wwPDB EM Validation Summary Report (i)

Nov 15, 2022 – 02:23 AM JST

PDB ID	:	6K42
EMDB ID	:	EMD-9912
Title	:	cryo-EM structure of alpha2BAR-Gi1 complex
Authors	:	Yuan, D.; Liu, Z.; Wang, H.W.; Kobilka, B.K.
Deposited on	:	2019-05-23
Resolution	:	4.10 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 (i) 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 (1)) were used in the production of this report:

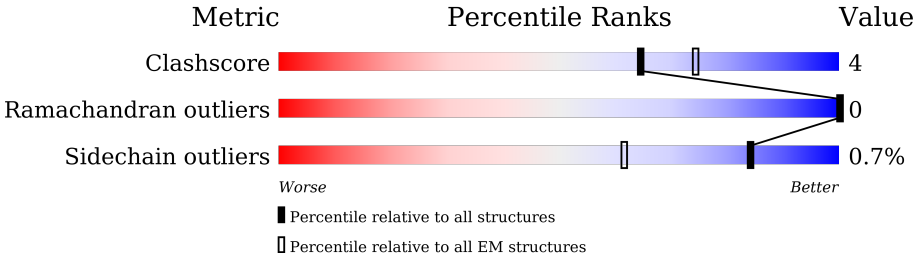
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 4.10 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 >=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	354	22% 51% 11% 38%
2	B	350	29% 87% 10% •
3	G	71	45% 70% 7% 23%
4	R	512	23% 45% 7% 47%
5	H	307	29% 68% 7% 24%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8816 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	218	1759	1122	293	332	12	0	0

- 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
			Total	C	N	O	S		
2	B	340	2616	1612	470	513	21	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	HIS	-	expression tag	UNP P62874
B	-8	HIS	-	expression tag	UNP P62874
B	-7	HIS	-	expression tag	UNP P62874
B	-6	HIS	-	expression tag	UNP P62874
B	-5	HIS	-	expression tag	UNP P62874
B	-4	HIS	-	expression tag	UNP P62874
B	-3	GLY	-	expression tag	UNP P62874
B	-2	SER	-	expression tag	UNP P62874
B	-1	SER	-	expression tag	UNP P62874
B	0	GLY	-	expression tag	UNP P62874
B	1	GLN	-	expression tag	UNP P62874

- 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
			Total	C	N	O	S		
3	G	55	424	266	75	80	3	0	0

- Molecule 4 is a protein called Alpha-2A adrenergic receptor,Endolysin,Alpha-2B adrenergic

receptor,Alpha-2B adrenergic receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	R	270	2201	1474	370	345	12	0	0

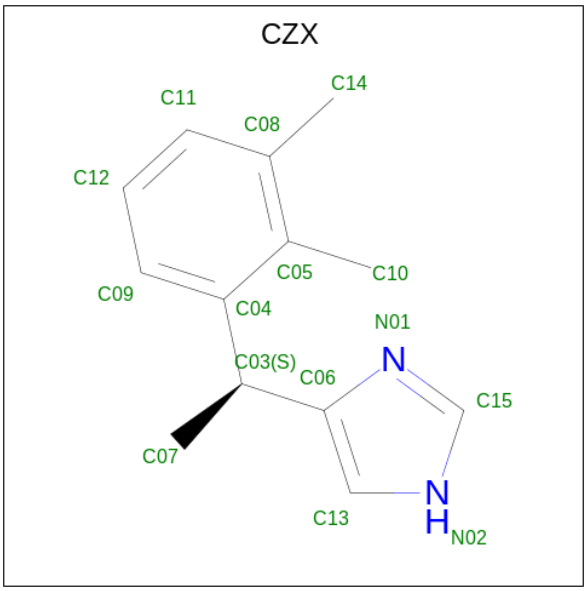
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-198	ASP	-	expression tag	UNP P08913
R	-197	ASP	-	expression tag	UNP P08913
R	-196	ASP	-	expression tag	UNP P08913
R	-195	ASP	-	expression tag	UNP P08913
R	-194	ALA	-	expression tag	UNP P08913
R	-193	HIS	-	expression tag	UNP P08913
R	-192	HIS	-	expression tag	UNP P08913
R	-191	HIS	-	expression tag	UNP P08913
R	-190	HIS	-	expression tag	UNP P08913
R	-189	HIS	-	expression tag	UNP P08913
R	-188	HIS	-	expression tag	UNP P08913
R	-160	GLU	-	linker	UNP P08913
R	-159	ASN	-	linker	UNP P08913
R	-158	LEU	-	linker	UNP P08913
R	-157	TYR	-	linker	UNP P08913
R	-156	PHE	-	linker	UNP P08913
R	-155	GLN	-	linker	UNP P08913
R	-154	GLY	-	linker	UNP P08913
R	-101	THR	CYS	conflict	UNP A0A097J809
R	-58	ALA	CYS	conflict	UNP A0A097J809

- Molecule 5 is a protein called scFv.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	H	233	1801	1143	300	348	10	1	0

- Molecule 6 is 4-[(1 {S})-1-(2,3-dimethylphenyl)ethyl]-1 {H}-imidazole (three-letter code: CZX) (formula: $C_{13}H_{16}N_2$) (labeled as "Ligand of Interest" by depositor).



