



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 08:09 AM UTC

PDB ID : 3DG2 / pdb_00003dg2
EMDB ID : EMD-1056
Title : Coordinates of 16S and 23S rRNAs fitted into the cryo-EM map of a pre-translocation complex
Authors : Gao, H.; LeBarron, J.; Frank, J.
Deposited on : 2008-06-12
Resolution : 10.00 Å (reported)
Based on initial models : 2AVY, 2AW4

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

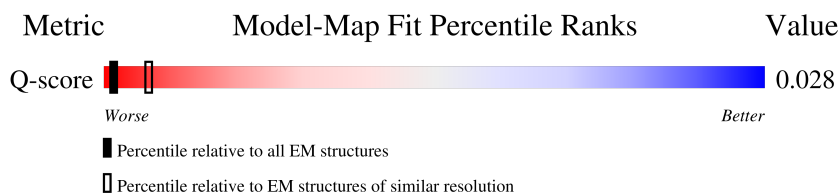
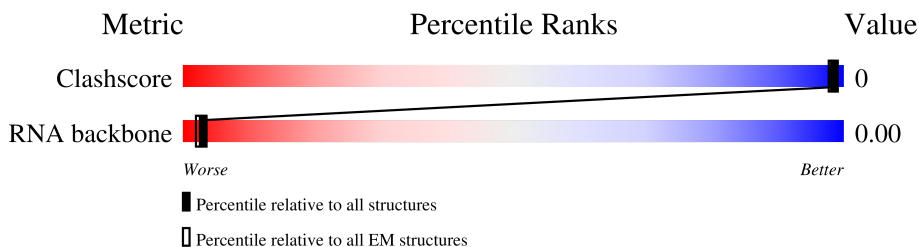
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.00 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	257 (8.50 - 9.50)

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	1542	35% 99% .
2	B	2904	43% 98% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4371 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 RNA chain called 16S Ribosomal RNA from E. coli.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A	1530	Total	P	0	1530
			1530	1530		

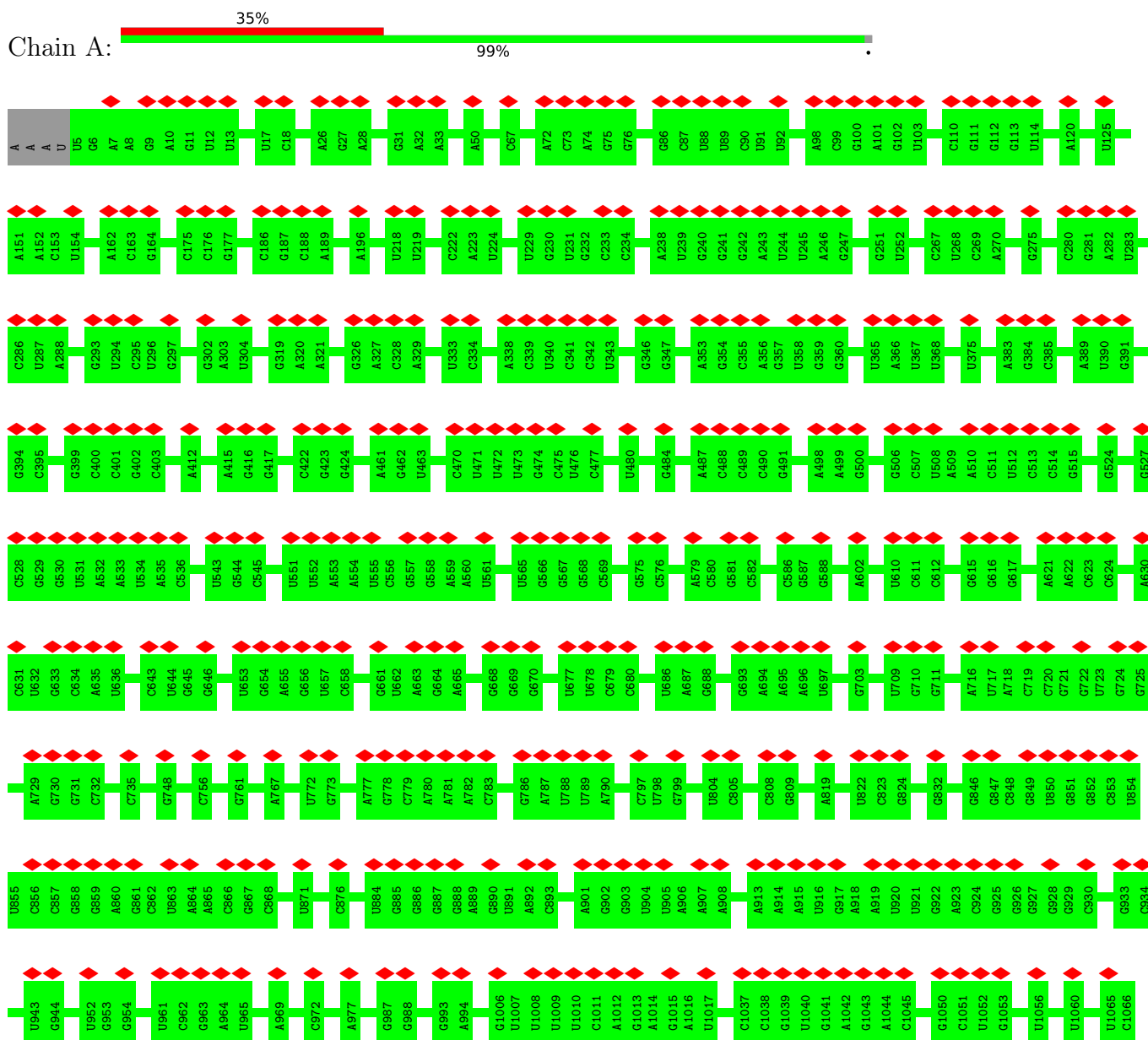
- Molecule 2 is a RNA chain called 23S Ribosomal RNA from E. coli.

