



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 03:00 AM UTC

PDB ID : 8TXB / pdb_00008txb
EMDB ID : EMD-41679
Title : Characterization of the Chlamydomonas Flagellar Mastigoneme Filament Structure at 3.9Å
Authors : Yue, W.; Kai, Z.
Deposited on : 2023-08-23
Resolution : 3.90 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

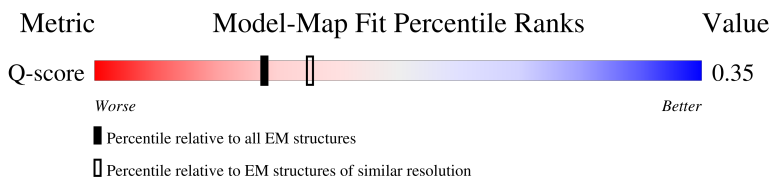
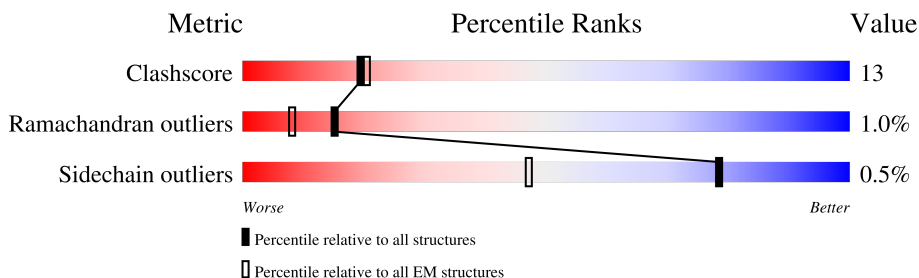
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1987	 69% 26% • 5%
1	B	1987	 69% 25% • 5%
1	C	1987	 71% 24% • 5%
1	D	1987	 71% 24% • 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 54748 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 Mastigoneme-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1894	Total	C	N	O	S	0	0
			13687	8643	2234	2727	83		
1	B	1894	Total	C	N	O	S	0	0
			13687	8643	2234	2727	83		
1	C	1894	Total	C	N	O	S	0	0
			13687	8643	2234	2727	83		
1	D	1894	Total	C	N	O	S	0	0
			13687	8643	2234	2727	83		

