



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 09:34 PM UTC

PDB ID : 6VYQ / pdb_00006vyq
EMDB ID : EMD-21468
Title : Escherichia coli transcription-translation complex A1 (TTC-A1) containing an 15 nt long mRNA spacer, NusG, and fMet-tRNAs at E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-27
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
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

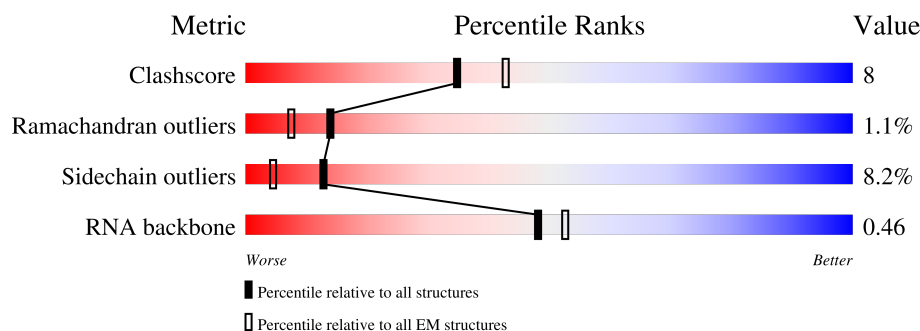
1 Overall quality at a glance

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.



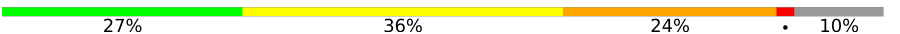
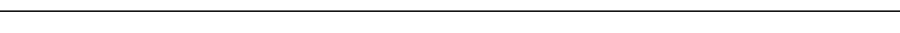
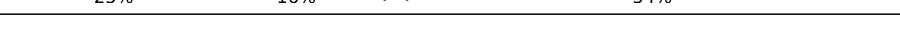
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	0	103	84% 15% .
2	1	110	75% 25%
3	2	100	85% 7% . 6%
4	3	104	84% 14% ..
5	4	94	97% .
6	5	36	25% 36% . 36%
7	6	36	39% 36% 25%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	7	32	
9	9	165	
10	A	76	
10	B	76	
11	AA	1341	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	C	75	
16	D	1542	
17	E	87	
18	F	71	
19	G	241	
20	H	557	
21	I	233	
22	J	206	
23	K	167	
24	L	135	
25	M	179	
26	N	130	
27	O	130	
28	P	99	
29	Q	129	
30	R	124	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
31	S	101	 90% 7% ...
32	T	89	 80% 17% ..
33	U	82	 88% 11% .
34	V	84	 87% 7% . 5%
35	W	92	 82% 8% . 10%
36	X	118	 75% 18% 5% .
37	Y	142	 38% 39% 19% ..
38	Z	121	 7% 12% 5% . 75%
39	a	2904	 73% 23% ..
40	b	85	 85% 5% 11%
41	c	78	 87% 9% ..
42	d	120	 80% 19% .
43	e	63	 87% 10% ..
44	f	59	 81% 15% ..
45	g	70	 80% 13% . 6%
46	h	273	 85% 13% ..
47	i	57	 77% 19% ..
48	j	209	 89% 11%
49	k	55	 89% 5% 5%
50	l	201	 85% 13% .
51	m	46	 78% 17% .
52	n	179	 75% 20% ..
53	o	65	 88% 8% ..
54	p	177	 90% 8% .
55	q	38	 87% 11% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
56	r	149	 88% 11% .
57	s	142	 81% 18% .
58	t	123	 80% 18% .
59	u	144	 88% 12%
60	v	136	 91% 8% .
61	w	127	 79% 15% 6%
62	x	117	 82% 16% ..
63	y	115	 89% 10% .
64	z	118	 84% 14% ..

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 300668 atoms, of which 124723 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 L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1632	498	844	148	142			

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			847	259	305	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 15 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	32	Total	C	H	N	O	P	0	0
			769	300	97	100	240	32		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AA	1322	Total	C	H	N	O	S	0	0
			20851	6539	10426	1817	2026	43		

- Molecule 12 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AB	98	Total	C	H	N	O	S	0	0
			1573	505	783	139	140	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	50		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	variant	UNP A0A4S1NBU2

- Molecule 15 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 16 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 17 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 18 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 20 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 21 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 22 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 23 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 24 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 25 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 26 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 27 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 28 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 29 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
30	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 31 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 32 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 33 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 34 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 35 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 36 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 37 is a protein called 50S ribosomal protein L11.

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

- Molecule 38 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 39 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	variant	GB 937521852

- Molecule 40 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 41 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 42 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 43 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 44 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 45 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 46 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 47 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 48 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 51 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 52 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 53 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 54 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 56 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 57 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 58 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 59 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 60 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 61 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 62 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	x	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 63 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 64 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	z	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 65 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
65	AE	1	Total	Mg	0
			1	1	

- Molecule 66 is ZINC ION (CCD ID: ZN) (formula: Zn).

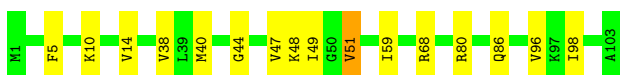
Mol	Chain	Residues	Atoms		AltConf
66	AE	2	Total	Zn	0
			2	2	

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 L21

Chain 0:  84% 15% .



- Molecule 2: 50S ribosomal protein L22

Chain 1:  75% 25%



- Molecule 3: 50S ribosomal protein L23

Chain 2:  85% 7% . 6%

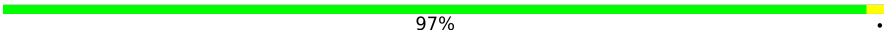


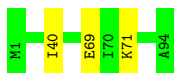
- Molecule 4: 50S ribosomal protein L24

Chain 3:  84% 14% ..



- Molecule 5: 50S ribosomal protein L25

Chain 4:  97% .



- Molecule 6: NT DNA

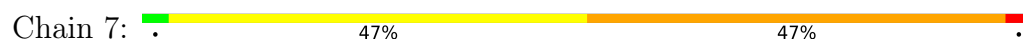
Chain 5:  25% 36% . 36%



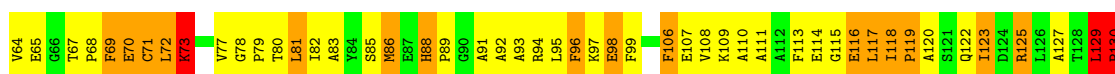
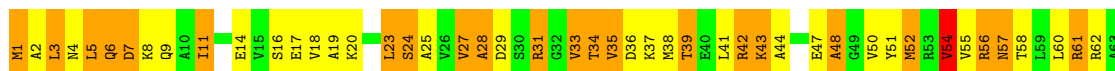
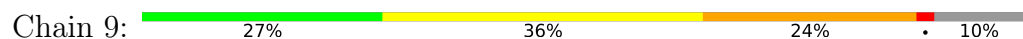
- Molecule 7: T DNA



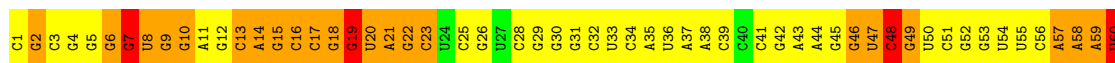
- Molecule 8: mRNA with 15 nt long spacer



