



wwPDB EM Validation Summary Report ⓘ

Nov 10, 2024 – 02:56 am GMT

PDB ID : 6SO5
EMDB ID : EMD-10266
Title : Homo sapiens WRB/CAML heterotetramer in complex with a TRC40 dimer
Authors : McDowell, M.A.; Heimes, M.; Wild, K.; Flemming, D.; Sinning, I.
Deposited on : 2019-08-29
Resolution : 4.20 Å(reported)
Based on initial model : 3SJA

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.dev113
MolProbity : 4.02b-467
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) : 2.39

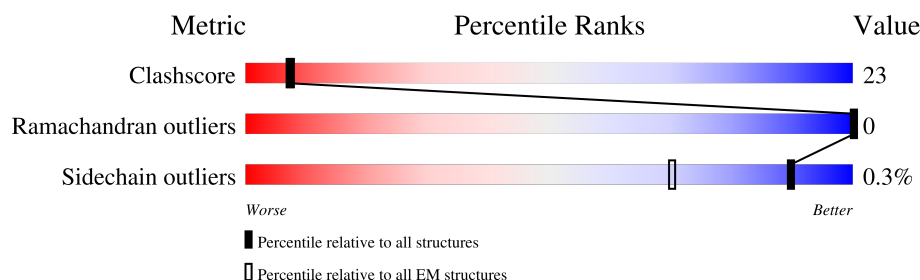
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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	A	360	<div> <div>18%</div> <div>46%</div> <div>41%</div> <div>13%</div> </div>
1	B	360	<div> <div>18%</div> <div>46%</div> <div>35%</div> <div>19%</div> </div>
2	C	184	<div> <div>33%</div> <div>39%</div> <div>39%</div> <div>22%</div> </div>
2	D	184	<div> <div>18%</div> <div>35%</div> <div>43%</div> <div>22%</div> </div>
3	E	127	<div> <div>33%</div> <div>37%</div> <div>44%</div> <div>19%</div> </div>
3	F	127	<div> <div>54%</div> <div>49%</div> <div>31%</div> <div>20%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8737 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 ATPase ASNA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	313	Total	C	N	O	S	0	0
			2464	1573	404	466	21		
1	B	292	Total	C	N	O	S	0	0
			2301	1472	376	435	18		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP O43681
A	0	ALA	-	expression tag	UNP O43681
A	349	GLY	-	expression tag	UNP O43681
A	350	SER	-	expression tag	UNP O43681
A	351	TRP	-	expression tag	UNP O43681
A	352	SER	-	expression tag	UNP O43681
A	353	HIS	-	expression tag	UNP O43681
A	354	PRO	-	expression tag	UNP O43681
A	355	GLN	-	expression tag	UNP O43681
A	356	PHE	-	expression tag	UNP O43681
A	357	GLU	-	expression tag	UNP O43681
A	358	LYS	-	expression tag	UNP O43681
B	-1	GLY	-	expression tag	UNP O43681
B	0	ALA	-	expression tag	UNP O43681
B	349	GLY	-	expression tag	UNP O43681
B	350	SER	-	expression tag	UNP O43681
B	351	TRP	-	expression tag	UNP O43681
B	352	SER	-	expression tag	UNP O43681
B	353	HIS	-	expression tag	UNP O43681
B	354	PRO	-	expression tag	UNP O43681
B	355	GLN	-	expression tag	UNP O43681
B	356	PHE	-	expression tag	UNP O43681
B	357	GLU	-	expression tag	UNP O43681
B	358	LYS	-	expression tag	UNP O43681

- Molecule 2 is a protein called Tail-anchored protein insertion receptor WRB.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	144	Total	C	N	O	S	0	0
			1160	757	198	195	10		
2	D	144	Total	C	N	O	S	0	0
			1160	757	198	195	10		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	175	GLY	-	expression tag	UNP O00258
C	176	SER	-	expression tag	UNP O00258
C	177	GLY	-	expression tag	UNP O00258
C	178	SER	-	expression tag	UNP O00258
C	179	LEU	-	expression tag	UNP O00258
C	180	GLU	-	expression tag	UNP O00258
C	181	VAL	-	expression tag	UNP O00258
C	182	LEU	-	expression tag	UNP O00258
C	183	PHE	-	expression tag	UNP O00258
C	184	GLN	-	expression tag	UNP O00258
D	175	GLY	-	expression tag	UNP O00258
D	176	SER	-	expression tag	UNP O00258
D	177	GLY	-	expression tag	UNP O00258
D	178	SER	-	expression tag	UNP O00258
D	179	LEU	-	expression tag	UNP O00258
D	180	GLU	-	expression tag	UNP O00258
D	181	VAL	-	expression tag	UNP O00258
D	182	LEU	-	expression tag	UNP O00258
D	183	PHE	-	expression tag	UNP O00258
D	184	GLN	-	expression tag	UNP O00258

- Molecule 3 is a protein called Calcium signal-modulating cyclophilin ligand.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	103	Total	C	N	O	S	0	0
			835	563	127	138	7		
3	F	101	Total	C	N	O	S	0	0
			816	551	122	136	7		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	185	MET	-	initiating methionine	UNP P49069
E	297	GLY	-	expression tag	UNP P49069
E	298	SER	-	expression tag	UNP P49069

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Chain	Residue	Modelled	Actual	Comment	Reference
E	299	GLY	-	expression tag	UNP P49069
E	300	SER	-	expression tag	UNP P49069
E	301	GLU	-	expression tag	UNP P49069
E	302	ASN	-	expression tag	UNP P49069
E	303	LEU	-	expression tag	UNP P49069
E	304	TYR	-	expression tag	UNP P49069
E	305	PHE	-	expression tag	UNP P49069
E	306	GLN	-	expression tag	UNP P49069
E	307	SER	-	expression tag	UNP P49069
E	308	GLY	-	expression tag	UNP P49069
E	309	SER	-	expression tag	UNP P49069
E	310	GLY	-	expression tag	UNP P49069
E	311	SER	-	expression tag	UNP P49069
F	185	MET	-	initiating methionine	UNP P49069
F	297	GLY	-	expression tag	UNP P49069
F	298	SER	-	expression tag	UNP P49069
F	299	GLY	-	expression tag	UNP P49069
F	300	SER	-	expression tag	UNP P49069
F	301	GLU	-	expression tag	UNP P49069
F	302	ASN	-	expression tag	UNP P49069
F	303	LEU	-	expression tag	UNP P49069
F	304	TYR	-	expression tag	UNP P49069
F	305	PHE	-	expression tag	UNP P49069
F	306	GLN	-	expression tag	UNP P49069
F	307	SER	-	expression tag	UNP P49069
F	308	GLY	-	expression tag	UNP P49069
F	309	SER	-	expression tag	UNP P49069
F	310	GLY	-	expression tag	UNP P49069
F	311	SER	-	expression tag	UNP P49069

