



wwPDB EM Validation Summary Report ⓘ

Jun 1, 2026 – 06:53 PM EDT

PDB ID : 9YFT / pdb_00009yft
EMDB ID : EMD-72905
Title : N4 Bacteriophage Asymmetric Tail Gating Complex
Authors : Bellis, N.F.; Cingolani, G.
Deposited on : 2025-09-26
Resolution : 3.61 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:

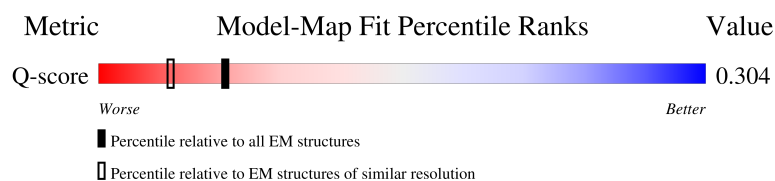
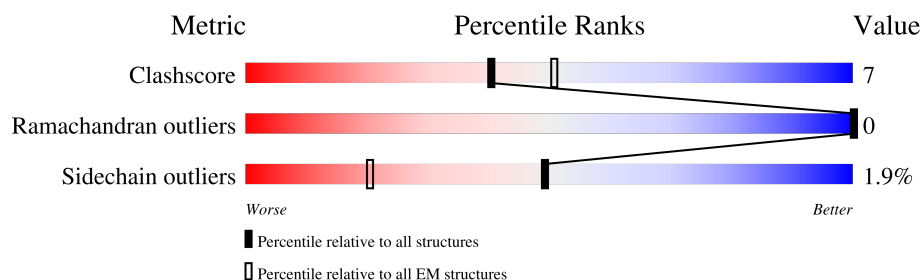
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.61 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	11801 (3.11 - 4.10)

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	FA	885	<p>9% 65% 16% 19%</p>
2	LA	1382	<p>17% 5% 78%</p>
3	TA	299	<p>19% 77%</p>
3	TB	299	<p>19% 77%</p>

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Mol	Chain	Length	Quality of chain
3	TC	299	 19% 77%
3	TD	299	 19% 77%
3	TE	299	 19% 77%
3	TF	299	 20% 77%
3	TG	299	 20% 77%
3	TH	299	 20% 77%
3	TI	299	 19% 77%
3	TJ	299	 19% 77%
3	TK	299	 19% 77%
3	TL	299	 19% 77%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14173 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 Gp53.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	FA	716	Total	C	N	O	S	0	0
			5606	3568	926	1093	19		

- Molecule 2 is a protein called Non-contractile tail sheath.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LA	300	Total	C	N	O	S	0	0
			2315	1456	388	462	9		

- Molecule 3 is a protein called Gp54.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	TA	68	Total	C	N	O	0	0
			521	325	88	108		
3	TB	68	Total	C	N	O	0	0
			521	325	88	108		
3	TC	68	Total	C	N	O	0	0
			521	325	88	108		
3	TD	68	Total	C	N	O	0	0
			521	325	88	108		
3	TE	68	Total	C	N	O	0	0
			521	325	88	108		
3	TF	68	Total	C	N	O	0	0
			521	325	88	108		
3	TG	68	Total	C	N	O	0	0
			521	325	88	108		
3	TH	68	Total	C	N	O	0	0
			521	325	88	108		
3	TI	68	Total	C	N	O	0	0
			521	325	88	108		
3	TJ	68	Total	C	N	O	0	0
			521	325	88	108		
3	TK	68	Total	C	N	O	0	0
			521	325	88	108		

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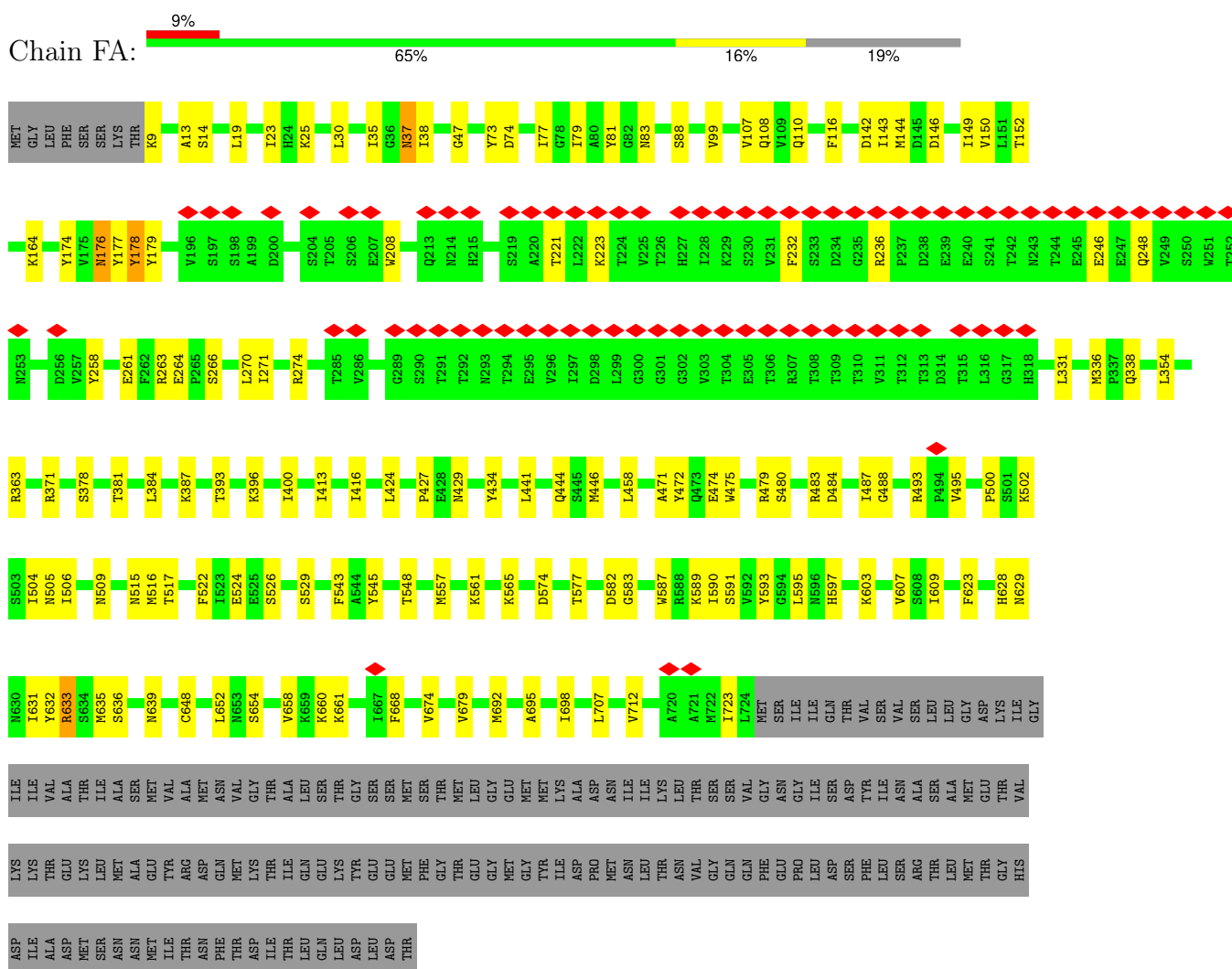
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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	TL	68	521	325	88	108	0	0

