



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 06:27 AM UTC

PDB ID : 9OAC / pdb_00009oac
EMDB ID : EMD-70279
Title : C5 reconstruction of the thermophilic bacteriophage P74-26 Portal Vertex
Authors : Sedivy, E.L.; Agnello, E.; Song, K.; Xu, C.; Kelch, B.A.
Deposited on : 2025-04-21
Resolution : 2.60 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

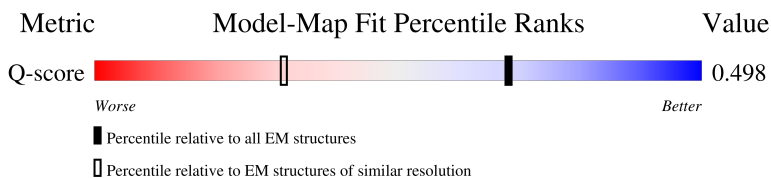
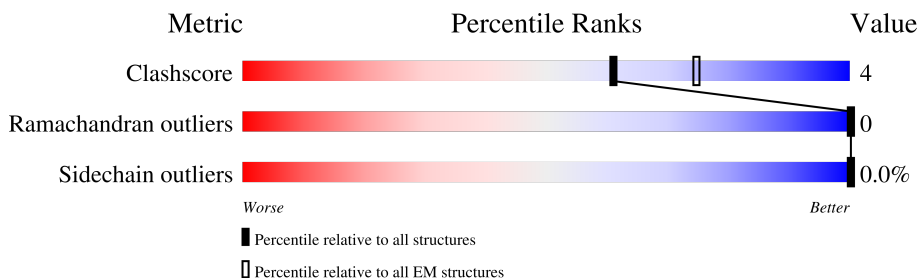
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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.



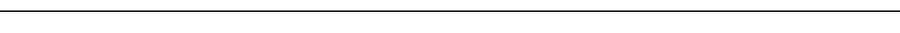
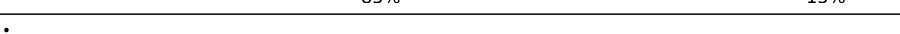
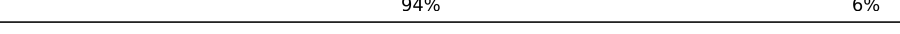
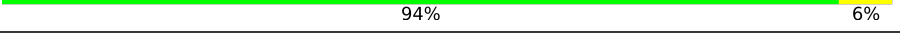
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	Aa	409	
1	Ab	409	
1	Ac	409	
1	Ad	409	

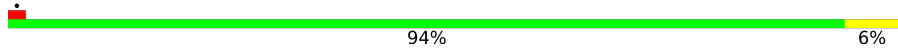
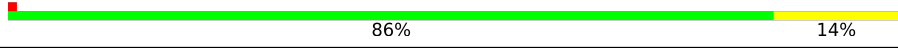
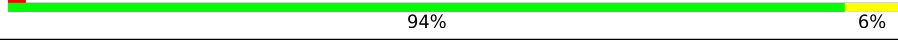
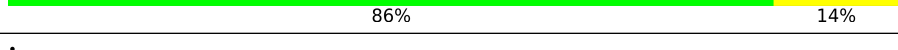
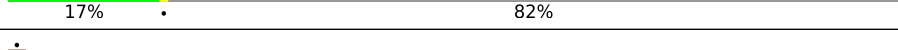
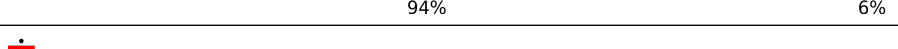
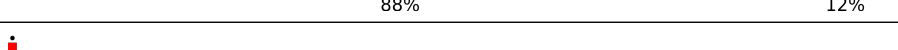
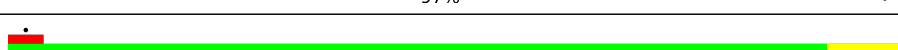
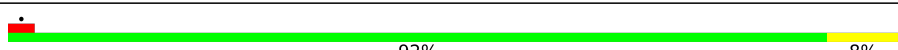
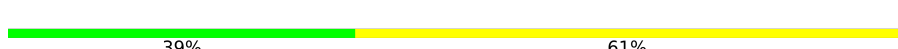
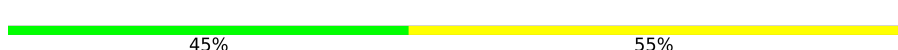
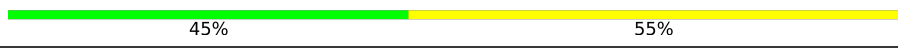
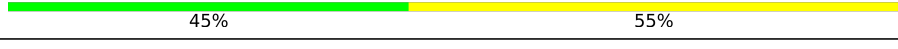
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Mol	Chain	Length	Quality of chain
1	Ae	409	
1	Af	409	
1	Ag	409	
1	Ah	409	
1	Ai	409	
1	Aj	409	
1	Ak	409	
1	Al	409	
1	Am	409	
1	An	409	
1	Ao	409	
1	Ap	409	
1	Aq	409	
1	Ar	409	
1	As	409	
1	At	409	
2	Ba	146	
2	Bb	146	
2	Bc	146	
2	Bd	146	
2	Be	146	
2	Bf	146	
2	Bg	146	
2	Bh	146	
2	Bi	146	

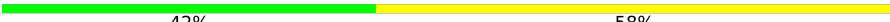
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Mol	Chain	Length	Quality of chain
2	Bj	146	
2	Bk	146	
2	Bl	146	
2	Bm	146	
2	Bn	146	
2	Bo	146	
2	Bp	146	
2	Bq	146	
2	Br	146	
2	Bs	146	
2	Bt	146	
3	Ca	73	
3	Cb	73	
3	Cc	73	
3	Cd	73	
3	Ce	73	
4	Ja	31	
4	Jc	31	
4	Je	31	
4	Jg	31	
4	Ji	31	
5	Jb	31	
5	Jd	31	
5	Jf	31	
5	Jh	31	

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Mol	Chain	Length	Quality of chain
5	Jj	31	 42% 58%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 70830 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 Major head protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	38	Total	C	N	O	S	0	0
			288	183	53	51	1		
1	Ab	382	Total	C	N	O	S	0	0
			3100	1999	527	569	5		
1	Ac	409	Total	C	N	O	S	0	0
			3303	2125	563	609	6		
1	Ad	233	Total	C	N	O	S	0	0
			1901	1232	320	346	3		
1	Ae	38	Total	C	N	O	S	0	0
			288	183	53	51	1		
1	Af	382	Total	C	N	O	S	0	0
			3100	1999	527	569	5		
1	Ag	409	Total	C	N	O	S	0	0
			3303	2125	563	609	6		
1	Ah	233	Total	C	N	O	S	0	0
			1901	1232	320	346	3		
1	Ai	38	Total	C	N	O	S	0	0
			288	183	53	51	1		
1	Aj	382	Total	C	N	O	S	0	0
			3100	1999	527	569	5		
1	Ak	409	Total	C	N	O	S	0	0
			3303	2125	563	609	6		
1	Al	233	Total	C	N	O	S	0	0
			1901	1232	320	346	3		
1	Am	38	Total	C	N	O	S	0	0
			288	183	53	51	1		
1	An	382	Total	C	N	O	S	0	0
			3100	1999	527	569	5		
1	Ao	409	Total	C	N	O	S	0	0
			3303	2125	563	609	6		
1	Ap	233	Total	C	N	O	S	0	0
			1901	1232	320	346	3		
1	Aq	38	Total	C	N	O	S	0	0
			288	183	53	51	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ar	382	Total	C	N	O	S	0	0
			3100	1999	527	569	5		
1	As	409	Total	C	N	O	S	0	0
			3303	2125	563	609	6		
1	At	233	Total	C	N	O	S	0	0
			1901	1232	320	346	3		

- Molecule 2 is a protein called P74-26 Head Decoration Protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ba	26	Total	C	N	O	S	0	0
			225	147	38	39	1		
2	Bb	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bc	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bd	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Be	26	Total	C	N	O	S	0	0
			225	147	38	39	1		
2	Bf	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bg	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bh	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bi	26	Total	C	N	O	S	0	0
			225	147	38	39	1		
2	Bj	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bk	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bl	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bm	26	Total	C	N	O	S	0	0
			225	147	38	39	1		
2	Bn	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bo	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bp	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Bq	26	Total	C	N	O	S	0	0
			225	147	38	39	1		
2	Br	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bs	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		
2	Bt	146	Total	C	N	O	S	0	0
			1161	756	197	205	3		

- Molecule 3 is a protein called Portal Vertex Protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ca	73	Total	C	N	O	S	0	0
			595	374	107	113	1		
3	Cb	73	Total	C	N	O	S	0	0
			595	374	107	113	1		
3	Cc	73	Total	C	N	O	S	0	0
			595	374	107	113	1		
3	Cd	73	Total	C	N	O	S	0	0
			595	374	107	113	1		
3	Ce	73	Total	C	N	O	S	0	0
			595	374	107	113	1		

- Molecule 4 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ja	31	Total	C	N	O	P	0	0
			620	310	62	217	31		
4	Jc	31	Total	C	N	O	P	0	0
			620	310	62	217	31		
4	Je	31	Total	C	N	O	P	0	0
			620	310	62	217	31		
4	Jg	31	Total	C	N	O	P	0	0
			620	310	62	217	31		
4	Ji	31	Total	C	N	O	P	0	0
			620	310	62	217	31		

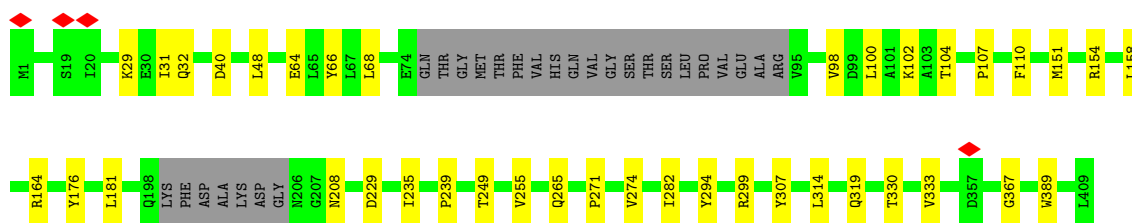
- Molecule 5 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Jb	31	Total	C	N	O	P	0	0
			651	310	155	155	31		

