



wwPDB EM Validation Summary Report ⓘ

Jul 27, 2026 – 06:03 PM EDT

PDB ID : 10SJ / pdb_000010sj
EMDB ID : EMD-75436
Title : 20S Alpha 3 Deletion proteasome core particle in complex with Blm10
Authors : Walsh Jr, R.M.; Rawson, S.; Fermin Perez, E.; Venclovaite, U.; Hanna, J.
Deposited on : 2026-02-05
Resolution : 3.70 Å (reported)
Based on initial model : 10QT

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.dev133
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) : 2.50

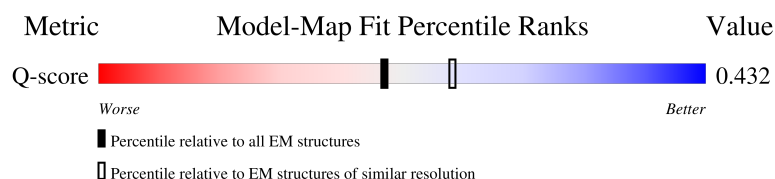
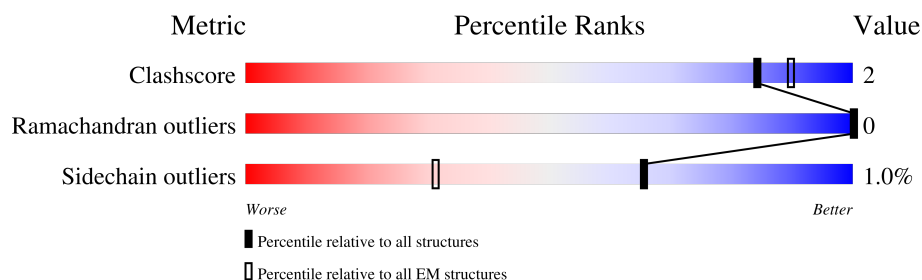
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



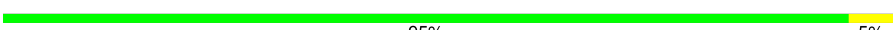
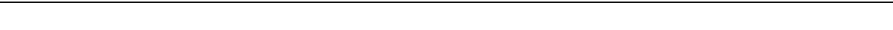
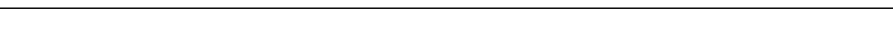
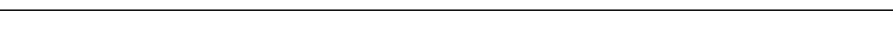
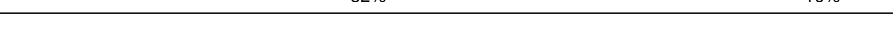
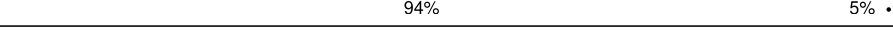
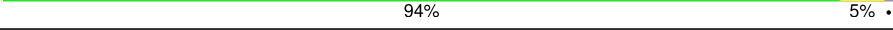
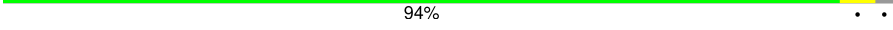
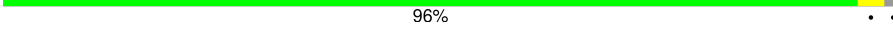
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	1	241	 84% 7% 8%
1	M	241	 83% 8% 8%
2	2	266	 79% 9% 12%
2	N	266	 79% 8% 12%

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Mol	Chain	Length	Quality of chain
3	A	252	 88% 6% 6%
3	O	252	 92% 6%
4	B	250	 94% 6%
4	P	250	 95% 5%
5	C	254	 90% 7%
5	D	254	 81% 11% 8%
5	Q	254	 86% 6% 7%
5	R	254	 86% 6% 8%
6	E	260	 88% 5% 7%
6	S	260	 87% 5% 7%
7	F	234	 92% 8%
7	T	234	 94% 6%
8	G	288	 82% 16%
8	U	288	 82% 16%
9	H	215	 87% 9%
9	V	215	 87% 9%
10	I	261	 78% 6% 16%
10	W	261	 80% 16%
11	J	205	 94% 5%
11	X	205	 94% 5%
12	K	198	 94% ..
12	Y	198	 96% ..
13	L	287	 70% 26%
13	Z	287	 70% 26%
14	CA	2167	 79% 6% 15%

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Mol	Chain	Length	Quality of chain
14	DA	2167	 A horizontal bar chart showing the quality of chain 14 (DA, length 2167). The bar is divided into three segments: a green segment representing 78%, a yellow segment representing 7%, and a grey segment representing 15%. The percentages are labeled below the bar.

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 158332 atoms, of which 79134 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 Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	221	Total	C	H	N	O	S	0	0
			3449	1110	1701	301	333	4		
1	M	221	Total	C	H	N	O	S	0	0
			3449	1110	1701	301	333	4		

- Molecule 2 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	233	Total	C	H	N	O	S	0	0
			3654	1154	1830	312	351	7		
2	N	233	Total	C	H	N	O	S	0	0
			3654	1154	1830	312	351	7		

- Molecule 3 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	A	238	Total	C	H	N	O	S	0	0
			3764	1198	1882	316	360	8		
3	O	238	Total	C	H	N	O	S	0	0
			3764	1198	1882	316	360	8		

- Molecule 4 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	249	Total	C	H	N	O	S	0	0
			3826	1214	1919	314	376	3		
4	P	249	Total	C	H	N	O	S	0	0
			3826	1214	1919	314	376	3		

- Molecule 5 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C	235	Total	C	H	N	O	S	0	0
			3698	1151	1856	322	365	4		
5	D	234	Total	C	H	N	O	S	0	0
			3687	1148	1851	321	363	4		
5	Q	235	Total	C	H	N	O	S	0	0
			3698	1151	1856	322	365	4		
5	R	234	Total	C	H	N	O	S	0	0
			3687	1148	1851	321	363	4		

- Molecule 6 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	E	241	Total	C	H	N	O	S	0	0
			3694	1163	1835	313	376	7		
6	S	241	Total	C	H	N	O	S	0	0
			3694	1163	1835	313	376	7		

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	F	234	Total	C	H	N	O	S	0	0
			3614	1134	1811	313	351	5		
7	T	234	Total	C	H	N	O	S	0	0
			3613	1134	1810	313	351	5		

- Molecule 8 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	G	242	Total	C	H	N	O	S	0	0
			3763	1199	1878	328	354	4		
8	U	242	Total	C	H	N	O	S	0	0
			3762	1199	1877	328	354	4		

- Molecule 9 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	H	195	Total	C	H	N	O	S	0	0
			2971	949	1468	249	298	7		
9	V	195	Total	C	H	N	O	S	0	0
			2971	949	1468	249	298	7		

- Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	I	220	Total	C	H	N	O	S	0	0
			3348	1054	1678	291	319	6		
10	W	220	Total	C	H	N	O	S	0	0
			3348	1054	1678	291	319	6		

- Molecule 11 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	J	203	Total	C	H	N	O	S	0	0
			3142	1007	1567	257	303	8		
11	X	203	Total	C	H	N	O	S	0	0
			3142	1007	1567	257	303	8		

- Molecule 12 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	K	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		
12	Y	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		

- Molecule 13 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	L	211	Total	C	H	N	O	S	0	0
			3229	1043	1590	279	310	7		
13	Z	211	Total	C	H	N	O	S	0	0
			3229	1043	1590	279	310	7		

- Molecule 14 is a protein called Proteasome activator BLM10.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	CA	1849	Total	C	H	N	O	S	0	0
			30198	9727	15133	2501	2768	69		
14	DA	1849	Total	C	H	N	O	S	0	0
			30198	9727	15133	2501	2768	69		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	-23	MET	-	initiating methionine	UNP P43583
CA	-22	HIS	-	expression tag	UNP P43583
CA	-21	HIS	-	expression tag	UNP P43583

