



wwPDB EM Validation Summary Report ⓘ

May 2, 2026 – 12:43 PM EDT

PDB ID : 9YNF / pdb_00009ynf
EMDB ID : EMD-73176
Title : Motor domain of human dynein-1 in post1 state
Authors : Yang, J.; Rao, Q.; Chai, P.; Zhang, K.
Deposited on : 2025-10-10
Resolution : 3.92 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

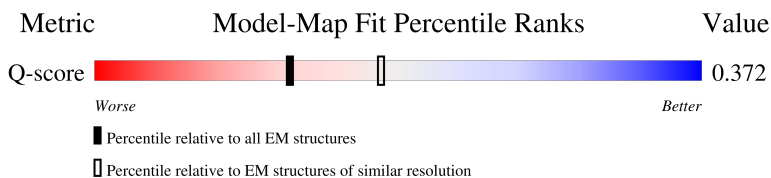
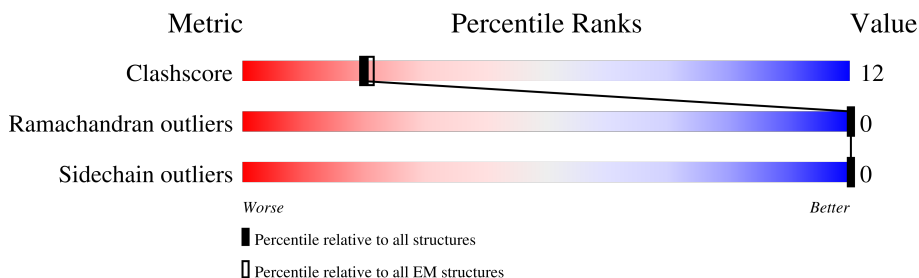
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

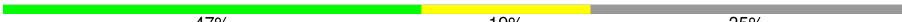
The reported resolution of this entry is 3.92 Å.

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	7862 (3.42 - 4.42)

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	4646	 47% 19% 35%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 24588 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 Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	3038	24471	15586	4225	4538	122	0	0

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



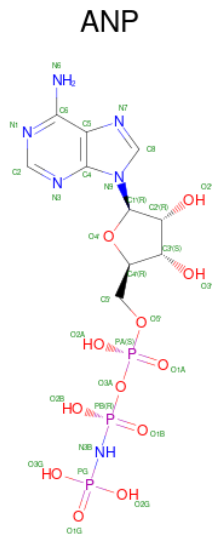
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	27	10	5	10	2	0
2	A	1	27	10	5	10	2	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $\text{C}_{10}\text{H}_{17}\text{N}_6\text{O}_{12}\text{P}_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total 31	C 10	N 6	O 12	P 3	0

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Mg	0
			1	1	

E2248	Y2086	E1984	W1838	Y1738	I1611	H1495	L1399	VAL	TRP	ARG	GLU	ALA	ASN	GLU	ASN	PHE
G2278	L2090	H1985	R1843	W1741	Y1618	K1496	V1400	ALA	GLU	PHE	PHE	LEU	LYS	LEU	LYS	ASN
H2282	L2093	S1986	F1844	Q1748	R1621	V1497	I1401	LEU	THR	GLN	THR	GLU	ASP	GLN	GLN	PHE
V2283	L2097	N1987	Q1860	L1749	F1626	S1503	L1403	LEU	LYS	PRO	PRO	ILE	ILE	VAL	VAL	LYS
I2287	K2115	I1997	M1861	V1750	P1627	M1507	A1407	Q1327	THR	SER	SER	ARG	PRO	ASN	GLN	VAL
Q2299	R2118	C1999	N1863	L1751	E1635	K1508	L1408	L1328	GLY	TRP	TRP	LYS	ASP	GLU	GLU	ASP
W2300	R2118	V2006	N1863	A1753	E1635	L1509	K1409	L1329	ASN	TYR	TYR	GLY	GLY	VAL	LEU	LEU
D2306	V2122	K2007	Y1872	L1756	L1638	K1514	D1410	V1332	ILE	ASP	ASP	THR	ALA	ASN	GLY	ILE
V2307	Q2125	S2009	Q1876	A1757	Q1651	F1516	R1411	E1335	PRO	ASN	ILE	ASP	LEU	PRO	VAL	ILE
W2311	E2129	P2010	D1877	W1758	Q1651	E1517	K1414	L1336	GLU	ILE	GLU	ASP	GLU	ARG	VAL	GLU
V2312	E2129	D2011	K1878	E1763	A1659	E1517	M1417	L1337	GLU	GLY	GLU	ASN	GLU	ILE	ARG	GLU
L2315	E2133	M2012	L1879	L1764	G1660	S1522	V1422	K1338	ALA	GLY	GLU	GLY	GLU	GLY	ALA	LYS
K2323	L2138	A2013	A1765	V1661	W1523	L1539	N1423	V1339	GLN	GLU	SER	THR	TYR	GLY	ALA	ILE
L2324	E2157	I2014	L1766	V1664	E1524	W1523	V1424	E1341	LEU	GLY	ASP	THR	GLY	ASP	LEU	GLY
R2332	L2141	F2016	W1769	I1665	D1525	K1526	V1426	D1344	THR	PHE	ALA	THR	VAL	VAL	ARG	GLU
L2335	L2149	M2017	G1770	V1673	L1527	L1527	S1427	K1347	GLY	ILE	ILE	SER	GLN	GLN	TRP	VAL
P2336	V2150	G2021	A1776	G1675	I1530	I1530	E1428	P1350	LYS	ARG	ARG	ALA	GLU	GLU	LYS	VAL
P2337	L2156	ALA	P1777	I1676	M1531	M1531	T1430	V1354	PHE	THR	THR	VAL	VAL	VAL	LEU	THR
M2338	L2157	GLY	W1785	S1677	A1532	A1532	L1431	Q1355	GLY	LYS	GLY	ASP	GLU	GLU	GLY	MET
V2339	L2157	ARG	L1789	S1678	F1534	F1534	G1432	P1356	ARG	ASP	PHE	THR	GLN	GLN	TRP	VAL
R2340	L2161	S2026	E1680	R1679	Q1541	Q1541	I1434	R1357	LYS	SER	ILE	GLY	LYS	LYS	ALA	THR
I2341	L2161	D2030	G1681	E1680	Q1541	Q1541	W1435	R1360	LYS	ALA	THR	VAL	VAL	VAL	VAL	LYS
M2342	R2172	K2033	L1792	E1682	I1550	I1550	D1438	Q1361	ASP	GLN	VAL	VAL	VAL	VAL	VAL	THR
V2345	G2173	F2036	A1793	K1687	A1555	A1555	Q1440	L1362	ARG	GLN	GLN	SER	LEU	LEU	GLY	PHE
A2354	R2179	D1933	Q1800	V1690	H1559	H1559	K1441	L1367	CYS	LYS	LYS	ASN	PRO	ASP	ILE	LEU
R2358	M2189	E1934	L1803	T1698	L1560	L1560	A1453	A1375	ALA	LYS	LYS	LEU	GLN	MET	MET	ASN
W2363	G2200	F1938	R1804	T1698	L1561	L1561	M1457	Q1378	LYS	GLN	ILE	TYR	THR	THR	THR	ASN
F2364	G2200	V1946	R1806	W1701	E1564	E1564	E1460	R1379	LYS	LYS	GLN	SER	ASP	ASP	ALA	GLN
L2369	G2209	C1949	H1810	M1709	I1571	I1571	E1461	A1380	ALA	ILE	PHE	TRP	MET	ARG	PRO	LYS
S2370	L2210	Q1950	L1811	T1712	K1580	K1580	K1464	A1383	GLU	GLN	LYS	LYS	GLN	GLN	VAL	VAL
M2373	T2214	V1951	T1812	T1712	K1581	K1581	V1469	S1382	LEU	GLU	GLU	GLU	VAL	VAL	SER	ASP
I2374	M2222	G1952	T1813	L1713	V1582	V1582	W1470	E1384	THR	ASP	VAL	VAL	GLY	GLY	HIS	ASP
M2377	S2228	A1953	E1814	A1714	S1583	S1583	W1470	F1385	ASP	ARG	GLU	LEU	ILE	ILE	LYS	LEU
L2382	G2229	W1954	L1815	K1715	K1584	K1584	Y1473	V1386	THR	ALA	LEU	SER	TYR	PRO	ASN	ASN
P2386	S2231	R1962	Q1818	E1719	M1589	M1589	E1474	Q1387	GLY	VAL	VAL	ARG	ASN	GLY	GLY	LEU
L2387	M2232	L1963	L1825	S1720	D1590	D1590	E1474	R1388	LEU	GLU	GLU	SER	ARG	LEU	GLY	LEU
L2387	M2232	E1964	L1825	V1721	V1591	V1591	L1475	K1391	LEU	THR	THR	GLY	GLY	GLY	PRO	GLU
Q2395	M2234	M1967	T1830	V1724	L1592	L1592	V1478	G1392	SER	THR	THR	ARG	GLN	GLU	LYS	TYR
R2396	M2235	V1975	D1831	E1725	H1593	H1593	L1486	Y1393	GLY	GLY	GLY	MET	GLY	GLY	ILE	ASN
R2397	K2239	I1978	M1832	E1725	I1594	I1594	L1486	M1394	GLU	ASP	ASP	LEU	GLY	GLY	LYS	LYS
			A1833	D1734	L1604	L1604	T1487	K1395	GLU	LEU	LEU	SER	ASN	ASN	ASN	PRO
			F1836	T1737	L1604	L1604	R1488	I1396	VAL	THR	THR	GLY	LYS	LYS	VAL	ILE
			E1837		L1608	L1608	F1494	M1398	ARG	ASP			GLN	TRP	VAL	VAL



