



wwPDB EM Validation Summary Report ⓘ

Jun 3, 2026 – 05:23 PM EDT

PDB ID : 9YH7 / pdb_00009yh7
EMDB ID : EMD-72963
Title : Composite structure of the sheathed flagellar motor in *Vibrio cholerae* adopting a higher FOMC conformation
Authors : Guo, W.B.; Yue, J.
Deposited on : 2025-09-30
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

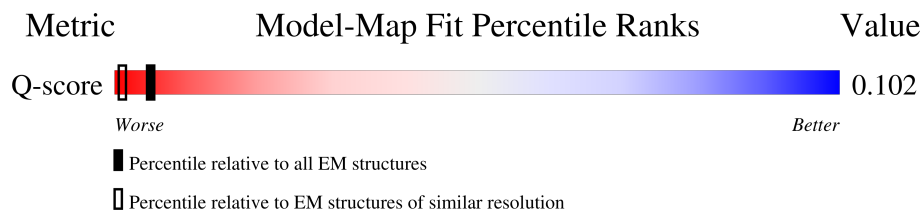
1 Overall quality at a glance

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 13 unique types of molecules in this entry. The entry contains 574924 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 Flagellar basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ab	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ac	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ad	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ae	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Af	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ag	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ah	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ai	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Aj	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ak	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Al	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Am	262	Total 1966	C 1215	N 339	O 403	S 9	0	0
1	An	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ao	262	Total 1969	C 1217	N 339	O 403	S 10	0	0
1	Ap	252	Total 1893	C 1173	N 323	O 387	S 10	0	0
1	Aq	262	Total 1969	C 1217	N 339	O 403	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ar	247	Total	C	N	O	S	0	0
			1863	1156	317	380	10		
1	As	262	Total	C	N	O	S	0	0
			1969	1217	339	403	10		
1	At	251	Total	C	N	O	S	0	0
			1889	1171	322	386	10		
1	Au	262	Total	C	N	O	S	0	0
			1969	1217	339	403	10		
1	Av	247	Total	C	N	O	S	0	0
			1859	1154	316	379	10		
1	Aw	262	Total	C	N	O	S	0	0
			1969	1217	339	403	10		
1	Ax	249	Total	C	N	O	S	0	0
			1876	1163	320	383	10		
1	Ay	248	Total	C	N	O	S	0	0
			1864	1158	316	380	10		
1	Az	249	Total	C	N	O	S	0	0
			1873	1161	319	383	10		
1	Bb	253	Total	C	N	O	S	0	0
			1900	1178	324	388	10		

- Molecule 2 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ba	241	Total	C	N	O	S	0	0
			1811	1112	327	361	11		
2	Bc	249	Total	C	N	O	S	0	0
			1870	1149	336	373	12		
2	Bd	244	Total	C	N	O	S	0	0
			1833	1125	331	365	12		
2	Bv	232	Total	C	N	O	S	0	0
			1737	1066	312	347	12		
2	Bw	249	Total	C	N	O	S	0	0
			1868	1147	336	373	12		

- Molecule 3 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Be	268	Total	C	N	O	S	0	0
			2045	1273	354	414	4		
3	Bf	268	Total	C	N	O	S	0	0
			2045	1273	354	414	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Bg	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bh	268	Total 2045	C 1273	N 354	O 414	S 4	0	0
3	Bi	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bj	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bk	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bl	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bm	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bn	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bo	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bp	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bq	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Br	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bs	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bt	270	Total 2065	C 1285	N 359	O 417	S 4	0	0
3	Bu	270	Total 2065	C 1285	N 359	O 417	S 4	0	0

- Molecule 4 is a protein called Flagellar L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Bx	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	By	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Bz	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ca	223	Total 1674	C 1027	N 290	O 353	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Cb	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cc	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cd	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ce	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cf	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cg	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ch	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ci	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cj	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ck	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cl	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cm	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cn	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Co	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cp	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cq	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cr	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cs	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Ct	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cu	223	Total 1674	C 1027	N 290	O 353	S 4	0	0
4	Cv	223	Total 1674	C 1027	N 290	O 353	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Cw	223	Total	C	N	O	S	0	0
			1674	1027	290	353	4		

- Molecule 5 is a protein called Flagellar P-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Cx	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Cy	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Cz	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Da	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Db	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dc	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dd	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	De	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Df	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dg	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dh	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Di	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dj	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dk	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dl	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dm	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dn	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Do	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Dp	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dq	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dr	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Ds	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dt	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Du	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dv	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		
5	Dw	316	Total	C	N	O	S	0	0
			2314	1457	404	446	7		

- Molecule 6 is a protein called Flagellar protein FlgT.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Dx	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Dy	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Dz	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ea	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eb	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ec	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ed	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ee	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ef	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eg	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eh	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	Ei	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ej	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ek	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	El	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Em	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	En	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eo	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ep	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eq	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Er	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Es	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Et	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Eu	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ev	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		
6	Ew	352	Total	C	N	O	S	0	0
			2770	1741	477	535	17		

- Molecule 7 is a protein called Sodium-type flagellar protein MotY.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ex	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
7	Ey	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		
7	Ez	257	Total	C	N	O	S	0	0
			2085	1312	362	404	7		
7	Fa	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	Fb	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fc	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fd	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fe	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Ff	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fg	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fh	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fi	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fj	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fk	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fl	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fm	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fn	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fo	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fp	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fq	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fr	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fs	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Ft	257	Total 2085	C 1312	N 362	O 404	S 7	0	0
7	Fu	258	Total 2080	C 1310	N 358	O 405	S 7	0	0
7	Fv	257	Total 2085	C 1312	N 362	O 404	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	Fw	258	Total	C	N	O	S	0	0
			2080	1310	358	405	7		

- Molecule 8 is a protein called Sodium-type flagellar protein MotX.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Fx	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Fy	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Fz	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Ga	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gb	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gc	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gd	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Ge	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gf	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gg	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gh	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gi	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gj	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gk	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gl	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gm	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gn	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Go	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	Gp	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gq	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gr	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gs	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gt	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gu	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		
8	Gv	183	Total	C	N	O	S	0	0
			1466	926	259	275	6		
8	Gw	183	Total	C	N	O	S	0	0
			1494	943	268	277	6		

- Molecule 9 is a protein called FlgP.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Gx	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Gy	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Gz	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Ha	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hb	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hc	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hd	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	He	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hf	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hg	12	Total	C	N	O	S	0	0
			105	66	19	19	1		
9	Hh	12	Total	C	N	O	S	0	0
			105	66	19	19	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	Hi	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hj	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hk	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hl	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hm	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hn	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ho	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hp	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hq	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hr	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hs	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ht	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hu	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hv	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hw	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hx	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hy	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Hz	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ia	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ib	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ic	12	Total 105	C 66	N 19	O 19	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	Id	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ie	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	If	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ig	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ih	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ii	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ij	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ik	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Il	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Im	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	In	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Io	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ip	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iq	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Ir	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Is	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	It	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iu	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iv	12	Total 105	C 66	N 19	O 19	S 1	0	0
9	Iw	12	Total 105	C 66	N 19	O 19	S 1	0	0

- Molecule 10 is a protein called Chemotaxis protein PomB.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ix	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Iy	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Iz	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Ja	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jb	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jc	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jd	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Je	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jf	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jg	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jh	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Ji	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jj	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jk	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jl	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jm	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jn	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jo	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jp	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jq	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jr	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Js	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	Jt	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Ju	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jv	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		
10	Jw	155	Total	C	N	O	S	0	0
			1231	758	229	241	3		

- Molecule 11 is a protein called FlgP.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Jx	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Jy	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Jz	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Ka	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kb	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kc	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kd	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Ke	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kf	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kg	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kh	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Ki	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kj	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kk	104	Total	C	N	O	S	0	0
			828	506	155	163	4		
11	Kl	104	Total	C	N	O	S	0	0
			828	506	155	163	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	Km	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kn	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ko	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kp	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kq	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kr	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ks	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kt	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ku	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kv	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kw	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kx	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ky	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Kz	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	La	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lb	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lc	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ld	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Le	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lf	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lg	104	Total 828	C 506	N 155	O 163	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	Lh	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Li	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lj	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lk	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ll	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lm	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ln	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lo	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lp	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lq	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lr	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ls	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lt	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lu	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lv	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lw	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lx	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ly	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Lz	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Ma	104	Total 828	C 506	N 155	O 163	S 4	0	0
11	Mb	104	Total 828	C 506	N 155	O 163	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	Mc	104	Total	C	N	O	S	0	0
			828	506	155	163	4		

