



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:32 AM UTC

PDB ID : 5NP0 / pdb_00005np0
EMDB ID : EMD-3669
Title : Closed dimer of human ATM (Ataxia telangiectasia mutated)
Authors : Baretic, D.; Pollard, H.K.; Fisher, D.I.; Johnson, C.M.; Santhanam, B.; Truman, C.M.; Kouba, T.; Fersht, A.R.; Phillips, C.; Williams, R.L.
Deposited on : 2017-04-13
Resolution : 5.70 Å(reported)
Based on initial model : 4JSP

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

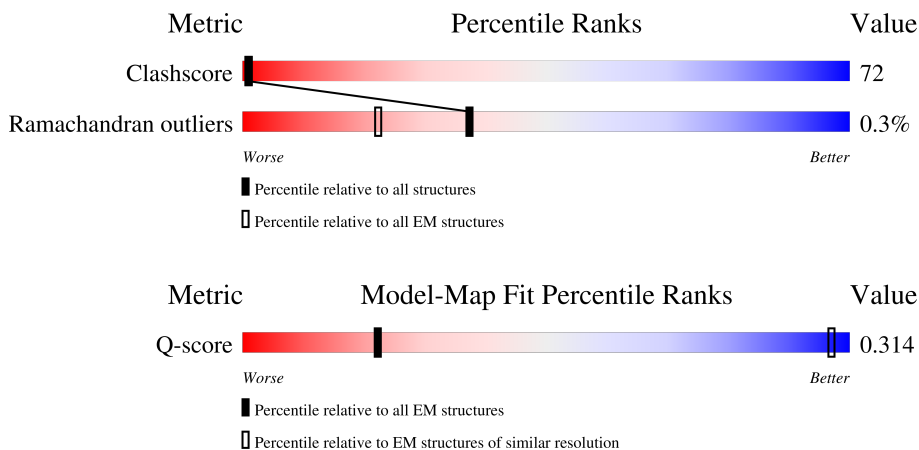
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.70 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	-
Q-score	-	25397	503 (5.20 - 6.20)

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	A	3066	
1	B	3066	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25074 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 Serine-protein kinase ATM.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	2528	Total	C	N	O	0	0
			12537	7481	2528	2528		
1	B	2528	Total	C	N	O	0	0
			12537	7481	2528	2528		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	initiating methionine	UNP Q13315
A	-8	ASP	-	expression tag	UNP Q13315
A	-7	TYR	-	expression tag	UNP Q13315
A	-6	LYS	-	expression tag	UNP Q13315
A	-5	ASP	-	expression tag	UNP Q13315
A	-4	ASP	-	expression tag	UNP Q13315
A	-3	ASP	-	expression tag	UNP Q13315
A	-2	ASP	-	expression tag	UNP Q13315
A	-1	LYS	-	expression tag	UNP Q13315
A	0	HIS	-	expression tag	UNP Q13315
B	-9	MET	-	initiating methionine	UNP Q13315
B	-8	ASP	-	expression tag	UNP Q13315
B	-7	TYR	-	expression tag	UNP Q13315
B	-6	LYS	-	expression tag	UNP Q13315
B	-5	ASP	-	expression tag	UNP Q13315
B	-4	ASP	-	expression tag	UNP Q13315
B	-3	ASP	-	expression tag	UNP Q13315
B	-2	ASP	-	expression tag	UNP Q13315
B	-1	LYS	-	expression tag	UNP Q13315
B	0	HIS	-	expression tag	UNP Q13315









