



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 02:46 PM UTC

PDB ID : 8SOK / pdb_00008sok
EMDB ID : EMD-40660
Title : Cryo-EM structure of human CST bound to POT1(ESDL)/TPP1 in the presence of telomeric ssDNA
Authors : Cai, S.W.
Deposited on : 2023-04-28
Resolution : 4.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

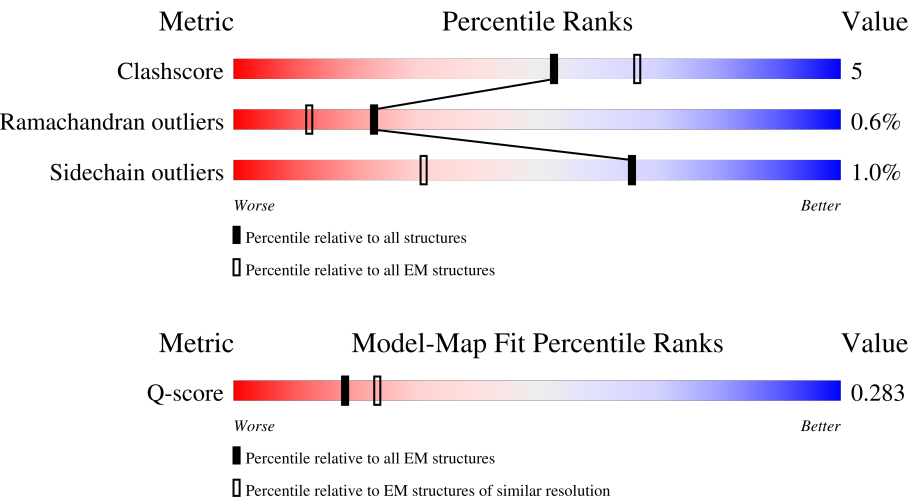
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	1613	
2	B	368	
3	C	123	
4	D	646	

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Mol	Chain	Length	Quality of chain
5	E	529	6% 13% 87%
6	F	18	22% 28% 6% 44%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 37162 atoms, of which 18588 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 CST complex subunit CTC1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1158	Total	C	H	N	O	S	0	0
			18208	5783	9160	1589	1625	51		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-395	MET	-	initiating methionine	UNP P0AEY0
A	-394	GLY	-	expression tag	UNP P0AEY0
A	-393	SER	-	expression tag	UNP P0AEY0
A	-392	SER	-	expression tag	UNP P0AEY0
A	-391	HIS	-	expression tag	UNP P0AEY0
A	-390	HIS	-	expression tag	UNP P0AEY0
A	-389	HIS	-	expression tag	UNP P0AEY0
A	-388	HIS	-	expression tag	UNP P0AEY0
A	-387	HIS	-	expression tag	UNP P0AEY0
A	-386	HIS	-	expression tag	UNP P0AEY0
A	-385	SER	-	expression tag	UNP P0AEY0
A	-384	SER	-	expression tag	UNP P0AEY0
A	-383	GLY	-	expression tag	UNP P0AEY0
A	-382	THR	-	expression tag	UNP P0AEY0
A	-15	LYS	-	linker	UNP P0AEY0
A	-14	LEU	-	linker	UNP P0AEY0
A	-13	VAL	-	linker	UNP P0AEY0
A	-12	GLU	-	linker	UNP P0AEY0
A	-11	LYS	-	linker	UNP P0AEY0
A	-10	TYR	-	linker	UNP P0AEY0
A	-9	LEU	-	linker	UNP P0AEY0
A	-8	GLU	-	linker	UNP P0AEY0
A	-7	VAL	-	linker	UNP P0AEY0
A	-6	LEU	-	linker	UNP P0AEY0
A	-5	PHE	-	linker	UNP P0AEY0
A	-4	GLN	-	linker	UNP P0AEY0
A	-3	GLY	-	linker	UNP P0AEY0
A	-2	PRO	-	linker	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	linker	UNP P0AEY0
A	0	SER	-	linker	UNP P0AEY0

- Molecule 2 is a protein called CST complex subunit STN1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	361	Total	C	H	N	O	S	0	0
			5825	1843	2914	499	557	12		

- Molecule 3 is a protein called CST complex subunit TEN1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	119	Total	C	H	N	O	S	0	0
			1897	595	955	169	171	7		

- Molecule 4 is a protein called Protection of telomeres protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	630	Total	C	H	N	O	S	0	0
			9937	3172	4965	832	942	26		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	MET	-	initiating methionine	UNP Q9NUX5
D	-6	HIS	-	expression tag	UNP Q9NUX5
D	-5	HIS	-	expression tag	UNP Q9NUX5
D	-4	HIS	-	expression tag	UNP Q9NUX5
D	-3	HIS	-	expression tag	UNP Q9NUX5
D	-2	HIS	-	expression tag	UNP Q9NUX5
D	-1	HIS	-	expression tag	UNP Q9NUX5
D	0	GLY	-	expression tag	UNP Q9NUX5
D	1	SER	-	expression tag	UNP Q9NUX5
D	320A	GLU	-	insertion	UNP Q9NUX5
D	320B	SER	-	insertion	UNP Q9NUX5
D	320C	ASP	-	insertion	UNP Q9NUX5
D	320D	LEU	-	insertion	UNP Q9NUX5

- Molecule 5 is a protein called TPP1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	67	Total	C	H	N	O	S	0	0
			972	302	480	83	100	7		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-277	MET	-	initiating methionine	UNP B6F2F5
E	-276	TRP	-	expression tag	UNP B6F2F5
E	-275	SER	-	expression tag	UNP B6F2F5
E	-274	HIS	-	expression tag	UNP B6F2F5
E	-273	PRO	-	expression tag	UNP B6F2F5
E	-272	GLN	-	expression tag	UNP B6F2F5
E	-271	PHE	-	expression tag	UNP B6F2F5
E	-270	GLU	-	expression tag	UNP B6F2F5
E	-269	LYS	-	expression tag	UNP B6F2F5
E	-268	GLY	-	expression tag	UNP B6F2F5
E	-267	GLY	-	expression tag	UNP B6F2F5
E	-266	GLY	-	expression tag	UNP B6F2F5
E	-265	SER	-	expression tag	UNP B6F2F5
E	-264	GLY	-	expression tag	UNP B6F2F5
E	-263	GLY	-	expression tag	UNP B6F2F5
E	-262	GLY	-	expression tag	UNP B6F2F5
E	-261	SER	-	expression tag	UNP B6F2F5
E	-260	GLY	-	expression tag	UNP B6F2F5
E	-259	GLY	-	expression tag	UNP B6F2F5
E	-258	SER	-	expression tag	UNP B6F2F5
E	-257	ALA	-	expression tag	UNP B6F2F5
E	-256	TRP	-	expression tag	UNP B6F2F5
E	-255	SER	-	expression tag	UNP B6F2F5
E	-254	HIS	-	expression tag	UNP B6F2F5
E	-253	PRO	-	expression tag	UNP B6F2F5
E	-252	GLN	-	expression tag	UNP B6F2F5
E	-251	PHE	-	expression tag	UNP B6F2F5
E	-250	GLU	-	expression tag	UNP B6F2F5
E	-249	LYS	-	expression tag	UNP B6F2F5
E	-8	GLU	-	linker	UNP B6F2F5
E	-7	ASN	-	linker	UNP B6F2F5
E	-6	LEU	-	linker	UNP B6F2F5
E	-5	TYR	-	linker	UNP B6F2F5
E	-4	PHE	-	linker	UNP B6F2F5
E	-3	GLN	-	linker	UNP B6F2F5
E	-2	GLY	-	linker	UNP B6F2F5
E	-1	GLY	-	linker	UNP B6F2F5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	SER	-	linker	UNP B6F2F5

- Molecule 6 is a DNA chain called DNA (5'-D(*TP*TP*AP*GP*GP*GP*TP*TP*AP*G)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	10	Total	C	H	N	O	P	0	0
			321	100	114	38	60	9		

- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

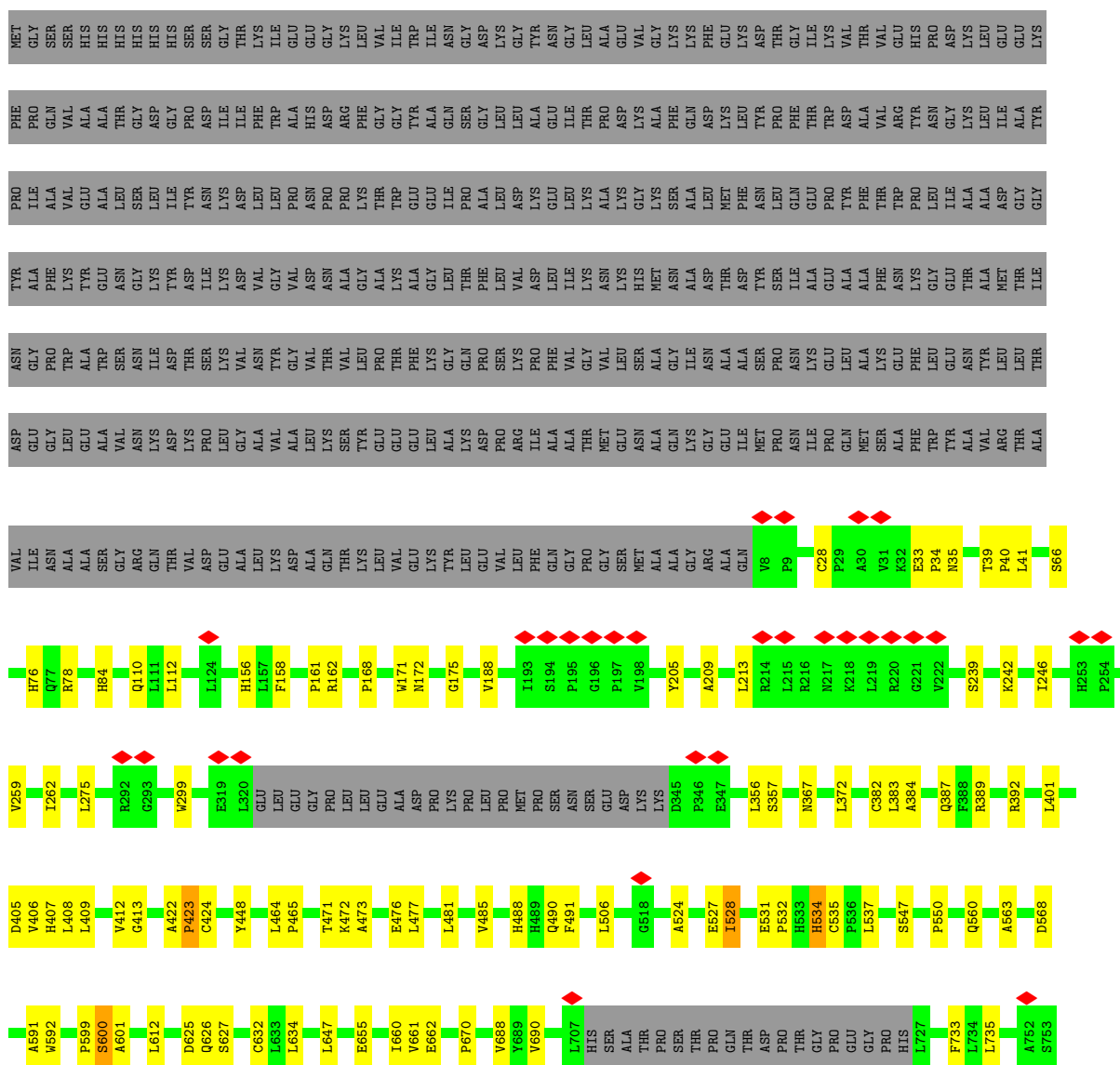
Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total	Zn	0
			1	1	
7	D	1	Total	Zn	0
			1	1	

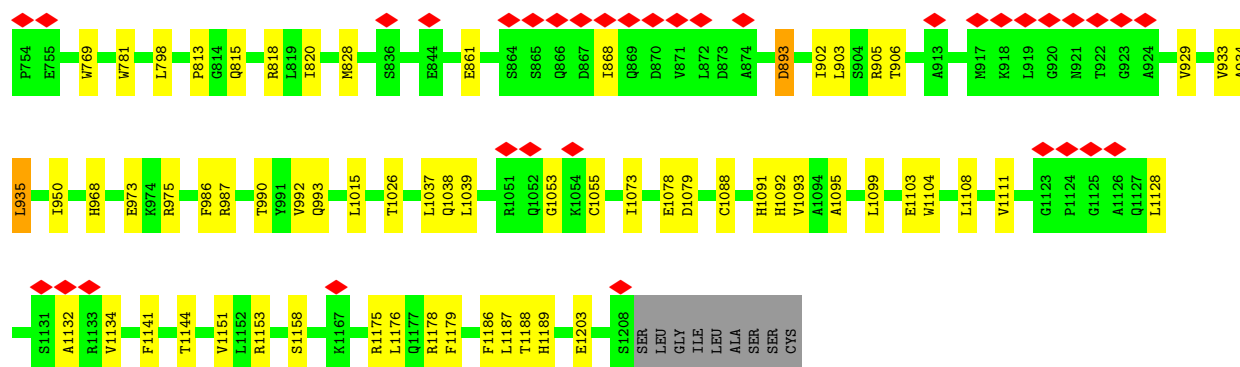
3 Residue-property plots

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.

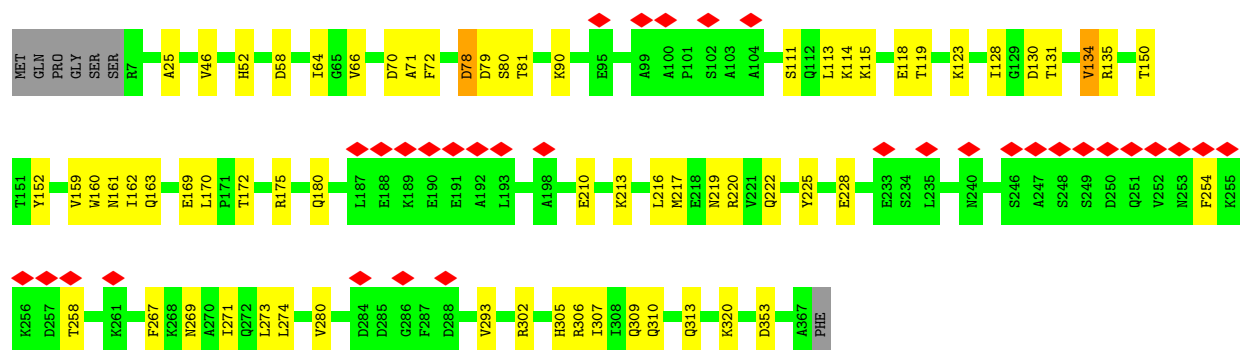
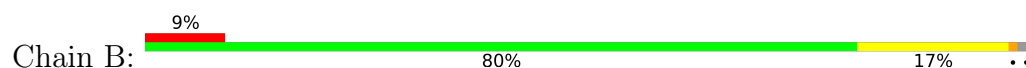
• Molecule 1: CST complex subunit CTC1

Chain A: 

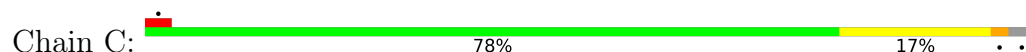




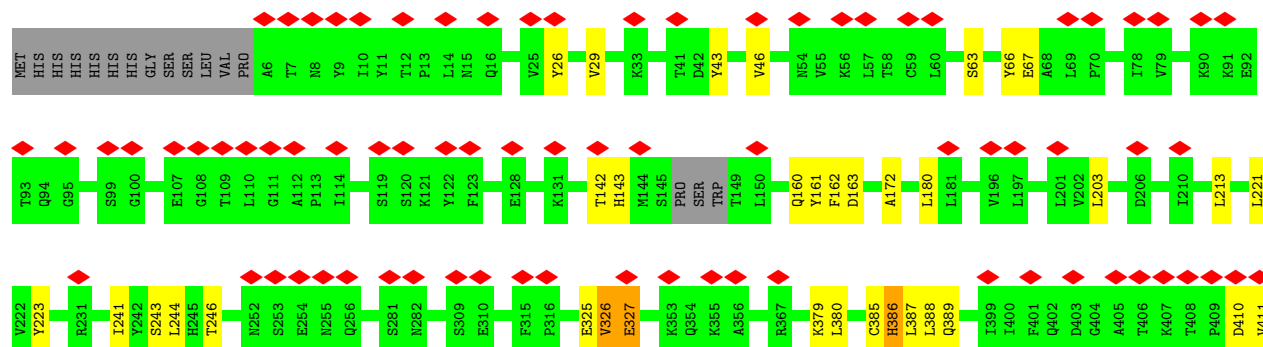
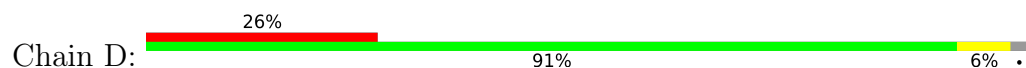
• Molecule 2: CST complex subunit STN1

