



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 12:17 AM UTC

PDB ID : 8RGZ / pdb_00008rgz
EMDB ID : EMD-19163
Title : Trimeric HSV-1F gB ectodomain in postfusion conformation with three bound HDIT101 Fab molecules.
Authors : Kalbermatter, D.; Seyfizadeh, N.; Imhof, T.; Ries, M.; Mueller, C.; Jenner, L.; Blumenschein, E.; Yendrzheyevskiy, A.; Moog, K.; Eckert, D.; Engel, R.; Diebolder, P.; Chami, M.; Krauss, J.; Schaller, T.; Arndt, M.
Deposited on : 2023-12-14
Resolution : 3.27 Å(reported)
Based on initial model : 2gum

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:

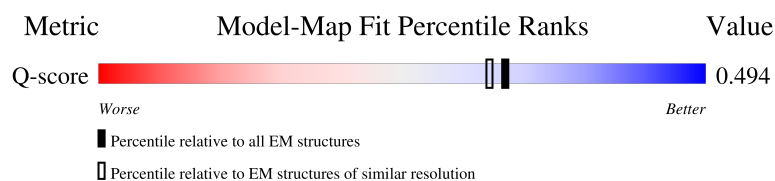
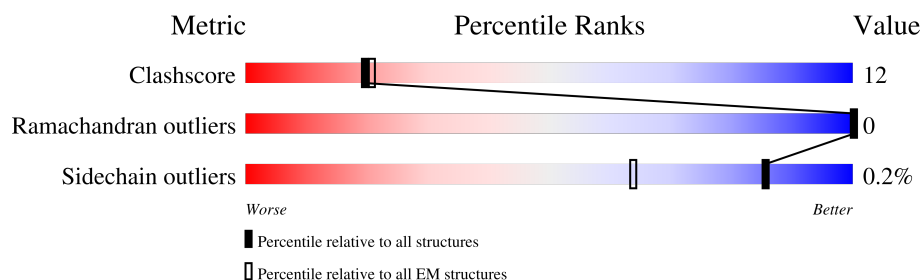
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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

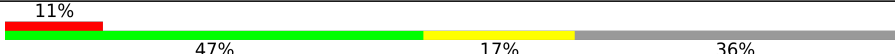
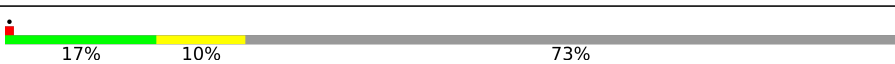
The reported resolution of this entry is 3.27 Å.

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.



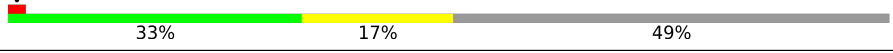
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14508 (2.77 - 3.77)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	906	
1	B	906	
1	C	906	
2	D	450	

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Mol	Chain	Length	Quality of chain
2	F	450	 16% 10% 73%
2	H	450	 15% 12% 73%
3	E	218	 36% 15% 49%
3	G	218	 33% 17% 49%
3	L	218	 36% 15% 49%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19545 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 Envelope glycoprotein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	583	Total	C	N	O	S	0	0
			4705	2969	829	885	22		
1	B	583	Total	C	N	O	S	0	0
			4705	2969	829	885	22		
1	C	583	Total	C	N	O	S	0	0
			4705	2969	829	885	22		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	PRO	-	insertion	UNP P06436
A	858	HIS	ARG	conflict	UNP P06436
A	905	ALA	-	expression tag	UNP P06436
A	906	ALA	-	expression tag	UNP P06436
B	6	PRO	-	insertion	UNP P06436
B	858	HIS	ARG	conflict	UNP P06436
B	905	ALA	-	expression tag	UNP P06436
B	906	ALA	-	expression tag	UNP P06436
C	6	PRO	-	insertion	UNP P06436
C	858	HIS	ARG	conflict	UNP P06436
C	905	ALA	-	expression tag	UNP P06436
C	906	ALA	-	expression tag	UNP P06436

- Molecule 2 is a protein called HDIT101 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	120	Total	C	N	O	S	0	0
			952	614	155	177	6		
2	H	120	Total	C	N	O	S	0	0
			952	614	155	177	6		
2	F	120	Total	C	N	O	S	0	0
			952	614	155	177	6		

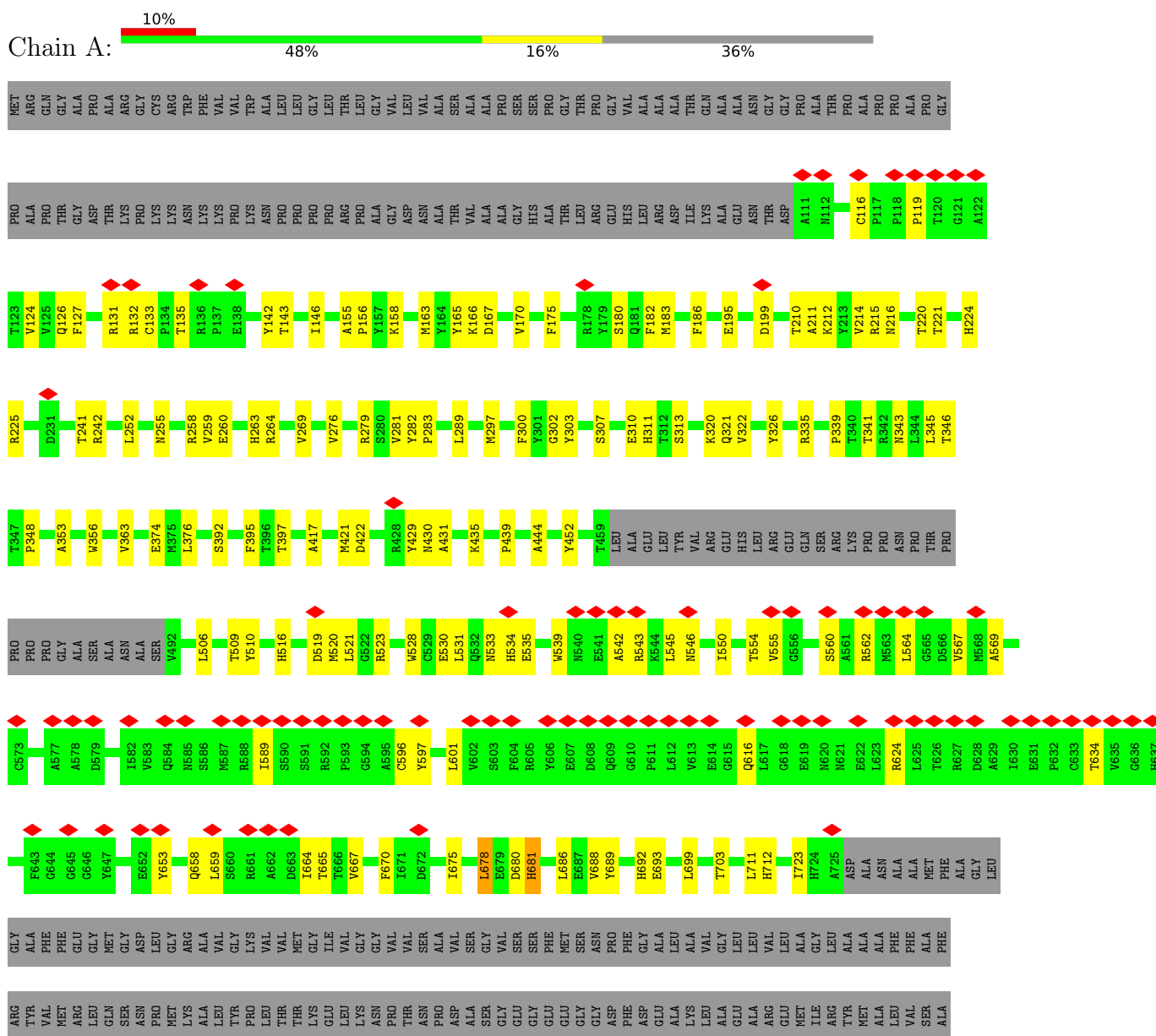
- Molecule 3 is a protein called HDIT101 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	111	Total	C	N	O	S	0	0
			858	546	144	165	3		
3	L	111	Total	C	N	O	S	0	0
			858	546	144	165	3		
3	G	111	Total	C	N	O	S	0	0
			858	546	144	165	3		

