



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 12:20 PM UTC

PDB ID : 3J2H / pdb_00003j2h
EMDB ID : EMD-5510
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 : 18.80 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

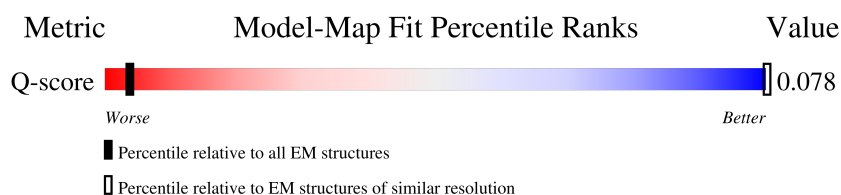
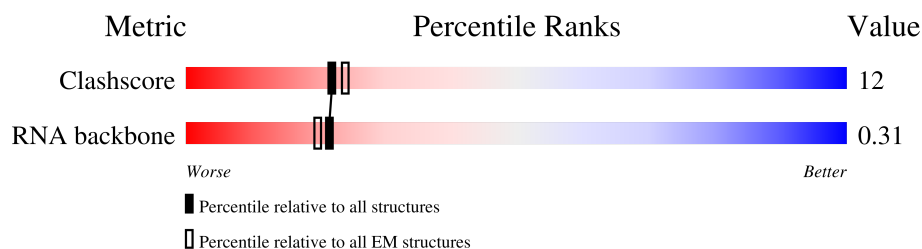
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 18.80 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	16 (18.30 - 19.20)

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		

A1502	G1442	C1382	U1202	G1142	A1082	C962	G902	U842	A782	G722
A1503	C1443	C1383	C1203	G1143	U1083	G963	G903	U843	C783	U723
G1504	U1444	C1384	A1204	G1144	G1084	A964	U904	A844	A784	G724
G1505	U1445	C1385	U1205	U1085	U1085	U965	U905	A845	G785	G725
U1506	U1446	G1386	G1206	A1146	U1086	G966	A906	G846	G786	G726
A1507	C1447	G1387	G1207	C1147	U1087	G967	A907	G847	A787	G727
A1508	A1447	G1388	C1267	U1148	G1088	A968	A908	U848	U788	A728
G1509	C1448	C1389	G1268	C1148	G1089	A969	A909	U849	U789	A729
C1510	U1450	A1269	A1209	A1150	U1090	C970	C910	U850	A790	G730
U1511	G1391	G1270	C1210	A1151	U1091	G971	U911	G851	G791	G731
U1512	A1392	A1271	U1211	A1152	A1092	C972	C912	G852	A792	C732
A1513	U1393	G1272	U1212	G1153	A1093	G973	A913	C853	U793	G733
G1514	A1394	C1273	A1213	G1154	G1094	A974	A914	U854	A794	G734
G1515	C1395	C1273	C1214	A1155	U1095	A975	A915	U855	C795	C735
G1516	A1396	A1274	G1215	G1156	C1096	G976	U916	C856	G796	G736
G1517	C1397	A1275	A1216	U1157	C1097	A977	G917	C857	C797	C737
A1518	G1457	G1276	C1217	C1158	G1098	A978	A918	G858	U798	G738
A1519	C1458	C1277	C1218	U1159	G1099	C979	A919	G859	G799	C739
C1520	G1459	G1278	A1219	C1160	C1100	C980	U920	A860	G800	U740
C1521	C1460	A1280	G1220	C1161	A1101	U981	U921	C861	U801	G741
G1522	G1461	C1281	G1222	C1162	A1102	U982	G922	C862	A802	G742
C1523	C1462	C1282	C1223	G1163	C1103	A983	A923	U863	G803	A743
C1524	G1463	U1283	U1224	U1165	G1104	C984	C924	A864	C744	C744
G1525	U1464	C1284	C1225	G1166	A1105	C985	G925	C865	C805	G745
G1526	U1465	A1285	G1226	A1167	C1107	U986	G926	C866	C806	A746
U1527	C1466	U1286	A1227	U1168	G1108	C987	G927	C867	A807	A747
U1528	A1467	A1287	C1228	C1169	C1109	G988	G928	C868	C808	G748
G1529	C1468	U1288	G1229	A1170	U1110	U989	G929	G869	G809	A749
A1530	U1469	A1289	A1230	C1171	A1111	C990	C930	U870	C810	C750
C1531	U1470	C1290	G1231	U1172	C1112	U991	G931	U871	C811	U751
C1532	U1471	G1291	U1232	U1173	C1113	U992	G932	A872	G812	G752
C1533	U1472	C1292	C1233	G1174	G993	C993	C933	C873	U813	A753
A1534	U1473	U1293	C1234	G1175	C1114	A994	C934	A874	C754	C754
	G1474	G1294	U1235	A1176	U1115	A995	C935	C875	A815	G755
	G1475	U1295	A1236	G1177	A1117	U997	A937	G876	C816	C756
	G1476	C1296	C1237	U1178	C1118	U998	A938	A877	G817	U757
	A1477	G1297	A1238	A1179	C1119	C999	C939	C878	G818	C758
	U1478	U1298	U1239	U1180	C1120	C999	G940	C879	A819	A759
	U1479	A1299	U1240	G1181	U1121	C1000	G941	C880	U820	G760
	C1480	G1300	G1241	U1182	U1122	G1001	G942	C881	G821	G761
	U1481	U1301	U1242	U1183	U1123	G1003	U943	C882	U822	G762
	U1482	C1302	C1243	U1184	G1124	G1004	G944	C883	C823	G763
	G1483	G1303	G1244	G1185	U1125	A1004	G945	C884	G824	C764
	U1484	C1304	C1245	U1186	U1126	A1005	A946	G885	A825	G765
	U1485	G1305	A1246	G1187	G1127	G1006	G947	G886	C826	A766
	U1486	A1306	U1247	U1188	C1128	U1007	C948	G887	U827	A767
	G1487	U1307	A1248	U1189	C1129	A889	A949	G888	U828	A768
	G1488	U1308	C1249	U1190	C1130	U1008	U950	A890	G829	G769
	G1489	G1309	A1250	A1191	G1131	U1009	G951	G890	A831	C770
	U1490	C1310	A1251	C1192	C1132	U1010	U952	A891	U832	G771
	A1491	A1311	A1252	G1193	G1133	C1011	G953	A892	G833	U772
	A1492	G1312	G1253	U1194	G1134	A1012	G954	C893	G834	G773
	A1493	U1313	U1254	C1195	U1135	G1013	G955	G894	U834	G774
	A1494	C1314	G1255	A1196	C1136	A1014	U956	G895	U835	G775
	A1495	U1315	A1256	U1197	C1137	G1015	U957	C896	G836	G776
	G1496	G1316	A1257	G1198	G1138	A1016	A898	G897	U837	A777
	G1497	C1317	G1258	U1199	C1139	U1017	A899	G898	G838	G778
	U1498	A1318	C1259	C1200	C1140	G1018	A900	C899	C839	C779
	U1499	C1319	G1260	U1201	U1141	G1019	A901	A900	A780	A780
	A1500	C1320	A1261	A1201	C1141	G1020	A902	A901	A781	A781
	C1501	U1321		A1081		A1021				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	11474	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	4.629	Depositor
Minimum map value	-7.414	Depositor
Average map value	-4.262	Depositor
Map value standard deviation	0.653	Depositor
Recommended contour level	-2.3	Depositor
Map size (Å)	375.0, 375.0, 375.0	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.0, 3.0, 3.0	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	2.05	818/36831 (2.2%)	2.10	1988/57458 (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	978

