



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 21, 2017 – 07:25 AM EDT

PDB ID : 5LZU  
EMDB ID: : EMD-4132  
Title : Structure of the mammalian ribosomal termination complex with accommodated eRF1  
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.  
Deposited on : unknown  
Resolution : 3.75 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

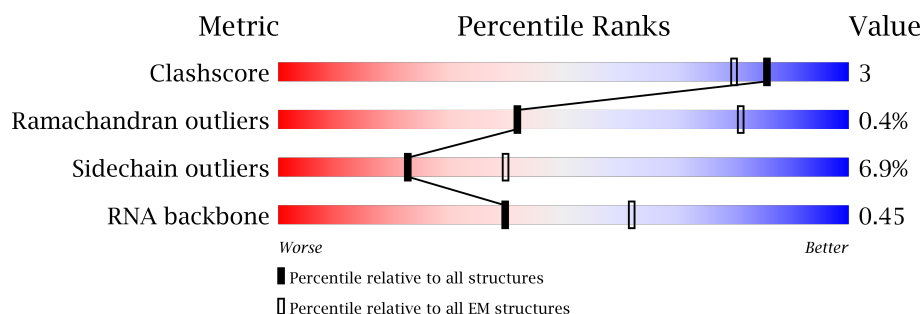
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.75 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.




















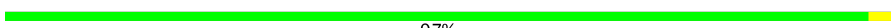







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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

Mol	Chain	Length	Quality of chain
1	A	257	80% 16% . .
2	B	403	85% 13% .
3	C	425	74% 11% 15%
4	D	297	90% 7% . .
5	E	291	66% 7% . 26%
6	F	247	82% 8% . 9%
7	G	319	63% 10% 27%
8	H	192	84% 15% .



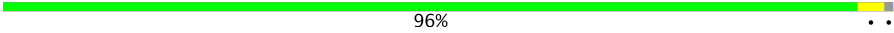
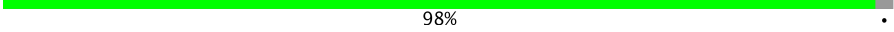



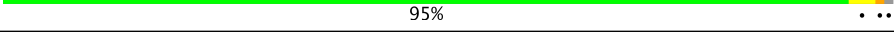


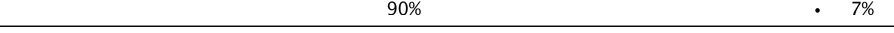
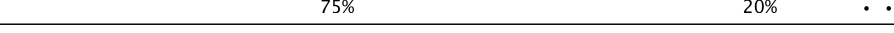
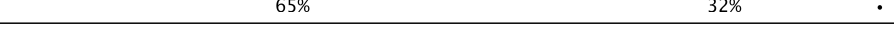


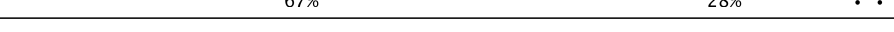









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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	245	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	






















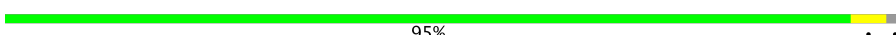


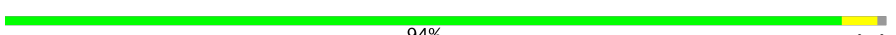
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Mol	Chain	Length	Quality of chain
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	102	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	318	
44	t	165	
45	2	76	
46	3	75	
47	5	3543	
48	7	120	
49	8	156	
50	9	1869	
51	AA	295	
52	BB	264	
53	CC	293	
54	DD	243	
55	EE	263	
56	FF	204	
57	GG	249	
58	HH	194	



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Mol	Chain	Length	Quality of chain
59	II	208	
60	JJ	194	
61	KK	165	
62	LL	158	
63	MM	132	
64	NN	151	
65	OO	168	
66	PP	145	
67	QQ	146	
68	RR	135	
69	SS	152	
70	TT	145	
71	UU	119	
72	VV	83	
73	WW	130	
74	XX	143	
75	YY	130	
76	ZZ	125	
77	aa	115	
78	bb	84	
79	cc	69	
80	dd	56	
81	ee	133	
82	ff	156	
83	gg	317	

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Mol	Chain	Length	Quality of chain
84	hh	15	 47% 53%
85	ii	459	 86% 5% 9%

## 2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 219122 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	379	VAL	-	expression tag	UNP G1SVW5
C	380	LYS	-	expression tag	UNP G1SVW5
C	381	LYS	-	expression tag	UNP G1SVW5
C	382	PRO	-	expression tag	UNP G1SVW5
C	383	ARG	-	expression tag	UNP G1SVW5
C	384	ALA	-	expression tag	UNP G1SVW5
C	385	VAL	-	expression tag	UNP G1SVW5
C	386	GLY	-	expression tag	UNP G1SVW5
C	387	ILE	-	expression tag	UNP G1SVW5
C	388	LYS	-	expression tag	UNP G1SVW5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	389	GLN	-	expression tag	UNP G1SVW5
C	390	LYS	-	expression tag	UNP G1SVW5
C	391	LYS	-	expression tag	UNP G1SVW5
C	392	LYS	-	expression tag	UNP G1SVW5
C	393	PRO	-	expression tag	UNP G1SVW5
C	394	VAL	-	expression tag	UNP G1SVW5
C	395	VAL	-	expression tag	UNP G1SVW5
C	396	GLY	-	expression tag	UNP G1SVW5
C	397	ARG	-	expression tag	UNP G1SVW5
C	398	LYS	-	expression tag	UNP G1SVW5
C	399	ALA	-	expression tag	UNP G1SVW5
C	400	ALA	-	expression tag	UNP G1SVW5
C	401	ALA	-	expression tag	UNP G1SVW5
C	402	ALA	-	expression tag	UNP G1SVW5
C	403	LYS	-	expression tag	UNP G1SVW5
C	404	LYS	-	expression tag	UNP G1SVW5
C	405	PRO	-	expression tag	UNP G1SVW5
C	406	ALA	-	expression tag	UNP G1SVW5
C	407	ALA	-	expression tag	UNP G1SVW5
C	408	ASP	-	expression tag	UNP G1SVW5
C	409	LYS	-	expression tag	UNP G1SVW5
C	410	LYS	-	expression tag	UNP G1SVW5
C	411	ALA	-	expression tag	UNP G1SVW5
C	412	ALA	-	expression tag	UNP G1SVW5
C	413	ASP	-	expression tag	UNP G1SVW5
C	414	LYS	-	expression tag	UNP G1SVW5
C	415	ARG	-	expression tag	UNP G1SVW5
C	416	ALA	-	expression tag	UNP G1SVW5
C	417	GLY	-	expression tag	UNP G1SVW5
C	418	PRO	-	expression tag	UNP G1SVW5
C	419	GLU	-	expression tag	UNP G1SVW5
C	420	ASP	-	expression tag	UNP G1SVW5
C	421	LYS	-	expression tag	UNP G1SVW5
C	422	LYS	-	expression tag	UNP G1SVW5
C	423	PRO	-	expression tag	UNP G1SVW5
C	424	ALA	-	expression tag	UNP G1SVW5
C	425	ALA	-	expression tag	UNP G1SVW5

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		



There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP G1SYJ6

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	1	MET	-	initiating methionine	UNP G1SV32
F	2	GLU	-	expression tag	UNP G1SV32
F	3	GLY	-	expression tag	UNP G1SV32
F	4	ALA	-	expression tag	UNP G1SV32
F	5	GLU	-	expression tag	UNP G1SV32

