



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 09:54 AM UTC

PDB ID : 9MOG / pdb_00009mog
EMDB ID : EMD-48459
Title : Structure of the distal part of the bacteriophage T4 tail
Authors : Fokine, A.; Zhu, J.; Klose, T.; Vago, F.; Arnaud, C.; Wang, Z.; Khare, B.;
Rossmann, M.G.; Chen, Z.; Sun, L.; Fang, Q.; Kuhn, R.; Rao, V.B.
Deposited on : 2024-12-26
Resolution : 3.60 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 : **FAILED**
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

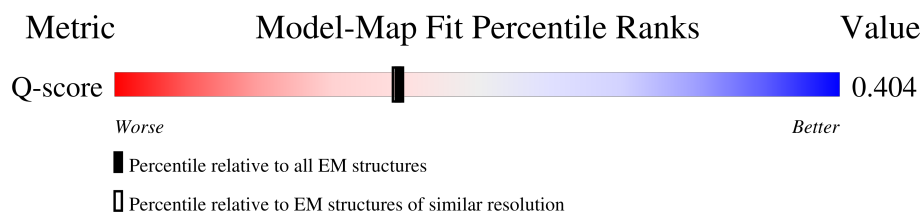
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	12797 (3.10 - 4.10)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 652117 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 gp12, short tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S0	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S1	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S2	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S3	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S4	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S5	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S6	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S7	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	S8	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	SA	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	SO	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	SP	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	SQ	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	Sv	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	Sw	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	Sx	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
1	Sy	526	Total 3945	C 2429	N 702	O 803	S 11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Sz	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		

- Molecule 2 is a protein called gp9, baseplate wedge tail fiber connector.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	T1	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T2	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T3	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T4	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T5	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T6	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T7	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T8	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	T9	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	TF	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	TG	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	TH	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	Td	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	Te	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	Tf	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	Tg	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	Th	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
2	Ti	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		

- Molecule 3 is a protein called gp11, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	UL	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	UM	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	UN	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Up	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Uq	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Ur	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Us	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Ut	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Uu	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	VL	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	VM	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	VN	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Vp	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Vq	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Vr	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Vs	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Vt	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
3	Vu	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		

- Molecule 4 is a protein called gp10, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	WI	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	WJ	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	WK	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Wj	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Wk	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Wl	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Wm	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Wn	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Wo	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	XI	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	XJ	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	XK	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Xj	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Xk	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Xl	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Xm	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Xn	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
4	Xo	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		

- Molecule 5 is a protein called gp7, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	YC	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
5	YX	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	YY	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
5	Yc	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
5	Yx	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
5	Yy	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		

- Molecule 6 is a protein called gp8, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	ZD	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
6	ZE	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
6	ZZ	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
6	Za	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
6	Zb	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
6	Zc	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
6	aD	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
6	aE	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
6	aZ	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
6	aa	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
6	ab	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
6	ac	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		

- Molecule 7 is a protein called gp18, tail sheath protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	b0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	b3	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	b4	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	b5	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	b6	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	b7	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	b8	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	b9	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	bN	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	bO	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	bP	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	bQ	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	bR	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	bY	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cA	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cB	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cC	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cD	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cE	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cF	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cG	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
7	cH	655	Total 5000	C 3152	N 841	O 996	S 11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	cI	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	cJ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	cK	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	cL	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	cM	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	cN	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	cO	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	cP	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
7	dS	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
7	dT	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
7	dU	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
7	dV	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
7	dW	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
7	dZ	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b0	109	ASN	SER	conflict	UNP A0A7S9SVW9
b0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b3	109	ASN	SER	conflict	UNP A0A7S9SVW9
b3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b4	109	ASN	SER	conflict	UNP A0A7S9SVW9
b4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b5	109	ASN	SER	conflict	UNP A0A7S9SVW9
b5	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
b5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b6	109	ASN	SER	conflict	UNP A0A7S9SVW9
b6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b7	109	ASN	SER	conflict	UNP A0A7S9SVW9
b7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b8	109	ASN	SER	conflict	UNP A0A7S9SVW9
b8	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b9	109	ASN	SER	conflict	UNP A0A7S9SVW9
b9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bN	109	ASN	SER	conflict	UNP A0A7S9SVW9
bN	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bN	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bO	109	ASN	SER	conflict	UNP A0A7S9SVW9
bO	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bO	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bP	109	ASN	SER	conflict	UNP A0A7S9SVW9
bP	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bP	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bQ	109	ASN	SER	conflict	UNP A0A7S9SVW9
bQ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bQ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bR	109	ASN	SER	conflict	UNP A0A7S9SVW9
bR	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bR	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bY	109	ASN	SER	conflict	UNP A0A7S9SVW9
bY	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bY	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cA	109	ASN	SER	conflict	UNP A0A7S9SVW9
cA	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cA	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cB	109	ASN	SER	conflict	UNP A0A7S9SVW9
cB	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cB	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cC	109	ASN	SER	conflict	UNP A0A7S9SVW9
cC	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cC	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cD	109	ASN	SER	conflict	UNP A0A7S9SVW9
cD	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
cD	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cE	109	ASN	SER	conflict	UNP A0A7S9SVW9
cE	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cE	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cF	109	ASN	SER	conflict	UNP A0A7S9SVW9
cF	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cF	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cG	109	ASN	SER	conflict	UNP A0A7S9SVW9
cG	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cG	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cH	109	ASN	SER	conflict	UNP A0A7S9SVW9
cH	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cH	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cI	109	ASN	SER	conflict	UNP A0A7S9SVW9
cI	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cI	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cJ	109	ASN	SER	conflict	UNP A0A7S9SVW9
cJ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cJ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cK	109	ASN	SER	conflict	UNP A0A7S9SVW9
cK	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cK	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cL	109	ASN	SER	conflict	UNP A0A7S9SVW9
cL	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cL	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cM	109	ASN	SER	conflict	UNP A0A7S9SVW9
cM	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cM	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cN	109	ASN	SER	conflict	UNP A0A7S9SVW9
cN	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cN	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cO	109	ASN	SER	conflict	UNP A0A7S9SVW9
cO	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cO	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cP	109	ASN	SER	conflict	UNP A0A7S9SVW9
cP	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cP	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dS	109	ASN	SER	conflict	UNP A0A7S9SVW9
dS	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dS	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dT	109	ASN	SER	conflict	UNP A0A7S9SVW9
dT	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
dT	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dU	109	ASN	SER	conflict	UNP A0A7S9SVW9
dU	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dU	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dV	109	ASN	SER	conflict	UNP A0A7S9SVW9
dV	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dV	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dW	109	ASN	SER	conflict	UNP A0A7S9SVW9
dW	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dW	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
dZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9

- Molecule 8 is a protein called gp6, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	eB	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
8	eU	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
8	eW	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
8	f9	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
8	fA	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
8	fB	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
8	fR	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
8	fS	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
8	fU	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
8	fW	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
8	fr	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
8	fs	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		

- Molecule 9 is a protein called gp5, baseplate central spike protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	gE	559	Total	C	N	O	S	0	0
			4321	2681	761	856	23		
9	gG	559	Total	C	N	O	S	0	0
			4321	2681	761	856	23		
9	gH	559	Total	C	N	O	S	0	0
			4321	2681	761	856	23		

- Molecule 10 is a protein called gp5.4, tip of the central spike.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	gd	96	Total	C	N	O	S	0	0
			709	447	120	139	3		

- Molecule 11 is a protein called gp19, tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	h1	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	h2	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hX	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	he	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hf	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hg	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hh	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hi	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hj	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	hk	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hl	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hm	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hn	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	ho	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hp	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hr	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hs	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	ht	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hu	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hv	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hw	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hx	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hy	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
11	hz	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

- Molecule 12 is a protein called gp27, baseplate hub protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	iC	375	Total	C	N	O	S	0	0
			3000	1916	491	575	18		
12	iD	375	Total	C	N	O	S	0	0
			3000	1916	491	575	18		
12	iF	375	Total	C	N	O	S	0	0
			3000	1916	491	575	18		