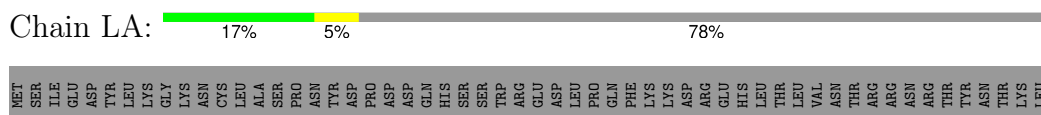
3 Residue-property plots

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.

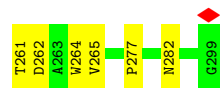
• Molecule 1: Gp53



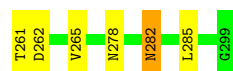
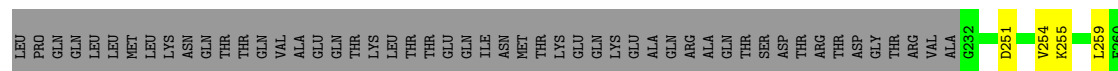
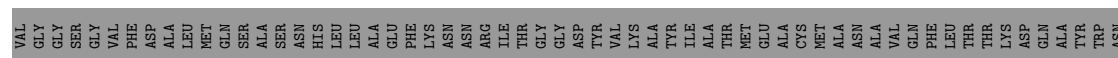
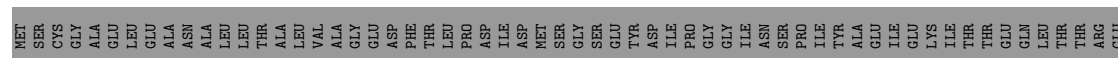
• Molecule 2: Non-contractile tail sheath



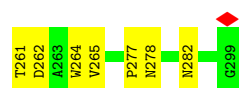
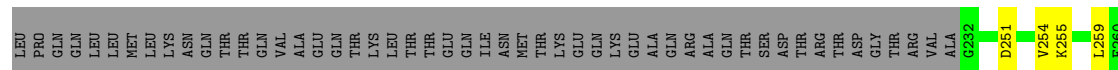
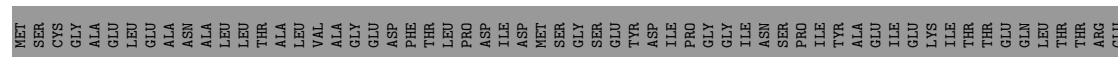




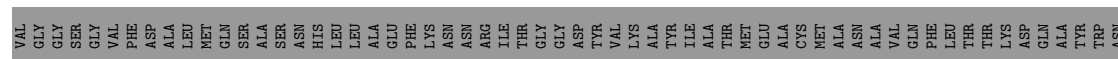
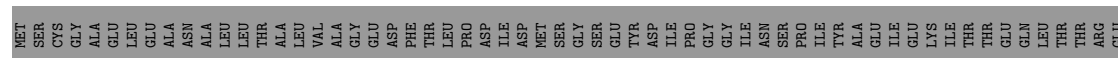
- Molecule 3: Gp54

