



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 06:35 AM EST

PDB ID : 3J9Z
EMDB ID : EMD-6315
Title : Activation of GTP Hydrolysis in mRNA-tRNA Translocation by Elongation Factor G
Authors : Li, W.; Liu, Z.; Koripella, R.K.; Langlois, R.; Sanyal, S.; Frank, J.
Deposited on : 2015-03-27
Resolution : 3.60 Å(reported)
Based on initial model : 3J0U

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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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) : 2.31.3

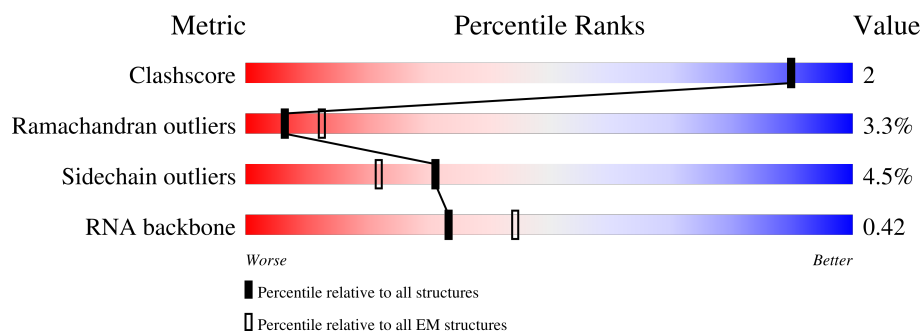
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.






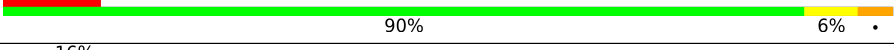


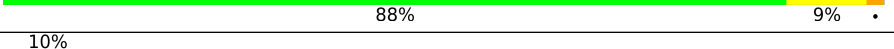
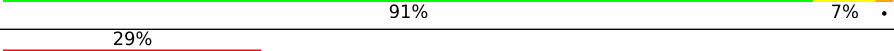
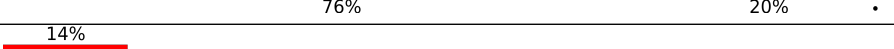
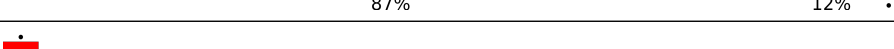
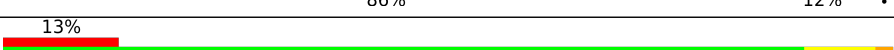

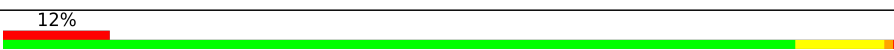

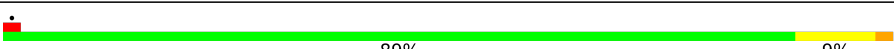

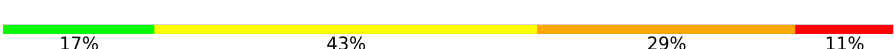



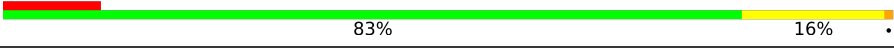
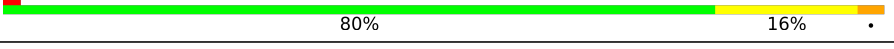

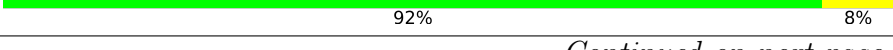

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 ≥ 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	SA	1542	
2	S6	77	
3	S7	74	
4	SJ	103	
5	SK	128	
6	SL	123	
7	SM	117	

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Mol	Chain	Length	Quality of chain
8	SN	100	
9	SO	88	
10	SP	82	
11	SQ	83	
12	SR	74	
13	SS	91	
14	SB	240	
15	ST	86	
16	SU	70	
17	SC	232	
18	SD	205	
19	SE	166	
20	SF	135	
21	SG	178	
22	SH	129	
23	SI	129	
24	S1	702	
25	LA	2904	
26	LB	120	
27	LC	234	
28	LM	114	
29	LN	272	
30	LO	117	
31	LP	103	
32	LQ	110	

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Mol	Chain	Length	Quality of chain
33	LR	100	
34	LS	103	
35	LT	94	
36	LU	84	
37	LV	77	
38	LD	164	
39	LW	63	
40	LX	209	
41	LY	58	
42	L1	56	
43	L2	54	
44	L3	46	
45	L4	64	
46	L5	38	
47	L6	201	
48	LE	141	
49	L7	178	
50	L8	176	
51	L9	149	
52	LF	142	
53	LG	123	
54	LH	144	
55	LI	136	
56	LJ	127	
57	LK	117	

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Mol	Chain	Length	Quality of chain
58	LZ	70	<p>26% 87% 9%</p>

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
59	GTP	S1	801	-	-	X	-

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 156714 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	SA	1542	Total	C	N	O	P	0	0
			33076	14754	6064	10717	1541		

- Molecule 2 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S6	77	Total	C	N	O	P	0	0
			1639	732	297	534	76		

- Molecule 3 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S7	74	Total	C	N	O	P	0	0
			1577	704	282	518	73		

- Molecule 4 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SJ	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SK	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 6 is a protein called 30S ribosomal protein S12.

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

- Molecule 7 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SM	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 8 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SN	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 9 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SO	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 10 is a protein called 30S ribosomal protein S16.

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

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SQ	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SR	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SS	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 14 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SB	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 15 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 16 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SU	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 17 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SC	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 18 is a protein called 30S ribosomal protein S4.

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

- Molecule 19 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SE	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 20 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SF	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 21 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SG	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 22 is a protein called 30S ribosomal protein S8.

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

- Molecule 23 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SI	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 24 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S1	702	Total	C	N	O	S	0	0
			5431	3420	938	1048	25		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S1	91	ALA	HIS	ENGINEERED MUTATION	UNP P0A6M8

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LA	2904	Total	C	N	O	P	0	0
			62333	27808	11464	20158	2903		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	1618	U	A	CONFLICT	GB 33357927
LA	2030	C	A	CONFLICT	GB 33357927

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LB	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 27 is a protein called 50S ribosomal protein L1.

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

- Molecule 28 is a protein called 50S ribosomal protein L19.

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

- Molecule 29 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LN	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 30 is a protein called 50S ribosomal protein L20.

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

- Molecule 31 is a protein called 50S ribosomal protein L21.

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

- Molecule 32 is a protein called 50S ribosomal protein L22.

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

- Molecule 33 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LR	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 34 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LS	103	Total	C	N	O	S	0	0
			789	498	148	143			

- Molecule 35 is a protein called 50S ribosomal protein L25.

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

- Molecule 36 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LU	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 37 is a protein called 50S ribosomal protein L28.

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

- Molecule 38 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LD	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 39 is a protein called 50S ribosomal protein L29.

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

- Molecule 40 is a protein called 50S ribosomal protein L3.

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

- Molecule 41 is a protein called 50S ribosomal protein L30.

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

- Molecule 42 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L1	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 43 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L2	54	Total	C	N	O	S	0	0
			441	284	81	76			

- Molecule 44 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L3	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 45 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	L4	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 46 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	L5	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 47 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L6	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 48 is a protein called 50S ribosomal protein L11.

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

- Molecule 49 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L7	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 50 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	L8	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 51 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	L9	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 52 is a protein called 50S ribosomal protein L13.

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

- Molecule 53 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LG	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 54 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LH	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 55 is a protein called 50S ribosomal protein L16.

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

- Molecule 56 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LJ	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

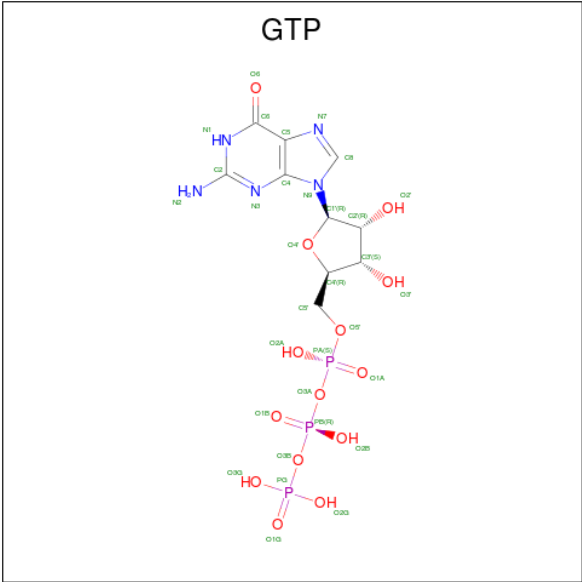
- Molecule 57 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LK	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 58 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LZ	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

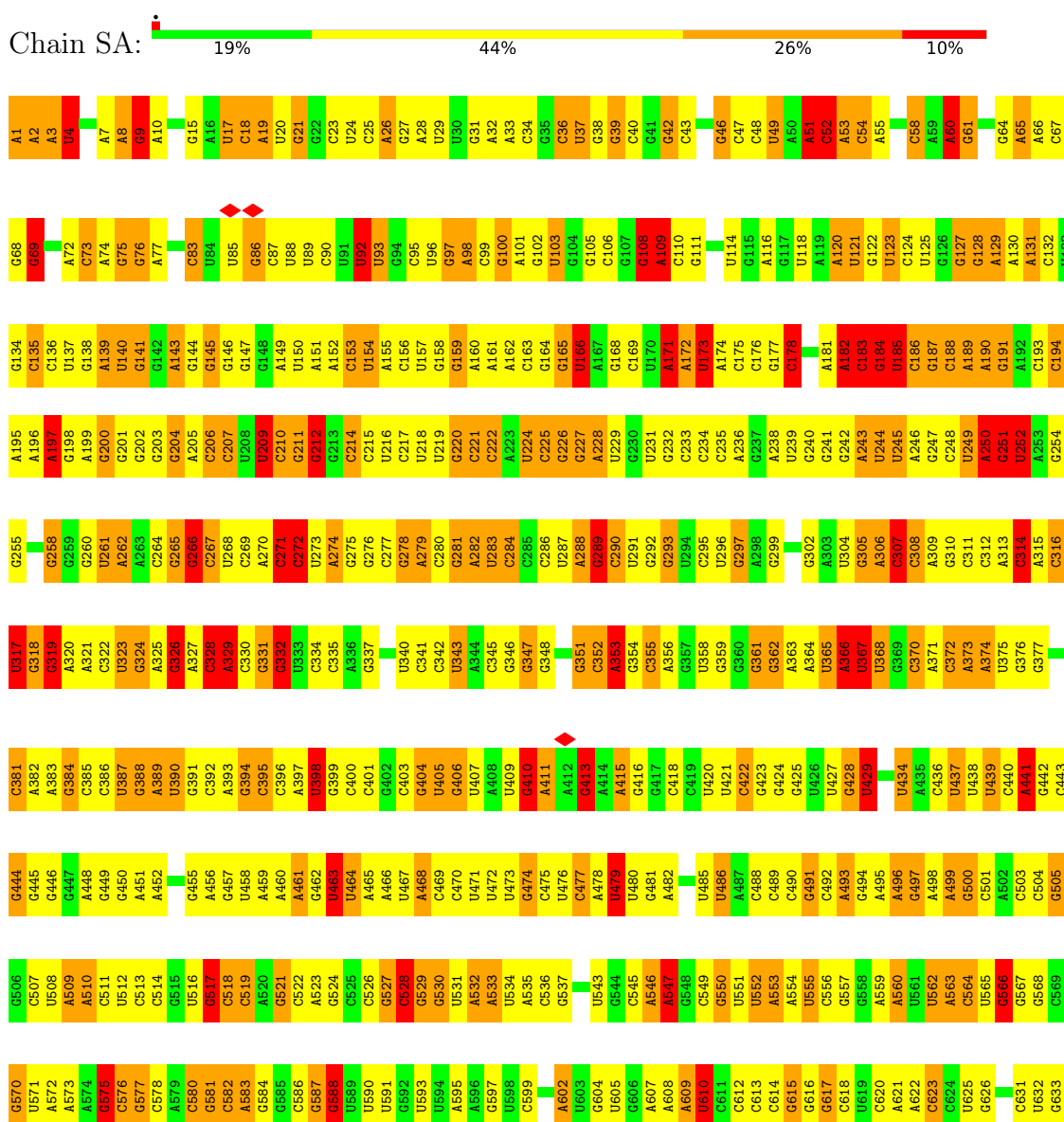


Mol	Chain	Residues	Atoms					AltConf
59	S1	1	Total	C	N	O	P	0
			32	10	5	14	3	

3 Residue-property plots

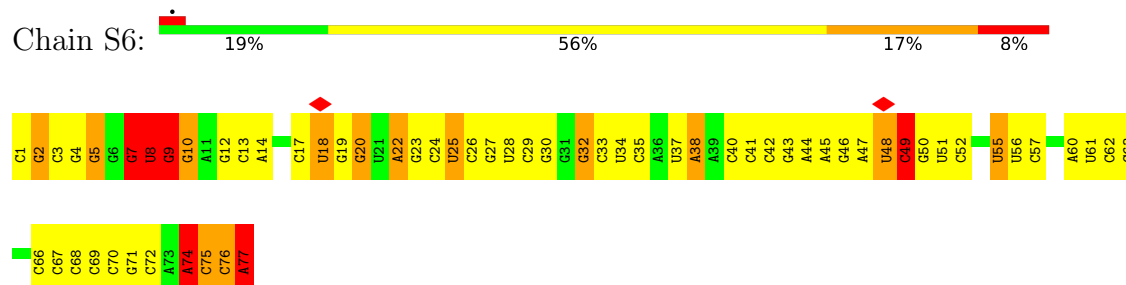
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S ribosomal RNA

