



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:45 AM UTC

PDB ID : 9KPD / pdb_00009kpd
EMDB ID : EMD-62484
Title : Cryo-EM structure of GPCR16-miniGs complex
Authors : Wang, X.; Wu, L.J.; Hua, T.; Liu, Z.J.
Deposited on : 2024-11-22
Resolution : 2.84 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:

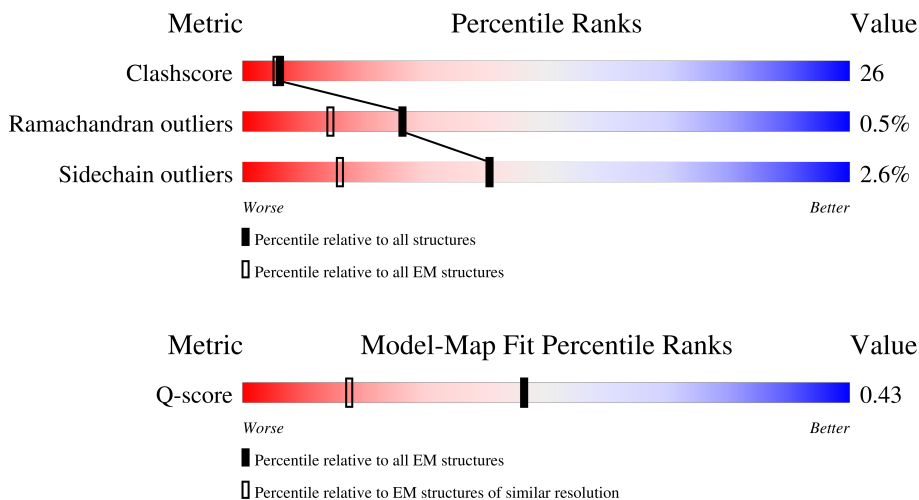
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.84 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11884 (2.34 - 3.34)

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	264	
2	B	366	
3	G	71	
4	N	135	

Continued on next page...

Mol	Chain	Length	Quality of chain
5	R	1011	6% 10% 12% 73%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8237 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Guanine nucleotide-binding protein G(s) subunit alpha isoforms short, Guanine nucleotide-binding protein G(s) subunit alpha isoforms short, Guanine nucleotide-binding protein G(t) subunit alpha-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	239	Total	C	N	O	S	0	0
			1961	1240	347	368	6		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP P63092
A	-9	ASP	-	expression tag	UNP P63092
A	-8	TYR	-	expression tag	UNP P63092
A	-7	LYS	-	expression tag	UNP P63092
A	-6	ASP	-	expression tag	UNP P63092
A	-5	ASP	-	expression tag	UNP P63092
A	-4	ASP	-	expression tag	UNP P63092
A	-3	ASP	-	expression tag	UNP P63092
A	-2	LYS	-	expression tag	UNP P63092
A	-1	GLU	-	expression tag	UNP P63092
A	0	ASN	-	expression tag	UNP P63092
A	1	LEU	-	expression tag	UNP P63092
A	2	TYR	-	expression tag	UNP P63092
A	3	PHE	-	expression tag	UNP P63092
A	4	GLN	-	expression tag	UNP P63092
A	5	SER	-	expression tag	UNP P63092
A	49	ASP	GLY	conflict	UNP P63092
A	50	ASN	GLU	conflict	UNP P63092
A	65	GLY	-	linker	UNP P63092
A	66	GLY	-	linker	UNP P63092
A	67	SER	-	linker	UNP P63092
A	67A	GLY	-	linker	UNP P63092
A	67B	GLY	-	linker	UNP P63092
A	67C	SER	-	linker	UNP P63092
A	67D	GLY	-	linker	UNP P63092
A	67E	GLY	-	linker	UNP P63092

- 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	341	Total	C	N	O	S	0	0
			2616	1612	470	513	21		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	341	GLY	-	expression tag	UNP P62873
B	342	SER	-	expression tag	UNP P62873
B	343	SER	-	expression tag	UNP P62873
B	344	GLY	-	expression tag	UNP P62873
B	345	GLY	-	expression tag	UNP P62873
B	346	GLY	-	expression tag	UNP P62873
B	347	GLY	-	expression tag	UNP P62873
B	348	SER	-	expression tag	UNP P62873
B	349	GLY	-	expression tag	UNP P62873
B	350	GLY	-	expression tag	UNP P62873
B	351	GLY	-	expression tag	UNP P62873
B	352	GLY	-	expression tag	UNP P62873
B	353	SER	-	expression tag	UNP P62873
B	354	SER	-	expression tag	UNP P62873
B	355	GLY	-	expression tag	UNP P62873
B	356	VAL	-	expression tag	UNP P62873
B	357	SER	-	expression tag	UNP P62873
B	358	GLY	-	expression tag	UNP P62873
B	359	TRP	-	expression tag	UNP P62873
B	360	ARG	-	expression tag	UNP P62873
B	361	LEU	-	expression tag	UNP P62873
B	362	PHE	-	expression tag	UNP P62873
B	363	LYS	-	expression tag	UNP P62873
B	364	LYS	-	expression tag	UNP P62873
B	365	ILE	-	expression tag	UNP P62873
B	366	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	57	Total	C	N	O	S	0	0
			436	273	77	83	3		

- Molecule 4 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	128	Total	C	N	O	S	0	0
			973	605	170	192	6		

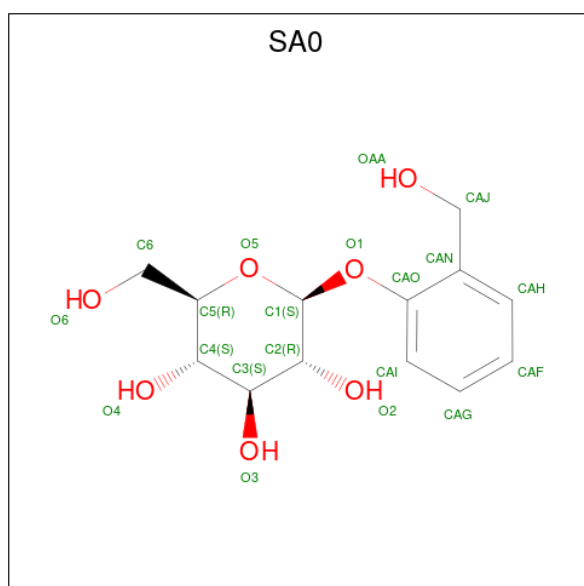
- Molecule 5 is a protein called Fusion protein 1,exo-alpha-sialidase,Taste receptor type 2 member 16,Fusion protein 2,exo-alpha-sialidase,Taste receptor type 2 member 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	270	Total	C	N	O	S	0	0
			2231	1504	355	355	17		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-3	GLY	-	linker	UNP A0A4J1WX37
R	-2	SER	-	linker	UNP A0A4J1WX37
R	-1	GLY	-	linker	UNP A0A4J1WX37
R	0	SER	-	linker	UNP A0A4J1WX37
R	1	GLY	-	linker	UNP A0A4J1WX37
R	133	CYS	SER	conflict	UNP Q9NYV7

