



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:52 PM UTC

PDB ID : 3DG0 / pdb_00003dg0
EMDB ID : EMD-1363
Title : Coordinates of 16S and 23S rRNAs fitted into the cryo-EM map of EF-G-bound translocation complex
Authors : Gao, H.; LeBarron, J.; Frank, J.
Deposited on : 2008-06-12
Resolution : 10.80 Å (reported)
Based on initial models : 2AW4, 2AVY

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

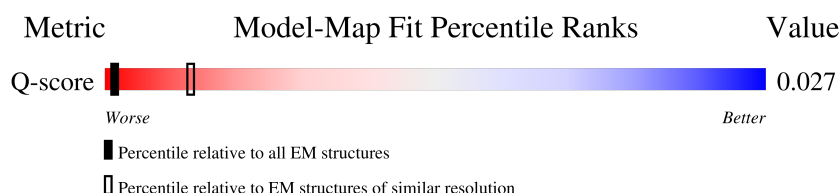
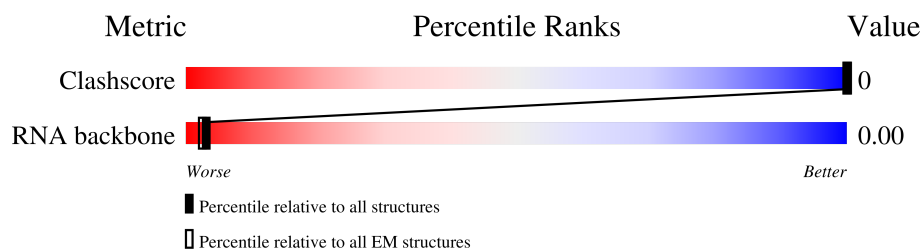
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.80 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	94 (10.40 - 11.40)

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

Mol	Chain	Length	Quality of chain
1	A	1542	
2	B	2904	

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		

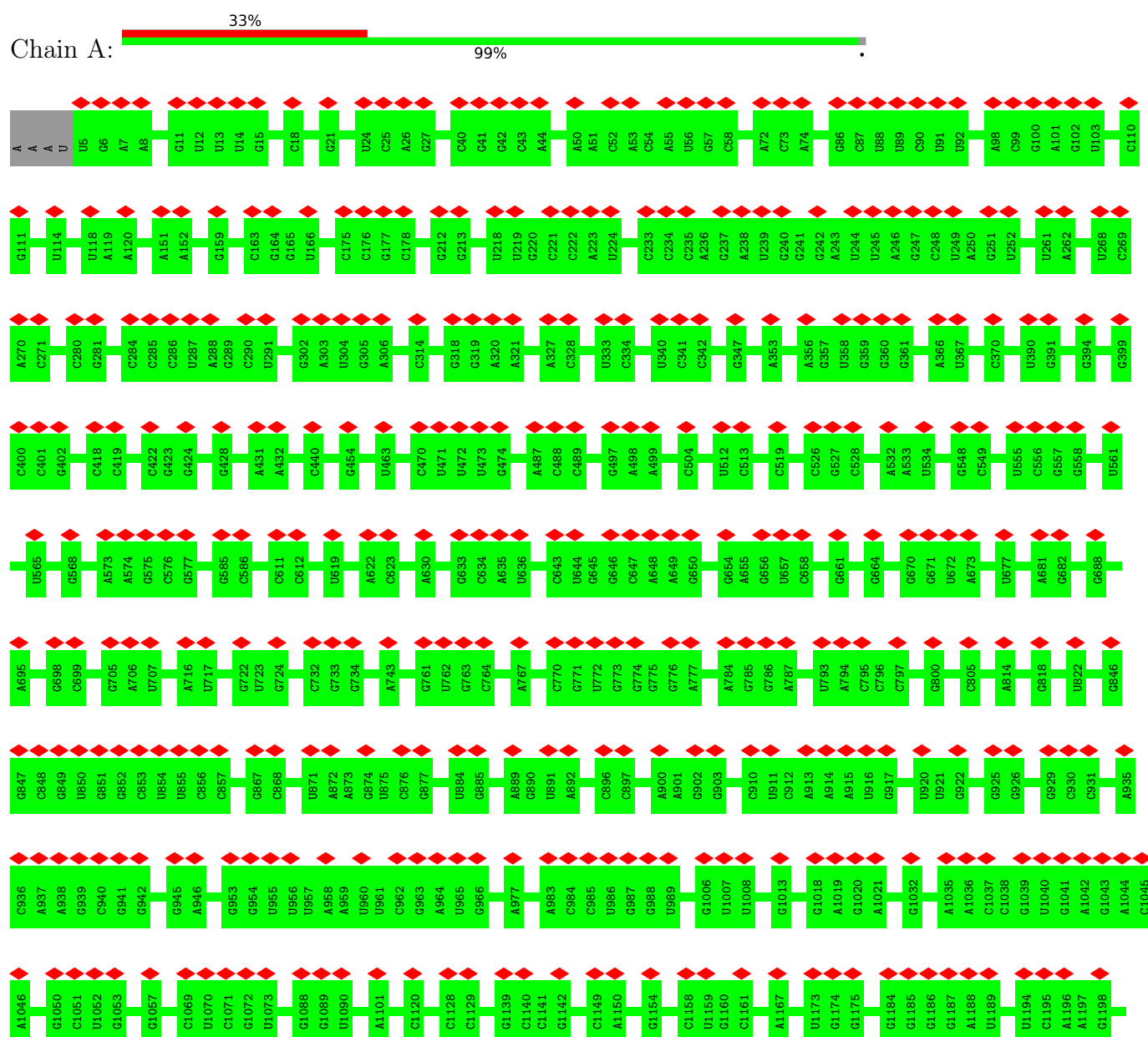
- Molecule 2 is a RNA chain called 23S Ribosomal RNA from E. coli.

