



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 07:47 AM EST

PDB ID : 3JA1
EMDB ID : EMD-6316
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 : 2015-03-30
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

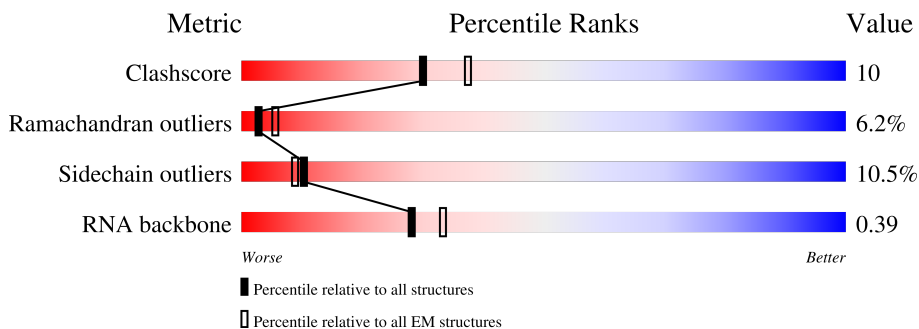
1 Overall quality at a glance

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	SS	91	<div> <div>10%</div> <div>53%</div> <div>30%</div> <div>13%</div> <div>.</div> </div>
2	SA	1542	<div> <div>15%</div> <div>40%</div> <div>45%</div> </div>
3	S1	47	<div> <div>47%</div> <div>26%</div> <div>70%</div> </div>
4	S2	77	<div> <div>14%</div> <div>40%</div> <div>45%</div> </div>
5	ST	86	<div> <div>5%</div> <div>67%</div> <div>26%</div> <div>7%</div> </div>
6	SU	70	<div> <div>27%</div> <div>51%</div> <div>29%</div> <div>16%</div> <div>.</div> </div>
7	SG	178	<div> <div>15%</div> <div>63%</div> <div>27%</div> <div>8%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
8	SH	129	
9	SI	129	
10	SJ	103	
11	SK	128	
12	SL	123	
13	SM	117	
14	SN	100	
15	SO	88	
16	SP	82	
17	SQ	83	
18	SB	240	
19	SC	232	
20	SD	205	
21	SE	166	
22	SF	135	
23	SR	74	
24	S3	702	
25	LB	120	
26	LA	2904	
27	LD	272	
28	LU	110	
29	LV	100	
30	LW	103	
31	LX	94	
32	LY	84	

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Mol	Chain	Length	Quality of chain
33	LZ	77	
34	L0	63	
35	L1	58	
36	L2	70	
37	LC	234	
38	LE	209	
39	L3	56	
40	L4	54	
41	L5	46	
42	L6	64	
43	L7	38	
44	LF	201	
45	LG	178	
46	LH	176	
47	LJ	164	
48	LN	144	
49	LK	141	
50	LL	142	
51	LI	149	
52	LO	136	
53	LP	127	
54	LM	123	
55	LQ	117	
56	LR	114	
57	LS	117	

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Mol	Chain	Length	Quality of chain
58	LT	103	<div><div></div><div>5%</div><div>64%</div><div>22%</div><div>13%</div><div></div></div>

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 156127 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 30S ribosomal protein S19.

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

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S1	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 4 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S2	77	Total	C	N	O	P	0	0
			1639	732	297	534	76		

- Molecule 5 is a protein called 30S ribosomal protein S20.

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

- Molecule 6 is a protein called 30S ribosomal protein S21.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

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

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

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

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S2.

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

- Molecule 19 is a protein called 30S ribosomal protein S3.

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

- Molecule 20 is a protein called 30S ribosomal protein S4.

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

- Molecule 21 is a protein called 30S ribosomal protein S5.

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

- Molecule 22 is a protein called 30S ribosomal protein S6.

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

- Molecule 23 is a protein called 30S ribosomal protein S18.

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

- Molecule 24 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S3	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
S3	91	ALA	HIS	ENGINEERED MUTATION	UNP P0A6M8

- Molecule 25 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LA	2904	Total	C	N	O	P	0	0
			62330	27807	11462	20158	2903		

There are 4 discrepancies between the modelled and reference sequences:

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

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Chain	Residue	Modelled	Actual	Comment	Reference
LA	1915	C	U	CONFLICT	GB 33357927
LA	2030	U	A	CONFLICT	GB 33357927
LA	2251	U	G	CONFLICT	GB 33357927

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L22.

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

- Molecule 29 is a protein called 50S ribosomal protein L23.

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

- Molecule 30 is a protein called 50S ribosomal protein L24.

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

- Molecule 31 is a protein called 50S ribosomal protein L25.

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

- Molecule 32 is a protein called 50S ribosomal protein L27.

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

- Molecule 33 is a protein called 50S ribosomal protein L28.

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

- Molecule 34 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 35 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 36 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 37 is a protein called 50S ribosomal protein L1.

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

- Molecule 38 is a protein called 50S ribosomal protein L3.

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

- Molecule 39 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	L3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 40 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	L4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 41 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	L5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 42 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 43 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 44 is a protein called 50S ribosomal protein L4.

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

- Molecule 45 is a protein called 50S ribosomal protein L5.

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

- Molecule 46 is a protein called 50S ribosomal protein L6.

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

- Molecule 47 is a protein called 50S ribosomal protein L10.

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

- Molecule 48 is a protein called 50S ribosomal protein L15.

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

- Molecule 49 is a protein called 50S ribosomal protein L11.

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

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

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

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

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

- Molecule 52 is a protein called 50S ribosomal protein L16.

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

- Molecule 53 is a protein called 50S ribosomal protein L17.

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

- Molecule 54 is a protein called 50S ribosomal protein L14.

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

- Molecule 55 is a protein called 50S ribosomal protein L18.

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

- Molecule 56 is a protein called 50S ribosomal protein L19.

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

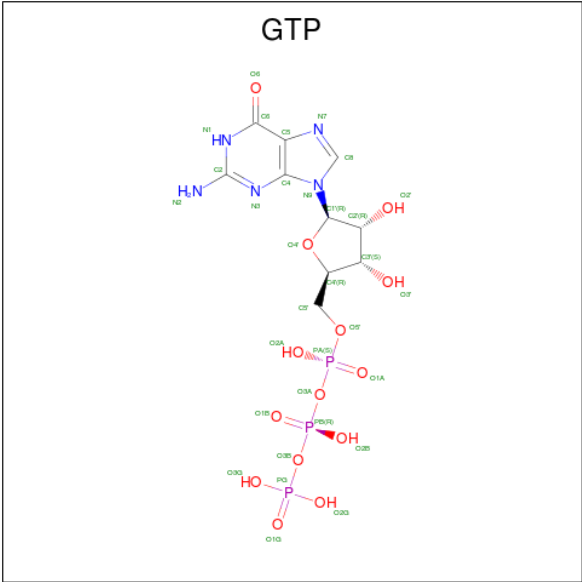
- Molecule 57 is a protein called 50S ribosomal protein L20.

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

- Molecule 58 is a protein called 50S ribosomal protein L21.

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

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

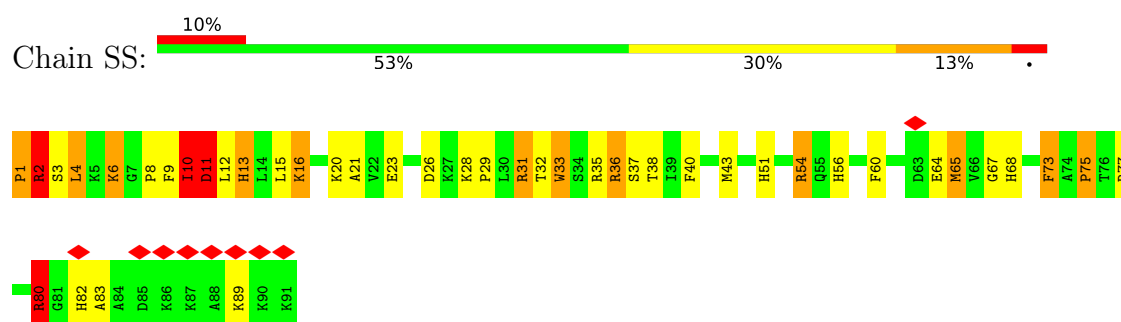


Mol	Chain	Residues	Atoms					AltConf
59	S3	1	Total	C	N	O	P	0
			32	10	5	14	3	

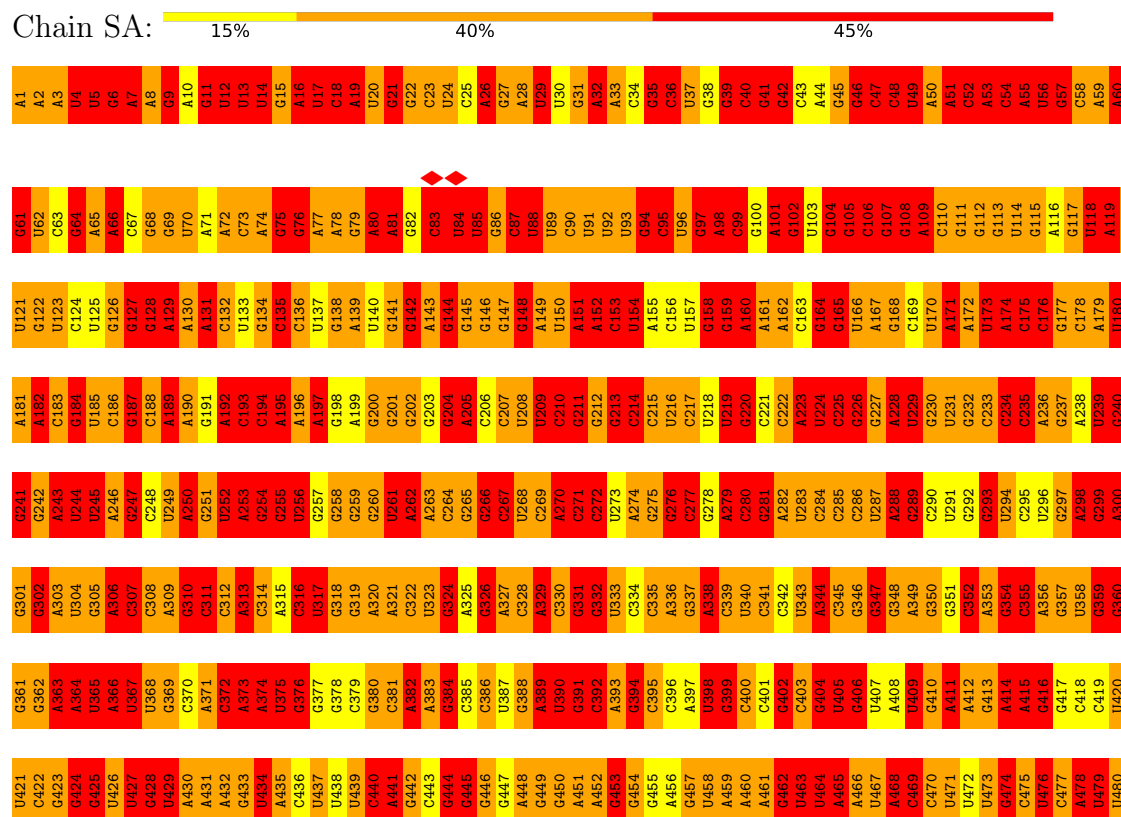
3 Residue-property plots

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.

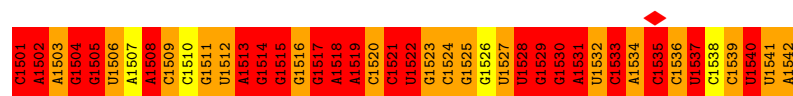
• Molecule 1: 30S ribosomal protein S19



• Molecule 2: 16S ribosomal RNA



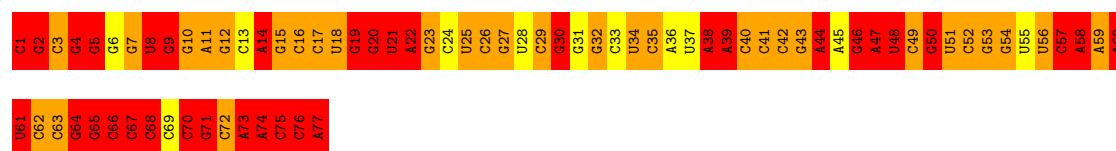
A1441	G601	G661	G721	A781	C841	A901	U961	A1021	A1081	G1141	A1201	A1261	U1321	U1381	A1441
G1442	A602	U662	G722	A782	U842	G902	C962	A1022	A1082	G1142	U1202	C1262	C1322	C1382	G1442
U1443	U603	C543	U723	C783	U843	G903	G963	U1023	U1083	G1143	C1203	C1263	C1323	C1383	U1443
C1444	G604	U664	U724	A784	G844	U904	U964	G1024	G1084	G1144	A1204	U1264	A1324	C1384	C1444
U1445	U605	C545	G725	G785	A845	U905	U965	U1025	U1085	A1145	U1205	G1265	U1325	G1385	U1445
A1446	G606	U666	G726	G786	A846	U906	U966	G1026	U1086	A1146	G1206	G1266	U1326	G1386	A1446
U1447	A607	U667	G727	U787	G847	A907	C967	G1027	G1087	C1147	G1207	G1267	C1327	G1387	U1447
C1448	U608	U668	A728	U788	G848	A908	U968	C1028	G1088	U1148	C1208	G1268	C1328	C1388	C1448
U1449	A609	C549	U729	U789	G849	A909	U969	U1029	U1089	U1149	C1209	A1269	A1329	C1389	U1449
C1450	U610	U650	G730	A790	U850	C910	C970	U1030	U1090	A1150	C1210	G1270	U1330	U1390	C1450
U1451	G611	U651	G731	G791	U851	U911	G971	U1031	U1091	A1151	U1211	A1271	G1331	U1391	U1451
A1452	C612	U552	C732	A792	G852	C912	C972	G1032	A1092	A1152	U1212	C1272	A1332	U1392	C1452
G1453	C613	A553	G733	U793	C853	C913	G973	G1033	A1093	G1153	C1213	C1273	A1333	U1393	U1453
U1454	C614	A554	G734	A794	U854	A914	A974	G1034	G1094	G1154	C1214	A1274	G1334	A1394	G1454
G1455	G615	U555	A675	C795	U855	A915	A975	A1035	U1095	A1155	G1215	A1275	U1335	C1395	U1455
A1456	U616	C556	A676	C796	C856	U916	G976	A1036	C1096	G1156	A1216	G1276	U1336	C1396	G1456
G1457	G617	U557	G737	C797	C857	A917	A977	C1037	C1097	A1157	C1217	G1277	G1337	C1397	U1457
U1458	C618	U558	U738	U798	G858	U918	A978	C1038	C1098	C1158	C1218	G1278	G1338	C1398	U1458
G1459	U619	A559	C739	G799	G859	A919	C979	G1039	U1099	U1159	U1219	G1279	A1339	C1399	U1459
C1460	C620	A560	U740	G800	A860	U920	C980	U1040	C1100	G1160	G1220	A1280	A1340	C1400	C1460
U1461	A621	U561	G741	U801	G861	U921	U981	G1041	A1101	C1161	G1221	C1281	U1341	C1401	U1461
A1462	C622	U562	A742	A802	C862	U922	U982	A1042	A1102	C1162	G1222	U1282	C1342	C1402	U1462
U1463	C623	A563	G743	G803	G863	A923	A983	G1043	C1103	C1163	C1223	U1283	G1343	C1403	U1463
G1464	C624	C564	U744	U804	U864	C924	C984	A1044	G1104	G1164	U1224	C1284	C1344	C1404	U1464
A1465	U625	U565	G745	C805	A865	C925	C985	G1045	A1105	U1165	U1225	A1285	U1345	G1405	A1465
C1466	C626	C566	A746	C806	C866	U926	U986	A1046	G1106	G1166	C1226	U1286	A1346	U1406	C1466
U1467	G627	U567	U747	A807	G867	U927	U987	C1047	C1107	A1167	G1227	A1287	G1347	U1407	U1467
A1478	U628	U568	G748	C808	C868	U928	C988	G1048	C1108	U1168	C1228	U1288	U1348	A1408	U1478
C1479	C629	A569	A749	U809	G869	U929	U989	U1049	C1109	A1179	U1229	A1289	A1349	C1409	C1479
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G1482	U632	A572	G752	C812	A872	C932	U992	U1052	C1112	C1172	U1232	C1292	C1352	C1412	G1482
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C1496	U646	U586	A766	C826	C886	U946	G1006	C1066	U1126	A1186	U1246	A1306	C1366	U1426	U1496
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U1500	G650	C590	C770	G830	A890	U950	U1010	U1070	A1130	G1190	A1250	G1310	G1370	A1430	C1500
G1501	C651	U591	G771	A831	C891	C951	C1011	C1071	G1131	A1191	A1251	A1311	G1371	G1431	G1501
A1502	U652	C592	U772	U832	U892	U952	A1012	G1072	C1132	C1192	A1252	G1312	U1372	A1432	U1502
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U1504	U654	A594	G774	U834	G894	U954	A1014	G1074	G1134	U1194	A1254	C1314	A1374	A1434	U1504
A1505	A655	C595	G775	U835	G895	U955	G1015	U1075	U1135	C1195	G1255	U1315	A1375	A1435	A1505
C1506	U656	U596	G776	C836	C896	U956	A1016	U1076	C1136	A1196	A1256	G1316	U1376	U1436	C1506
G1507	C657	C597	U777	U837	C897	U957	U1017	G1077	C1137	A1197	A1257	C1317	A1377	A1437	G1507
U1508	U658	U598	G778	C838	C898	U958	G1018	U1078	G1138	G1198	G1258	G1318	C1378	G1438	U1508
A1509	C659	A599	C779	U839	C899	A959	A1019	U1079	G1139	U1199	C1259	A1319	G1379	A1439	A1509
G1540	C660	A600	C720	C840	A900	U960	G1020	A1080	C1140	C1200	G1260	C1320	U1380	U1440	A1500



