



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 07:31 pm GMT

PDB ID : 4CSU  
EMDB ID : EMD-2605  
Title : Cryo-EM structures of the 50S ribosome subunit bound with ObgE  
Authors : Feng, B.; Mandava, C.S.; Guo, Q.; Wang, J.; Cao, W.; Li, N.; Zhang, Y.;  
Zhang, Y.; Wang, Z.; Wu, J.; Sanyal, S.; Lei, J.; Gao, N.  
Deposited on : 2014-03-10  
Resolution : 5.50 Å (reported)  
Based on initial model : 3OFC

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

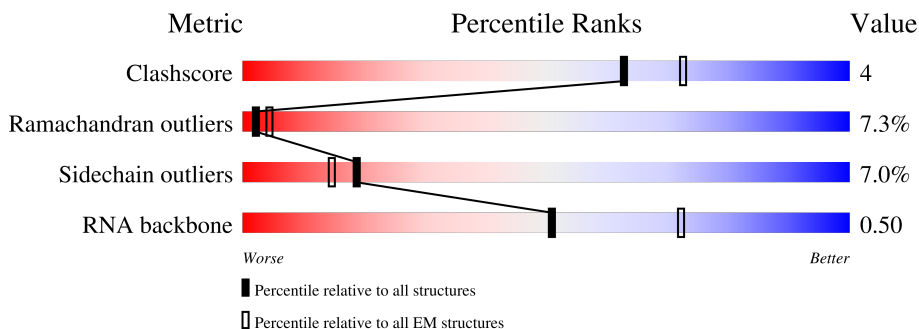
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.50 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	0	77	
2	1	63	
3	2	58	
4	3	56	
5	4	54	
6	5	234	
7	6	46	


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Mol	Chain	Length	Quality of chain
8	7	64	
9	8	38	
10	9	390	
11	A	118	
12	B	2903	
13	C	272	
14	D	209	
15	E	201	
16	F	178	
17	G	176	
18	H	149	
19	I	141	
20	J	142	
21	K	123	
22	L	143	
23	M	136	
24	N	127	
25	O	116	
26	P	114	
27	Q	117	
28	R	103	
29	S	110	
30	T	100	
31	U	103	
32	W	94	

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Mol	Chain	Length	Quality of chain
33	Y	84	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a small red segment at the beginning, followed by a large green segment (60%), a yellow segment (27%), an orange segment (7%), and a small grey segment at the end (6%).</p>

## 2 Entry composition [i](#)

There are 33 unique types of molecules in this entry. The entry contains 94625 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 protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	77	625	388	129	106	2	0	0

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	63	509	313	99	95	2	0	0

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	58	449	281	87	79	2	0	0

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	56	444	269	94	80	1	0	0

- Molecule 5 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	4	51	410	263	76	71	0	1

- Molecule 6 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	234	1733	1081	315	330	7	0	0

- Molecule 7 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	46	377	228	90	57	2	0	0

- Molecule 8 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	64	504	323	105	74	2	0	0

- Molecule 9 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	8	38	302	185	65	48	4	0	0

- Molecule 10 is a protein called GTPASE OBGE/CGTA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	9	334	2541	1596	448	485	12	0	1

- Molecule 11 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	A	115	2455	1097	451	795	112	0	0

- Molecule 12 is a RNA chain called 23S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	B	2903	62317	27801	11467	20147	2902	0	0

- Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	C	272	2083	1288	424	364	7	0	1

- Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	D	209	1565	979	288	294	4	0	0

- Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	E	201	1552	974	283	290	5	0	0

- Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	F	178	1420	905	251	258	6	0	0

- Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	G	176	1317	827	243	245	2	0	1

- Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	H	149	1111	699	197	214	1	0	0

- Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	I	69	495	303	90	99	3	0	0

- Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	J	142	1129	714	212	199	4	0	0

- Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	K	122	932	582	180	164	6	0	1

- Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	L	143	1045	649	206	189	1	0	0

- Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	M	136	1074	686	205	177	6	0	0

- Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	N	121	961	593	197	166	5	0	1

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	O	116	892	552	178	162	0	0

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	P	114	917	574	179	163	1	0	0

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	Q	117	947	604	192	151	0	0

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L21.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	R	103	816	516	153	145	2	0	0

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	S	110	857	532	166	156	3	0	0

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	T	94	739	466	140	131	2	0	1

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	U	102	758	479	143	136	0	3

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	W	94	753	479	137	134	3	0	0

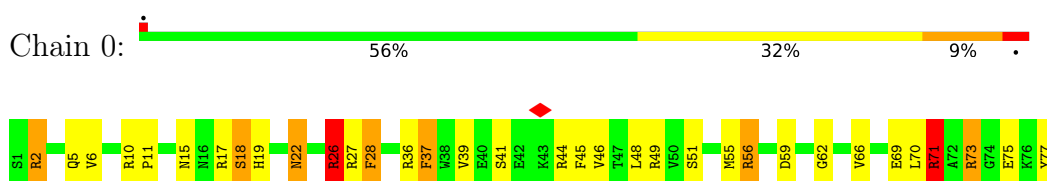
- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Y	79	596	367	120	108	1	0	0

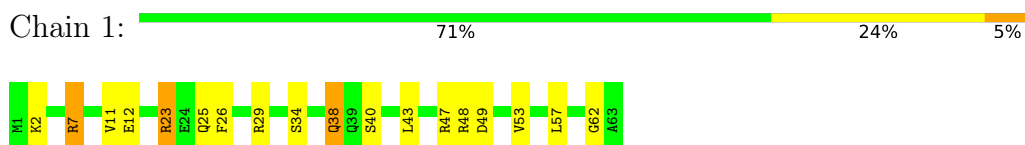
### 3 Residue-property plots [i](#)

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.

