



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:03 AM UTC

PDB ID : 3DG4 / pdb_00003dg4
EMDB ID : EMD-1184
Title : Coordinates of 16S and 23S rRNAs fitted into the cryo-EM map of RF1-bound termination complex
Authors : Gao, H.; LeBarron, J.; Frank, J.
Deposited on : 2008-06-12
Resolution : 12.80 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

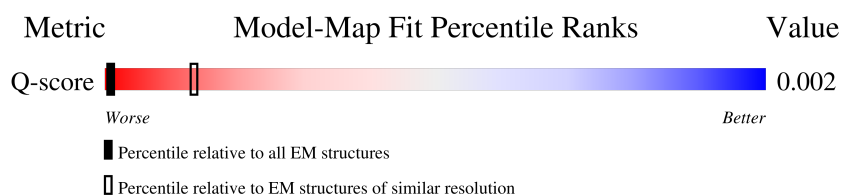
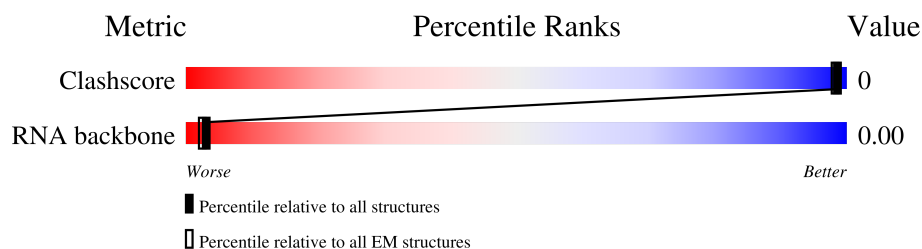
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 12.80 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	60 (12.30 - 13.30)

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		

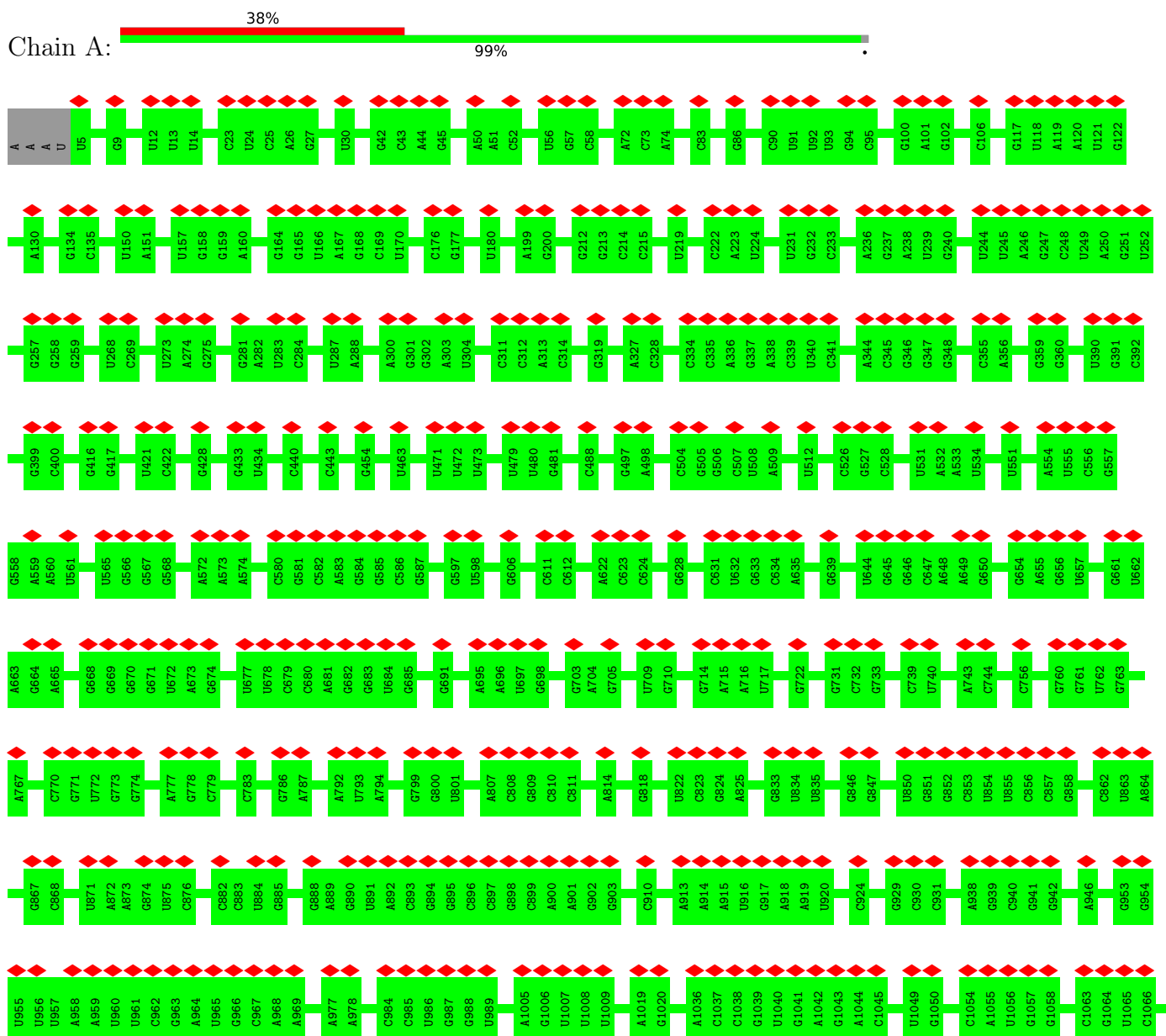
- Molecule 2 is a RNA chain called 23S RibosomaL RNA from E. coli.

