



wwPDB EM Validation Summary Report ⓘ

May 7, 2026 – 01:31 pm BST

PDB ID : 9QT4 / pdb_00009qt4
EMDB ID : EMD-53346
Title : CryoEM structure of Arabidopsis TIR-NLR WRR4A tetramer in complex with effector CCG40 (focused refinement)
Authors : Zhao, H.; Lukyanova, N.; Selvaraj, M.; Jones, J.
Deposited on : 2025-04-07
Resolution : 4.00 Å(reported)
Based on initial model : .

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

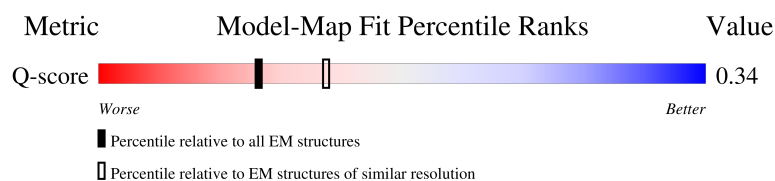
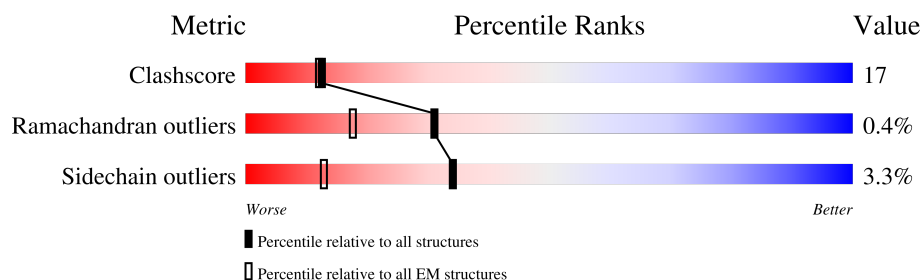
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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	P	216	
1	Q	216	
1	R	216	
1	S	216	

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Mol	Chain	Length	Quality of chain
2	A	1007	<div><div><div></div><div></div><div></div></div><div>43%22%35%</div></div>
2	B	1007	<div><div><div></div><div></div><div></div></div><div>42%22%35%</div></div>
2	C	1007	<div><div><div></div><div></div><div></div></div><div>43%21%35%</div></div>
2	D	1007	<div><div><div></div><div></div><div></div></div><div>41%23%35%</div></div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 23228 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 CCG40.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	P	77	Total	C	N	O	S	0	0
			583	362	101	115	5		
1	Q	77	Total	C	N	O	S	0	0
			583	362	101	115	5		
1	R	77	Total	C	N	O	S	0	0
			583	362	101	115	5		
1	S	77	Total	C	N	O	S	0	0
			583	362	101	115	5		

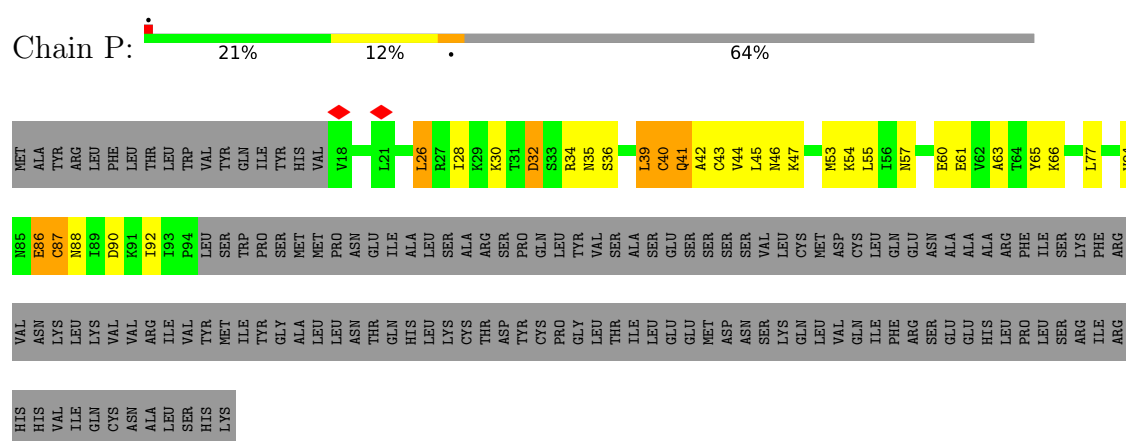
- Molecule 2 is a protein called Disease resistance protein ADR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		
2	B	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		
2	C	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		
2	D	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		

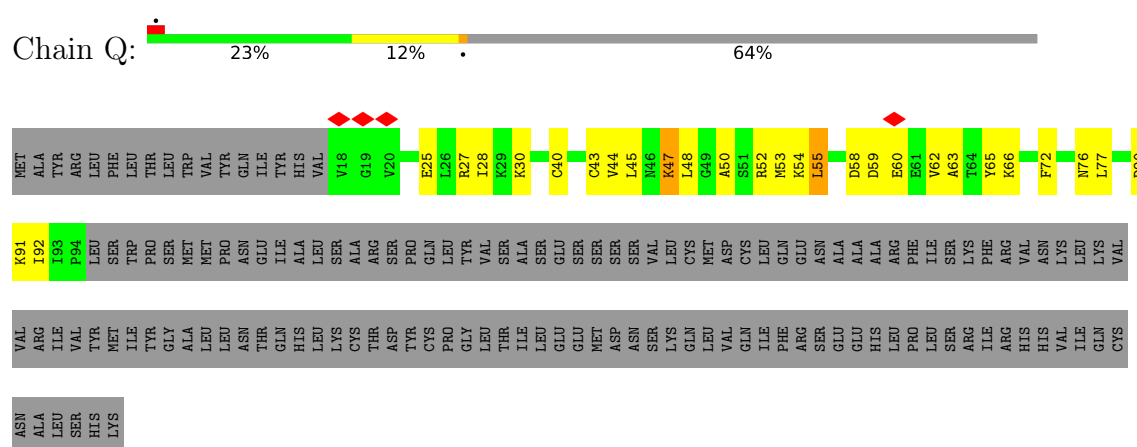
3 Residue-property plots [i](#)

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.

