



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2025 – 03:10 pm GMT

PDB ID : 8RCM
EMDB ID : EMD-19055
Title : Escherichia coli paused disome complex (Non-rotated disome interface class 2)
Authors : Fluegel, T.; Schacherl, M.
Deposited on : 2023-12-06
Resolution : 3.59 Å(reported)
Based on initial model : 7N1P

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 : **FAILED**
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41

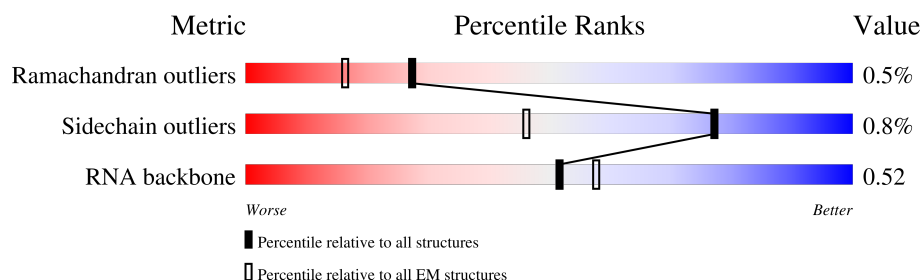
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.59 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.



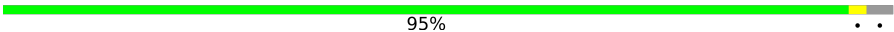



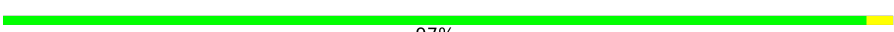







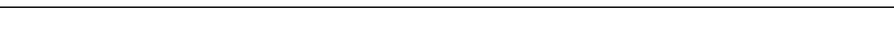

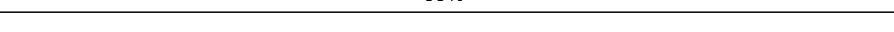
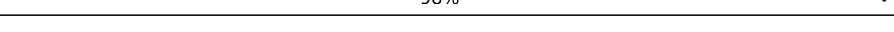
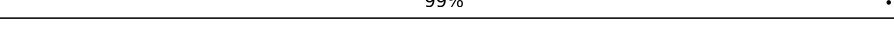
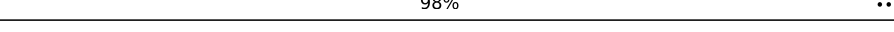



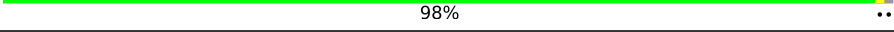
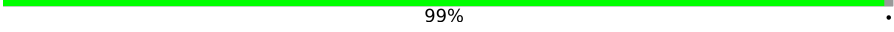
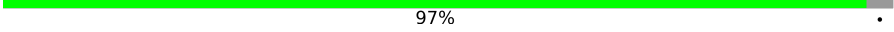
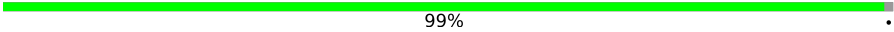
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	12	78	
2	32	59	
3	4	70	
4	62	65	
5	71	2904	
5	72	2904	
6	82	120	
7	A1	1542	
7	A2	1542	

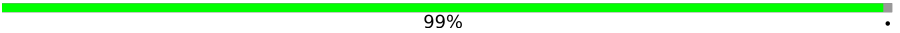
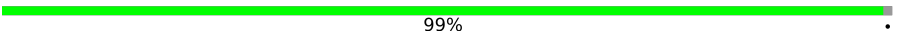
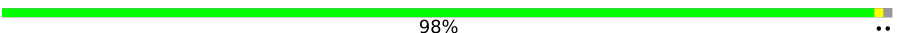
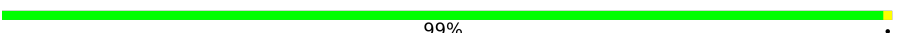
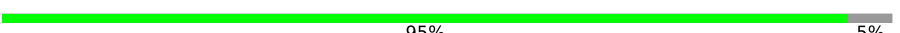















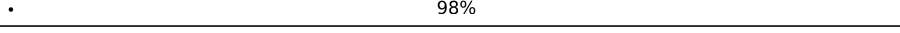

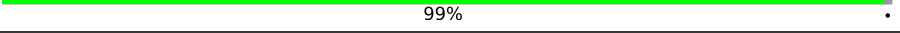
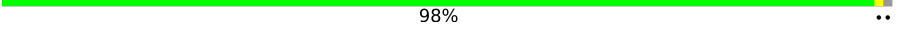
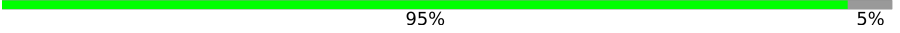
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Mol	Chain	Length	Quality of chain
8	B	241	 95% . .
8	B2	241	 92% . 6%
9	C1	233	 90% . 9%
9	C2	233	 91% 9%
10	D1	206	 97% .
10	D2	206	 99% .
11	E1	167	 95% 5%
11	E2	167	 95% 5%
12	F1	135	 79% 21%
12	F2	135	 77% . 21%
13	G1	179	 87% 13%
13	G2	179	 82% . 14%
14	H1	130	 99% .
14	H2	130	 99% .
15	I1	130	 98% .
15	I2	130	 99% .
16	J1	103	 98% ..
16	J2	103	 88% 9% .
17	K1	129	 87% . 11%
17	K2	129	 90% . 9%
18	L1	124	 98% ..
18	L2	124	 99% .
19	M1	118	 97% .
19	M2	118	 99% .
20	N1	101	 97% ..

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Mol	Chain	Length	Quality of chain
20	N2	101	 99% .
21	O1	89	 99% .
21	O2	89	 98% ..
22	P1	82	 99% .
23	Q1	84	 95% 5%
23	Q2	84	 94% . 5%
24	R1	75	 88% . 9%
24	R2	75	 93% 5% .
25	S1	92	 89% . 10%
25	S2	92	 90% 10%
26	T1	87	 92% 7% .
27	U1	71	 96% . .
27	U2	71	 96% . .
28	V2	64	 27% 62% . 9%
29	W	76	 59% 30% 11%
30	W1	76	 29% 17% . 53%
31	X2	77	 56% 38% 6%
32	Y1	76	 38% 8% . 53%
33	Y2	76	 66% 30% .
34	Z1	557	 . 98%
35	a2	234	 57% 43%
36	b2	273	 99% .
37	e2	179	 98% ..
38	g2	55	 95% 5%
39	h2	136	 100%

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Mol	Chain	Length	Quality of chain
40	i2	149	<div><div></div><div>97%</div><div></div></div>
41	l2	46	<div><div></div><div>98%</div><div></div></div>
42	o2	144	<div><div></div><div>33%</div><div></div><div></div><div>65%</div><div></div></div>
43	p	10	<div><div></div><div>70%</div><div></div><div></div><div>30%</div><div></div></div>
44	r2	117	<div><div></div><div>99%</div><div></div></div>
45	z2	85	<div><div></div><div>89%</div><div></div><div></div><div>11%</div><div></div></div>

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 188215 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	12	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	32	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	67	Total	C	N	O	S	0	0
			529	328	100	95	6		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	62	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	71	19	Total	C	N	O	P	0	0
			406	182	73	132	19		
5	72	2904	Total	C	N	O	P	0	0
			62355	27824	11468	20159	2904		

- Molecule 6 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	82	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 7 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A1	1542	Total	C	N	O	P	0	0
			33092	14767	6064	10719	1542		
7	A2	1537	Total	C	N	O	P	0	0
			32990	14721	6049	10683	1537		

- Molecule 8 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	233	Total	C	N	O	S	0	0
			1815	1145	325	337	8		
8	B2	227	Total	C	N	O	S	0	0
			1776	1123	318	327	8		

- Molecule 9 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C1	213	Total	C	N	O	S	0	0
			1665	1054	312	295	4		
9	C2	212	Total	C	N	O	S	0	0
			1658	1049	311	294	4		

- Molecule 10 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D1	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		
10	D2	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 11 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E1	158	Total	C	N	O	S	0	0
			1166	725	220	215	6		
11	E2	158	Total	C	N	O	S	0	0
			1166	725	220	215	6		

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F1	106	Total	C	N	O	S	0	0
			862	545	156	154	7		
12	F2	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G1	155	Total	C	N	O	S	0	0
			1228	767	237	220	4		
13	G2	154	Total	C	N	O	S	0	0
			1214	756	235	219	4		

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H1	129	Total	C	N	O	S	0	0
			979	616	173	184	6		
14	H2	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 15 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I1	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		
15	I2	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 16 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J1	102	Total	C	N	O	S	0	0
			817	509	157	150	1		
16	J2	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K1	115	Total	C	N	O	S	0	0
			857	528	168	158	3		
17	K2	118	Total	C	N	O	S	0	0
			884	545	175	161	3		

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L1	123	Total	C	N	O	S	0	0
			955	590	196	165	4		
18	L2	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 19 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M1	115	Total	C	N	O	S	0	0
			891	552	179	157	3		
19	M2	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N1	100	Total	C	N	O	S	0	0
			805	499	164	139	3		
20	N2	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 21 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O1	88	Total	C	N	O	S	0	0
			714	439	144	130	1		
21	O2	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P1	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q1	80	Total	C	N	O	S	0	0
			648	411	121	113	3		
23	Q2	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 24 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R1	68	Total	C	N	O	S	0	0
			566	357	110	98	1		
24	R2	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 25 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S1	83	Total	C	N	O	S	0	0
			663	424	126	111	2		
25	S2	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 26 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T1	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 27 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U1	70	Total	C	N	O	S	0	0
			590	366	125	98	1		
27	U2	70	Total	C	N	O	S	0	0
			584	363	122	98	1		

- Molecule 28 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V2	58	Total	C	N	O	P	0	0
			1250	559	237	396	58		

- Molecule 29 is a RNA chain called tRNA-Trp (P-site).

