



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 10:12 PM UTC

PDB ID : 8WOE / pdb_00008woe
EMDB ID : EMD-37684
Title : Cryo-EM structure of the intact flagellar motor-hook complex in the CW state
Authors : Tan, J.X.; Zhang, L.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2023-10-07
Resolution : 4.30 Å(reported)
Based on initial models : ?, .

This is a Full wwPDB EM Validation 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

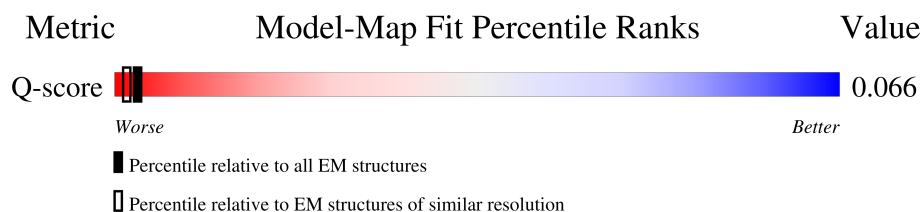
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 614043 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	0	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	1	252	Total	C	N	O	S	0	0
			1894	1172	331	385	6		
1	2	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	3	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	4	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	5	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	6	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	7	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	8	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	9	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	AF	254	Total	C	N	O	S	0	0
			1903	1175	334	389	5		
1	AG	255	Total	C	N	O	S	0	0
			1911	1181	335	390	5		
1	AH	256	Total	C	N	O	S	0	0
			1919	1186	336	391	6		
1	AI	254	Total	C	N	O	S	0	0
			1903	1175	334	389	5		
1	AJ	255	Total	C	N	O	S	0	0
			1911	1181	335	390	5		
1	AK	243	Total	C	N	O	S	0	0
			1823	1127	318	373	5		
1	AL	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AM	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	AN	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	ZA	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZB	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZC	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZD	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZE	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		

- Molecule 2 is a protein called Flagellar L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	B	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	C	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	D	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	E	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	F	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	G	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	H	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	I	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	J	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	K	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	L	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	N	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	O	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	P	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	Q	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	R	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	S	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	T	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	U	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	V	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	W	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	X	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	Y	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
2	Z	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		

- Molecule 3 is a protein called Flagellar basal body rod protein FlgB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A0	123	Total	C	N	O	S	0	0
			950	588	172	185	5		
3	A6	134	Total	C	N	O	S	0	0
			1030	633	189	203	5		
3	A7	121	Total	C	N	O	S	0	0
			942	583	172	182	5		
3	A8	125	Total	C	N	O	S	0	0
			967	598	177	187	5		
3	A9	127	Total	C	N	O	S	0	0
			982	606	182	189	5		

- Molecule 4 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A1	91	Total	C	N	O	S	0	0
			672	415	121	129	7		
4	A2	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
4	A3	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
4	A4	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
4	A5	92	Total	C	N	O	S	0	0
			679	420	122	130	7		
4	Az	59	Total	C	N	O	S	0	0
			429	265	74	83	7		

- Molecule 5 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AA	248	Total	C	N	O	S	0	0
			1804	1106	324	367	7		
5	AB	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
5	AC	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
5	AD	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
5	AE	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

- Molecule 6 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AO	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AP	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AQ	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AR	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AS	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AT	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	AU	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AV	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AW	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AX	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AY	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AZ	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Aa	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ac	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ad	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ae	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Af	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ag	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ah	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ai	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Aj	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ak	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Al	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Am	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	An	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ao	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ap	164	Total 1275	C 776	N 237	O 259	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	BG	13	Total 81	C 50	N 15	O 16		0	0
6	BH	16	Total 103	C 64	N 19	O 20		0	0
6	BI	20	Total 133	C 83	N 23	O 27		0	0
6	BJ	16	Total 103	C 64	N 19	O 20		0	0
6	BK	21	Total 140	C 88	N 24	O 28		0	0
6	BL	16	Total 103	C 64	N 19	O 20		0	0
6	BM	21	Total 140	C 88	N 24	O 28		0	0
6	BN	16	Total 103	C 64	N 19	O 20		0	0
6	BO	20	Total 133	C 83	N 23	O 27		0	0
6	BP	16	Total 103	C 64	N 19	O 20		0	0
6	BQ	21	Total 140	C 88	N 24	O 28		0	0
6	BR	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	BS	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	BT	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	BU	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	BV	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	BW	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	BX	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	UI	155	Total 1172	C 733	N 211	O 226	S 2	0	0
6	UJ	155	Total 1172	C 733	N 211	O 226	S 2	0	0
6	UK	155	Total 1172	C 733	N 211	O 226	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	UL	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UM	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UN	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UO	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UP	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	WA	113	Total	C	N	O	S	0	0
			849	534	148	166	1		
6	WB	111	Total	C	N	O	S	0	0
			836	526	146	163	1		
6	WC	108	Total	C	N	O	S	0	0
			812	510	142	159	1		
6	WD	110	Total	C	N	O	S	0	0
			827	522	144	160	1		
6	WE	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WF	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WG	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WH	95	Total	C	N	O	S	0	0
			703	439	126	137	1		
6	WI	95	Total	C	N	O	S	0	0
			703	439	126	137	1		
6	WJ	99	Total	C	N	O	S	0	0
			737	462	131	143	1		
6	WK	98	Total	C	N	O	S	0	0
			729	456	130	142	1		
6	WL	85	Total	C	N	O	S	0	0
			622	389	110	122	1		
6	WM	82	Total	C	N	O	S	0	0
			596	372	107	116	1		
6	WN	84	Total	C	N	O	S	0	0
			611	380	109	121	1		
6	WO	96	Total	C	N	O	S	0	0
			714	448	127	138	1		
6	WP	100	Total	C	N	O	S	0	0
			741	464	132	144	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	WQ	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WR	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WS	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WT	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WU	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WV	110	Total	C	N	O	S	0	0
			827	521	144	161	1		
6	WW	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	DE	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	DL	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	B0	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	B3	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	EH	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	EO	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	EV	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	Ba	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	Bh	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	Bo	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	Bv	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	Ea	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	CG	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
6	CN	27	Total	C	N	O	S	0	0
			224	135	44	42	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	CU	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Cb	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ci	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Cp	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Cw	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Eb	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ec	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ed	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ee	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ef	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Eg	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Eh	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ei	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ej	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ek	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	El	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Em	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	En	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Eo	27	Total 224	C 135	N 44	O 42	S 3	0	0
6	Ep	27	Total 224	C 135	N 44	O 42	S 3	0	0

- Molecule 7 is a protein called Flagellar biosynthetic protein FliQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ab	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	Aq	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	Ar	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	As	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

- Molecule 8 is a protein called Flagellar biosynthetic protein FliR.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	At	253	Total	C	N	O	S	0	0
			1945	1305	307	318	15		

- Molecule 9 is a protein called Flagellar biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Au	207	Total	C	N	O	S	0	0
			1605	1072	249	272	12		
9	Av	209	Total	C	N	O	S	0	0
			1626	1086	252	276	12		
9	Aw	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
9	Ax	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
9	Ay	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

- Molecule 10 is a protein called Flagellar basal-body rod protein FlgC.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BA	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
10	BB	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
10	BC	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
10	BD	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
10	BE	133	Total	C	N	O	S	0	0
			969	604	167	193	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	BF	133	Total	C	N	O	S	0	0
			969	604	167	193	5		

- Molecule 11 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	ZF	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZG	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZH	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZI	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZJ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZK	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZL	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZM	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZN	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZO	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZP	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZQ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZR	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZS	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZT	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZU	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZV	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZW	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	ZX	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZY	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	ZZ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Za	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Zb	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Zc	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Zd	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Ze	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Zf	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Zg	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
11	Zh	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

- Molecule 12 is a protein called Flagellar P-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	a	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	b	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	c	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	d	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	e	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	f	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	g	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	h	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	i	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	j	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	k	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	l	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	m	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	n	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	o	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	p	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	q	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	r	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	s	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	t	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	u	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	v	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	w	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	x	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	y	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
12	z	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		

- Molecule 13 is a protein called Flagellar motor switch protein FliN.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	C3	87	Total	C	N	O	S	0	0
			675	427	118	126	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	C4	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	C5	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	C8	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	C9	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DD	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DI	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DJ	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DK	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DM	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DN	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DO	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DP	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DQ	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DR	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DS	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DT	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DU	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DV	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	DW	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Da	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Db	87	Total 675	C 427	N 118	O 126	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	Dc	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Dg	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Dh	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Di	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Dm	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Dn	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Do	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Ds	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Dt	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Du	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Dy	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Dz	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	D1	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	D5	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	D6	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	D7	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EA	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EB	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	B1	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	B2	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	B7	87	Total 675	C 427	N 118	O 126	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	B8	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	B9	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EE	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EF	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EG	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EL	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EM	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EN	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	ES	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	ET	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EU	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	EZ	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	BY	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	BZ	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Be	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bf	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bg	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bl	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bm	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bn	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bs	87	Total 675	C 427	N 118	O 126	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	Bt	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bu	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Bz	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	C1	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	C2	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CD	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CE	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CF	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CK	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CL	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CM	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CR	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CS	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CT	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CY	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	CZ	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Ca	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Cf	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Cg	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Ch	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Cm	87	Total 675	C 427	N 118	O 126	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	Cn	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Co	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Ct	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Cu	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	Cv	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FC	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FD	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FE	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FF	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FG	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FH	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FI	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FJ	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FK	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FL	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FM	87	Total 675	C 427	N 118	O 126	S 4	0	0
13	FN	87	Total 675	C 427	N 118	O 126	S 4	0	0

