



wwPDB EM Validation Summary Report ⓘ

May 19, 2025 – 01:27 AM EDT

PDB ID : 6CMO / pdb_00006cmo
EMDB ID : EMD-7517
Title : Rhodopsin-Gi complex
Authors : Kang, Y.; Kuybeda, O.; de Waal, P.W.; Mukherjee, S.; Van Eps, N.; Dutka, P.; Zhou, X.E.; Bartesaghi, A.; Erramilli, S.; Morizumi, T.; Gu, X.; Yin, Y.; Liu, P.; Jiang, Y.; Meng, X.; Zhao, G.; Melcher, K.; Earnst, O.P.; Kossiakoff, A.A.; Subramaniam, S.; Xu, H.E.
Deposited on : 2018-03-05
Resolution : 4.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.43.1

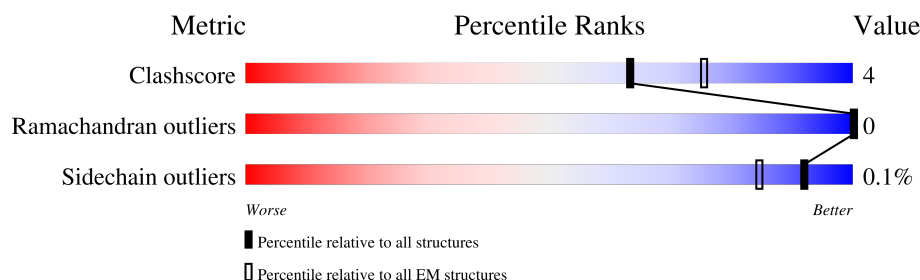
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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	R	463	<div> <div>60%</div> <div>61% 9% 30%</div> </div>
2	A	354	<div> <div>73%</div> <div>86% 13%</div> </div>
3	B	345	<div> <div>44%</div> <div>87% 11% .</div> </div>
4	G	68	<div> <div>74%</div> <div>75% 10% 15%</div> </div>
5	L	215	<div> <div>78%</div> <div>85% 13% .</div> </div>
6	H	239	<div> <div>87%</div> <div>92% 5% .</div> </div>
7	C	2	<div> <div>100%</div> <div>100%</div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11834 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 chimera protein of Soluble cytochrome b562 and Rhodopsin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	323	Total	C	N	O	S	0	0
			2567	1714	393	434	26		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-139	PHE	-	expression tag	UNP P0ABE7
R	-138	ALA	-	expression tag	UNP P0ABE7
R	-137	ASP	-	expression tag	UNP P0ABE7
R	-136	TYR	-	expression tag	UNP P0ABE7
R	-135	LYS	-	expression tag	UNP P0ABE7
R	-134	ASP	-	expression tag	UNP P0ABE7
R	-133	ASP	-	expression tag	UNP P0ABE7
R	-132	ASP	-	expression tag	UNP P0ABE7
R	-131	ASP	-	expression tag	UNP P0ABE7
R	-130	ALA	-	expression tag	UNP P0ABE7
R	-129	LYS	-	expression tag	UNP P0ABE7
R	-128	LEU	-	expression tag	UNP P0ABE7
R	-127	GLN	-	expression tag	UNP P0ABE7
R	-126	THR	-	expression tag	UNP P0ABE7
R	-125	MET	-	expression tag	UNP P0ABE7
R	-124	HIS	-	expression tag	UNP P0ABE7
R	-123	HIS	-	expression tag	UNP P0ABE7
R	-122	HIS	-	expression tag	UNP P0ABE7
R	-121	HIS	-	expression tag	UNP P0ABE7
R	-120	HIS	-	expression tag	UNP P0ABE7
R	-119	HIS	-	expression tag	UNP P0ABE7
R	-118	HIS	-	expression tag	UNP P0ABE7
R	-117	HIS	-	expression tag	UNP P0ABE7
R	-116	HIS	-	expression tag	UNP P0ABE7
R	-115	HIS	-	expression tag	UNP P0ABE7
R	-114	GLU	-	expression tag	UNP P0ABE7
R	-113	ASN	-	expression tag	UNP P0ABE7
R	-112	LEU	-	expression tag	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-111	TYR	-	expression tag	UNP P0ABE7
R	-110	PHE	-	expression tag	UNP P0ABE7
R	-109	GLN	-	expression tag	UNP P0ABE7
R	-108	GLY	-	expression tag	UNP P0ABE7
R	-107	GLY	-	expression tag	UNP P0ABE7
R	-106	THR	-	expression tag	UNP P0ABE7
R	-99	TRP	MET	conflict	UNP P0ABE7
R	-4	ILE	HIS	conflict	UNP P0ABE7
R	0	LEU	-	linker	UNP P0ABE7
R	1	MET	-	linker	UNP P0ABE7
R	2	CYS	-	linker	UNP P0ABE7
R	113	GLN	GLU	conflict	UNP P08100
R	257	TYR	MET	conflict	UNP P08100
R	282	CYS	ASN	conflict	UNP P08100

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	354	Total	C	N	O	S	0	0
			2834	1790	481	544	19		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	ALA	GLY	conflict	UNP P63096
A	326	SER	ALA	conflict	UNP P63096

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	340	Total	C	N	O	S	0	0
			2616	1612	470	513	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P54311
B	-3	GLY	-	expression tag	UNP P54311
B	-2	SER	-	expression tag	UNP P54311
B	-1	LEU	-	expression tag	UNP P54311
B	0	LEU	-	expression tag	UNP P54311

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLN	-	expression tag	UNP P54311

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	58	Total	C	N	O	S	0	0
			444	277	79	85	3		

- Molecule 5 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	211	Total	C	N	O	S	0	0
			1602	997	270	329	6		

