



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:35 PM UTC

PDB ID : 6WDJ / pdb_00006wdj
EMDB ID : EMD-21638
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Non-cognate Structure V-A1)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

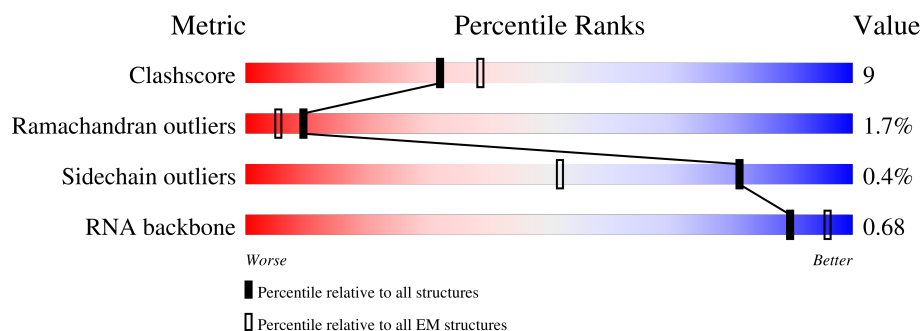
1 Overall quality at a glance

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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	b	271	76% 23% .
2	c	209	69% 30%
3	d	201	75% 24%
4	e	177	70% 29% .
5	f	176	78% 22% .
6	g	149	68% 29% .
7	h	131	55% 37% 7% .

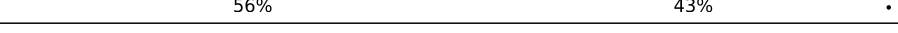
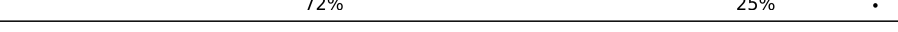
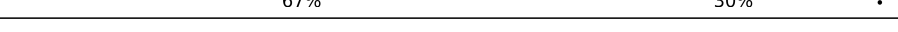
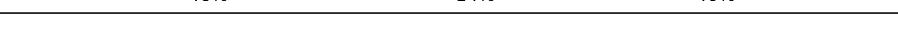
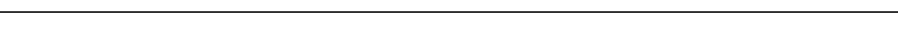
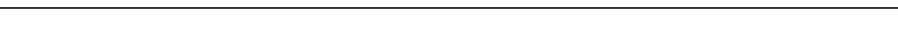
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Mol	Chain	Length	Quality of chain
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	
29	E	64	
30	F	38	
31	G	225	
32	H	206	

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Mol	Chain	Length	Quality of chain
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	
54	2	120	
55	5	77	
55	6	77	
56	4	18	

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Mol	Chain	Length	Quality of chain
57	7	76	72% 22% 5%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 150211 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

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

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	t	93	Total	C	N	O	S	0
			739	466	139	132	2	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

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

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

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

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C	50	Total	C	N	O	0	0
			410	263	75	72		

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

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

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

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	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
2	120	A	-	insertion	GB 1266961702

- | Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|---------|---------|-------|
| 55 | 5 | 77 | Total
1640 | C
732 | N
297 | O
535 | P
76 | 0 | 0 |
| 55 | 6 | 77 | Total
1640 | C
732 | N
297 | O
535 | P
76 | 0 | 0 |

- | Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|---------|----------|---------|---------|-------|
| 56 | 4 | 18 | Total
388 | C
175 | N
77 | O
119 | P
17 | 0 | 0 |

- | Mol | Chain | Residues | Atoms | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|---|
| 57 | 7 | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1619 | 723 | 290 | 531 | 75 | | |

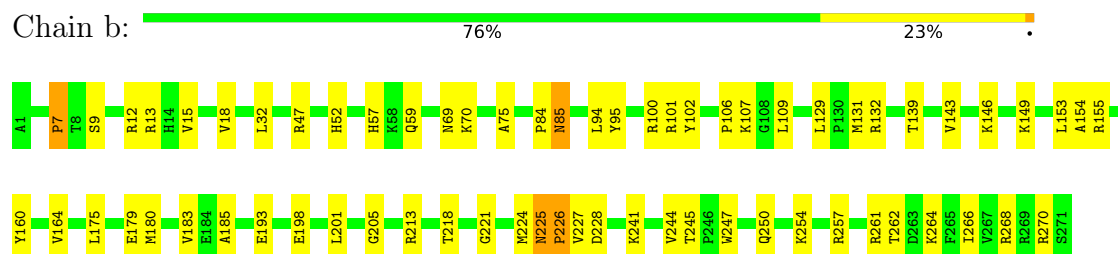
- FME
-
- Chemical structure diagram of FME (Farnesyl pyrophosphate). The structure shows a central carbon atom bonded to a hydroxyl group (OXT), a carboxylate group (CA(S)), a sulfonate group (S), and a methyl group (CB). The sulfonate group is further bonded to a chain (CE) and a sulfur atom (SD). The carboxylate group is bonded to a nitrogen atom (N) which is part of a pyrophosphate group (O1).

Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

3 Residue-property plots

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.

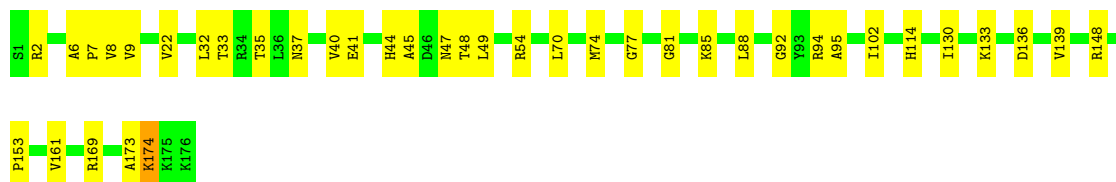
• Molecule 1: 50S ribosomal protein L2





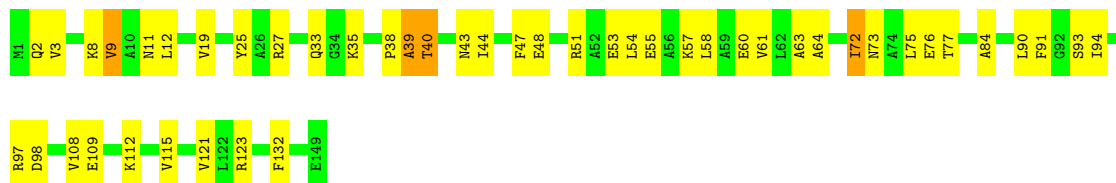
• Molecule 5: 50S ribosomal protein L6

Chain f: 78% 22% .



