



# wwPDB EM Validation Summary Report ⓘ

Mar 11, 2024 – 10:12 AM JST

PDB ID : 8WU1  
EMDB ID : EMD-37849  
Title : Cryo-EM structure of CB1-beta-arrestin1 complex  
Authors : Liao, Y.; Zhang, H.; Shen, Q.; Cai, C.  
Deposited on : 2023-10-19  
Resolution : 3.20 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

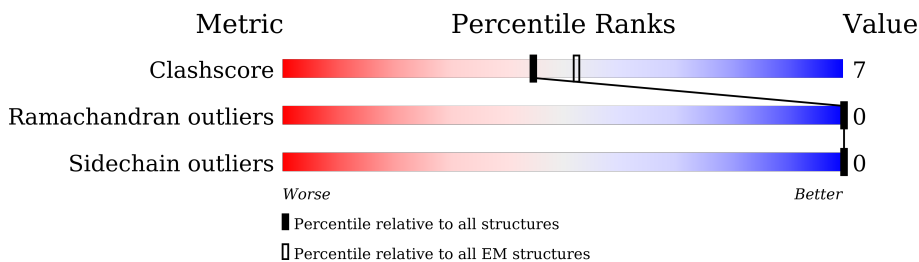
EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 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 3.20 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	C	393	79% 12% 9%
2	H	238	8% 74% 8% 19%
3	L	215	14% 80% 5% 15%
4	R	443	47% 16% 37%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7250 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 Beta-arrestin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	C	358	2577	1656	452	460	9	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	169	GLU	ARG	engineered mutation	UNP P17870
C	386	ALA	ILE	engineered mutation	UNP P17870
C	387	ALA	VAL	engineered mutation	UNP P17870
C	388	ALA	PHE	engineered mutation	UNP P17870

- Molecule 2 is a protein called Fab30 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	193	1314	831	220	258	5	0	0

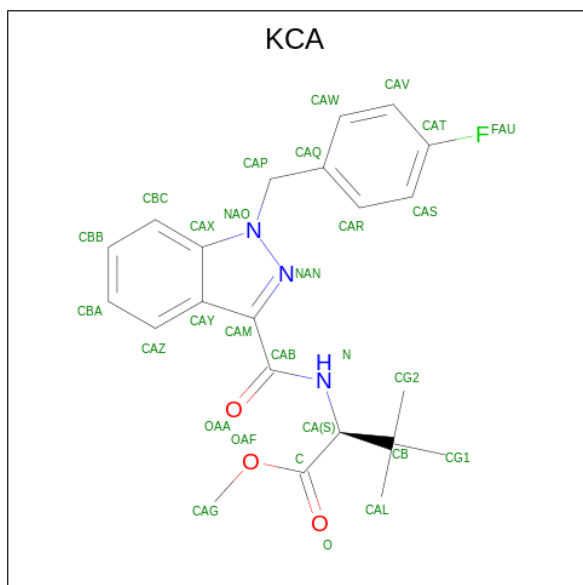
- Molecule 3 is a protein called Fab30 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L	183	1191	737	205	245	4	0	0

- Molecule 4 is a protein called Cannabinoid receptor 1, Vasopressin V2 receptor.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
4	R	280	2139	1402	346	372	6	13	0	0

- Molecule 5 is methyl N-{1-[(4-fluorophenyl)methyl]-1H-indazole-3-carbonyl}-3-methyl-L-valinate (three-letter code: KCA) (formula: C<sub>22</sub>H<sub>24</sub>FN<sub>3</sub>O<sub>3</sub>).

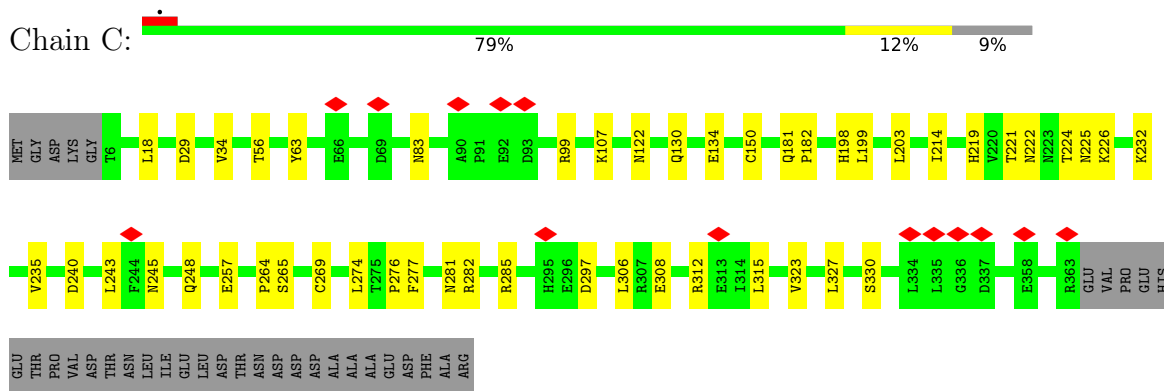


Mol	Chain	Residues	Atoms					AltConf
			Total	C	F	N	O	
5	R	1	29	22	1	3	3	0

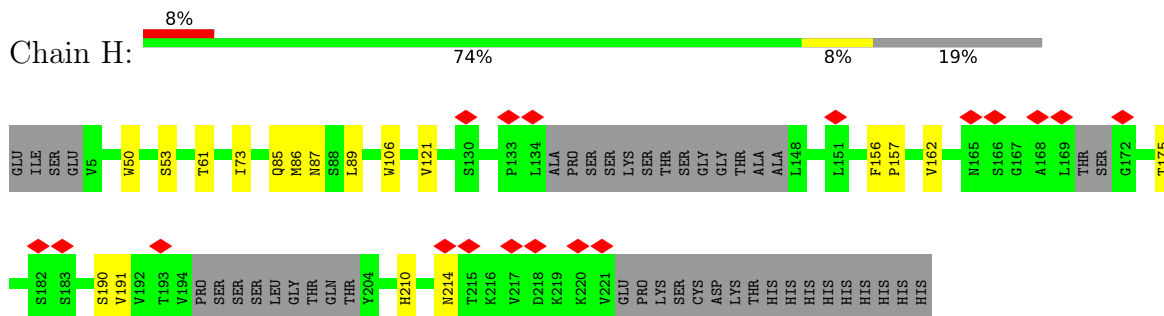
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

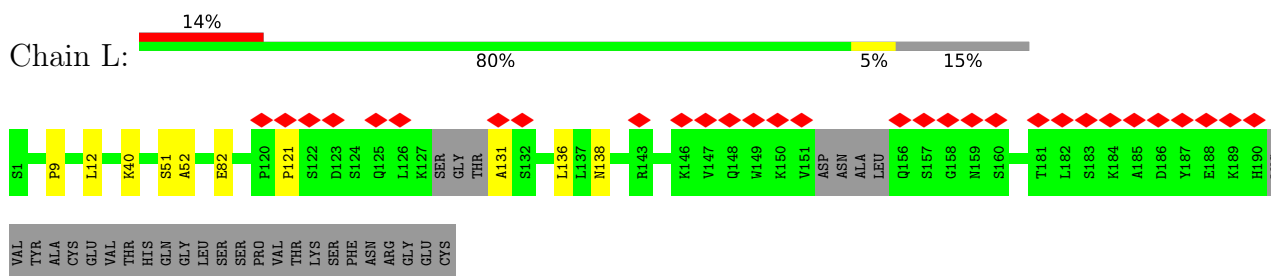
- Molecule 1: Beta-arrestin-1



- Molecule 2: Fab30 heavy chain



- Molecule 3: Fab30 light chain



- Molecule 4: Cannabinoid receptor 1, Vasopressin V2 receptor



MET LYS SER ILE LEU ASP GLY LEU ALA THR ASP THR PHE ARG THR ILE THR ASP LEU LEU VAL TYR VAL GLY SER ASN ASP ILE GLN TYR ASP GLU ASP ILE GLY ASP MET MET ALA SER LYS LEU GLY TYR PHE MET PRO GLN LYS PHE PRO LEU THR SER PHE ARG GLY SER PRO PHE GLN GLU

