



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:38 PM UTC

PDB ID : 4CSU / pdb_00004csu
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

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:

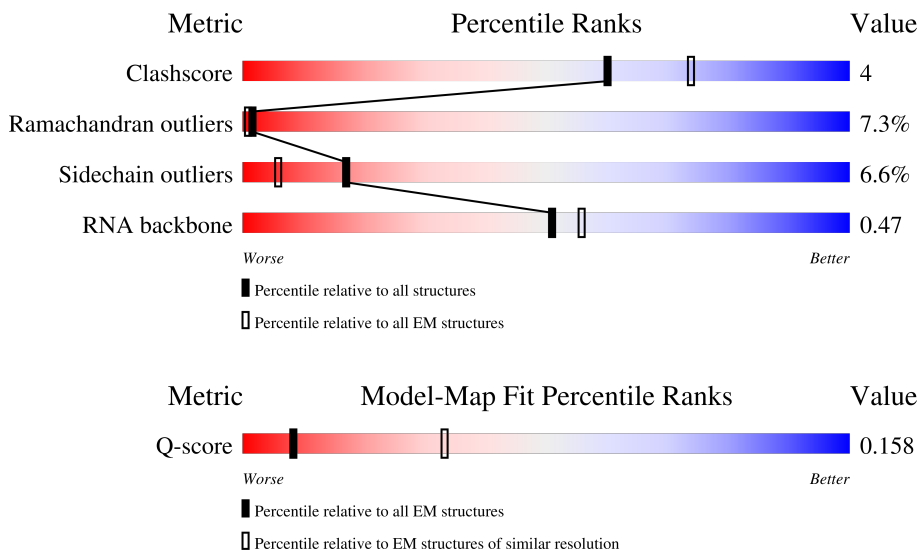
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance 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)	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	520 (5.00 - 6.00)

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	0	77	
2	1	63	
3	2	58	

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Mol	Chain	Length	Quality of chain
4	3	56	11% 45% 38% 18%
5	4	54	17% 41% 48% 6% 6%
6	5	234	91% 39% 53% 7%
7	6	46	33% 50% 11% 7%
8	7	64	34% 45% 14% 6%
9	8	38	39% 47% 13%
10	9	390	22% 24% 40% 15% 6% 14%
11	A	118	8% 31% 49% 10%
12	B	2903	8% 35% 37% 20%
13	C	272	36% 54% 9%
14	D	209	39% 48% 11%
15	E	201	36% 49% 13%
16	F	178	40% 46% 12%
17	G	176	39% 51% 10%
18	H	149	64% 38% 50% 11%
19	I	141	6% 26% 19% 51%
20	J	142	36% 50% 12%
21	K	123	33% 51% 14%
22	L	143	37% 54% 8%
23	M	136	36% 52% 11%
24	N	127	30% 50% 13% 5%
25	O	116	42% 51% 6%
26	P	114	38% 48% 12%
27	Q	117	39% 50% 9%
28	R	103	32% 54% 12%

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Mol	Chain	Length	Quality of chain
29	S	110	 32% 51% 14% •
30	T	100	 31% 45% 16% • 6%
31	U	103	 44% 41% 13% ••
32	W	94	 39% 53% 7%
33	Y	84	 33% 46% 14% 6%

2 Entry composition

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
28	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

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

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

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

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

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

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

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

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

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

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

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.

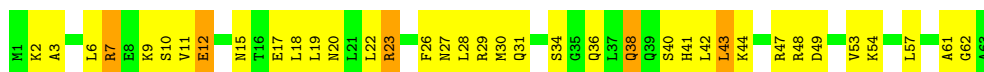
- Molecule 1: 50S RIBOSOMAL PROTEIN L28

Chain 0: 



- Molecule 2: 50S RIBOSOMAL PROTEIN L29

Chain 1: 




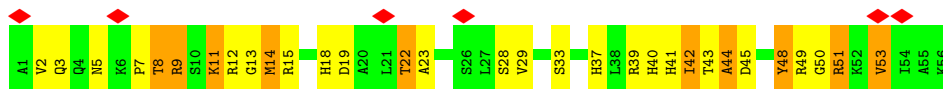
- Molecule 3: 50S RIBOSOMAL PROTEIN L30

Chain 2: 



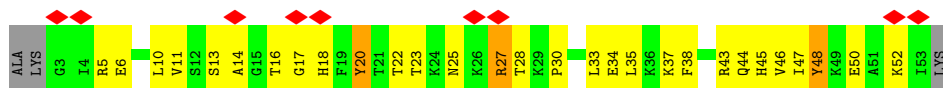
- Molecule 4: 50S RIBOSOMAL PROTEIN L32

Chain 3: 

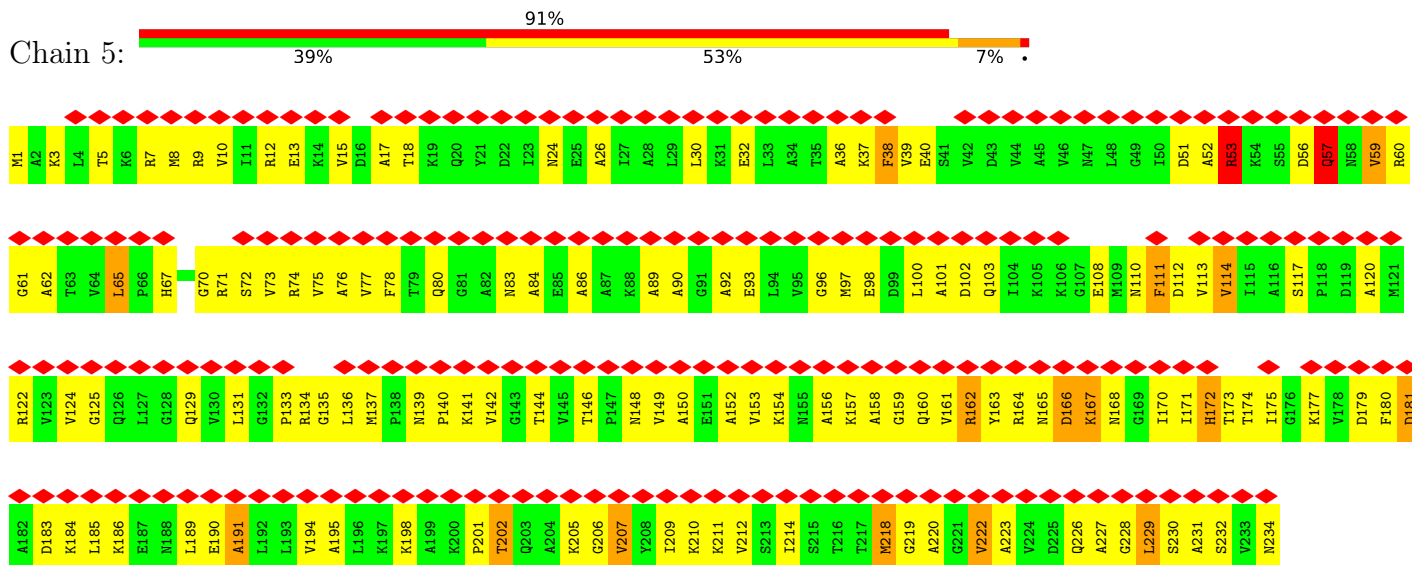


- Molecule 5: 50S RIBOSOMAL PROTEIN L33

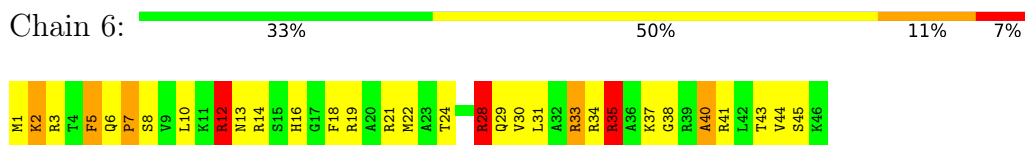
Chain 4: 



