



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:05 PM UTC

PDB ID : 2YKR / pdb_00002ykr
EMDB ID : EMD-1884
Title : 30S ribosomal subunit with RsgA bound in the presence of GMPPNP
Authors : Guo, Q.; Yuan, Y.; Xu, Y.; Feng, B.; Liu, L.; Chen, K.; Lei, J.; Gao, N.
Deposited on : 2011-05-30
Resolution : 9.80 Å(reported)
Based on initial models : 3OFA, 2RCN

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

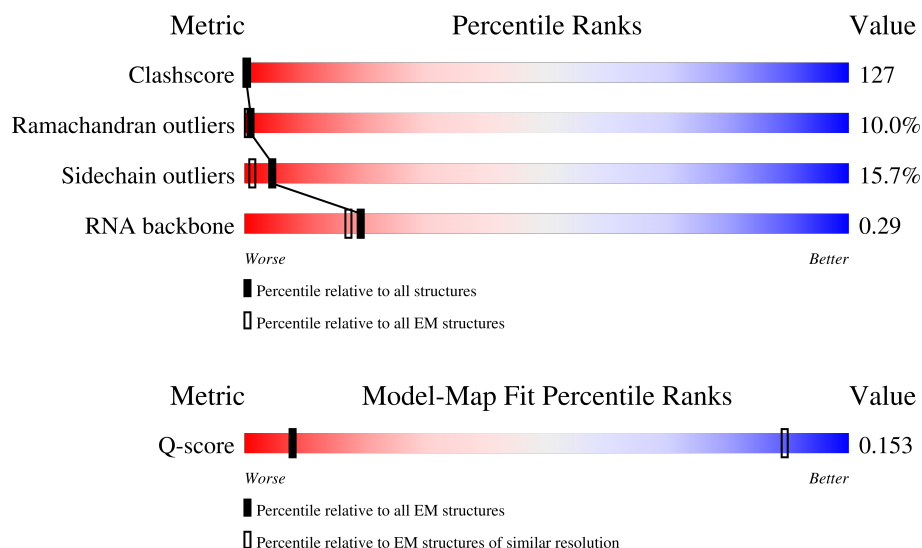
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.80 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.



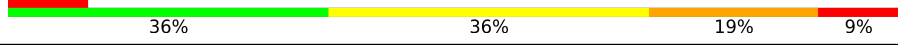
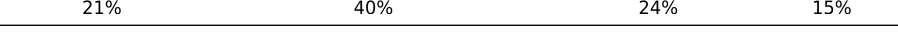
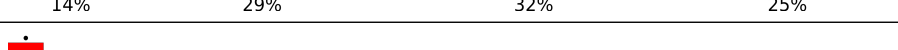
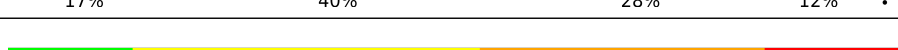
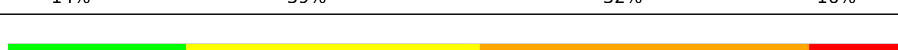
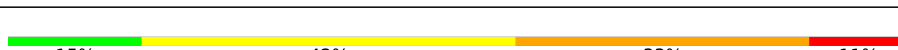
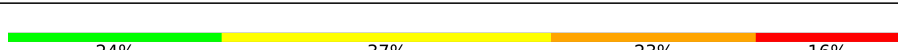
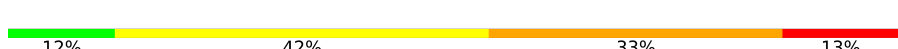
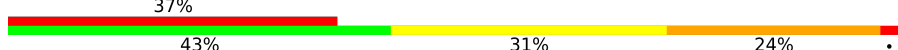
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	157 (9.30 - 10.30)

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	A	1533	
2	B	218	
3	C	206	

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Mol	Chain	Length	Quality of chain
4	D	205	
5	E	150	
6	F	100	
7	G	151	
8	H	129	
9	I	127	
10	J	98	
11	K	117	
12	L	123	
13	M	114	
14	N	100	
15	O	88	
16	P	82	
17	Q	80	
18	R	55	
19	S	79	
20	T	85	
21	U	51	
22	W	350	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 53633 atoms, of which 0 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	A	1533	Total	C	N	O	P	0	0
			32892	14671	6036	10653	1532		

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	150	Total	C	N	O	S	0	0
			1106	687	211	202	6		

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	97	Total	C	N	O	S	0	1
			775	483	161	128	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	39	ASP	GLU	conflict	UNP B7M1M1

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

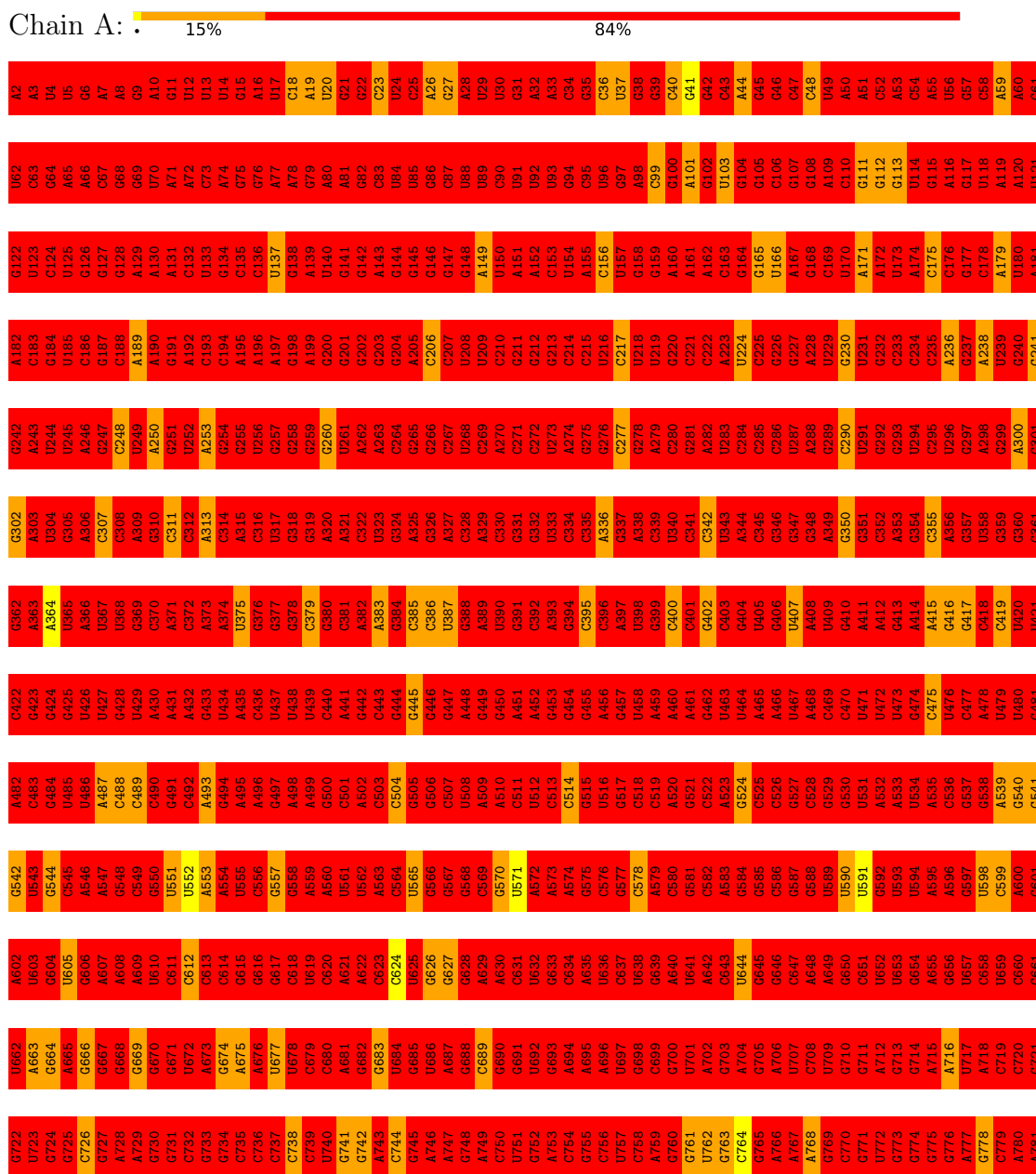
- Molecule 22 is a protein called PUTATIVE RIBOSOME BIOGENESIS GTPASE RSGA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	282	Total	C	N	O	S	0	4
			2186	1378	388	410	10		

3 Residue-property plots

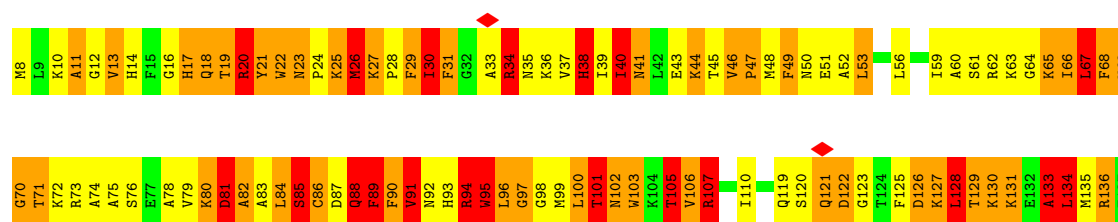
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

