



## wwPDB EM Validation Summary Report ⓘ

Apr 26, 2025 – 12:14 PM EDT

PDB ID : 9DUM / pdb\_00009dum  
EMDB ID : EMD-47170  
Title : Human PELP1-WDR18-TEX10 complex  
Authors : Huang, J.; Tong, L.  
Deposited on : 2024-10-03  
Resolution : 3.56 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)

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<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.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
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) : 2.43.1

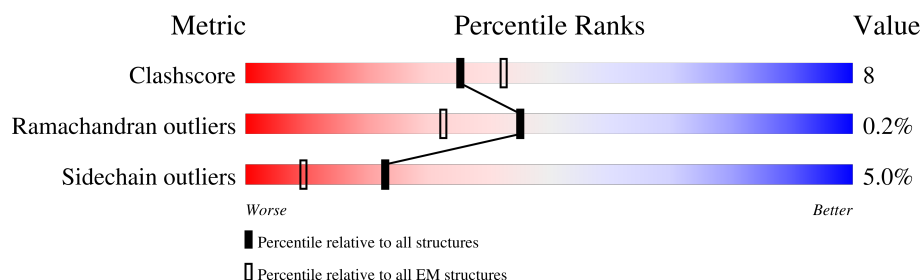
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.56 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  $\geq 3$ , 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	A	434	
1	B	434	
2	C	644	
2	D	644	
3	G	931	
3	H	931	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22662 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 WD repeat-containing protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	358	Total	C	N	O	S	0	0
			2718	1725	468	505	20		
1	B	376	Total	C	N	O	S	0	0
			2872	1819	500	533	20		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP Q9BV38
A	0	ASN	-	expression tag	UNP Q9BV38
B	-1	SER	-	expression tag	UNP Q9BV38
B	0	ASN	-	expression tag	UNP Q9BV38

- Molecule 2 is a protein called Proline-, glutamic acid- and leucine-rich protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	481	Total	C	N	O	S	0	0
			3655	2320	646	660	29		
2	D	485	Total	C	N	O	S	0	0
			3683	2337	653	664	29		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	SER	-	expression tag	UNP Q8IZL8
C	0	ASN	-	expression tag	UNP Q8IZL8
D	-1	SER	-	expression tag	UNP Q8IZL8
D	0	ASN	-	expression tag	UNP Q8IZL8

- Molecule 3 is a protein called Testis-expressed protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	710	Total	C	N	O	S	0	0
			5690	3691	971	1004	24		
3	G	505	Total	C	N	O	S	0	0
			4044	2605	699	722	18		

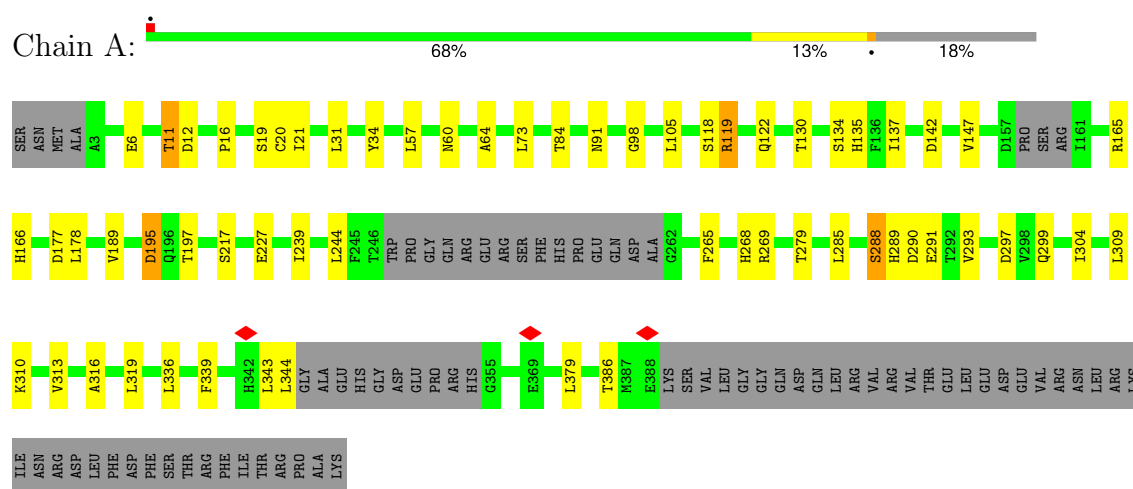
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	SER	-	expression tag	UNP Q9NXF1
H	0	ASN	-	expression tag	UNP Q9NXF1
G	-1	SER	-	expression tag	UNP Q9NXF1
G	0	ASN	-	expression tag	UNP Q9NXF1

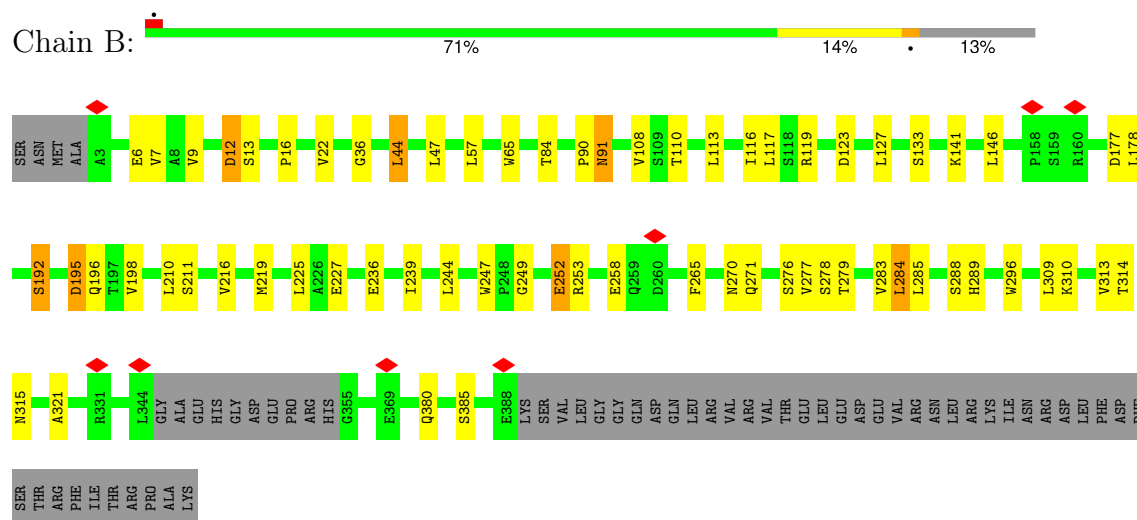
### 3 Residue-property plots

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: WD repeat-containing protein 18