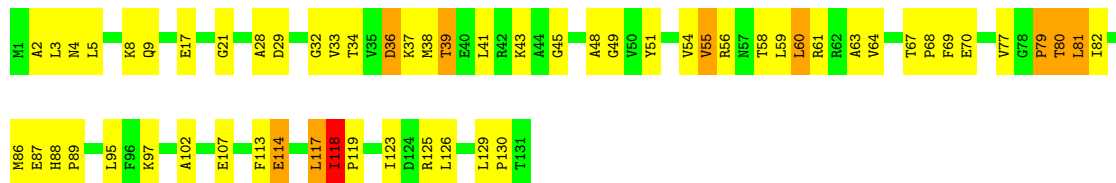
• Molecule 6: 50S ribosomal protein L9

Chain g: 68% 29% .



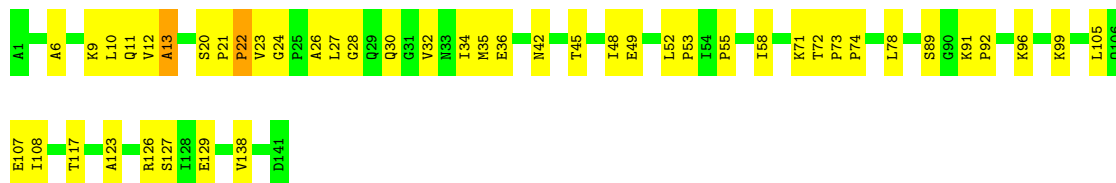
• Molecule 7: 50S ribosomal protein L10

Chain h: 55% 37% 7% .



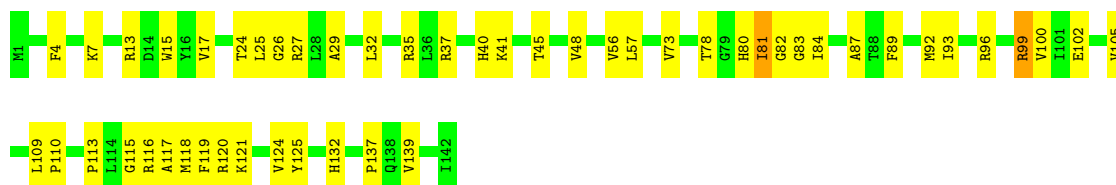
• Molecule 8: 50S ribosomal protein L11

Chain i: 67% 31% .



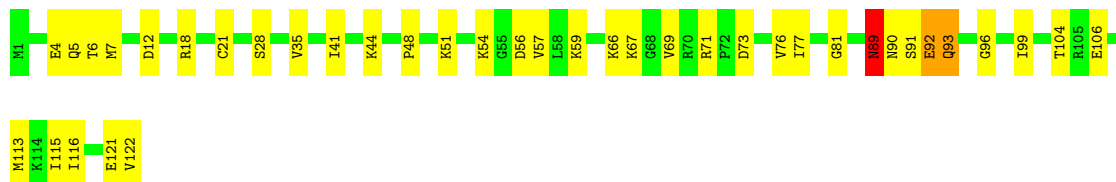
• Molecule 9: 50S ribosomal protein L13

Chain j: 65% 34% .



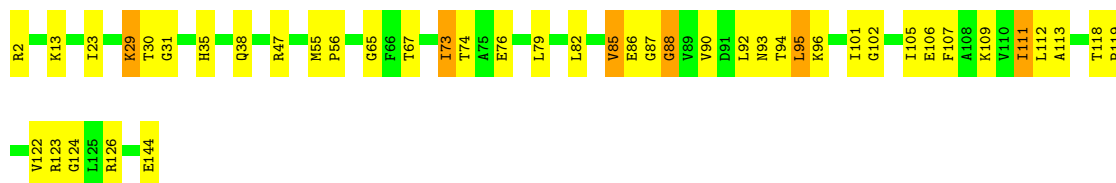
- Molecule 10: 50S ribosomal protein L14

Chain k: 68% 30% ..



- Molecule 11: 50S ribosomal protein L15

Chain l: 69% 27% .



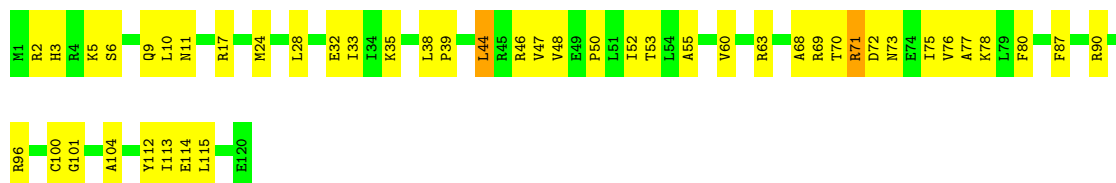
- Molecule 12: 50S ribosomal protein L16

Chain m: 74% 25% .



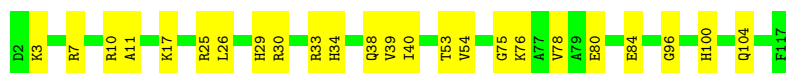
- Molecule 13: 50S ribosomal protein L17

Chain n: 62% 37% .

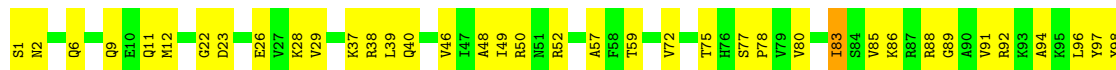


- Molecule 14: 50S ribosomal protein L18

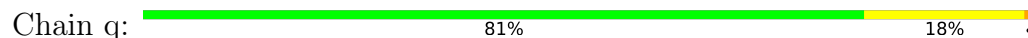
Chain o: 79% 21%



- Molecule 15: 50S ribosomal protein L19



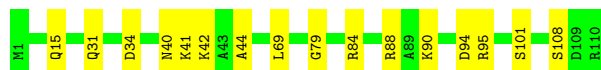
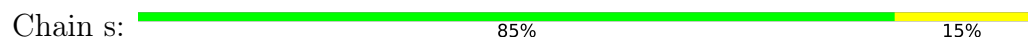
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25

Chain v:  65% 35%



- Molecule 22: 50S ribosomal protein L27

Chain w:  72% 28%



- Molecule 23: 50S ribosomal protein L28

Chain x:  74% 25%



- Molecule 24: 50S ribosomal protein L29

Chain y:  73% 25%



- Molecule 25: 50S ribosomal protein L30

Chain z:  74% 26%



- Molecule 26: 50S ribosomal protein L32

Chain B:  68% 32%



- Molecule 27: 50S ribosomal protein L33

Chain C:  70% 28%



- Molecule 28: 50S ribosomal protein L34

Chain D:  80% 15% .



- Molecule 29: 50S ribosomal protein L35

Chain E:  64% 34% .



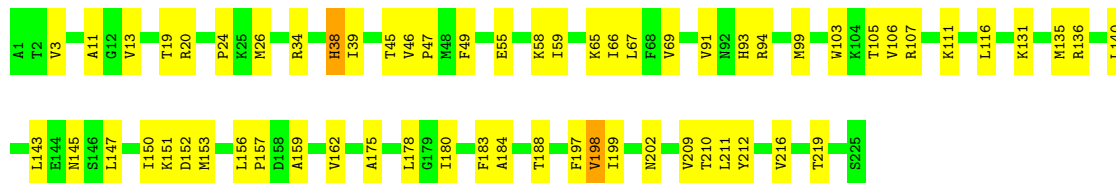
- Molecule 30: 50S ribosomal protein L36

Chain F:  68% 29% .