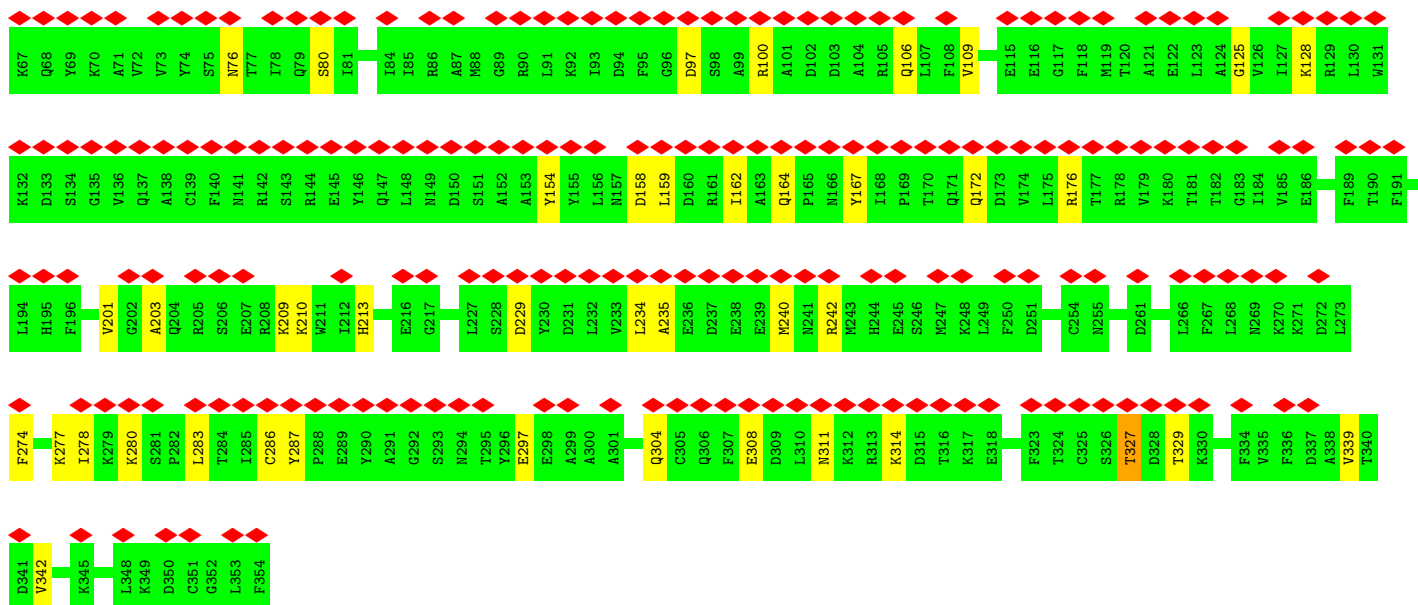
- Molecule 6 is a protein called Fab Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	230	Total	C	N	O	S	0	0
			1743	1113	284	338	8		

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

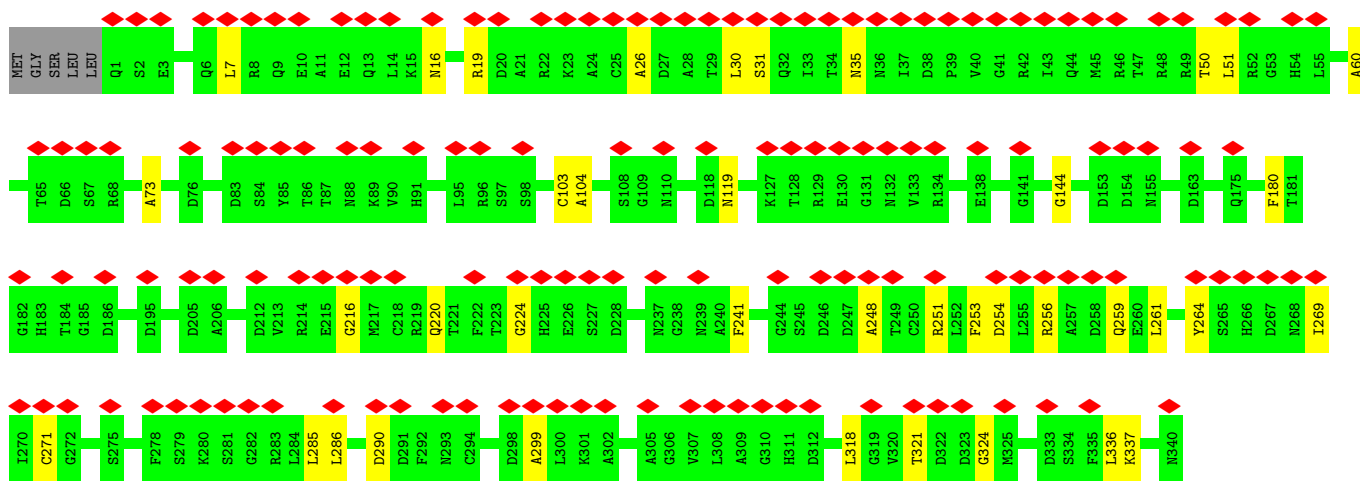


Mol	Chain	Residues	Atoms				AltConf	Trace
7	C	2	Total	C	N	O	0	0
			28	16	2	10		



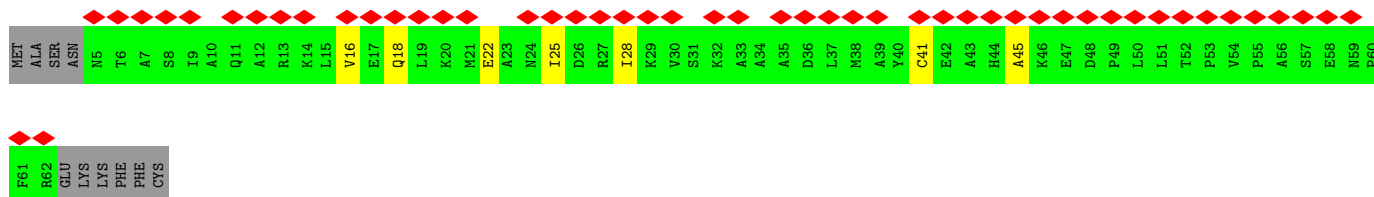
• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B: 44% 87% 11%