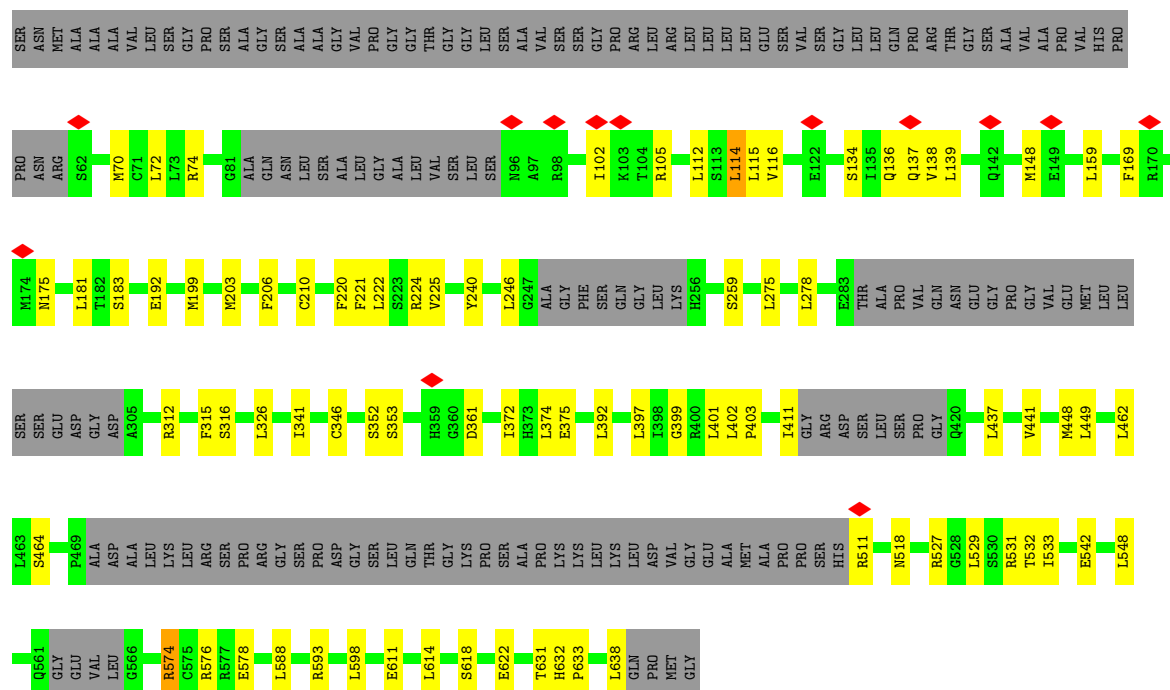


- Molecule 1: WD repeat-containing protein 18

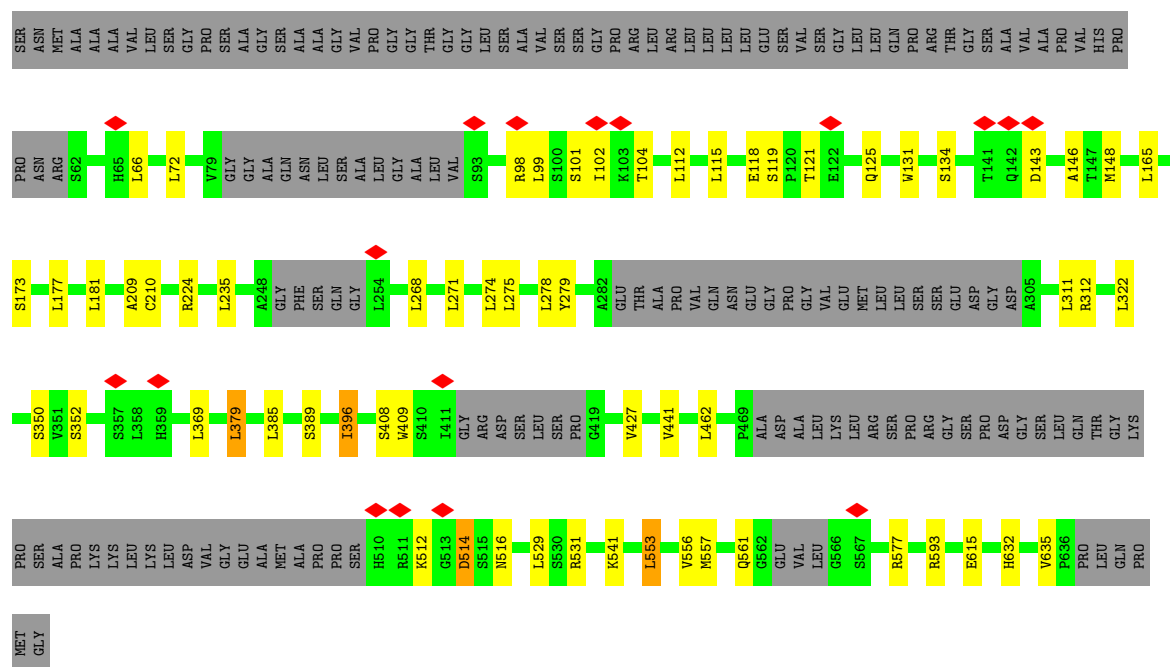


- Molecule 2: Proline-, glutamic acid- and leucine-rich protein 1

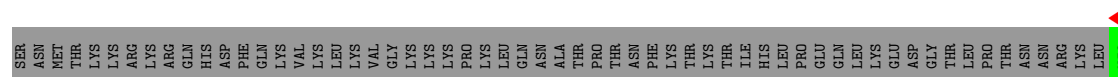
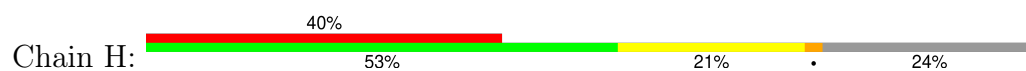




• Molecule 2: Proline-, glutamic acid- and leucine-rich protein 1



• Molecule 3: Testis-expressed protein 10





N890	H818	L713	T595	L502	V442	TRP	ILE	GLU	ALA	SER	VAL	ILE
I891	L819	S714	I599	I503	S443	ARG	GLN	ASP	GLY	ILE	GLN	ASP
T892	R820	P715	I599	I503	LEU	LYS	LEU	SER	SER	LEU	LEU	LEU
T893	K821	V716	P602	A505	ALA	ASN	GLN	PRO	GLY	LEU	GLN	GLN
L894	R822	L717	A606	V507	ALA	TYR	LEU	LEU	ARG	LEU	PHE	LEU
L894	R823	L718	A606	T508	ALA	LEU	ILE	ILE	ARG	LEU	ALA	MET
S896	K824	L727	R617	L509	THR	ASP	GLU	CYS	GLU	VAL	PRO	HIS
S896	L825	L727	L618	L510	THR	PHE	GLN	TRP	SER	GLY	LYS	TYR
G897	W626	V732	L618	Q511	GLN	LYS	TRP	TRP	GLU	GLU	ILE	ILE
S898	G827	V732	L618	Q511	GLN	LYS	TRP	TRP	GLU	GLU	ILE	ILE
S898	V830	V736	L625	Q512	ASP	HIS	VAL	VAL	GLY	GLY	ARG	ASN
V899	V830	F737	P626	Q512	ASP	HIS	GLU	GLU	LEU	LEU	ARG	ASN
Q900	V837	F737	S627	R513	CYS	PHE	ALA	ALA	PRO	PRO	PHE	ALA
E901	V837	Q749	L628	G514	SER	MET	VAL	VAL	GLU	GLU	GLN	GLN
Q902	R841	Q749	P629	L515	ILE	ARG	PRO	PRO	LYS	LYS	SER	GLN
W903	L842	L752	D631	I516	E458	PHE	GLN	GLN	GLU	GLU	SER	SER
L904	M843	L753	L632	L517	M459	PRO	ALA	ALA	ASN	ASN	LYS	ALA
T905	L844	Q754	L633	P518	I460	TYR	THR	THR	HIS	HIS	GLY	PHE
D906	Q845	L761	M642	V519	R461	VAL	PRO	PRO	ALA	ALA	ILE	PRO
L907	Q845	L761	M642	R520	K462	LYS	VAL	VAL	THR	THR	LEU	LEU
H908	R848	L764	S646	T521	F463	GLU	GLY	GLY	THR	THR	VAL	VAL
Y909	V849	V766	L649	L522	V464	ILE	ASN	ASN	SER	SER	VAL	VAL
C910	N850	V767	R660	F527	T465	THR	GLY	GLY	SER	ASP	ALA	ASP
F911	R851	P768	R660	F527	E466	LYS	ASN	ILE	GLN	GLN	HIS	LEU
N912	V852	D769	S770	Y631	T467	HIS	LYS	GLY	D275	D275	GLN	LEU
Y913	G853	T771	G665	Q532	T468	ARG	LYS	ARG	Q276	Q276	SER	SER
Y914	P854	A772	W666	T533	L468	GLY	PRO	GLU	I279	I279	TRP	ALA
I915	E855	G773	K667	E534	E469	GLU	PRO	LEU	Q250	Q250	ILE	THR
T916	E856	V778	Y668	E535	D470	PRO	ASN	VAL	E283	E283	SER	HIS
G917	L857	V778	S669	L536	G471	ASN	GLN	MET	N290	N290	VAL	ILE
HIS	P858	H785	A670	ARG	S472	LYS	GLN	GLN	R298	R298	PRO	GLY
PRO	V859	V789	K671	SER	R473	ILE	VAL	VAL	TYR	TYR	GLY	ILE
GLY	V859	V789	D672	CYS	L474	LYS	GLN	GLN	ARG	ARG	ASN	SER
PRO	L863	S790	N673	PHE	N475	HIS	VAL	VAL	LEU	LEU	GLN	LEU
ALA	L864	E791	L684	ARG	S476	THR	ILE	ILE	VAL	VAL	ASP	ILE
ALA	R865	L866	L684	Y543	K477	VAL	THR	THR	GLY	GLY	SER	LEU
ALA	L866	L866	L684	R544	Q478	LEU	VAL	VAL	LEU	LEU	GLN	GLY
VAL	L867	A798	F691	S545	L479	SER	ASN	ASN	LEU	LEU	LYS	LYS
VAL	L868	S799	S692	K546	N480	ASN	ASN	TRP	SER	ARG	TRP	VAL
TYR	Q869	S799	K693	K546	R481	ASN	ASN	TRP	LEU	LEU	ARG	THR
TYR	H870	C800	E694	S549	L482	ILE	LYS	LYS	GLY	GLY	THR	ALA
TYR	A871	Y802	E695	S549	L483	LEU	LEU	LEU	VAL	VAL	ASP	ALA
TYR	A871	S803	L696	W551	L483	SER	LYS	LYS	ASP	ASP	ILE	PHE
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR	GLY	GLY	GLY	GLY	LEU	THR
TYR	A871	L604	L696	W551	L483	THR						



