



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2025 – 08:20 AM EDT

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.dev117
Mogul : 2022.3.0, CSD as543be (2022)
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) : 2.42

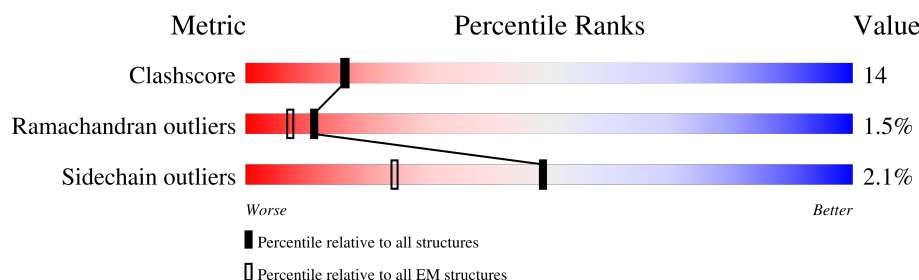
1 Overall quality at a glance

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)
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	739	
1	M	739	
1	Q	739	
2	B	345	
3	E	345	
4	C	746	
4	K	746	
5	L	441	

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Mol	Chain	Length	Quality of chain
6	N	425	<div><div></div><div>65%</div><div>24%</div><div>•</div><div>9%</div></div>
7	O	7	<div><div></div><div>57%</div><div>86%</div><div>14%</div></div>
8	P	295	<div><div></div><div>19%</div><div>••</div><div>78%</div></div>
9	Z	135	<div><div></div><div>•</div><div>80%</div><div>20%</div></div>

2 Entry composition

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		

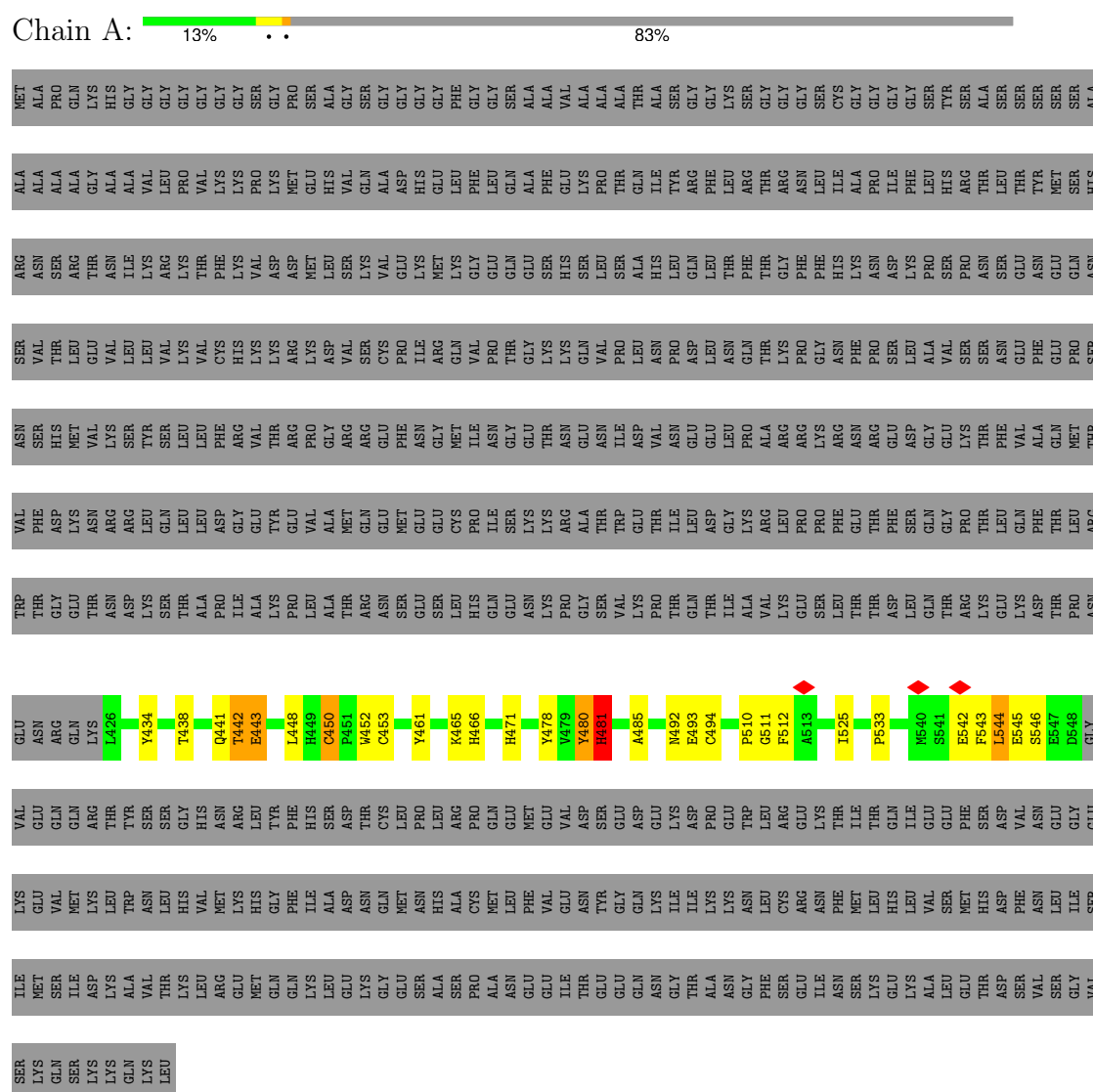
- Molecule 9 is a protein called SUZ12.

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

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: Polycomb protein SUZ12



• Molecule 1: Polycomb protein SUZ12



GLU	MET	GLN	GLN	LYS	GLN	LEU	GLU	LYS	GLY	GLU	GLU	ALA	SER	ALA	SER	PRO	ASN	GLU	GLU	THR	ILE	GLU	THR	GLN	GLN	GLY	GLY	PHE	SER	SER	GLU	ILE	ASN	ALA	ALA	LYS	GLU	GLU	THR	ASP	VAL	SER	SER	GLY	VAL	VAL	SER	SER	LYS	GLN	GLN	LYS	LYS	LYS	LYS	LEU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 1: Polycomb protein SUZ12

