



wwPDB EM Validation Summary Report ⓘ

Nov 7, 2022 – 02:18 AM EST

PDB ID : 6DNC
EMDB ID : EMD-7970
Title : E.coli RF1 bound to E.coli 70S ribosome in response to UAU sense A-site codon
Authors : Svidritskiy, E.; Demo, G.; Korostelev, A.A.
Deposited on : 2018-06-06
Resolution : 3.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

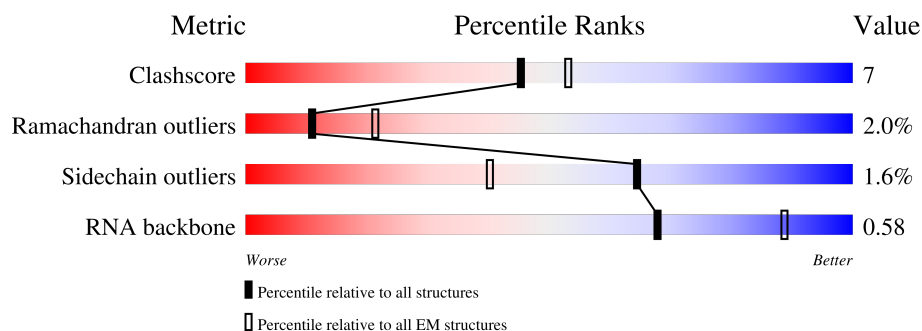
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.















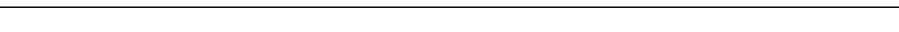

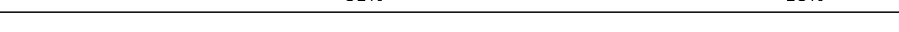

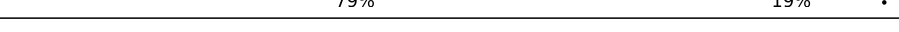








Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	1539	64% 33% .
2	B	2903	66% 30% .
3	C	120	62% 36% .
4	D	77	45% 49% 5%
4	LA	77	69% 27% .
5	E	234	70% 24% 6%
6	F	273	79% 19% .












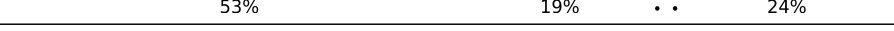







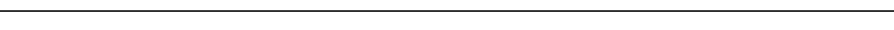

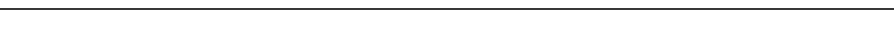
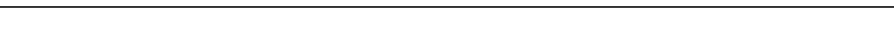


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
7	G	209	 81% 18% .
8	H	201	 83% 16% .
9	I	179	 77% 22% .
10	J	177	 79% 19% ..
11	K	149	 69% 30% .
12	L	165	 52% 24% .. 21%
13	M	142	 68% 29% ..
14	N	142	 83% 16% .
15	O	123	 79% 18% ..
16	P	144	 81% 17% ..
17	Q	136	 89% 10% .
18	R	127	 66% 28% . 6%
19	S	117	 79% 19% ..
20	T	115	 81% 18% .
21	U	118	 82% 17% .
22	V	103	 79% 19% .
23	W	110	 83% 15% .
24	X	100	 87% 6% 7%
25	Y	104	 83% 15% .
26	Z	94	 87% 13%
27	AA	85	 74% 14% 12%
28	BA	78	 91% 8% .
29	CA	63	 86% 14%
30	DA	59	 81% 17% .
31	EA	70	 74% 19% . 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
32	FA	57	 79% 19% .
33	GA	55	 89% . 9%
34	HA	46	 76% 22% .
35	IA	65	 82% 15% . .
36	JA	38	 74% 24% .
37	KA	27	 41% 30% 30%
38	MA	362	 73% 20% . 5%
39	OA	241	 77% 15% . 7%
40	PA	233	 67% 20% . 12%
41	QA	206	 77% 21% .
42	RA	167	 71% 22% . 6%
43	SA	131	 53% 19% . . 24%
44	TA	156	 90% 7% .
45	UA	130	 81% 18% .
46	VA	130	 72% 25% . .
47	WA	103	 61% 32% . 5%
48	XA	129	 73% 16% . 10%
49	YA	124	 68% 27% 5% .
50	ZA	118	 71% 25% . .
51	AB	102	 53% 29% 14% . .
52	BB	89	 83% 16% .
53	CB	82	 71% 27% .
54	DB	84	 70% 23% . 5%
55	EB	75	 75% 11% . 13%
56	FB	92	 61% 24% . 14%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
57	GB	87	<div><div></div><div>87%</div><div>10%</div><div></div></div>
58	HB	71	<div><div></div><div>55%</div><div>32%</div><div></div><div>•</div><div>8%</div></div>

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 152438 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	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2903	Total	C	N	O	P	0	0
			62318	27801	11468	20147	2902		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	747	C	U	conflict	GB 1036415628
B	1847	G	A	conflict	GB 1036415628

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	120	A	-	expression tag	GB 1370526515

- Molecule 4 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
4	LA	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 5 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	220	Total	C	N	O	S	0	0
			1637	1023	298	310	6		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

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

- Molecule 11 is a protein called 50S ribosomal protein L9.

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

- Molecule 12 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 13 is a protein called 50S ribosomal protein L11.

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

- Molecule 14 is a protein called 50S ribosomal protein L13.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 17 is a protein called 50S ribosomal protein L16.

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

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 19 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 20 is a protein called 50S ribosomal protein L19.

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

- Molecule 21 is a protein called 50S ribosomal protein L20.

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

- Molecule 22 is a protein called 50S ribosomal protein L21.

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

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 28 is a protein called 50S ribosomal protein L28.

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

- Molecule 29 is a protein called 50S ribosomal protein L29.

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

- Molecule 30 is a protein called 50S ribosomal protein L30.

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

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	EA	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 32 is a protein called 50S ribosomal protein L32.

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

- Molecule 33 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	GA	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 34 is a protein called 50S ribosomal protein L34.

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

- Molecule 35 is a protein called 50S ribosomal protein L35.

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

- Molecule 36 is a protein called 50S ribosomal protein L36.

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

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	KA	19	Total	C	N	O	P	0	0
			412	186	83	125	18		

- Molecule 38 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	MA	344	Total	C	N	O	S	0	0
			2714	1656	507	538	13		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MA	361	LEU	-	expression tag	UNP B7MKB3
MA	362	GLU	-	expression tag	UNP B7MKB3

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	OA	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	PA	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	RA	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SA	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 44 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	TA	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	VA	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 47 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	WA	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 48 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	XA	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 49 is a protein called 30S ribosomal protein S12.

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

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	ZA	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AB	101	Total	C	N	O	S	0	0
			810	502	165	140	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AB	35	ALA	-	insertion	UNP B7MCS2

- Molecule 52 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 53 is a protein called 30S ribosomal protein S16.

