



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 30, 2017 – 09:39 PM EDT

PDB ID : 5MYJ
EMDB ID: : EMD-3581
Title : Structure of 70S ribosome from *Lactococcus lactis*
Authors : Franken, L.E.; Oostergetel, G.T.; Pijning, T.; Puri, P.; Boekema, E.J.; Poolman, B.; Guskov, A.
Deposited on : unknown
Resolution : 5.60 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

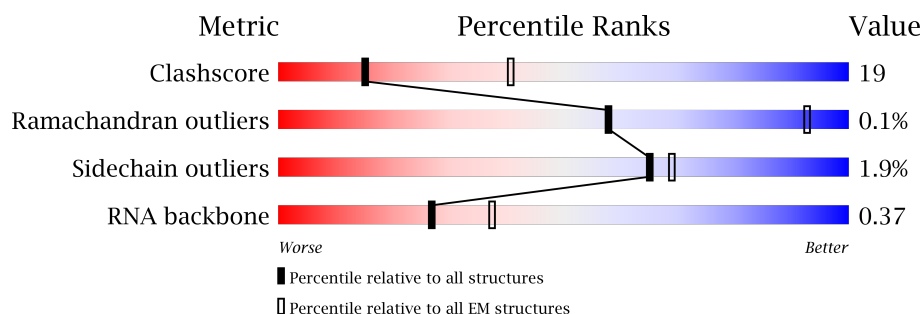
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.60 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.




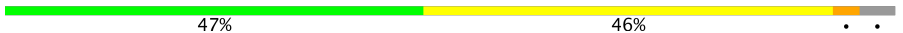





















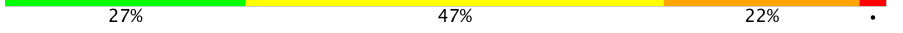
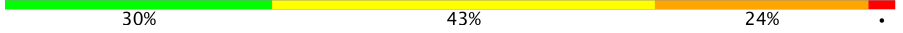
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	AA	1535	23% 46% 27% .
2	AB	255	59% 28% 12%
3	AC	217	50% 47% .
4	AD	203	44% 53% ..
5	AE	168	56% 36% . 7%
6	AF	97	49% 51%
7	AG	155	52% 45% ..
8	AH	132	54% 44% ..

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Mol	Chain	Length	Quality of chain
9	AI	130	
10	AJ	102	
11	AK	127	
12	AL	137	
13	AM	121	
14	AN	61	
15	AO	89	
16	AP	90	
17	AQ	86	
18	AR	81	
19	AS	92	
20	AT	77	
21	AU	58	
22	B0	64	
23	B1	69	
24	B2	59	
25	B3	81	
26	B4	57	
27	B5	49	
28	B6	44	
29	B7	66	
30	B8	38	
31	BA	2897	
32	BB	115	
33	BD	276	

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Mol	Chain	Length	Quality of chain
34	BE	207	
35	BF	208	
36	BG	180	
37	BH	178	
38	BM	148	
39	BN	122	
40	BO	147	
41	BP	137	
42	BQ	126	
43	BR	115	
44	BS	114	
45	BT	119	
46	BU	104	
47	BV	115	
48	BW	97	
49	BX	101	
50	BZ	94	
51	A	185	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 140480 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	AA	1535	Total	C	N	O	P	0	0
			32911	14689	6018	10669	1535		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	224	Total	C	N	O	S	0	0
			1774	1129	311	326	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	211	Total	C	N	O	S	0	0
			1648	1042	302	301	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	200	Total	C	N	O	S	0	0
			1610	1014	298	294	4		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	156	Total	C	N	O	S	0	0
			1133	711	212	209	1		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	97	Total	C	N	O	S	0	0
			797	507	132	156	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	152	Total	C	N	O	S	0	0
			1207	748	236	217	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	130	Total	C	N	O	S	0	0
			1009	641	178	188	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	129	Total	C	N	O	S	0	0
			983	606	199	176	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			794	501	145	146	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	118	Total	C	N	O	S	0	0
			857	530	165	160	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	136	Total	C	N	O	S	0	0
			1054	656	215	180	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	111	Total	C	N	O	S	0	0
			873	535	174	162	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	59	Total	C	N	O	S	0	0
			471	296	94	76	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	87	Total	C	N	O	S	0	0
			708	442	140	125	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	86	Total	C	N	O	S	0	0
			688	433	127	126	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	82	Total	C	N	O	S	0	0
			675	423	126	124	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	68	Total	C	N	O	S	0	0
			549	349	105	94	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	82	Total	C	N	O	S	0	0
			660	419	121	118	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	71	Total	C	N	O	S	0	0
			542	333	107	101	1		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AU	56	Total	C	N	O	0	0
			440	269	95	76		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B0	61	Total	C	N	O	S	0	0
			477	299	91	86	1		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	B1	67	Total	C	N	O	0	0
			533	334	95	104		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B2	58	Total	C	N	O	S	0	0
			424	269	77	77	1		

- Molecule 25 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B3	79	Total	C	N	O	S	0	0
			642	408	110	122	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	B4	53	Total	C	N	O	0	0
			437	270	92	75		

- Molecule 27 is a protein called 50S ribosomal protein L33 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B5	47	Total	C	N	O	S	0	0
			365	225	72	64	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B6	44	Total	C	N	O	S	0	0
			362	219	86	55	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B7	64	Total	C	N	O	S	0	0
			530	327	120	80	3		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B8	36	Total	C	N	O	S	0	0
			292	182	62	44	4		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BA	2897	Total	C	N	O	P	0	0
			62143	27749	11409	20088	2897		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	135	U	C	conflict	GB 124491690
BA	376	A	G	conflict	GB 124491690
BA	1239	A	G	conflict	GB 124491690
BA	1489	C	U	conflict	GB 124491690

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BB	115	Total	C	N	O	P	0	0
			2455	1097	439	804	115		

- Molecule 33 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BD	272	Total	C	N	O	S	0	0
			2041	1264	397	371	9		

- Molecule 34 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BE	205	Total	C	N	O	S	0	0
			1522	957	282	279	4		

- Molecule 35 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BF	206	Total	C	N	O	S	0	0
			1563	980	284	299			

- Molecule 36 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BG	176	Total	C	N	O	S	0	0
			1367	867	238	256	6		

- Molecule 37 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BH	174	Total	C	N	O	S	0	0
			1303	811	237	251	4		

- Molecule 38 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BM	147	Total	C	N	O	S	0	0
			1127	714	203	205	5		

- Molecule 39 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BN	121	Total	C	N	O	S	0	0
			895	563	165	166	1		

- Molecule 40 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BO	146	Total	C	N	O	S	0	0
			1066	650	210	205	1		

- Molecule 41 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BP	134	Total	C	N	O	S	0	0
			1061	675	206	174	6		

- Molecule 42 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BQ	125	Total	C	N	O	S	0	0
			990	613	188	186	3		

- Molecule 43 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BR	115	Total	C	N	O	S	0	0
			872	542	164	165	1		

- Molecule 44 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BS	114	Total	C	N	O	S	0	0
			923	578	186	158	1		

- Molecule 45 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BT	117	Total	C	N	O	S	0	0
			945	601	186	154	4		

- Molecule 46 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BU	101	Total	C	N	O	0	0
			783	501	138	144		

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BV	112	Total	C	N	O	S	0	0
			853	536	160	156	1		

- Molecule 48 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BW	88	Total	C	N	O	S	0	0
			689	441	116	130	2		

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BX	99	Total	C	N	O	S	0	0
			747	474	136	136	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	75	Total	C	N	O	S	0	0
			562	345	110	106	1		