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	1	MET	-	initiating methionine	UNP G1STW0
G	2	SER	-	expression tag	UNP G1STW0
G	3	SER	-	expression tag	UNP G1STW0
G	4	TYR	-	expression tag	UNP G1STW0
G	5	ARG	-	expression tag	UNP G1STW0
G	6	LEU	-	expression tag	UNP G1STW0
G	7	GLY	-	expression tag	UNP G1STW0
G	8	TYR	-	expression tag	UNP G1STW0
G	9	CYS	-	expression tag	UNP G1STW0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	10	MET	-	expression tag	UNP G1STW0
G	11	LYS	-	expression tag	UNP G1STW0
G	12	GLU	-	expression tag	UNP G1STW0
G	13	GLU	-	expression tag	UNP G1STW0
G	14	ARG	-	expression tag	UNP G1STW0
G	15	HIS	-	expression tag	UNP G1STW0
G	16	ASN	-	expression tag	UNP G1STW0
G	17	LEU	-	expression tag	UNP G1STW0
G	18	VAL	-	expression tag	UNP G1STW0
G	19	LEU	-	expression tag	UNP G1STW0
G	20	CYS	-	expression tag	UNP G1STW0
G	21	LEU	-	expression tag	UNP G1STW0
G	22	TRP	-	expression tag	UNP G1STW0
G	23	SER	-	expression tag	UNP G1STW0
G	24	GLN	-	expression tag	UNP G1STW0
G	25	SER	-	expression tag	UNP G1STW0
G	26	PRO	-	expression tag	UNP G1STW0
G	27	GLY	-	expression tag	UNP G1STW0
G	28	ILE	-	expression tag	UNP G1STW0
G	29	LEU	-	expression tag	UNP G1STW0
G	30	ASN	-	expression tag	UNP G1STW0
G	31	SER	-	expression tag	UNP G1STW0
G	32	LYS	-	expression tag	UNP G1STW0
G	33	CYS	-	expression tag	UNP G1STW0
G	34	LEU	-	expression tag	UNP G1STW0
G	35	TRP	-	expression tag	UNP G1STW0
G	36	PRO	-	expression tag	UNP G1STW0
G	37	PHE	-	expression tag	UNP G1STW0
G	38	THR	-	expression tag	UNP G1STW0
G	39	ASN	-	expression tag	UNP G1STW0
G	40	ILE	-	expression tag	UNP G1STW0
G	41	HIS	-	expression tag	UNP G1STW0
G	42	LEU	-	expression tag	UNP G1STW0
G	43	LEU	-	expression tag	UNP G1STW0
G	44	VAL	-	expression tag	UNP G1STW0
G	45	GLY	-	expression tag	UNP G1STW0
G	46	ALA	-	expression tag	UNP G1STW0
G	47	LEU	-	expression tag	UNP G1STW0
G	48	PRO	-	expression tag	UNP G1STW0
G	49	ARG	-	expression tag	UNP G1STW0
G	50	GLU	-	expression tag	UNP G1STW0
G	51	GLY	-	expression tag	UNP G1STW0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	52	ALA	-	expression tag	UNP G1STW0
G	53	GLY	-	expression tag	UNP G1STW0
G	54	GLY	-	expression tag	UNP G1STW0
G	55	ALA	-	expression tag	UNP G1STW0
G	56	TRP	-	expression tag	UNP G1STW0
G	57	GLY	-	expression tag	UNP G1STW0
G	58	GLY	-	expression tag	UNP G1STW0
G	59	GLY	-	expression tag	UNP G1STW0
G	60	ARG	-	expression tag	UNP G1STW0
G	61	SER	-	expression tag	UNP G1STW0
G	62	GLU	-	expression tag	UNP G1STW0
G	63	GLN	-	expression tag	UNP G1STW0
G	64	LEU	-	expression tag	UNP G1STW0
G	65	PRO	-	expression tag	UNP G1STW0
G	66	THR	-	expression tag	UNP G1STW0
G	67	CYS	-	expression tag	UNP G1STW0
G	68	SER	-	expression tag	UNP G1STW0
G	69	THR	-	expression tag	UNP G1STW0
G	70	THR	-	expression tag	UNP G1STW0
G	71	HIS	-	expression tag	UNP G1STW0
G	72	HIS	-	expression tag	UNP G1STW0
G	73	ASP	-	expression tag	UNP G1STW0
G	74	PHE	-	expression tag	UNP G1STW0
G	75	THR	-	expression tag	UNP G1STW0
G	76	TRP	-	expression tag	UNP G1STW0
G	77	ASP	-	expression tag	UNP G1STW0
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	GLN	conflict	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	227	ALA	-	expression tag	UNP G1SGR6
b	228	PRO	-	expression tag	UNP G1SGR6
b	229	VAL	-	expression tag	UNP G1SGR6
b	230	PRO	-	expression tag	UNP G1SGR6
b	231	ALA	-	expression tag	UNP G1SGR6
b	232	GLN	-	expression tag	UNP G1SGR6
b	233	ALA	-	expression tag	UNP G1SGR6
b	234	PRO	-	expression tag	UNP G1SGR6
b	235	PRO	-	expression tag	UNP G1SGR6
b	236	LYS	-	expression tag	UNP G1SGR6
b	237	GLY	-	expression tag	UNP G1SGR6
b	238	ALA	-	expression tag	UNP G1SGR6
b	239	GLN	-	expression tag	UNP G1SGR6

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Chain	Residue	Modelled	Actual	Comment	Reference
b	240	PRO	-	expression tag	UNP G1SGR6
b	241	PRO	-	expression tag	UNP G1SGR6
b	242	ALA	-	expression tag	UNP G1SGR6
b	243	LYS	-	expression tag	UNP G1SGR6
b	244	ALA	-	expression tag	UNP G1SGR6
b	245	PRO	-	expression tag	UNP G1SGR6

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	117	LYS	-	expression tag	UNP G1U945

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called 60s ribosomal protein l41.



Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 46 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 47 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 48 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 49 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 50 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	9	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 51 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 52 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 54 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 55 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 56 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 57 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 59 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 60 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
60	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 61 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 62 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 63 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 64 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
OO	-16	MET	-	initiating methionine	UNP G1T1F0
OO	-15	LYS	-	expression tag	UNP G1T1F0
OO	-14	ALA	-	expression tag	UNP G1T1F0
OO	-13	ARG	-	expression tag	UNP G1T1F0
OO	-12	ALA	-	expression tag	UNP G1T1F0
OO	-11	LEU	-	expression tag	UNP G1T1F0
OO	-10	SER	-	expression tag	UNP G1T1F0
OO	-9	GLY	-	expression tag	UNP G1T1F0
OO	-8	SER	-	expression tag	UNP G1T1F0
OO	-7	GLY	-	expression tag	UNP G1T1F0
OO	-6	VAL	-	expression tag	UNP G1T1F0
OO	-5	ARG	-	expression tag	UNP G1T1F0

- Molecule 66 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	PP	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 67 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 68 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 69 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 70 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 71 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 72 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 73 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 75 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 76 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 77 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 79 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 80 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 81 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 82 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 83 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 84 is a RNA chain called mRNA (UGA stop codon).

Mol	Chain	Residues	Atoms					AltConf	Trace
84	hh	15	Total	C	N	O	P	0	0
			317	142	54	106	15		

- Molecule 85 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	ii	418	Total	C	N	O	S	0	0
			3295	2095	561	627	12		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	-21	MET	-	initiating methionine	UNP P62495
ii	-20	ARG	-	expression tag	UNP P62495
ii	-19	GLY	-	expression tag	UNP P62495
ii	-18	SER	-	expression tag	UNP P62495
ii	-17	HIS	-	expression tag	UNP P62495
ii	-16	HIS	-	expression tag	UNP P62495
ii	-15	HIS	-	expression tag	UNP P62495
ii	-14	HIS	-	expression tag	UNP P62495
ii	-13	HIS	-	expression tag	UNP P62495
ii	-12	HIS	-	expression tag	UNP P62495
ii	-11	GLY	-	expression tag	UNP P62495
ii	-10	MET	-	expression tag	UNP P62495
ii	-9	ALA	-	expression tag	UNP P62495
ii	-8	SER	-	expression tag	UNP P62495
ii	-7	GLU	-	expression tag	UNP P62495
ii	-6	ASN	-	expression tag	UNP P62495
ii	-5	LEU	-	expression tag	UNP P62495
ii	-4	TYR	-	expression tag	UNP P62495
ii	-3	PHE	-	expression tag	UNP P62495
ii	-2	GLN	-	expression tag	UNP P62495
ii	-1	GLY	-	expression tag	UNP P62495
ii	0	SER	-	expression tag	UNP P62495

