wwPDB EM Validation Summary Report

Nov 4, 2024 – 09:09 AM JST

PDB ID	:	7WU2
EMDB ID	:	EMD-32817
Title	:	Cryo-EM structure of the adhesion GPCR ADGRD1 in complex with miniGs
Authors	:	Qu, X.; Qiu, N.; Wang, M.; Zhao, Q.; Wu, B.
Deposited on	:	2022-02-05
Resolution	:	2.80 Å(reported)

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:

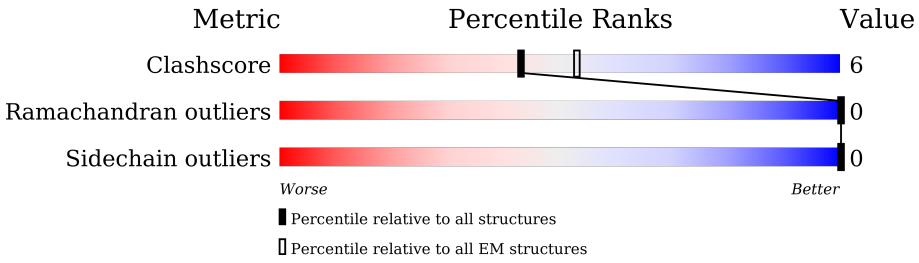
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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 <=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	243	70% 16% 14%
2	B	351	83% 13%
3	C	71	18% 75% 21%
4	N	162	57% 22% 21%
5	R	348	6% 68% 12% 20%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7829 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	210	Total	C	N	O	S	0	0
			1734	1099	311	318	6		

- 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	339	Total	C	N	O	S	0	0
			2586	1595	465	505	21		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	MET	-	expression tag	UNP P62873
B	-9	HIS	-	expression tag	UNP P62873
B	-8	HIS	-	expression tag	UNP P62873
B	-7	HIS	-	expression tag	UNP P62873
B	-6	HIS	-	expression tag	UNP P62873
B	-5	HIS	-	expression tag	UNP P62873
B	-4	HIS	-	expression tag	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 Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	56	Total	C	N	O	S	0	0
			423	266	73	81	3		

- Molecule 4 is a protein called Nanobody Nb35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	128	Total	C	N	O	S	0	0
			971	604	170	191	6		

- Molecule 5 is a protein called Adhesion G-protein coupled receptor D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	277	Total	C	N	O	S	0	0
			2115	1404	342	355	14		

There are 65 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	526	MET	-	initiating methionine	UNP Q6QNK2
R	527	LYS	-	expression tag	UNP Q6QNK2
R	528	THR	-	expression tag	UNP Q6QNK2
R	529	ILE	-	expression tag	UNP Q6QNK2
R	530	ILE	-	expression tag	UNP Q6QNK2
R	531	ALA	-	expression tag	UNP Q6QNK2
R	532	LEU	-	expression tag	UNP Q6QNK2
R	533	SER	-	expression tag	UNP Q6QNK2
R	534	TYR	-	expression tag	UNP Q6QNK2
R	535	ILE	-	expression tag	UNP Q6QNK2
R	536	PHE	-	expression tag	UNP Q6QNK2
R	537	CYS	-	expression tag	UNP Q6QNK2
R	538	LEU	-	expression tag	UNP Q6QNK2
R	539	VAL	-	expression tag	UNP Q6QNK2
R	540	PHE	-	expression tag	UNP Q6QNK2
R	541	ALA	-	expression tag	UNP Q6QNK2
R	542	GLY	-	expression tag	UNP Q6QNK2
R	543	ALA	-	expression tag	UNP Q6QNK2
R	544	PRO	-	expression tag	UNP Q6QNK2
R	828	GLU	-	expression tag	UNP Q6QNK2
R	829	PHE	-	expression tag	UNP Q6QNK2
R	830	LEU	-	expression tag	UNP Q6QNK2
R	831	GLU	-	expression tag	UNP Q6QNK2
R	832	VAL	-	expression tag	UNP Q6QNK2
R	833	LEU	-	expression tag	UNP Q6QNK2
R	834	PHE	-	expression tag	UNP Q6QNK2
R	835	GLN	-	expression tag	UNP Q6QNK2
R	836	GLY	-	expression tag	UNP Q6QNK2
R	837	PRO	-	expression tag	UNP Q6QNK2