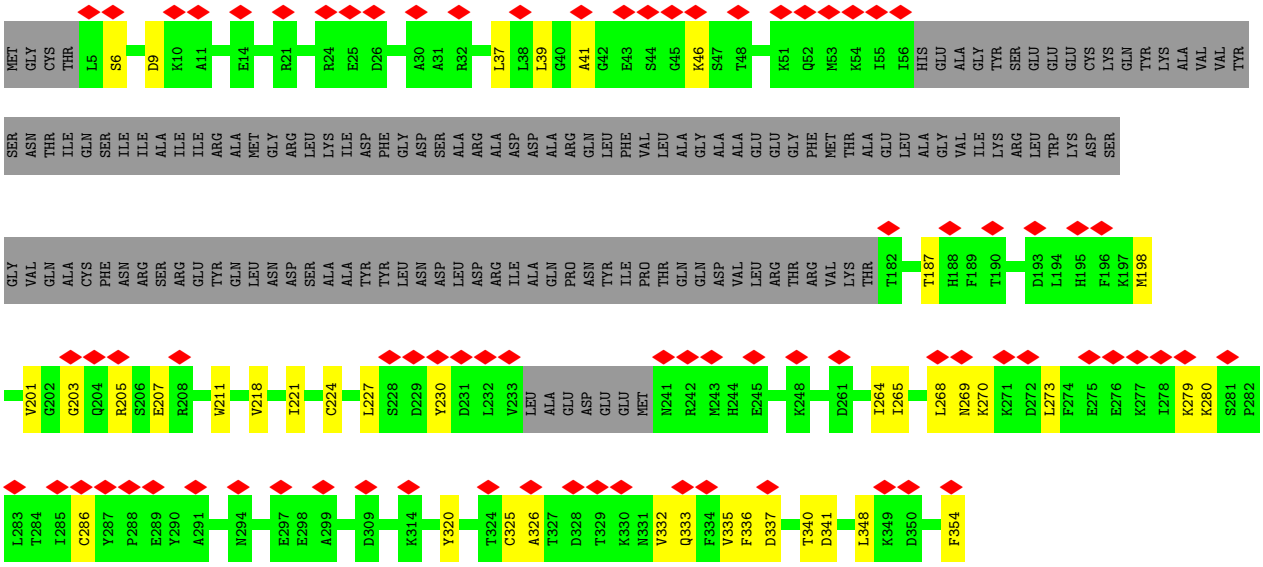
Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
6	R	1	15	13	2	0

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.

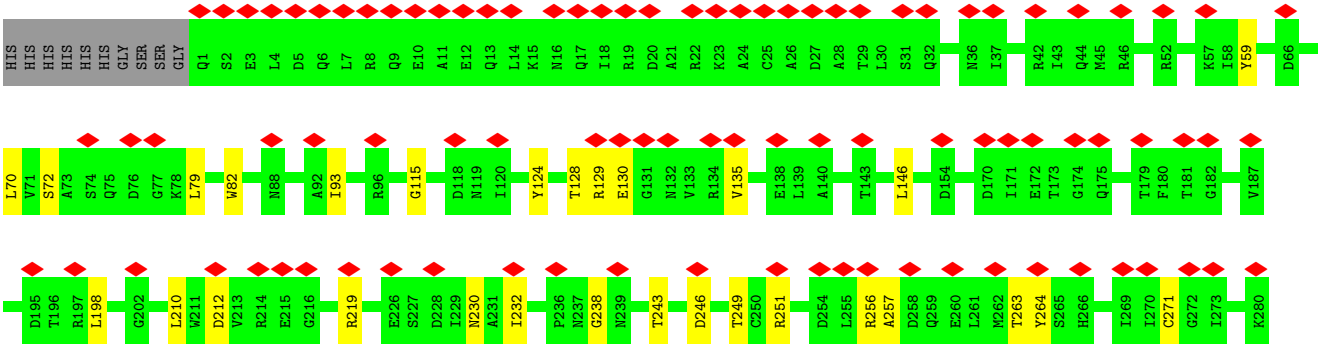
• Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1

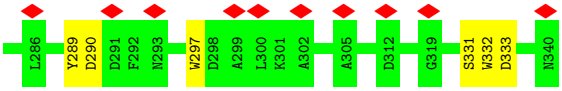
Chain A: 22% 51% 11% 38%



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

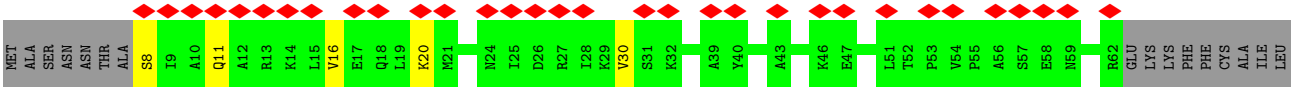
Chain B: 29% 87% 10%





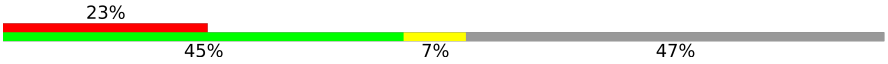
• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

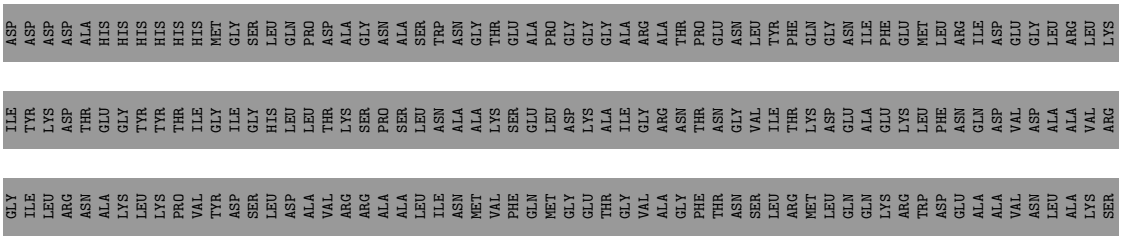
Chain G:

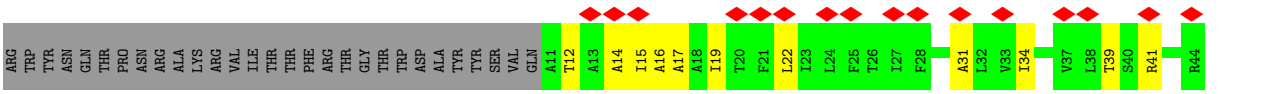


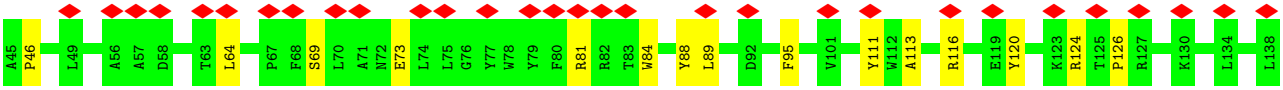
• Molecule 4: Alpha-2A adrenergic receptor,Endolysin,Alpha-2B adrenergic receptor,Alpha-2B adrenergic receptor

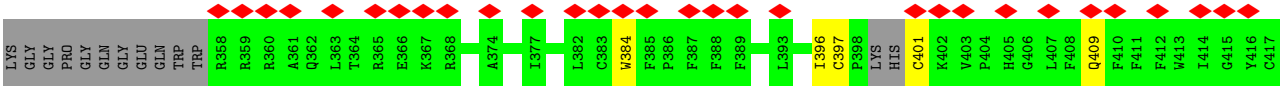
Chain R:

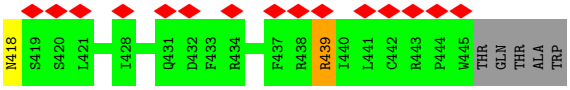






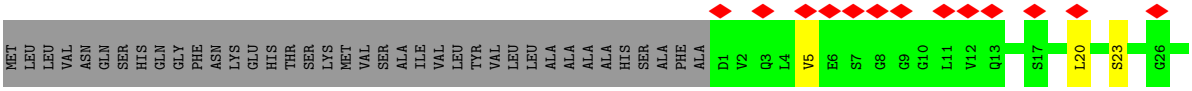


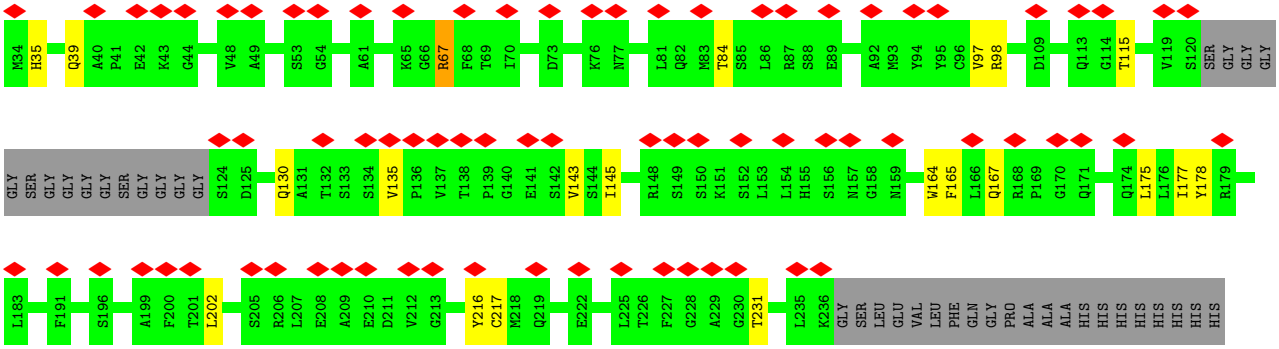




• Molecule 5: scFv

Chain H:




M34 H35 Q39 A40 P41 E42 K43 G44 V48 A49 S53 G54 A61 K65 G66 R67 F68 T69 I70 D73 K76 N77 L81 Q82 M83 T84 S85 L86 R87 S88 E89 A92 M93 Y94 Y95 C96 V97 R98 D109 Q113 G114 T115 V119 S120 SER GLY GLY GLY
GLY SER GLY GLY GLY SER GLY GLY GLY GLY S124 D125 Q130 A131 T132 S133 S134 V135 P136 V137 T138 P139 G140 E141 S142 V143 S144 T145 R148 S149 S150 K151 S152 L153 L154 H155 S156 N157 G158 N159 W164 F165 L166 Q167 R168 P169 G170 Q171 Q174 L175 L176 I177 Y178 R179
L183 F191 S196 A199 F200 T201 L202 S205 R206 L207 E208 A209 E210 D211 V212 G213 Y216 C217 M218 Q219 E222 L225 T226 F227 G228 A229 G230 T231 L235 K236 GLY SER LEU GLU VAL LEU PHE GLN GLY PRO ALA ALA ALA HIS HIS HIS HIS HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	235982	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.702	Depositor
Minimum map value	-0.558	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.131	Depositor
Map size (Å)	336.24, 336.24, 336.24	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4009999, 1.4009999, 1.4009999	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: CZX

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	0/1788	0.50	0/2396
2	B	0.25	0/2663	0.52	0/3609
3	G	0.23	0/430	0.43	0/580
4	R	0.30	0/2262	0.53	0/3077
5	H	0.26	0/1848	0.54	0/2504
All	All	0.27	0/8991	0.52	0/12166

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	1759	0	1759	21	0
2	B	2616	0	2521	19	0
3	G	424	0	436	3	0
4	R	2201	0	2289	19	0
5	H	1801	0	1742	12	0
6	R	15	0	0	0	0
All	All	8816	0	8747	73	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 73 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)
2:B:249:THR:HA	2:B:264:TYR:O	1.83	0.77
4:R:384:TRP:HE1	4:R:418:ASN:HD22	1.33	0.76
1:A:333:GLN:O	1:A:336:PHE:HB3	1.90	0.72
5:H:39:GLN:HE22	5:H:167:GLN:HE22	1.46	0.62
1:A:224:CYS:SG	1:A:269:ASN:ND2	2.73	0.62