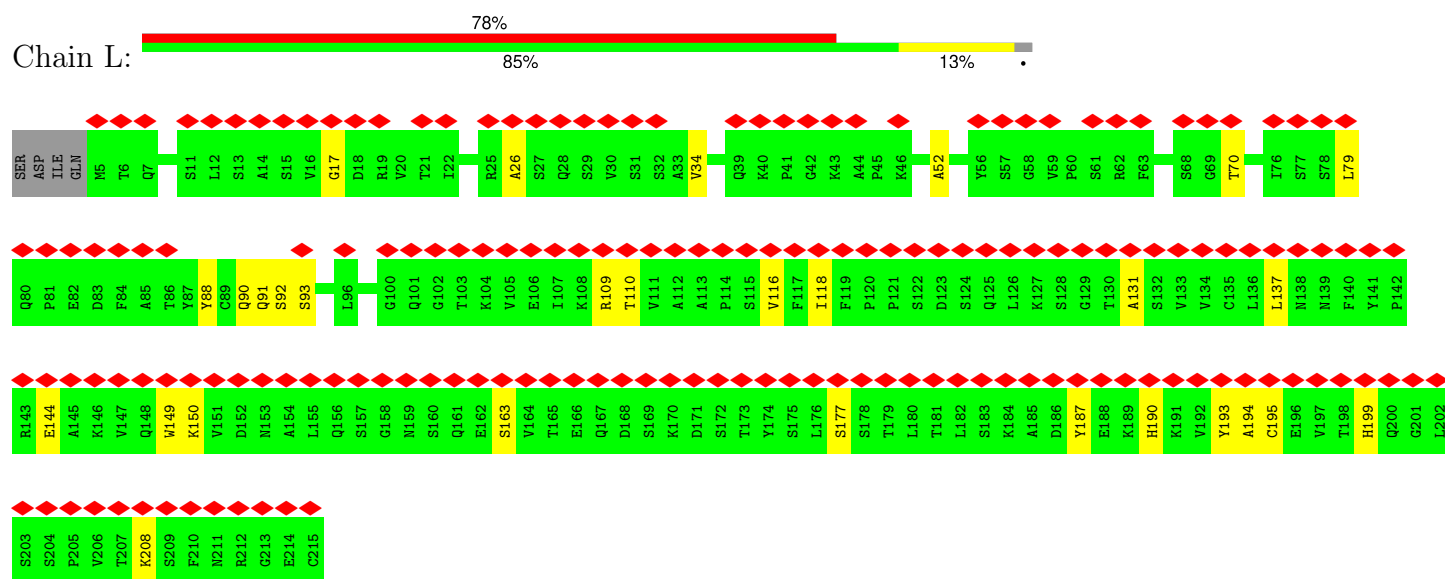


• Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

Chain G: 74% 75% 10% 15%



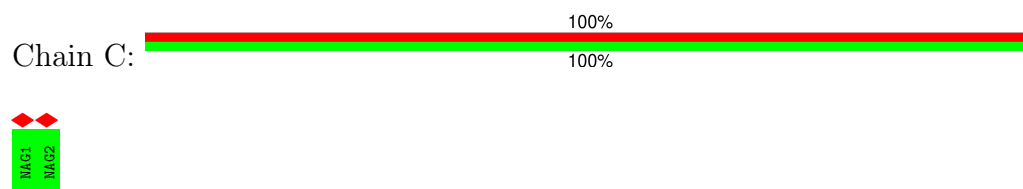
• Molecule 5: Fab light chain



• Molecule 6: Fab Heavy chain



• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	227386	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.92	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	0.207	Depositor
Minimum map value	-0.128	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.063	Depositor
Map size (\AA)	278.528, 278.528, 278.528	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.088, 1.088, 1.088	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: NAG

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	R	0.29	0/2649	0.67	1/3611 (0.0%)
2	A	0.23	0/2881	0.63	3/3874 (0.1%)
3	B	0.19	0/2663	0.51	0/3609
4	G	0.19	0/450	0.51	0/608
5	L	0.17	0/1634	0.50	0/2215
6	H	0.16	0/1794	0.47	0/2449
All	All	0.22	0/12071	0.57	4/16366 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	297	GLU	N-CA-C	5.84	118.12	111.11
1	R	43	TYR	CA-CB-CG	5.47	123.74	113.90
2	A	327	THR	CA-C-N	5.04	127.74	120.38
2	A	327	THR	C-N-CA	5.04	127.74	120.38

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	R	2567	0	2553	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2834	0	2813	25	0
3	B	2616	0	2521	22	0
4	G	444	0	454	6	0
5	L	1602	0	1565	16	0
6	H	1743	0	1684	7	0
7	C	28	0	25	0	0
All	All	11834	0	11615	94	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 94 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)
1:R:115:PHE:O	1:R:119:LEU:HB2	1.91	0.70
1:R:87:VAL:O	1:R:91:PHE:HB2	1.93	0.68
5:L:90:GLN:HE22	5:L:92:SER:HB2	1.60	0.66
2:A:209:LYS:HG2	2:A:210:LYS:HG3	1.79	0.64
1:R:125:LEU:HD11	1:R:215:PRO:HG3	1.80	0.63

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	R	321/463 (69%)	319 (99%)	2 (1%)	0	100	100
2	A	352/354 (99%)	344 (98%)	8 (2%)	0	100	100
3	B	338/345 (98%)	335 (99%)	3 (1%)	0	100	100
4	G	56/68 (82%)	56 (100%)	0	0	100	100
5	L	209/215 (97%)	205 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	H	228/239 (95%)	226 (99%)	2 (1%)	0	100	100
All	All	1504/1684 (89%)	1485 (99%)	19 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	R	275/391 (70%)	275 (100%)	0	100	100
2	A	306/306 (100%)	305 (100%)	1 (0%)	91	91
3	B	283/287 (99%)	283 (100%)	0	100	100
4	G	47/56 (84%)	47 (100%)	0	100	100
5	L	186/190 (98%)	186 (100%)	0	100	100
6	H	193/202 (96%)	193 (100%)	0	100	100
All	All	1290/1432 (90%)	1289 (100%)	1 (0%)	92	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	283	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
5	L	200	GLN
6	H	87	ASN
6	H	85	GLN
3	B	220	GLN
5	L	138	ASN

