



# wwPDB EM Validation Summary Report ⓘ

Oct 21, 2024 – 04:25 AM EDT

PDB ID : 8FYH  
EMDB ID : EMD-29578  
Title : G4 RNA-mediated PRC2 dimer  
Authors : Song, J.; Kasinath, V.  
Deposited on : 2023-01-26  
Resolution : 3.40 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

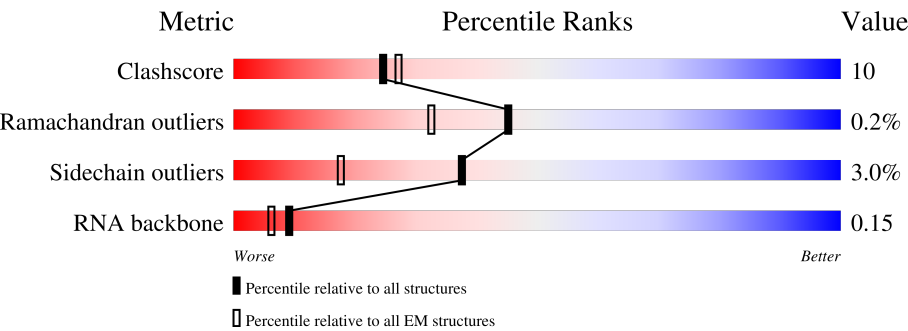
EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.40 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.



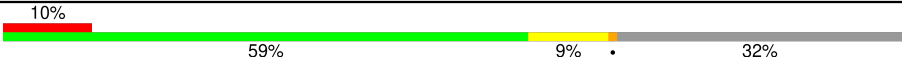
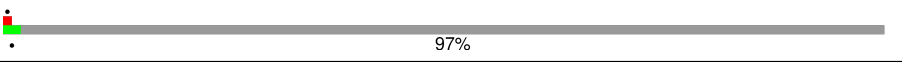
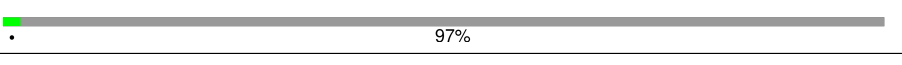



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	B	739	<div><div>13%</div><div>51%</div><div>8%</div><div>41%</div></div>
1	H	739	<div><div>51%</div><div>7%</div><div>41%</div></div>
2	C	441	<div><div>71%</div><div>12%</div><div>17%</div></div>
2	I	441	<div><div>69%</div><div>14%</div><div>17%</div></div>
3	D	425	<div><div>9%</div><div>73%</div><div>18%</div><div>8%</div></div>
3	J	425	<div><div>80%</div><div>12%</div><div>8%</div></div>
4	A	751	<div><div>12%</div><div>58%</div><div>10%</div><div>32%</div></div>

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Mol	Chain	Length	Quality of chain
4	G	751	
5	E	1238	
5	K	1238	
6	F	517	
6	L	517	
7	M	24	

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 25833 atoms, of which 195 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	B	433	Total	C	N	O	S	0	0
			2931	1851	557	510	13		
1	H	433	Total	C	N	O	S	0	0
			2931	1851	557	510	13		

- Molecule 2 is a protein called Polycomb protein EED.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	367	Total	C	N	O	S	0	0
			2654	1689	477	477	11		
2	I	367	Total	C	N	O	S	0	0
			2654	1689	477	477	11		

- Molecule 3 is a protein called Histone-binding protein RBBP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	392	Total	C	N	O	S	0	0
			2722	1729	494	497	2		
3	J	392	Total	C	N	O	S	0	0
			2722	1729	494	497	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	514	Total	C	N	O	S	0	0
			3425	2148	625	621	31		
4	G	514	Total	C	N	O	S	0	0
			3425	2148	625	621	31		

- Molecule 5 is a protein called protein Jumonji isoform X3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	31	Total	C	N	O	S	0	0
			187	114	35	37	1		
5	K	31	Total	C	N	O	S	0	0
			187	114	35	37	1		

- Molecule 6 is a protein called Zinc finger protein AEBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	109	Total	C	N	O	S	0	0
			696	439	134	122	1		
6	L	109	Total	C	N	O	S	0	0
			696	439	134	122	1		

- Molecule 7 is a RNA chain called G4 RNA.

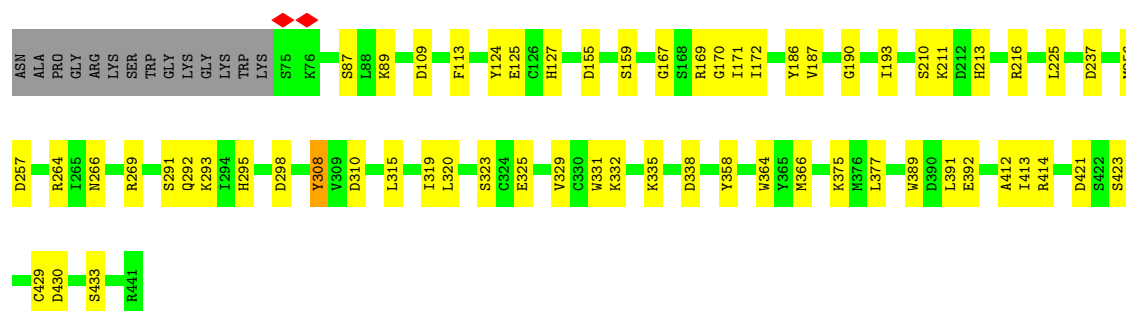
Mol	Chain	Residues	Atoms						AltConf	Trace
7	M	18	Total	C	H	N	O	P	0	0
			589	176	195	78	124	16		

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

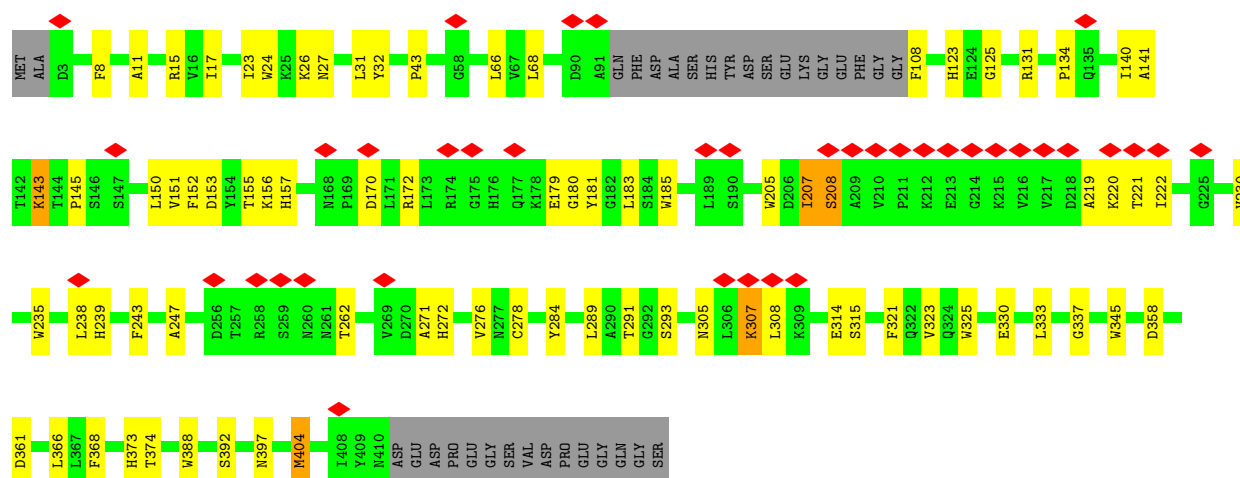
Mol	Chain	Residues	Atoms		AltConf
8	A	7	Total	Zn	0
			7	7	
8	G	7	Total	Zn	0
			7	7	