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

- Molecule 54 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DB	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	EB	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	FB	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 57 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	GB	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

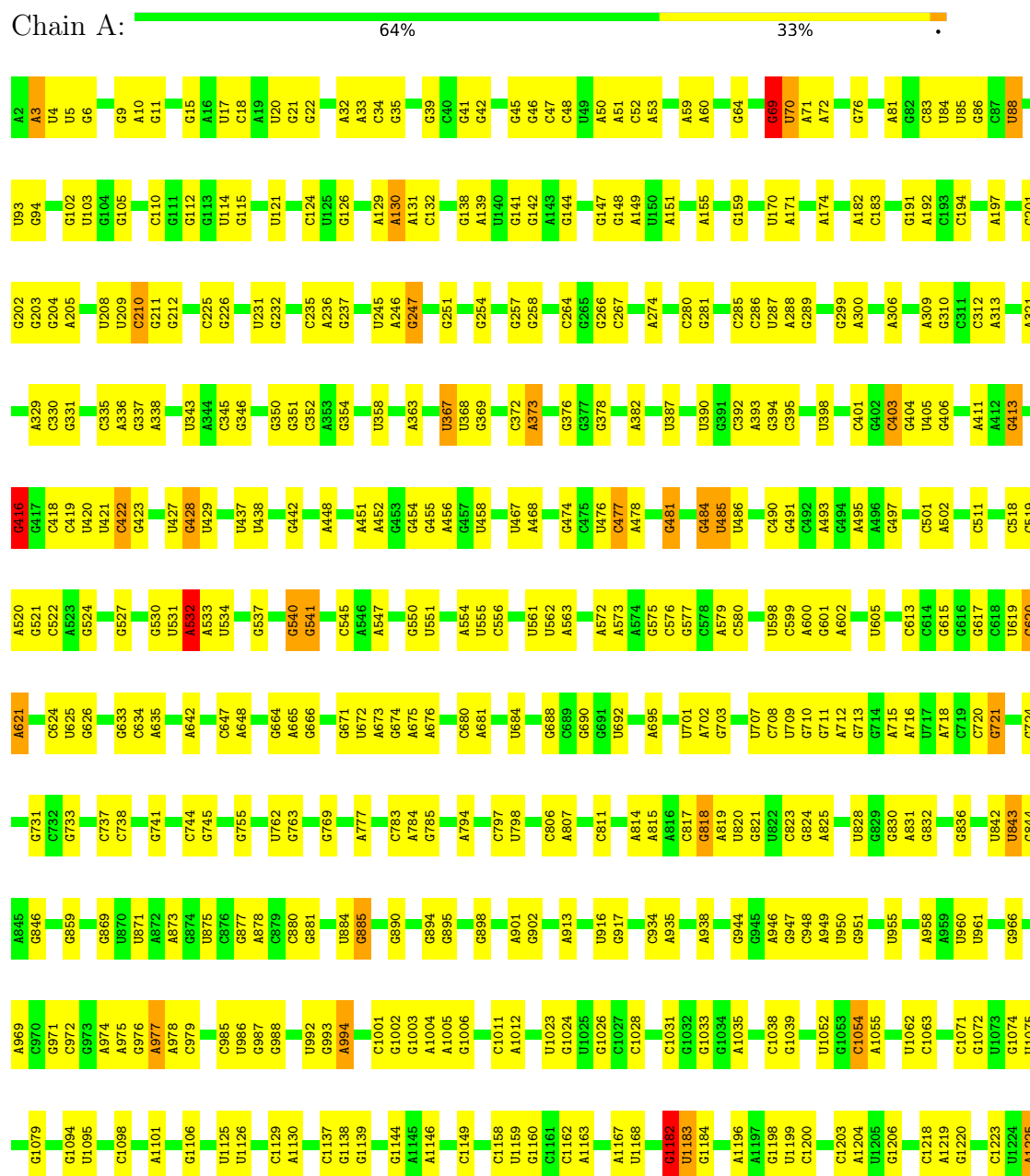
- Molecule 58 is a protein called 30S ribosomal protein S21.

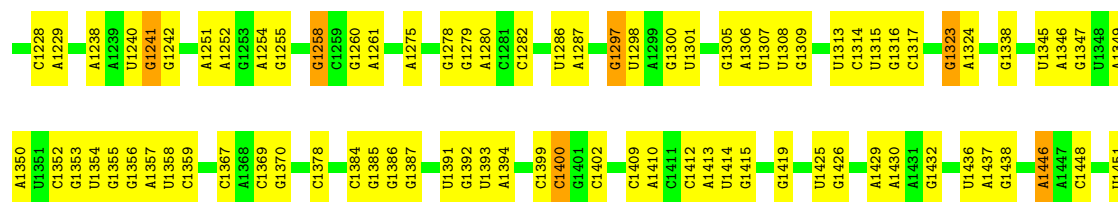
Mol	Chain	Residues	Atoms					AltConf	Trace
58	HB	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