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 ⓘ

2 monosaccharides 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	$\# Z > 2$
7	NAG	C	1	7,1	14,14,15	0.32	0	17,19,21	0.54	0
7	NAG	C	2	7	14,14,15	0.29	0	17,19,21	0.54	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
7	NAG	C	1	7,1	-	4/6/23/26	0/1/1/1
7	NAG	C	2	7	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	1	NAG	O5-C5-C6-O6
7	C	1	NAG	C4-C5-C6-O6

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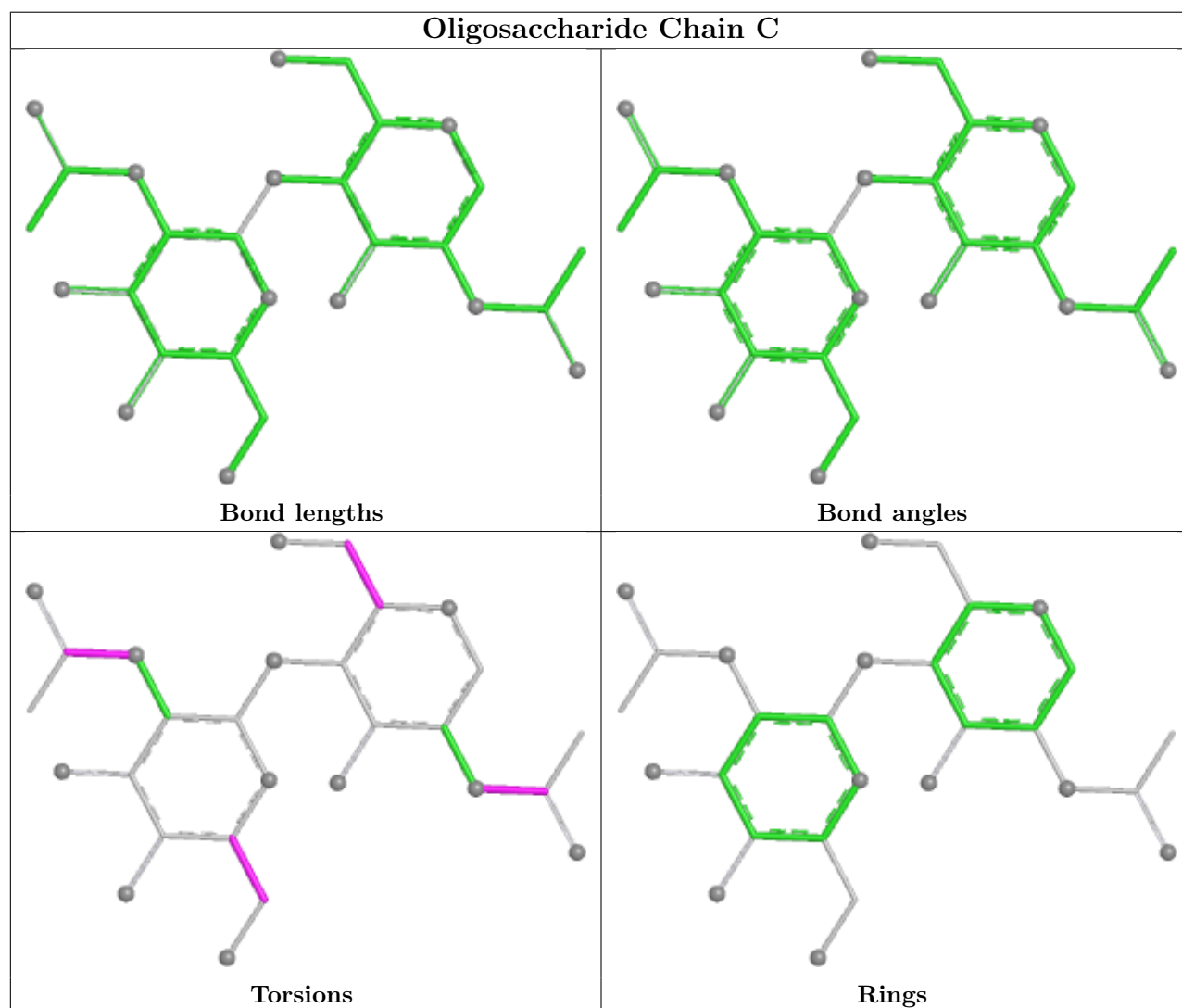
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Mol	Chain	Res	Type	Atoms
7	C	1	NAG	C8-C7-N2-C2
7	C	1	NAG	O7-C7-N2-C2
7	C	2	NAG	C8-C7-N2-C2

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 oligosaccharide.



5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

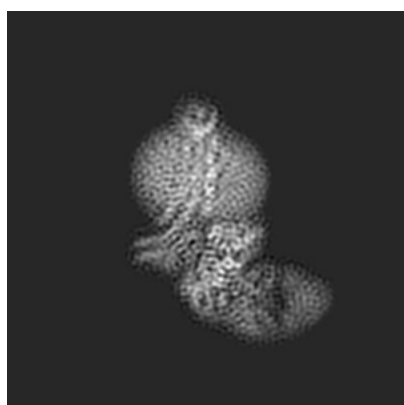
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7517. These allow visual inspection of the internal detail of the map and identification of artifacts.

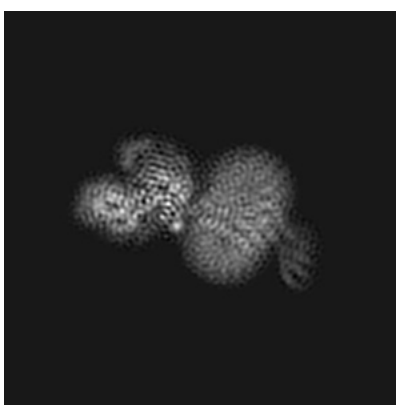
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

