



wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 05:25 PM JST

PDB ID : 8IY9
EMDB ID : EMD-35817
Title : Structure of Niacin-GPR109A-G protein complex
Authors : Yadav, M.K.; Sarma, P.; Chami, M.; Banerjee, R.; Shukla, A.K.
Deposited on : 2023-04-04
Resolution : 3.37 Å(reported)
Based on initial model : .

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
buster-report : 1.1.7 (2018)
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

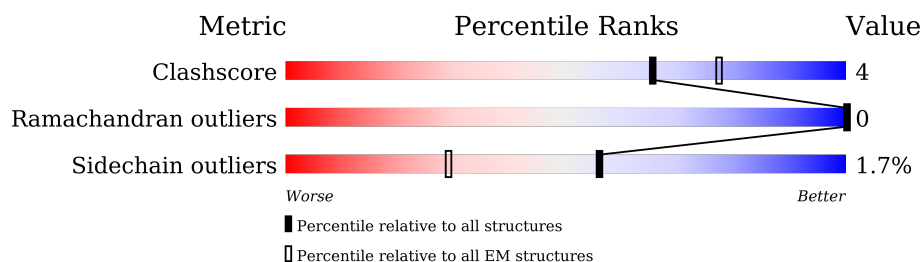
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





The reported resolution of this entry is 3.37 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	A	240	 80% 7% 13%
2	B	350	 89% 7% .
3	G	71	 72% 7% 21%
4	H	248	 89% . 7%
5	R	419	 62% 9% 29%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8121 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(o) subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	208	Total	C	N	O	S	0	0
			1551	997	263	283	8		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP P09471
A	-10	GLY	-	expression tag	UNP P09471
A	-9	HIS	-	expression tag	UNP P09471
A	-8	HIS	-	expression tag	UNP P09471
A	-7	HIS	-	expression tag	UNP P09471
A	-6	HIS	-	expression tag	UNP P09471
A	-5	HIS	-	expression tag	UNP P09471
A	-4	HIS	-	expression tag	UNP P09471
A	-3	GLU	-	expression tag	UNP P09471
A	-2	ASN	-	expression tag	UNP P09471
A	-1	LEU	-	expression tag	UNP P09471
A	0	TYR	-	expression tag	UNP P09471
A	1	PHE	-	expression tag	UNP P09471
A	2	GLN	-	expression tag	UNP P09471
A	3	GLY	-	expression tag	UNP P09471
A	4	THR	-	expression tag	UNP P09471
A	5	LEU	-	expression tag	UNP P09471
A	42	ASP	GLY	engineered mutation	UNP P09471
A	43	ASN	GLU	engineered mutation	UNP P09471
A	172	ILE	-	linker	UNP P09471
A	173	HIS	-	linker	UNP P09471
A	174	GLY	-	linker	UNP P09471
A	175	GLY	-	linker	UNP P09471
A	176	SER	-	linker	UNP P09471
A	177	GLY	-	linker	UNP P09471
A	178	GLY	-	linker	UNP P09471
A	179	SER	-	linker	UNP P09471

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Chain	Residue	Modelled	Actual	Comment	Reference
A	180	GLY	-	linker	UNP P09471
A	181	GLY	-	linker	UNP P09471
A	227	ASP	ALA	engineered mutation	UNP P09471
A	230	ASP	GLY	engineered mutation	UNP P09471
A	?	-	ASP	deletion	UNP P09471
A	?	-	GLN	deletion	UNP P09471
A	?	-	VAL	deletion	UNP P09471
A	?	-	LEU	deletion	UNP P09471
A	?	-	HIS	deletion	UNP P09471
A	?	-	GLU	deletion	UNP P09471
A	?	-	ASP	deletion	UNP P09471
A	?	-	GLU	deletion	UNP P09471
A	?	-	THR	deletion	UNP P09471
A	?	-	THR	deletion	UNP P09471
A	332	ALA	ILE	engineered mutation	UNP P09471
A	335	ILE	VAL	engineered mutation	UNP P09471

- 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
			2399	1488	437	459	15		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	MET	-	initiating methionine	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	HIS	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873
B	2	SER	-	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	G	56	Total	C	N	O	S	0	0
			392	247	68	75	2		

- Molecule 4 is a protein called ScFv16 (Antibody Fragment).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	231	Total	C	N	O	S	0	0
			1655	1049	279	320	7		

- Molecule 5 is a protein called Hydroxycarboxylic acid receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	297	Total	C	N	O	S	0	0
			2115	1388	364	348	15		

There are 35 discrepancies between the modelled and reference sequences:

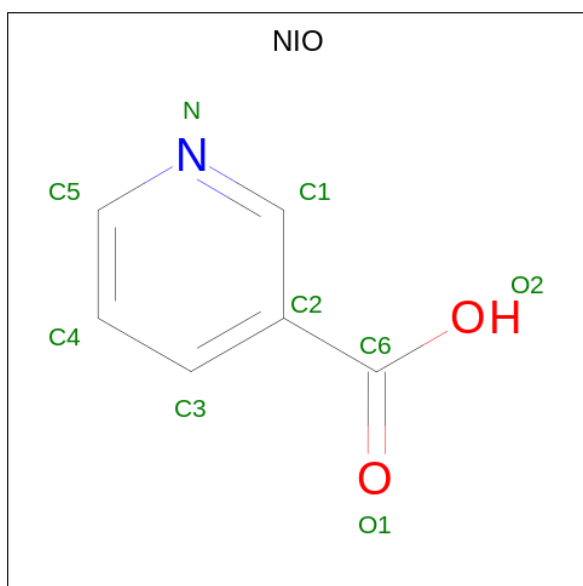
Chain	Residue	Modelled	Actual	Comment	Reference
R	-55	MET	-	initiating methionine	UNP P08173
R	-54	GLY	-	expression tag	UNP P08173
R	-53	LYS	-	expression tag	UNP P08173
R	-52	THR	-	expression tag	UNP P08173
R	-51	ILE	-	expression tag	UNP P08173
R	-50	ILE	-	expression tag	UNP P08173
R	-49	ALA	-	expression tag	UNP P08173
R	-48	LEU	-	expression tag	UNP P08173
R	-47	SER	-	expression tag	UNP P08173
R	-46	TYR	-	expression tag	UNP P08173
R	-45	ILE	-	expression tag	UNP P08173
R	-44	PHE	-	expression tag	UNP P08173
R	-43	CYS	-	expression tag	UNP P08173
R	-42	LEU	-	expression tag	UNP P08173
R	-41	VAL	-	expression tag	UNP P08173
R	-40	PHE	-	expression tag	UNP P08173
R	-39	ALA	-	expression tag	UNP P08173
R	-38	ASP	-	expression tag	UNP P08173
R	-37	TYR	-	expression tag	UNP P08173
R	-36	LYS	-	expression tag	UNP P08173
R	-35	ASP	-	expression tag	UNP P08173
R	-34	ASP	-	expression tag	UNP P08173
R	-33	ASP	-	expression tag	UNP P08173
R	-32	ASP	-	expression tag	UNP P08173
R	-31	ALA	-	expression tag	UNP P08173

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-8	LEU	-	linker	UNP P08173
R	-7	GLU	-	linker	UNP P08173
R	-6	VAL	-	linker	UNP P08173
R	-5	LEU	-	linker	UNP P08173
R	-4	PHE	-	linker	UNP P08173
R	-3	GLN	-	linker	UNP P08173
R	-2	GLY	-	linker	UNP P08173
R	-1	PRO	-	linker	UNP P08173
R	0	GLY	-	linker	UNP P08173
R	1	SER	-	linker	UNP P08173

- Molecule 6 is NICOTINIC ACID (three-letter code: NIO) (formula: $C_6H_5NO_2$) (labeled as "Ligand of Interest" by depositor).