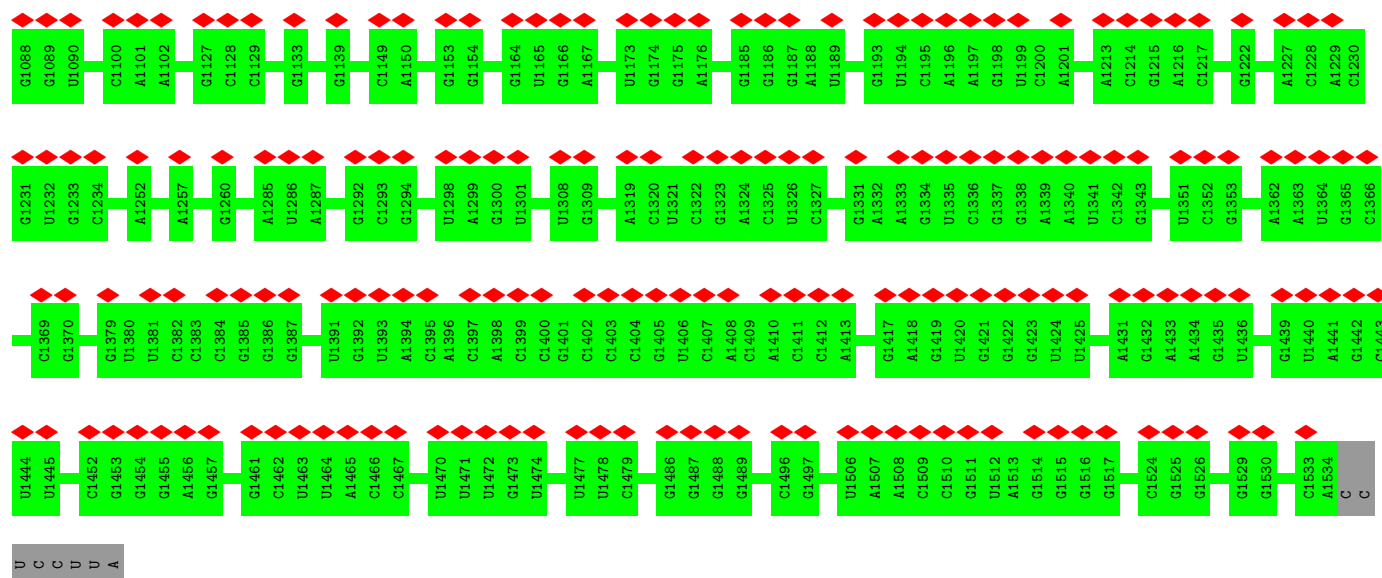
Mol	Chain	Residues	Atoms		AltConf	Trace
2	B	2841	Total	P	0	2841
			2841	2841		

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.

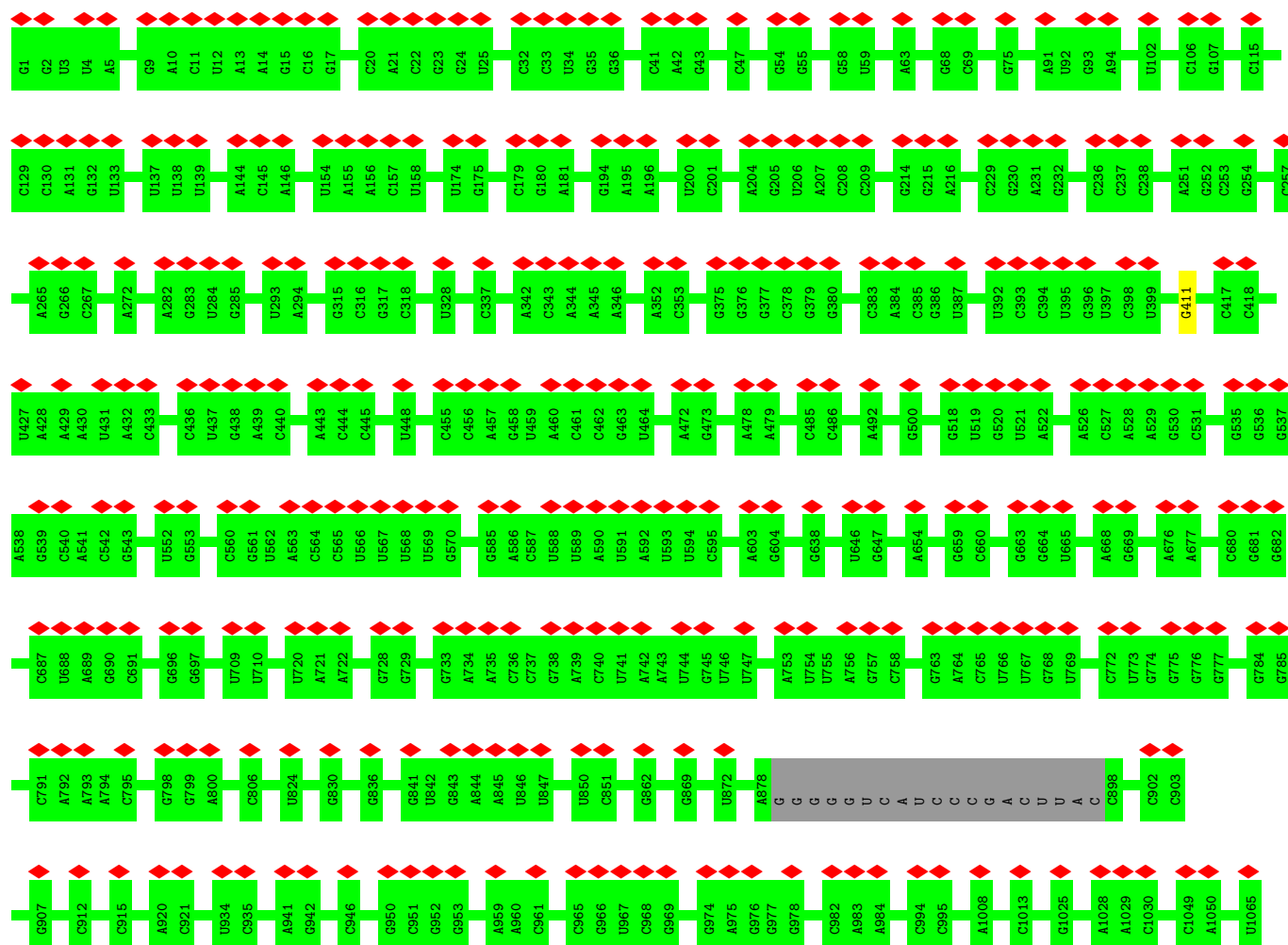
- Molecule 1: 16S Ribosomal RNA from E. coli