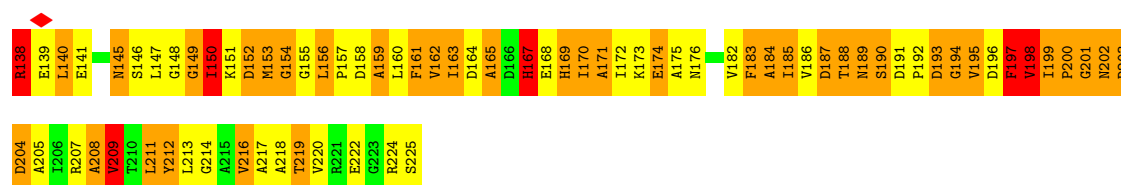
• Molecule 1: 16S rRNA



A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795	A796	A797	A798	A799	A800	A801	A802	A803	A804	A805	A806	A807	A808	A809	A810	A811	A812	A813	A814	A815	A816	A817	A818	A819	A820	A821	A822	A823	A824	A825	A826	A827	A828	A829	A830	A831	A832	A833	A834	A835	A836	A837	A838	A839	A840	A841
U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901
G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961
C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	A1000	A1001	A1002	A1003	A1004	A1005	A1006	A1007	A1008	A1009	A1010	A1011	A1012	A1013	A1014	A1015	A1016	A1017	A1018	A1019	A1020	A1021
A1022	A1023	A1024	A1025	A1026	A1027	A1028	A1029	A1030	A1031	A1032	A1033	A1034	A1035	A1036	A1037	A1038	A1039	A1040	A1041	A1042	A1043	A1044	A1045	A1046	A1047	A1048	A1049	A1050	A1051	A1052	A1053	A1054	A1055	A1056	A1057	A1058	A1059	A1060	A1061	A1062	A1063	A1064	A1065	A1066	A1067	A1068	A1069	A1070	A1071	A1072	A1073	A1074	A1075	A1076	A1077	A1078	A1079	A1080	A1081
A1082	A1083	A1084	A1085	A1086	A1087	A1088	A1089	A1090	A1091	A1092	A1093	A1094	A1095	A1096	A1097	A1098	A1099	A1100	A1101	A1102	A1103	A1104	A1105	A1106	A1107	A1108	A1109	A1110	A1111	A1112	A1113	A1114	A1115	A1116	A1117	A1118	A1119	A1120	A1121	A1122	A1123	A1124	A1125	A1126	A1127	A1128	A1129	A1130	A1131	A1132	A1133	A1134	A1135	A1136	A1137	A1138	A1139	A1140	A1141
G1142	G1143	G1144	G1145	G1146	G1147	G1148	G1149	G1150	G1151	G1152	G1153	G1154	G1155	G1156	G1157	G1158	G1159	G1160	G1161	G1162	G1163	G1164	G1165	G1166	G1167	G1168	G1169	G1170	G1171	G1172	G1173	G1174	G1175	G1176	G1177	G1178	G1179	G1180	G1181	G1182	G1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	G1191	G1192	G1193	G1194	G1195	G1196	G1197	G1198	G1199	G1200	A1201
U1202	U1203	U1204	U1205	U1206	U1207	U1208	U1209	U1210	U1211	U1212	U1213	U1214	U1215	U1216	U1217	U1218	U1219	U1220	U1221	U1222	U1223	U1224	U1225	U1226	U1227	U1228	U1229	U1230	U1231	U1232	U1233	U1234	U1235	U1236	U1237	U1238	U1239	U1240	U1241	U1242	U1243	U1244	U1245	U1246	U1247	U1248	U1249	U1250	U1251	U1252	U1253	U1254	U1255	U1256	U1257	U1258	U1259	U1260	A1261
C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	U1321
C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	A1381
G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	G1400	G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1440	A1441
G1442	G1443	G1444	G1445	G1446	G1447	G1448	G1449	G1450	G1451	G1452	G1453	G1454	G1455	G1456	G1457	G1458	G1459	G1460	G1461	G1462	G1463	G1464	G1465	G1466	G1467	G1468	G1469	G1470	G1471	G1472	G1473	G1474	G1475	G1476	G1477	G1478	G1479	G1480	G1481	G1482	G1483	G1484	G1485	G1486	G1487	G1488	G1489	G1490	G1491	G1492	G1493	G1494	G1495	G1496	G1497	G1498	G1499	G1500	C1501
A1502	A1503	A1504	A1505	A1506	A1507	A1508	A1509	A1510	A1511	A1512	A1513	A1514	A1515	A1516	A1517	A1518	A1519	A1520	A1521	A1522	A1523	A1524	A1525	A1526	A1527	A1528	A1529	A1530	A1531	A1532	A1533	A1534	A1535	A1536	A1537	A1538	A1539	A1540	A1541	A1542	A1543	A1544	A1545	A1546	A1547	A1548	A1549	A1550	A1551	A1552	A1553	A1554	A1555	A1556	A1557	A1558	A1559	A1560	A1561