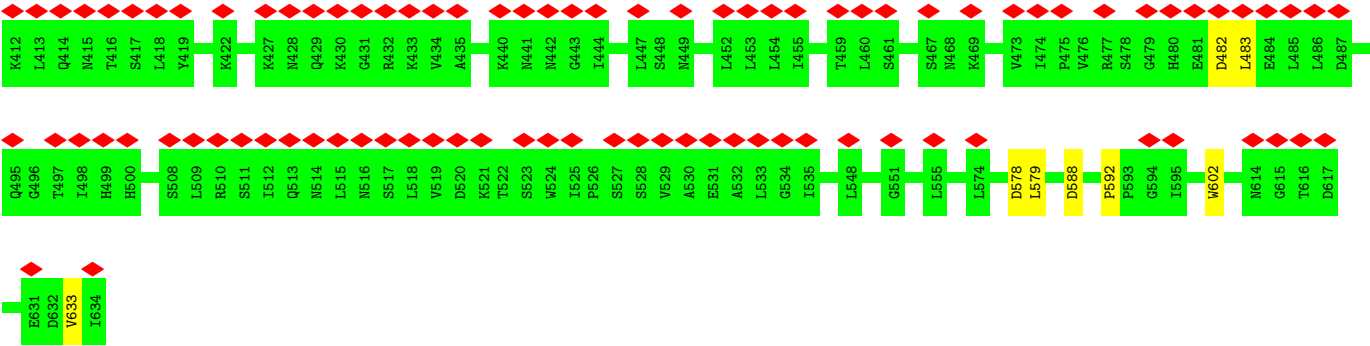


• Molecule 3: CST complex subunit TEN1

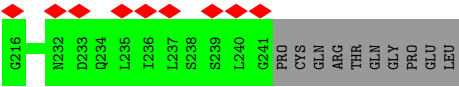
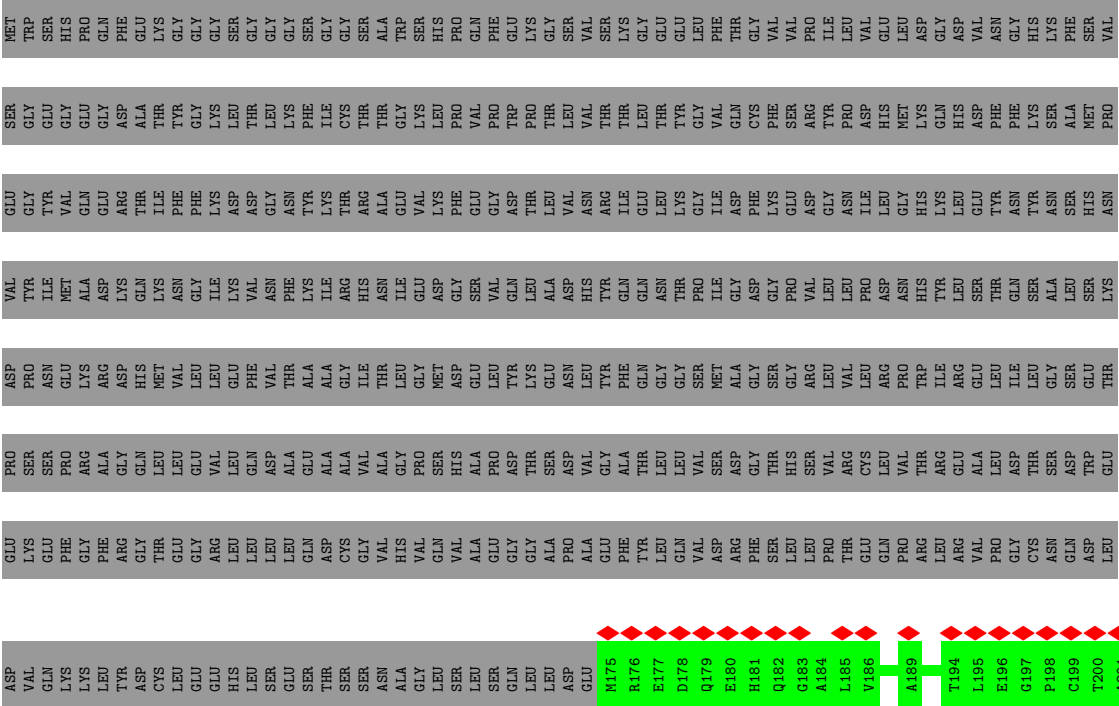


• Molecule 4: Protection of telomeres protein 1





• Molecule 5: TPP1



• Molecule 6: DNA (5'-D(*TP*TP*AP*GP*GP*GP*TP*TP*AP*G)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76359	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 ($e^-/\text{\AA}^2$)	50.3	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.737	Depositor
Minimum map value	-0.985	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	302.72, 302.72, 302.72	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86, 0.86, 0.86	Depositor

5 Model quality

5.1 Standard geometry

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	A	0.28	0/9283	0.48	0/12656
2	B	0.20	0/2966	0.36	0/4010
3	C	0.21	0/960	0.40	0/1299
4	D	0.18	0/5077	0.39	0/6890
5	E	0.13	0/500	0.32	0/681
6	F	0.44	0/232	0.69	1/358 (0.3%)
All	All	0.24	0/19018	0.44	1/25894 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	F	1	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	3	DA	C4'-C3'-O3'	5.97	118.95	110.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	F	3	DA	C3'

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9048	9160	9142	116	0
2	B	2911	2914	2911	39	0
3	C	942	955	953	18	0
4	D	4972	4965	4953	28	0
5	E	492	480	479	0	0
6	F	207	114	116	5	0
7	A	1	0	0	0	0
7	D	1	0	0	0	0
All	All	18574	18588	18554	198	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 5.

The worst 5 of 198 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)
2:B:130:ASP:OD1	2:B:131:THR:N	2.08	0.86
1:A:382:CYS:SG	1:A:383:LEU:N	2.51	0.84
1:A:407:HIS:ND1	1:A:537:LEU:O	2.23	0.71
3:C:14:GLU:N	3:C:14:GLU:OE1	2.27	0.68
2:B:135:ARG:O	2:B:150:THR:N	2.26	0.67

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1152/1613 (71%)	1003 (87%)	139 (12%)	10 (1%)	14	49
2	B	359/368 (98%)	325 (90%)	33 (9%)	1 (0%)	36	70
3	C	117/123 (95%)	109 (93%)	8 (7%)	0	100	100
4	D	626/646 (97%)	579 (92%)	45 (7%)	2 (0%)	36	70
5	E	65/529 (12%)	63 (97%)	2 (3%)	0	100	100
All	All	2319/3279 (71%)	2079 (90%)	227 (10%)	13 (1%)	23	58

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	547	SER
1	A	563	ALA
1	A	600	SER
2	B	80	SER
4	D	326	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	1016/1383 (74%)	1003 (99%)	13 (1%)	61	72
2	B	326/332 (98%)	323 (99%)	3 (1%)	70	76
3	C	104/107 (97%)	102 (98%)	2 (2%)	50	67
4	D	565/587 (96%)	562 (100%)	3 (0%)	81	82
5	E	56/447 (12%)	56 (100%)	0	100	100
All	All	2067/2856 (72%)	2046 (99%)	21 (1%)	65	76

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	134	VAL
3	C	94	LEU
4	D	387	LEU

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Mol	Chain	Res	Type
4	D	26	TYR
3	C	78	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	495	GLN
4	D	623	GLN
5	E	234	GLN
2	B	301	HIS
4	D	8	ASN

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](#)

Of 2 ligands modelled in this entry, 2 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 [i](#)

There are no chain breaks in this entry.

