



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 01:04 PM UTC

PDB ID : 5KC2 / pdb_00005kc2
EMDB ID : EMD-8235
Title : Negative stain structure of Vps15/Vps34 complex
Authors : Kirsten, M.L.; Zhang, L.; Ohashi, Y.; Perisic, O.; Williams, R.L.; Sachse, C.
Deposited on : 2016-06-04
Resolution : 28.00 Å(reported)

This is a Full wwPDB EM Validation 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
MolProbity : 4-5-2 with Phenix2.0
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

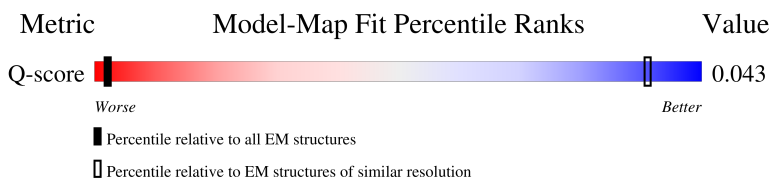
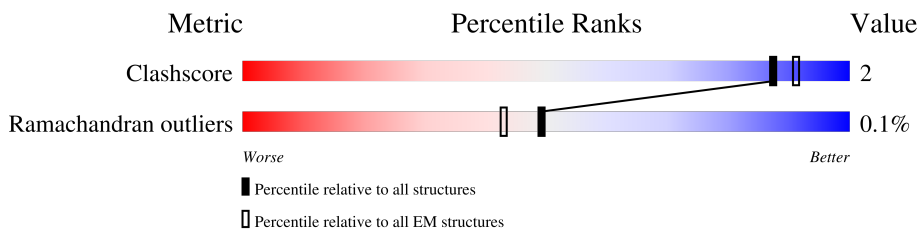
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 28.00 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	-
Q-score	-	25397	11 (27.70 - 28.40)

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	C	875	 85% 5% 11%
2	B	1454	 81% 16%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9967 atoms, of which 0 are hydrogens and 0 are deuteriums.

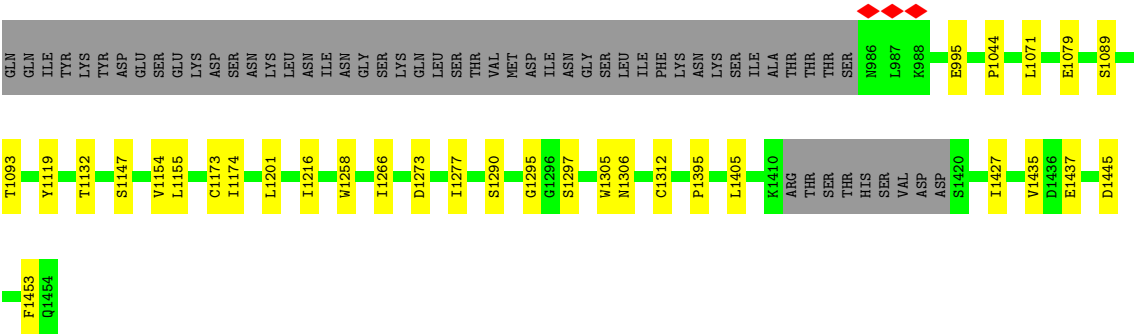
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Phosphatidylinositol 3-kinase VPS34.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	C	783	Total	C	N	O	0	0
			3888	2322	783	783		

- Molecule 2 is a protein called Serine/threonine-protein kinase VPS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	1224	Total	C	N	O	0	0
			6079	3631	1224	1224		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14172	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	0.187	Depositor
Minimum map value	-0.034	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.018	Depositor
Map size ($\text{\AA}$)	397.28, 397.28, 397.28	wwPDB
Map dimensions	104, 104, 104	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.82, 3.82, 3.82	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	C	0.33	0/3885	1.15	32/5418 (0.6%)
2	B	0.30	0/6069	0.95	25/8456 (0.3%)
All	All	0.32	0/9954	1.03	57/13874 (0.4%)

There are no bond length outliers.