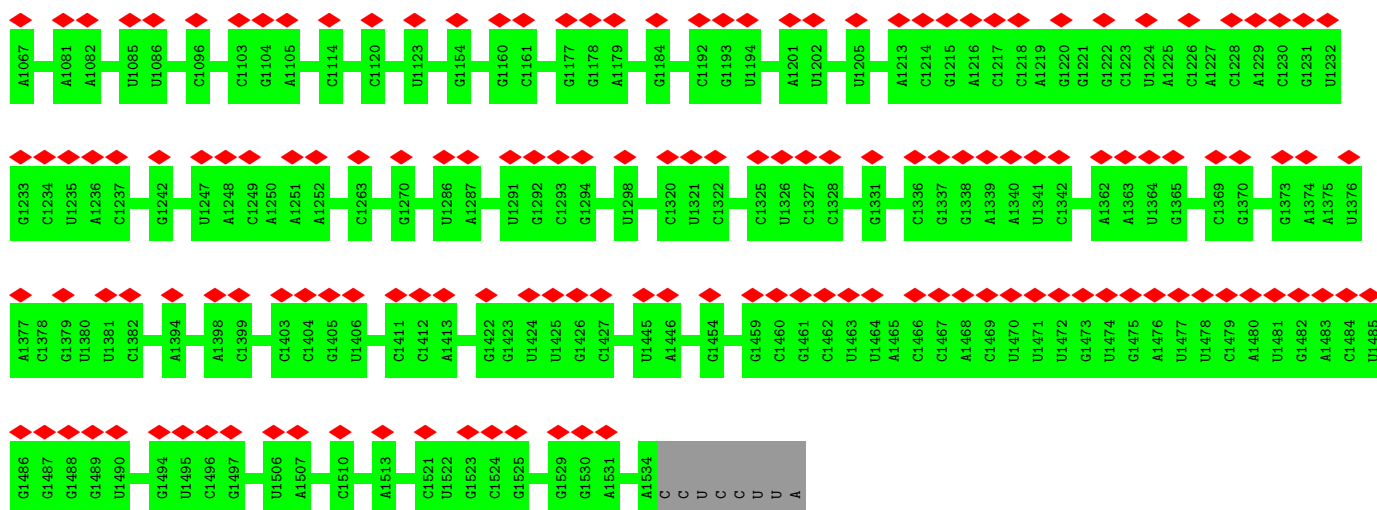
Mol	Chain	Residues	Atoms		AltConf	Trace
2	B	2841	Total	P	0	2841
			2841	2841		

3 Residue-property plots

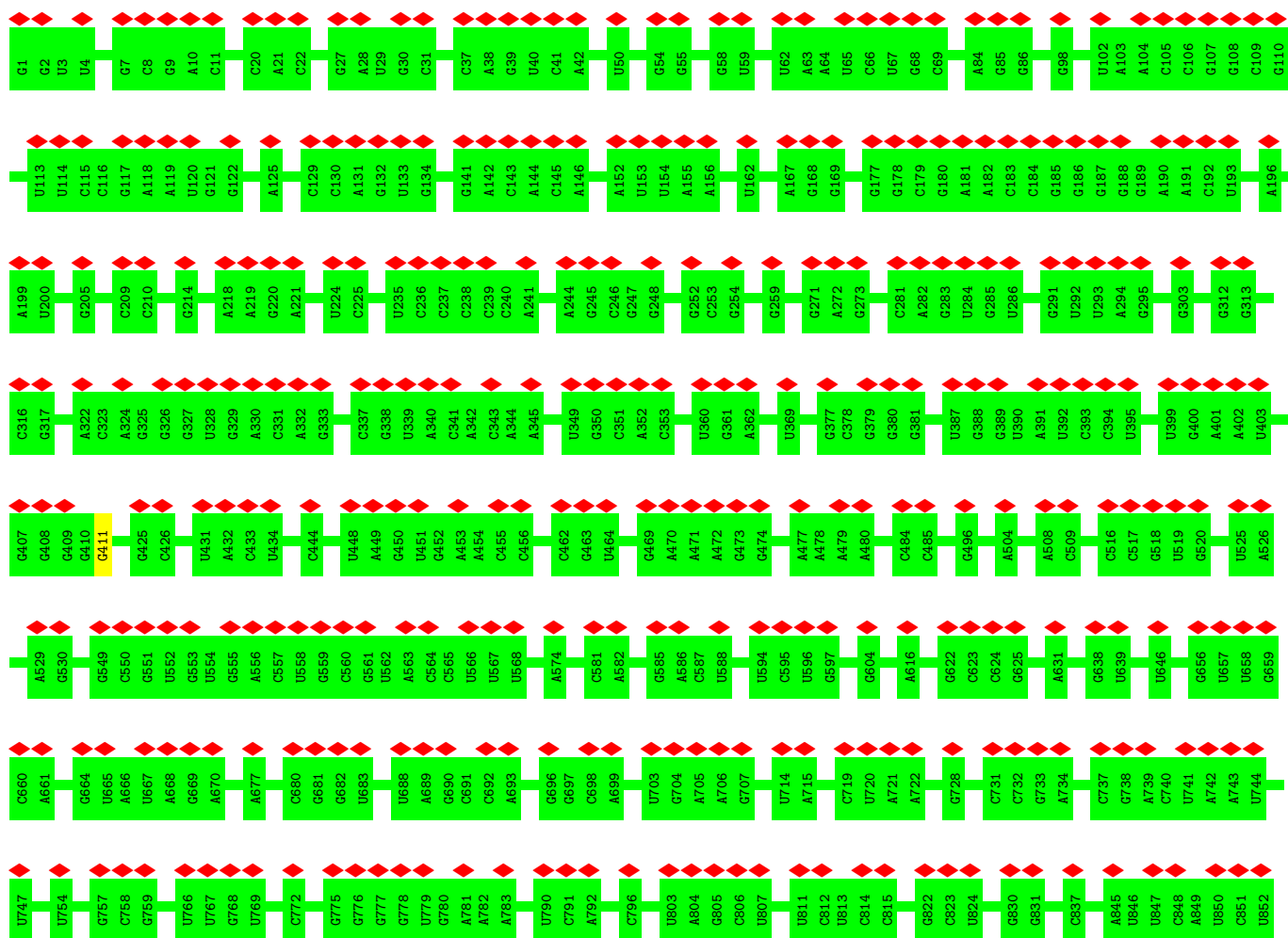
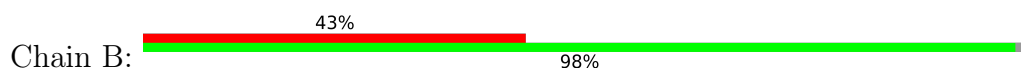
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 16S Ribosomal RNA from E. coli





