



wwPDB EM Validation Summary Report ⓘ

Nov 11, 2024 – 08:09 PM JST

PDB ID : 7WVX
EMDB ID : EMD-32861
Title : Cryo-EM structure of the human formyl peptide receptor 2 in complex with fhumanin and Gi2
Authors : Zhu, Y.; Lin, X.; Zong, X.; Han, S.; Zhao, Q.; Wu, B.
Deposited on : 2022-02-11
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
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

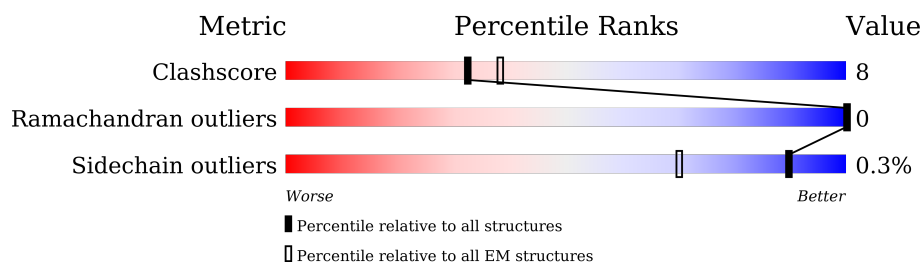
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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 $\leq 5\%$. 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	L	24	 50% 12% 38%
2	R	513	 44% 14% 42%
3	A	355	 53% 7% 39%
4	B	351	 73% 23% .
5	C	71	 58% 17% 25%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7070 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 Humanin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L	15	Total	C	N	O	S	0	0
			114	73	18	21	2		

- Molecule 2 is a protein called Soluble cytochrome b562,N-formyl peptide receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	299	Total	C	N	O	S	0	0
			2331	1571	373	371	16		

There are 65 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-118	GLY	-	expression tag	UNP P0ABE7
R	-117	ALA	-	expression tag	UNP P0ABE7
R	-116	PRO	-	expression tag	UNP P0ABE7
R	-109	TRP	MET	conflict	UNP P0ABE7
R	-14	ILE	HIS	conflict	UNP P0ABE7
R	-10	LEU	-	linker	UNP P0ABE7
R	-9	GLY	-	linker	UNP P0ABE7
R	-8	SER	-	linker	UNP P0ABE7
R	-7	GLY	-	linker	UNP P0ABE7
R	-6	SER	-	linker	UNP P0ABE7
R	-5	GLU	-	linker	UNP P0ABE7
R	-4	ASN	-	linker	UNP P0ABE7
R	-3	LEU	-	linker	UNP P0ABE7
R	-2	TYR	-	linker	UNP P0ABE7
R	-1	PHE	-	linker	UNP P0ABE7
R	0	GLN	-	linker	UNP P0ABE7
R	1	SER	-	linker	UNP P0ABE7
R	211	LEU	SER	engineered mutation	UNP P25090
R	348	PHE	-	expression tag	UNP P25090
R	349	LEU	-	expression tag	UNP P25090
R	350	GLU	-	expression tag	UNP P25090

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Chain	Residue	Modelled	Actual	Comment	Reference
R	351	VAL	-	expression tag	UNP P25090
R	352	LEU	-	expression tag	UNP P25090
R	353	PHE	-	expression tag	UNP P25090
R	354	GLN	-	expression tag	UNP P25090
R	355	GLY	-	expression tag	UNP P25090
R	356	PRO	-	expression tag	UNP P25090
R	357	GLY	-	expression tag	UNP P25090
R	358	SER	-	expression tag	UNP P25090
R	359	TRP	-	expression tag	UNP P25090
R	360	SER	-	expression tag	UNP P25090
R	361	HIS	-	expression tag	UNP P25090
R	362	PRO	-	expression tag	UNP P25090
R	363	GLN	-	expression tag	UNP P25090
R	364	PHE	-	expression tag	UNP P25090
R	365	GLU	-	expression tag	UNP P25090
R	366	LYS	-	expression tag	UNP P25090
R	367	GLY	-	expression tag	UNP P25090
R	368	SER	-	expression tag	UNP P25090
R	369	GLY	-	expression tag	UNP P25090
R	370	ALA	-	expression tag	UNP P25090
R	371	GLY	-	expression tag	UNP P25090
R	372	ALA	-	expression tag	UNP P25090
R	373	SER	-	expression tag	UNP P25090
R	374	ALA	-	expression tag	UNP P25090
R	375	GLY	-	expression tag	UNP P25090
R	376	SER	-	expression tag	UNP P25090
R	377	TRP	-	expression tag	UNP P25090
R	378	SER	-	expression tag	UNP P25090
R	379	HIS	-	expression tag	UNP P25090
R	380	PRO	-	expression tag	UNP P25090
R	381	GLN	-	expression tag	UNP P25090
R	382	PHE	-	expression tag	UNP P25090
R	383	GLU	-	expression tag	UNP P25090
R	384	LYS	-	expression tag	UNP P25090
R	385	GLY	-	expression tag	UNP P25090
R	386	SER	-	expression tag	UNP P25090
R	387	ASP	-	expression tag	UNP P25090
R	388	TYR	-	expression tag	UNP P25090
R	389	LYS	-	expression tag	UNP P25090
R	390	ASP	-	expression tag	UNP P25090
R	391	ASP	-	expression tag	UNP P25090
R	392	ASP	-	expression tag	UNP P25090