- Molecule 6 is 2-(hydroxymethyl)phenyl beta-D-glucopyranoside (CCD ID: SA0) (formula: C₁₃H₁₈O₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
6	R	1	Total	C	O	0
			20	13	7	

THR	LEU	TRP	ASN	GLY	ASN	LYS	ILE	ILE	ASP	GLU	ARG	LEU	ILE	THR	THR	ASN	ASP	GLY	HIS	GLY	PHE	SER	MET	LEU	PHE	LEU	PHE	ILE	VAL	THR	THR	GLY	ASP	GLN																							
MET	ALA	GLN	ILE	GLU	GLU	VAL	PHE	LYS	VAL	VAL	VAL	THR	PRO	VAL	ASP	ASP	HIS	HIS	VAL	VAL	SER	SER	LEU	LEU	LEU	VAL	VAL	ILE	THR	THR	VAL	THR	GLY																								
Y266	GLU	GLN	THR	ALA	ALA	TYR	ASN	LEU	ASP	GLN	VAL	LEU	GLU	GLN	GLY	GLY	VAL	VAL	VAL	VAL	SER	SER	LEU	LEU	LEU	GLN	ASN	LYS	GLY	VAL	THR	ASP	GLN																								
K205	Q206	I207	Q208	H209	H210	S211	T212	G213	H214	C215	N216	P217	S218	R222	F223	T224	A225	L226	R227	S228	L229	A230	V231	L232	F233	I234	V235	F236	T237	S238	Y239	F240	L241	T242	I243	L244	L245	T246	I247	I248	G249	T250	L251	F252	D253	K254	R255	C256	W257	L258	W259	V260	W261	E262	A263	F264	V265
I141	I142	P143	S144	A145	G146	N148	Y149	I150	Q151	I152	Q153	L154	L155	T156	MET	GLU	HIS	LEU	PRO	ARG	ASN	SER	THR	VAL	THR	ASP	LYS	LEU	E171	M172	F173	H174	Q175	Y176	Q177	F178	Q179	A180	H181	T182	V183	A184	L185	V186	I187	F188	I189	I190	S195	T196	I197	F198	L199	M200	A201	S202	L203

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	122713	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.741	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	266.24, 266.24, 266.24	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	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: SA0

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	0.31	1/1999 (0.1%)	0.43	3/2689 (0.1%)
2	B	0.21	0/2663	0.35	0/3610
3	G	0.16	0/442	0.37	0/597
4	N	0.21	0/993	0.37	0/1345
5	R	1.48	42/2296 (1.8%)	1.19	34/3130 (1.1%)
All	All	0.80	43/8393 (0.5%)	0.70	37/11371 (0.3%)

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	240	PHE	CA-C	-8.10	1.41	1.52
5	R	224	THR	C-O	-7.80	1.15	1.24
5	R	101	VAL	C-O	-7.41	1.15	1.24
5	R	99	LEU	CA-C	-7.12	1.44	1.52
5	R	71	TYR	CA-C	-6.87	1.44	1.52

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	240	PHE	N-CA-C	-7.98	101.36	112.45
5	R	66	ASN	N-CA-C	7.71	119.47	111.14
5	R	280	SER	CA-C-N	7.51	129.22	119.84
5	R	280	SER	C-N-CA	7.51	129.22	119.84
5	R	229	LEU	N-CA-C	-7.41	103.28	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1961	0	1932	82	0
2	B	2616	0	2518	93	0
3	G	436	0	448	11	0
4	N	973	0	938	26	0
5	R	2231	0	2312	232	0
6	R	20	0	18	2	0
All	All	8237	0	8166	426	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 26.

The worst 5 of 426 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:48:ILE:HD11	5:R:98:LEU:CD2	1.54	1.37
5:R:142:ILE:CG1	5:R:143:PRO:HD3	1.54	1.36
1:A:60:MET:CE	1:A:86:MET:HE1	1.62	1.27
5:R:142:ILE:HG13	5:R:143:PRO:CD	1.70	1.20
5:R:252:PHE:CZ	5:R:257:TRP:CD1	2.37	1.13

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	235/264 (89%)	227 (97%)	8 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	339/366 (93%)	327 (96%)	12 (4%)	0	100	100
3	G	55/71 (78%)	54 (98%)	1 (2%)	0	100	100
4	N	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
5	R	266/1011 (26%)	240 (90%)	21 (8%)	5 (2%)	6	13
All	All	1021/1847 (55%)	972 (95%)	44 (4%)	5 (0%)	26	43

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	R	62	ALA
5	R	257	TRP
5	R	77	VAL
5	R	258	LEU
5	R	136	ILE

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	213/234 (91%)	212 (100%)	1 (0%)	81	90
2	B	283/298 (95%)	282 (100%)	1 (0%)	84	92
3	G	46/58 (79%)	46 (100%)	0	100	100
4	N	106/113 (94%)	104 (98%)	2 (2%)	50	73
5	R	252/879 (29%)	233 (92%)	19 (8%)	12	27
All	All	900/1582 (57%)	877 (97%)	23 (3%)	41	65

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	R	240	PHE
5	R	260	VAL
5	R	258	LEU

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Mol	Chain	Res	Type
5	R	261	TRP
5	R	61	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
5	R	60	GLN
5	R	209	HIS
5	R	67	ASN
5	R	210	HIS
5	R	177	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	SA0	R	501	-	21,21,21	0.23	0	29,29,29	0.48	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	SA0	R	501	-	-	1/8/28/28	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