- Molecule 13 is a protein called gp29, tape measure protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	ja	20	Total	C	N	O	S	0	0
			137	84	22	30	1		
13	jb	20	Total	C	N	O	S	0	0
			137	84	22	30	1		
13	jc	20	Total	C	N	O	S	0	0
			137	84	22	30	1		

- Molecule 14 is a protein called gp53, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k3	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
14	k4	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
14	k7	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
14	k8	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
14	kV	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
14	lV	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		

- Molecule 15 is a protein called gp25, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	m1	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
15	m2	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
15	m5	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
15	m6	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
15	mT	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
15	nT	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		

- Molecule 16 is a protein called gp48, baseplate protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	o0	358	Total	C	N	O	S	0	0
			2749	1714	467	559	9		
16	o1	314	Total	C	N	O	S	0	0
			2436	1523	414	491	8		
16	o2	314	Total	C	N	O	S	0	0
			2436	1523	414	491	8		
16	o6	314	Total	C	N	O	S	0	0
			2436	1523	414	491	8		
16	pA	358	Total	C	N	O	S	0	0
			2749	1714	467	559	9		
16	pB	358	Total	C	N	O	S	0	0
			2749	1714	467	559	9		

- Molecule 17 is a protein called gp54, baseplate protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q3	207	Total	C	N	O	S	0	0
			1650	1037	280	321	12		
17	q4	207	Total	C	N	O	S	0	0
			1650	1037	280	321	12		
17	q5	213	Total	C	N	O	S	0	0
			1693	1064	287	330	12		
17	q7	213	Total	C	N	O	S	0	0
			1693	1064	287	330	12		
17	q8	207	Total	C	N	O	S	0	0
			1650	1037	280	321	12		
17	q9	213	Total	C	N	O	S	0	0
			1693	1064	287	330	12		

- Molecule 18 is a protein called unassigned peptide A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	rc	25	Total	C	N	O	0	0
			125	75	25	25		
18	rd	25	Total	C	N	O	0	0
			125	75	25	25		
18	re	25	Total	C	N	O	0	0
			125	75	25	25		
18	rf	25	Total	C	N	O	0	0
			125	75	25	25		
18	rg	25	Total	C	N	O	0	0
			125	75	25	25		
18	rh	25	Total	C	N	O	0	0
			125	75	25	25		

- Molecule 19 is a protein called unassigned peptide B.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	sQ	18	Total	C	N	O	0	0
			90	54	18	18		
19	sT	18	Total	C	N	O	0	0
			90	54	18	18		
19	sU	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 20 is a protein called unassigned peptide C.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	tS	10	Total	C	N	O	0	0
			50	30	10	10		
20	tX	10	Total	C	N	O	0	0
			50	30	10	10		
20	tY	10	Total	C	N	O	0	0
			50	30	10	10		

- Molecule 21 is a protein called unassigned peptide D.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	uR	7	Total	C	N	O	0	0
			35	21	7	7		
21	uV	7	Total	C	N	O	0	0
			35	21	7	7		
21	uW	7	Total	C	N	O	0	0
			35	21	7	7		

- Molecule 22 is a protein called unassigned peptide E.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	vZ	9	Total	C	N	O	0	0
			45	27	9	9		
22	va	9	Total	C	N	O	0	0
			45	27	9	9		
22	vb	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 23 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
23	S0	1	Total 1	Zn 1	0
23	S1	1	Total 1	Zn 1	0
23	S4	1	Total 1	Zn 1	0
23	SA	1	Total 1	Zn 1	0
23	SQ	1	Total 1	Zn 1	0
23	Sv	1	Total 1	Zn 1	0

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	113800	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 ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.101	Depositor
Minimum map value	-0.072	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	646.4, 646.4, 646.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.616, 1.616, 1.616	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

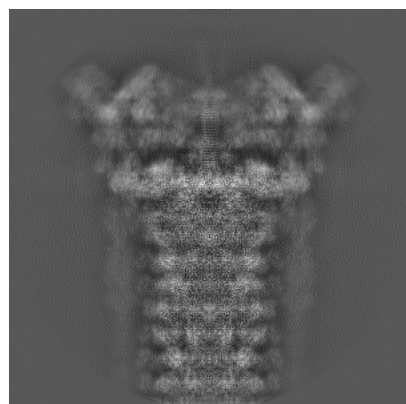
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48459. These allow visual inspection of the internal detail of the map and identification of artifacts.

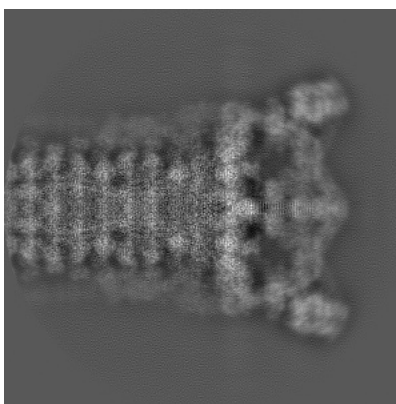
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

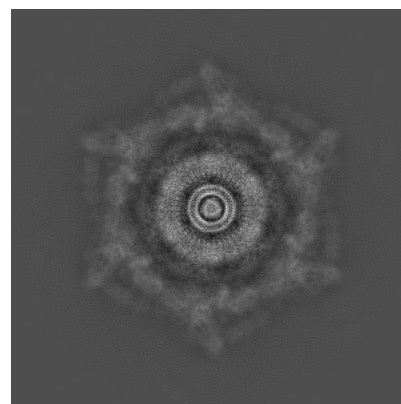
5.1.1 Primary map



X

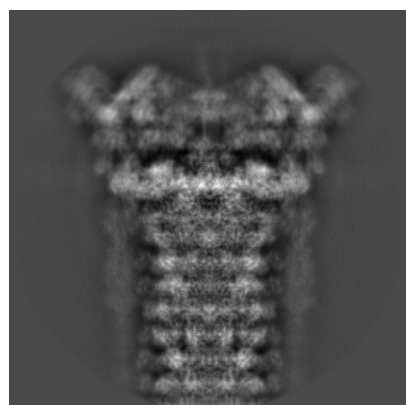


Y

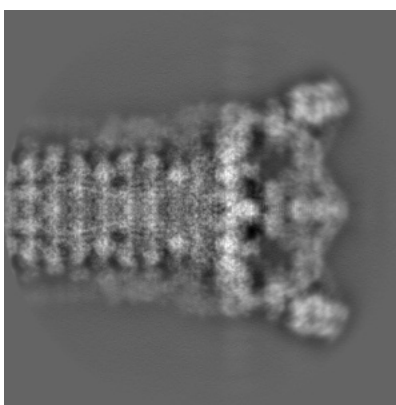


Z

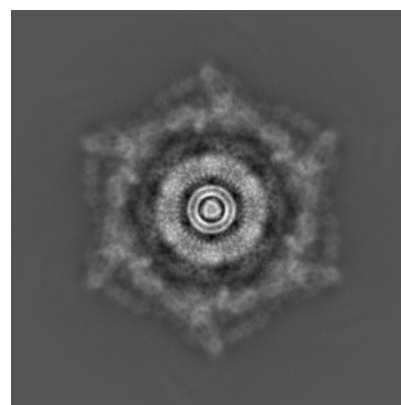
5.1.2 Raw map



X



Y



Z

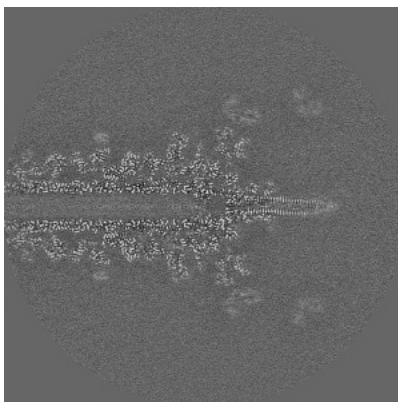
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

