



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 04:02 PM UTC

PDB ID : 6C24 / pdb_00006c24
EMDB ID : EMD-7335
Title : Cryo-EM structure of PRC2 bound to cofactors AEBP2 and JARID2 in the Extended Active State
Authors : Kasinath, V.; Faini, M.; Poepsel, S.; Reif, D.; Feng, A.; Stjepanovic, G.; Aebersold, R.; Nogales, E.
Deposited on : 2018-01-06
Resolution : 3.50 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
Mogul : 2022.3.0, CSD as543be (2022)
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

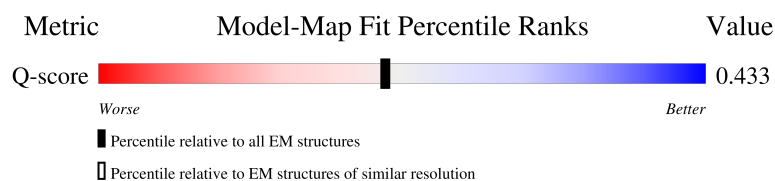
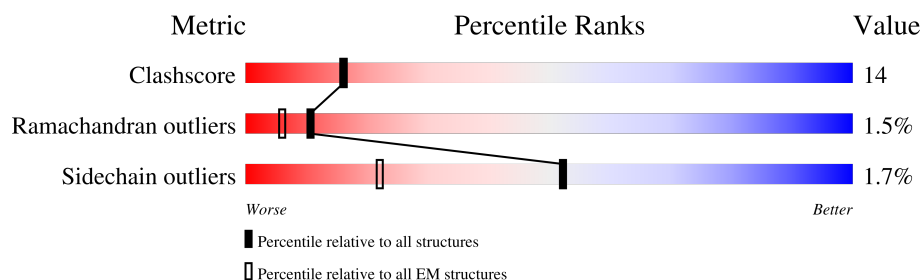
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	739	
1	M	739	
1	Q	739	
2	B	345	

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Mol	Chain	Length	Quality of chain
3	E	345	92%
4	C	746	7% 17% 80%
4	K	746	35% 8% 56%
5	L	441	55% 25% 18%
6	N	425	64% 24% 9%
7	O	7	57% 86% 14%
8	P	295	19% 78%
9	Z	135	80% 20%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 13346 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 Polycomb protein SUZ12.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	123	Total	C	N	O	S	0	0
			867	555	157	149	6		
1	M	122	Total	C	N	O	S	0	0
			962	609	169	175	9		
1	Q	66	Total	C	N	O	S	0	0
			496	315	94	85	2		

- Molecule 2 is a protein called Protein Jumonji.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	7	Total	C	N	O	0	0
			52	35	9	8		

- Molecule 3 is a protein called Protein Jumonji.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	27	Total	C	N	O	S	0	0
			184	112	32	39	1		

- Molecule 4 is a protein called Histone-lysine N-methyltransferase EZH2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	325	Total	C	N	O	S	0	0
			2406	1514	426	436	30		
4	C	148	Total	C	N	O	S	0	0
			1227	779	218	223	7		

- Molecule 5 is a protein called Polycomb protein EED.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	362	Total	C	N	O	S	0	0
			2881	1829	506	526	20		

- Molecule 6 is a protein called Histone-binding protein RBBP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	386	Total	C	N	O	S	0	0
			3062	1933	524	595	10		

- Molecule 7 is a protein called JARID2-substrate.

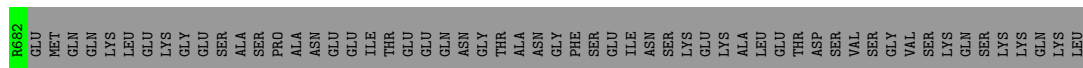
Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	7	Total	C	N	O	0	0
			51	33	11	7		

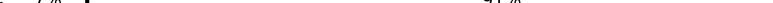
- Molecule 8 is a protein called Zinc finger protein AEBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	64	Total	C	N	O	S	0	0
			484	304	91	87	2		

- Molecule 9 is a protein called SUZ12.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Z	135	Total	C	N	O	0	0
			674	404	135	135		



Chain Q:  7% 91%

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

- Molecule 2: Protein Jumonji

Chain B: 98%

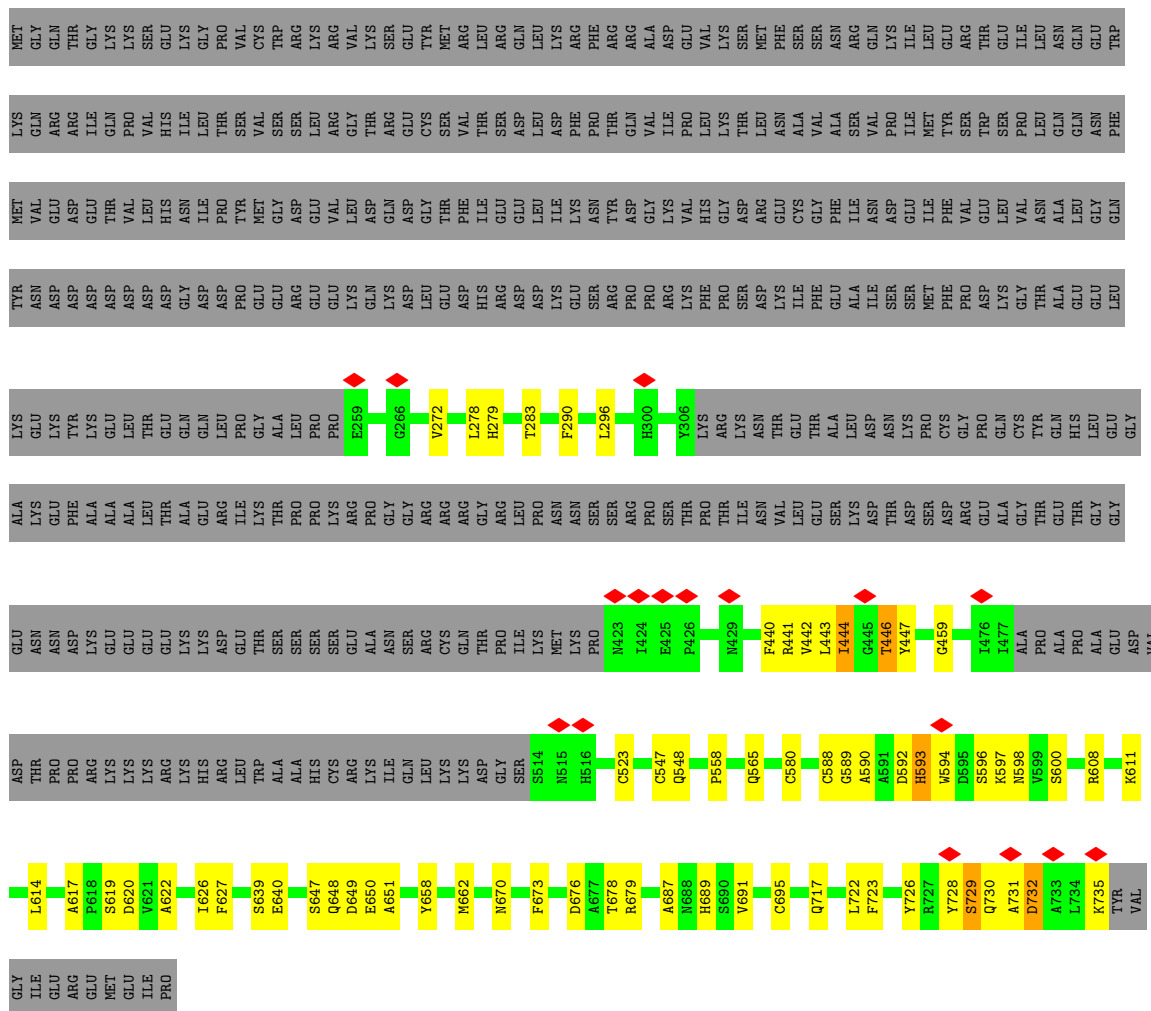
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- Molecule 3: Protein Jumonji

