



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 06:11 AM UTC

PDB ID : 5ADY / pdb_00005ady
EMDB ID : EMD-3133
Title : Cryo-EM structures of the 50S ribosome subunit bound with HflX
Authors : Zhang, Y.; Mandava, C.S.; Cao, W.; Li, X.; Zhang, D.; Li, N.; Zhang, Y.;
Zhang, X.; Qin, Y.; Mi, K.; Lei, J.; Sanyal, S.; Gao, N.
Deposited on : 2015-08-25
Resolution : 4.50 Å(reported)
Based on initial model : 3FIK

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:

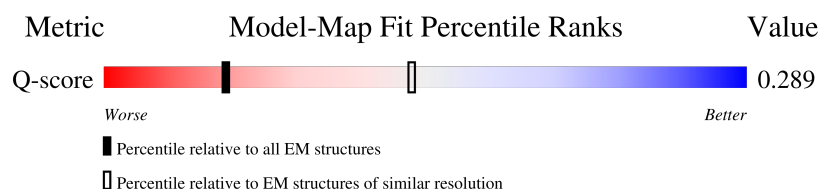
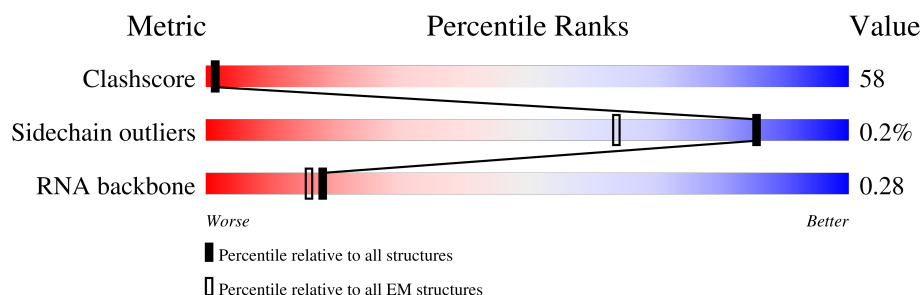
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.50 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	57	
2	1	55	
3	2	46	
4	3	65	

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Mol	Chain	Length	Quality of chain
5	4	38	
6	5	234	
7	6	426	
8	7	165	
9	A	120	
10	B	2903	
11	C	273	
12	D	209	
13	E	201	
14	F	179	
15	G	177	
16	H	149	
17	I	142	
18	J	142	
19	K	123	
20	L	144	
21	M	136	
22	N	127	
23	O	117	
24	P	115	
25	Q	118	
26	R	103	
27	S	110	
28	T	100	
29	U	104	

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Mol	Chain	Length	Quality of chain
30	V	94	
31	W	85	
32	X	78	
33	Y	63	
34	Z	59	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	GNP	6	527	-	-	X	-

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 97364 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 L32.

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

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	51	Total	C	N	O	0	1
			410	263	76	71		

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

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

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

- Molecule 7 is a protein called GTPASE HFLX.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	426	Total	C	N	O	S	0	0
			3403	2129	624	641	9		

- Molecule 8 is a protein called 50S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	164	Total	C	N	O	S	0	1
			1231	775	220	229	7		

- Molecule 9 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 10 is a RNA chain called 23S RRNA.

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

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	264	C	G	conflict	GB 731469900
B	542	C	U	conflict	GB 731469900
B	846	U	C	conflict	GB 731469900
B	1211	C	U	conflict	GB 731469900
B	1220	G	A	conflict	GB 731469900
B	1229	C	U	conflict	GB 731469900
B	1723	G	A	conflict	GB 731469900
B	1725	U	C	conflict	GB 731469900
B	1726	C	G	conflict	GB 731469900
B	1727	C	A	conflict	GB 731469900
B	1730	C	U	conflict	GB 731469900
B	1733	G	U	conflict	GB 731469900
B	1734	G	C	conflict	GB 731469900
B	1735	A	G	conflict	GB 731469900
B	2794	C	U	conflict	GB 731469900
B	2796	U	C	conflict	GB 731469900
B	2799	A	G	conflict	GB 731469900

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2802	G	A	conflict	GB 731469900

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L2.

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

- Molecule 12 is a protein called 50S RIBOSOMAL PROTEIN L3.

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

- Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L4.

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

- Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L5.

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

- Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L9.

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

- Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L13.

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

- Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	122	Total	C	N	O	S	0	1
			931	582	180	164	5		

- Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L15.

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

- Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L16.

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

- Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L17.

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

- Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L18.

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

- Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L19.

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

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L20.

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

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L21.

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

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L22.

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

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L23.

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

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	103	Total	C	N	O	S	0	1
			780	492	147	141			

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L25.

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

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L27.

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

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L28.

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

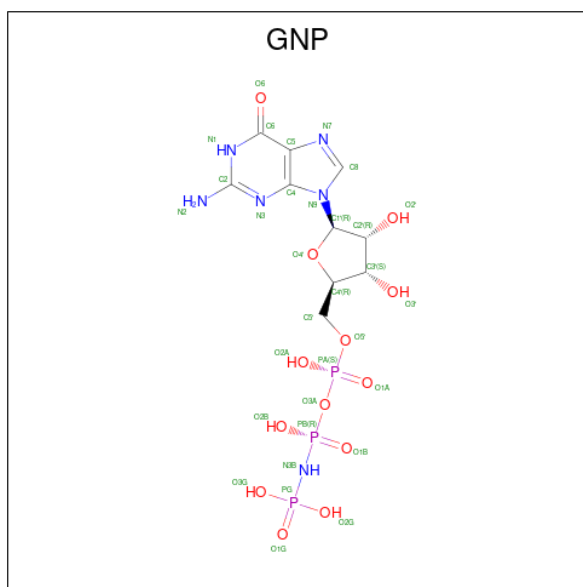
- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L29.

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

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L30.

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

- Molecule 35 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
35	6	1	Total	C	N	O	P	0
			32	10	6	13	3	

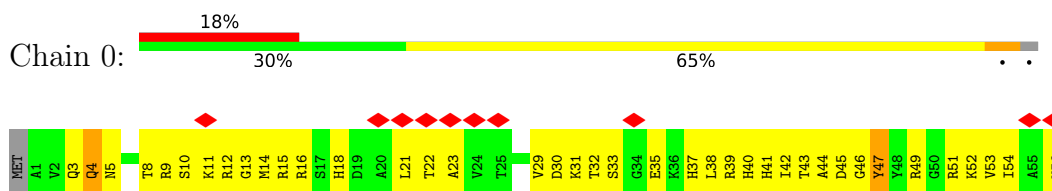
- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	6	1	Total	Mg	0
			1	1	

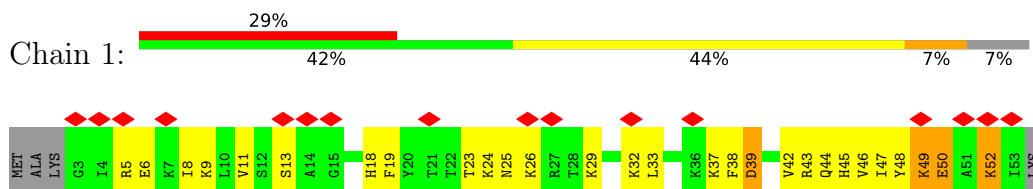
3 Residue-property plots [i](#)

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.

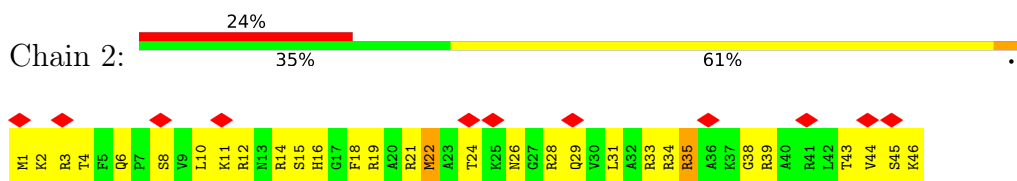
- Molecule 1: 50S RIBOSOMAL PROTEIN L32



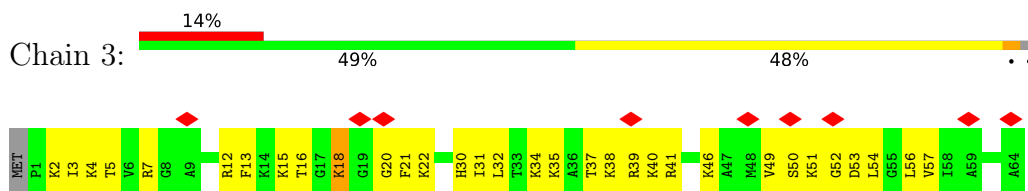
- Molecule 2: 50S RIBOSOMAL PROTEIN L33



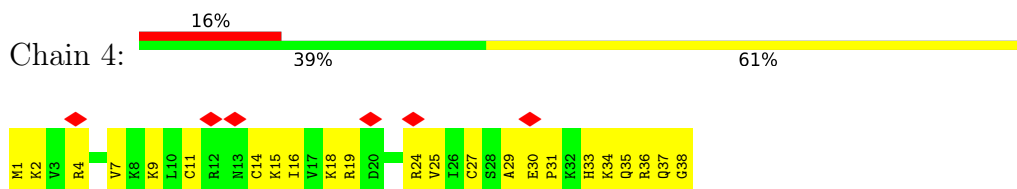
- Molecule 3: 50S RIBOSOMAL PROTEIN L34



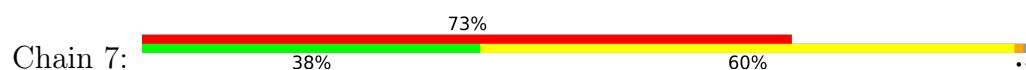
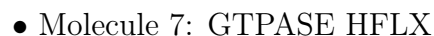
- Molecule 4: 50S RIBOSOMAL PROTEIN L35