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	LEU	VAL	conflict	UNP Q8LRM7
A	142	LEU	THR	conflict	UNP Q8LRM7
A	143	ALA	GLY	conflict	UNP Q8LRM7
A	144	SER	LEU	conflict	UNP Q8LRM7
A	145	LYS	GLU	conflict	UNP Q8LRM7
A	146	THR	ASP	conflict	UNP Q8LRM7
A	147	VAL	GLY	conflict	UNP Q8LRM7
A	149	ILE	HIS	conflict	UNP Q8LRM7
A	150	TYR	LEU	conflict	UNP Q8LRM7
A	151	VAL	CYS	conflict	UNP Q8LRM7
A	517	ARG	LYS	conflict	UNP Q8LRM7
A	530	GLU	GLY	conflict	UNP Q8LRM7
A	619	THR	ALA	conflict	UNP Q8LRM7
A	800	SER	THR	conflict	UNP Q8LRM7
A	820	SER	PHE	conflict	UNP Q8LRM7
A	?	-	GLY	deletion	UNP Q8LRM7
A	?	-	THR	deletion	UNP Q8LRM7
A	?	-	PRO	deletion	UNP Q8LRM7
A	?	-	GLY	deletion	UNP Q8LRM7
A	?	-	PRO	deletion	UNP Q8LRM7
A	?	-	TYR	deletion	UNP Q8LRM7
A	?	-	PHE	deletion	UNP Q8LRM7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP Q8LRM7
A	1399	LYS	ARG	conflict	UNP Q8LRM7
A	?	-	PRO	deletion	UNP Q8LRM7
A	?	-	GLU	deletion	UNP Q8LRM7
A	1868	PRO	ALA	conflict	UNP Q8LRM7
A	1897	PRO	GLN	conflict	UNP Q8LRM7
A	1914	PRO	ARG	conflict	UNP Q8LRM7
A	1915	PRO	ARG	conflict	UNP Q8LRM7
A	1917	PRO	HIS	conflict	UNP Q8LRM7
A	1919	SER	ALA	conflict	UNP Q8LRM7
A	1920	PRO	ARG	conflict	UNP Q8LRM7
A	1921	PRO	ARG	conflict	UNP Q8LRM7
A	1924	ASN	THR	conflict	UNP Q8LRM7
A	1925	ARG	ALA	conflict	UNP Q8LRM7
A	1926	SER	LEU	conflict	UNP Q8LRM7
A	1935	SER	PRO	conflict	UNP Q8LRM7
A	1978	ASP	-	expression tag	UNP Q8LRM7
A	1979	ALA	-	expression tag	UNP Q8LRM7
A	1980	GLU	-	expression tag	UNP Q8LRM7
A	1981	MET	-	expression tag	UNP Q8LRM7
A	1982	GLN	-	expression tag	UNP Q8LRM7
A	1983	PRO	-	expression tag	UNP Q8LRM7
A	1984	GLN	-	expression tag	UNP Q8LRM7
A	1985	ASP	-	expression tag	UNP Q8LRM7
A	1986	ASP	-	expression tag	UNP Q8LRM7
A	1987	GLU	-	expression tag	UNP Q8LRM7
B	141	LEU	VAL	conflict	UNP Q8LRM7
B	142	LEU	THR	conflict	UNP Q8LRM7
B	143	ALA	GLY	conflict	UNP Q8LRM7
B	144	SER	LEU	conflict	UNP Q8LRM7
B	145	LYS	GLU	conflict	UNP Q8LRM7
B	146	THR	ASP	conflict	UNP Q8LRM7
B	147	VAL	GLY	conflict	UNP Q8LRM7
B	149	ILE	HIS	conflict	UNP Q8LRM7
B	150	TYR	LEU	conflict	UNP Q8LRM7
B	151	VAL	CYS	conflict	UNP Q8LRM7
B	517	ARG	LYS	conflict	UNP Q8LRM7
B	530	GLU	GLY	conflict	UNP Q8LRM7
B	619	THR	ALA	conflict	UNP Q8LRM7
B	800	SER	THR	conflict	UNP Q8LRM7
B	820	SER	PHE	conflict	UNP Q8LRM7
B	?	-	GLY	deletion	UNP Q8LRM7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	THR	deletion	UNP Q8LRM7
B	?	-	PRO	deletion	UNP Q8LRM7
B	?	-	GLY	deletion	UNP Q8LRM7
B	?	-	PRO	deletion	UNP Q8LRM7
B	?	-	TYR	deletion	UNP Q8LRM7
B	?	-	PHE	deletion	UNP Q8LRM7
B	?	-	LEU	deletion	UNP Q8LRM7
B	1399	LYS	ARG	conflict	UNP Q8LRM7
B	?	-	PRO	deletion	UNP Q8LRM7
B	?	-	GLU	deletion	UNP Q8LRM7
B	1868	PRO	ALA	conflict	UNP Q8LRM7
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B	1914	PRO	ARG	conflict	UNP Q8LRM7
B	1915	PRO	ARG	conflict	UNP Q8LRM7
B	1917	PRO	HIS	conflict	UNP Q8LRM7
B	1919	SER	ALA	conflict	UNP Q8LRM7
B	1920	PRO	ARG	conflict	UNP Q8LRM7
B	1921	PRO	ARG	conflict	UNP Q8LRM7
B	1924	ASN	THR	conflict	UNP Q8LRM7
B	1925	ARG	ALA	conflict	UNP Q8LRM7
B	1926	SER	LEU	conflict	UNP Q8LRM7
B	1935	SER	PRO	conflict	UNP Q8LRM7
B	1978	ASP	-	expression tag	UNP Q8LRM7
B	1979	ALA	-	expression tag	UNP Q8LRM7
B	1980	GLU	-	expression tag	UNP Q8LRM7
B	1981	MET	-	expression tag	UNP Q8LRM7
B	1982	GLN	-	expression tag	UNP Q8LRM7
B	1983	PRO	-	expression tag	UNP Q8LRM7
B	1984	GLN	-	expression tag	UNP Q8LRM7
B	1985	ASP	-	expression tag	UNP Q8LRM7
B	1986	ASP	-	expression tag	UNP Q8LRM7
B	1987	GLU	-	expression tag	UNP Q8LRM7
C	141	LEU	VAL	conflict	UNP Q8LRM7
C	142	LEU	THR	conflict	UNP Q8LRM7
C	143	ALA	GLY	conflict	UNP Q8LRM7
C	144	SER	LEU	conflict	UNP Q8LRM7
C	145	LYS	GLU	conflict	UNP Q8LRM7
C	146	THR	ASP	conflict	UNP Q8LRM7
C	147	VAL	GLY	conflict	UNP Q8LRM7
C	149	ILE	HIS	conflict	UNP Q8LRM7
C	150	TYR	LEU	conflict	UNP Q8LRM7
C	151	VAL	CYS	conflict	UNP Q8LRM7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	517	ARG	LYS	conflict	UNP Q8LRM7
C	530	GLU	GLY	conflict	UNP Q8LRM7
C	619	THR	ALA	conflict	UNP Q8LRM7
C	800	SER	THR	conflict	UNP Q8LRM7
C	820	SER	PHE	conflict	UNP Q8LRM7
C	?	-	GLY	deletion	UNP Q8LRM7
C	?	-	THR	deletion	UNP Q8LRM7
C	?	-	PRO	deletion	UNP Q8LRM7
C	?	-	GLY	deletion	UNP Q8LRM7
C	?	-	PRO	deletion	UNP Q8LRM7
C	?	-	TYR	deletion	UNP Q8LRM7
C	?	-	PHE	deletion	UNP Q8LRM7
C	?	-	LEU	deletion	UNP Q8LRM7
C	1399	LYS	ARG	conflict	UNP Q8LRM7
C	?	-	PRO	deletion	UNP Q8LRM7
C	?	-	GLU	deletion	UNP Q8LRM7
C	1868	PRO	ALA	conflict	UNP Q8LRM7
C	1897	PRO	GLN	conflict	UNP Q8LRM7
C	1914	PRO	ARG	conflict	UNP Q8LRM7
C	1915	PRO	ARG	conflict	UNP Q8LRM7
C	1917	PRO	HIS	conflict	UNP Q8LRM7
C	1919	SER	ALA	conflict	UNP Q8LRM7
C	1920	PRO	ARG	conflict	UNP Q8LRM7
C	1921	PRO	ARG	conflict	UNP Q8LRM7
C	1924	ASN	THR	conflict	UNP Q8LRM7
C	1925	ARG	ALA	conflict	UNP Q8LRM7
C	1926	SER	LEU	conflict	UNP Q8LRM7
C	1935	SER	PRO	conflict	UNP Q8LRM7
C	1978	ASP	-	expression tag	UNP Q8LRM7
C	1979	ALA	-	expression tag	UNP Q8LRM7
C	1980	GLU	-	expression tag	UNP Q8LRM7
C	1981	MET	-	expression tag	UNP Q8LRM7
C	1982	GLN	-	expression tag	UNP Q8LRM7
C	1983	PRO	-	expression tag	UNP Q8LRM7
C	1984	GLN	-	expression tag	UNP Q8LRM7
C	1985	ASP	-	expression tag	UNP Q8LRM7
C	1986	ASP	-	expression tag	UNP Q8LRM7
C	1987	GLU	-	expression tag	UNP Q8LRM7
D	141	LEU	VAL	conflict	UNP Q8LRM7
D	142	LEU	THR	conflict	UNP Q8LRM7
D	143	ALA	GLY	conflict	UNP Q8LRM7
D	144	SER	LEU	conflict	UNP Q8LRM7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	145	LYS	GLU	conflict	UNP Q8LRM7
D	146	THR	ASP	conflict	UNP Q8LRM7
D	147	VAL	GLY	conflict	UNP Q8LRM7
D	149	ILE	HIS	conflict	UNP Q8LRM7
D	150	TYR	LEU	conflict	UNP Q8LRM7
D	151	VAL	CYS	conflict	UNP Q8LRM7
D	517	ARG	LYS	conflict	UNP Q8LRM7
D	530	GLU	GLY	conflict	UNP Q8LRM7
D	619	THR	ALA	conflict	UNP Q8LRM7
D	800	SER	THR	conflict	UNP Q8LRM7
D	820	SER	PHE	conflict	UNP Q8LRM7
D	?	-	GLY	deletion	UNP Q8LRM7
D	?	-	THR	deletion	UNP Q8LRM7
D	?	-	PRO	deletion	UNP Q8LRM7
D	?	-	GLY	deletion	UNP Q8LRM7
D	?	-	PRO	deletion	UNP Q8LRM7
D	?	-	TYR	deletion	UNP Q8LRM7
D	?	-	PHE	deletion	UNP Q8LRM7
D	?	-	LEU	deletion	UNP Q8LRM7
D	1399	LYS	ARG	conflict	UNP Q8LRM7
D	?	-	PRO	deletion	UNP Q8LRM7
D	?	-	GLU	deletion	UNP Q8LRM7
D	1868	PRO	ALA	conflict	UNP Q8LRM7
D	1897	PRO	GLN	conflict	UNP Q8LRM7
D	1914	PRO	ARG	conflict	UNP Q8LRM7
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D	1917	PRO	HIS	conflict	UNP Q8LRM7
D	1919	SER	ALA	conflict	UNP Q8LRM7
D	1920	PRO	ARG	conflict	UNP Q8LRM7
D	1921	PRO	ARG	conflict	UNP Q8LRM7
D	1924	ASN	THR	conflict	UNP Q8LRM7
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D	1980	GLU	-	expression tag	UNP Q8LRM7
D	1981	MET	-	expression tag	UNP Q8LRM7
D	1982	GLN	-	expression tag	UNP Q8LRM7
D	1983	PRO	-	expression tag	UNP Q8LRM7
D	1984	GLN	-	expression tag	UNP Q8LRM7
D	1985	ASP	-	expression tag	UNP Q8LRM7