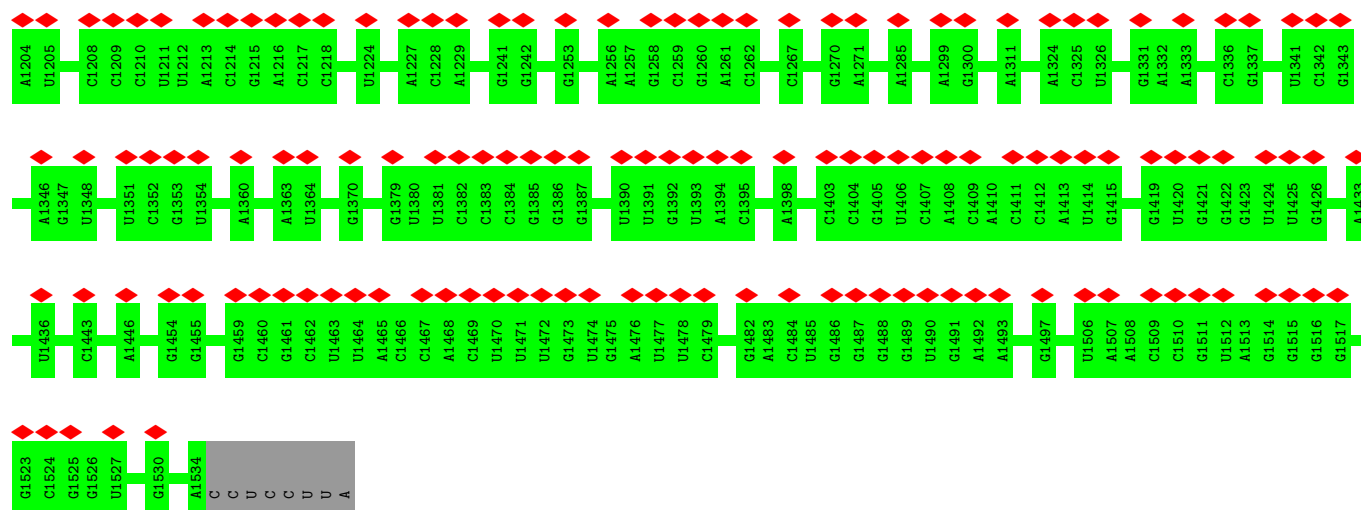
Mol	Chain	Residues	Atoms		AltConf	Trace
2	B	2841	Total	P	0	2841
			2841	2841		