- Molecule 14 is a protein called Flagellar motor switch protein FliG.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C6	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	DA	310	Total 2428	C 1515	N 430	O 474	S 9	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	DG	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	DY	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	De	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	Dk	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	Dq	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	Dw	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	D3	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	D9	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	B5	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	EC	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	EJ	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	EQ	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	EX	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	Bc	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	Bj	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	Bq	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	Bx	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	CB	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	CI	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	CP	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
14	CW	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	Cd	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	Ck	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	Cr	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	Cy	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	Ex	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	Ey	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	Ez	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	E1	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	E2	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	E3	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
14	E4	310	Total 2428	C 1515	N 430	O 474	S 9	0	0

- Molecule 15 is a protein called Chemotaxis protein CheY.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	C7	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	DB	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	DH	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	DZ	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Df	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Dl	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Dr	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Dx	129	Total 991	C 634	N 165	O 185	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
15	D4	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	D0	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	B6	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	ED	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	EK	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	ER	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	EY	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Bd	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Bk	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Br	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	By	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	CC	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	CJ	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	CQ	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	CX	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Ce	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Cl	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Cs	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	Cz	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	E6	129	Total 991	C 634	N 165	O 185	S 7	0	0
15	E7	129	Total 991	C 634	N 165	O 185	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
15	E8	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
15	E9	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
15	E0	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
15	FA	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
15	FB	129	Total	C	N	O	S	0	0
			991	634	165	185	7		

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C7	13	LYS	ASP	engineered mutation	UNP P0A2D5
C7	106	TRP	TYR	engineered mutation	UNP P0A2D5
DB	13	LYS	ASP	engineered mutation	UNP P0A2D5
DB	106	TRP	TYR	engineered mutation	UNP P0A2D5
DH	13	LYS	ASP	engineered mutation	UNP P0A2D5
DH	106	TRP	TYR	engineered mutation	UNP P0A2D5
DZ	13	LYS	ASP	engineered mutation	UNP P0A2D5
DZ	106	TRP	TYR	engineered mutation	UNP P0A2D5
Df	13	LYS	ASP	engineered mutation	UNP P0A2D5
Df	106	TRP	TYR	engineered mutation	UNP P0A2D5
Dl	13	LYS	ASP	engineered mutation	UNP P0A2D5
Dl	106	TRP	TYR	engineered mutation	UNP P0A2D5
Dr	13	LYS	ASP	engineered mutation	UNP P0A2D5
Dr	106	TRP	TYR	engineered mutation	UNP P0A2D5
Dx	13	LYS	ASP	engineered mutation	UNP P0A2D5
Dx	106	TRP	TYR	engineered mutation	UNP P0A2D5
D4	13	LYS	ASP	engineered mutation	UNP P0A2D5
D4	106	TRP	TYR	engineered mutation	UNP P0A2D5
D0	13	LYS	ASP	engineered mutation	UNP P0A2D5
D0	106	TRP	TYR	engineered mutation	UNP P0A2D5
B6	13	LYS	ASP	engineered mutation	UNP P0A2D5
B6	106	TRP	TYR	engineered mutation	UNP P0A2D5
ED	13	LYS	ASP	engineered mutation	UNP P0A2D5
ED	106	TRP	TYR	engineered mutation	UNP P0A2D5
EK	13	LYS	ASP	engineered mutation	UNP P0A2D5
EK	106	TRP	TYR	engineered mutation	UNP P0A2D5
ER	13	LYS	ASP	engineered mutation	UNP P0A2D5
ER	106	TRP	TYR	engineered mutation	UNP P0A2D5
EY	13	LYS	ASP	engineered mutation	UNP P0A2D5

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Chain	Residue	Modelled	Actual	Comment	Reference
EY	106	TRP	TYR	engineered mutation	UNP P0A2D5
Bd	13	LYS	ASP	engineered mutation	UNP P0A2D5
Bd	106	TRP	TYR	engineered mutation	UNP P0A2D5
Bk	13	LYS	ASP	engineered mutation	UNP P0A2D5
Bk	106	TRP	TYR	engineered mutation	UNP P0A2D5
Br	13	LYS	ASP	engineered mutation	UNP P0A2D5
Br	106	TRP	TYR	engineered mutation	UNP P0A2D5
By	13	LYS	ASP	engineered mutation	UNP P0A2D5
By	106	TRP	TYR	engineered mutation	UNP P0A2D5
CC	13	LYS	ASP	engineered mutation	UNP P0A2D5
CC	106	TRP	TYR	engineered mutation	UNP P0A2D5
CJ	13	LYS	ASP	engineered mutation	UNP P0A2D5
CJ	106	TRP	TYR	engineered mutation	UNP P0A2D5
CQ	13	LYS	ASP	engineered mutation	UNP P0A2D5
CQ	106	TRP	TYR	engineered mutation	UNP P0A2D5
CX	13	LYS	ASP	engineered mutation	UNP P0A2D5
CX	106	TRP	TYR	engineered mutation	UNP P0A2D5
Ce	13	LYS	ASP	engineered mutation	UNP P0A2D5
Ce	106	TRP	TYR	engineered mutation	UNP P0A2D5
Cl	13	LYS	ASP	engineered mutation	UNP P0A2D5
Cl	106	TRP	TYR	engineered mutation	UNP P0A2D5
Cs	13	LYS	ASP	engineered mutation	UNP P0A2D5
Cs	106	TRP	TYR	engineered mutation	UNP P0A2D5
Cz	13	LYS	ASP	engineered mutation	UNP P0A2D5
Cz	106	TRP	TYR	engineered mutation	UNP P0A2D5
E6	13	LYS	ASP	engineered mutation	UNP P0A2D5
E6	106	TRP	TYR	engineered mutation	UNP P0A2D5
E7	13	LYS	ASP	engineered mutation	UNP P0A2D5
E7	106	TRP	TYR	engineered mutation	UNP P0A2D5
E8	13	LYS	ASP	engineered mutation	UNP P0A2D5
E8	106	TRP	TYR	engineered mutation	UNP P0A2D5
E9	13	LYS	ASP	engineered mutation	UNP P0A2D5
E9	106	TRP	TYR	engineered mutation	UNP P0A2D5
E0	13	LYS	ASP	engineered mutation	UNP P0A2D5
E0	106	TRP	TYR	engineered mutation	UNP P0A2D5
FA	13	LYS	ASP	engineered mutation	UNP P0A2D5
FA	106	TRP	TYR	engineered mutation	UNP P0A2D5
FB	13	LYS	ASP	engineered mutation	UNP P0A2D5
FB	106	TRP	TYR	engineered mutation	UNP P0A2D5

- Molecule 16 is a protein called Flagellar motor switch protein FliM.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	C0	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	DC	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	DF	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	DX	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Dd	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Dj	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Dp	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Dv	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	D2	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	D8	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	B4	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	EI	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	EP	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	EW	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Bb	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Bi	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Bp	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Bw	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	CA	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	CH	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	CO	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	CV	301	Total 2431	C 1549	N 437	O 440	S 5	0	0

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Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Cc	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Cj	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Cq	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Cx	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Eq	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Er	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Es	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Et	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Eu	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Ev	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	Ew	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
16	E5	301	Total 2431	C 1549	N 437	O 440	S 5	0	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, C34	Depositor
Number of particles used	26921	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.415	Depositor
Minimum map value	-0.224	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	1008.00006, 1008.00006, 1008.00006	wwPDB
Map dimensions	840, 840, 840	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	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.

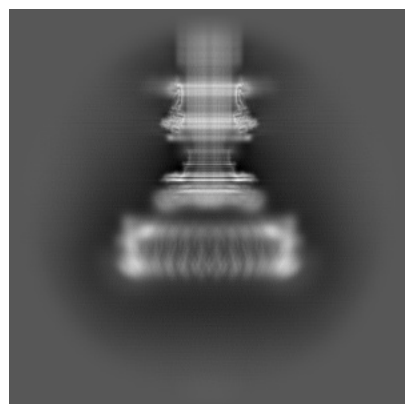
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37684. These allow visual inspection of the internal detail of the map and identification of artifacts.