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	822	ASP	CA-C-N	11.41	134.10	119.84
1	C	822	ASP	C-N-CA	11.41	134.10	119.84
1	C	120	ILE	CA-C-N	-10.55	109.69	120.98
1	C	120	ILE	C-N-CA	-10.55	109.69	120.98
1	C	40	ASN	CA-C-N	10.49	130.10	119.82
1	C	40	ASN	C-N-CA	10.49	130.10	119.82
1	C	16	VAL	CA-C-N	9.92	130.66	120.14
1	C	16	VAL	C-N-CA	9.92	130.66	120.14
1	C	740	THR	CA-C-N	8.97	128.71	119.56
1	C	740	THR	C-N-CA	8.97	128.71	119.56
1	C	275	ASP	CA-C-N	8.79	129.22	120.52
1	C	275	ASP	C-N-CA	8.79	129.22	120.52
2	B	1079	GLU	CA-C-N	8.40	128.90	119.32
2	B	1079	GLU	C-N-CA	8.40	128.90	119.32
1	C	177	LEU	CA-C-N	8.06	127.64	118.85
1	C	177	LEU	C-N-CA	8.06	127.64	118.85
1	C	77	THR	CA-C-N	7.62	129.36	119.84
1	C	77	THR	C-N-CA	7.62	129.36	119.84
2	B	440	ALA	N-CA-C	-7.30	103.64	112.54
2	B	46	ASP	CA-C-N	7.20	128.83	119.84
2	B	46	ASP	C-N-CA	7.20	128.83	119.84
1	C	51	PHE	CA-C-N	6.92	127.47	120.14
1	C	51	PHE	C-N-CA	6.92	127.47	120.14
2	B	1044	PRO	CA-C-N	6.88	126.48	119.19
2	B	1044	PRO	C-N-CA	6.88	126.48	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	313	TYR	CA-C-N	6.79	124.61	119.66
1	C	313	TYR	C-N-CA	6.79	124.61	119.66
1	C	761	PHE	CA-C-N	6.75	127.34	120.38
1	C	761	PHE	C-N-CA	6.75	127.34	120.38
2	B	844	ILE	CA-C-N	6.39	126.02	119.56
2	B	844	ILE	C-N-CA	6.39	126.02	119.56
2	B	12	SER	CA-C-N	6.32	126.50	120.31
2	B	12	SER	C-N-CA	6.32	126.50	120.31
1	C	115	ASN	N-CA-C	6.31	120.86	111.96
1	C	298	LYS	CA-C-N	6.27	126.45	120.31
1	C	298	LYS	C-N-CA	6.27	126.45	120.31
2	B	58	LYS	CA-C-N	6.11	125.73	119.56
2	B	58	LYS	C-N-CA	6.11	125.73	119.56
1	C	593	CYS	CA-C-N	6.06	125.78	119.05
1	C	593	CYS	C-N-CA	6.06	125.78	119.05
2	B	1119	TYR	N-CA-C	6.01	119.56	107.41
2	B	995	GLU	CA-C-N	5.91	126.38	119.99
2	B	995	GLU	C-N-CA	5.91	126.38	119.99
1	C	213	LEU	CA-C-N	-5.82	114.63	120.21
1	C	213	LEU	C-N-CA	-5.82	114.63	120.21
2	B	92	ILE	N-CA-C	5.71	115.86	107.75
1	C	822	ASP	N-CA-C	-5.70	105.85	113.25
2	B	763	GLN	CA-C-N	5.59	124.94	118.85
2	B	763	GLN	C-N-CA	5.59	124.94	118.85
2	B	1093	THR	CA-C-N	5.50	125.52	119.90
2	B	1093	THR	C-N-CA	5.50	125.52	119.90
2	B	1089	SER	CA-C-N	5.33	125.31	120.03
2	B	1089	SER	C-N-CA	5.33	125.31	120.03
1	C	314	PRO	CA-C-N	5.24	124.87	119.05
1	C	314	PRO	C-N-CA	5.24	124.87	119.05
2	B	660	LEU	CA-C-N	5.14	124.76	119.56
2	B	660	LEU	C-N-CA	5.14	124.76	119.56

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	C	3888	0	1633	15	0
2	B	6079	0	2576	14	0
All	All	9967	0	4209	28	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 2.

All (28) 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:C:6:ILE:HA	1:C:212:GLU:HA	1.68	0.75
1:C:130:PHE:HA	1:C:136:THR:HA	1.68	0.74
1:C:65:LYS:H	1:C:105:SER:HA	1.60	0.67
1:C:23:LYS:HA	1:C:89:ASP:H	1.61	0.64
1:C:140:GLY:HA2	1:C:209:PRO:HA	1.83	0.61
1:C:115:ASN:H	1:C:120:ILE:HA	1.67	0.58
1:C:592:VAL:HA	1:C:611:PHE:HA	1.87	0.55
1:C:54:SER:HA	1:C:115:ASN:HA	1.86	0.55
2:B:1277:ILE:HA	2:B:1295:GLY:HA3	1.89	0.55
2:B:1071:LEU:HA	2:B:1453:PHE:HA	1.89	0.55
1:C:25:LEU:HA	1:C:204:LEU:HA	1.88	0.55
2:B:1258:TRP:HA	2:B:1266:ILE:H	1.72	0.54
2:B:1132:THR:H	2:B:1147:SER:HA	1.73	0.54
2:B:1290:SER:HA	2:B:1306:ASN:HA	1.88	0.54
2:B:1305:TRP:HA	2:B:1312:CYS:HA	1.90	0.52
2:B:1155:LEU:HA	2:B:1173:CYS:HA	1.94	0.49
1:C:45:LEU:O	1:C:49:ASN:N	2.33	0.48
2:B:1395:PRO:HA	2:B:1405:LEU:HA	1.96	0.46
1:C:219:GLU:H	2:B:439:THR:CB	2.30	0.45
1:C:17:PRO:HA	1:C:97:ARG:HA	1.98	0.45
1:C:141:PHE:HA	1:C:207:GLU:HA	2.00	0.44
1:C:11:SER:CB	1:C:217:PHE:H	2.30	0.43
2:B:1201:LEU:HA	2:B:1216:ILE:H	1.84	0.43
1:C:65:LYS:HA	1:C:104:SER:C	2.44	0.41
2:B:1273:ASP:H	2:B:1297:SER:HA	1.86	0.41
2:B:1154:VAL:O	2:B:1174:ILE:N	2.50	0.40
2:B:1435:VAL:C	2:B:1437:GLU:H	2.28	0.40
2:B:1427:ILE:HA	2:B:1445:ASP:HA	2.04	0.40

