



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 02:59 AM UTC

PDB ID : 6YLF / pdb_00006ylf
EMDB ID : EMD-10837
Title : Rix1-Rea1 pre-60S particle - Rea1, body 3 (rigid body refinement, composite structure of Rea1 ring and tail)
Authors : Kater, L.; Beckmann, R.
Deposited on : 2020-04-07
Resolution : 4.20 Å (reported)
Based on initial models : 6OR5, 6HYD, 6QTA, 6HYP

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

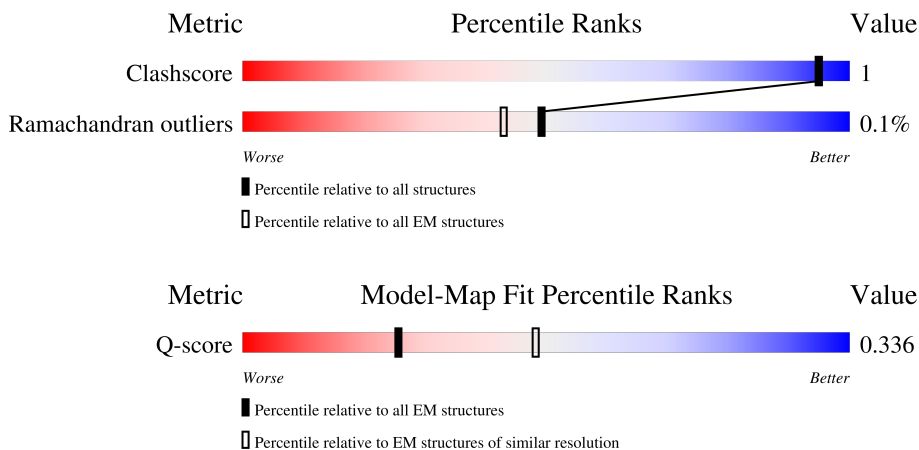
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	AP1	4910	
2	xP1	515	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18362 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.

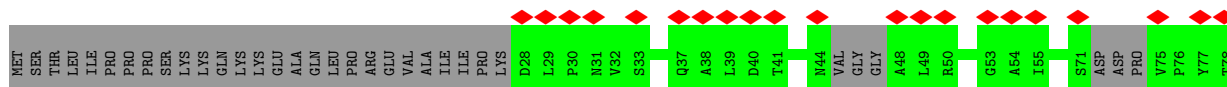
- Molecule 1 is a protein called Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	AP1	3629	Total	C	N	O	0	0
			18010	10752	3629	3629		

- Molecule 2 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	xP1	71	Total	C	N	O	0	0
			352	210	71	71		





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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	55397	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 ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.143	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	370.65, 370.65, 370.65	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	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	AP1	0.30	0/17970	0.68	3/25013 (0.0%)
2	xP1	0.26	0/346	0.56	0/473
All	All	0.30	0/18316	0.68	3/25486 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AP1	0	14

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	AP1	3567	PRO	N-CA-CB	7.94	111.14	102.72
1	AP1	3594	PRO	N-CA-CB	7.11	110.72	103.25
1	AP1	255	ILE	CA-C-O	-5.47	114.64	120.39

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AP1	1742	PRO	Peptide
1	AP1	1850	HIS	Peptide
1	AP1	2147	PRO	Peptide
1	AP1	223	LEU	Peptide
1	AP1	2443	ASN	Peptide
1	AP1	2595	LEU	Peptide
1	AP1	2972	PRO	Peptide
1	AP1	3515	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	AP1	4000	LEU	Peptide
1	AP1	406	GLU	Peptide
1	AP1	4749	GLY	Peptide
1	AP1	947	ASN	Peptide
1	AP1	948	THR	Peptide
1	AP1	95	ILE	Peptide

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	AP1	18010	0	7839	27	0
2	xP1	352	0	145	1	0
All	All	18362	0	7984	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 1.