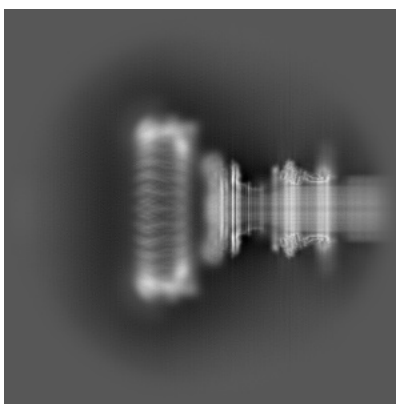
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

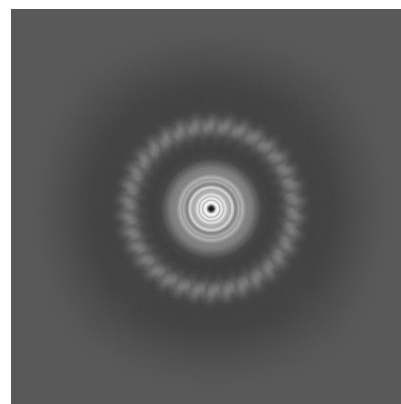
5.1.1 Primary map



X

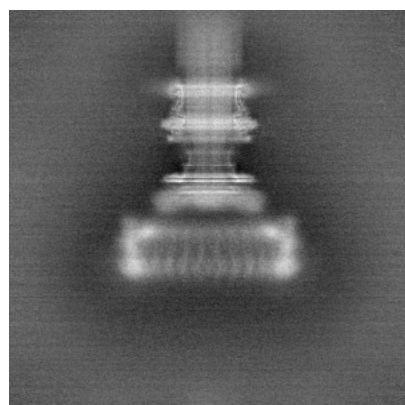


Y

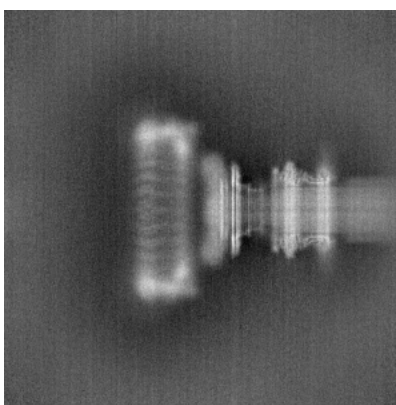


Z

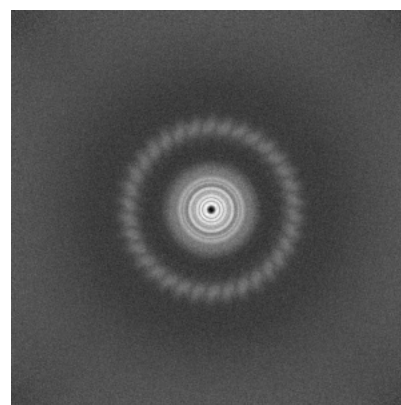
5.1.2 Raw map



X



Y

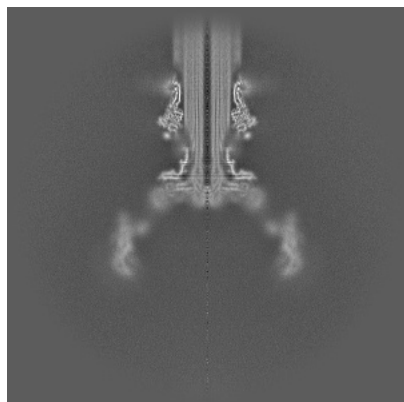


Z

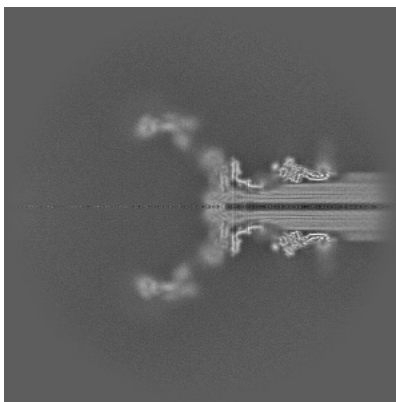
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

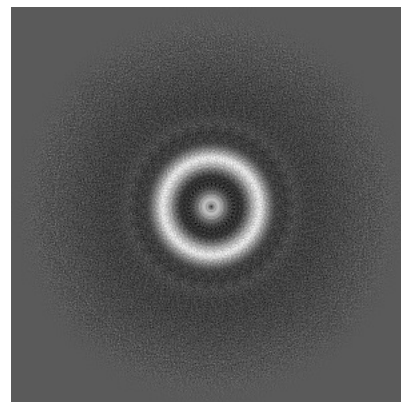
5.2.1 Primary map



X Index: 420



Y Index: 420

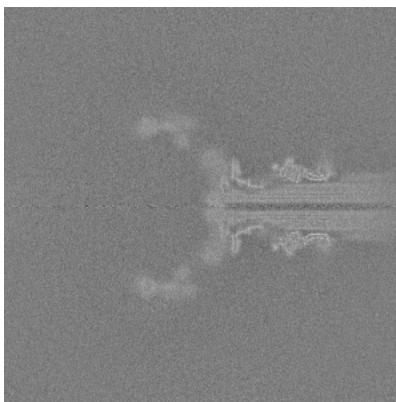


Z Index: 420

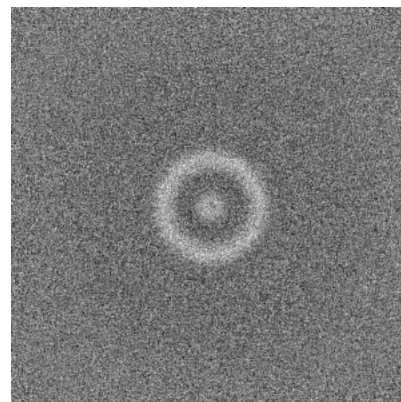
5.2.2 Raw map



X Index: 420



Y Index: 420

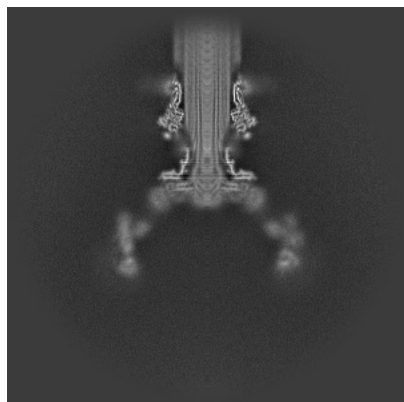


Z Index: 420

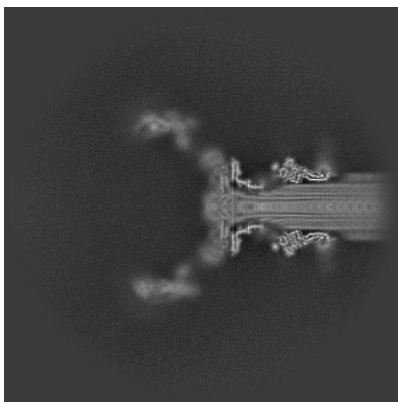
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

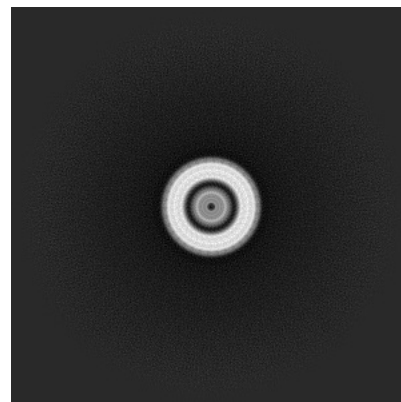
5.3.1 Primary map



X Index: 431



Y Index: 431

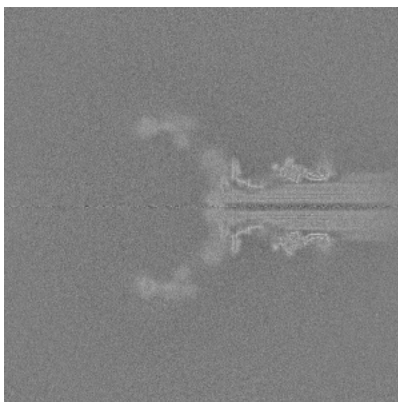


Z Index: 481

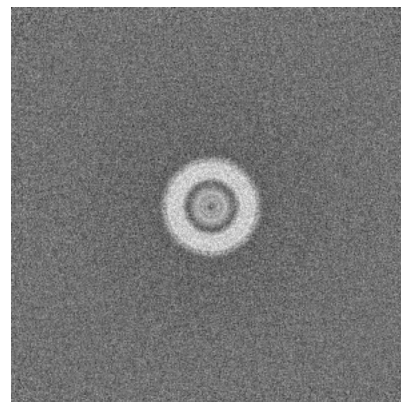
5.3.2 Raw map



X Index: 420



Y Index: 420

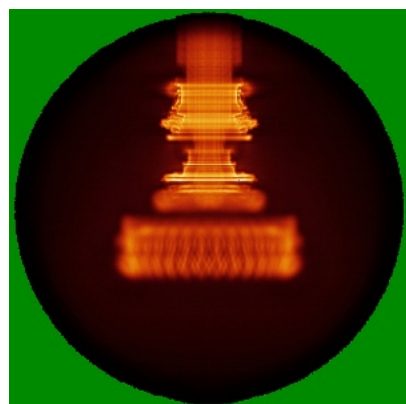


Z Index: 481

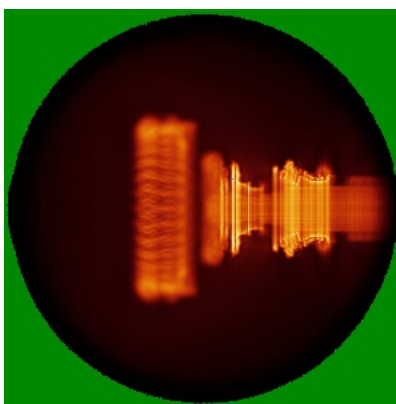
The images above show the largest variance slices of the map in three orthogonal directions.

