wwPDB EM Validation Summary Report (i)

Oct 12, 2026 – 04:19 am BST

PDB ID	:	9T25 / pdb_00009t25
EMDB ID	:	EMD-55460
Title	:	yeast core m6A Methyltransferase Complex (ycMTC)
Authors	:	Lassandro, M.; Swuec, P.; Casanal, A.
Deposited on	:	2025-10-22
Resolution	:	2.62 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 (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:

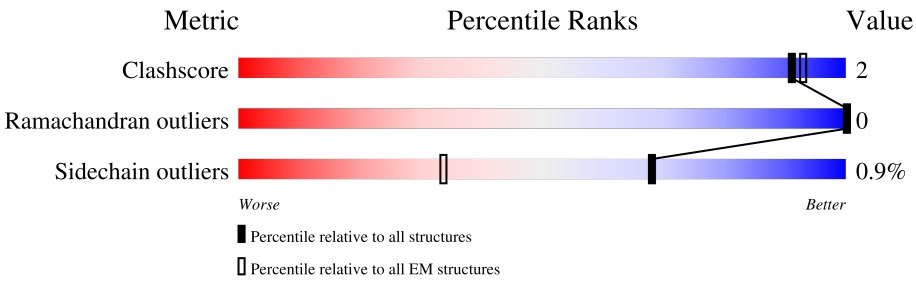
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

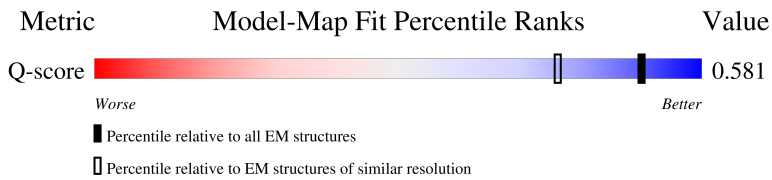
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.62 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	8810 (2.12 - 3.12)

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	E	366	9% 38% · 59%
1	F	366	20% 43% · 54%
1	G	366	11% 43% · 57%
1	H	366	17% 39% · 59%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	I	298	11% 15% 84%
3	A	600	17% 74% 23%
4	B	335	19% 73% 5% 22%
5	C	909	20% 60% 36%
5	D	909	29% 57% 39%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 20638 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 Protein MUM2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	F	168	1367	854	236	272	5	0	0
1	E	150	1207	754	207	242	4	0	0
1	G	158	1285	805	221	255	4	0	0
1	H	149	1203	752	206	241	4	0	0

- Molecule 2 is a protein called Sporulation-specific with a leucine zipper motif protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	I	47	376	234	64	76	2	0	0

- Molecule 3 is a protein called N(6)-adenosine-methyltransferase IME4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	A	462	3788	2428	653	694	13	0	0

- Molecule 4 is a protein called Karyogamy protein KAR4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	B	261	2128	1368	363	388	9	0	0

- Molecule 5 is a protein called Protein virilizer.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	582	4754	3103	761	879	11	0	0

Continued on next page...

Continued from previous page...

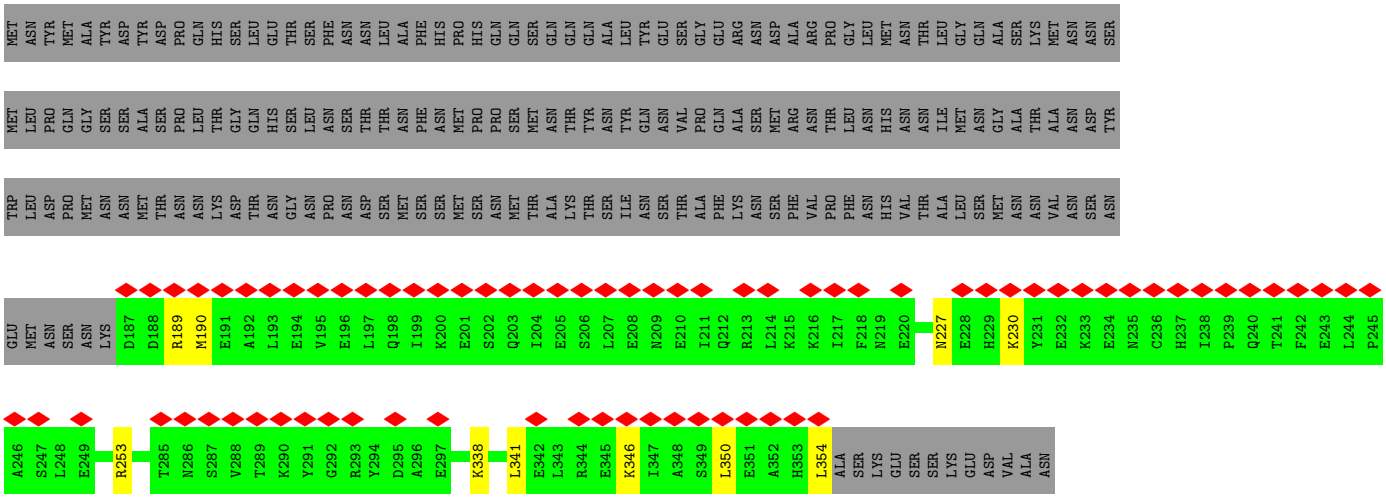
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	553	4530	2977	718	824	11	0	0

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.

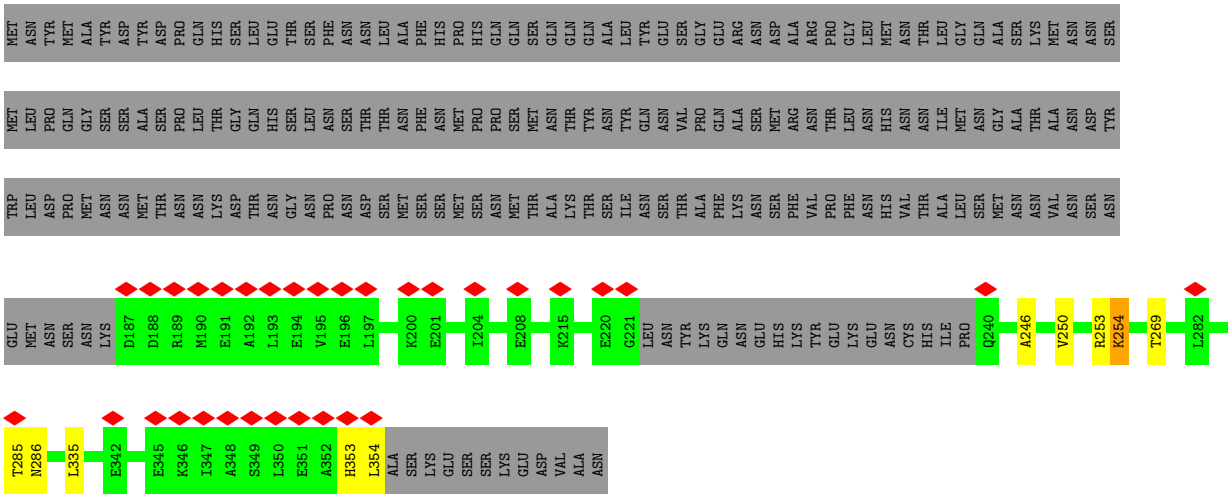
- Molecule 1: Protein MUM2

Chain F:



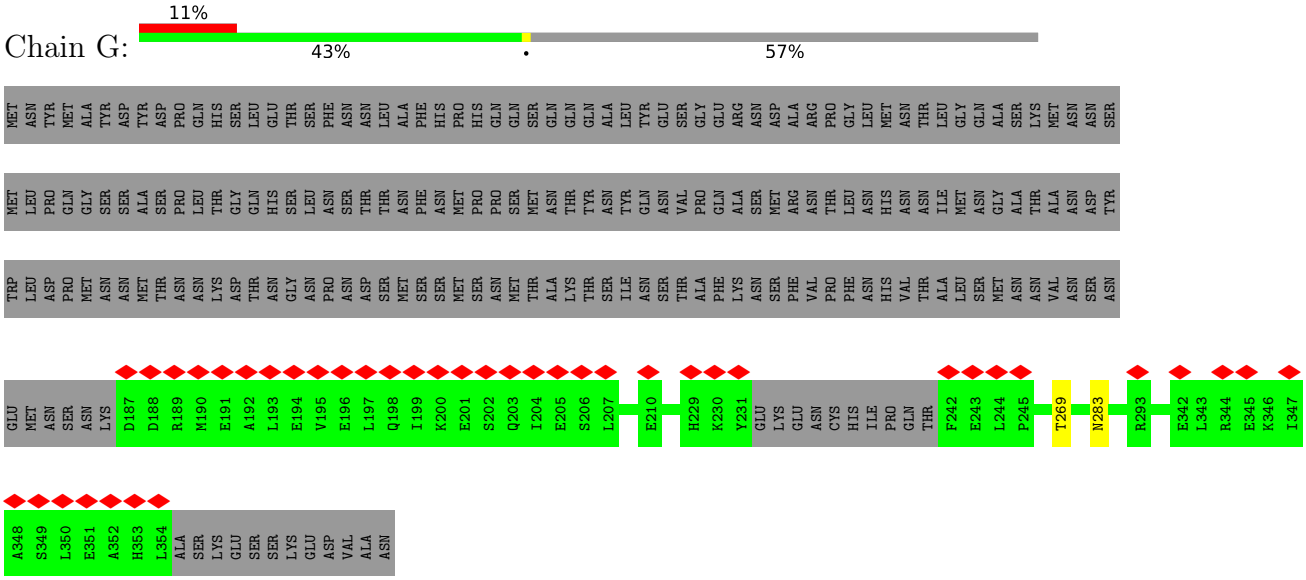
- Molecule 1: Protein MUM2

Chain E:



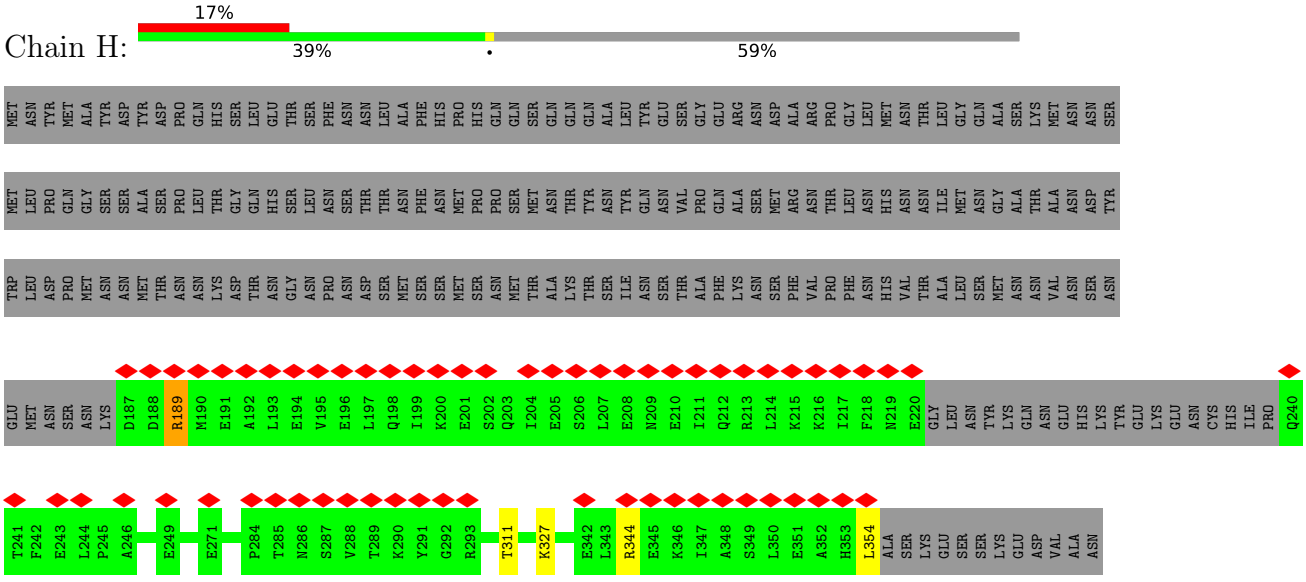
- Molecule 1: Protein MUM2

Chain G:



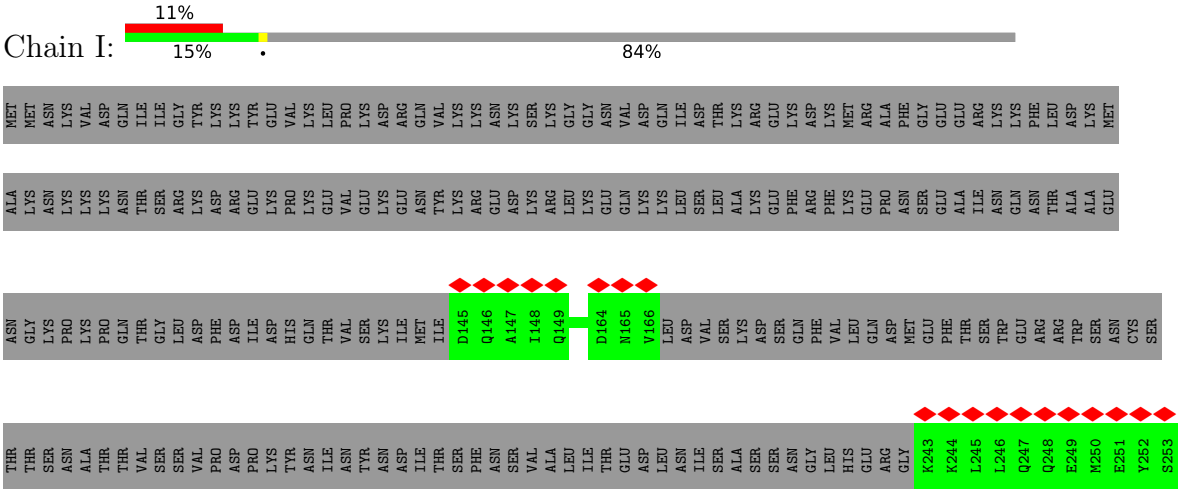
• Molecule 1: Protein MUM2

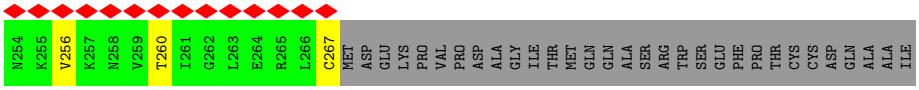
Chain H:



• Molecule 2: Sporulation-specific with a leucine zipper motif protein 1

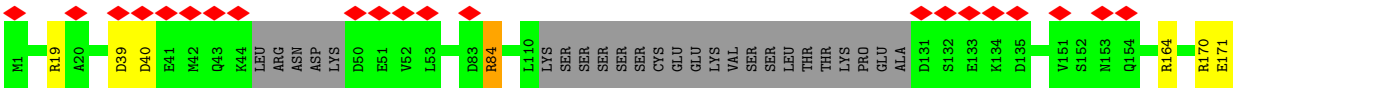
Chain I:

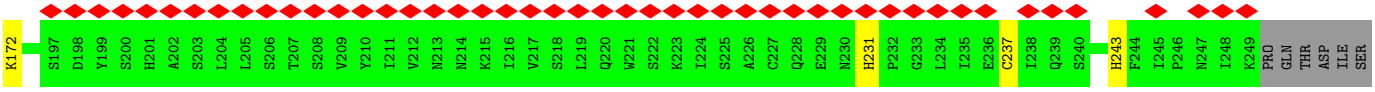


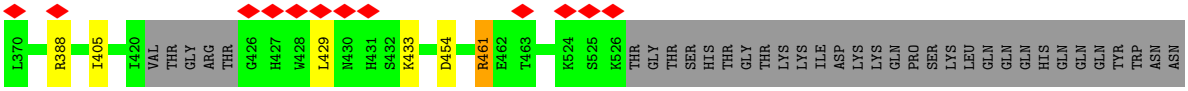


- Molecule 3: N(6)-adenosine-methyltransferase IME4

Chain A:

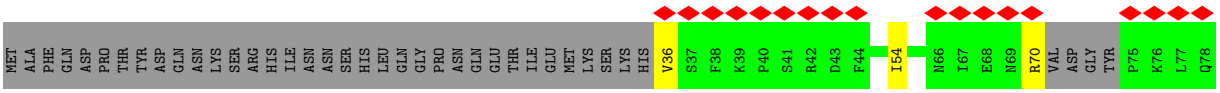


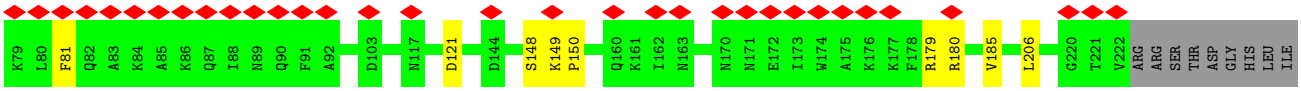


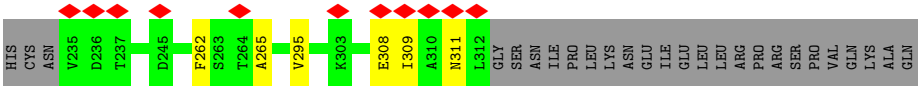


- Molecule 4: Karyogamy protein KAR4

Chain B:

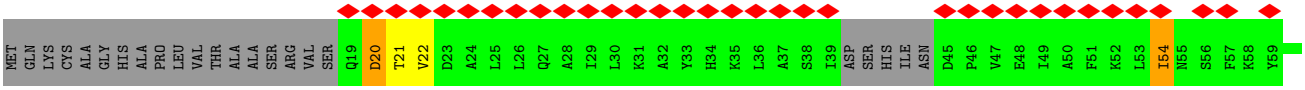


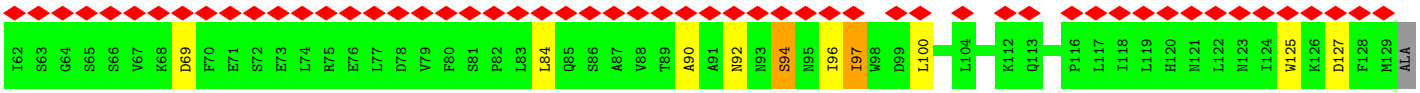


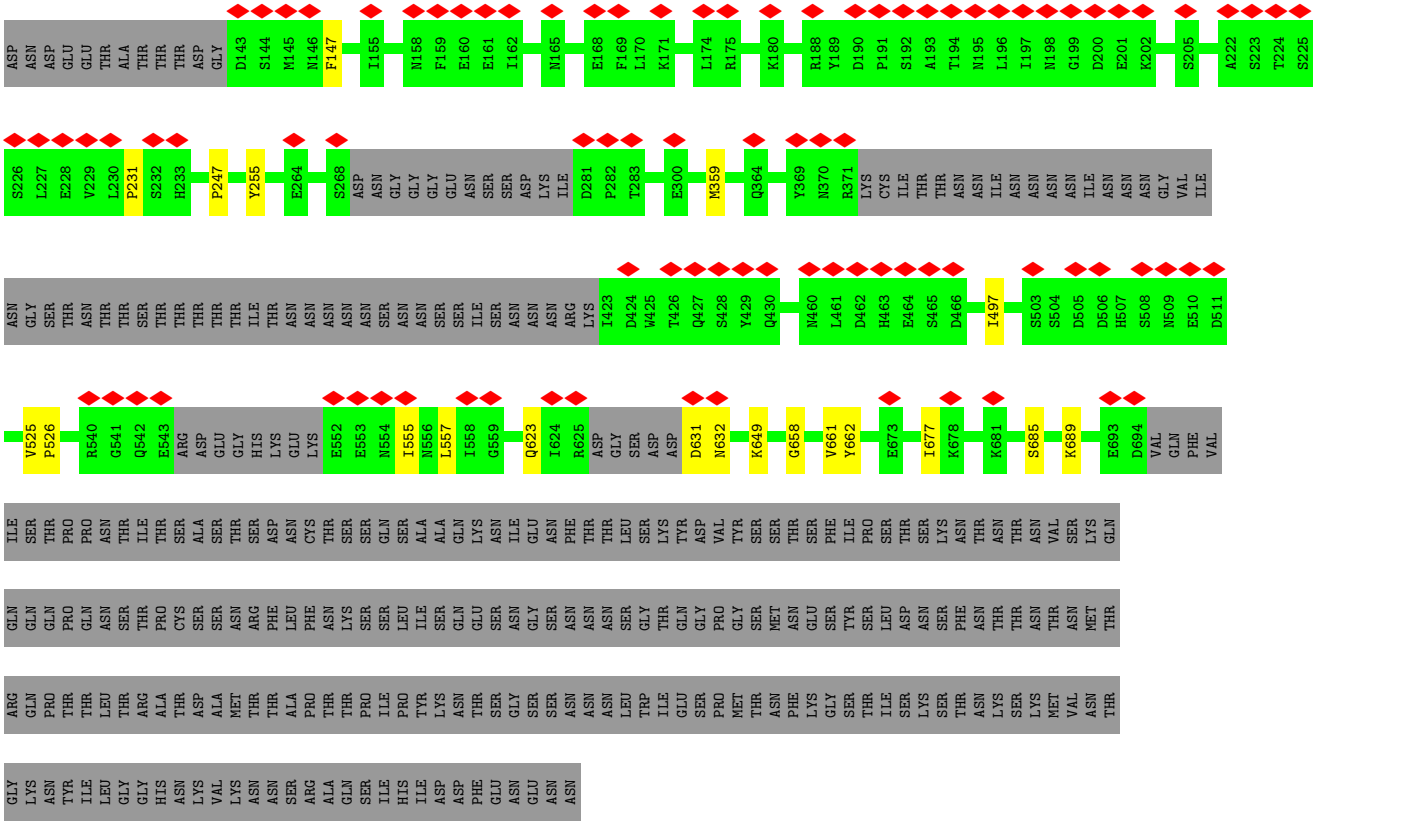


- Molecule 5: Protein virilizer

Chain C:

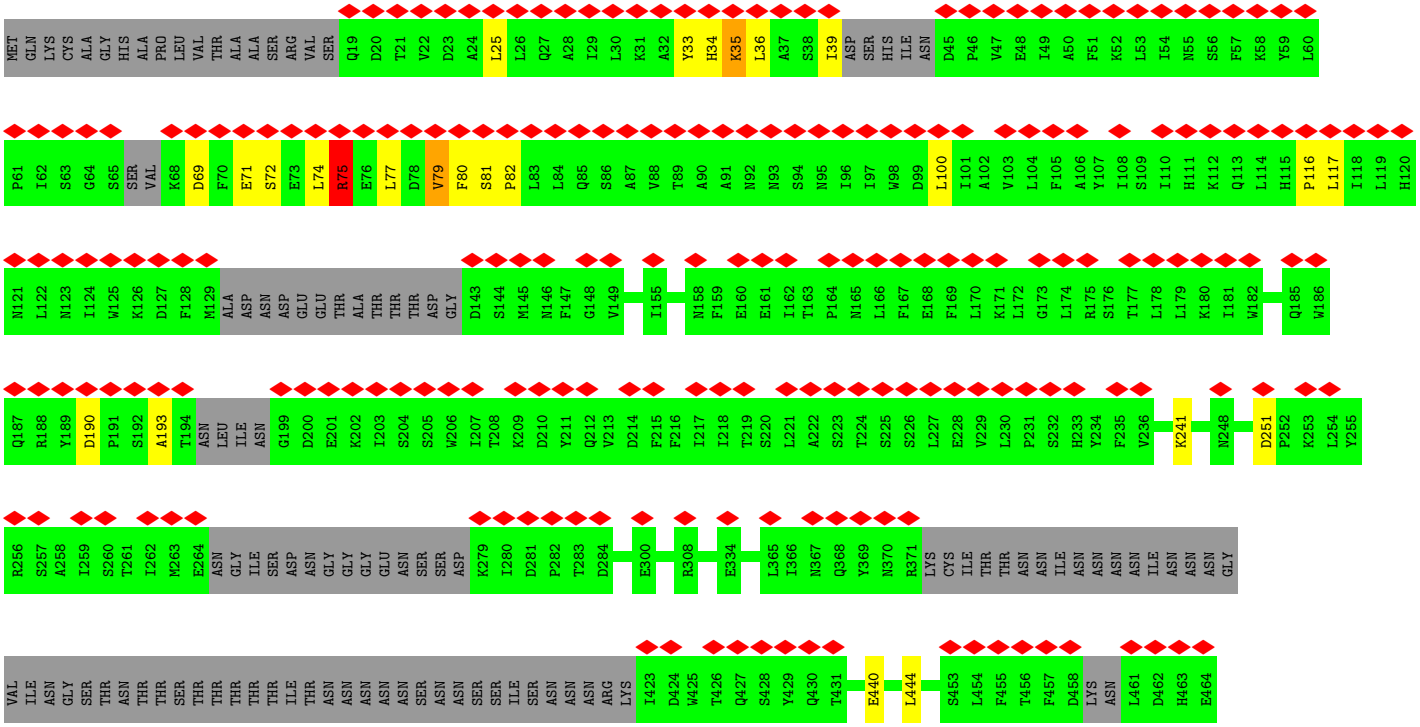


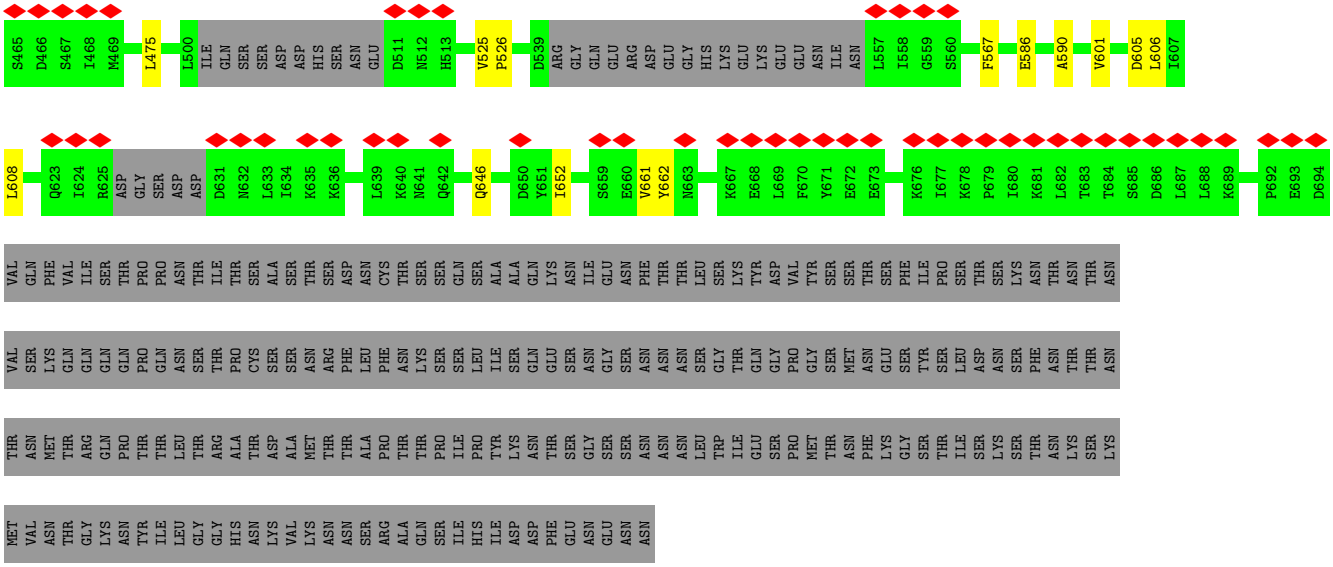




- Molecule 5: Protein virilizer

Chain D:




S465 D466 S467 I468 M469 L475 L500 ILE GLN SER SER ASP ASP HIS SER ASN GLU D511 N512 H513 V525 P526 D539 ARG GLY GLN GLU ARG ASP GLU GLY HIS LYS GLU LYS GLU GLU ASN ILE ASN L557 I558 G559 S560 F567 E586 A590 V601 D605 L606 I607
L608 Q623 I624 R625 ASP GLY SER ASP ASP D631 N632 L633 I634 K635 K636 L639 K640 N641 Q642 Q646 D650 Y651 I652 S659 E660 V661 Y662 N663 K667 E668 L669 F670 Y671 E672 E673 K676 I677 K678 P679 I680 K681 L682 T683 T684 S685 D686 L687 L688 K689 P692 E693 D694
VAL GLN PHE VAL ILE SER THR PRO PRO ASN THR ILE THR SER ALA SER THR SER ASP ASN CYS THR SER SER GLN SER ALA ALA GLN LYS ASN ILE GLU ASN PHE THR THR LEU SER LYS TYR ASP VAL TYR SER SER THR SER PHE ILE PRO SER THR SER LYS ASN THR THR ASN
VAL SER LYS GLN GLN GLN GLN PRO GLN ASN SER THR PRO CYS SER SER ASN ARG PHE LEU PHE ASN LYS SER SER LEU ILE SER GLN GLU SER ASN GLY SER ASN ASN ASN SER GLY THR GLN GLY PRO GLY SER MET ASN GLU SER TYR SER LEU ASP ASN SER PHE ASN THR THR ASN
THR ASN MET THR ARG GLN PRO THR THR LEU THR ARG ALA THR ASP ALA MET THR THR ALA PRO THR THR PRO ILE PRO TYR LYS ASN THR SER GLY SER SER ASN ASN ASN LEU TRP ILE GLU GLU SER PRO MET THR ASN PHE LYS GLY SER THR ILE SER LYS SER THR ASN LYS SER LYS
MET VAL ASN THR GLY LYS ASN TYR ILE LEU GLY GLY HIS ASN LYS VAL LYS ASN ASN SER ARG ALA GLN SER ILE HIS ILE ASP ASP PHE GLU ASN GLU ASN ASN

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	236407	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.077	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	286.5, 286.5, 286.5	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.955, 0.955, 0.955	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	E	0.58	0/1216	1.01	1/1627 (0.1%)
1	F	0.53	0/1382	1.01	0/1852
1	G	0.55	0/1297	1.02	0/1735
1	H	0.53	0/1212	0.99	0/1622
2	I	0.50	0/377	1.00	0/506
3	A	0.58	0/3872	1.00	5/5237 (0.1%)
4	B	0.61	0/2182	1.01	0/2962
5	C	0.57	0/4855	0.99	5/6585 (0.1%)
5	D	0.55	0/4626	0.94	2/6269 (0.0%)
All	All	0.57	0/21019	0.99	13/28395 (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
1	E	0	1
1	F	0	2
1	H	0	2
3	A	0	8
4	B	0	2
5	D	0	1
All	All	0	16

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	231	PRO	N-CA-C	7.55	123.30	113.86
5	D	251	ASP	CA-CB-CG	6.36	118.96	112.60
3	A	454	ASP	CA-CB-CG	6.06	118.66	112.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	94	SER	N-CA-C	-5.96	104.86	111.71
3	A	231	HIS	CA-CB-CG	5.86	119.66	113.80

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	164	ARG	Sidechain
3	A	19	ARG	Peptide
3	A	84	ARG	Sidechain
1	F	189	ARG	Sidechain
1	F	253	ARG	Sidechain

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	E	1207	0	1237	8	0
1	F	1367	0	1387	6	0
1	G	1285	0	1310	4	0
1	H	1203	0	1234	3	0
2	I	376	0	383	3	0
3	A	3788	0	3763	7	0
4	B	2128	0	2123	9	0
5	C	4754	0	4826	18	0
5	D	4530	0	4628	24	0
All	All	20638	0	20891	68	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 2.

