



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 03:44 PM UTC

PDB ID : 3J2G / pdb_00003j2g
EMDB ID : EMD-5509
Title : Dissecting the in vivo assembly of the 30S ribosomal subunit reveals the role of RimM
Authors : Guo, Q.; Goto, S.; Chen, Y.; Muto, A.; Himeno, H.; Deng, H.; Lei, J.; Gao, N.
Deposited on : 2012-09-28
Resolution : 16.50 Å (reported)
Based on initial model : 3OFA

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

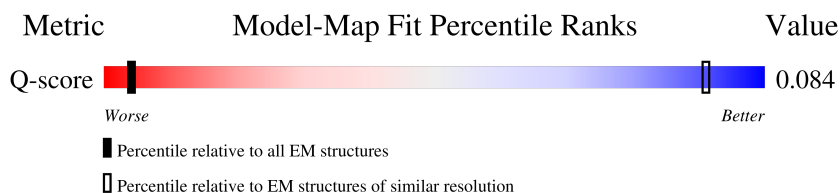
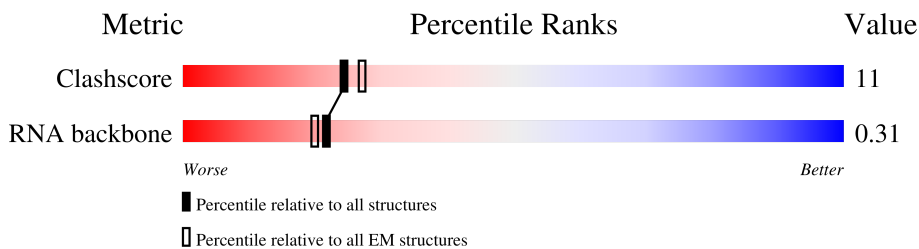
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

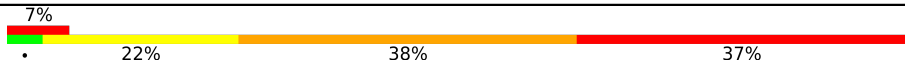
The reported resolution of this entry is 16.50 Å.

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	55 (16.00 - 17.00)

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	N	1533	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 49446 atoms, of which 16554 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.

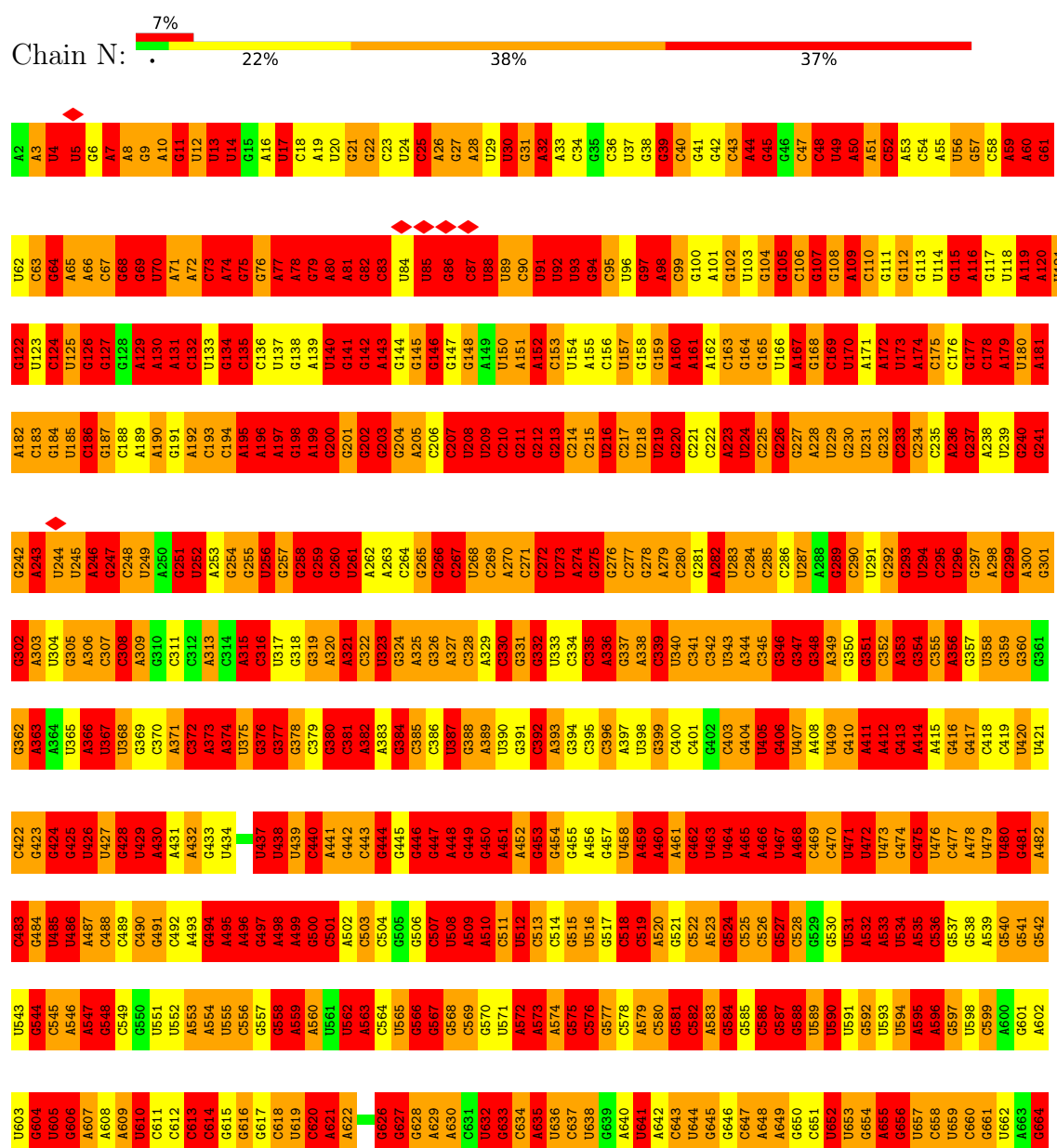
- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	N	1533	Total	C	H	N	O	P	0	0
			49446	14671	16554	6036	10653	1532		