3 Residue-property plots

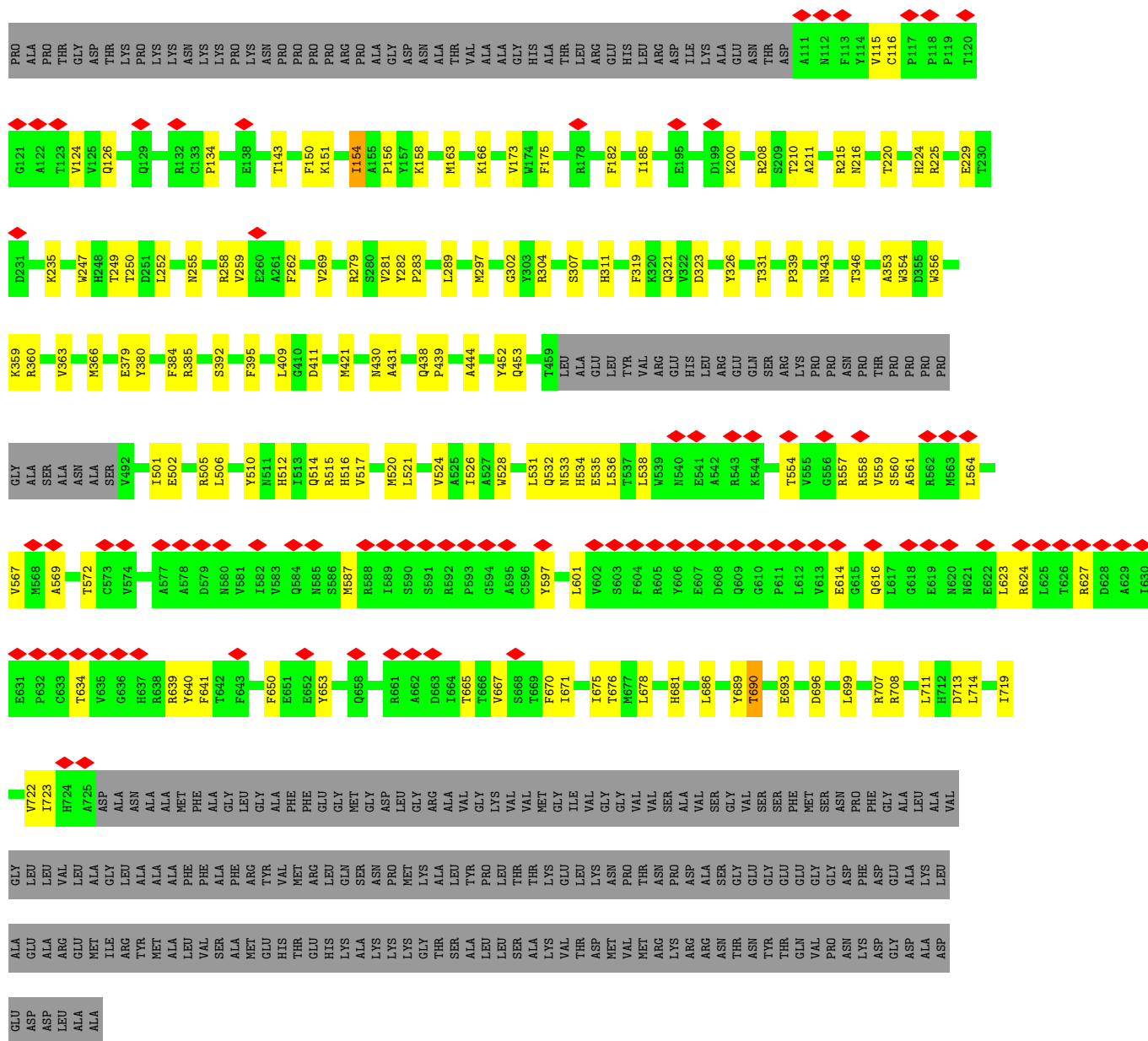
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Envelope glycoprotein B

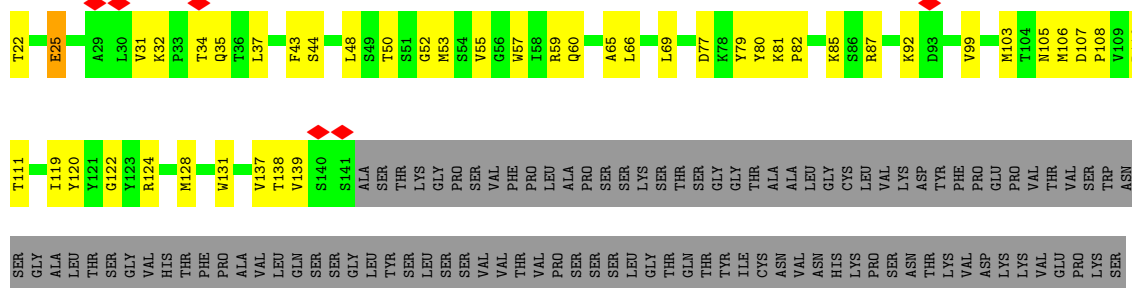


Chain B:



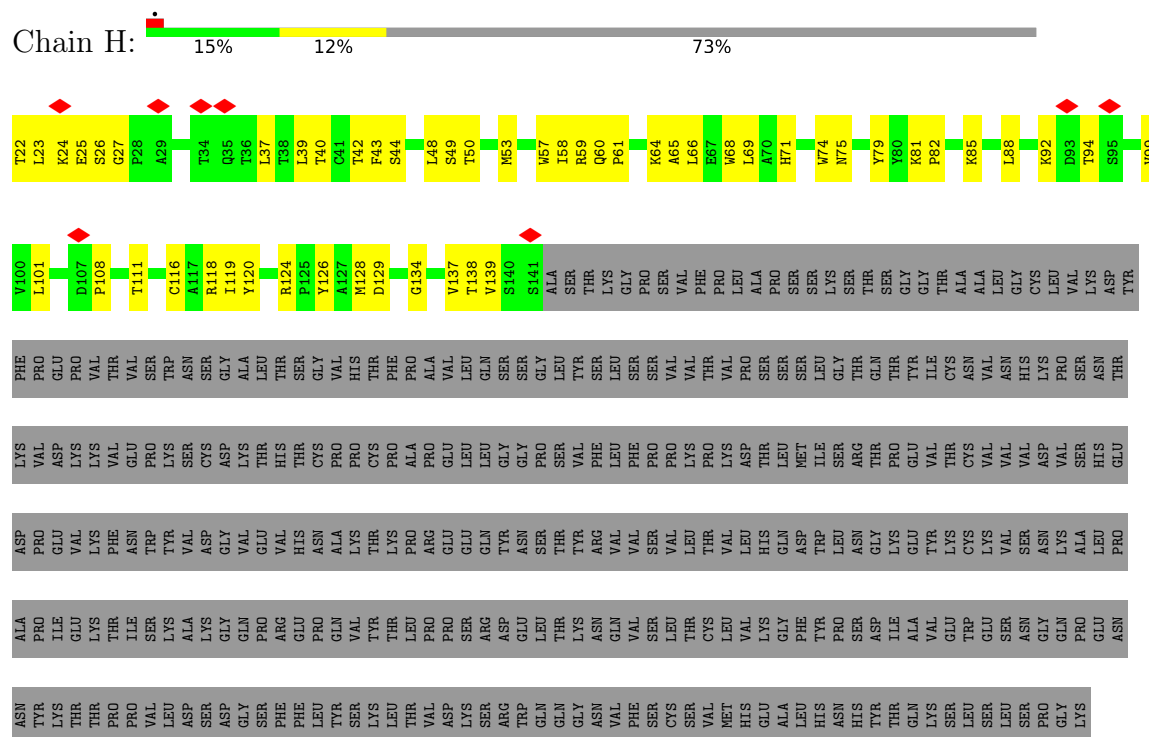


• Molecule 2: HDIT101 Fab heavy chain

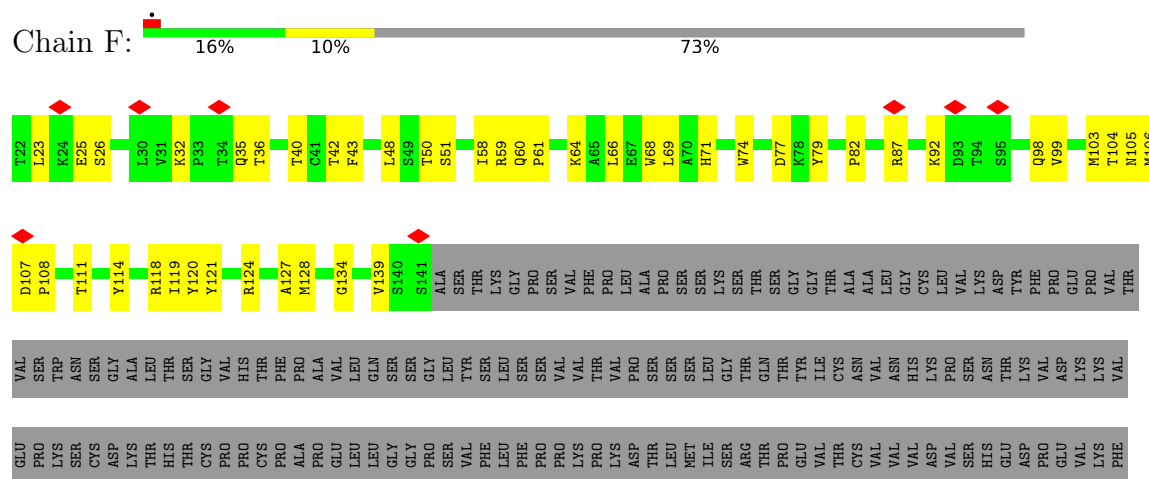


[illegible]