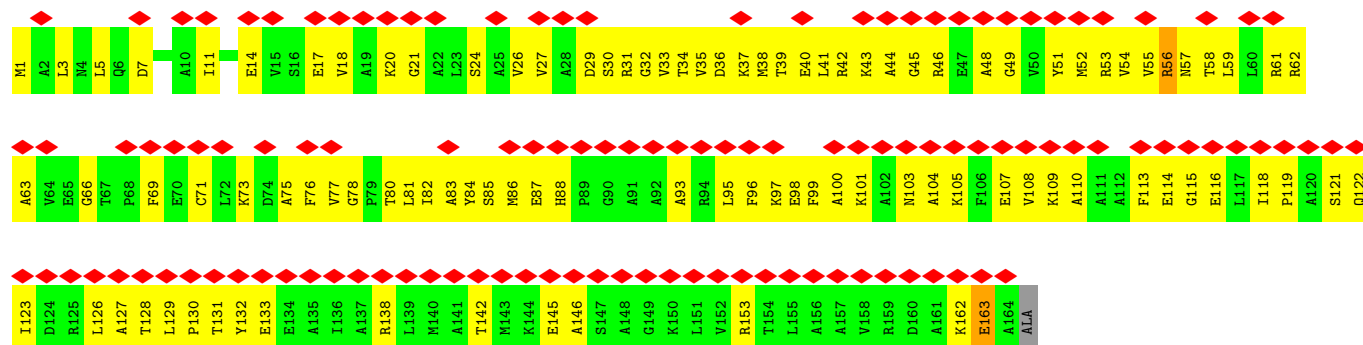


- Molecule 5: 50S RIBOSOMAL PROTEIN L36



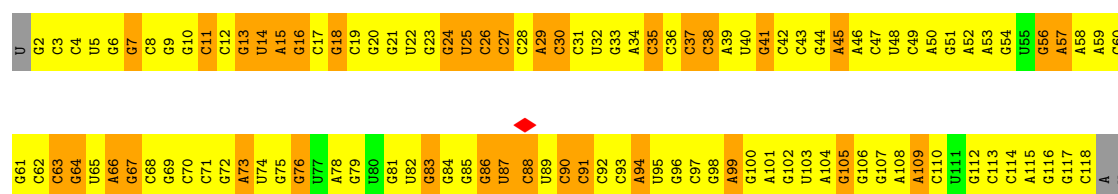
- Molecule 6: 50S RIBOSOMAL PROTEIN L1





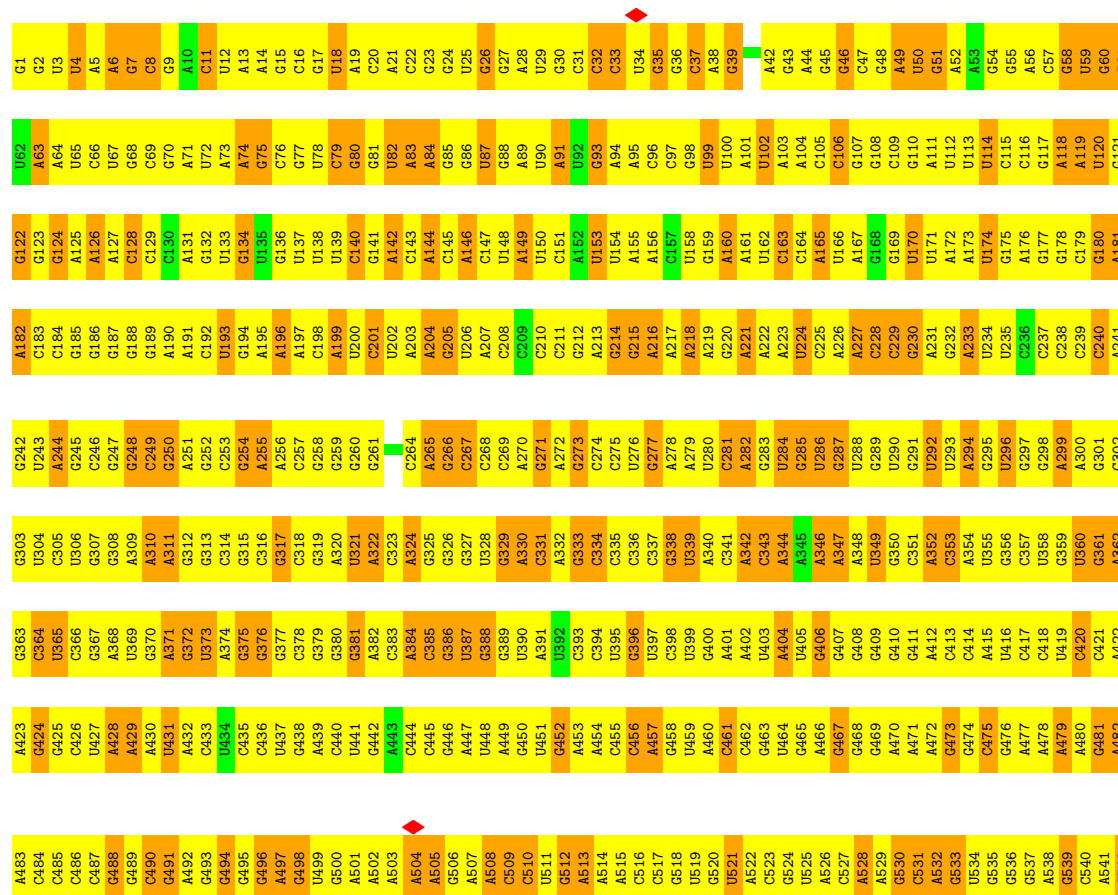
• Molecule 9: 5S RRNA

Chain A: 64% 30%



• Molecule 10: 23S RRNA

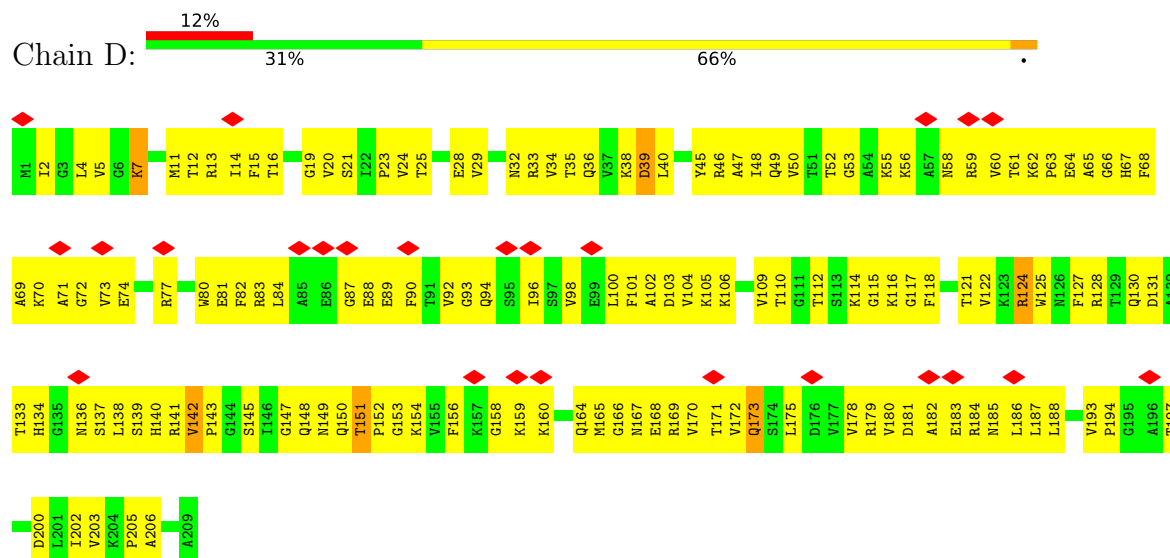
Chain B: 63% 34%



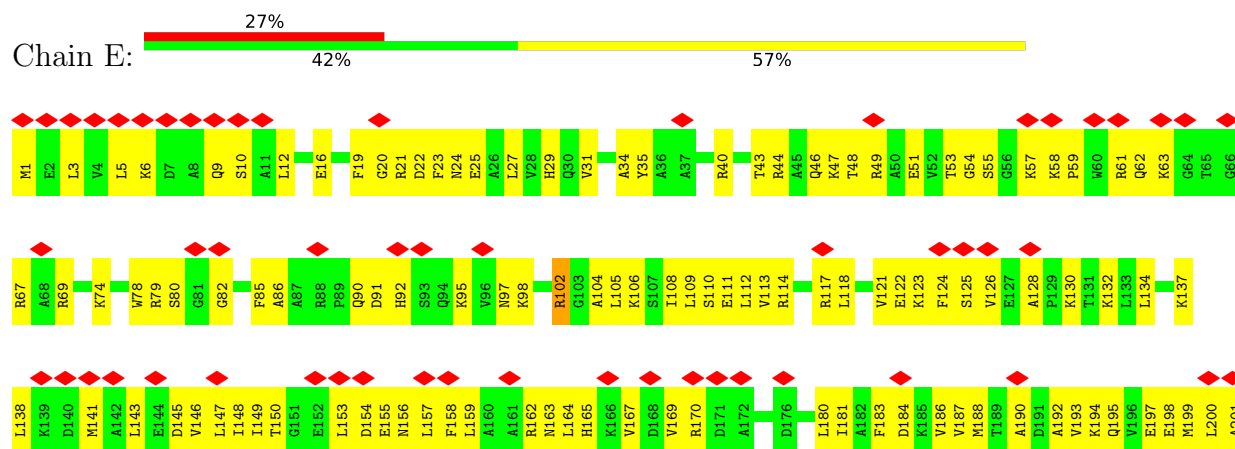
C1447	C1386	U1326	A1265	A1205	C1145	A1085	U1023	U963	C903	C843	A783	C723	G663	A603	C543
G1448	A1387	A1327	G1266	G1206	C1146	A1086	G1024	G964	G904	A844	G784	U724	G664	G604	C544
C1449	C1388	A1328	G1267	G1207	A1147	A1087	G1025	G965	A905	A845	G785	G725	G665	G605	U545
U1450	U1329	A1268	A1268	C1208	U1148	A1088	G1026	G966	U906	U846	C786	G726	U666	U546	C546
C1451	C1330	U1269	A1269	G1209	G1149	A1089	A1027	U967	G907	U847	C787	A727	G667	U607	A547
C1452	G1331	G1270	C1150	G1090	C1150	A1091	A1028	G968	C908	C848	U788	G728	G668	A608	G548
C1453	C1332	G1271	A1151	C1092	A1151	A1092	C1029	G969	A909	A849	U789	G729	G669	A609	G549
C1454	C1333	A1272	C1152	G1212	C1152	C1092	C1030	U970	A910	U850	U790	A730	A670	C610	C550
G1455	C1334	U1273	A1153	G1213	C1153	G1093	G1031	G971	A911	C851	G791	C731	C671	G611	G551
C1456	C1335	A1274	C1154	A1214	G1154	U1094	A1032	A872	C912	U852	U792	C732	C672	G612	U552
U1457	A1396	A1275	A1155	G1215	A1155	A1095	U1033	A973	C913	C853	A793	G733	C673	A613	G553
C1458	U1397	G1276	A1156	G1216	A1156	A1096	G1034	G974	G914	C854	A794	A734	G674	A614	U554
C1459	C1338	G1277	G1157	U1097	G1157	A1097	U1035	A975	C915	G855	C795	A735	A675	U615	G555
U1460	C1339	C1278	C1158	G1218	C1158	A1098	G1036	G976	G916	G856	C796	C736	A676	A616	A556
C1461	U1400	U1279	U1159	U1219	U1159	G1099	G1037	G977	A917	G857	G797	C737	A677	G617	C557
C1462	G1341	G1280	G1160	G1220	G1160	C1100	A1038	G978	A918	G858	G798	G738	C678	G618	U558
C1463	A1342	G1281	C1161	G1221	C1161	U1101	U1039	A979	U919	G859	G799	A739	G679	G619	G559
G1464	A1403	G1282	G1162	U1222	G1162	C1102	A1040	A980	A920	U860	A800	C740	C680	G620	C560
C1465	C1404	G1283	G1163	G1223	G1163	A1103	G1041	A981	C921	A861	G801	U741	G681	A621	G561
U1466	C1405	U1466	C1164	U1224	C1164	C1104	G1042	C982	C922	G862	A802	A742	G682	G622	U562
U1467	U1406	G1346	A1165	G1225	A1165	U1105	C1045	A983	G923	A863	U803	A743	G683	C623	A563
U1468	G1407	A1287	G1166	A1226	G1166	G1106	C1045	A984	G924	A864	A804	U744	G684	C624	C564
A1469	C1348	G1288	G1227	C1167	G1167	U1107	G1046	C985	A925	C865	G805	G745	A685	G625	C565
A1470	U1409	C1289	G1228	G1228	G1168	U1108	G1047	C986	G926	A866	C806	U746	A686	A626	U566
C1471	C1350	C1290	A1169	A1229	U1169	C1109	A1048	C987	A927	C867	U807	U747	C687	A627	U567
C1472	G1351	C1291	C1170	C1230	G1170	G1110	C1049	A988	A928	U868	C808	G748	U688	G628	U568
C1473	U1352	G1292	C1171	U1231	G1171	A1111	A1050	C989	U929	G869	C809	A749	A689	G629	U569
U1474	A1413	C1293	C1172	G1232	C1172	G1112	G1051	A990	G930	U870	U810	A750	G690	G630	G570
G1475	C1354	U1294	C1173	C1233	U1173	U1113	U1052	C991	U931	U871	U811	A751	C691	A631	U571