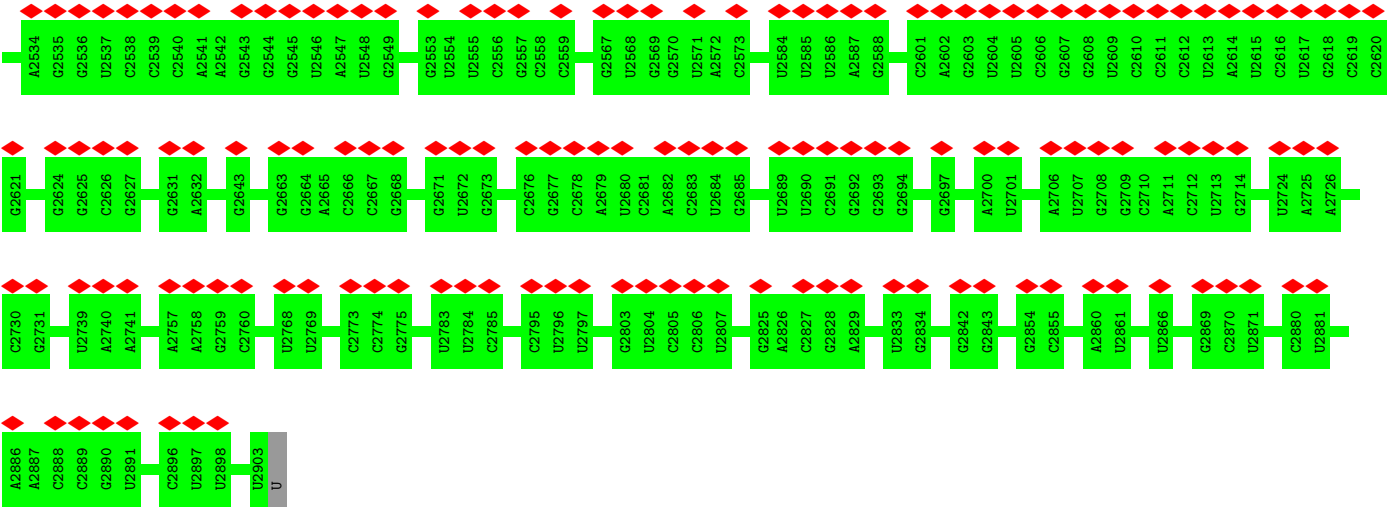


• Molecule 2: 23S Ribosomal RNA from E. coli

Chain B: 35% 98% .