- Molecule 3: mRNA



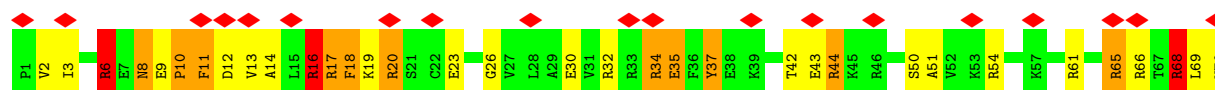
- Molecule 4: P/E-tRNA



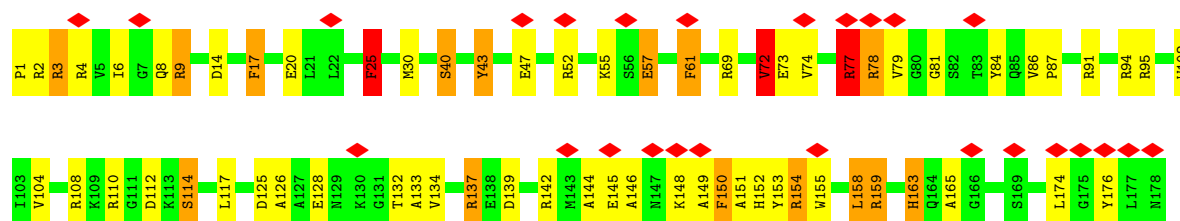
- Molecule 5: 30S ribosomal protein S20



- Molecule 6: 30S ribosomal protein S21

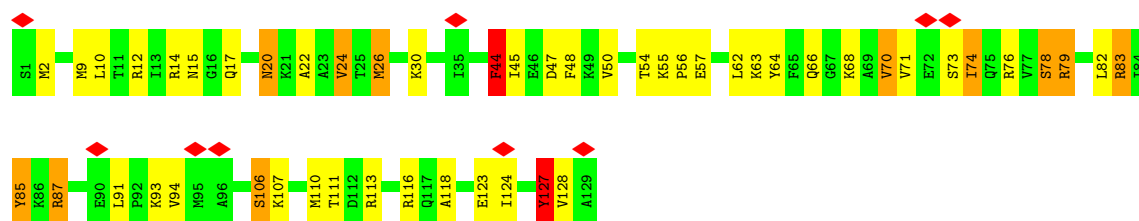


- Molecule 7: 30S ribosomal protein S7

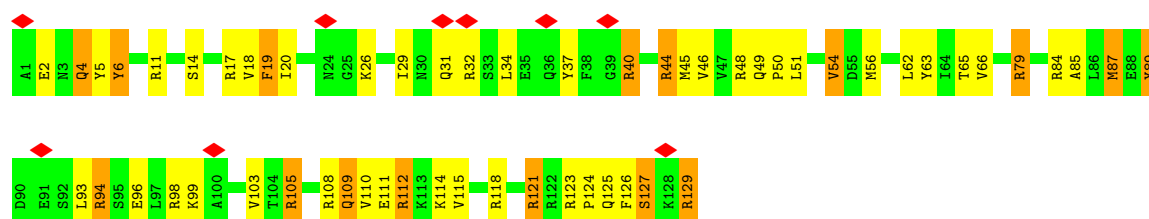


- Molecule 8: 30S ribosomal protein S8

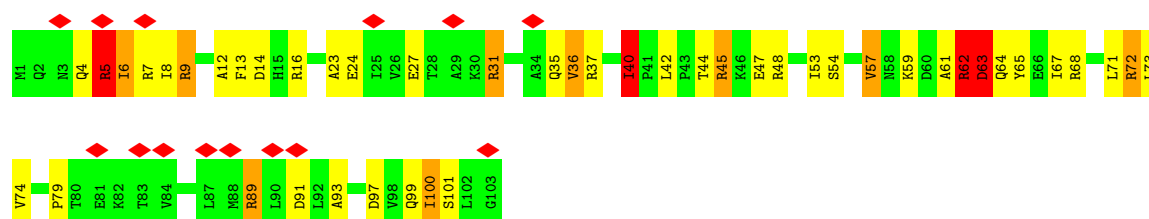




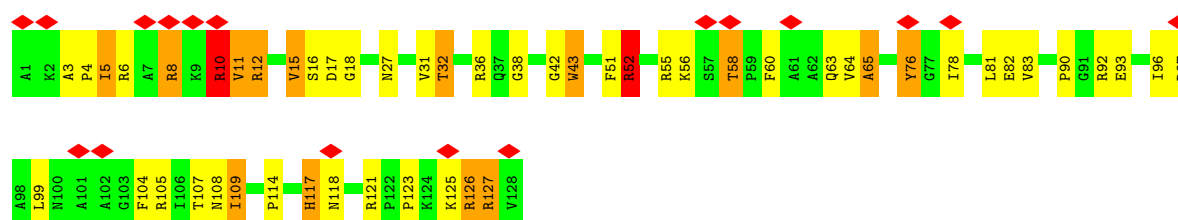
• Molecule 9: 30S ribosomal protein S9



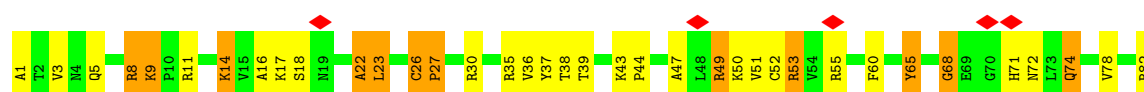
• Molecule 10: 30S ribosomal protein S10

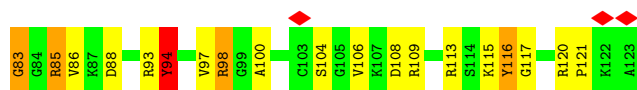


• Molecule 11: 30S ribosomal protein S11



• Molecule 12: 30S ribosomal protein S12

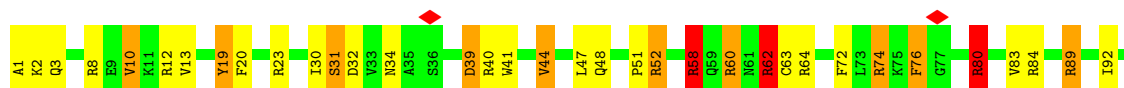




- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14



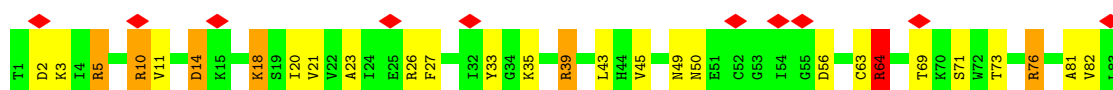
- Molecule 15: 30S ribosomal protein S15



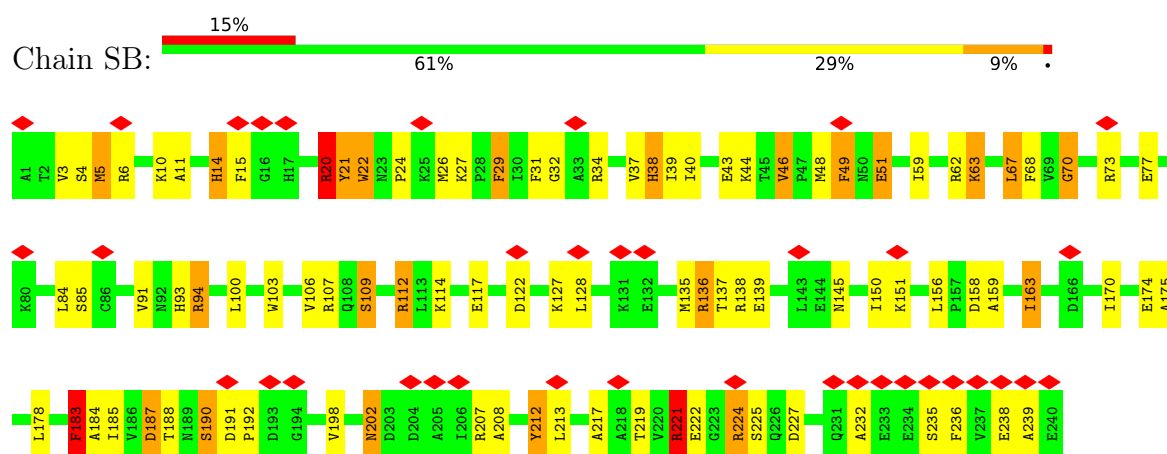
- Molecule 16: 30S ribosomal protein S16



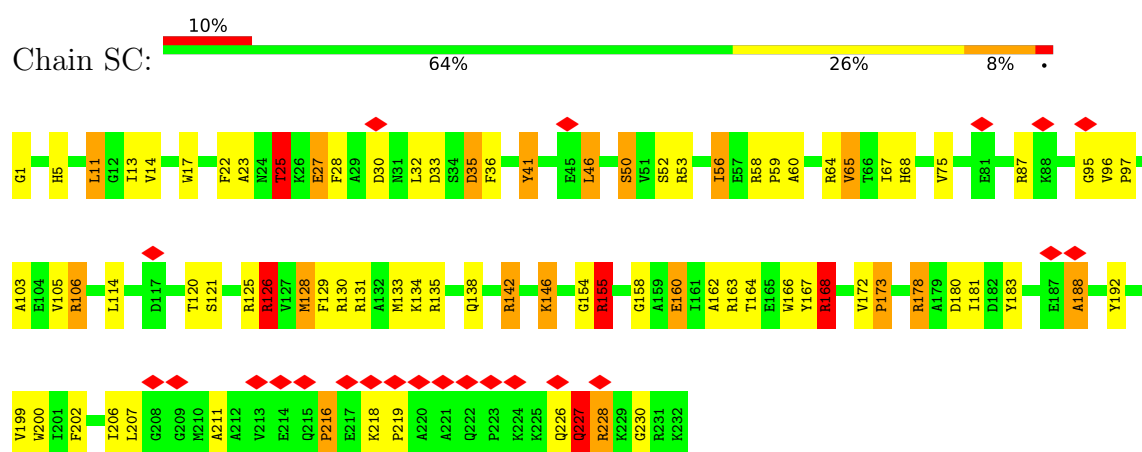
- Molecule 17: 30S ribosomal protein S17