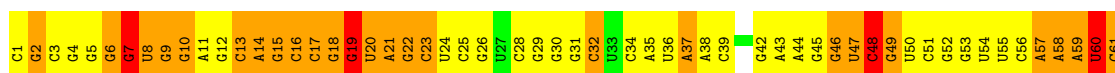
- Molecule 9: 50S ribosomal protein L10



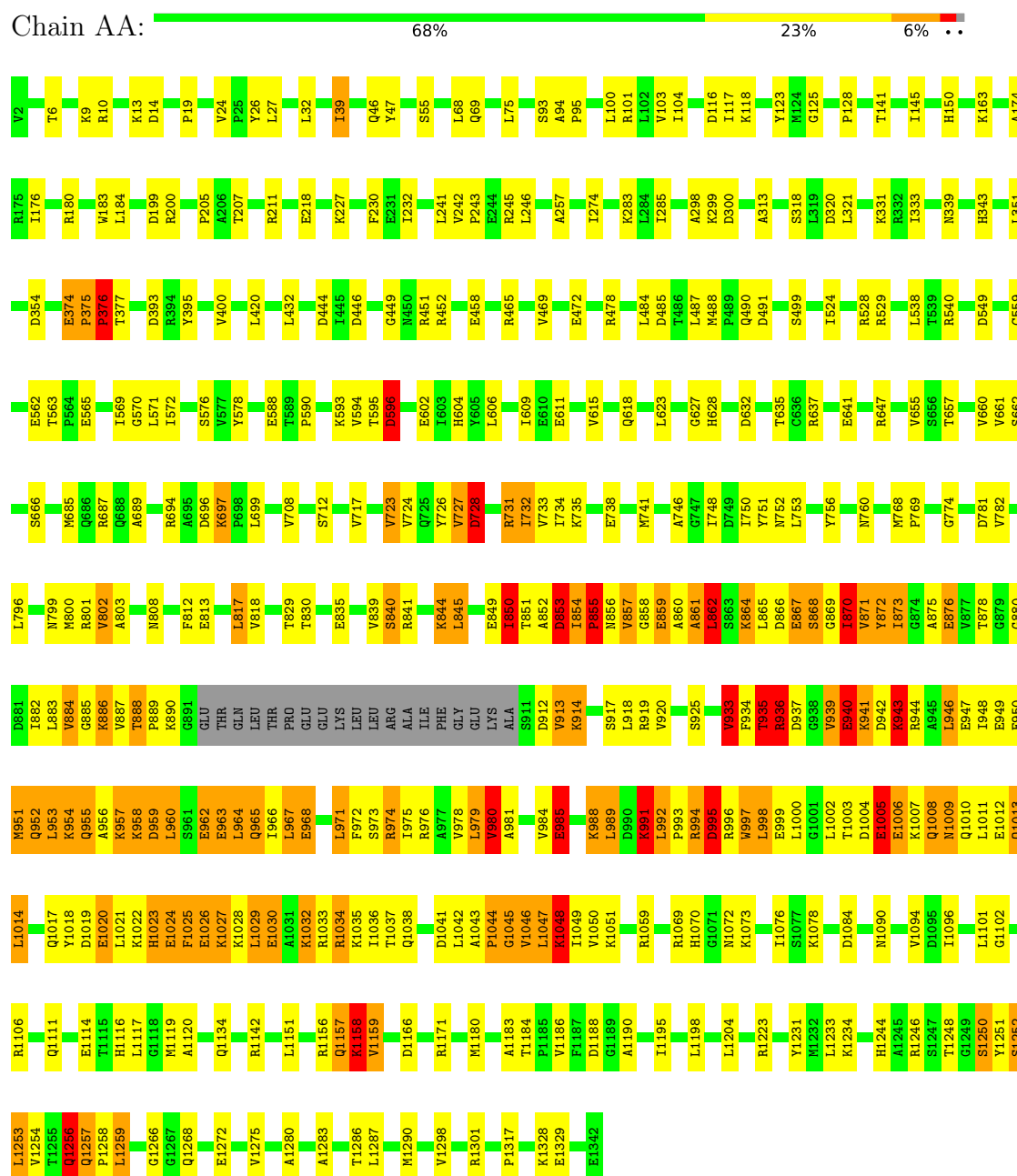
- Molecule 10: E-site and P-site tRNA (fMet)



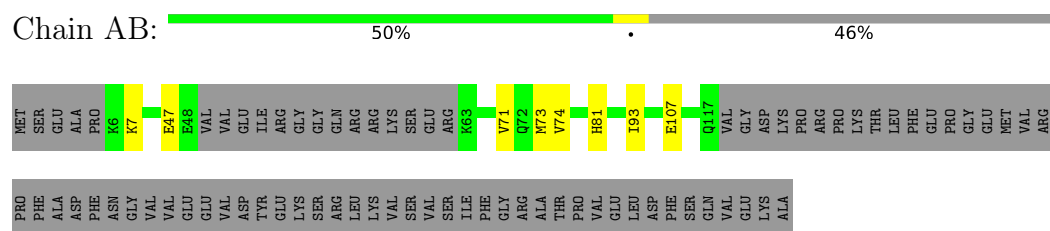
- Molecule 10: E-site and P-site tRNA (fMet)



