



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 02:34 AM UTC

PDB ID : 9PAW / pdb_00009paw
EMDB ID : EMD-71448
Title : Cryo-EM structure of the engineered HflK/C variant stabilized in the closed conformation via disulfide bond crosslinking.
Authors : Iqbal, N.; Ghanbarpour, A.
Deposited on : 2025-06-25
Resolution : 2.93 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

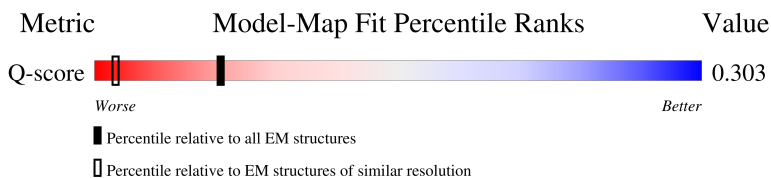
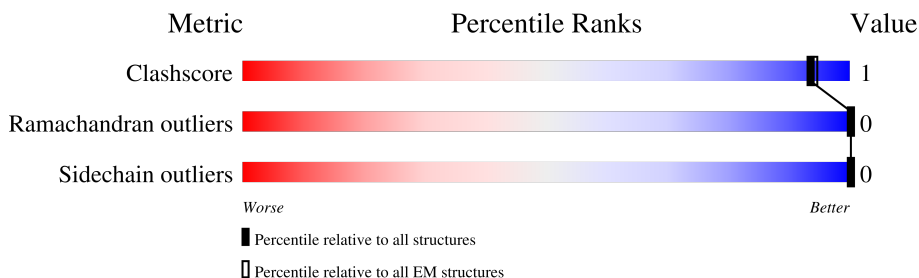
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.93 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	13037 (2.43 - 3.43)

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	XA	419	
1	XC	419	
1	XE	419	
1	XG	419	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	XI	419	
1	XK	419	
1	XM	419	
1	XO	419	
1	XQ	419	
1	XS	419	
1	XU	419	
1	XW	419	
2	XB	334	
2	XD	334	
2	XF	334	
2	XH	334	
2	XJ	334	
2	XL	334	
2	XN	334	
2	XP	334	
2	XR	334	
2	XT	334	
2	XV	334	
2	XX	334	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 103604 atoms, of which 51782 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 HflK.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	XA	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XC	260	Total	C	H	N	O	S	0	0
			4147	1298	2074	365	402	8		
1	XE	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XG	260	Total	C	H	N	O	S	0	0
			4147	1298	2074	365	402	8		
1	XI	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XK	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XM	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XO	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XQ	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XS	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XU	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		
1	XW	259	Total	C	H	N	O	S	0	0
			4140	1296	2071	364	401	8		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XA	270	CYS	ALA	conflict	UNP P0ABC8
XA	283	CYS	ALA	conflict	UNP P0ABC8
XC	270	CYS	ALA	conflict	UNP P0ABC8
XC	283	CYS	ALA	conflict	UNP P0ABC8
XE	270	CYS	ALA	conflict	UNP P0ABC8
XE	283	CYS	ALA	conflict	UNP P0ABC8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
XG	270	CYS	ALA	conflict	UNP P0ABC8
XG	283	CYS	ALA	conflict	UNP P0ABC8
XI	270	CYS	ALA	conflict	UNP P0ABC8
XI	283	CYS	ALA	conflict	UNP P0ABC8
XK	270	CYS	ALA	conflict	UNP P0ABC8
XK	283	CYS	ALA	conflict	UNP P0ABC8
XM	270	CYS	ALA	conflict	UNP P0ABC8
XM	283	CYS	ALA	conflict	UNP P0ABC8
XO	270	CYS	ALA	conflict	UNP P0ABC8
XO	283	CYS	ALA	conflict	UNP P0ABC8
XQ	270	CYS	ALA	conflict	UNP P0ABC8
XQ	283	CYS	ALA	conflict	UNP P0ABC8
XS	270	CYS	ALA	conflict	UNP P0ABC8
XS	283	CYS	ALA	conflict	UNP P0ABC8
XU	270	CYS	ALA	conflict	UNP P0ABC8
XU	283	CYS	ALA	conflict	UNP P0ABC8
XW	270	CYS	ALA	conflict	UNP P0ABC8
XW	283	CYS	ALA	conflict	UNP P0ABC8

- Molecule 2 is a protein called Modulator of FtsH protease HflC.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	XB	279	Total	C	H	N	O	S	0	0
			4479	1401	2236	405	427	10		
2	XD	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XF	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XH	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XJ	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XL	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XN	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XP	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XR	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XT	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms						AltConf	Trace
2	XV	280	Total	C	H	N	O	S	0	0
			4495	1406	2245	406	428	10		
2	XX	279	Total	C	H	N	O	S	0	0
			4481	1401	2238	405	427	10		

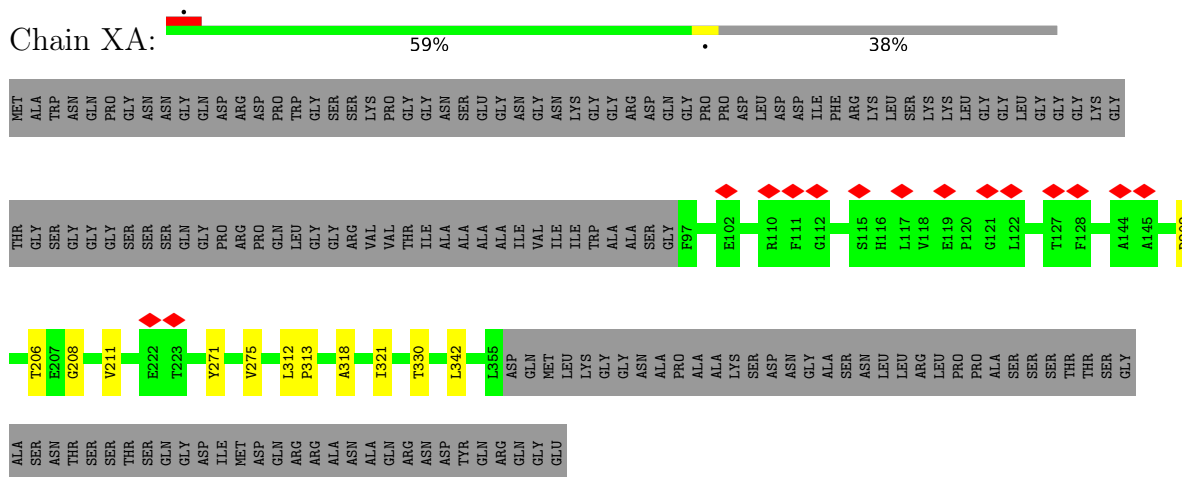
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XB	233	CYS	ALA	conflict	UNP P0ABC5
XB	264	CYS	ALA	conflict	UNP P0ABC5
XD	233	CYS	ALA	conflict	UNP P0ABC5
XD	264	CYS	ALA	conflict	UNP P0ABC5
XF	233	CYS	ALA	conflict	UNP P0ABC5
XF	264	CYS	ALA	conflict	UNP P0ABC5
XH	233	CYS	ALA	conflict	UNP P0ABC5
XH	264	CYS	ALA	conflict	UNP P0ABC5
XJ	233	CYS	ALA	conflict	UNP P0ABC5
XJ	264	CYS	ALA	conflict	UNP P0ABC5
XL	233	CYS	ALA	conflict	UNP P0ABC5
XL	264	CYS	ALA	conflict	UNP P0ABC5
XN	233	CYS	ALA	conflict	UNP P0ABC5
XN	264	CYS	ALA	conflict	UNP P0ABC5
XP	233	CYS	ALA	conflict	UNP P0ABC5
XP	264	CYS	ALA	conflict	UNP P0ABC5
XR	233	CYS	ALA	conflict	UNP P0ABC5
XR	264	CYS	ALA	conflict	UNP P0ABC5
XT	233	CYS	ALA	conflict	UNP P0ABC5
XT	264	CYS	ALA	conflict	UNP P0ABC5
XV	233	CYS	ALA	conflict	UNP P0ABC5
XV	264	CYS	ALA	conflict	UNP P0ABC5
XX	233	CYS	ALA	conflict	UNP P0ABC5
XX	264	CYS	ALA	conflict	UNP P0ABC5

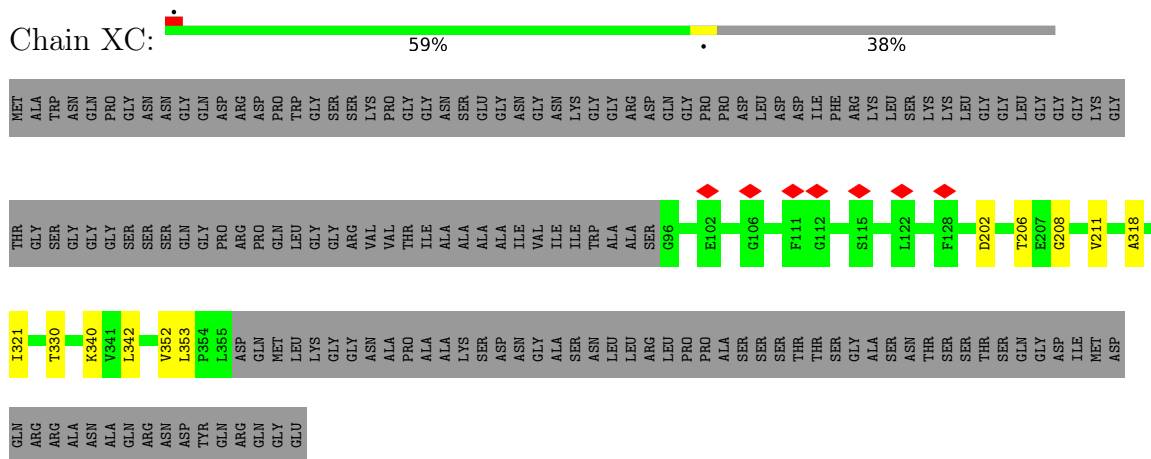
3 Residue-property plots [i](#)

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.