Chain Q: 7% . 91%

ILE	GLY	LEU	ASN	THR	ALA	MET
VAL	ARG	ALA	THR	PHE	ALA	ALA
GLU	ARG	ARG	LEU	THR	ALA	GLN
SER	PRO	ARG	PRO	PHE	GLY	HIS
LEU	PHE	ARG	ASN	HIS	ALA	GLY
THR	GLU	ASN	PHE	LYS	VAL	GLY
THR	THR	ARG	PRO	ASN	LEU	GLY
ASP	PHE	ARG	SER	ASP	PRO	GLY
LEU	SER	ASP	LEU	LYS	VAL	GLY
GLN	GLN	GLY	ALA	PRO	LYS	GLY
THR	GLY	GLU	VAL	SER	LYS	GLY
ARG	THR	LYS	PRO	PRO	PRO	SER
GLU	THR	THR	SER	ASN	LYS	GLY
GLU	LEU	PHE	ASN	SER	MET	PRO
LYS	GLN	VAL	GLU	GLU	GLU	SER
ASP	PHE	ALA	PHE	ASN	HIS	ALA
THR	THR	GLN	GLU	GLU	VAL	GLY
PRO	LEU	MET	PRO	GLN	GLN	SER
PRO	ARG	THR	ASN	ASN	ARG1	GLY
GLU	TRP	VAL	SER	SER	F90	GLY
ASN	THR	PHE	SER	VAL	T94	GLY
ARG	GLY	ASP	HIS	THR	R103	PHE
GLN	GLU	LYS	MET	LEU	I106	GLY
THR	THR	ASN	VAL	GLU	I109	ALA
GLM	THR	LYS	THR	GLU	F110	VAL
LYS	ASN	ARG	VAL	VAL	L111	ALA
LEU	ASP	ASP	PHE	CYS	L115	ALA
ILE	LYS	LEU	TYR	HIS	T116	ALA
PHE	ASP	GLN	SER	VAL	Y117	THR
TYR	ALA	GLU	VAL	LYS	I127	ALA
ASN	LYS	TYR	THR	LYS	R128	ALA
ASN	PRO	GLU	ARG	ARG	K130	THR
ASN	LEU	VAL	PRO	LYS	I131	ALA
THR	ALA	ALA	GLY	ASP	R129	THR
THR	THR	MET	ARG	VAL	K136	LYS
GLM	ARG	GLN	ARG	SER	T131	GLY
GLN	ASN	GLU	GLU	CYS	F140	GLY
THR	SER	MET	PHE	PRO	K140	SER
GLU	GLU	GLU	ASN	ILE	G146	CYS
ALA	SER	GLU	GLY	GLN	GLU	GLY
ASP	HIS	ILE	ASN	VAL	GLN	GLY
LEU	GLN	PRO	ILE	VAL	GLU	GLY
ASP	GLN	ILE	ASN	PRO	GLN	GLY
THR	GLU	THR	GLY	THR	GLU	GLY
HIS	ASN	LYS	GLY	LYS	GLU	GLY
CYS	LYS	LYS	THR	GLY	SER	THR
PRO	PRO	ARG	ASN	LYS	HIS	TYR
TRP	GLY	ALA	GLU	GLN	SER	THR
CYS	SER	THR	ASN	VAL	LEU	ALA
THR	VAL	TRP	ILE	PRO	SER	ALA
LEU	LYS	TRP	ASP	LEU	SER	SER
ASN	PRO	THR	VAL	ASN	HIS	SER
CYS	THR	ILE	ASN	PRO	LEU	SER
THR	THR	THR	GLU	ASP	GLN	ALA
ARG	THR	ASP	THR	LEU	THR	ALA

[illegible]

- Molecule 2: Protein Jumonji

Chain B: 98%

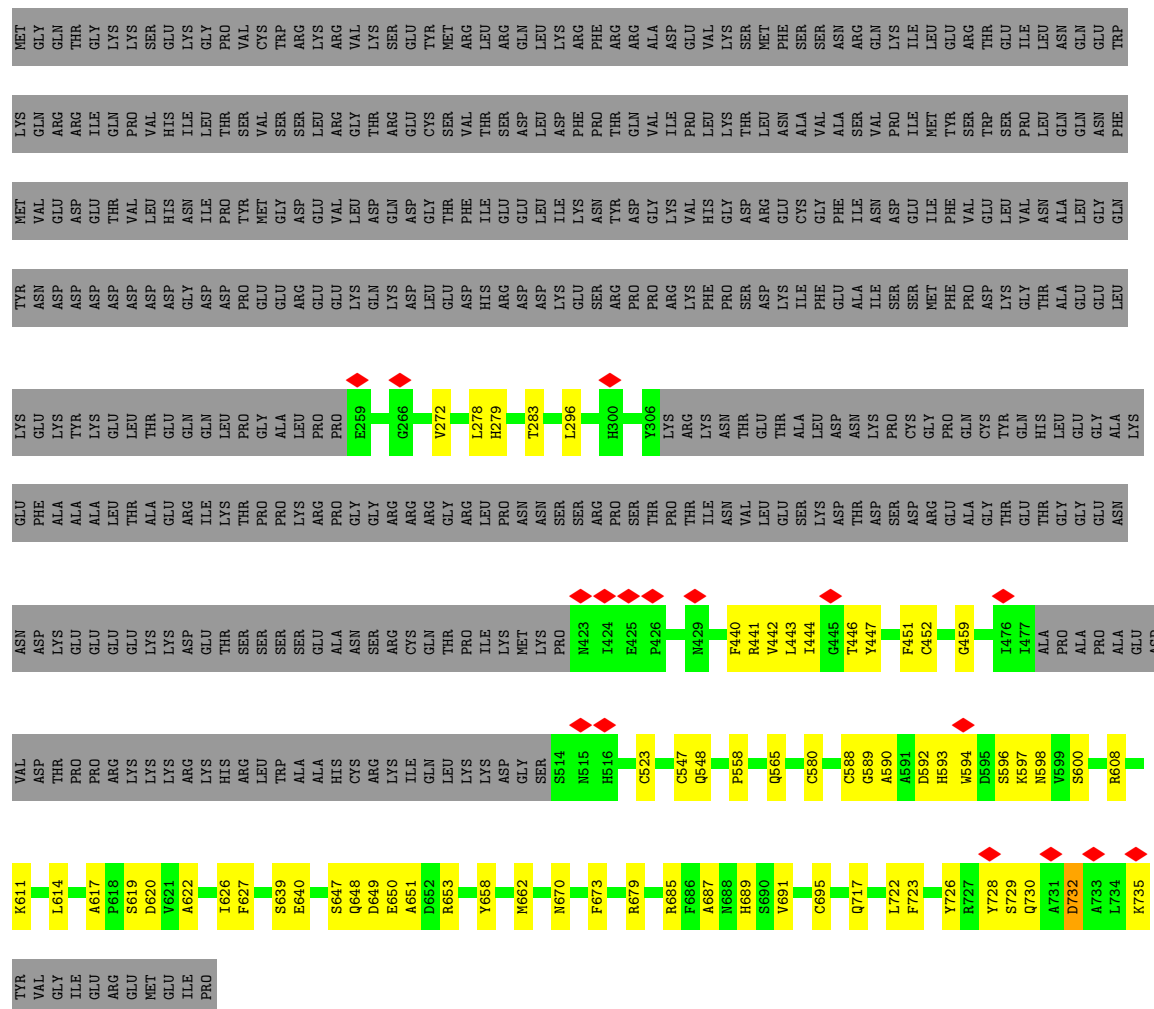
[illegible]

- Molecule 3: Protein Jumonji

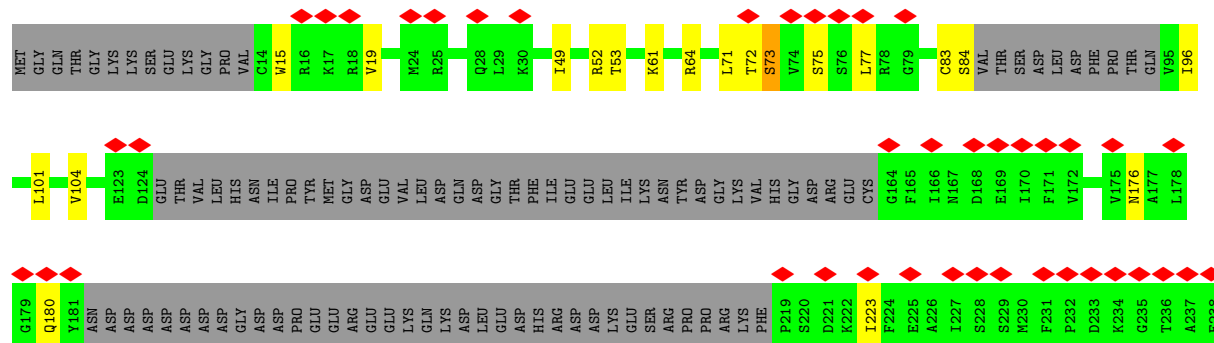
Chain E: 5% .. 92%

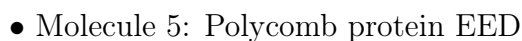
[illegible]

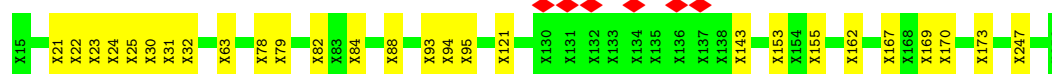
Chain K:



Chain C:







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 (\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 (\AA)	0.84, 0.84, 0.84	Depositor

5 Model quality

5.1 Standard geometry

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	0.53	0/890	0.78	1/1219 (0.1%)
1	M	0.48	0/983	0.70	0/1328
1	Q	1.18	3/506 (0.6%)	0.89	1/687 (0.1%)
2	B	0.48	0/40	0.38	0/53
3	E	0.46	0/185	1.04	0/250
4	C	0.42	0/1247	0.69	1/1669 (0.1%)
4	K	0.42	0/2466	0.64	1/3352 (0.0%)
5	L	0.62	0/2956	0.79	1/4012 (0.0%)
6	N	0.64	0/3146	0.77	4/4291 (0.1%)
7	O	0.52	0/51	0.71	0/66
8	P	0.46	0/492	0.79	0/666
All	All	0.59	3/12962 (0.0%)	0.75	9/17593 (0.1%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	146	GLY	C-O	21.12	1.57	1.23
1	Q	146	GLY	CA-C	7.68	1.64	1.51
1	Q	146	GLY	N-CA	6.97	1.56	1.46

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	146	GLY	CA-C-O	-6.82	108.32	120.60
4	C	73	SER	N-CA-C	-6.73	92.82	111.00
6	N	404	MET	CB-CG-SD	-6.49	92.94	112.40
6	N	79	LEU	CB-CG-CD2	-6.09	100.65	111.00
5	L	405	THR	N-CA-C	5.65	126.25	111.00

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	16	0
1	Q	496	0	450	10	0
2	B	52	0	49	0	0
3	E	184	0	172	10	0
4	C	1227	0	1249	16	0
4	K	2406	0	2120	70	0
5	L	2881	0	2760	131	0
6	N	3062	0	2908	79	0
7	O	51	0	54	11	0
8	P	484	0	476	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	Z	674	0	166	19	0
All	All	13346	0	12038	355	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 355 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 [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	121/739 (16%)	85 (70%)	30 (25%)	6 (5%)	1	16
1	M	120/739 (16%)	105 (88%)	13 (11%)	2 (2%)	7	36
1	Q	64/739 (9%)	45 (70%)	18 (28%)	1 (2%)	8	38
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	49
5	L	360/441 (82%)	299 (83%)	57 (16%)	4 (1%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	N	382/425 (90%)	326 (85%)	53 (14%)	3 (1%)	16	51
7	O	5/7 (71%)	4 (80%)	1 (20%)	0	100	100
8	P	62/295 (21%)	43 (69%)	18 (29%)	1 (2%)	8	38
All	All	1602/5567 (29%)	1329 (83%)	249 (16%)	24 (2%)	11	39

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%)	62	79
1	M	101/646 (16%)	100 (99%)	1 (1%)	73	84
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%)	18 (95%)	1 (5%)	19	46
4	C	138/667 (21%)	138 (100%)	0	100	100
4	K	233/667 (35%)	231 (99%)	2 (1%)	75	86
5	L	311/392 (79%)	302 (97%)	9 (3%)	37	64
6	N	341/375 (91%)	329 (96%)	12 (4%)	31	59
7	O	3/3 (100%)	3 (100%)	0	100	100
8	P	50/263 (19%)	49 (98%)	1 (2%)	50	72
All	All	1316/4894 (27%)	1289 (98%)	27 (2%)	49	71

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	N	35	VAL
6	N	79	LEU
6	N	393	VAL
6	N	68	LEU
6	N	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
4	C	117	GLN
8	P	290	GLN
6	N	226	HIS
6	N	192	HIS
6	N	328	HIS

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

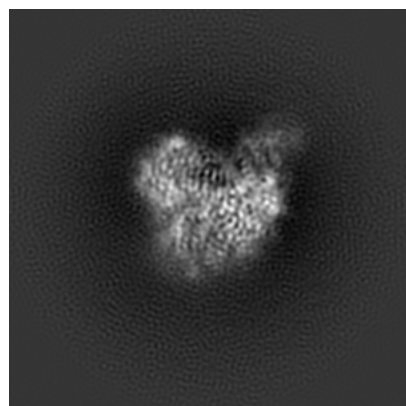
6 Map visualisation [i](#)

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.

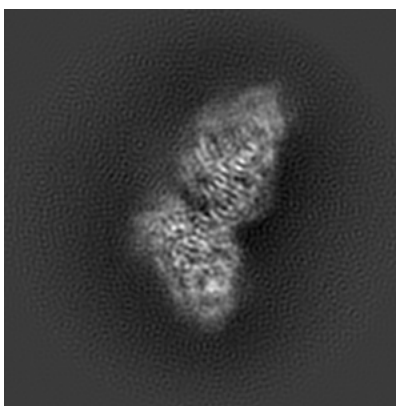
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

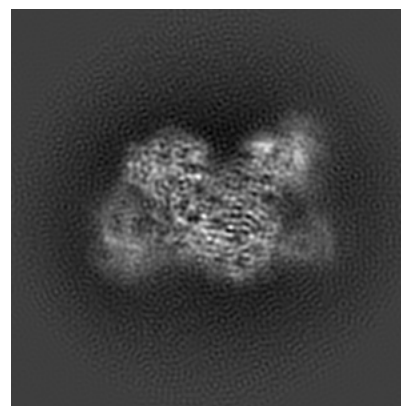
6.1.1 Primary map



X

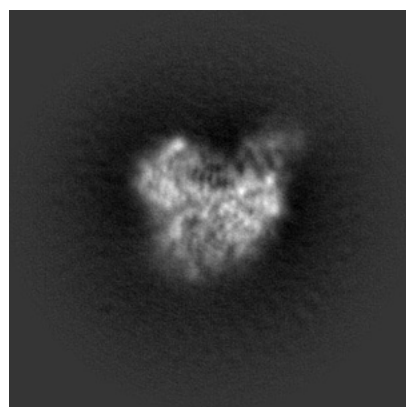


Y

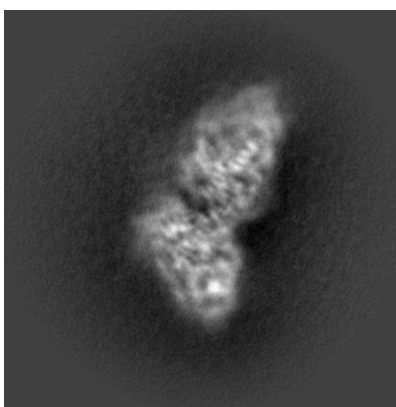


Z

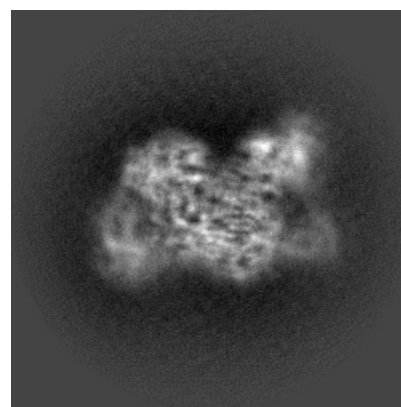
6.1.2 Raw map



X



Y

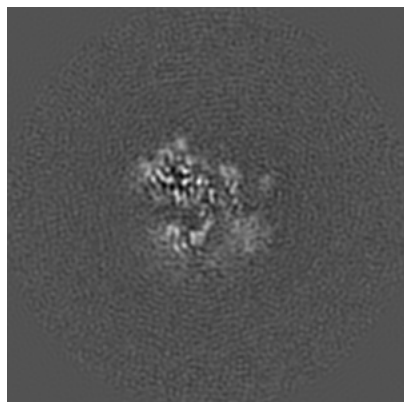


Z

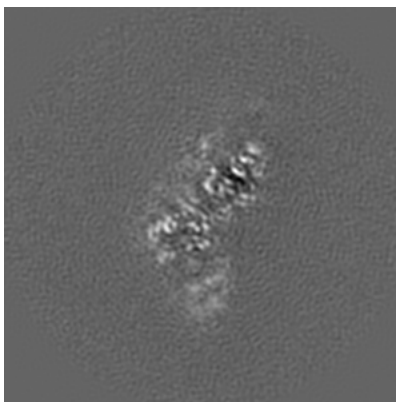
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