• Molecule 2: 23S Ribosomal RNA from E. coli



A2059	A2060	G2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	G2069	A2070	A2071	C2072	C2073	U2074	U2075	U2076	A2077	G2078	U2079	A2080	U2081	U2085	U2086	G2087	A2088	C2089	A2090	G2093	A2094	A2095	C2096	A2097	U2098	U2099	G2100	A2101	G2102	C2103	U2106	G2107	G2110	U	G	U	G	A	A	G	U	A	U	A	G	C																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
C1958	G1959	A1960	U1963	G1964	C1965	A1966	C1967	A1970	G1975	U1976	A1977	C1985	C1986	A1987	G1988	G1989	C1996	G2004	A2005	C2006	U2007	C2008	A2009	G2012	U2017	G2018	C2023	G2024	C2025	U2026	G2027	U2028	G2029	A2030	A2033	U2034	G2035	C2044	C2045	G2046	C2047	G2048	G2049	C2050	G2053	A2054																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
C1874	A1877	G1878	C1879	G1884	A1885	U1886	C1887	G1888	A1889	A1890	C1893	C1894	C1895	U1896	U1897	U1898	A1899	A1900	A1901	C1909	G1910	U1911	A1912	A1913	C1914	U1915	A1916	U1917	G1921	G1922	U1926	G1929	G1930	U1931	A1932	G1933	C1934	G1935	U1943	U1946	C1947	G1948	G1949	G1950	A1953	G1954	U1955	U1956	C1957																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
G1770	C1771	A1772	A1773	A1784	A1785	A1786	A1787	C1788	A1794	C1795	U1796	G1797	U1798	G1799	C1800	A1801	C1804	A1805	C1806	G1807	A1808	A1809	A1810	G1811	U1812	U1820	A1821	G1826	A1829	C1830	G1831	C1832	C1833	U1834	G1835	C1838	G1839	G1840	U1841	G1842	C1843	G1850	U1851	U1859	G1860	G1861	G1862	G1863	G1873																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
U1680	G1681	U1682	U1683	G1684	C1685	G1686	G1687	U1688	A1689	A1690	C1691	U1692	G1695	G1702	G1703	C1706	G1707	C1708	U1709	A1713	G1718	G1719	U1720	G1721	G1731	C1732	G1733	G1734	A1735	U1736	G1737	G1738	A1739	G1740	A1745	A1746	U1747	C1748	A1749	G1842	C1843	G1850	U1851	U1859	G1860	G1861	G1862	G1863	G1873																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
C1592	A1593	A1597	A1598	G1601	U1602	A1603	A1608	A1609	C1612	G1613	A1618	G1619	G1620	G1623	U1624	C1625	A1626	G1627	G1628	U1629	A1632	U1636	G1645	G1646	U1647	U1648	G1649	A1650	A1654	A1655	C1656	G1659	G1660	G1661	U1662	G1663	G1666	G1667	A1668	A1669	G1673	G1674	C1675	A1676	A1677																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											

G	A2211	G2286	G2399	U2491	U2584	U2698	G2812
G	A2212	A2287	G2400	U2492	U2585	C2704	A2813
A	U2213	A2288	U2401	U2493	U2586	A2705	A2814
G	C2214	G2289	U2402	G2494	A2587	A2706	C2815
C	C2215		A2407	G2495	A2588	U2707	G2816
U	G2216	C2295	U2296	C2496	A2589	G2708	U2817
U	G2217	U2297	A2297	A2497	A2590	G2709	
	G2218	U2298	U2299	C2498	C2591	G2710	A2823
		G2221	U2299	U2504	U2592	A2711	G2828
	G2138	G2222	G2413	U2505	U2593	C2712	A2829
	U2139	G2223	G2414	U2506	U2594	U2713	
	G2140	G2224	G2415		C2595		A2835
	G2141	G2225	C2417		U2596	G2716	U2836
	A2142	C2226	A2418	C2510	G2597	C2717	A2837
		A2227	U2419	U2511		G2718	
	G2146	G2228	C2420	U2512	A2602	G2719	G2840
	A2147	G2229	C2421	U2513	G2603	U2720	C2841
	G2148	U2230	C2422	U2514	U2604	A2721	
			U2423		U2605		G2844
	G2156	G2235	A2426	U2519	C2606	U2724	
	C2157	U2236		C2520		A2725	G2848
	A	U2237	A2433	C2521	U2609	A2726	
	G	G2238	A2434	U2522	C2610	A2727	
	C	G2239	A2435	G2523		U2728	A2851
	G	U2240	G2436	U2524	U2613	G2729	G2852
	A	A2241	G2437	G2525	G2621	C2730	C2853
	C		U2438	A2530	U2622	G2731	
	C		U2439		G2623	G2732	C2863
	U	U2245	C2440	G2535	G2630	A2733	
	U	G2246	U2441	U2536	G2631	A2734	G2875
	A		C2442	U2537	A2632	G2735	A2886
	A	G2251	C2443	C2538	G2633	A2736	
	A			G2544	A2634	U2741	C2889
	U	C2254	U2449	U2553	A2635	G2742	G2890
	A	G2255	A2451	G2554	G2636	U2743	U2891
	C	G2256	A2452	G2555	U2637	G2744	G2892
	C	U2257	A2453		G2638	C2745	
	A	C2258	G2454	C2558	A2639	U2753	C2901
	C		A2356	C2559	U2640	U2754	C2902
			G2357	A2560	G2641	C2755	U2903
		C2264	A2358	U2561	U2642		U
				U2562	C2649	G2763	
		A2267	C2362	U2563	U2650	A2764	
		A2268	C2363	A2564	C2651	C2773	
		G2269	C2364	A2565			G2777
		A2270	G2365	A2566	C2676	G2778	
		G2271	G2366	A2567	G2677	U2779	
		U2272	G2367	U2568	C2678	G2780	
		A2273	C2368	U2569	G2685		A2800
		A2274	A2376	G2570	G2686		G2801
		C2275		U2571			G2802
		G2276	U2387	G2470			G2803
		G2277	A2388	A2471			U2804
		A2278	G2389	G2472			C2805
		G2279	U2390	U2473			
		A2281	G2391	U2474			
		G2282	U2392	G2481			
		C2283	A2392	G2484			
		A2284		G2487			
		C2285					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52181	Depositor
Resolution determination method	Not provided	
CTF correction method	CTF correction of 3D map	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	49696	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	250.773	Depositor
Minimum map value	-142.587	Depositor
Average map value	1.513	Depositor
Map value standard deviation	24.331	Depositor
Recommended contour level	43.4	Depositor
Map size ($\text{\AA}$)	366.6, 366.6, 366.6	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	2.82, 2.82, 2.82	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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1530	0	0	0	0
2	B	2841	0	0	1	0
All	All	4371	0	0	1	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 0.