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:AP1:263:LYS:HA	1:AP1:274:LYS:O	1.74	0.87
1:AP1:263:LYS:CA	1:AP1:274:LYS:O	2.40	0.69
1:AP1:263:LYS:CB	1:AP1:274:LYS:O	2.45	0.65
1:AP1:1779:LEU:O	1:AP1:1783:PHE:N	2.30	0.64
1:AP1:2178:GLU:O	1:AP1:2182:GLU:N	2.37	0.57
1:AP1:1237:ILE:O	1:AP1:1241:TYR:N	2.36	0.57
1:AP1:447:MET:O	1:AP1:451:ARG:N	2.39	0.56
1:AP1:1401:GLY:O	1:AP1:1405:GLY:N	2.39	0.55
1:AP1:2043:ALA:O	1:AP1:2047:ASN:N	2.41	0.54
1:AP1:3789:HIS:O	1:AP1:3793:LYS:N	2.40	0.53
1:AP1:1900:TYR:O	1:AP1:1902:SER:N	2.43	0.52
1:AP1:540:ILE:O	1:AP1:544:VAL:N	2.42	0.49
1:AP1:2871:VAL:O	1:AP1:2875:GLU:N	2.42	0.49
1:AP1:2227:SER:O	1:AP1:2234:SER:N	2.45	0.47
1:AP1:2861:ILE:O	1:AP1:2865:THR:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP1:2470:ARG:O	1:AP1:2474:ASN:N	2.42	0.47
1:AP1:1888:THR:O	1:AP1:1891:ASP:N	2.48	0.46
1:AP1:1314:GLU:O	1:AP1:1318:LYS:N	2.48	0.46
1:AP1:2218:SER:O	1:AP1:2220:SER:N	2.49	0.46
1:AP1:978:TYR:O	1:AP1:982:ARG:N	2.48	0.45
2:xP1:81:CYS:N	2:xP1:90:ASP:O	2.49	0.45
1:AP1:474:PHE:O	1:AP1:476:ILE:N	2.49	0.44
1:AP1:2785:VAL:O	1:AP1:2789:SER:N	2.48	0.43
1:AP1:1873:LYS:O	1:AP1:1877:ASN:N	2.50	0.43
1:AP1:2149:LYS:O	1:AP1:2152:ASP:N	2.53	0.42
1:AP1:263:LYS:O	1:AP1:274:LYS:N	2.53	0.42
1:AP1:2415:TYR:O	1:AP1:2418:ALA:N	2.53	0.41
1:AP1:3305:VAL:O	1:AP1:3309:LEU:N	2.53	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	AP1	3549/4910 (72%)	3232 (91%)	313 (9%)	4 (0%)	48	82
2	xP1	59/515 (12%)	53 (90%)	6 (10%)	0	100	100
All	All	3608/5425 (66%)	3285 (91%)	319 (9%)	4 (0%)	49	82

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AP1	241	PRO
1	AP1	3594	PRO
1	AP1	280	ASP
1	AP1	948	THR

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AP1	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AP1	3595:LEU	C	3599:ARG	N	4.97
1	AP1	3575:LEU	C	3579:VAL	N	3.43
1	AP1	3587:MET	C	3591:ARG	N	3.23

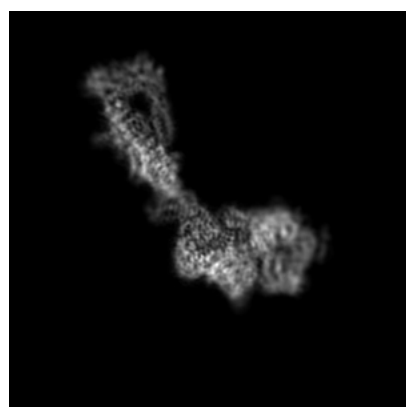
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10837. These allow visual inspection of the internal detail of the map and identification of artifacts.

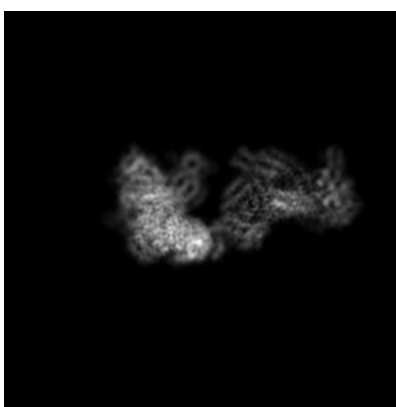
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