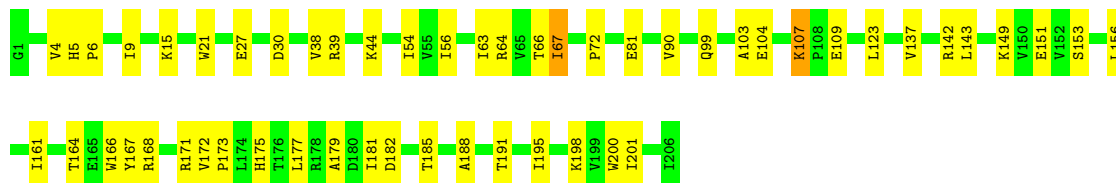
- Molecule 31: 30S ribosomal protein S2

Chain G:  72% 27% .



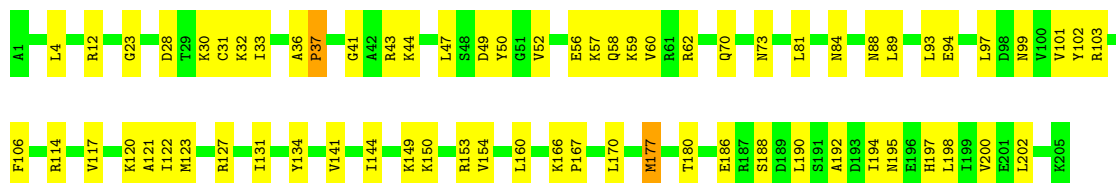
- Molecule 32: 30S ribosomal protein S3

Chain H:  74% 25% .

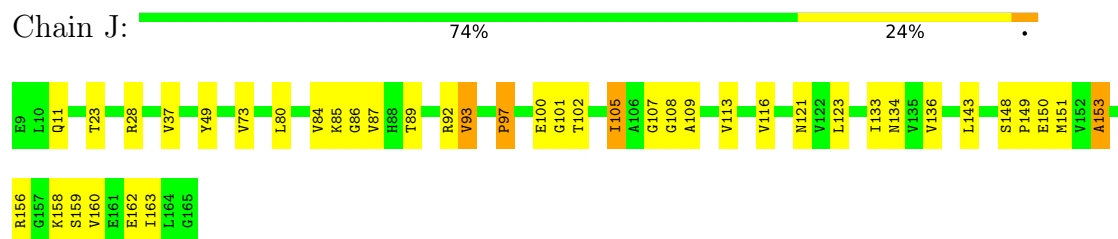


- Molecule 33: 30S ribosomal protein S4

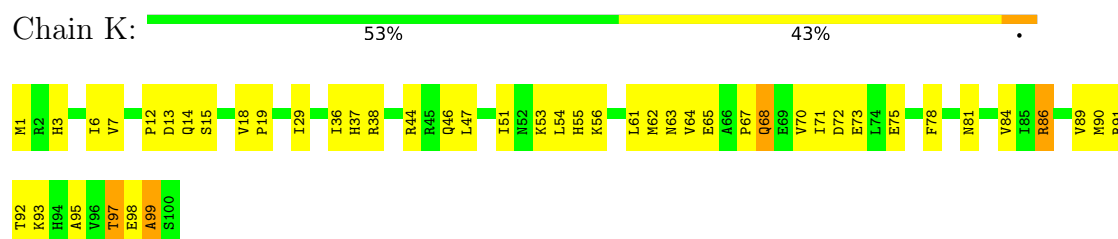
Chain I:  67% 32% .



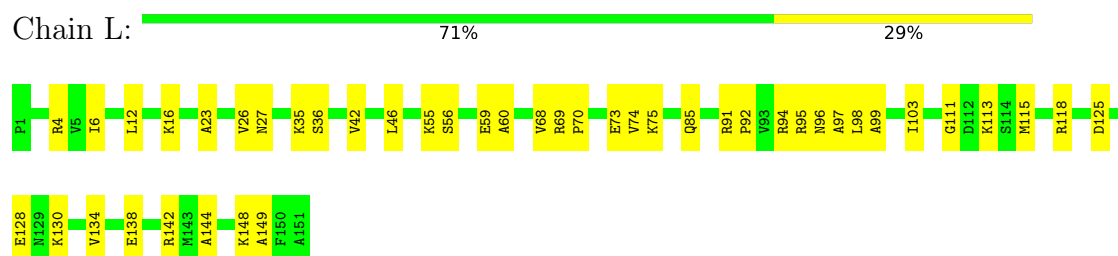
- Molecule 34: 30S ribosomal protein S5



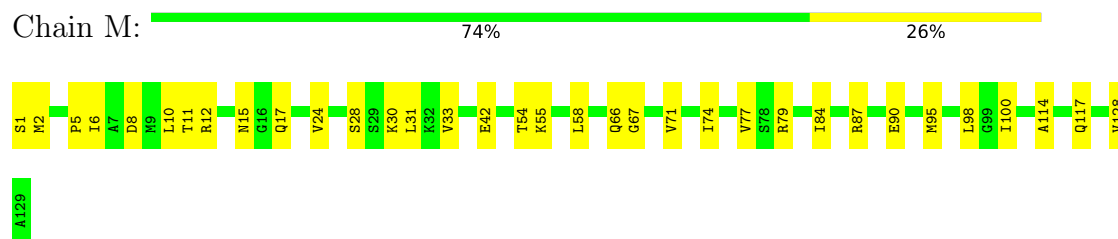
- Molecule 35: 30S ribosomal protein S6



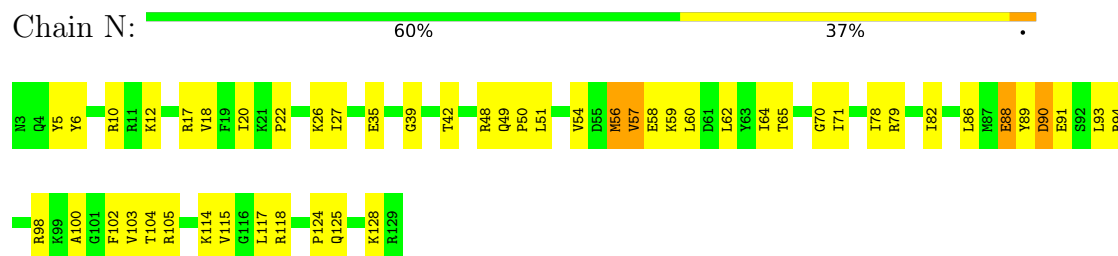
- Molecule 36: 30S ribosomal protein S7



- Molecule 37: 30S ribosomal protein S8

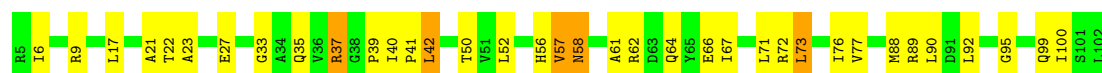


- Molecule 38: 30S ribosomal protein S9



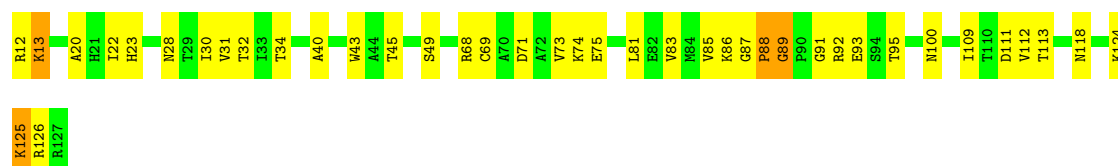
- Molecule 39: 30S ribosomal protein S10