ASN	VAL	L2523	E2457	D2395	T2333	L2270	R2136	Q2069	L2001	V1941	F1870	ILE	D1725	I1643
VAL	PRO	A2524	D2458	T2396	Y2334	F2271	D2137	N2070	Q2002	A1942	T1871	ASN	C1726	T1644
LYS	GLN	A2525	R2459	Q2397	T2335	E2272	ARG	L2071	D2003	K1943	S1872	LEU	W1727	M1644
GLN	GLN	R2526	K2460	Q2398	E2336	E2273	GLU	G2072	L2004	K1944	C1873	TRP	K1728	V1645
SER	SER	N2527	R2461	Q2399	C2337	A2274	PHE	L2005	L2005	A1945	L1874	ILE	S1731	K1646
THR	THR	G2528	F2462	R2400	L2338	L2275	S2141	C2074	L2006	Q1946	F1877	P1797	S1731	L1647
GLN	GLN	L2401	L2463	E2402	R2339	F2276	T2142	H2075	E2007	S1947	S1877		A1732	V1648
LEU	LEU	C2464	E2403	E2402	V2340	Q2277	F2143	L2076	E2008	C1948	S1878	A1812	A1733	V1649
D2595	D2595	M2465	A2466	M2405	G2342	L2278		L2077	Y2009	A1949	Q1879	F1813	T1734	N1650
E2596	E2596	G2533	V2467	Q2406	N2343	Q2280	S2146	S2078	R2010	A1950	T1880	L1814	T1735	M1657
D2597	D2597	G2534	E2468	K2406	N2344	Q2281	L2147	S2079	S2011	H1951	S1881	S1816	C1736	A1658
R2598	R2598	K2468	N2469	S2407	N2345	Q2280	K2148	S2079	R2011	A1952	T1882	S1816	L1737	F1657
T2599	T2599	S2407	Y2470	S2408	L2345	Q2282	Y2143	L2081	G2013	T1953	S1883	G1817	K1738	L1659
E2600	E2600				D2216	F2217	A2150	K2082	E2014	A1954	T1884	G1818	N1739	N1660
D2601	D2601				S2218	L2219	R2151	G2083	P2015	L1955	T1885		K1738	N1659
A2602	A2602				F2219	Q2220	V2152	L2084	D2016	L1956	F1886	E1822	A1741	T1662
N2603	N2603				Q2220	Q2221	K2153	D2085	D2017	L1957	A1887	L1741	A1742	G1663
R2604	R2604				E2221	E2221	E2154	D2086	L2018	A1958	N1888	L1824	T1743	E1664
L2605	L2605				P2222	P2222	V2155	E2087	Y2019	E1959	S1891	Q1825	K1744	K1665
T2606	T2606				L2223	L2223	E2156			I1960	E1892	L1826	T1745	E1666
C2607	C2607				K2224	K2224	E2157			I1961	E1892	L1827	G1746	V1667
T2608	T2608				A2225	A2225	M2158	W2091	C2021	A1962	K1828	L1868		E1669
L2609	L2609				L2226	L2226	C2159	C2092	G2022	D1963	C1900	F1749		
K2610	K2610				E2295	A2296	K2160	E2094	Q2028	K1964	L1901	W1750		
R2611	R2611				Q2297	R2297	R2161	L2095	P2029	E1751	D1902	E1751	E1751	G1676
S2612	S2612				Q2297	Q2297	E2096	E2096	L2030	S1966	K1903	E1832	L1752	E1677
T2612	T2612				Q2298	V2228	P2171	E2097	T2031	K1967	K1904	E1833	Y1753	V1678
					L2230	L2230	E2164			D1968	S1905	K1894	K1754	E1679
Q2615	Q2615				E2231	E2231	Y2167	L2098	R2032	L2033	S1905	T1835	E1680	G1680
M2616	M2616				L2232	L2232	S2168	H2099	L2033	D1969	Q1906	K1894	K1754	E1680
V2617	V2617				L2234	L2234	L2169	Y2100	R2034	Q1970	T1907	D1836	T1756	I1681
K2618	K2618				E2235	E2235	Y2170	A2102	Y2036	K1972	N1909	Q1839	T1757	E1682
S2619	S2619				E2236	E2236	P2171	A2103	E2037	K1973	L1910		D1758	F1683
T2620	T2620						T2172	W2104	L2038	S1974	A1911	L1842	L1764	I1686
E2621	E2621				S2242	Q2243	L2173	R2105	E2039	L1975	V1912		Q1765	A1687
A2622	A2622				Q2243	Q2243	S2174	N2106		PHE	V1913	L1845		I1688
L2623	L2623				C2246	C2246	R2175	M2107	W2042	GLU	D1914	L1846	R1768	
C2624	C2624				L2247	L2247	L2176		G2043	GLU	Y1915	H1847	T1769	Y1696
D2625	D2625				L2247	L2247	Q2177		K2044	GLU	M1916	D1848	S1770	
A2626	A2626				K2248	K2248	A2178		A2045	GLY	R1917	T1849		
V2627	V2627				D2249	D2249	L2179		L2046	SER	R1918	L1850	ARG	L1702
L2628	L2628				L2250	L2250	G2180		L2047	GLN		L1850	LYS	F1703
T2629	T2629				L2251	L2251			W2047	SER		L1851	LYS	E1704
L2630	L2630				L2251	L2251	E2183	LYS	T2048	GLN	S1923	K1852	PHE	D1705
A2631	A2631				L2252	L2252	S2184	VAL	Y2049	THR	G1925	D1853	LEU	K1706
N2632	N2632				K2253	K2253	Q2184	GLU	D2050	THR	S1924	T1854	LEU	E1707
L2633	L2633				H2254	H2254	E2187	GLY	L2051	ILE	T1926	N1855	VAL	E1707
LEU	LEU				L2255	L2255	E2187	THR	E2052	SER	T1927	E1856	ARG	L1708
D2634	D2634				L2256	L2256	L2188			SER	F1928	S1857	PRO	
ALA	ALA				D2320	D2320	S2123			SER			ARG	
THR	THR				A2321	A2321	R2124			LEU	W1713	PHE	THR	F1712
LYS	LYS				E2321	E2321	R2191	H2125	S2058	SER	D1930	L1859	ASP	M1714
PRO	PRO				L2322	L2322	SER	E2126	T2057	GLU	D1930	L1860	LYS	L1715
GLU	GLU				K2323	K2323	VAL	S2127	R2060	LYS	F1932	L1861	GLU	T1716
TRP	TRP				A2324	A2324			Q2061	ASN		L1862	ASN	Y1717
LYS	LYS				ALA	ALA	T2194			LYS				
ARG	ARG				ASN	ASN	Q2197		A2062	LYS		S1863	PRO	L1718
ARG	ARG				ASN	ASN	L2188					S1864	PHE	N1719
F2616	F2616				L2388	L2388			G2063	E1995	D1935	T1864	GLY	T1720
L2617	L2617				D2448	D2448	L2198		L2064	T1997	L1936	H1865	GLY	N1720
R2642	R2642				E2449	E2449	S2199	L2132	L2065	E1996	N1937	L1866	GLY	T1721
					A2391	A2391	S2328	L2133	Q2066	G1998	Y1938	Q1867	LEU	L1722
L2618	L2618				R2390	R2390	S2328	L2267	K2330				ASP	N1723
S2619	S2619				A2391	A2391	L2330		L2331					
M2620	M2620				R2392	R2392	L2330		Q2067					
ILE	ILE				L2452	L2452	L2453		L2068					
T2645	T2645				L2453	L2453	L2454							
N2646	N2646				A2454	A2454								
L2647	L2647				L2455	L2455								
					K2456	K2456								