Mol	Chain	Residues	Atoms						AltConf	Trace
29	W	76	Total	C	N	O	P	S	0	0
			1630	730	286	536	76	2		

- Molecule 30 is a RNA chain called tRNA-Phe (P-site).

Mol	Chain	Residues	Atoms						AltConf	Trace
30	W1	36	Total	C	N	O	P	S	0	0
			781	352	143	248	36	2		

- Molecule 31 is a RNA chain called tRNA-Arg (E-site).

Mol	Chain	Residues	Atoms						AltConf	Trace
31	X2	77	Total	C	N	O	P	S	0	0
			1654	740	297	538	77	2		

- Molecule 32 is a RNA chain called tRNA-Val (A-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y1	36	Total	C	N	O	P	0	0
			778	348	142	252	36		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y1	34	CM0	U	variant	GB 1847302804

- Molecule 33 is a RNA chain called tRNA-Ala (A-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y2	76	Total	C	N	O	P	0	0
			1628	726	293	533	76		

- Molecule 34 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	Z1	9	Total	C	N	O	0	0
			75	49	10	16		

- Molecule 35 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a2	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 36 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b2	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 37 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e2	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 38 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	g2	52	Total	C	N	O	0	0
			427	275	78	74		

- Molecule 39 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h2	136	Total	C	N	O	S	1	0
			1085	692	209	178	6		

- Molecule 40 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i2	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 42 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o2	51	Total	C	N	O	S	0	0
			377	231	83	62	1		

- Molecule 43 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	p	10	Total	C	N	O	0	0
			76	47	18	11		

- Molecule 44 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r2	116	Total	C	N	O	0	0
			891	552	178	161		

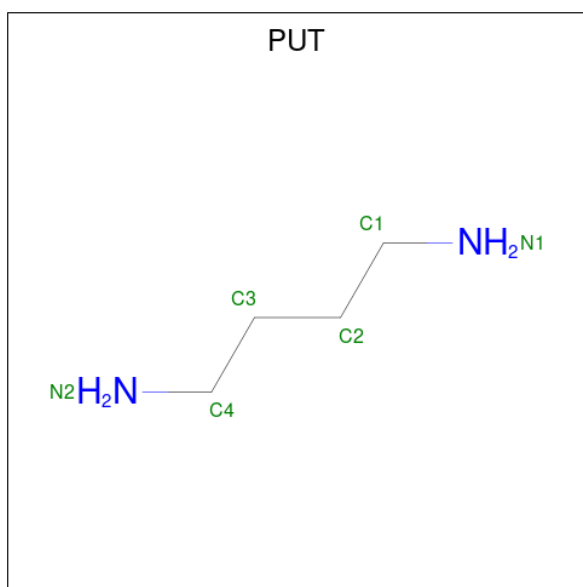
- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	z2	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 46 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	4	1	Total	Zn	0
			1	1	
46	B	1	Total	Zn	0
			1	1	

- Molecule 47 is 1,4-DIAMINOBTUTANE (three-letter code: PUT) (formula: C₄H₁₂N₂).

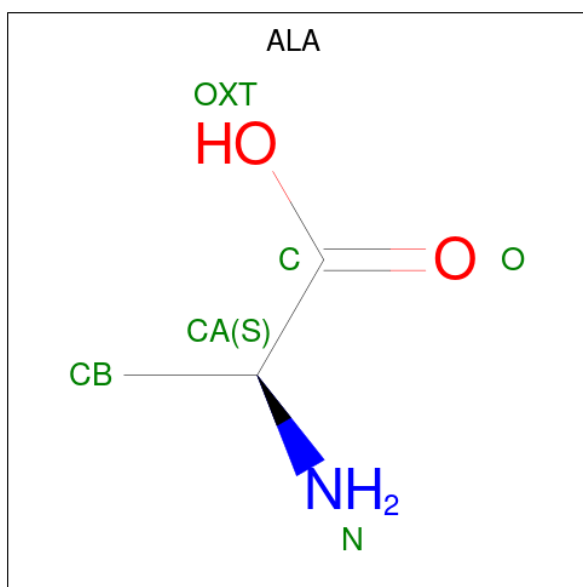


Mol	Chain	Residues	Atoms			AltConf
47	72	1	Total	C	N	0
			6	4	2	
47	72	1	Total	C	N	0
			6	4	2	

- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	72	191	Total	Mg	0
			191	191	
48	82	1	Total	Mg	0
			1	1	
48	A1	59	Total	Mg	0
			59	59	
48	A2	42	Total	Mg	0
			42	42	
48	V2	1	Total	Mg	0
			1	1	
48	W	1	Total	Mg	0
			1	1	
48	Y2	1	Total	Mg	0
			1	1	

- Molecule 49 is ALANINE (three-letter code: ALA) (formula: C₃H₇NO₂).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
49	Y2	1	5	3	1	1	0

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: 50S ribosomal protein L28

Chain 12:  96% ..



- Molecule 2: 50S ribosomal protein L30

Chain 32:  95% ..



- Molecule 3: Large ribosomal subunit protein bL31A

Chain 4:  91% . .



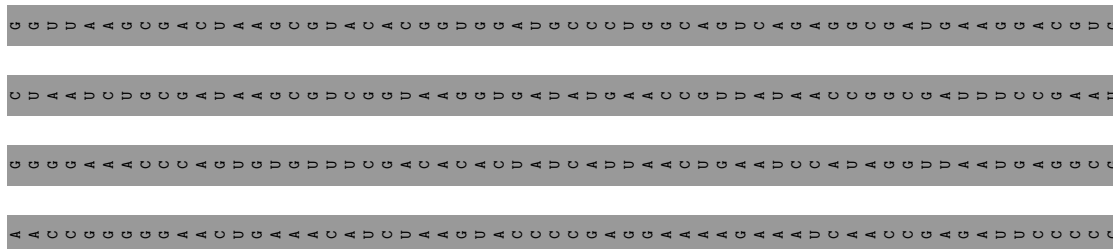
- Molecule 4: 50S ribosomal protein L35

Chain 62:  97% ..

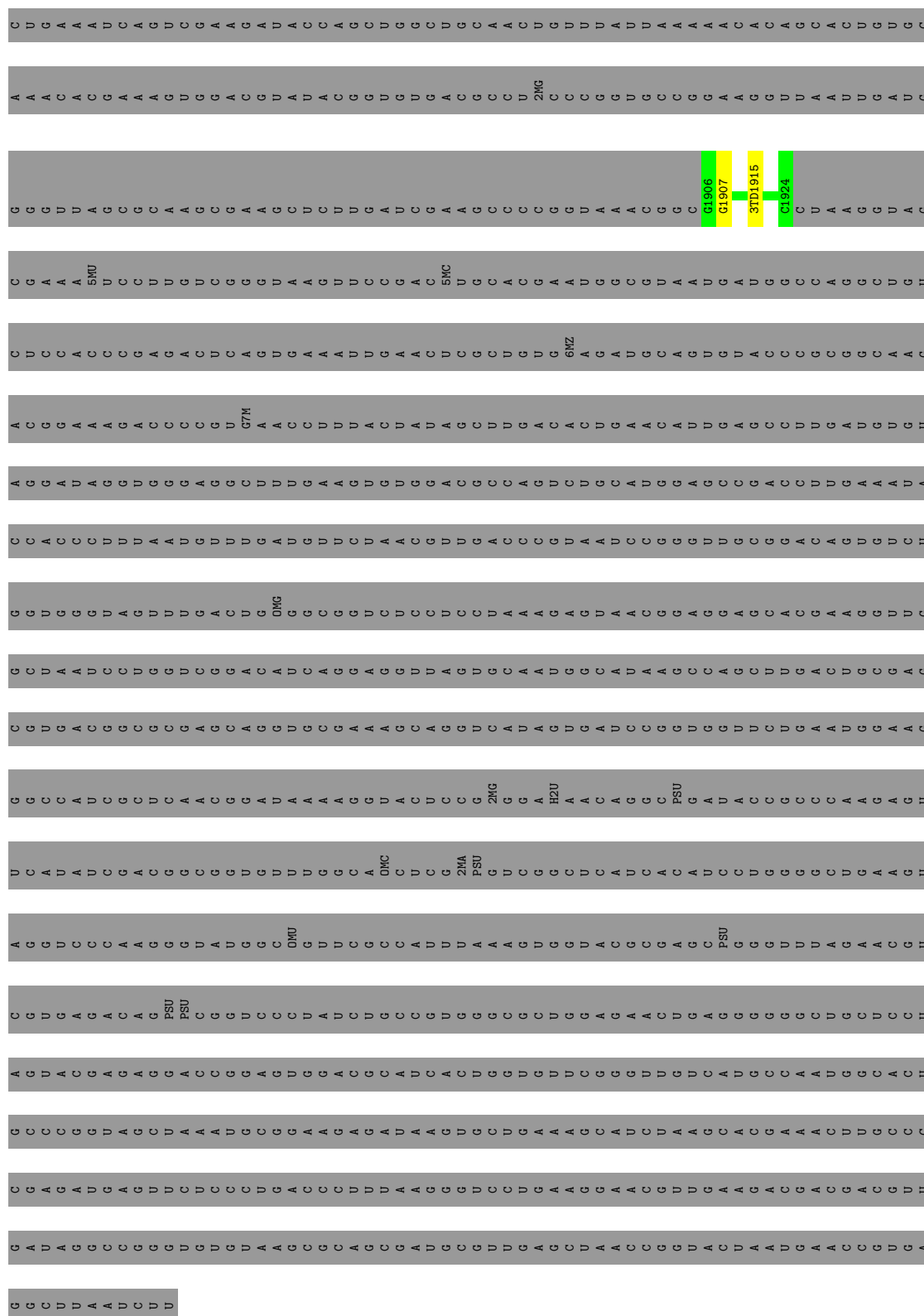


- Molecule 5: 23S ribosomal RNA


Chain 71:  99% .