All (1) 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)
2:B:411:G:P	2:B:2407:A:P	2.88	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	0/1542	-	-
2	B	0/2904	-	-
All	All	0/4446	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 [i](#)

There are no chain breaks in this entry.

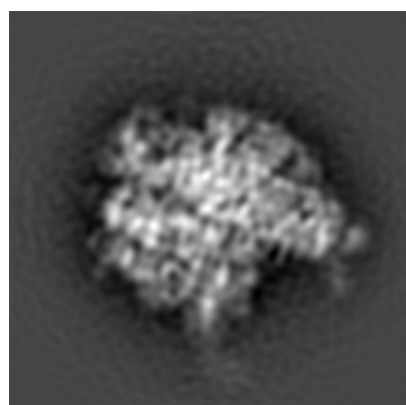
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1056. These allow visual inspection of the internal detail of the map and identification of artifacts.

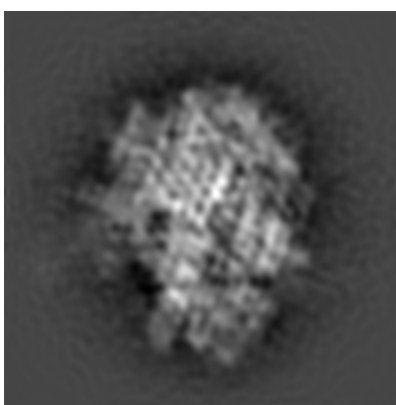
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

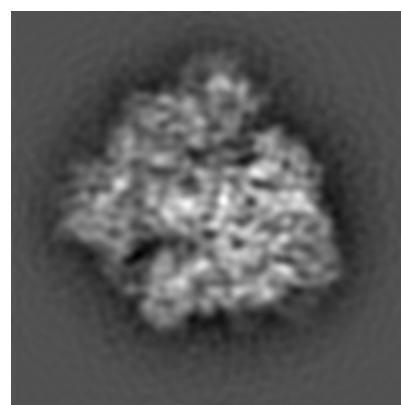
6.1.1 Primary map



X



Y

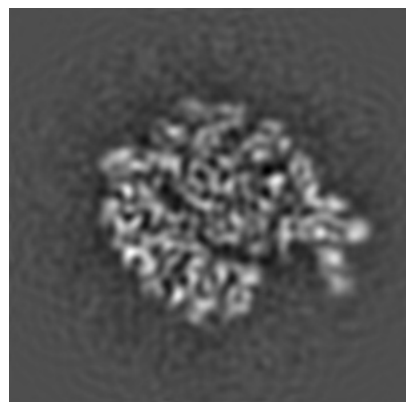


Z

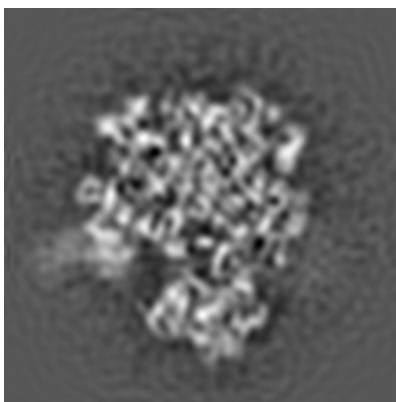
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

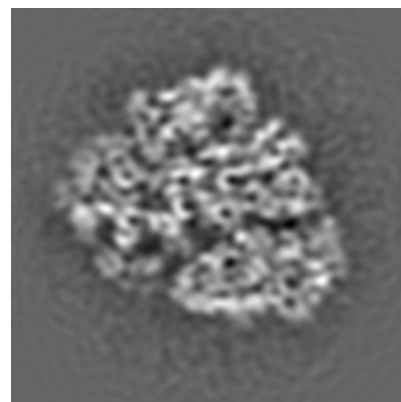
6.2.1 Primary map



X Index: 65



Y Index: 65

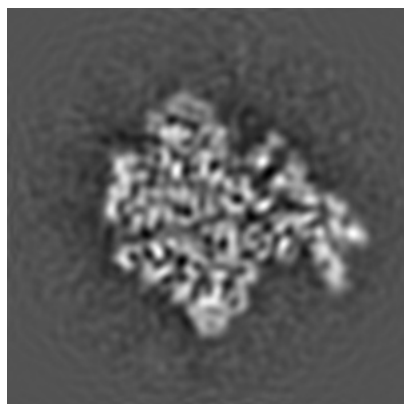


Z Index: 65

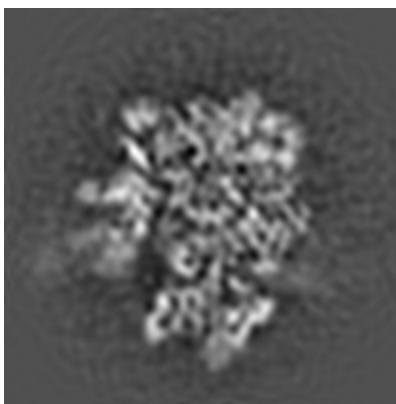
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

