



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 06:19 PM UTC

PDB ID : 3J29 / pdb_00003j29
EMDB ID : EMD-5501
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 : 14.00 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

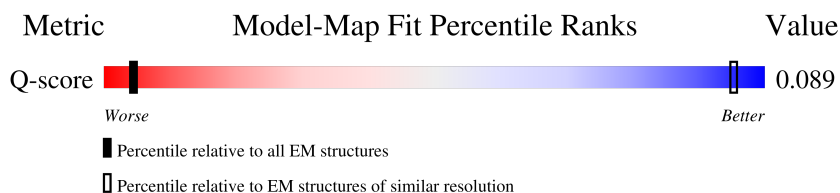
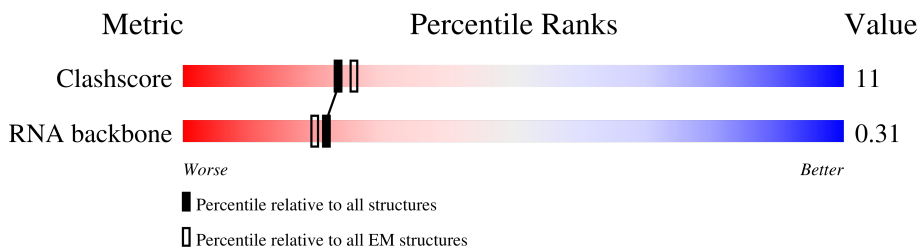
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 14.00 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 (13.50 - 14.50)

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.

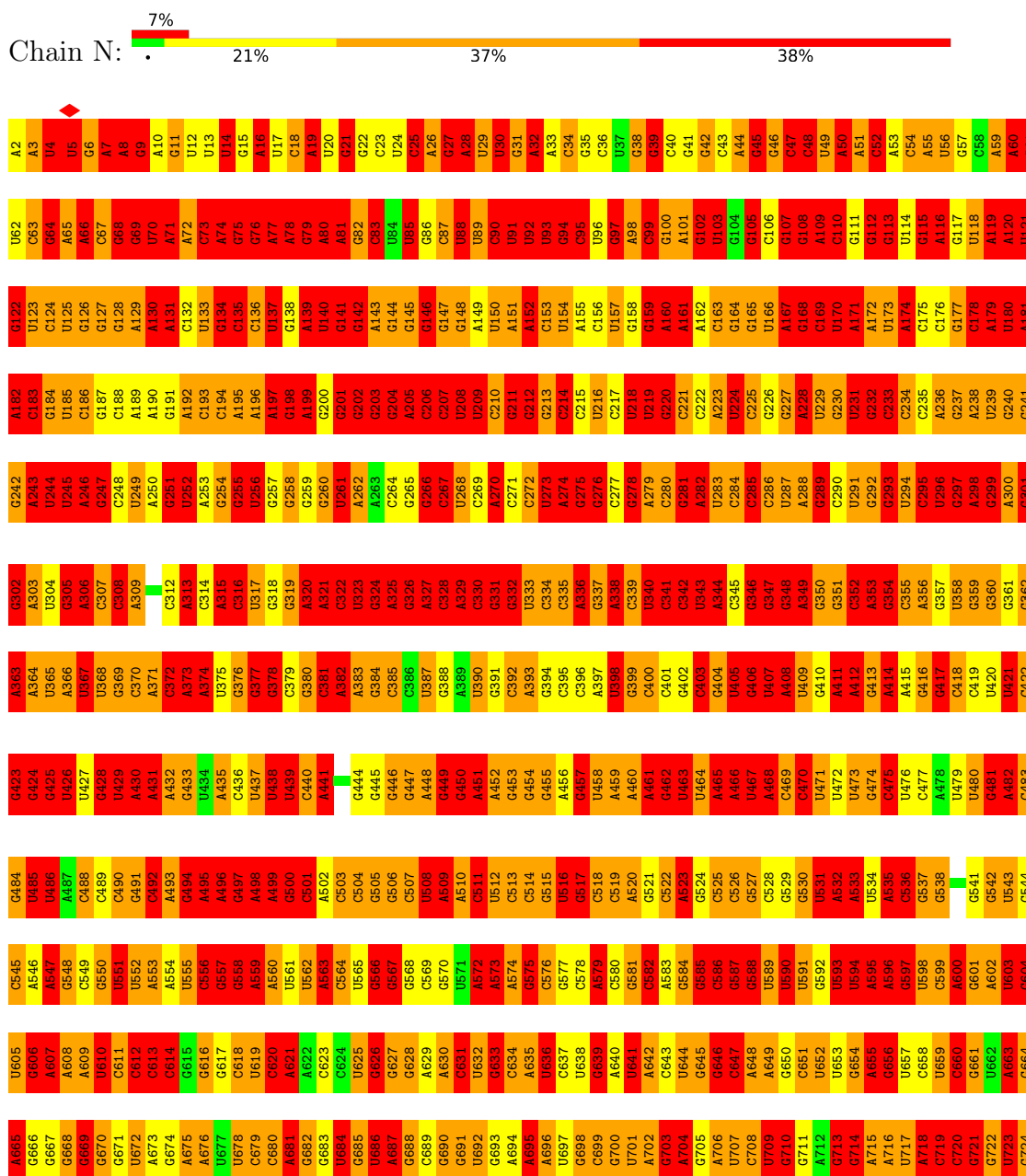
- Molecule 1 is a RNA chain called 16S rRNA.