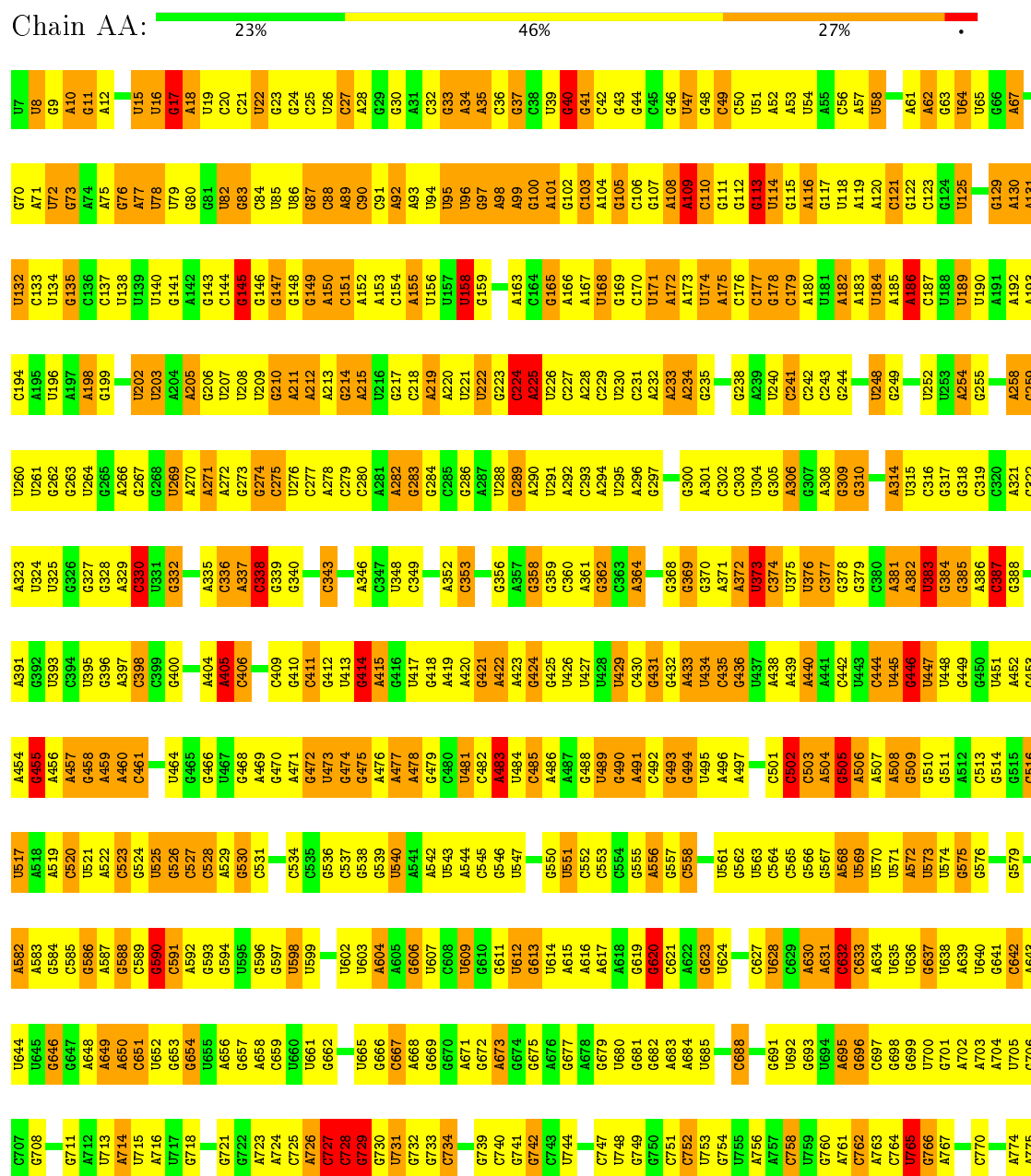
- Molecule 51 is a protein called Ribosome hibernation promotion factor.


Mol	Chain	Residues	Atoms					AltConf	Trace
51	A	159	Total	C	N	O	S	0	0
			1128	698	209	218	3		

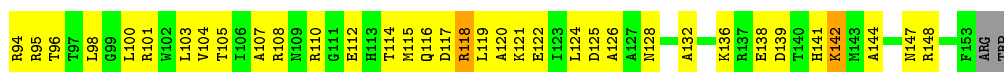
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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

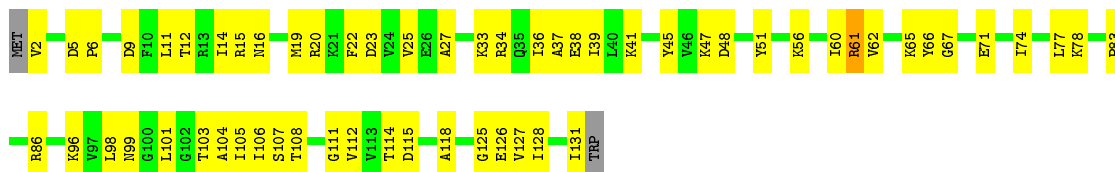


Chain AG:  52% 45%



• Molecule 8: 30S ribosomal protein S8

Chain AH: 54% 44% ..



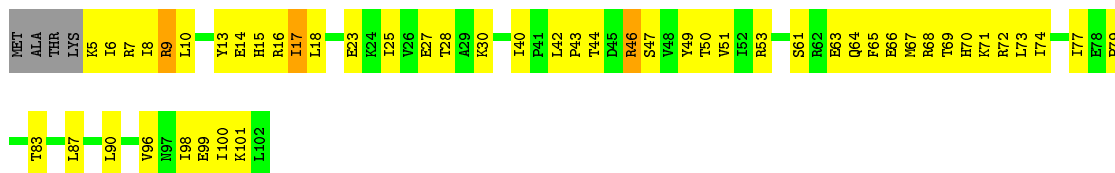
• Molecule 9: 30S ribosomal protein S9

Chain AI: 45% 53% ..



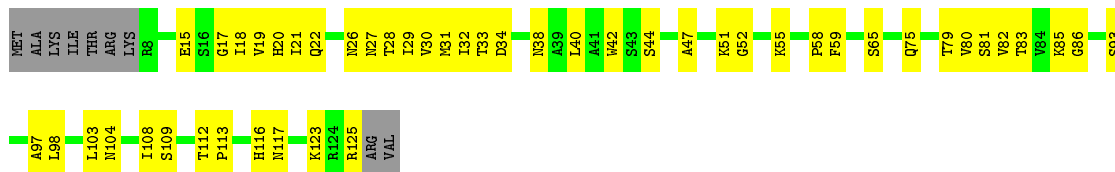
• Molecule 10: 30S ribosomal protein S10

Chain AJ: 47% 46% . .



• Molecule 11: 30S ribosomal protein S11

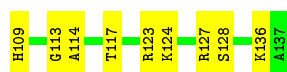
Chain AK: 55% 38% 7%



• Molecule 12: 30S ribosomal protein S12

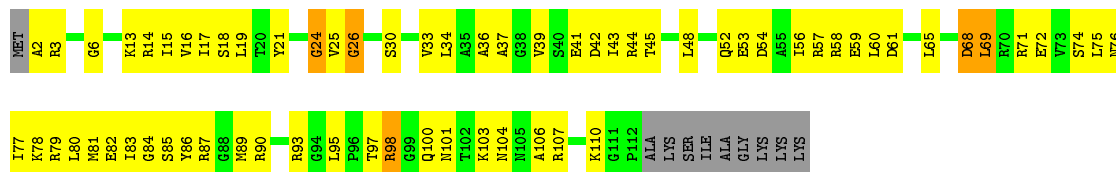
Chain AL: 65% 34% .