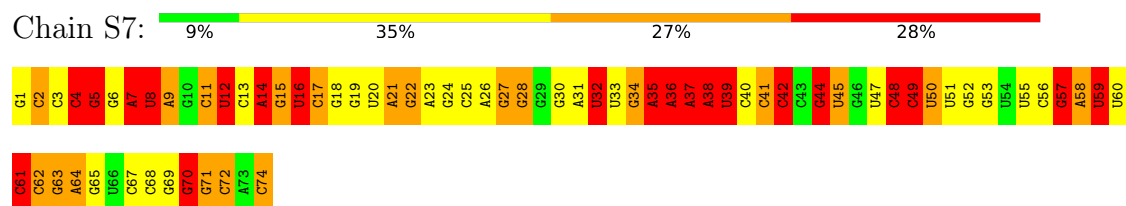




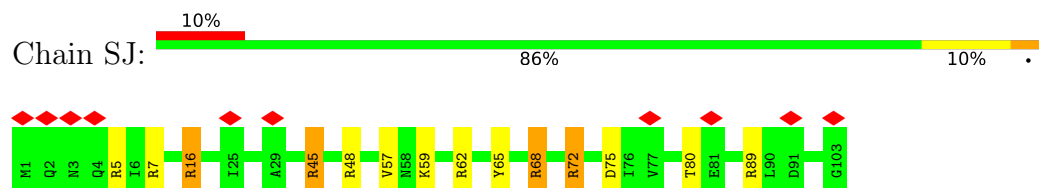
- Molecule 2: P-tRNA



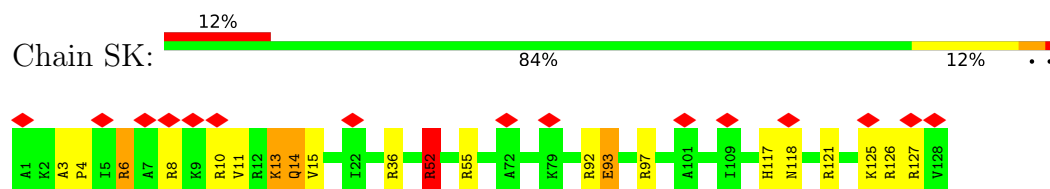
- Molecule 3: E-tRNA



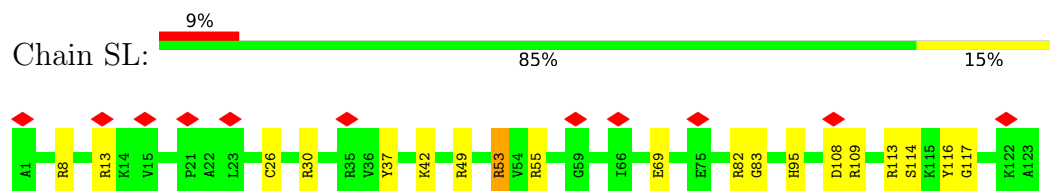
- Molecule 4: 30S ribosomal protein S10



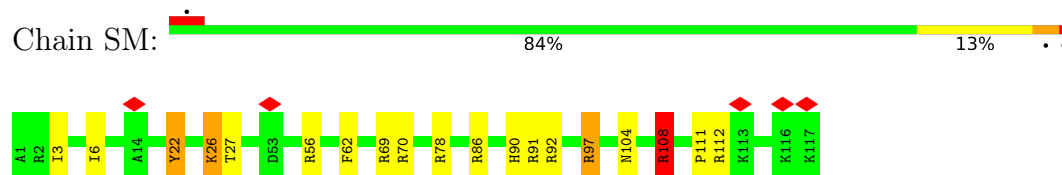
- Molecule 5: 30S ribosomal protein S11




- Molecule 6: 30S ribosomal protein S12

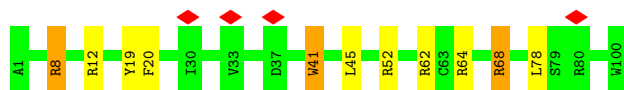


- Molecule 7: 30S ribosomal protein S13




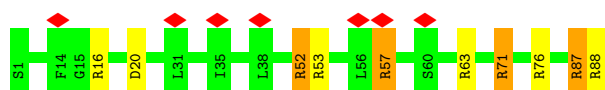
- Molecule 8: 30S ribosomal protein S14

Chain SN:  89% 8%




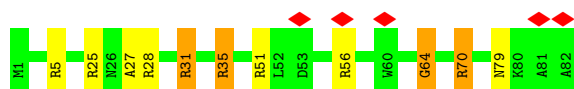
- Molecule 9: 30S ribosomal protein S15

Chain SO:  89% 7% 5%

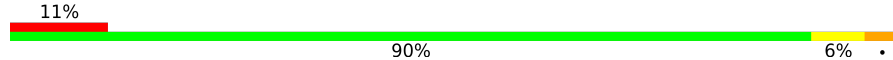


- Molecule 10: 30S ribosomal protein S16

Chain SP:  87% 9% 5%




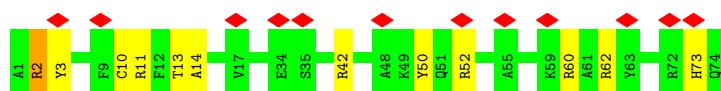
- Molecule 11: 30S ribosomal protein S17

Chain SQ:  90% 6%




- Molecule 12: 30S ribosomal protein S18

Chain SR:  84% 15%




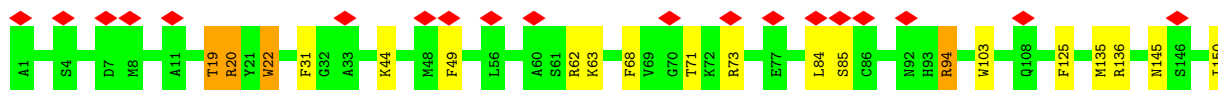
- Molecule 13: 30S ribosomal protein S19

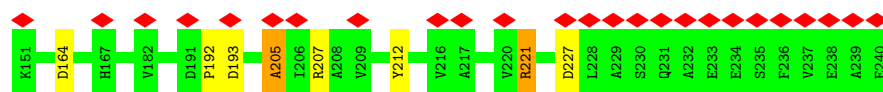
Chain SS:  84% 15%



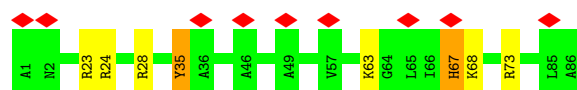
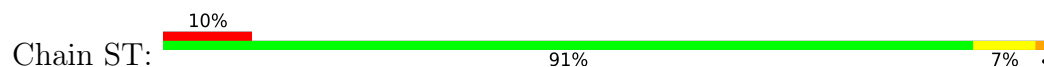
- Molecule 14: 30S ribosomal protein S2

Chain SB:  88% 9%

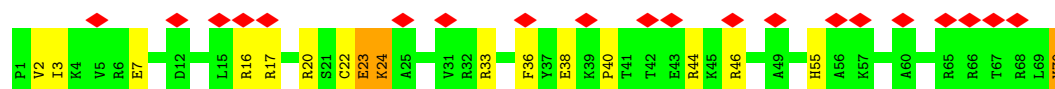
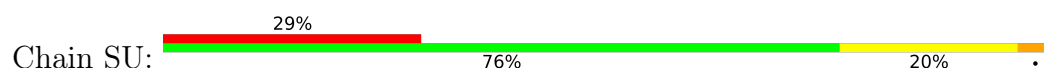




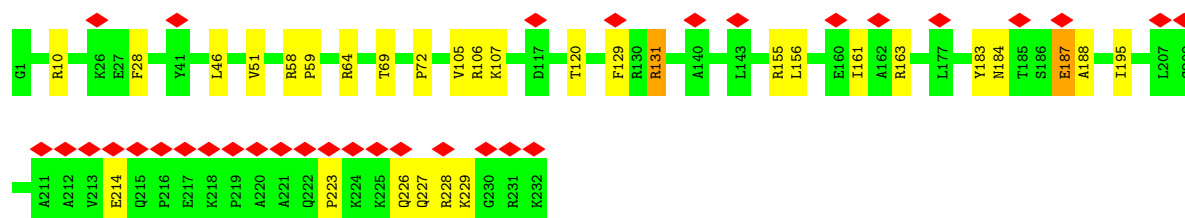
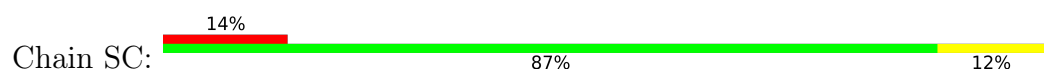
- Molecule 15: 30S ribosomal protein S20



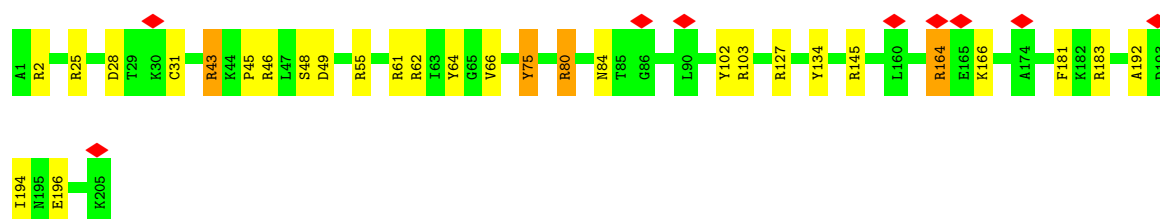
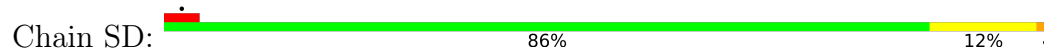
- Molecule 16: 30S ribosomal protein S21