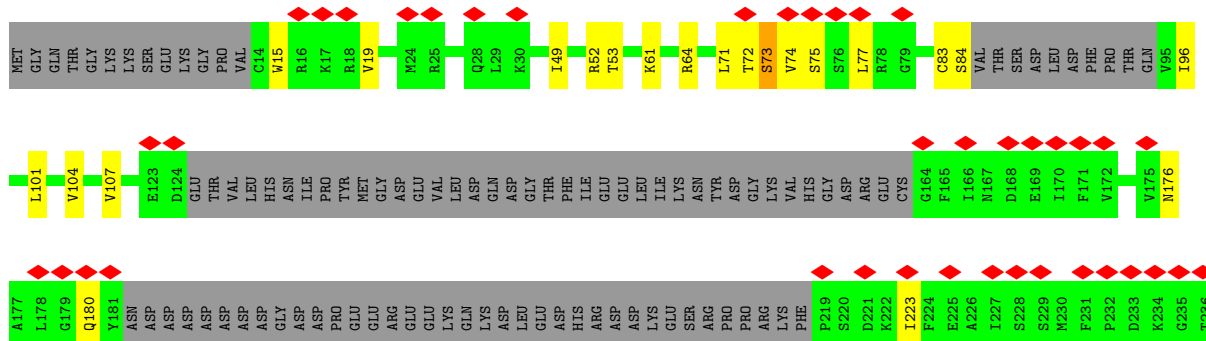
Chain E: 92%

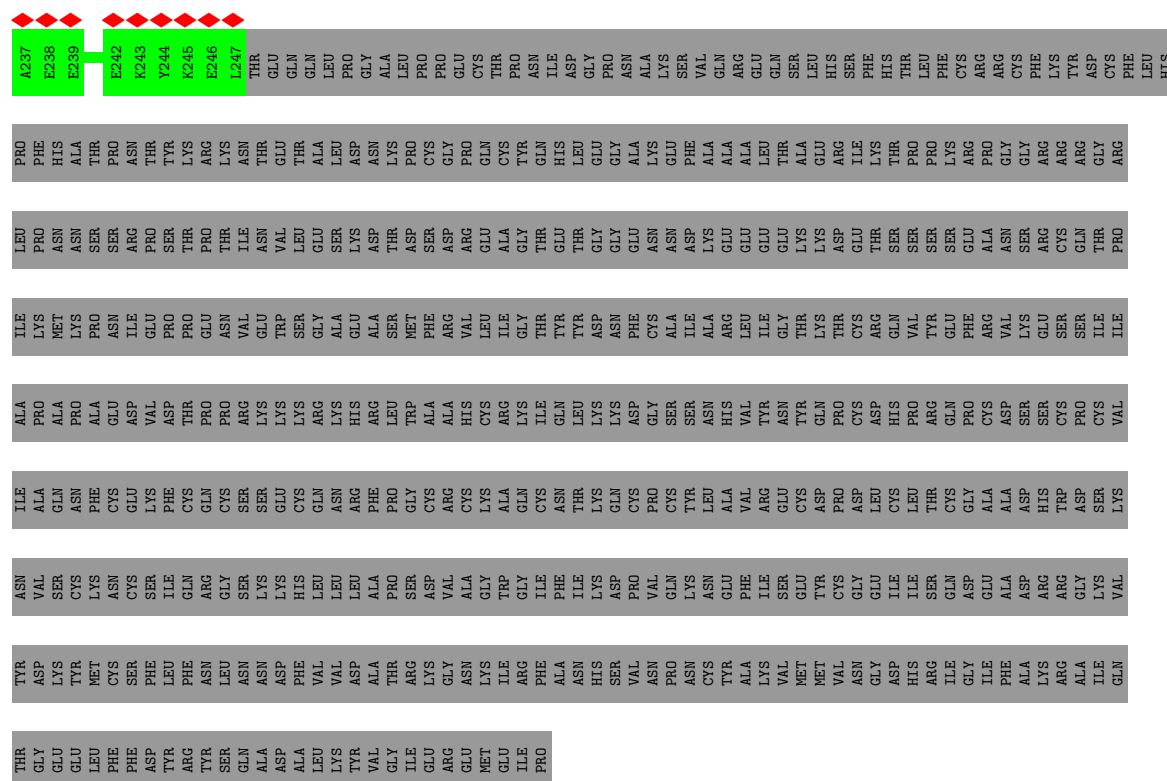
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Chain K:

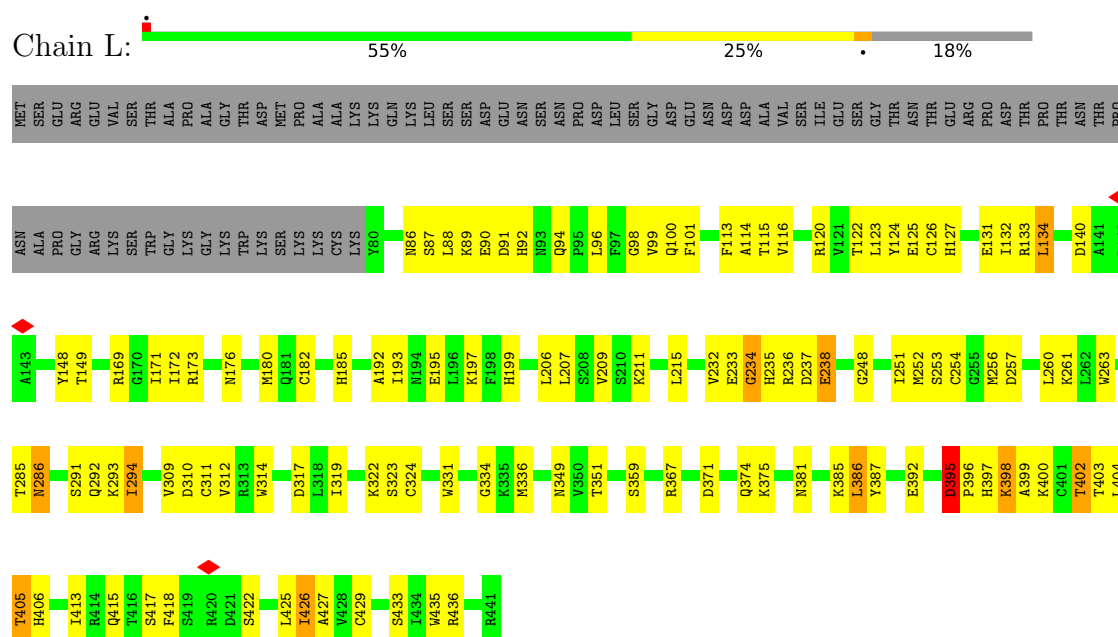


Chain C:

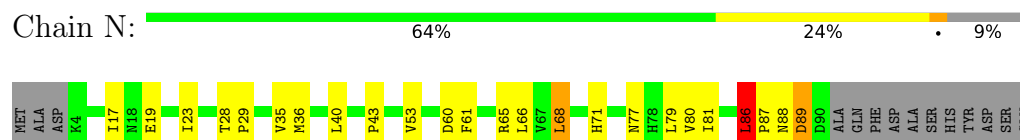


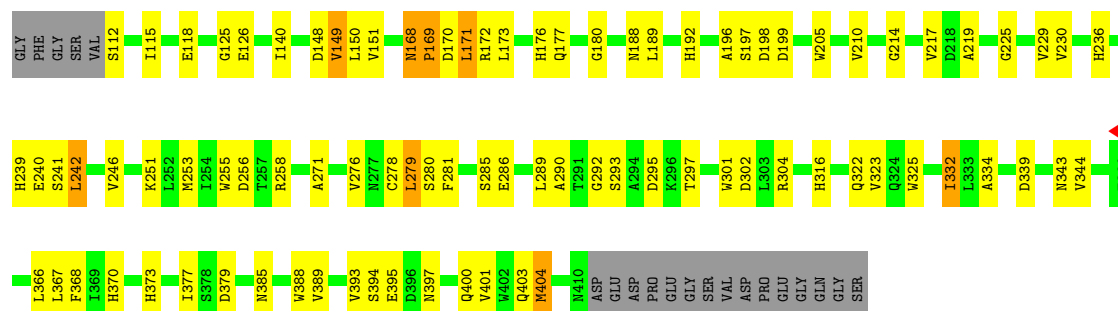


- Molecule 5: Polycomb protein EED

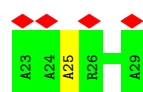
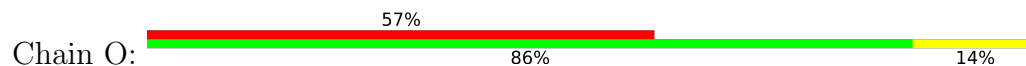