The worst 5 of 818 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	404	G	C2'-C1'	-9.72	1.38	1.53
1	N	669	G	P-O5'	-9.63	1.45	1.59
1	N	353	A	C2'-C1'	-8.86	1.40	1.53
1	N	1205	U	C1'-N1	8.85	1.61	1.48
1	N	350	G	C1'-N9	8.72	1.61	1.48

The worst 5 of 1988 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	1248	A	P-O5'-C5'	18.01	147.91	120.90
1	N	1399	C	P-O3'-C3'	17.73	146.79	120.20
1	N	1242	G	P-O5'-C5'	17.63	147.35	120.90
1	N	1531	A	P-O5'-C5'	17.49	147.14	120.90
1	N	94	G	P-O3'-C3'	16.80	145.39	120.20

There are no chirality outliers.

5 of 978 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	3	A	Sidechain
1	N	4	U	Sidechain
1	N	5	U	Sidechain
1	N	6	G	Sidechain
1	N	9	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	16521	569	0
All	All	32892	16554	16521	569	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 12.

The worst 5 of 569 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:32:A:H4'	1:N:48:C:H42	1.50	0.75
1:N:594:U:C4	1:N:595:A:C6	2.74	0.75
1:N:338:A:H61	1:N:351:G:H1	1.36	0.73
1:N:116:A:H61	1:N:313:A:H1'	1.53	0.73
1:N:197:A:H2	1:N:198:G:C4	2.08	0.70

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%)	459 (29%)	152 (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 152 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	1189	U
1	N	1432	G
1	N	1224	U
1	N	1319	A
1	N	1532	U

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.