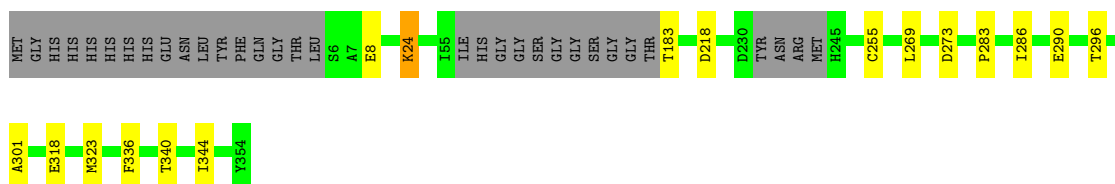
Mol	Chain	Residues	Atoms				AltConf
6	R	1	Total	C	N	O	0
			9	6	1	2	

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.

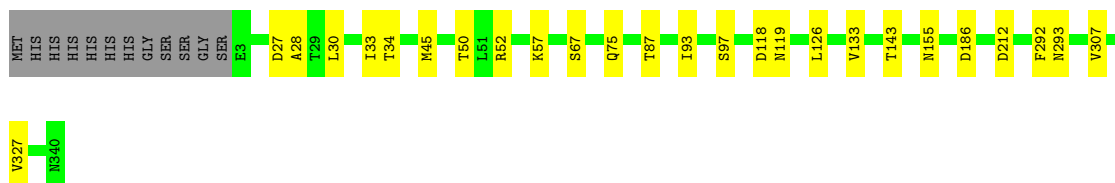
- Molecule 1: Guanine nucleotide-binding protein G(o) subunit alpha

Chain A: 



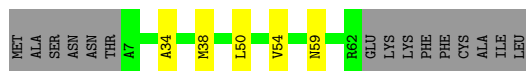
- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B: 




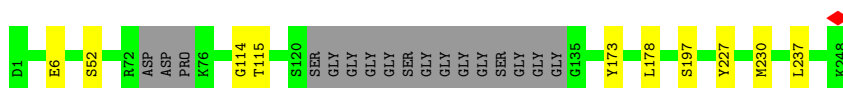
- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

Chain G: 



- Molecule 4: ScFv16 (Antibody Fragment)

Chain H: 



- Molecule 5: Hydroxycarboxylic acid receptor 2



MET	GLY	LYS	THR	ILE	ILE	ALA	LEU	SER	TYR	ILE	PHE	CYS	LEU	VAL	PHE	ASP	ALA	ASP	TYR	LYS	ASP	ASP	ASP	ALA	ALA	ASN	PHE	THR	PRO	VAL	ASN	GLY	SER	SER	GLY	ASN	GLN	VAL	ARG	LEU	VAL	THR	SER	SER	SER	LEU	LEU	GLU	VAL	LEU	PHE	GLN	PRO	GLY	SER	ASN	ARG	HIS
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HIS	LEU	GLN	D8	H9	F10	L11	N17	C18	D23	D24	F25	I26	V27	L34	F40	G41	L42	L43	A48	H55	S58	F82	R90	M103	L104	Q112	I116	P132	G173	A174	N175	C183	A191	S208	L215	M220	I230	T231	F232
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T233	M234	V235	L245	P246	S247	V248	T260	C266	A275	T279	F282	M285	D290	P291	Y294	P299	P302	N303	F304	PHE	SER	THR	LEU	ILE	ASN	ARG	CYS	LEU	GLN	ARG	LYS	MET	THR	GLY	GLU	PRO	ASP	ASN	ASN	ARG	SER	THR	VAL	GLU	LEU	THR	GLY
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ASP	PRO	ASN	LYS	THR	ARG	GLY	ALA	PRO	PRO	GLU	ALA	LEU	MET	ALA	ASN	SER	GLY	GLU	PRO	TRP	SER	PRO	SER	TYR	LEU	GLY	PRO	THR	SER	PRO
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1011301	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.392	Depositor
Minimum map value	-2.228	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.18	Depositor
Map size (\AA)	316.0832, 316.0832, 316.0832	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.2347, 1.2347, 1.2347	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: NIO

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	0.34	0/1577	0.62	0/2131
2	B	0.33	0/2446	0.60	0/3338
3	G	0.31	0/398	0.55	0/544
4	H	0.35	0/1697	0.56	0/2315
5	R	0.33	0/2170	0.61	0/2975
All	All	0.33	0/8288	0.60	0/11303

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	A	1551	0	1472	13	0
2	B	2399	0	2128	20	0
3	G	392	0	371	4	0
4	H	1655	0	1471	7	0
5	R	2115	0	1889	21	0
6	R	9	0	4	0	0
All	All	8121	0	7335	58	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 58 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:18:CYS:HA	5:R:183:CYS:HB3	1.66	0.77
5:R:175:ASN:O	5:R:175:ASN:OD1	2.12	0.68
5:R:23:ASP:OD1	5:R:24:ASP:N	2.28	0.67
5:R:282:PHE:O	5:R:285:MET:N	2.32	0.62
2:B:27:ASP:OD1	2:B:28:ALA:N	2.34	0.61

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	202/240 (84%)	196 (97%)	6 (3%)	0	100	100
2	B	336/350 (96%)	321 (96%)	15 (4%)	0	100	100
3	G	54/71 (76%)	54 (100%)	0	0	100	100
4	H	225/248 (91%)	218 (97%)	7 (3%)	0	100	100
5	R	295/419 (70%)	289 (98%)	6 (2%)	0	100	100
All	All	1112/1328 (84%)	1078 (97%)	34 (3%)	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	150/206 (73%)	145 (97%)	5 (3%)	33	59
2	B	219/291 (75%)	217 (99%)	2 (1%)	75	86
3	G	36/58 (62%)	36 (100%)	0	100	100
4	H	160/201 (80%)	158 (99%)	2 (1%)	65	79
5	R	186/375 (50%)	182 (98%)	4 (2%)	47	69
All	All	751/1131 (66%)	738 (98%)	13 (2%)	56	74

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	52	SER
4	H	197	SER
5	R	294	TYR
5	R	208	SER
5	R	234	MET

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	266	HIS
2	B	268	ASN
5	R	112	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand 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	$\# Z > 2$
6	NIO	R	401	-	9,9,9	0.17	0	11,11,11	0.31	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
6	NIO	R	401	-	-	0/4/4/4	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