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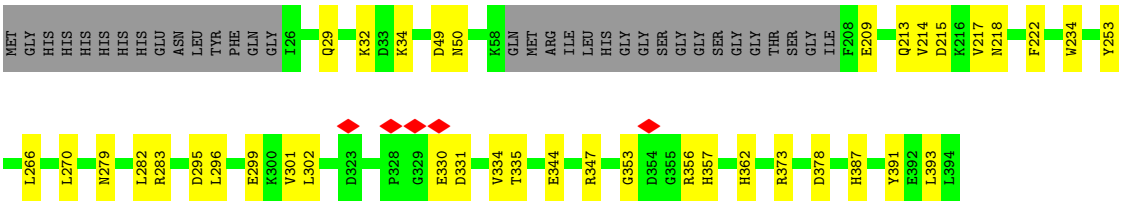
Chain	Residue	Modelled	Actual	Comment	Reference
R	838	TRP	-	expression tag	UNP Q6QNK2
R	839	SER	-	expression tag	UNP Q6QNK2
R	840	HIS	-	expression tag	UNP Q6QNK2
R	841	PRO	-	expression tag	UNP Q6QNK2
R	842	GLN	-	expression tag	UNP Q6QNK2
R	843	PHE	-	expression tag	UNP Q6QNK2
R	844	GLU	-	expression tag	UNP Q6QNK2
R	845	LYS	-	expression tag	UNP Q6QNK2
R	846	GLY	-	expression tag	UNP Q6QNK2
R	847	GLY	-	expression tag	UNP Q6QNK2
R	848	GLY	-	expression tag	UNP Q6QNK2
R	849	SER	-	expression tag	UNP Q6QNK2
R	850	GLY	-	expression tag	UNP Q6QNK2
R	851	GLY	-	expression tag	UNP Q6QNK2
R	852	GLY	-	expression tag	UNP Q6QNK2
R	853	SER	-	expression tag	UNP Q6QNK2
R	854	GLY	-	expression tag	UNP Q6QNK2
R	855	GLY	-	expression tag	UNP Q6QNK2
R	856	SER	-	expression tag	UNP Q6QNK2
R	857	ALA	-	expression tag	UNP Q6QNK2
R	858	TRP	-	expression tag	UNP Q6QNK2
R	859	SER	-	expression tag	UNP Q6QNK2
R	860	HIS	-	expression tag	UNP Q6QNK2
R	861	PRO	-	expression tag	UNP Q6QNK2
R	862	GLN	-	expression tag	UNP Q6QNK2
R	863	PHE	-	expression tag	UNP Q6QNK2
R	864	GLU	-	expression tag	UNP Q6QNK2
R	865	LYS	-	expression tag	UNP Q6QNK2
R	866	ASP	-	expression tag	UNP Q6QNK2
R	867	TYR	-	expression tag	UNP Q6QNK2
R	868	LYS	-	expression tag	UNP Q6QNK2
R	869	ASP	-	expression tag	UNP Q6QNK2
R	870	ASP	-	expression tag	UNP Q6QNK2
R	871	ASP	-	expression tag	UNP Q6QNK2
R	872	ASP	-	expression tag	UNP Q6QNK2
R	873	LYS	-	expression tag	UNP Q6QNK2

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.

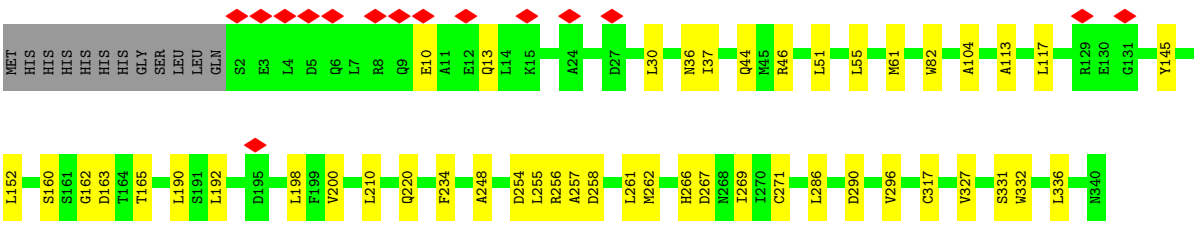
• Molecule 1: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

Chain A:



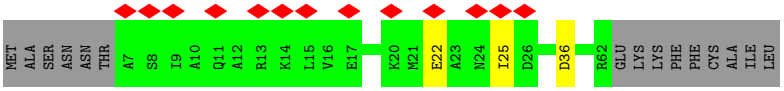
• Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B:



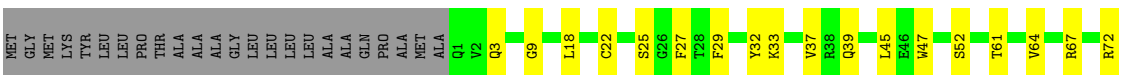
• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

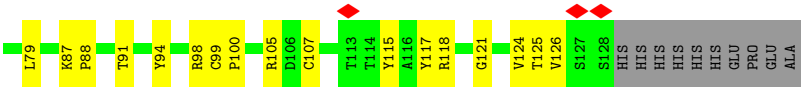
Chain C:



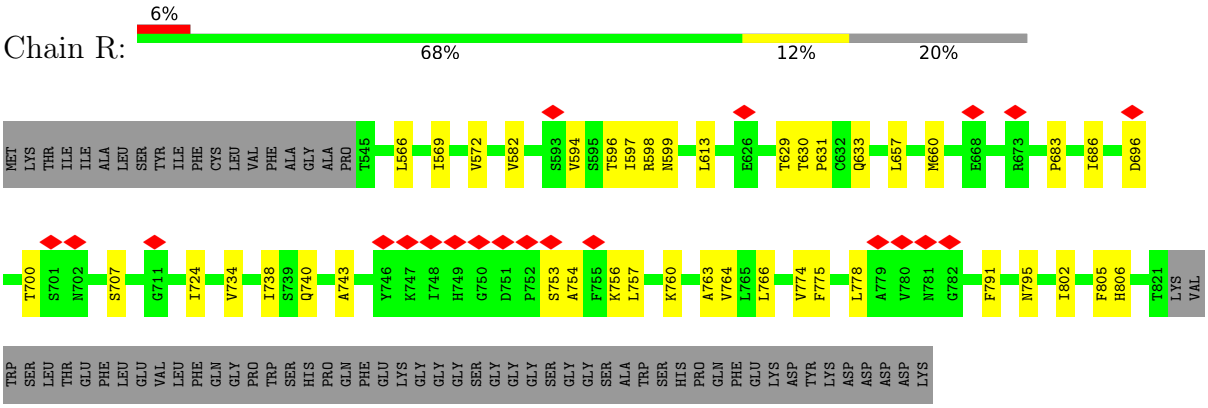
• Molecule 4: Nanobody Nb35

Chain N:





• Molecule 5: Adhesion G-protein coupled receptor D1



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1266674	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 ($e^-/Å^2$)	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.118	Depositor
Minimum map value	-0.066	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0115	Depositor
Map size (Å)	274.176, 274.176, 274.176	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.071, 1.071, 1.071	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	0.26	0/1771	0.50	0/2390
2	B	0.24	0/2633	0.52	0/3571
3	C	0.23	0/429	0.37	0/580
4	N	0.25	0/991	0.50	0/1342
5	R	0.24	0/2168	0.43	0/2958
All	All	0.25	0/7992	0.48	0/10841

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	1734	0	1683	25	0
2	B	2586	0	2478	30	0
3	C	423	0	430	2	0
4	N	971	0	933	22	0
5	R	2115	0	2165	25	0
All	All	7829	0	7689	99	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.

The worst 5 of 99 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)
5:R:596:THR:O	5:R:599:ASN:ND2	2.20	0.73
2:B:271:CYS:HB2	2:B:290:ASP:HB2	1.75	0.68
2:B:160:SER:HB3	2:B:190:LEU:HD23	1.76	0.66
4:N:64:VAL:HG12	4:N:67:ARG:HH21	1.62	0.65
1:A:34:LYS:HA	2:B:55:LEU:HD21	1.79	0.64

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	206/243 (85%)	205 (100%)	1 (0%)	0	100	100
2	B	337/351 (96%)	331 (98%)	6 (2%)	0	100	100
3	C	54/71 (76%)	53 (98%)	1 (2%)	0	100	100
4	N	126/162 (78%)	121 (96%)	5 (4%)	0	100	100
5	R	275/348 (79%)	267 (97%)	8 (3%)	0	100	100
All	All	998/1175 (85%)	977 (98%)	21 (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	185/214 (86%)	185 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	277/293 (94%)	277 (100%)	0	100	100
3	C	44/58 (76%)	44 (100%)	0	100	100
4	N	105/130 (81%)	105 (100%)	0	100	100
5	R	227/290 (78%)	227 (100%)	0	100	100
All	All	838/985 (85%)	838 (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
2	B	32	GLN
2	B	340	ASN
5	R	806	HIS

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.

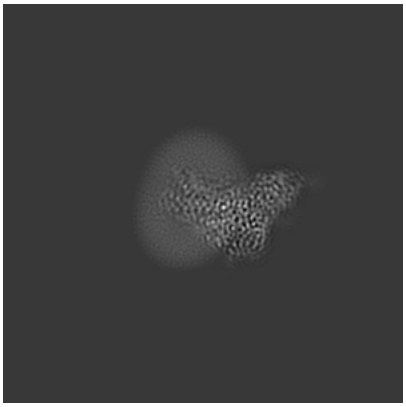
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32817. These allow visual inspection of the internal detail of the map and identification of artifacts.

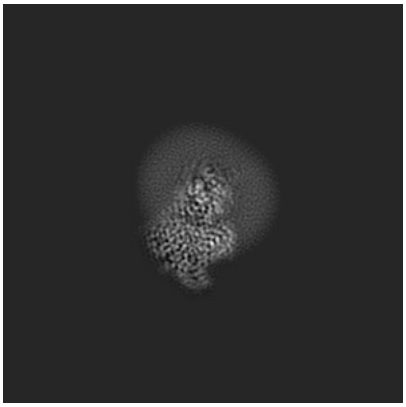
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

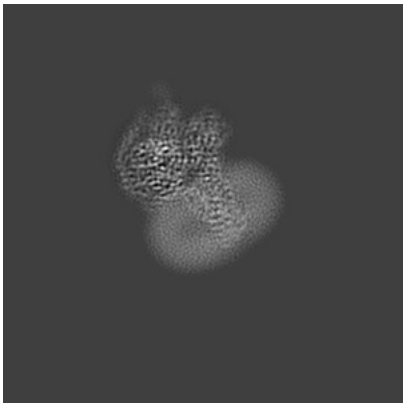
6.1.1 Primary map



X



Y

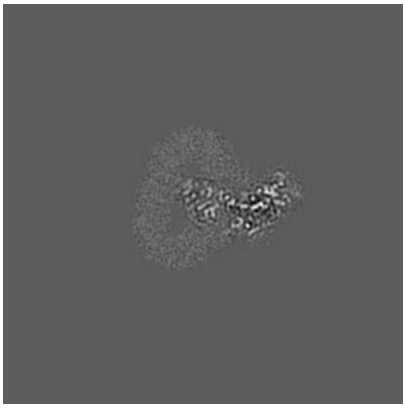


Z

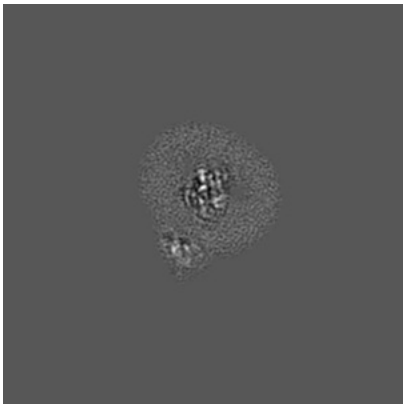
The images above show the map projected in three orthogonal directions.