Chain O:  63% 32% 5%



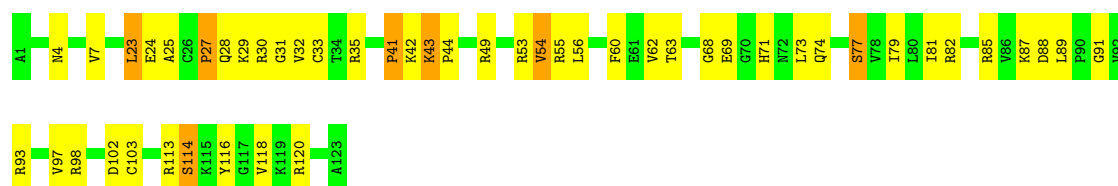
- Molecule 40: 30S ribosomal protein S11

Chain P:  66% 31% 3%



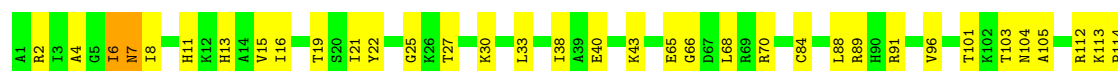
- Molecule 41: 30S ribosomal protein S12

Chain Q:  60% 34% 6%



- Molecule 42: 30S ribosomal protein S13

Chain R:  69% 29% 2%



- Molecule 43: 30S ribosomal protein S14

Chain S:  59% 38% 3%

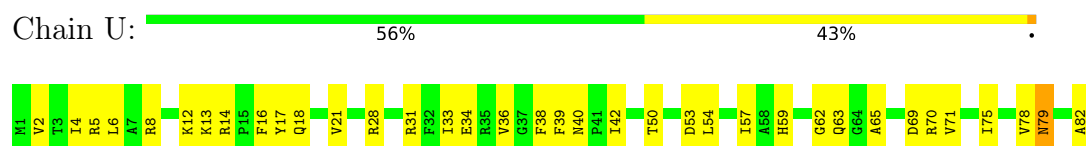


- Molecule 44: 30S ribosomal protein S15

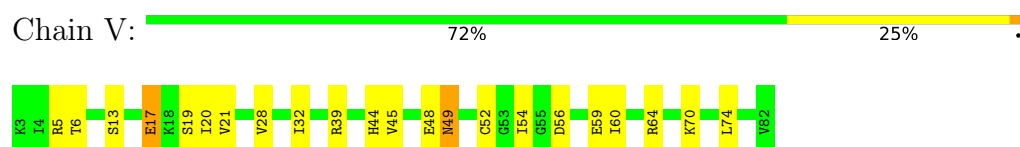
Chain T:  77% 22% 1%



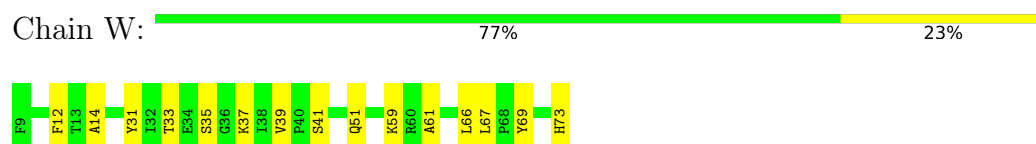
- Molecule 45: 30S ribosomal protein S16



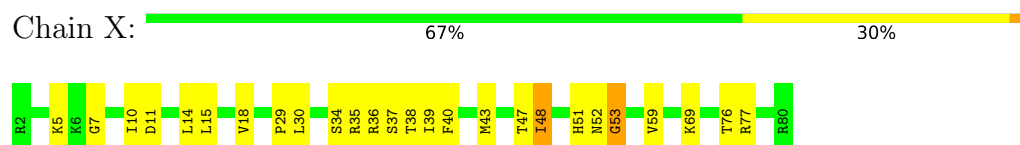
- Molecule 46: 30S ribosomal protein S17



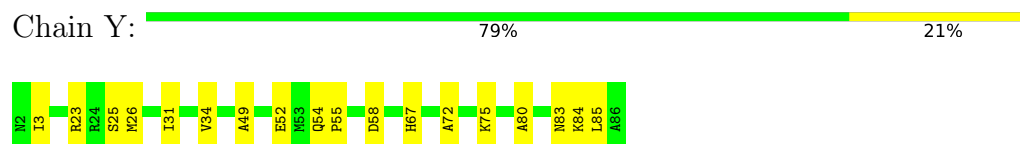
- Molecule 47: 30S ribosomal protein S18



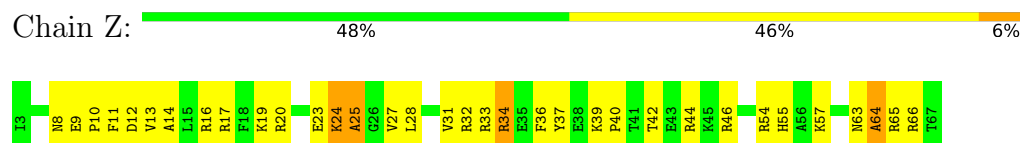
- Molecule 48: 30S ribosomal protein S19



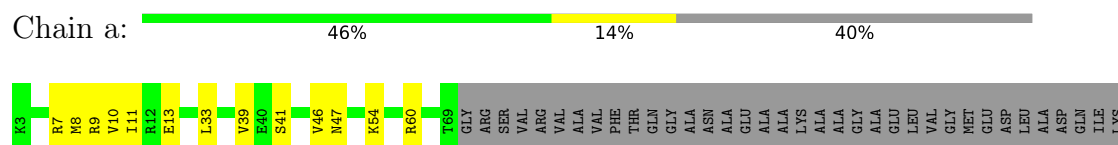
- Molecule 49: 30S ribosomal protein S20

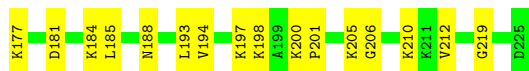
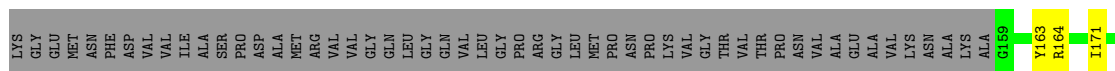