LYS MET THR ALA GLY ASP ASN PRO GLN VAL PRO THR ALA ASP GLN VAL ASN ILE THR LEU PHE TYR ASN LYS GLU ASN GLU ASN ILE GLN CYS GLY ASN PHE MET ASP ILE CYS PHE M109 M112 P113 S114 Q115 Q116 T128 L132 E133

M134 R145 I156 D163 L164 D184 T197 A198 T201 G205 F208 L209 I212 H219 H221 P231 V234 M240 I243 V246 I247 A248 W255 N256 C257 GLU LYS LEU GLN SER VAL C264 S265 F268 T271 D272 E273 L276 W279 L280 G281

V282 V285 I290 L298 A301 H304 A305 V306 H307 M308 I309 O310 ARG GLY THR GLN LYS SER ILE ILE HIS THR SER GLU ASP GLY VAL GLN VAL THR ARG PRO GLN ALA MET D338 R340 T344 L345 V346 L347 I348 L349 V350 V351 L352 I353 I354 C355

H356 G357 P358 L359 L360 R363 V367 H371 L374 V378 C386 N389 V392 I395 I396 Y397 R400 H406 A407 F408 ARG SER MET PHE PRO CYS ALA ARG GLY ARG THR PRO PRO SER LEU PRO GLN ASP E428 S423 C430 T431 T432 A433 S434 S435 S436

D440 THR SER SER

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110196	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 ( $e^-/\text{\AA}^2$ )	52	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.046	Depositor
Minimum map value	-0.025	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0035	Depositor
Map size (Å)	238.08, 238.08, 238.08	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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: KCA, TPO, SEP

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	C	0.31	0/2634	0.50	0/3605
2	H	0.32	0/1344	0.48	0/1846
3	L	0.29	0/1211	0.49	0/1665
4	R	0.26	0/2122	0.47	0/2893
All	All	0.29	0/7311	0.48	0/10009

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	C	2577	0	2458	31	0
2	H	1314	0	1136	13	0
3	L	1191	0	1016	7	0
4	R	2139	0	2107	48	0
5	R	29	0	0	0	0
All	All	7250	0	6717	95	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 7.



The worst 5 of 95 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:R:359:LEU:HD11	4:R:386:CYS:HB2	1.67	0.74
3:L:40:LYS:NZ	3:L:82:GLU:O	2.21	0.72
4:R:272:ASP:OD1	4:R:273:GLU:N	2.23	0.72
1:C:130:GLN:NE2	1:C:282:ARG:O	2.24	0.71
1:C:240:ASP:OD1	1:C:248:GLN:NE2	2.26	0.68

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	356/393 (91%)	341 (96%)	15 (4%)	0	100	100
2	H	185/238 (78%)	177 (96%)	8 (4%)	0	100	100
3	L	177/215 (82%)	169 (96%)	8 (4%)	0	100	100
4	R	266/443 (60%)	253 (95%)	13 (5%)	0	100	100
All	All	984/1289 (76%)	940 (96%)	44 (4%)	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	C	248/347 (72%)	248 (100%)	0	100	100
2	H	122/201 (61%)	122 (100%)	0	100	100
3	L	110/190 (58%)	110 (100%)	0	100	100
4	R	214/388 (55%)	214 (100%)	0	100	100
All	All	694/1126 (62%)	694 (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 (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	130	GLN
4	R	310	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

6 non-standard protein/DNA/RNA residues are 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
4	TPO	R	432	4	8,10,11	1.56	1 (12%)	10,14,16	1.87	1 (10%)
4	SEP	R	434	4	8,9,10	1.50	1 (12%)	8,12,14	1.38	1 (12%)
4	SEP	R	435	4	8,9,10	1.51	1 (12%)	8,12,14	1.45	2 (25%)
4	SEP	R	429	4	8,9,10	1.53	1 (12%)	8,12,14	1.67	2 (25%)
4	SEP	R	436	4	8,9,10	1.55	1 (12%)	8,12,14	1.50	2 (25%)
4	TPO	R	431	4	8,10,11	1.11	0	10,14,16	1.79	1 (10%)

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
4	TPO	R	432	4	-	1/9/11/13	-
4	SEP	R	434	4	-	0/5/8/10	-
4	SEP	R	435	4	-	2/5/8/10	-
4	SEP	R	429	4	-	1/5/8/10	-
4	SEP	R	436	4	-	1/5/8/10	-
4	TPO	R	431	4	-	2/9/11/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	R	436	SEP	P-O1P	3.37	1.61	1.50
4	R	429	SEP	P-O1P	3.35	1.61	1.50
4	R	435	SEP	P-O1P	3.30	1.61	1.50
4	R	432	TPO	P-O1P	3.30	1.61	1.50
4	R	434	SEP	P-O1P	3.29	1.61	1.50

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	432	TPO	P-OG1-CB	-5.23	107.40	123.21
4	R	431	TPO	P-OG1-CB	-4.92	108.34	123.21
4	R	429	SEP	P-OG-CB	-3.21	109.45	118.30
4	R	434	SEP	P-OG-CB	-2.94	110.19	118.30
4	R	429	SEP	OG-CB-CA	2.89	110.95	108.14

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	R	429	SEP	N-CA-CB-OG
4	R	431	TPO	O-C-CA-CB
4	R	432	TPO	O-C-CA-CB
4	R	436	SEP	N-CA-CB-OG
4	R	435	SEP	CB-OG-P-O1P

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	R	435	SEP	1	0
4	R	431	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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
5	KCA	R	501	-	28,31,31	5.08	18 (64%)	32,45,45	1.75	7 (21%)

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
5	KCA	R	501	-	-	8/20/24/24	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	501	KCA	CAW-CAV	8.90	1.55	1.38
5	R	501	KCA	CAS-CAR	8.73	1.54	1.38
5	R	501	KCA	CAV-CAT	8.62	1.54	1.37
5	R	501	KCA	CBC-CAX	8.54	1.58	1.41
5	R	501	KCA	CAS-CAT	8.53	1.53	1.37

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	501	KCA	OAF-C-CA	6.17	119.88	111.39
5	R	501	KCA	CB-CA-N	-4.42	106.31	111.84
5	R	501	KCA	CAP-NAO-NAN	2.62	125.15	117.77
5	R	501	KCA	OAF-C-O	-2.27	119.41	123.84
5	R	501	KCA	CAW-CAV-CAT	2.24	120.68	118.36

There are no chirality outliers.