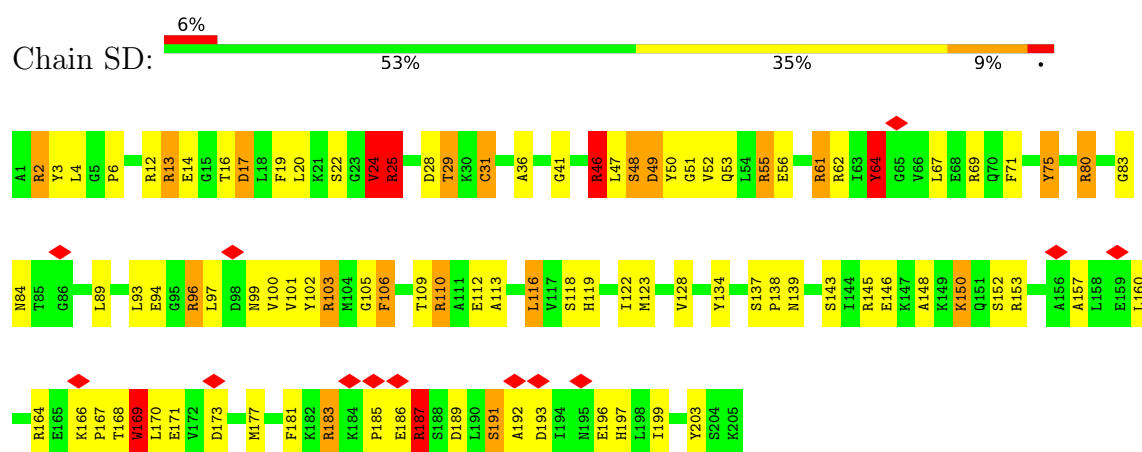
- Molecule 18: 30S ribosomal protein S2



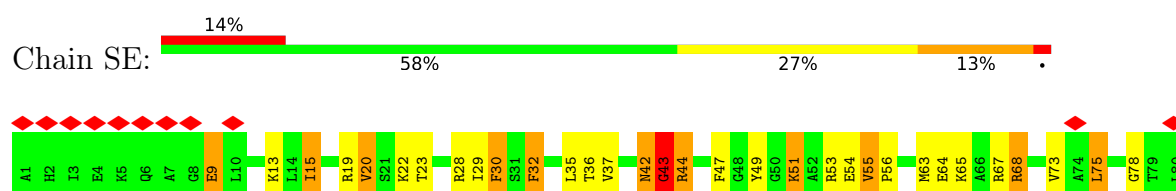
• Molecule 19: 30S ribosomal protein S3

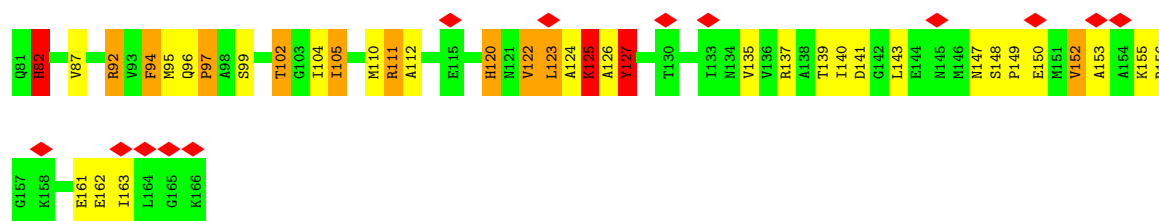


• Molecule 20: 30S ribosomal protein S4

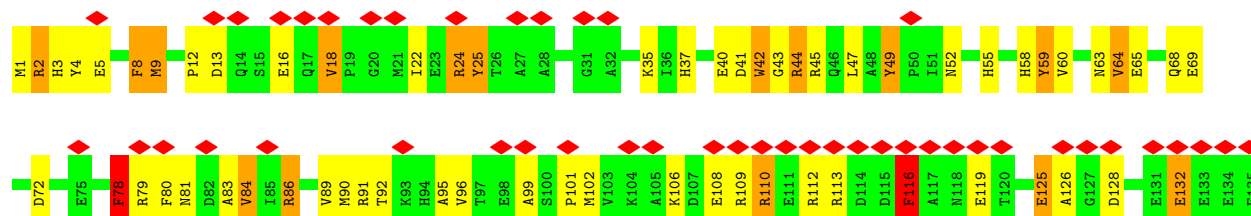


• Molecule 21: 30S ribosomal protein S5





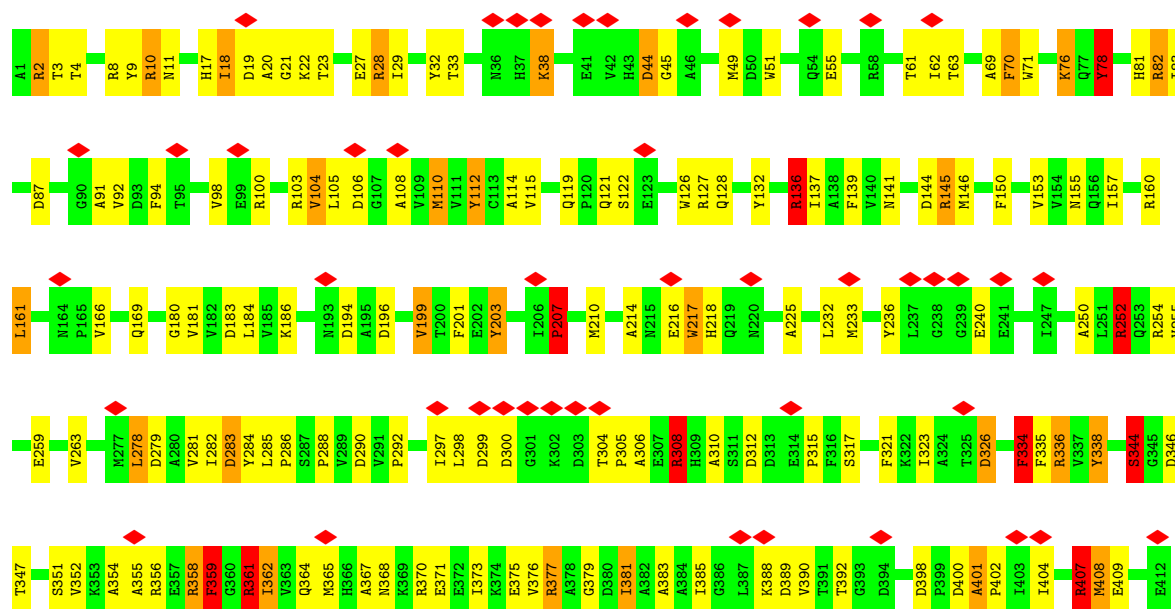
- Molecule 22: 30S ribosomal protein S6

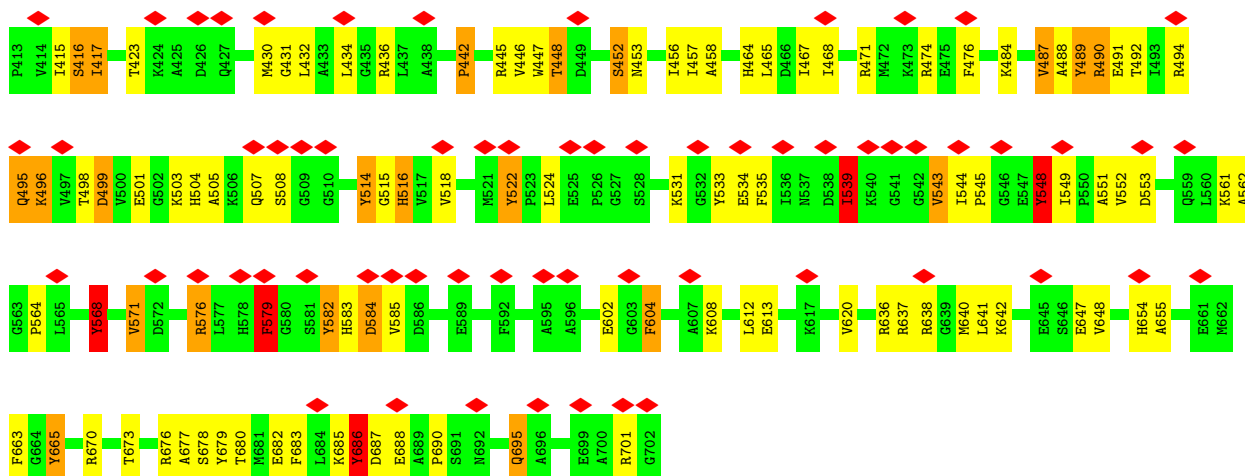


- Molecule 23: 30S ribosomal protein S18

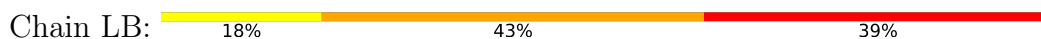


- Molecule 24: Elongation factor G

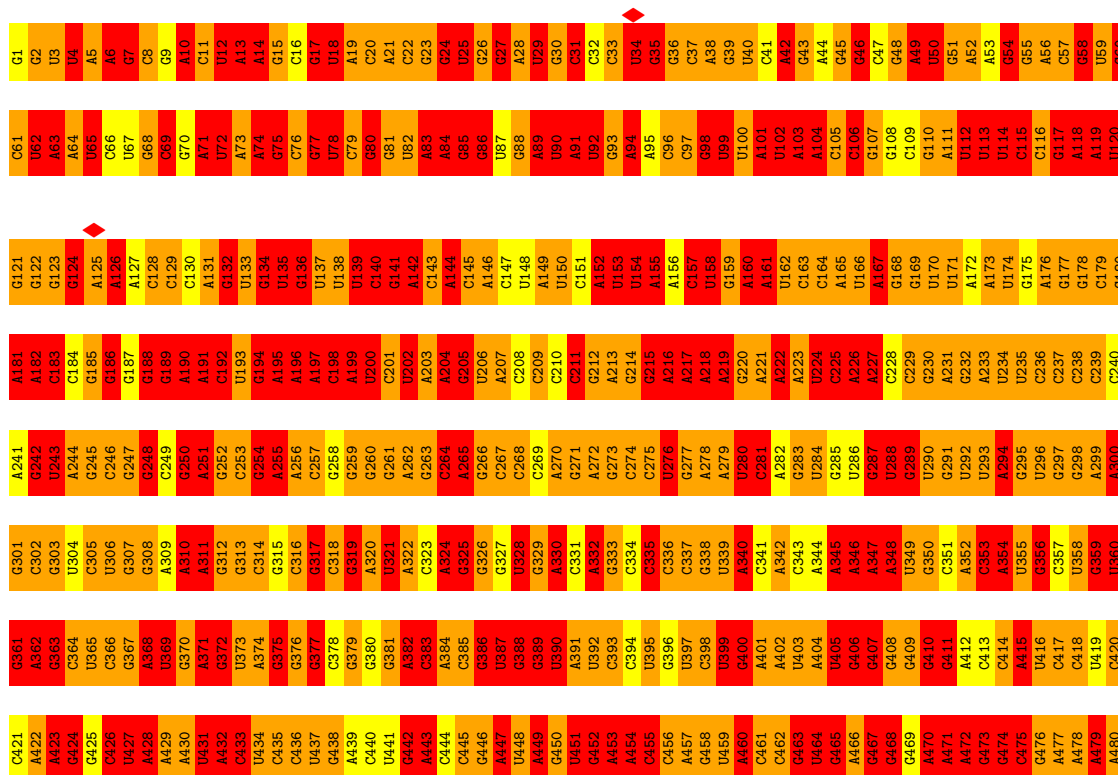




• Molecule 25: 5S ribosomal RNA

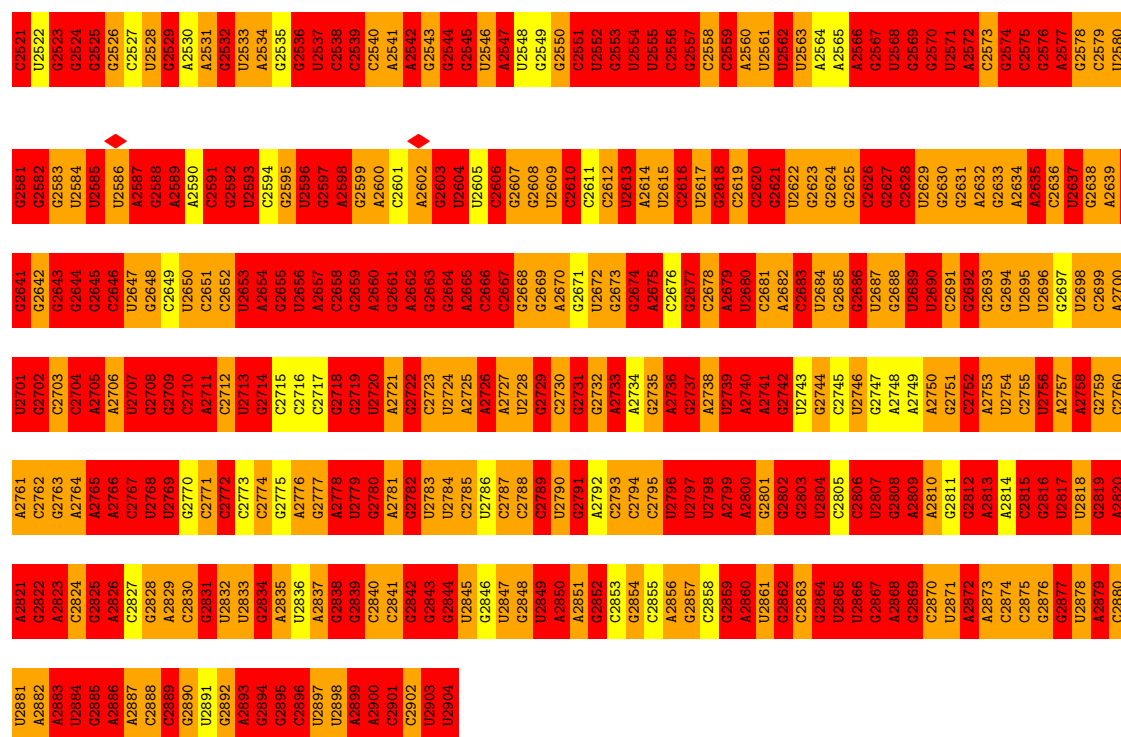


• Molecule 26: 23S ribosomal RNA

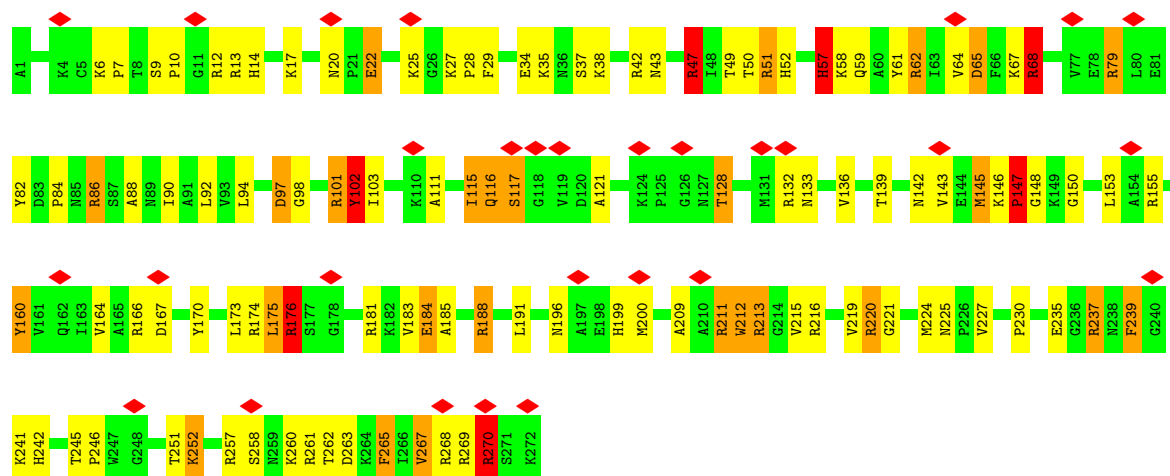


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U1443	A1383	C1323	U1263	U1203	A1143	U1083	U1023	G963	C903	G843	A763	C723	G663	A603	G543	A483
U1444	A1384	C1324	U1264	G1204	A1144	U1084	G1024	U964	G904	A844	G764	U724	G664	G604	C544	A484
G1445	A1385	U1325	A1265	G1205	C1145	A1085	G1025	G965	U905	U845	G765	G725	U665	G605	U545	C485
G1446	C1386	G1326	G1266	G1206	C1146	A1086	G1026	G966	U906	U846	G766	G726	U666	U606	U546	C486
C1447	A1387	A1327	U1267	C1207	A1147	G1087	A1027	U967	G907	U847	G767	A727	U667	U607	A547	C487
G1448	G1388	A1328	A1268	C1208	U1148	A1088	A1028	C968	C908	C848	A768	G728	U668	A608	G548	G488
G1449	G1389	U1329	A1269	U1209	U1149	A1089	A1029	G969	U909	A849	A769	G729	U669	A609	G549	G489
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C1451	U1391	G1331	C1271	C1211	A1151	G1091	G1031	G971	A911	C851	C791	C731	C671	G611	G551	G491
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C1454	U1394	G1334	A1274	A1214	G1154	U1094	G1034	G974	G914	C854	A794	A754	G674	A614	U554	G494
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A1499	A1439	U1379	G1319	U1259	U1199	G1139	C1079	U1019	A959	C897	U839	G779	A719	G659	A599	G539
G1500	U1440	G1380	C1320	A1260	C1200	C1140	A1080	A1020	A960	C898	C840	G780	U720	C660	G600	C540