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Jx	?	-	VAL	deletion	UNP Q9KQ01
Jy	?	-	VAL	deletion	UNP Q9KQ01
Jz	?	-	VAL	deletion	UNP Q9KQ01
Ka	?	-	VAL	deletion	UNP Q9KQ01
Kb	?	-	VAL	deletion	UNP Q9KQ01
Kc	?	-	VAL	deletion	UNP Q9KQ01
Kd	?	-	VAL	deletion	UNP Q9KQ01
Ke	?	-	VAL	deletion	UNP Q9KQ01
Kf	?	-	VAL	deletion	UNP Q9KQ01
Kg	?	-	VAL	deletion	UNP Q9KQ01
Kh	?	-	VAL	deletion	UNP Q9KQ01
Ki	?	-	VAL	deletion	UNP Q9KQ01
Kj	?	-	VAL	deletion	UNP Q9KQ01
Kk	?	-	VAL	deletion	UNP Q9KQ01
Kl	?	-	VAL	deletion	UNP Q9KQ01
Km	?	-	VAL	deletion	UNP Q9KQ01
Kn	?	-	VAL	deletion	UNP Q9KQ01
Ko	?	-	VAL	deletion	UNP Q9KQ01
Kp	?	-	VAL	deletion	UNP Q9KQ01
Kq	?	-	VAL	deletion	UNP Q9KQ01
Kr	?	-	VAL	deletion	UNP Q9KQ01
Ks	?	-	VAL	deletion	UNP Q9KQ01
Kt	?	-	VAL	deletion	UNP Q9KQ01
Ku	?	-	VAL	deletion	UNP Q9KQ01
Kv	?	-	VAL	deletion	UNP Q9KQ01
Kw	?	-	VAL	deletion	UNP Q9KQ01
Kx	?	-	VAL	deletion	UNP Q9KQ01
Ky	?	-	VAL	deletion	UNP Q9KQ01
Kz	?	-	VAL	deletion	UNP Q9KQ01
La	?	-	VAL	deletion	UNP Q9KQ01
Lb	?	-	VAL	deletion	UNP Q9KQ01
Lc	?	-	VAL	deletion	UNP Q9KQ01
Ld	?	-	VAL	deletion	UNP Q9KQ01
Le	?	-	VAL	deletion	UNP Q9KQ01
Lf	?	-	VAL	deletion	UNP Q9KQ01
Lg	?	-	VAL	deletion	UNP Q9KQ01

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Chain	Residue	Modelled	Actual	Comment	Reference
Lh	?	-	VAL	deletion	UNP Q9KQ01
Li	?	-	VAL	deletion	UNP Q9KQ01
Lj	?	-	VAL	deletion	UNP Q9KQ01
Lk	?	-	VAL	deletion	UNP Q9KQ01
Ll	?	-	VAL	deletion	UNP Q9KQ01
Lm	?	-	VAL	deletion	UNP Q9KQ01
Ln	?	-	VAL	deletion	UNP Q9KQ01
Lo	?	-	VAL	deletion	UNP Q9KQ01
Lp	?	-	VAL	deletion	UNP Q9KQ01
Lq	?	-	VAL	deletion	UNP Q9KQ01
Lr	?	-	VAL	deletion	UNP Q9KQ01
Ls	?	-	VAL	deletion	UNP Q9KQ01
Lt	?	-	VAL	deletion	UNP Q9KQ01
Lu	?	-	VAL	deletion	UNP Q9KQ01
Lv	?	-	VAL	deletion	UNP Q9KQ01
Lw	?	-	VAL	deletion	UNP Q9KQ01
Lx	?	-	VAL	deletion	UNP Q9KQ01
Ly	?	-	VAL	deletion	UNP Q9KQ01
Lz	?	-	VAL	deletion	UNP Q9KQ01
Ma	?	-	VAL	deletion	UNP Q9KQ01
Mb	?	-	VAL	deletion	UNP Q9KQ01
Mc	?	-	VAL	deletion	UNP Q9KQ01

- Molecule 12 is a protein called FlgO domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Md	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Me	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mf	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mg	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mh	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mi	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mj	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Mk	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	MI	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mm	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mn	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mo	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mp	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mq	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mr	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ms	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mt	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mu	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mv	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mw	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mx	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	My	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Mz	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Na	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nb	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nc	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nd	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ne	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nf	190	Total 1482	C 928	N 260	O 287	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	Ng	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nh	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ni	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nj	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nk	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nl	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nm	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nn	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	No	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Np	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nq	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nr	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ns	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nt	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nu	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nv	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nw	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nx	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Ny	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Nz	190	Total 1482	C 928	N 260	O 287	S 7	0	0
12	Oa	190	Total 1482	C 928	N 260	O 287	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	Ob	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Oc	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Od	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Oe	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Of	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Og	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Oh	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		
12	Oi	190	Total	C	N	O	S	0	0
			1482	928	260	287	7		

- Molecule 13 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Oj	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ok	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ol	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Om	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	On	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oo	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Op	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oq	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Or	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Os	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ot	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	Ou	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ov	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ow	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ox	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oy	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Oz	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pa	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pb	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pc	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pd	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pe	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pf	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pg	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Ph	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pi	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pj	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pk	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pl	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pm	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pn	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Po	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	Pp	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		
13	Pq	144	Total	C	N	O	S	0	0
			1134	702	201	230	1		

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, C26	Depositor
Number of particles used	5068	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 ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.766	Depositor
Minimum map value	-0.700	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	640.63995, 640.63995, 640.63995	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.43, 1.43, 1.43	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](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

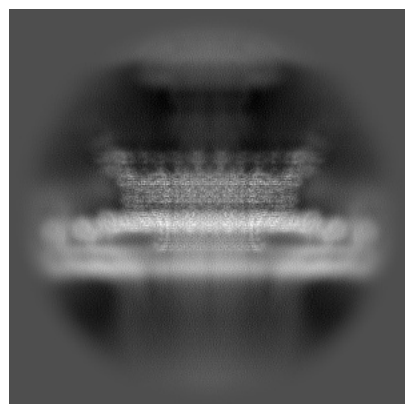
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72963. These allow visual inspection of the internal detail of the map and identification of artifacts.

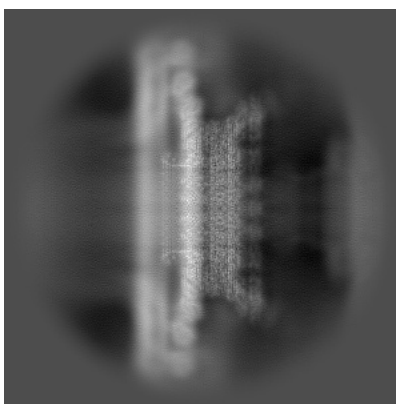
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

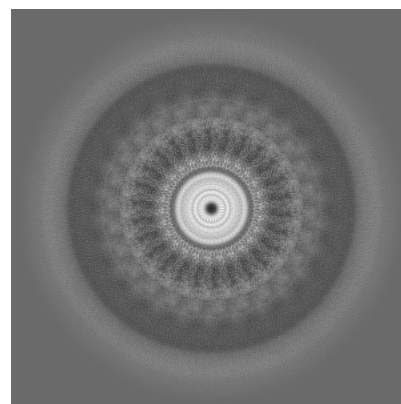
5.1.1 Primary map



X

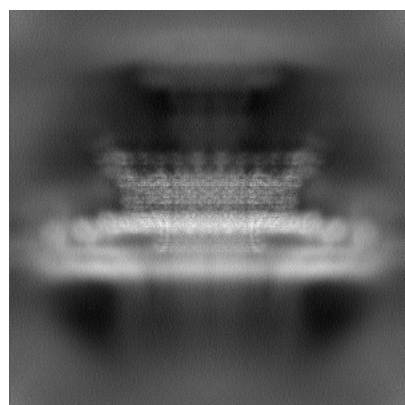


Y

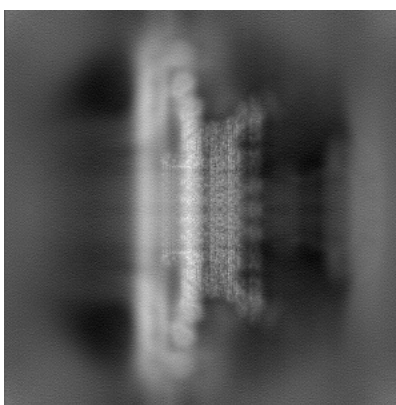


Z

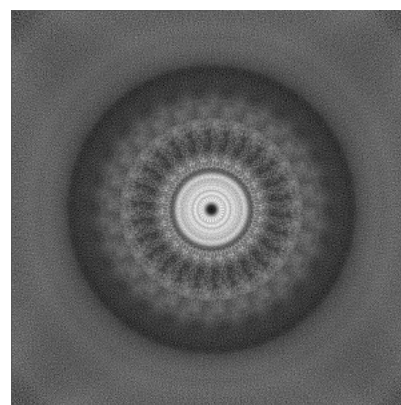
5.1.2 Raw map



X



Y

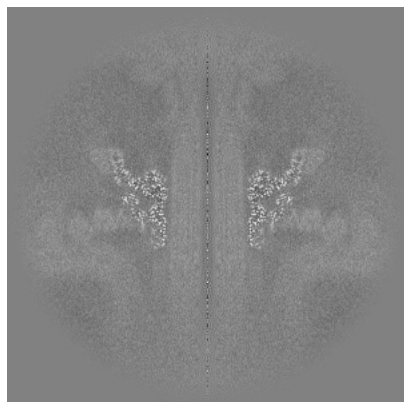


Z

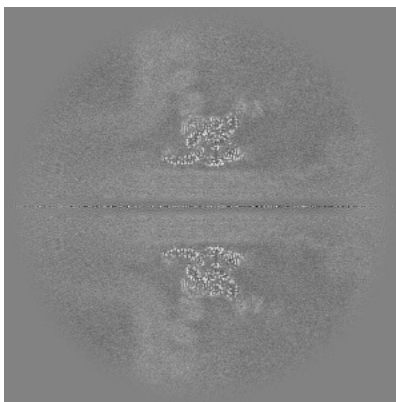
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