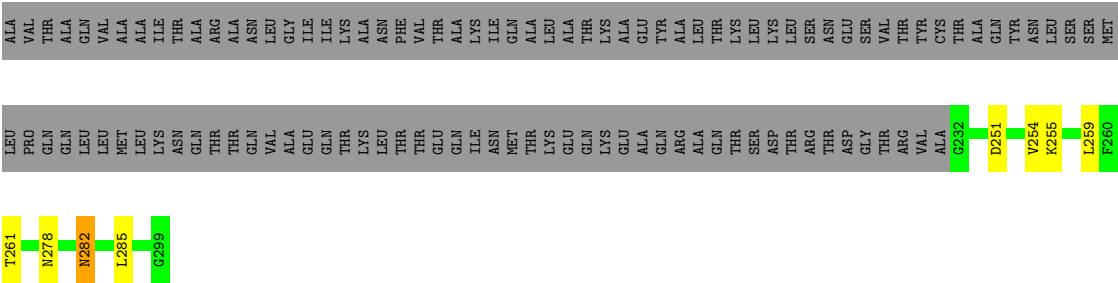


- Molecule 3: Gp54

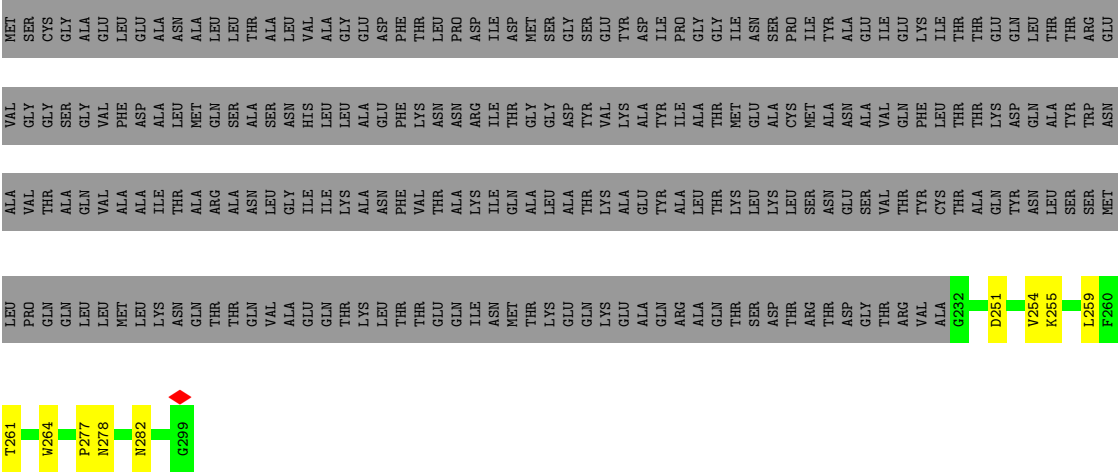


- Molecule 3: Gp54





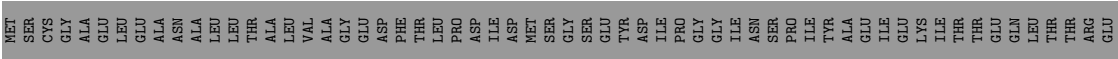
• Molecule 3: Gp54



• Molecule 3: Gp54



• Molecule 3: Gp54



T261	LEU	ALA	VAL	MET
D262	PRO	THR	GLY	GLY
V265	GLN	THR	SER	CYS
M278	LEU	GLN	GLY	ALA
N282	LEU	VAL	VAL	GLU
L285	MET	ALA	PHE	LEU
G299	LYS	ALA	ASP	GLU
	ASN	THR	ALA	ALA
	GLN	ILE	LEU	ASN
	THR	ALA	MET	ALA
	THR	ARG	GLN	LEU
	GLN	ASN	SER	LEU
	VAL	LEU	ALA	THR
	ALA	GLY	SER	ALA
	GLU	ILE	ASN	VAL
	GLN	ILE	LEU	ALA
	THR	ALA	LEU	GLY
	LYS	ALA	ASP	GLU
	LEU	PHE	THR	ASP
	THR	VAL	LYS	THR
	GLU	THR	ASN	LEU
	GLN	THR	ASN	PRO
	ILE	ALA	ARG	ASP
	ASN	ILE	ILE	ASP
	MET	GLN	THR	MET
	THR	ALA	GLY	SER
	LYS	LEU	GLY	SER
	GLU	ALA	ASP	GLY
	GLN	THR	VAL	GLU
	ALA	ALA	THR	ILE
	ARG	LEU	ILE	PRO
	ALA	THR	THR	GLY
	GLN	LYS	THR	GLY
	THR	LYS	MET	ILE
	SER	LEU	GLU	ASN
	ASP	LYS	ALA	SER
	THR	LEU	CYS	PRO
	ARG	SER	MET	ILE
	THR	ASN	ALA	TYR
	ASP	GLU	ASN	ALA
	GLY	SER	ALA	GLU
	THR	VAL	VAL	ILE
	ARG	THR	GLN	GLU
	VAL	TYR	PHE	LYS
	ALA	THR	LEU	ILE
		THR	THR	THR
		ALA	THR	THR
		GLN	LYS	GLU
		TYR	ASP	GLN
		ASN	GLN	LEU
		ASN	ALA	THR
		SER	TYR	THR
		SER	ALA	THR
		MET	TRP	CYS
			ASN	GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18434	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.749	Depositor
Minimum map value	-0.428	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.115	Depositor
Map size (Å)	266.262, 268.65, 657.894	wwPDB
Map dimensions	551, 225, 223	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.194, 1.194, 1.194	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	FA	0.09	0/5736	0.29	0/7798
2	LA	0.08	0/2369	0.28	0/3233
3	TA	0.09	0/528	0.23	0/712
3	TB	0.09	0/528	0.23	0/712
3	TC	0.09	0/528	0.23	0/712
3	TD	0.09	0/528	0.23	0/712
3	TE	0.09	0/528	0.23	0/712
3	TF	0.09	0/528	0.23	0/712
3	TG	0.09	0/528	0.23	0/712
3	TH	0.09	0/528	0.23	0/712
3	TI	0.09	0/528	0.23	0/712
3	TJ	0.09	0/528	0.23	0/712
3	TK	0.09	0/528	0.23	0/712
3	TL	0.09	0/528	0.23	0/712
All	All	0.09	0/14441	0.26	0/19575

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 [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	FA	5606	0	5480	85	0
2	LA	2315	0	2209	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	TA	521	0	517	8	0
3	TB	521	0	517	9	0
3	TC	521	0	517	8	0
3	TD	521	0	517	8	0
3	TE	521	0	517	8	0
3	TF	521	0	517	7	0
3	TG	521	0	517	7	0
3	TH	521	0	517	8	0
3	TI	521	0	517	9	0
3	TJ	521	0	517	10	0
3	TK	521	0	517	8	0
3	TL	521	0	517	8	0
All	All	14173	0	13893	195	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 7.