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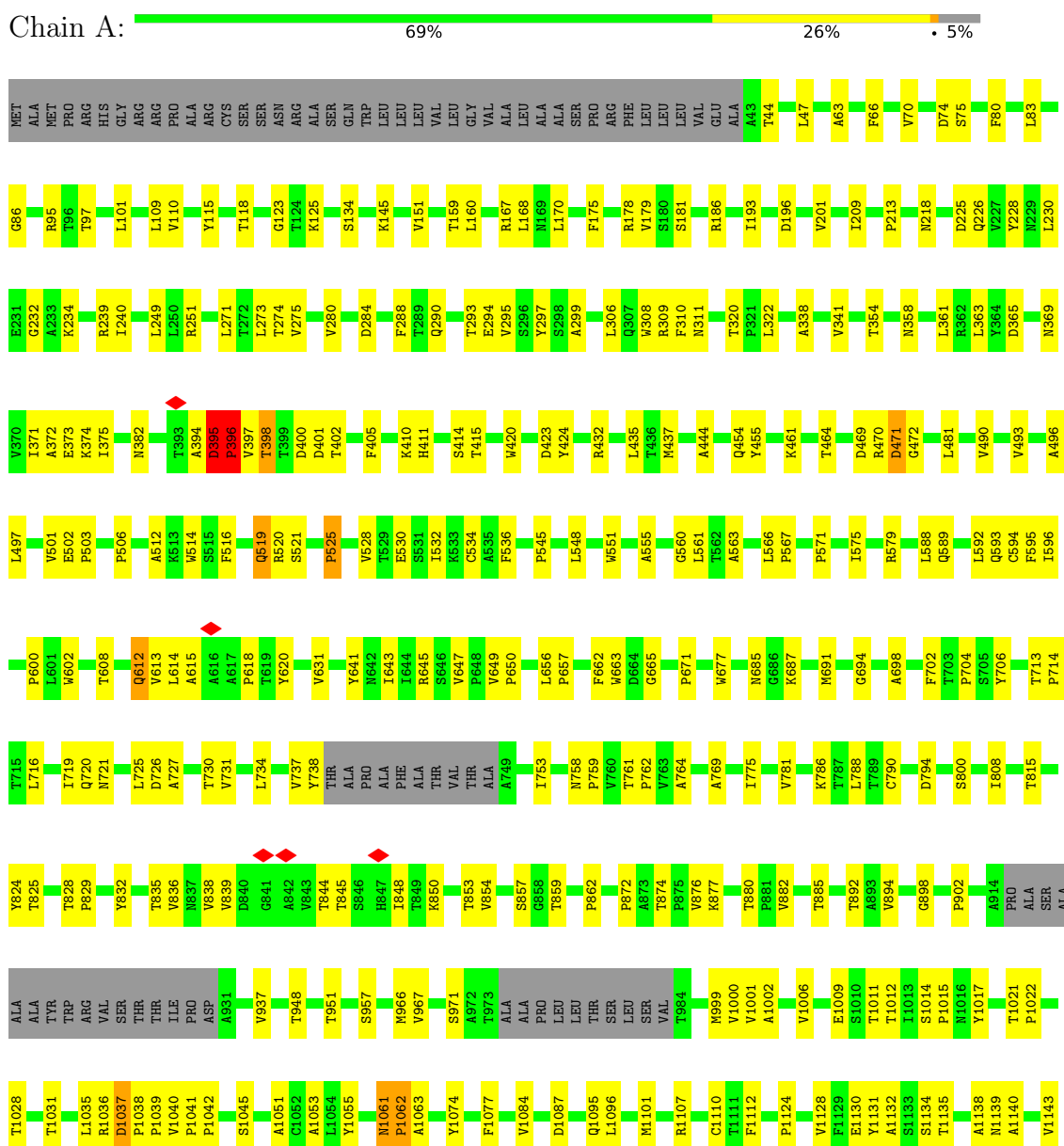
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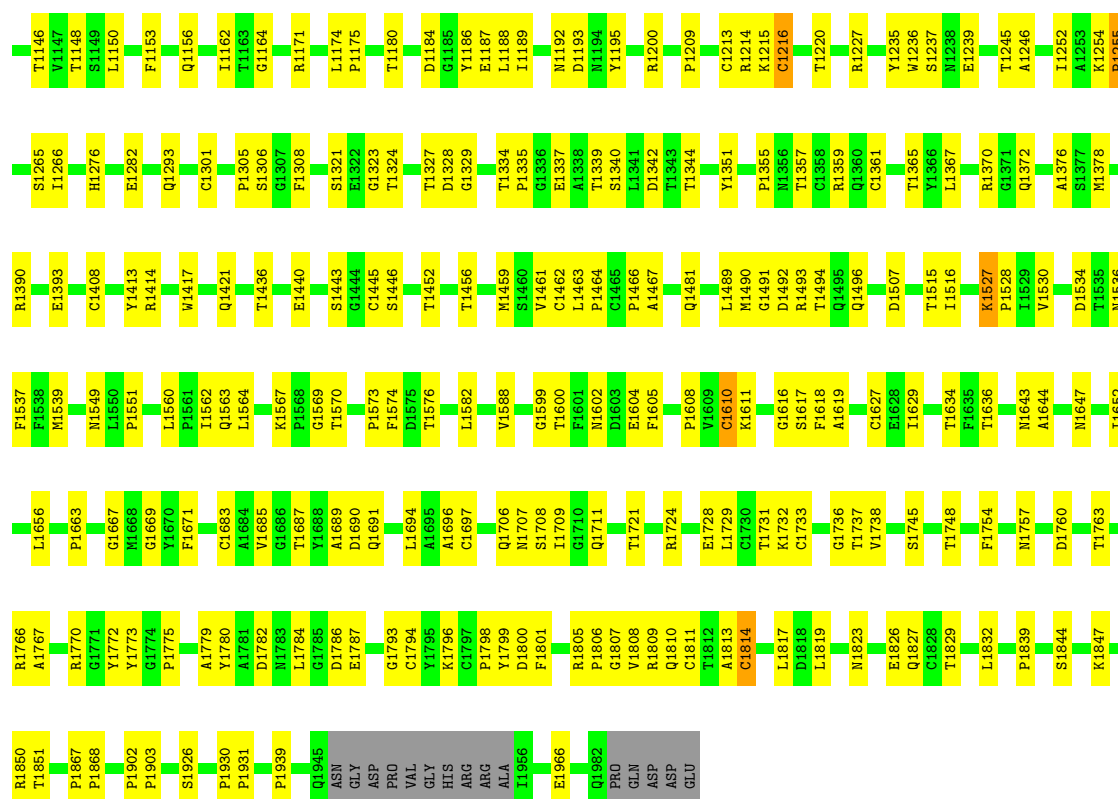
Chain	Residue	Modelled	Actual	Comment	Reference
D	1986	ASP	-	expression tag	UNP Q8LRM7
D	1987	GLU	-	expression tag	UNP Q8LRM7