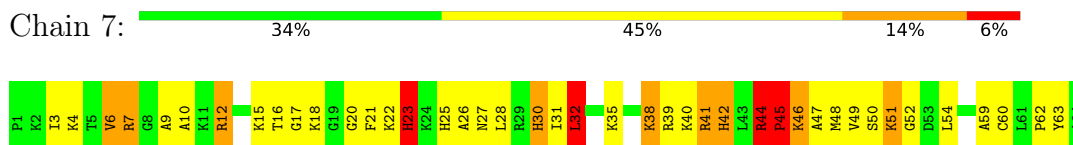
- Molecule 6: 50S RIBOSOMAL PROTEIN L1



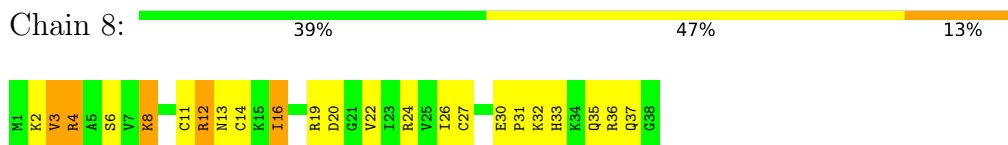
- Molecule 7: 50S RIBOSOMAL PROTEIN L34



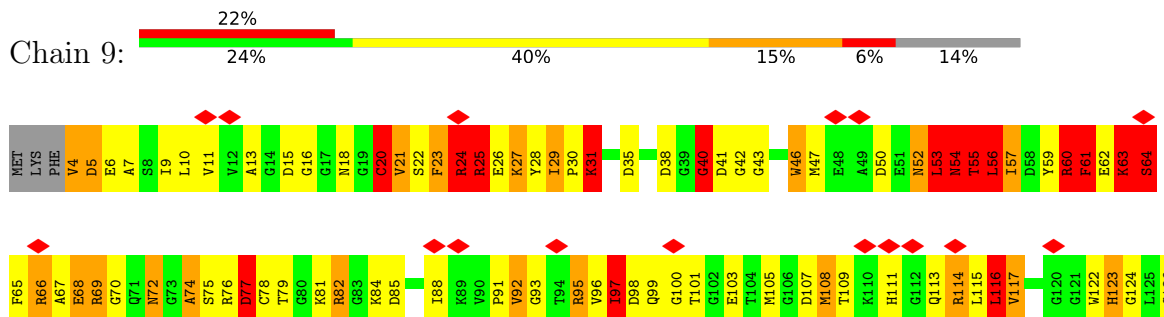
- Molecule 8: 50S RIBOSOMAL PROTEIN L35



- Molecule 9: 50S RIBOSOMAL PROTEIN L36

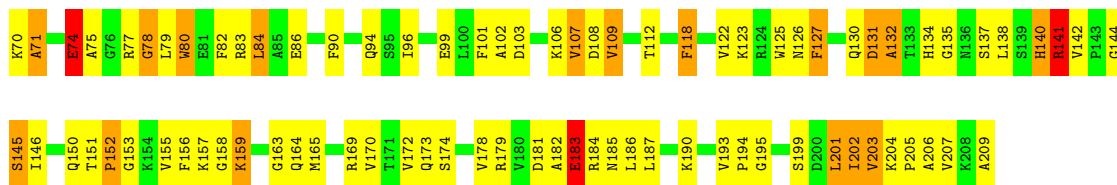


- Molecule 10: GTPASE OBGE/CGTA

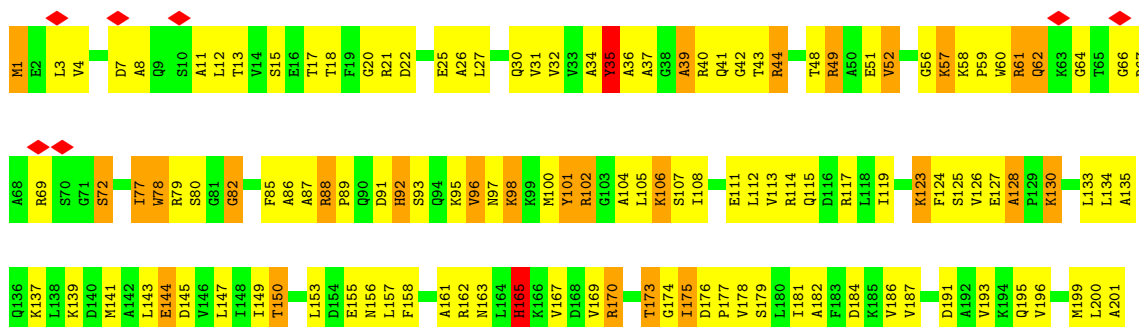


A1393	G1332	G1271	G1211	C1150	A1080	C1030	U970	A910	U850	U790	A730	G669	A609	G549	C489	A439
U1394	G1333	A1272	G1212	C1151	G1091	G1031	G971	A911	C851	C791	C731	A670	C610	C559	C490	A430
A1395	A1334	U1273	A1213	C1152	C1092	A1032	A972	C912	U852	A792	G732	C671	C611	G551	G491	U431
U1396	C1335	A1274	A1214	C1153	G1093	U1033	A973	U913	C853	A793	G733	C672	G612	U552	A492	A432
A1397	A1336	A1275	G1215	A1155	A1094	U1034	A974	G914	C854	A794	G734	C673	A613	G553	G493	C433
C1398	G1337	A1276	G1216	A1156	A1095	U1035	A975	G915	C855	A795	G735	C674	A614	U554	G494	U434
U1399	C1338	G1277	U1217	G1157	A1096	G1036	G976	G916	C856	C796	G736	A675	U615	G555	G495	C435
U1400	G1339	U1278	G1218	C1158	U1097	G1037	G977	A917	C857	C797	G737	A676	A616	A556	G496	C436
U1401	U1219	G1280	U1219	C1159	A1098	G1038	G978	A918	C858	G798	G738	A677	G617	C557	U437	U437
U1402	G1341	U1281	G1220	C1160	G1099	A1039	A979	U919	C859	G799	G739	G678	G618	U558	G498	G438
A1403	A1342	U1282	C1221	C1161	U1100	A1040	A980	A920	U860	A800	C740	C679	G619	U559	U439	A439
C1404	G1343	G1283	U1222	G1162	C1101	G1041	A981	C921	A861	S801	U741	G681	G620	G560	G500	C440
U1405	U1344	A1284	G1223	G1163	U1102	G1042	C982	C922	C862	A802	U742	G682	A621	A561	A501	U441
U1406	C1345	A1285	U1224	C1164	A1103	C1043	A983	G923	A863	U803	A743	U683	G622	U562	A502	G442
G1407	G1346	A1286	G1225	A1165	C1104	C1044	A984	G924	S864	A904	U744	G684	G623	A563	A503	A443
G1408	A1347	A1287	A1226	C1166	U1105	C1045	C985	A925	C865	A805	G745	A685	C624	C564	A504	C444
U1409	C1348	G1288	G1227	C1167	G1106	A1046	C986	G926	A866	C806	U746	U686	G625	C565	A505	G445
G1410	C1349	C1289	A1228	G1168	G1107	G1047	C987	A927	C867	U807	U747	U687	A626	G566	G506	G446
U1411	C1350	C1290	C1229	A1169	U1108	A1048	A988	A928	U868	G808	G748	U688	A627	U567	A507	A447
U1412	C1351	C1291	A1230	G1170	C1109	C1049	C989	U929	S869	S809	A749	A689	G628	U568	A508	U448
A1413	U1352	G1292	U1231	G1171	G1110	A1050	A990	G930	U870	U810	A750	G690	G629	U569	C509	A449
U1414	A1353	C1293	C1232	C1172	A1111	G1051	C991	U931	U871	U811	A751	C691	G630	G570	C510	G450
U1415	A1354	U1294	G1233	C1173	G1112	C1052	C992	U932	U872	C812	A752	C692	A631	U571	U511	U451
G1416	G1355	C1295	U1234	U1174	U1113	C1053	G993	G933	C873	U813	A753	A693	A632	A572	G512	G452
G1417	G1356	G1296	G1235	A1175	C1114	A1054	C994	U934	C874	C814	U754	U694	A633	U573	A513	A453
G1418	C1357	C1297	G1236	U1176	G1115	G1055	C995	C935	S875	C815	U755	G695	C634	A574	A514	A454
A1419	G1358	C1298	A1237	C1177	G1116	A1056	A996	A936	C876	C816	A756	G696	C635	A575	A515	C455
U1420	A1359	U1299	G1238	G1178	C1117	A1057	G997	C937	A877	C817	A757	G697	C636	U576	C516	C456
G1421	G1360	G1300	U1239	C1179	U1118	U1058	C998	G938	A878	C818	A758	C698	A637	G577	C517	A457
A1422	G1361	A1301	G1240	U1180	C1119	G1059	U999	G939	G879	A819	A759	A699	G638	G578	G518	G458
G1423	C1362	A1302	A1241	U1181	G1120	U1060	A1000	G940	S880	A820	G760	G700	U639	U579	U519	U459
U1424	C1363	G1303	U1242	G1182	C1121	U1061	A1001	A941	S881	A821	A761	G701	C640	U580	A520	A460
G1425	G1364	A1304	C1243	U1183	G1122	G1062	G1002	G942	S882	G822	U762	G702	U641	U581	U521	C461
A1426	A1365	C1305	A1244	U1184	C1123	G1063	U1003	A943	S883	C823	A763	G703	A642	A582	A522	C462
U1427	C1366	G1306	G1245	G1185	G1124	A1064	G1004	C944	U884	U824	A764	U704	A643	G583	C523	G463
C1428	A1367	A1307	A1246	G1186	G1125	U1065	C1005	A945	C885	A825	C765	A705	A644	C584	U524	U464
G1429	G1368	U1308	A1247	G1187	A1126	U1066	C1006	C946	A886	U826	U766	A706	C645	G585	U525	G465
U1430	G1369	G1309	G1248	U1188	A1127	A1067	C1007	A947	U887	U827	U767	G707	U646	A586	A526	A466
A1431	C1370	G1310	U1249	U1189	G1128	G1068	A1008	C948	C888	U828	G768	G708	G647	C587	C527	G467
A1432	G1371	G1311	G1250	A1190	A1129	U1069	A1009	G949	C889	A829	U769	U709	G648	U588	A528	G468
A1433	G1372	U1312	C1251	G1191	U1130	A1070	A1010	G950	C890	G830	G770	U710	C649	U589	A529	G469
G1373	U1373	U1313	G1252	G1192	G1131	G1071	G1011	C951	S891	G831	G771	G711	C650	A590	G530	A470
U1374	C1374	C1314	A1253	G1193	U1132	C1072	A1012	G952	A892	U832	C772	G712	G651	U591	C531	A471
G1375	G1375	U1315	U1254	A1194	A1133	A1073	C1013	G953	C893	A833	U773	G713	U652	A592	A532	A472
C1437	G1376	U1316	U1255	G1195	A1134	G1074	A1014	G954	U894	G834	G774	U714	U653	U593	G533	G473
U1438	A1378	G1317	G1256	C1196	C1135	C1075	U1015	U955	A895	C835	G775	A715	A654	U594	U534	G474
A1439	U1379	U1318	C1257	G1197	G1136	A1076	G1016	G956	A896	G836	G776	A716	A655	C595	G535	C475
U1440	G1380	C1319	U1258	U1198	G1137	A1077	G1017	C957	C897	C837	G777	C717	G656	U596	G536	G476
G1441	A1381	C1320	G1259	U1199	U1138	U1078	U1018	U958	C898	C838	G778	A718	G657	G537	G537	A477
U1442	G1382	A1321	A1260	C1200	G1139	C1079	U1019	A959	A899	U839	U779	C719	U658	U598	A538	A478
U1443	A1383	A1322	C1261	U1201	C1140	A1080	A1020	A960	A900	C840	G780	U720	G659	A599	C539	A479
G1444	C1384	U1323	A1262	U1202	U1141	U1081	A1021	C961	C901	S841	A781	A721	C660	A599	G540	A480
A1445	A1385	G1324	U1263	C1203	A1142	U1082	G1022	G962	C902	U842	A782	A722	A661	C601	A541	G481
C1446	G1386	U1325	A1264	U1204	A1143	U1083	U1023	U963	C903	G843	A783	C723	G662	A602	C542	A482
A1447	A1387	U1326	A1265	A1205	A1144	A1084	G1024	C964	S904	A844	G784	U724	G663	A603	G543	A483
G1448	C1388	A1327	G1266	G1206	C1145	A1085	A1025	C965	A905	A845	G785	G725	G664	G604	C544	C484
U1449	G1389	A1328	U1267	C1207	C1146	A1086	G1026	G966	U906	U846	C786	G726	U665	G605	U545	C485
U1450	U1390	U1329	A1268	U1208	A1147	U1087	A1027	U967	G907	U847	A787	A727	A666	U606	U546	C486
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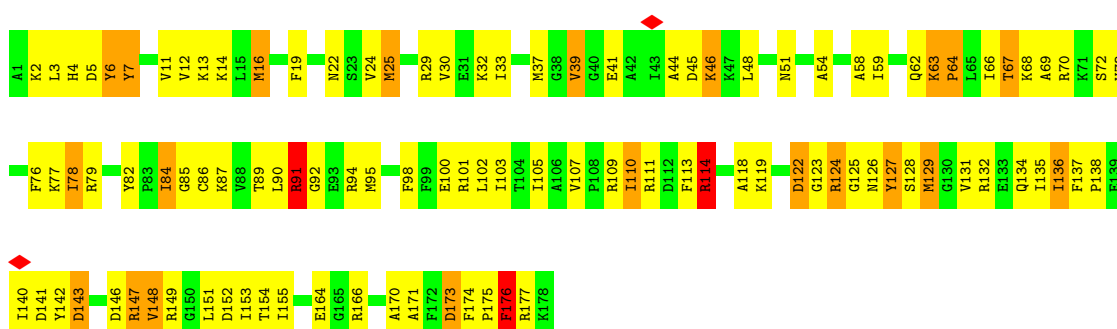
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• Molecule 15: 50S RIBOSOMAL PROTEIN L4