The worst 5 of 195 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LA:1177:THR:OG1	3:TI:282:ASN:ND2	2.21	0.74
1:FA:144:MET:HG2	1:FA:146:ASP:H	1.53	0.72
1:FA:413:ILE:HD13	1:FA:652:LEU:HD23	1.76	0.68
1:FA:529:SER:O	1:FA:587:TRP:NE1	2.28	0.66
2:LA:1347:THR:HA	2:LA:1351:GLY:HA2	1.78	0.66

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	FA	714/885 (81%)	673 (94%)	41 (6%)	0	100	100
2	LA	298/1382 (22%)	280 (94%)	18 (6%)	0	100	100
3	TA	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TB	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TC	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TD	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TE	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TF	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TG	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TH	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TI	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TJ	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TK	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
3	TL	66/299 (22%)	65 (98%)	1 (2%)	0	100	100
All	All	1804/5855 (31%)	1733 (96%)	71 (4%)	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	FA	616/763 (81%)	603 (98%)	13 (2%)	47	62
2	LA	251/1155 (22%)	247 (98%)	4 (2%)	55	66
3	TA	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TB	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TC	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TD	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TE	57/244 (23%)	56 (98%)	1 (2%)	51	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	TF	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TG	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TH	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TI	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TJ	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TK	57/244 (23%)	56 (98%)	1 (2%)	51	65
3	TL	57/244 (23%)	56 (98%)	1 (2%)	51	65
All	All	1551/4846 (32%)	1522 (98%)	29 (2%)	49	64

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	LA	1124	VAL
3	TK	282	ASN
3	TA	282	ASN
3	TH	282	ASN
2	LA	1350	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
3	TC	296	ASN
3	TK	296	ASN
3	TE	296	ASN
3	TL	296	ASN
3	TI	296	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 [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-72905. These allow visual inspection of the internal detail of the map and identification of artifacts.

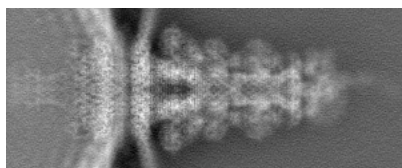
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

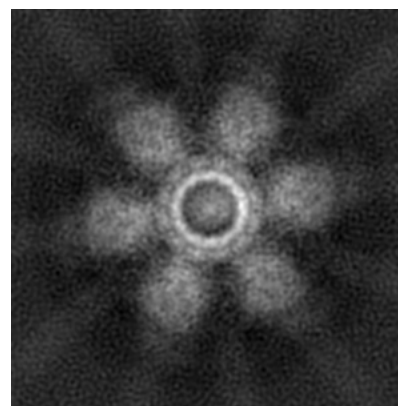
6.1.1 Primary map



X

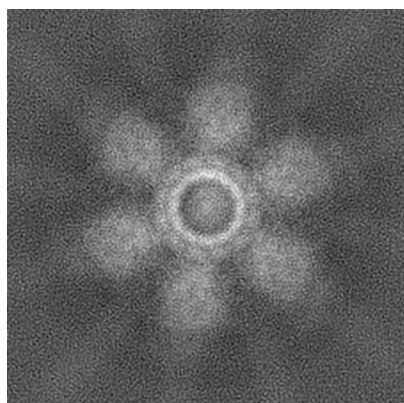


Y



Z

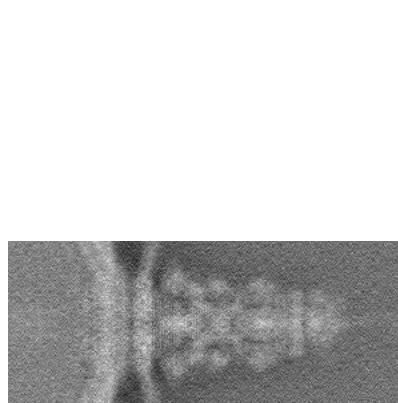
6.1.2 Raw map



X



Y

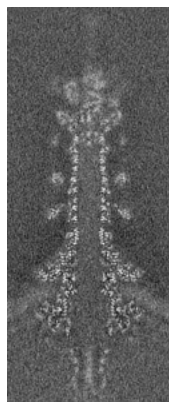


Z

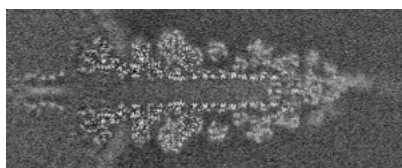
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