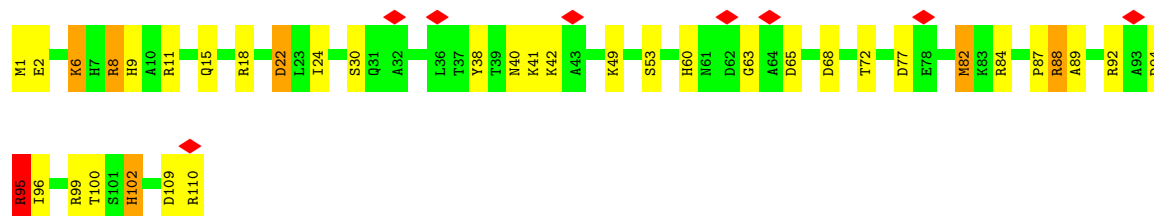
A2481	U2401	G2341	A2281	G2221	C2161	A2101	U2041	A1981	G1921	G1861	A1801	C1741	G1681	U1621	G1501
C2462	U2402	C2342	G2282	C2222	G2162	G2102	A2042	U1962	G1922	G1862	A1802	U1742	G1682	U1622	A1502
C2463	C2403	G2343	A2283	G2223	A2163	C2103	C2043	G1983	U1923	G1863	A1803	U1743	G1683	U1623	A1503
C2464	U2404	U2344	A2284	G2224	C2164	C2104	C2044	G1984	U1924	U1864	A1804	A1744	U1684	U1624	A1504
C2465	G2405	G2345	C2285	A2225	C2165	U2105	C2045	C1985	U1925	U1865	A1805	A1745	C1685	C1625	A1505
C2466	G2406	A2346	G2286	C2226	U2166	U2106	G2046	C1986	U1926	A1866	A1806	A1746	C1686	A1626	A1506
C2467	A2407	C2347	A2287	G2227	U2167	G2107	C2047	A1987	U1927	G1867	A1807	U1747	G1687	G1627	C1507
A2468	U2408	U2348	A2288	G2228	C2168	A2108	G2048	G1988	U1928	G1868	A1808	C1748	U1688	G1628	A1508
A2469	G2409	G2349	G2289	U2229	A2169	U2109	G2049	G1989	U1929	U1869	A1809	U1749	A1689	U1629	A1509
G2470	G2410	C2350	G2290	G2230	A2170	G2110	C2050	C1990	G1930	C1870	A1810	G1750	A1690	G1630	G1510
A2471	A2411	G2351	U2291	U2231	A2171	U2111	A2051	U1991	U1931	A1871	G1811	U1751	A1691	G1631	G1511
G2472	A2412	A2352	U2292	C2232	U2172	G2112	A2052	G1992	A1932	A1872	U1812	C1752	U1692	A1632	C1512
U2473	G2413	G2353	G2293	U2233	A2173	U2113	G2053	U1993	G1933	A1873	G1813	G1753	U1693	G1633	U1513
U2474	G2414	C2354	G2294	G2234	C2174	A2114	A2054	C1994	C1934	C1874	G1814	A1754	C1694	A1634	G1514
C2475	G2415	G2355	G2295	G2235	C2175	G2115	C2055	U1995	G1935	U1875	A1815	A1755	C1695	U1635	A1515
A2476	C2416	U2356	U2296	U2236	A2176	G2116	G2056	C1996	A1936	A1876	G1816	G1756	U1696	U1636	G1516
U2477	G2417	G2357	A2297	G2237	C2177	A2117	G2057	U1997	A1937	A1877	U1817	A1757	C1697	U1637	G1517
A2478	A2418	A2358	G2298	G2238	C2178	U2118	A2058	G1998	A1938	A1878	U1818	U1758	A1698	C1638	C1518
U2479	U2419	G2359	U2299	G2239	C2179	A2119	A2059	G1999	U1939	C1879	A1819	A1759	A1699	A1639	A1519
C2480	G2420	C2360	C2300	U2240	U2180	G2120	A2060	C2000	U1940	U1880	U1820	C1760	A1700	A1640	U1520
G2481	G2421	G2361	C2301	A2241	U2181	G2121	C2061	C2001	C1941	C1881	A1821	C1761	A1701	A1641	G1521
A2482	C2422	C2362	U2302	G2242	U2182	U2122	A2062	G2002	C1942	U1882	G1822	A1762	G1702	G1642	A1522
C2483	U2423	G2363	G2303	U2243	A2183	G2123	C2063	A2003	U1943	U1883	G1823	G1763	G1703	G1643	U1523
G2484	C2424	C2364	G2304	U2244	A2184	G2124	G2064	G2004	U1944	G1884	G1824	C1764	C1704	C1644	G1524
A2485	A2425	G2365	U2305	U2245	U2185	G2125	C2065	A2005	G1945	U1885	U1825	U1765	U1705	G1645	A1525
C2486	A2426	A2366	C2306	G2246	G2186	A2126	C2066	C2006	U1946	U1886	G1826	G1766	C1706	C1646	C1526
G2487	G2427	G2367	G2307	A2247	U2187	G2127	G2067	U2007	C1947	C1887	U1827	G1767	G1707	U1647	G1527
A2488	C2428	C2368	G2308	G2248	U2188	G2128	U2068	C2008	G1948	U1888	G1828	C1768	A1528	A1528	A1528
A2489	G2429	A2369	A2309	U2249	U2189	C2129	G2069	A2009	U1949	A1889	A1829	U1769	A1589	G1529	G1529
G2490	A2430	G2370	C2310	G2250	U2190	U2130	A2070	G2010	G1950	A1890	A1830	G1770	G1710	A1650	A1530
U2491	U2431	G2371	A2311	U2251	A2191	U2131	A2071	U2011	U1951	G1891	G1831	C1771	A1711	G1651	C1531
U2492	A2432	U2372	U2312	G2252	U2192	U2132	C2072	G2012	A1952	C1892	C1832	A1772	U1712	A1652	A1532
U2493	A2433	G2373	C2313	G2253	G2193	G2133	C2073	A2013	A1953	C1893	G1833	C1773	A1713	G1653	C1533
G2494	A2434	C2374	A2314	G2254	U2194	A2134	U2074	A2014	G1954	C1894	U1834	C1774	U1714	A1654	U1534
A2495	A2435	G2375	G2315	G2255	U2195	A2135	U2075	A2015	U1955	C1895	A1835	G1775	G1715	A1655	A1535
C2496	G2436	G2376	G2316	G2256	C2196	G2136	U2076	U2016	U1956	G1896	C1836	G1776	U1716	C1656	A1536
A2497	G2437	A2377	A2317	U2257	U2197	U2137	A2077	U2017	C1957	G1897	C1837	U1777	A1717	U1657	G1537
U2498	U2438	A2378	A2318	C2258	A2198	G2138	C2078	G2018	C1958	U1898	C1838	U1778	G1718	C1658	G1538
C2499	A2439	G2379	G2319	U2259	A2199	U2139	U2079	A2019	G1959	A1899	G1839	U1779	G1719	G1659	U1539
U2500	C2440	C2380	U2320	C2260	C2200	G2140	A2080	A2020	A1960	A1900	G1840	A1780	U1720	G1660	G1540
G2501	U2441	A2381	U2321	C2261	G2201	G2141	U2081	C2021	C1961	A1901	U1841	U1781	G1721	G1661	C1541
C2502	C2442	C2382	A2322	U2262	U2202	A2142	A2082	U2022	C1962	C1902	G1842	U1782	A1722	G1662	U1542
G2503	G2443	G2383	C2323	C2263	U2203	C2143	G2083	C2023	U1963	G1903	C1843	A1783	G1723	G1663	G1543
U2504	G2444	U2384	U2324	C2264	G2204	G2144	C2084	G2024	G1964	G1904	C1844	A1784	G1724	A1664	A1544
G2505	G2445	C2385	G2325	U2265	A2205	C2145	U2085	C2025	C1965	G1905	G1845	A1785	U1725	A1665	A1545
U2506	G2446	A2386	C2326	A2266	C2206	C2146	U2086	U2026	A1966	G1906	G1846	A1786	C1726	G1666	G1546
C2507	G2447	U2387	A2327	G2267	C2207	A2147	G2087	G2027	C1967	G1907	A1847	A1787	C1727	G1667	C1547
A2508	U2448	A2388	A2328	A2268	C2208	G2148	A2088	U2028	G1968	C1908	A1848	A1788	U1728	A1668	A1548
G2509	U2449	G2389	U2329	G2269	G2209	U2149	C2089	G2029	A1969	G1909	G1849	A1789	U1729	A1669	A1549
C2510	A2450	U2390	G2330	A2270	U2210	C2150	A2090	U2030	A1970	G1910	G1850	C1790	G1730	C1670	A1550
U2511	A2451	G2391	G2331	G2271	A2211	U2151	C2091	A2031	U1971	U1911	U1851	A1791	C1731	U1671	A1551
C2512	A2452	C2392	C2332	U2272	A2212	G2152	U2092	G2032	G1972	A1912	U1852	G1792	C1732	A1672	A1552
A2513	U2453	U2393	A2333	C2273	U2213	C2153	G2093	A2033	G1973	A1913	A1853	C1793	G1733	G1673	A1553
U2514	G2454	C2394	U2334	A2274	C2214	A2054	A2094	U2034	C1974	C1914	A1854	A1794	G1734	G1674	U1554
C2515	G2455	C2395	A2335	G2275	U2215	U2155	A2095	G2035	G1975	C1915	U1855	G1795	A1735	C1675	G1555
A2516	C2456	G2396	C2336	G2276	G2216	C2156	C2096	G2036	U1976	U1916	U1856	U1796	U1736	A1676	C1556
C2517	U2457	G2397	G2337	G2277	G2217	G2157	A2097	A2037	A1977	U1917	C1857	G1797	G1737	A1677	C1557
U2518	A2458	U2398	C2338	A2278	U2218	A2158	U2098	G2038	A1978	A1918	A1858	U1798	G1738	A1678	C1558
A2519	G2459	G2399	C2339	G2279	G2219	C2159	U2099	U2039	U1979	A1919	U1859	A1799	G1739	A1679	U1559
C2520	U2460	G2400	A2340	G2280	U2220	C2160	G2100	G2040	G1980	C1920	G1860	C1800	G1740	U1680	G1560



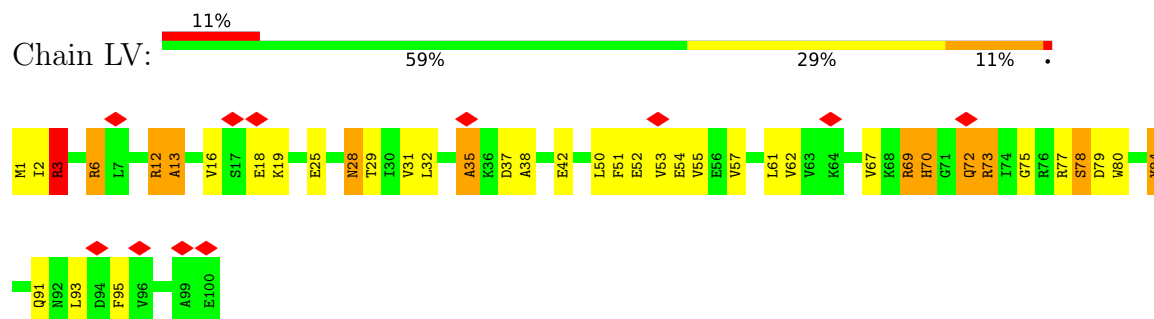
• Molecule 27: 50S ribosomal protein L2



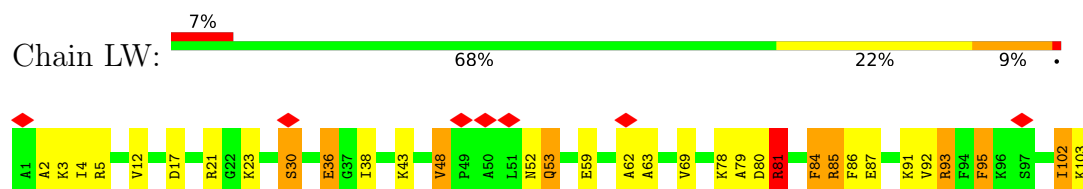
• Molecule 28: 50S ribosomal protein L22



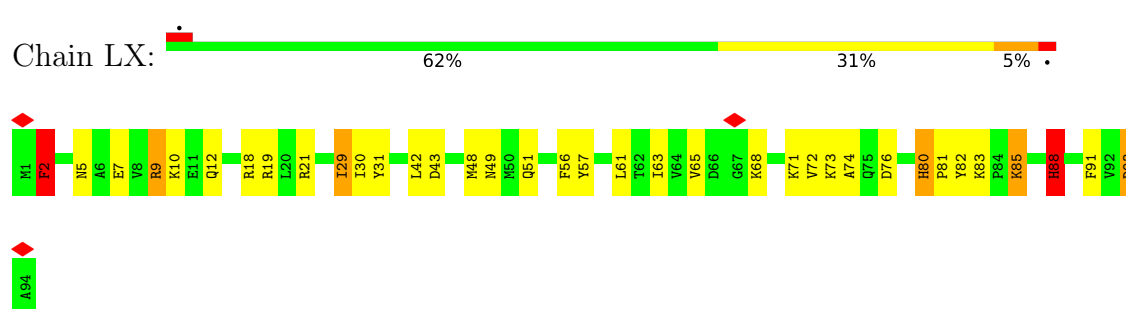
- Molecule 29: 50S ribosomal protein L23



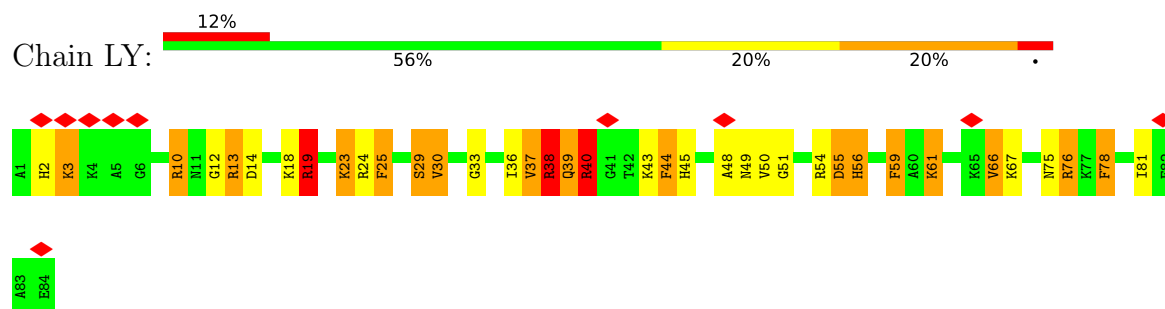
- Molecule 30: 50S ribosomal protein L24



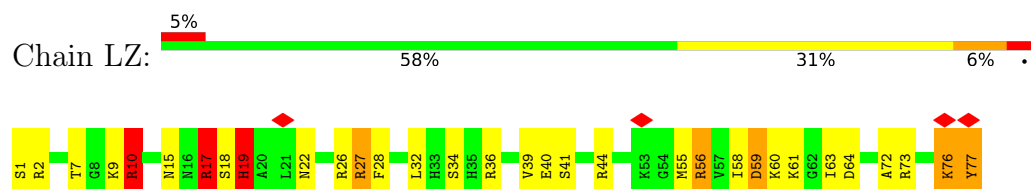
- Molecule 31: 50S ribosomal protein L25



- Molecule 32: 50S ribosomal protein L27



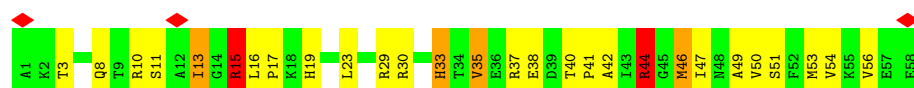
- Molecule 33: 50S ribosomal protein L28



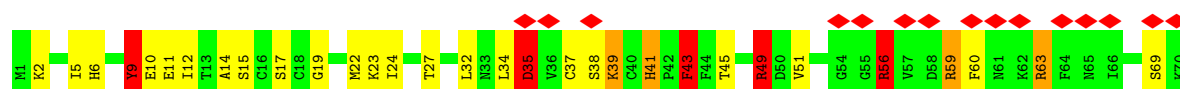
- Molecule 34: 50S ribosomal protein L29



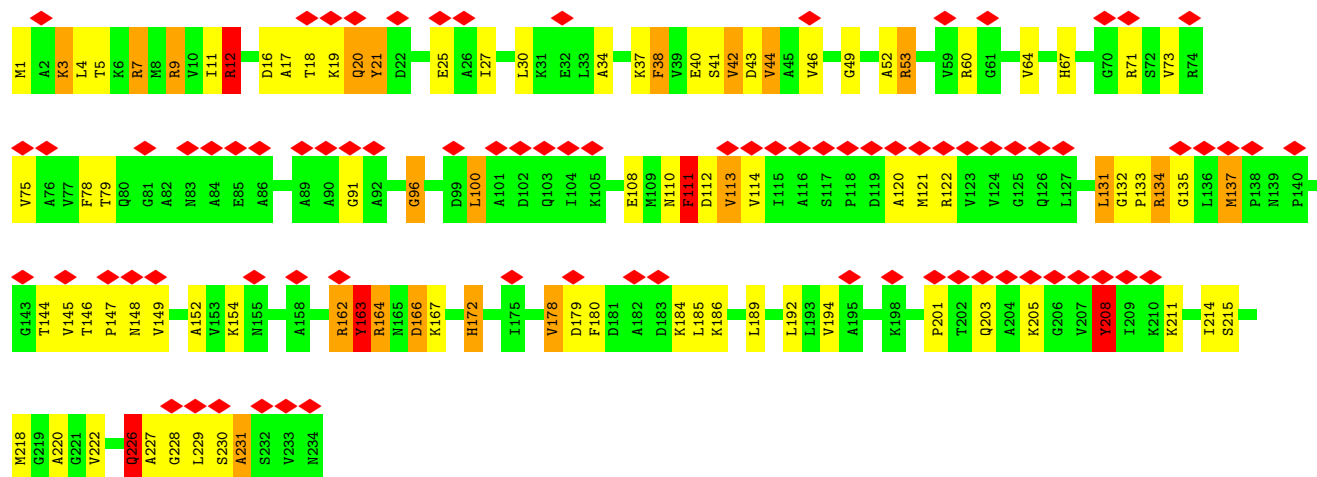
- Molecule 35: 50S ribosomal protein L30



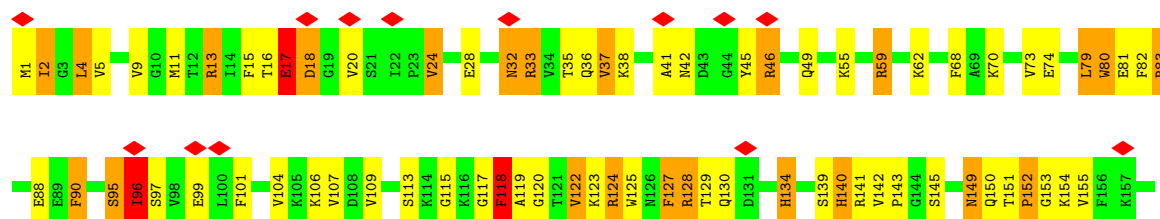
- Molecule 36: 50S ribosomal protein L31

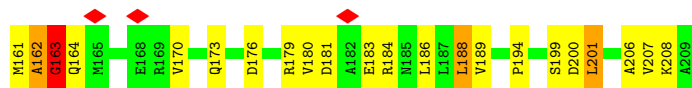


- Molecule 37: 50S ribosomal protein L1

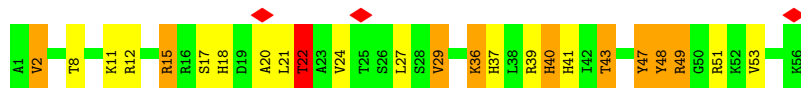


- Molecule 38: 50S ribosomal protein L3





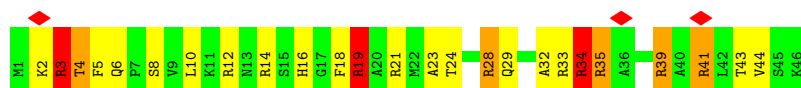
- Molecule 39: 50S ribosomal protein L32



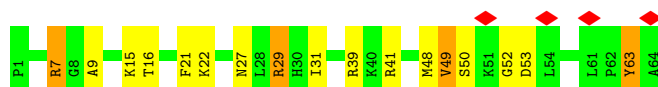
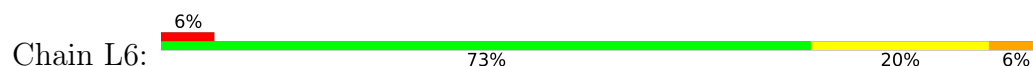
- Molecule 40: 50S ribosomal protein L33



- Molecule 41: 50S ribosomal protein L34



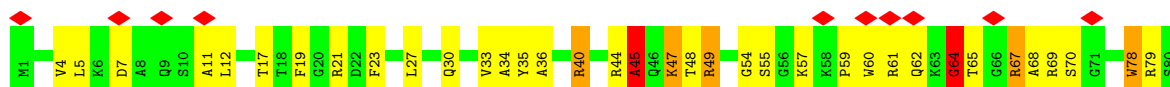
- Molecule 42: 50S ribosomal protein L35

