



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:50 PM BST

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 PDB ID : 3J0U

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

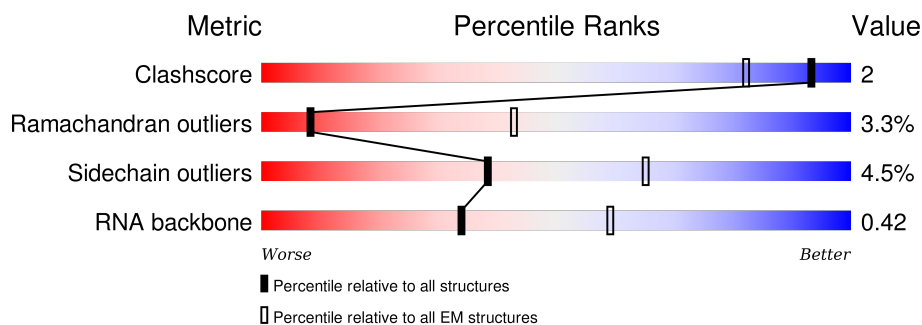
1 Overall quality at a glance

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.













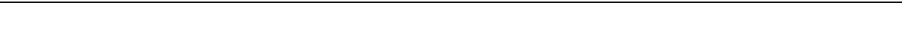

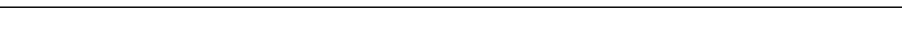
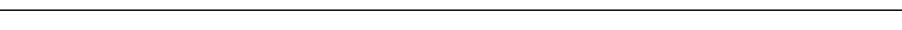











Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	SA	1542	19% 44% 26% 10%
2	S6	77	19% 56% 17% 8%
3	S7	74	9% 35% 27% 28%
4	SJ	103	86% 10% .
5	SK	128	84% 13% ..
6	SL	123	85% 15% .
7	SM	117	84% 13% ..
8	SN	100	89% 8% .










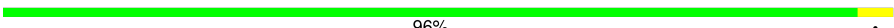















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Mol	Chain	Length	Quality of chain
9	SO	88	 89% 7% 5%
10	SP	82	 87% 9% 5%
11	SQ	83	 90% 6% .
12	SR	74	 84% 15% .
13	SS	91	 84% 15% .
14	SB	240	 88% 9% .
15	ST	86	 91% 7% .
16	SU	70	 76% 20% .
17	SC	232	 87% 12% .
18	SD	205	 86% 12% .
19	SE	166	 90% 8% .
20	SF	135	 89% 10% ..
21	SG	178	 89% 10% ..
22	SH	129	 88% 10% .
23	SI	129	 89% 9% .
24	S1	702	 87% 12% .
25	LA	2904	 17% 43% 29% 11%
26	LB	120	 19% 51% 24% 6%
27	LC	234	 85% 13% .
28	LM	114	 82% 12% 5%
29	LN	272	 83% 16% .
30	LO	117	 80% 16% .
31	LP	103	 83% 14% ..
32	LQ	110	 92% 8%
33	LR	100	 86% 14%

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Mol	Chain	Length	Quality of chain
34	LS	103	 85% 12% .
35	LT	94	 90% 7% .
36	LU	84	 70% 24% 5% .
37	LV	77	 88% 10% .
38	LD	164	 93% 7%
39	LW	63	 87% 10% .
40	LX	209	 83% 12% .
41	LY	58	 91% 5% .
42	L1	56	 80% 18% .
43	L2	54	 96% .
44	L3	46	 76% 15% 7% .
45	L4	64	 91% 8% .
46	L5	38	 92% . 5%
47	L6	201	 87% 11% .
48	LE	141	 91% 8% .
49	L7	178	 75% 21% .
50	L8	176	 88% 11% .
51	L9	149	 87% 12% .
52	LF	142	 85% 13% .
53	LG	123	 82% 16% .
54	LH	144	 84% 13% .
55	LI	136	 91% 7% .
56	LJ	127	 80% 17% .
57	LK	117	 85% 15% .
58	LZ	70	 87% 9% .

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		

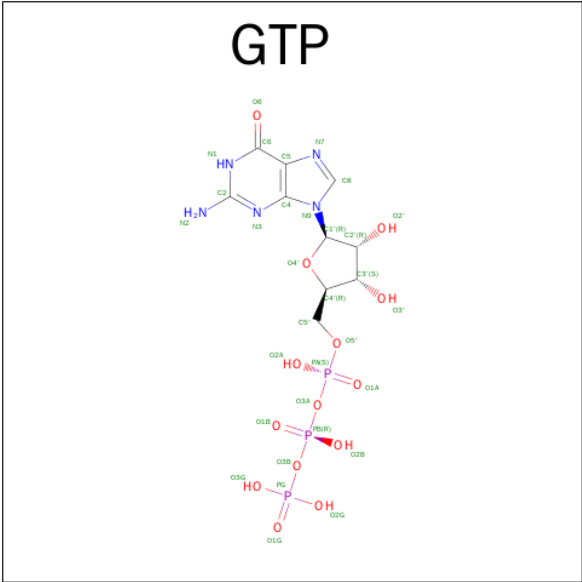
- Molecule 57 is a protein called 50S ribosomal protein L18.

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).