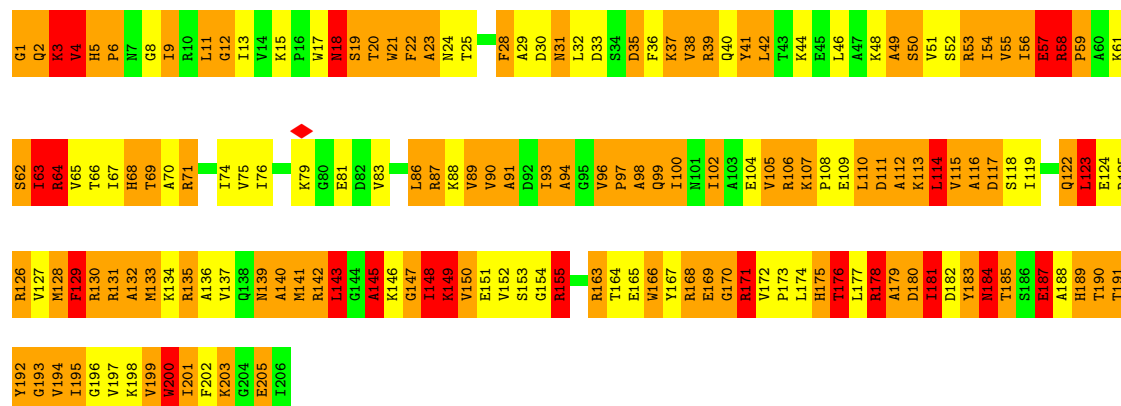
● Molecule 2: 30S RIBOSOMAL PROTEIN S2





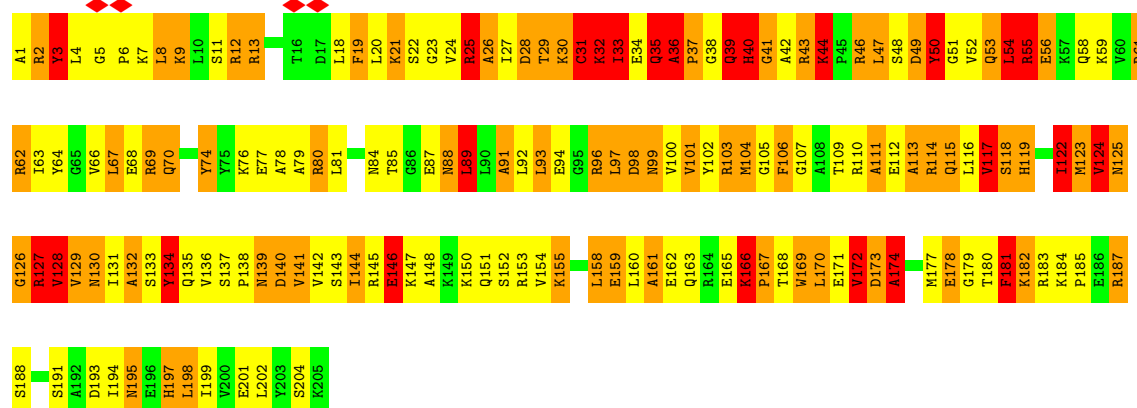
• Molecule 3: 30S RIBOSOMAL PROTEIN S3

Chain C: 18% 28% 43% 11%



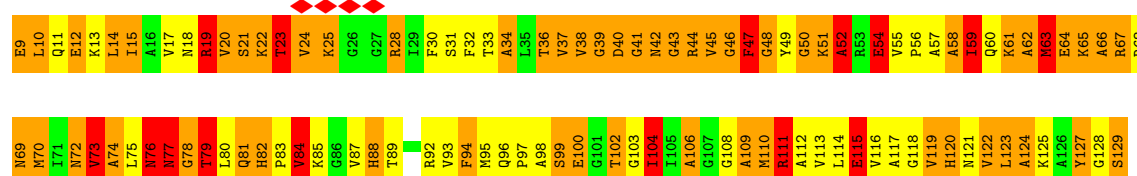
• Molecule 4: 30S RIBOSOMAL PROTEIN S4

Chain D: 17% 38% 33% 12%



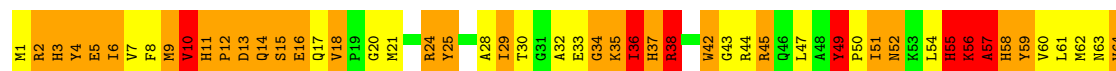
• Molecule 5: 30S RIBOSOMAL PROTEIN S5

Chain E: 13% 33% 43% 11%

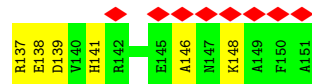
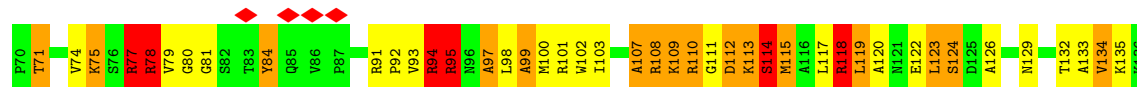
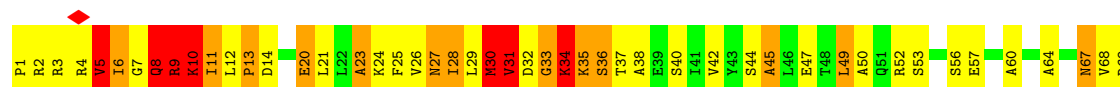




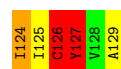
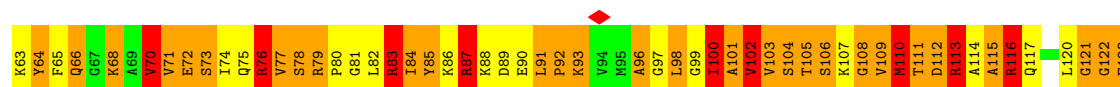
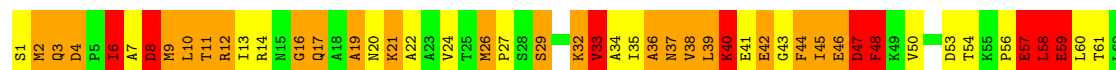
• Molecule 6: 30S RIBOSOMAL PROTEIN S6



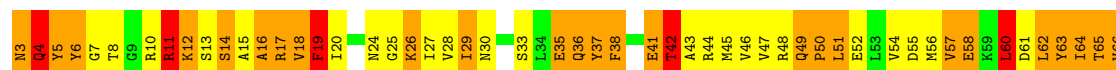
• Molecule 7: 30S RIBOSOMAL PROTEIN S7



• Molecule 8: 30S RIBOSOMAL PROTEIN S8

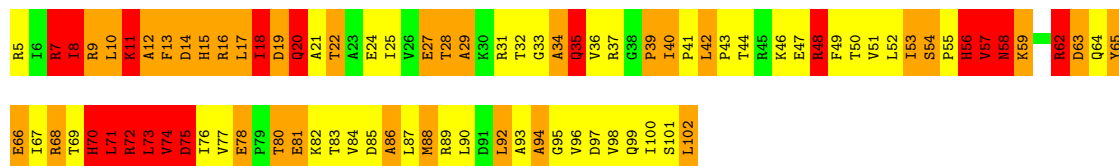
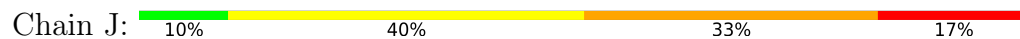


• Molecule 9: 30S RIBOSOMAL PROTEIN S9

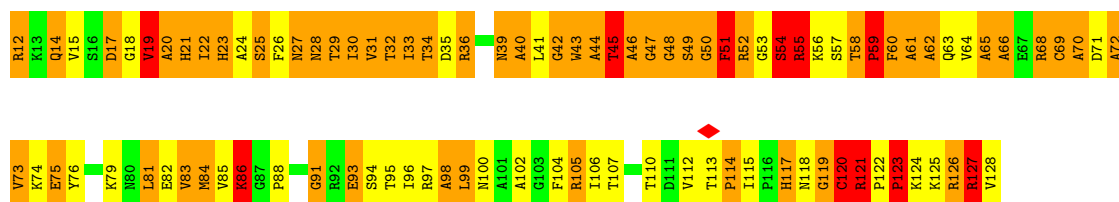




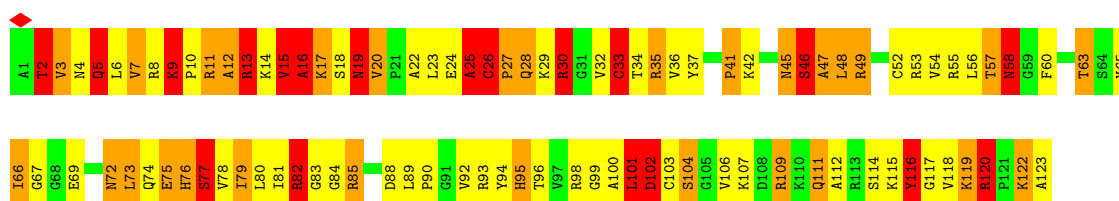
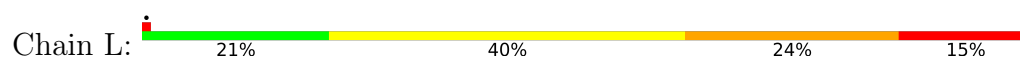
• Molecule 10: 30S RIBOSOMAL PROTEIN S10



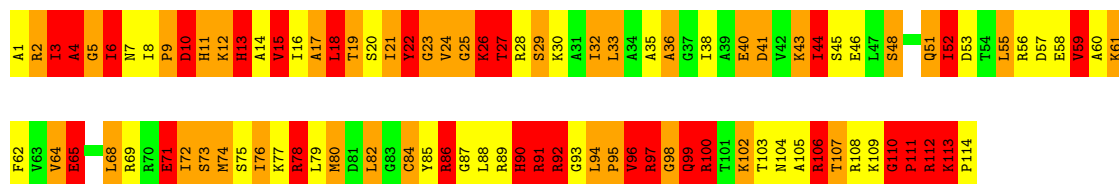
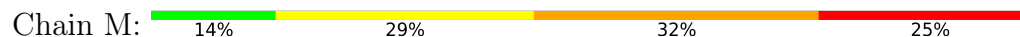
• Molecule 11: 30S RIBOSOMAL PROTEIN S11



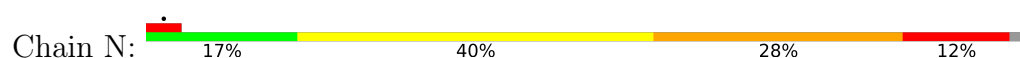
• Molecule 12: 30S RIBOSOMAL PROTEIN S12

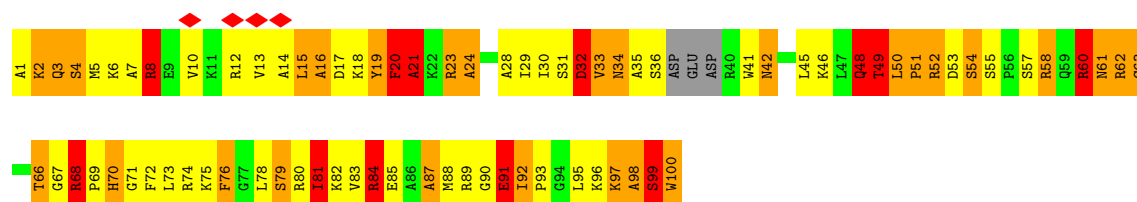


• Molecule 13: 30S RIBOSOMAL PROTEIN S13



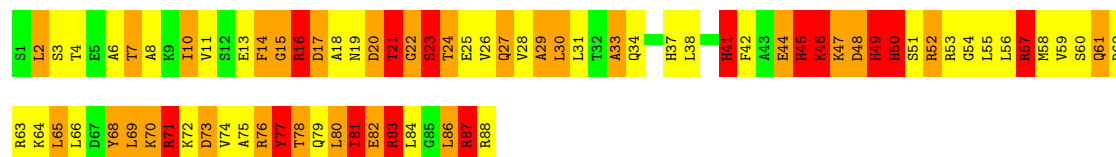
• Molecule 14: 30S RIBOSOMAL PROTEIN S14





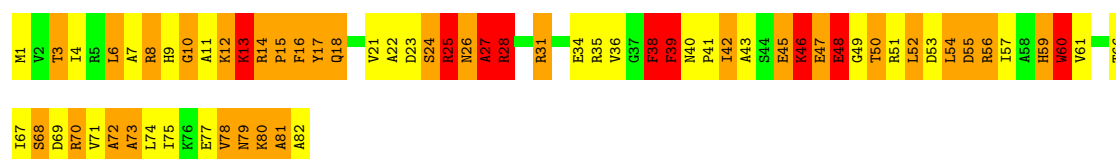
• Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain O: 14% 39% 32% 16%