F4615	A4421	Q4346	I4233	P4118	D3999
W4516	K4422	M4347	S4234	R4000	
E4518	L4423	M4348	P4235	T4127	A4004
	L4424	L4349	P4239	E4129	A4005
		E4350		I4130	H4006
	R4428	D4351	A4242		V4009
		E4352	L4243	K4133	S4010
	L4431	D4353	K4244		T4011
		ASP		M4137	L4012
	V4434	LEU	H4247	L4138	L4013
		TYR		L4139	G4014
	V4437	ALA			E4015
	C4438	ALA	R4255	P4149	S4019
	K4443	GLU	V4256	P4150	
	K4444	THR	D4257		E4022
		GLU	R4263	V4153	
	L4448	LYS	L4264		V4031
		LYS	L4265	R4159	
	L4451	THR	R4266	T4160	E4034
	L4452	ARG	T4267		V4035
	N4453	THR	F4268	P4165	
	E4454	ASP	F4269		L4042
		SER	L4269	R4168	M4043
	L4455	THR	E4270		
	V4456	THR	R4271	K4171	V4055
	K4457	SER		E4175	Q4065
		ASP	R4276	R4176	
	L4460	GLY	S4277	A4177	S4068
	P4461	ARG	F4278	R4178	I4071
	R4462	PRO		L4179	F4077
			L4284		A4080
	M4473	A4375		W4185	
	T4474	T4379	V4288	F4186	I4084
		L4380		H4187	
	Q4477	H4381	I4294	I4189	V4088
	N4478	T4382	Q4295	Q4191	
	S4480	T4383	M4296	E4192	
	D4481	A4384	P4297	L4199	M4095
	F4482	S4385			L4096
	S4483	M4386	I4300	Y4205	
	E4484	K4387	R4301	E4206	
	R4485	L4388	R4302	L4212	H4100
	L4486	H4389	E4303	A4215	P4103
		I4391		D4217	G4104
	K4487	L4390	V4306		W4105
	Q4488		Q4307	D4220	L4106
		L4395	K4308	L4223	Q4107
				D4224	L4109
	I4492	K4399	D4314		F4110
			T4315		K4111
	A4496	V4402			
	A4497	E4403	R4329		
		N4404	V4330		
	L4504	I4405			
	K4505	K4406	Q4336		
	N4506	D4407			
	I4507		I4340		
		F4410			
	G4513	R4411			
	L4514	F4412	M4343	A4227	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	326895	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	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)	2600	Depositor
Magnification	45000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.624	Depositor
Minimum map value	-1.305	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	444.416, 444.416, 444.416	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.736, 1.736, 1.736	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, ADP, MG, ANP

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	0.13	0/24989	0.34	0/33856

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	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2597	PRO	Peptide

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	A	24471	0	24528	609	0
2	A	54	0	24	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	31	0	12	6	0
4	A	31	0	13	4	0
5	A	1	0	0	0	0
All	All	24588	0	24577	609	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 12.

The worst 5 of 609 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:3194:LEU:HD22	1:A:3500:MET:HE3	1.57	0.87
1:A:2603:MET:HE2	4:A:4703:ANP:H5'2	1.60	0.82
1:A:2387:LEU:HB3	1:A:2467:ARG:HH21	1.44	0.80
1:A:3817:SER:HB3	1:A:4349:LEU:HD21	1.63	0.80
1:A:2386:PRO:HA	1:A:2416:GLN:HE22	1.47	0.79

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	A	3028/4646 (65%)	2937 (97%)	91 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	2703/4125 (66%)	2703 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3837	HIS
1	A	4078	ASN
1	A	4532	ASN
1	A	3931	GLN
1	A	4098	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](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ANP	A	4703	-	33,33,33	2.34	6 (18%)	45,52,52	1.44	6 (13%)
2	ADP	A	4704	-	28,29,29	1.41	4 (14%)	43,45,45	1.82	9 (20%)
3	ATP	A	4702	5	32,33,33	0.42	0	48,52,52	0.32	0
2	ADP	A	4701	-	28,29,29	1.42	5 (17%)	43,45,45	1.79	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ANP	A	4703	-	-	7/18/38/38	0/3/3/3
2	ADP	A	4704	-	-	4/16/32/32	0/3/3/3
3	ATP	A	4702	5	-	7/22/38/38	0/3/3/3
2	ADP	A	4701	-	-	4/16/32/32	0/3/3/3

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4703	ANP	PB-O3A	9.14	1.70	1.59
4	A	4703	ANP	PG-N3B	6.20	1.79	1.63
4	A	4703	ANP	PG-O1G	4.80	1.53	1.46
2	A	4704	ADP	C5-C4	4.65	1.47	1.39
2	A	4701	ADP	C5-C4	4.65	1.47	1.39

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4704	ADP	C5-C4-N3	-5.93	118.55	126.72
2	A	4701	ADP	C5-C4-N3	-5.64	118.94	126.72
2	A	4704	ADP	N3-C4-N9	4.58	134.96	127.17
4	A	4703	ANP	O2B-PB-O1B	4.52	119.57	109.87
2	A	4701	ADP	N3-C4-N9	4.50	134.82	127.17

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	4701	ADP	O4'-C4'-C5'-O5'
2	A	4704	ADP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
3	A	4702	ATP	PB-O3B-PG-O3G
3	A	4702	ATP	C5'-O5'-PA-O3A
4	A	4703	ANP	PB-N3B-PG-O1G

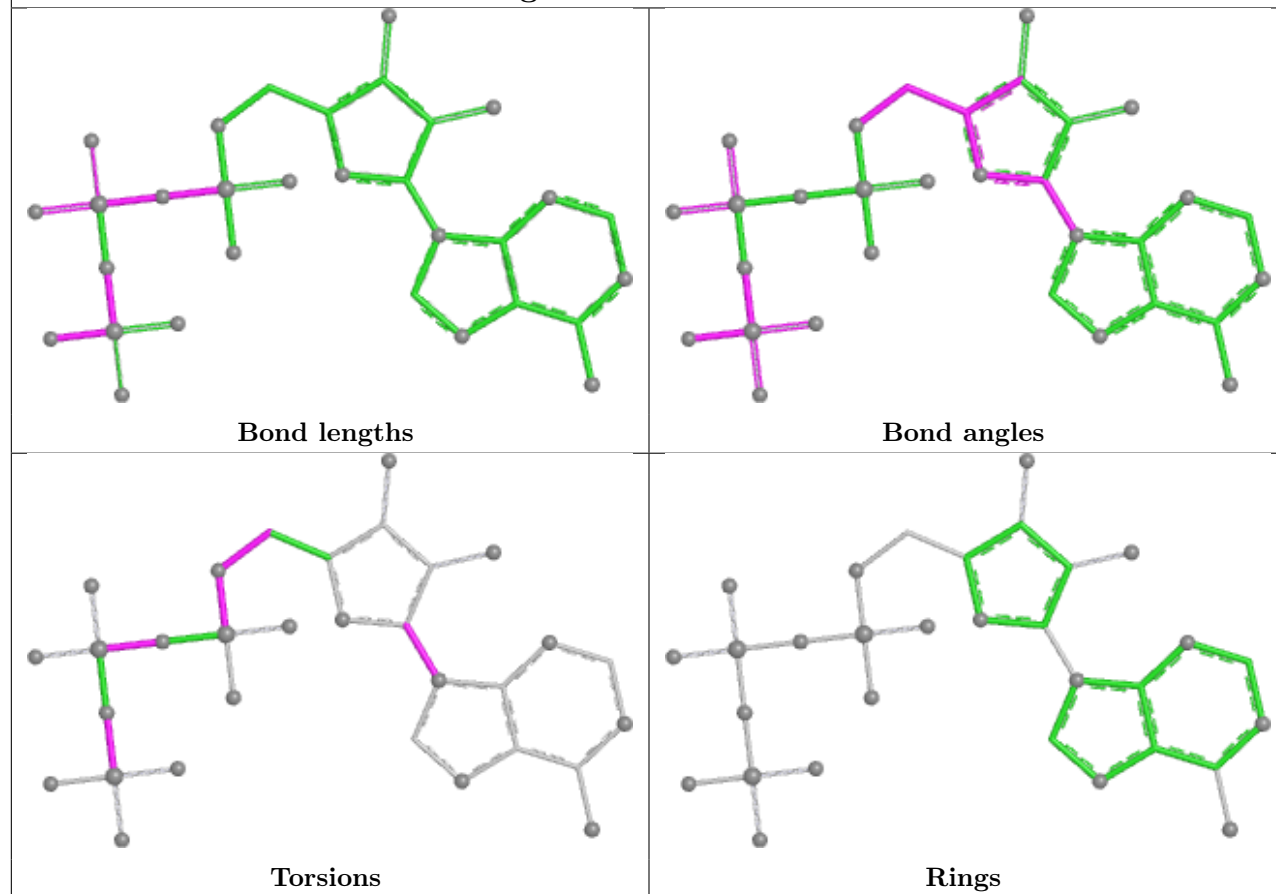
There are no ring outliers.

