



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:35 PM UTC

PDB ID : 6WDK / pdb_00006wdk
EMDB ID : EMD-21639
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Non-cognate Structure V-A2)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.60 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

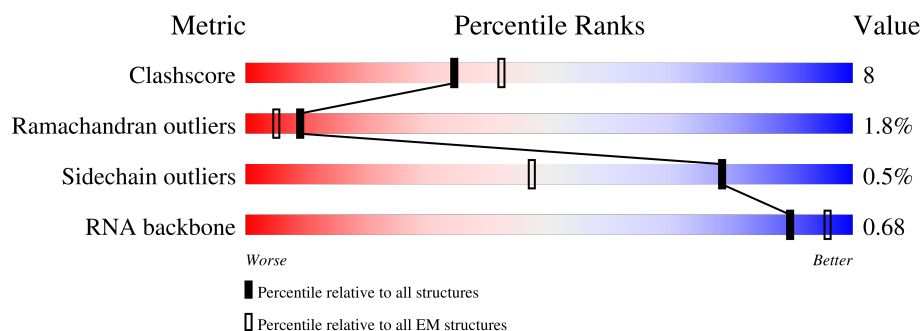
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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	73% 26% .
2	c	209	77% 22%
3	d	201	75% 24% .
4	e	177	71% 27% .
5	f	176	82% 17% .
6	g	149	70% 30%
7	h	131	63% 32% ..

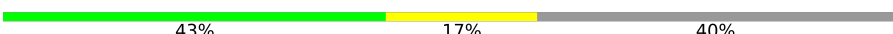
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Mol	Chain	Length	Quality of chain
8	i	141	 71% 28% .
9	j	142	 77% 22% .
10	k	122	 69% 27% .
11	l	143	 78% 20% .
12	m	136	 71% 28% .
13	n	120	 67% 33%
14	o	116	 78% 18% .
15	p	114	 68% 29% .
16	q	117	 79% 21%
17	r	103	 75% 20% 5%
18	s	110	 66% 33% .
19	t	93	 78% 20% .
20	u	102	 71% 28% .
21	v	94	 72% 28%
22	w	75	 87% 13%
23	x	77	 84% 16%
24	y	63	 73% 25% .
25	z	58	 76% 24%
26	B	56	 73% 27%
27	C	50	 94% 6%
28	D	46	 72% 28%
29	E	64	 78% 20% .
30	F	38	 61% 34% 5%
31	G	225	 80% 20%
32	H	206	 73% 27%

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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	74% 20% 7%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 150222 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

- Molecule 55 is a RNA chain called tRNA^fMet.

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

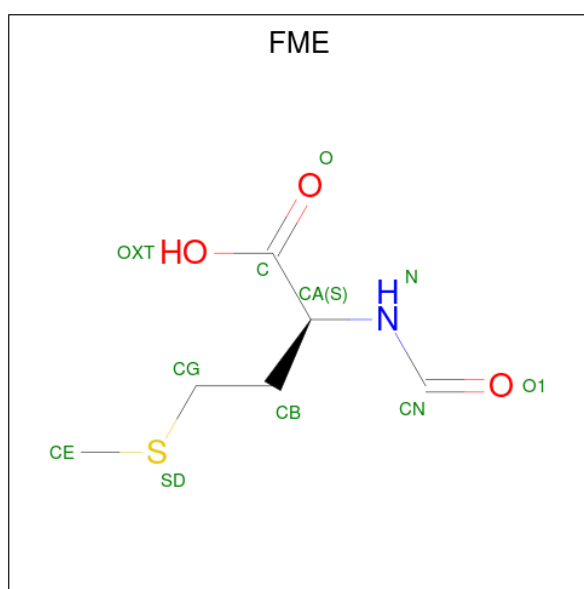
- Molecule 56 is a RNA chain called mRNA.

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

- Molecule 57 is a RNA chain called tRNA^Phe.

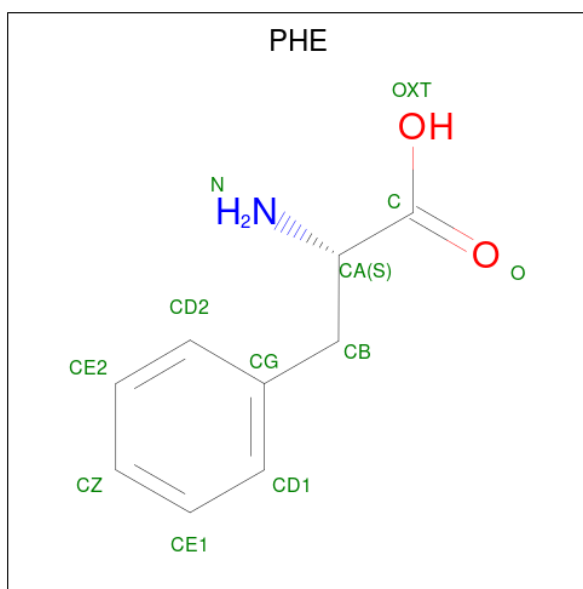
Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



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

- Molecule 59 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).