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 rRNA



A1446	G1386	C1265	U1205	A1145	U1085	U1025	U905	A945	G785	G725	A665
A1447	G1387	G1266	G1206	A1146	U1086	G1026	A906	G846	G786	C726	G665
A1448	C1388	G1267	G1207	A1147	G1087	G1027	A907	G847	A787	C727	G667
C1449	C1389	G1268	C1208	U1148	G1088	C1028	A908	G848	A788	A728	G668
U1450	U1390	A1269	C1209	C1149	G1089	C1029	A909	G849	A789	A729	G669
U1451	U1391	G1270	C1210	A1150	U1090	U1029	C910	U850	A790	G730	G670
U1452	G1392	A1271	U1211	A1151	U1091	U1030	U911	G851	G791	G731	G671
G1453	U1393	G1272	U1212	A1152	A1092	C1031	C912	G852	A792	C732	U672
G1454	C1394	C1273	C1213	G1153	A1093	C1032	A913	G853	U793	A673	A673
G1454	U1395	A1274	C1214	G1154	U1094	G1032	A914	U854	A794	G734	G674
G1455	U1395	A1275	G1215	A1155	U1095	G1033	A915	U855	C795	C735	A675
G1456	C1397	G1276	A1216	G1156	C1096	G1034	U916	C856	C796	C736	A676
G1457	U1398	G1277	C1217	A1157	C1097	G1034	U917	C857	C797	C737	U677
G1458	C1399	G1278	C1218	U1158	C1098	A1035	A918	C858	U798	C738	U678
G1459	U1400	A1279	A1219	U1159	G1099	A1036	A919	G859	G799	C739	C679
C1460	C1281	G1280	G1220	G1160	C1100	C1037	U920	A860	U740	C680	G681
G1461	G1343	C1282	G1221	C1161	A1101	C1038	U921	G861	U801	G741	A681
G1462	U1283	G1222	G1222	C1162	A1102	U1039	G922	C862	A802	G742	G682
C1463	C1284	U1224	C1223	A1163	C1103	U1040	A923	U863	G803	A743	G683
G1465	U1345	A1245	U1224	G1164	G1104	G1041	C924	A864	U804	C744	U684
U1464	A1346	A1246	A1225	U1165	A1105	G1042	G925	A865	C805	C745	G685
U1465	G1347	U1286	G1226	G1166	G1106	A1043	G926	C866	C806	A746	U686
U1466	U1348	A1287	A1227	A1167	C1107	G1043	G927	U867	A807	A747	A687
A1467	A1349	C1288	C1228	U1168	G1108	A1044	G928	C868	C808	G748	G688
C1467	U1351	A1229	A1229	A1169	C1109	U1045	G929	U869	G809	A749	C689
A1468	C1352	G1290	C1230	A1170	A1110	C1046	C930	U870	C810	C750	G690
A1469	G1353	U1291	G1231	A1171	A1111	A1047	C931	U871	U751	C751	G691
U1470	C1354	C1292	U1232	C1172	C1112	G1048	C932	A872	G812	C752	U692
U1471	G1355	C1293	G1233	U1173	C1113	U1049	C933	A873	U813	A753	G693
U1472	G1356	G1294	G1234	G1174	C1114	G983	C934	G874	A814	C754	A694
U1473	C1357	U1295	U1235	G1175	U1115	C1050	A935	U875	A815	G755	A695
U1474	A1357	C1296	A1236	A1176	U1116	C1051	C936	C876	A816	C756	A696
U1475	U1358	G1297	C1237	G1177	U1117	A996	A937	G877	C817	U757	U697
U1476	C1359	U1298	A1238	U1178	C1118	G1052	A938	A878	G818	C758	G698
U1477	A1360	A1299	A1239	A1179	C1119	C1054	G939	A879	A819	A759	C699
U1478	G1361	G1300	U1240	A1180	C1120	U1056	C940	G880	U820	G760	G700
U1479	A1362	C1301	G1241	G1181	U1121	G1057	G941	G881	G821	G761	U701
U1480	U1364	C1302	G1242	G1182	U1122	C1058	G942	C882	U822	U762	A702
U1481	G1365	G1303	C1243	U1183	U1123	G1059	U943	C883	C823	G763	G703
U1482	C1366	G1304	G1244	G1184	G1124	U1060	G944	U884	G824	C764	A704
U1483	C1367	G1305	G1245	G1185	U1125	G1061	G945	G885	A825	G765	G705
U1484	U1368	U1306	A1246	G1186	G1126	U1062	G946	G886	C826	A766	A706
U1485	C1369	U1307	U1247	G1187	G1127	G1063	G947	G887	U827	A767	U707
U1486	G1370	G1308	A1248	A1188	C1128	G1064	C948	G888	U828	A768	C708
U1487	U1371	C1309	C1249	U1189	C1129	U1065	A949	A889	G829	G769	U709
U1488	G1372	A1250	A1251	A1190	A1130	G1066	U950	G890	G830	C770	G710
U1489	A1373	G1312	G1252	A1191	G1131	A1067	G951	U891	G831	G771	G711
U1490	A1374	U1313	G1253	G1192	C1132	U1068	U952	A892	G832	U772	A712
U1491	A1375	C1314	A1254	G1193	G1133	U1069	G953	G893	G833	G773	G713
U1492	U1376	U1315	G1255	U1194	G1134	U1070	G954	G894	U834	G774	G714
U1493	A1377	G1316	G1256	C1195	U1135	C1071	U955	G895	U835	G775	A715
U1494	C1378	C1317	A1257	A1196	C1136	G1072	U956	C896	G836	G776	A716
U1495	G1379	U1318	G1258	A1197	C1137	U1073	U957	C897	U837	G777	A717
U1496	U1380	A1319	C1259	U1198	G1138	U1074	A958	G898	G838	G778	U718
U1497	U1381	C1320	C1260	C1200	G1139	U1075	A899	C899	C839	C779	C719
U1498	C1382	U1321	G1261	A1201	C1140	U1076	U960	A900	C840	A780	G720
U1499	C1383	G1322	C1262	U1202	G1141	G1077	U961	A901	C841	A781	G721
A1500	C1384	A1324	C1263	C1203	G1142	U1078	C962	G902	U842	A782	G722
A1501	G1385		U1264	A1204	G1143	G1079	A964	G903	U843	C783	U723
A1502					G1144	A1080		U904	G844	A784	G724
A1503						A1081					
A1504						U1082					
A1505						U1083					
						G1084					