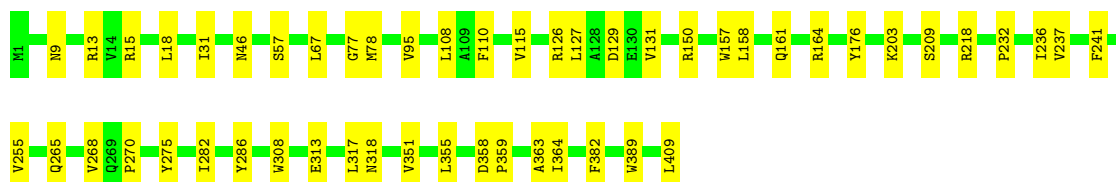
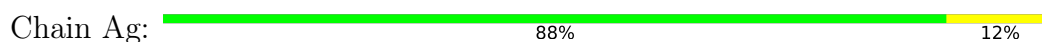
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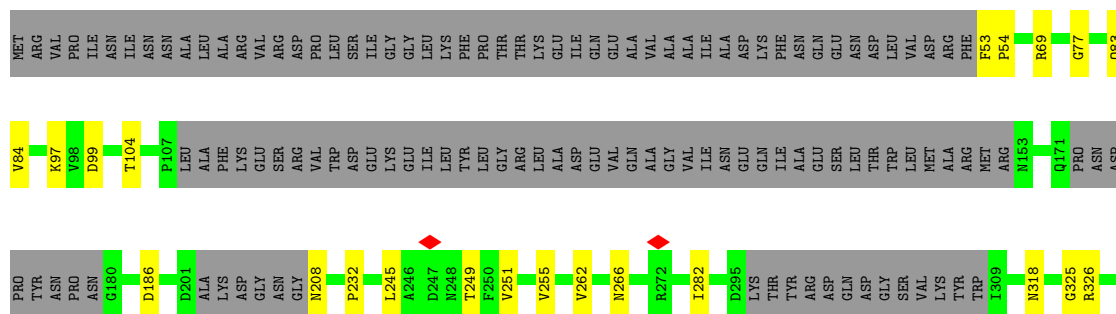
Mol	Chain	Residues	Atoms					AltConf	Trace
5	Jd	31	Total 651	C 310	N 155	O 155	P 31	0	0
5	Jf	31	Total 651	C 310	N 155	O 155	P 31	0	0
5	Jh	31	Total 651	C 310	N 155	O 155	P 31	0	0
5	Jj	31	Total 651	C 310	N 155	O 155	P 31	0	0



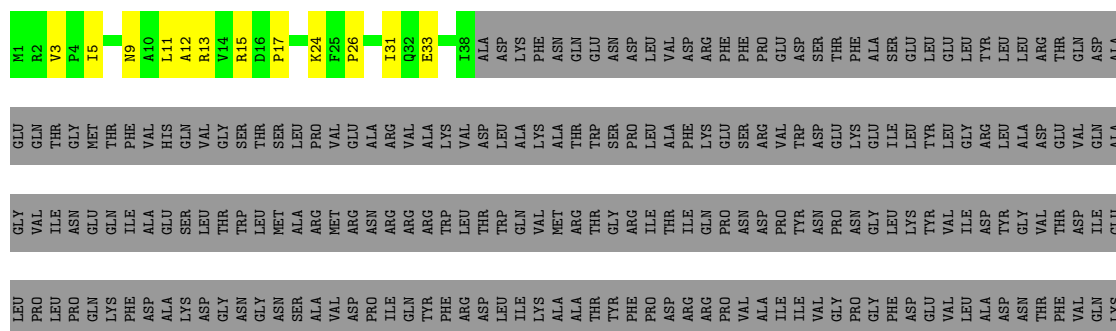
- Molecule 1: Major head protein



- Molecule 1: Major head protein

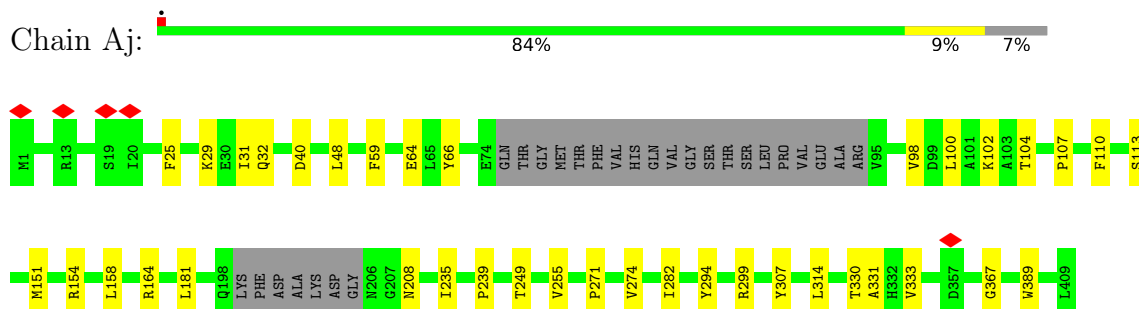


- Molecule 1: Major head protein

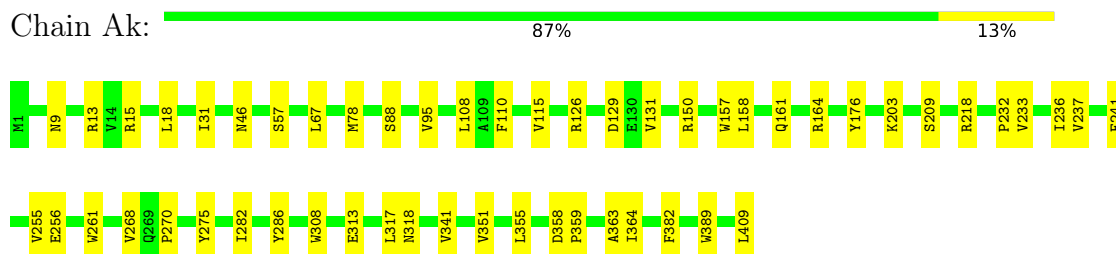


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LEU	ILE	VAL	GLU	TYR	ASN	GLN	SER	THR	GLY	PRO	PHE	VAL	GLY	THR	TYR	GLN	ALA	VAL	HIS	VAL	ALA	ASN	GLY	TYR	GLN	ARG	VAL	GLN	ASN	GLY	TYR	THR	ALA	PRO	ARG	GLU	VAL	ALA	ASN	GLY	LEU	PRO	VAL	GLY	THR	LEU	GLN	ASP	VAL	HIS	TYR	LEU	GLN	ASP	THR	TYR	ARG	PRO	ASP	GLN	TYR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

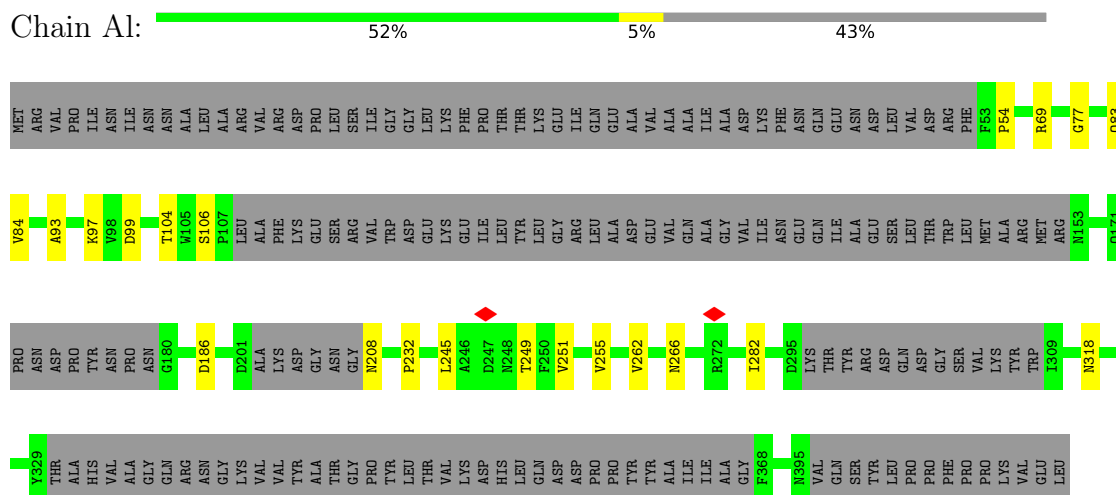
- Molecule 1: Major head protein



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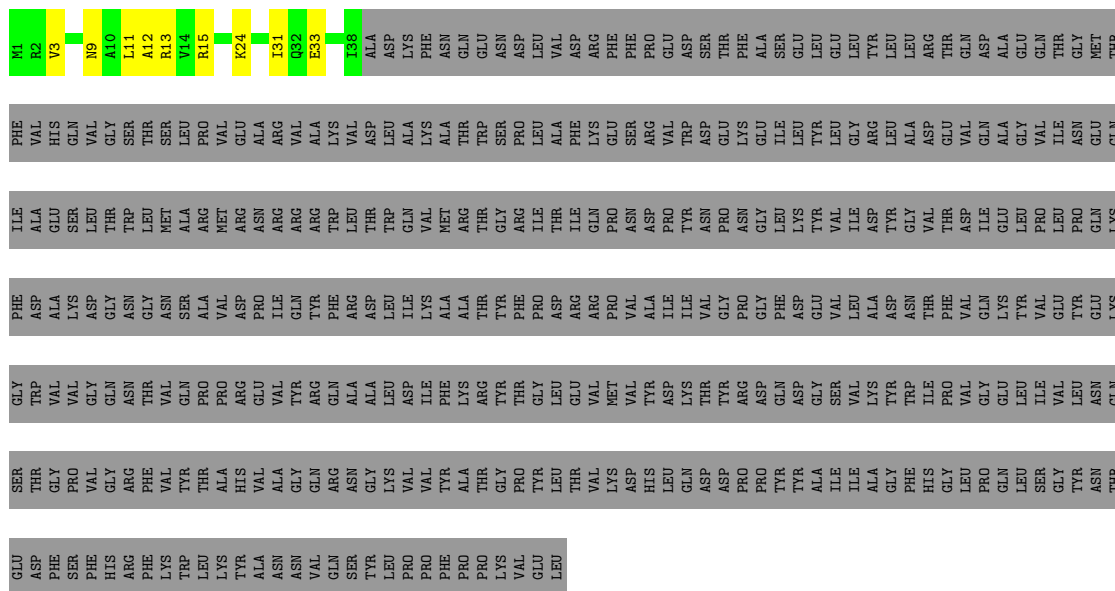


