



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:58 AM UTC

PDB ID : 8Z9M / pdb_00008z9m
EMDB ID : EMD-39863
Title : Cryo-EM structure of dimeric WDR11-FAM91A1 complex
Authors : Jia, G.W.; Deng, Q.H.; Su, Z.M.; Jia, D.
Deposited on : 2024-04-23
Resolution : 3.30 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.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

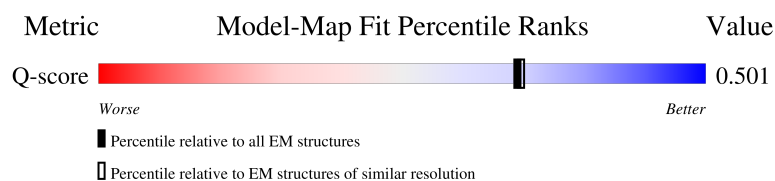
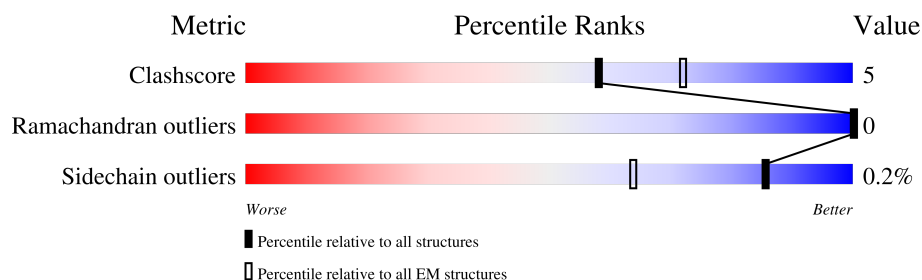
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	847	 6% 34% 5% 61%
1	C	847	 6% 34% 5% 61%
2	B	1224	 1% 76% 11% 13%
2	D	1224	 1% 75% 12% 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22016 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 Protein FAM91A1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	328	Total	C	N	O	S	0	0
			2607	1679	453	463	12		
1	A	332	Total	C	N	O	S	0	0
			2640	1700	457	471	12		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	MET	-	initiating methionine	UNP Q658Y4
C	-7	HIS	-	expression tag	UNP Q658Y4
C	-6	HIS	-	expression tag	UNP Q658Y4
C	-5	HIS	-	expression tag	UNP Q658Y4
C	-4	HIS	-	expression tag	UNP Q658Y4
C	-3	HIS	-	expression tag	UNP Q658Y4
C	-2	HIS	-	expression tag	UNP Q658Y4
C	-1	HIS	-	expression tag	UNP Q658Y4
C	0	HIS	-	expression tag	UNP Q658Y4
A	-8	MET	-	initiating methionine	UNP Q658Y4
A	-7	HIS	-	expression tag	UNP Q658Y4
A	-6	HIS	-	expression tag	UNP Q658Y4
A	-5	HIS	-	expression tag	UNP Q658Y4
A	-4	HIS	-	expression tag	UNP Q658Y4
A	-3	HIS	-	expression tag	UNP Q658Y4
A	-2	HIS	-	expression tag	UNP Q658Y4
A	-1	HIS	-	expression tag	UNP Q658Y4
A	0	HIS	-	expression tag	UNP Q658Y4

- Molecule 2 is a protein called WD repeat-containing protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	1064	Total	C	N	O	S	0	0
			8394	5352	1442	1551	49		

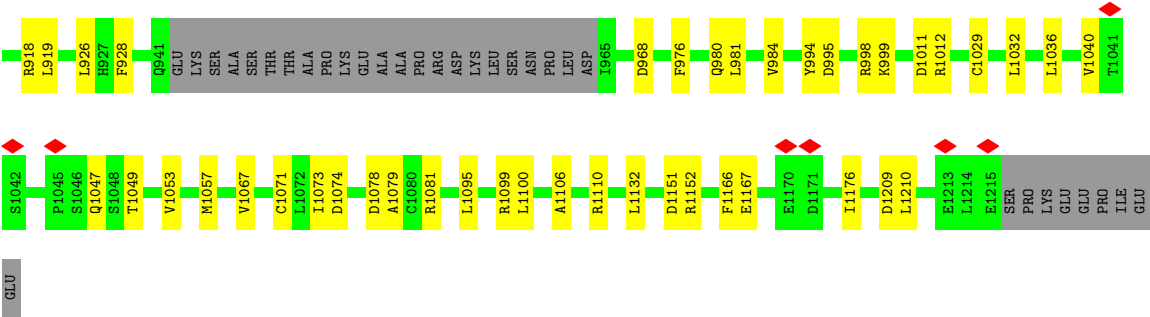
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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1062	8375	5341	1439	1546	49	0	0