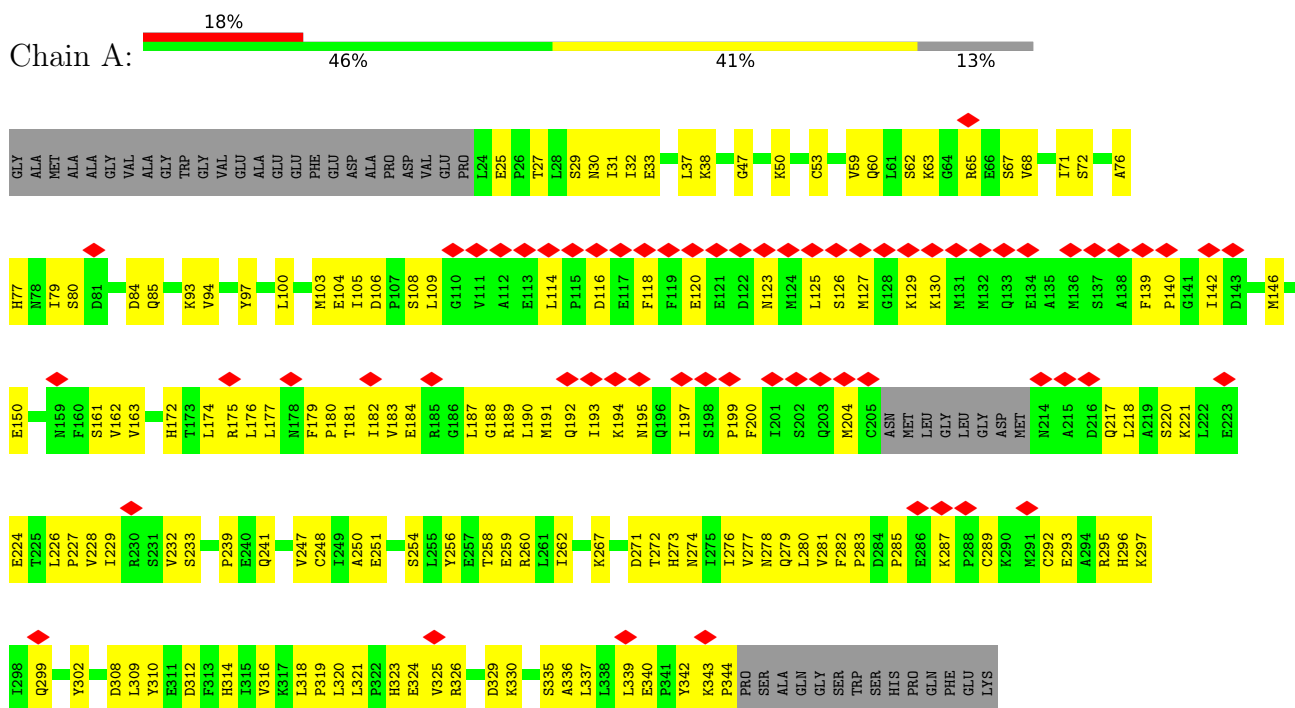
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
4	A	1	Total Zn 1 1	0