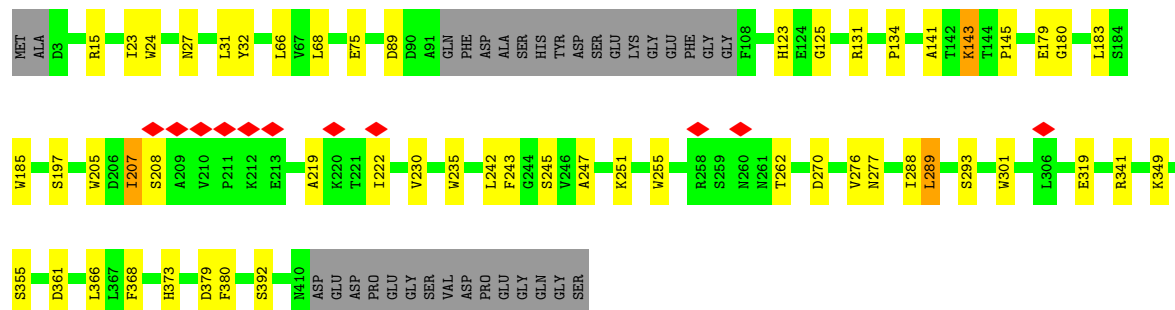
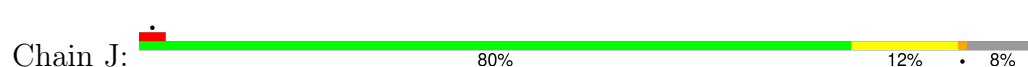




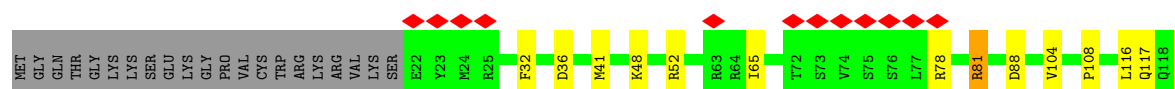
• Molecule 3: Histone-binding protein RBBP4



• Molecule 3: Histone-binding protein RBBP4

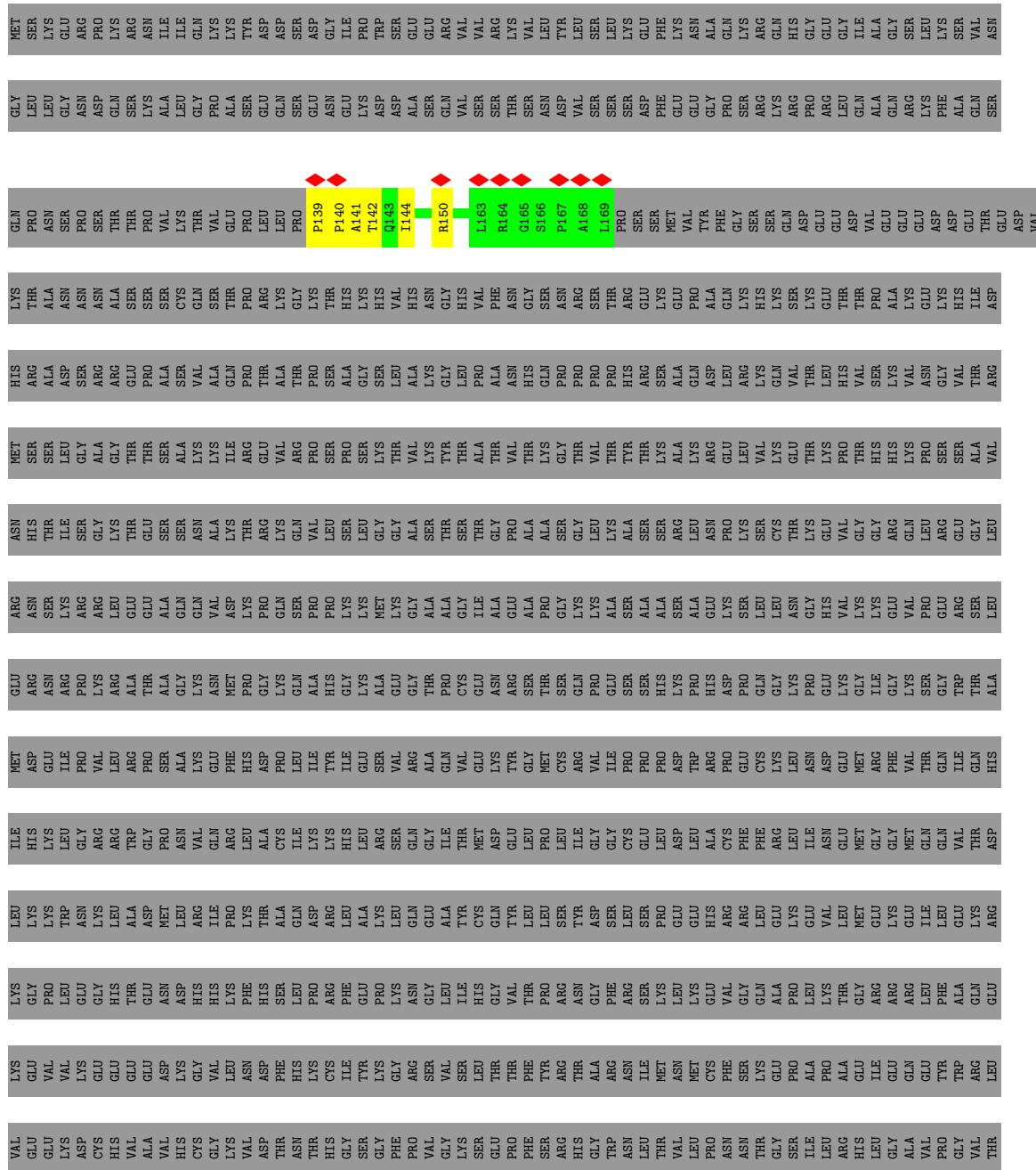


• Molecule 4: Histone-lysine N-methyltransferase EZH2











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

- Molecule 6: Zinc finger protein AEBP2

Chain F:  17% 79%

[illegible]

- Molecule 6: Zinc finger protein AEBP2

Response	Percentage
Doing a good job	19%
Doing a bad job	79%

- Molecule 7: G4 RNA

Chain M: 

A diagram showing a sequence of 22 nodes (G1 to A) arranged in a row. Nodes G1, G2, G3, G7, G8, G9, G13, G14, G15, G19, G20, and G21 are yellow. Nodes U4, U6, U10, U16, and U22 are orange. Nodes A, A6, A8, A18, and A22 are grey. Red diamonds are placed above nodes G1, G2, G3, G7, G8, G9, G13, G14, G15, G19, G20, and G21.

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	217196	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.052	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	319.03198, 319.03198, 319.03198	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06344, 1.06344, 1.06344	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: ZN

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	B	0.24	0/2992	0.46	0/4081
1	H	0.24	0/2992	0.45	0/4081
2	C	0.26	0/2727	0.47	0/3734
2	I	0.25	0/2727	0.47	0/3734
3	D	0.25	0/2806	0.45	0/3863
3	J	0.24	0/2806	0.45	0/3863
4	A	0.26	0/3495	0.46	0/4779
4	G	0.25	0/3495	0.45	0/4779
5	E	0.26	0/190	0.54	0/261
5	K	0.26	0/190	0.54	0/261
6	F	0.24	0/715	0.48	0/987
6	L	0.24	0/715	0.47	0/987
7	M	1.07	0/440	1.17	0/682
All	All	0.28	0/26290	0.48	0/36092

There are no bond length outliers.

There are no bond angle outliers.