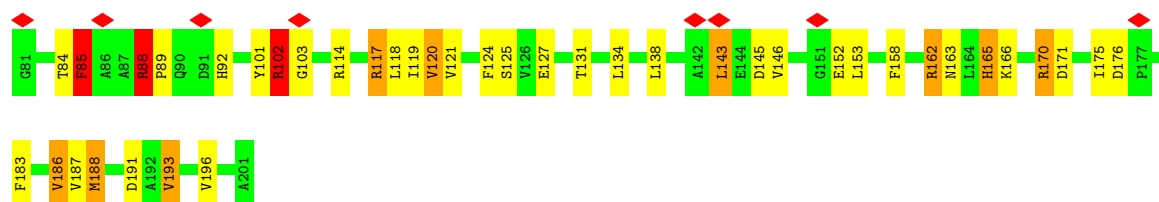


- Molecule 43: 50S ribosomal protein L36



- Molecule 44: 50S ribosomal protein L4

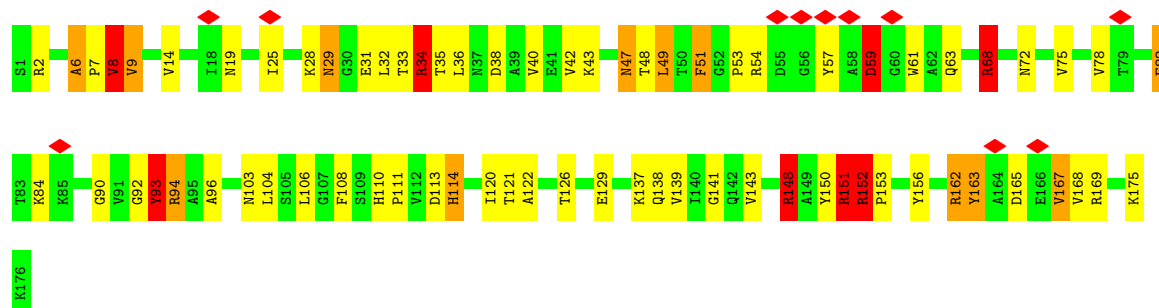




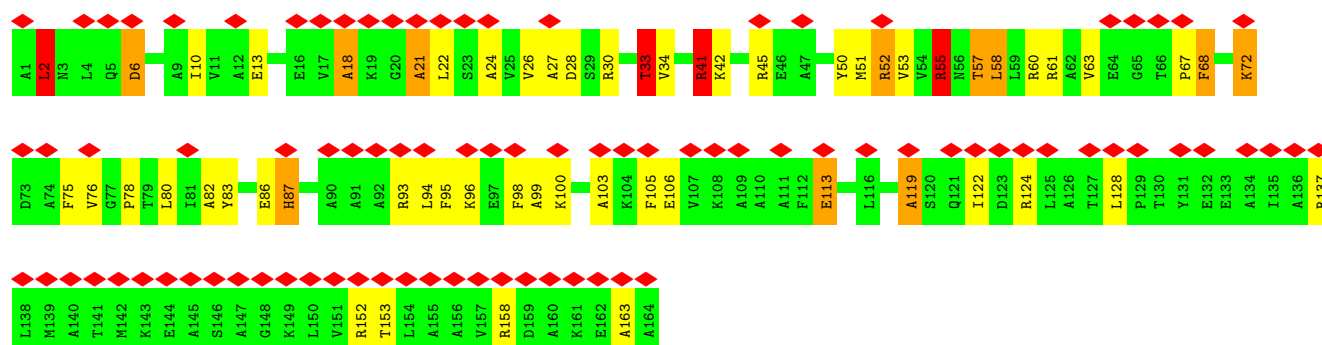
• Molecule 45: 50S ribosomal protein L5



• Molecule 46: 50S ribosomal protein L6

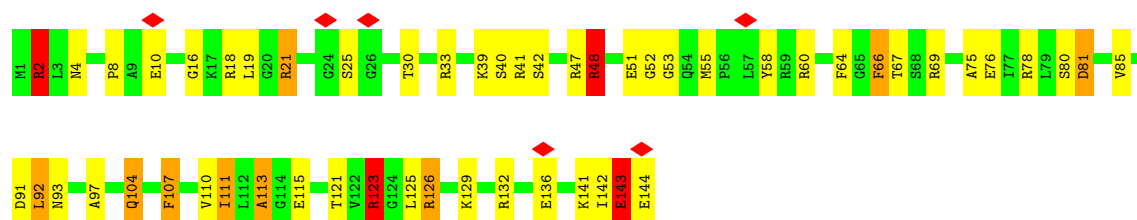


• Molecule 47: 50S ribosomal protein L10



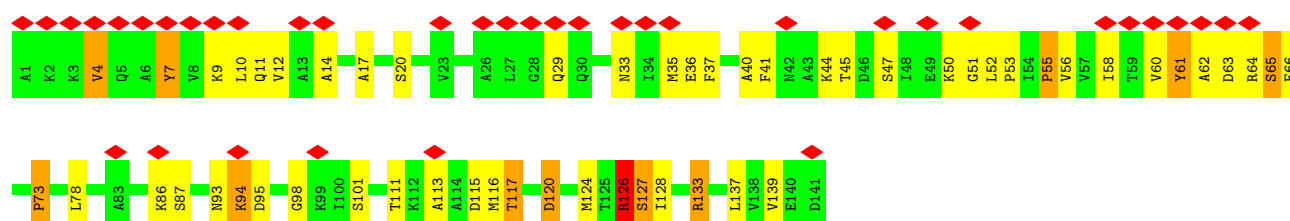
- Molecule 48: 50S ribosomal protein L15

Chain LN:  62% 28% 6%



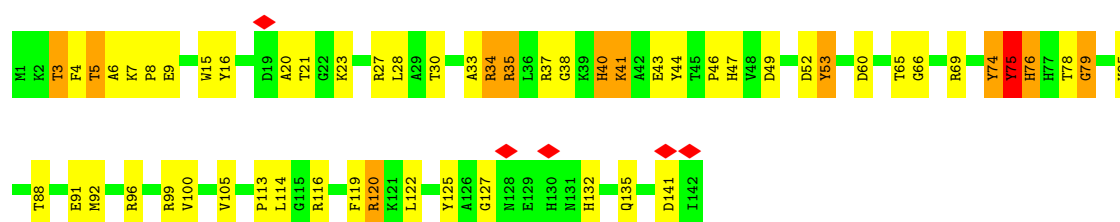
- Molecule 49: 50S ribosomal protein L11

Chain LK:  27% 61% 30% 8%




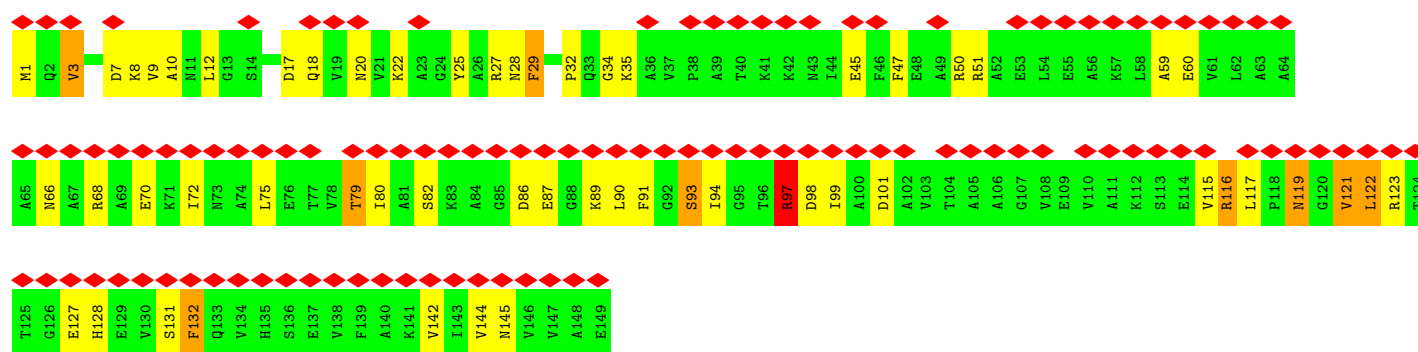
- Molecule 50: 50S ribosomal protein L13

Chain LL:  60% 32% 8%



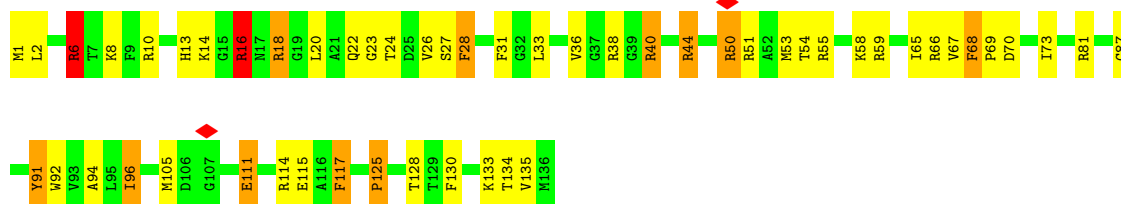
- Molecule 51: 50S ribosomal protein L9

Chain LI:  75% 62% 32% 6%



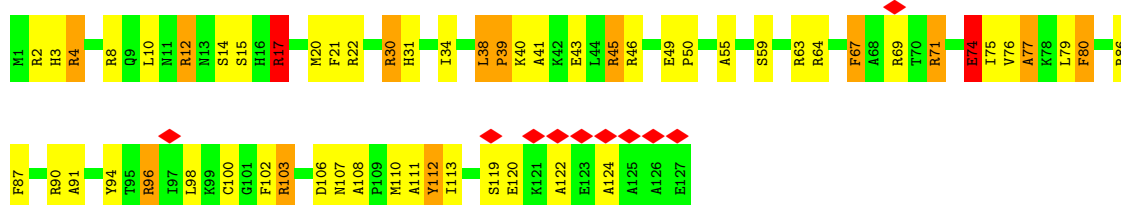
- Molecule 52: 50S ribosomal protein L16

Chain LO:  61% 29% 8%



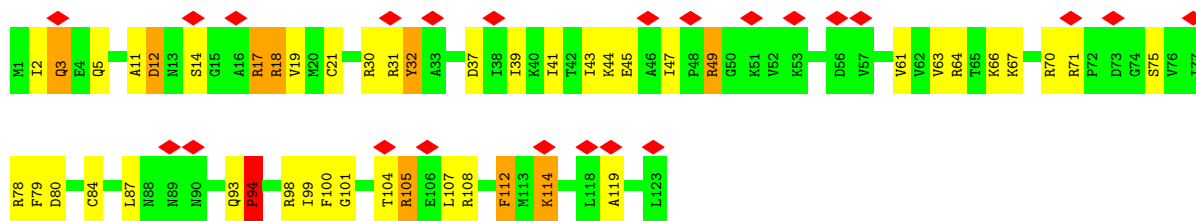
- Molecule 53: 50S ribosomal protein L17

Chain LP:  8% 54% 34% 10%



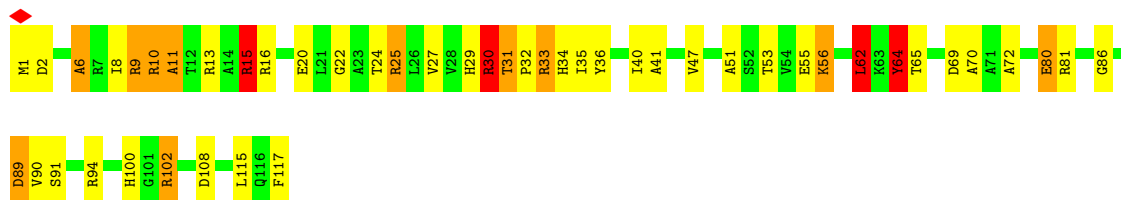
- Molecule 54: 50S ribosomal protein L14

Chain LM:  19% 62% 30% 7%



- Molecule 55: 50S ribosomal protein L18

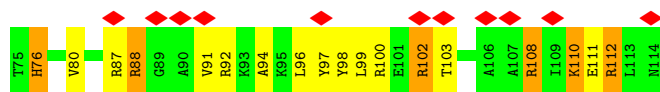
Chain LQ:  59% 28% 9%



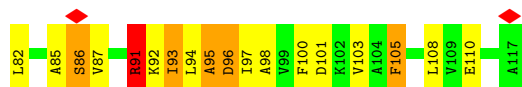
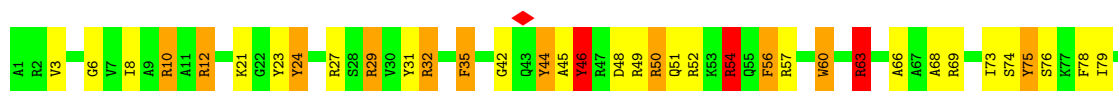
- Molecule 56: 50S ribosomal protein L19

Chain LR:  19% 53% 32% 13%

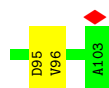
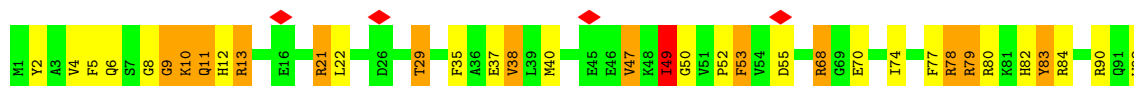




- Molecule 57: 50S ribosomal protein L20



- Molecule 58: 50S ribosomal protein L21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	50000	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	0.207	Depositor
Minimum map value	-0.084	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	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	SS	1.56	2/744 (0.3%)	2.24	33/995 (3.3%)
2	SA	3.39	5085/37035 (13.7%)	3.51	8259/57774 (14.3%)
3	S1	3.38	150/1108 (13.5%)	3.59	243/1724 (14.1%)
4	S2	3.42	257/1831 (14.0%)	3.58	423/2853 (14.8%)
5	ST	1.63	4/676 (0.6%)	2.23	33/895 (3.7%)
6	SU	1.70	5/598 (0.8%)	2.73	30/792 (3.8%)
7	SG	1.68	10/1422 (0.7%)	2.09	48/1908 (2.5%)
8	SH	1.58	5/989 (0.5%)	2.10	33/1326 (2.5%)
9	SI	1.67	6/1048 (0.6%)	2.18	43/1394 (3.1%)
10	SJ	1.65	8/835 (1.0%)	2.13	34/1127 (3.0%)
11	SK	1.67	8/982 (0.8%)	2.23	33/1323 (2.5%)
12	SL	1.66	6/969 (0.6%)	2.28	46/1300 (3.5%)
13	SM	1.61	3/919 (0.3%)	2.36	43/1226 (3.5%)
14	SN	1.59	6/817 (0.7%)	2.23	36/1088 (3.3%)
15	SO	1.56	5/724 (0.7%)	2.20	29/966 (3.0%)
16	SP	1.56	4/659 (0.6%)	2.17	25/884 (2.8%)
17	SQ	1.66	3/681 (0.4%)	2.07	20/913 (2.2%)
18	SB	1.61	10/1904 (0.5%)	2.05	63/2565 (2.5%)
19	SC	1.60	8/1852 (0.4%)	2.10	50/2490 (2.0%)
20	SD	1.65	17/1665 (1.0%)	2.20	62/2227 (2.8%)
21	SE	1.60	8/1239 (0.6%)	2.11	38/1664 (2.3%)
22	SF	1.65	8/1121 (0.7%)	2.34	42/1509 (2.8%)
23	SR	1.71	9/637 (1.4%)	2.26	25/851 (2.9%)
24	S3	1.63	40/5532 (0.7%)	2.11	178/7485 (2.4%)
25	LB	3.37	384/2869 (13.4%)	3.42	601/4474 (13.4%)
26	LA	3.49	10162/69808 (14.6%)	3.51	15513/108905 (14.2%)
27	LD	1.64	14/2131 (0.7%)	2.20	72/2863 (2.5%)
28	LU	1.50	3/864 (0.3%)	2.05	25/1156 (2.2%)
29	LV	1.62	6/794 (0.8%)	2.08	29/1060 (2.7%)
30	LW	1.58	4/797 (0.5%)	2.12	17/1062 (1.6%)
31	LX	1.61	4/766 (0.5%)	2.09	29/1025 (2.8%)
32	LY	1.71	4/642 (0.6%)	2.27	25/848 (2.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	1.74	6/635 (0.9%)	2.24	24/848 (2.8%)
34	L0	1.56	2/510 (0.4%)	2.31	24/677 (3.5%)
35	L1	1.56	2/453 (0.4%)	2.22	19/605 (3.1%)
36	L2	1.57	1/559 (0.2%)	2.11	15/745 (2.0%)
37	LC	1.62	11/1748 (0.6%)	2.15	59/2355 (2.5%)
38	LE	1.66	10/1586 (0.6%)	2.14	61/2134 (2.9%)
39	L3	1.63	2/450 (0.4%)	1.98	9/599 (1.5%)
40	L4	1.67	4/448 (0.9%)	2.12	11/594 (1.9%)
41	L5	1.66	1/380 (0.3%)	2.65	31/498 (6.2%)
42	L6	1.53	1/513 (0.2%)	2.02	14/676 (2.1%)
43	L7	1.53	0/303	2.12	9/397 (2.3%)
44	LF	1.66	10/1571 (0.6%)	2.07	53/2113 (2.5%)
45	LG	1.60	5/1444 (0.3%)	2.28	64/1937 (3.3%)
46	LH	1.62	8/1343 (0.6%)	2.17	53/1816 (2.9%)
47	LJ	1.60	4/1247 (0.3%)	2.08	46/1679 (2.7%)
48	LN	1.56	5/1062 (0.5%)	2.24	42/1413 (3.0%)
49	LK	1.58	6/1046 (0.6%)	2.07	33/1410 (2.3%)
50	LL	1.71	10/1152 (0.9%)	2.19	45/1551 (2.9%)
51	LI	1.58	4/1122 (0.4%)	2.10	30/1515 (2.0%)
52	LO	1.63	9/1093 (0.8%)	2.27	29/1460 (2.0%)
53	LP	1.69	11/1021 (1.1%)	2.21	45/1364 (3.3%)
54	LM	1.59	2/956 (0.2%)	2.32	35/1279 (2.7%)
55	LQ	1.67	6/910 (0.7%)	2.00	28/1219 (2.3%)
56	LR	1.72	8/929 (0.9%)	2.27	32/1242 (2.6%)
57	LS	1.62	6/960 (0.6%)	2.27	39/1278 (3.1%)
58	LT	1.62	2/829 (0.2%)	2.18	32/1107 (2.9%)
All	All	2.97	16384/168928 (9.7%)	3.17	27062/251183 (10.8%)

