



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 03:35 AM UTC

PDB ID : 3J28 / pdb_00003j28
EMDB ID : EMD-5500
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 : 12.90 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

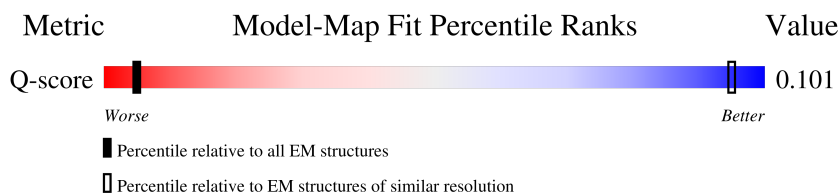
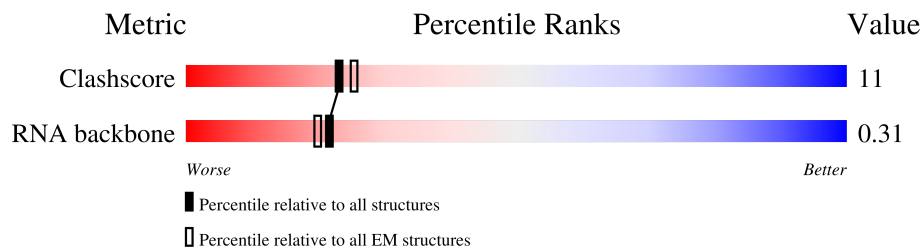
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 12.90 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	58 (12.40 - 13.40)

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	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.

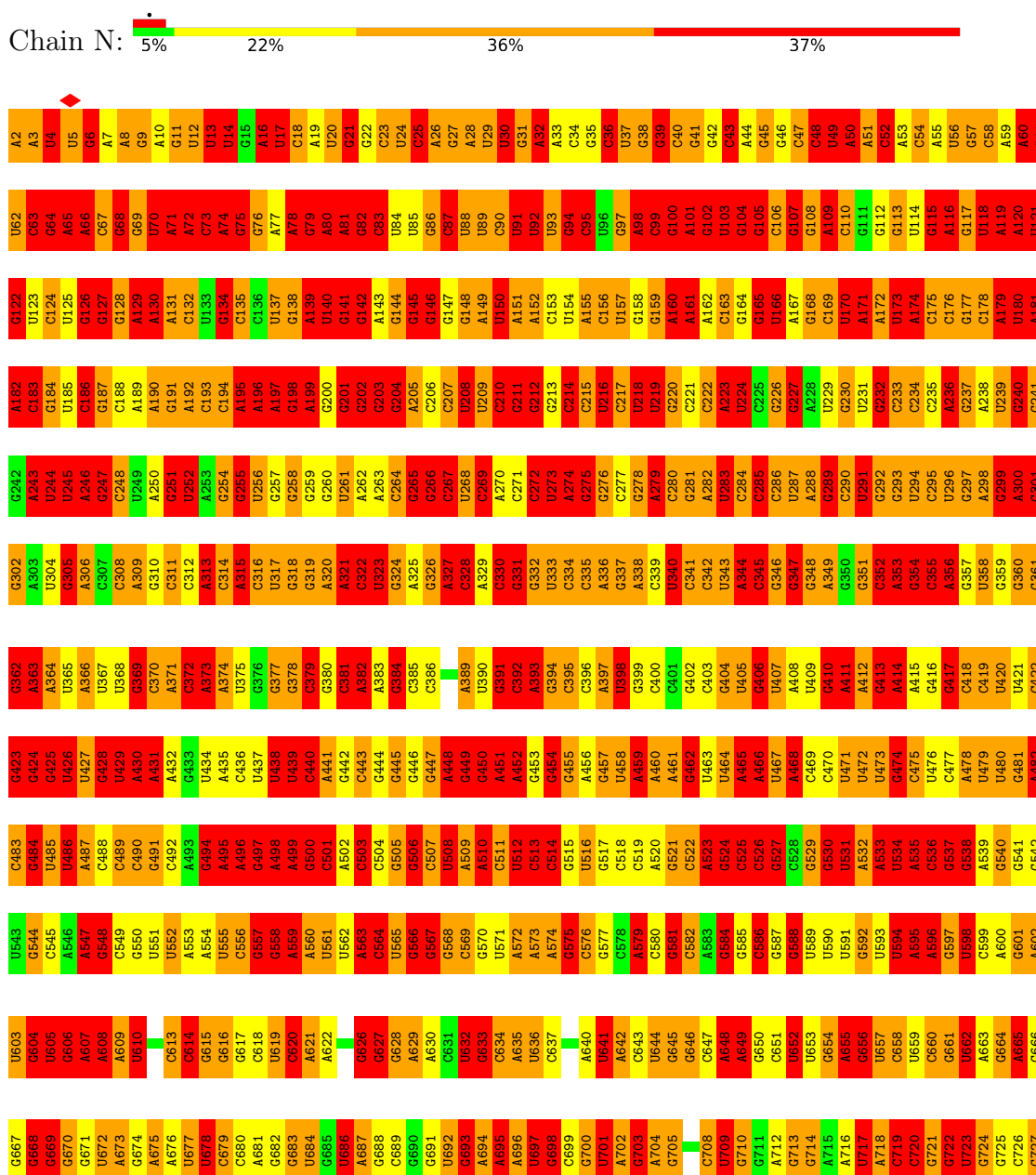
- Molecule 1 is a RNA chain called 16S rRNA.