- Molecule 17: 30S ribosomal protein S3



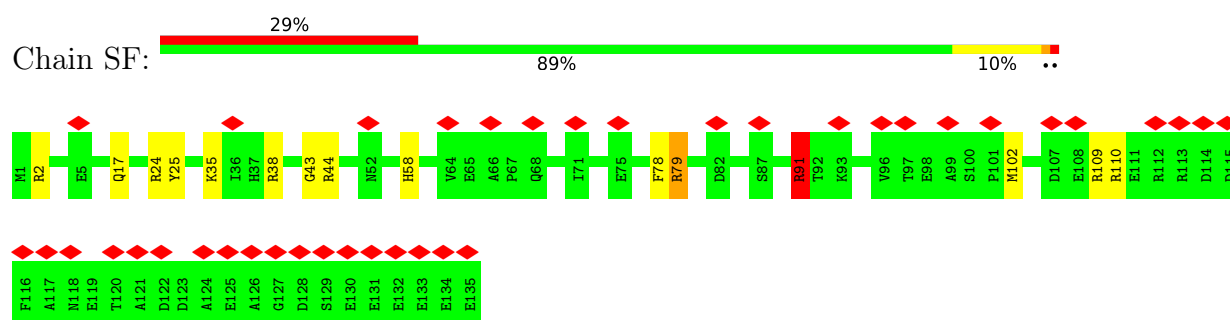
- Molecule 18: 30S ribosomal protein S4



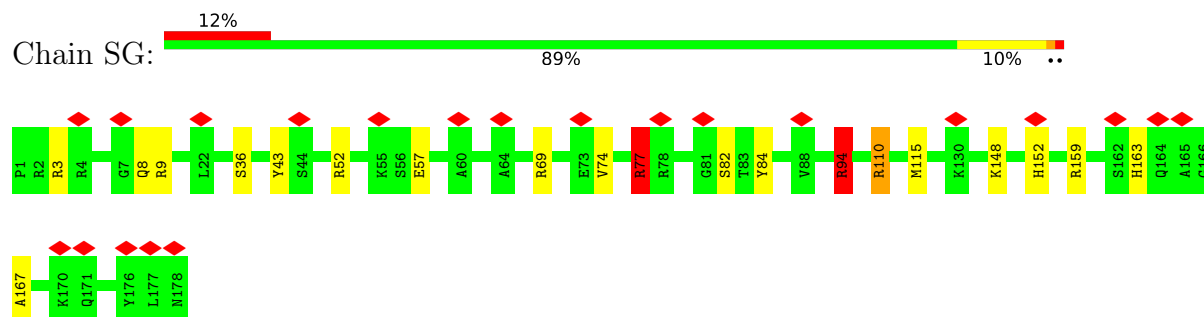
- Molecule 19: 30S ribosomal protein S5



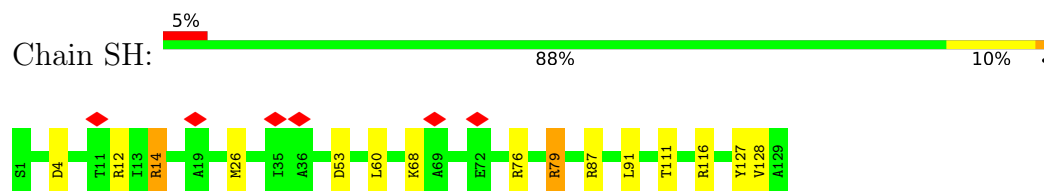
- Molecule 20: 30S ribosomal protein S6



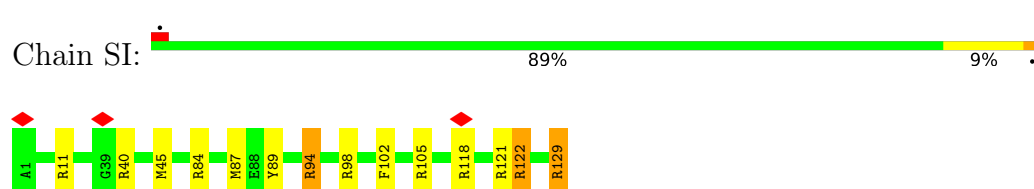
- Molecule 21: 30S ribosomal protein S7



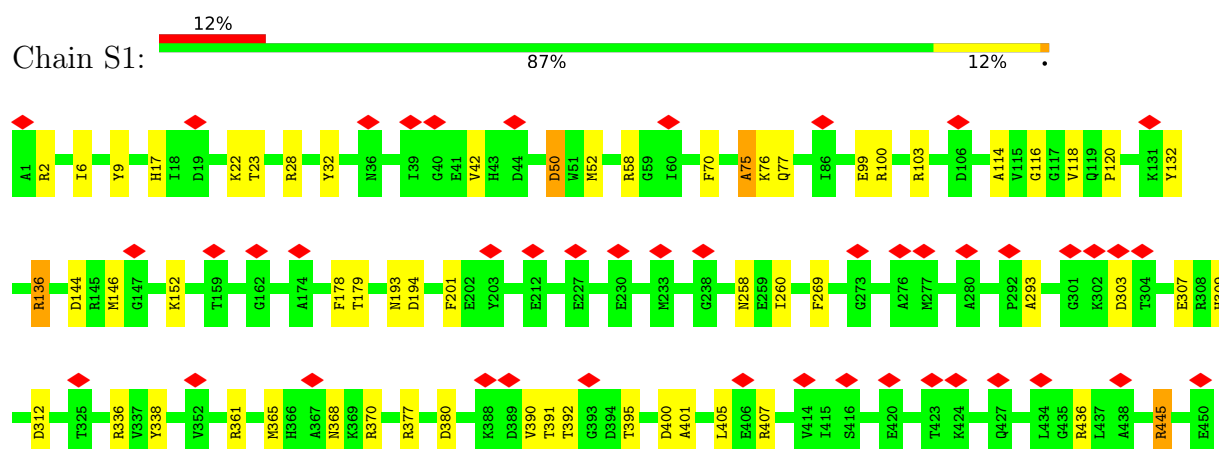
- Molecule 22: 30S ribosomal protein S8

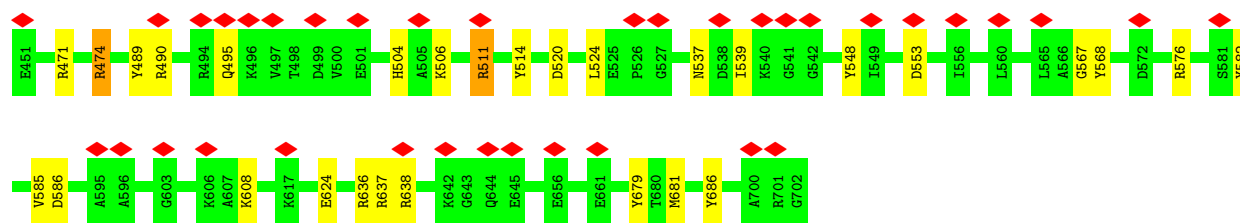


- Molecule 23: 30S ribosomal protein S9



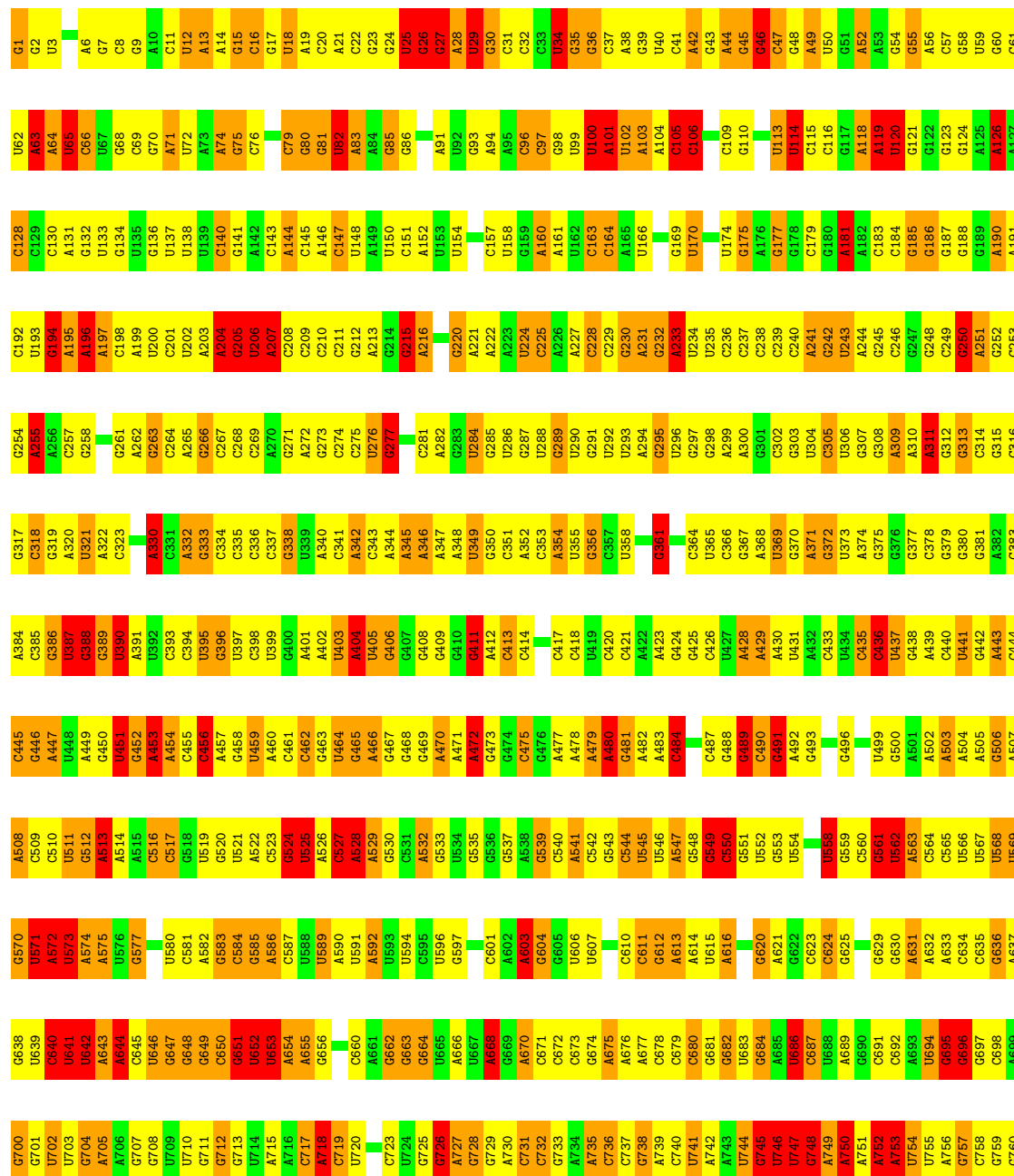
- Molecule 24: Elongation factor G





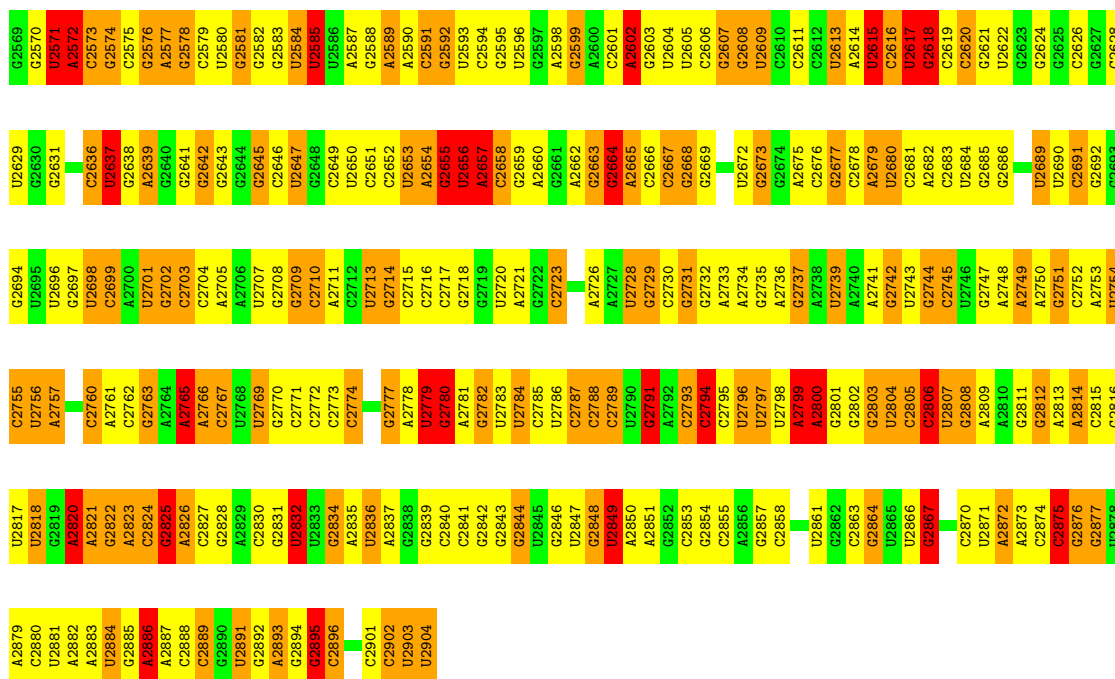
• Molecule 25: 23S ribosomal RNA

Chain LA: 17% 43% 29% 11%



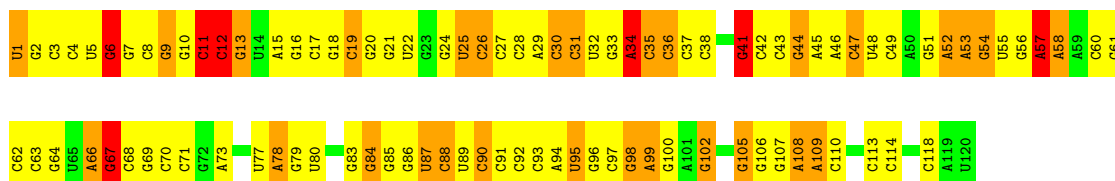
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U1578	U1579	G1514	C1386	C1447	C1385	G1324	U1262	C1200	U1141	U1077	U1011	A825	G763
A1579	A1580	G1515	C1387	G1448	C1386	U1325	U1263	U1201	U1325	U1078	U1012	G850	G764
G1581	G1582	G1516	G1388	G1449	U1326	U1326	A1264	G1202	A1142	C1079	C1013	U826	U765
C1583	C1584	G1517	G1389	C1450	A1327	A1265	G1266	U1203	A1143	A1080	A1014	U828	U766
U1585	U1586	C1518	U1390	G1452	A1328	U1267	U1267	A1204	A1144	U1081	U1015	A829	U767
G1587	G1588	C1519	U1391	A1453	U1329	U1268	A1268	U1205	C1145	U1082	G1016	G830	G769
A1590	A1591	C1520	U1392	C1454	C1330	G1269	G1269	U1083	C1146	U1083	U1019	A833	U773
C1592	C1593	G1521	A1393	U1455	G1331	C1270	C1270	A1084	A1147	A1084	A1020	G834	G774
A1594	A1595	A1522	U1394	U1457	G1332	C1271	C1271	A1086	G1149	A1086	A1021	G835	G775
U1596	U1597	U1523	A1395	U1458	G1333	A1272	A1272	G1087	C1150	G1087	G1022	G836	G776
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C1612	C1613	A1528	U1400	C1463	G1339	G1277	G1277	U1094	A1155	U1094	A1027	U842	G780
U1614	U1615	G1529	G1401	U1467	U1340	C1278	C1278	A1095	A1156	A1095	A1028	G843	A781
C1616	C1617	C1530	U1402	U1468	G1341	G1281	G1281	U1217	G1157	A1096	A1029	A844	A782
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C1621	C1622	C1532	C1404	A1470	G1343	U1283	U1283	U1219	U1159	A1098	G1031	U846	G784
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C1629	C1630	C1536	U1408	U1474	A1347	A1287	A1287	G1223	G1163	A973	U1035	C851	A788
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U1765													