- Molecule 11: DNA-directed RNA polymerase subunit beta



- Molecule 12: Transcription termination/antitermination protein NusG



- Molecule 13: DNA-directed RNA polymerase subunit alpha

Frequency	Percentage
Daily	52%
Weekly	14%
Monthly	30%
Other	14%

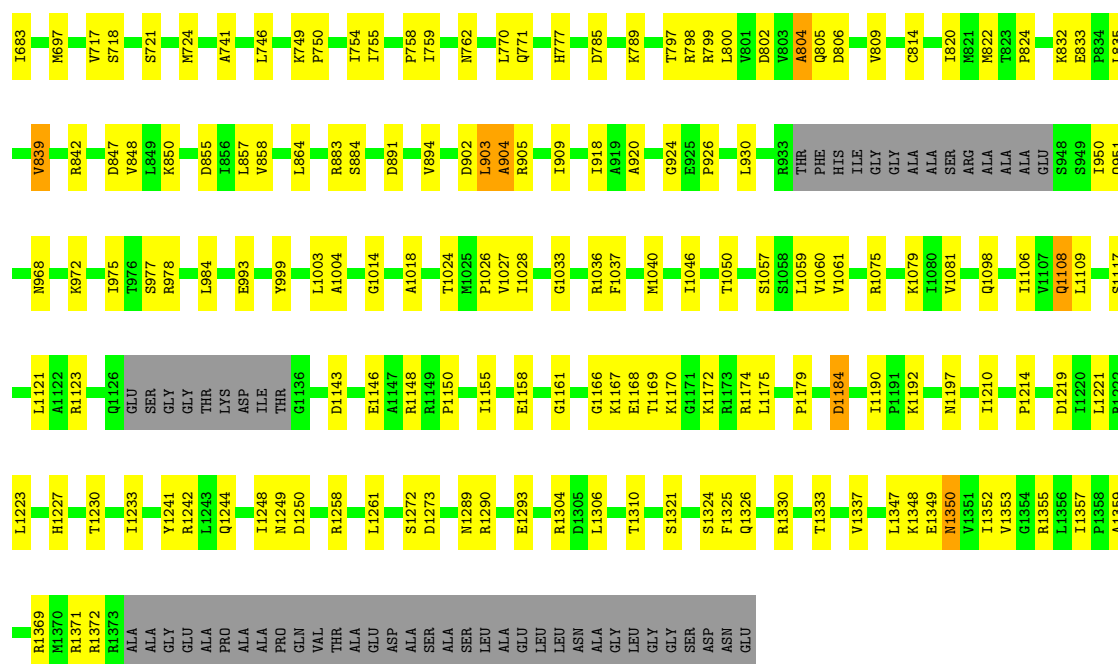


Device Type	Percentage
Smartphones	53%
Tablets	16%
Other mobile devices	31%



Response	Percentage
Used	67%
Not used	24%
Don't know	5%





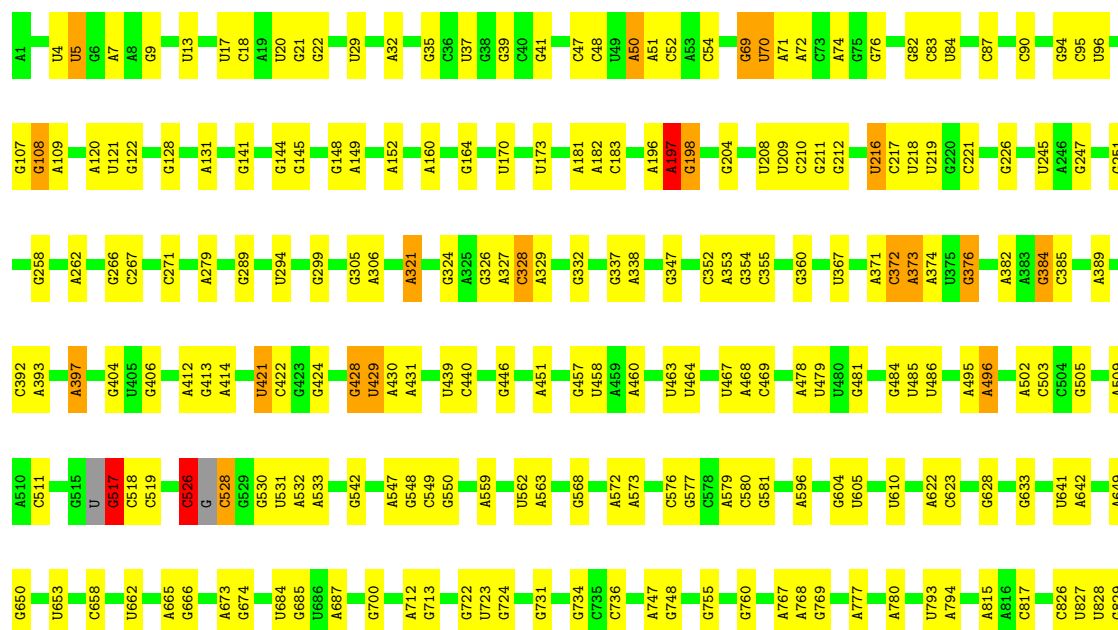
- Molecule 15: 30S ribosomal protein S18

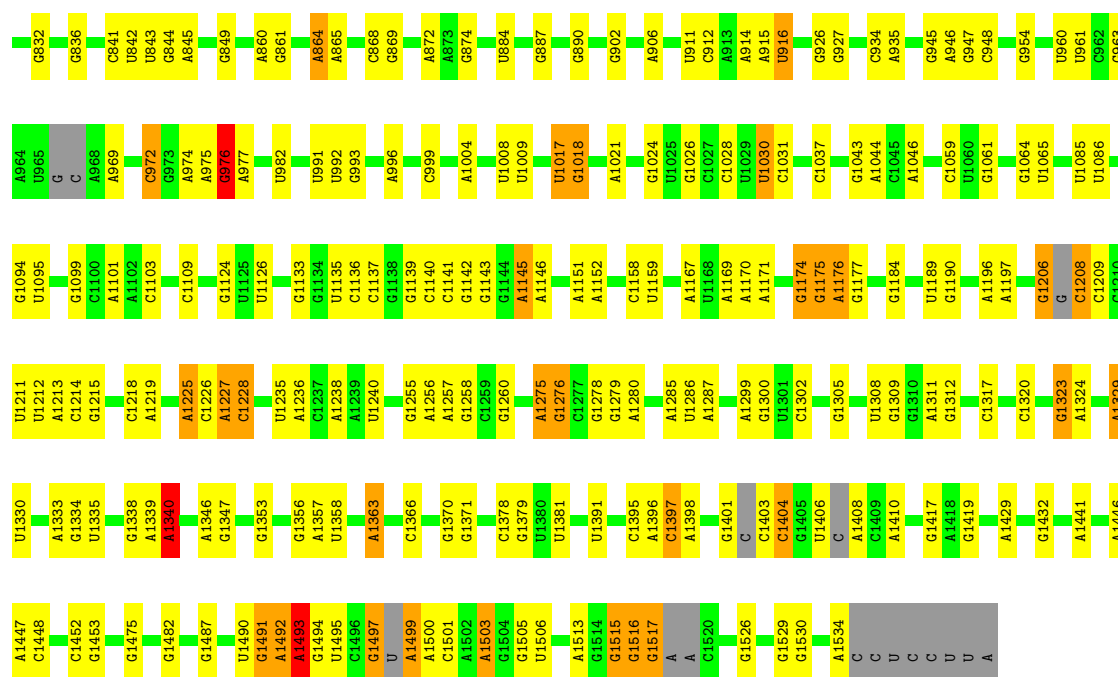
Chain C: 72% 15% 12%



- Molecule 16: 16S rRNA

Chain D: 70% 25% 5%





• Molecule 17: 30S ribosomal protein S20

Chain E: 87% 10% ..



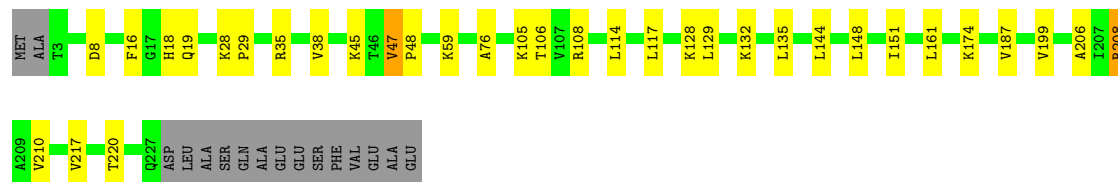
• Molecule 18: 30S ribosomal protein S21

Chain F: 87% 10% ..