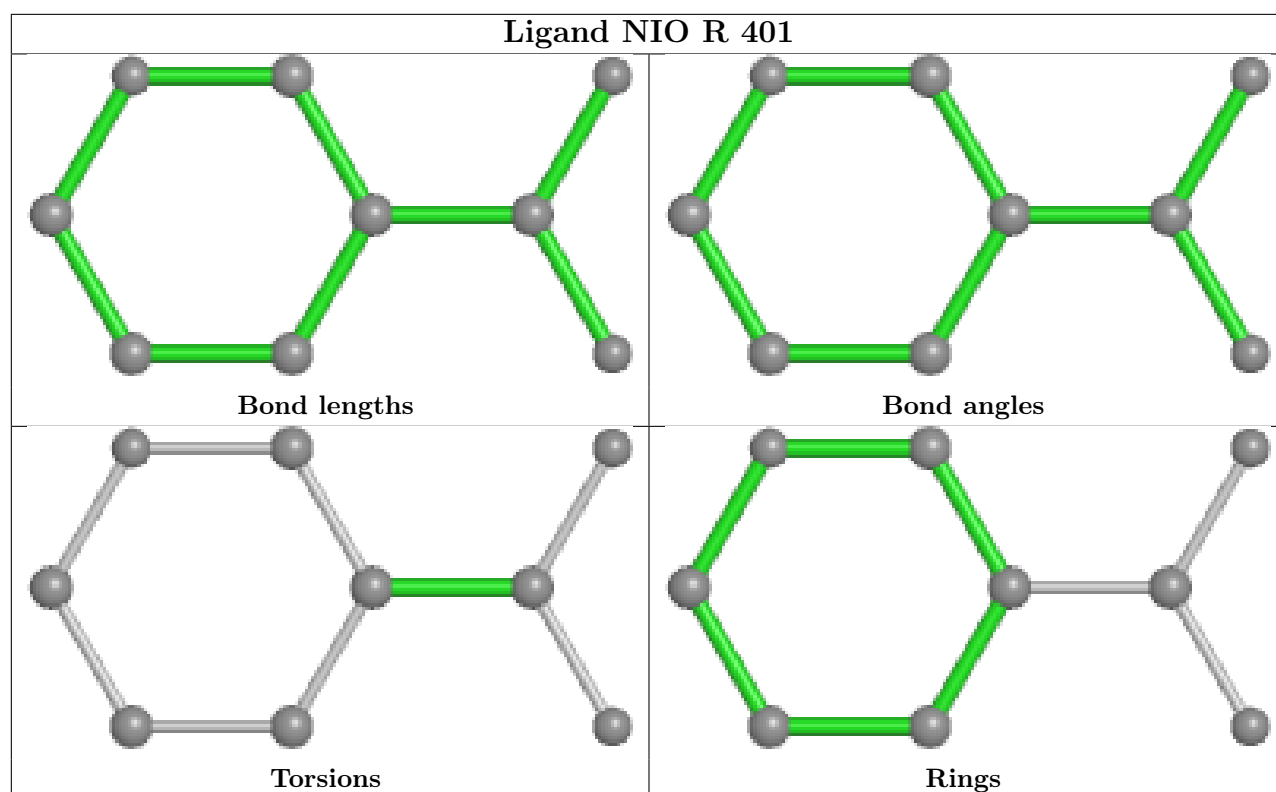
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

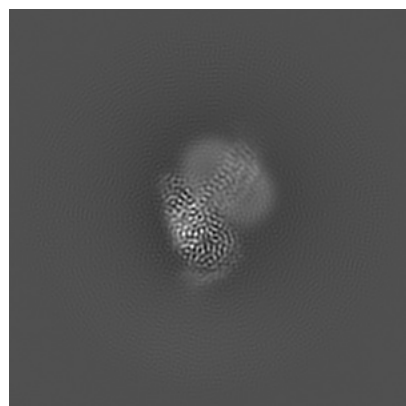
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35817. These allow visual inspection of the internal detail of the map and identification of artifacts.

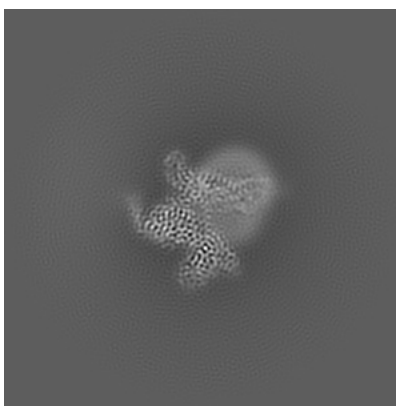
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

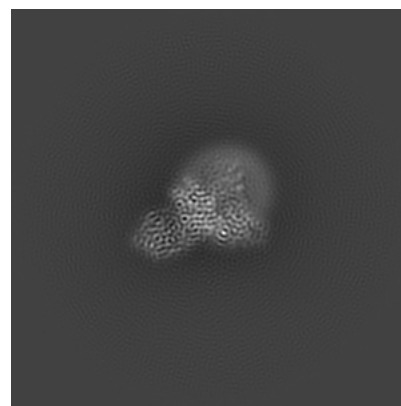
6.1.1 Primary map



X

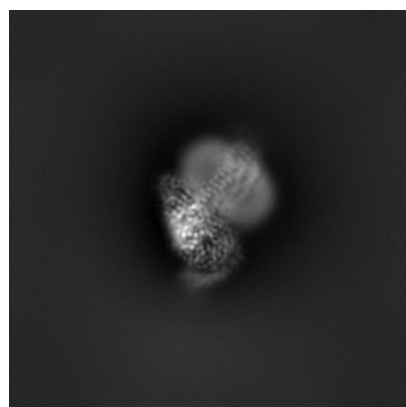


Y

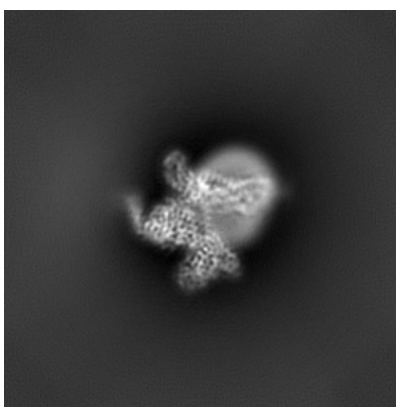


Z

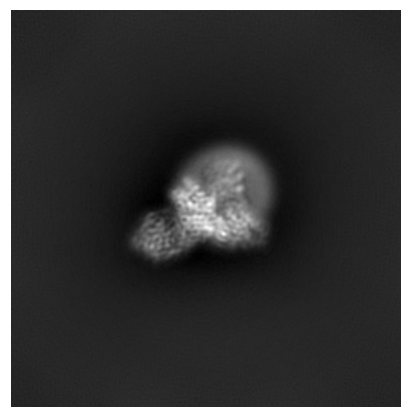
6.1.2 Raw map



X



Y

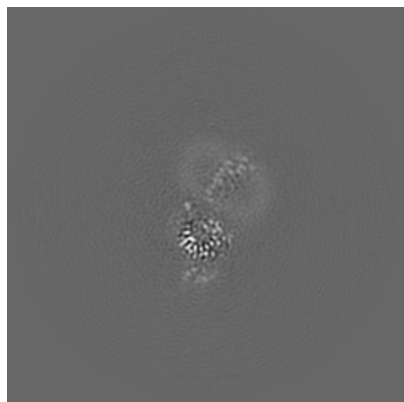


Z

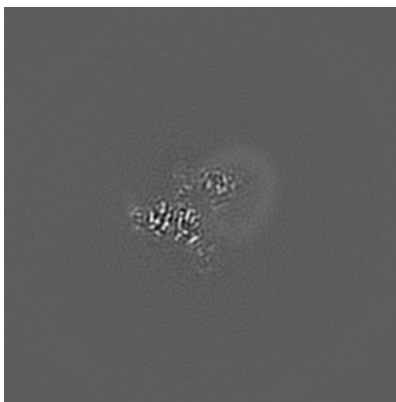
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