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	B	2931	0	2277	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	2931	0	2277	45	0
2	C	2654	0	2262	44	0
2	I	2654	0	2262	50	0
3	D	2722	0	2173	97	0
3	J	2722	0	2173	40	0
4	A	3425	0	2699	84	0
4	G	3425	0	2699	78	0
5	E	187	0	148	7	0
5	K	187	0	148	1	0
6	F	696	0	500	20	0
6	L	696	0	500	8	0
7	M	394	195	200	22	0
8	A	7	0	0	0	0
8	G	7	0	0	0	0
All	All	25638	195	20318	476	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 10.

The worst 5 of 476 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:B:467:LEU:HD13	1:B:476:PHE:CE2	1.54	1.41
3:D:156:LYS:HZ3	3:D:157:HIS:CD2	1.43	1.36
2:I:308:TYR:OH	2:I:364:TRP:HB3	1.22	1.35
3:D:156:LYS:NZ	3:D:157:HIS:CD2	1.95	1.34
2:I:366:MET:HE2	2:I:414:ARG:HD3	1.14	1.13

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	B	411/739 (56%)	390 (95%)	20 (5%)	1 (0%)	44	72
1	H	411/739 (56%)	383 (93%)	27 (7%)	1 (0%)	44	72
2	C	365/441 (83%)	345 (94%)	20 (6%)	0	100	100
2	I	365/441 (83%)	346 (95%)	19 (5%)	0	100	100
3	D	388/425 (91%)	362 (93%)	24 (6%)	2 (0%)	25	54
3	J	388/425 (91%)	364 (94%)	23 (6%)	1 (0%)	37	66
4	A	500/751 (67%)	466 (93%)	33 (7%)	1 (0%)	44	72
4	G	500/751 (67%)	466 (93%)	32 (6%)	2 (0%)	30	60
5	E	29/1238 (2%)	22 (76%)	7 (24%)	0	100	100
5	K	29/1238 (2%)	21 (72%)	8 (28%)	0	100	100
6	F	105/517 (20%)	92 (88%)	13 (12%)	0	100	100
6	L	105/517 (20%)	93 (89%)	12 (11%)	0	100	100
All	All	3596/8222 (44%)	3350 (93%)	238 (7%)	8 (0%)	45	72

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	669	ILE
3	D	207	ILE
1	H	669	ILE
4	A	65	ILE
3	J	207	ILE

### 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	B	205/646 (32%)	200 (98%)	5 (2%)	44	66
1	H	205/646 (32%)	198 (97%)	7 (3%)	32	57
2	C	229/392 (58%)	223 (97%)	6 (3%)	41	64
2	I	229/392 (58%)	225 (98%)	4 (2%)	56	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	211/375 (56%)	206 (98%)	5 (2%)	44	66
3	J	211/375 (56%)	208 (99%)	3 (1%)	62	77
4	A	256/672 (38%)	244 (95%)	12 (5%)	22	49
4	G	256/672 (38%)	243 (95%)	13 (5%)	20	46
5	E	14/1079 (1%)	14 (100%)	0	100	100
5	K	14/1079 (1%)	14 (100%)	0	100	100
6	F	42/417 (10%)	40 (95%)	2 (5%)	21	48
6	L	42/417 (10%)	41 (98%)	1 (2%)	44	66
All	All	1914/7162 (27%)	1856 (97%)	58 (3%)	37	61

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	269	LEU
4	G	658	ARG
1	H	557	TYR
4	G	654	ASP
4	G	549	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	305	ASN
4	A	332	HIS
2	C	204	ASN
2	C	221	GLN
3	D	157	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	M	16/24 (66%)	8 (50%)	4 (25%)

5 of 8 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	M	4	U

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Mol	Chain	Res	Type
7	M	7	G
7	M	8	G
7	M	10	U
7	M	16	U

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	M	6	A
7	M	7	G
7	M	18	A
7	M	19	G

## 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](#)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

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.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

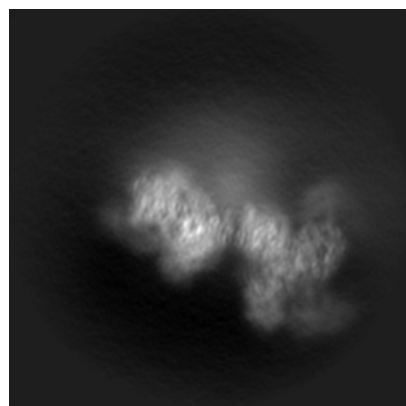
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29578. These allow visual inspection of the internal detail of the map and identification of artifacts.

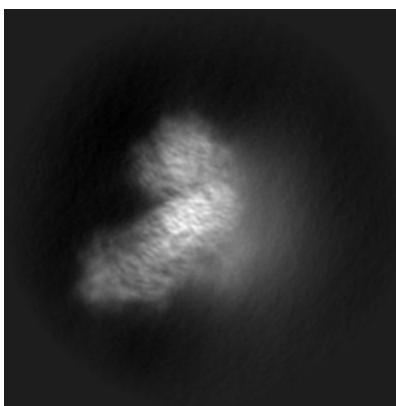
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

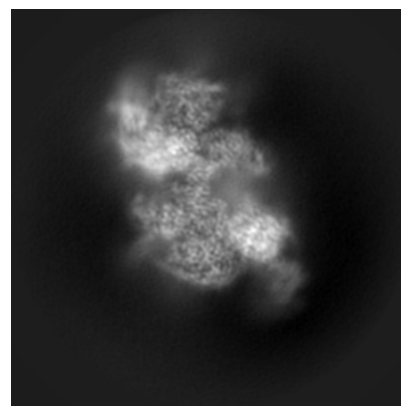
#### 6.1.1 Primary map



X

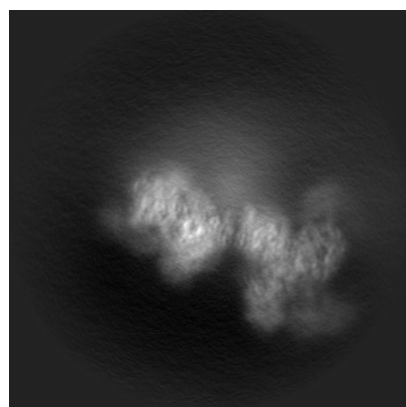


Y

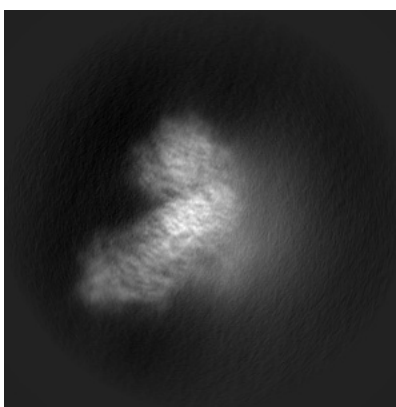


Z

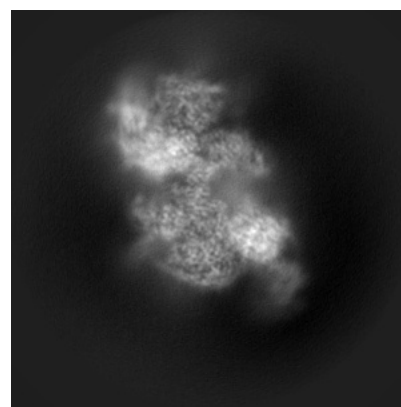
#### 6.1.2 Raw map



X



Y

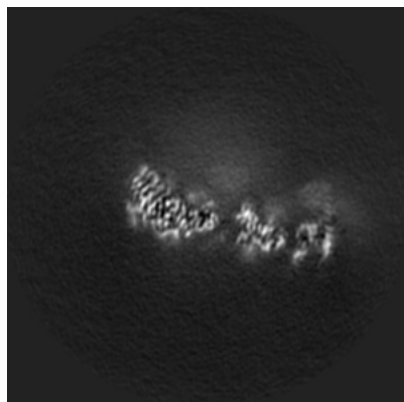


Z

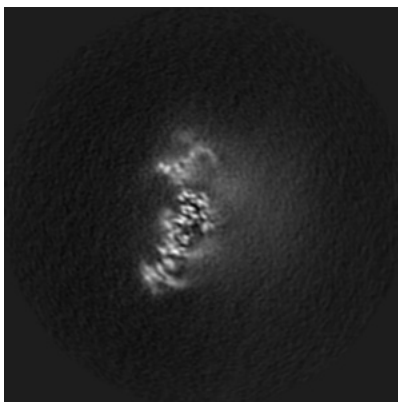
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