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Chain	Residue	Modelled	Actual	Comment	Reference
CA	-20	HIS	-	expression tag	UNP P43583
CA	-19	HIS	-	expression tag	UNP P43583
CA	-18	HIS	-	expression tag	UNP P43583
CA	-17	HIS	-	expression tag	UNP P43583
CA	-16	HIS	-	expression tag	UNP P43583
CA	-15	HIS	-	expression tag	UNP P43583
CA	-14	HIS	-	expression tag	UNP P43583
CA	-13	HIS	-	expression tag	UNP P43583
CA	-12	HIS	-	expression tag	UNP P43583
CA	-11	HIS	-	expression tag	UNP P43583
CA	-10	THR	-	expression tag	UNP P43583
CA	-9	ALA	-	expression tag	UNP P43583
CA	-8	ASN	-	expression tag	UNP P43583
CA	-7	ASN	-	expression tag	UNP P43583
CA	-6	ASP	-	expression tag	UNP P43583
CA	-5	ASP	-	expression tag	UNP P43583
CA	-4	ASP	-	expression tag	UNP P43583
CA	-3	ILE	-	expression tag	UNP P43583
CA	-2	LYS	-	expression tag	UNP P43583
CA	-1	SER	-	expression tag	UNP P43583
CA	0	PRO	-	expression tag	UNP P43583
DA	-23	MET	-	initiating methionine	UNP P43583
DA	-22	HIS	-	expression tag	UNP P43583
DA	-21	HIS	-	expression tag	UNP P43583
DA	-20	HIS	-	expression tag	UNP P43583
DA	-19	HIS	-	expression tag	UNP P43583
DA	-18	HIS	-	expression tag	UNP P43583
DA	-17	HIS	-	expression tag	UNP P43583
DA	-16	HIS	-	expression tag	UNP P43583
DA	-15	HIS	-	expression tag	UNP P43583
DA	-14	HIS	-	expression tag	UNP P43583
DA	-13	HIS	-	expression tag	UNP P43583
DA	-12	HIS	-	expression tag	UNP P43583
DA	-11	HIS	-	expression tag	UNP P43583
DA	-10	THR	-	expression tag	UNP P43583
DA	-9	ALA	-	expression tag	UNP P43583
DA	-8	ASN	-	expression tag	UNP P43583
DA	-7	ASN	-	expression tag	UNP P43583
DA	-6	ASP	-	expression tag	UNP P43583
DA	-5	ASP	-	expression tag	UNP P43583
DA	-4	ASP	-	expression tag	UNP P43583
DA	-3	ILE	-	expression tag	UNP P43583

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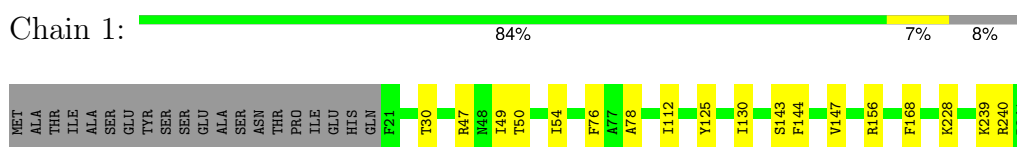
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Chain	Residue	Modelled	Actual	Comment	Reference
DA	-2	LYS	-	expression tag	UNP P43583
DA	-1	SER	-	expression tag	UNP P43583
DA	0	PRO	-	expression tag	UNP P43583

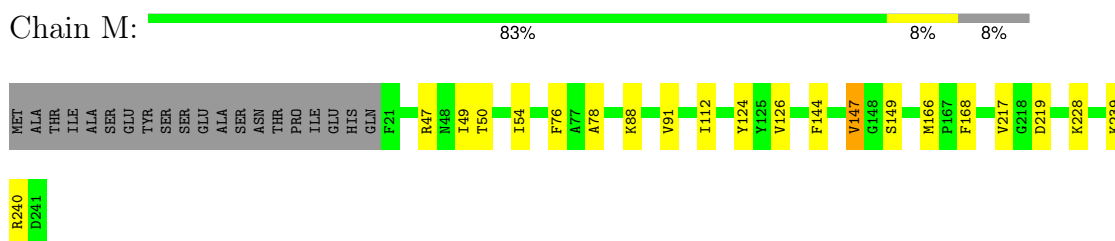
3 Residue-property plots [i](#)

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.

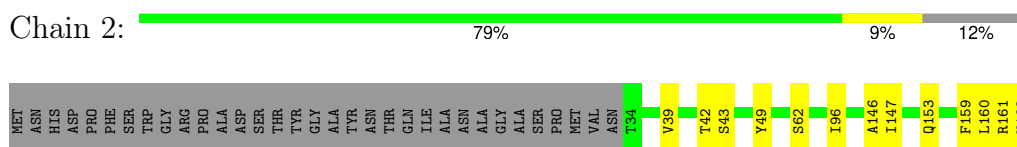
• Molecule 1: Proteasome subunit beta type-6



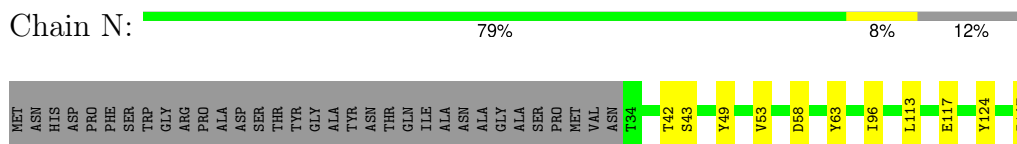
• Molecule 1: Proteasome subunit beta type-6



• Molecule 2: Proteasome subunit beta type-7



• Molecule 2: Proteasome subunit beta type-7



- Molecule 3: Proteasome subunit alpha type-1

Chain A:  88% 6% 6%

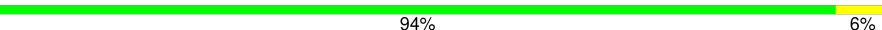


- Molecule 3: Proteasome subunit alpha type-1

Chain O:  92% 6%



- Molecule 4: Proteasome subunit alpha type-2

Chain B:  94% 6%



- Molecule 4: Proteasome subunit alpha type-2

Chain P:  95% 5%



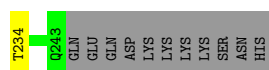
- Molecule 5: Proteasome subunit alpha type-4

Chain C:  90% 7%



- Molecule 5: Proteasome subunit alpha type-4

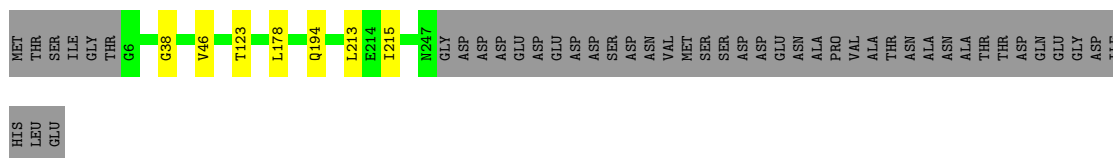
Chain D:  81% 11% 8%



- Molecule 5: Proteasome subunit alpha type-4

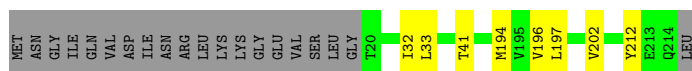
Chain Q:  86% 6% 7%

Chain U:  82% 16%



- Molecule 9: Proteasome subunit beta type-1

Chain H:  87% 9%



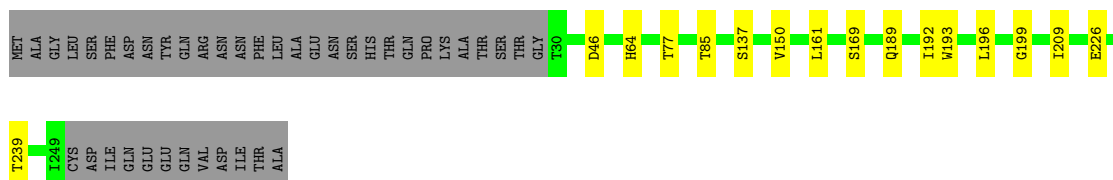
- Molecule 9: Proteasome subunit beta type-1

Chain V:  87% 9%



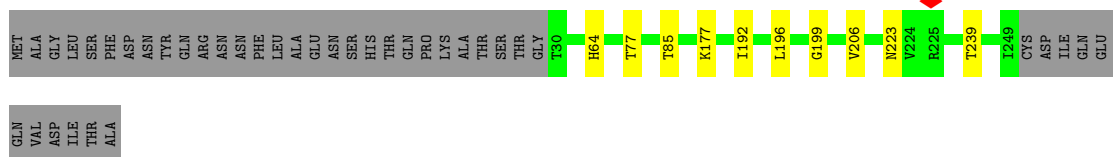
- Molecule 10: Proteasome subunit beta type-2

Chain I:  78% 6% 16%



- Molecule 10: Proteasome subunit beta type-2

Chain W:  80% 16%



- Molecule 11: Proteasome subunit beta type-3

Chain J:  94% 5%



- Molecule 11: Proteasome subunit beta type-3

MET
SER
D3
I11
T88
F124
E132
T141 A142
L146
M149
S168
Q169
A170
D205

- | | | | | | | | | | | | | |
|----|----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|
| M1 | V9 | A50 | L88 | S91 | I119 | T124 | K125 | V126 | F195 | GLN | ALA | GLN |
|----|----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|