3 Residue-property plots [i](#)

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

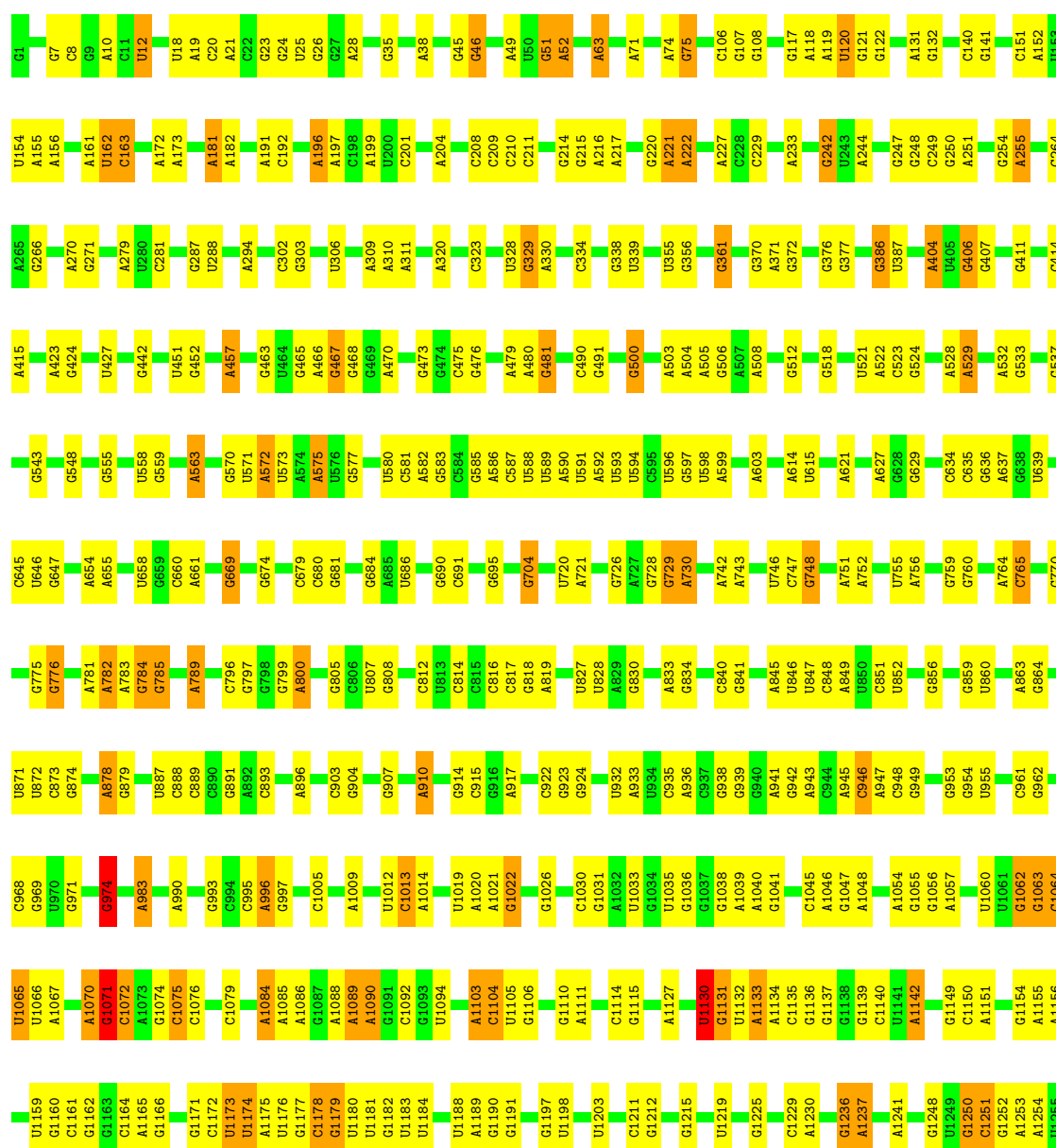
• Molecule 1: 16S ribosomal RNA





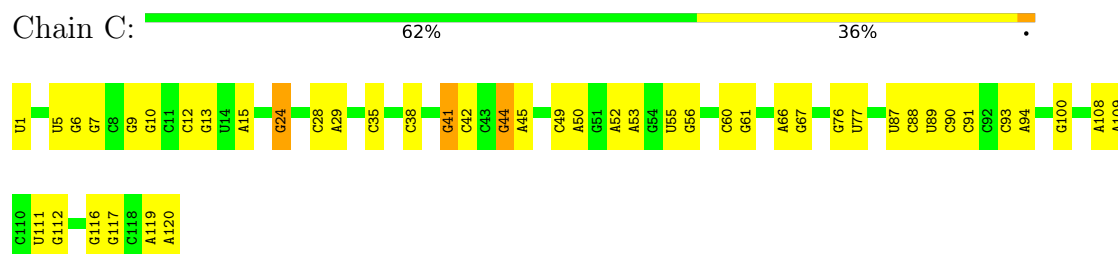
• Molecule 2: 23S ribosomal RNA

Chain B:  66%  30% •

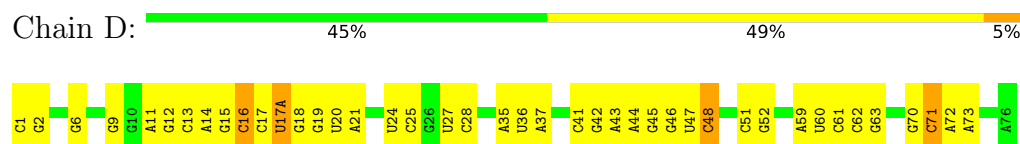


U2898	A2765	C2640	U2519	U2402	G2303	A2212	G2093	A2009	A1889	U1779	G1651	G1521	U1390	G1266
A2899	C2772	G2641	C2520	C2403	G2304	U2213	C2096	G2010	A1890	U1780	A1652	A1522	A1395	C1257
U2903	A2778	G2685	G2532	A2406	C2306	C2215	U2106	A2013	A1899	U1781	G1653	G1523	U1405	U1268
	U2779	A2682	C2539	C2417	A2309	G2217	G2107	A2014	A1900	A1784	G1659	C1526	U1406	A1260
	G2791			A2418	C2310	U2220	U2111	A2015	A1901		A1664	G1527		A1265
		A2685	G2544	C2422	A2311	G2221	G2112	U2022	G1906	A1791	A1665	A1535	G1416	G1271
	U2798	U2546	G2545	U2423	U2312	G2222	G2113	C2023	G1907	G1792	G1666	C1536	C1428	U1272
	A2799	G2673	U2547	U2423	A2313	G2223	A2114	C2024	C1908	C1793	G1667	G1537		U1273
	A2800	G2674		G2428	A2314	G2224	G2115	C2025	C1909	A1794	G1668	G1538	G1433	A1274
			U2554	G2429	G2315	A2225	G2116	U2026	U1911	U1796	A1669	U1539	A1434	A1275
	G2808	U2680	U2555	A2430	A2317	A2225	A2117	G2027	A1912	G1797		G1540	A1434	
		C2681	C2556		U2320	U2229	U2118	U2028	A1913		G1674	A1544	G1435	C1278
	G2812	A2682	G2557	A2435	U2321	G2230	A2119	G2029	G1914	C1800		A1544	G1436	C1279
	A2813		C2558		U2321	U2231	G2120	A2030	A1801	A1801	G1682	A1548	C1437	U1291
	C2815	G2685		U2441	U2324	G2232	G2121	C2031	U1917	A1802	C1685	A1549	U1438	C1292
	G2816	U2687	A2566	C2442	G2325	U2233	U2122	C2032	A1918	A1808	C1686	C1550	U1440	
	U2817	G2688	G2567	C2443	C2326	G2234	G2123	A2033	A1919	A1809		A1551	G1441	C1295
	U2818	U2689	A2572	G2444	A2327	G2238	G2124	U2034	G1929	G1823	G1695	G1555	U1442	G1296
	G2819	U2690			A2328		G2125	A2037	G1930	G1813		G1558	U1443	G1300
	A2820		G2576	A2448	U2329	A2241	G2127	G2038	G1934	C1816	A1698	C1558	G1444	A1301
	A2821				G2330	G2242	G2128	U2039	G1935	G1817	G1699	U1559	G1445	A1302
				G2455	A2333	U2243	G2129	G2040	A1936	U1818		G1560	G1446	
	G2828	U2707		C2456	U2334	U2244	U2130	U2041	A1937		C1704	G1566	C1447	C1306
	C2830	G2708	G2582	C2466	U2334	U2245	U2131	A2042	A1937	G1823	A1705	U1566	G1448	A1307
	G2831	G2709	U2585		A2340	G2246	U2132	C2043	A1938	G1823	U1709	G1567	G1449	
	U2832		U2586	G2470	G2341	A2247	G2133	C2047	U1944	G1824	G1710	G1568	G1454	U1316
	U2833	G2714	A2587	A2471		A2247		G2048	C1947	U1825		A1569	G1317	
					C2350	G2250	C2145	G2048	G1947	G1826	G1715	A1590	C1461	A1321
	A2837	G2718	C2590	C2475	G2355	G2251	C2146	G2049	G1948	G1827	U1729	A1591	G1464	
	G2838	G2719	C2591	A2476	G2355	G2252	A2147	A2051	C2050	G1828	C1730	C1592	G1465	A1328
	G2848	U2477	U2592	U2477	C2359	C2264	G2157	A2052	G1954	A1829	G1731	A1593		
	U2849	A2478	U2593	A2478	G2360	A2265	G2158	C2055	U1955	G1830			U1468	G1332
			C2594		G2361	A2266	C2160	G2056	C1957	C1837	U1738	A1597		
		C2723		C2483	G2361	A2267	C2161	G2056	C1958		A1739	A1598	G1475	G1343
	G2853	A2726	G2597	G2488	C2368	A2268	G2162	A2060	G1959	U1841	A1744	U1599	C1344	U1344
	G2854	A2727	A2598		A2369		G2162	G2061	C1967	C1843	A1745	C1600	G1478	C1345
	U2861	G2729	A2600	C2498	U2372	G2271	U2166	A2062	C1967	G1844		G1601	G1482	C1363
	C2862		C2601	U2500	G2373	A2273	A2170	C2065	A1970	G1845	C1748	C1604	G1364	G1364
	G2867		A2602	C2501	G2373	C2283	A2171	C2066	U1971		A1749	C1605	A1490	A1365
	A2868	G2737	U2603	G2502	C2380	A2284	U2172		G1972	A1848	A1754	C1606		
		A2738	U2605	A2503	A2381	G2285	A2173	G2069	G1973	G1849	A1755	C1607	C1499	G1368
	A2872		U2609	G2504	G2382	G2286	A2176	A2070	C1985	G1857	G1756	A1608	G1500	G1369
				G2505	G2383	A2287		A2071			A1757		A1504	
	C2875	G2744	U2613	U2506	U2384		A2183	C2072	U1991	G1860	U1758	C1611		G1377
	G2876		A2514	G2508	C2385	U2291	A2184	U2075	G1992	G1861	A1616	A1598	A1508	A1378
	A2879	A2748	U2615	G2509	G2391	G2293	A2198	A2077	U1993	G1870	C1764	C1606	A1509	U1379
	C2880						A2199	A2077		A1871	U1765	U1636	G1510	A1383
	U2881	C2755	U2629	U2514	G2396	U2296	A2199	A2077	C1996	G1871	G1766	A1637		
	A2882	U2756	G2630	C2515	C2397	A2297	A2199	U2086	C1997	A1880	G1767		U1513	C1386
		U2757		A2516	U2398	A2298	G2204	G2087	A1998	U1881		C1646	G1514	A1387
	U2884		G2638	C2517	G2399		A2211	A2088	G2002		A1773	U1647	A1515	G1388
			A2639	A2518		U2302					C1774			G1389