U1506	A1507	A1508	C1509	C1510	G1511	U1512	A1513	G1514	G1515	G1516	G1517	A1518	A1519	C1520	C1521	U1522	G1523	C1524	G1525	G1526	U1527	U1528	G1529	G1530	A1531	U1532	C1533	A1534
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25631	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Weiner filter	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	59000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	4.704	Depositor
Minimum map value	-7.202	Depositor
Average map value	-4.377	Depositor
Map value standard deviation	0.601	Depositor
Recommended contour level	-2.3	Depositor
Map size ($\text{\AA}$)	375.0, 375.0, 375.0	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.00, 3.00, 3.00	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	N	2.07	851/36831 (2.3%)	2.10	2008/57458 (3.5%)

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	N	0	956

The worst 5 of 851 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	896	C	P-O5'	-9.89	1.45	1.59
1	N	245	U	C5'-C4'	9.70	1.65	1.51
1	N	711	G	C2'-C1'	-9.32	1.39	1.53
1	N	79	G	C5'-C4'	9.28	1.65	1.51
1	N	1433	A	C1'-N9	9.27	1.61	1.48

The worst 5 of 2008 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	438	U	P-O3'-C3'	23.36	155.24	120.20
1	N	547	A	P-O3'-C3'	18.06	147.28	120.20
1	N	184	G	P-O5'-C5'	17.93	147.79	120.90
1	N	264	C	P-O5'-C5'	17.49	147.14	120.90
1	N	776	G	P-O5'-C5'	17.36	146.94	120.90

There are no chirality outliers.

5 of 956 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	10	A	Sidechain
1	N	11	G	Sidechain
1	N	4	U	Sidechain
1	N	5	U	Sidechain
1	N	7	A	Sidechain

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	N	32892	16554	16536	530	0
All	All	32892	16554	16536	530	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 11.

The worst 5 of 530 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:N:858:G:H1	1:N:869:G:H2'	1.53	0.74
1:N:1240:U:C6	1:N:1241:G:H5'	2.26	0.70
1:N:67:C:H2'	1:N:68:G:C8	2.27	0.70
1:N:594:U:C4	1:N:595:A:C6	2.80	0.69
1:N:909:A:H2	1:N:1487:G:H21	1.40	0.68

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	N	1532/1533 (99%)	458 (29%)	150 (9%)

5 of 458 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	N	3	A
1	N	4	U
1	N	5	U
1	N	6	G
1	N	8	A

5 of 150 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	1197	A
1	N	1498	U
1	N	1228	C
1	N	1337	G
1	N	412	A

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 ⓘ

There are no chain breaks in this entry.

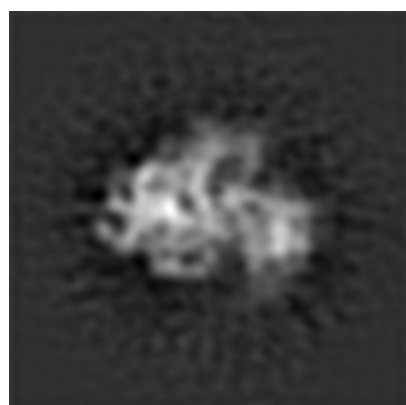
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5509. These allow visual inspection of the internal detail of the map and identification of artifacts.

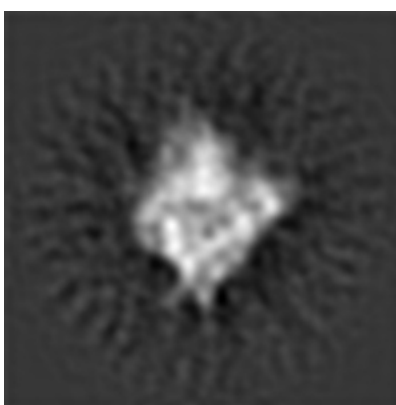
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