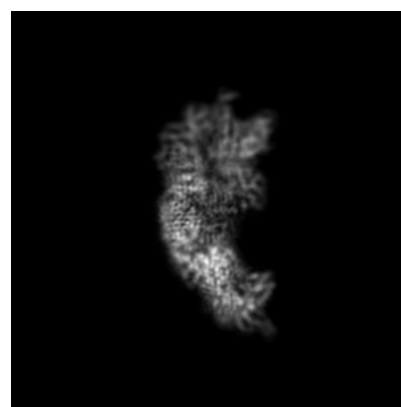
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

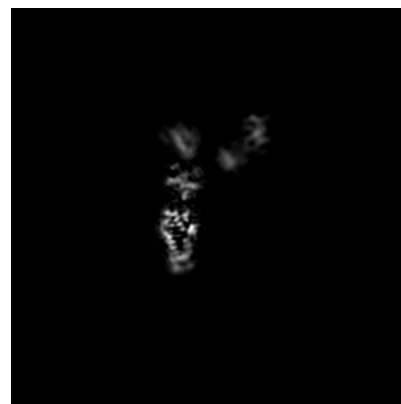
6.2.1 Primary map



X Index: 175



Y Index: 175



Z Index: 175

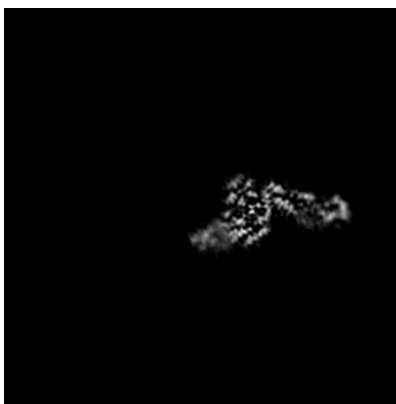
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

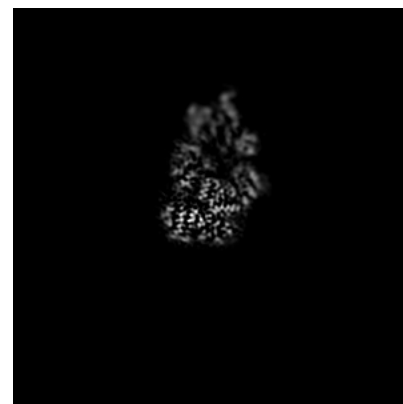
6.3.1 Primary map



X Index: 188



Y Index: 132

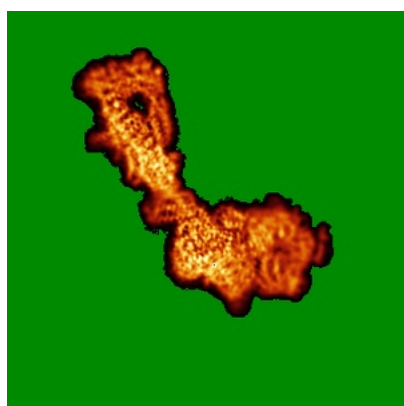


Z Index: 133

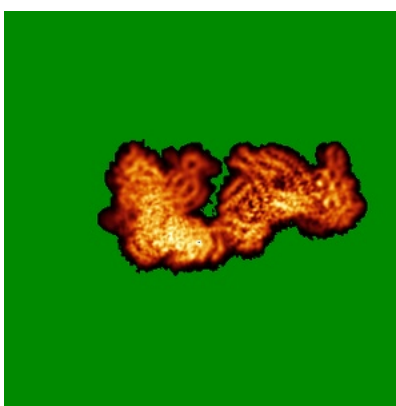
The images above show the largest variance slices of the map in three orthogonal directions.

