wwPDB EM Validation Summary Report (i)

May 16, 2024 – 01:07 PM JST

PDB ID	:	8JPN
EMDB ID	:	EMD-36484
Title	:	Cryo-EM structure of succinate receptor bound to cis-epoxysuccinic acid coupling to Gi
Authors	:	Wang, T.X.; Tang, W.Q.; Li, F.H.; Wang, J.Y.
Deposited on	:	2023-06-12
Resolution	:	2.90 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:

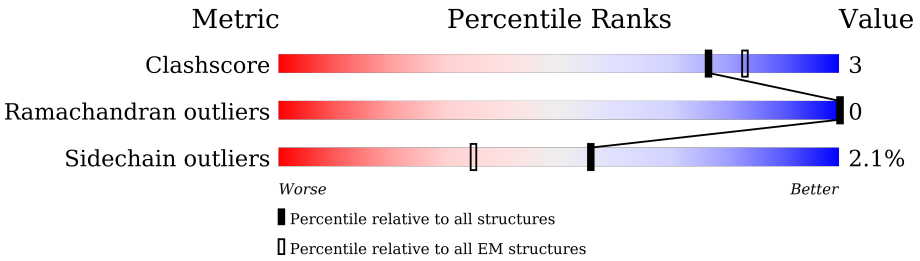
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.90 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	63% • 36%
2	B	377	• 84% 7% 9%
3	C	71	8% 80% • 18%
4	R	658	38% 7% 55%
5	S	286	76% 5% 18%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8557 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	227	1713	1098	288	316	11	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	342	2528	1563	445	499	21	0	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	MET	-	initiating methionine	UNP P62873
B	-9	HIS	-	expression tag	UNP P62873
B	-8	HIS	-	expression tag	UNP P62873
B	-7	HIS	-	expression tag	UNP P62873
B	-6	HIS	-	expression tag	UNP P62873
B	-5	HIS	-	expression tag	UNP P62873
B	-4	HIS	-	expression tag	UNP P62873
B	-3	GLY	-	expression tag	UNP P62873
B	-2	SER	-	expression tag	UNP P62873
B	-1	LEU	-	expression tag	UNP P62873
B	0	LEU	-	expression tag	UNP P62873
B	1	GLN	-	expression tag	UNP P62873
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
			Total	C	N	O	S		
3	C	58	397	250	69	76	2	0	0

- Molecule 4 is a protein called Soluble cytochrome b562,Succinate receptor 1,Oplophorus-luciferin 2-monooxygenase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	R	296	2187	1454	356	369	8	0	0

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-162	MET	-	initiating methionine	UNP P0ABE7
R	-161	LYS	-	expression tag	UNP P0ABE7
R	-160	THR	-	expression tag	UNP P0ABE7
R	-159	ILE	-	expression tag	UNP P0ABE7
R	-158	ILE	-	expression tag	UNP P0ABE7
R	-157	ALA	-	expression tag	UNP P0ABE7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	-156	LEU	-	expression tag	UNP P0ABE7
R	-155	SER	-	expression tag	UNP P0ABE7
R	-154	TYR	-	expression tag	UNP P0ABE7
R	-153	ILE	-	expression tag	UNP P0ABE7
R	-152	PHE	-	expression tag	UNP P0ABE7
R	-151	CYS	-	expression tag	UNP P0ABE7
R	-150	LEU	-	expression tag	UNP P0ABE7
R	-149	VAL	-	expression tag	UNP P0ABE7
R	-148	PHE	-	expression tag	UNP P0ABE7
R	-147	ALA	-	expression tag	UNP P0ABE7
R	-146	ASP	-	expression tag	UNP P0ABE7
R	-145	TYR	-	expression tag	UNP P0ABE7
R	-144	LYS	-	expression tag	UNP P0ABE7
R	-143	ASP	-	expression tag	UNP P0ABE7
R	-142	ASP	-	expression tag	UNP P0ABE7
R	-141	ASP	-	expression tag	UNP P0ABE7
R	-140	ASP	-	expression tag	UNP P0ABE7
R	-139	ALA	-	expression tag	UNP P0ABE7
R	-138	GLY	-	expression tag	UNP P0ABE7
R	-137	ARG	-	expression tag	UNP P0ABE7
R	-136	ALA	-	expression tag	UNP P0ABE7
R	-135	HIS	-	expression tag	UNP P0ABE7
R	-134	HIS	-	expression tag	UNP P0ABE7
R	-133	HIS	-	expression tag	UNP P0ABE7
R	-132	HIS	-	expression tag	UNP P0ABE7
R	-131	HIS	-	expression tag	UNP P0ABE7
R	-130	HIS	-	expression tag	UNP P0ABE7
R	-129	HIS	-	expression tag	UNP P0ABE7
R	-128	HIS	-	expression tag	UNP P0ABE7
R	-127	HIS	-	expression tag	UNP P0ABE7
R	-126	HIS	-	expression tag	UNP P0ABE7
R	-125	GLU	-	expression tag	UNP P0ABE7
R	-124	ASN	-	expression tag	UNP P0ABE7
R	-123	LEU	-	expression tag	UNP P0ABE7
R	-122	TYR	-	expression tag	UNP P0ABE7
R	-121	PHE	-	expression tag	UNP P0ABE7
R	-120	GLN	-	expression tag	UNP P0ABE7
R	-119	SER	-	expression tag	UNP P0ABE7
R	-118	GLY	-	expression tag	UNP P0ABE7
R	-117	ALA	-	expression tag	UNP P0ABE7
R	-116	PRO	-	expression tag	UNP P0ABE7
R	-109	TRP	MET	conflict	UNP P0ABE7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	-14	ILE	HIS	conflict	UNP P0ABE7
R	-10	LEU	-	linker	UNP P0ABE7
R	-9	LEU	-	linker	UNP P0ABE7
R	-8	GLU	-	linker	UNP P0ABE7
R	-7	VAL	-	linker	UNP P0ABE7
R	-6	LEU	-	linker	UNP P0ABE7
R	-5	PHE	-	linker	UNP P0ABE7
R	-4	GLN	-	linker	UNP P0ABE7
R	-3	GLY	-	linker	UNP P0ABE7
R	-2	PRO	-	linker	UNP P0ABE7
R	-1	GLU	-	linker	UNP P0ABE7
R	0	PHE	-	linker	UNP P0ABE7
R	46	PHE	TYR	conflict	UNP Q9BXA5
R	49	LEU	ILE	conflict	UNP Q9BXA5
R	51	CYS	SER	conflict	UNP Q9BXA5
R	67	ILE	VAL	conflict	UNP Q9BXA5
R	175	TYR	PHE	conflict	UNP Q9BXA5
R	221	LEU	VAL	conflict	UNP Q9BXA5
R	304	GLU	ASP	conflict	UNP Q9BXA5
R	309	LYS	GLN	conflict	UNP Q9BXA5
R	321	ARG	SER	conflict	UNP Q9BXA5
R	335	ALA	-	linker	UNP Q9BXA5
R	336	ALA	-	linker	UNP Q9BXA5
R	337	ALA	-	linker	UNP Q9BXA5
R	338	VAL	-	linker	UNP Q9BXA5
R	342	GLU	ALA	conflict	UNP Q9GV45
R	349	GLU	GLN	conflict	UNP Q9GV45
R	353	ALA	GLY	conflict	UNP Q9GV45
R	356	LEU	GLN	conflict	UNP Q9GV45
R	365	VAL	LEU	conflict	UNP Q9GV45
R	369	LEU	PHE	conflict	UNP Q9GV45
R	371	ASN	ALA	conflict	UNP Q9GV45
R	373	ALA	GLY	conflict	UNP Q9GV45
R	381	ARG	LYS	conflict	UNP Q9GV45
R	382	ILE	VAL	conflict	UNP Q9GV45
R	384	ARG	LEU	conflict	UNP Q9GV45
R	389	ALA	GLY	conflict	UNP Q9GV45
R	392	ILE	ALA	conflict	UNP Q9GV45
R	405	ALA	GLY	conflict	UNP Q9GV45
R	406	ASP	PHE	conflict	UNP Q9GV45
R	409	ALA	GLY	conflict	UNP Q9GV45
R	410	GLN	LEU	conflict	UNP Q9GV45

Continued on next page...

