



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:53 PM BST

PDB ID : 5AKA
EMDB ID: : EMD-2917
Title : EM structure of ribosome-SRP-FtsY complex in closed state
Authors : vonLoeffelholz, O.; Jiang, Q.; Ariosa, A.; Karuppasamy, M.; Huard, K.;
Berger, I.; Shan, S.; Schaffitzel, C.
Deposited on : 2015-03-03
Resolution : 5.70 Å(reported)

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 : unknown
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

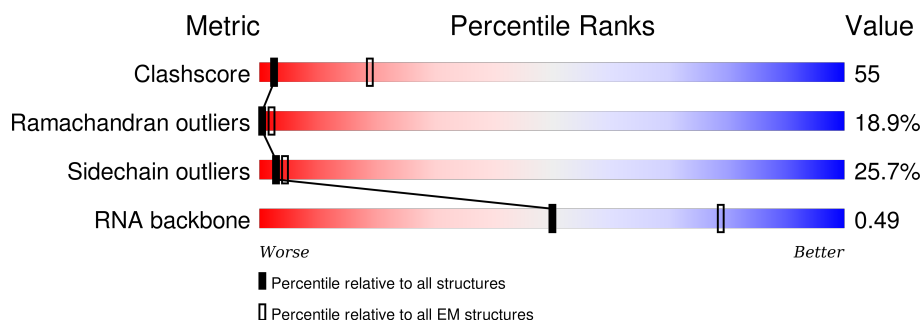
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.70 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.




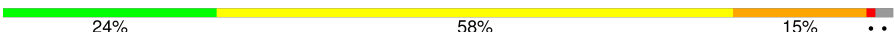


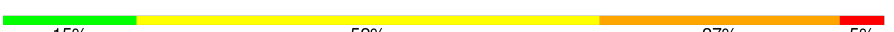
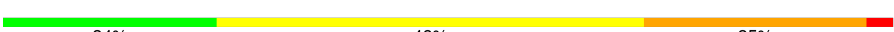
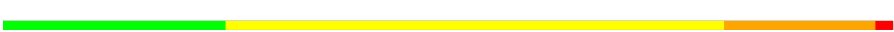





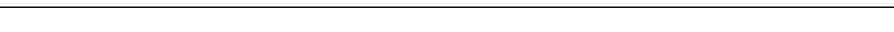

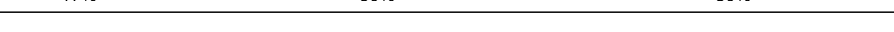

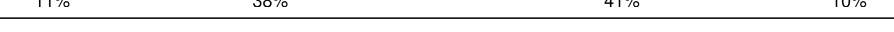


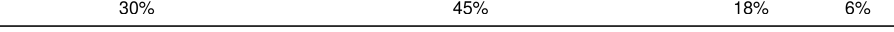




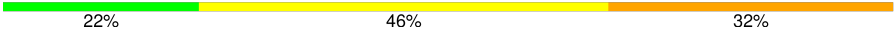
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	0	56	16% 52% 20% 13%
2	1	54	17% 46% 35% .
3	2	46	28% 46% 26%
4	3	64	23% 42% 33% .
5	4	38	21% 37% 39% .
6	5	109	44% 50% 6%
7	6	8	88% 13%
8	7	74	55% 43% .

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Mol	Chain	Length	Quality of chain
9	A	120	
10	B	2904	
11	C	273	
12	D	209	
13	E	201	
14	F	178	
15	G	176	
16	H	149	
17	I	141	
18	J	142	
19	K	123	
20	L	144	
21	M	136	
22	N	127	
23	O	117	
24	P	114	
25	Q	117	
26	R	103	
27	S	110	
28	T	100	
29	U	103	
30	V	94	
31	W	84	
32	X	63	
33	Y	58	

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Mol	Chain	Length	Quality of chain
34	Z	70	<div> <div></div> <div>21%</div> <div>43%</div> <div>23%</div> <div>13%</div> </div>

2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 92737 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S RIBOSOMAL PROTEIN L32.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	54	Total	C	N	O	0	0
			441	284	81	76		

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

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

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

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

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

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

- Molecule 6 is a protein called SIGNAL RECOGNITION PARTICLE PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	109	Total	C	N	O	S	0	0
			850	523	159	153	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	406	SER	CYS	CONFLICT	UNP P0AGD7

- Molecule 7 is a protein called ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	6	8	Total	C	N	O	0	0
			41	24	8	9		

- Molecule 8 is a RNA chain called 4.5 S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	74	Total	C	N	O	P	0	0
			1591	709	298	511	73		

- Molecule 9 is a RNA chain called LARGE RIBOSOMAL SUBUNIT RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	117	Total	C	N	O	P	0	0
			2507	1116	459	815	117		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	2841	Total	C	N	O	P	0	0
			60995	27210	11229	19715	2841		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	2798	U	UNK	CONFLICT	GB 731469900
B	2800	A	UNK	CONFLICT	GB 731469900

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	138	Total	C	N	O	S	0	0
			1002	623	197	181	1		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

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

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

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

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

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L29.

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

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L30.

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

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L31.

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

- Molecule 35 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	B	110	Total	Mg	0
			110	110	

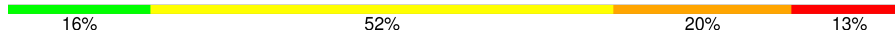
- Molecule 36 is water.

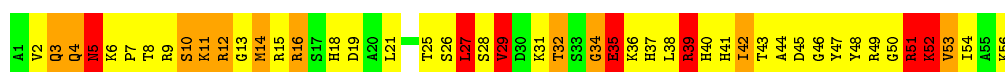
Mol	Chain	Residues	Atoms		AltConf
36	B	497	Total	O	0
			497	497	
36	C	1	Total	O	0
			1	1	
36	E	5	Total	O	0
			5	5	
36	L	2	Total	O	0
			2	2	
36	N	1	Total	O	0
			1	1	

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: 50S RIBOSOMAL PROTEIN L32

Chain 0: 



- Molecule 2: 50S RIBOSOMAL PROTEIN L33

Chain 1: 

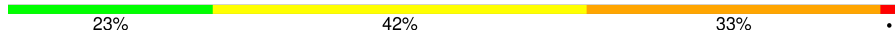


- Molecule 3: 50S RIBOSOMAL PROTEIN L34

Chain 2: 

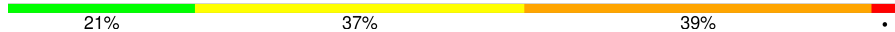


- Molecule 4: 50S RIBOSOMAL PROTEIN L35

Chain 3: 



- Molecule 5: 50S RIBOSOMAL PROTEIN L36

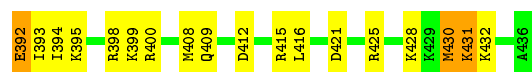
Chain 4: 