LEU	LEU	CYS	VAL	TYR	LEU	MET
GLY	GLY	ILE	GLN	ASP	VAL	HIS
PHE	PHE	ALA	ALA	SER	LYS	HIS
ALA	ALA	VAL	GLY	LEU	HIS	HIS
HIS	HIS	PRO	TYR	PRO	VAL	HIS
LYS	LYS	PRO	ILE	ASN	LYS	HIS
GLY	GLY	LEU	THR	THR	ASP	HIS
GLN	GLN	GLU	GLU	PHE	GLU	HIS
VAL	VAL	PHE	ASP	ALA	ARG	MET
ILE	ILE	VAL	ILE	ASP	ARG	ASN
ASN	ASN	MET	LYS	CYS	TYR	ILE
LEU	LEU	ASN	ILE	LEU	TYR	ASP
ASP	ASP	ARG	CYS	ARG	GLU	VAL
GLN	GLN	VAL	THR	LEU	GLU	GLY
LEU	LEU	LEU	LEU	LEU	LEU	PHE
HIS	HIS	GLY	PRO	GLY	LEU	HIS
SER	SER	ASP	GLU	ILE	LYS	ILE
SER	SER	PHE	CYS	GLY	TYR	ARG
TRP	TRP	THR	LYS	ARG	SER	HIS
LYS	LYS	GLU	ALA	ASN	ARG	ASN
ASN	ASN	THR	VAL	GLN	ASP	TYR
VAL	VAL	LEU	ASP	TYR	HIS	PRO
PRO	PRO	LEU	LYS	ILE	LEU	TRP
SER	SER	TYR	ILE	ASP	MET	ASN
VAL	VAL	LYS	ASP	LEU	LEU	LYS
ASN	ASN	ILE	ASP	MET	TYR	LEU
ARG	ARG	PHE	GLY	ASN	PRO	PRO
LEU	LEU	VAL	GLY	GLN	TYR	ALA
LYS	LYS	SER	PRO	CYS	HIS	ASN
SER	SER	ILE	GLN	ARG	LEU	VAL
THR	THR	ASP	LEU	SER	SER	ARG
LEU	LEU	GLU	SER	SER	ASP	GLN
PRO	PRO	HIS	GLY	LYS	ILE	LEU
GLN	GLN	THR	SER	PHE	GLY	GLY
ASN	ASN	ASN	LEU	LYS	VAL	ASN
VAL	VAL	VAL	VAL	THR	ILE	GLN
SER	SER	ALA	VAL	LYS	ARG	ARG
SER	SER	ASN	HIS	THR	ILE	GLU
TRP	TRP	VAL	SER	ALA	THR	TYR
GLY	GLY	VAL	THR	ARG	PRO	GLU
GLY	GLY	GLU	TYR	LEU	PHE	LEU
GLU	GLU	ILE	ASN	LEU	SER	TYR
SER	SER	ASP	LYS	PRO	TYR	LEU
ARG	ARG	LEU	GLY	ILE	THR	TYR
SER	SER	PHE	PHE	LYS	GLY	TYR
PRO	PRO	LEU	ILE	TYR	ILE	ILE
VAL	VAL	VAL	THR	SER	MET	ARG
VAL	VAL	LYS	LEU	LEU	GLU	ARG
GLN	GLN	ASN	ASP	ILE	ASP	ASN
ALA	ALA	ALA	VAL	ALA	ILE	GLN
SER	SER	VAL	PRO	ILE	MET	LEU
SER	SER	SER	ILE	GLU	ASN	ARG
ALA	ALA	MET	ILE	ALA	SER	TYR
THR	THR	TYR	ASP	TRP	GLU	ARG
ASP	ASP	CYS	ASP	ASP	LYS	ASN
THR	THR	ARG	SER	VAL	SER	THR

CYS	ASN	ARG	SER	ARG	ASN	SER	SER	SER	GLY	V401	S402	S409	C411	P414	V415	G416	V417	L418	Q419	N420	K421	S426	L427	D428	E440	H441	ARG	GLY	SER	ILE	L447	L459	P464	M460	I481	K482	T492	E510	L511	L526	M538	N539	M540	
MET	LEU	PRO	TYR	THR	VAL	ASN	F8	K9	C39	H40	L54	L57	E58	I78	R85	L86	V98	D99	D130	N139	Y157	K199	S204	SER	PRO	HIS	SER	SER	PRO	HIS	ASN	LYS	LEU	ALA	THR	ALA	THR	GLY	ALA	LYS	LEU	ASN	LYS	VAL