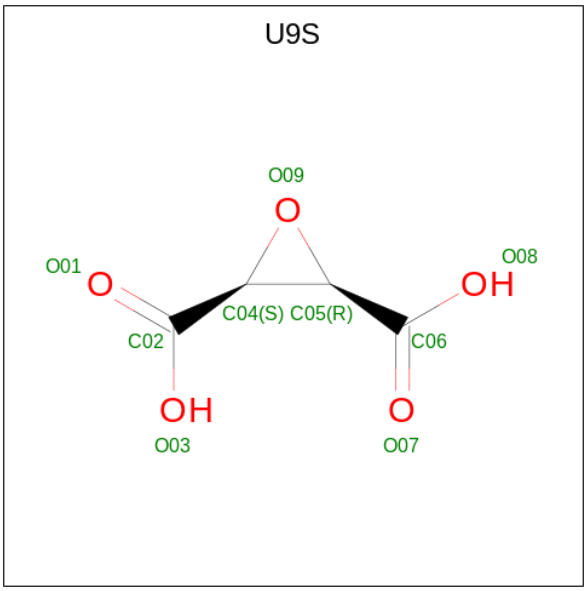
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	413	GLU	MET	conflict	UNP Q9GV45
R	414	VAL	ILE	conflict	UNP Q9GV45
R	428	VAL	ILE	conflict	UNP Q9GV45
R	431	PRO	HIS	conflict	UNP Q9GV45
R	445	LEU	ILE	conflict	UNP Q9GV45
R	446	ASN	ASP	conflict	UNP Q9GV45
R	453	GLU	PRO	conflict	UNP Q9GV45
R	462	LYS	GLN	conflict	UNP Q9GV45
R	476	ILE	TYR	conflict	UNP Q9GV45
R	482	THR	ASN	conflict	UNP Q9GV45
R	487	MET	LEU	conflict	UNP Q9GV45
R	495	SER	GLY	conflict	UNP Q9GV45

- Molecule 5 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	S	234	1723	1100	289	324	10	0	0

- Molecule 6 is (2R,3S)-oxirane-2,3-dicarboxylic acid (three-letter code: U9S) (formula: $C_4H_4O_5$) (labeled as "Ligand of Interest" by depositor).



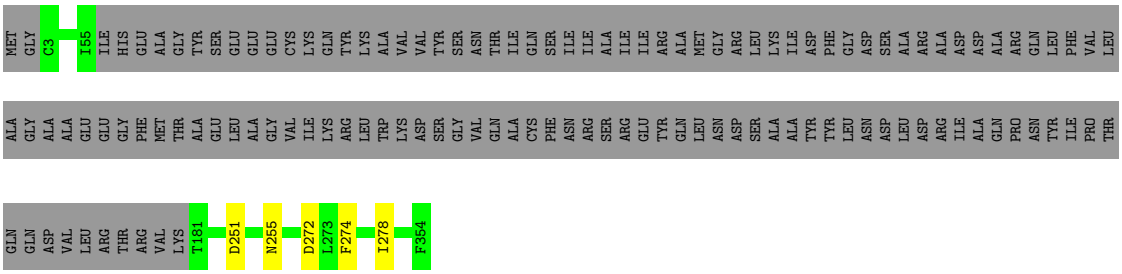
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
6	R	1	9	4	5	0

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.

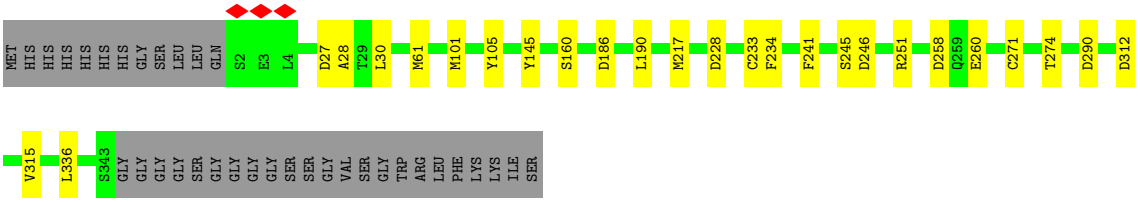
• Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1

Chain A:



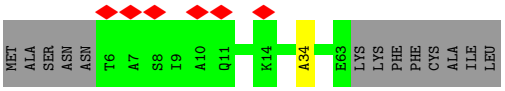
• Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B:



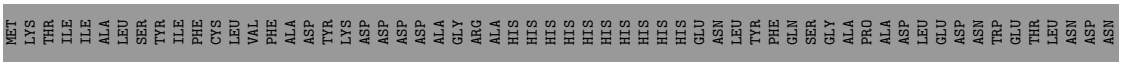
• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

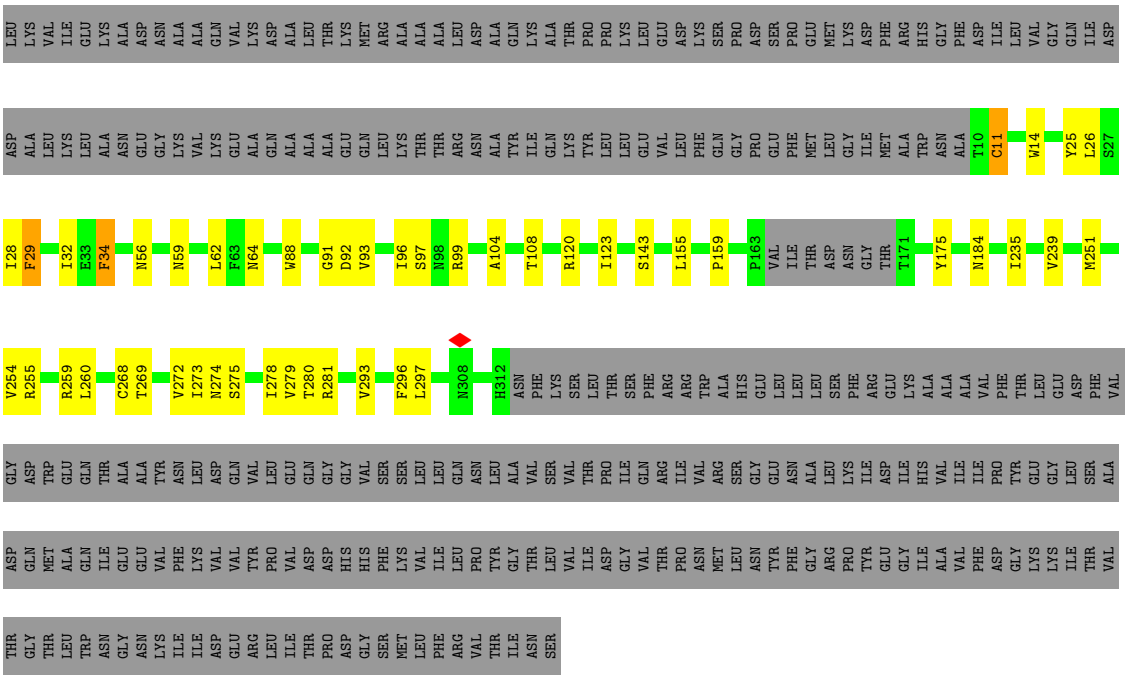
Chain C:



• Molecule 4: Soluble cytochrome b562,Succinate receptor 1,Oplophorus-luciferin 2-monooxygenase catalytic subunit

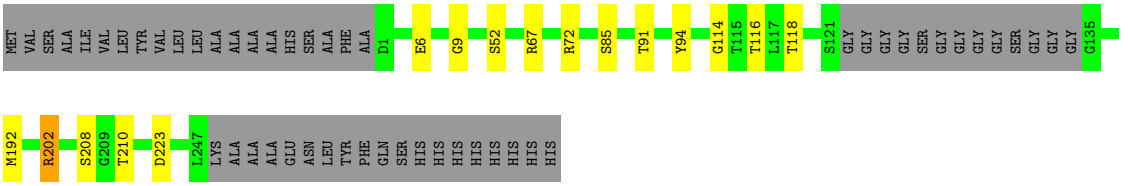
Chain R:





- Molecule 5: scFv16

Chain S:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	278158	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.487	Depositor
Minimum map value	-1.272	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	269.6, 269.6, 269.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.674, 0.674, 0.674	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: U9S

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	0/1743	0.43	0/2350
2	B	0.27	0/2575	0.53	0/3504
3	C	0.24	0/403	0.42	0/554
4	R	0.28	0/2246	0.47	0/3087
5	S	0.30	0/1767	0.54	0/2405
All	All	0.28	0/8734	0.49	0/11900

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	1713	0	1622	2	0
2	B	2528	0	2353	10	0
3	C	397	0	366	1	0
4	R	2187	0	2019	28	0
5	S	1723	0	1606	9	0
6	R	9	0	0	0	0
All	All	8557	0	7966	49	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 3.

