wwPDB EM Validation Summary Report (i)

May 19, 2024 – 10:30 PM JST

PDB ID	:	7DD9
EMDB ID	:	EMD-30650
Title	:	Cryo-EM structure of the Ams1 and Nbr1 complex
Authors	:	Zhang, J.; Ye, K.
Deposited on	:	2020-10-28
Resolution	:	2.40 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

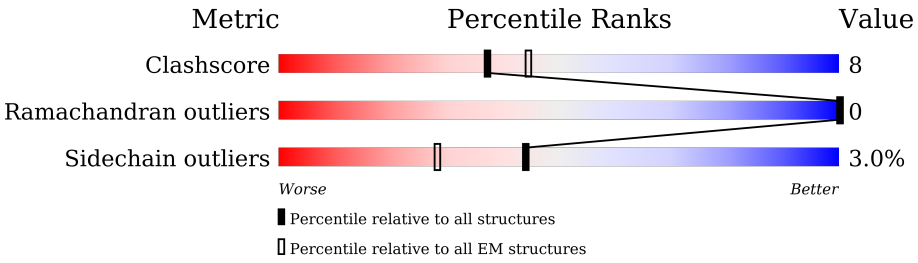
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	1584	57% 14% 29%
1	C	1584	56% 14% 29%
1	E	1584	56% 14% 29%
1	G	1584	57% 14% 29%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 37149 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 Alpha-mannosidase,ZZ-type zinc finger-containing protein P3 5G2.11c,Maltose/maltodextrin-binding periplasmic protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1129	Total	C	N	O	S	0	0
			9047	5777	1528	1694	48		
1	C	1129	Total	C	N	O	S	0	0
			9047	5777	1528	1694	48		
1	E	1129	Total	C	N	O	S	0	0
			9047	5777	1528	1694	48		
1	G	1129	Total	C	N	O	S	0	0
			9047	5777	1528	1694	48		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1078	GLY	-	linker	UNP Q9UT61
A	1079	PHE	-	linker	UNP Q9UT61
A	1080	LYS	-	linker	UNP Q9UT61
A	1081	LYS	-	linker	UNP Q9UT61
A	1082	ALA	-	linker	UNP Q9UT61
A	1083	SER	-	linker	UNP Q9UT61
A	1084	SER	-	linker	UNP Q9UT61
A	1085	SER	-	linker	UNP Q9UT61
A	1086	ASP	-	linker	UNP Q9UT61
A	1087	ASN	-	linker	UNP Q9UT61
A	1088	LYS	-	linker	UNP Q9UT61
A	1089	GLU	-	linker	UNP Q9UT61
A	1090	GLN	-	linker	UNP Q9UT61
C	1078	GLY	-	linker	UNP Q9UT61
C	1079	PHE	-	linker	UNP Q9UT61
C	1080	LYS	-	linker	UNP Q9UT61
C	1081	LYS	-	linker	UNP Q9UT61
C	1082	ALA	-	linker	UNP Q9UT61
C	1083	SER	-	linker	UNP Q9UT61
C	1084	SER	-	linker	UNP Q9UT61
C	1085	SER	-	linker	UNP Q9UT61

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1086	ASP	-	linker	UNP Q9UT61
C	1087	ASN	-	linker	UNP Q9UT61
C	1088	LYS	-	linker	UNP Q9UT61
C	1089	GLU	-	linker	UNP Q9UT61
C	1090	GLN	-	linker	UNP Q9UT61
E	1078	GLY	-	linker	UNP Q9UT61
E	1079	PHE	-	linker	UNP Q9UT61
E	1080	LYS	-	linker	UNP Q9UT61
E	1081	LYS	-	linker	UNP Q9UT61
E	1082	ALA	-	linker	UNP Q9UT61
E	1083	SER	-	linker	UNP Q9UT61
E	1084	SER	-	linker	UNP Q9UT61
E	1085	SER	-	linker	UNP Q9UT61
E	1086	ASP	-	linker	UNP Q9UT61
E	1087	ASN	-	linker	UNP Q9UT61
E	1088	LYS	-	linker	UNP Q9UT61
E	1089	GLU	-	linker	UNP Q9UT61
E	1090	GLN	-	linker	UNP Q9UT61
G	1078	GLY	-	linker	UNP Q9UT61
G	1079	PHE	-	linker	UNP Q9UT61
G	1080	LYS	-	linker	UNP Q9UT61
G	1081	LYS	-	linker	UNP Q9UT61
G	1082	ALA	-	linker	UNP Q9UT61
G	1083	SER	-	linker	UNP Q9UT61
G	1084	SER	-	linker	UNP Q9UT61
G	1085	SER	-	linker	UNP Q9UT61
G	1086	ASP	-	linker	UNP Q9UT61
G	1087	ASN	-	linker	UNP Q9UT61
G	1088	LYS	-	linker	UNP Q9UT61
G	1089	GLU	-	linker	UNP Q9UT61
G	1090	GLN	-	linker	UNP Q9UT61

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
2	A	3	Total Zn 3 3	0
2	C	3	Total Zn 3 3	0
2	E	3	Total Zn 3 3	0

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Mol	Chain	Residues	Atoms		AltConf
2	G	3	Total 3	Zn 3	0

- Molecule 3 is water.

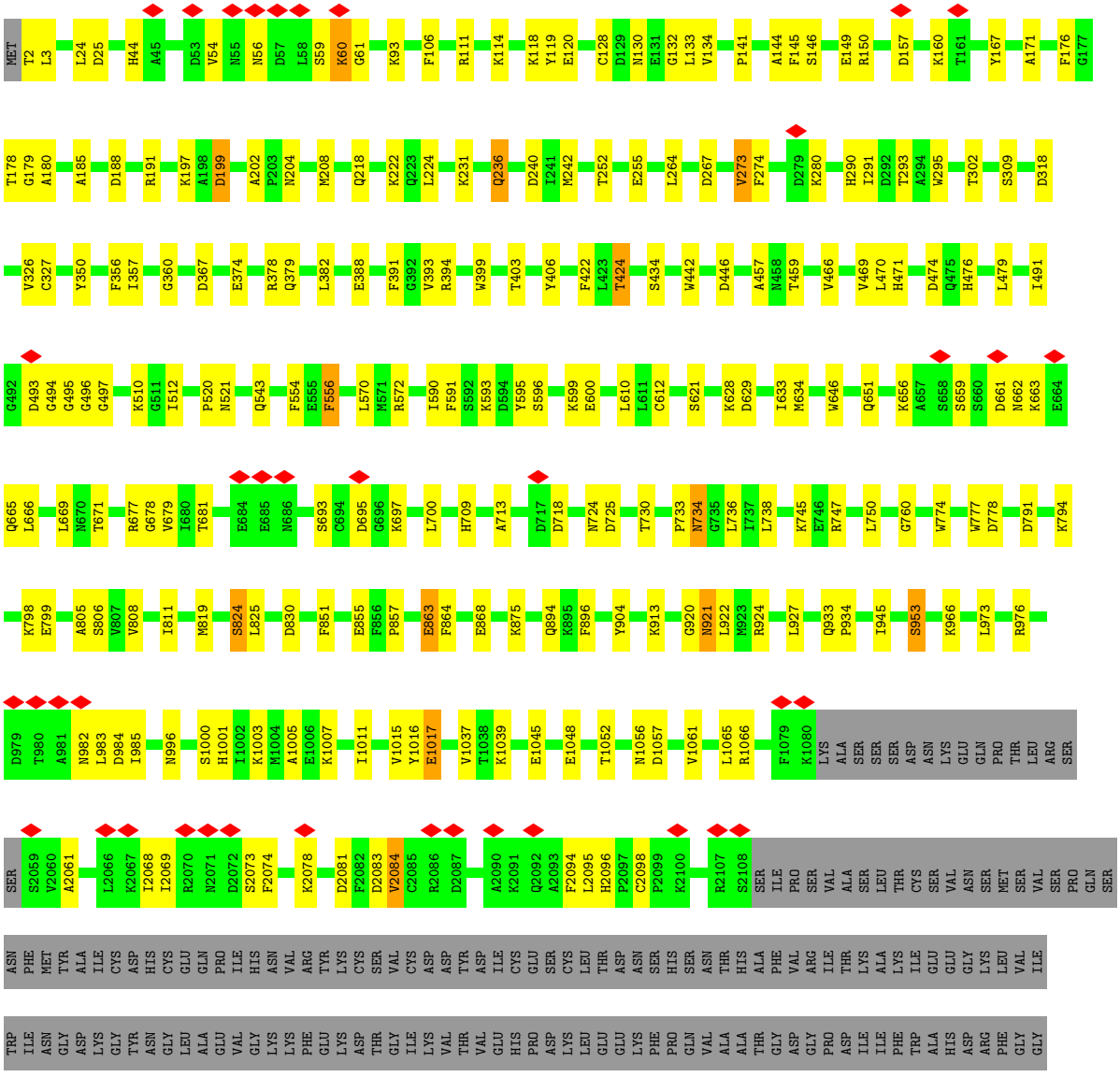
Mol	Chain	Residues	Atoms		AltConf
3	A	238	Total 238	O 238	0
3	C	238	Total 238	O 238	0
3	E	236	Total 236	O 236	0
3	G	237	Total 237	O 237	0