- Molecule 1: Major head protein

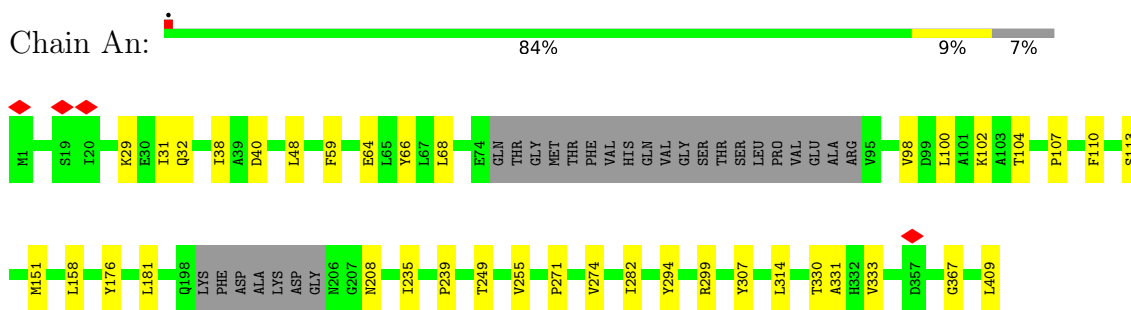


- Molecule 1: Major head protein

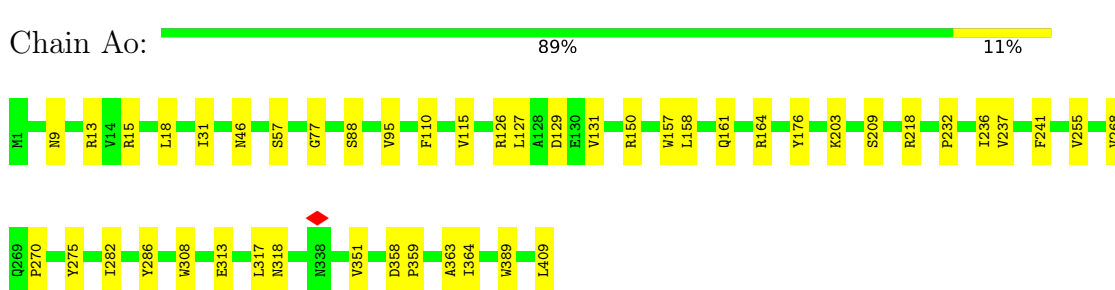




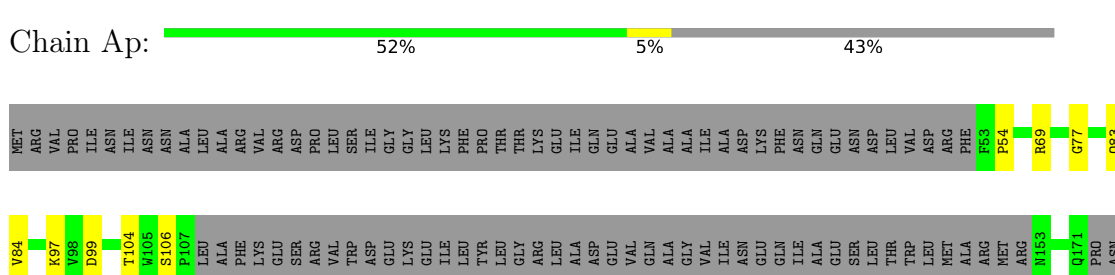
- Molecule 1: Major head protein

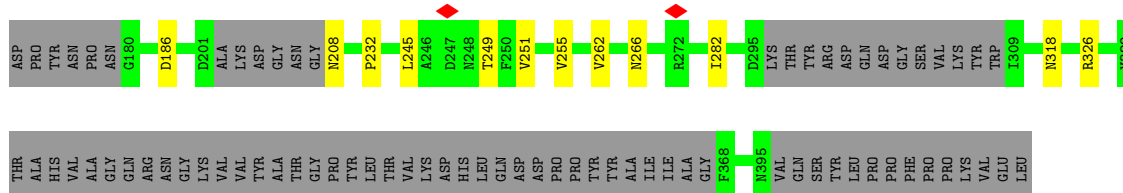


- Molecule 1: Major head protein



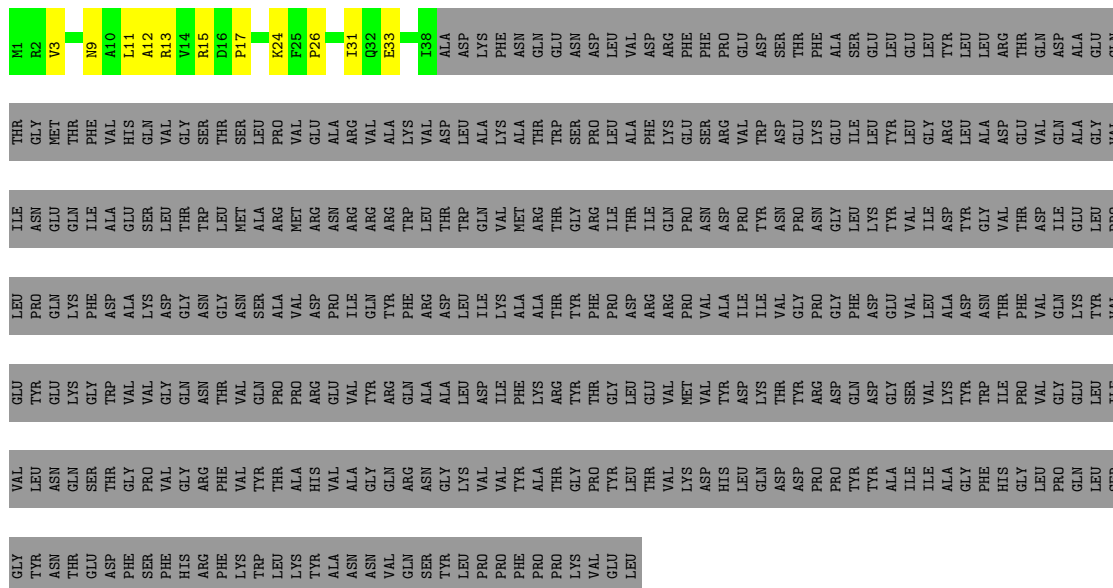
- Molecule 1: Major head protein





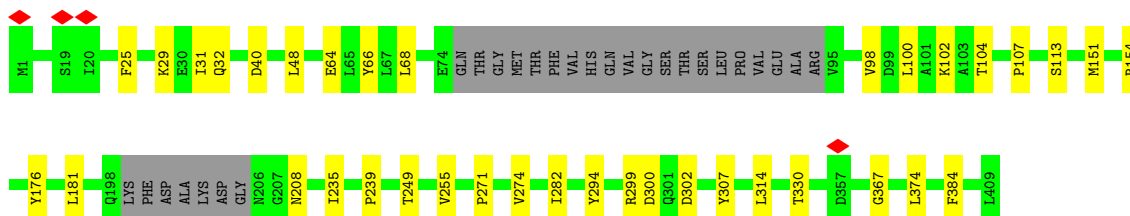
• Molecule 1: Major head protein

Chain Aq: 7% 91%



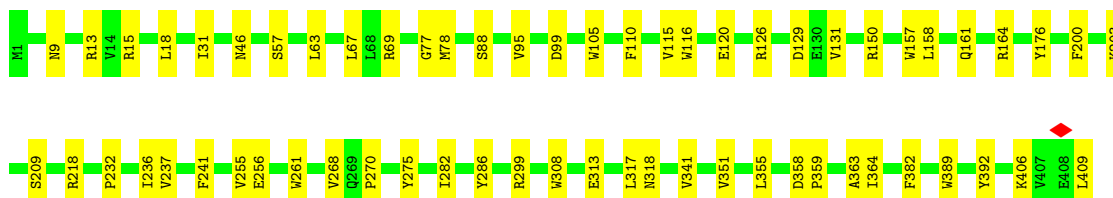
• Molecule 1: Major head protein

Chain Ar: 84% 9% 7%

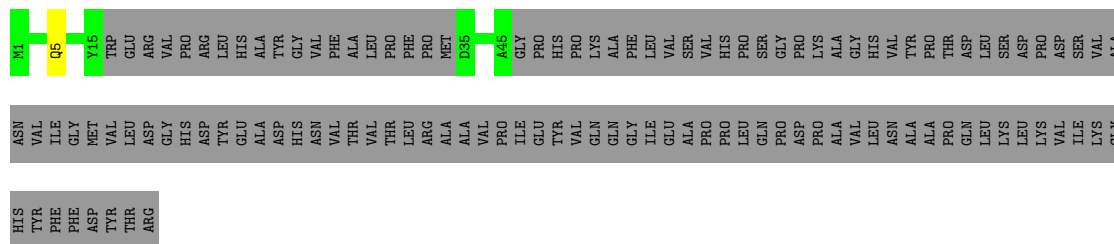


• Molecule 1: Major head protein

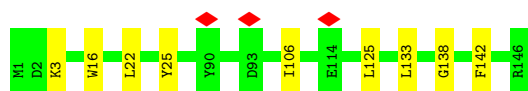
Chain As: 85% 15%



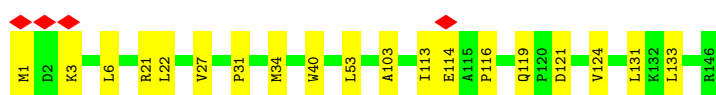
● Molecule 2: P74-26 Head Decoration Protein

Chain Be:  17% 82%

● Molecule 2: P74-26 Head Decoration Protein

Chain Bf:  94% 6%

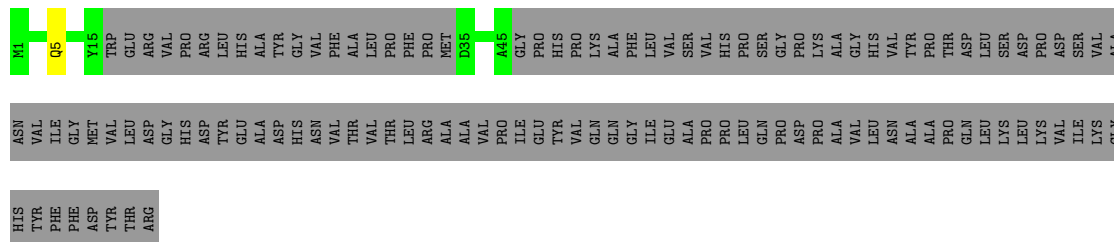
● Molecule 2: P74-26 Head Decoration Protein

Chain Bg:  87% 13%

● Molecule 2: P74-26 Head Decoration Protein

Chain Bh:  88% 12%

● Molecule 2: P74-26 Head Decoration Protein

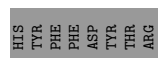
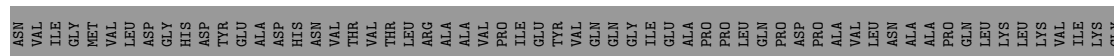
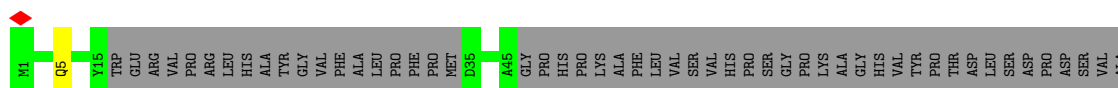
Chain Bi:  17% 82%

● Molecule 2: P74-26 Head Decoration Protein

Chain Bj:  94% 6%



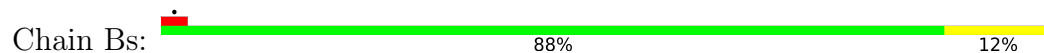
• Molecule 2: P74-26 Head Decoration Protein



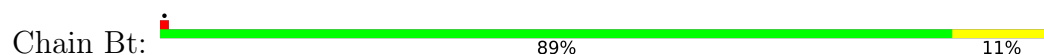
• Molecule 2: P74-26 Head Decoration Protein



• Molecule 2: P74-26 Head Decoration Protein



• Molecule 2: P74-26 Head Decoration Protein

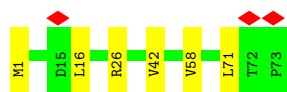


• Molecule 3: Portal Vertex Protein



• Molecule 3: Portal Vertex Protein





- Molecule 3: Portal Vertex Protein



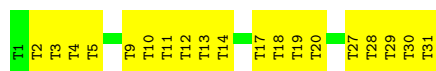
- Molecule 3: Portal Vertex Protein



- Molecule 3: Portal Vertex Protein



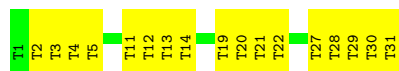
- Molecule 4: DNA (31-MER)



- Molecule 4: DNA (31-MER)

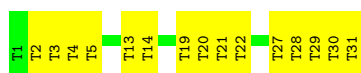


- Molecule 4: DNA (31-MER)



- Molecule 4: DNA (31-MER)

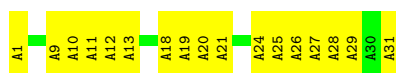




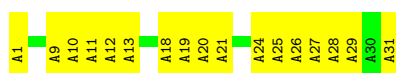
• Molecule 4: DNA (31-MER)



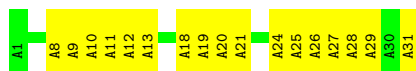
• Molecule 5: DNA (31-MER)



• Molecule 5: DNA (31-MER)