The worst 5 of 49 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:S:94:TYR:O	5:S:114:GLY:HA2	1.88	0.73
1:A:251:ASP:OD1	1:A:255:ASN:ND2	2.33	0.61
4:R:56:ASN:OD1	4:R:59:ASN:ND2	2.34	0.60
4:R:88:TRP:NE1	4:R:91:GLY:O	2.34	0.59
5:S:52:SER:O	5:S:72:ARG:NH1	2.38	0.56

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	223/354 (63%)	220 (99%)	3 (1%)	0	100	100
2	B	340/377 (90%)	328 (96%)	12 (4%)	0	100	100
3	C	56/71 (79%)	56 (100%)	0	0	100	100
4	R	292/658 (44%)	281 (96%)	11 (4%)	0	100	100
5	S	230/286 (80%)	218 (95%)	12 (5%)	0	100	100
All	All	1141/1746 (65%)	1103 (97%)	38 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	168/305 (55%)	167 (99%)	1 (1%)	86	96
2	B	261/308 (85%)	253 (97%)	8 (3%)	40	74
3	C	35/58 (60%)	35 (100%)	0	100	100
4	R	203/576 (35%)	195 (96%)	8 (4%)	32	66
5	S	175/229 (76%)	174 (99%)	1 (1%)	86	96
All	All	842/1476 (57%)	824 (98%)	18 (2%)	56	81

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	R	175	TYR
5	S	202	ARG
4	R	281	ARG
2	B	336	LEU
4	R	159	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
4	R	59	ASN

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	U9S	R	501	-	9,9,9	1.36	0	11,13,13	1.65	3 (27%)

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	U9S	R	501	-	-	3/6/13/13	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	R	501	U9S	C05-O09-C04	2.39	64.18	61.94
6	R	501	U9S	O09-C04-C02	2.10	119.62	116.19
6	R	501	U9S	O09-C05-C04	-2.07	57.86	59.03

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	R	501	U9S	O01-C02-C04-C05
6	R	501	U9S	O01-C02-C04-O09
6	R	501	U9S	O03-C02-C04-C05

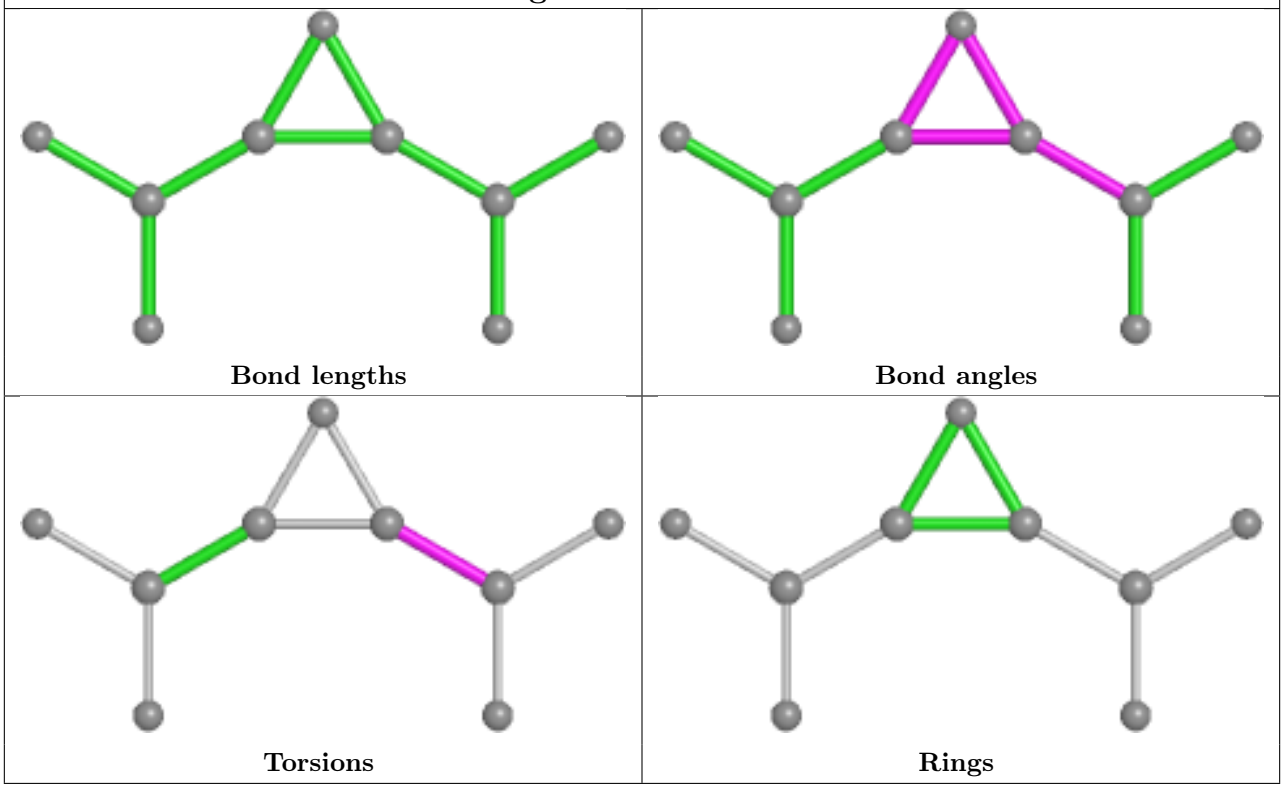
There are no ring outliers.

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 U9S 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.

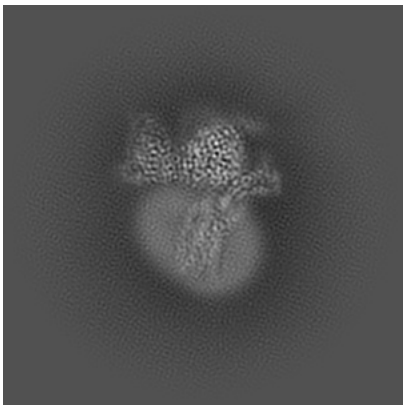
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-36484. These allow visual inspection of the internal detail of the map and identification of artifacts.

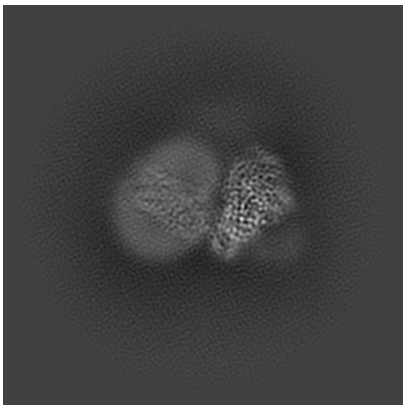
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