The worst 5 of 68 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)
5:C:94:SER:HA	5:C:97:ILE:HD12	1.77	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:71:GLU:CG	5:D:116:PRO:HG2	2.25	0.66
5:D:71:GLU:O	5:D:75:ARG:HG3	1.97	0.64
5:D:71:GLU:CD	5:D:116:PRO:HG2	2.28	0.58
1:F:338:LYS:HA	1:F:341:LEU:HD12	1.86	0.58

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	E	146/366 (40%)	143 (98%)	3 (2%)	0	100	100
1	F	166/366 (45%)	165 (99%)	1 (1%)	0	100	100
1	G	154/366 (42%)	153 (99%)	1 (1%)	0	100	100
1	H	145/366 (40%)	144 (99%)	1 (1%)	0	100	100
2	I	43/298 (14%)	41 (95%)	2 (5%)	0	100	100
3	A	450/600 (75%)	441 (98%)	9 (2%)	0	100	100
4	B	255/335 (76%)	243 (95%)	12 (5%)	0	100	100
5	C	568/909 (62%)	549 (97%)	19 (3%)	0	100	100
5	D	531/909 (58%)	514 (97%)	17 (3%)	0	100	100
All	All	2458/4515 (54%)	2393 (97%)	65 (3%)	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	E	134/329 (41%)	133 (99%)	1 (1%)	76	89
1	F	152/329 (46%)	151 (99%)	1 (1%)	76	89
1	G	142/329 (43%)	142 (100%)	0	100	100
1	H	134/329 (41%)	132 (98%)	2 (2%)	57	79
2	I	45/274 (16%)	45 (100%)	0	100	100
3	A	419/546 (77%)	419 (100%)	0	100	100
4	B	241/309 (78%)	237 (98%)	4 (2%)	53	76
5	C	550/846 (65%)	545 (99%)	5 (1%)	70	86
5	D	523/846 (62%)	516 (99%)	7 (1%)	61	81
All	All	2340/4137 (57%)	2320 (99%)	20 (1%)	68	86

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	D	241	LYS
1	E	254	LYS
1	H	327	LYS
1	H	311	THR
5	C	96	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
5	D	185	GLN
5	D	326	HIS
5	D	305	GLN
5	D	339	GLN
4	B	51	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.

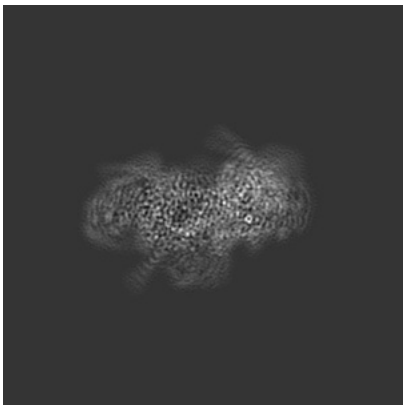
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-55460. These allow visual inspection of the internal detail of the map and identification of artifacts.

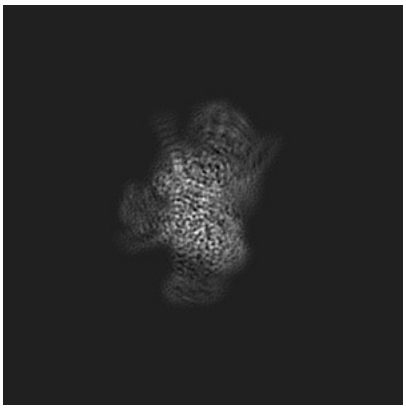
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

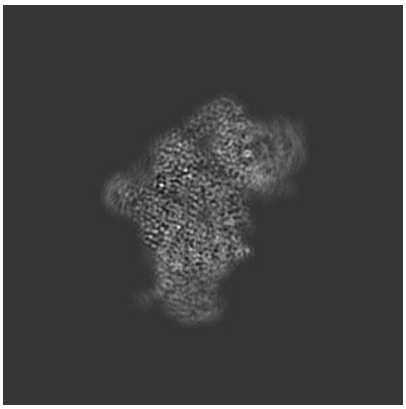
6.1.1 Primary map



X

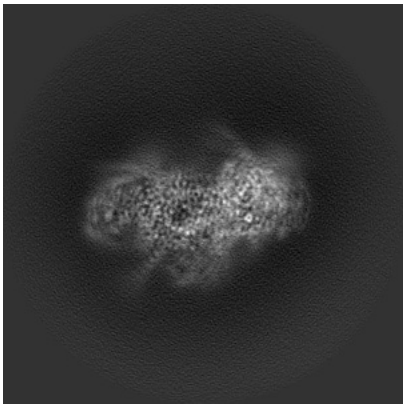


Y

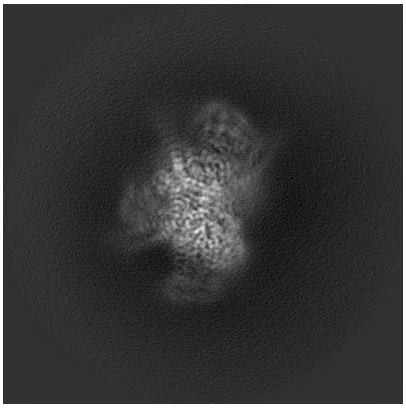


Z

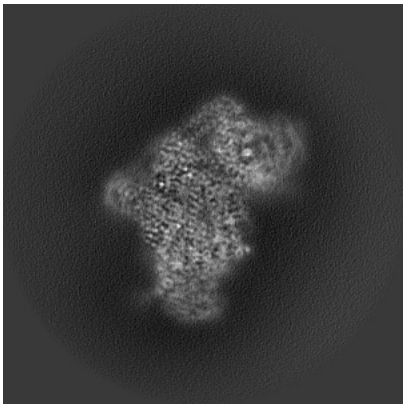
6.1.2 Raw map



X



Y

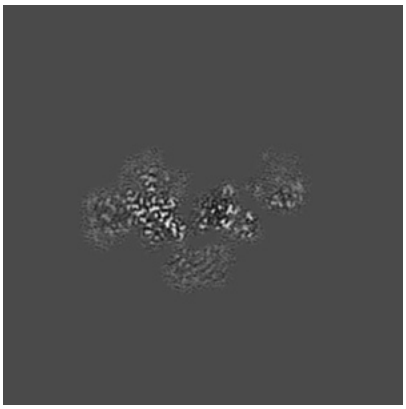


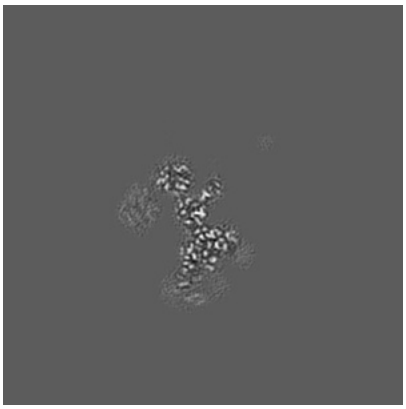
Z

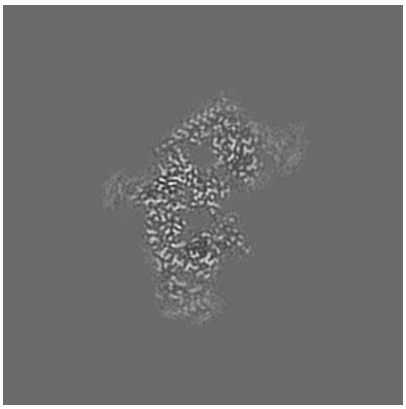
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

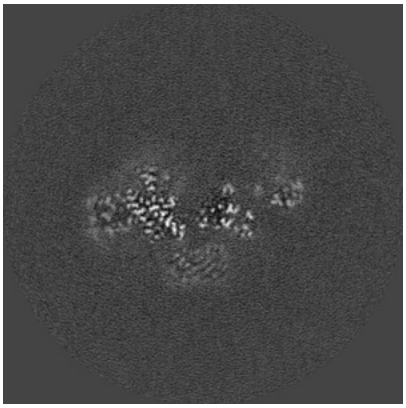
6.2.1 Primary map

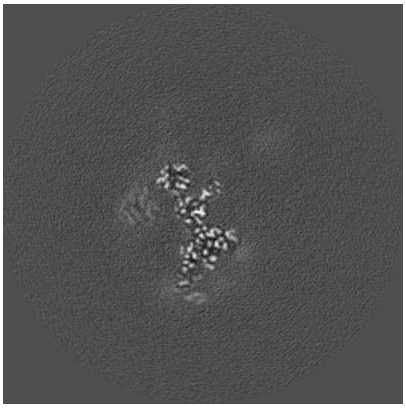

X Index: 150

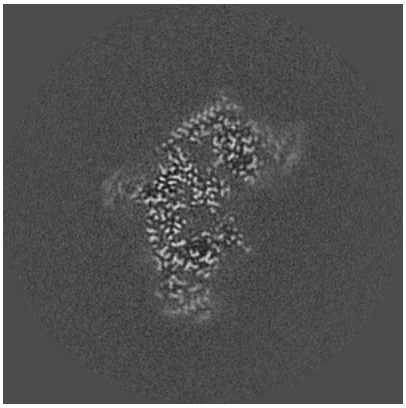

Y Index: 150


Z Index: 150

6.2.2 Raw map


X Index: 150

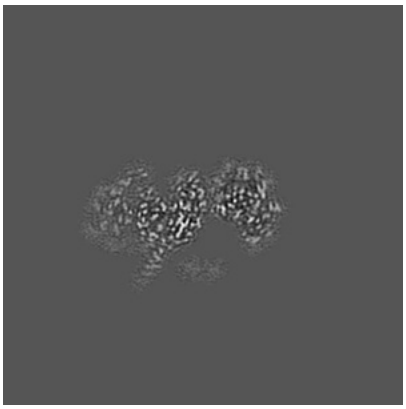

Y Index: 150


Z Index: 150

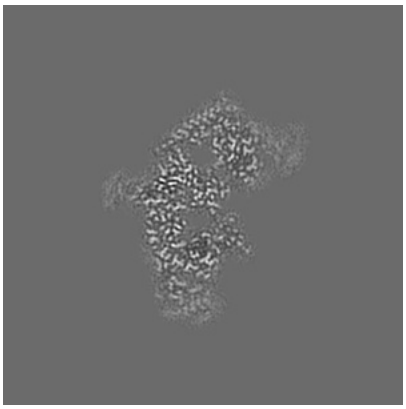
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