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G2510	U2449	U2329	A2266	A2205	C2143	A2082	C2021	A1900	U1834	C1774	C1708	C1644
G2511	A2450	G2330	A2267	G2206	G2144	G2083	U2022	A1901	G1836	U1775	U1709	G1645
A2512	A2451	G2331	G2268	C2207	C2145	C2084	C2023	A1902	C1837	G1776		C1646
A2513	G2452	C2332	G2269	G2208	G2146	U2085	G2024	G1903	U1838	U1777	A1713	U1647
G2514	A2453	A2333	A2270	C2209	A2147	U2086	C2025	G1904	U1839	U1778	U1714	U1648
G2515	G2454	U2334	G2271	U2210	G2148	G2087	U2026	C1905	G1840	U1779	G1715	G1649
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G2517	C2456	A2336	A2273	A2212	C2150	C2089	U2028	A1966	G1842	U1781	G1717	A1652
U2518	G2457	G2337	A2274	U2213	U2151	G2091	G2029	A1968	G1843	U1782	G1718	G1651
G2458	U2519	C2338	C2275	C2214	G2152	C2092	C2030	A1969	U1844	A1784	G1719	G1652
C2520	A2459	C2339	G2276	G2215	C2153	G2093	A2031	U1970	G1845	U1785	U1720	C1656
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U2522		G2341	A2278	G2217	U2155	A2095	A2033	U1972	G1847	A1787	A1722	C1658
G2523	G2463	C2342	G2279	U2218	G2156	C2096	U2034	G1973	A1848	C1788	G1723	G1659
G2464	G2464	U2343	G2280	G2219	G2157		C2035	A1974	G1849	U1789	G1724	G1660
G2524	G2465	U2344	A2281	U2220	A2158	G1975	C2036	U1915	G1850	C1790	U1725	G1661
G2525	C2466	G2345	G2282	G2221	G2159	U1976	A2037	A1916	U1851	G1791	C1726	U1662
G2526	G2467	A2346	C2283	C2222	C2160	U1977	C2038	U1917	U1852	G1792	C1727	G1663
U2528	A2468	C2347	A2284	G2223	C2161	A1978	U2041	A1918	U1853	G1793	C1728	A1664
G2529	G2469	U2348	G2285	G2224	G2162	U1979	A2042	A1919	A1854	U1794	U1729	A1665
U2530	G2470	G2349	G2286	A2225	A2163	G1980	C2043	C1920	U1855	C1795	C1730	G1666
A2531	A2471	C2350	A2287	C2226	C2164	A1981	C2044	G1921	U1856	U1796	G1731	G1667
G2532	G2472	G2351	A2288	A2227	C2165	U1982	C2045	G1922	U1857	G1797	G1732	A1668
U2533	U2473	A2352	G2289	G2228		G1983	G2046	U1923		U1798	G1733	A1669
G2474	U2474	G2353	U2229	U2229	A2169	G1984	G2047	C1924	G1862	U1799	G1734	C1670
A2534	G2475	C2354	G2230	U2230	A2170	C1985	C2048	U1925	G1863	C1800	A1735	U1671
G2535	G2476	G2355	G2231	U2231	A2171	U1986	G2049	U1926	U1864	A1801	U1736	A1672
G2536	U2477	A2356	C2295	G2232	U2172	A1987	C2050	C1927	U1865	U1802	G1737	G1673
G2537	A2478	G2357	U2296	U2233	A2173	G1988	A2051	A1928	U1866	A1803	G1738	G1674
C2538	U2479	A2358	A2297		C2174	G1989	A2052	G1929	U1867	C1804	A1739	C1675
U2539	C2480	C2359	A2297	U2236	C2175	U1991	A2053	G1930	C1867	U1805	G1740	A1676
G2540	A2481	G2360	G2297	G2237	A2176	G1992	G2054	U1931	C1868	G1806	C1741	A1677
A2542	U2482	C2361	G2298	G2238	C2177	U1993	C2055	G1932	U1869	U1807	U1742	A1678
G2543	G2483	G2362	U2302	G2239	C2178	C1994	C2056	G1933	C1870	A1809	G1743	U1679
G2544	G2484	C2363	G2303	U2240	C2179	U1995	G2057	U1934	A1871	A1808	A1744	U1680
G2545	G2485	G2364	G2304	A2241	U2180	U1996	G2058	G1935	A1872	A1809	A1745	G1681
U2546	C2486	G2365	U2305	G2242	U2181	C1997	A2059	G1936	G1873	A1810	A1746	G1682
G2487	G2487	A2366	C2306	U2243	U2182	A1998	A2060	A1937	C1874	U1812	U1747	U1683
U2548	G2488	G2367	G2307	U2244	A2183	C1999	G2061	U1938	G1875	G1813	G1748	G1684
G2549	U2489	C2368	G2308	U2245	U2184	G2000	G2062	U1939	A1876	G1814		C1685
G2550	G2490	A2369	A2309	G2246	U2185	C2001	C2063	U1940		U1815	G1752	C1686
C2551	U2491	G2370	C2310	A2247	U2186	G2002	C2064	C1941	C1879	A1816	G1756	U1687
U2552	U2492	C2371	A2311	C2248	U2187	A2003	C2065	C1942	U1880	G1817	A1757	U1688
G2553	U2493	U2372	U2312	U2249	U2188	G2004	C2066	U1943	C1881	U1758	U1759	A1689
U2554	G2494	C2373	C2313	G2250	U2189		G2067	U1944	U1882	A1819	C1760	A1690
U2555	G2495	G2374	A2314	G2251	G2190	C2006	G2068	G1945		U1821	U1692	U1691
G2496	A2496	C2375	G2315	G2252	A2191	U2007	U2069	U1946	U1886	U1822	C1761	U1693
U2497	G2497	A2376	G2316	G2253	U2192	C2008	G2070	G1947	C1887	G1823	G1762	C1694
G2498	C2498	G2377	A2317	G2254	C2193	A2009	A2071	U1948	G1888	U1824	G1763	G1695
C2559	U2500	A2378	G2318	G2255	U2194	G2010	C2072	G1949	A1889	G1825	G1764	G1696
A2560	G2501	G2379	G2319	G2256	U2195	U2011	A2073	G1950	U1890	U1826	U1765	G1697
C2501	C2501	U2320	G2320	G2257	C2196	G2012	C2074	U1951	A1891	G1827	G1766	A1698
G2502	U2502	U2321	U2321	C2258	U2197	A2013	U2074	A1952	C1892	U1828	G1767	G1699
A2503	G2503	G2382	G2322	U2259	A2198	A2014	U2075	G1953	C1894	U1829	G1768	
G2504	U2504	C2383	G2323	C2260	A2199	A2015	U2076	A1954	C1895	A1829	U1769	G1703
G2505	G2505	U2384	U2324	C2261	A2199	U2016	A2077	U1955	C1896	G1830	G1770	C1704
U2506	G2506	C2385	C2325	U2262	C2200	U2017	C2078	U1956	G1897	U1831	C1771	A1705
A2566	G2507	A2386	U2202	G2263	U2201	G2018	U2079	U1957	U1898	C1832	A1772	C1706
G2568	G2508	U2387	U2203	C2264	U2202	A2019	A2080	C1958				



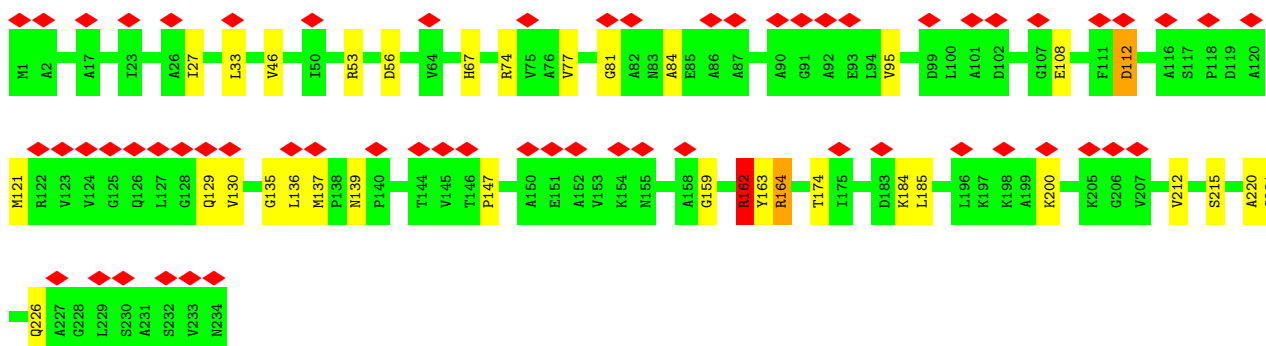
- Molecule 26: 5S ribosomal RNA

Chain LB: 19% 51% 24% 6%



- Molecule 27: 50S ribosomal protein L1

Chain LC: 26% 85% 13%

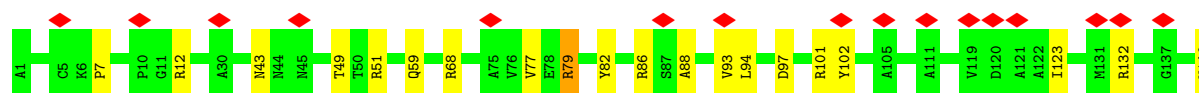
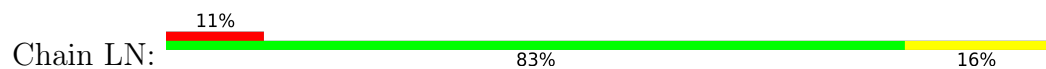


- Molecule 28: 50S ribosomal protein L19

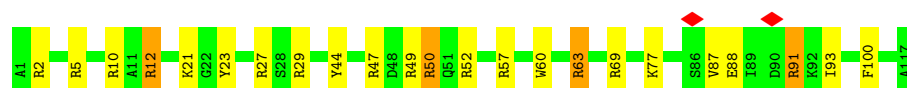
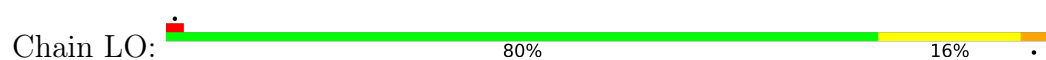
Chain LM: 9% 82% 12% 5%



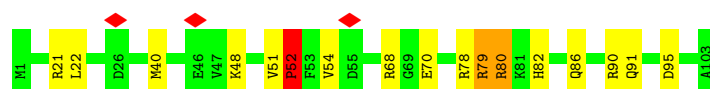
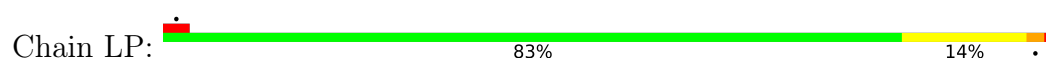
- Molecule 29: 50S ribosomal protein L2



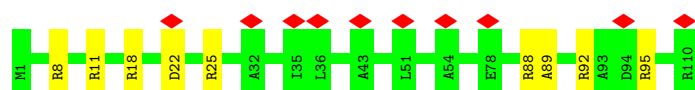
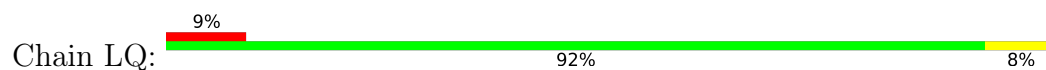
- Molecule 30: 50S ribosomal protein L20



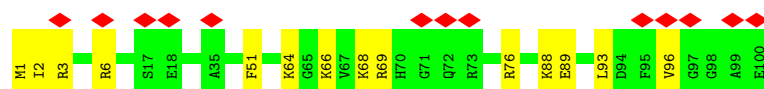
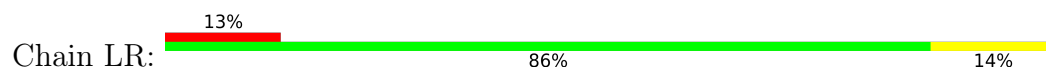
- Molecule 31: 50S ribosomal protein L21



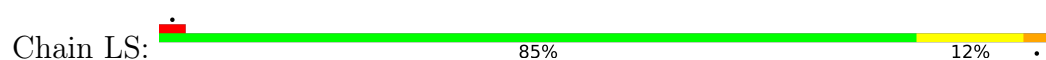
- Molecule 32: 50S ribosomal protein L22

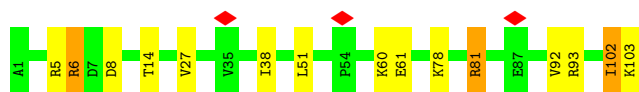


- Molecule 33: 50S ribosomal protein L23

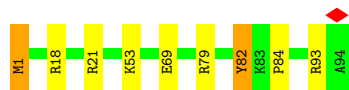
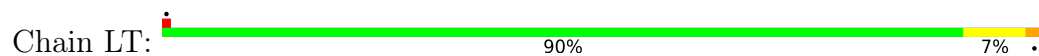


- Molecule 34: 50S ribosomal protein L24

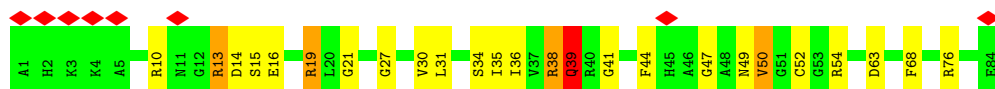




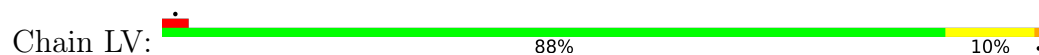
- Molecule 35: 50S ribosomal protein L25



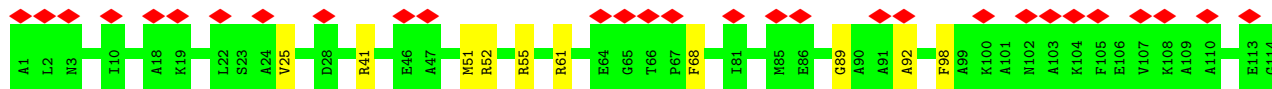
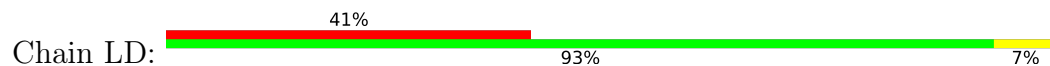
- Molecule 36: 50S ribosomal protein L27



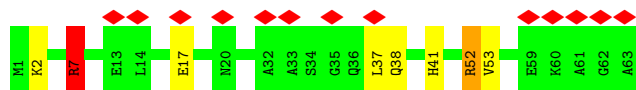
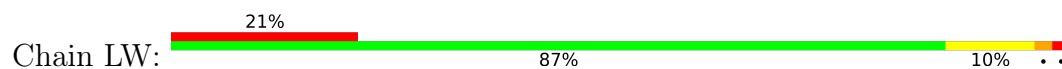
- Molecule 37: 50S ribosomal protein L28



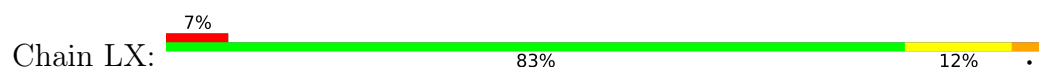
- Molecule 38: 50S ribosomal protein L10

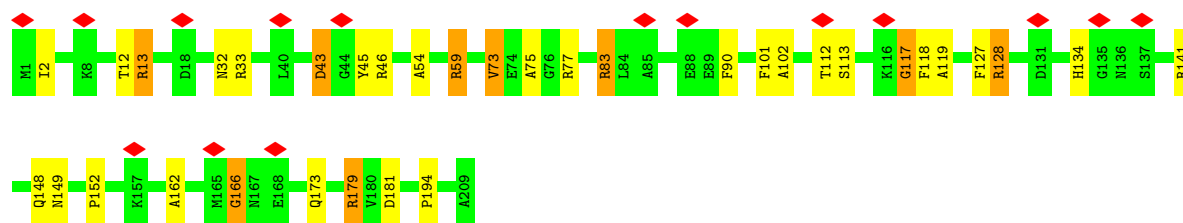


- Molecule 39: 50S ribosomal protein L29

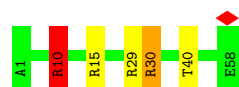


- Molecule 40: 50S ribosomal protein L3

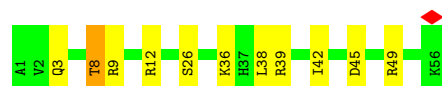
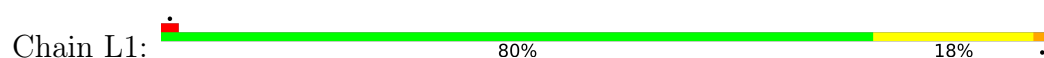




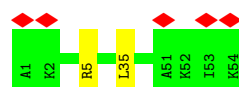
- Molecule 41: 50S ribosomal protein L30



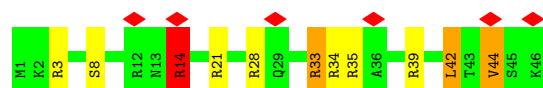
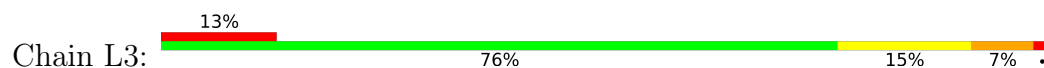
- Molecule 42: 50S ribosomal protein L32