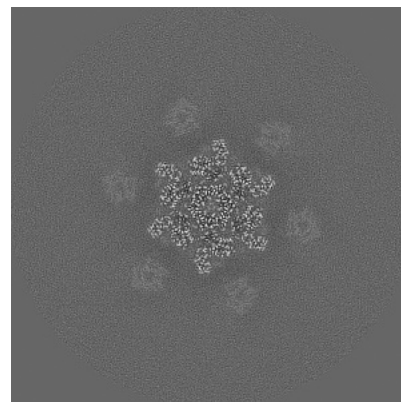
5.2.1 Primary map



X Index: 200

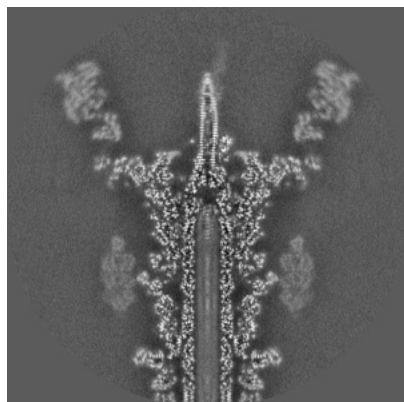


Y Index: 200

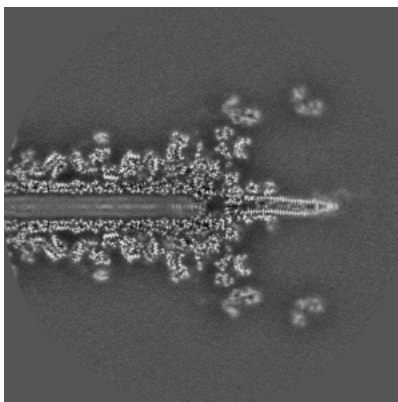


Z Index: 200

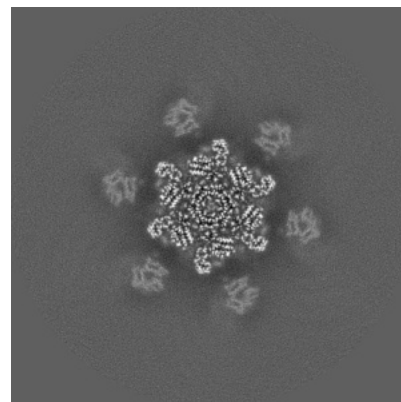
5.2.2 Raw map



X Index: 200



Y Index: 200

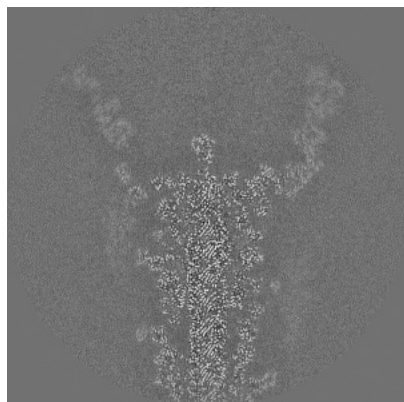


Z Index: 200

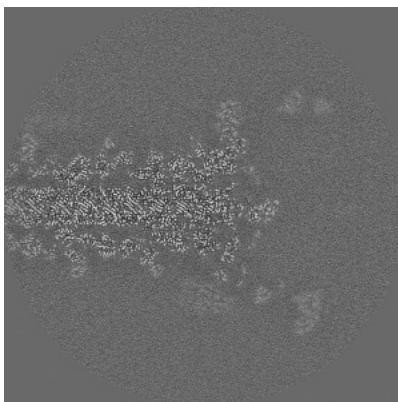
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

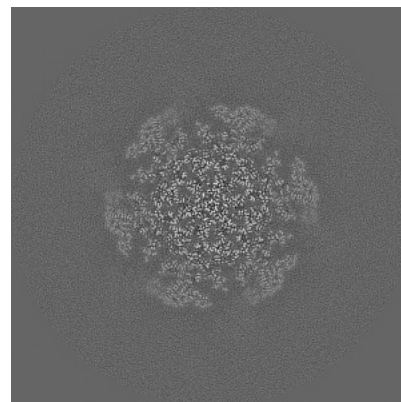
5.3.1 Primary map



X Index: 215

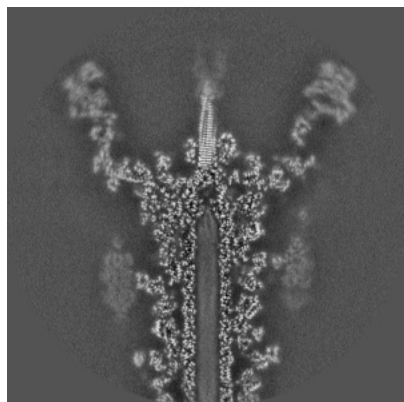


Y Index: 215

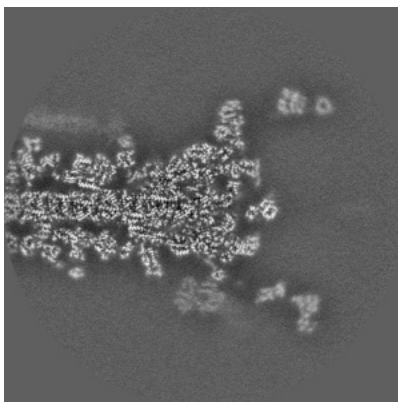


Z Index: 224

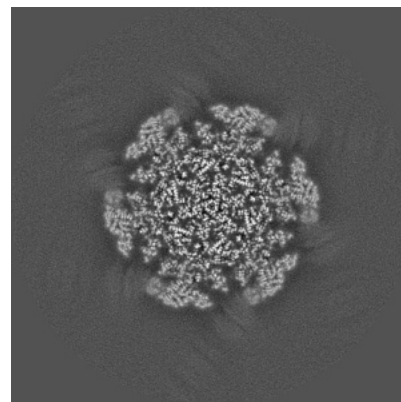
5.3.2 Raw map



X Index: 195



Y Index: 220

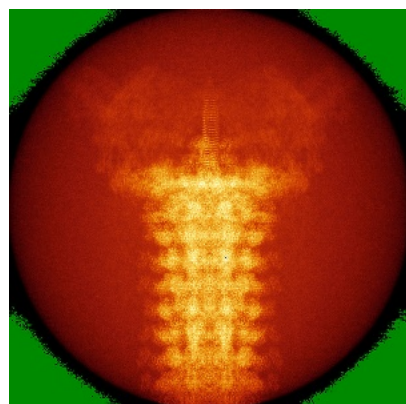


Z Index: 224

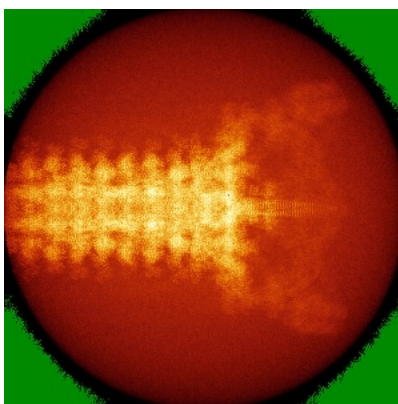
The images above show the largest variance slices of the map in three orthogonal directions.