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Chain	Residue	Modelled	Actual	Comment	Reference
R	393	ASP	-	expression tag	UNP P25090
R	394	LYS	-	expression tag	UNP P25090

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	215	Total	C	N	O	S	0	0
			1680	1081	283	305	11		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ASN	SER	engineered mutation	UNP P04899
A	204	ALA	GLY	engineered mutation	UNP P04899
A	246	ALA	GLU	engineered mutation	UNP P04899
A	327	SER	ALA	engineered mutation	UNP P04899

- 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	338	Total	C	N	O	S	0	0
			2557	1583	455	499	20		

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

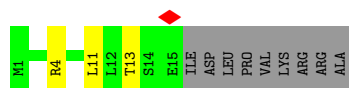
- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	53	Total	C	N	O	S	0	0
			388	246	68	71	3		

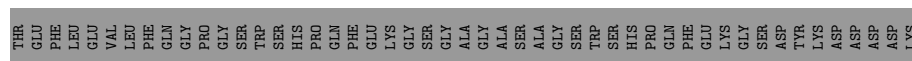
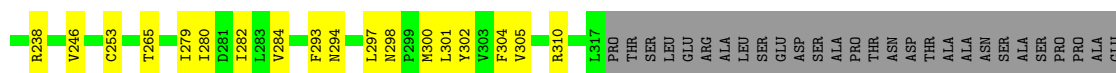
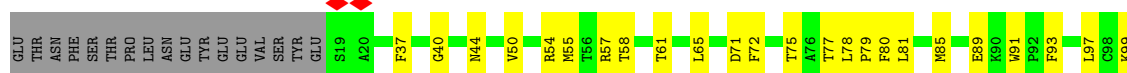
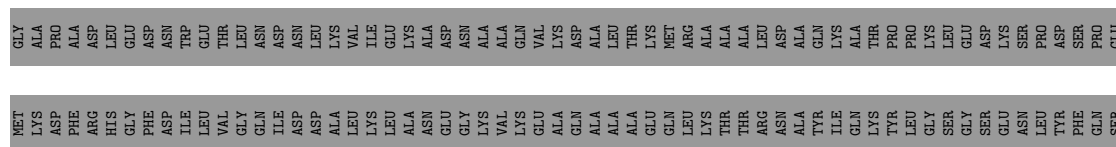
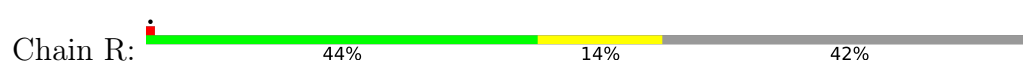
3 Residue-property plots

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.

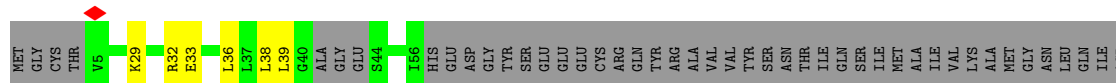
- Molecule 1: Humanin



- Molecule 2: Soluble cytochrome b562,N-formyl peptide receptor 2



- Molecule 3: Guanine nucleotide-binding protein G(i) subunit alpha-2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1398841	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 ($e^-/\text{\AA}^2$)	2.1875	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.261	Depositor
Minimum map value	-0.154	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.021	Depositor
Map size (\AA)	267.52, 267.52, 267.52	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.045, 1.045, 1.045	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	L	0.23	0/105	0.53	0/141
2	R	0.25	0/2396	0.42	0/3274
3	A	0.24	0/1709	0.39	0/2296
4	B	0.24	0/2604	0.45	0/3539
5	C	0.24	0/394	0.36	0/535
All	All	0.24	0/7208	0.42	0/9785

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 [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	L	114	0	119	2	0
2	R	2331	0	2433	50	0
3	A	1680	0	1653	19	0
4	B	2557	0	2427	51	0
5	C	388	0	383	8	0
All	All	7070	0	7015	117	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 8.

