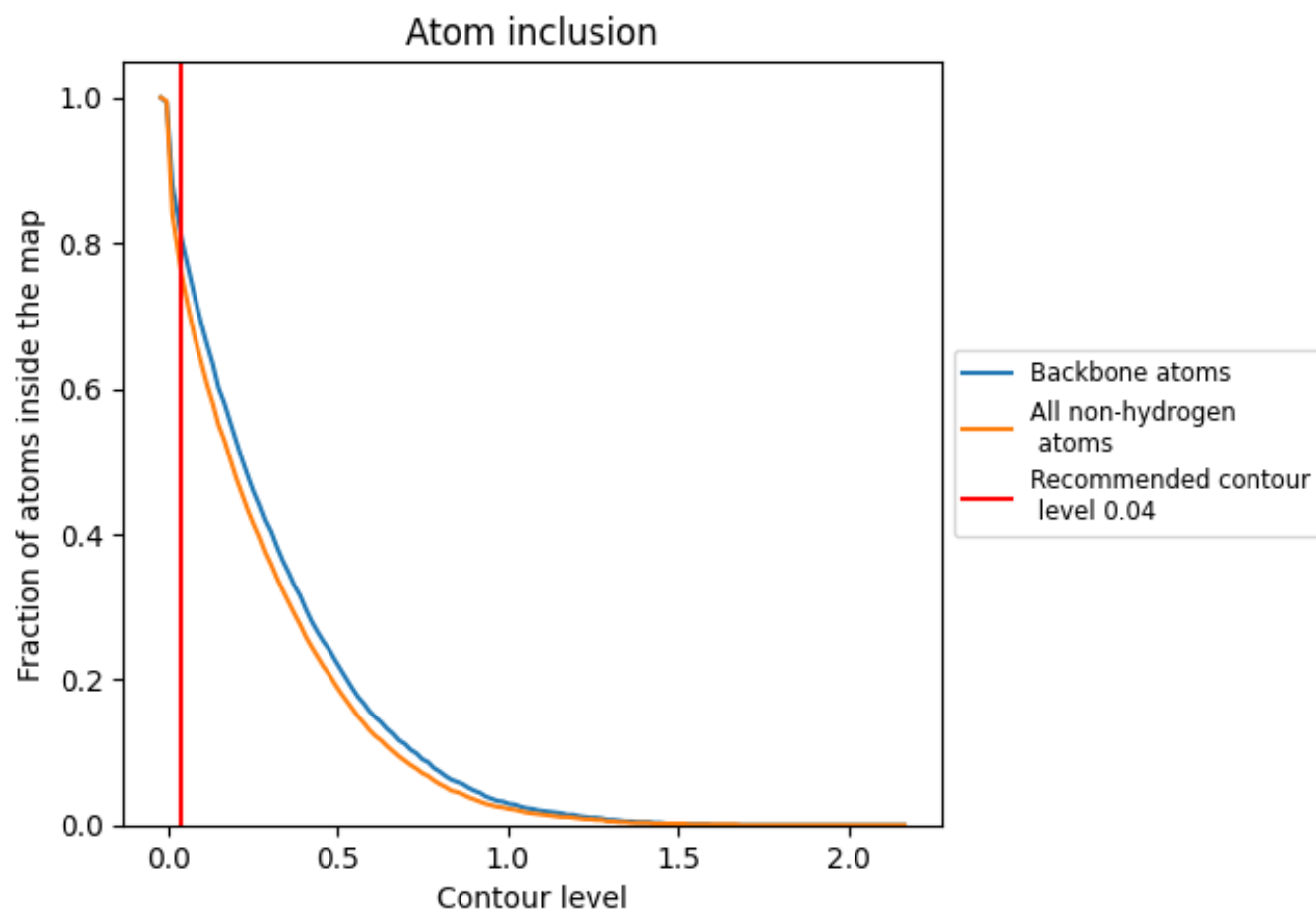
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 81% of all backbone atoms, 76% 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	<div></div> 0.7580	<div></div> 0.3160
B	<div></div> 0.7520	<div></div> 0.3000
C	<div></div> 0.7780	<div></div> 0.3400
D	<div></div> 0.3570	<div></div> 0.1490
E	<div></div> 0.8080	<div></div> 0.3400
R	<div></div> 0.7830	<div></div> 0.3150