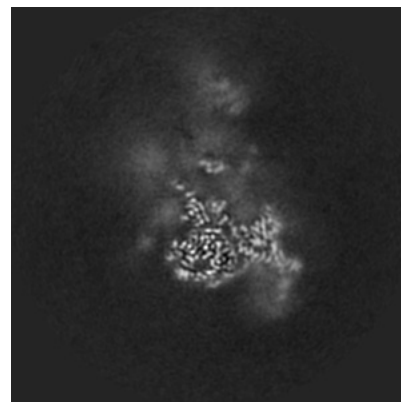
### 6.2.1 Primary map



X Index: 150

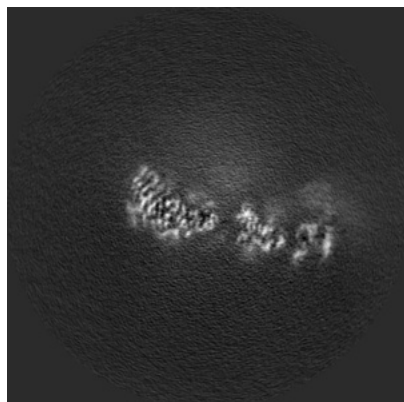


Y Index: 150

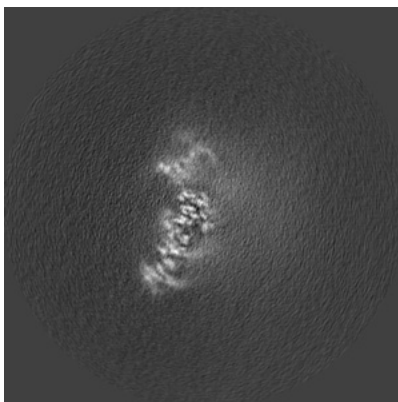


Z Index: 150

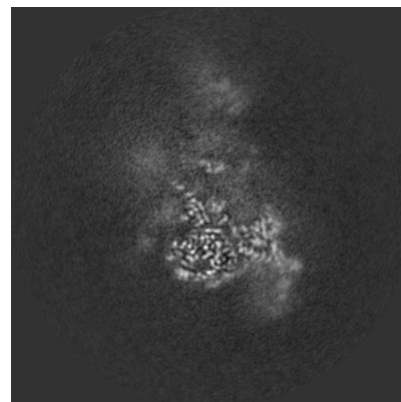
### 6.2.2 Raw map



X Index: 150



Y Index: 150

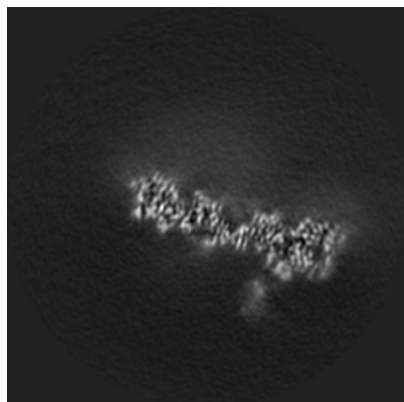


Z Index: 150

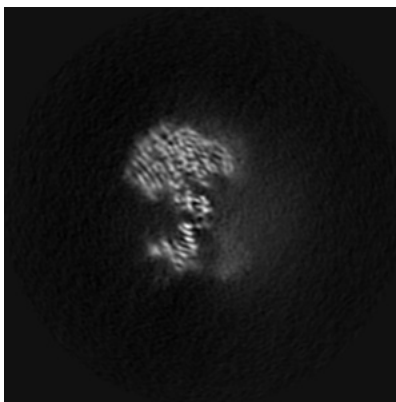
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

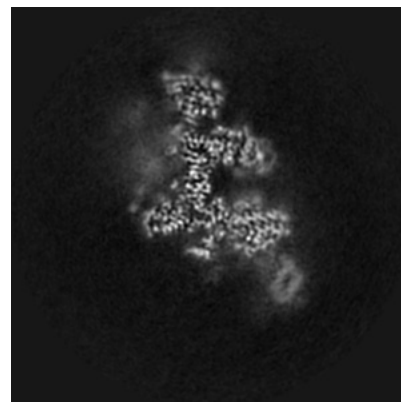
### 6.3.1 Primary map



X Index: 136

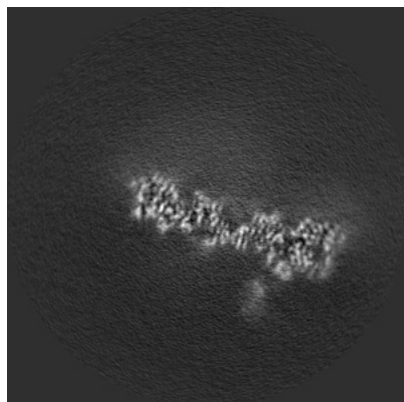


Y Index: 132

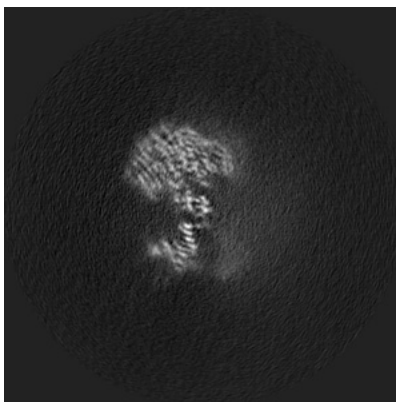


Z Index: 132

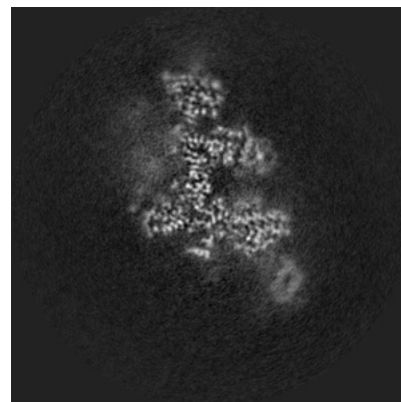
### 6.3.2 Raw map



X Index: 136



Y Index: 132

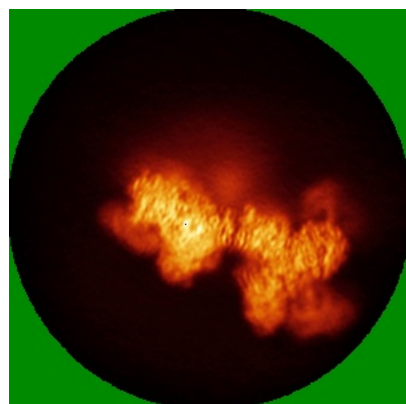


Z Index: 132

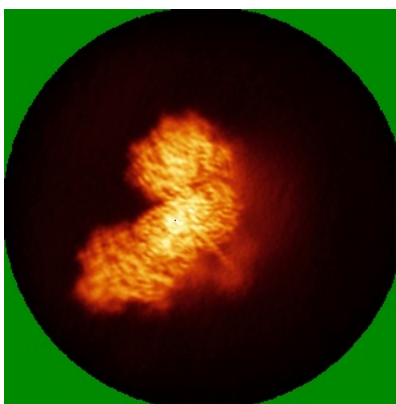
The images above show the largest variance slices of the map in three orthogonal directions.