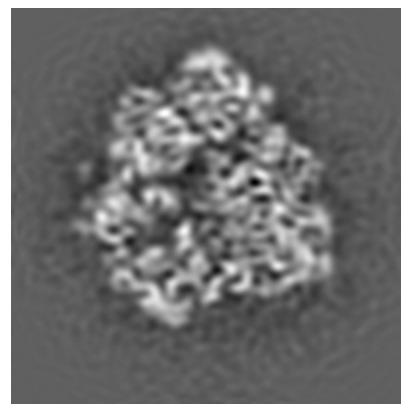
6.3.1 Primary map



X Index: 68



Y Index: 68

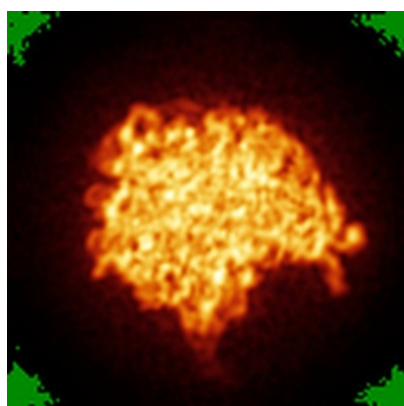


Z Index: 58

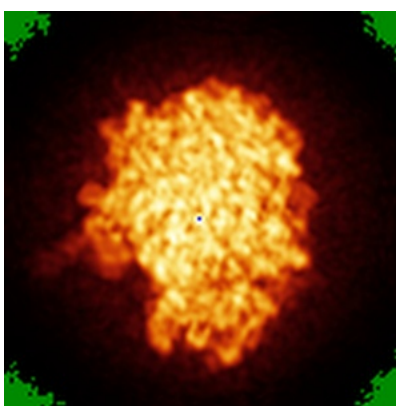
The images above show the largest variance slices of the map in three orthogonal directions.

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

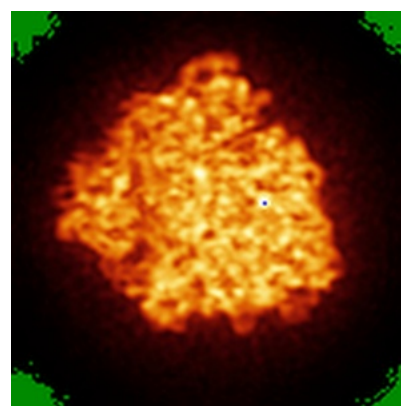
6.4.1 Primary map



X



Y

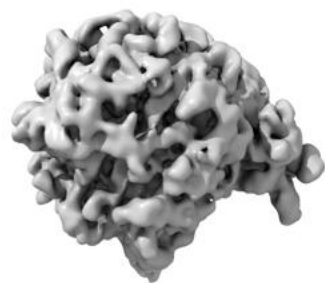


Z

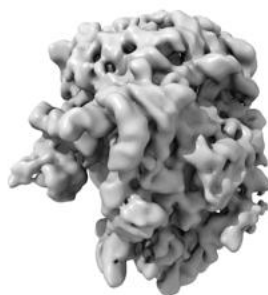
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

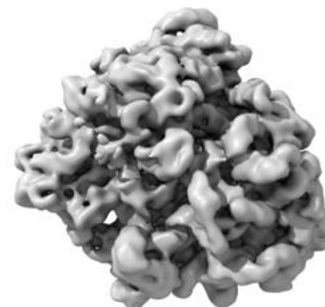
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 43.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