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	232473	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 ($e^-/\text{\AA}^2$)	58.47	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2992	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.844	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.16	Depositor
Map size ($\text{\AA}$)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.85, 0.85, 0.85	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	A	0.21	0/2695	0.45	1/3644 (0.0%)
1	C	0.11	0/2662	0.27	0/3599
2	B	0.10	0/8552	0.29	0/11610
2	D	0.09	0/8572	0.26	0/11639
All	All	0.12	0/22481	0.30	1/30492 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	744	ILE	N-CA-C	-5.12	107.76	112.83

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	2640	0	2677	24	0
1	C	2607	0	2645	27	0
2	B	8375	0	8397	81	0
2	D	8394	0	8411	87	0
All	All	22016	0	22130	209	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 5.

The worst 5 of 209 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)
2:D:1029:CYS:SG	2:B:1029:CYS:SG	2.66	0.94
1:A:406:MET:HE1	1:A:412:LEU:HD11	1.69	0.75
2:D:1032:LEU:CD2	2:B:1036:LEU:HD22	2.19	0.73
2:D:260:MET:HE3	2:D:273:LEU:HD21	1.72	0.71
2:D:1054:ALA:HB2	2:D:1069:LEU:HD22	1.74	0.69

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	316/847 (37%)	300 (95%)	16 (5%)	0	100	100
1	C	312/847 (37%)	303 (97%)	9 (3%)	0	100	100
2	B	1046/1224 (86%)	1015 (97%)	31 (3%)	0	100	100
2	D	1048/1224 (86%)	1010 (96%)	38 (4%)	0	100	100
All	All	2722/4142 (66%)	2628 (96%)	94 (4%)	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	298/758 (39%)	292 (98%)	6 (2%)	48	68
1	C	294/758 (39%)	294 (100%)	0	100	100
2	B	928/1073 (86%)	928 (100%)	0	100	100
2	D	931/1073 (87%)	931 (100%)	0	100	100
All	All	2451/3662 (67%)	2445 (100%)	6 (0%)	85	88

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	749	LEU
1	A	751	ARG
1	A	752	LYS
1	A	457	ASP
1	A	456	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	1047	GLN
2	B	124	ASN
2	B	1123	GLN
2	B	120	GLN
2	B	125	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

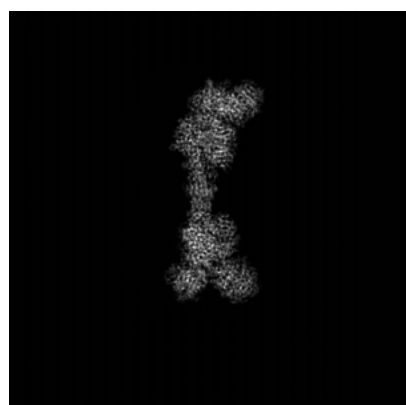
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39863. These allow visual inspection of the internal detail of the map and identification of artifacts.

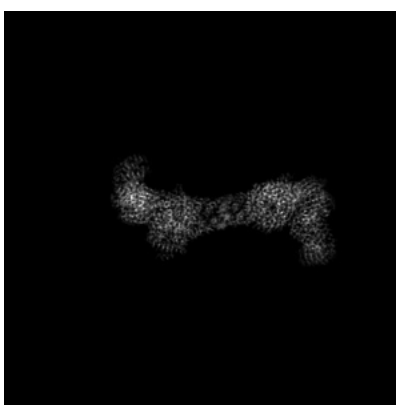
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

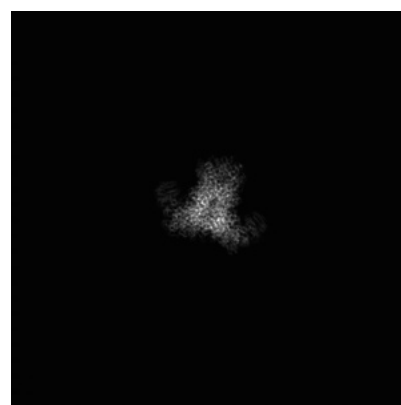
6.1.1 Primary map



X



Y



Z

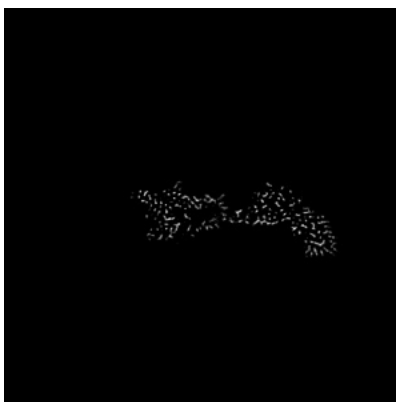
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