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	212/354 (60%)	199 (94%)	13 (6%)	0	100	100
2	B	338/350 (97%)	321 (95%)	17 (5%)	0	100	100
3	G	53/71 (75%)	51 (96%)	2 (4%)	0	100	100
4	R	262/512 (51%)	251 (96%)	11 (4%)	0	100	100
5	H	230/307 (75%)	214 (93%)	16 (7%)	0	100	100
All	All	1095/1594 (69%)	1036 (95%)	59 (5%)	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	194/305 (64%)	194 (100%)	0	100	100
2	B	283/291 (97%)	283 (100%)	0	100	100
3	G	45/58 (78%)	45 (100%)	0	100	100
4	R	235/427 (55%)	230 (98%)	5 (2%)	53	72
5	H	198/247 (80%)	195 (98%)	3 (2%)	65	79
All	All	955/1328 (72%)	947 (99%)	8 (1%)	84	88

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	H	98	ARG
5	H	67[B]	ARG
4	R	439	ARG
4	R	396	ILE
5	H	67[A]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
4	R	30	ASN
4	R	167	ASN
5	H	167	GLN
4	R	418	ASN
2	B	311	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 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	$\#\|Z\| > 2$
6	CZX	R	501	-	11,16,16	5.57	6 (54%)	15,22,22	0.94	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	CZX	R	501	-	-	1/7/8/8	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	501	CZX	C09-C04	10.18	1.53	1.39
6	R	501	CZX	C04-C05	7.30	1.53	1.41
6	R	501	CZX	C08-C05	6.89	1.53	1.40
6	R	501	CZX	C12-C09	6.84	1.53	1.38
6	R	501	CZX	C12-C11	6.82	1.53	1.38

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	R	501	CZX	C07-C03-C06-C13

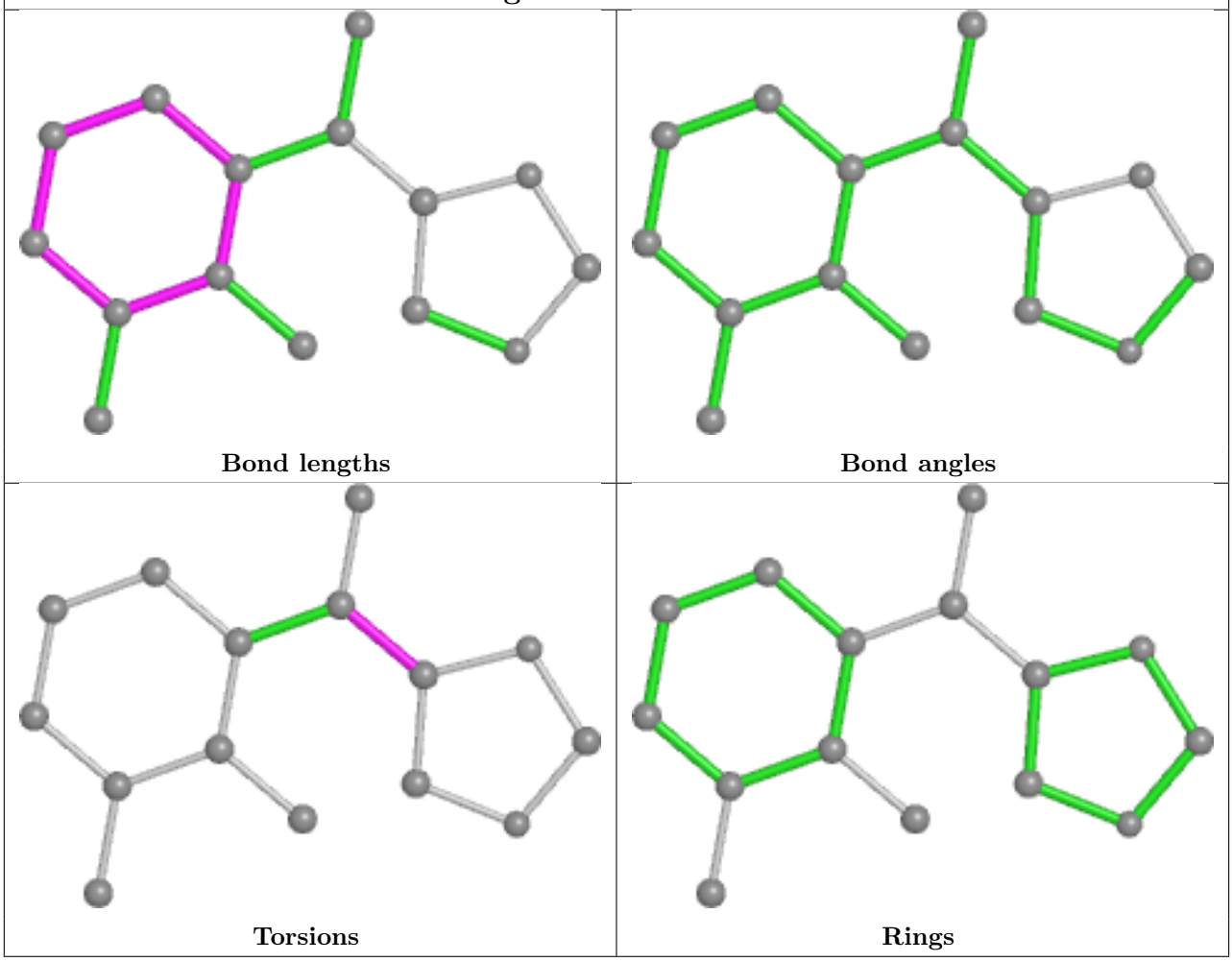
There are no ring outliers.