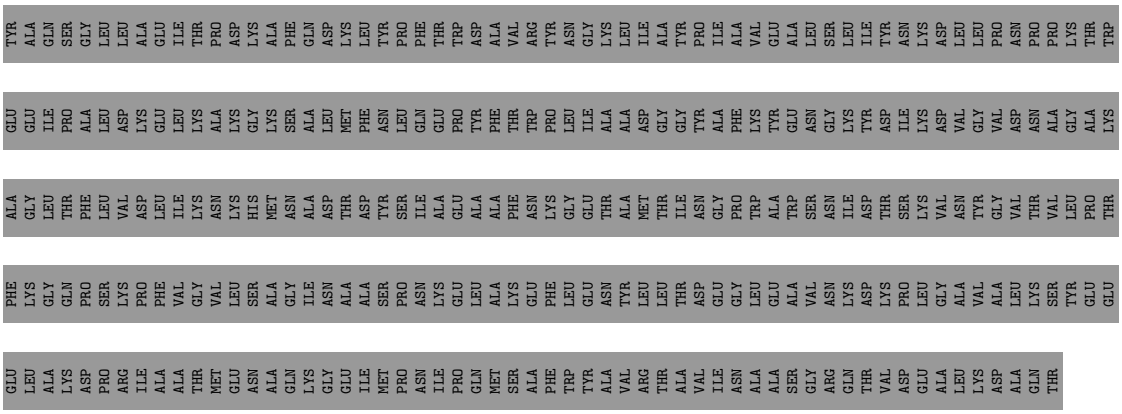
3 Residue-property plots (i)

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: Alpha-mannosidase,ZZ-type zinc finger-containing protein P35G2.11c,Maltose/maltodextrin-binding periplasmic protein

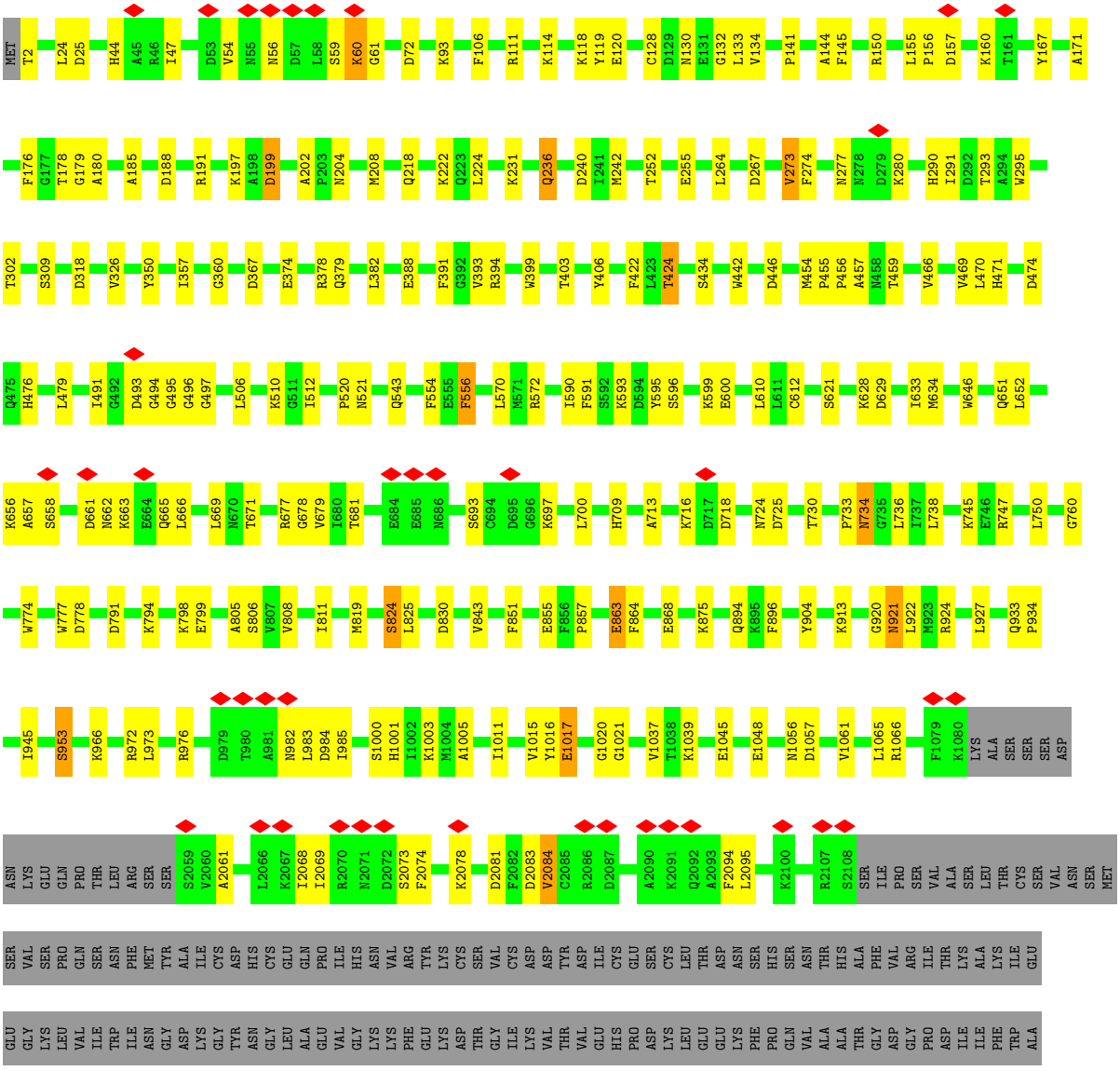
Chain A:

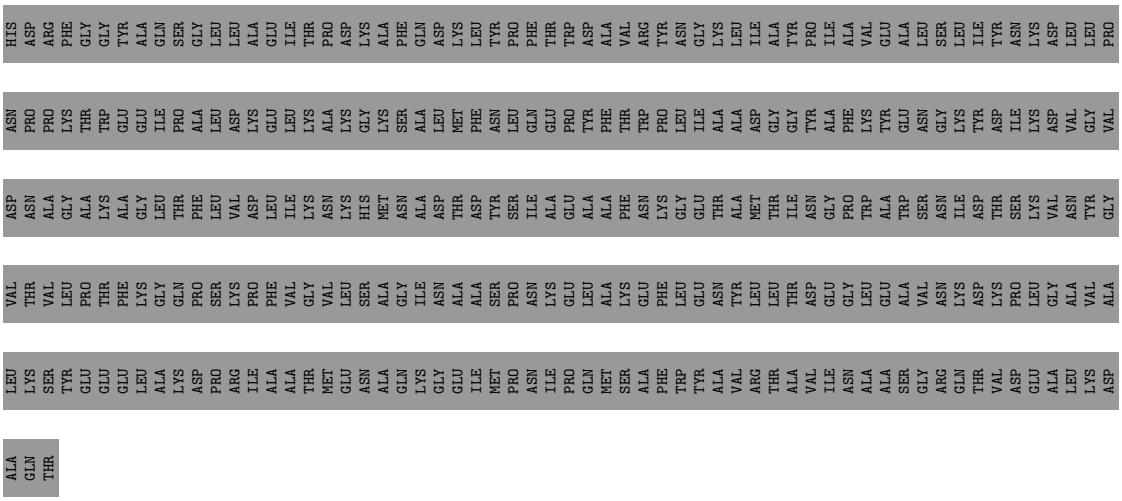




• Molecule 1: Alpha-mannosidase,ZZ-type zinc finger-containing protein P35G2.11c,Maltose/maltodextrin-binding periplasmic protein