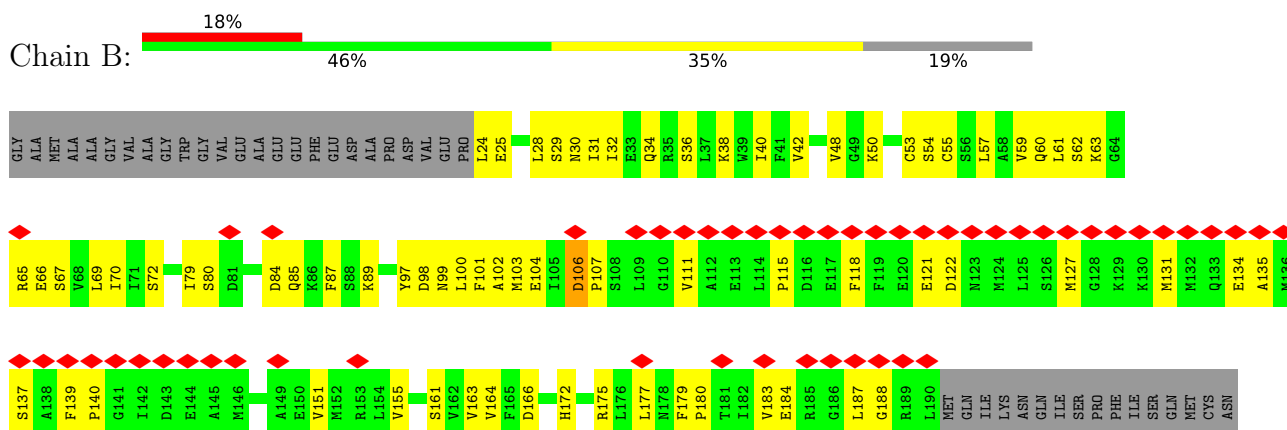
3 Residue-property plots

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

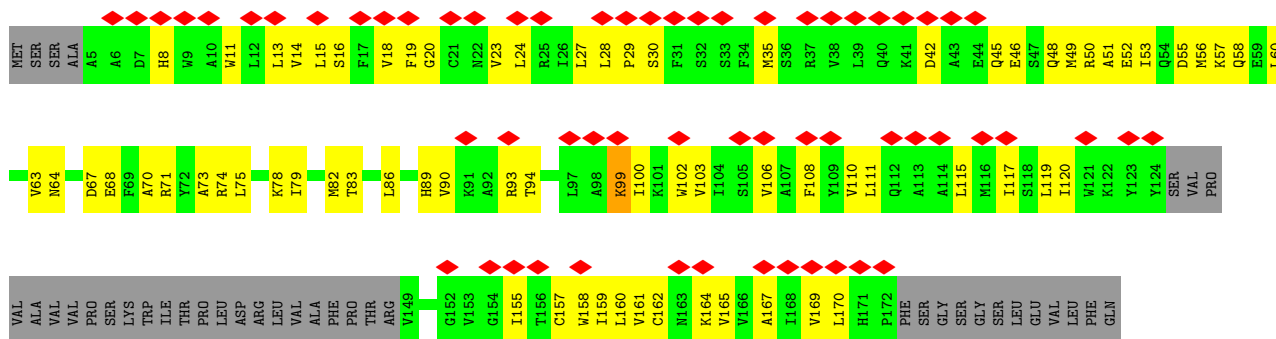
• Molecule 1: ATPase ASNA1



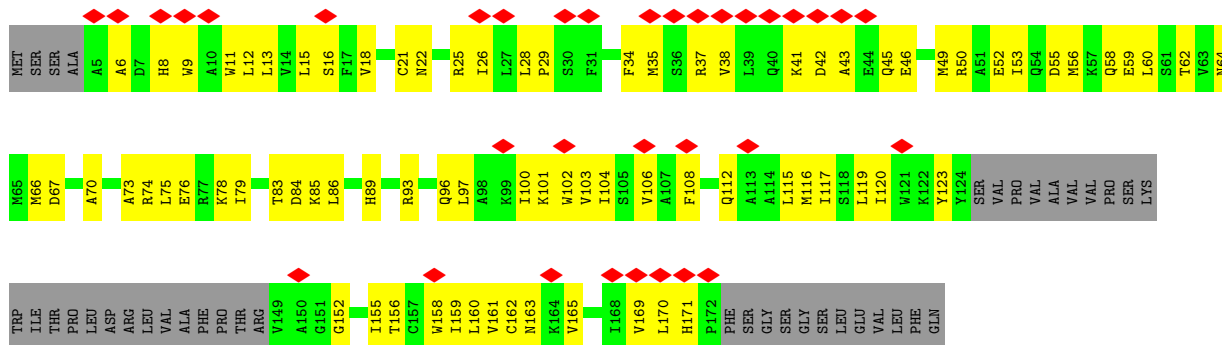
• Molecule 1: ATPase ASNA1



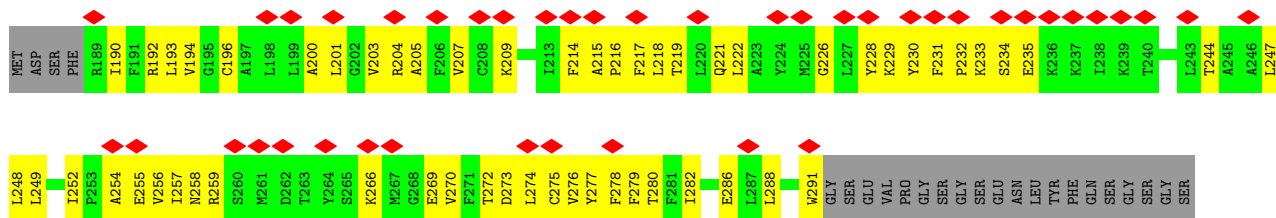
- Molecule 2: Tail-anchored protein insertion receptor WRB



- Molecule 2: Tail-anchored protein insertion receptor WRB

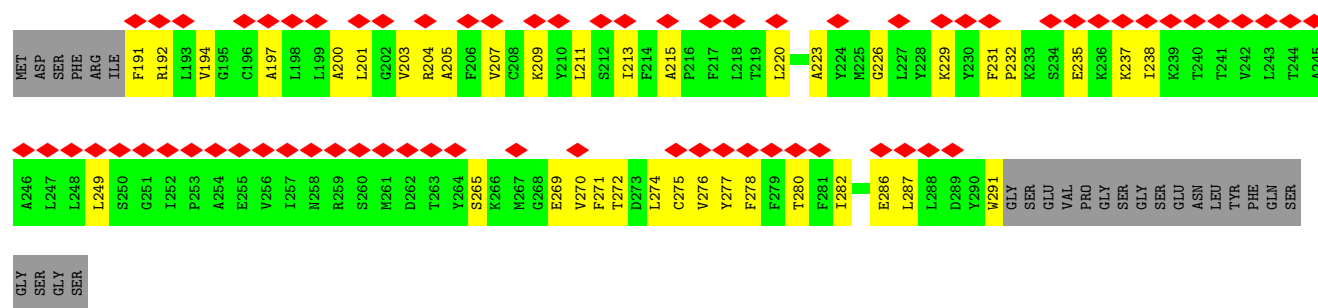


- Molecule 3: Calcium signal-modulating cyclophilin ligand



- Molecule 3: Calcium signal-modulating cyclophilin ligand

Government	Percentage
Current Government	54%
Opposition	49%
Current Government	31%
Opposition	20%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	225244	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.6	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.057	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	233.28, 233.28, 233.28	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.81, 0.81, 0.81	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: ZN

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	0.35	0/2511	0.48	0/3390
1	B	0.35	0/2346	0.49	1/3168 (0.0%)
2	C	0.28	0/1183	0.45	0/1597
2	D	0.31	0/1183	0.48	0/1597
3	E	0.30	0/857	0.52	1/1159 (0.1%)
3	F	0.28	0/838	0.45	0/1134
All	All	0.33	0/8918	0.48	2/12045 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	106	ASP	CB-CG-OD1	5.98	123.69	118.30
3	E	275	CYS	CA-CB-SG	5.04	123.08	114.00

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	2464	0	2488	114	0
1	B	2301	0	2322	96	0
2	C	1160	0	1209	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1160	0	1209	66	0
3	E	835	0	862	58	0
3	F	816	0	838	36	0
4	A	1	0	0	0	0
All	All	8737	0	8928	408	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 23.

The worst 5 of 408 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)
3:E:219:THR:CG2	3:E:277:TYR:CE2	1.97	1.44
3:E:219:THR:HG23	3:E:277:TYR:CZ	1.52	1.43
3:E:219:THR:HG23	3:E:277:TYR:CE2	1.58	1.33
3:E:219:THR:HG21	3:E:277:TYR:CE2	1.92	1.03
3:E:219:THR:HG21	3:E:277:TYR:CD2	2.01	0.95

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	309/360 (86%)	275 (89%)	34 (11%)	0	100	100
1	B	288/360 (80%)	250 (87%)	38 (13%)	0	100	100
2	C	140/184 (76%)	137 (98%)	3 (2%)	0	100	100
2	D	140/184 (76%)	131 (94%)	9 (6%)	0	100	100
3	E	101/127 (80%)	88 (87%)	13 (13%)	0	100	100
3	F	99/127 (78%)	86 (87%)	13 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1077/1342 (80%)	967 (90%)	110 (10%)	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	A	280/313 (90%)	278 (99%)	2 (1%)	81	86
1	B	261/313 (83%)	261 (100%)	0	100	100
2	C	125/160 (78%)	124 (99%)	1 (1%)	79	84
2	D	125/160 (78%)	125 (100%)	0	100	100
3	E	90/109 (83%)	90 (100%)	0	100	100
3	F	88/109 (81%)	88 (100%)	0	100	100
All	All	969/1164 (83%)	966 (100%)	3 (0%)	90	92