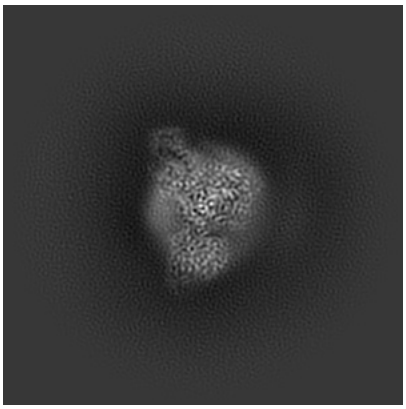
6.1.1 Primary map



X

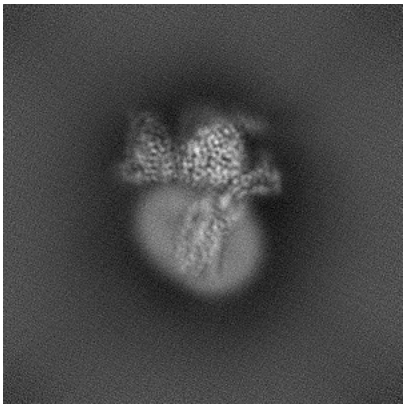


Y

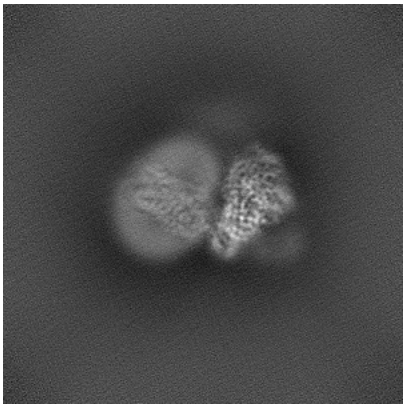


Z

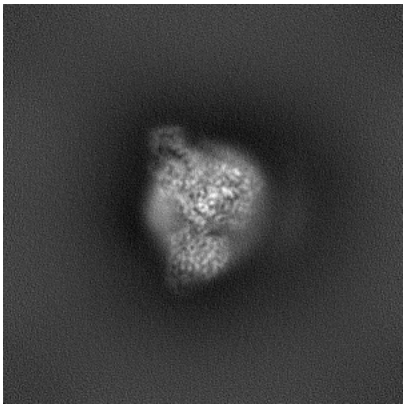
6.1.2 Raw map



X



Y

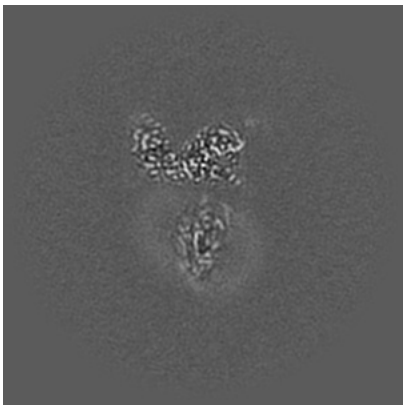


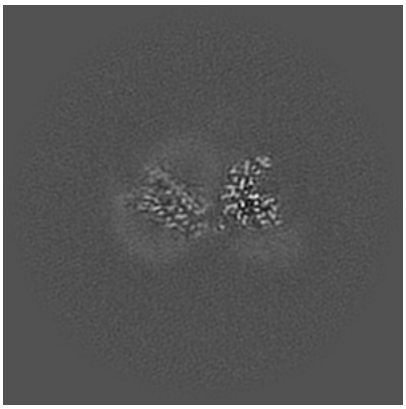
Z

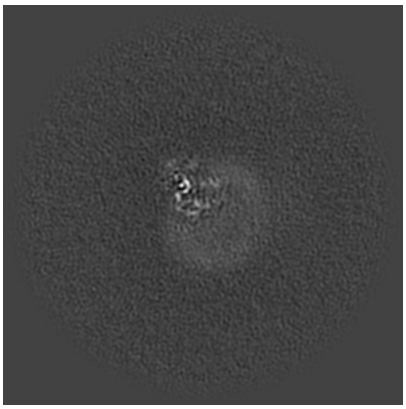
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

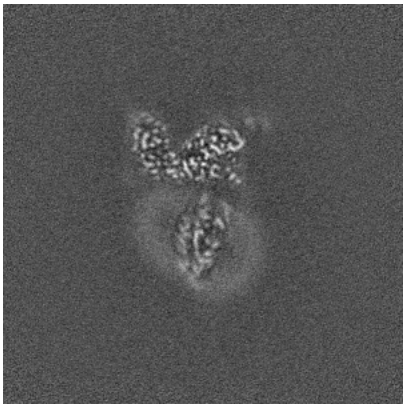
6.2.1 Primary map

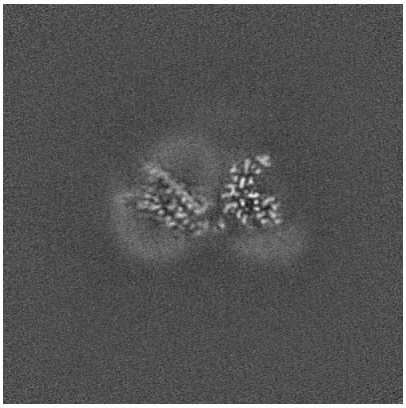

X Index: 200

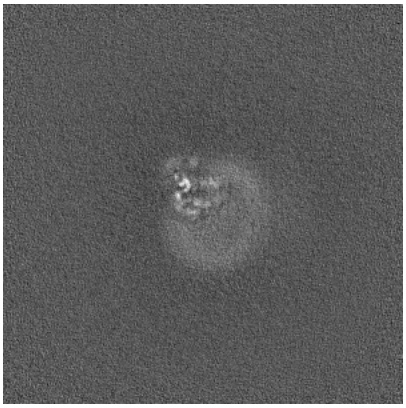

Y Index: 200


Z Index: 200

6.2.2 Raw map


X Index: 200

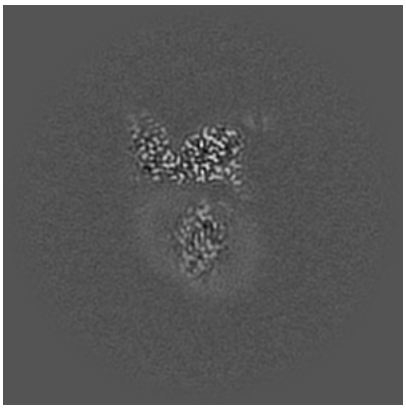

Y Index: 200


Z Index: 200

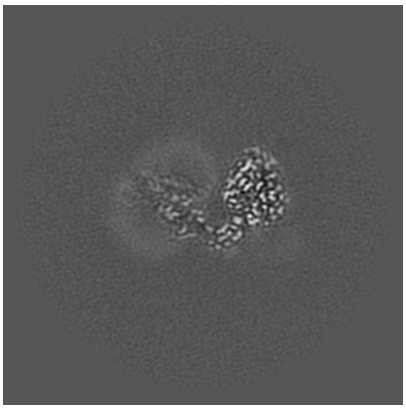
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