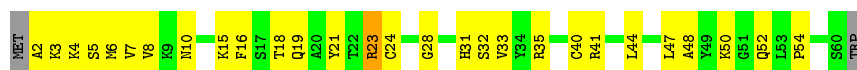
- Molecule 13: 30S ribosomal protein S13

Chain AM: 36% 51% 8%



- Molecule 14: 30S ribosomal protein S14 type Z

Chain AN: 51% 44% 2%



- Molecule 15: 30S ribosomal protein S15

Chain AO: 56% 42% 2%



- Molecule 16: 30S ribosomal protein S16

Chain AP: 56% 39% 2%



- Molecule 17: 30S ribosomal protein S17

Chain AQ: 55% 40% 5%

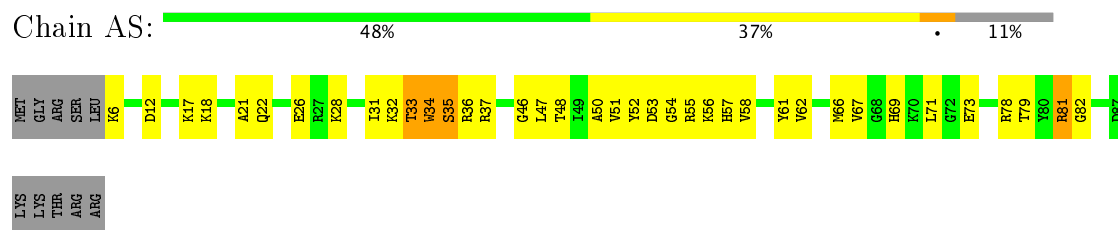


- Molecule 18: 30S ribosomal protein S18

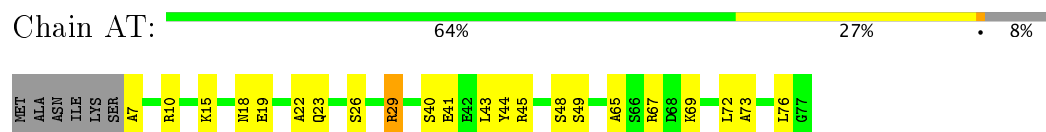
Chain AR: 51% 33% 16%



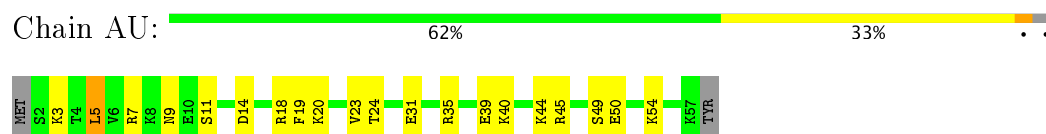
- Molecule 19: 30S ribosomal protein S19



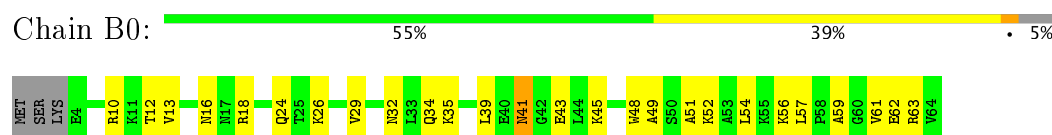
- Molecule 20: 30S ribosomal protein S20



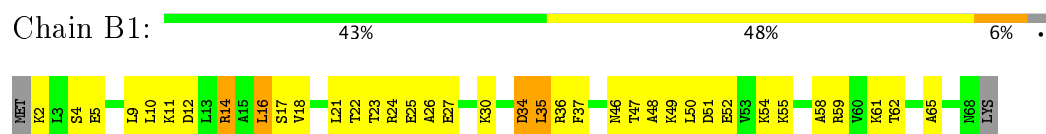
- Molecule 21: 30S ribosomal protein S21



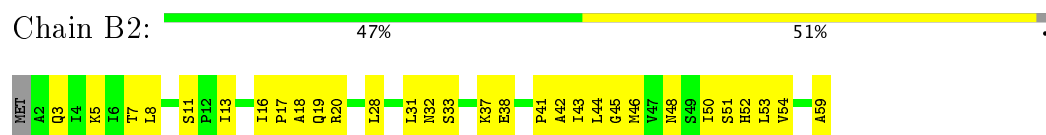
- Molecule 22: 50S ribosomal protein L28



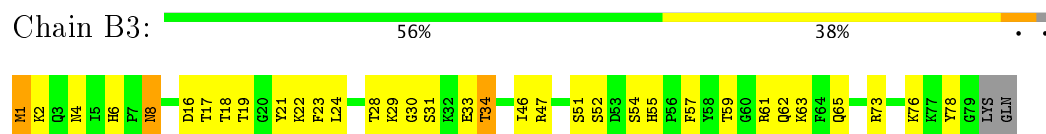
- Molecule 23: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L30



- Molecule 25: 50S ribosomal protein L31 type B



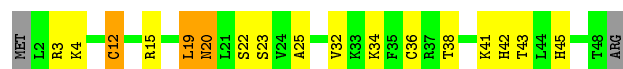
- Molecule 26: 50S ribosomal protein L32

Chain B4: 



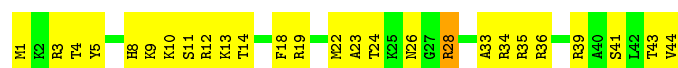
- Molecule 27: 50S ribosomal protein L33 3

Chain B5: 



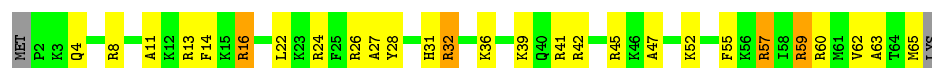
- Molecule 28: 50S ribosomal protein L34

Chain B6: 



- Molecule 29: 50S ribosomal protein L35

Chain B7: 

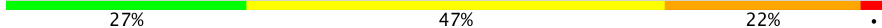


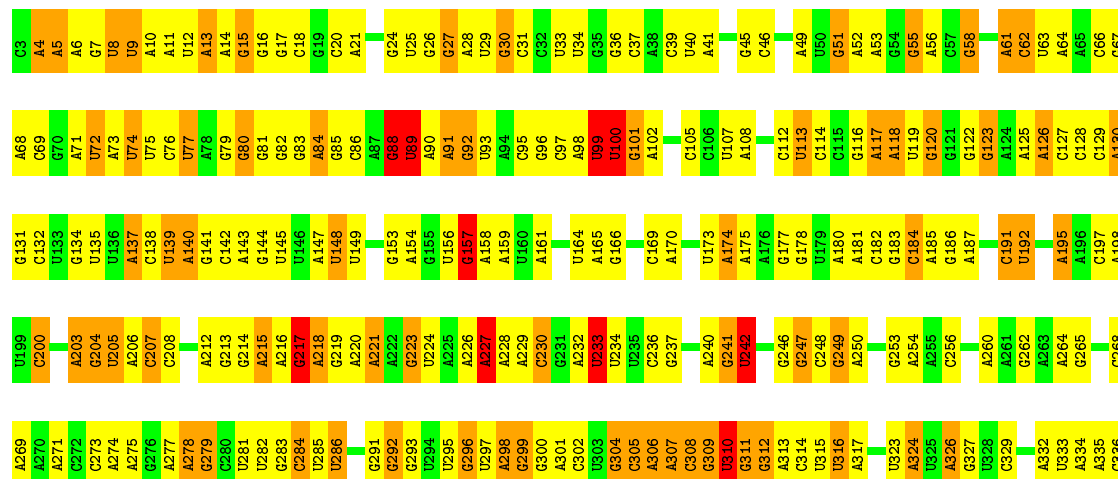
- Molecule 30: 50S ribosomal protein L36