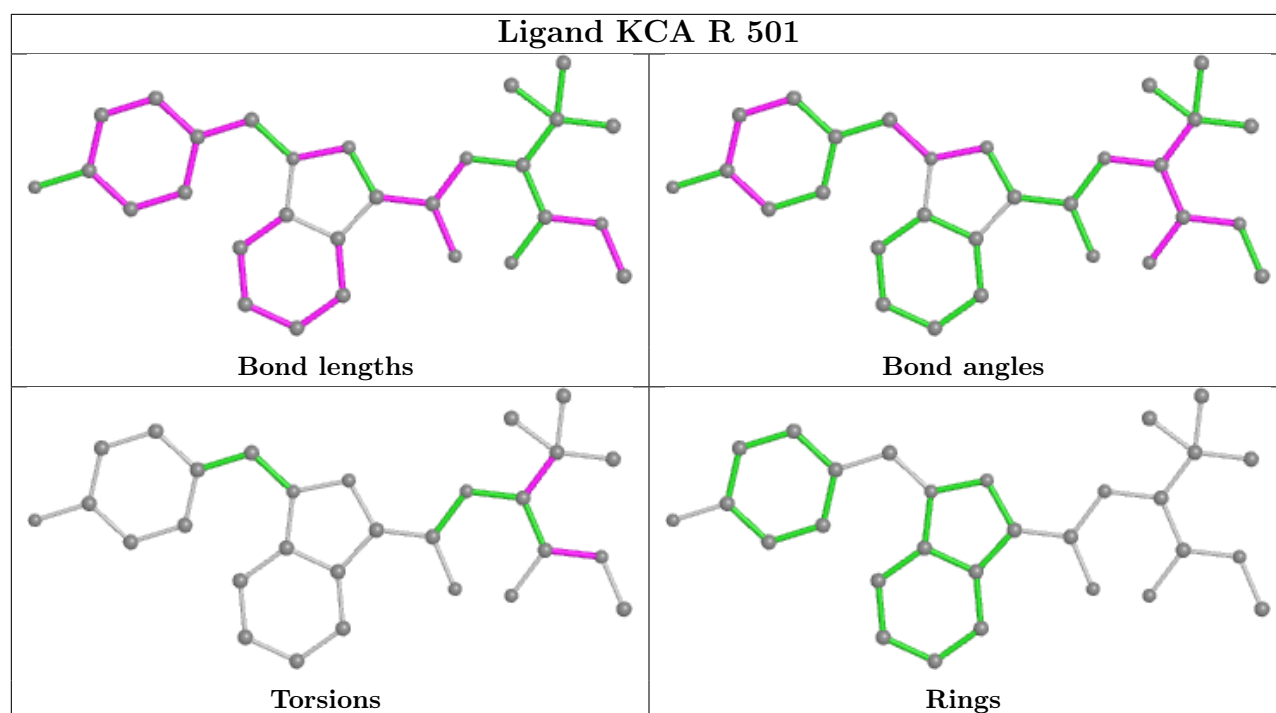
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	R	501	KCA	CA-C-OAF-CAG
5	R	501	KCA	O-C-OAF-CAG
5	R	501	KCA	N-CA-CB-CG2
5	R	501	KCA	N-CA-CB-CG1
5	R	501	KCA	C-CA-CB-CG2

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.

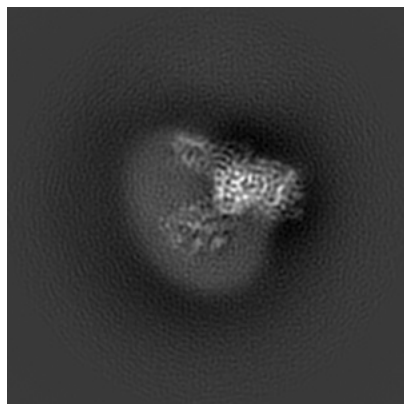
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37849. These allow visual inspection of the internal detail of the map and identification of artifacts.

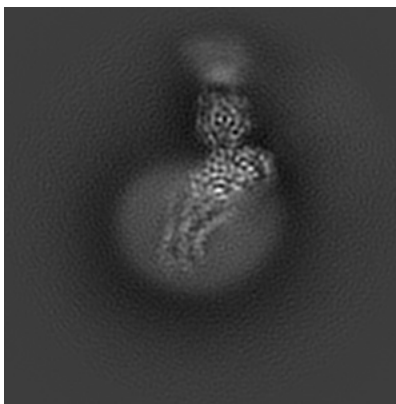
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

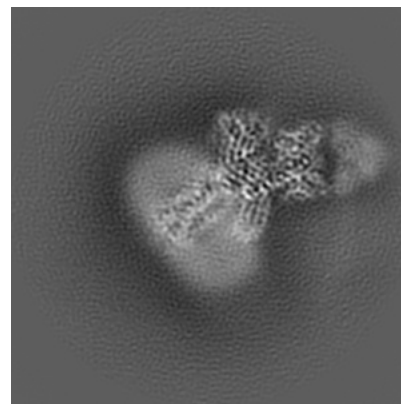
#### 6.1.1 Primary map



X

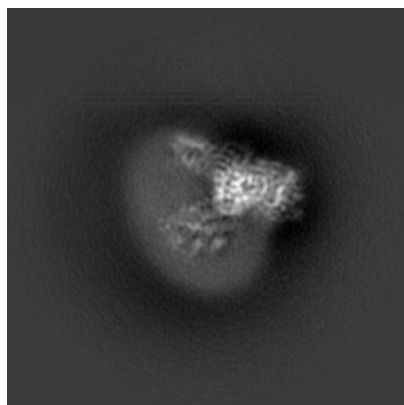


Y

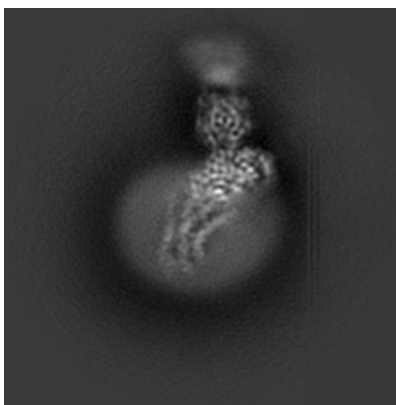


Z

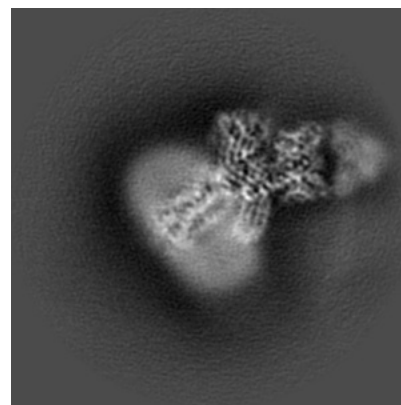
#### 6.1.2 Raw map



X



Y

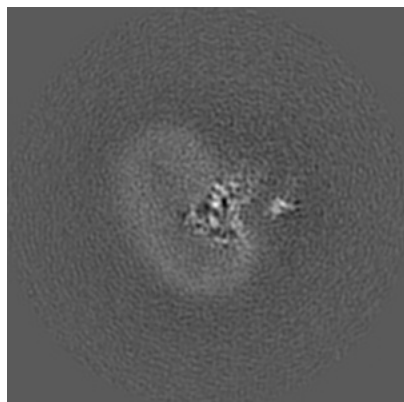


Z

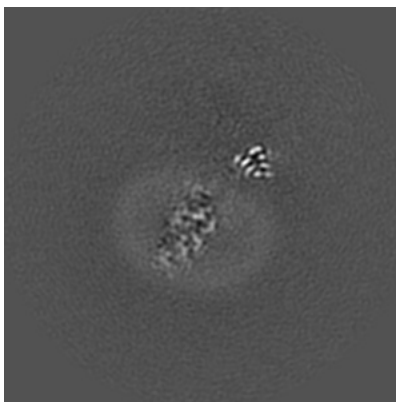
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