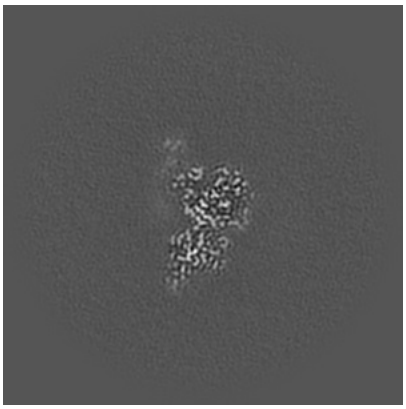
6.3.1 Primary map



X Index: 198

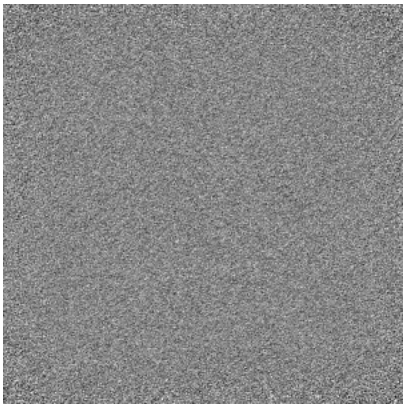


Y Index: 216

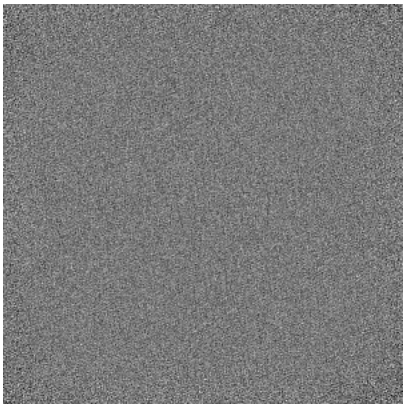


Z Index: 239

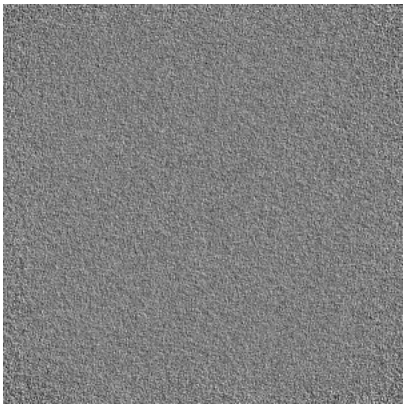
6.3.2 Raw map



X Index: 0



Y Index: 0

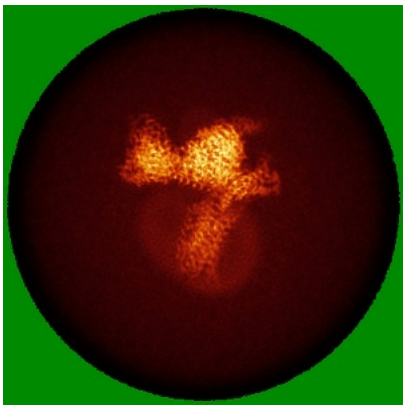


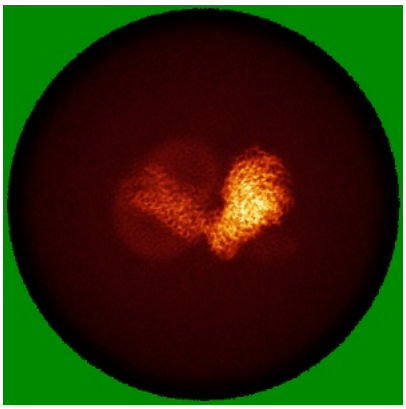
Z Index: 0

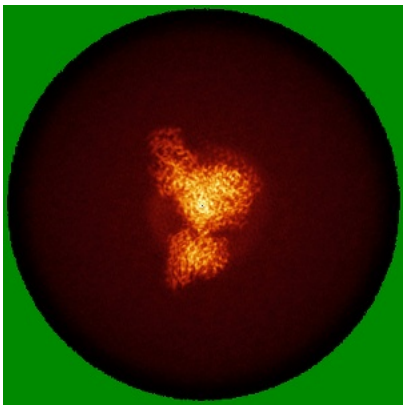
The images above show the largest variance slices of the map in three orthogonal directions.

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

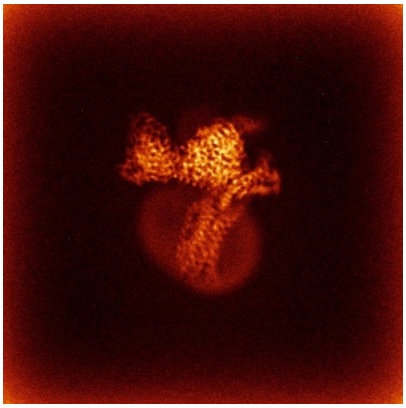
6.4.1 Primary map

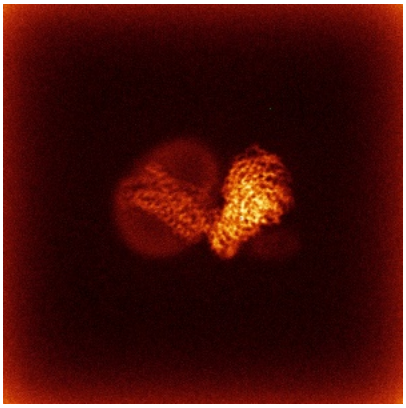

X

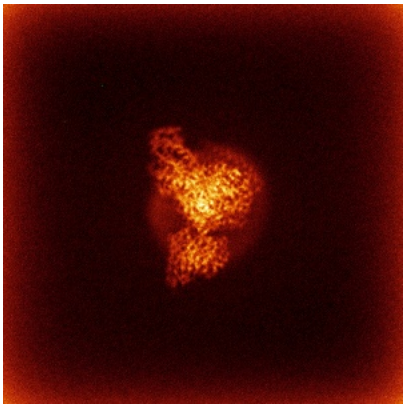

Y


Z

6.4.2 Raw map


X

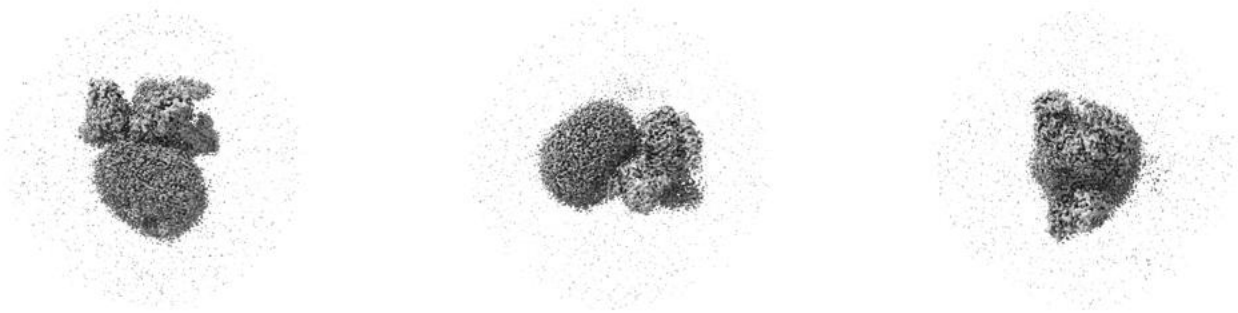

Y


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)

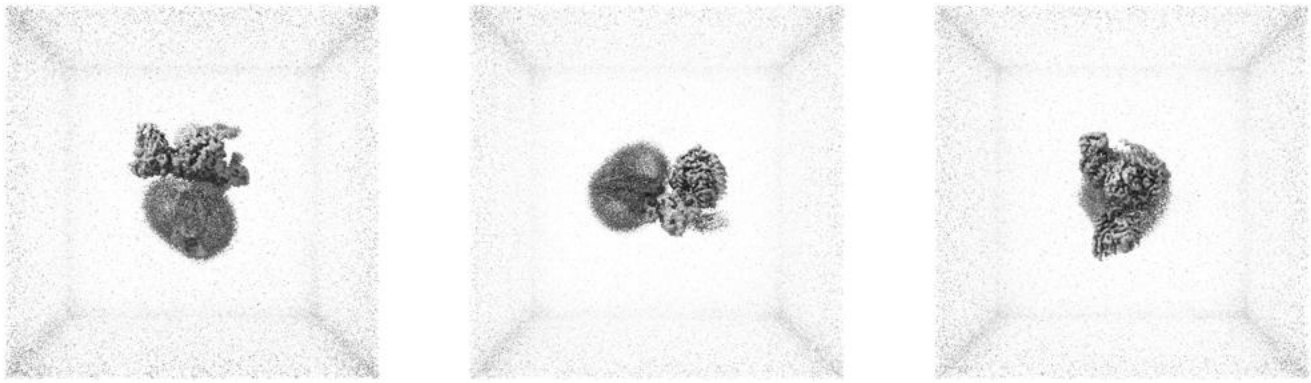
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



X Y Z

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.