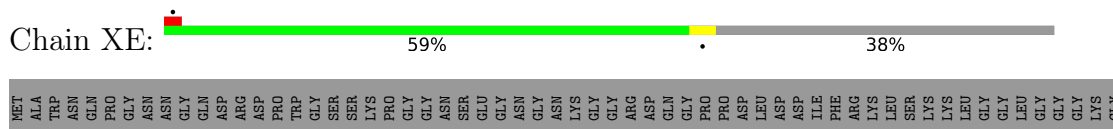
• Molecule 1: Protein HflK



• Molecule 1: Protein HflK

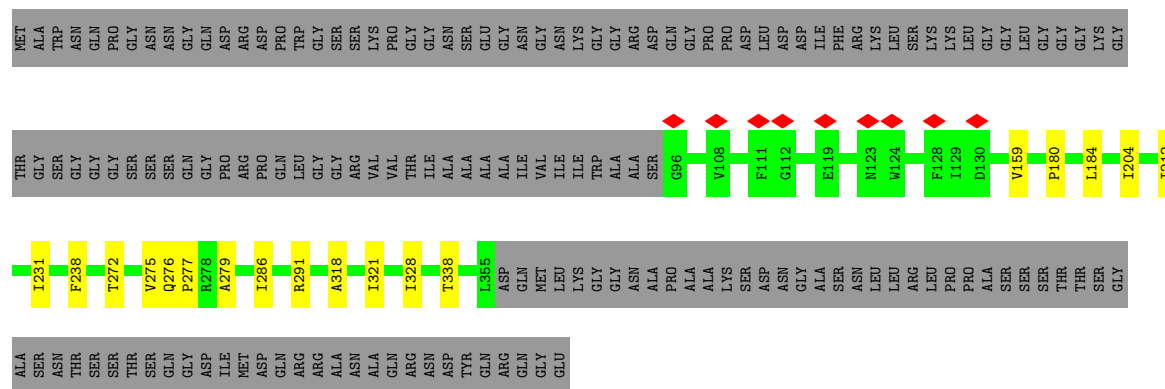


• Molecule 1: Protein HflK



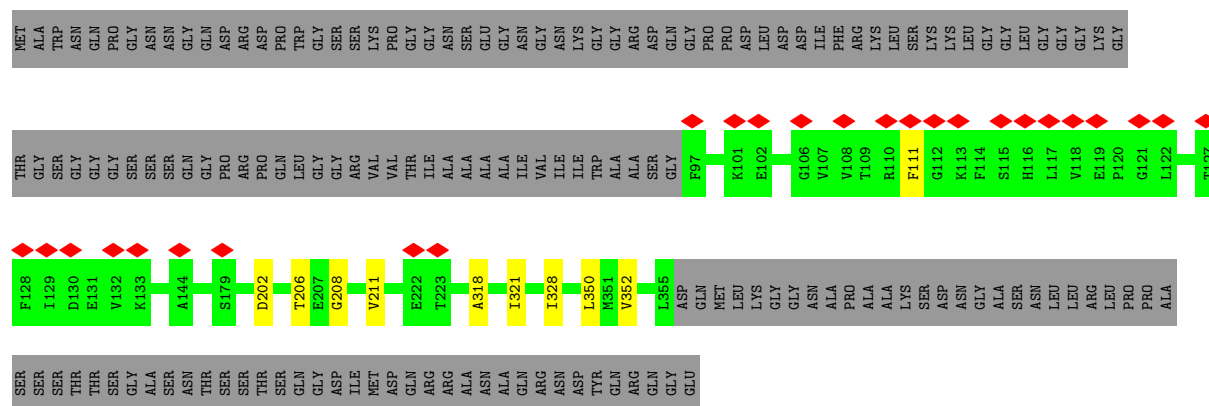
- Molecule 1: Protein HflK

Chain XG: 



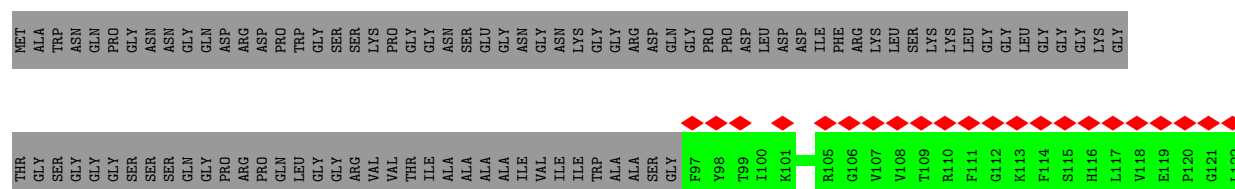
- Molecule 1: Protein HflK

Chain XI: 

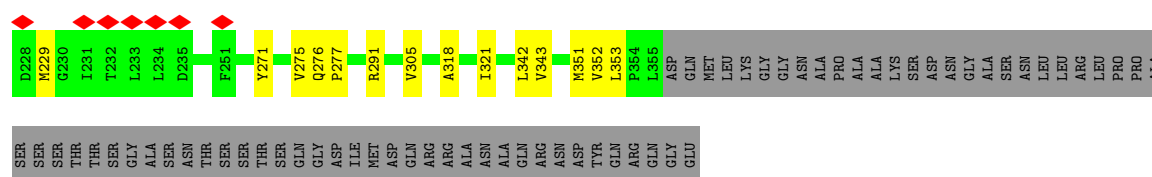
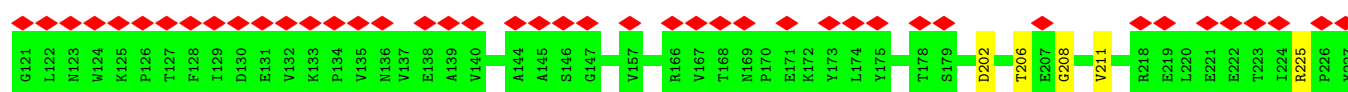
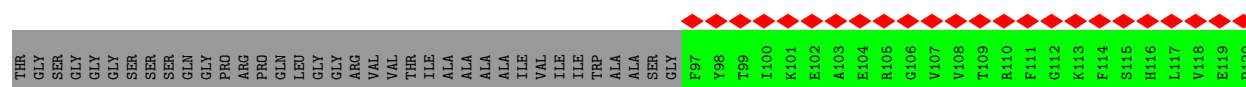
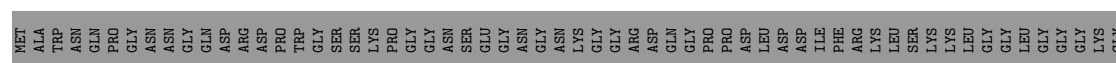


- Molecule 1: Protein HflK

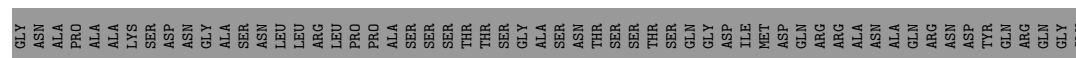
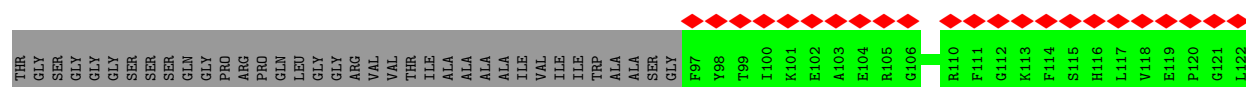
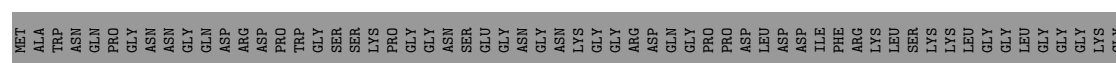
Chain XK: 