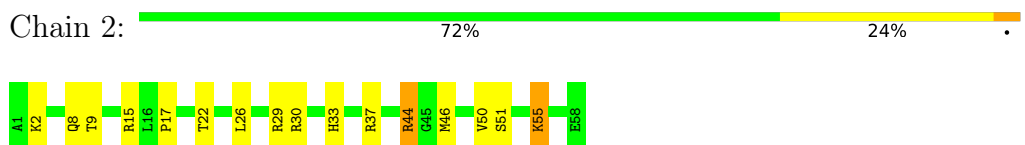
- Molecule 1: 50S RIBOSOMAL PROTEIN L28



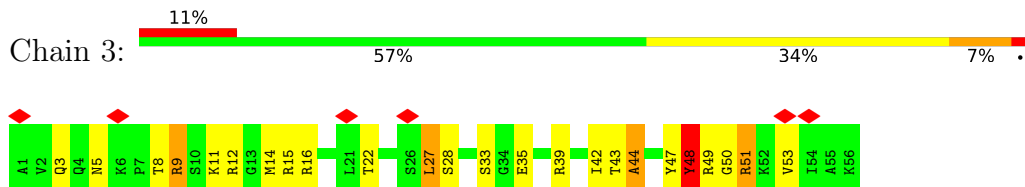
- Molecule 2: 50S RIBOSOMAL PROTEIN L29



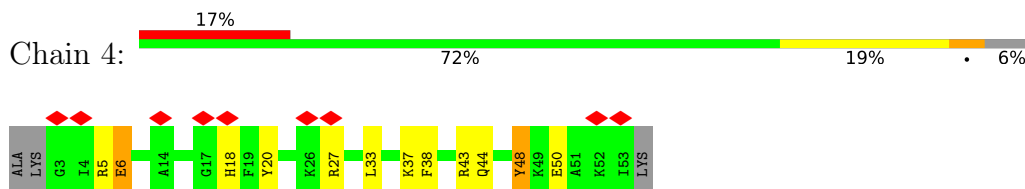
- Molecule 3: 50S RIBOSOMAL PROTEIN L30



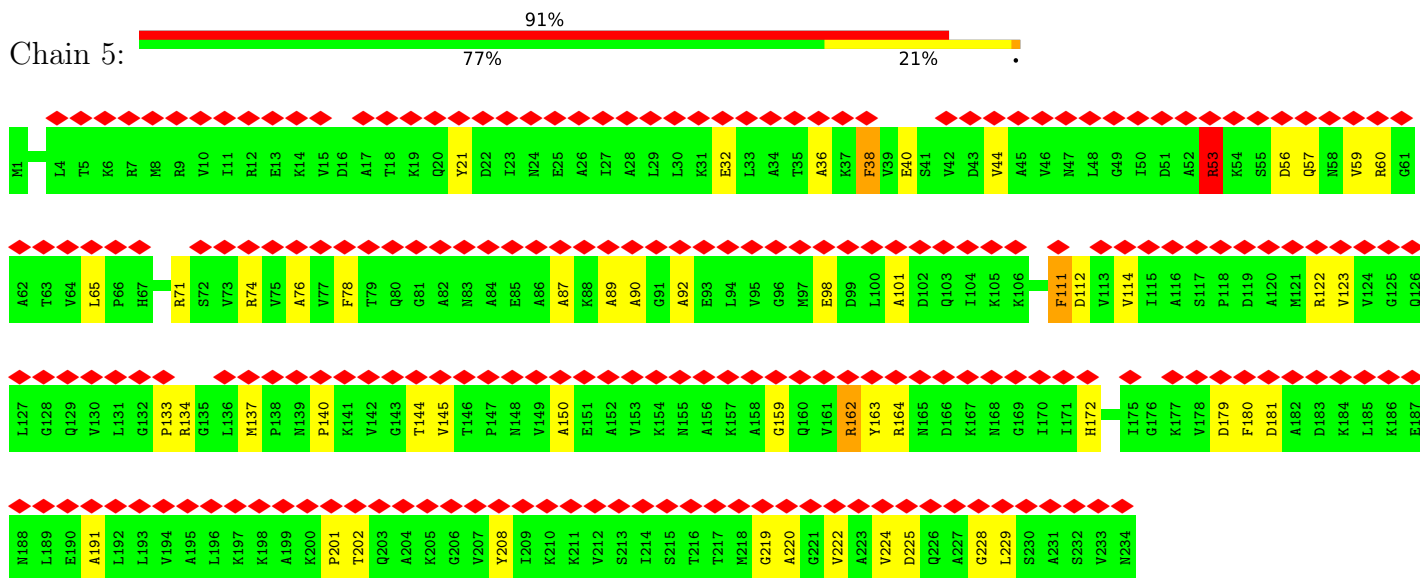
- Molecule 4: 50S RIBOSOMAL PROTEIN L32



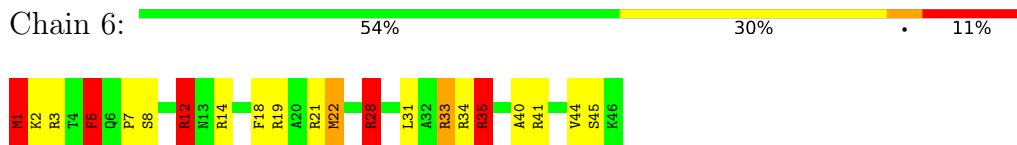
- Molecule 5: 50S RIBOSOMAL PROTEIN L33



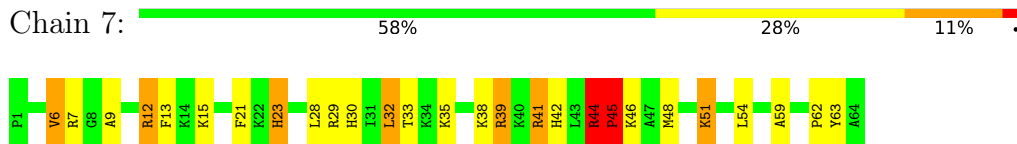
- Molecule 6: 50S RIBOSOMAL PROTEIN L1



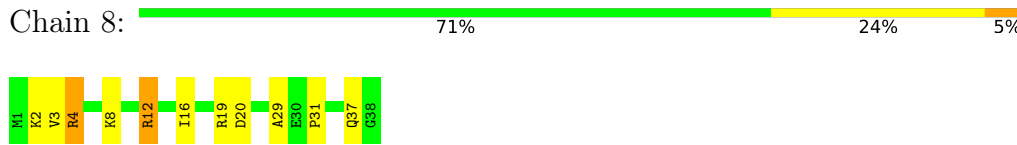
• Molecule 7: 50S RIBOSOMAL PROTEIN L34



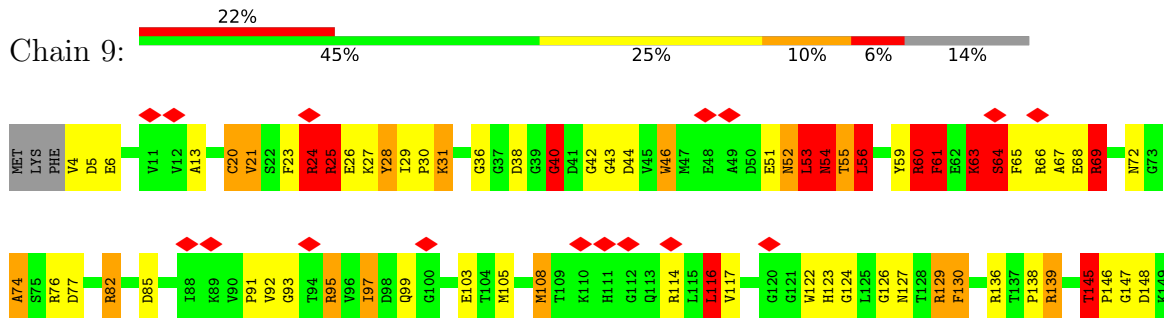
• Molecule 8: 50S RIBOSOMAL PROTEIN L35

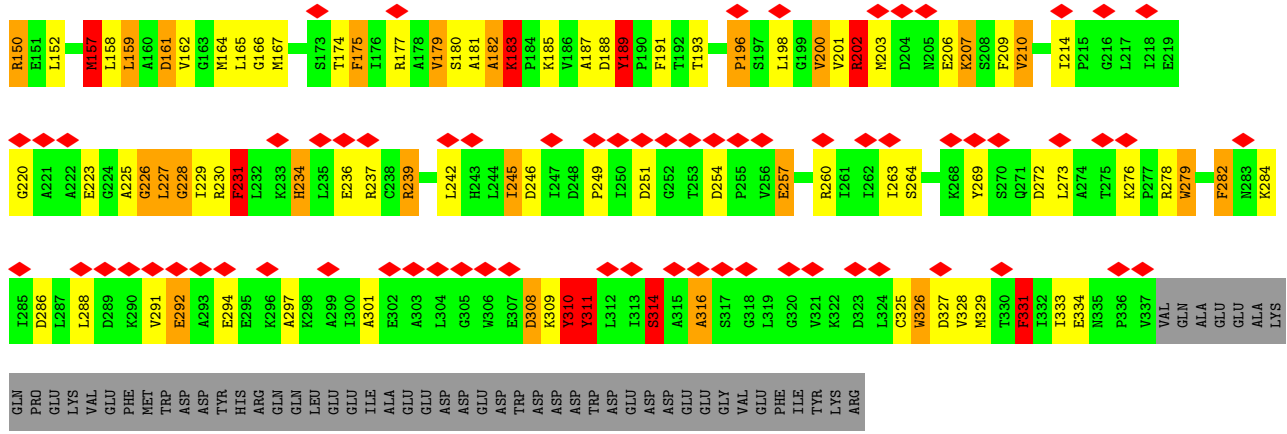


• Molecule 9: 50S RIBOSOMAL PROTEIN L36



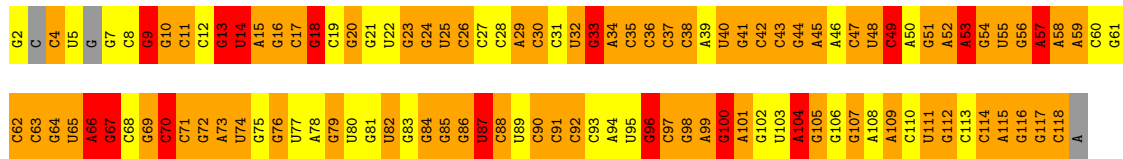
• Molecule 10: GTPASE OBGE/CGTA





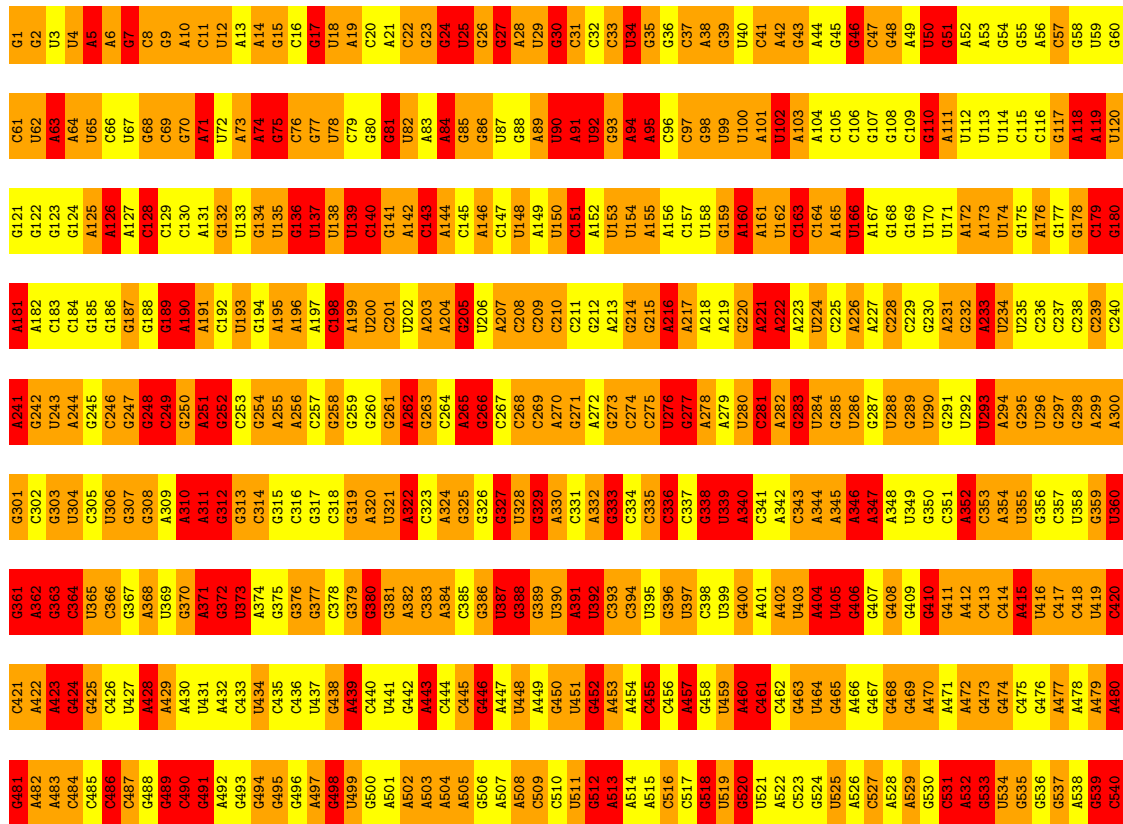
• Molecule 11: 5S RRNA

Chain A: 28% 57% 13%



• Molecule 12: 23S RRNA

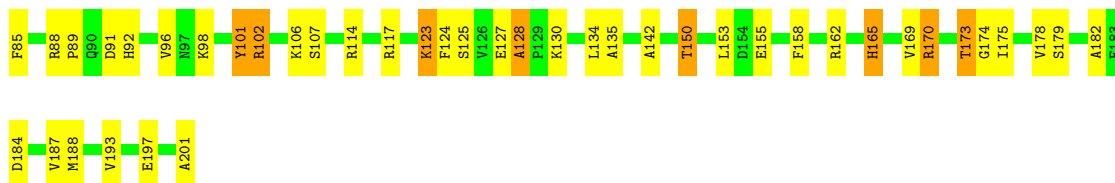
Chain B: 31% 45% 25%



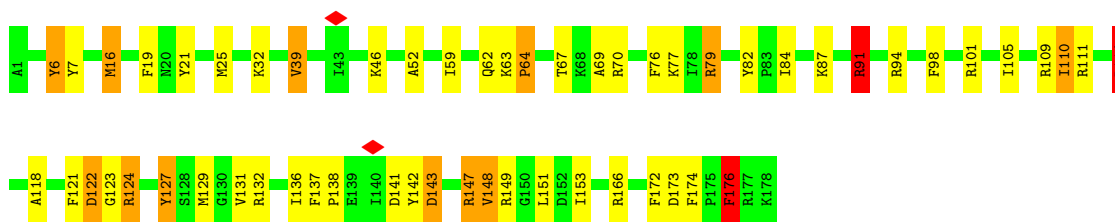
G1501	G1441	G1381	A1321	C1261	U1201	U1141	U1081	A1021	C961	C901	G841	A781	A721	A661	C601	A541
A1502	U1442	G1382	A1322	A1262	G1202	A1142	U1082	G1022	G962	C902	U842	A782	A722	A662	A602	C542
A1503	U1443	A1383	G1323	A1263	U1203	A1143	U1083	U1023	U963	C903	G843	A783	A723	A663	A603	C543
A1504	U1444	A1384	G1324	A1264	A1204	A1144	A1084	G1024	U964	C904	A844	A784	A724	A664	A604	C544
A1505	G1445	A1385	A1325	A1265	G1205	A1145	A1085	G1025	G965	C905	A845	A785	A725	A665	U605	U545
U1506	G1446	C1386	U1326	G1266	G1206	C1146	A1086	G1026	G966	U906	U846	A786	A726	A666	U606	A546
C1507	G1447	A1387	A1327	U1267	C1207	A1147	G1087	A1027	U967	C907	U847	A787	A727	A667	U607	A547
A1508	G1448	G1388	A1328	A1268	U1208	U1148	A1088	A1028	C968	C908	C848	A788	A728	A668	A608	C548
A1509	G1449	G1389	U1329	A1269	U1209	U1149	A1089	A1029	G969	A909	C849	A789	A729	A669	A609	C549
G1510	G1450	A1390	G1330	C1270	G1210	A1150	A1090	G1030	U970	A910	U850	A790	A730	A670	C610	G510
C1511	G1451	U1391	G1331	G1271	G1211	A1151	A1091	G1031	U971	A911	C851	A791	A731	A671	C611	G511
C1512	G1452	A1392	G1332	U1272	G1212	A1152	A1092	G1032	A972	C912	U852	A792	A732	A672	U612	U512
A1513	G1453	A1393	G1333	U1273	A1213	C1153	G1093	U1033	A973	U913	C853	A793	A733	A673	A613	G513
G1514	G1454	U1394	G1334	A1274	A1214	G1154	U1094	G1034	G974	C914	C854	A794	A734	A674	A614	U514
A1515	G1455	A1395	C1335	A1275	G1215	A1155	A1095	U1035	A975	C915	G855	A795	A735	A675	U615	G515
G1516	G1456	U1396	A1336	A1276	G1216	A1156	A1096	G1036	G976	C916	C856	A796	A736	A676	A616	A516
U1517	U1457	U1397	G1337	G1277	U1217	G1157	U1097	G1037	G977	A917	C857	A797	A737	A677	U617	U517
C1518	G1458	A1398	G1338	C1278	G1218	A1158	A1098	G1038	G978	A918	C858	A798	A738	A678	G618	U518
G1519	G1459	C1399	G1339	G1279	U1219	U1159	G1099	A1039	A979	U919	C859	A799	A739	A679	U619	G519
U1520	U1460	U1400	U1340	G1280	G1220	C1160	C1100	A1040	A980	A920	U860	A800	A740	A680	C620	C560
G1521	C1461	G1401	G1341	G1281	G1221	C1161	U1101	G1041	A981	A921	A861	A801	A741	A681	A621	G561
A1522	C1462	U1402	A1342	U1282	U1222	G1162	C1102	G1042	C982	C922	C862	A802	A742	A682	G622	U562
U1523	C1463	A1403	G1343	G1283	G1223	A1163	A1103	C1043	A983	G923	A863	U803	A743	U683	C623	A563
G1524	G1464	C1404	U1344	A1284	U1224	C1164	C1104	C1044	A984	C924	C864	A804	A744	A684	C624	C564
A1525	G1465	U1405	C1345	A1285	G1225	A1165	U1105	C1045	A985	A925	C865	G805	A745	A685	G625	G565