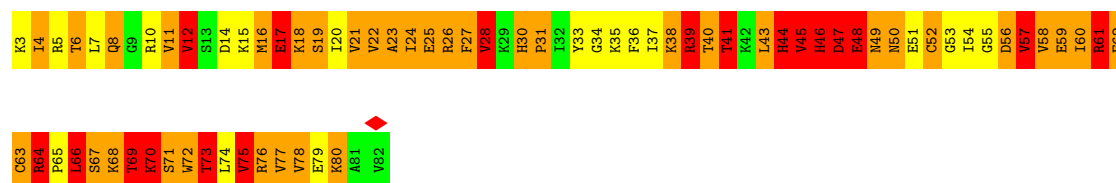
• Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain P: 20% 33% 37% 11%



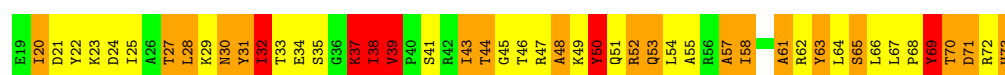
• Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain Q: 9% 24% 45% 22%



• Molecule 18: 30S RIBOSOMAL PROTEIN S18

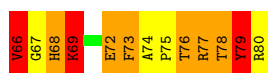
Chain R: 15% 42% 33% 11%



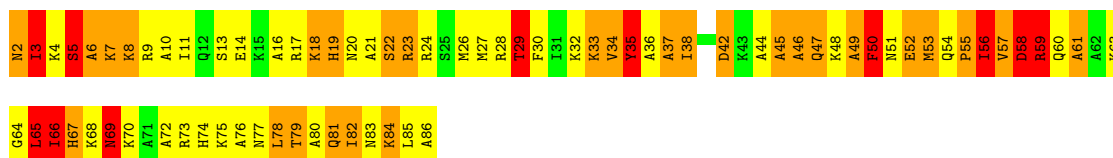
• Molecule 19: 30S RIBOSOMAL PROTEIN S19

Chain S: 24% 37% 23% 16%

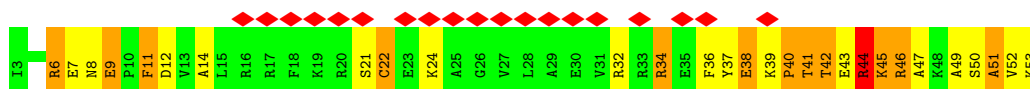
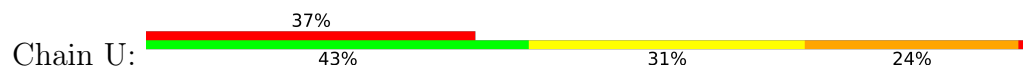




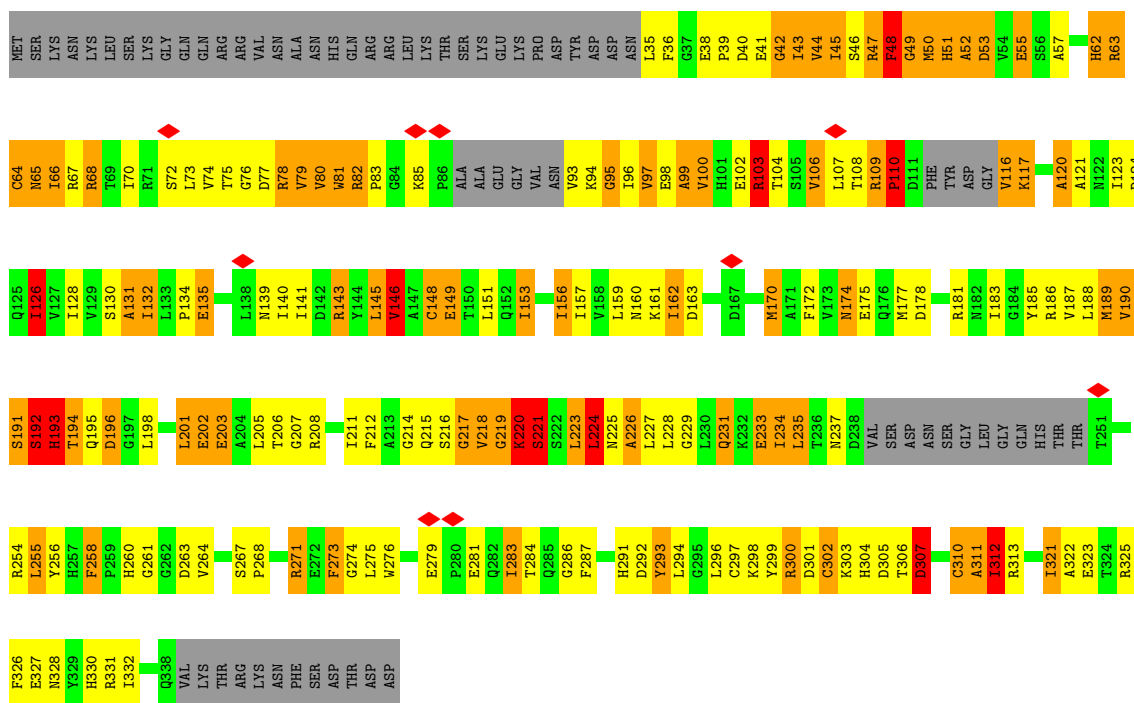
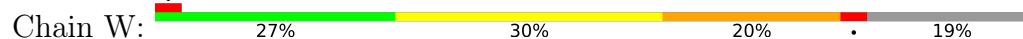
• Molecule 20: 30S RIBOSOMAL PROTEIN S20



• Molecule 21: 30S RIBOSOMAL PROTEIN S21



• Molecule 22: PUTATIVE RIBOSOME BIOGENESIS GTPASE RSGA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	77483	Depositor
Resolution determination method	Not provided	
CTF correction method	MAPS FROM EACH DEFOCUS GROUP	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	3850	Depositor
Magnification	59000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	19.771	Depositor
Minimum map value	-6.451	Depositor
Average map value	0.106	Depositor
Map value standard deviation	1.371	Depositor
Recommended contour level	3.16	Depositor
Map size ($\text{\AA}$)	362.5, 362.5, 362.5	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	2.9, 2.9, 2.9	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	A	2.49	2421/36831 (6.6%)	2.77	4596/57458 (8.0%)
2	B	2.06	55/1736 (3.2%)	2.57	158/2338 (6.8%)
3	C	2.30	85/1652 (5.1%)	2.46	134/2225 (6.0%)
4	D	2.14	66/1665 (4.0%)	2.48	118/2227 (5.3%)
5	E	2.44	67/1119 (6.0%)	2.56	98/1504 (6.5%)
6	F	2.13	31/836 (3.7%)	2.45	61/1128 (5.4%)
7	G	1.85	22/1196 (1.8%)	2.29	86/1602 (5.4%)
8	H	2.19	44/989 (4.4%)	2.55	84/1326 (6.3%)
9	I	2.12	36/1034 (3.5%)	2.55	95/1375 (6.9%)
10	J	2.19	30/797 (3.8%)	2.67	82/1077 (7.6%)
11	K	2.37	48/893 (5.4%)	2.51	71/1205 (5.9%)
12	L	2.10	32/969 (3.3%)	2.50	76/1300 (5.8%)
13	M	2.37	42/893 (4.7%)	2.79	95/1193 (8.0%)
14	N	1.90	17/786 (2.2%)	2.56	68/1045 (6.5%)
15	O	2.27	25/722 (3.5%)	2.81	82/964 (8.5%)
16	P	2.10	19/659 (2.9%)	2.61	64/884 (7.2%)
17	Q	2.70	50/658 (7.6%)	3.06	84/881 (9.5%)
18	R	1.99	14/463 (3.0%)	2.50	40/621 (6.4%)
19	S	1.79	9/653 (1.4%)	2.32	47/877 (5.4%)
20	T	2.13	26/671 (3.9%)	2.86	76/888 (8.6%)
21	U	1.66	4/431 (0.9%)	2.30	22/570 (3.9%)
22	W	1.96	65/2223 (2.9%)	2.21	124/3008 (4.1%)
All	All	2.37	3208/57876 (5.5%)	2.69	6361/85696 (7.4%)

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	A	0	1238
2	B	0	14
3	C	0	16

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	15
5	E	0	6
6	F	0	7
7	G	0	4
8	H	0	12
9	I	0	15
10	J	0	6
11	K	0	10
12	L	0	7
13	M	0	13
14	N	0	9
15	O	0	9
16	P	0	5
17	Q	0	7
18	R	0	4
19	S	0	8
20	T	0	5
21	U	0	2
22	W	0	7
All	All	0	1419

The worst 5 of 3208 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	O	22	GLY	CA-C	-15.77	1.41	1.52
1	A	1171	A	P-O5'	-14.75	1.37	1.59
1	A	70	U	O3'-P	-14.17	1.40	1.61
1	A	76	G	P-O5'	-13.99	1.38	1.59
1	A	737	C	P-O5'	-13.52	1.39	1.59

The worst 5 of 6361 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1399	C	P-O3'-C3'	37.32	176.18	120.20
1	A	1139	G	P-O3'-C3'	37.29	176.13	120.20
1	A	76	G	P-O5'-C5'	36.24	175.25	120.90
1	A	90	C	P-O5'-C5'	32.53	169.70	120.90
1	A	306	A	P-O3'-C3'	30.91	166.56	120.20

There are no chirality outliers.