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



A1507	A1447	G1387	G1266	G1206	A1146	U1086	G1026	G966	A906	G846	G786	G726
A1508	C1448	C1388	C1267	G1207	C1147	G1087	C1027	C967	A907	G847	G787	G727
C1509	C1449	C1389	C1268	C1208	U1148	G1088	C1028	A968	A908	C848	G788	A728
C1510	U1450	U1390	A1269	C1209	C1149	G1089	U1029	A969	A909	U850	U789	A729
G1511	U1451	U1391	G1270	U1211	A1151	U1091	U1030	C970	C910	G851	A790	G730
U1512	C1452	A1332	U1212	U1212	A1152	A1092	U1031	G971	C912	G852	G791	G731
A1513	U1393	A1333	C1273	U1213	G1153	A1093	G1032	C972	A913	G853	A792	G732
G1514	A1334	U1335	A1274	C1214	U1154	G1094	G1033	G973	A914	U854	U793	G733
G1515	A1336	G1336	G1275	G1215	A1155	U1095	G1034	A974	A915	U855	G794	G734
G1516	C1337	C1277	G1276	G1216	G1156	C1096	G1035	A975	U916	C856	C795	G735
A1517	G1338	C1278	G1277	G1217	A1157	C1097	A1036	G976	G917	G857	C796	G736
A1518	A1339	G1279	G1278	C1217	U1158	U1098	U1035	A977	A918	G858	C797	G737
C1519	A1340	A1280	A1280	A1219	U1159	G1099	A1036	A978	A919	G859	C798	G738
A1520	U1341	C1281	C1281	C1219	G1160	C1100	C1037	C979	U920	A860	G799	G739
C1521	C1342	C1282	C1282	G1221	C1161	A1101	C1038	C980	U921	C980	G800	U740
U1522	G1343	U1283	G1283	G1222	C1162	A1102	G1039	U981	U922	C862	U801	G741
G1523	C1344	C1284	C1284	G1223	A1163	C1103	U1040	A983	A923	U863	A802	G742
G1524	U1345	A1285	A1285	U1224	G1164	G1104	U1041	C984	C924	A864	G803	A743
G1525	A1346	U1286	U1286	U1225	U1165	A1105	G1042	C985	G925	A865	U804	G744
G1526	G1347	A1287	C1287	C1226	A1166	G1106	G1043	U986	G927	C866	G805	G745
U1527	U1464	U1348	A1288	C1227	A1167	C1107	G1044	G987	G928	C867	C806	A746
U1528	A1465	A1349	A1289	C1228	U1168	G1108	U1045	G988	G929	C868	A807	A747
G1530	C1467	A1350	G1290	A1229	A1169	C1109	U1046	U989	G930	G869	G808	G748
A1531	C1467	U1351	U1291	C1230	A1170	A1110	A1047	U870	G931	U870	G809	A749
C1532	U1471	C1411	G1292	G1231	A1171	A1111	G1048	A872	C932	U871	C810	C750
C1533	U1472	C1412	C1293	U1232	C1172	C1112	G1049	U992	G933	A873	C811	U751
A1534	U1473	A1413	U1295	G1233	U1173	U1113	G1050	G993	G934	U874	U813	G752
	U1474	A1414	C1296	C1234	G1174	C1114	G1051	A994	A935	U875	A814	C754
	U1475	G1415	G1297	U1235	A1175	U1115	G1052	C995	C936	C876	A815	C755
	U1476	G1416	U1298	U1236	A1176	U1116	C1053	A996	A837	C877	A816	C756
	U1477	G1417	A1299	C1237	G1177	A1117	G1054	U997	A938	A878	C817	U757
	U1478	A1418	G1300	A1238	U1178	U1118	A1055	C998	G939	C879	A818	C758
	U1479	G1419	U1301	U1239	A1179	C1119	U1056	C999	C940	C880	A819	A759
	U1480	U1420	A1302	G1241	G1181	U1121	G1057	A1000	G941	U820	U820	G760
	U1481	G1421	C1303	C1242	G1182	U1122	G1058	C1001	G942	G882	G821	G761
	U1482	G1422	G1304	C1243	U1183	U1123	C1059	G1002	U943	C883	U822	U762
	U1483	G1423	G1305	G1244	G1184	U1124	G1060	G885	G944	C823	G823	G763
	U1484	G1424	U1306	C1245	G1185	U1125	G1061	C886	G945	G824	C764	G764
	U1485	U1425	U1307	U1246	G1186	G1126	U1062	C887	G946	A825	A825	G765
	U1486	G1426	G1308	U1247	G1187	G1127	G1063	A1004	G947	C826	A766	A766
	U1487	G1427	G1309	U1248	U1188	C1128	C1064	A889	A948	U827	A767	A767
	U1488	A1428	A1310	A1249	U1189	G1129	U1065	G890	U950	U828	A768	A768
	U1489	A1429	C1312	A1250	G1190	A1130	C1066	U891	G829	G829	G776	G776
	U1490	G1430	U1313	A1251	A1191	G1131	A1072	G892	G830	G830	C777	C777
	U1491	A1431	C1314	G1252	C1192	C1132	G1073	U893	A831	A831	U777	U777
	U1492	A1432	U1315	G1253	G1193	G1133	U1074	G894	G832	G832	G778	G778
	U1493	A1433	G1316	A1254	U1194	U1134	U1075	A900	C840	C840	C779	C779
	U1494	A1434	C1317	G1255	C1195	U1135	U1076	A901	C841	C841	A780	A780
	U1495	A1435	C1318	A1256	A1196	C1136	G1077	U902	G902	U842	U842	A781
	U1496	A1436	U1319	A1257	A1197	G1137	U1078	G903	U903	U843	C783	C783
	U1497	A1437	C1320	G1258	U1198	G1138	G1079	U904	U904	G844	A845	A845
	U1498	A1438	C1321	C1259	U1199	G1139	U1080	A1021	G962	U845		
	U1499	A1439	U1322	G1260	C1200	C1140	A1081	A1022	G963			
	U1500	A1440	C1323	A1261	U1202	G1142	A1082	U1023	U965			
	U1501	A1441	A1324	C1262	C1203	G1143	U1083	G1024				
	U1502	A1442	G1325	U1264	A1204	G1144	G1084	U1025				
	U1503	A1443	U1326	C1265	U1205	A1145	U1085					
	U1504	A1444										
	U1505	A1445										
	U1506	A1446										