Chain B8: 



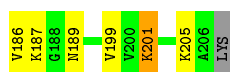
- Molecule 31: 23S ribosomal RNA

Chain BA: 

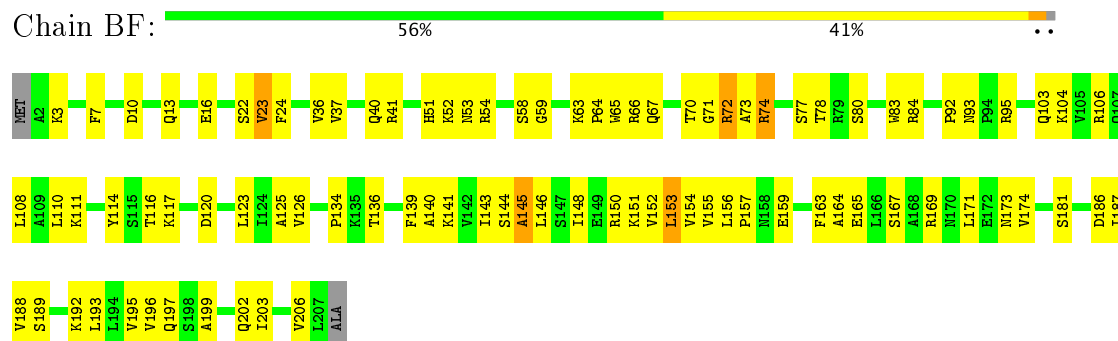




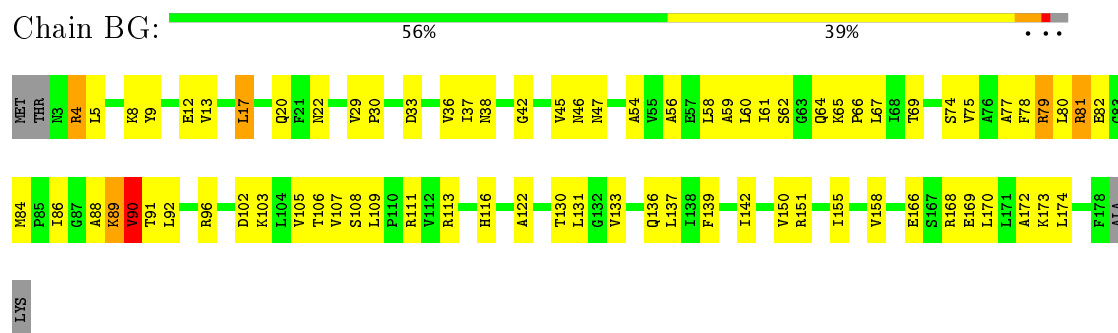

A2438	G2374	U2310	C2240	G2169	A2037	C1967	U1902	C1768	A1706	A1637	A1565	U1503	G1440
G2375	G2376	G2311	G2241	G2172	G2038	G1968	A1903	C1769	A1707	A1638	C1566	G1504	G1441
A2443	A2377	G2312	G2242	G2173	G2039	C1969	A1904	A1770	U1708	A1639	G1567	G1505	A1442
C2444	G2378	A2314	C2244	G2174	C2040	A1970	G1908	A1771	U1709	G1640	G1568	G1506	A1443
G2445	G2379	A2315	C2245	A2175	G2042	G1972	G1909	G1772	A1710	G1641	U1569	U1507	C1444
U2447	A2380	U2316	U2247	U2176	G2043	A1973	G1910	G1773	G1713	A1643	G1573	G1508	G1445
A2448	A2381	C2317	U2248	A2177	U2044	A1974	G1911	A1774	C1714	A1644	A1575	U1510	U1446
G2449	G2318	A2318	U2249	C2178	U2045	A1975	A1916	C1776	G1715	A1645	A1576	G1511	A1448
G2450	A2319	A2118	A2046	G1976	C2047	G1977	A1917	A1777	G1716	A1647	C1578	G1512	G1451
A2451	G2386	C2181	C2048	G1978	C2049	G1979	G1918	U1778	U1717	G1648	U1579	G1513	G1452
U2452	C2387	C2182	G2049	G1979	G2050	A1980	A1920	U1780	A1718	G1649	G1580	G1514	G1453
A2454	A2388	C2183	G2050	A1981	C2051	A1982	A1921	U1781	A1719	U1650	G1582	G1515	G1454
G2455	C2389	U2184	C2052	A1986	G2053	U1987	A1922	A1782	G1720	A1651	A1583	U1516	G1455
C2456	U2390	A2123	G2054	U1988	C2055	U1989	A1923	G1783	U1721	A1652	U1584	U1517	G1456
U2464	U2391	G2188	C2056	G1989	G2057	C1994	G1925	G1784	U1722	G1657	U1585	G1518	G1457
C2465	C2392	C2189	A2055	G1990	G2058	U1991	A1926	A1786	G1724	G1658	C1589	A1522	G1458
G2466	G2393	U2190	G2059	C1992	C2060	U1993	G1927	A1787	G1725	C1659	C1590	A1523	C1459
C2467	U2394	G2191	C2061	C1994	U1994	C2000	A1928	C1790	A1727	A1660	C1591	U1524	A1460
A2470	U2397	G2192	C2062	U1995	C2063	U1996	C1928	G1791	G1728	A1661	G1592	G1525	G1461
C2471	C2398	G2193	G2064	U1997	G2065	C2001	C1929	G1792	A1729	A1662	A1596	A1527	U1462
A2472	A2401	G2194	A2064	C1998	G2066	C2002	A1930	G1793	U1730	G1663	A1597	U1528	A1463
A2473	U2402	A2197	G2067	U1999	A2068	C2003	A1931	G1794	A1743	A1664	G1598	U1529	G1464
G2474	G2403	U2198	G2068	C2000	A2069	C2004	A1932	G1795	A1744	A1665	A1599	U1530	G1465
U2475	C2404	G2199	G2070	C2001	C2070	G2005	G1933	G1796	A1745	A1666	A1600	C1531	U1467
G2476	G2405	C2200	A2071	C2002	C2071	G2006	U1934	G1797	A1746	C1667	A1601	U1532	A1468
U2477	A2406	G2201	G2072	G2003	C2072	G2007	A1936	U1798	C1737	U1668	A1602	C1533	
A2480	C2407	A2202	A2073	G2004	A2074	A2007	G1937	U1799	U1738	C1669	G1603	U1534	A1473
C2481	G2408	A2203	G2075	G2005	C2075	C2008	A1938	G1800	G1740	U1606		U1535	U1474
A2482	C2409	C2204	A2076	G2006	A2076	A2009	G1939	G1801	A1741	C1607	U1536	U1537	G1475
G2483	G2410	G2205	A2077	A2007	C2077	C2010	A1940	U1802	G1742	U1608	A1538	C1477	C1476
A2486	A2411	C2206	G2076	U1942	C2077	U2011	A1941	U1803	U1743	A1609	C1539	A1478	G1479
C2487	U2412	G2207	G2077	U1943	C2077	C2012	U1942	A1804	A1744	G1610	U1540	U1541	U1480
G2488	G2413	C2208	U2078	U1944	C2078	C2013	U1944	A1805	A1745	C1611	U1542	U1543	U1481
U2494	A2414	U2209	U2079	C2012	U2079	G2013	C1945	A1806	A1746	G1612	U1544	A1482	A1483
G2495	G2415	C2210	U2080	C2013	C2080	G2016	C1946	C1807	A1747	U1683	A1614	U1545	U1484
U2496	A2416	G2211	U2081	C2014	A2081	A2017	U1947	U1808	G1748	C1687	A1615	G1546	G1485
G2497	G2417	U2212	U2082	C2015	A2082	A2018	U1948	U1814	C1749	U1688	A1616	U1547	G1486
A2498	C2420	A2213	U2083	C2016	U2083	A2019	G1949	U1815	A1750	U1689	G1617	G1548	A1487
G2499	A2422	G2214	U2084	C2017	U2084	A2020	U1950	A1816	C1751	U1690	U1618	U1549	U1488
C2500	U2423	A2215	G2091	U2022	U2090	U2021	C1951	A1817	G1752	U1691	C1619	G1550	C1489
A2501	C2424	U2216	U2092	U2023	A2092	U2024	G1952	U1818	C1753	U1692	A1620	A1551	U1490
C2502	G2425	C2217	U2093	U2024	U2093	A2025	G1953	G1819	G1754	U1693	U1621	U1552	U1491
U2503	G2426	G2218	U2094	U2025	A2094	G2026	U1954	U1820	C1755	A1694	A1622	G1553	G1492
C2505	U2427	C2219	U2095	U2026	U2095	U2027	U1955	A1821	C1756	G1695	U1623	G1554	G1493
G2506	A2428	U2220	U2096	U2027	U2096	A2028	A1956	U1822	G1758	C1624	C1625	U1555	U1494
A2507	C2429	G2221	U2097	C2028	G2097	C2029	U1957	A1823	U1759	U1697	U1626	G1556	C1495
U2508	A2430	U2222	A2098	C2029	A2098	C2030	G1958	G1824	G1760	A1698	A1627	A1557	U1496
C2509	G2431	C2223	U2099	U2030	U2099	U2031	U1959	A1825	U1761	C1699	U1628	U1558	A1497
U2510	G2432	G2224	G2100	U2031	U2100	G2032	C1961	A1826	A1762	U1700	G1629	G1559	A1498
G2511	A2433	U2225	A2101	U2032	A2101	G2033	C1962	G1827	U1763	G1701	U1630	C1560	G1499
G2512	U2434	C2226	C2102	G2033	C2102	G2034	G1963	U1828	A1764	G1702	U1631	A1561	C1500
C2516	A2435	G2227	C2103	U2034	U2103	A2035	A1964	G1829	G1765	G1703	A1632	U1562	A1501
		U2228	U2104	C2035	U2104	C1965	A1900	U1830	G1766	A1704			G1502
		A2239	G2105	G2036	G2105	C2036	C1966	C1832	C1767	A1705			