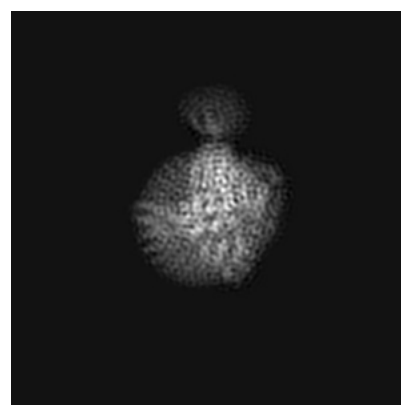
6.1.1 Primary map



X



Y

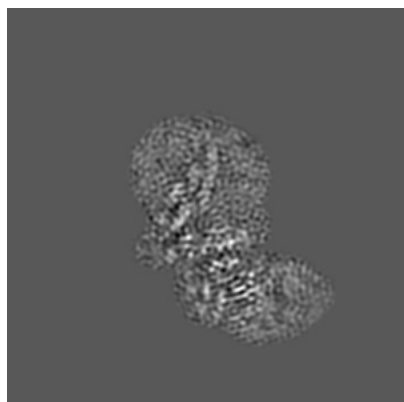


Z

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

6.2 Central slices [i](#)

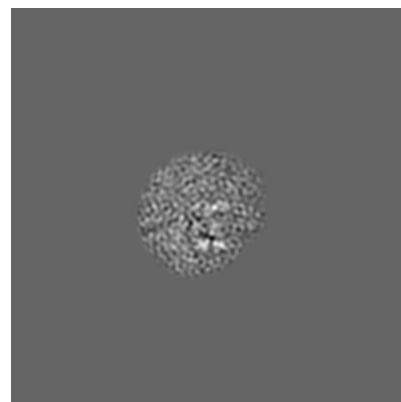
6.2.1 Primary map



X Index: 128



Y Index: 128

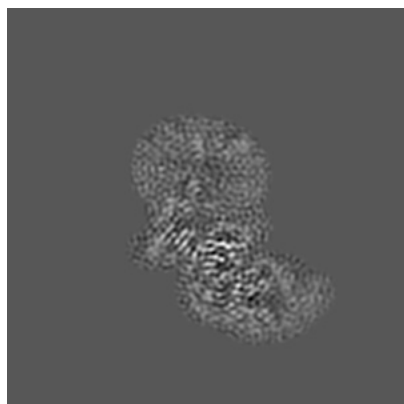


Z Index: 128

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

6.3 Largest variance slices [i](#)

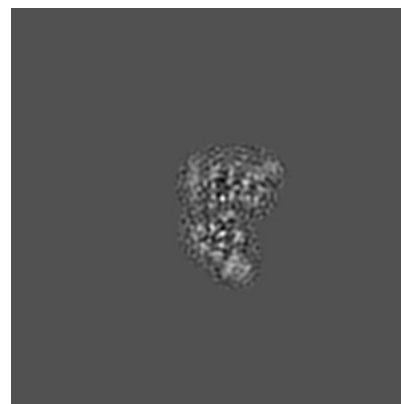
6.3.1 Primary map



X Index: 132



Y Index: 130

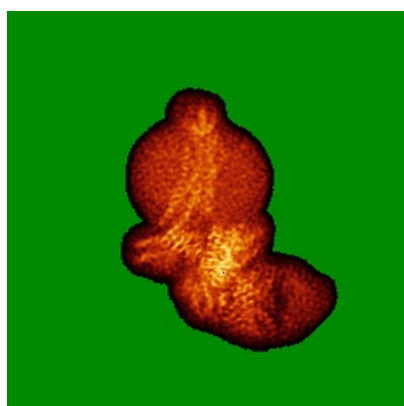


Z Index: 108

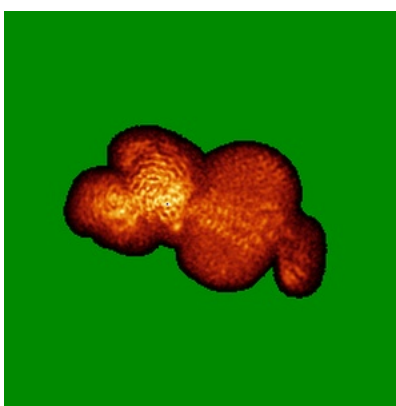
The images above show the largest variance slices of the map in three orthogonal directions.

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

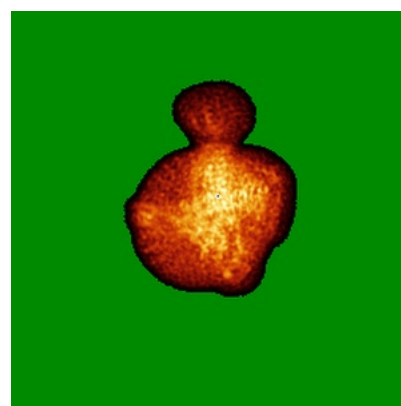
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.063. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