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26670	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	3.844	Depositor
Minimum map value	-6.202	Depositor
Average map value	-3.839	Depositor
Map value standard deviation	0.520	Depositor
Recommended contour level	-2.8	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	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	851/36831 (2.3%)	2.09	2031/57458 (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	984

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	172	A	O3'-P	-9.47	1.47	1.61
1	N	765	G	O3'-P	-9.20	1.47	1.61
1	N	1149	C	C1'-N1	8.85	1.61	1.48
1	N	1491	G	C5'-C4'	8.81	1.64	1.51
1	N	1136	C	C1'-N1	8.74	1.60	1.47

The worst 5 of 2031 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	1399	C	P-O3'-C3'	19.93	150.10	120.20
1	N	484	G	P-O3'-C3'	17.91	147.06	120.20
1	N	1362	A	P-O3'-C3'	17.42	146.33	120.20
1	N	1242	G	P-O5'-C5'	17.16	146.64	120.90
1	N	172	A	P-O3'-C3'	16.43	144.85	120.20

There are no chirality outliers.

5 of 984 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	2	A	Sidechain
1	N	4	U	Sidechain
1	N	5	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	16524	542	0
All	All	32892	16554	16524	542	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 542 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:67:C:H2'	1:N:68:G:C8	2.21	0.76
1:N:664:G:H22	1:N:741:G:H1	1.34	0.76
1:N:858:G:H1	1:N:869:G:H2'	1.50	0.75
1:N:507:C:H3'	1:N:508:U:H5''	1.70	0.74
1:N:840:C:H1'	1:N:843:U:H3	1.51	0.74

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%)	459 (29%)	148 (9%)

5 of 459 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 148 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	1191	A
1	N	1498	U
1	N	1228	C
1	N	1337	G
1	N	366	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-5501. These allow visual inspection of the internal detail of the map and identification of artifacts.

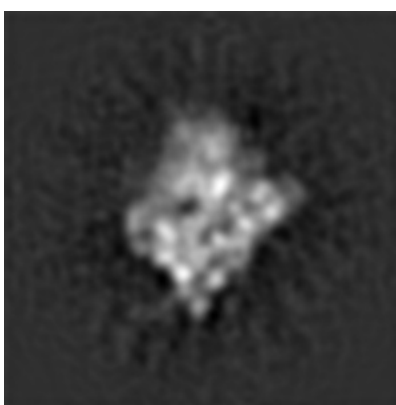
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

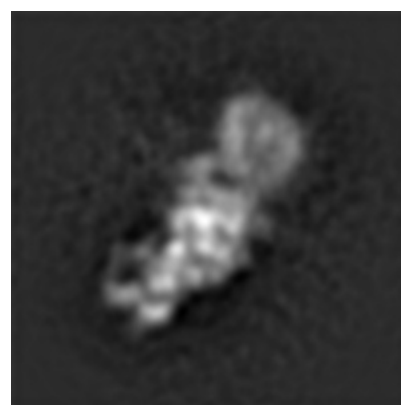
6.1.1 Primary map



X



Y

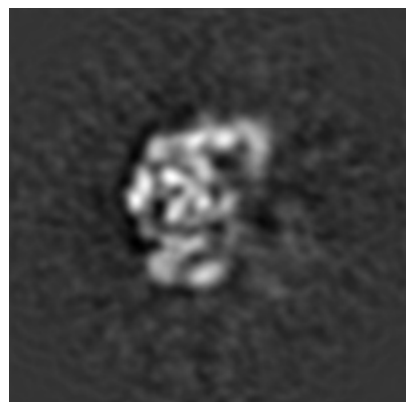


Z

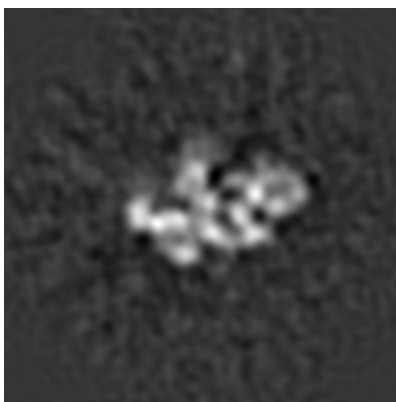
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