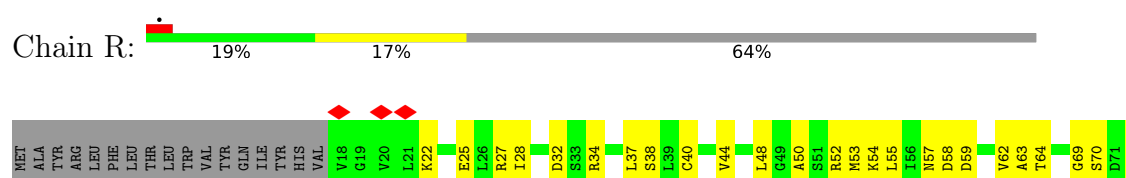
• Molecule 1: CCG40



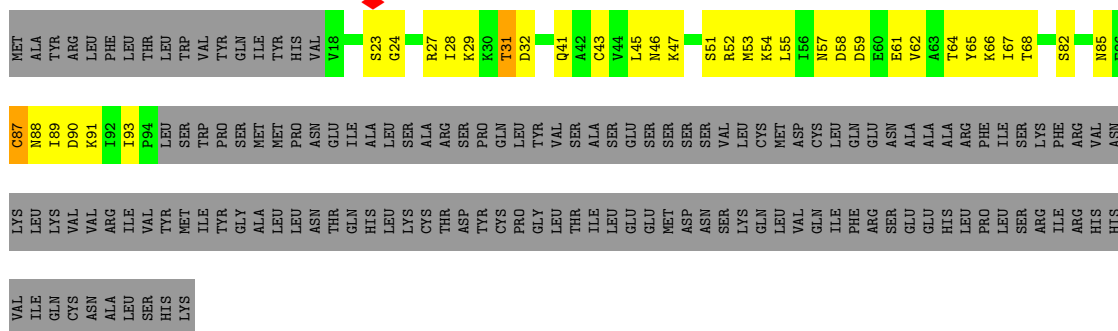
• Molecule 1: CCG40



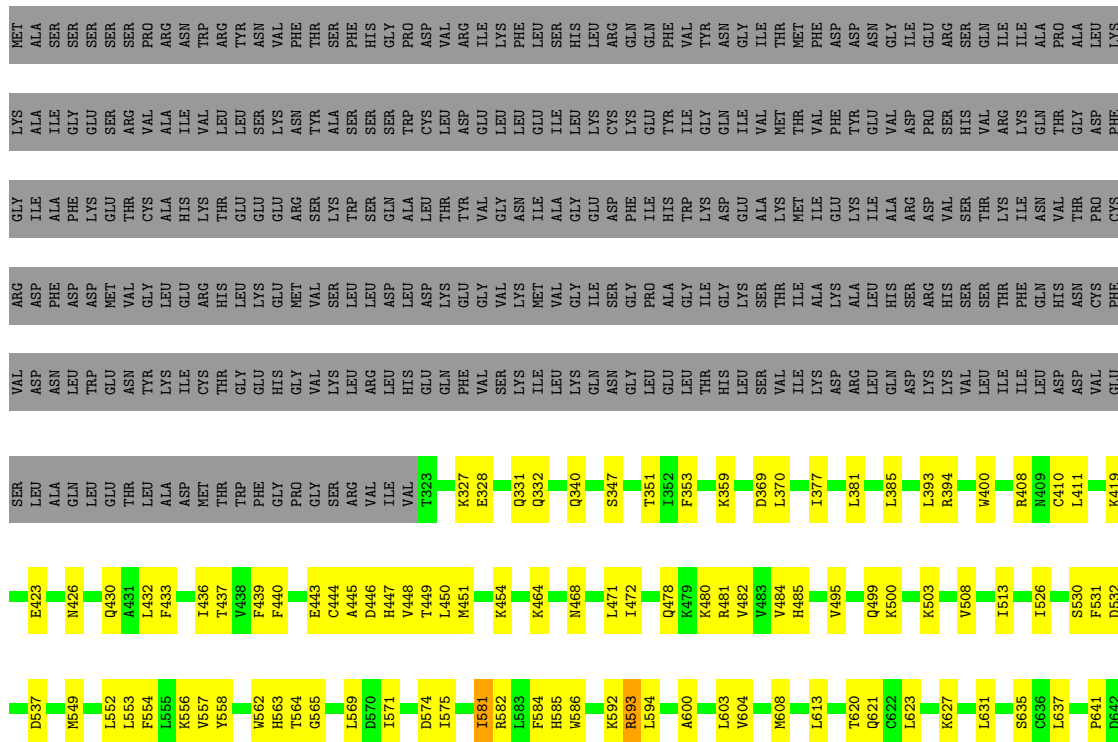
• Molecule 1: CCG40

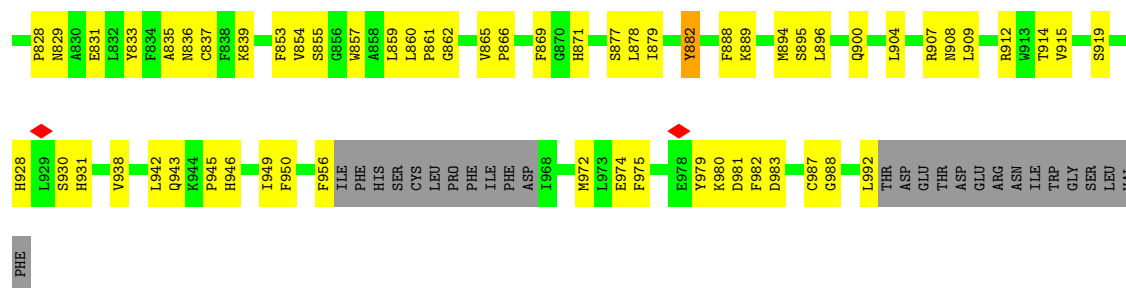


- Molecule 1: CCG40



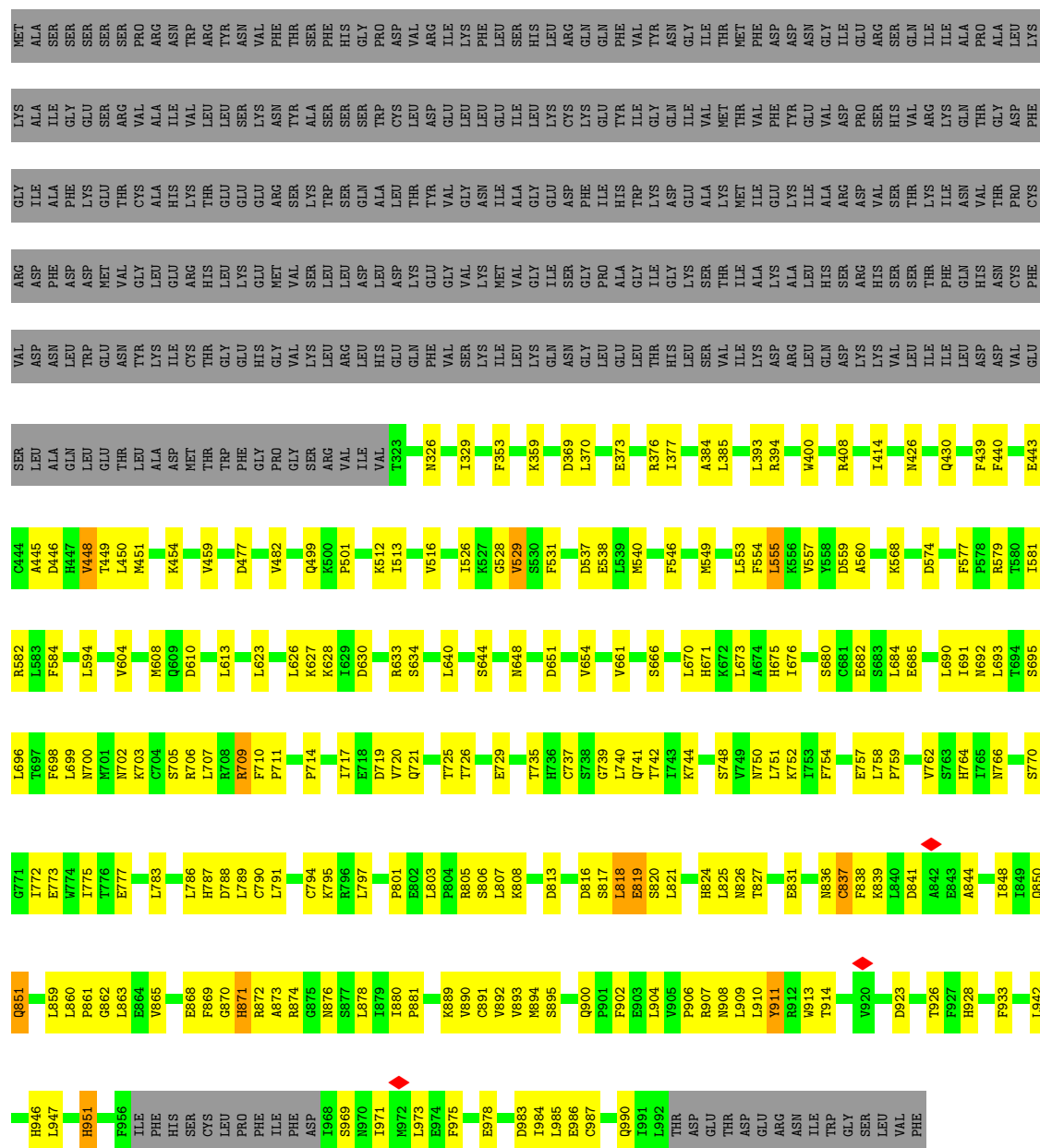
- Molecule 2: Disease resistance protein ADR2