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- | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|
| ASP | ASP | ASP | ASP | ASN | ASN | CYS | ASP | LYS | LYS | ILE | ALA | ARG | HIS | T76 | T77 | T78 | V91 | L116 | A125 | W130 | V151 | A152 | L161 | K182 | T195 | I286 | GLY | |
| MET | GLN | ALA | ILE | ALA | ASP | PHE | SER | VAL | VAL | PRO | ASN | ARG | LEU | VAL | GLU | LEU | GLN | TYR | ASN | GLU | LEU | ASP | PHE | VAL | THR | GLY | ALA | SER | GLN | PHE | ARG | ALA | PRO | SER | LEU | THR | VAL | PRO | PRO | ILE | ALA | SER | PRO | GLN | GLN | THR | THR | HIS | THR |

- [illegible]

- [illegible]



V1581	R1752	A1958
A1602	GLU	Q1972
L1606	SER	T1983
F1610	ASP	V1995
V1619	ALA	R2009
L1638	A1757	I2013
C1648	S1762	I2017
GLU	P1779	R2033
L1650	D1780	G2066
N1664	V1781	V2075
K1665	V1789	A2093
ASP	H1792	A2103
ASP	P1793	T2106
K1668	Y1794	K2111
M1671	V1797	D2132
I1672	I1817	L2137
M1673	S1818	Y2141
S1674	D1819	Y2142
V1675	M1829	A2143
L1693	ASP	
ASP	PRO	
LYS	ASP	
R1696	GLY	
F1699	L1834	
F1703	I1856	
L1708	V1863	
H1714	P1868	
D1715	F1871	
A1716	I1872	
F1717	K1873	
E1718	T1874	
I1719	D1875	
W1720	Y1876	
L1723	F1877	
A1724	Y1878	
W1725	I1883	
W1726	M1890	
L1727	L1911	
F1740	K1918	
W1745	D1919	
ALA	L1935	
ASP	V1957	
GLY		
M1749		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46626	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 ($e^-/\text{\AA}^2$)	50.253	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.075	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00238	Depositor
Map size (Å)	571.2, 571.2, 571.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1	0.24	0/1786	0.45	0/2408
1	M	0.21	0/1786	0.34	0/2408
2	2	0.22	0/1855	0.35	0/2514
2	N	0.21	0/1855	0.34	0/2514
3	A	0.19	0/1919	0.33	0/2599
3	O	0.19	0/1919	0.31	0/2599
4	B	0.20	0/1944	0.35	0/2632
4	P	0.19	0/1944	0.31	0/2632
5	C	0.15	0/1870	0.43	0/2532
5	D	0.16	0/1864	0.40	0/2524
5	Q	0.16	0/1870	0.43	0/2532
5	R	0.17	0/1864	0.43	0/2524
6	E	0.19	0/1885	0.39	0/2540
6	S	0.19	0/1885	0.39	0/2540
7	F	0.20	0/1831	0.36	0/2473
7	T	0.19	0/1831	0.32	0/2473
8	G	0.20	0/1925	0.37	0/2599
8	U	0.20	0/1925	0.30	0/2599
9	H	0.23	0/1532	0.31	0/2076
9	V	0.22	0/1532	0.30	0/2076
10	I	0.23	0/1701	0.41	0/2307
10	W	0.21	0/1701	0.32	0/2307
11	J	0.23	0/1605	0.37	0/2166
11	X	0.22	0/1605	0.32	0/2166
12	K	0.19	0/1589	0.32	0/2142
12	Y	0.19	0/1589	0.30	0/2142
13	L	0.21	0/1676	0.31	0/2269
13	Z	0.20	0/1676	0.31	0/2269
14	CA	0.16	0/15398	0.34	0/20843
14	DA	0.16	0/15398	0.36	0/20843
All	All	0.19	0/80760	0.36	0/109248

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
5	D	0	2
6	E	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	D	127	ARG	Sidechain
5	D	197	ARG	Sidechain
6	E	72	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	1	1748	1701	1700	10	0
1	M	1748	1701	1700	13	0
2	2	1824	1830	1829	14	0
2	N	1824	1830	1829	12	0
3	A	1882	1882	1881	9	0
3	O	1882	1882	1881	3	0
4	B	1907	1919	1917	11	0
4	P	1907	1919	1917	8	0
5	C	1842	1856	1855	7	0
5	D	1836	1851	1850	16	0
5	Q	1842	1856	1855	9	0
5	R	1836	1851	1850	14	0
6	E	1859	1835	1834	9	0
6	S	1859	1835	1834	8	0
7	F	1803	1811	1809	10	0
7	T	1803	1810	1809	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	G	1885	1878	1876	3	0
8	U	1885	1877	1876	4	0
9	H	1503	1468	1467	7	0
9	V	1503	1468	1467	6	0
10	I	1670	1678	1676	10	0
10	W	1670	1678	1676	6	0
11	J	1575	1567	1566	6	0
11	X	1575	1567	1566	6	0
12	K	1561	1569	1569	6	0
12	Y	1561	1569	1569	2	0
13	L	1639	1590	1589	7	0
13	Z	1639	1590	1589	5	0
14	CA	15065	15133	15118	70	0
14	DA	15065	15133	15118	93	0
All	All	79198	79134	79072	361	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 2.

The worst 5 of 361 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)
14:DA:1957:VAL:HG12	14:DA:1958:ALA:N	1.96	0.78
1:1:49:ILE:HD12	10:I:196:LEU:HD11	1.65	0.77
5:R:110:THR:HG22	5:R:135:ILE:HD12	1.73	0.69
1:1:47:ARG:HD3	1:1:49:ILE:HD11	1.75	0.68
14:DA:1957:VAL:CG1	14:DA:1958:ALA:N	2.58	0.66

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	1	219/241 (91%)	213 (97%)	6 (3%)	0	100	100
1	M	219/241 (91%)	211 (96%)	8 (4%)	0	100	100
2	2	231/266 (87%)	220 (95%)	11 (5%)	0	100	100
2	N	231/266 (87%)	224 (97%)	7 (3%)	0	100	100
3	A	236/252 (94%)	232 (98%)	4 (2%)	0	100	100
3	O	236/252 (94%)	232 (98%)	4 (2%)	0	100	100
4	B	247/250 (99%)	245 (99%)	2 (1%)	0	100	100
4	P	247/250 (99%)	244 (99%)	3 (1%)	0	100	100
5	C	233/254 (92%)	218 (94%)	15 (6%)	0	100	100
5	D	232/254 (91%)	224 (97%)	8 (3%)	0	100	100
5	Q	233/254 (92%)	222 (95%)	11 (5%)	0	100	100
5	R	232/254 (91%)	221 (95%)	11 (5%)	0	100	100
6	E	239/260 (92%)	231 (97%)	8 (3%)	0	100	100
6	S	239/260 (92%)	234 (98%)	5 (2%)	0	100	100
7	F	232/234 (99%)	230 (99%)	2 (1%)	0	100	100
7	T	232/234 (99%)	228 (98%)	4 (2%)	0	100	100
8	G	240/288 (83%)	233 (97%)	7 (3%)	0	100	100
8	U	240/288 (83%)	230 (96%)	10 (4%)	0	100	100
9	H	193/215 (90%)	189 (98%)	4 (2%)	0	100	100
9	V	193/215 (90%)	190 (98%)	3 (2%)	0	100	100
10	I	218/261 (84%)	213 (98%)	5 (2%)	0	100	100
10	W	218/261 (84%)	214 (98%)	4 (2%)	0	100	100
11	J	201/205 (98%)	194 (96%)	7 (4%)	0	100	100
11	X	201/205 (98%)	195 (97%)	6 (3%)	0	100	100
12	K	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
12	Y	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
13	L	209/287 (73%)	207 (99%)	2 (1%)	0	100	100
13	Z	209/287 (73%)	207 (99%)	2 (1%)	0	100	100
14	CA	1823/2167 (84%)	1773 (97%)	50 (3%)	0	100	100
14	DA	1823/2167 (84%)	1772 (97%)	51 (3%)	0	100	100
All	All	9892/11264 (88%)	9624 (97%)	268 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	184/201 (92%)	179 (97%)	5 (3%)	39	59
1	M	184/201 (92%)	180 (98%)	4 (2%)	45	63
2	2	199/224 (89%)	198 (100%)	1 (0%)	81	80
2	N	199/224 (89%)	196 (98%)	3 (2%)	57	68
3	A	204/210 (97%)	202 (99%)	2 (1%)	68	74
3	O	204/210 (97%)	203 (100%)	1 (0%)	81	80
4	B	208/209 (100%)	208 (100%)	0	100	100
4	P	208/209 (100%)	207 (100%)	1 (0%)	81	80
5	C	209/226 (92%)	208 (100%)	1 (0%)	81	80
5	D	208/226 (92%)	207 (100%)	1 (0%)	81	80
5	Q	209/226 (92%)	205 (98%)	4 (2%)	50	65
5	R	208/226 (92%)	208 (100%)	0	100	100
6	E	198/215 (92%)	194 (98%)	4 (2%)	48	64
6	S	198/215 (92%)	194 (98%)	4 (2%)	48	64
7	F	193/193 (100%)	191 (99%)	2 (1%)	68	74
7	T	193/193 (100%)	191 (99%)	2 (1%)	68	74
8	G	200/239 (84%)	199 (100%)	1 (0%)	81	80
8	U	200/239 (84%)	200 (100%)	0	100	100
9	H	161/178 (90%)	161 (100%)	0	100	100
9	V	161/178 (90%)	160 (99%)	1 (1%)	78	79
10	I	179/214 (84%)	175 (98%)	4 (2%)	45	63
10	W	179/214 (84%)	177 (99%)	2 (1%)	65	73
11	J	171/173 (99%)	169 (99%)	2 (1%)	63	72
11	X	171/173 (99%)	169 (99%)	2 (1%)	63	72
12	K	173/175 (99%)	173 (100%)	0	100	100
12	Y	173/175 (99%)	172 (99%)	1 (1%)	78	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	L	169/235 (72%)	168 (99%)	1 (1%)	78	79
13	Z	169/235 (72%)	168 (99%)	1 (1%)	78	79
14	CA	1707/1986 (86%)	1691 (99%)	16 (1%)	70	75
14	DA	1707/1986 (86%)	1688 (99%)	19 (1%)	65	73
All	All	8726/9808 (89%)	8641 (99%)	85 (1%)	65	74