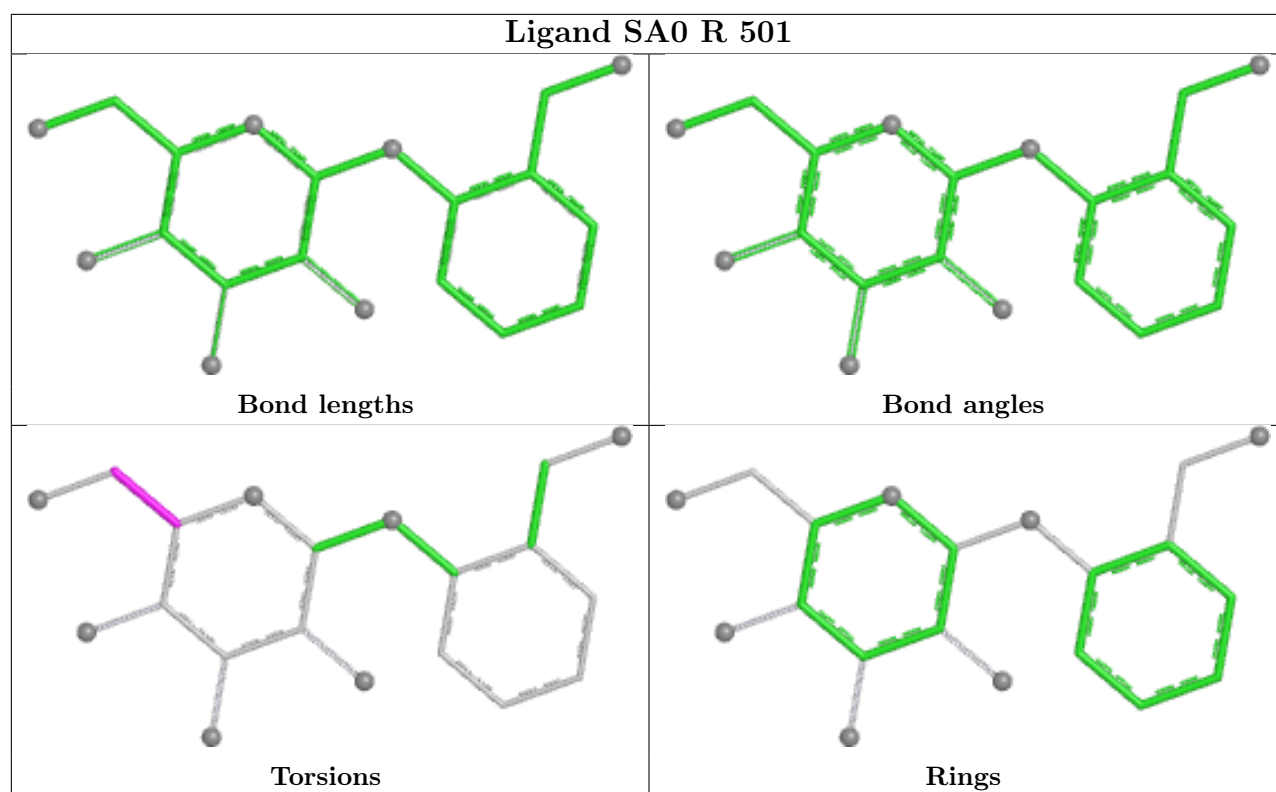
Mol	Chain	Res	Type	Atoms
6	R	501	SA0	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	501	SA0	2	0

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.

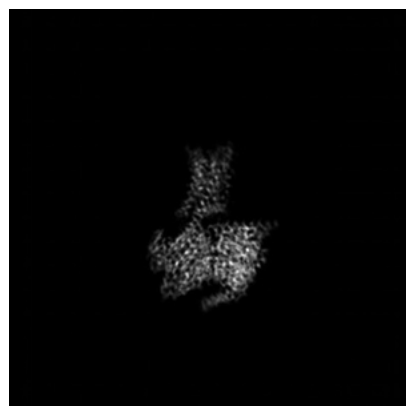
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62484. 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](#)

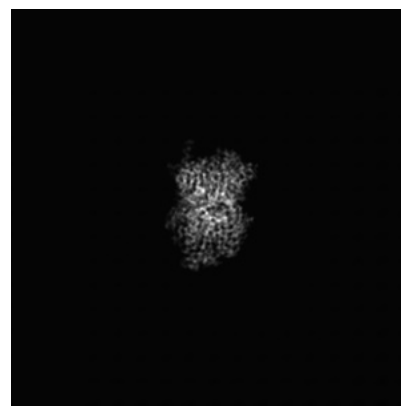
6.1.1 Primary map



X

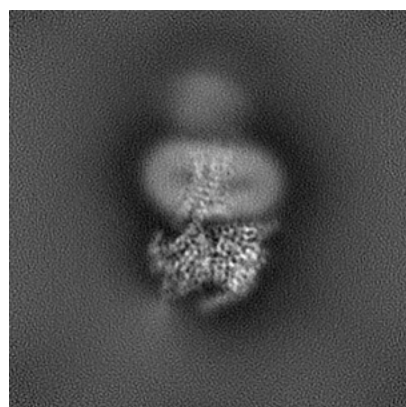


Y

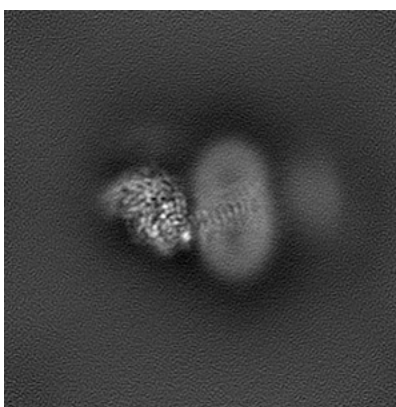


Z

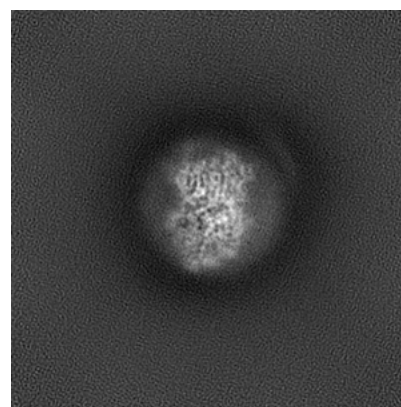
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