C1526	U1466	U1406	G1346	A1286	A1226	G1166	G1106	A1046	C986	G926	A866	C806	A746	U686	A626	U566
U1527	U1467	G1407	A1347	A1287	G1227	C1167	U1107	G1047	A987	A927	C867	U807	A747	A687	A627	U567
A1528	G1468	U1408	G1348	G1288	G1228	A1168	U1108	A1048	A988	A928	U868	A808	A748	U688	G628	G568
G1529	U1469	A1409	C1349	A1289	A1229	A1169	C1109	A1049	A989	U929	C869	A809	A749	A689	G629	U569
U1530	U1470	G1410	C1350	C1290	U1230	C1170	G1110	A1050	A990	G930	U870	A810	A750	G690	G630	U570
C1531	G1471	U1411	C1351	C1291	U1231	G1171	A1111	C1051	C991	U931	U871	U811	A751	C691	A631	U571
G1532	C1472	U1412	U1352	G1292	G1232	C1172	G1112	C1052	C992	U932	U872	C812	A752	C692	A632	A572
C1533	U1473	A1413	A1353	C1293	U1233	U1173	U1113	C1053	G993	A933	C873	U813	A753	A693	A633	U573
U1534	U1474	C1414	C1354	C1294	U1234	U1174	G1114	A1054	C994	U934	C874	C814	A754	A694	C634	A574
A1535	G1475	U1415	G1355	C1295	G1235	A1175	G1115	G1055	C995	C935	C875	C815	A755	G695	G635	A575
G1536	U1476	G1416	G1356	G1296	U1236	U1176	G1116	G1056	A996	A936	C876	C816	A756	G696	G636	U576
C1537	U1477	U1417	C1357	C1297	U1237	G1177	C1117	A1057	G997	U937	C877	C817	A757	G697	A637	G577
G1538	G1478	G1418	G1358	C1298	G1238	C1178	C1118	U1058	C998	G938	A878	C818	A758	C698	G638	G578
U1539	U1479	A1419	A1359	G1299	U1239	U1179	U1119	G1059	U999	C940	C879	A819	A759	A699	U639	U579
G1540	C1480	U1420	G1360	G1300	U1240	U1180	G1120	U1060	A1000	G940	C880	A820	A760	G700	C640	U580
C1541	U1481	G1421	G1361	A1301	A1241	U1181	C1121	U1061	A1001	A941	C881	A821	A761	G701	U641	C581
U1542	G1482	G1422	C1362	A1302	U1242	G1182	G1122	G1062	G1002	G942	C882	G822	U762	U702	U642	A582
G1543	U1483	G1423	G1363	G1303	C1243	U1183	C1123	G1063	A1003	A943	C883	C823	A763	U703	A643	G583
A1544	U1484	G1424	G1364	A1304	A1244	U1184	G1124	C1064	U1004	C944	U884	U824	A764	G704	A644	C584
U1545	U1485	G1425	A1365	C1305	G1245	G1185	G1125	U1065	C1005	A945	C885	A825	A765	A705	C645	G585
G1546	U1486	G1426	G1366	G1306	A1246	U1186	A1126	U1066	C1006	C946	A886	U826	A766	A706	U646	A586
A1547	U1487	A1427	A1367	A1307	U1247	G1187	A1127	A1067	C1007	A947	U887	U827	U767	G707	U647	G587
C1548	U1488	C1428	G1368	A1308	G1248	U1188	G1128	G1068	A1008	C948	C888	U828	A768	G708	G648	U588
U1549	G1489	G1429	G1369	G1309	U1249	U1189	A1129	A1069	A1009	G949	C889	A829	U769	U709	G649	U589
C1550	U1490	U1430	C1370	G1310	G1250	G1190	U1130	A1070	U1010	C950	C890	G830	A770	U710	C650	A590
A1551	G1491	A1431	G1371	G1311	C1251	G1191	G1131	G1071	G1011	C951	C891	G831	A771	G711	C651	U591
G1552	U1491	G1432	U1372	U1312	G1252	G1192	U1132	C1072	U1012	G952	A892	U832	A772	G712	U652	A592
U1553	G1492	A1433	A1373	G1313	A1253	G1193	A1133	A1073	C1013	G953	C893	A833	U773	G713	U653	U593
A1554	C1493	U1434	G1374	C1314	A1254	A1194	A1134	G1074	A1014	G954	U894	U834	A774	U714	A654	G594
G1555	U1494	G1435	U1375	G1315	U1255	G1195	C1135	C1075	U1015	U955	U895	A835	A775	A715	A655	C595
A1495	G1495	G1436	G1376	U1316	G1256	G1196	G1136	C1076	G1016	G956	A896	U836	A776	A716	G656	U596
U1497	U1496	C1437	G1377	G1317	C1257	G1197	G1137	A1077	G1017	C957	C897	C837	A777	G717	U657	G597
C1498	U1497	U1438	A1378	U1318	U1258	U1198	G1138	U1078	U1018	U958	C898	C838	A778	A718	U658	U598
G1499	U1498	G1439	G1379	C1319	G1259	U1199	G1139	C1079	U1019	A959	C899	U839	A779	A719	U659	A599
U1559	C1499	U1440	G1380	C1320	A1260	C1200	C1140	A1080	A1020	A960	A900	C840	A780	U720	C660	G600
G1560	G1500															