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

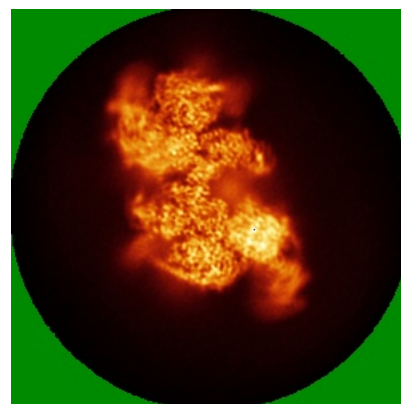
### 6.4.1 Primary map



X

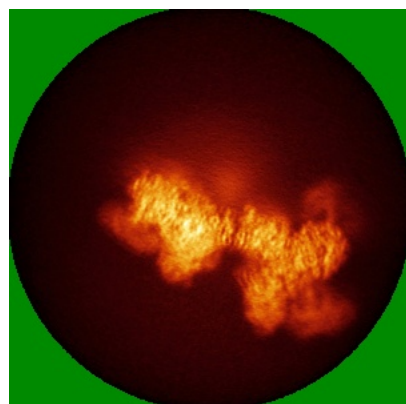


Y

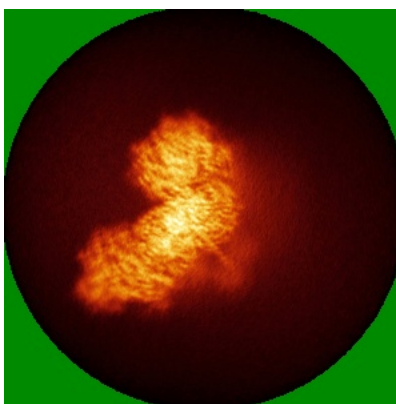


Z

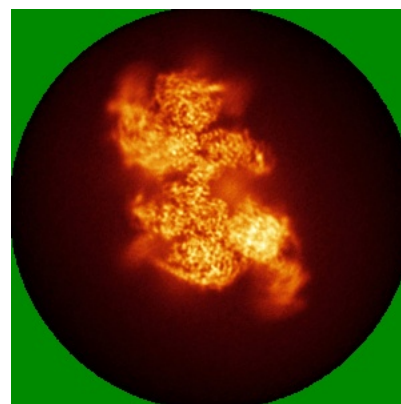
### 6.4.2 Raw map



X



Y



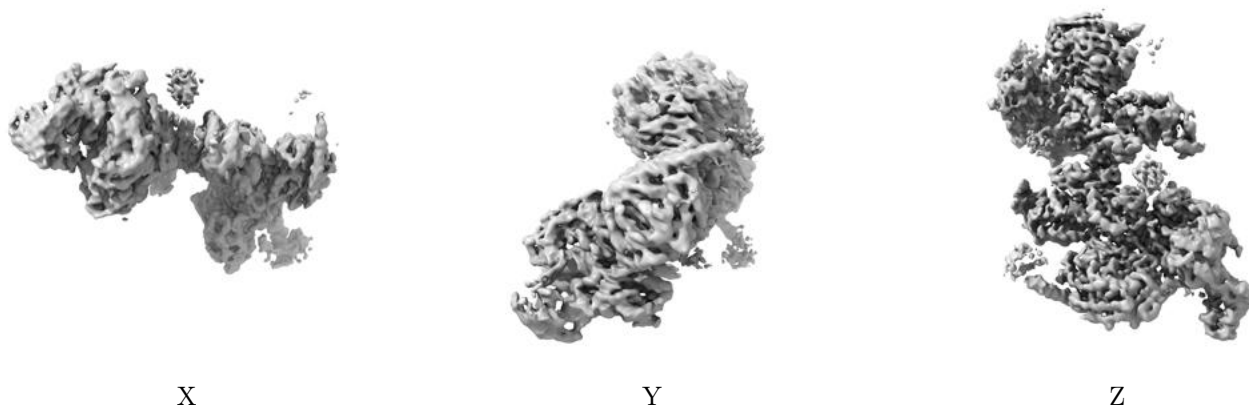
Z

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.



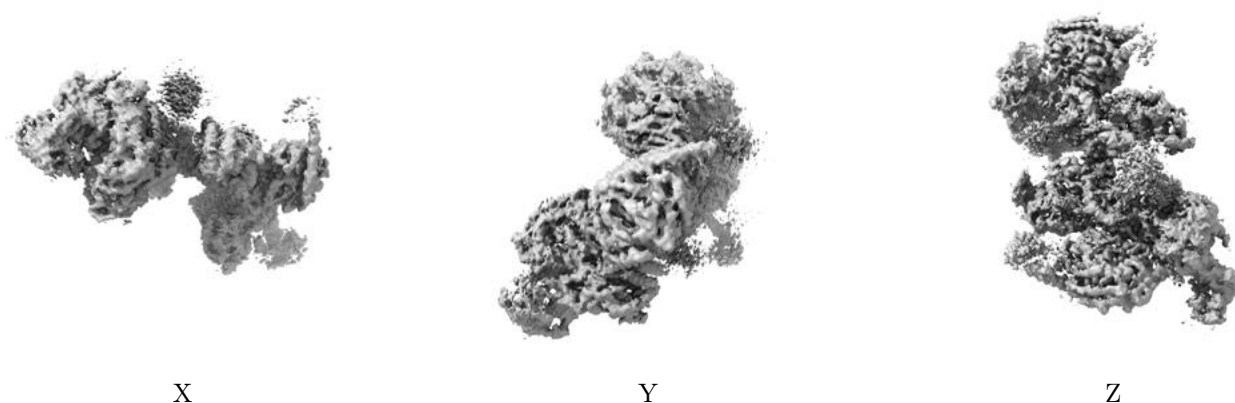
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. 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.

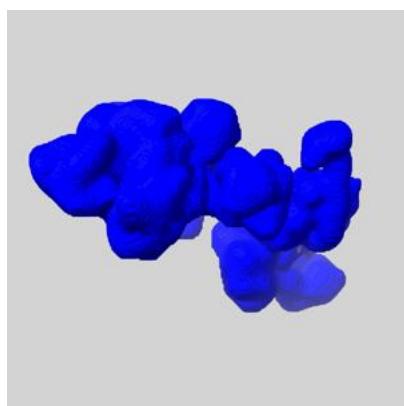
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

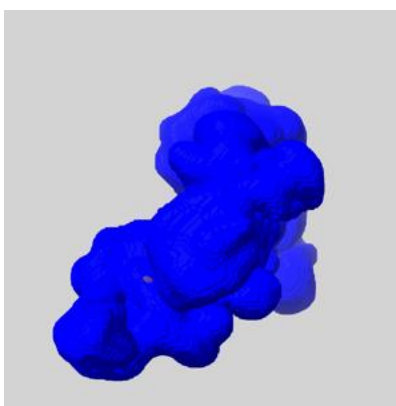
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

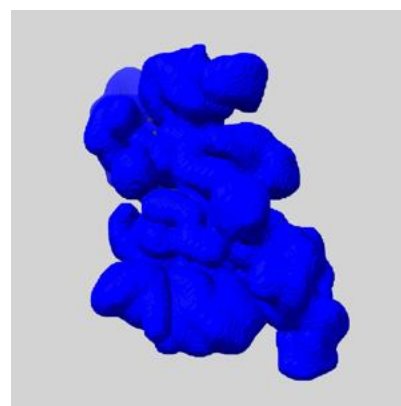
### 6.6.1 emd\_29578\_msk\_1.map [i](#)