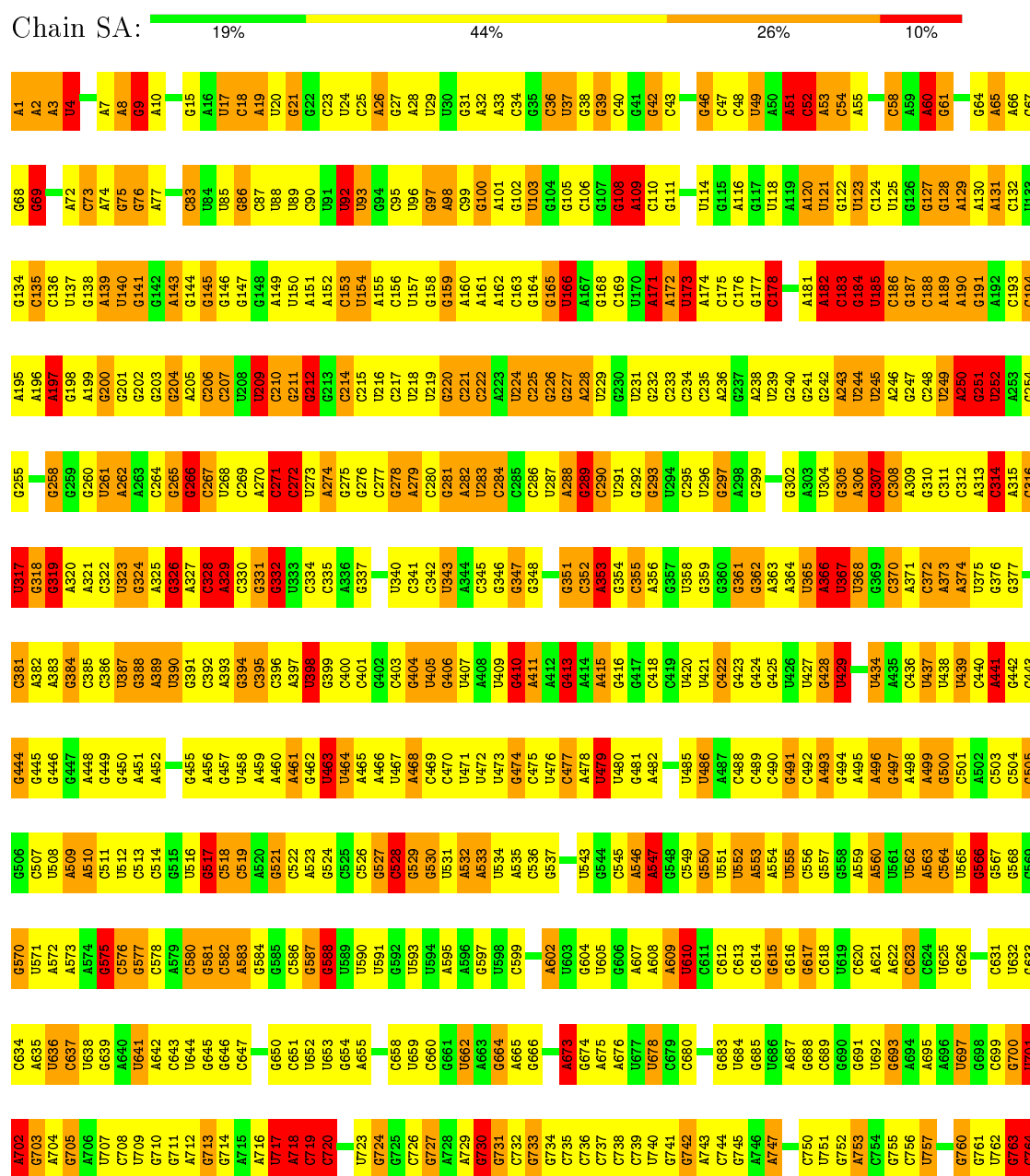


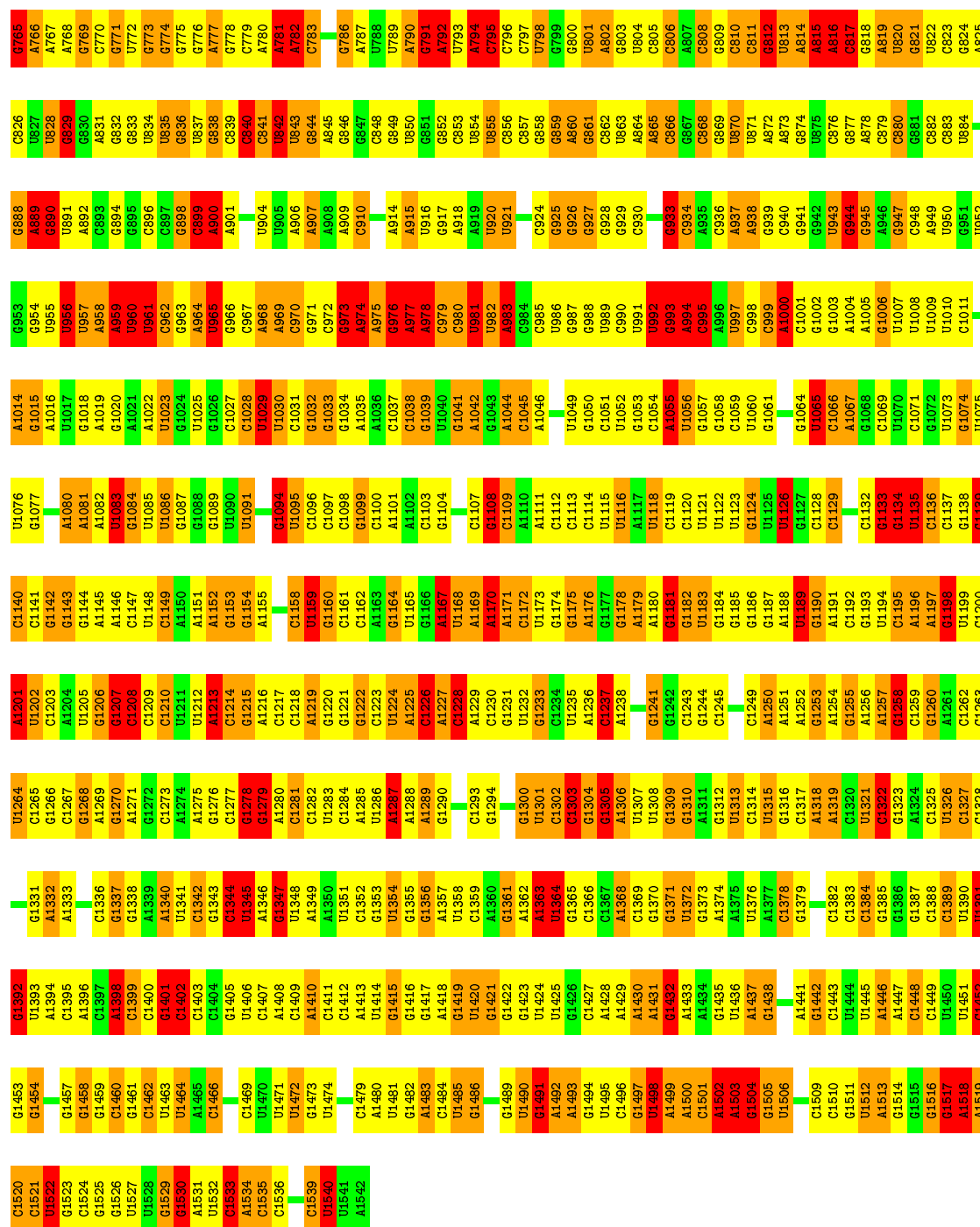
Mol	Chain	Residues	Atoms					AltConf
59	S1	1	Total	C	N	O	P	0
			32	10	5	14	3	