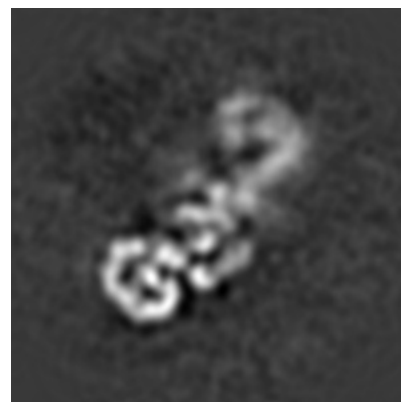
6.2.1 Primary map



X Index: 62



Y Index: 62

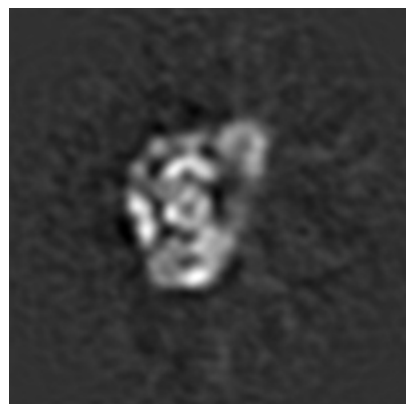


Z Index: 62

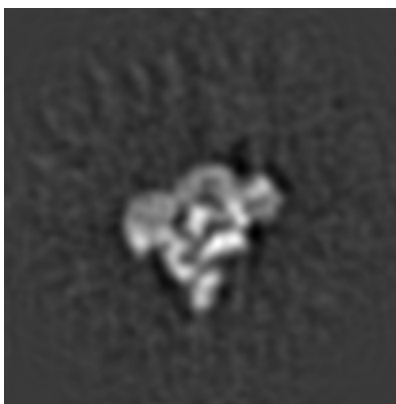
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

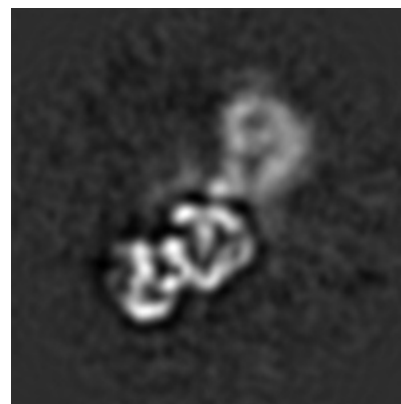
6.3.1 Primary map



X Index: 59



Y Index: 50

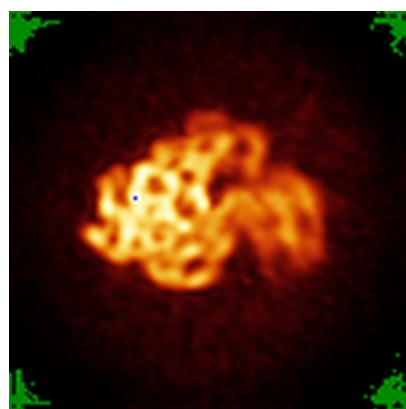


Z Index: 65

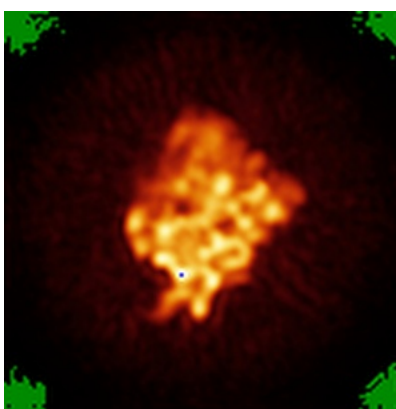
The images above show the largest variance slices of the map in three orthogonal directions.

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

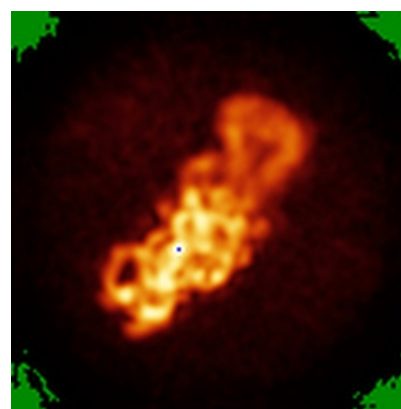
6.4.1 Primary map



X



Y

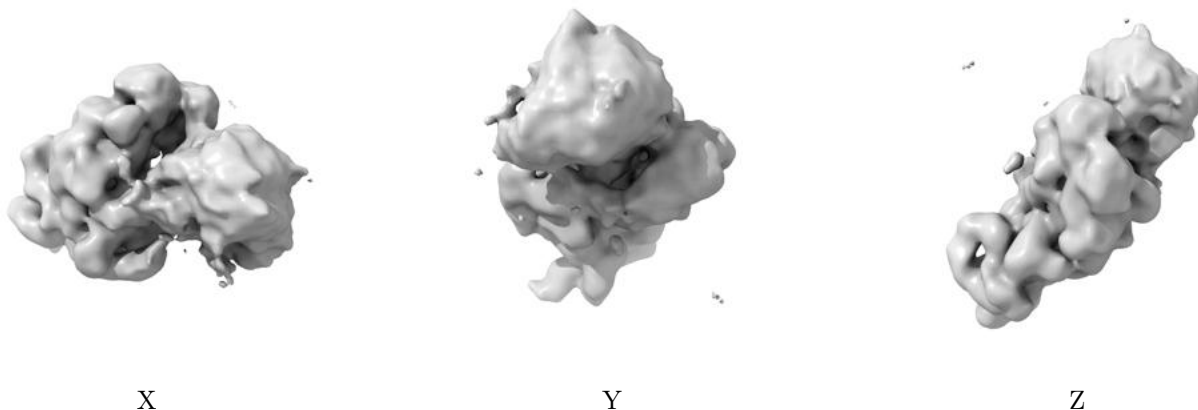


Z

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.