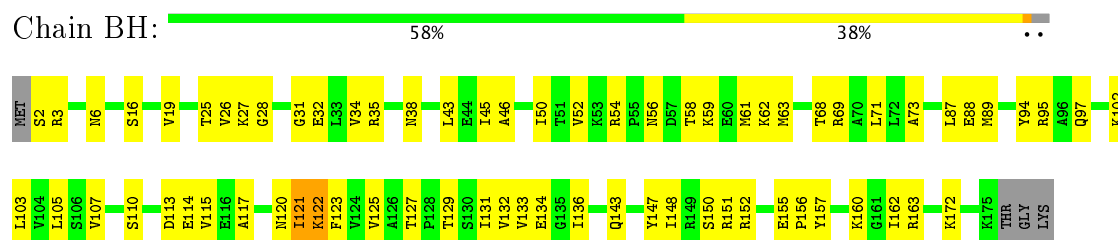
• Molecule 35: 50S ribosomal protein L4



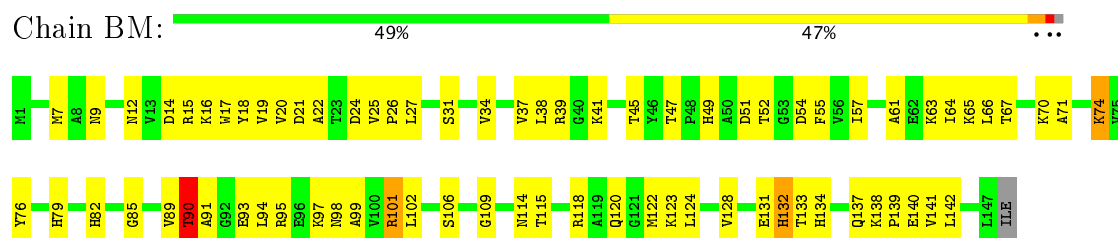
• Molecule 36: 50S ribosomal protein L5



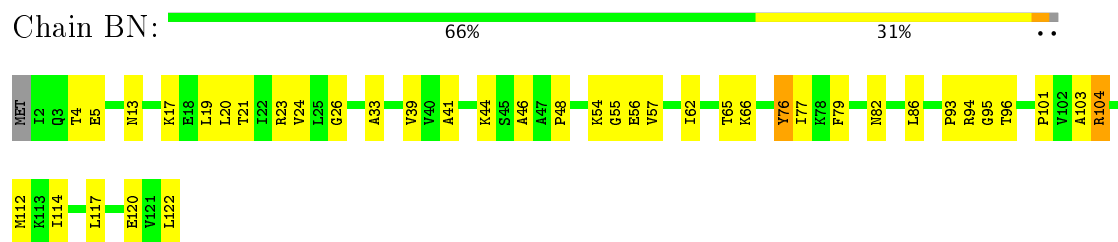
• Molecule 37: 50S ribosomal protein L6



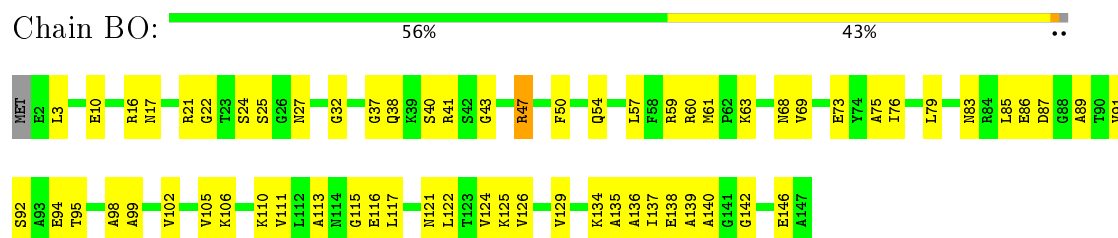
• Molecule 38: 50S ribosomal protein L13



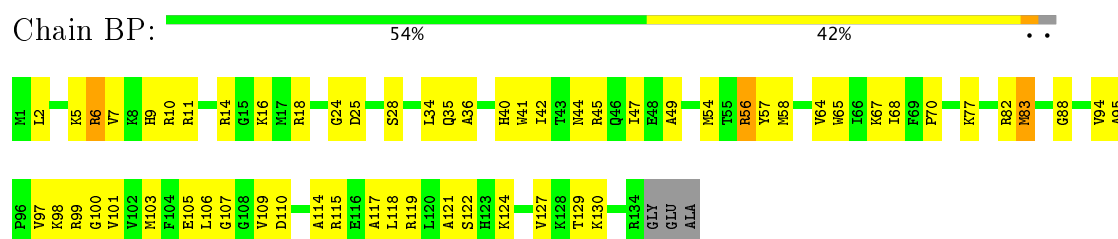
• Molecule 39: 50S ribosomal protein L14