U1066	G1179	G1421	G1560	G1699	C1822	U2007	G2110	C	A2274	U2431
A1067	U1180	G1426	A1591	G1703	G1823	C2008	U	C	C2275	A2432
G1068	U1181	A1427	C1592	G1707	G1824	G2012	G		G2276	A2433
A1073	G1187	C1428	C1593	G1708	U1825	A2019	A		U2296	A2434
G1074	U1188	G1429	U1594	C1709	G1826	A2020	C		A2297	A2435
C1075	A1189	A1430	A1608	U1720	G1831	C2023	U		A2309	G2436
C1076	G1190	A1431	A1609	G1721	C1832	G2024	A		C2313	A2439
U1077	G1191	A1432	G1613	G1724	U1833	C2025	G		A2314	U2440
U1078	G1192	A1433	A1614	G1724	U1834	C2025	U		G2323	U2441
C1079	G1193	A1434	G1615	G1724	G1835	A2030	G		G2324	C2442
U1080	A1194	G1436	G1619	G1730	G1836	G2033	G		U2193	C2443
A1090	G1195	C1437	G1620	G1734	G1840	U2033	A		U2194	U2449
G1091	C1196	U1440	G1625	A1735	U1841	U2034	C		A2198	C2452
C1092	U1197	U1441	A1626	G1744	G1842	G2035	U		G2204	A2453
G1093	U1198	U1442	G1627	A1745	C1843	G2038	C		U2210	G2454
U1094	C1200	U1446	G1628	A1746	G1844	C2047	U		A2211	G2455
C1104	U1201	G1446	U1629	U1747	G1846	G2048	G2133		U2212	A2461
U1105	A1204	C1447	A1640	C1748	A1847	G2049	G2140		U2213	C2462
C1114	A1205	U1448	A1641	A1749	G1857	C2050	G2141		G2217	C2463
G1115	G1206	G1449	A1642	U1758	U1858	C2055	A2142		G2222	G2464
G1116	C1207	G1450	G1643	C1761	U1859	G2055	G2143		A2222	C2465
C1117	G1218	A1353	G1644	A1762	G1860	A2059	G2144		A2227	G2472
G1118	U1219	A1354	G1645	G1763	G1878	A2060	G2148		G2228	U2473
U1119	G1220	A1355	G1646	C1764	C1879	G2061	U2149		U2229	C2480
G1120	C1221	G1357	G1660	A1772	U1880	A2062	C2150		G2230	G2481
C1121	G1229	C1361	G1661	A1773	G1884	C2063	G2151		U2231	A2482
G1125	A1230	C1362	U1662	U1777	C1893	C2064	G2152		G2239	G2484
A1126	G1232	C1363	G1663	U1778	C1894	C2065	A2154		U2240	G2485
A1127	C1233	A1367	G1671	A1787	U1898	C2066	G2155		A2241	C2486
G1128	G1248	G1368	A1672	C1793	A1899	G2067	G2156		G2246	G2487
A1133	U1255	G1369	C1675	A1794	U1901	U2068	G2157		A2247	A2385
A1134	G1258	U1374	A1676	C1795	C1902	G2069	A		C2248	A2386
C1145	U1259	C1375	A1677	U1796	G1903	C2073	G		U2249	U2387
C1146	A1260	C1376	G1682	C1800	U1907	U2074	C		G2250	A2388
A1147	G1261	G1377	U1683	A1801	C1908	U2079	U		U2081	G2389
U1148	A1262	A1378	C1536	U1808	C1909	A2080	C		U2082	U2390
G1149	U1263	A1392	G1537	A1809	U1910	U2081	G		G2252	G2391
C1150	G1263	A1393	U1538	A1810	U1911	U2082	U		G2253	C2396
G1160	U1273	U1400	C1538	U1796	A1912	C2083	A		C2254	G2397
C1161	A1274	G1401	G1539	C1800	U1916	C2084	C		G2255	U2398
A1165	A1275	U1402	C1541	A1801	U1917	U2085	U		G2256	G2399
G1166	A1276	A1403	U1552	U1808	U1918	G2087	A		A2407	
C1167	C1290	C1404	A1553	A1809	A1919	A2090	C		G2414	G2414
G1168	C1291	G1410	U1554	U1810	C1920	C2103	C		G2415	G2415
U1173	G1292	U1411	G1555	G1811	G1925	C2104	U		C2416	C2416
U1174	C1293	U1412	C1556	U1812	U1926	U2105	A		A2418	G2418
A1175	U1294	A1419	C1557	G1813	C1934	G2106	C		C2422	
U1176	A1302	A1419	C1558	A1821		G2107	A			
G1177	G1303		U1559							



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24622	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	225.713	Depositor
Minimum map value	-115.182	Depositor
Average map value	4.811	Depositor
Map value standard deviation	21.585	Depositor
Recommended contour level	50.8	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	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	3.16	0.44

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.

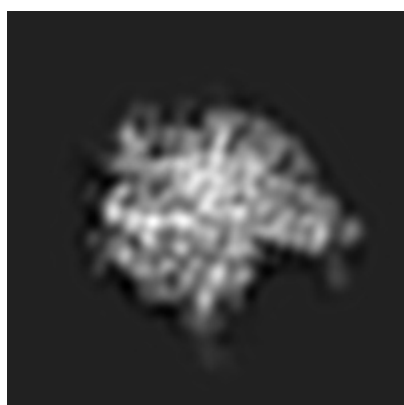
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1184. These allow visual inspection of the internal detail of the map and identification of artifacts.

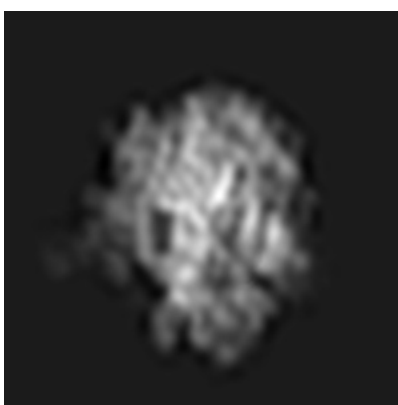
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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: 67

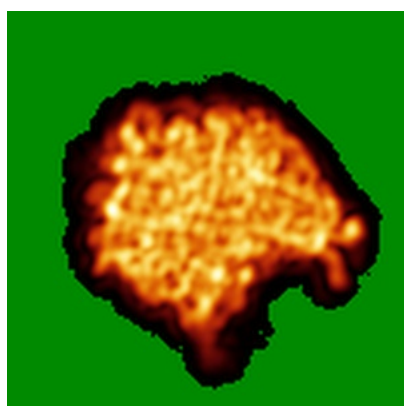


Z Index: 60

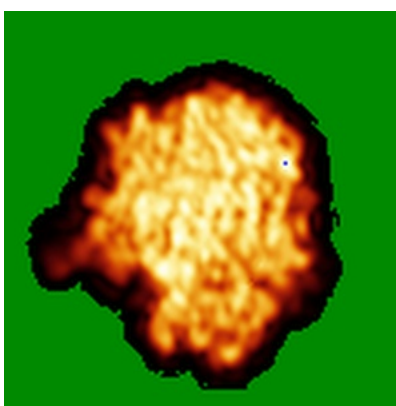
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