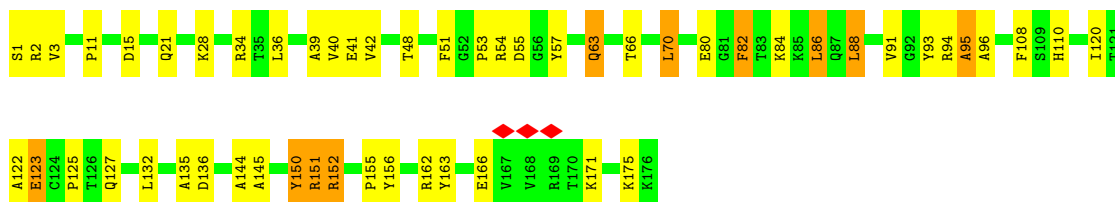




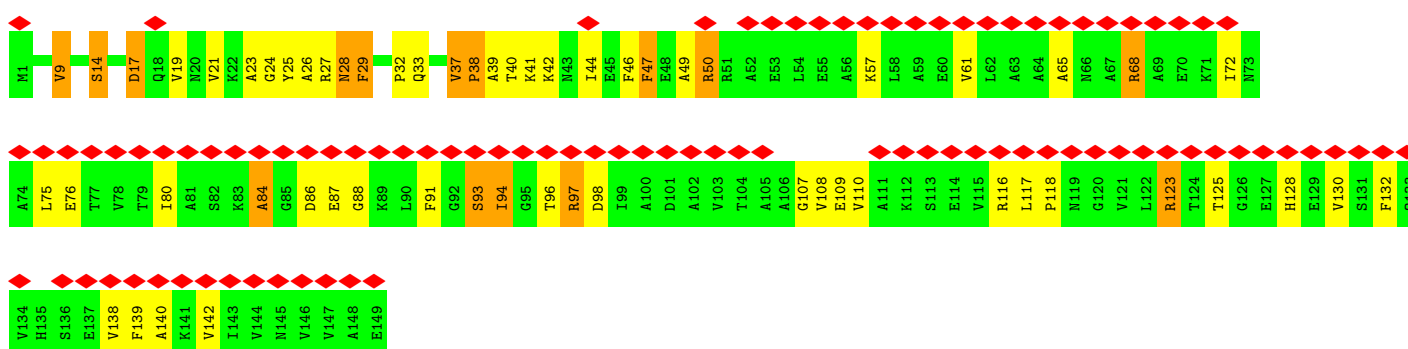
• Molecule 16: 50S RIBOSOMAL PROTEIN L5



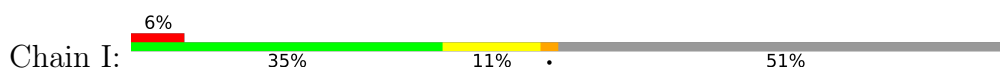
• Molecule 17: 50S RIBOSOMAL PROTEIN L6



• Molecule 18: 50S RIBOSOMAL PROTEIN L9

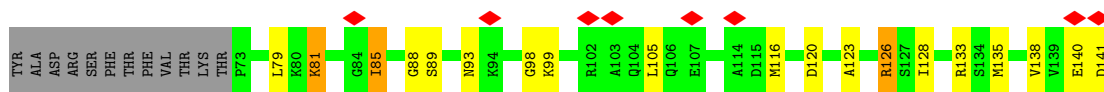


• Molecule 19: 50S RIBOSOMAL PROTEIN L11

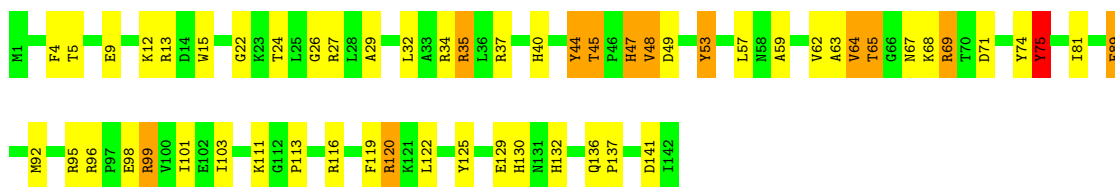


ALA	LYS	VAL	GLN	ALA	TYR	VAL	LYS	GLN	VAL	ALA	ALA	GLY	MET	ALA	ASN	PRO	SER	PRO	PRO	VAL	GLY	ALA	ALA	LEU	GLY	GLN	GLN	GLY	VAL	ASN	ILE	MET	GLU	PHE	CYS	LYS	ALA	PHE	ASN	ALA	LEU	THR	ASP	ILE	GLU	LYS	GLY	LEU	PRO	ILE	PRO	VAL	VAL	THR	THR	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

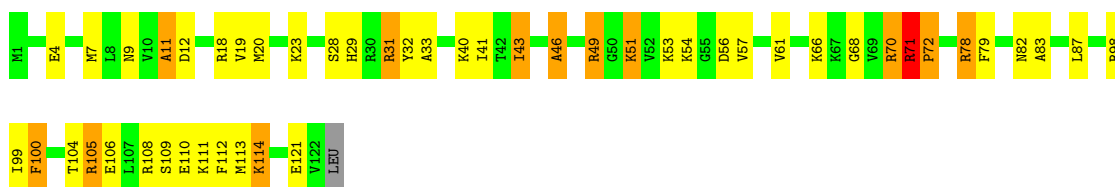




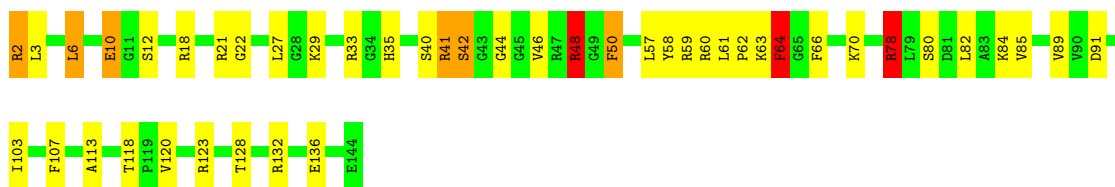
• Molecule 20: 50S RIBOSOMAL PROTEIN L13



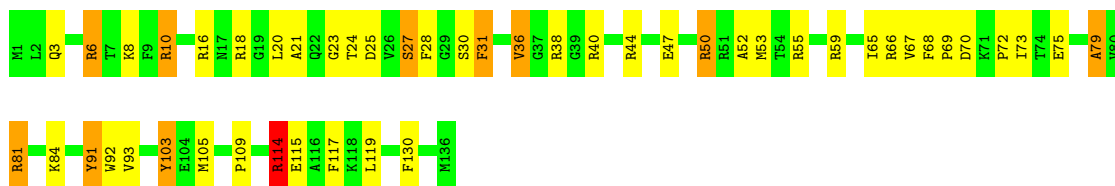
• Molecule 21: 50S RIBOSOMAL PROTEIN L14



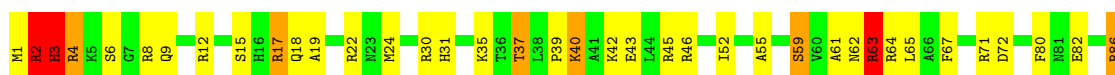
• Molecule 22: 50S RIBOSOMAL PROTEIN L15



• Molecule 23: 50S RIBOSOMAL PROTEIN L16



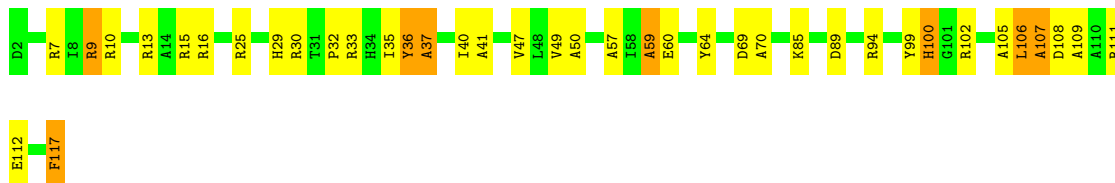
• Molecule 24: 50S RIBOSOMAL PROTEIN L17





- Molecule 25: 50S RIBOSOMAL PROTEIN L18

Chain O: 66% 27% 7%



- Molecule 26: 50S RIBOSOMAL PROTEIN L19

Chain P: 66% 25% 7%



- Molecule 27: 50S RIBOSOMAL PROTEIN L20

Chain Q: 60% 32% 7%



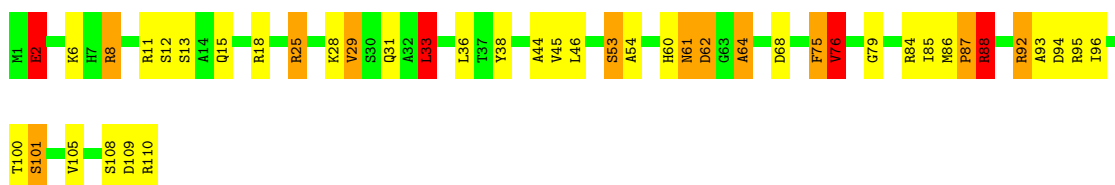
- Molecule 28: 50S RIBOSOMAL PROTEIN L21

Chain R: 66% 25% 8%

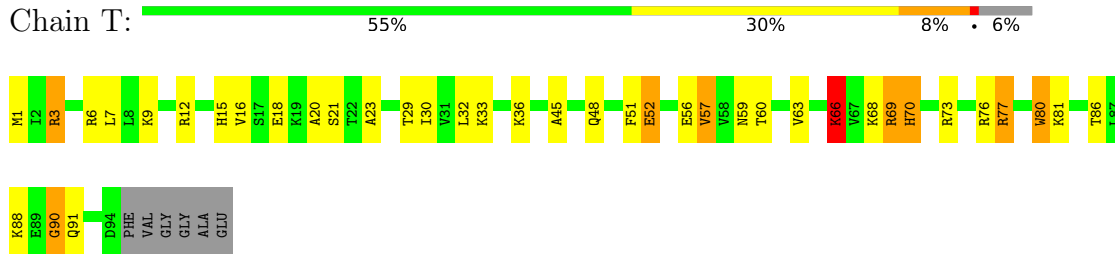


- Molecule 29: 50S RIBOSOMAL PROTEIN L22

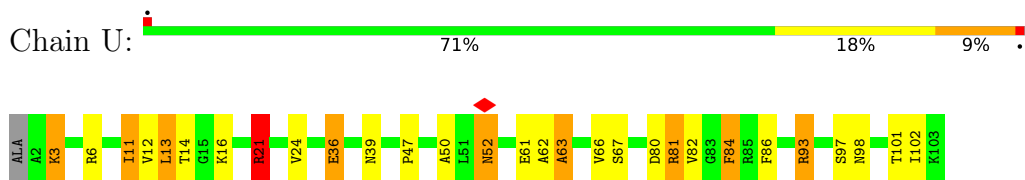
Chain S: 60% 26% 10%



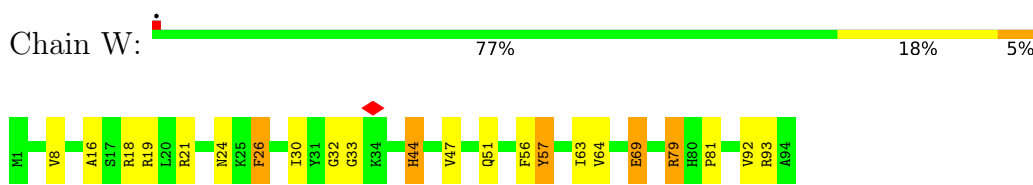
• Molecule 30: 50S RIBOSOMAL PROTEIN L23