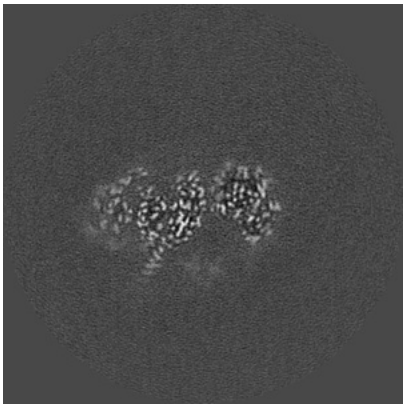
6.3.1 Primary map

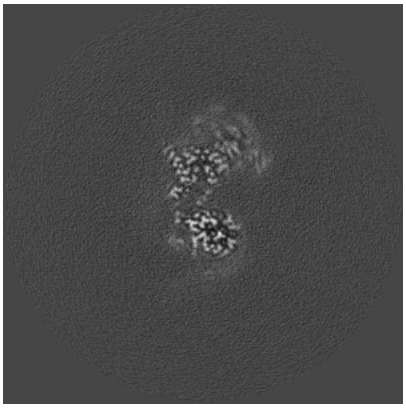

X Index: 131

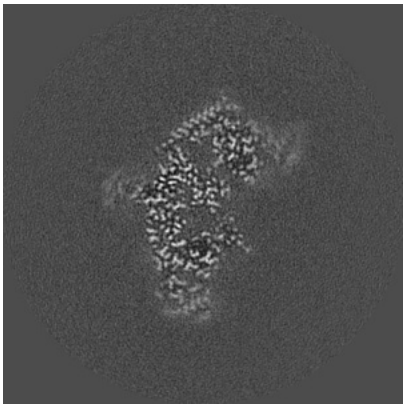
Y Index: 183


Z Index: 150

6.3.2 Raw map


X Index: 131

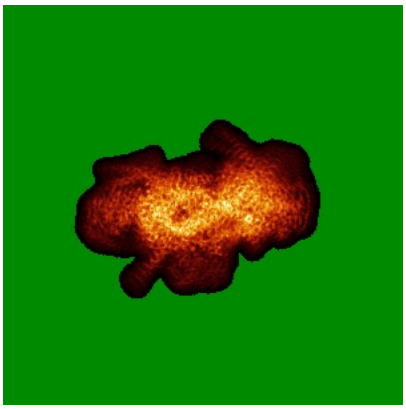

Y Index: 176

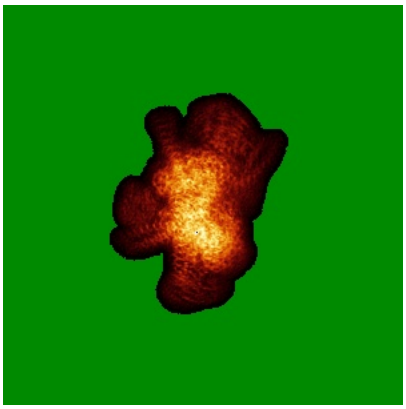

Z Index: 150

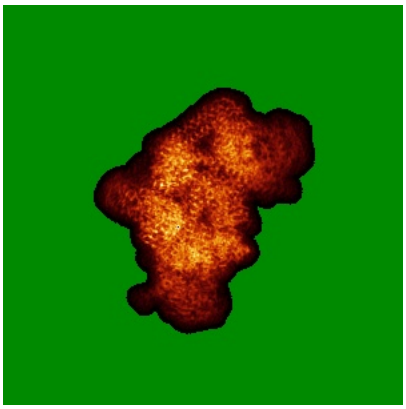
The images above show the largest variance slices of the map in three orthogonal directions.

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

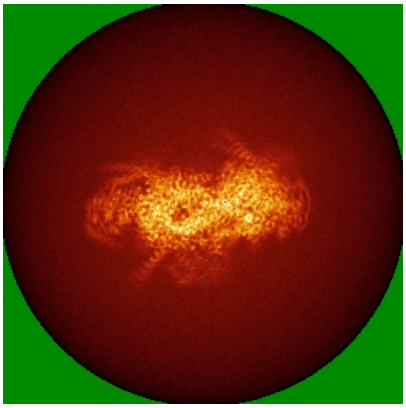
6.4.1 Primary map

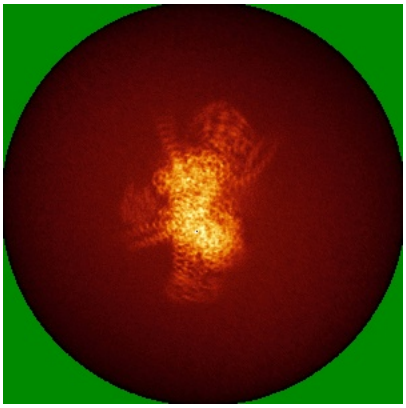

X

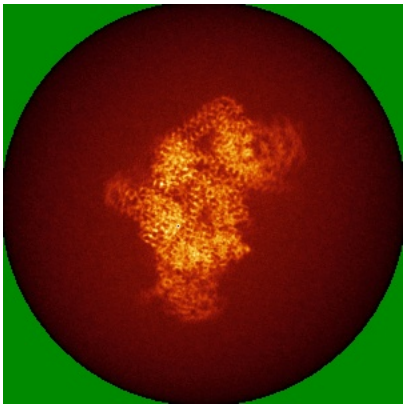

Y


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 0.015. 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.

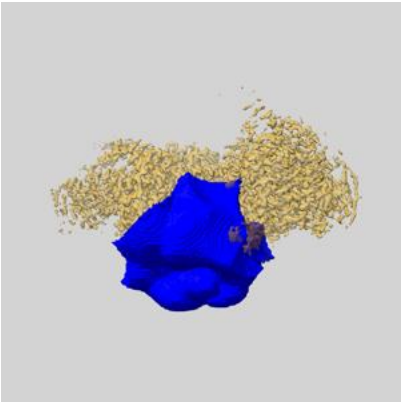
6.6 Mask visualisation (i)

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

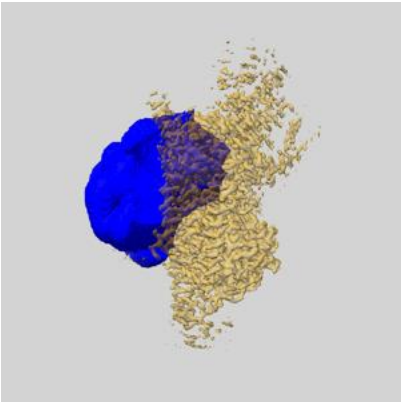
A mask typically either:

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

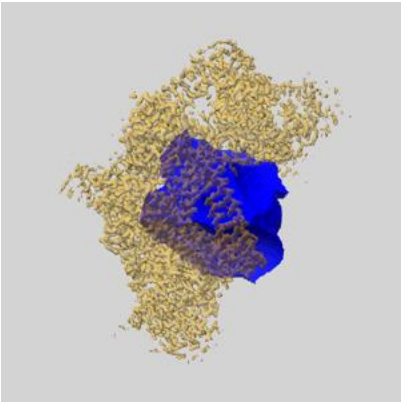
6.6.1 emd_55460_msk_1.map (i)



X

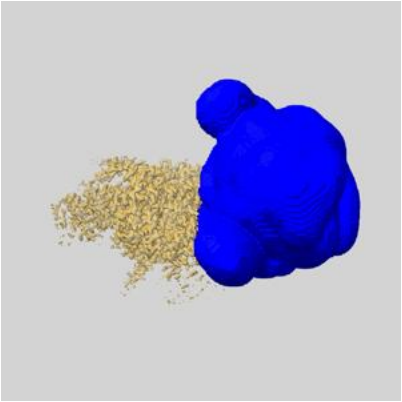


Y

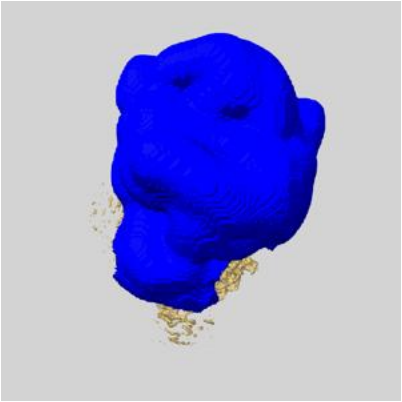


Z

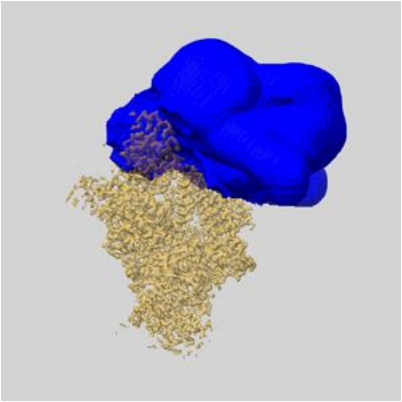
6.6.2 emd_55460_msk_2.map (i)