- Molecule 5: 23S ribosomal RNA

Chain 72:  83% 17%

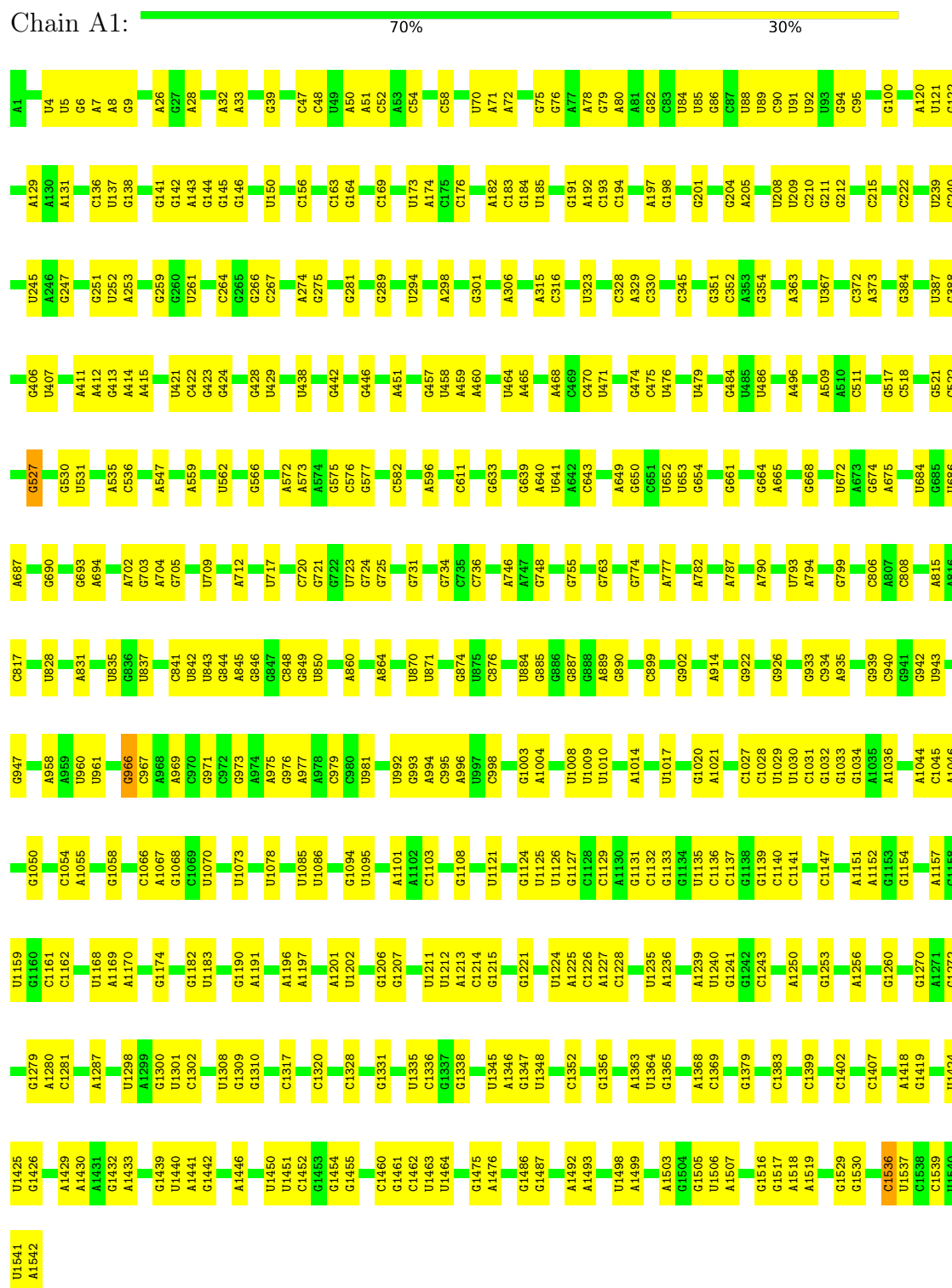
A2765	A2547	G2391	G2093	3TD1915	A1610	A1395	C1161	C961	A793	G512	A222	G1
A2778	U2548	U2402	U2098	C1920	A1618	U1396	A1169	G962	G784	A513	G248	A10
U2779	G2549	C2403	U2099	G1929	G1619	G1416	G1417	G874	G785	C527	G252	G15
U2798	U2552	A2406	A2101	G1930	U1647	G1418	C1172	A983	A789	A532	C275	U34
A2800	U2553	G2410	C2104	A1937	U1648	A1419	U1173	A983	G805	A547	U276	G43
U2818	U2554	U2423	U2109	A1938	U1649	A1420	U1174	C995	C812	A278	G277	A44
A2820	U2555	G2424	U2110	U1939	G1674	C1428	A1175	A996	A819	G548	A279	G45
A2821	G2556	A2425	U2111	U1940	C1675	A1434	G1177	U999	U827	G549	G46	G46
U2832	U2571	G2429	G2112	U1955	G1715	A1452	C1178	C1005	G830	A563	G283	G85
U2835	A2572	A2430	U2113	U1956	C1727	A1453	U1180	G1211	G830	U573	U284	U71
U2835	C2573	U2431	A2114	A1960	G1728	C1461	G1212	U1012	A845	A574	U286	A71
U2861	A2278	A2278	G2116	C1962	U1729	C1461	G1235	C1013	U846	A575	A311	A74
U2867	A2279	A2279	U2118	U1963	C1730	G1475	G1236	A1020	U847	G578	A330	G75
A2873	C2283	A2287	G2120	G1964	G1731	U1476	G1247	A1021	G888	A603	A345	A101
A2879	A2287	U2305	A2126	C1965	G1738	G1482	U1249	G1026	G859	A613	A352	A102
C2880	U2308	U2308	U2130	A1966	C1764	C1488	G1250	U1033	G869	A614	C353	A103
A2883	G2309	G2309	U2131	C1967	A1773	G1489	A1046	A1046	A878	U615	G359	G110
U2885	C2310	C2310	U2132	U1971	U1782	A1490	G1047	G1047	G883	A637	U360	A118
A2886	A2311	A2311	A2134	G1975	A1783	G1492	G1055	U1081	U884	C645	G361	A119
U2891	U2312	U2312	U2139	U1982	A1785	A1494	G1266	A1083	C885	U646	A362	U120
U2904	G2319	G2319	G2140	U1982	A1786	U1497	A1262	U1060	U887	G647	G386	A125
U2603	U2320	U2320	G2141	U1991	A1791	A1503	G1266	A1070	U888	A654	G134	G134
U2604	A2321	A2321	C2145	U1992	G1799	A1508	G1271	U1081	G891	A655	U395	U135
U2605	A2322	A2322	C2146	G1993	C1800	A1509	U1273	U1082	U895	C671	G396	U139
U2608	G2325	G2325	U2149	C1997	A1801	A1515	G1300	A1085	U896	U686	A401	G141
U2613	A2333	A2333	A2154	U2022	G1807	A1524	A1301	A1086	C902	C717	A404	A142
U2615	A2336	A2336	A2158	C2023	A1808	G1524	U1313	A1087	G907	G726	U405	U158
U2629	G2345	G2345	C2161	A2030	C1816	A1532	A1321	A1088	A910	A412	A412	G159
U2630	C2346	C2346	G2162	G2032	G1835	U1539	U1329	A1089	G917	G729	C455	C163
G2683	C2347	C2347	A2163	A2033	A1847	A1566	C1345	A1090	A917	A730	C456	U174
U2689	C2350	C2350	C2165	C2043	A1848	A1569	U1352	U1097	U919	G745	A457	G178
U2690	G2361	G2361	U2166	C2055	C1870	A1578	U1352	U1130	U919	U747	A470	G177
G2714	U2372	U2372	U2167	G2056	A1871	U1579	U1352	U1131	U931	G748	G473	A181
A2726	C2375	C2375	A2170	A2059	A1872	A1579	A1365	G1131	U932	A751	G481	A196
G2732	G2379	G2379	A2171	A2060	G1873	A1580	A1336	A1133	C937	A764	A491	A199
A2733	G2383	G2383	U2182	A2062	A1901	G1581	U1379	C1135	A941	C765	A504	G215
U2743	C2385	C2385	A2183	G2069	G1906	G1582	G1380	G1136	C946	G775	A505	A216
G2744	U2394	U2394	A2198	C2072	G1907	U1584	A1383	A1142	U955	G776	G506	A216
A2748	G2395	G2395	A2198	C2072	A1913	A1608	A1609	G1149		A782	C509	A221