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	267	LYS
1	A	274	ASN
2	C	99	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	172	HIS
1	B	235	GLN
3	E	258	ASN
2	D	22	ASN
2	D	163	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

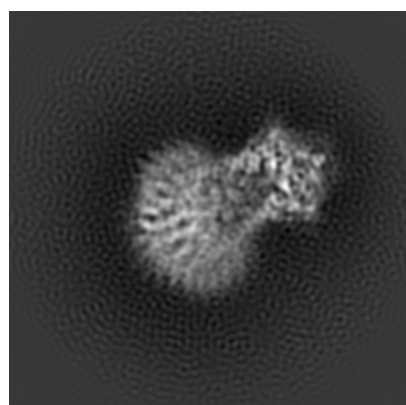
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10266. These allow visual inspection of the internal detail of the map and identification of artifacts.

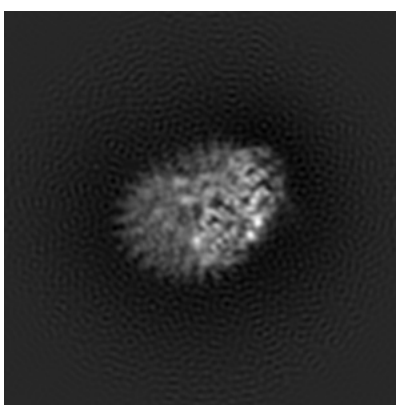
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

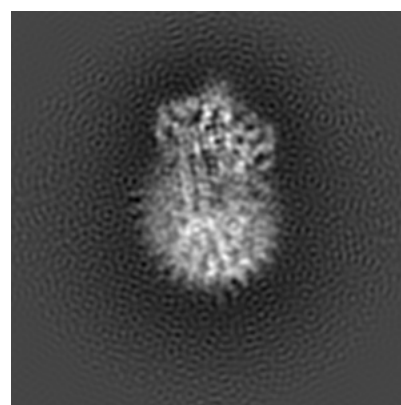
6.1.1 Primary map



X



Y

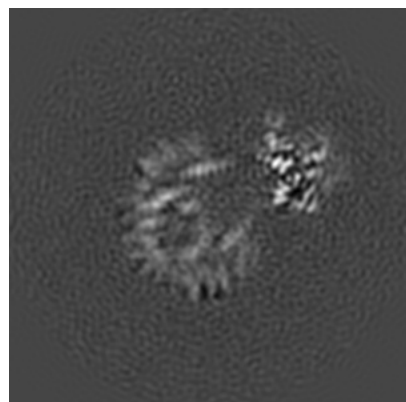


Z

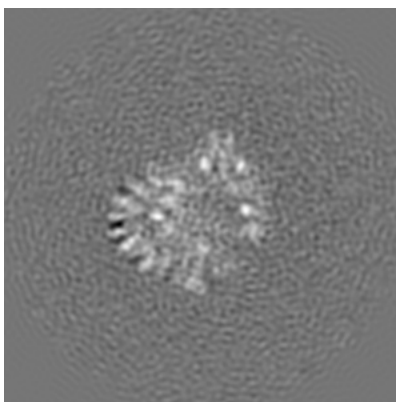
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

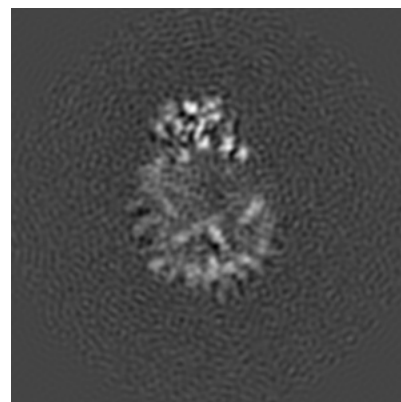
6.2.1 Primary map



X Index: 144



Y Index: 144

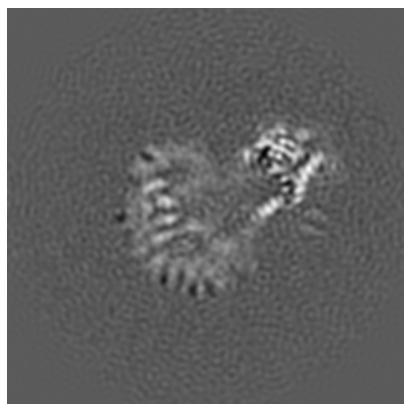


Z Index: 144

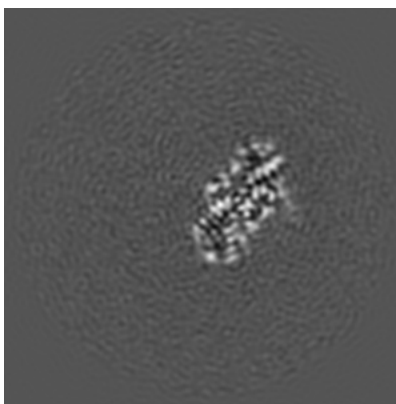
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

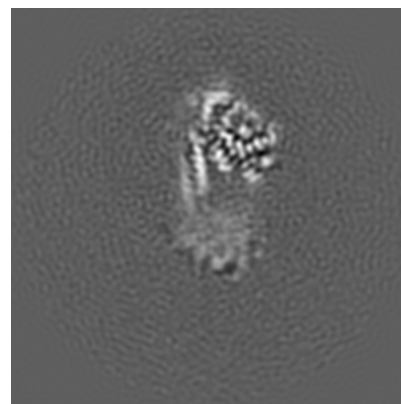
6.3.1 Primary map



X Index: 155



Y Index: 196

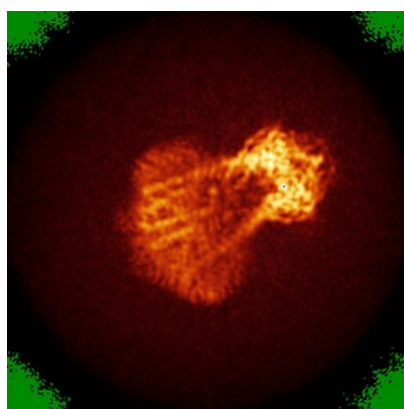


Z Index: 181

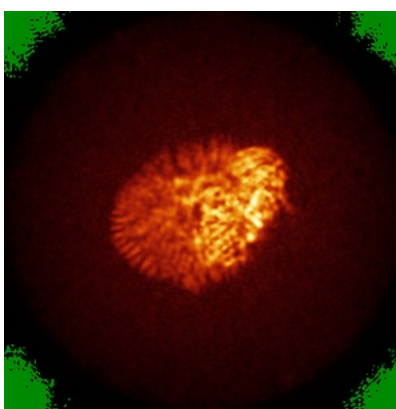
The images above show the largest variance slices of the map in three orthogonal directions.