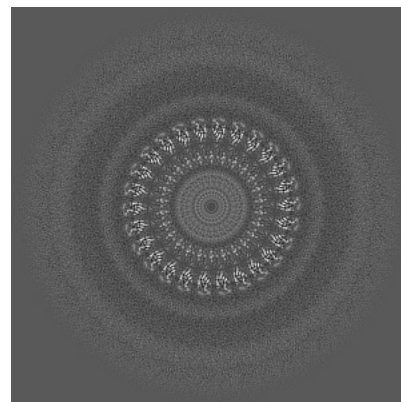
5.2.1 Primary map



X Index: 224

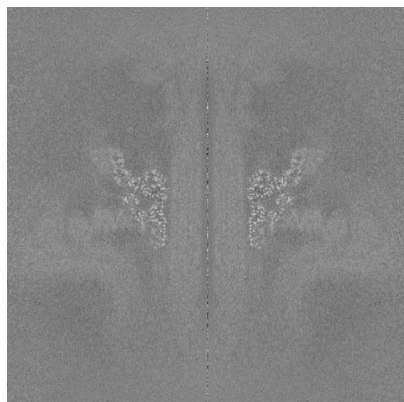


Y Index: 224

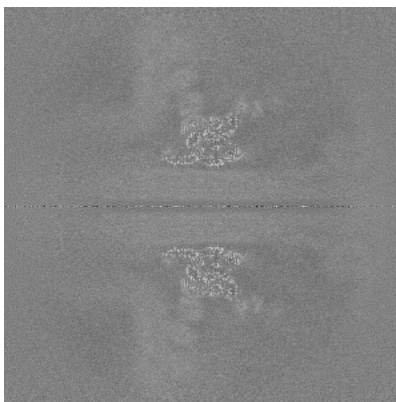


Z Index: 224

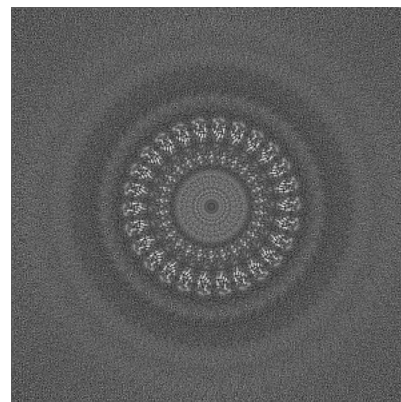
5.2.2 Raw map



X Index: 224



Y Index: 224

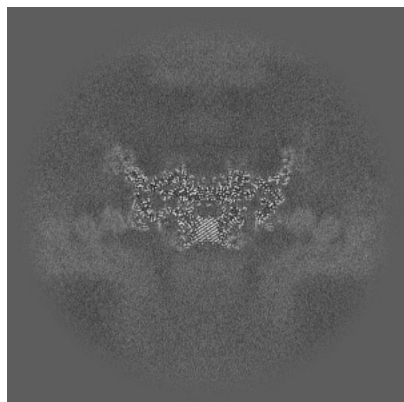


Z Index: 224

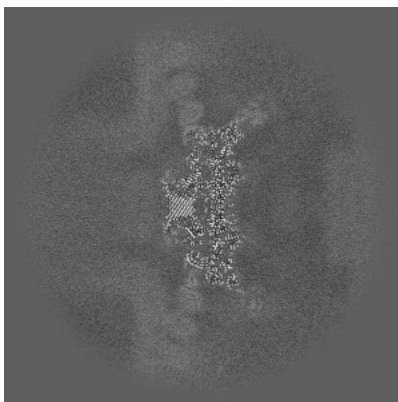
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

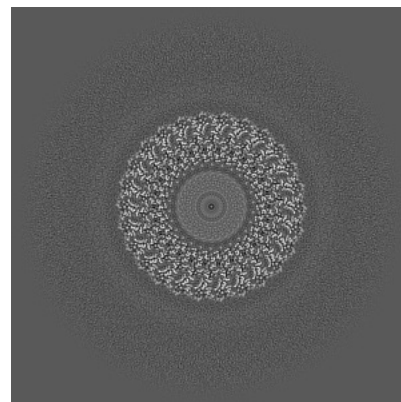
5.3.1 Primary map



X Index: 176

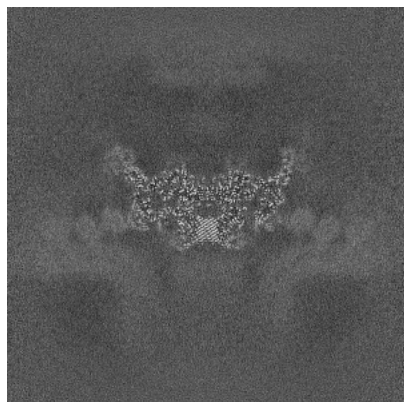


Y Index: 272

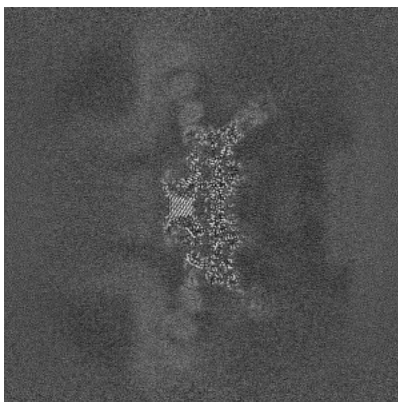


Z Index: 254

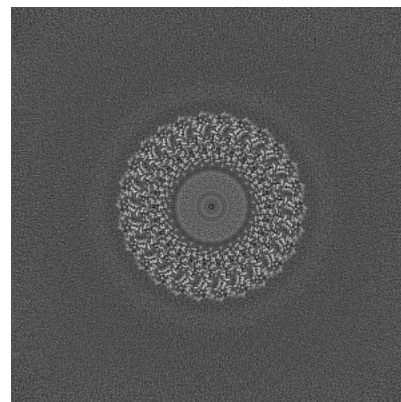
5.3.2 Raw map



X Index: 176



Y Index: 272

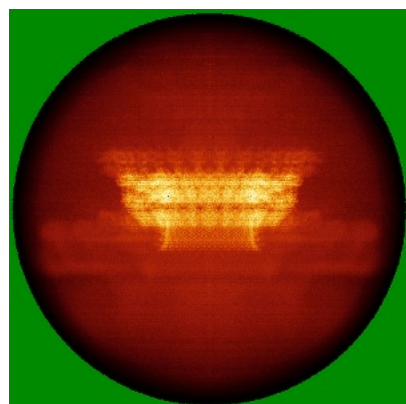


Z Index: 254

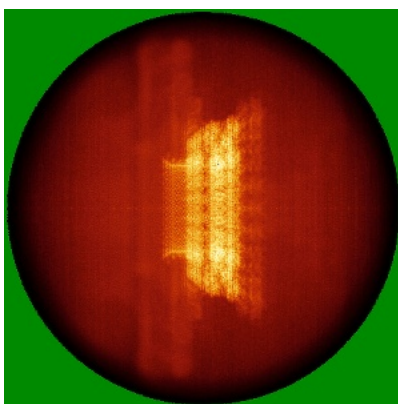
The images above show the largest variance slices of the map in three orthogonal directions.