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

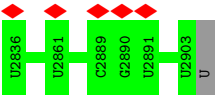




• Molecule 2: 23S Ribosomal RNA from E. coli



G2644	U2650	C2667	G2673	G2677	C2678	A2679	U2684	G2685	U2689	U2690	C2691	U2701	U2707	G2708	G2709	U2713	C2716	C2717	A2721	U2724	A2725	A2726	U2739	G2744	A2757	A2764	A2765	U2768	U2769	C2773	A2776	G2803	U2804	C2805	A2813	A2823													
G2543	G2544	G2545	U2546	A2547	U2548	G2549	G2553	C2556	C2559	A2566	G2567	U2568	G2569	G2582	G2583	U2584	U2585	U2586	A2587	G2595	G2599	A2600	C2601	A2602	G2603	U2604	U2605	C2606	G2607	G2608	U2609	C2610	U2613	A2614	U2615	C2616	U2617	U2622	G2625	G2630	G2631	A2632	A2635	C2636	G2642	G2643			
C2417	G2421	C2422	A2433	A2434	A2435	G2436	G2437	C2440	U2441	C2442	C2443	U2449	A2450	A2451	C2452	G2455	C2462	C2463	G2472	G2481	A2482	C2483	G2484	G2485	C2486	G2487	G2490	U2491	U2492	U2493	G2494	U2505	U2506	C2510	U2511	C2512	U2519	C2520	G2525	G2535	G2536	C2539	C2540						
G2255	G2256	U2257	C2258	A2270	G2271	U2272	A2273	A2274	G2279	G2280	U2296	A2297	A2298	U2299	C2300	C2301	U2302	A2309	A2322	G2323	U2324	G2325	C2326	A2327	G2330	C2338	C2339	A2340	G2341	U2356	G2357	A2358	G2363	C2364	C2380	A2381	C2382	G2383	U2387	G2391	U2402	G2413	G2414	G2415	C2416				
G	A	C	U	U	G	A	A	U	A	C	C2179	U2180	U2181	U2185	G2186	U2187	U2188	U2189	G2190	G2193	U2194	U2195	G2201	A2205	U2213	C2214	C2215	G2216	G2217	G2218	A2227	G2228	U2229	G2230	U2231	C2232	U2233	G2239	U2240	A2241	G2242	U2243	G2246	C2254					
C2078	U2079	A2080	U2081	U2085	U2086	C2103	C2104	U2105	U2106	G2107	A2108	U2109	G2110	U	G	U	A	G	A	G	U	G	G	G	A	C	C	U	U	U	G2133	A2134	G2141	A2142	A2147	G2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A	G	C	C
G1973	C1974	G1975	U1976	A1977	C1978	U1979	G1984	A1987	C1990	U1993	C1996	C1997	A1998	C2001	G2004	G2012	A2020	G2024	G2027	U2028	G2029	A2030	A2033	U2034	G2035	C2045	G2046	C2047	G2048	G2049	C2050	A2059	A2060	G2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	G2069	A2070	C2073					
C1874	G1875	A1876	A1877	G1878	C1879	U1880	C1881	U1882	U1883	G1884	G1888	A1889	A1890	G1891	C1892	C1893	C1894	A1899	A1900	A1901	G1904	C1908	C1909	G1910	U1911	C1914	U1915	A1916	U1917	A1918	U1923	C1924	C1925	U1931	G1935	A1936	A1937	A1938	U1939	U1943	C1957	C1958	G1959	A1960	U1963	G1968			
A1744	A1745	A1746	U1747	A1748	A1749	G1750	U1758	C1761	A1762	G1763	C1764	C1768	U1769	G1770	C1771	A1772	A1773	G1776	U1777	A1787	C1788	A1794	C1795	U1796	C1800	A1801	G1807	A1810	G1811	U1812	U1820	A1821	C1822	G1826	A1829	C1833	U1834	G1835	G1840	U1841	G1849	G1873							
A1608	A1609	G1613	G1619	G1623	U1624	G1627	C1638	C1646	A1650	A1654	A1655	G1659	G1660	G1661	U1662	G1663	A1672	G1673	G1674	C1675	A1676	A1677	U1683	G1684	C1691	U1692	U1693	C1694	G1695	G1699	G1702	G1703	C1706	G1707	C1708	U1720	G1721	C1730	G1733	G1734	A1735								
G1422	G1423	C1428	G1432	A1433	A1434	G1436	U1443	G1464	G1465	U1466	U1467	U1468	A1469	A1470	G1471	G1478	U1481	G1482	A1490	G1500	G1501	A1502	G1516	G1517	C1518	G1537	G1538	U1539	A1551	A1552	A1553	U1554	G1555	C1556	U1559	G1560	C1564	C1565	G1588	U1589	A1590	A1591	C1592						
C1270	U1273	A1274	A1275	A1276	C1289	C1290	C1291	G1292	C1293	U1294	C1295	G1296	C1297	C1298	A1301	A1302	C1315	A1322	C1323	G1324	C1330	G1334	C1335	A1336	G1346	A1347	C1348	C1349	G1355	G1356	C1357	G1361	G1368	G1369	C1370	G1371	U1372	A1378	G1382	U1396	G1418	A1419	A1420	G1421					
G1128	A1129	U1130	A1133	G1136	G1145	G1149	C1150	C1167	U1176	C1177	G1178	G1179	U1180	U1181	U1184	G1185	G1193	A1194	G1195	C1200	G1218	U1219	G1220	A1226	G1227	A1230	U1231	U1240	A1241	U1242	A1247	G1248	U1249	A1253	G1259	A1260	C1261	A1262	U1267										



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	
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	253.154	Depositor
Minimum map value	-116.942	Depositor
Average map value	2.691	Depositor
Map value standard deviation	25.799	Depositor
Recommended contour level	56.8	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	0	0
All	All	4371	0	0	0	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.

There are no clashes within the asymmetric unit.

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.

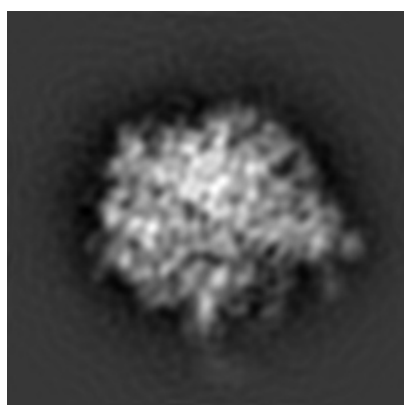
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1363. These allow visual inspection of the internal detail of the map and identification of artifacts.

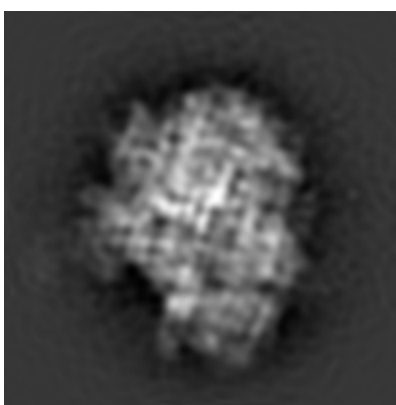
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

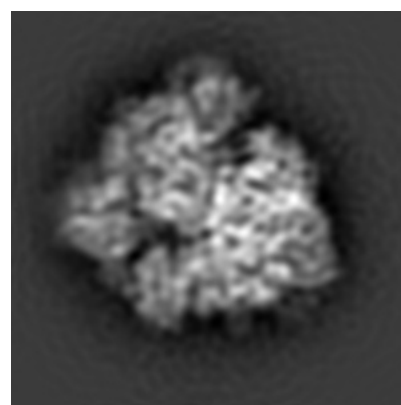
6.1.1 Primary map



X



Y

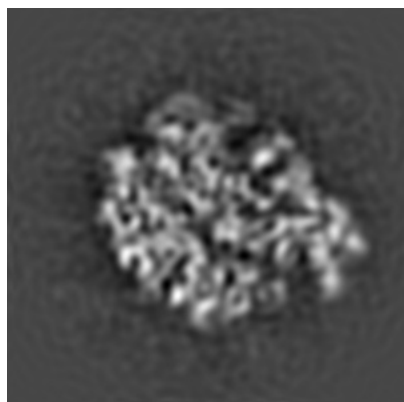


Z

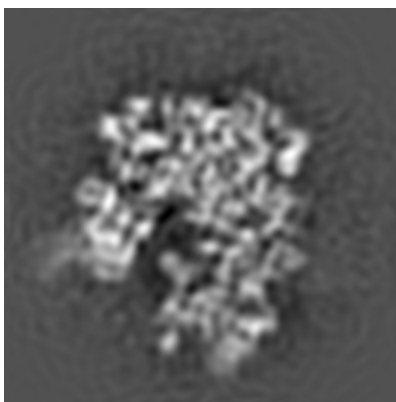
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

