



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:33 PM UTC

PDB ID : 3J2A / pdb_00003j2a
EMDB ID : EMD-5502
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 : 13.10 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:

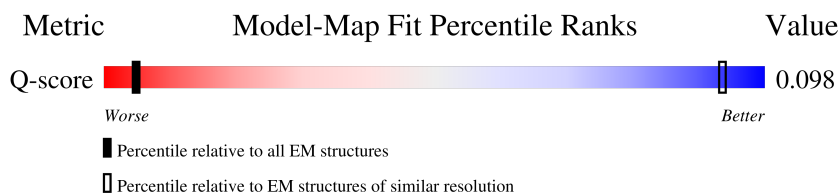
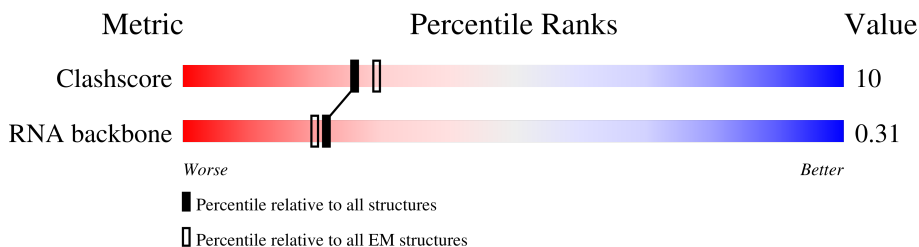
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 13.10 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	61 (12.60 - 13.60)

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.

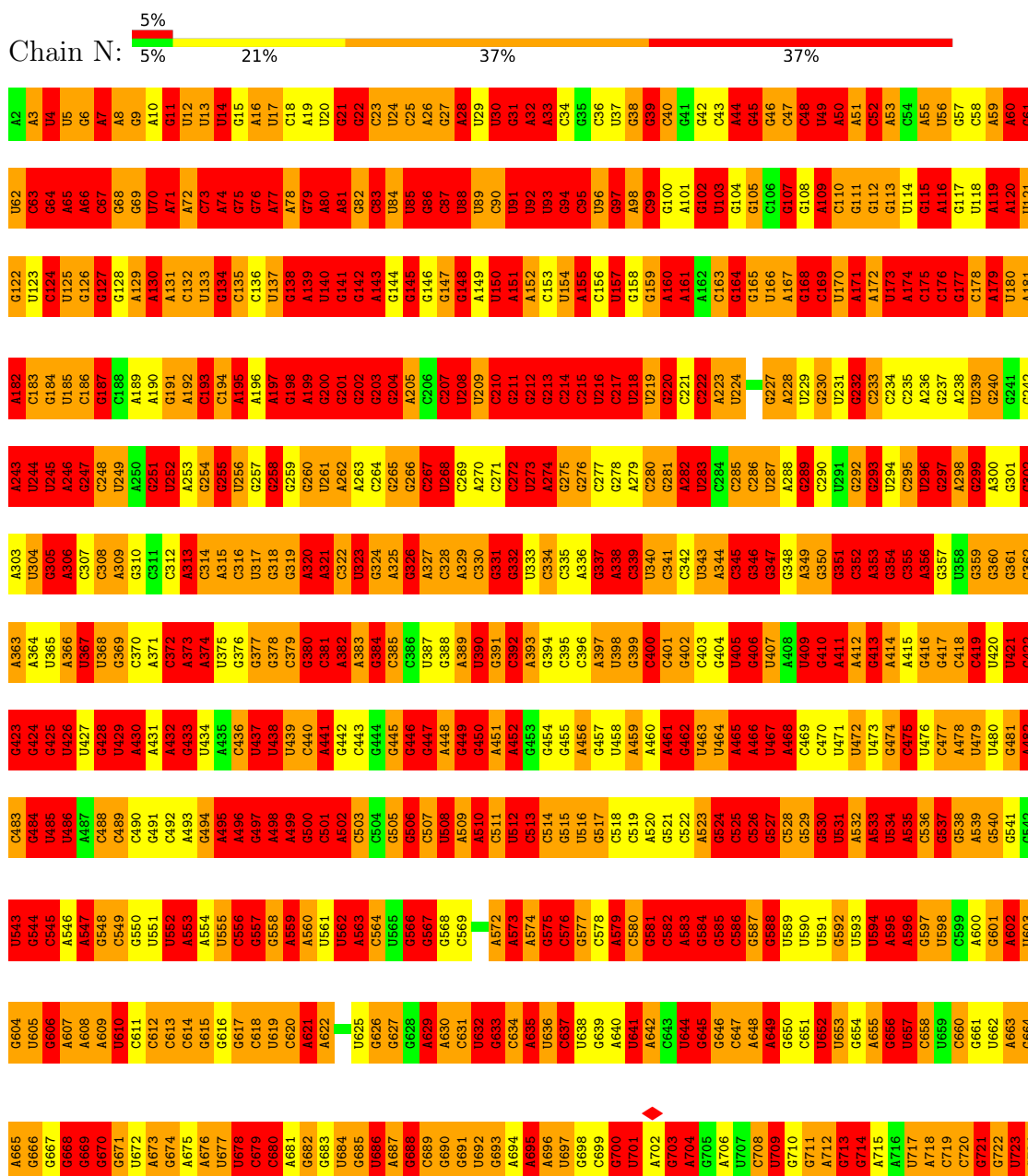
- Molecule 1 is a RNA chain called 16S rRNA.