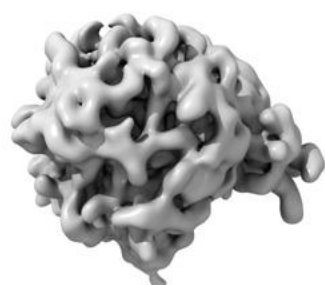


Z

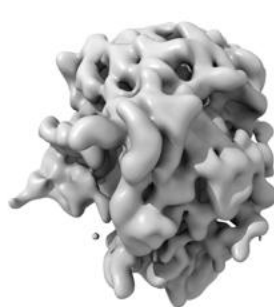
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

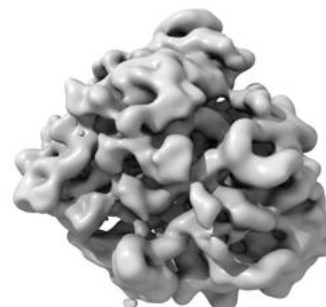
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 50.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

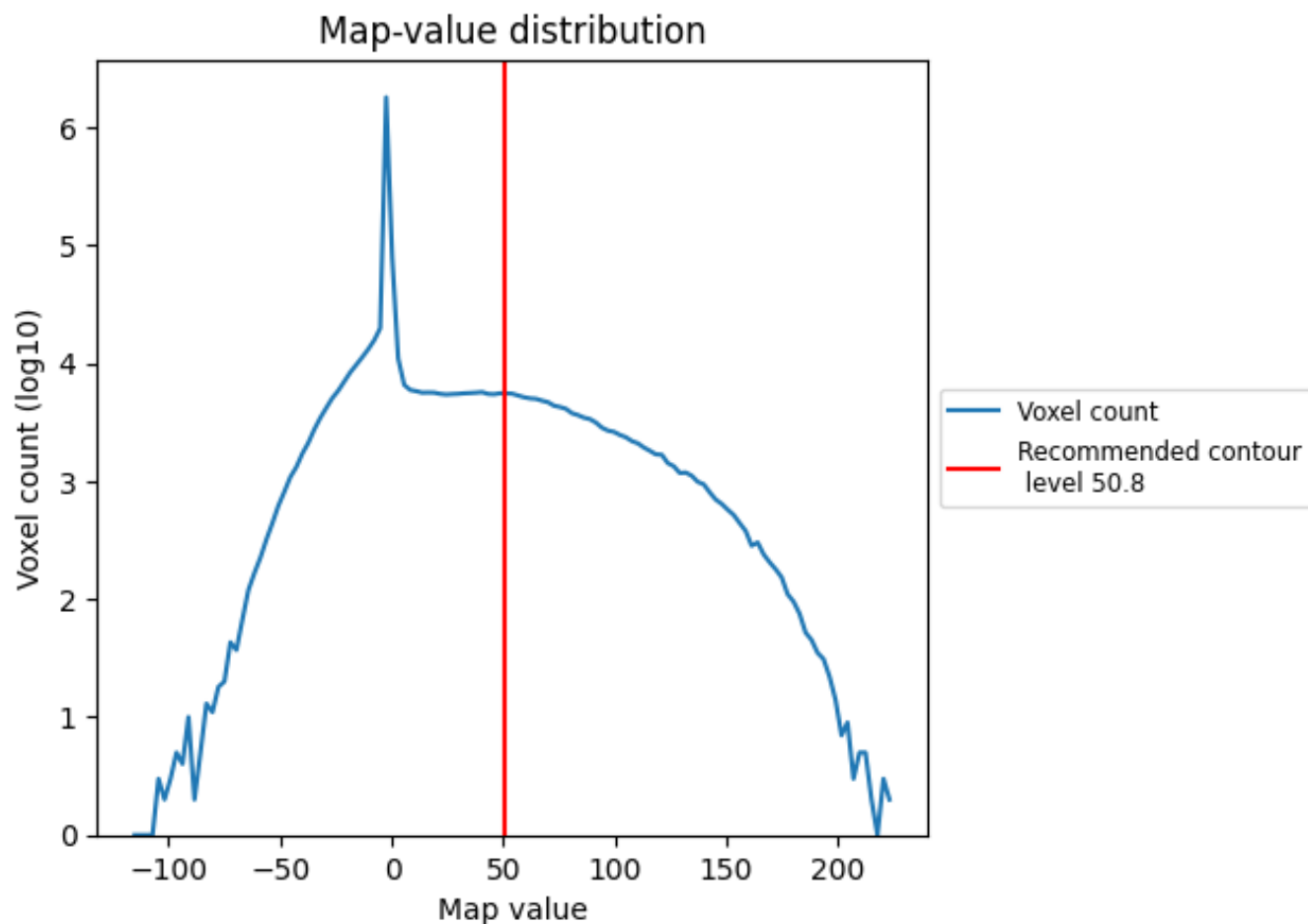
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