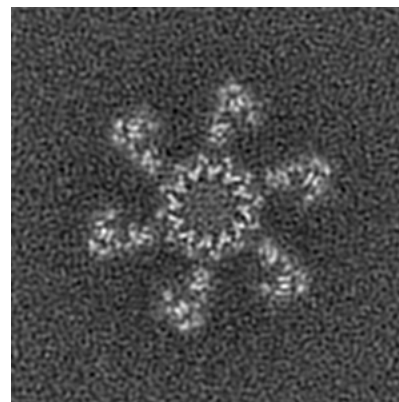
6.2.1 Primary map



X Index: 111

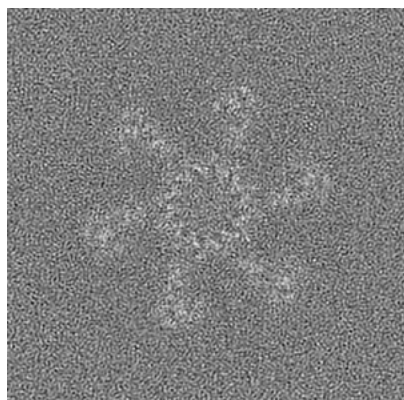


Y Index: 112

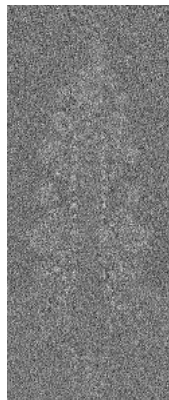


Z Index: 275

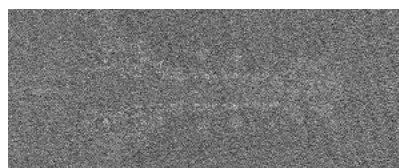
6.2.2 Raw map



X Index: 275



Y Index: 112



Z Index: 111

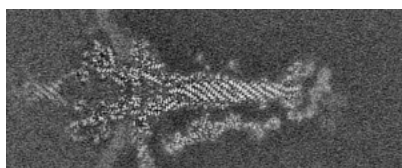
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

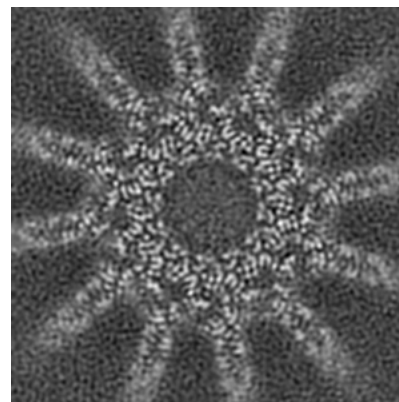
6.3.1 Primary map



X Index: 129

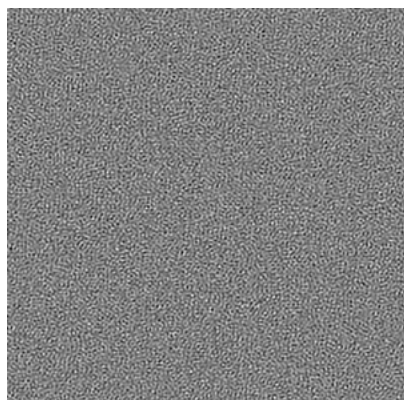


Y Index: 94

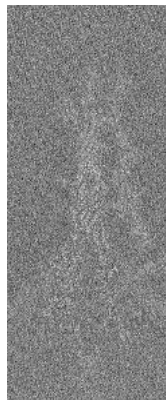


Z Index: 189

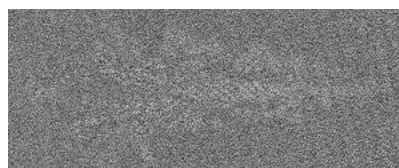
6.3.2 Raw map



X Index: 544



Y Index: 129



Z Index: 129

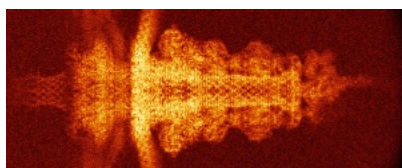
The images above show the largest variance slices of the map in three orthogonal directions.

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

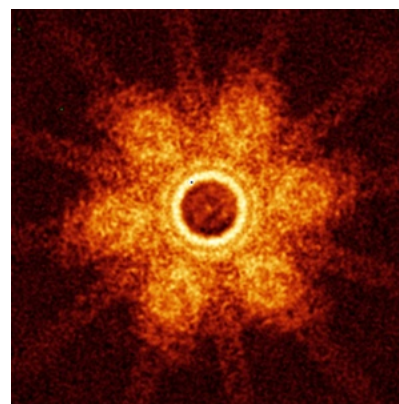
6.4.1 Primary map



X

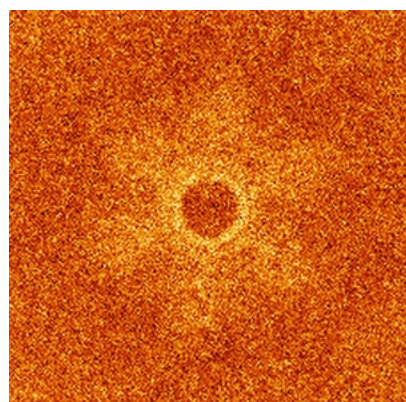


Y



Z

6.4.2 Raw map



X



Y



Z

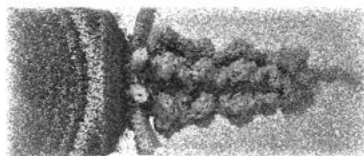
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

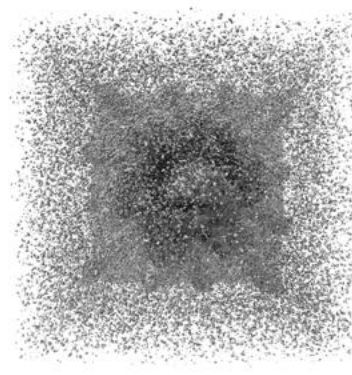
6.5.1 Primary map



X



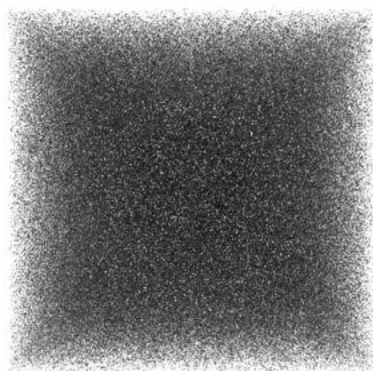
Y



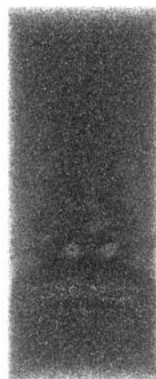
Z

The images above show the 3D surface view of the map at the recommended contour level 0.115. 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