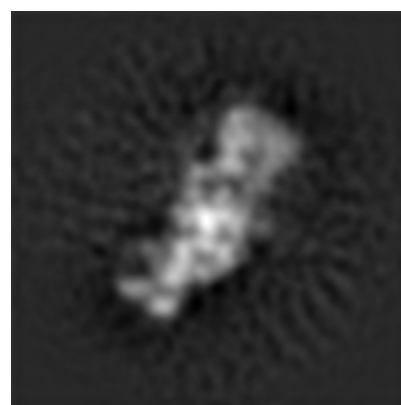
6.1.1 Primary map



X



Y

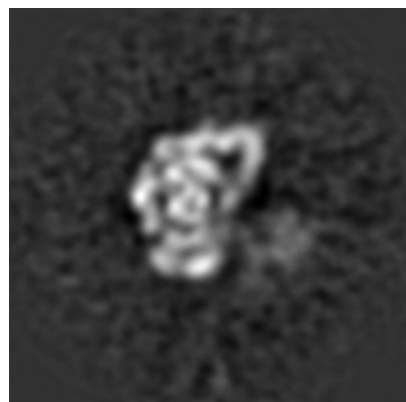


Z

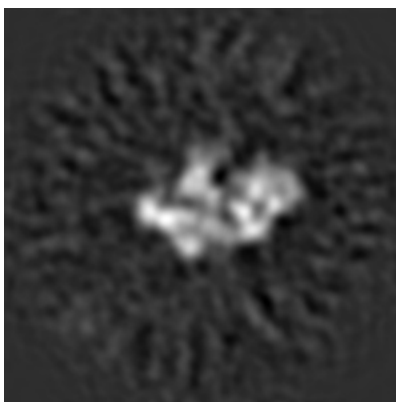
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

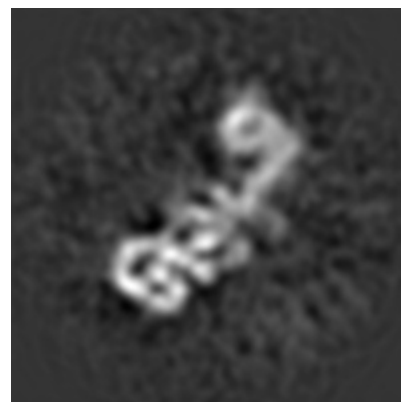
6.2.1 Primary map



X Index: 62



Y Index: 62

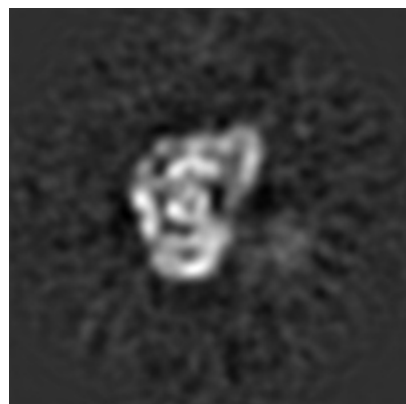


Z Index: 62

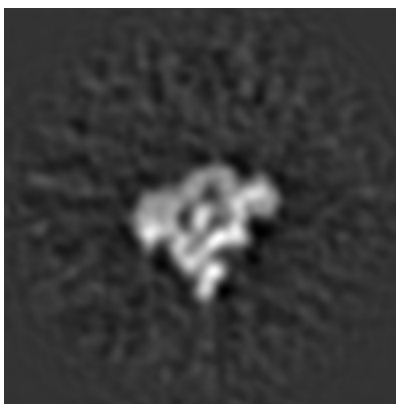
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

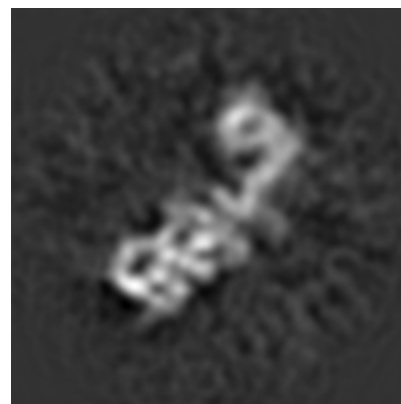
6.3.1 Primary map



X Index: 60



Y Index: 50

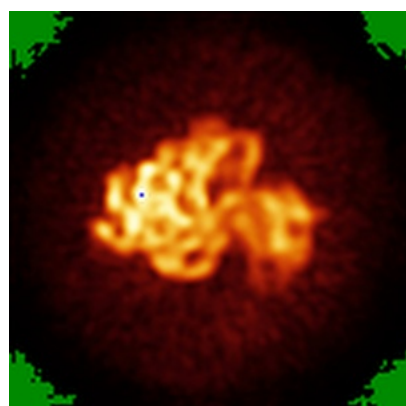


Z Index: 61

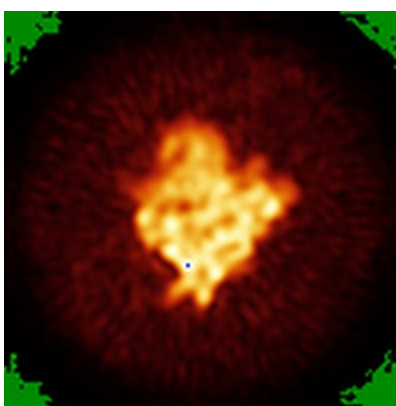
The images above show the largest variance slices of the map in three orthogonal directions.