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

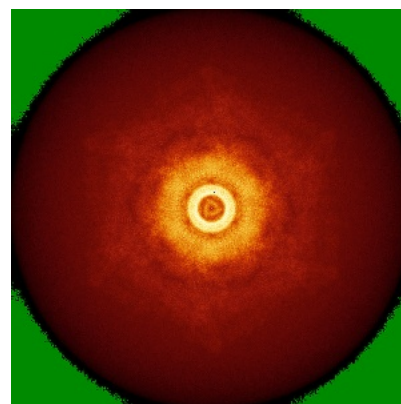
5.4.1 Primary map



X

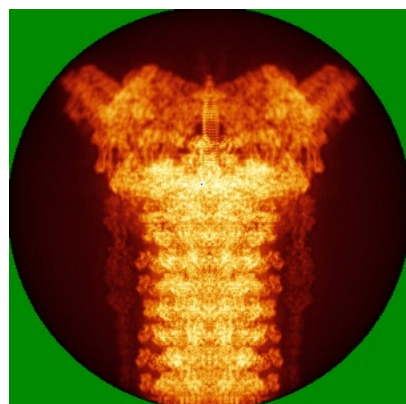


Y

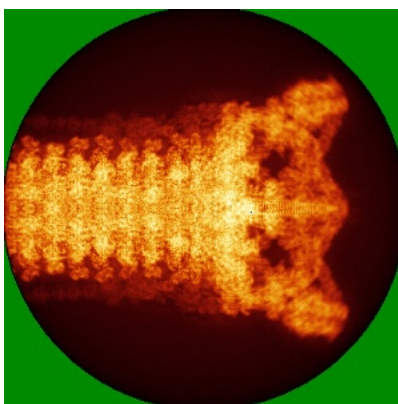


Z

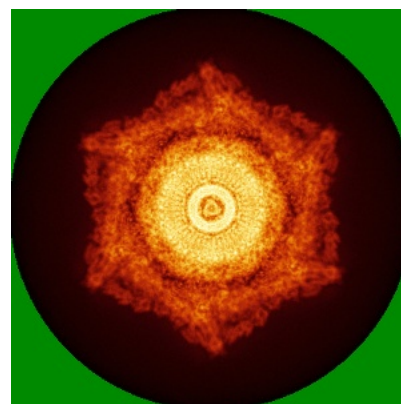
5.4.2 Raw map



X



Y

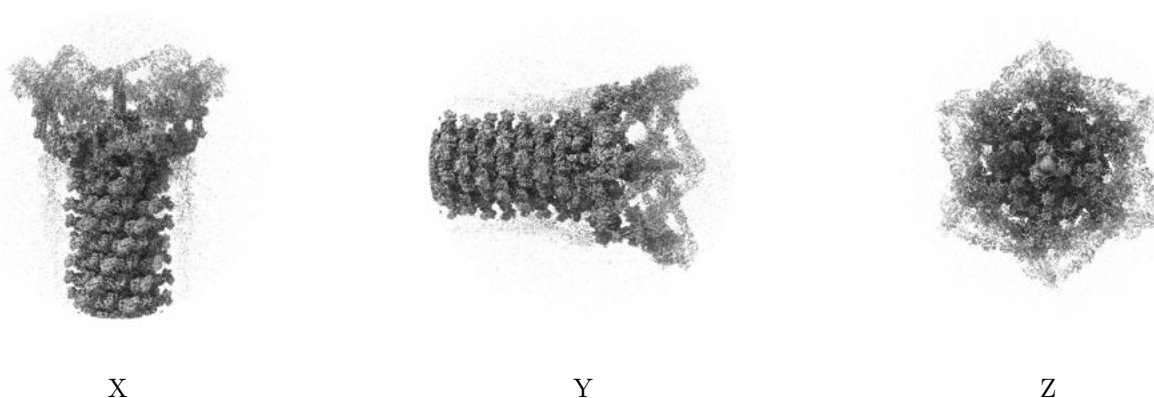


Z

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.

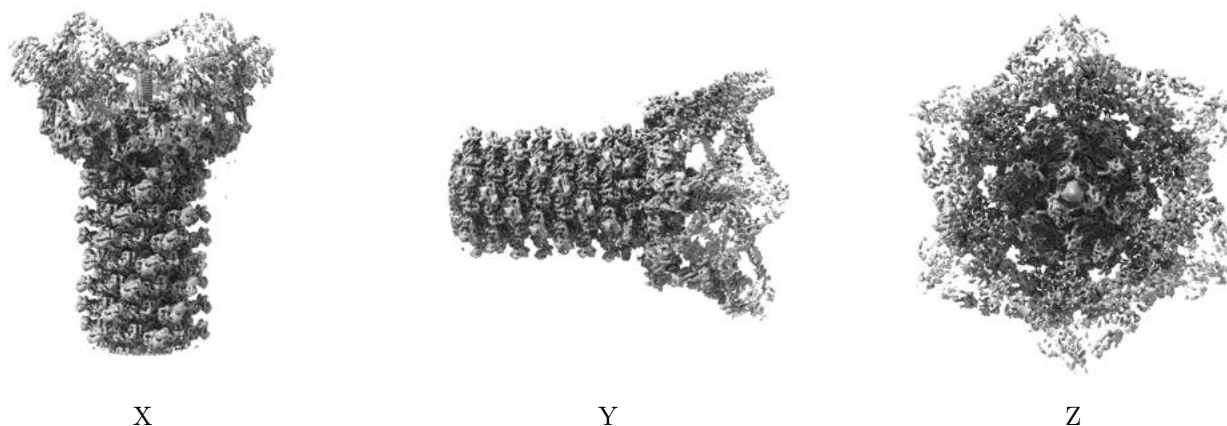
5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

5.5.2 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.

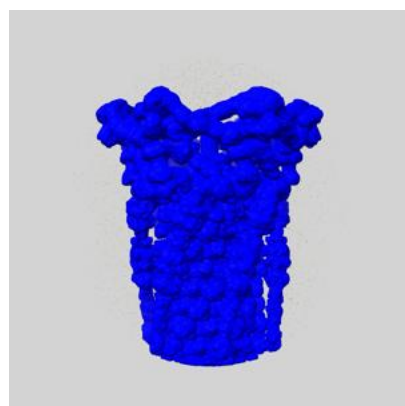
5.6 Mask visualisation [i](#)

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

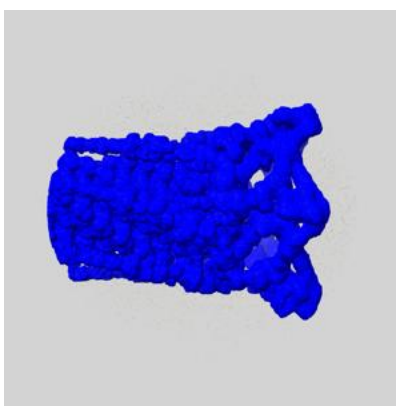
A mask typically either:

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

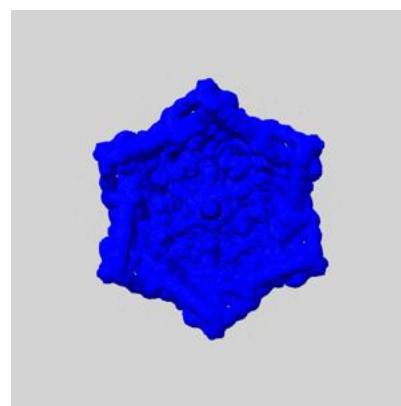
5.6.1 emd_48459_msk_1.map [i](#)