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	CA	1318	ILE
14	DA	606	GLU
14	CA	1673	MET
14	CA	2006	VAL
14	DA	926	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
11	X	38	ASN
14	CA	527	ASN
12	Y	146	HIS
14	CA	103	ASN
14	CA	664	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

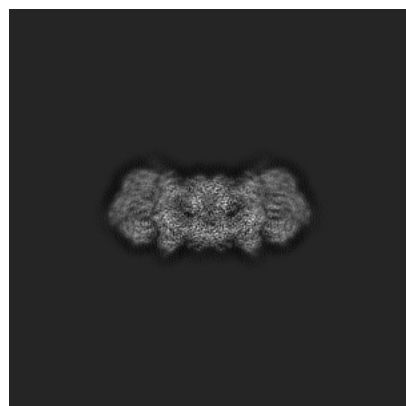
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75436. These allow visual inspection of the internal detail of the map and identification of artifacts.

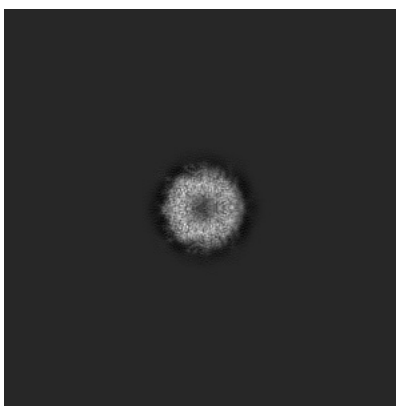
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

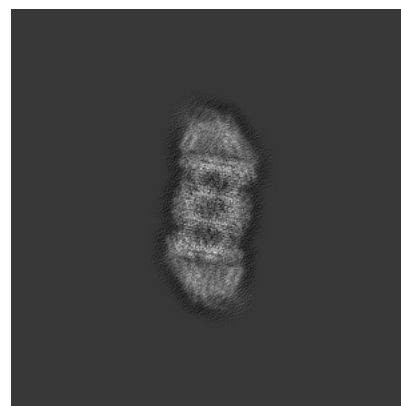
6.1.1 Primary map



X

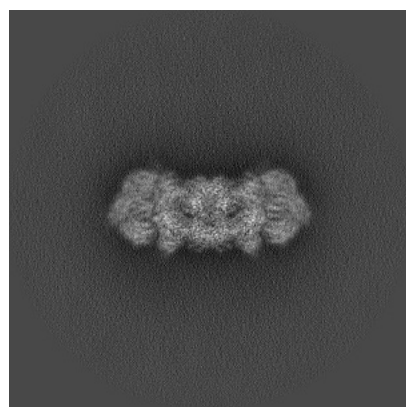


Y

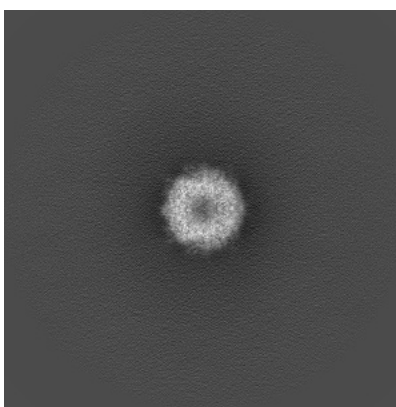


Z

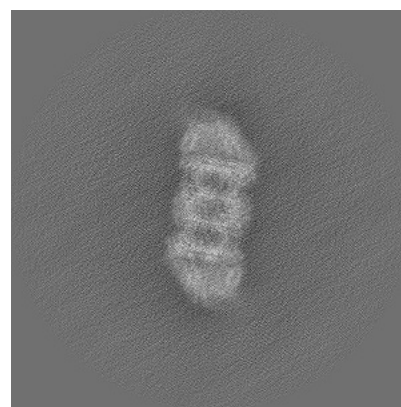
6.1.2 Raw map



X



Y

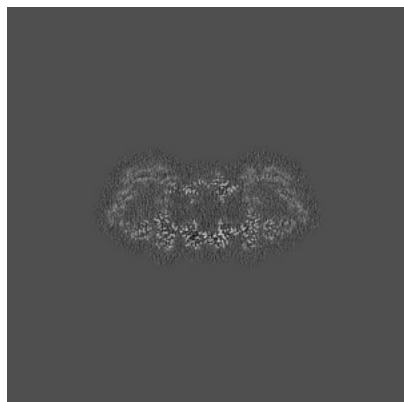


Z

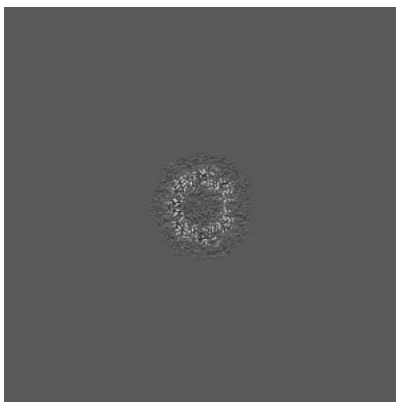
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

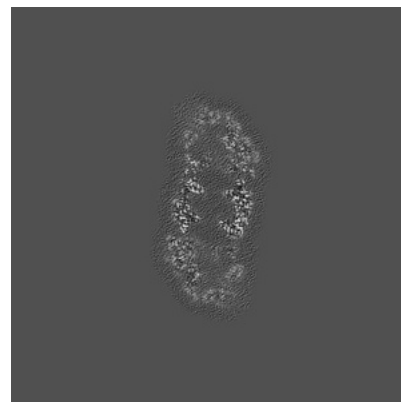
6.2.1 Primary map



X Index: 240

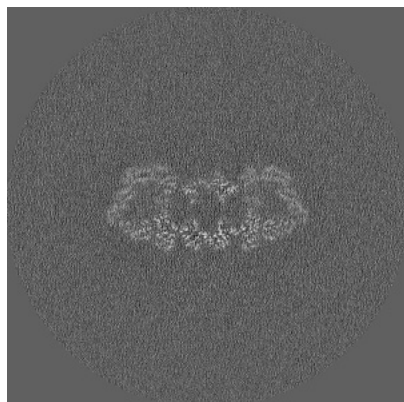


Y Index: 240

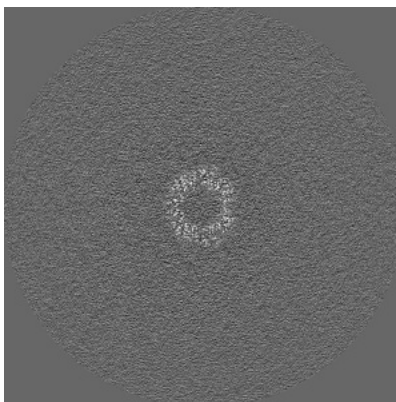


Z Index: 240

6.2.2 Raw map



X Index: 240



Y Index: 240

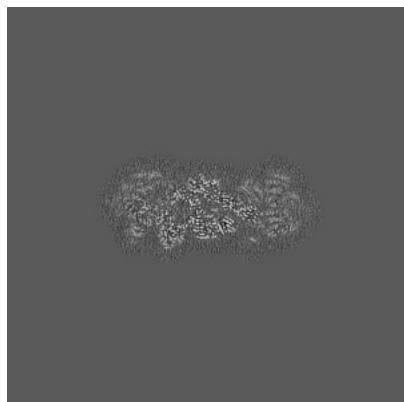


Z Index: 240

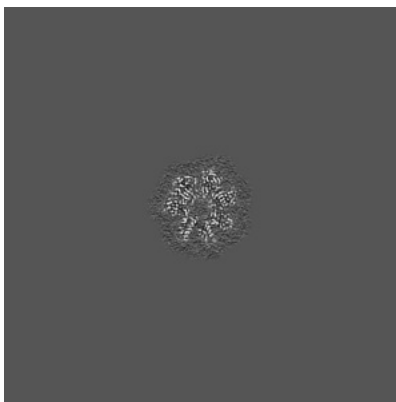
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