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	C	777/875 (89%)	721 (93%)	54 (7%)	2 (0%)	36	72
2	B	1204/1454 (83%)	1109 (92%)	95 (8%)	0	100	100
All	All	1981/2329 (85%)	1830 (92%)	149 (8%)	2 (0%)	49	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	29	LYS
1	C	753	ILE

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

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.

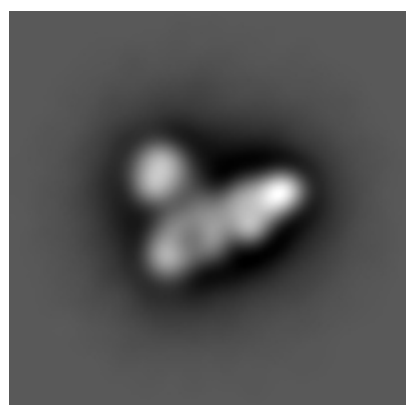
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8235. These allow visual inspection of the internal detail of the map and identification of artifacts.

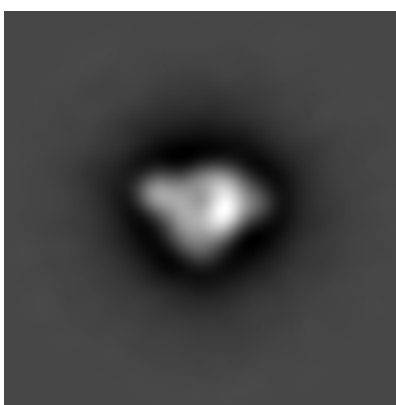
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

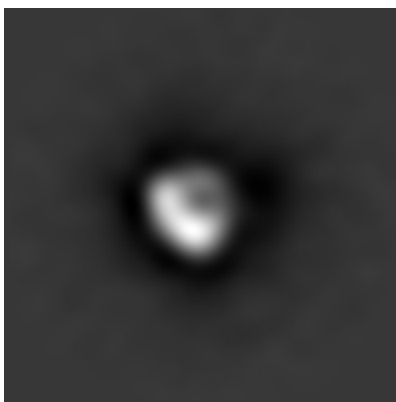
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 52



Y Index: 52



Z Index: 52

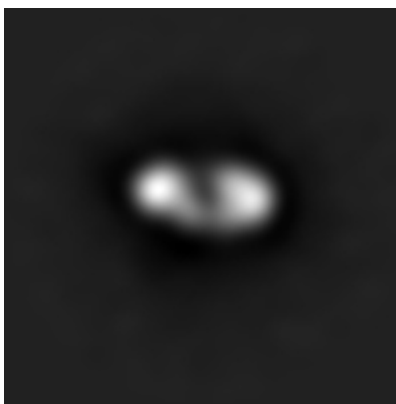
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

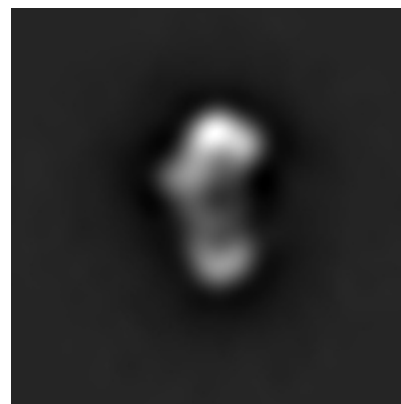
6.3.1 Primary map



X Index: 55



Y Index: 40



Z Index: 56

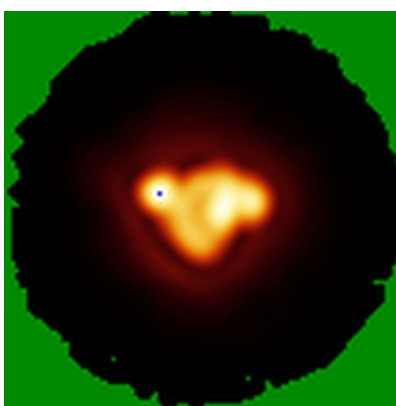
The images above show the largest variance slices of the map in three orthogonal directions.