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



C1510	U1450	U1390	U1330	G1270	G1210	A1150	U1090	U1030	C970	A908	C848	U788	A728
G1511	U1451	U1391	G1331	A1271	U1211	A1151	U1091	C1031	G971	A909	G849	U789	A729
U1512	A1532	G1392	A1332	G1272	U1212	A1152	A1092	G1032	C972	C910	U850	A790	A730
A1513	U1333	U1333	C1273	A1213	U1213	G1153	A1093	G1033	G973	U911	G851	G791	G731
G1514	A1394	A1394	C1274	A1214	G1214	G1154	G1094	A1034	A974	A912	G852	A792	C732
G1515	C1395	A1395	U1335	A1275	G1215	A1155	U1095	A1035	A975	C913	C853	U793	G733
G1516	A1396	A1396	C1336	G1276	A1216	G1156	C1096	A1036	G976	A914	U854	A794	G734
G1517	C1397	G1397	G1337	C1277	C1217	A1157	C1097	C1037	A977	A915	U855	A795	C735
A1518	A1398	A1398	G1338	G1278	C1218	C1158	C1098	C1038	A978	U916	C856	C796	C736
U1519	A1399	A1399	A1339	G1279	A1219	U1159	G1099	U1039	C979	G917	C857	C797	C737
C1520	A1400	A1400	A1340	A1280	G1220	U1160	C1100	U1040	C980	A918	C858	U798	C738
C1521	G1401	G1401	U1341	C1281	G1221	C1161	A1101	G1041	U981	A919	G859	G799	C739
U1522	C1402	C1402	C1342	C1282	G1222	C1162	A1102	A1042	U982	U920	A860	U740	U740
G1523	C1403	U1283	G1343	U1283	C1223	A1163	C1103	G1043	A983	U921	C861	G741	G741
C1524	C1404	C1284	C1344	C1284	U1224	G1164	G1104	A1044	C984	G922	C862	G742	G742
G1525	G1405	A1285	U1345	A1285	A1225	U1165	A1105	C1045	C985	A923	U863	G803	G743
G1526	U1406	U1286	A1346	A1286	C1226	G1166	G1106	A1046	U986	G924	A864	U804	C744
U1527	G1407	A1287	G1347	A1287	G1227	A1167	C1107	G1047	U987	G925	A865	C805	G745
A1528	A1408	A1288	U1348	A1288	C1228	U1168	G1108	G1048	G988	G926	C866	C806	A746
U1529	A1409	A1289	A1349	A1289	A1229	A1169	G1109	U1049	U989	G927	C867	A747	A747
G1530	C1409	A1290	A1350	G1290	C1230	A1170	A1110	G1050	G928	U928	C868	C808	G748
A1531	A1410	U1291	U1351	G1291	G1231	A1171	A1111	C1051	C929	G929	G869	A749	A749
U1532	C1411	G1292	C1352	G1292	U1232	C1172	C1112	U1052	U991	C930	U870	C810	C750
C1533	U1471	C1293	G1353	G1293	U1233	U1173	C1113	G1053	U992	C931	U871	G811	U751
A1534	A1412	C1294	U1354	G1294	G1233	G1174	C1114	C1054	G993	G932	A872	G812	G752
	U1472	U1295	G1355	U1295	C1234	G1175	U1115	A1055	A994	C933	A873	U813	A753
	G1473	C1296	G1356	C1296	U1235	A1176	U1116	U1056	C995	C934	G874	A814	C754
	U1474	G1297	U1357	G1297	A1236	G1177	G1057	G1057	A996	A935	U875	A815	G755
	G1475	U1298	U1358	U1298	C1237	G1178	U1118	G1058	U997	C936	C876	A816	C756
	A1476	A1299	C1359	A1299	A1238	A1179	U1119	C1059	C998	A937	U877	C817	U757
	U1477	G1300	G1361	G1300	A1239	A1180	C1120	U1060	C999	A938	A878	G818	G758
	U1478	U1301	G1362	U1301	G1241	G1181	U1121	G1061	C1001	G939	C879	A819	A759
	C1479	C1302	A1363	C1302	G1242	U1182	U1122	U1062	C940	C940	C880	U820	G760
	A1480	G1303	U1364	G1303	C1243	U1183	U1123	C1063	G941	G941	G881	G821	G761
	U1481	G1304	G1365	G1304	G1244	U1184	G1124	G1064	G942	G942	C882	U822	U762
	A1482	G1305	G1366	G1305	G1245	G1185	U1125	U1065	U943	C883	C883	G823	G763
	A1483	A1306	C1367	A1306	A1246	G1186	U1126	C1066	G944	G944	U884	G824	C764
	C1484	U1307	U1368	U1307	U1247	G1187	G1127	A1067	G945	G945	G885	A825	G765
	U1485	G1308	A1369	U1308	A1248	A1188	C1128	G1068	A946	A946	C886	A826	A766
	C1486	G1309	G1370	G1309	C1249	U1189	C1129	C1069	U947	G947	G887	U827	A767
	A1487	A1310	G1371	A1310	A1250	G1190	A1130	U1070	C948	C948	G888	U828	A768
	U1488	A1311	U1372	A1311	A1251	A1191	G1131	C1071	A949	A949	A889	G829	G769
	G1489	G1312	U1373	G1312	A1252	C1192	C1132	G1072	U950	U950	U890	G830	C770
	U1490	U1313	C1374	U1313	G1253	G1193	G1133	U1073	C951	C951	G891	A831	G771
	G1491	C1314	A1375	C1314	A1254	U1194	U1134	G1074	U952	U952	A892	G832	U772
	A1492	G1315	U1376	G1315	A1255	C1195	U1135	U1075	G953	G953	C893	G833	G773
	U1493	G1316	A1377	G1316	A1256	A1196	C1136	G1076	G954	G954	G894	U834	G774
	G1494	C1317	U1378	C1317	A1257	A1197	G1137	G1077	U955	U955	G895	U835	G775
	U1495	A1318	G1379	A1318	A1258	G1198	G1138	U1078	U956	U956	C896	G836	G776
	C1496	G1319	U1380	G1319	C1259	U1199	G1139	G1079	U957	U957	C897	U837	A777
	A1497	C1320	A1381	C1320	G1260	C1200	C1140	A1080	U960	U960	C898	G838	G778
	U1498	A1321	U1382	A1321	A1261	A1201	G1141	A1081	U961	U961	C899	C839	C779
	A1499	C1322	C1383	C1322	C1262	U1202	G1142	A1082	C962	C962	A900	C840	A780
	U1500	G1323	U1384	G1323	C1263	C1203	U1143	U1083	G963	G963	A901	C841	A781
	C1501	A1324	C1385	A1324	U1264	G1144	G1144	G1084	U1022	U1022	G902	U842	A782
	U1502	G1325	A1386	G1325	C1265	A1204	G1145	U1085	A1023	A1023	G903	U843	C783
	A1503	U1326	G1387	U1326	G1266	G1205	A1146	U1086	G1024	G1024	U904	C844	A784
	U1504	C1327	U1388	C1327	G1267	U1147	U1147	G1087	G966	G966	U905	A845	G785
	G1505	A1328	C1389	A1328	G1268	C1206	U1148	U1088	C967	C967	A906	G846	A786
	U1506	G1329		A1329	A1269	C1208	U1149	G1089	A968	A968	G847	G847	A787
	A1507					C1209	C1149		C1027	C1027			
	U1508								U1029	U1029			
	C1509												