E3007	R3008	V3009	L3010	M3011	R3012	L3013	Q3014	E3015	K3016	L3017	K3018	G3019	V3020												G3023	T3024	V3025	L3026	S3027	V3028	G3029	G3030	Q3031	V3032	N3033	L3034	L3035	I3036	Q3037	Q3038	A3039	L3040	D3041	P3042	K3043	N3044	L3045	S3046	R3047	L3048	F3049	G3050	G3051	K3052	K3053	A3054	W3055	V3056							
S2941	Q2942			L2945	L2946	T2947	L2948	V2949	E2950	V2951	L2952			P2956	L2957	F2958			T2961	M2962	N2963			K2966	A2967	L2968	Y2969	L2970	Q2971	Q2972	P2974	E2975	D2976			E2979	L2980	H2981	PRO	THR	LEU	ASN	ALA	ASP	ASP	GLN	GLU	CYS	LYS	ARG	ASN	LEU	SER	ASP	L2998	D2999	Q3000	S3001	F3002	N3003	K3004	V3005	A3006		
V2862	Q2863		L2866	G2867			H2872			N2875	L2876	L2877	L2878	N2879	E2880	Q2881	S2882	A2883	E2884	L2885	V2886	H2887	L2888			F2894	E2895	L2899	N2900	L2910	L2911	Q2828	P2829	V2830			Y2833	E2834	C2835			F2839	L2840	D2841	P2842	A2843	L2844	W2845	F2846	E2847	R2848	L2849	N2850	A2851	Y2852	L2853	E2932	K2933	T2934	M2935	E2936	V2937	M2938	R2939	N2940
P2648	A2649	D2650	T2654	K2657	N2658	L2659	E2660	D2661			P2665	T2666			L2669	T2674	Y2677	T2682	L2683	Q2684	S2685	F2686			E2689	F2690	R2691	L2692	A2693			V2696	P2699	K2700	L2701	L2702	D2703	C2704	V2705	G2706	S2707	D2708	G2709	L2710	E2711	R2712	R2713	Q2714	L2715	V2716			R2719	D2720	L2721	L2722	Q2724								
D2725	A2726	V2727	M2728	Q2729	V2730	L2731	F2732	Q2733	M2734	C2735	N2736	T2737	L2738	L2739	Q2740	R2741	N2742	T2743	E2744	T2745	R2746	K2747	R2748	K2749			V2757	V2758	S2761	R2691	Q2762	R2763	S2764	G2765	V2766	L2767	E2768			G2772	L2773	C2774	P2775	L2776	G2777	E2778	F2779	L2780	V2781	N2782	N2783	E2784	D2785	G2786	A2787	H2788	K2789			P2793	L2794	N2795			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25315	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.1	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	35714	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	428.99997, 428.99997, 428.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.43, 1.43, 1.43	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	0.71	4/12490 (0.0%)	1.04	52/17349 (0.3%)
1	B	0.71	4/12490 (0.0%)	1.04	54/17349 (0.3%)
All	All	0.71	8/24980 (0.0%)	1.04	106/34698 (0.3%)

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	53
1	B	0	53
All	All	0	106

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1650	ASN	CA-C	-8.96	1.40	1.52
1	A	1650	ASN	CA-C	-8.92	1.40	1.52
1	B	2169	LEU	N-CA	-5.38	1.40	1.46
1	A	2169	LEU	N-CA	-5.29	1.40	1.46
1	B	3028	VAL	C-O	-5.09	1.18	1.24

The worst 5 of 106 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1053	ASP	CA-C-N	-20.39	97.81	119.83
1	A	1053	ASP	C-N-CA	-20.39	97.81	119.83
1	B	1053	ASP	CA-C-N	-20.38	97.82	119.83
1	B	1053	ASP	C-N-CA	-20.38	97.82	119.83
1	B	1353	GLU	CA-C-N	19.84	144.63	119.84

There are no chirality outliers.

5 of 106 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1001	LEU	Peptide
1	A	1053	ASP	Peptide
1	A	39	THR	Peptide
1	A	497	SER	Peptide
1	A	646	SER	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	12537	0	5446	1290	0
1	B	12537	0	5446	1289	0
All	All	25074	0	10892	2578	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 72.

The worst 5 of 2578 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:B:2095:LEU:O	1:B:2099:HIS:N	1.93	1.02
1:B:3013:LEU:O	1:B:3017:LEU:N	1.92	1.02
1:A:2068:LEU:O	1:A:2072:GLY:N	1.93	1.01
1:A:3013:LEU:O	1:A:3017:LEU:N	1.92	1.01
1:A:1955:LEU:O	1:A:1959:GLU:N	1.94	1.01

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	2435/3066 (79%)	2231 (92%)	197 (8%)	7 (0%)	36	72
1	B	2435/3066 (79%)	2232 (92%)	196 (8%)	7 (0%)	36	72
All	All	4870/6132 (79%)	4463 (92%)	393 (8%)	14 (0%)	37	72

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1367	ASP
1	A	1376	PRO
1	A	1378	PRO
1	B	1367	ASP
1	B	1376	PRO

5.3.2 Protein sidechains [i](#)

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

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3
1	B	3

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	305:SER	C	306:THR	N	6.20
1	B	305:SER	C	306:THR	N	6.20
1	A	163:GLN	C	164:TRP	N	3.12
1	B	163:GLN	C	164:TRP	N	3.12
1	A	1394:SER	C	1395:ASN	N	2.99

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3669. These allow visual inspection of the internal detail of the map and identification of artifacts.

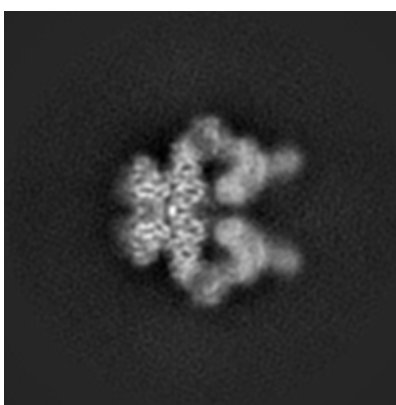
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