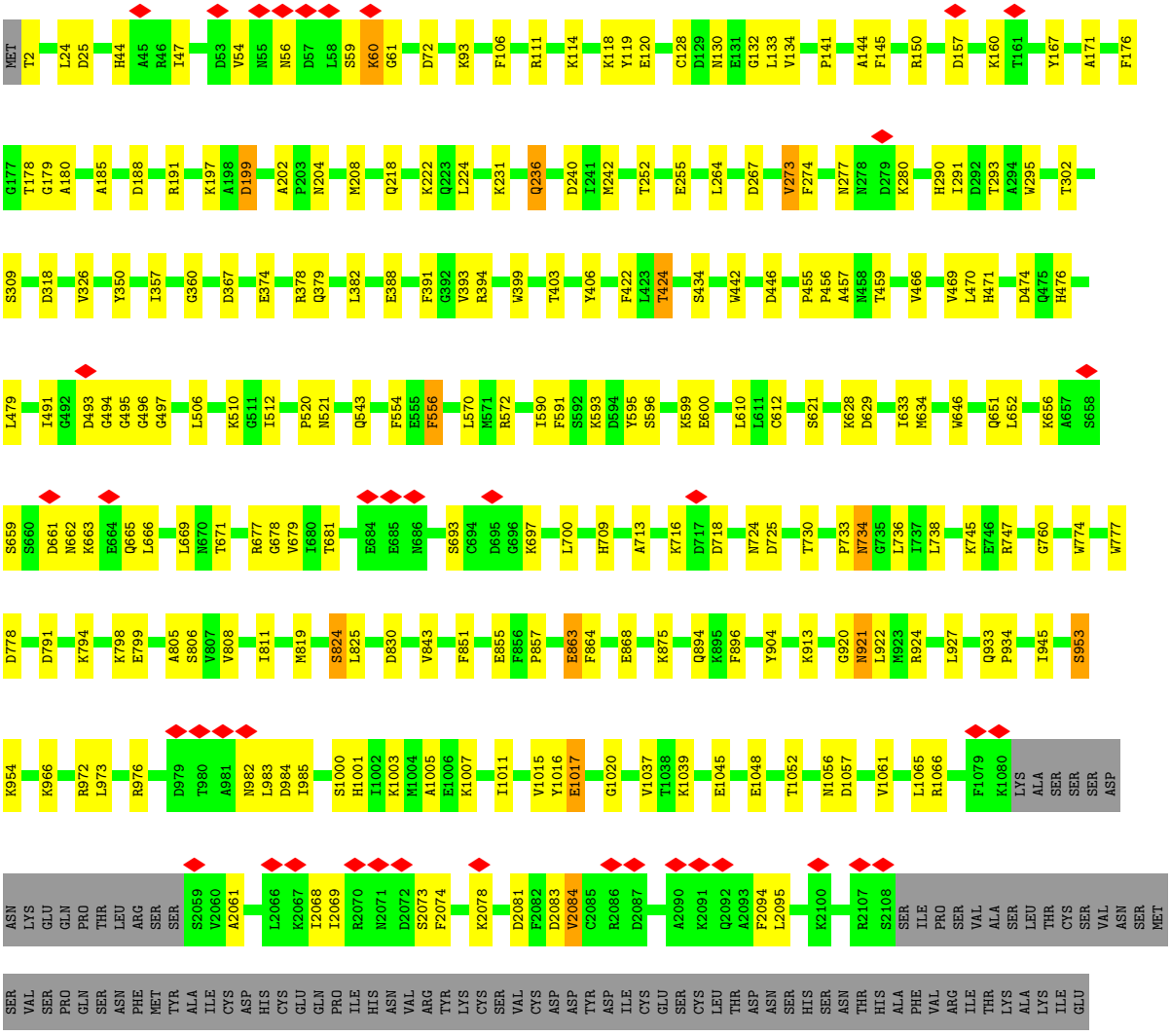
Chain C:

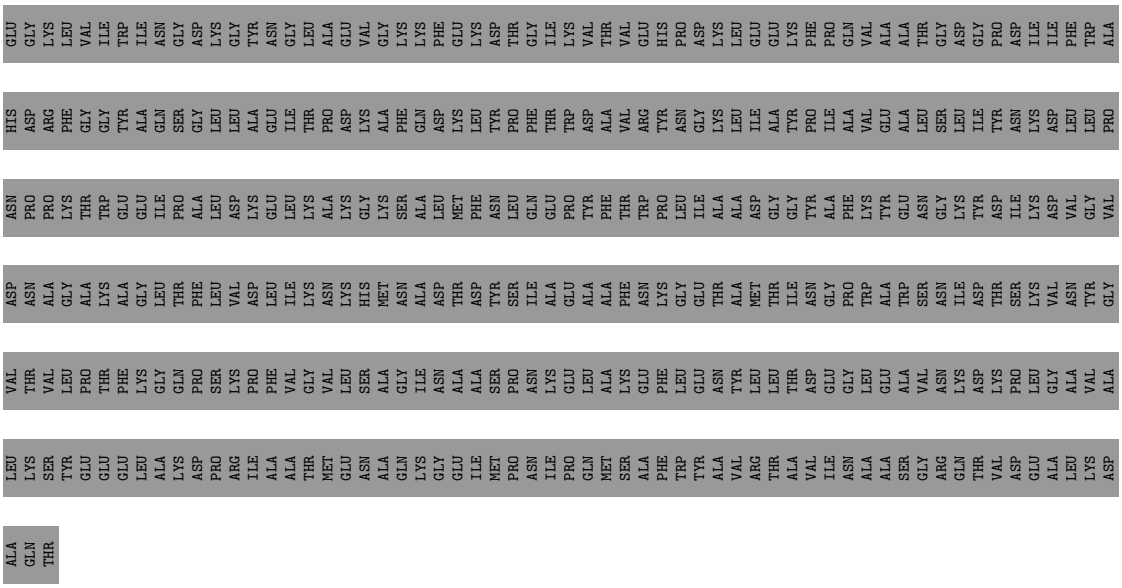




• Molecule 1: Alpha-mannosidase,ZZ-type zinc finger-containing protein P35G2.11c,Maltose/maltodextrin-binding periplasmic protein

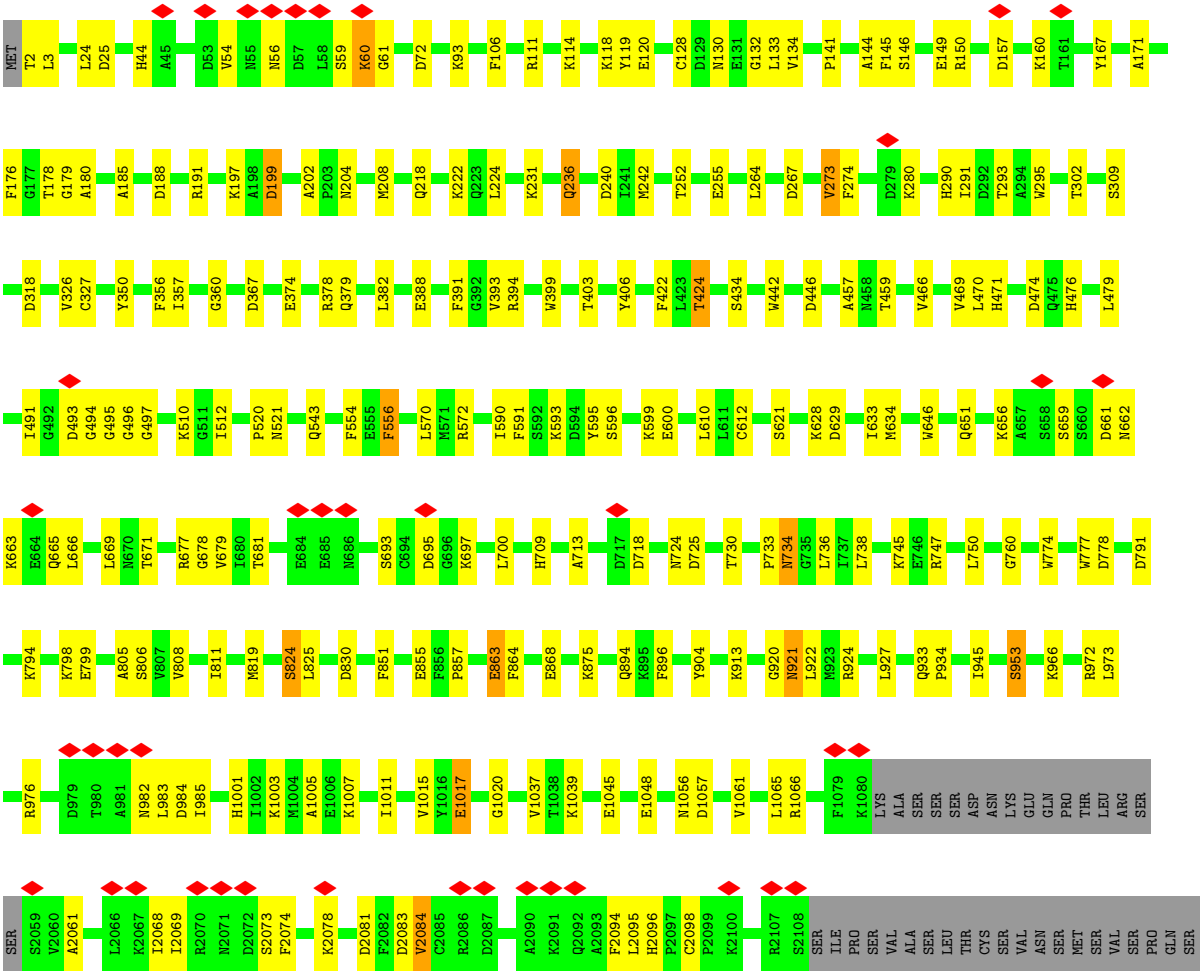
Chain E:

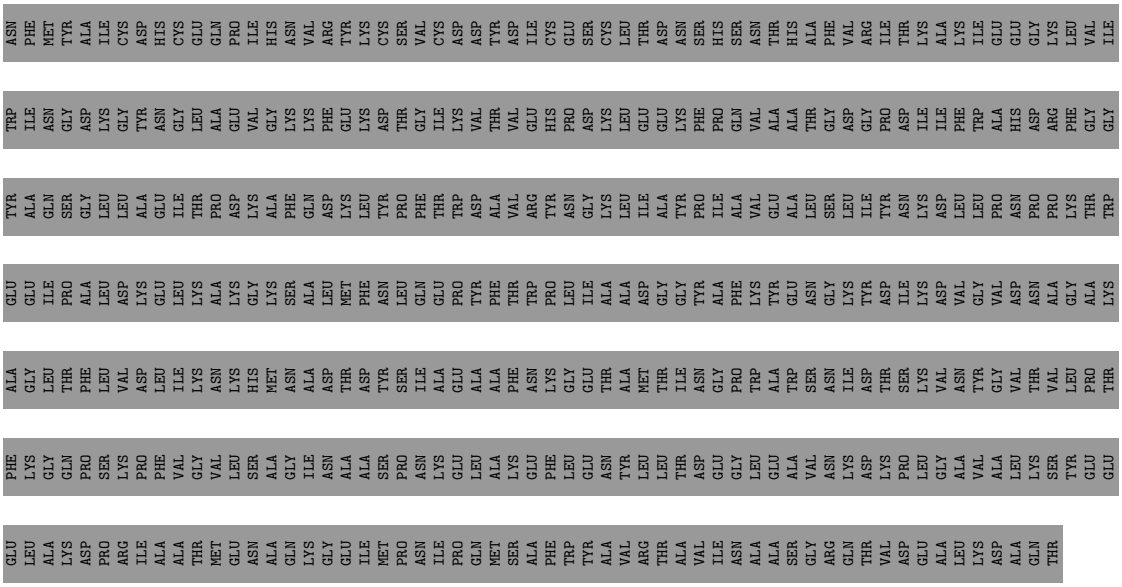




• Molecule 1: Alpha-mannosidase,ZZ-type zinc finger-containing protein P35G2.11c,Maltose/maltodextrin-binding periplasmic protein