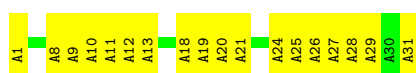
• Molecule 5: DNA (31-MER)



• Molecule 5: DNA (31-MER)



• Molecule 5: DNA (31-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	40773	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.0571	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.902	Depositor
Minimum map value	-0.497	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.050	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	Aa	0.13	0/291	0.33	0/394
1	Ab	0.16	0/3182	0.26	0/4333
1	Ac	0.17	0/3391	0.31	0/4618
1	Ad	0.13	0/1949	0.25	0/2647
1	Ae	0.13	0/291	0.33	0/394
1	Af	0.16	0/3182	0.26	0/4333
1	Ag	0.16	0/3391	0.30	0/4618
1	Ah	0.13	0/1949	0.26	0/2647
1	Ai	0.13	0/291	0.33	0/394
1	Aj	0.16	0/3182	0.26	0/4333
1	Ak	0.17	0/3391	0.30	0/4618
1	Al	0.13	0/1949	0.25	0/2647
1	Am	0.13	0/291	0.33	0/394
1	An	0.16	0/3182	0.26	0/4333
1	Ao	0.16	0/3391	0.30	0/4618
1	Ap	0.13	0/1949	0.25	0/2647
1	Aq	0.13	0/291	0.33	0/394
1	Ar	0.16	0/3182	0.26	0/4333
1	As	0.16	0/3391	0.30	0/4618
1	At	0.13	0/1949	0.25	0/2647
2	Ba	0.13	0/231	0.22	0/311
2	Bb	0.17	0/1203	0.32	0/1648
2	Bc	0.16	0/1203	0.27	0/1648
2	Bd	0.16	0/1203	0.29	0/1648
2	Be	0.13	0/231	0.22	0/311
2	Bf	0.16	0/1203	0.32	0/1648
2	Bg	0.15	0/1203	0.26	0/1648
2	Bh	0.16	0/1203	0.29	0/1648
2	Bi	0.13	0/231	0.21	0/311
2	Bj	0.16	0/1203	0.32	0/1648
2	Bk	0.16	0/1203	0.27	0/1648
2	Bl	0.17	0/1203	0.29	0/1648
2	Bm	0.13	0/231	0.23	0/311
2	Bn	0.17	0/1203	0.32	0/1648

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Bo	0.15	0/1203	0.26	0/1648
2	Bp	0.17	0/1203	0.29	0/1648
2	Bq	0.13	0/231	0.23	0/311
2	Br	0.16	0/1203	0.32	0/1648
2	Bs	0.15	0/1203	0.26	0/1648
2	Bt	0.16	0/1203	0.29	0/1648
3	Ca	0.16	0/609	0.32	0/826
3	Cb	0.16	0/609	0.28	0/826
3	Cc	0.16	0/609	0.28	0/826
3	Cd	0.16	0/609	0.28	0/826
3	Ce	0.16	0/609	0.28	0/826
4	Ja	0.23	0/681	0.60	0/1050
4	Jc	0.24	0/681	0.60	0/1050
4	Je	0.24	0/681	0.60	0/1050
4	Jg	0.24	0/681	0.60	0/1050
4	Ji	0.23	0/681	0.60	0/1050
5	Jb	0.21	0/743	0.44	0/1143
5	Jd	0.21	0/743	0.44	0/1143
5	Jf	0.21	0/743	0.44	0/1143
5	Jh	0.21	0/743	0.44	0/1143
5	Jj	0.21	0/743	0.44	0/1143
All	All	0.16	0/73430	0.32	0/101330

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	Aa	288	0	313	8	0
1	Ab	3100	0	3055	29	0
1	Ac	3303	0	3255	34	0
1	Ad	1901	0	1862	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Ae	288	0	313	8	0
1	Af	3100	0	3055	28	0
1	Ag	3303	0	3255	38	0
1	Ah	1901	0	1862	17	0
1	Ai	288	0	313	10	0
1	Aj	3100	0	3055	26	0
1	Ak	3303	0	3255	36	0
1	Al	1901	0	1862	18	0
1	Am	288	0	313	9	0
1	An	3100	0	3055	26	0
1	Ao	3303	0	3255	33	0
1	Ap	1901	0	1862	17	0
1	Aq	288	0	313	10	0
1	Ar	3100	0	3055	26	0
1	As	3303	0	3255	42	0
1	At	1901	0	1862	16	0
2	Ba	225	0	212	1	0
2	Bb	1161	0	1129	6	0
2	Bc	1161	0	1129	10	0
2	Bd	1161	0	1129	11	0
2	Be	225	0	212	1	0
2	Bf	1161	0	1129	6	0
2	Bg	1161	0	1129	11	0
2	Bh	1161	0	1129	11	0
2	Bi	225	0	212	1	0
2	Bj	1161	0	1129	6	0
2	Bk	1161	0	1129	11	0
2	Bl	1161	0	1129	14	0
2	Bm	225	0	212	2	0
2	Bn	1161	0	1129	6	0
2	Bo	1161	0	1129	11	0
2	Bp	1161	0	1129	14	0
2	Bq	225	0	212	1	0
2	Br	1161	0	1129	6	0
2	Bs	1161	0	1129	10	0
2	Bt	1161	0	1129	11	0
3	Ca	595	0	584	2	0
3	Cb	595	0	584	4	0
3	Cc	595	0	584	5	0
3	Cd	595	0	584	5	0
3	Ce	595	0	584	4	0
4	Ja	620	0	373	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Jc	620	0	373	12	0
4	Je	620	0	373	12	0
4	Jg	620	0	373	11	0
4	Ji	620	0	373	12	0
5	Jb	651	0	342	11	0
5	Jd	651	0	342	12	0
5	Jf	651	0	342	13	0
5	Jh	651	0	342	10	0
5	Jj	651	0	342	12	0
All	All	70830	0	66915	599	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 4.

The worst 5 of 599 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:Ah:186:ASP:H	2:Bh:1:MET:HG3	1.57	0.69
1:Ad:186:ASP:H	2:Bd:1:MET:HG3	1.59	0.68
1:At:186:ASP:H	2:Bt:1:MET:HG3	1.60	0.67
1:Al:186:ASP:H	2:Bl:1:MET:HG3	1.59	0.66
1:Aj:181:LEU:HD21	2:Bh:31:PRO:HB2	1.78	0.65

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	Aa	36/409 (9%)	33 (92%)	3 (8%)	0	100	100
1	Ab	376/409 (92%)	364 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ac	407/409 (100%)	399 (98%)	8 (2%)	0	100	100
1	Ad	221/409 (54%)	218 (99%)	3 (1%)	0	100	100
1	Ae	36/409 (9%)	33 (92%)	3 (8%)	0	100	100
1	Af	376/409 (92%)	364 (97%)	12 (3%)	0	100	100
1	Ag	407/409 (100%)	399 (98%)	8 (2%)	0	100	100
1	Ah	221/409 (54%)	218 (99%)	3 (1%)	0	100	100
1	Ai	36/409 (9%)	33 (92%)	3 (8%)	0	100	100
1	Aj	376/409 (92%)	364 (97%)	12 (3%)	0	100	100
1	Ak	407/409 (100%)	399 (98%)	8 (2%)	0	100	100
1	Al	221/409 (54%)	218 (99%)	3 (1%)	0	100	100
1	Am	36/409 (9%)	33 (92%)	3 (8%)	0	100	100
1	An	376/409 (92%)	364 (97%)	12 (3%)	0	100	100
1	Ao	407/409 (100%)	399 (98%)	8 (2%)	0	100	100
1	Ap	221/409 (54%)	218 (99%)	3 (1%)	0	100	100
1	Aq	36/409 (9%)	33 (92%)	3 (8%)	0	100	100
1	Ar	376/409 (92%)	364 (97%)	12 (3%)	0	100	100
1	As	407/409 (100%)	399 (98%)	8 (2%)	0	100	100
1	At	221/409 (54%)	218 (99%)	3 (1%)	0	100	100
2	Ba	22/146 (15%)	21 (96%)	1 (4%)	0	100	100
2	Bb	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
2	Bc	144/146 (99%)	144 (100%)	0	0	100	100
2	Bd	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
2	Be	22/146 (15%)	21 (96%)	1 (4%)	0	100	100
2	Bf	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
2	Bg	144/146 (99%)	144 (100%)	0	0	100	100
2	Bh	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
2	Bi	22/146 (15%)	21 (96%)	1 (4%)	0	100	100
2	Bj	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
2	Bk	144/146 (99%)	144 (100%)	0	0	100	100
2	Bl	144/146 (99%)	143 (99%)	1 (1%)	0	100	100
2	Bm	22/146 (15%)	21 (96%)	1 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Bn	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
2	Bo	144/146 (99%)	144 (100%)	0	0	100	100
2	Bp	144/146 (99%)	143 (99%)	1 (1%)	0	100	100
2	Bq	22/146 (15%)	21 (96%)	1 (4%)	0	100	100
2	Br	144/146 (99%)	138 (96%)	6 (4%)	0	100	100
2	Bs	144/146 (99%)	144 (100%)	0	0	100	100
2	Bt	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
3	Ca	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
3	Cb	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
3	Cc	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
3	Cd	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
3	Ce	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
All	All	7825/11465 (68%)	7647 (98%)	178 (2%)	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	Aa	31/352 (9%)	31 (100%)	0	100	100
1	Ab	330/352 (94%)	330 (100%)	0	100	100
1	Ac	352/352 (100%)	352 (100%)	0	100	100
1	Ad	204/352 (58%)	204 (100%)	0	100	100
1	Ae	31/352 (9%)	31 (100%)	0	100	100
1	Af	330/352 (94%)	330 (100%)	0	100	100
1	Ag	352/352 (100%)	352 (100%)	0	100	100
1	Ah	204/352 (58%)	204 (100%)	0	100	100
1	Ai	31/352 (9%)	31 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Aj	330/352 (94%)	330 (100%)	0	100	100
1	Ak	352/352 (100%)	352 (100%)	0	100	100
1	Al	204/352 (58%)	204 (100%)	0	100	100
1	Am	31/352 (9%)	31 (100%)	0	100	100
1	An	330/352 (94%)	330 (100%)	0	100	100
1	Ao	352/352 (100%)	352 (100%)	0	100	100
1	Ap	204/352 (58%)	204 (100%)	0	100	100
1	Aq	31/352 (9%)	31 (100%)	0	100	100
1	Ar	330/352 (94%)	330 (100%)	0	100	100
1	As	352/352 (100%)	352 (100%)	0	100	100
1	At	204/352 (58%)	204 (100%)	0	100	100
2	Ba	23/123 (19%)	23 (100%)	0	100	100
2	Bb	123/123 (100%)	123 (100%)	0	100	100
2	Bc	123/123 (100%)	123 (100%)	0	100	100
2	Bd	123/123 (100%)	123 (100%)	0	100	100
2	Be	23/123 (19%)	23 (100%)	0	100	100
2	Bf	123/123 (100%)	123 (100%)	0	100	100
2	Bg	123/123 (100%)	123 (100%)	0	100	100
2	Bh	123/123 (100%)	122 (99%)	1 (1%)	73	88
2	Bi	23/123 (19%)	23 (100%)	0	100	100
2	Bj	123/123 (100%)	123 (100%)	0	100	100
2	Bk	123/123 (100%)	123 (100%)	0	100	100
2	Bl	123/123 (100%)	123 (100%)	0	100	100
2	Bm	23/123 (19%)	23 (100%)	0	100	100
2	Bn	123/123 (100%)	123 (100%)	0	100	100
2	Bo	123/123 (100%)	123 (100%)	0	100	100
2	Bp	123/123 (100%)	122 (99%)	1 (1%)	73	88
2	Bq	23/123 (19%)	23 (100%)	0	100	100
2	Br	123/123 (100%)	123 (100%)	0	100	100
2	Bs	123/123 (100%)	123 (100%)	0	100	100
2	Bt	123/123 (100%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Ca	62/62 (100%)	62 (100%)	0	100	100
3	Cb	62/62 (100%)	62 (100%)	0	100	100
3	Cc	62/62 (100%)	62 (100%)	0	100	100
3	Cd	62/62 (100%)	62 (100%)	0	100	100
3	Ce	62/62 (100%)	62 (100%)	0	100	100
All	All	6855/9810 (70%)	6853 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Bh	99	THR
2	Bp	99	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	Bj	14	GLN
3	Ca	56	GLN
2	Bk	139	HIS
2	Bo	139	HIS
3	Cb	56	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.