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



Mol	Chain	Residues	Atoms		AltConf
86	P	1	Total 1	Mg 1	0
86	g	1	Total 1	Mg 1	0
86	j	1	Total 1	Mg 1	0
86	Q	1	Total 1	Mg 1	0
86	e	1	Total 1	Mg 1	0
86	B	1	Total 1	Mg 1	0
86	I	1	Total 1	Mg 1	0
86	V	1	Total 1	Mg 1	0
86	7	5	Total 5	Mg 5	0
86	a	1	Total 1	Mg 1	0
86	5	169	Total 169	Mg 169	0
86	8	3	Total 3	Mg 3	0
86	9	71	Total 71	Mg 71	0
86	hh	1	Total 1	Mg 1	0

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	p	1	Total 1	Zn 1	0
87	g	1	Total 1	Zn 1	0
87	j	1	Total 1	Zn 1	0
87	dd	1	Total 1	Zn 1	0
87	ff	1	Total 1	Zn 1	0
87	aa	1	Total 1	Zn 1	0

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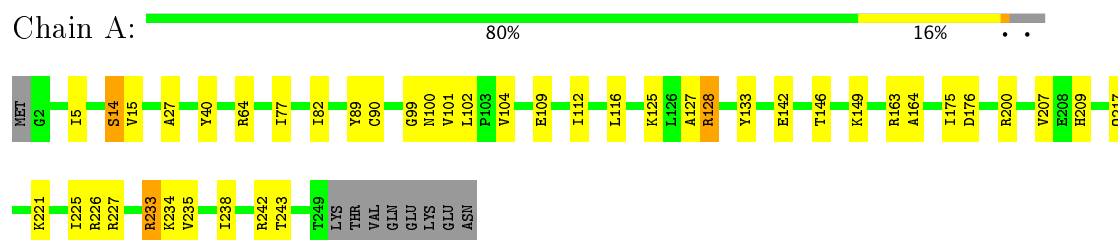
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Mol	Chain	Residues	Atoms		AltConf
87	o	1	Total 1	Zn 1	0
87	m	1	Total 1	Zn 1	0

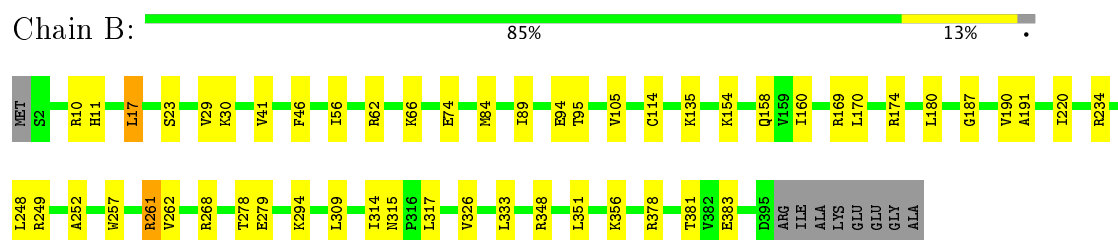
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

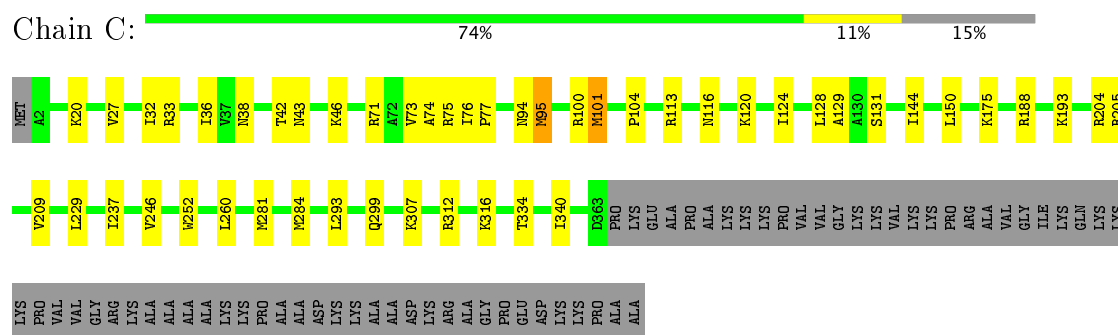
#### • Molecule 1: uL2



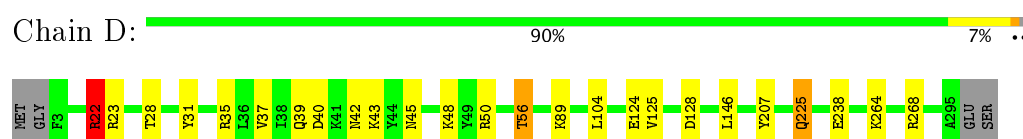
#### • Molecule 2: uL3



#### • Molecule 3: uL4

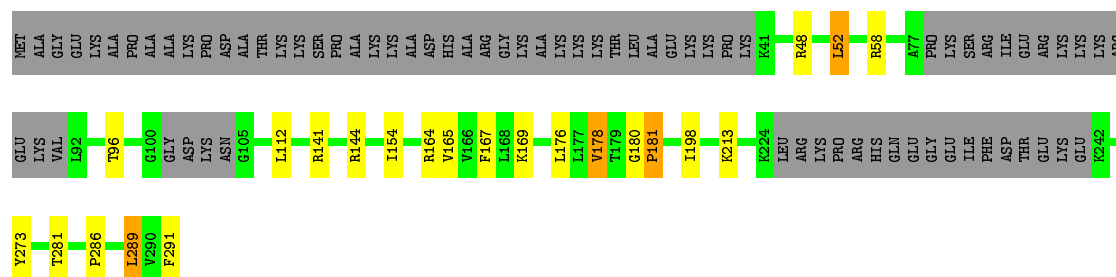


#### • Molecule 4: 60S ribosomal protein L5

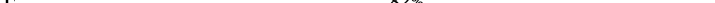


#### • Molecule 5: 60S ribosomal protein L6

Chain E:  66% 7% 26%



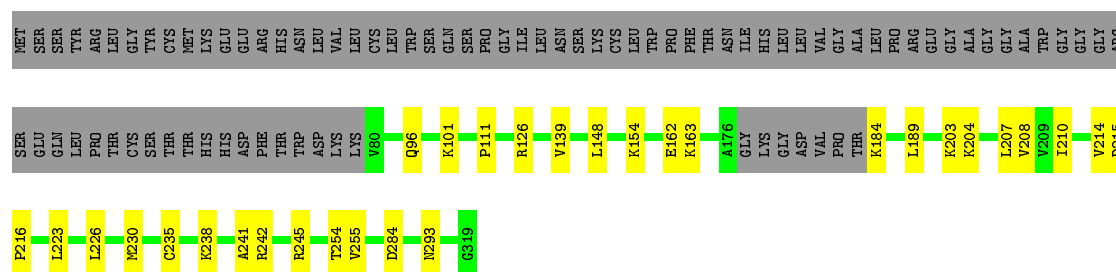
- Molecule 6: uL30

Chain F:  82% 8% 9%



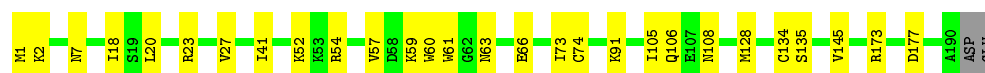
- Molecule 7: eL8

Chain G:  63% 10% 27%



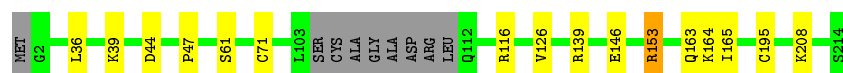
- Molecule 8: uL6

Chain H:  84% 15%



- Molecule 9: uL16

Chain I:  88% 7% .