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

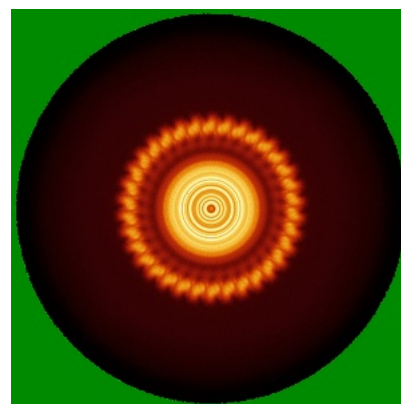
5.4.1 Primary map



X

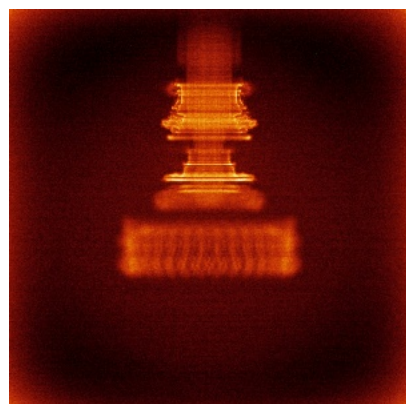


Y

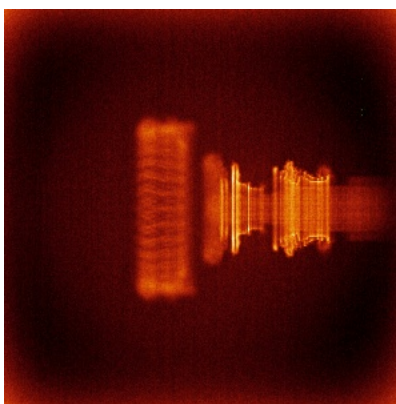


Z

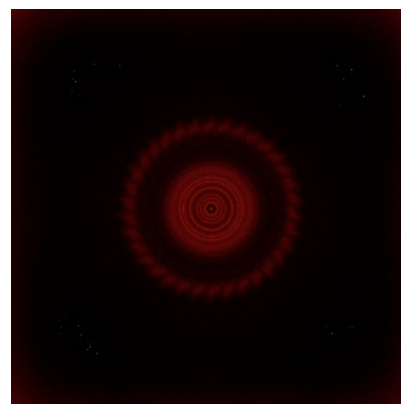
5.4.2 Raw map



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.

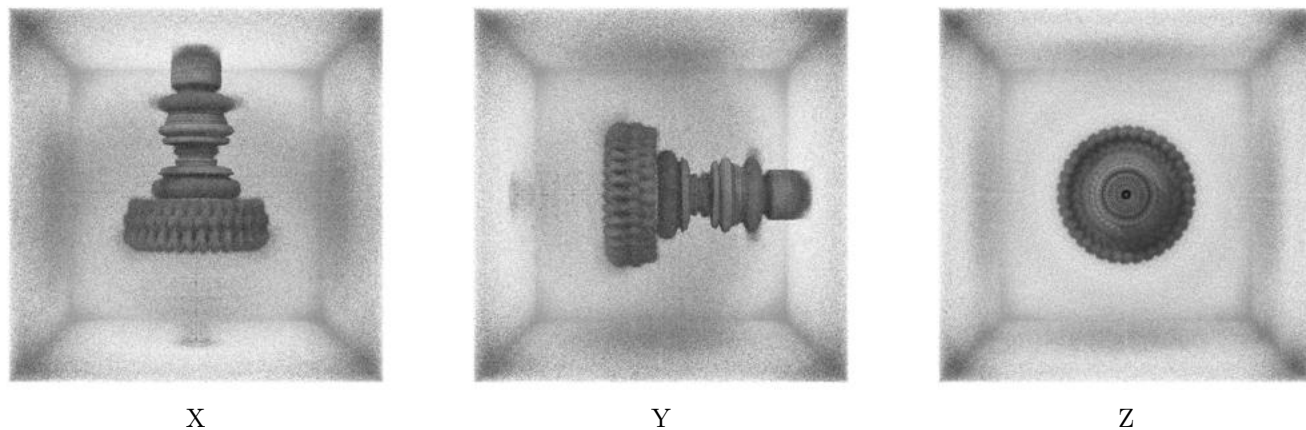
5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

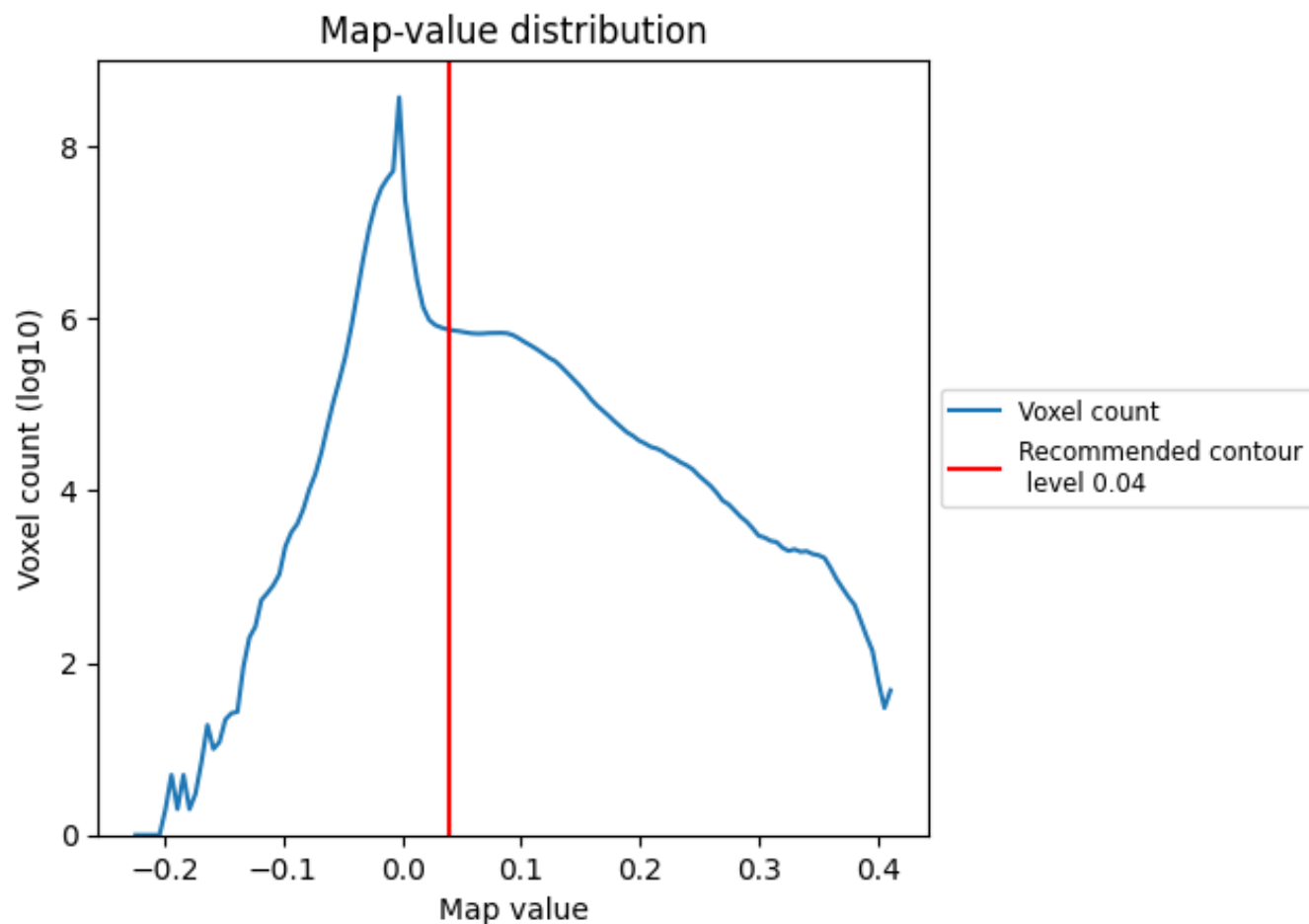
5.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