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

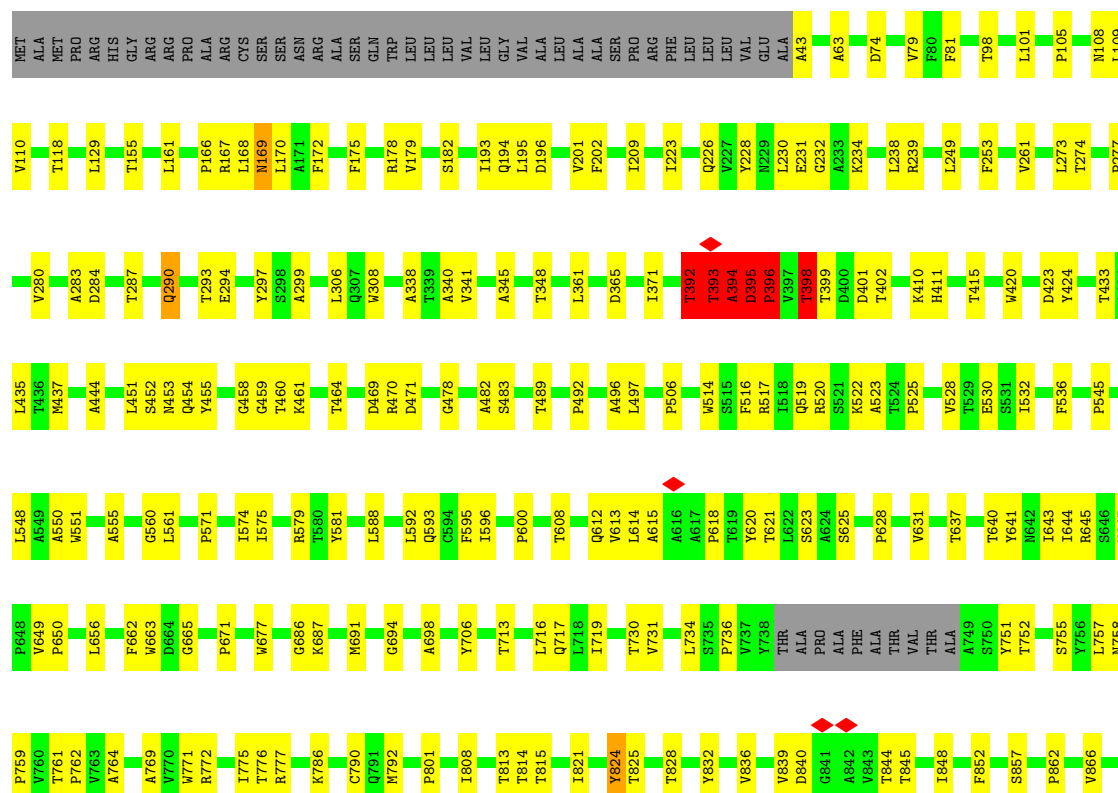
- Molecule 1: Mastigoneme-like protein

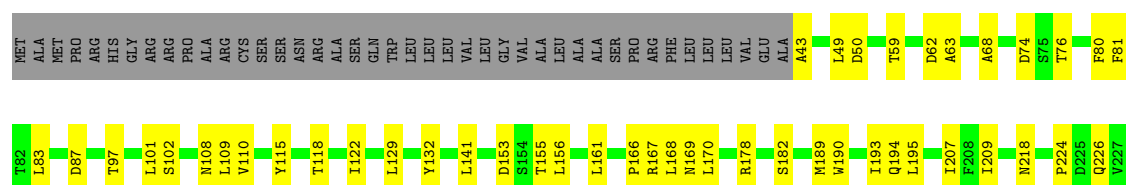




• Molecule 1: Mastigoneme-like protein

Chain B: 69% 25% 5%





L1842	L1843	P1867	P1868	P1883	P1902	P1903	P1920	P1921	S1926	S1935	P1939	Q1945	ASN	GLY	ASP	PRO	VAL	GLY	HIS	ARG	ARG	ALA	T1956	Q1982	PRO	GLN	ASP	ASP	GLU																		
S1745	Q1746	C1747	T1748	P1749	F1754	A1758	P1759	D1760	S1761	R1766	A1767	C1768	P1769	G1770	G1771	Y1772	Y1773	D1786	E1787	K1796	C1797	P1798	Y1799	D1800	A1803	D1804	R1805	P1806	G1807	V1808	R1809	C1814	P1815	L1816	L1817	D1818	L1819	N1823	L1824	V1825	E1826	T1829	L1832	G1833	S1834	P1839	
S1617	F1618	E1628	T1634	F1635	T1636	A1644	T1645	F1646	M1647	I1652	Y1654	L1656	A1660	Q1661	P1663	M1668	Q1672	C1680	C1683	A1684	V1685	G1686	T1687	L1694	Q1706	M1707	S1708	I1709	K1715	M1719	G1720	T1721	Y1722	S1723	R1724	T1731	K1732	C1733	P1734	T1737	V1738	S1740					
D1482	R1493	T1494	M1497	A1498	L1499	N1503	M1506	R1512	A1513	Y1514	T1515	M1519	V1520	A1526	K1527	V1530	F1537	F1538	M1539	T1548	N1549	T1555	G1569	P1573	F1574	T1578	L1586	T1587	V1588	Y1594	M1602	D1603	E1604	F1605	S1606	P1607	P1608	V1609	C1613	G1616							
C1361	N1364	T1365	Y1366	M1378	N1379	V1397	S1398	K1399	C1405	Q1406	P1410	R1414	N1415	F1418	Q1421	L1422	G1423	T1436	T1439	E1440	S1443	G1444	C1445	P1450	G1451	T1452	Y1453	A1454	P1455	T1456	F1457	M1459	C1462	L1463	P1464	C1465	P1466	T1469	G1485	T1486	L1489						
G1211	Q1212	C1213	R1214	K1215	C1216	T1220	M1223	D1224	C1228	I1229	P1230	E1239	C1247	T1251	I1252	A1253	K1254	P1255	A1256	A1257	H1276	E1282	K1285	K1286	K1289	F1292	Q1293	P1294	N1295	T1299	V1300	C1304	S1310	T1311	S1312	Y1325	H1326	T1327	D1328	T1350	Y1351	C1358					
N1061	P1062	T1070	D1071	F1077	V1080	T1081	T1082	A1083	V1084	A1085	T1086	D1087	D1093	L1096	R1097	C1110	T1111	F1112	L1115	V1128	F1129	E1130	Y1131	A1138	N1139	A1140	V1143	A1144	D1145	L1150	P1165	L1174	P1175	F1178	Y1186	E1187	Y1195	V1199	R1200	V1201	A1202						
S973	A972	T973	ALA	PRD	LEU	LEU	THR	LEU	THR	SER	VAL	T984	Q987	L988	M999	V1000	A1001	V1006	E1009	T1010	T1011	T1012	I1013	S1014	P1015	P1022	T1028	T1031	F1032	T1033	L1034	A1035	D1037	P1038	P1041	P1042	S1045	Q1049	F1050	A1051	Y1055	Q1058	N1059	V1060			
K877	T880	P881	T882	T883	T884	T885	P886	T889	V894	P902	I903	N909	G910	A914	ALA	SER	ALA	ALA	ALA	ALA	TRP	TYR	T814	T828	P829	Y832	V836	V837	V838	V839	D840	G841	T844	T845	S846	H847	V854	L855	A856	S857	Q858	T859	P872	A873	T874	P875	V876
Y228	E231	K234	P244	F253	T254	P255	V261	L271	V280	D284	F288	T289	Q290	E294	Y297	S298	A299	L306	Q307	W308	N311	E319	A338	V341	R360	L361	R362	L363	Y364	D365	V370	A372	I375	Y385	L389	T393											
T398	D401	A404	F405	S406	A407	K410	T415	V418	W419	W420	T421	I422	D423	R432	T433	A434	L435	T436	M437	N439	A444	P445	N446	Q454	T464	L465	R466	L467	Y468	D469	R470	D471	G472	G478	L481	A486	L497	F504	S505	P506	F516	R517	I518				
Q519	E530	K533	C534	A535	P536	P545	W551	A555	N556	G560	I565	I570	P571	I574	R579	L588	L592	F595	I596	P600	Q612	V613	L614	A615	P618	T619	Y620	S623	V631	Y641	N642	I643	R645	P650	P654	S655											
L656	P657	L658	L659	W663	D664	G665	P671	T672	T673	D674	A675	G676	W677	L680	A681	M685	G686	T689	M691	A692	S695	C700	T701	F702	T703	P704	P600	Y706	T713	L716	Q717	L718	I719	Q720	F723	T730	P736	V737	Y738	THR	ALA	ALA	PHE	ALA	THR		
VAL	THR	ALA	A749	I753	N758	P759	V760	T761	P762	T763	D764	A765	A769	I773	W774	I775	L788	T789	C790	D794	S800	T814	T828	P829	Y832	V836	V837	V838	V839	D840	G841	T844	T845	S846	H847	V854	L855	A856	S857	Q858	T859	P872	A873	T874	P875	V876	