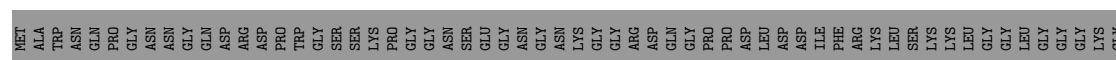
- Molecule 1: Protein HflK

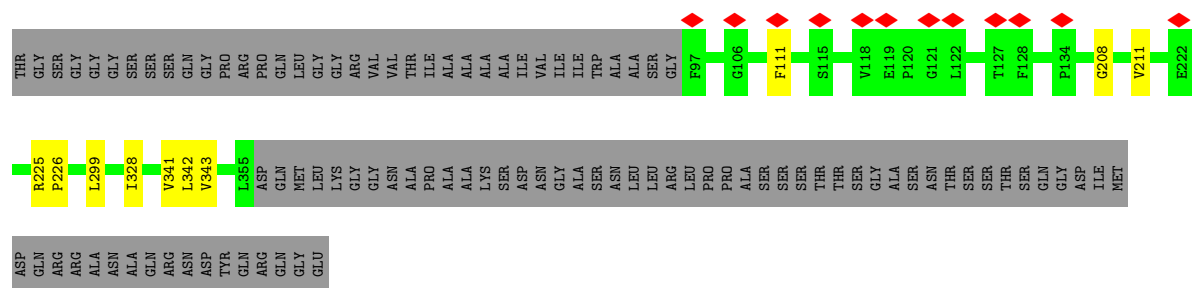


- Molecule 1: Protein HflK

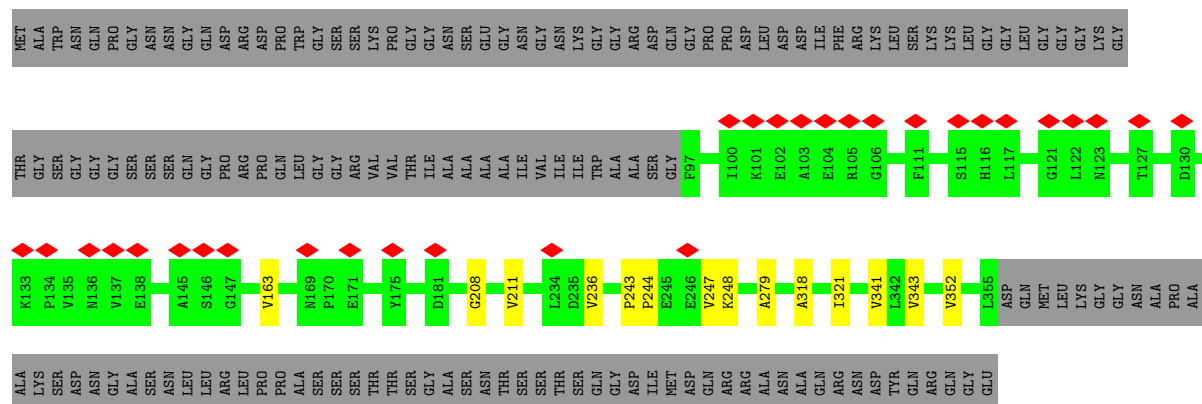


- Molecule 1: Protein HflK

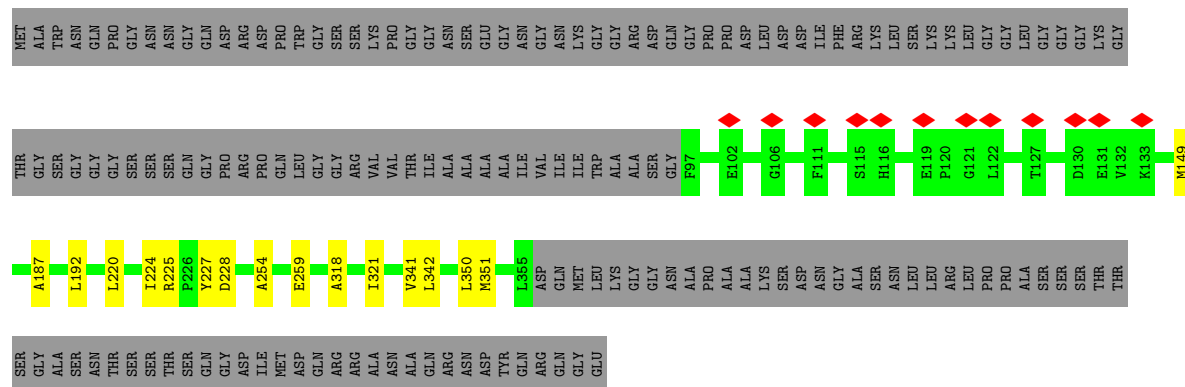




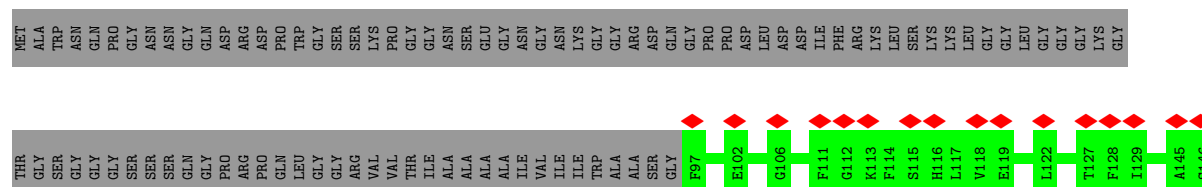
- Molecule 1: Protein HflK




- Molecule 1: Protein HflK

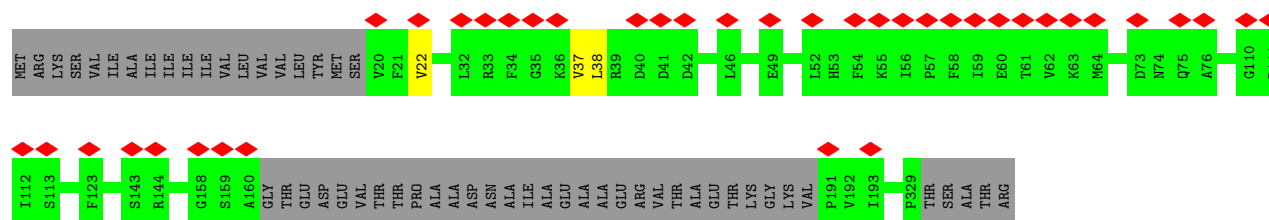


- Molecule 1: Protein HflK




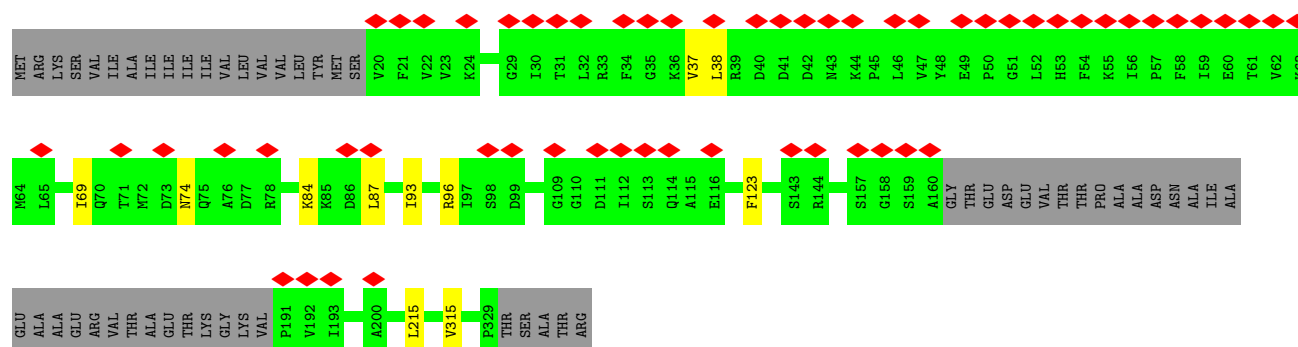
- Molecule 2: Modulator of FtsH protease HflC

Chain XJ: 




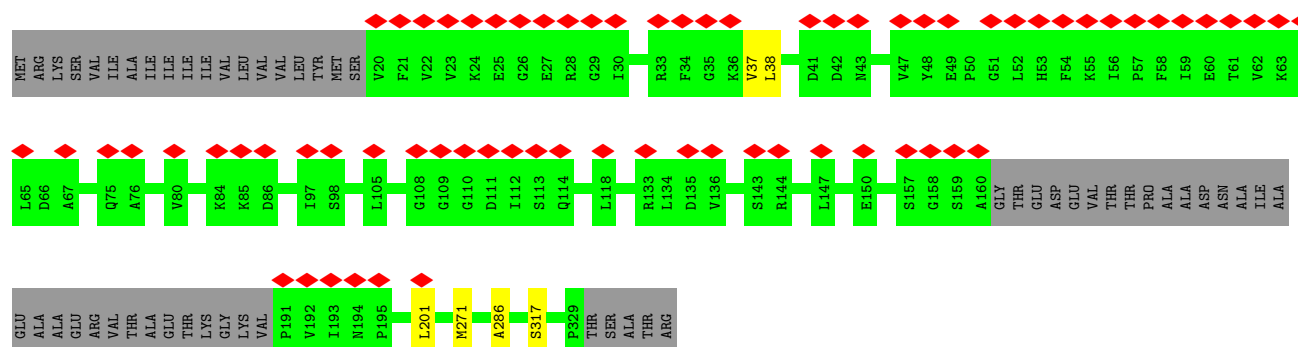
- Molecule 2: Modulator of FtsH protease HflC

Chain XL: 




- Molecule 2: Modulator of FtsH protease HflC

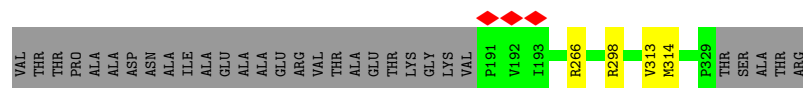
Chain XN: 



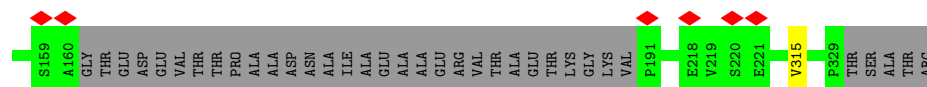
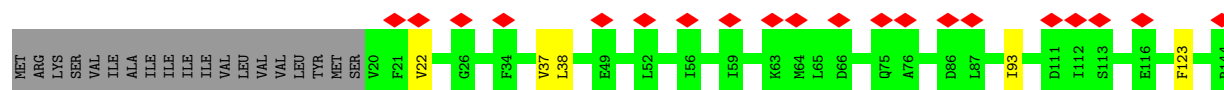
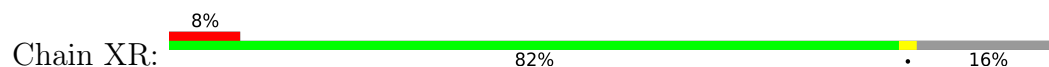
- Molecule 2: Modulator of FtsH protease HflC

Chain XP: 

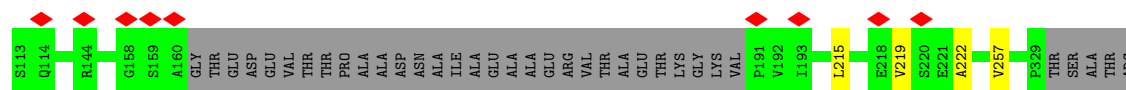
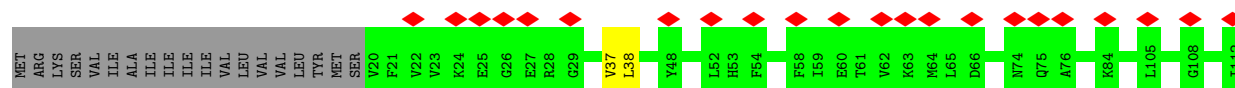
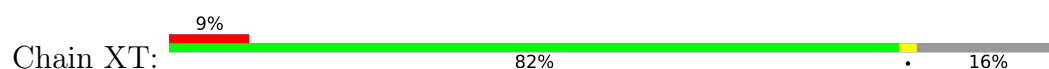




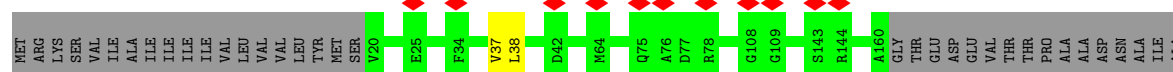
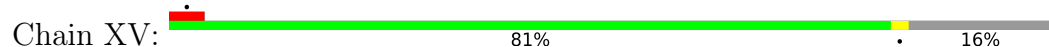
- Molecule 2: Modulator of FtsH protease HflC



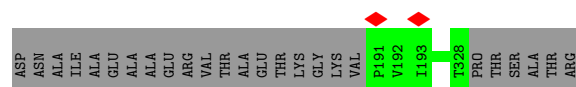
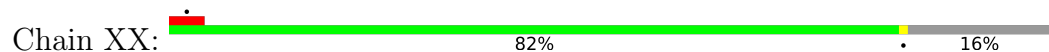
- Molecule 2: Modulator of FtsH protease HflC



- Molecule 2: Modulator of FtsH protease HflC



- Molecule 2: Modulator of FtsH protease HflC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	299919	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; Patch CTF estimation, cryoSPARC	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.19	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1750	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.893	Depositor
Minimum map value	-0.941	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.235	Depositor
Map size (\AA)	442.86722, 442.86722, 442.86722	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1533, 1.1533, 1.1533	Depositor