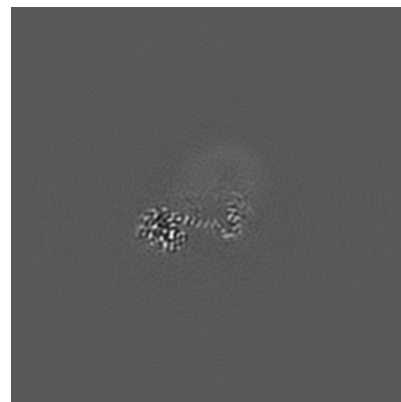
6.2.1 Primary map



X Index: 128

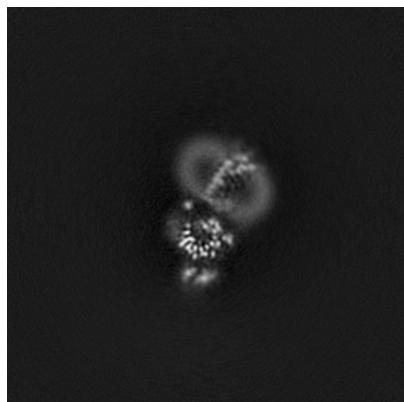


Y Index: 128

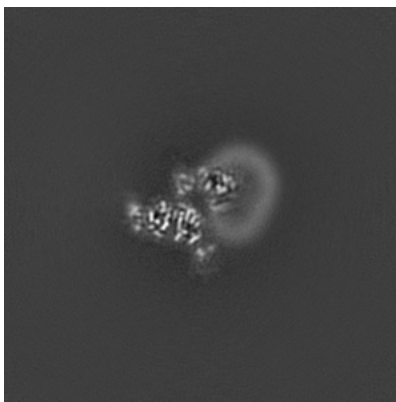


Z Index: 128

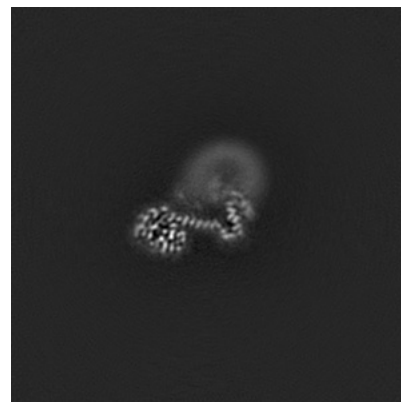
6.2.2 Raw map



X Index: 128



Y Index: 128

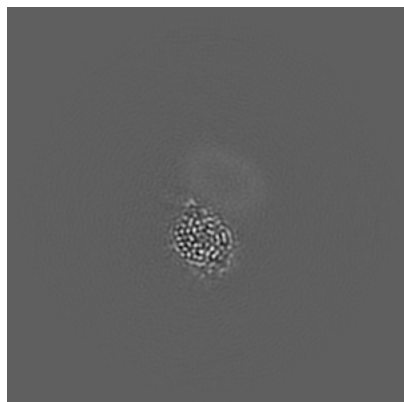


Z Index: 128

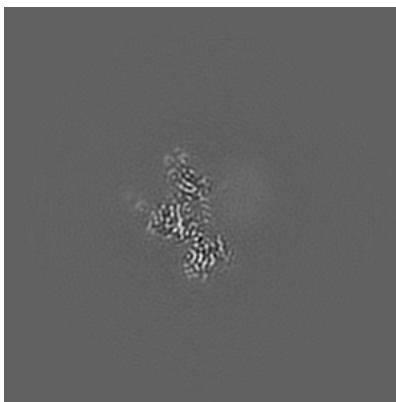
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

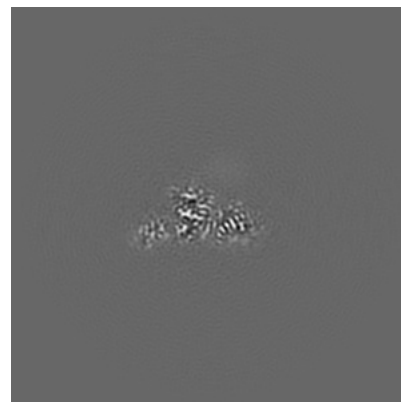
6.3.1 Primary map



X Index: 118

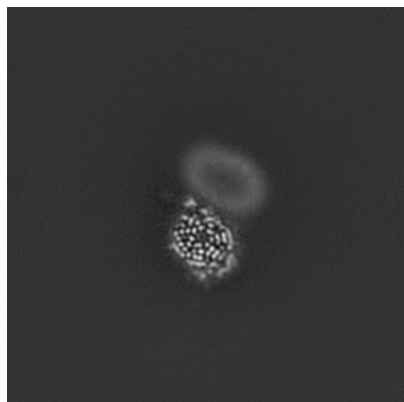


Y Index: 115

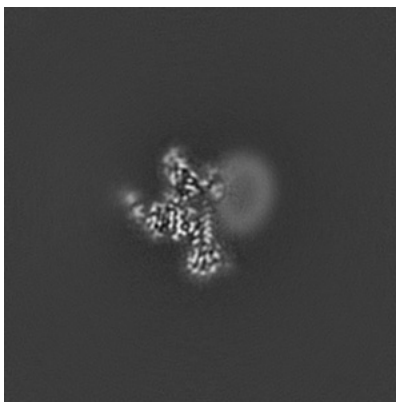


Z Index: 117

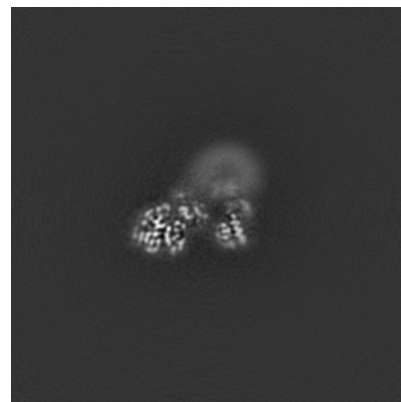
6.3.2 Raw map



X Index: 118



Y Index: 119

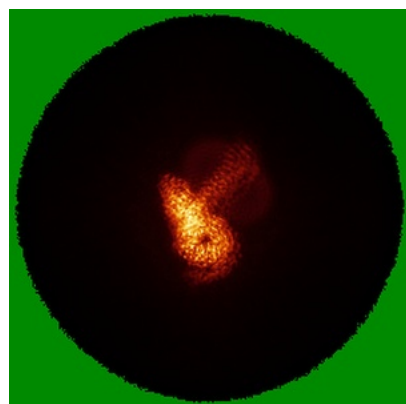


Z Index: 125

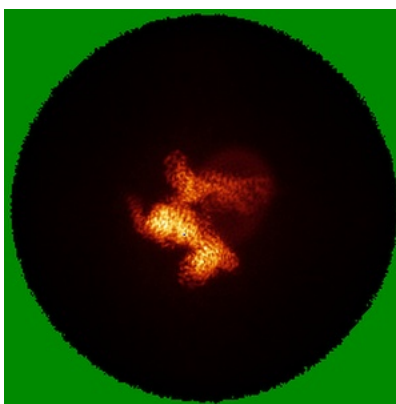
The images above show the largest variance slices of the map in three orthogonal directions.