X



Y

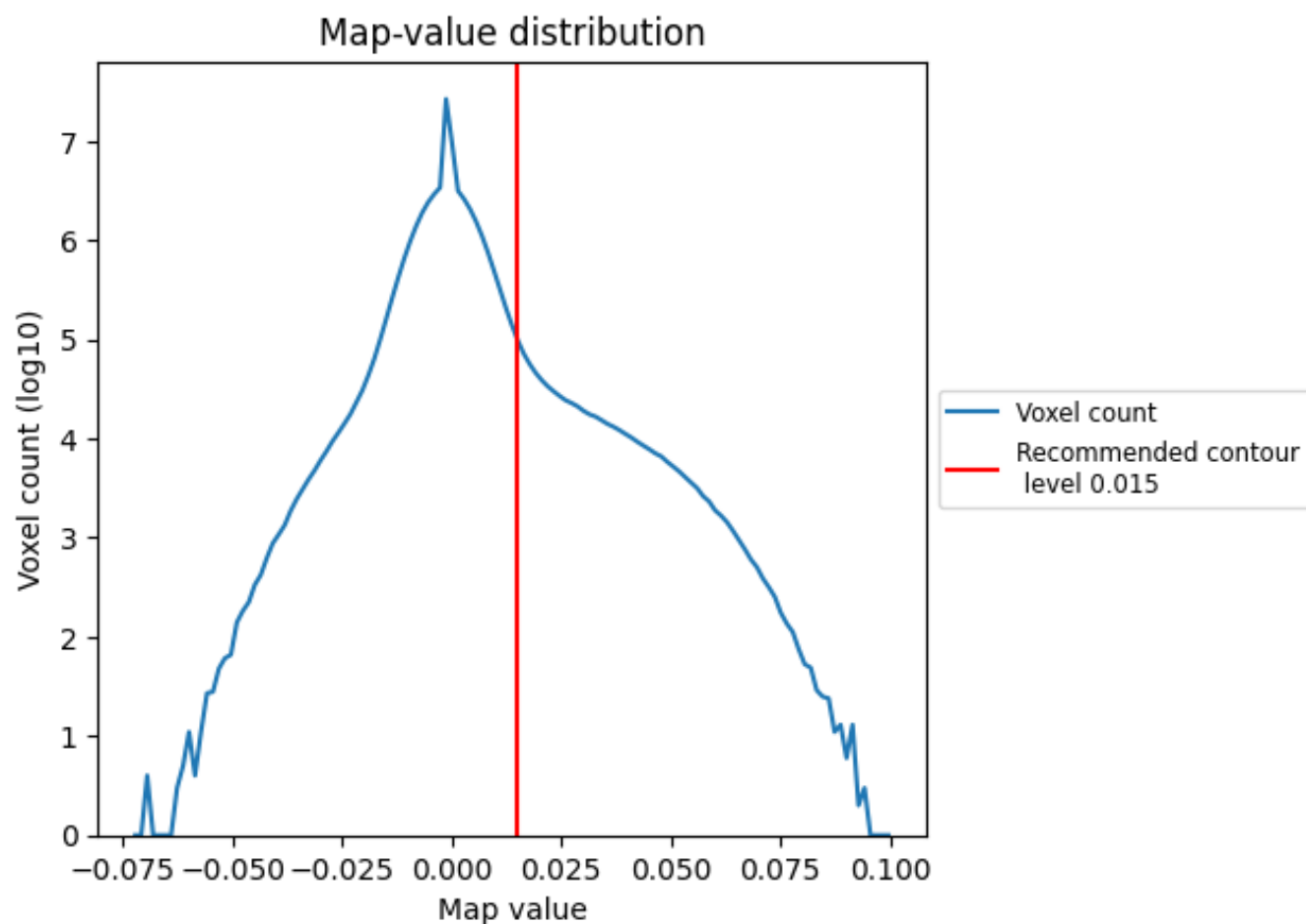


Z

6 Map analysis [i](#)

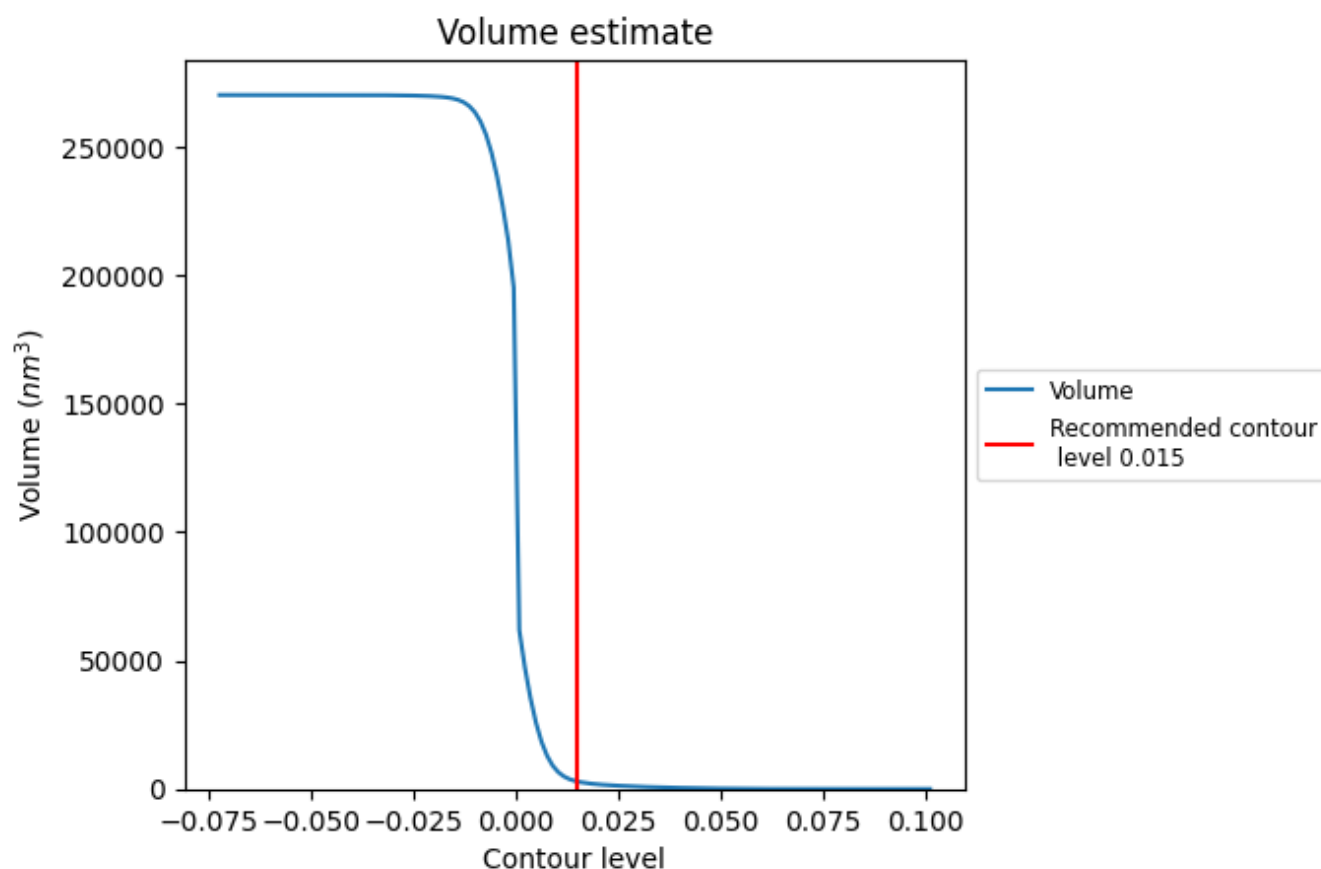
This section contains the results of statistical analysis of the map.

6.1 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.