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	268599	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	51	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.296	Depositor
Minimum map value	-1.700	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.284	Depositor
Map size (Å)	324.9, 324.9, 324.9	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.21	0/2777	0.39	2/3777 (0.1%)
1	B	0.21	0/2940	0.42	1/4002 (0.0%)
2	C	0.12	0/3720	0.26	0/5043
2	D	0.12	0/3748	0.27	0/5079
3	G	0.14	0/4124	0.33	0/5597
3	H	0.18	0/5799	0.41	1/7860 (0.0%)
All	All	0.17	0/23108	0.35	4/31358 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	530	ILE	N-CA-C	-8.70	104.68	113.47
1	A	195	ASP	CA-CB-CG	6.67	119.27	112.60
1	B	195	ASP	CA-CB-CG	6.12	118.72	112.60
1	A	290	ASP	CA-CB-CG	5.62	118.22	112.60

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2718	0	2708	26	0
1	B	2872	0	2846	40	0
2	C	3655	0	3772	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3683	0	3805	39	0
3	G	4044	0	4169	71	0
3	H	5690	0	5920	150	0
All	All	22662	0	23220	352	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 8.

The worst 5 of 352 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)
3:H:503:ILE:HD11	3:H:530:ILE:HD11	1.29	1.13
3:H:527:PHE:HA	3:H:530:ILE:HG22	1.34	1.07
3:H:503:ILE:HD11	3:H:530:ILE:CD1	1.95	0.97
1:B:270:ASN:ND2	3:H:742:VAL:HG13	1.81	0.94
3:H:527:PHE:CA	3:H:530:ILE:HG22	1.97	0.94

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	350/434 (81%)	325 (93%)	25 (7%)	0	100	100
1	B	372/434 (86%)	342 (92%)	30 (8%)	0	100	100
2	C	467/644 (72%)	457 (98%)	10 (2%)	0	100	100
2	D	471/644 (73%)	457 (97%)	14 (3%)	0	100	100
3	G	497/931 (53%)	447 (90%)	49 (10%)	1 (0%)	44	74
3	H	688/931 (74%)	652 (95%)	32 (5%)	4 (1%)	22	56
All	All	2845/4018 (71%)	2680 (94%)	160 (6%)	5 (0%)	45	74

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	180	SER
3	H	355	VAL
3	H	132	GLU
3	G	532	GLN
3	H	532	GLN

### 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	303/370 (82%)	283 (93%)	20 (7%)	14	42
1	B	319/370 (86%)	301 (94%)	18 (6%)	17	46
2	C	408/528 (77%)	389 (95%)	19 (5%)	22	51
2	D	411/528 (78%)	399 (97%)	12 (3%)	37	64
3	G	458/845 (54%)	436 (95%)	22 (5%)	21	51
3	H	646/845 (76%)	611 (95%)	35 (5%)	18	47
All	All	2545/3486 (73%)	2419 (95%)	126 (5%)	23	49

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	66	LEU
3	G	555	LEU
3	H	122	LEU
3	G	549	SER
3	G	805	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
3	G	566	ASN
3	G	886	GLN

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Mol	Chain	Res	Type
3	G	585	ASN
3	G	725	GLN
2	C	164	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

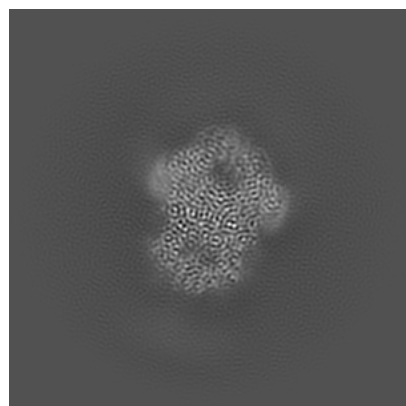
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47170. These allow visual inspection of the internal detail of the map and identification of artifacts.

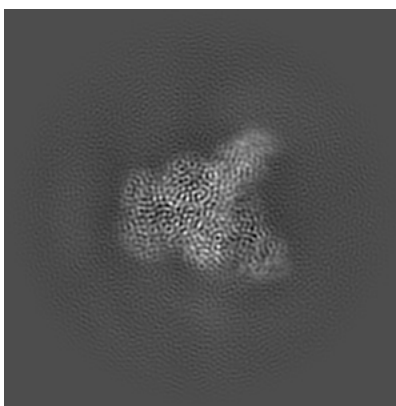
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