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

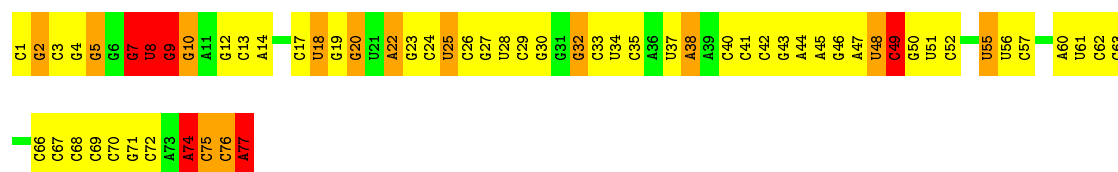
• Molecule 1: 16S ribosomal RNA



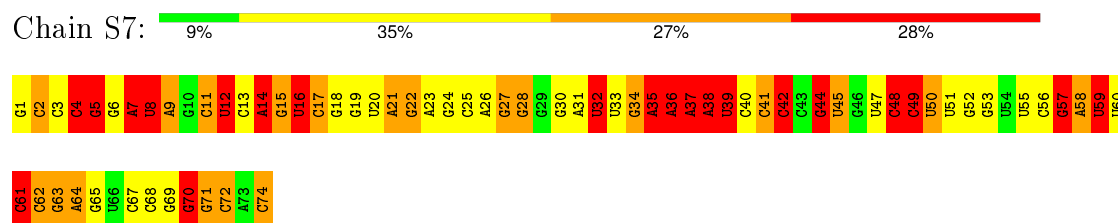


• Molecule 2: P-tRNA

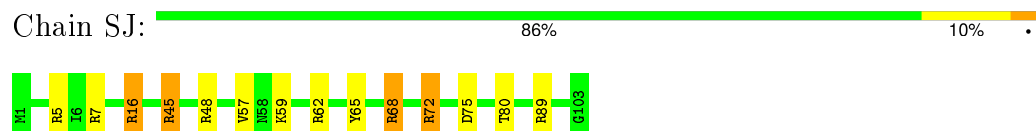
Chain S6: 19% 56% 17% 8%



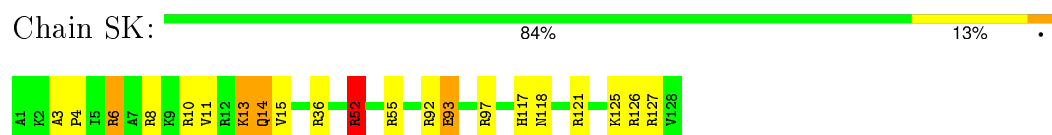
- Molecule 3: E-tRNA



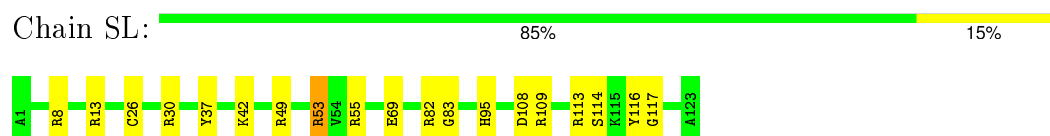
- Molecule 4: 30S ribosomal protein S10



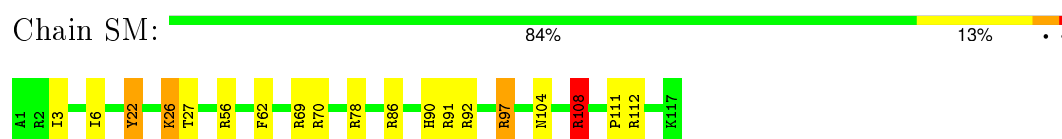
- Molecule 5: 30S ribosomal protein S11



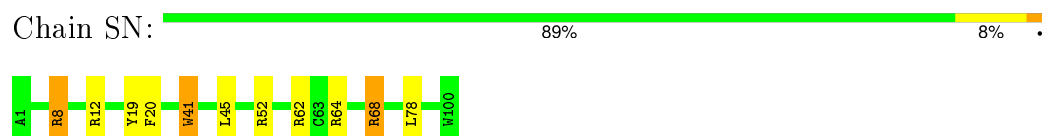
- Molecule 6: 30S ribosomal protein S12



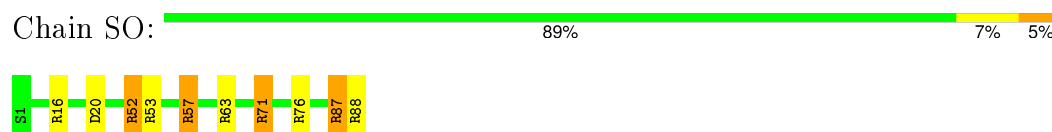
- Molecule 7: 30S ribosomal protein S13



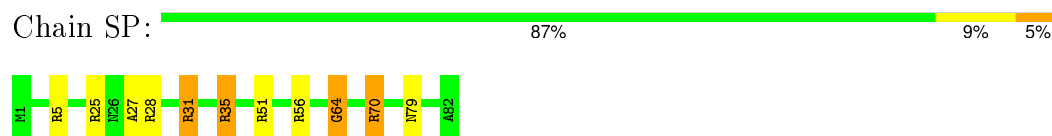