4 monomers are involved in 17 short contacts:

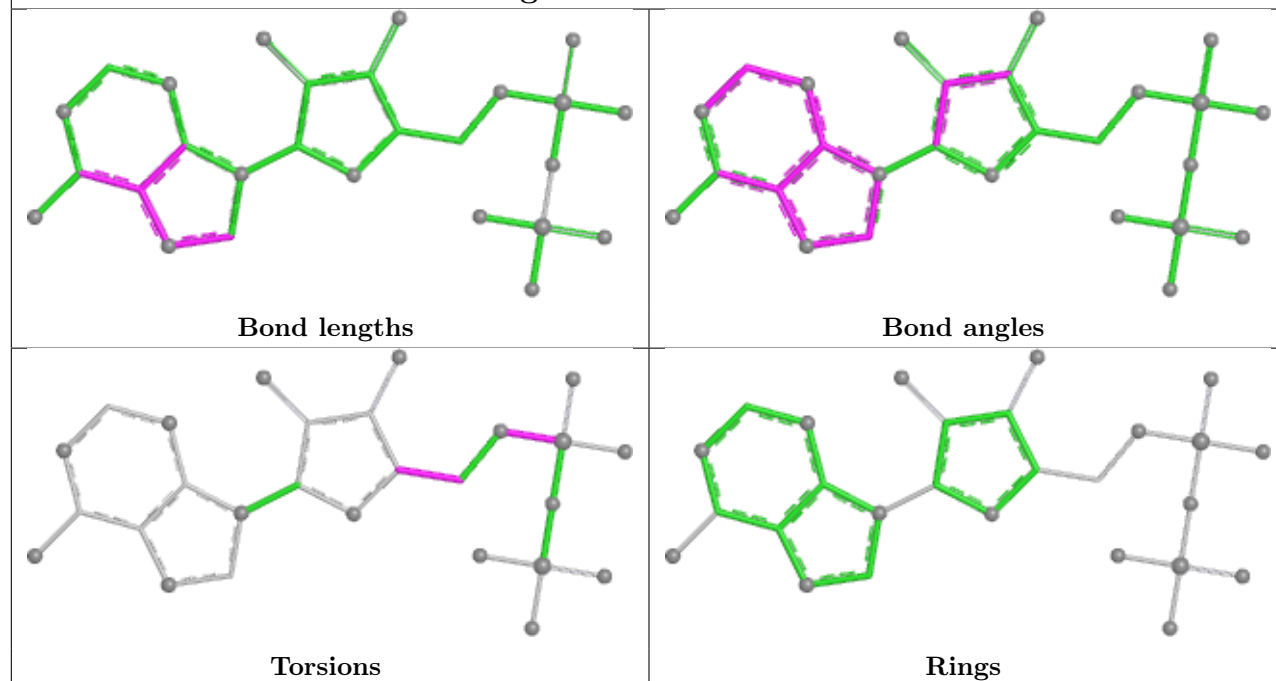
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	4703	ANP	4	0
2	A	4704	ADP	3	0
3	A	4702	ATP	6	0
2	A	4701	ADP	4	0

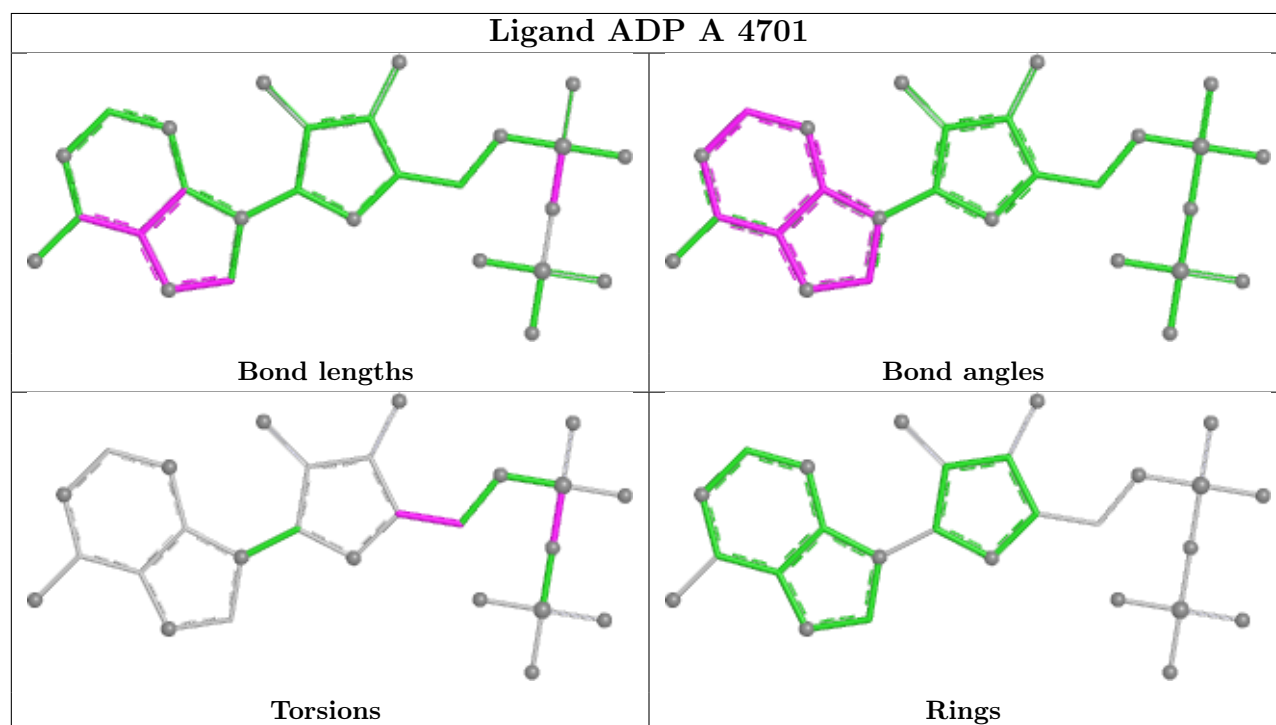
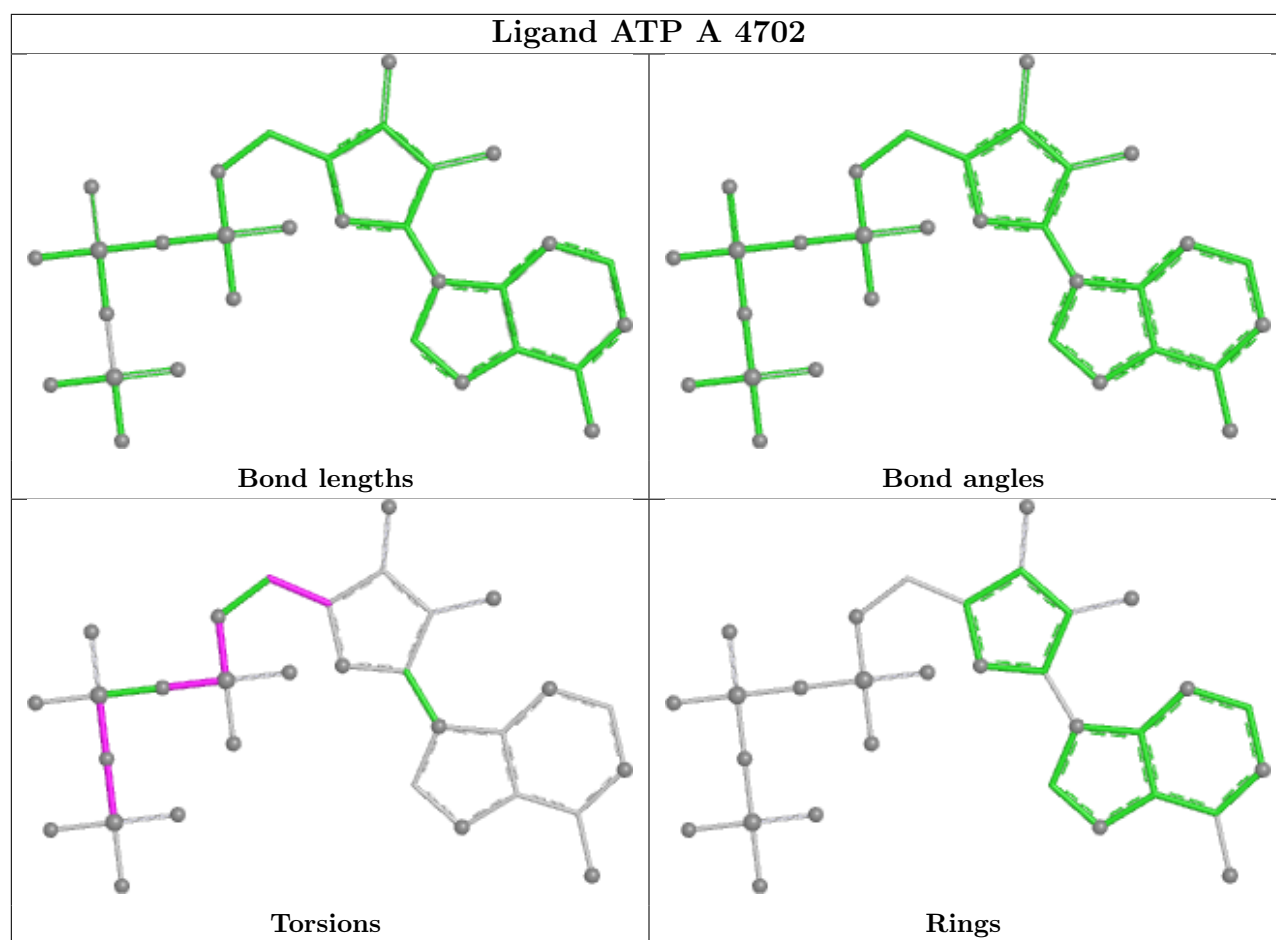
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ANP A 4703



