



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:16 AM UTC

PDB ID : 3J2B / pdb_00003j2b
EMDB ID : EMD-5503
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 : 13.60 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

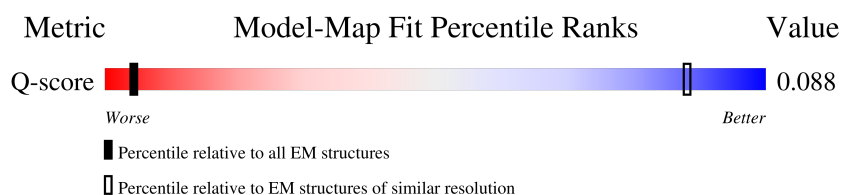
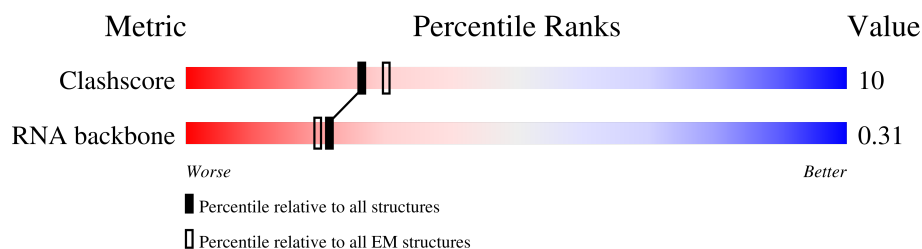
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 13.60 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	66 (13.10 - 14.10)

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.

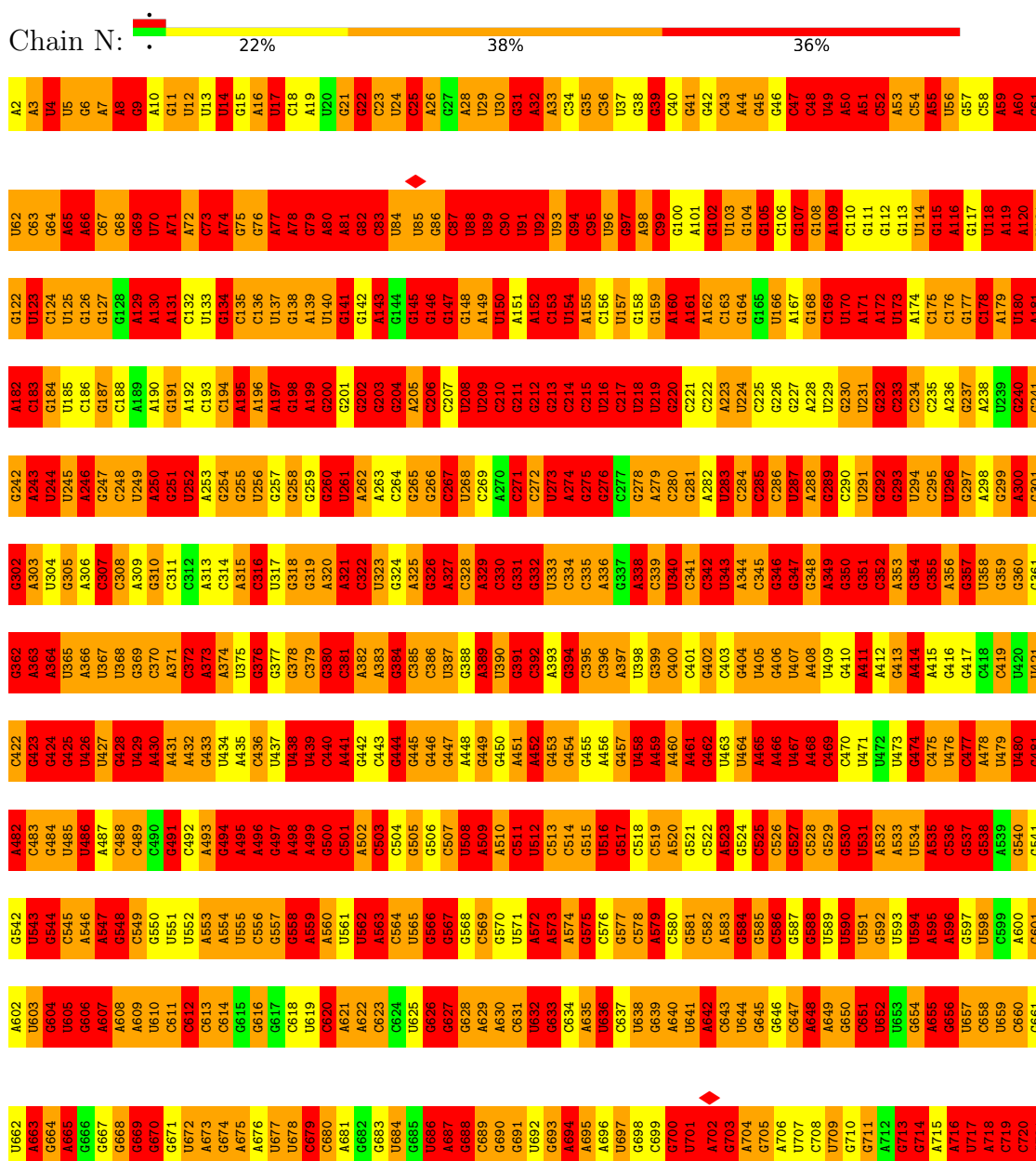
- Molecule 1 is a RNA chain called 16S rRNA.