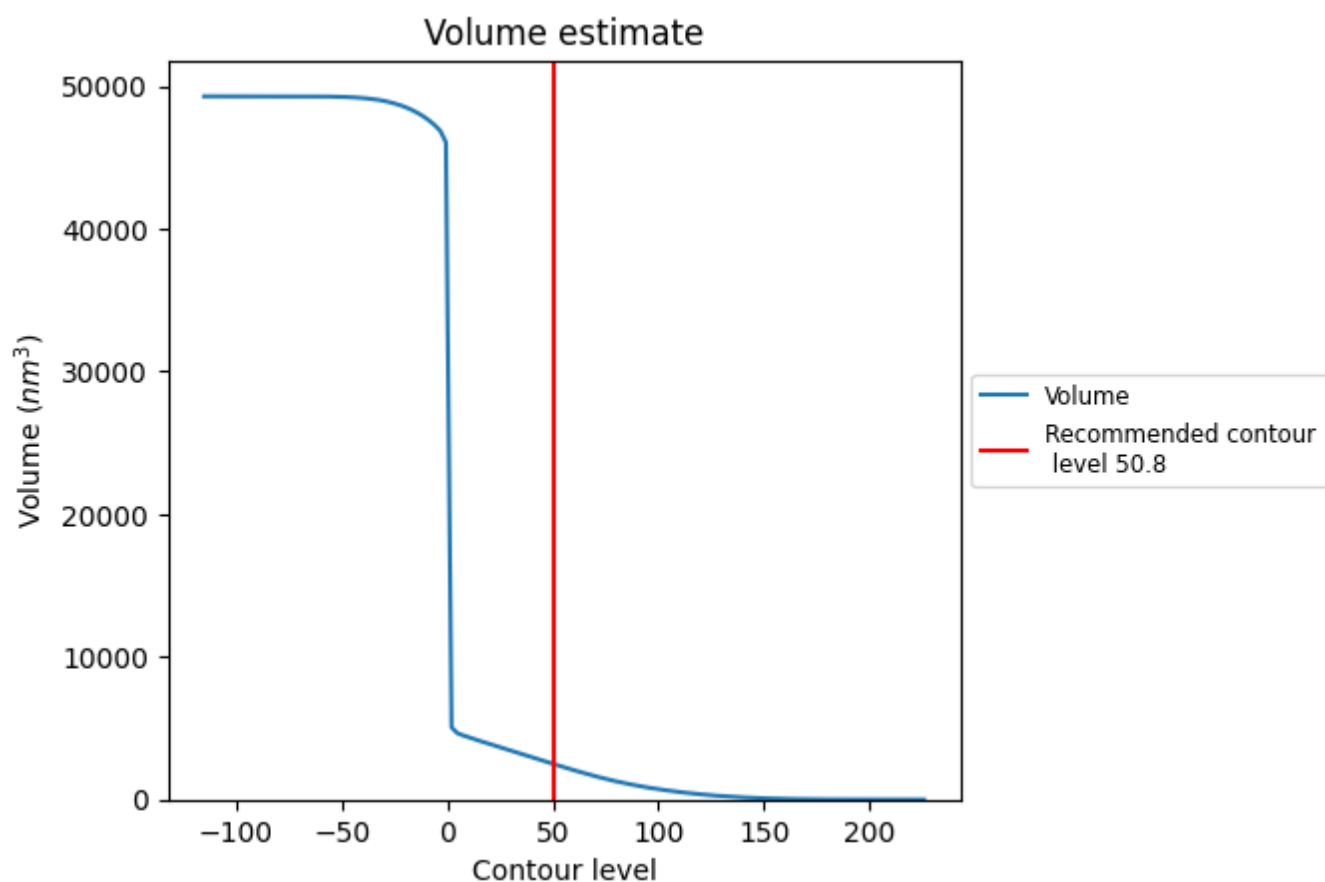
This section contains the results of statistical analysis of the map.

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.

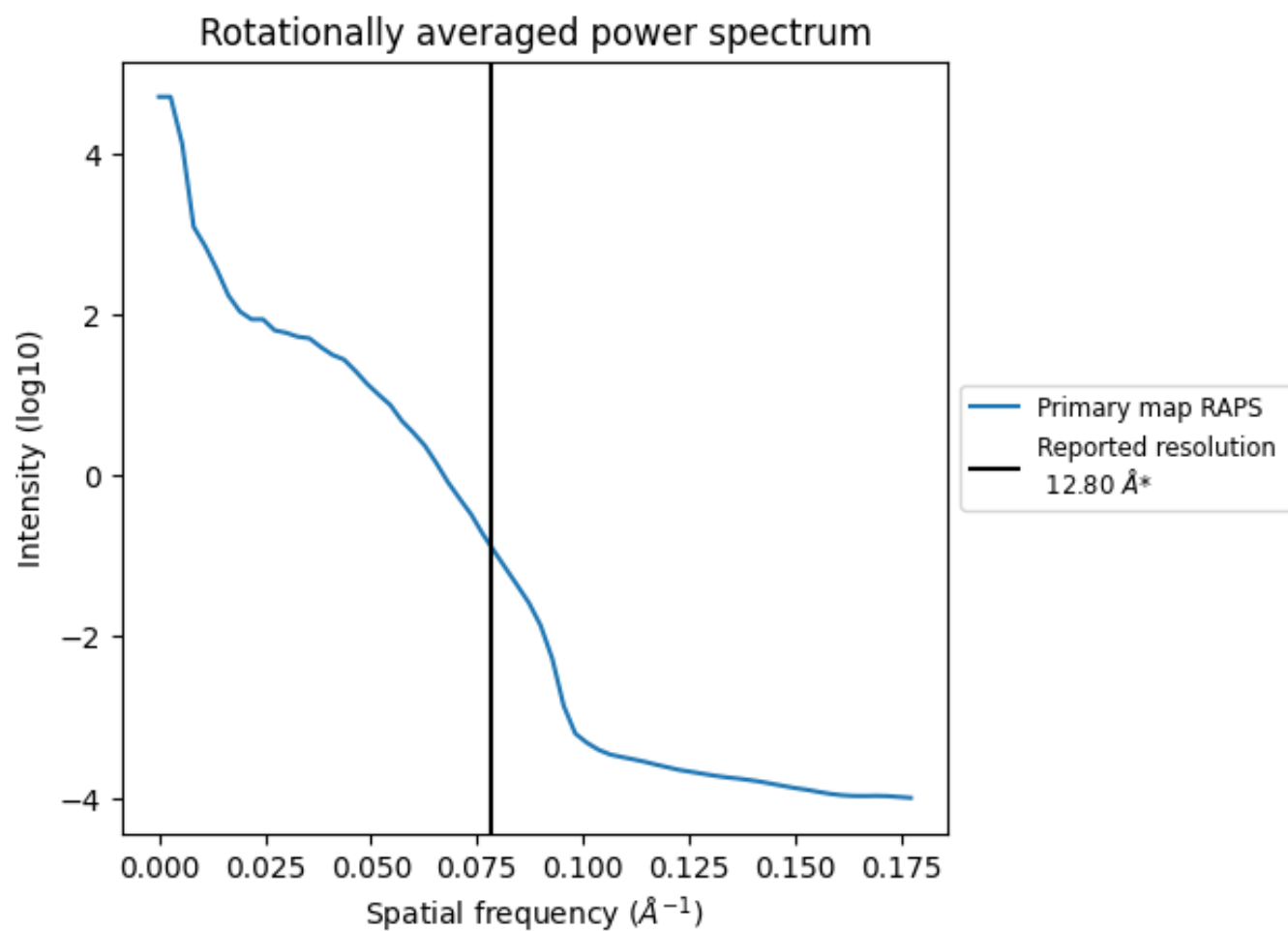
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2469 nm³; this corresponds to an approximate mass of 2230 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 0.078 Å⁻¹