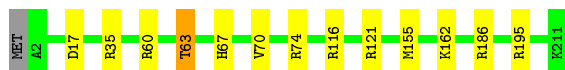
- Molecule 10: uL5

Chain J:  86% 10%



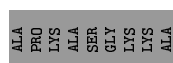
- Molecule 11: eL13

Chain L: 93% 6%



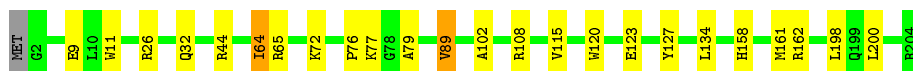
- Molecule 12: eL14

Chain M: 51% 11% 37%



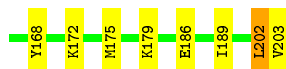
- Molecule 13: Ribosomal protein L15

Chain N: 88% 11%



- Molecule 14: uL13

Chain O: 79% 16% 5%



- Molecule 15: uL22

Chain P: 74% 8% 17%

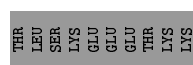
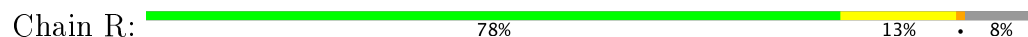


- Molecule 16: eL18

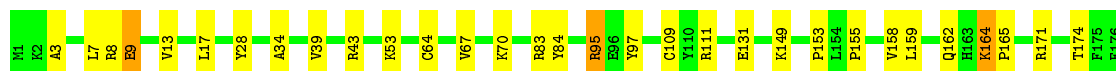
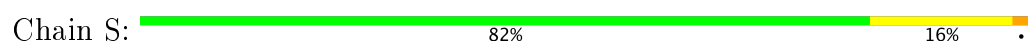
Chain Q: 87% 12% 1%



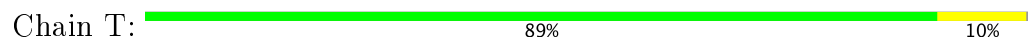
- Molecule 17: eL19



- Molecule 18: eL20



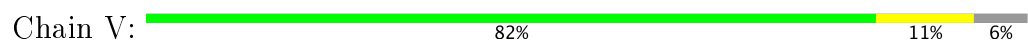
- Molecule 19: eL21



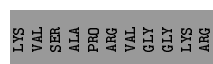
- Molecule 20: eL22



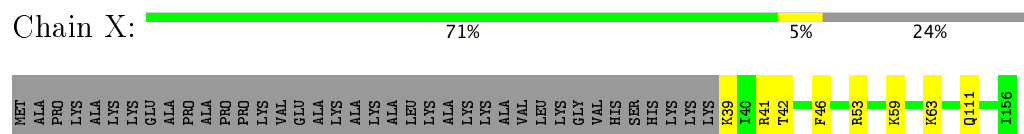
- Molecule 21: uL14



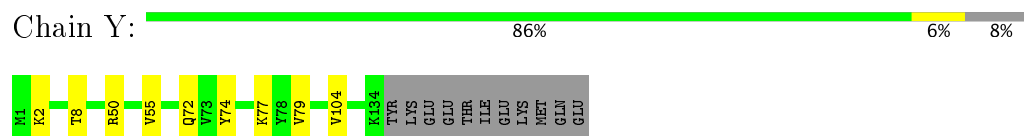
- Molecule 22: eL24



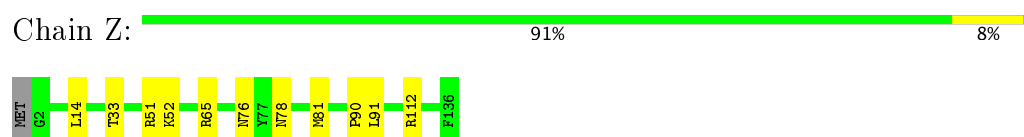
- Molecule 23: uL23



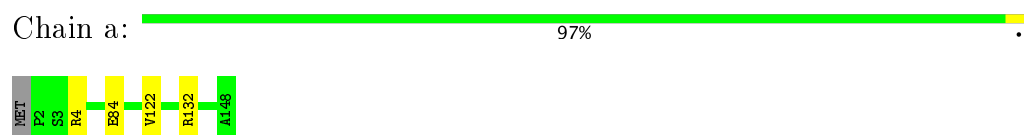
- Molecule 24: uL24



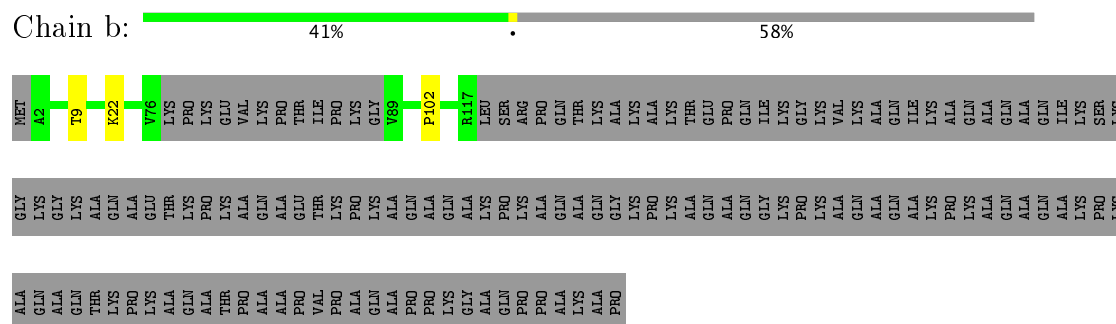
- Molecule 25: 60S ribosomal protein L27



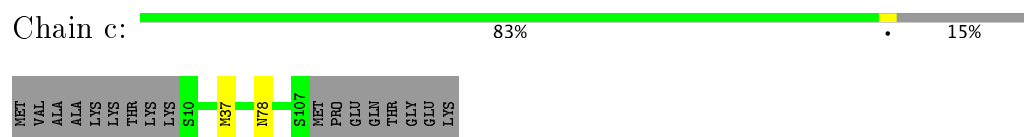
- Molecule 26: uL15



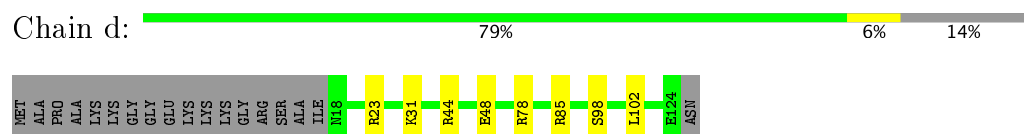
- Molecule 27: eL29



- Molecule 28: eL30

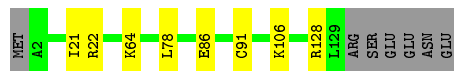


- Molecule 29: eL31



- Molecule 30: eL32

Chain e:  89% 6% 5%



- Molecule 31: eL33

Chain f:  92% 7% .



- Molecule 32: eL34

Chain g:  93% . .



- Molecule 33: uL29

Chain h:  95% . .




- Molecule 34: 60S ribosomal protein L36

Chain i:  94% . .



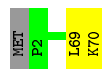
- Molecule 35: Ribosomal protein L37

Chain j:  82% 6% 11%



- Molecule 36: eL38

Chain k:  96% . .



- Molecule 37: eL39

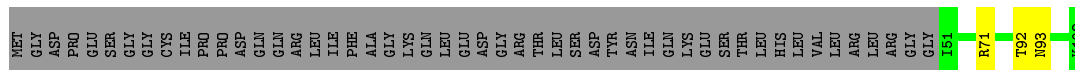
Chain l:  98% .





- Molecule 38: eL40

Chain m: 48% . 49%



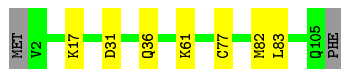
- Molecule 39: 60s ribosomal protein l41

Chain n: 92% 8%



- Molecule 40: eL42

Chain o: 92% 7% .



- Molecule 41: eL43

Chain p: 95% . .