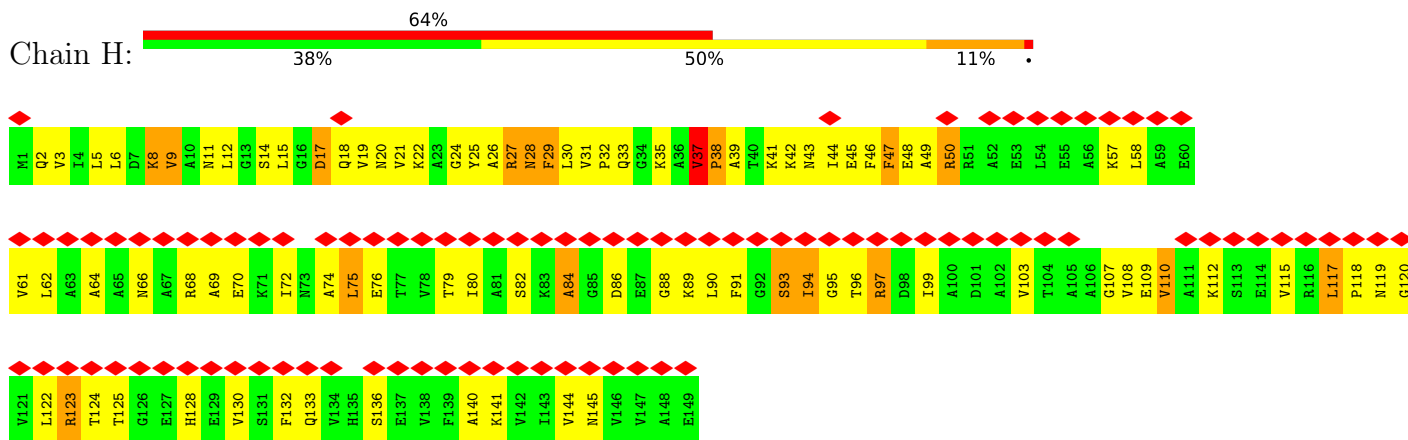
• Molecule 16: 50S RIBOSOMAL PROTEIN L5



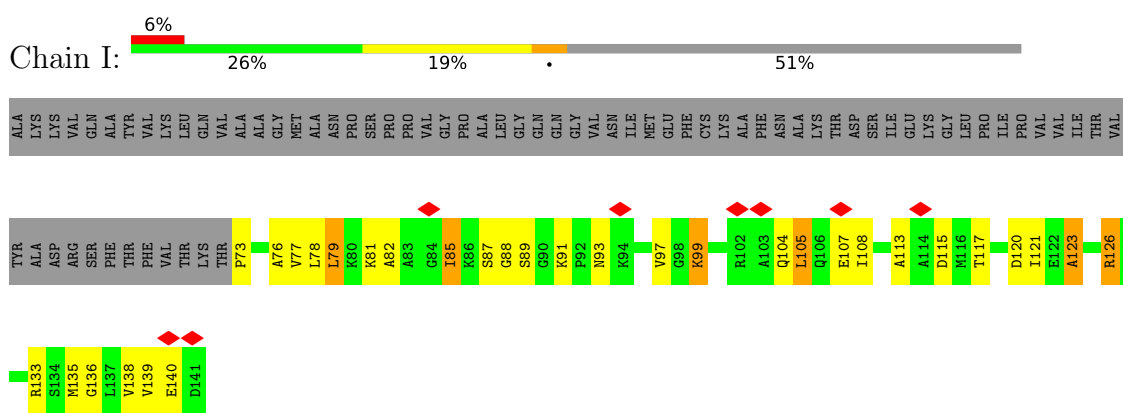
• Molecule 17: 50S RIBOSOMAL PROTEIN L6



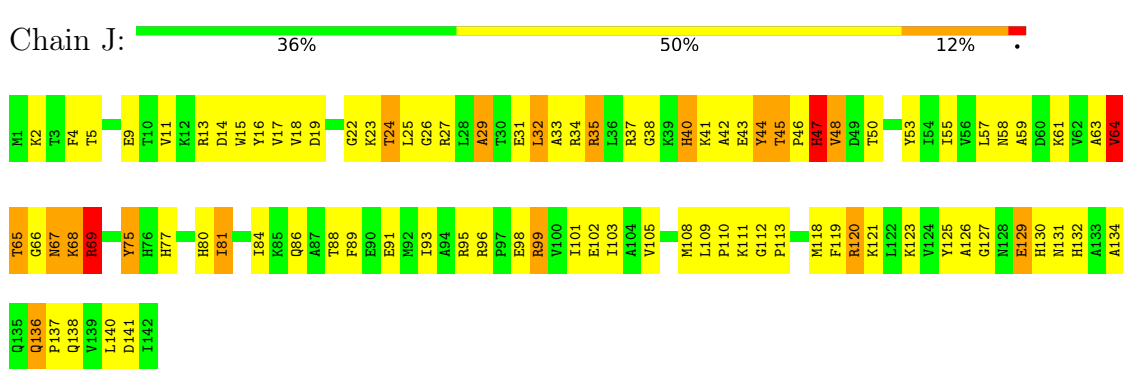
• Molecule 18: 50S RIBOSOMAL PROTEIN L9



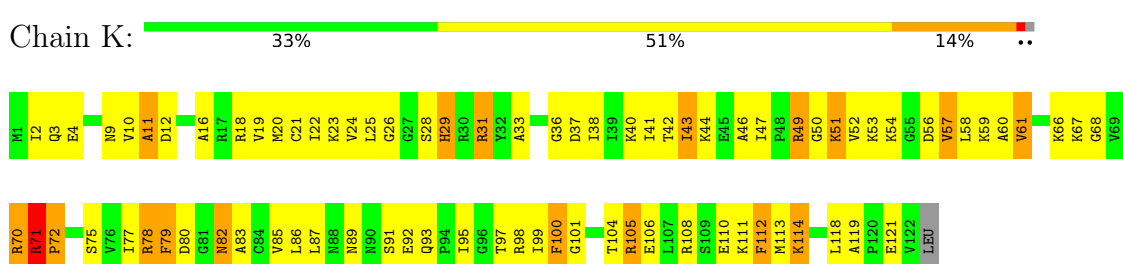
• Molecule 19: 50S RIBOSOMAL PROTEIN L11