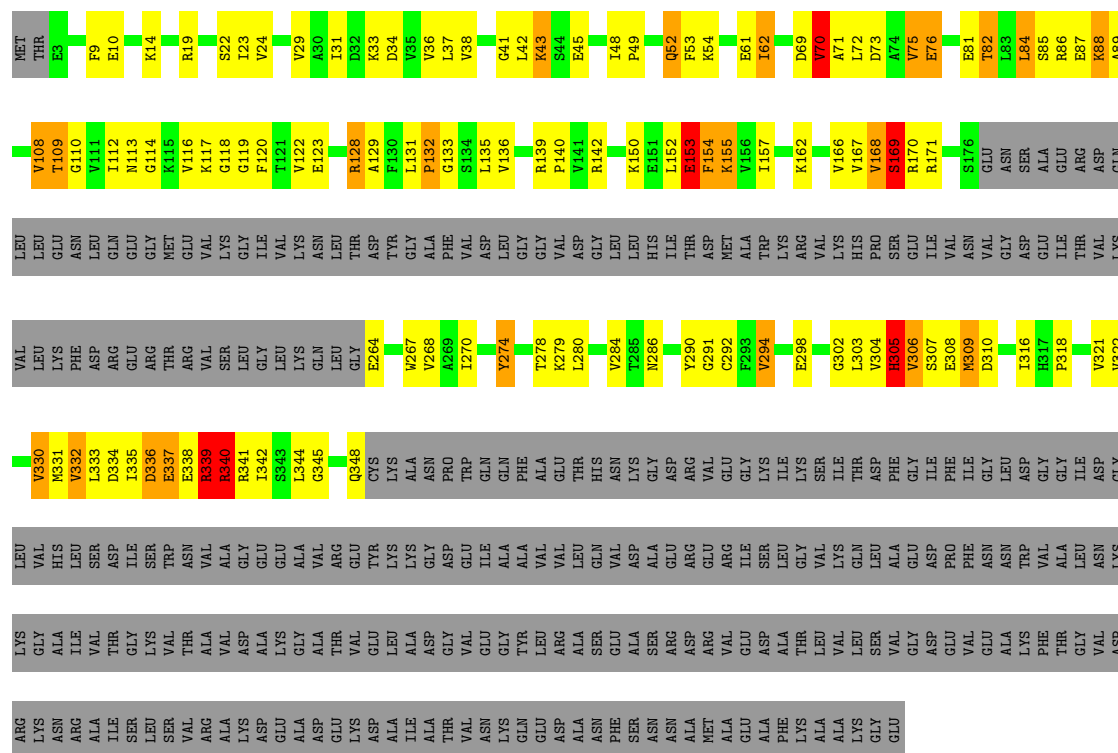
• Molecule 19: 30S ribosomal protein S2

Chain G: 79% 13% 7%

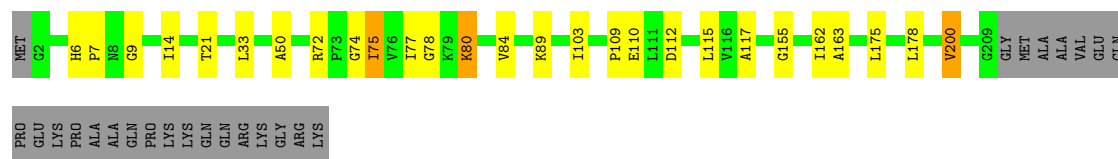
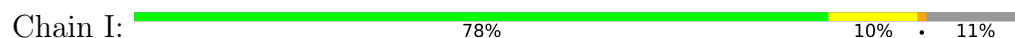


• Molecule 20: 30S ribosomal protein S1

Chain H: 25% 16% 54%



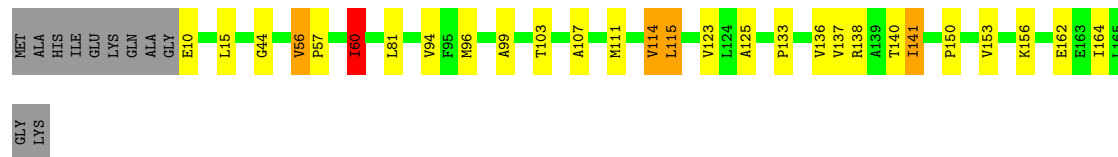
- Molecule 21: 30S ribosomal protein S3



- Molecule 22: 30S ribosomal protein S4

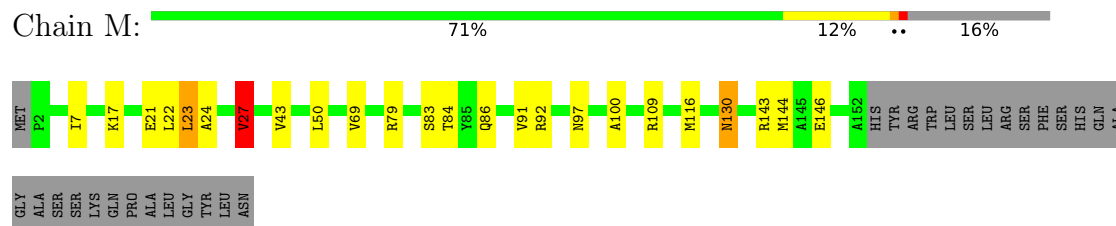


- Molecule 23: 30S ribosomal protein S5

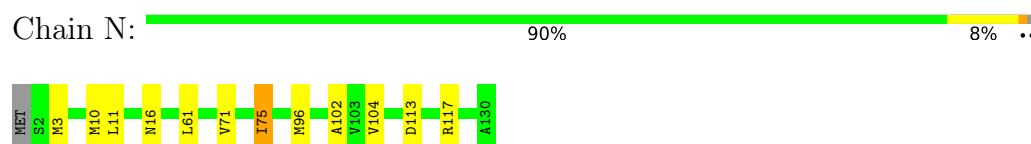


- Molecule 24: 30S ribosomal protein S6

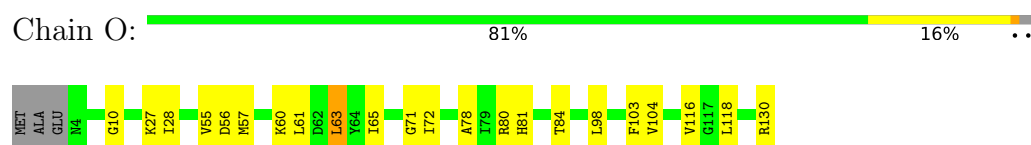
- Molecule 25: 30S ribosomal protein S7



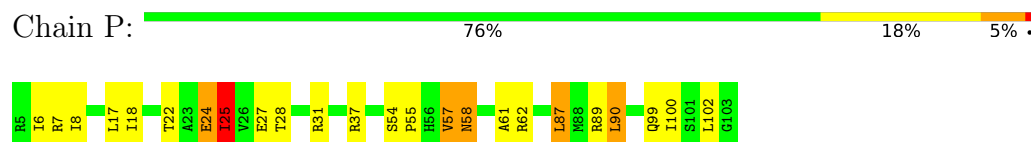
- Molecule 26: 30S ribosomal protein S8



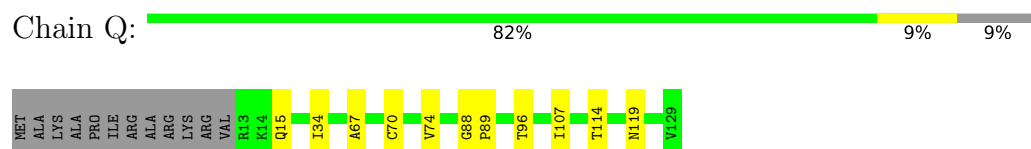
- Molecule 27: 30S ribosomal protein S9



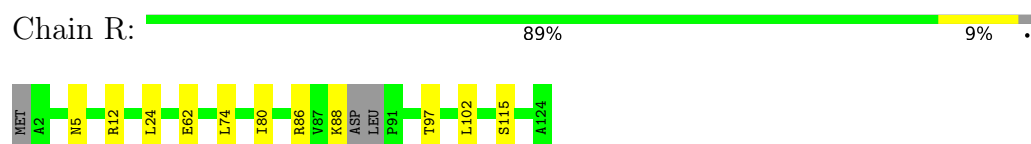
- Molecule 28: 30S ribosomal protein S10



- Molecule 29: 30S ribosomal protein S11



- Molecule 30: 30S ribosomal protein S12



- Molecule 31: 30S ribosomal protein S14

Chain S:  90% 7% ...