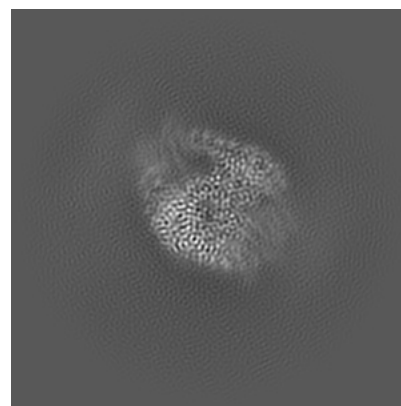
#### 6.1.1 Primary map



X

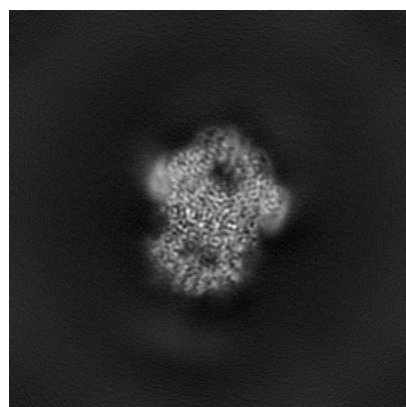


Y

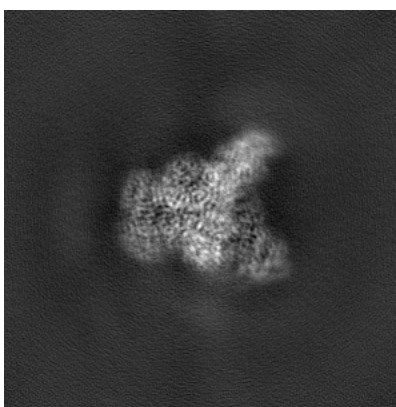


Z

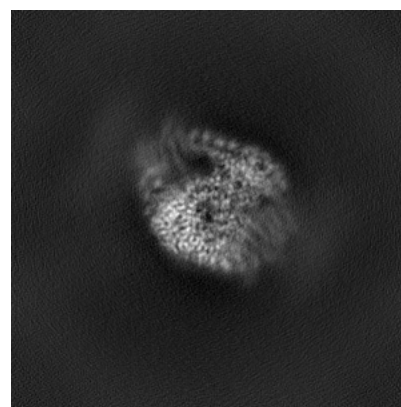
#### 6.1.2 Raw map



X



Y

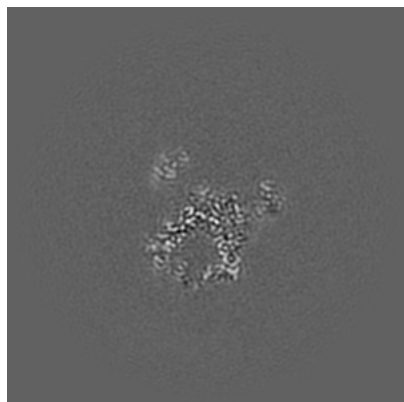


Z

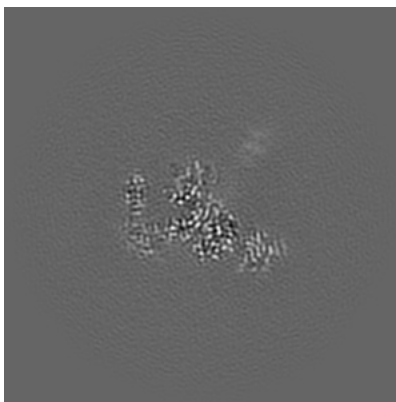
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