- Molecule 2: HDIT101 Fab heavy chain



- Molecule 2: HDIT101 Fab heavy chain



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

• Molecule 3: HDIT101 Fab light chain

Chain E: 

I21	V22	M23	T24	Q25	P31	V32	T33	E36	P37	I40	R43	S44	S45	Q46	S47	I48	V49	H50	Y60	L61	L70	Y73	S89	T96	I99	S100	R101	Y110	Y111	C112	F113	Q114	G115	S116	H117	V118	P119	W120	S121	F122	G123	Q124	K131	ARG	THR	VAL	ALA					
ALA	PRO	SER	VAL	SER	ILE	PHE	PRO	PRO	SER	ASP	GLU	GLN	LEU	LYS	GLY	THR	ALA	LYS	VAL	SER	VAL	TYR	PRO	ARG	GLU	ALA	LYS	VAL	GLN	TRP	LYS	VAL	ASN	ALA	GLN	LEU	SER	GLY	ASN	SER	GLN	SER	VAL	THR	GLU	GLN	ASP	SER	LYS	THR	VAL	SER
THR	TYR	SER	LEU	SER	SER	THR	LEU	THR	THR	SER	LYS	ALA	ASP	TYR	GLY	THR	LYS	HIS	VAL	THR	GLN	ASN	PRO	SER	GLU	VAL	THR	LYS	GLN	PHE	ASN	ARG	GLY	GLU	CYS																	

• Molecule 3: HDIT101 Fab light chain

Chain L: 

I21	V22	M23	Q25	L28	S39	I40	R43	S44	Q46	V49	T55	Y56	L57	Y60	L61	Q62	L70	Y73	R85	T93	D94	F95	T96	L97	K98	F105	D106	V109	Y110	F113	Q114	G115	P119	W120	S121	F122	G123	Q124	T126	K127	K131			
ARG	THR	VAL	ALA	PRO	SER	VAL	PHE	PRO	PRO	PRO	SER	ASP	GLU	GLN	LEU	LYS	VAL	THR	ALA	SER	VAL	VAL	CYS	LEU	LEU	ASN	ASN	PHE	THR	PRO	ARG	GLU	ALA	GLN	SER	GLY	ASN	SER	GLN	VAL	THR	GLU	GLN	ASP
SER	LYS	ASP	SER	THR	TYR	SER	LEU	LEU	THR	THR	LEU	LYS	LYS	VAL	VAL	VAL	CYS	GLY	THR	HIS	GLN	LEU	SER	PRO	VAL	THR	LYS	PHE	ASN	VAL	ASN	ALA	LEU	SER	GLY	ASN	GLN	VAL	THR	GLU	GLN	ASP		

• Molecule 3: HDIT101 Fab light chain

Chain G: 

THR	GLU	GLN	ASP	SER	LYS	ASP	SER	THR	THR	TYR	SER	LEU	SER	THR	LEU	THR	LEU	LYS	ALA	ASP	TYR	GLU	LYS	HIS	VAL	THR	ASN	PHE	GLY	LEU	SER	PRO	GLU	VAL	THR	LYS	SER	PHE	ASN	ARG	GLY	GLU	CYS										
Q124	G125	K131	ARG	THR	VAL	ALA	ALA	PRO	PRO	SER	VAL	PHE	ILE	PHE	PRO	PRO	SER	ASP	GLU	GLN	LEU	LYS	SER	GLY	THR	ALA	SER	VAL	CYS	LEU	LEU	ASN	ASN	PHE	TYR	PRO	ARG	GLU	ALA	LYS	VAL	GLN	TRP	LYS	VAL	ASP	ASN	ALA	LEU	GLN	SER	GLY	ASN
I21	V22	Q25	T33	E36	P37	I40	S44	Q46	S47	I48	V49	N52	T55	Y56	E58	M59	Y60	L61	Q62	L70	L71	I72	Y73	F79	S80	R85	F95	T96	E105	D106	Y110	Y111	C112	F113	Q114	G115	S116	H117	V118	P119	W120	S121	F122										

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23330	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.131	Depositor
Minimum map value	-0.086	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0175	Depositor
Map size (Å)	386.28, 386.28, 386.28	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2876, 1.2876, 1.2876	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	A	0.72	4/4823 (0.1%)	0.73	0/6554
1	B	0.73	5/4823 (0.1%)	0.74	2/6554 (0.0%)
1	C	0.71	4/4823 (0.1%)	0.73	1/6554 (0.0%)
2	D	0.57	0/980	0.67	0/1338
2	F	0.59	0/980	0.72	0/1338
2	H	0.63	0/980	0.71	0/1338
3	E	0.53	0/881	0.64	0/1197
3	G	0.55	1/881 (0.1%)	0.68	0/1197
3	L	0.56	0/881	0.67	0/1197
All	All	0.68	14/20052 (0.1%)	0.72	3/27267 (0.0%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	681	HIS	CE1-NE2	9.05	1.41	1.32
1	C	690	THR	C-N	8.30	1.44	1.33
1	A	681	HIS	CE1-NE2	8.03	1.40	1.32
1	A	712	HIS	CE1-NE2	7.95	1.40	1.32
1	C	681	HIS	CE1-NE2	7.03	1.39	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	719	ILE	N-CA-C	7.27	117.40	110.42
1	B	217	ASN	OD1-CG-ND2	-5.99	116.61	122.60
1	C	690	THR	O-C-N	5.53	129.09	122.79

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	4705	0	4522	135	0
1	B	4705	0	4522	142	0
1	C	4705	0	4522	141	0
2	D	952	0	939	37	0
2	F	952	0	939	35	0
2	H	952	0	939	40	0
3	E	858	0	836	26	0
3	G	858	0	836	32	0
3	L	858	0	836	23	0
All	All	19545	0	18891	479	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 12.

The worst 5 of 479 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:B:505:ARG:NH1	1:C:686:LEU:HB3	1.97	0.79
1:B:670:PHE:CE1	1:C:536:LEU:HD11	2.18	0.79
1:B:528:TRP:CH2	1:C:531:LEU:HD22	2.19	0.77
3:E:37:PRO:HA	3:E:99:ILE:O	1.85	0.76
1:B:539:TRP:HZ2	1:C:534:HIS:CD2	2.03	0.76

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	579/906 (64%)	563 (97%)	16 (3%)	0	100	100
1	B	579/906 (64%)	567 (98%)	12 (2%)	0	100	100
1	C	579/906 (64%)	564 (97%)	15 (3%)	0	100	100
2	D	118/450 (26%)	116 (98%)	2 (2%)	0	100	100
2	F	118/450 (26%)	113 (96%)	5 (4%)	0	100	100
2	H	118/450 (26%)	114 (97%)	4 (3%)	0	100	100
3	E	109/218 (50%)	107 (98%)	2 (2%)	0	100	100
3	G	109/218 (50%)	106 (97%)	3 (3%)	0	100	100
3	L	109/218 (50%)	106 (97%)	3 (3%)	0	100	100
All	All	2418/4722 (51%)	2356 (97%)	62 (3%)	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	A	506/745 (68%)	504 (100%)	2 (0%)	84	85
1	B	506/745 (68%)	506 (100%)	0	100	100
1	C	506/745 (68%)	505 (100%)	1 (0%)	87	88
2	D	105/404 (26%)	104 (99%)	1 (1%)	68	77
2	F	105/404 (26%)	105 (100%)	0	100	100
2	H	105/404 (26%)	105 (100%)	0	100	100
3	E	98/194 (50%)	98 (100%)	0	100	100
3	G	98/194 (50%)	98 (100%)	0	100	100
3	L	98/194 (50%)	98 (100%)	0	100	100
All	All	2127/4029 (53%)	2123 (100%)	4 (0%)	85	88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	124	VAL
1	A	678	LEU
2	D	25	GLU
1	C	154	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	217	ASN
1	B	532	GLN
1	C	709	ASN
1	B	514	GLN
1	C	172	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 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.