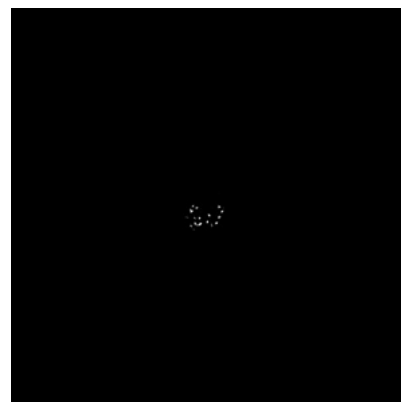
6.2.1 Primary map



X Index: 240



Y Index: 240

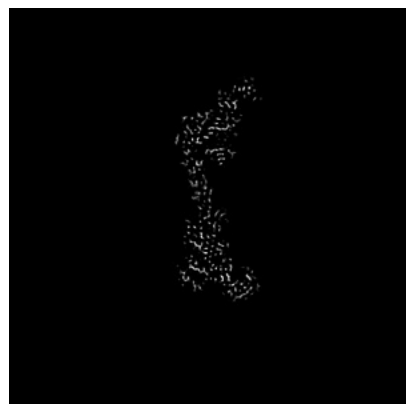


Z Index: 240

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: 250



Y Index: 228

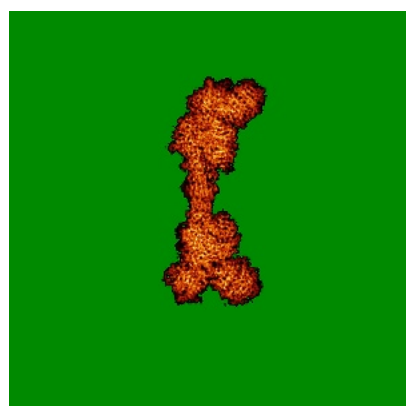


Z Index: 166

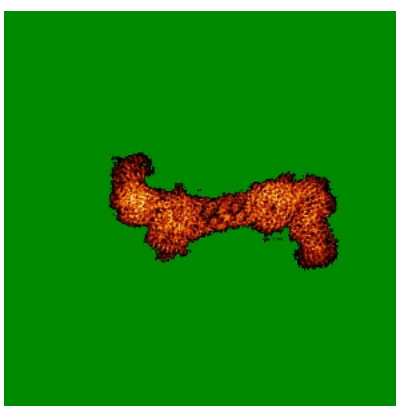
The images above show the largest variance slices of the map in three orthogonal directions.

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

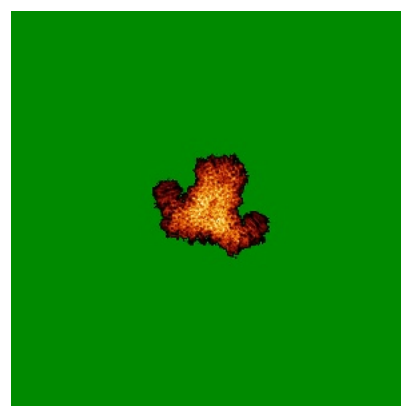
6.4.1 Primary map



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

This section was not generated.