6.2 Central slices

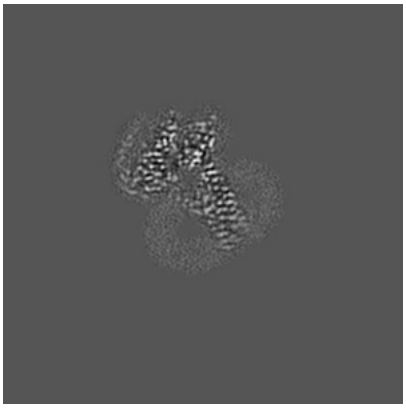
6.2.1 Primary map



X Index: 128



Y Index: 128



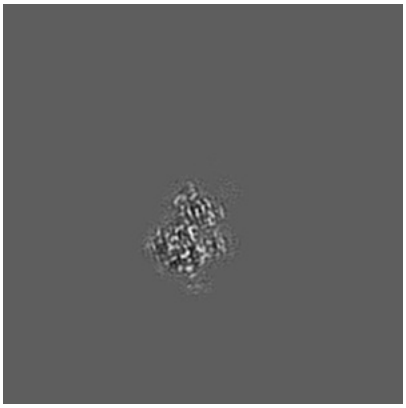
Z Index: 128

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

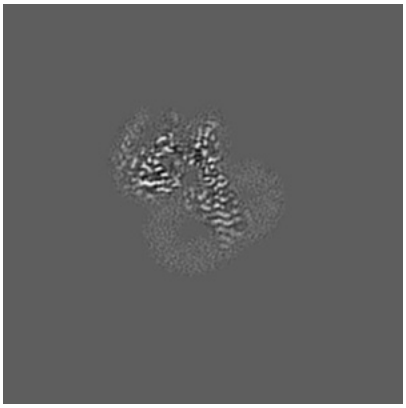
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 102



Y Index: 159

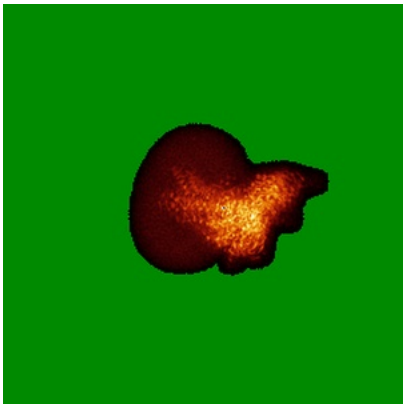


Z Index: 125

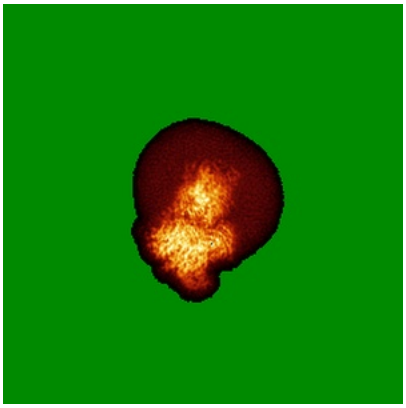
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

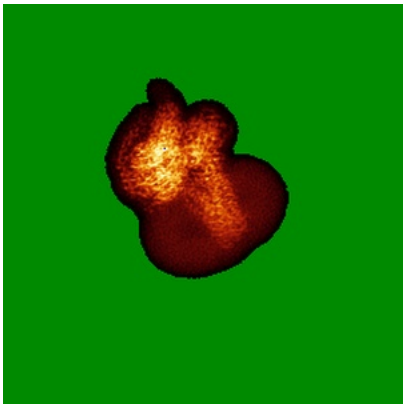
6.4.1 Primary map



X



Y

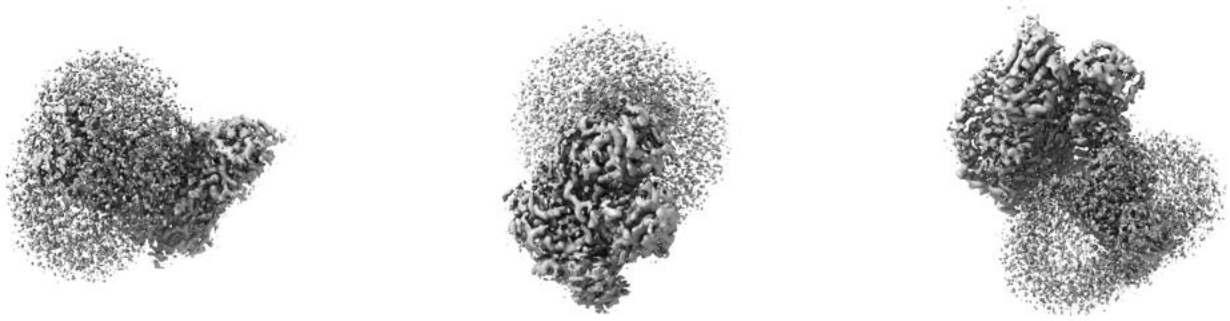


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0115. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