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

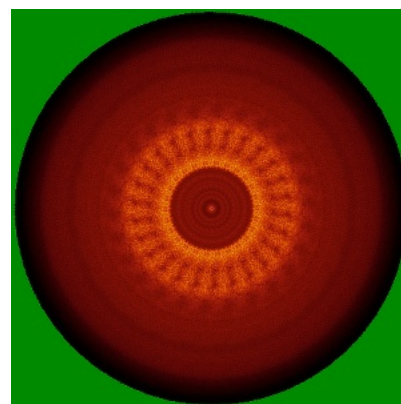
5.4.1 Primary map



X

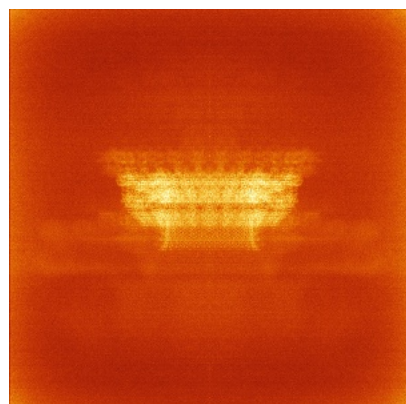


Y

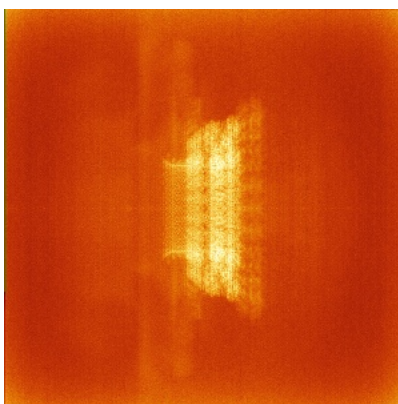


Z

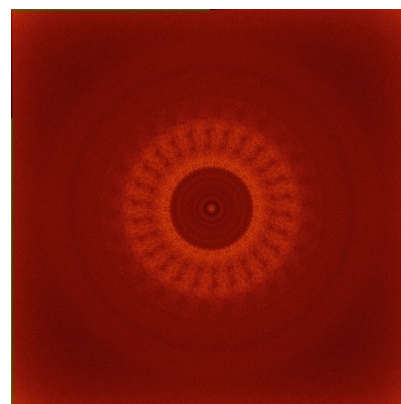
5.4.2 Raw map



X



Y

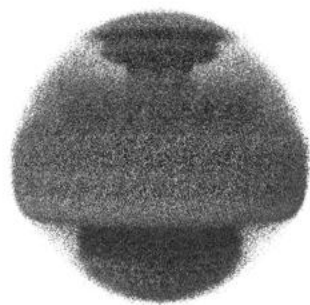


Z

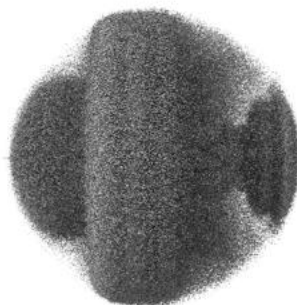
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

5.5 Orthogonal surface views [i](#)

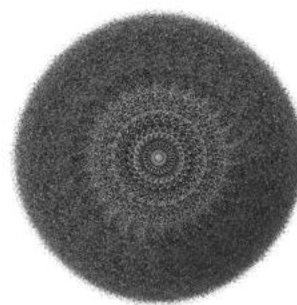
5.5.1 Primary map



X



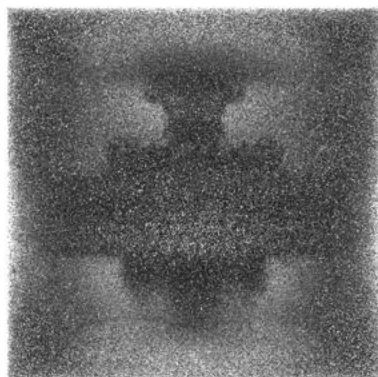
Y



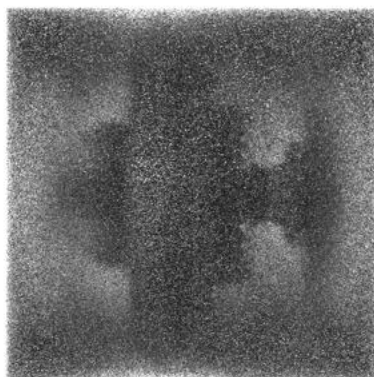
Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

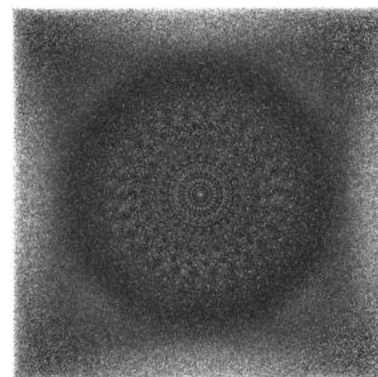
5.5.2 Raw map



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.

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_72963_msk_1.map [i](#)