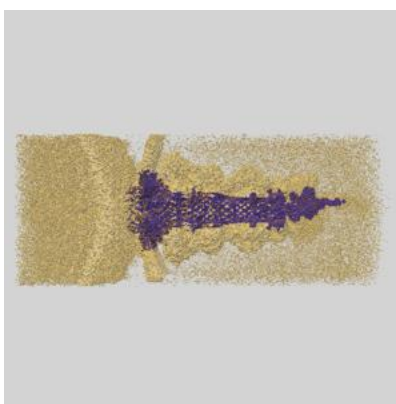
A mask typically either:

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

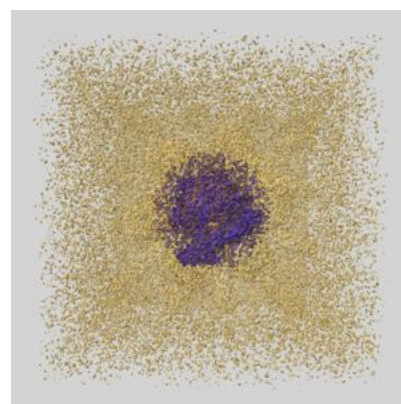
6.6.1 emd_72905_msk_1.map [i](#)



X



Y

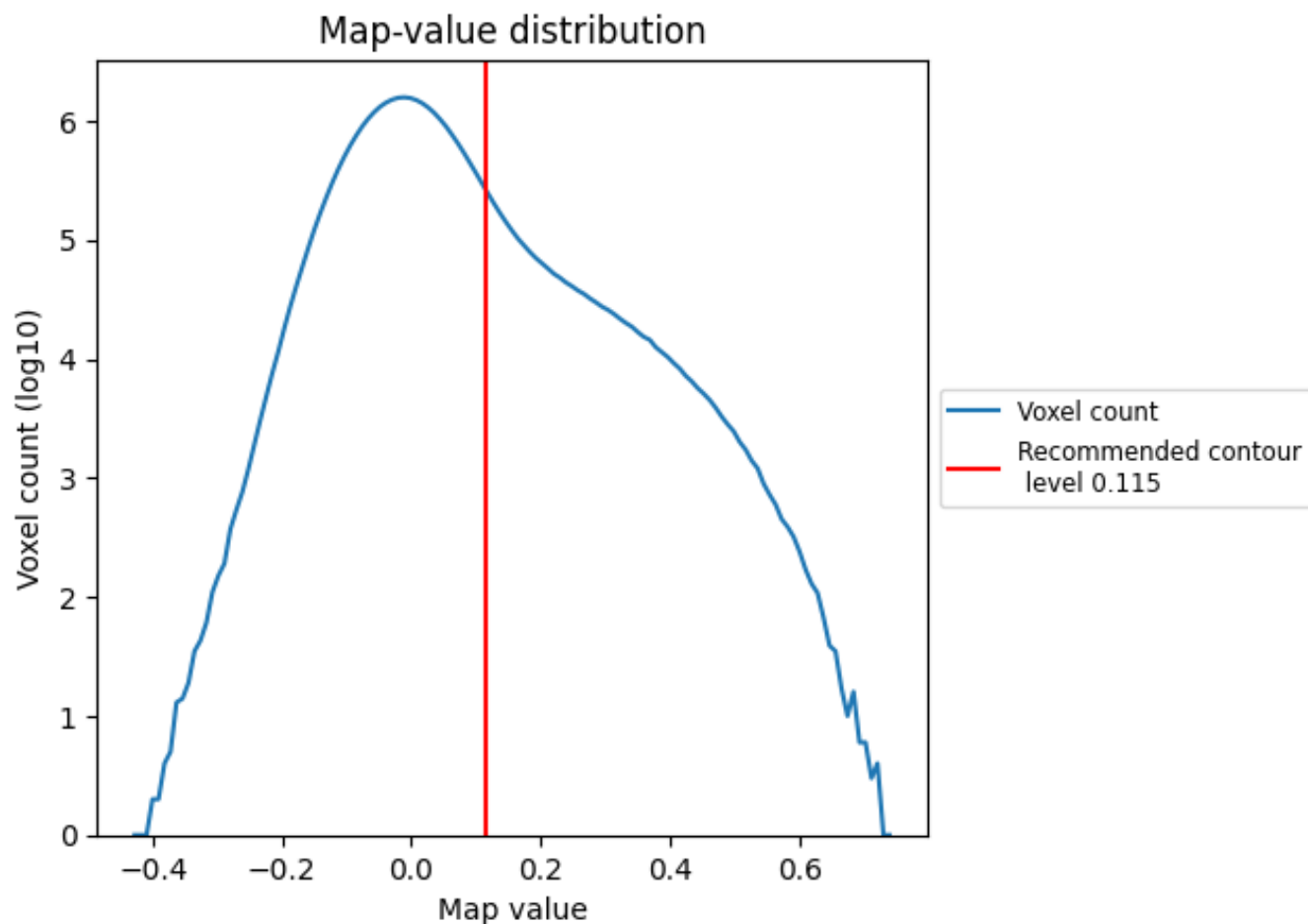


Z

7 Map analysis [i](#)

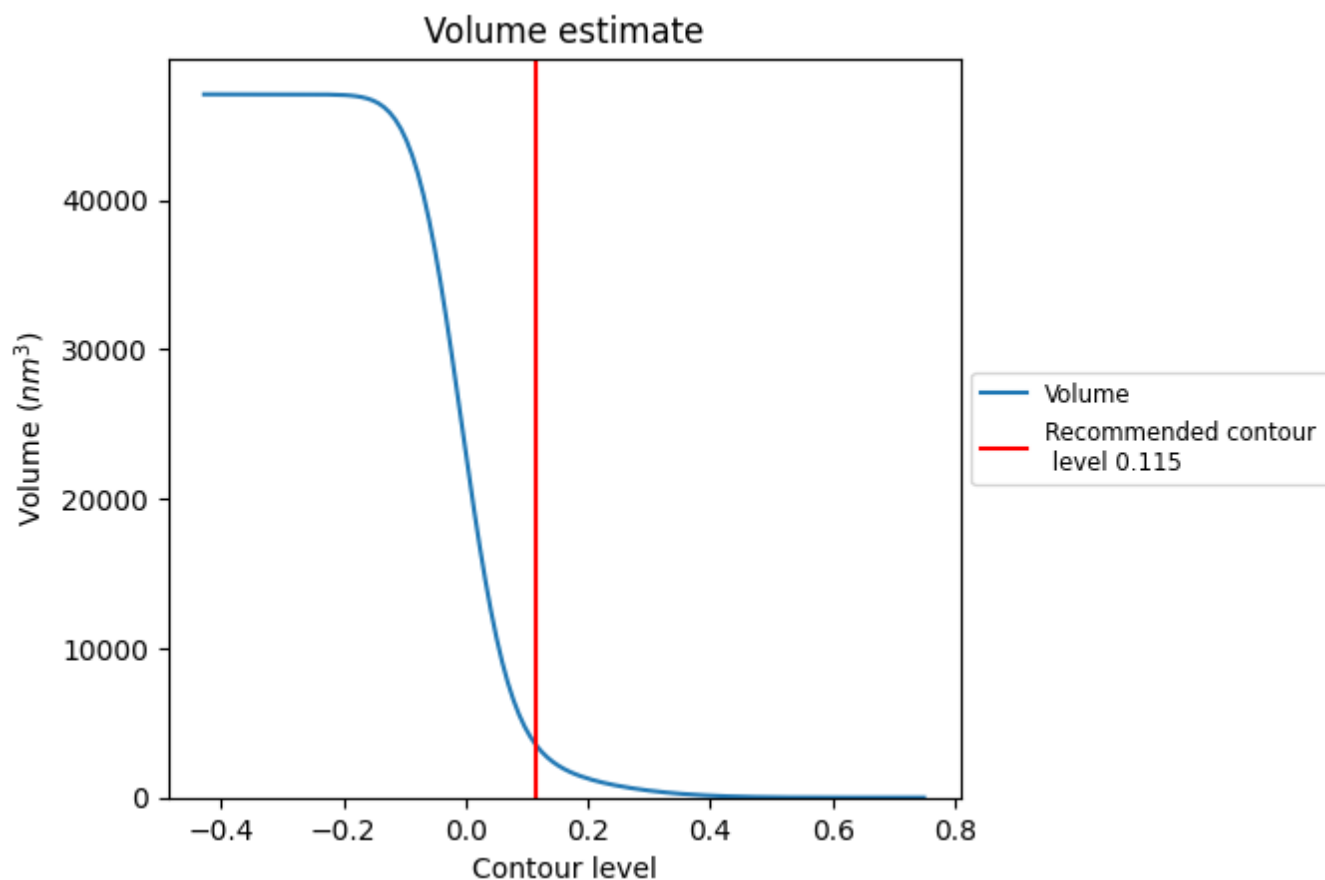
This section contains the results of statistical analysis of the map.