K877	T880	P881	T882	T883	T884	T885	P886	T889	V894	P902	I903	N909	G910	A914	ALA	SER	ALA	ALA	ALA	TRP	TYR	T814	T828	P829	Y832	V836	V837	V838	V839	D840	G841	T844	T845	S846	H847	V854	L855	A856	S857	Q858	T859	P872	A873	T874	P875	V876	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70074	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.733	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.023	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.0728	Depositor
Map size ($\text{\AA}$)	229.8, 229.8, 919.2	wwPDB
Map dimensions	200, 200, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.149, 1.149, 1.149	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.31	6/14067 (0.0%)	0.59	15/19393 (0.1%)
1	B	0.44	10/14067 (0.1%)	0.68	28/19393 (0.1%)
1	C	0.34	6/14067 (0.0%)	0.55	13/19393 (0.1%)
1	D	0.34	6/14067 (0.0%)	0.60	18/19393 (0.1%)
All	All	0.36	28/56268 (0.0%)	0.61	74/77572 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	10
1	C	0	1
1	D	0	2
All	All	0	17

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	396	PRO	CG-CD	-28.56	0.53	1.50
1	C	396	PRO	CG-CD	-26.53	0.60	1.50
1	D	1769	PRO	CG-CD	-20.89	0.79	1.50
1	B	1769	PRO	CG-CD	-20.21	0.82	1.50
1	A	396	PRO	CB-CG	19.48	2.47	1.49

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	396	PRO	CB-CG-CD	-33.14	0.04	106.10
1	D	1769	PRO	N-CD-CG	-26.92	62.81	103.20
1	B	1769	PRO	CB-CG-CD	-21.61	36.95	106.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1769	PRO	CA-CB-CG	-20.80	64.99	104.50
1	B	1769	PRO	N-CD-CG	-19.02	74.66	103.20

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1527	LYS	Peptide
1	A	395	ASP	Peptide
1	A	397	VAL	Peptide
1	A	398	THR	Peptide
1	B	392	THR	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	13687	0	13241	374	0
1	B	13687	0	13241	344	0
1	C	13687	0	13241	353	0
1	D	13687	0	13241	323	0
All	All	54748	0	52964	1354	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 1354 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:532:ILE:HD11	1:A:594:CYS:HB3	1.47	0.97
1:A:1515:THR:HG21	1:C:1192:ASN:HD22	1.40	0.85
1:C:659:LEU:HB2	1:C:719:ILE:O	1.76	0.85
1:C:401:ASP:OD1	1:C:402:THR:N	2.10	0.85
1:A:358:ASN:HB3	1:A:375:ILE:HD11	1.58	0.84

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1884/1987 (95%)	1738 (92%)	132 (7%)	14 (1%)	18	53
1	B	1884/1987 (95%)	1725 (92%)	133 (7%)	26 (1%)	9	38
1	C	1884/1987 (95%)	1727 (92%)	139 (7%)	18 (1%)	12	45
1	D	1884/1987 (95%)	1726 (92%)	137 (7%)	21 (1%)	11	43
All	All	7536/7948 (95%)	6916 (92%)	541 (7%)	79 (1%)	15	45

5 of 79 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	398	THR
1	A	1062	PRO
1	A	1143	VAL
1	B	169	ASN
1	B	393	THR

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1488/1571 (95%)	1482 (100%)	6 (0%)	84	83
1	B	1488/1571 (95%)	1477 (99%)	11 (1%)	76	78
1	C	1488/1571 (95%)	1485 (100%)	3 (0%)	87	87
1	D	1488/1571 (95%)	1479 (99%)	9 (1%)	78	80
All	All	5952/6284 (95%)	5923 (100%)	29 (0%)	78	82

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

Mol	Chain	Res	Type
1	B	1748	THR
1	D	1769	PRO
1	C	162	GLN
1	D	1497	MET
1	B	1804	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1372	GLN
1	D	1506	ASN
1	C	1480	GLN
1	D	847	HIS
1	D	1757	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

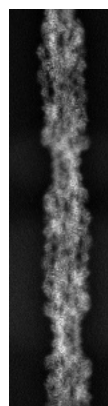
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41679. These allow visual inspection of the internal detail of the map and identification of artifacts.