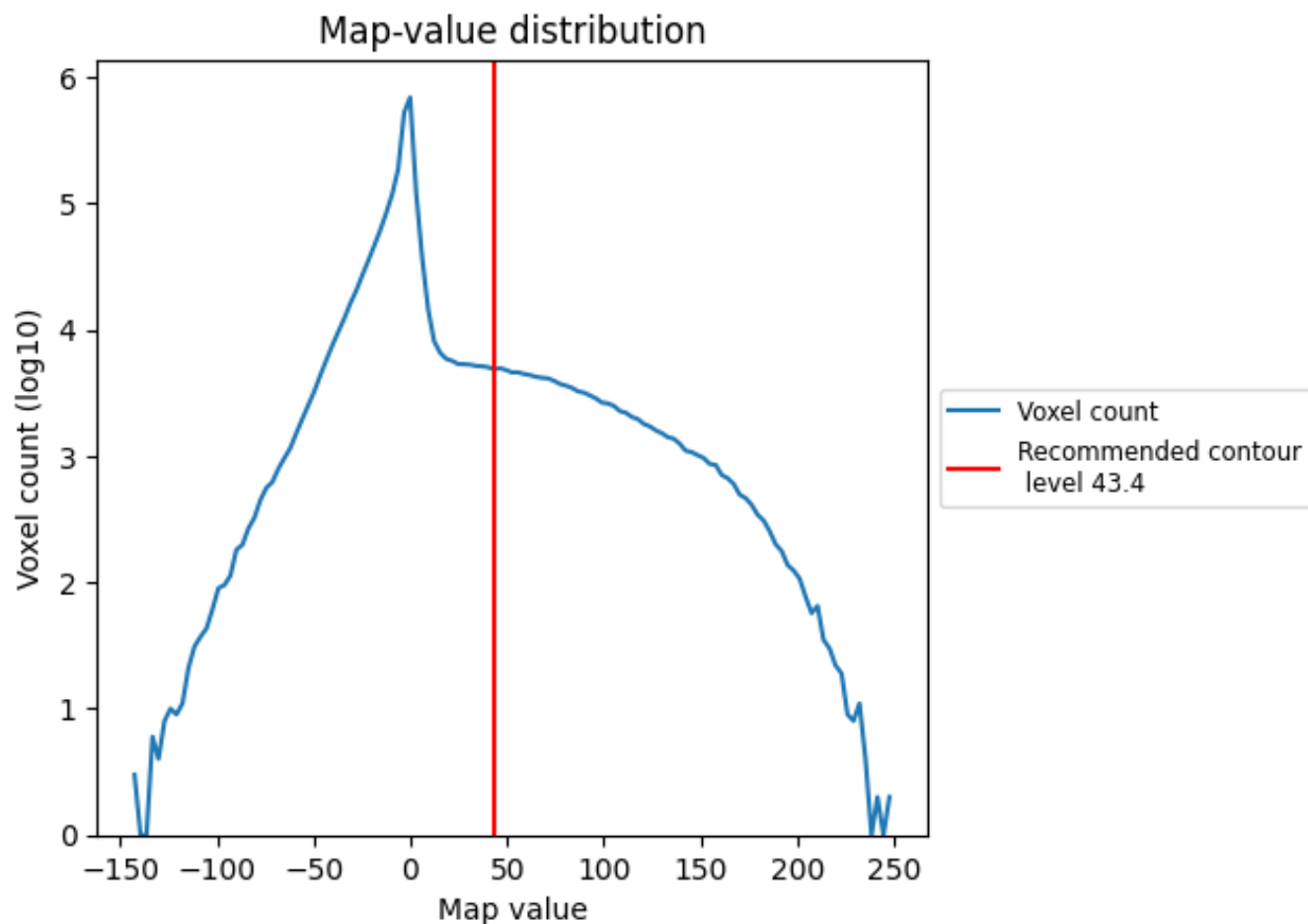
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

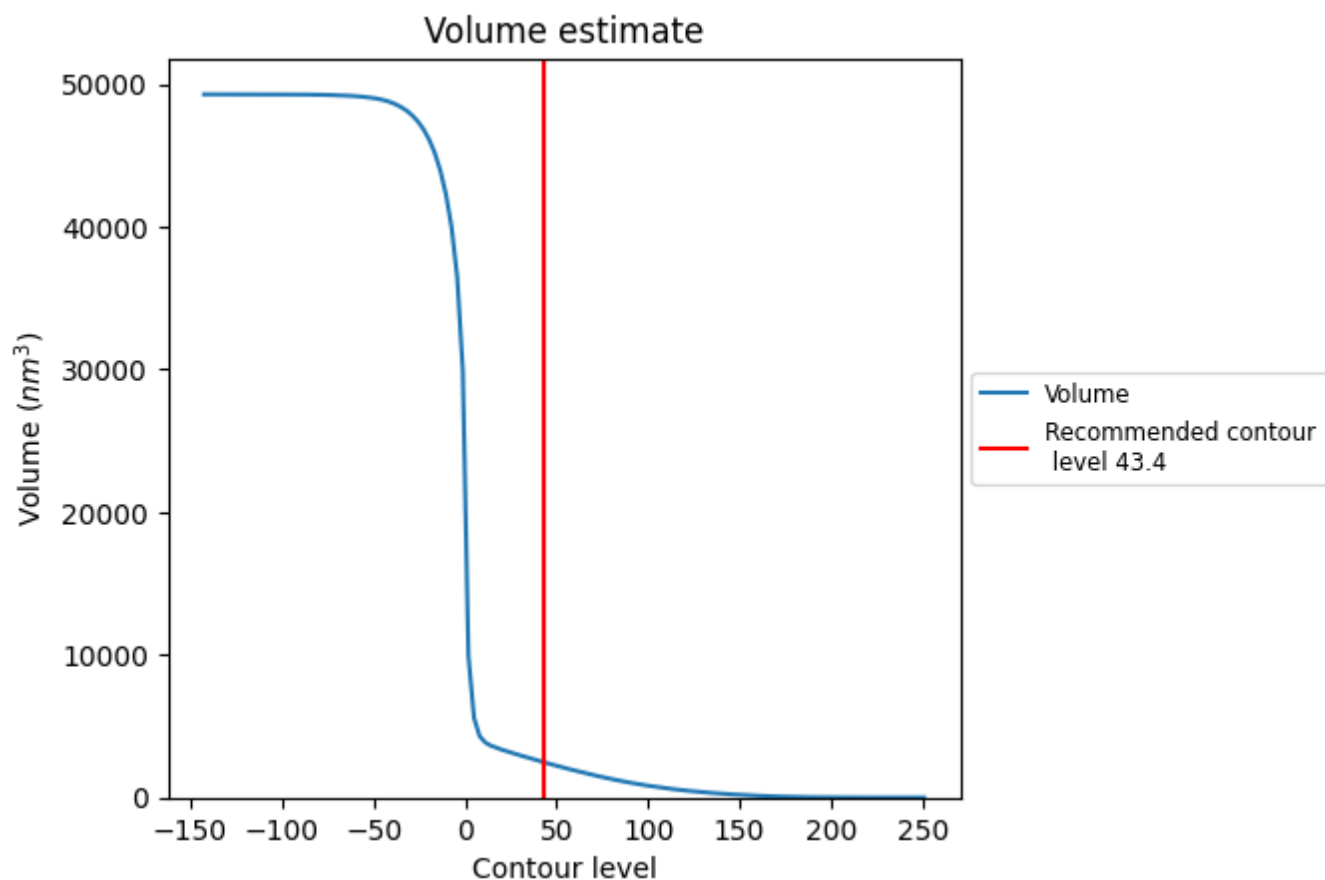
This section contains the results of statistical analysis of the map.