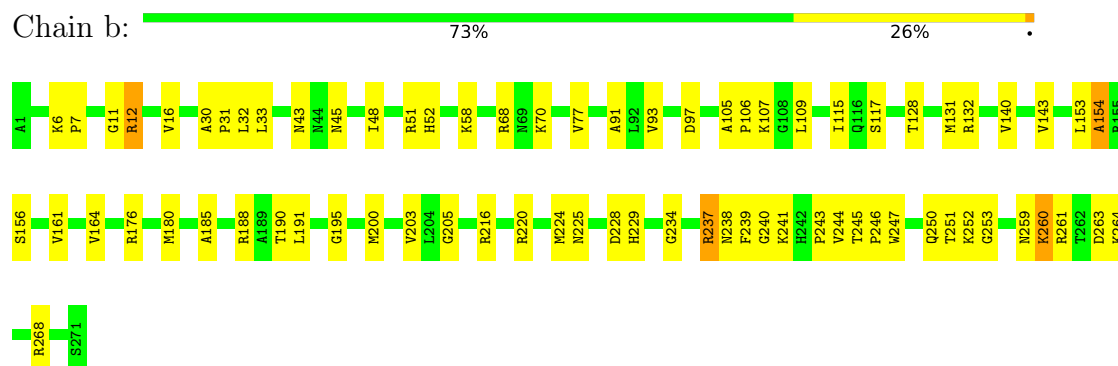


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
59	7	1	11	9	1	1	0

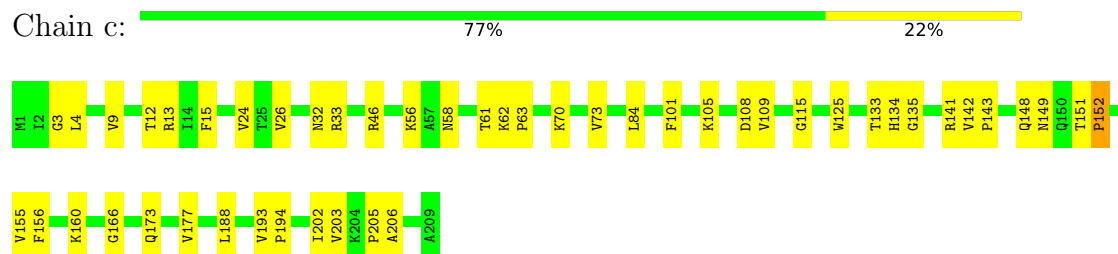
3 Residue-property plots

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.

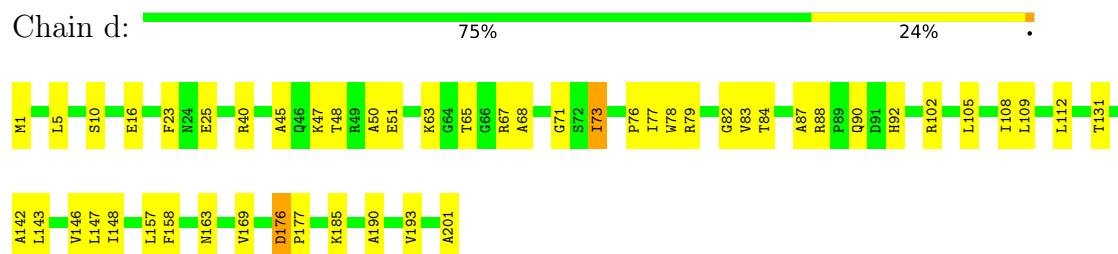
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

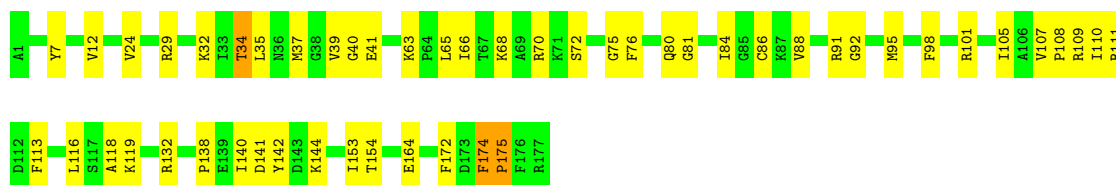


- Molecule 3: 50S ribosomal protein L4



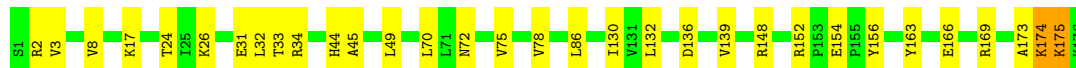
- Molecule 4: 50S ribosomal protein L5





- Molecule 5: 50S ribosomal protein L6

Chain f: 82% 17%



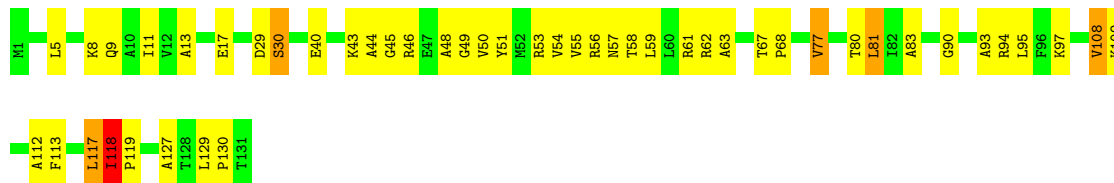
- Molecule 6: 50S ribosomal protein L9

Chain g: 70% 30%



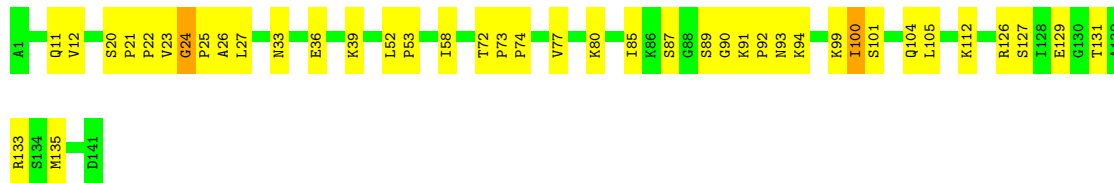
- Molecule 7: 50S ribosomal protein L10

Chain h: 63% 32%



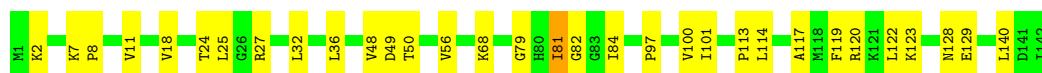
- Molecule 8: 50S ribosomal protein L11

Chain i: 71% 28%

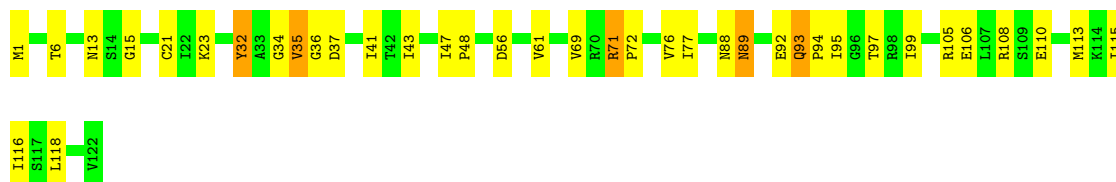


- Molecule 9: 50S ribosomal protein L13

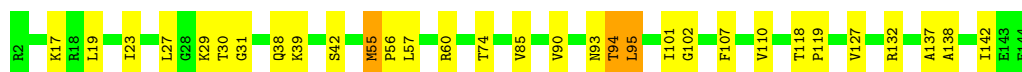
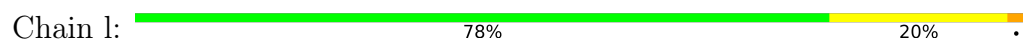
Chain j: 77% 22%