• Molecule 6: 5S ribosomal RNA

Chain 82:  78% 21%

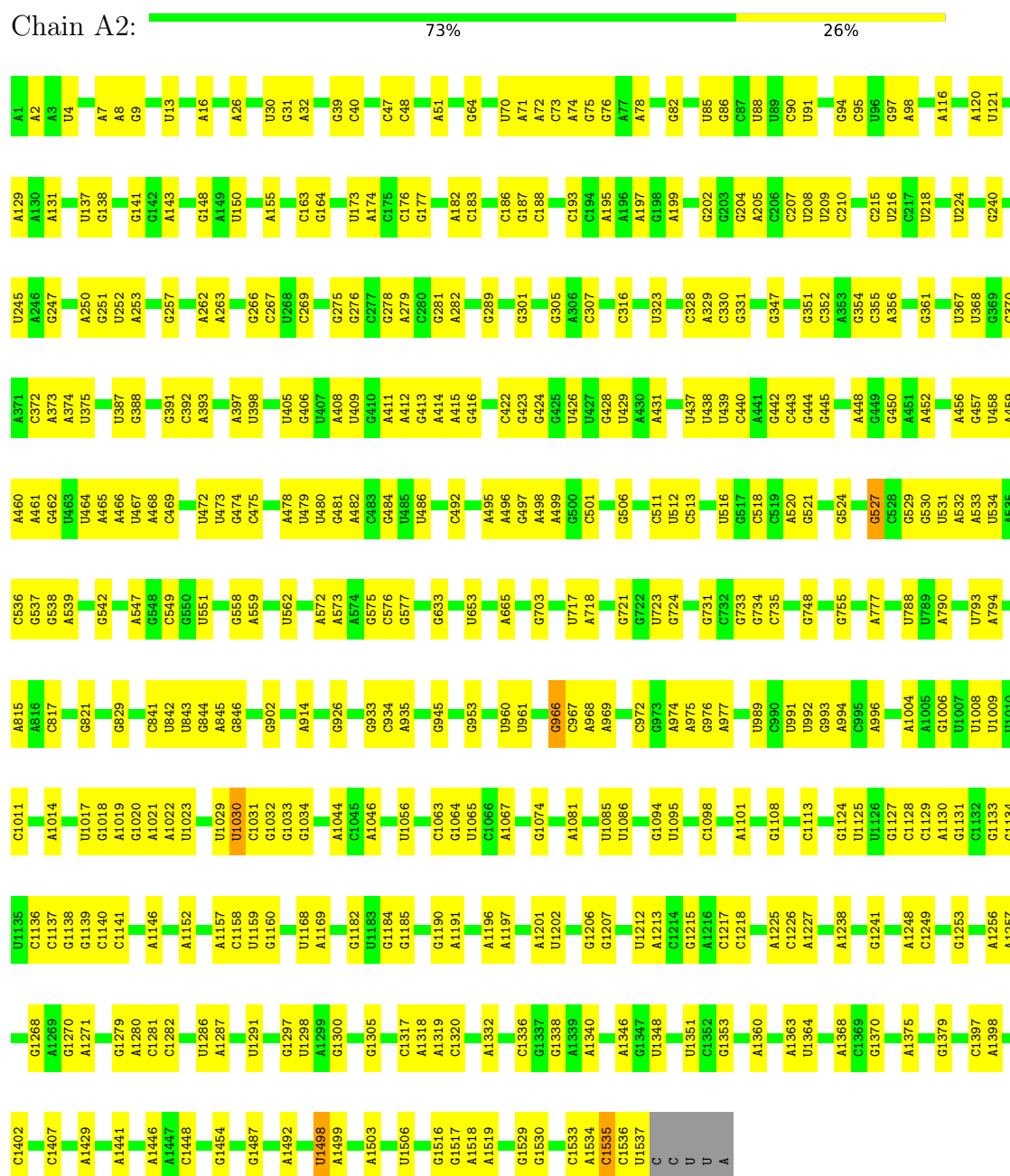


• Molecule 7: 16S ribosomal RNA



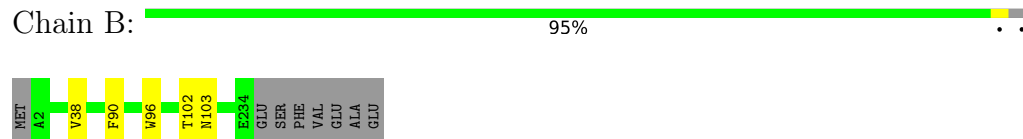
• Molecule 7: 16S ribosomal RNA

Chain A2:



- Molecule 8: Small ribosomal subunit protein uS2

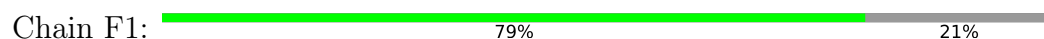
Chain B:

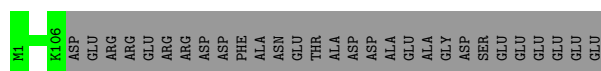


- Molecule 8: Small ribosomal subunit protein uS2

Chain B2:

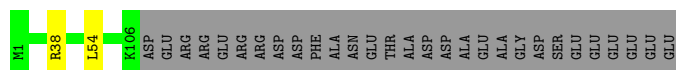






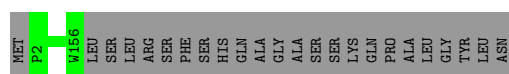
- Molecule 12: 30S ribosomal protein S6

Chain F2: 77% 21%



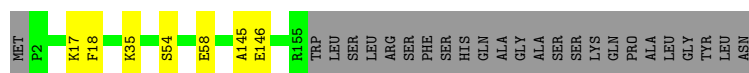
- Molecule 13: 30S ribosomal protein S7

Chain G1: 87% 13%



- Molecule 13: 30S ribosomal protein S7

Chain G2: 82% 14%



- Molecule 14: Small ribosomal subunit protein uS8

Chain H1: 99% .



- Molecule 14: Small ribosomal subunit protein uS8

Chain H2: 99% .



- Molecule 15: Small ribosomal subunit protein uS9

Chain I1: 98% .



- Molecule 15: Small ribosomal subunit protein uS9

Chain I2: 99% .



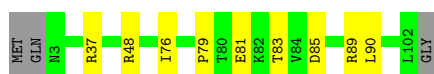
- Molecule 16: 30S ribosomal protein S10

Chain J1: 98% ..



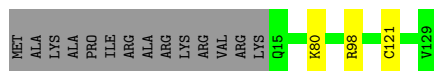
- Molecule 16: 30S ribosomal protein S10

Chain J2: 88% 9% .



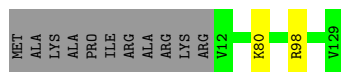
- Molecule 17: Small ribosomal subunit protein uS11

Chain K1: 87% . 11%



- Molecule 17: Small ribosomal subunit protein uS11

Chain K2: 90% . 9%



- Molecule 18: Small ribosomal subunit protein uS12

Chain L1: 98% ..



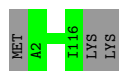
- Molecule 18: Small ribosomal subunit protein uS12

Chain L2: 99% .



- Molecule 19: Small ribosomal subunit protein uS13

Chain M1: 97% .



- Molecule 19: Small ribosomal subunit protein uS13

Chain M2: 99% .



- Molecule 20: Small ribosomal subunit protein uS14

Chain N1: 97% ..



- Molecule 20: Small ribosomal subunit protein uS14

Chain N2: 99% .



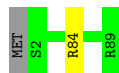
- Molecule 21: 30S ribosomal protein S15

Chain O1: 99% .



- Molecule 21: 30S ribosomal protein S15

Chain O2: 98% ..



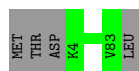
- Molecule 22: 30S ribosomal protein S16

Chain P1: 99% .