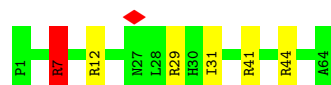
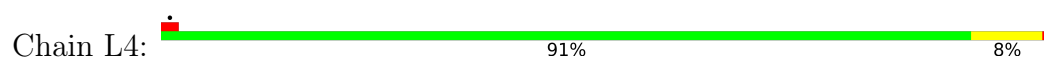
- Molecule 43: 50S ribosomal protein L33



- Molecule 44: 50S ribosomal protein L34

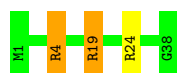


- Molecule 45: 50S ribosomal protein L35

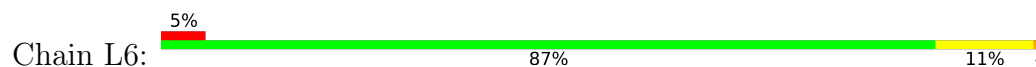


- Molecule 46: 50S ribosomal protein L36

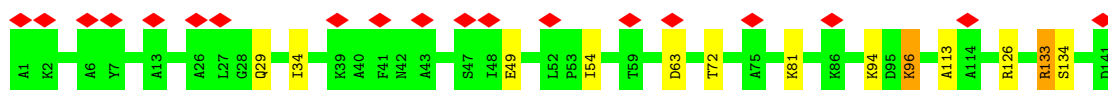




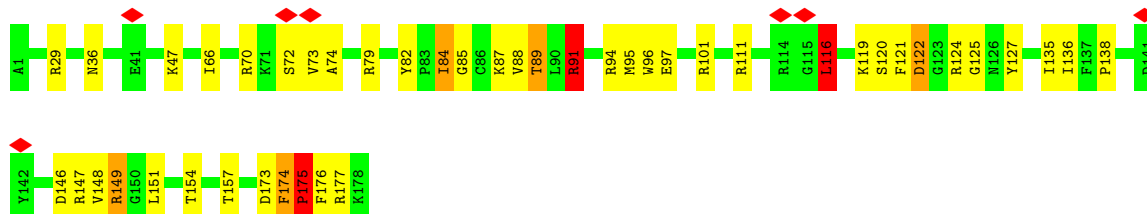
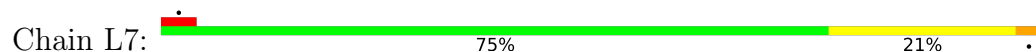
- Molecule 47: 50S ribosomal protein L4



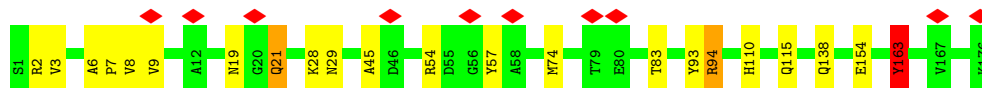
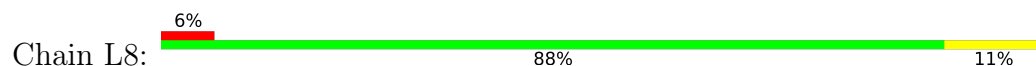
- Molecule 48: 50S ribosomal protein L11



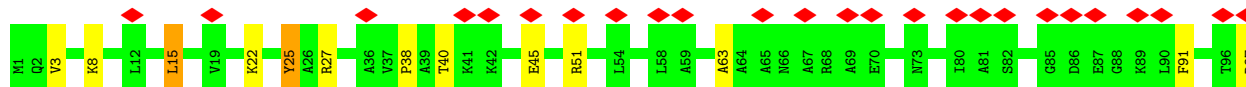
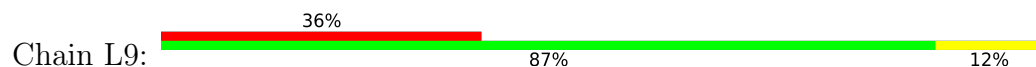
- Molecule 49: 50S ribosomal protein L5




- Molecule 50: 50S ribosomal protein L6

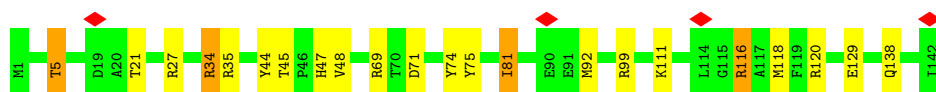


- Molecule 51: 50S ribosomal protein L9




- Molecule 52: 50S ribosomal protein L13

Chain LF:  85% 13%




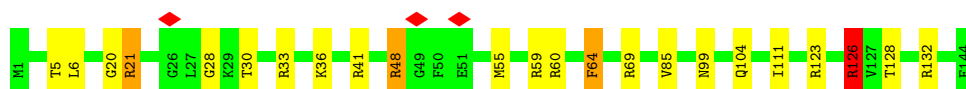
- Molecule 53: 50S ribosomal protein L14

Chain LG:  11% 82% 16%



- Molecule 54: 50S ribosomal protein L15

Chain LH:  84% 13%




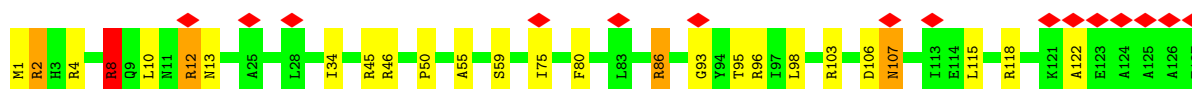
- Molecule 55: 50S ribosomal protein L16

Chain LI:  91% 7%




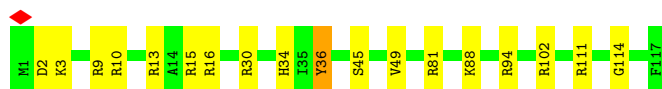
- Molecule 56: 50S ribosomal protein L17

Chain LJ:  12% 80% 17%




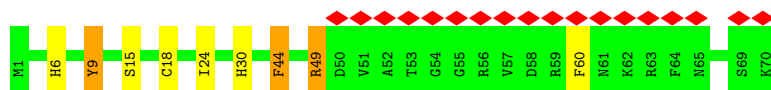
- Molecule 57: 50S ribosomal protein L18

Chain LK:  85% 15%



- Molecule 58: 50S ribosomal protein L31

Chain LZ:  26% 87% 9%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	90000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTFFIND3 and CTFIT	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	58000	Depositor
Image detector	DIRECT ELECTRON DE-12 (4k x 3k)	Depositor
Maximum map value	0.305	Depositor
Minimum map value	-0.154	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.03	Depositor
Map size (\AA)	377.99997, 377.99997, 377.99997	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	SA	1.54	172/37035 (0.5%)	1.91	1570/57774 (2.7%)
2	S6	1.44	5/1831 (0.3%)	1.81	72/2853 (2.5%)
3	S7	1.36	4/1762 (0.2%)	1.97	89/2746 (3.2%)
4	SJ	0.73	0/835	1.28	10/1127 (0.9%)
5	SK	0.75	0/982	1.30	11/1323 (0.8%)
6	SL	0.75	0/969	1.37	9/1300 (0.7%)
7	SM	0.70	0/919	1.33	10/1226 (0.8%)
8	SN	0.73	0/817	1.36	8/1088 (0.7%)
9	SO	0.70	0/724	1.35	12/966 (1.2%)
10	SP	0.73	0/659	1.41	12/884 (1.4%)
11	SQ	0.74	0/681	1.24	5/913 (0.5%)
12	SR	0.76	0/637	1.37	8/851 (0.9%)
13	SS	0.70	0/744	1.28	5/995 (0.5%)
14	SB	0.71	0/1904	1.22	16/2565 (0.6%)
15	ST	0.69	0/676	1.15	3/895 (0.3%)
16	SU	0.84	0/598	1.53	8/792 (1.0%)
17	SC	0.74	0/1852	1.19	7/2490 (0.3%)
18	SD	0.70	0/1665	1.33	16/2227 (0.7%)
19	SE	0.74	0/1239	1.16	2/1664 (0.1%)
20	SF	0.75	0/1121	1.26	6/1509 (0.4%)
21	SG	0.75	0/1422	1.29	12/1908 (0.6%)
22	SH	0.71	0/989	1.22	8/1326 (0.6%)
23	SI	0.75	0/1048	1.35	17/1394 (1.2%)
24	S1	0.70	0/5532	1.21	27/7485 (0.4%)
25	LA	1.66	473/69812 (0.7%)	1.93	2989/108912 (2.7%)
26	LB	1.39	6/2869 (0.2%)	1.84	112/4474 (2.5%)
27	LC	0.70	0/1748	1.21	7/2355 (0.3%)
28	LM	0.77	0/929	1.33	12/1242 (1.0%)
29	LN	0.74	0/2131	1.38	16/2863 (0.6%)
30	LO	0.70	0/960	1.46	18/1278 (1.4%)
31	LP	0.76	0/829	1.21	6/1107 (0.5%)
32	LQ	0.74	0/864	1.28	9/1156 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LR	0.73	0/794	1.22	6/1060 (0.6%)
34	LS	0.71	0/797	1.19	6/1062 (0.6%)
35	LT	0.71	0/766	1.18	4/1025 (0.4%)
36	LU	0.78	0/642	1.34	6/848 (0.7%)
37	LV	0.76	0/635	1.32	7/848 (0.8%)
38	LD	0.73	0/1247	1.15	3/1679 (0.2%)
39	LW	0.72	0/510	1.22	4/677 (0.6%)
40	LX	0.77	0/1586	1.35	16/2134 (0.7%)
41	LY	0.68	0/453	1.40	4/605 (0.7%)
42	L1	0.71	0/450	1.28	1/599 (0.2%)
43	L2	0.75	0/448	1.13	1/594 (0.2%)
44	L3	0.77	0/380	1.61	9/498 (1.8%)
45	L4	0.66	0/513	1.28	3/676 (0.4%)
46	L5	0.81	0/303	1.35	3/397 (0.8%)
47	L6	0.71	0/1571	1.27	11/2113 (0.5%)
48	LE	0.68	0/1046	1.19	4/1410 (0.3%)
49	L7	0.73	0/1444	1.35	18/1937 (0.9%)
50	L8	0.70	0/1343	1.20	9/1816 (0.5%)
51	L9	0.71	0/1122	1.16	8/1515 (0.5%)
52	LF	0.77	0/1152	1.30	10/1551 (0.6%)
53	LG	0.78	0/956	1.32	6/1279 (0.5%)
54	LH	0.72	0/1062	1.35	13/1413 (0.9%)
55	LI	0.75	0/1093	1.33	12/1460 (0.8%)
56	LJ	0.75	0/1021	1.36	12/1364 (0.9%)
57	LK	0.73	0/910	1.32	12/1219 (1.0%)
58	LZ	0.71	0/559	1.23	4/745 (0.5%)
All	All	1.38	660/169586 (0.4%)	1.75	5304/252212 (2.1%)

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
1	SA	2	423
2	S6	0	16
3	S7	0	31
4	SJ	0	7
5	SK	0	5
6	SL	0	9
7	SM	0	4
8	SN	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	SO	0	4
10	SP	0	4
11	SQ	0	4
12	SR	0	3
13	SS	0	2
14	SB	0	3
15	ST	0	2
16	SU	0	3
17	SC	0	7
18	SD	0	6
19	SE	0	8
20	SF	0	6
21	SG	0	4
22	SH	0	3
23	SI	0	4
24	S1	0	19
25	LA	1	941
26	LB	0	21
27	LC	0	4
28	LM	0	5
29	LN	0	9
30	LO	0	4
31	LP	0	1
32	LQ	0	2
34	LS	0	3
35	LT	0	2
36	LU	0	5
37	LV	0	3
38	LD	0	3
39	LW	0	4
40	LX	0	10
41	LY	0	1
42	L1	0	2
44	L3	0	5
45	L4	0	3
46	L5	0	1
47	L6	0	6
48	LE	0	1
49	L7	0	8
50	L8	0	3
51	L9	0	2
52	LF	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
53	LG	0	4
54	LH	0	5
55	LI	0	1
56	LJ	0	6
57	LK	0	3
58	LZ	0	4
All	All	3	1660

The worst 5 of 660 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	SA	1513	A	N9-C4	-11.15	1.31	1.37
1	SA	781	A	N9-C4	-10.92	1.31	1.37
1	SA	900	A	N9-C4	-10.30	1.31	1.37
25	LA	2571	U	O3'-P	-10.16	1.49	1.61
25	LA	750	A	N9-C4	-10.00	1.31	1.37

The worst 5 of 5304 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	LA	2030	C	C6-N1-C2	-27.21	109.42	120.30
25	LA	2251	G	O4'-C1'-N9	26.55	129.44	108.20
25	LA	1900	A	P-O3'-C3'	25.97	150.87	119.70
1	SA	51	A	P-O3'-C3'	25.23	149.97	119.70
25	LA	2656	U	C2-N3-C4	-22.74	113.35	127.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	SA	1498	U	C4',C3'
25	LA	2251	G	C1'

5 of 1660 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	SA	20	U	Sidechain
1	SA	21	G	Sidechain
1	SA	33	A	Sidechain
1	SA	4	U	Sidechain
1	SA	9	G	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SA	33076	0	16648	111	0
2	S6	1639	0	837	1	0
3	S7	1577	0	800	5	0
4	SJ	825	0	865	0	0
5	SK	965	0	997	3	0
6	SL	955	0	1019	1	0
7	SM	910	0	981	2	0
8	SN	805	0	847	1	0
9	SO	716	0	742	0	0
10	SP	649	0	666	0	0
11	SQ	672	0	716	0	0
12	SR	626	0	651	0	0
13	SS	727	0	769	2	0
14	SB	1872	0	1885	1	0
15	ST	670	0	722	3	0
16	SU	590	0	631	0	0
17	SC	1822	0	1913	2	0
18	SD	1643	0	1710	1	0
19	SE	1225	0	1273	1	0
20	SF	1101	0	1050	1	0
21	SG	1400	0	1449	2	0
22	SH	979	0	1034	1	0
23	SI	1036	0	1084	0	0
24	S1	5431	0	5403	16	0
25	LA	62333	0	31349	251	0
26	LB	2566	0	1302	10	0
27	LC	1733	0	1824	6	0
28	LM	917	0	965	1	0
29	LN	2092	0	2170	6	0
30	LO	947	0	1022	1	0
31	LP	816	0	839	2	0
32	LQ	857	0	922	0	0
33	LR	787	0	846	0	0
34	LS	789	0	847	1	0
35	LT	753	0	780	0	0
36	LU	634	0	656	3	0
37	LV	625	0	655	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	LD	1233	0	1283	1	0
39	LW	509	0	543	2	0
40	LX	1565	0	1616	1	0
41	LY	449	0	491	1	0
42	L1	444	0	461	5	0
43	L2	441	0	485	0	0
44	L3	377	0	418	0	0
45	L4	504	0	574	0	0
46	L5	302	0	343	0	0
47	L6	1552	0	1619	3	0
48	LE	1032	0	1088	0	0
49	L7	1420	0	1460	4	0
50	L8	1323	0	1374	1	0
51	L9	1111	0	1148	0	0
52	LF	1129	0	1162	6	0
53	LG	947	0	1023	5	0
54	LH	1053	0	1129	2	0
55	LI	1074	0	1157	1	0
56	LJ	1008	0	1045	4	0
57	LK	900	0	935	0	0
58	LZ	549	0	552	1	0
59	S1	32	0	12	15	0
All	All	156714	0	108787	450	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 2.