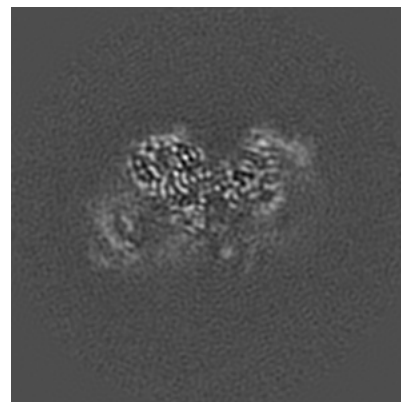
6.2.1 Primary map



X Index: 144

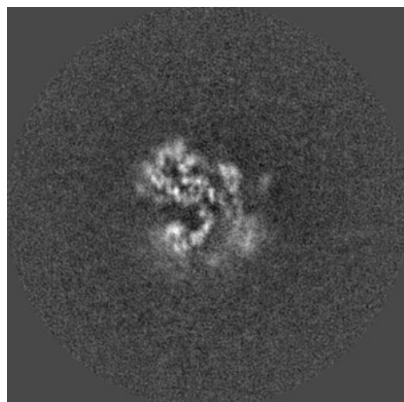


Y Index: 144

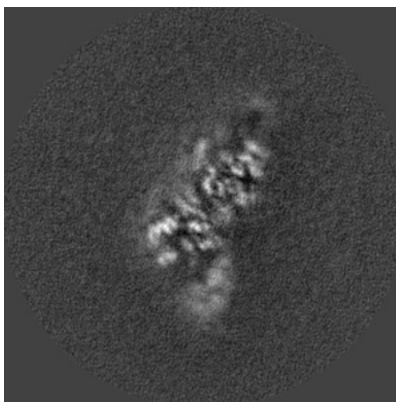


Z Index: 144

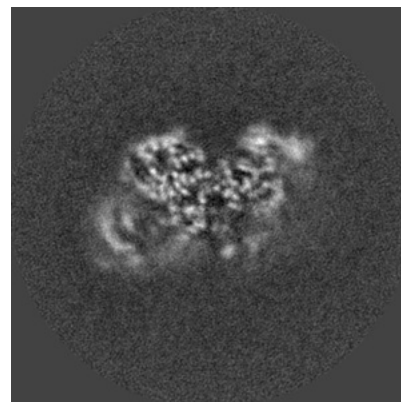
6.2.2 Raw map



X Index: 144



Y Index: 144

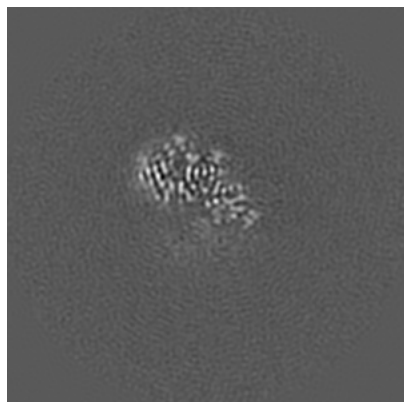


Z Index: 144

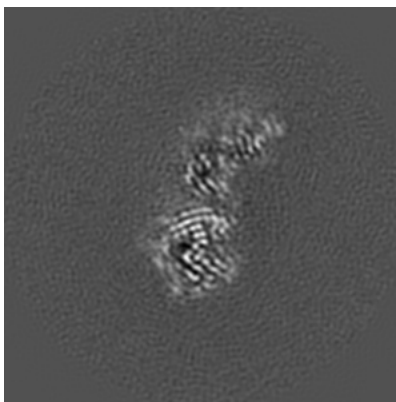
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

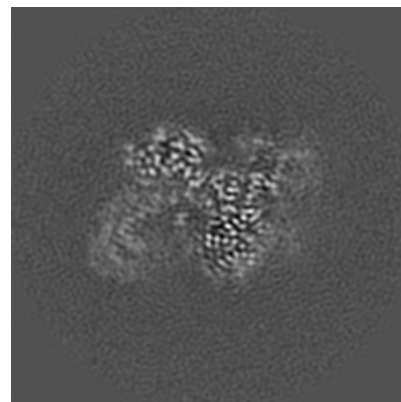
6.3.1 Primary map



X Index: 159

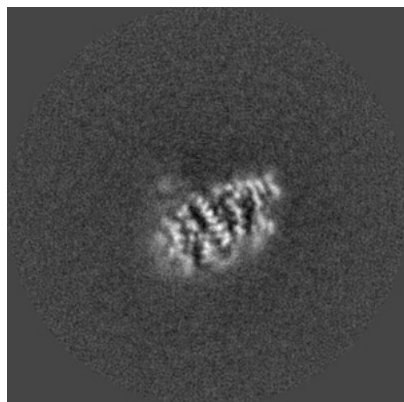


Y Index: 167

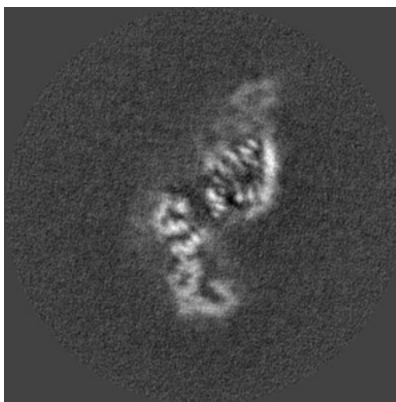


Z Index: 156

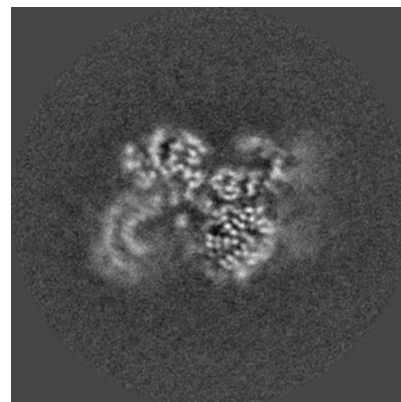
6.3.2 Raw map



X Index: 129



Y Index: 121

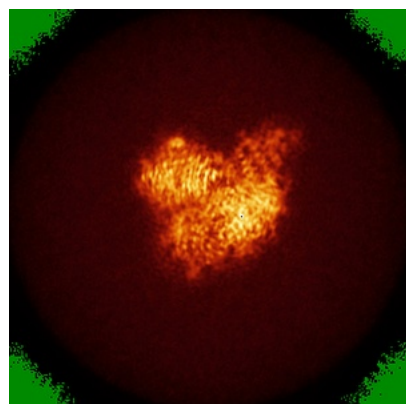


Z Index: 157

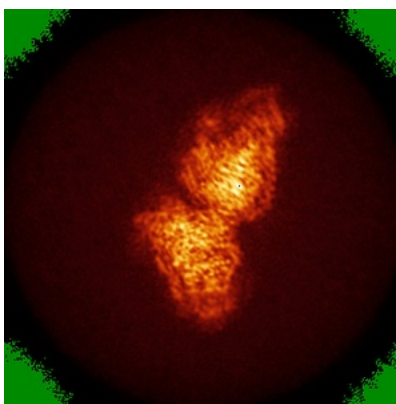
The images above show the largest variance slices of the map in three orthogonal directions.