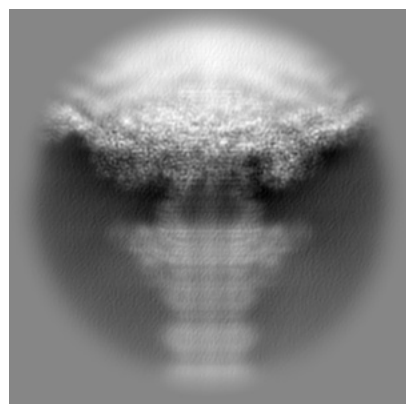
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70279. These allow visual inspection of the internal detail of the map and identification of artifacts.

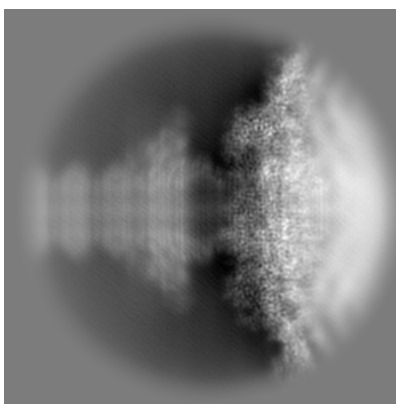
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

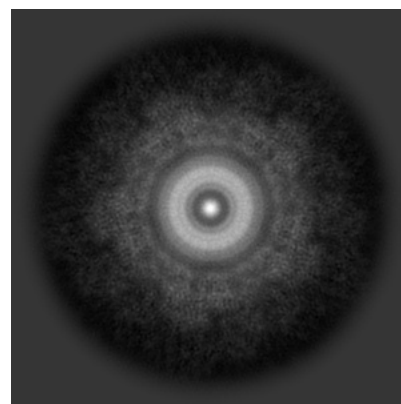
6.1.1 Primary map



X

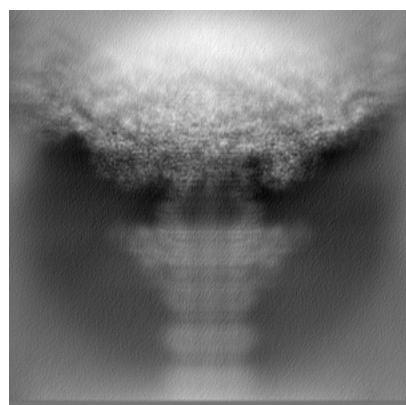


Y

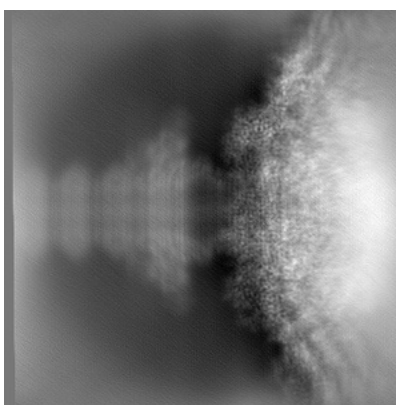


Z

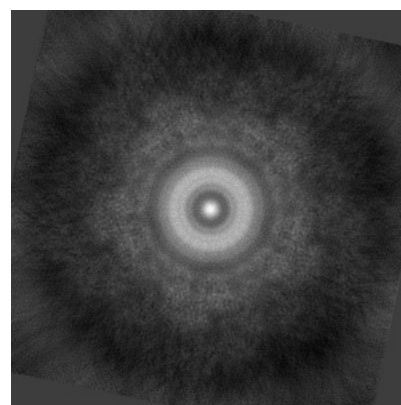
6.1.2 Raw map



X



Y

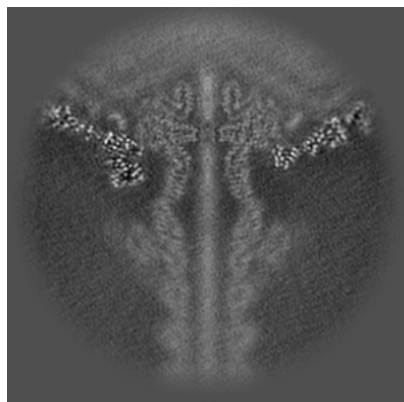


Z

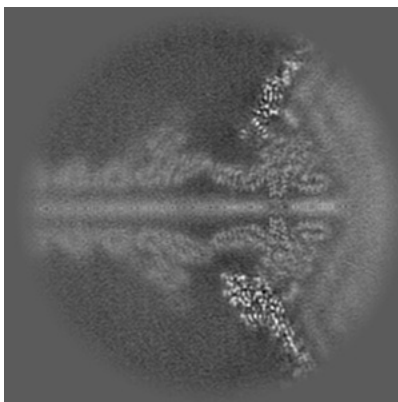
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

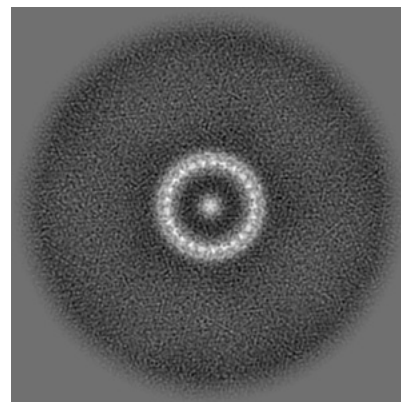
6.2.1 Primary map



X Index: 180

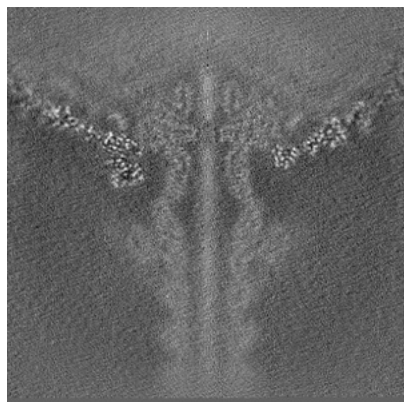


Y Index: 180

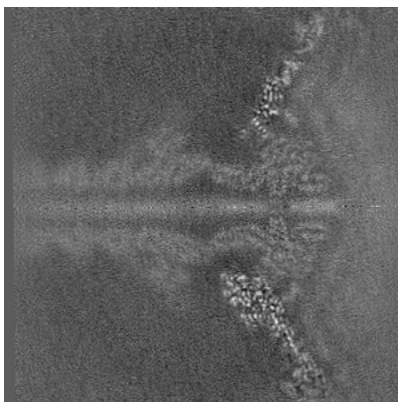


Z Index: 180

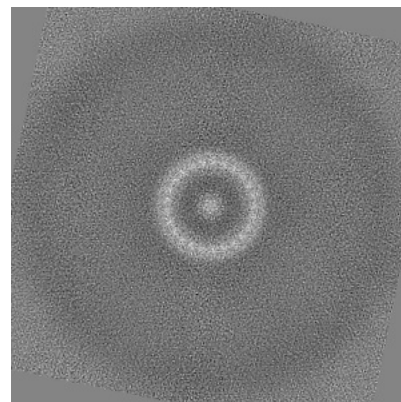
6.2.2 Raw map



X Index: 180



Y Index: 180

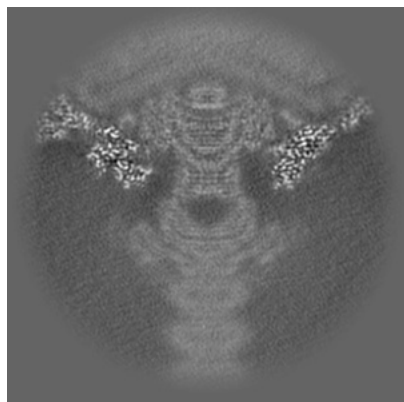


Z Index: 180

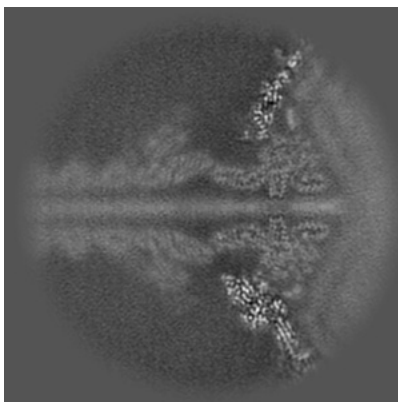
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

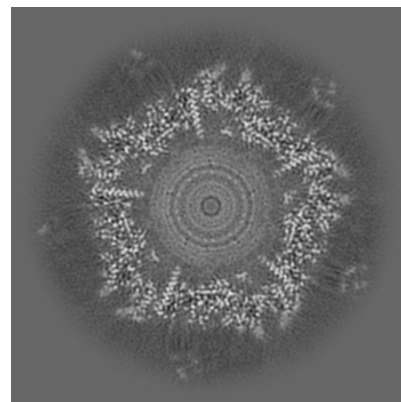
6.3.1 Primary map



X Index: 155

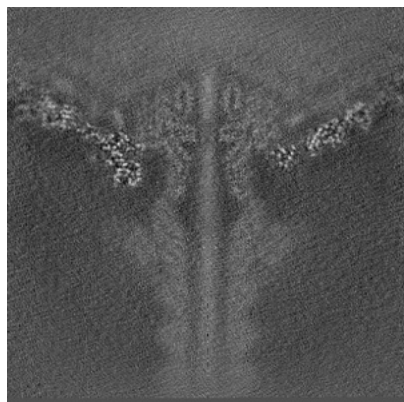


Y Index: 178

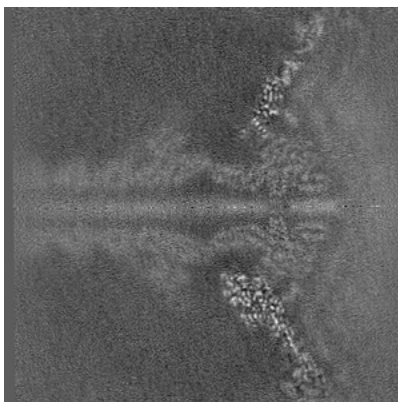


Z Index: 239

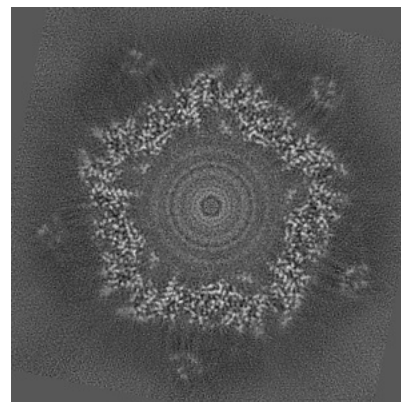
6.3.2 Raw map



X Index: 178



Y Index: 180

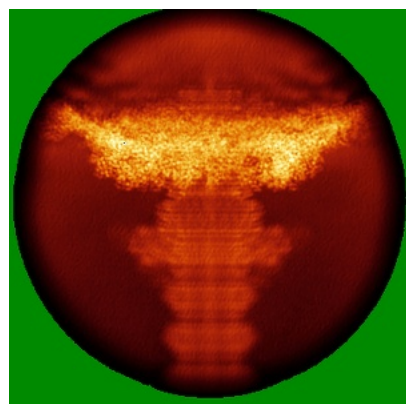


Z Index: 240

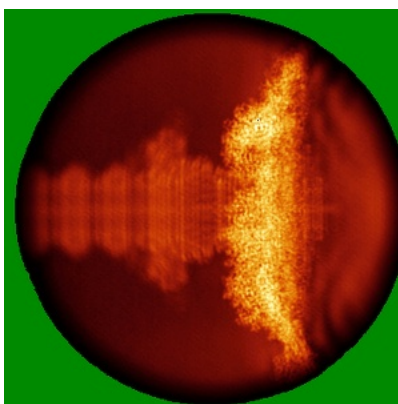
The images above show the largest variance slices of the map in three orthogonal directions.