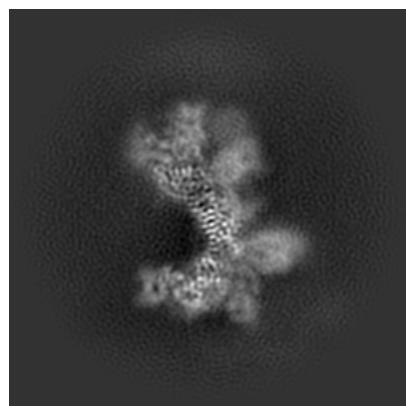
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40660. These allow visual inspection of the internal detail of the map and identification of artifacts.

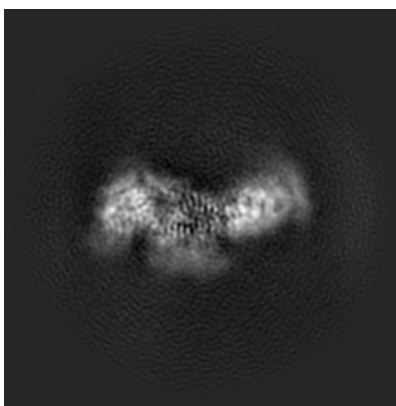
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

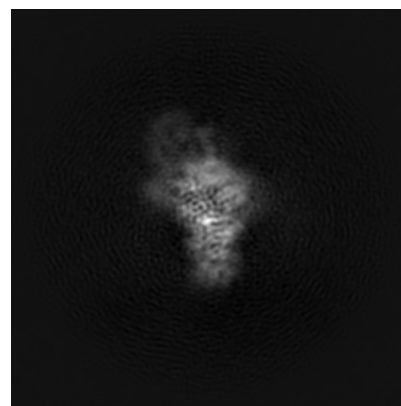
6.1.1 Primary map



X

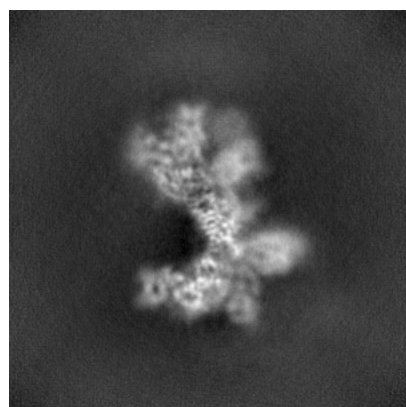


Y

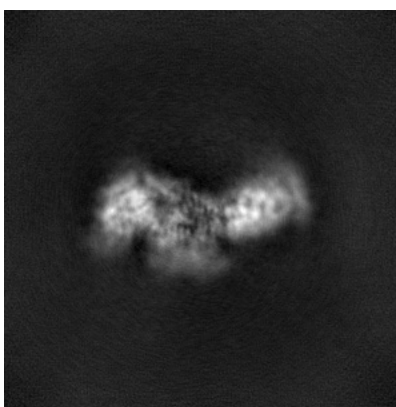


Z

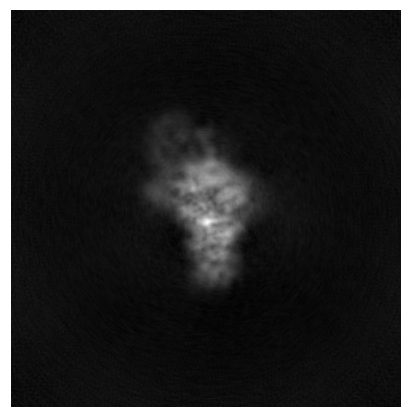
6.1.2 Raw map



X



Y

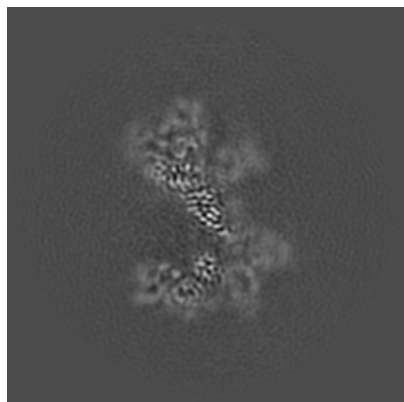


Z

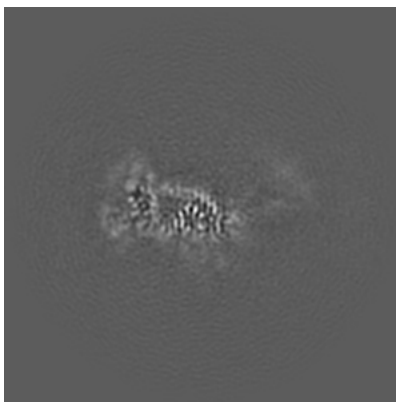
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

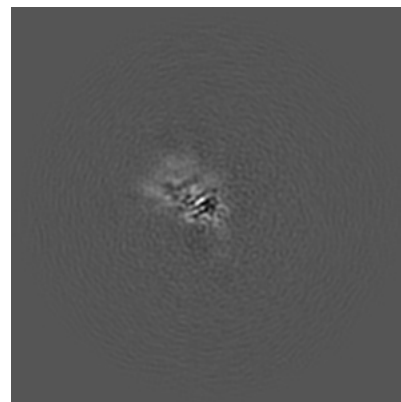
6.2.1 Primary map



X Index: 176

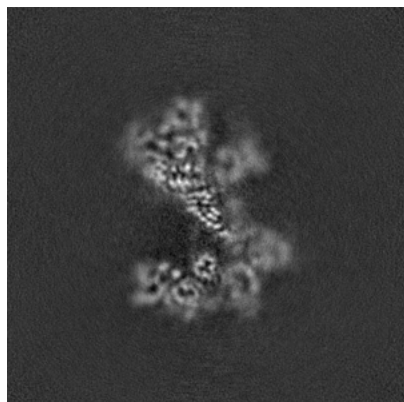


Y Index: 176

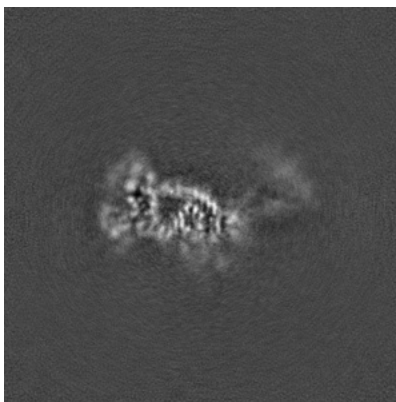


Z Index: 176

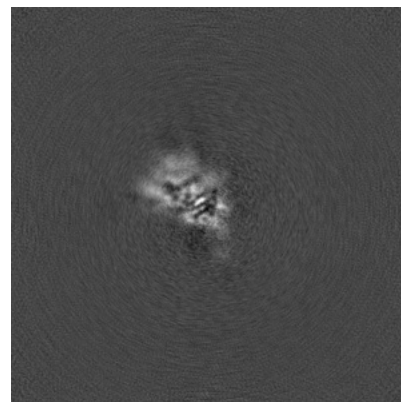
6.2.2 Raw map



X Index: 176



Y Index: 176

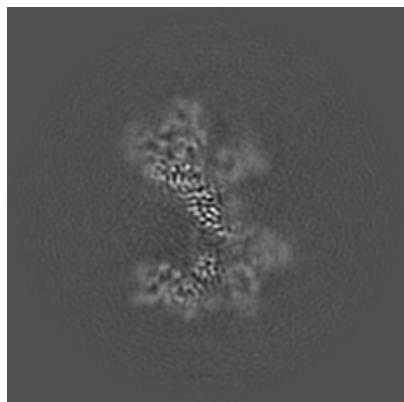


Z Index: 176

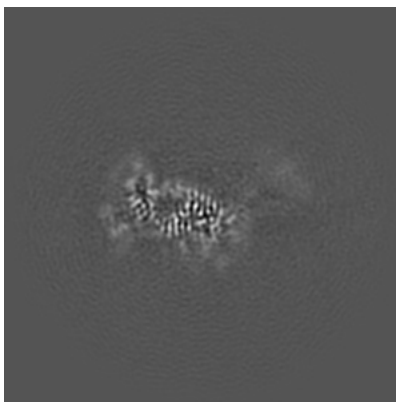
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