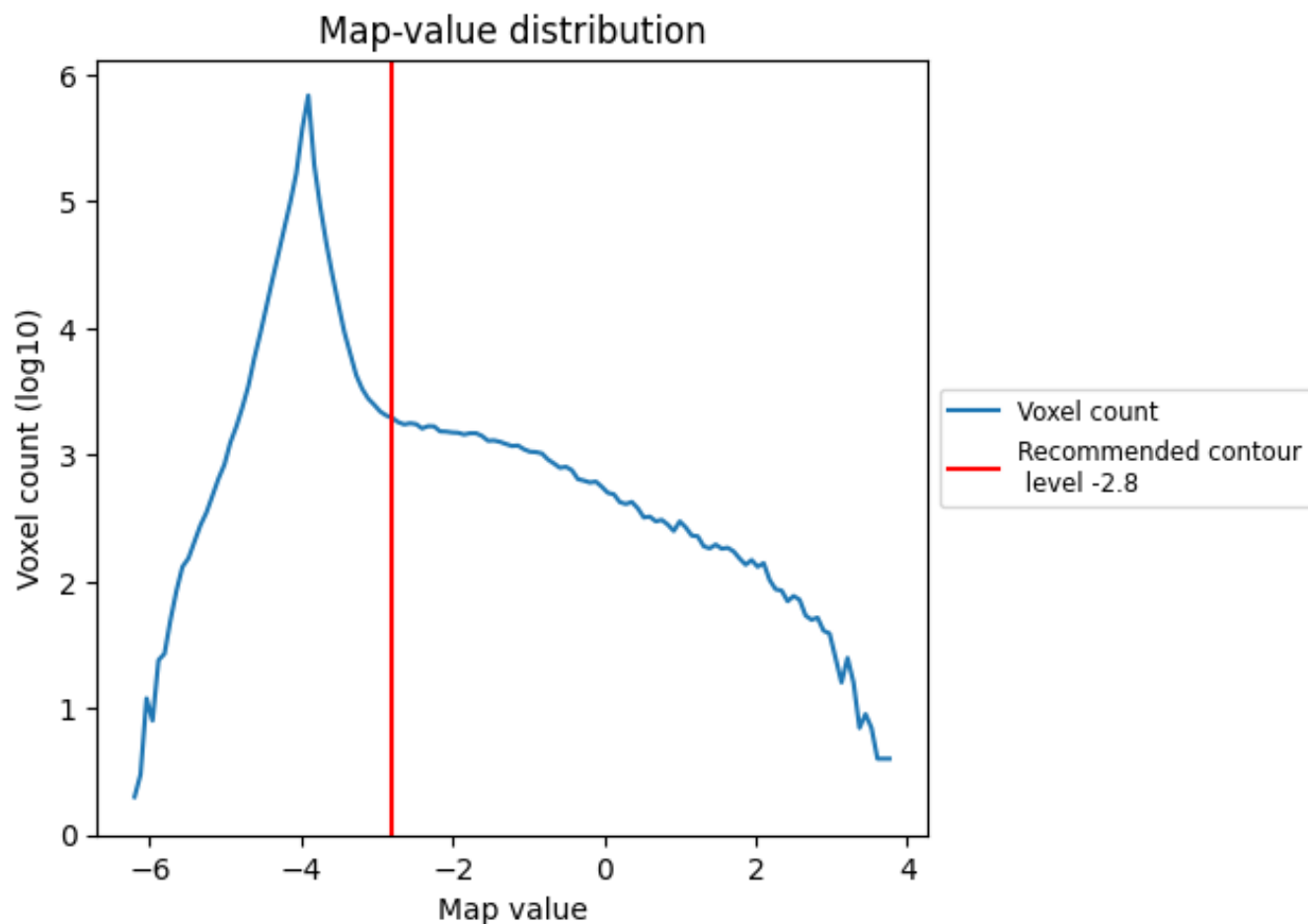
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