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.

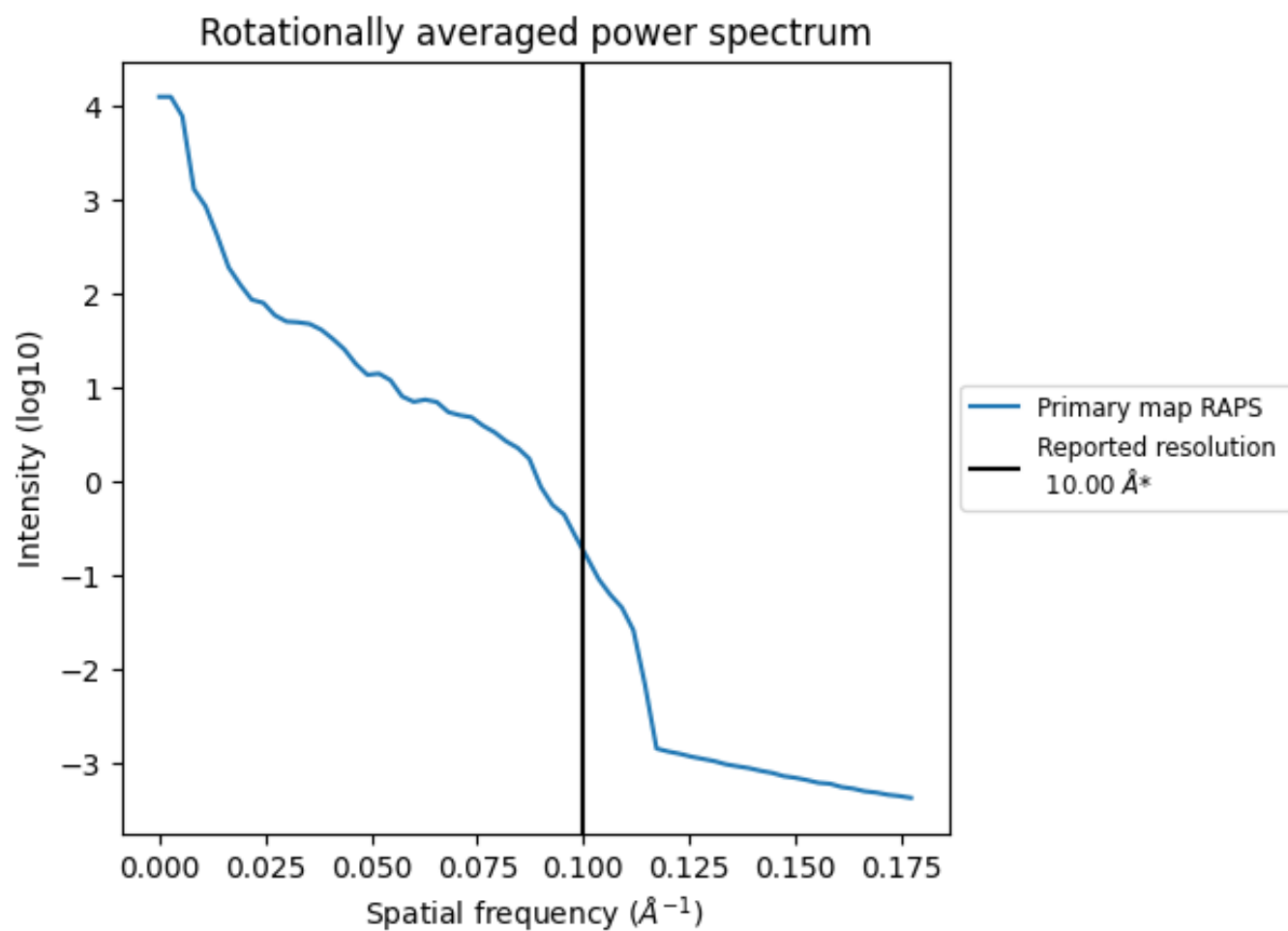
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2462 nm³; this corresponds to an approximate mass of 2224 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 0.100 Å⁻¹

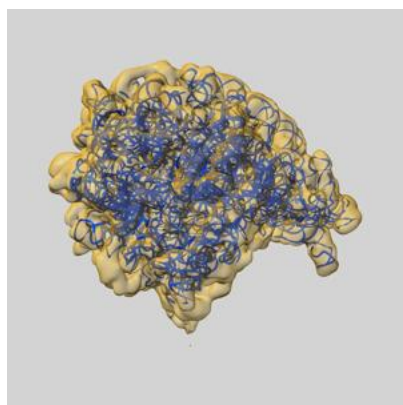
8 Fourier-Shell correlation

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

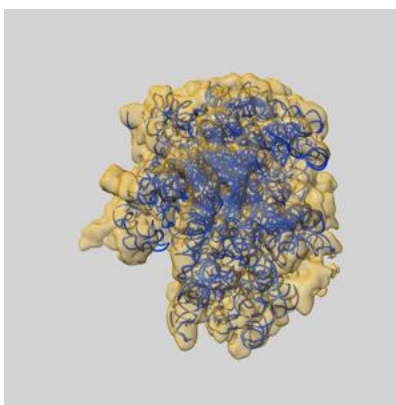
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1056 and PDB model 3DG2. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

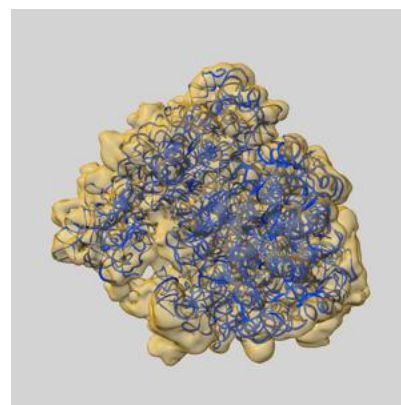
9.1 Map-model overlay [i](#)