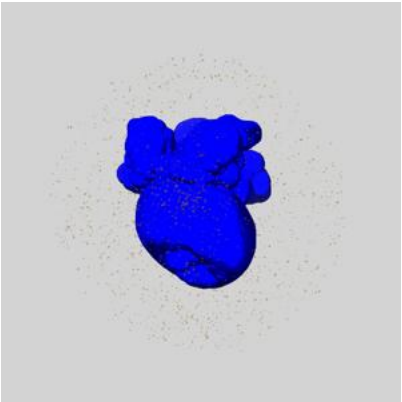
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

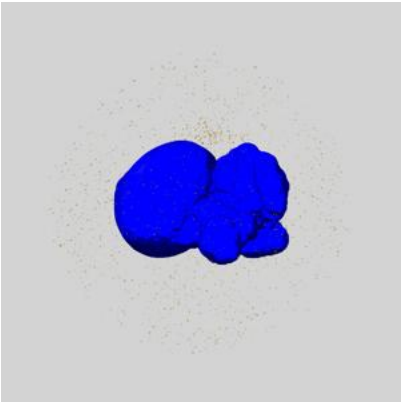
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

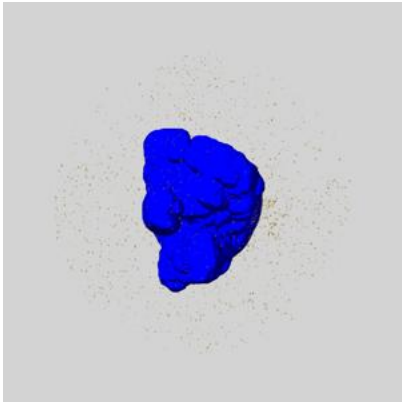
6.6.1 emd_36484_msk_1.map (i)



X



Y

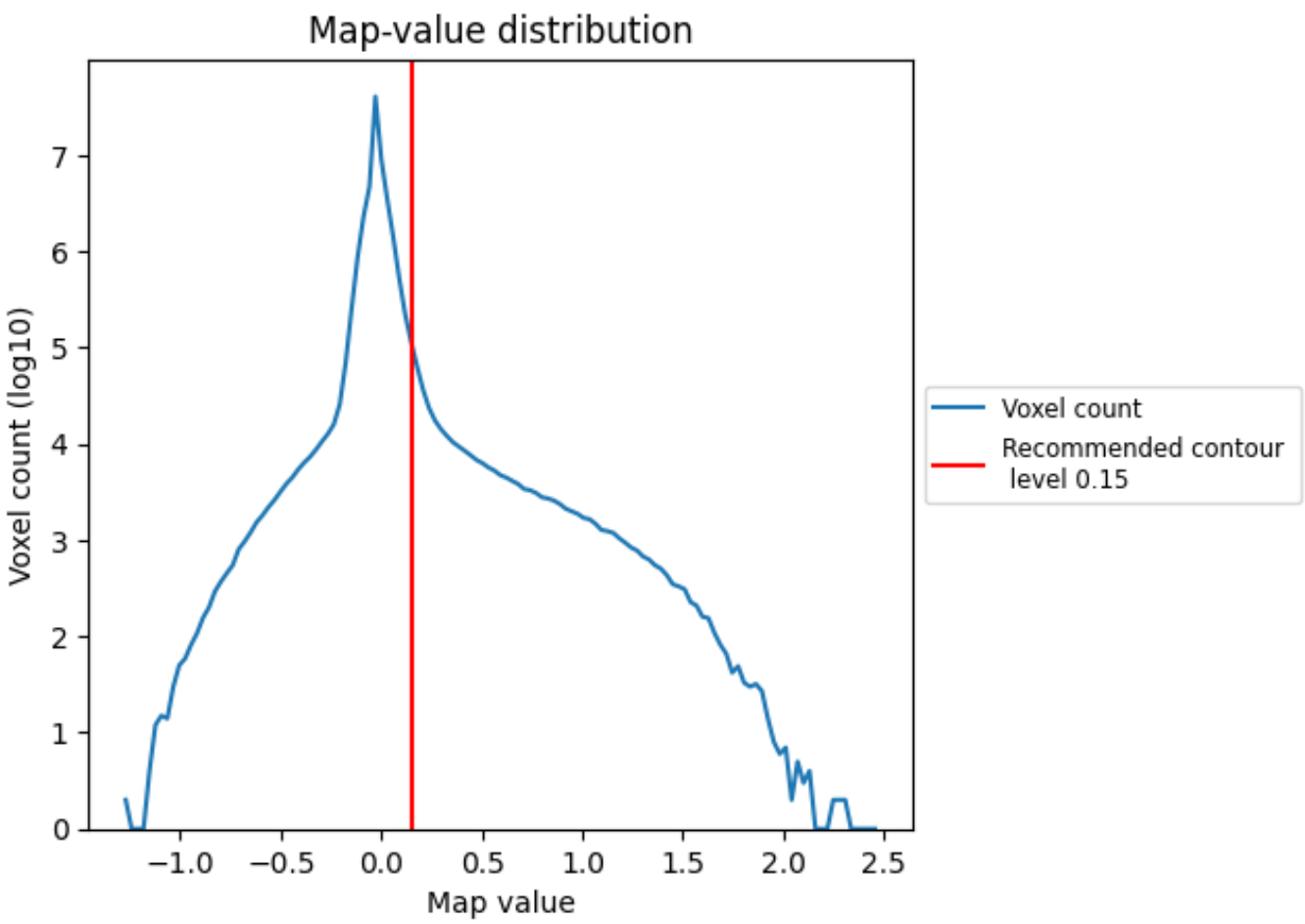


Z

7 Map analysis (i)

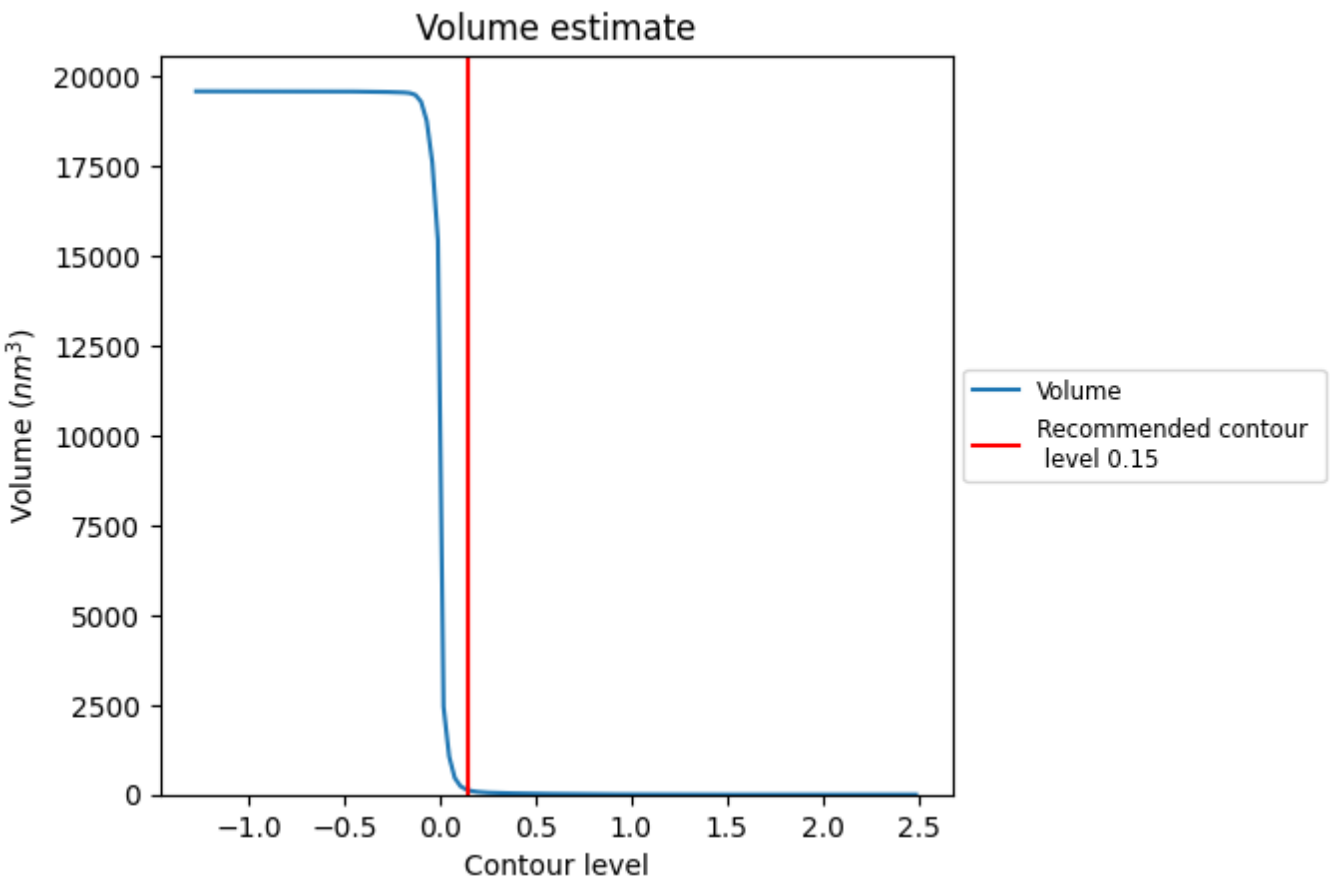
This section contains the results of statistical analysis of the map.