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 then 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.

Ligand CZX R 501



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-9912. 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

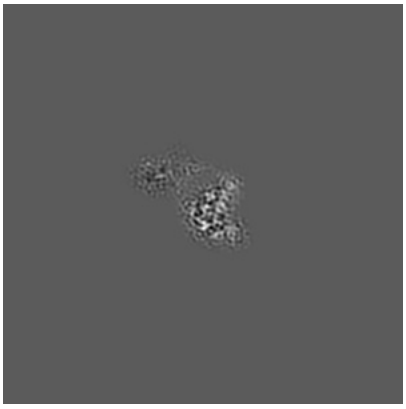
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map

X Index: 120

Y Index: 120



Z Index: 120

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: 120

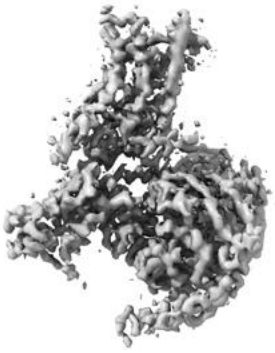
Y Index: 130

Z Index: 103

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.131. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

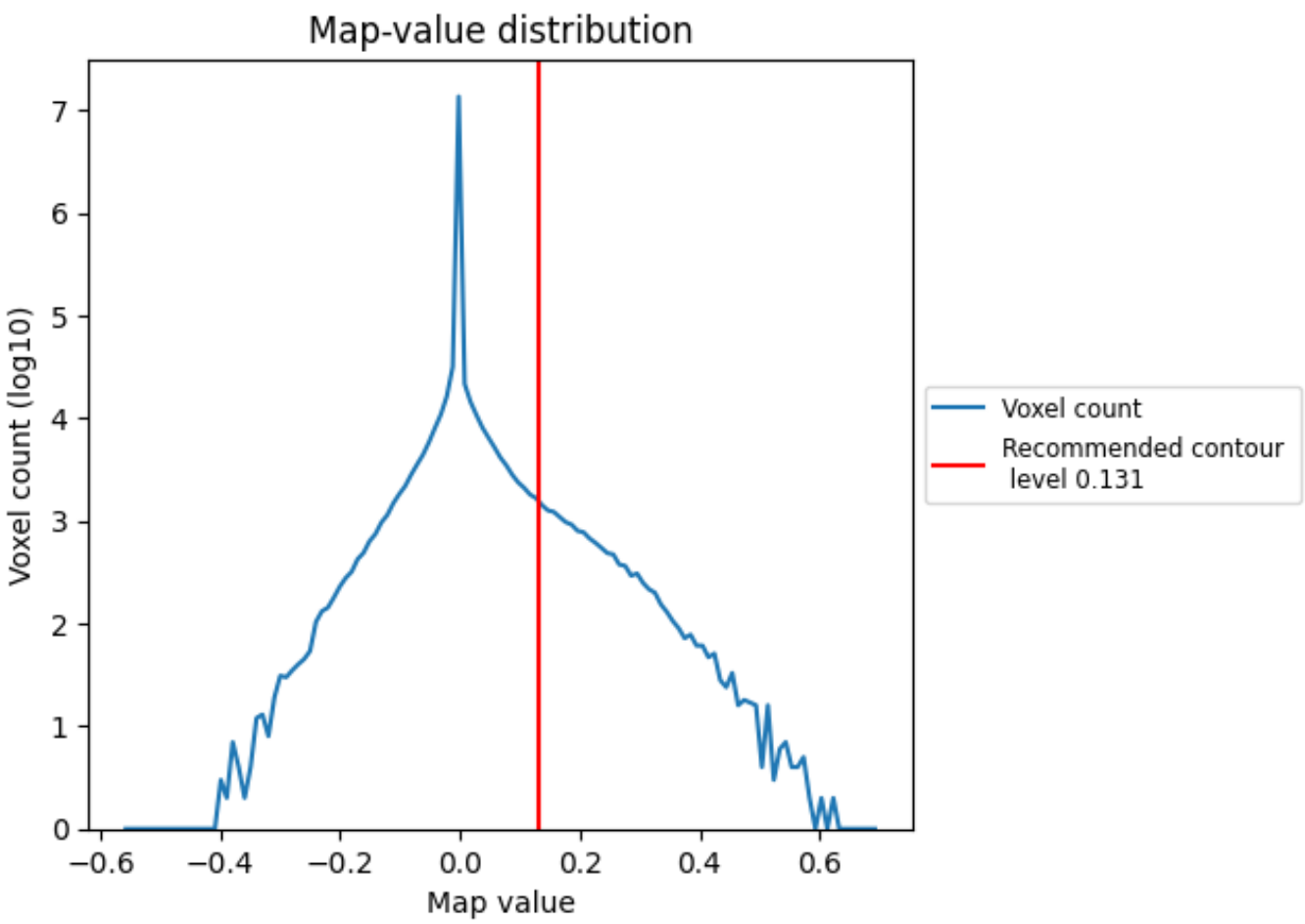
6.5 Mask visualisation (i)