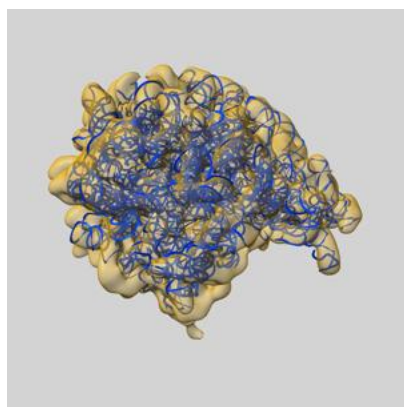
8 Fourier-Shell correlation

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

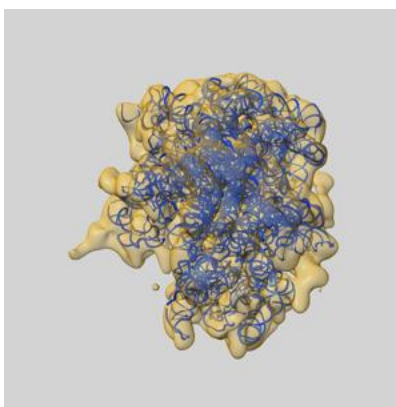
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1184 and PDB model 3DG4. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

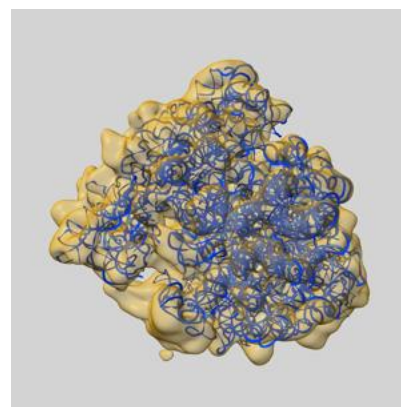
9.1 Map-model overlay [i](#)