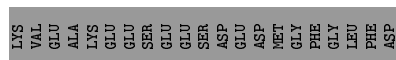
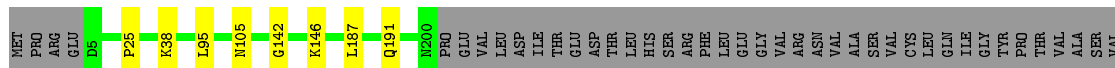
- Molecule 42: eL28

Chain r: 85% 6% 9%

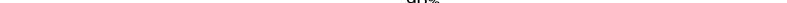


- Molecule 43: uL10

Chain s: 59% . 38%



- Molecule 44: uL11

Chain t:  90% • 7%



- Molecule 45: P-site tRNA

Chain 2:  75% 20% .



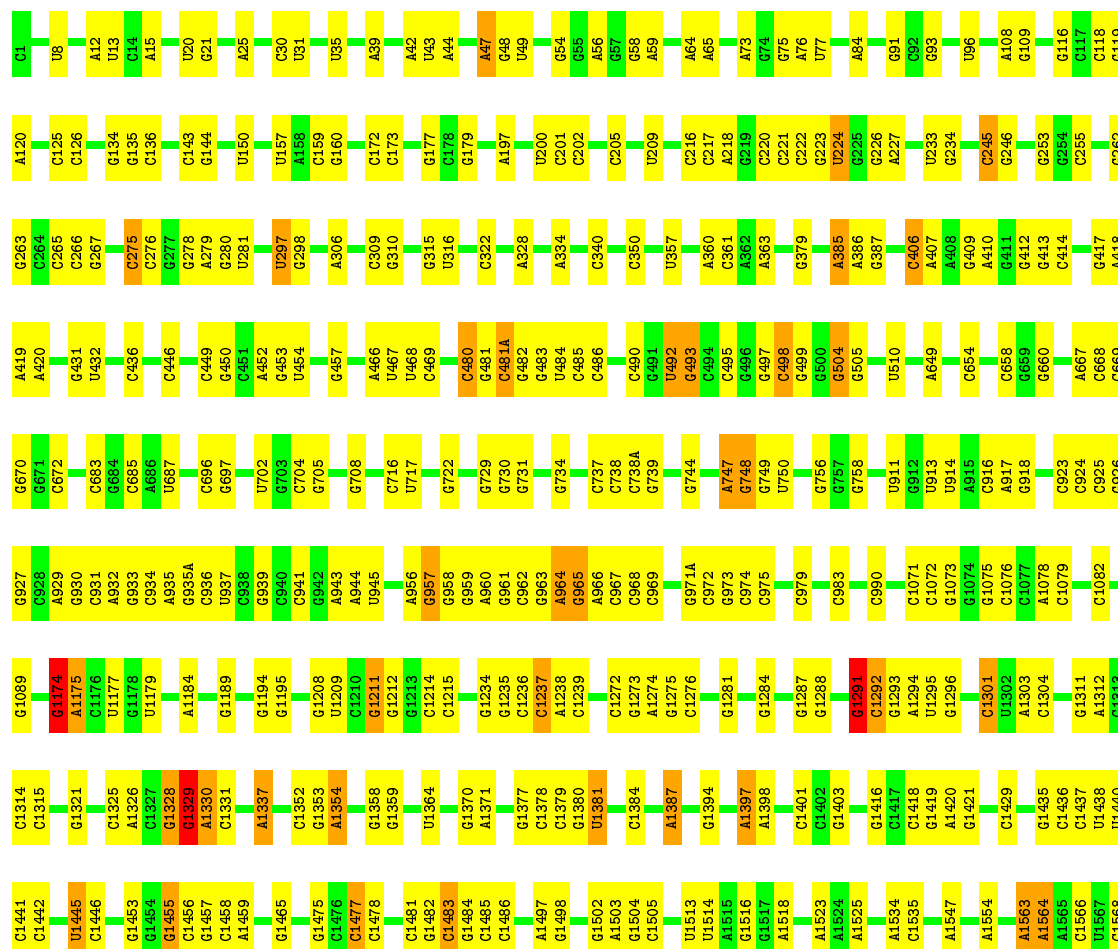
- Molecule 46: E-site tRNA

Chain 3:  65% 32%

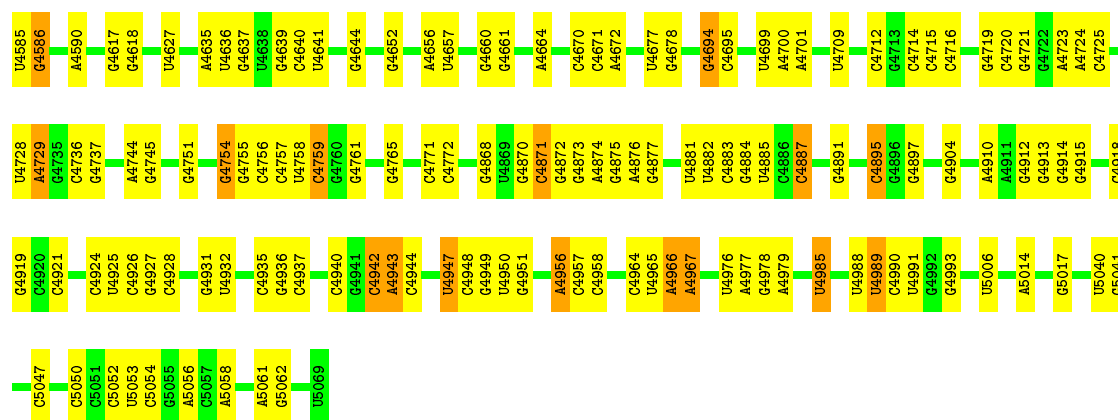


- Molecule 47: 28S ribosomal RNA

Chain 5:  68% 28% .