- Molecule 32: 30S ribosomal protein S15

Chain T:  80% 17% ..



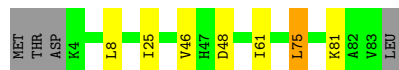
- Molecule 33: 30S ribosomal protein S16

Chain U:  88% 11% •



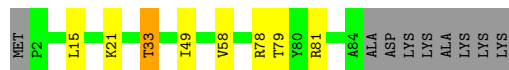
- Molecule 34: 30S ribosomal protein S17

Chain V:  87% 7% • 5%



- Molecule 35: 30S ribosomal protein S19

Chain W:  82% 8% • 10%



- Molecule 36: 30S ribosomal protein S13

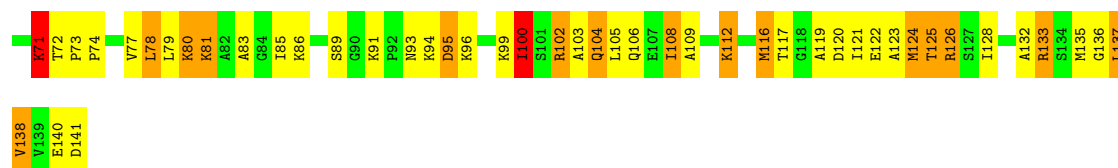
Chain X:  75% 18% 5% •



- Molecule 37: 50S ribosomal protein L11

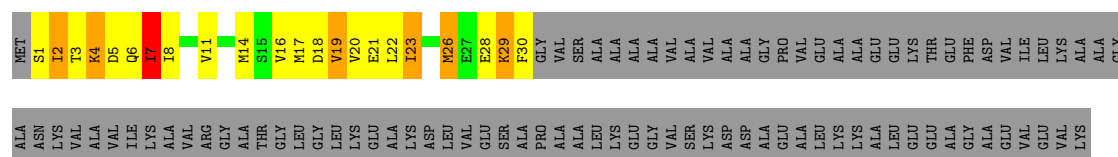
Chain Y:  38% 39% 19% ..





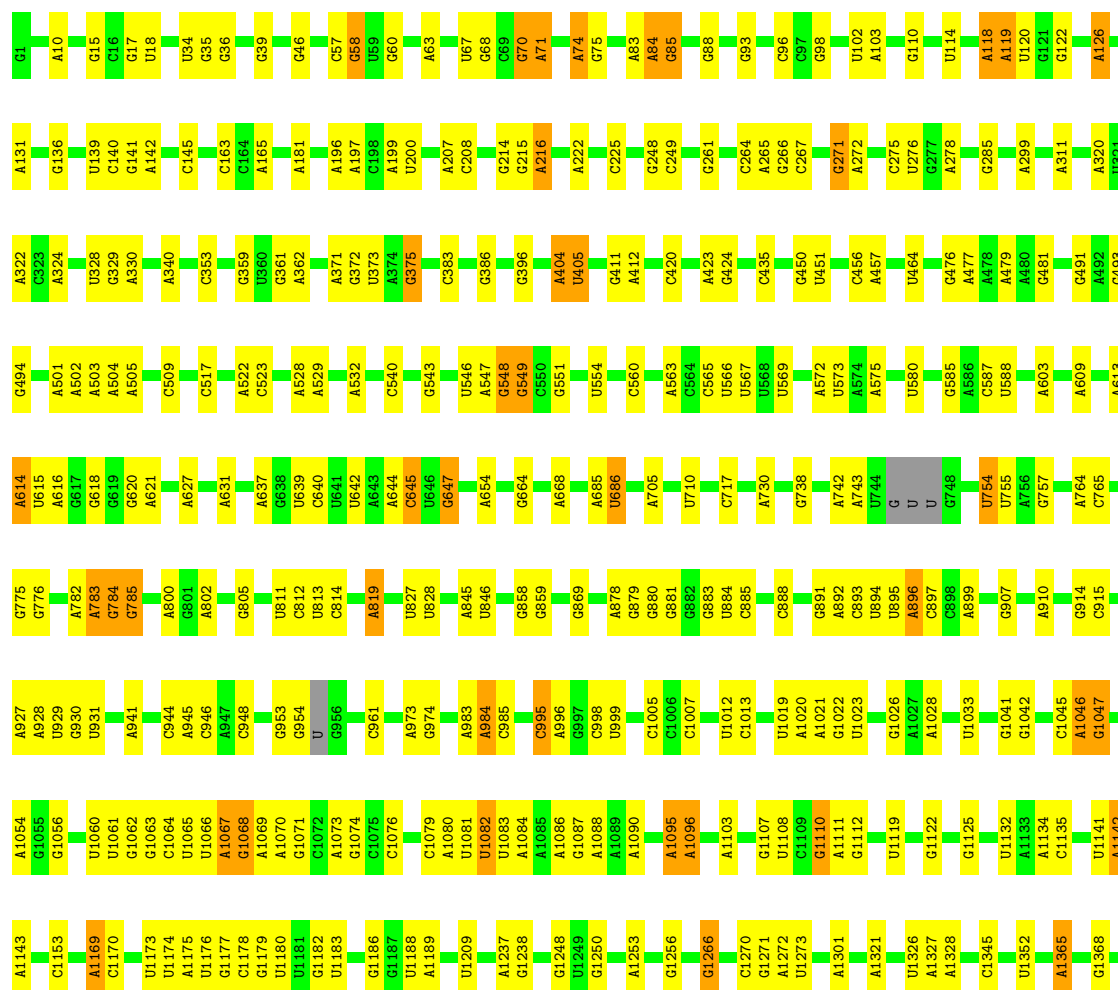
- Molecule 38: 50S ribosomal protein L7/L12