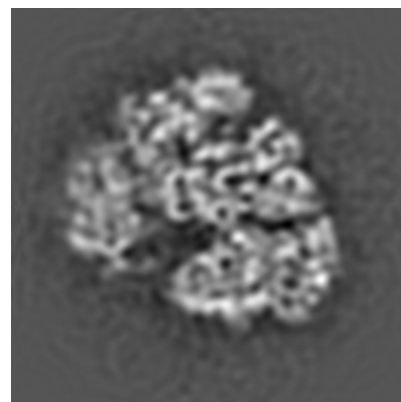
6.2.1 Primary map



X Index: 65



Y Index: 65

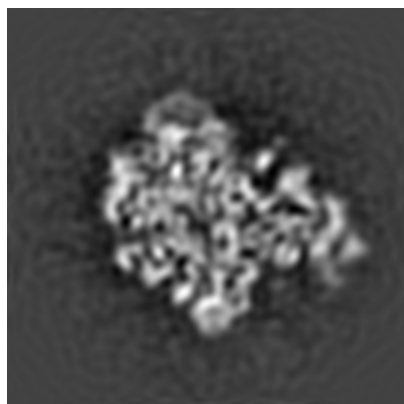


Z Index: 65

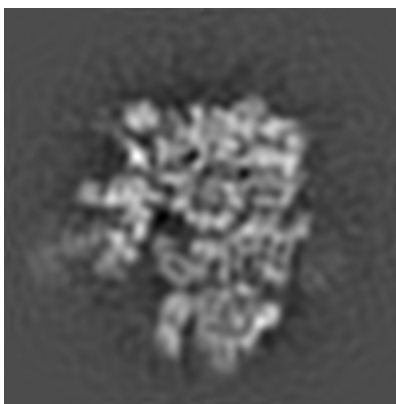
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

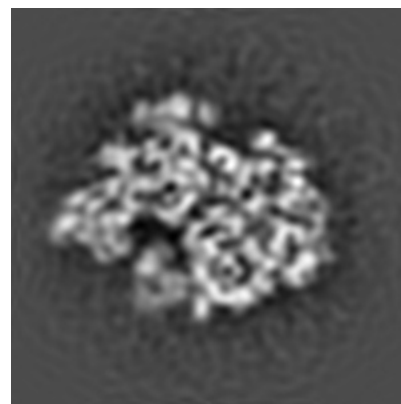
6.3.1 Primary map



X Index: 67



Y Index: 68

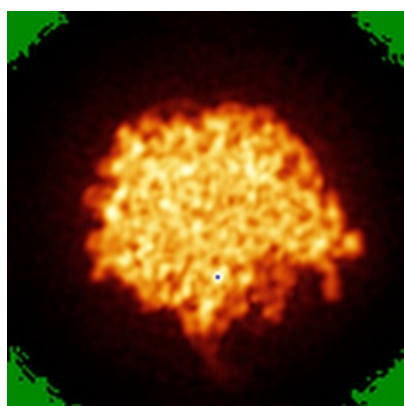


Z Index: 79

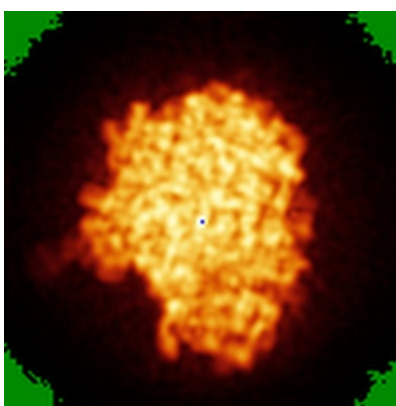
The images above show the largest variance slices of the map in three orthogonal directions.

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

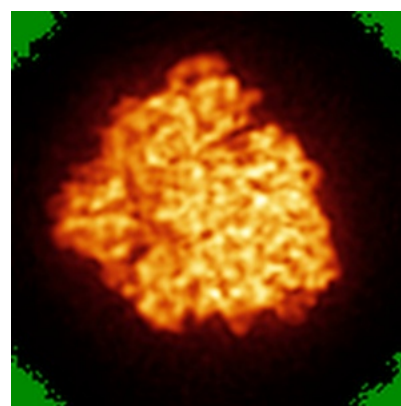
6.4.1 Primary map



X



Y

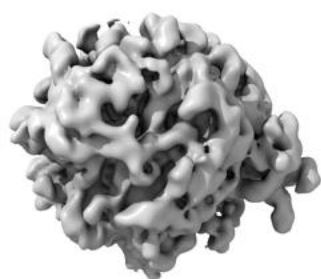


Z

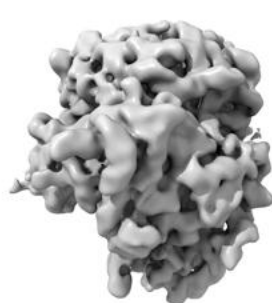
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