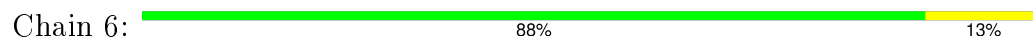
- Molecule 6: SIGNAL RECOGNITION PARTICLE PROTEIN

Chain 5: 

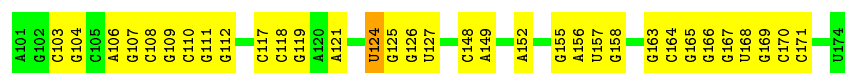




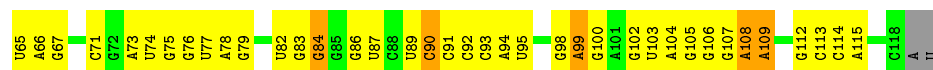
- Molecule 7: ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA



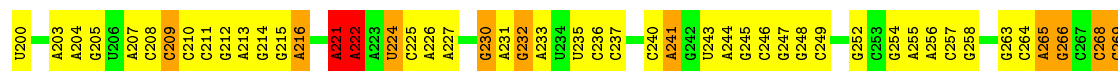
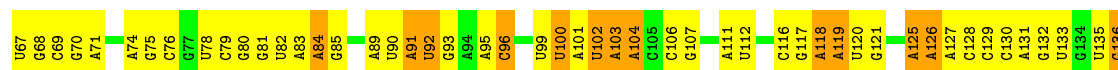
- Molecule 8: 4.5 S RNA