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



A1502	G1442	C1382	C1262	U1202	A1082	A1022	C862	G902	U842	A782	G722
A1503	C1443	C1383	C1263	C1203	U1083	U1023	G863	G903	U843	C783	U723
G1504	U1444	C1384	C1264	A1204	G1084	G1024	A964	U904	G844	C784	G724
G1505	U1445	C1385	C1265	U1205	U1085	U1025	U965	U905	A845	A784	G725
U1506	G1446	C1386	G1266	G1206	U1086	G1026	G966	A906	G846	G786	G726
A1507	C1447	C1387	C1267	G1207	G1087	G1027	G967	A907	G847	A787	G727
A1508	C1448	C1388	G1268	C1208	U1088	C1028	A968	A908	U848	U788	A728
G1509	C1449	A1389	A1269	C1209	G1089	U1029	A969	A909	G849	U789	A729
C1510	C1449	C1390	G1270	C1210	U1090	U1030	C970	C910	U850	A790	A730
G1511	U1450	G1391	A1271	U1211	U1091	C1031	G971	U911	G851	G791	G731
U1512	C1451	A1392	G1272	U1212	A1092	G1032	C972	C912	G852	A792	C732
A1513	U1451	C1393	C1273	A1213	A1093	G1033	G973	A913	C853	U793	G733
G1514	C1452	A1394	A1274	C1214	G1094	G1034	A974	A914	U854	A794	G734
G1515	C1453	C1395	A1275	G1215	U1095	A1035	A975	A915	U855	C785	C735
G1516	A1454	A1396	C1276	A1216	C1096	A1036	G976	U916	C856	C786	C736
G1517	C1455	C1397	C1277	C1217	U1097	G1037	A977	U917	C857	C787	C737
A1518	G1456	G1398	G1278	C1218	C1098	C1038	A978	A918	G858	U788	C738
A1519	C1457	A1399	G1279	A1219	U1099	G1039	C979	A919	G859	G799	C739
C1520	G1458	A1400	A1280	G1220	C1100	U1040	C980	A920	A860	G800	U740
U1521	C1459	C1401	C1281	G1221	A1101	G1041	U981	U921	C861	U801	G741
G1522	C1460	C1402	U1282	C1222	A1102	A1042	U982	G922	C862	A802	G742
C1523	G1461	C1403	U1283	C1223	C1103	G1043	A983	C923	U863	G803	A743
G1524	U1462	C1404	G1284	U1224	G1104	A1044	C984	C924	A864	U804	C744
G1525	C1463	U1405	A1285	A1225	A1105	C1045	C985	G925	A865	C805	G745
G1526	U1464	G1406	U1286	C1226	G1106	A1046	U986	G926	C866	C806	A746
U1527	C1465	C1407	A1287	A1227	C1107	G1047	G987	G927	C867	A807	A747
U1528	A1466	A1408	A1288	C1228	U1108	G1048	C988	G928	C868	C808	G748
G1529	C1466	U1409	A1289	A1229	C1109	U1049	U989	G929	G869	G809	A749
G1530	A1467	C1410	G1290	C1230	A1110	G1050	C990	C930	U870	C810	C750
A1531	C1467	U1411	U1291	G1231	U1111	C1051	U991	C931	U871	C811	U751
U1532	A1468	C1412	G1292	U1232	C1112	U1052	U992	G932	A872	G812	G752
C1533	C1469	U1413	C1293	G1233	G1113	G1053	G993	C933	U873	U813	A753
A1534	U1470	A1414	G1294	C1234	C1114	C1054	A994	G934	G874	A814	C754
	U1471	G1415	U1295	U1235	U1115	A1055	C995	A935	U875	A815	G755
	U1472	G1416	C1296	A1236	U1116	U1056	A996	G936	C876	A816	C756
	G1473	G1417	G1297	C1237	A1117	G1057	U997	A937	G877	C817	U757
	U1474	A1418	U1298	A1238	U1118	C1058	C998	A938	A878	G818	C758
	G1475	C1419	A1299	U1239	C1119	C1059	C999	G939	C879	A819	A759
A1476	U1420	G1361	G1300	U1240	C1120	U1060	A1000	C940	C880	U820	G760
U1477	A1362	A1362	U1301	G1241	U1121	G1061	C881	G941	G881	G821	G761
U1478	G1421	A1363	C1302	G1242	U1122	U1062	C882	G942	C882	U822	U762
U1479	G1422	U1364	C1303	C1243	U1123	C1063	C883	U943	C883	G823	G763
C1479	G1423	G1365	G1304	G1244	G1124	G1064	U884	G944	U884	G824	C764
A1480	U1424	C1366	A1305	C1245	U1125	U1065	G885	G945	G885	A825	G765
U1481	G1425	C1367	U1307	U1246	G1126	C1066	A946	A946	C886	C826	A766
G1426	U1426	A1368	U1308	A1248	C1128	A1067	G947	G947	G887	U827	A767
U1482	C1369	C1369	G1309	C1249	U1129	C1068	U888	C948	G888	U828	G768
A1483	G1370	G1370	C1310	A1250	C1129	C1069	A889	U950	A889	G829	C769
C1484	A1427	G1371	A1311	A1251	A1130	U1070	U890	U951	G890	G830	C770
U1485	A1429	U1372	G1312	A1252	C1132	G1071	U891	G952	U891	A831	G771
G1486	A1430	G1373	U1313	G1253	G1133	G1072	A892	U953	A892	G832	U772
C1487	A1375	A1375	C1314	A1254	G1134	G1073	C893	G954	C893	G833	G773
G1488	U1376	U1376	U1315	G1255	U1135	U1074	G894	U955	U894	U834	G774
G1489	A1431	A1431	U1316	A1256	U1136	U1075	G895	G956	G895	U835	G775
U1490	G1432	C1377	C1317	A1257	C1137	G1076	G896	U957	C896	G836	G776
G1491	A1433	G1378	U1318	A1258	G1138	G1077	U897	U958	U897	U837	A777
U1492	G1434	G1379	C1319	G1259	U1139	U1078	C898	A959	C898	G838	G778
A1493	U1380	U1380	A1436	G1260	G1140	G1079	C899	U960	C899	G839	C779
G1494	A1437	U1381	C1320	G1261	C1141	A1080	A900	U961	A900	C840	A780
U1495	G1438										
C1496	U1440										
U1497	A1441										
U1498											
A1499											
A1500											
C1501											