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	SS	0	11
2	SA	0	979
3	S1	0	36
4	S2	0	48
5	ST	0	5
6	SU	0	11
7	SG	0	19
8	SH	0	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	SI	0	7
10	SJ	0	9
11	SK	0	7
12	SL	0	10
13	SM	0	8
14	SN	0	11
15	SO	0	7
16	SP	0	9
17	SQ	0	6
18	SB	0	13
19	SC	0	11
20	SD	0	18
21	SE	0	11
22	SF	0	12
23	SR	0	9
24	S3	0	38
25	LB	0	68
26	LA	5	1948
27	LD	0	24
28	LU	0	8
29	LV	0	5
30	LW	0	8
31	LX	0	5
32	LY	0	8
33	LZ	0	7
34	L0	0	2
35	L1	0	3
36	L2	0	9
37	LC	0	17
38	LE	0	15
39	L3	0	5
40	L4	0	4
41	L5	0	7
42	L6	0	2
43	L7	0	4
44	LF	0	10
45	LG	0	15
46	LH	0	13
47	LJ	0	10
48	LN	0	12
49	LK	0	10
50	LL	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
51	LI	0	7
52	LO	0	8
53	LP	0	10
54	LM	0	9
55	LQ	0	14
56	LR	0	11
57	LS	0	12
58	LT	0	8
All	All	5	3608

The worst 5 of 16384 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	SA	199	A	N7-C5	-23.19	1.25	1.39
26	LA	727	A	N7-C5	-22.32	1.25	1.39
26	LA	1791	A	N9-C4	-20.53	1.25	1.37
2	SA	298	A	N7-C5	-20.39	1.27	1.39
26	LA	743	A	N7-C5	-19.99	1.27	1.39

The worst 5 of 27062 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	SF	44	ARG	NE-CZ-NH1	30.21	135.41	120.30
26	LA	826	U	P-O3'-C3'	28.10	153.42	119.70
26	LA	2451	A	O4'-C1'-N9	27.95	130.56	108.20
26	LA	1005	C	C6-N1-C2	-25.59	110.06	120.30
26	LA	2899	A	N1-C6-N6	23.91	132.94	118.60

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
26	LA	2451	A	C1'
26	LA	2503	A	C2'
26	LA	2504	U	C3',C2'
26	LA	2575	C	C4'

5 of 3608 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	SS	1	PRO	Peptide
1	SS	10	ILE	Peptide
1	SS	2	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	SS	3	SER	Peptide
1	SS	8	PRO	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	SS	727	0	769	10	0
2	SA	33076	0	16190	637	0
3	S1	993	0	496	16	0
4	S2	1639	0	816	32	0
5	ST	670	0	722	2	0
6	SU	590	0	631	6	0
7	SG	1400	0	1449	13	0
8	SH	979	0	1034	5	0
9	SI	1036	0	1084	9	0
10	SJ	825	0	865	9	0
11	SK	965	0	997	13	0
12	SL	955	0	1019	10	0
13	SM	910	0	981	9	0
14	SN	805	0	847	5	0
15	SO	716	0	742	4	0
16	SP	649	0	666	3	0
17	SQ	672	0	716	2	0
18	SB	1872	0	1885	15	0
19	SC	1822	0	1913	13	0
20	SD	1643	0	1710	21	0
21	SE	1225	0	1273	18	0
22	SF	1101	0	1050	11	0
23	SR	626	0	651	6	0
24	S3	5431	0	5403	46	0
25	LB	2566	0	1269	48	0
26	LA	62330	0	30424	1516	0
27	LD	2092	0	2170	21	0
28	LU	857	0	922	5	0
29	LV	787	0	846	5	0
30	LW	789	0	847	9	0
31	LX	753	0	780	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	LY	634	0	655	16	0
33	LZ	625	0	655	2	0
34	L0	509	0	543	5	0
35	L1	449	0	491	3	0
36	L2	549	0	552	5	0
37	LC	1733	0	1824	19	0
38	LE	1565	0	1616	21	0
39	L3	444	0	461	8	0
40	L4	441	0	485	4	0
41	L5	377	0	418	7	0
42	L6	504	0	574	3	0
43	L7	302	0	343	3	0
44	LF	1552	0	1619	18	0
45	LG	1420	0	1460	16	0
46	LH	1323	0	1374	6	0
47	LJ	1233	0	1283	6	0
48	LN	1053	0	1129	7	0
49	LK	1032	0	1088	3	0
50	LL	1129	0	1162	9	0
51	LI	1111	0	1148	6	0
52	LO	1074	0	1157	17	0
53	LP	1008	0	1045	10	0
54	LM	947	0	1023	6	0
55	LQ	900	0	935	9	0
56	LR	917	0	965	5	0
57	LS	947	0	1022	15	0
58	LT	816	0	839	7	0
59	S3	32	0	12	0	0
All	All	156127	0	107045	2623	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 10.

The worst 5 of 2623 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)
21:SE:123:LEU:HD13	21:SE:124:ALA:H	1.44	0.83
2:SA:1381:U:H1'	7:SG:152:HIS:CE1	2.16	0.80
26:LA:1853:A:H61	26:LA:2087:G:H1'	1.47	0.80
26:LA:1965:C:C2	26:LA:1966:A:H2'	2.18	0.78
2:SA:803:G:C5	2:SA:804:U:C4	2.72	0.78

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	SS	89/91 (98%)	71 (80%)	13 (15%)	5 (6%)	2	19
5	ST	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
6	SU	68/70 (97%)	46 (68%)	14 (21%)	8 (12%)	0	5
7	SG	176/178 (99%)	154 (88%)	14 (8%)	8 (4%)	2	23
8	SH	127/129 (98%)	103 (81%)	16 (13%)	8 (6%)	1	17
9	SI	127/129 (98%)	99 (78%)	22 (17%)	6 (5%)	2	22
10	SJ	101/103 (98%)	83 (82%)	11 (11%)	7 (7%)	1	14
11	SK	126/128 (98%)	102 (81%)	18 (14%)	6 (5%)	2	22
12	SL	121/123 (98%)	95 (78%)	14 (12%)	12 (10%)	0	8
13	SM	115/117 (98%)	97 (84%)	11 (10%)	7 (6%)	1	17
14	SN	98/100 (98%)	81 (83%)	12 (12%)	5 (5%)	2	20
15	SO	86/88 (98%)	76 (88%)	7 (8%)	3 (4%)	3	30
16	SP	80/82 (98%)	72 (90%)	4 (5%)	4 (5%)	2	21
17	SQ	81/83 (98%)	67 (83%)	9 (11%)	5 (6%)	1	17
18	SB	238/240 (99%)	212 (89%)	14 (6%)	12 (5%)	2	21
19	SC	230/232 (99%)	196 (85%)	18 (8%)	16 (7%)	1	14
20	SD	203/205 (99%)	166 (82%)	26 (13%)	11 (5%)	2	19
21	SE	164/166 (99%)	127 (77%)	24 (15%)	13 (8%)	1	11
22	SF	133/135 (98%)	114 (86%)	11 (8%)	8 (6%)	1	17
23	SR	72/74 (97%)	57 (79%)	10 (14%)	5 (7%)	1	14
24	S3	700/702 (100%)	611 (87%)	61 (9%)	28 (4%)	3	26
27	LD	270/272 (99%)	215 (80%)	42 (16%)	13 (5%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	LU	108/110 (98%)	95 (88%)	11 (10%)	2 (2%)	8	42
29	LV	98/100 (98%)	75 (76%)	13 (13%)	10 (10%)	0	7
30	LW	101/103 (98%)	84 (83%)	12 (12%)	5 (5%)	2	21
31	LX	92/94 (98%)	83 (90%)	5 (5%)	4 (4%)	2	24
32	LY	82/84 (98%)	57 (70%)	15 (18%)	10 (12%)	0	5
33	LZ	75/77 (97%)	63 (84%)	10 (13%)	2 (3%)	5	35
34	L0	61/63 (97%)	51 (84%)	8 (13%)	2 (3%)	4	31
35	L1	56/58 (97%)	45 (80%)	7 (12%)	4 (7%)	1	14
36	L2	68/70 (97%)	44 (65%)	15 (22%)	9 (13%)	0	4
37	LC	232/234 (99%)	192 (83%)	29 (12%)	11 (5%)	2	22
38	LE	207/209 (99%)	151 (73%)	34 (16%)	22 (11%)	0	7
39	L3	54/56 (96%)	40 (74%)	7 (13%)	7 (13%)	0	5
40	L4	52/54 (96%)	45 (86%)	5 (10%)	2 (4%)	3	27
41	L5	44/46 (96%)	34 (77%)	7 (16%)	3 (7%)	1	15
42	L6	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	9	46
43	L7	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	4
44	LF	199/201 (99%)	163 (82%)	21 (11%)	15 (8%)	1	12
45	LG	176/178 (99%)	133 (76%)	26 (15%)	17 (10%)	0	8
46	LH	174/176 (99%)	127 (73%)	29 (17%)	18 (10%)	0	7
47	LJ	162/164 (99%)	143 (88%)	11 (7%)	8 (5%)	2	21
48	LN	142/144 (99%)	116 (82%)	22 (16%)	4 (3%)	5	34
49	LK	139/141 (99%)	114 (82%)	17 (12%)	8 (6%)	1	18
50	LL	140/142 (99%)	116 (83%)	14 (10%)	10 (7%)	1	14
51	LI	147/149 (99%)	121 (82%)	16 (11%)	10 (7%)	1	15
52	LO	134/136 (98%)	111 (83%)	14 (10%)	9 (7%)	1	15
53	LP	125/127 (98%)	109 (87%)	10 (8%)	6 (5%)	2	22
54	LM	121/123 (98%)	91 (75%)	18 (15%)	12 (10%)	0	8
55	LQ	115/117 (98%)	108 (94%)	5 (4%)	2 (2%)	9	45
56	LR	112/114 (98%)	79 (70%)	17 (15%)	16 (14%)	0	4
57	LS	115/117 (98%)	104 (90%)	5 (4%)	6 (5%)	2	20
58	LT	101/103 (98%)	87 (86%)	11 (11%)	3 (3%)	4	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7019/7125 (98%)	5781 (82%)	805 (12%)	433 (6%)	3	17

5 of 433 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	SS	11	ASP
1	SS	37	SER
1	SS	75	PRO
6	SU	10	PRO
6	SU	18	PHE

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	
1	SS	78/78 (100%)	65 (83%)	13 (17%)	2	14
5	ST	65/65 (100%)	60 (92%)	5 (8%)	13	45
6	SU	60/60 (100%)	54 (90%)	6 (10%)	7	35
7	SG	146/146 (100%)	134 (92%)	12 (8%)	11	42
8	SH	104/104 (100%)	90 (86%)	14 (14%)	4	23
9	SI	106/106 (100%)	91 (86%)	15 (14%)	3	21
10	SJ	90/90 (100%)	80 (89%)	10 (11%)	6	31
11	SK	98/98 (100%)	90 (92%)	8 (8%)	11	42
12	SL	103/103 (100%)	97 (94%)	6 (6%)	20	55
13	SM	95/95 (100%)	81 (85%)	14 (15%)	3	20
14	SN	83/83 (100%)	78 (94%)	5 (6%)	19	54
15	SO	76/76 (100%)	69 (91%)	7 (9%)	9	39
16	SP	65/65 (100%)	58 (89%)	7 (11%)	6	32
17	SQ	77/77 (100%)	75 (97%)	2 (3%)	46	74
18	SB	198/198 (100%)	183 (92%)	15 (8%)	13	45
19	SC	189/189 (100%)	170 (90%)	19 (10%)	7	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	SD	172/172 (100%)	152 (88%)	20 (12%)	5	29
21	SE	125/125 (100%)	111 (89%)	14 (11%)	6	30
22	SF	116/116 (100%)	103 (89%)	13 (11%)	6	30
23	SR	64/64 (100%)	58 (91%)	6 (9%)	8	38
24	S3	575/575 (100%)	514 (89%)	61 (11%)	6	32
27	LD	217/217 (100%)	188 (87%)	29 (13%)	4	23
28	LU	93/93 (100%)	82 (88%)	11 (12%)	5	28
29	LV	84/84 (100%)	77 (92%)	7 (8%)	11	42
30	LW	84/84 (100%)	80 (95%)	4 (5%)	25	60
31	LX	78/78 (100%)	70 (90%)	8 (10%)	7	34
32	LY	62/62 (100%)	54 (87%)	8 (13%)	4	24
33	LZ	67/67 (100%)	55 (82%)	12 (18%)	2	11
34	L0	55/55 (100%)	49 (89%)	6 (11%)	6	32
35	L1	48/48 (100%)	39 (81%)	9 (19%)	1	9
36	L2	62/62 (100%)	52 (84%)	10 (16%)	2	16
37	LC	181/181 (100%)	164 (91%)	17 (9%)	8	38
38	LE	164/164 (100%)	143 (87%)	21 (13%)	4	24
39	L3	47/47 (100%)	43 (92%)	4 (8%)	10	41
40	L4	48/48 (100%)	44 (92%)	4 (8%)	11	42
41	L5	38/38 (100%)	35 (92%)	3 (8%)	12	44
42	L6	51/51 (100%)	48 (94%)	3 (6%)	19	55
43	L7	34/34 (100%)	32 (94%)	2 (6%)	19	55
44	LF	165/165 (100%)	153 (93%)	12 (7%)	14	46
45	LG	149/149 (100%)	133 (89%)	16 (11%)	6	32
46	LH	137/137 (100%)	119 (87%)	18 (13%)	4	23
47	LJ	122/122 (100%)	109 (89%)	13 (11%)	6	32
48	LN	103/103 (100%)	87 (84%)	16 (16%)	2	18
49	LK	109/109 (100%)	93 (85%)	16 (15%)	3	20
50	LL	116/116 (100%)	108 (93%)	8 (7%)	15	49
51	LI	114/114 (100%)	99 (87%)	15 (13%)	4	23
52	LO	109/109 (100%)	96 (88%)	13 (12%)	5	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	LP	103/103 (100%)	95 (92%)	8 (8%)	12	44
54	LM	104/104 (100%)	99 (95%)	5 (5%)	25	60
55	LQ	87/87 (100%)	80 (92%)	7 (8%)	12	43
56	LR	99/99 (100%)	87 (88%)	12 (12%)	5	26
57	LS	89/89 (100%)	78 (88%)	11 (12%)	4	26
58	LT	84/84 (100%)	78 (93%)	6 (7%)	14	48
All	All	5788/5788 (100%)	5182 (90%)	606 (10%)	10	33

5 of 606 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	LH	51	PHE
55	LQ	56	LYS
47	LJ	2	LEU
46	LH	49	LEU
49	LK	133	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
44	LF	41	GLN
53	LP	3	HIS
45	LG	20	ASN
50	LL	47	HIS
53	LP	107	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	SA	1541/1542 (99%)	362 (23%)	122 (7%)
25	LB	119/120 (99%)	21 (17%)	9 (7%)
26	LA	2903/2904 (99%)	645 (22%)	221 (7%)
3	S1	46/47 (97%)	36 (78%)	12 (26%)
4	S2	77/77 (100%)	20 (25%)	10 (12%)
All	All	4686/4690 (99%)	1084 (23%)	374 (7%)