X

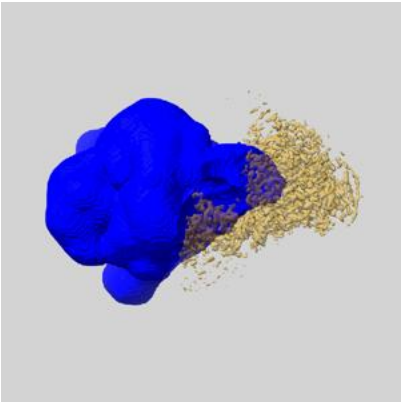


Y

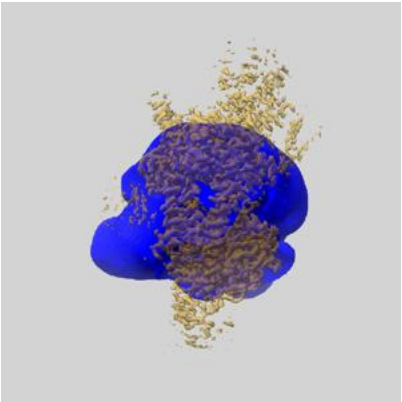


Z

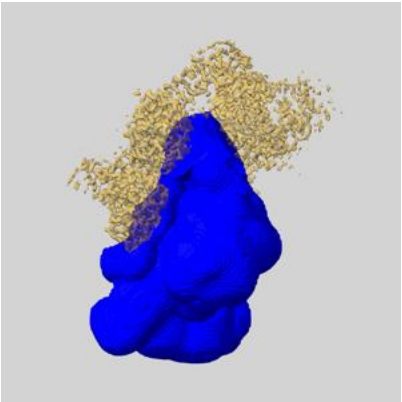
6.6.3 emd_55460_msk_3.map



X

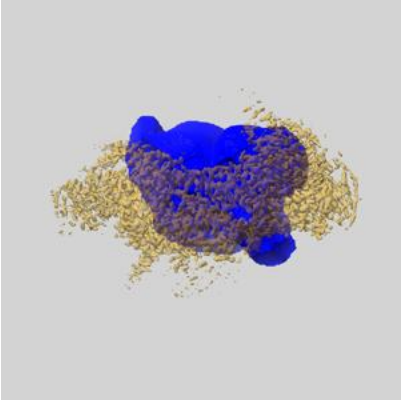


Y

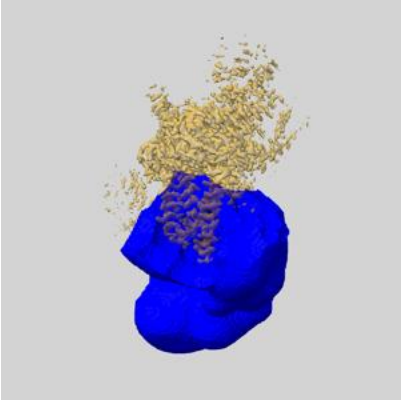


Z

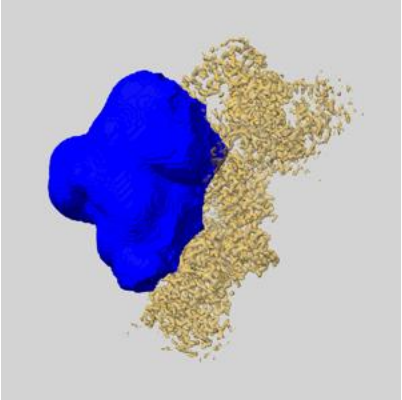
6.6.4 emd_55460_msk_4.map



X

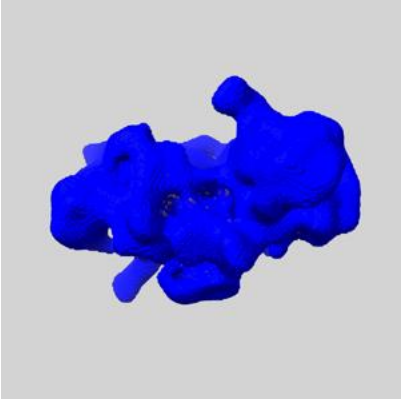


Y

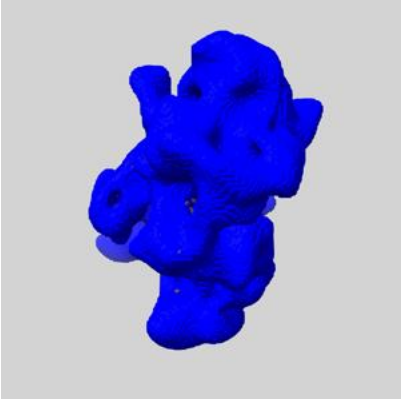


Z

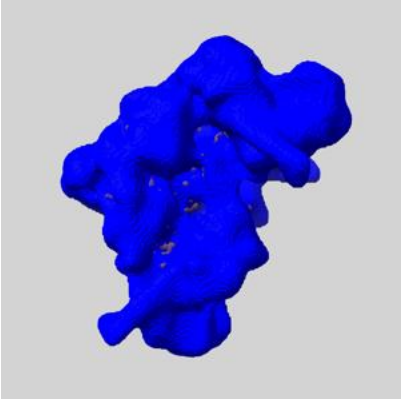
6.6.5 emd_55460_msk_5.map



X



Y

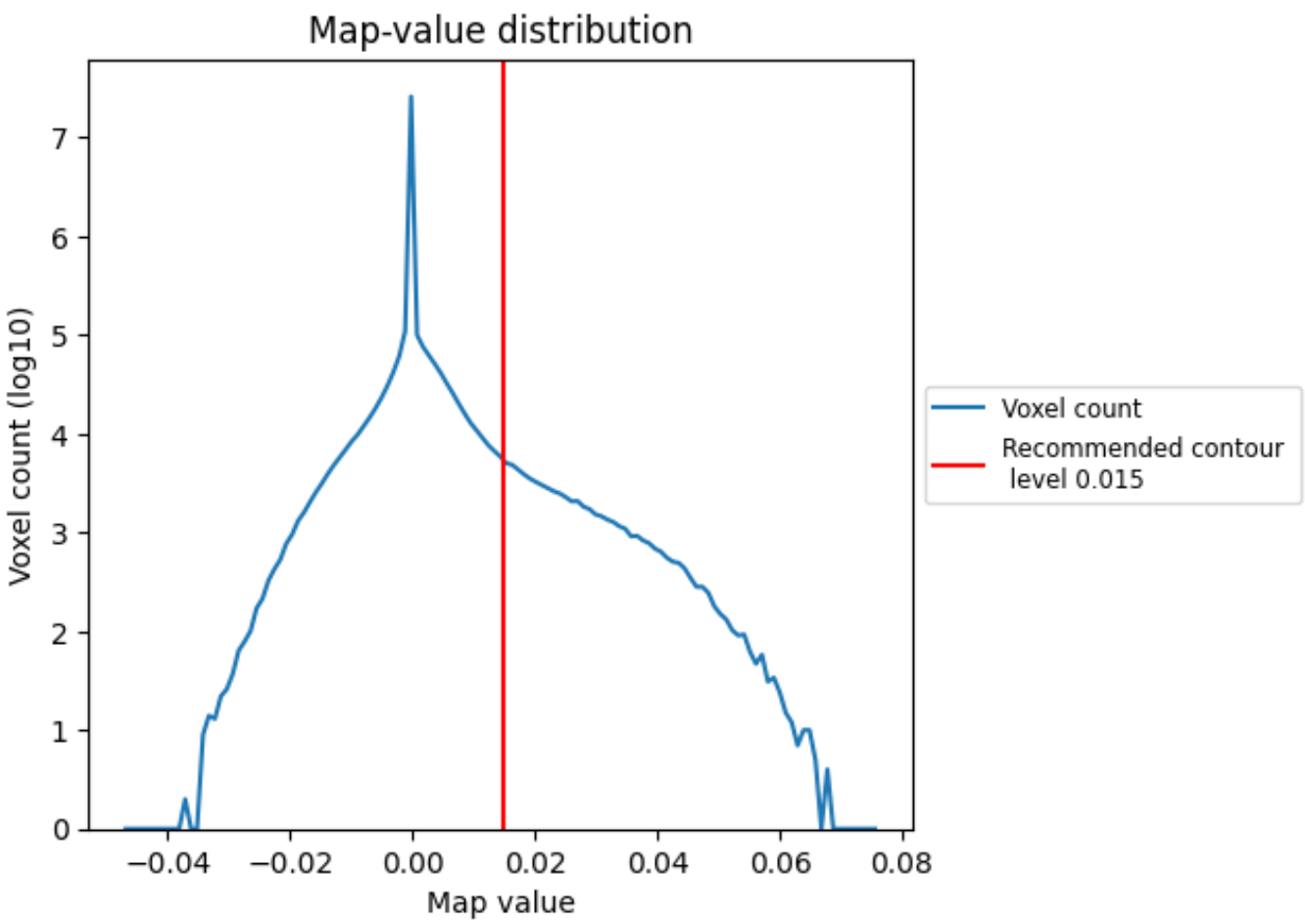


Z

7 Map analysis (i)

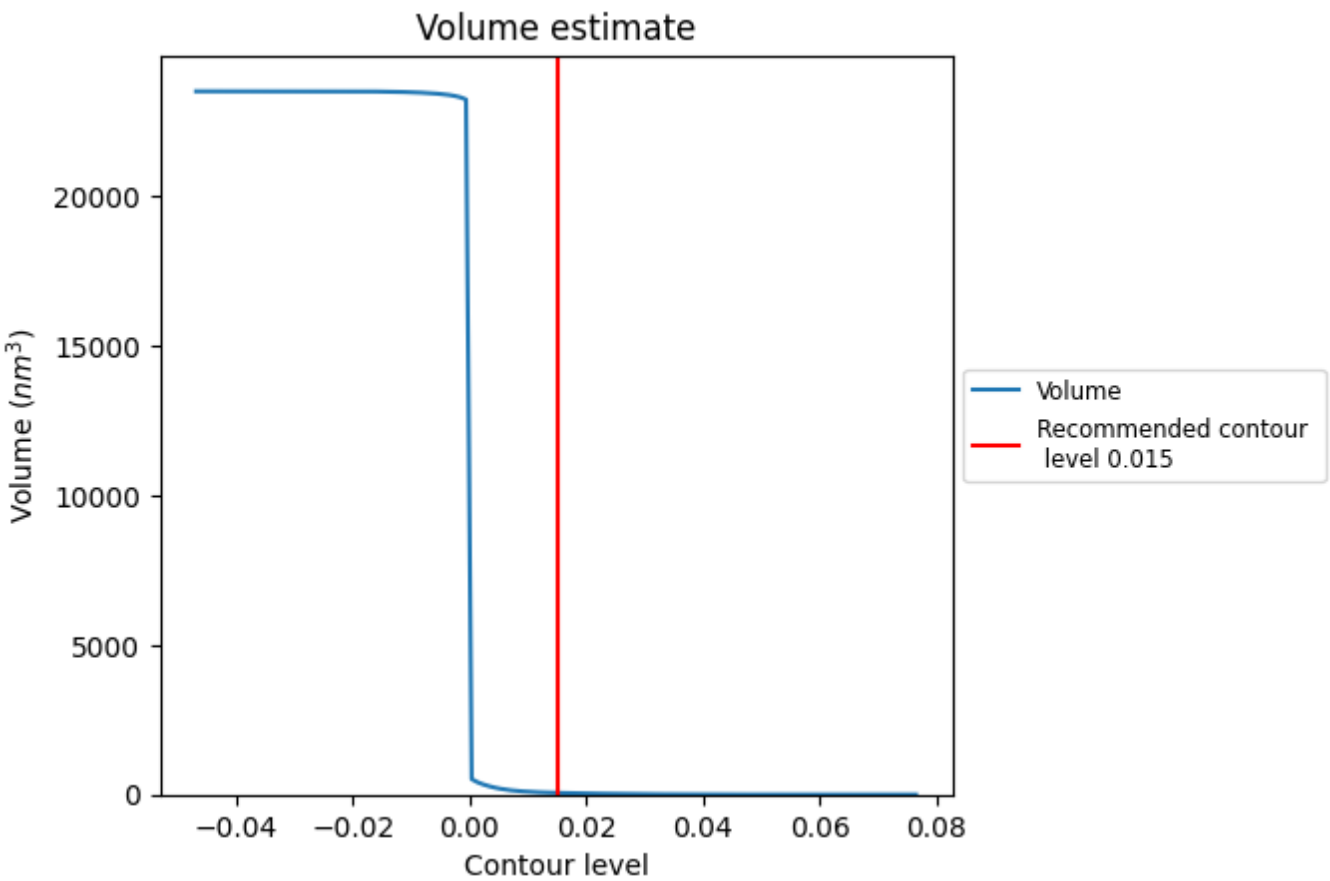
This section contains the results of statistical analysis of the map.