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30892	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	5.345	Depositor
Minimum map value	-7.752	Depositor
Average map value	-4.176	Depositor
Map value standard deviation	0.605	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	2.07	842/36831 (2.3%)	2.08	1964/57458 (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	935

The worst 5 of 842 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	798	U	C5'-C4'	11.05	1.67	1.51
1	N	628	G	O4'-C1'	9.81	1.56	1.41
1	N	1352	C	C2'-C1'	-9.04	1.39	1.53
1	N	773	G	C1'-N9	8.94	1.61	1.48
1	N	737	C	P-O5'	-8.92	1.46	1.59

The worst 5 of 1964 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	94	G	P-O3'-C3'	18.98	148.67	120.20
1	N	1362	A	P-O3'-C3'	18.48	147.92	120.20
1	N	47	C	P-O3'-C3'	17.90	147.06	120.20
1	N	119	A	P-O3'-C3'	17.48	146.43	120.20
1	N	1530	G	P-O3'-C3'	17.35	146.22	120.20

There are no chirality outliers.

5 of 935 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	11	G	Sidechain
1	N	4	U	Sidechain
1	N	5	U	Sidechain
1	N	8	A	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	16532	491	0
All	All	32892	16554	16532	491	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 491 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:1123:U:H3	1:N:1150:A:H61	1.28	0.81
1:N:688:G:C8	1:N:688:G:H5''	2.18	0.78
1:N:1255:G:H2'	1:N:1279:G:H1	1.54	0.72
1:N:1240:U:C6	1:N:1241:G:H5'	2.24	0.71
1:N:50:A:H1'	1:N:52:C:C6	2.27	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%)	459 (29%)	162 (10%)

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 162 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	1064	G
1	N	1331	G
1	N	1129	C
1	N	1197	A
1	N	1364	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.

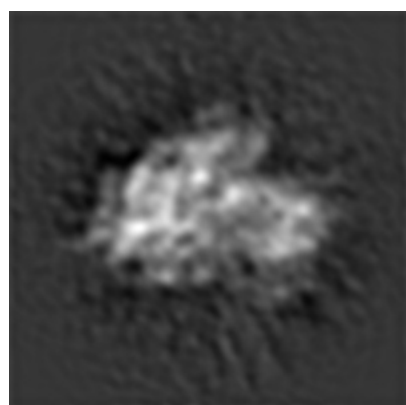
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5503. These allow visual inspection of the internal detail of the map and identification of artifacts.