- Molecule 6: Histone-binding protein RBBP4

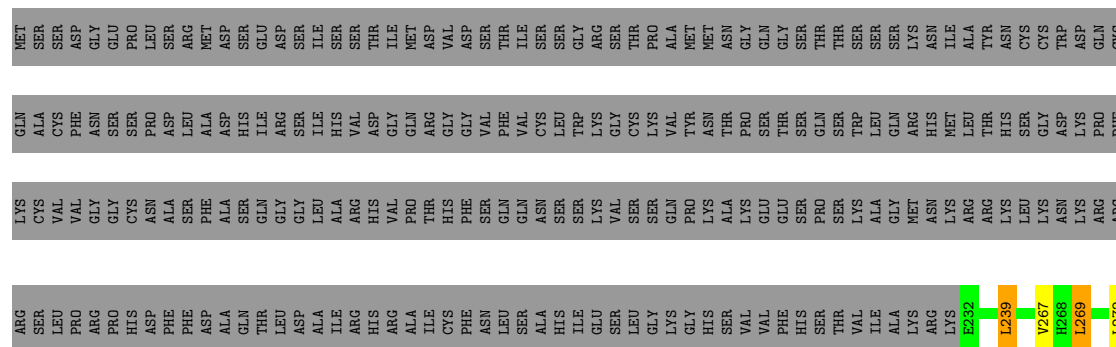




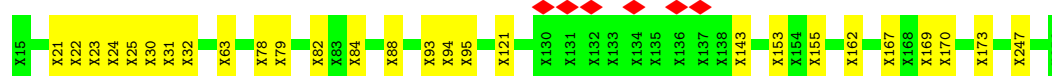
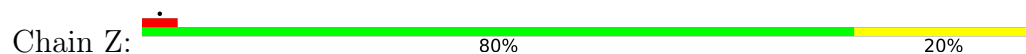
- Molecule 7: JARID2-substrate



- Molecule 8: Zinc finger protein AEBP2



- Molecule 9: SUZ12



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	249696	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.378	Depositor
Minimum map value	-0.202	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0383	Depositor
Map size ($\text{\AA}$)	241.92, 241.92, 241.92	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.84, 0.84, 0.84	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: M3L

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	0.69	0/890	0.99	1/1219 (0.1%)
1	M	0.60	0/983	0.98	1/1328 (0.1%)
1	Q	1.17	3/506 (0.6%)	1.12	3/687 (0.4%)
2	B	0.41	0/40	0.42	0/53
3	E	0.71	0/185	1.44	6/250 (2.4%)
4	C	0.56	0/1247	0.85	3/1669 (0.2%)
4	K	0.56	0/2466	0.82	5/3352 (0.1%)
5	L	0.85	0/2956	0.96	5/4012 (0.1%)
6	N	0.87	2/3146 (0.1%)	0.94	7/4291 (0.2%)
7	O	0.61	0/51	0.62	0/66
8	P	0.65	0/492	1.04	1/666 (0.2%)
All	All	0.76	5/12962 (0.0%)	0.94	32/17593 (0.2%)

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	A	0	4
1	M	0	1
4	K	0	1
5	L	0	1
6	N	0	1
8	P	0	1
9	Z	0	1
All	All	0	10

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	146	GLY	C-O	16.95	1.57	1.23
1	Q	146	GLY	N-CA	6.85	1.56	1.45
1	Q	146	GLY	CA-C	6.72	1.64	1.52
6	N	334	ALA	CA-C	-5.60	1.45	1.52
6	N	36	MET	CA-C	-5.39	1.47	1.53

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	405	THR	N-CA-C	14.13	126.25	108.45
4	C	73	SER	N-CA-C	-8.62	92.82	107.99
4	K	444	ILE	N-CA-C	8.60	118.61	110.53
3	E	157	PHE	N-CA-C	-8.36	98.11	110.23
5	L	395	ASP	C-N-CD	6.96	135.92	120.60

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	441	GLN	Peptide
1	A	478	TYR	Peptide
1	A	480	TYR	Peptide
1	A	481	HIS	Peptide
4	K	723	PHE	Peptide

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	867	0	736	21	0
1	M	962	0	898	18	0
1	Q	496	0	450	10	0
2	B	52	0	49	0	0
3	E	184	0	172	11	0
4	C	1227	0	1249	16	0
4	K	2406	0	2120	71	0
5	L	2881	0	2760	131	0
6	N	3062	0	2908	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	O	51	0	54	10	0
8	P	484	0	476	6	0
9	Z	674	0	166	19	0
All	All	13346	0	12038	363	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 14.

The worst 5 of 363 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)
9:Z:25:UNK:CB	9:Z:247:UNK:H	1.19	1.50
4:K:728:TYR:CE1	7:O:25:ALA:HB1	1.52	1.42
9:Z:25:UNK:CB	9:Z:247:UNK:N	1.76	1.37
4:K:440:PHE:O	4:K:444:ILE:HG12	1.23	1.36
4:K:728:TYR:CE1	7:O:25:ALA:CB	2.10	1.33

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	A	121/739 (16%)	85 (70%)	30 (25%)	6 (5%)	1	15
1	M	120/739 (16%)	105 (88%)	13 (11%)	2 (2%)	7	35
1	Q	64/739 (9%)	45 (70%)	18 (28%)	1 (2%)	7	36
2	B	4/345 (1%)	4 (100%)	0	0	100	100
3	E	25/345 (7%)	15 (60%)	6 (24%)	4 (16%)	0	2
4	C	140/746 (19%)	128 (91%)	12 (9%)	0	100	100
4	K	319/746 (43%)	275 (86%)	41 (13%)	3 (1%)	14	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	L	360/441 (82%)	299 (83%)	57 (16%)	4 (1%)	11	43
6	N	382/425 (90%)	326 (85%)	53 (14%)	3 (1%)	16	49
7	O	5/7 (71%)	4 (80%)	1 (20%)	0	100	100
8	P	62/295 (21%)	43 (69%)	18 (29%)	1 (2%)	7	36
All	All	1602/5567 (29%)	1329 (83%)	249 (16%)	24 (2%)	11	37

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	442	THR
1	A	481	HIS
3	E	160	PHE
5	L	238	GLU
1	M	581	VAL

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	73/646 (11%)	72 (99%)	1 (1%)	59	71
1	M	101/646 (16%)	101 (100%)	0	100	100
1	Q	45/646 (7%)	45 (100%)	0	100	100
2	B	2/294 (1%)	2 (100%)	0	100	100
3	E	19/295 (6%)	19 (100%)	0	100	100
4	C	138/667 (21%)	138 (100%)	0	100	100
4	K	233/667 (35%)	232 (100%)	1 (0%)	84	81
5	L	311/392 (79%)	303 (97%)	8 (3%)	40	62
6	N	341/375 (91%)	329 (96%)	12 (4%)	32	57
7	O	3/3 (100%)	3 (100%)	0	100	100
8	P	50/263 (19%)	49 (98%)	1 (2%)	48	67
All	All	1316/4894 (27%)	1293 (98%)	23 (2%)	52	70

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	N	115	ILE
6	N	242	LEU
6	N	230	VAL
6	N	279	LEU
5	L	286	ASN

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	M	655	ASN
6	N	192	HIS
1	Q	120	HIS
6	N	329	ASN
8	P	290	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue 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	$\# Z > 2$
2	M3L	B	116	2	10,11,12	0.57	0	9,14,16	0.46	0

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
2	M3L	B	116	2	-	0/9/10/12	-

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.