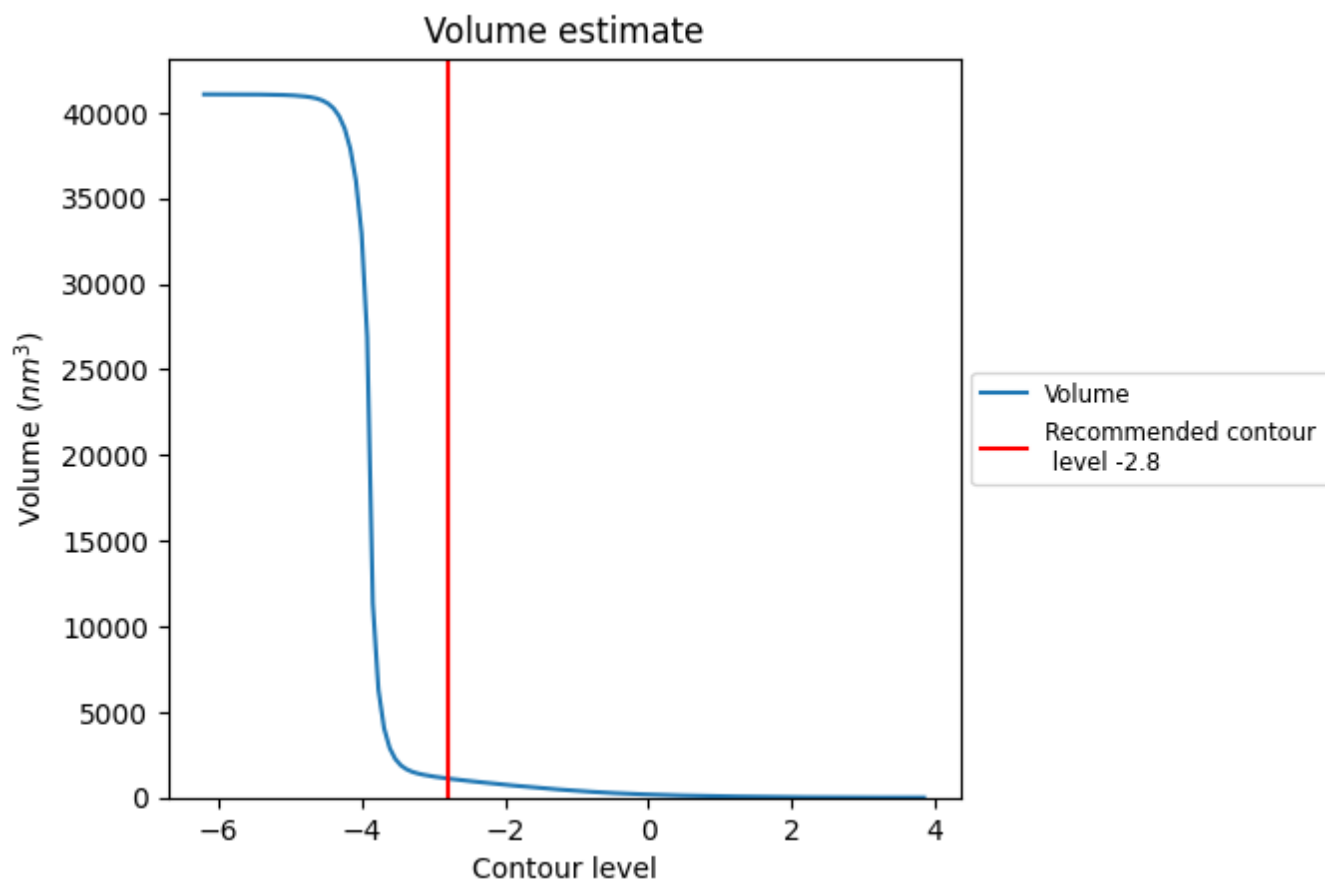
This section contains the results of statistical analysis of the map.

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.

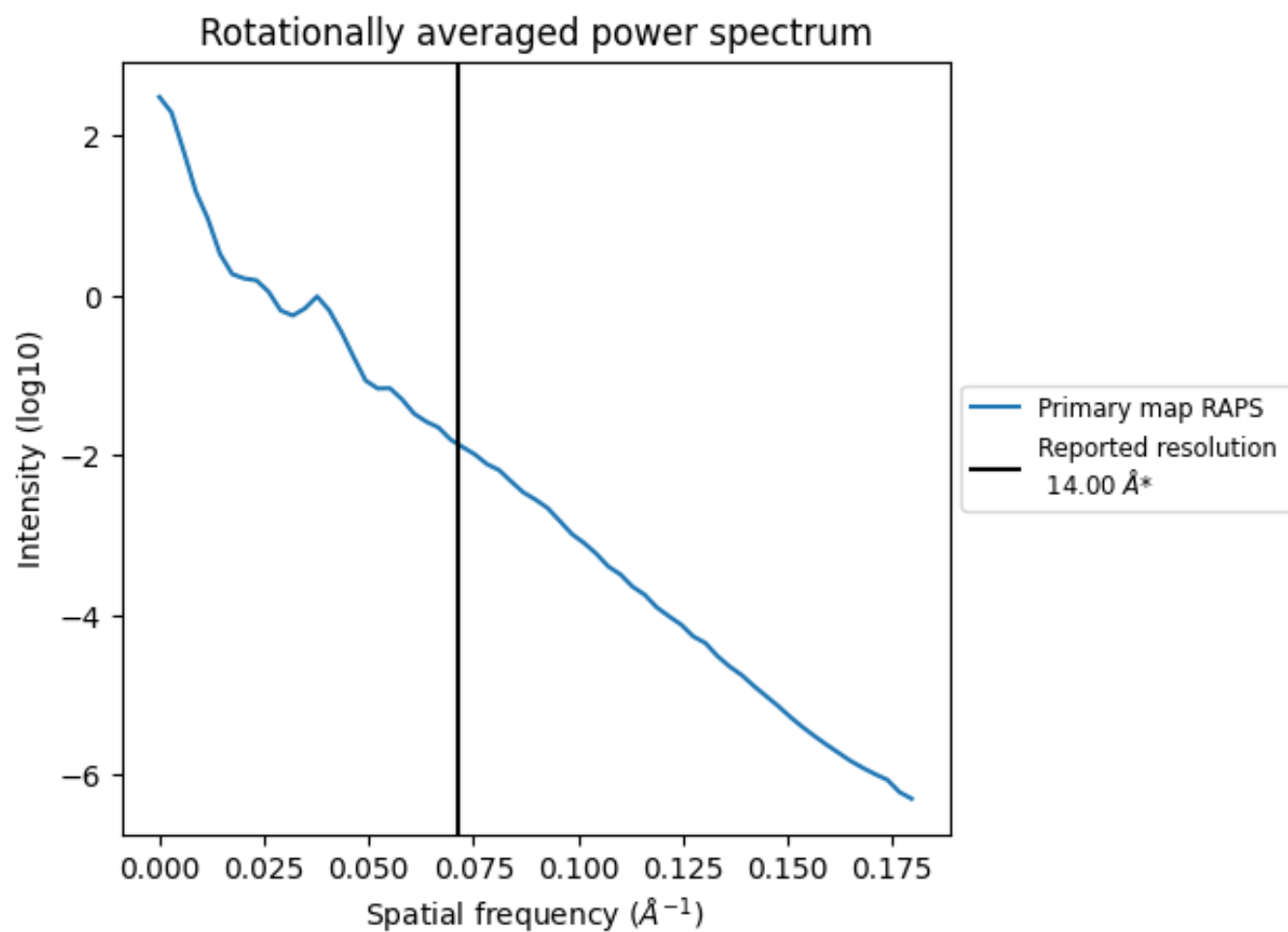
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1112 nm³; this corresponds to an approximate mass of 1005 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 0.071 Å⁻¹