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

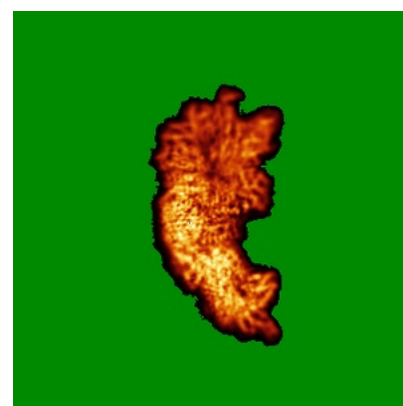
6.4.1 Primary map



X



Y

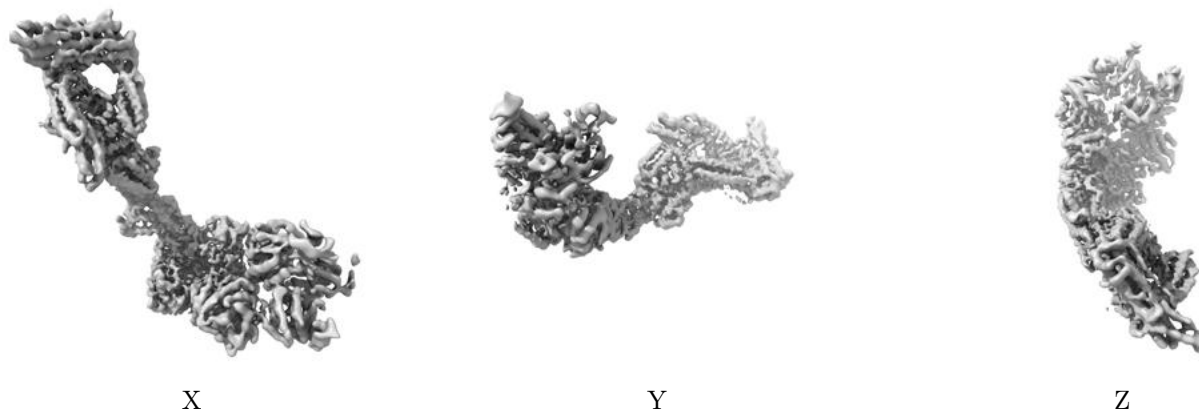


Z

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

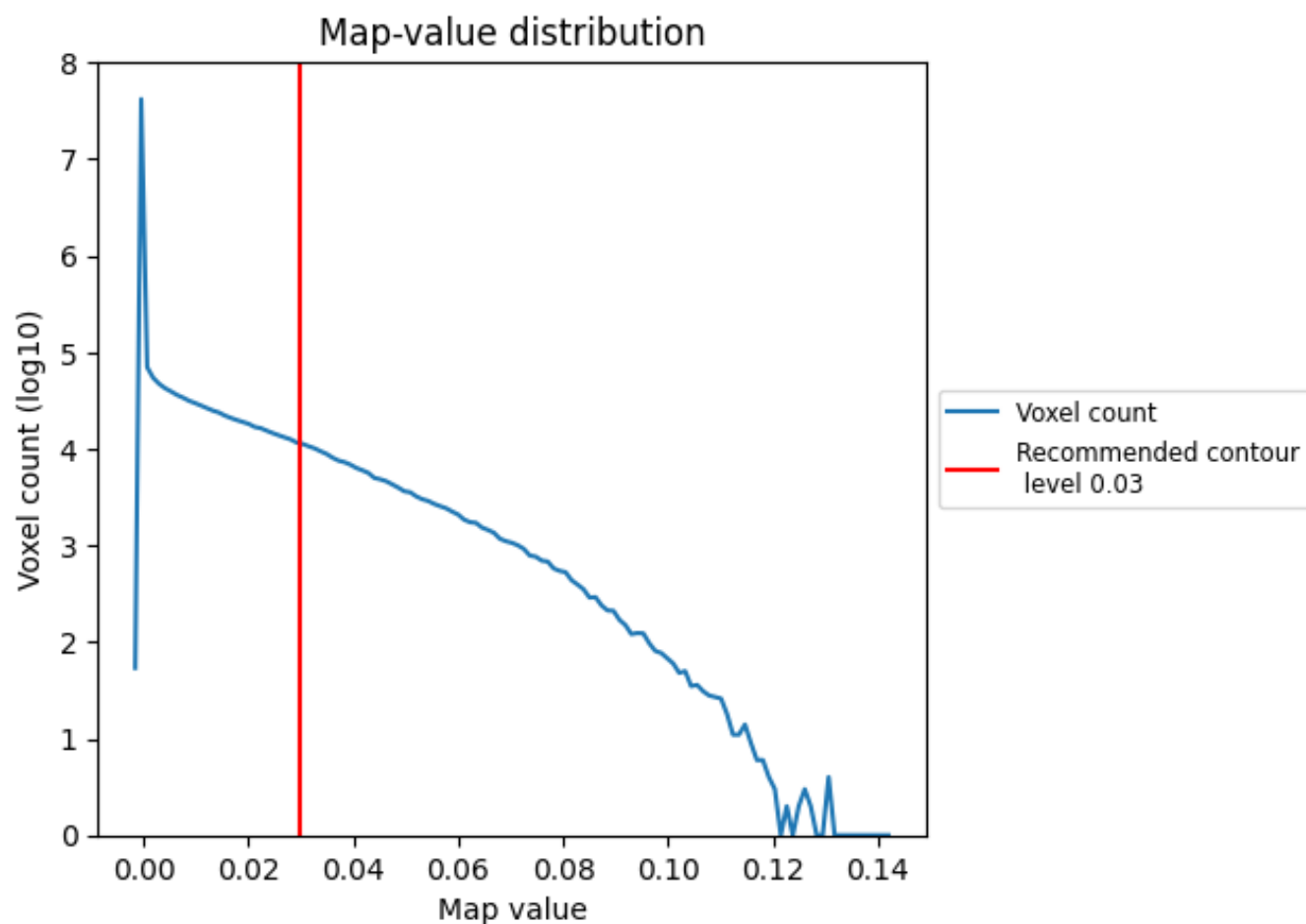
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