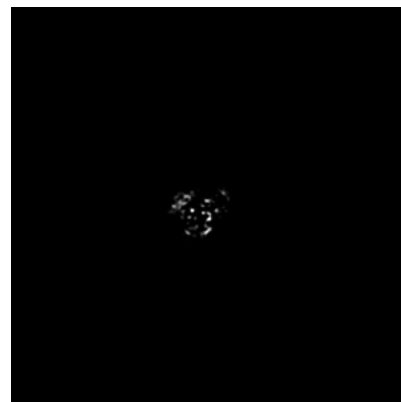
6.2.1 Primary map



X Index: 128

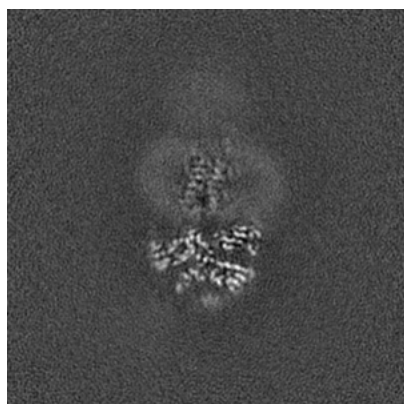


Y Index: 128

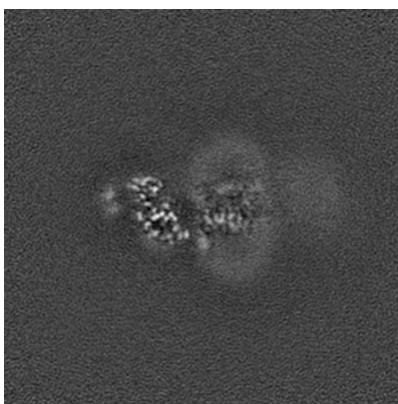


Z Index: 128

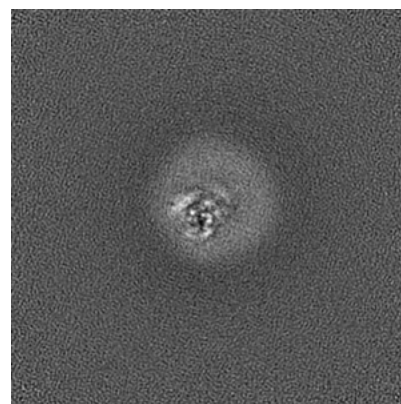
6.2.2 Raw map



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: 123

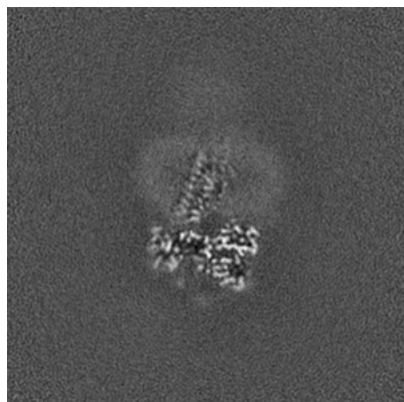


Y Index: 145

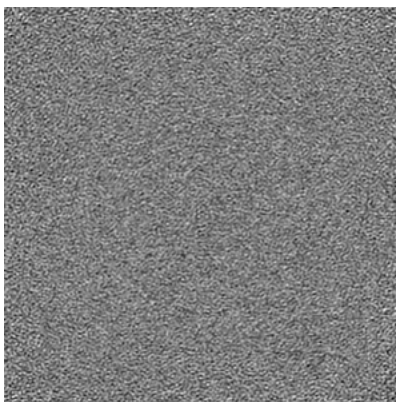


Z Index: 89

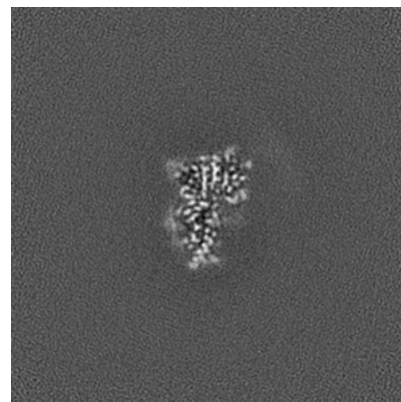
6.3.2 Raw map



X Index: 123



Y Index: 0

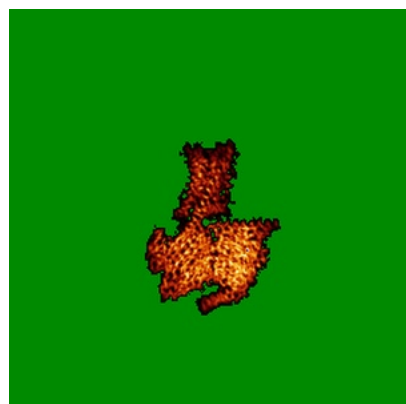


Z Index: 102

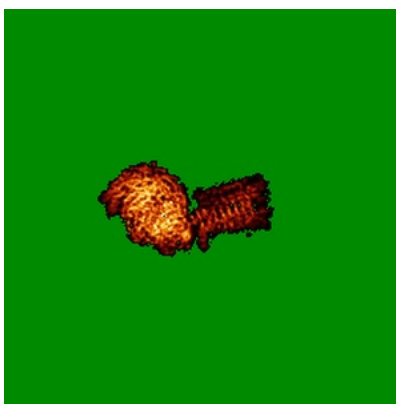
The images above show the largest variance slices of the map in three orthogonal directions.

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

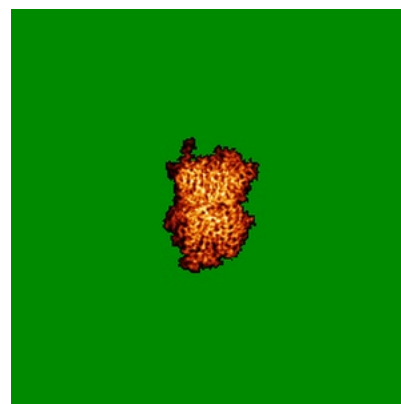
6.4.1 Primary map



X

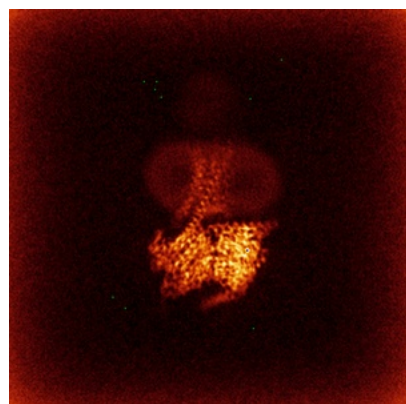


Y

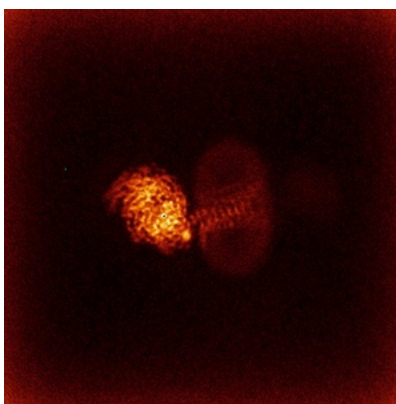


Z

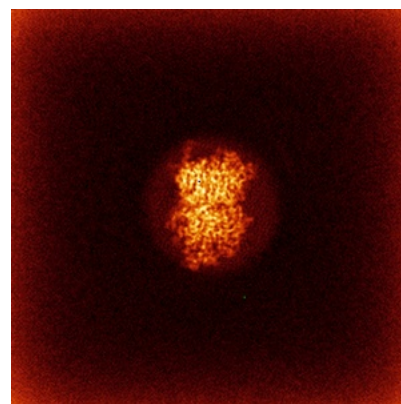
6.4.2 Raw map



X



Y

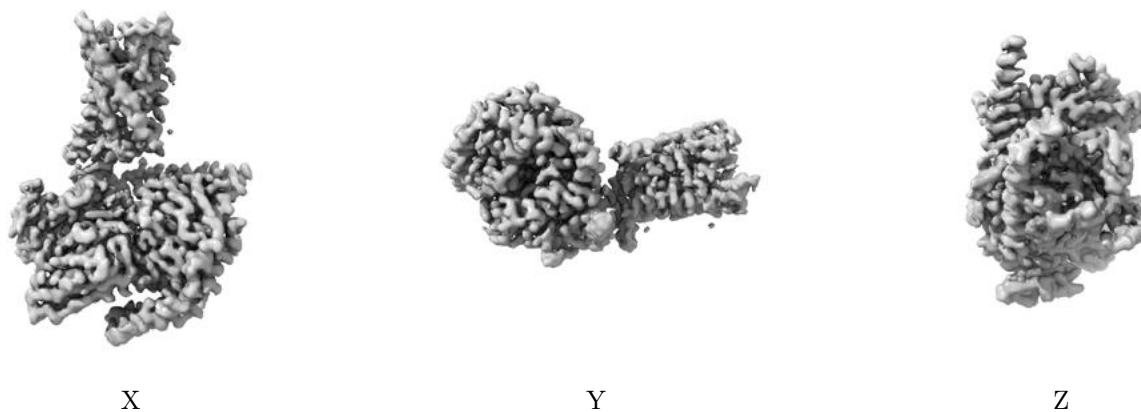


Z

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.