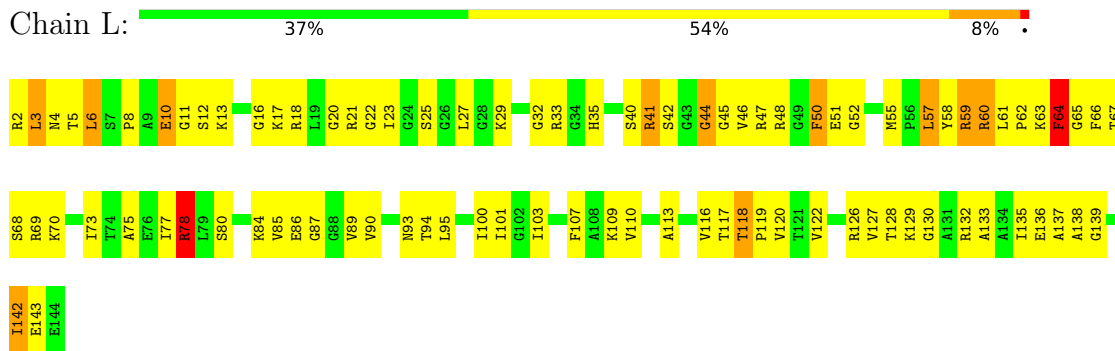
• Molecule 20: 50S RIBOSOMAL PROTEIN L13



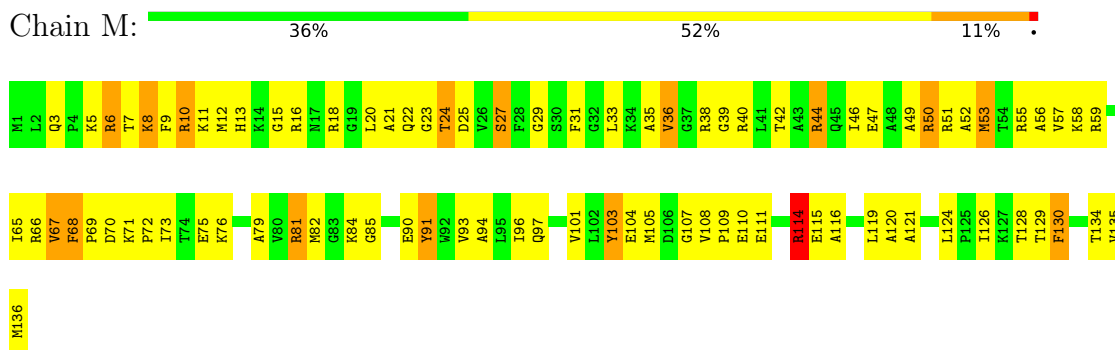
• Molecule 21: 50S RIBOSOMAL PROTEIN L14



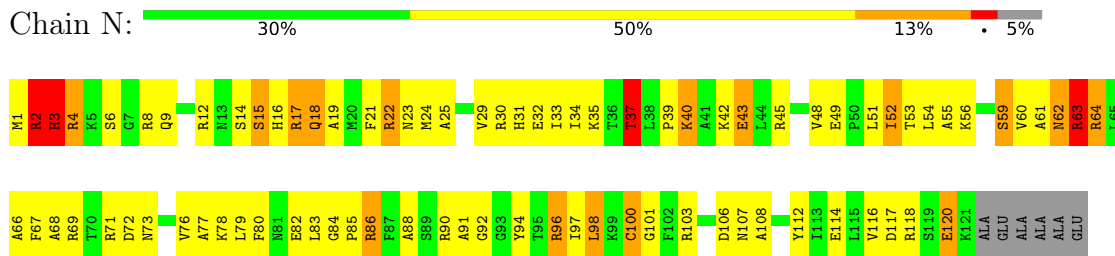
• Molecule 22: 50S RIBOSOMAL PROTEIN L15



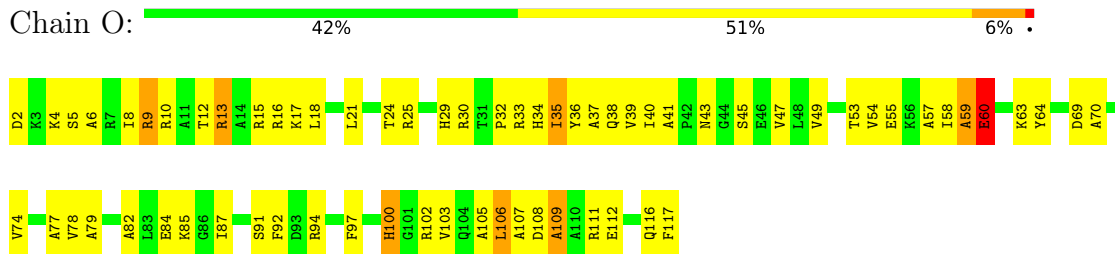
- Molecule 23: 50S RIBOSOMAL PROTEIN L16



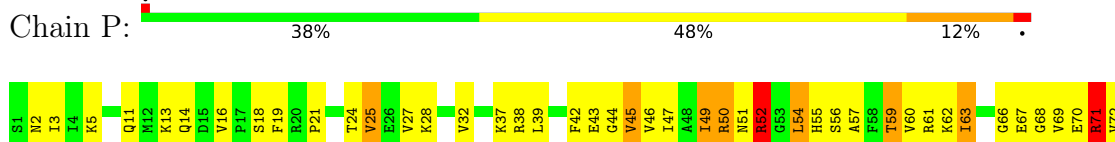
- Molecule 24: 50S RIBOSOMAL PROTEIN L17

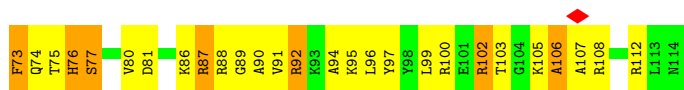


- Molecule 25: 50S RIBOSOMAL PROTEIN L18

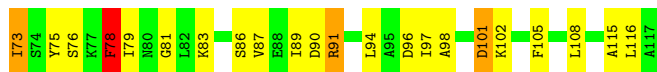
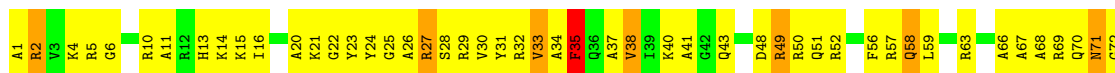
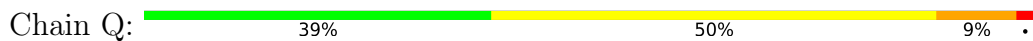


- Molecule 26: 50S RIBOSOMAL PROTEIN L19

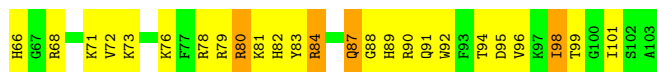
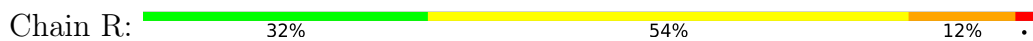




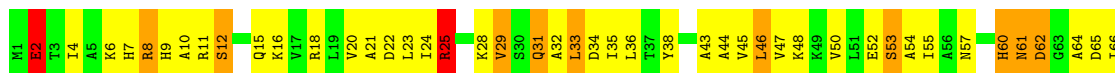
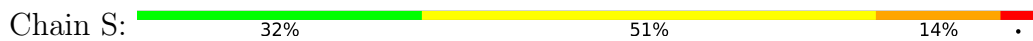
• Molecule 27: 50S RIBOSOMAL PROTEIN L20



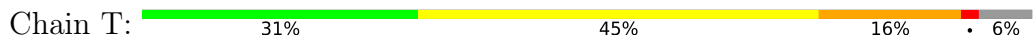
• Molecule 28: 50S RIBOSOMAL PROTEIN L21