Ligand ADP A 4704





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

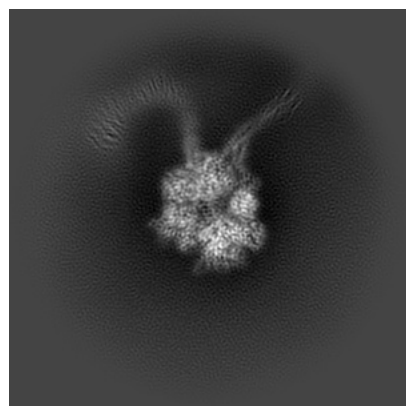
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73176. These allow visual inspection of the internal detail of the map and identification of artifacts.

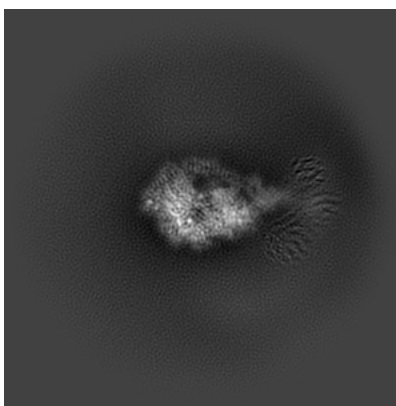
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

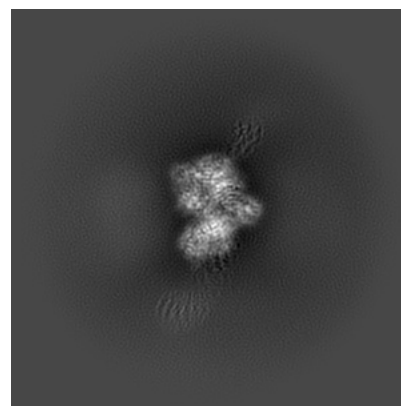
6.1.1 Primary map



X

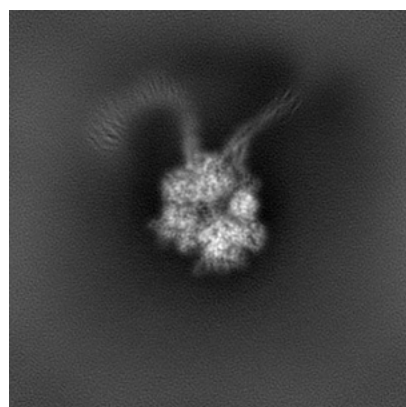


Y

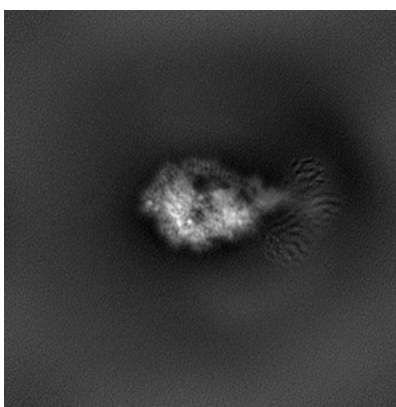


Z

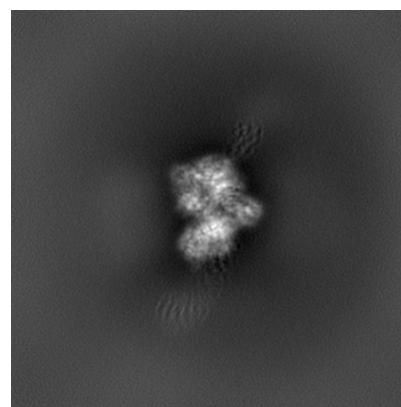
6.1.2 Raw map



X



Y

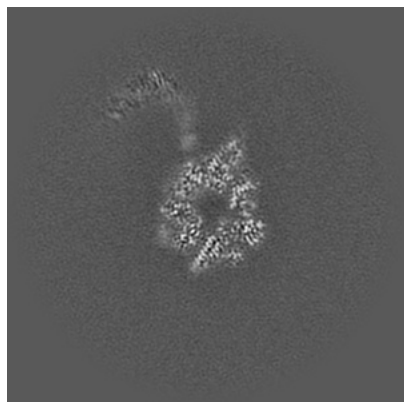


Z

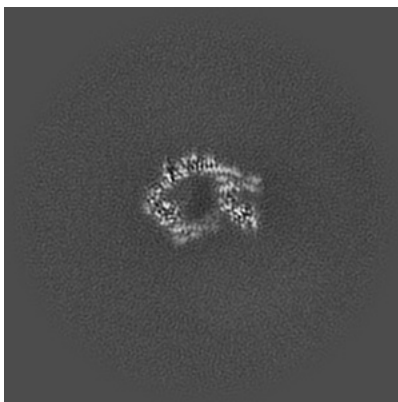
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

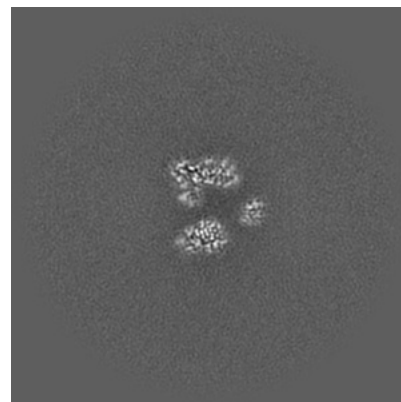
6.2.1 Primary map



X Index: 128

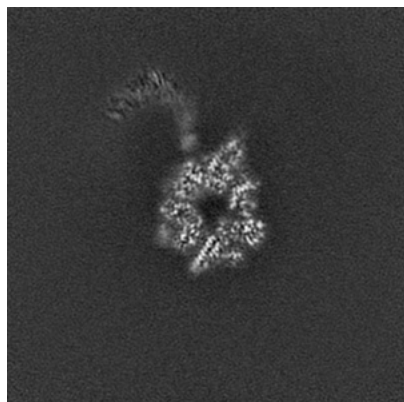


Y Index: 128

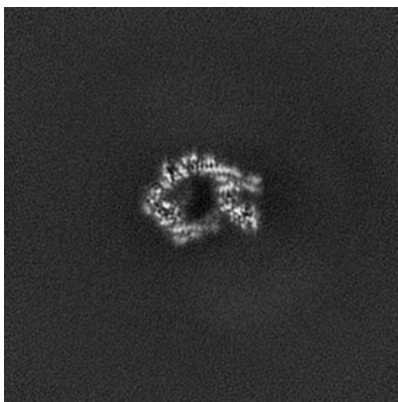


Z Index: 128

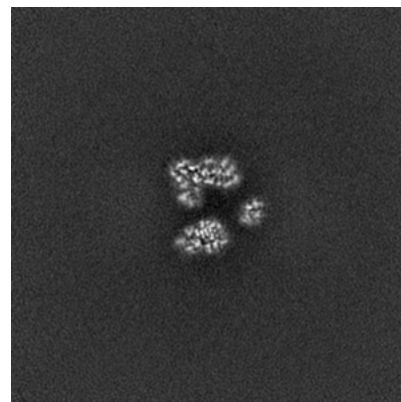
6.2.2 Raw map



X Index: 128



Y Index: 128

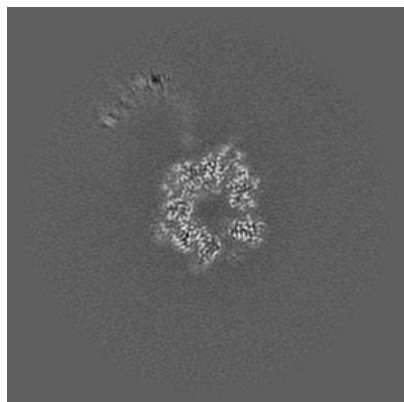


Z Index: 128

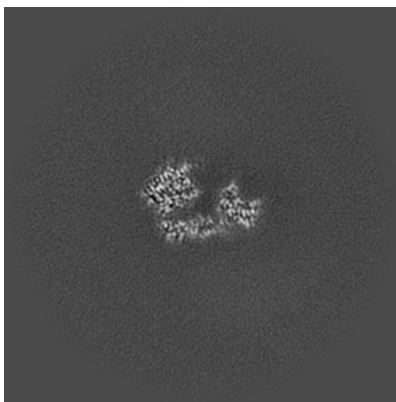
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