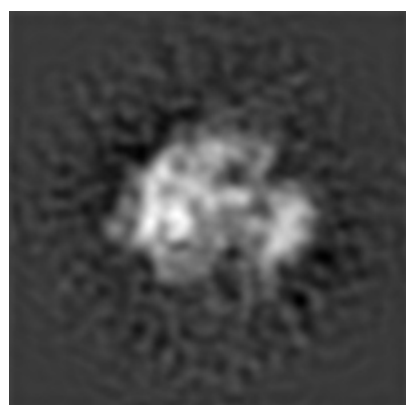
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5510. These allow visual inspection of the internal detail of the map and identification of artifacts.

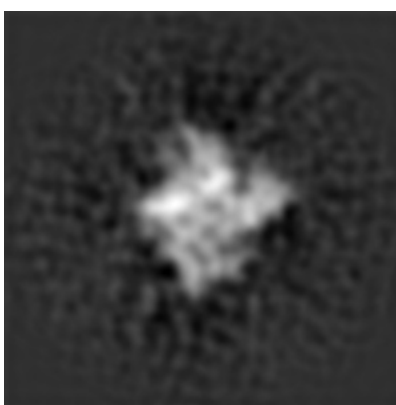
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

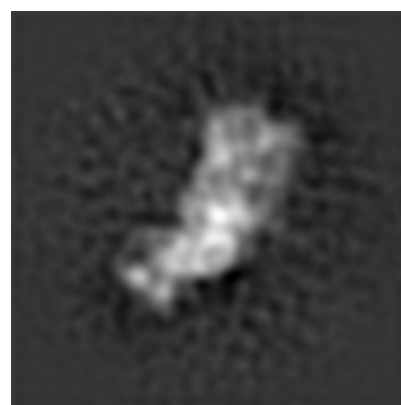
6.1.1 Primary map



X



Y

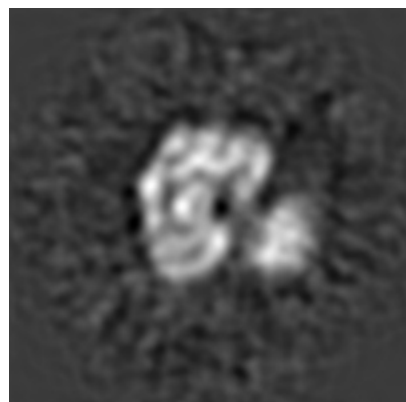


Z

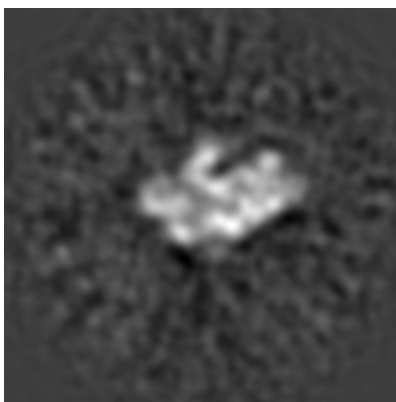
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

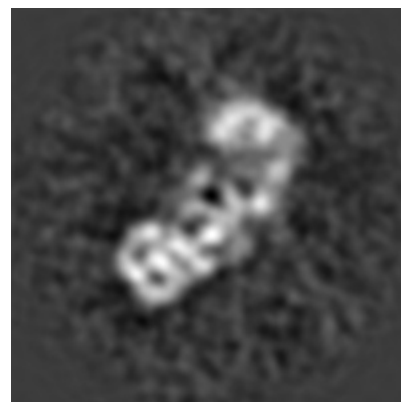
6.2.1 Primary map



X Index: 62



Y Index: 62

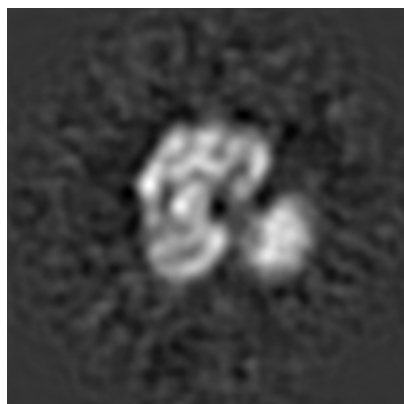


Z Index: 62

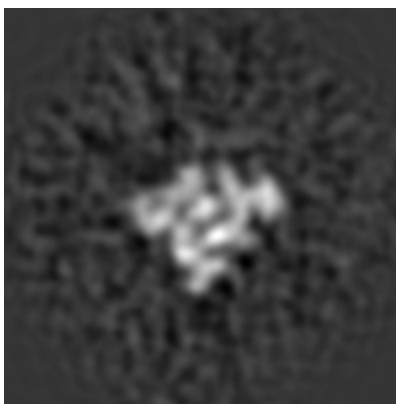
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