5 of 1084 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	SA	3	A
2	SA	4	U
2	SA	5	U
2	SA	8	A
2	SA	9	G

5 of 374 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	LA	1061	U
26	LA	1818	U
26	LA	1133	A
26	LA	1392	A
26	LA	2042	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	S3	801	-	26,34,34	1.72	6 (23%)	32,54,54	2.46	6 (18%)

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	S3	801	-	-	0/18/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	S3	801	GTP	C8-N7	-5.15	1.26	1.35
59	S3	801	GTP	C5-C4	-2.51	1.36	1.43
59	S3	801	GTP	O4'-C4'	2.33	1.50	1.45
59	S3	801	GTP	C6-N1	2.31	1.41	1.37
59	S3	801	GTP	PG-O2G	-2.17	1.46	1.54

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	S3	801	GTP	PA-O3A-PB	-8.72	102.91	132.83
59	S3	801	GTP	PB-O3B-PG	-7.87	105.81	132.83
59	S3	801	GTP	O5'-PA-O1A	-3.25	96.38	109.07
59	S3	801	GTP	O4'-C1'-C2'	-3.21	102.24	106.93
59	S3	801	GTP	O4'-C4'-C3'	-2.78	99.61	105.11

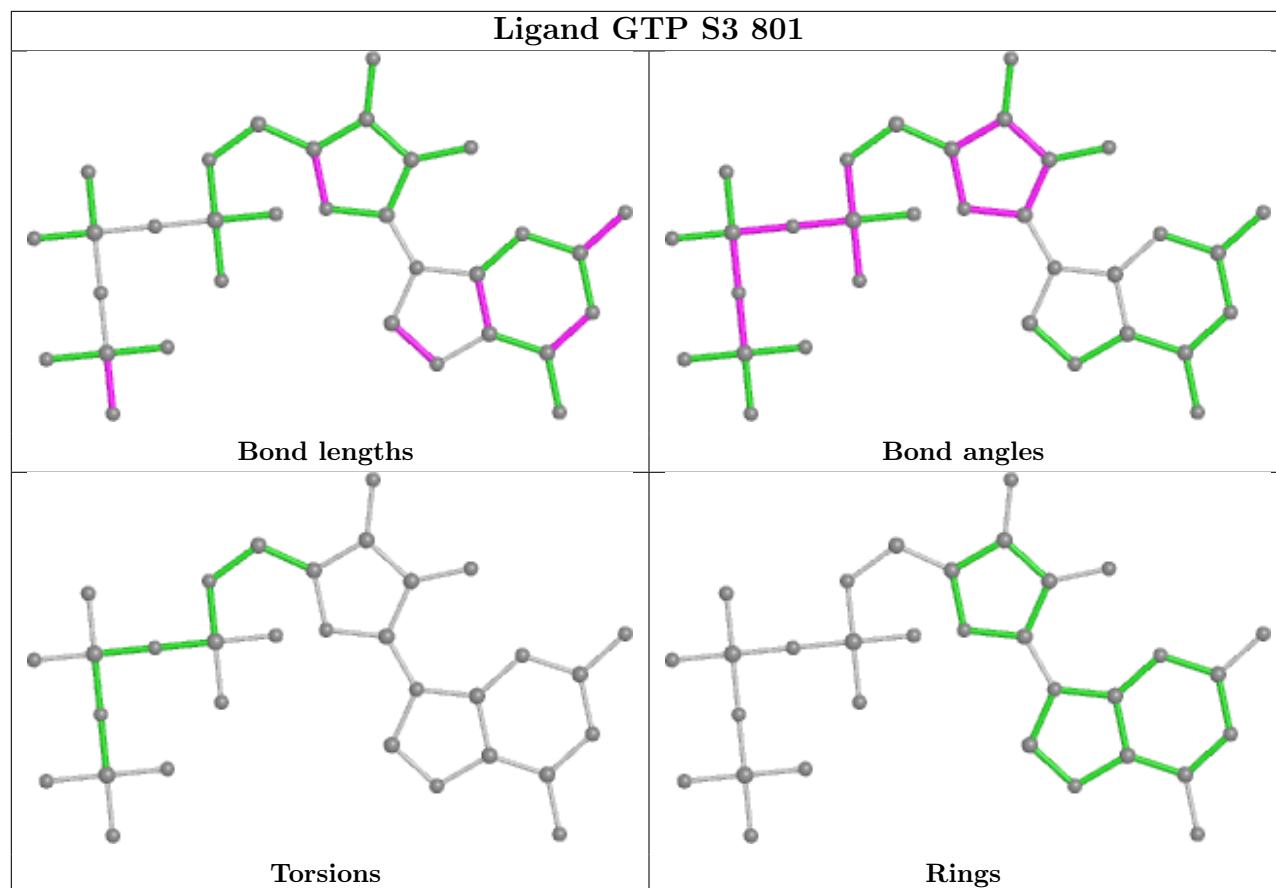
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

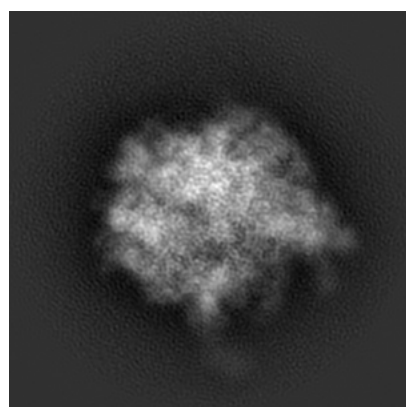
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6316. These allow visual inspection of the internal detail of the map and identification of artifacts.

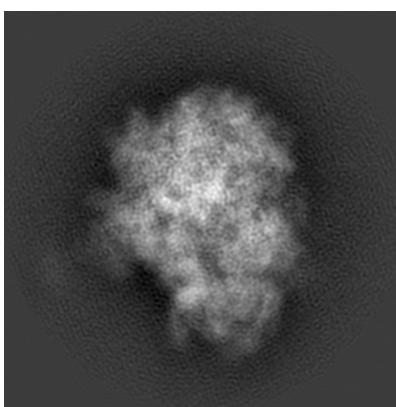
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

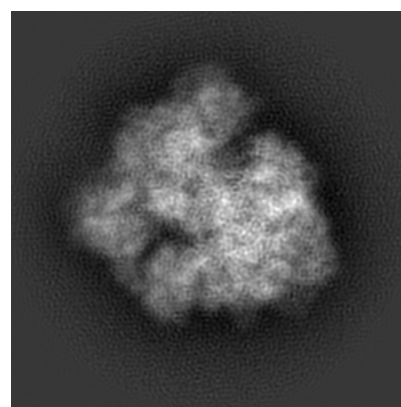
6.1.1 Primary map



X



Y

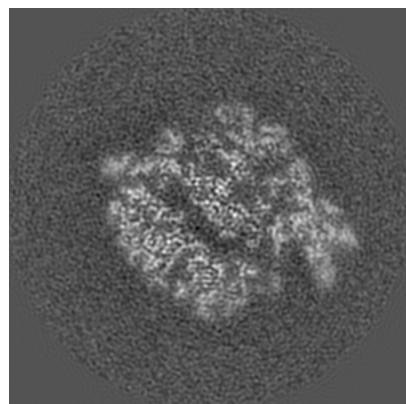


Z

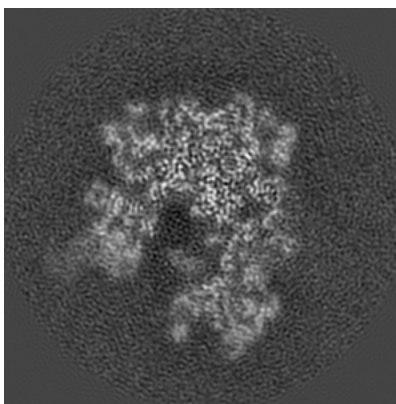
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

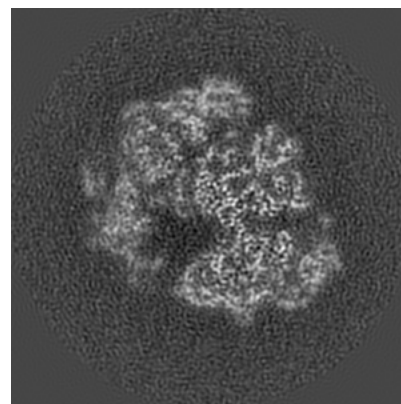
6.2.1 Primary map



X Index: 180



Y Index: 180

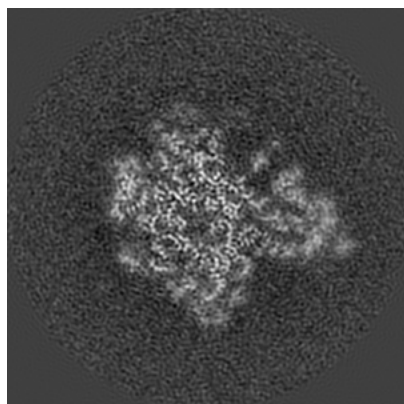


Z Index: 180

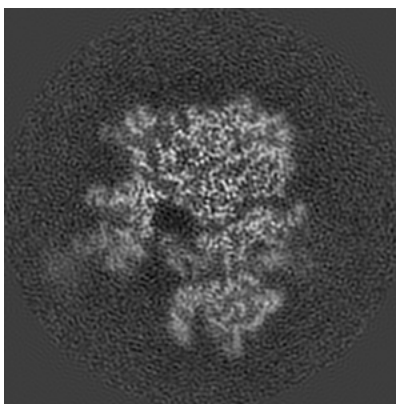
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

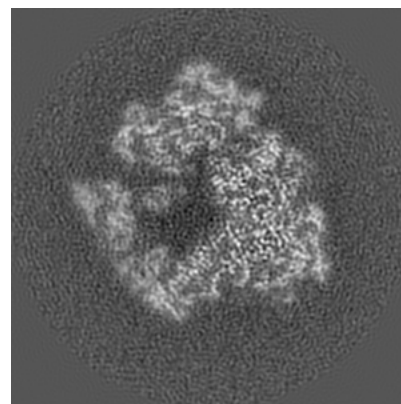
6.3.1 Primary map



X Index: 191



Y Index: 188



Z Index: 161

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

6.4 Orthogonal surface views [i](#)

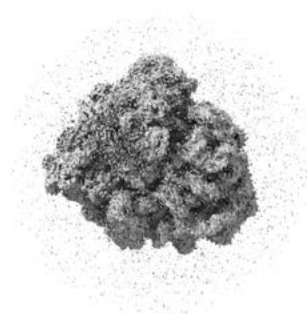
6.4.1 Primary map



X



Y



Z

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

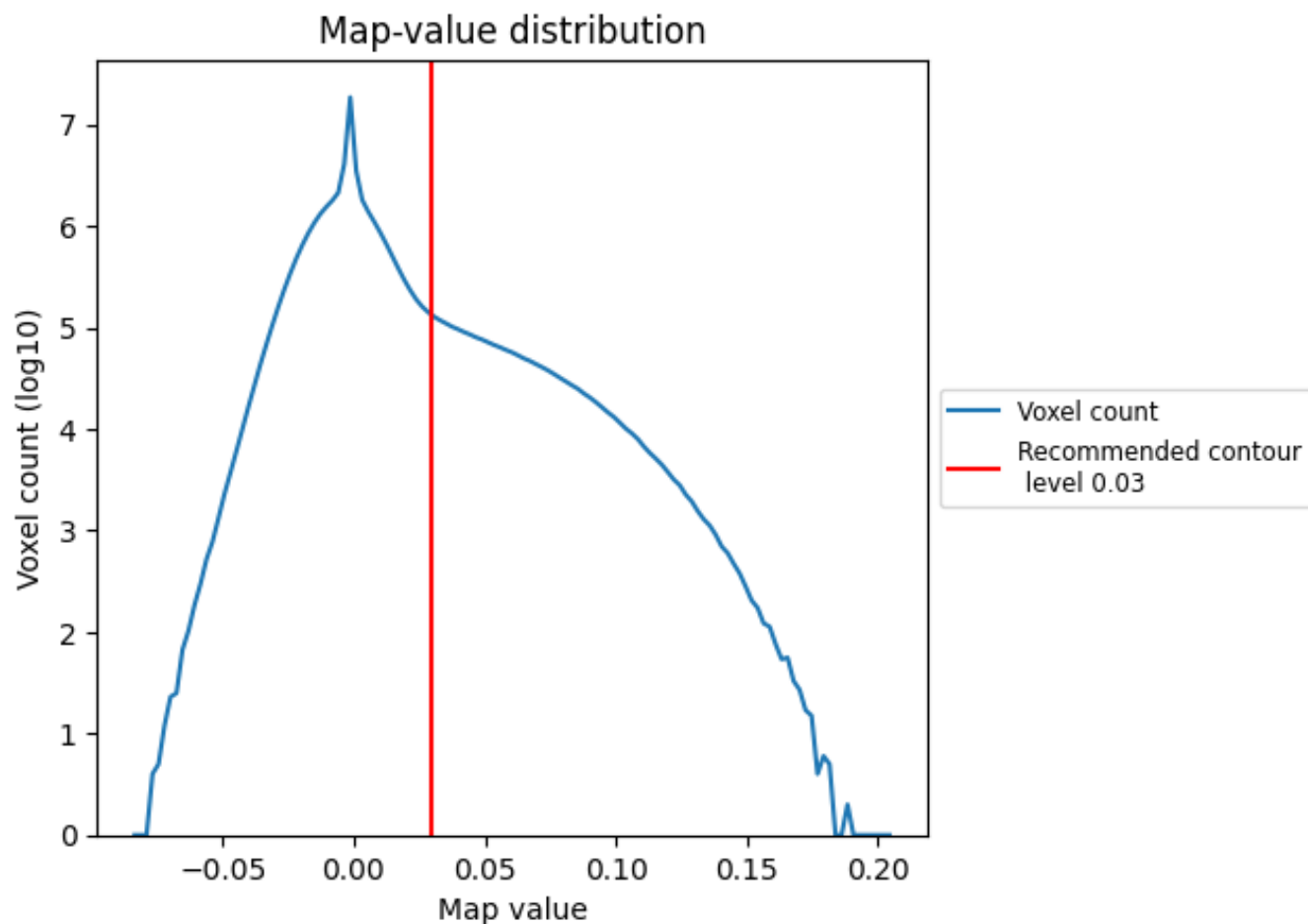
6.5 Mask visualisation

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

7 Map analysis [i](#)

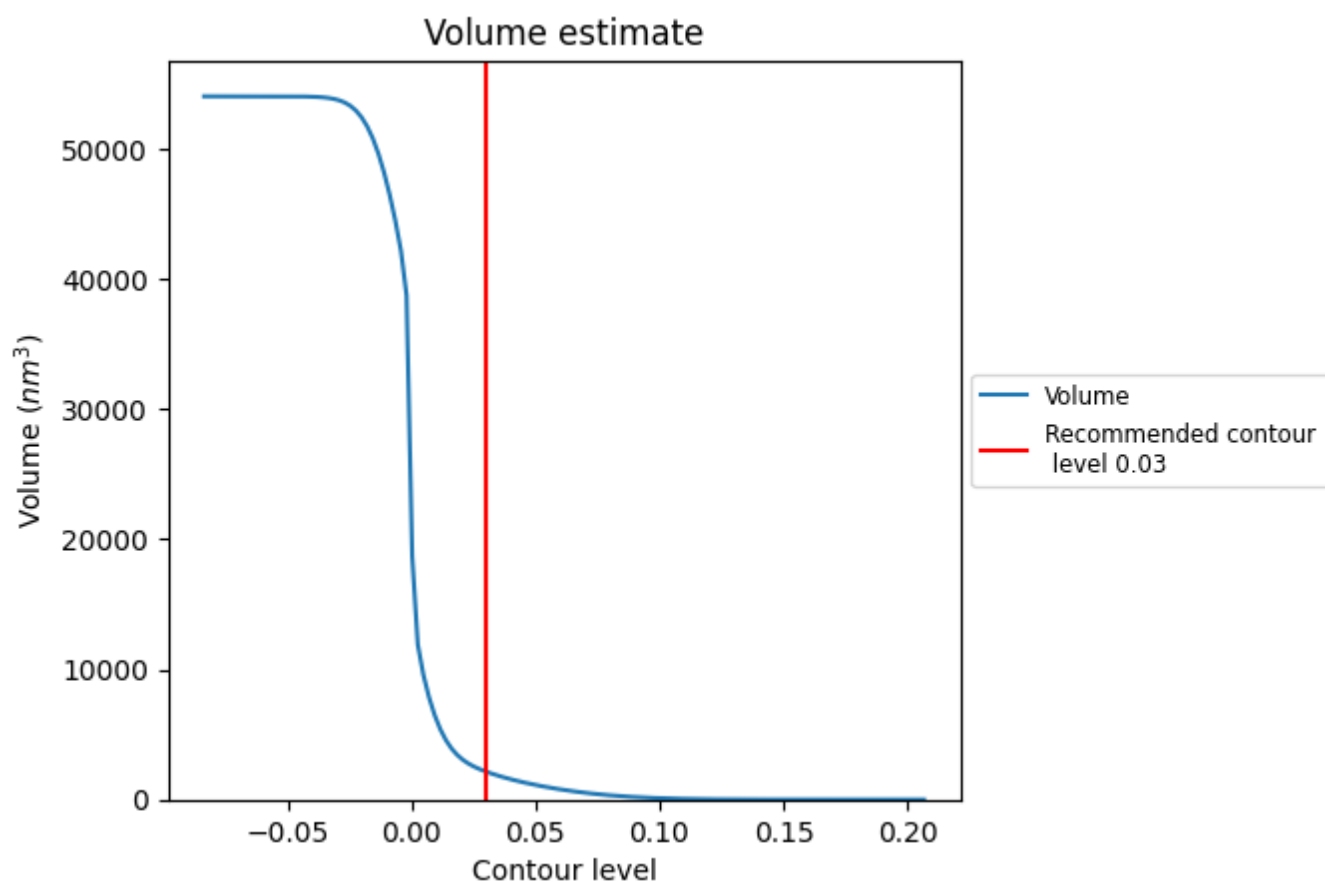
This section contains the results of statistical analysis of the map.