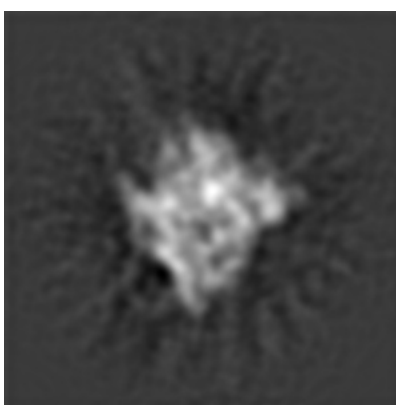
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

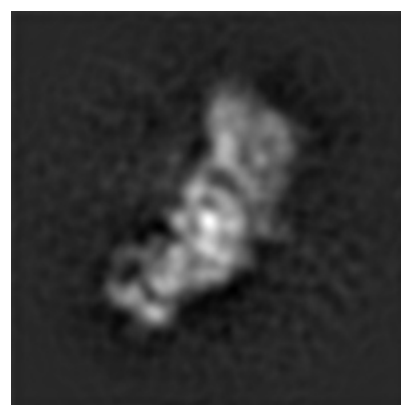
6.1.1 Primary map



X



Y

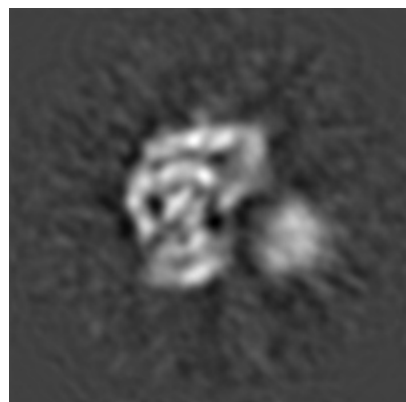


Z

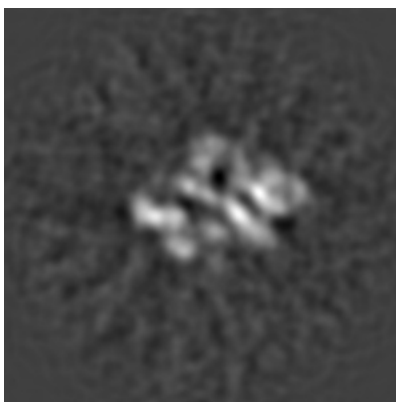
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

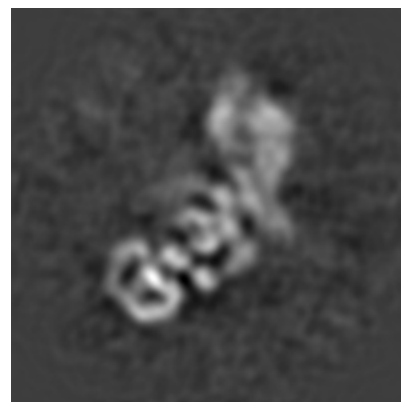
6.2.1 Primary map



X Index: 62



Y Index: 62

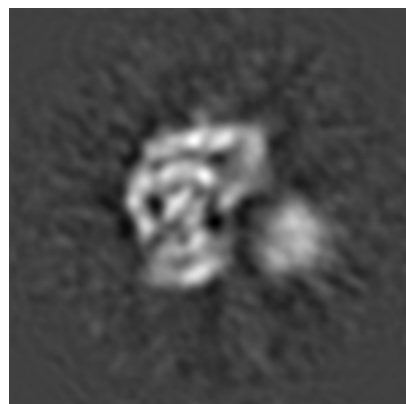


Z Index: 62

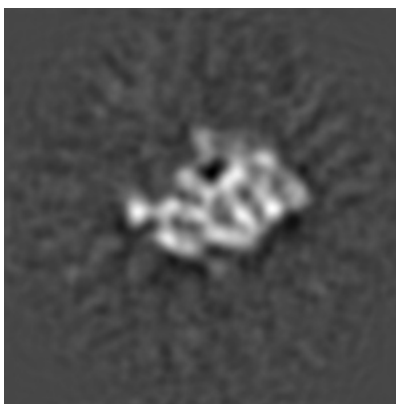
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