- Molecule 9: LARGE RIBOSOMAL SUBUNIT RNA



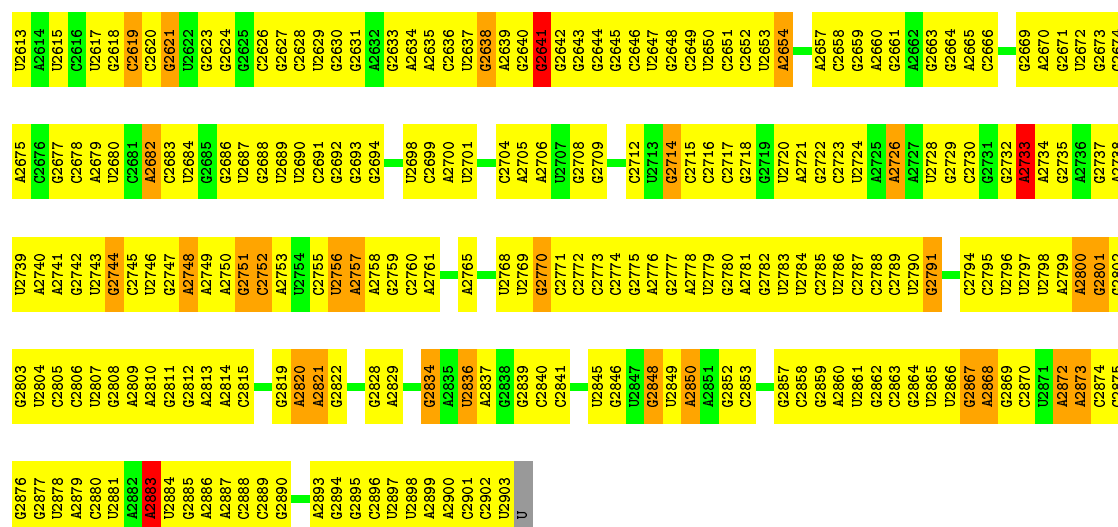
- Molecule 10: 23S RNA



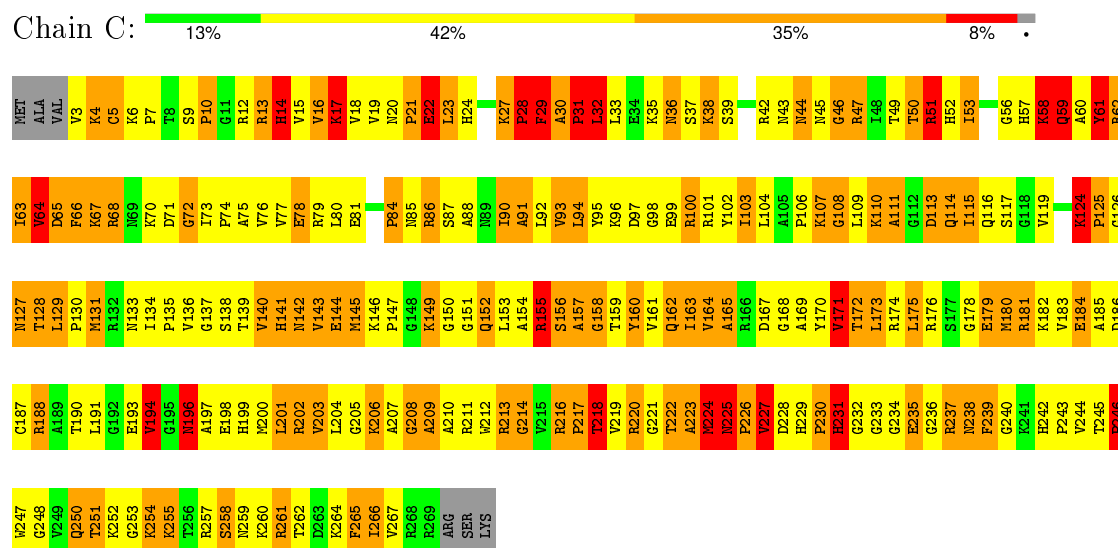

WORLDWIDE PDB
 PROTEIN DATA BANK

EMDataBank
 Unified Data Resource for 3DEM

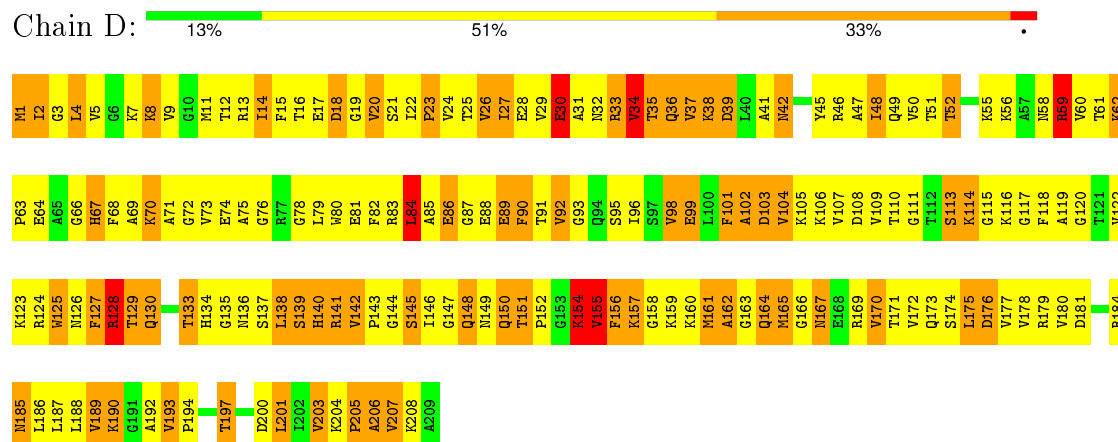
C2538	A2469	G2396	U2321	U2259	G2190	G	C2066	C1997	A1927	U1851	U1782	A1717	A1652	A1580	C1518
C2539	G2470	G2397	A2322	C2260	A2191	C	G2067	A1996	A1928	U1852	A1783	G1718	G1653	A1581	G1519
C2540	A2471	G2398	G2323	C2261	U2192	U	U2068	C1999	G1929	A1853	A1784	G1719	A1654	U1583	U1520
	G2472	G2399	G2324	U2262	G2193	U	G2069	C2000	G1930	A1854	A1785	U1720	A1655	U1584	G1521
G2543	C2475	G2400	G2325	C2263	U2194	U	A2070	C2001	U1932	U1855	A1786	G1721	C1656	C1585	A1522
G2544	A2476	U2401		C2264	U2195		A2071		A1933	U1856	A1787	U1722	C1657	A1586	U1523
G2545	U2477	U2402	A2328	U2265	C2196		C2072	U2007	G1933	G1857	C1788	G1723	C1658	G1587	G1524
A2547	A2478		U2329	A2266	U2197		C2073	C2008	C1934		A1789	G1724		G1588	A1525
U2548	U2479		G2330	A2267	A2198		U2074	A2009	G1935		G1790	U1725	G1661	U1589	C1526
			G2331	A2268	A2199		U2075		A1936	U1864	A1791	G1726	G1662	A1590	G1527
			C2332	G2269	C2200		U2076	U2011	A1937	U1865	G1792	C1727	G1663	A1591	A1528
			A2333	A2270	G2201		A2077		A1938	A1866	C1793	C1728	A1664	C1592	G1529
G2553	C2483	G2412	U2334	G2271	U2203		C2078	A2014	U1939	A1867	A1794	U1728	A1665	A1593	G1530
U2554	G2413	G2415	A2335	U2272	G2204		U2079	A2015	U1940	C1868	C1795	C1730	G1666	U1594	C1531
U2555	G2485	G2416	A2336	A2273	C2143		A2080			C1869	U1796	G1732	G1667	C1595	A1532
C2556		C2415	A2337	A2274	C2144		U2081	U2017	U1943	A1870	G1797	C1733	A1596	A1596	C1533
C2557	U2489	C2416	G2337	A2275	C2145		G2082		U1944	U1872	U1798	G1734	A1669	A1597	U1534
C2558	G2490	C2416	C2338	C2276	C2146		A2083	A2019	U1946	A1873	C1800	A1735	C1670	A1598	U1535
	U2491	U2419	C2339	G2277	A2147		G2084		C1947	C1874	A1801	U1736	A1672	U1599	C1536
U2563	U2492	C2420	A2340	G2277	C2148		U2085	U2022	U1952	C1875	A1802	G1737	G1673	C1600	G1537
	U2493		G2341	A2278	U2210		C2086	C2023	C1954	U1876	A1803	G1738	C1674	G1601	U1538
A2566		U2423	U2344		A2211		U2087	G2029	U1955	C1881	U1810	U1742		C1606	U1542
G2567	C2498	C2424	G2345	G2282	U2212		G2088	A2030	U1956	A1882	U1811	G1743	G1681	C1607	G1543
G2568	C2499	A2425	C2346	C2283	U2213		A2089	C2025	C1957	A1883	U1812	U1744	G1682	A1608	A1544
G2569	U2500	A2426	A2347	A2284	G2214	A	A2090	C2026	C1958	U1884	G1813	A1745	U1683	A1610	G1546
G2570	C2501	C2427	C2347	C2285	C2215	C	A2091	G2027	C1959	A1885	G1814	A1746	C1685	C1611	C1547
U2571	G2502	G2428	U2348	G2286	G2216	C	C2092	U2028	C1960		U1815	U1747	C1686	G1612	A1548
A2572	A2503	G2429	G2349	A2287	G2217	C	U2093	U2029	U1963	G1888	C1816	C1748	G1687	G1613	A1549
G2573	U2504	A2430	C2350	A2288	G2218	G	G2094	G2035	U1964	A1889	U1817	U1749	G1688	C1616	C1550
G2574	G2505		G2351	G2289	U2219	A	A2095	A2037	G1965	A1890	U1818	U1750	U1689	A1551	A1552
G2575	U2506		A2352	G2290	U2220	C	A2096	G2038	C1966		U1820	C1752	A1690	A1553	
G2576	G2507	A2434	C2353	U2291	G2221	C	C2097	U2039	A1967	U1898	A1821	G1753	C1691	U1554	
A2577		U2438	G2354	U2292	G2222	C	A2098	G2040	C1967		C1822	U1754	U1692	G1622	G1555
U2578		G2439	G2355	G2293	C2223	G	U2099	U2041		A1901	G1823	U1755	U1693	G1623	C1556
G2579	U2511	C2440	C2364	G2294	G2224	A	G2100	A2042	U1970	C1902	G1824	G1756	C1694	U1624	C1557
G2581	A2513	U2441	G2365	C2295	A2225	C	A2101	C2043	U1971	G1903	U1825	A1757	G1695		C1558
	C2514	C2442		U2296	G2226	U	G2102	C2044	G1972	C1904	G1826	U1758	G1696	U1629	
C2585	C2515	C2443	A2369	A2297	A2227	U	C2103		C1973	G1905	U1827	A1759			G1560
U2586	A2516	G2444	G2370	A2298	G2228	U	C2104	U2045		G1906	G1828			G1633	C1561
A2587	G2445	G2446	G2371	U2299	U2229	G	C2105	A2046	U1979	C1909	A1829	A1762	A1701	A1634	U1562
	U2518	G2447	U2372	C2301	G2230	A	U2106		G1980	C1910	G1830	G1763	G1702	A1635	U1563
A2590	U2519	G2448	G2373	U2302	U2231	A			A1981		C1832	U1765	G1703	U1636	C1564
C2591	C2520	U2449	C2374	C2303	C2232	U	G2110			A1913	C1833	G1766	A1705	A1637	C1565
G2592	C2521	U2449		G2304		A	U		G1986	C1914			C1706	C1639	A1566
	U2522	A2450	G2379	U2305	U2236	C	G	C2047	A1987		G1838	C1771	G1707	A1640	G1567
G2597	G2523		C2380	C2306	G2237	C	U	G2048	G1988	U1917		A1772	C1708	A1641	G1568
A2598	G2524			G2307	G2238	C	A	G2049	G1989	A1918	G1842	A1773	U1709	A1569	
G2599	G2525	G2455	G2383	C2308	U2239	A	A	C2050	C1990	A1919	C1843	C1774	G1710	G1642	A1570
A2600	G2526	G2456	U2384	A2309	U2240	C	G	A2051	C1991	C1920	C1844	U1775	A1711	G1645	A1572
C2601	C2527	U2457	C2385	C2310	G2242	C	G	A2052	G1992	G1921	G1845	G1776		C1646	C1573
A2602	U2528	G2458	A2386	A2311	U2243	A	U	A2054	U1993	G1922	G1846			U1647	C1574
G2603	G2603	A2459	U2387	U2312	U2243	U	A	C2055	U1994	G1923	A1847			U1648	
U2604	A2530	U2460	G2388	C2313	G2246	A	G	C2056	G1995	U1924	A1848			G1649	
G2605	A2531	U2461	G2389	A2314	A2247	G	G								U1578
G2606	G2532	C2462	U2390	G2315	C2248	U	U	A2060	G1992	G1922					
	U2533		G2391	C2316	U2249	U	G	A2061	U1993	G1922					
G2608	A2534	C2465	A2392	A2317	G2250	G	G	A2062	U1994	G1922					
U2609	G2535	C2466	G2393	G2318	G2251	G	G	C2063	U1995	U1923					
C2610	G2536	U2467	C2394	U2187	G2251	A	A	C2064	U1996	C1924					
	U2537	A2468	C2395	U2188	C2258	G	G								
				U2189											