The worst 5 of 117 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)
4:B:271:CYS:HB2	4:B:290:ASP:HB2	1.68	0.76
4:B:250:CYS:HB2	4:B:264:TYR:HB2	1.70	0.73
3:A:38:LEU:HD11	3:A:199:MET:HE3	1.71	0.72
4:B:310:GLY:O	4:B:337:LYS:NZ	2.25	0.67
2:R:298:ASN:O	2:R:302:TYR:HB2	1.95	0.66

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	L	13/24 (54%)	11 (85%)	2 (15%)	0	100	100
2	R	297/513 (58%)	291 (98%)	6 (2%)	0	100	100
3	A	207/355 (58%)	205 (99%)	2 (1%)	0	100	100
4	B	336/351 (96%)	328 (98%)	8 (2%)	0	100	100
5	C	51/71 (72%)	50 (98%)	1 (2%)	0	100	100
All	All	904/1314 (69%)	885 (98%)	19 (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	L	12/20 (60%)	11 (92%)	1 (8%)	9	28
2	R	252/432 (58%)	252 (100%)	0	100	100
3	A	176/309 (57%)	176 (100%)	0	100	100
4	B	269/293 (92%)	268 (100%)	1 (0%)	89	96
5	C	37/58 (64%)	37 (100%)	0	100	100
All	All	746/1112 (67%)	744 (100%)	2 (0%)	90	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	4	ARG
4	B	134	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
5	C	18	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	FME	L	1	1	8,9,10	0.94	0	7,9,11	0.88	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	FME	L	1	1	-	2/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	L	1	FME	CA-CB-CG-SD
1	L	1	FME	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

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.

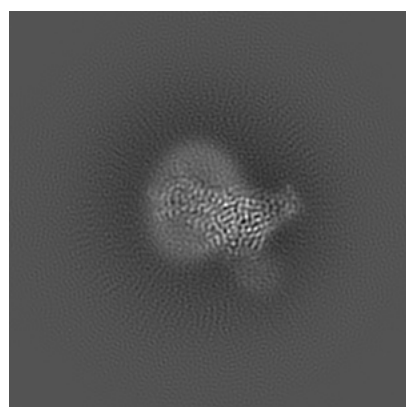
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32861. These allow visual inspection of the internal detail of the map and identification of artifacts.

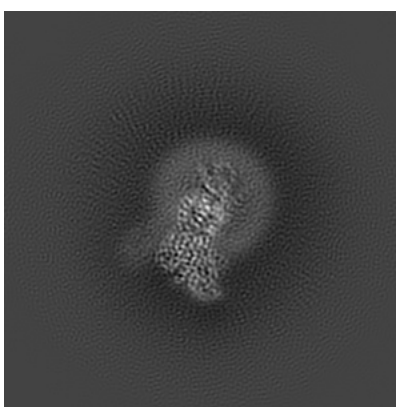
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

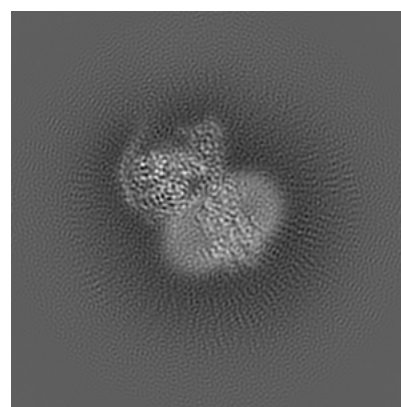
6.1.1 Primary map



X



Y

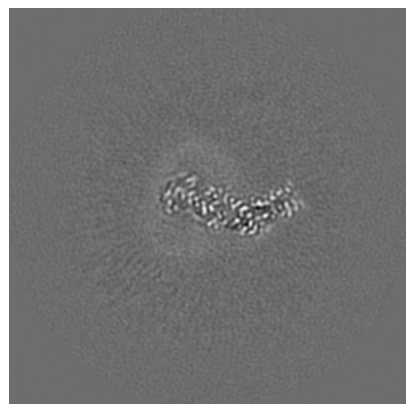


Z

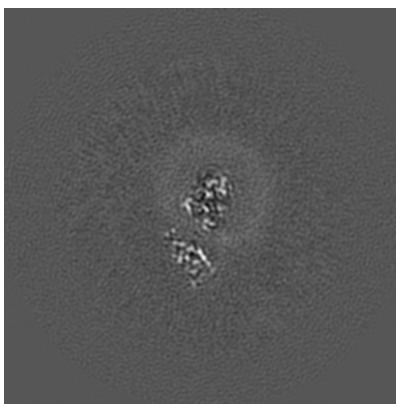
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