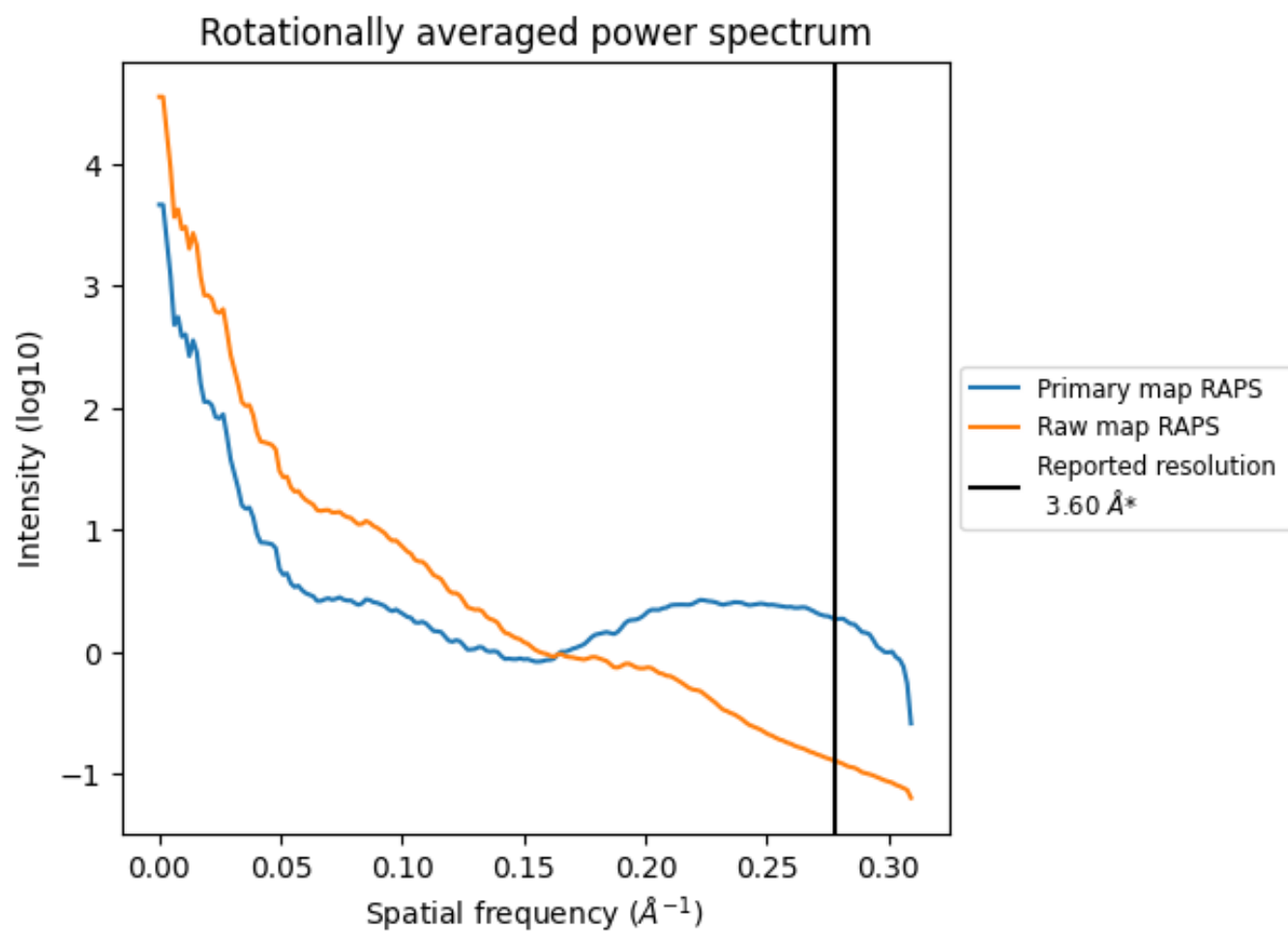
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 2938 nm³; this corresponds to an approximate mass of 2654 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.

6.3 Rotationally averaged power spectrum ⓘ

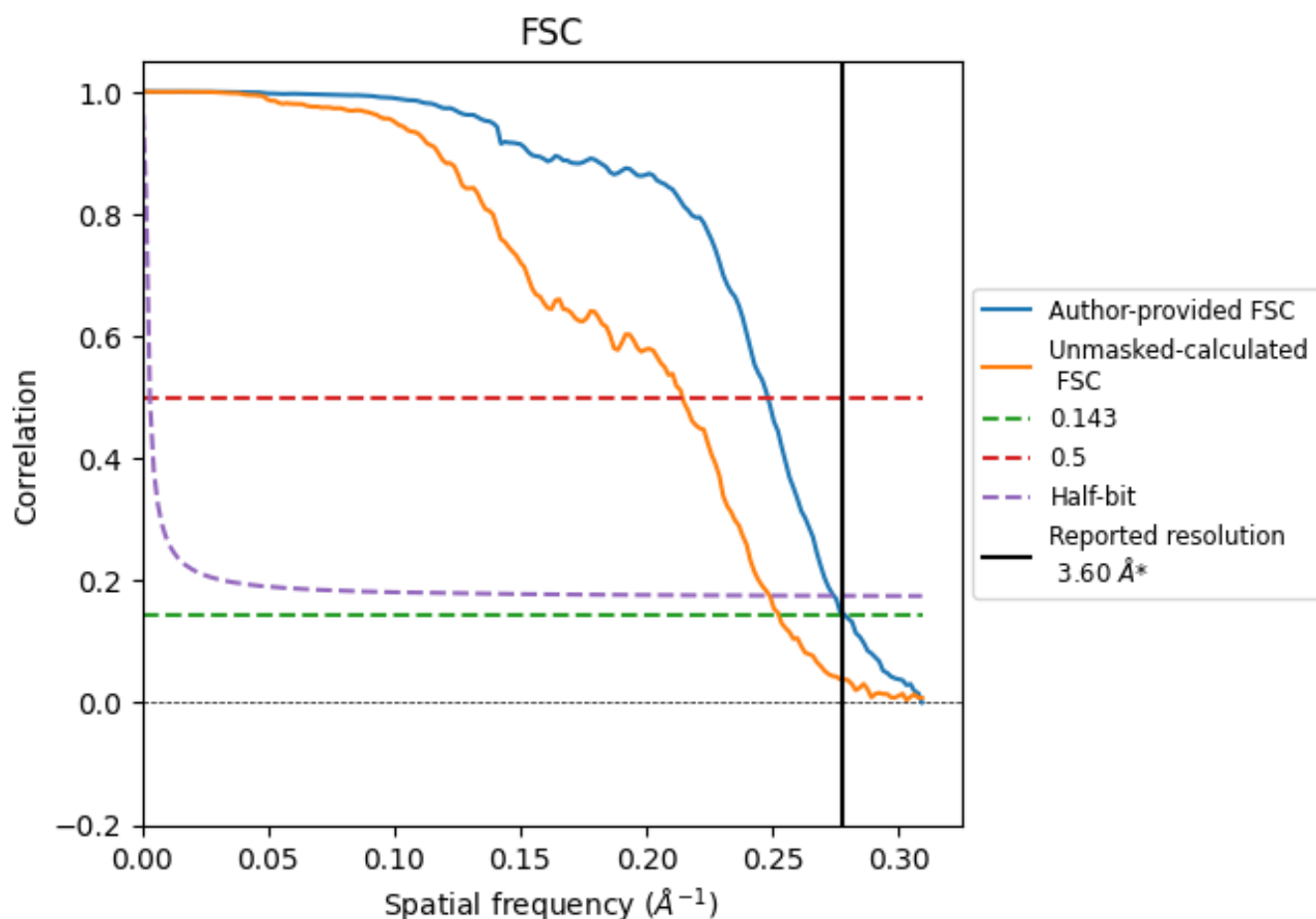


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

7 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.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

7.2 Resolution estimates [i](#)

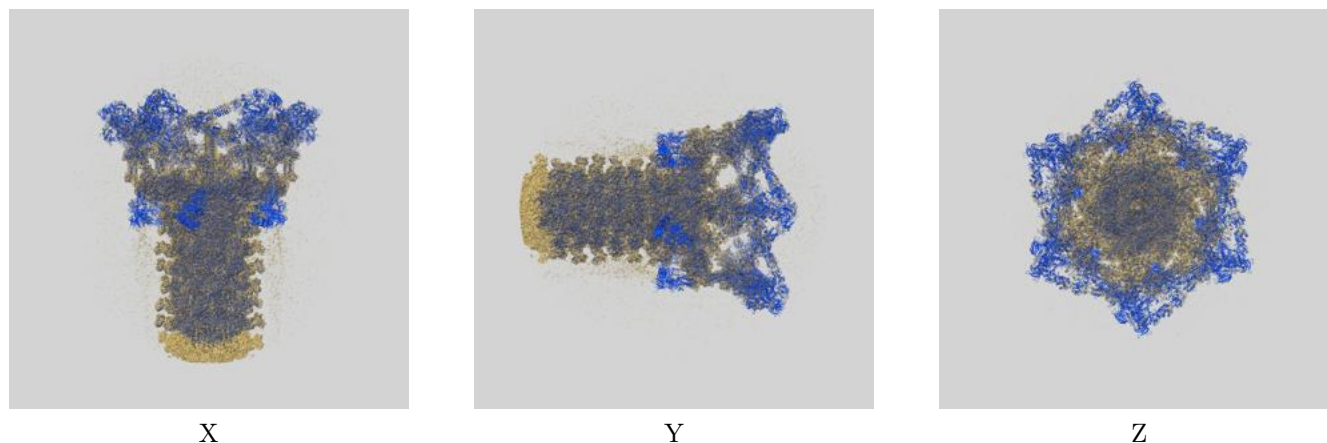
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	4.03	3.64
Unmasked-calculated*	3.96	4.67	4.02