• Molecule 2: Disease resistance protein ADR2

Chain C: 43% 21% 35%



• Molecule 2: Disease resistance protein ADR2



MET	LYS	GLY	ARG	VAL	SER	F439	K566	A674	L751	F834	W913	THR
ALA	ILE	PHE	ASP	ASN	PHE	F440	K567	H675	K752	A835	G917	ASP
SER	GLU	LEU	ASP	TRP	ASP	E443	K568	I676	I753	N836	D923	GLU
SER	GLU	LEU	ASP	GLU	ASP	C444	D570	C681	Y754	C837	I927	ARG
SER	THR	THR	MET	ASN	VAL	H447	I571	E682	Y755	F838	D923	ASN
PRO	VAL	CYS	VAL	GLY	GLY			S683	T756	E843	F927	ILE
ARG	ALA	ALA	THR	LEU	THR			L684	P759	A844	H928	TRP
ASN	VAL	ASN	GLY	GLY	LEU			E685		R845	L929	GLY
VAL	LYS	LYS	LEU	GLU	ASP	L450	R582	L685		R846	S930	SER
PHE	ASN	ARG	MET	GLY	ILE	M451	F584	V686	S762	A847	H931	LEU
THR	ALA	THR	VAL	THR	CYS	K454	F585	I687	S763	I848	M932	VAL
SER	LYS	THR	LYS	GLY	THR	K454	K586	P688	H764	I849	F933	
LYS	TRP	GLY	LEU	LYS	TRP	K464	S587	S689	I765	G850		
THR	GLU	GLU	GLY	GLY	PHE	I472	A588	L690	N766	Q851	S937	
GLN	GLU	GLU	PRO	GLY	GLY	Q478	Y589	L693	I767	S852	Y938	
ALA	LEU	GLY	VAL	GLY	ARG		S590		S768	F853	H939	
ASP	LEU	THR	LYS	LEU	LEU		R593	L696	S770		L942	
PRO	GLY	TRP	LEU	ARG	VAL	R481	L594		G771	A858		
LYS	GLY	GLN	LEU	LEU	ILE	V482	F599	L699	I772	L859	P945	
THR	ASP	ALA	LEU	ASP	VAL	V483		N700		L860	H946	
GLY	CYS	LEU	GLY	TRP	GLU	V484		M701	H784	P861	L947	
ILE	ASP	THR	LYS	GLY	GLN		L603	N702	N785	G862	F948	
LEU	VAL	THR	GLY	THR	PHE	V485	V604	C704	L786	L863	I949	
GLY	GLY	VAL	GLY	GLY	VAL	Q499	S686	S705	H787	V685	F950	
ASP	LYS	VAL	GLY	ILE	GLY		V606		L788	P866	H951	
ARG	CYS	GLY	ILE	GLY	VAL	I506	E618	R708	C790	E868	S952	
LYS	GLY	GLY	ILE	GLY	SER	L507	Q621	R709	L791	H871	F956	
GLN	THR	GLY	PRO	GLY	LYS	F363	L623	F710	S792	R874	ILE	
THR	LYS	ASP	ALA	GLY	LEU	D369	L626	T711	G793		PHE	
VAL	TRP	PHE	GLY	THR	LEU	L517	L629	T712	C794	L878	HIS	
LYS	LYS	VAL	LYS	LYS	THR	A520		T713		I879	SER	
ASN	GLY	ASP	ILE	ILE	THR		C636	S716	L797		CYS	
GLY	GLN	GLY	LYS	ALA	HIS	I377	L637	I717	V798	L803	LEU	
ILE	ILE	ILE	LYS	THR	GLY	L385	T638	E718		P804	PRO	
THR	VAL	THR	ASP	MET	THR	F531	E639	D719	L807	R805	PHE	
ALA	VAL	LYS	ASP	ILE	ALA		L643	T725	R806	S806	ILE	
LYS	GLY	ASP	ARG	LYS	LYS	I536	S656	E728	K807	L807	ASP	
ASP	THR	VAL	ASP	VAL	LYS	D399	L660	L729	R808	R809		
ASN	GLY	LYS	ASN	GLY	LYS	E537	V661	L730	L810	L810	E974	
THR	GLY	ALA	GLN	THR	ASP	R408	E662	P731	Q811	A812		
MET	VAL	ARG	ASP	THR	ASP	L539	L663	A732	A812	D813	S977	
THR	ASP	ASP	ASP	VAL	ASP	D412	P664	S733	S820	S820	E978	
ALA	PRO	VAL	ASP	VAL	LYS	K419	S666	T734	L821	L821	Y979	
ARG	SER	SER	GLU	THR	LYS	E423	L667	H736	N822	N822	K980	
SER	GLN	GLN	SER	GLN	ASN	L432	V557	C737	L825	L825	D981	
ILE	LYS	ILE	THR	ILE	VAL	F433	L670	S738			F982	
ALA	THR	VAL	ARG	GLN	HIS	I436	L673		P828	P828	D983	
PRO	GLY	THR	GLY	VAL	THR	T437			N829	N829	G988	
LYS	PHE	ASP	ASP	VAL	CYS	V438			L910	L910	I991	
									Y911	Y911	L992	
									THR	THR	ASP	
									GLU	GLU	GLU	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	34546	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	331.2, 331.2, 331.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	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	P	0.35	0/586	0.70	1/786 (0.1%)
1	Q	0.28	0/586	0.53	0/786
1	R	0.16	0/586	0.44	0/786
1	S	0.18	0/586	0.49	0/786
2	A	0.19	0/5332	0.52	2/7224 (0.0%)
2	B	0.18	0/5332	0.52	2/7224 (0.0%)
2	C	0.19	0/5332	0.51	0/7224
2	D	0.23	0/5332	0.57	4/7224 (0.1%)
All	All	0.20	0/23672	0.53	9/32040 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	938	VAL	N-CA-C	-7.23	106.05	111.90
1	P	32	ASP	N-CA-C	-6.93	105.16	112.93
2	D	807	LEU	N-CA-C	-6.48	100.83	110.23
2	A	931	HIS	N-CA-C	-6.25	105.64	113.20
2	A	835	ALA	N-CA-C	-5.38	107.27	112.97

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	P	583	0	601	31	0
1	Q	583	0	601	19	0
1	R	583	0	601	26	0
1	S	583	0	601	34	0
2	A	5224	0	5248	171	0
2	B	5224	0	5248	173	0
2	C	5224	0	5248	155	0
2	D	5224	0	5248	195	0
All	All	23228	0	23396	783	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 17.

The worst 5 of 783 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:D:731:PRO:HG2	2:D:754:PHE:HB2	1.47	0.95
2:D:768:SER:HA	2:D:791:LEU:HG	1.53	0.89
2:D:714:PRO:HG2	2:D:717:ILE:HG13	1.54	0.89
2:D:507:LEU:HB3	2:D:513:ILE:HG12	1.55	0.89
2:B:678:MET:HE1	2:B:684:LEU:HD22	1.57	0.86

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	P	75/216 (35%)	67 (89%)	8 (11%)	0	100	100
1	Q	75/216 (35%)	66 (88%)	9 (12%)	0	100	100
1	R	75/216 (35%)	66 (88%)	9 (12%)	0	100	100
1	S	75/216 (35%)	66 (88%)	8 (11%)	1 (1%)	9	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	655/1007 (65%)	580 (88%)	72 (11%)	3 (0%)	24	60
2	B	655/1007 (65%)	578 (88%)	77 (12%)	0	100	100
2	C	655/1007 (65%)	573 (88%)	77 (12%)	5 (1%)	16	52
2	D	655/1007 (65%)	573 (88%)	79 (12%)	3 (0%)	24	60
All	All	2920/4892 (60%)	2569 (88%)	339 (12%)	12 (0%)	31	65

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	819	GLU
2	D	837	CYS
2	C	851	GLN
2	C	890	VAL
1	S	87	CYS

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	P	68/196 (35%)	61 (90%)	7 (10%)	7	25
1	Q	68/196 (35%)	64 (94%)	4 (6%)	18	42
1	R	68/196 (35%)	66 (97%)	2 (3%)	37	58
1	S	68/196 (35%)	67 (98%)	1 (2%)	57	70
2	A	597/907 (66%)	582 (98%)	15 (2%)	42	62
2	B	597/907 (66%)	580 (97%)	17 (3%)	38	60
2	C	597/907 (66%)	577 (97%)	20 (3%)	32	55
2	D	597/907 (66%)	575 (96%)	22 (4%)	30	52
All	All	2660/4412 (60%)	2572 (97%)	88 (3%)	34	56

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	710	PHE
2	D	554	PHE
2	C	818	LEU
2	C	951	HIS
2	D	629	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	473	HIS
2	D	931	HIS
2	C	625	ASN
2	D	784	HIS
2	C	551	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](#)

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.

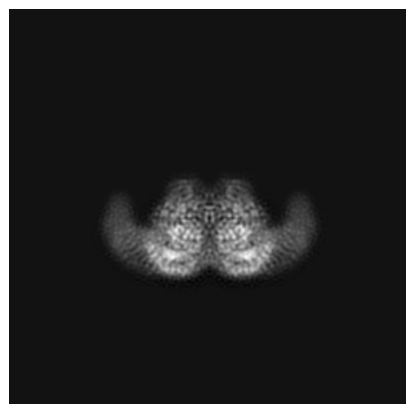
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53346. These allow visual inspection of the internal detail of the map and identification of artifacts.