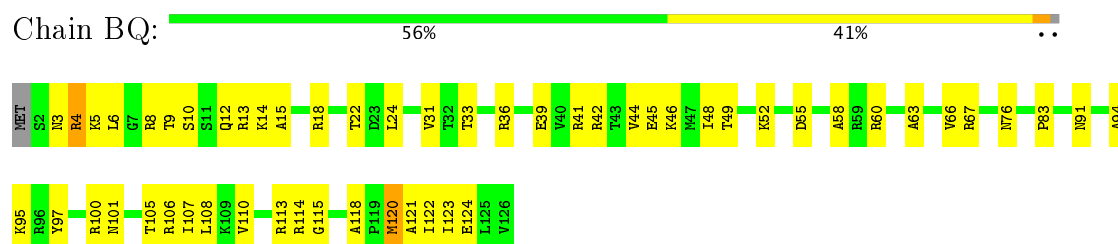
- Molecule 40: 50S ribosomal protein L15



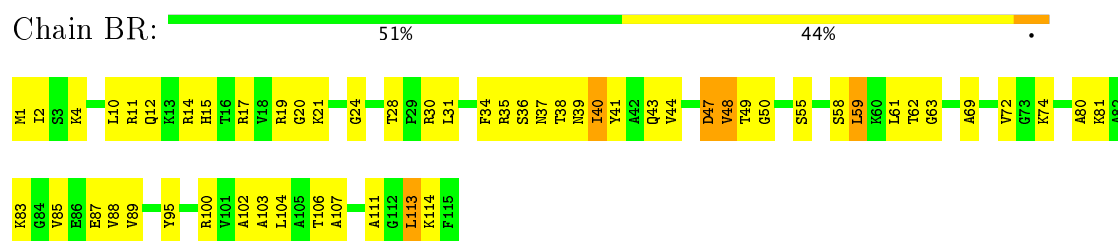
- Molecule 41: 50S ribosomal protein L16



- Molecule 42: 50S ribosomal protein L17

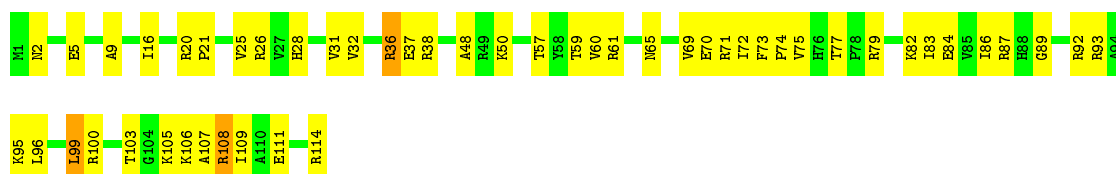


- Molecule 43: 50S ribosomal protein L18



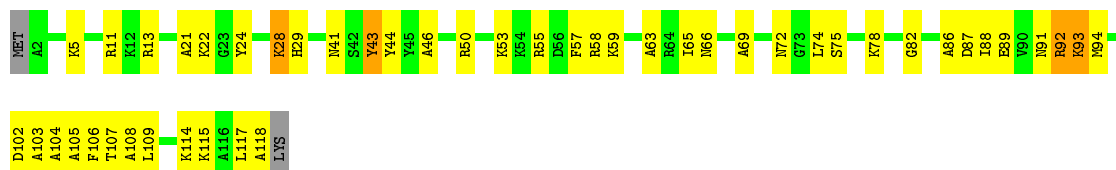
- Molecule 44: 50S ribosomal protein L19





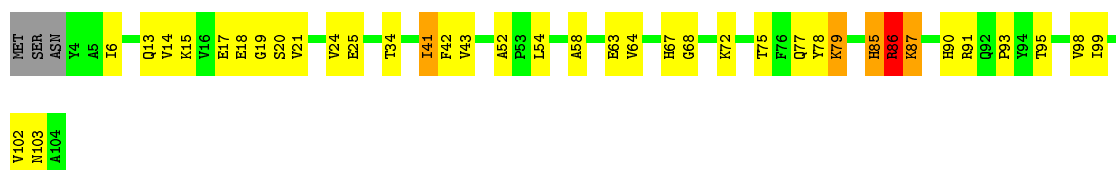
- Molecule 45: 50S ribosomal protein L20

Chain BT: 59% 36%



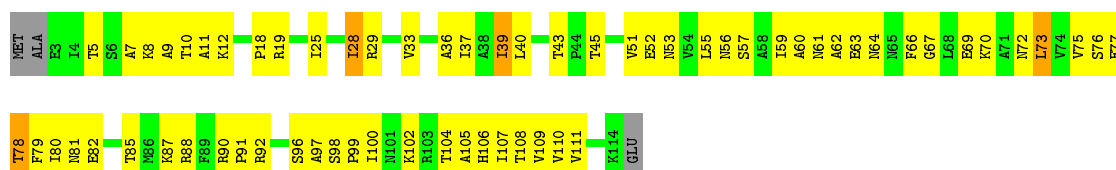
- Molecule 46: 50S ribosomal protein L21

Chain BU: 61% 32%



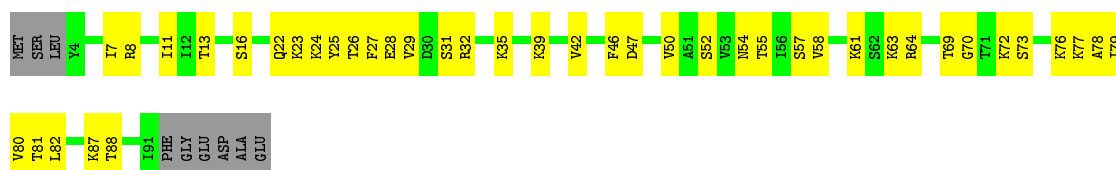
- Molecule 47: 50S ribosomal protein L22

Chain BV: 41% 53%



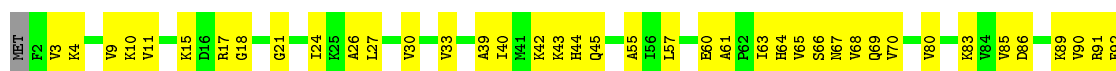
- Molecule 48: 50S ribosomal protein L23

Chain BW: 47% 43% 9%



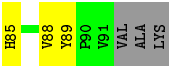
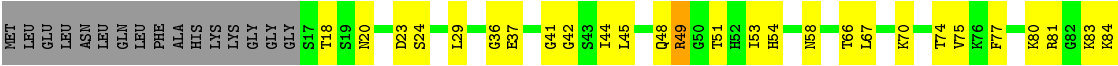
- Molecule 49: 50S ribosomal protein L24