5 Model quality

5.1 Standard geometry

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	XA	0.07	0/2101	0.20	0/2844
1	XC	0.07	0/2105	0.22	0/2849
1	XE	0.07	0/2101	0.21	0/2844
1	XG	0.08	0/2105	0.23	0/2849
1	XI	0.07	0/2101	0.21	0/2844
1	XK	0.07	0/2101	0.22	0/2844
1	XM	0.07	0/2101	0.21	0/2844
1	XO	0.06	0/2101	0.20	0/2844
1	XQ	0.08	0/2101	0.21	0/2844
1	XS	0.06	0/2101	0.21	0/2844
1	XU	0.09	0/2101	0.27	0/2844
1	XW	0.06	0/2101	0.21	0/2844
2	XB	0.06	0/2277	0.18	0/3057
2	XD	0.06	0/2284	0.19	0/3067
2	XF	0.06	0/2284	0.19	0/3067
2	XH	0.06	0/2284	0.18	0/3067
2	XJ	0.06	0/2284	0.19	0/3067
2	XL	0.06	0/2284	0.20	0/3067
2	XN	0.06	0/2284	0.19	0/3067
2	XP	0.06	0/2284	0.19	0/3067
2	XR	0.06	0/2284	0.19	0/3067
2	XT	0.06	0/2284	0.20	0/3067
2	XV	0.06	0/2284	0.20	0/3067
2	XX	0.06	0/2276	0.20	0/3055
All	All	0.07	0/52613	0.20	0/70920

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	XA	2069	2071	2071	7	0
1	XC	2073	2074	2074	8	0
1	XE	2069	2071	2071	8	0
1	XG	2073	2074	2074	14	0
1	XI	2069	2071	2071	6	0
1	XK	2069	2071	2071	6	0
1	XM	2069	2071	2071	15	0
1	XO	2069	2071	2071	8	0
1	XQ	2069	2071	2071	9	0
1	XS	2069	2071	2071	10	0
1	XU	2069	2071	2071	13	0
1	XW	2069	2071	2071	5	0
2	XB	2243	2236	2236	5	0
2	XD	2250	2245	2245	7	0
2	XF	2250	2245	2245	5	0
2	XH	2250	2245	2245	8	0
2	XJ	2250	2245	2245	2	0
2	XL	2250	2245	2245	9	0
2	XN	2250	2245	2245	5	0
2	XP	2250	2245	2245	5	0
2	XR	2250	2245	2245	4	0
2	XT	2250	2245	2245	4	0
2	XV	2250	2245	2245	6	0
2	XX	2243	2238	2238	2	0
All	All	51822	51782	51782	132	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 1.

The worst 5 of 132 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:XU:187:ALA:HB2	1:XU:225:ARG:NH1	2.06	0.69
1:XU:187:ALA:HB1	1:XU:224:ILE:HD12	1.80	0.63
1:XC:340:LYS:HG2	2:XD:316:MET:HE1	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XO:350:LEU:HD22	1:XQ:343:VAL:HG21	1.86	0.56
1:XE:318:ALA:HB1	1:XE:321:ILE:HG22	1.89	0.55

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	XA	257/419 (61%)	243 (95%)	14 (5%)	0	100	100
1	XC	258/419 (62%)	239 (93%)	19 (7%)	0	100	100
1	XE	257/419 (61%)	237 (92%)	20 (8%)	0	100	100
1	XG	258/419 (62%)	245 (95%)	13 (5%)	0	100	100
1	XI	257/419 (61%)	242 (94%)	15 (6%)	0	100	100
1	XK	257/419 (61%)	243 (95%)	14 (5%)	0	100	100
1	XM	257/419 (61%)	237 (92%)	20 (8%)	0	100	100
1	XO	257/419 (61%)	240 (93%)	17 (7%)	0	100	100
1	XQ	257/419 (61%)	240 (93%)	17 (7%)	0	100	100
1	XS	257/419 (61%)	237 (92%)	20 (8%)	0	100	100
1	XU	257/419 (61%)	239 (93%)	18 (7%)	0	100	100
1	XW	257/419 (61%)	246 (96%)	11 (4%)	0	100	100
2	XB	275/334 (82%)	266 (97%)	9 (3%)	0	100	100
2	XD	276/334 (83%)	269 (98%)	7 (2%)	0	100	100
2	XF	276/334 (83%)	266 (96%)	10 (4%)	0	100	100
2	XH	276/334 (83%)	269 (98%)	7 (2%)	0	100	100
2	XJ	276/334 (83%)	268 (97%)	8 (3%)	0	100	100
2	XL	276/334 (83%)	267 (97%)	9 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	XN	276/334 (83%)	264 (96%)	12 (4%)	0	100	100
2	XP	276/334 (83%)	266 (96%)	10 (4%)	0	100	100
2	XR	276/334 (83%)	269 (98%)	7 (2%)	0	100	100
2	XT	276/334 (83%)	269 (98%)	7 (2%)	0	100	100
2	XV	276/334 (83%)	265 (96%)	11 (4%)	0	100	100
2	XX	275/334 (82%)	261 (95%)	14 (5%)	0	100	100
All	All	6396/9036 (71%)	6087 (95%)	309 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	XA	223/338 (66%)	223 (100%)	0	100	100
1	XC	223/338 (66%)	223 (100%)	0	100	100
1	XE	223/338 (66%)	223 (100%)	0	100	100
1	XG	223/338 (66%)	223 (100%)	0	100	100
1	XI	223/338 (66%)	223 (100%)	0	100	100
1	XK	223/338 (66%)	223 (100%)	0	100	100
1	XM	223/338 (66%)	223 (100%)	0	100	100
1	XO	223/338 (66%)	223 (100%)	0	100	100
1	XQ	223/338 (66%)	223 (100%)	0	100	100
1	XS	223/338 (66%)	223 (100%)	0	100	100
1	XU	223/338 (66%)	223 (100%)	0	100	100
1	XW	223/338 (66%)	223 (100%)	0	100	100
2	XB	241/285 (85%)	241 (100%)	0	100	100
2	XD	242/285 (85%)	242 (100%)	0	100	100
2	XF	242/285 (85%)	242 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	XH	242/285 (85%)	242 (100%)	0	100	100
2	XJ	242/285 (85%)	242 (100%)	0	100	100
2	XL	242/285 (85%)	242 (100%)	0	100	100
2	XN	242/285 (85%)	242 (100%)	0	100	100
2	XP	242/285 (85%)	242 (100%)	0	100	100
2	XR	242/285 (85%)	242 (100%)	0	100	100
2	XT	242/285 (85%)	242 (100%)	0	100	100
2	XV	242/285 (85%)	242 (100%)	0	100	100
2	XX	241/285 (85%)	241 (100%)	0	100	100
All	All	5578/7476 (75%)	5578 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	XM	284	GLN
1	XW	349	ASN
2	XP	305	ASN
1	XW	237	ASN
1	XO	349	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

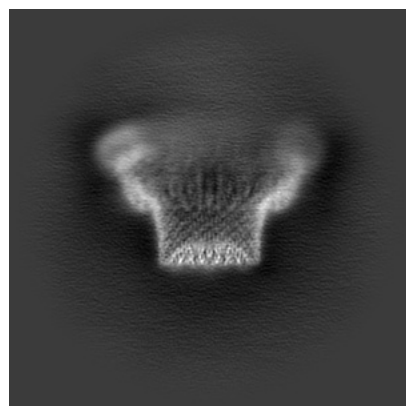
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71448. These allow visual inspection of the internal detail of the map and identification of artifacts.

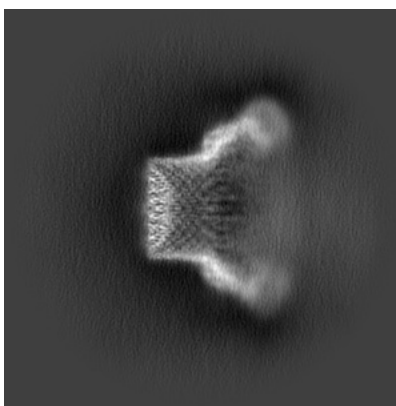
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

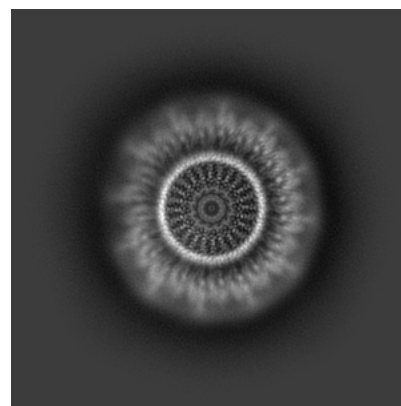
6.1.1 Primary map



X

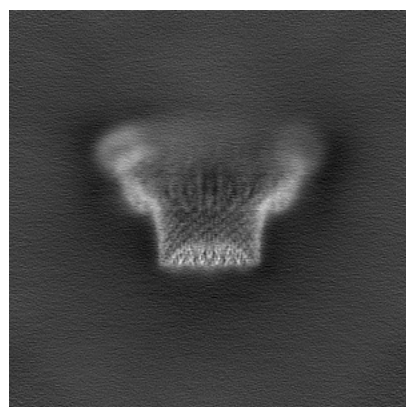


Y

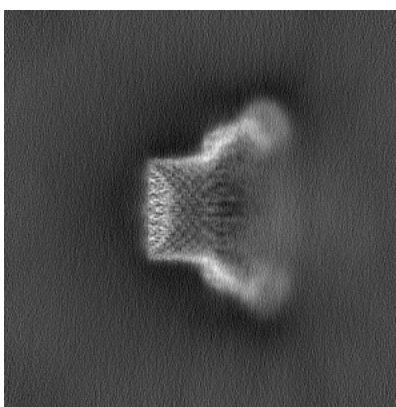


Z

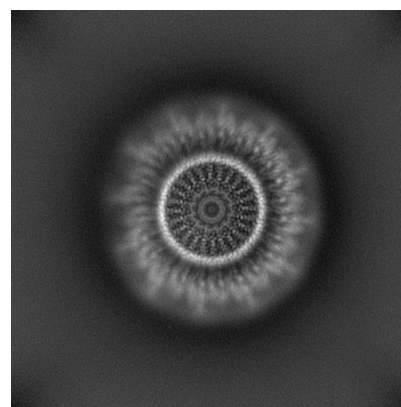
6.1.2 Raw map



X



Y

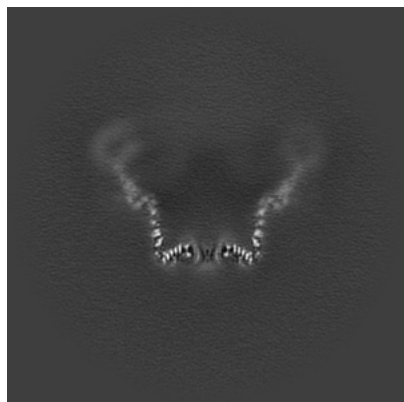


Z

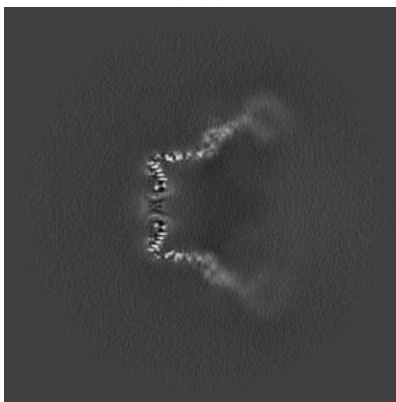
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