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

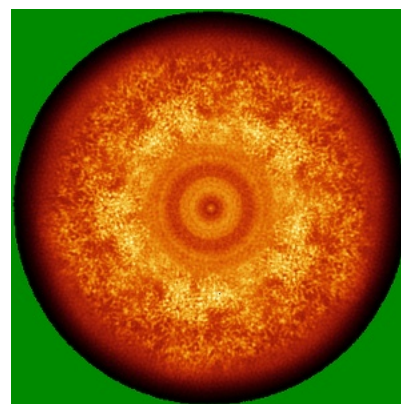
6.4.1 Primary map



X

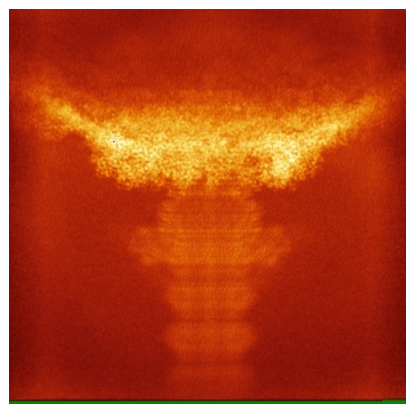


Y

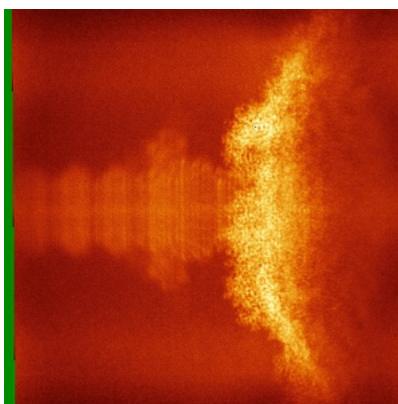


Z

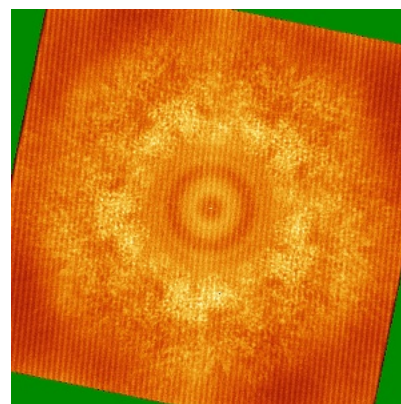
6.4.2 Raw map



X



Y



Z

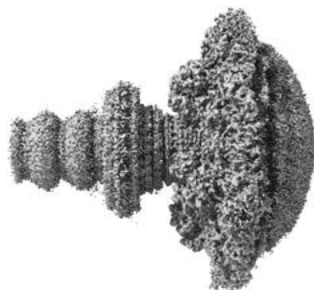
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

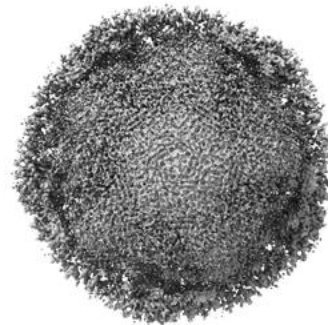
6.5.1 Primary map



X



Y



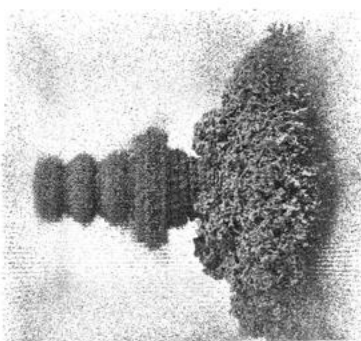
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

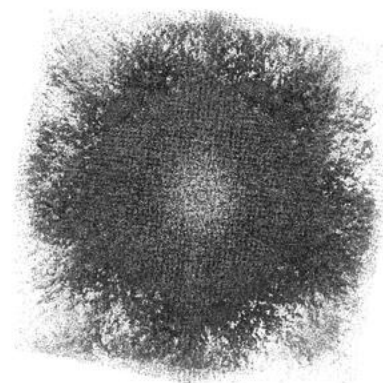
6.5.2 Raw map



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.

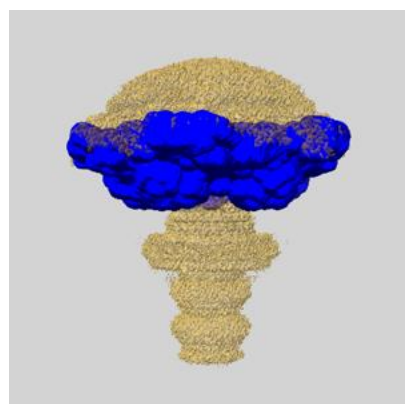
6.6 Mask visualisation [i](#)

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

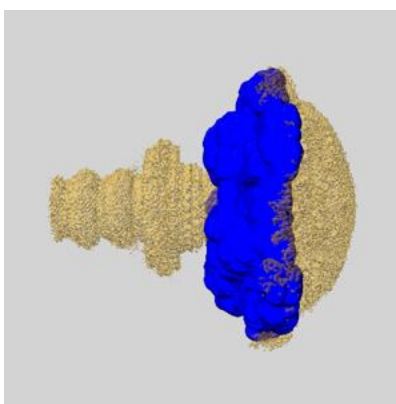
A mask typically either:

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

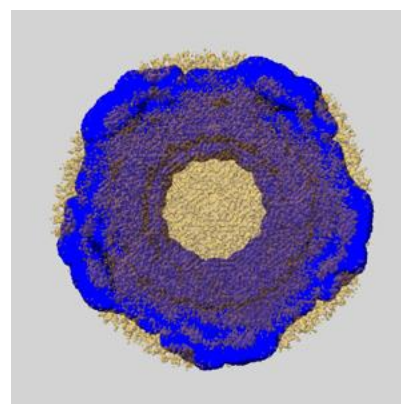
6.6.1 emd_70279_msk_1.map [i](#)