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

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



G1505	U1445	G1385	C1325	G1265	U1205	A1145	U1085	U1025	U965	U905	A845	G785	G725
U1506	A1446	G1386	U1326	G1266	G1206	A1146	U1086	G1026	G966	A906	G846	G786	C726
A1507	A1447	G1387	C1327	C1267	G1207	C1147	G1087	C1027	C967	A907	G847	A787	G727
A1508	C1448	G1388	C1328	C1268	C1208	U1148	G1088	G1028	A968	A908	G848	A788	A728
C1509	C1449	A1389	A1329	A1269	C1209	C1149	G1089	U1029	U969	A909	G849	A789	A729
C1510	U1450	U1390	U1330	G1270	C1210	U1150	U1090	U1030	C970	C910	U850	A790	G730
U1511	U1451	U1391	G1331	A1271	U1211	A1151	U1091	G1031	G971	U911	G851	G731	C731
U1512	U1452	G1392	A1332	G1272	U1212	A1152	A1092	G1032	C972	C912	G852	C732	C732
A1513	G1453	U1393	G1333	C1273	G1213	G1153	A1093	G1033	G973	A913	C853	A793	G733
G1514	G1454	A1394	A1334	A1274	C1214	G1154	G1094	A1034	A974	A914	U854	A794	G734
G1515	G1455	C1395	U1335	A1275	G1215	A1155	U1095	A1035	A975	A915	U855	C795	C735
G1516	G1456	A1396	G1336	G1276	C1216	G1156	A1096	A1036	G976	U916	G856	C796	C736
G1517	G1457	C1397	G1337	C1277	U1217	C1157	C1097	G1037	A977	G917	G857	C797	C737
A1518	A1458	A1398	G1338	G1278	C1218	C1158	C1098	C1038	A978	A918	G858	C798	C738
A1519	G1459	U1399	A1339	G1279	U1219	U1159	U1099	G1039	C979	A919	G859	C799	C739
C1520	G1458	C1400	A1340	A1280	G1220	U1160	C1100	U1040	C980	A920	G860	U740	U740
C1521	G1459	G1401	G1341	C1281	G1221	C1161	A1101	U1041	U981	U921	G861	U801	G741
U1522	C1460	C1402	C1342	C1282	G1222	G1162	A1102	A1042	U982	G922	C862	A802	G742
G1523	C1461	C1403	G1343	U1283	G1223	A1163	C1103	G1043	A983	A923	G863	G803	A743
C1524	G1462	C1404	C1344	C1284	U1224	G1164	G1104	A1044	C984	C924	A864	U804	C744
G1525	C1463	C1405	U1345	A1285	A1225	U1165	A1105	C1045	C985	G925	A865	C805	C745
G1526	U1463	G1406	A1346	U1286	C1226	G1166	G1106	A1046	U986	G926	C866	C806	A746
U1527	U1464	U1406	G1347	A1287	A1227	A1167	C1107	G1047	G987	G927	G867	A807	A747
U1528	U1465	C1407	U1348	A1288	C1228	U1168	G1108	G1048	G988	G928	C868	C808	G748
G1529	A1466	C1408	A1349	A1289	A1229	U1169	C1109	U1049	U989	G929	G869	G809	A749
G1530	C1466	C1409	A1350	G1290	C1230	A1170	A1110	G1050	C990	C930	U870	C810	C750
A1531	C1467	C1410	U1351	U1291	G1231	A1171	A1111	U1051	U991	C931	U871	C811	U751
C1532	A1468	A1410	C1352	G1292	C1232	C1172	C1112	U1052	U992	C932	A872	G812	G752
C1533	C1469	C1411	G1353	C1293	G1233	U1173	C1113	G1053	G993	G933	A873	U813	A754
U1470	U1471	C1412	U1354	G1294	C1234	G1174	C1114	C1054	A994	C934	G874	A814	C754
U1471	U1472	C1413	G1355	U1295	U1235	G1175	U1115	A1055	C995	C935	U875	A815	G755
U1472	U1473	G1414	G1356	G1296	A1236	A1176	U1116	U1056	A996	C936	C876	A816	C756
G1473	U1474	G1415	A1357	G1297	C1237	G1177	A1117	G1057	U997	C937	G877	C817	U757
U1474	G1475	G1416	U1358	U1298	A1238	G1178	U1118	G1058	C998	A938	A878	C818	C758
G1475	G1476	G1417	C1359	A1299	A1239	A1179	C1119	C1059	C999	G939	C879	A819	A759
U1476	G1477	A1418	A1360	G1300	U1240	A1180	C1120	U1060	A1000	C940	C880	U820	G760
U1477	U1478	A1419	G1361	U1301	G1241	G1181	U1121	G1061	C1001	G941	G881	G821	G761
U1478	C1479	C1420	A1362	C1302	G1242	G1182	U1122	U1062	G1002	C942	C882	U822	U762
C1480	U1481	U1421	A1363	C1303	U1243	U1183	U1123	C1063	G1003	U943	C883	C823	G763
U1481	G1482	G1422	G1364	G1304	G1244	G1184	G1124	G1064	A1004	G944	U884	G824	C764
G1482	G1483	G1423	G1365	G1305	C1245	G1185	U1125	U1065	A1005	G945	G885	A825	G765
C1484	U1485	G1424	C1366	A1306	A1246	G1186	U1126	C1066	G1006	A946	G886	C826	A766
U1485	G1486	G1425	G1367	U1307	U1247	G1187	G1127	A1067	U1007	G947	G887	U827	A767
G1486	G1487	A1428	A1374	U1308	A1248	U1188	C1128	G1068	U1008	C948	G888	U828	A768
G1487	G1488	A1429	A1375	U1309	C1249	U1189	C1129	C1069	U1009	A949	A889	G829	G769
G1488	A1431	A1430	U1376	G1310	A1250	U1190	A1130	C1070	G1010	U950	A889	G830	C770
G1489	G1432	G1431	A1377	A1311	A1251	A1191	G1131	C1071	C1011	G951	U891	A831	G771
U1490	A1433	C1427	C1378	G1312	U1252	C1192	C1132	G1072	A1012	U952	A892	G832	U772
G1491	A1434	U1428	G1379	U1313	G1253	G1193	G1133	U1073	G1013	G953	C893	G833	G773
A1492	U1435	A1428	A1374	C1314	A1254	U1194	G1134	G1074	A1014	G954	G894	U834	G774
A1493	U1436	A1429	A1375	U1315	A1255	C1195	U1135	U1075	G1015	U955	G895	U835	G775
G1494	A1437	A1430	U1376	G1316	A1256	A1196	C1136	G1076	A1016	U956	C896	G836	G776
U1495	G1438	A1431	A1377	C1317	A1257	U1197	G1137	C1077	U1017	U957	C897	U837	A777
G1496	G1439	G1432	C1378	G1318	U1258	A1198	G1138	U1078	G1018	U958	G898	G838	G778
G1497	U1440	A1433	A1379	A1319	G1259	U1199	G1139	G1079	A1019	A959	C899	C839	C779
U1498	U1441	A1434	U1380	C1320	G1260	U1200	G1140	A1080	U1020	U960	A900	G840	A780
A1499	U1442	U1435	U1381	U1321	A1261	A1201	C1141	A1081	A1021	U961	A901	C841	A781
A1500	C1443	C1382	C1382	C1322	C1262	U1202	G1142	A1082	A1022	C962	G902	U842	A782
A1502	U1444	C1383	A1384	G1323	C1263	C1203	G1143	U1083	A1023	G963	G903	U843	C783
A1503		C1384		A1324	U1264	A1204	G1144	G1084	G1024	A964	U904	G844	A784