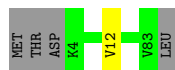
- Molecule 23: Small ribosomal subunit protein uS17

Chain Q1: 95% 5%



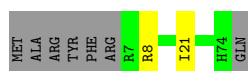
- Molecule 23: Small ribosomal subunit protein uS17

Chain Q2: 94% 5%



- Molecule 24: Small ribosomal subunit protein bS18

Chain R1: 88% 9%



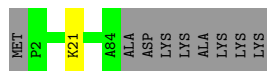
- Molecule 24: Small ribosomal subunit protein bS18

Chain R2: 93% 5%



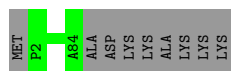
- Molecule 25: Small ribosomal subunit protein uS19

Chain S1: 89% 10%



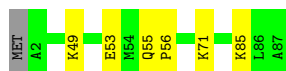
- Molecule 25: Small ribosomal subunit protein uS19

Chain S2: 90% 10%



- Molecule 26: Small ribosomal subunit protein bS20

Chain T1: 92% 7%



- Molecule 27: 30S ribosomal protein S21

Chain U1: 96%



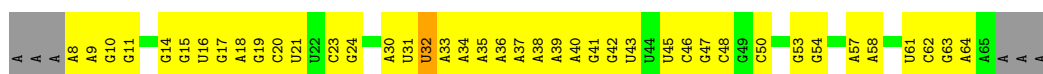
- Molecule 27: 30S ribosomal protein S21

Chain U2: 96%



- Molecule 28: messenger RNA

Chain V2: 27% 62% 9%



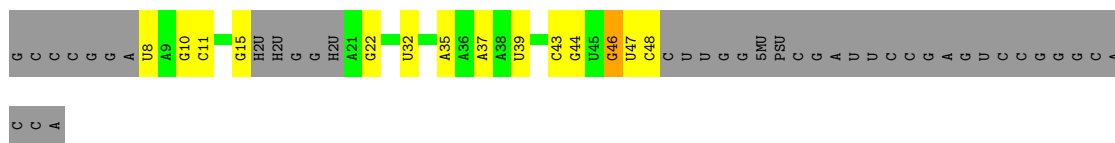
- Molecule 29: tRNA-Trp (P-site)

Chain W: 59% 30% 11%



- Molecule 30: tRNA-Phe (P-site)

Chain W1: 29% 17% 53%



- Molecule 31: tRNA-Arg (E-site)

Chain X2: 56% 38% 6%



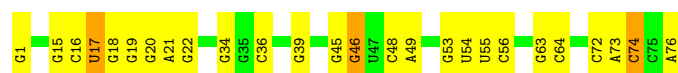
- Molecule 32: tRNA-Val (A-site)

Chain Y1: 38% 8% 53%



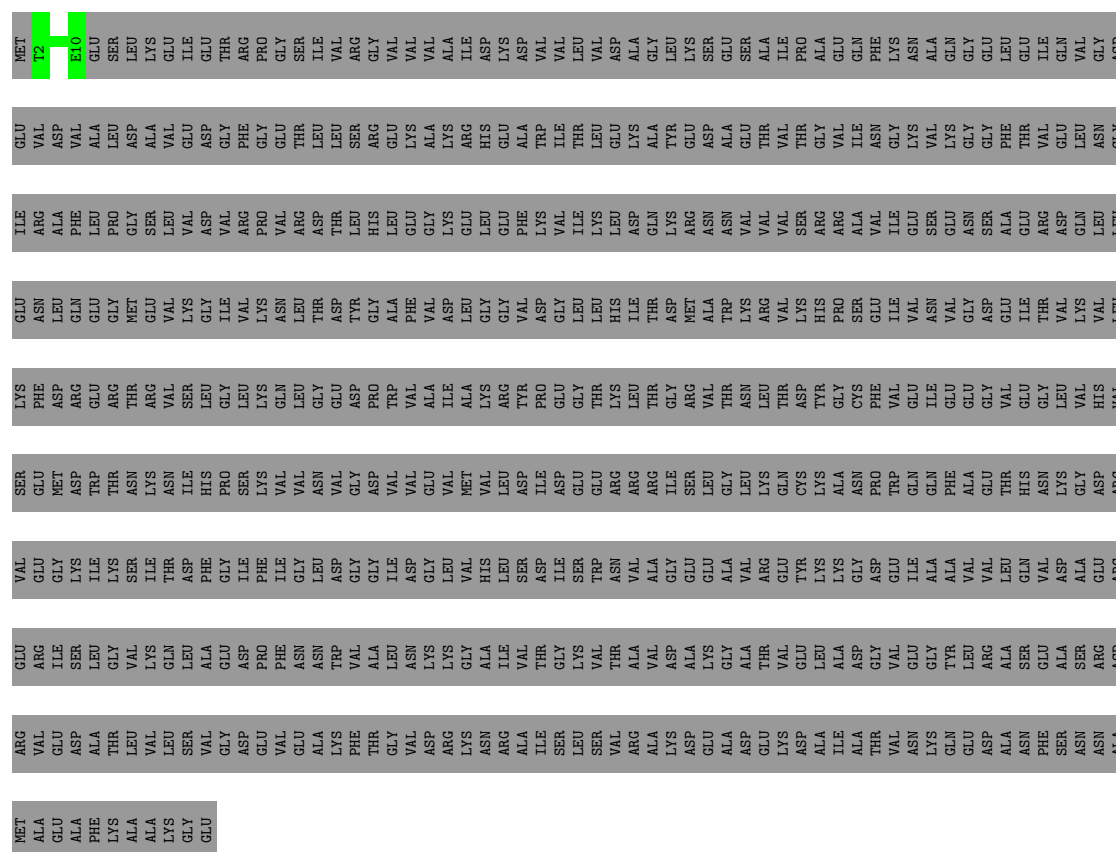
- Molecule 33: tRNA-Ala (A-site)

Chain Y2:  66% 30%



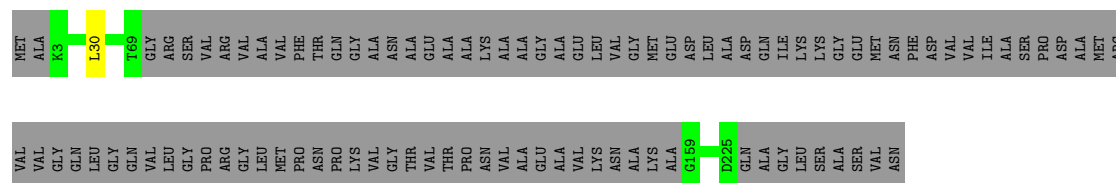
- Molecule 34: 30S ribosomal protein S1

Chain Z1:  98%



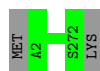
- Molecule 35: Large ribosomal subunit protein uL1

Chain a2:  57% 43%



- Molecule 36: 50S ribosomal protein L2

Chain b2:  99%



- Molecule 37: 50S ribosomal protein L5

Chain e2: 98% ..



- Molecule 38: 50S ribosomal protein L33

Chain g2: 95% 5%



- Molecule 39: 50S ribosomal protein L16

Chain h2: 100%

There are no outlier residues recorded for this chain.

- Molecule 40: 50S ribosomal protein L9

Chain i2: 97% .



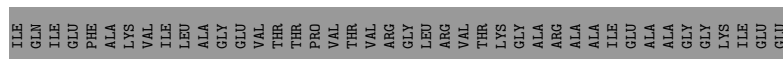
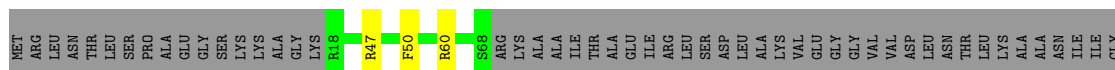
- Molecule 41: 50S ribosomal protein L34

Chain l2: 98% .



- Molecule 42: 50S ribosomal protein L15

Chain o2: 33% . 65%



- Molecule 43: Nascent chain

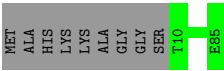
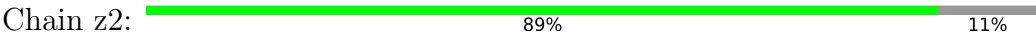
Chain p: 70% 30%



- Molecule 44: 50S ribosomal protein L18



- Molecule 45: 50S ribosomal protein L27



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	29998	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, 2MA, 3TD, PSU, ZN, 5MC, 1MG, RSP, OMG, 2MG, CM0, OMU, 5MU, PUT, 6MZ, H2U, OMC, MIA, MA6, G7M, UR3, 4SU, 3AU, 4OC, 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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	12	0.24	0/635	0.60	0/848
2	32	0.22	0/453	0.53	0/605
3	4	0.27	0/539	0.63	1/721 (0.1%)
4	62	2.74	1/513 (0.2%)	0.80	2/676 (0.3%)
5	71	0.18	0/429	0.69	0/664
5	72	0.20	1/69306 (0.0%)	0.70	16/108116 (0.0%)
6	82	0.22	1/2872 (0.0%)	0.74	2/4478 (0.0%)
7	A1	0.25	0/36794	0.77	2/57392 (0.0%)
7	A2	0.25	0/36681	0.75	5/57217 (0.0%)
8	B	0.24	0/1846	0.52	0/2488
8	B2	0.25	0/1807	0.48	0/2435
9	C1	0.25	0/1692	0.55	0/2280
9	C2	0.26	0/1685	0.56	0/2270
10	D1	0.25	0/1665	0.53	0/2227
10	D2	0.25	0/1665	0.55	0/2227
11	E1	0.27	0/1179	0.52	0/1584
11	E2	0.26	0/1179	0.53	0/1584
12	F1	0.24	0/881	0.51	0/1189
12	F2	0.25	0/881	0.50	0/1189
13	G1	0.25	0/1246	0.53	0/1672
13	G2	0.25	0/1230	0.56	0/1649
14	H1	0.26	0/989	0.53	0/1326
14	H2	0.26	0/989	0.54	0/1326
15	I1	0.25	0/1034	0.58	0/1375
15	I2	0.26	0/1048	0.58	0/1394
16	J1	0.25	0/827	0.60	0/1117
16	J2	0.35	0/813	0.75	0/1100
17	K1	0.25	0/873	0.55	0/1180
17	K2	0.26	0/900	0.56	0/1215
18	L1	0.27	0/969	0.61	0/1300
18	L2	0.26	0/969	0.61	0/1300