U1476	G1355	C1295	U1174	U1234	A1175	C1114	A1054	G992	A932	U872	C812	A752	C692	A632	A572
A1477	C1417	G1296	A1175	G1235	C1176	G1115	A1055	G993	A933	C873	U813	A753	A693	A633	U573
G1478	G1418	C1297	U1176	U1236	U1177	C1116	G1056	C994	U934	G874	C814	U754	C694	C634	A574
C1479	C1358	C1298	G1177	A1237	C1178	C1117	A1057	C995	C935	G875	C815	U755	G695	C635	A575
A1480	A1420	G1299	C1178	G1238	C1179	C1118	U1058	A996	A936	C876	C816	A756	C696	G636	U576
G1481	G1421	G1300	U1179	U1239	G1179	U1119	G1059	G997	C937	A877	C817	G757	G697	A637	G577
U1482	C1361	A1301	U1180	U1240	U1180	G1120	U1060	C998	G938	A878	C818	G758	C698	G638	G578
G1483	G1423	A1302	A1302	A1241	U1181	C1121	G1061	U999	G939	G879	A819	G759	U639	A639	U579
C1424	C1363	G1303	U1242	U1242	U1182	G1122	G1062	A1000	G940	G880	A820	G760	G700	C640	U580
G1425	G1364	A1304	C1243	C1243	U1183	C1123	G1063	A1001	A941	C881	A821	A761	G701	U641	C581
U1486	A1365	C1306	A1244	A1244	C1184	G1124	C1064	G1002	G942	C882	G822	U762	U702	U642	A582
A1487	A1427	C1306	G1245	G1245	U1185	G1125	U1065	G1003	A943	G883	C823	G763	U703	A643	G583
C1488	C1367	A1307	A1246	A1246	G1186	A1126	U1066	U1004	C944	U884	U824	A764	G704	A644	C584
A1489	G1368	A1308	A1247	A1247	G1187	A1127	A1067	C1005	A945	C885	A825	C765	A705	C645	G585
C1490	C1369	G1309	G1248	G1248	U1188	G1128	G1068	C1006	C946	C886	U826	U766	A706	U646	A586
G1491	A1430	G1310	U1249	U1249	A1189	A1129	A1069	C1007	A947	A887	U827	U767	G707	G647	C587
C1492	C1370	G1310	G1310	G1250	A1190	G1130	A1070	A1008	C948	U887	U828	G768	G708	A648	U588
A1493	G1432	G1311	G1311	G1251	G1191	U1131	G1071	A1009	C949	C888	A829	U769	U709	G649	U589
C1494	A1433	U1312	U1312	G1251	G1191	G1132	C1072	A1010	G950	C889	G830	G770	U710	C650	A590
A1495	A1434	U1313	G1313	G1252	G1192	U1132	A1073	G1011	C951	G831	G771	C771	G711	G651	U591
U1496	C1435	A1253	G1314	G1253	G1193	A1134	G1074	G952	C952	U832	U832	C772	G712	U652	A592
C1497	G1375	C1315	A1254	A1254	A1194	C1135	C1075	G953	G953	A833	U773	G773	G713	U653	U593
C1498	C1376	U1316	U1255	G1255	G1195	G1136	C1076	G954	C954	G834	G774	A774	U714	A654	U594
A1499	G1377	G1317	G1317	C1257	C1196	G1137	A1077	U1015	U955	C835	C775	G775	A715	A655	C595
C1500	A1439	U1318	U1318	U1257	G1197	G1138	U1078	G956	C956	C836	G776	G776	G716	G656	U596
U1501	U1440	C1319	U1258	U1258	U1198	G1139	C1079	G1017	C957	U894	C837	C777	C717	G657	G597
A1502	G1380	C1320	G1259	U1259	U1199	U1139	U1078	G1018	U958	U895	C837	G778	G718	U658	U598
C1503	A1381	A1321	C1260	C1200	U1199	C1140	A1080	U1018	U958	A896	U838	U779	A719	U658	A599
A1504	C1382	A1322	U1201	U1201	C1200	U1141	U1081	U1019	A959	U897	U839	G780	C719	G659	A599
U1505	A1383	C1323	G1202	G1202	U1202	A1142	U1082	A1020	A960	C897	C840	G780	U720	C660	G600
C1506	A1384	U1263	U1263	G1203	G1203	A1143	U1083	A1021	C961	C898	G841	A781	A721	A661	C601
C1507	C1446	U1325	A1264	A1264	A1204	A1144	A1084	G1022	G962	A900	U842	A782	A722	G662	A602
										C902					