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

7 Map analysis (i)

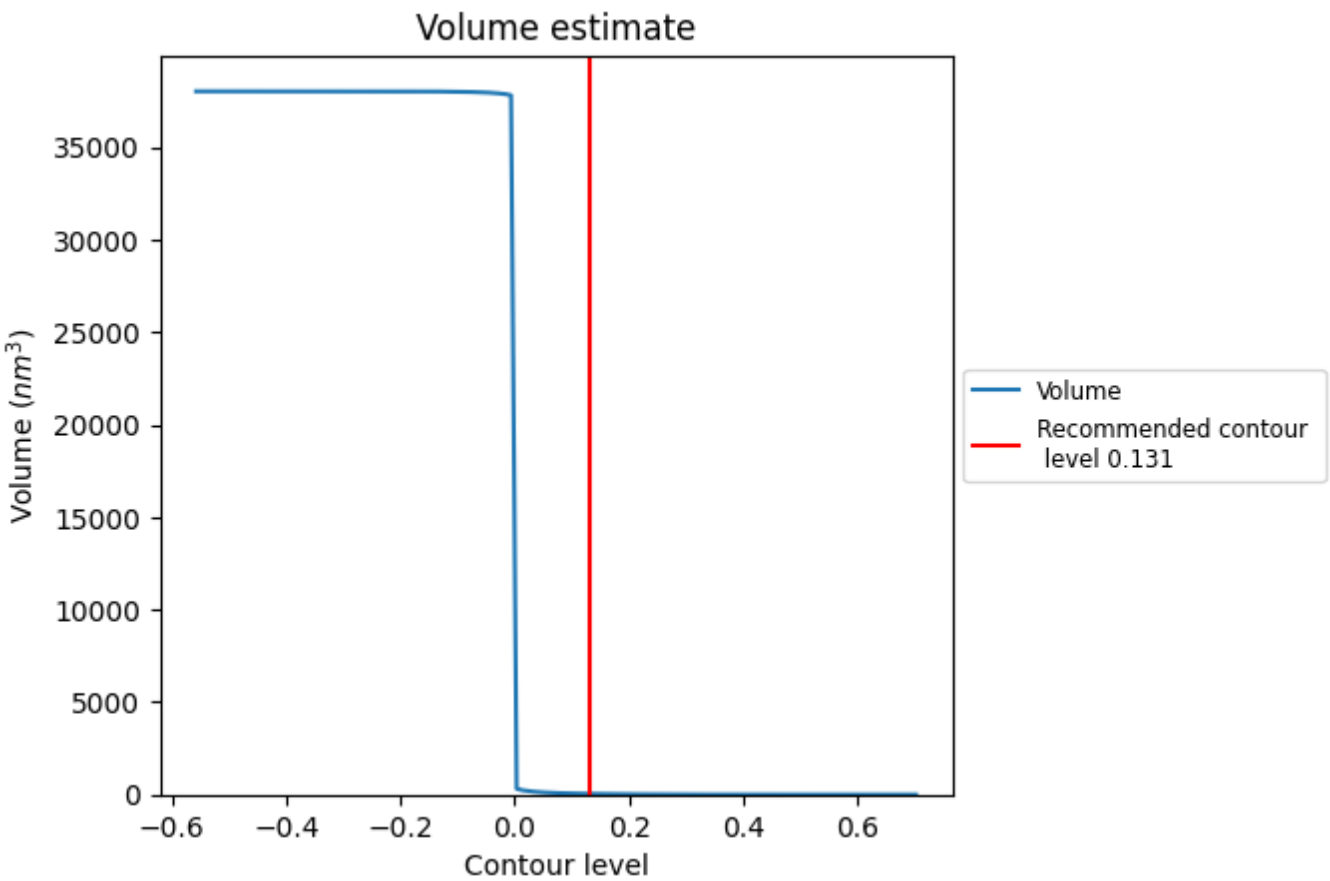
This section contains the results of statistical analysis of the map.

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.

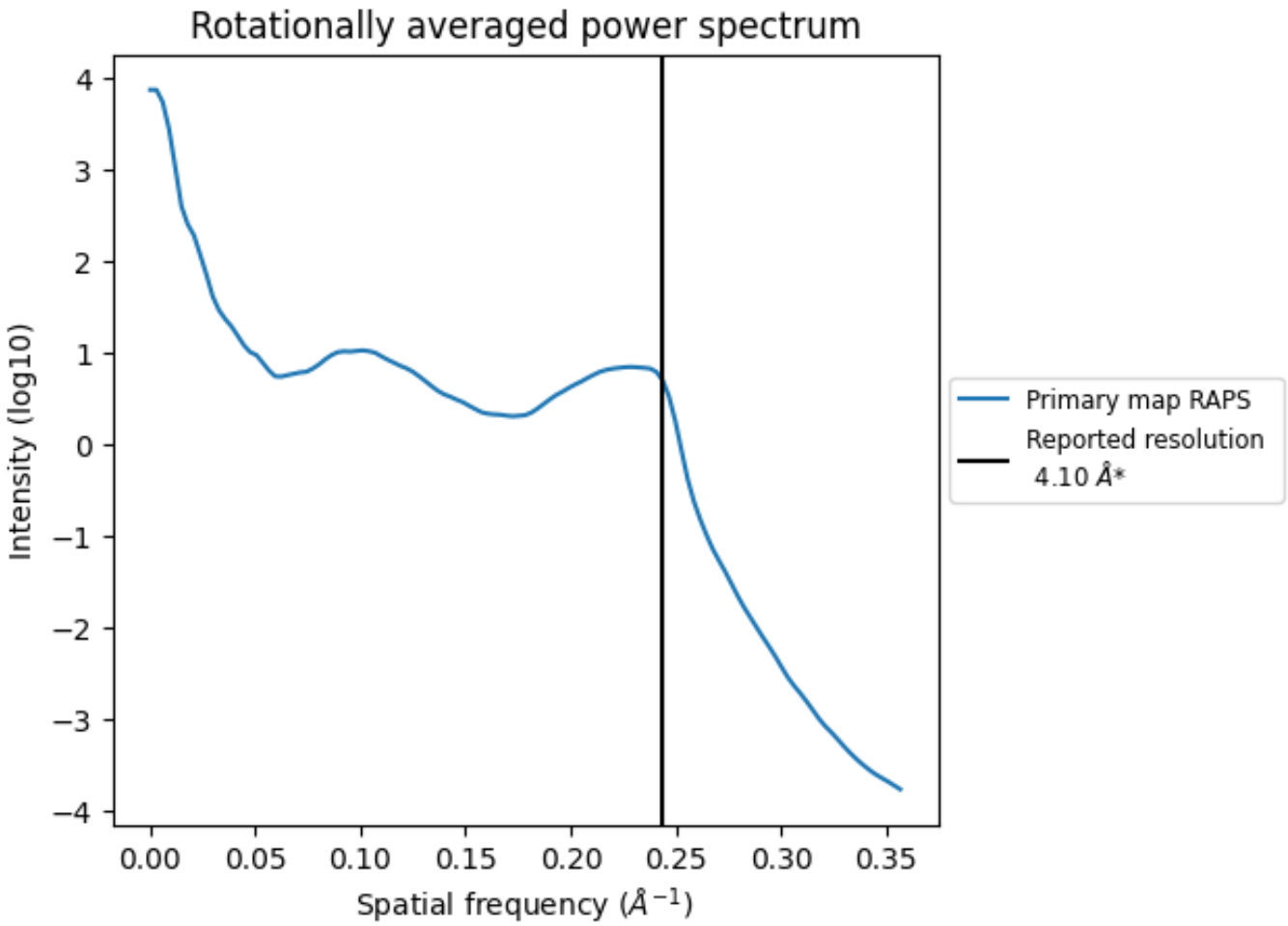
7.2 Volume estimate (i)