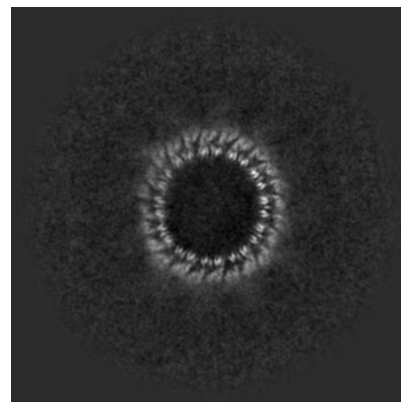
6.2.1 Primary map



X Index: 192

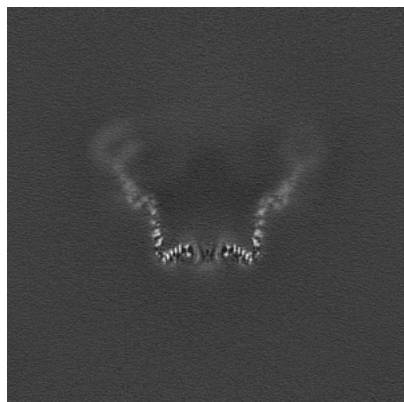


Y Index: 192

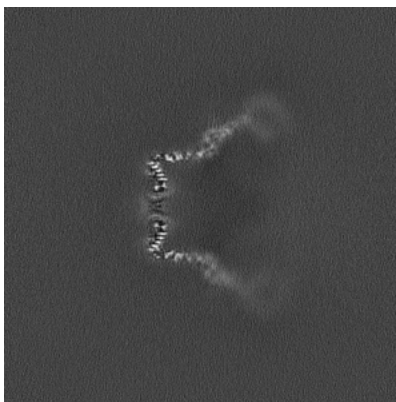


Z Index: 192

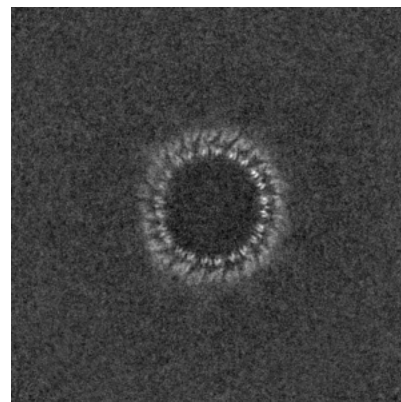
6.2.2 Raw map



X Index: 192



Y Index: 192

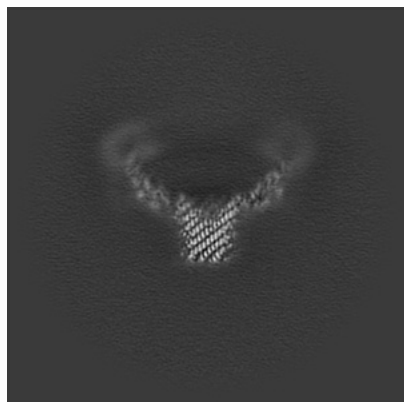


Z Index: 192

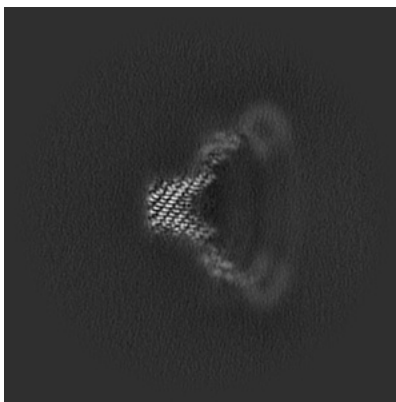
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

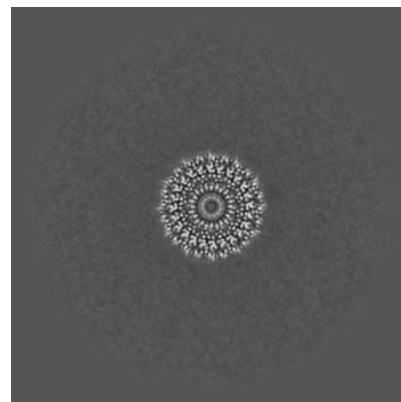
6.3.1 Primary map



X Index: 238

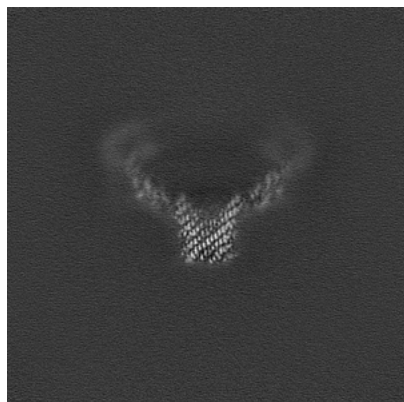


Y Index: 146

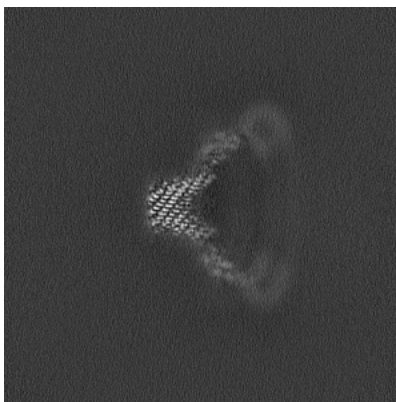


Z Index: 146

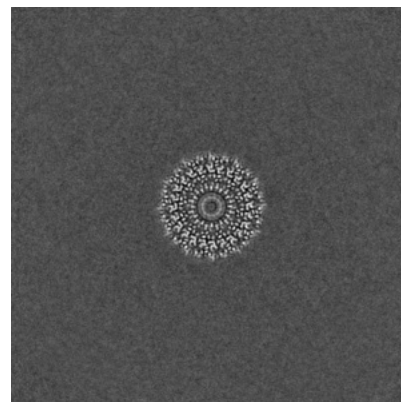
6.3.2 Raw map



X Index: 237



Y Index: 146

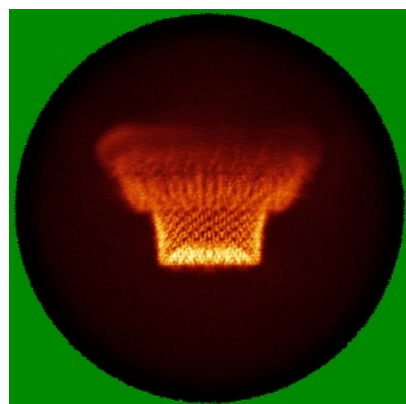


Z Index: 146

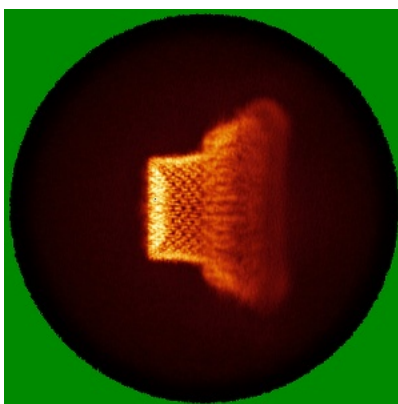
The images above show the largest variance slices of the map in three orthogonal directions.