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

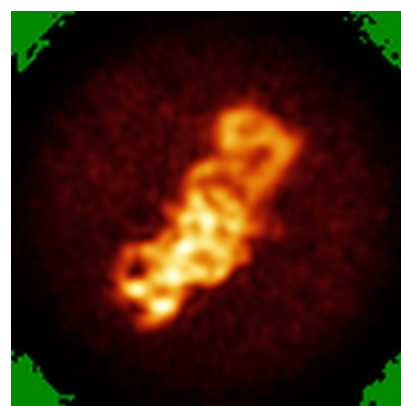
6.4.1 Primary map



X



Y

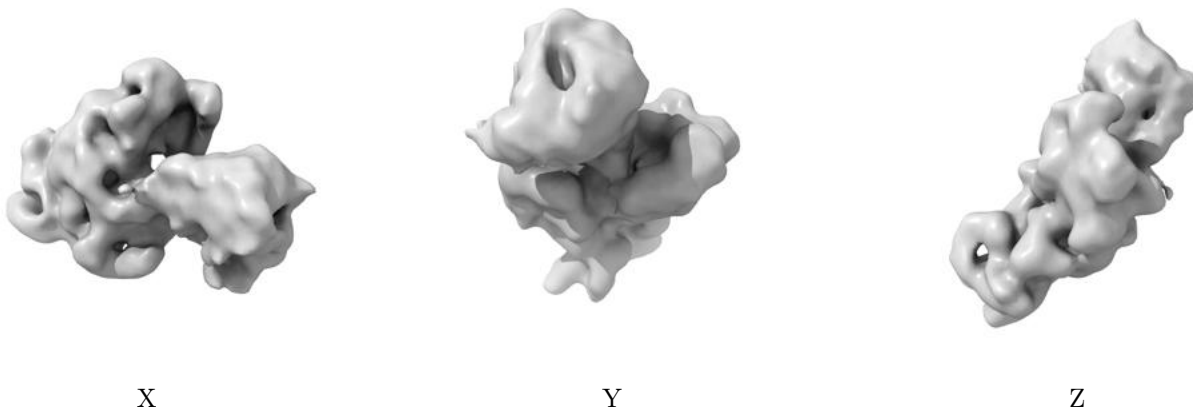


Z

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

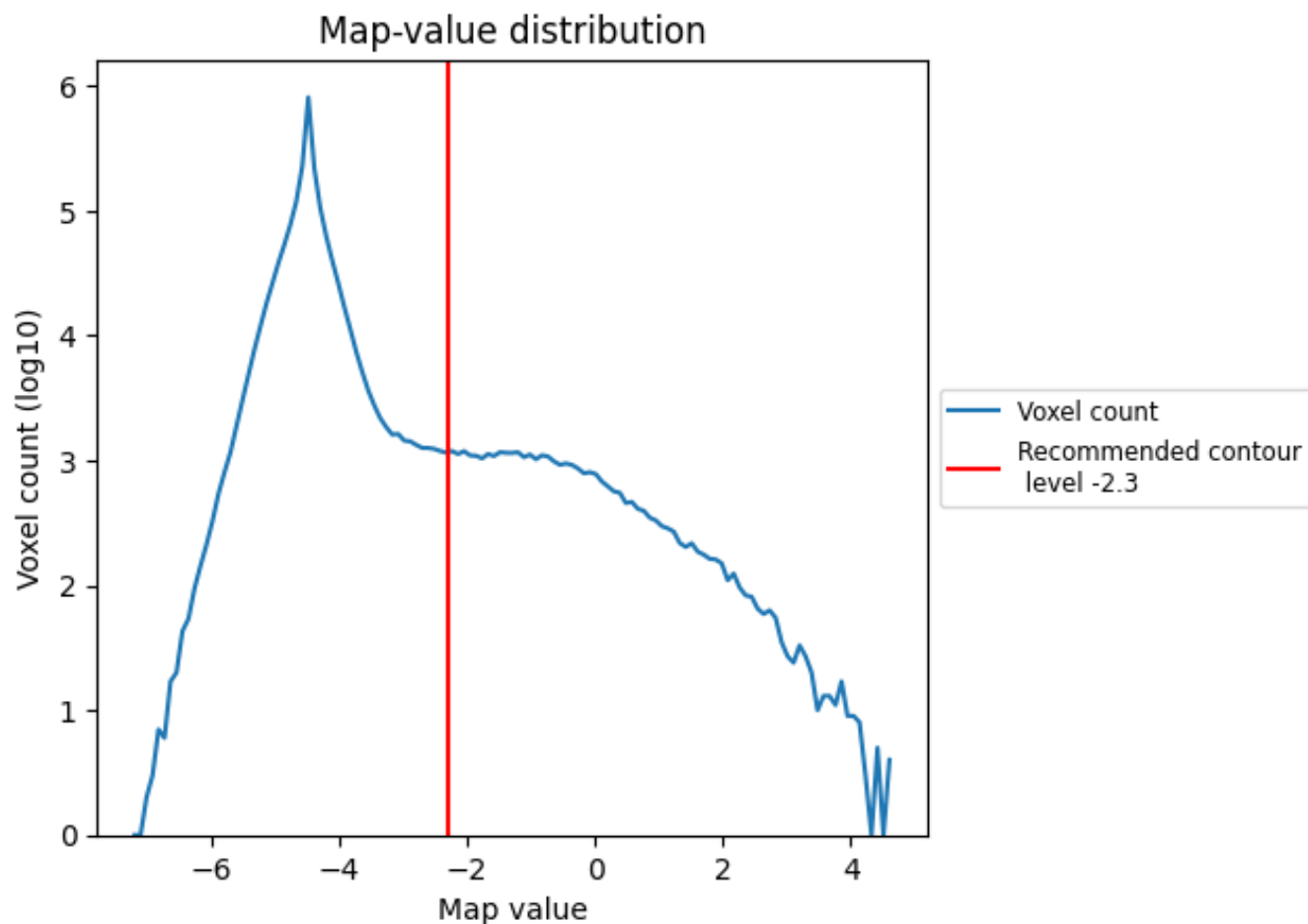
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