- Molecule 10: 50S ribosomal protein L14



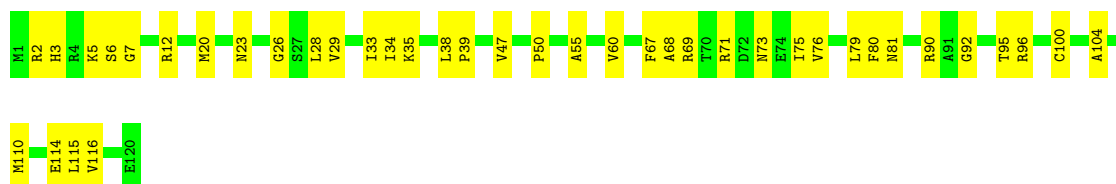
- Molecule 11: 50S ribosomal protein L15



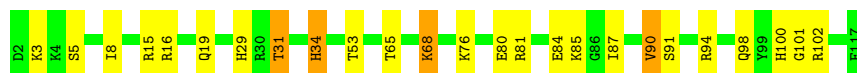
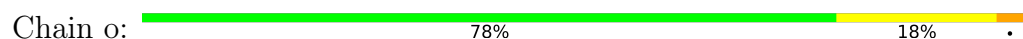
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17

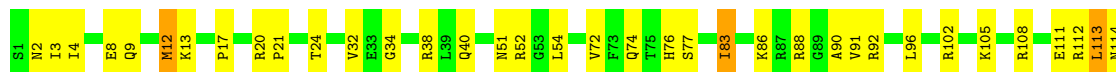


- Molecule 14: 50S ribosomal protein L18



- Molecule 15: 50S ribosomal protein L19

Chain p:  68% 29% .



- Molecule 16: 50S ribosomal protein L20

Chain q:  79% 21%



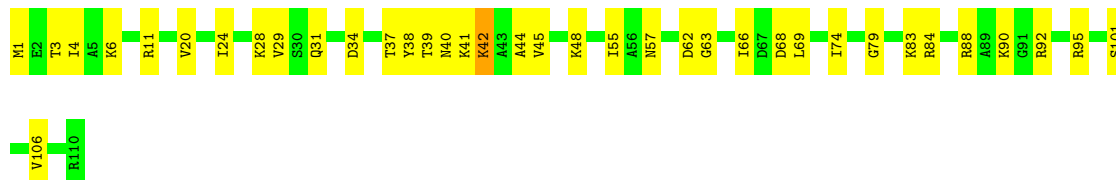
- Molecule 17: 50S ribosomal protein L21

Chain r:  75% 20% 5%



- Molecule 18: 50S ribosomal protein L22

Chain s:  66% 33% .



- Molecule 19: 50S ribosomal protein L23

Chain t:  78% 20% .



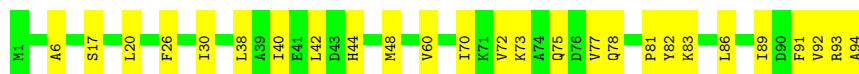
- Molecule 20: 50S ribosomal protein L24

Chain u:  71% 28% .



- Molecule 21: 50S ribosomal protein L25

Chain v:  72% 28%



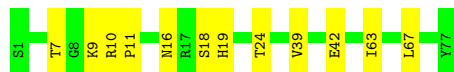
- Molecule 22: 50S ribosomal protein L27

Chain w:  87% 13%



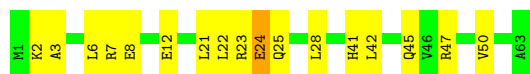
- Molecule 23: 50S ribosomal protein L28

Chain x:  84% 16%



- Molecule 24: 50S ribosomal protein L29

Chain y:  73% 25% .



- Molecule 25: 50S ribosomal protein L30

Chain z:  76% 24%

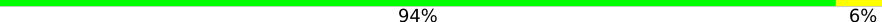


- Molecule 26: 50S ribosomal protein L32

Chain B:  73% 27%



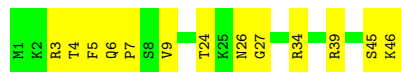
- Molecule 27: 50S ribosomal protein L33

Chain C:  94% 6%



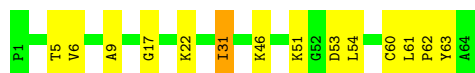
- Molecule 28: 50S ribosomal protein L34

Chain D:  72% 28%



- Molecule 29: 50S ribosomal protein L35

Chain E:  78% 20% .