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

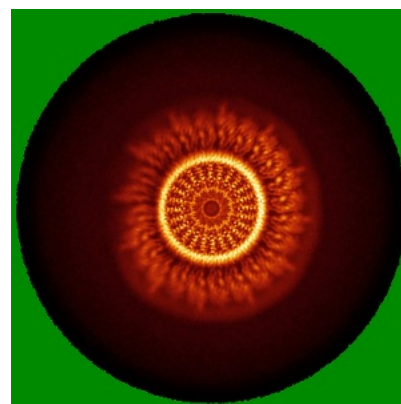
6.4.1 Primary map



X

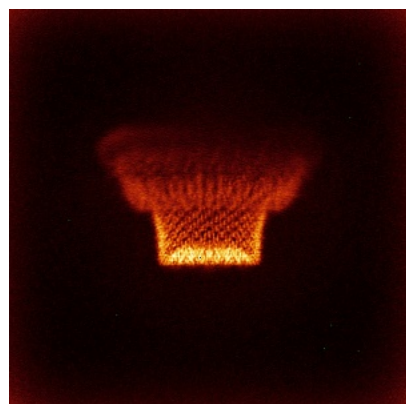


Y

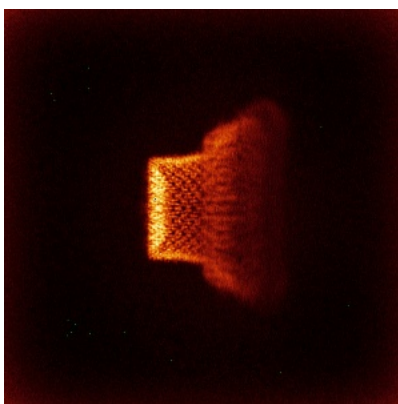


Z

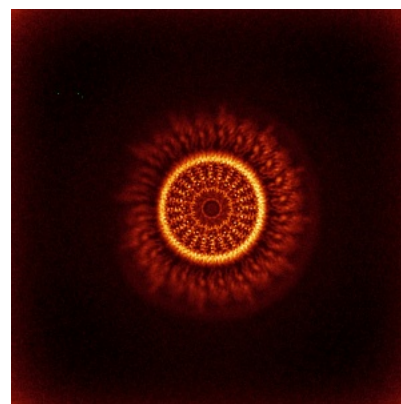
6.4.2 Raw map



X



Y

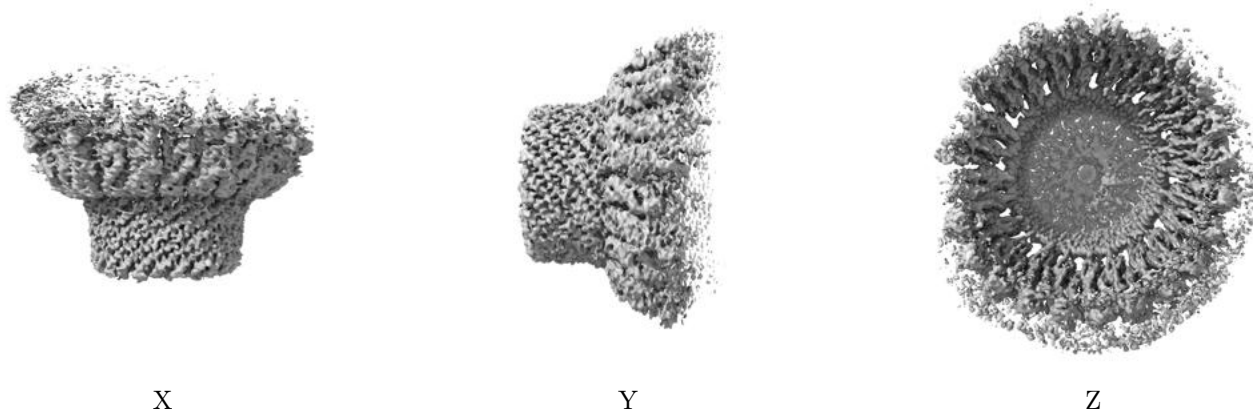


Z

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.

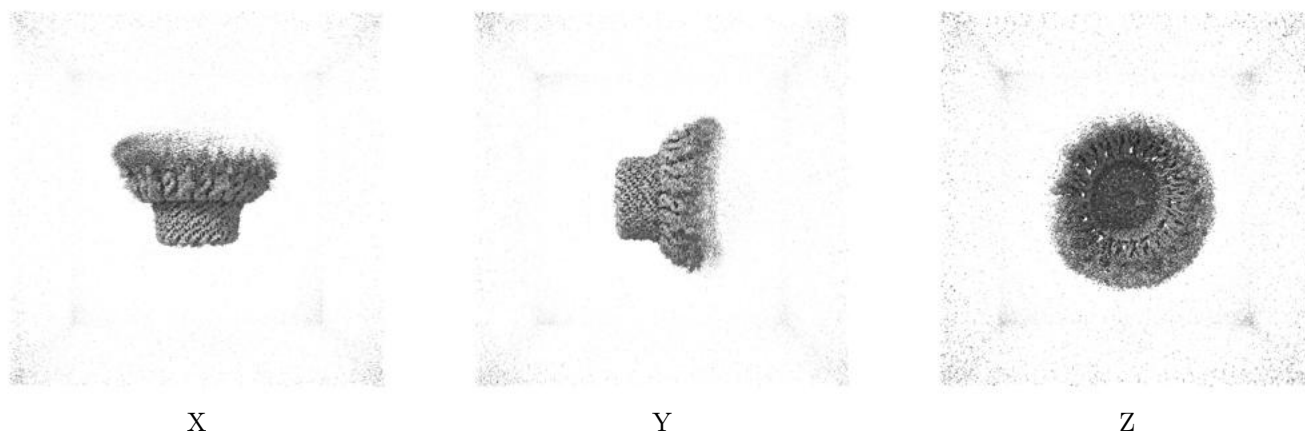
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.235. 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.

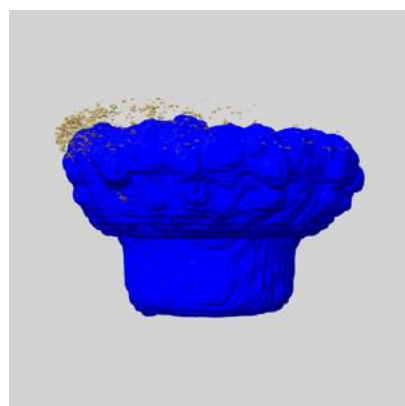
6.6 Mask visualisation [i](#)

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

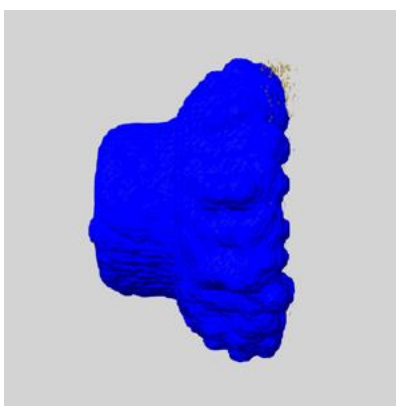
A mask typically either:

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

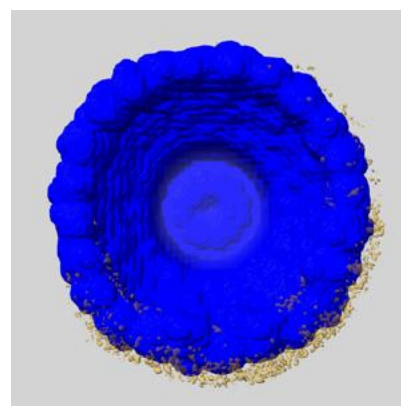
6.6.1 emd_71448_msk_1.map [i](#)