X



Y

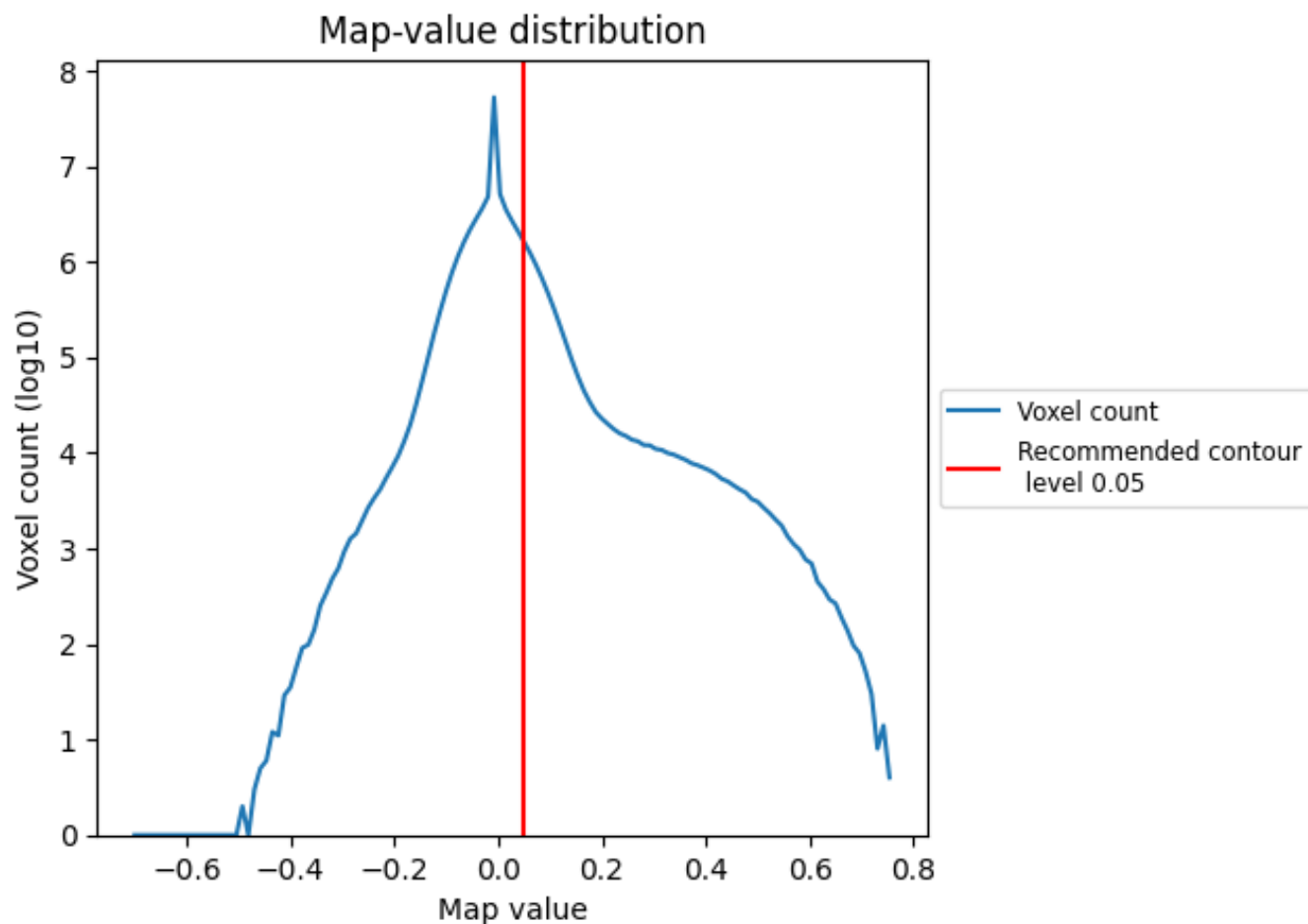


Z

6 Map analysis [i](#)

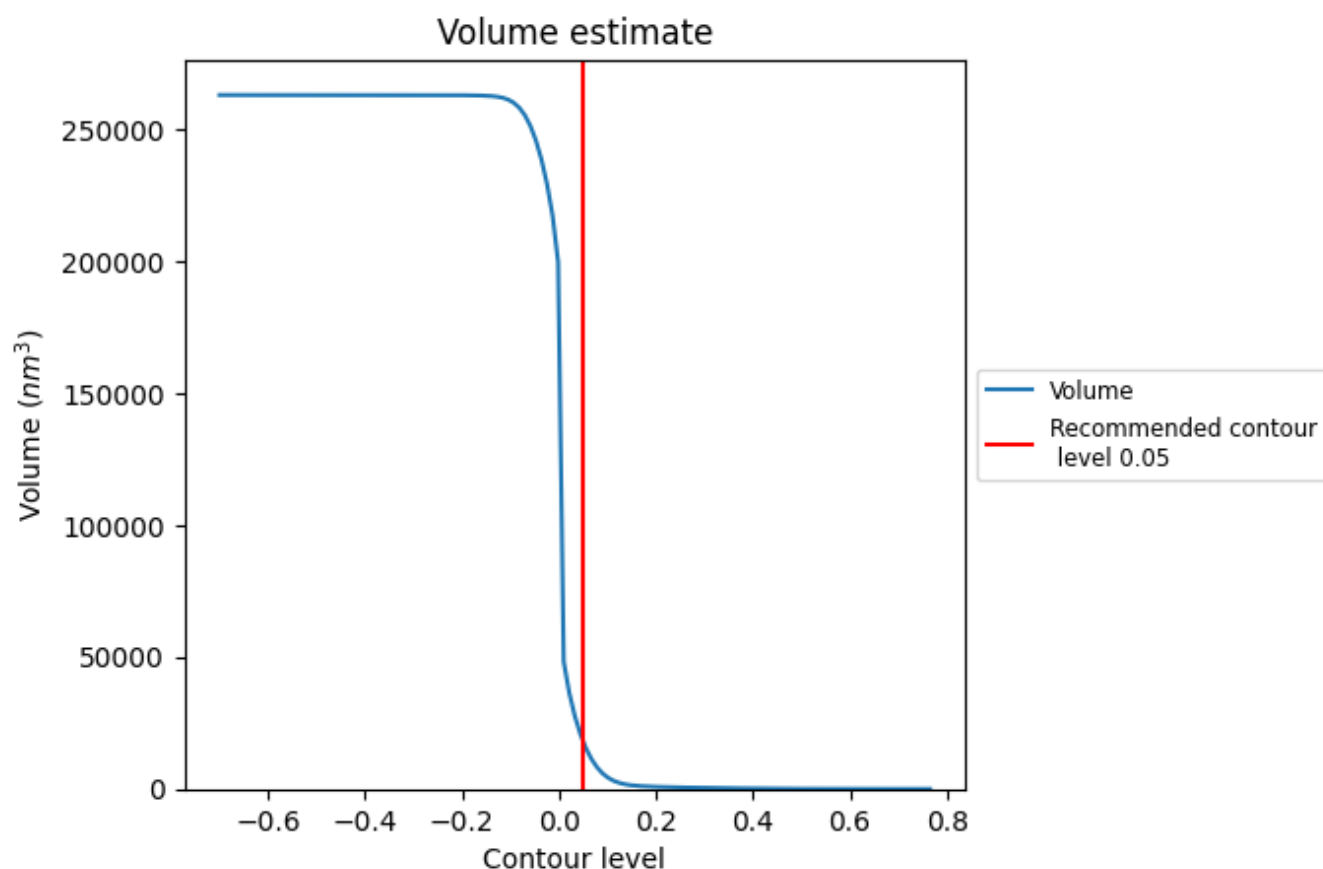
This section contains the results of statistical analysis of the map.

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.

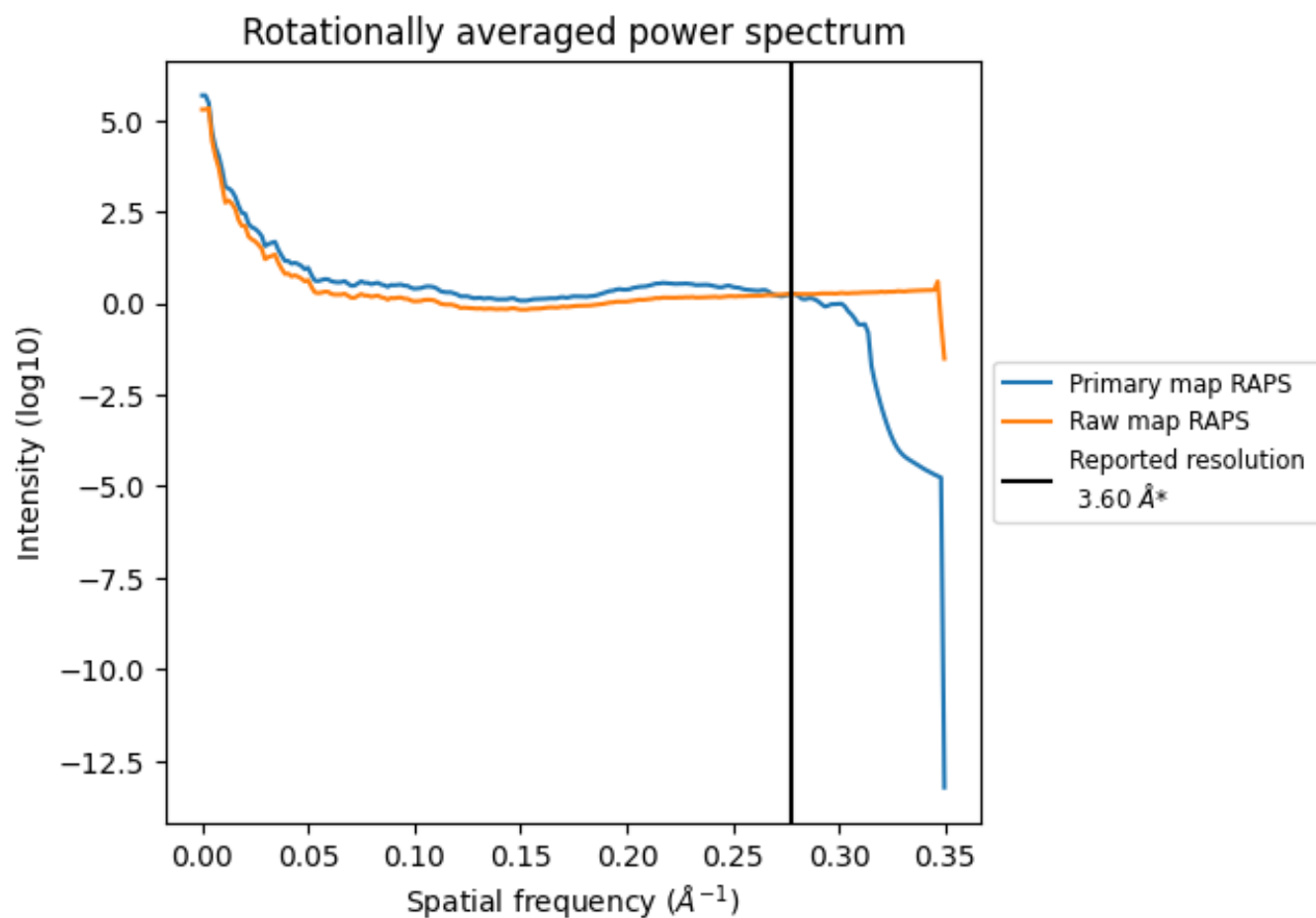
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 18044 nm^3 ; this corresponds to an approximate mass of 16299 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 ⓘ