5.5 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
9	Z	6

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Z	182:UNK	C	247:UNK	N	39.28
1	Z	45:UNK	C	55:UNK	N	34.04
1	Z	67:UNK	C	77:UNK	N	29.09
1	Z	138:UNK	C	143:UNK	N	26.06
1	Z	99:UNK	C	120:UNK	N	9.78

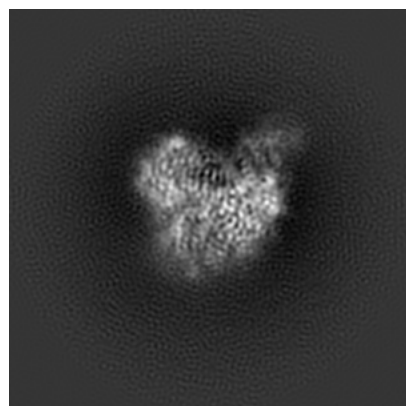
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7335. These allow visual inspection of the internal detail of the map and identification of artifacts.

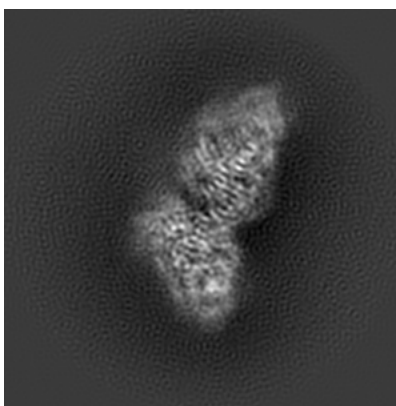
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

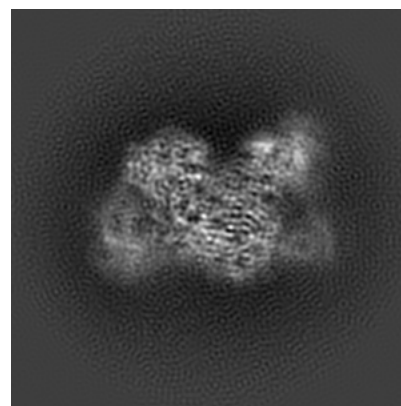
6.1.1 Primary map



X

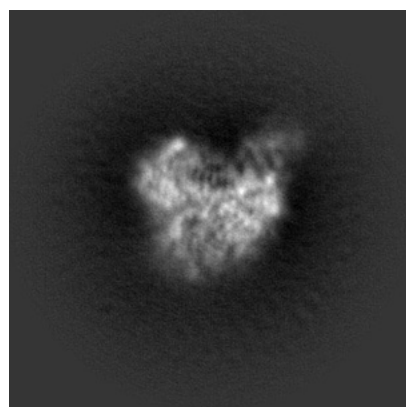


Y

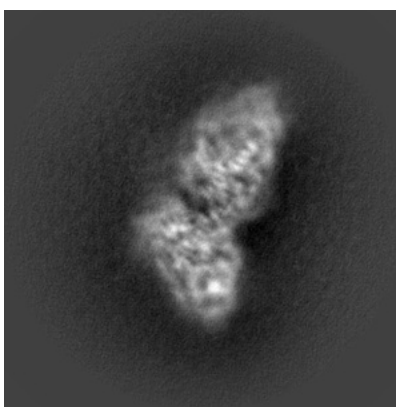


Z

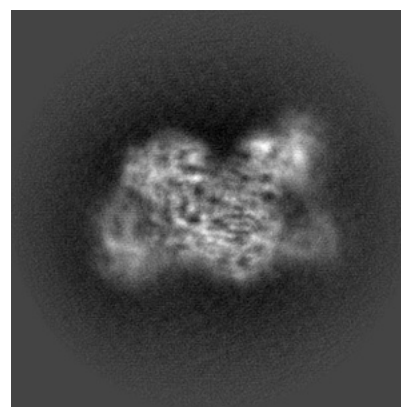
6.1.2 Raw map



X



Y

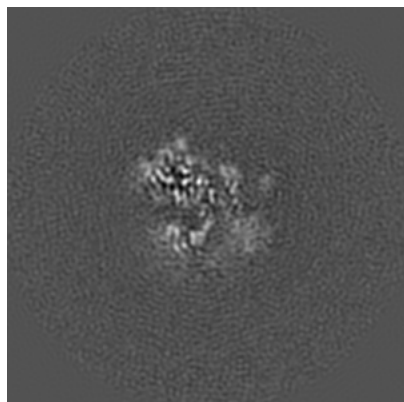


Z

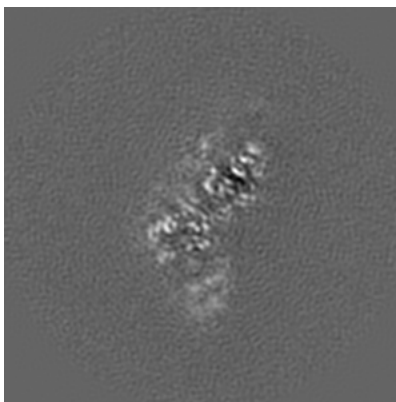
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

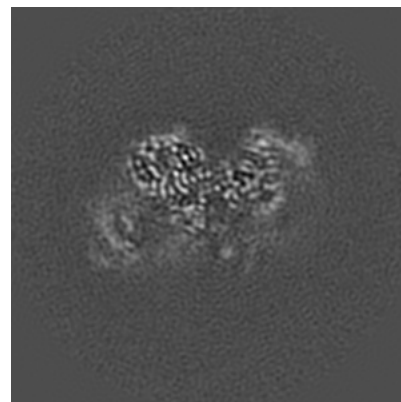
6.2.1 Primary map



X Index: 144

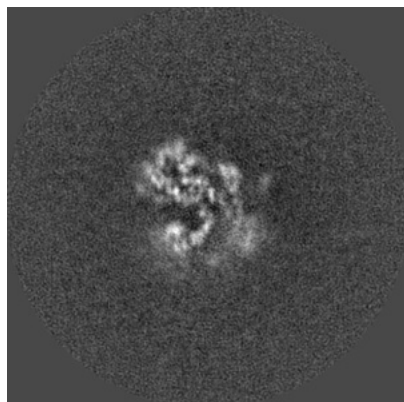


Y Index: 144

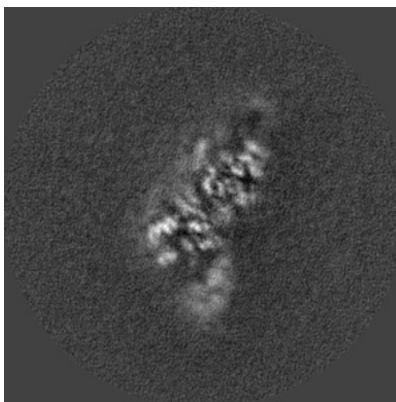


Z Index: 144

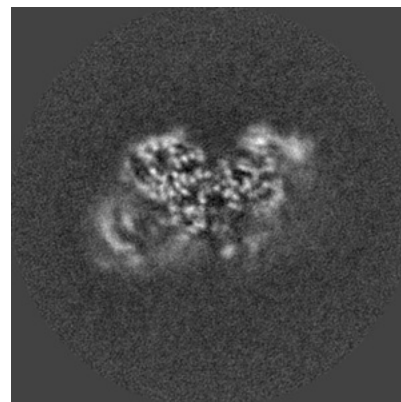
6.2.2 Raw map



X Index: 144



Y Index: 144

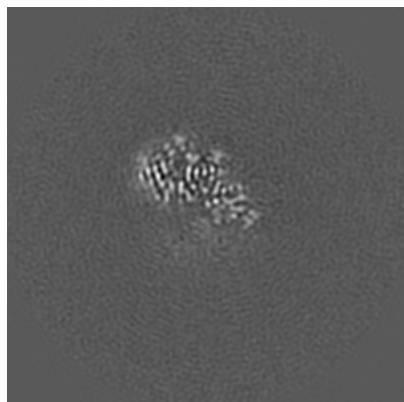


Z Index: 144

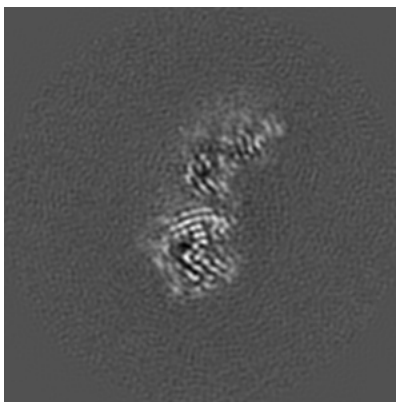
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