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.

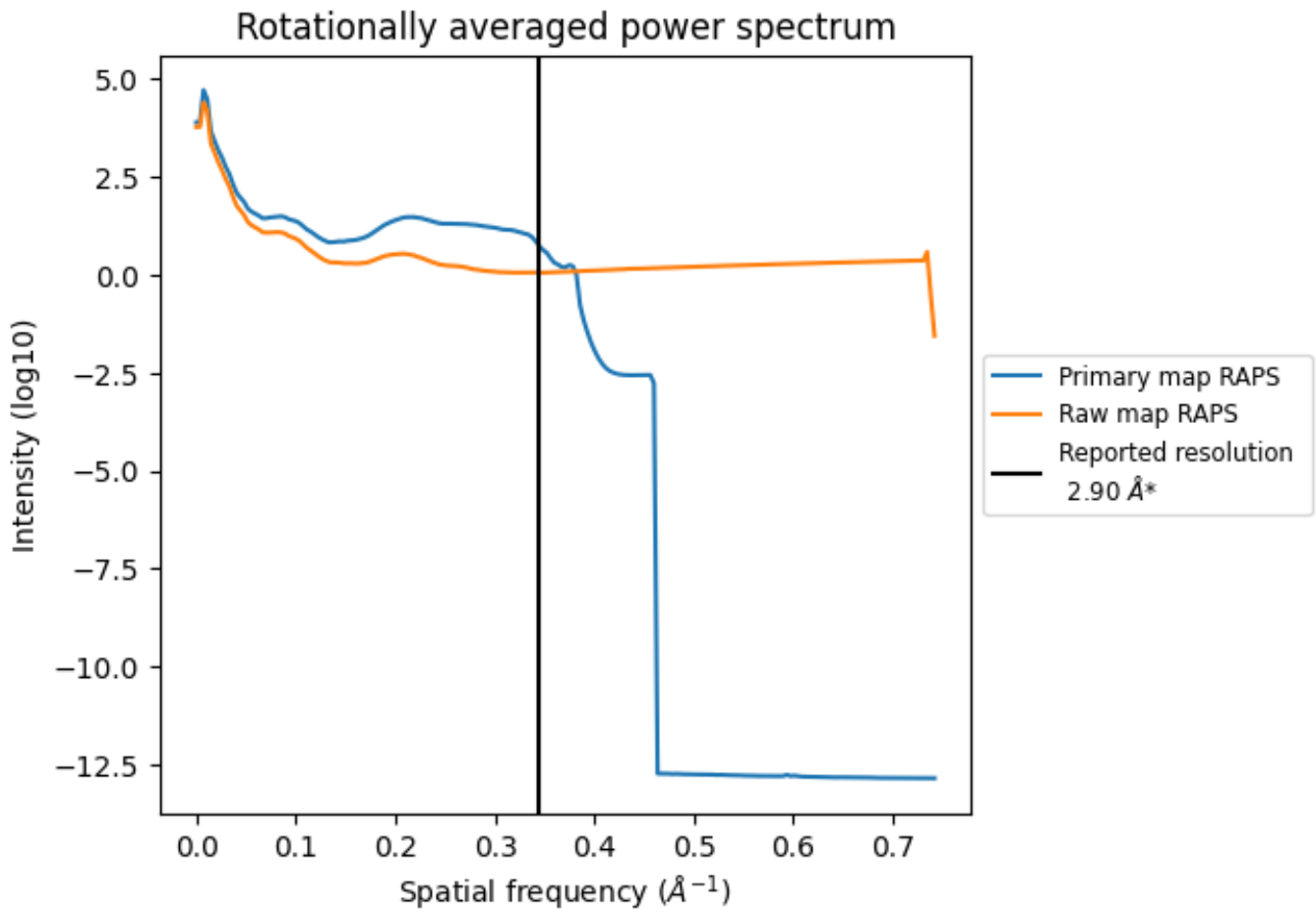
7.2 Volume estimate (i)



The volume at the recommended contour level is 125 nm^3; this corresponds to an approximate mass of 113 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)

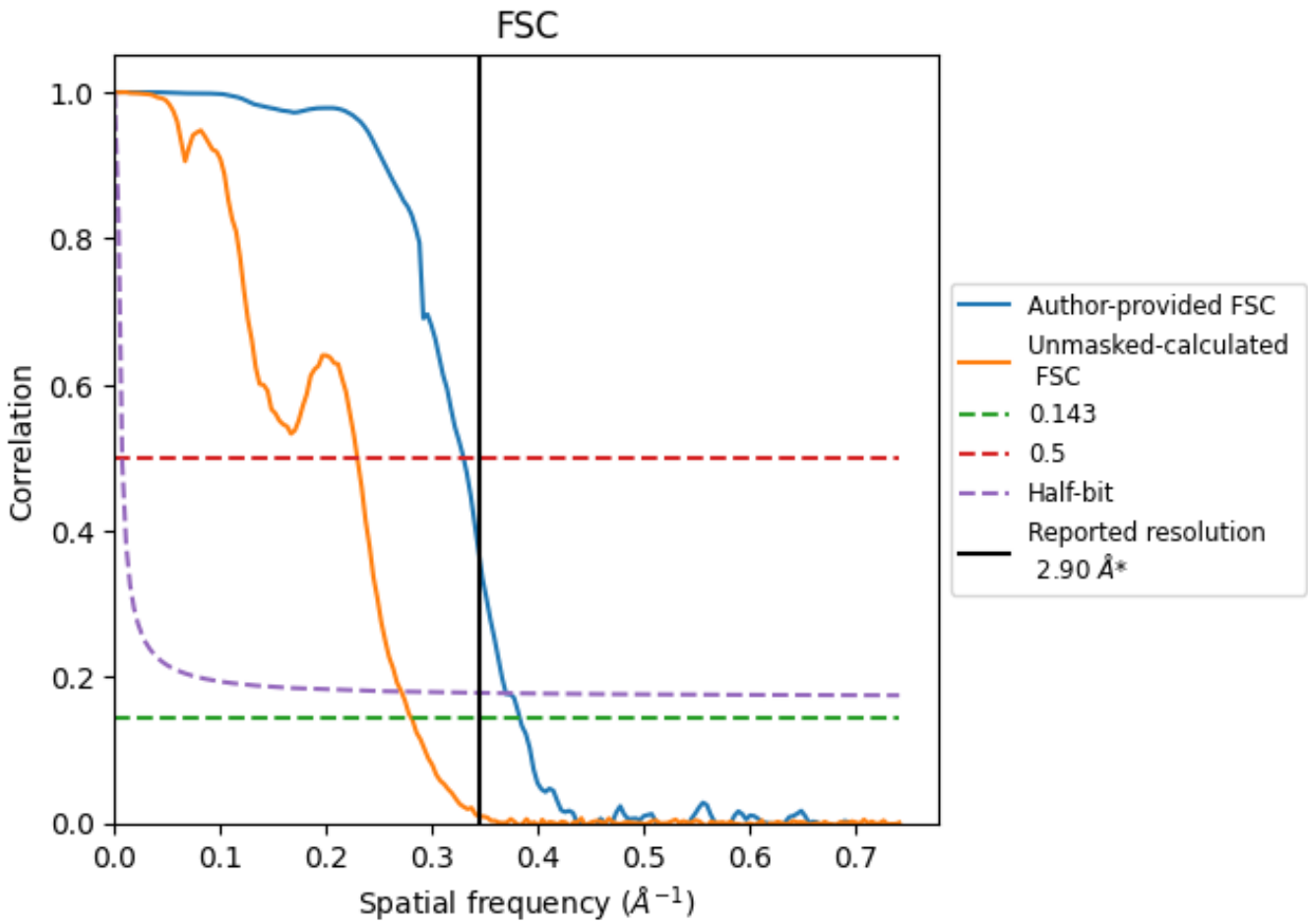


*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

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 0.345 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.61	3.03	2.70
Unmasked-calculated*	3.56	4.36	3.69