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.

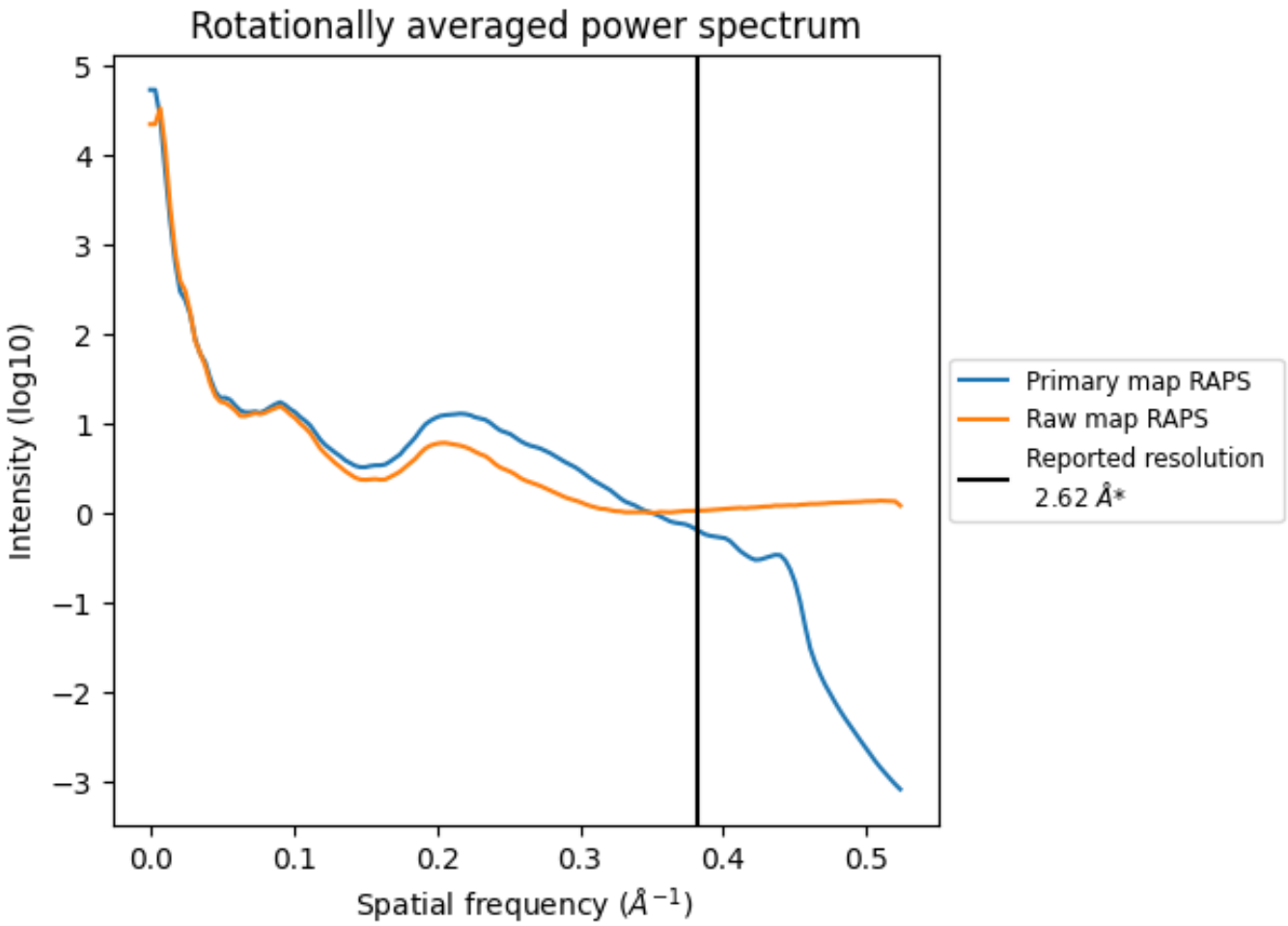
7.2 Volume estimate (i)



The volume at the recommended contour level is 56 nm^3; this corresponds to an approximate mass of 51 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)

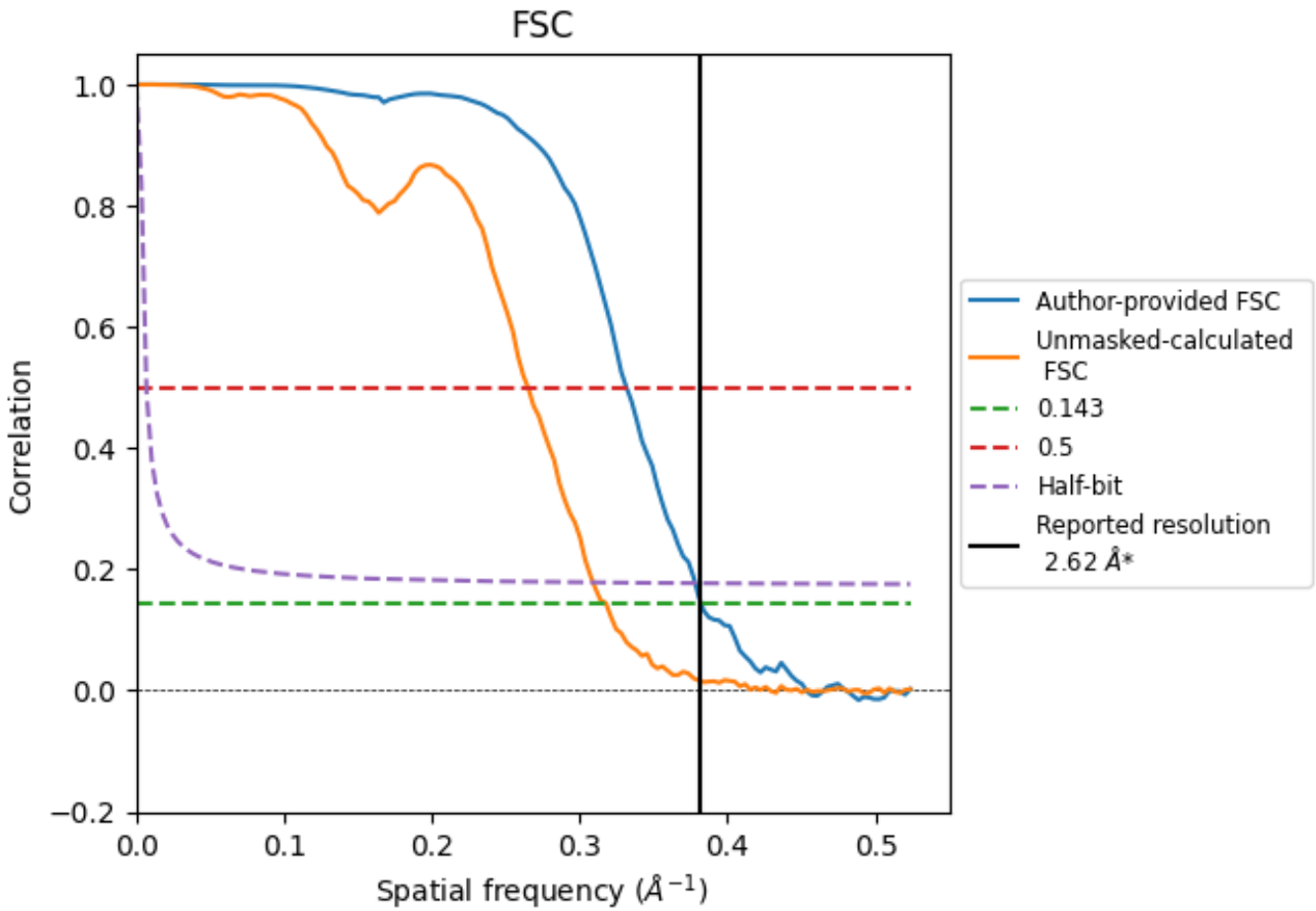


*Reported resolution corresponds to spatial frequency of 0.382 Å^{-1}

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 0.382 Å^{-1}

8.2 Resolution estimates (i)

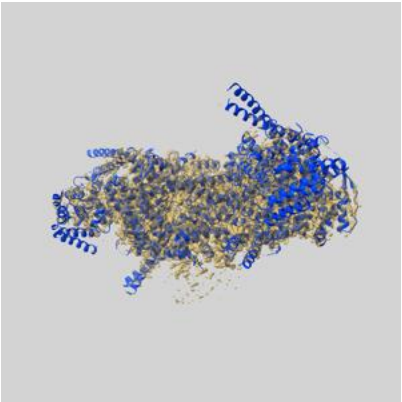
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.62	-	-
Author-provided FSC curve	2.62	3.02	2.64
Unmasked-calculated*	3.15	3.77	3.24