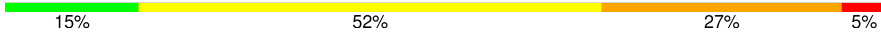
• Molecule 11: 50S RIBOSOMAL PROTEIN L2

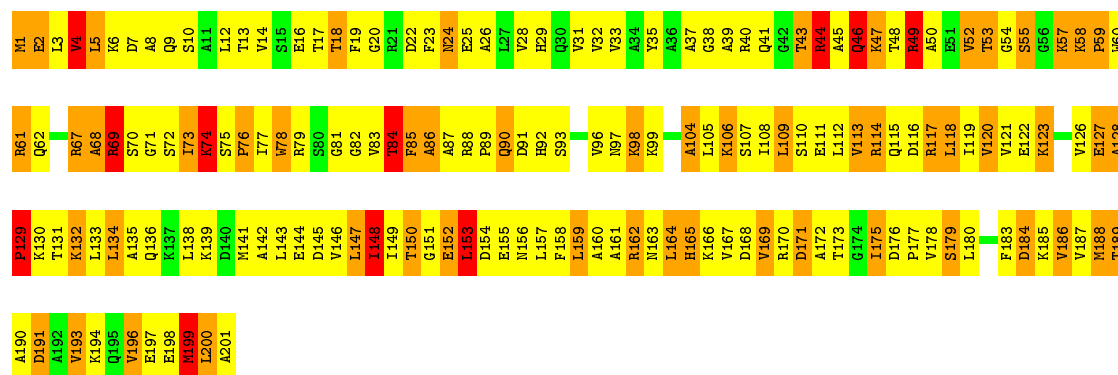


- Molecule 12: 50S RIBOSOMAL PROTEIN L3



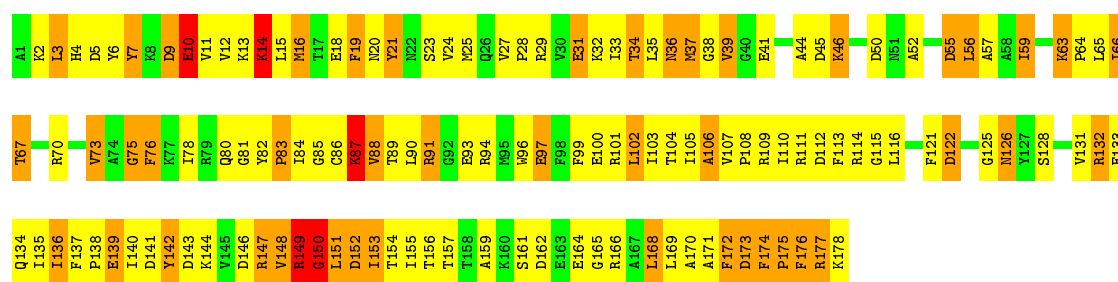
- Molecule 13: 50S RIBOSOMAL PROTEIN L4

Chain E: 



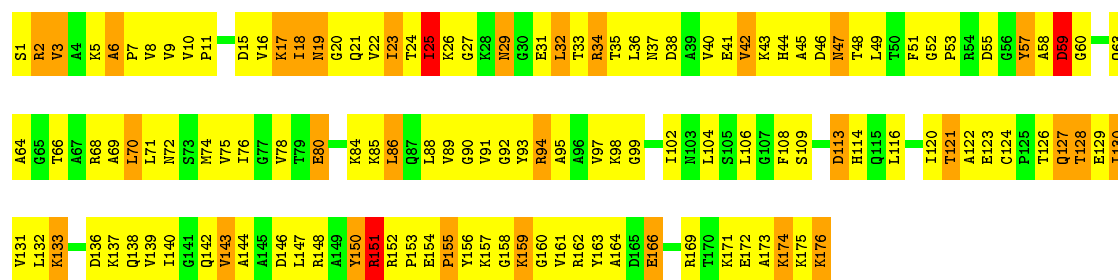
• Molecule 14: 50S RIBOSOMAL PROTEIN L5

Chain F: 



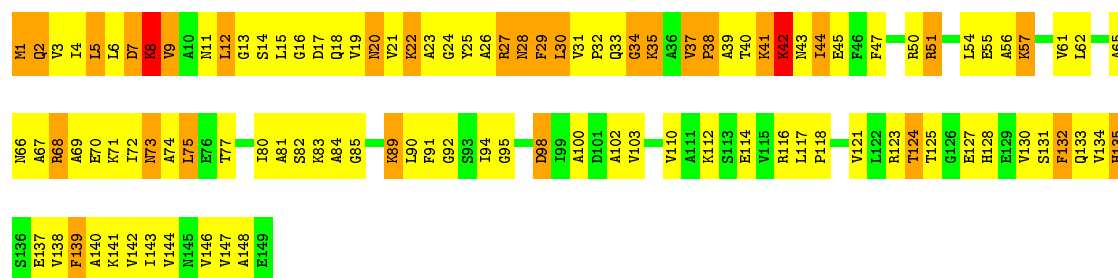
• Molecule 15: 50S RIBOSOMAL PROTEIN L6

Chain G: 