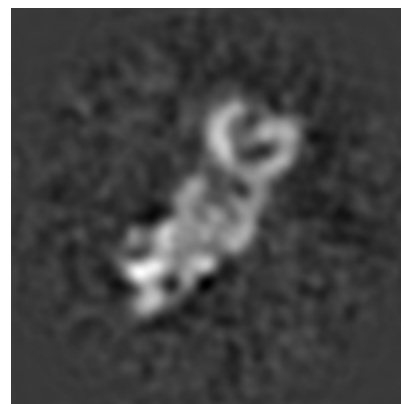
6.3.1 Primary map



X Index: 63



Y Index: 53

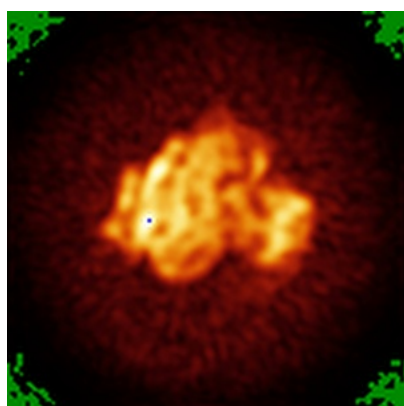


Z Index: 58

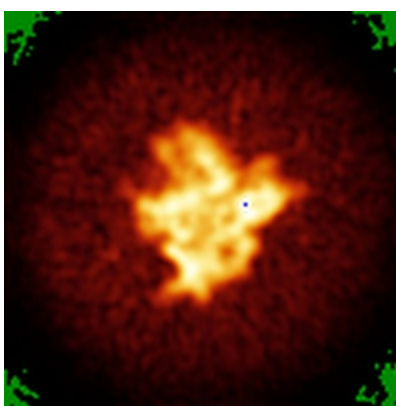
The images above show the largest variance slices of the map in three orthogonal directions.

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

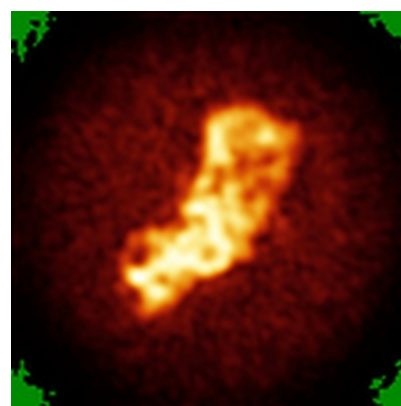
6.4.1 Primary map



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.

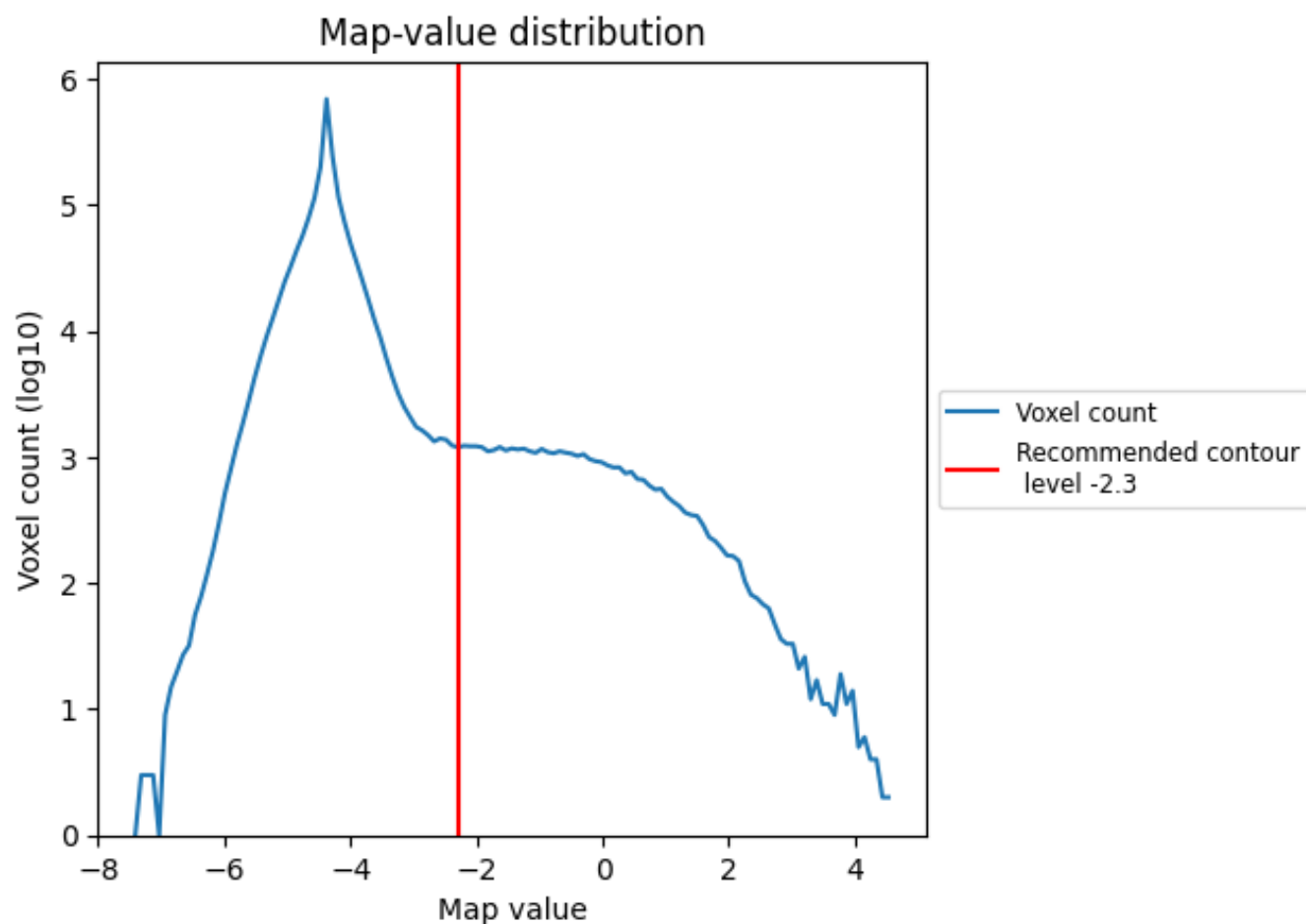
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