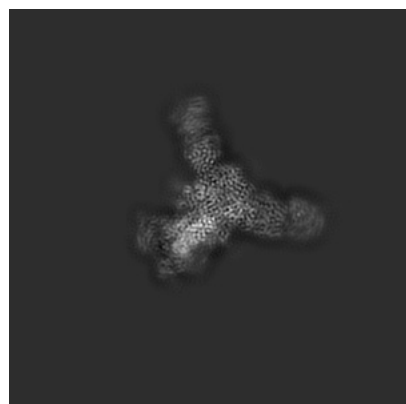
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19163. These allow visual inspection of the internal detail of the map and identification of artifacts.

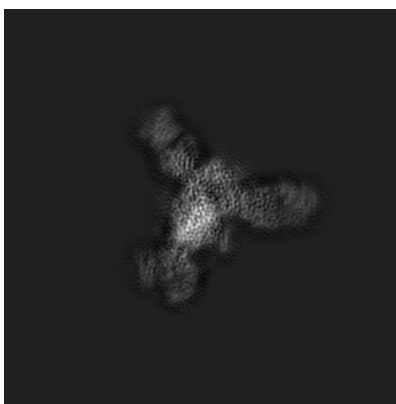
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

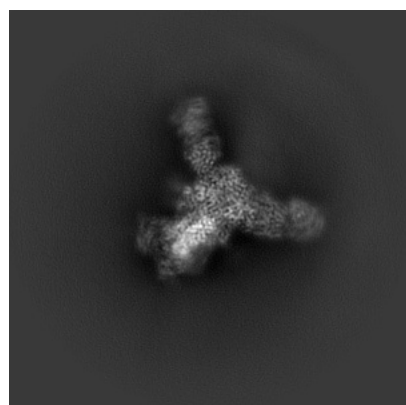


Y

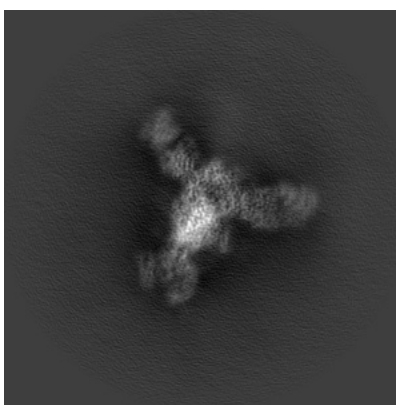


Z

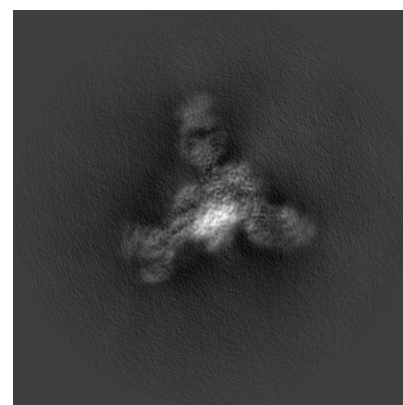
6.1.2 Raw map



X



Y

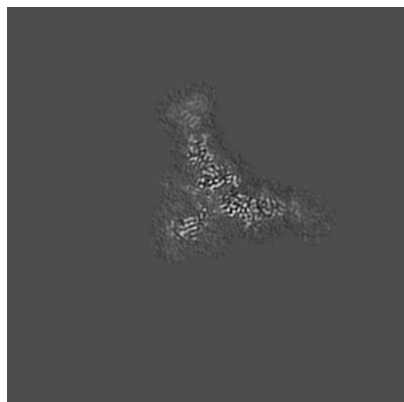


Z

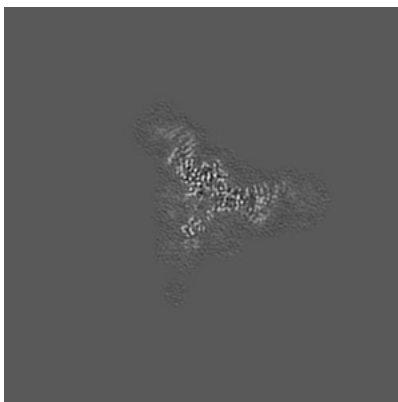
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

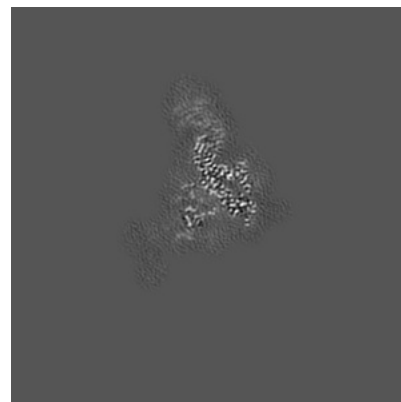
6.2.1 Primary map



X Index: 150

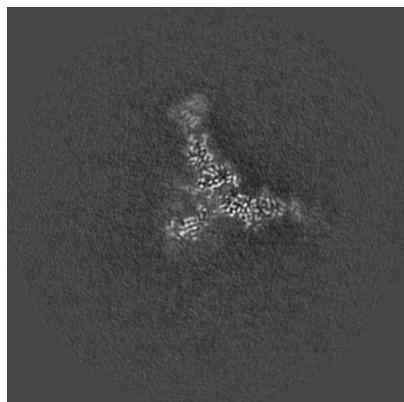


Y Index: 150

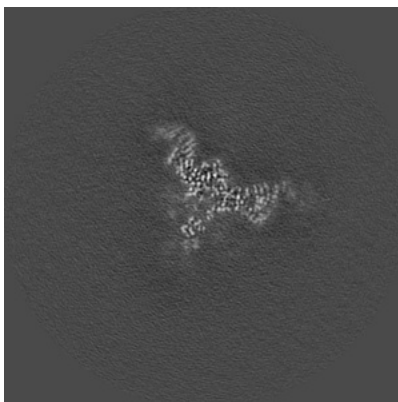


Z Index: 150

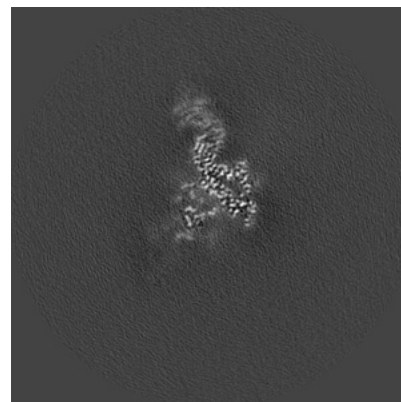
6.2.2 Raw map



X Index: 150



Y Index: 150

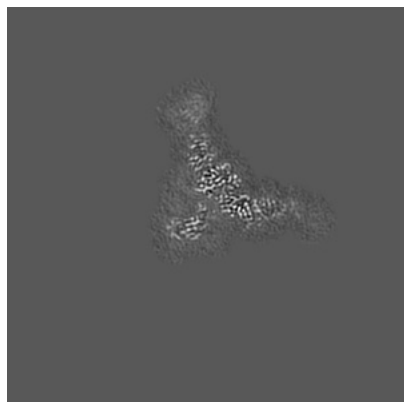


Z Index: 150

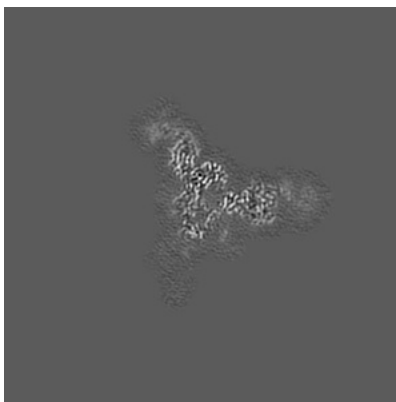
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