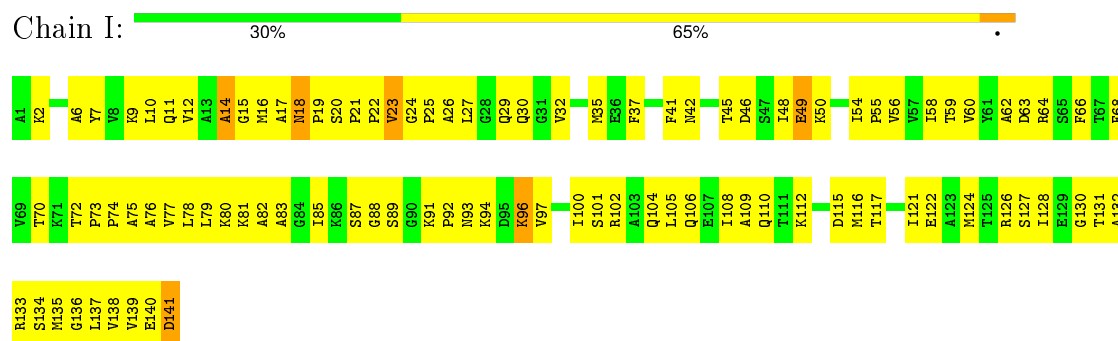


• Molecule 16: 50S RIBOSOMAL PROTEIN L9

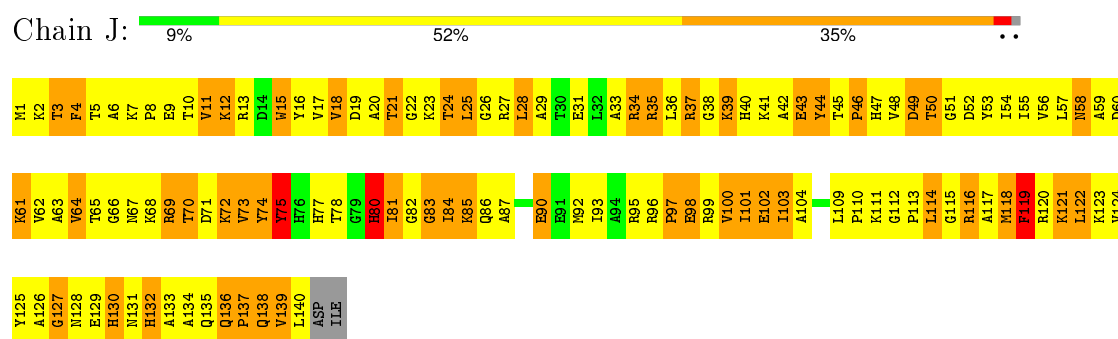
Chain H: 



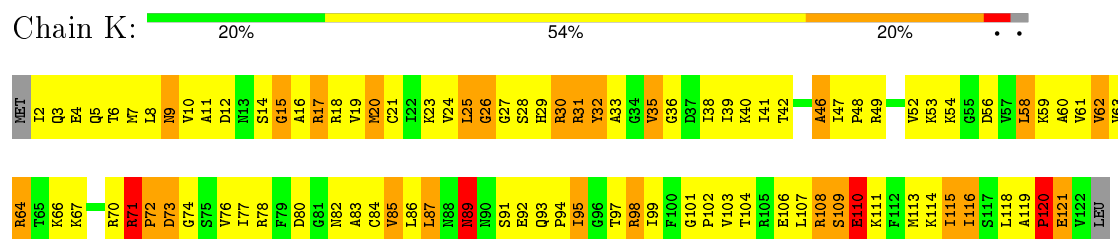
- Molecule 17: 50S RIBOSOMAL PROTEIN L11



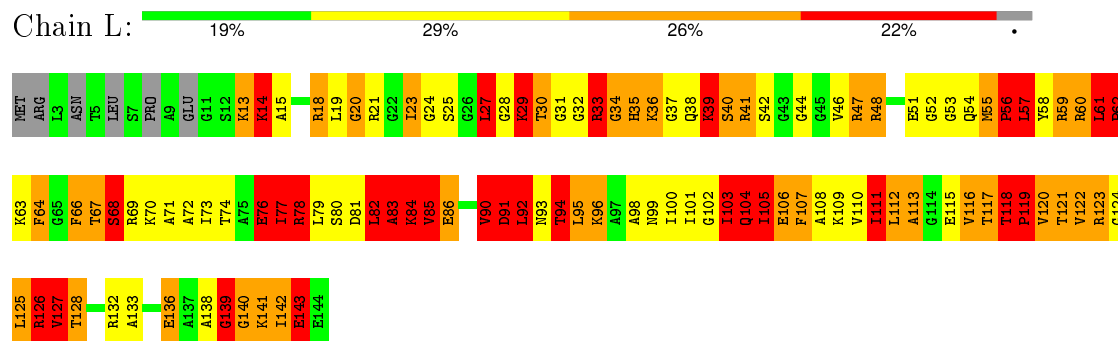
- Molecule 18: 50S RIBOSOMAL PROTEIN L13



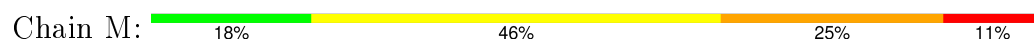
- Molecule 19: 50S RIBOSOMAL PROTEIN L14

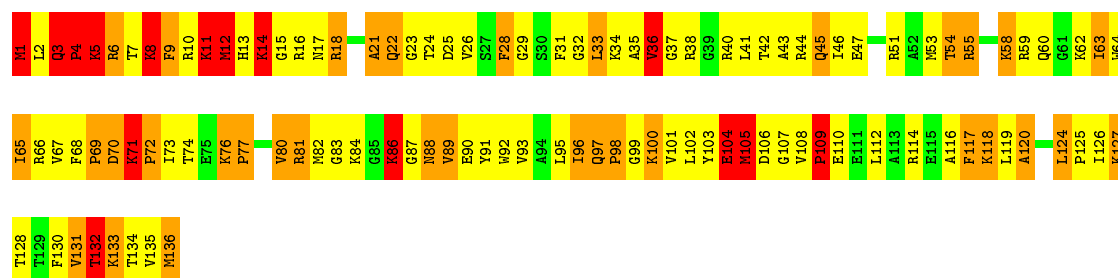


- Molecule 20: 50S RIBOSOMAL PROTEIN L15



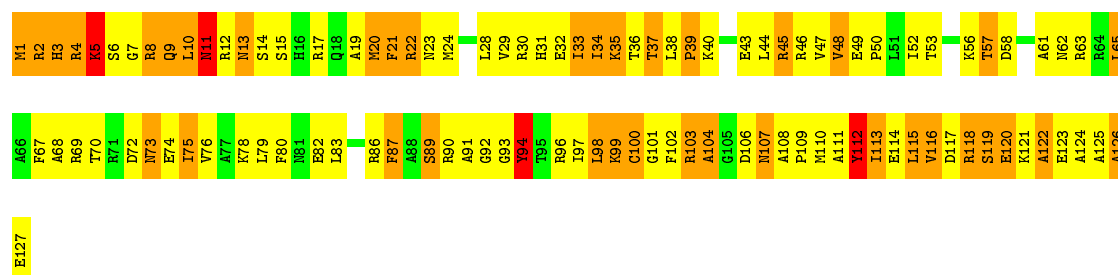
- Molecule 21: 50S RIBOSOMAL PROTEIN L16