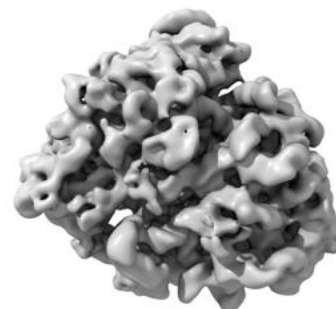
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 56.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

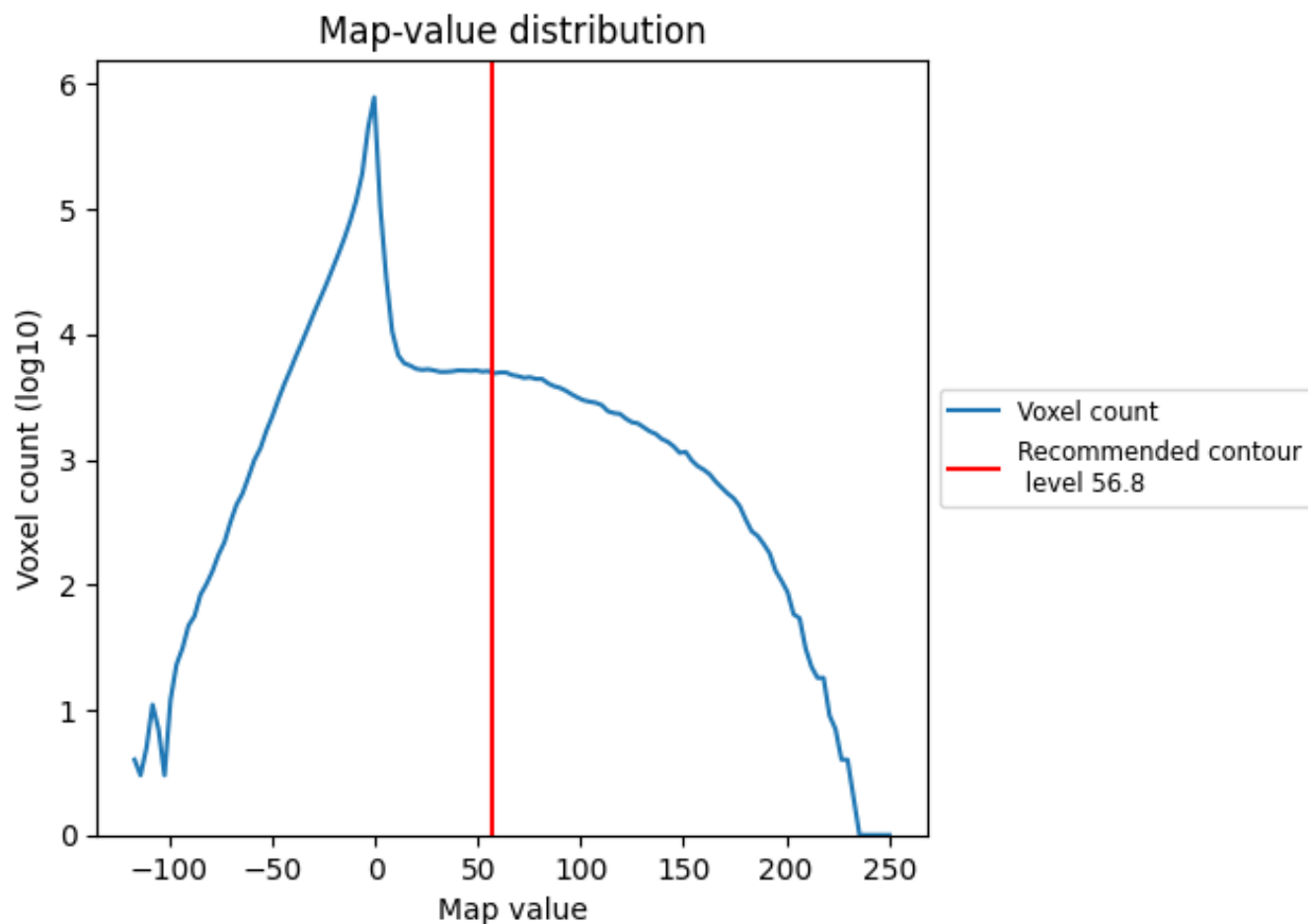
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