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

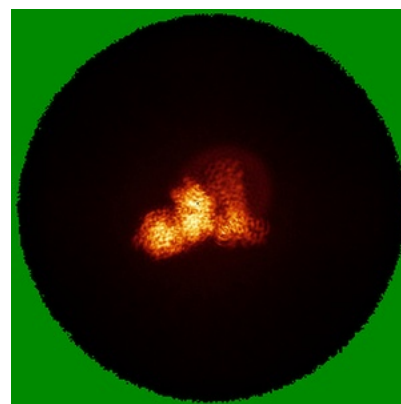
6.4.1 Primary map



X

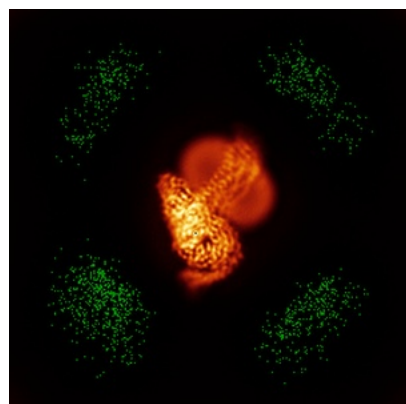


Y

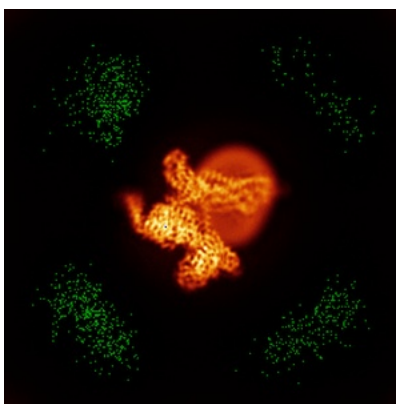


Z

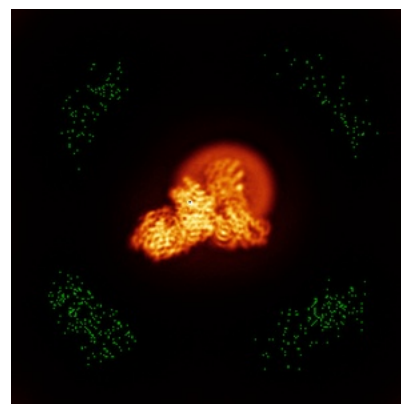
6.4.2 Raw map



X



Y

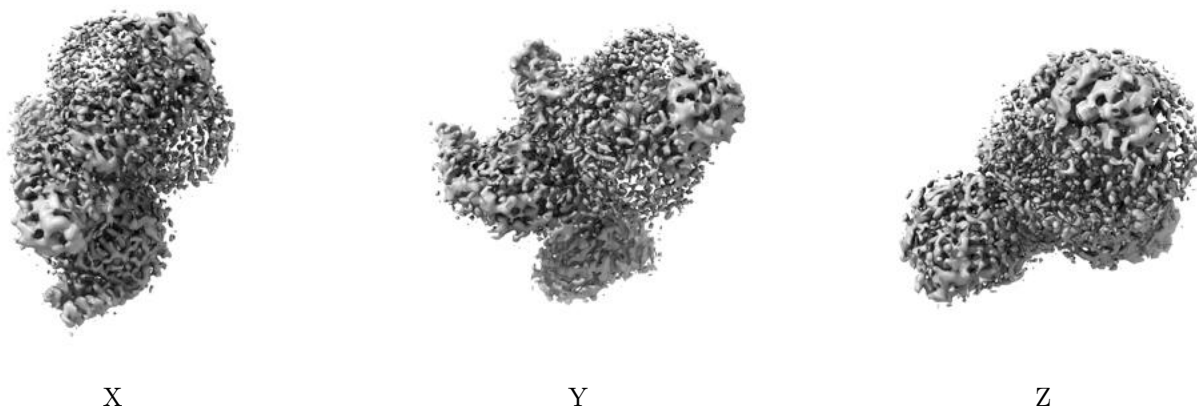


Z

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

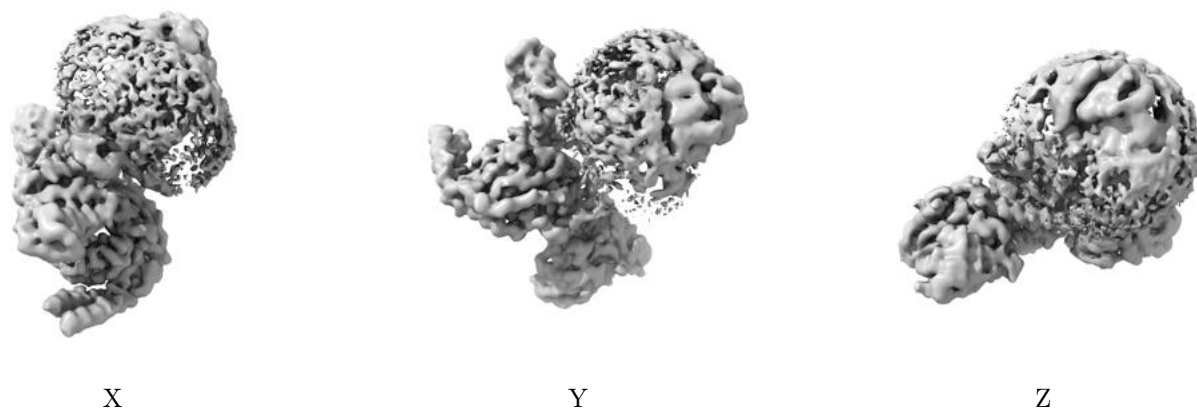
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

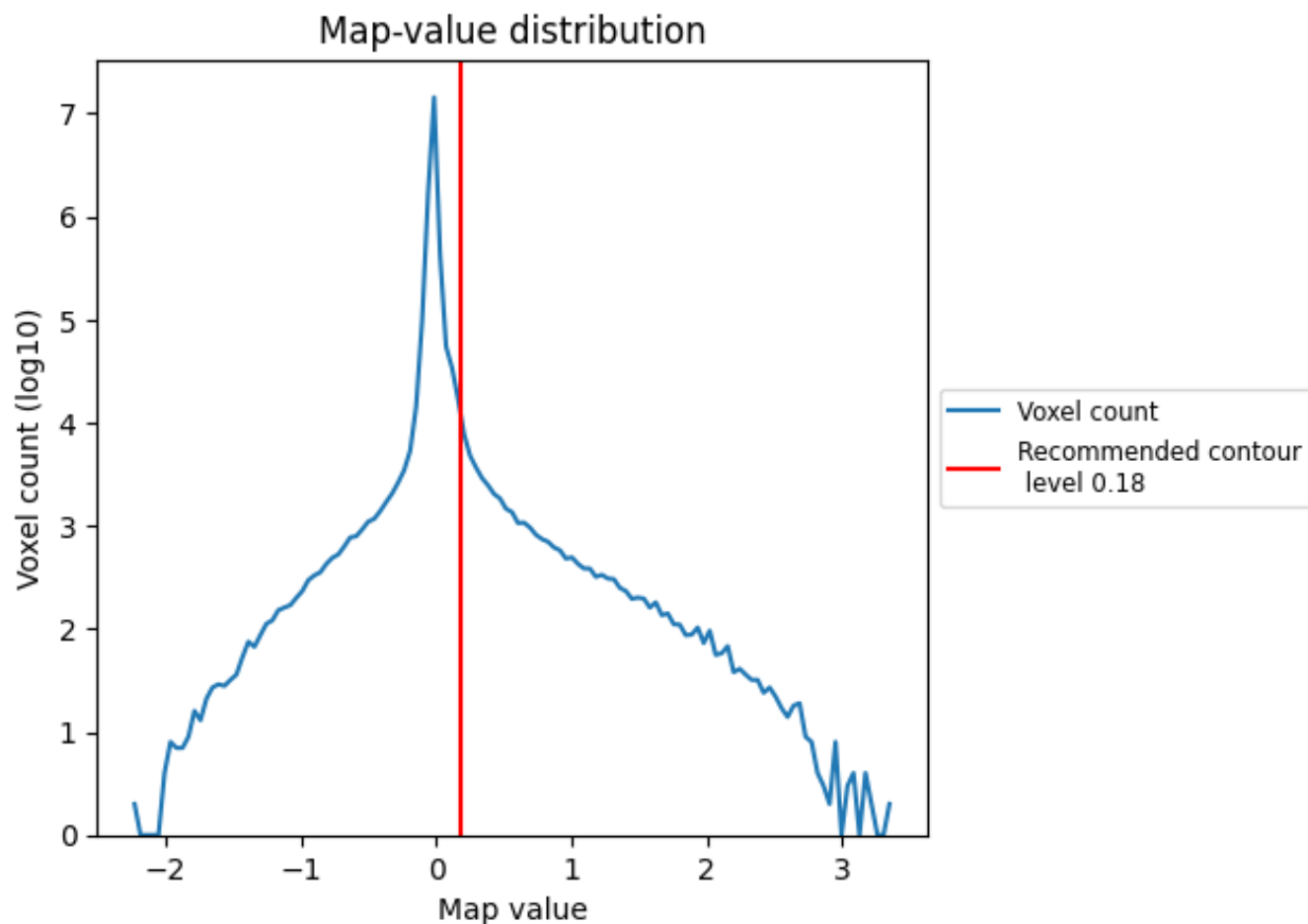
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