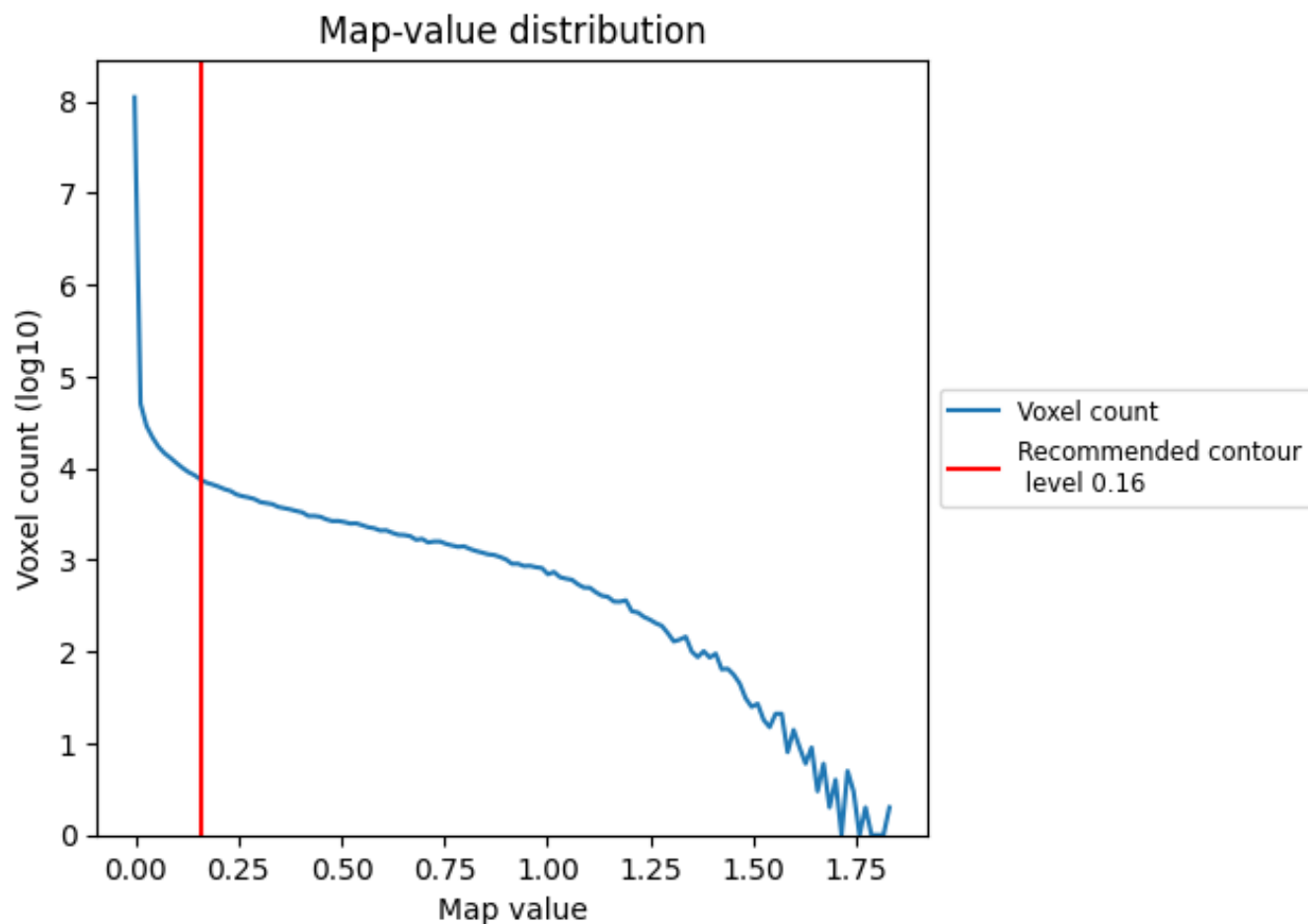
6.6 Mask visualisation

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

7 Map analysis [i](#)

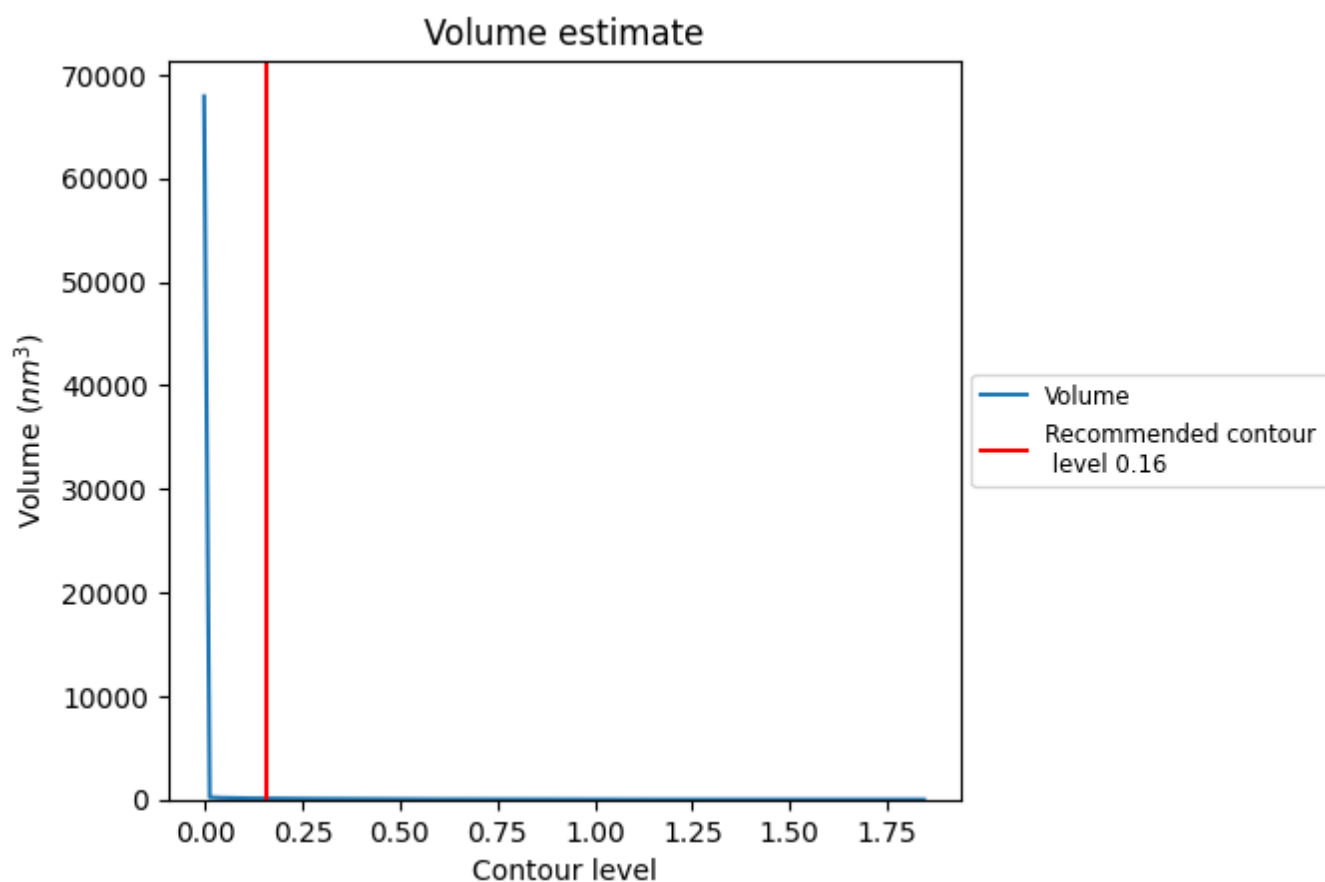
This section contains the results of statistical analysis of the map.