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

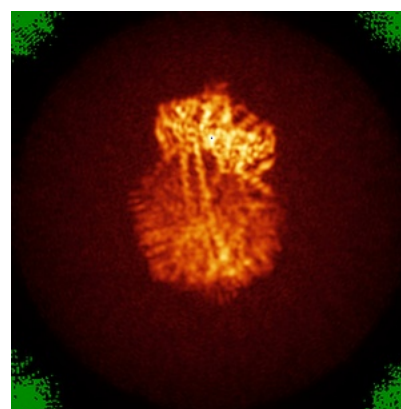
6.4.1 Primary map



X



Y

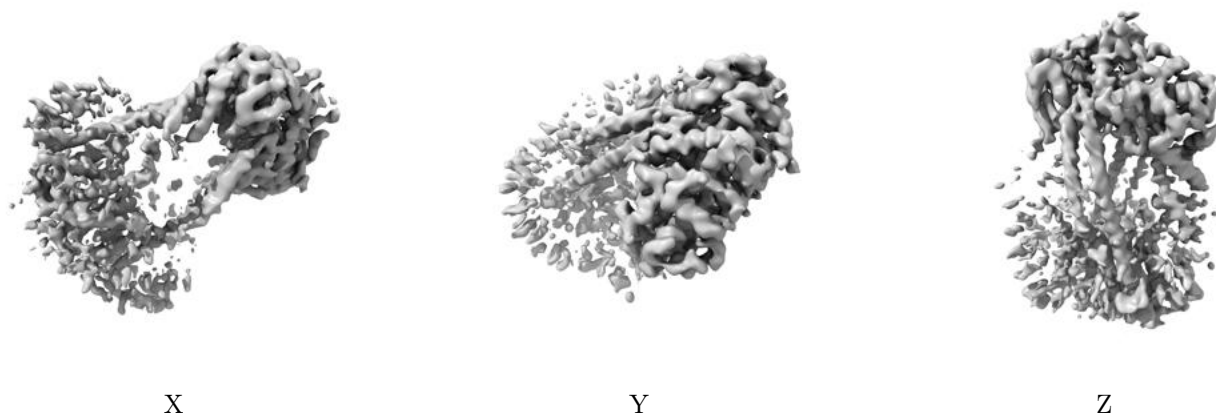


Z

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 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

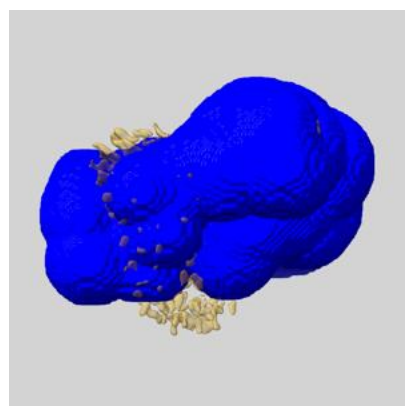
6.6 Mask visualisation [i](#)

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

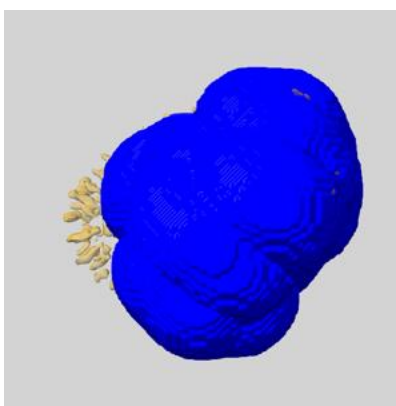
A mask typically either:

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

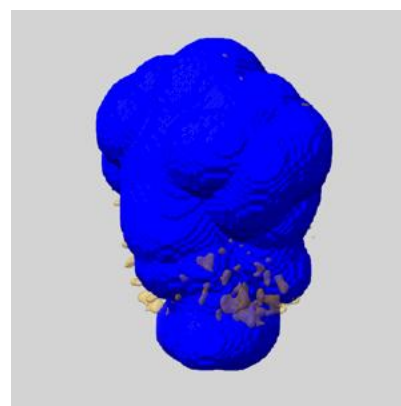
6.6.1 emd_10266_msk_1.map [i](#)