Chain BX: 55% 43%

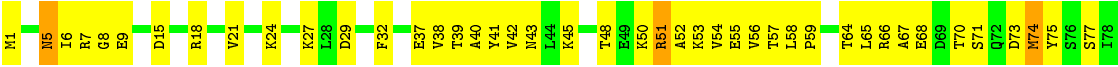




- Molecule 50: 50S ribosomal protein L27



- Molecule 51: Ribosome hibernation promotion factor



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43530	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	AA	0.68	0/36854	1.35	448/57482 (0.8%)
10	AJ	0.30	0/805	0.69	2/1084 (0.2%)
11	AK	0.33	0/870	0.63	0/1175
12	AL	0.35	0/1070	0.72	0/1433
13	AM	0.38	0/880	0.80	2/1176 (0.2%)
14	AN	0.32	0/479	0.56	0/637
15	AO	0.31	0/718	0.62	0/958
16	AP	0.33	0/699	0.56	0/938
17	AQ	0.33	0/684	0.66	0/915
18	AR	0.36	0/554	0.75	0/740
19	AS	0.36	0/676	0.68	0/911
2	AB	0.32	0/1805	0.65	0/2442
20	AT	0.32	0/545	0.59	0/723
21	AU	0.31	0/443	0.61	1/583 (0.2%)
22	B0	0.39	0/483	0.75	0/649
23	B1	0.40	0/534	0.96	2/713 (0.3%)
24	B2	0.36	0/427	0.72	0/575
25	B3	0.39	0/659	0.86	0/888
26	B4	0.44	0/447	0.66	0/599
27	B5	0.38	0/368	0.72	0/489
28	B6	0.38	0/366	0.71	0/481
29	B7	0.37	0/538	0.75	0/704
3	AC	0.32	0/1674	0.62	0/2259
30	B8	0.37	0/297	0.64	0/396
31	BA	0.86	7/69612 (0.0%)	1.37	856/108576 (0.8%)
32	BB	0.75	1/2746 (0.0%)	1.29	22/4278 (0.5%)
33	BD	0.41	0/2071	0.80	2/2789 (0.1%)
34	BE	0.44	0/1544	0.79	2/2079 (0.1%)
35	BF	0.39	0/1586	0.72	1/2145 (0.0%)
36	BG	0.40	0/1385	0.84	2/1866 (0.1%)
37	BH	0.37	0/1317	0.66	0/1776
38	BM	0.40	0/1147	0.74	0/1549
39	BN	0.41	0/904	0.75	1/1215 (0.1%)
4	AD	0.34	0/1639	0.62	0/2205

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	BO	0.39	0/1072	0.72	0/1430
41	BP	0.43	0/1084	0.64	0/1450
42	BQ	0.39	0/998	0.79	0/1338
43	BR	0.42	0/881	0.83	3/1184 (0.3%)
44	BS	0.38	0/935	0.70	1/1255 (0.1%)
45	BT	0.47	0/958	0.70	1/1273 (0.1%)
46	BU	0.46	0/796	0.82	2/1070 (0.2%)
47	BV	0.39	0/862	0.76	1/1164 (0.1%)
48	BW	0.37	0/697	0.62	0/935
49	BX	0.40	0/755	0.75	0/1013
5	AE	0.34	0/1143	0.63	0/1540
50	BZ	0.37	0/570	0.75	1/760 (0.1%)
51	A	0.36	0/1138	0.64	0/1538
6	AF	0.40	0/809	0.77	2/1089 (0.2%)
7	AG	0.31	0/1224	0.61	0/1649
8	AH	0.35	0/1020	0.58	0/1374
9	AI	0.30	0/995	0.71	0/1334
All	All	0.71	8/152763 (0.0%)	1.23	1352/228824 (0.6%)

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	AJ	0	1
11	AK	0	2
13	AM	0	4
14	AN	0	2
19	AS	0	3
2	AB	0	1
22	B0	0	1
23	B1	0	3
24	B2	0	2
25	B3	0	3
26	B4	0	1
27	B5	0	1
3	AC	0	1
33	BD	0	4
34	BE	0	4
35	BF	0	2
36	BG	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
37	BH	0	1
38	BM	0	4
39	BN	0	2
4	AD	0	2
43	BR	0	2
44	BS	0	1
45	BT	0	1
46	BU	0	4
47	BV	0	2
48	BW	0	1
49	BX	0	1
6	AF	0	1
9	AI	0	1
All	All	0	61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	BA	2480	A	N9-C4	-5.85	1.34	1.37
31	BA	1719	A	N9-C4	-5.55	1.34	1.37
31	BA	1089	A	N9-C4	-5.36	1.34	1.37
32	BB	21	A	N9-C4	-5.19	1.34	1.37
31	BA	542	A	N9-C4	5.19	1.41	1.37

The worst 5 of 1352 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	BA	1503	U	N3-C2-O2	-17.92	109.66	122.20
1	AA	1310	C	C2-N1-C1'	13.33	133.47	118.80
31	BA	2117	C	N1-C2-O2	13.13	126.78	118.90
31	BA	2117	C	C2-N1-C1'	12.12	132.14	118.80
31	BA	568	U	C5-C6-N1	12.06	128.73	122.70

There are no chirality outliers.

5 of 61 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	4	ILE	Peptide
3	AC	207	LEU	Peptide
4	AD	187	ASN	Peptide
4	AD	201	LYS	Peptide

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Mol	Chain	Res	Type	Group
6	AF	51	GLU	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	AA	32911	0	16551	930	0
2	AB	1774	0	1820	83	0
3	AC	1648	0	1704	81	0
4	AD	1610	0	1632	100	0
5	AE	1133	0	1205	48	0
6	AF	797	0	795	35	0
7	AG	1207	0	1235	64	0
8	AH	1009	0	1068	46	0
9	AI	983	0	1025	59	0
10	AJ	794	0	841	48	0
11	AK	857	0	886	45	0
12	AL	1054	0	1141	40	0
13	AM	873	0	912	70	0
14	AN	471	0	499	25	0
15	AO	708	0	737	32	0
16	AP	688	0	716	34	0
17	AQ	675	0	704	28	0
18	AR	549	0	599	26	0
19	AS	660	0	658	35	0
20	AT	542	0	577	26	0
21	AU	440	0	448	14	0
22	B0	477	0	503	18	0
23	B1	533	0	572	25	0
24	B2	424	0	471	19	0
25	B3	642	0	620	31	0
26	B4	437	0	444	17	0
27	B5	365	0	389	15	0
28	B6	362	0	400	31	0
29	B7	530	0	573	28	0
30	B8	292	0	320	14	0
31	BA	62143	0	31234	1411	0
32	BB	2455	0	1236	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	BD	2041	0	2142	102	0
34	BE	1522	0	1608	69	0
35	BF	1563	0	1606	77	0
36	BG	1367	0	1417	60	0
37	BH	1303	0	1343	54	0
38	BM	1127	0	1176	50	0
39	BN	895	0	951	29	0
40	BO	1066	0	1109	58	0
41	BP	1061	0	1111	48	0
42	BQ	990	0	1037	47	0
43	BR	872	0	911	52	0
44	BS	923	0	983	41	0
45	BT	945	0	1012	40	0
46	BU	783	0	818	32	0
47	BV	853	0	915	57	0
48	BW	689	0	738	32	0
49	BX	747	0	808	32	0
50	BZ	562	0	567	29	0
51	A	1128	0	992	93	0
All	All	140480	0	93759	3990	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 19.

The worst 5 of 3990 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)
1:AA:1439:G:N2	1:AA:1475:A:N7	1.81	1.28
31:BA:1487:A:C2	31:BA:2706:G:N1	2.06	1.23
2:AB:207:ILE:HD11	51:A:144:GLU:O	1.48	1.11
2:AB:207:ILE:CD1	51:A:145:GLU:HA	1.84	1.07
31:BA:2312:G:N1	31:BA:2315:A:C2	2.22	1.06