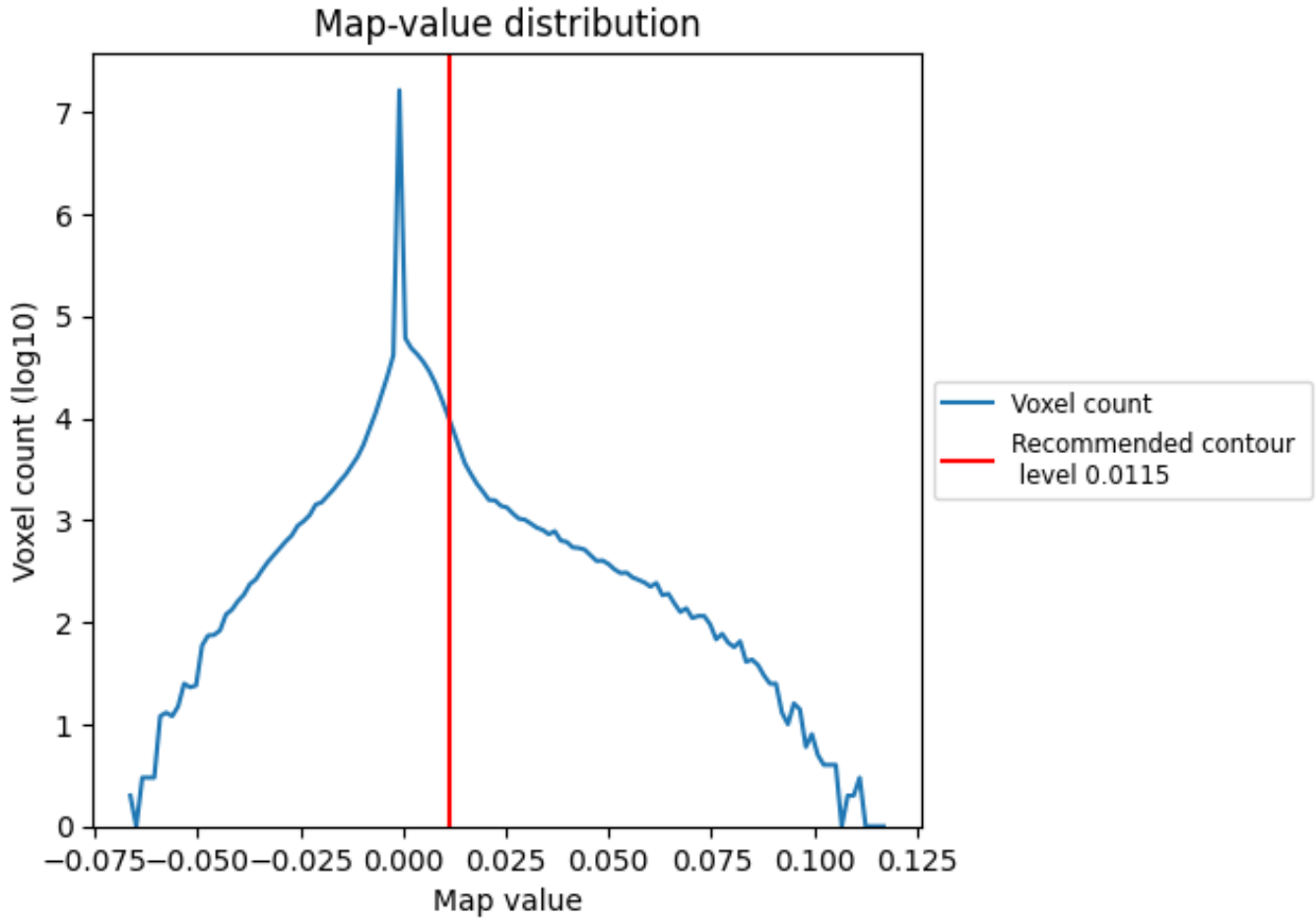
6.6 Mask visualisation (i)