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	M1	0.24	0/900	0.58	0/1204
19	M2	0.24	0/919	0.58	0/1226
20	N1	0.25	0/817	0.57	0/1088
20	N2	0.25	0/817	0.58	0/1088
21	O1	0.23	0/722	0.57	0/964
21	O2	0.23	0/722	0.59	0/964
22	P1	0.26	0/659	0.61	0/884
23	Q1	0.27	0/657	0.58	0/881
23	Q2	0.25	0/657	0.56	0/881
24	R1	0.26	0/575	0.57	0/770
24	R2	0.25	0/637	0.60	0/851
25	S1	0.25	0/680	0.51	0/915
25	S2	0.26	0/680	0.52	0/915
26	T1	0.25	0/676	0.52	0/895
27	U1	0.26	0/598	0.62	0/792
27	U2	0.25	0/592	0.58	0/785
28	V2	0.32	0/1402	0.89	3/2185 (0.1%)
29	W	0.40	1/1604 (0.1%)	0.89	6/2496 (0.2%)
30	W1	0.19	0/747	0.73	0/1161
31	X2	0.52	3/1628 (0.2%)	0.85	2/2526 (0.1%)
32	Y1	0.19	0/786	0.81	0/1216
33	Y2	0.37	1/1725 (0.1%)	0.79	1/2687 (0.0%)
34	Z1	0.26	0/76	0.33	0/101
35	a2	0.24	0/1033	0.48	0/1387
36	b2	0.26	0/2121	0.60	0/2852
37	e2	0.25	0/1444	0.52	0/1937
38	g2	0.25	0/434	0.51	0/576
39	h2	0.25	0/1104	0.57	0/1474
40	i2	0.25	0/1122	0.51	0/1515
41	l2	0.24	0/380	0.63	0/498
42	o2	3.39	6/383 (1.6%)	1.19	2/501 (0.4%)
43	p	0.65	0/77	0.89	0/104
44	r2	0.25	0/901	0.59	0/1209
45	z2	0.26	0/589	0.54	0/779
All	All	0.31	14/203453 (0.0%)	0.71	42/306451 (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
10	D1	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	D2	0	1
16	J2	0	4
17	K1	0	1
17	K2	0	1
21	O2	0	1
22	P1	0	1
43	p	0	1
All	All	0	12

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	62	52	LYS	CB-CG	61.69	3.19	1.52
42	o2	50	PHE	CE2-CZ	32.50	1.99	1.37
42	o2	50	PHE	CD1-CE1	31.53	2.02	1.39
42	o2	50	PHE	CE1-CZ	29.60	1.93	1.37
42	o2	50	PHE	CD2-CE2	27.74	1.94	1.39

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	W	73	G	P-O3'-C3'	-11.35	106.08	119.70
5	72	937	C	O4'-C1'-N1	10.58	116.67	108.20
4	62	52	LYS	CB-CG-CD	10.07	137.78	111.60
4	62	52	LYS	CA-CB-CG	9.46	134.22	113.40
5	72	1939	5MU	P-O3'-C3'	-8.63	109.35	119.70

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	D1	104	ARG	Sidechain
10	D1	15	GLU	Peptide
10	D2	104	ARG	Sidechain
16	J2	37	ARG	Sidechain
16	J2	48	ARG	Sidechain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
1	12	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
2	32	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	7	35
3	4	65/70 (93%)	52 (80%)	13 (20%)	0	100	100
4	62	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
8	B	231/241 (96%)	193 (84%)	34 (15%)	4 (2%)	7	37
8	B2	225/241 (93%)	189 (84%)	36 (16%)	0	100	100
9	C1	211/233 (91%)	186 (88%)	23 (11%)	2 (1%)	14	48
9	C2	210/233 (90%)	184 (88%)	26 (12%)	0	100	100
10	D1	203/206 (98%)	181 (89%)	21 (10%)	1 (0%)	25	59
10	D2	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
11	E1	156/167 (93%)	152 (97%)	4 (3%)	0	100	100
11	E2	156/167 (93%)	152 (97%)	4 (3%)	0	100	100
12	F1	104/135 (77%)	104 (100%)	0	0	100	100
12	F2	104/135 (77%)	79 (76%)	23 (22%)	2 (2%)	6	35
13	G1	153/179 (86%)	151 (99%)	2 (1%)	0	100	100
13	G2	152/179 (85%)	122 (80%)	24 (16%)	6 (4%)	2	21
14	H1	127/130 (98%)	127 (100%)	0	0	100	100
14	H2	127/130 (98%)	127 (100%)	0	0	100	100
15	I1	125/130 (96%)	103 (82%)	22 (18%)	0	100	100
15	I2	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
16	J1	100/103 (97%)	92 (92%)	8 (8%)	0	100	100
16	J2	98/103 (95%)	86 (88%)	9 (9%)	3 (3%)	3	26
17	K1	113/129 (88%)	97 (86%)	15 (13%)	1 (1%)	14	48
17	K2	116/129 (90%)	100 (86%)	15 (13%)	1 (1%)	14	48
18	L1	121/124 (98%)	114 (94%)	6 (5%)	1 (1%)	16	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	L2	121/124 (98%)	116 (96%)	5 (4%)	0	100	100
19	M1	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
19	M2	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
20	N1	98/101 (97%)	87 (89%)	11 (11%)	0	100	100
20	N2	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
21	O1	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
21	O2	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
22	P1	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
23	Q1	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
23	Q2	78/84 (93%)	75 (96%)	2 (3%)	1 (1%)	10	41
24	R1	66/75 (88%)	60 (91%)	5 (8%)	1 (2%)	8	39
24	R2	72/75 (96%)	52 (72%)	19 (26%)	1 (1%)	9	40
25	S1	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
25	S2	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
26	T1	84/87 (97%)	79 (94%)	3 (4%)	2 (2%)	5	30
27	U1	68/71 (96%)	57 (84%)	11 (16%)	0	100	100
27	U2	68/71 (96%)	59 (87%)	7 (10%)	2 (3%)	3	27
34	Z1	7/557 (1%)	7 (100%)	0	0	100	100
35	a2	130/234 (56%)	124 (95%)	6 (5%)	0	100	100
36	b2	269/273 (98%)	264 (98%)	5 (2%)	0	100	100
37	e2	176/179 (98%)	172 (98%)	4 (2%)	0	100	100
38	g2	50/55 (91%)	50 (100%)	0	0	100	100
39	h2	135/136 (99%)	135 (100%)	0	0	100	100
40	i2	147/149 (99%)	116 (79%)	29 (20%)	2 (1%)	9	40
41	l2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
42	o2	49/144 (34%)	45 (92%)	4 (8%)	0	100	100
43	p	8/10 (80%)	4 (50%)	2 (25%)	2 (25%)	0	0
44	r2	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
45	z2	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
All	All	6096/7240 (84%)	5606 (92%)	457 (8%)	33 (0%)	27	59

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C1	15	VAL
13	G2	18	PHE
13	G2	35	LYS
13	G2	54	SER
13	G2	146	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	
1	12	67/68 (98%)	65 (97%)	2 (3%)	36	63
2	32	48/49 (98%)	47 (98%)	1 (2%)	48	71
3	4	60/62 (97%)	58 (97%)	2 (3%)	33	61
4	62	51/52 (98%)	51 (100%)	0	100	100
8	B	192/199 (96%)	191 (100%)	1 (0%)	86	93
8	B2	189/199 (95%)	184 (97%)	5 (3%)	41	65
9	C1	173/190 (91%)	172 (99%)	1 (1%)	84	92
9	C2	172/190 (90%)	171 (99%)	1 (1%)	84	92
10	D1	172/173 (99%)	169 (98%)	3 (2%)	56	75
10	D2	172/173 (99%)	171 (99%)	1 (1%)	84	92
11	E1	120/126 (95%)	120 (100%)	0	100	100
11	E2	120/126 (95%)	120 (100%)	0	100	100
12	F1	92/116 (79%)	92 (100%)	0	100	100
12	F2	92/116 (79%)	92 (100%)	0	100	100
13	G1	128/147 (87%)	128 (100%)	0	100	100
13	G2	127/147 (86%)	126 (99%)	1 (1%)	79	88
14	H1	104/105 (99%)	104 (100%)	0	100	100
14	H2	104/105 (99%)	104 (100%)	0	100	100
15	I1	105/107 (98%)	105 (100%)	0	100	100
15	I2	106/107 (99%)	106 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	J1	89/90 (99%)	88 (99%)	1 (1%)	70	83
16	J2	88/90 (98%)	86 (98%)	2 (2%)	45	68
17	K1	88/99 (89%)	87 (99%)	1 (1%)	70	83
17	K2	91/99 (92%)	91 (100%)	0	100	100
18	L1	103/104 (99%)	103 (100%)	0	100	100
18	L2	103/104 (99%)	103 (100%)	0	100	100
19	M1	93/96 (97%)	93 (100%)	0	100	100
19	M2	95/96 (99%)	95 (100%)	0	100	100
20	N1	83/84 (99%)	81 (98%)	2 (2%)	44	67
20	N2	83/84 (99%)	83 (100%)	0	100	100
21	O1	76/77 (99%)	76 (100%)	0	100	100
21	O2	76/77 (99%)	76 (100%)	0	100	100
22	P1	65/65 (100%)	65 (100%)	0	100	100
23	Q1	74/78 (95%)	74 (100%)	0	100	100
23	Q2	74/78 (95%)	74 (100%)	0	100	100
24	R1	59/65 (91%)	58 (98%)	1 (2%)	56	75
24	R2	64/65 (98%)	61 (95%)	3 (5%)	22	51
25	S1	72/79 (91%)	71 (99%)	1 (1%)	62	79
25	S2	72/79 (91%)	72 (100%)	0	100	100
26	T1	65/66 (98%)	61 (94%)	4 (6%)	15	44
27	U1	60/61 (98%)	58 (97%)	2 (3%)	33	61
27	U2	59/61 (97%)	59 (100%)	0	100	100
34	Z1	8/461 (2%)	8 (100%)	0	100	100
35	a2	110/181 (61%)	109 (99%)	1 (1%)	75	87
36	b2	216/218 (99%)	216 (100%)	0	100	100
37	e2	149/150 (99%)	147 (99%)	2 (1%)	65	81
38	g2	47/49 (96%)	47 (100%)	0	100	100
39	h2	110/109 (101%)	110 (100%)	0	100	100
40	i2	114/114 (100%)	111 (97%)	3 (3%)	41	65
41	l2	38/38 (100%)	37 (97%)	1 (3%)	41	65
42	o2	35/103 (34%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	p	5/5 (100%)	5 (100%)	0	100	100
44	r2	86/87 (99%)	86 (100%)	0	100	100
45	z2	58/63 (92%)	58 (100%)	0	100	100
All	All	5102/5932 (86%)	5060 (99%)	42 (1%)	77	88