• Molecule 29: 50S RIBOSOMAL PROTEIN L22

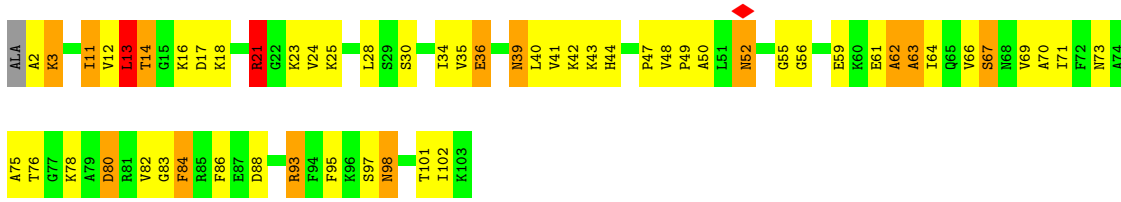


• Molecule 30: 50S RIBOSOMAL PROTEIN L23

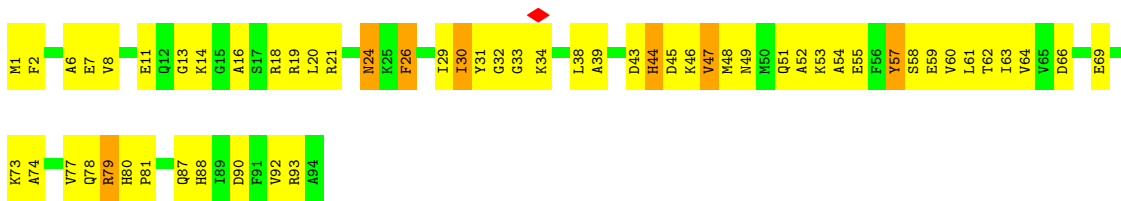


• Molecule 31: 50S RIBOSOMAL PROTEIN L24

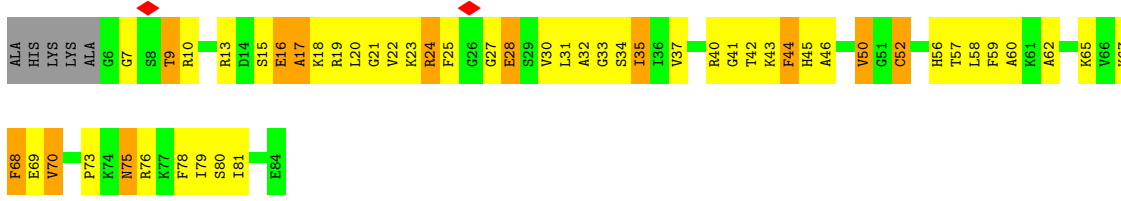




• Molecule 32: 50S RIBOSOMAL PROTEIN L25



• 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 (\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 (\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	2.48	37/635 (5.8%)	2.60	50/848 (5.9%)
2	1	2.33	21/510 (4.1%)	2.58	42/677 (6.2%)
3	2	2.53	24/453 (5.3%)	2.44	33/605 (5.5%)
4	3	2.46	20/450 (4.4%)	2.53	26/599 (4.3%)
5	4	2.26	20/417 (4.8%)	2.33	22/556 (4.0%)
6	5	2.32	74/1748 (4.2%)	2.48	126/2355 (5.4%)
7	6	2.41	18/380 (4.7%)	2.54	26/498 (5.2%)
8	7	2.43	29/513 (5.7%)	2.53	34/676 (5.0%)
9	8	2.43	17/303 (5.6%)	2.43	21/397 (5.3%)
10	9	2.38	127/2584 (4.9%)	2.68	238/3487 (6.8%)
11	A	2.02	60/2744 (2.2%)	1.93	113/4276 (2.6%)
12	B	2.00	1362/69796 (2.0%)	1.89	2603/108888 (2.4%)
13	C	2.37	92/2122 (4.3%)	2.53	148/2854 (5.2%)
14	D	2.33	77/1586 (4.9%)	2.50	103/2134 (4.8%)
15	E	2.31	58/1571 (3.7%)	2.54	128/2113 (6.1%)
16	F	2.29	54/1444 (3.7%)	2.49	94/1937 (4.9%)
17	G	2.31	51/1336 (3.8%)	2.42	89/1805 (4.9%)
18	H	2.39	57/1122 (5.1%)	2.56	80/1515 (5.3%)
19	I	2.23	17/497 (3.4%)	2.54	30/662 (4.5%)
20	J	2.37	59/1152 (5.1%)	2.46	88/1551 (5.7%)
21	K	2.37	46/941 (4.9%)	2.54	71/1260 (5.6%)
22	L	2.37	49/1054 (4.6%)	2.50	73/1403 (5.2%)
23	M	2.41	56/1093 (5.1%)	2.31	57/1460 (3.9%)
24	N	2.41	50/974 (5.1%)	2.54	83/1303 (6.4%)
25	O	2.38	42/902 (4.7%)	2.44	52/1209 (4.3%)
26	P	2.35	47/929 (5.1%)	2.41	53/1242 (4.3%)
27	Q	2.27	33/960 (3.4%)	2.61	83/1278 (6.5%)
28	R	2.44	42/829 (5.1%)	2.45	61/1107 (5.5%)
29	S	2.55	46/864 (5.3%)	2.58	71/1156 (6.1%)
30	T	2.30	29/745 (3.9%)	2.58	59/996 (5.9%)
31	U	2.34	35/764 (4.6%)	2.31	41/1019 (4.0%)
32	W	2.41	34/766 (4.4%)	2.40	49/1025 (4.8%)
33	Y	2.29	21/603 (3.5%)	2.44	36/797 (4.5%)
All	All	2.12	2804/102787 (2.7%)	2.07	4883/153688 (3.2%)

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 2804 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	15	ARG	CD-NE	11.30	1.62	1.46
20	J	80	HIS	ND1-CE1	10.95	1.43	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	W	69	GLU	CA-C	-10.74	1.39	1.52
22	L	35	HIS	ND1-CE1	10.49	1.43	1.32
29	S	85	ILE	C-N	10.37	1.44	1.33

The worst 5 of 4883 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	1780	A	P-O3'-C3'	18.20	147.50	120.20
10	9	234	HIS	CA-CB-CG	14.29	128.09	113.80
12	B	890	C	P-O3'-C3'	14.25	141.58	120.20
12	B	827	U	P-O3'-C3'	13.32	140.18	120.20
12	B	277	G	P-O5'-C5'	12.98	140.38	120.90

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	5	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	8	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	68	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	523	0
13	C	2083	0	2157	14	0
14	D	1565	0	1616	9	0
15	E	1552	0	1619	7	0
16	F	1420	0	1460	9	0
17	G	1317	0	1364	7	0
18	H	1111	0	1148	4	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	9	0
23	M	1074	0	1157	8	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	709	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 709 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%)	1	14
2	1	61/63 (97%)	50 (82%)	8 (13%)	3 (5%)	1	15
3	2	56/58 (97%)	50 (89%)	5 (9%)	1 (2%)	6	33
4	3	54/56 (96%)	43 (80%)	4 (7%)	7 (13%)	0	4
5	4	49/54 (91%)	43 (88%)	4 (8%)	2 (4%)	2	17
6	5	232/234 (99%)	197 (85%)	25 (11%)	10 (4%)	2	17
7	6	44/46 (96%)	33 (75%)	8 (18%)	3 (7%)	1	11
8	7	62/64 (97%)	47 (76%)	10 (16%)	5 (8%)	1	9
9	8	36/38 (95%)	27 (75%)	7 (19%)	2 (6%)	1	14
10	9	332/390 (85%)	261 (79%)	43 (13%)	28 (8%)	0	8
13	C	270/272 (99%)	216 (80%)	31 (12%)	23 (8%)	0	8
14	D	207/209 (99%)	160 (77%)	34 (16%)	13 (6%)	1	12
15	E	199/201 (99%)	163 (82%)	16 (8%)	20 (10%)	0	7
16	F	176/178 (99%)	135 (77%)	22 (12%)	19 (11%)	0	6
17	G	172/176 (98%)	126 (73%)	31 (18%)	15 (9%)	0	8
18	H	147/149 (99%)	112 (76%)	21 (14%)	14 (10%)	0	8
19	I	67/141 (48%)	65 (97%)	0	2 (3%)	3	22
20	J	140/142 (99%)	108 (77%)	20 (14%)	12 (9%)	0	8
21	K	120/123 (98%)	98 (82%)	16 (13%)	6 (5%)	1	15
22	L	141/143 (99%)	115 (82%)	17 (12%)	9 (6%)	1	12
23	M	134/136 (98%)	112 (84%)	16 (12%)	6 (4%)	2	16
24	N	119/127 (94%)	94 (79%)	17 (14%)	8 (7%)	1	11
25	O	114/116 (98%)	88 (77%)	20 (18%)	6 (5%)	1	14
26	P	112/114 (98%)	84 (75%)	19 (17%)	9 (8%)	1	9
27	Q	115/117 (98%)	95 (83%)	12 (10%)	8 (7%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	R	101/103 (98%)	83 (82%)	14 (14%)	4 (4%)	2	18
29	S	108/110 (98%)	87 (81%)	11 (10%)	10 (9%)	0	8
30	T	92/100 (92%)	68 (74%)	16 (17%)	8 (9%)	0	8
31	U	96/103 (93%)	73 (76%)	15 (16%)	8 (8%)	0	9
32	W	92/94 (98%)	78 (85%)	11 (12%)	3 (3%)	3	20
33	Y	77/84 (92%)	54 (70%)	15 (20%)	8 (10%)	0	6
All	All	3800/4018 (95%)	3026 (80%)	498 (13%)	276 (7%)	1	10