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

7 Map analysis

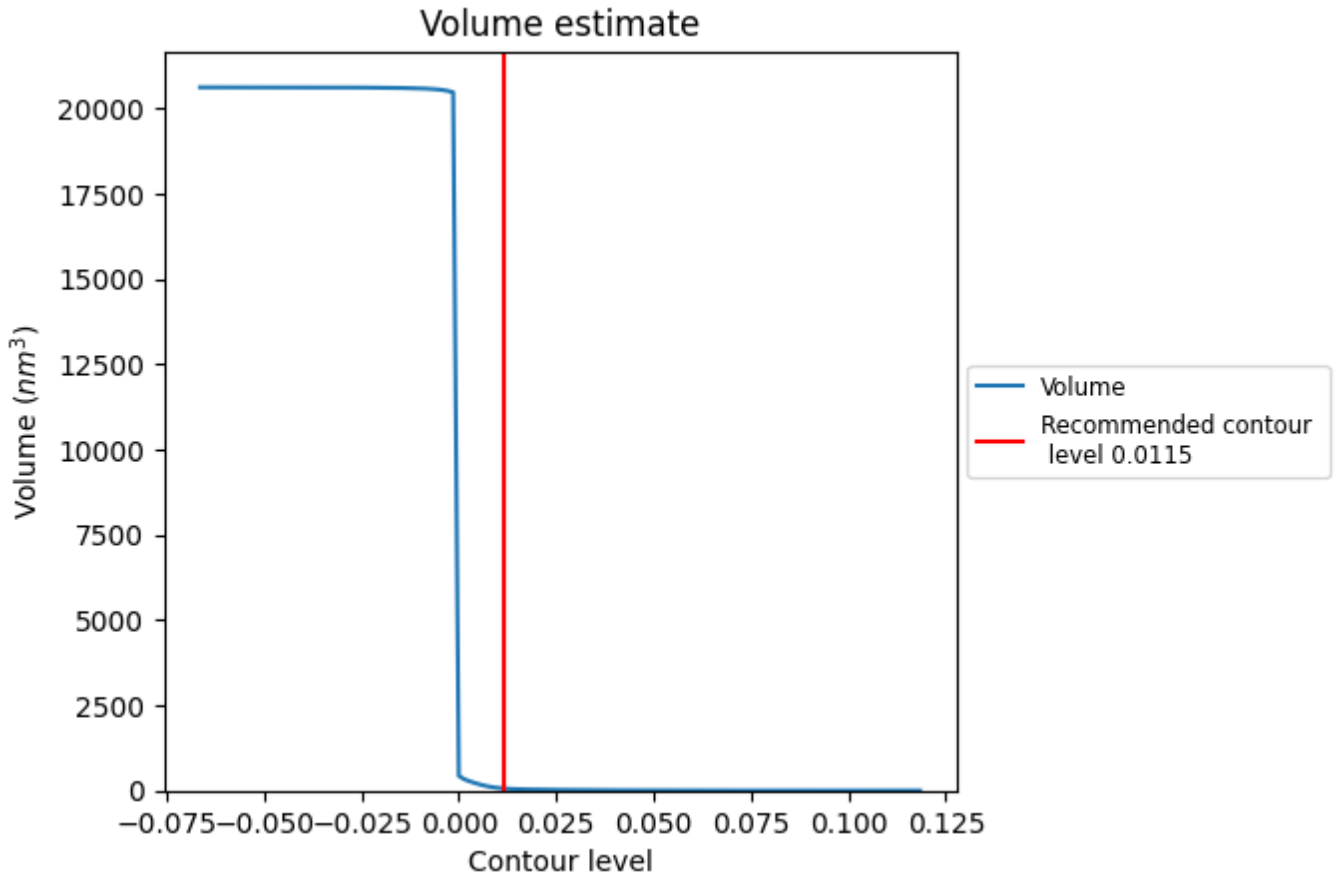
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

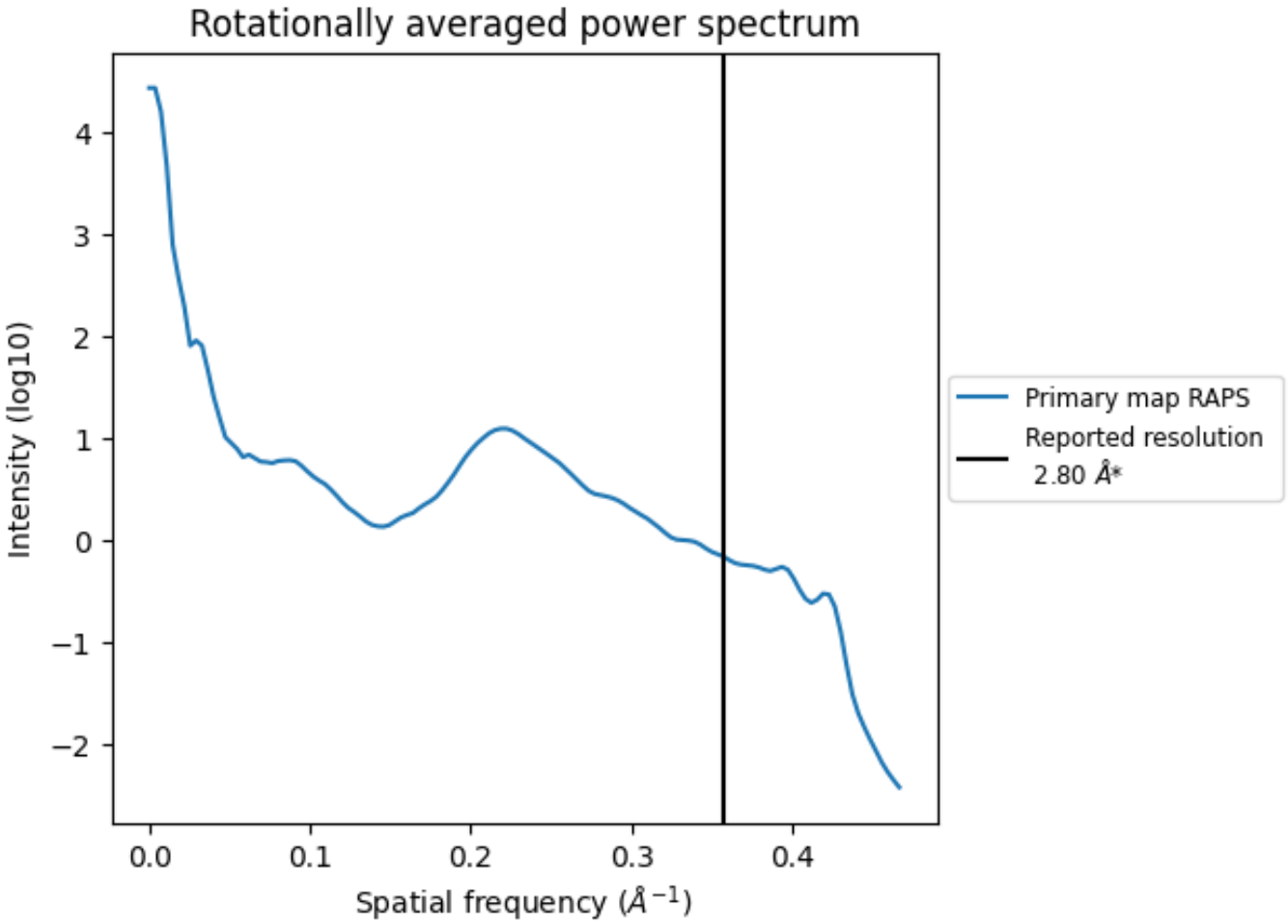
7.2 Volume estimate (i)