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	S1	21	LYS
35	a2	30	LEU
26	T1	49	LYS
26	T1	85	LYS
37	e2	178	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
20	N2	43	ASN
42	o2	38	GLN
44	r2	38	GLN
42	o2	35	HIS
13	G2	86	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	V2	58/64 (90%)	38 (65%)	8 (13%)
29	W	74/76 (97%)	23 (31%)	4 (5%)
30	W1	33/76 (43%)	8 (24%)	2 (6%)
31	X2	73/77 (94%)	28 (38%)	5 (6%)
32	Y1	32/76 (42%)	4 (12%)	2 (6%)
33	Y2	75/76 (98%)	23 (30%)	2 (2%)
5	71	17/2904 (0%)	1 (5%)	0
5	72	2899/2904 (99%)	455 (15%)	32 (1%)
6	82	119/120 (99%)	21 (17%)	4 (3%)
7	A1	1538/1542 (99%)	449 (29%)	37 (2%)
7	A2	1533/1542 (99%)	399 (26%)	33 (2%)
All	All	6451/9457 (68%)	1449 (22%)	129 (1%)

5 of 1449 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	71	1907	G
5	72	10	A
5	72	15	G
5	72	34	U
5	72	44	A

5 of 129 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	W	18	G
30	W1	43	C
7	A1	421	U
7	A1	412	A
31	X2	22	A