- Molecule 50: 30S ribosomal protein S21



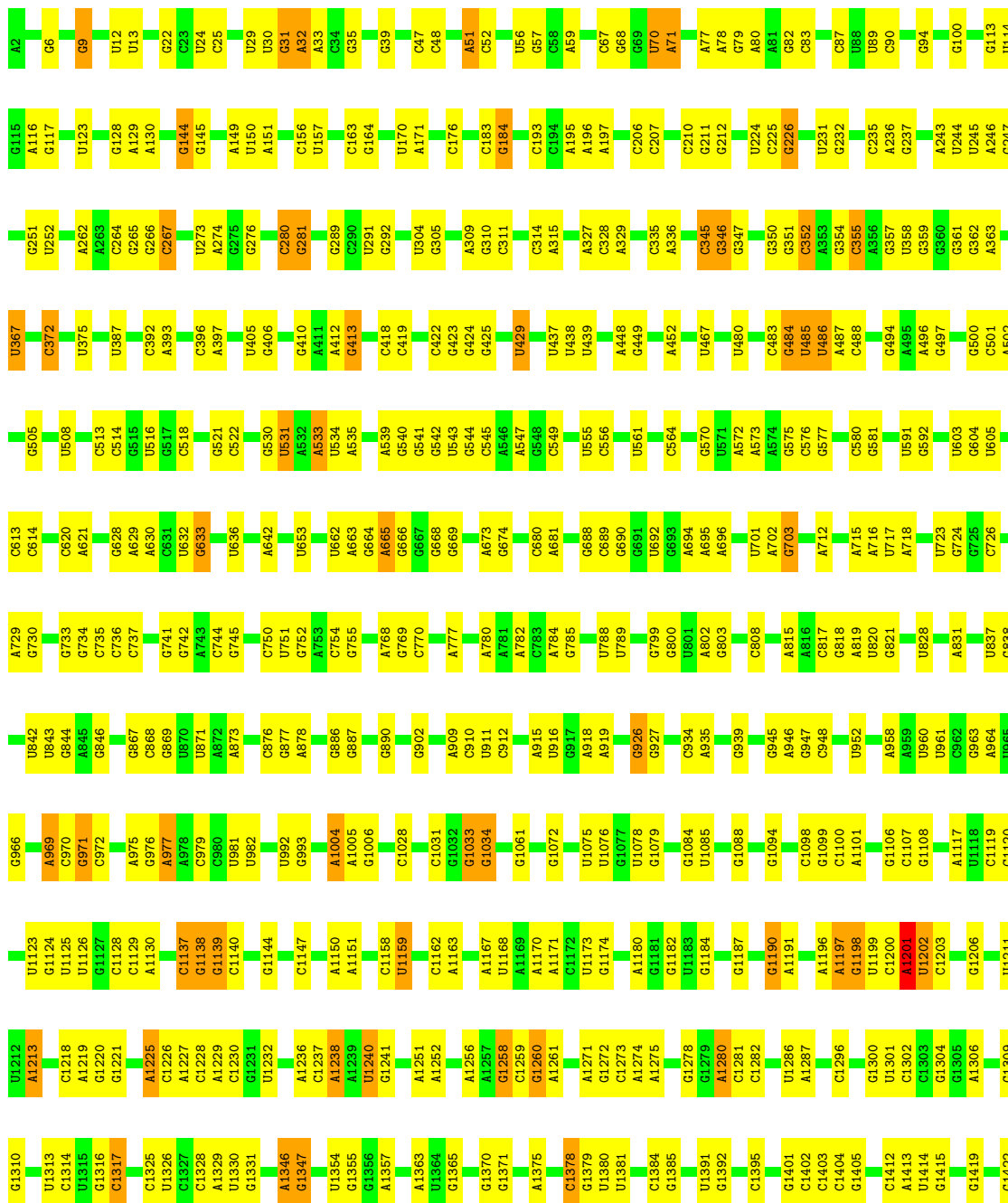
- Molecule 51: 50S ribosomal protein L1

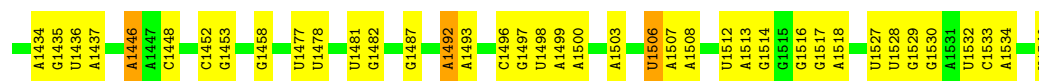




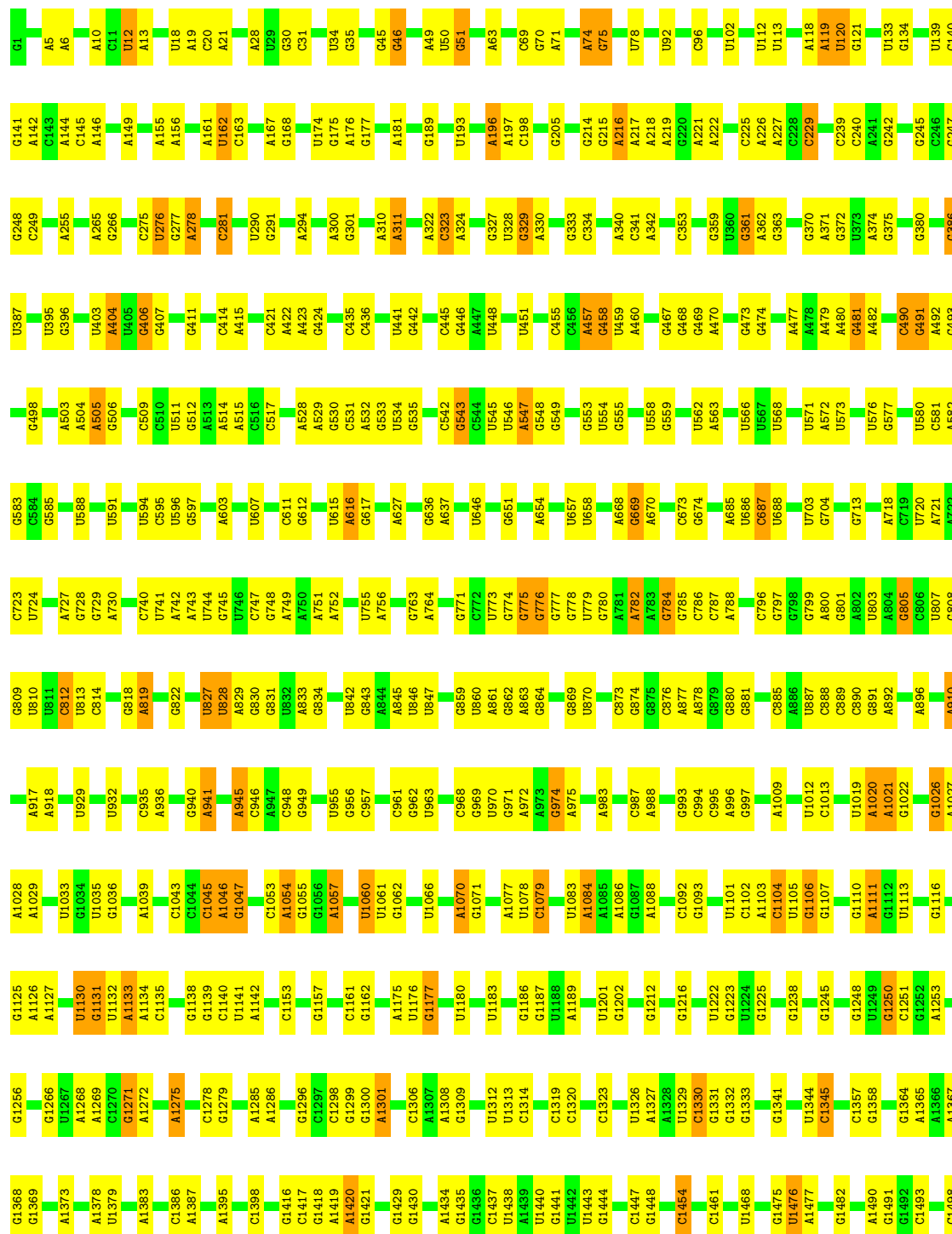
• Molecule 52: 16S ribosomal RNA

Chain 3: 66% 30% .





• Molecule 53: 23S ribosomal RNA



C1507	C1615	C1748	U1856	A1970	A2080	U2182	A2267	G2357	G2442	A2541	G2640	A2758	G2859
A1508	A1616	A1749	G1857	U1971	U2081	A2183	A2268	A2358	C2443	G2545	G2641	G2759	A2860
A1509	G1645	G1753	U1858	G1972	U2086	A2184	G2270	G2360	G2444	U2546	G2642	A2761	U2861
G1510	C1646	U1647	G1860	A1978	G2087	U2185	G2271	G2364	A2448	U2547	G2644	A2764	G2862
A1515	U1648	U1758	A1871	U1979	A2088	U2186	U2272	C2365	A2451	G2549	G2646	A2765	G2867
A1522	G1651	A1759	A1872	G1980	A2094	C2196	G2277	A2366	A2452	G2553	U2647	A2778	A2868
U1523	G1652	C1760	G1873	G1989	A2095	A2197	A2278	G2367	A2453	U2554	U2655	U2779	A2872
G1524	A1654	A1761	C1874	U1991	C2096	A2198	G2279	C2368	G2454	G2559	U2656	G2780	G2875
A1535	A1655	G1763	G1875	G1992	C2104	A2199	G2280	G2369	G2455	A2560	A2660	A2781	G2876
C1536	C1658	C1764	G1884	U1993	U2105	C2200	C2283	G2370	C2456	A2566	G2661	U2784	G2879
G1537	G1658	U1765	A1885	U1996	U2106	G2201	G2286	G2371	U2457	G2567	G2662	C2785	C2880
U1538	A1664	G1766	G1888	C1997	G2107	U2202	A2287	G2373	A2458	A2572	U2663	G2786	U2881
U1539	A1665	A1772	A1889	U1997	G2110	U2203	A2288	A2376	A2467	G2573	U2664	C2787	A2882
G1540	G1666	C1773	A1890	U2011	U2111	G2204	U2292	A2377	A2468	G2574	U2665	G2788	G2883
A1549	A1669	A1774	A1899	G2012	G2112	C2208	G2293	C2380	C2475	U2580	A2666	C2789	U2884
C1550	U1674	U1775	A1900	A2013	U2113	G2209	U2296	A2381	A2476	G2582	G2667	U2790	G2890
U1554	G1674	G1776	A1901	A2014	A2114	U2210	A2297	G2382	A2477	G2583	U2668	G2791	A2893
G1555	A1679	A1780	C1902	U2022	G2115	A2211	U2302	U2383	A2478	U2585	U2669	U2797	U2903
U1559	U1680	A1786	G1906	G2023	U2118	C2215	G2303	G2384	C2480	G2586	G2670	C2794	
G1560	G1681	C1790	C1907	G2024	G2120	G2216	U2304	G2385	G2481	U2587	U2671	C2795	