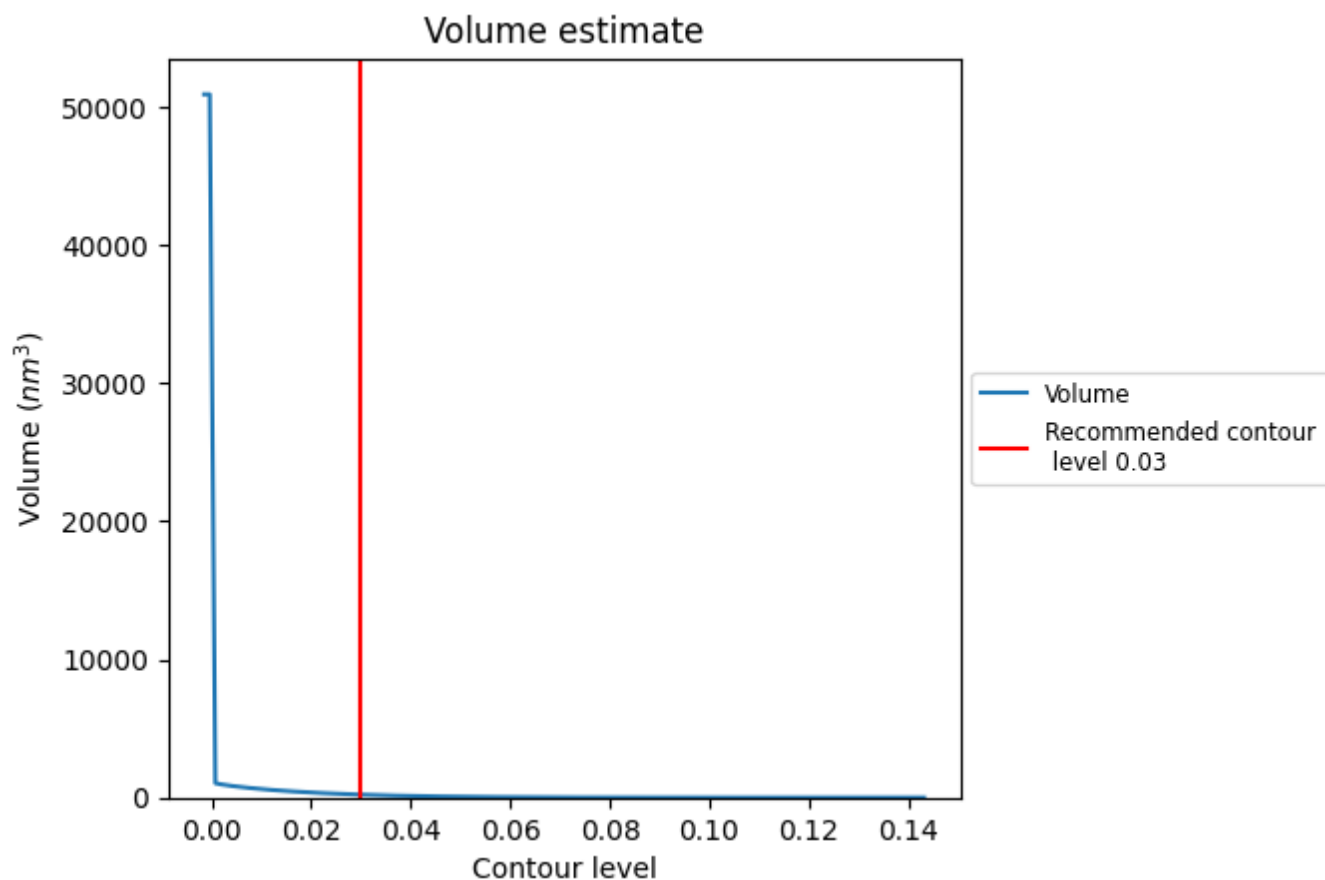
This section contains the results of statistical analysis of the map.