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

8 Map-model fit [i](#)

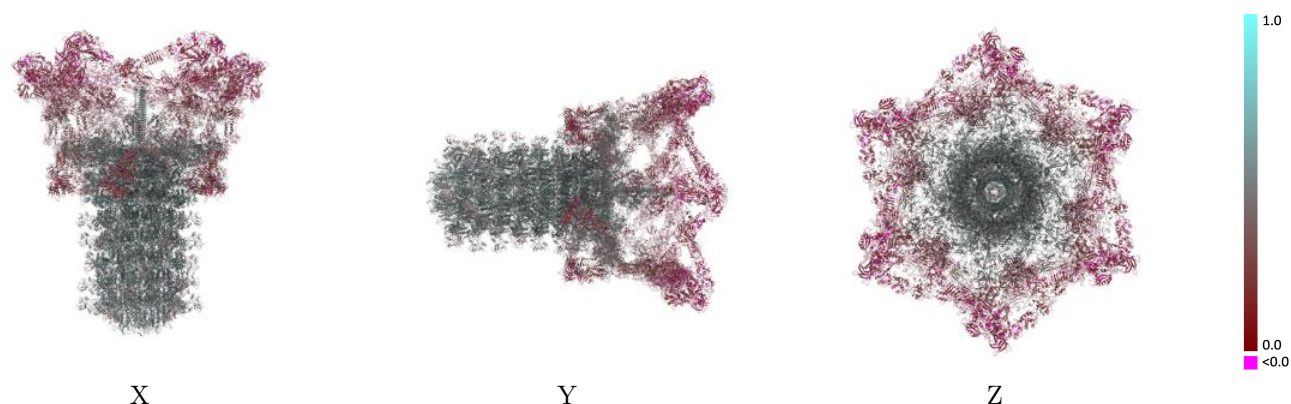
This section contains information regarding the fit between EMDB map EMD-48459 and PDB model 9MOG. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



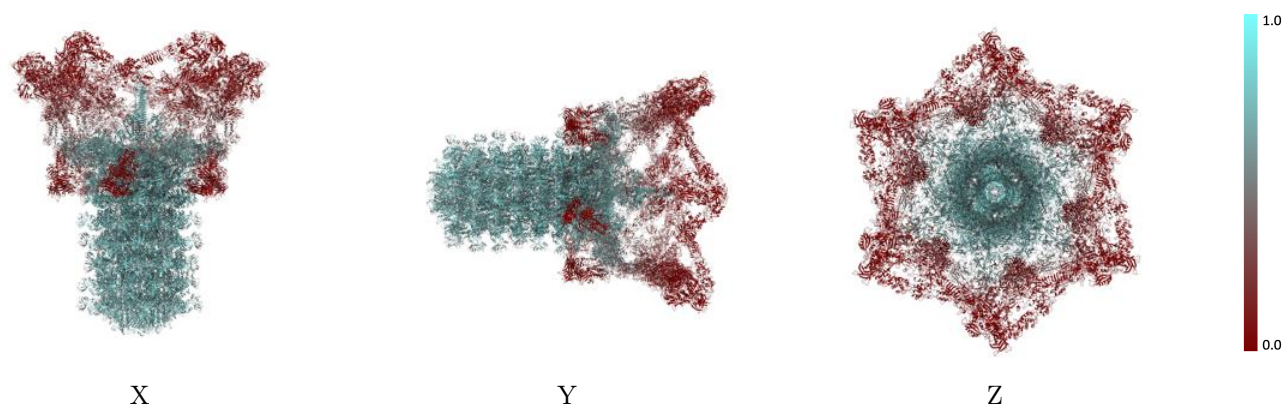
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



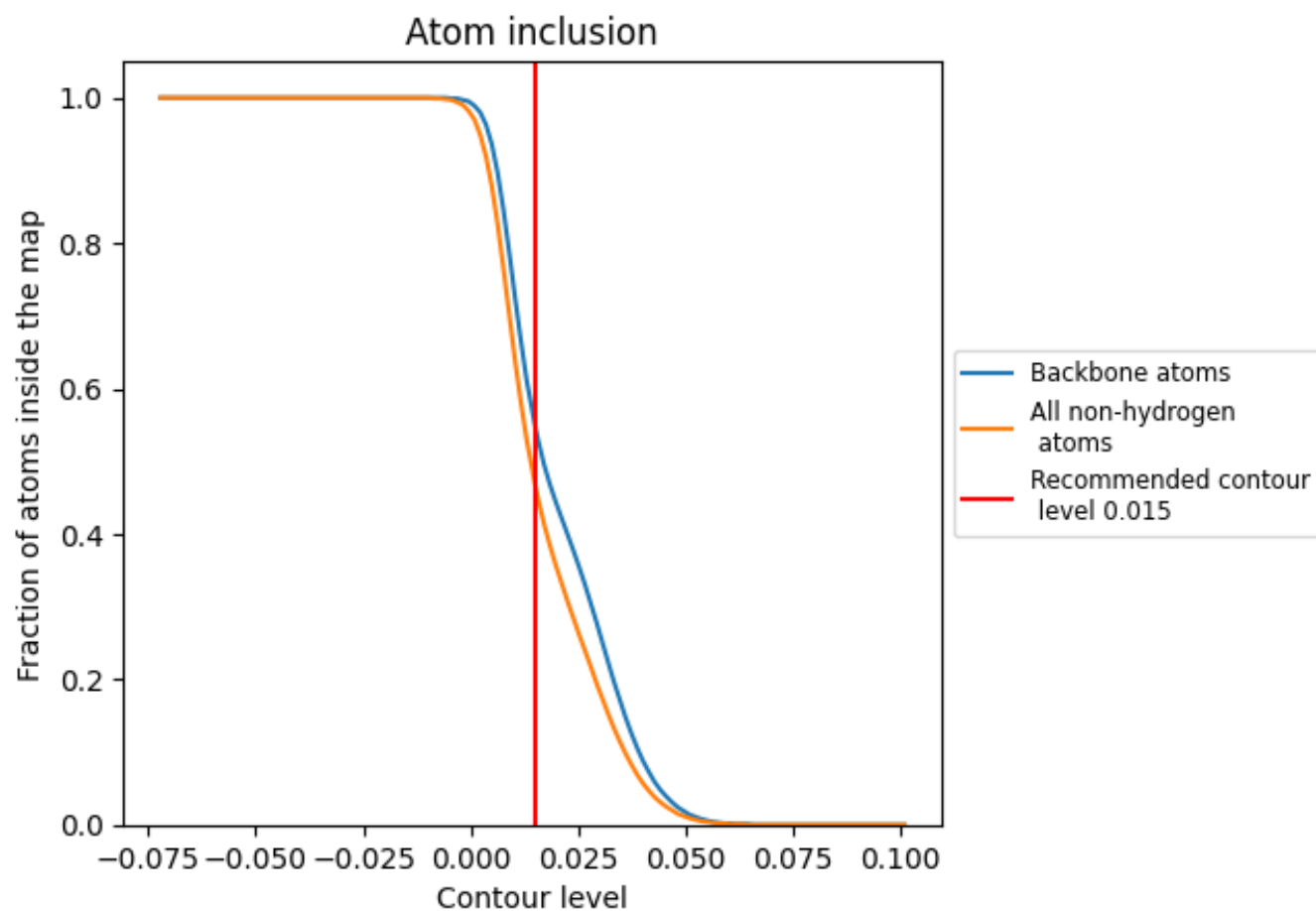
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