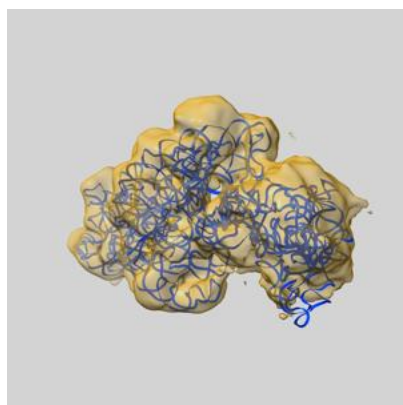
8 Fourier-Shell correlation

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

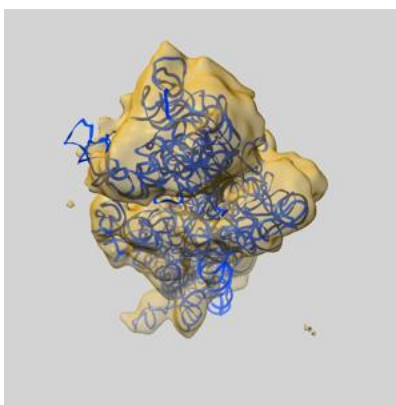
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5501 and PDB model 3J29. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

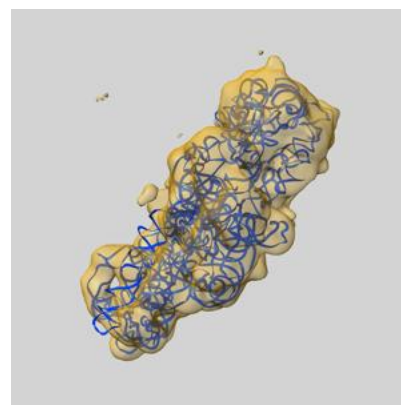
9.1 Map-model overlay [i](#)