5 of 1419 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2	A	Sidechain
1	A	3	A	Sidechain
1	A	4	U	Sidechain
1	A	5	U	Sidechain
1	A	6	G	Sidechain

5.2 Too-close contacts ⓘ

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	A	32892	0	16464	9852	0
2	B	1705	0	1732	217	0
3	C	1625	0	1699	211	0
4	D	1643	0	1710	182	0
5	E	1106	0	1148	148	0
6	F	818	0	808	113	0
7	G	1182	0	1240	128	0
8	H	979	0	1034	141	0
9	I	1022	0	1070	133	0
10	J	787	0	828	133	0
11	K	877	0	887	165	0
12	L	955	0	1019	108	0
13	M	884	0	944	128	0
14	N	775	0	827	117	0
15	O	714	0	737	112	0
16	P	649	0	666	71	0
17	Q	649	0	691	145	0
18	R	456	0	478	58	0
19	S	638	0	665	79	0
20	T	665	0	714	113	0
21	U	426	0	449	19	0
22	W	2186	0	2180	109	0
All	All	53633	0	37990	11571	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 127.

The worst 5 of 11571 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:A:429:U:H5'	4:D:8:LEU:HD13	1.45	0.99
1:A:688:G:H5''	1:A:688:G:C8	1.99	0.98
1:A:82:G:H22	1:A:84:U:H3	1.11	0.95
1:A:450:G:H1	1:A:483:C:H42	1.13	0.95
1:A:1469:C:H5'	1:A:1469:C:C6	2.02	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	216/218 (99%)	149 (69%)	41 (19%)	26 (12%)	0	4
3	C	204/206 (99%)	158 (78%)	28 (14%)	18 (9%)	0	8
4	D	203/205 (99%)	139 (68%)	41 (20%)	23 (11%)	0	5
5	E	148/150 (99%)	104 (70%)	25 (17%)	19 (13%)	0	4
6	F	98/100 (98%)	75 (76%)	16 (16%)	7 (7%)	1	11
7	G	149/151 (99%)	118 (79%)	20 (13%)	11 (7%)	1	10
8	H	127/129 (98%)	90 (71%)	26 (20%)	11 (9%)	0	9
9	I	125/127 (98%)	83 (66%)	25 (20%)	17 (14%)	0	4
10	J	96/98 (98%)	74 (77%)	10 (10%)	12 (12%)	0	4
11	K	115/117 (98%)	81 (70%)	20 (17%)	14 (12%)	0	4
12	L	121/123 (98%)	85 (70%)	22 (18%)	14 (12%)	0	5
13	M	112/114 (98%)	82 (73%)	16 (14%)	14 (12%)	0	4
14	N	93/100 (93%)	61 (66%)	21 (23%)	11 (12%)	0	4
15	O	86/88 (98%)	65 (76%)	16 (19%)	5 (6%)	1	14
16	P	80/82 (98%)	58 (72%)	13 (16%)	9 (11%)	0	5
17	Q	78/80 (98%)	55 (70%)	16 (20%)	7 (9%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	R	53/55 (96%)	33 (62%)	12 (23%)	8 (15%)	0	3
19	S	77/79 (98%)	61 (79%)	12 (16%)	4 (5%)	1	15
20	T	83/85 (98%)	64 (77%)	14 (17%)	5 (6%)	1	13
21	U	49/51 (96%)	28 (57%)	11 (22%)	10 (20%)	0	2
22	W	274/350 (78%)	236 (86%)	25 (9%)	13 (5%)	2	16
All	All	2587/2708 (96%)	1899 (73%)	430 (17%)	258 (10%)	1	7

5 of 258 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	11	ALA
2	B	18	GLN
2	B	23	ASN
2	B	27	LYS
2	B	30	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	180/180 (100%)	154 (86%)	26 (14%)	3	13
3	C	170/170 (100%)	144 (85%)	26 (15%)	3	12
4	D	172/172 (100%)	147 (86%)	25 (14%)	3	13
5	E	113/113 (100%)	94 (83%)	19 (17%)	2	10
6	F	87/87 (100%)	72 (83%)	15 (17%)	2	9
7	G	124/124 (100%)	111 (90%)	13 (10%)	6	21
8	H	104/104 (100%)	83 (80%)	21 (20%)	1	7
9	I	105/105 (100%)	87 (83%)	18 (17%)	2	10
10	J	86/86 (100%)	71 (83%)	15 (17%)	2	9
11	K	90/90 (100%)	73 (81%)	17 (19%)	1	8
12	L	103/103 (100%)	86 (84%)	17 (16%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	92/92 (100%)	73 (79%)	19 (21%)	1	6
14	N	79/83 (95%)	71 (90%)	8 (10%)	7	23
15	O	76/76 (100%)	66 (87%)	10 (13%)	4	15
16	P	65/65 (100%)	55 (85%)	10 (15%)	2	12
17	Q	74/74 (100%)	50 (68%)	24 (32%)	0	2
18	R	48/48 (100%)	44 (92%)	4 (8%)	10	30
19	S	70/70 (100%)	58 (83%)	12 (17%)	2	10
20	T	65/65 (100%)	55 (85%)	10 (15%)	2	12
21	U	44/44 (100%)	42 (96%)	2 (4%)	24	46
22	W	238/302 (79%)	206 (87%)	32 (13%)	4	14
All	All	2185/2253 (97%)	1842 (84%)	343 (16%)	4	12

5 of 343 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	N	46	LYS
18	R	69	TYR
14	N	100	TRP
17	Q	8	GLN
20	T	27	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
15	O	45	HIS
18	R	73	HIS
22	W	291	HIS
15	O	49	HIS
17	Q	8	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1532/1533 (99%)	489 (31%)	200 (13%)

5 of 489 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	A
1	A	4	U
1	A	5	U
1	A	6	G
1	A	7	A

5 of 200 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	817	C
1	A	1087	G
1	A	1533	C
1	A	845	A
1	A	974	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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	70:U	O3'	71:A	P	1.39

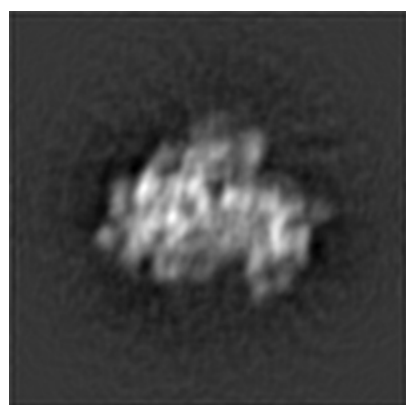
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1884. These allow visual inspection of the internal detail of the map and identification of artifacts.

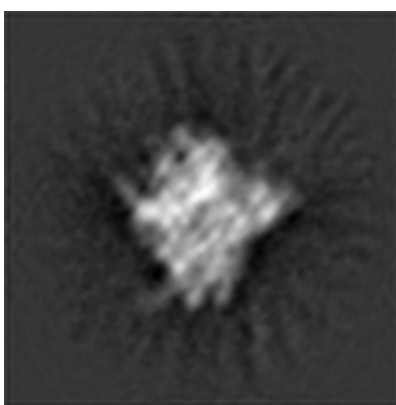
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

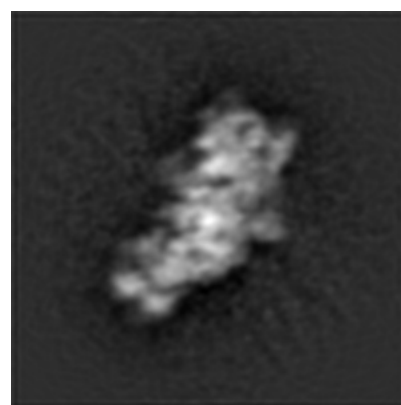
6.1.1 Primary map



X



Y

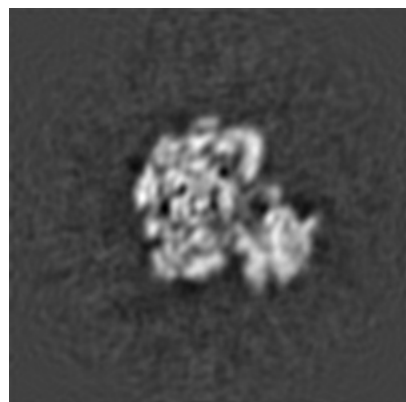


Z

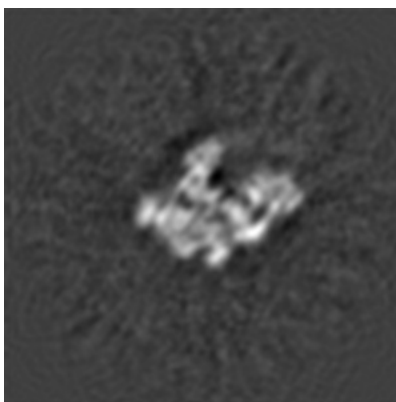
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