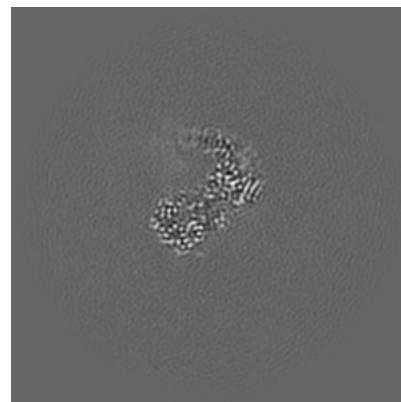
### 6.2.1 Primary map



X Index: 150

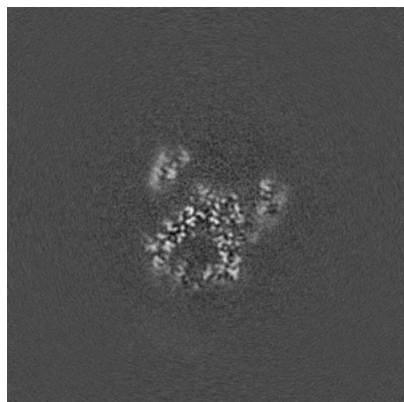


Y Index: 150

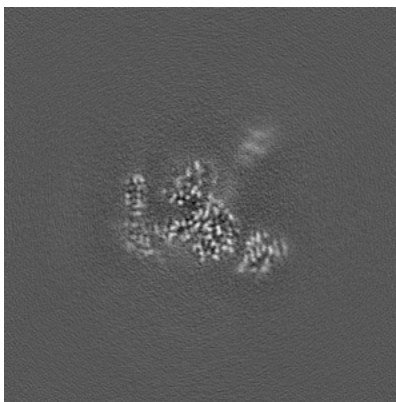


Z Index: 150

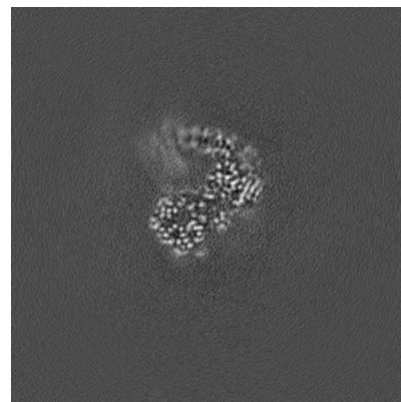
### 6.2.2 Raw map



X Index: 150



Y Index: 150



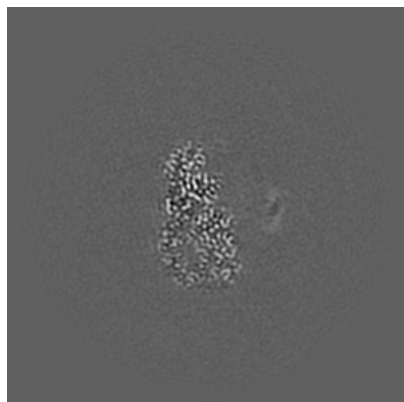
Z Index: 150

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

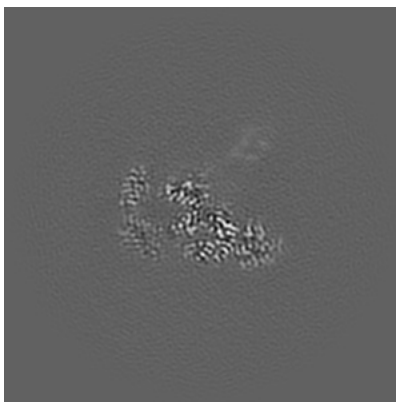


## 6.3 Largest variance slices [i](#)

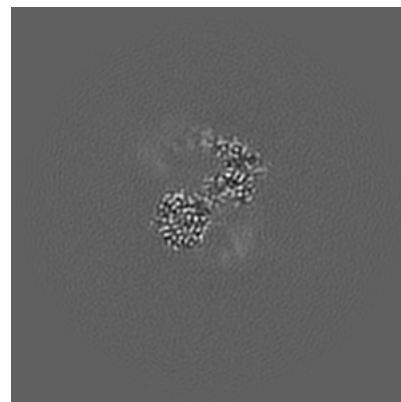
### 6.3.1 Primary map



X Index: 133

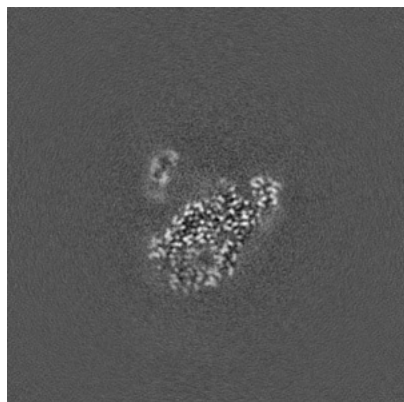


Y Index: 144

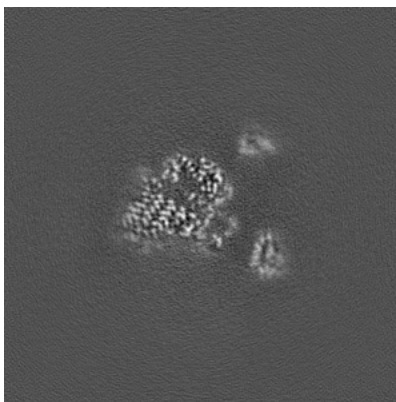


Z Index: 157

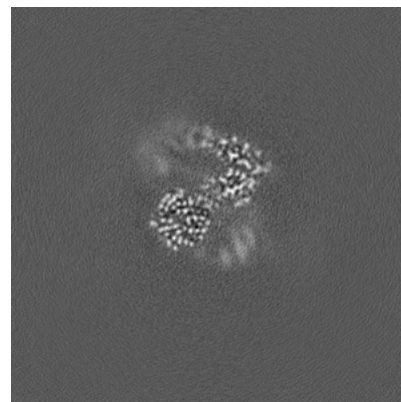
### 6.3.2 Raw map



X Index: 158



Y Index: 161



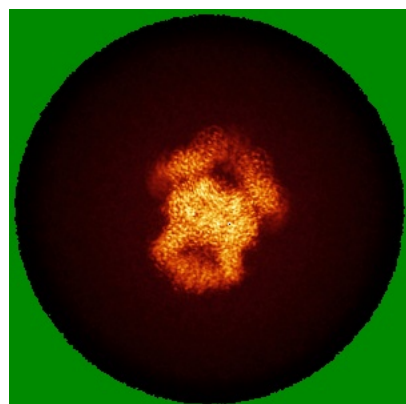
Z Index: 158

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

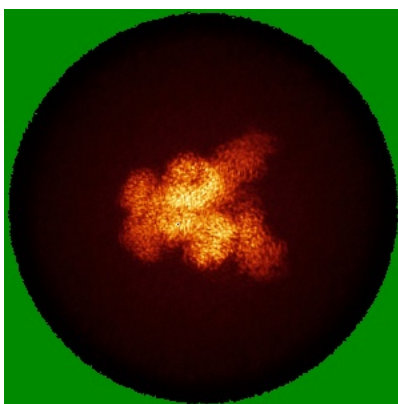


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

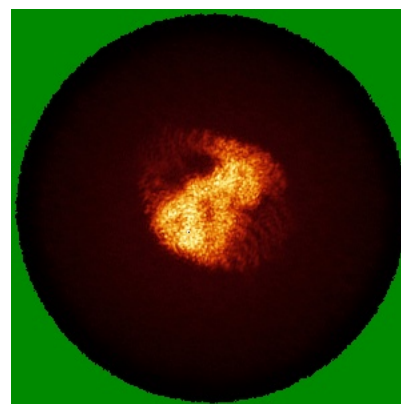
### 6.4.1 Primary map



X

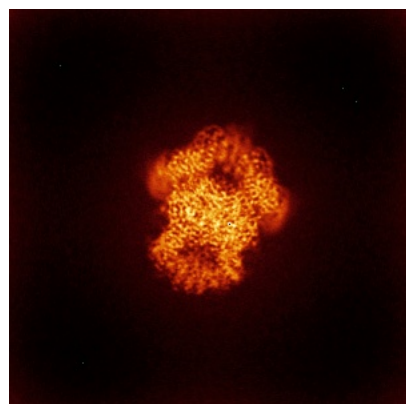


Y

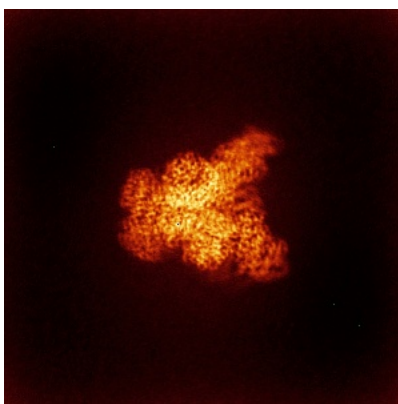


Z

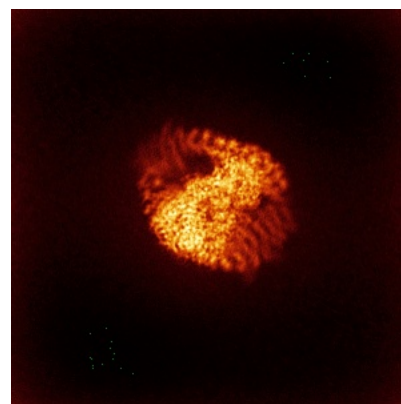
### 6.4.2 Raw map



X



Y

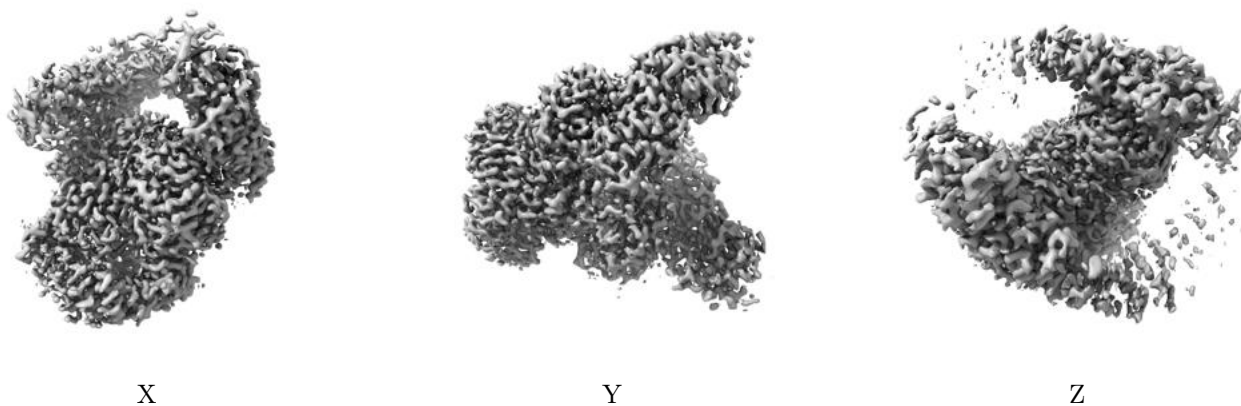


Z

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.

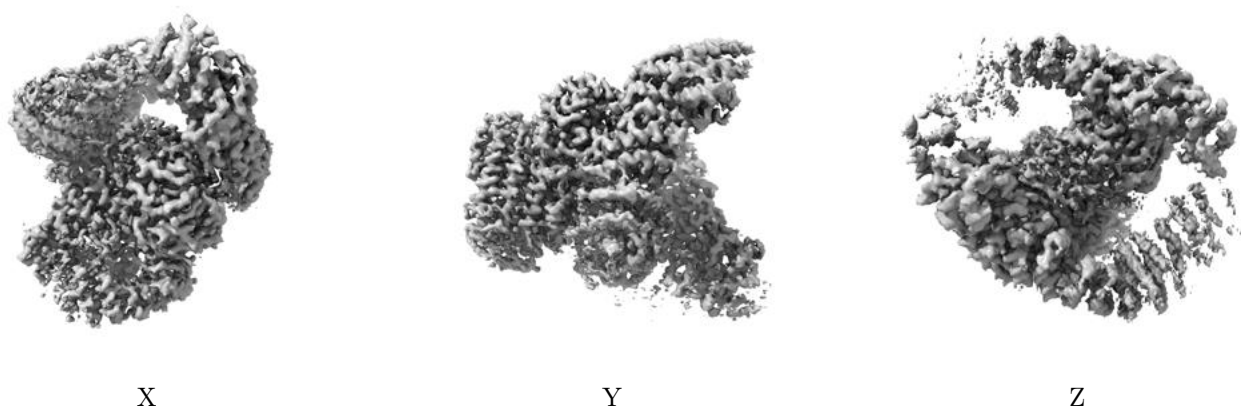
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.284. 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.