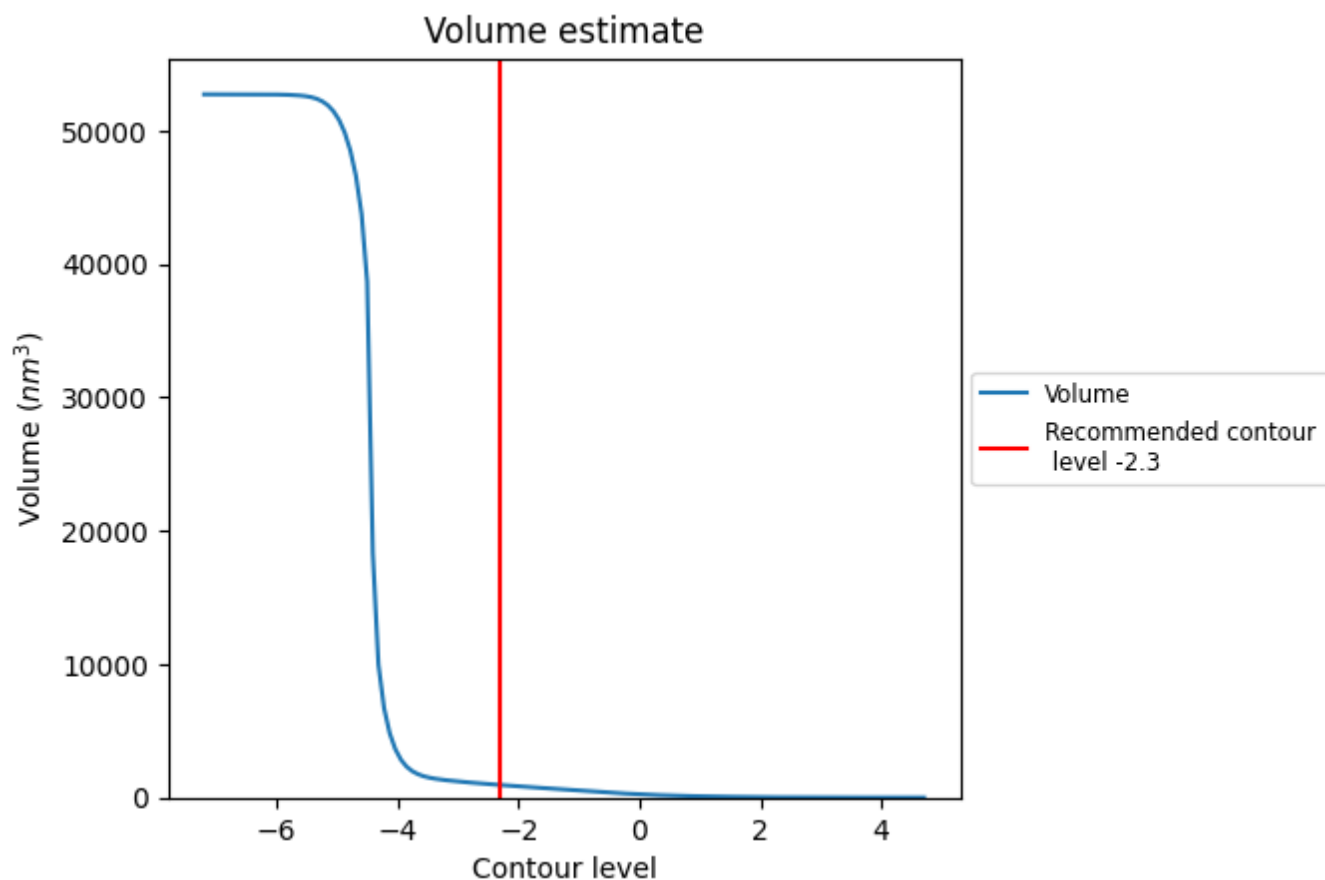
This section contains the results of statistical analysis of the map.

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.

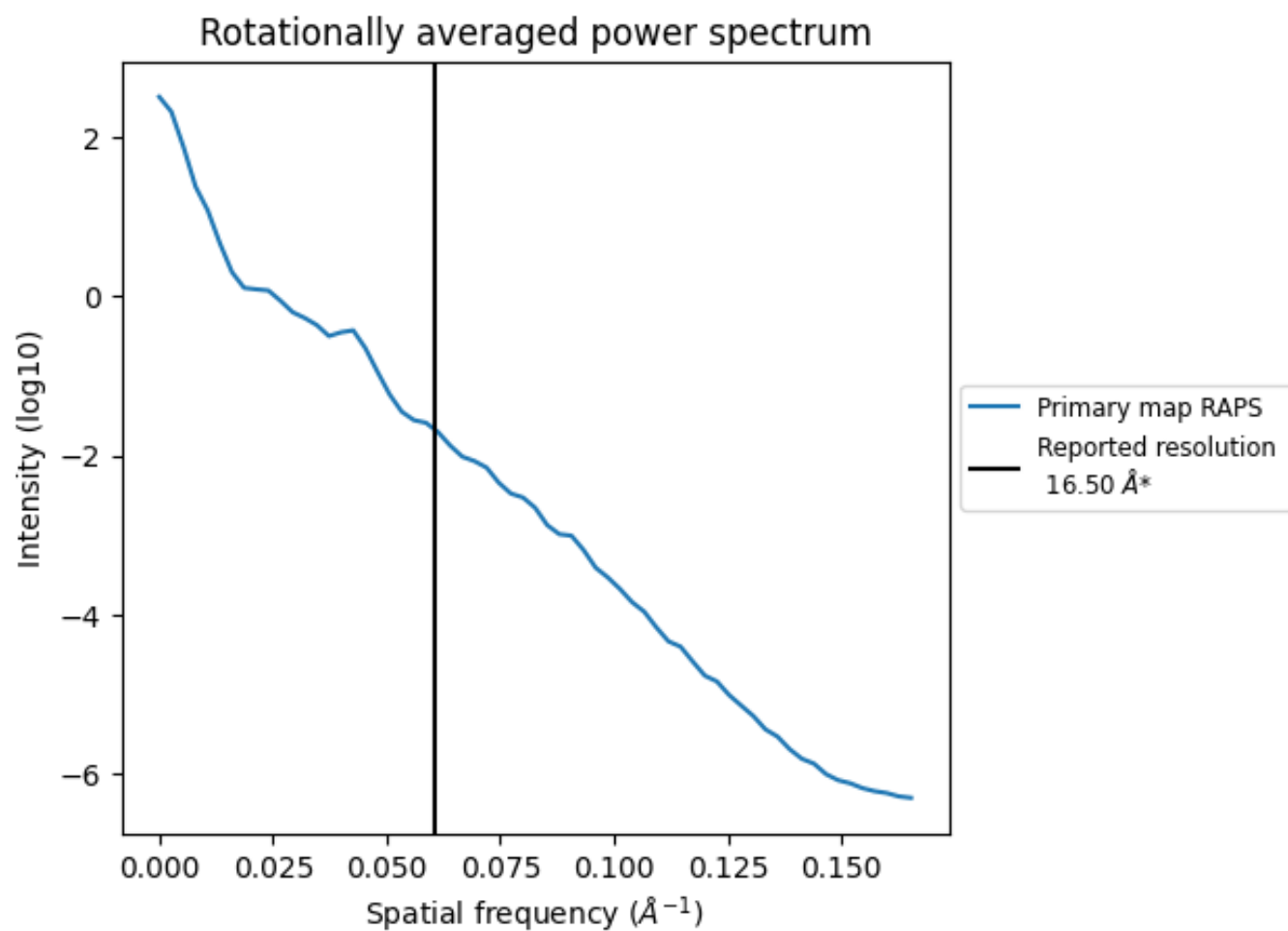
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 943 nm³; this corresponds to an approximate mass of 851 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 0.061 Å⁻¹