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32152	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	4.191	Depositor
Minimum map value	-6.676	Depositor
Average map value	-4.024	Depositor
Map value standard deviation	0.567	Depositor
Recommended contour level	-2.8	Depositor
Map size (Å)	345.0, 345.0, 345.0	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.76, 2.76, 2.76	Depositor

5 Model quality

5.1 Standard geometry

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	2.05	814/36831 (2.2%)	2.08	1954/57458 (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	948

The worst 5 of 814 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	1181	G	C1'-N9	11.15	1.63	1.47
1	N	1240	U	C1'-N1	10.94	1.64	1.48
1	N	1485	U	C1'-N1	10.46	1.64	1.48
1	N	11	G	C4'-C3'	9.35	1.66	1.52
1	N	1229	A	C5'-C4'	9.24	1.65	1.51

The worst 5 of 1954 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	1362	A	P-O3'-C3'	23.49	155.43	120.20
1	N	94	G	P-O3'-C3'	19.62	149.63	120.20
1	N	1242	G	P-O5'-C5'	18.54	148.72	120.90
1	N	982	U	P-O3'-C3'	18.00	147.20	120.20
1	N	1173	U	P-O5'-C5'	17.83	147.65	120.90

There are no chirality outliers.

5 of 948 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	10	A	Sidechain
1	N	2	A	Sidechain
1	N	4	U	Sidechain
1	N	5	U	Sidechain
1	N	6	G	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	16511	547	0
All	All	32892	16554	16511	547	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 547 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:664:G:H22	1:N:741:G:H1	1.31	0.76
1:N:596:A:H61	1:N:644:U:H3	1.37	0.73
1:N:116:A:H61	1:N:313:A:H1'	1.56	0.70
1:N:67:C:H2'	1:N:68:G:C8	2.26	0.70
1:N:381:C:C5	1:N:382:A:C5	2.81	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 ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	N	1532/1533 (99%)	469 (30%)	150 (9%)

5 of 469 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	1190	G
1	N	1440	U
1	N	1201	A
1	N	1319	A
1	N	428	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

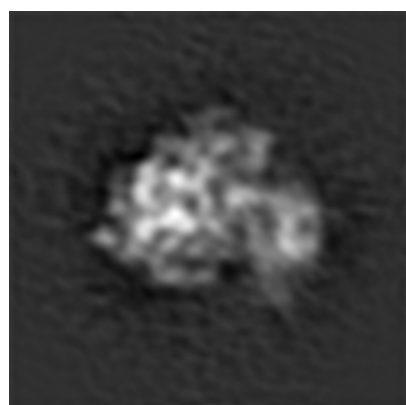
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5500. These allow visual inspection of the internal detail of the map and identification of artifacts.

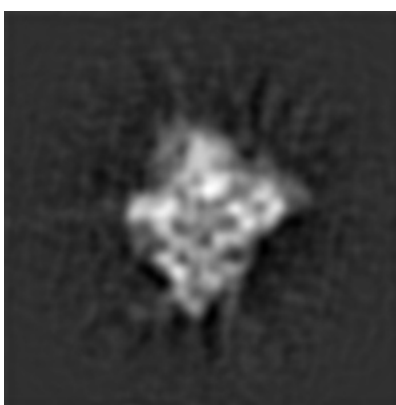
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