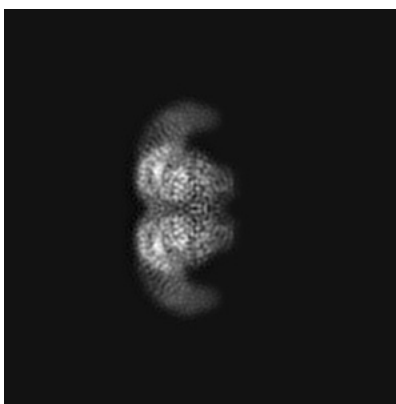
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

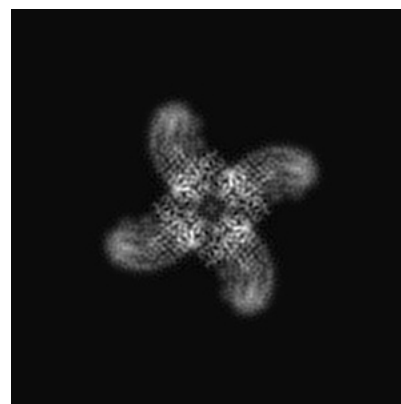
6.1.1 Primary map



X

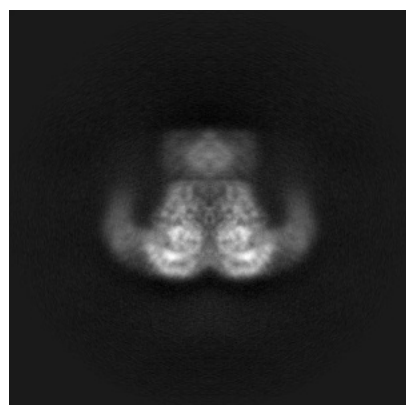


Y

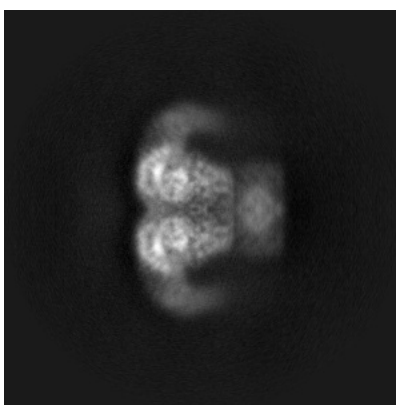


Z

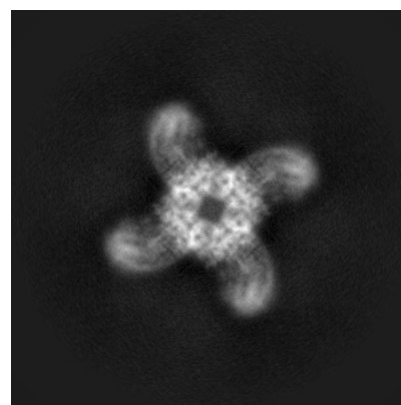
6.1.2 Raw map



X



Y



Z

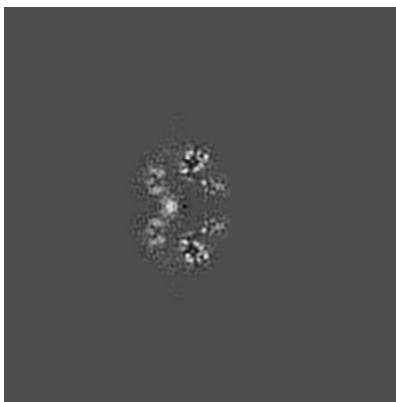
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

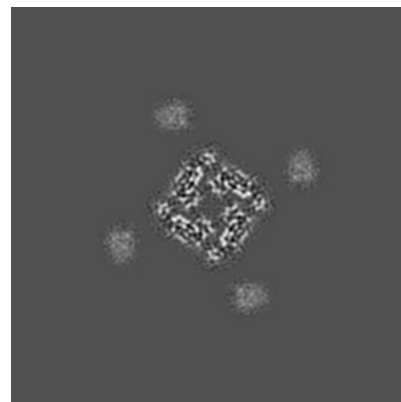
6.2.1 Primary map



X Index: 200

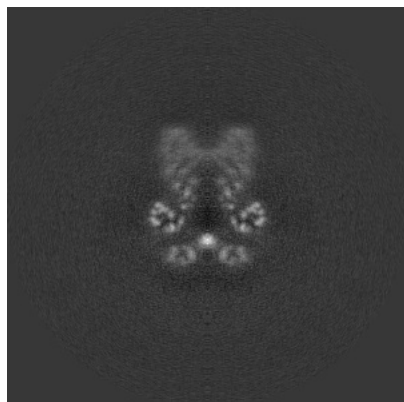


Y Index: 200

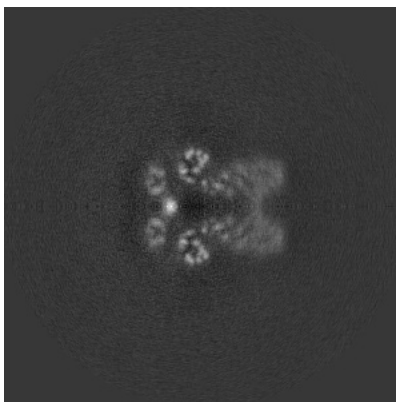


Z Index: 200

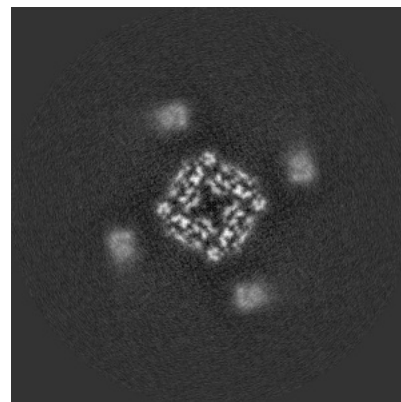
6.2.2 Raw map



X Index: 200



Y Index: 200

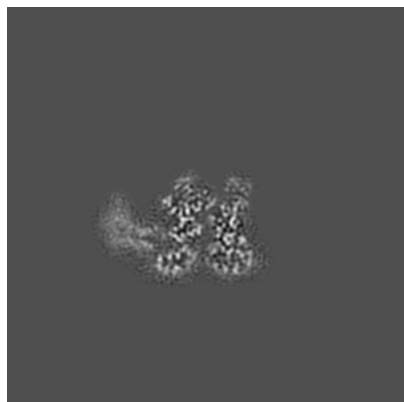


Z Index: 200

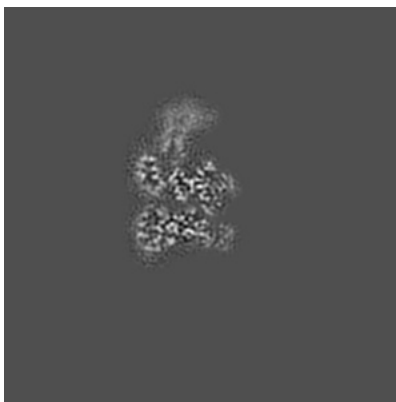
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