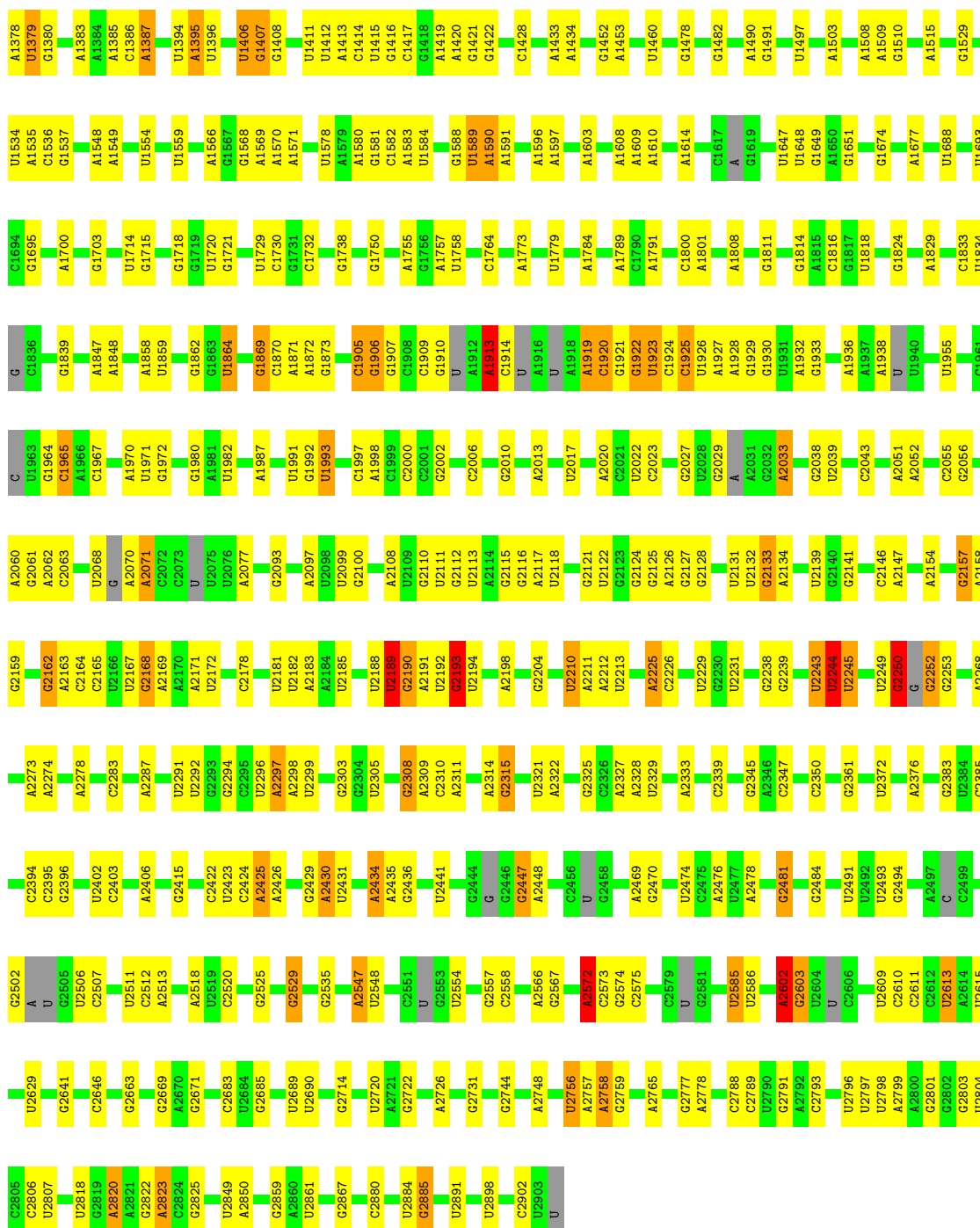
Chain Z: 7% 12% 5% 75%



- Molecule 39: 23S rRNA

Chain a: 73% 23%





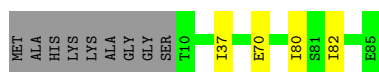
- Molecule 40: 50S ribosomal protein L27

Chain b:

85%

5%

11%



- Molecule 41: 50S ribosomal protein L28

Chain c:  87% 9% ..



- Molecule 42: 5S rRNA

Chain d:  80% 19% .



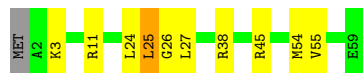
- Molecule 43: 50S ribosomal protein L29

Chain e:  87% 10% ..



- Molecule 44: 50S ribosomal protein L30

Chain f:  81% 15% ..



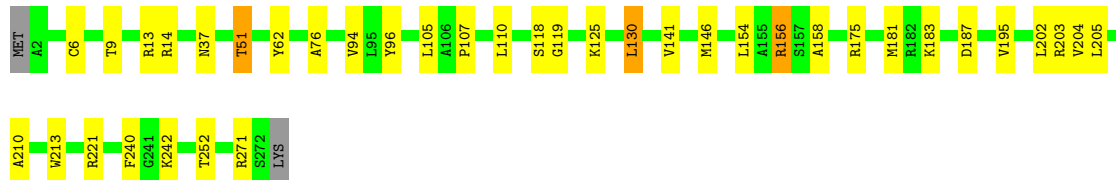
- Molecule 45: 50S ribosomal protein L31

Chain g:  80% 13% • 6%



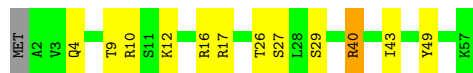
- Molecule 46: 50S ribosomal protein L2

Chain h:  85% 13% ..



- Molecule 47: 50S ribosomal protein L32

Chain i:  77% 19% ..



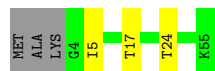
- Molecule 48: 50S ribosomal protein L3

Chain j:  89% 11%



- Molecule 49: 50S ribosomal protein L33

Chain k:  89% 5% 5%



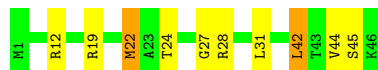
- Molecule 50: 50S ribosomal protein L4

Chain l:  85% 13% .



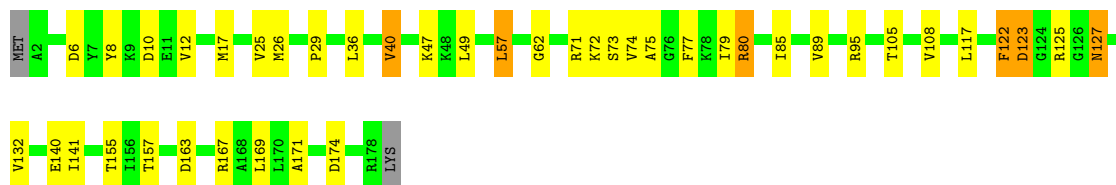
- Molecule 51: 50S ribosomal protein L34

Chain m:  78% 17% .



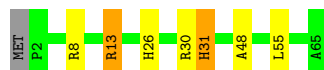
- Molecule 52: 50S ribosomal protein L5

Chain n:  75% 20% ..



- Molecule 53: 50S ribosomal protein L35

Chain o:  88% 8% ..



- Molecule 54: 50S ribosomal protein L6

Chain p:  90% 8% .