Chain G:




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

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	296884	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.228	Depositor
Minimum map value	-0.136	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	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	0.40	0/9281	0.49	0/12593
1	C	0.40	0/9281	0.49	0/12593
1	E	0.40	0/9281	0.49	0/12593
1	G	0.40	0/9281	0.49	0/12593
All	All	0.40	0/37124	0.49	0/50372

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	9047	0	8788	146	0
1	C	9047	0	8788	153	0
1	E	9047	0	8788	150	0
1	G	9047	0	8788	146	0
2	A	3	0	0	0	0
2	C	3	0	0	0	0
2	E	3	0	0	0	0
2	G	3	0	0	0	0
3	A	238	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	238	0	0	1	0
3	E	236	0	0	1	0
3	G	237	0	0	2	0
All	All	37149	0	35152	583	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 583 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:PHE:CE2	1:A:424:THR:HG21	2.17	0.79
1:G:422:PHE:CE2	1:G:424:THR:HG21	2.18	0.79
1:C:422:PHE:CE2	1:C:424:THR:HG21	2.18	0.79
1:E:422:PHE:CE2	1:E:424:THR:HG21	2.18	0.79
1:A:2069:ILE:HG21	1:A:2073:SER:HB3	1.66	0.78

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	1125/1584 (71%)	1045 (93%)	80 (7%)	0	100	100
1	C	1125/1584 (71%)	1045 (93%)	80 (7%)	0	100	100
1	E	1125/1584 (71%)	1045 (93%)	80 (7%)	0	100	100
1	G	1125/1584 (71%)	1045 (93%)	80 (7%)	0	100	100
All	All	4500/6336 (71%)	4180 (93%)	320 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	1000/1378 (73%)	970 (97%)	30 (3%)	41	61
1	C	1000/1378 (73%)	971 (97%)	29 (3%)	42	62
1	E	1000/1378 (73%)	970 (97%)	30 (3%)	41	61
1	G	1000/1378 (73%)	971 (97%)	29 (3%)	42	62
All	All	4000/5512 (73%)	3882 (97%)	118 (3%)	44	61

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2084	VAL
1	G	953	SER
1	E	628	LYS
1	G	921	ASN
1	G	556	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	665	GLN
1	E	744	HIS
1	G	744	HIS
1	G	236	GLN
1	C	236	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 12 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.

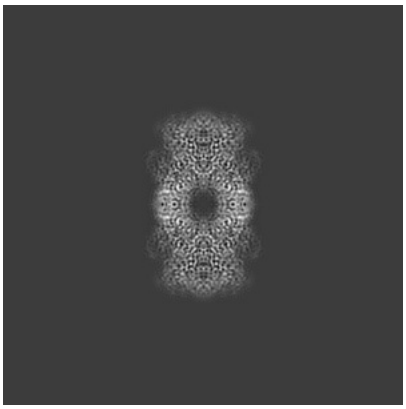
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-30650. These allow visual inspection of the internal detail of the map and identification of artifacts.

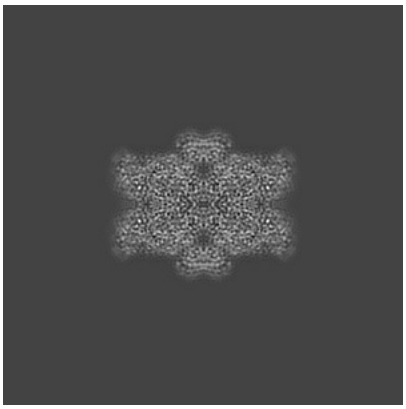
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

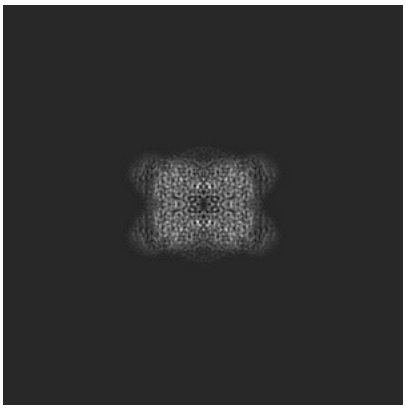
6.1.1 Primary map



X

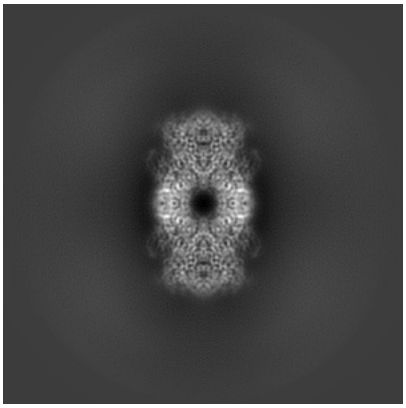


Y

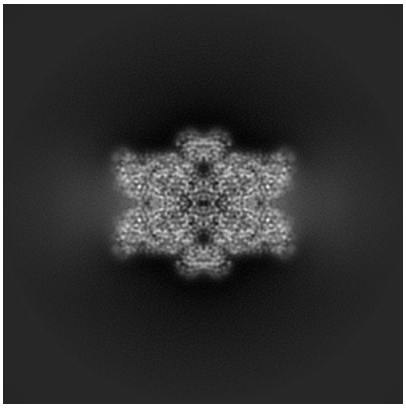


Z

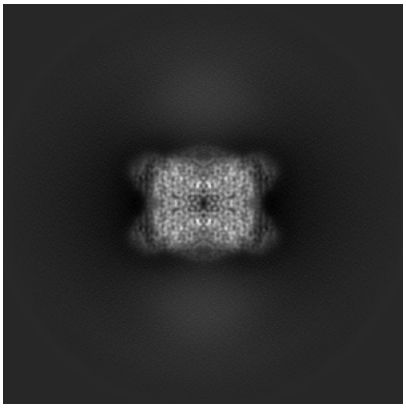
6.1.2 Raw map



X



Y

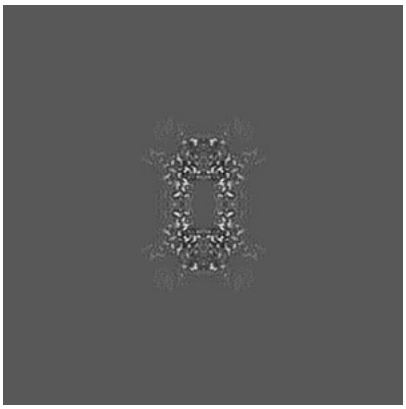


Z

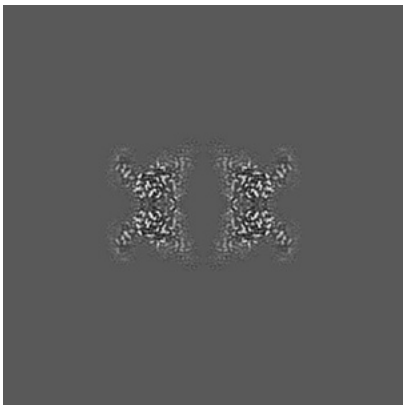
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