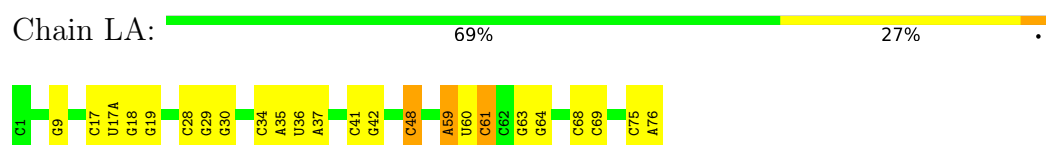
- Molecule 3: 5S ribosomal RNA



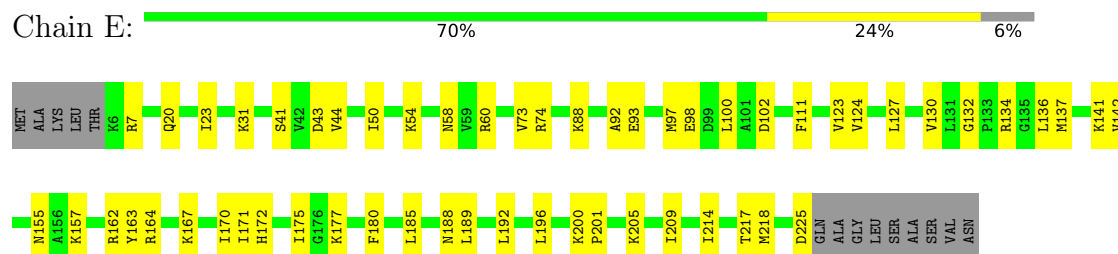
- Molecule 4: tRNA(fMet)



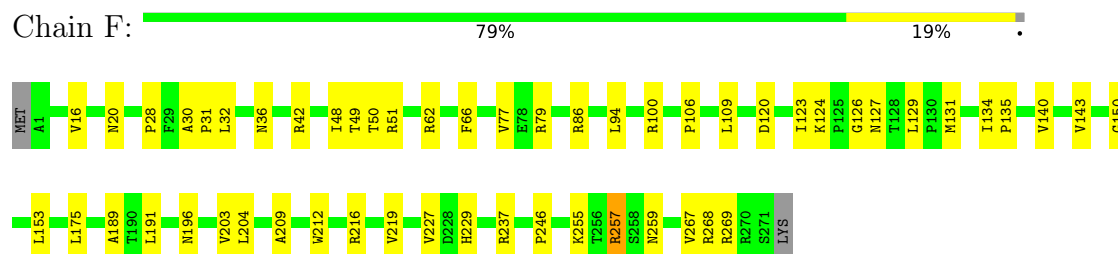
- Molecule 4: tRNA(fMet)



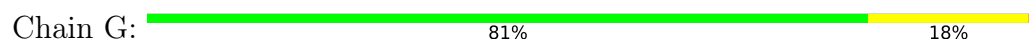
- Molecule 5: 50S ribosomal protein L1



- Molecule 6: 50S ribosomal protein L2



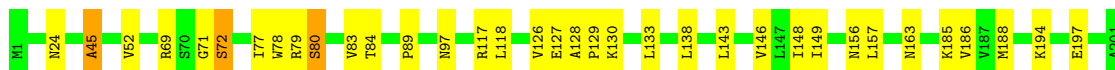
- Molecule 7: 50S ribosomal protein L3





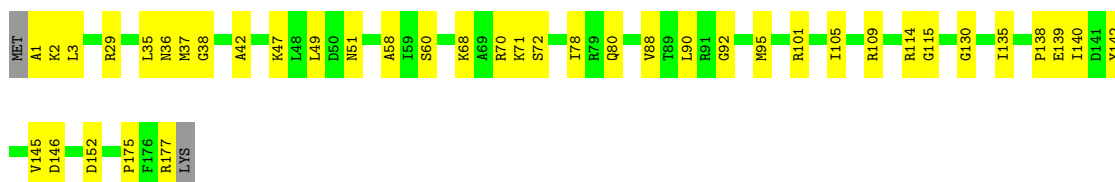
- Molecule 8: 50S ribosomal protein L4

Chain H: 83% 16% .



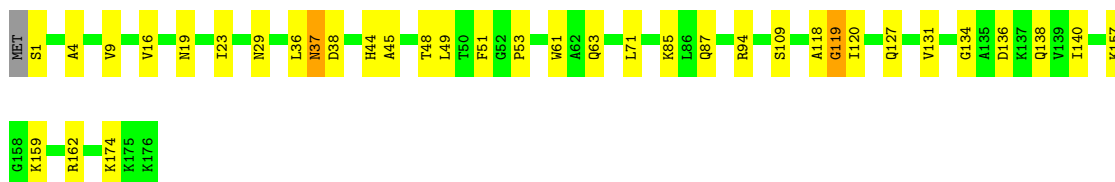
- Molecule 9: 50S ribosomal protein L5

Chain I: 77% 22% .



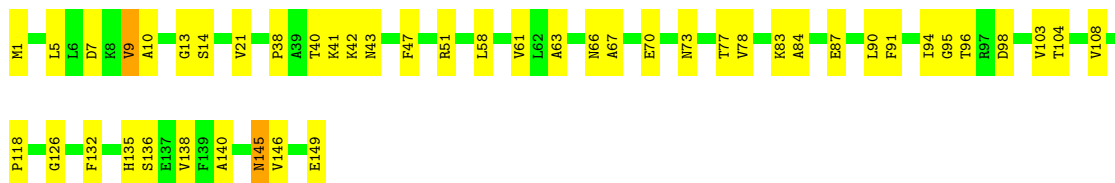
- Molecule 10: 50S ribosomal protein L6

Chain J: 79% 19% ..