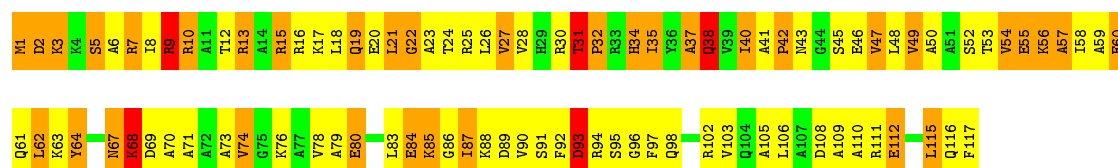
• Molecule 22: 50S RIBOSOMAL PROTEIN L17

Chain N: 17% 50% 30%



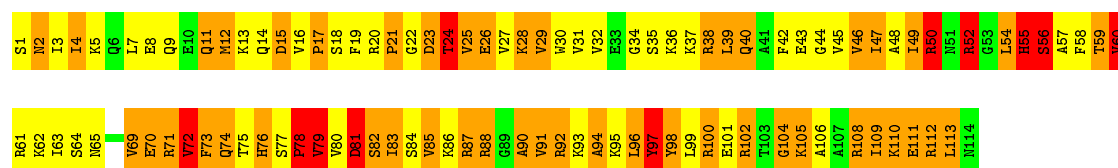
• Molecule 23: 50S RIBOSOMAL PROTEIN L18

Chain O: 20% 46% 30%



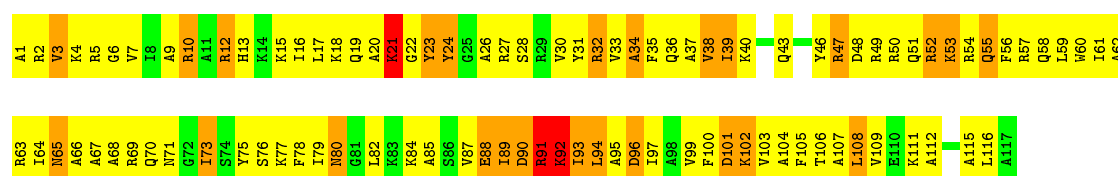
• Molecule 24: 50S RIBOSOMAL PROTEIN L19

Chain P: 11% 38% 41% 10%

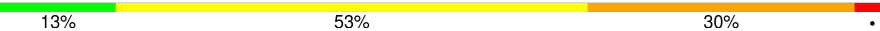


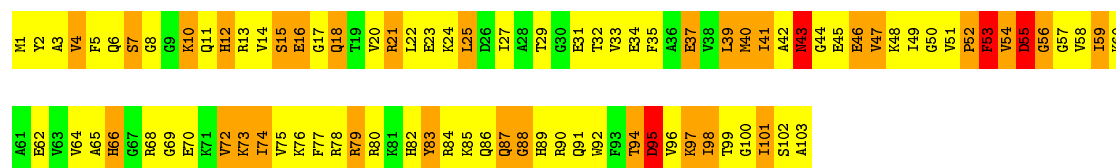
• Molecule 25: 50S RIBOSOMAL PROTEIN L20

Chain Q: 16% 60% 21%



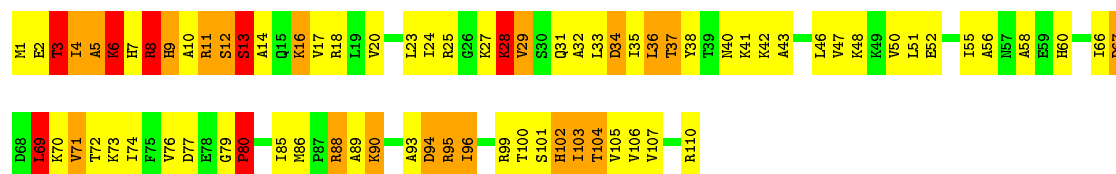
• Molecule 26: 50S RIBOSOMAL PROTEIN L21

Chain R: 




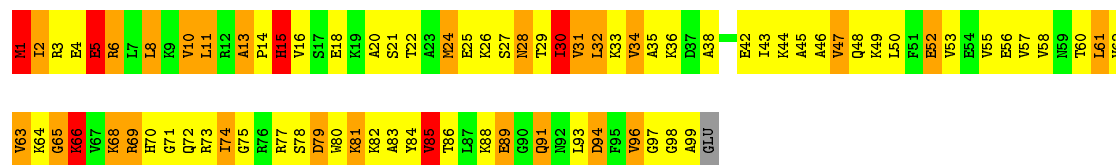
• Molecule 27: 50S RIBOSOMAL PROTEIN L22

Chain S: 




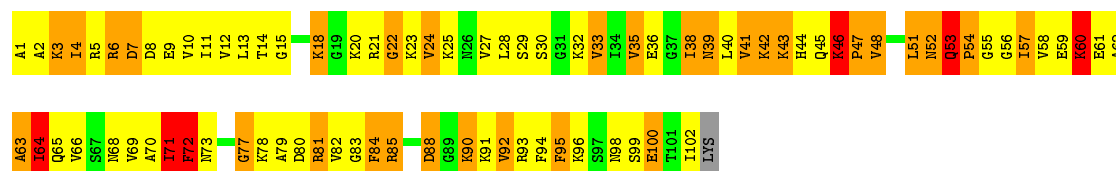
• Molecule 28: 50S RIBOSOMAL PROTEIN L23

Chain T: 




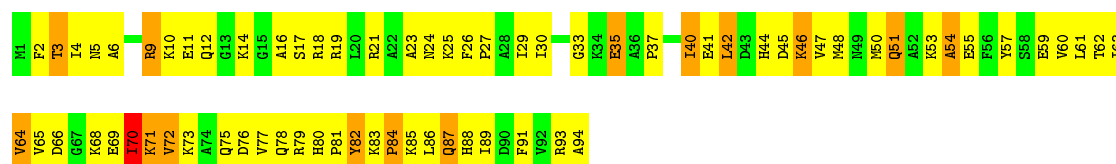
• Molecule 29: 50S RIBOSOMAL PROTEIN L24

Chain U: 

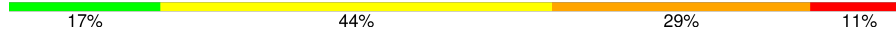


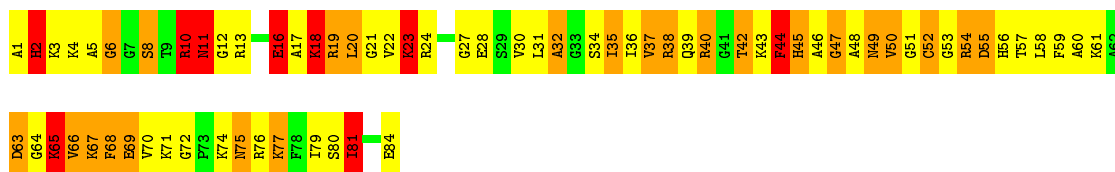
• Molecule 30: 50S RIBOSOMAL PROTEIN L25