A1566	G1682	A1791	G1908	G2029	G2121	C2220	U2305	G2389	U2489	U2588	U2672	C2796	
U1569	U1683	U1796	C1909	A2030	U2122	G2221	U2306	U2390	U2490	G2589	G2673	U2797	
A1569	G1684	G1797	G1910	G2031	G2123	G2222	A2309	U2391	G2491	G2590	U2674	A2799	
A1570	C1685	U1798	A1912	G2032	G2124	G2223	G2310	U2392	U2492	G2591	G2675	A2800	
A1571	G1686	G1799	A1913	U2034	G2125	G2224	A2311	U2393	C2493	G2592	U2676	G2801	
A1580	G1687	C1800	U1917	G2035	A2126	A2225	U2312	G2394	C2494	A2602	U2677	U2802	
G1581	G1695	A1801	A1918	C2036	G2127	C2226	G2319	U2402	G2502	U2609	G2714	G2803	
U1584	G1696	A1802	A1919	U2039	U2132	C2232	A2322	A2406	U2504	U2613	G2715	G2804	
C1585	A1698	A1803	G1929	G2041	G2133	U2233	G2323	A2407	G2505	A2614	G2716	G2805	
G1587	G1699	A1808	G1930	C2042	A2134	G2234	U2324	A2412	G2508	U2615	G2717	G2806	
U1594	A1713	A1809	A1936	G2043	U2139	G2238	G2325	G2413	C2512	G2618	G2718	G2807	
C1595	U1715	A1810	A1937	G2048	G2141	U2243	C2326	G2414	G2513	U2619	G2719	G2808	
A1596	G1721	G1811	A1938	G2049	A2142	U2244	A2328	G2415	U2514	G2620	U2720	G2809	
A1597	U1729	U1818	U1943	A2052	A2147	U2245	G2329	A2418	C2515	G2621	U2721	G2810	
U1599	C1730	A1821	U1944	G2055	G2149	G2246	G2330	U2419	A2516	G2622	U2722	G2811	
G1601	G1736	C1822	G1948	G2056	C2150	U2247	G2331	C2420	A2517	G2623	U2723	G2812	
C1606	U1737	U1827	U1955	A2060	G2156	U2248	U2334	U2423	A2518	G2624	U2724	G2813	
C1607	G1738	G1828	U1956	G2061	G2157	U2257	G2337	C2424	G2526	U2625	G2725	G2814	
A1608	A1739	A1829	C1957	A2062	G2162	C2258	U2344	A2425	C2527	U2626	G2726	G2815	
G1611	G1740	C1830	G1957	C2066	A2163	U2259	G2345	G2429	U2528	U2627	U2727	G2816	
C1612	C1741	G1831	U1963	G2067	C2164	C2260	U2348	A2430	A2530	G2628	A2728	G2817	
G1613	U1742	G1837	G1965	U2068	U2172	C2263	U2349	U2431	G2533	G2629	G2729	G2818	
A1614	G1743	A1837	A1966	G2069	A2173	C2264	C2350	A2432	A2534	U2630	G2730	G2819	
	A1744	A1854	C1967	C2072	C2174	U2265	G2351	A2435	C2539	G2631	U2731	G2820	
					C2175	A2266	U2356	U2441	C2540	U2632	U2732	G2821	