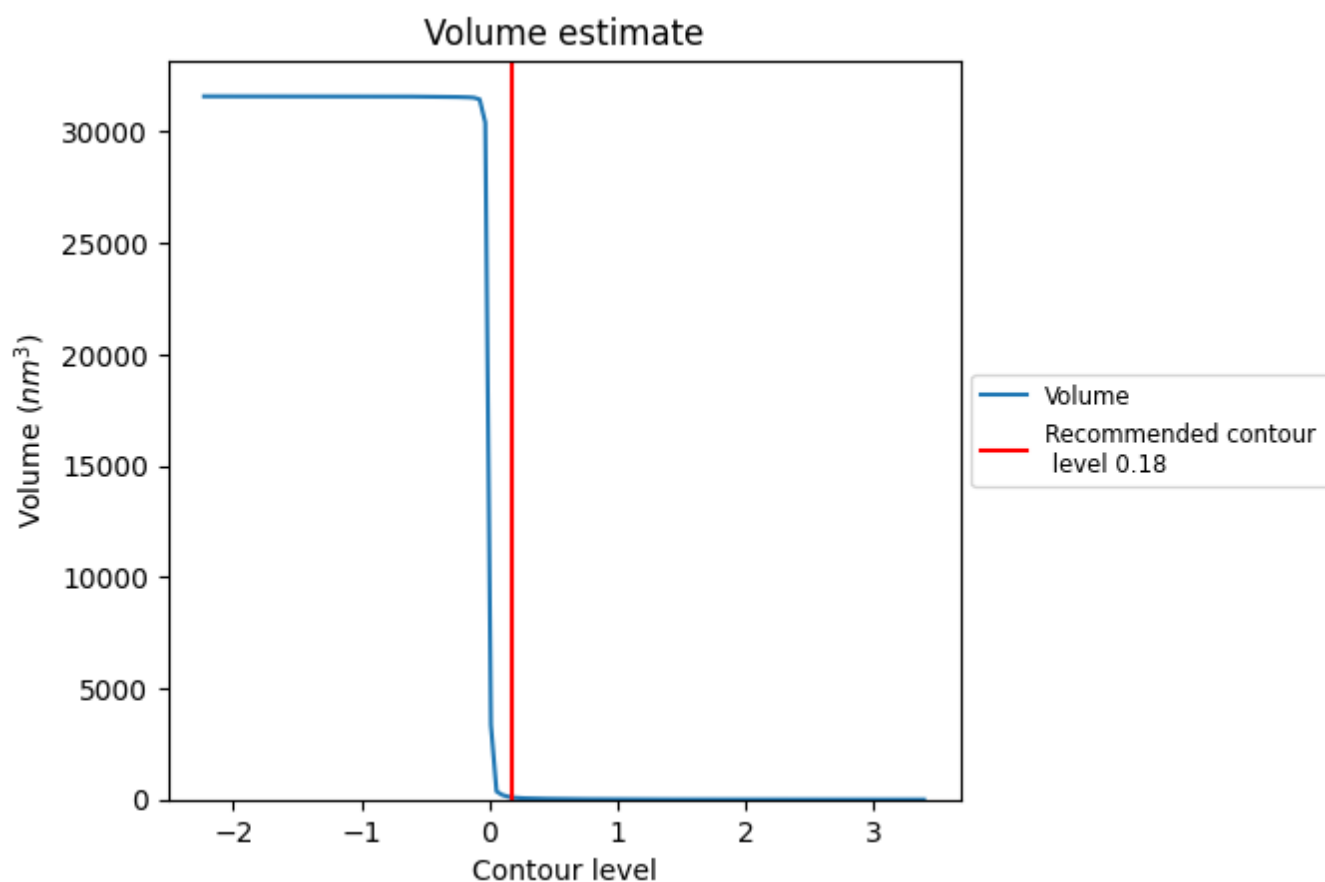
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

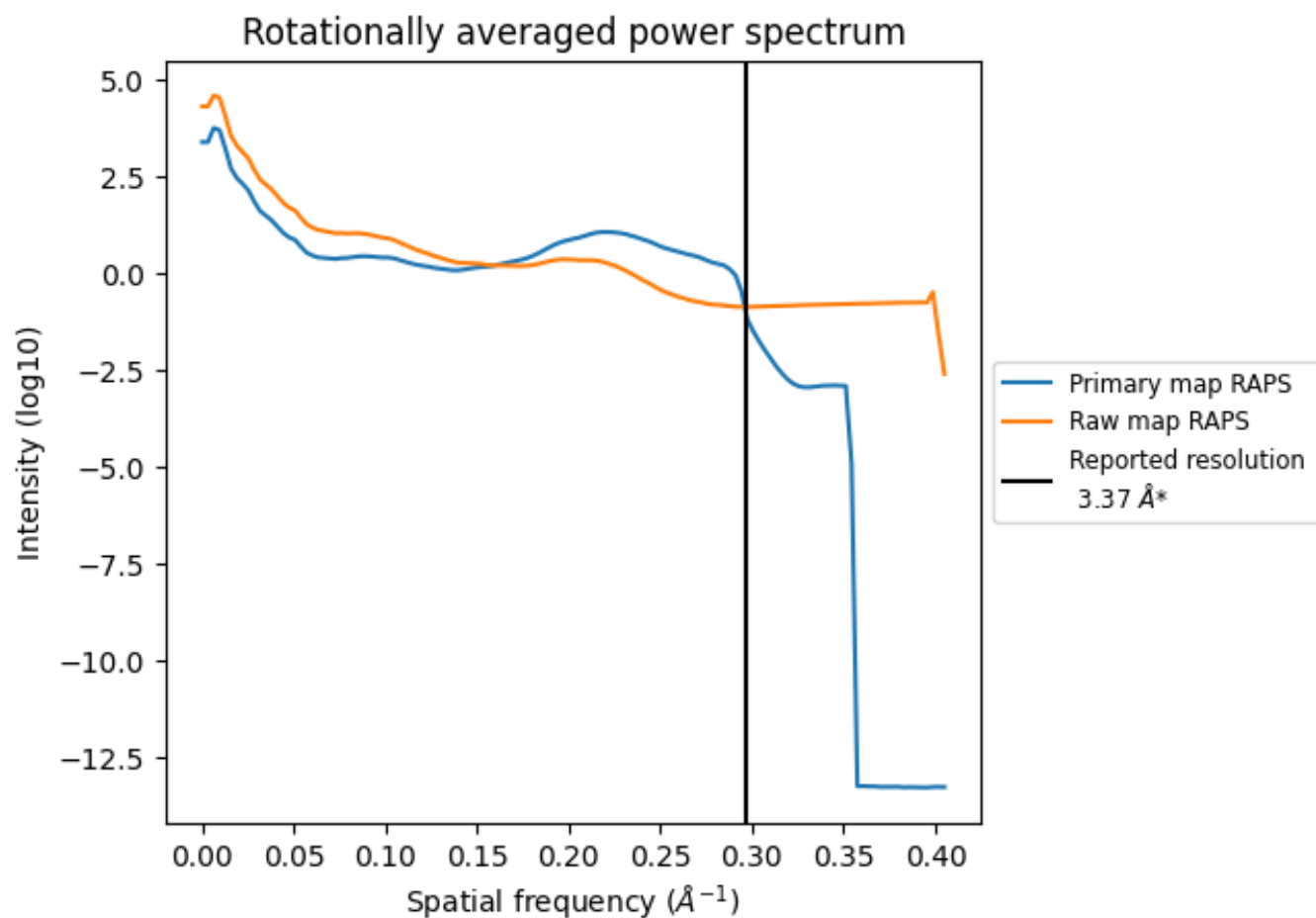
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 95 nm³; this corresponds to an approximate mass of 86 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 ⓘ