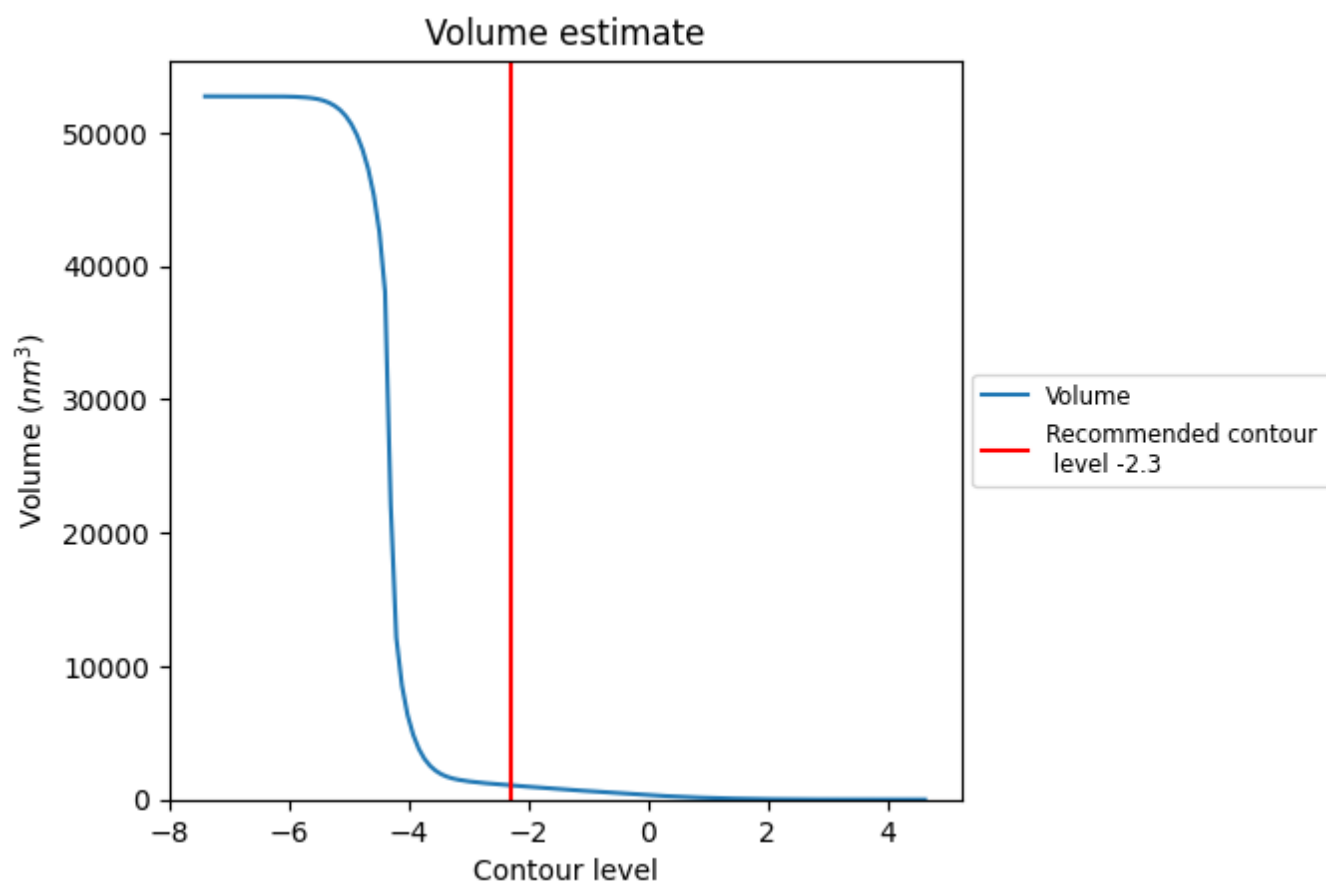
This section contains the results of statistical analysis of the map.