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	
2	AB	222/255 (87%)	194 (87%)	28 (13%)	0	100	100
3	AC	209/217 (96%)	177 (85%)	32 (15%)	0	100	100
4	AD	198/203 (98%)	163 (82%)	34 (17%)	1 (0%)	32	74
5	AE	154/168 (92%)	138 (90%)	16 (10%)	0	100	100
6	AF	95/97 (98%)	73 (77%)	22 (23%)	0	100	100
7	AG	150/155 (97%)	136 (91%)	14 (9%)	0	100	100
8	AH	128/132 (97%)	110 (86%)	18 (14%)	0	100	100
9	AI	127/130 (98%)	104 (82%)	23 (18%)	0	100	100
10	AJ	96/102 (94%)	82 (85%)	14 (15%)	0	100	100
11	AK	116/127 (91%)	102 (88%)	14 (12%)	0	100	100
12	AL	134/137 (98%)	110 (82%)	24 (18%)	0	100	100
13	AM	109/121 (90%)	82 (75%)	27 (25%)	0	100	100
14	AN	57/61 (93%)	44 (77%)	13 (23%)	0	100	100
15	AO	85/89 (96%)	72 (85%)	13 (15%)	0	100	100
16	AP	84/90 (93%)	74 (88%)	10 (12%)	0	100	100
17	AQ	80/86 (93%)	65 (81%)	15 (19%)	0	100	100
18	AR	66/81 (82%)	53 (80%)	13 (20%)	0	100	100
19	AS	80/92 (87%)	61 (76%)	19 (24%)	0	100	100
20	AT	69/77 (90%)	57 (83%)	12 (17%)	0	100	100
21	AU	54/58 (93%)	46 (85%)	8 (15%)	0	100	100
22	B0	59/64 (92%)	45 (76%)	14 (24%)	0	100	100
23	B1	65/69 (94%)	51 (78%)	14 (22%)	0	100	100
24	B2	56/59 (95%)	45 (80%)	11 (20%)	0	100	100
25	B3	77/81 (95%)	52 (68%)	25 (32%)	0	100	100
26	B4	51/57 (90%)	43 (84%)	8 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	B5	45/49 (92%)	32 (71%)	12 (27%)	1 (2%)	8	45
28	B6	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
29	B7	62/66 (94%)	51 (82%)	11 (18%)	0	100	100
30	B8	34/38 (90%)	32 (94%)	2 (6%)	0	100	100
33	BD	270/276 (98%)	193 (72%)	77 (28%)	0	100	100
34	BE	203/207 (98%)	164 (81%)	39 (19%)	0	100	100
35	BF	204/208 (98%)	157 (77%)	46 (22%)	1 (0%)	32	74
36	BG	174/180 (97%)	137 (79%)	36 (21%)	1 (1%)	28	71
37	BH	172/178 (97%)	144 (84%)	28 (16%)	0	100	100
38	BM	145/148 (98%)	119 (82%)	25 (17%)	1 (1%)	25	68
39	BN	119/122 (98%)	99 (83%)	20 (17%)	0	100	100
40	BO	144/147 (98%)	117 (81%)	27 (19%)	0	100	100
41	BP	132/137 (96%)	120 (91%)	12 (9%)	0	100	100
42	BQ	123/126 (98%)	109 (89%)	14 (11%)	0	100	100
43	BR	113/115 (98%)	90 (80%)	22 (20%)	1 (1%)	20	63
44	BS	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
45	BT	115/119 (97%)	103 (90%)	12 (10%)	0	100	100
46	BU	99/104 (95%)	67 (68%)	32 (32%)	0	100	100
47	BV	110/115 (96%)	99 (90%)	11 (10%)	0	100	100
48	BW	86/97 (89%)	78 (91%)	8 (9%)	0	100	100
49	BX	97/101 (96%)	73 (75%)	24 (25%)	0	100	100
50	BZ	73/94 (78%)	64 (88%)	9 (12%)	0	100	100
51	A	155/185 (84%)	130 (84%)	25 (16%)	0	100	100
All	All	5450/5778 (94%)	4487 (82%)	957 (18%)	6 (0%)	58	88

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	BM	132	HIS
4	AD	202	MET
27	B5	12	CYS
35	BF	23	VAL
36	BG	82	GLU

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	
2	AB	190/213 (89%)	187 (98%)	3 (2%)	68	85
3	AC	168/172 (98%)	166 (99%)	2 (1%)	75	88
4	AD	172/175 (98%)	170 (99%)	2 (1%)	75	88
5	AE	115/126 (91%)	113 (98%)	2 (2%)	66	85
6	AF	84/84 (100%)	81 (96%)	3 (4%)	40	69
7	AG	125/128 (98%)	122 (98%)	3 (2%)	54	78
8	AH	111/113 (98%)	109 (98%)	2 (2%)	64	84
9	AI	99/100 (99%)	98 (99%)	1 (1%)	80	90
10	AJ	89/92 (97%)	88 (99%)	1 (1%)	78	89
11	AK	89/97 (92%)	88 (99%)	1 (1%)	78	89
12	AL	113/114 (99%)	113 (100%)	0	100	100
13	AM	93/100 (93%)	92 (99%)	1 (1%)	78	89
14	AN	50/53 (94%)	49 (98%)	1 (2%)	60	82
15	AO	74/76 (97%)	74 (100%)	0	100	100
16	AP	77/81 (95%)	75 (97%)	2 (3%)	51	76
17	AQ	76/80 (95%)	75 (99%)	1 (1%)	73	87
18	AR	59/69 (86%)	59 (100%)	0	100	100
19	AS	70/79 (89%)	69 (99%)	1 (1%)	71	86
20	AT	53/58 (91%)	52 (98%)	1 (2%)	62	82
21	AU	42/53 (79%)	41 (98%)	1 (2%)	54	78
22	B0	52/56 (93%)	52 (100%)	0	100	100
23	B1	58/60 (97%)	57 (98%)	1 (2%)	66	85
24	B2	48/49 (98%)	48 (100%)	0	100	100
25	B3	69/71 (97%)	68 (99%)	1 (1%)	71	86
26	B4	46/50 (92%)	46 (100%)	0	100	100
27	B5	41/43 (95%)	39 (95%)	2 (5%)	29	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	B6	37/37 (100%)	36 (97%)	1 (3%)	50	74
29	B7	54/56 (96%)	48 (89%)	6 (11%)	7	30
30	B8	34/35 (97%)	34 (100%)	0	100	100
33	BD	219/223 (98%)	214 (98%)	5 (2%)	56	79
34	BE	162/164 (99%)	156 (96%)	6 (4%)	39	68
35	BF	170/171 (99%)	168 (99%)	2 (1%)	75	88
36	BG	150/154 (97%)	147 (98%)	3 (2%)	60	82
37	BH	140/147 (95%)	139 (99%)	1 (1%)	87	93
38	BM	122/123 (99%)	118 (97%)	4 (3%)	43	70
39	BN	93/95 (98%)	90 (97%)	3 (3%)	44	71
40	BO	107/109 (98%)	106 (99%)	1 (1%)	82	91
41	BP	106/107 (99%)	102 (96%)	4 (4%)	38	67
42	BQ	104/105 (99%)	102 (98%)	2 (2%)	62	82
43	BR	90/90 (100%)	89 (99%)	1 (1%)	78	89
44	BS	98/98 (100%)	95 (97%)	3 (3%)	45	72
45	BT	90/92 (98%)	88 (98%)	2 (2%)	57	80
46	BU	85/88 (97%)	84 (99%)	1 (1%)	75	88
47	BV	92/94 (98%)	90 (98%)	2 (2%)	57	80
48	BW	77/84 (92%)	77 (100%)	0	100	100
49	BX	83/85 (98%)	82 (99%)	1 (1%)	75	88
50	BZ	59/73 (81%)	59 (100%)	0	100	100
51	A	93/163 (57%)	89 (96%)	4 (4%)	33	64
All	All	4528/4785 (95%)	4444 (98%)	84 (2%)	65	82

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	B7	57	ARG
34	BE	144	MET
47	BV	5	THR
33	BD	63	ARG
33	BD	243	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
25	B3	65	GLN
33	BD	213	HIS
48	BW	22	GLN
26	B4	40	HIS
33	BD	11	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1534/1535 (99%)	663 (43%)	8 (0%)
31	BA	2896/2897 (99%)	1094 (37%)	20 (0%)
32	BB	114/115 (99%)	45 (39%)	0
All	All	4544/4547 (99%)	1802 (39%)	28 (0%)

5 of 1802 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	8	U
1	AA	9	G
1	AA	10	A
1	AA	11	G
1	AA	15	U

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	BA	932	U
31	BA	1285	U
31	BA	2273	G
31	BA	980	A
31	BA	1281	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.