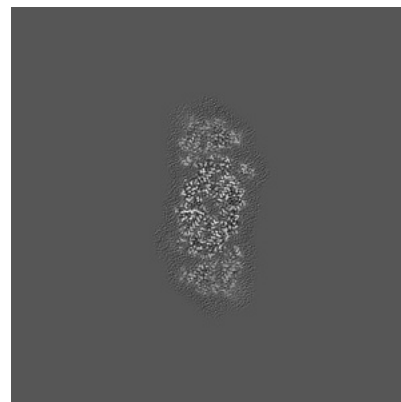
6.3.1 Primary map



X Index: 217

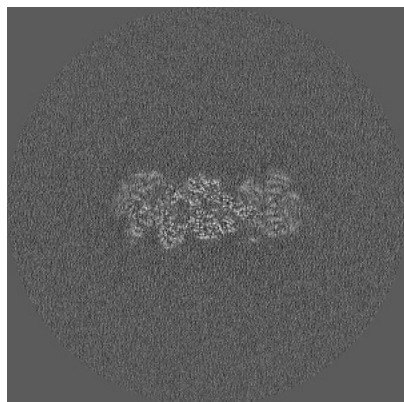


Y Index: 222

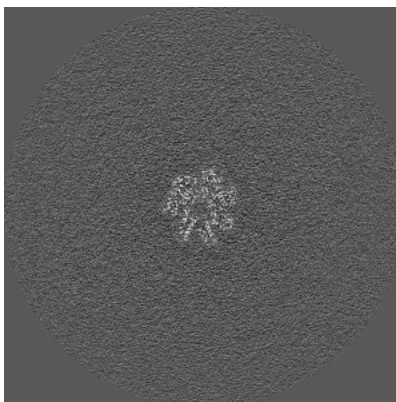


Z Index: 215

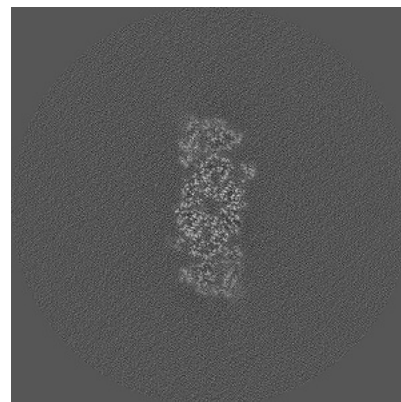
6.3.2 Raw map



X Index: 217



Y Index: 222

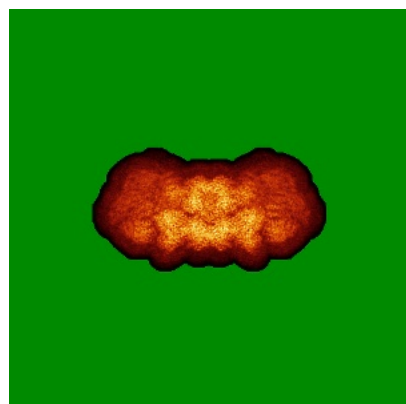


Z Index: 216

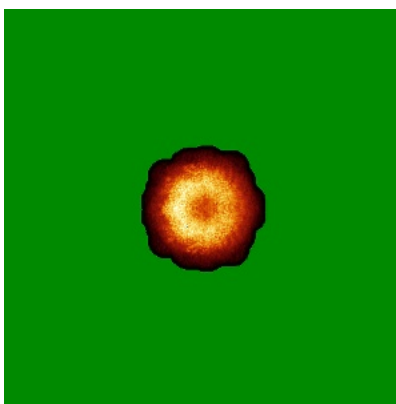
The images above show the largest variance slices of the map in three orthogonal directions.

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

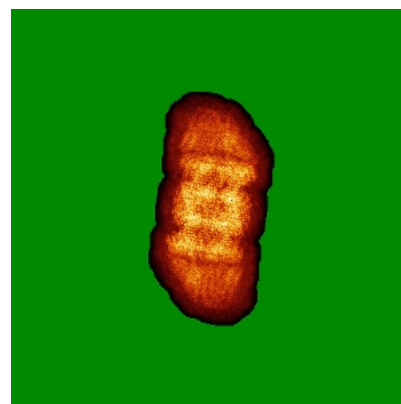
6.4.1 Primary map



X

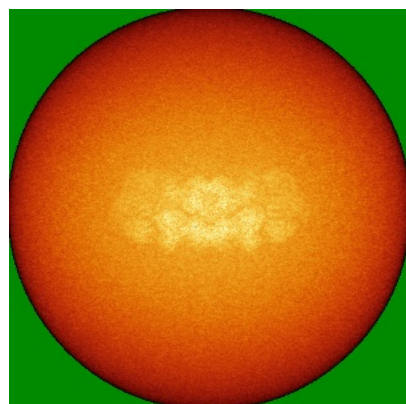


Y

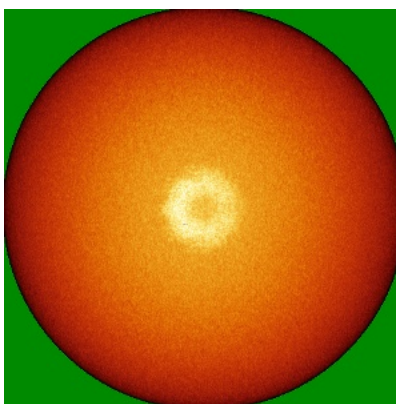


Z

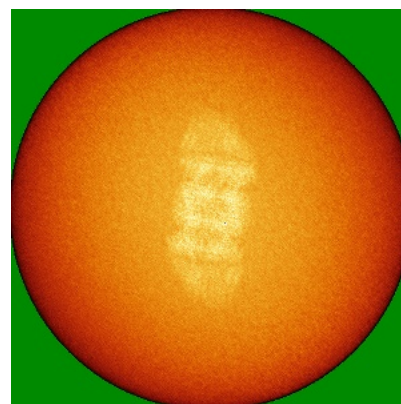
6.4.2 Raw map



X



Y

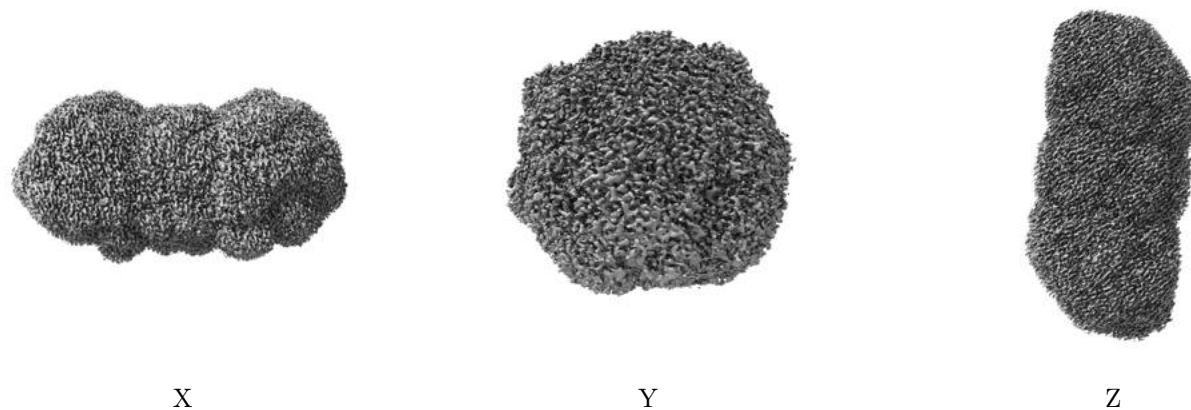


Z

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

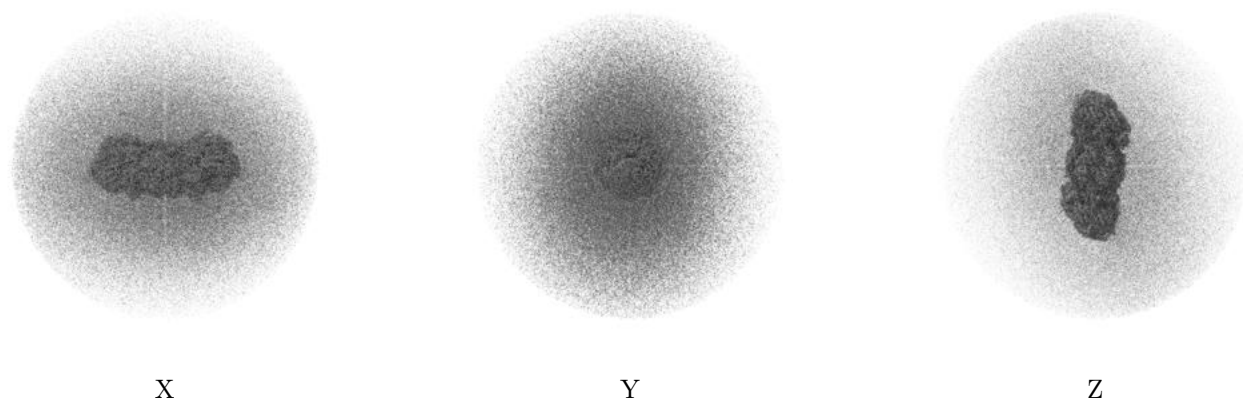
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00238. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