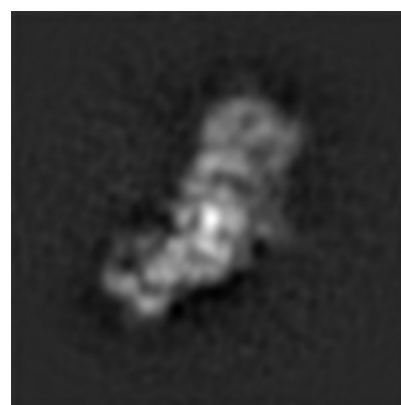
6.1.1 Primary map



X



Y

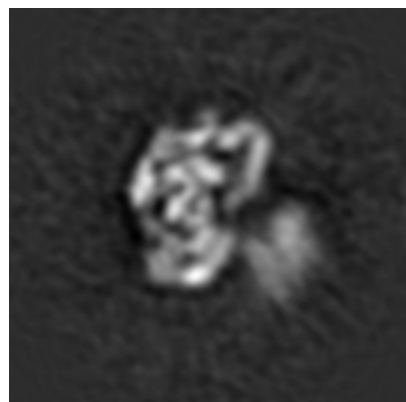


Z

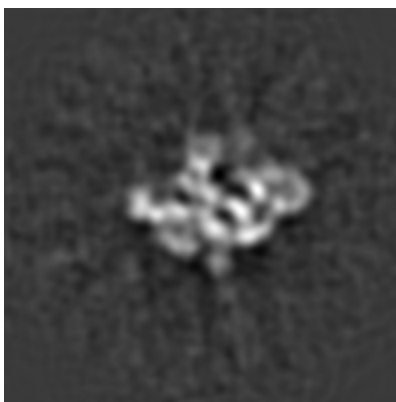
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

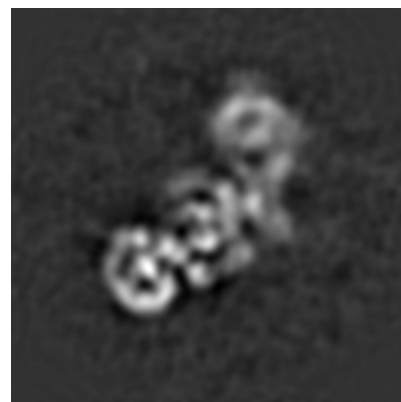
6.2.1 Primary map



X Index: 62



Y Index: 62

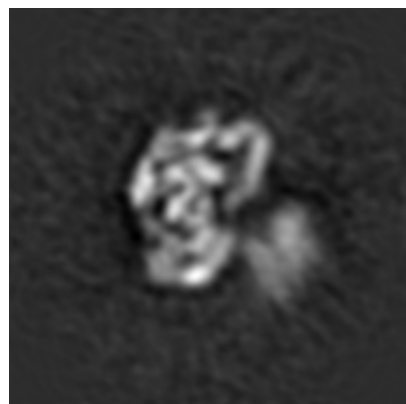


Z Index: 62

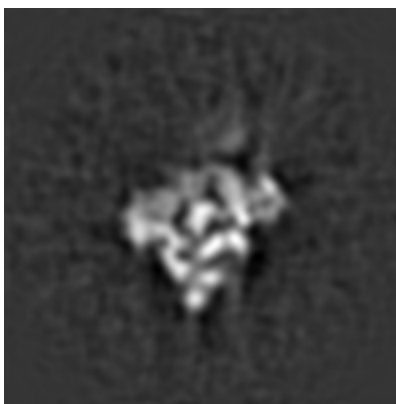
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

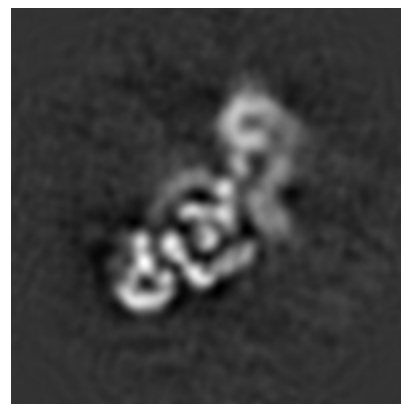
6.3.1 Primary map



X Index: 62



Y Index: 51



Z Index: 64

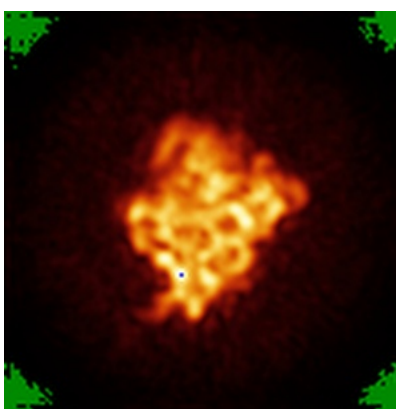
The images above show the largest variance slices of the map in three orthogonal directions.