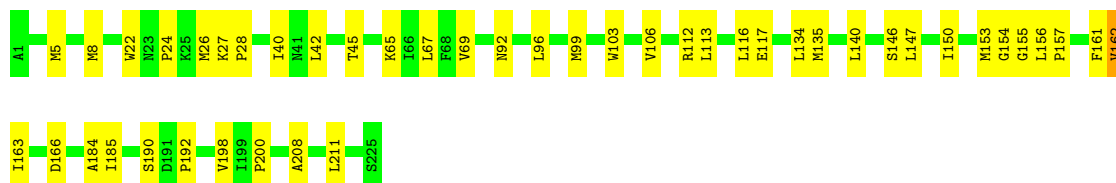
- Molecule 30: 50S ribosomal protein L36

Chain F:  61% 34% 5%



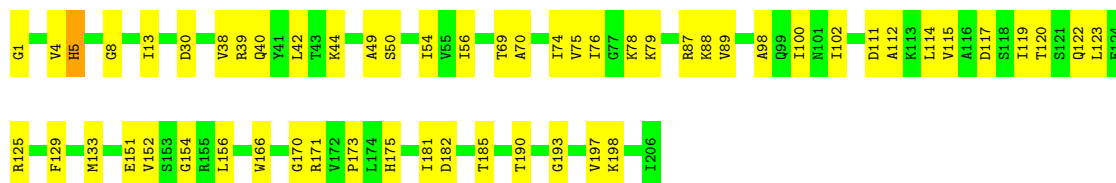
- Molecule 31: 30S ribosomal protein S2

Chain G:  80% 20%



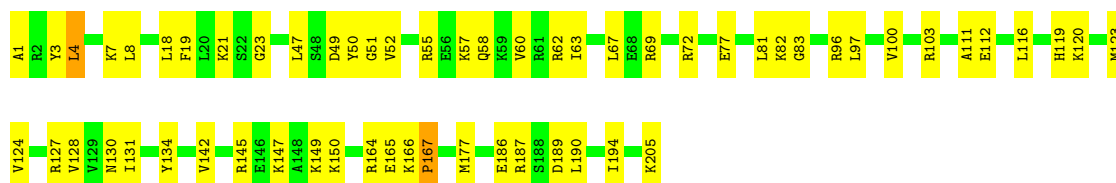
- Molecule 32: 30S ribosomal protein S3

Chain H:  73% 27%



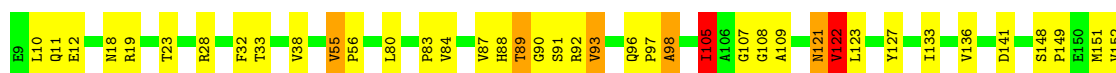
- Molecule 33: 30S ribosomal protein S4

Chain I:  71% 28% .



- Molecule 34: 30S ribosomal protein S5

Chain J:  73% 22% . .





- Molecule 35: 30S ribosomal protein S6

Chain K: 62% 32% 6%



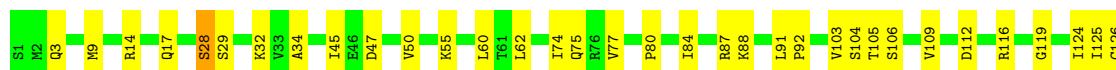
- Molecule 36: 30S ribosomal protein S7

Chain L: 63% 34% .



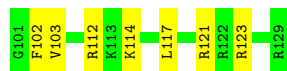
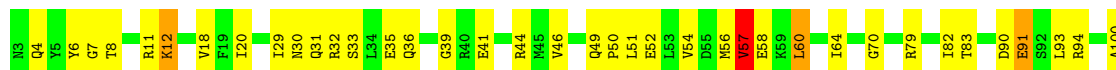
- Molecule 37: 30S ribosomal protein S8

Chain M: 74% 26% .



- Molecule 38: 30S ribosomal protein S9

Chain N: 65% 32% ..

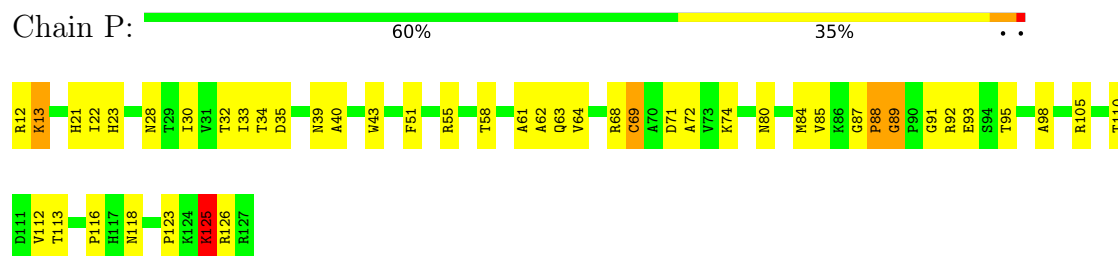


- Molecule 39: 30S ribosomal protein S10

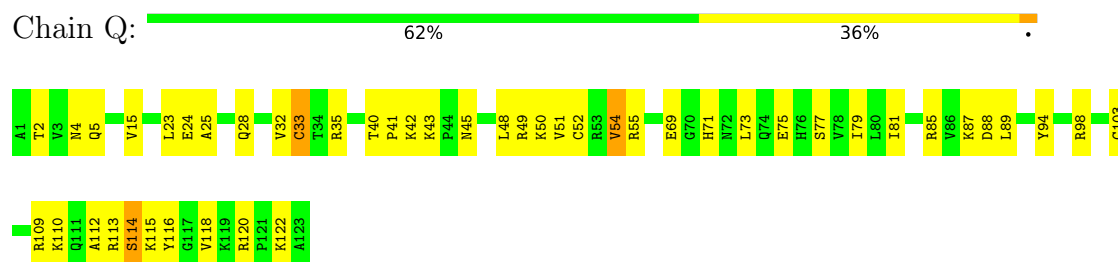
Chain O: 67% 30% ..



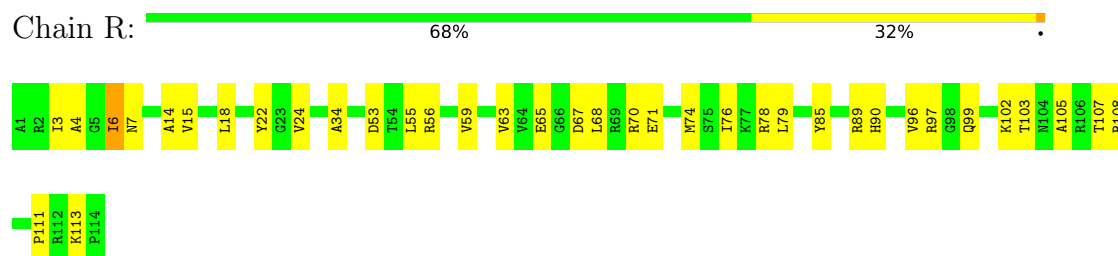
- Molecule 40: 30S ribosomal protein S11