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30262	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Weiner filter	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	80000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	4.176	Depositor
Minimum map value	-6.630	Depositor
Average map value	-3.903	Depositor
Map value standard deviation	0.568	Depositor
Recommended contour level	-2.8	Depositor
Map size (\AA)	345.0, 345.0, 345.0	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.76, 2.76, 2.76	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	2.06	820/36831 (2.2%)	2.09	1930/57458 (3.4%)

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	937

The worst 5 of 820 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	1246	A	C5'-C4'	10.50	1.67	1.51
1	N	592	G	C4'-C3'	10.01	1.67	1.52
1	N	586	C	C4'-C3'	9.64	1.67	1.52
1	N	1022	A	C4'-C3'	9.22	1.66	1.52
1	N	481	G	C4'-C3'	9.11	1.66	1.53

The worst 5 of 1930 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	438	U	P-O3'-C3'	22.22	153.54	120.20
1	N	94	G	P-O3'-C3'	18.14	147.41	120.20
1	N	547	A	P-O3'-C3'	17.31	146.17	120.20
1	N	555	U	P-O3'-C3'	17.31	146.16	120.20
1	N	789	U	P-O5'-C5'	16.94	146.30	120.90

There are no chirality outliers.

5 of 937 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	11	G	Sidechain
1	N	12	U	Sidechain
1	N	4	U	Sidechain
1	N	7	A	Sidechain
1	N	8	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	16528	504	0
All	All	32892	16554	16528	504	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 10.

The worst 5 of 504 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:928:G:H21	1:N:1533:C:H42	1.24	0.85
1:N:67:C:H2'	1:N:68:G:C8	2.13	0.83
1:N:50:A:H1'	1:N:52:C:C6	2.23	0.73
1:N:1266:G:H21	1:N:1269:A:H8	1.39	0.70
1:N:1394:A:H3'	1:N:1395:C:H5'	1.74	0.69

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%)	472 (30%)	145 (9%)

5 of 472 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	7	A

5 of 145 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	1228	C
1	N	1530	G
1	N	1282	C
1	N	1363	A
1	N	430	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.

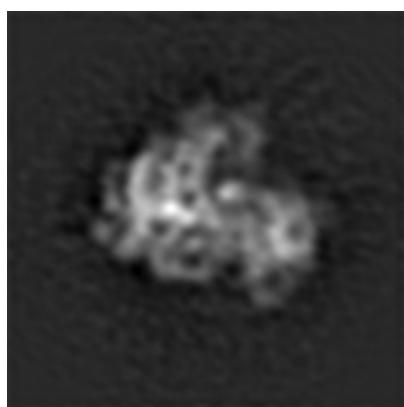
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5502. These allow visual inspection of the internal detail of the map and identification of artifacts.

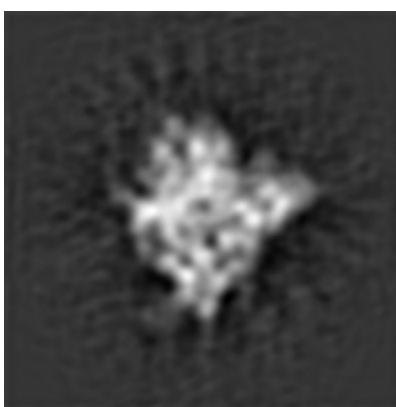
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