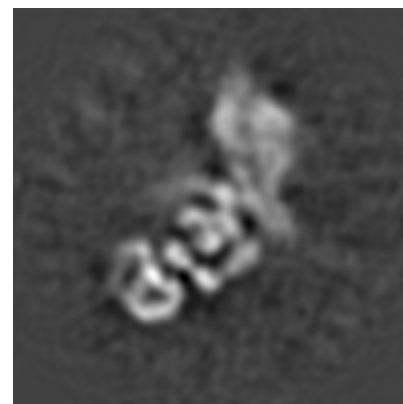
6.3.1 Primary map



X Index: 62



Y Index: 58

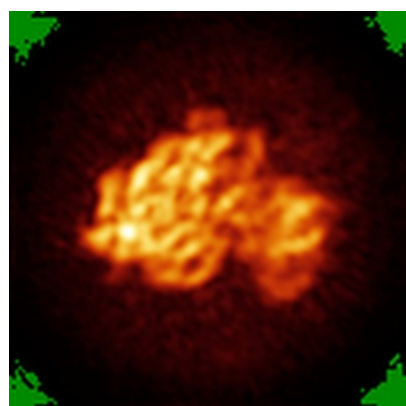


Z Index: 63

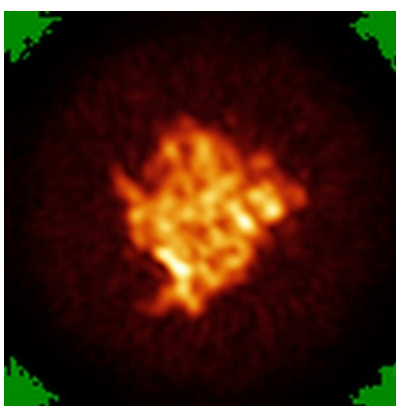
The images above show the largest variance slices of the map in three orthogonal directions.

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

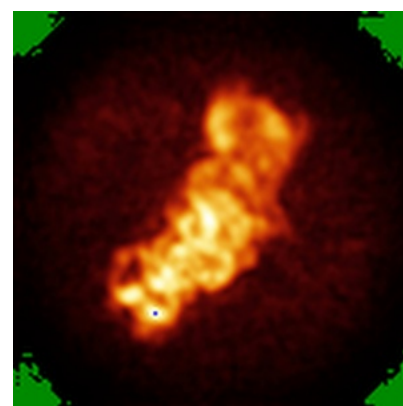
6.4.1 Primary map



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

This section was not generated.