Chain V: 

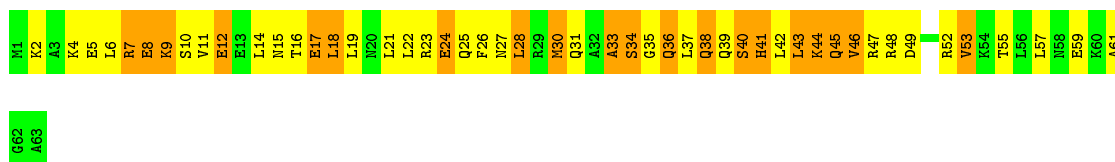
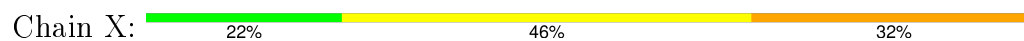


• Molecule 31: 50S RIBOSOMAL PROTEIN L27

Chain W: 



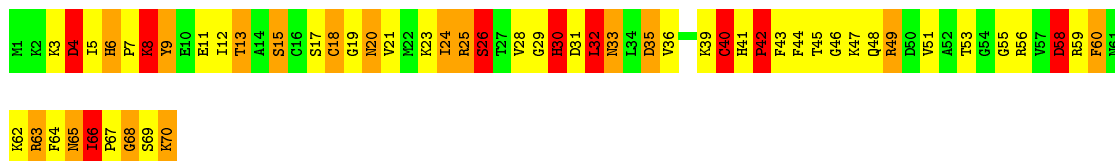
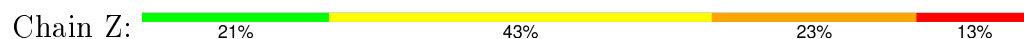
• Molecule 32: 50S RIBOSOMAL PROTEIN L29



• Molecule 33: 50S RIBOSOMAL PROTEIN L30



• Molecule 34: 50S RIBOSOMAL PROTEIN L31



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PER MICROGRAPH	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	24	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	Depositor
Image detector	FEL FALCON II	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0	0.53	1/450 (0.2%)	1.15	7/599 (1.2%)
10	B	0.32	11/68314 (0.0%)	0.77	54/106569 (0.1%)
11	C	0.40	0/2092	0.88	7/2813 (0.2%)
12	D	0.40	0/1586	0.80	2/2134 (0.1%)
13	E	0.45	1/1571 (0.1%)	0.88	6/2113 (0.3%)
14	F	0.33	0/1444	0.87	5/1937 (0.3%)
15	G	0.31	0/1343	0.69	0/1816
16	H	0.27	0/1122	0.59	0/1515
17	I	0.26	0/1046	0.58	0/1410
18	J	0.41	1/1135 (0.1%)	0.72	3/1529 (0.2%)
19	K	0.35	0/939	0.99	2/1258 (0.2%)
2	1	0.36	0/448	0.71	0/594
20	L	0.71	0/1006	1.61	29/1331 (2.2%)
21	M	0.48	0/1093	1.03	8/1460 (0.5%)
22	N	0.34	0/1021	0.78	4/1364 (0.3%)
23	O	0.30	0/910	0.67	1/1219 (0.1%)
24	P	0.55	0/929	1.40	16/1242 (1.3%)
25	Q	0.41	0/960	0.86	2/1278 (0.2%)
26	R	1.06	6/829 (0.7%)	1.42	13/1107 (1.2%)
27	S	0.28	0/864	0.69	1/1156 (0.1%)
28	T	0.38	0/784	0.77	4/1048 (0.4%)
29	U	0.48	0/787	0.74	3/1051 (0.3%)
3	2	0.33	0/380	0.64	0/498
30	V	0.30	0/766	0.53	0/1025
31	W	0.36	0/642	0.96	5/848 (0.6%)
32	X	0.29	0/509	0.81	1/674 (0.1%)
33	Y	0.30	0/453	0.64	0/605
34	Z	0.48	0/559	1.04	5/745 (0.7%)
4	3	0.47	0/513	0.96	1/676 (0.1%)
5	4	0.40	0/303	0.73	0/397
6	5	0.24	0/855	0.38	0/1124
7	6	0.37	0/40	0.26	0/53

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	7	0.13	0/1781	0.63	0/2779
9	A	0.27	0/2803	0.74	0/4371
All	All	0.35	20/100277 (0.0%)	0.80	179/150338 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	55
11	C	0	3
18	J	0	2
20	L	0	1
24	P	0	1
25	Q	0	1
26	R	0	1
All	All	0	64

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	R	53	PHE	CB-CG	17.81	1.81	1.51
26	R	54	VAL	N-CA	-11.64	1.23	1.46
26	R	54	VAL	CA-CB	11.12	1.78	1.54
10	B	2196	C	O3'-P	10.16	1.73	1.61
10	B	2052	A	C4'-C3'	-8.24	1.44	1.53

The worst 5 of 179 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	2791	G	O5'-P-OP1	-28.73	76.22	110.70
10	B	2791	G	O5'-P-OP2	18.24	132.59	110.70
26	R	53	PHE	CA-C-N	-17.34	79.05	117.20
26	R	54	VAL	CB-CA-C	15.12	140.12	111.40
10	B	2790	U	OP1-P-O3'	14.24	136.52	105.20

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	B	136	G	Sidechain
10	B	139	U	Sidechain
10	B	142	A	Sidechain
10	B	143	C	Sidechain
10	B	51	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	0	444	0	461	105	0
2	1	441	0	485	68	0
3	2	377	0	418	50	0
4	3	504	0	574	108	0
5	4	302	0	343	45	0
6	5	850	0	897	94	0
7	6	41	0	39	1	0
8	7	1591	0	806	24	0
9	A	2507	0	1270	86	0
10	B	60995	0	30659	4167	0
11	C	2053	0	2122	432	0
12	D	1565	0	1616	377	0
13	E	1552	0	1617	282	0
14	F	1420	0	1460	167	0
15	G	1323	0	1374	165	0
16	H	1111	0	1148	190	0
17	I	1032	0	1088	199	0
18	J	1112	0	1147	217	0
19	K	930	0	1000	119	0
20	L	1002	0	1070	287	0
21	M	1074	0	1157	244	0
22	N	1008	0	1036	232	0
23	O	900	0	935	129	0
24	P	917	0	965	205	0
25	Q	947	0	1022	173	0
26	R	816	0	838	166	0
27	S	857	0	922	120	0
28	T	777	0	840	129	0
29	U	779	0	831	255	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	V	753	0	780	104	0
31	W	634	0	656	157	0
32	X	509	0	541	68	0
33	Y	449	0	491	57	0
34	Z	549	0	552	114	0
35	B	110	0	0	0	0
36	B	497	0	0	17	0
36	C	1	0	0	0	0
36	E	5	0	0	0	0
36	L	2	0	0	0	0
36	N	1	0	0	0	0
All	All	92737	0	61160	8372	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 55.