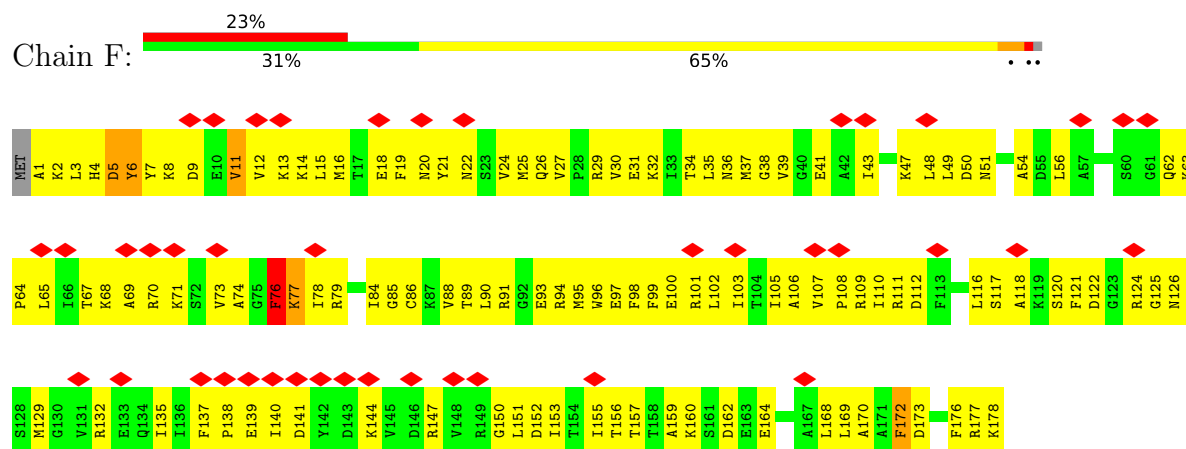
- Molecule 12: 50S RIBOSOMAL PROTEIN L3



- Molecule 13: 50S RIBOSOMAL PROTEIN L4

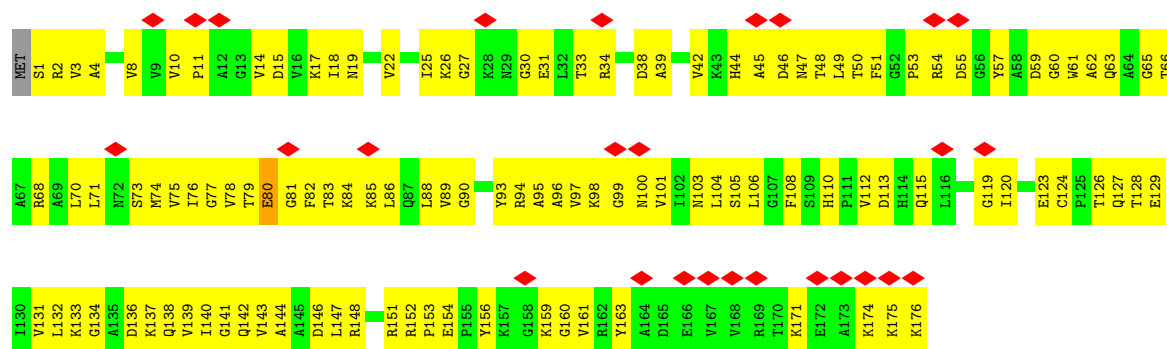


- Molecule 14: 50S RIBOSOMAL PROTEIN L5

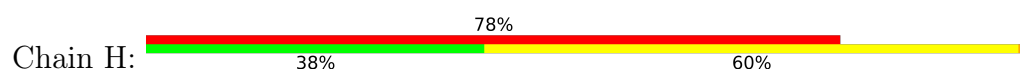


- Molecule 15: 50S RIBOSOMAL PROTEIN L6

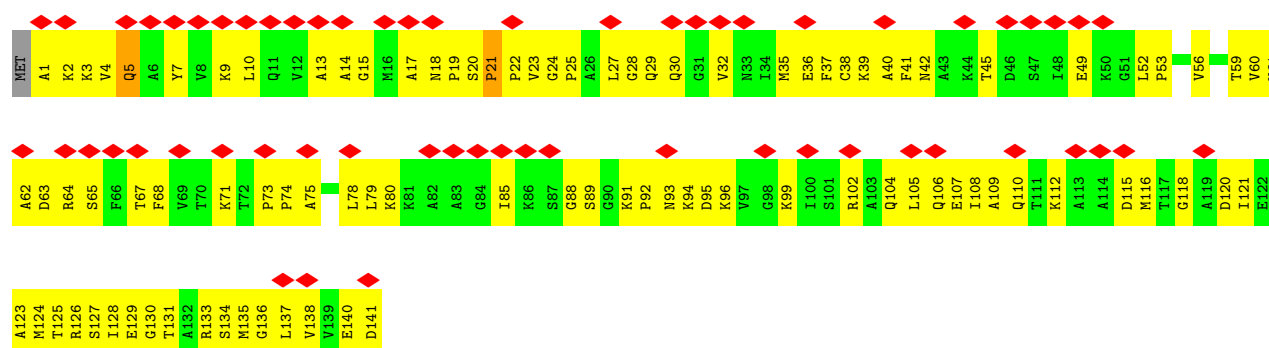




• Molecule 16: 50S RIBOSOMAL PROTEIN L9

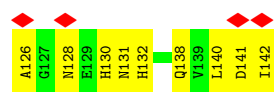


• Molecule 17: 50S RIBOSOMAL PROTEIN L11

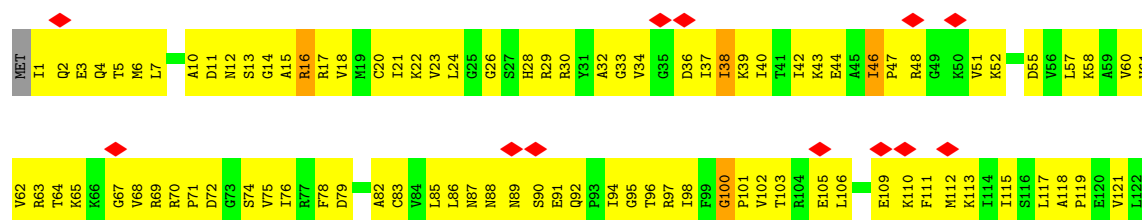


• Molecule 18: 50S RIBOSOMAL PROTEIN L13

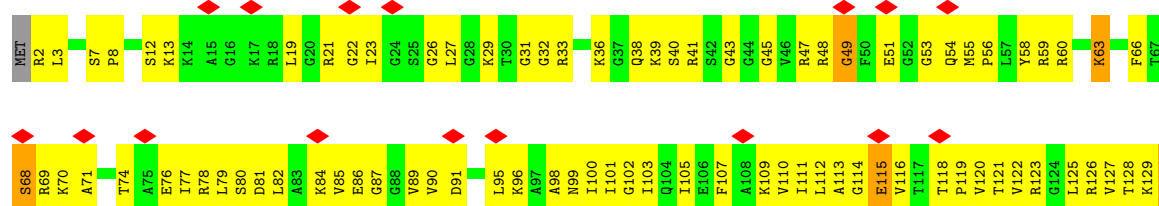




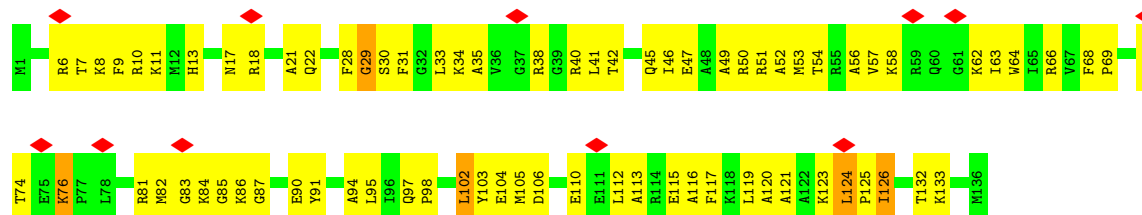
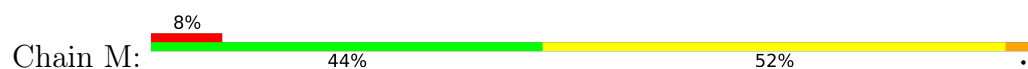
• Molecule 19: 50S RIBOSOMAL PROTEIN L14



• Molecule 20: 50S RIBOSOMAL PROTEIN L15



• Molecule 21: 50S RIBOSOMAL PROTEIN L16

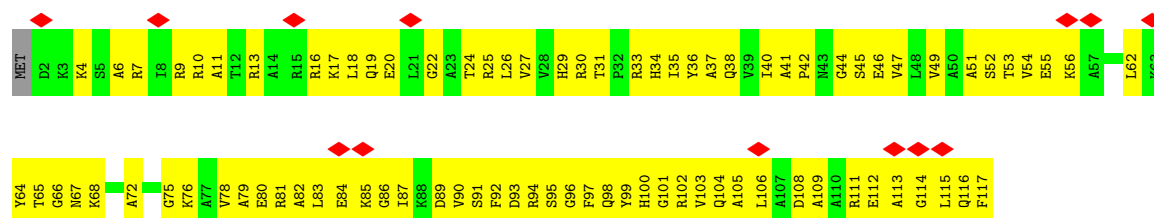


• Molecule 22: 50S RIBOSOMAL PROTEIN L17

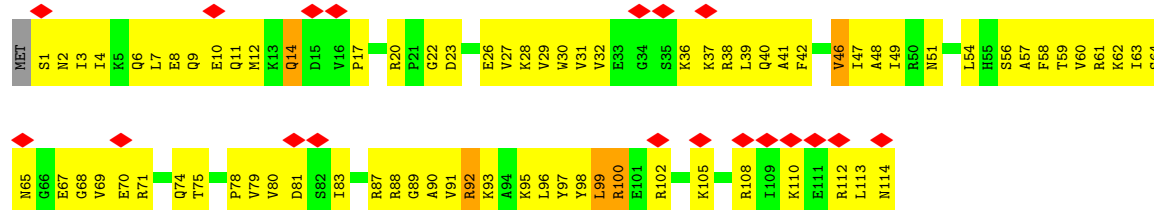




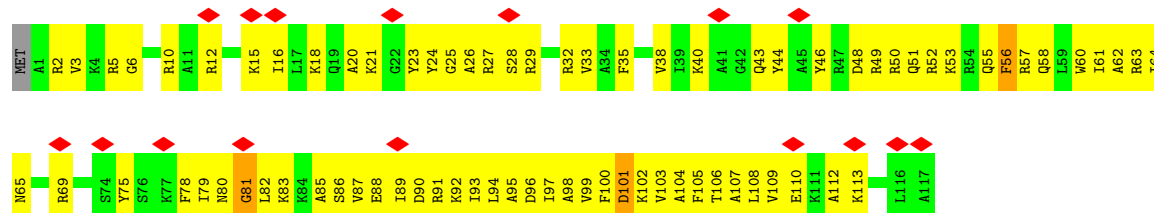
• Molecule 23: 50S RIBOSOMAL PROTEIN L18



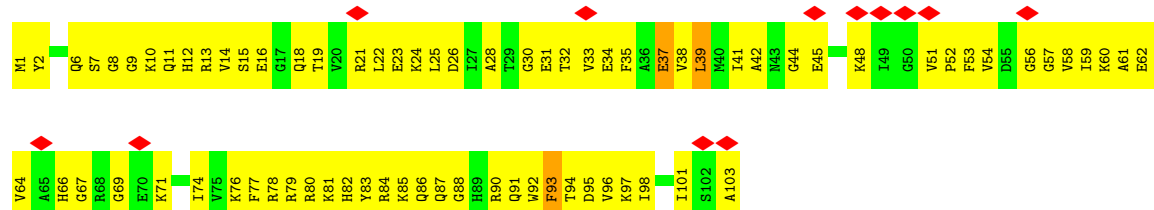
• Molecule 24: 50S RIBOSOMAL PROTEIN L19



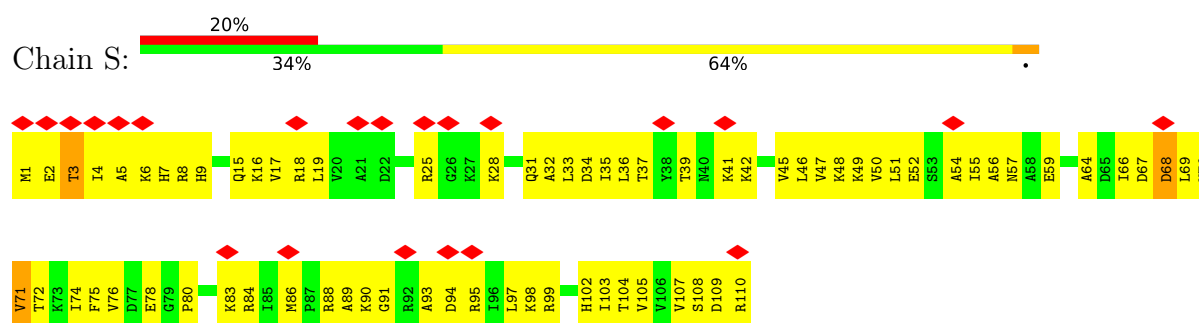
• Molecule 25: 50S RIBOSOMAL PROTEIN L20



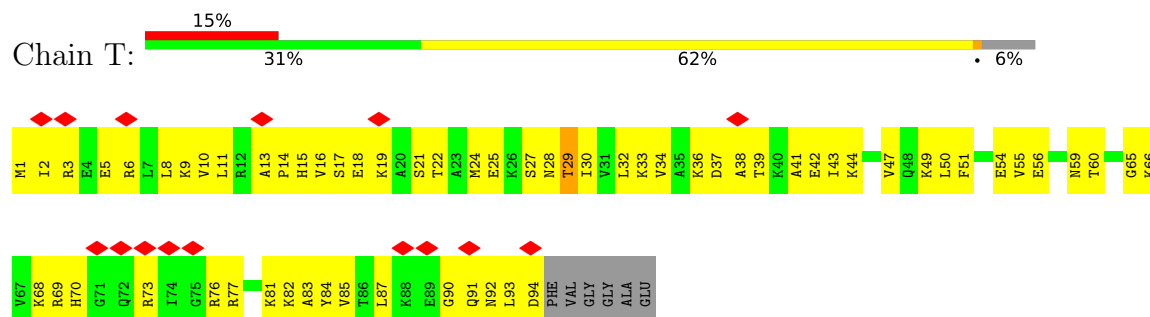
• Molecule 26: 50S RIBOSOMAL PROTEIN L21



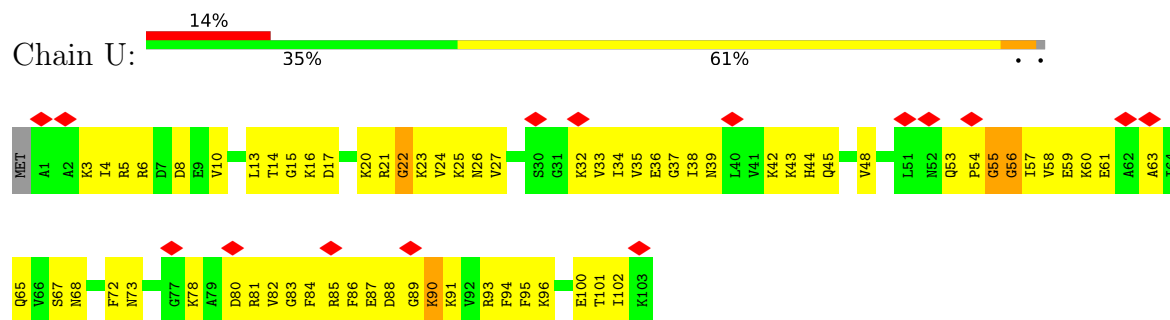
• Molecule 27: 50S RIBOSOMAL PROTEIN L22



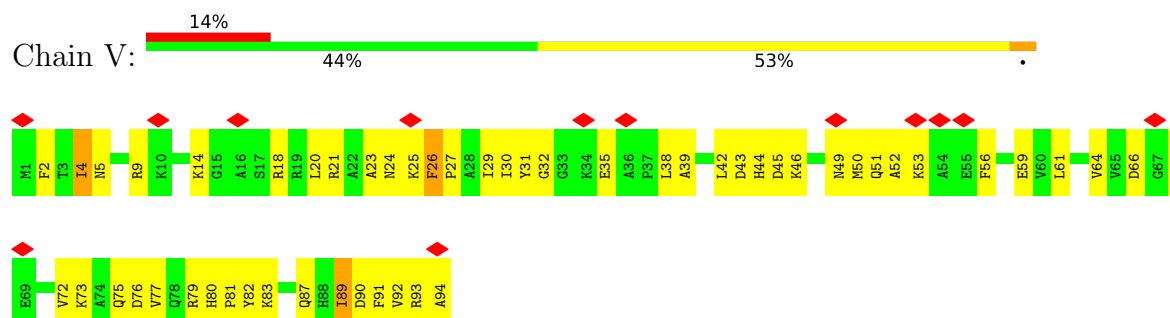
• Molecule 28: 50S RIBOSOMAL PROTEIN L23