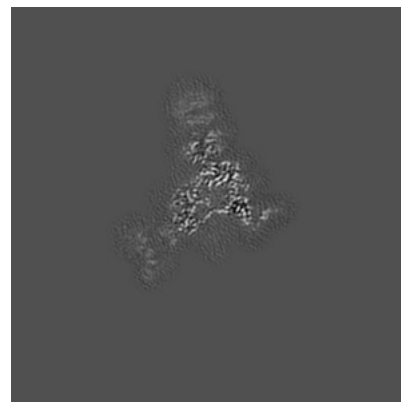
6.3.1 Primary map



X Index: 151

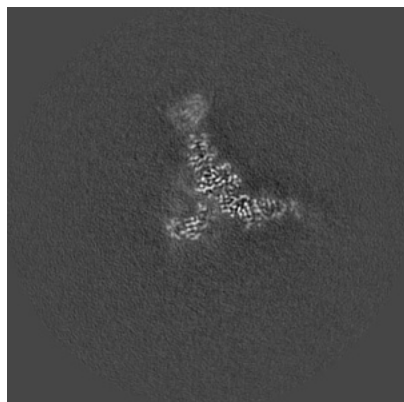


Y Index: 146

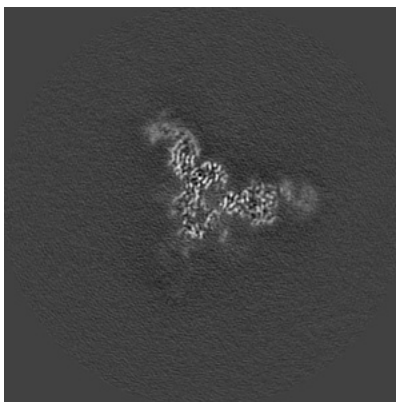


Z Index: 144

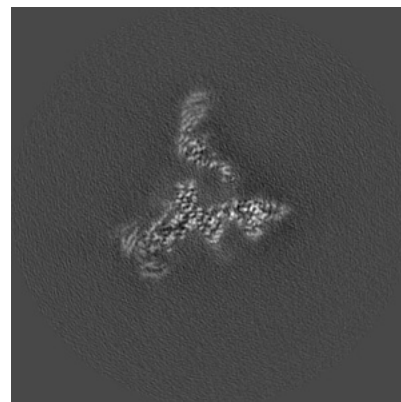
6.3.2 Raw map



X Index: 151



Y Index: 146

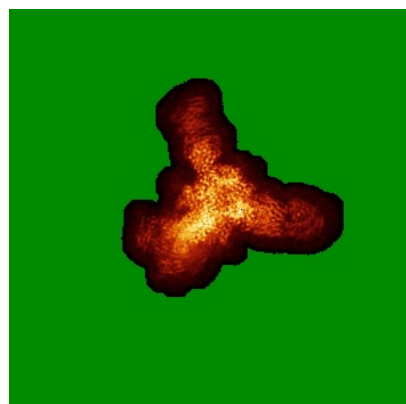


Z Index: 137

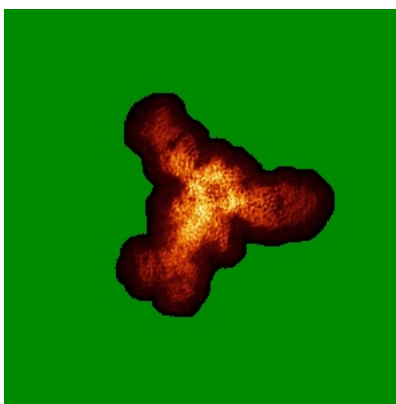
The images above show the largest variance slices of the map in three orthogonal directions.

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

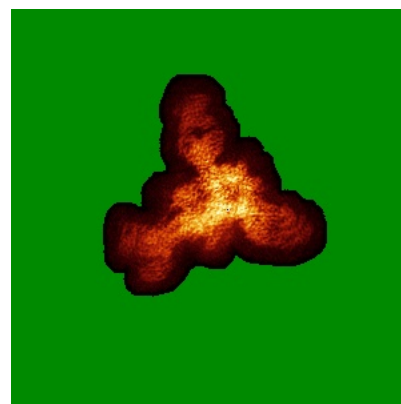
6.4.1 Primary map



X

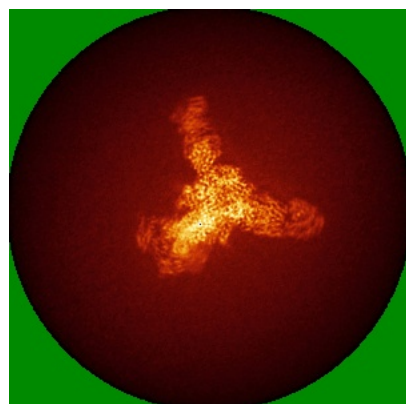


Y

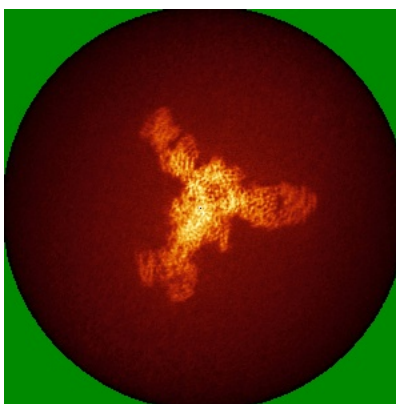


Z

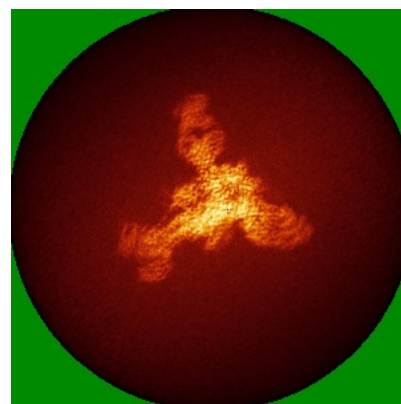
6.4.2 Raw map



X



Y

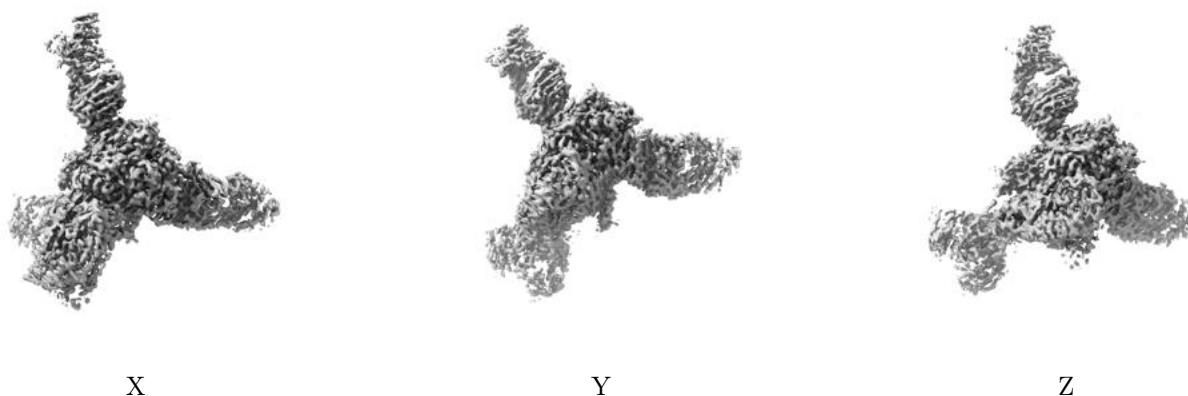


Z

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.

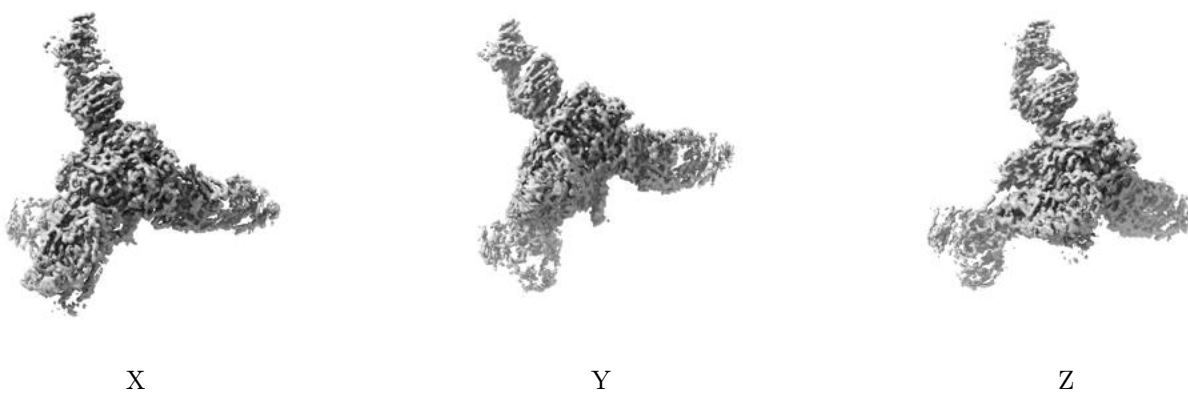
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0175. 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.