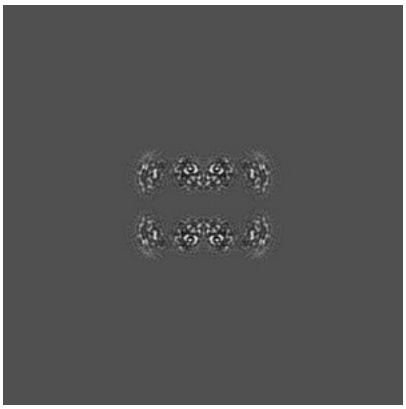
6.2.1 Primary map



X Index: 160

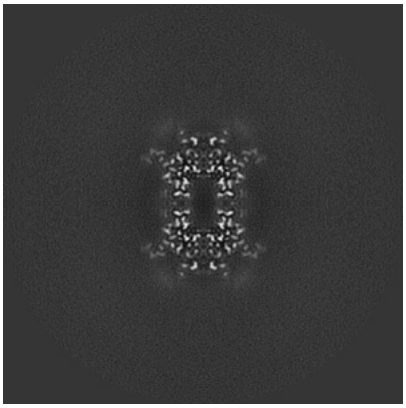


Y Index: 160

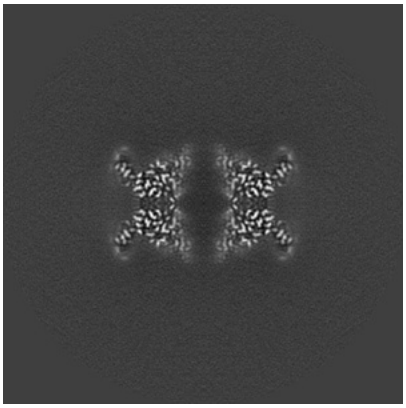


Z Index: 160

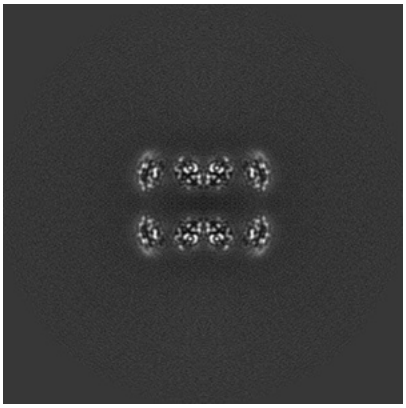
6.2.2 Raw map



X Index: 160



Y Index: 160

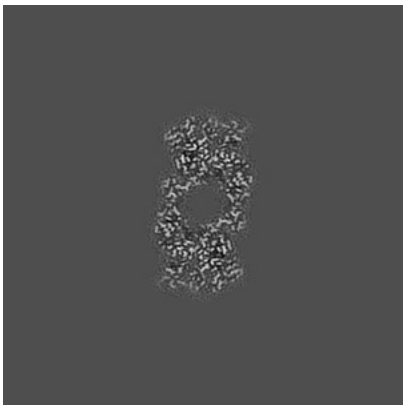


Z Index: 160

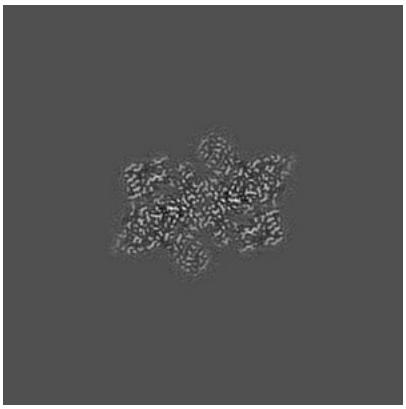
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

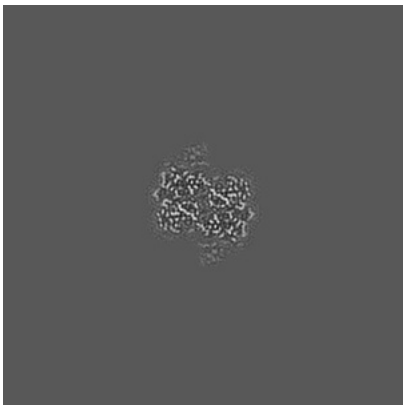
6.3.1 Primary map



X Index: 182

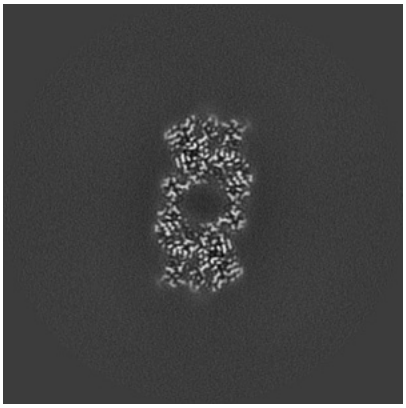


Y Index: 177

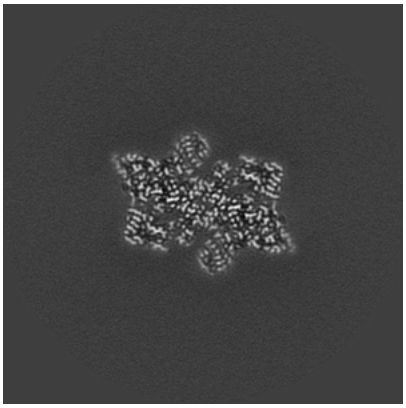


Z Index: 124

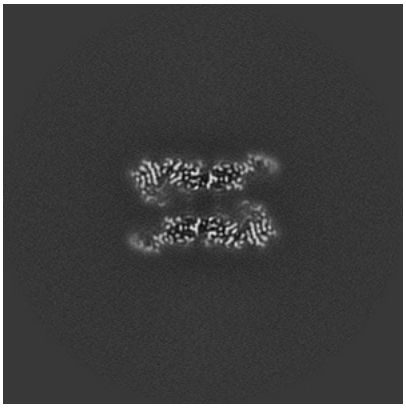
6.3.2 Raw map



X Index: 182



Y Index: 143

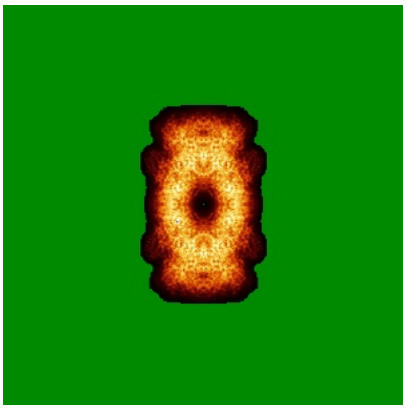


Z Index: 149

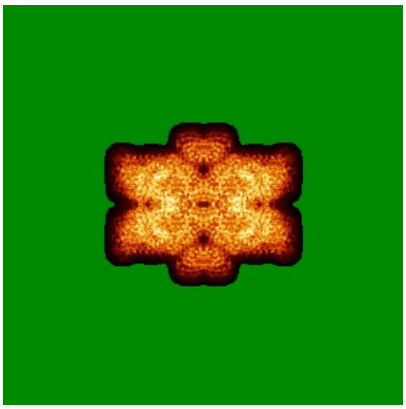
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

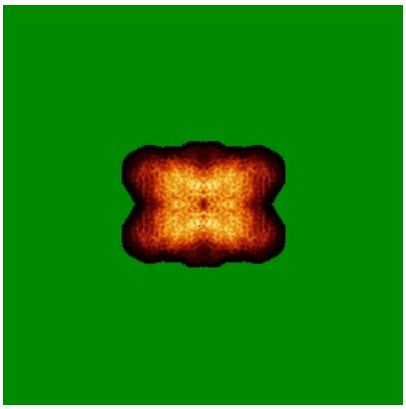
6.4.1 Primary map



X

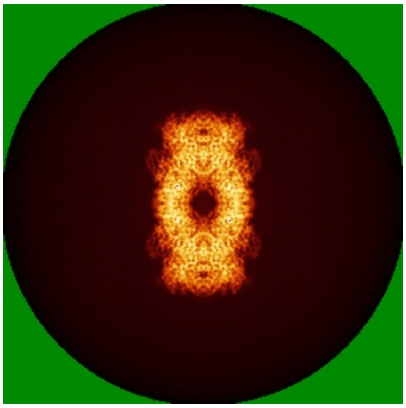


Y

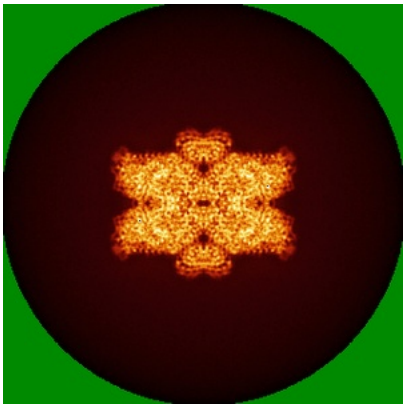


Z

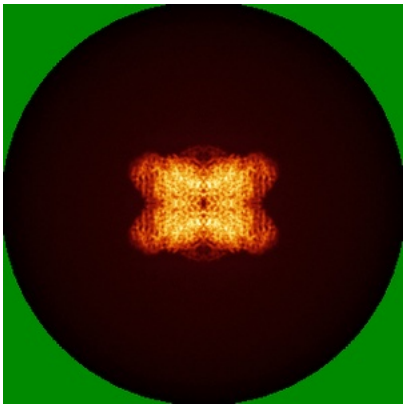
6.4.2 Raw map



X



Y

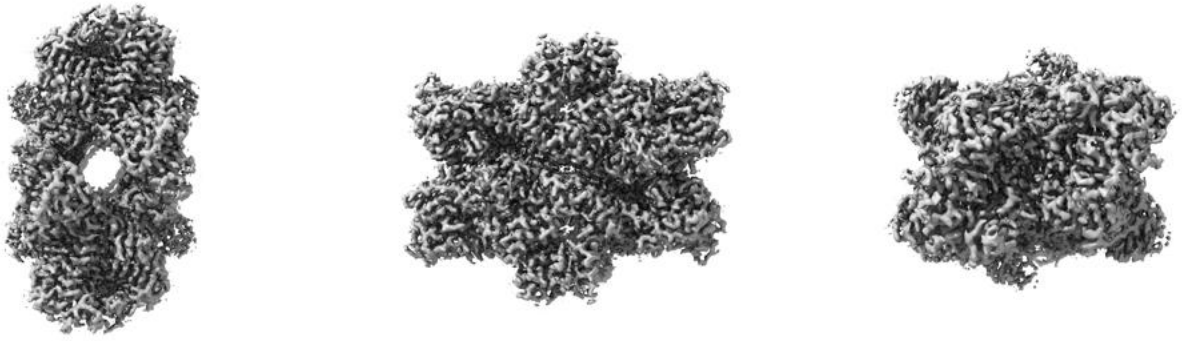


Z

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)