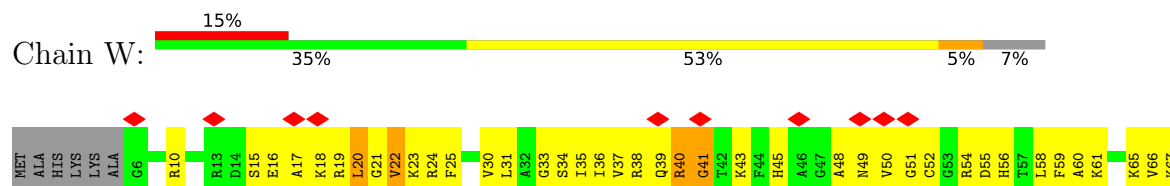
• Molecule 29: 50S RIBOSOMAL PROTEIN L24



• Molecule 30: 50S RIBOSOMAL PROTEIN L25

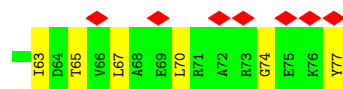
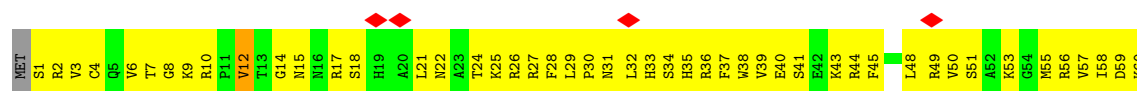


• Molecule 31: 50S RIBOSOMAL PROTEIN L27

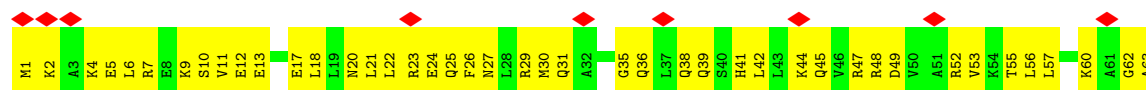




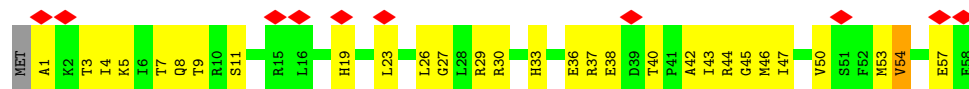
• Molecule 32: 50S RIBOSOMAL PROTEIN L28



• Molecule 33: 50S RIBOSOMAL PROTEIN L29



• Molecule 34: 50S RIBOSOMAL PROTEIN L30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	384206	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
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	75000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	5.850	Depositor
Minimum map value	-2.336	Depositor
Average map value	0.040	Depositor
Map value standard deviation	0.416	Depositor
Recommended contour level	1.4	Depositor
Map size ($\text{\AA}$)	349.77, 349.77, 349.77	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1659, 1.1659, 1.1659	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GNP

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	0.84	0/450	1.09	2/599 (0.3%)
2	1	0.78	1/417 (0.2%)	1.05	4/556 (0.7%)
3	2	0.96	0/380	1.26	4/498 (0.8%)
4	3	0.91	0/513	1.15	2/676 (0.3%)
5	4	0.84	0/303	1.13	0/397
6	5	0.50	0/1748	1.01	8/2355 (0.3%)
7	6	0.76	0/3456	1.18	20/4675 (0.4%)
8	7	0.56	1/1245 (0.1%)	0.97	2/1677 (0.1%)
9	A	0.47	0/2800	0.47	0/4367
10	B	0.55	0/69796	0.51	0/108888
11	C	0.85	1/2122 (0.0%)	1.14	11/2854 (0.4%)
12	D	0.87	0/1586	1.11	6/2134 (0.3%)
13	E	0.81	0/1571	1.06	4/2113 (0.2%)
14	F	0.60	0/1444	1.07	9/1937 (0.5%)
15	G	0.78	0/1343	1.08	5/1816 (0.3%)
16	H	0.61	0/1122	1.00	2/1515 (0.1%)
17	I	0.58	0/1046	1.10	3/1410 (0.2%)
18	J	0.87	0/1152	1.13	8/1551 (0.5%)
19	K	0.83	1/940 (0.1%)	1.23	7/1260 (0.6%)
20	L	0.80	0/1054	1.18	9/1403 (0.6%)
21	M	0.91	0/1093	1.15	7/1460 (0.5%)
22	N	0.91	1/974 (0.1%)	1.12	5/1303 (0.4%)
23	O	0.77	0/902	1.11	1/1209 (0.1%)
24	P	0.78	0/929	1.08	5/1242 (0.4%)
25	Q	0.98	0/960	1.15	2/1278 (0.2%)
26	R	0.76	0/829	1.11	5/1107 (0.5%)
27	S	0.95	0/864	1.24	7/1156 (0.6%)
28	T	0.83	1/745 (0.1%)	1.15	2/996 (0.2%)
29	U	0.75	1/788 (0.1%)	1.16	6/1053 (0.6%)
30	V	0.82	0/766	1.18	4/1025 (0.4%)
31	W	0.88	0/603	1.19	4/797 (0.5%)
32	X	0.84	0/635	1.04	1/848 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.77	0/510	0.98	0/677
34	Z	0.84	0/453	1.15	2/605 (0.3%)
All	All	0.63	7/105539 (0.0%)	0.73	157/157437 (0.1%)

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
6	5	0	1
13	E	0	1
14	F	0	1
24	P	0	1
25	Q	0	1
All	All	0	5

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	C	271	SER	C-N	-7.49	1.22	1.33
29	U	102	ILE	C-N	-7.40	1.23	1.33
28	T	93	LEU	C-N	-7.37	1.23	1.33
2	1	52	LYS	C-N	-7.30	1.23	1.33
22	N	120	GLU	C-N	-7.10	1.23	1.33

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	6	372	LEU	CA-C-N	13.63	134.42	120.38
7	6	372	LEU	C-N-CA	13.63	134.42	120.38
18	J	4	PHE	N-CA-C	-9.70	98.72	111.71
30	V	26	PHE	CA-C-N	9.13	129.18	119.78
30	V	26	PHE	C-N-CA	9.13	129.18	119.78

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	5	59	VAL	Peptide
13	E	59	PRO	Peptide

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Mol	Chain	Res	Type	Group
14	F	76	PHE	Peptide
24	P	14	GLN	Peptide
25	Q	101	ASP	Peptide

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	0	444	0	461	53	0
2	1	410	0	440	41	0
3	2	377	0	418	43	0
4	3	504	0	574	56	0
5	4	302	0	343	36	0
6	5	1733	0	1823	208	0
7	6	3403	0	3433	407	0
8	7	1231	0	1282	128	0
9	A	2504	0	1271	247	0
10	B	62317	0	31345	6174	0
11	C	2083	0	2157	255	0
12	D	1565	0	1616	240	0
13	E	1552	0	1619	132	0
14	F	1420	0	1460	172	0
15	G	1323	0	1374	140	0
16	H	1111	0	1148	200	0
17	I	1032	0	1088	148	0
18	J	1129	0	1162	153	0
19	K	931	0	1003	117	0
20	L	1045	0	1117	124	0
21	M	1074	0	1157	110	0
22	N	961	0	1000	110	0
23	O	892	0	923	133	0
24	P	917	0	965	107	0
25	Q	947	0	1022	144	0
26	R	816	0	839	112	0
27	S	857	0	922	102	0
28	T	739	0	807	76	0
29	U	780	0	834	90	0
30	V	753	0	780	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	W	596	0	610	95	0
32	X	625	0	655	94	0
33	Y	509	0	543	56	0
34	Z	449	0	491	25	0
35	6	32	0	13	23	0
36	6	1	0	0	0	0
All	All	97364	0	66695	9177	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 58.

The worst 5 of 9177 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)
16:H:68:ARG:CD	16:H:132:PHE:CE1	1.84	1.55
16:H:68:ARG:HG3	16:H:132:PHE:CD2	1.40	1.55
16:H:68:ARG:HG3	16:H:132:PHE:CE2	1.37	1.53
16:H:68:ARG:HD2	16:H:132:PHE:CE1	1.43	1.52
7:6:365:VAL:CG2	7:6:405:ARG:NH2	1.69	1.43

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	47/48 (98%)	47 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
6	5	181/181 (100%)	181 (100%)	0	100	100
7	6	364/364 (100%)	361 (99%)	3 (1%)	73	77
8	7	123/123 (100%)	123 (100%)	0	100	100
11	C	216/218 (99%)	216 (100%)	0	100	100
12	D	164/164 (100%)	163 (99%)	1 (1%)	78	80
13	E	165/165 (100%)	165 (100%)	0	100	100
14	F	149/150 (99%)	149 (100%)	0	100	100
15	G	137/138 (99%)	137 (100%)	0	100	100
16	H	114/114 (100%)	113 (99%)	1 (1%)	70	76
17	I	109/110 (99%)	109 (100%)	0	100	100
18	J	116/116 (100%)	116 (100%)	0	100	100
19	K	102/104 (98%)	102 (100%)	0	100	100
20	L	102/103 (99%)	102 (100%)	0	100	100
21	M	109/109 (100%)	109 (100%)	0	100	100
22	N	100/103 (97%)	100 (100%)	0	100	100
23	O	86/87 (99%)	86 (100%)	0	100	100
24	P	99/100 (99%)	99 (100%)	0	100	100
25	Q	89/90 (99%)	88 (99%)	1 (1%)	65	74
26	R	84/84 (100%)	84 (100%)	0	100	100
27	S	93/93 (100%)	92 (99%)	1 (1%)	65	74
28	T	80/84 (95%)	80 (100%)	0	100	100
29	U	83/85 (98%)	83 (100%)	0	100	100
30	V	78/78 (100%)	78 (100%)	0	100	100
31	W	59/63 (94%)	59 (100%)	0	100	100
32	X	67/68 (98%)	67 (100%)	0	100	100
33	Y	55/55 (100%)	55 (100%)	0	100	100
34	Z	48/49 (98%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3387/3419 (99%)	3380 (100%)	7 (0%)	85 85

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	D	151	THR
16	H	68	ARG
27	S	71	VAL
25	Q	56	PHE
7	6	365	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
22	N	81	ASN
28	T	28	ASN
24	P	51	ASN
26	R	86	GLN
30	V	5	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	2902/2903 (99%)	1015 (34%)	56 (1%)
9	A	116/120 (96%)	35 (30%)	2 (1%)
All	All	3018/3023 (99%)	1050 (34%)	58 (1%)

5 of 1050 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	7	G
9	A	11	C
9	A	13	G
9	A	14	U
9	A	15	A

5 of 58 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	1385	A

Continued on next page...