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

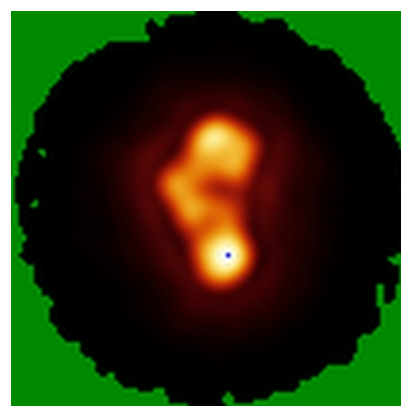
6.4.1 Primary map



X



Y

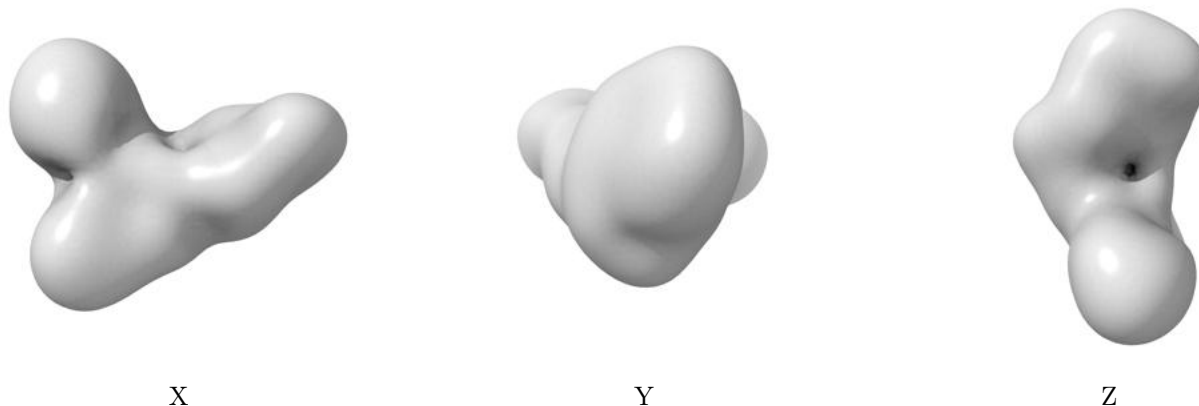


Z

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

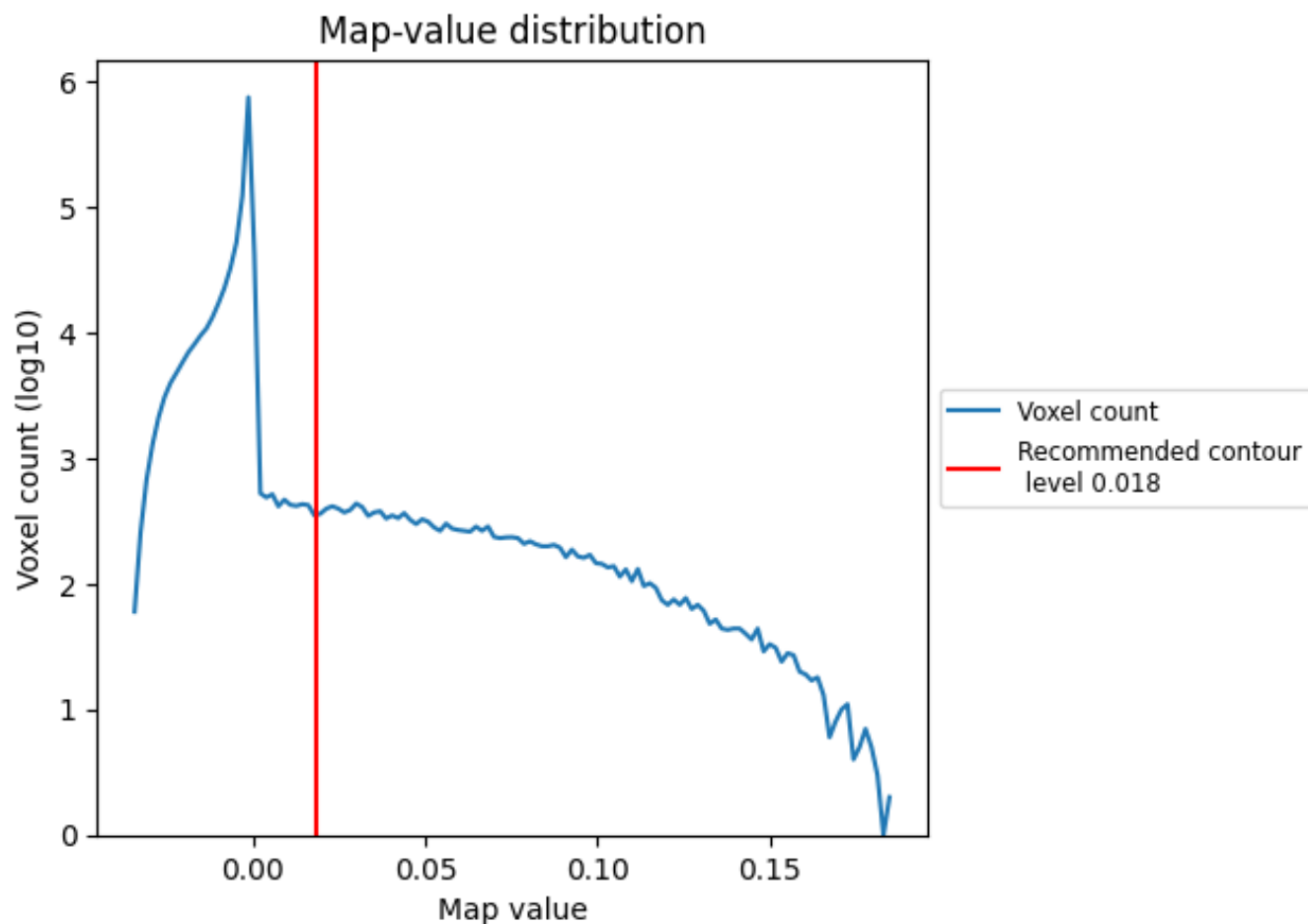
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