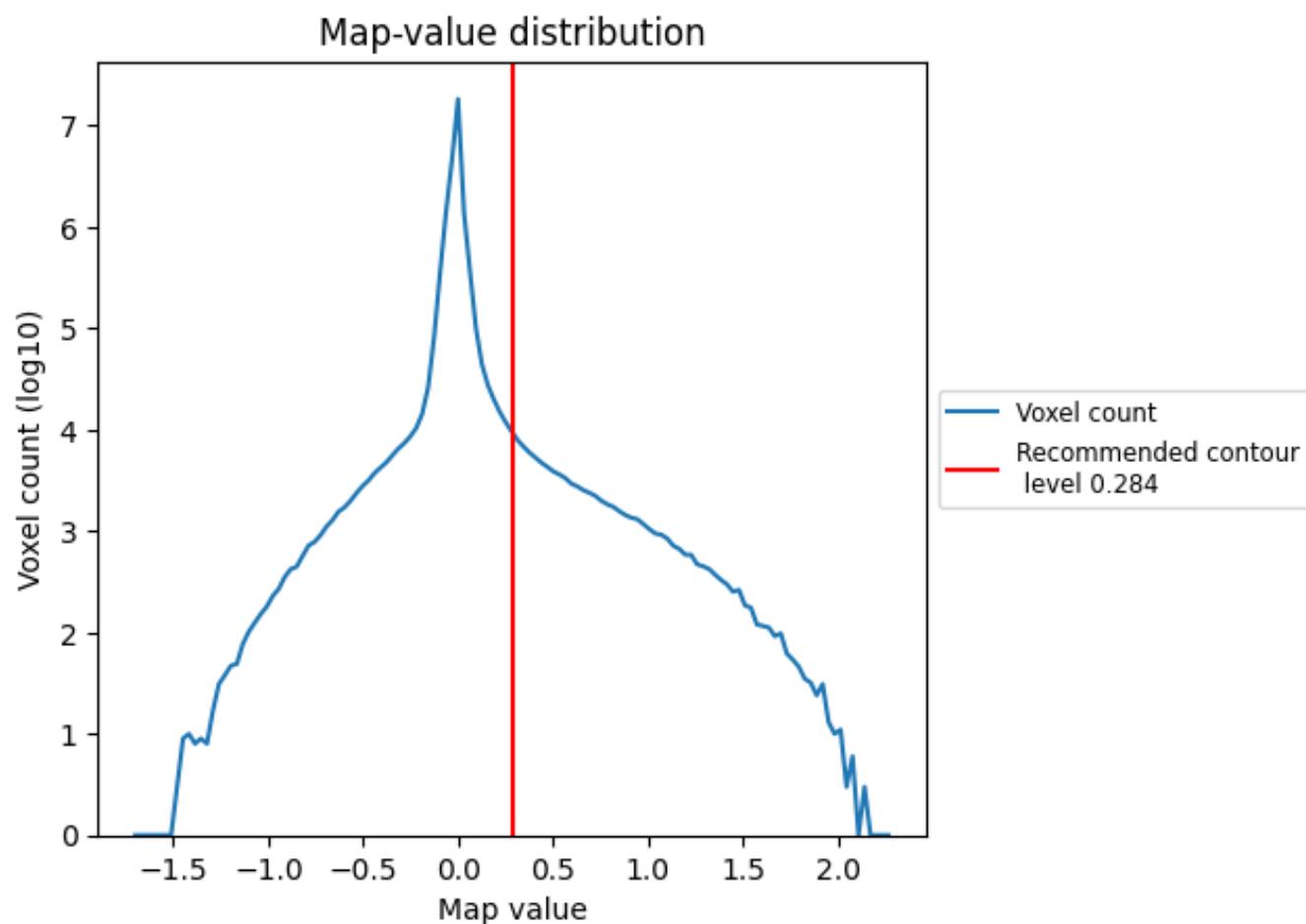
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

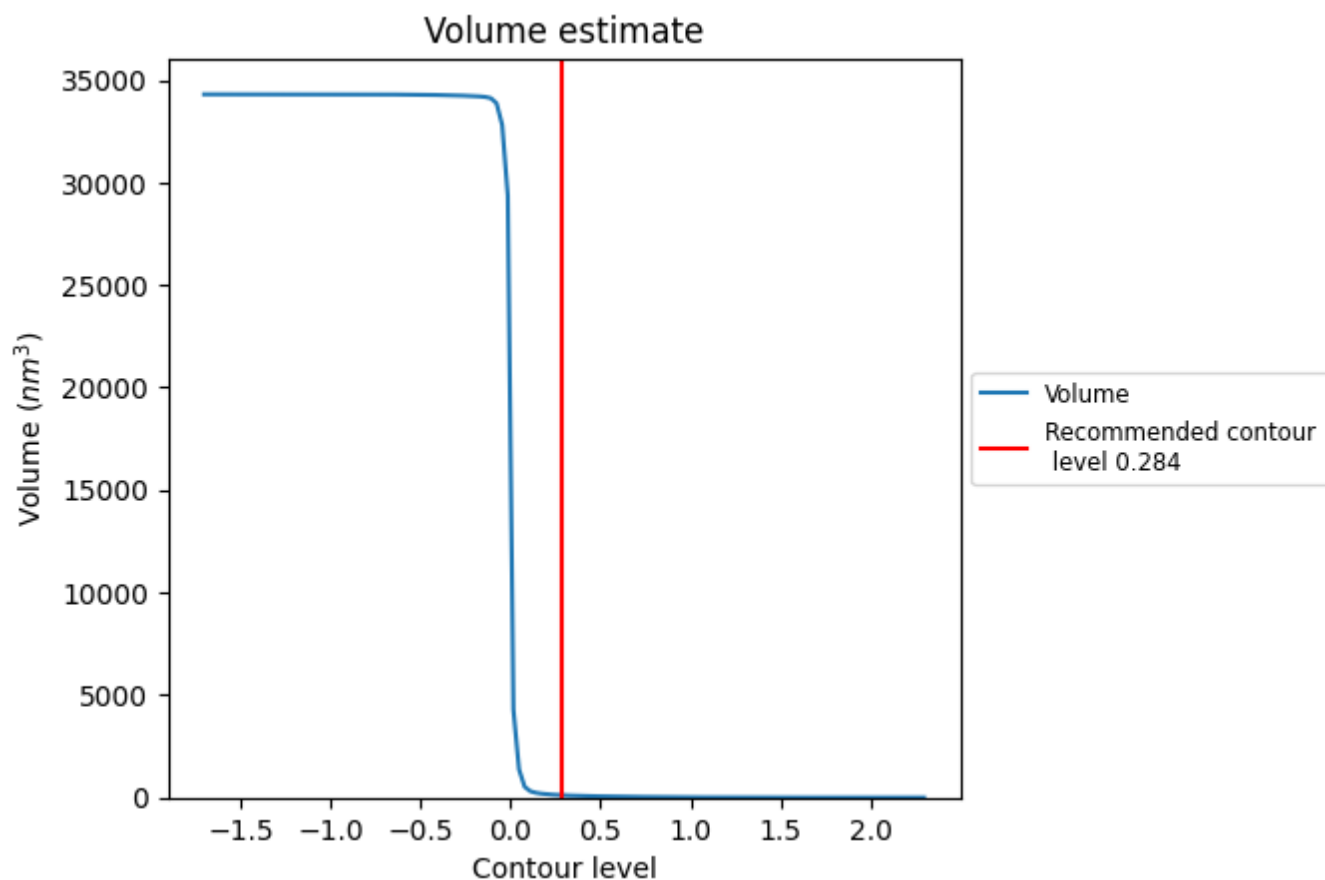
This section contains the results of statistical analysis of the map.