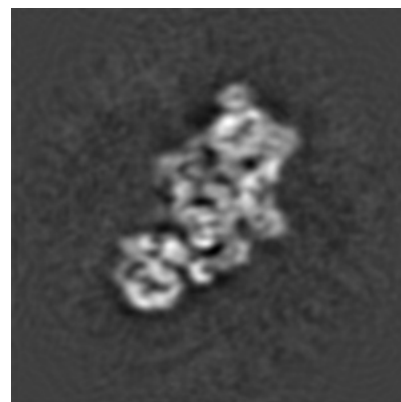
6.2.1 Primary map



X Index: 62



Y Index: 62

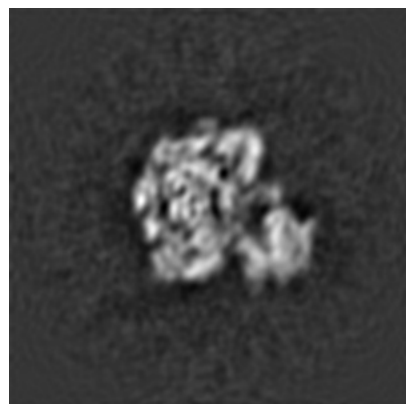


Z Index: 62

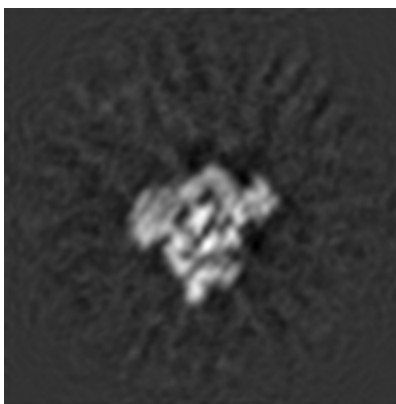
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

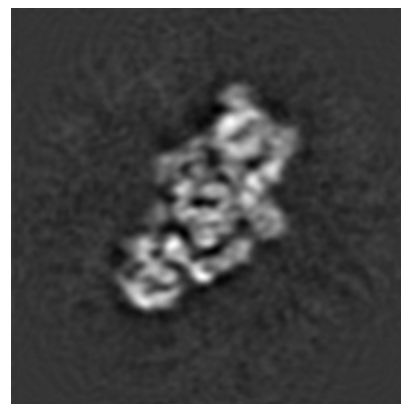
6.3.1 Primary map



X Index: 61



Y Index: 51

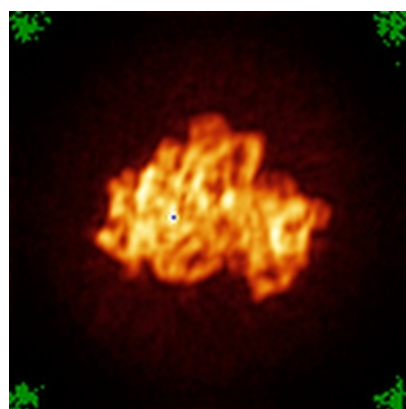


Z Index: 63

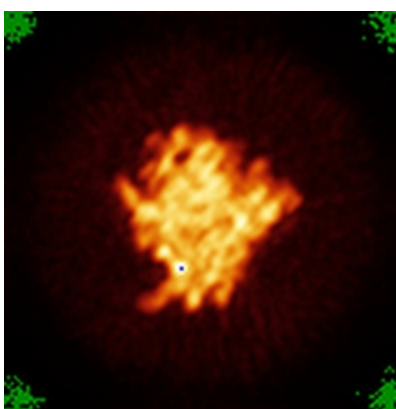
The images above show the largest variance slices of the map in three orthogonal directions.

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

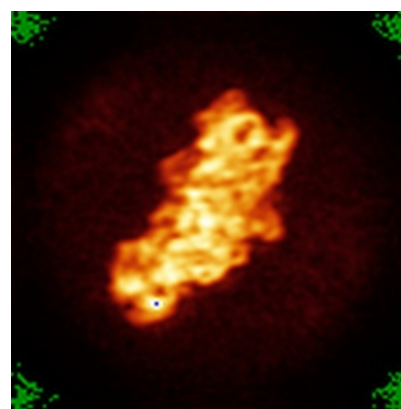
6.4.1 Primary map



X



Y

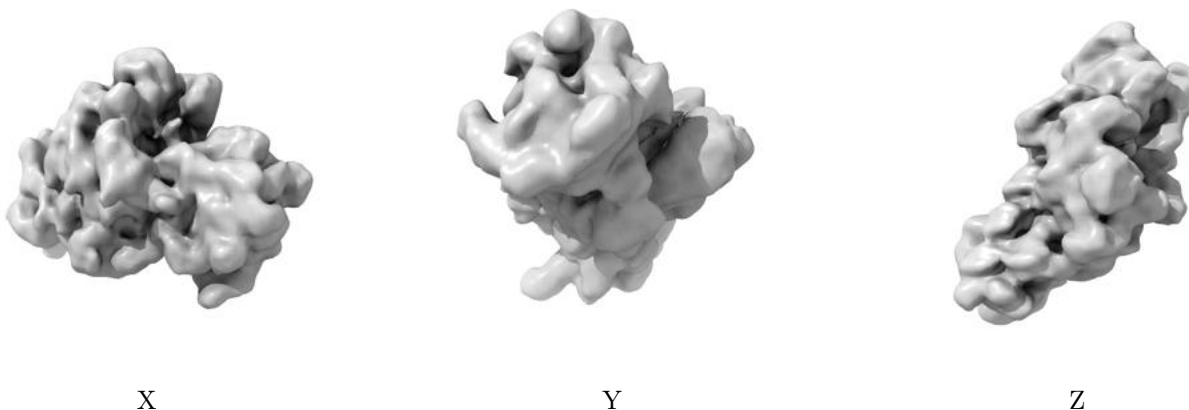


Z

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

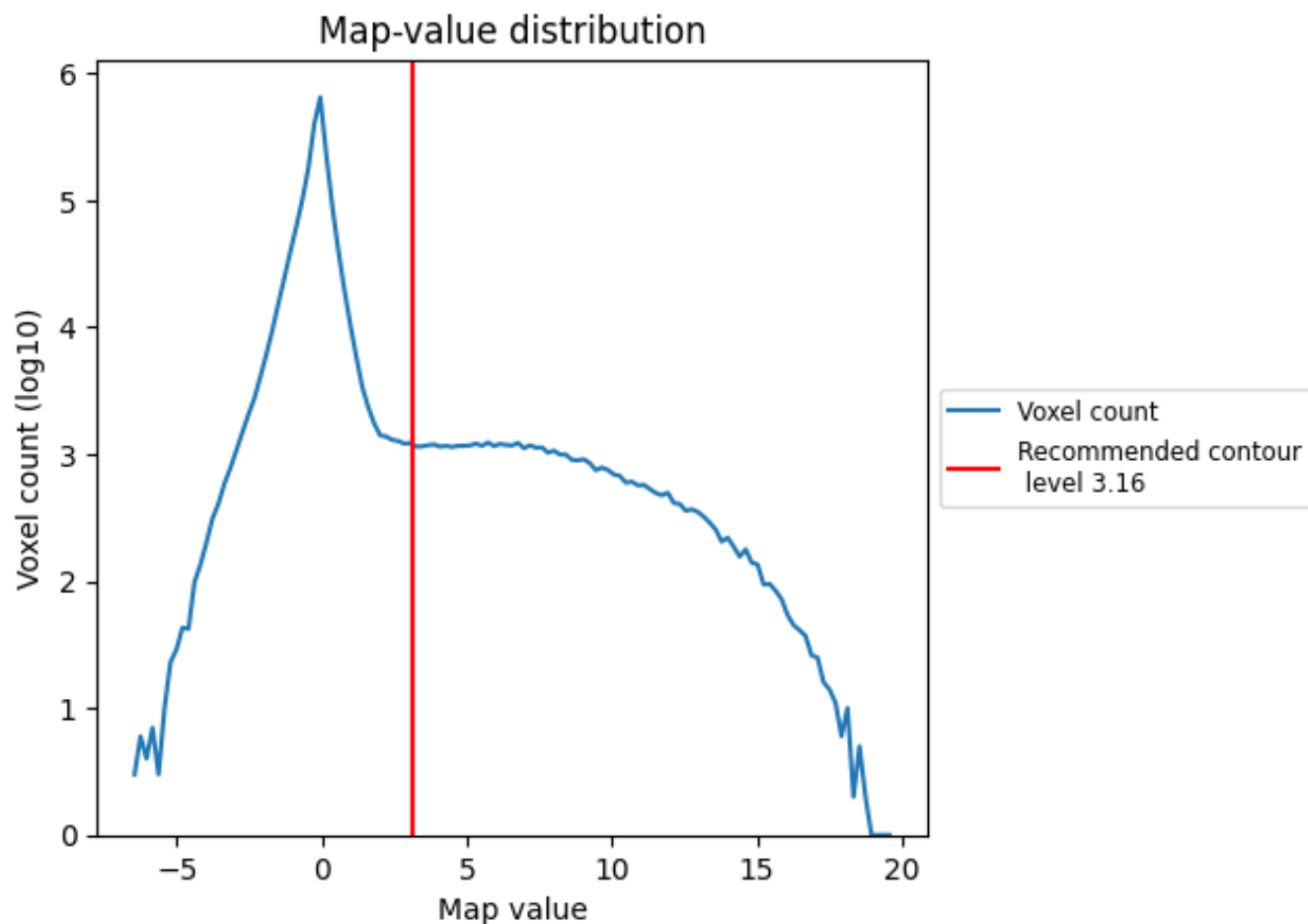
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