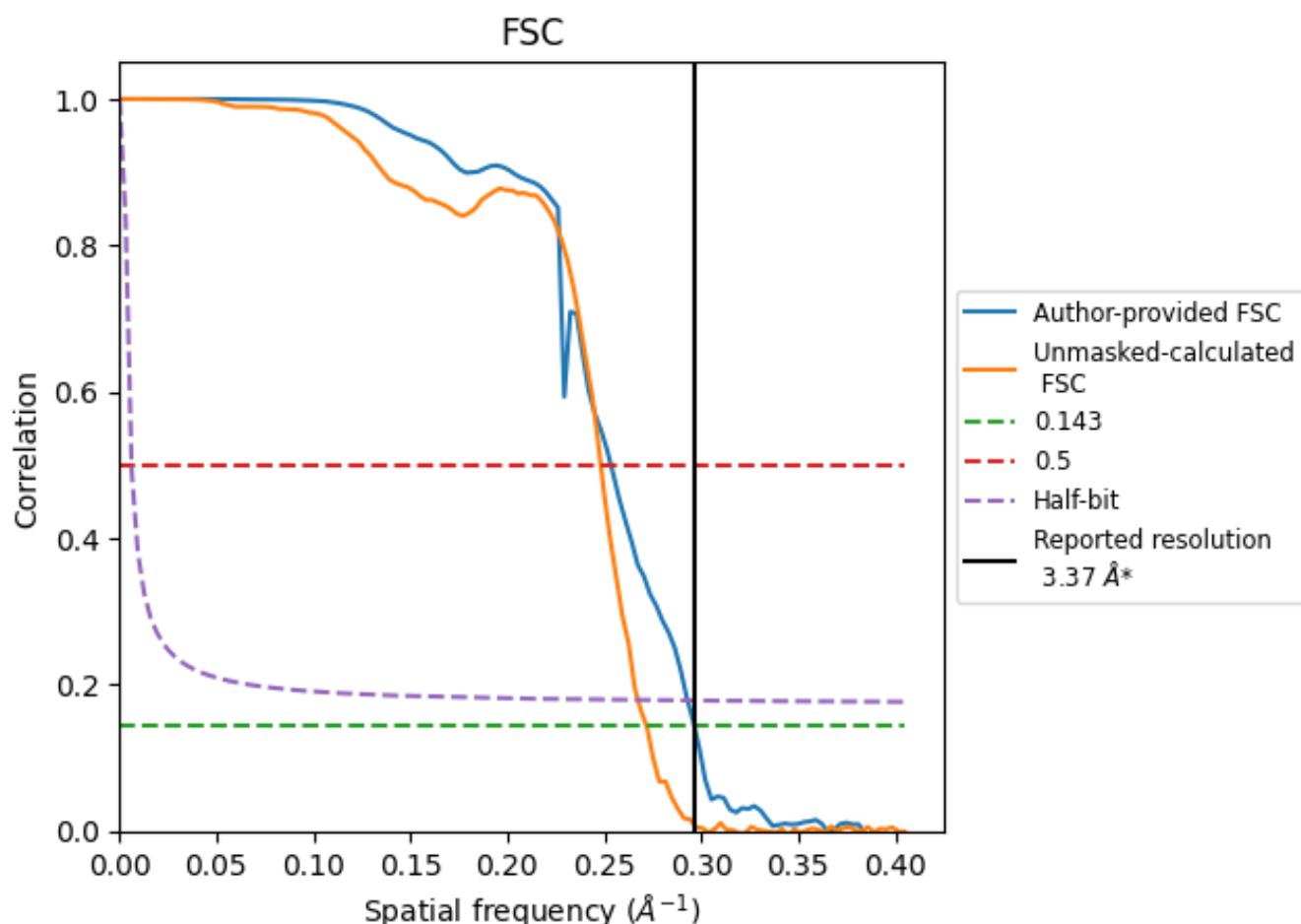


*Reported resolution corresponds to spatial frequency of 0.297 \AA^{-1}

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 0.297 Å⁻¹

8.2 Resolution estimates [i](#)

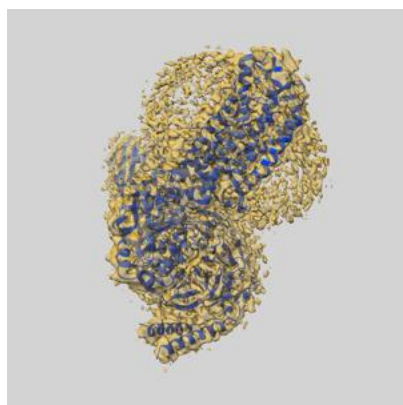
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.37	-	-
Author-provided FSC curve	3.37	3.95	3.41
Unmasked-calculated*	3.68	4.03	3.74

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

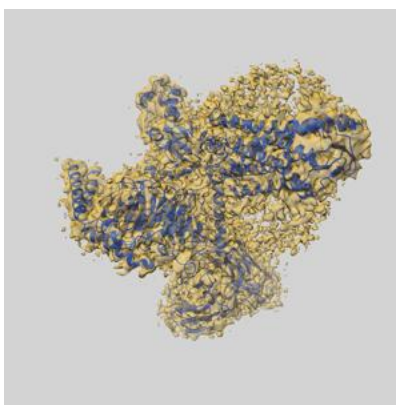
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35817 and PDB model 8IY9. Per-residue inclusion information can be found in section 3 on page 7.