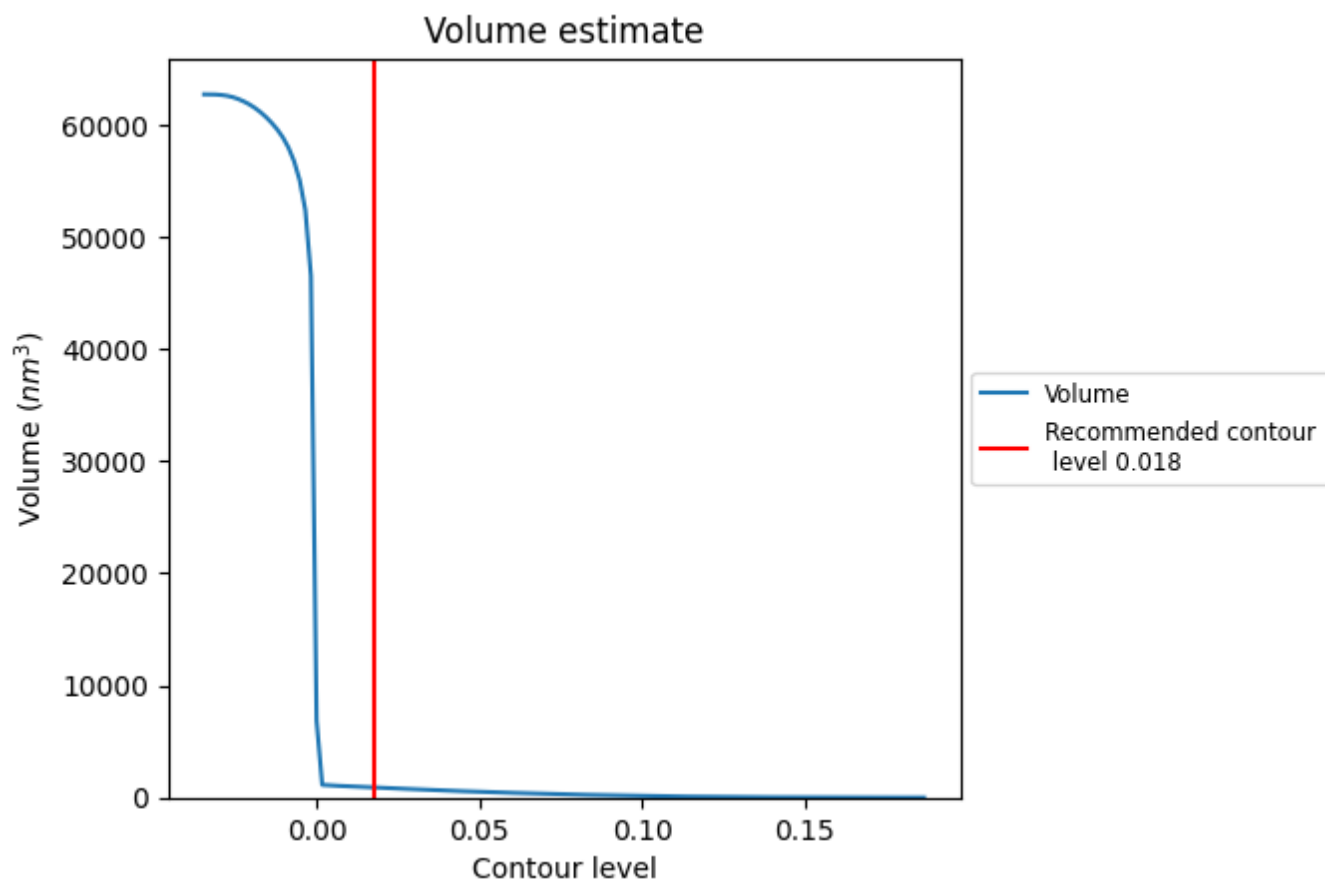
This section contains the results of statistical analysis of the map.