The worst 5 of 450 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)
24:S1:22:LYS:CE	59:S1:801:GTP:O3G	2.13	0.97
24:S1:23:THR:N	59:S1:801:GTP:O2B	2.08	0.86
24:S1:22:LYS:HE3	59:S1:801:GTP:O3G	1.76	0.85
21:SG:77:ARG:HE	21:SG:152:HIS:CD2	2.05	0.74
24:S1:144:ASP:CG	59:S1:801:GTP:HN1	1.89	0.74

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SJ	101/103 (98%)	98 (97%)	0	3 (3%)	4	33
5	SK	126/128 (98%)	104 (82%)	17 (14%)	5 (4%)	3	26
6	SL	121/123 (98%)	109 (90%)	10 (8%)	2 (2%)	9	45
7	SM	115/117 (98%)	101 (88%)	9 (8%)	5 (4%)	2	24
8	SN	98/100 (98%)	88 (90%)	9 (9%)	1 (1%)	15	55
9	SO	86/88 (98%)	83 (96%)	1 (1%)	2 (2%)	6	38
10	SP	80/82 (98%)	72 (90%)	4 (5%)	4 (5%)	2	21
11	SQ	81/83 (98%)	71 (88%)	8 (10%)	2 (2%)	5	36
12	SR	72/74 (97%)	58 (81%)	11 (15%)	3 (4%)	3	25
13	SS	89/91 (98%)	74 (83%)	10 (11%)	5 (6%)	2	19
14	SB	238/240 (99%)	217 (91%)	13 (6%)	8 (3%)	3	31
15	ST	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	13	51
16	SU	68/70 (97%)	52 (76%)	11 (16%)	5 (7%)	1	13
17	SC	230/232 (99%)	212 (92%)	13 (6%)	5 (2%)	6	39
18	SD	203/205 (99%)	177 (87%)	18 (9%)	8 (4%)	3	27
19	SE	164/166 (99%)	149 (91%)	13 (8%)	2 (1%)	13	51
20	SF	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	19	59
21	SG	176/178 (99%)	158 (90%)	15 (8%)	3 (2%)	9	45
22	SH	127/129 (98%)	121 (95%)	4 (3%)	2 (2%)	9	46
23	SI	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
24	S1	700/702 (100%)	632 (90%)	45 (6%)	23 (3%)	4	31
27	LC	232/234 (99%)	206 (89%)	19 (8%)	7 (3%)	4	33
28	LM	112/114 (98%)	99 (88%)	10 (9%)	3 (3%)	5	35
29	LN	270/272 (99%)	244 (90%)	16 (6%)	10 (4%)	3	28
30	LO	115/117 (98%)	108 (94%)	4 (4%)	3 (3%)	5	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	LP	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	7	41
32	LQ	108/110 (98%)	102 (94%)	5 (5%)	1 (1%)	17	57
33	LR	98/100 (98%)	84 (86%)	9 (9%)	5 (5%)	2	20
34	LS	101/103 (98%)	89 (88%)	8 (8%)	4 (4%)	3	26
35	LT	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	14	53
36	LU	82/84 (98%)	56 (68%)	15 (18%)	11 (13%)	0	4
37	LV	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
38	LD	162/164 (99%)	154 (95%)	7 (4%)	1 (1%)	25	64
39	LW	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
40	LX	207/209 (99%)	168 (81%)	25 (12%)	14 (7%)	1	15
41	LY	56/58 (97%)	52 (93%)	3 (5%)	1 (2%)	8	43
42	L1	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	3	28
43	L2	52/54 (96%)	44 (85%)	7 (14%)	1 (2%)	8	42
44	L3	44/46 (96%)	39 (89%)	2 (4%)	3 (7%)	1	15
45	L4	62/64 (97%)	59 (95%)	2 (3%)	1 (2%)	9	46
46	L5	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
47	L6	199/201 (99%)	172 (86%)	18 (9%)	9 (4%)	2	23
48	LE	139/141 (99%)	123 (88%)	12 (9%)	4 (3%)	4	33
49	L7	176/178 (99%)	137 (78%)	21 (12%)	18 (10%)	0	7
50	L8	174/176 (99%)	156 (90%)	9 (5%)	9 (5%)	2	20
51	L9	147/149 (99%)	132 (90%)	9 (6%)	6 (4%)	3	26
52	LF	140/142 (99%)	122 (87%)	16 (11%)	2 (1%)	11	48
53	LG	121/123 (98%)	107 (88%)	12 (10%)	2 (2%)	9	45
54	LH	142/144 (99%)	129 (91%)	5 (4%)	8 (6%)	2	19
55	LI	134/136 (98%)	122 (91%)	10 (8%)	2 (2%)	10	47
56	LJ	125/127 (98%)	110 (88%)	9 (7%)	6 (5%)	2	22
57	LK	115/117 (98%)	107 (93%)	5 (4%)	3 (3%)	5	35
58	LZ	68/70 (97%)	56 (82%)	10 (15%)	2 (3%)	4	33
All	All	7019/7125 (98%)	6254 (89%)	534 (8%)	231 (3%)	6	31

5 of 231 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	SK	125	LYS
7	SM	62	PHE
16	SU	7	GLU
18	SD	48	SER
18	SD	134	TYR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SJ	90/90 (100%)	89 (99%)	1 (1%)	73	88
5	SK	98/98 (100%)	92 (94%)	6 (6%)	18	53
6	SL	103/103 (100%)	101 (98%)	2 (2%)	57	80
7	SM	95/95 (100%)	89 (94%)	6 (6%)	18	53
8	SN	83/83 (100%)	81 (98%)	2 (2%)	49	75
9	SO	76/76 (100%)	75 (99%)	1 (1%)	69	86
10	SP	65/65 (100%)	65 (100%)	0	100	100
11	SQ	77/77 (100%)	75 (97%)	2 (3%)	46	74
12	SR	64/64 (100%)	62 (97%)	2 (3%)	40	71
13	SS	78/78 (100%)	75 (96%)	3 (4%)	33	66
14	SB	198/198 (100%)	189 (96%)	9 (4%)	27	62
15	ST	65/65 (100%)	64 (98%)	1 (2%)	65	84
16	SU	60/60 (100%)	54 (90%)	6 (10%)	7	35
17	SC	189/189 (100%)	178 (94%)	11 (6%)	20	55
18	SD	172/172 (100%)	165 (96%)	7 (4%)	30	64
19	SE	125/125 (100%)	118 (94%)	7 (6%)	21	56
20	SF	116/116 (100%)	112 (97%)	4 (3%)	37	69
21	SG	146/146 (100%)	141 (97%)	5 (3%)	37	69
22	SH	104/104 (100%)	99 (95%)	5 (5%)	25	60
23	SI	106/106 (100%)	104 (98%)	2 (2%)	57	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	S1	575/575 (100%)	549 (96%)	26 (4%)	27	62
27	LC	181/181 (100%)	171 (94%)	10 (6%)	21	57
28	LM	99/99 (100%)	91 (92%)	8 (8%)	11	43
29	LN	217/217 (100%)	207 (95%)	10 (5%)	27	61
30	LO	89/89 (100%)	84 (94%)	5 (6%)	21	56
31	LP	84/84 (100%)	75 (89%)	9 (11%)	6	32
32	LQ	93/93 (100%)	92 (99%)	1 (1%)	73	88
33	LR	84/84 (100%)	79 (94%)	5 (6%)	19	54
34	LS	84/84 (100%)	80 (95%)	4 (5%)	25	60
35	LT	78/78 (100%)	74 (95%)	4 (5%)	24	58
36	LU	62/62 (100%)	57 (92%)	5 (8%)	11	43
37	LV	67/67 (100%)	65 (97%)	2 (3%)	41	71
38	LD	122/122 (100%)	120 (98%)	2 (2%)	62	83
39	LW	55/55 (100%)	53 (96%)	2 (4%)	35	67
40	LX	164/164 (100%)	157 (96%)	7 (4%)	29	63
41	LY	48/48 (100%)	46 (96%)	2 (4%)	30	63
42	L1	47/47 (100%)	44 (94%)	3 (6%)	17	52
43	L2	48/48 (100%)	48 (100%)	0	100	100
44	L3	38/38 (100%)	36 (95%)	2 (5%)	22	58
45	L4	51/51 (100%)	49 (96%)	2 (4%)	32	65
46	L5	34/34 (100%)	33 (97%)	1 (3%)	42	72
47	L6	165/165 (100%)	160 (97%)	5 (3%)	41	71
48	LE	109/109 (100%)	101 (93%)	8 (7%)	14	46
49	L7	149/149 (100%)	138 (93%)	11 (7%)	13	46
50	L8	137/137 (100%)	130 (95%)	7 (5%)	24	58
51	L9	114/114 (100%)	106 (93%)	8 (7%)	15	48
52	LF	116/116 (100%)	112 (97%)	4 (3%)	37	69
53	LG	104/104 (100%)	98 (94%)	6 (6%)	20	55
54	LH	103/103 (100%)	98 (95%)	5 (5%)	25	59
55	LI	109/109 (100%)	106 (97%)	3 (3%)	43	72
56	LJ	103/103 (100%)	98 (95%)	5 (5%)	25	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	LK	87/87 (100%)	82 (94%)	5 (6%)	20	55
58	LZ	62/62 (100%)	59 (95%)	3 (5%)	25	60
All	All	5788/5788 (100%)	5526 (96%)	262 (4%)	31	62

5 of 262 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	LF	34	ARG
53	LG	41	ILE
58	LZ	44	PHE
24	S1	377	ARG
24	S1	312	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
30	LO	43	GLN
52	LF	47	HIS
36	LU	56	HIS
50	L8	115	GLN
36	LU	45	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	SA	1542/1542 (100%)	308 (19%)	87 (5%)
2	S6	76/77 (98%)	13 (17%)	4 (5%)
25	LA	2903/2904 (99%)	557 (19%)	141 (4%)
26	LB	119/120 (99%)	20 (16%)	11 (9%)
3	S7	73/74 (98%)	29 (39%)	7 (9%)
All	All	4713/4717 (99%)	927 (19%)	250 (5%)

5 of 927 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	SA	2	A
1	SA	3	A
1	SA	4	U
1	SA	7	A

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Mol	Chain	Res	Type
1	SA	8	A

5 of 250 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	LA	428	A
25	LA	2473	U
25	LA	1142	A
25	LA	2452	C
25	LA	2835	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](#)

1 ligand is modelled in this entry.

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	$\# Z > 2$
59	GTP	S1	801	-	26,34,34	1.81	3 (11%)	32,54,54	2.02	8 (25%)

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
59	GTP	S1	801	-	-	2/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	S1	801	GTP	C5-C6	-6.84	1.33	1.47
59	S1	801	GTP	C5-C4	-3.59	1.33	1.43
59	S1	801	GTP	O4'-C1'	2.02	1.43	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	S1	801	GTP	PB-O3B-PG	-6.78	109.56	132.83
59	S1	801	GTP	PA-O3A-PB	-3.75	119.94	132.83
59	S1	801	GTP	C2-N1-C6	-3.73	118.24	125.10
59	S1	801	GTP	C5-C6-N1	3.17	119.55	113.95
59	S1	801	GTP	C8-N7-C5	2.69	108.12	102.99

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	S1	801	GTP	O4'-C4'-C5'-O5'
59	S1	801	GTP	C3'-C4'-C5'-O5'

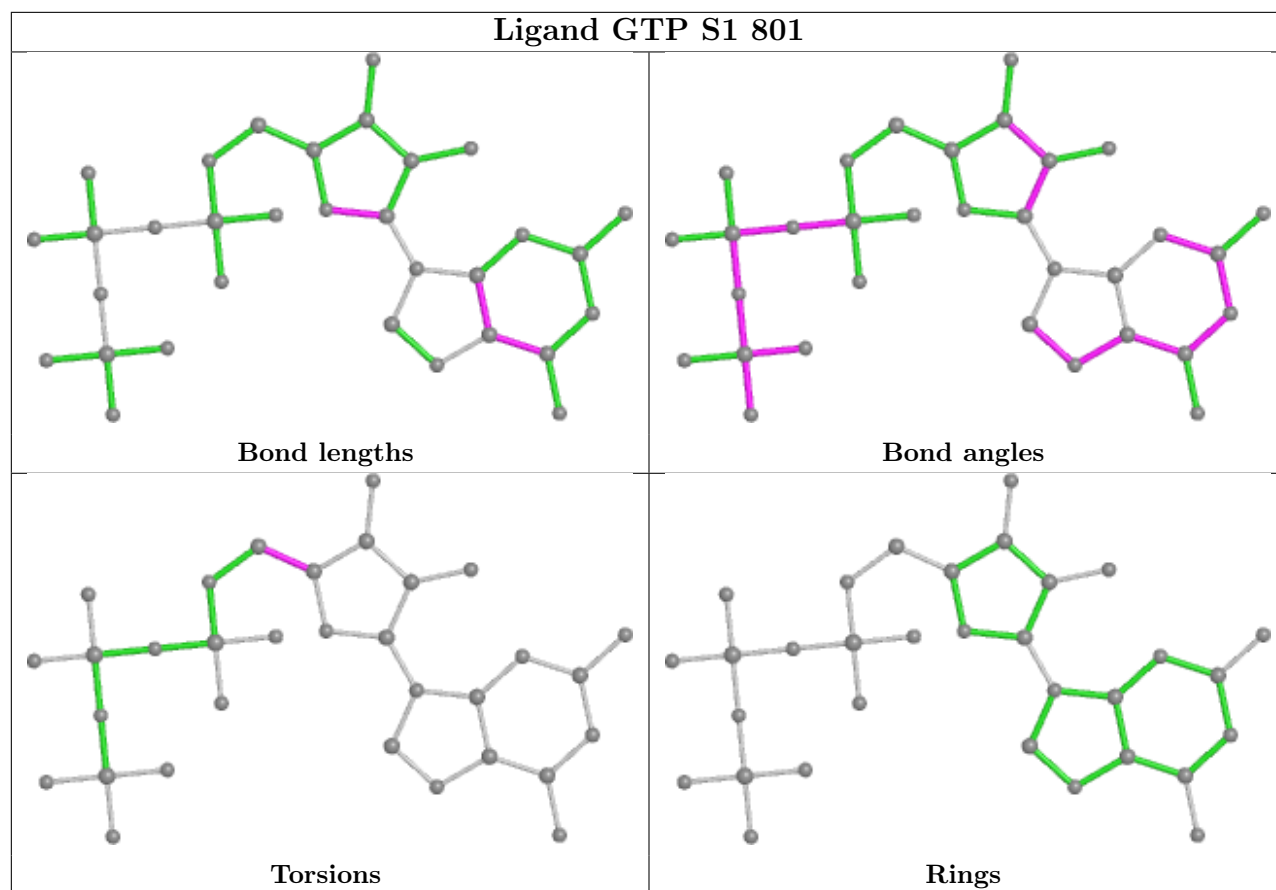
There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	S1	801	GTP	15	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.