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

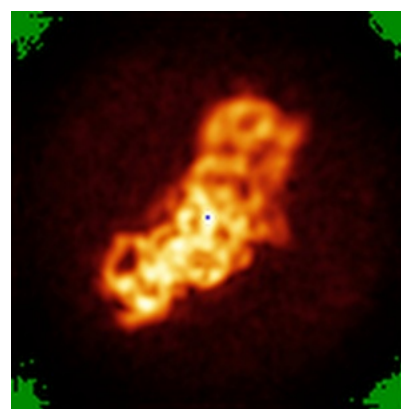
6.4.1 Primary map



X



Y

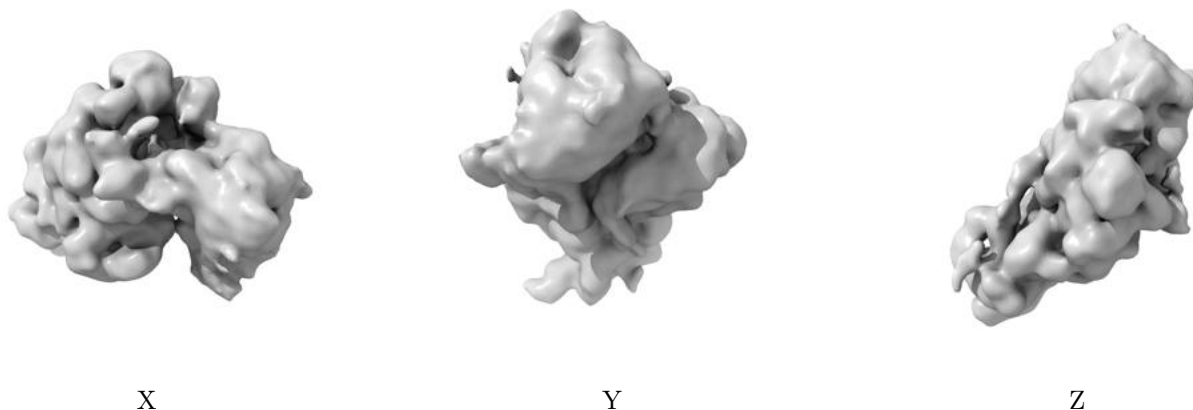


Z

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.

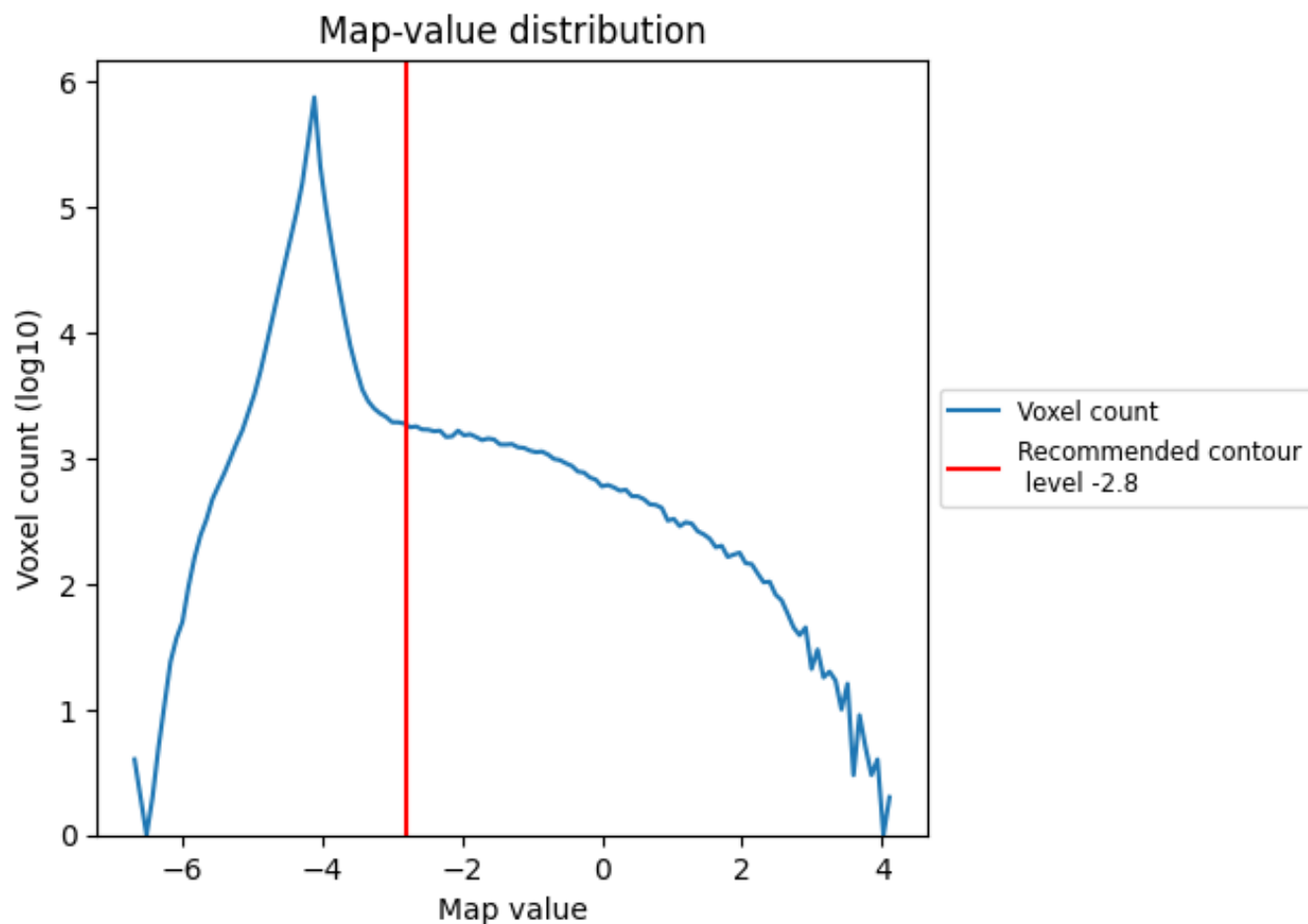
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