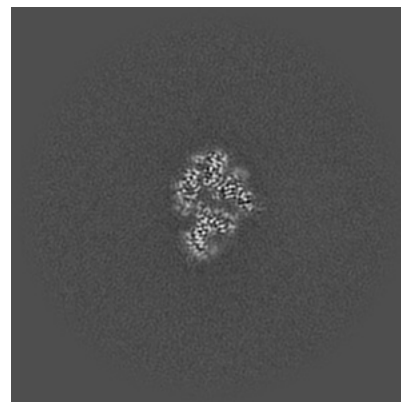
6.3.1 Primary map



X Index: 125

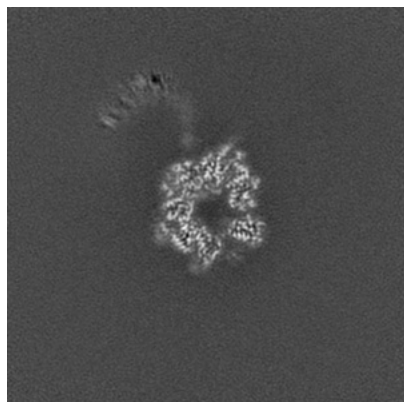


Y Index: 135

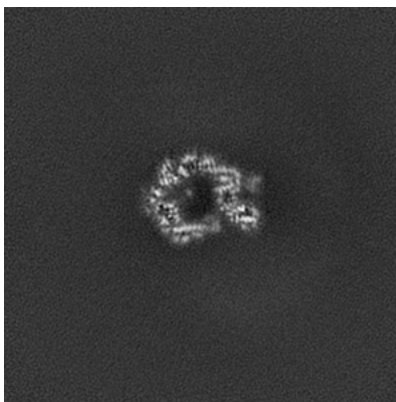


Z Index: 112

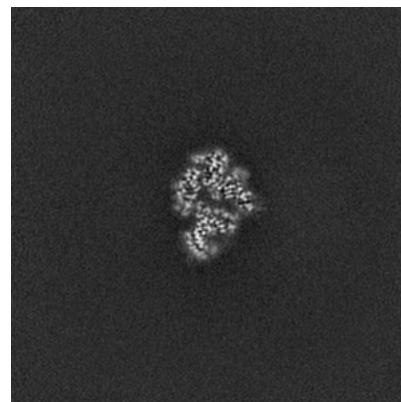
6.3.2 Raw map



X Index: 125



Y Index: 129

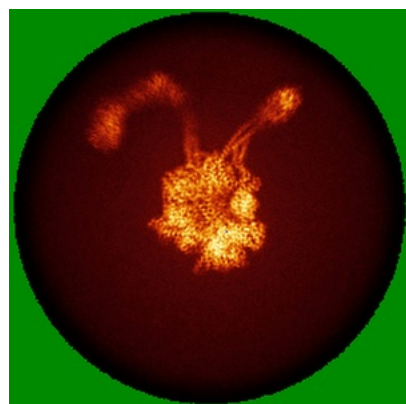


Z Index: 112

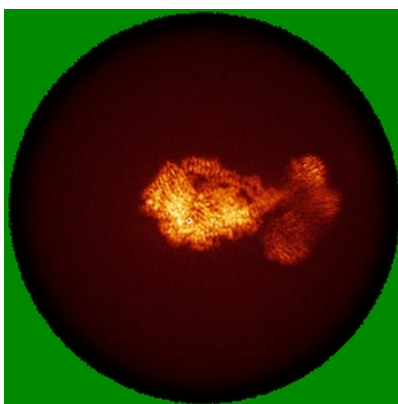
The images above show the largest variance slices of the map in three orthogonal directions.

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

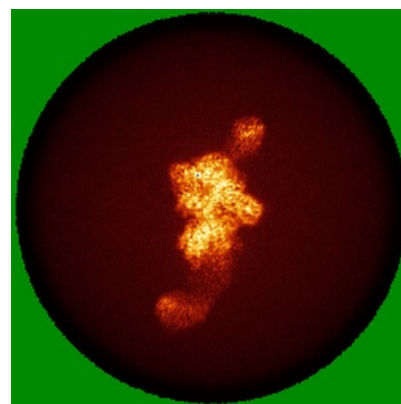
6.4.1 Primary map



X

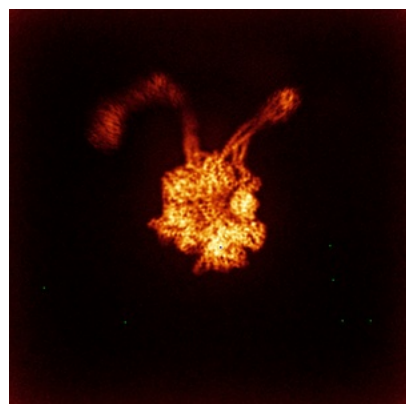


Y

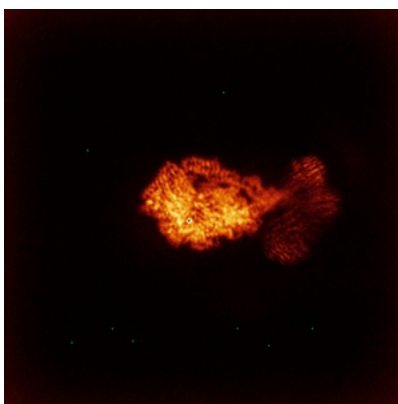


Z

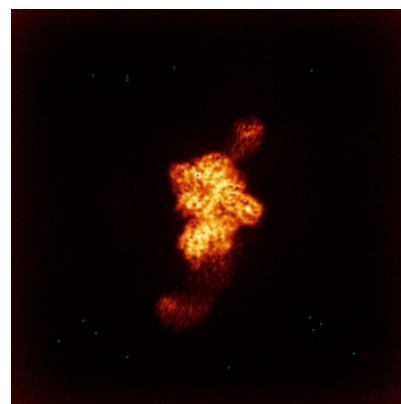
6.4.2 Raw map



X



Y

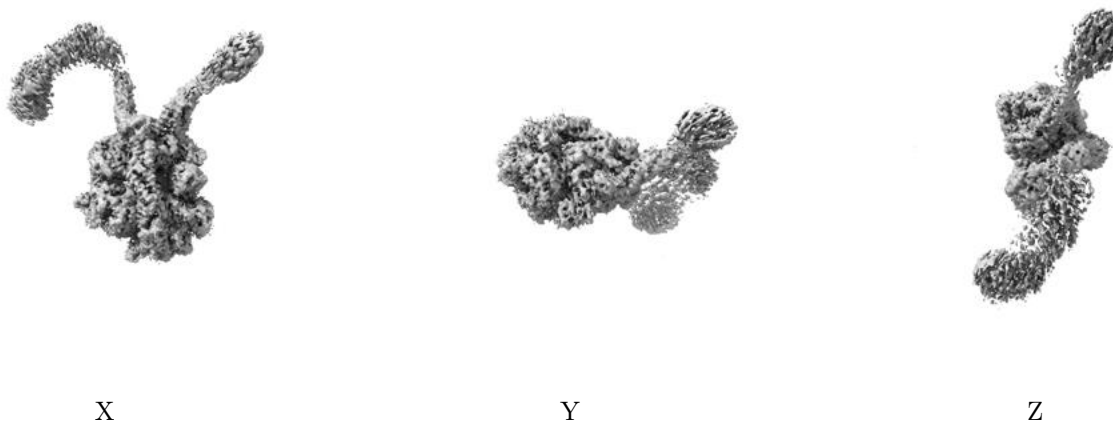


Z

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.