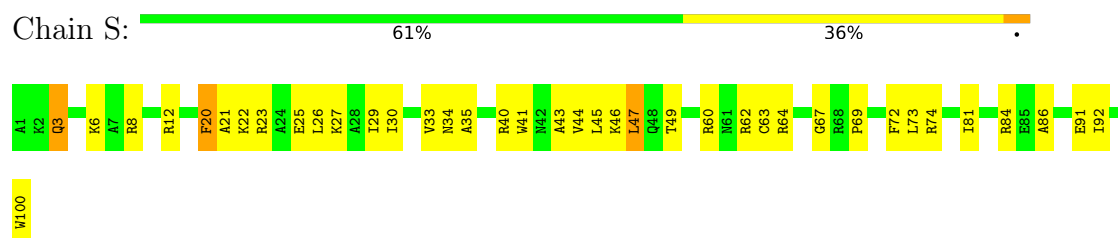
- Molecule 41: 30S ribosomal protein S12



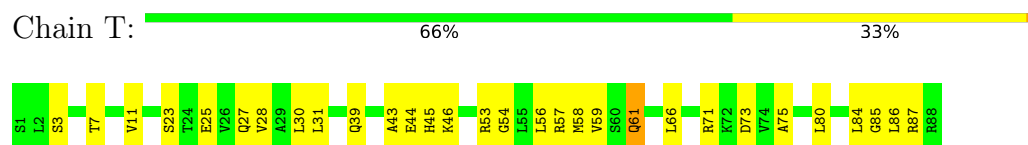
- Molecule 42: 30S ribosomal protein S13



- Molecule 43: 30S ribosomal protein S14



- Molecule 44: 30S ribosomal protein S15



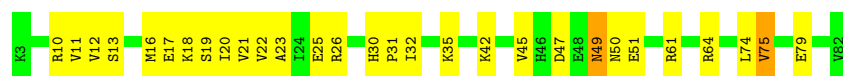
- Molecule 45: 30S ribosomal protein S16