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.

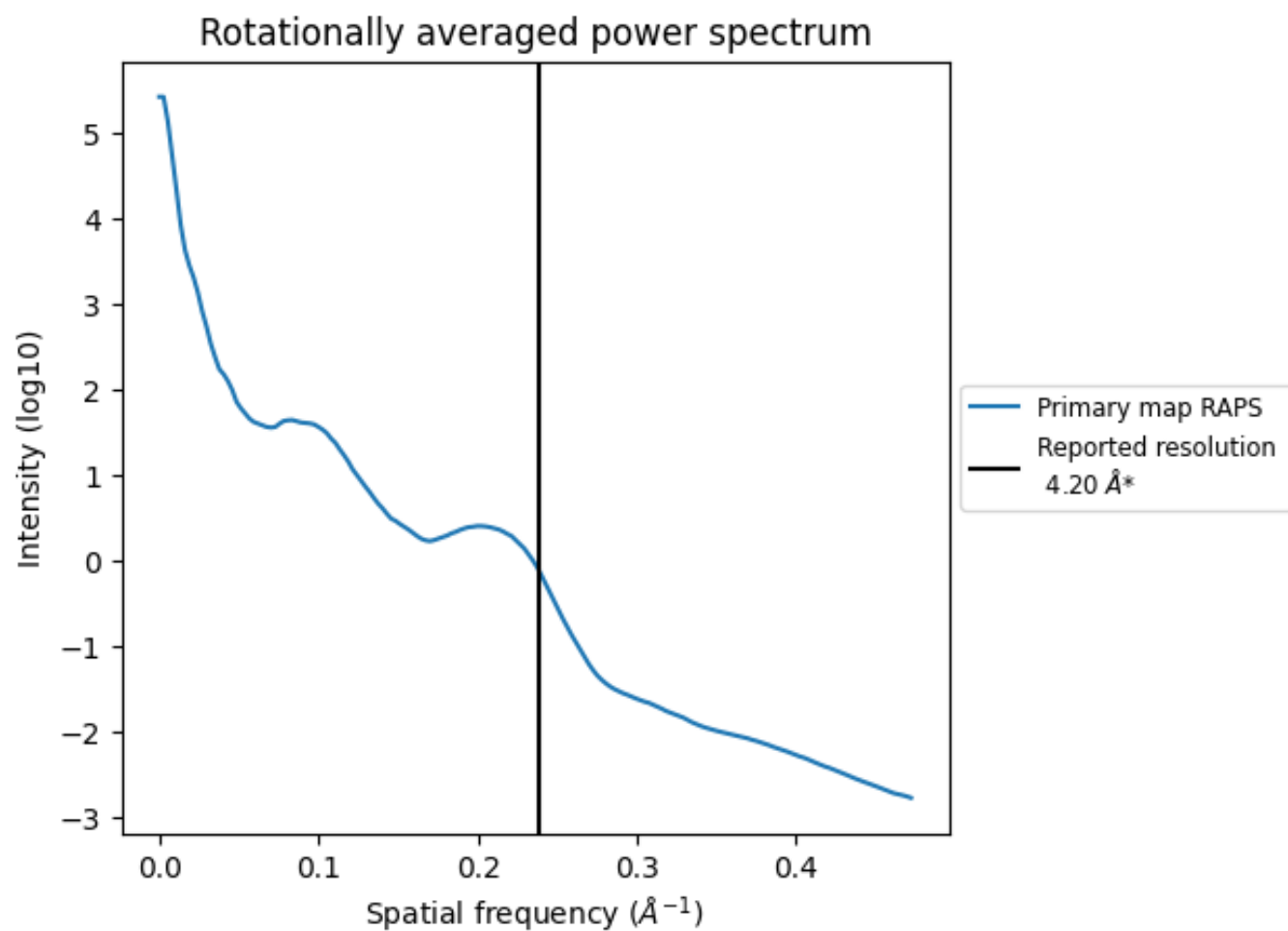
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 210 nm³; this corresponds to an approximate mass of 189 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.