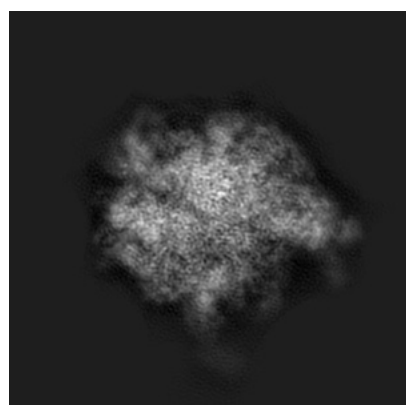
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6315. These allow visual inspection of the internal detail of the map and identification of artifacts.

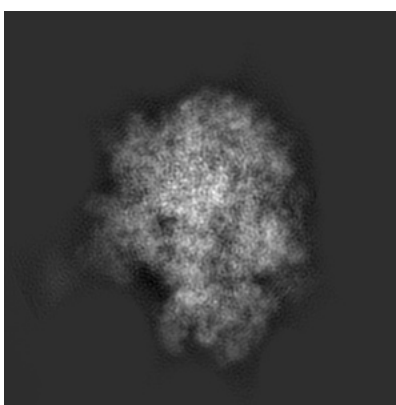
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

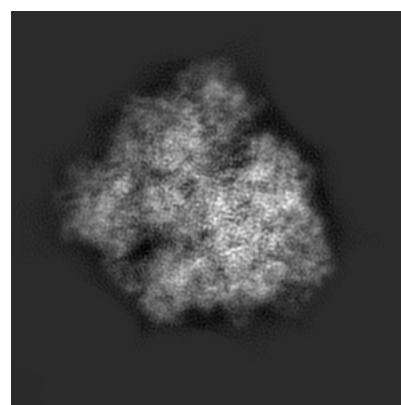
6.1.1 Primary map



X



Y

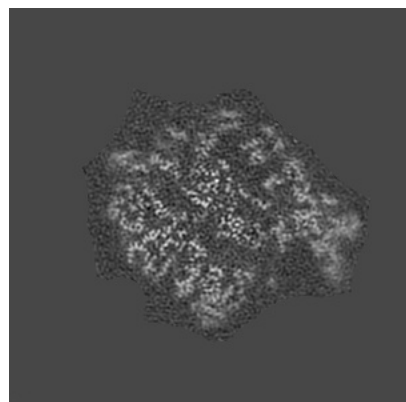


Z

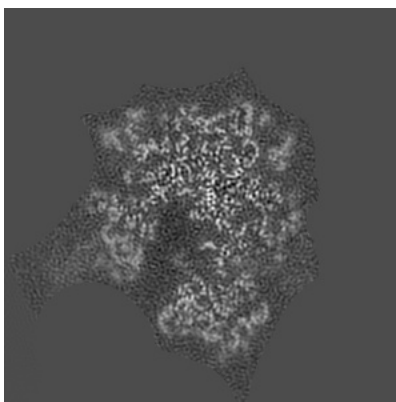
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

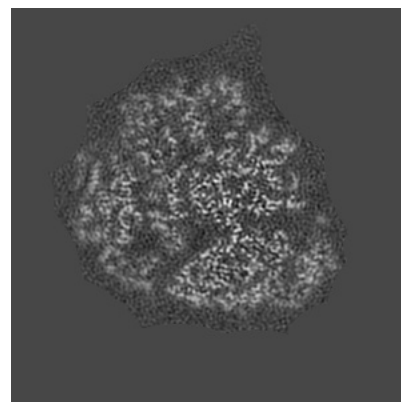
6.2.1 Primary map



X Index: 180



Y Index: 180

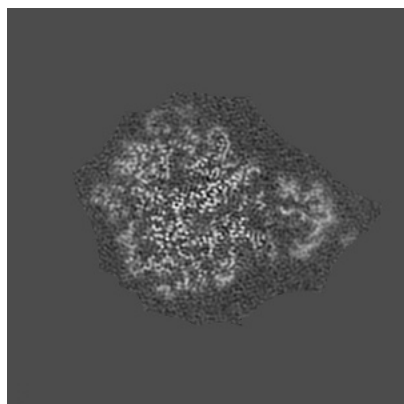


Z Index: 180

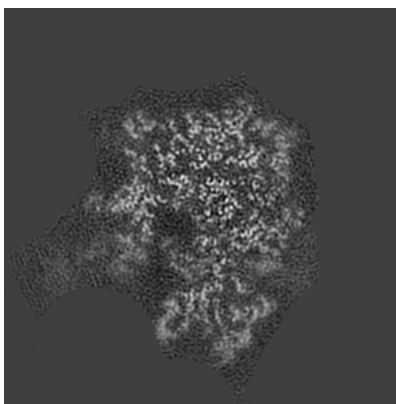
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ

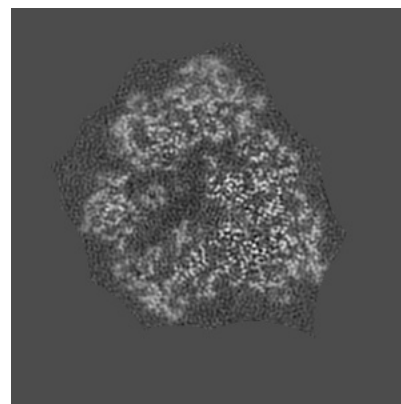
6.3.1 Primary map



X Index: 201



Y Index: 187



Z Index: 164

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

6.4 Orthogonal surface views ⓘ

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

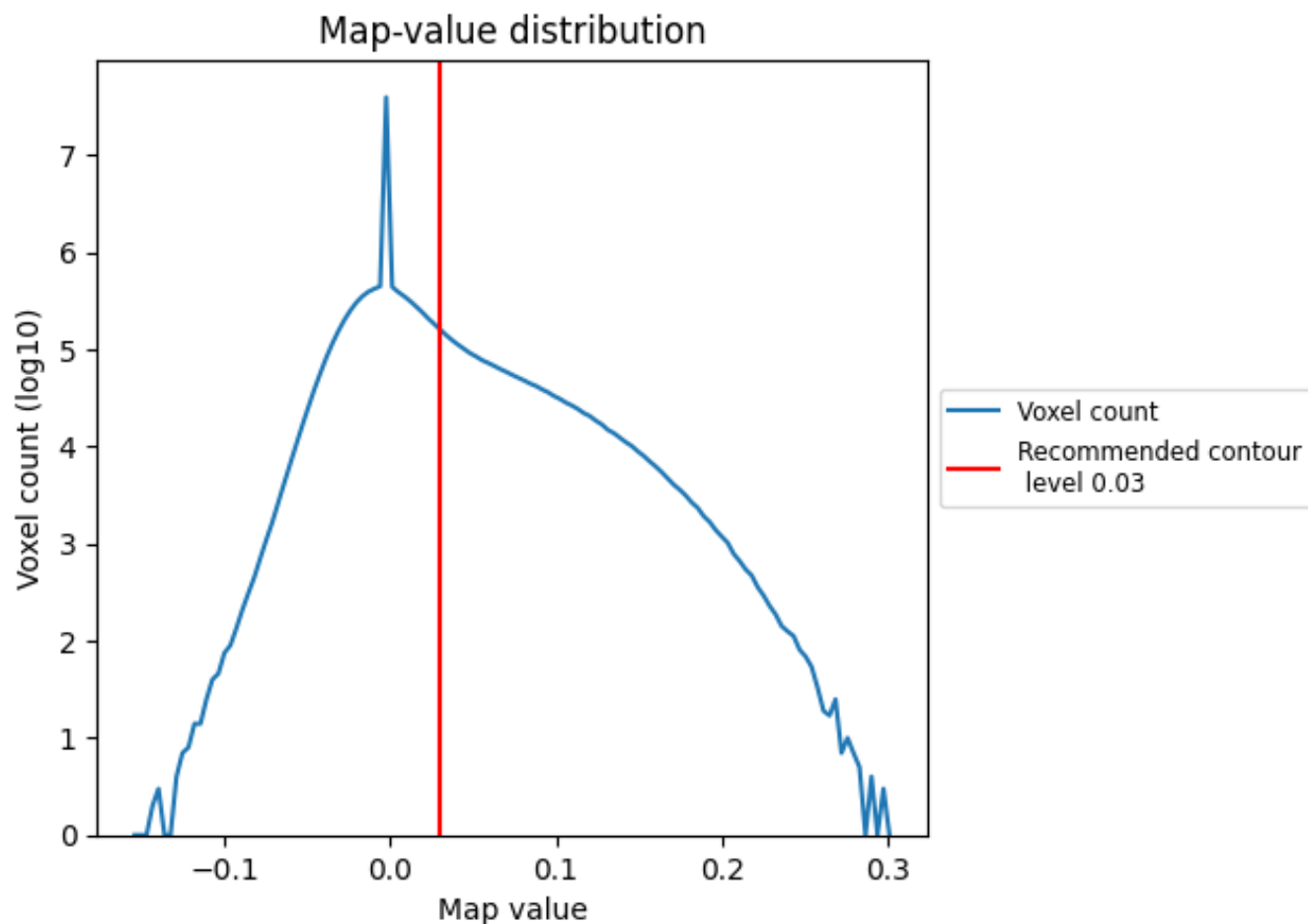
6.5 Mask visualisation

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

7 Map analysis [i](#)

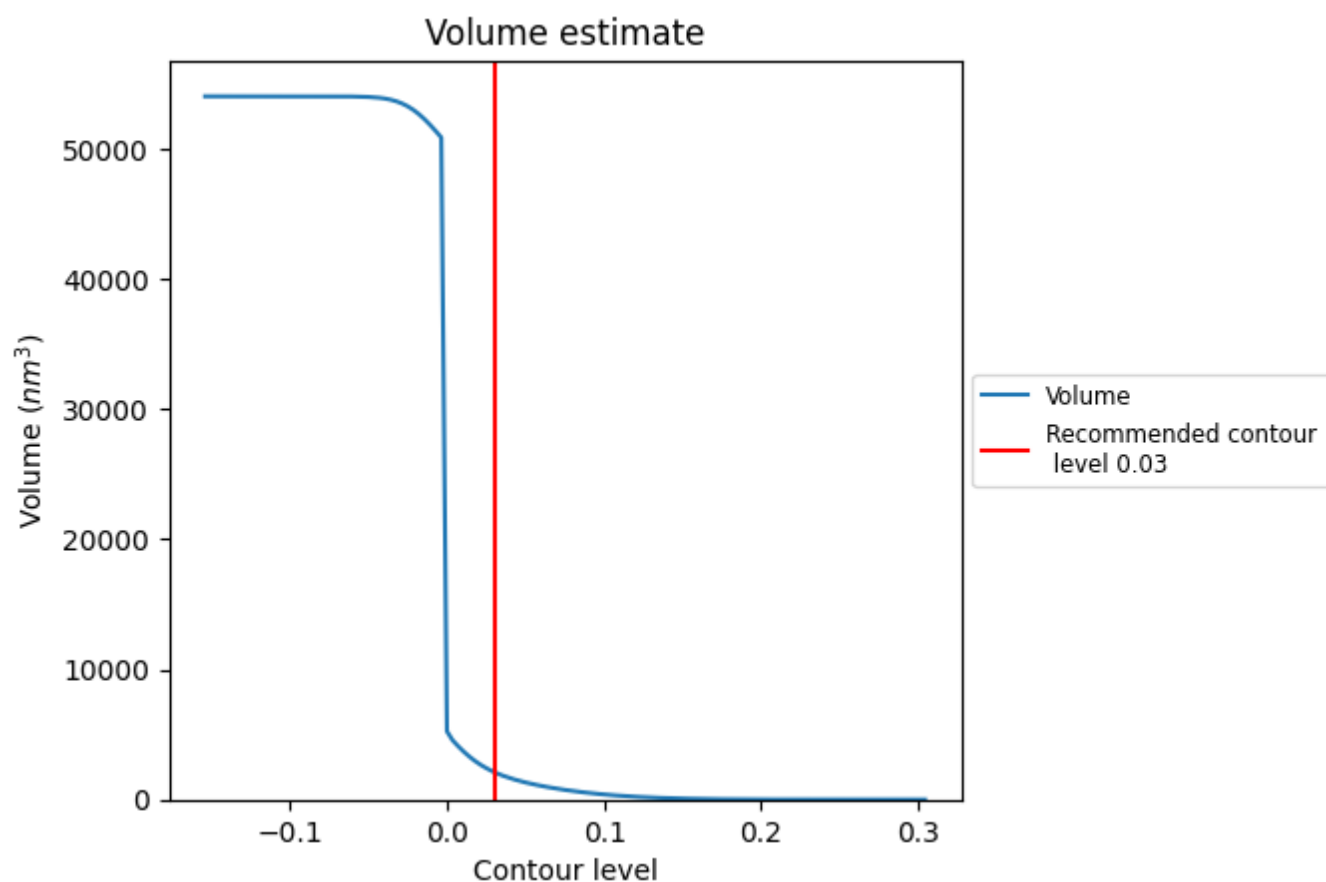
This section contains the results of statistical analysis of the map.