6 Map analysis [i](#)

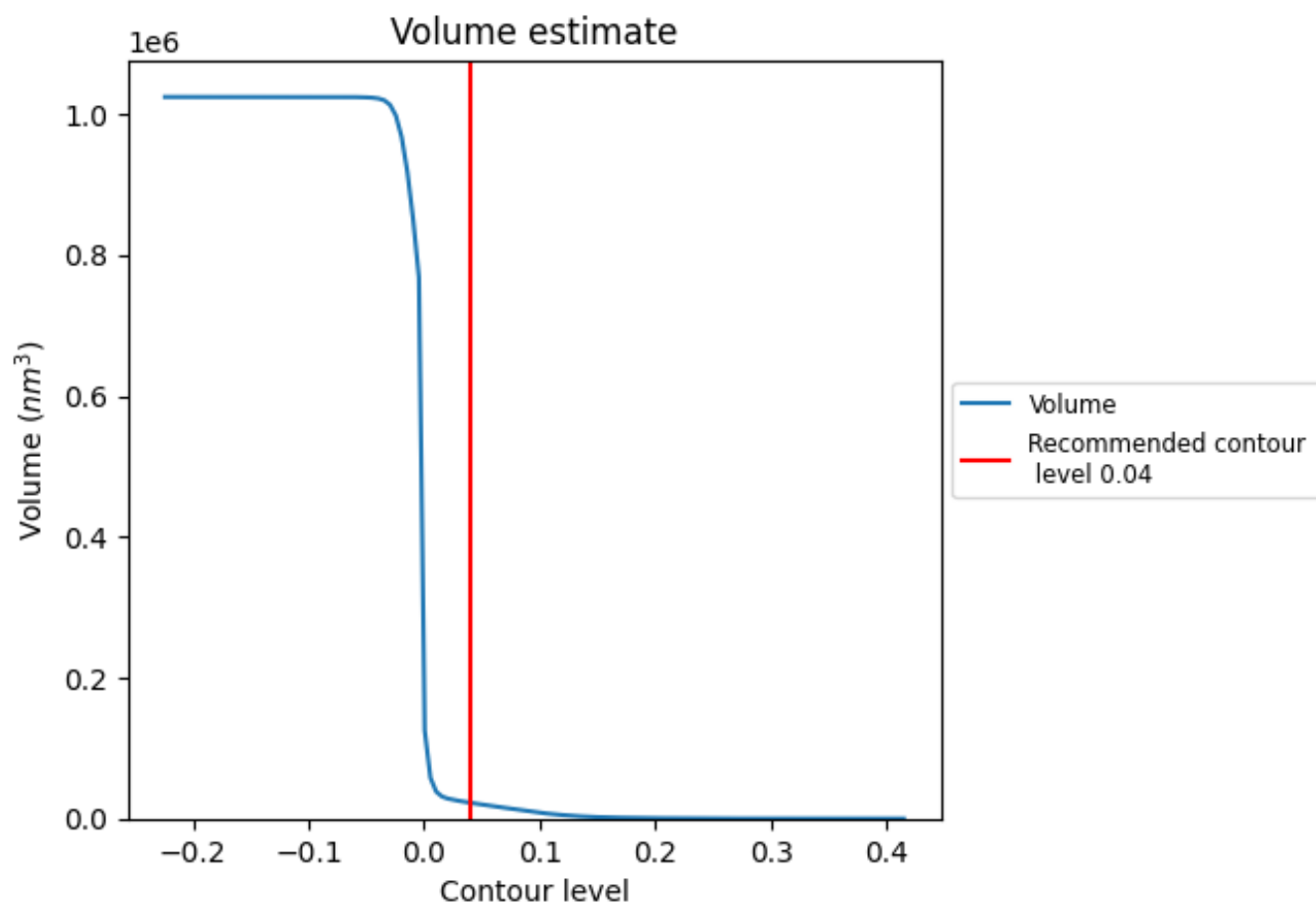
This section contains the results of statistical analysis of the map.

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.

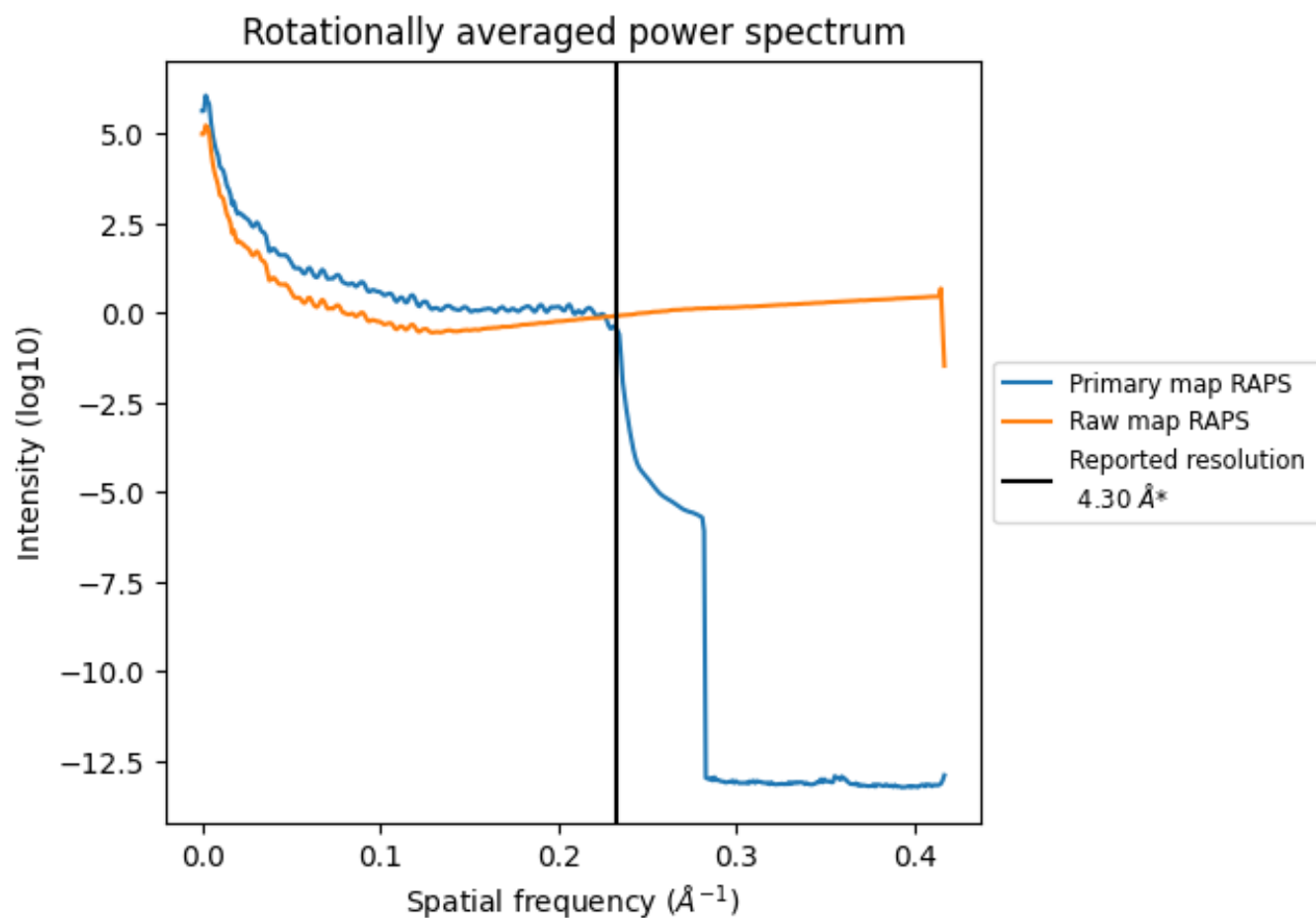
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 22548 nm³; this corresponds to an approximate mass of 20368 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 ⓘ