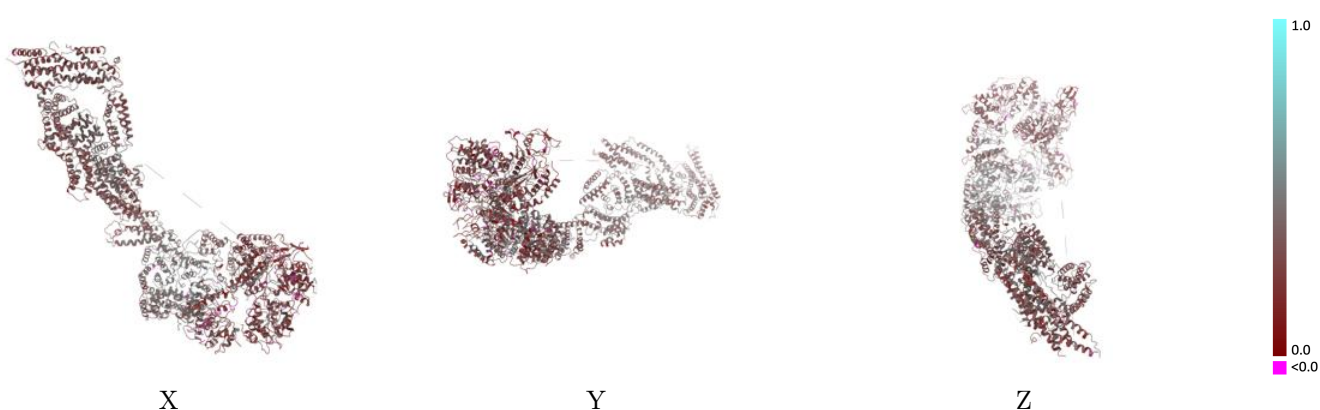
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10837 and PDB model 6YLF. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

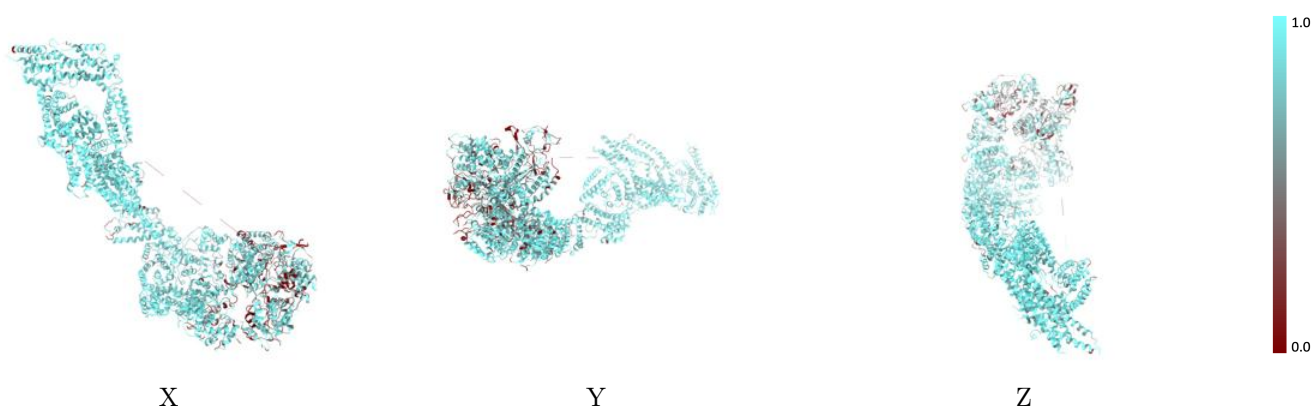
This section was not generated.