X



Y



Z

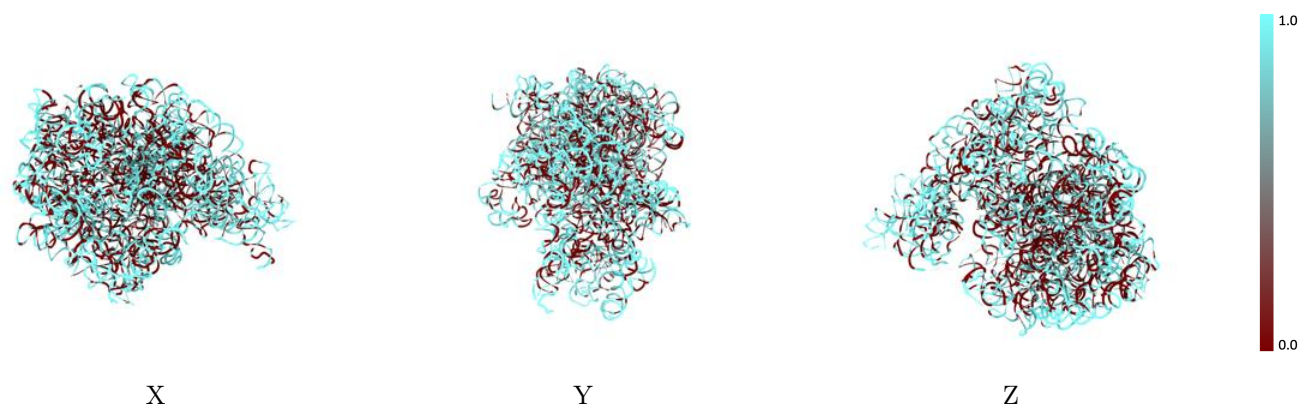
The images above show the 3D surface view of the map at the recommended contour level 43.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



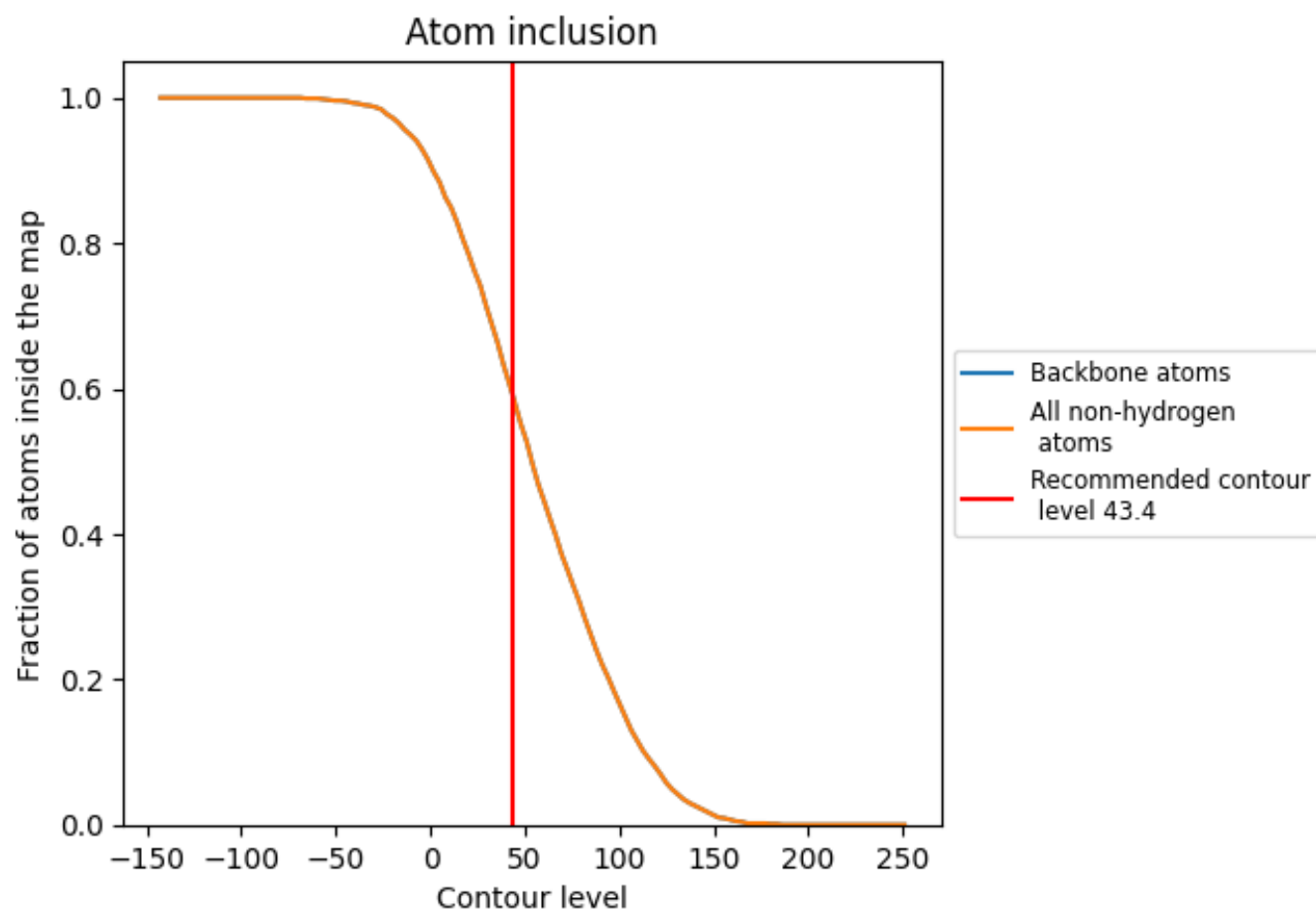
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (43.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 59% 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 (43.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5930	0.0280
A	0.6450	0.0320
B	0.5640	0.0260