X



Y

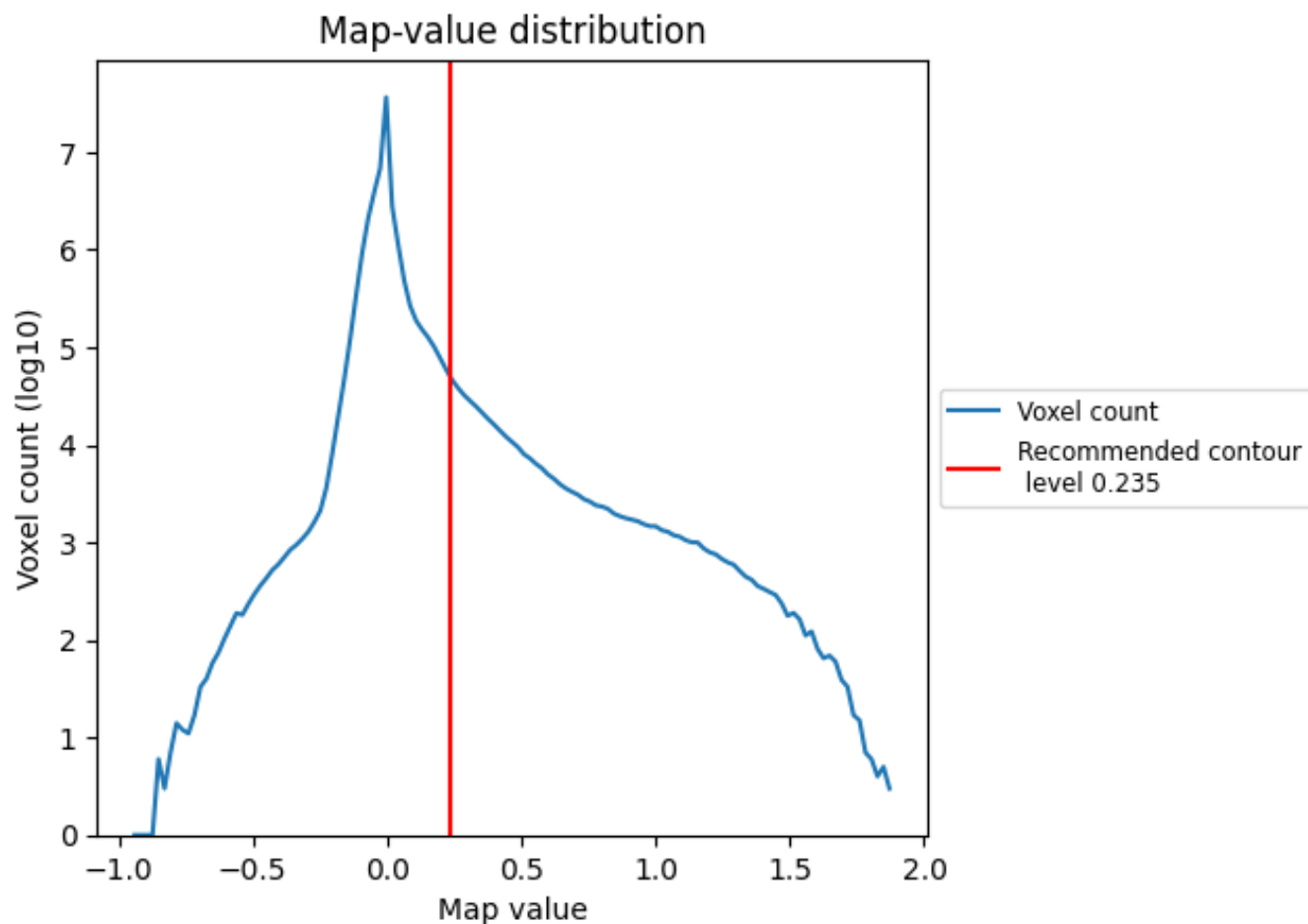


Z

7 Map analysis [i](#)

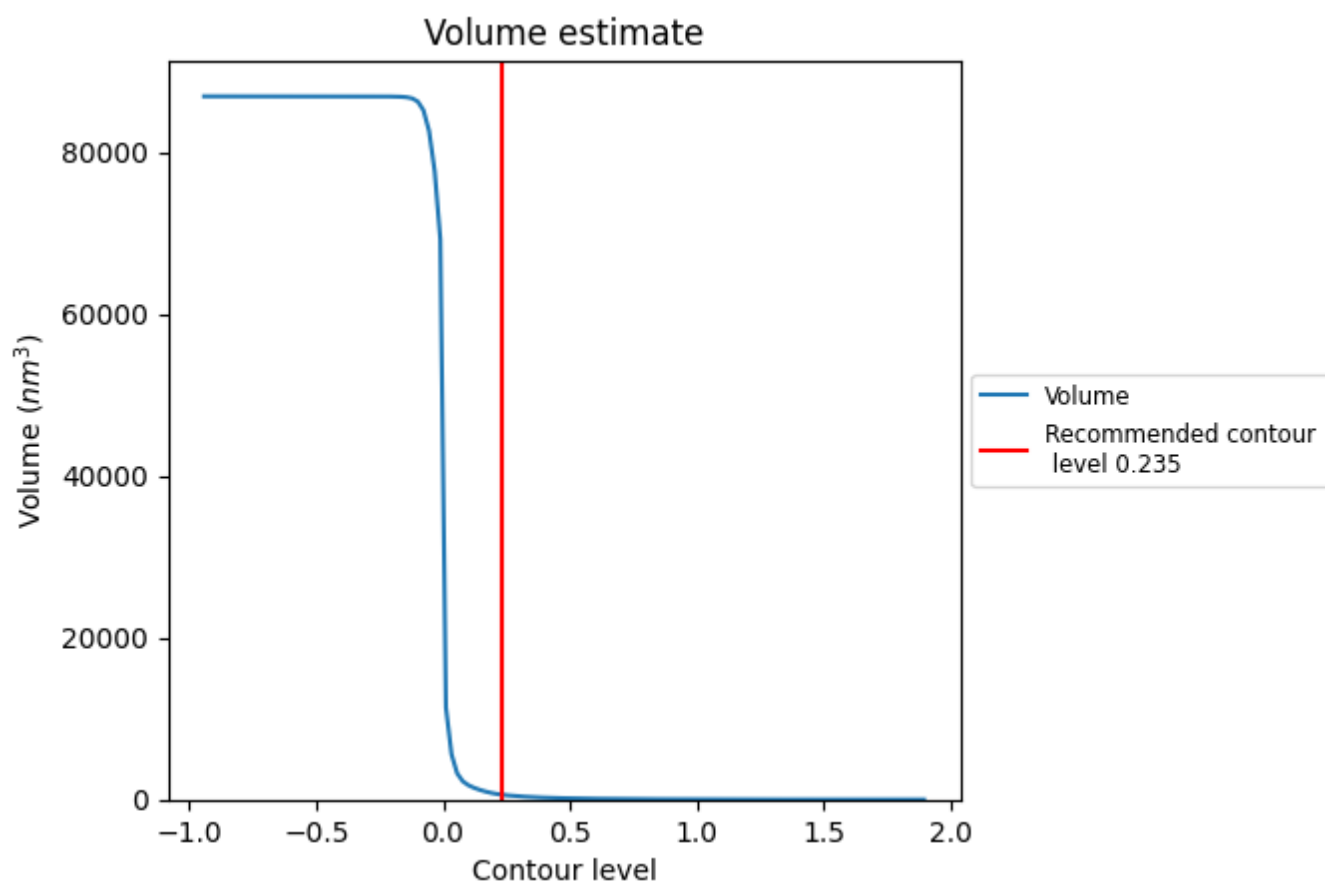
This section contains the results of statistical analysis of the map.

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.

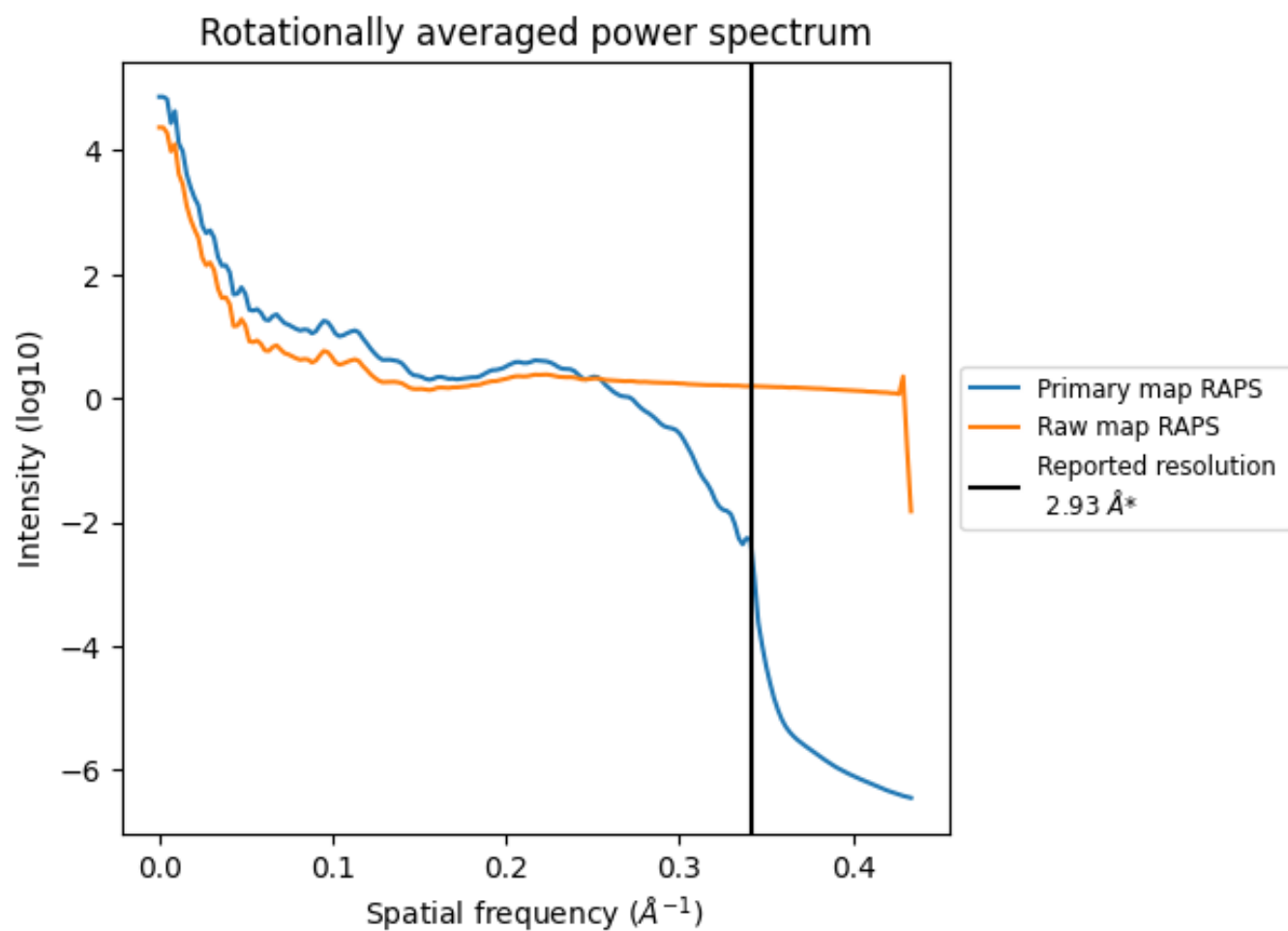
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 587 nm³; this corresponds to an approximate mass of 530 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 ⓘ