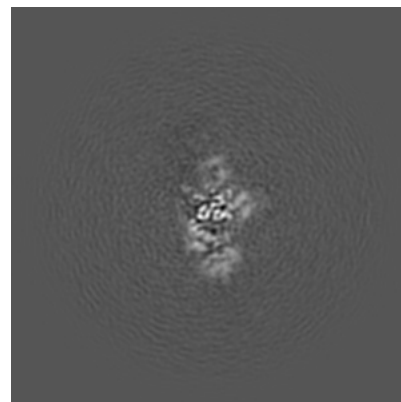
6.3.1 Primary map



X Index: 175

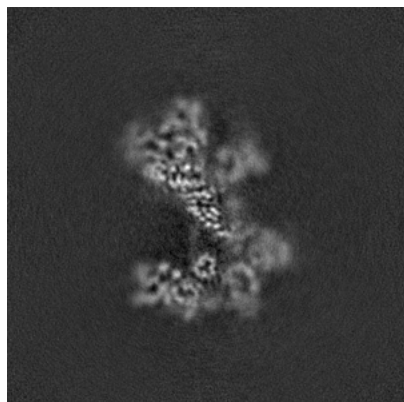


Y Index: 178

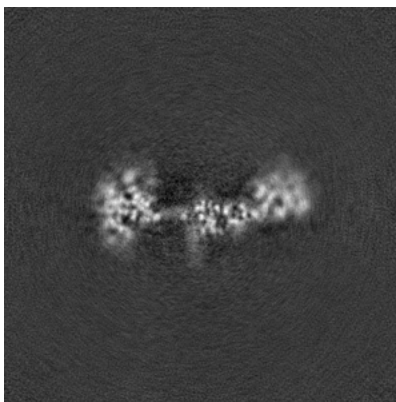


Z Index: 114

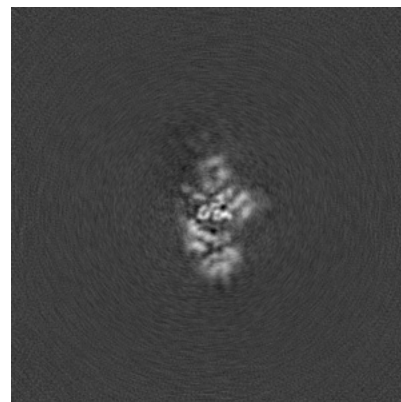
6.3.2 Raw map



X Index: 175



Y Index: 166

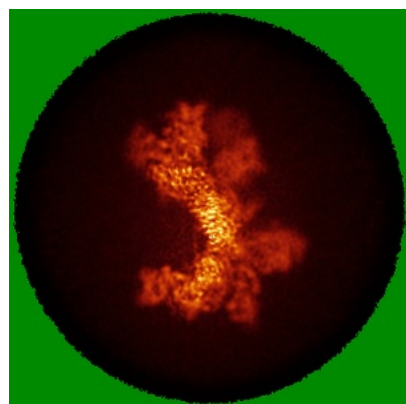


Z Index: 114

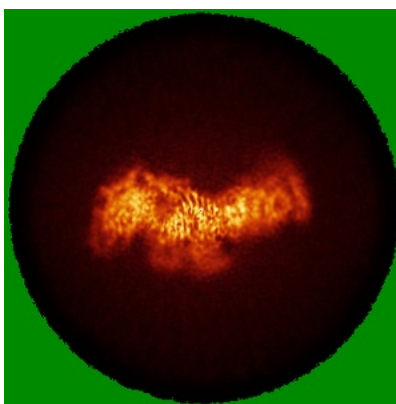
The images above show the largest variance slices of the map in three orthogonal directions.

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

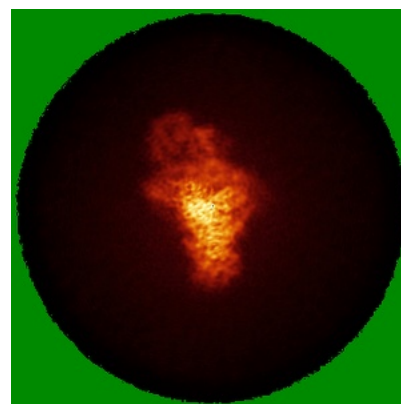
6.4.1 Primary map



X

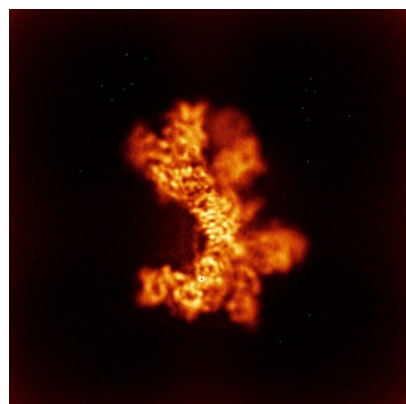


Y

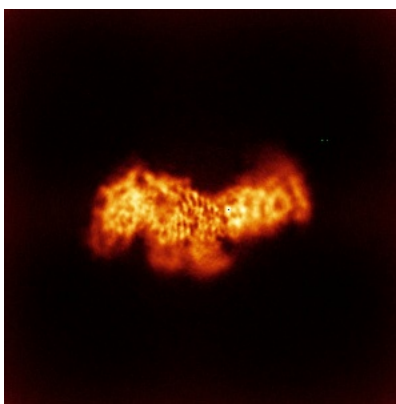


Z

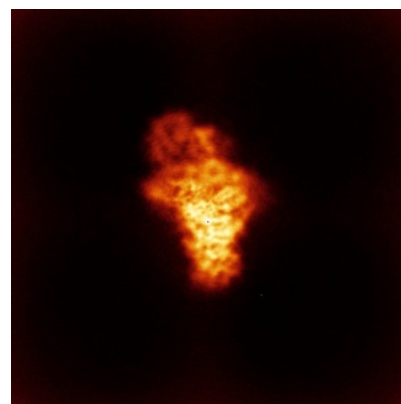
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



X



Y



Z

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.

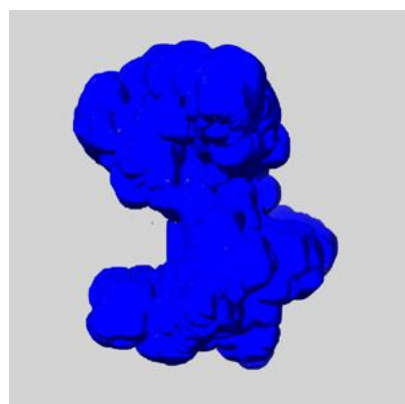
6.6 Mask visualisation [i](#)

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

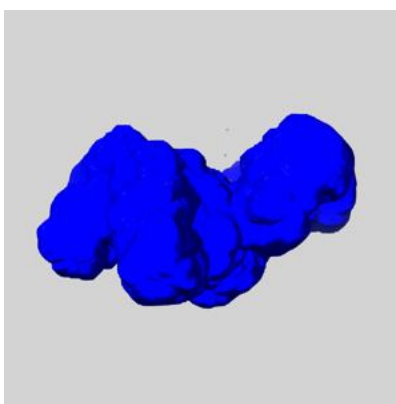
A mask typically either:

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

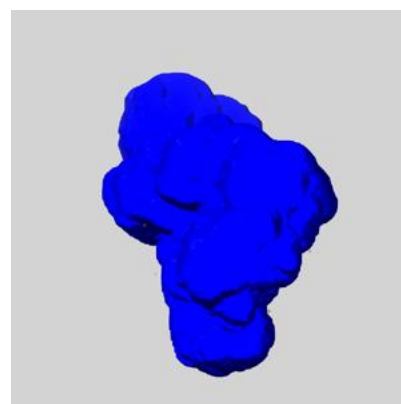
6.6.1 emd_40660_msk_1.map [i](#)