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

73 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	MA6	A2	1518	7	18,26,27	1.07	2 (11%)	19,38,41	3.37	3 (15%)
7	UR3	A2	1498	7	19,22,23	2.73	8 (42%)	26,32,35	1.28	1 (3%)
31	RSP	X2	33	31	17,21,22	4.14	7 (41%)	22,30,33	0.77	0
5	OMG	72	2251	29,5	18,26,27	2.84	7 (38%)	19,38,41	1.52	4 (21%)
31	G7M	X2	47	31	20,26,27	2.81	7 (35%)	17,39,42	1.20	1 (5%)
30	4SU	W1	8	30	18,21,22	3.77	7 (38%)	26,30,33	2.20	4 (15%)
5	5MU	72	747	5	19,22,23	0.25	0	28,32,35	0.67	0
31	PSU	X2	56	31	18,21,22	0.88	1 (5%)	22,30,33	0.73	0
30	PSU	W1	39	30	18,21,22	4.66	8 (44%)	22,30,33	1.82	5 (22%)
7	MA6	A1	1518	7	18,26,27	1.07	2 (11%)	19,38,41	3.43	3 (15%)
7	UR3	A1	1498	7	19,22,23	2.74	8 (42%)	26,32,35	1.28	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	OMU	72	2552	5	19,22,23	3.21	8 (42%)	26,31,34	1.69	5 (19%)
5	2MG	72	2445	5	18,26,27	2.81	7 (38%)	16,38,41	1.40	3 (18%)
31	H2U	X2	17	31	18,21,22	3.09	5 (27%)	21,30,33	1.98	5 (23%)
7	2MG	A2	966	7	18,26,27	2.83	7 (38%)	16,38,41	1.34	3 (18%)
30	MIA	W1	37	30	24,31,32	2.34	3 (12%)	26,44,47	2.63	7 (26%)
7	2MG	A1	966	7	18,26,27	2.84	7 (38%)	16,38,41	1.41	3 (18%)
7	2MG	A2	1516	7	18,26,27	2.81	7 (38%)	16,38,41	1.37	3 (18%)
33	5MU	Y2	54	33	19,22,23	0.23	0	28,32,35	0.25	0
5	PSU	72	746	5,48	18,21,22	0.84	1 (5%)	22,30,33	0.92	1 (4%)
32	6MZ	Y1	37	32	18,25,26	2.06	4 (22%)	16,36,39	2.41	4 (25%)
5	PSU	72	2605	5	18,21,22	4.64	8 (44%)	22,30,33	1.82	5 (22%)
30	G7M	W1	46	30	20,26,27	2.81	7 (35%)	17,39,42	1.14	1 (5%)
29	PSU	W	55	29	18,21,22	0.88	1 (5%)	22,30,33	0.73	0
7	MA6	A2	1519	7	18,26,27	1.07	2 (11%)	19,38,41	3.44	3 (15%)
5	5MU	72	1939	5	19,22,23	0.28	0	28,32,35	0.24	0
30	PSU	W1	32	30	18,21,22	4.66	8 (44%)	22,30,33	1.82	5 (22%)
33	PSU	Y2	55	33	18,21,22	0.88	1 (5%)	22,30,33	0.65	0
5	PSU	72	2457	5	18,21,22	4.65	8 (44%)	22,30,33	1.89	5 (22%)
7	2MG	A1	1516	7	18,26,27	2.84	7 (38%)	16,38,41	1.36	3 (18%)
5	PSU	72	2604	5	18,21,22	4.64	8 (44%)	22,30,33	1.85	5 (22%)
7	2MG	A2	1207	7	18,26,27	2.82	7 (38%)	16,38,41	1.36	3 (18%)
7	G7M	A2	527	7	20,26,27	2.79	8 (40%)	17,39,42	1.02	1 (5%)
5	5MC	72	1962	5	18,22,23	4.01	7 (38%)	26,32,35	1.07	2 (7%)
5	PSU	72	955	5	18,21,22	4.65	8 (44%)	22,30,33	1.89	5 (22%)
29	H2U	W	17	29	18,21,22	3.06	5 (27%)	21,30,33	2.00	5 (23%)
7	2MG	A1	1207	7	18,26,27	2.83	7 (38%)	16,38,41	1.34	3 (18%)
7	4OC	A2	1402	7	20,23,24	3.24	8 (40%)	26,32,35	0.91	1 (3%)
7	4OC	A1	1402	7	20,23,24	3.23	8 (40%)	26,32,35	0.93	1 (3%)
29	PSU	W	32	29	18,21,22	4.61	8 (44%)	22,30,33	1.91	5 (22%)
7	5MC	A2	1407	7	18,22,23	4.01	7 (38%)	26,32,35	0.96	2 (7%)
7	5MC	A2	967	7	18,22,23	4.03	7 (38%)	26,32,35	1.01	2 (7%)
33	H2U	Y2	17	33	18,21,22	3.07	5 (27%)	21,30,33	2.03	5 (23%)
7	5MC	A1	1407	7	18,22,23	4.01	7 (38%)	26,32,35	1.01	2 (7%)
5	3TD	72	1915	5	19,22,23	4.05	7 (36%)	21,32,35	1.76	3 (14%)
29	G7M	W	46	29	20,26,27	2.80	7 (35%)	17,39,42	1.13	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	H2U	X2	21	31	18,21,22	3.08	5 (27%)	21,30,33	2.02	5 (23%)
7	G7M	A1	527	7	20,26,27	2.79	8 (40%)	17,39,42	1.03	1 (5%)
5	1MG	72	745	5	18,26,27	2.75	6 (33%)	19,39,42	1.42	3 (15%)
5	PSU	72	2504	5,48	18,21,22	4.67	8 (44%)	22,30,33	1.85	5 (22%)
29	5MU	W	54	29	19,22,23	0.27	0	28,32,35	0.49	0
5	6MZ	72	2030	5	18,25,26	2.07	4 (22%)	16,36,39	2.32	3 (18%)
31	4SU	X2	8	31	18,21,22	3.79	7 (38%)	26,30,33	2.29	4 (15%)
5	2MA	72	2503	5,48	19,25,26	3.56	6 (31%)	21,37,40	3.65	4 (19%)
7	5MC	A1	967	7	18,22,23	4.03	7 (38%)	26,32,35	1.01	2 (7%)
5	OMC	72	2498	5,48	19,22,23	3.31	8 (42%)	26,31,34	0.80	0
33	G7M	Y2	46	33	20,26,27	2.81	8 (40%)	17,39,42	1.08	1 (5%)
29	4SU	W	8	29	18,21,22	3.78	7 (38%)	26,30,33	2.26	5 (19%)
5	2MG	72	1835	5	18,26,27	2.81	7 (38%)	16,38,41	1.41	3 (18%)
7	MA6	A1	1519	7	18,26,27	1.06	2 (11%)	19,38,41	3.41	3 (15%)
29	H2U	W	16	29	18,21,22	3.05	5 (27%)	21,30,33	2.00	5 (23%)
5	6MZ	72	1618	5	18,25,26	2.03	2 (11%)	16,36,39	2.28	4 (25%)
5	PSU	72	2580	5	18,21,22	4.63	8 (44%)	22,30,33	1.86	6 (27%)
31	2MA	X2	38	31	19,25,26	3.64	6 (31%)	21,37,40	3.63	3 (14%)
31	3AU	X2	48	31	24,28,29	2.82	8 (33%)	33,40,43	1.29	3 (9%)
5	H2U	72	2449	5,48	18,21,22	3.05	5 (27%)	21,30,33	2.04	5 (23%)
31	5MU	X2	55	31	19,22,23	0.25	0	28,32,35	0.38	0
32	CM0	Y1	34	32	23,26,27	3.72	6 (26%)	27,37,40	1.54	2 (7%)
29	H2U	W	20	29	18,21,22	3.05	5 (27%)	21,30,33	2.02	5 (23%)
32	7MG	Y1	46	32	22,26,27	3.88	10 (45%)	29,39,42	2.07	9 (31%)
5	G7M	72	2069	5	20,26,27	2.78	7 (35%)	17,39,42	1.06	1 (5%)
29	MIA	W	37	29	24,31,32	2.30	3 (12%)	26,44,47	2.49	7 (26%)
5	3TD	71	1915	5	19,22,23	4.07	7 (36%)	21,32,35	1.66	2 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MA6	A2	1518	7	-	0/7/29/30	0/3/3/3
7	UR3	A2	1498	7	-	2/7/25/26	0/2/2/2
31	RSP	X2	33	31	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	OMG	72	2251	29,5	-	3/5/27/28	0/3/3/3
31	G7M	X2	47	31	-	3/3/25/26	0/3/3/3
30	4SU	W1	8	30	-	2/7/25/26	0/2/2/2
5	5MU	72	747	5	-	0/7/25/26	0/2/2/2
31	PSU	X2	56	31	-	1/7/25/26	0/2/2/2
30	PSU	W1	39	30	-	0/7/25/26	0/2/2/2
7	MA6	A1	1518	7	-	3/7/29/30	0/3/3/3
7	UR3	A1	1498	7	-	2/7/25/26	0/2/2/2
5	OMU	72	2552	5	-	0/9/27/28	0/2/2/2
5	2MG	72	2445	5	-	0/5/27/28	0/3/3/3
31	H2U	X2	17	31	-	6/7/38/39	0/2/2/2
7	2MG	A2	966	7	-	0/5/27/28	0/3/3/3
30	MIA	W1	37	30	-	6/11/33/34	0/3/3/3
7	2MG	A1	966	7	-	0/5/27/28	0/3/3/3
7	2MG	A2	1516	7	-	0/5/27/28	0/3/3/3
33	5MU	Y2	54	33	-	0/7/25/26	0/2/2/2
5	PSU	72	746	5,48	-	3/7/25/26	0/2/2/2
32	6MZ	Y1	37	32	-	2/5/27/28	0/3/3/3
5	PSU	72	2605	5	-	0/7/25/26	0/2/2/2
30	G7M	W1	46	30	-	3/3/25/26	0/3/3/3
29	PSU	W	55	29	-	0/7/25/26	0/2/2/2
7	MA6	A2	1519	7	-	2/7/29/30	0/3/3/3
5	5MU	72	1939	5	-	0/7/25/26	0/2/2/2
30	PSU	W1	32	30	-	0/7/25/26	0/2/2/2
33	PSU	Y2	55	33	-	0/7/25/26	0/2/2/2
5	PSU	72	2457	5	-	0/7/25/26	0/2/2/2
7	2MG	A1	1516	7	-	0/5/27/28	0/3/3/3
5	PSU	72	2604	5	-	0/7/25/26	0/2/2/2
7	2MG	A2	1207	7	-	0/5/27/28	0/3/3/3
7	G7M	A2	527	7	-	3/3/25/26	0/3/3/3
5	5MC	72	1962	5	-	0/7/25/26	0/2/2/2
5	PSU	72	955	5	-	0/7/25/26	0/2/2/2
29	H2U	W	17	29	-	1/7/38/39	0/2/2/2
7	2MG	A1	1207	7	-	0/5/27/28	0/3/3/3
7	4OC	A2	1402	7	-	1/9/29/30	0/2/2/2
7	4OC	A1	1402	7	-	0/9/29/30	0/2/2/2
29	PSU	W	32	29	-	0/7/25/26	0/2/2/2
7	5MC	A2	1407	7	-	0/7/25/26	0/2/2/2
7	5MC	A2	967	7	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	H2U	Y2	17	33	-	7/7/38/39	0/2/2/2
7	5MC	A1	1407	7	-	0/7/25/26	0/2/2/2
5	3TD	72	1915	5	-	2/7/25/26	0/2/2/2
29	G7M	W	46	29	-	2/3/25/26	0/3/3/3
31	H2U	X2	21	31	-	1/7/38/39	0/2/2/2
7	G7M	A1	527	7	-	1/3/25/26	0/3/3/3
5	1MG	72	745	5	-	0/3/25/26	0/3/3/3
5	PSU	72	2504	5,48	-	0/7/25/26	0/2/2/2
29	5MU	W	54	29	-	2/7/25/26	0/2/2/2
5	6MZ	72	2030	5	-	3/5/27/28	0/3/3/3
31	4SU	X2	8	31	-	2/7/25/26	0/2/2/2
5	2MA	72	2503	5,48	-	0/3/25/26	0/3/3/3
7	5MC	A1	967	7	-	0/7/25/26	0/2/2/2
5	OMC	72	2498	5,48	-	2/9/27/28	0/2/2/2
33	G7M	Y2	46	33	-	2/3/25/26	0/3/3/3
29	4SU	W	8	29	-	2/7/25/26	0/2/2/2
5	2MG	72	1835	5	-	0/5/27/28	0/3/3/3
7	MA6	A1	1519	7	-	3/7/29/30	0/3/3/3
29	H2U	W	16	29	-	1/7/38/39	0/2/2/2
5	6MZ	72	1618	5	-	4/5/27/28	0/3/3/3
5	PSU	72	2580	5	-	0/7/25/26	0/2/2/2
31	2MA	X2	38	31	-	3/3/25/26	0/3/3/3
31	3AU	X2	48	31	-	4/16/34/35	0/2/2/2
5	H2U	72	2449	5,48	-	0/7/38/39	0/2/2/2
31	5MU	X2	55	31	-	3/7/25/26	0/2/2/2
32	CM0	Y1	34	32	-	2/12/30/31	0/2/2/2
29	H2U	W	20	29	-	2/7/38/39	0/2/2/2
32	7MG	Y1	46	32	-	1/7/37/38	0/3/3/3
5	G7M	72	2069	5	-	2/3/25/26	0/3/3/3
29	MIA	W	37	29	-	1/11/33/34	0/3/3/3
5	3TD	71	1915	5	-	1/7/25/26	0/2/2/2

The worst 5 of 417 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	Y1	34	CM0	C6-C5	12.68	1.48	1.34
5	72	1915	3TD	C6-C5	12.65	1.50	1.35
5	71	1915	3TD	C6-C5	12.64	1.50	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	W1	39	PSU	C6-C5	12.18	1.49	1.35
5	72	2504	PSU	C6-C5	12.15	1.49	1.35

The worst 5 of 216 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	72	2503	2MA	C1'-N9-C4	14.99	152.98	126.64
31	X2	38	2MA	C1'-N9-C4	14.78	152.60	126.64
7	A2	1519	MA6	N1-C6-N6	-12.61	103.78	117.06
7	A1	1519	MA6	N1-C6-N6	-12.36	104.05	117.06
7	A2	1518	MA6	N1-C6-N6	-12.30	104.11	117.06

There are no chirality outliers.

5 of 98 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A1	1518	MA6	C5-C6-N6-C9
7	A1	1518	MA6	C5-C6-N6-C10
7	A1	1519	MA6	C3'-C4'-C5'-O5'
7	A2	1402	4OC	C1'-C2'-O2'-CM2
7	A2	1498	UR3	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 301 ligands modelled in this entry, 298 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	PUT	72	3002	-	5,5,5	0.25	0	4,4,4	0.55	0
47	PUT	72	3001	-	5,5,5	0.25	0	4,4,4	0.51	0
49	ALA	Y2	102	33	3,4,5	0.53	0	2,4,6	1.62	1 (50%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	PUT	72	3002	-	-	0/3/3/3	-
47	PUT	72	3001	-	-	1/3/3/3	-
49	ALA	Y2	102	33	-	0/0/2/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	Y2	102	ALA	O-C-CA	-2.29	117.03	124.28

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
47	72	3001	PUT	C1-C2-C3-C4

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.