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Mol	Chain	Res	Type
10	B	2810	A
10	B	1779	U
10	B	2808	G
10	B	2389	G

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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	GNP	6	527	36	34,34,34	2.25	8 (23%)	47,54,54	1.24	6 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	GNP	6	527	36	-	4/18/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	6	527	GNP	PA-O3A	-7.99	1.50	1.59
35	6	527	GNP	PB-O3A	-7.13	1.50	1.59
35	6	527	GNP	PB-O2B	-3.54	1.47	1.56
35	6	527	GNP	PG-O1G	3.03	1.50	1.46
35	6	527	GNP	PG-N3B	-2.35	1.57	1.63

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	6	527	GNP	O2B-PB-O1B	3.66	117.71	109.87
35	6	527	GNP	O3G-PG-O1G	-3.33	105.11	113.45
35	6	527	GNP	O2G-PG-O3G	3.07	115.85	107.59
35	6	527	GNP	C2'-C3'-C4'	-2.96	96.89	102.61
35	6	527	GNP	C2'-C1'-N9	-2.86	105.29	113.25

There are no chirality outliers.

All (4) torsion outliers are listed below:

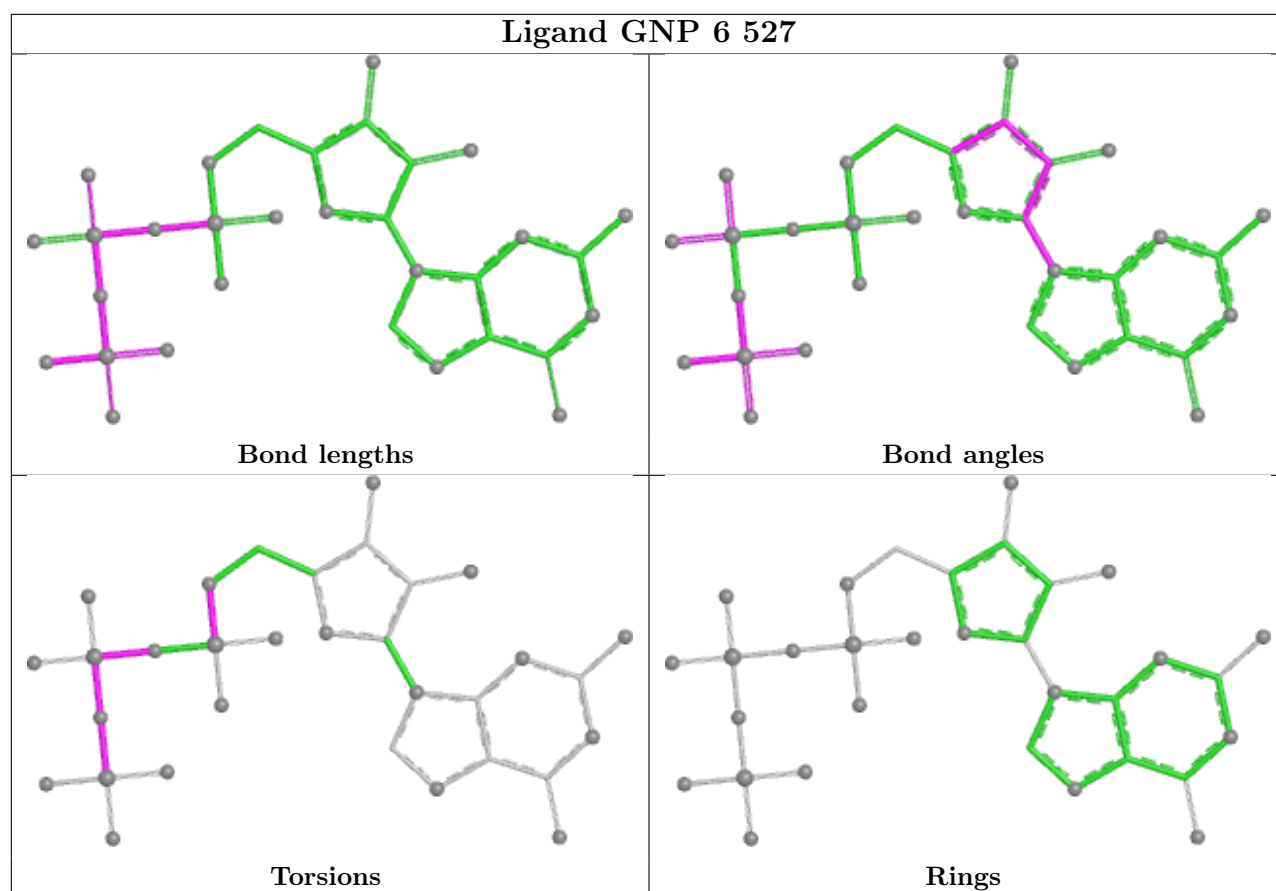
Mol	Chain	Res	Type	Atoms
35	6	527	GNP	PB-N3B-PG-O1G
35	6	527	GNP	PG-N3B-PB-O1B
35	6	527	GNP	C5'-O5'-PA-O1A
35	6	527	GNP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	6	527	GNP	23	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

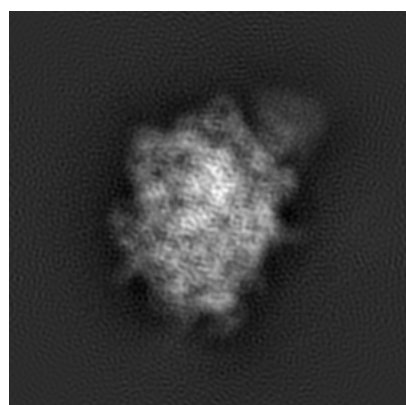
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3133. These allow visual inspection of the internal detail of the map and identification of artifacts.

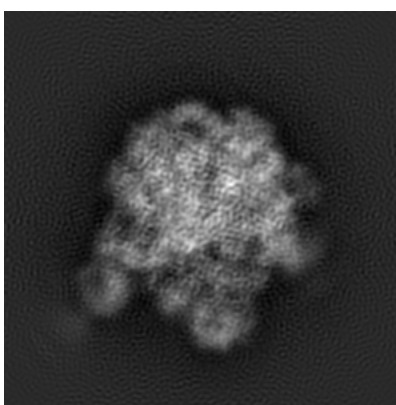
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

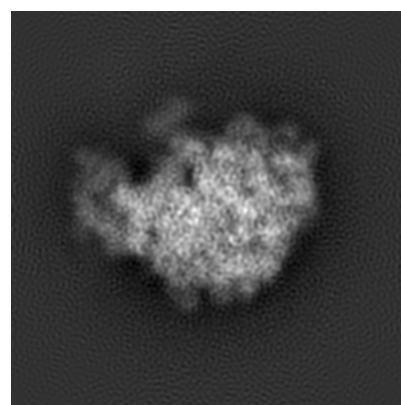
6.1.1 Primary map



X



Y

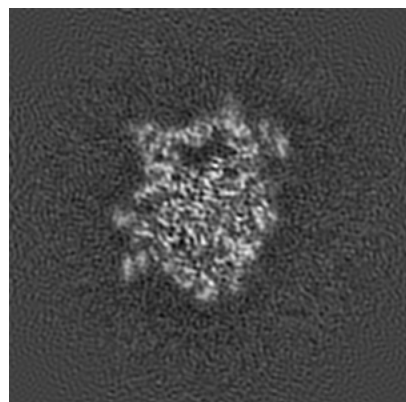


Z

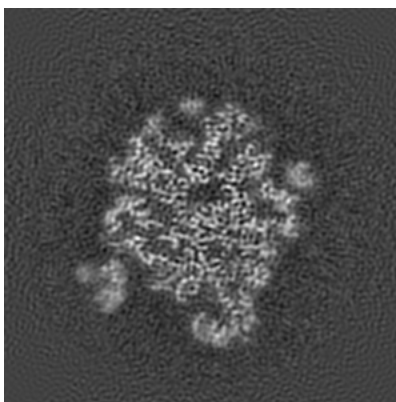
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

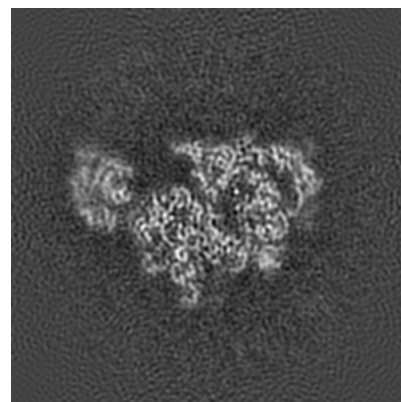
6.2.1 Primary map



X Index: 150



Y Index: 150

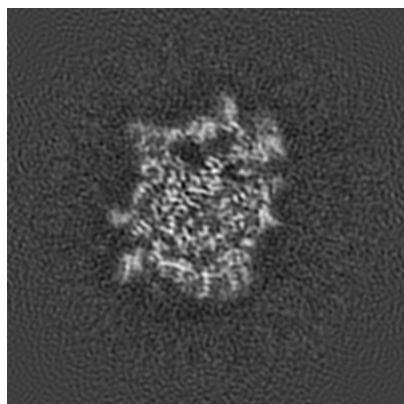


Z Index: 150

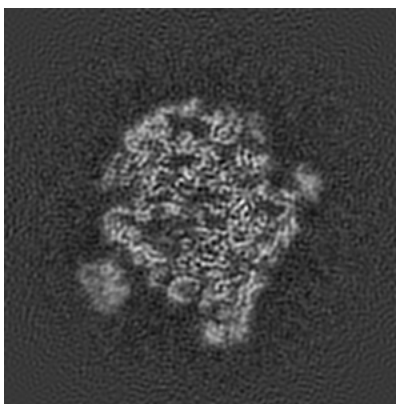
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

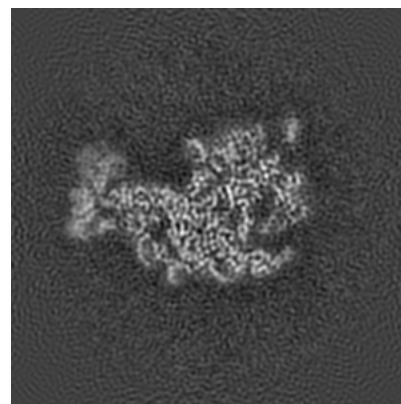
6.3.1 Primary map



X Index: 153



Y Index: 155

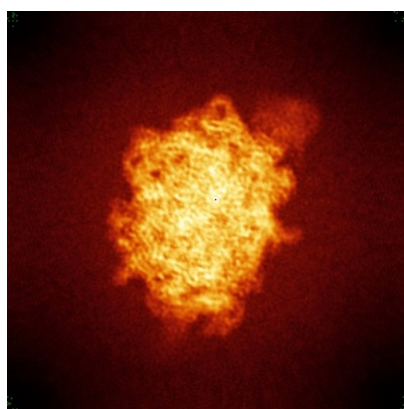


Z Index: 164

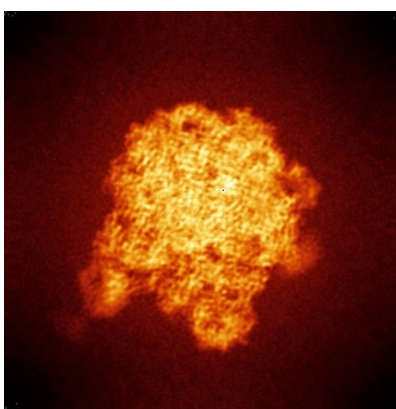
The images above show the largest variance slices of the map in three orthogonal directions.