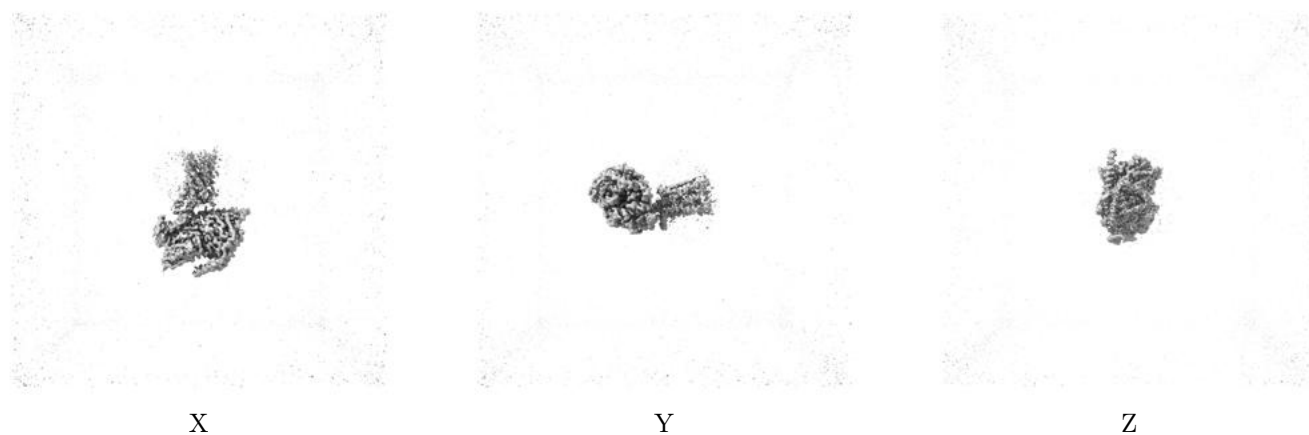
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

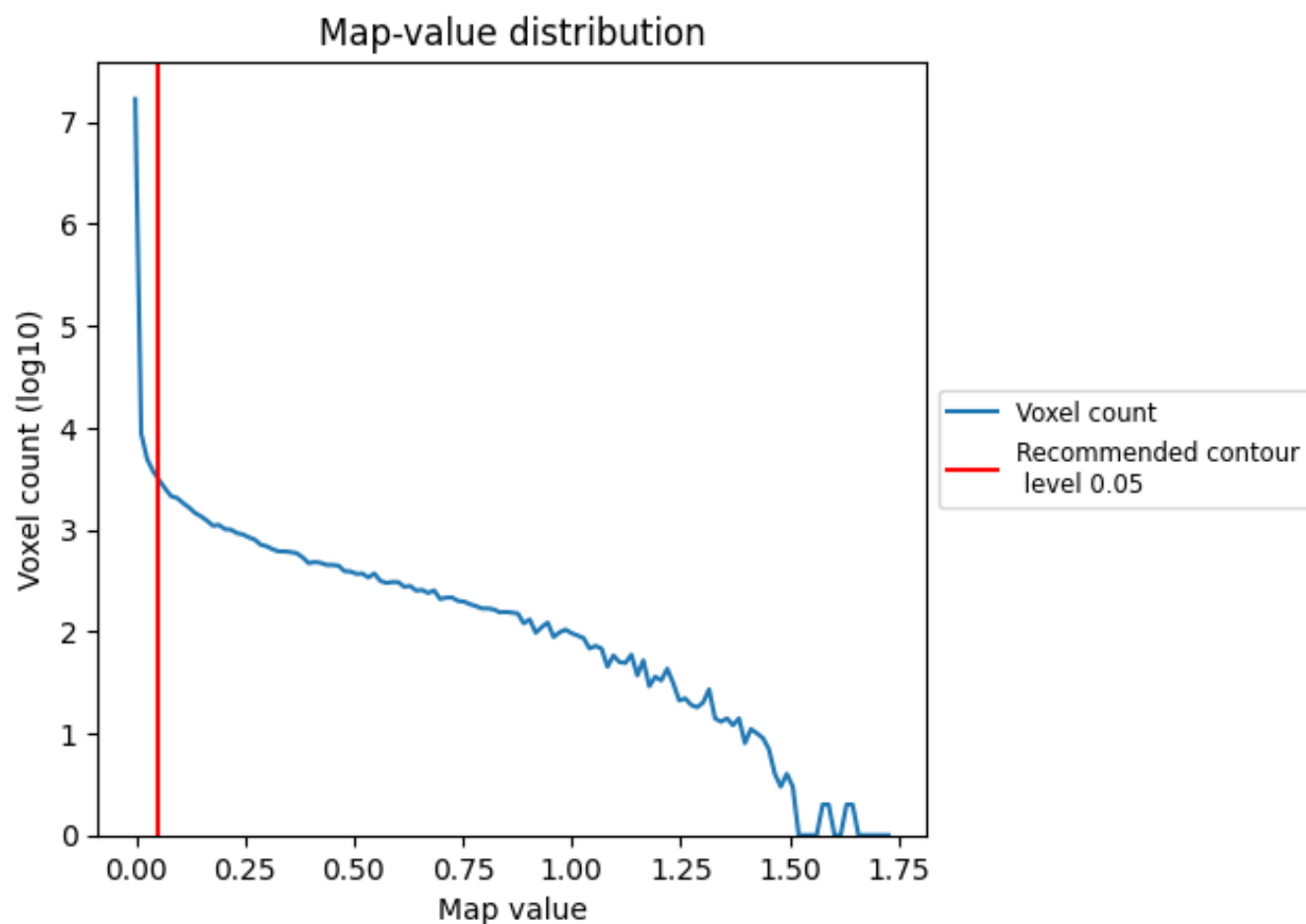
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