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.

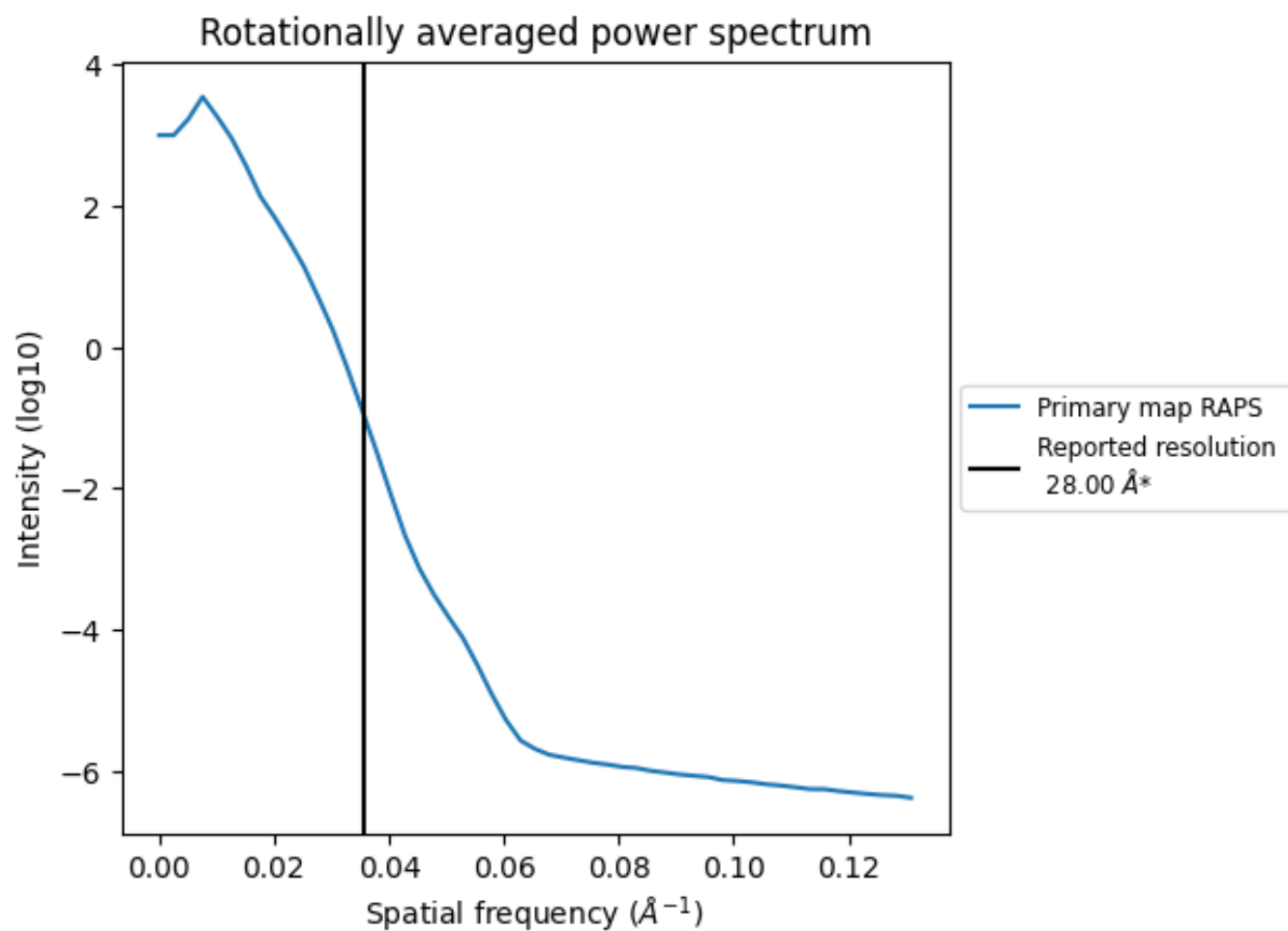
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 892 nm³; this corresponds to an approximate mass of 805 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 0.036 $\text{\AA}^{-1}$