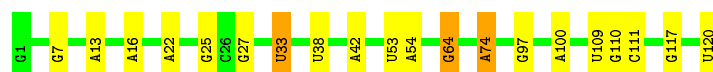


U4463	G4331	A3816	C3700	G2863	U2734	G2618	U2467	G2321	C2081	C1977	G1855	C1740	G1574
A4464	C4332	A3817	G3703	A2864	G2735	G2619	U2468	G2321	G2082	C1978	C1856	G1741	G1575
U4471	C4335	G3819	U3704	C2875	U2740	G2620	C2469	G2331	U2084	A1979	C1856	A1742	U1578
G4475	A4336	G3820	G3710	G2876	A2743	U2625	G2470	G2333	G2085	U1980	A1867	G1750	G1586
C4476	A4339	A3821	A3711	G2884	A2744	U2626	G2471	G2348	A2088	A1983	A1868	U1753	G1590
A4488	G4339	G3822	A3712	U2891	A2745	U2627	G2474	A2349	G2089	A1984	G1869	U1754	C1590
U4489	C4340	A3829	G3722	G2896	A2755	G2638	G2475	U2348	U2090	U1985	U1882	U1755	U1591
G4495	A4350	G3830	A3723	G2897	A2756	U2639	G2479	C2351	G2091	C1987	G1883	U1756	G1592
U4499	C4354	U3831	A3724	U2899	G2760	G2640	G2483	A2363	G2093	U1988	U1889	U1757	U1596
G4499	A4355	U3832	G3725	C3598	U2761	A2641	G2485	G2364	C2094	A1990	U1890	G1760	U1596
U4500	A4355	G3839	U3729	G3598	U2762	A2647	U2485	G2366	A2095	A1991	A1892	G1761	G1612
C4508	G4373	U3840	U3730	A3604	G2763	G2647	G2485	C2366	G2096	U1992	C1893	G1762	A1613
U4509	A4377	A3845	A3732	C3605	A2764	G2658	C2488	A2367	G2098	C1993	C1763	G1764	G1624
A4511	A4378	U3851	A3733	G3615	U2769	A2659	C2489	A2368	G2099	U1997	A1897	G1768	G1625
U4512	A4380	U3859	C3739	U3616	C2772	A2660	U2490	U2369	G2100	A1907	A1908	C1772	G1626
A4513	C4387	A3860	G3740	G3617	U2772	G2663	G2493	A2370	G2102	U1909	G1910	U1773	C1628
U4518	A4390	G3867	A3748	A3621	C2786	G2669	U2495	A2374	A2103	G2003	G1918	A1776	A1631
G4520	G4391	U3877	C3749	C3622	U2787	C2670	U2495	G2394	A2105	G2005	U1918	A1632	A1632
U4524	A4394	A3877	G3753	G3625	U2788	G2673	A2502	A2396	A2106	U2006	G1919	G1633	G1634
U4526	U4395	C3878	C3754	G3626	A2789	G2674	G2503	G2397	A2107	G2007	C1920	A1780	A1634
U4531	A4397	G3879	G3755	A3630	U2790	A2676	G2504	A2398	A2109	U2008	C1921	U1781	C1635
U4548	C4398	U3888	A3759	A3635	A2798	G2680	A2513	U2408	G2259	C2011	A1923	C1785	C1640
G4548	G4401	G3889	A3760	U3644	A2806	G2681	G2521	G2416	G2260	A2013	U1930	A1787	G1641
U4549	A4415	G3897	A3763	G3645	A2807	U2686	G2521	A2417	G2261	G2014	C1931	G1799	A1653
U4555	U4419	G3898	A3766	A3646	G2808	G2688	A2529	A2418	G2262	G2024	G1932	U1800	G1654
C4560	U4420	A3901	A3772	G3647	G2809	C2689	U2530	C2419	G2265	A2025	A1934	A1801	C1655
G4561	C4421	G3904	U3772	A3648	C2814	G2694	A2537	A2422	U2267	G2034	A1939	A1804	U1656
U4563	A4422	A3905	U3773	A3652	U2819	A2695	G2546	A2417	A2269	C2035	G1940	A1805	C1662
A4564	U4423	A3906	A3774	G3654	U2826	A2696	G2547	A2418	C2269	C2036	A1941	G1818	A1667
C4565	G4427	G3907	A3775	G3659	U2827	U2707	A2553	C2422	G2274	G2046	U1947	G1819	A1668
U4566	U4437	A3908	G3776	A3662	U2828	G2709	U2554	A2423	G2275	U2048	G1948	U1820	A1669
G4567	U4438	U3914	G3777	G3673	U2829	G2710	G2555	G2424	G2276	G1951	G1952	U1821	G1670
U4570	U4439	U3915	A3779	G3674	U2835	G2711	G2564	A2428	G2277	C2052	U1957	C1676	C1676
G4572	A4440	G3916	G3780	G3674	A2835	G2712	A2565	A2429	A2279	C2053	A1958	C1678	C1678
U4573	U4441	C3919	A3783	C3685	G2838	C2716	G2566	G2433	G2280	G2055	U1959	C1828	A1679
U4574	G4444	C3919	A3785	U3690	U2838	U2716	G2566	G2433	U2281	A2057	A1960	G1833	G1691
G4575	U4448	U3927	U3786	G3691	G2841	C2719	C2571	A2438	A2282	C2062	G1961	U1834	G1691
U4578	A4449	G3939	G3809	A3692	G2842	G2720	U2575	G2439	C2289	G2063	A1962	G1835	G1724
U4580	U4450	C3943	G3811	U3693	G2855	G2721	U2575	U2440	C2290	G2064	C1963	A1837	U1725
G4581	C4453	A3943	G3812	C3696	G2856	G2724	C2583	C2441	A2300	G2068	A1965	G1840	U1726
C4582	U4458	U4067	A3813	U3697	A2857	A2725	A2587	U2447	G2301	A2069	C1966	C1841	G1733
A4584	U4458	U4068	U3814	G3698	A2858	G2726	A2587	U2447	A2313	U2070	A1967	G1842	U1735
		U4069	G3815	C3699	G2862	C2733	A2601	G2450	G2314	U1852	G1976	U1852	



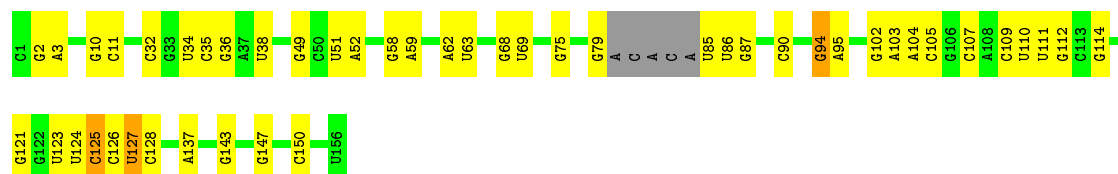
• Molecule 48: 5S ribosomal RNA

Chain 7: 83% 14% .