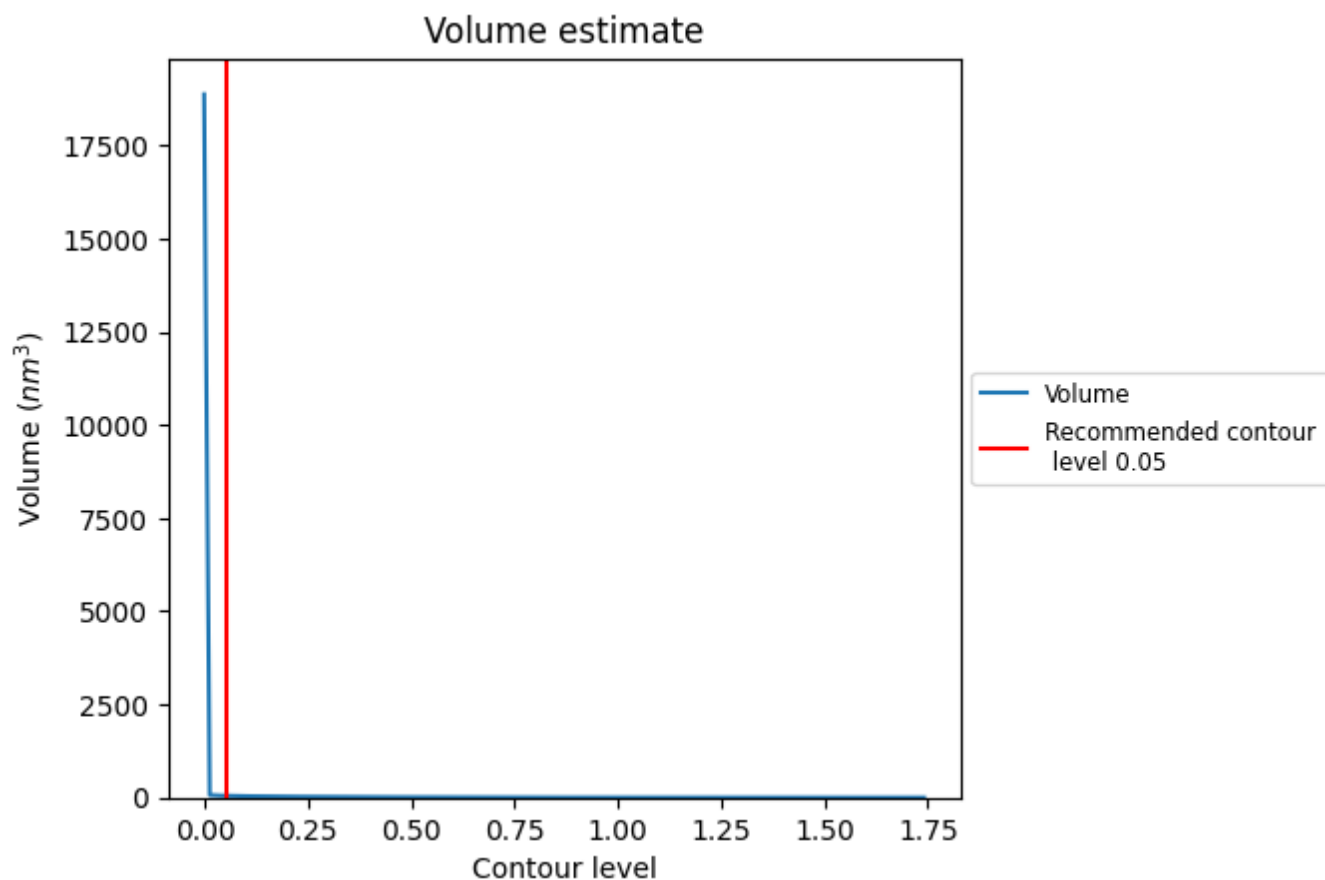
This section contains the results of statistical analysis of the map.

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.

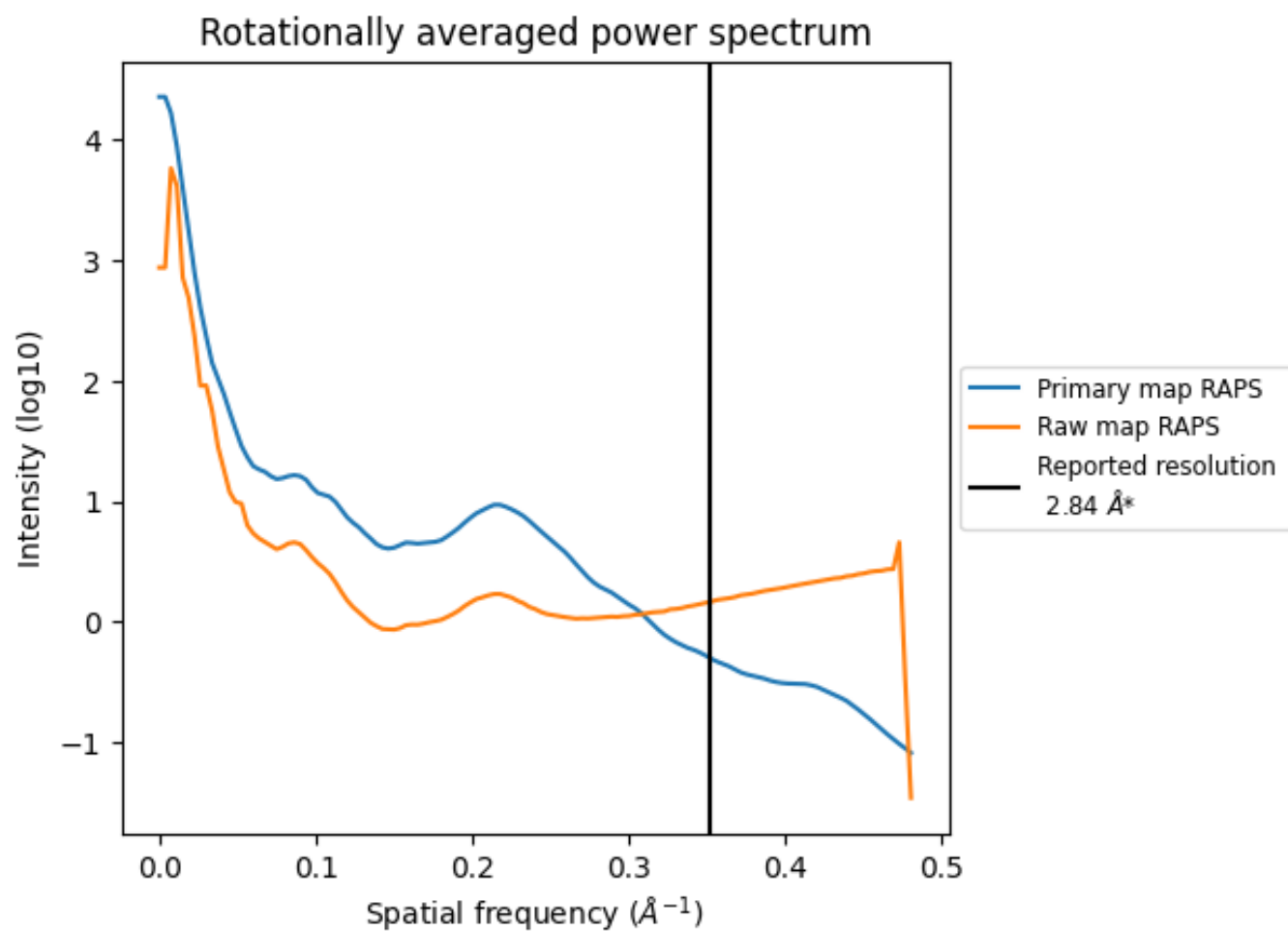
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 48 nm^3 ; this corresponds to an approximate mass of 44 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 ⓘ