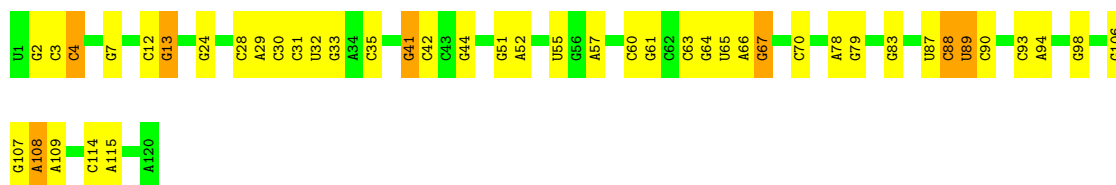
● Molecule 54: 5S ribosomal RNA

Chain 2:

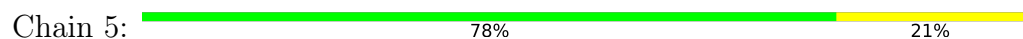
62%

32%

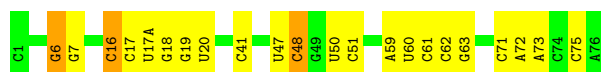
6%



- Molecule 55: tRNA^{fMet}



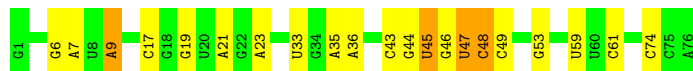
- Molecule 55: tRNA^{fMet}



- Molecule 56: mRNA



- Molecule 57: tRNA^{Phe}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6847	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k 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: FME

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	b	0.28	0/2122	0.91	4/2852 (0.1%)
2	c	0.29	0/1586	0.88	5/2134 (0.2%)
3	d	0.29	0/1571	0.86	1/2113 (0.0%)
4	e	0.29	0/1435	0.88	4/1926 (0.2%)
5	f	0.29	0/1343	0.80	1/1816 (0.1%)
6	g	0.30	0/1122	0.98	5/1515 (0.3%)
7	h	0.34	0/1002	1.06	12/1350 (0.9%)
8	i	0.34	0/1046	1.00	8/1410 (0.6%)
9	j	0.28	0/1152	0.82	4/1551 (0.3%)
10	k	0.28	0/948	0.94	3/1268 (0.2%)
11	l	0.29	0/1054	0.97	5/1403 (0.4%)
12	m	0.29	0/1093	0.84	1/1460 (0.1%)
13	n	0.30	0/974	0.95	6/1301 (0.5%)
14	o	0.29	0/902	0.87	2/1209 (0.2%)
15	p	0.28	0/929	0.78	1/1242 (0.1%)
16	q	0.28	0/960	0.88	2/1278 (0.2%)
17	r	0.27	0/829	0.89	2/1107 (0.2%)
18	s	0.28	0/864	0.88	1/1156 (0.1%)
19	t	0.28	0/745	0.78	0/994
20	u	0.28	0/788	0.90	4/1051 (0.4%)
21	v	0.28	0/766	0.82	0/1025
22	w	0.27	0/582	0.82	0/769
23	x	0.27	0/635	0.78	1/848 (0.1%)
24	y	0.27	0/510	0.95	3/677 (0.4%)
25	z	0.28	0/453	0.81	1/605 (0.2%)
26	B	0.29	0/450	0.81	0/599
27	C	0.32	0/417	0.95	2/554 (0.4%)
28	D	0.32	0/380	0.91	0/498
29	E	0.30	0/513	0.86	1/676 (0.1%)
30	F	0.29	0/303	0.87	0/397
31	G	0.28	0/1788	0.87	5/2408 (0.2%)
32	H	0.29	0/1652	0.88	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.95	7/2227 (0.3%)
34	J	0.29	0/1170	0.89	3/1573 (0.2%)
35	K	0.30	0/836	0.85	1/1128 (0.1%)
36	L	0.29	0/1196	0.90	1/1602 (0.1%)
37	M	0.28	0/989	0.92	0/1326
38	N	0.30	0/1034	0.95	4/1375 (0.3%)
39	O	0.31	0/797	0.95	3/1077 (0.3%)
40	P	0.30	0/886	0.97	4/1195 (0.3%)
41	Q	0.29	0/969	0.96	3/1300 (0.2%)
42	R	0.31	0/893	0.91	2/1193 (0.2%)
43	S	0.29	0/817	0.90	4/1088 (0.4%)
44	T	0.28	0/722	0.88	4/964 (0.4%)
45	U	0.30	0/659	0.94	4/884 (0.5%)
46	V	0.28	0/658	0.87	1/881 (0.1%)
47	W	0.32	0/545	0.85	0/731
48	X	0.32	0/653	0.87	1/877 (0.1%)
49	Y	0.30	0/671	0.94	2/888 (0.2%)
50	Z	0.32	0/551	1.02	4/728 (0.5%)
51	a	0.31	0/1034	0.80	0/1387
52	3	0.40	0/36963	0.50	3/57662 (0.0%)
53	1	0.39	0/69796	0.50	0/108888
54	2	0.40	0/2872	0.50	0/4479
55	5	0.39	0/1832	0.48	0/2855
55	6	0.40	0/1832	0.51	0/2855
56	4	0.40	0/436	0.49	0/679
57	7	0.39	0/1809	0.47	0/2819
All	All	0.37	0/163199	0.63	141/244078 (0.1%)

There are no bond length outliers.