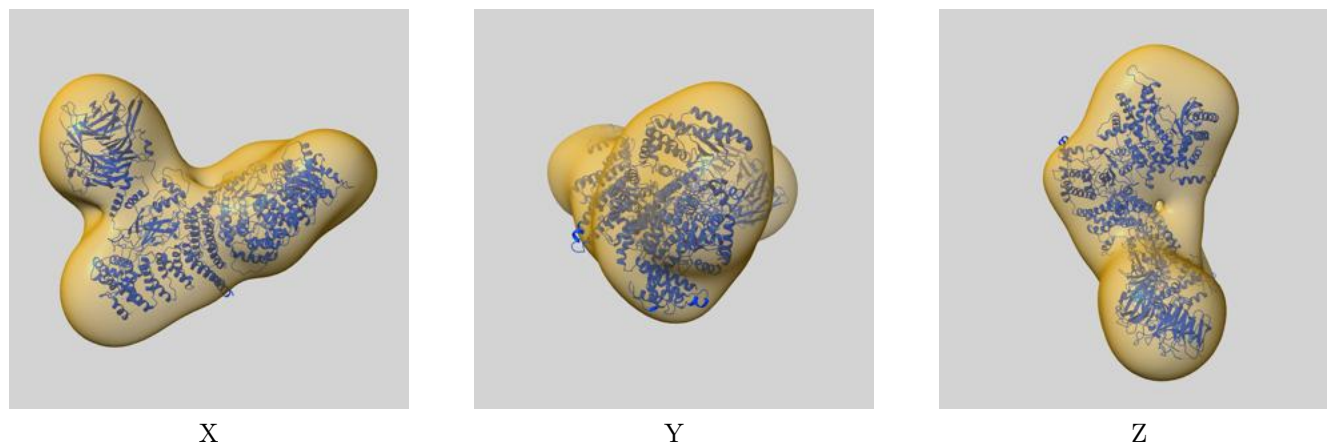
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

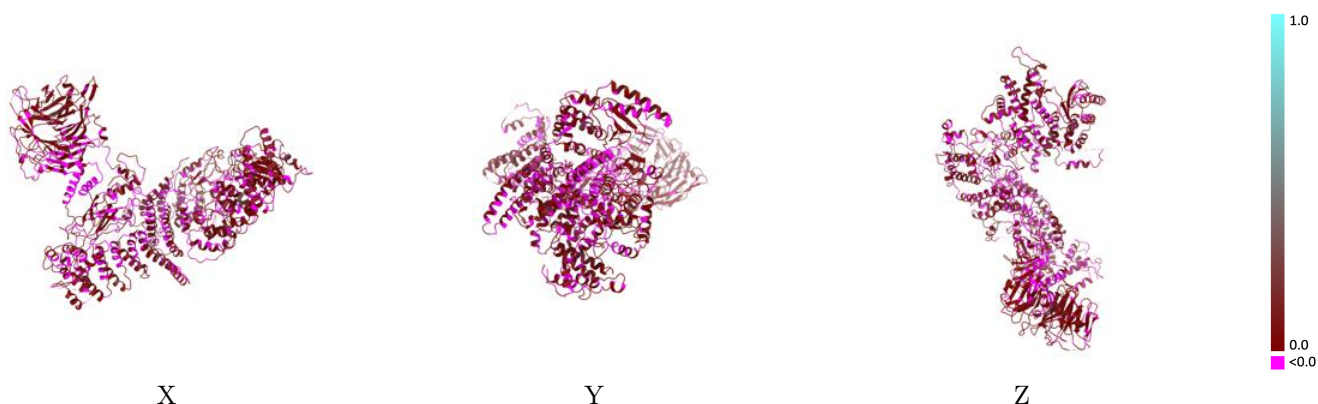
This section contains information regarding the fit between EMDB map EMD-8235 and PDB model 5KC2. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



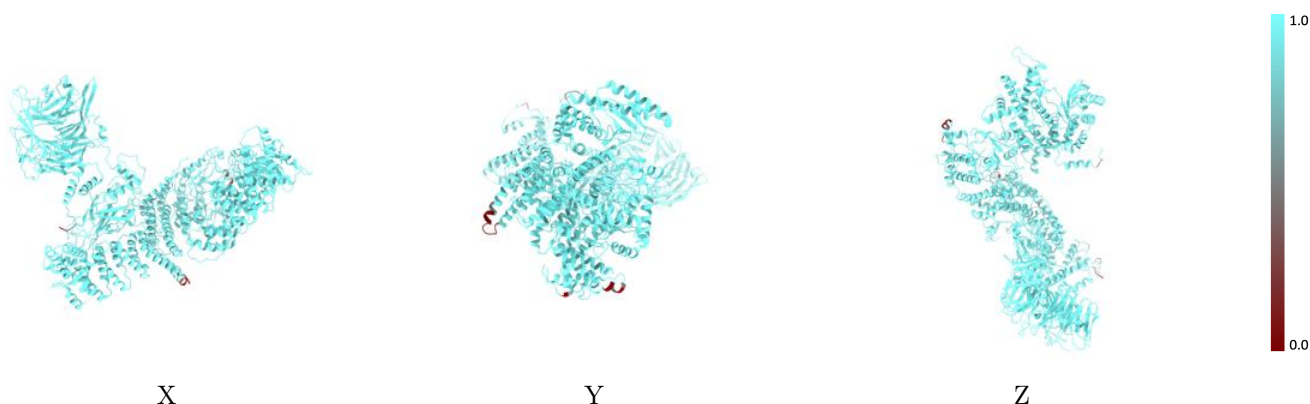
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