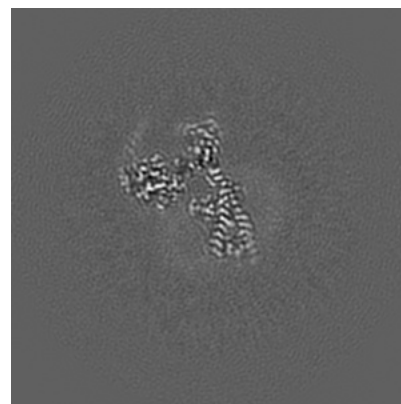
6.2.1 Primary map



X Index: 128



Y Index: 128

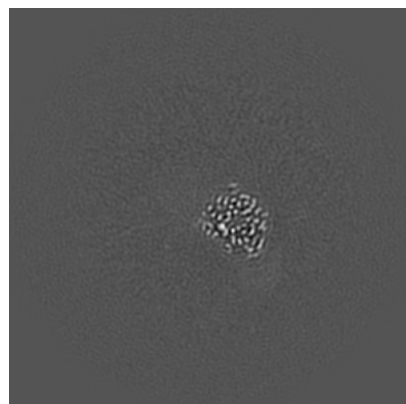


Z Index: 128

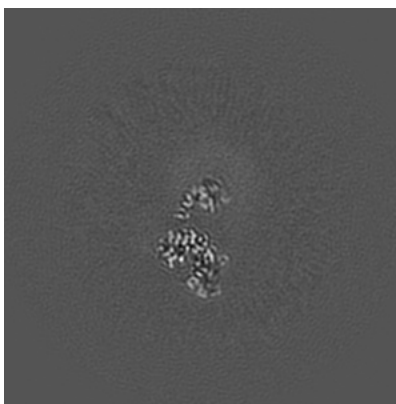
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

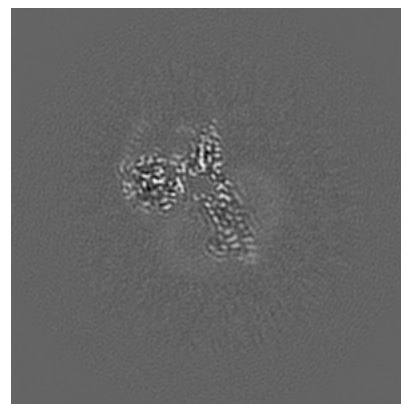
6.3.1 Primary map



X Index: 95



Y Index: 143

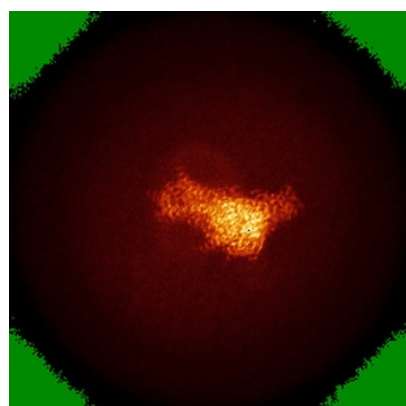


Z Index: 125

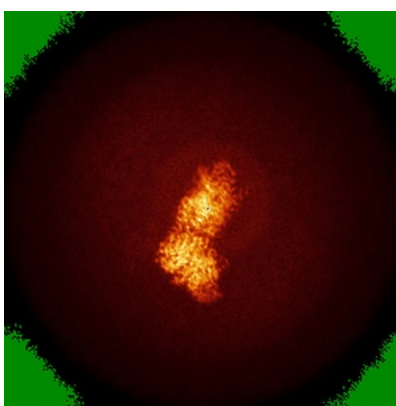
The images above show the largest variance slices of the map in three orthogonal directions.