The volume at the recommended contour level is 42 nm^3; this corresponds to an approximate mass of 38 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 0.244 Å^{-1}

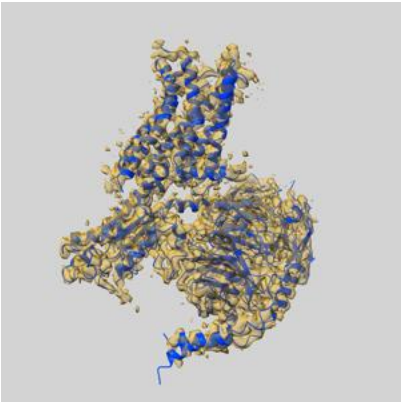
8 Fourier-Shell correlation (i)

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

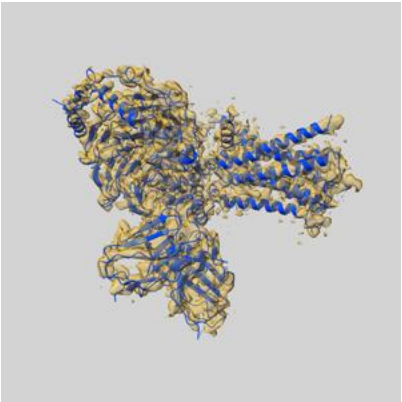
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-9912 and PDB model 6K42. Per-residue inclusion information can be found in section 3 on page 6.

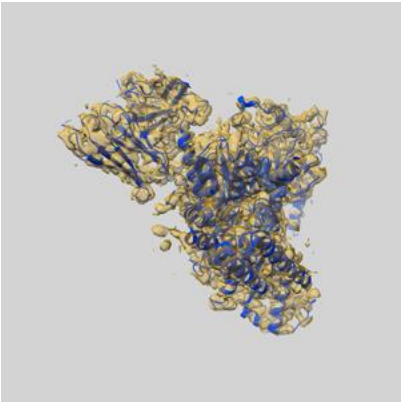
9.1 Map-model overlay (i)