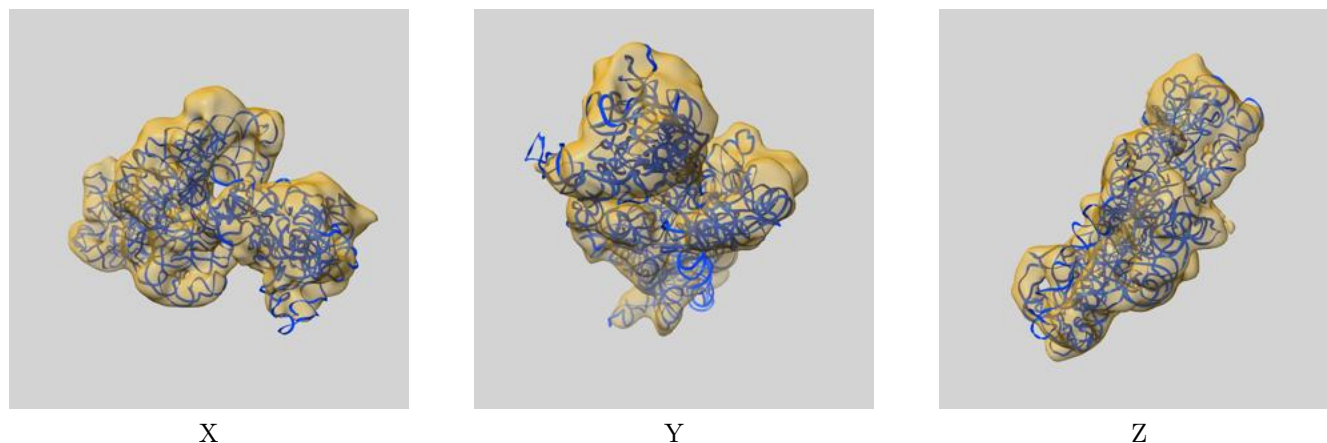
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

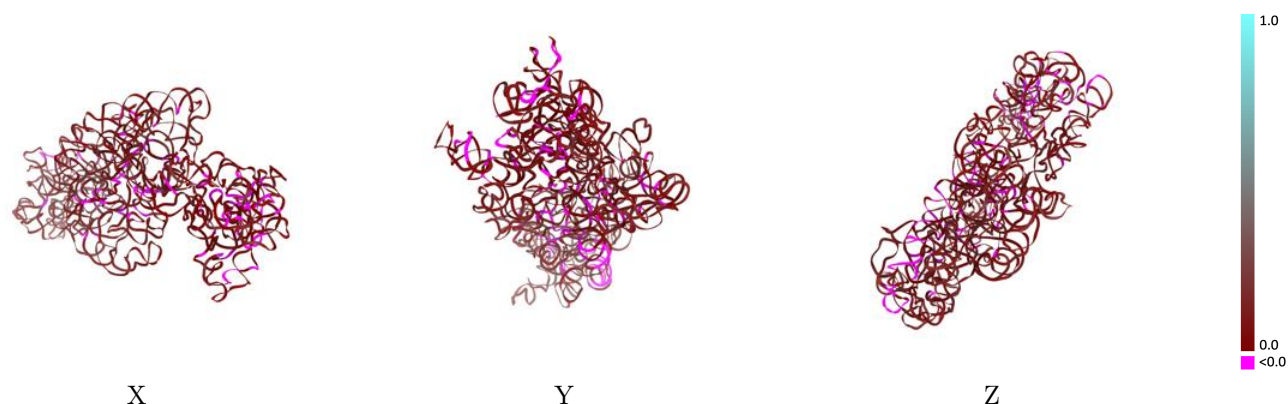
This section contains information regarding the fit between EMDB map EMD-5509 and PDB model 3J2G. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