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.

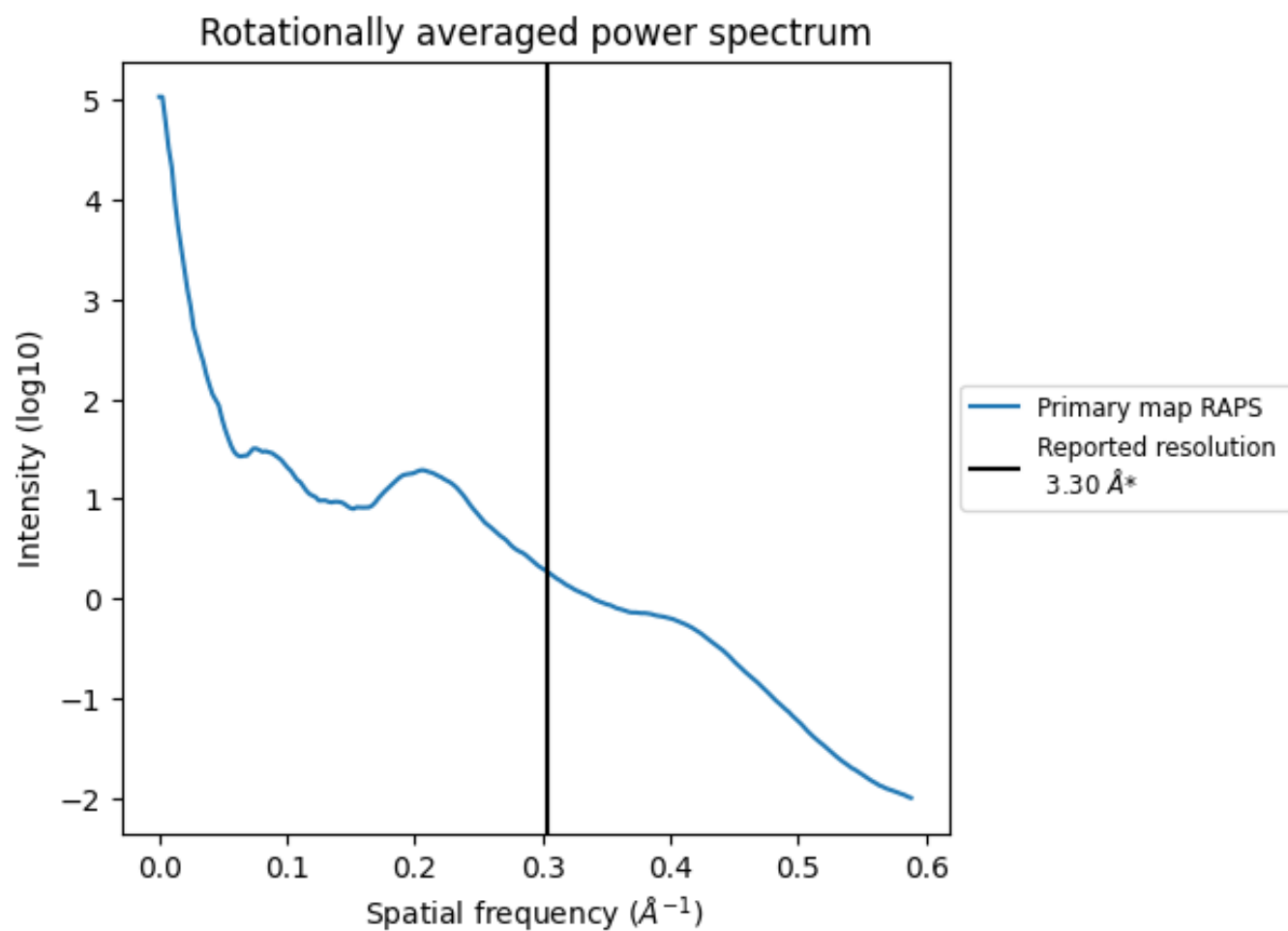
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 103 nm³; this corresponds to an approximate mass of 93 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 0.303 Å⁻¹