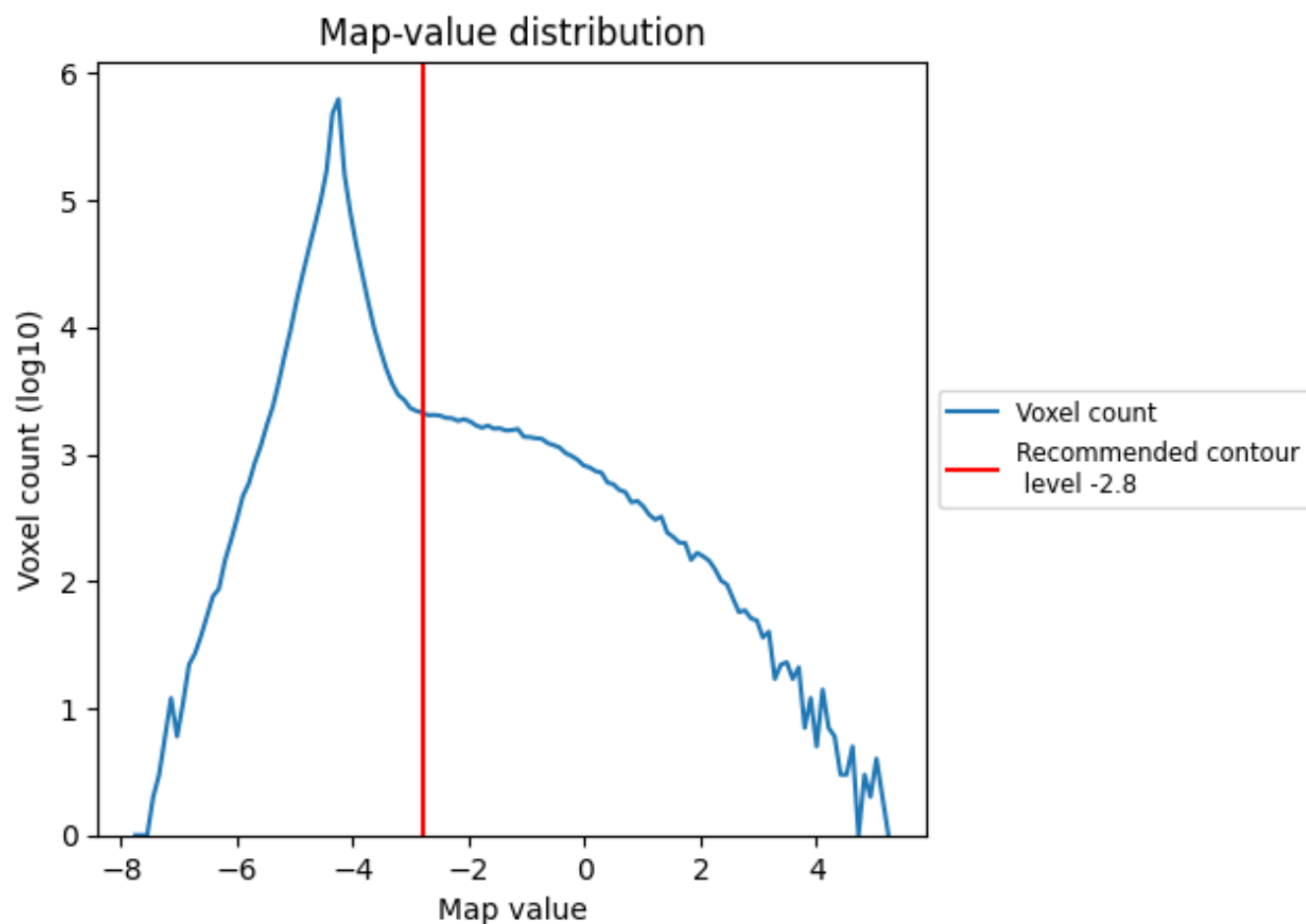
6.6 Mask visualisation

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

7 Map analysis [i](#)

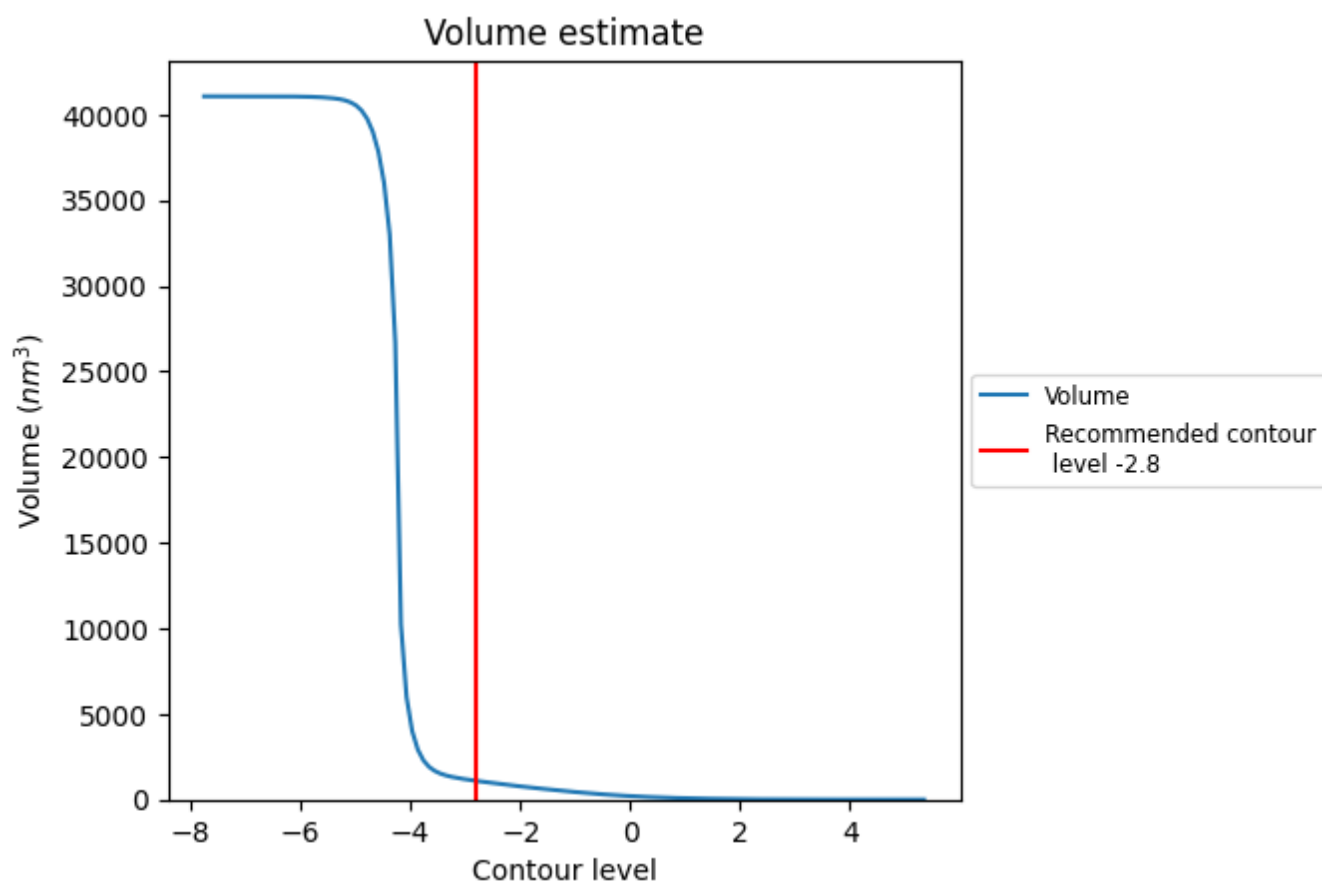
This section contains the results of statistical analysis of the map.

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.