X



Y

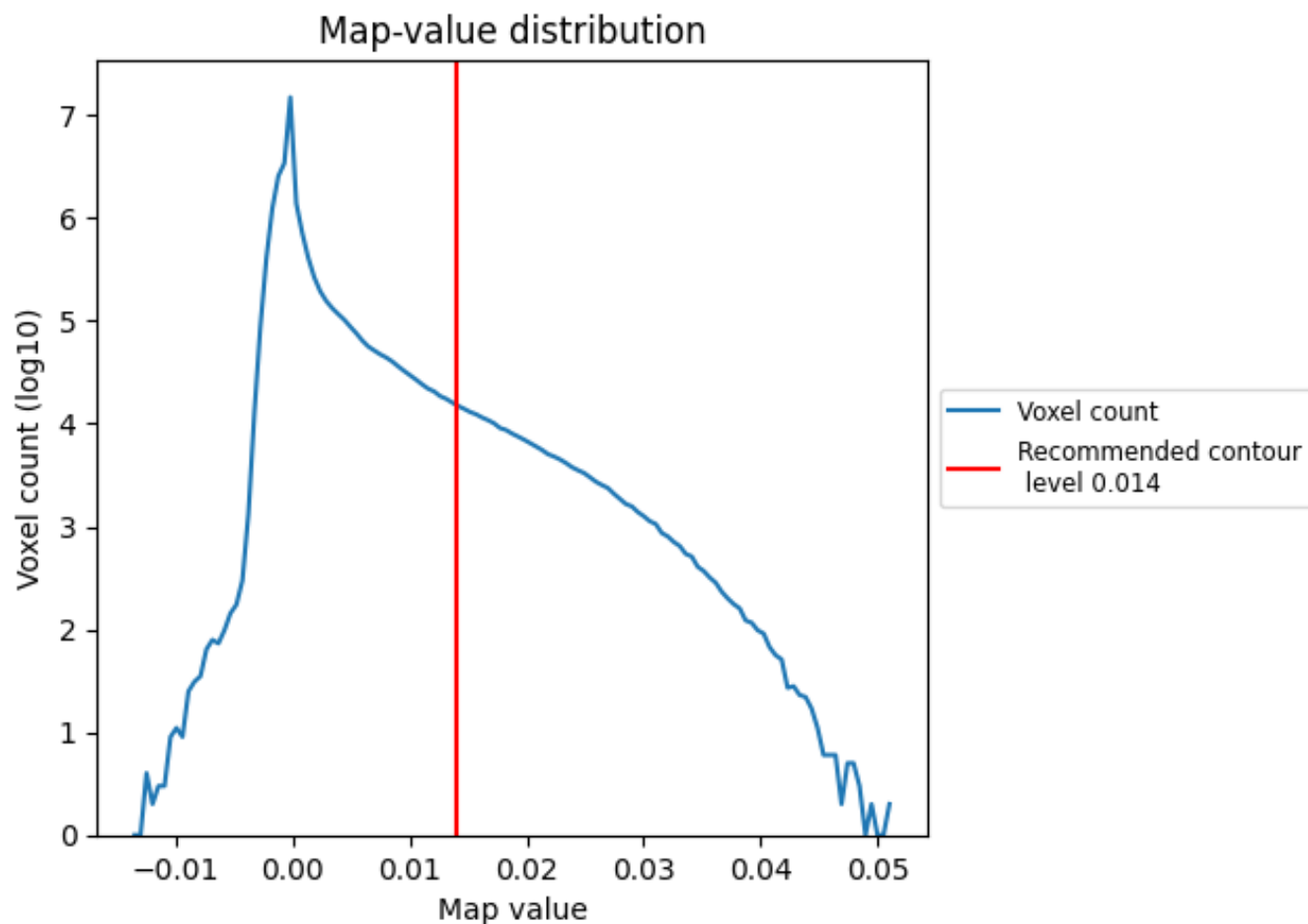


Z

## 7 Map analysis [i](#)

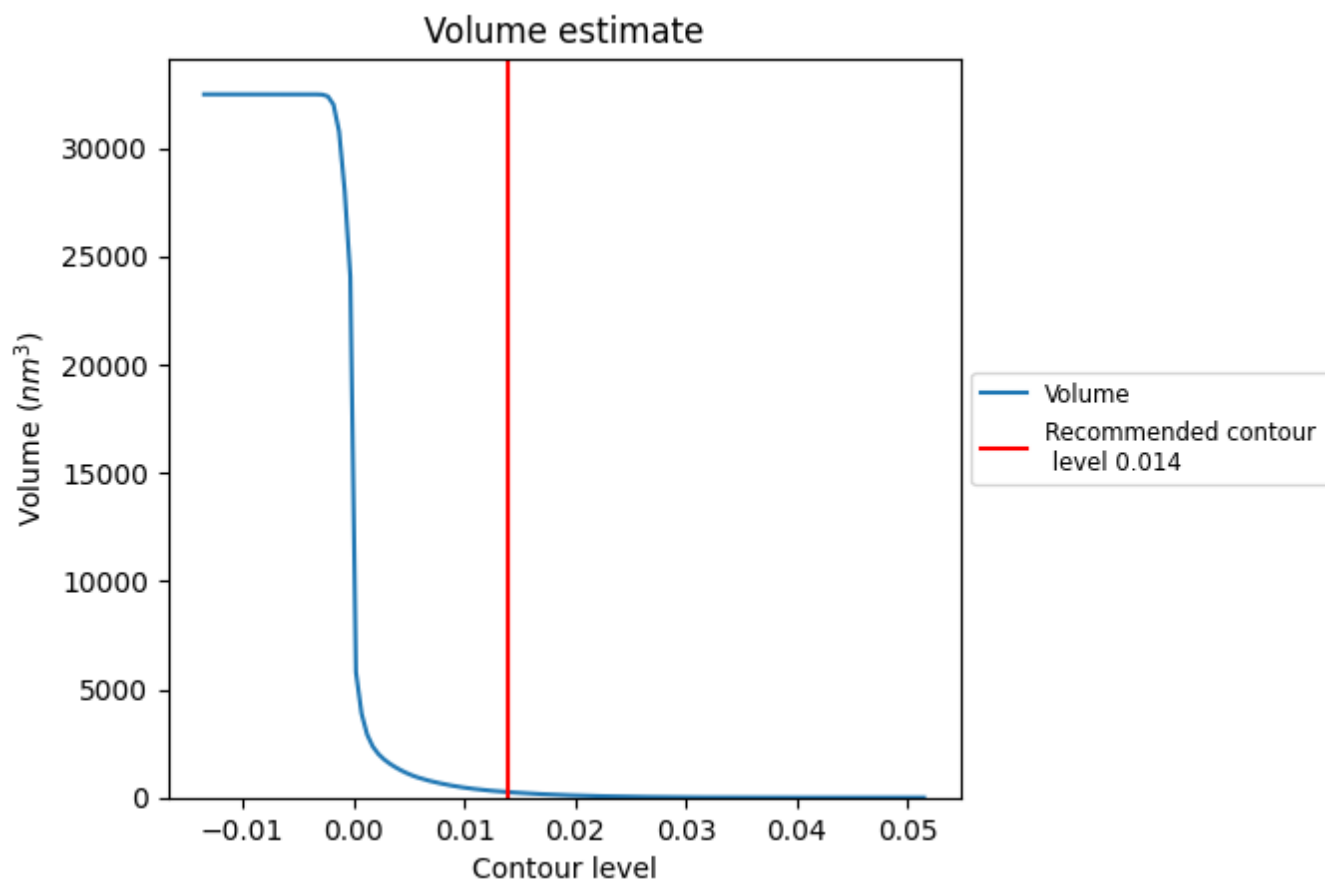
This section contains the results of statistical analysis of the map.