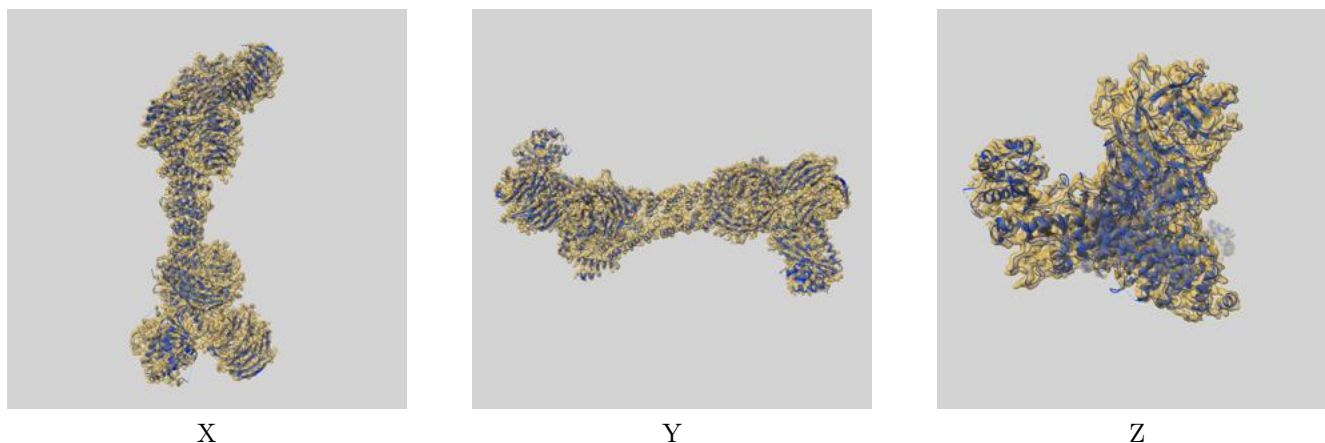
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

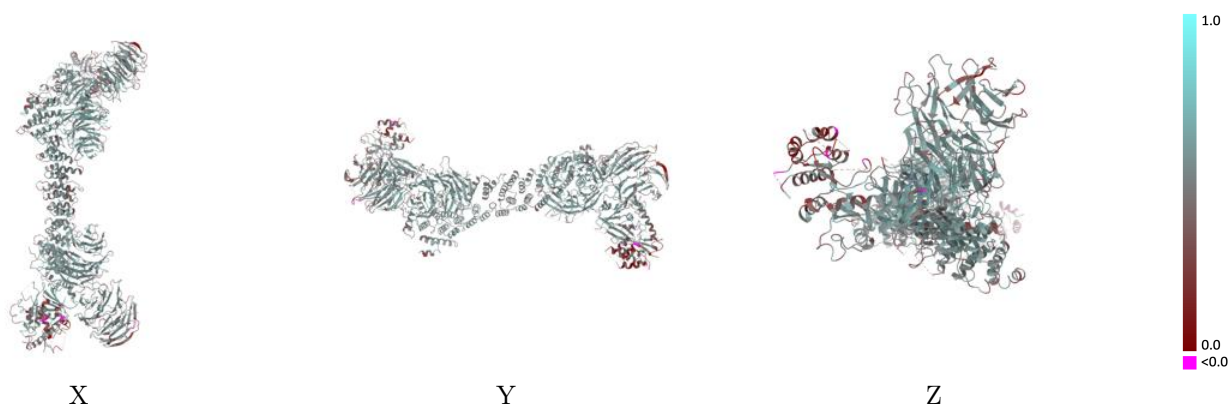
This section contains information regarding the fit between EMDB map EMD-39863 and PDB model 8Z9M. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.16 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](#)