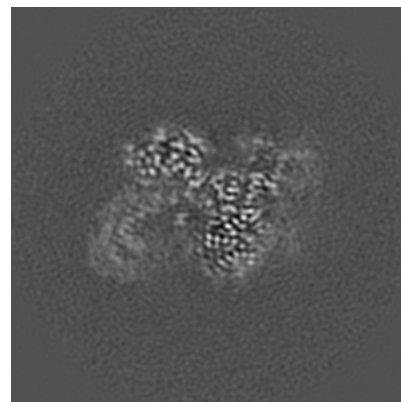
6.3.1 Primary map



X Index: 159

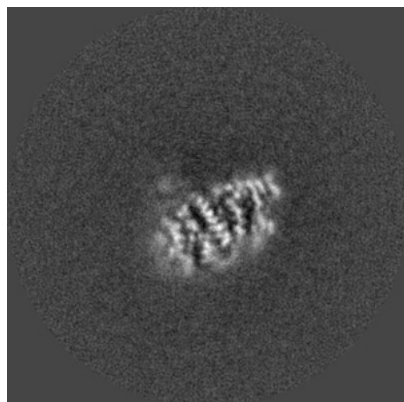


Y Index: 167

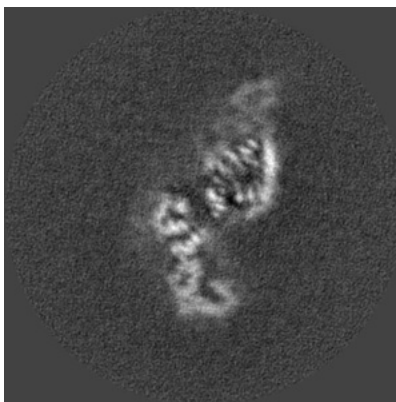


Z Index: 156

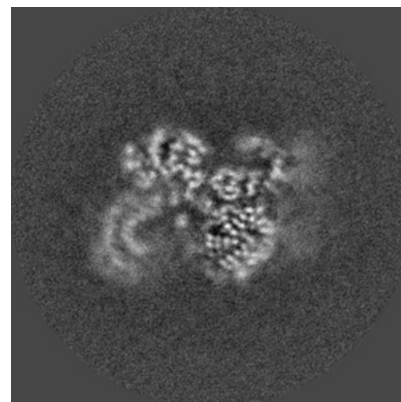
6.3.2 Raw map



X Index: 129



Y Index: 121

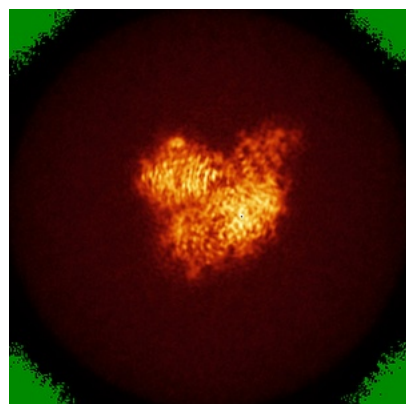


Z Index: 157

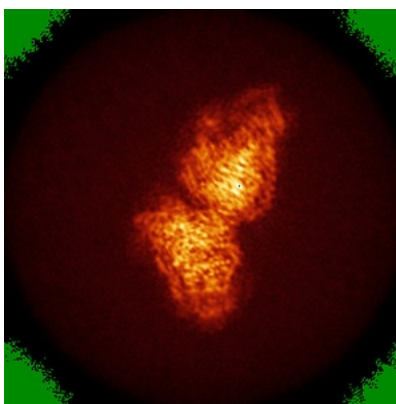
The images above show the largest variance slices of the map in three orthogonal directions.

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

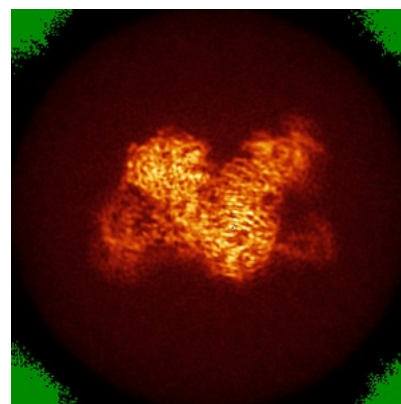
6.4.1 Primary map



X

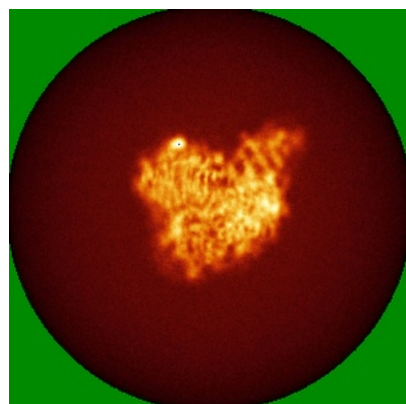


Y

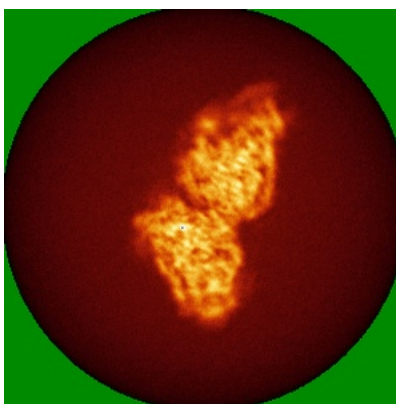


Z

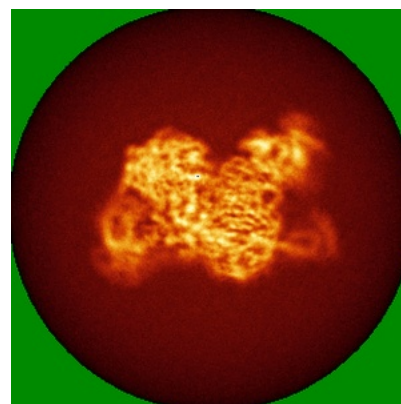
6.4.2 Raw map



X



Y

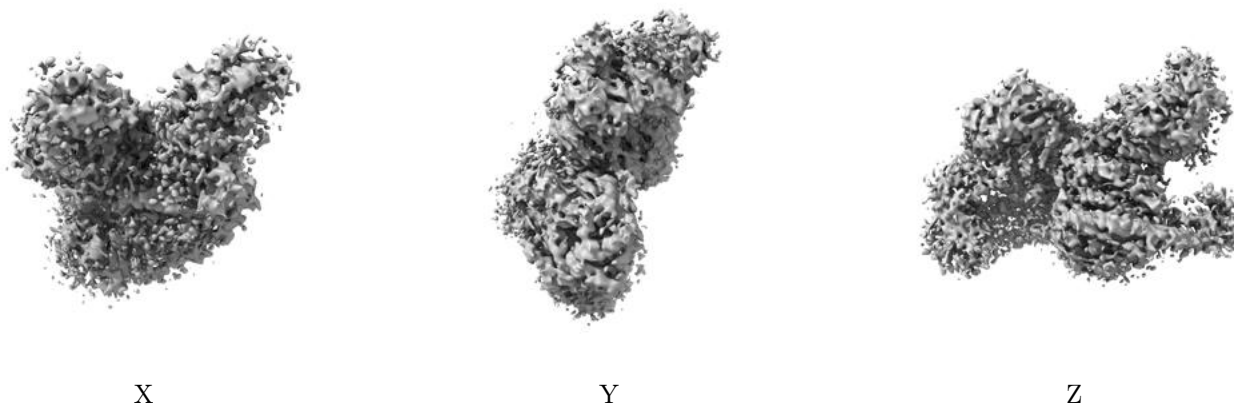


Z

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.