X



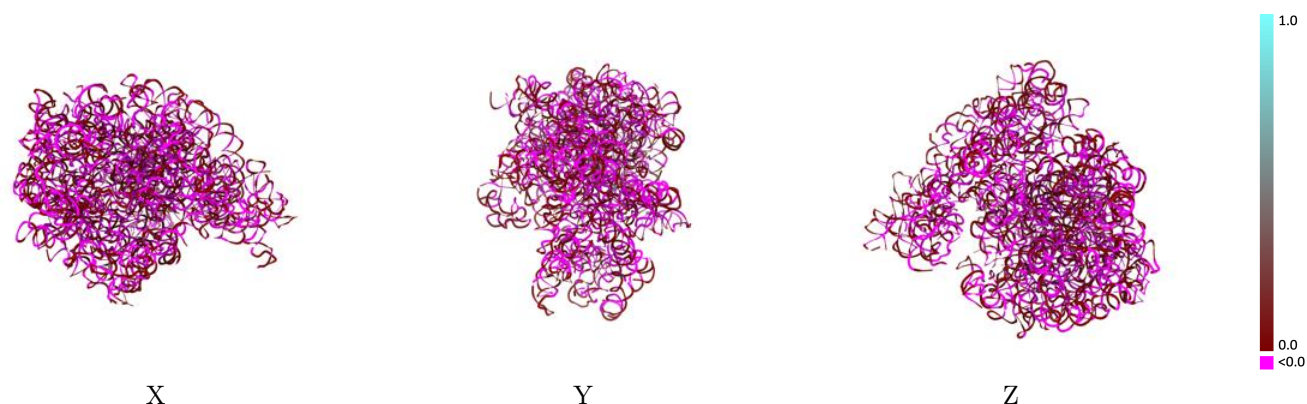
Y



Z

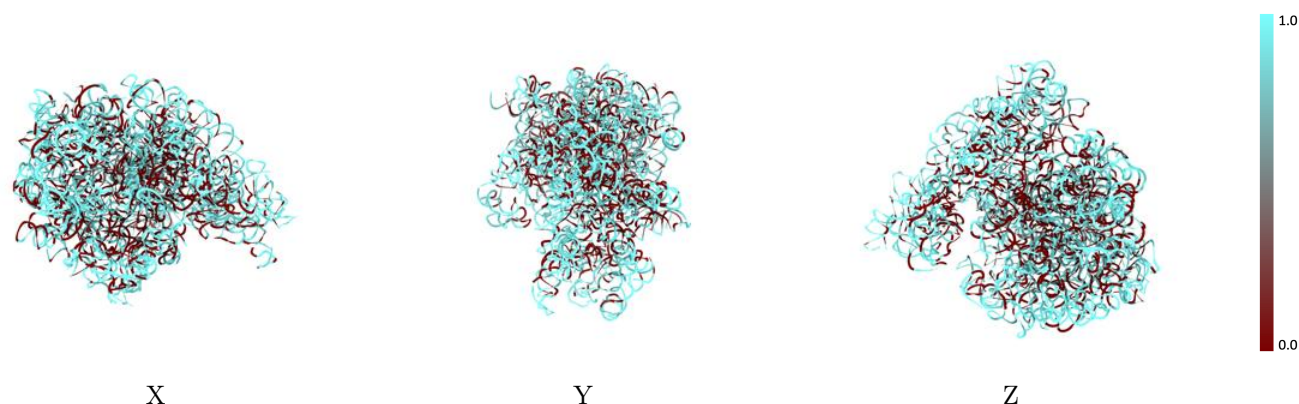
The images above show the 3D surface view of the map at the recommended contour level 50.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



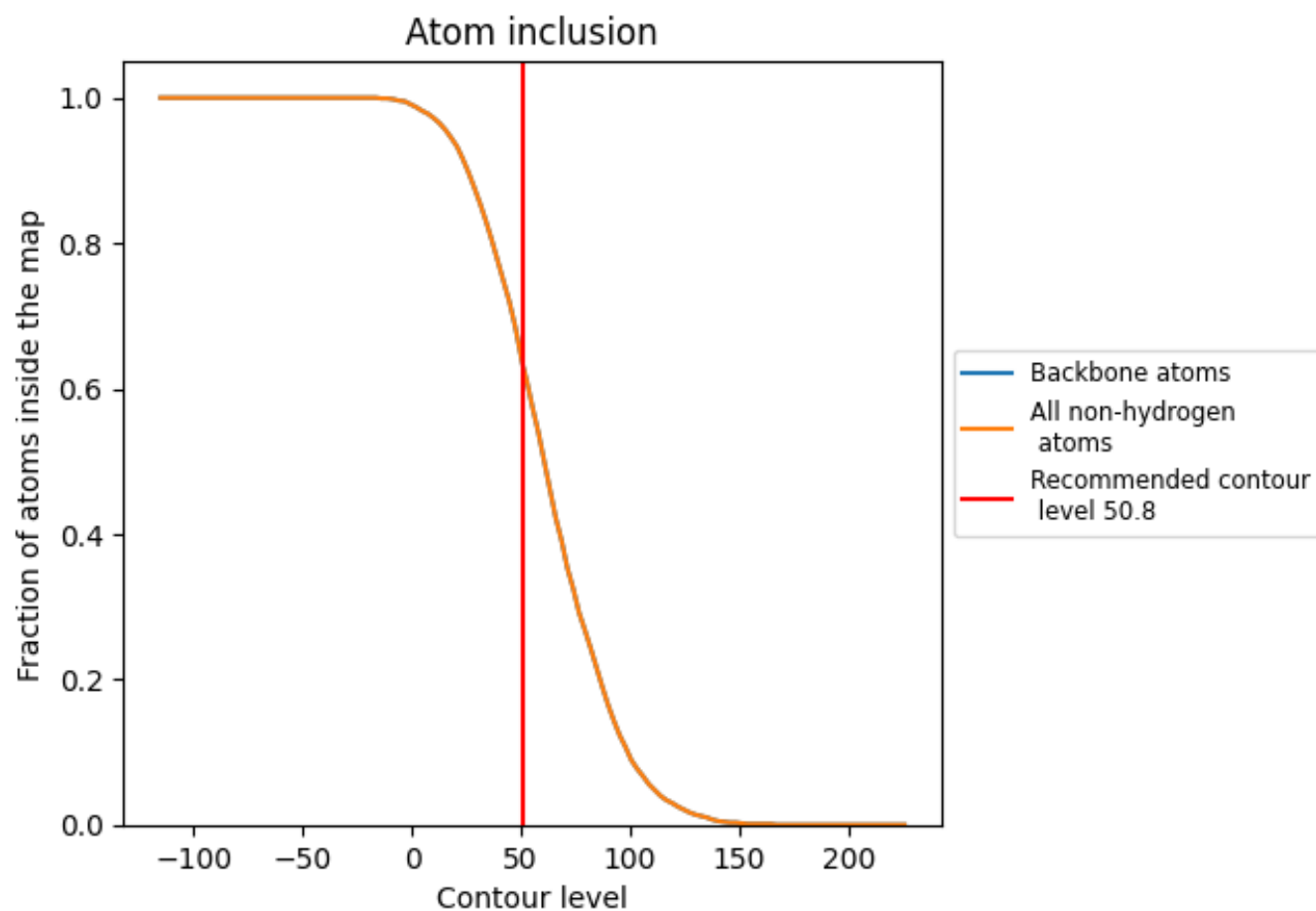
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (50.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 63% 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 (50.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6320	0.0020
A	0.6180	0.0010
B	0.6390	0.0030