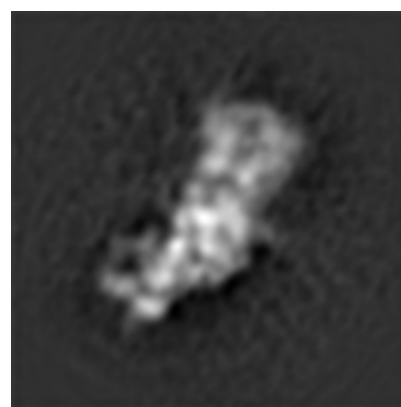
6.1.1 Primary map



X



Y

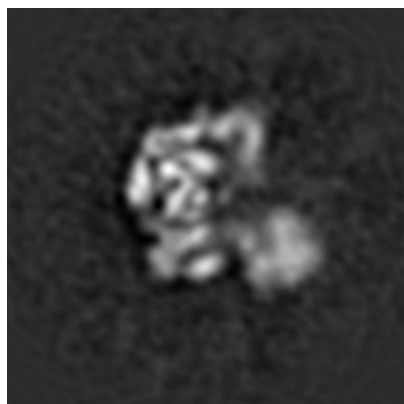


Z

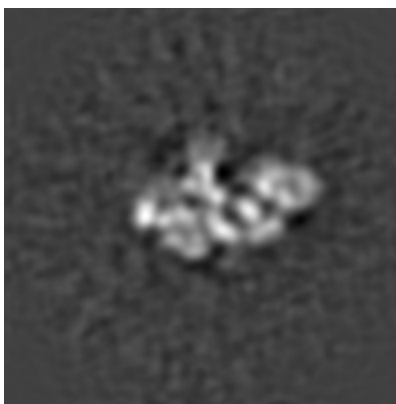
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

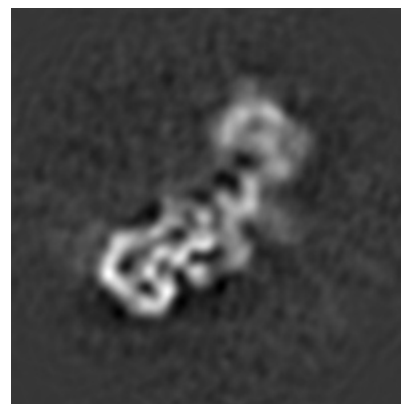
6.2.1 Primary map



X Index: 62



Y Index: 62

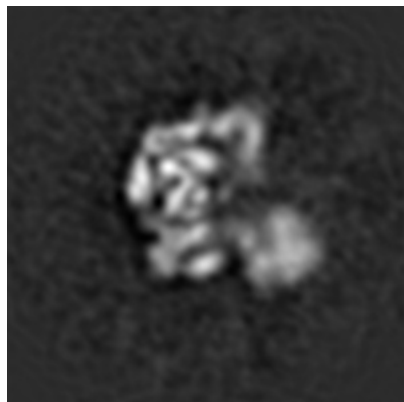


Z Index: 62

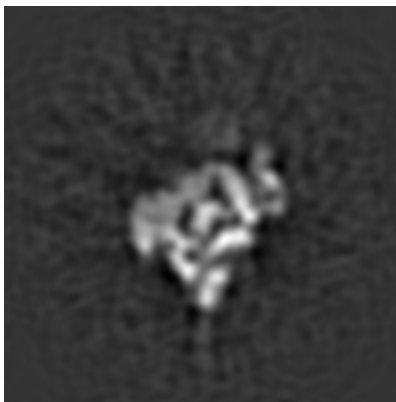
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

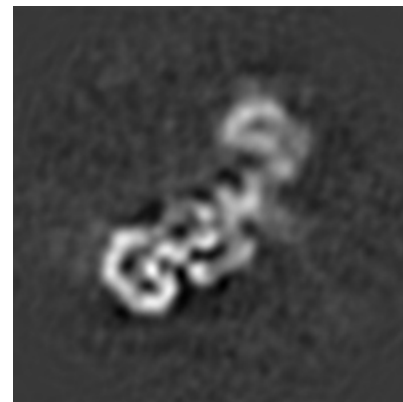
6.3.1 Primary map



X Index: 62



Y Index: 51

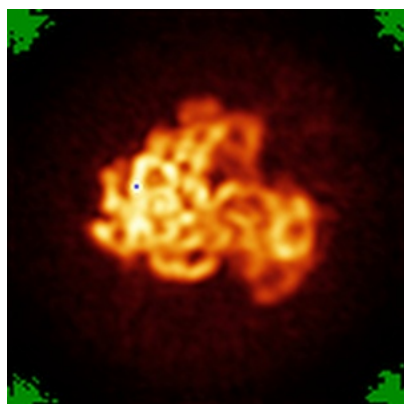


Z Index: 63

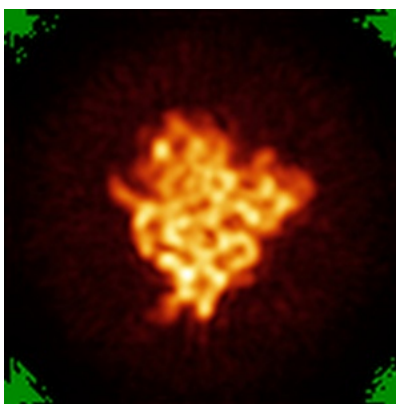
The images above show the largest variance slices of the map in three orthogonal directions.