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.15 differs from the reported value 2.62 by more than 10 %

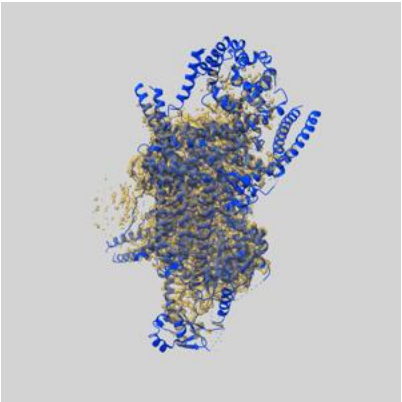
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-55460 and PDB model 9T25. Per-residue inclusion information can be found in section 3 on page 6.

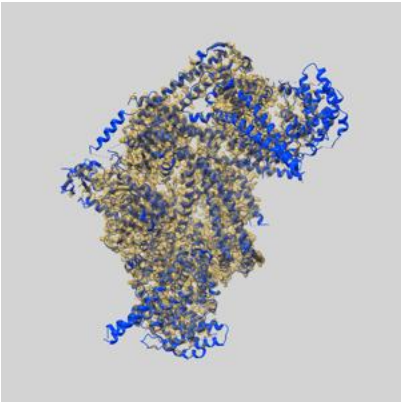
9.1 Map-model overlay (i)



X



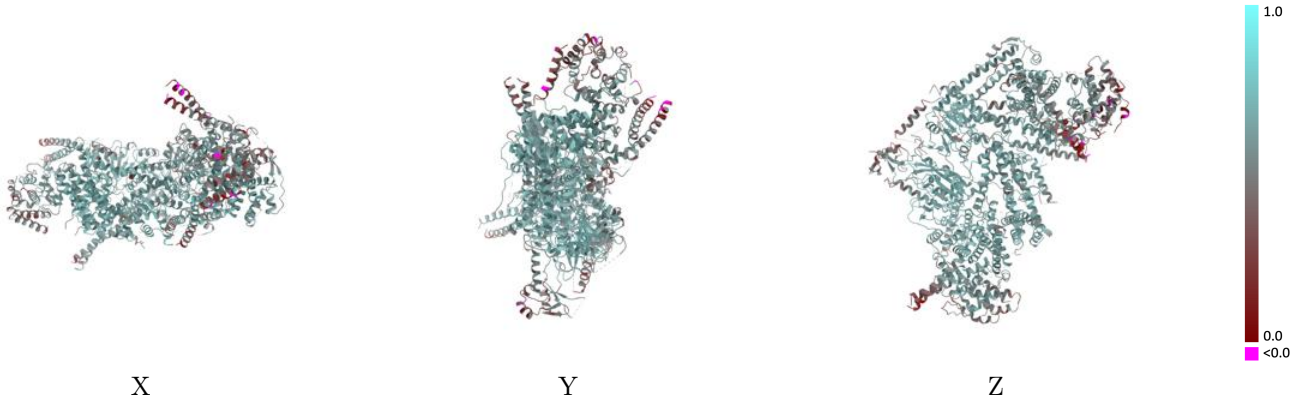
Y



Z

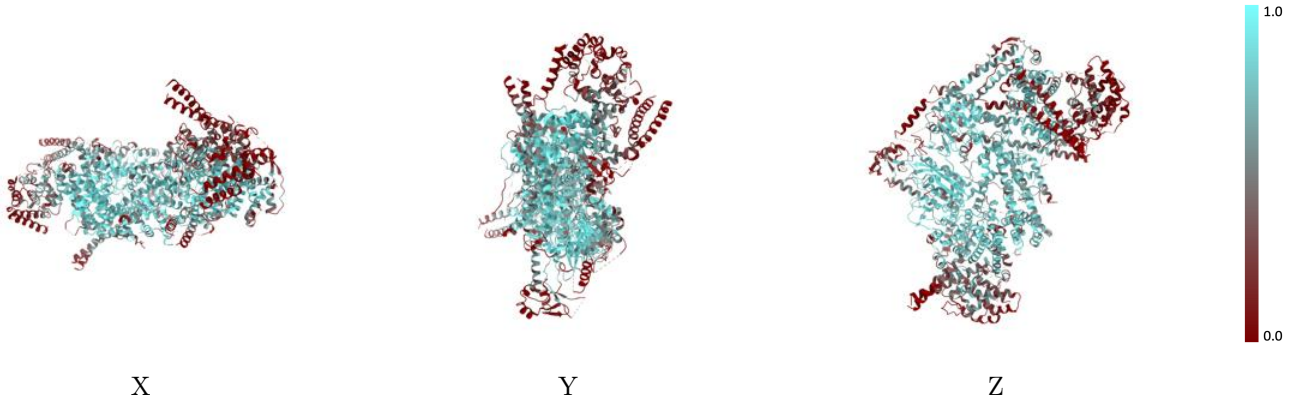
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



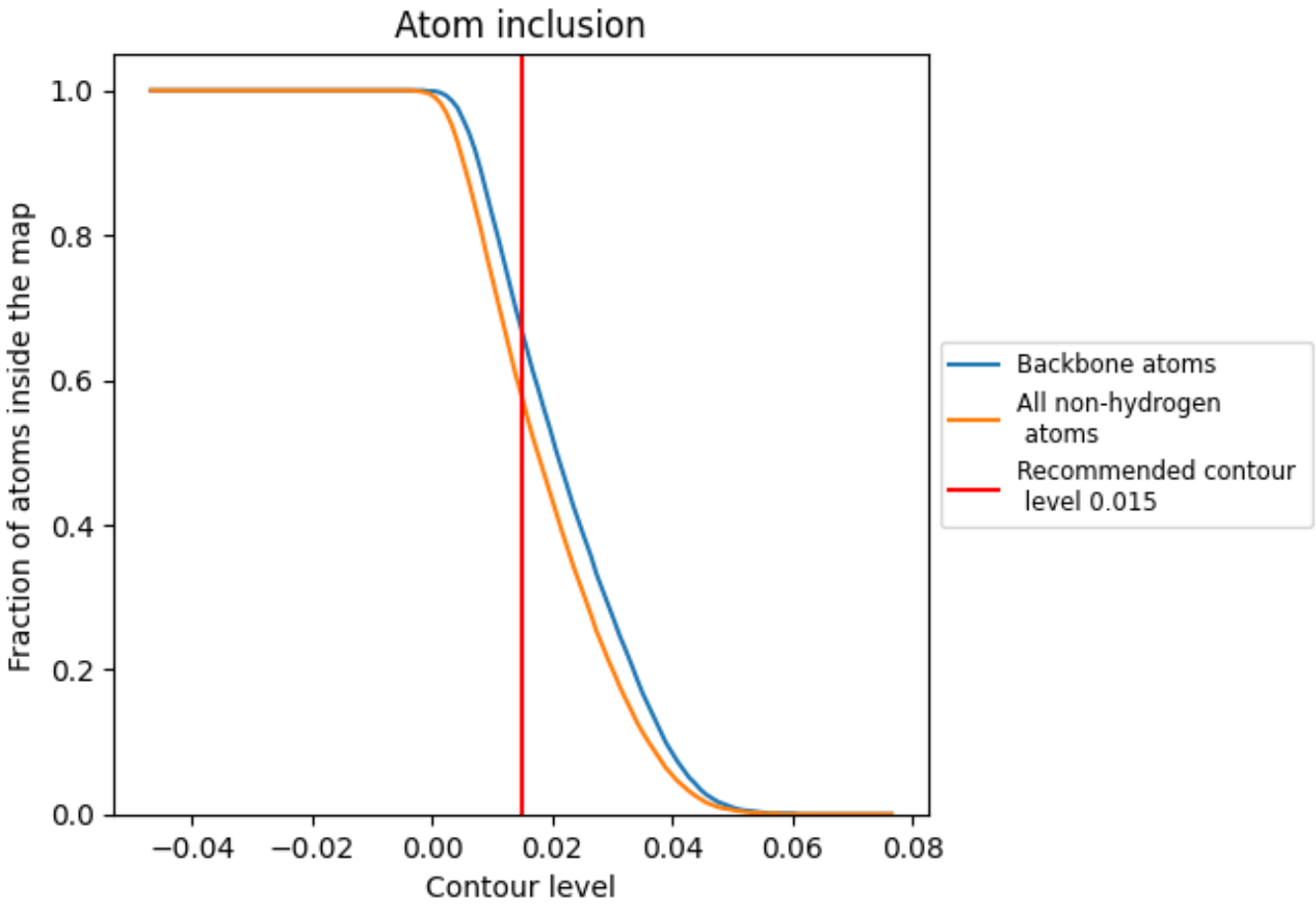
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion (i)



At the recommended contour level, 67% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5760	0.5810
A	0.6890	0.6120
B	0.6780	0.6090
C	0.6060	0.6010
D	0.4680	0.5540
E	0.6510	0.6130
F	0.4310	0.5240
G	0.6090	0.5790
H	0.4920	0.5430
I	0.2230	0.4110