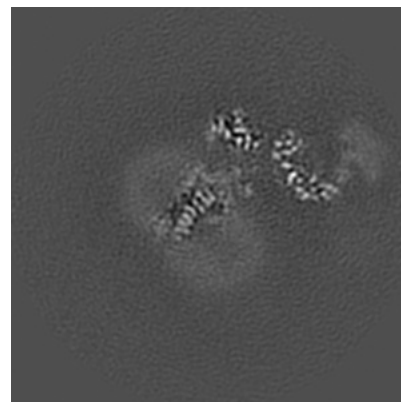
### 6.2.1 Primary map



X Index: 128

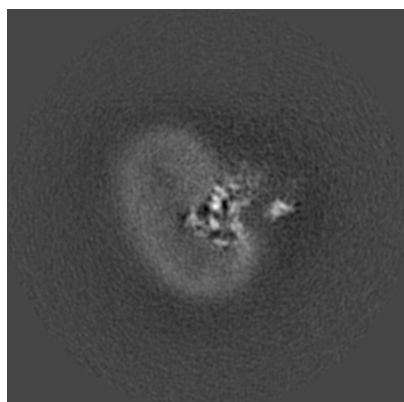


Y Index: 128

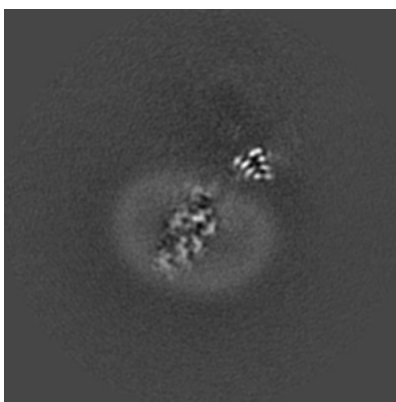


Z Index: 128

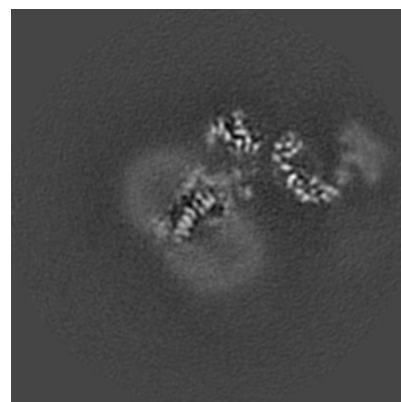
### 6.2.2 Raw map



X Index: 128



Y Index: 128



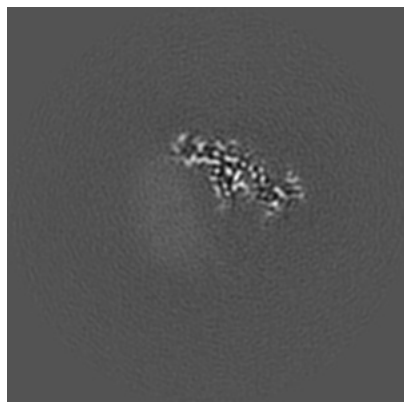
Z Index: 128

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

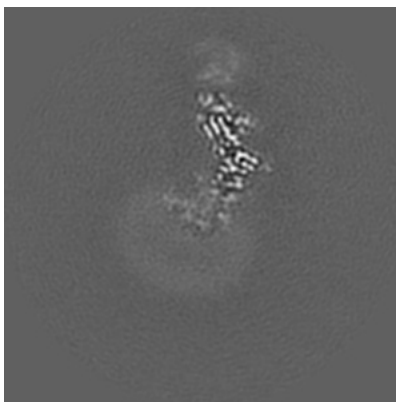


## 6.3 Largest variance slices [i](#)

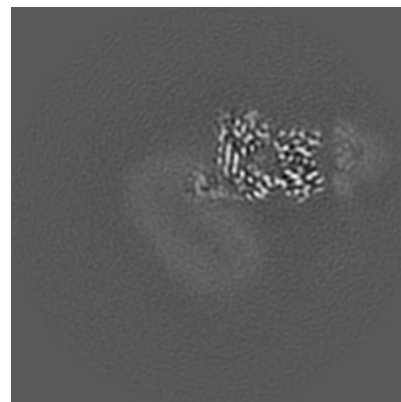
### 6.3.1 Primary map



X Index: 152

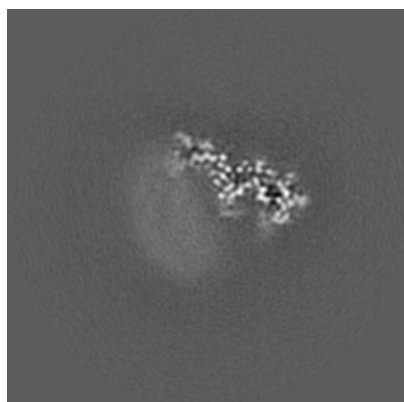


Y Index: 146

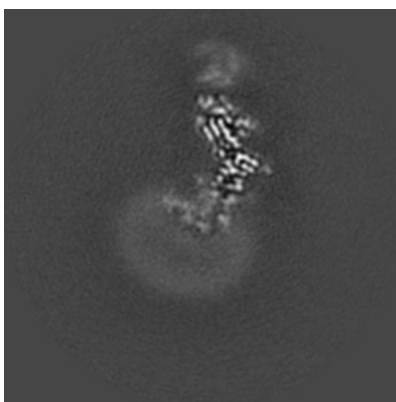


Z Index: 139

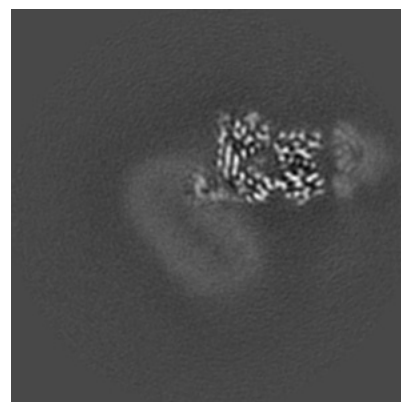
### 6.3.2 Raw map



X Index: 148



Y Index: 146

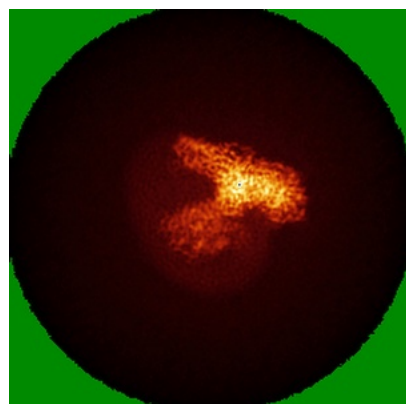


Z Index: 139

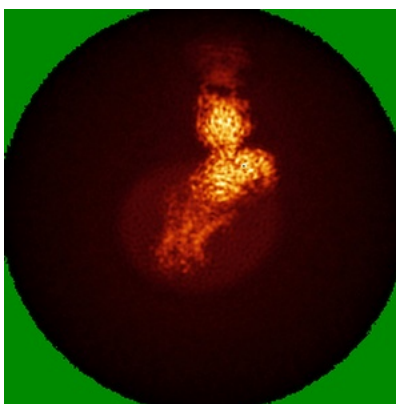
The images above show the largest variance slices of the map in three orthogonal directions.