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

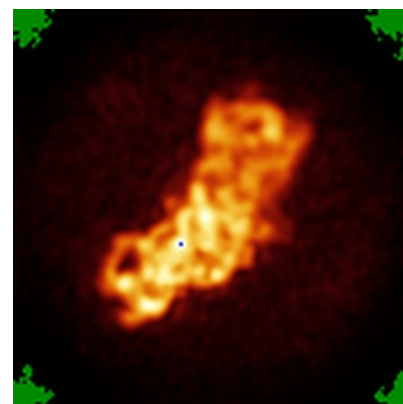
6.4.1 Primary map



X



Y

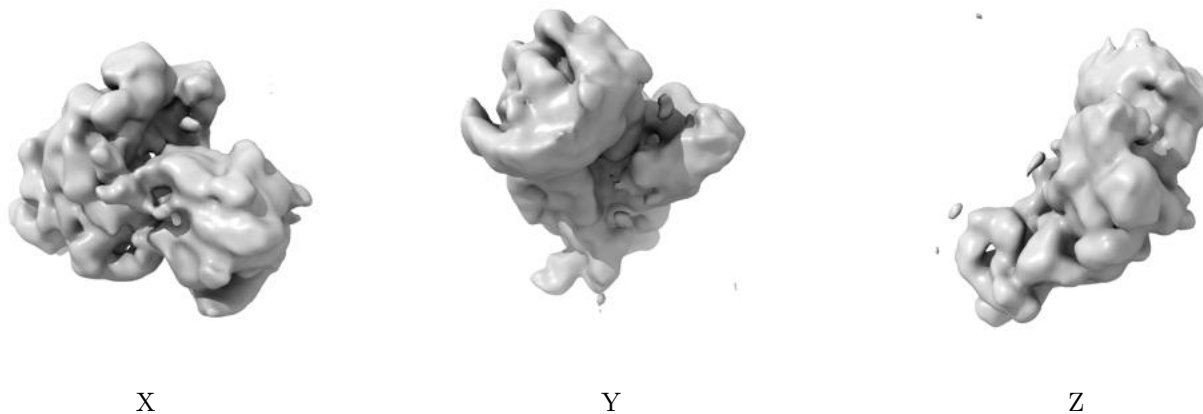


Z

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

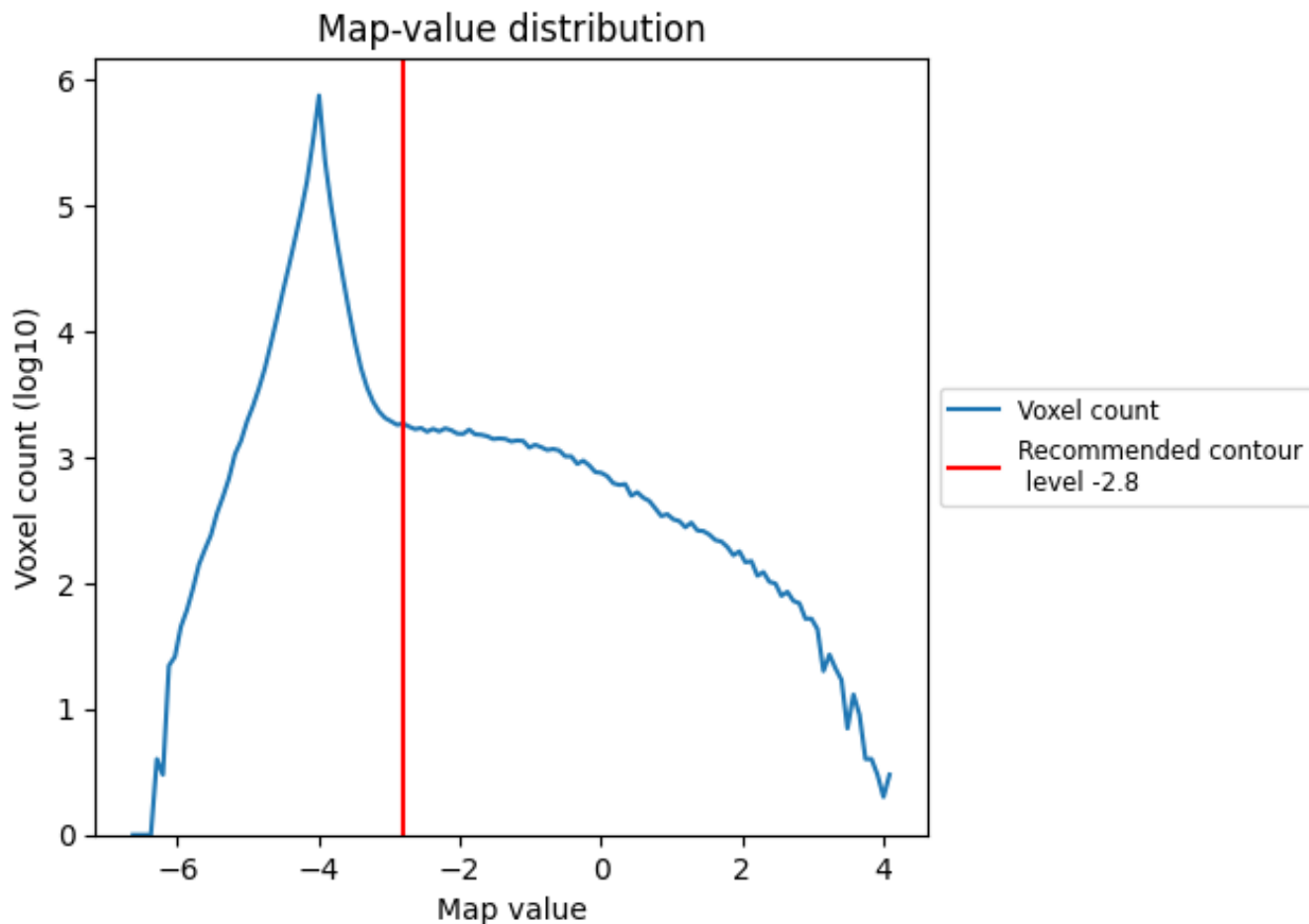
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