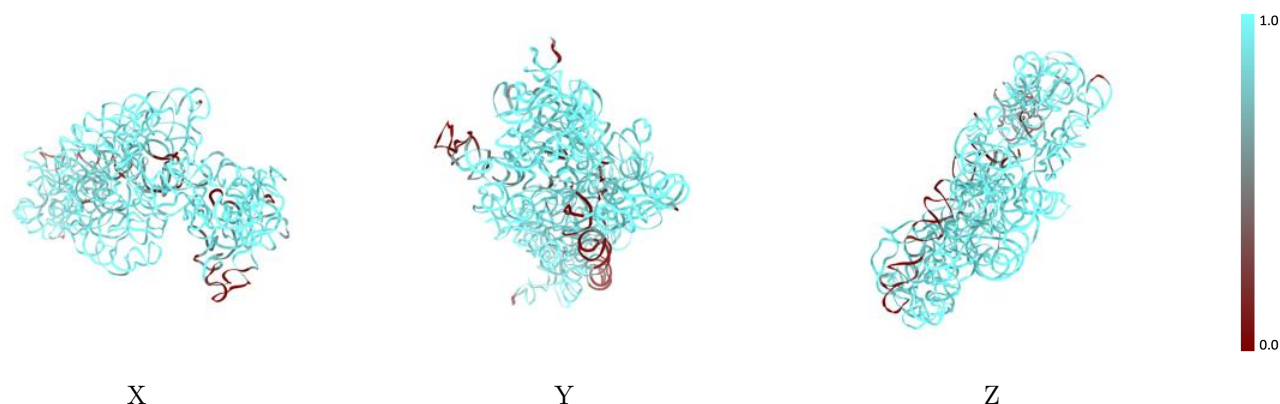
The images above show the 3D surface view of the map at the recommended contour level -2.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



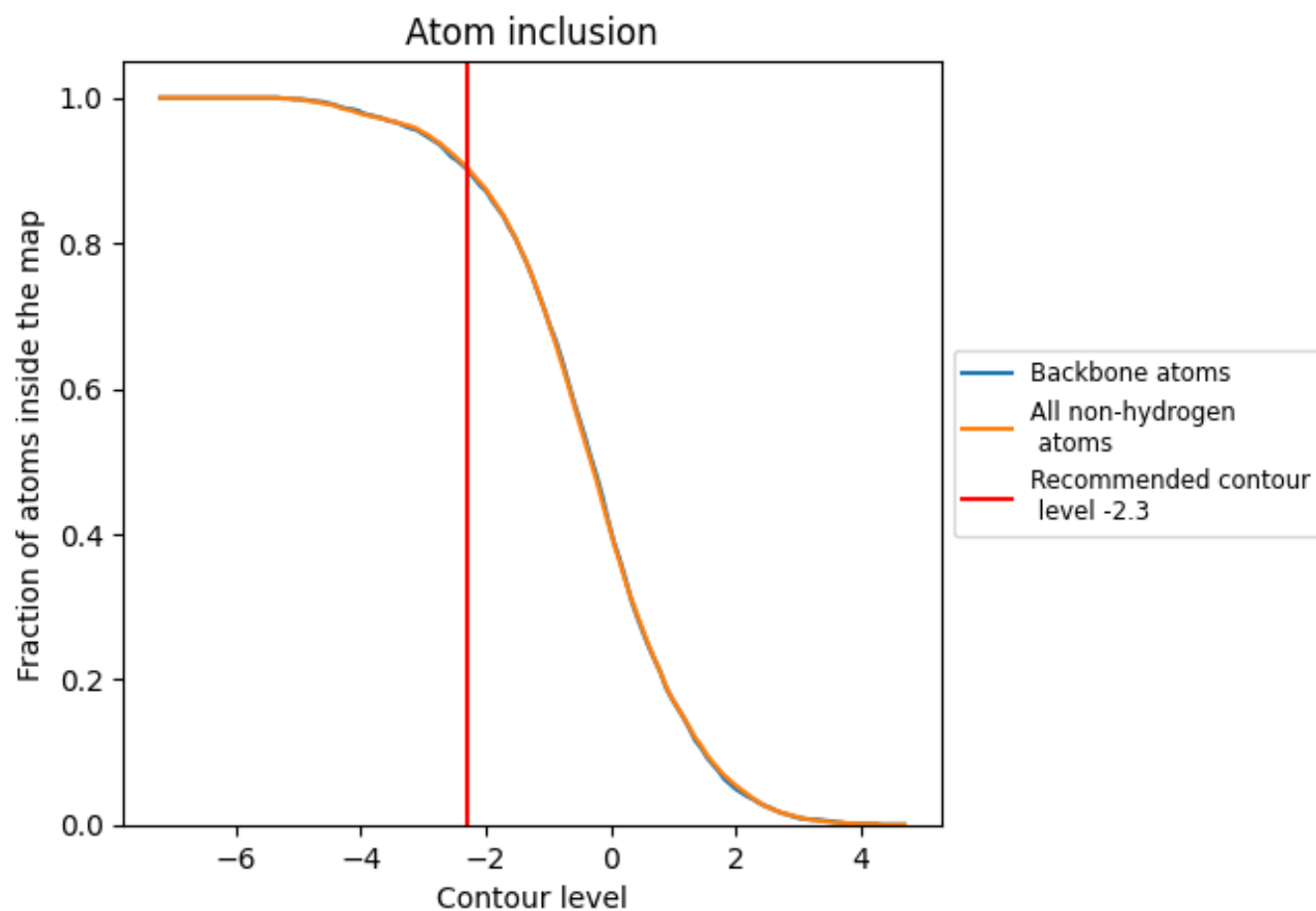
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (-2.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (-2.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9040	0.0840
N	0.9050	0.0840