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

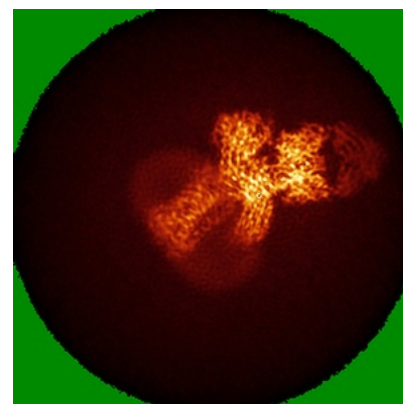
### 6.4.1 Primary map



X

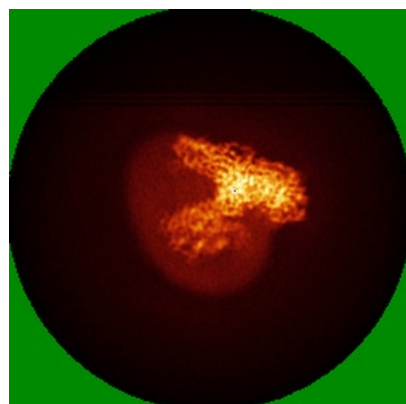


Y

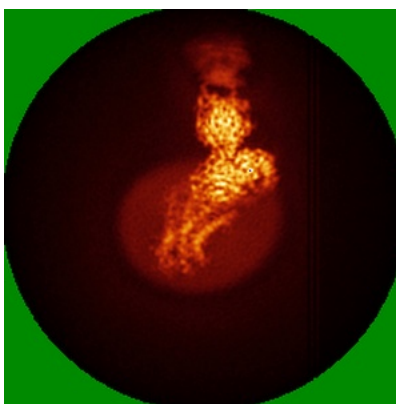


Z

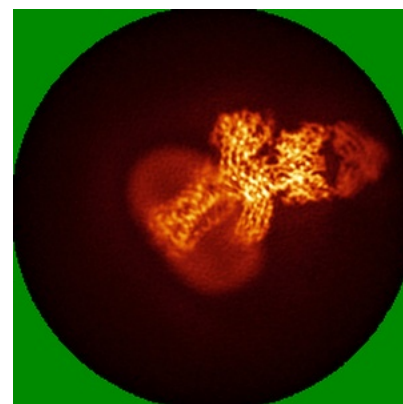
### 6.4.2 Raw map



X



Y

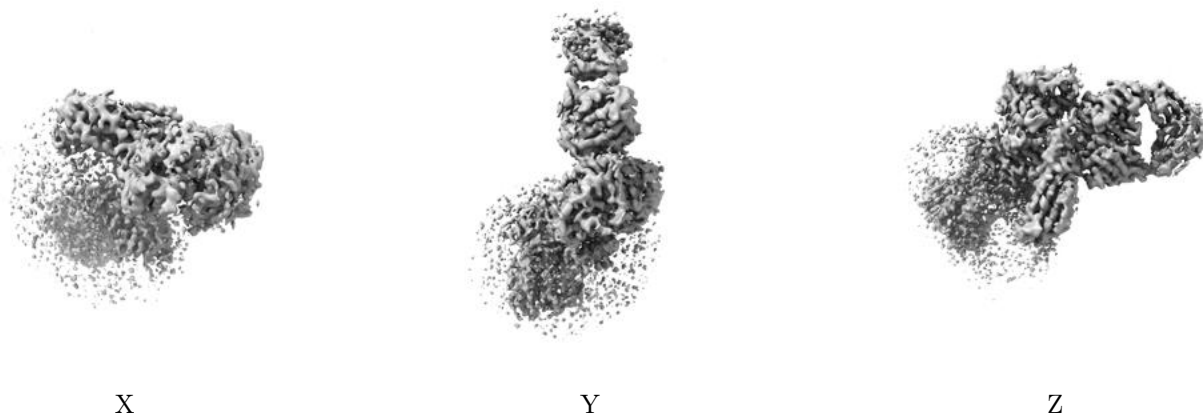


Z

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.

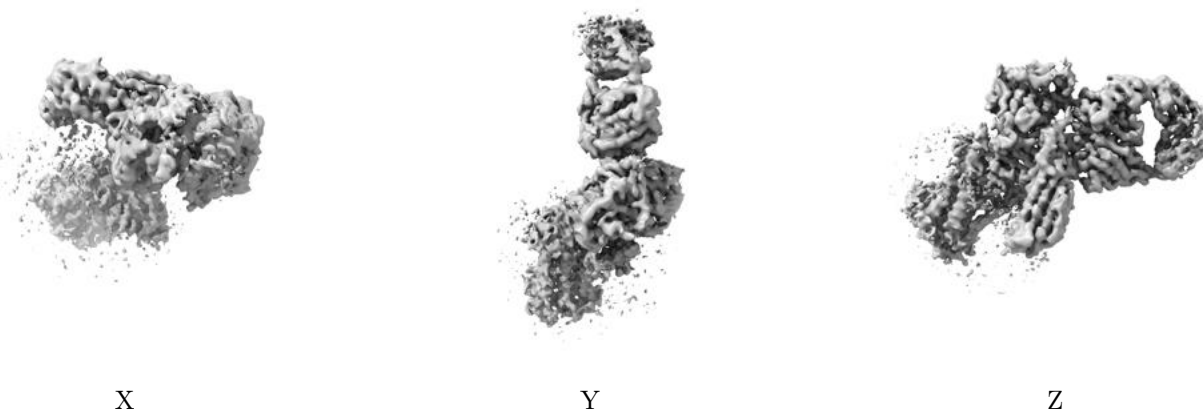
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0035. 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.

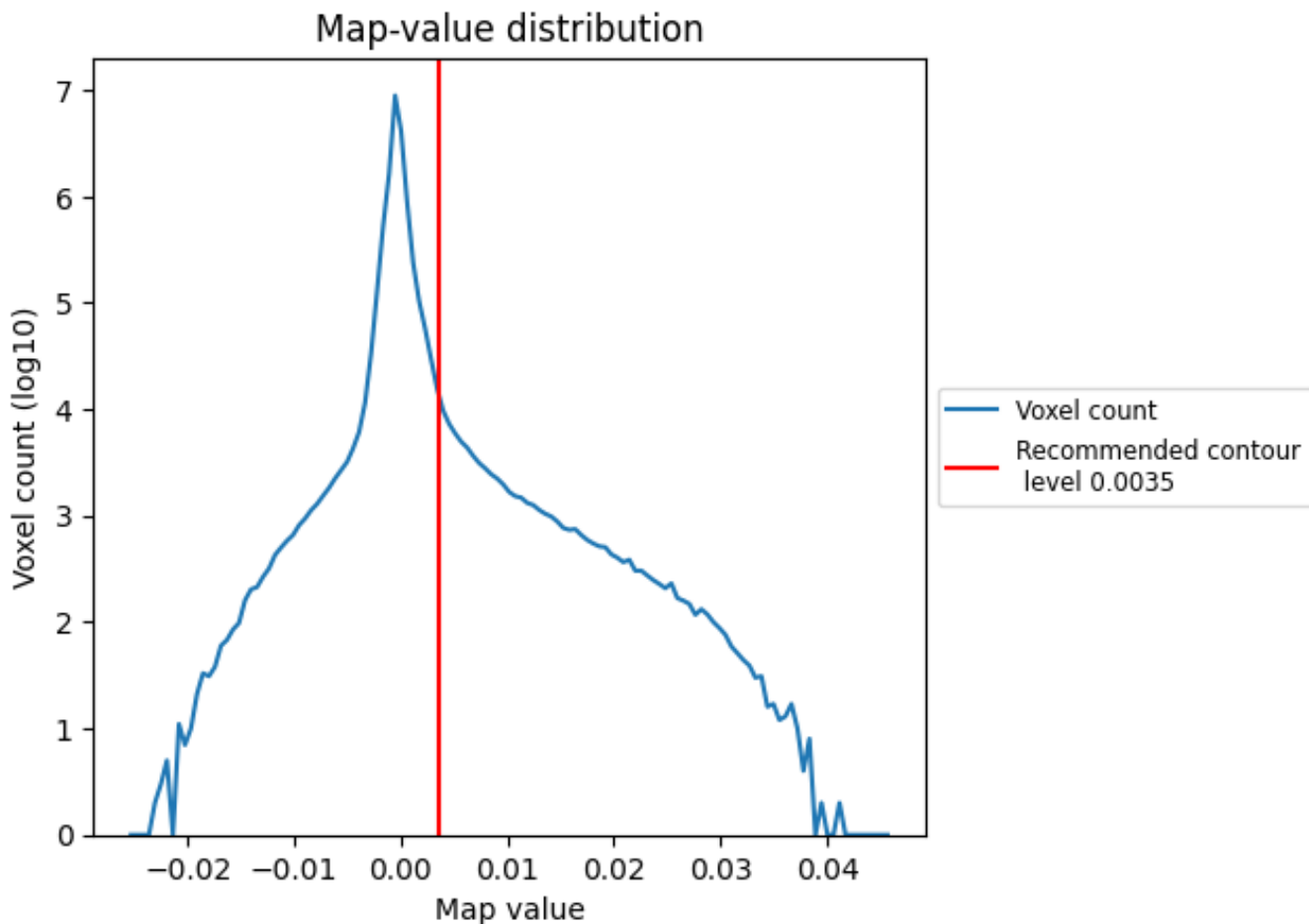
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