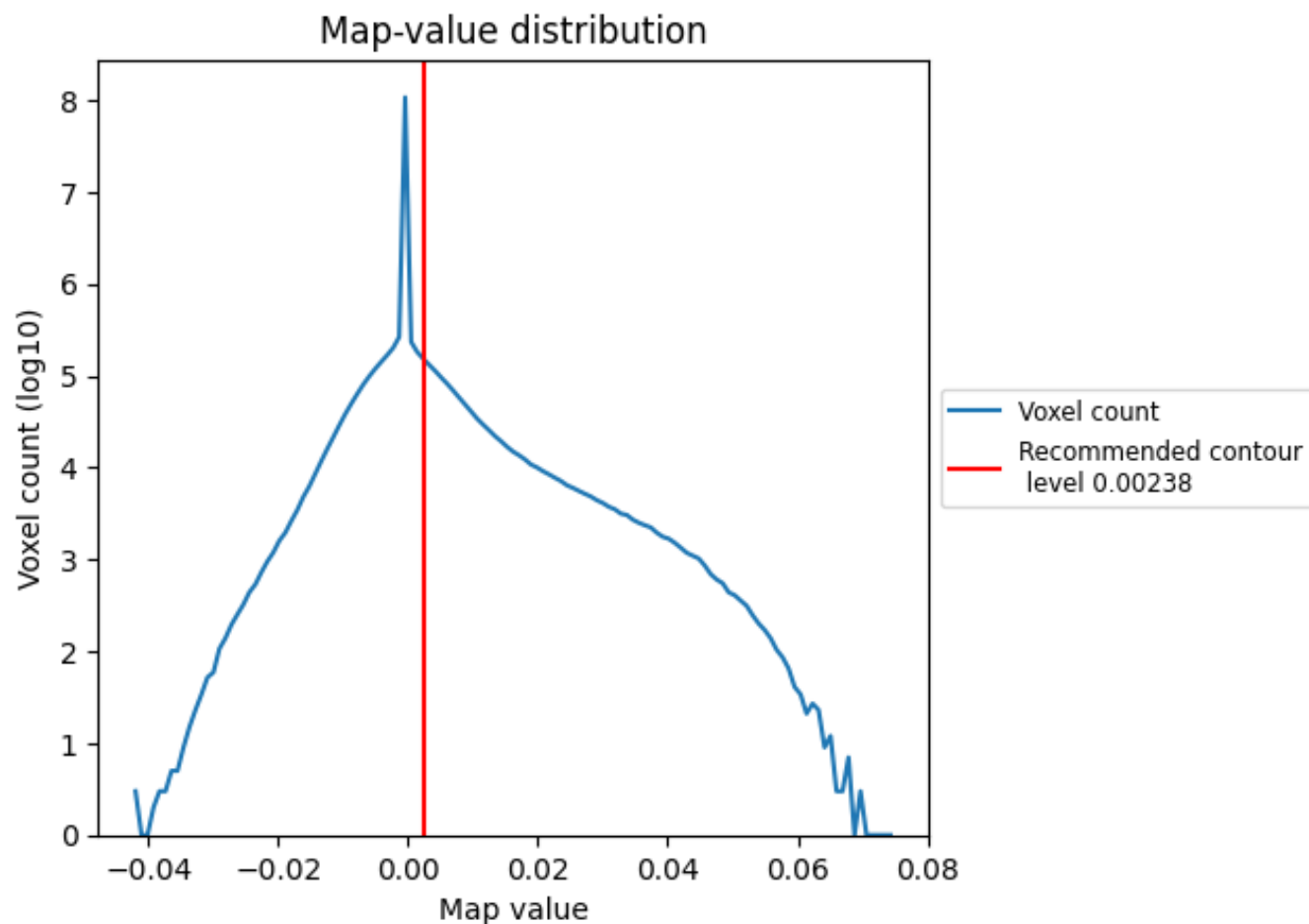
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

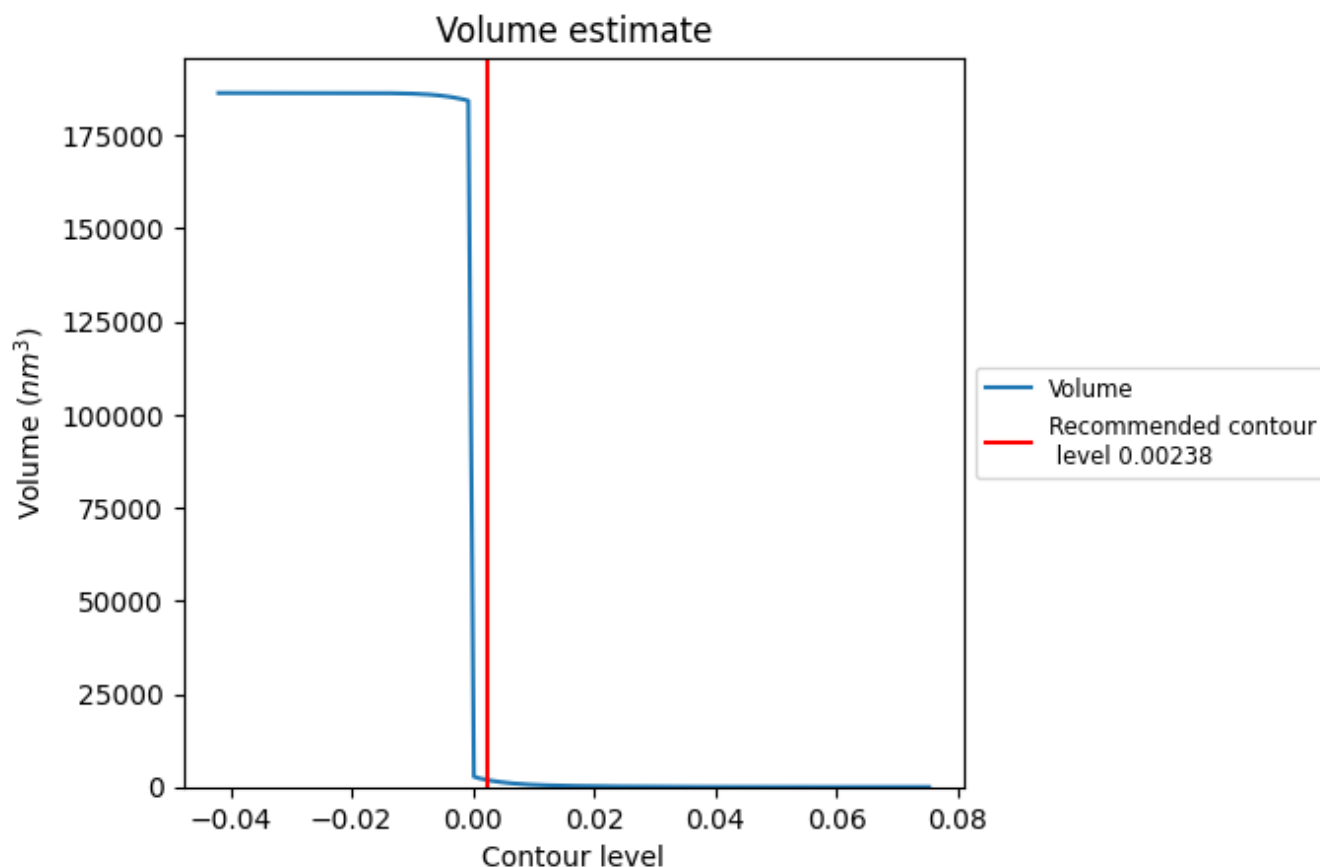
This section contains the results of statistical analysis of the map.

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.