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

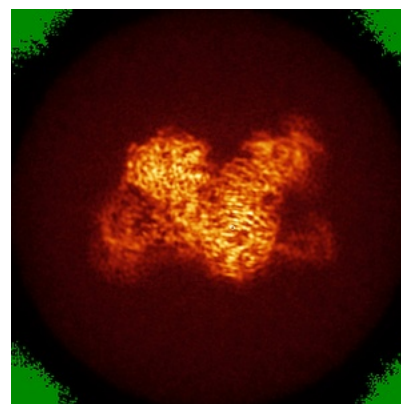
6.4.1 Primary map



X

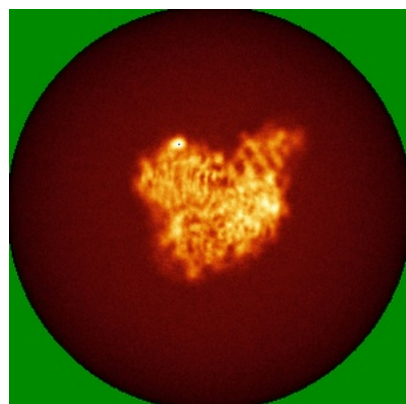


Y

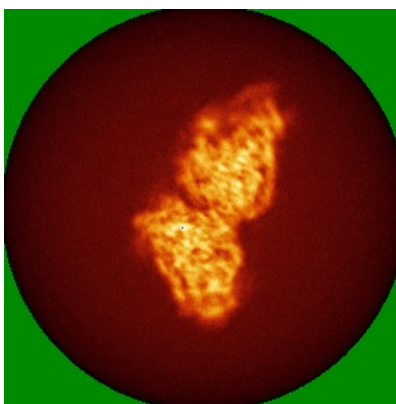


Z

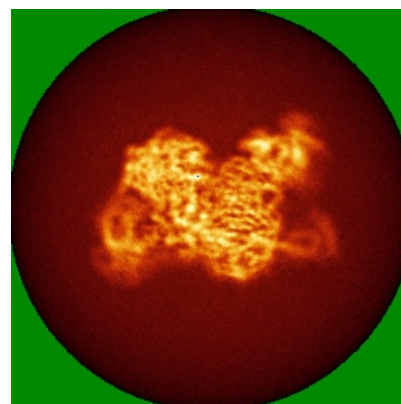
6.4.2 Raw map



X



Y

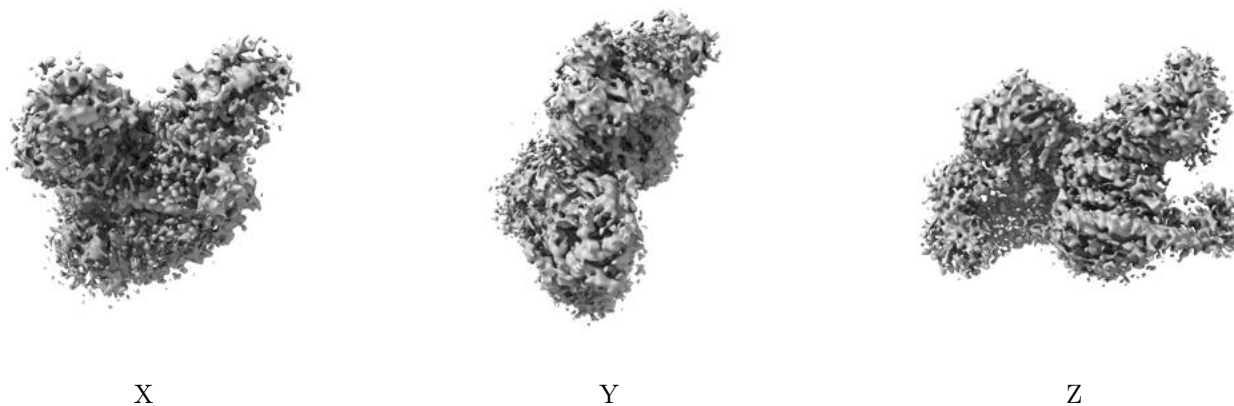


Z

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.

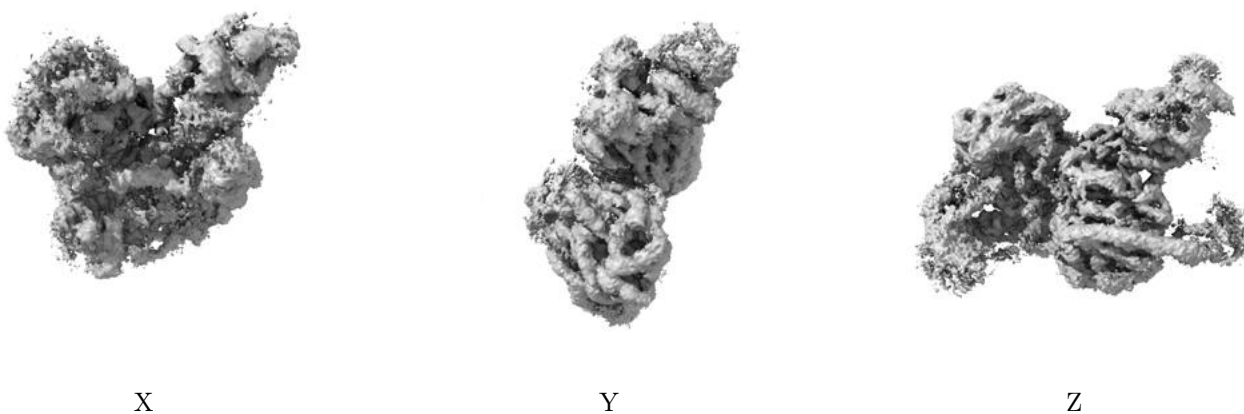
6.5 Orthogonal surface views [i](#)

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.

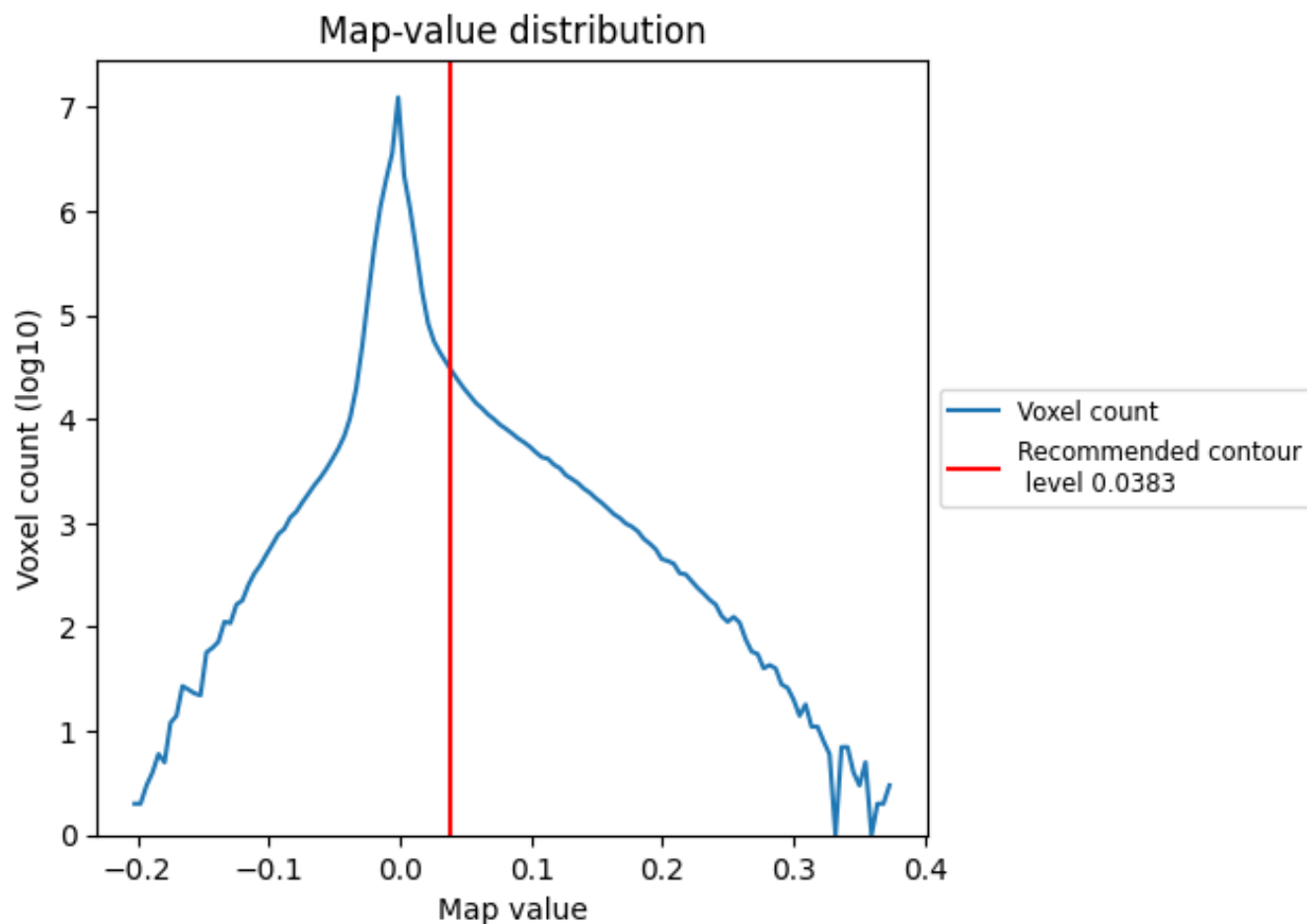
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