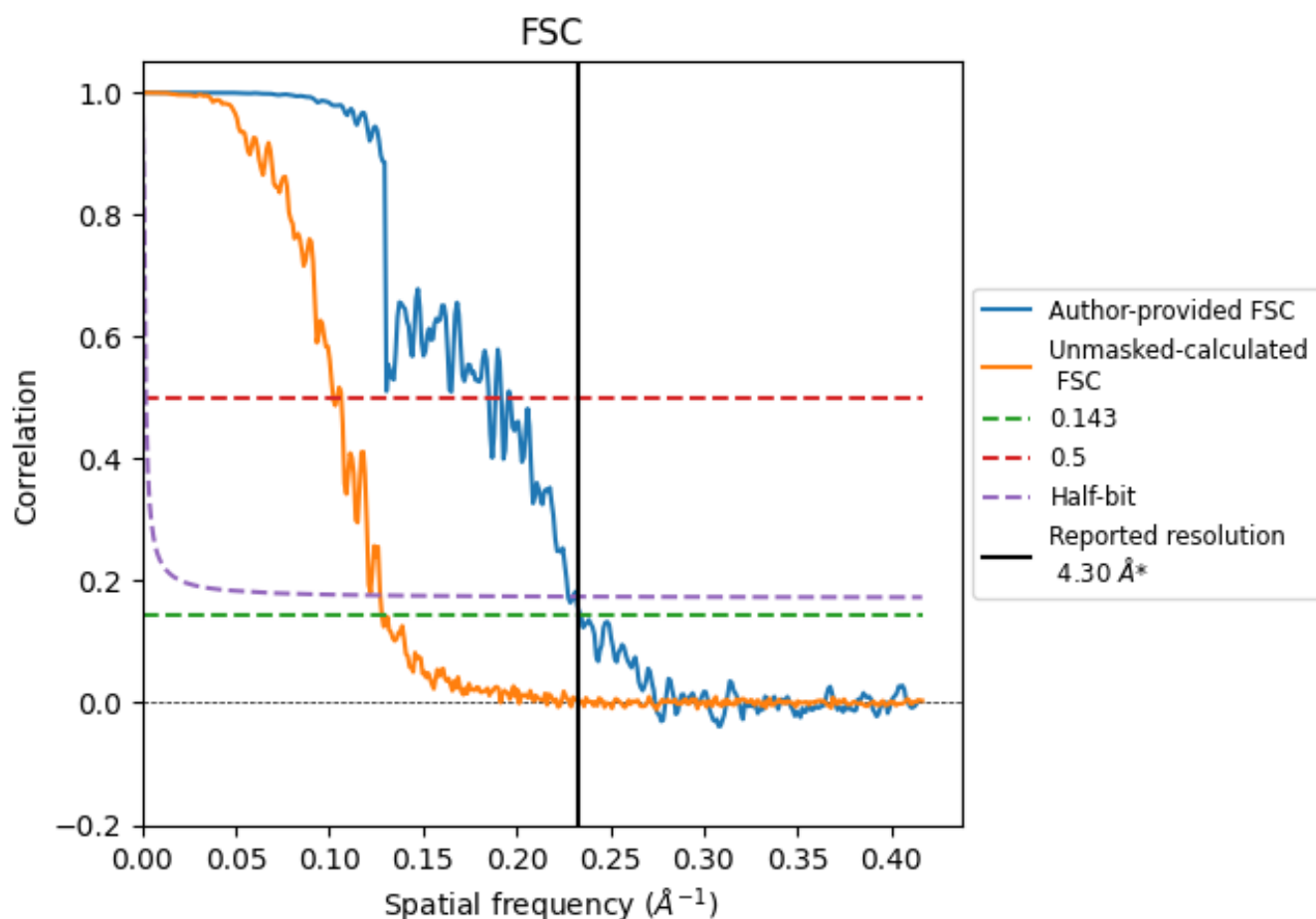


*Reported resolution corresponds to spatial frequency of 0.233 $\text{\AA}^{-1}$

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 0.233 $\text{\AA}^{-1}$

7.2 Resolution estimates [i](#)

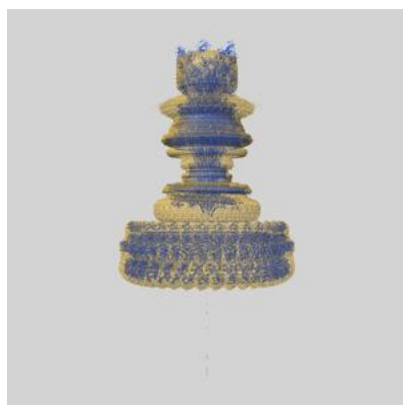
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.27	5.40	4.39
Unmasked-calculated*	7.81	9.80	7.86

*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 7.81 differs from the reported value 4.3 by more than 10 %

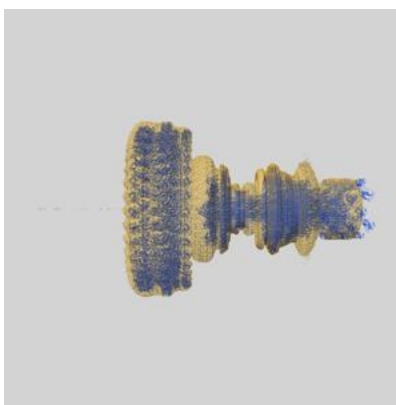
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37684 and PDB model 8WOE. Per-residue inclusion information can be found in section ?? on page ??.

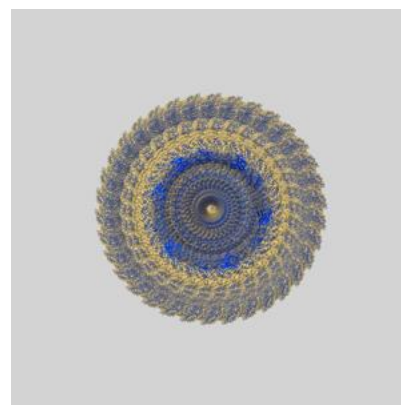
8.1 Map-model overlay [i](#)



X



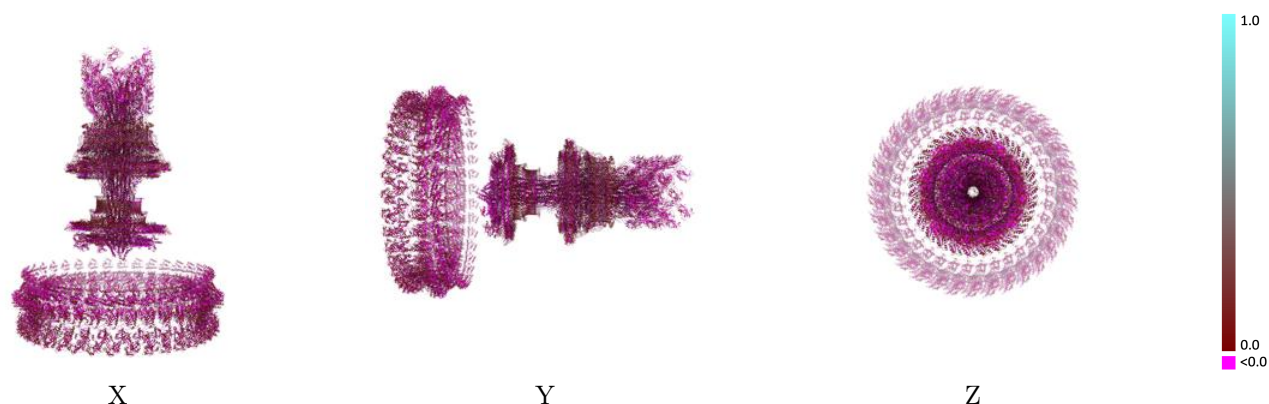
Y



Z

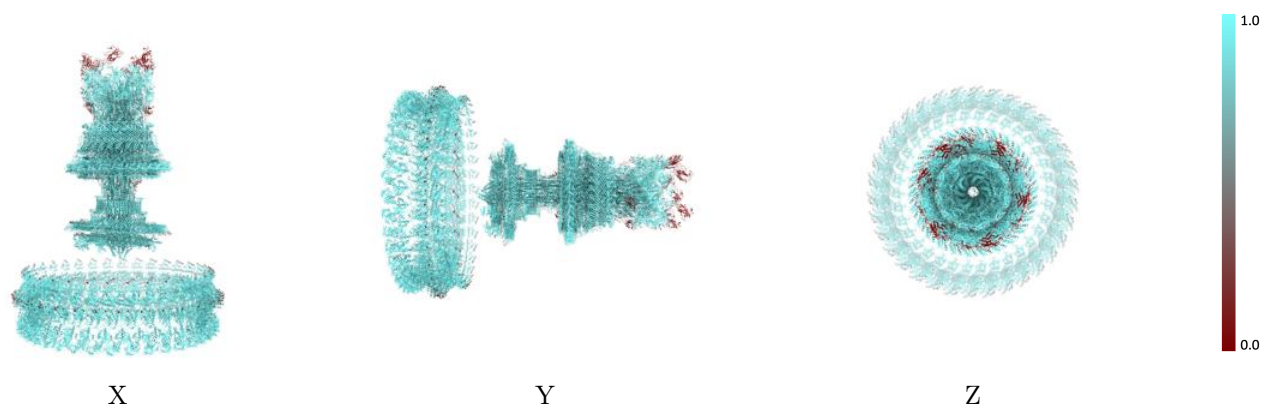
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



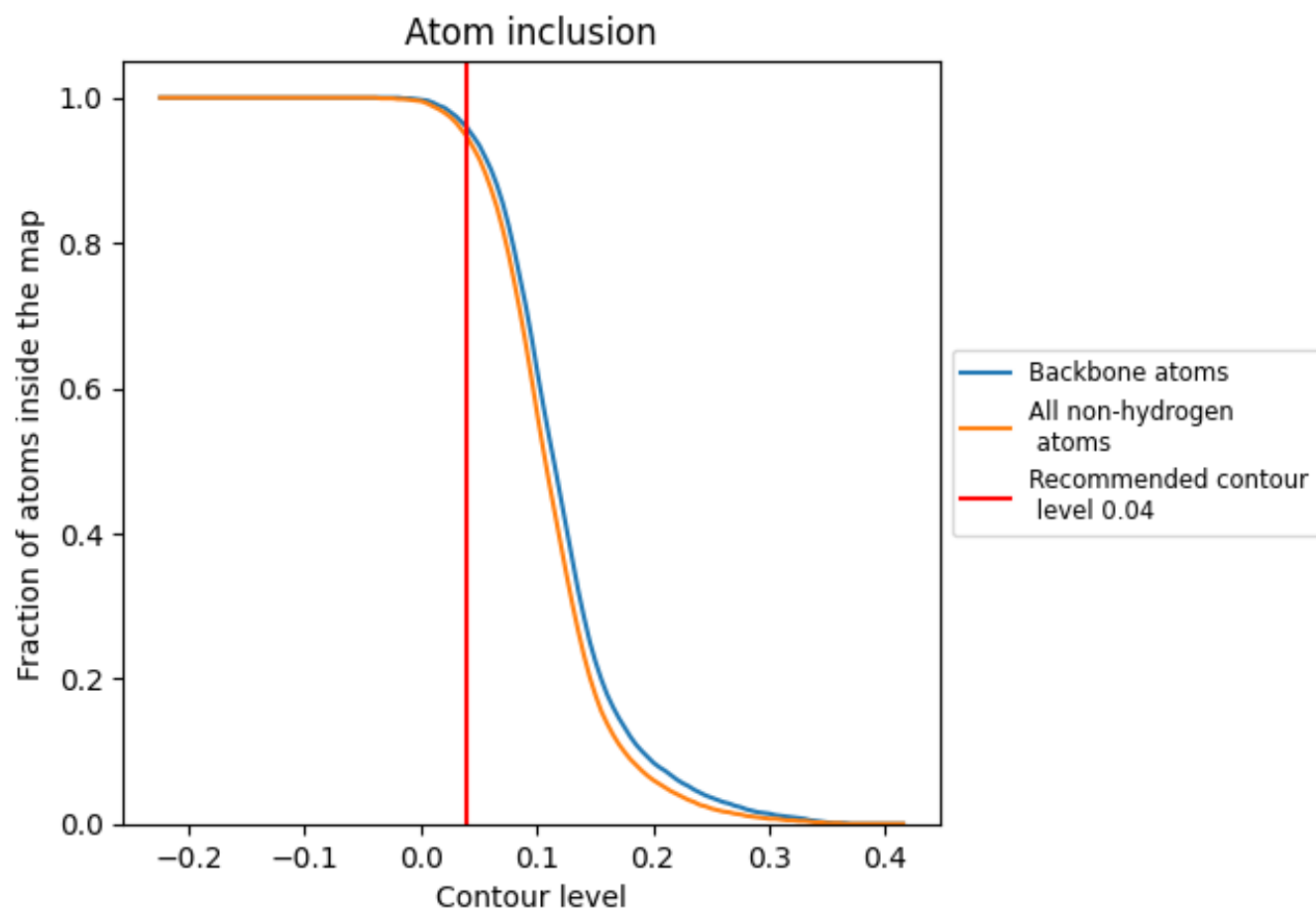
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