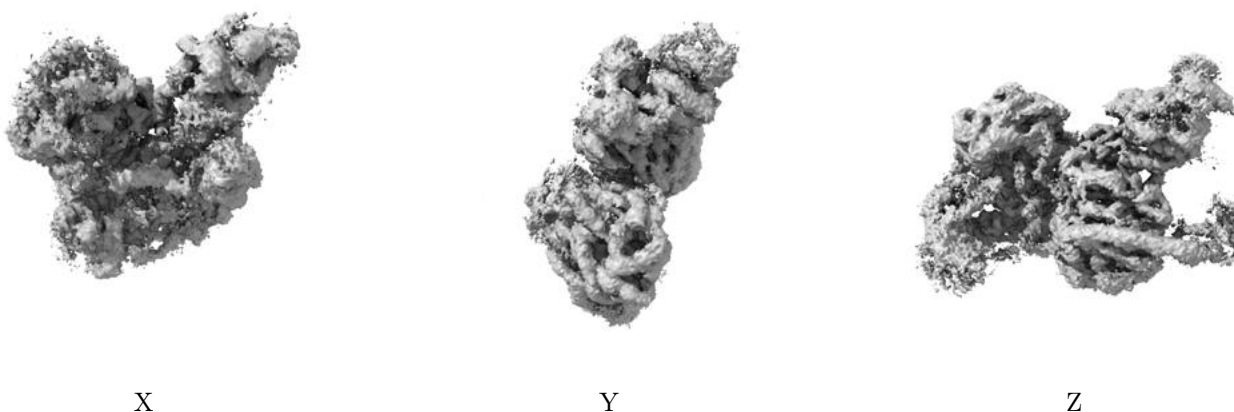
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0383. 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



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.

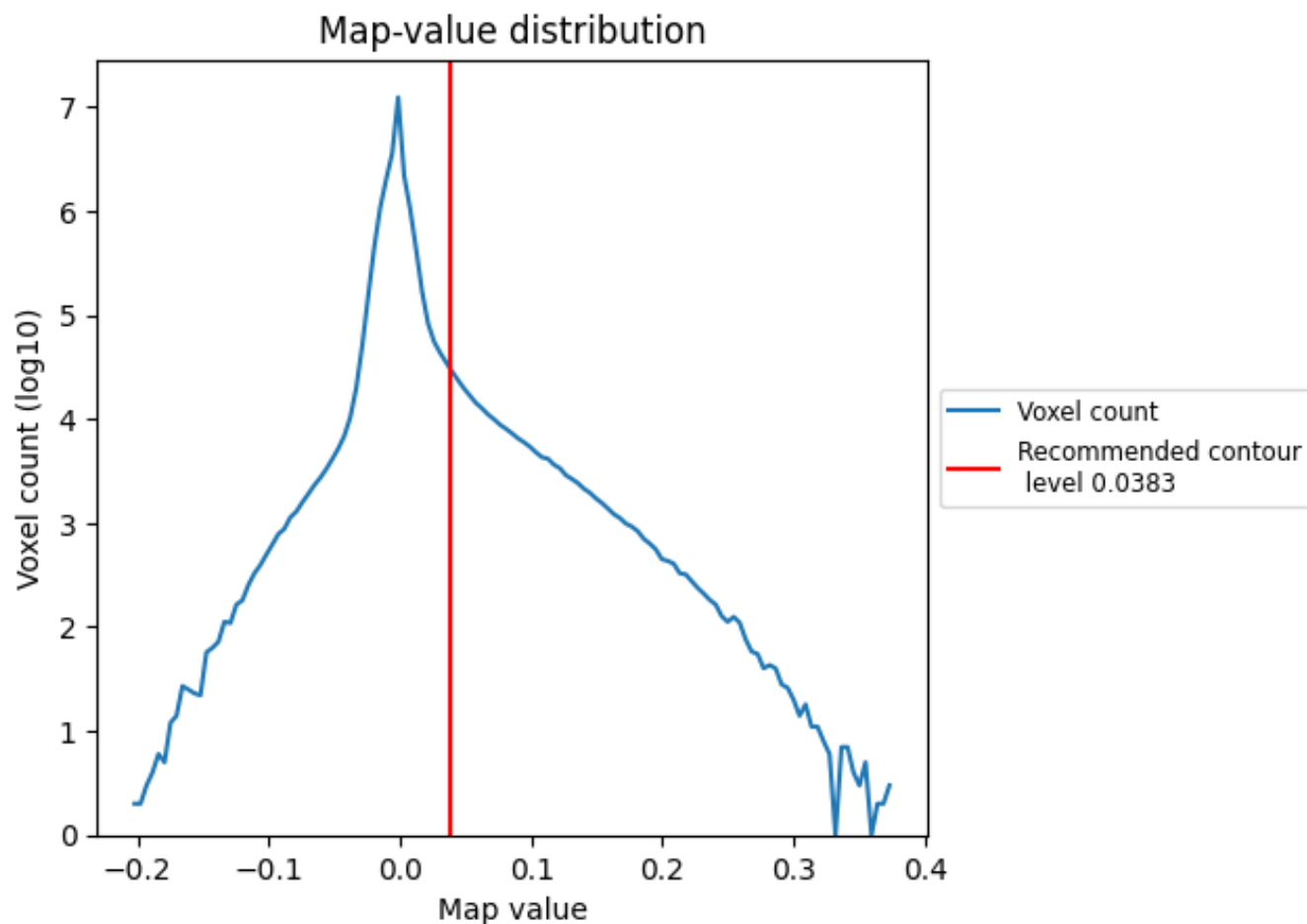
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

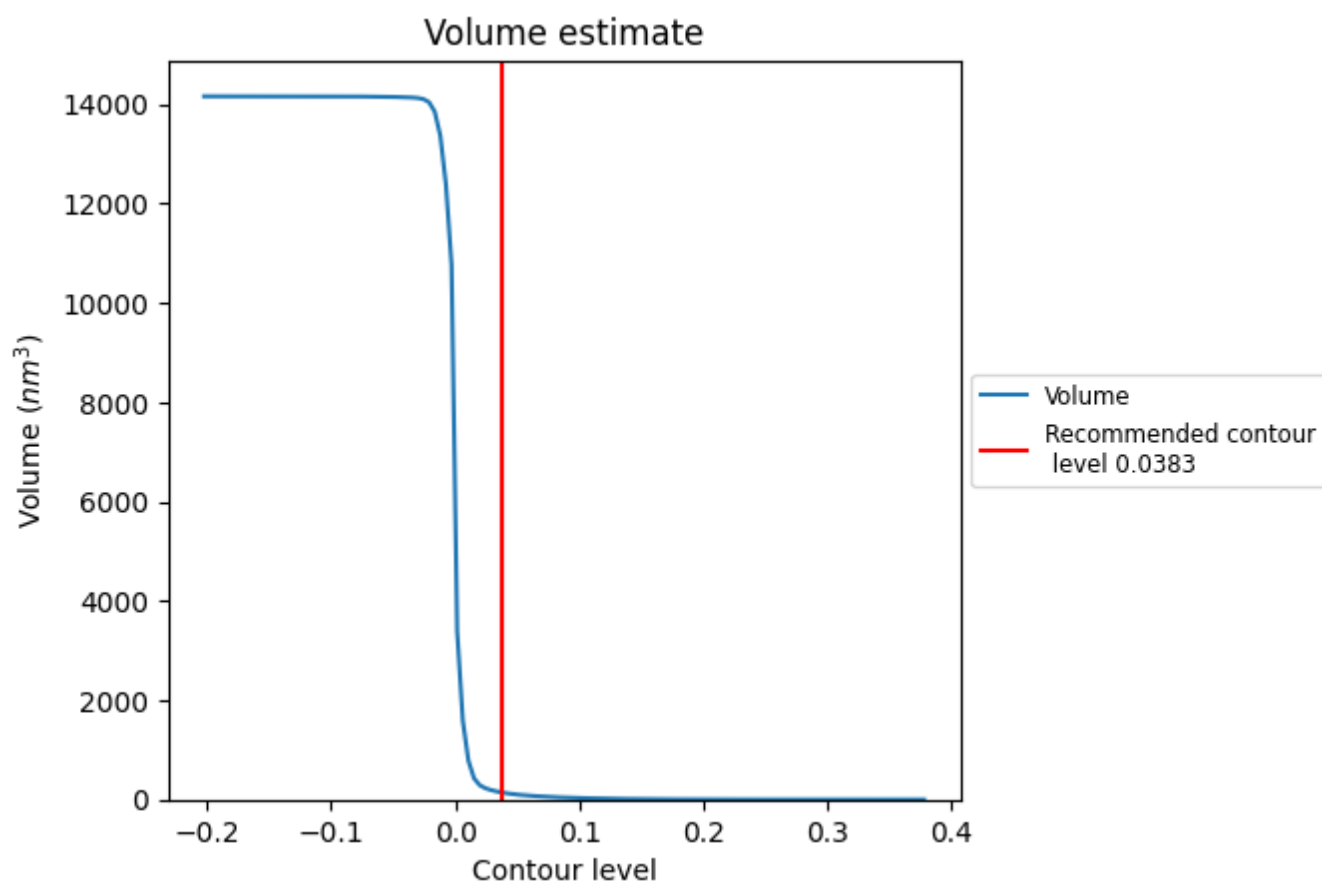
This section contains the results of statistical analysis of the map.