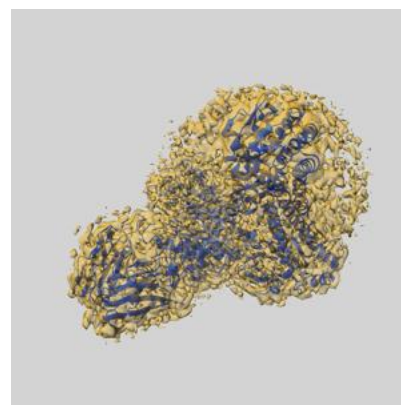
9.1 Map-model overlay [i](#)



X



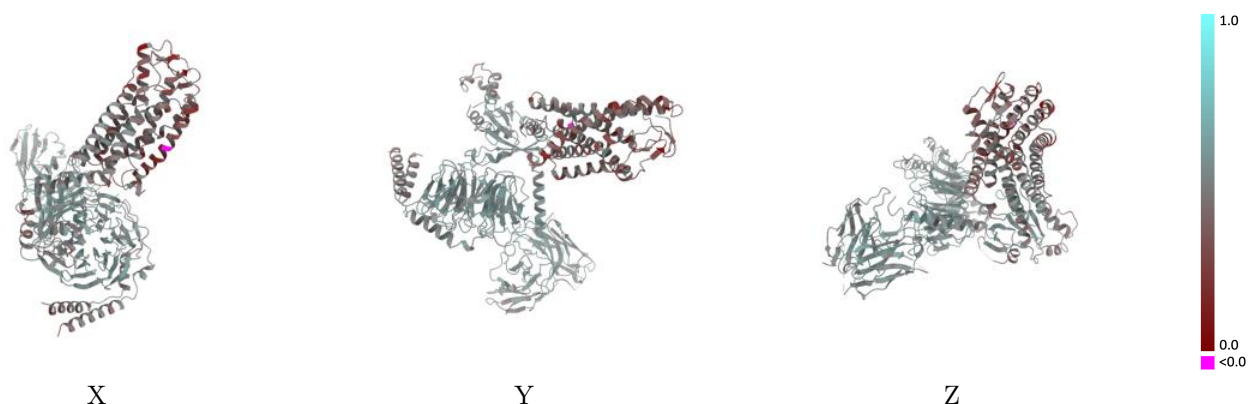
Y



Z

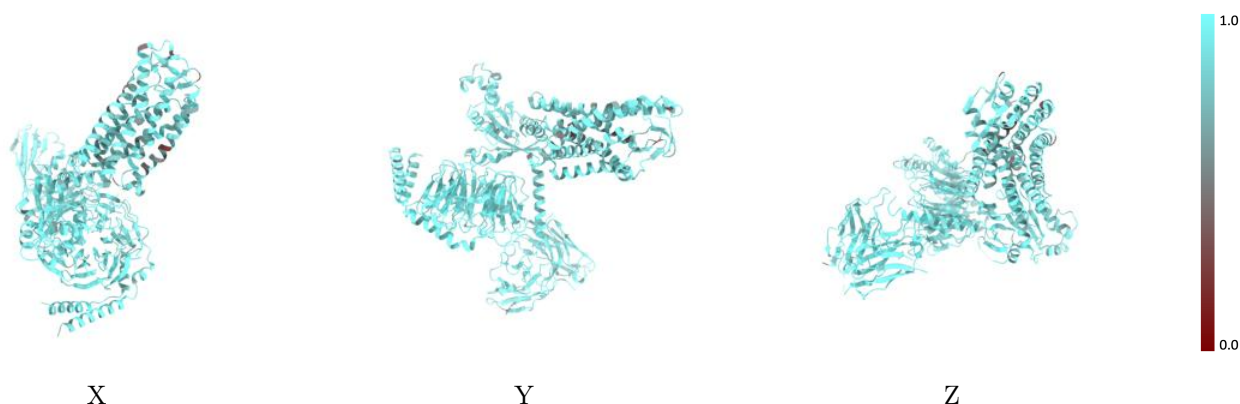
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



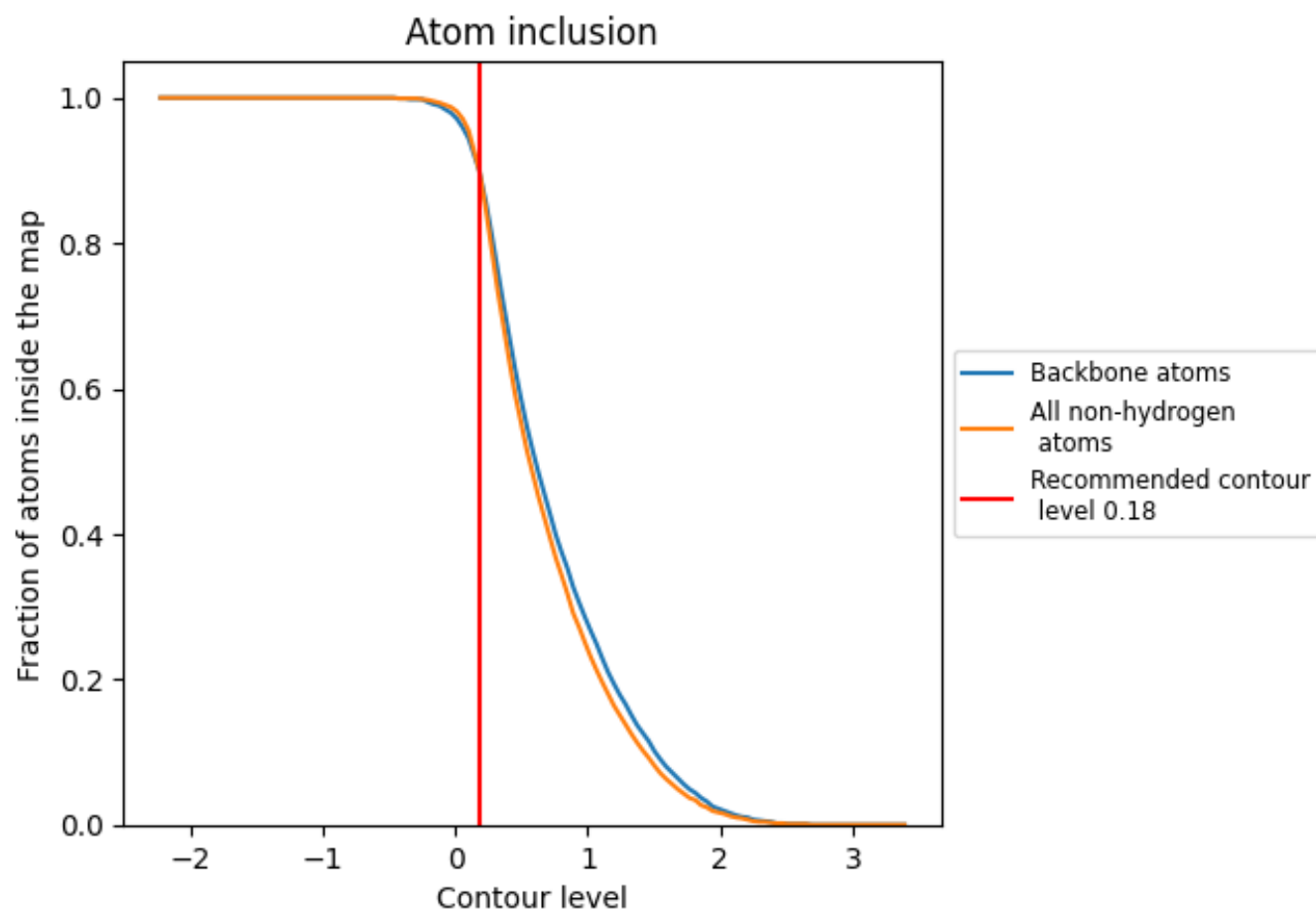
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9000	<div></div> 0.4940
A	<div></div> 0.8990	<div></div> 0.5040
B	<div></div> 0.9320	<div></div> 0.5400
G	<div></div> 0.9070	<div></div> 0.4820
H	<div></div> 0.9240	<div></div> 0.5280
R	<div></div> 0.8440	<div></div> 0.4110