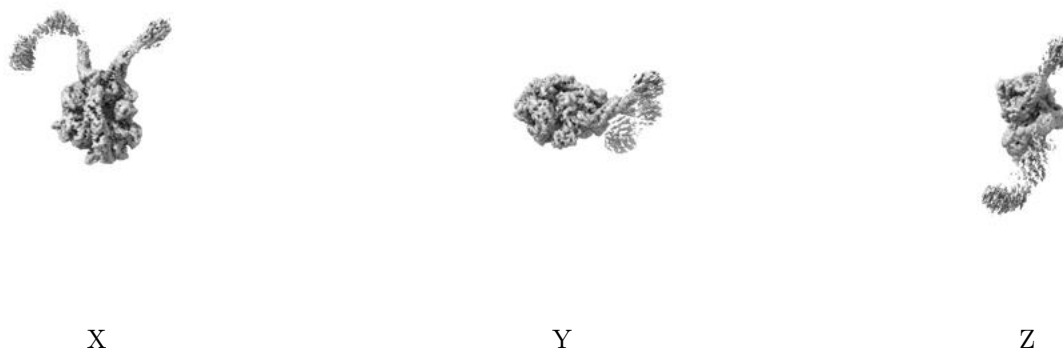
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

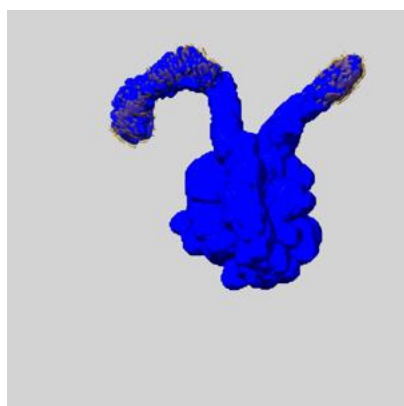
6.6 Mask visualisation [i](#)

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

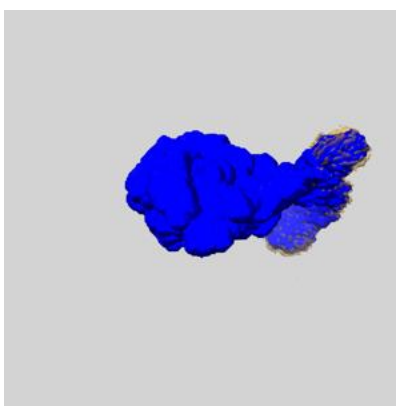
A mask typically either:

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

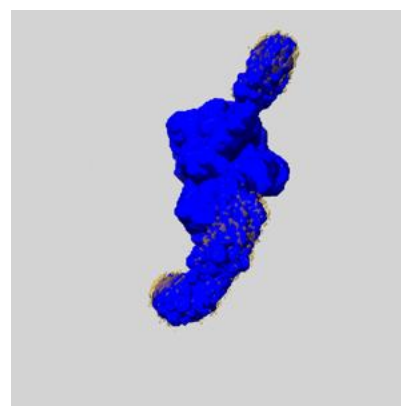
6.6.1 emd_73176_msk_1.map [i](#)



X



Y

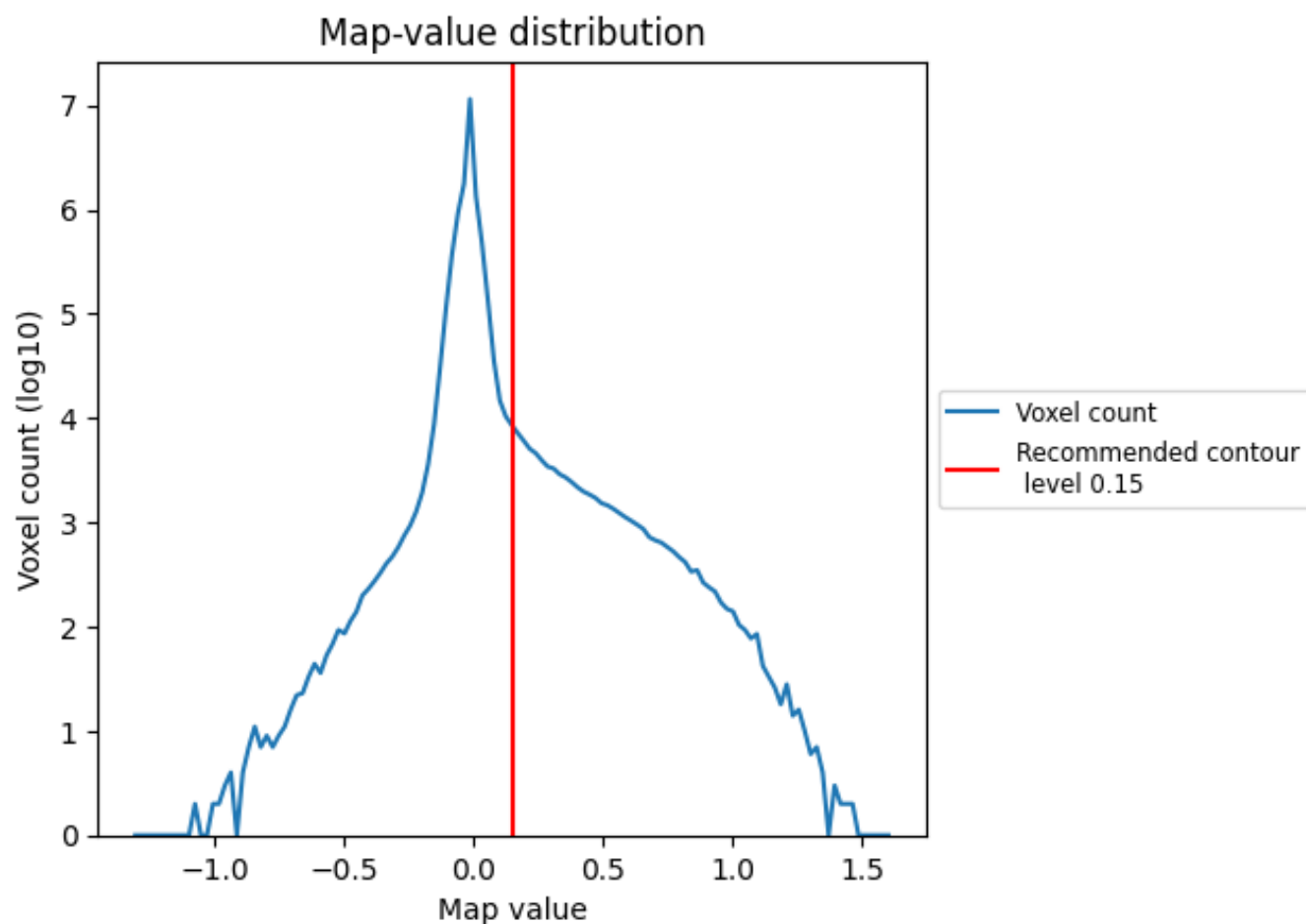


Z

7 Map analysis [i](#)

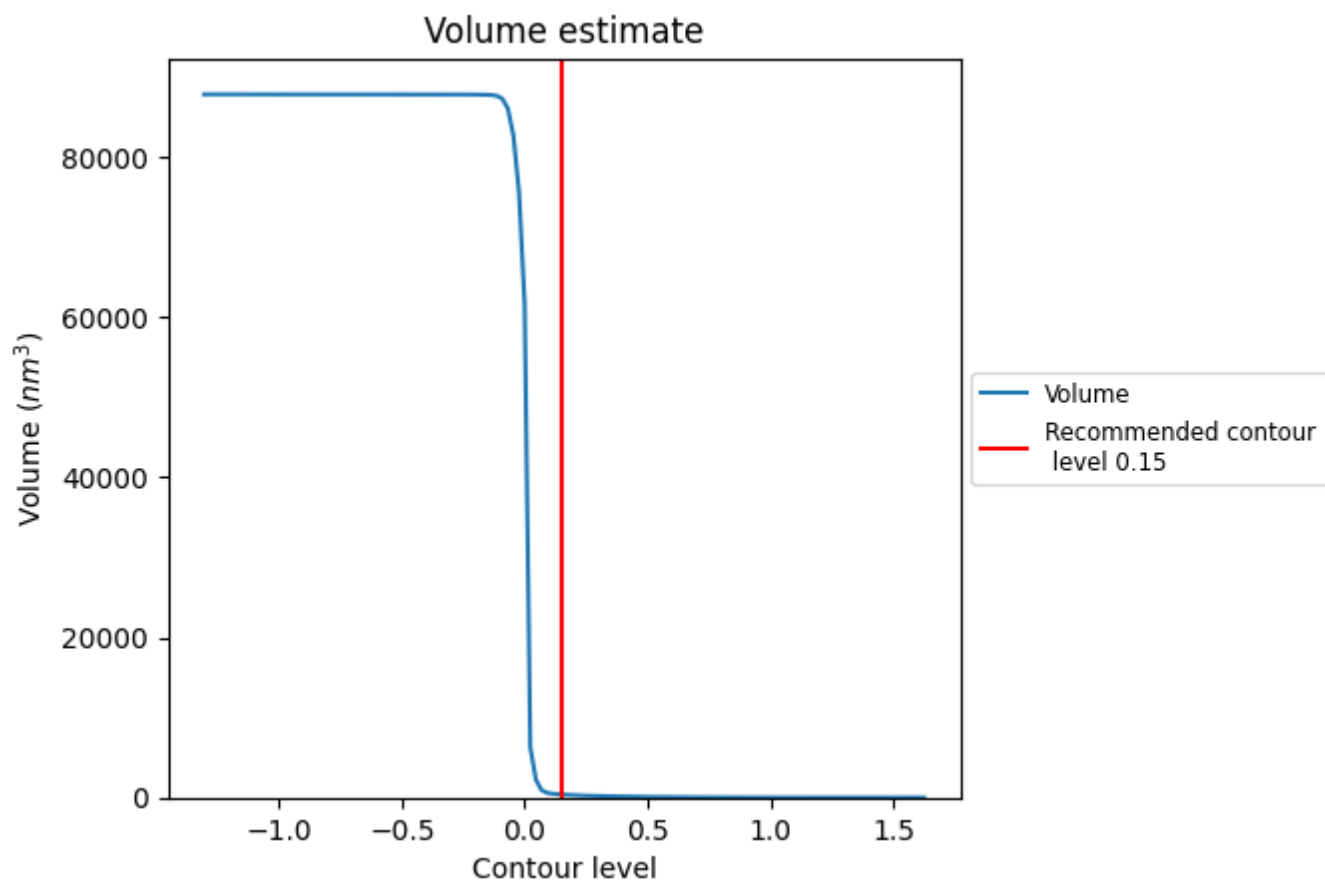
This section contains the results of statistical analysis of the map.