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

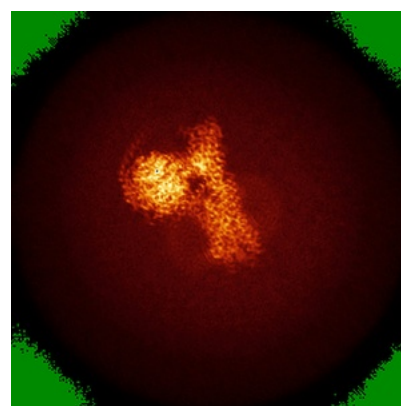
6.4.1 Primary map



X



Y

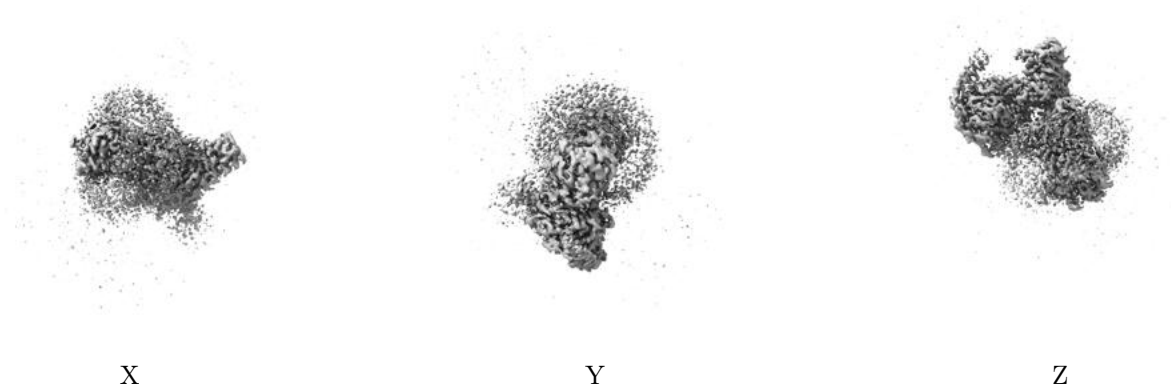


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

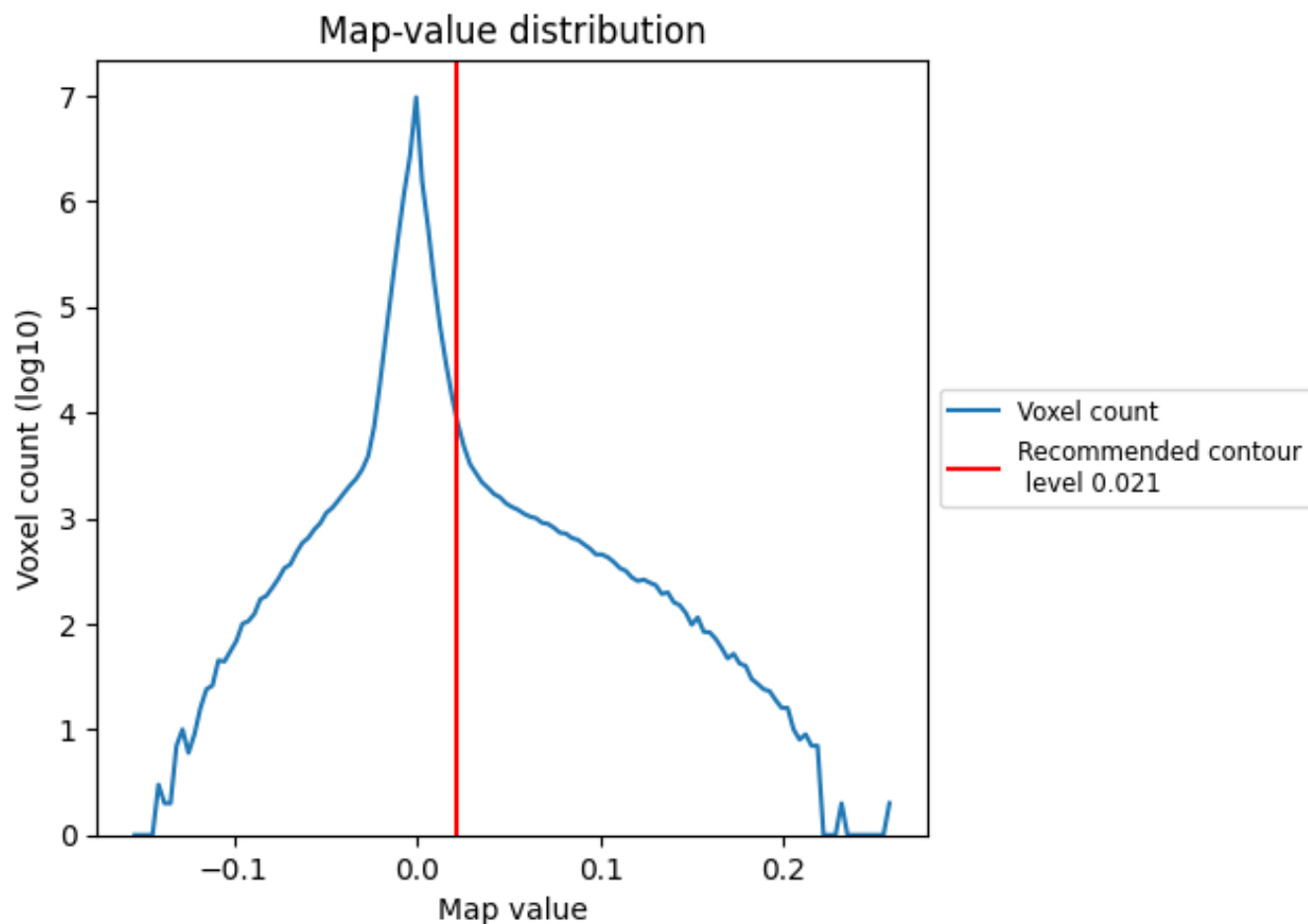
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