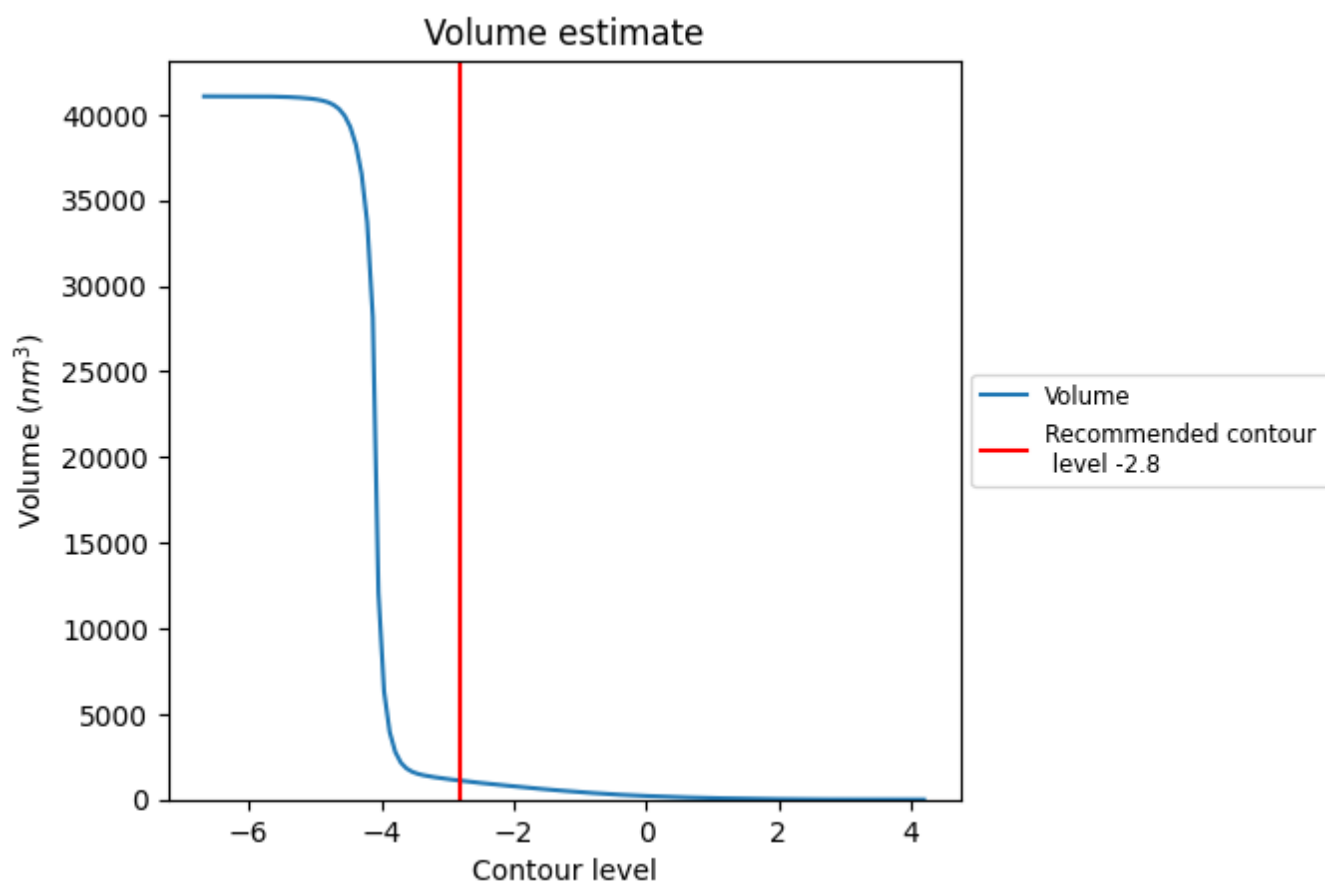
This section contains the results of statistical analysis of the map.

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.

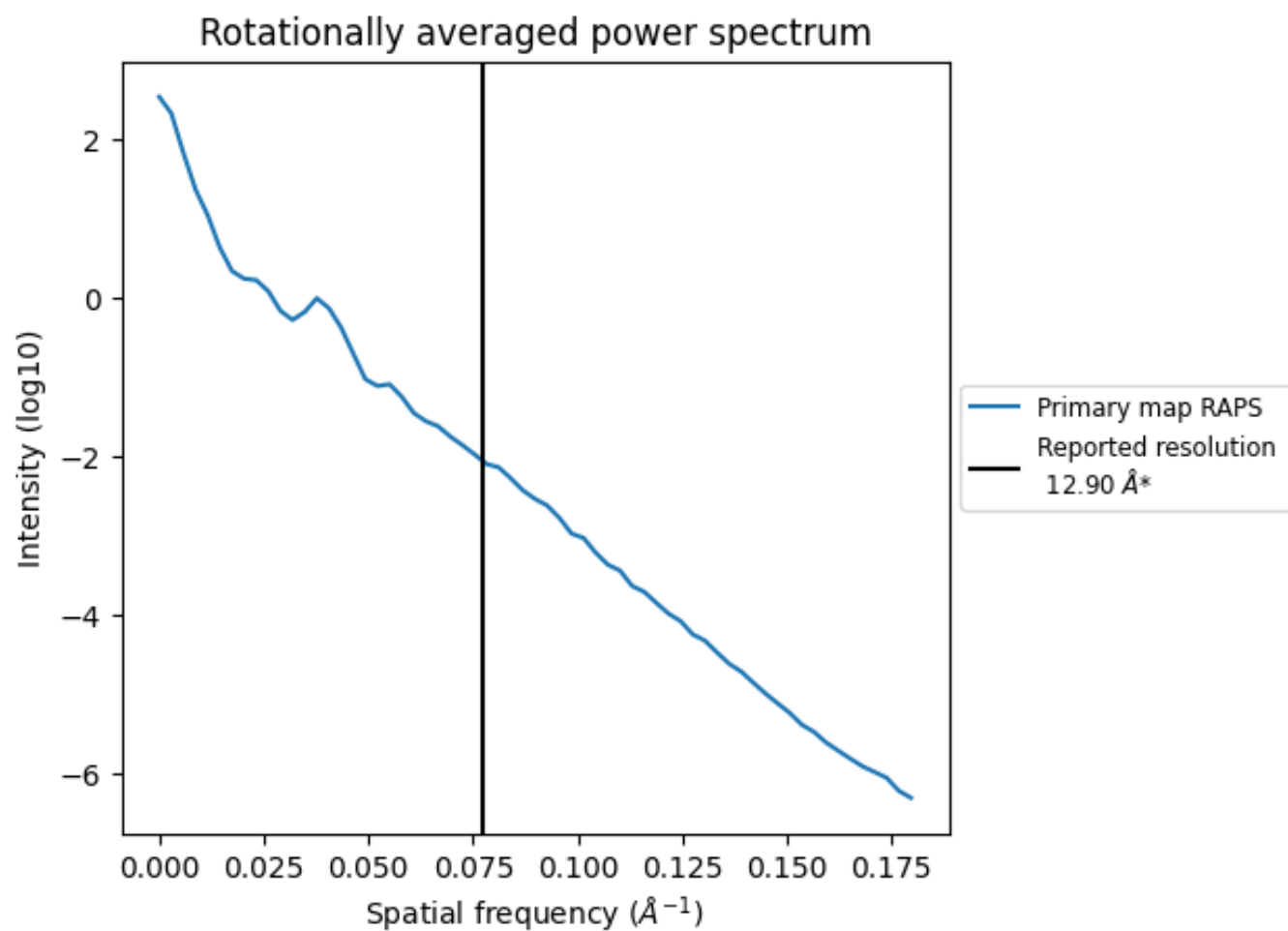
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1102 nm³; this corresponds to an approximate mass of 995 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