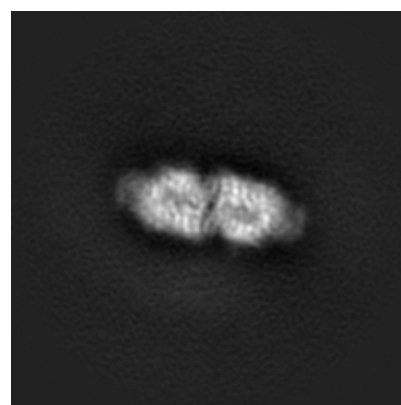
6.1.1 Primary map



X



Y

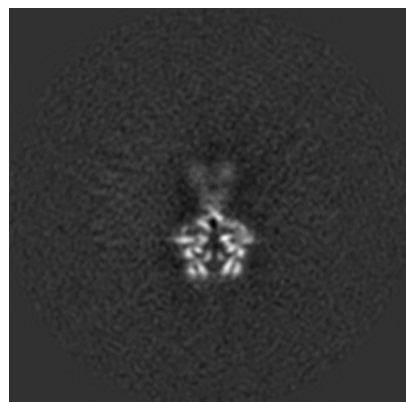


Z

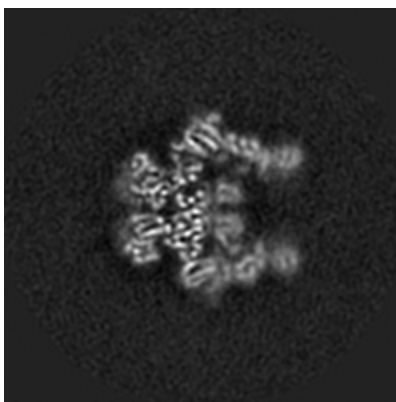
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

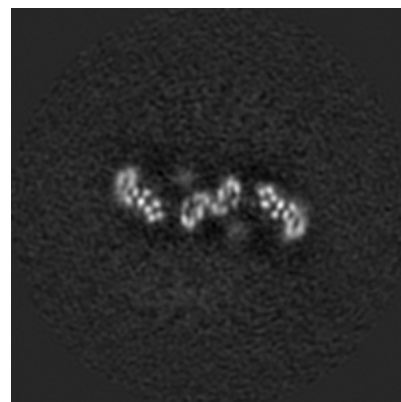
6.2.1 Primary map



X Index: 150



Y Index: 150

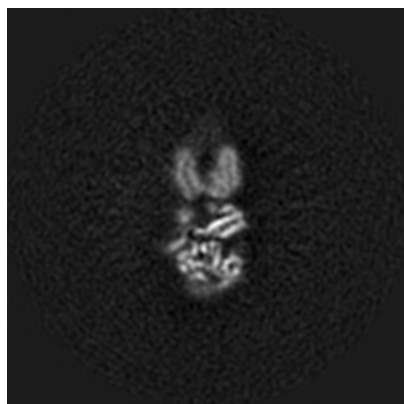


Z Index: 150

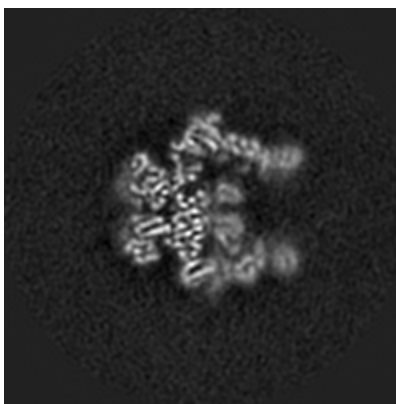
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

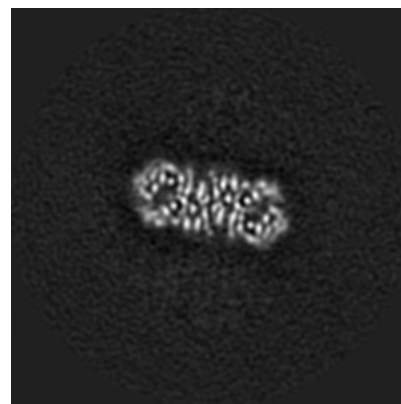
6.3.1 Primary map



X Index: 168



Y Index: 149

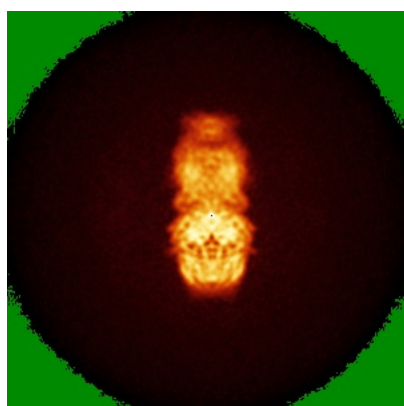


Z Index: 133

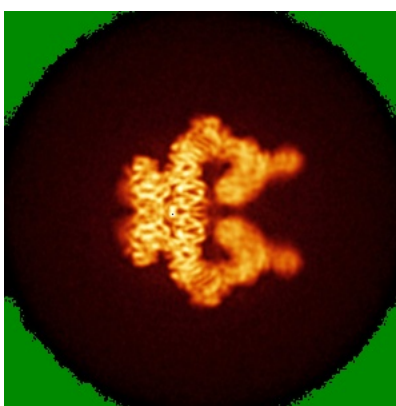
The images above show the largest variance slices of the map in three orthogonal directions.

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

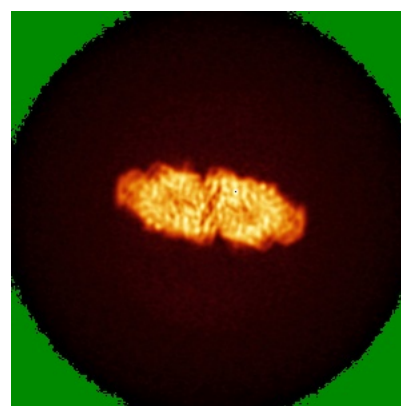
6.4.1 Primary map



X



Y

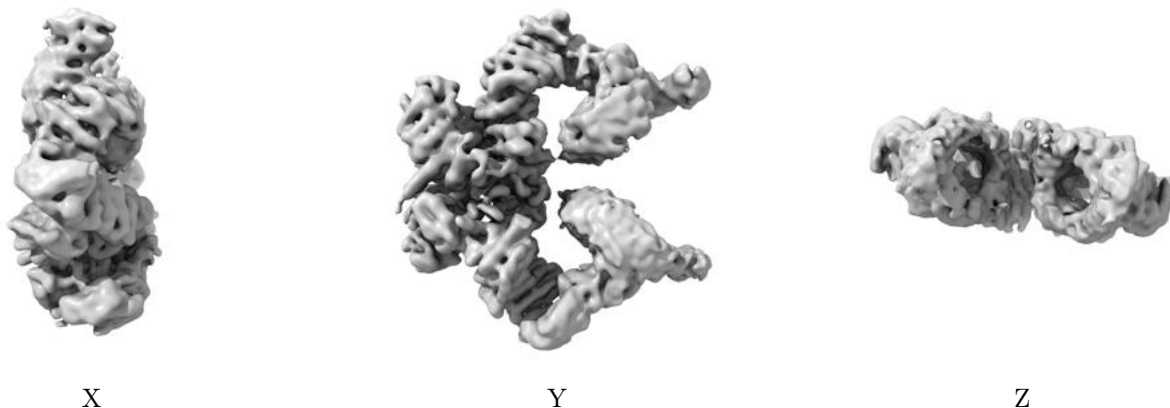


Z

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 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