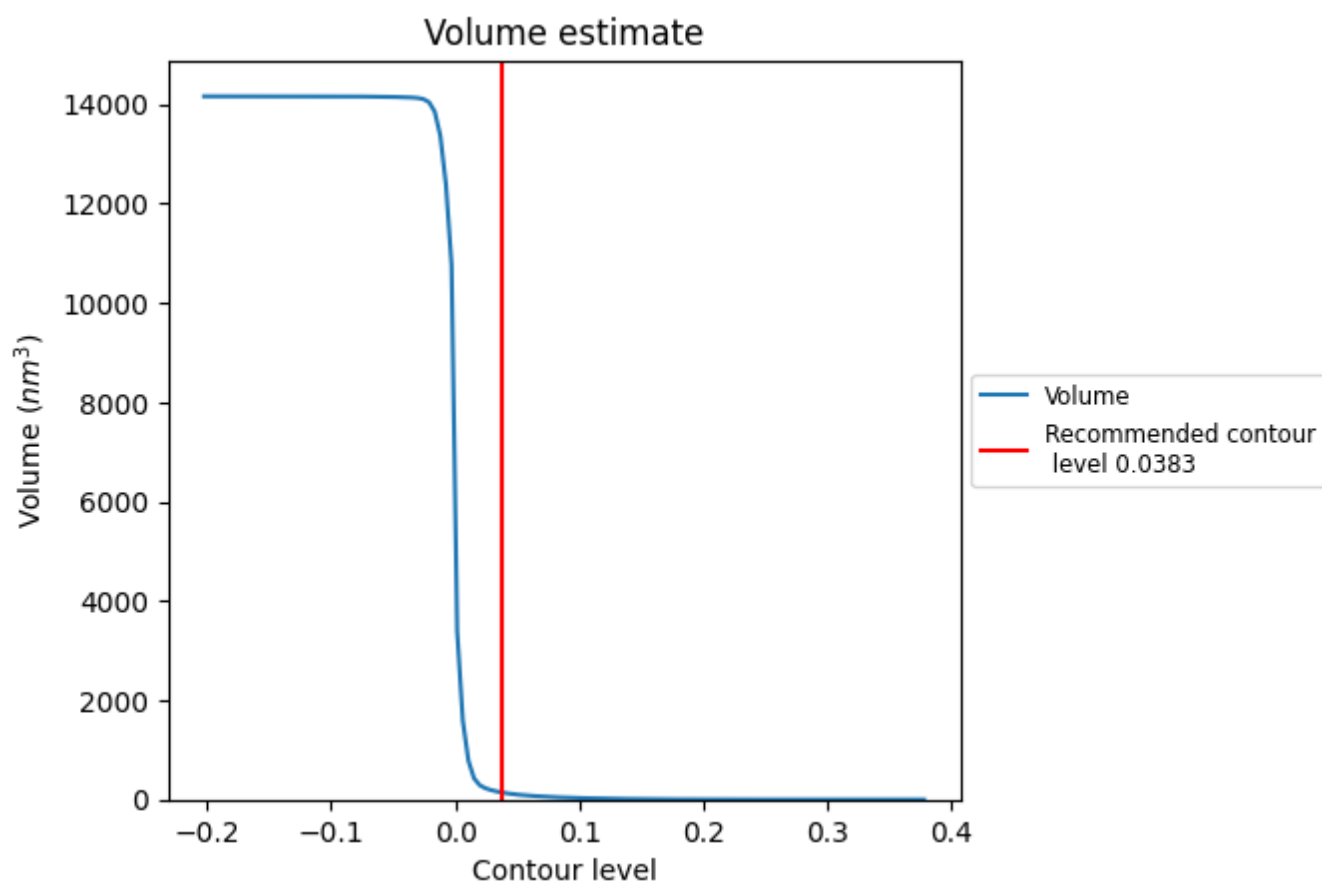
This section contains the results of statistical analysis of the map.

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.

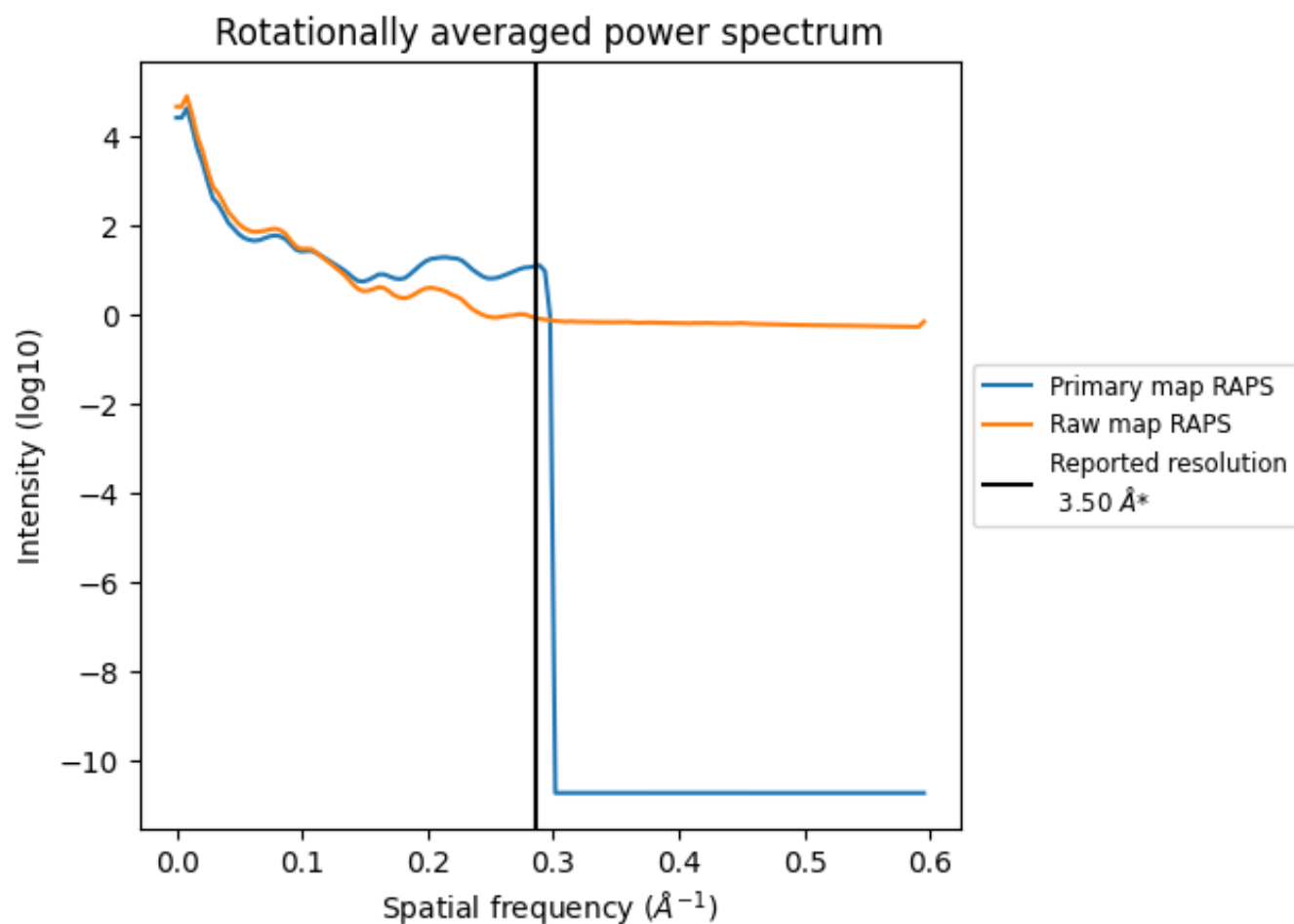
7.2 Volume estimate [i](#)