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%)	64 (96%)	3 (4%)	24	46
2	1	55/55 (100%)	52 (94%)	3 (6%)	19	41
3	2	48/48 (100%)	45 (94%)	3 (6%)	16	37
4	3	47/47 (100%)	46 (98%)	1 (2%)	47	65
5	4	45/48 (94%)	43 (96%)	2 (4%)	25	47
6	5	181/181 (100%)	173 (96%)	8 (4%)	25	47
7	6	38/38 (100%)	38 (100%)	0	100	100
8	7	51/51 (100%)	48 (94%)	3 (6%)	18	39
9	8	34/34 (100%)	31 (91%)	3 (9%)	9	28
10	9	268/321 (84%)	235 (88%)	33 (12%)	4	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	C	216/217 (100%)	207 (96%)	9 (4%)	26	48
14	D	164/164 (100%)	147 (90%)	17 (10%)	7	22
15	E	165/165 (100%)	154 (93%)	11 (7%)	15	36
16	F	149/149 (100%)	141 (95%)	8 (5%)	20	41
17	G	136/137 (99%)	128 (94%)	8 (6%)	18	39
18	H	114/114 (100%)	104 (91%)	10 (9%)	9	28
19	I	51/109 (47%)	47 (92%)	4 (8%)	11	32
20	J	116/116 (100%)	108 (93%)	8 (7%)	14	36
21	K	102/104 (98%)	98 (96%)	4 (4%)	28	49
22	L	102/102 (100%)	94 (92%)	8 (8%)	11	32
23	M	109/109 (100%)	99 (91%)	10 (9%)	8	26
24	N	100/103 (97%)	95 (95%)	5 (5%)	22	43
25	O	86/86 (100%)	81 (94%)	5 (6%)	18	39
26	P	99/99 (100%)	97 (98%)	2 (2%)	48	66
27	Q	89/89 (100%)	86 (97%)	3 (3%)	32	54
28	R	84/84 (100%)	78 (93%)	6 (7%)	13	35
29	S	93/93 (100%)	86 (92%)	7 (8%)	12	33
30	T	80/84 (95%)	71 (89%)	9 (11%)	5	19
31	U	81/84 (96%)	77 (95%)	4 (5%)	22	43
32	W	78/78 (100%)	75 (96%)	3 (4%)	29	50
33	Y	59/62 (95%)	53 (90%)	6 (10%)	7	23
All	All	3107/3238 (96%)	2901 (93%)	206 (7%)	17	37

5 of 206 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	H	37	VAL
22	L	117	THR
32	W	51	GLN
18	H	94	ILE
20	J	69	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
21	K	82	ASN
27	Q	58	GLN
22	L	4	ASN
24	N	81	ASN
28	R	86	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%)	547 (18%)	96 (3%)
All	All	3014/3021 (99%)	568 (18%)	99 (3%)

5 of 568 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 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](#)

There are no chain breaks in this entry.

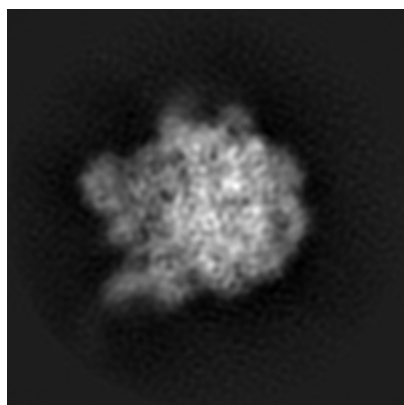
6 Map visualisation [i](#)

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.

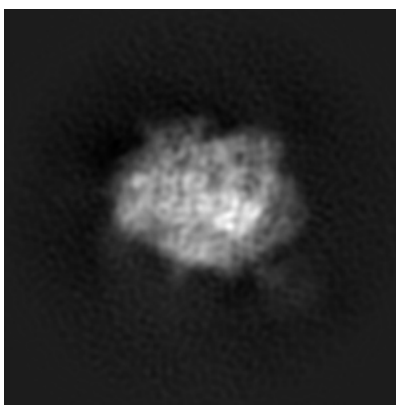
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

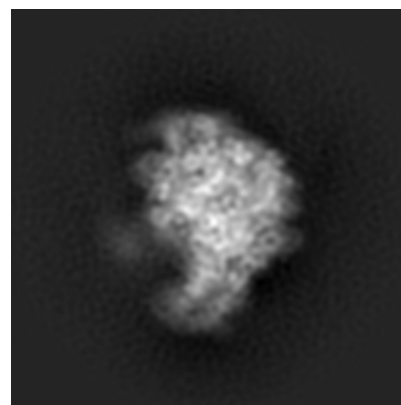
6.1.1 Primary map



X



Y

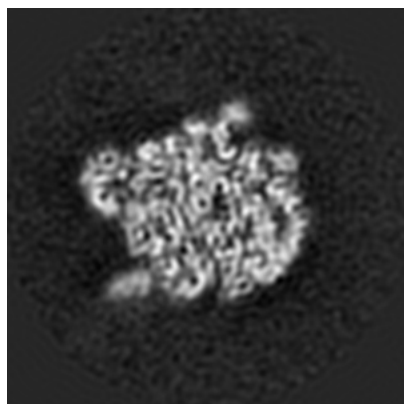


Z

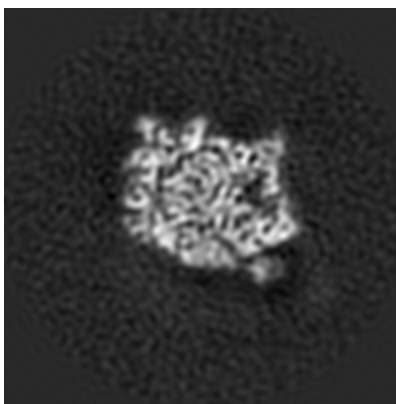
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

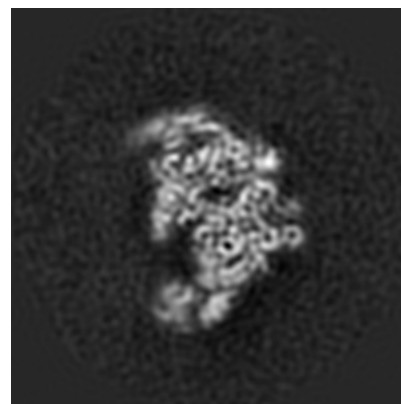
6.2.1 Primary map



X Index: 128



Y Index: 128

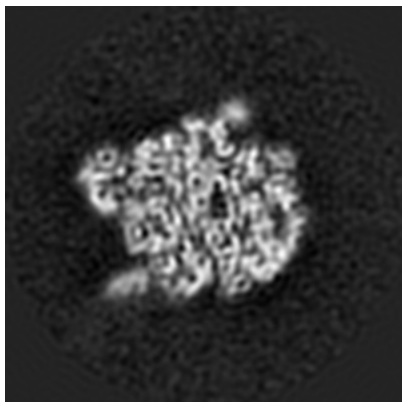


Z Index: 128

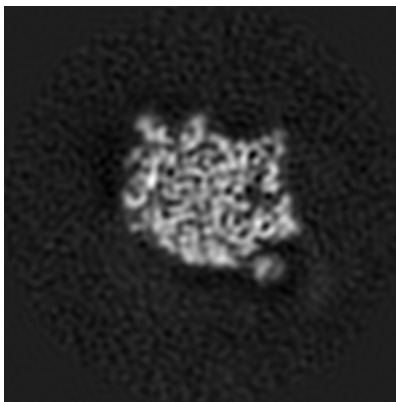
The images above show central slices of the map in three orthogonal directions.

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

6.3.1 Primary map



X Index: 129



Y Index: 126

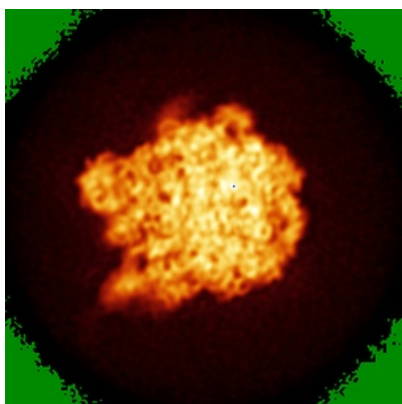


Z Index: 143

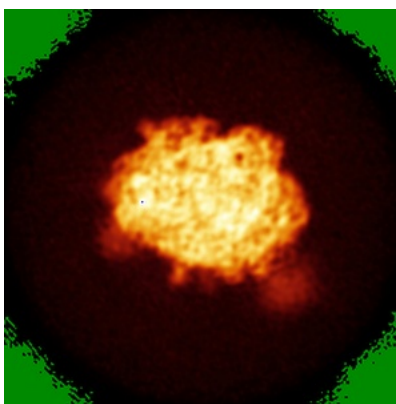
The images above show the largest variance slices of the map in three orthogonal directions.