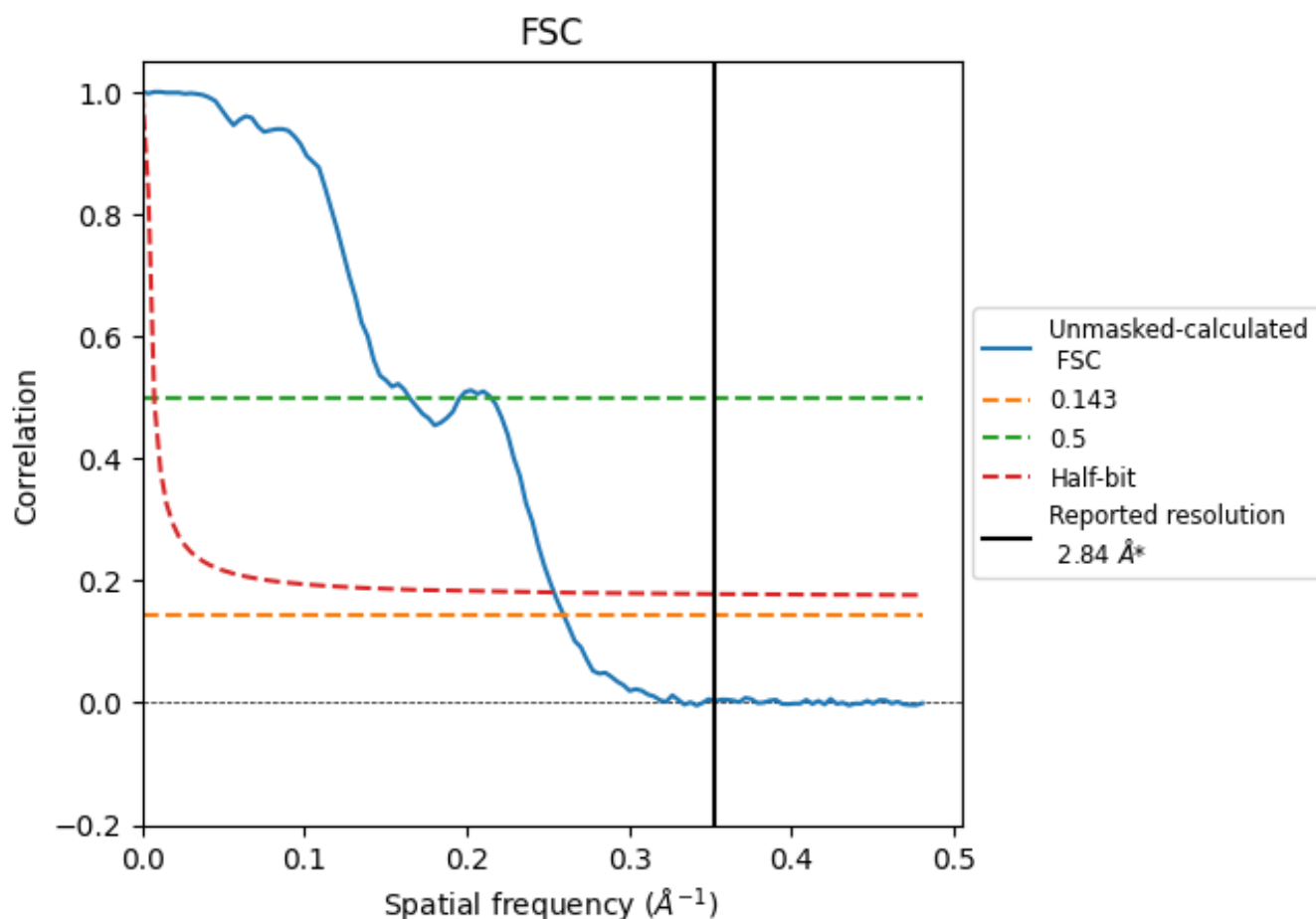


*Reported resolution corresponds to spatial frequency of 0.352 $\text{\AA}^{-1}$

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 0.352 Å⁻¹

8.2 Resolution estimates [i](#)

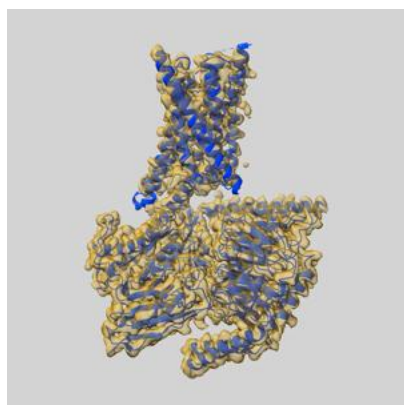
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.85	6.08	3.94

*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 3.85 differs from the reported value 2.84 by more than 10 %

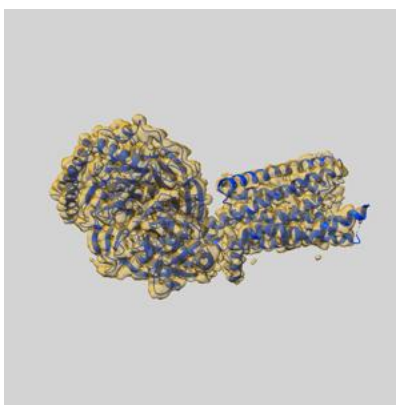
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-62484 and PDB model 9KPD. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

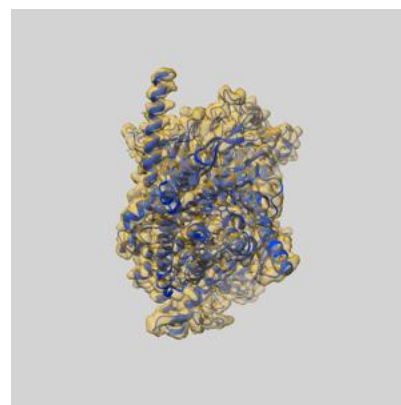
9.1 Map-model overlay [i](#)