Chain U:  66% 29% 5%



- Molecule 46: 30S ribosomal protein S17

Chain V:  64% 34% 2%



- Molecule 47: 30S ribosomal protein S18

Chain W:  72% 26% 2%



- Molecule 48: 30S ribosomal protein S19

Chain X:  66% 34% 0%



- Molecule 49: 30S ribosomal protein S20

Chain Y:  71% 29% 0%

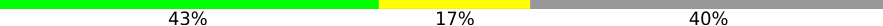


- Molecule 50: 30S ribosomal protein S21

Chain Z:  57% 37% 6%



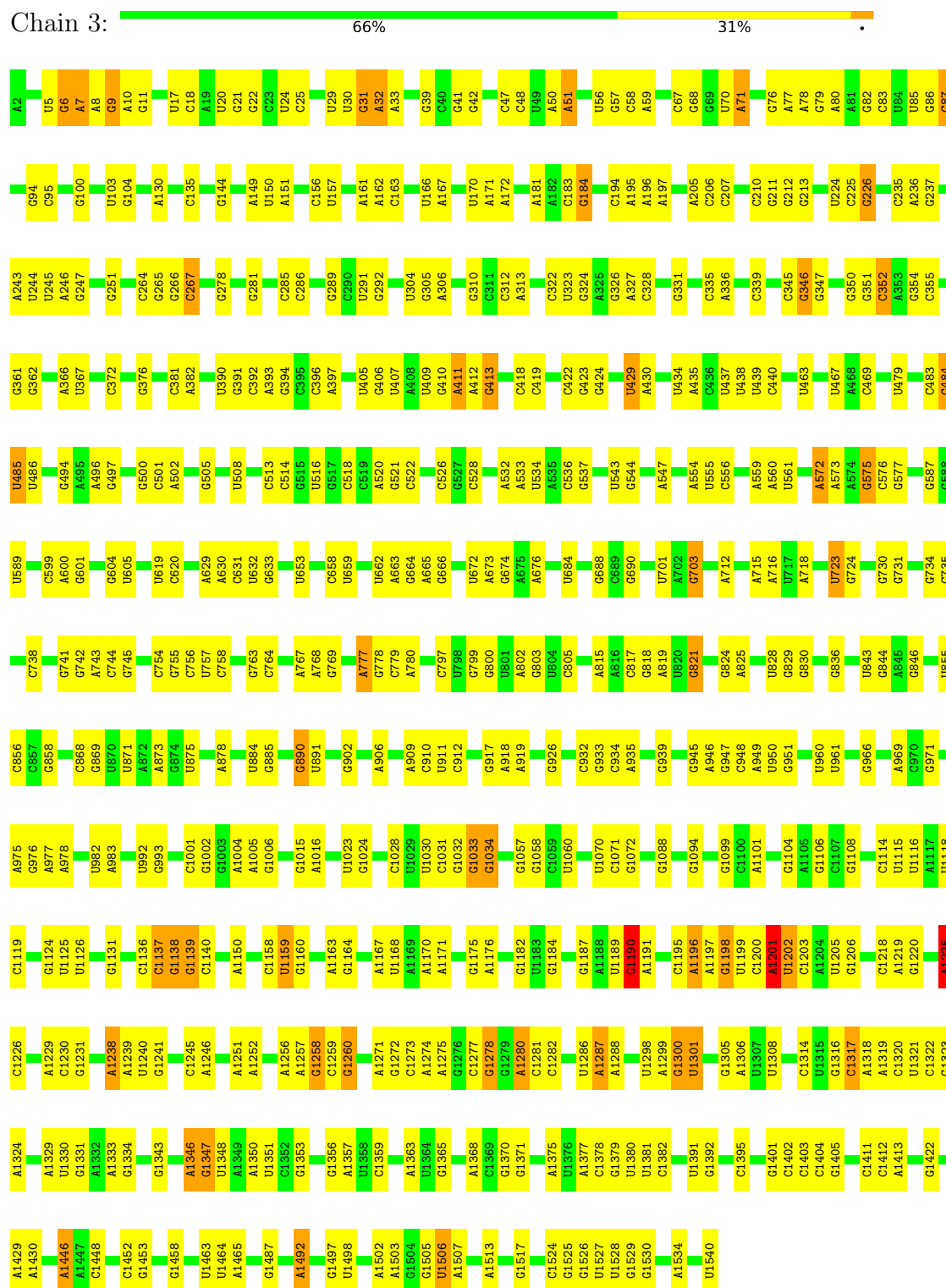
- Molecule 51: 50S ribosomal protein L1

Chain a:  43% 17% 40%



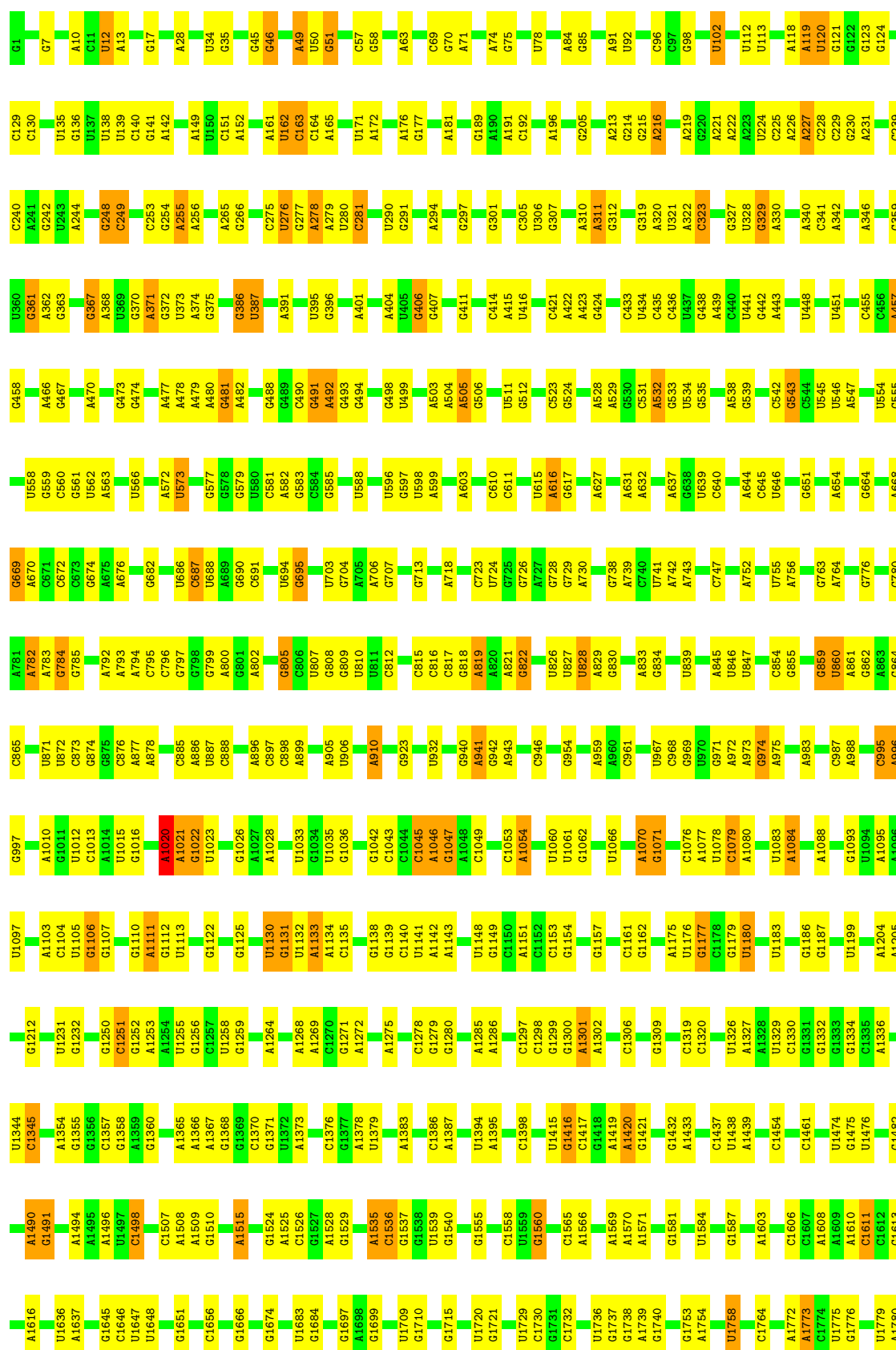
ALA GLU LEU VAL GLY MET GLU ASP LEU ALA ASP ILE LYS LYS GLY A28 L29 MET ASN PHE ASP VAL ILE ALA SER PRO ASP ALA MET ARG VAL VAL GLY GLN LEU GLY GLN VAL LEU GLY ARG VAL MET PHE PRO ASN PRO LYS VAL ALA THR VAL THR ASN VAL ALA GLU

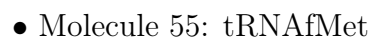
- Molecule 52: 16S ribosomal RNA



- Molecule 53: 23S ribosomal RNA

Chain 1:  65% 30% 5%







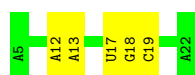
- Molecule 55: tRNAfMet

Chain 6: 73% 23% .