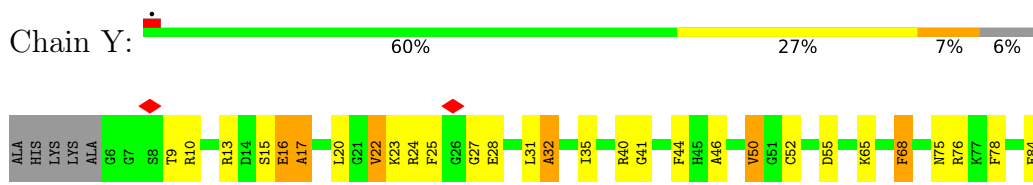
• Molecule 31: 50S RIBOSOMAL PROTEIN L24



• Molecule 32: 50S RIBOSOMAL PROTEIN L25



• Molecule 33: 50S RIBOSOMAL PROTEIN L27



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	102814	Depositor
Resolution determination method	Not provided	
CTF correction method	INDIVIDUAL PARTICLES	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	0.191	Depositor
Minimum map value	-0.046	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.045	Depositor
Map size ( $\text{\AA}$ )	384.0, 384.0, 384.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.5, 1.5, 1.5	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	0	1.91	12/635 (1.9%)	2.26	26/848 (3.1%)
2	1	1.71	3/510 (0.6%)	1.90	8/677 (1.2%)
3	2	1.85	8/453 (1.8%)	1.91	10/605 (1.7%)
4	3	1.79	6/450 (1.3%)	2.16	16/599 (2.7%)
5	4	1.66	1/417 (0.2%)	1.93	5/556 (0.9%)
6	5	1.69	15/1748 (0.9%)	1.91	38/2355 (1.6%)
7	6	1.86	6/380 (1.6%)	2.24	15/498 (3.0%)
8	7	1.76	6/513 (1.2%)	1.99	14/676 (2.1%)
9	8	1.77	4/303 (1.3%)	1.84	3/397 (0.8%)
10	9	1.75	31/2584 (1.2%)	2.10	81/3487 (2.3%)
11	A	3.31	347/2744 (12.6%)	3.75	664/4276 (15.5%)
12	B	3.41	9451/69796 (13.5%)	3.79	16403/108888 (15.1%)
13	C	1.82	28/2122 (1.3%)	2.15	58/2854 (2.0%)
14	D	1.74	16/1586 (1.0%)	1.95	36/2134 (1.7%)
15	E	1.77	16/1571 (1.0%)	2.04	50/2113 (2.4%)
16	F	1.79	13/1444 (0.9%)	2.00	35/1937 (1.8%)
17	G	1.72	7/1336 (0.5%)	1.90	26/1805 (1.4%)
18	H	1.80	17/1122 (1.5%)	2.05	42/1515 (2.8%)
19	I	1.61	4/497 (0.8%)	1.98	9/662 (1.4%)
20	J	1.74	7/1152 (0.6%)	2.02	42/1551 (2.7%)
21	K	1.77	10/941 (1.1%)	2.00	29/1260 (2.3%)
22	L	1.81	17/1054 (1.6%)	2.02	32/1403 (2.3%)
23	M	1.84	20/1093 (1.8%)	1.97	26/1460 (1.8%)
24	N	1.80	11/974 (1.1%)	2.02	28/1303 (2.1%)
25	O	1.79	9/902 (1.0%)	2.02	28/1209 (2.3%)
26	P	1.77	9/929 (1.0%)	2.06	24/1242 (1.9%)
27	Q	1.81	11/960 (1.1%)	2.20	45/1278 (3.5%)
28	R	1.78	9/829 (1.1%)	2.04	24/1107 (2.2%)
29	S	1.83	13/864 (1.5%)	2.05	31/1156 (2.7%)
30	T	1.69	4/745 (0.5%)	2.01	22/996 (2.2%)
31	U	1.71	5/764 (0.7%)	1.86	11/1019 (1.1%)
32	W	1.76	8/766 (1.0%)	1.92	13/1025 (1.3%)
33	Y	1.76	5/603 (0.8%)	2.03	15/797 (1.9%)
All	All	3.02	10129/102787 (9.9%)	3.41	17909/153688 (11.7%)

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	0	0	2
2	1	0	2
3	2	0	1
4	3	0	2
5	4	0	2
6	5	0	3
7	6	0	6
8	7	0	3
9	8	0	1
10	9	0	27
11	A	0	55
12	B	0	1482
13	C	0	9
14	D	0	4
15	E	0	5
16	F	0	6
17	G	0	4
18	H	0	2
20	J	0	6
21	K	0	7
22	L	0	2
23	M	0	7
24	N	0	7
25	O	0	5
26	P	0	3
27	Q	0	4
28	R	0	5
29	S	0	3
30	T	0	2
31	U	0	2
32	W	0	3
33	Y	0	3
All	All	0	1675

The worst 5 of 10129 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	2225	A	N7-C5	-20.53	1.26	1.39
12	B	2105	U	C2-N3	19.07	1.51	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	1853	A	N7-C5	-18.25	1.28	1.39
12	B	548	G	N7-C5	-17.75	1.28	1.39
12	B	1501	G	C6-N1	17.64	1.51	1.39

The worst 5 of 17909 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	751	A	N1-C6-N6	26.85	134.71	118.60
12	B	370	G	N1-C6-O6	26.32	135.69	119.90
12	B	928	A	N1-C6-N6	24.76	133.45	118.60
12	B	2360	G	N1-C6-O6	24.64	134.69	119.90
12	B	668	A	N1-C6-N6	24.57	133.34	118.60

There are no chirality outliers.

5 of 1675 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	37	PHE	Sidechain
1	0	56	ARG	Sidechain
2	1	23	ARG	Sidechain
2	1	7	ARG	Sidechain
3	2	44	ARG	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	0	625	0	655	4	0
2	1	509	0	543	1	0
3	2	449	0	491	0	0
4	3	444	0	461	3	0
5	4	410	0	440	2	0
6	5	1733	0	1824	6	0
7	6	377	0	418	3	0
8	7	504	0	574	8	0
9	8	302	0	343	1	0
10	9	2541	0	2555	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	A	2455	0	1253	15	0
12	B	62317	0	31306	522	0
13	C	2083	0	2157	14	0
14	D	1565	0	1616	9	0
15	E	1552	0	1619	6	0
16	F	1420	0	1460	8	0
17	G	1317	0	1364	7	0
18	H	1111	0	1148	2	0
19	I	495	0	525	4	0
20	J	1129	0	1162	7	0
21	K	932	0	1003	9	0
22	L	1045	0	1117	8	0
23	M	1074	0	1157	7	0
24	N	961	0	1000	8	0
25	O	892	0	923	3	0
26	P	917	0	965	13	0
27	Q	947	0	1022	4	0
28	R	816	0	839	5	0
29	S	857	0	922	9	0
30	T	739	0	807	7	0
31	U	758	0	807	8	0
32	W	753	0	780	1	0
33	Y	596	0	610	5	0
All	All	94625	0	63866	702	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 4.

The worst 5 of 702 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)
12:B:1481:U:H3	12:B:1511:G:H21	1.23	0.85
12:B:2267:A:H61	12:B:2271:G:H1	1.25	0.79
30:T:20:ALA:H	30:T:23:ALA:HB3	1.50	0.75
10:9:279:TRP:CG	10:9:328:VAL:HG13	2.21	0.75
12:B:2507:C:H41	12:B:2576:G:H22	1.35	0.74

There are no symmetry-related clashes.



## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	
1	0	75/77 (97%)	61 (81%)	10 (13%)	4 (5%)	2	19
2	1	61/63 (97%)	50 (82%)	8 (13%)	3 (5%)	2	20
3	2	56/58 (97%)	50 (89%)	5 (9%)	1 (2%)	8	40
4	3	54/56 (96%)	43 (80%)	4 (7%)	7 (13%)	0	5
5	4	49/54 (91%)	43 (88%)	4 (8%)	2 (4%)	3	22
6	5	232/234 (99%)	197 (85%)	25 (11%)	10 (4%)	2	22
7	6	44/46 (96%)	33 (75%)	8 (18%)	3 (7%)	1	15
8	7	62/64 (97%)	47 (76%)	10 (16%)	5 (8%)	1	12
9	8	36/38 (95%)	27 (75%)	7 (19%)	2 (6%)	2	18
10	9	332/390 (85%)	261 (79%)	43 (13%)	28 (8%)	1	11
13	C	270/272 (99%)	216 (80%)	31 (12%)	23 (8%)	1	11
14	D	207/209 (99%)	160 (77%)	34 (16%)	13 (6%)	1	16
15	E	199/201 (99%)	163 (82%)	16 (8%)	20 (10%)	0	9
16	F	176/178 (99%)	135 (77%)	22 (12%)	19 (11%)	0	8
17	G	172/176 (98%)	126 (73%)	31 (18%)	15 (9%)	1	11
18	H	147/149 (99%)	112 (76%)	21 (14%)	14 (10%)	0	10
19	I	67/141 (48%)	65 (97%)	0	2 (3%)	4	28
20	J	140/142 (99%)	108 (77%)	20 (14%)	12 (9%)	1	11
21	K	120/123 (98%)	98 (82%)	16 (13%)	6 (5%)	2	20
22	L	141/143 (99%)	115 (82%)	17 (12%)	9 (6%)	1	16
23	M	134/136 (98%)	112 (84%)	16 (12%)	6 (4%)	2	22
24	N	119/127 (94%)	94 (79%)	17 (14%)	8 (7%)	1	15
25	O	114/116 (98%)	88 (77%)	20 (18%)	6 (5%)	2	19
26	P	112/114 (98%)	84 (75%)	19 (17%)	9 (8%)	1	12
27	Q	115/117 (98%)	95 (83%)	12 (10%)	8 (7%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	R	101/103 (98%)	83 (82%)	14 (14%)	4 (4%)	3	23
29	S	108/110 (98%)	87 (81%)	11 (10%)	10 (9%)	0	10
30	T	92/100 (92%)	68 (74%)	16 (17%)	8 (9%)	1	11
31	U	96/103 (93%)	73 (76%)	15 (16%)	8 (8%)	1	12
32	W	92/94 (98%)	78 (85%)	11 (12%)	3 (3%)	4	26
33	Y	77/84 (92%)	54 (70%)	15 (20%)	8 (10%)	0	8
All	All	3800/4018 (95%)	3026 (80%)	498 (13%)	276 (7%)	2	13