- Molecule 8: 30S ribosomal protein S14



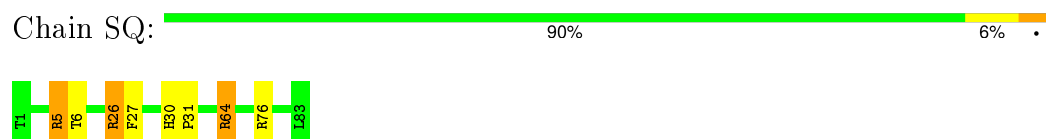
- Molecule 9: 30S ribosomal protein S15



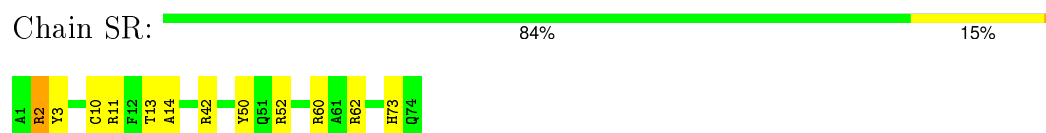
- Molecule 10: 30S ribosomal protein S16



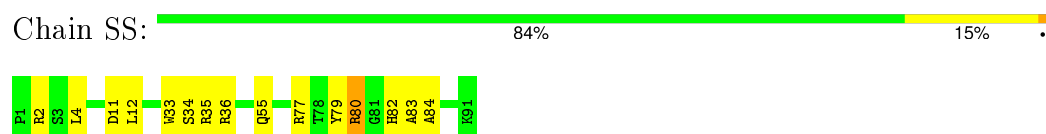
- Molecule 11: 30S ribosomal protein S17



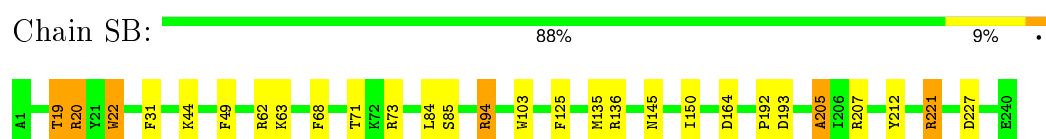
- Molecule 12: 30S ribosomal protein S18



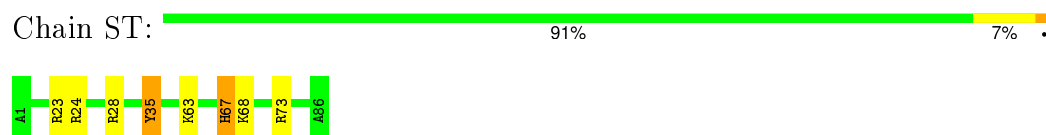
- Molecule 13: 30S ribosomal protein S19



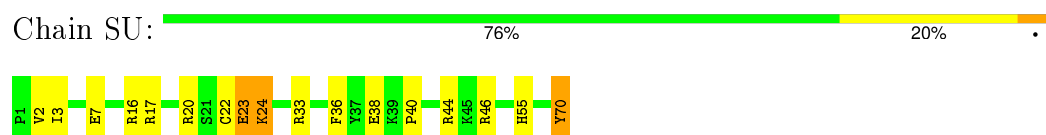
- Molecule 14: 30S ribosomal protein S2



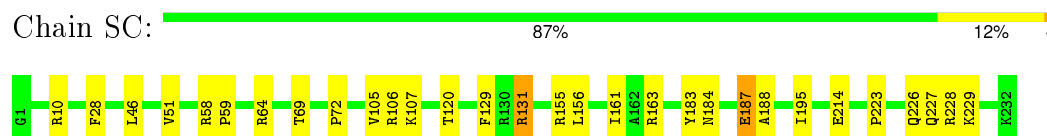
- Molecule 15: 30S ribosomal protein S20



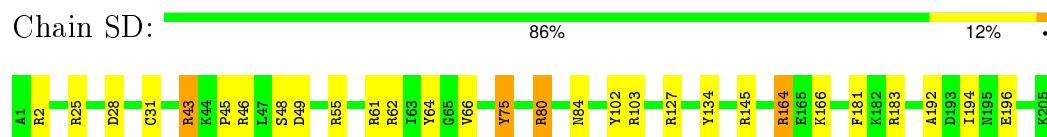
- Molecule 16: 30S ribosomal protein S21