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 3505 nm³; this corresponds to an approximate mass of 3166 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

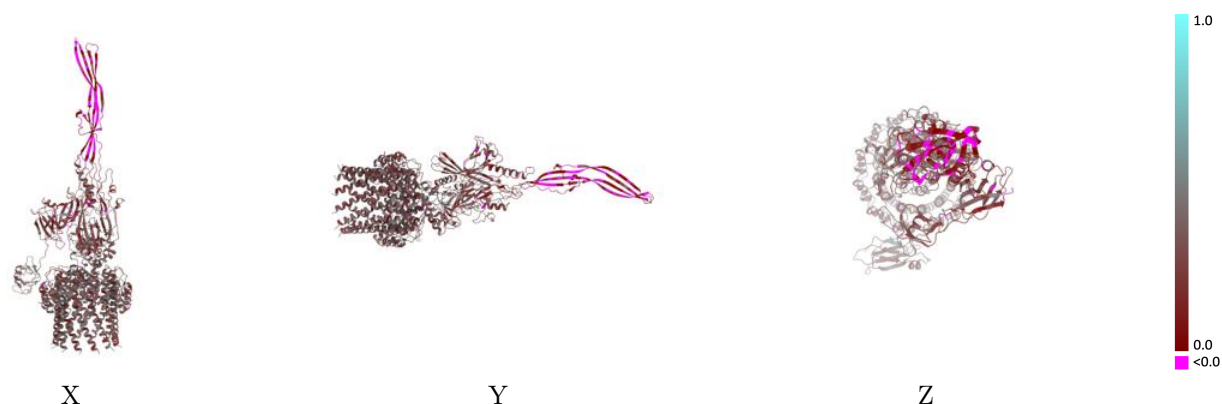
This section contains information regarding the fit between EMDB map EMD-72905 and PDB model 9YFT. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