X



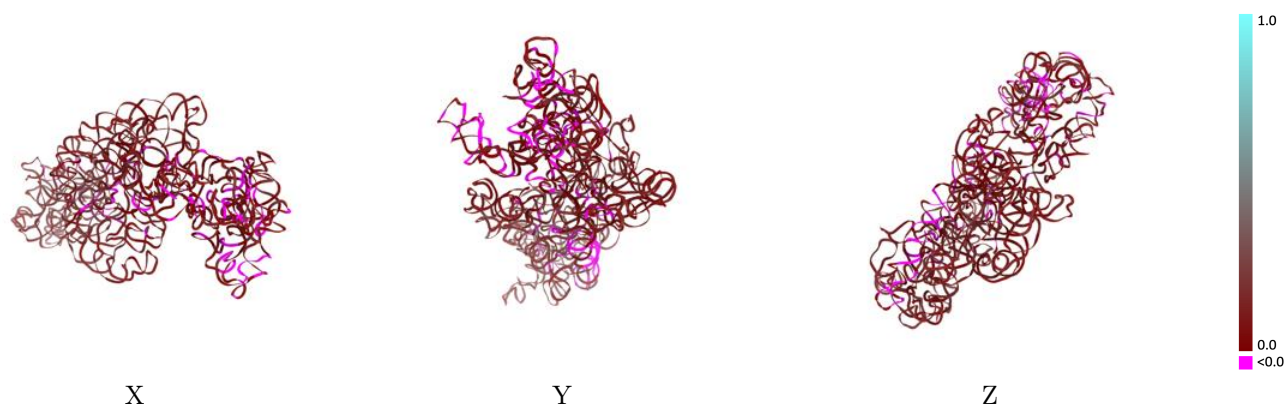
Y



Z

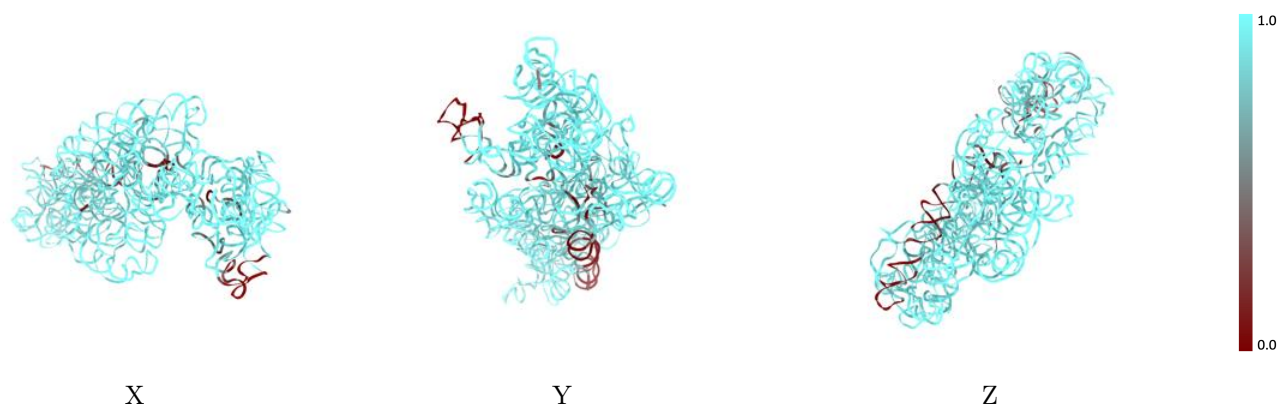
The images above show the 3D surface view of the map at the recommended contour level -2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



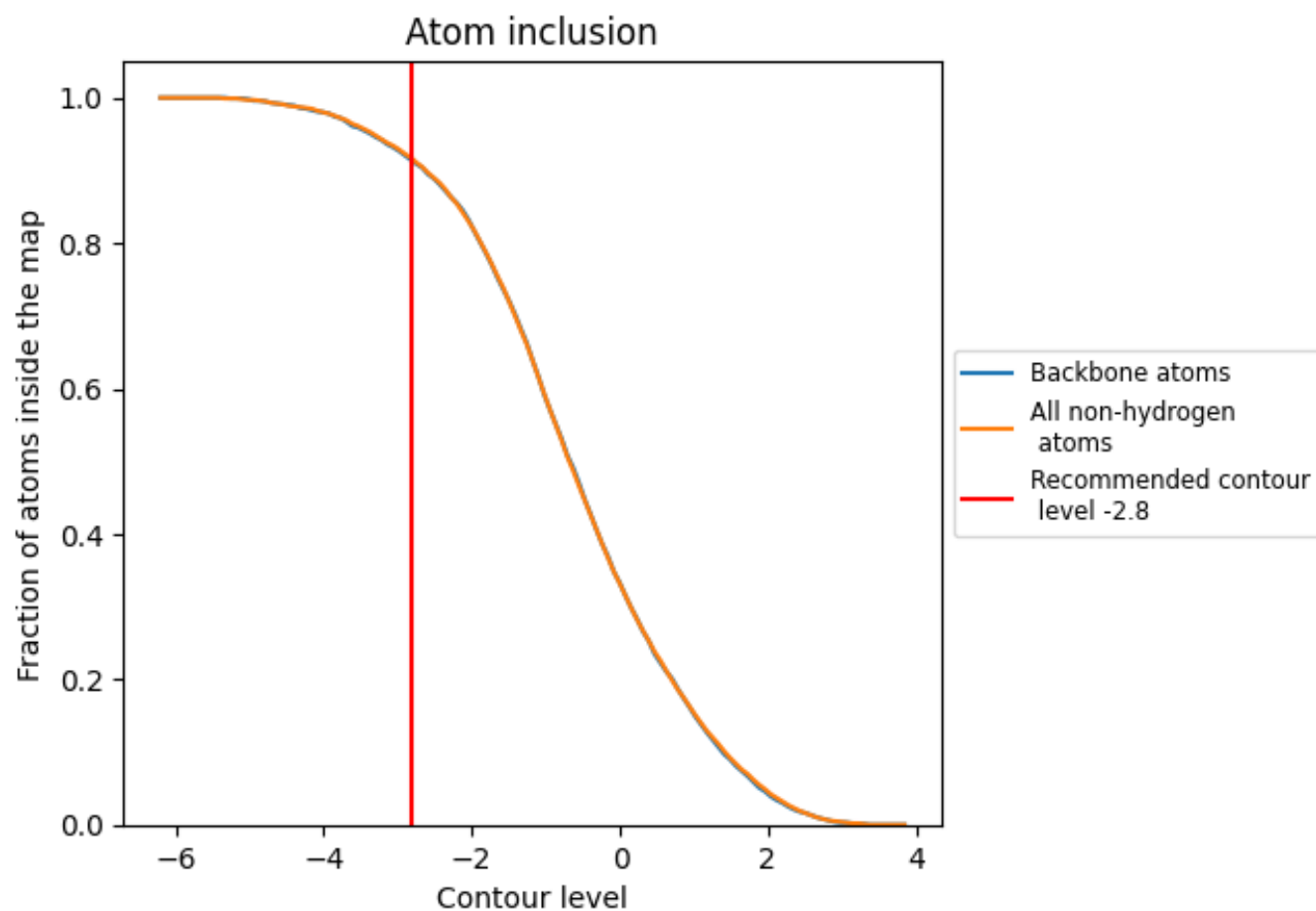
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 91% of all backbone atoms, 92% 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	0.9160	0.0890
N	0.9160	0.0890