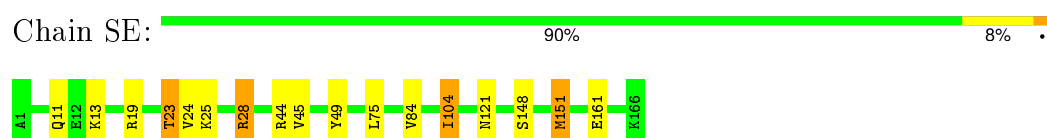
- Molecule 17: 30S ribosomal protein S3



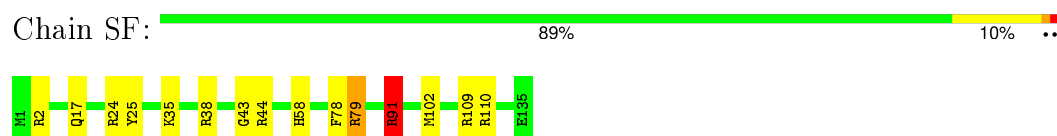
- Molecule 18: 30S ribosomal protein S4



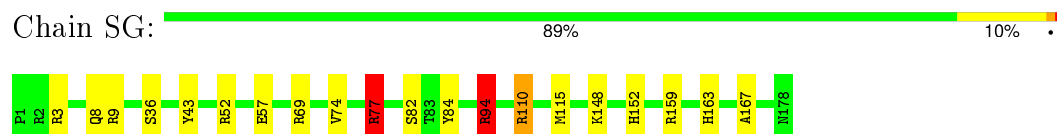
- Molecule 19: 30S ribosomal protein S5



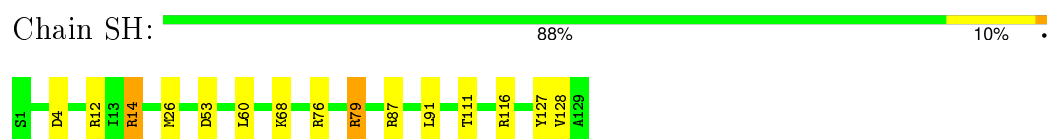
- Molecule 20: 30S ribosomal protein S6



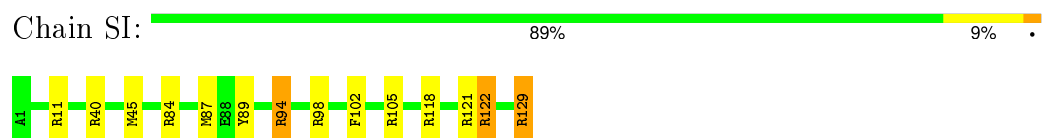
- Molecule 21: 30S ribosomal protein S7



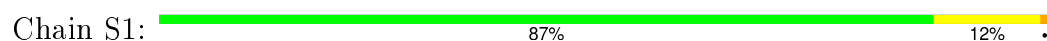
- Molecule 22: 30S ribosomal protein S8



- Molecule 23: 30S ribosomal protein S9



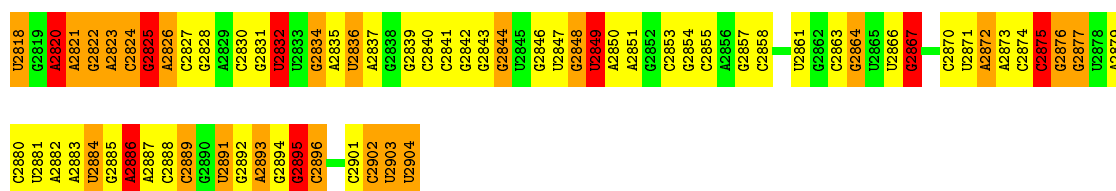
- Molecule 24: Elongation factor G





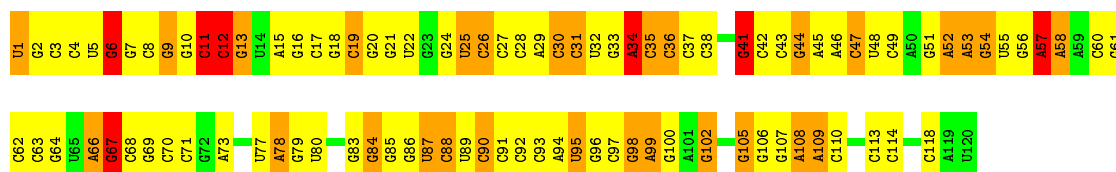
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C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	C1973	C1974	C1975	C1976	C1977	C1978	C1979	C1980	C1981	C1982	C1983	C1984	C1985	C1986	C1987	C1988	C1989	C1990	C1991	C1992	C1993	C1994	C1995	C1996	C1997	C1998	C1999	C2000	C2001	C2002	C2003	C2004	C2005	C2006	C2007	C2008	C2009	C2010	C2011	C2012	C2013	C2014	C2015	C2016	C2017	C2018	C2019	C2020					
A1900	A1901	A1902	A1903	A1904	A1905	A1906	A1907	A1908	A1909	A1910	A1911	A1912	A1913	A1914	A1915	A1916	A1917	A1918	A1919	A1920	A1921	A1922	A1923	A1924	A1925	A1926	A1927	A1928	A1929	A1930	A1931	A1932	A1933	A1934	A1935	A1936	A1937	A1938	A1939	A1940	A1941	A1942	A1943	A1944	A1945	A1946	A1947	A1948	A1949	A1950	A1951	A1952	A1953	A1954	A1955	A1956	A1957	A1958	A1959						
U1834	U1835	U1836	U1837	U1838	U1839	U1840	U1841	U1842	U1843	U1844	U1845	U1846	U1847	U1848	U1849	U1850	U1851	U1852	U1853	U1854	U1855	U1856	U1857	U1858	U1859	U1860	U1861	U1862	U1863	U1864	U1865	U1866	U1867	U1868	U1869	U1870	U1871	U1872	U1873	U1874	U1875	U1876	U1877	U1878	U1879	U1880	U1881	U1882	U1883	U1884	U1885	U1886	U1887	U1888	U1889	U1890	U1891	U1892	U1893	U1894	U1895	U1896	U1897	U1898	U1899