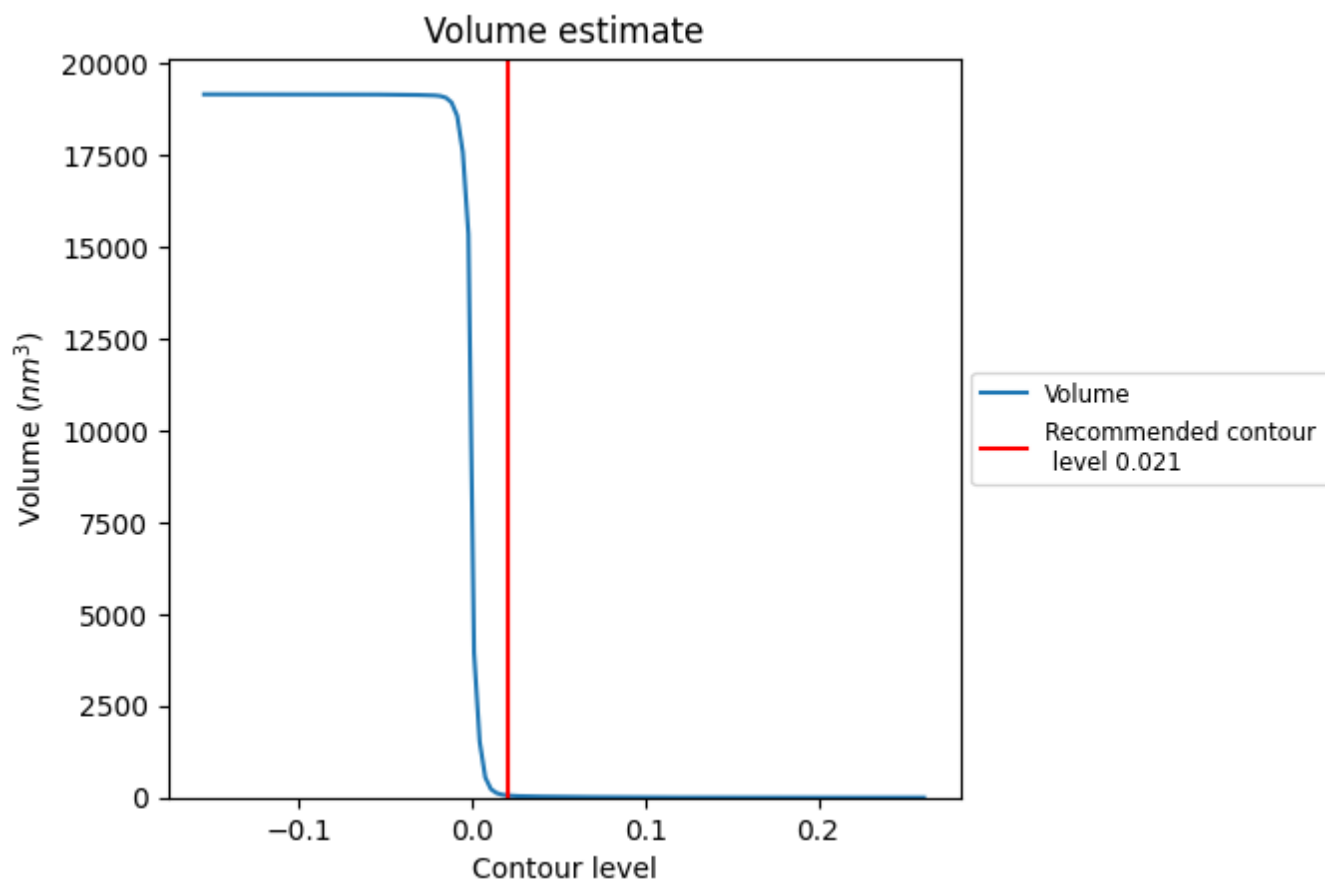
This section contains the results of statistical analysis of the map.

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.

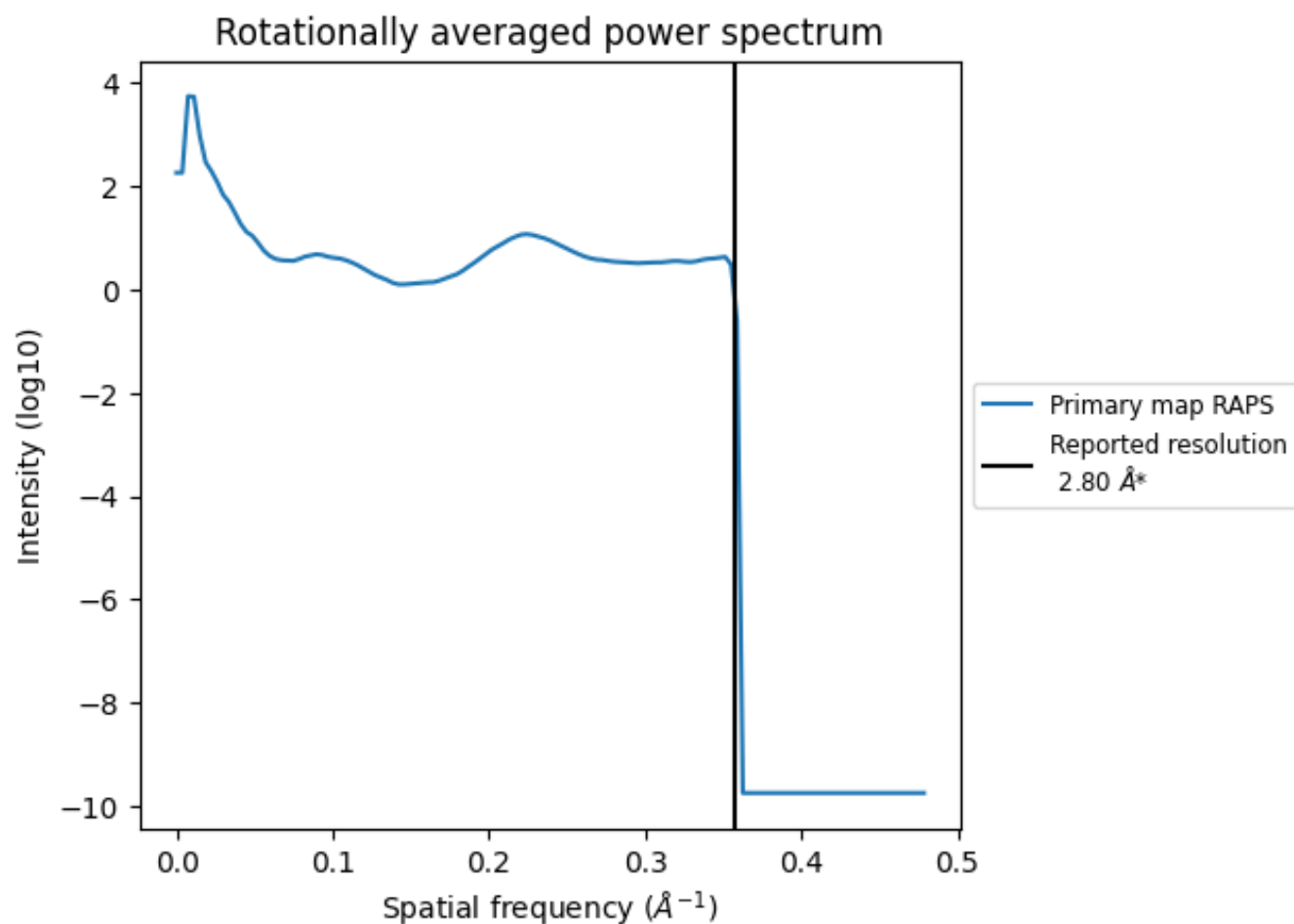
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 56 nm³; this corresponds to an approximate mass of 50 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 0.357 Å⁻¹