X



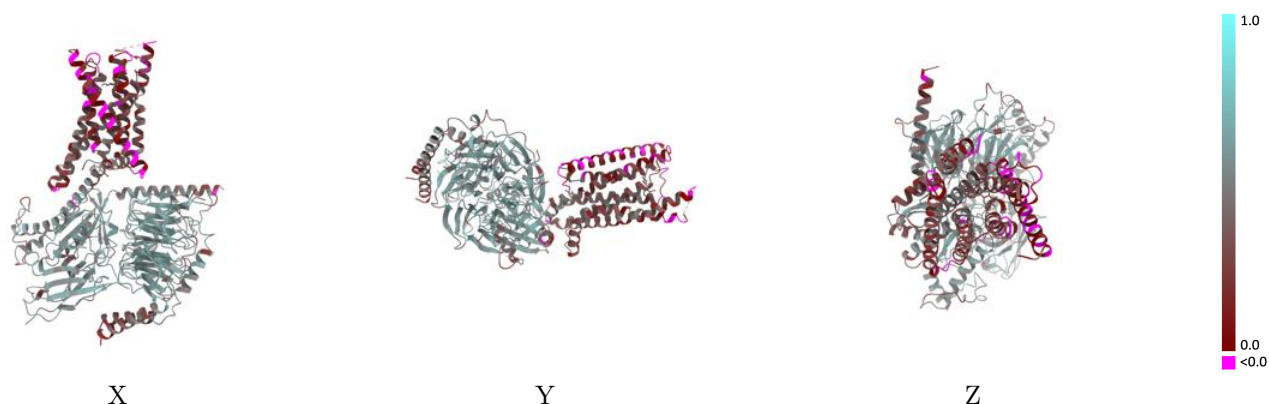
Y



Z

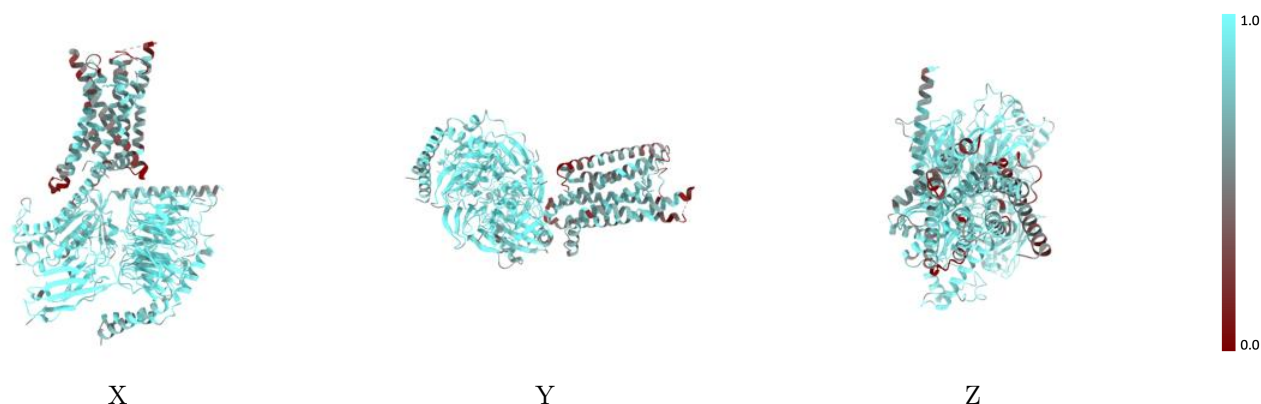
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



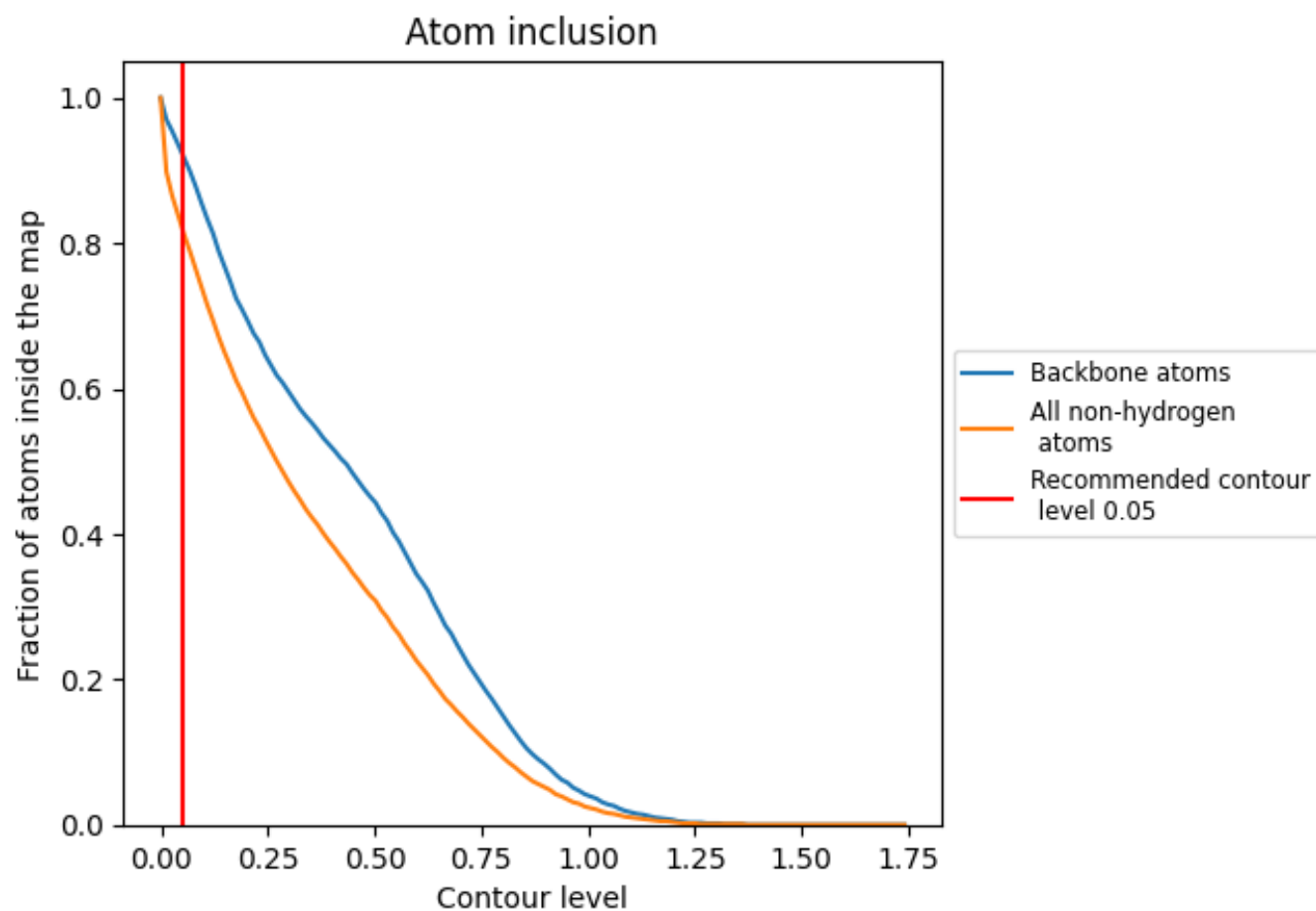
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8180	0.4300
A	0.8660	0.4820
B	0.9230	0.5400
G	0.8020	0.4240
N	0.9370	0.5270
R	0.6050	0.2160