X



Y

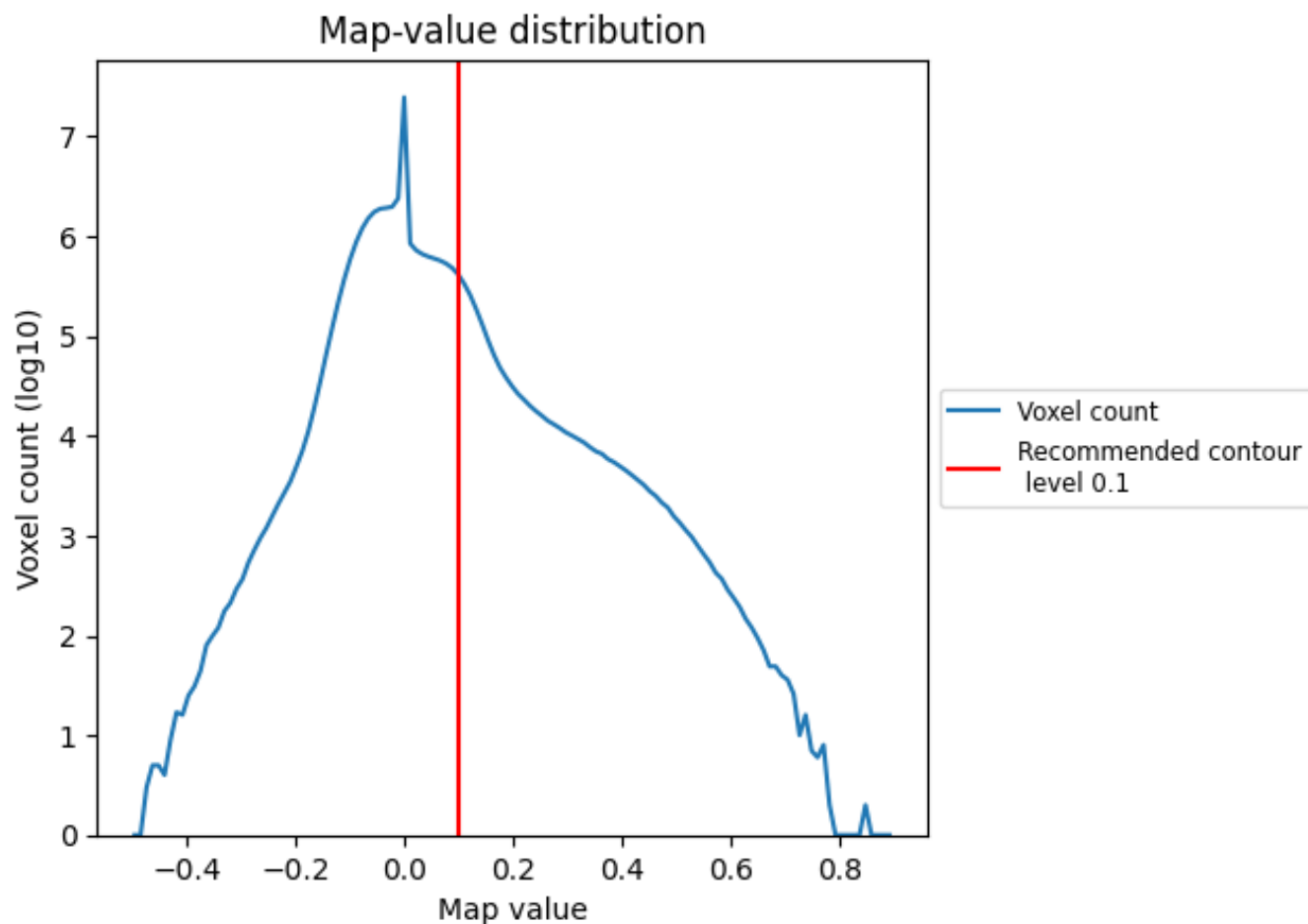


Z

7 Map analysis [i](#)

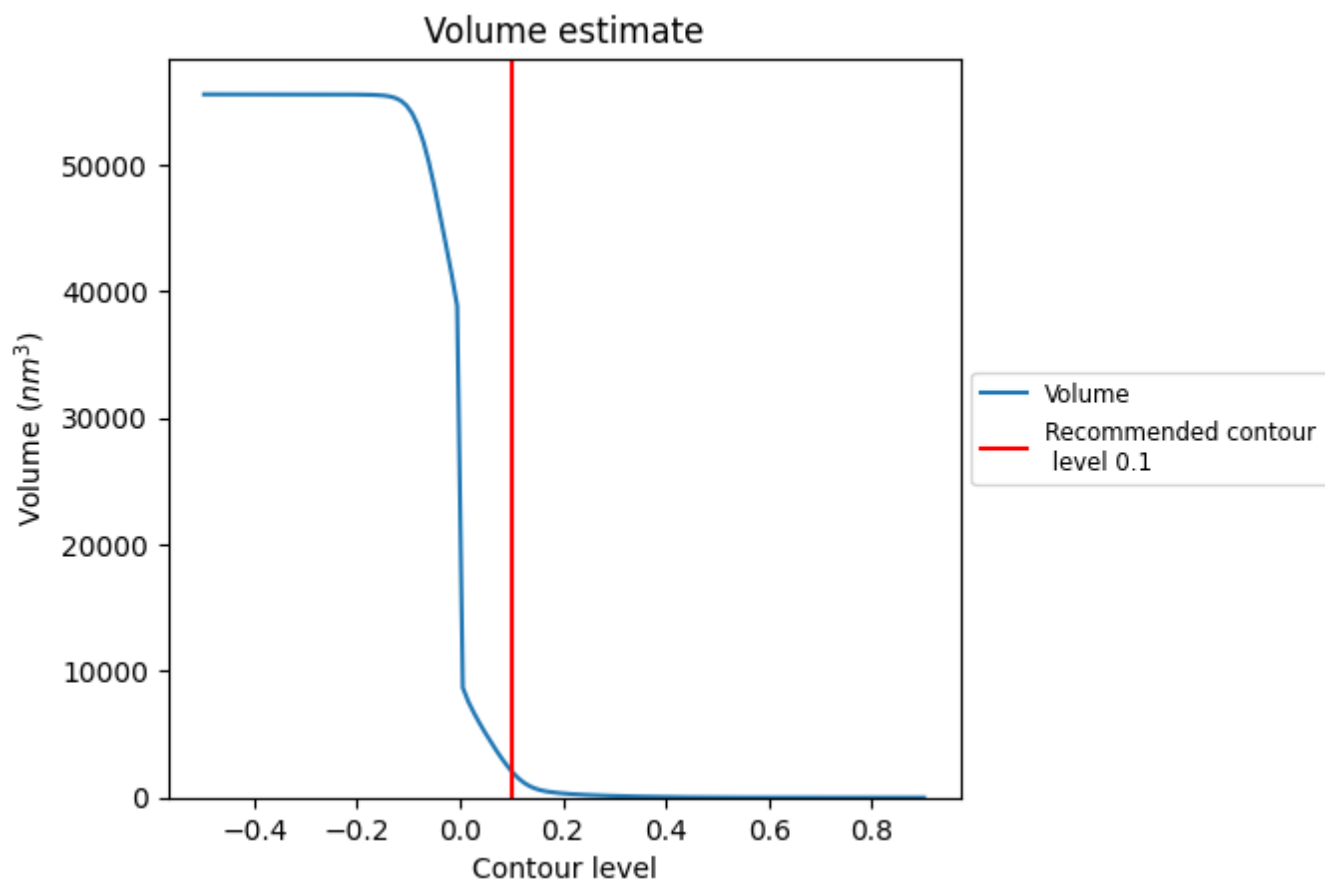
This section contains the results of statistical analysis of the map.

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.

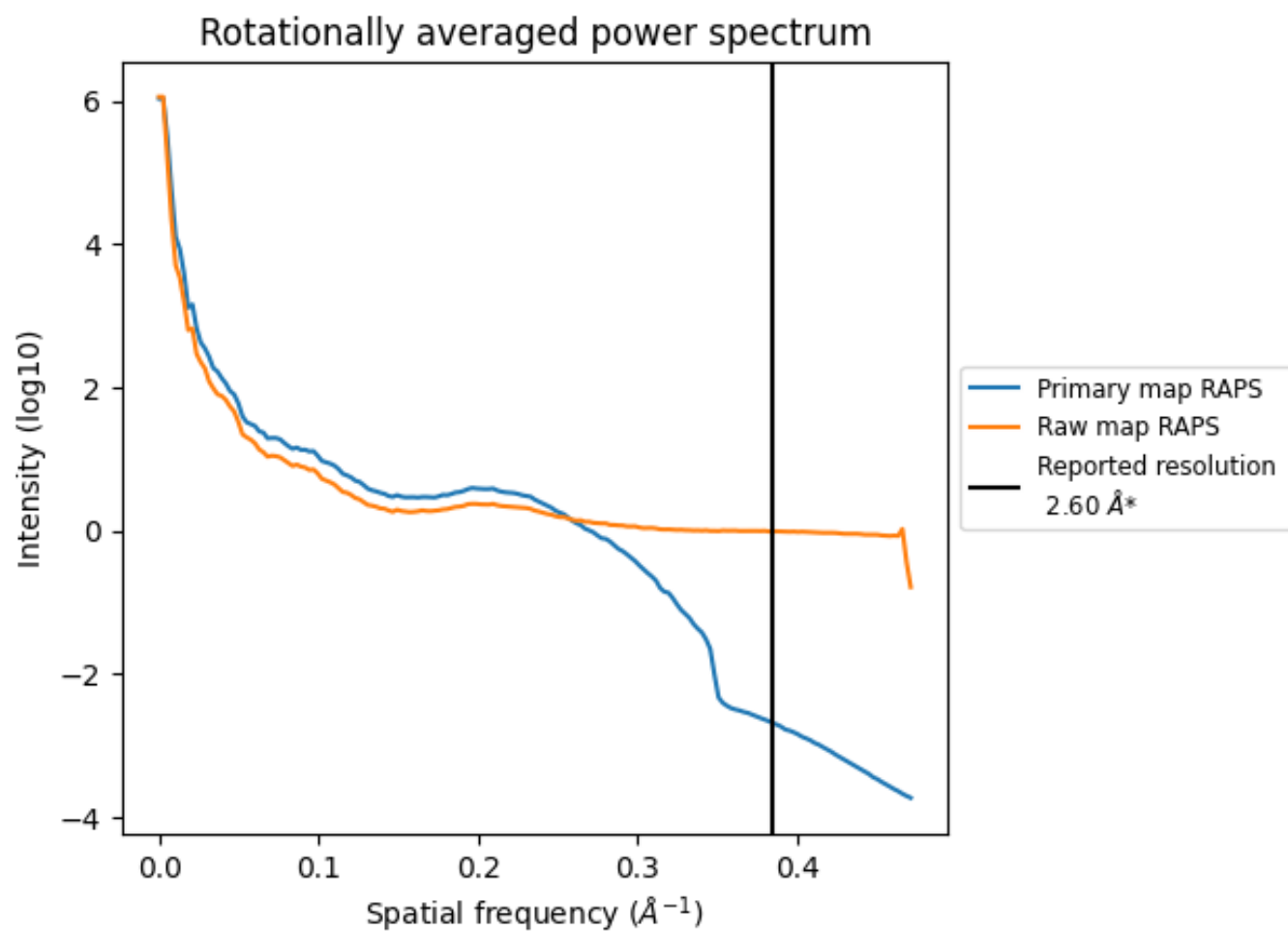
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2108 nm^3 ; this corresponds to an approximate mass of 1904 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 ⓘ

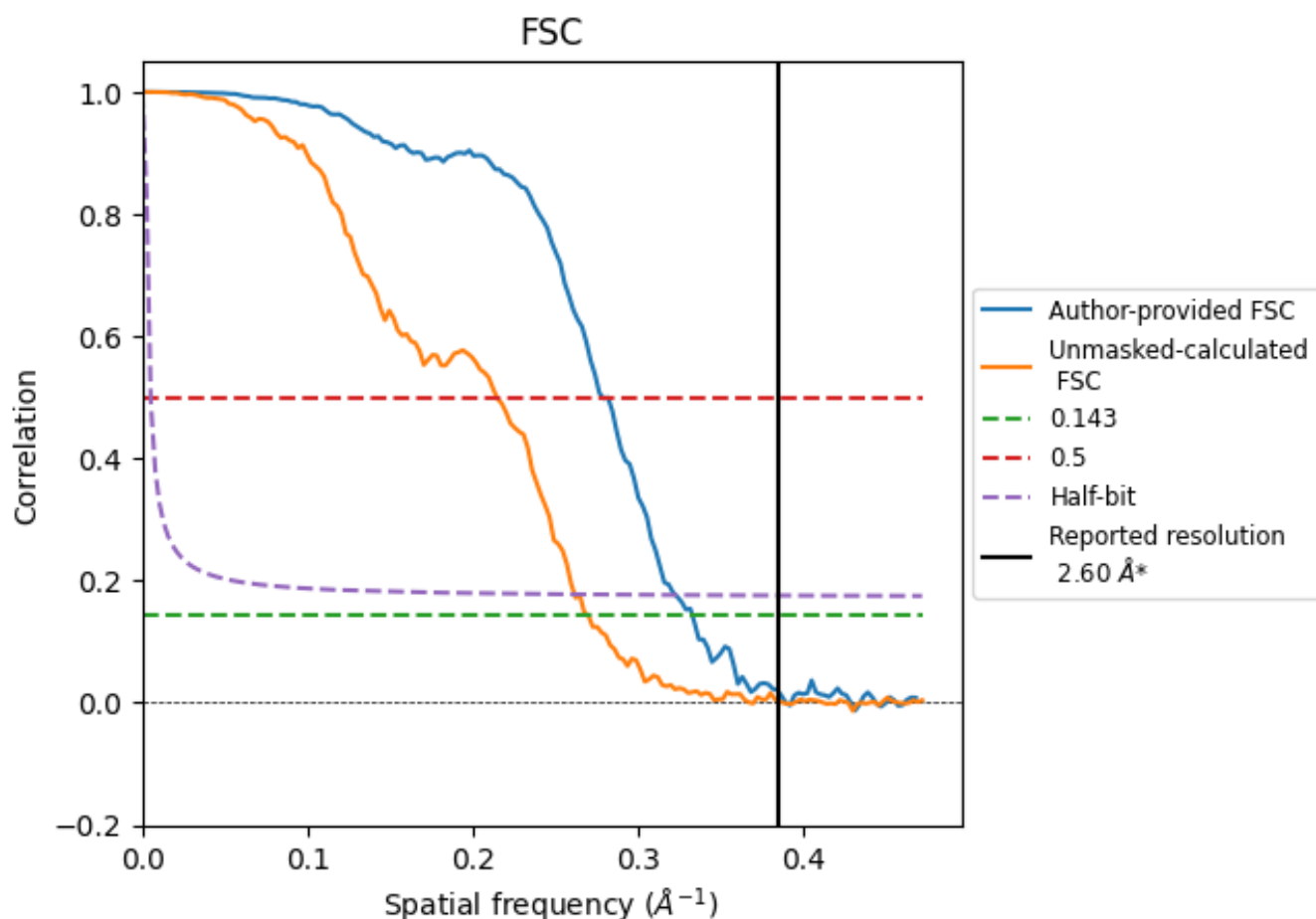


*Reported resolution corresponds to spatial frequency of 0.385 $\text{\AA}^{-1}$

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 $0.385 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	3.01	3.59	3.10
Unmasked-calculated*	3.71	4.66	3.83