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.

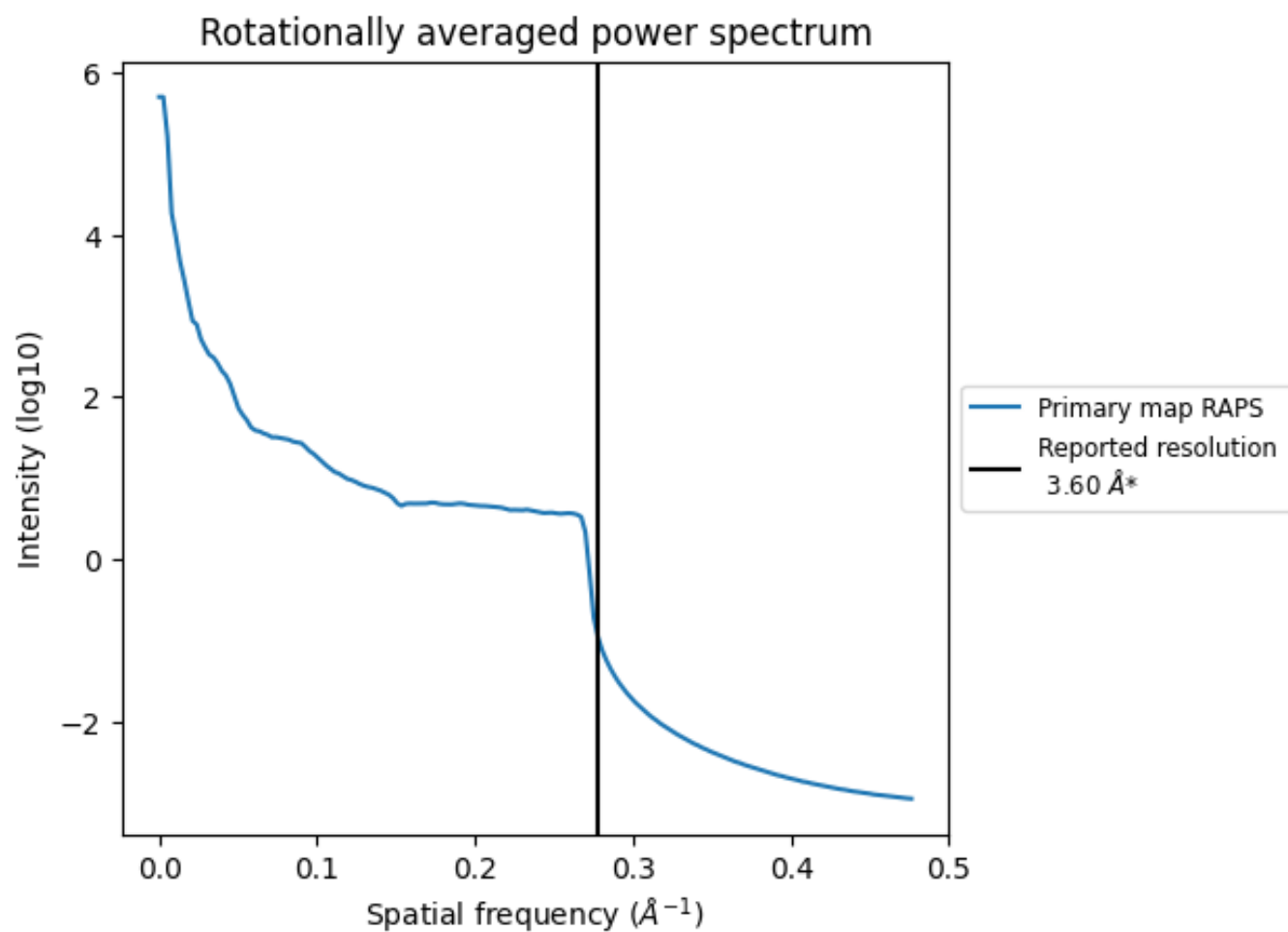
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2119 nm³; this corresponds to an approximate mass of 1915 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 0.278 Å⁻¹

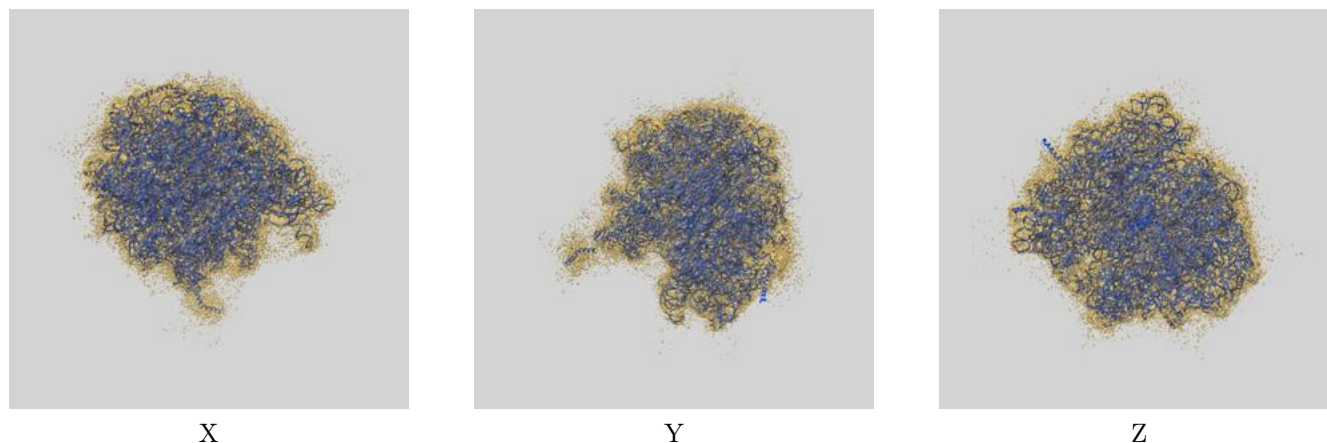
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6315 and PDB model 3J9Z. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



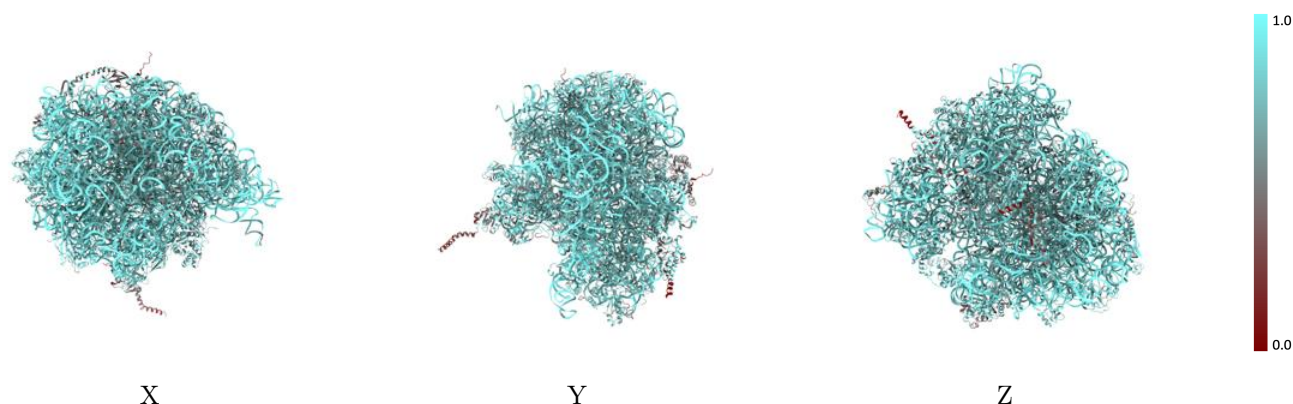
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



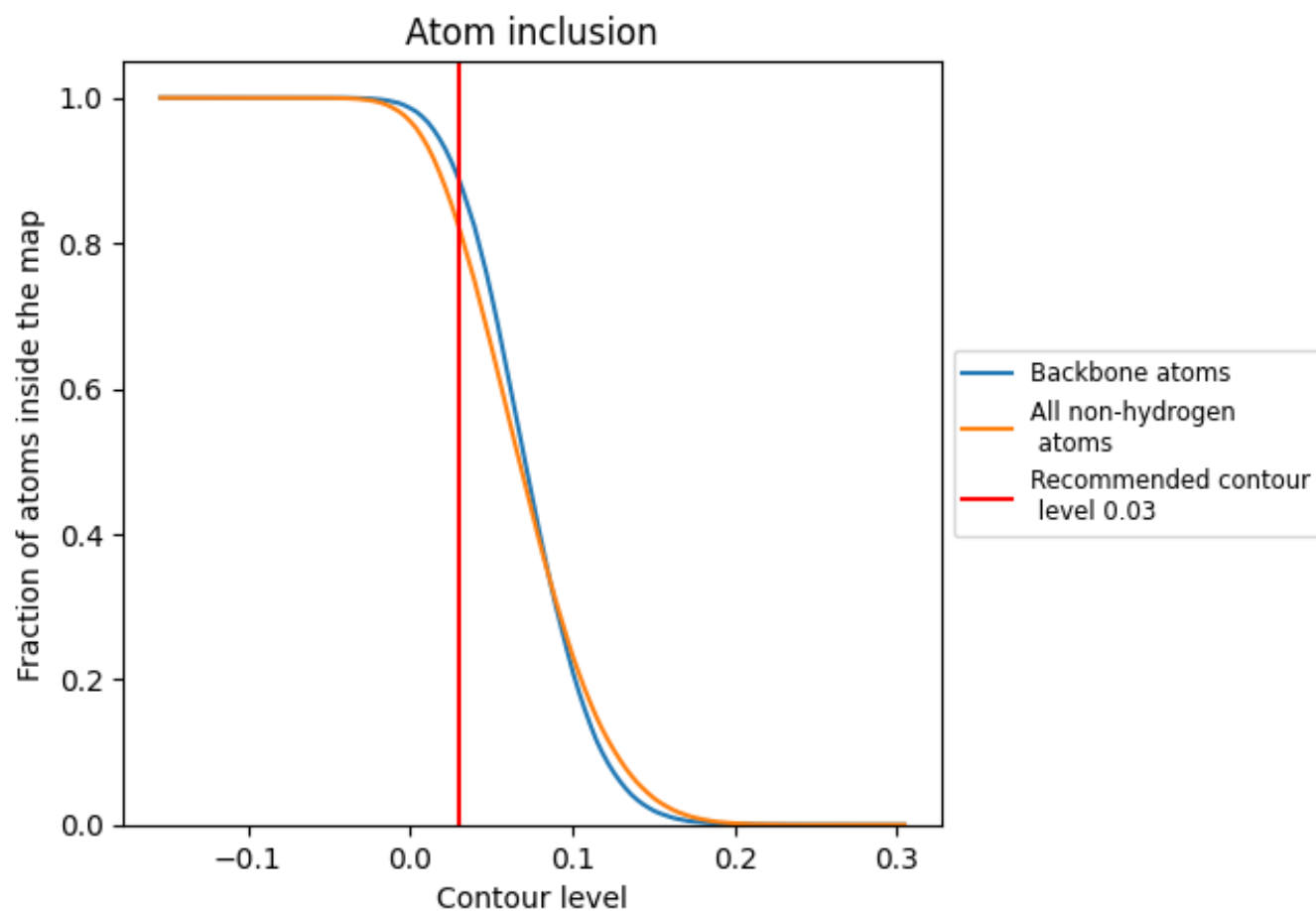
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 82% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8208	 0.1940
L1	 0.7383	 0.1660
L2	 0.7575	 0.2300
L3	 0.6761	 0.1490
L4	 0.7719	 0.2340
L5	 0.7877	 0.2560
L6	 0.7566	 0.1840
L7	 0.8163	 0.2540
L8	 0.8019	 0.2460
L9	 0.5100	 0.1070
LA	 0.8748	 0.2050
LB	 0.9630	 0.2750
LC	 0.6101	 0.1060
LD	 0.4942	 0.1870
LE	 0.7123	 0.1980
LF	 0.7909	 0.2260
LG	 0.6443	 0.1730
LH	 0.7812	 0.2110
LI	 0.8081	 0.2900
LJ	 0.6835	 0.1270
LK	 0.8530	 0.2540
LM	 0.6858	 0.1430
LN	 0.6742	 0.1470
LO	 0.7952	 0.2170
LP	 0.7880	 0.2220
LQ	 0.7141	 0.1760
LR	 0.6783	 0.1130
LS	 0.7902	 0.1340
LT	 0.8496	 0.3110
LU	 0.7282	 0.2380
LV	 0.7354	 0.1800
LW	 0.6801	 0.0770
LX	 0.7224	 0.1850
LY	 0.7986	 0.2660
LZ	 0.6413	 0.1850



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Chain	Atom inclusion	Q-score
S1	 0.7013	 0.1850
S6	 0.8652	 0.2260
S7	 0.8098	 0.1550
SA	 0.8843	 0.1920
SB	 0.6415	 0.1240
SC	 0.6851	 0.1890
SD	 0.7723	 0.1700
SE	 0.6683	 0.1570
SF	 0.5728	 0.0870
SG	 0.7072	 0.1740
SH	 0.7156	 0.1140
SI	 0.7603	 0.1720
SJ	 0.7000	 0.1970
SK	 0.6909	 0.1670
SL	 0.7134	 0.1850
SM	 0.7938	 0.2500
SN	 0.7997	 0.2190
SO	 0.6797	 0.0970
SP	 0.7576	 0.1140
SQ	 0.6982	 0.1110
SR	 0.6762	 0.1380
SS	 0.7609	 0.2490
ST	 0.7267	 0.1220
SU	 0.5982	 0.1600