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 ⓘ

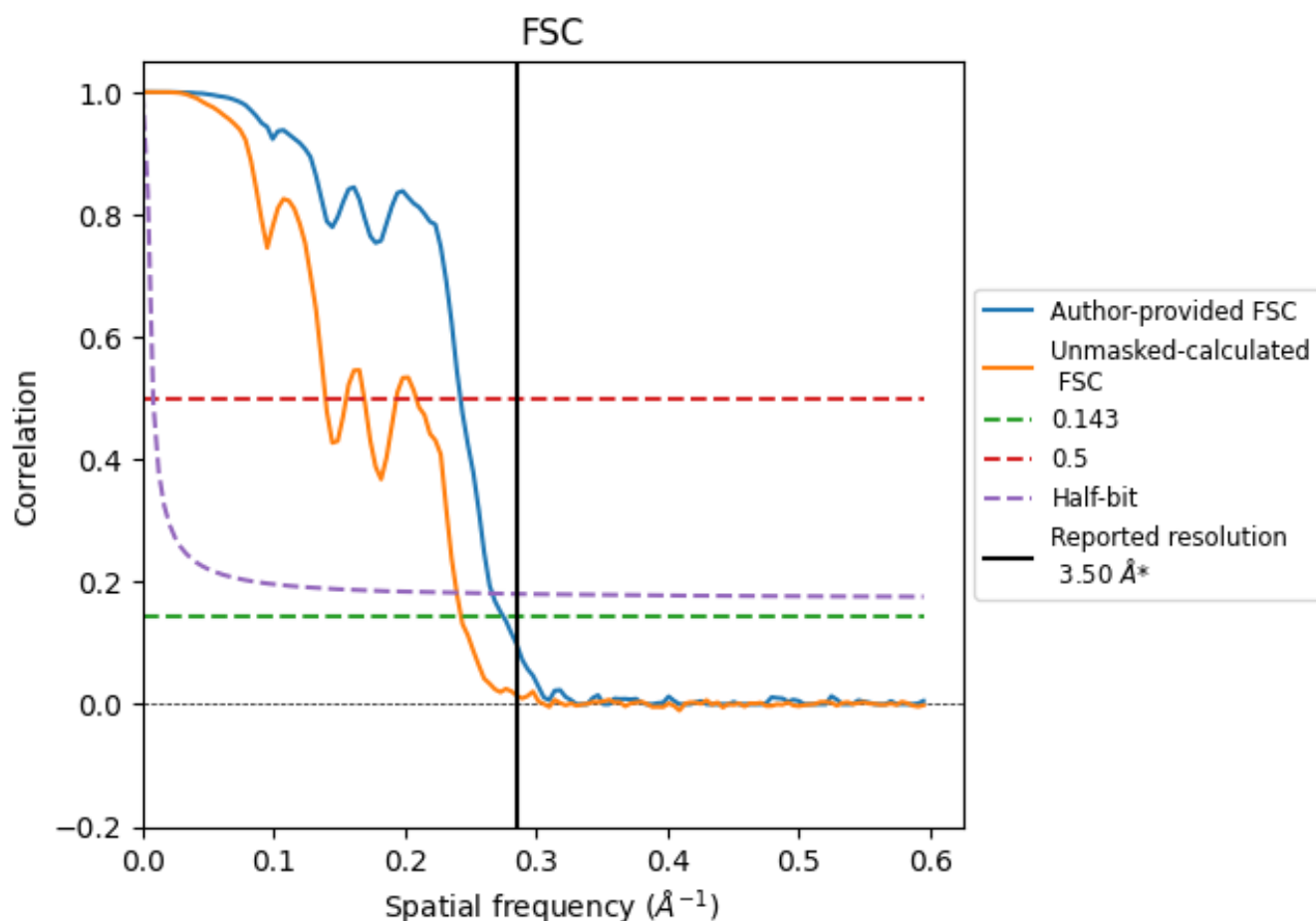


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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](#)

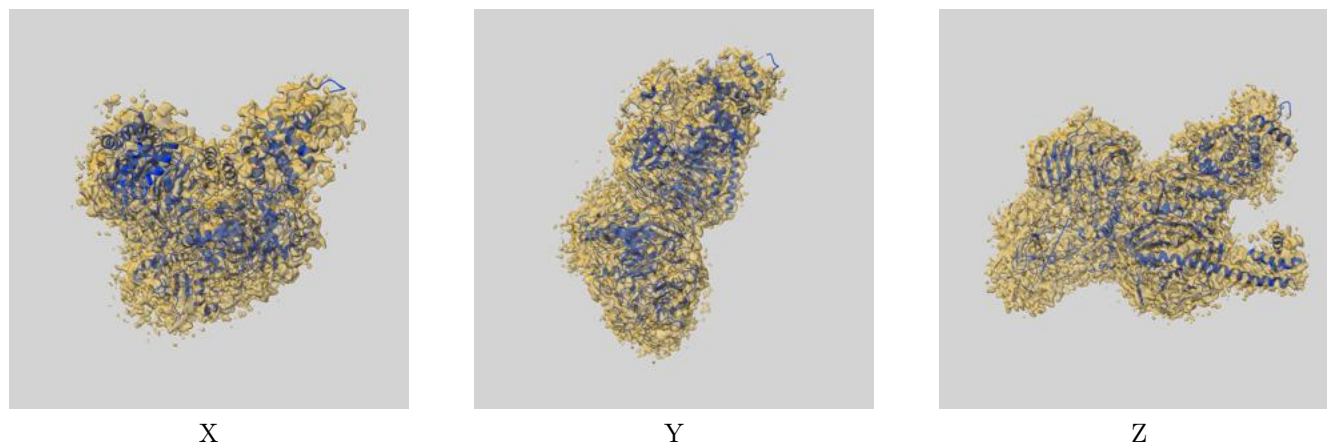
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.64	4.13	3.75
Unmasked-calculated*	4.12	7.17	4.17

*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](#)