5 of 276 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	73	ARG
3	2	9	THR
4	3	3	GLN
6	5	40	GLU
10	9	54	ASN

### 5.3.2 Protein sidechains [i](#)

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	
1	0	67/67 (100%)	60 (90%)	7 (10%)	7	26
2	1	55/55 (100%)	51 (93%)	4 (7%)	14	40
3	2	48/48 (100%)	46 (96%)	2 (4%)	30	54
4	3	47/47 (100%)	44 (94%)	3 (6%)	17	44
5	4	45/48 (94%)	43 (96%)	2 (4%)	28	53
6	5	181/181 (100%)	179 (99%)	2 (1%)	73	84
7	6	38/38 (100%)	35 (92%)	3 (8%)	12	38
8	7	51/51 (100%)	45 (88%)	6 (12%)	5	21
9	8	34/34 (100%)	31 (91%)	3 (9%)	10	33
10	9	268/321 (84%)	231 (86%)	37 (14%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	C	216/217 (100%)	208 (96%)	8 (4%)	34	58
14	D	164/164 (100%)	146 (89%)	18 (11%)	6	24
15	E	165/165 (100%)	156 (94%)	9 (6%)	21	48
16	F	149/149 (100%)	143 (96%)	6 (4%)	31	56
17	G	136/137 (99%)	128 (94%)	8 (6%)	19	46
18	H	114/114 (100%)	105 (92%)	9 (8%)	12	38
19	I	51/109 (47%)	46 (90%)	5 (10%)	8	28
20	J	116/116 (100%)	108 (93%)	8 (7%)	15	42
21	K	102/104 (98%)	95 (93%)	7 (7%)	15	42
22	L	102/102 (100%)	95 (93%)	7 (7%)	15	42
23	M	109/109 (100%)	98 (90%)	11 (10%)	7	27
24	N	100/103 (97%)	93 (93%)	7 (7%)	15	41
25	O	86/86 (100%)	82 (95%)	4 (5%)	26	52
26	P	99/99 (100%)	94 (95%)	5 (5%)	24	50
27	Q	89/89 (100%)	84 (94%)	5 (6%)	21	47
28	R	84/84 (100%)	79 (94%)	5 (6%)	19	46
29	S	93/93 (100%)	89 (96%)	4 (4%)	29	54
30	T	80/84 (95%)	72 (90%)	8 (10%)	7	27
31	U	81/84 (96%)	76 (94%)	5 (6%)	18	45
32	W	78/78 (100%)	74 (95%)	4 (5%)	24	50
33	Y	59/62 (95%)	54 (92%)	5 (8%)	10	35
All	All	3107/3238 (96%)	2890 (93%)	217 (7%)	19	41

5 of 217 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	G	88	LEU
21	K	61	VAL
30	T	48	GLN
18	H	19	VAL
19	I	105	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
21	K	29	HIS
25	O	34	HIS
22	L	38	GLN
24	N	3	HIS
27	Q	58	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	112/118 (94%)	21 (18%)	3 (2%)
12	B	2902/2903 (99%)	540 (18%)	96 (3%)
All	All	3014/3021 (99%)	561 (18%)	99 (3%)

5 of 561 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	9	G
11	A	13	G
11	A	14	U
11	A	16	G
11	A	26	C

5 of 99 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	B	1786	A
12	B	2133	G
12	B	1847	A
12	B	2051	A
12	B	2158	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 monosaccharides 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](#)

There are no chain breaks in this entry.

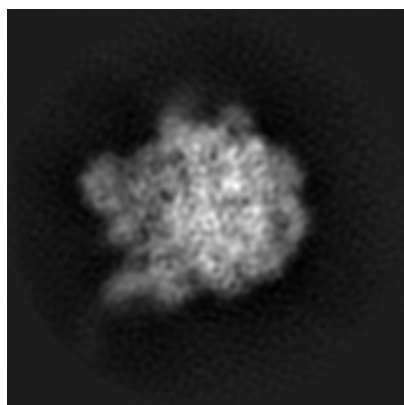
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2605. These allow visual inspection of the internal detail of the map and identification of artifacts.

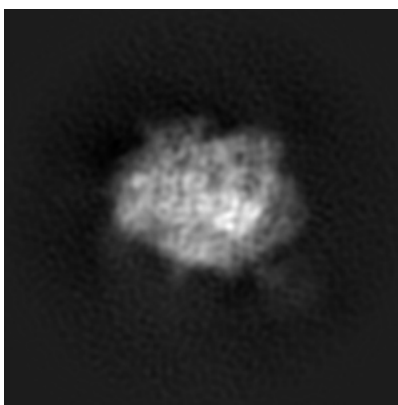
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

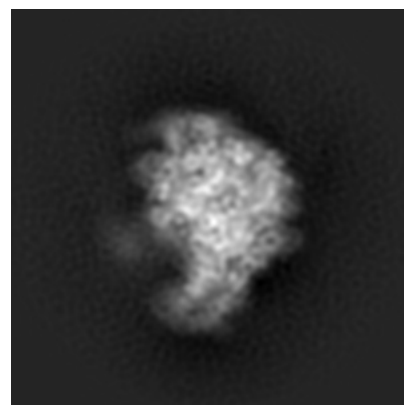
#### 6.1.1 Primary map



X



Y

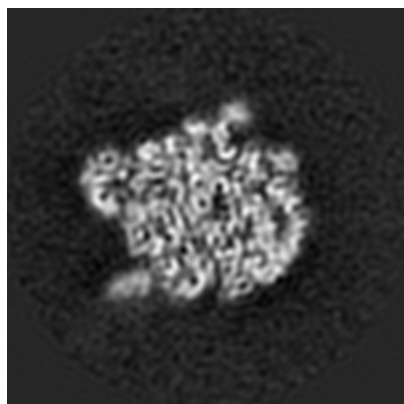


Z

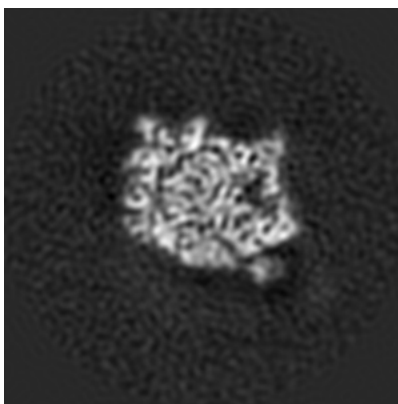
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

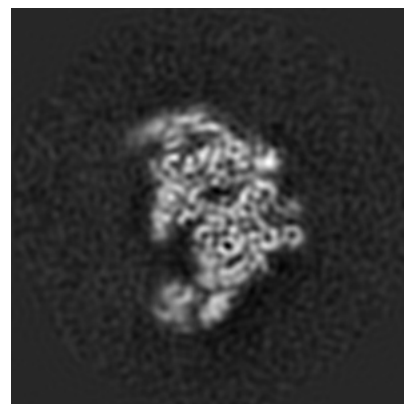
#### 6.2.1 Primary map



X Index: 128



Y Index: 128

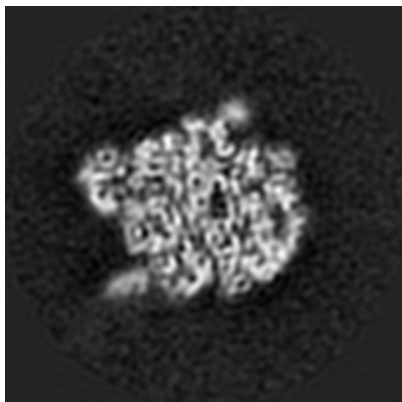


Z Index: 128

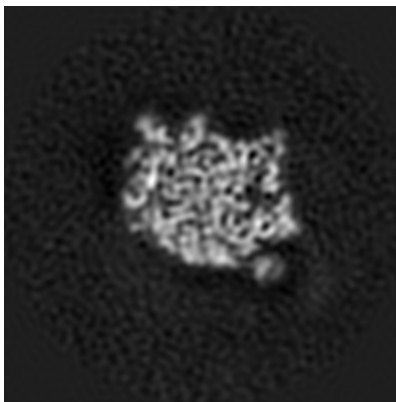
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 129



Y Index: 126

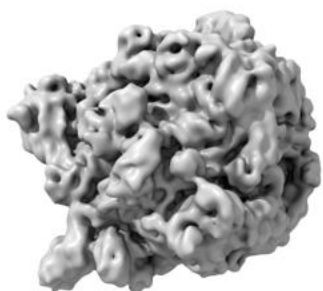


Z Index: 143

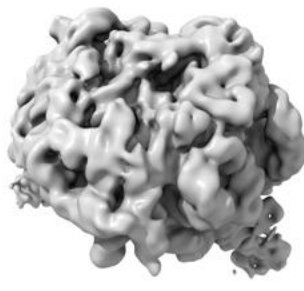
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

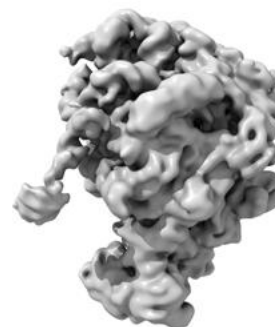
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