### 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.

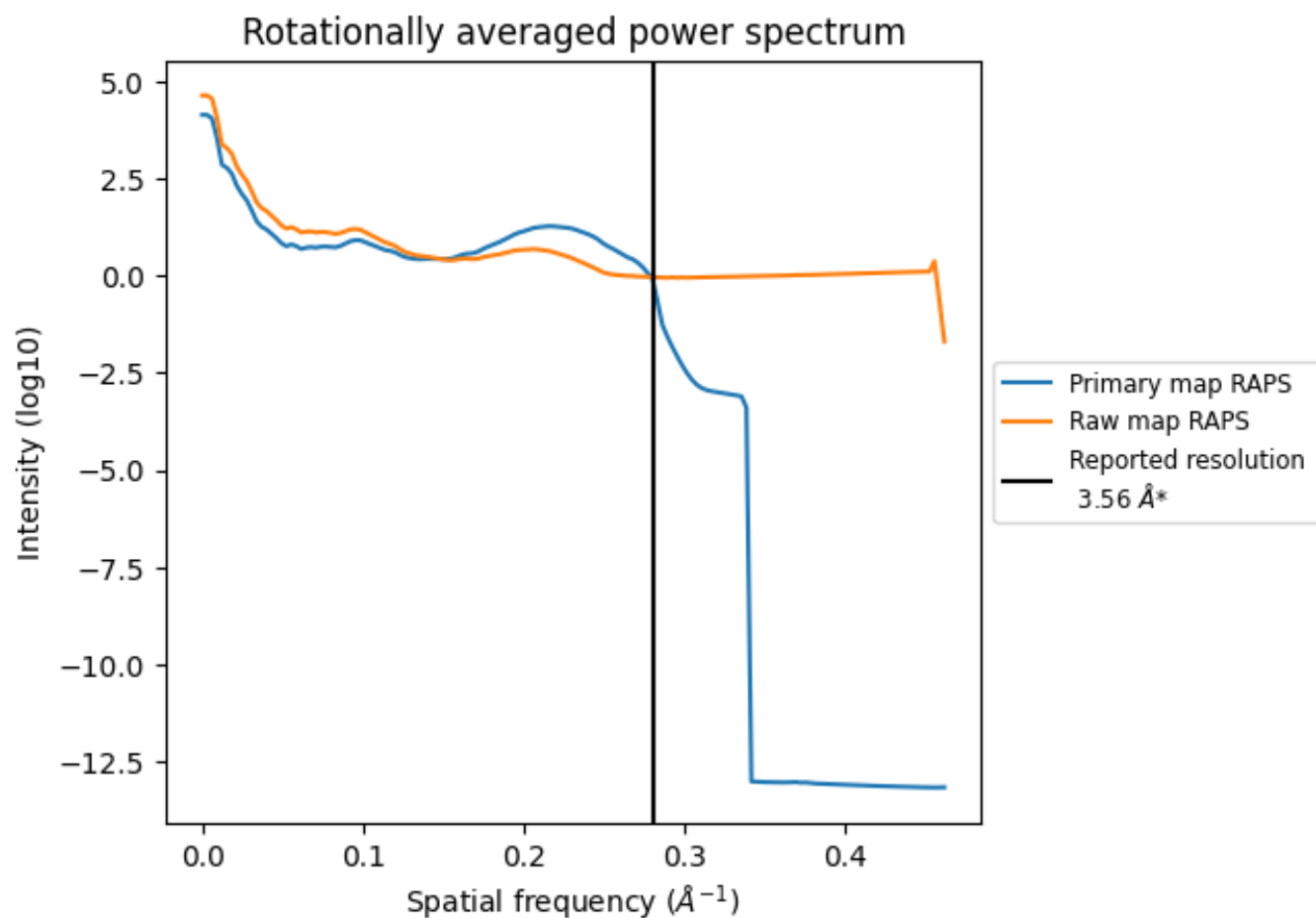
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 115 nm<sup>3</sup>; this corresponds to an approximate mass of 104 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 ⓘ

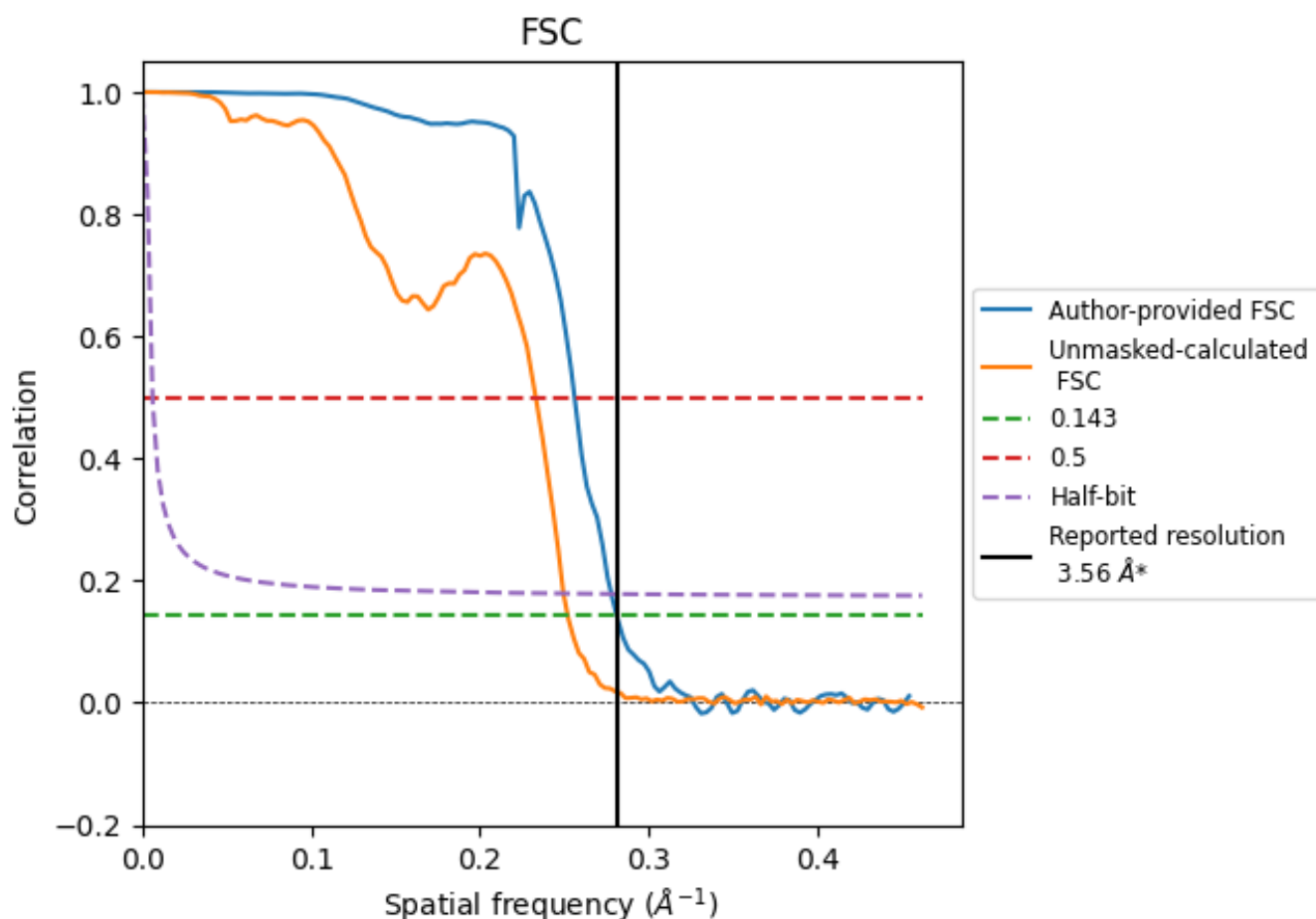


\*Reported resolution corresponds to spatial frequency of 0.281 Å<sup>-1</sup>

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

## 8.2 Resolution estimates [i](#)

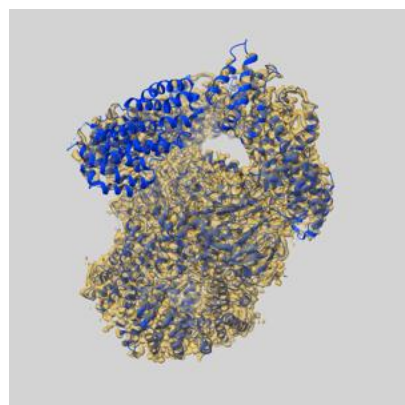
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.56	-	-
Author-provided FSC curve	3.56	3.91	3.60
Unmasked-calculated*	3.97	4.29	4.01

\*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 3.97 differs from the reported value 3.56 by more than 10 %

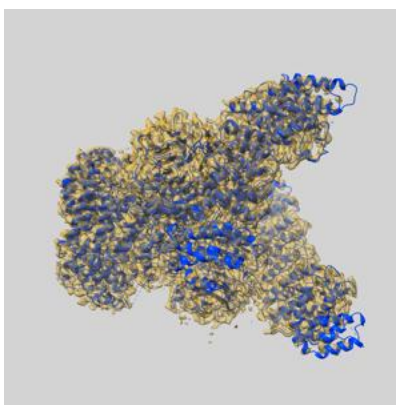
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47170 and PDB model 9DUM. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

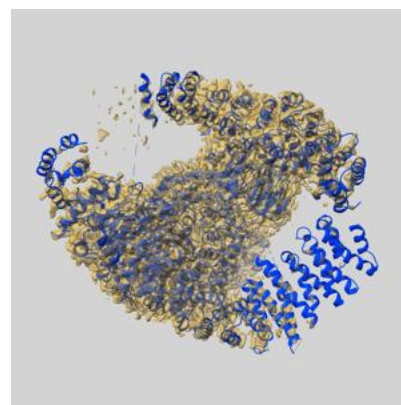
### 9.1 Map-model overlay [i](#)