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

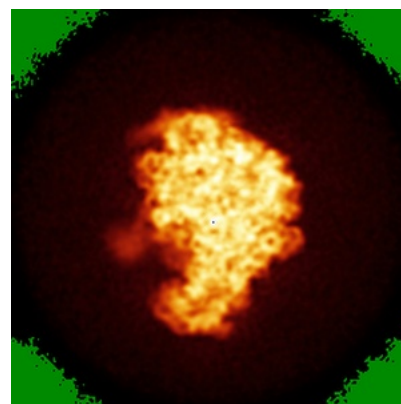
6.4.1 Primary map



X



Y

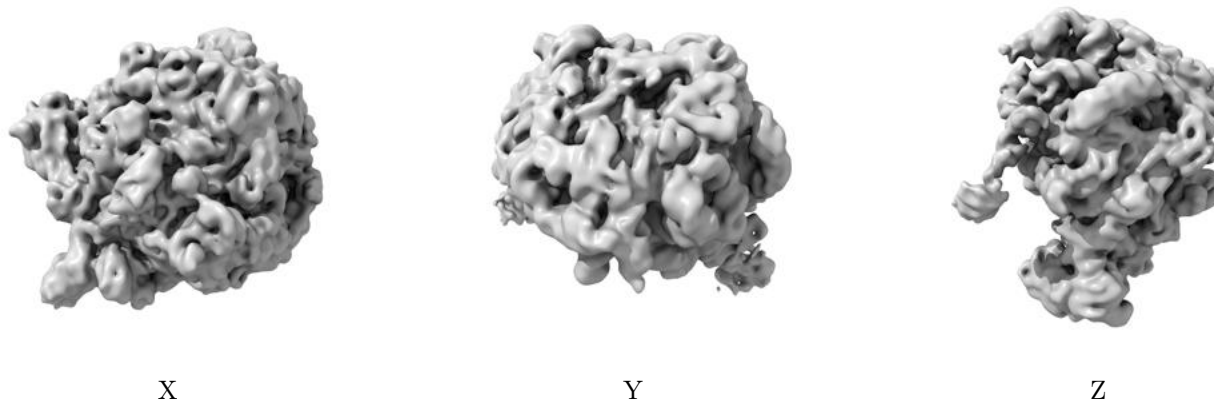


Z

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

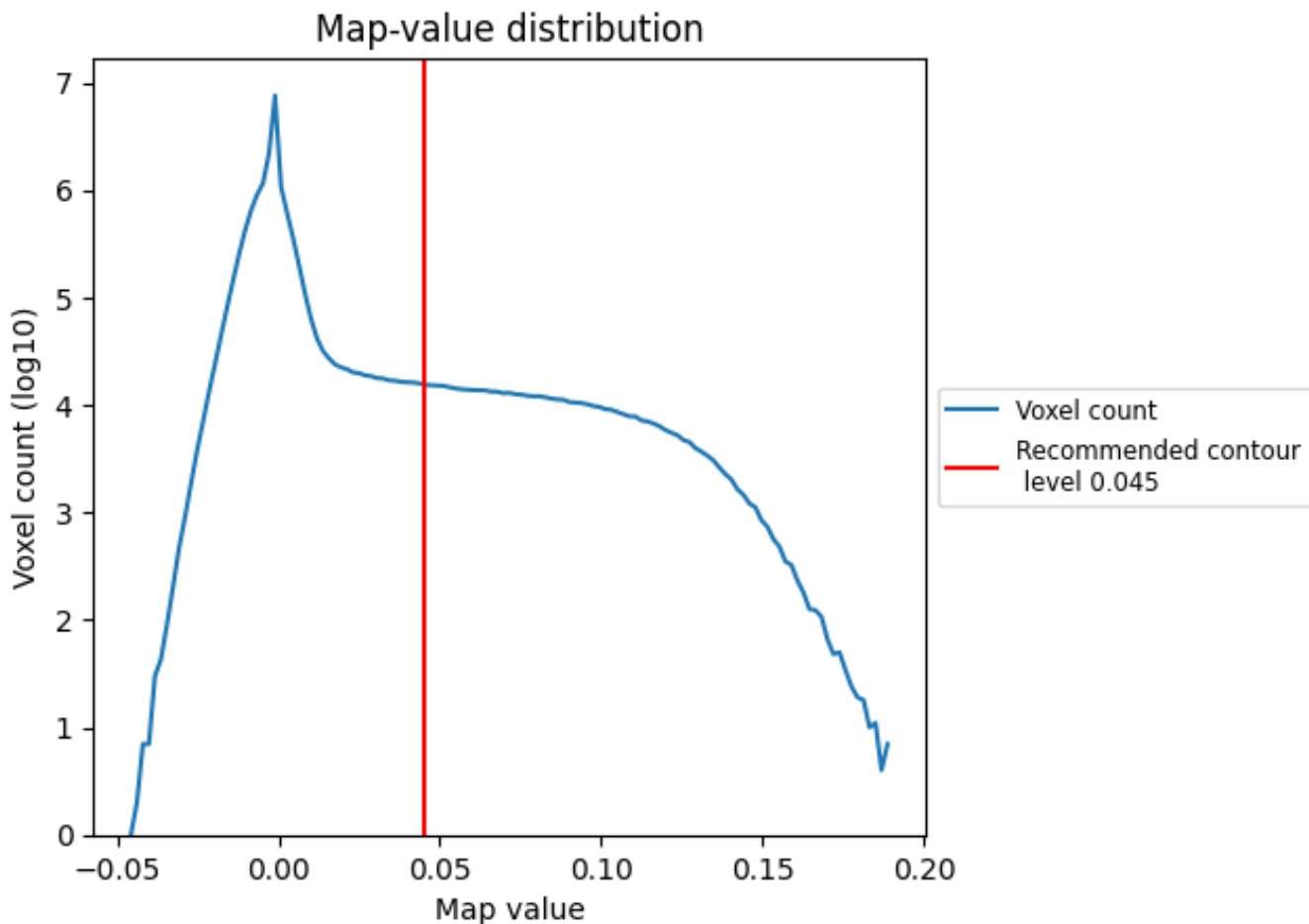
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

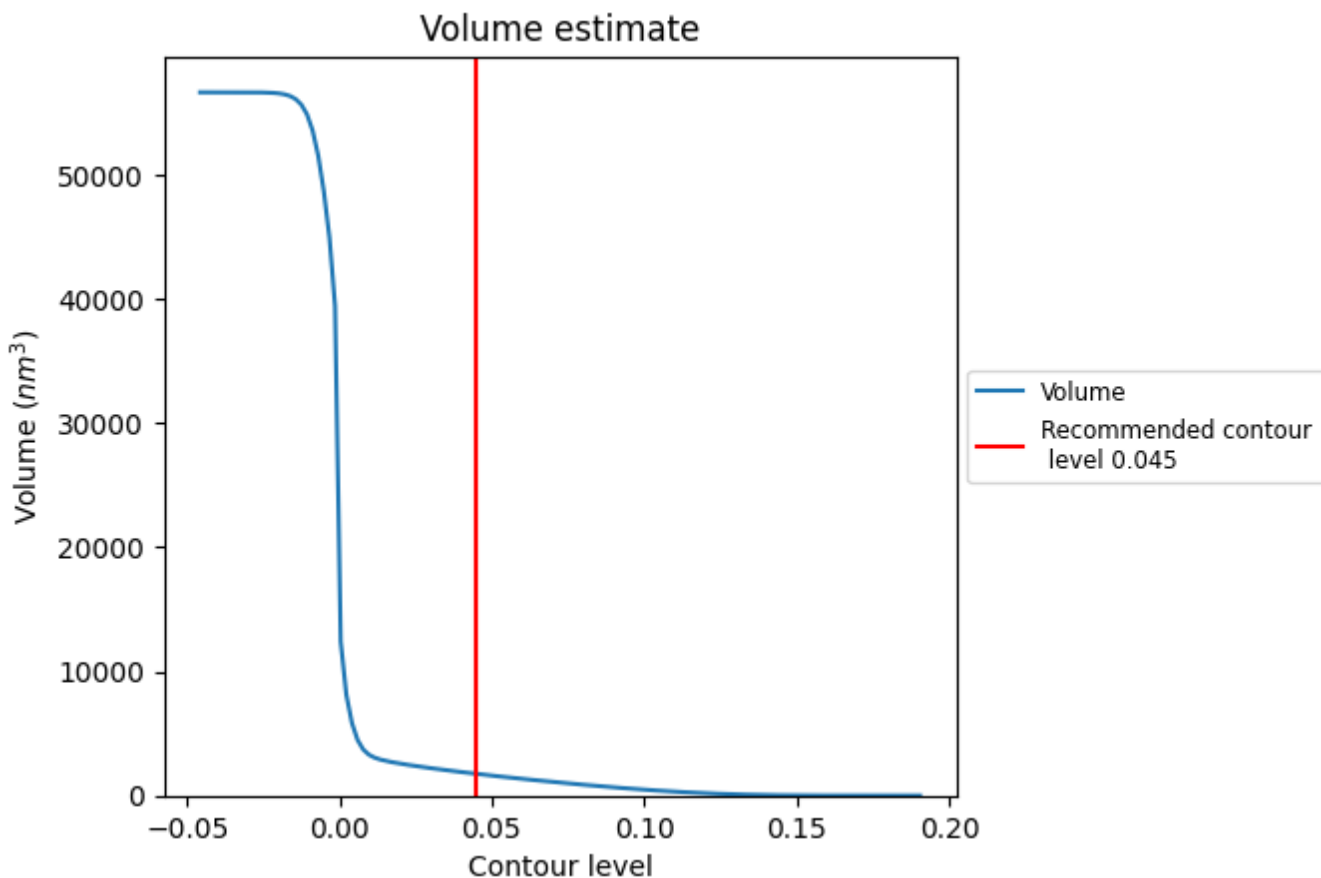
This section contains the results of statistical analysis of the map.

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.