X



Y

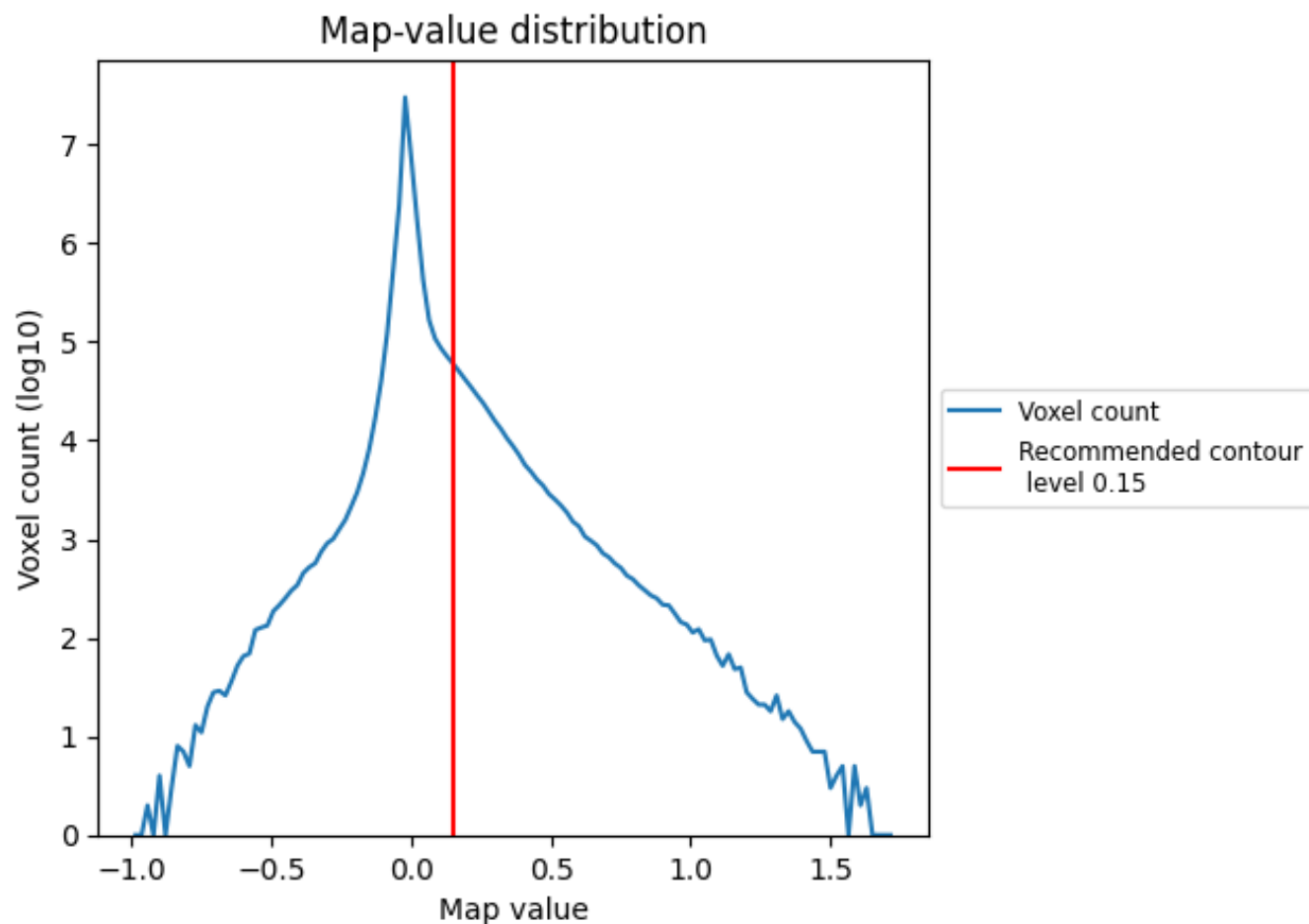


Z

7 Map analysis [i](#)

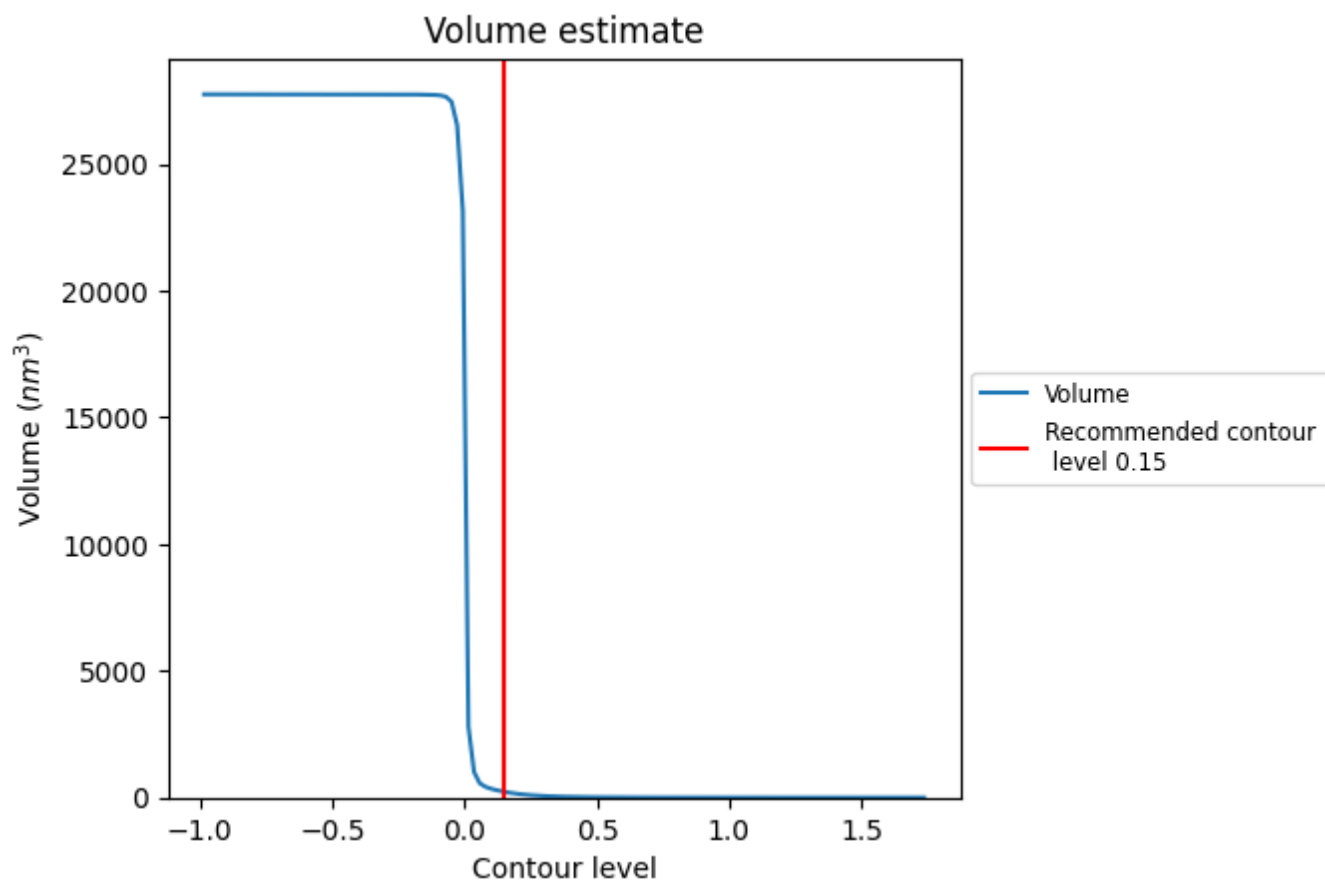
This section contains the results of statistical analysis of the map.

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.