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.

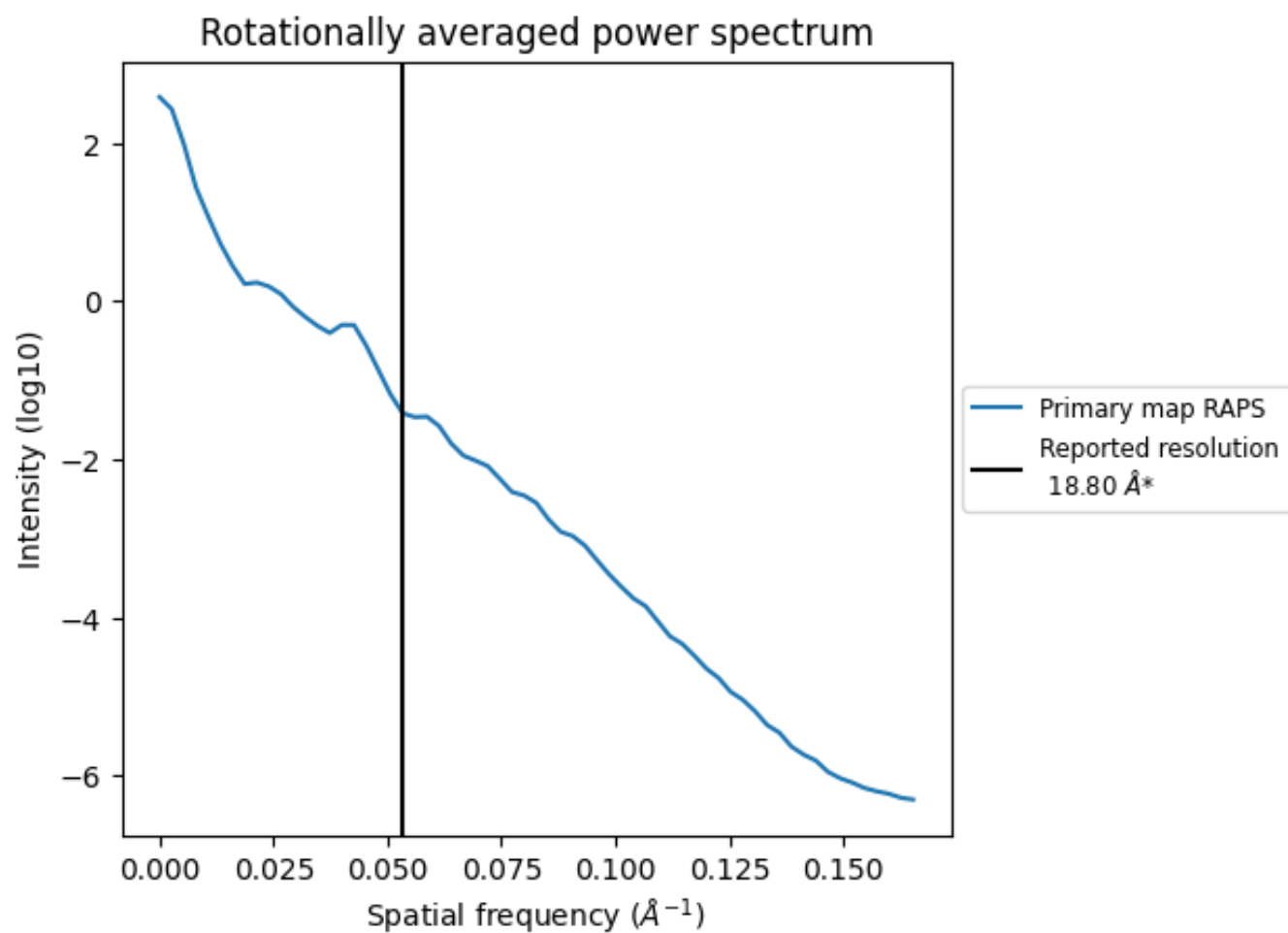
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1065 nm³; this corresponds to an approximate mass of 962 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 0.053 Å⁻¹