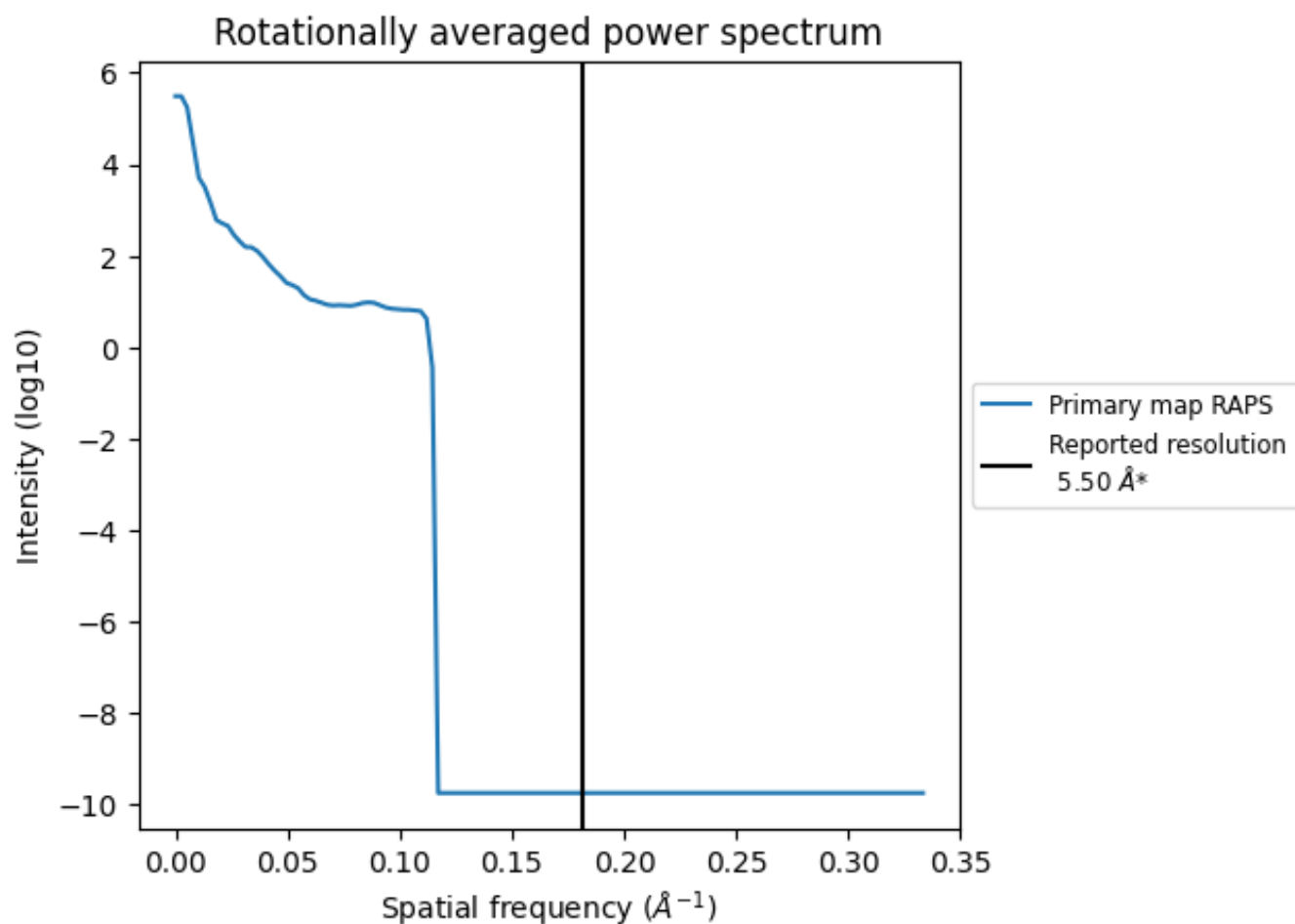
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1748 nm³; 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\AA^{-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-2605 and PDB model 4CSU. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

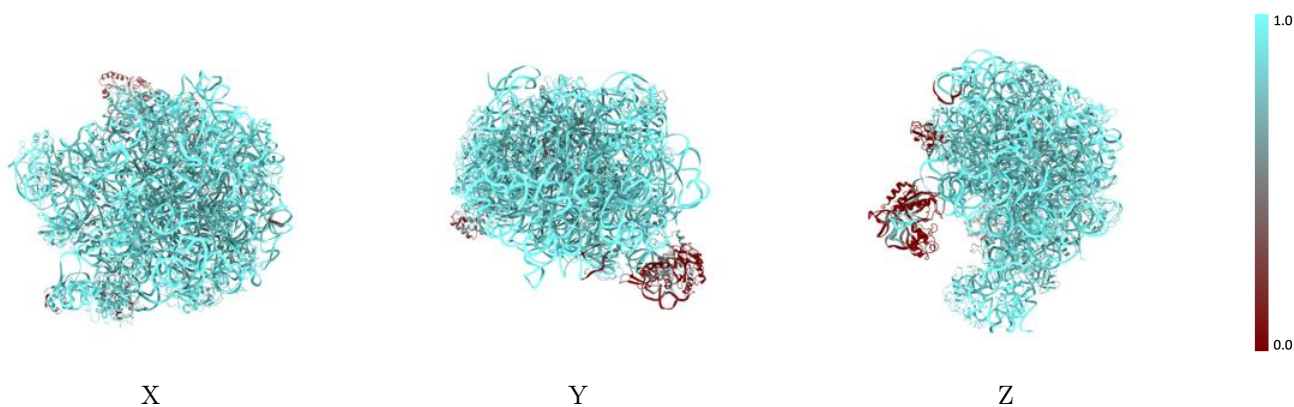
This section was not generated.

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



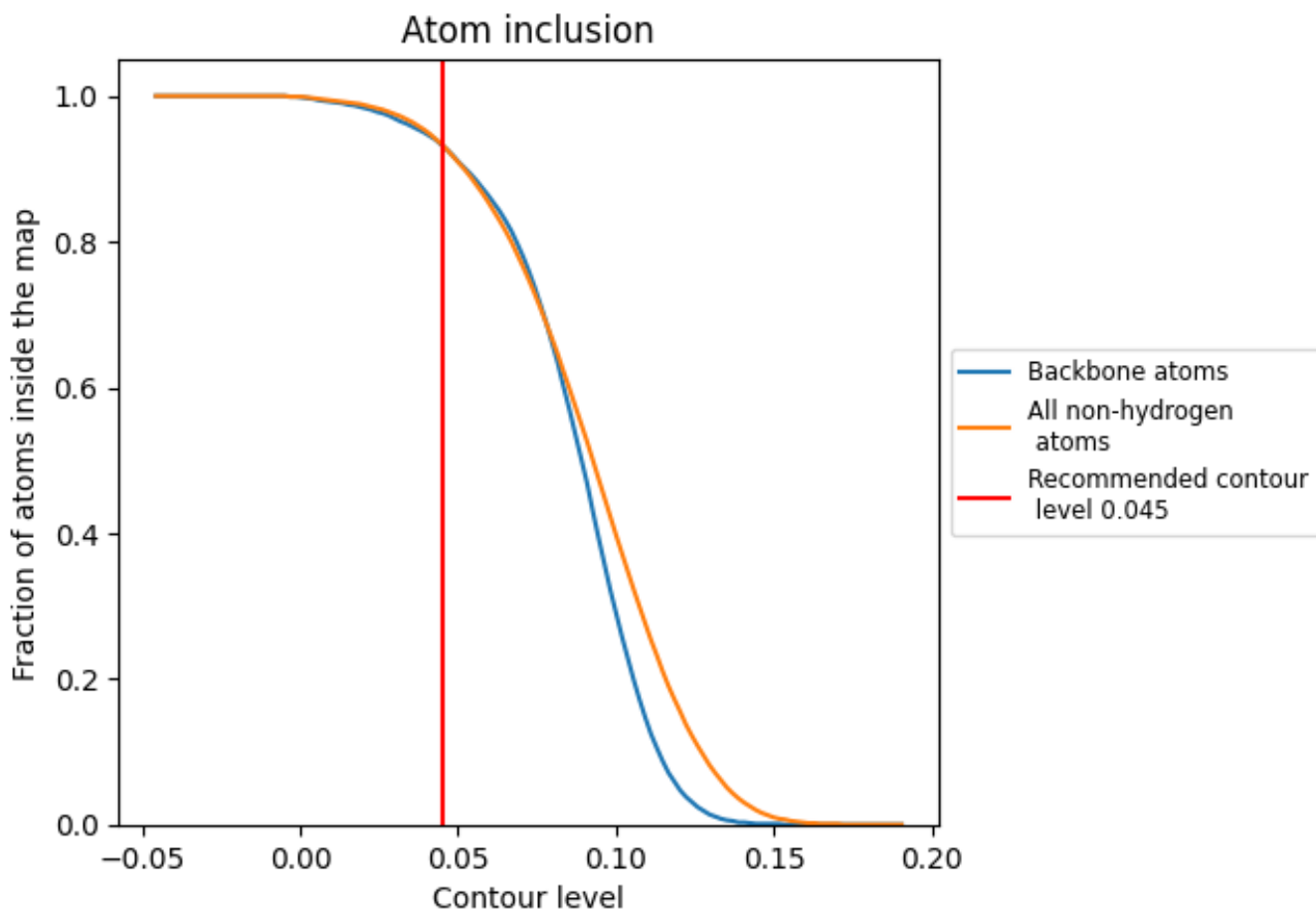
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	 0.9330	 0.1580
0	 0.9020	 0.1240
1	 0.9860	 0.1510
2	 0.9150	 0.1450
3	 0.8510	 0.0740
4	 0.7790	 0.0940
5	 0.0840	 0.0310
6	 0.9350	 0.1170
7	 0.9330	 0.1150
8	 0.9730	 0.0750
9	 0.6850	 0.1020
A	 0.9980	 0.1940
B	 0.9730	 0.1770
C	 0.9440	 0.1260
D	 0.9600	 0.1280
E	 0.9070	 0.1380
F	 0.9530	 0.1170
G	 0.9250	 0.1390
H	 0.3160	 0.0780
I	 0.8100	 0.0820
J	 0.9560	 0.1520
K	 0.9610	 0.1330
L	 0.9490	 0.1220
M	 0.9600	 0.1390
N	 0.9320	 0.1200
O	 0.9820	 0.1260
P	 0.9460	 0.1390
Q	 0.9390	 0.1150
R	 0.9440	 0.1360
S	 0.9220	 0.1300
T	 0.9540	 0.1280
U	 0.9560	 0.1220
W	 0.9250	 0.1430
Y	 0.9240	 0.0970