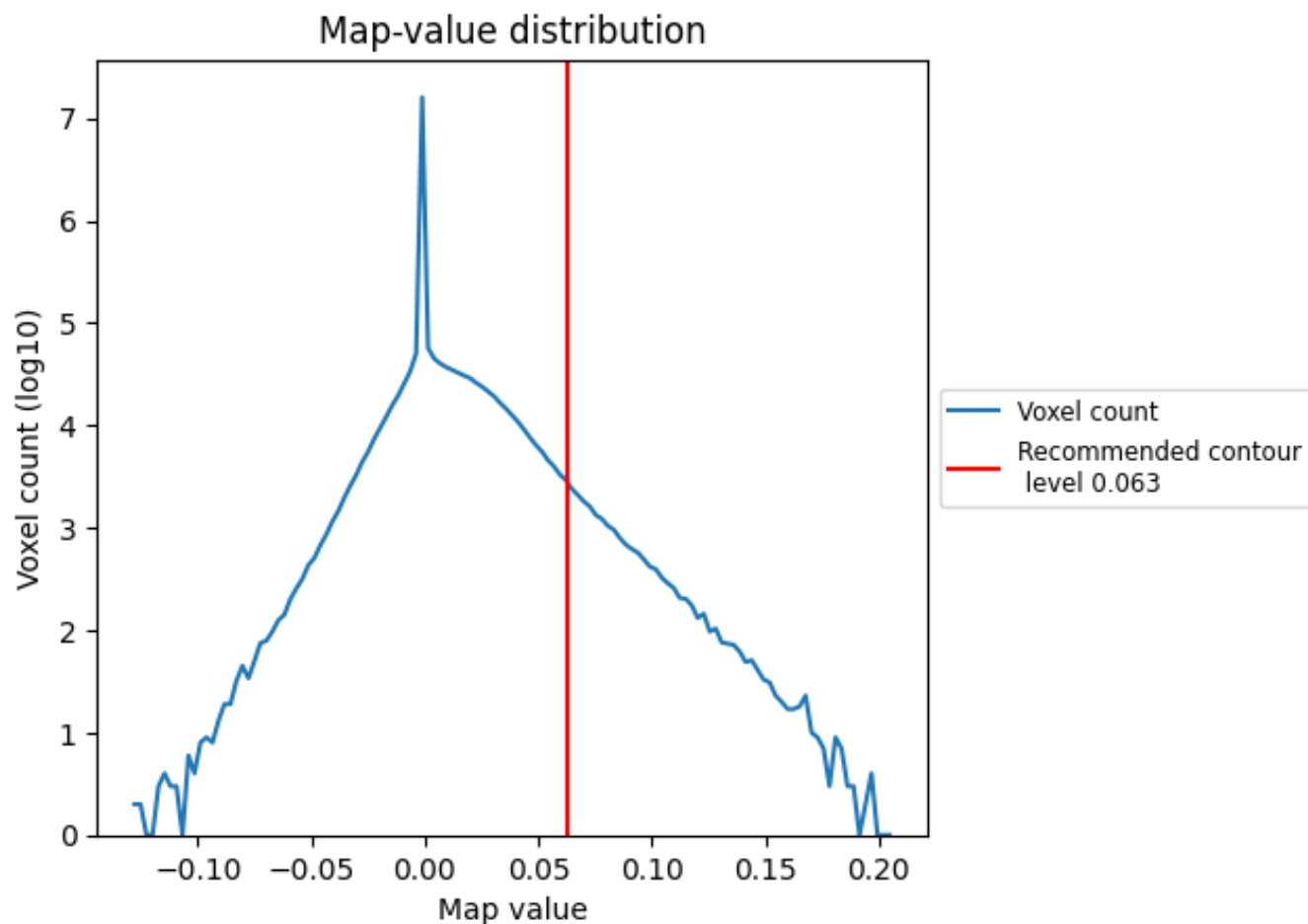
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

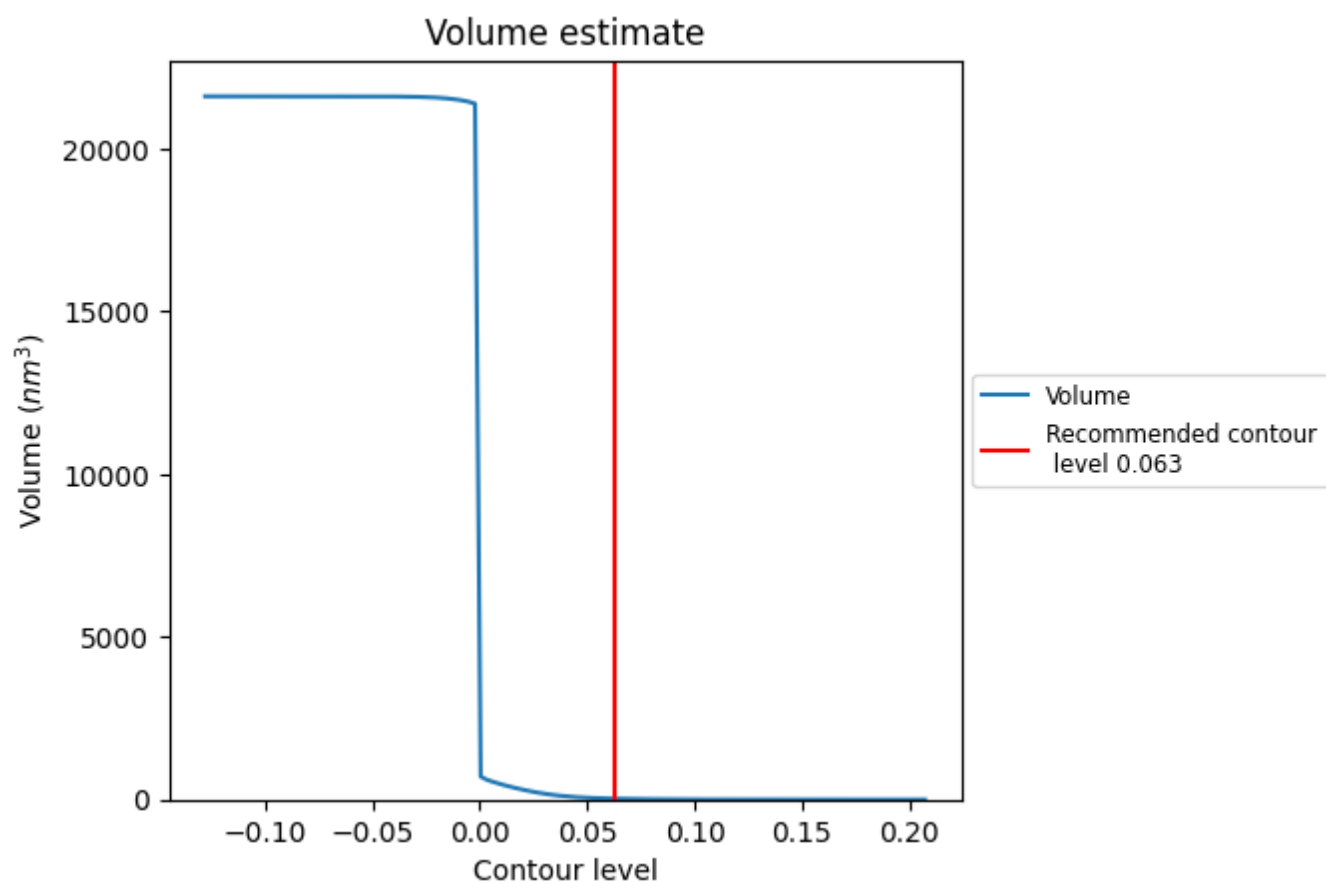
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