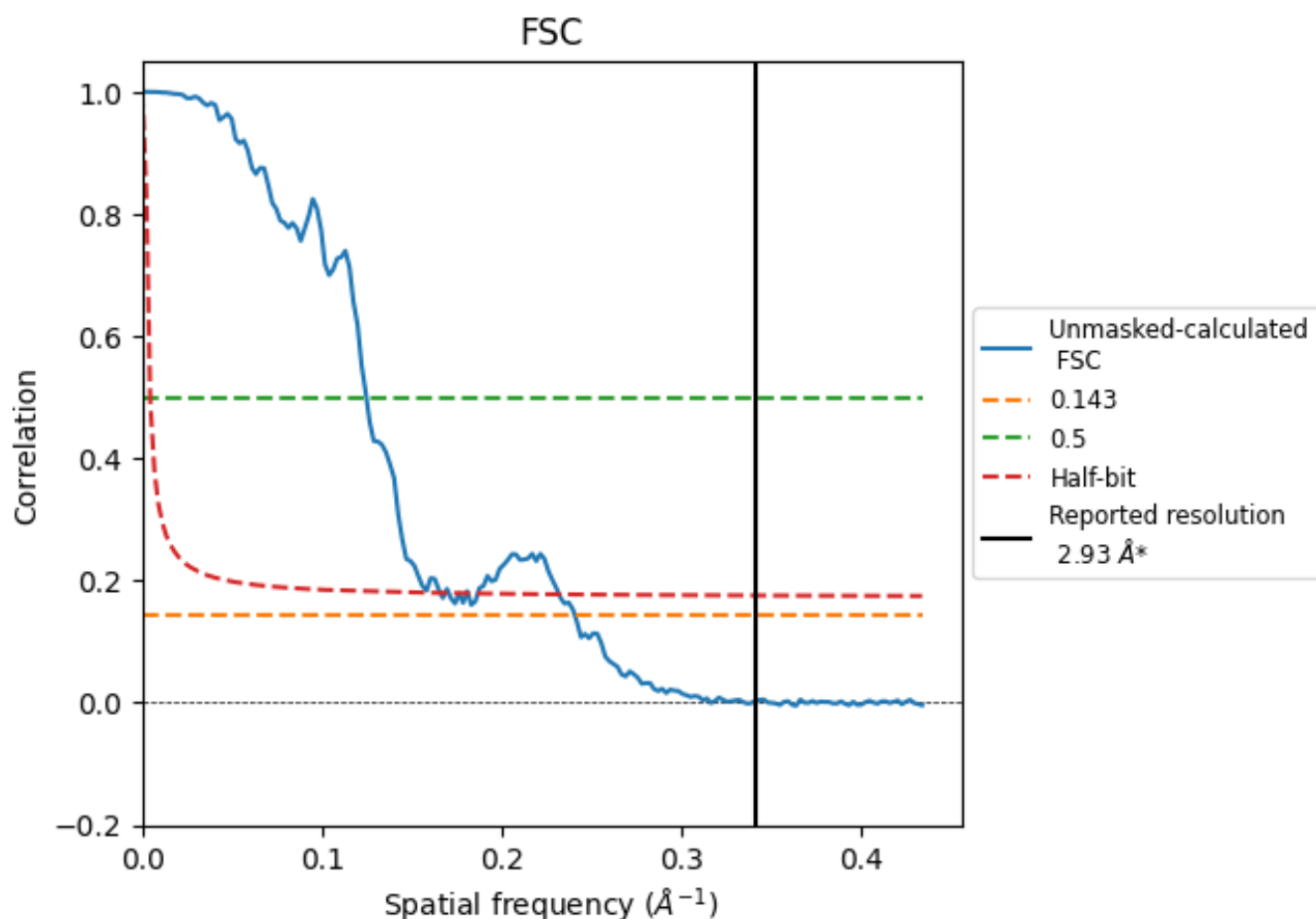


*Reported resolution corresponds to spatial frequency of 0.341 Å⁻¹

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 0.341 Å⁻¹

8.2 Resolution estimates [i](#)

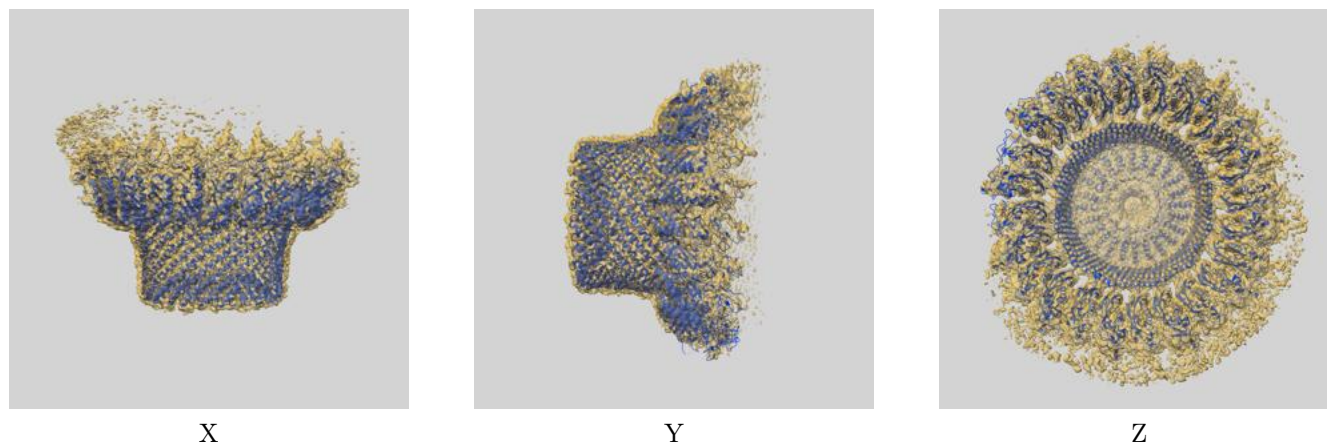
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.93	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.16	8.03	6.04

*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 4.16 differs from the reported value 2.93 by more than 10 %

9 Map-model fit [i](#)

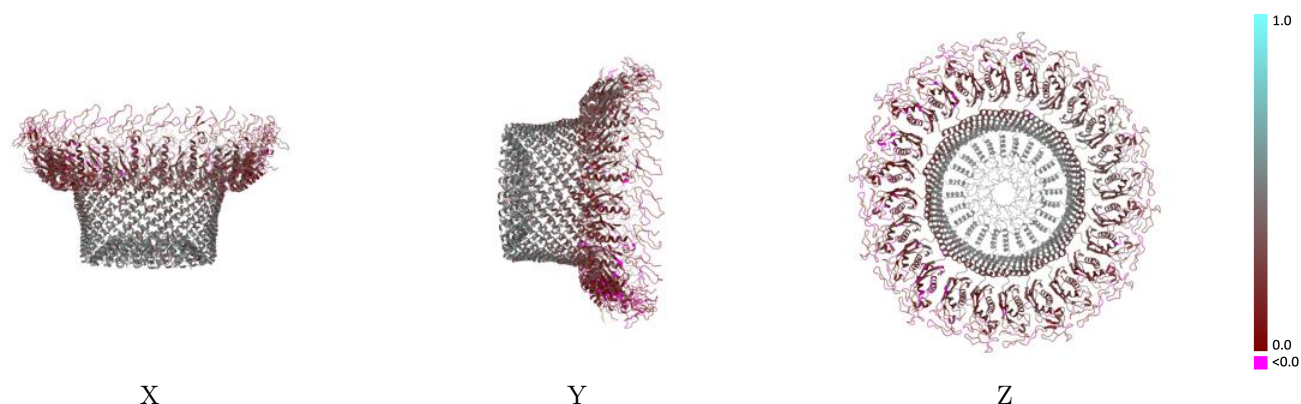
This section contains information regarding the fit between EMDB map EMD-71448 and PDB model 9PAW. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



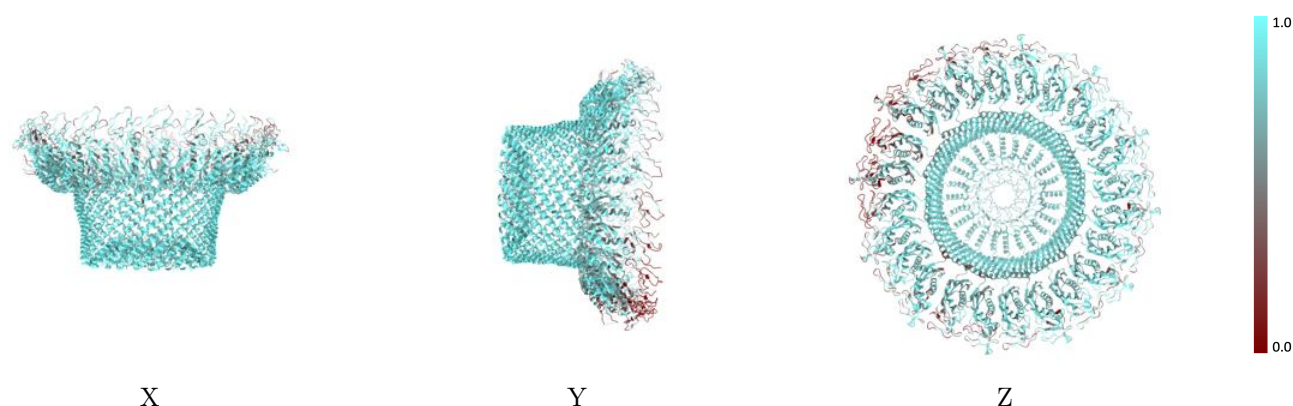
The images above show the 3D surface view of the map at the recommended contour level 0.235 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



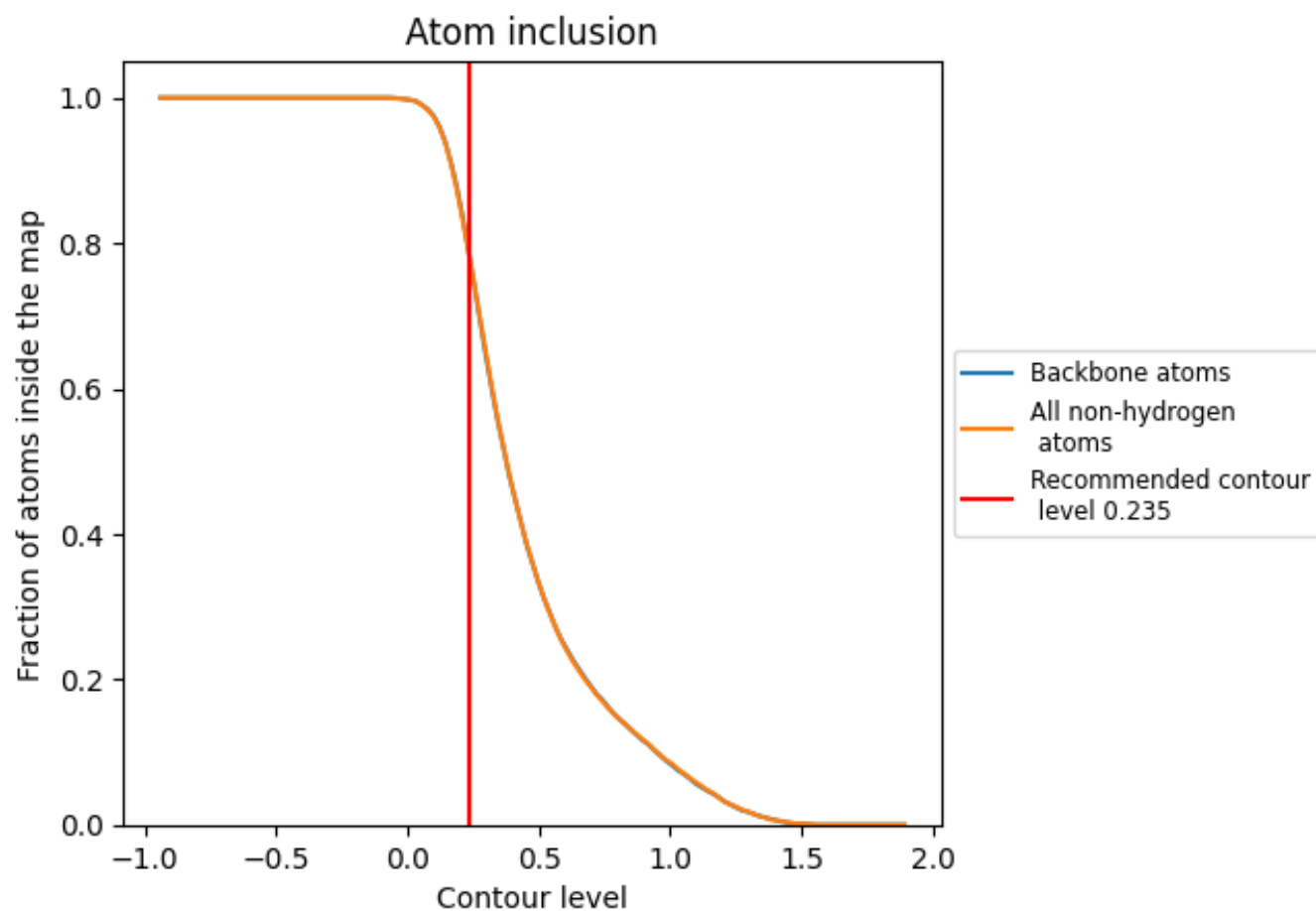
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.235).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 78% 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 (0.235) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.3030
XA	 0.8310	 0.3140
XB	 0.8460	 0.3290
XC	 0.8640	 0.3480
XD	 0.8610	 0.3500
XE	 0.8720	 0.3770
XF	 0.8470	 0.3360
XG	 0.8470	 0.3440
XH	 0.8330	 0.3210
XI	 0.7720	 0.3010
XJ	 0.7620	 0.2910
XK	 0.7180	 0.2770
XL	 0.6930	 0.2640
XM	 0.6150	 0.2590
XN	 0.6540	 0.2590
XO	 0.7210	 0.2650
XP	 0.8020	 0.2910
XQ	 0.8180	 0.2920
XR	 0.8020	 0.2620
XS	 0.7540	 0.2830
XT	 0.7680	 0.2820
XU	 0.8090	 0.3170
XV	 0.8190	 0.3160
XW	 0.8180	 0.3120
XX	 0.8350	 0.2940