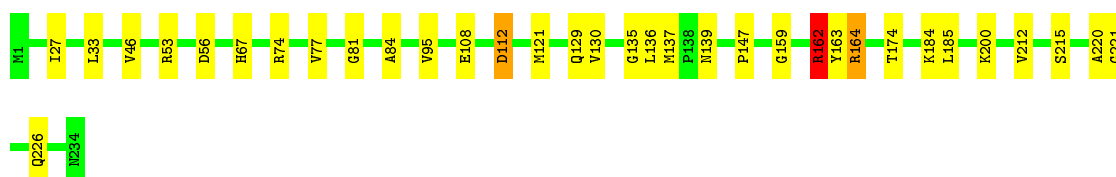
- Molecule 26: 5S ribosomal RNA

Chain LB: 19% 51% 24% 6%



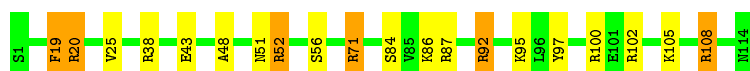
- Molecule 27: 50S ribosomal protein L1

Chain LC: 85% 13%



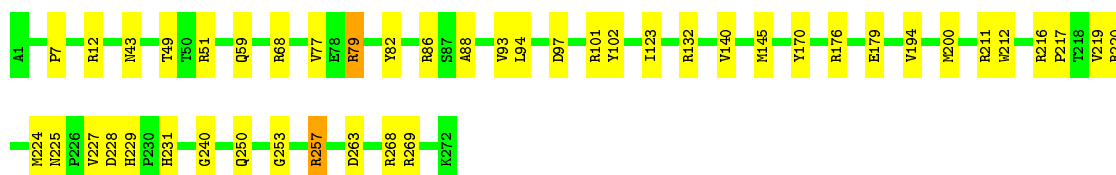
- Molecule 28: 50S ribosomal protein L19

Chain LM: 82% 12% 5%



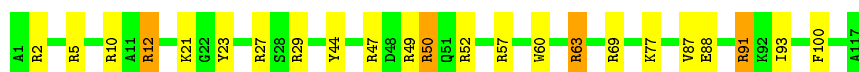
- Molecule 29: 50S ribosomal protein L2

Chain LN: 83% 16%




- Molecule 30: 50S ribosomal protein L20

Chain LO: 80% 16%



- Molecule 31: 50S ribosomal protein L21

Chain LP:  83% 14% ..




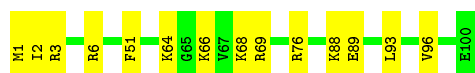
- Molecule 32: 50S ribosomal protein L22

Chain LQ:  92% 8%




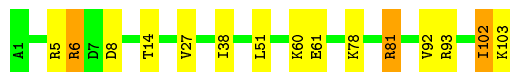
- Molecule 33: 50S ribosomal protein L23

Chain LR:  86% 14%



- Molecule 34: 50S ribosomal protein L24

Chain LS:  85% 12% •



- Molecule 35: 50S ribosomal protein L25

Chain LT:  90% 7% •




- Molecule 36: 50S ribosomal protein L27

Chain LU:  70% 24% 5% •



- Molecule 37: 50S ribosomal protein L28

Chain LV:  88% 10% •



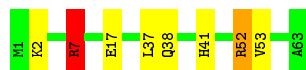
- Molecule 38: 50S ribosomal protein L10

Chain LD:  93% 7%



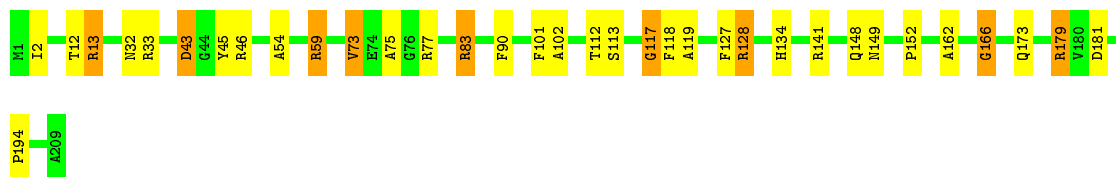
- Molecule 39: 50S ribosomal protein L29

Chain LW: 87% 10% . .



- Molecule 40: 50S ribosomal protein L3

Chain LX: 83% 12% .



- Molecule 41: 50S ribosomal protein L30

Chain LY: 91% 5% . .



- Molecule 42: 50S ribosomal protein L32

Chain L1: 80% 18% .



- Molecule 43: 50S ribosomal protein L33

Chain L2: 96% .



- Molecule 44: 50S ribosomal protein L34

Chain L3: 76% 15% 7% .



- Molecule 45: 50S ribosomal protein L35

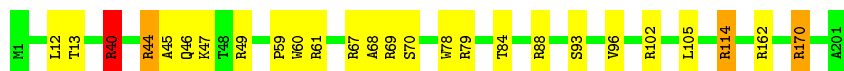
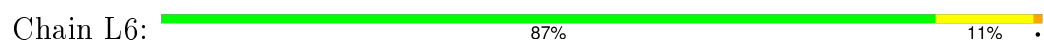
Chain L4: 91% 8% .



- Molecule 46: 50S ribosomal protein L36



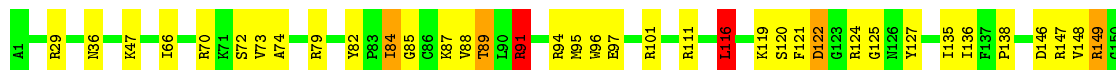
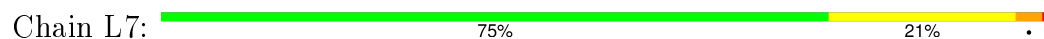
- Molecule 47: 50S ribosomal protein L4



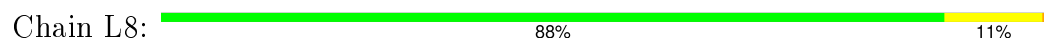
- Molecule 48: 50S ribosomal protein L11



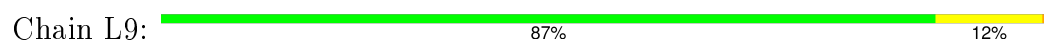
- Molecule 49: 50S ribosomal protein L5



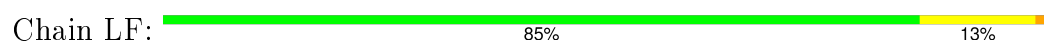
- Molecule 50: 50S ribosomal protein L6



- Molecule 51: 50S ribosomal protein L9



- Molecule 52: 50S ribosomal protein L13





- Molecule 53: 50S ribosomal protein L14

Chain LG: 82% 16% ..



- Molecule 54: 50S ribosomal protein L15

Chain LH: 84% 13% ..



- Molecule 55: 50S ribosomal protein L16

Chain LI: 91% 7% .