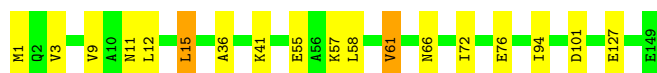
- Molecule 55: 50S ribosomal protein L36

Chain q: 87% 11%



- Molecule 56: 50S ribosomal protein L9

Chain r: 88% 11%



- Molecule 57: 50S ribosomal protein L13

Chain s: 81% 18%



- Molecule 58: 50S ribosomal protein L14

Chain t: 80% 18%



- Molecule 59: 50S ribosomal protein L15

Chain u: 88% 12%



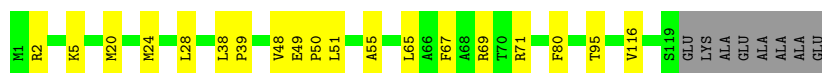
- Molecule 60: 50S ribosomal protein L16

Chain v: 91% 8%



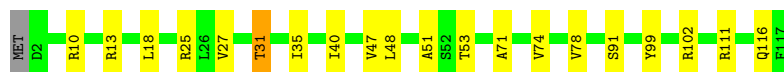
- Molecule 61: 50S ribosomal protein L17

Chain w: 79% 15% 6%



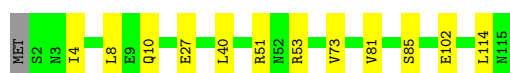
- Molecule 62: 50S ribosomal protein L18

Chain x: 82% 16% ..



- Molecule 63: 50S ribosomal protein L19

Chain y: 89% 10% .



- Molecule 64: 50S ribosomal protein L20

Chain z: 84% 14% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27378	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	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: MG, ZN

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	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.56	2/747 (0.3%)	0.81	2/1160 (0.2%)
9	9	1.15	3/1131 (0.3%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.87	9/2821 (0.3%)
11	AA	0.67	13/10591 (0.1%)	0.96	54/14289 (0.4%)
12	AB	0.43	1/808 (0.1%)	0.70	2/1088 (0.2%)
13	AC	0.60	3/1808 (0.2%)	0.73	9/2450 (0.4%)
13	AD	0.39	0/1789	0.55	0/2425
14	AE	0.54	7/10545 (0.1%)	0.74	23/14236 (0.2%)
15	C	0.66	0/553	1.14	2/743 (0.3%)
16	D	0.40	9/36610 (0.0%)	0.75	39/57091 (0.1%)
17	E	0.76	0/675	1.32	0/895
18	F	0.71	0/597	1.20	0/792
19	G	0.65	0/1791	1.08	1/2413 (0.0%)
20	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
21	I	0.58	0/1663	0.98	0/2241
22	J	0.63	0/1665	1.08	0/2227
23	K	0.63	1/1165 (0.1%)	1.06	2/1568 (0.1%)
24	L	0.58	0/867	0.94	0/1171
25	M	0.68	0/1195	1.19	3/1602 (0.2%)
26	N	0.55	0/989	0.91	0/1326
27	O	0.58	0/1034	1.02	1/1375 (0.1%)
28	P	0.60	0/800	1.11	4/1082 (0.4%)
29	Q	0.55	0/893	0.91	0/1205
30	R	0.49	0/952	0.81	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.64	0/817	1.11	1/1088 (0.1%)
32	T	0.69	0/722	1.21	0/964
33	U	0.58	0/659	0.99	0/884
34	V	0.45	0/657	0.73	0/881
35	W	0.51	0/680	0.83	0/915
36	X	0.67	0/909	1.21	3/1215 (0.2%)
37	Y	1.03	0/1046	1.08	0/1410
38	Z	1.02	0/227	1.13	0/304
39	a	0.40	3/69247 (0.0%)	0.75	55/107985 (0.1%)
40	b	0.50	0/589	0.76	0/779
41	c	0.63	0/635	0.97	0/848
42	d	0.37	0/2872	0.69	0/4478
43	e	0.69	0/502	1.19	0/667
44	f	0.62	0/452	1.02	0/605
45	g	0.55	0/531	0.99	1/709 (0.1%)
46	h	0.54	0/2121	0.85	0/2852
47	i	0.52	0/450	0.94	0/599
48	j	0.60	0/1586	0.87	0/2134
49	k	0.47	0/433	0.80	0/576
50	l	0.61	0/1571	1.03	1/2113 (0.0%)
51	m	0.68	0/380	1.22	0/498
52	n	0.62	0/1434	1.18	10/1926 (0.5%)
53	o	0.64	0/513	1.10	1/676 (0.1%)
54	p	0.58	0/1333	0.89	0/1805
55	q	0.50	0/303	0.88	0/397
56	r	0.63	0/1122	0.97	1/1515 (0.1%)
57	s	0.68	0/1152	1.02	2/1551 (0.1%)
58	t	0.57	0/955	0.88	0/1279
59	u	0.55	0/1062	0.96	1/1413 (0.1%)
60	v	0.59	0/1093	0.97	0/1460
61	w	0.67	0/964	1.13	0/1289
62	x	0.61	0/902	1.09	0/1209
63	y	0.53	0/929	0.79	0/1242
64	z	0.80	0/960	1.25	0/1278
All	All	0.50	48/189180 (0.0%)	0.84	267/278836 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	A	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	2
11	AA	0	10
14	AE	0	5
20	H	0	3
36	X	0	1
All	All	0	23

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.24	1.70	1.47
11	AA	374	GLU	C-N	17.58	1.54	1.33
11	AA	850	ILE	N-CA	-13.14	1.29	1.46
14	AE	93	THR	CA-C	12.17	1.69	1.52
20	H	169	SER	N-CA	11.79	1.61	1.46

The worst 5 of 267 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	O3'-P-O5'	17.46	130.20	104.00
11	AA	727	VAL	N-CA-C	-17.13	95.15	110.74
20	H	88	LYS	CA-C-N	16.94	143.59	120.38
20	H	88	LYS	C-N-CA	16.94	143.59	120.38
10	B	29	G	C3'-C2'-O2'	15.99	134.69	110.70

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	205	PRO	Peptide
11	AA	594	VAL	Peptide
11	AA	595	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	260	261	20	0
7	6	542	305	306	24	0
8	7	672	97	332	82	0
9	9	1117	0	1153	164	0
10	A	1620	826	826	169	0
10	B	1620	813	827	138	0
11	AA	10425	10426	10428	384	0
12	AB	790	783	783	7	0
13	AC	1786	1813	1813	77	0
13	AD	1767	1789	1789	46	0
14	AE	10388	10612	10611	369	0
15	C	544	559	560	23	0
16	D	32703	16423	16459	222	0
17	E	669	719	719	4	0
18	F	589	629	629	8	0
19	G	1760	1785	1785	47	0
20	H	1730	1454	1454	213	0
21	I	1636	1710	1710	40	0
22	J	1643	1707	1707	29	0
23	K	1152	1196	1196	20	0
24	L	848	846	846	3	0
25	M	1181	1235	1235	32	0
26	N	979	1031	1031	6	0
27	O	1022	1070	1070	11	0
28	P	790	831	831	37	0
29	Q	877	887	887	4	0
30	R	939	1001	1001	5	0
31	S	805	844	844	5	0
32	T	714	734	734	7	0
33	U	649	666	666	3	0
34	V	648	691	691	4	0
35	W	663	688	688	2	0
36	X	900	964	964	57	0
37	Y	1032	0	1088	84	0
38	Z	227	0	237	18	0
39	a	61841	31077	31123	293	0
40	b	582	599	599	2	0
41	c	625	652	652	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	d	2569	1301	1301	5	0
43	e	501	531	531	4	0
44	f	448	488	488	6	0
45	g	522	520	520	11	0
46	h	2082	2154	2154	18	0
47	i	444	459	458	6	0
48	j	1565	1617	1616	14	0
49	k	426	464	464	0	0
50	l	1552	1619	1619	13	0
51	m	377	418	418	10	0
52	n	1410	1443	1444	28	0
53	o	504	572	572	3	0
54	p	1313	1358	1358	7	0
55	q	302	343	343	2	0
56	r	1111	1148	1148	5	0
57	s	1129	1162	1162	14	0
58	t	946	1023	1023	12	0
59	u	1053	1129	1129	8	0
60	v	1074	1157	1157	5	0
61	w	951	994	994	7	0
62	x	892	923	923	10	0
63	y	917	962	962	4	0
64	z	947	1020	1019	13	0
65	AE	1	0	0	0	0
66	AE	2	0	0	0	0
All	All	175945	124723	127534	2414	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 8.