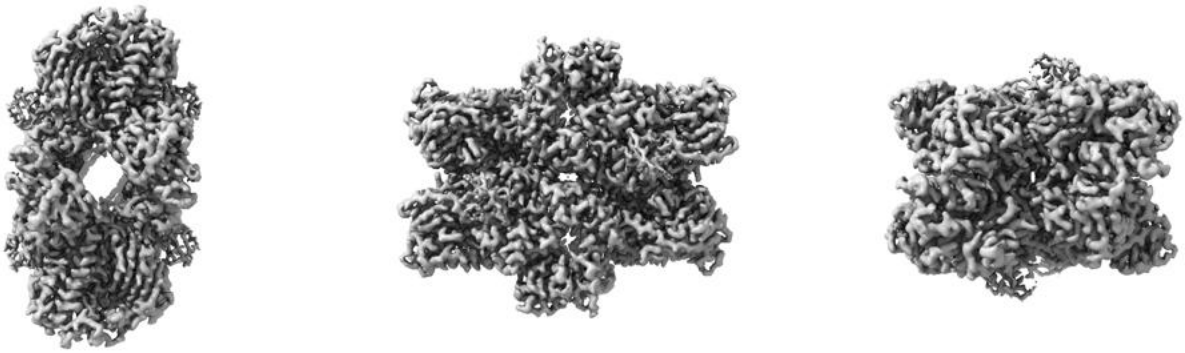
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. 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.

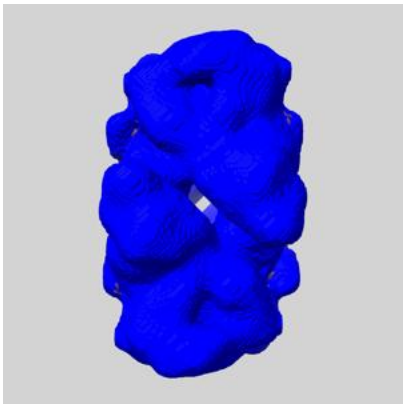
6.6 Mask visualisation (i)

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

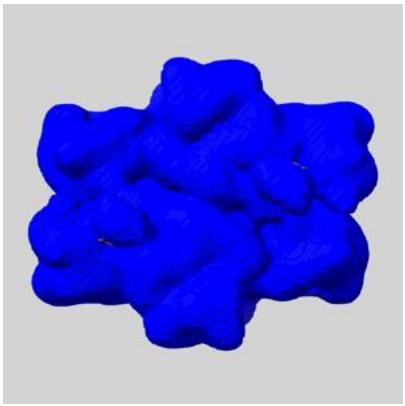
A mask typically either:

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

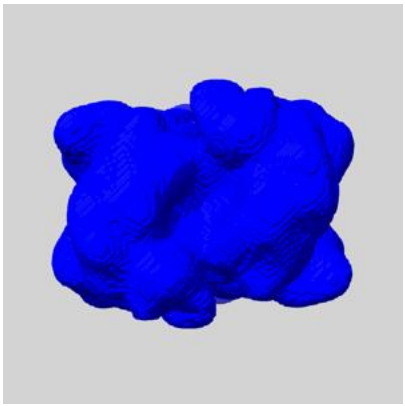
6.6.1 emd_30650_msk_1.map (i)



X



Y

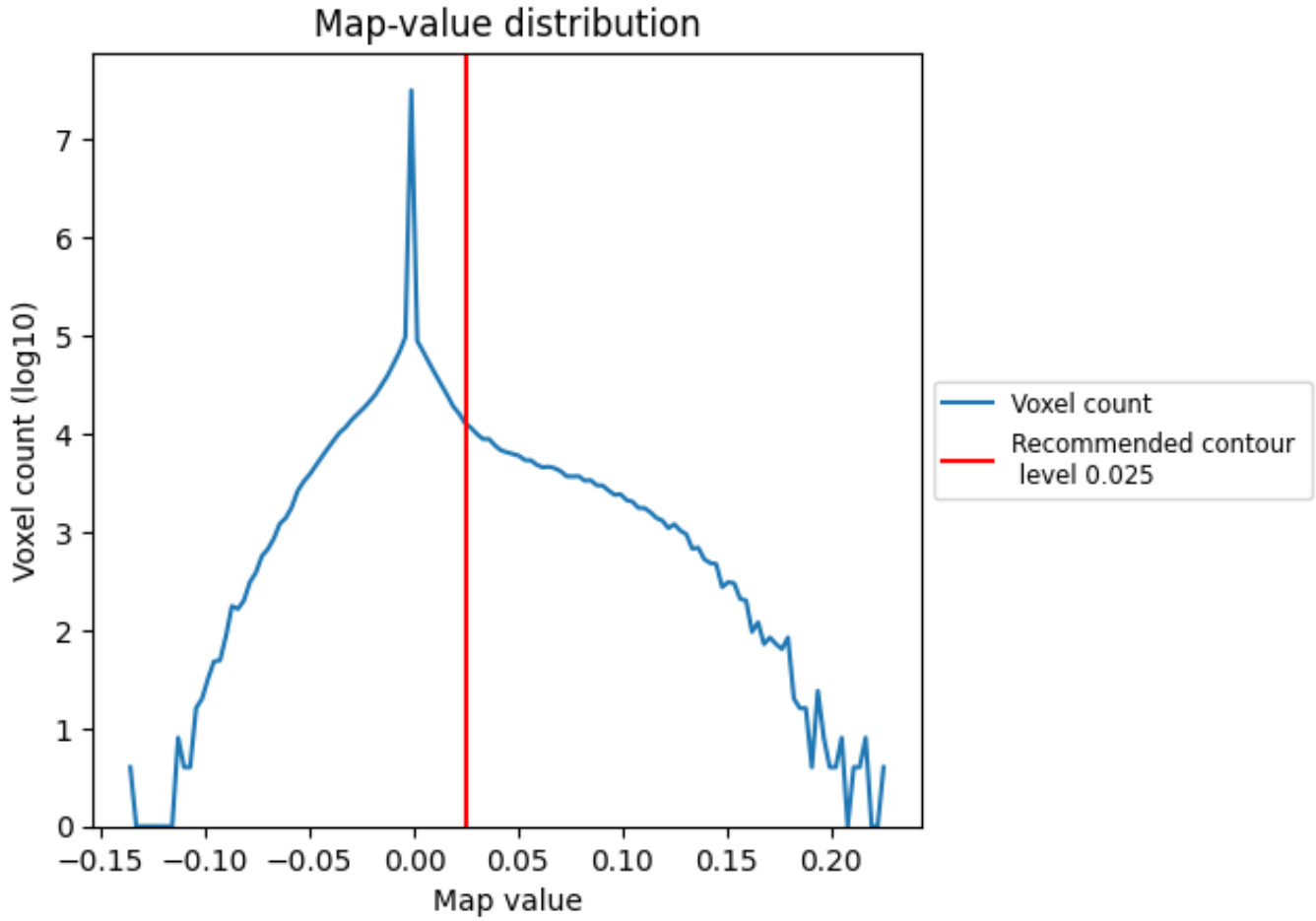


Z

7 Map analysis

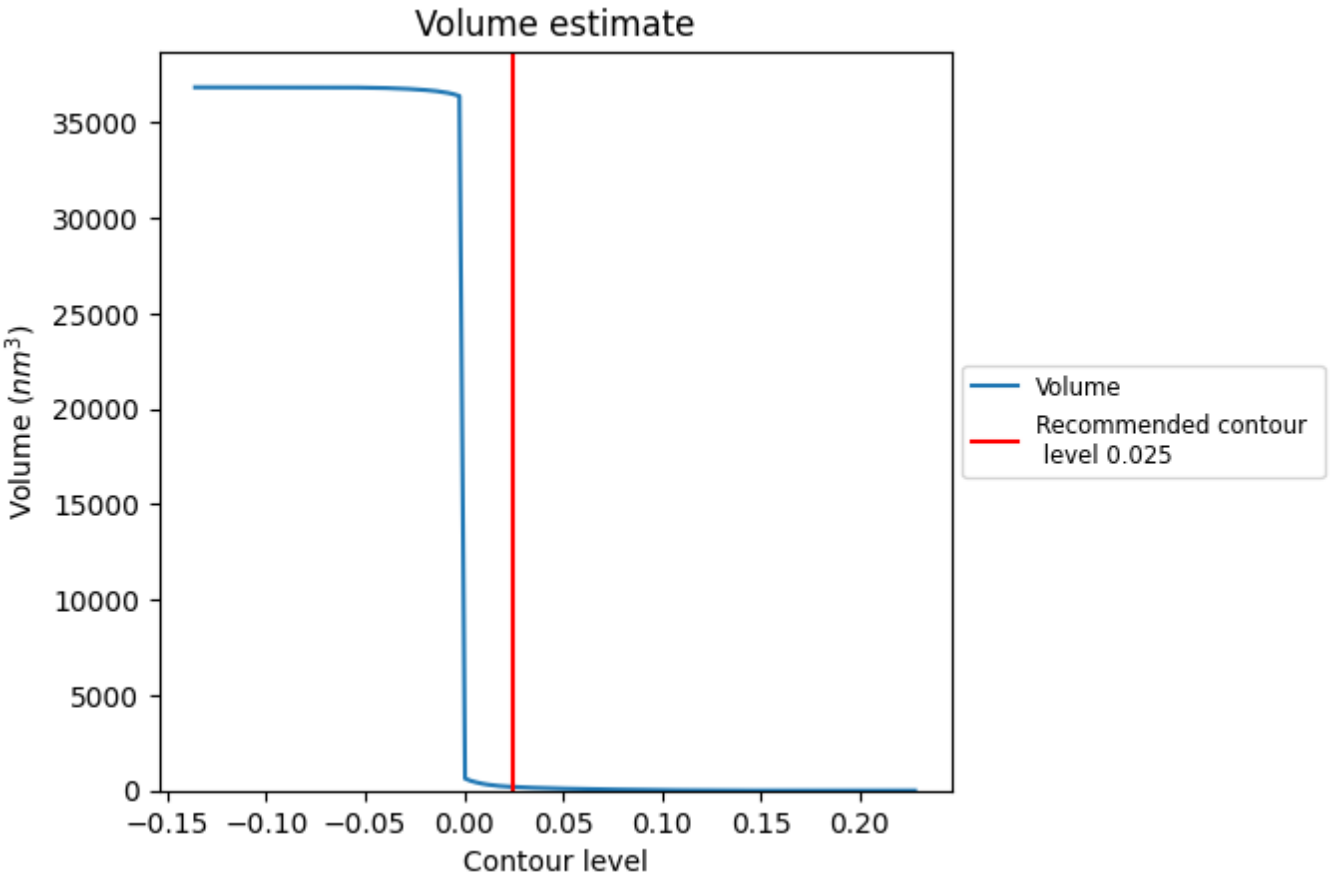
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