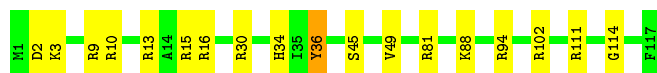
- Molecule 56: 50S ribosomal protein L17

Chain LJ: 80% 17% ..



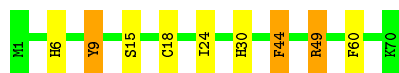
- Molecule 57: 50S ribosomal protein L18

Chain LK: 85% 15% .



- Molecule 58: 50S ribosomal protein L31

Chain LZ: 87% 9% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	90000	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	CTFFIND3 and CTFIT	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	55000	Depositor
Image detector	DIRECT ELECTRON DE-12 (4k x 3k)	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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	SA	1.54	172/37035 (0.5%)	1.91	1570/57774 (2.7%)
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%)
2	S6	1.44	5/1831 (0.3%)	1.81	72/2853 (2.5%)
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%)
3	S7	1.36	4/1762 (0.2%)	1.97	89/2746 (3.2%)
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%)
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	LW	0.72	0/510	1.22	4/677 (0.6%)
4	SJ	0.73	0/835	1.28	10/1127 (0.9%)
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%)
5	SK	0.75	0/982	1.30	11/1323 (0.8%)
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%)
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%)
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
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

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Mol	Chain	#Chirality outliers	#Planarity outliers
17	SC	0	7
18	SD	0	6
19	SE	0	8
2	S6	0	16
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
3	S7	0	31
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
4	SJ	0	7
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
5	SK	0	5
50	L8	0	3
51	L9	0	2
52	LF	0	6
53	LG	0	4
54	LH	0	5
55	LI	0	1
56	LJ	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
57	LK	0	3
58	LZ	0	4
6	SL	0	9
7	SM	0	4
8	SN	0	5
9	SO	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%)	5	44
5	SK	126/128 (98%)	104 (82%)	17 (14%)	5 (4%)	4	35
6	SL	121/123 (98%)	109 (90%)	10 (8%)	2 (2%)	11	55
7	SM	115/117 (98%)	101 (88%)	9 (8%)	5 (4%)	3	33
8	SN	98/100 (98%)	88 (90%)	9 (9%)	1 (1%)	19	66
9	SO	86/88 (98%)	83 (96%)	1 (1%)	2 (2%)	8	50
10	SP	80/82 (98%)	72 (90%)	4 (5%)	4 (5%)	3	29
11	SQ	81/83 (98%)	71 (88%)	8 (10%)	2 (2%)	7	48
12	SR	72/74 (97%)	58 (81%)	11 (15%)	3 (4%)	3	33
13	SS	89/91 (98%)	74 (83%)	10 (11%)	5 (6%)	2	26
14	SB	238/240 (99%)	217 (91%)	13 (6%)	8 (3%)	5	41
15	ST	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	16	62
16	SU	68/70 (97%)	52 (76%)	11 (16%)	5 (7%)	1	18
17	SC	230/232 (99%)	212 (92%)	13 (6%)	5 (2%)	8	51
18	SD	203/205 (99%)	177 (87%)	18 (9%)	8 (4%)	4	36
19	SE	164/166 (99%)	149 (91%)	13 (8%)	2 (1%)	16	62
20	SF	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	24	69
21	SG	176/178 (99%)	158 (90%)	15 (8%)	3 (2%)	11	55
22	SH	127/129 (98%)	121 (95%)	4 (3%)	2 (2%)	12	56
23	SI	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
24	S1	700/702 (100%)	632 (90%)	45 (6%)	23 (3%)	5	41
27	LC	232/234 (99%)	206 (89%)	19 (8%)	7 (3%)	5	44
28	LM	112/114 (98%)	99 (88%)	10 (9%)	3 (3%)	6	46
29	LN	270/272 (99%)	244 (90%)	16 (6%)	10 (4%)	4	38
30	LO	115/117 (98%)	108 (94%)	4 (4%)	3 (3%)	7	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	LP	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	9	53
32	LQ	108/110 (98%)	102 (94%)	5 (5%)	1 (1%)	21	67
33	LR	98/100 (98%)	84 (86%)	9 (9%)	5 (5%)	2	28
34	LS	101/103 (98%)	89 (88%)	8 (8%)	4 (4%)	4	35
35	LT	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	17	64
36	LU	82/84 (98%)	56 (68%)	15 (18%)	11 (13%)	0	6
37	LV	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
38	LD	162/164 (99%)	154 (95%)	7 (4%)	1 (1%)	30	74
39	LW	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
40	LX	207/209 (99%)	168 (81%)	25 (12%)	14 (7%)	1	21
41	LY	56/58 (97%)	52 (93%)	3 (5%)	1 (2%)	11	54
42	L1	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	4	38
43	L2	52/54 (96%)	44 (85%)	7 (14%)	1 (2%)	10	53
44	L3	44/46 (96%)	39 (89%)	2 (4%)	3 (7%)	1	21
45	L4	62/64 (97%)	59 (95%)	2 (3%)	1 (2%)	12	56
46	L5	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
47	L6	199/201 (99%)	172 (86%)	18 (9%)	9 (4%)	3	31
48	LE	139/141 (99%)	123 (88%)	12 (9%)	4 (3%)	6	44
49	L7	176/178 (99%)	137 (78%)	21 (12%)	18 (10%)	1	11
50	L8	174/176 (99%)	156 (90%)	9 (5%)	9 (5%)	2	27
51	L9	147/149 (99%)	132 (90%)	9 (6%)	6 (4%)	3	34
52	LF	140/142 (99%)	122 (87%)	16 (11%)	2 (1%)	14	59
53	LG	121/123 (98%)	107 (88%)	12 (10%)	2 (2%)	11	55
54	LH	142/144 (99%)	129 (91%)	5 (4%)	8 (6%)	2	26
55	LI	134/136 (98%)	122 (91%)	10 (8%)	2 (2%)	13	57
56	LJ	125/127 (98%)	110 (88%)	9 (7%)	6 (5%)	3	30
57	LK	115/117 (98%)	107 (93%)	5 (4%)	3 (3%)	7	46
58	LZ	68/70 (97%)	56 (82%)	10 (15%)	2 (3%)	6	44
All	All	7019/7125 (98%)	6254 (89%)	534 (8%)	231 (3%)	8	41