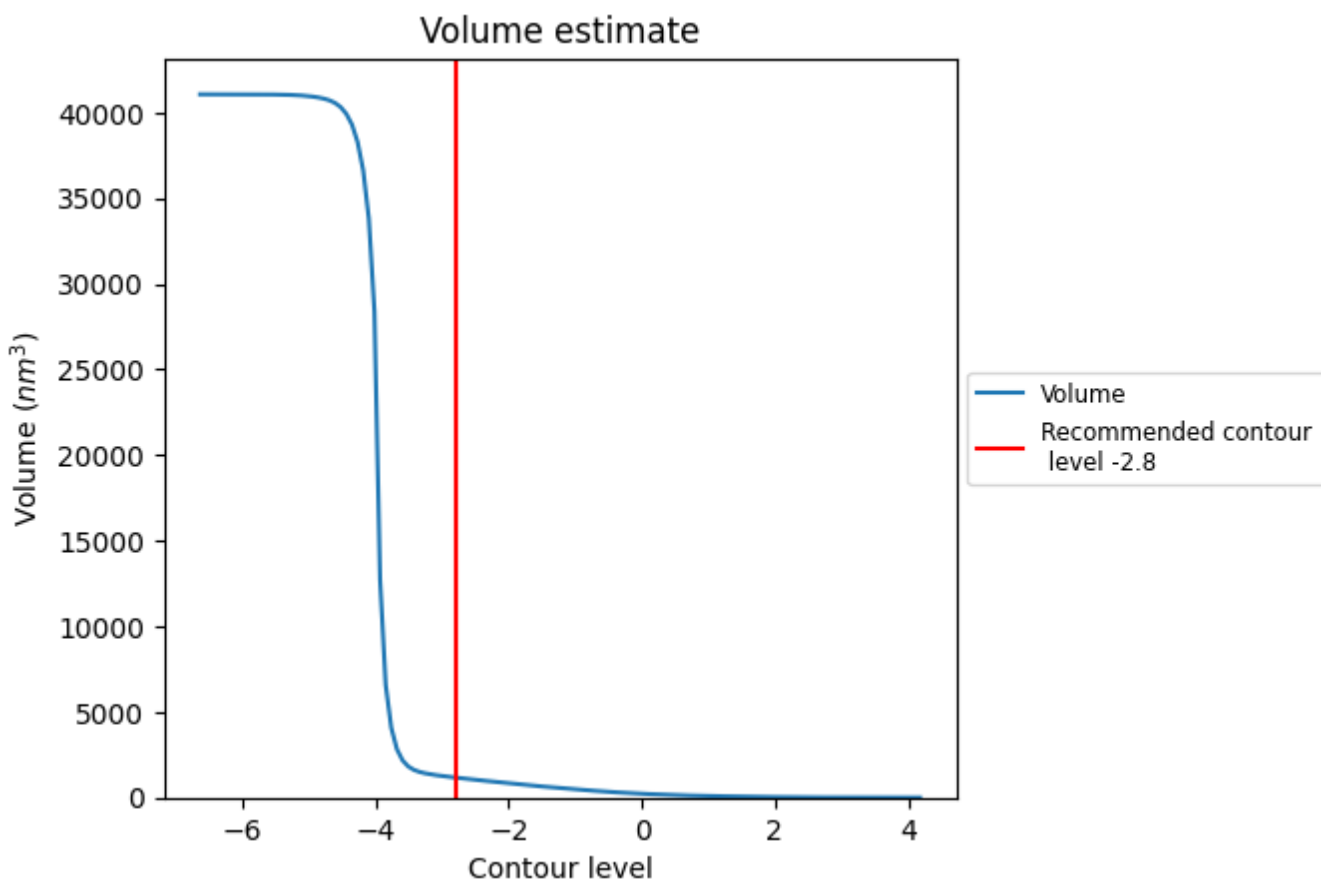
This section contains the results of statistical analysis of the map.

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.

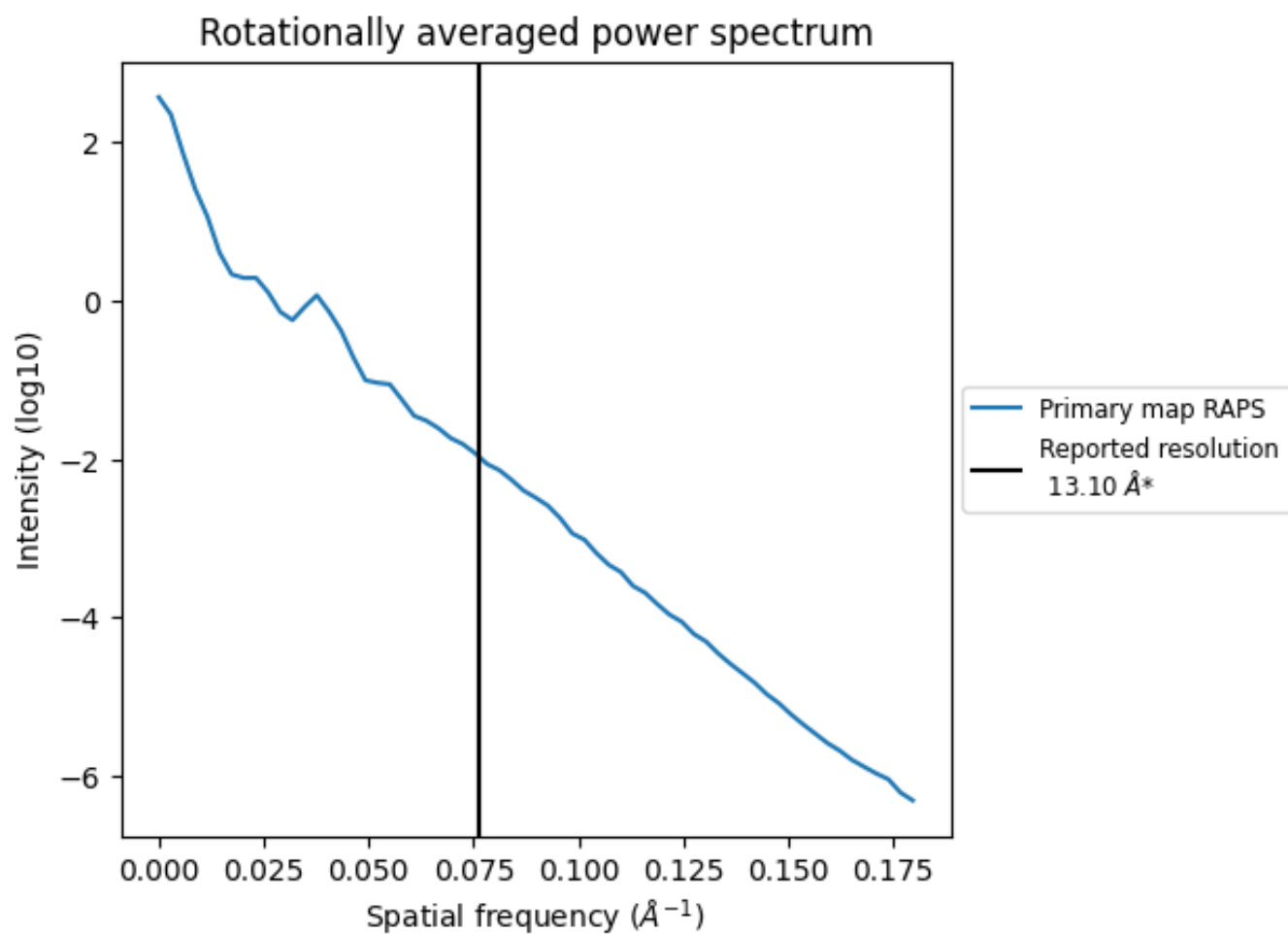
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1168 nm³; this corresponds to an approximate mass of 1055 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.076 Å⁻¹