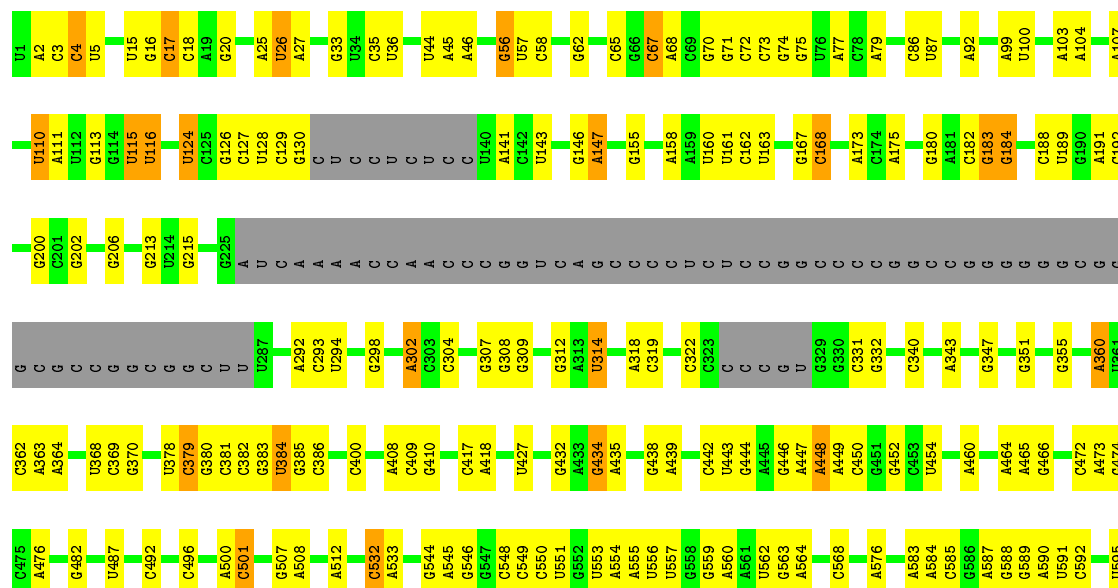
• Molecule 49: 5.8S ribosomal RNA

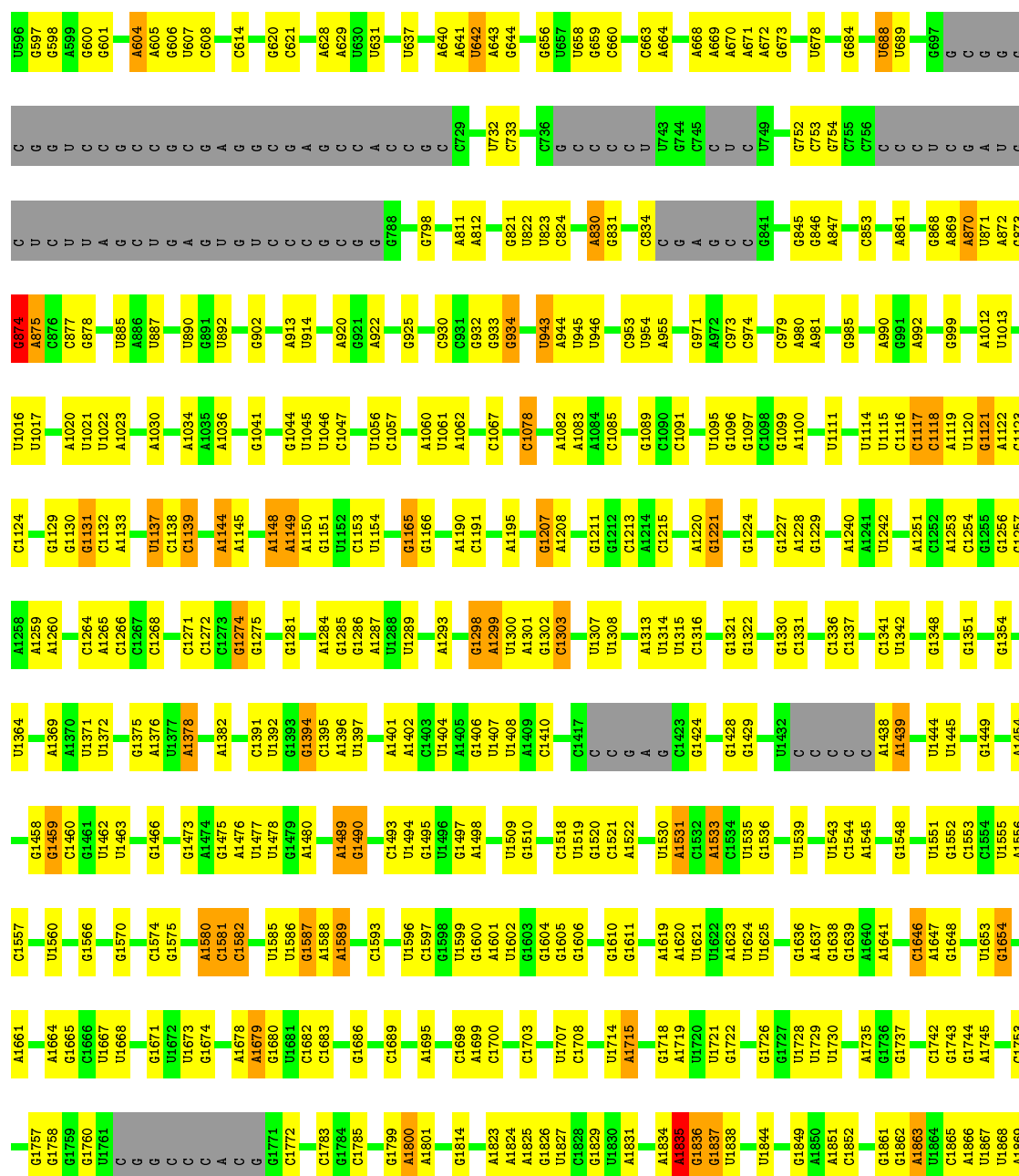
Chain 8: 67% 28% . .



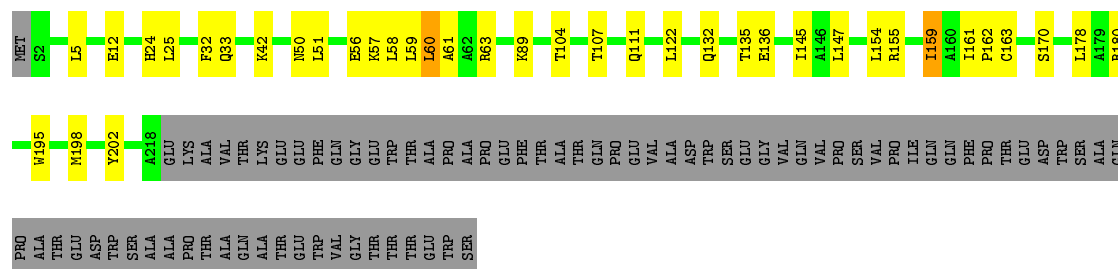
• Molecule 50: 18S ribosomal RNA

Chain 9: 59% 28% . 9%






- Molecule 51: uS2




- Molecule 52: 40S ribosomal protein S3a

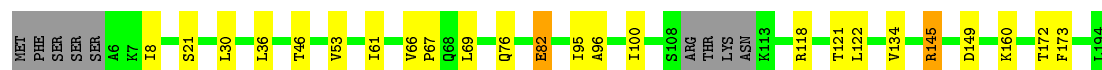


Chain GG:  84% 10% 5%




- Molecule 58: eS7

Chain HH:  83% 11% 5%




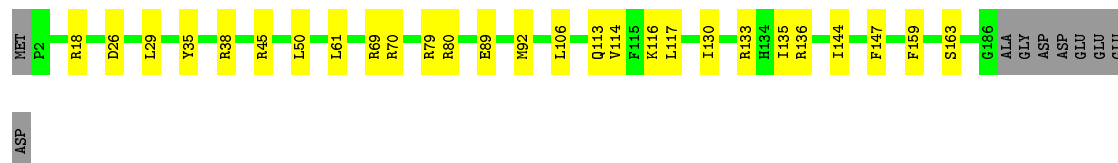
- Molecule 59: 40S ribosomal protein S8

Chain II:  83% 15% 2%



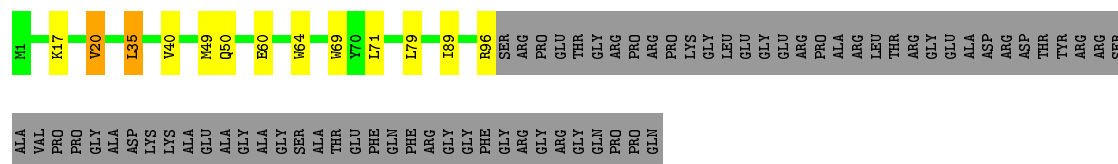
- Molecule 60: Ribosomal protein S9 (Predicted)

Chain JJ:  81% 14% 5%




- Molecule 61: eS10

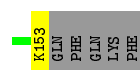
Chain KK:  50% 7% 42%



- Molecule 62: uS17

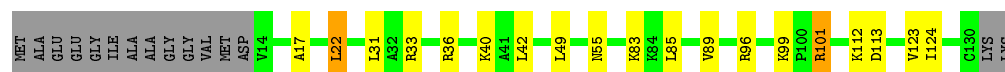
Chain LL:  75% 15% 9%





- Molecule 63: 40S ribosomal protein S12

Chain MM: 74% 13% 11%



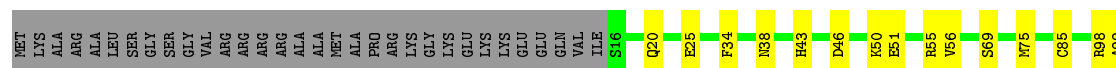
- Molecule 64: uS15

Chain NN: 81% 15% ..



- Molecule 65: uS11

Chain OO: 68% 12% 19%



- Molecule 66: uS19

Chain PP: 70% 10% 17%



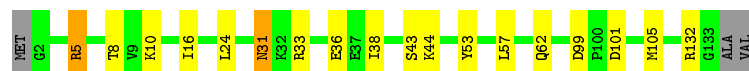
- Molecule 67: uS9

Chain QQ: 89% 8% .



- Molecule 68: eS17

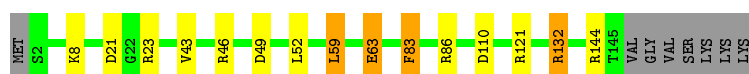
Chain RR: 84% 12% ..