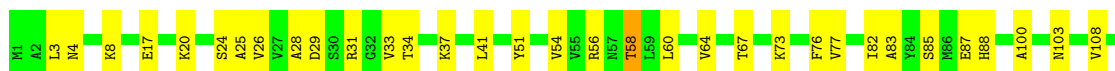
- Molecule 11: 50S ribosomal protein L9

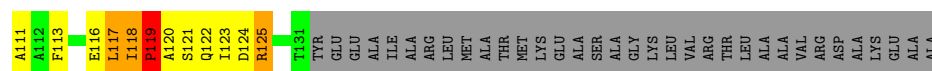
Chain K: 69% 30% .



- Molecule 12: 50S ribosomal protein L10

Chain L: 52% 24% .. 21%





- Molecule 13: 50S ribosomal protein L11

Chain M: 68% 29% ..



- Molecule 14: 50S ribosomal protein L13

Chain N: 83% 16% ..



- Molecule 15: 50S ribosomal protein L14

Chain O: 79% 18% ..



- Molecule 16: 50S ribosomal protein L15

Chain P: 81% 17% ..



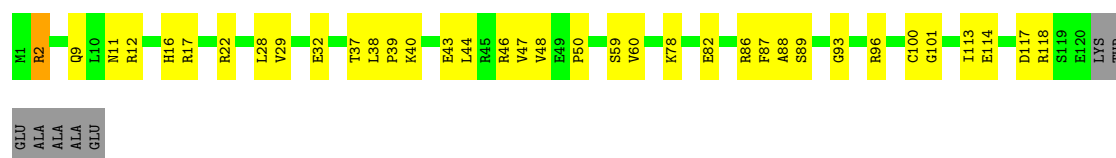
- Molecule 17: 50S ribosomal protein L16

Chain Q: 89% 10% ..




- Molecule 18: 50S ribosomal protein L17

Chain R: 66% 28% 6%




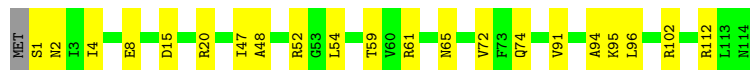
- Molecule 19: 50S ribosomal protein L18

Chain S:  79% 19% ..




- Molecule 20: 50S ribosomal protein L19

Chain T:  81% 18% .




- Molecule 21: 50S ribosomal protein L20

Chain U:  82% 17% .




- Molecule 22: 50S ribosomal protein L21

Chain V:  79% 19% .




- Molecule 23: 50S ribosomal protein L22

Chain W:  83% 15% .




- Molecule 24: 50S ribosomal protein L23

Chain X:  87% 6% 7%




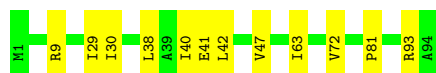
- Molecule 25: 50S ribosomal protein L24

Chain Y:  83% 15% .




- Molecule 26: 50S ribosomal protein L25

Chain Z:  87% 13%



- Molecule 27: 50S ribosomal protein L27

Chain AA:  74% 14% 12%




- Molecule 28: 50S ribosomal protein L28

Chain BA:  91% 8%




- Molecule 29: 50S ribosomal protein L29

Chain CA:  86% 14%




- Molecule 30: 50S ribosomal protein L30

Chain DA:  81% 17%




- Molecule 31: 50S ribosomal protein L31

Chain EA:  74% 19% 6%



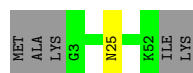
- Molecule 32: 50S ribosomal protein L32

Chain FA:  79% 19%




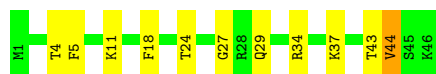
- Molecule 33: 50S ribosomal protein L33

Chain GA:  89% 9%




- Molecule 34: 50S ribosomal protein L34

Chain HA:  76% 22%



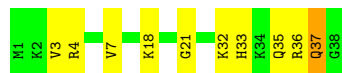
- Molecule 35: 50S ribosomal protein L35

Chain IA:  82% 15%



- Molecule 36: 50S ribosomal protein L36

Chain JA:  74% 24%




- Molecule 37: mRNA

Chain KA:  41% 30% 30%




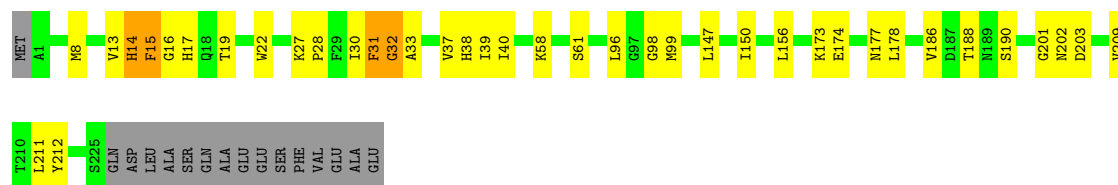
- Molecule 38: Peptide chain release factor 1