## 6.5 Mask visualisation

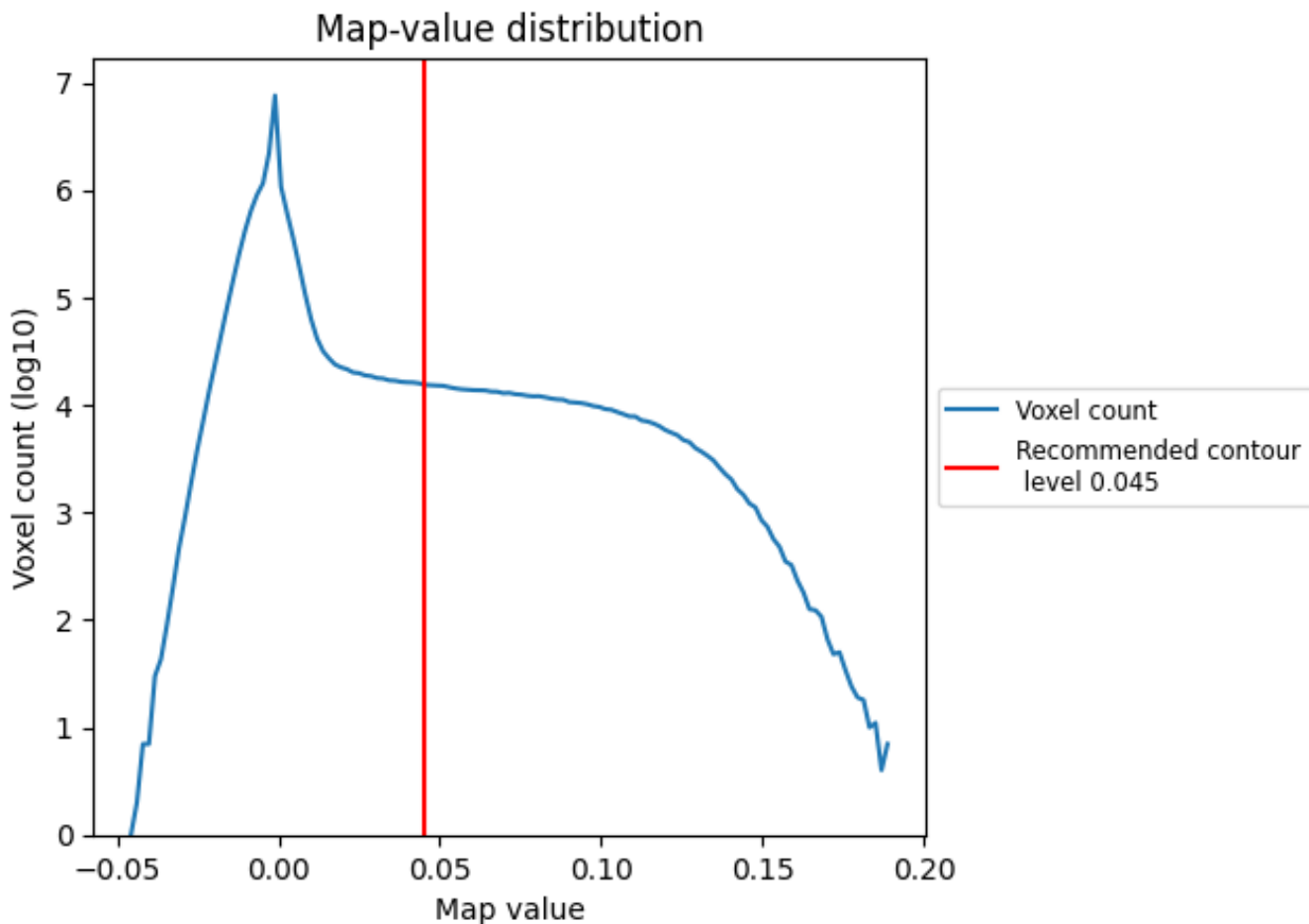
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

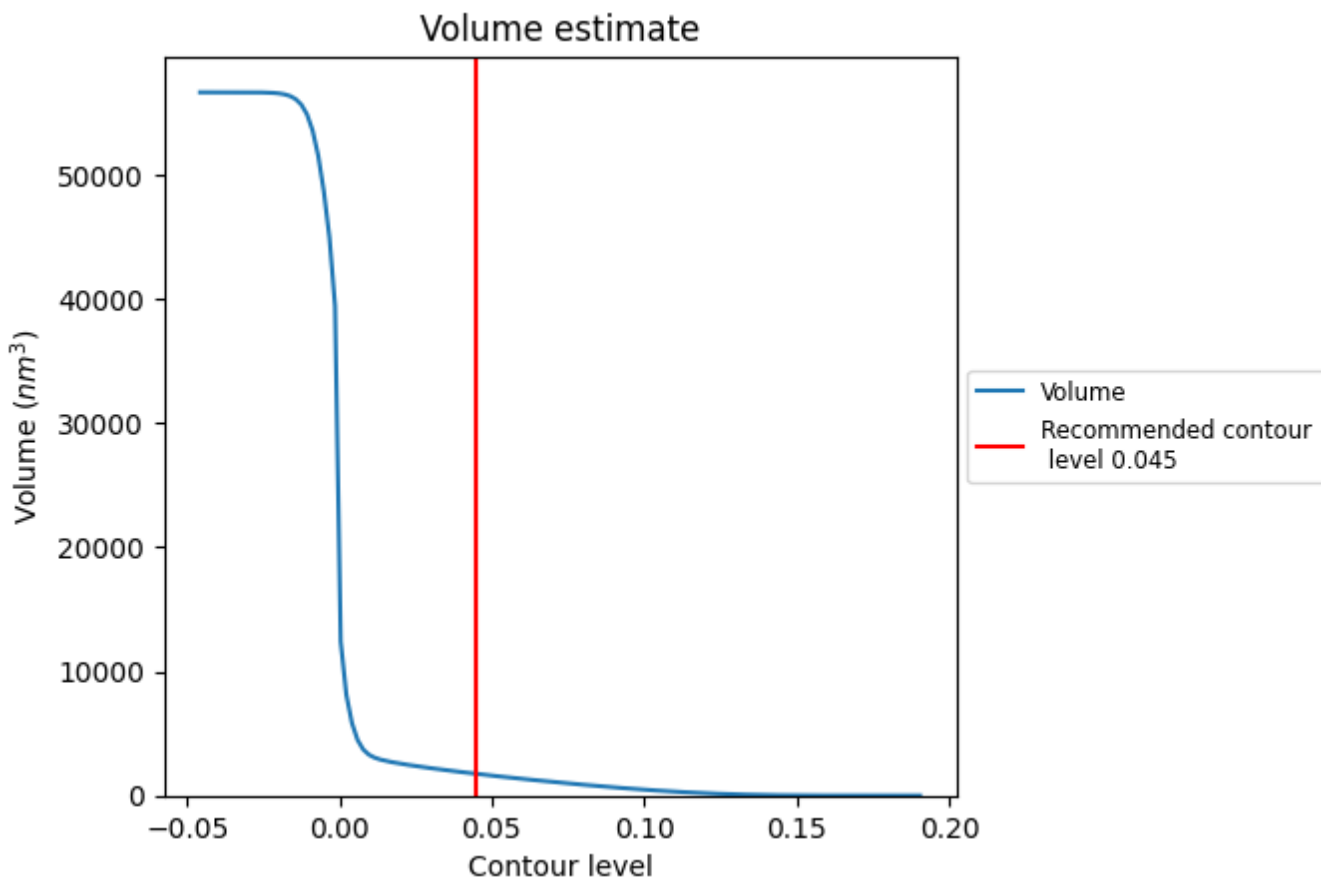
This section contains the results of statistical analysis of the map.

### 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.

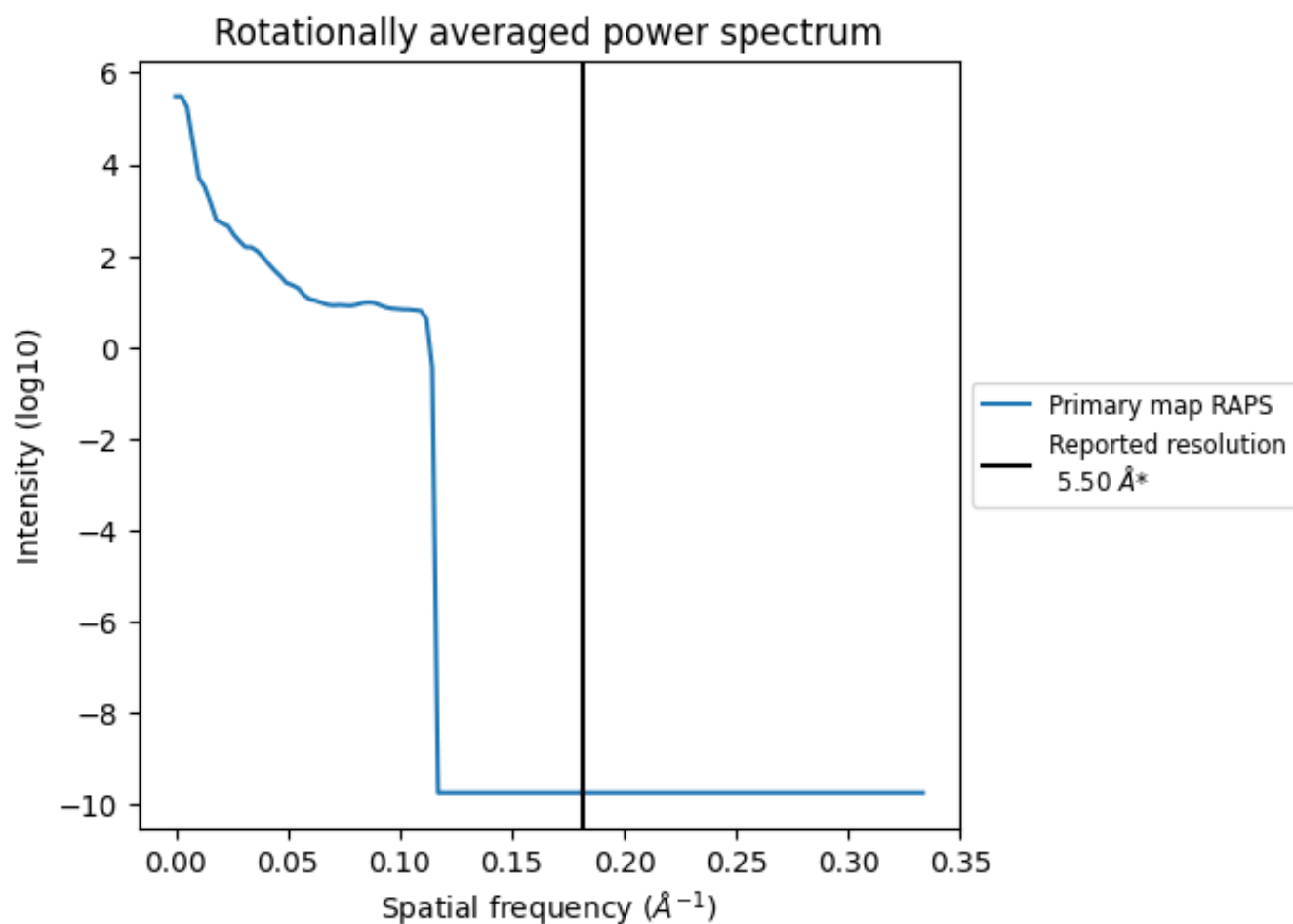
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1748  $\text{nm}^3$ ; this corresponds to an approximate mass of 1579 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 i