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



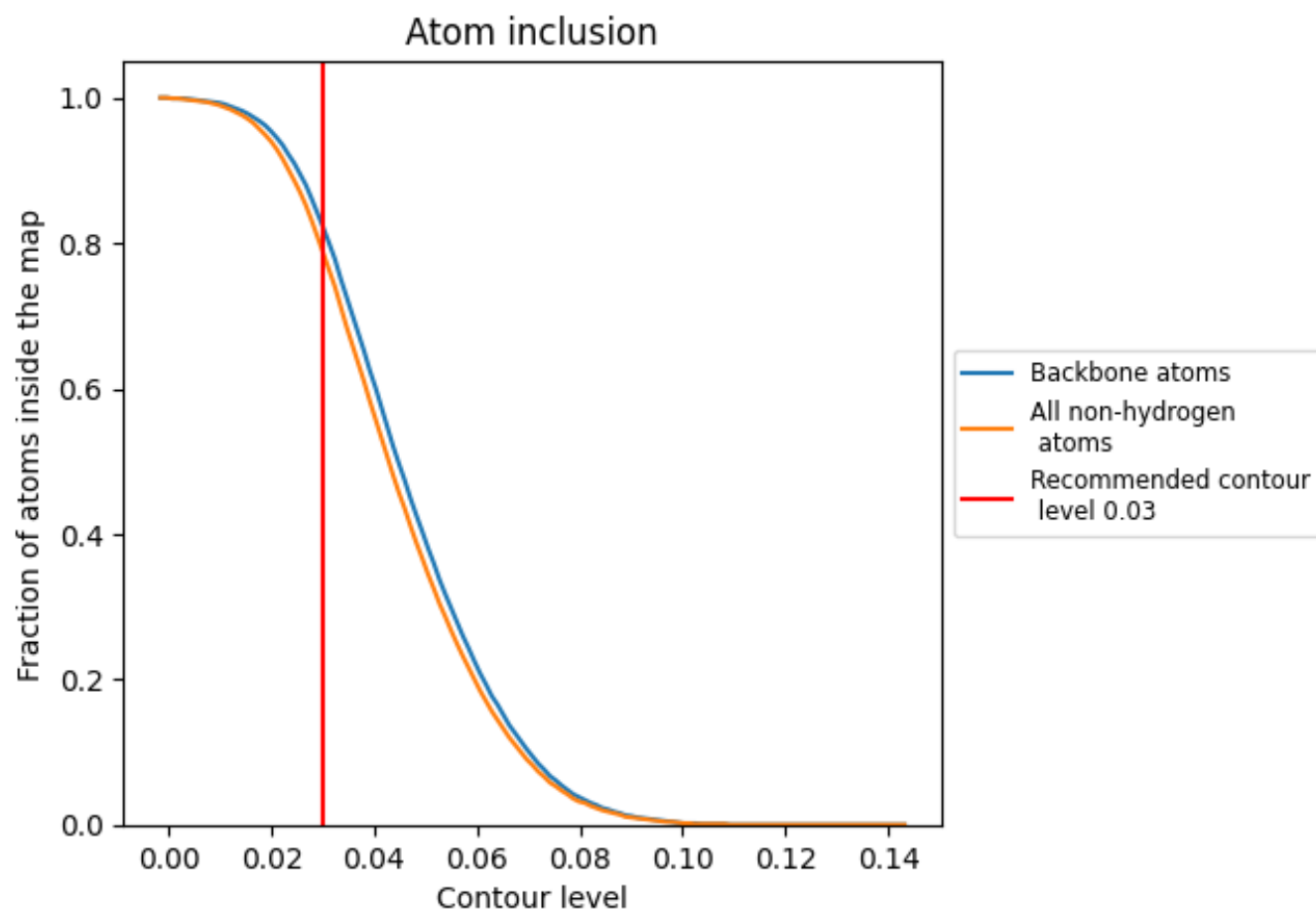
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 79% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7890	0.3360
AP1	0.7950	0.3380
xP1	0.4800	0.2400