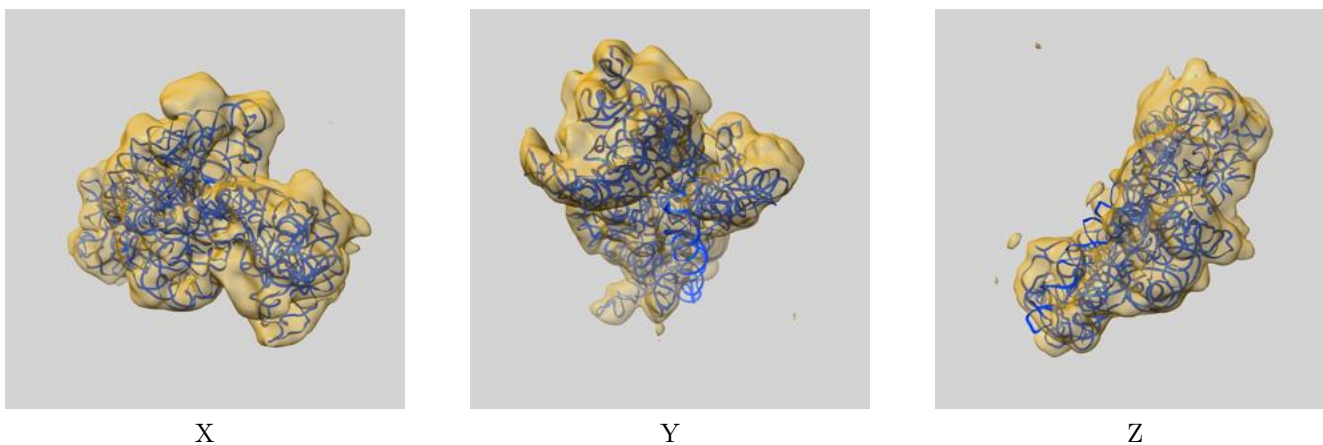
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

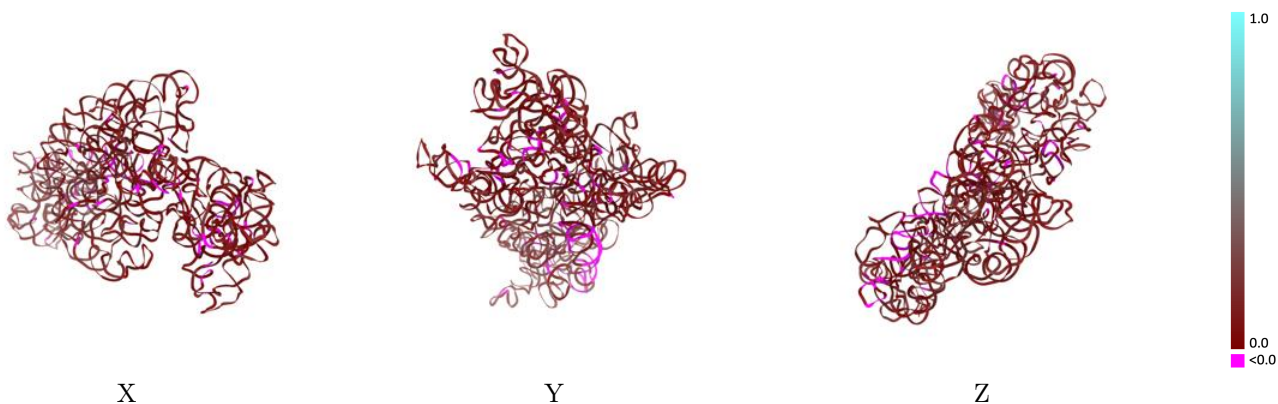
This section contains information regarding the fit between EMDB map EMD-5502 and PDB model 3J2A. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