Chain MA:  73% 20% 5%



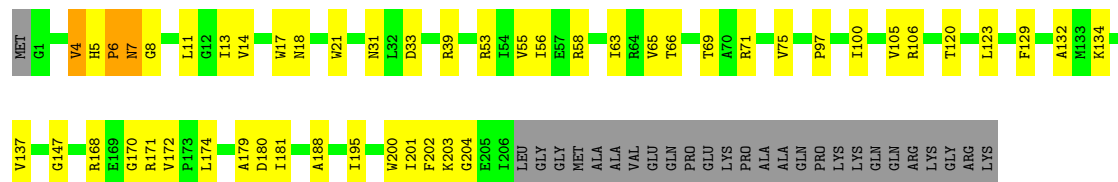
- Molecule 39: 30S ribosomal protein S2

Chain OA:  77% 15% 7%



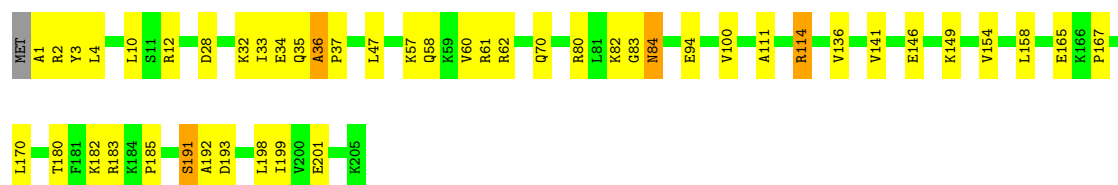
- Molecule 40: 30S ribosomal protein S3

Chain PA: 67% 20% 12%



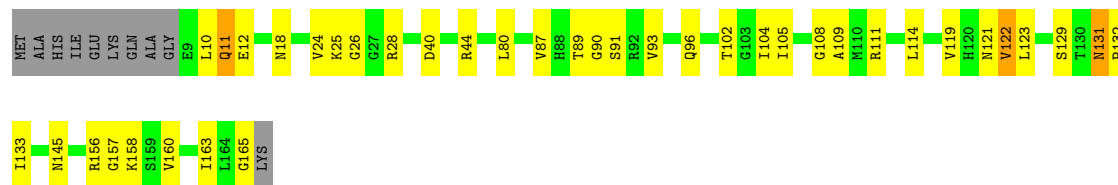
- Molecule 41: 30S ribosomal protein S4

Chain QA: 77% 21% 2%



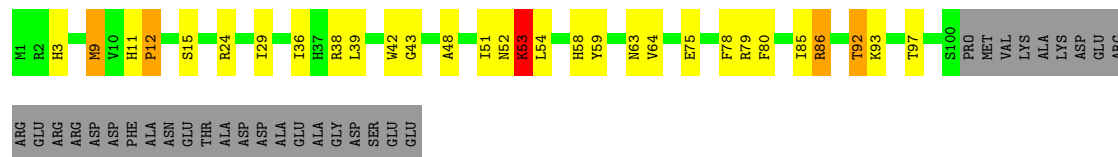
- Molecule 42: 30S ribosomal protein S5

Chain RA: 71% 22% 6%



- Molecule 43: 30S ribosomal protein S6

Chain SA: 53% 19% 24%



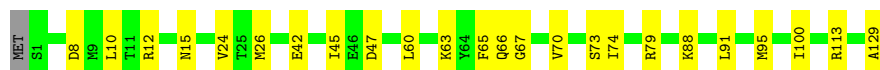
- Molecule 44: 30S ribosomal protein S7

Chain TA: 90% 7% 3%



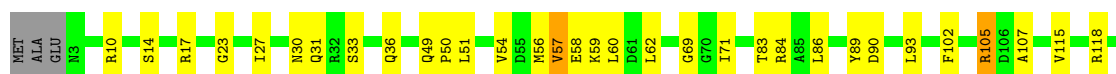
- Molecule 45: 30S ribosomal protein S8

Chain UA: 81% 18% .



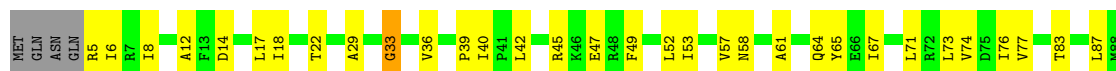
- Molecule 46: 30S ribosomal protein S9

Chain VA: 72% 25% . .



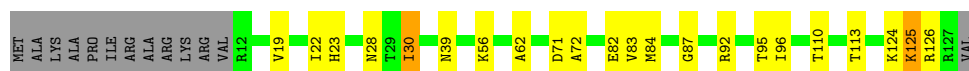
- Molecule 47: 30S ribosomal protein S10

Chain WA: 61% 32% 5%



- Molecule 48: 30S ribosomal protein S11

Chain XA: 73% 16% 10%



- Molecule 49: 30S ribosomal protein S12

Chain YA: 68% 27% 5%



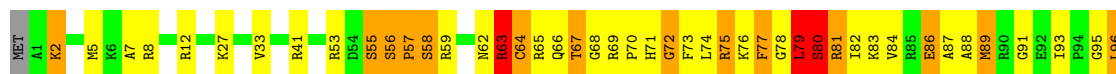
- Molecule 50: 30S ribosomal protein S13

Chain ZA:  71% 25% ..




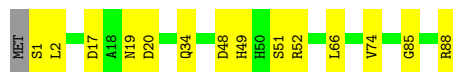
- Molecule 51: 30S ribosomal protein S14

Chain AB:  53% 29% 14% ..



- Molecule 52: 30S ribosomal protein S15

Chain BB:  83% 16% .



- Molecule 53: 30S ribosomal protein S16

Chain CB:  71% 27% .




- Molecule 54: 30S ribosomal protein S17

Chain DB:  70% 23% . 5%



- Molecule 55: 30S ribosomal protein S18

Chain EB:  75% 11% . 13%

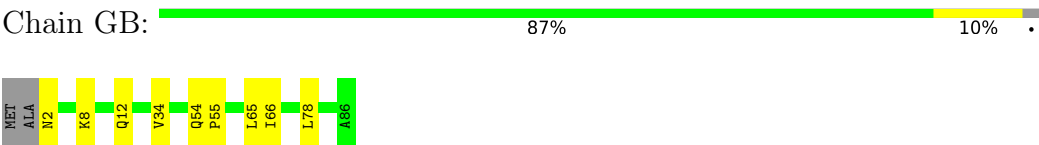


- Molecule 56: 30S ribosomal protein S19

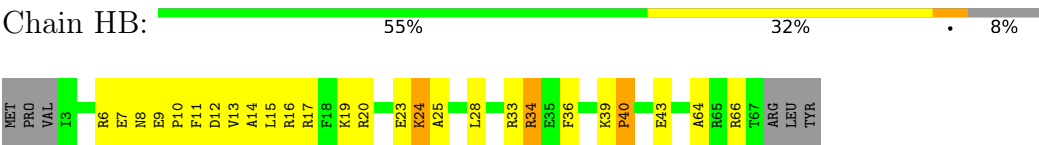
Chain FB:  61% 24% . 14%



● Molecule 57: 30S ribosomal protein S20



● Molecule 58: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	639088	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	0.5	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	22000	Depositor
Image detector	GATAN K2 SUMMIT (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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.43	0/36963	0.70	4/57662 (0.0%)
2	B	0.42	1/69797 (0.0%)	0.70	11/108890 (0.0%)
3	C	0.41	0/2872	0.71	1/4479 (0.0%)
4	D	0.40	0/1832	0.68	0/2855
4	LA	0.39	0/1832	0.67	0/2855
5	E	0.37	0/1652	0.60	0/2227
6	F	0.34	0/2121	0.69	0/2852
7	G	0.35	0/1586	0.64	0/2134
8	H	0.36	0/1571	0.65	0/2113
9	I	0.39	0/1434	0.64	0/1926
10	J	0.35	0/1343	0.64	1/1816 (0.1%)
11	K	0.45	0/1122	0.73	0/1515
12	L	0.51	0/1001	0.81	2/1350 (0.1%)
13	M	0.47	0/1046	0.69	0/1410
14	N	0.33	0/1152	0.60	0/1551
15	O	0.34	0/947	0.66	0/1268
16	P	0.34	0/1054	0.64	0/1403
17	Q	0.37	0/1093	0.66	0/1460
18	R	0.38	0/973	0.70	0/1301
19	S	0.35	0/902	0.59	0/1209
20	T	0.35	0/929	0.65	0/1242
21	U	0.39	0/960	0.65	0/1278
22	V	0.37	0/829	0.71	1/1107 (0.1%)
23	W	0.36	0/864	0.70	1/1156 (0.1%)
24	X	0.37	0/744	0.61	0/994
25	Y	0.36	0/787	0.66	0/1051
26	Z	0.34	0/766	0.57	0/1025
27	AA	0.35	0/582	0.61	0/769
28	BA	0.35	0/635	0.64	0/848
29	CA	0.36	0/510	0.69	0/677
30	DA	0.32	0/453	0.63	0/605
31	EA	0.45	0/531	0.64	0/709
32	FA	0.33	0/450	0.61	0/599
33	GA	0.34	0/416	0.59	0/554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	HA	0.37	0/380	0.65	0/498
35	IA	0.34	0/513	0.66	0/676
36	JA	0.45	0/303	0.74	0/397
37	KA	0.40	0/464	0.69	0/723
38	MA	0.85	0/2751	0.67	1/3703 (0.0%)
39	OA	0.55	1/1787 (0.1%)	0.80	3/2408 (0.1%)
40	PA	0.45	1/1651 (0.1%)	0.68	1/2225 (0.0%)
41	QA	0.38	0/1665	0.66	0/2227
42	RA	0.45	0/1169	0.78	1/1573 (0.1%)
43	SA	0.40	0/835	0.77	1/1128 (0.1%)
44	TA	0.36	0/1195	0.60	0/1602
45	UA	0.33	0/989	0.63	0/1326
46	VA	0.40	0/1034	0.66	0/1375
47	WA	0.36	0/796	0.70	0/1077
48	XA	0.35	0/885	0.65	0/1195
49	YA	0.38	0/969	0.76	1/1300 (0.1%)
50	ZA	0.40	0/892	0.66	0/1193
51	AB	0.88	4/822 (0.5%)	1.12	4/1095 (0.4%)
52	BB	0.37	0/722	0.65	0/964
53	CB	0.36	0/659	0.67	0/884
54	DB	0.34	0/657	0.67	0/881
55	EB	0.42	0/544	0.62	0/731
56	FB	0.38	0/652	0.64	0/877
57	GB	0.34	0/671	0.52	0/888
58	HB	0.49	0/550	0.78	0/728
All	All	0.43	7/165304 (0.0%)	0.70	33/246564 (0.0%)