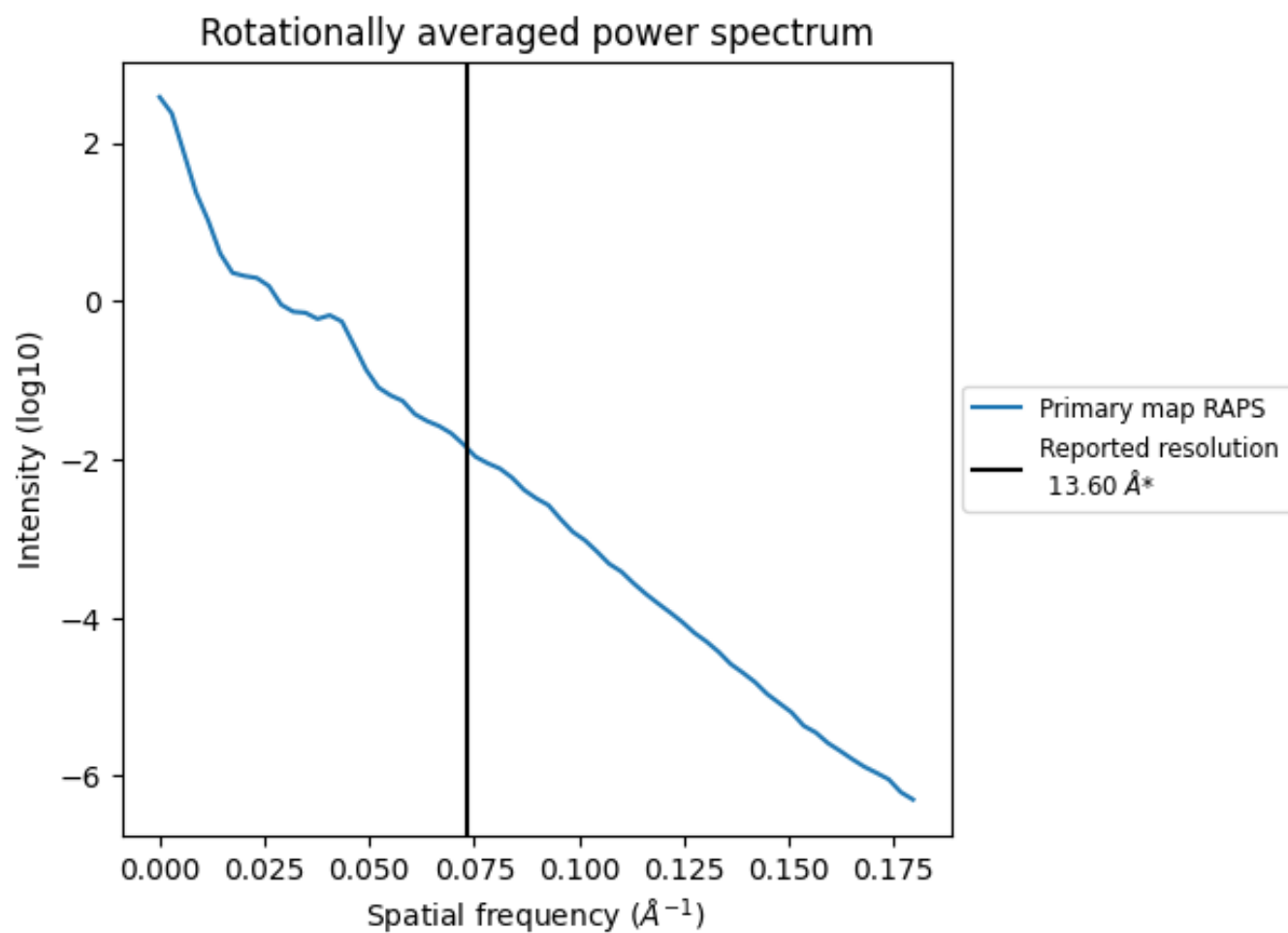
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1092 nm^3 ; this corresponds to an approximate mass of 986 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 0.074 Å⁻¹

8 Fourier-Shell correlation

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

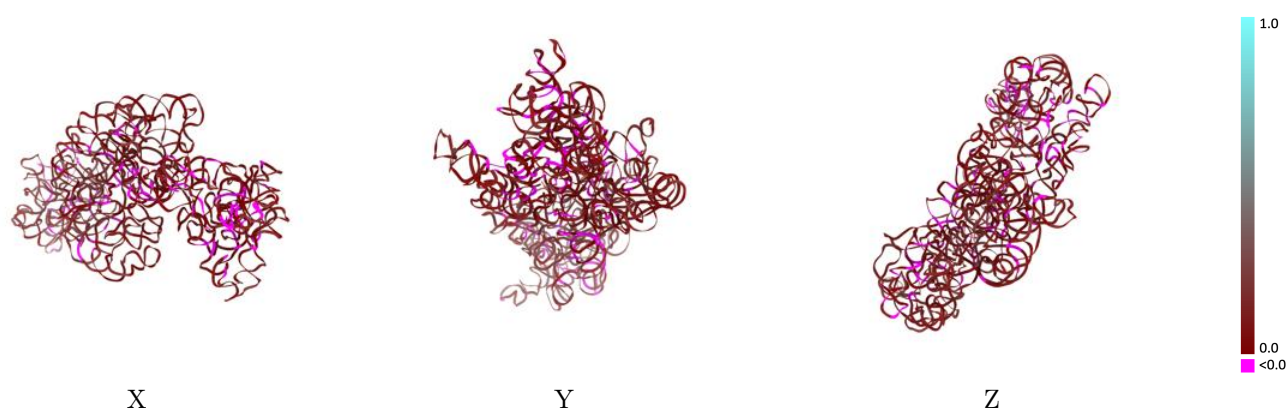
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5503 and PDB model 3J2B. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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