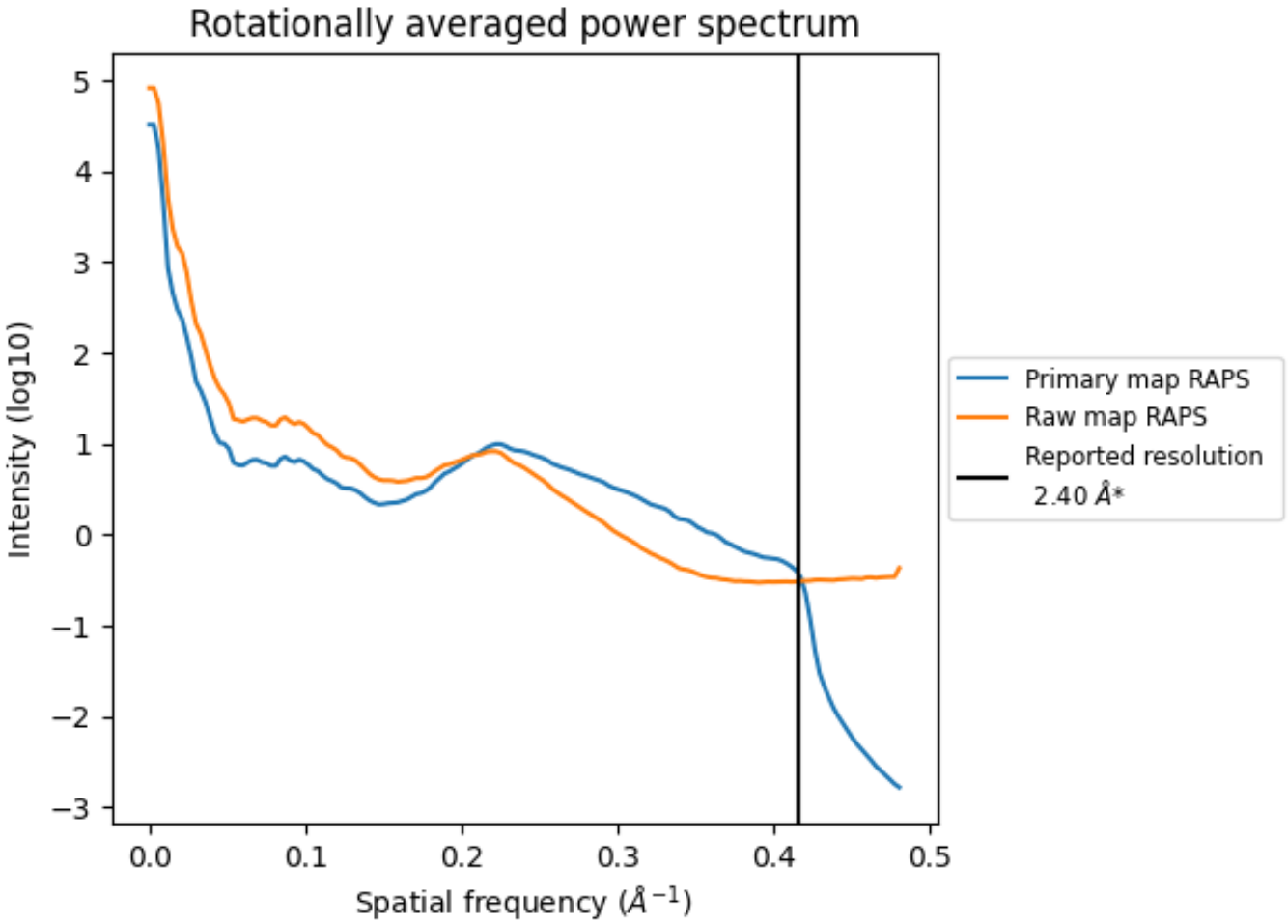
7.2 Volume estimate (i)



The volume at the recommended contour level is 190 nm^3; this corresponds to an approximate mass of 172 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 (i)

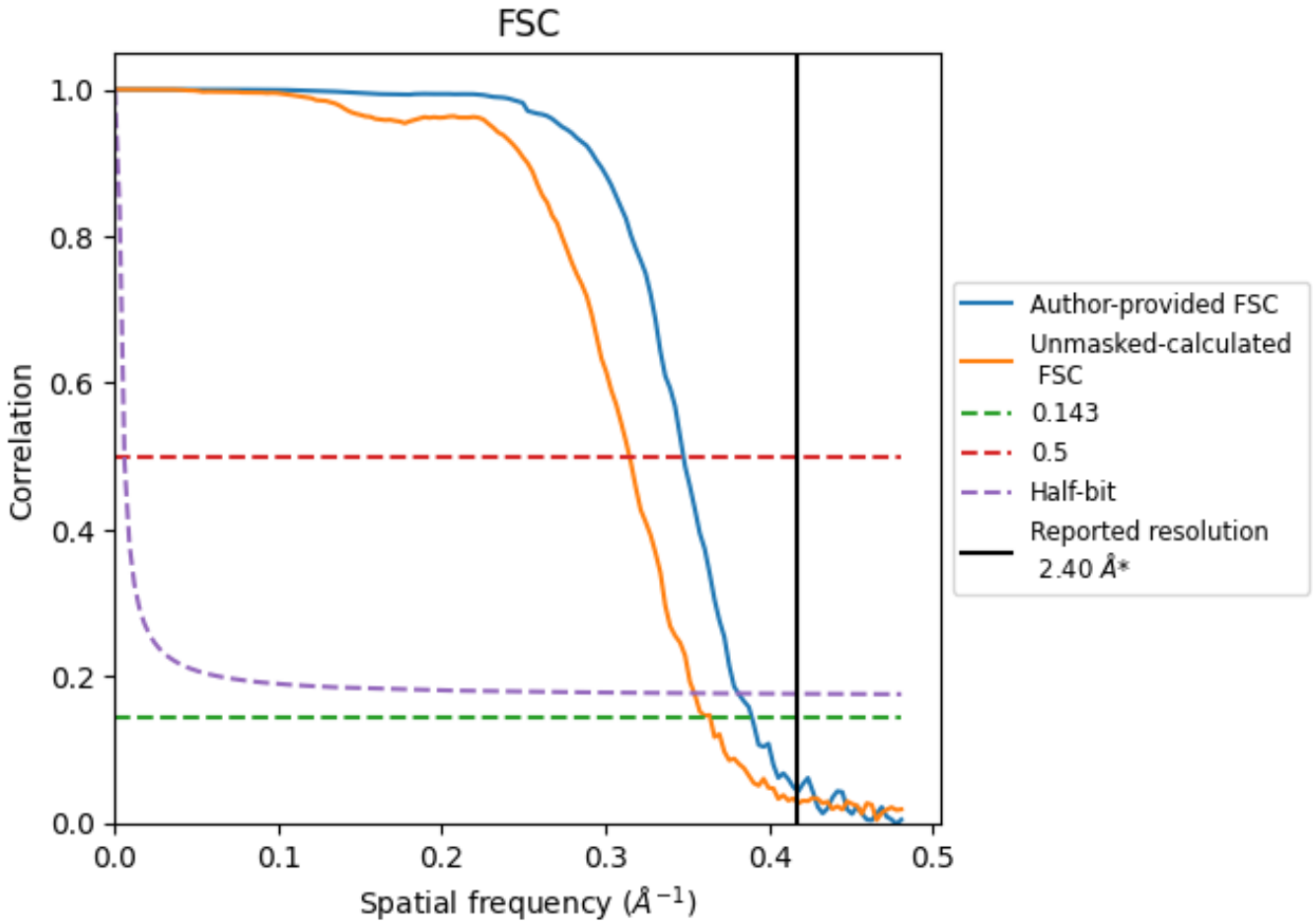


*Reported resolution corresponds to spatial frequency of 0.417 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.417 Å^{-1}