\*Reported resolution corresponds to spatial frequency of 0.182 Å<sup>-1</sup>

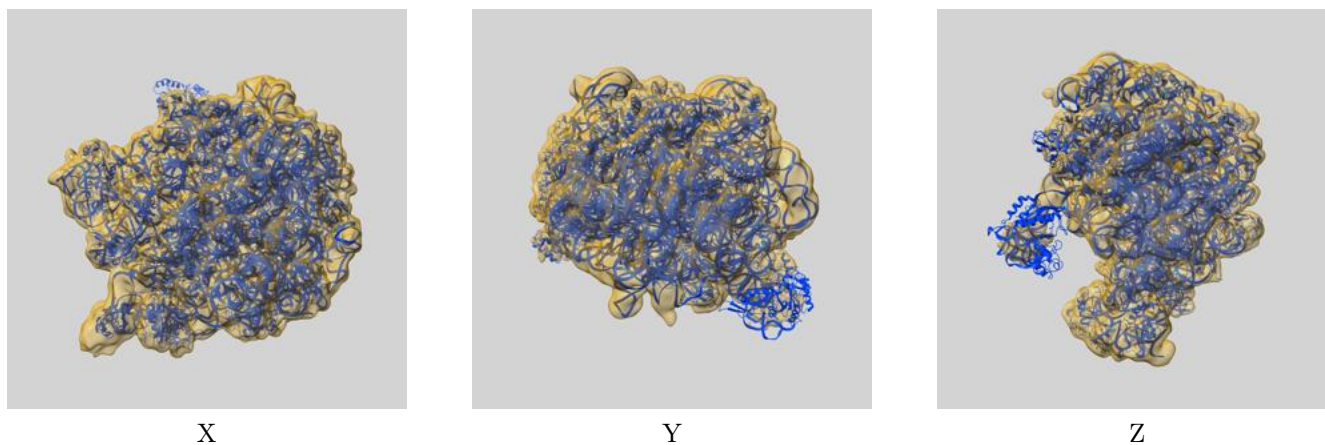
## 8 Fourier-Shell correlation

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-2605 and PDB model 4CSU. Per-residue inclusion information can be found in section 3 on page 10.

### 9.1 Map-model overlay [i](#)



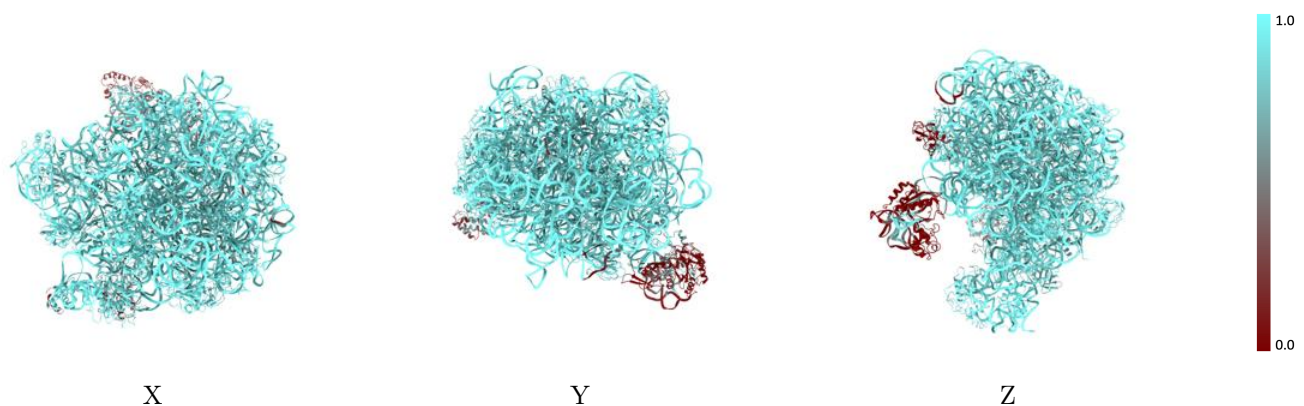
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



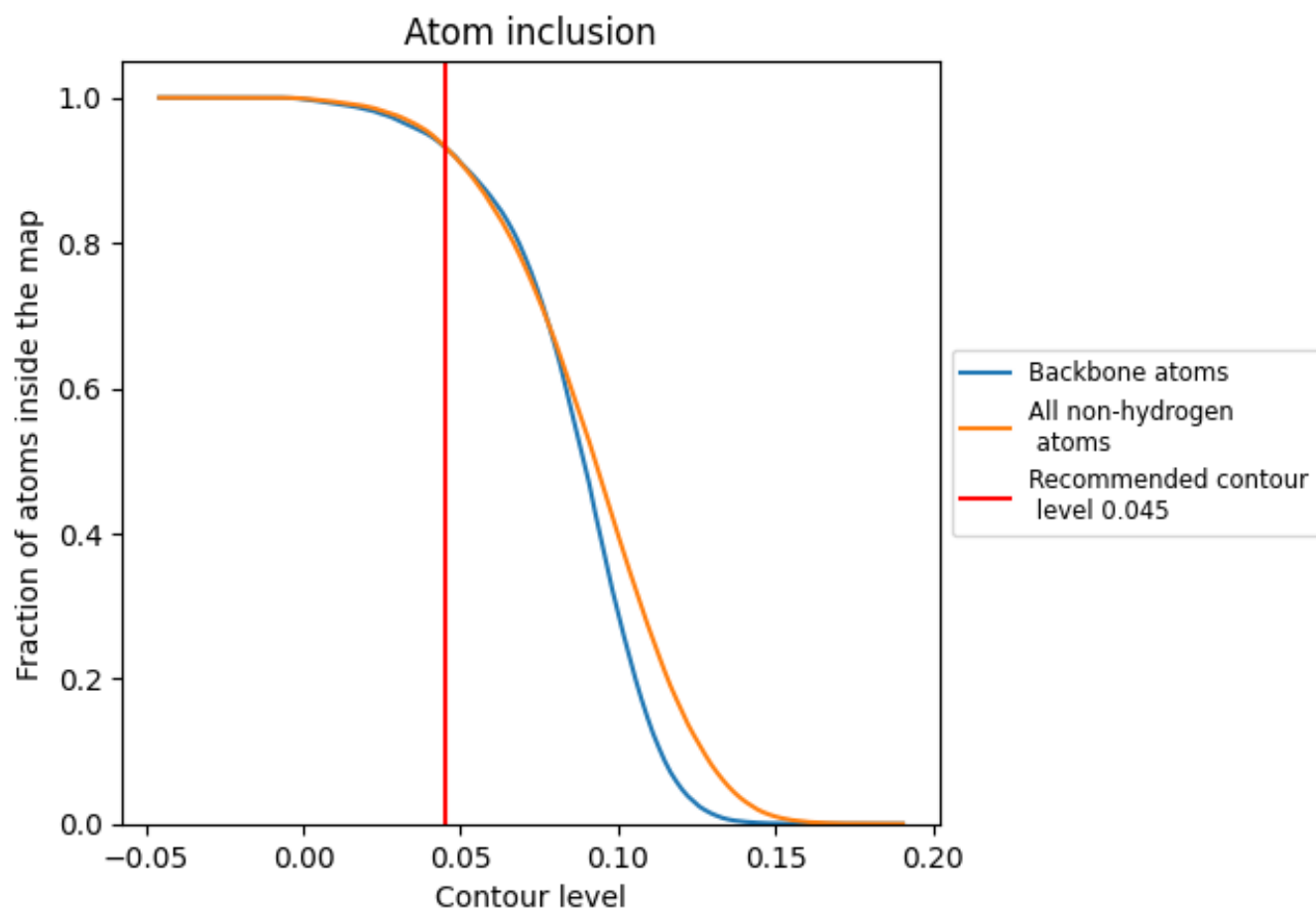
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).





































































## 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9326	 0.1580
0	 0.9018	 0.1240
1	 0.9859	 0.1510
2	 0.9153	 0.1450
3	 0.8505	 0.0740
4	 0.7786	 0.0940
5	 0.0843	 0.0310
6	 0.9352	 0.1170
7	 0.9328	 0.1150
8	 0.9726	 0.0750
9	 0.6847	 0.1020
A	 0.9984	 0.1940
B	 0.9728	 0.1770
C	 0.9440	 0.1260
D	 0.9597	 0.1280
E	 0.9072	 0.1380
F	 0.9530	 0.1170
G	 0.9249	 0.1390
H	 0.3157	 0.0780
I	 0.8098	 0.0820
J	 0.9564	 0.1520
K	 0.9614	 0.1330
L	 0.9488	 0.1220
M	 0.9597	 0.1390
N	 0.9317	 0.1200
O	 0.9815	 0.1260
P	 0.9459	 0.1390
Q	 0.9394	 0.1150
R	 0.9435	 0.1360
S	 0.9222	 0.1300
T	 0.9544	 0.1280
U	 0.9559	 0.1220
W	 0.9255	 0.1430
Y	 0.9241	 0.0970