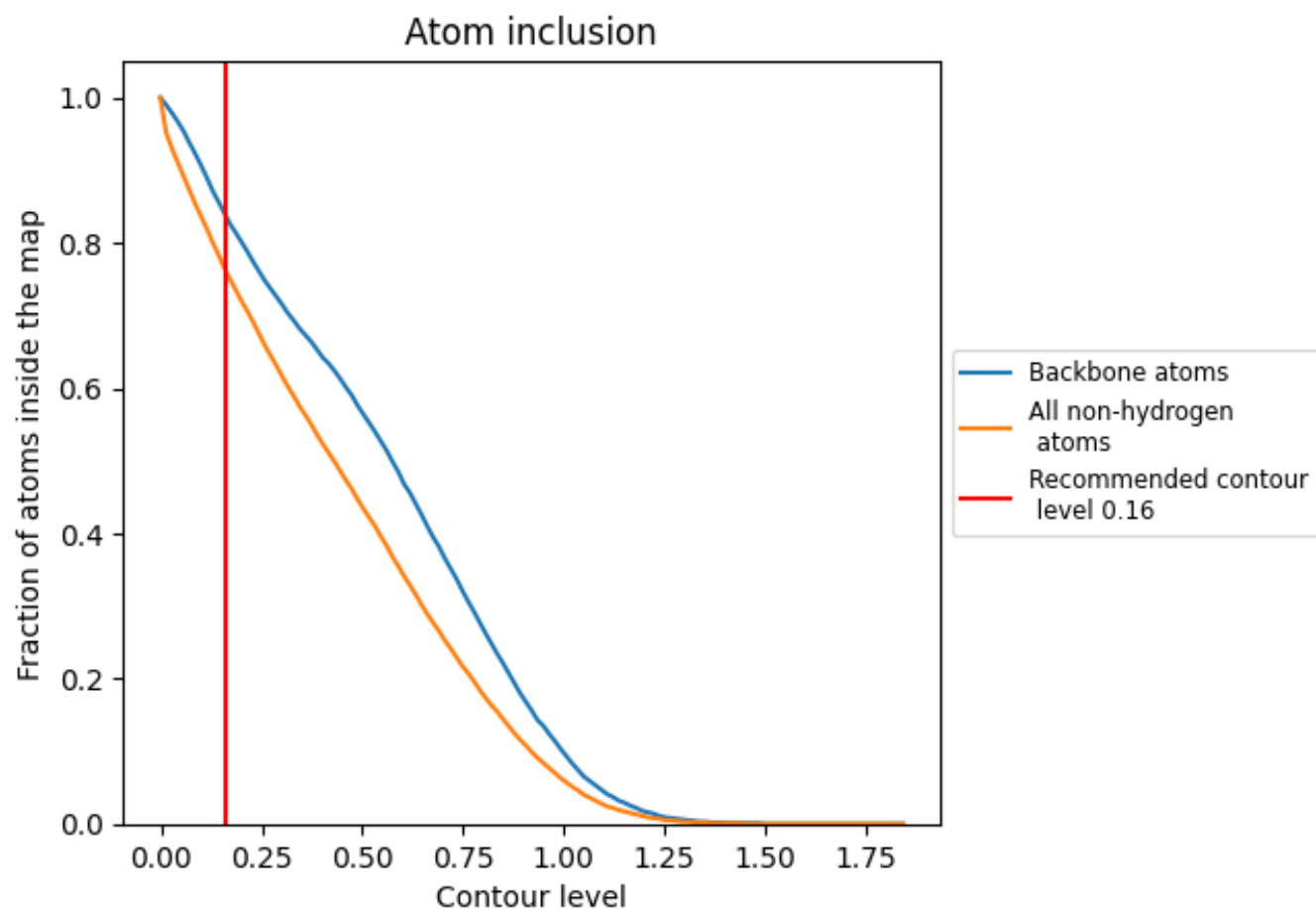


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 76% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7620	0.5010
A	0.7000	0.4590
B	0.7830	0.5100
C	0.6840	0.4510
D	0.7850	0.5200