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.

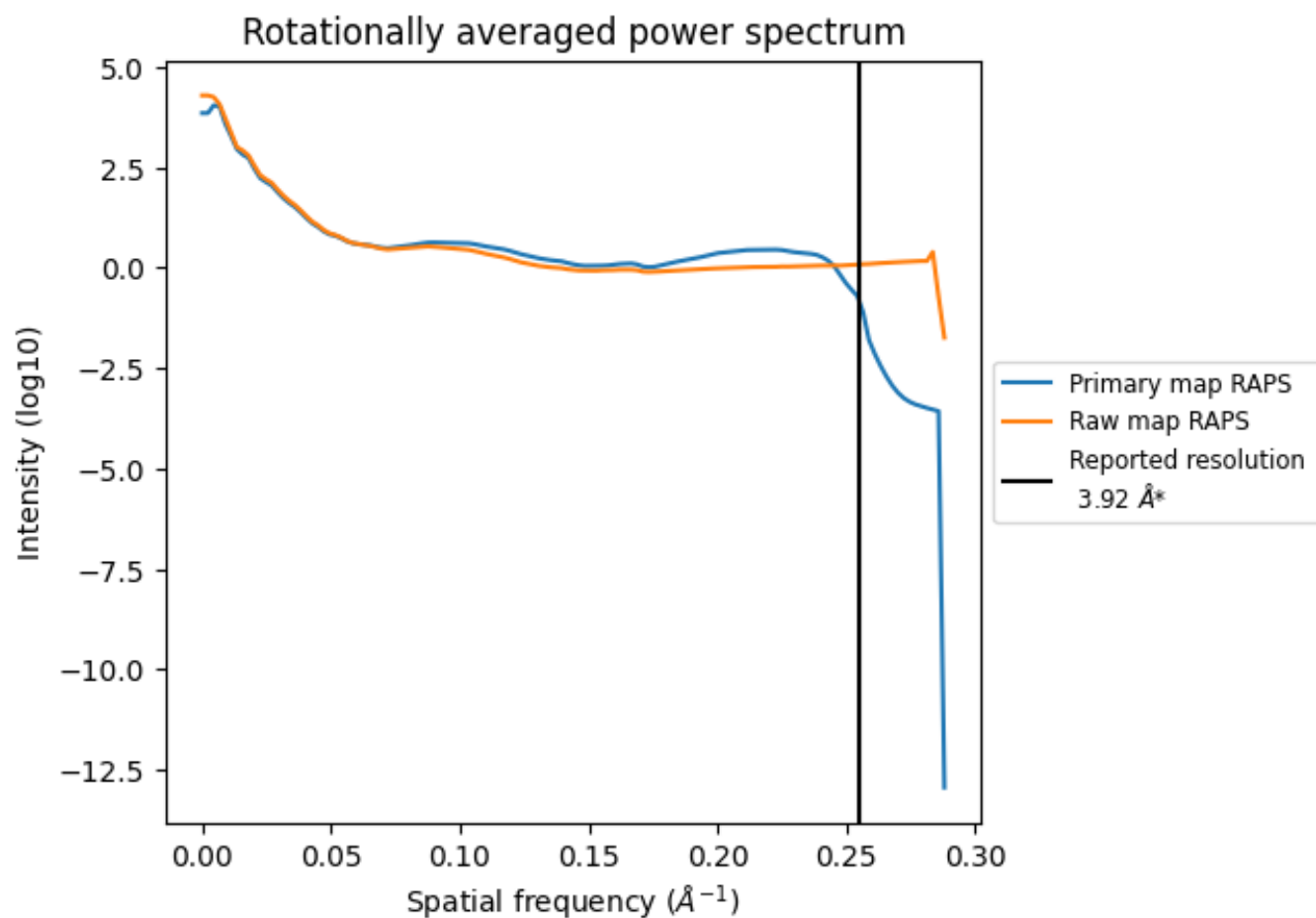
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 383 nm³; this corresponds to an approximate mass of 346 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 ⓘ