The worst 5 of 2414 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)
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.61
15:C:12:ARG:HG3	20:H:264:GLU:CB	1.30	1.53
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.47
9:9:31:ARG:NE	39:a:1054:A:H5'	1.31	1.46
11:AA:1026:GLU:HG3	16:D:1030:U:C2	1.54	1.41

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	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	43
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12	43
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	7
11	AA	1318/1341 (98%)	1150 (87%)	136 (10%)	32 (2%)	4	29
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100	100
13	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14	45
13	AD	226/329 (69%)	212 (94%)	14 (6%)	0	100	100
14	AE	1329/1407 (94%)	1200 (90%)	120 (9%)	9 (1%)	18	50
15	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
17	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
18	F	68/71 (96%)	68 (100%)	0	0	100	100
19	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	18
21	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	24	56
22	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
23	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	52
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	43
25	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	50
26	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	48
27	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	48
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	12	43
29	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	34

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
31	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
32	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	76 (95%)	3 (4%)	1 (1%)	9	38
34	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
35	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
36	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	6	34
37	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	8
38	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	12
40	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
41	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
43	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
44	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
45	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
46	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	60
47	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
48	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
49	k	50/55 (91%)	50 (100%)	0	0	100	100
50	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	56
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	42
53	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
54	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
55	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
56	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
57	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
58	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
59	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
60	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
61	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
62	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
64	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	45
All	All	9368/10481 (89%)	8607 (92%)	659 (7%)	102 (1%)	14	42

5 of 102 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	8	31
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	39
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	48
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	44
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	53
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1140/1156 (99%)	1027 (90%)	113 (10%)	7	30
12	AB	86/158 (54%)	85 (99%)	1 (1%)	63	72
13	AC	198/286 (69%)	183 (92%)	15 (8%)	12	38
13	AD	196/286 (68%)	193 (98%)	3 (2%)	57	68
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	15	42
15	C	57/65 (88%)	55 (96%)	2 (4%)	32	54
17	E	65/66 (98%)	61 (94%)	4 (6%)	16	44
18	F	60/61 (98%)	57 (95%)	3 (5%)	22	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	G	187/199 (94%)	174 (93%)	13 (7%)	14	41
20	H	137/461 (30%)	124 (90%)	13 (10%)	8	31
21	I	171/190 (90%)	163 (95%)	8 (5%)	23	48
22	J	172/173 (99%)	164 (95%)	8 (5%)	23	48
23	K	119/126 (94%)	111 (93%)	8 (7%)	15	42
24	L	91/116 (78%)	84 (92%)	7 (8%)	12	38
25	M	124/147 (84%)	113 (91%)	11 (9%)	9	33
26	N	104/105 (99%)	101 (97%)	3 (3%)	37	57
27	O	105/107 (98%)	99 (94%)	6 (6%)	18	45
28	P	86/86 (100%)	77 (90%)	9 (10%)	6	28
29	Q	90/99 (91%)	88 (98%)	2 (2%)	45	63
30	R	101/104 (97%)	95 (94%)	6 (6%)	18	44
31	S	83/84 (99%)	79 (95%)	4 (5%)	23	48
32	T	76/77 (99%)	65 (86%)	11 (14%)	3	17
33	U	65/65 (100%)	60 (92%)	5 (8%)	12	38
34	V	74/78 (95%)	71 (96%)	3 (4%)	27	52
35	W	72/79 (91%)	66 (92%)	6 (8%)	10	35
36	X	94/96 (98%)	87 (93%)	7 (7%)	13	39
37	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1
38	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
40	b	58/63 (92%)	57 (98%)	1 (2%)	53	67
41	c	67/68 (98%)	64 (96%)	3 (4%)	24	49
43	e	54/55 (98%)	51 (94%)	3 (6%)	19	46
44	f	48/49 (98%)	43 (90%)	5 (10%)	7	28
45	g	59/62 (95%)	54 (92%)	5 (8%)	10	35
46	h	216/218 (99%)	199 (92%)	17 (8%)	11	37
47	i	47/48 (98%)	41 (87%)	6 (13%)	4	21
48	j	164/164 (100%)	156 (95%)	8 (5%)	22	48
49	k	47/49 (96%)	44 (94%)	3 (6%)	16	43
50	l	165/165 (100%)	151 (92%)	14 (8%)	10	35
51	m	38/38 (100%)	36 (95%)	2 (5%)	20	46

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	n	148/150 (99%)	130 (88%)	18 (12%)	5	22
53	o	51/52 (98%)	47 (92%)	4 (8%)	11	37
54	p	136/138 (99%)	130 (96%)	6 (4%)	25	50
55	q	34/34 (100%)	31 (91%)	3 (9%)	9	33
56	r	114/114 (100%)	102 (90%)	12 (10%)	6	28
57	s	116/116 (100%)	106 (91%)	10 (9%)	10	34
58	t	104/104 (100%)	97 (93%)	7 (7%)	15	42
59	u	103/103 (100%)	96 (93%)	7 (7%)	14	42
60	v	109/109 (100%)	105 (96%)	4 (4%)	30	54
61	w	99/103 (96%)	91 (92%)	8 (8%)	11	36
62	x	86/87 (99%)	80 (93%)	6 (7%)	14	41
63	y	99/100 (99%)	91 (92%)	8 (8%)	11	36
64	z	89/90 (99%)	85 (96%)	4 (4%)	24	49
All	All	7791/8659 (90%)	7150 (92%)	641 (8%)	13	36

5 of 641 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Z	3	THR
55	q	26	ILE
38	Z	30	PHE
38	Z	2	ILE
48	j	99	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
46	h	70	ASN
47	i	5	GLN
55	q	35	GLN
14	AE	469	HIS
14	AE	424	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)
16	D	1515/1542 (98%)	289 (19%)	35 (2%)
39	a	2859/2904 (98%)	541 (18%)	0
42	d	119/120 (99%)	17 (14%)	0
8	7	31/32 (96%)	21 (67%)	3 (9%)
All	All	4674/4750 (98%)	932 (19%)	50 (1%)

5 of 932 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-9	G
8	7	-8	U
8	7	-7	U
8	7	-5	U
8	7	-4	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	532	A
16	D	1109	C
16	D	1493	A
16	D	562	U
16	D	793	U

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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-21468. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal 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.