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

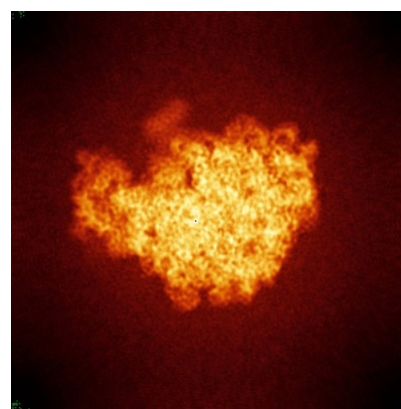
6.4.1 Primary map



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

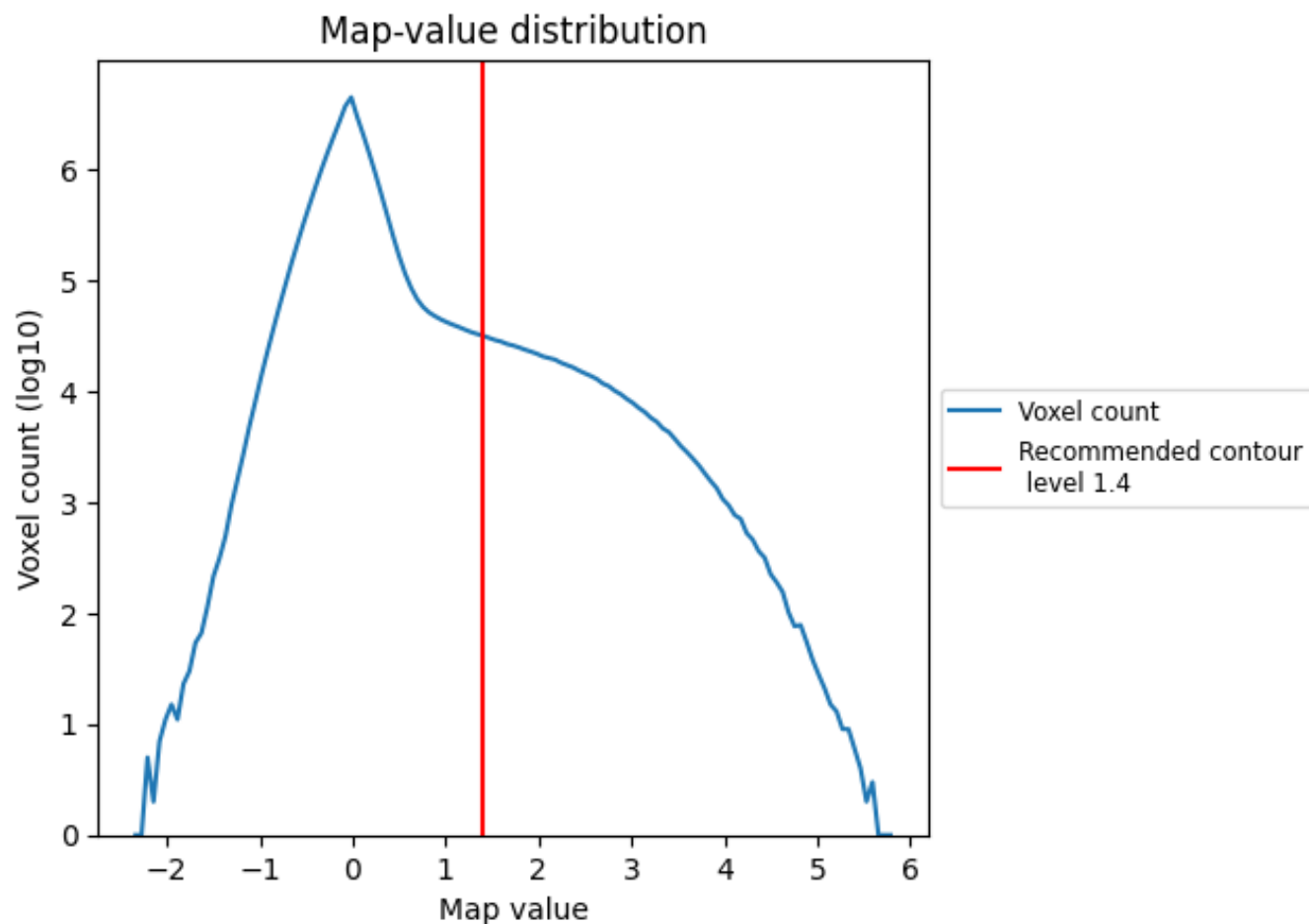
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

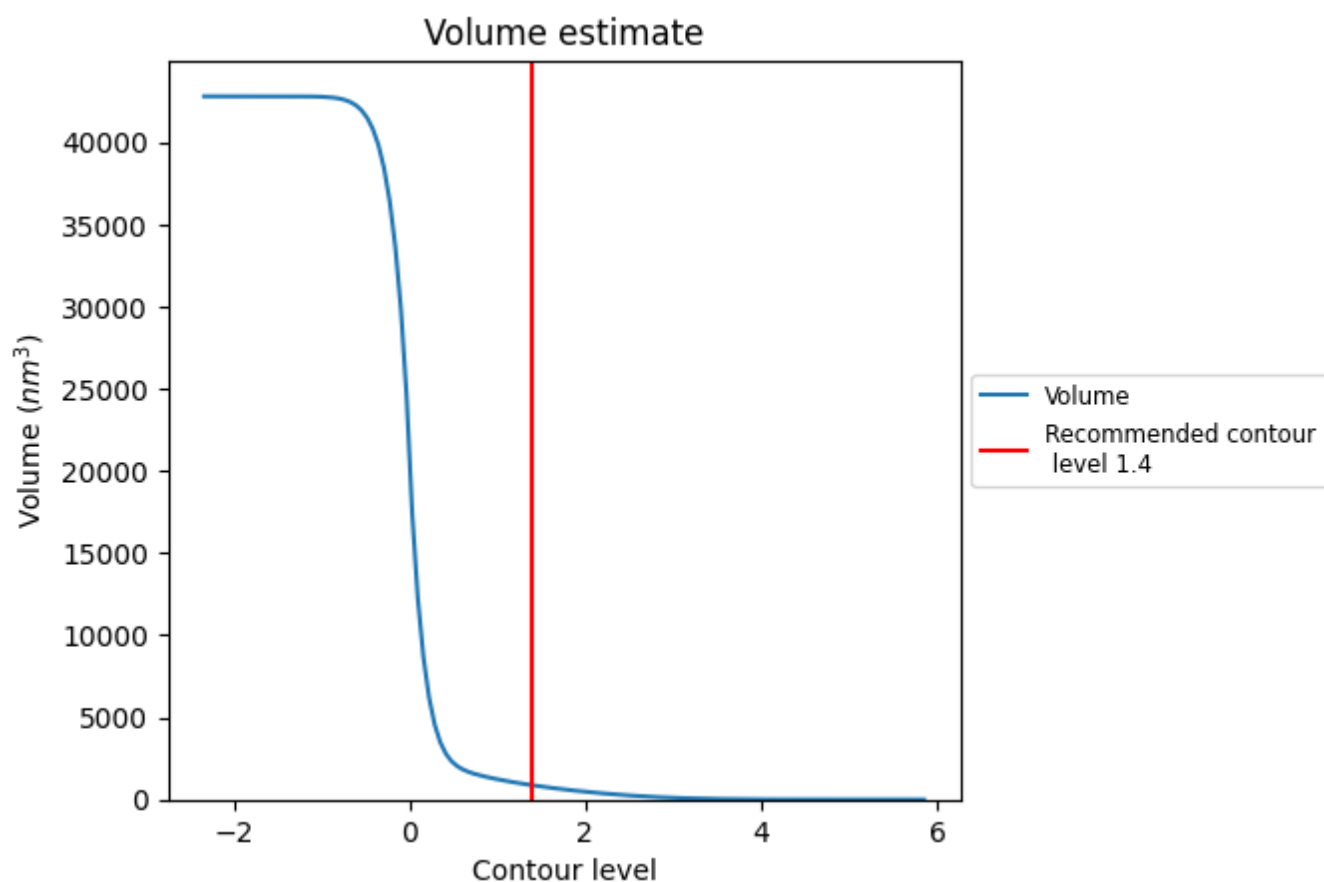
This section contains the results of statistical analysis of the map.

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.

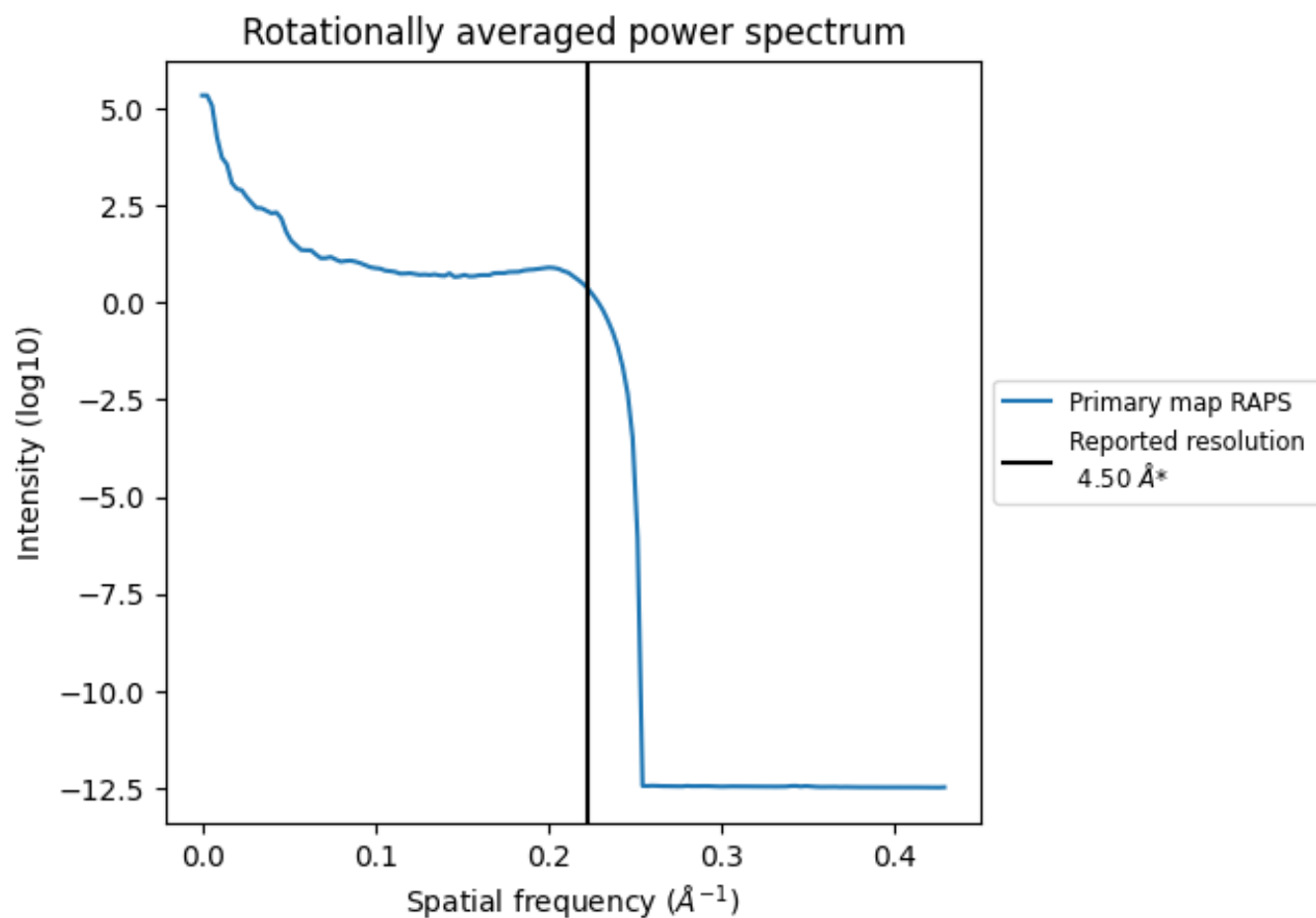
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 869 nm³; this corresponds to an approximate mass of 785 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 0.222 $\text{\AA}^{-1}$