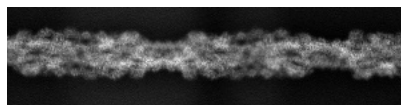
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

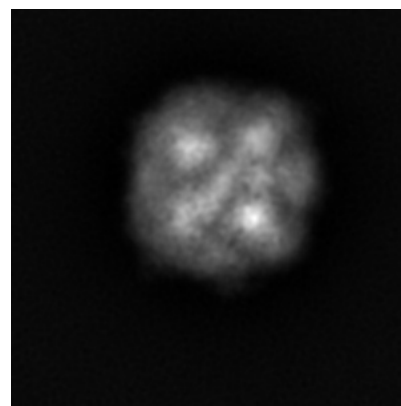
6.1.1 Primary map



X



Y

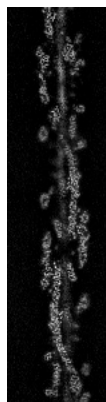


Z

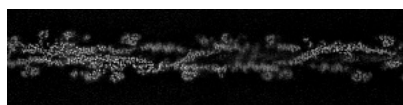
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

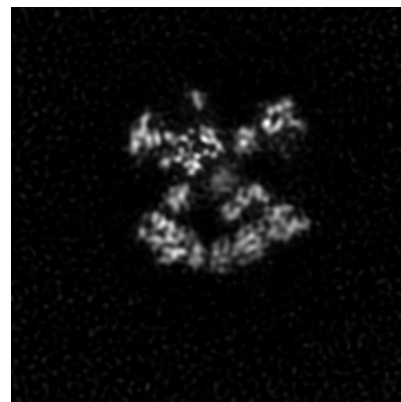
6.2.1 Primary map



X Index:
100



Y Index: 100

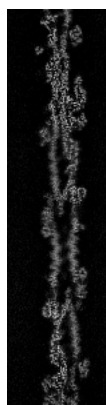


Z Index: 400

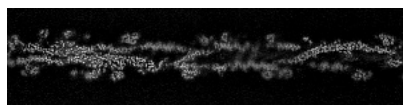
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

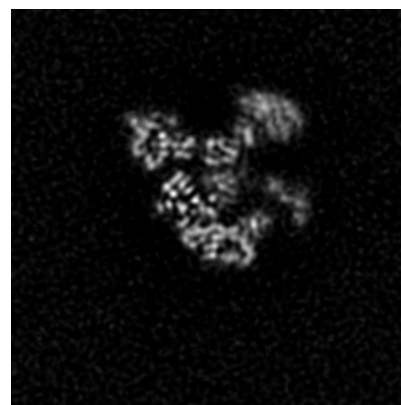
6.3.1 Primary map



X Index:
122



Y Index: 99

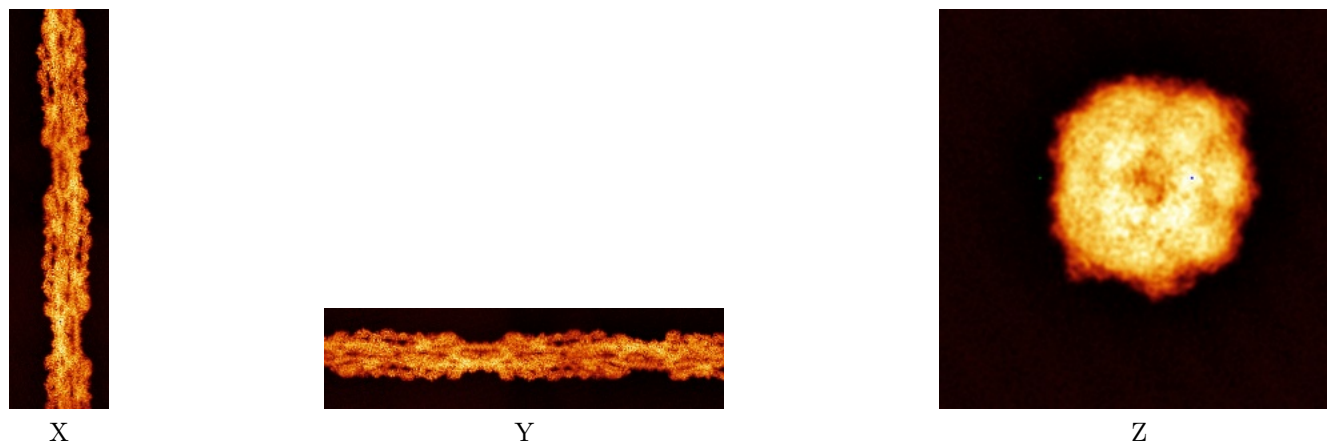


Z Index: 264

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

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

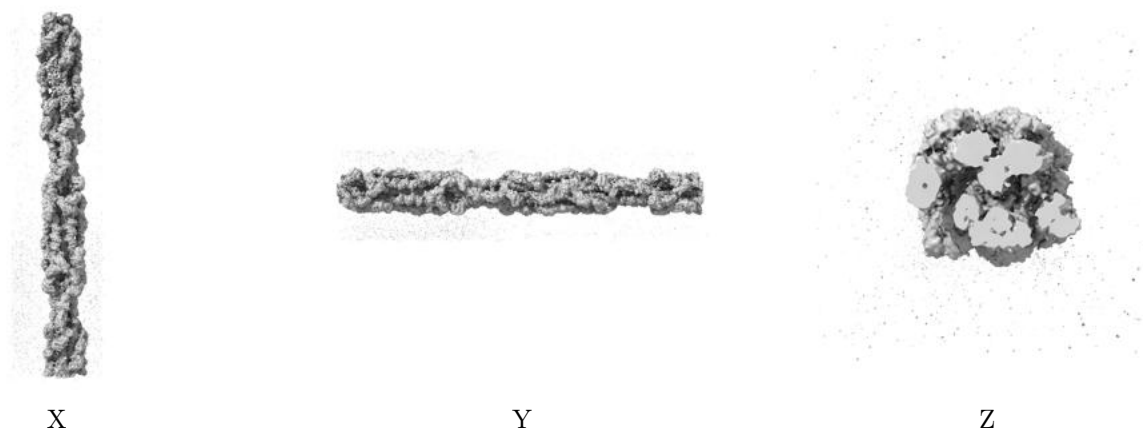
6.4.1 Primary map



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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0728. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