X



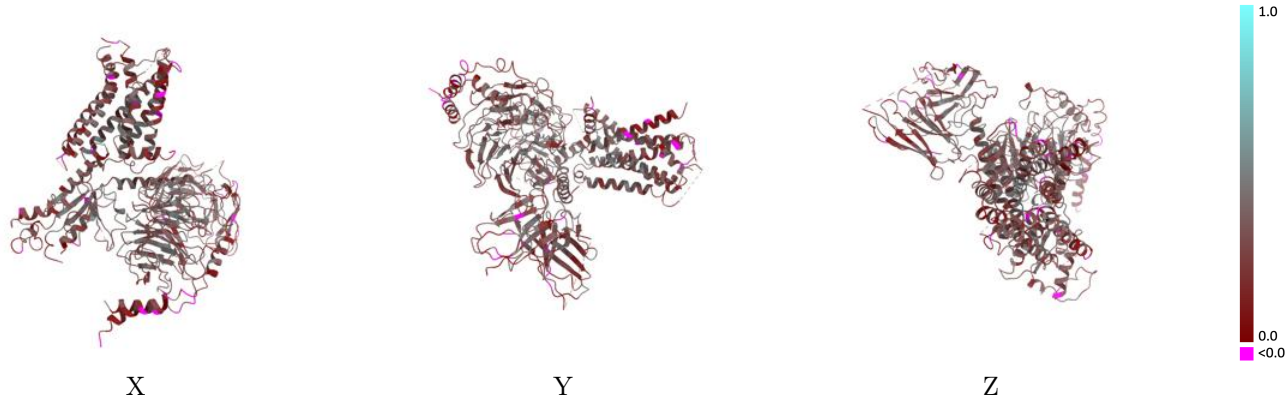
Y



Z

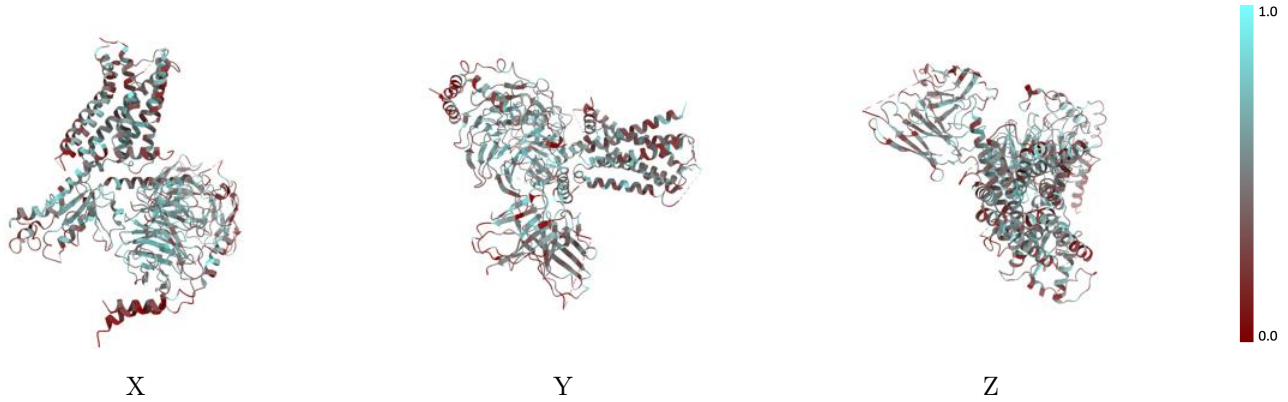
The images above show the 3D surface view of the map at the recommended contour level 0.131 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



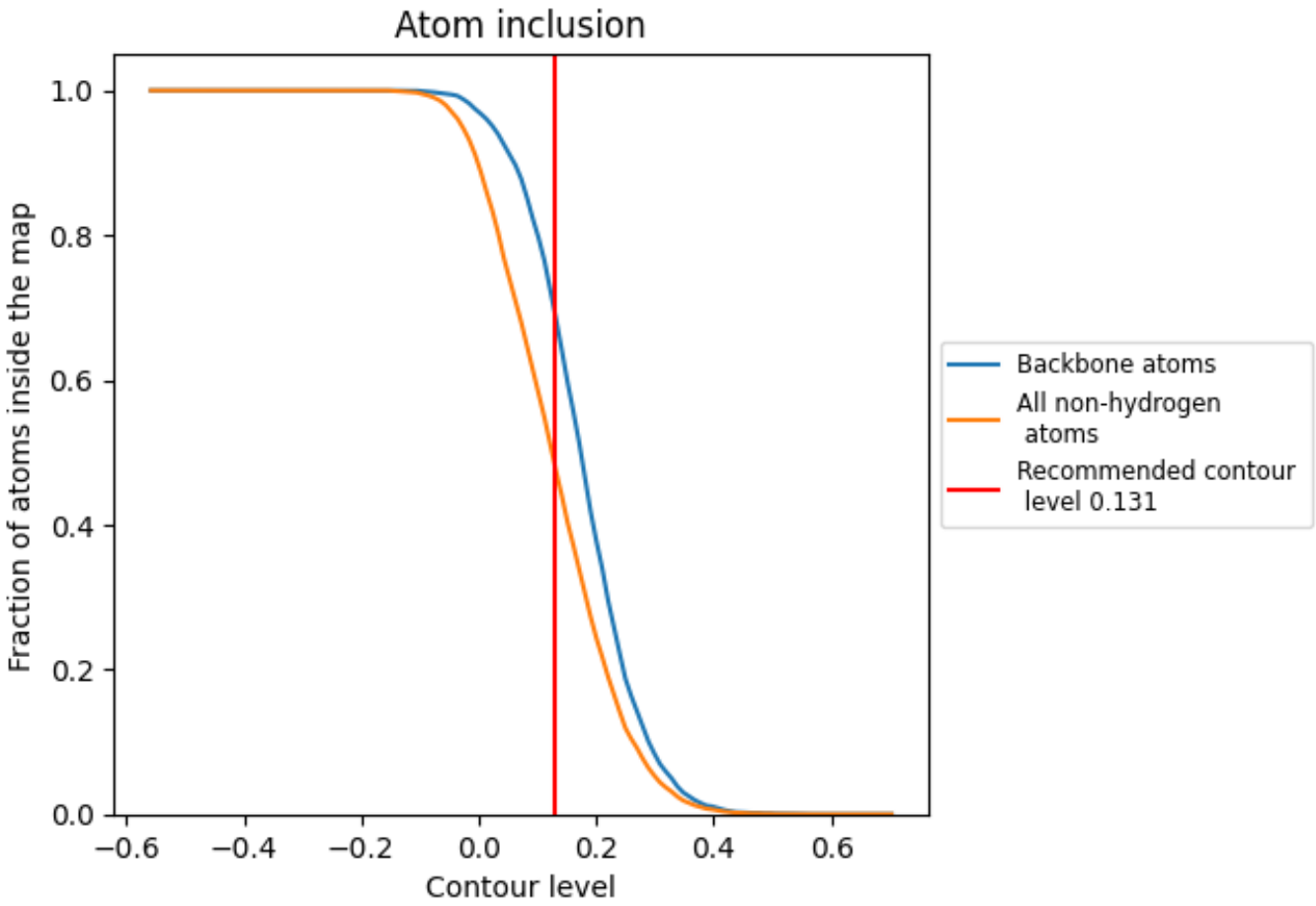
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.131).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 48% 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 (0.131) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4751	0.2990
A	0.4709	0.3060
B	0.5235	0.3250
G	0.3717	0.2480
H	0.4643	0.2850
R	0.4498	0.2850