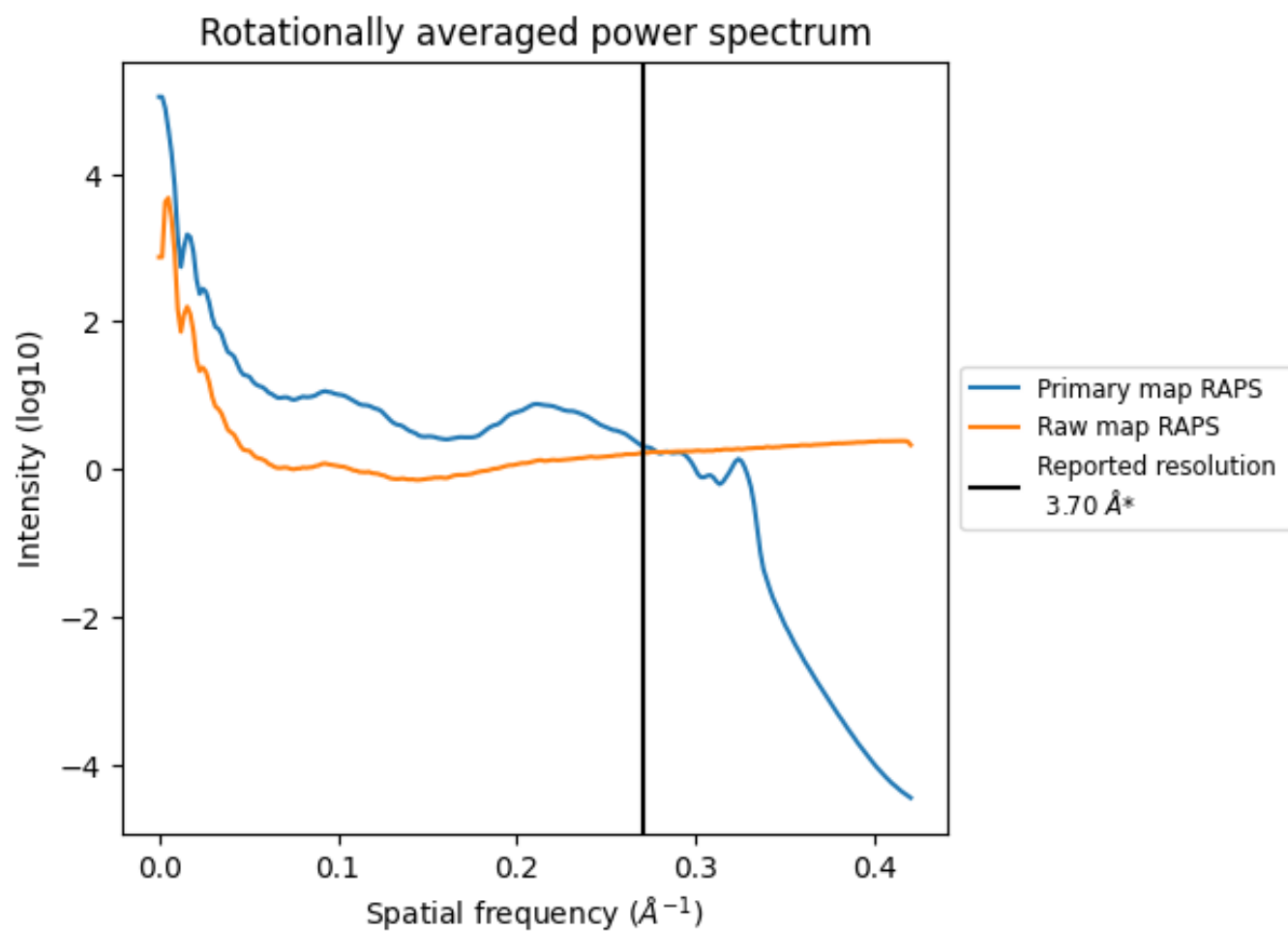
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1866 nm^3 ; this corresponds to an approximate mass of 1686 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](#)

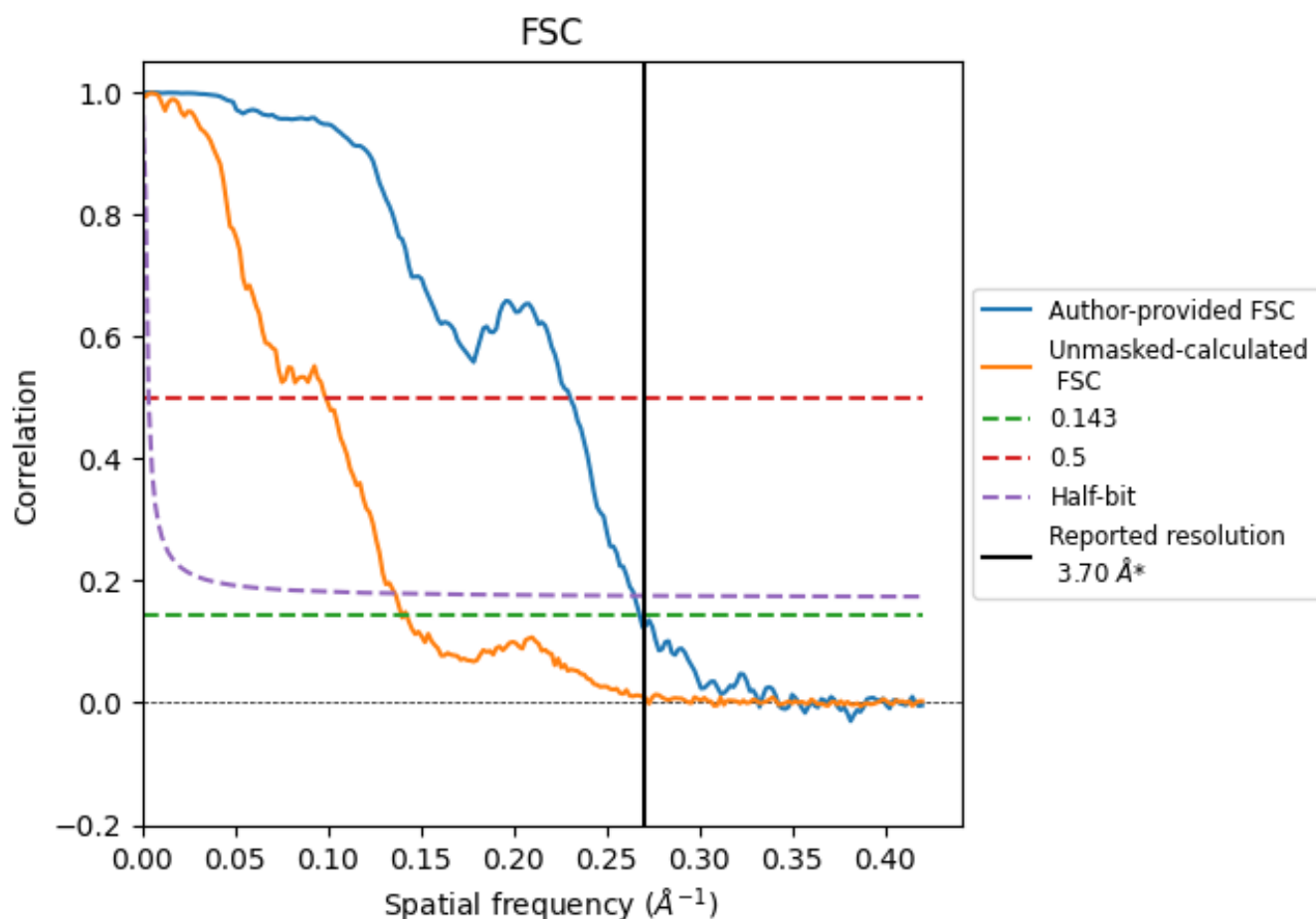


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

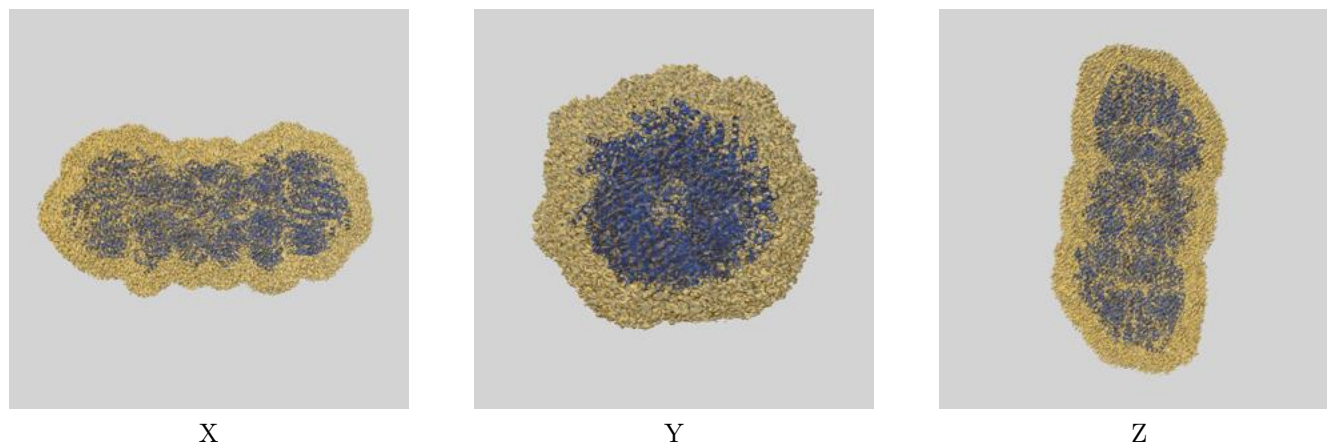
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.73	4.34	3.77
Unmasked-calculated*	7.16	10.11	7.34