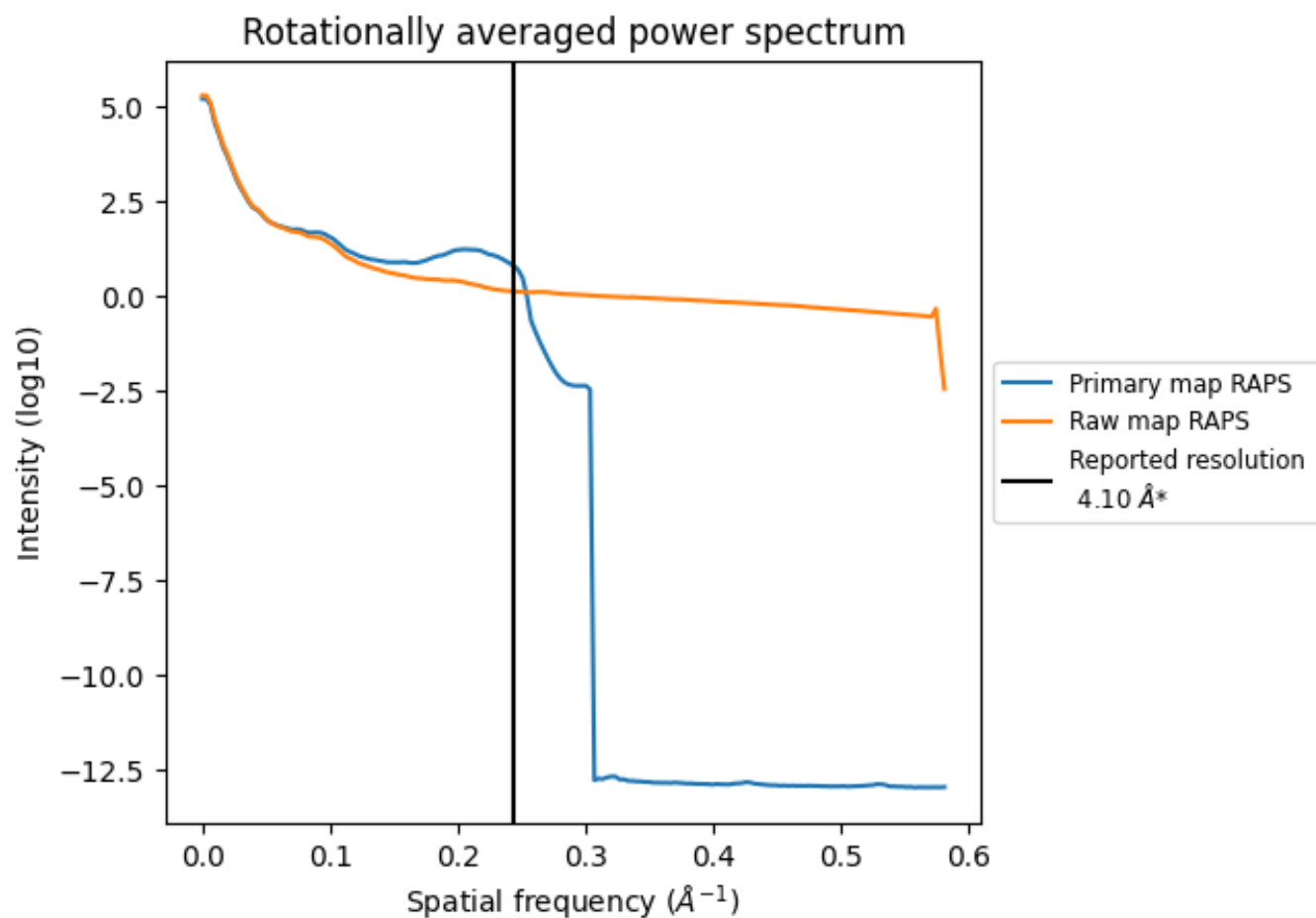
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 227 nm³; this corresponds to an approximate mass of 205 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 ⓘ

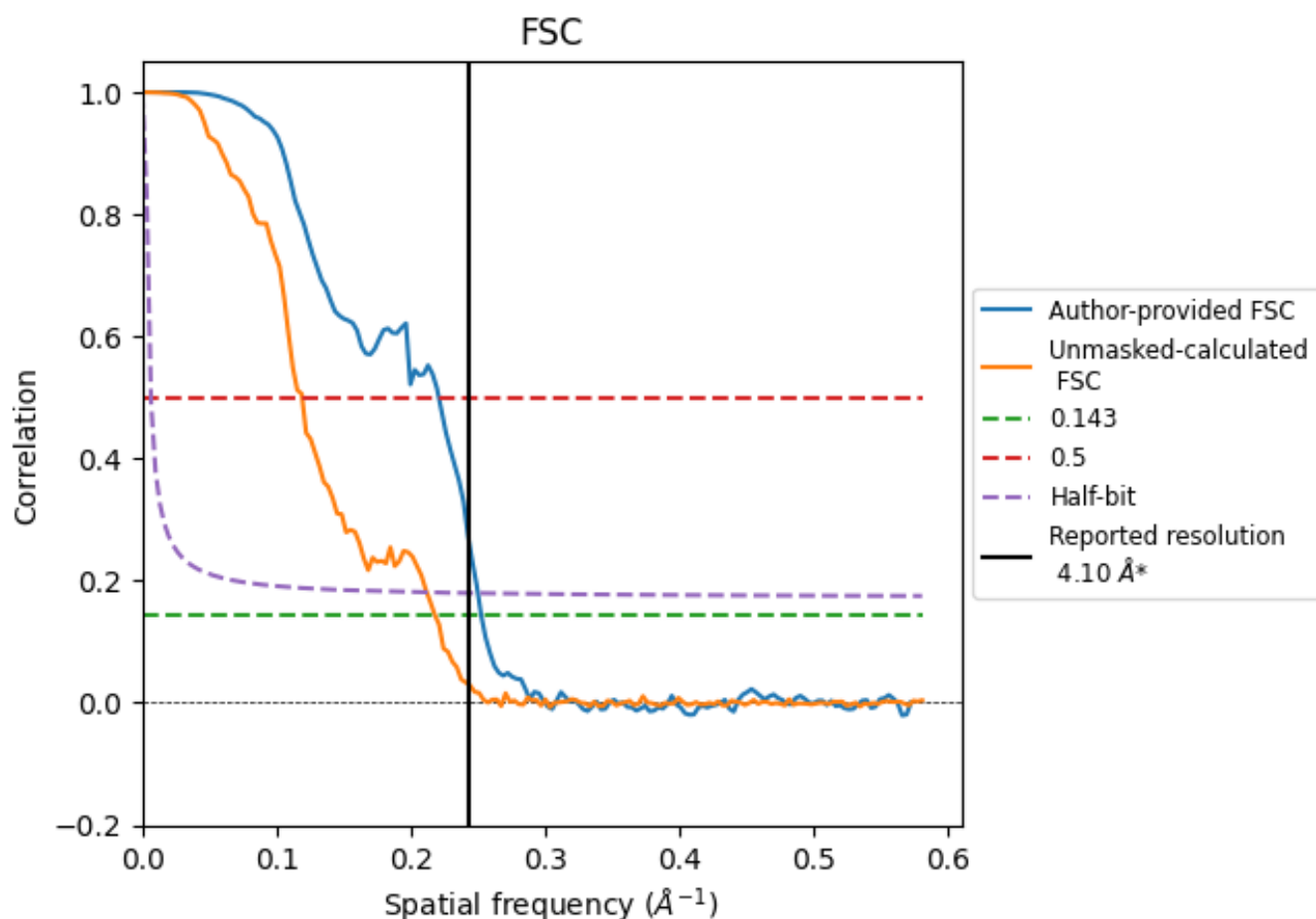


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 $0.244 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

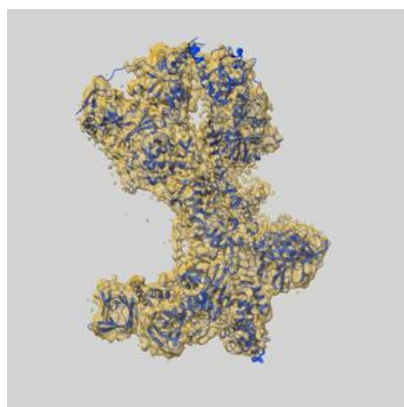
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	3.96	4.52	4.00
Unmasked-calculated*	4.58	8.39	4.71

*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 4.58 differs from the reported value 4.1 by more than 10 %

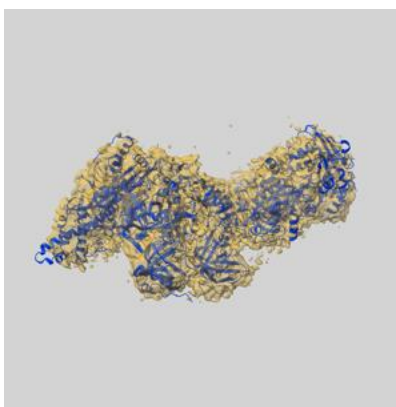
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40660 and PDB model 8SOK. Per-residue inclusion information can be found in section [3](#) on page [8](#).