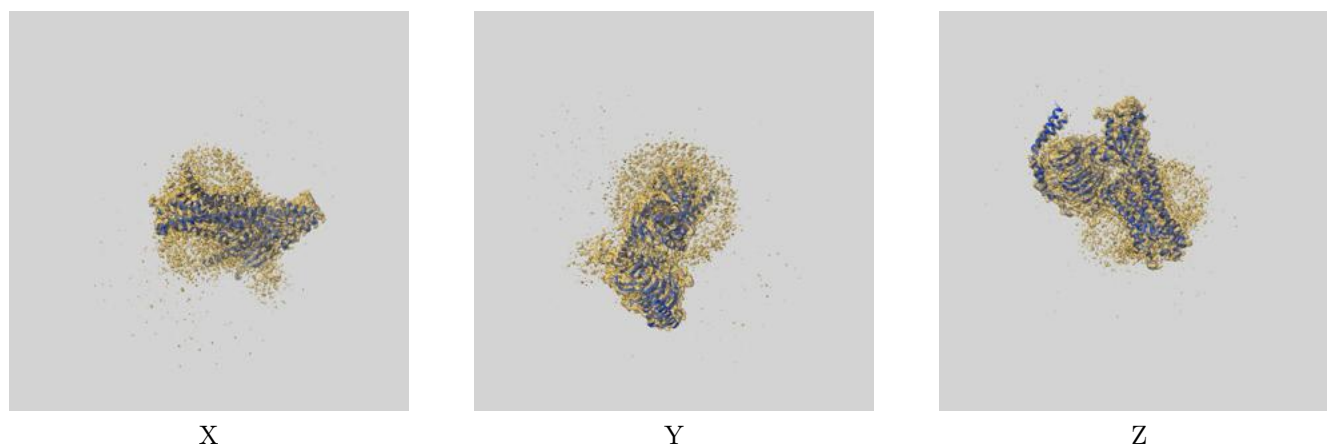
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32861 and PDB model 7WVX. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



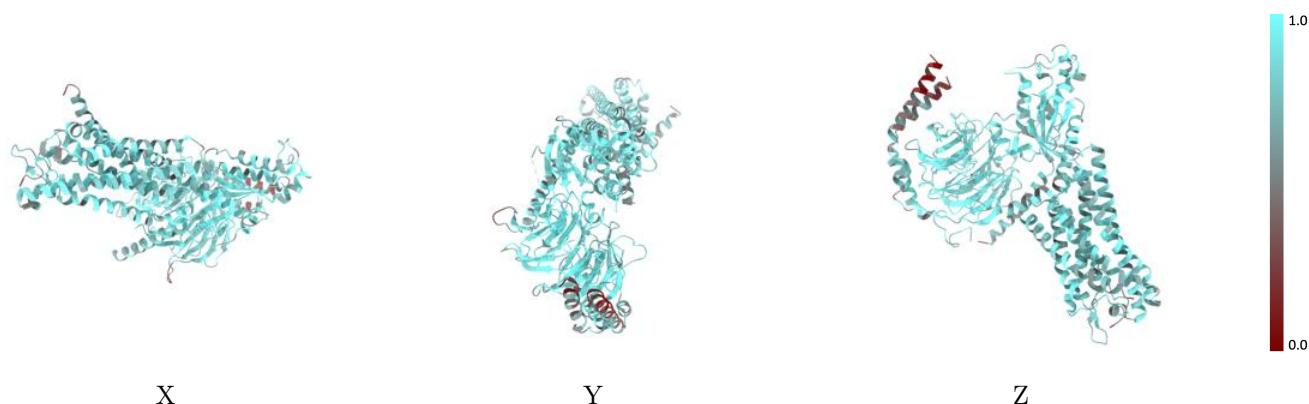
The images above show the 3D surface view of the map at the recommended contour level 0.021 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