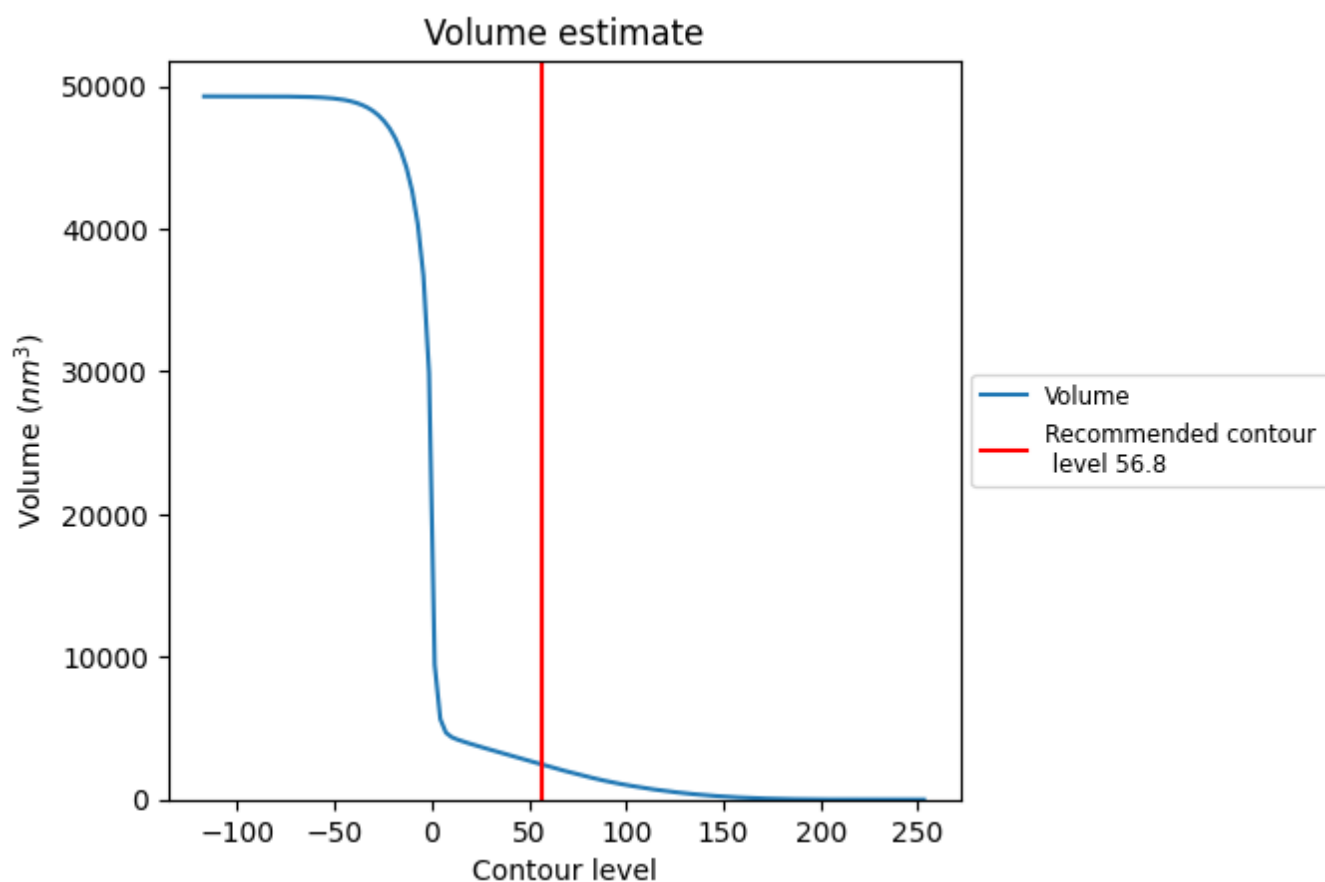
This section contains the results of statistical analysis of the map.

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.

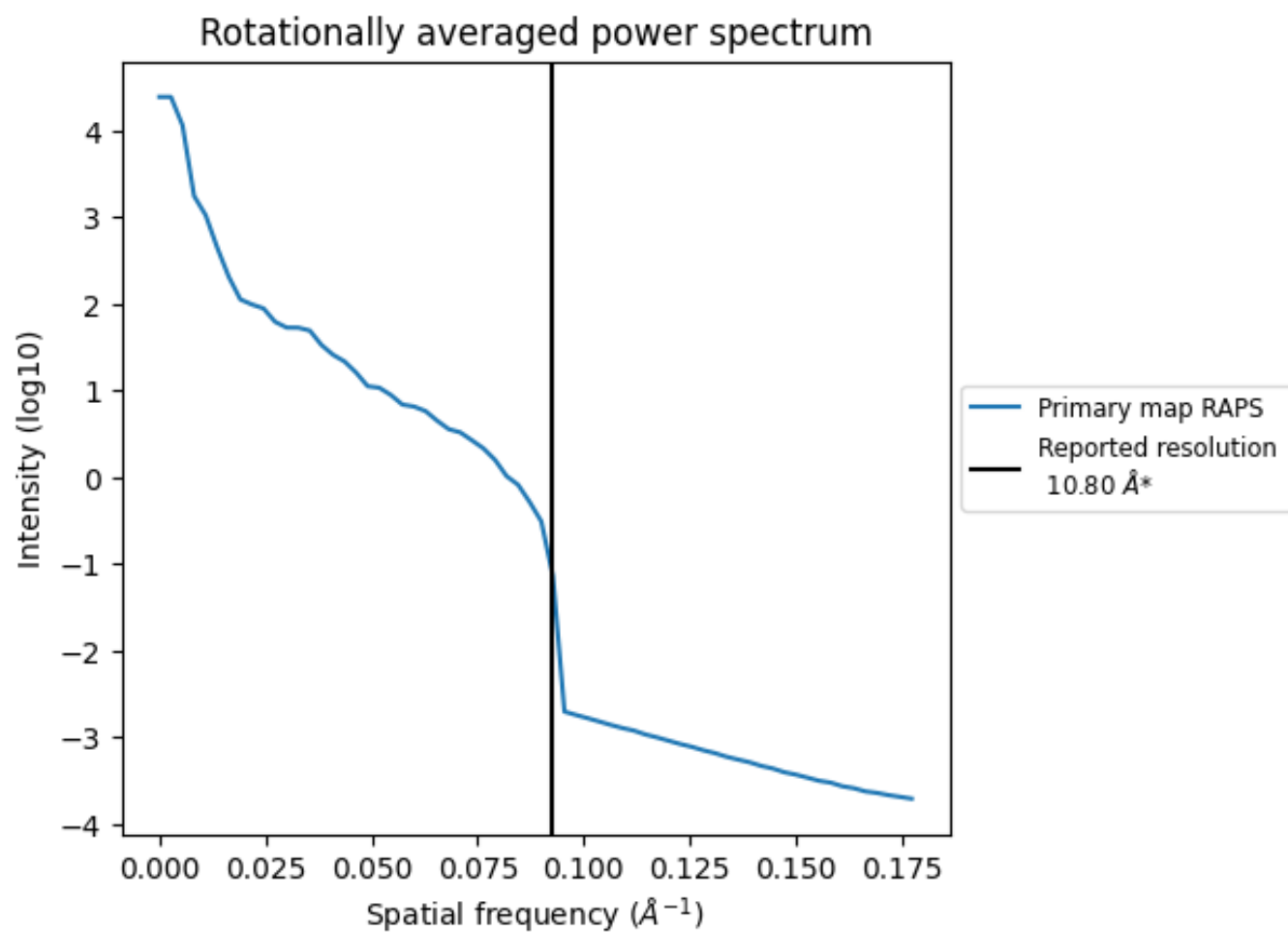
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2453 nm³; this corresponds to an approximate mass of 2216 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 0.093 Å⁻¹