8.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.0660
0	 0.9630	 0.0640
1	 0.9600	 0.0700
2	 0.9620	 0.0710
3	 0.9620	 0.0670
4	 0.9560	 0.0560
5	 0.9560	 0.0480
6	 0.9570	 0.0700
7	 0.9660	 0.0710
8	 0.9720	 0.0770
9	 0.9740	 0.0690
A	 0.9370	 0.1470
A0	 0.9020	 0.0500
A1	 0.8930	 0.0440
A2	 0.9510	 0.0550
A3	 0.9540	 0.0720
A4	 0.9590	 0.1040
A5	 0.9510	 0.0930
A6	 0.8340	 0.0610
A7	 0.8770	 0.0350
A8	 0.8850	 0.0360
A9	 0.8790	 0.0380
AA	 0.8630	 0.0360
AB	 0.8980	 0.0310
AC	 0.9290	 0.0380
AD	 0.9510	 0.0550
AE	 0.9590	 0.0710
AF	 0.9670	 0.0760
AG	 0.9660	 0.0660
AH	 0.9710	 0.0590
AI	 0.9670	 0.0480
AJ	 0.9690	 0.0690
AK	 0.9730	 0.0660
AL	 0.9680	 0.0800
AM	 0.9690	 0.0620



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Chain	Atom inclusion	Q-score
AN	 0.9590	 0.0450
AO	 0.9620	 0.0790
AP	 0.9750	 0.1060
AQ	 0.9780	 0.1230
AR	 0.9740	 0.1190
AS	 0.9290	 0.0700
AT	 0.9320	 0.0710
AU	 0.9330	 0.0790
AV	 0.9450	 0.0910
AW	 0.9550	 0.1070
AX	 0.9680	 0.1250
AY	 0.9730	 0.1440
AZ	 0.9770	 0.1450
Aa	 0.9770	 0.1370
Ab	 0.9870	 0.0060
Ac	 0.9650	 0.0970
Ad	 0.9540	 0.0750
Ae	 0.9420	 0.0550
Af	 0.9220	 0.0390
Ag	 0.9110	 0.0280
Ah	 0.8980	 0.0200
Ai	 0.8930	 0.0130
Aj	 0.8920	 0.0120
Ak	 0.8960	 0.0120
Al	 0.9010	 0.0150
Am	 0.9110	 0.0190
An	 0.9210	 0.0240
Ao	 0.9380	 0.0320
Ap	 0.9470	 0.0510
Aq	 1.0000	 -0.0100
Ar	 1.0000	 0.0070
As	 0.9940	 0.0470
At	 0.9950	 0.0390
Au	 0.9690	 0.0360
Av	 0.9840	 0.0330
Aw	 0.9770	 0.0160
Ax	 0.9580	 0.0210
Ay	 0.9240	 0.0430
Az	 0.9110	 0.0700
B	 0.9360	 0.1430
B0	 0.9910	 0.0380
B1	 0.9940	 0.1100

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Chain	Atom inclusion	Q-score
B2	 0.9920	 0.0680
B3	 0.9910	 0.0420
B4	 0.9880	 0.0820
B5	 0.9740	 0.0320
B6	 0.8860	 0.0460
B7	 0.9970	 0.0820
B8	 0.9940	 0.1080
B9	 0.9920	 0.0710
BA	 0.9450	 0.0370
BB	 0.9490	 0.0440
BC	 0.9530	 0.0250
BD	 0.9790	 0.0710
BE	 0.9890	 0.0930
BF	 0.9940	 0.0690
BG	 1.0000	 0.0830
BH	 0.8450	 0.0020
BI	 0.5710	 -0.0320
BJ	 0.8350	 -0.0060
BK	 0.6860	 -0.0090
BL	 0.8640	 -0.0320
BM	 0.8210	 0.0250
BN	 0.9710	 0.0730
BO	 0.9320	 0.1020
BP	 0.9610	 0.0190
BQ	 0.8570	 0.0660
BR	 0.9820	 0.1300
BS	 0.9740	 0.1260
BT	 0.9660	 0.1160
BU	 0.9480	 0.1040
BV	 0.9380	 0.0920
BW	 0.9330	 0.0800
BX	 0.9290	 0.0720
BY	 0.9940	 0.1110
BZ	 0.9920	 0.0700
Ba	 0.9910	 0.0390
Bb	 0.9870	 0.0820
Bc	 0.9730	 0.0320
Bd	 0.8770	 0.0430
Be	 0.9950	 0.0790
Bf	 0.9940	 0.1120
Bg	 0.9920	 0.0670
Bh	 0.9910	 0.0380

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Chain	Atom inclusion	Q-score
Bi	 0.9870	 0.0820
Bj	 0.9730	 0.0320
Bk	 0.8760	 0.0440
Bl	 0.9950	 0.0790
Bm	 0.9940	 0.1080
Bn	 0.9920	 0.0690
Bo	 0.9910	 0.0370
Bp	 0.9870	 0.0830
Bq	 0.9720	 0.0310
Br	 0.8730	 0.0450
Bs	 0.9970	 0.0810
Bt	 0.9940	 0.1050
Bu	 0.9920	 0.0700
Bv	 0.9910	 0.0420
Bw	 0.9870	 0.0830
Bx	 0.9730	 0.0330
By	 0.8770	 0.0450
Bz	 0.9950	 0.0810
C	 0.9410	 0.1460
C0	 0.9880	 0.0800
C1	 0.9970	 0.0790
C2	 0.9940	 0.1060
C3	 0.9920	 0.0720
C4	 0.9970	 0.0790
C5	 0.9940	 0.1050
C6	 0.9720	 0.0320
C7	 0.8770	 0.0370
C8	 0.9950	 0.0780
C9	 0.9940	 0.1080
CA	 0.9880	 0.0820
CB	 0.9740	 0.0320
CC	 0.8820	 0.0450
CD	 0.9950	 0.0810
CE	 0.9940	 0.1100
CF	 0.9920	 0.0700
CG	 0.9910	 0.0360
CH	 0.9880	 0.0820
CI	 0.9720	 0.0300
CJ	 0.8800	 0.0420
CK	 0.9970	 0.0810
CL	 0.9940	 0.1100
CM	 0.9920	 0.0710

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Chain	Atom inclusion	Q-score
CN	 0.9910	 0.0410
CO	 0.9880	 0.0820
CP	 0.9730	 0.0310
CQ	 0.8810	 0.0420
CR	 0.9970	 0.0790
CS	 0.9940	 0.1110
CT	 0.9920	 0.0730
CU	 0.9910	 0.0430
CV	 0.9870	 0.0810
CW	 0.9730	 0.0310
CX	 0.8730	 0.0430
CY	 0.9970	 0.0820
CZ	 0.9940	 0.1070
Ca	 0.9920	 0.0710
Cb	 0.9910	 0.0410
Cc	 0.9870	 0.0810
Cd	 0.9730	 0.0320
Ce	 0.8770	 0.0420
Cf	 0.9970	 0.0810
Cg	 0.9920	 0.1080
Ch	 0.9920	 0.0700
Ci	 0.9910	 0.0380
Cj	 0.9870	 0.0820
Ck	 0.9730	 0.0310
Cl	 0.8740	 0.0420
Cm	 0.9940	 0.0780
Cn	 0.9920	 0.1070
Co	 0.9920	 0.0710
Cp	 0.9910	 0.0360
Cq	 0.9870	 0.0820
Cr	 0.9730	 0.0330
Cs	 0.8780	 0.0400
Ct	 0.9950	 0.0790
Cu	 0.9940	 0.1080
Cv	 0.9920	 0.0720
Cw	 0.9910	 0.0420
Cx	 0.9870	 0.0810
Cy	 0.9740	 0.0320
Cz	 0.8770	 0.0410
D	 0.9350	 0.1440
D0	 0.8770	 0.0380
D1	 0.9920	 0.0690