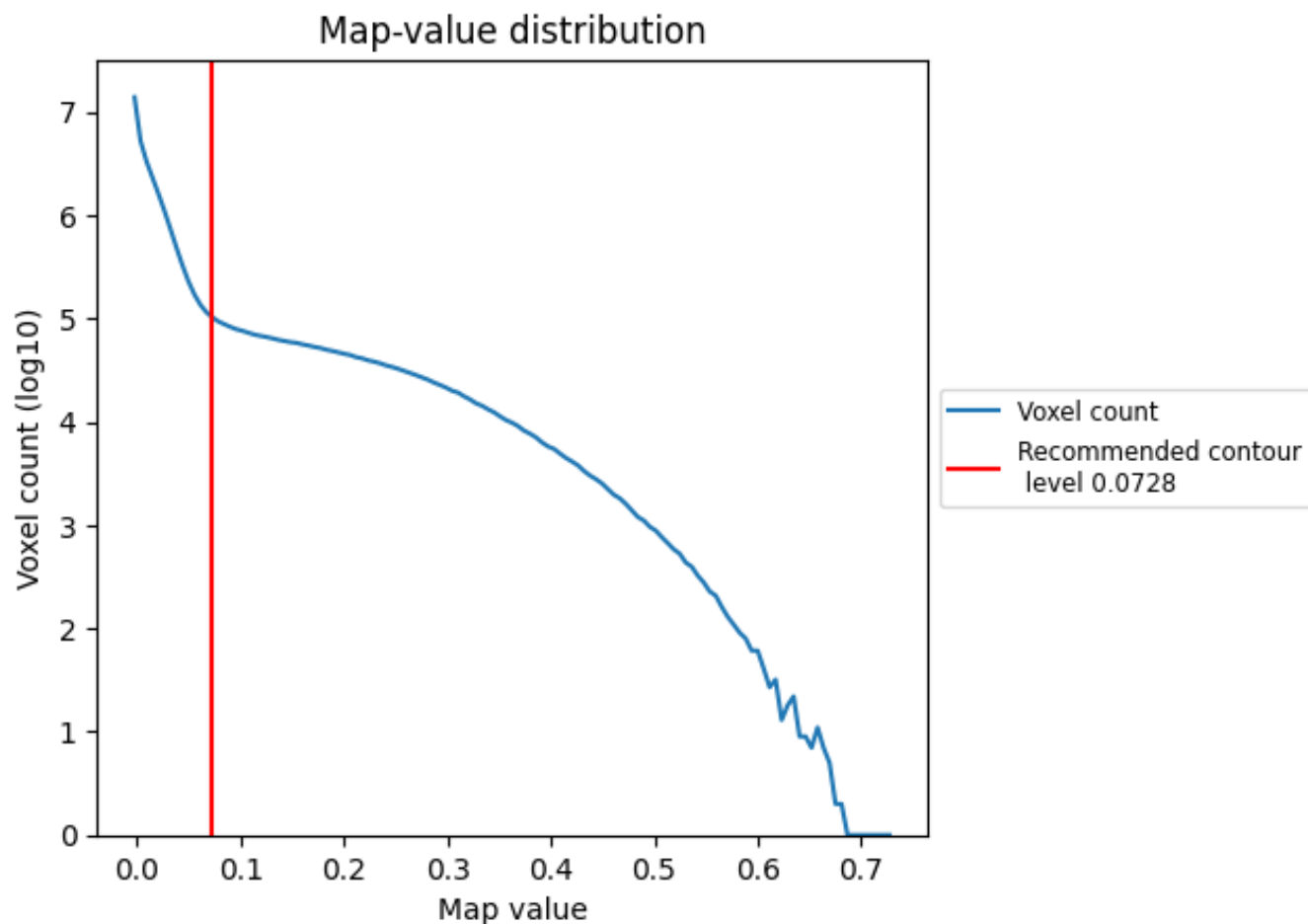
6.6 Mask visualisation

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

7 Map analysis [i](#)

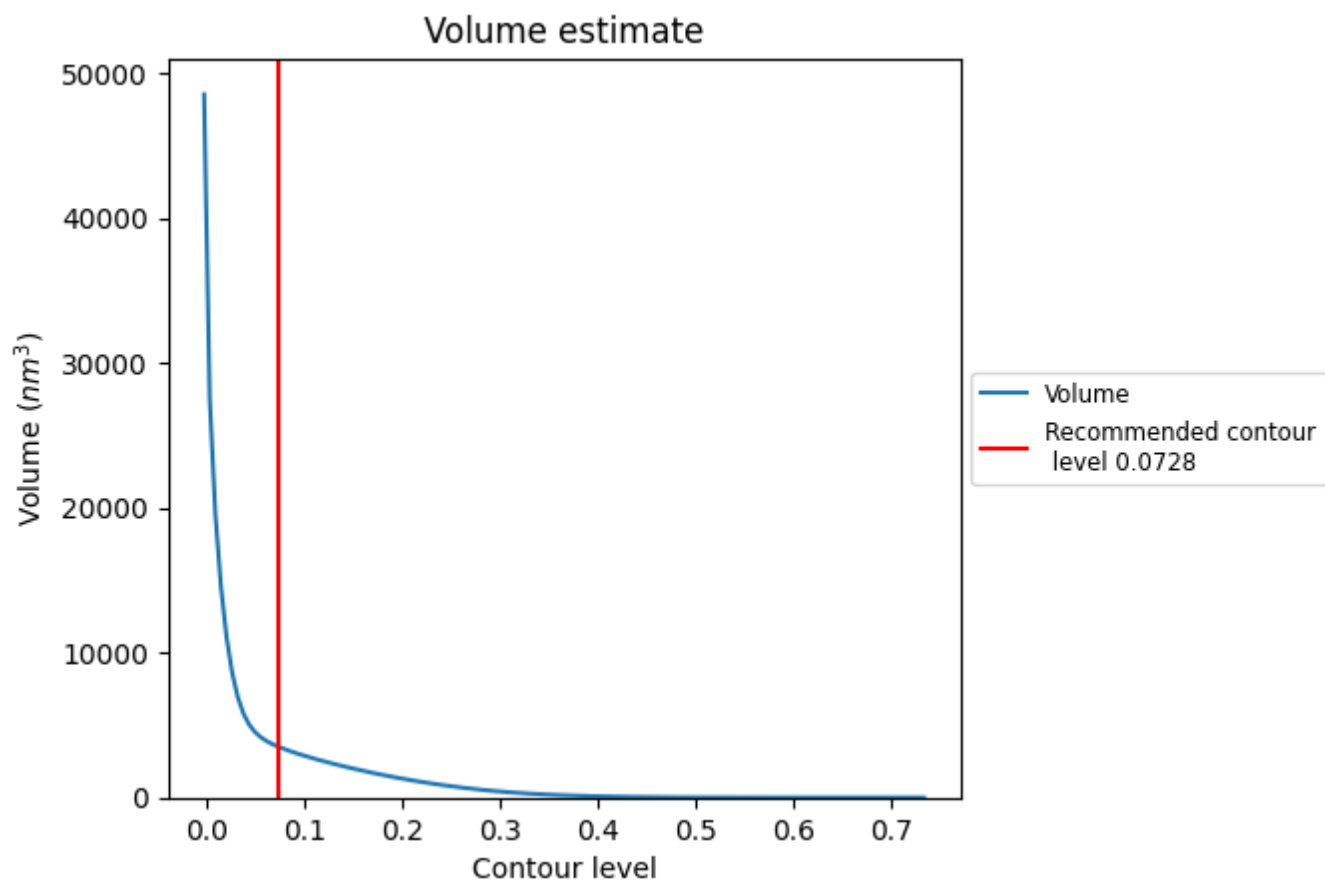
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3533 nm³; this corresponds to an approximate mass of 3192 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