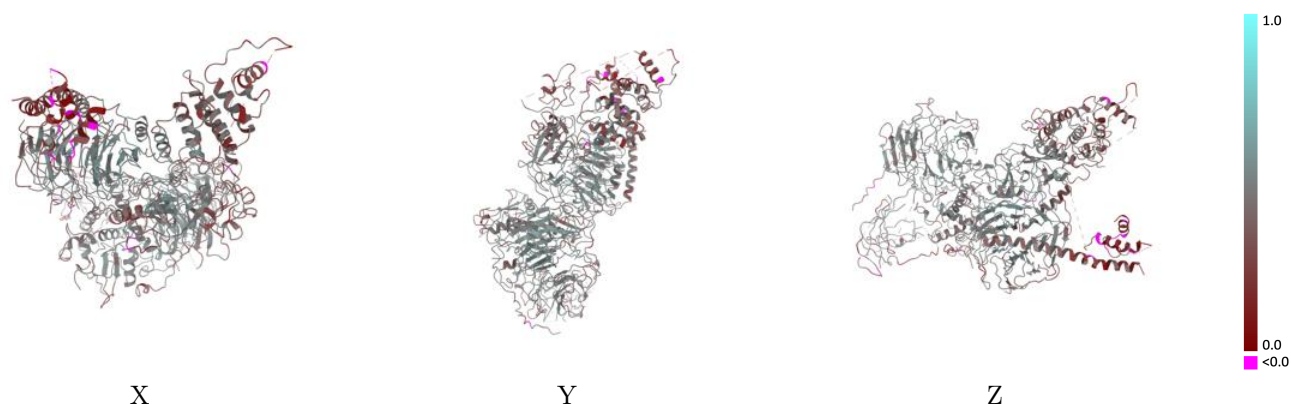
This section contains information regarding the fit between EMDB map EMD-7335 and PDB model 6C24. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



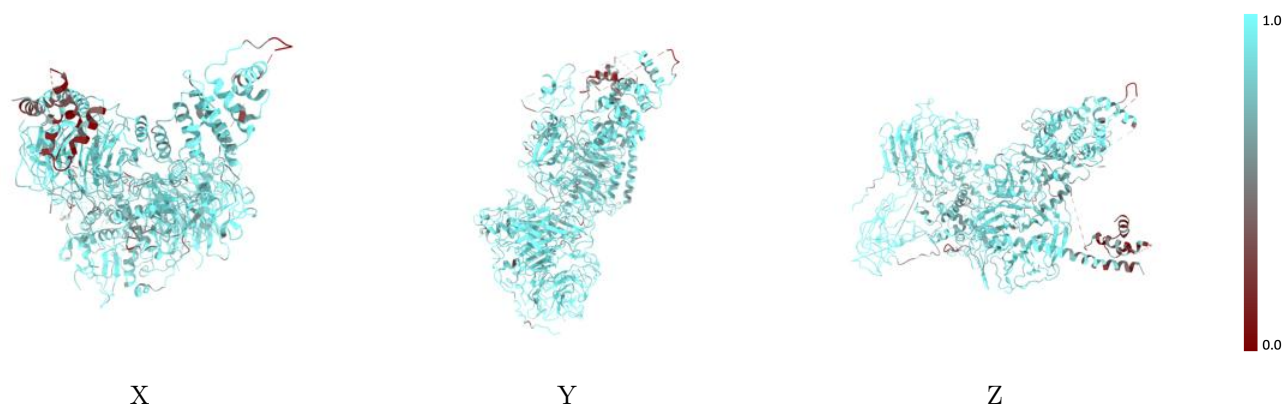
The images above show the 3D surface view of the map at the recommended contour level 0.0383 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



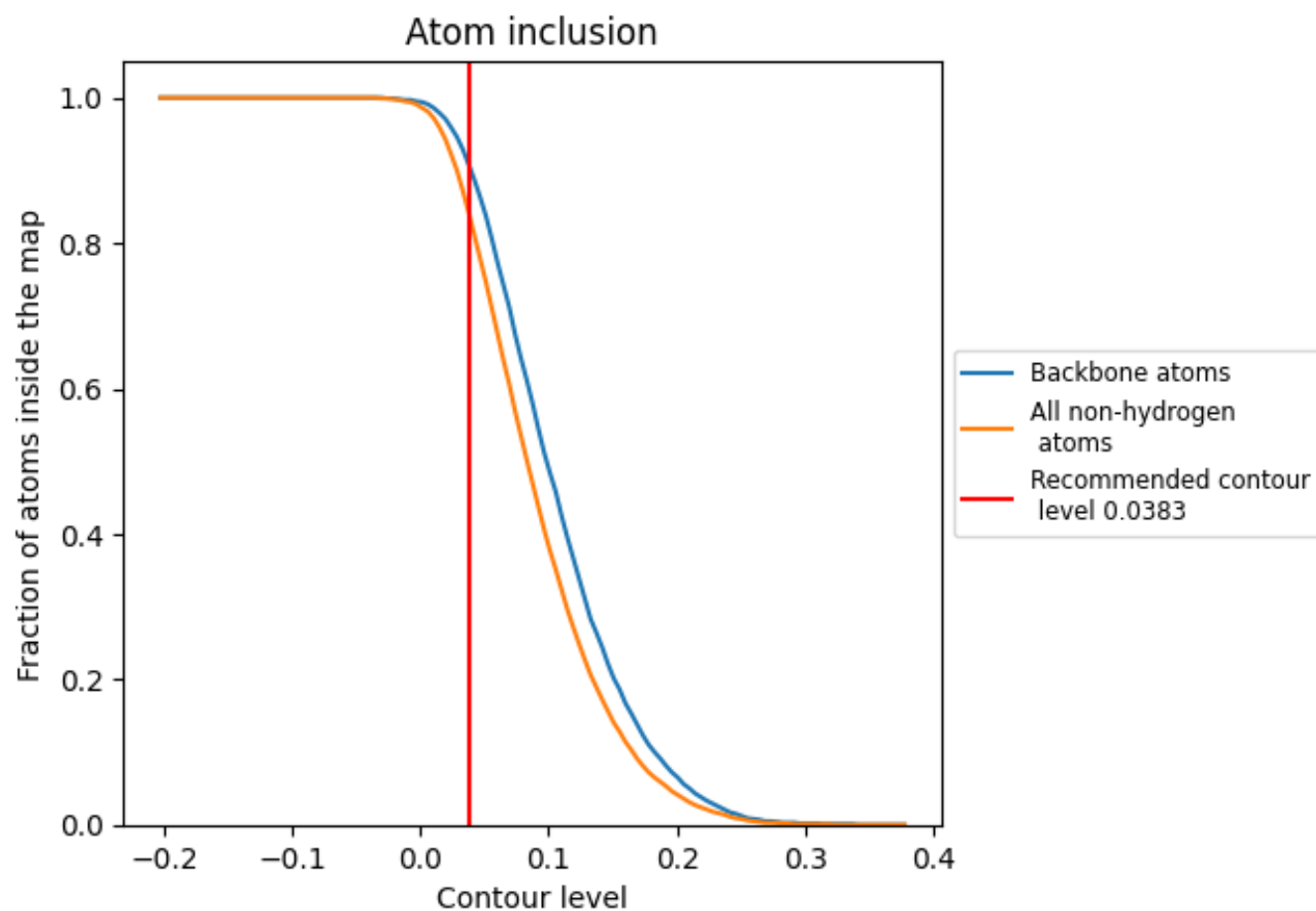
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	<div></div> 0.8390	<div></div> 0.4330
A	<div></div> 0.8770	<div></div> 0.4430
B	<div></div> 0.7880	<div></div> 0.4460
C	<div></div> 0.5600	<div></div> 0.2870
E	<div></div> 0.8740	<div></div> 0.3800
K	<div></div> 0.8200	<div></div> 0.3970
L	<div></div> 0.8800	<div></div> 0.4770
M	<div></div> 0.8410	<div></div> 0.4270
N	<div></div> 0.8920	<div></div> 0.4800
O	<div></div> 0.4900	<div></div> 0.3420
P	<div></div> 0.8210	<div></div> 0.4340
Q	<div></div> 0.8960	<div></div> 0.4690
Z	<div></div> 0.9270	<div></div> 0.4060

1.0

0.0

<0.0