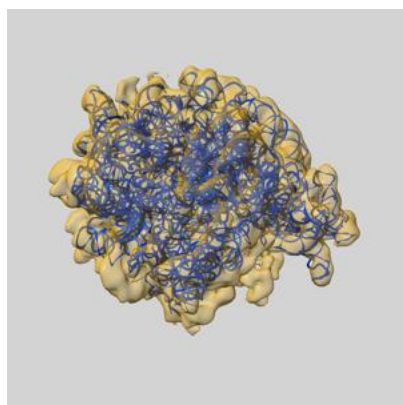
8 Fourier-Shell correlation

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

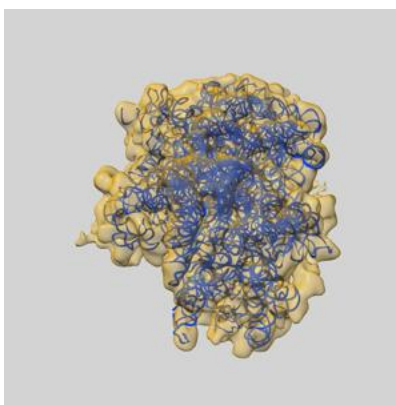
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1363 and PDB model 3DG0. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

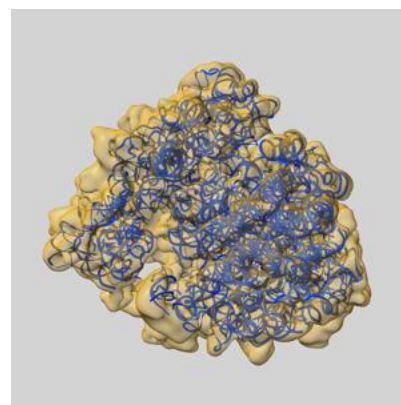
9.1 Map-model overlay [i](#)