X



Y

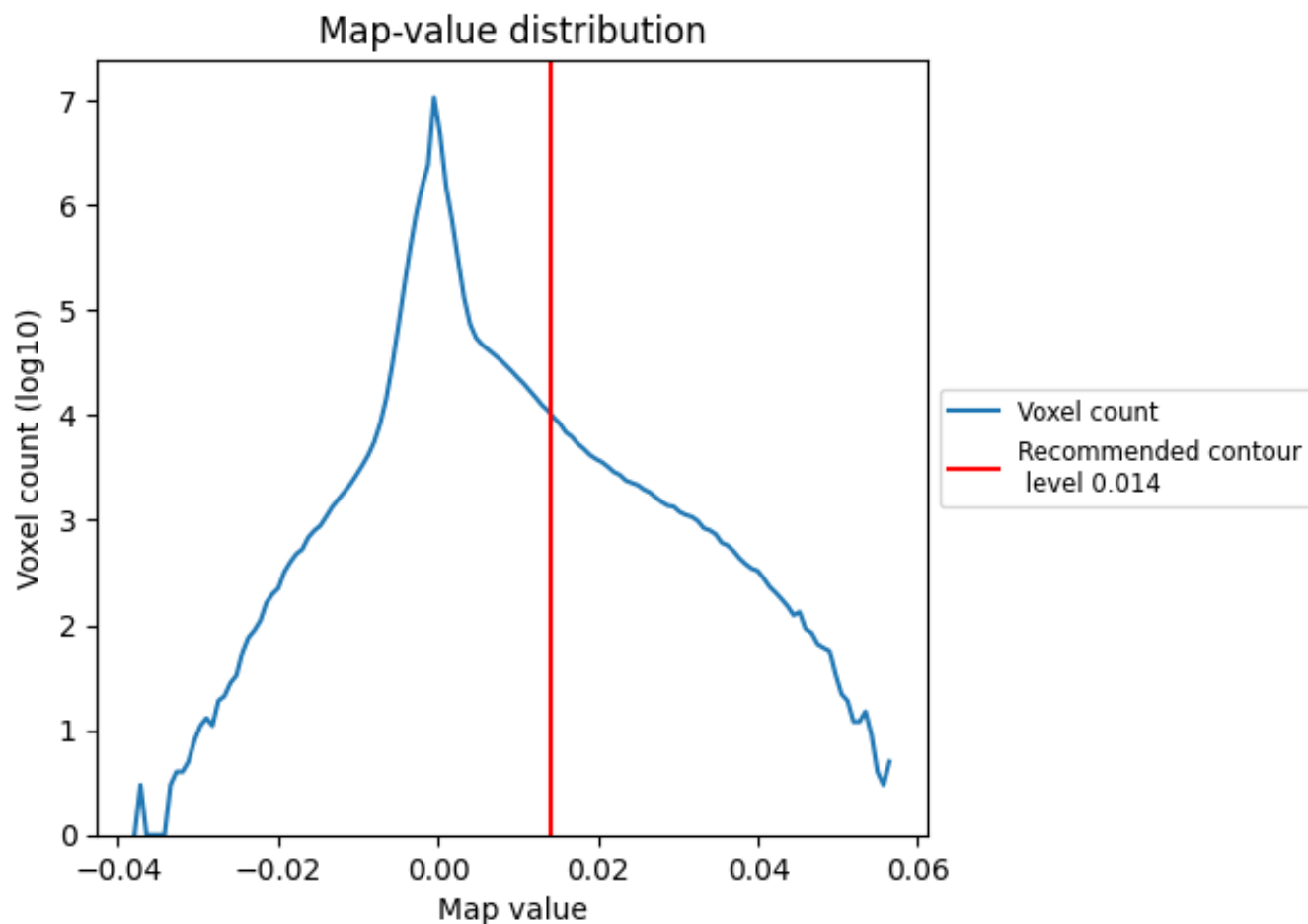


Z

7 Map analysis [i](#)

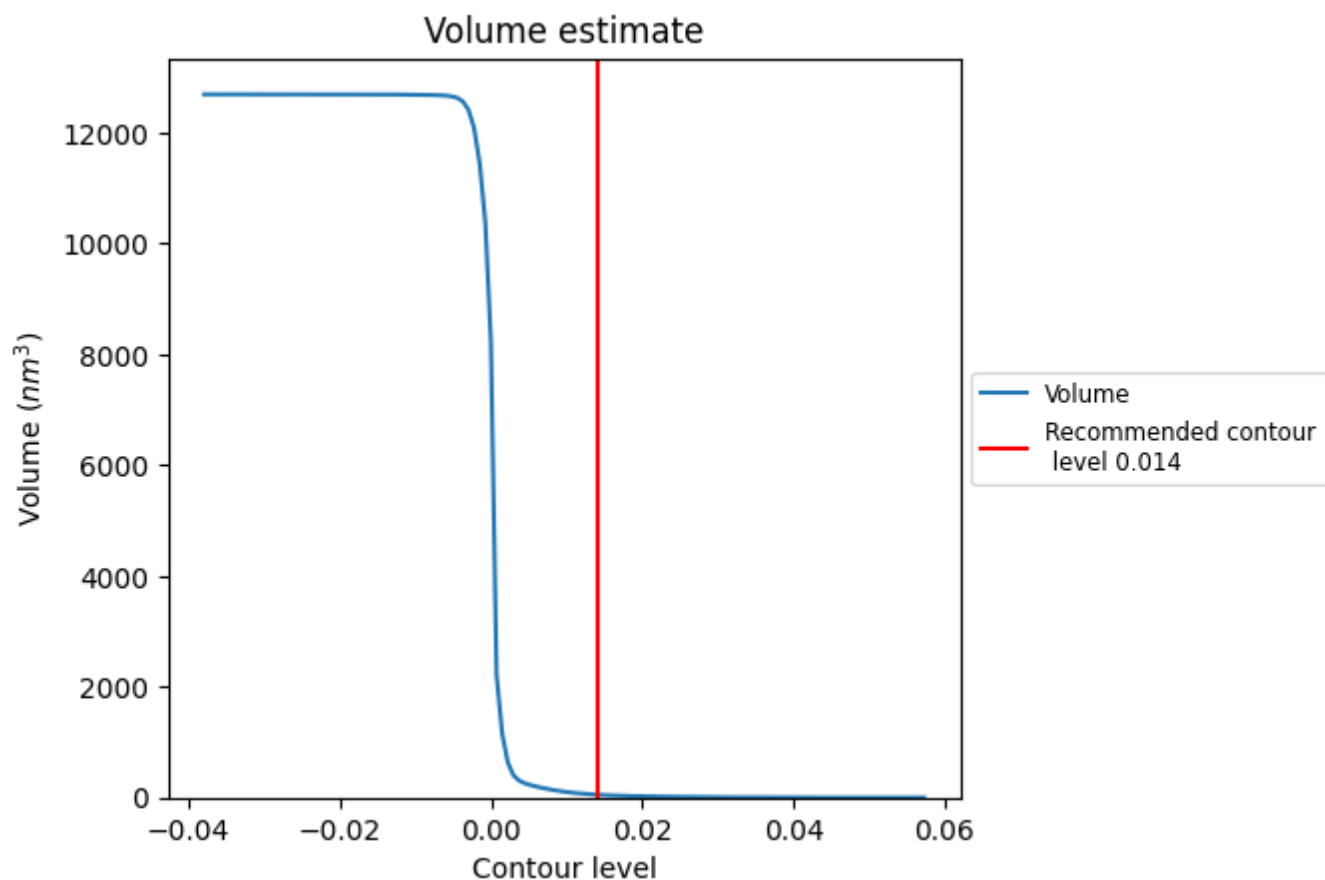
This section contains the results of statistical analysis of the map.

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.