8.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 47% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.4690	 0.4040
S0	 0.0420	 0.1890
S1	 0.0590	 0.2030
S2	 0.0580	 0.1830
S3	 0.0560	 0.1970
S4	 0.0570	 0.2040
S5	 0.0580	 0.1910
S6	 0.0600	 0.1860
S7	 0.0590	 0.1820
S8	 0.0600	 0.1920
SA	 0.0550	 0.1920
SO	 0.0640	 0.1960
SP	 0.0600	 0.1830
SQ	 0.0500	 0.1960
Sv	 0.0570	 0.2010
Sw	 0.0590	 0.1960
Sx	 0.0590	 0.1860
Sy	 0.0630	 0.1790
Sz	 0.0570	 0.1960
T1	 0.0190	 0.2460
T2	 0.0190	 0.2560
T3	 0.0180	 0.2570
T4	 0.0200	 0.2460
T5	 0.0200	 0.2430
T6	 0.0230	 0.2630
T7	 0.0320	 0.2640
T8	 0.0220	 0.2580
T9	 0.0310	 0.2790
TF	 0.0170	 0.2440
TG	 0.0260	 0.2610
TH	 0.0270	 0.2780
Td	 0.0220	 0.2400
Te	 0.0240	 0.2420
Tf	 0.0230	 0.2580
Tg	 0.0330	 0.2620



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Chain	Atom inclusion	Q-score
Th	0.0230	0.2640
Ti	0.0280	0.2760
UL	0.0270	0.1850
UM	0.0190	0.1690
UN	0.0260	0.1630
Up	0.0220	0.1830
Uq	0.0230	0.1750
Ur	0.0250	0.1580
Us	0.0210	0.1640
Ut	0.0360	0.1680
Uu	0.0290	0.1560
VL	0.0220	0.1790
VM	0.0240	0.1590
VN	0.0300	0.1690
Vp	0.0210	0.1850
Vq	0.0300	0.1800
Vr	0.0240	0.1550
Vs	0.0160	0.1640
Vt	0.0330	0.1680
Vu	0.0330	0.1610
WI	0.1340	0.2510
WJ	0.1610	0.2510
WK	0.1630	0.2650
Wj	0.1360	0.2540
Wk	0.1340	0.2500
Wl	0.1580	0.2640
Wm	0.1580	0.2510
Wn	0.1520	0.2590
Wo	0.1610	0.2640
XI	0.1370	0.2480
XJ	0.1540	0.2600
XK	0.1560	0.2600
Xj	0.1370	0.2510
Xk	0.1360	0.2490
Xl	0.1550	0.2610
Xm	0.1650	0.2500
Xn	0.1560	0.2600
Xo	0.1630	0.2610
YC	0.5110	0.4190
YX	0.5230	0.4210
YY	0.5130	0.4190
Yc	0.5180	0.4190

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Chain	Atom inclusion	Q-score
Yx	 0.5130	 0.4190
Yy	 0.5160	 0.4180
ZD	 0.5180	 0.4190
ZE	 0.6070	 0.4770
ZZ	 0.5250	 0.4250
Za	 0.5040	 0.4170
Zb	 0.6070	 0.4740
Zc	 0.6030	 0.4770
aD	 0.5220	 0.4270
aE	 0.6080	 0.4720
aZ	 0.5270	 0.4290
aa	 0.5210	 0.4210
ab	 0.6120	 0.4730
ac	 0.6140	 0.4750
b0	 0.6990	 0.5000
b3	 0.6620	 0.4880
b4	 0.6540	 0.4830
b5	 0.6660	 0.4880
b6	 0.6580	 0.4820
b7	 0.6650	 0.4860
b8	 0.7020	 0.5000
b9	 0.7030	 0.4990
bN	 0.7160	 0.5180
bO	 0.7150	 0.5190
bP	 0.7180	 0.5220
bQ	 0.7140	 0.5170
bR	 0.7150	 0.5170
bY	 0.7150	 0.5200
cA	 0.7000	 0.4970
cB	 0.6960	 0.5000
cC	 0.7110	 0.5050
cD	 0.7100	 0.5060
cE	 0.6580	 0.4850
cF	 0.6990	 0.4970
cG	 0.7070	 0.5060
cH	 0.7010	 0.5040
cI	 0.7090	 0.5030
cJ	 0.7120	 0.5070
cK	 0.7090	 0.5060
cL	 0.7030	 0.5020
cM	 0.7000	 0.5040
cN	 0.7030	 0.5020

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Chain	Atom inclusion	Q-score
cO	 0.6970	 0.5030
cP	 0.7050	 0.5040
dS	 0.7200	 0.5230
dT	 0.7080	 0.5160
dU	 0.7230	 0.5230
dV	 0.7070	 0.5180
dW	 0.7250	 0.5210
dZ	 0.7060	 0.5170
eB	 0.6930	 0.5040
eU	 0.6930	 0.5080
eW	 0.6870	 0.5030
f9	 0.6960	 0.5080
fA	 0.6930	 0.5020
fB	 0.6890	 0.5050
fR	 0.6950	 0.5080
fS	 0.6970	 0.5090
fU	 0.6870	 0.5070
fW	 0.6920	 0.5030
fr	 0.6970	 0.5070
fs	 0.6890	 0.5050
gE	 0.7630	 0.5270
gG	 0.7660	 0.5280
gH	 0.7660	 0.5320
gd	 0.4620	 0.3220
h1	 0.7530	 0.5420
h2	 0.7560	 0.5430
hI	 0.7500	 0.5450
hJ	 0.7370	 0.5400
hK	 0.7510	 0.5440
hL	 0.7520	 0.5430
hM	 0.7590	 0.5430
hX	 0.7400	 0.5400
he	 0.6810	 0.5200
hf	 0.6890	 0.5250
hg	 0.6850	 0.5200
hh	 0.6790	 0.5200
hi	 0.6870	 0.5220
hj	 0.7290	 0.5300
hk	 0.7330	 0.5280
hl	 0.7330	 0.5350
hm	 0.7180	 0.5280
hn	 0.7370	 0.5310

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Chain	Atom inclusion	Q-score
ho	 0.7630	 0.5460
hp	 0.7490	 0.5380
hq	 0.7610	 0.5420
hr	 0.7600	 0.5410
hs	 0.7610	 0.5400
ht	 0.6810	 0.5190
hu	 0.7260	 0.5290
hv	 0.7560	 0.5430
hw	 0.7590	 0.5410
hx	 0.7640	 0.5460
hy	 0.7540	 0.5380
hz	 0.7560	 0.5450
iC	 0.7410	 0.5500
iD	 0.7460	 0.5490
iF	 0.7460	 0.5510
ja	 0.6930	 0.5360
jb	 0.6790	 0.5300
jc	 0.6930	 0.5190
k3	 0.7310	 0.5280
k4	 0.7290	 0.5290
k7	 0.7290	 0.5310
k8	 0.7320	 0.5280
kV	 0.7280	 0.5310
lV	 0.7360	 0.5290
m1	 0.6870	 0.5190
m2	 0.6120	 0.5020
m5	 0.6800	 0.5200
m6	 0.6040	 0.5030
mT	 0.6070	 0.5010
nT	 0.6790	 0.5160
o0	 0.6560	 0.5310
o1	 0.6070	 0.5080
o2	 0.6150	 0.5110
o6	 0.6080	 0.5110
pA	 0.6700	 0.5370
pB	 0.6660	 0.5300
q3	 0.7390	 0.5420
q4	 0.7450	 0.5420
q5	 0.7400	 0.5450
q7	 0.7430	 0.5460
q8	 0.7440	 0.5470
q9	 0.7430	 0.5450

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Chain	Atom inclusion	Q-score
rc	 0.8000	 0.5480
rd	 0.8240	 0.5430
re	 0.7920	 0.5290
rf	 0.8000	 0.5480
rg	 0.8080	 0.5310
rh	 0.8080	 0.5370
sQ	 0.6220	 0.5320
sT	 0.5890	 0.5290
sU	 0.6000	 0.5100
tS	 0.7600	 0.5060
tX	 0.6600	 0.4860
tY	 0.7000	 0.5000
uR	 0.6290	 0.5540
uV	 0.7140	 0.5230
uW	 0.6860	 0.5260
vZ	 0.8440	 0.5900
va	 0.8440	 0.5800
vb	 0.8000	 0.5640