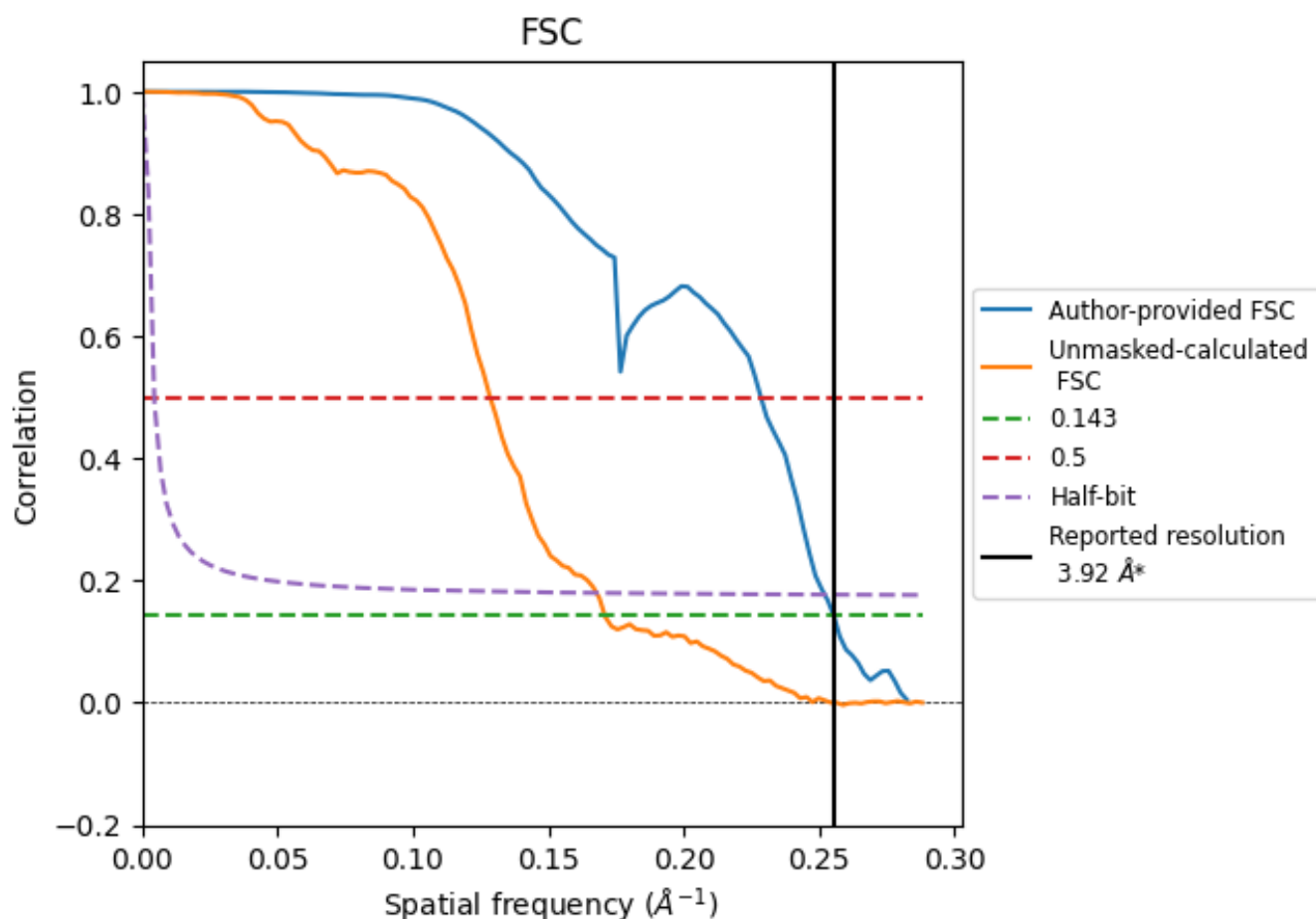


*Reported resolution corresponds to spatial frequency of 0.255 Å⁻¹

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 0.255 \AA^{-1}

8.2 Resolution estimates [i](#)

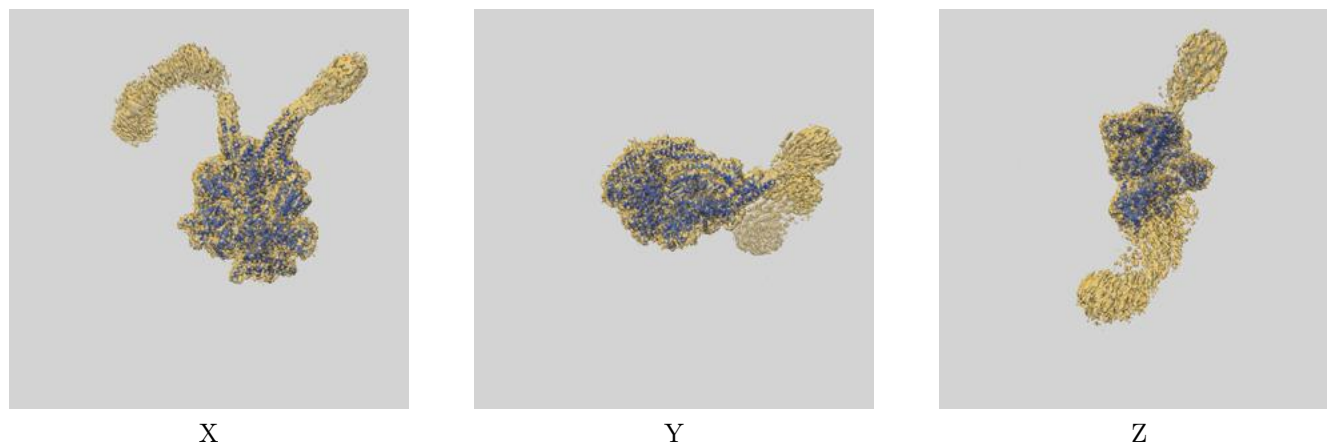
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.92	-	-
Author-provided FSC curve	3.92	4.38	3.97
Unmasked-calculated*	5.85	7.79	5.96

*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 5.85 differs from the reported value 3.92 by more than 10 %

9 Map-model fit [i](#)

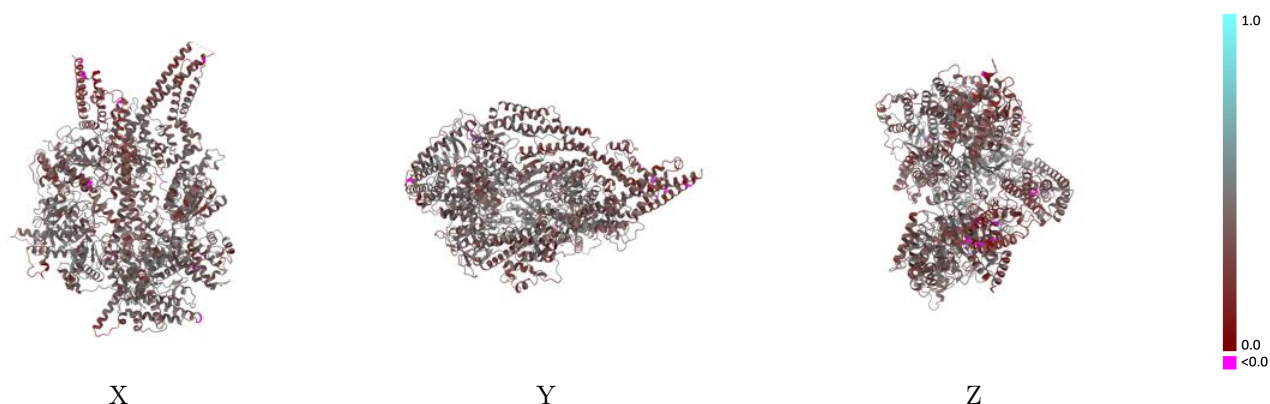
This section contains information regarding the fit between EMDB map EMD-73176 and PDB model 9YNF. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



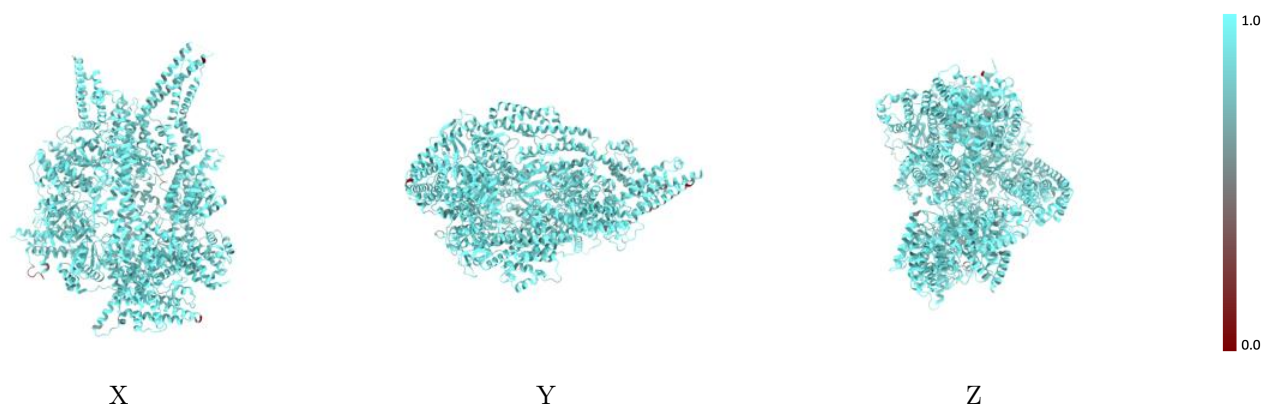
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



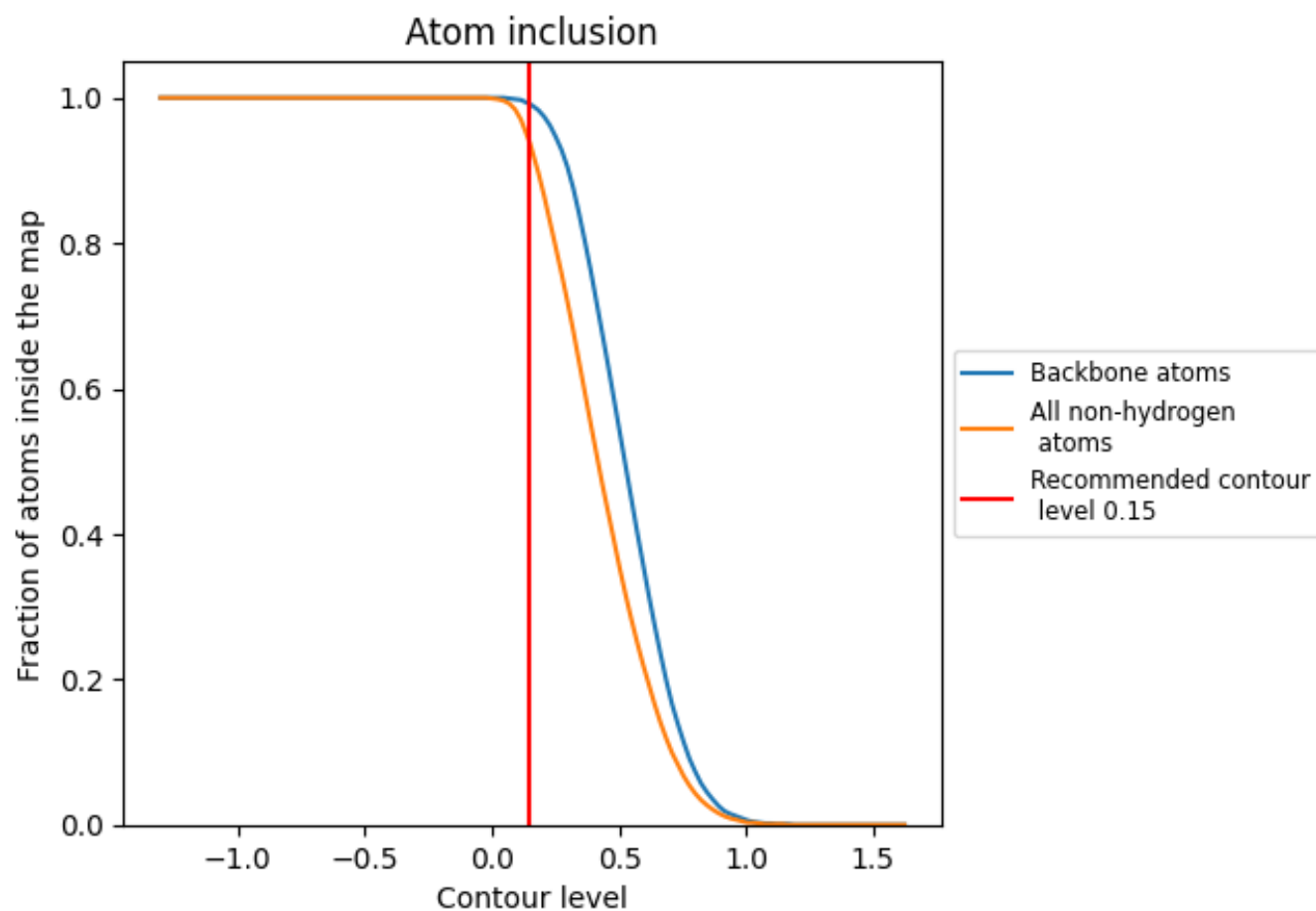
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 94% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9370	<div><div></div></div> 0.3720
A	<div><div></div></div> 0.9370	<div><div></div></div> 0.3720