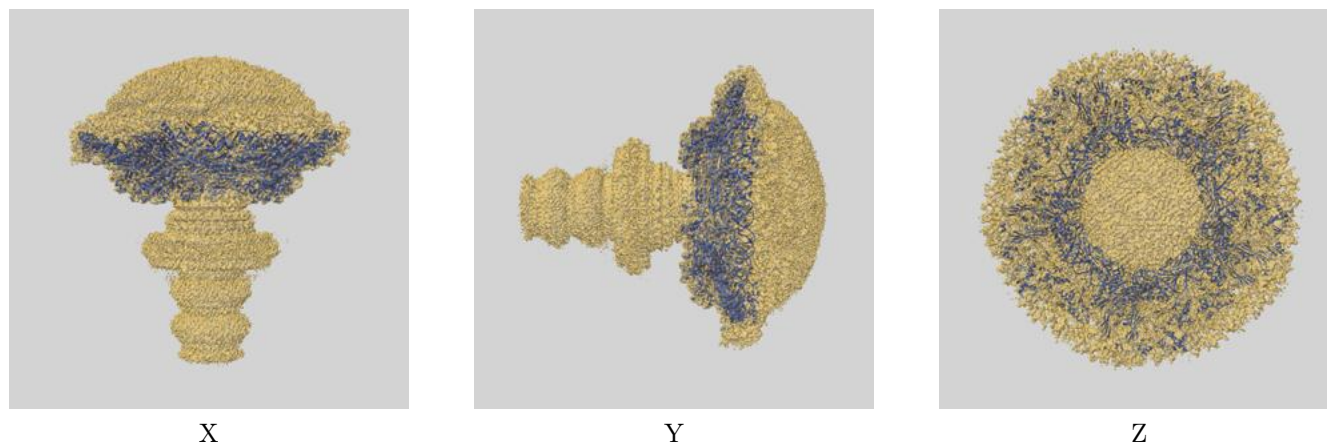
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.01 differs from the reported value 2.6 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.71 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

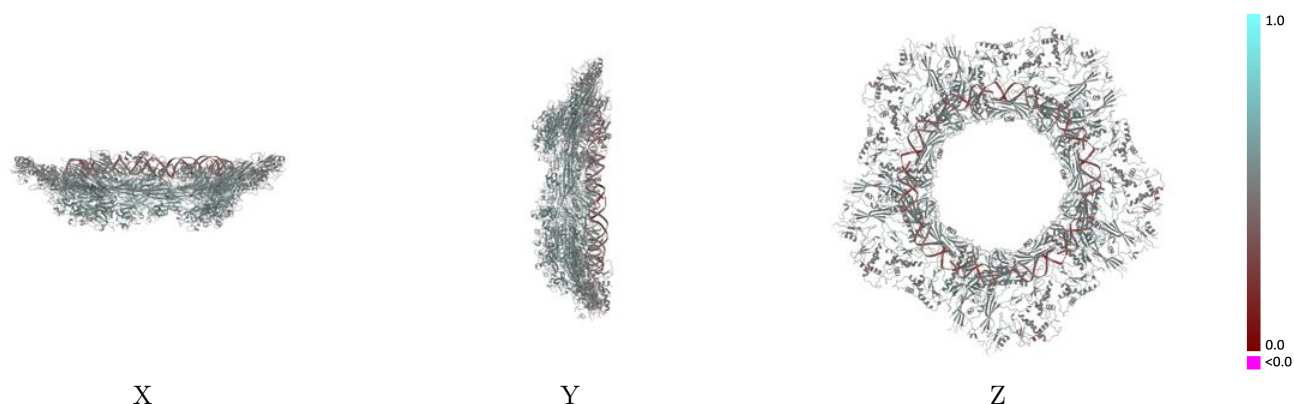
This section contains information regarding the fit between EMDB map EMD-70279 and PDB model 9OAC. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



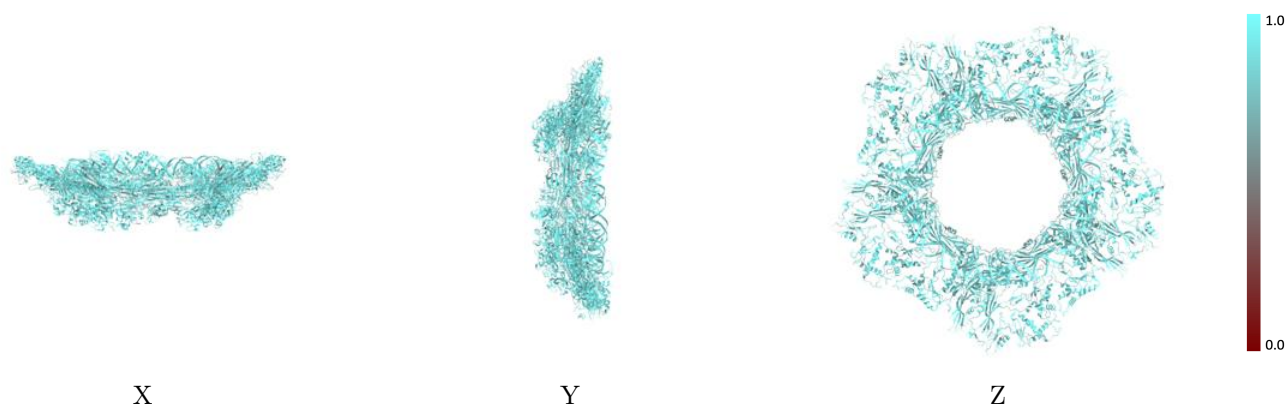
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



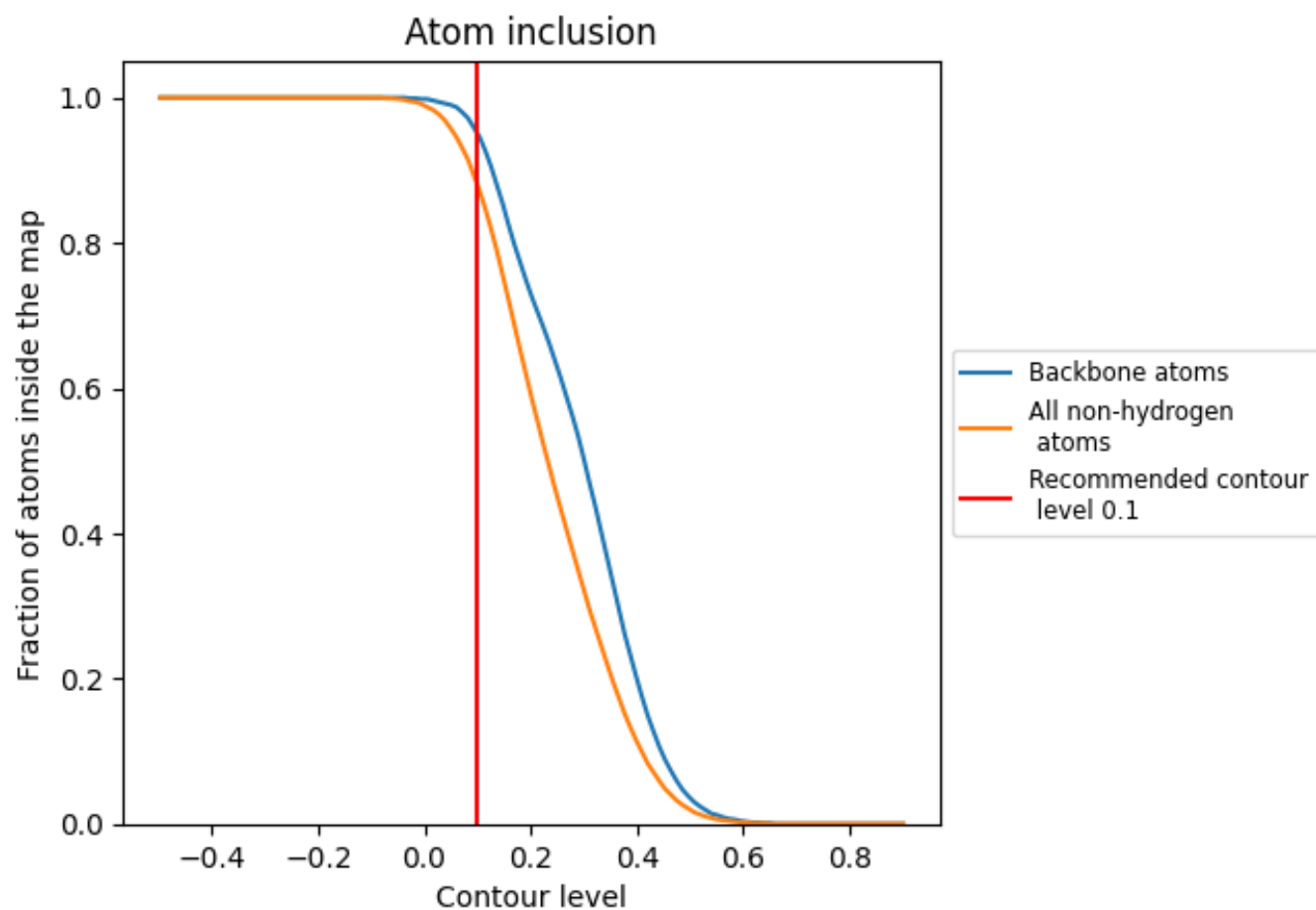
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.4980
Aa	 0.8370	 0.4910
Ab	 0.8840	 0.5150
Ac	 0.8990	 0.5220
Ad	 0.8650	 0.4750
Ae	 0.8580	 0.4940
Af	 0.8880	 0.5140
Ag	 0.8920	 0.5240
Ah	 0.8810	 0.4820
Ai	 0.8510	 0.4980
Aj	 0.8930	 0.5110
Ak	 0.8980	 0.5240
Al	 0.8680	 0.4820
Am	 0.8510	 0.5000
An	 0.8850	 0.5140
Ao	 0.8890	 0.5220
Ap	 0.8720	 0.4830
Aq	 0.8480	 0.5020
Ar	 0.8930	 0.5140
As	 0.8880	 0.5220
At	 0.8510	 0.4790
Ba	 0.7890	 0.5010
Bb	 0.9070	 0.5250
Bc	 0.8810	 0.5260
Bd	 0.9120	 0.5240
Be	 0.8030	 0.4970
Bf	 0.8970	 0.5210
Bg	 0.8720	 0.5270
Bh	 0.9060	 0.5280
Bi	 0.7940	 0.4930
Bj	 0.9080	 0.5210
Bk	 0.8910	 0.5290
Bl	 0.9170	 0.5300
Bm	 0.7940	 0.5020
Bn	 0.9090	 0.5270



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Chain	Atom inclusion	Q-score
Bo	 0.8750	 0.5260
Bp	 0.9130	 0.5310
Bq	 0.7940	 0.5050
Br	 0.8970	 0.5220
Bs	 0.8810	 0.5250
Bt	 0.9020	 0.5250
Ca	 0.8380	 0.5280
Cb	 0.8170	 0.5290
Cc	 0.8360	 0.5290
Cd	 0.8240	 0.5280
Ce	 0.8270	 0.5270
Ja	 0.8160	 0.3150
Jb	 0.8690	 0.3500
Jc	 0.8160	 0.3110
Jd	 0.8500	 0.3520
Je	 0.8190	 0.3120
Jf	 0.8630	 0.3500
Jg	 0.8210	 0.3120
Jh	 0.8590	 0.3520
Ji	 0.8160	 0.3130
Jj	 0.8620	 0.3530