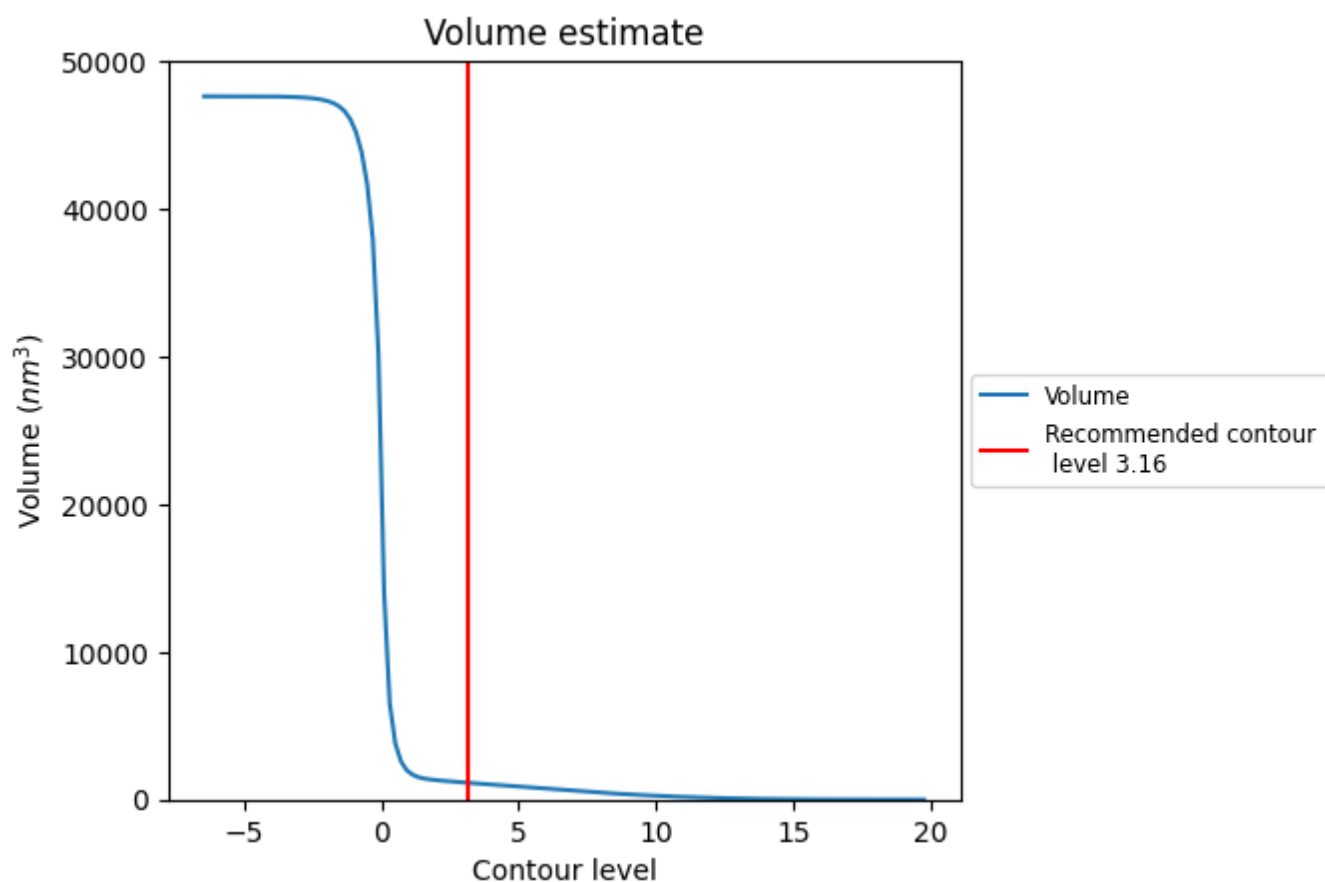
This section contains the results of statistical analysis of the map.

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.

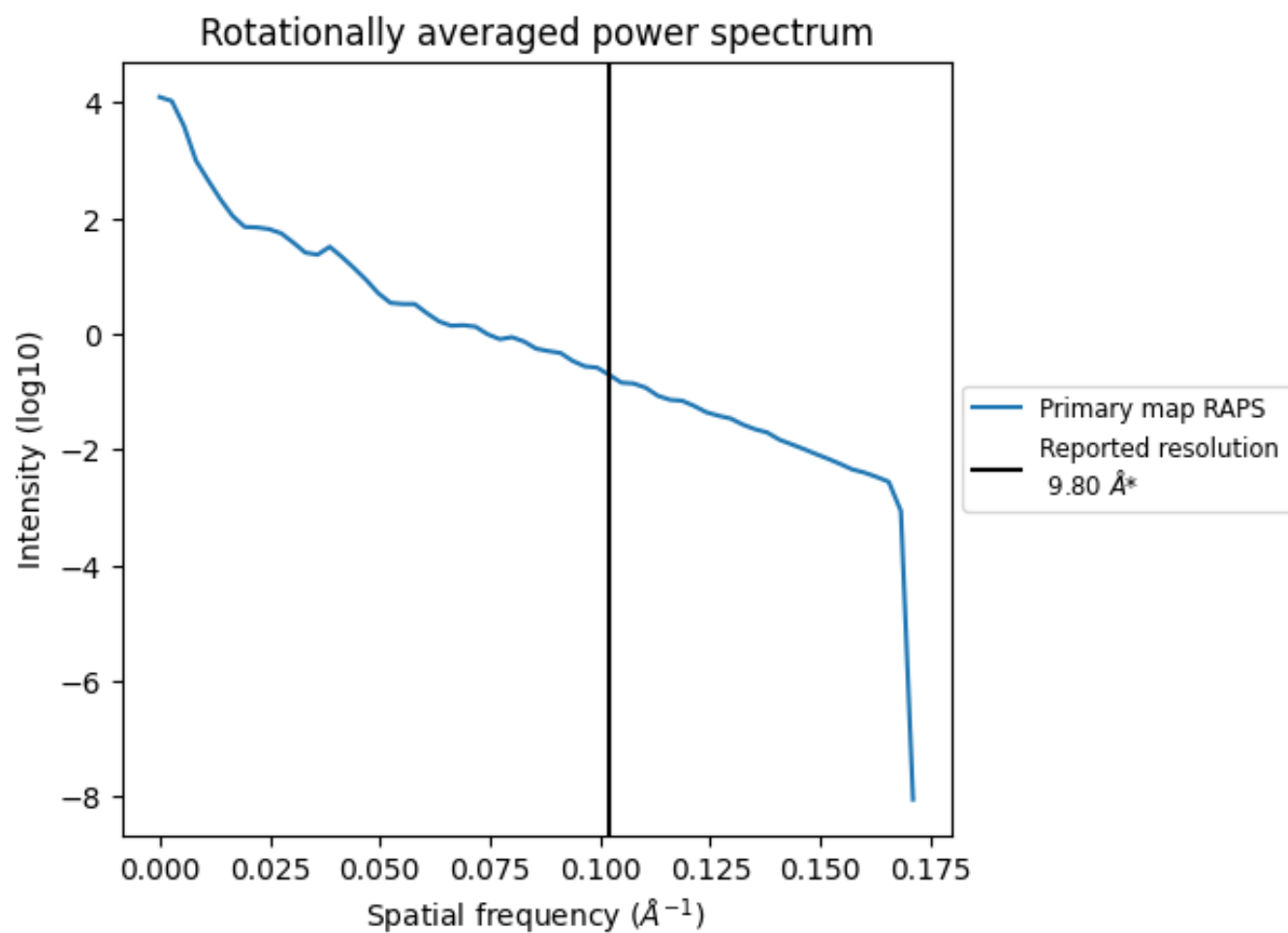
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1134 nm³; this corresponds to an approximate mass of 1025 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 0.102 Å⁻¹

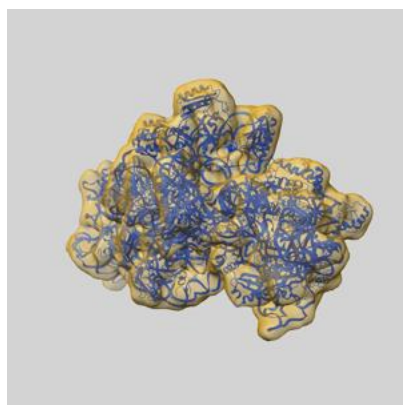
8 Fourier-Shell correlation

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

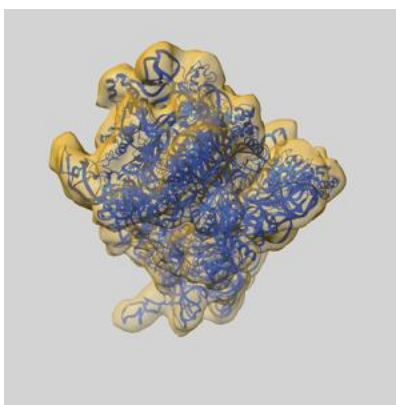
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1884 and PDB model 2YKR. Per-residue inclusion information can be found in section [3](#) on page [8](#).