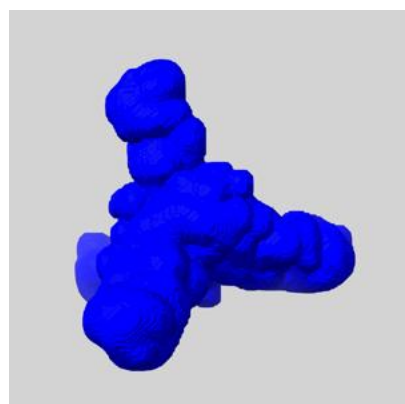
6.6 Mask visualisation [i](#)

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

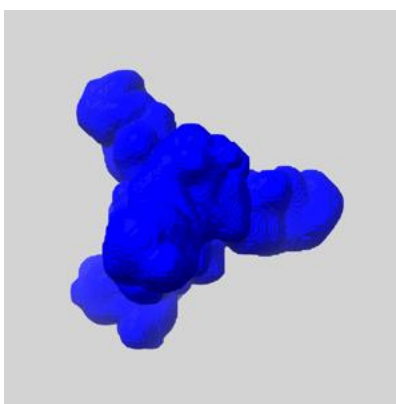
A mask typically either:

- 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_19163_msk_1.map [i](#)



X



Y

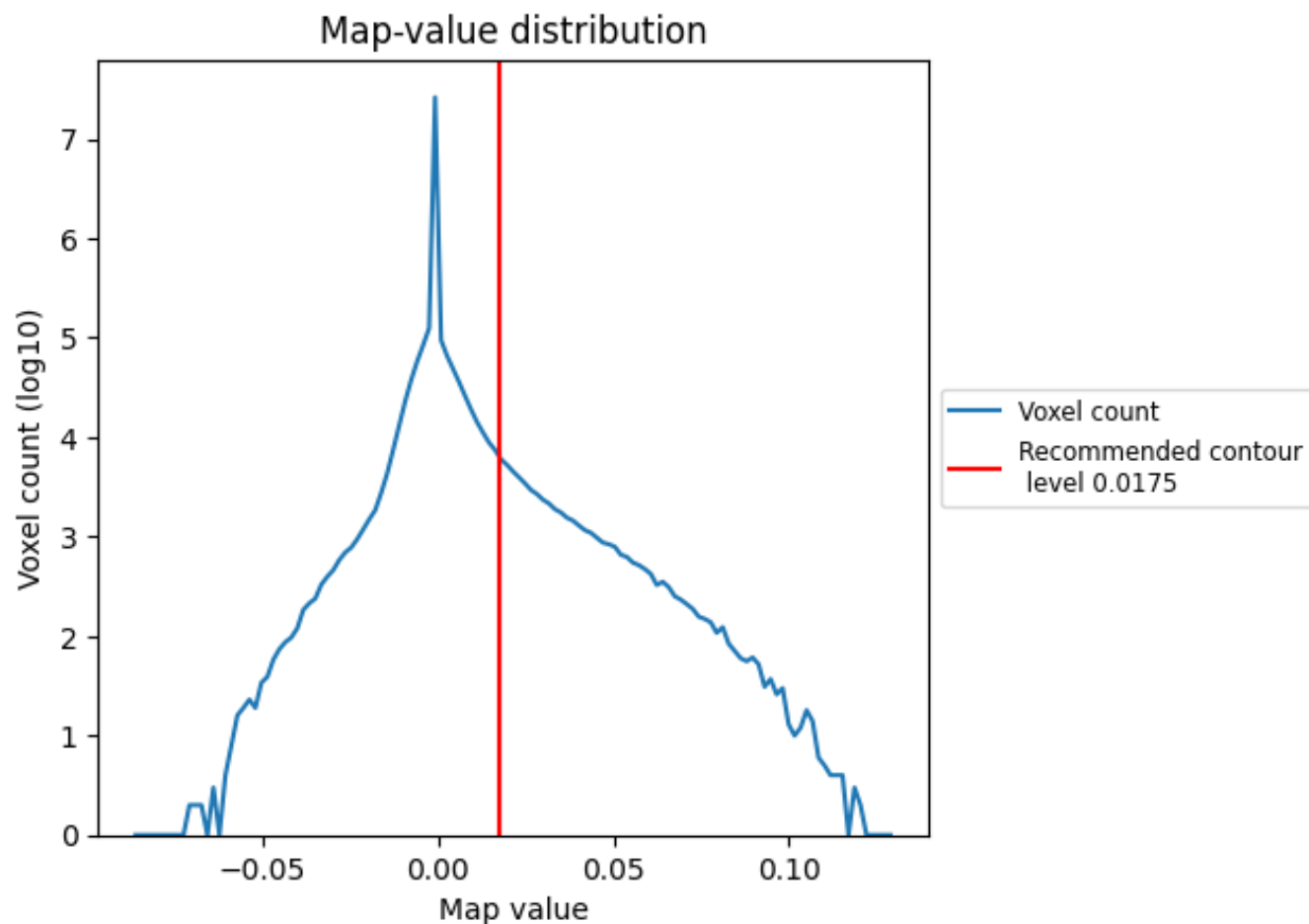


Z

7 Map analysis [i](#)

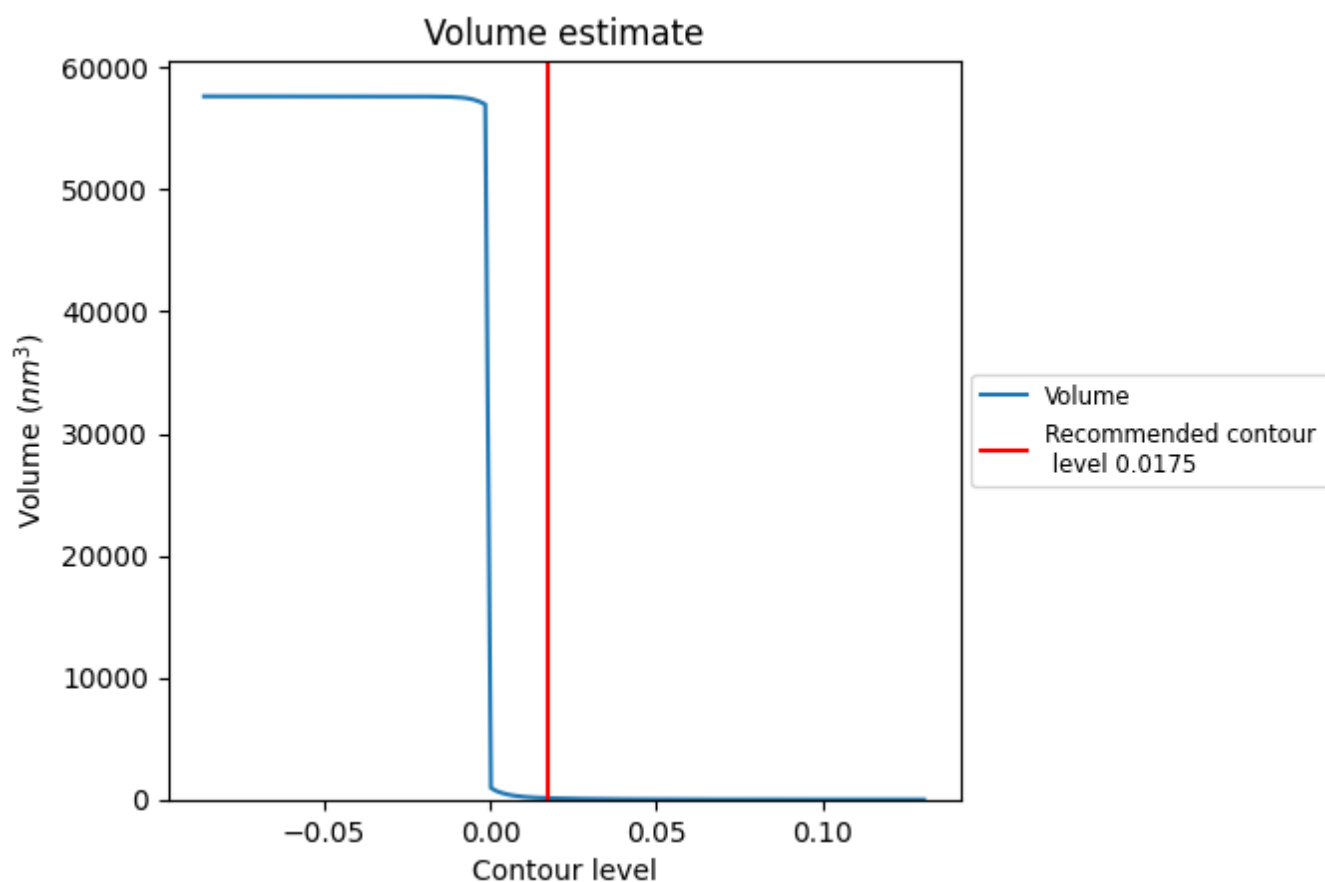
This section contains the results of statistical analysis of the map.