X



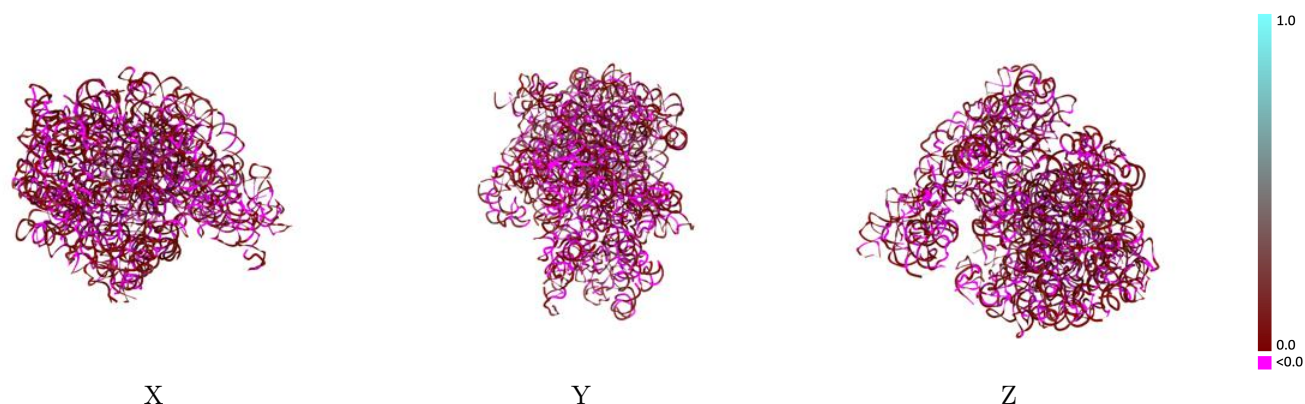
Y



Z

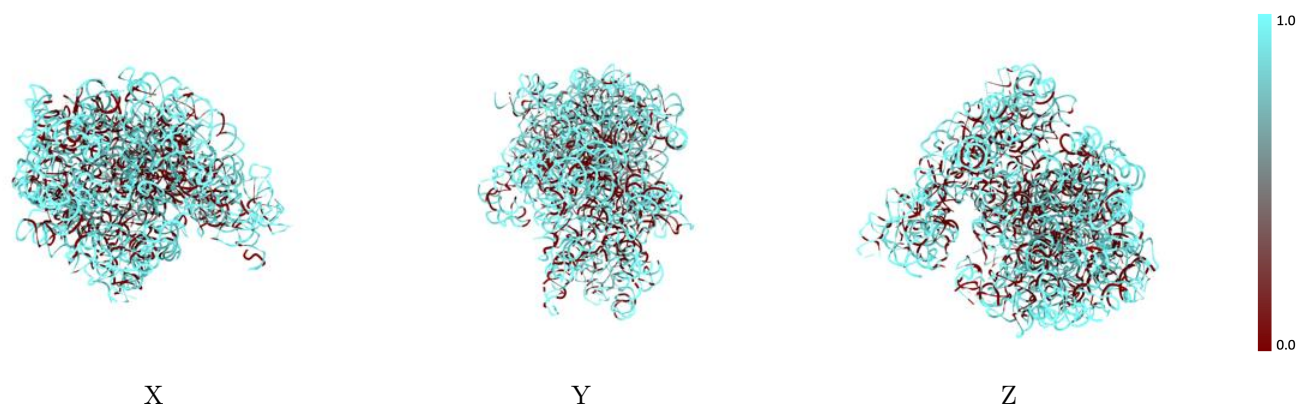
The images above show the 3D surface view of the map at the recommended contour level 56.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



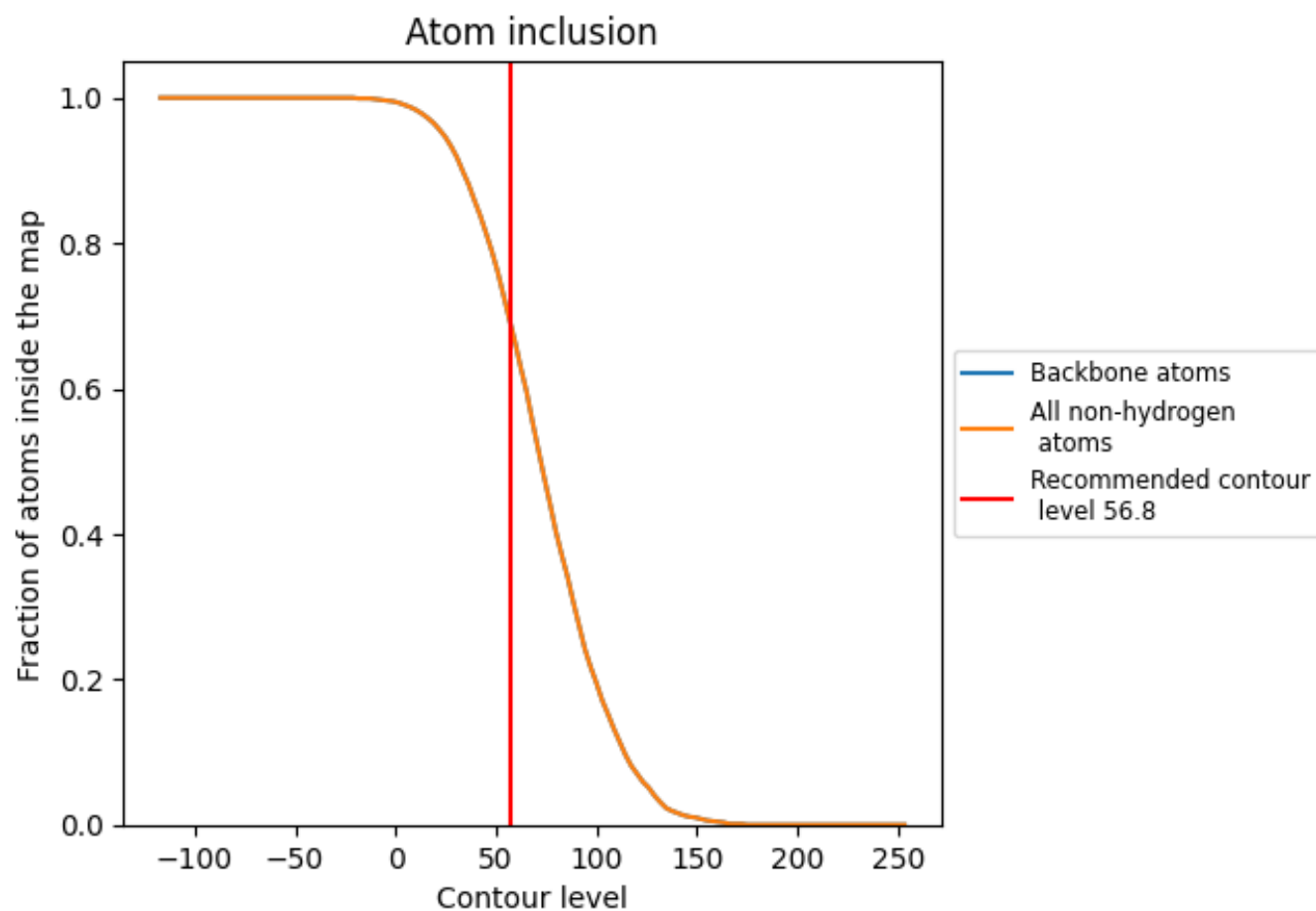
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (56.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 69% 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 (56.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6930	0.0270
A	0.6630	0.0240
B	0.7100	0.0290