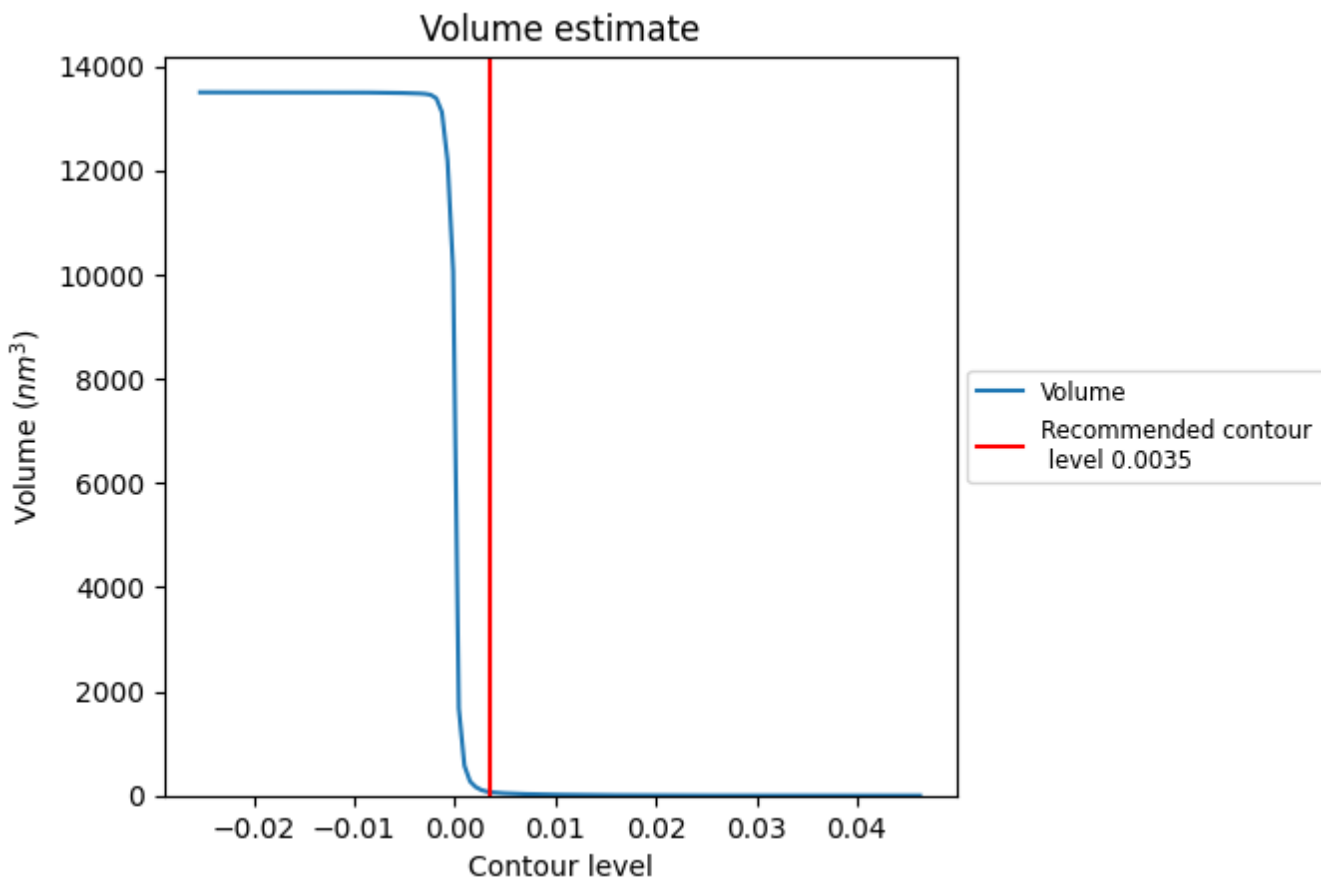
This section contains the results of statistical analysis of the map.

### 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.

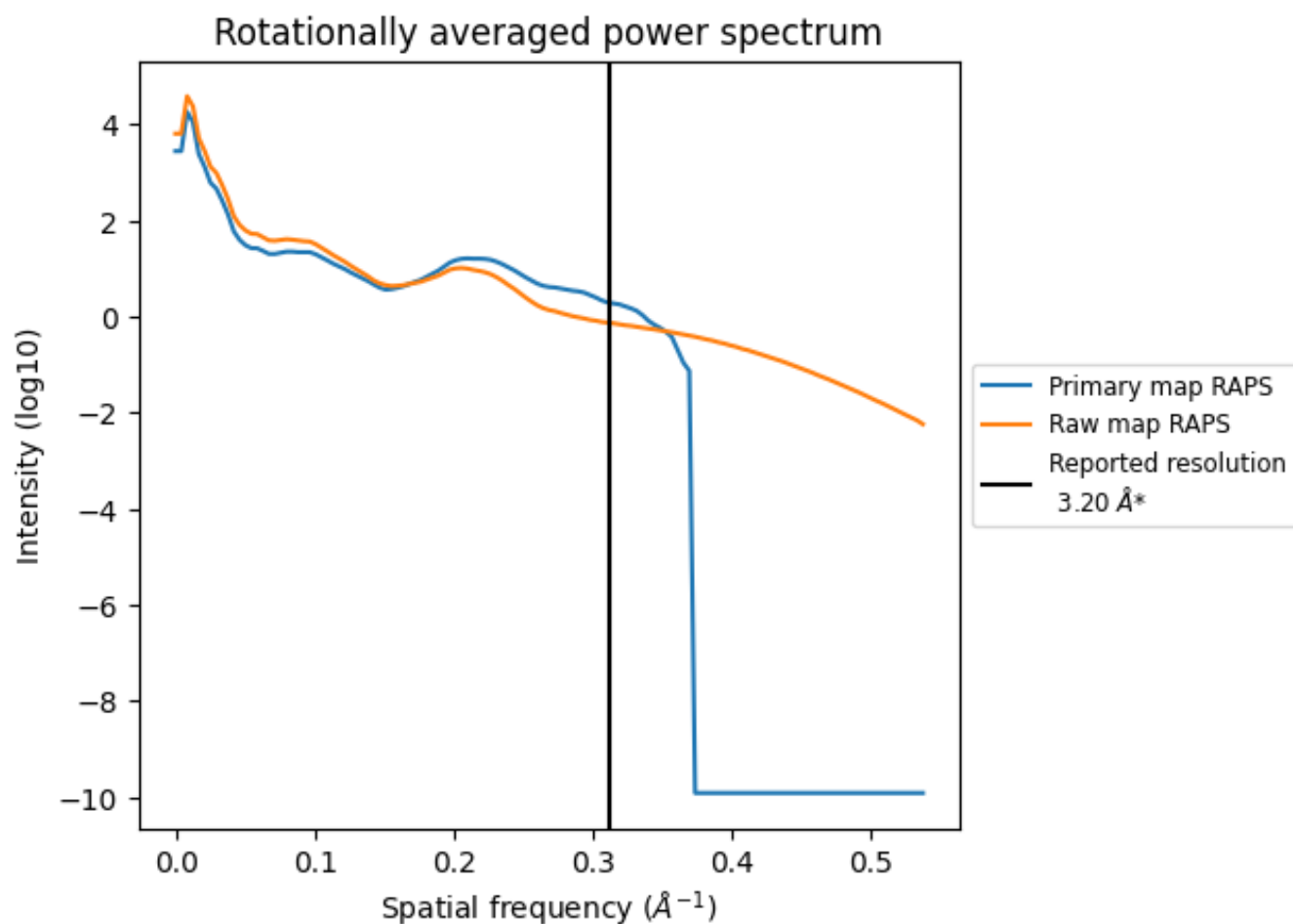
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 68  $\text{nm}^3$ ; this corresponds to an approximate mass of 61 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