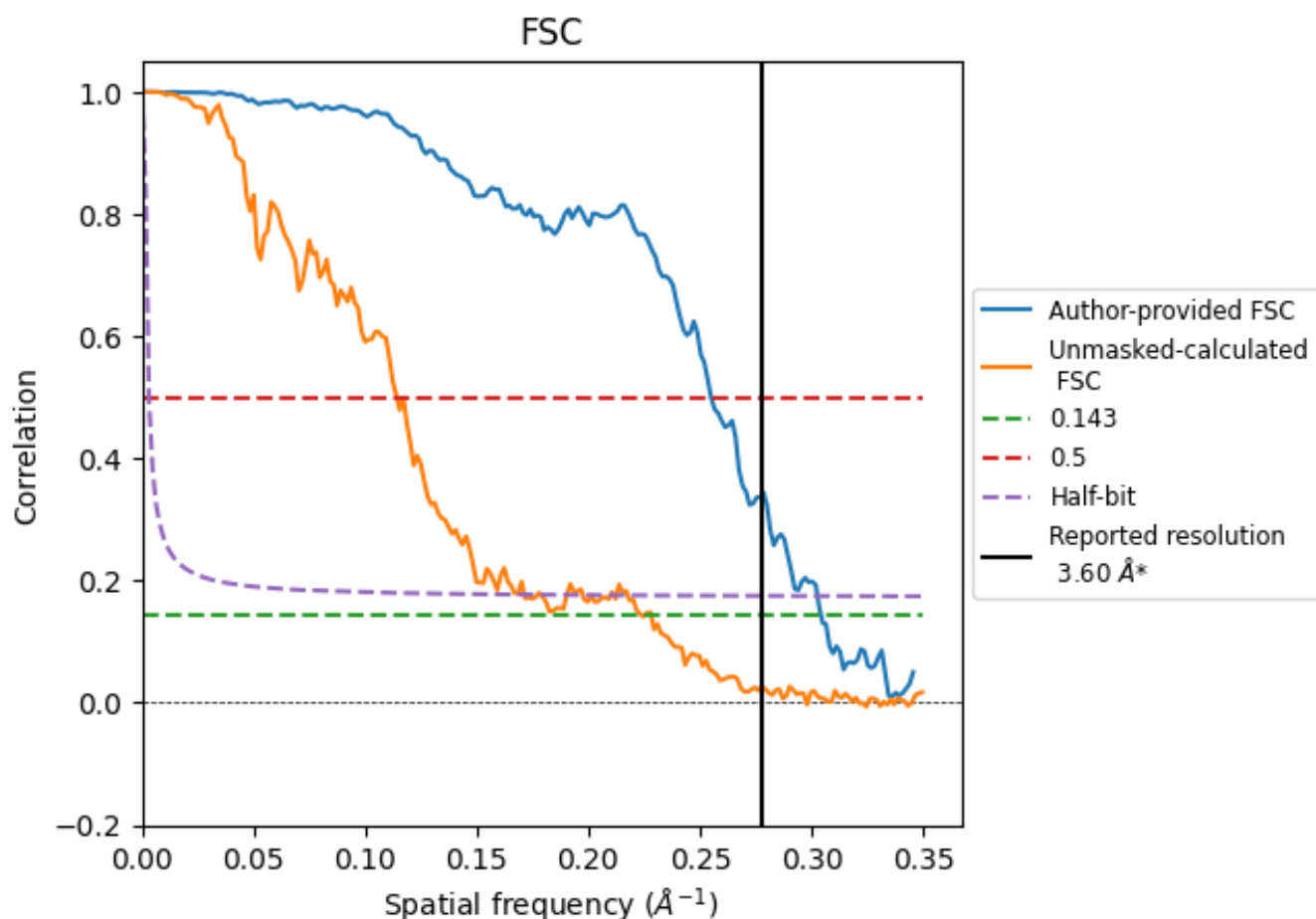


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 \AA^{-1}

7.2 Resolution estimates [i](#)

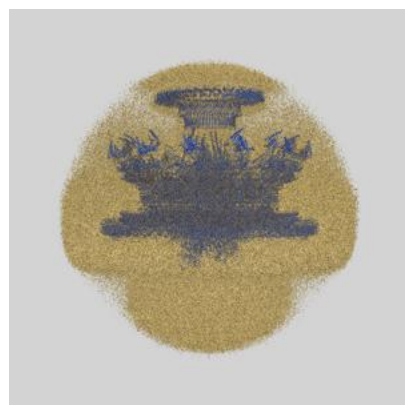
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.29	3.92	3.30
Unmasked-calculated*	4.46	8.76	5.83

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.46 differs from the reported value 3.6 by more than 10 %

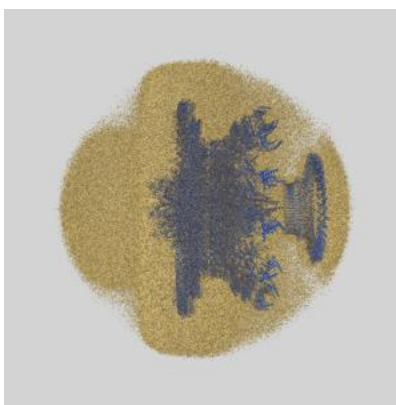
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72963 and PDB model 9YH7. Per-residue inclusion information can be found in section ?? on page ??.

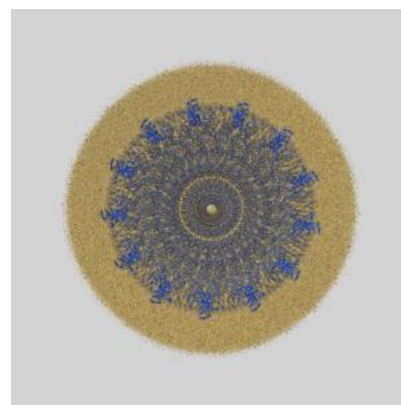
8.1 Map-model overlay [i](#)



X



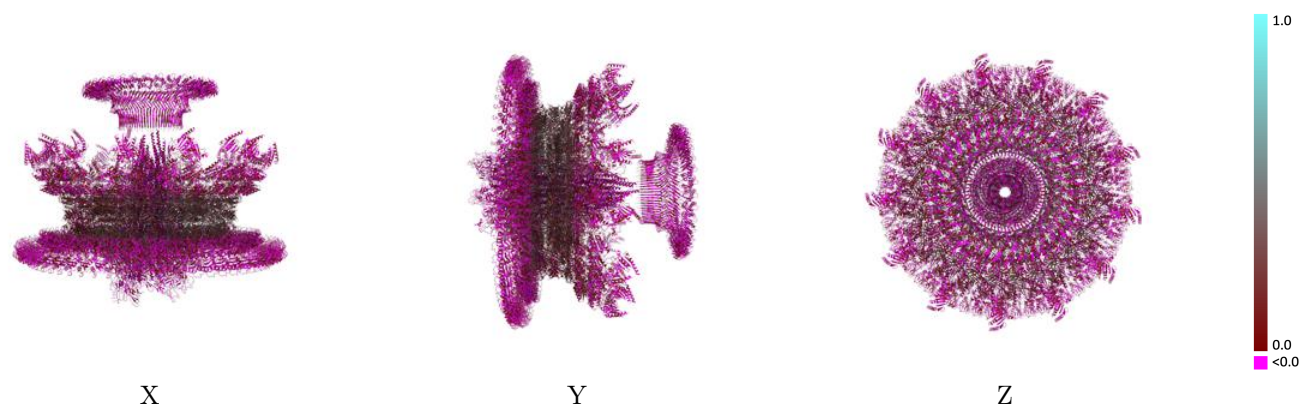
Y



Z

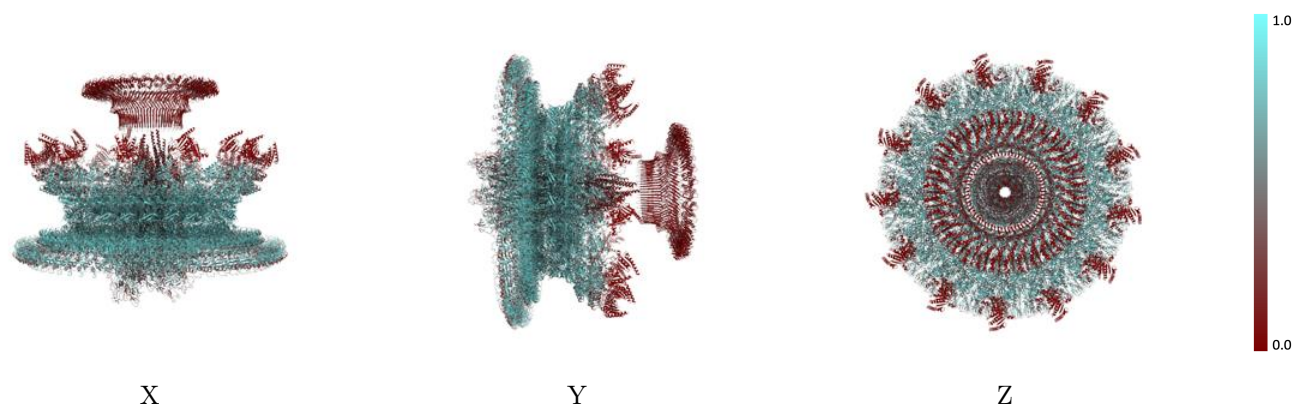
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



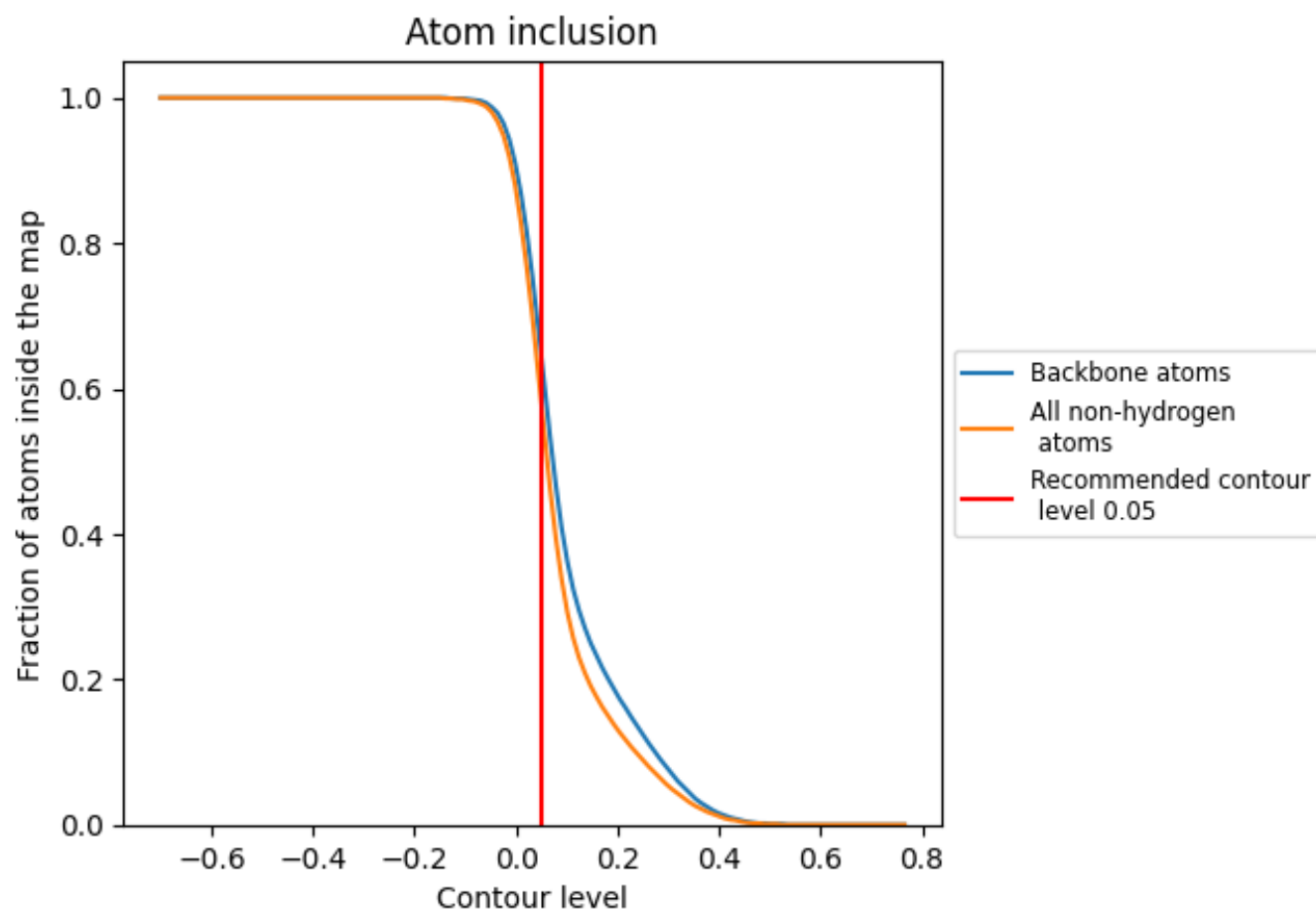
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