The volume at the recommended contour level is 61 nm^3; this corresponds to an approximate mass of 55 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 (i)



*Reported resolution corresponds to spatial frequency of 0.357 $Å^{-1}$

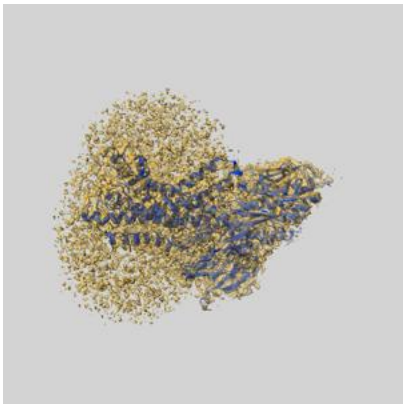
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

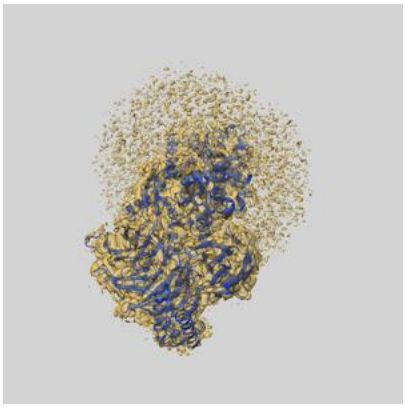
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-32817 and PDB model 7WU2. Per-residue inclusion information can be found in section 3 on page 6.

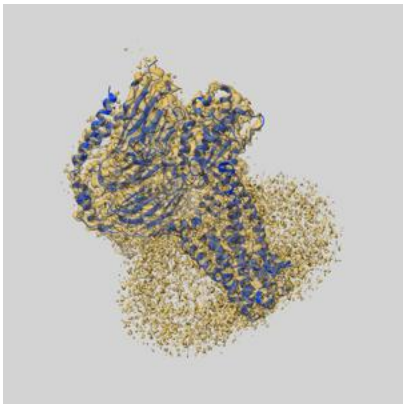
9.1 Map-model overlay



X



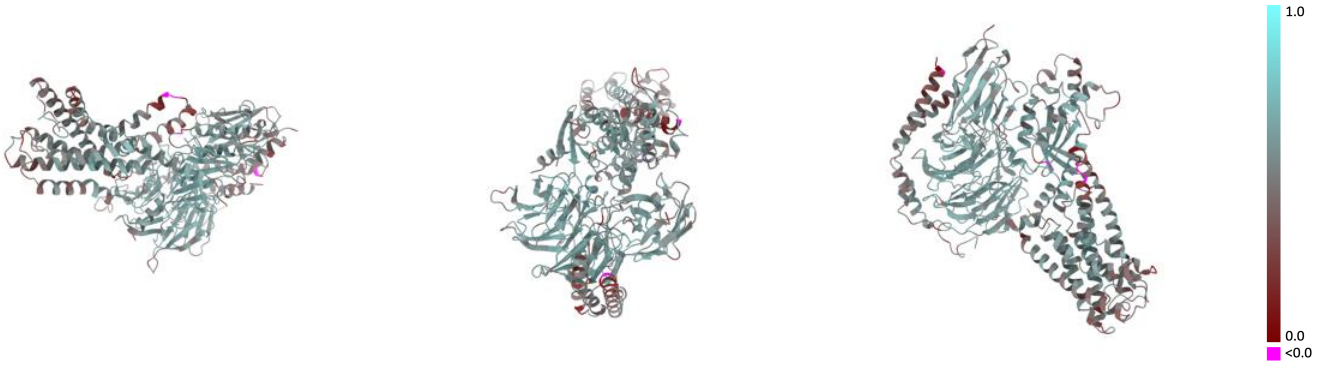
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0115 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.