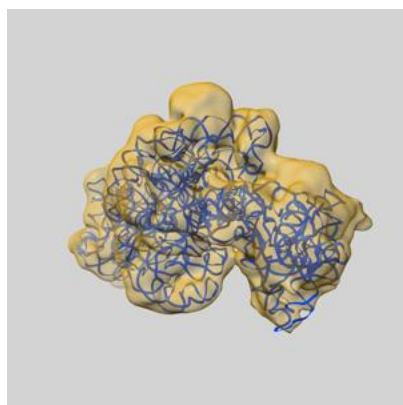
8 Fourier-Shell correlation ⓘ

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

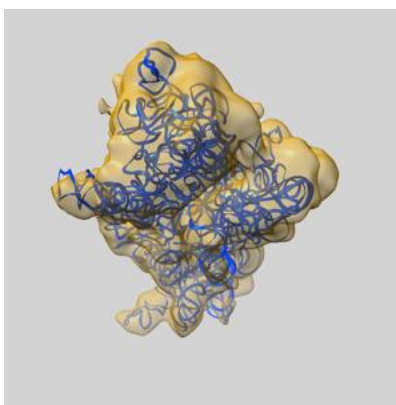
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5500 and PDB model 3J28. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

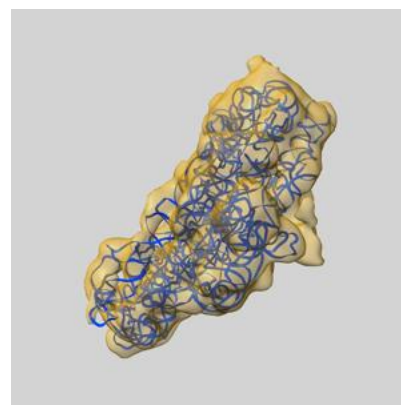
9.1 Map-model overlay [i](#)