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.

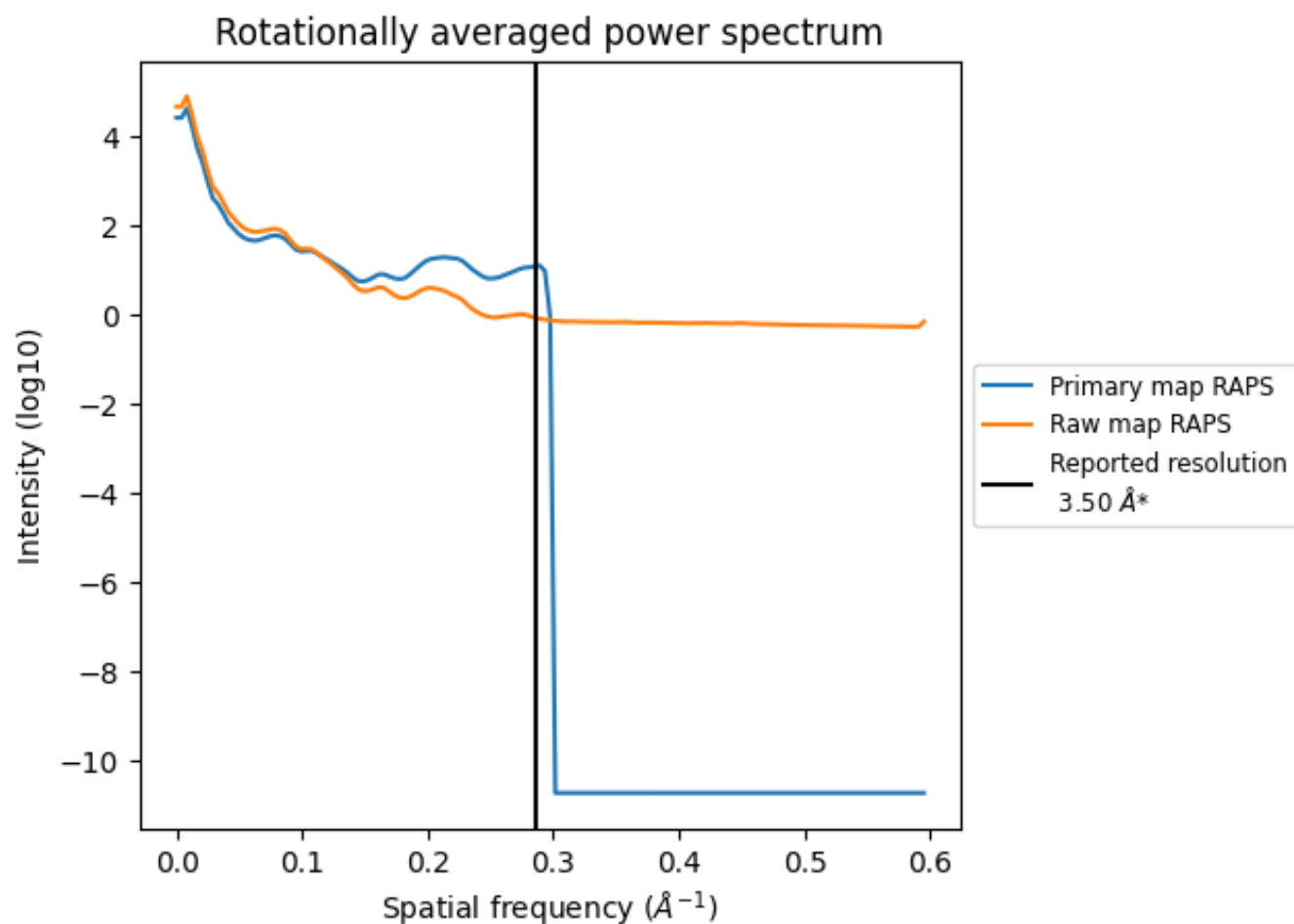
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm³; this corresponds to an approximate mass of 126 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 ⓘ