### 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.

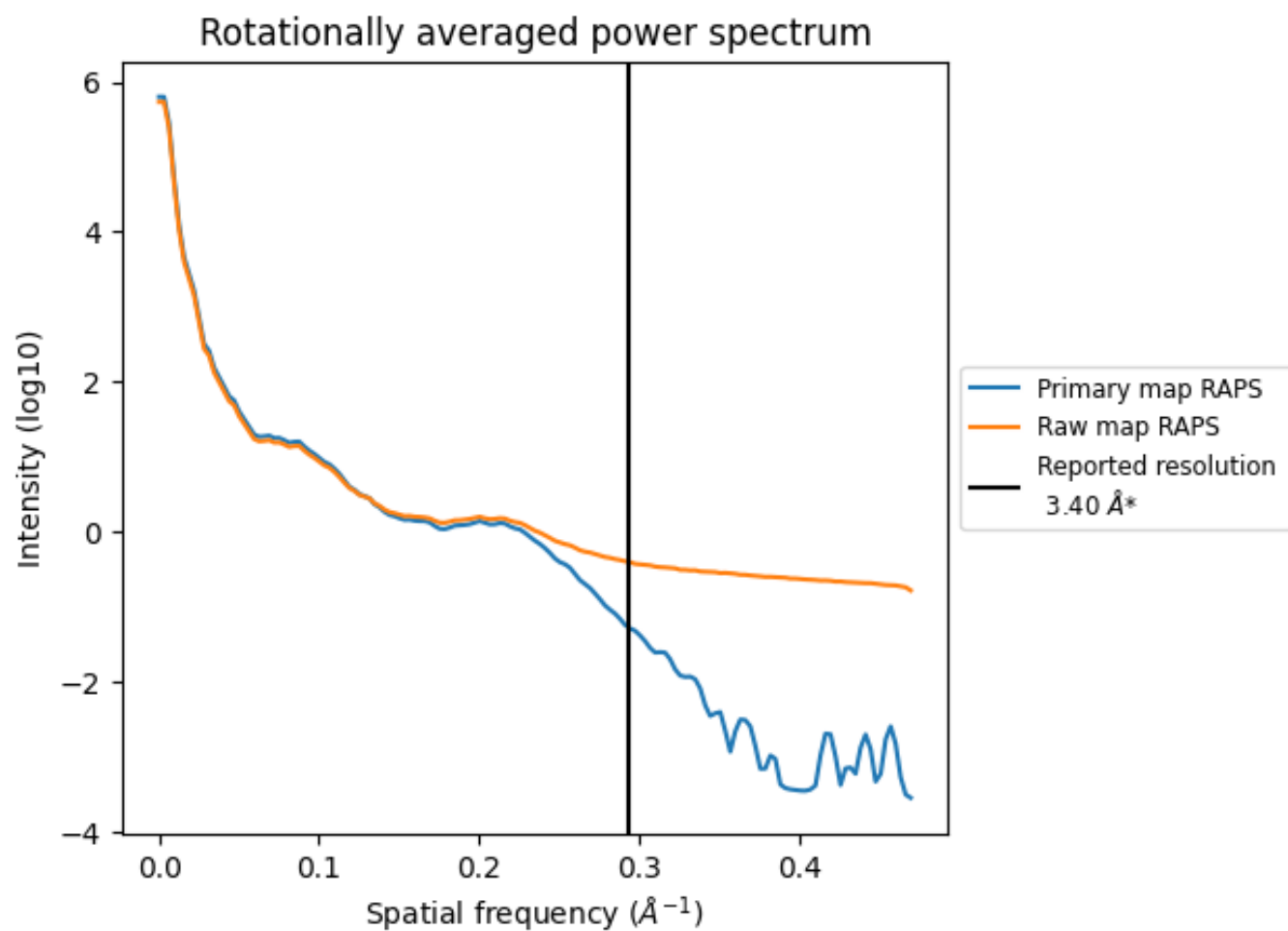
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 250 nm<sup>3</sup>; this corresponds to an approximate mass of 226 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 ⓘ

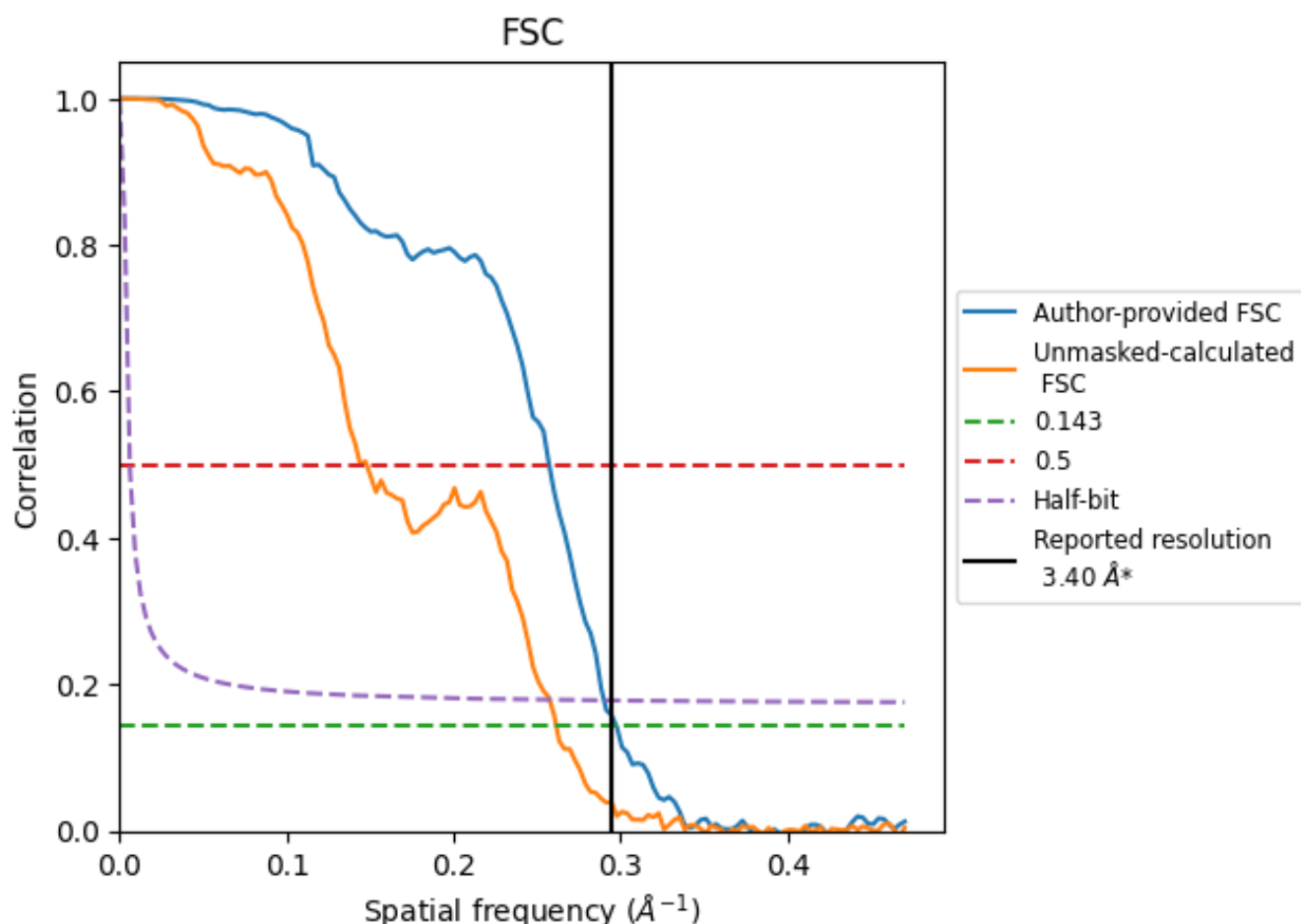


\*Reported resolution corresponds to spatial frequency of 0.294 Å<sup>-1</sup>

## 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  $0.294 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

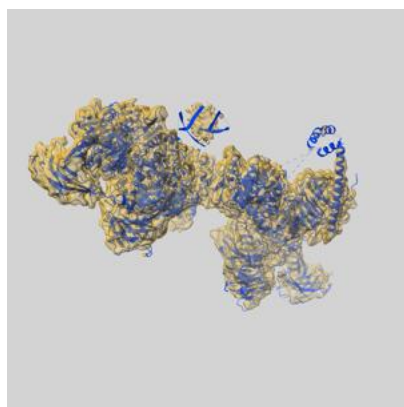
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.36	3.89	3.45
Unmasked-calculated*	3.82	6.93	3.88