- Molecule 56: mRNA

Chain 4: 72% 28%



- Molecule 57: tRNAPhe

Chain 7: 74% 20% 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	11041	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	0.90	4/2852 (0.1%)
2	c	0.28	0/1586	0.83	2/2134 (0.1%)
3	d	0.28	0/1571	0.85	4/2113 (0.2%)
4	e	0.30	0/1435	0.89	5/1926 (0.3%)
5	f	0.29	0/1343	0.85	1/1816 (0.1%)
6	g	0.30	0/1122	0.92	0/1515
7	h	0.34	0/1002	0.97	3/1350 (0.2%)
8	i	0.34	0/1046	0.94	3/1410 (0.2%)
9	j	0.28	0/1152	0.86	2/1551 (0.1%)
10	k	0.27	0/948	0.93	4/1268 (0.3%)
11	l	0.29	0/1054	0.90	4/1403 (0.3%)
12	m	0.28	0/1093	0.78	0/1460
13	n	0.30	0/974	0.90	3/1301 (0.2%)
14	o	0.28	0/902	0.86	1/1209 (0.1%)
15	p	0.28	0/929	0.83	0/1242
16	q	0.28	0/960	0.88	2/1278 (0.2%)
17	r	0.29	0/829	0.79	1/1107 (0.1%)
18	s	0.27	0/864	0.90	4/1156 (0.3%)
19	t	0.26	0/745	0.78	1/994 (0.1%)
20	u	0.27	0/788	0.87	0/1051
21	v	0.27	0/766	0.76	0/1025
22	w	0.27	0/582	0.80	0/769
23	x	0.27	0/635	0.85	2/848 (0.2%)
24	y	0.27	0/510	0.91	1/677 (0.1%)
25	z	0.29	0/453	0.78	0/605
26	B	0.28	0/450	0.77	0/599
27	C	0.32	0/417	0.82	0/554
28	D	0.32	0/380	1.03	3/498 (0.6%)
29	E	0.28	0/513	0.89	1/676 (0.1%)
30	F	0.30	0/303	0.89	2/397 (0.5%)
31	G	0.30	0/1788	0.87	3/2408 (0.1%)
32	H	0.30	0/1652	0.89	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.29	0/1665	0.88	2/2227 (0.1%)
34	J	0.31	0/1170	0.93	5/1573 (0.3%)
35	K	0.31	0/836	0.95	3/1128 (0.3%)
36	L	0.28	0/1196	0.94	5/1602 (0.3%)
37	M	0.28	0/989	0.86	3/1326 (0.2%)
38	N	0.29	0/1034	0.89	3/1375 (0.2%)
39	O	0.33	0/797	0.90	0/1077
40	P	0.31	0/886	0.92	3/1195 (0.3%)
41	Q	0.30	0/969	0.99	3/1300 (0.2%)
42	R	0.30	0/893	0.92	4/1193 (0.3%)
43	S	0.29	0/817	0.88	2/1088 (0.2%)
44	T	0.28	0/722	0.91	4/964 (0.4%)
45	U	0.31	0/659	0.91	2/884 (0.2%)
46	V	0.26	0/658	0.99	3/881 (0.3%)
47	W	0.32	0/545	1.01	4/731 (0.5%)
48	X	0.32	0/653	0.90	1/877 (0.1%)
49	Y	0.29	0/671	0.93	4/888 (0.5%)
50	Z	0.34	0/551	1.01	3/728 (0.4%)
51	a	0.30	0/1034	0.79	0/1387
52	3	0.40	0/36963	0.50	5/57662 (0.0%)
53	1	0.39	0/69796	0.50	2/108888 (0.0%)
54	2	0.40	0/2872	0.50	0/4479
55	5	0.40	0/1832	0.47	0/2855
55	6	0.40	0/1832	0.52	0/2855
56	4	0.40	0/436	0.49	0/679
57	7	0.39	0/1809	0.48	0/2819
All	All	0.37	0/163199	0.62	123/244078 (0.1%)

There are no bond length outliers.

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	V	75	VAL	N-CA-C	-11.00	102.10	111.56
1	b	259	ASN	N-CA-C	-8.62	104.79	114.62
50	Z	21	SER	N-CA-C	-8.37	102.63	112.92
28	D	6	GLN	CA-C-N	8.15	128.17	119.78
28	D	6	GLN	C-N-CA	8.15	128.17	119.78

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	56	0
2	c	1565	0	1616	34	0
3	d	1552	0	1619	33	0
4	e	1411	0	1447	41	0
5	f	1323	0	1374	28	0
6	g	1111	0	1148	31	0
7	h	989	0	1025	38	0
8	i	1032	0	1088	41	0
9	j	1129	0	1162	25	0
10	k	939	0	1012	25	0
11	l	1045	0	1117	20	0
12	m	1074	0	1157	29	0
13	n	961	0	1000	26	0
14	o	892	0	923	22	0
15	p	917	0	965	31	0
16	q	947	0	1022	19	0
17	r	816	0	839	23	0
18	s	857	0	922	25	0
19	t	739	0	807	15	0
20	u	780	0	834	19	0
21	v	753	0	780	17	0
22	w	575	0	592	8	0
23	x	625	0	655	9	0
24	y	509	0	543	14	0
25	z	449	0	491	9	0
26	B	444	0	461	13	0
27	C	410	0	440	2	0
28	D	377	0	418	8	0
29	E	504	0	574	10	0
30	F	302	0	343	13	0
31	G	1757	0	1787	30	0
32	H	1625	0	1699	35	0
33	I	1643	0	1710	40	0
34	J	1157	0	1199	25	0
35	K	818	0	808	28	0
36	L	1182	0	1240	43	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	32	0
39	O	787	0	828	26	0
40	P	870	0	878	39	0
41	Q	955	0	1019	36	0
42	R	884	0	944	24	0
43	S	805	0	847	30	0
44	T	714	0	737	20	0
45	U	649	0	666	22	0
46	V	649	0	691	19	0
47	W	536	0	552	11	0
48	X	638	0	665	18	0
49	Y	665	0	714	14	0
50	Z	545	0	579	26	0
51	a	1027	0	1092	26	0
52	3	33012	0	16618	355	0
53	1	62317	0	31346	669	0
54	2	2568	0	1303	44	0
55	5	1640	0	836	10	0
55	6	1640	0	837	11	0
56	4	388	0	197	1	0
57	7	1619	0	821	11	0
58	5	10	0	10	0	0
59	7	11	0	8	0	0
All	All	150222	0	101266	2038	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 2038 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'	1.28	1.15
8:i:25:PRO:HB2	53:1:1095:A:H61	1.12	1.14
9:j:100:VAL:HG13	9:j:101:ILE:HD12	1.41	1.00
8:i:91:LYS:HE2	8:i:91:LYS:HA	1.47	0.94
12:m:12:MET:HA	53:1:910:A:H62	1.31	0.94