The worst 5 of 141 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	95	LEU	N-CA-C	-8.72	102.07	112.89
12	m	110	GLU	N-CA-C	7.75	121.67	111.75
2	c	150	GLN	N-CA-C	7.71	120.58	111.71
20	u	96	LYS	N-CA-C	-7.64	100.23	110.55
7	h	114	GLU	N-CA-C	7.53	119.18	110.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	47	0
2	c	1565	0	1616	46	0
3	d	1552	0	1619	38	0
4	e	1411	0	1447	45	0
5	f	1323	0	1374	30	0
6	g	1111	0	1148	29	0
7	h	989	0	1025	51	0
8	i	1032	0	1088	34	0
9	j	1129	0	1162	40	0
10	k	939	0	1012	25	0
11	l	1045	0	1117	33	0
12	m	1074	0	1157	23	0
13	n	961	0	1000	31	0
14	o	892	0	923	18	0
15	p	917	0	965	36	0
16	q	947	0	1022	20	0
17	r	816	0	839	23	0
18	s	857	0	922	12	0
19	t	739	0	807	19	0
20	u	780	0	834	16	0
21	v	753	0	780	23	0
22	w	575	0	592	19	0
23	x	625	0	655	15	0
24	y	509	0	543	14	0
25	z	449	0	491	14	0
26	B	444	0	461	13	0
27	C	410	0	440	9	0
28	D	377	0	418	7	0
29	E	504	0	574	18	0
30	F	302	0	343	16	0
31	G	1757	0	1787	41	0
32	H	1625	0	1699	40	0
33	I	1643	0	1710	48	0
34	J	1157	0	1199	25	0
35	K	818	0	808	40	0
36	L	1182	0	1240	32	0
37	M	979	0	1034	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	40	0
39	O	787	0	828	31	0
40	P	870	0	878	26	0
41	Q	955	0	1019	38	0
42	R	884	0	944	29	0
43	S	805	0	847	28	0
44	T	714	0	737	13	0
45	U	649	0	666	26	0
46	V	649	0	691	16	0
47	W	536	0	552	10	0
48	X	638	0	665	18	0
49	Y	665	0	714	14	0
50	Z	545	0	579	21	0
51	a	1027	0	1092	24	0
52	3	33012	0	16618	354	0
53	1	62317	0	31346	725	0
54	2	2568	0	1303	41	0
55	5	1640	0	836	8	0
55	6	1640	0	837	17	0
56	4	388	0	197	2	0
57	7	1619	0	822	10	0
58	5	10	0	10	0	0
All	All	150211	0	101259	2169	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 9.

The worst 5 of 2169 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)
53:1:45:G:H5''	53:1:46:G:H5'	1.24	1.15
42:R:113:LYS:HG3	42:R:114:PRO:HD3	1.35	1.08
34:J:107:GLY:HA3	52:3:9:G:H5'	1.43	1.00
30:F:32:LYS:HE3	53:1:2478:A:H5'	1.47	0.93
52:3:484:G:H4'	52:3:485:U:H5''	1.54	0.90

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	229 (85%)	36 (13%)	4 (2%)	8	36
2	c	207/209 (99%)	186 (90%)	21 (10%)	0	100	100
3	d	199/201 (99%)	178 (89%)	19 (10%)	2 (1%)	12	43
4	e	175/177 (99%)	151 (86%)	22 (13%)	2 (1%)	11	42
5	f	174/176 (99%)	159 (91%)	14 (8%)	1 (1%)	21	52
6	g	147/149 (99%)	130 (88%)	15 (10%)	2 (1%)	9	37
7	h	129/131 (98%)	100 (78%)	23 (18%)	6 (5%)	2	18
8	i	139/141 (99%)	118 (85%)	19 (14%)	2 (1%)	9	37
9	j	140/142 (99%)	130 (93%)	9 (6%)	1 (1%)	18	50
10	k	120/122 (98%)	105 (88%)	12 (10%)	3 (2%)	4	29
11	l	141/143 (99%)	117 (83%)	18 (13%)	6 (4%)	2	19
12	m	134/136 (98%)	116 (87%)	15 (11%)	3 (2%)	5	31
13	n	118/120 (98%)	101 (86%)	14 (12%)	3 (2%)	4	29
14	o	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
15	p	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
16	q	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
17	r	101/103 (98%)	86 (85%)	13 (13%)	2 (2%)	6	32
18	s	108/110 (98%)	96 (89%)	11 (10%)	1 (1%)	14	45
19	t	91/93 (98%)	82 (90%)	8 (9%)	1 (1%)	11	42
20	u	100/102 (98%)	83 (83%)	15 (15%)	2 (2%)	6	32
21	v	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
22	w	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
23	x	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
24	y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
27	C	48/50 (96%)	44 (92%)	1 (2%)	3 (6%)	1	14
28	D	44/46 (96%)	39 (89%)	4 (9%)	1 (2%)	5	30
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	35
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
31	G	223/225 (99%)	206 (92%)	17 (8%)	0	100	100
32	H	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
33	I	203/205 (99%)	183 (90%)	18 (9%)	2 (1%)	12	43
34	J	155/157 (99%)	126 (81%)	23 (15%)	6 (4%)	2	21
35	K	98/100 (98%)	75 (76%)	20 (20%)	3 (3%)	3	26
36	L	149/151 (99%)	134 (90%)	14 (9%)	1 (1%)	18	50
37	M	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
38	N	125/127 (98%)	104 (83%)	18 (14%)	3 (2%)	4	29
39	O	96/98 (98%)	73 (76%)	17 (18%)	6 (6%)	1	14
40	P	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	19
41	Q	121/123 (98%)	98 (81%)	17 (14%)	6 (5%)	1	17
42	R	112/114 (98%)	99 (88%)	10 (9%)	3 (3%)	4	27
43	S	98/100 (98%)	79 (81%)	16 (16%)	3 (3%)	3	26
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
45	U	80/82 (98%)	64 (80%)	15 (19%)	1 (1%)	9	38
46	V	78/80 (98%)	63 (81%)	12 (15%)	3 (4%)	2	22
47	W	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
48	X	77/79 (98%)	63 (82%)	11 (14%)	3 (4%)	2	21
49	Y	83/85 (98%)	77 (93%)	6 (7%)	0	100	100
50	Z	63/65 (97%)	43 (68%)	13 (21%)	7 (11%)	0	5
51	a	130/223 (58%)	123 (95%)	7 (5%)	0	100	100
All	All	5919/6112 (97%)	5168 (87%)	651 (11%)	100 (2%)	9	34

5 of 100 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL

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Mol	Chain	Res	Type
7	h	113	PHE
7	h	118	ILE
10	k	89	ASN

5.3.2 Protein sidechains [i](#)

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	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	100 (100%)	0	100	100
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	75
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	65
11	l	102/102 (100%)	100 (98%)	2 (2%)	48	64
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	74
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	97 (98%)	2 (2%)	48	64
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	72
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	37 (97%)	1 (3%)	40	60
29	E	51/51 (100%)	50 (98%)	1 (2%)	48	64
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	79
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	76
35	K	87/87 (100%)	85 (98%)	2 (2%)	44	62
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4888 (100%)	20 (0%)	81	81

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	H	81	GLU
35	K	73	GLU
39	O	73	LEU
35	K	97	THR
13	n	10	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
32	H	5	HIS
34	J	131	ASN
48	X	68	HIS
32	H	31	ASN
33	I	115	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	140 (9%)	4 (0%)
53	1	2902/2903 (99%)	338 (11%)	9 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	8 (10%)	0
55	6	76/77 (98%)	8 (10%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	12 (16%)	0
All	All	4803/4810 (99%)	521 (10%)	14 (0%)

5 of 521 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1020	A
53	1	1130	U
54	2	88	C
53	1	2326	C
53	1	2391	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	FME	5	101	55	8,9,10	0.60	0	8,9,11	0.86	0

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
58	FME	5	101	55	-	1/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	5	101	FME	CB-CA-N-CN

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.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-21638. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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 standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 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.