8.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 58% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5780	 0.1020
Aa	 0.4740	 -0.0100
Ab	 0.5140	 0.0030
Ac	 0.5540	 0.0140
Ad	 0.5520	 0.0130
Ae	 0.5500	 0.0130
Af	 0.5420	 0.0160
Ag	 0.4770	 -0.0280
Ah	 0.5350	 -0.0020
Ai	 0.5160	 -0.0140
Aj	 0.5560	 0.0350
Ak	 0.5040	 0.0150
Al	 0.5570	 0.0240
Am	 0.5250	 0.0170
An	 0.4680	 -0.0100
Ao	 0.4340	 -0.0120
Ap	 0.4170	 0.0080
Aq	 0.5250	 0.0220
Ar	 0.4810	 0.0290
As	 0.5350	 0.0270
At	 0.4750	 0.0190
Au	 0.5420	 0.0140
Av	 0.4740	 -0.0000
Aw	 0.5420	 0.0200
Ax	 0.5050	 0.0090
Ay	 0.3800	 0.0130
Az	 0.3660	 -0.0100
Ba	 0.2530	 0.0150
Bb	 0.3440	 0.0040
Bc	 0.2520	 0.0230
Bd	 0.2700	 0.0110
Be	 0.4990	 0.0120
Bf	 0.4820	 -0.0010
Bg	 0.4620	 -0.0120
Bh	 0.5150	 0.0150























































































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Chain	Atom inclusion	Q-score
Bi	0.4780	0.0030
Bj	0.5360	0.0260
Bk	0.4460	-0.0100
Bl	0.5280	0.0100
Bm	0.5150	0.0160
Bn	0.5240	0.0150
Bo	0.5120	0.0060
Bp	0.5130	0.0120
Bq	0.5160	-0.0130
Br	0.5370	0.0140
Bs	0.5170	0.0170
Bt	0.5160	0.0150
Bu	0.5000	-0.0030
Bv	0.3200	-0.0020
Bw	0.3120	0.0180
Bx	0.7360	0.2270
By	0.7430	0.2360
Bz	0.7380	0.2310
Ca	0.7430	0.2290
Cb	0.7480	0.2290
Cc	0.7430	0.2280
Cd	0.7410	0.2340
Ce	0.7550	0.2410
Cf	0.7490	0.2450
Cg	0.7550	0.2520
Ch	0.7570	0.2600
Ci	0.7600	0.2660
Cj	0.7690	0.2730
Ck	0.7720	0.2760
Cl	0.7770	0.2870
Cm	0.7850	0.2940
Cn	0.7960	0.3040
Co	0.7950	0.3130
Cp	0.7920	0.3130
Cq	0.7970	0.3040
Cr	0.7950	0.3120
Cs	0.7850	0.3080
Ct	0.7800	0.2940
Cu	0.7750	0.2790
Cv	0.7640	0.2660
Cw	0.7500	0.2490
Cx	0.7940	0.2940





















































































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Chain	Atom inclusion	Q-score
Cy	 0.7840	 0.2750
Cz	 0.7690	 0.2610
Da	 0.7660	 0.2480
Db	 0.7530	 0.2350
Dc	 0.7480	 0.2260
Dd	 0.7320	 0.2160
De	 0.7330	 0.2140
Df	 0.7270	 0.2100
Dg	 0.7340	 0.2100
Dh	 0.7270	 0.2110
Di	 0.7330	 0.2140
Dj	 0.7360	 0.2120
Dk	 0.7480	 0.2190
Dl	 0.7530	 0.2220
Dm	 0.7550	 0.2330
Dn	 0.7640	 0.2410
Do	 0.7790	 0.2600
Dp	 0.7850	 0.2770
Dq	 0.7950	 0.2940
Dr	 0.8020	 0.3030
Ds	 0.8150	 0.3140
Dt	 0.8080	 0.3200
Du	 0.8120	 0.3220
Dv	 0.8050	 0.3160
Dw	 0.8000	 0.3070
Dx	 0.7300	 0.1800
Dy	 0.7090	 0.1750
Dz	 0.7320	 0.1840
Ea	 0.7290	 0.1800
Eb	 0.7320	 0.1790
Ec	 0.7280	 0.1770
Ed	 0.7310	 0.1900
Ee	 0.7430	 0.1930
Ef	 0.7450	 0.1990
Eg	 0.7590	 0.2060
Eh	 0.7670	 0.2180
Ei	 0.7810	 0.2340
Ej	 0.7880	 0.2520
Ek	 0.7980	 0.2590
El	 0.8060	 0.2670
Em	 0.8040	 0.2630
En	 0.8020	 0.2620





















































































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Chain	Atom inclusion	Q-score
Eo	 0.7890	 0.2500
Ep	 0.7850	 0.2390
Eq	 0.7670	 0.2210
Er	 0.7690	 0.2140
Es	 0.7560	 0.2020
Et	 0.7380	 0.1990
Eu	 0.7330	 0.1880
Ev	 0.7340	 0.1900
Ew	 0.7310	 0.1820
Ex	 0.7290	 0.1570
Ey	 0.7340	 0.1710
Ez	 0.7250	 0.1470
Fa	 0.7510	 0.1930
Fb	 0.7310	 0.1500
Fc	 0.7720	 0.2020
Fd	 0.7270	 0.1510
Fe	 0.7700	 0.2030
Ff	 0.7220	 0.1570
Fg	 0.7650	 0.1980
Fh	 0.7320	 0.1580
Fi	 0.7480	 0.1810
Fj	 0.7290	 0.1550
Fk	 0.7380	 0.1660
Fl	 0.7290	 0.1590
Fm	 0.7180	 0.1520
Fn	 0.7290	 0.1600
Fo	 0.6990	 0.1510
Fp	 0.7260	 0.1670
Fq	 0.6970	 0.1550
Fr	 0.7150	 0.1620
Fs	 0.7000	 0.1520
Ft	 0.7180	 0.1670
Fu	 0.7120	 0.1550
Fv	 0.7190	 0.1620
Fw	 0.7180	 0.1600
Fx	 0.5660	 0.0830
Fy	 0.5340	 0.0660
Fz	 0.5530	 0.0780
Ga	 0.5280	 0.0520
Gb	 0.5620	 0.0750
Gc	 0.5230	 0.0490
Gd	 0.5570	 0.0810





















































































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Chain	Atom inclusion	Q-score
Ge	 0.5290	 0.0600
Gf	 0.5580	 0.0840
Gg	 0.5340	 0.0630
Gh	 0.5540	 0.0920
Gi	 0.5420	 0.0660
Gj	 0.5580	 0.0970
Gk	 0.5480	 0.0770
Gl	 0.5720	 0.1110
Gm	 0.5560	 0.0820
Gn	 0.5760	 0.1220
Go	 0.5430	 0.0820
Gp	 0.5980	 0.1370
Gq	 0.5610	 0.0950
Gr	 0.6100	 0.1350
Gs	 0.5500	 0.0940
Gt	 0.5960	 0.1260
Gu	 0.5470	 0.0900
Gv	 0.5790	 0.1040
Gw	 0.5430	 0.0760
Gx	 0.6210	 0.0860
Gy	 0.5340	 0.0670
Gz	 0.5920	 0.0600
Ha	 0.5730	 0.0760
Hb	 0.6120	 0.0820
Hc	 0.6020	 0.0920
Hd	 0.5630	 0.0590
He	 0.5150	 0.0260
Hf	 0.5530	 0.0530
Hg	 0.4950	 0.0540
Hh	 0.5920	 0.0930
Hi	 0.5440	 0.0450
Hj	 0.5530	 0.0630
Hk	 0.6500	 0.1110
Hl	 0.6120	 0.0610
Hm	 0.6500	 0.1100
Hn	 0.6800	 0.1140
Ho	 0.6310	 0.1470
Hp	 0.6700	 0.1610
Hq	 0.6700	 0.1330
Hr	 0.6600	 0.1140
HS	 0.7180	 0.1530
Ht	 0.7380	 0.1450