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.

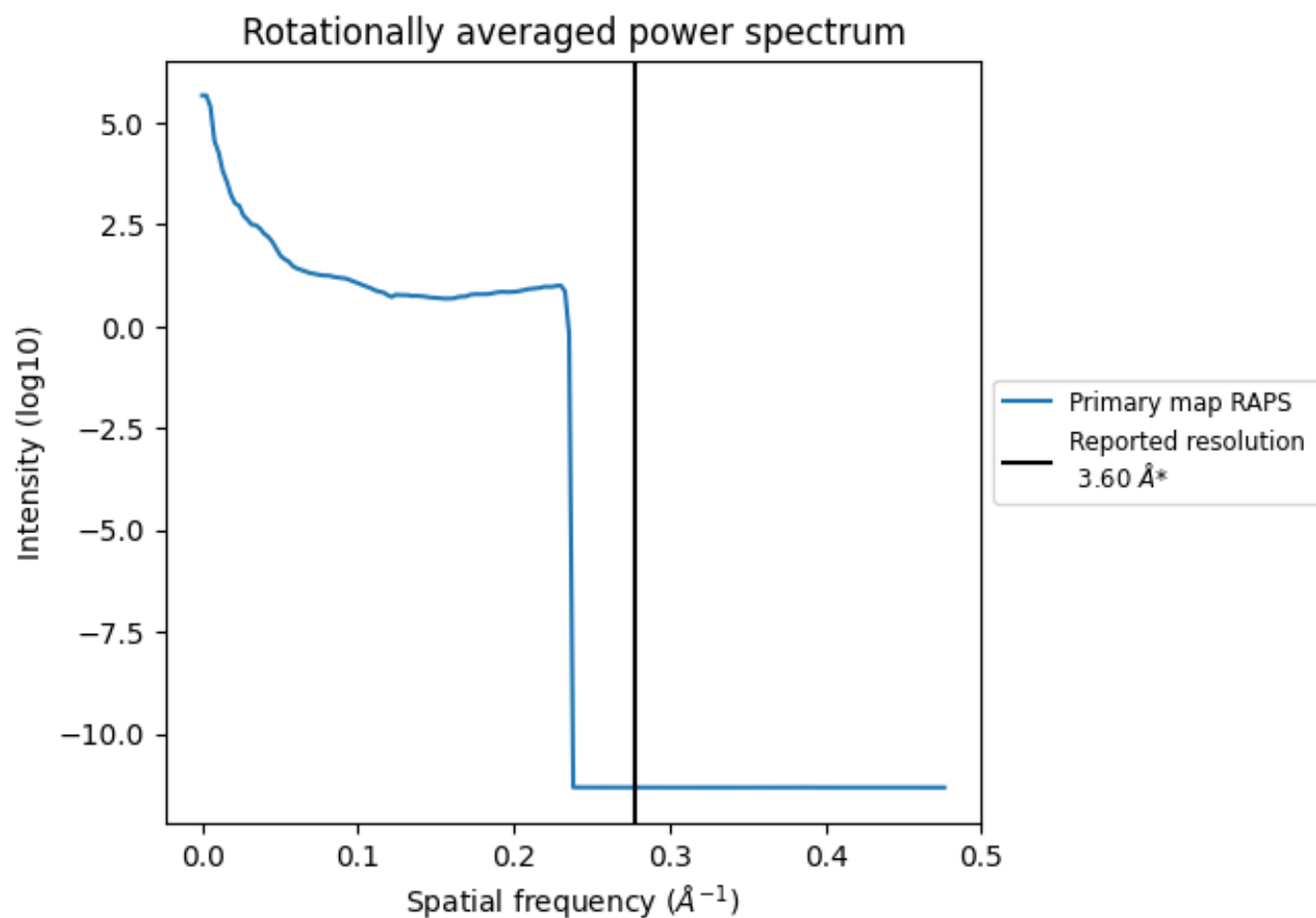
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2151 nm³; this corresponds to an approximate mass of 1943 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 \AA^{-1}

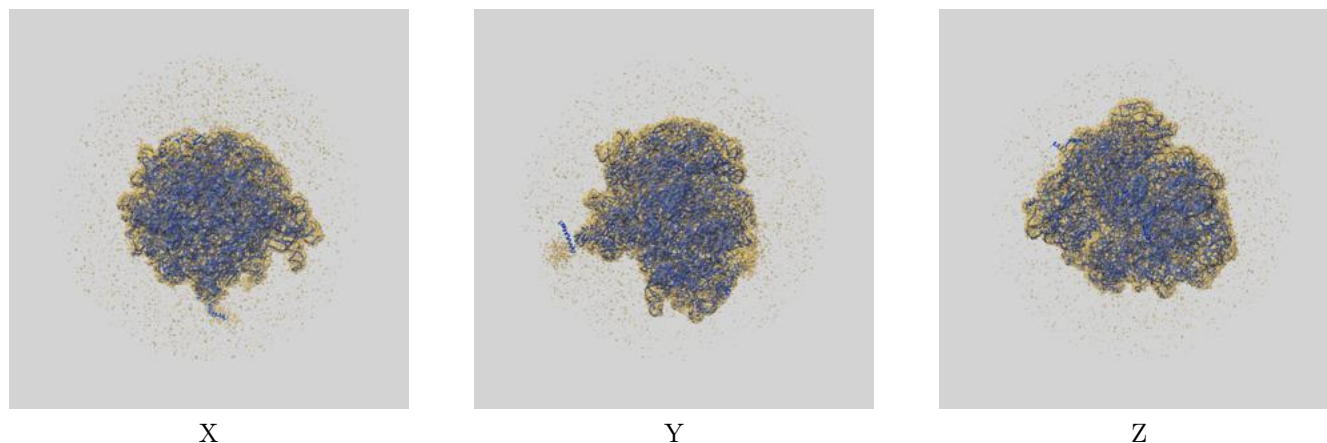
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

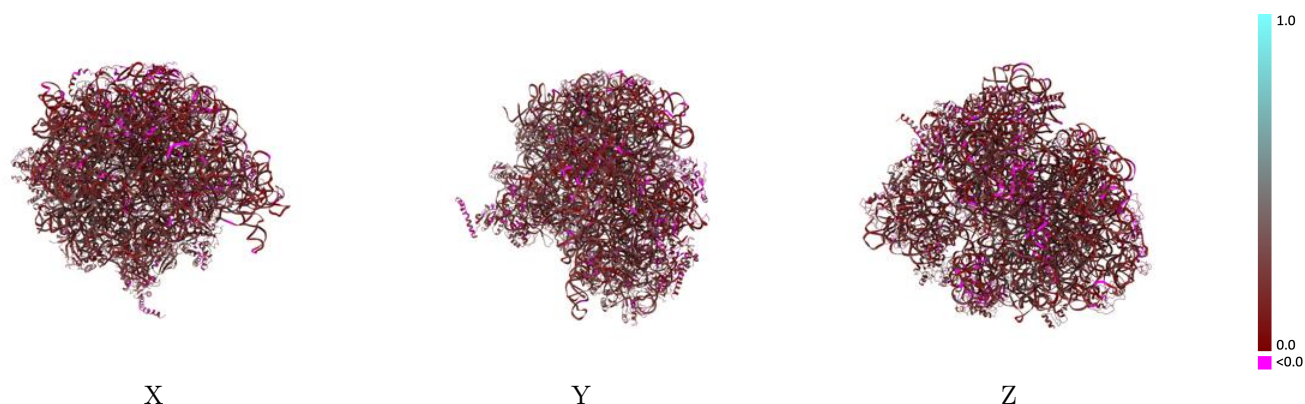
This section contains information regarding the fit between EMDB map EMD-6316 and PDB model 3JA1. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



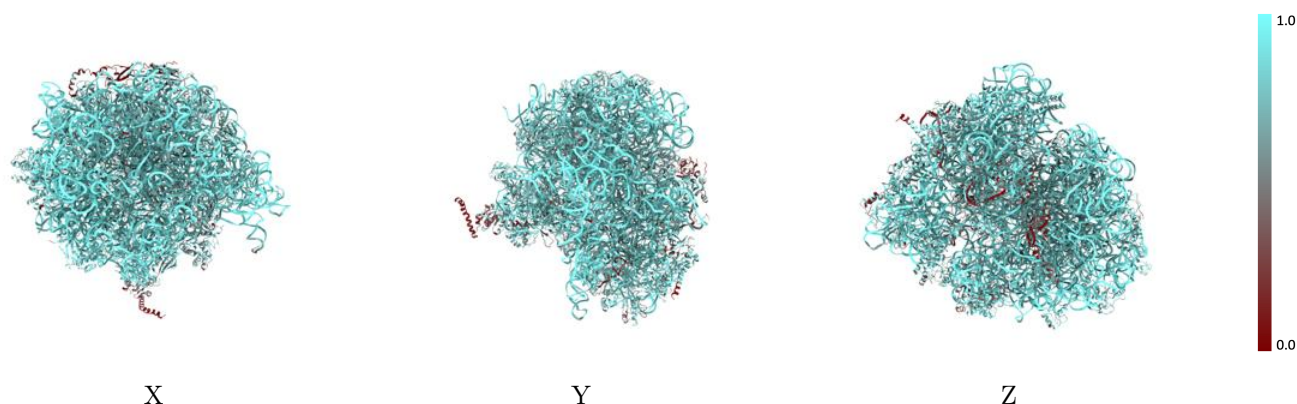
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



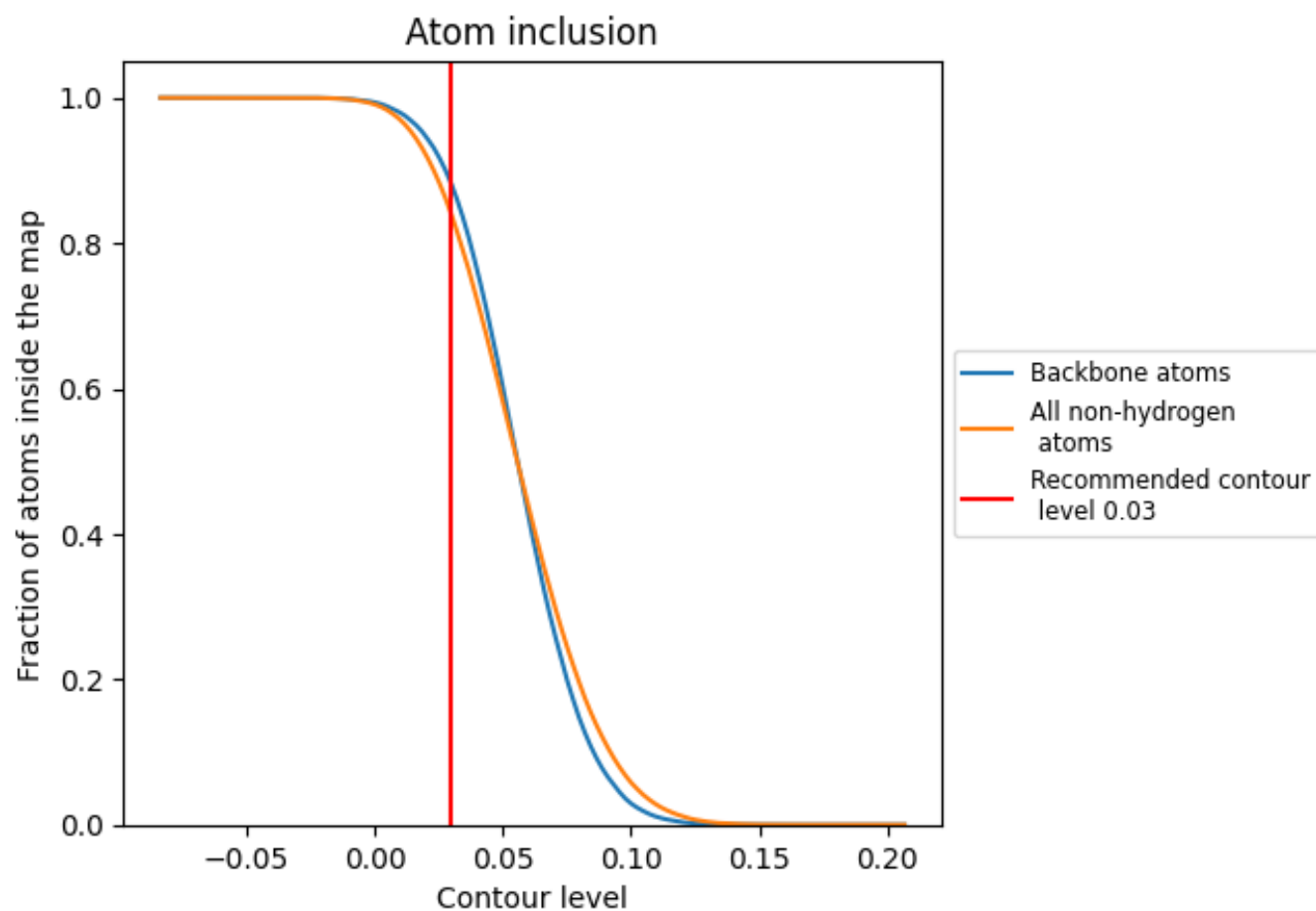
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 88% of all backbone atoms, 84% 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	 0.8382	 0.1980
L0	 0.6982	 0.0780
L1	 0.7941	 0.2550
L2	 0.7100	 0.2320
L3	 0.8131	 0.2120
L4	 0.8014	 0.2200
L5	 0.7127	 0.1580
L6	 0.8310	 0.2520
L7	 0.8390	 0.2520
LA	 0.9057	 0.2080
LB	 0.9634	 0.2520
LC	 0.5673	 0.1420
LD	 0.7034	 0.1620
LE	 0.7477	 0.2040
LF	 0.7467	 0.1930
LG	 0.7990	 0.2160
LH	 0.7972	 0.2420
LI	 0.2464	 0.0930
LJ	 0.3823	 0.1930
LK	 0.6223	 0.1940
LL	 0.8145	 0.2350
LM	 0.6193	 0.1840
LN	 0.8066	 0.2280
LO	 0.8129	 0.2710
LP	 0.7753	 0.1480
LQ	 0.8967	 0.2430
LR	 0.6622	 0.1500
LS	 0.8282	 0.2360
LT	 0.8118	 0.2220
LU	 0.7356	 0.1850
LV	 0.6939	 0.1090
LW	 0.8185	 0.1440
LX	 0.8415	 0.2880
LY	 0.7767	 0.2540
LZ	 0.7587	 0.1900



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Chain	Atom inclusion	Q-score
S1	 0.4401	 0.1220
S2	 0.8658	 0.1970
S3	 0.6696	 0.2040
SA	 0.9164	 0.1960
SB	 0.6687	 0.1540
SC	 0.7291	 0.2070
SD	 0.7937	 0.1780
SE	 0.7074	 0.1600
SF	 0.5420	 0.0470
SG	 0.6777	 0.1610
SH	 0.7281	 0.1580
SI	 0.8107	 0.1870
SJ	 0.7175	 0.1920
SK	 0.6984	 0.1770
SL	 0.7101	 0.2180
SM	 0.7301	 0.2250
SN	 0.8282	 0.2130
SO	 0.7478	 0.1270
SP	 0.8022	 0.1580
SQ	 0.7302	 0.1010
SR	 0.7282	 0.1310
SS	 0.7454	 0.2230
ST	 0.7893	 0.1410
SU	 0.6036	 0.1850