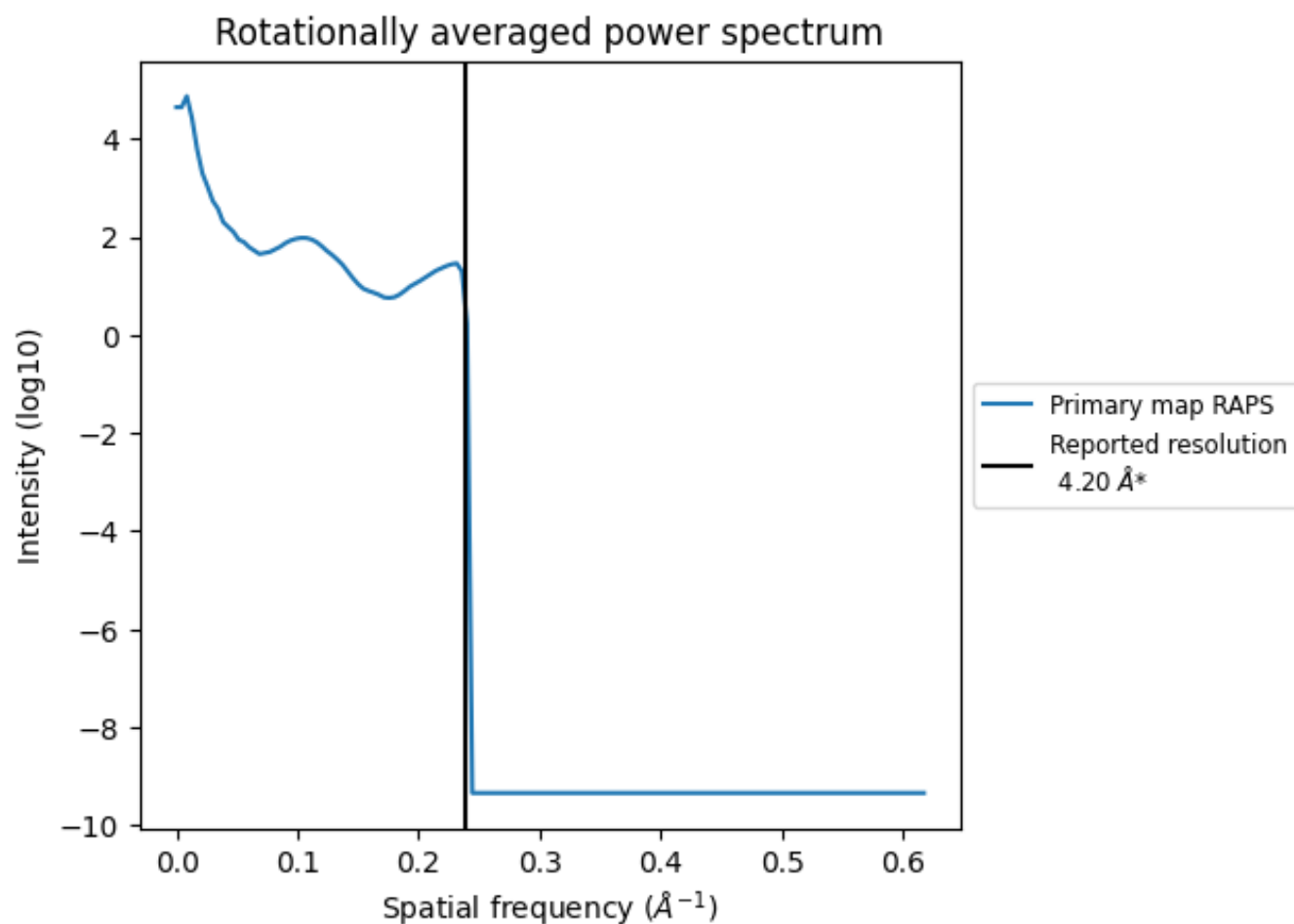
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 51 nm³; this corresponds to an approximate mass of 46 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 0.238 Å⁻¹

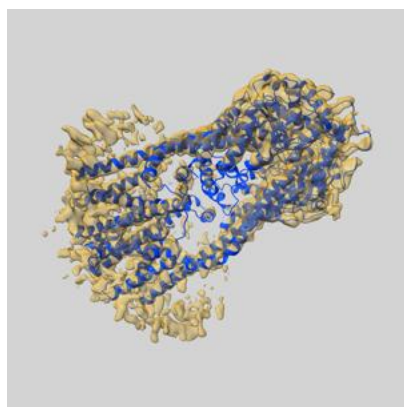
8 Fourier-Shell correlation ⓘ

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

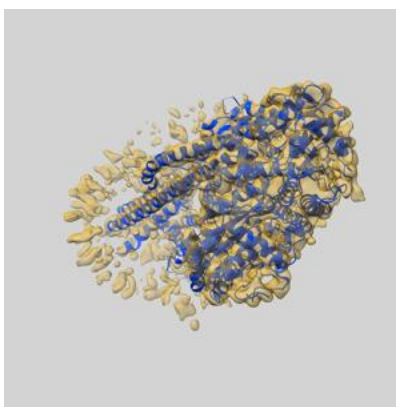
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10266 and PDB model 6SO5. Per-residue inclusion information can be found in section [3](#) on page [6](#).

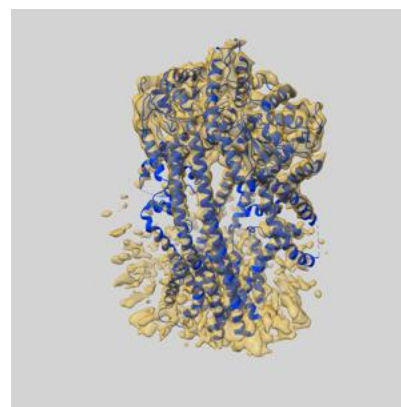
9.1 Map-model overlay [i](#)