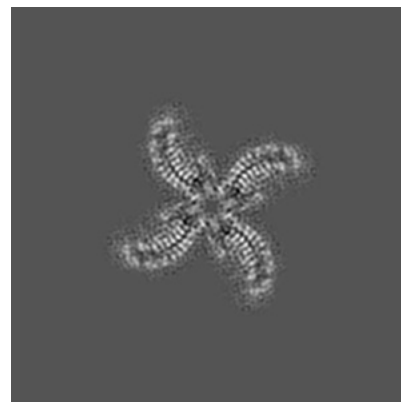
6.3.1 Primary map



X Index: 225

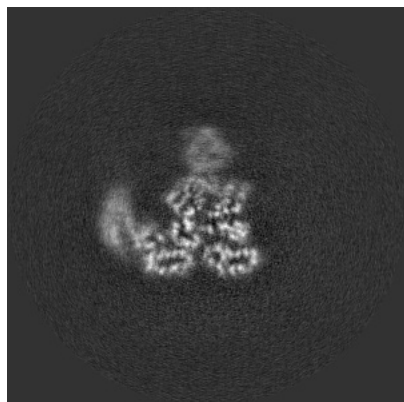


Y Index: 225

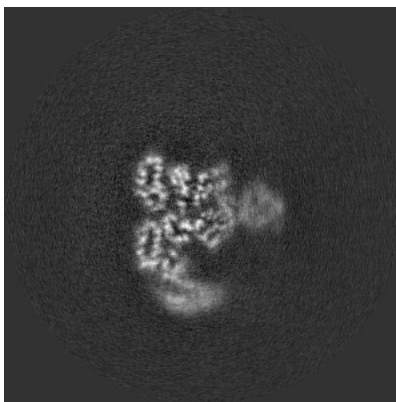


Z Index: 152

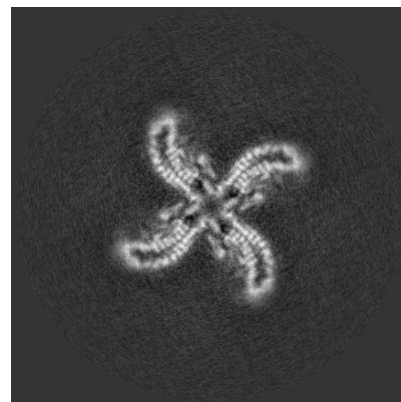
6.3.2 Raw map



X Index: 232



Y Index: 168

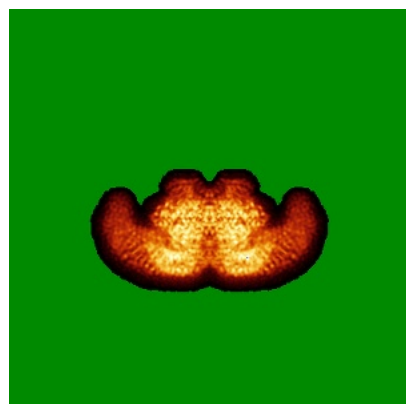


Z Index: 153

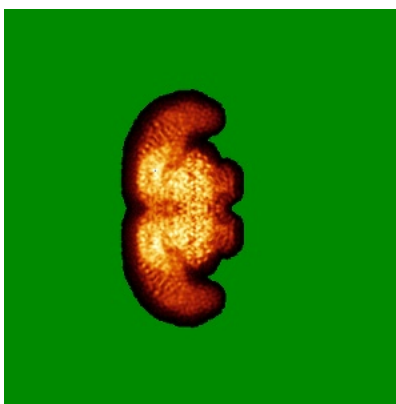
The images above show the largest variance slices of the map in three orthogonal directions.

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

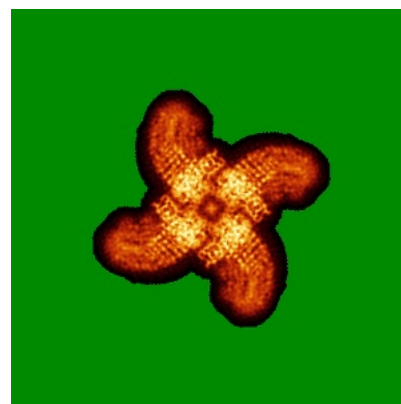
6.4.1 Primary map



X

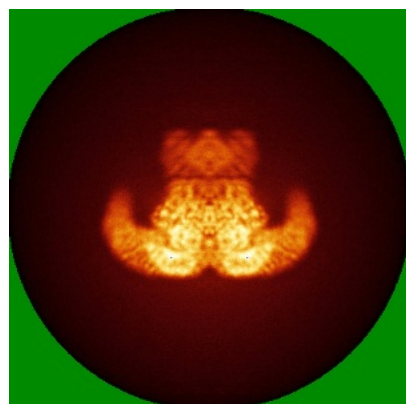


Y

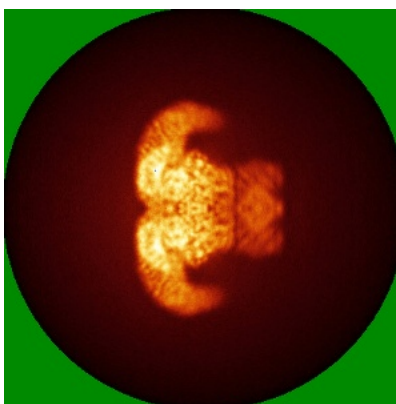


Z

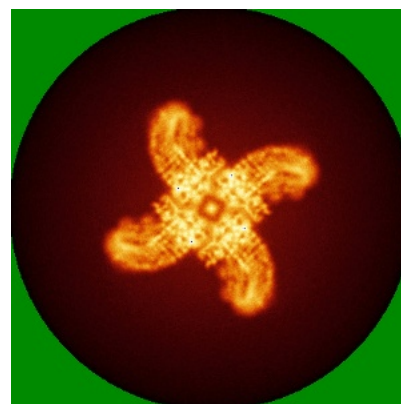
6.4.2 Raw map



X



Y

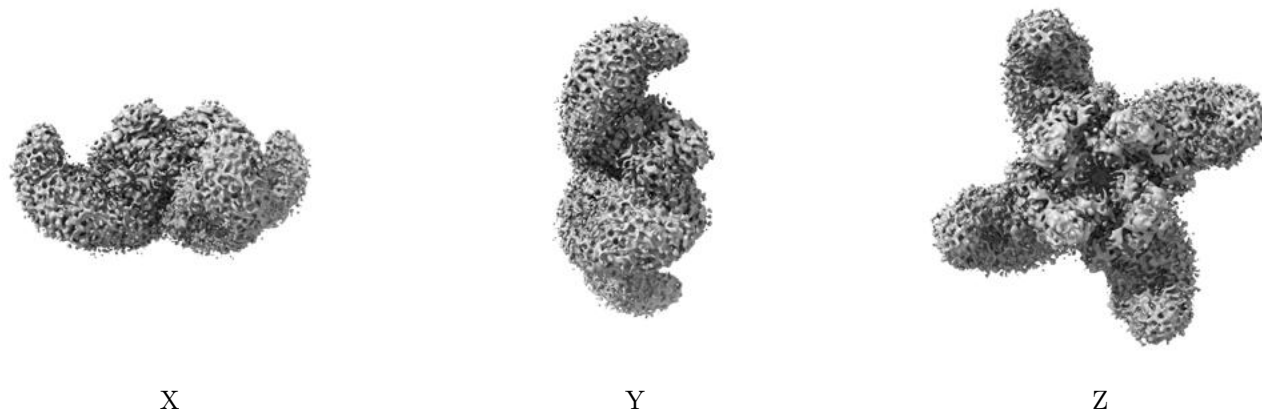


Z

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.

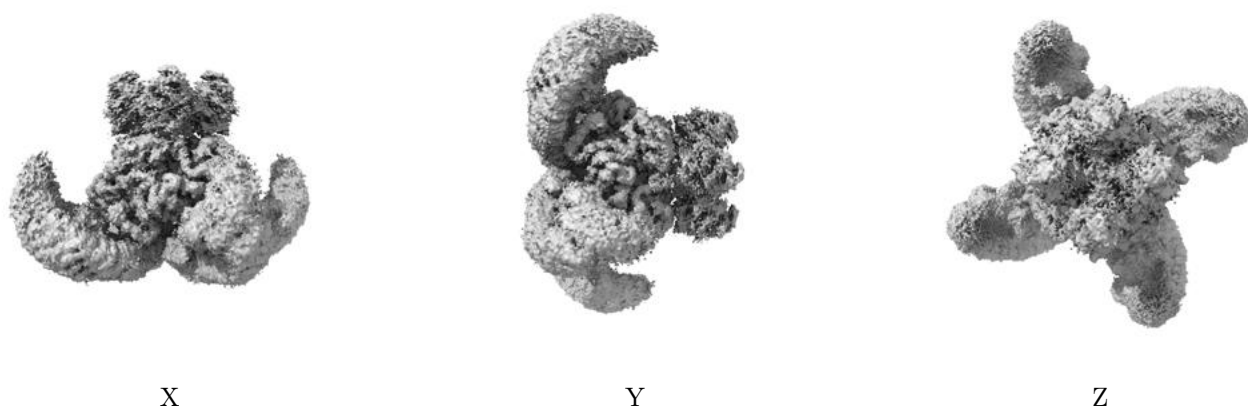
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

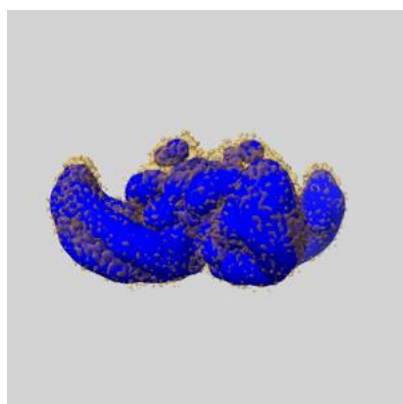
6.6 Mask visualisation [i](#)

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

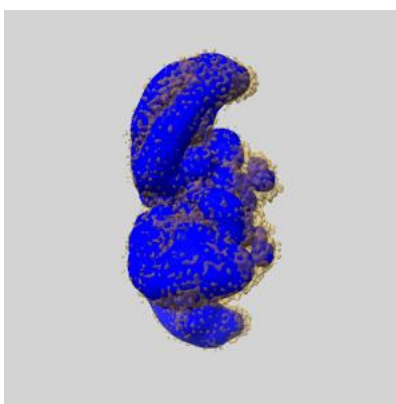
A mask typically either:

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

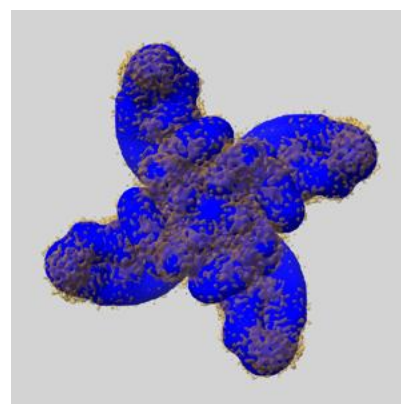
6.6.1 emd_53346_msk_1.map [i](#)