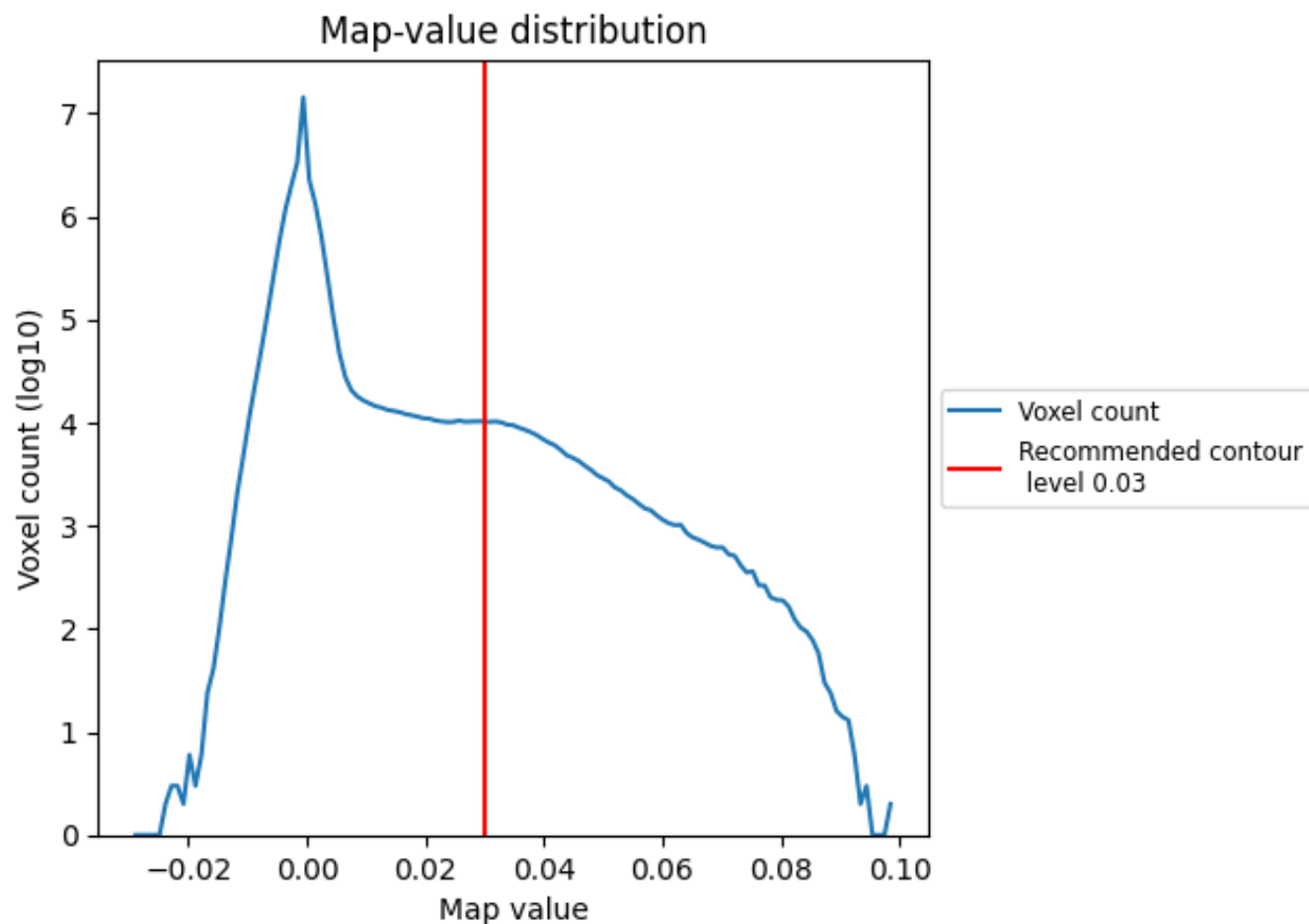
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