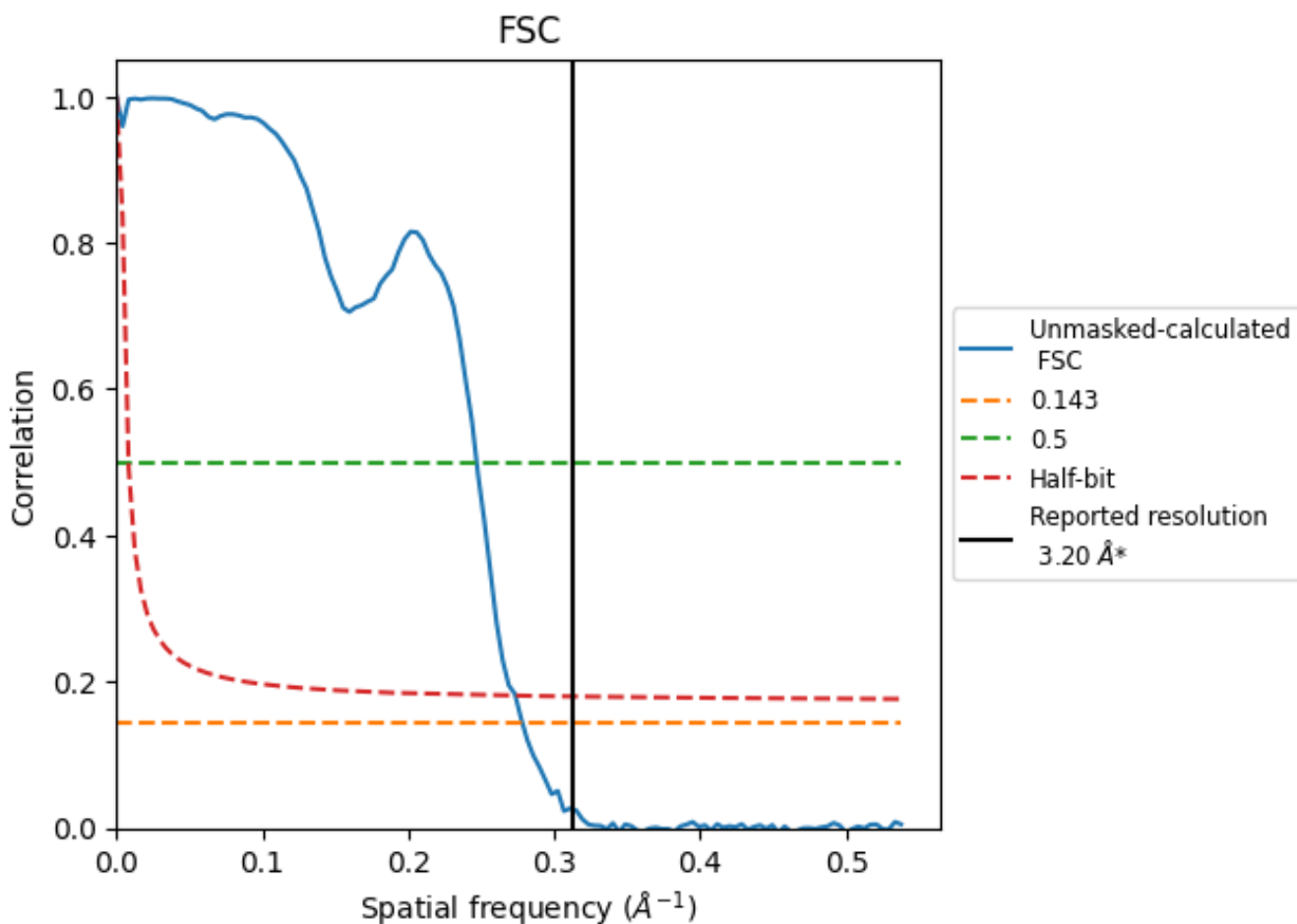


\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

## 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 0.312 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.59	4.05	3.66

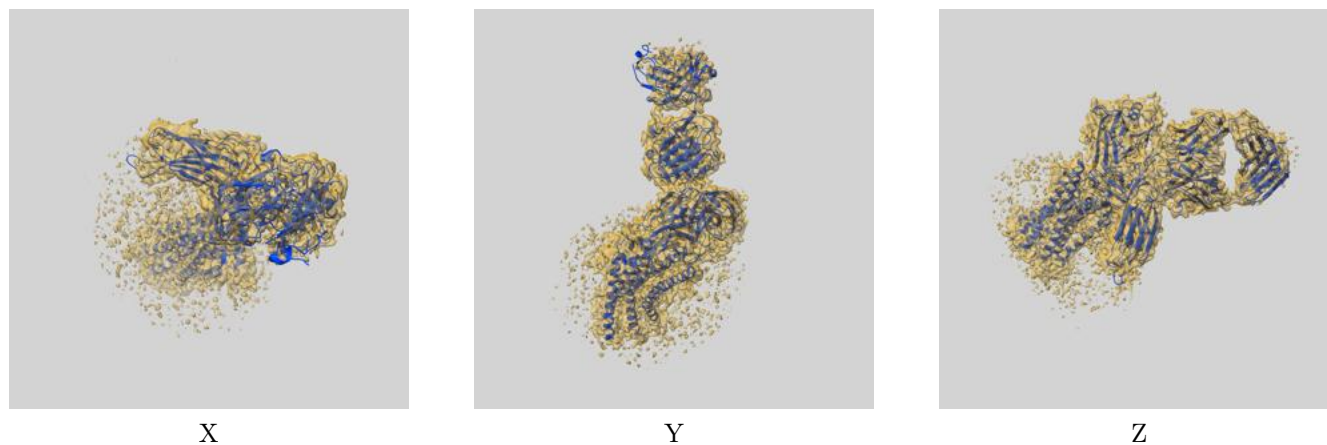
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.59 differs from the reported value 3.2 by more than 10 %