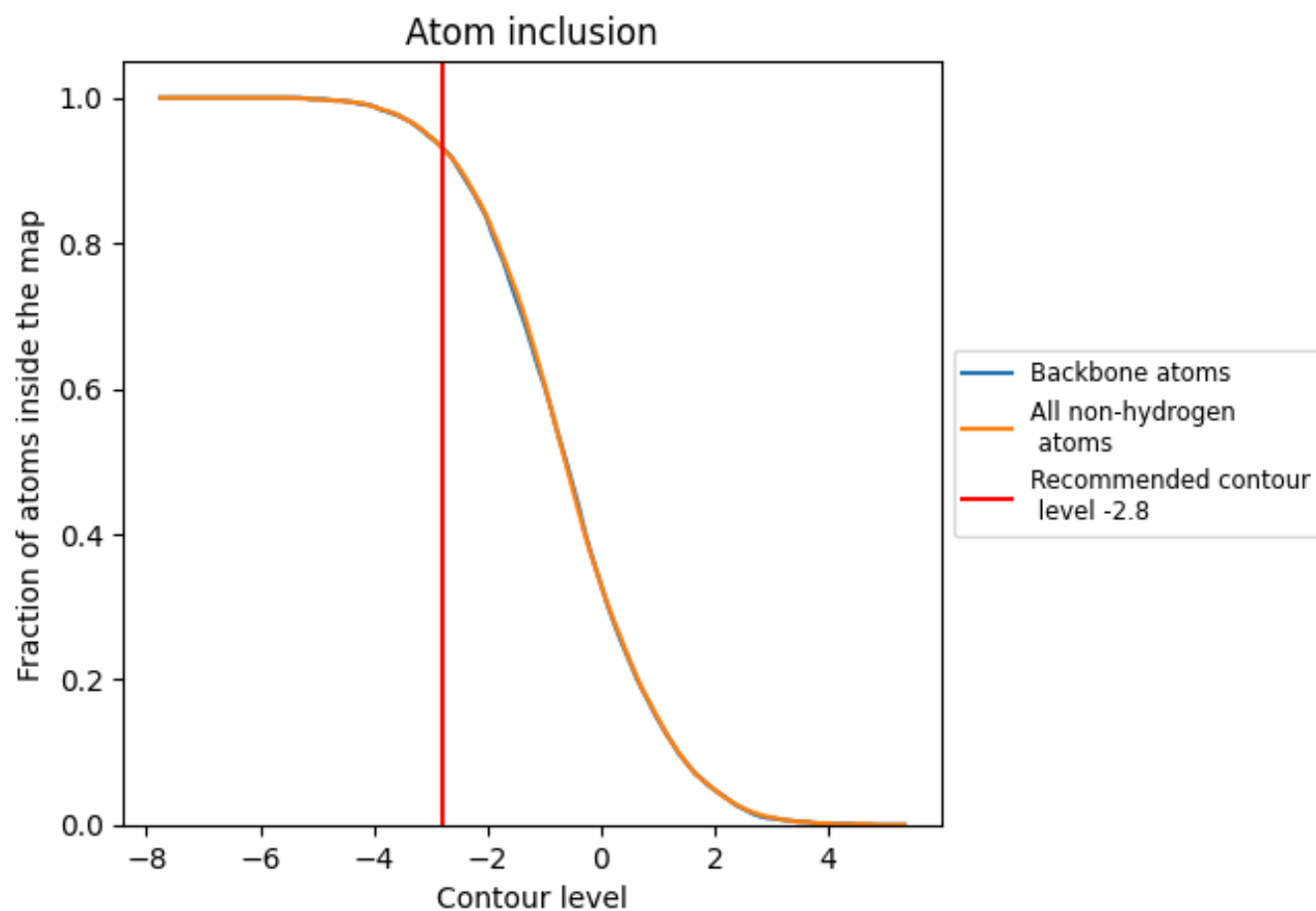


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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	0.9310	0.0880
N	0.9310	0.0880