\*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 3.82 differs from the reported value 3.4 by more than 10 %

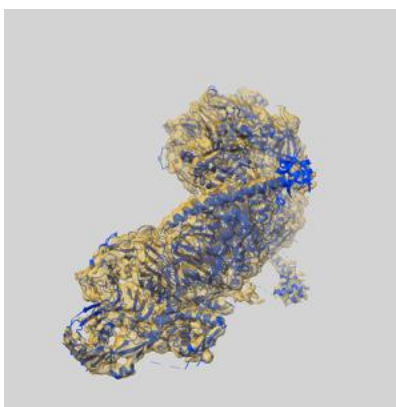
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29578 and PDB model 8FYH. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

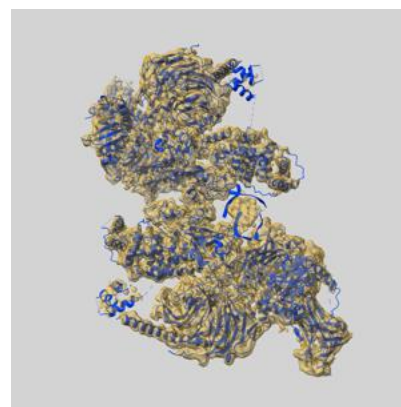
### 9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.014 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.

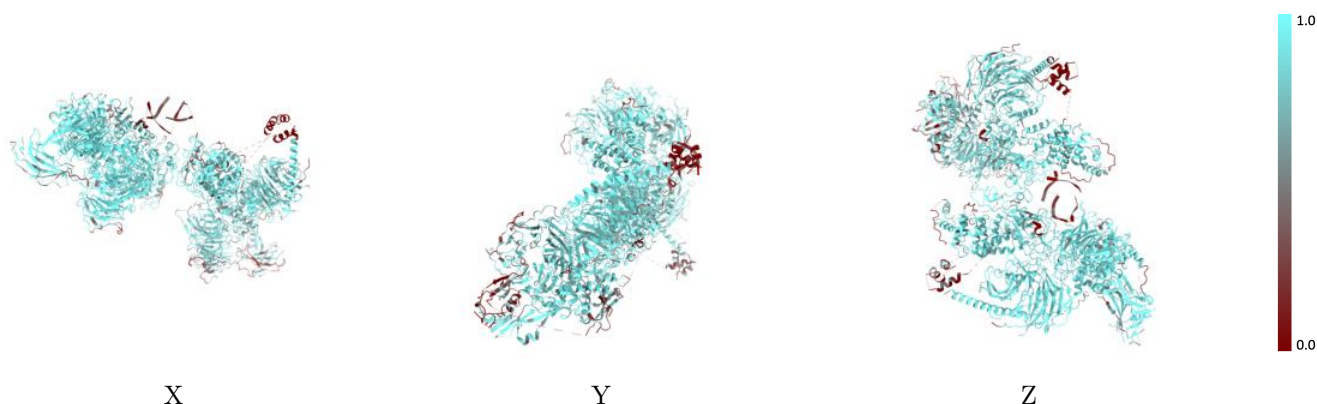


## 9.2 Q-score mapped to coordinate model [i](#)



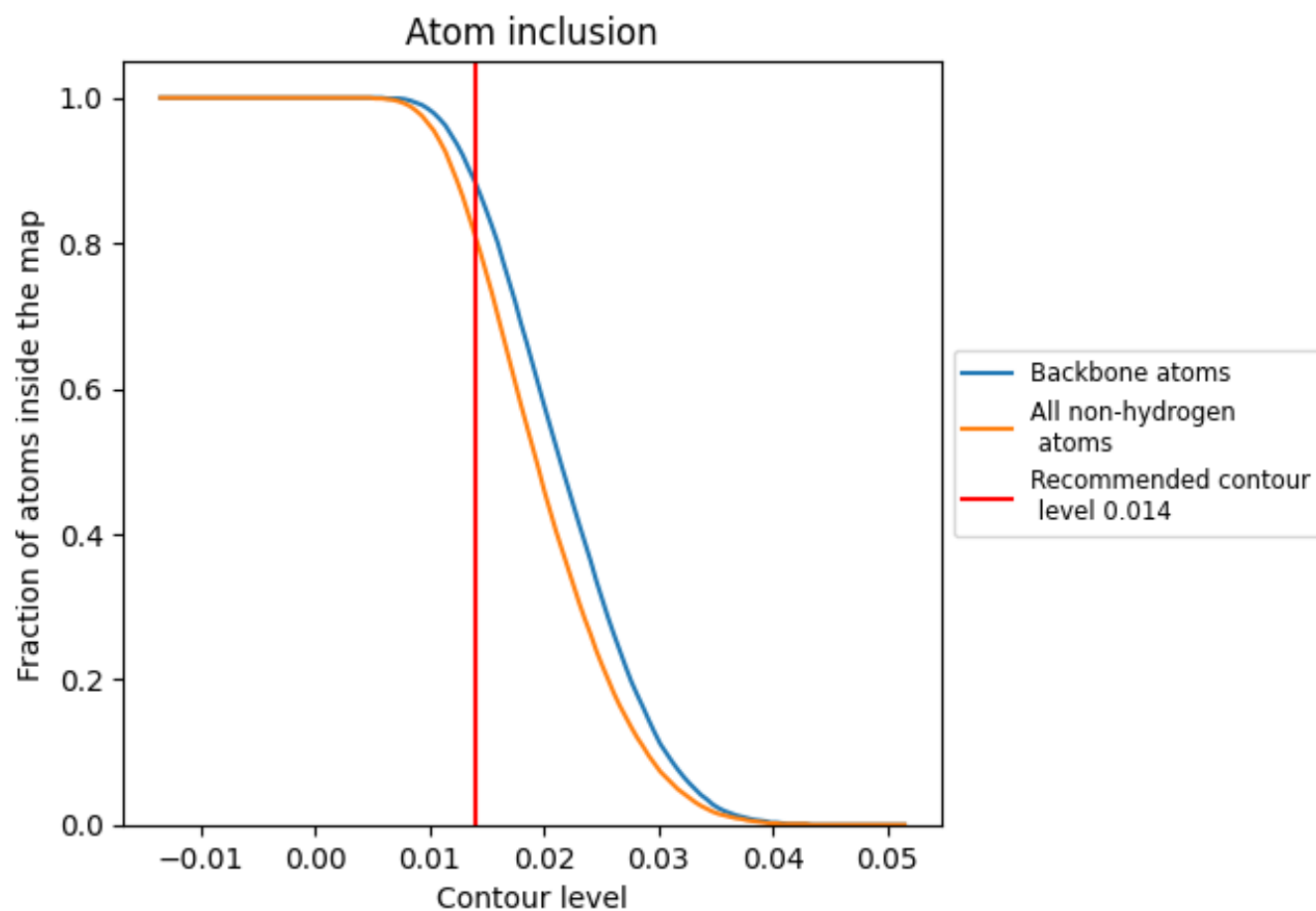
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).





























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 81% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8100	 0.4000
A	 0.7510	 0.4020
B	 0.6970	 0.3520
C	 0.8270	 0.4550
D	 0.7850	 0.3390
E	 0.6590	 0.3140
F	 0.8040	 0.3610
G	 0.7930	 0.4200
H	 0.8570	 0.4010
I	 0.9180	 0.4810
J	 0.9210	 0.4180
K	 0.8320	 0.3710
L	 0.9350	 0.4200
M	 0.2440	 0.0310