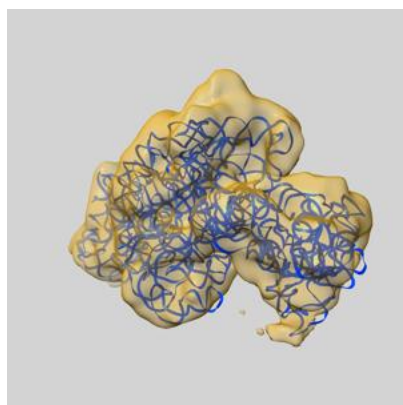
8 Fourier-Shell correlation

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

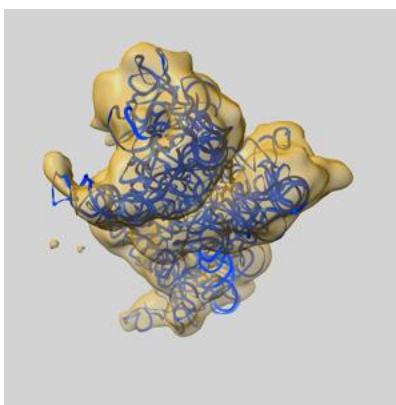
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5510 and PDB model 3J2H. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

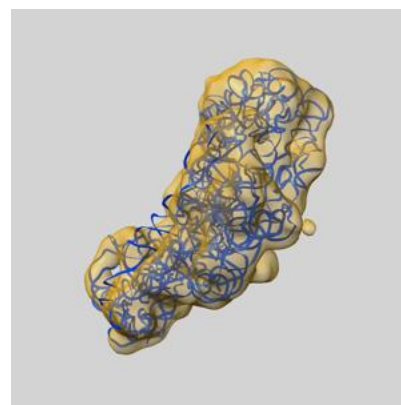
9.1 Map-model overlay [i](#)



X



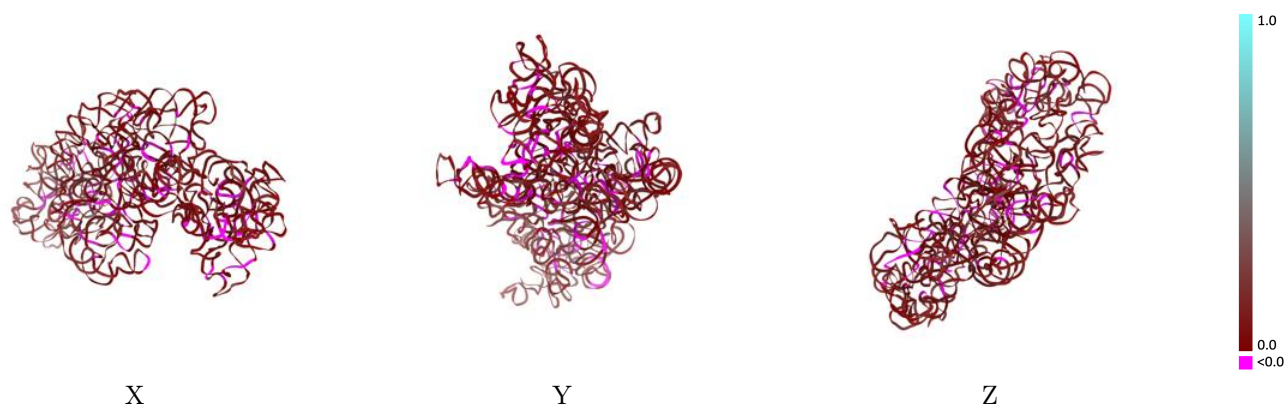
Y



Z

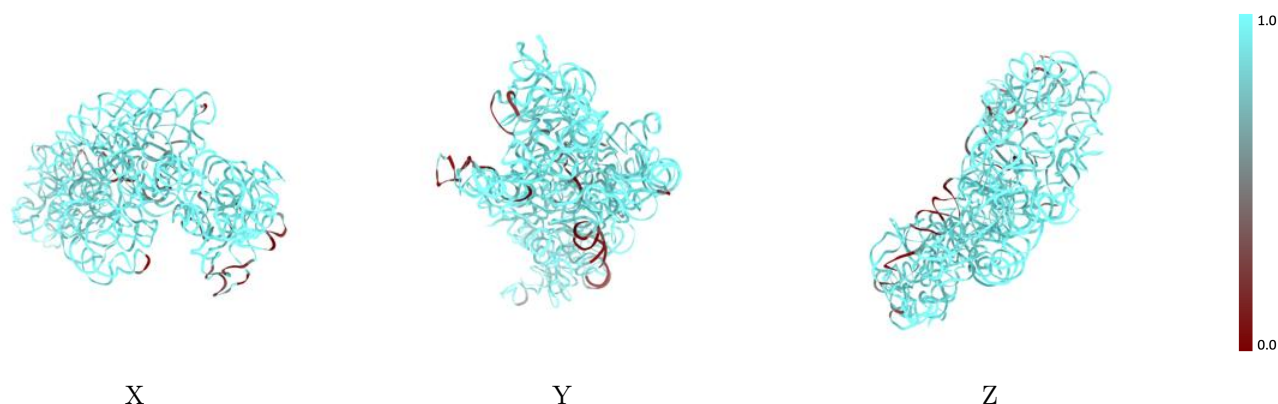
The images above show the 3D surface view of the map at the recommended contour level -2.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