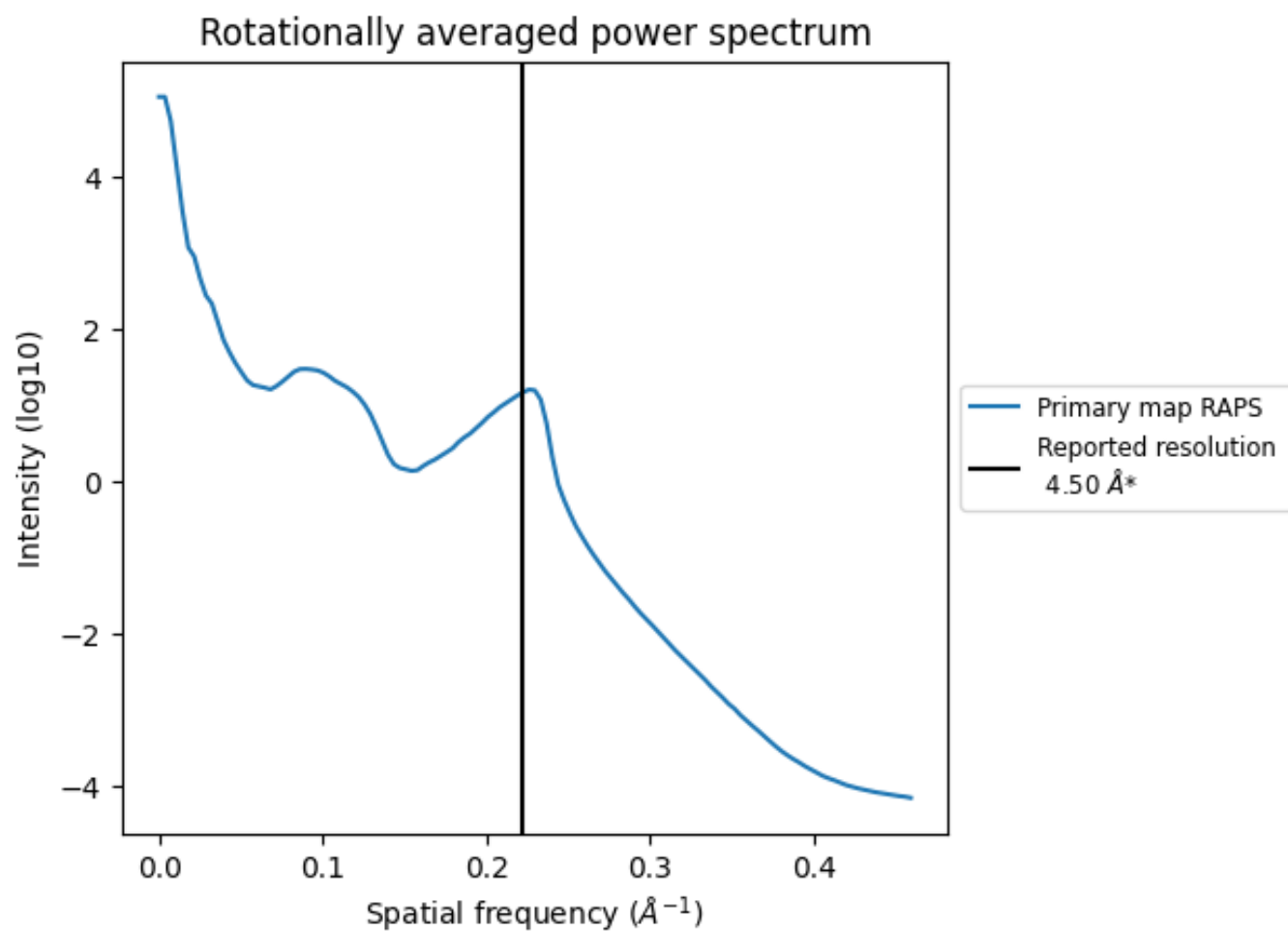
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 27 nm³; this corresponds to an approximate mass of 24 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 0.222 Å⁻¹

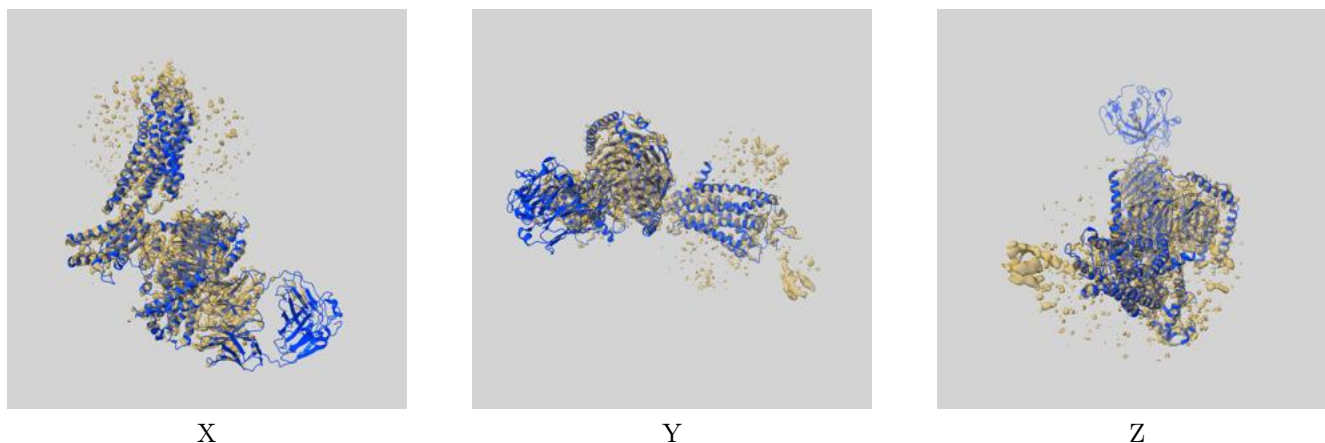
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7517 and PDB model 6CMO. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