X



Y

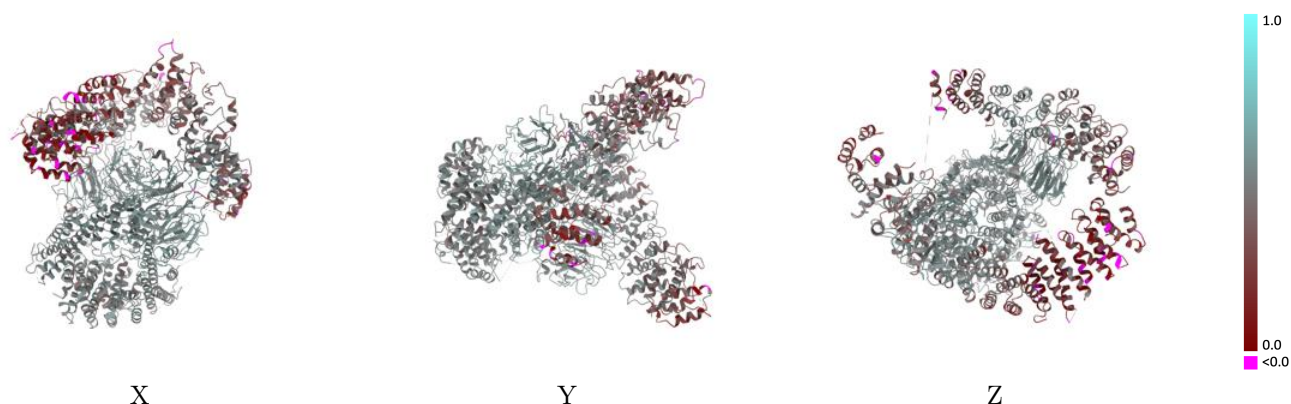


Z

The images above show the 3D surface view of the map at the recommended contour level 0.284 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.

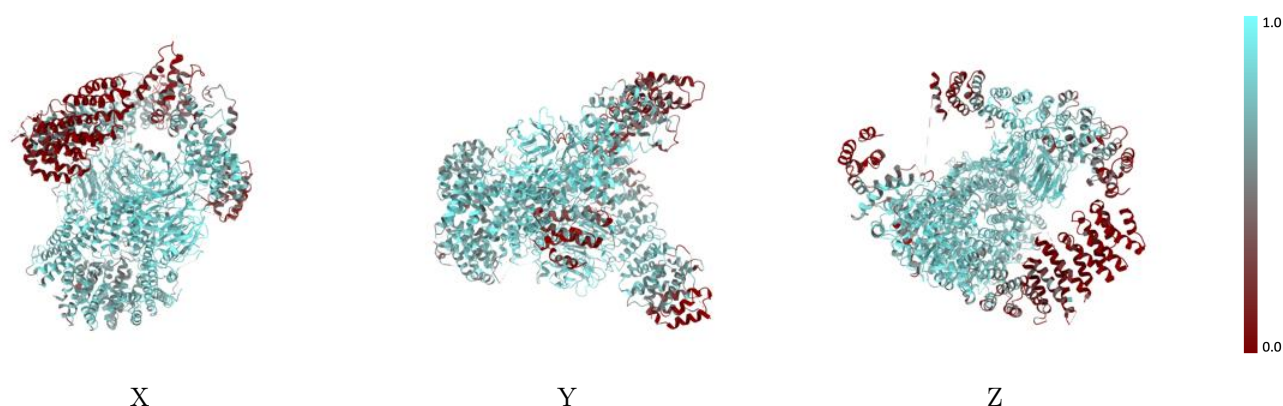


## 9.2 Q-score mapped to coordinate model [i](#)



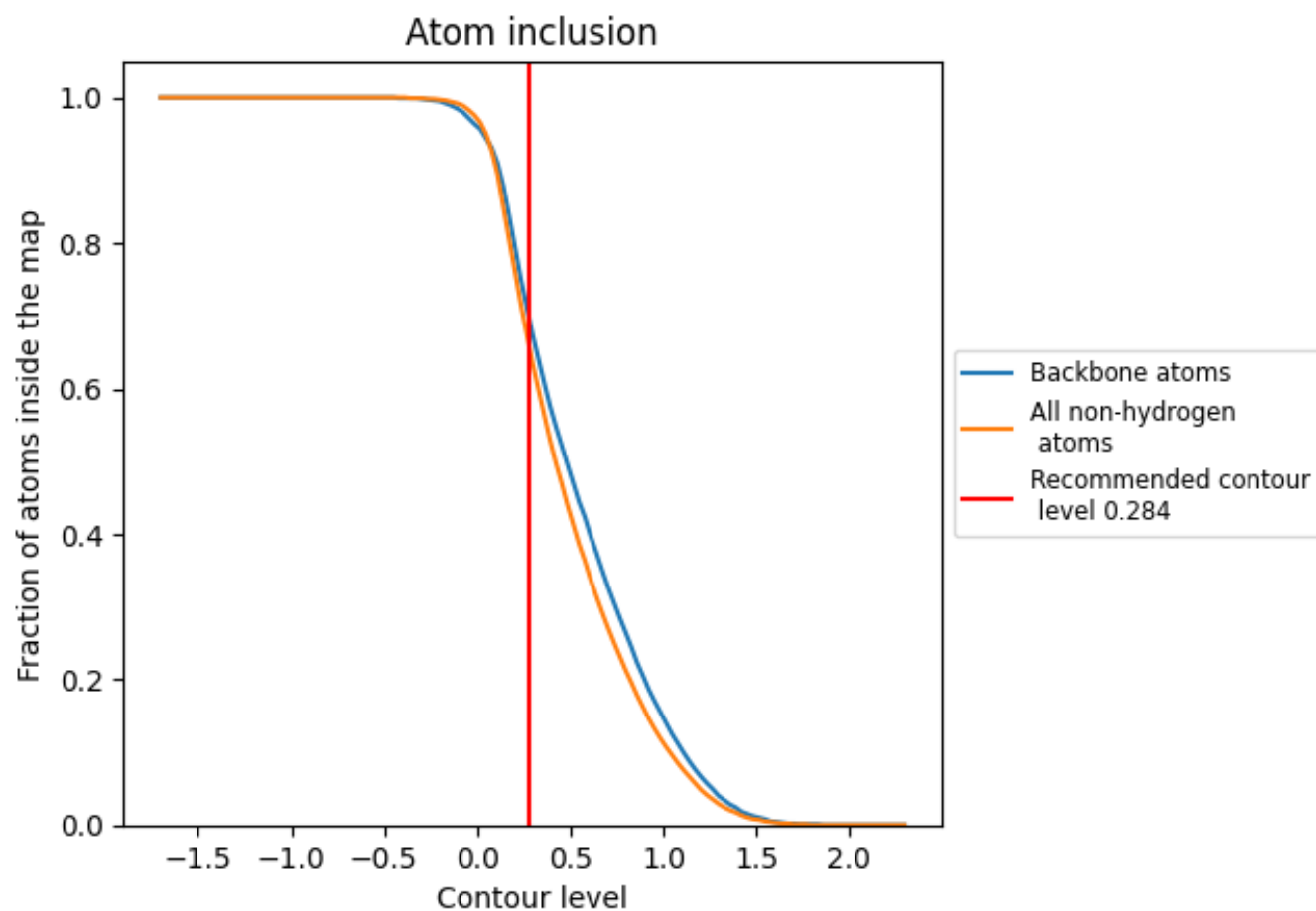
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.284).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 65% 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 (0.284) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6520	<div></div> 0.4530
A	<div></div> 0.8470	<div></div> 0.5450
B	<div></div> 0.8260	<div></div> 0.5390
C	<div></div> 0.7830	<div></div> 0.5190
D	<div></div> 0.7780	<div></div> 0.5160
G	<div></div> 0.5410	<div></div> 0.3940
H	<div></div> 0.3840	<div></div> 0.3240

1.0

0.0

<0.0