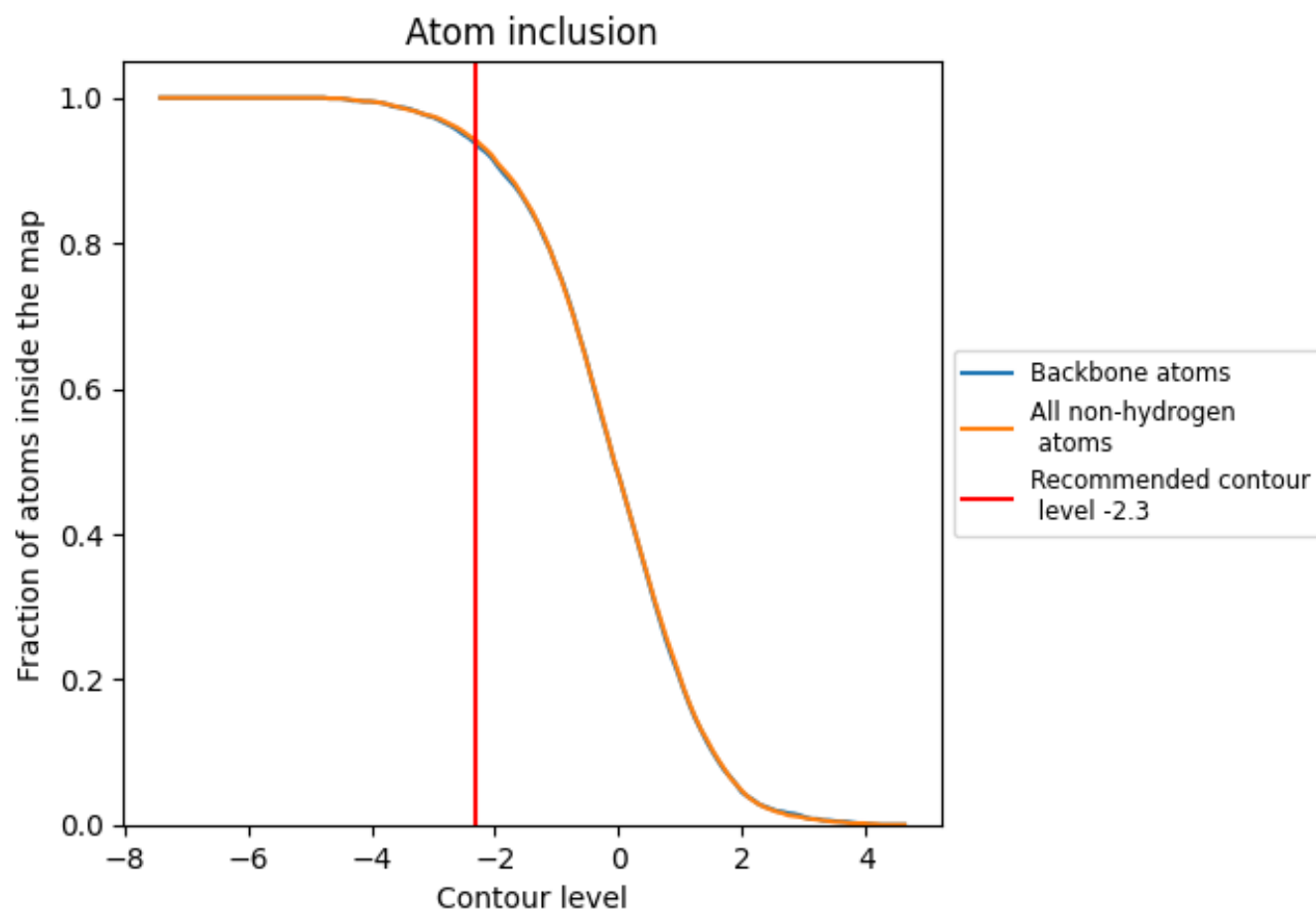
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 94% of all backbone atoms, 94% 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	0.9410	0.0780
N	0.9420	0.0780