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%)	80	92
5	SK	98/98 (100%)	92 (94%)	6 (6%)	23	65
6	SL	103/103 (100%)	101 (98%)	2 (2%)	65	88
7	SM	95/95 (100%)	89 (94%)	6 (6%)	22	64
8	SN	83/83 (100%)	81 (98%)	2 (2%)	57	85
9	SO	76/76 (100%)	75 (99%)	1 (1%)	76	91
10	SP	65/65 (100%)	65 (100%)	0	100	100
11	SQ	77/77 (100%)	75 (97%)	2 (3%)	54	83
12	SR	64/64 (100%)	62 (97%)	2 (3%)	47	81
13	SS	78/78 (100%)	75 (96%)	3 (4%)	40	77
14	SB	198/198 (100%)	189 (96%)	9 (4%)	34	74
15	ST	65/65 (100%)	64 (98%)	1 (2%)	72	90
16	SU	60/60 (100%)	54 (90%)	6 (10%)	9	43
17	SC	189/189 (100%)	178 (94%)	11 (6%)	25	66
18	SD	172/172 (100%)	165 (96%)	7 (4%)	37	75
19	SE	125/125 (100%)	118 (94%)	7 (6%)	26	68
20	SF	116/116 (100%)	112 (97%)	4 (3%)	44	80
21	SG	146/146 (100%)	141 (97%)	5 (3%)	44	80
22	SH	104/104 (100%)	99 (95%)	5 (5%)	31	72
23	SI	106/106 (100%)	104 (98%)	2 (2%)	65	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	S1	575/575 (100%)	549 (96%)	26 (4%)	34	74
27	LC	181/181 (100%)	171 (94%)	10 (6%)	27	68
28	LM	99/99 (100%)	91 (92%)	8 (8%)	15	54
29	LN	217/217 (100%)	207 (95%)	10 (5%)	33	73
30	LO	89/89 (100%)	84 (94%)	5 (6%)	26	68
31	LP	84/84 (100%)	75 (89%)	9 (11%)	8	40
32	LQ	93/93 (100%)	92 (99%)	1 (1%)	80	92
33	LR	84/84 (100%)	79 (94%)	5 (6%)	24	65
34	LS	84/84 (100%)	80 (95%)	4 (5%)	31	72
35	LT	78/78 (100%)	74 (95%)	4 (5%)	29	70
36	LU	62/62 (100%)	57 (92%)	5 (8%)	15	54
37	LV	67/67 (100%)	65 (97%)	2 (3%)	48	82
38	LD	122/122 (100%)	120 (98%)	2 (2%)	70	90
39	LW	55/55 (100%)	53 (96%)	2 (4%)	42	78
40	LX	164/164 (100%)	157 (96%)	7 (4%)	35	75
41	LY	48/48 (100%)	46 (96%)	2 (4%)	36	75
42	L1	47/47 (100%)	44 (94%)	3 (6%)	22	63
43	L2	48/48 (100%)	48 (100%)	0	100	100
44	L3	38/38 (100%)	36 (95%)	2 (5%)	28	69
45	L4	51/51 (100%)	49 (96%)	2 (4%)	39	77
46	L5	34/34 (100%)	33 (97%)	1 (3%)	50	82
47	L6	165/165 (100%)	160 (97%)	5 (3%)	48	82
48	LE	109/109 (100%)	101 (93%)	8 (7%)	17	58
49	L7	149/149 (100%)	138 (93%)	11 (7%)	17	57
50	L8	137/137 (100%)	130 (95%)	7 (5%)	29	70
51	L9	114/114 (100%)	106 (93%)	8 (7%)	19	60
52	LF	116/116 (100%)	112 (97%)	4 (3%)	44	80
53	LG	104/104 (100%)	98 (94%)	6 (6%)	25	66
54	LH	103/103 (100%)	98 (95%)	5 (5%)	31	71
55	LI	109/109 (100%)	106 (97%)	3 (3%)	51	82
56	LJ	103/103 (100%)	98 (95%)	5 (5%)	31	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	LK	87/87 (100%)	82 (94%)	5 (6%)	25	67
58	LZ	62/62 (100%)	59 (95%)	3 (5%)	31	72
All	All	5788/5788 (100%)	5526 (96%)	262 (4%)	38	74

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

Mol	Chain	Res	Type
28	LM	19	PHE
31	LP	79	ARG
54	LH	55	MET
28	LM	71	ARG
29	LN	250	GLN

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

Mol	Chain	Res	Type
29	LN	229	HIS
36	LU	45	HIS
51	L9	135	HIS
30	LO	43	GLN
36	LU	56	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	386	G
25	LA	1061	U
25	LA	2797	U
25	LA	453	A
25	LA	620	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	1.61	6 (23%)	29,54,54	1.89	5 (17%)

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	-	-	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	S1	801	GTP	C6-C5	-3.79	1.33	1.41
59	S1	801	GTP	C5-C4	-2.92	1.33	1.40
59	S1	801	GTP	PG-O3G	-2.18	1.47	1.54
59	S1	801	GTP	PG-O2G	-2.18	1.47	1.54
59	S1	801	GTP	C2-N1	2.33	1.39	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	S1	801	GTP	N3-C2-N1	-5.95	119.46	127.56
59	S1	801	GTP	C4'-O4'-C1'	-5.36	103.96	109.64
59	S1	801	GTP	C5-C6-N1	-3.04	119.55	123.52
59	S1	801	GTP	C6-N1-C2	2.01	118.24	115.88
59	S1	801	GTP	O3G-PG-O2G	2.44	116.41	107.44

There are no chirality outliers.

There are no torsion outliers.

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

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.