X



Y

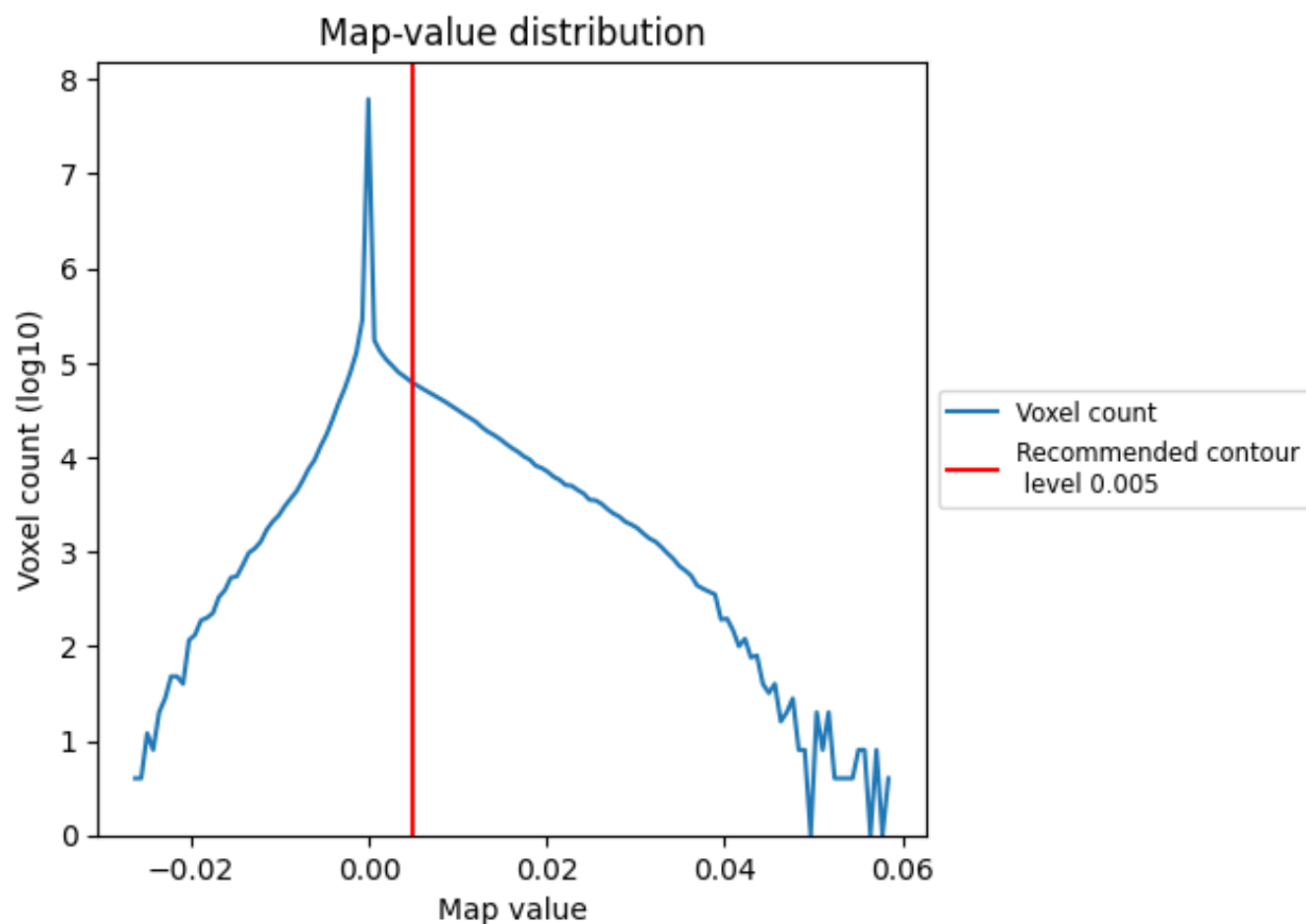


Z

7 Map analysis [i](#)

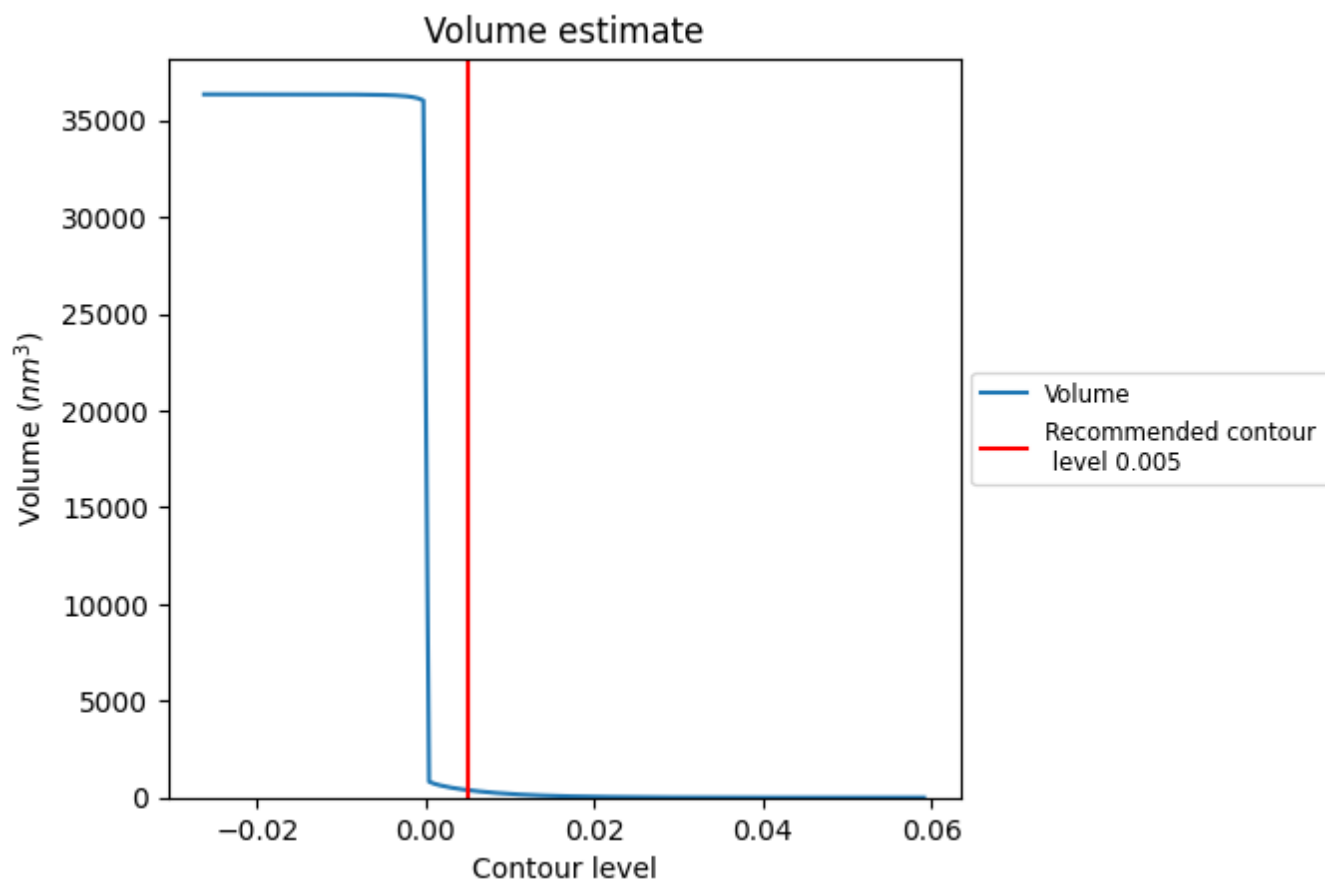
This section contains the results of statistical analysis of the map.

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.