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Chain	Atom inclusion	Q-score
D2	 0.9870	 0.0810
D3	 0.9730	 0.0300
D4	 0.8730	 0.0380
D5	 0.9940	 0.0790
D6	 0.9940	 0.1060
D7	 0.9920	 0.0690
D8	 0.9870	 0.0820
D9	 0.9730	 0.0310
DA	 0.9740	 0.0300
DB	 0.8840	 0.0370
DC	 0.9880	 0.0810
DD	 0.9920	 0.0700
DE	 0.9910	 0.0410
DF	 0.9880	 0.0810
DG	 0.9740	 0.0310
DH	 0.8800	 0.0420
DI	 0.9950	 0.0800
DJ	 0.9940	 0.1070
DK	 0.9920	 0.0690
DL	 0.9910	 0.0360
DM	 0.9920	 0.0700
DN	 0.9920	 0.0720
DO	 0.9920	 0.0710
DP	 0.9920	 0.0720
DQ	 0.9920	 0.0690
DR	 0.9920	 0.0710
DS	 0.9920	 0.0710
DT	 0.9920	 0.0670
DU	 0.9970	 0.0800
DV	 0.9940	 0.1040
DW	 0.9920	 0.0710
DX	 0.9880	 0.0810
DY	 0.9730	 0.0300
DZ	 0.8800	 0.0410
Da	 0.9970	 0.0800
Db	 0.9940	 0.1060
Dc	 0.9920	 0.0700
Dd	 0.9880	 0.0810
De	 0.9720	 0.0290
Df	 0.8810	 0.0370
Dg	 0.9950	 0.0800
Dh	 0.9940	 0.1030

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Chain	Atom inclusion	Q-score
Di	 0.9920	 0.0700
Dj	 0.9870	 0.0820
Dk	 0.9730	 0.0300
Dl	 0.8800	 0.0380
Dm	 0.9970	 0.0820
Dn	 0.9920	 0.1060
Do	 0.9920	 0.0720
Dp	 0.9870	 0.0800
Dq	 0.9720	 0.0290
Dr	 0.8760	 0.0390
Ds	 0.9970	 0.0830
Dt	 0.9940	 0.1050
Du	 0.9920	 0.0700
Dv	 0.9870	 0.0790
Dw	 0.9730	 0.0310
Dx	 0.8790	 0.0380
Dy	 0.9970	 0.0820
Dz	 0.9920	 0.1060
E	 0.9410	 0.1370
E0	 0.8750	 0.0390
E1	 0.9730	 0.0310
E2	 0.9730	 0.0310
E3	 0.9730	 0.0310
E4	 0.9720	 0.0300
E5	 0.9870	 0.0810
E6	 0.8810	 0.0390
E7	 0.8790	 0.0390
E8	 0.8780	 0.0380
E9	 0.8720	 0.0400
EA	 0.9950	 0.0810
EB	 0.9940	 0.1080
EC	 0.9720	 0.0330
ED	 0.8820	 0.0420
EE	 0.9970	 0.0800
EF	 0.9940	 0.1080
EG	 0.9920	 0.0680
EH	 0.9910	 0.0400
EI	 0.9880	 0.0810
EJ	 0.9720	 0.0320
EK	 0.8830	 0.0410
EL	 0.9970	 0.0820
EM	 0.9940	 0.1080

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Chain	Atom inclusion	Q-score
EN	 0.9920	 0.0710
EO	 0.9910	 0.0380
EP	 0.9880	 0.0820
EQ	 0.9730	 0.0300
ER	 0.8790	 0.0430
ES	 0.9970	 0.0810
ET	 0.9940	 0.1050
EU	 0.9920	 0.0700
EV	 0.9910	 0.0380
EW	 0.9870	 0.0810
EX	 0.9740	 0.0310
EY	 0.8730	 0.0440
EZ	 0.9970	 0.0820
Ea	 0.9910	 0.0400
Eb	 0.9910	 0.0390
Ec	 0.9910	 0.0370
Ed	 0.9910	 0.0410
Ee	 0.9910	 0.0430
Ef	 0.9910	 0.0420
Eg	 0.9910	 0.0400
Eh	 0.9910	 0.0410
Ei	 0.9910	 0.0430
Ej	 0.9910	 0.0430
Ek	 0.9910	 0.0420
El	 0.9910	 0.0420
Em	 0.9910	 0.0370
En	 0.9910	 0.0390
Eo	 0.9910	 0.0390
Ep	 0.9910	 0.0410
Eq	 0.9870	 0.0800
Er	 0.9870	 0.0810
Es	 0.9880	 0.0820
Et	 0.9870	 0.0820
Eu	 0.9870	 0.0810
Ev	 0.9870	 0.0820
Ew	 0.9870	 0.0820
Ex	 0.9720	 0.0310
Ey	 0.9730	 0.0310
Ez	 0.9730	 0.0290
F	 0.9400	 0.1370
FA	 0.8750	 0.0390
FB	 0.8720	 0.0370

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Chain	Atom inclusion	Q-score
FC	 0.9970	 0.0770
FD	 0.9970	 0.0810
FE	 0.9970	 0.0780
FF	 0.9970	 0.0780
FG	 0.9950	 0.0780
FH	 0.9950	 0.0760
FI	 0.9940	 0.1080
FJ	 0.9940	 0.1060
FK	 0.9940	 0.1040
FL	 0.9940	 0.1060
FM	 0.9940	 0.1060
FN	 0.9910	 0.1050
G	 0.9380	 0.1350
H	 0.9270	 0.1260
I	 0.9320	 0.1250
J	 0.9320	 0.1310
K	 0.9250	 0.1270
L	 0.9310	 0.1300
M	 0.9320	 0.1390
N	 0.9280	 0.1400
O	 0.9320	 0.1430
P	 0.9300	 0.1450
Q	 0.9270	 0.1460
R	 0.9320	 0.1450
S	 0.9280	 0.1430
T	 0.9260	 0.1340
U	 0.9260	 0.1350
UI	 0.9360	 0.0490
UJ	 0.8960	 0.0090
UK	 0.9260	 0.0530
UL	 0.9260	 0.0540
UM	 0.9890	 -0.0010
UN	 0.9710	 0.0110
UO	 0.9670	 0.0410
UP	 0.9440	 0.0470
V	 0.9310	 0.1360
W	 0.9290	 0.1290
WA	 0.9710	 0.0730
WB	 0.9830	 0.0770
WC	 0.9800	 0.0500
WD	 0.9770	 0.0590
WE	 0.9280	 0.0460

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Chain	Atom inclusion	Q-score
WF	 0.9610	 0.0770
WG	 0.9650	 0.0590
WH	 0.9710	 0.0900
WI	 0.9160	 0.0950
WJ	 0.9780	 0.0620
WK	 0.9900	 0.0270
WL	 0.9870	 -0.0210
WM	 0.9630	 -0.0210
WN	 0.9470	 -0.0240
WO	 0.9390	 -0.0120
WP	 0.9550	 -0.0220
WQ	 0.9670	 -0.0370
WR	 0.9790	 0.0110
WS	 0.9840	 -0.0140
WT	 0.9850	 0.0440
WU	 0.9930	 0.0540
WV	 0.9940	 0.0760
WW	 0.9990	 0.0740
X	 0.9310	 0.1380
Y	 0.9320	 0.1400
Z	 0.9380	 0.1440
ZA	 0.9800	 0.0510
ZB	 0.9730	 0.0500
ZC	 0.9800	 0.0600
ZD	 0.9840	 0.0610
ZE	 0.9850	 0.0580
ZF	 0.7050	 0.0240
ZG	 0.7380	 0.0300
ZH	 0.7700	 0.0230
ZI	 0.8220	 0.0400
ZJ	 0.9000	 0.0460
ZK	 0.9360	 0.0390
ZL	 0.9480	 0.0130
ZM	 0.9360	 0.0410
ZN	 0.9380	 0.0410
ZO	 0.9600	 0.0390
ZP	 0.9680	 0.0320
ZQ	 0.9760	 0.0280
ZR	 0.9660	 0.0280
ZS	 0.9540	 0.0280
ZT	 0.9630	 0.0360
ZU	 0.9720	 0.0270

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Chain	Atom inclusion	Q-score
ZV	 0.9710	 0.0330
ZW	 0.9530	 0.0160
ZX	 0.9180	 0.0250
ZY	 0.8790	 0.0320
ZZ	 0.8510	 0.0130
Za	 0.8220	 0.0190
Zb	 0.7790	 0.0210
Zc	 0.7410	 0.0330
Zd	 0.7020	 0.0120
Ze	 0.6730	 0.0270
Zf	 0.6350	 0.0300
Zg	 0.6210	 0.0330
Zh	 0.6050	 0.0180
a	 0.9660	 0.1240
b	 0.9680	 0.1300
c	 0.9660	 0.1280
d	 0.9640	 0.1270
e	 0.9650	 0.1130
f	 0.9640	 0.1140
g	 0.9650	 0.1160
h	 0.9610	 0.1030
i	 0.9630	 0.1090
j	 0.9620	 0.1150
k	 0.9620	 0.1130
l	 0.9670	 0.1210
m	 0.9640	 0.1210
n	 0.9620	 0.1290
o	 0.9640	 0.1300
p	 0.9620	 0.1220
q	 0.9660	 0.1240
r	 0.9610	 0.1200
s	 0.9580	 0.1080
t	 0.9570	 0.1070
u	 0.9580	 0.1040
v	 0.9550	 0.0950
w	 0.9550	 0.0960
x	 0.9630	 0.1090
y	 0.9590	 0.1170
z	 0.9620	 0.1170