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

8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

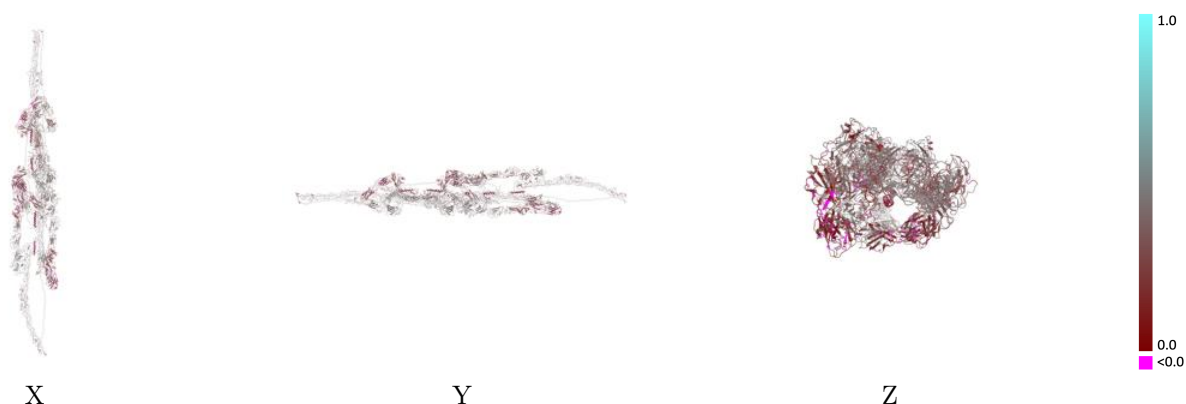
This section contains information regarding the fit between EMDB map EMD-41679 and PDB model 8TXB. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0728 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



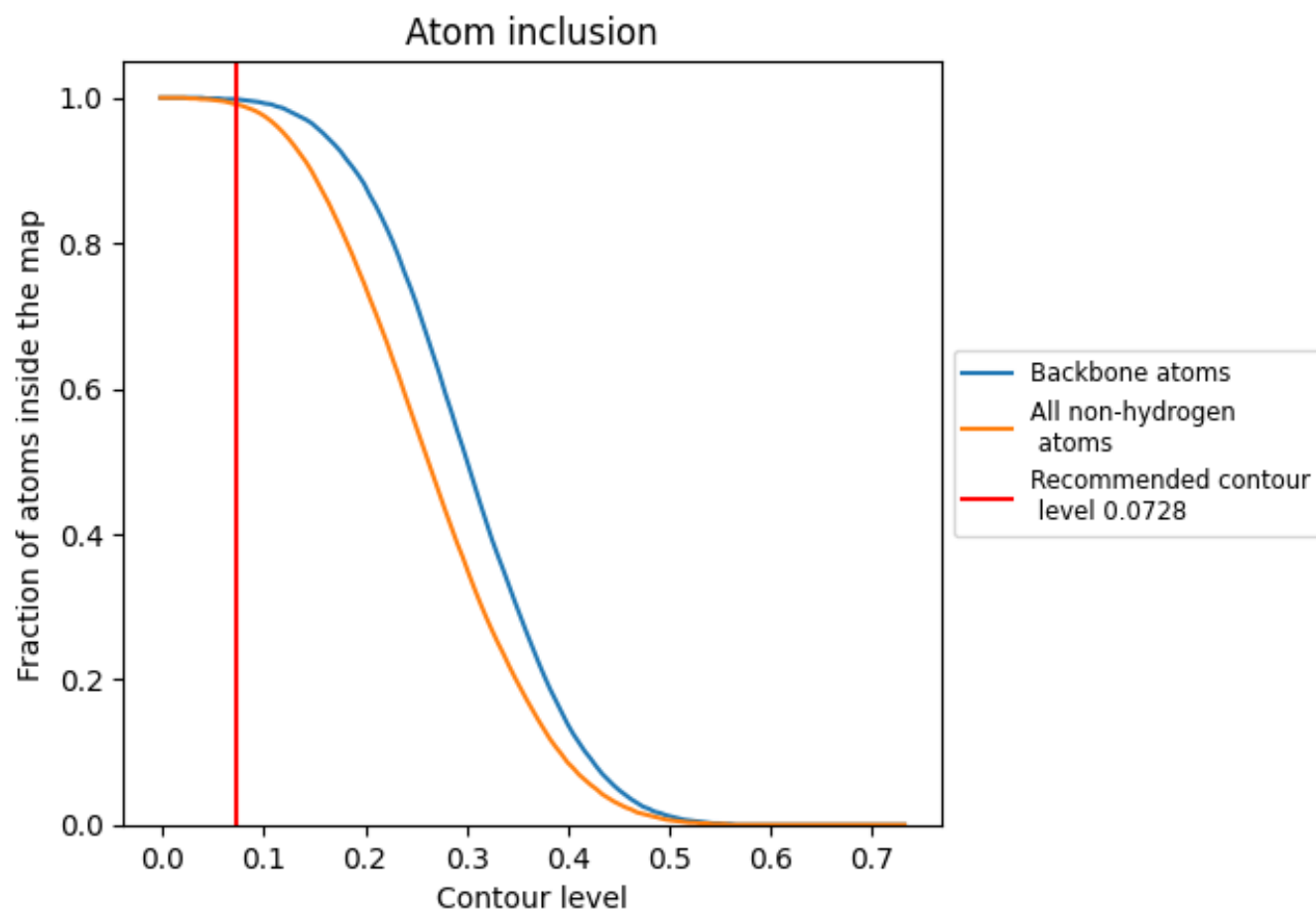
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0728).

9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0728) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9910	0.3500
A	0.9910	0.3490
B	0.9930	0.3620
C	0.9930	0.3500
D	0.9880	0.3360