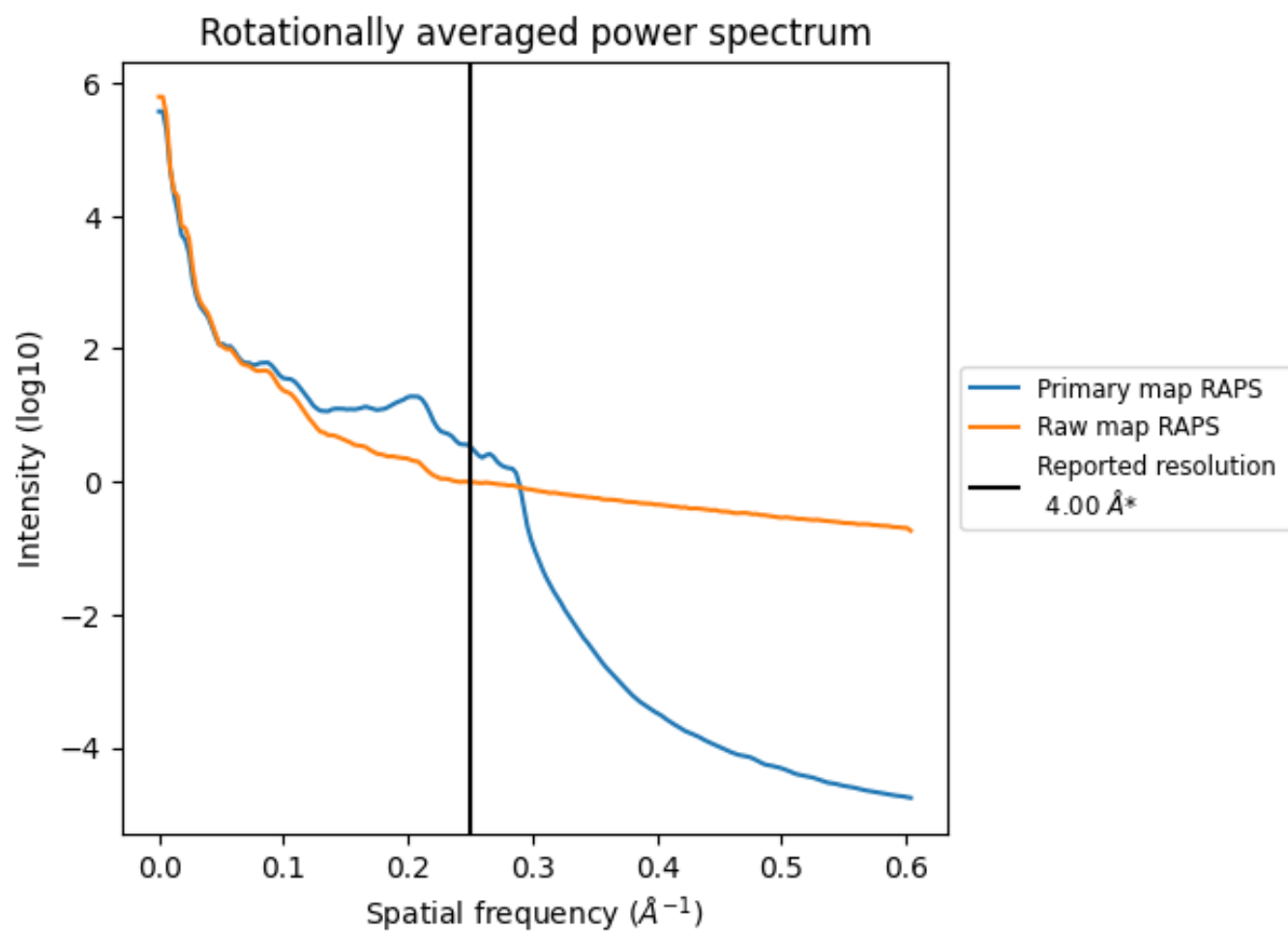
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 386 nm³; this corresponds to an approximate mass of 348 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 ⓘ

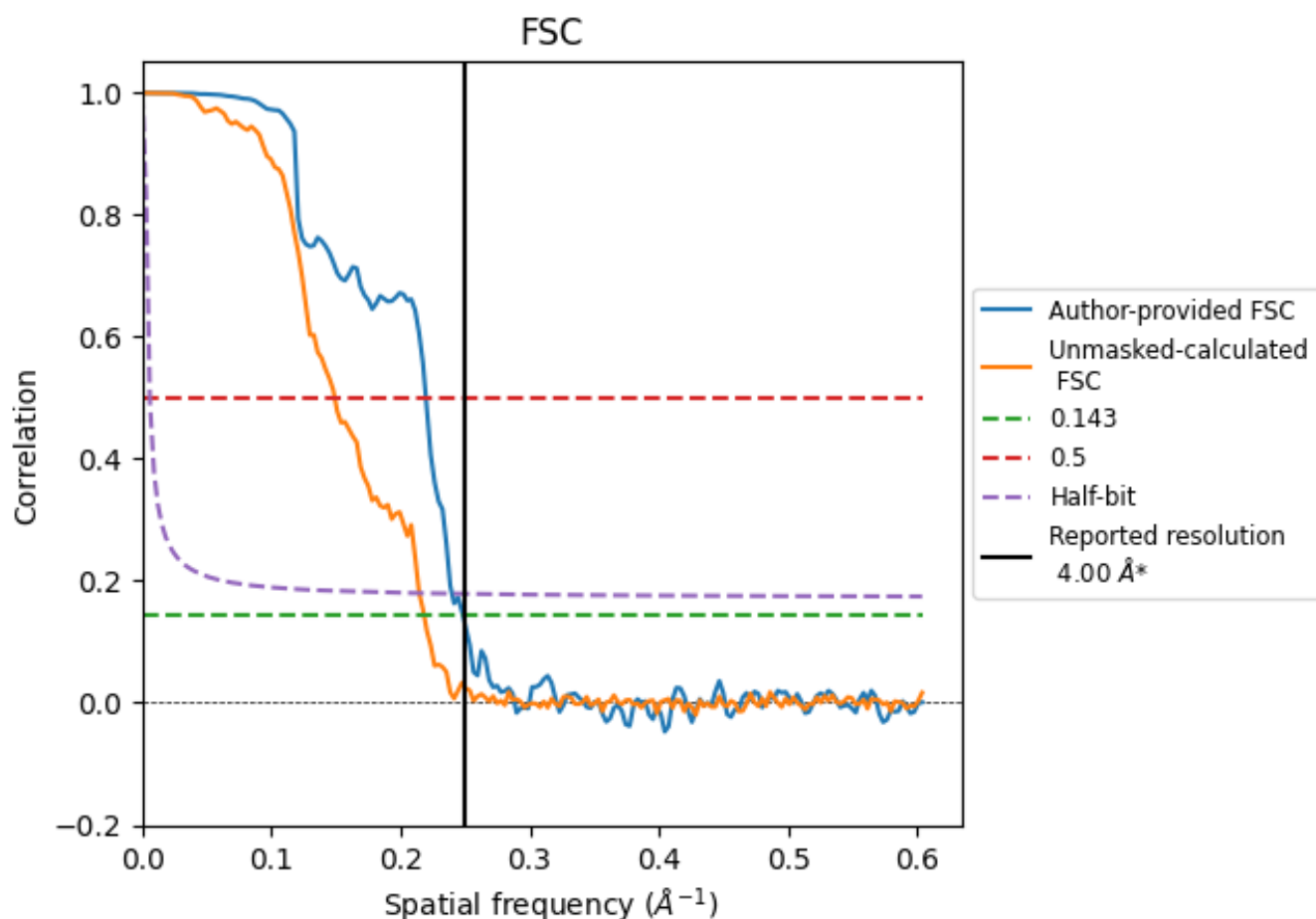


*Reported resolution corresponds to spatial frequency of 0.250 \AA^{-1}

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 0.250 \AA^{-1}

8.2 Resolution estimates [i](#)

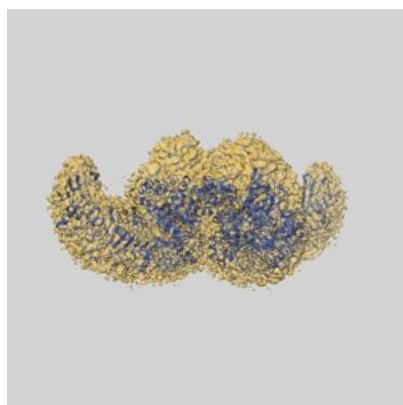
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.03	4.55	4.17
Unmasked-calculated*	4.58	6.71	4.66

*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 4.0 by more than 10 %

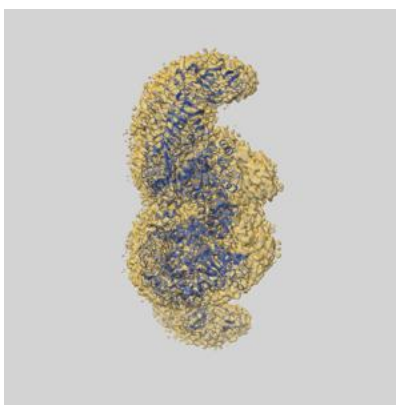
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53346 and PDB model 9QT4. Per-residue inclusion information can be found in section [3](#) on page [5](#).