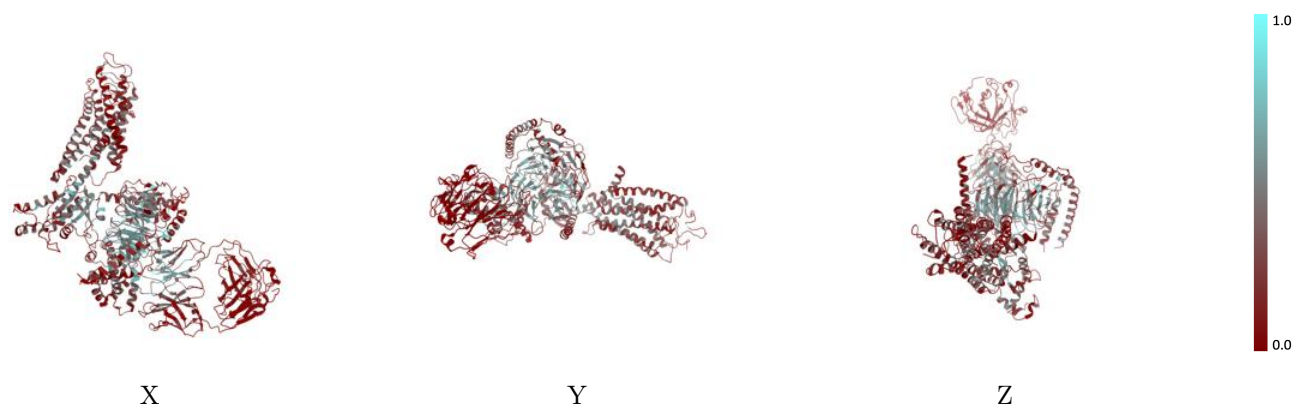
The images above show the 3D surface view of the map at the recommended contour level 0.063 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



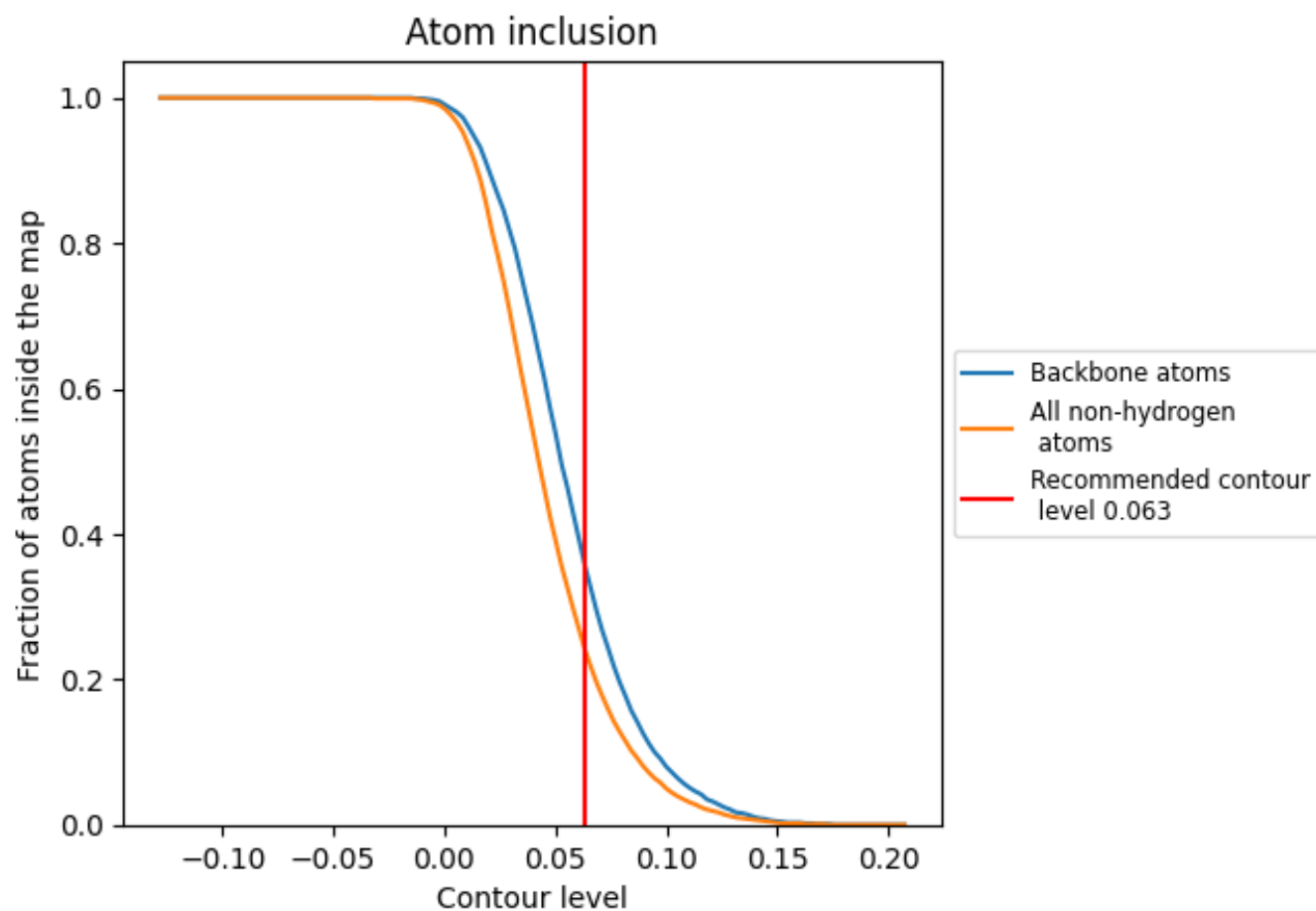
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.063).

9.4 Atom inclusion [i](#)



At the recommended contour level, 36% of all backbone atoms, 24% 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 (0.063) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.2450</div>	<div><div></div>0.3150</div>
A	<div><div></div>0.2500</div>	<div><div></div>0.3040</div>
B	<div><div></div>0.4230</div>	<div><div></div>0.4030</div>
C	<div><div></div>0.0710</div>	<div><div></div>0.3520</div>
G	<div><div></div>0.1780</div>	<div><div></div>0.2740</div>
H	<div><div></div>0.1190</div>	<div><div></div>0.2770</div>
L	<div><div></div>0.1780</div>	<div><div></div>0.3050</div>
R	<div><div></div>0.1990</div>	<div><div></div>0.2780</div>

1.0

0.0

<0.0