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%)	240 (89%)	24 (9%)	5 (2%)	6	33
2	c	207/209 (99%)	181 (87%)	26 (13%)	0	100	100
3	d	199/201 (99%)	185 (93%)	13 (6%)	1 (0%)	24	57
4	e	175/177 (99%)	152 (87%)	22 (13%)	1 (1%)	21	54
5	f	174/176 (99%)	163 (94%)	9 (5%)	2 (1%)	11	43
6	g	147/149 (99%)	129 (88%)	16 (11%)	2 (1%)	9	38
7	h	129/131 (98%)	98 (76%)	26 (20%)	5 (4%)	2	20
8	i	139/141 (99%)	120 (86%)	18 (13%)	1 (1%)	18	51
9	j	140/142 (99%)	130 (93%)	9 (6%)	1 (1%)	18	51
10	k	120/122 (98%)	97 (81%)	19 (16%)	4 (3%)	3	24
11	l	141/143 (99%)	116 (82%)	22 (16%)	3 (2%)	5	31
12	m	134/136 (98%)	123 (92%)	8 (6%)	3 (2%)	5	30
13	n	118/120 (98%)	97 (82%)	20 (17%)	1 (1%)	16	49
14	o	114/116 (98%)	103 (90%)	9 (8%)	2 (2%)	6	34
15	p	112/114 (98%)	97 (87%)	14 (12%)	1 (1%)	14	46
16	q	115/117 (98%)	106 (92%)	8 (7%)	1 (1%)	14	46
17	r	101/103 (98%)	83 (82%)	14 (14%)	4 (4%)	2	20
18	s	108/110 (98%)	99 (92%)	7 (6%)	2 (2%)	6	33
19	t	91/93 (98%)	81 (89%)	9 (10%)	1 (1%)	11	43
20	u	100/102 (98%)	86 (86%)	10 (10%)	4 (4%)	2	20
21	v	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
22	w	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
23	x	75/77 (97%)	69 (92%)	5 (7%)	1 (1%)	9	39
24	y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
25	z	56/58 (97%)	52 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	49 (91%)	4 (7%)	1 (2%)	6	33
27	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
28	D	44/46 (96%)	41 (93%)	1 (2%)	2 (4%)	2	17
29	E	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	7	36
30	F	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	26
31	G	223/225 (99%)	200 (90%)	22 (10%)	1 (0%)	30	61
32	H	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
33	I	203/205 (99%)	176 (87%)	23 (11%)	4 (2%)	6	32
34	J	155/157 (99%)	126 (81%)	22 (14%)	7 (4%)	2	17
35	K	98/100 (98%)	76 (78%)	18 (18%)	4 (4%)	2	19
36	L	149/151 (99%)	132 (89%)	14 (9%)	3 (2%)	6	32
37	M	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	49
38	N	125/127 (98%)	101 (81%)	18 (14%)	6 (5%)	2	16
39	O	96/98 (98%)	77 (80%)	14 (15%)	5 (5%)	1	15
40	P	114/116 (98%)	95 (83%)	14 (12%)	5 (4%)	2	18
41	Q	121/123 (98%)	95 (78%)	20 (16%)	6 (5%)	1	16
42	R	112/114 (98%)	96 (86%)	12 (11%)	4 (4%)	2	22
43	S	98/100 (98%)	85 (87%)	12 (12%)	1 (1%)	12	45
44	T	86/88 (98%)	75 (87%)	10 (12%)	1 (1%)	10	41
45	U	80/82 (98%)	70 (88%)	9 (11%)	1 (1%)	9	39
46	V	78/80 (98%)	62 (80%)	14 (18%)	2 (3%)	4	27
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	36
48	X	77/79 (98%)	66 (86%)	10 (13%)	1 (1%)	9	39
49	Y	83/85 (98%)	79 (95%)	3 (4%)	1 (1%)	10	41
50	Z	63/65 (97%)	40 (64%)	19 (30%)	4 (6%)	1	12
51	a	130/223 (58%)	126 (97%)	4 (3%)	0	100	100
All	All	5919/6112 (97%)	5162 (87%)	649 (11%)	108 (2%)	9	34

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
7	h	108	VAL

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Mol	Chain	Res	Type
7	h	118	ILE
11	l	31	GLY
11	l	85	VAL

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%)	164 (100%)	0	100	100
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%)	98 (98%)	2 (2%)	48	66
8	i	109/109 (100%)	108 (99%)	1 (1%)	70	76
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	75
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	75
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	76
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	64
15	p	99/99 (100%)	97 (98%)	2 (2%)	48	66
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	74
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100

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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%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	33 (97%)	1 (3%)	37	60
31	G	186/186 (100%)	185 (100%)	1 (0%)	81	80
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	172 (100%)	0	100	100
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	77
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	74
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	75
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	73
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	75
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	73
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	71
47	W	56/56 (100%)	55 (98%)	1 (2%)	51	68
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%)	53 (96%)	2 (4%)	31	56
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4883 (100%)	25 (0%)	78	80

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	J	105	ILE
39	O	89	ARG
50	Z	37	TYR
37	M	75	GLN
41	Q	75	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 130 such sidechains are listed below:

Mol	Chain	Res	Type
46	V	8	GLN
48	X	56	HIS
14	o	116	GLN
14	o	19	GLN
49	Y	51	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	138 (8%)	2 (0%)
53	1	2902/2903 (99%)	335 (11%)	11 (0%)
54	2	119/120 (99%)	10 (8%)	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%)	11 (14%)	0
All	All	4803/4810 (99%)	513 (10%)	14 (0%)

5 of 513 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	22	G
52	3	31	G

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](#)

2 ligands 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	$\# Z > 2$
59	PHE	7	101	57	10,11,12	0.69	0	8,13,15	0.29	0
58	FME	5	101	55	8,9,10	0.50	0	8,9,11	0.82	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
59	PHE	7	101	57	-	0/5/6/8	0/1/1/1
58	FME	5	101	55	-	2/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	5	101	FME	O1-CN-N-CA
58	5	101	FME	O-C-CA-CB

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-21639. 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.