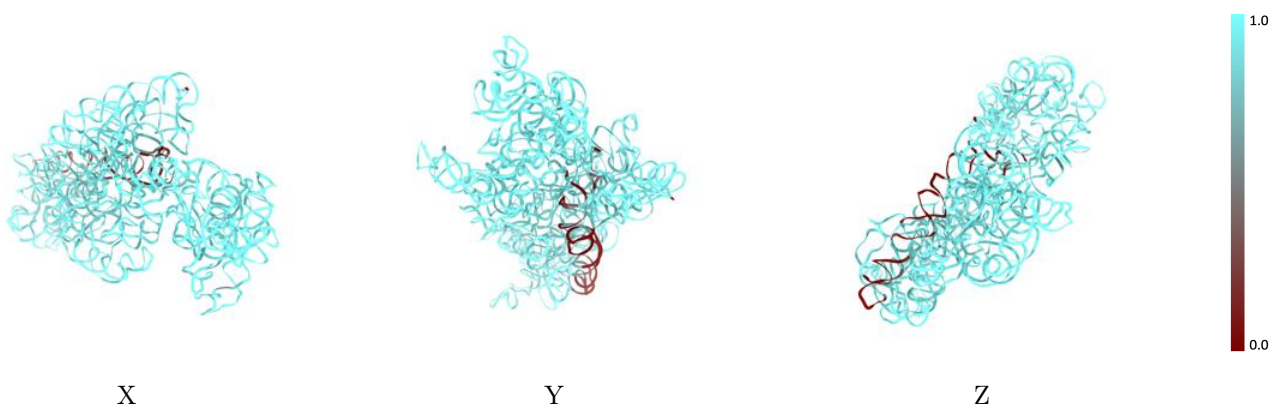
The images above show the 3D surface view of the map at the recommended contour level -2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



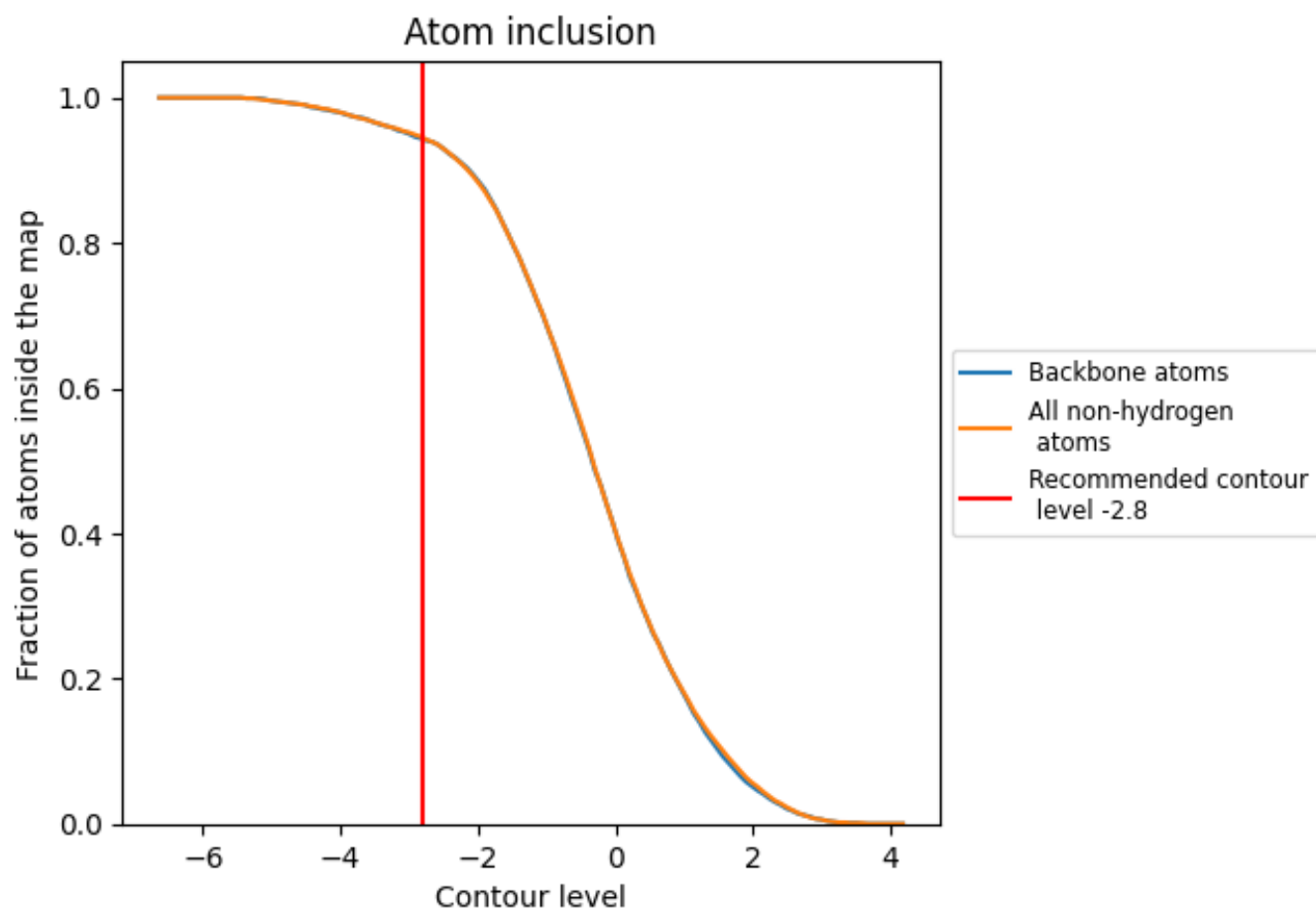
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (-2.8).





9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (-2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9450	 0.0980
N	 0.9450	 0.0980