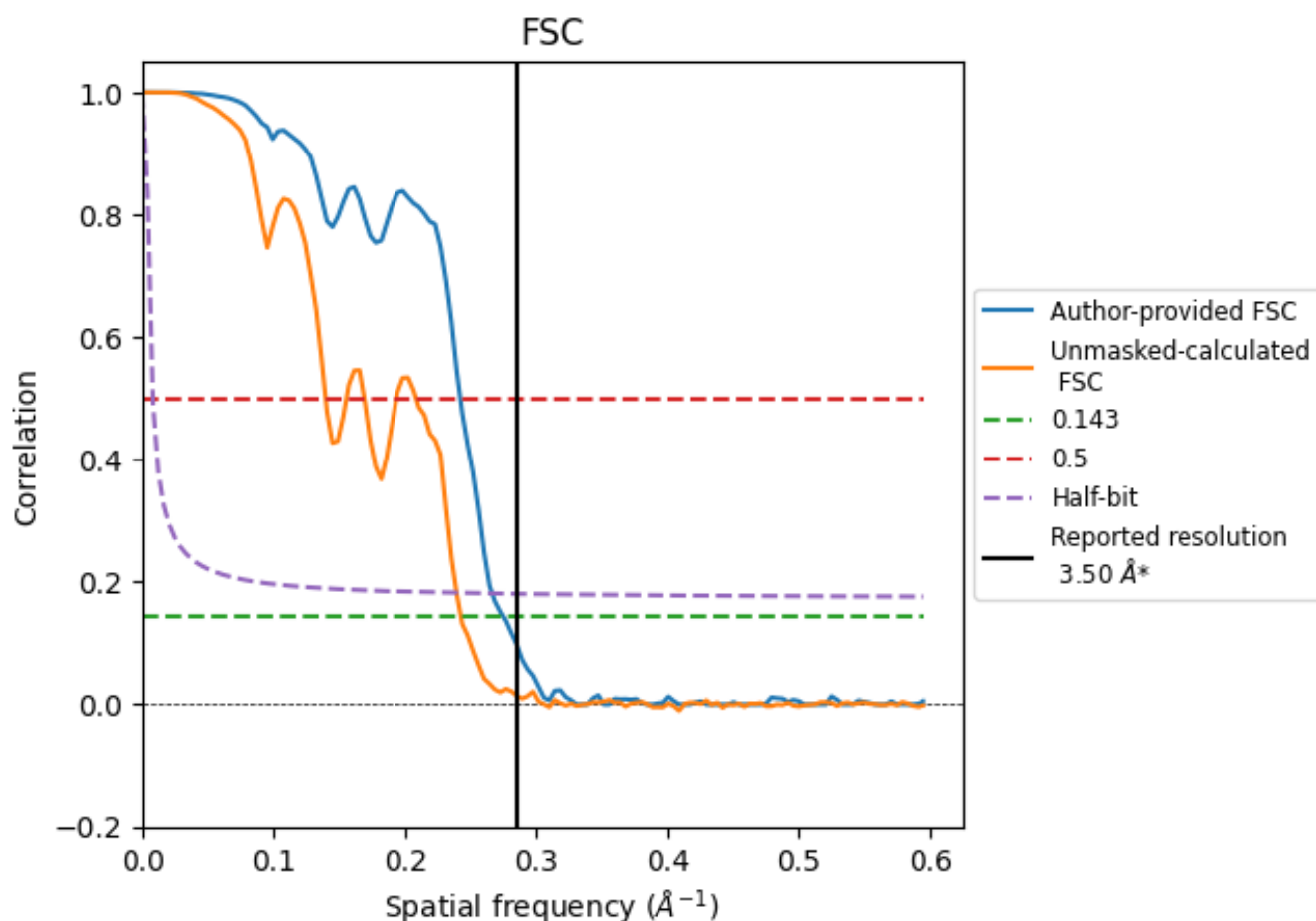


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

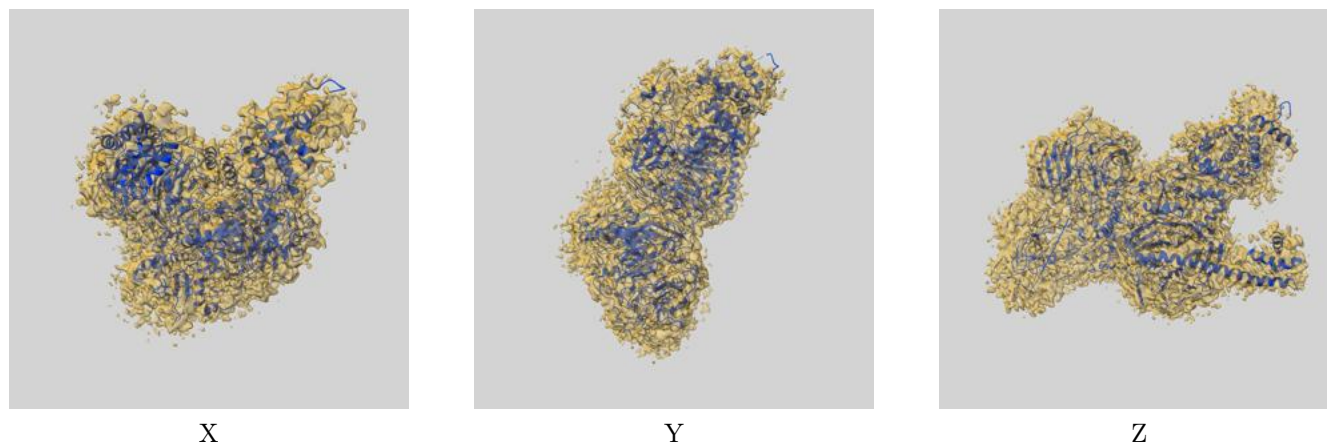
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.64	4.13	3.75
Unmasked-calculated*	4.12	7.17	4.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.12 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7335 and PDB model 6C24. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



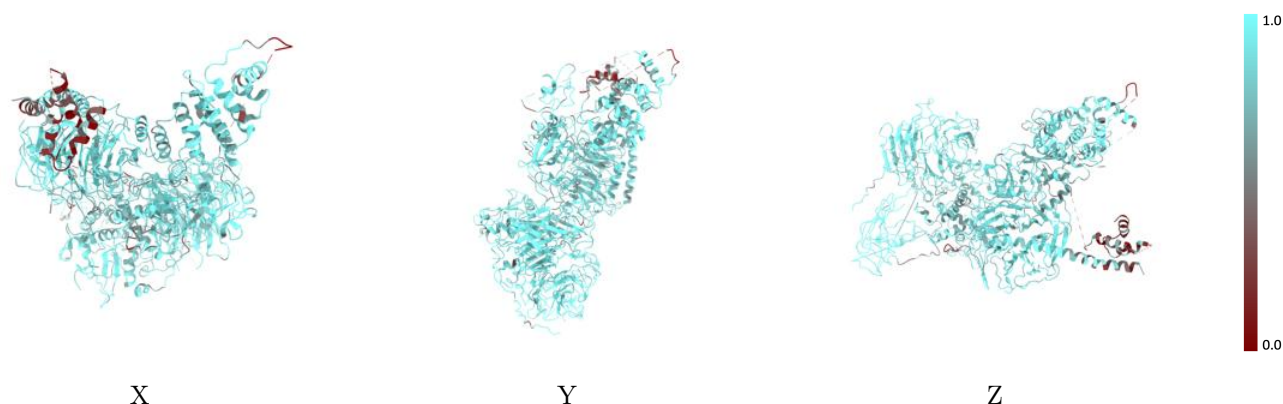
The images above show the 3D surface view of the map at the recommended contour level 0.0383 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



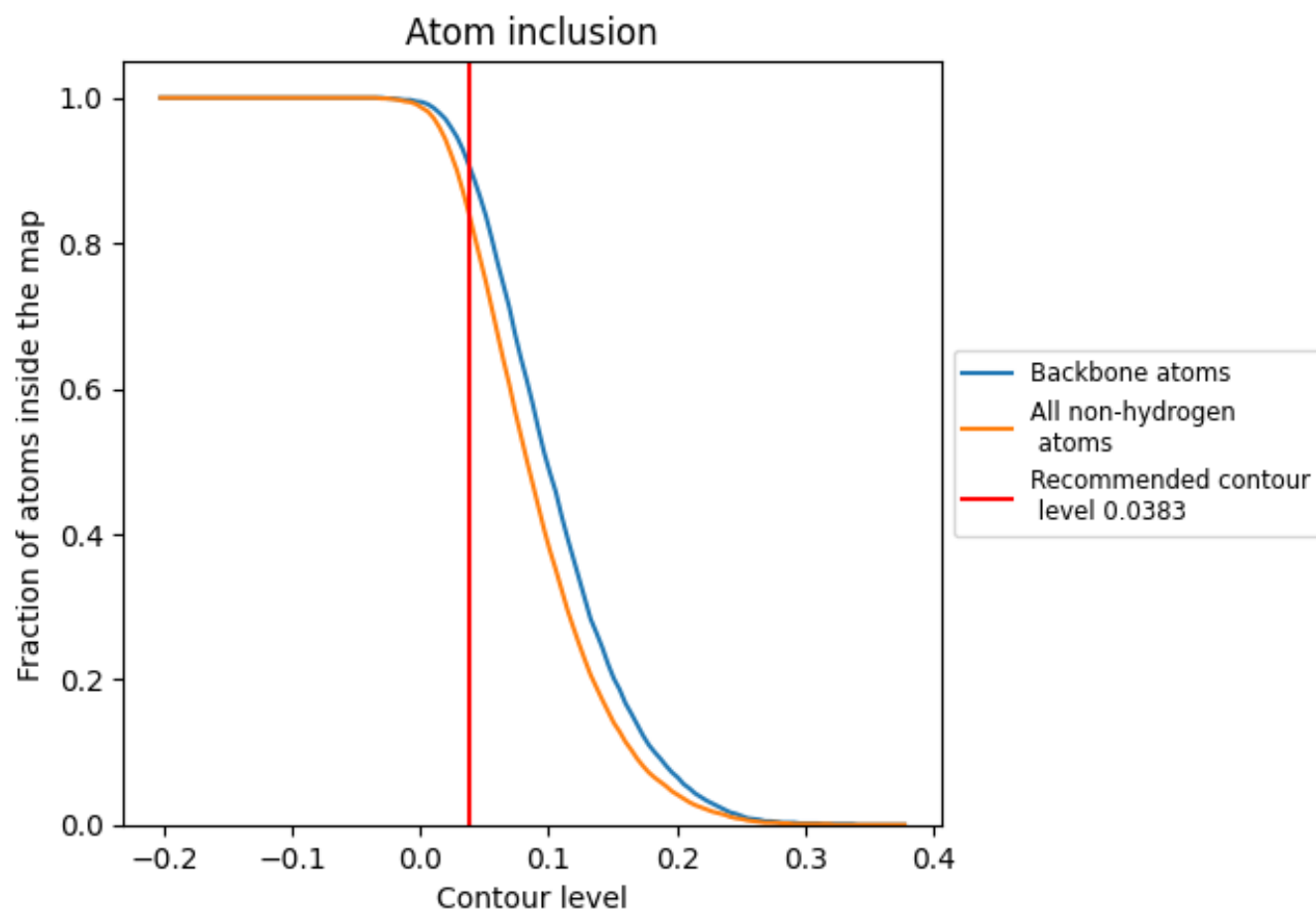
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0383).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 84% 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 (0.0383) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8390	0.4330
A	0.8770	0.4430
B	0.7880	0.4460
C	0.5600	0.2870
E	0.8740	0.3800
K	0.8200	0.3970
L	0.8800	0.4770
M	0.8410	0.4270
N	0.8920	0.4800
O	0.4900	0.3420
P	0.8210	0.4340
Q	0.8960	0.4690
Z	0.9270	0.4060