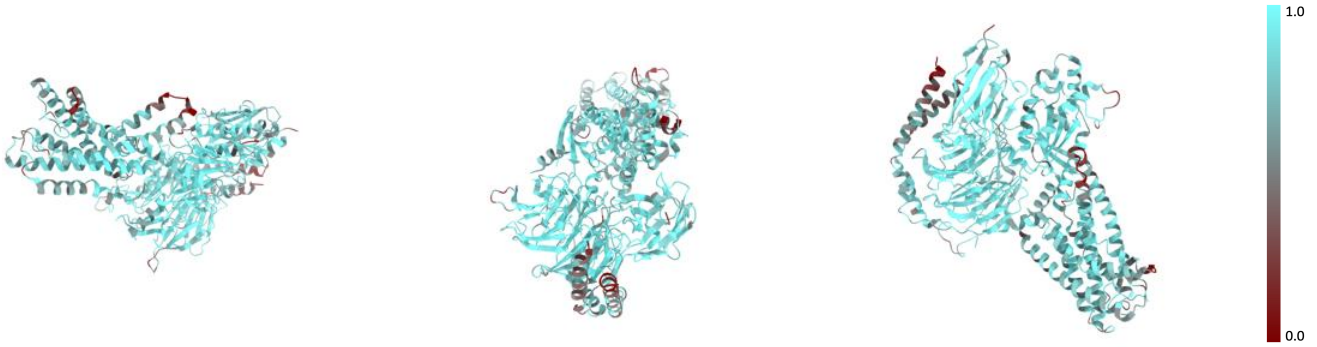
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

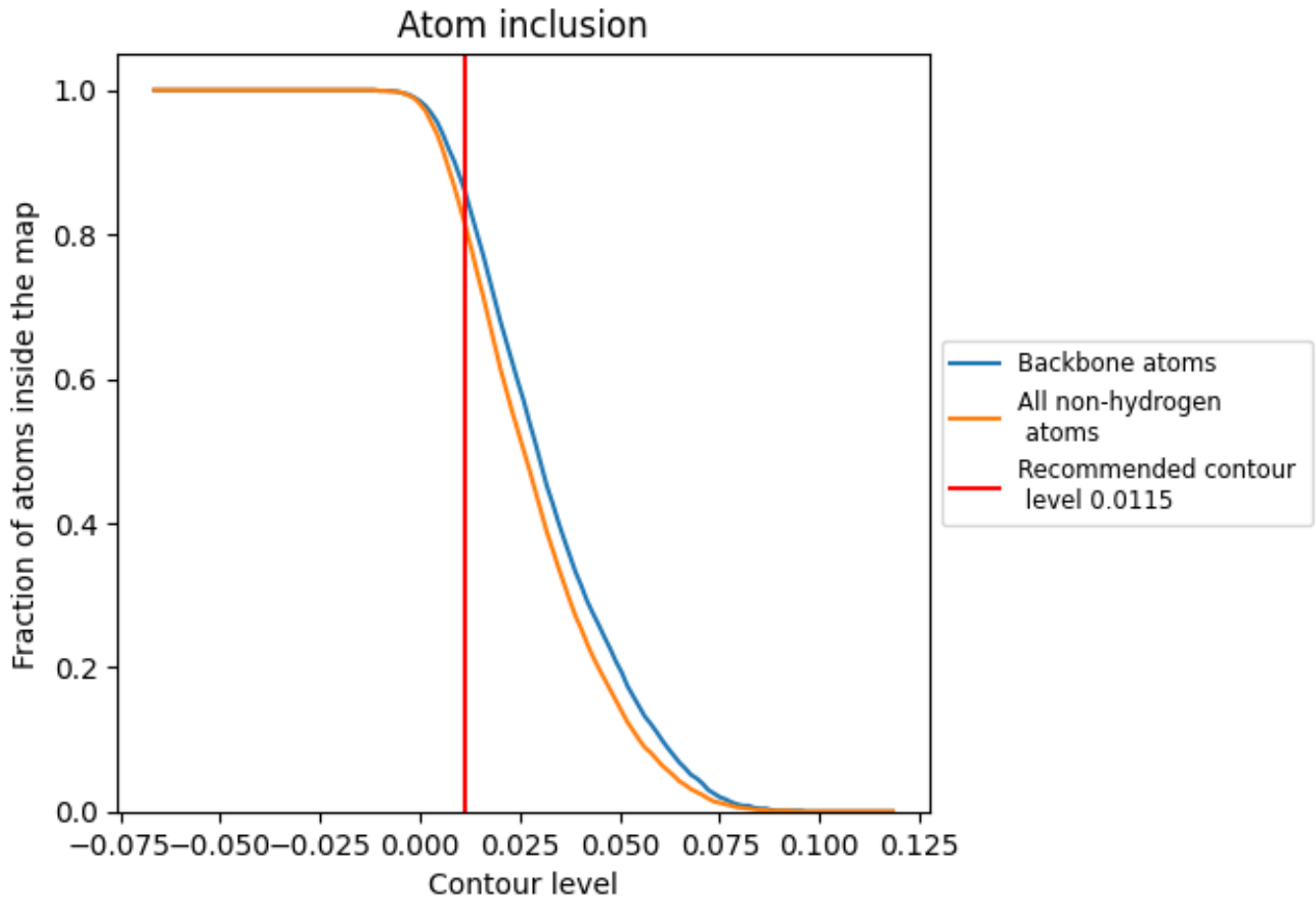
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0115).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 81% 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 (0.0115) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8110	0.5300
A	0.8480	0.5440
B	0.8640	0.5710
C	0.6390	0.4440
N	0.8410	0.5440
R	0.7370	0.4780