## 9 Map-model fit [i](#)

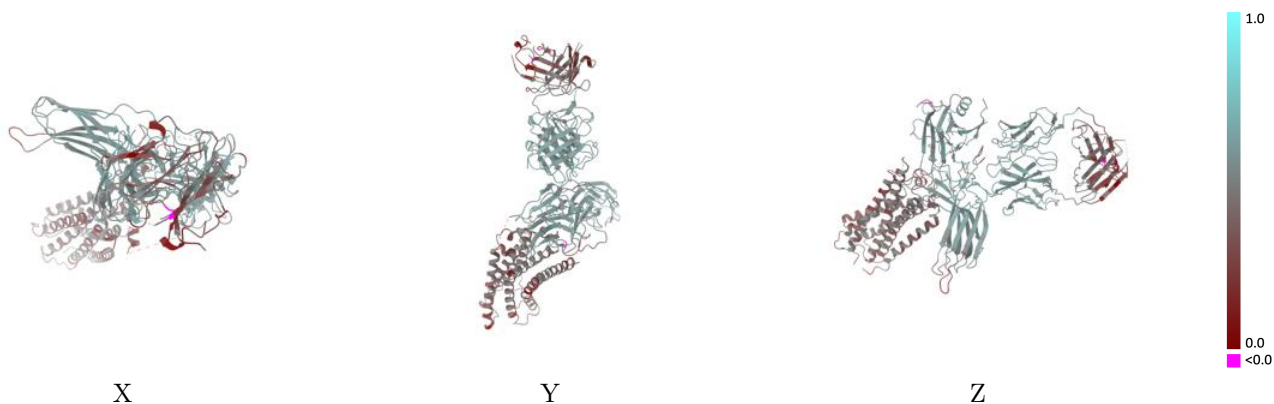
This section contains information regarding the fit between EMDB map EMD-37849 and PDB model 8WU1. Per-residue inclusion information can be found in section [3](#) on page [5](#).

### 9.1 Map-model overlay [i](#)



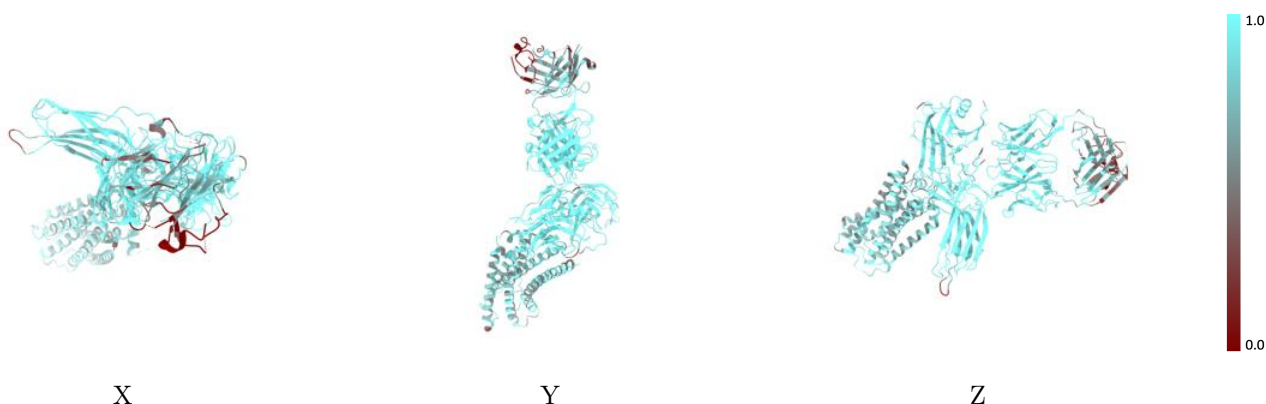
The images above show the 3D surface view of the map at the recommended contour level 0.0035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



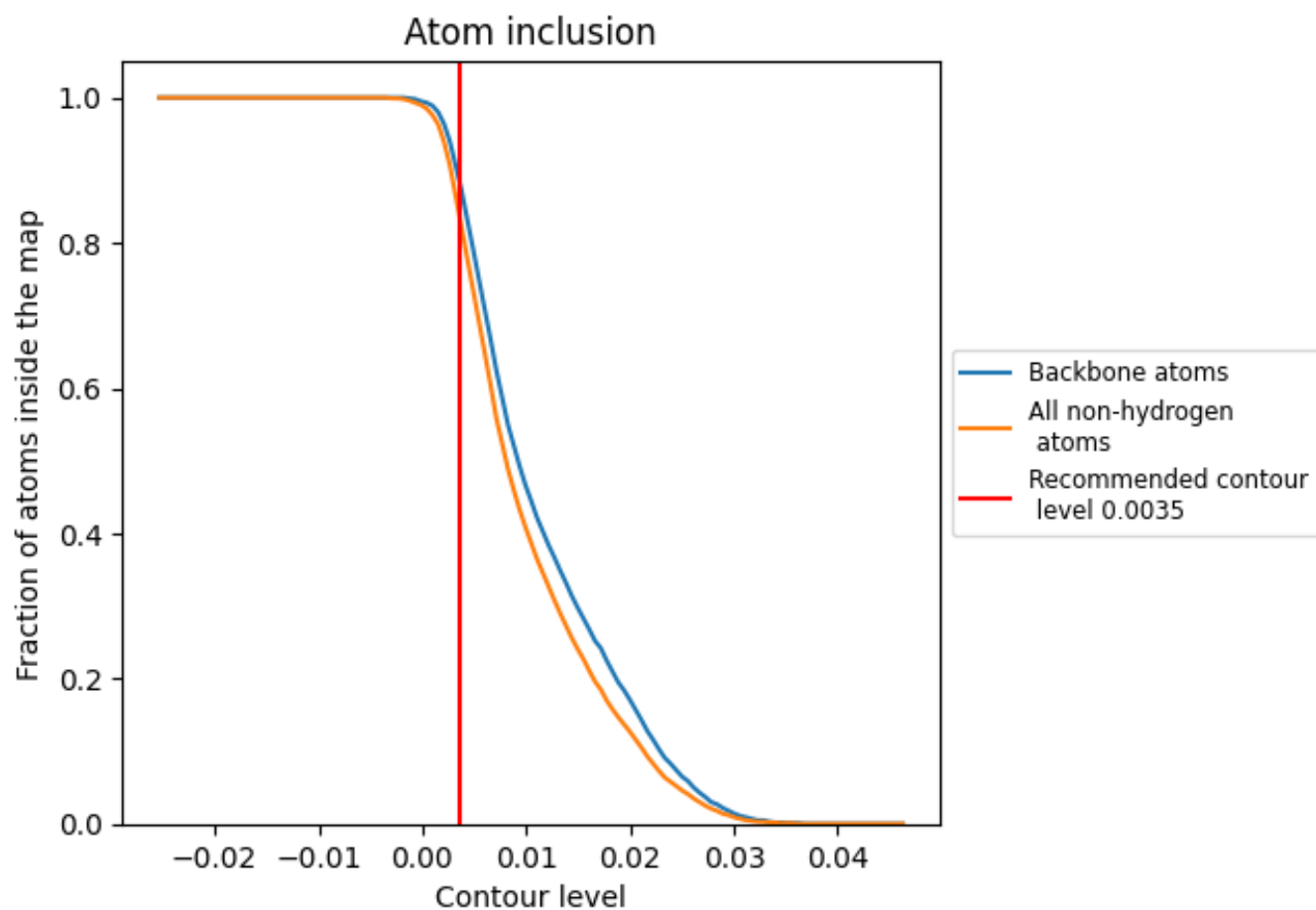
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0035).











## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.0035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8430	 0.4730
C	 0.9140	 0.5300
H	 0.8390	 0.5020
L	 0.7780	 0.4820
R	 0.7970	 0.3830