X



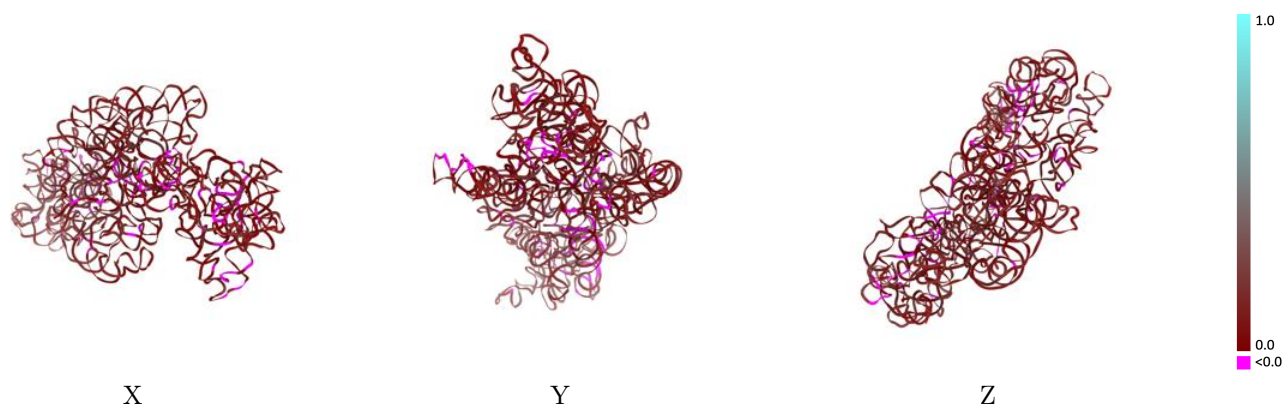
Y



Z

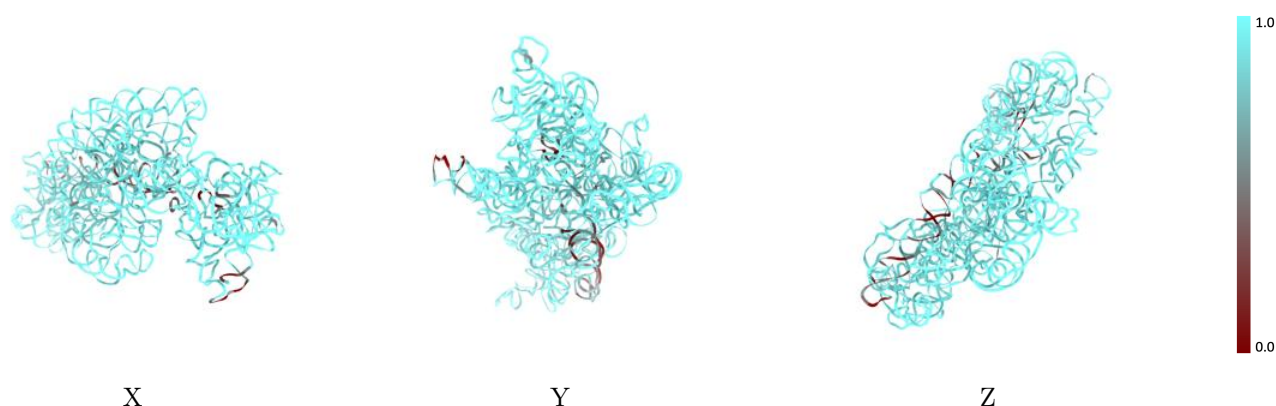
The images above show the 3D surface view of the map at the recommended contour level -2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



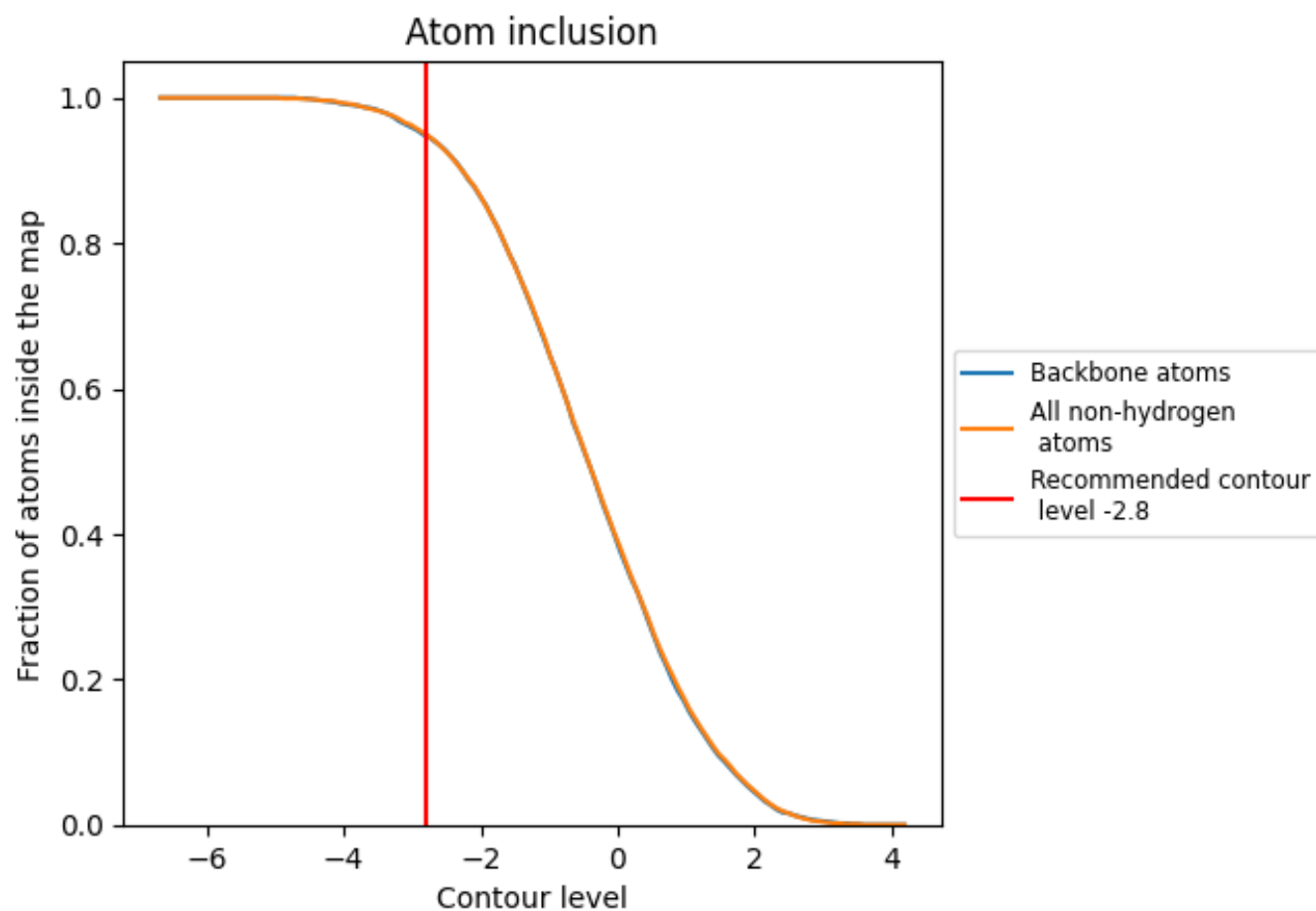
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 95% of all backbone atoms, 95% 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 (-2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9500	0.1010
N	0.9500	0.1010