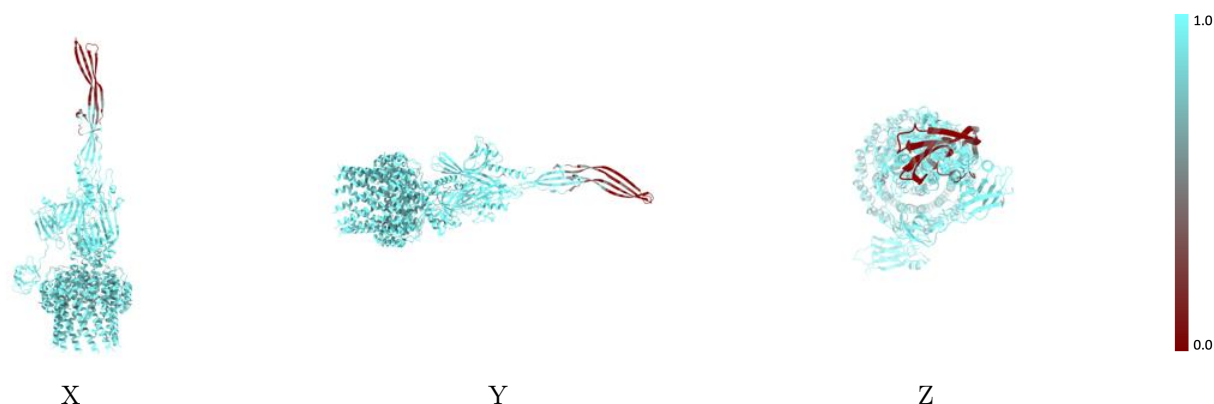
The images above show the 3D surface view of the map at the recommended contour level 0.115 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



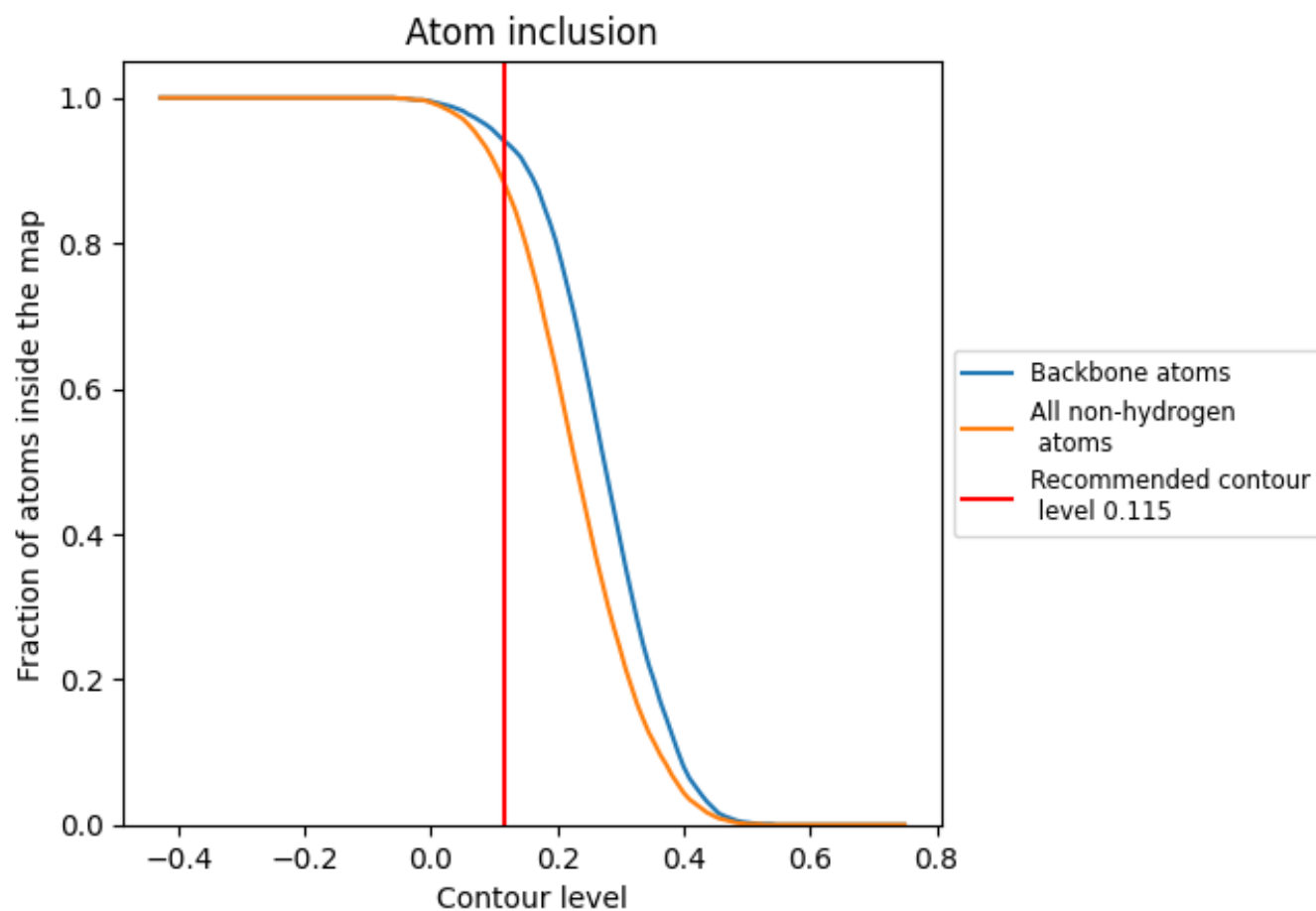
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.115).































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.115) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8840	 0.3040
FA	 0.8480	 0.2680
LA	 0.9610	 0.2970
TA	 0.8760	 0.3420
TB	 0.8840	 0.3400
TC	 0.8740	 0.3240
TD	 0.9030	 0.3410
TE	 0.8950	 0.3570
TF	 0.8880	 0.3290
TG	 0.9050	 0.3520
TH	 0.8880	 0.3360
TI	 0.8780	 0.3300
TJ	 0.8840	 0.3330
TK	 0.8890	 0.3360
TL	 0.8910	 0.3390