*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 7.16 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

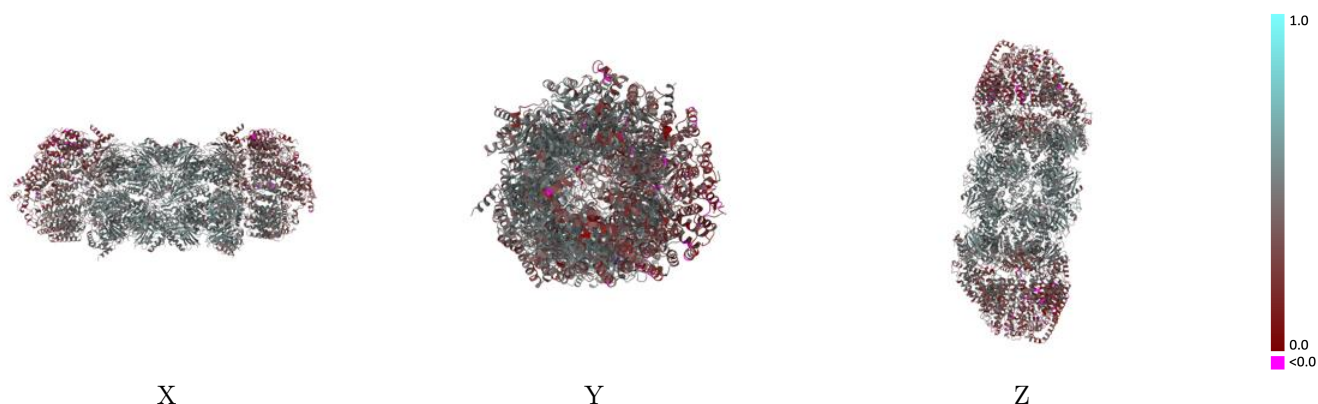
This section contains information regarding the fit between EMDB map EMD-75436 and PDB model 10SJ. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



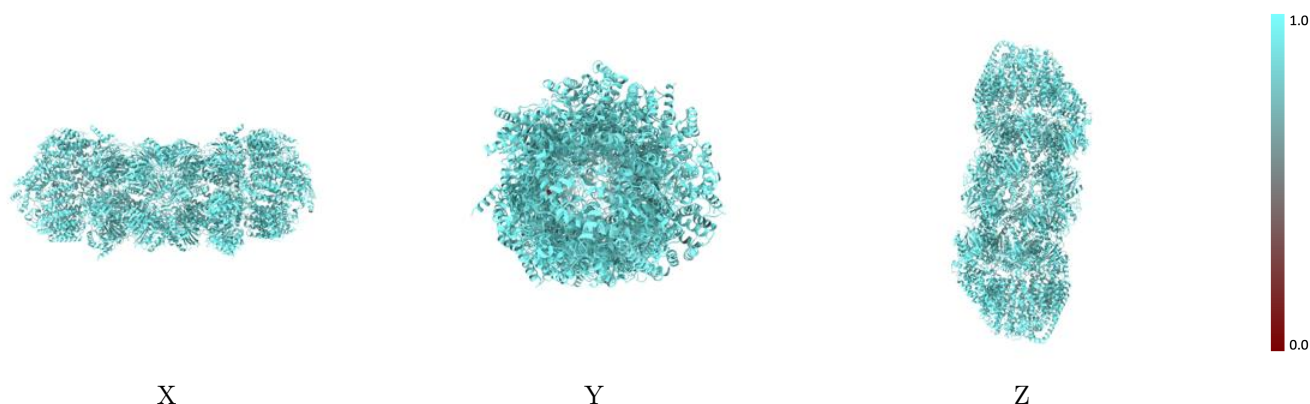
The images above show the 3D surface view of the map at the recommended contour level 0.00238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



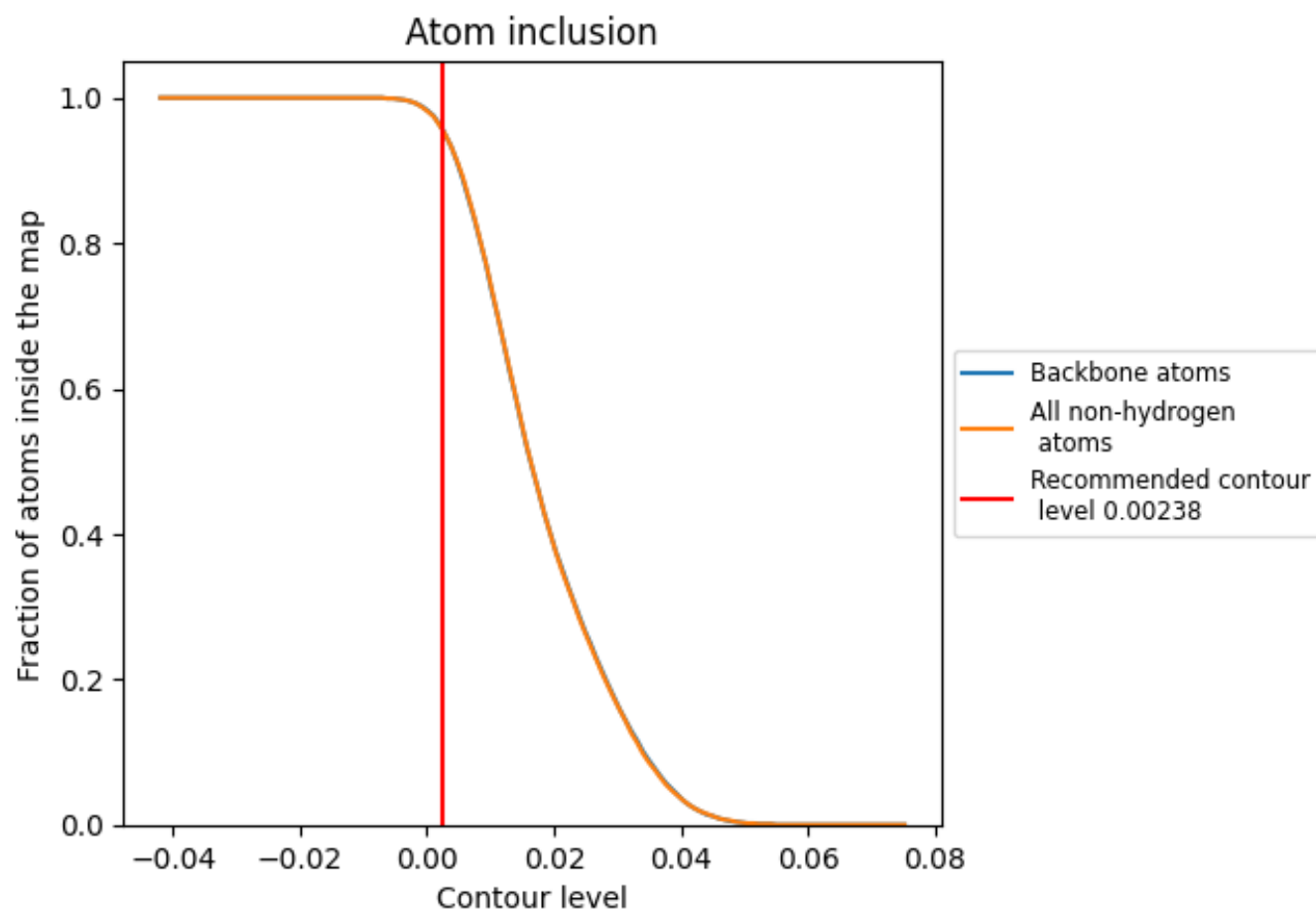
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00238).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.00238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.4320
1	 0.9780	 0.5100
2	 0.9740	 0.5180
A	 0.9710	 0.4940
B	 0.9570	 0.4730
C	 0.9510	 0.3890
CA	 0.9410	 0.3510
D	 0.9520	 0.3750
DA	 0.9380	 0.3460
E	 0.9710	 0.4790
F	 0.9690	 0.4950
G	 0.9760	 0.4920
H	 0.9670	 0.5190
I	 0.9790	 0.5040
J	 0.9760	 0.5130
K	 0.9690	 0.4920
L	 0.9760	 0.5110
M	 0.9730	 0.5080
N	 0.9750	 0.5170
O	 0.9770	 0.4980
P	 0.9630	 0.4780
Q	 0.9540	 0.4000
R	 0.9520	 0.3730
S	 0.9650	 0.4740
T	 0.9690	 0.4960
U	 0.9770	 0.4940
V	 0.9780	 0.5210
W	 0.9780	 0.5190
X	 0.9790	 0.5180
Y	 0.9730	 0.4920
Z	 0.9710	 0.5100