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	A	0	10
2	B	0	33
3	C	0	1
4	D	0	1
All	All	0	45

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	OA	31	PHE	C-O	7.44	1.37	1.23
51	AB	77	PHE	CB-CG	7.04	1.63	1.51
51	AB	63	ARG	CB-CG	6.01	1.68	1.52
40	PA	97	PRO	N-CD	5.77	1.55	1.47
51	AB	86	GLU	C-O	5.27	1.33	1.23

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	OA	32	GLY	N-CA-C	12.97	145.52	113.10
51	AB	79	LEU	CA-CB-CG	12.43	143.88	115.30
39	OA	31	PHE	C-N-CA	-9.34	102.70	122.30
12	L	119	PRO	N-CA-C	-8.80	89.22	112.10
2	B	974	G	N9-C1'-C2'	7.74	124.07	114.00

There are no chirality outliers.

5 of 45 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	G	Sidechain
1	A	350	G	Sidechain
1	A	416	G	Sidechain
1	A	532	A	Sidechain
1	A	563	A	Sidechain

5.2 Too-close contacts [i](#)

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	A	33012	0	16618	278	0
2	B	62318	0	31346	532	0
3	C	2568	0	1303	25	0
4	D	1640	0	837	28	0
4	LA	1640	0	837	15	0
5	E	1637	0	1719	40	0
6	F	2082	0	2157	36	0
7	G	1565	0	1616	32	0
8	H	1552	0	1619	27	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	I	1410	0	1447	24	0
10	J	1323	0	1374	22	0
11	K	1111	0	1148	24	0
12	L	988	0	1025	37	0
13	M	1032	0	1088	32	0
14	N	1129	0	1162	18	0
15	O	938	0	1012	16	0
16	P	1045	0	1117	16	0
17	Q	1074	0	1157	12	0
18	R	960	0	1000	26	0
19	S	892	0	923	16	0
20	T	917	0	965	16	0
21	U	947	0	1022	20	0
22	V	816	0	839	17	0
23	W	857	0	922	13	0
24	X	738	0	807	5	0
25	Y	779	0	834	8	0
26	Z	753	0	780	9	0
27	AA	575	0	592	8	0
28	BA	625	0	655	3	0
29	CA	509	0	543	5	0
30	DA	449	0	491	6	0
31	EA	522	0	524	9	0
32	FA	444	0	461	8	0
33	GA	409	0	440	1	0
34	HA	377	0	418	8	0
35	IA	504	0	574	11	0
36	JA	302	0	343	10	0
37	KA	412	0	207	7	0
38	MA	2714	0	2636	60	0
39	OA	1756	0	1787	27	0
40	PA	1624	0	1699	37	0
41	QA	1643	0	1710	35	0
42	RA	1156	0	1199	24	0
43	SA	817	0	808	22	0
44	TA	1181	0	1240	4	0
45	UA	979	0	1034	14	0
46	VA	1022	0	1070	21	0
47	WA	786	0	828	25	0
48	XA	869	0	878	16	0
49	YA	955	0	1019	30	0
50	ZA	883	0	944	21	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	AB	810	0	852	57	0
52	BB	714	0	737	6	0
53	CB	649	0	666	18	0
54	DB	648	0	691	13	0
55	EB	535	0	552	7	0
56	FB	637	0	665	16	0
57	GB	665	0	714	5	0
58	HB	544	0	579	18	0
All	All	152438	0	104230	1687	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 7.

The worst 5 of 1687 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)
38:MA:77:MET:CE	38:MA:77:MET:SD	2.04	1.45
39:OA:32:GLY:O	39:OA:38:HIS:HA	1.51	1.08
39:OA:33:ALA:HA	39:OA:37:VAL:O	1.52	1.08
12:L:119:PRO:CD	12:L:120:ALA:H	1.63	1.03
51:AB:73:PHE:HA	51:AB:78:GLY:HA2	1.07	1.03

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	
5	E	218/234 (93%)	185 (85%)	32 (15%)	1 (0%)	29	66
6	F	269/273 (98%)	229 (85%)	40 (15%)	0	100	100
7	G	207/209 (99%)	177 (86%)	27 (13%)	3 (1%)	11	45