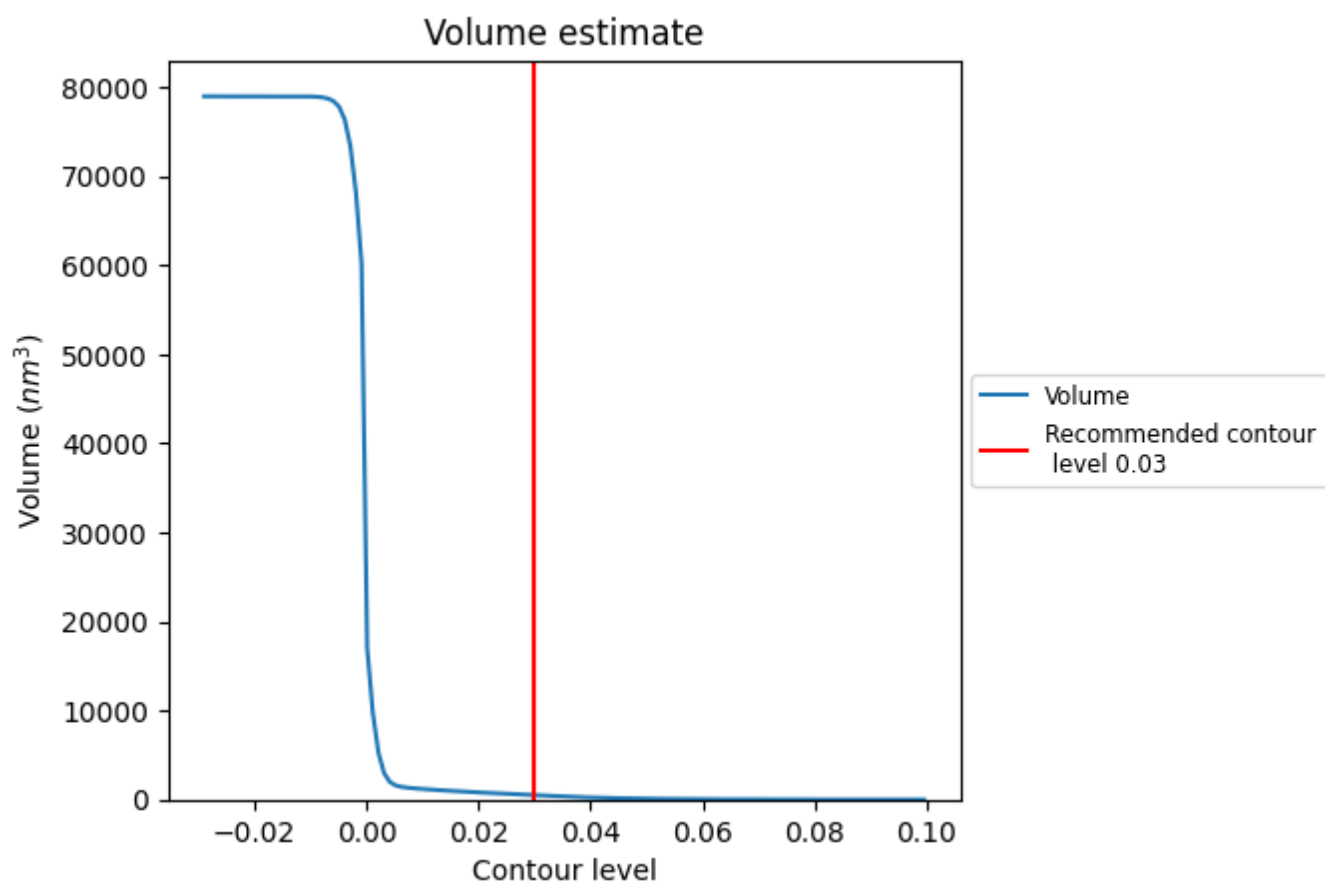
This section contains the results of statistical analysis of the map.

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.

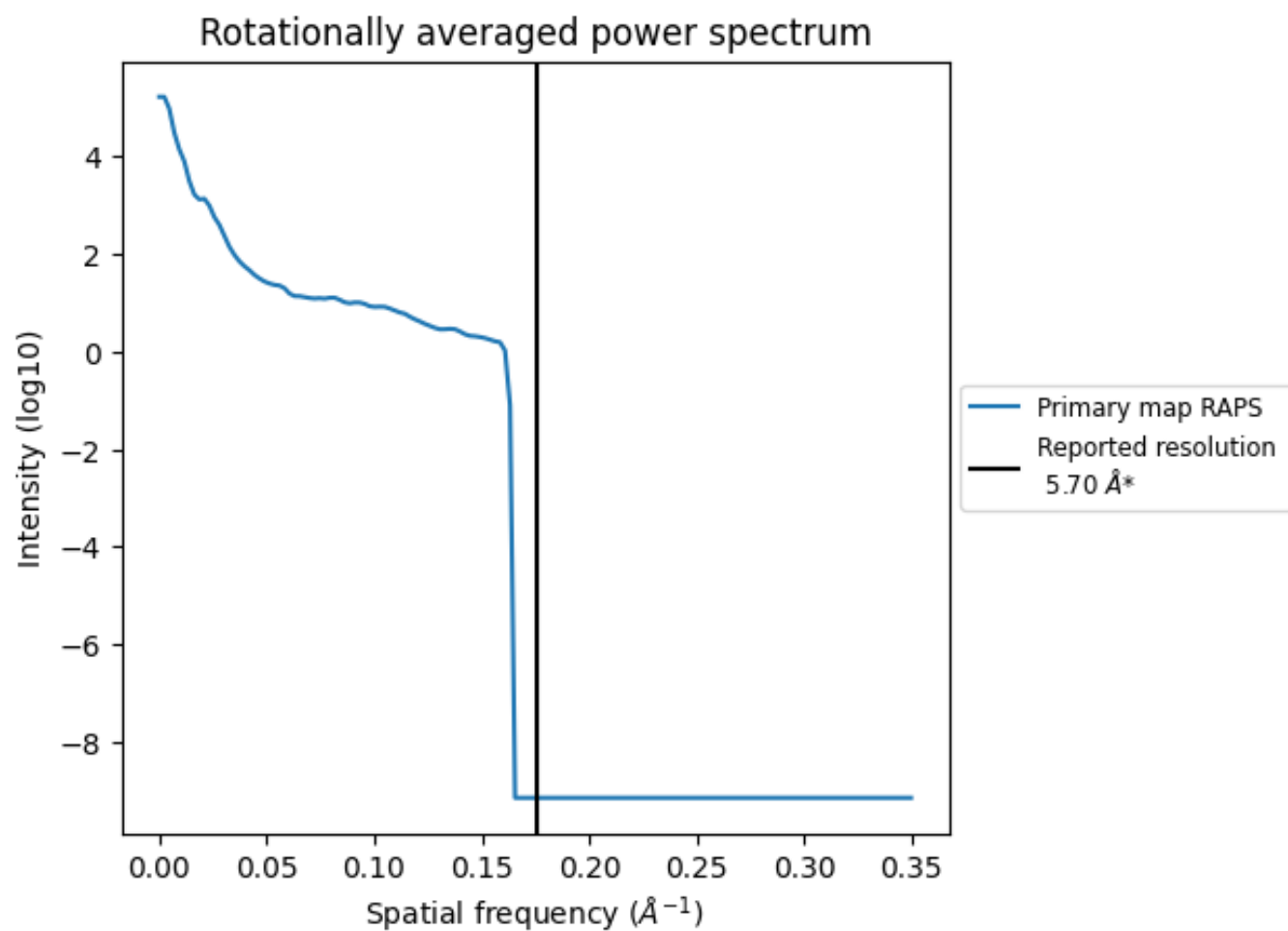
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 502 nm^3 ; this corresponds to an approximate mass of 454 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 ⓘ