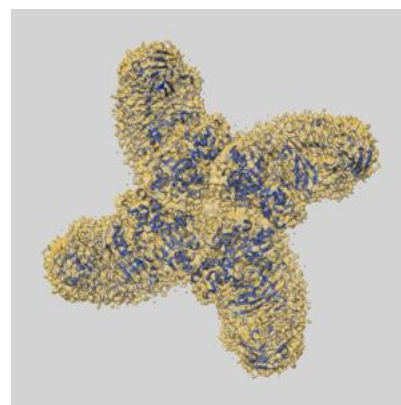
9.1 Map-model overlay [i](#)



X



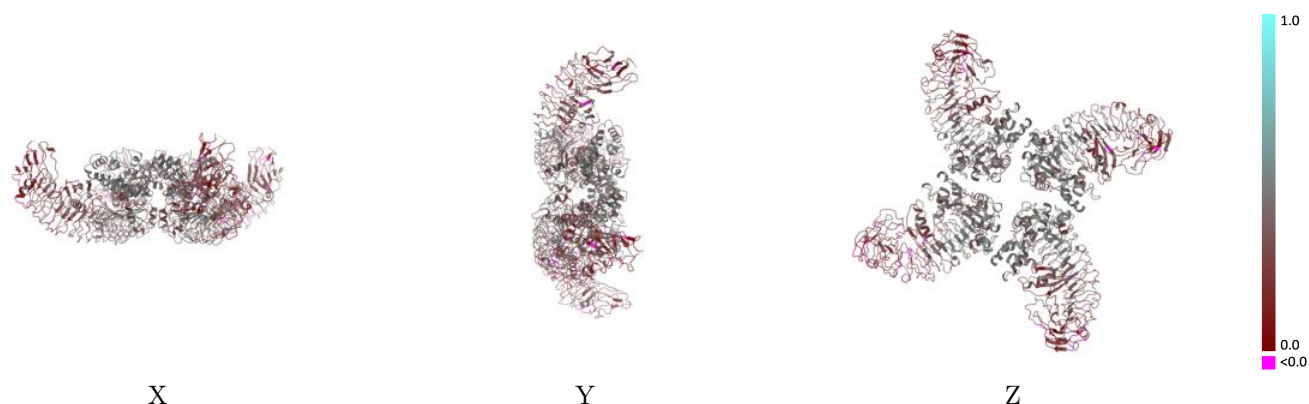
Y



Z

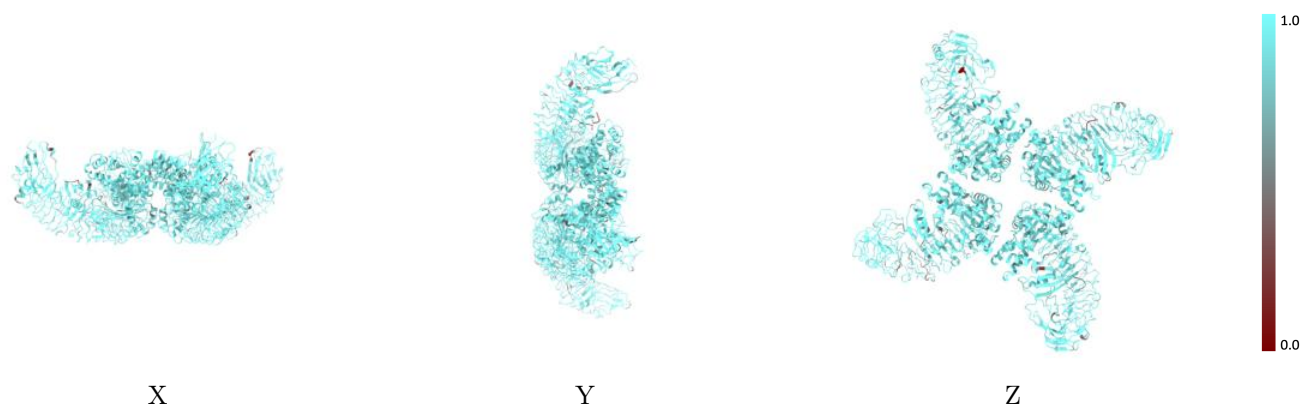
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



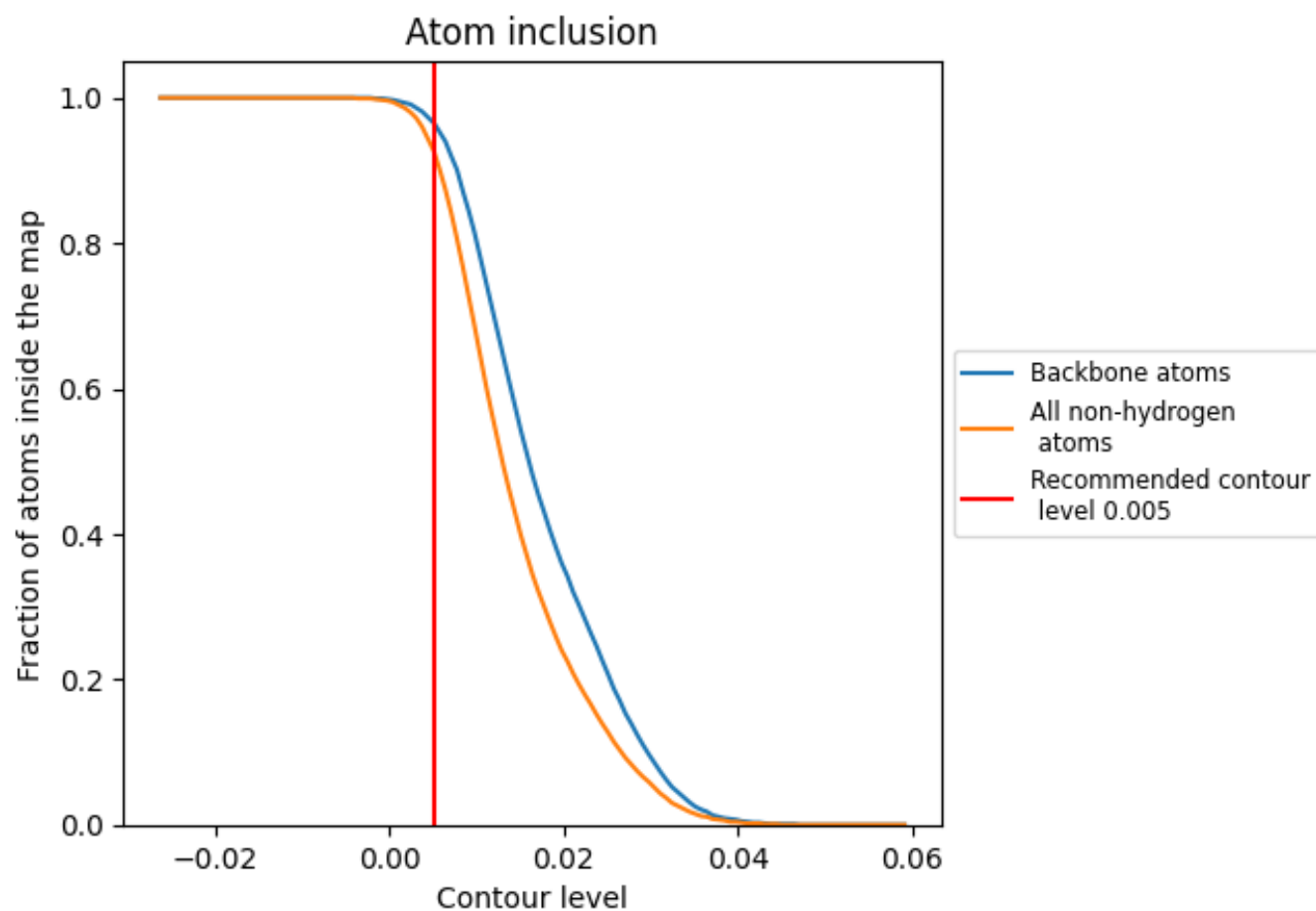
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9290	<div><div></div></div> 0.3400
A	<div><div></div></div> 0.9380	<div><div></div></div> 0.3480
B	<div><div></div></div> 0.9360	<div><div></div></div> 0.3540
C	<div><div></div></div> 0.9390	<div><div></div></div> 0.3480
D	<div><div></div></div> 0.9240	<div><div></div></div> 0.3310
P	<div><div></div></div> 0.8800	<div><div></div></div> 0.2910
Q	<div><div></div></div> 0.8590	<div><div></div></div> 0.2850
R	<div><div></div></div> 0.8720	<div><div></div></div> 0.2970
S	<div><div></div></div> 0.9010	<div><div></div></div> 0.2980

1.0

0.0

<0.0