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.

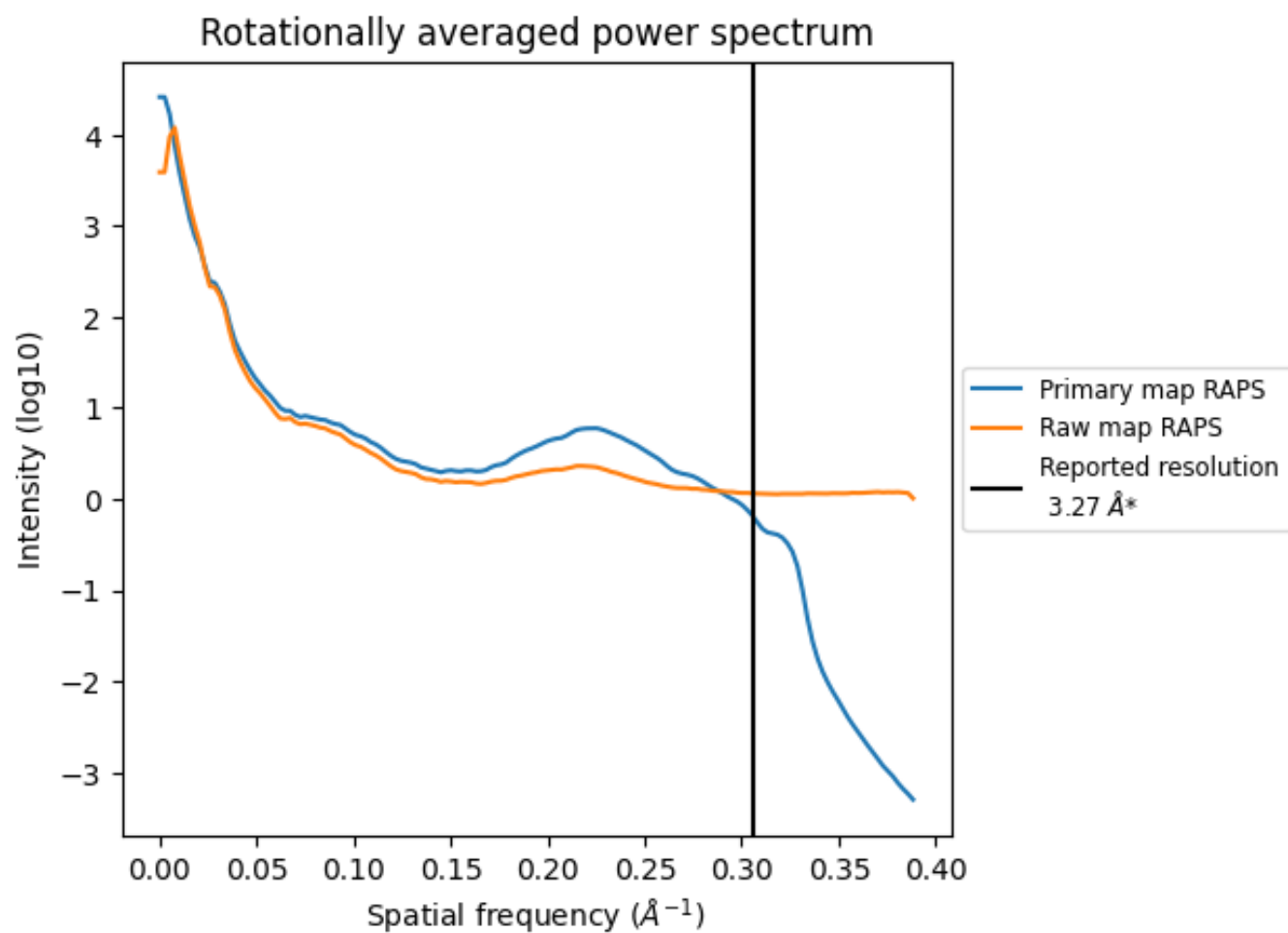
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 118 nm³; this corresponds to an approximate mass of 107 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 ⓘ

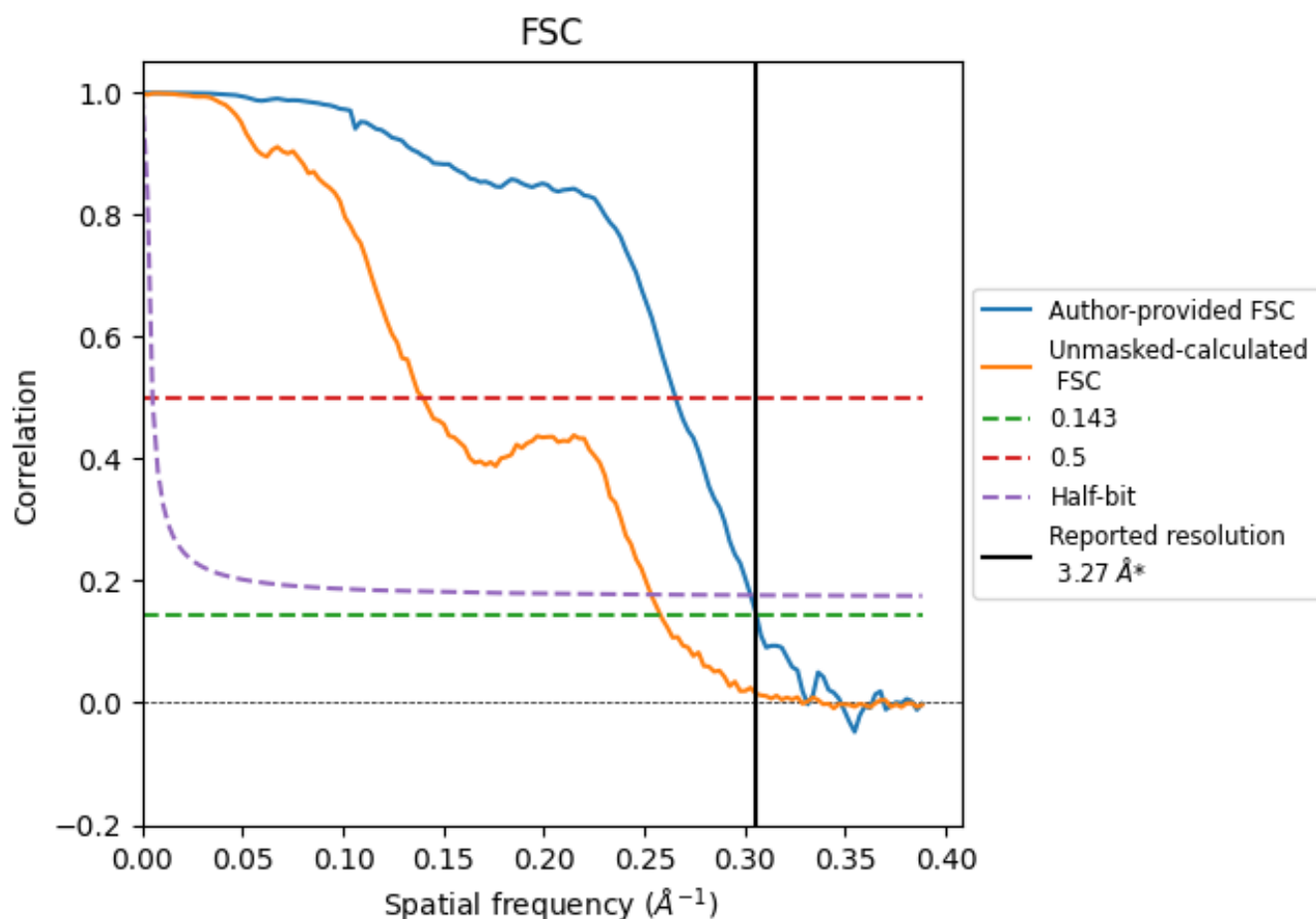


*Reported resolution corresponds to spatial frequency of 0.306 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.306 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