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Chain	Atom inclusion	Q-score
Hu	 0.6800	 0.1120
Hv	 0.6700	 0.1100
Hw	 0.5920	 0.0910
Hx	 0.8450	 0.2200
Hy	 0.7960	 0.2100
Hz	 0.8450	 0.1840
Ia	 0.8250	 0.2180
Ib	 0.8250	 0.1370
Ic	 0.7090	 0.0920
Id	 0.7770	 0.1110
Ie	 0.7480	 0.0980
If	 0.7860	 0.1430
Ig	 0.7380	 0.1170
Ih	 0.8250	 0.1590
Ii	 0.7860	 0.1730
Ij	 0.7770	 0.1610
Ik	 0.8160	 0.1670
Il	 0.7670	 0.1530
Im	 0.8160	 0.1260
In	 0.7480	 0.1480
Io	 0.7960	 0.1910
Ip	 0.7380	 0.1940
Iq	 0.7860	 0.1960
Ir	 0.7280	 0.1680
Is	 0.7770	 0.2050
It	 0.7180	 0.1120
Iu	 0.8450	 0.2410
Iv	 0.7860	 0.2410
Iw	 0.8930	 0.2830
Ix	 0.0480	 0.0020
Iy	 0.0510	 0.0290
Iz	 0.0420	 0.0100
Ja	 0.0660	 0.0340
Jb	 0.0440	 -0.0010
Jc	 0.0590	 0.0180
Jd	 0.0440	 0.0010
Je	 0.0530	 0.0090
Jf	 0.0450	 0.0050
Jg	 0.0570	 0.0050
Jh	 0.0440	 0.0070
Ji	 0.0560	 0.0210
Jj	 0.0510	 0.0090





















































































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Chain	Atom inclusion	Q-score
Jk	0.0550	0.0260
Jl	0.0470	0.0030
Jm	0.0510	0.0390
Jn	0.0450	0.0070
Jo	0.0570	0.0400
Jp	0.0420	0.0100
Jq	0.0610	0.0280
Jr	0.0420	0.0090
Js	0.0630	0.0260
Jt	0.0450	0.0040
Ju	0.0580	0.0250
Jv	0.0540	0.0000
Jw	0.0610	0.0270
Jx	0.6840	0.0330
Jy	0.6920	0.0430
Jz	0.6850	0.0180
Ka	0.6910	0.0290
Kb	0.6910	0.0210
Kc	0.7200	0.0550
Kd	0.6880	0.0350
Ke	0.6890	0.0090
Kf	0.6590	-0.0180
Kg	0.6730	0.0130
Kh	0.6880	0.0120
Ki	0.6970	0.0500
Kj	0.6740	-0.0080
Kk	0.6680	0.0190
Kl	0.6730	0.0190
Km	0.6790	0.0280
Kn	0.6500	-0.0010
Ko	0.6670	-0.0090
Kp	0.6580	0.0150
Kq	0.6700	0.0130
Kr	0.6780	0.0190
Ks	0.6450	-0.0320
Kt	0.6340	0.0030
Ku	0.6360	-0.0080
Kv	0.6650	0.0160
Kw	0.6440	-0.0080
Kx	0.6690	-0.0010
Ky	0.6650	0.0350
Kz	0.6800	0.0170





















































































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Chain	Atom inclusion	Q-score
La	 0.6670	 0.0280
Lb	 0.6650	 -0.0190
Lc	 0.6630	 0.0220
Ld	 0.6530	 -0.0080
Le	 0.6850	 0.0340
Lf	 0.6970	 0.0140
Lg	 0.6840	 0.0290
Lh	 0.7120	 0.0600
Li	 0.6790	 0.0030
Lj	 0.7020	 0.0460
Lk	 0.7160	 0.0560
Ll	 0.6840	 0.0240
Lm	 0.6820	 0.0060
Ln	 0.6880	 0.0150
Lo	 0.7310	 0.0620
Lp	 0.6940	 0.0390
Lq	 0.6700	 0.0110
Lr	 0.6540	 0.0040
Ls	 0.6620	 0.0260
Lt	 0.6780	 0.0170
Lu	 0.6970	 0.0470
Lv	 0.6650	 0.0320
Lw	 0.6910	 0.0470
Lx	 0.6780	 0.0300
Ly	 0.6790	 0.0020
Lz	 0.7070	 0.0430
Ma	 0.6930	 0.0550
Mb	 0.6780	 0.0240
Mc	 0.6700	 0.0140
Md	 0.5530	 0.0040
Me	 0.6030	 0.0290
Mf	 0.5640	 -0.0120
Mg	 0.5820	 0.0110
Mh	 0.5870	 0.0180
Mi	 0.5950	 0.0240
Mj	 0.5820	 0.0070
Mk	 0.5770	 0.0090
Ml	 0.5830	 0.0110
Mm	 0.6090	 0.0350
Mn	 0.5800	 0.0330
Mo	 0.5730	 0.0060
Mp	 0.5580	 -0.0010











































































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Chain	Atom inclusion	Q-score
Mq	 0.6010	 0.0320
Mr	 0.5720	 -0.0020
Ms	 0.5960	 0.0300
Mt	 0.5640	 0.0020
Mu	 0.5970	 0.0330
Mv	 0.5980	 0.0250
Mw	 0.5710	 0.0090
Mx	 0.5670	 0.0090
My	 0.5550	 -0.0090
Mz	 0.5860	 0.0160
Na	 0.5400	 -0.0150
Nb	 0.5790	 0.0180
Nc	 0.5920	 0.0170
Nd	 0.5940	 0.0300
Ne	 0.5820	 0.0240
Nf	 0.5660	 -0.0010
Ng	 0.5650	 0.0080
Nh	 0.5690	 0.0090
Ni	 0.5750	 0.0050
Nj	 0.5590	 -0.0140
Nk	 0.5640	 0.0020
Nl	 0.5970	 0.0150
Nm	 0.5920	 0.0150
Nn	 0.5920	 0.0220
No	 0.5530	 -0.0080
Np	 0.5600	 -0.0000
Nq	 0.6110	 0.0390
Nr	 0.5770	 -0.0110
Ns	 0.5800	 0.0160
Nt	 0.5930	 0.0180
Nu	 0.5910	 0.0210
Nv	 0.5840	 0.0050
Nw	 0.5600	 0.0050
Nx	 0.5690	 0.0030
Ny	 0.5860	 0.0330
Nz	 0.5580	 0.0230
Oa	 0.5770	 0.0180
Ob	 0.5800	 0.0150
Oc	 0.5840	 0.0240
Od	 0.5950	 0.0300
Oe	 0.5800	 0.0180
Of	 0.5830	 0.0090

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Chain	Atom inclusion	Q-score
Og	 0.5810	 0.0030
Oh	 0.5700	 -0.0050
Oi	 0.5620	 0.0030
Oj	 0.0770	 -0.0230
Ok	 0.0870	 -0.0130
Ol	 0.0830	 -0.0220
Om	 0.0850	 -0.0110
On	 0.0930	 0.0070
Oo	 0.0770	 -0.0060
Op	 0.0770	 -0.0070
Oq	 0.0950	 0.0050
Or	 0.1030	 0.0130
Os	 0.0920	 0.0110
Ot	 0.0830	 0.0150
Ou	 0.0950	 -0.0110
Ov	 0.1010	 0.0110
Ow	 0.1010	 0.0150
Ox	 0.1040	 0.0100
Oy	 0.1010	 -0.0260
Oz	 0.1020	 0.0130
Pa	 0.1150	 0.0260
Pb	 0.0770	 -0.0300
Pc	 0.1020	 -0.0020
Pd	 0.0940	 -0.0060
Pe	 0.1170	 0.0070
Pf	 0.0970	 0.0020
Pg	 0.0770	 0.0050
Ph	 0.0910	 0.0070
Pi	 0.0970	 -0.0010
Pj	 0.0970	 0.0170
Pk	 0.0750	 -0.0080
Pl	 0.0960	 0.0220
Pm	 0.0840	 0.0130
Pn	 0.0990	 0.0110
Po	 0.0850	 0.0040
Pp	 0.0880	 0.0110
Pq	 0.0870	 -0.0150