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	199/201 (99%)	176 (88%)	19 (10%)	4 (2%)	7	39
9	I	175/179 (98%)	150 (86%)	23 (13%)	2 (1%)	14	50
10	J	174/177 (98%)	151 (87%)	20 (12%)	3 (2%)	9	42
11	K	147/149 (99%)	123 (84%)	19 (13%)	5 (3%)	3	30
12	L	129/165 (78%)	88 (68%)	34 (26%)	7 (5%)	2	20
13	M	139/142 (98%)	114 (82%)	21 (15%)	4 (3%)	4	32
14	N	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	22	59
15	O	120/123 (98%)	97 (81%)	20 (17%)	3 (2%)	5	35
16	P	141/144 (98%)	120 (85%)	19 (14%)	2 (1%)	11	45
17	Q	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	10	44
18	R	118/127 (93%)	92 (78%)	24 (20%)	2 (2%)	9	42
19	S	114/117 (97%)	103 (90%)	8 (7%)	3 (3%)	5	34
20	T	112/115 (97%)	92 (82%)	19 (17%)	1 (1%)	17	54
21	U	115/118 (98%)	101 (88%)	13 (11%)	1 (1%)	17	54
22	V	101/103 (98%)	85 (84%)	14 (14%)	2 (2%)	7	39
23	W	108/110 (98%)	90 (83%)	15 (14%)	3 (3%)	5	33
24	X	91/100 (91%)	81 (89%)	10 (11%)	0	100	100
25	Y	100/104 (96%)	80 (80%)	17 (17%)	3 (3%)	4	32
26	Z	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
27	AA	73/85 (86%)	65 (89%)	8 (11%)	0	100	100
28	BA	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
29	CA	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	9	43
30	DA	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
31	EA	64/70 (91%)	52 (81%)	11 (17%)	1 (2%)	9	43
32	FA	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
33	GA	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
34	HA	44/46 (96%)	34 (77%)	9 (20%)	1 (2%)	6	36
35	IA	62/65 (95%)	50 (81%)	11 (18%)	1 (2%)	9	43
36	JA	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	5	33
38	MA	340/362 (94%)	292 (86%)	45 (13%)	3 (1%)	17	54
39	OA	223/241 (92%)	202 (91%)	19 (8%)	2 (1%)	17	54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	PA	204/233 (88%)	177 (87%)	25 (12%)	2 (1%)	15	51
41	QA	203/206 (98%)	174 (86%)	21 (10%)	8 (4%)	3	27
42	RA	155/167 (93%)	121 (78%)	27 (17%)	7 (4%)	2	23
43	SA	98/131 (75%)	73 (74%)	20 (20%)	5 (5%)	2	21
44	TA	149/156 (96%)	125 (84%)	21 (14%)	3 (2%)	7	39
45	UA	127/130 (98%)	111 (87%)	14 (11%)	2 (2%)	9	43
46	VA	125/130 (96%)	98 (78%)	23 (18%)	4 (3%)	4	31
47	WA	96/103 (93%)	73 (76%)	19 (20%)	4 (4%)	3	25
48	XA	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	17	54
49	YA	121/124 (98%)	96 (79%)	19 (16%)	6 (5%)	2	22
50	ZA	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	8	41
51	AB	99/102 (97%)	64 (65%)	25 (25%)	10 (10%)	0	7
52	BB	86/89 (97%)	71 (83%)	13 (15%)	2 (2%)	6	36
53	CB	80/82 (98%)	63 (79%)	16 (20%)	1 (1%)	12	47
54	DB	78/84 (93%)	63 (81%)	12 (15%)	3 (4%)	3	27
55	EB	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
56	FB	77/92 (84%)	63 (82%)	14 (18%)	0	100	100
57	GB	83/87 (95%)	79 (95%)	4 (5%)	0	100	100
58	HB	63/71 (89%)	44 (70%)	14 (22%)	5 (8%)	1	12
All	All	6412/6790 (94%)	5417 (84%)	868 (14%)	127 (2%)	11	39

5 of 127 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	83	VAL
9	I	2	LYS
10	J	119	GLY
11	K	9	VAL
11	K	10	ALA

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	
5	E	171/181 (94%)	168 (98%)	3 (2%)	59	77
6	F	216/218 (99%)	209 (97%)	7 (3%)	39	65
7	G	164/164 (100%)	163 (99%)	1 (1%)	86	93
8	H	165/165 (100%)	163 (99%)	2 (1%)	71	84
9	I	148/150 (99%)	146 (99%)	2 (1%)	67	82
10	J	137/138 (99%)	134 (98%)	3 (2%)	52	72
11	K	114/114 (100%)	112 (98%)	2 (2%)	59	77
12	L	100/123 (81%)	97 (97%)	3 (3%)	41	66
13	M	109/110 (99%)	106 (97%)	3 (3%)	43	67
14	N	116/116 (100%)	115 (99%)	1 (1%)	78	88
15	O	103/104 (99%)	102 (99%)	1 (1%)	76	86
16	P	102/103 (99%)	100 (98%)	2 (2%)	55	74
17	Q	109/109 (100%)	108 (99%)	1 (1%)	78	88
18	R	100/104 (96%)	99 (99%)	1 (1%)	76	86
19	S	86/87 (99%)	84 (98%)	2 (2%)	50	71
20	T	99/100 (99%)	98 (99%)	1 (1%)	76	86
21	U	89/90 (99%)	89 (100%)	0	100	100
22	V	84/84 (100%)	84 (100%)	0	100	100
23	W	93/93 (100%)	92 (99%)	1 (1%)	73	85
24	X	80/84 (95%)	80 (100%)	0	100	100
25	Y	83/85 (98%)	83 (100%)	0	100	100
26	Z	78/78 (100%)	78 (100%)	0	100	100
27	AA	57/63 (90%)	57 (100%)	0	100	100
28	BA	67/68 (98%)	66 (98%)	1 (2%)	65	81
29	CA	55/55 (100%)	54 (98%)	1 (2%)	59	77
30	DA	48/49 (98%)	48 (100%)	0	100	100
31	EA	59/62 (95%)	58 (98%)	1 (2%)	60	79
32	FA	47/48 (98%)	46 (98%)	1 (2%)	53	74
33	GA	45/49 (92%)	45 (100%)	0	100	100
34	HA	38/38 (100%)	38 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	IA	51/52 (98%)	51 (100%)	0	100	100
36	JA	34/34 (100%)	34 (100%)	0	100	100
38	MA	284/302 (94%)	279 (98%)	5 (2%)	59	77
39	OA	186/199 (94%)	186 (100%)	0	100	100
40	PA	170/190 (90%)	165 (97%)	5 (3%)	42	66
41	QA	172/173 (99%)	170 (99%)	2 (1%)	71	84
42	RA	119/126 (94%)	116 (98%)	3 (2%)	47	70
43	SA	87/112 (78%)	85 (98%)	2 (2%)	50	71
44	TA	124/129 (96%)	123 (99%)	1 (1%)	81	89
45	UA	104/105 (99%)	104 (100%)	0	100	100
46	VA	105/107 (98%)	103 (98%)	2 (2%)	57	76
47	WA	86/90 (96%)	85 (99%)	1 (1%)	71	84
48	XA	89/99 (90%)	87 (98%)	2 (2%)	52	72
49	YA	103/104 (99%)	99 (96%)	4 (4%)	32	60
50	ZA	92/96 (96%)	91 (99%)	1 (1%)	73	85
51	AB	83/84 (99%)	76 (92%)	7 (8%)	11	40
52	BB	76/77 (99%)	74 (97%)	2 (3%)	46	69
53	CB	65/65 (100%)	61 (94%)	4 (6%)	18	49
54	DB	74/78 (95%)	73 (99%)	1 (1%)	67	82
55	EB	56/65 (86%)	55 (98%)	1 (2%)	59	77
56	FB	70/79 (89%)	69 (99%)	1 (1%)	67	82
57	GB	65/66 (98%)	64 (98%)	1 (2%)	65	81
58	HB	55/61 (90%)	54 (98%)	1 (2%)	59	77
All	All	5312/5525 (96%)	5226 (98%)	86 (2%)	64	80

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	TA	121	ASN
51	AB	79	LEU
46	VA	105	ARG
49	YA	93	ARG
52	BB	19	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
39	OA	177	ASN
50	ZA	99	GLN
41	QA	88	ASN
44	TA	121	ASN
53	CB	40	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	222 (14%)	5 (0%)
2	B	2902/2903 (99%)	387 (13%)	8 (0%)
3	C	119/120 (99%)	18 (15%)	1 (0%)
37	KA	18/27 (66%)	3 (16%)	0
4	D	76/77 (98%)	10 (13%)	0
4	LA	76/77 (98%)	8 (10%)	0
All	All	4729/4743 (99%)	648 (13%)	14 (0%)

5 of 648 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	A
1	A	6	G
1	A	9	G
1	A	22	G
1	A	32	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	1020	A
2	B	1130	U
3	C	66	A
2	B	2326	C
2	B	2756	U

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 [i](#)

There are no monosaccharides 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.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-7970. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal surface views

This section was not generated.

6.5 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.