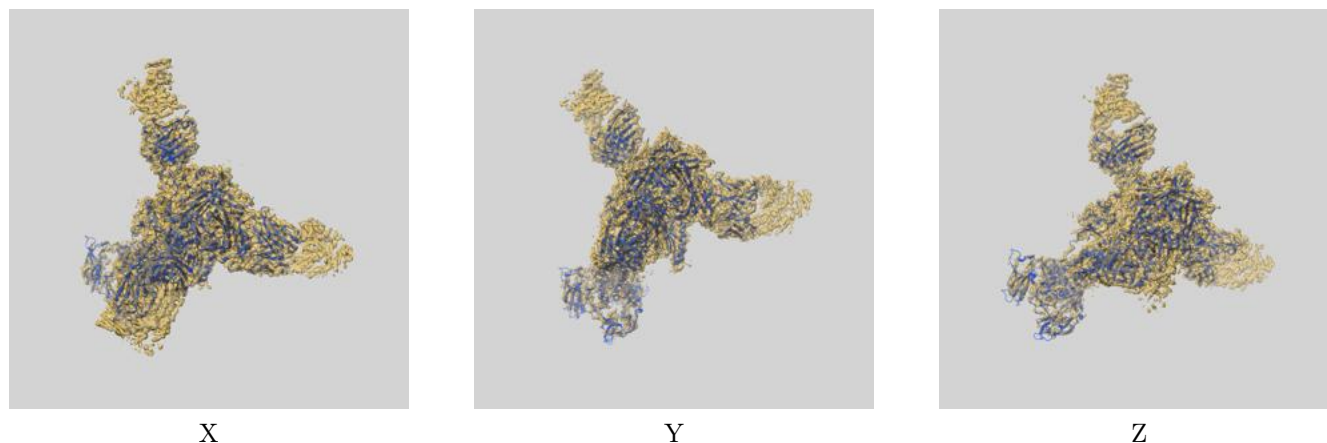
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.27	-	-
Author-provided FSC curve	3.27	3.77	3.30
Unmasked-calculated*	3.87	7.15	3.95

*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 3.87 differs from the reported value 3.27 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19163 and PDB model 8RGZ. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



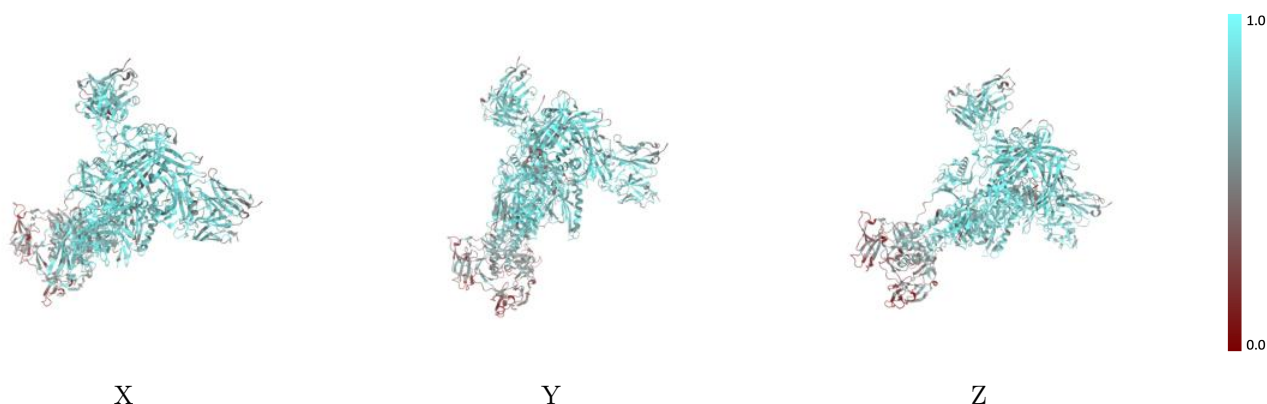
The images above show the 3D surface view of the map at the recommended contour level 0.0175 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



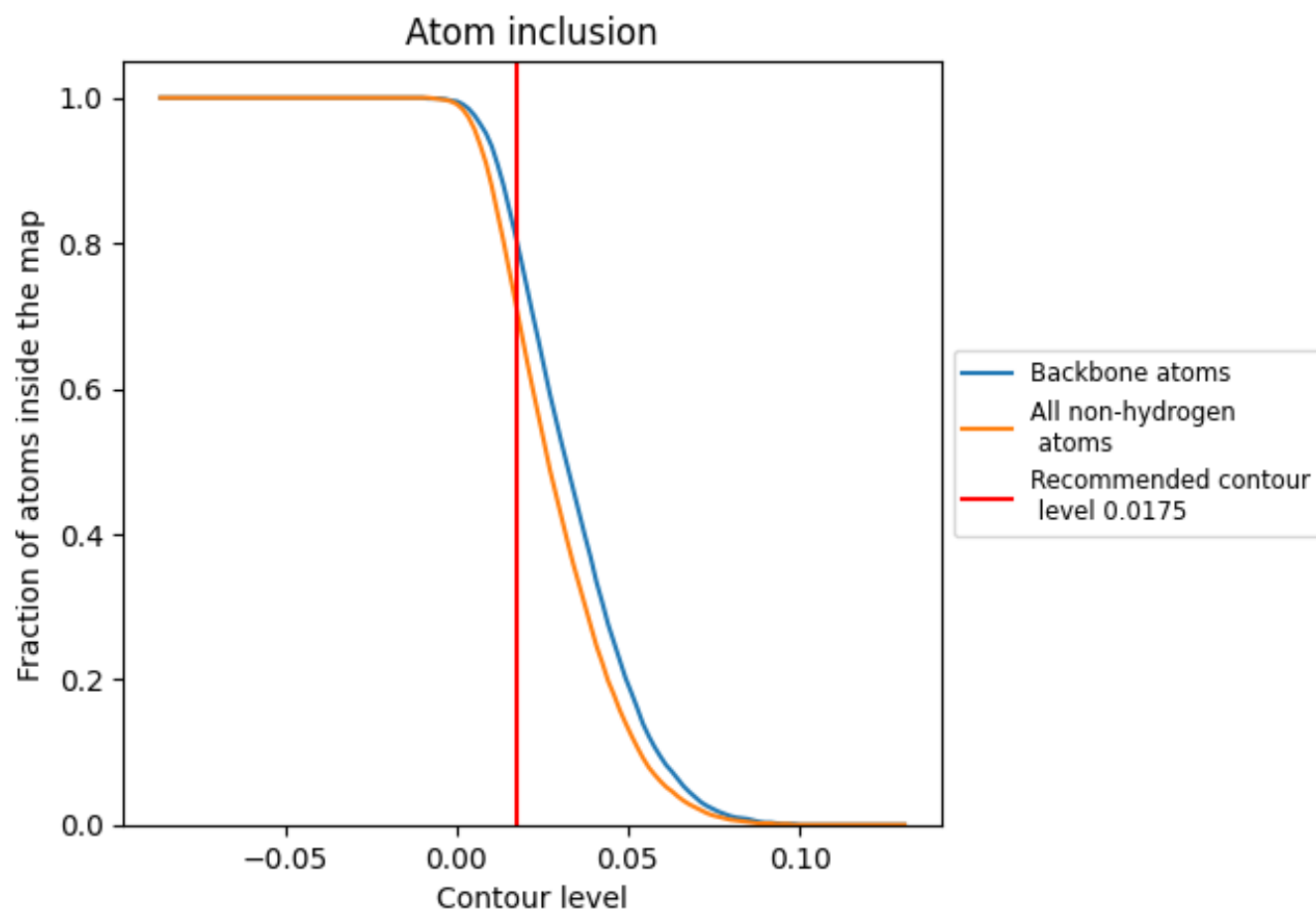
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0175).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 71% 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 (0.0175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7120	0.4940
A	0.7000	0.4930
B	0.6970	0.4910
C	0.6980	0.4920
D	0.7430	0.5070
E	0.7580	0.4990
F	0.7190	0.4950
G	0.7370	0.4960
H	0.7530	0.5050
L	0.7770	0.5020

1.0

0.0

<0.0