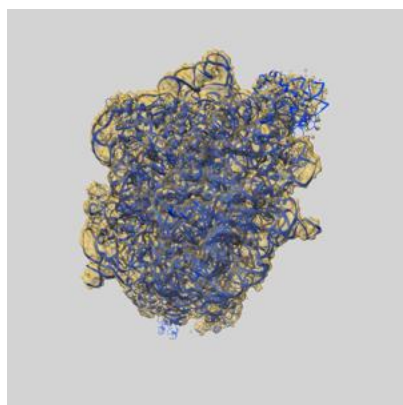
8 Fourier-Shell correlation

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

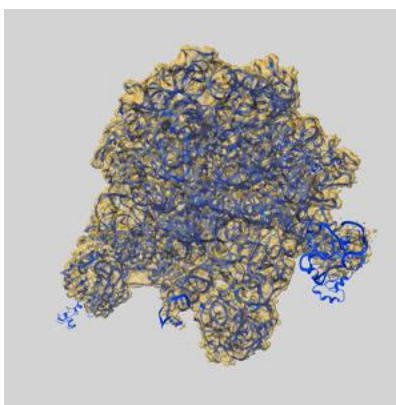
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3133 and PDB model 5ADY. Per-residue inclusion information can be found in section [3](#) on page [12](#).

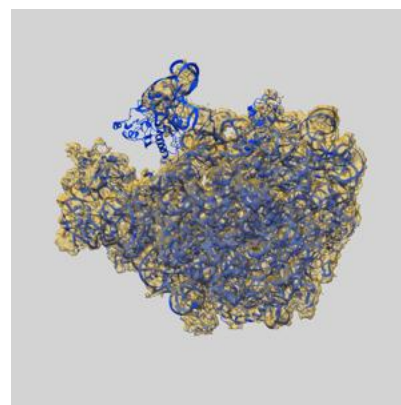
9.1 Map-model overlay [i](#)



X



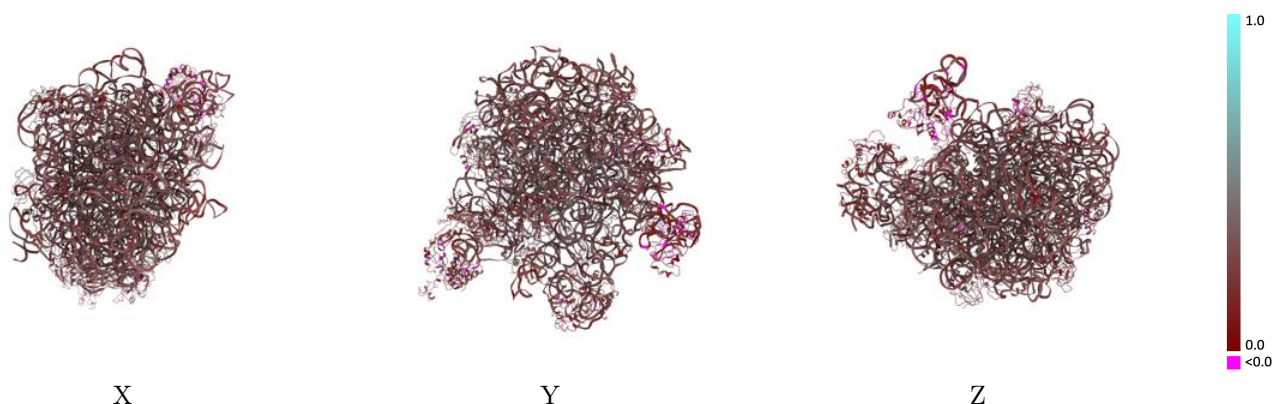
Y



Z

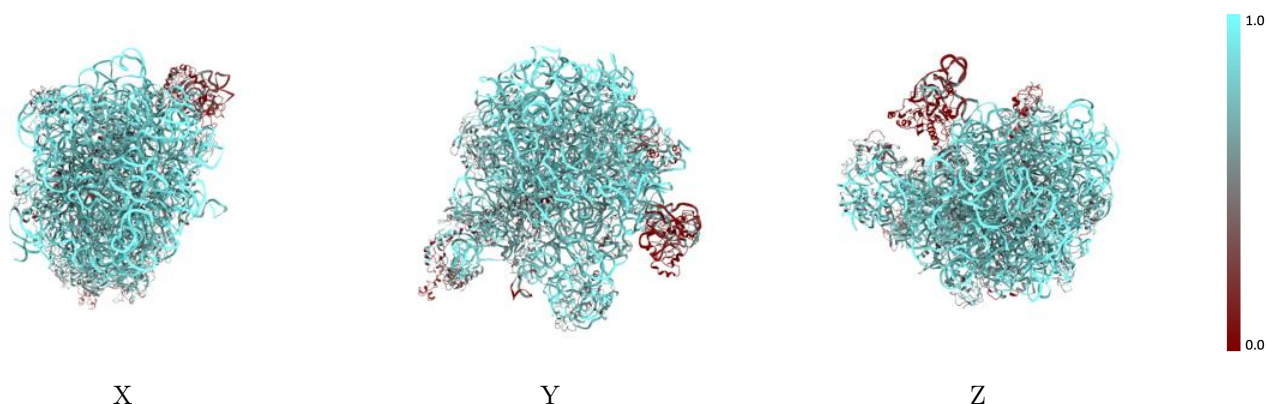
The images above show the 3D surface view of the map at the recommended contour level 1.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



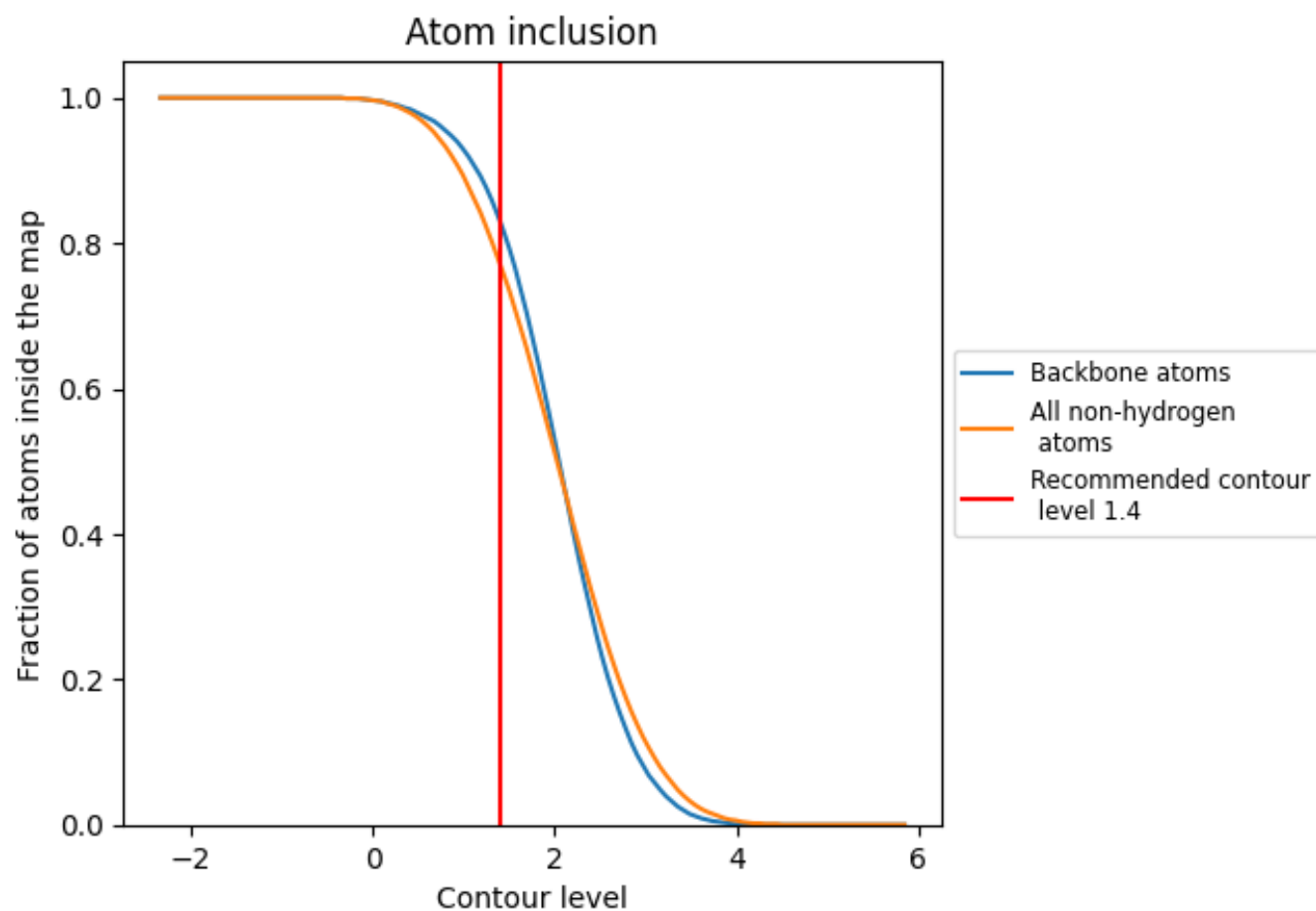
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 77% 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 (1.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7710	 0.2890
0	 0.6660	 0.2990
1	 0.5420	 0.2310
2	 0.6250	 0.2920
3	 0.6350	 0.3150
4	 0.6230	 0.2650
5	 0.0560	 0.1520
6	 0.5360	 0.2530
7	 0.2290	 0.2080
A	 0.8950	 0.2860
B	 0.8720	 0.3020
C	 0.6840	 0.2940
D	 0.6630	 0.2870
E	 0.5540	 0.2820
F	 0.5940	 0.2280
G	 0.6170	 0.2780
H	 0.2260	 0.2040
I	 0.4870	 0.2160
J	 0.6160	 0.2920
K	 0.6410	 0.2870
L	 0.6680	 0.3000
M	 0.6610	 0.3040
N	 0.6870	 0.2840
O	 0.6960	 0.2500
P	 0.6330	 0.2850
Q	 0.6760	 0.2910
R	 0.6690	 0.2970
S	 0.6300	 0.2850
T	 0.6580	 0.2900
U	 0.6470	 0.2460
V	 0.6300	 0.2810
W	 0.6190	 0.2700
X	 0.6290	 0.2970
Y	 0.6620	 0.2380
Z	 0.6160	 0.3110