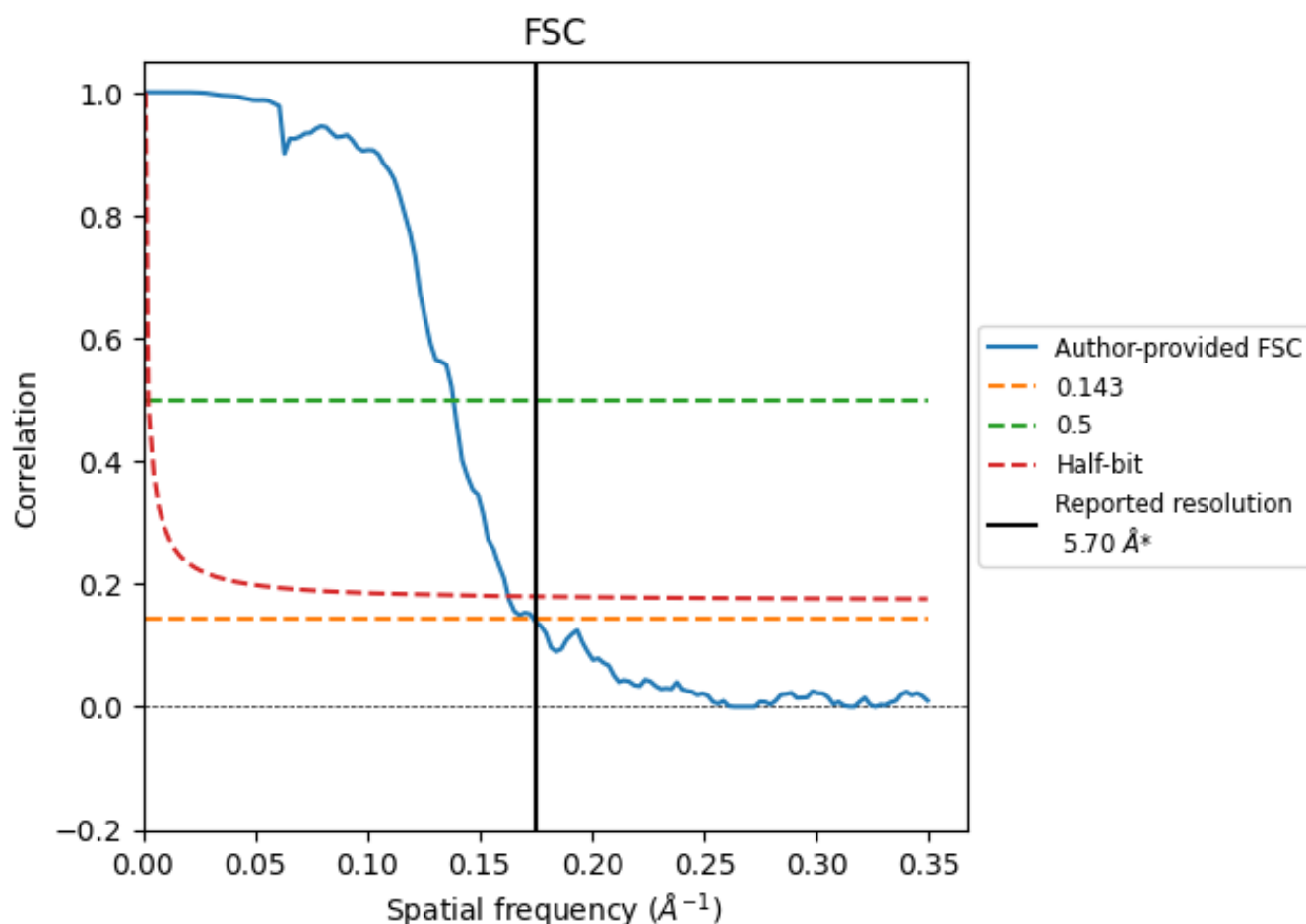


*Reported resolution corresponds to spatial frequency of 0.175 Å⁻¹

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 0.175 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.70	-	-
Author-provided FSC curve	5.75	7.23	6.14
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

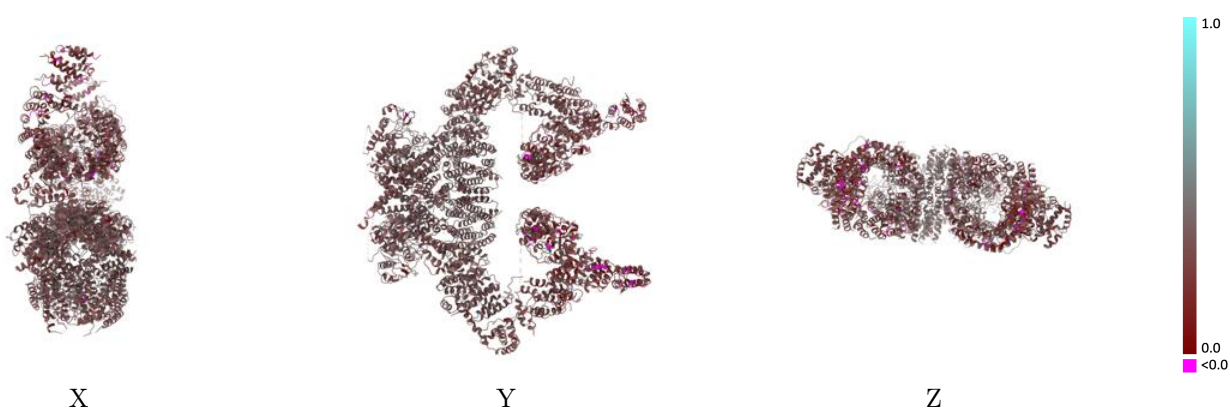
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3669 and PDB model 5NP0. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