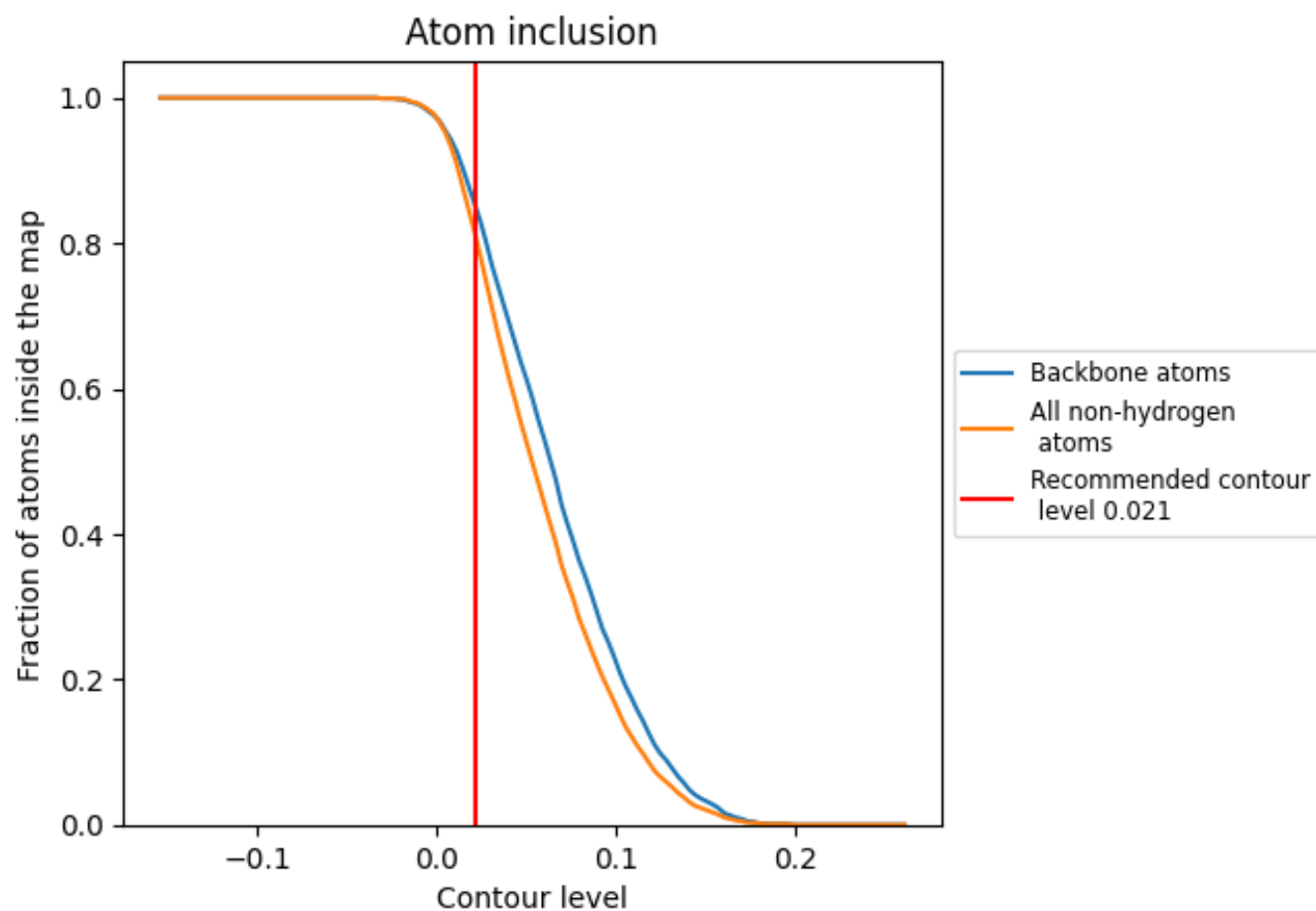
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.021).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8150	<div></div> 0.5100
A	<div></div> 0.8360	<div></div> 0.5250
B	<div></div> 0.8420	<div></div> 0.5330
C	<div></div> 0.6920	<div></div> 0.4570
L	<div></div> 0.6430	<div></div> 0.4180
R	<div></div> 0.7980	<div></div> 0.4880