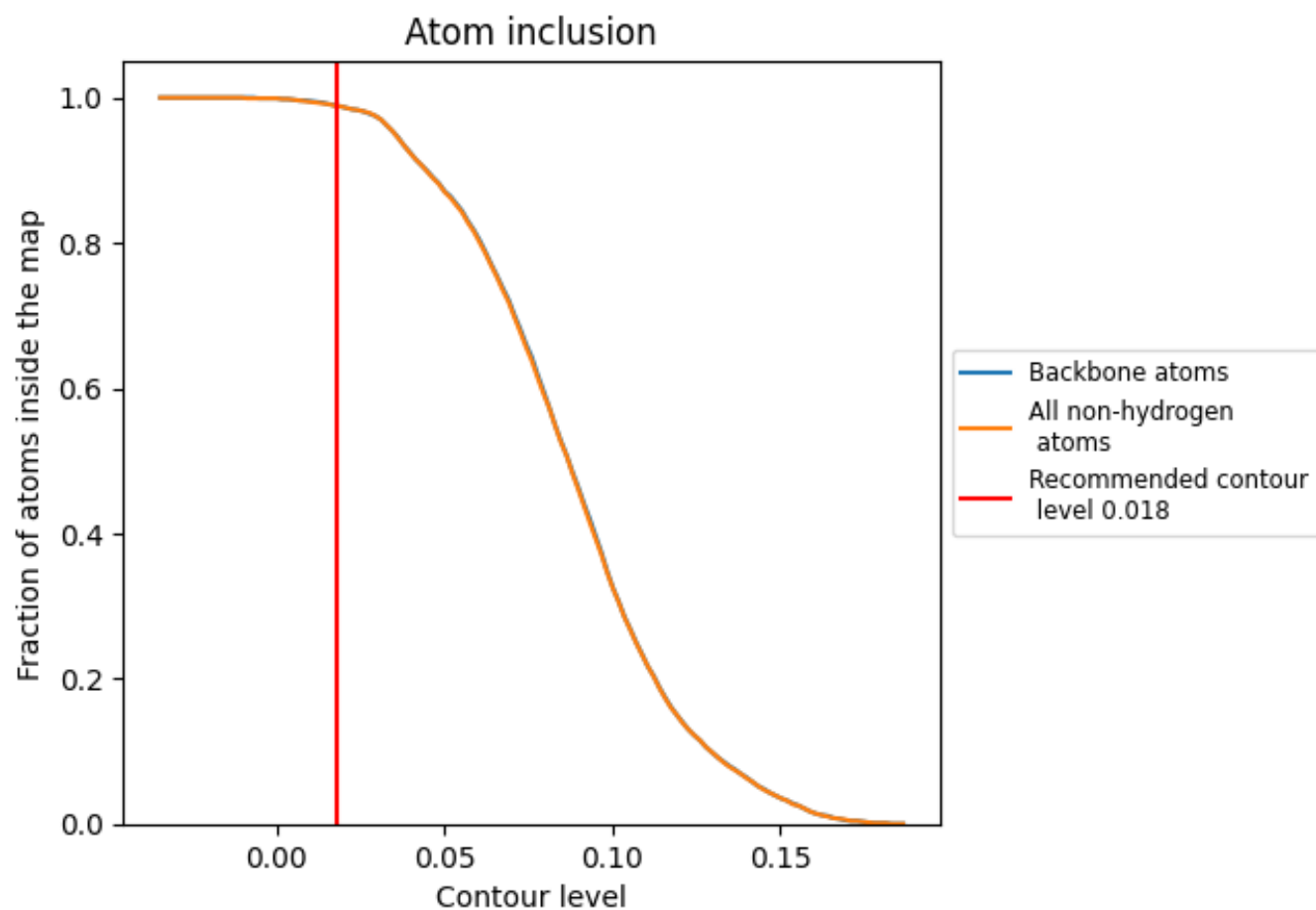
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9880	0.0430
B	0.9820	0.0460
C	0.9970	0.0380