The worst 5 of 8372 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)
10:B:1062:G:H21	17:I:134:SER:CB	1.09	1.62
10:B:1059:G:C5'	17:I:117:THR:HG23	1.22	1.60
26:R:54:VAL:CB	26:R:54:VAL:CA	1.78	1.59
26:R:53:PHE:CB	26:R:53:PHE:CG	1.81	1.58
10:B:80:G:C5'	10:B:346:A:C8	1.88	1.53

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	0	54/56 (96%)	30 (56%)	15 (28%)	9 (17%)	0 5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1	52/54 (96%)	19 (36%)	23 (44%)	10 (19%)	0	3
3	2	44/46 (96%)	23 (52%)	14 (32%)	7 (16%)	0	5
4	3	62/64 (97%)	30 (48%)	25 (40%)	7 (11%)	0	10
5	4	36/38 (95%)	18 (50%)	9 (25%)	9 (25%)	0	2
6	5	107/109 (98%)	83 (78%)	19 (18%)	5 (5%)	3	32
7	6	6/8 (75%)	5 (83%)	1 (17%)	0	100	100
11	C	265/273 (97%)	103 (39%)	82 (31%)	80 (30%)	0	0
12	D	207/209 (99%)	90 (44%)	69 (33%)	48 (23%)	0	2
13	E	199/201 (99%)	98 (49%)	60 (30%)	41 (21%)	0	3
14	F	176/178 (99%)	95 (54%)	48 (27%)	33 (19%)	0	3
15	G	174/176 (99%)	118 (68%)	39 (22%)	17 (10%)	1	14
16	H	147/149 (99%)	85 (58%)	47 (32%)	15 (10%)	1	13
17	I	139/141 (99%)	124 (89%)	11 (8%)	4 (3%)	6	43
18	J	138/142 (97%)	67 (49%)	42 (30%)	29 (21%)	0	3
19	K	119/123 (97%)	71 (60%)	32 (27%)	16 (13%)	0	7
20	L	132/144 (92%)	55 (42%)	36 (27%)	41 (31%)	0	0
21	M	134/136 (98%)	69 (52%)	37 (28%)	28 (21%)	0	3
22	N	125/127 (98%)	71 (57%)	34 (27%)	20 (16%)	0	5
23	O	115/117 (98%)	64 (56%)	26 (23%)	25 (22%)	0	2
24	P	112/114 (98%)	39 (35%)	36 (32%)	37 (33%)	0	0
25	Q	115/117 (98%)	81 (70%)	22 (19%)	12 (10%)	1	12
26	R	101/103 (98%)	44 (44%)	31 (31%)	26 (26%)	0	1
27	S	108/110 (98%)	63 (58%)	27 (25%)	18 (17%)	0	5
28	T	97/100 (97%)	41 (42%)	39 (40%)	17 (18%)	0	4
29	U	100/103 (97%)	30 (30%)	47 (47%)	23 (23%)	0	2
30	V	92/94 (98%)	62 (67%)	22 (24%)	8 (9%)	1	17
31	W	82/84 (98%)	29 (35%)	26 (32%)	27 (33%)	0	0
32	X	60/63 (95%)	28 (47%)	20 (33%)	12 (20%)	0	3
33	Y	56/58 (97%)	29 (52%)	17 (30%)	10 (18%)	0	4
34	Z	68/70 (97%)	29 (43%)	26 (38%)	13 (19%)	0	3
All	All	3422/3507 (98%)	1793 (52%)	982 (29%)	647 (19%)	0	3

5 of 647 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	10	SER
1	0	29	VAL
1	0	35	GLU
2	1	46	VAL
3	2	4	THR

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	0	47/47 (100%)	31 (66%)	16 (34%)	0	2
2	1	48/48 (100%)	33 (69%)	15 (31%)	0	2
3	2	38/38 (100%)	27 (71%)	11 (29%)	0	3
4	3	51/51 (100%)	33 (65%)	18 (35%)	0	1
5	4	34/34 (100%)	22 (65%)	12 (35%)	0	1
6	5	92/92 (100%)	89 (97%)	3 (3%)	45	76
11	C	213/218 (98%)	145 (68%)	68 (32%)	0	2
12	D	164/164 (100%)	112 (68%)	52 (32%)	0	2
13	E	165/165 (100%)	115 (70%)	50 (30%)	0	3
14	F	149/149 (100%)	119 (80%)	30 (20%)	1	11
15	G	137/137 (100%)	105 (77%)	32 (23%)	1	7
16	H	114/114 (100%)	87 (76%)	27 (24%)	1	7
17	I	109/109 (100%)	106 (97%)	3 (3%)	51	78
18	J	114/116 (98%)	84 (74%)	30 (26%)	0	5
19	K	102/104 (98%)	78 (76%)	24 (24%)	1	7
20	L	97/103 (94%)	57 (59%)	40 (41%)	0	0
21	M	109/109 (100%)	77 (71%)	32 (29%)	0	3
22	N	103/103 (100%)	78 (76%)	25 (24%)	1	6
23	O	87/87 (100%)	58 (67%)	29 (33%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	P	99/99 (100%)	77 (78%)	22 (22%)	1	9
25	Q	89/89 (100%)	66 (74%)	23 (26%)	0	5
26	R	84/84 (100%)	68 (81%)	16 (19%)	2	13
27	S	93/93 (100%)	72 (77%)	21 (23%)	1	8
28	T	83/84 (99%)	60 (72%)	23 (28%)	0	4
29	U	83/84 (99%)	58 (70%)	25 (30%)	0	3
30	V	78/78 (100%)	66 (85%)	12 (15%)	3	22
31	W	62/62 (100%)	46 (74%)	16 (26%)	0	5
32	X	55/55 (100%)	40 (73%)	15 (27%)	0	4
33	Y	48/48 (100%)	36 (75%)	12 (25%)	1	6
34	Z	62/62 (100%)	43 (69%)	19 (31%)	0	3
All	All	2809/2826 (99%)	2088 (74%)	721 (26%)	3	6

5 of 721 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	H	77	THR
20	L	57	LEU
31	W	40	ARG
17	I	96	LYS
18	J	139	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
17	I	11	GLN
19	K	82	ASN
32	X	36	GLN
17	I	29	GLN
18	J	80	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	2837/2904 (97%)	552 (19%)	19 (0%)
8	7	73/74 (98%)	3 (4%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	A	116/120 (96%)	23 (19%)	0
All	All	3026/3098 (97%)	578 (19%)	19 (0%)

5 of 578 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	121	A
8	7	124	U
8	7	168	U
9	A	11	C
9	A	12	C

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	1236	G
10	B	1301	A
10	B	2282	G
10	B	1210	G
10	B	2336	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 110 ligands modelled in this entry, 110 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.