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.61 differs from the reported value 2.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.56 differs from the reported value 2.9 by more than 10 %

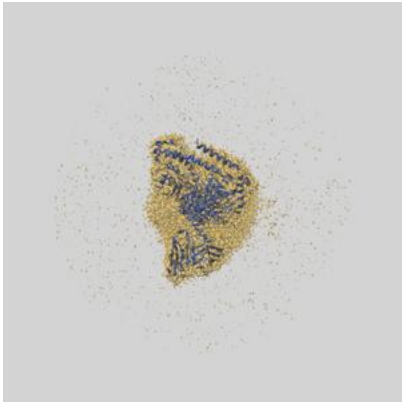
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-36484 and PDB model 8JPN. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay (i)

X

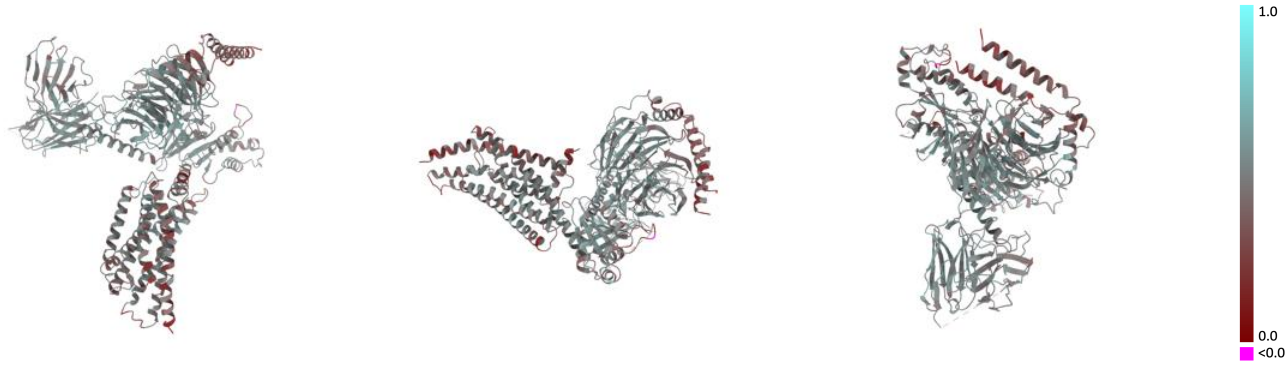
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15 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.

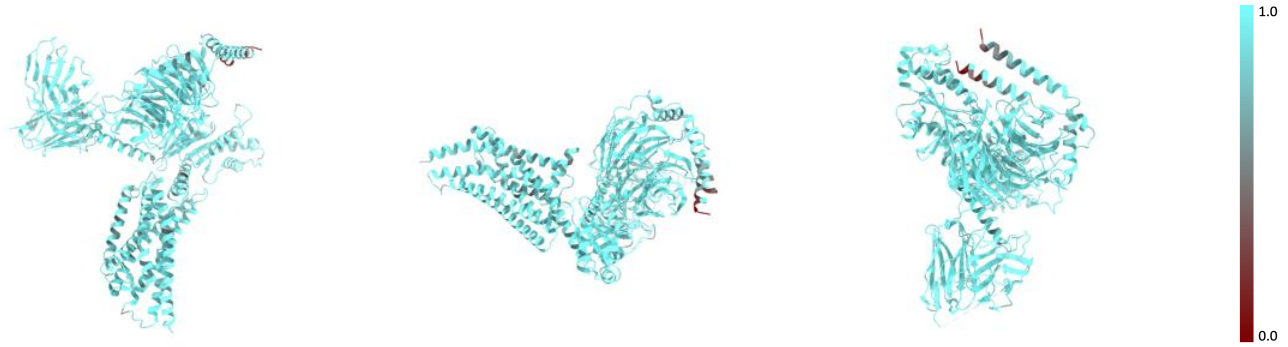
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

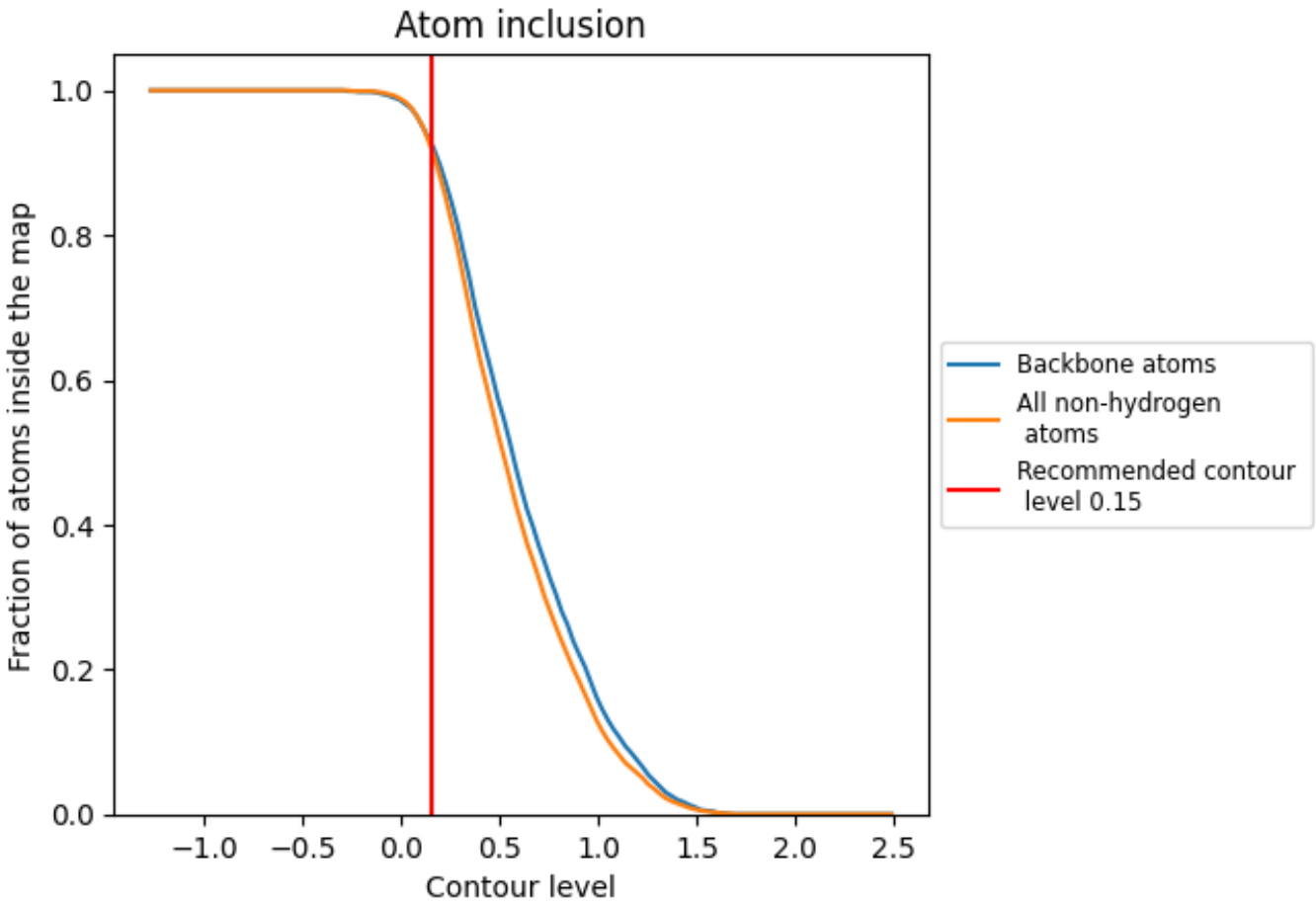
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.15).

9.4 Atom inclusion (i)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9210	0.4810
A	0.9230	0.4870
B	0.9360	0.5000
C	0.8160	0.4270
R	0.9060	0.4400
S	0.9410	0.5110