8.2 Resolution estimates (i)

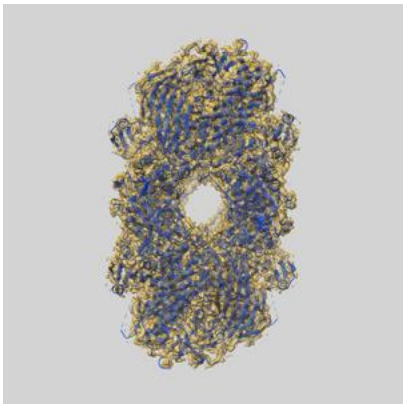
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.57	2.88	2.62
Unmasked-calculated*	2.75	3.18	2.82

*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 2.75 differs from the reported value 2.4 by more than 10 %

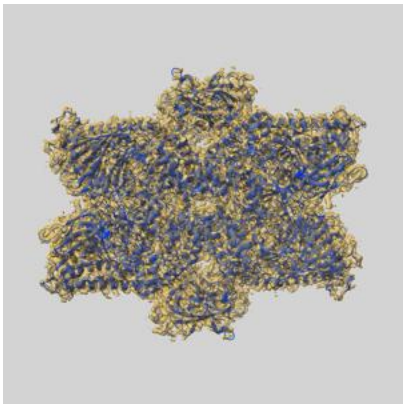
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-30650 and PDB model 7DD9. Per-residue inclusion information can be found in section 3 on page 6.

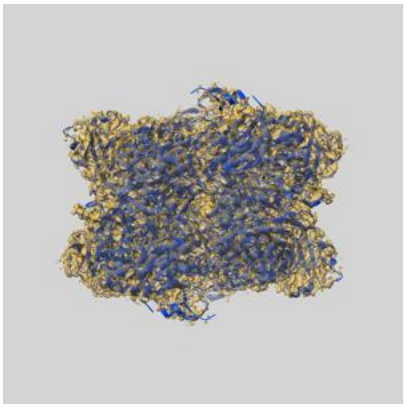
9.1 Map-model overlay



X



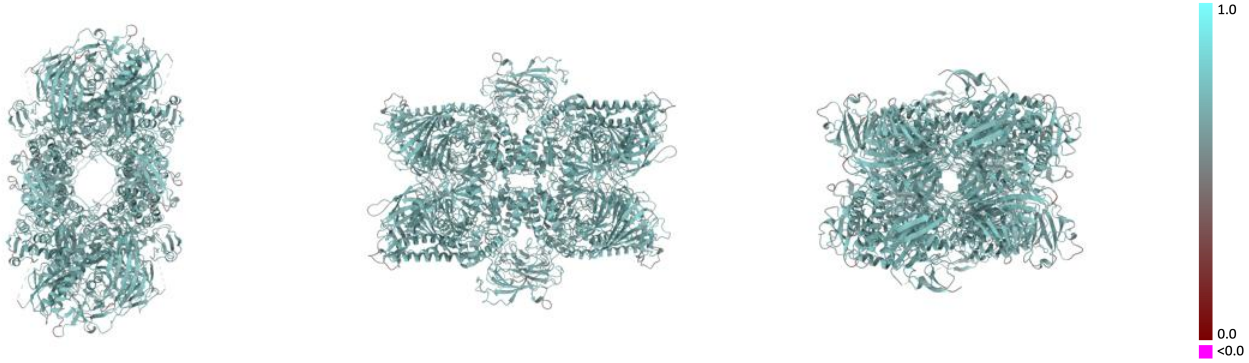
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025 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.

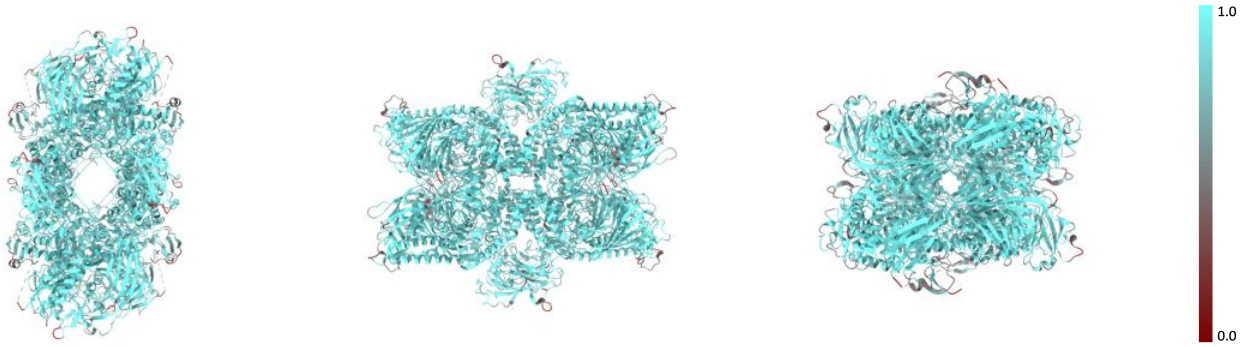
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

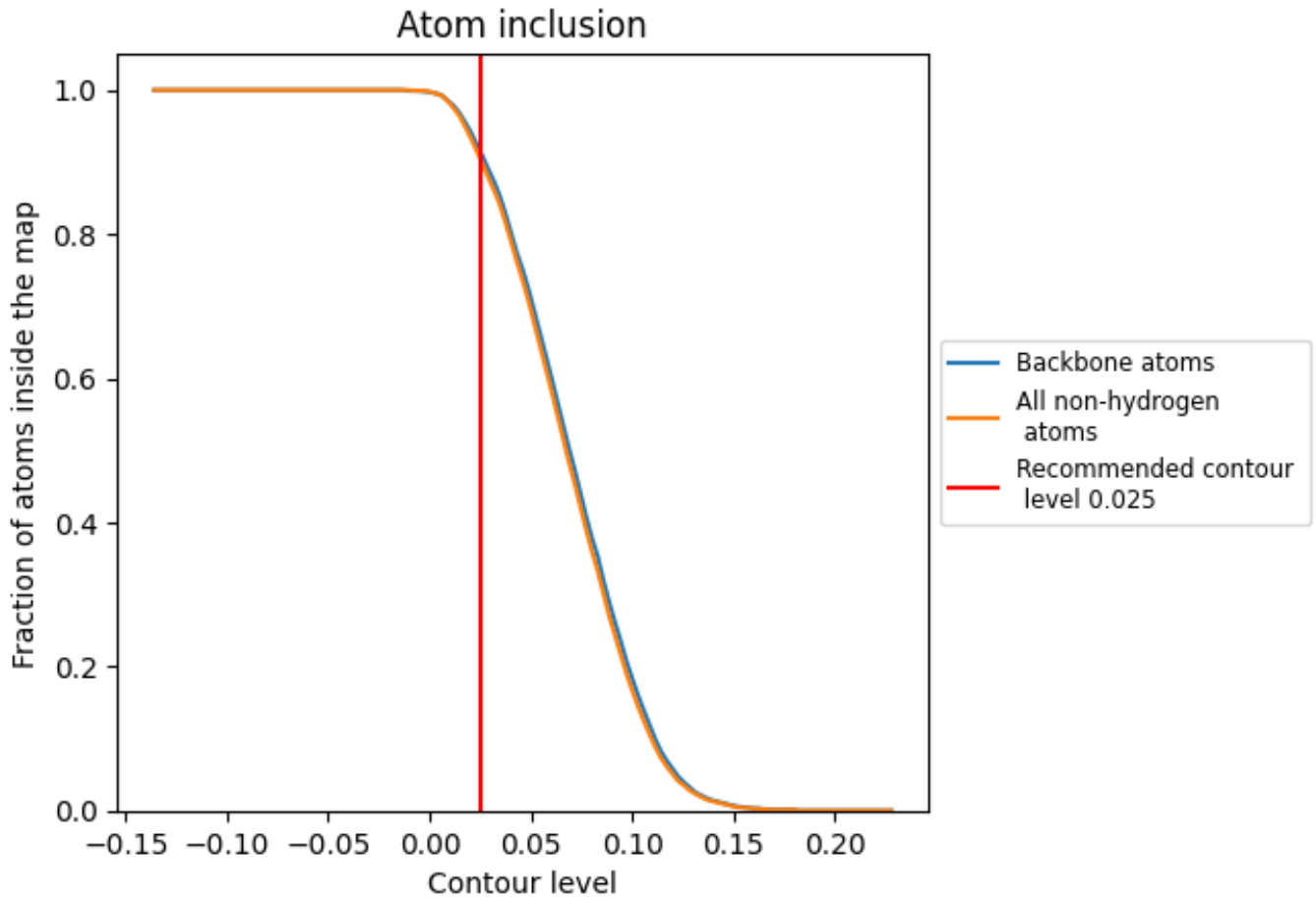
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.025).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9050	0.6680
A	0.9060	0.6690
C	0.9060	0.6680
E	0.9060	0.6680
G	0.9060	0.6680