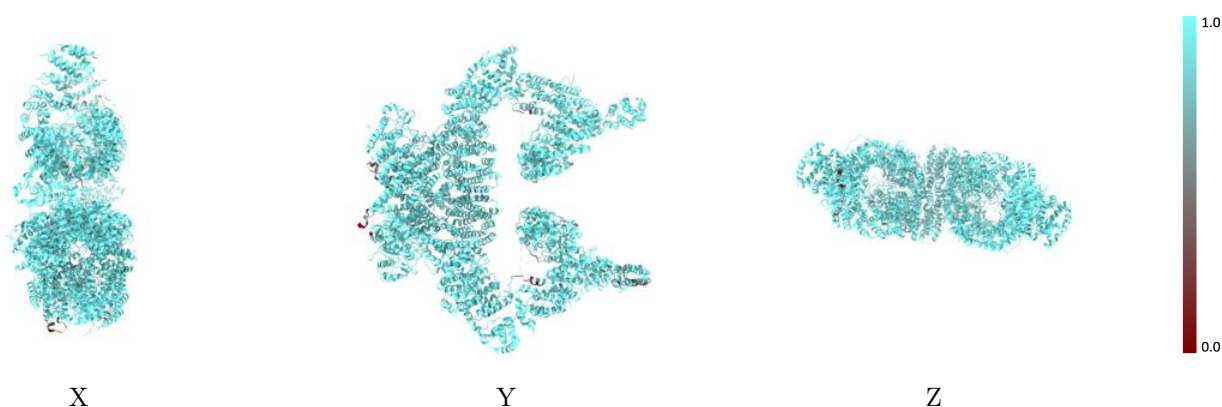
This section was not generated.

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



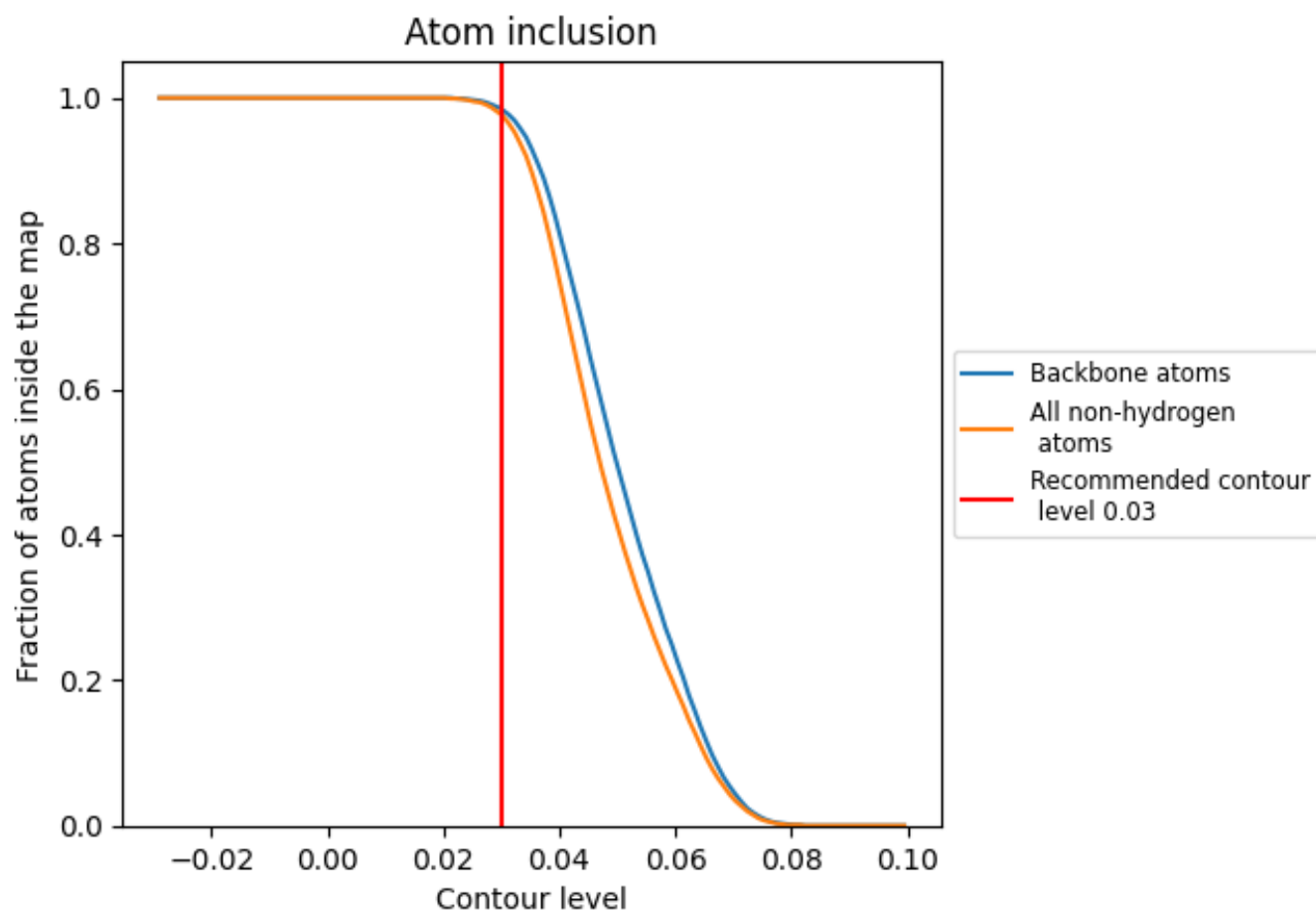
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9770	0.3140
A	0.9690	0.3110
B	0.9850	0.3160