X



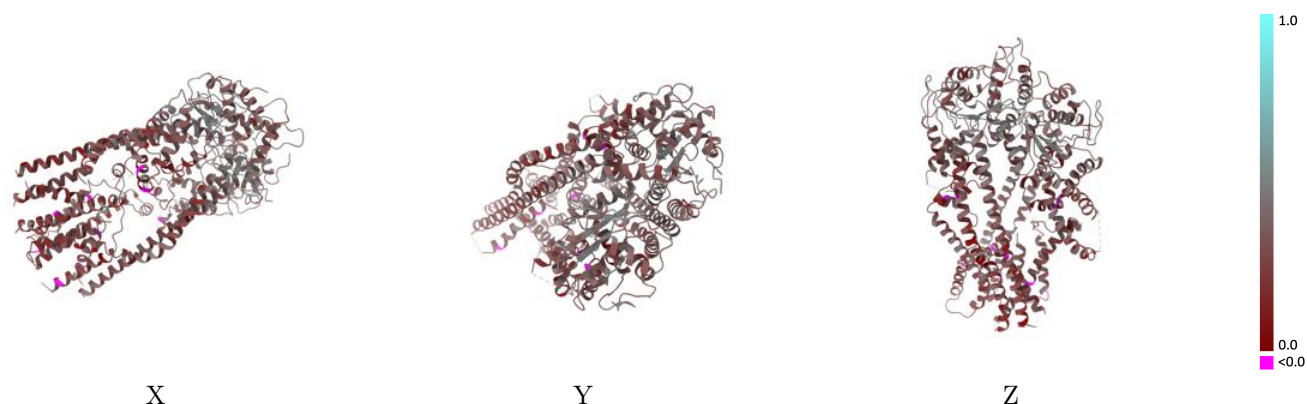
Y



Z

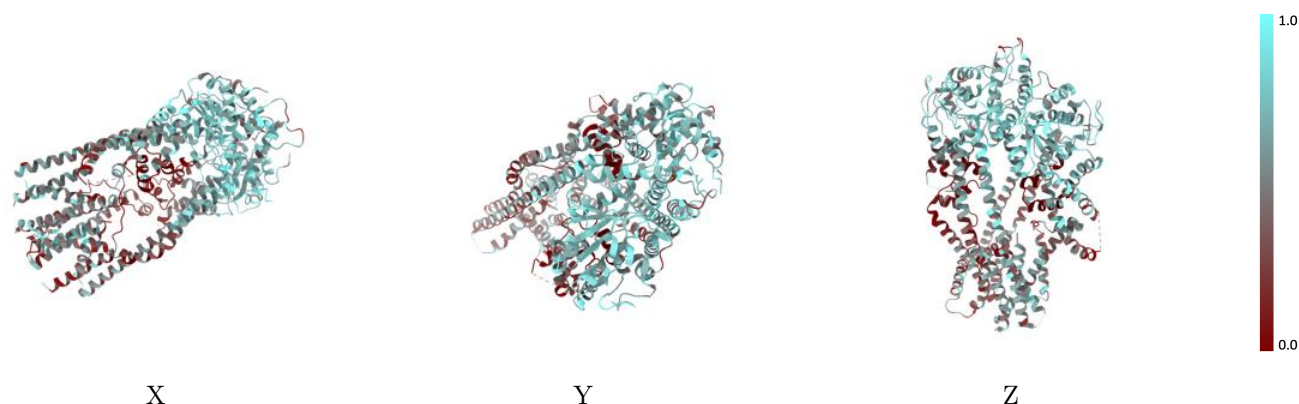
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



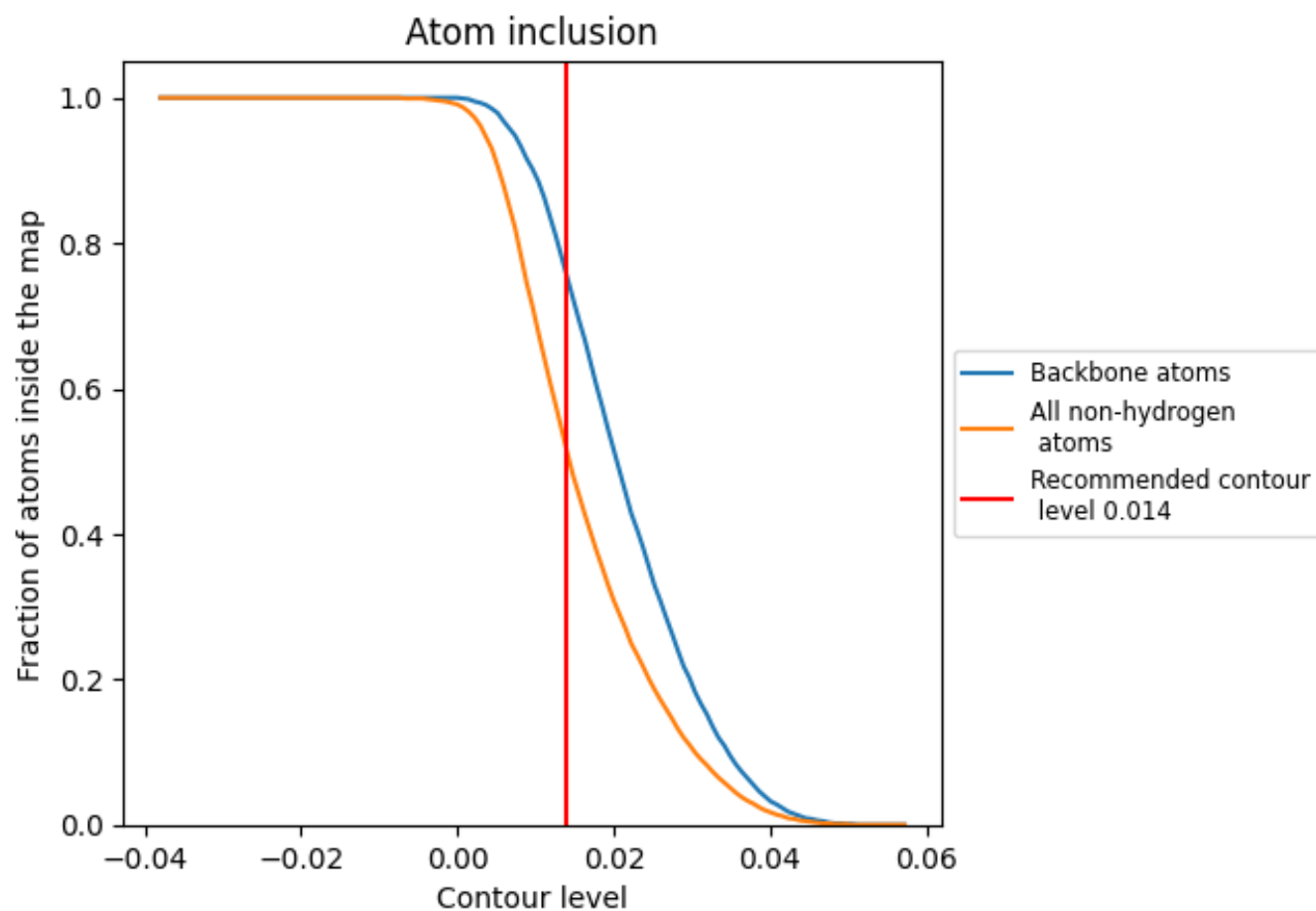
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 52% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5150	<div></div> 0.3260
A	<div></div> 0.5880	<div></div> 0.3660
B	<div></div> 0.5670	<div></div> 0.3670
C	<div></div> 0.4540	<div></div> 0.2900
D	<div></div> 0.5300	<div></div> 0.2750
E	<div></div> 0.4510	<div></div> 0.2730
F	<div></div> 0.2790	<div></div> 0.2620