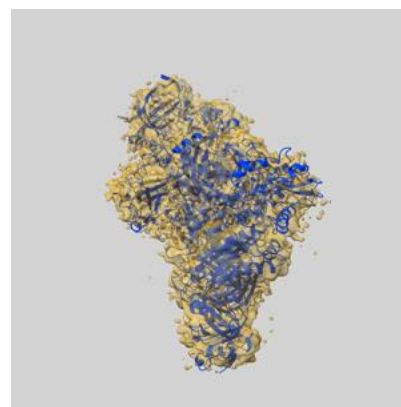
9.1 Map-model overlay [i](#)



X



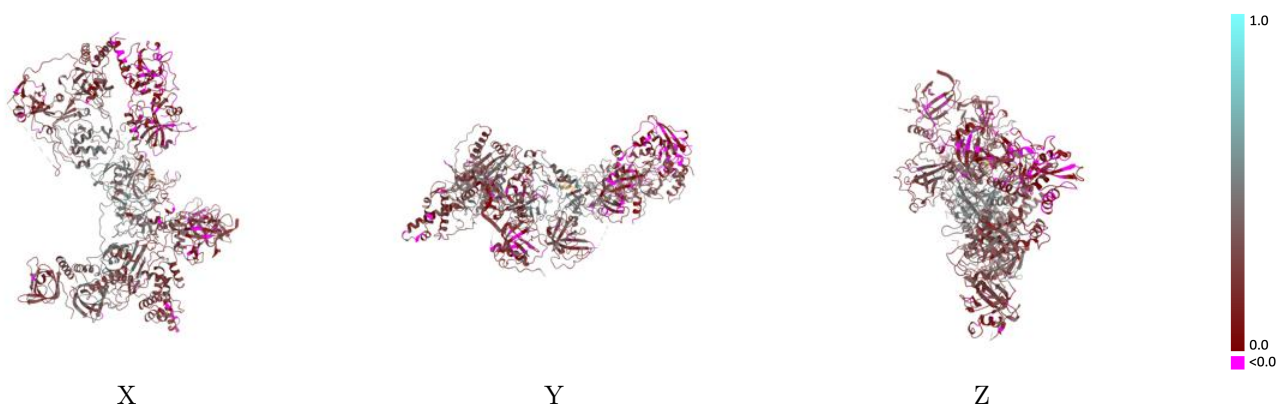
Y



Z

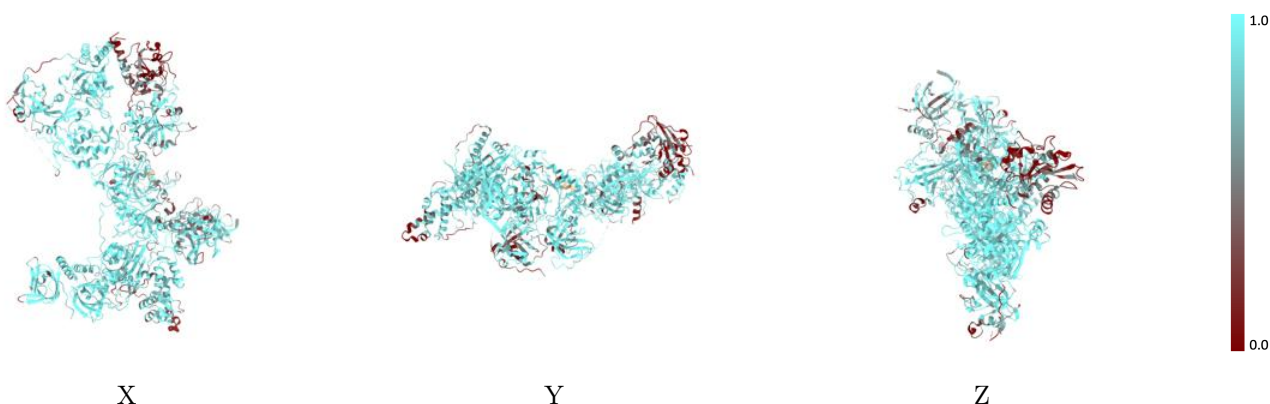
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



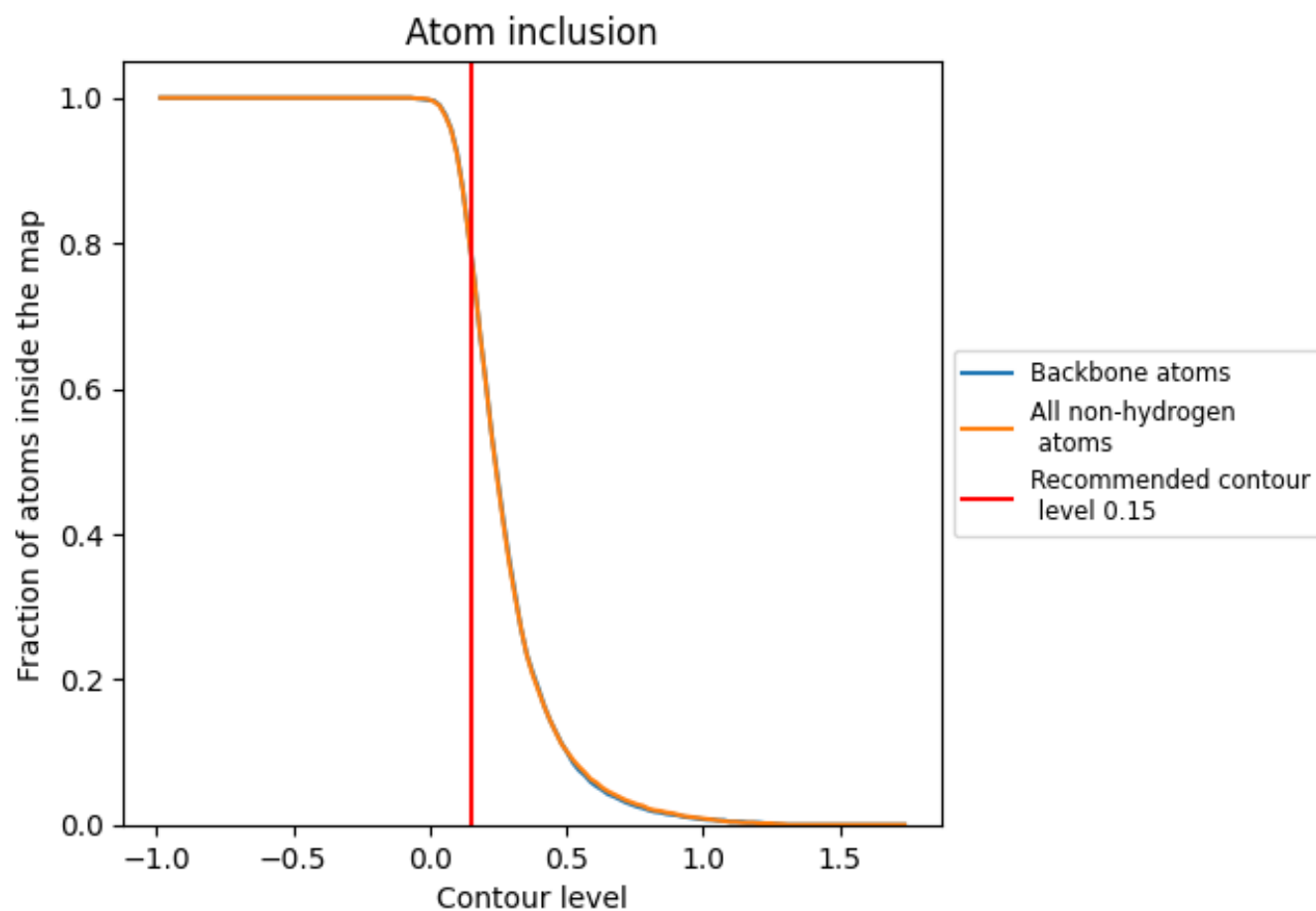
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7870	0.2830
A	0.8780	0.3520
B	0.8110	0.3030
C	0.8690	0.2760
D	0.6330	0.1690
E	0.4900	0.0990
F	0.8790	0.1910

1.0

0.0

<0.0