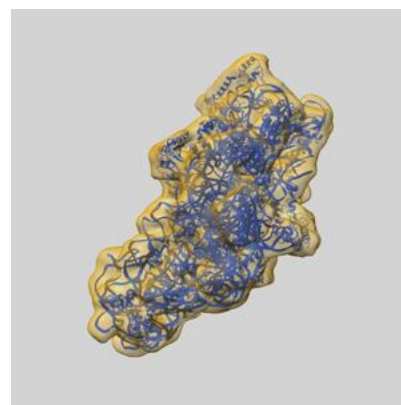
9.1 Map-model overlay [i](#)



X



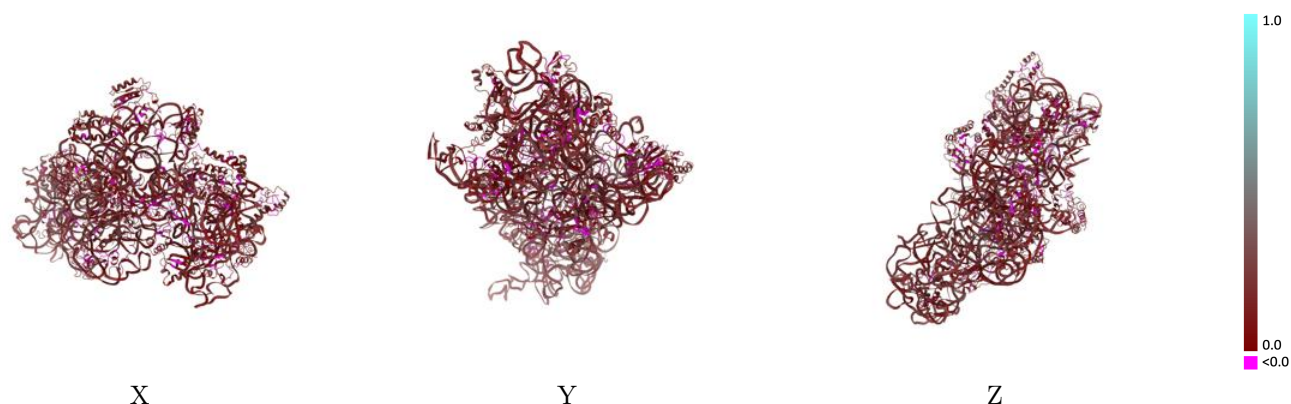
Y



Z

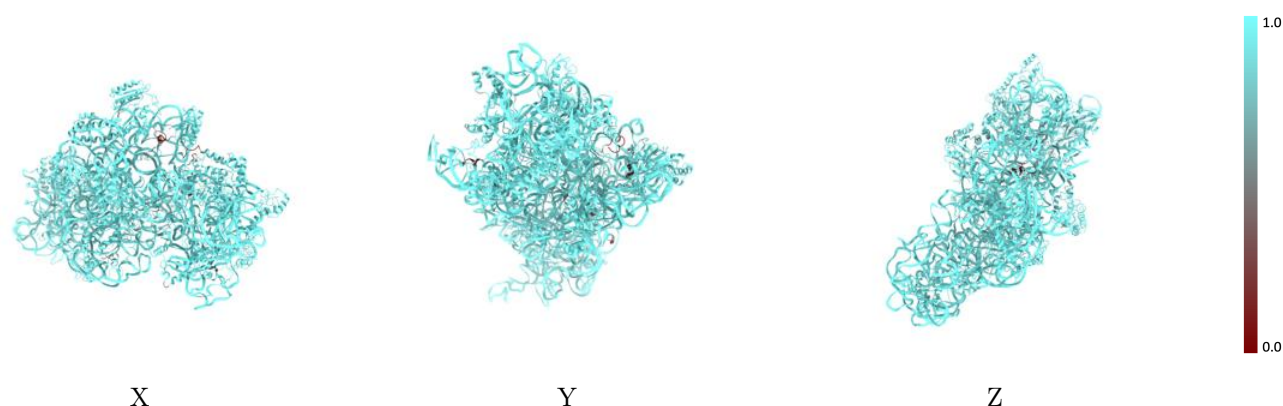
The images above show the 3D surface view of the map at the recommended contour level 3.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



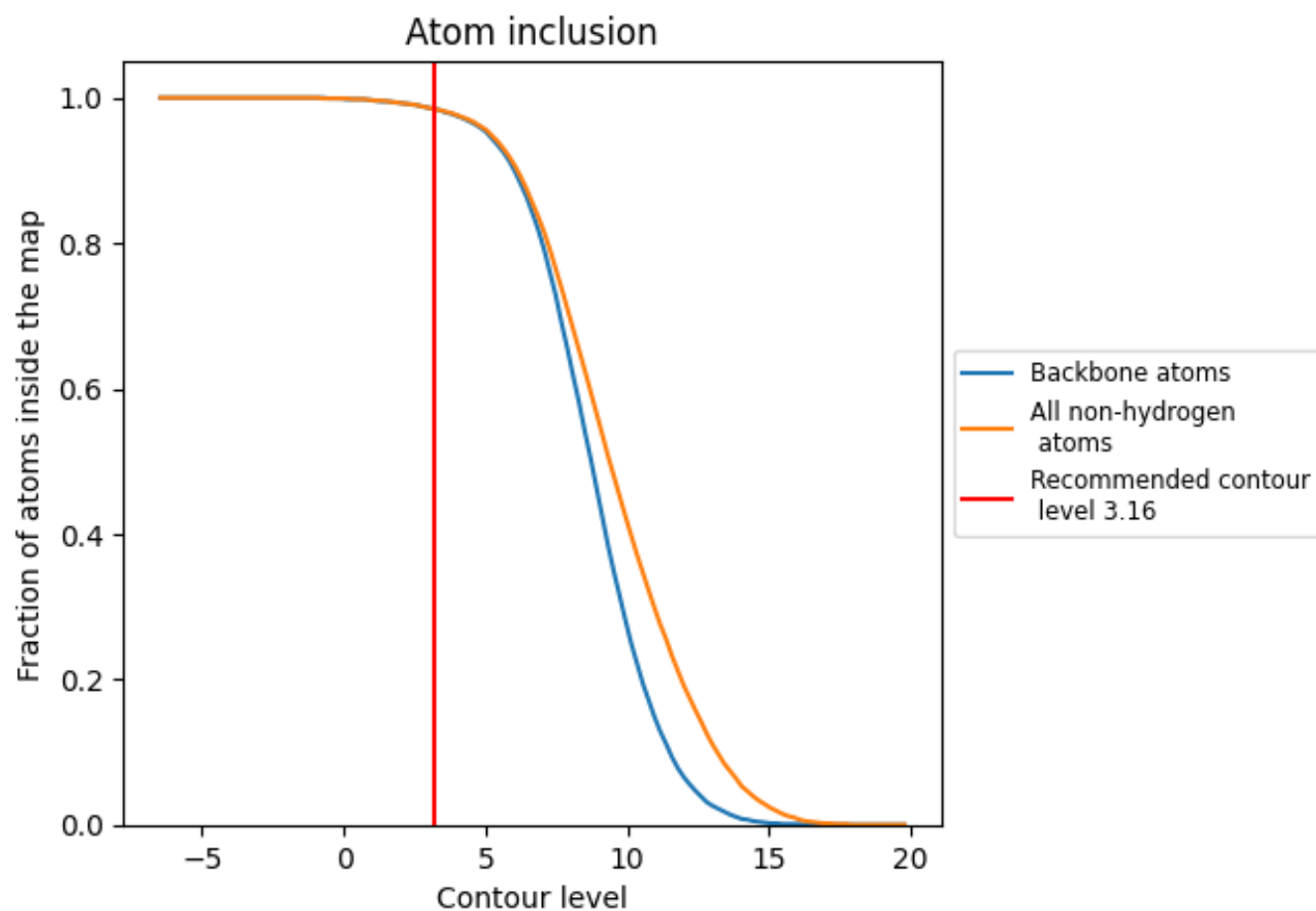
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.16).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (3.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.1530
A	 0.9990	 0.1730
B	 0.9700	 0.1270
C	 0.9850	 0.1370
D	 0.9760	 0.1140
E	 0.9800	 0.1420
F	 0.9650	 0.1330
G	 0.8990	 0.1010
H	 0.9830	 0.1310
I	 0.9910	 0.1110
J	 0.9650	 0.0940
K	 0.9800	 0.1120
L	 0.9870	 0.1060
M	 0.9950	 0.1390
N	 0.9560	 0.0920
O	 0.9940	 0.1460
P	 0.9950	 0.1050
Q	 0.9730	 0.1290
R	 1.0000	 0.1060
S	 0.9970	 0.1010
T	 0.9990	 0.1300
U	 0.5600	 0.0310
W	 0.9350	 0.1390