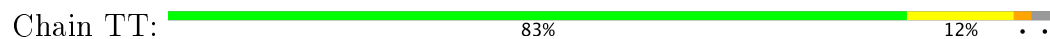
- Molecule 69: uS13

Chain SS: 85% 7% 5%

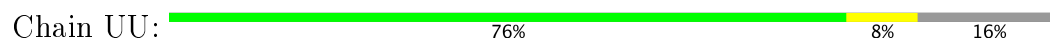




- Molecule 70: eS19



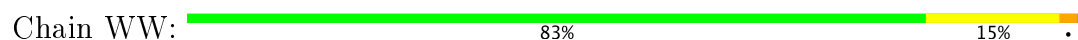
- Molecule 71: uS10



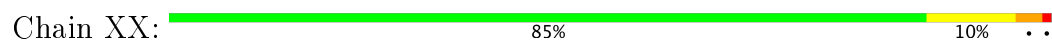
- Molecule 72: eS21



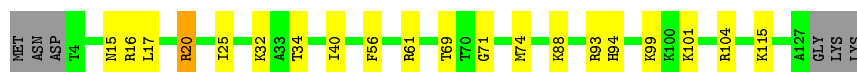
- Molecule 73: uS8



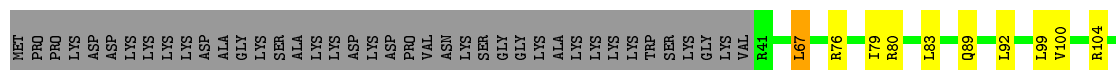
- Molecule 74: uS12

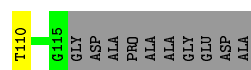


- Molecule 75: eS24



- Molecule 76: eS25





- Molecule 77: eS26

Chain aa: 80% 8% 12%



- Molecule 78: 40S ribosomal protein S27

Chain bb: 89% 10%



- Molecule 79: eS28

Chain cc: 80% 10% 10%



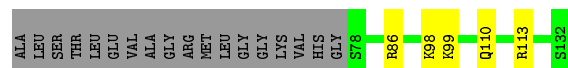
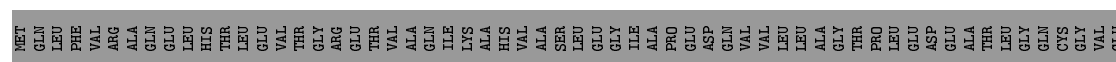
- Molecule 80: uS14

Chain dd: 95%



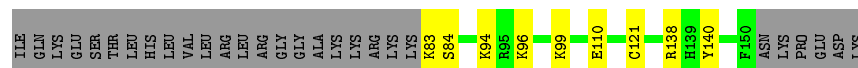
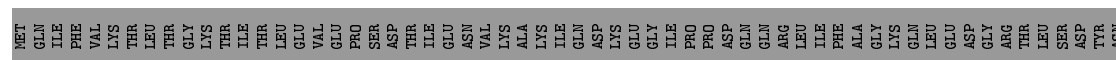
- Molecule 81: eS30

Chain ee: 38% 6% 59%



- Molecule 82: eS31

Chain ff: 38% 6% 56%



- Molecule 83: RACK1

Chain gg: 

94%

..

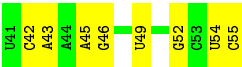


- Molecule 84: mRNA (UGA stop codon)

Chain hh: 

47%

53%



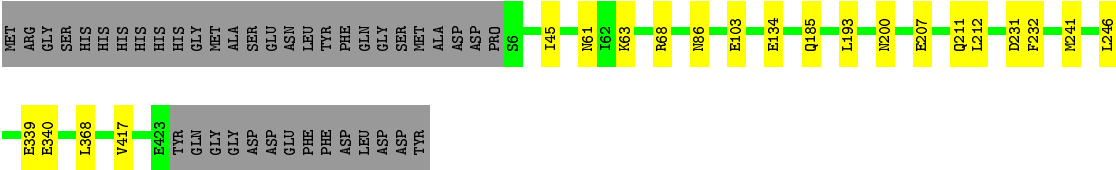
- Molecule 85: Eukaryotic peptide chain release factor subunit 1

Chain ii: 

86%

5%

9%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	13852	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 ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (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: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	0.47	0/1936	0.77	1/2596 (0.0%)
10	J	0.42	0/1385	0.67	1/1852 (0.1%)
11	L	0.55	0/1733	0.78	0/2316
12	M	0.59	1/1158 (0.1%)	0.79	0/1547
13	N	0.51	0/1746	0.79	0/2338
14	O	0.58	0/1662	0.81	2/2222 (0.1%)
15	P	0.53	0/1268	0.73	0/1700
16	Q	0.54	0/1539	0.86	0/2054
17	R	0.59	1/1524 (0.1%)	0.79	1/2013 (0.0%)
18	S	0.53	1/1501 (0.1%)	0.75	0/2012
19	T	0.48	0/1326	0.71	1/1770 (0.1%)
2	B	0.49	0/3240	0.74	1/4339 (0.0%)
20	U	0.42	0/823	0.62	0/1104
21	V	0.50	0/993	0.72	0/1332
22	W	0.42	0/873	0.63	0/1158
23	X	0.45	0/984	0.68	0/1323
24	Y	0.42	0/1132	0.66	0/1504
25	Z	0.46	0/1130	0.65	0/1507
26	a	0.50	0/1191	0.75	0/1590
27	b	0.47	0/861	0.69	0/1138
28	c	0.42	0/771	0.65	0/1034
29	d	0.47	0/903	0.75	0/1216
3	C	0.52	0/2937	0.77	0/3946
30	e	0.49	0/1071	0.77	0/1429
31	f	0.45	0/895	0.77	0/1198
32	g	0.43	0/916	0.73	0/1220
33	h	0.57	0/1021	0.77	1/1348 (0.1%)
34	i	0.45	0/841	0.69	0/1112
35	j	0.57	0/720	0.83	0/952
36	k	0.45	0/575	0.61	0/761
37	l	0.57	0/459	0.76	0/608
38	m	0.49	0/435	0.76	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	n	0.63	0/240	0.91	0/305
4	D	0.55	1/2437 (0.0%)	0.75	1/3264 (0.0%)
40	o	0.50	0/864	0.71	0/1140
41	p	0.55	0/718	0.78	0/953
42	r	0.49	0/1010	0.75	0/1354
43	s	0.44	0/1530	0.58	0/2064
44	t	0.47	0/1173	0.68	0/1579
45	2	0.40	1/1803 (0.1%)	0.72	2/2801 (0.1%)
46	3	0.24	0/1777	0.66	0/2763
47	5	0.39	3/84974 (0.0%)	0.71	22/132512 (0.0%)
48	7	0.38	0/2858	0.66	0/4455
49	8	0.39	0/3581	0.68	0/5577
5	E	0.42	0/1762	0.67	0/2362
50	9	0.34	1/40516 (0.0%)	0.72	12/63102 (0.0%)
51	AA	0.44	0/1747	0.68	0/2374
52	BB	0.40	0/1756	0.66	0/2350
53	CC	0.42	0/1753	0.70	0/2369
54	DD	0.45	0/1796	0.69	0/2417
55	EE	0.44	0/2118	0.73	0/2849
56	FF	0.43	0/1492	0.68	0/2005
57	GG	0.40	0/1946	0.72	0/2590
58	HH	0.41	0/1510	0.64	0/2022
59	II	0.47	0/1715	0.74	2/2287 (0.1%)
6	F	0.56	0/1911	0.76	1/2549 (0.0%)
60	JJ	0.43	0/1550	0.76	0/2069
61	KK	0.45	0/834	0.61	0/1125
62	LL	0.45	0/1195	0.78	0/1597
63	MM	0.44	0/918	0.64	0/1233
64	NN	0.41	0/1226	0.70	0/1649
65	OO	0.41	0/1029	0.80	1/1380 (0.1%)
66	PP	0.42	0/1017	0.74	1/1358 (0.1%)
67	QQ	0.40	0/1146	0.68	0/1534
68	RR	0.43	0/1082	0.65	0/1452
69	SS	0.40	0/1208	0.71	0/1618
7	G	0.47	0/1910	0.70	0/2569
70	TT	0.49	1/1115 (0.1%)	0.69	1/1493 (0.1%)
71	UU	0.51	2/805 (0.2%)	0.70	0/1081
72	VV	0.51	1/643 (0.2%)	0.75	0/860
73	WW	0.46	0/1051	0.74	0/1406
74	XX	0.45	0/1116	0.76	1/1490 (0.1%)
75	YY	0.41	0/1028	0.68	0/1366
76	ZZ	0.39	0/604	0.71	0/810
77	aa	0.43	0/828	0.78	0/1109

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	bb	0.41	0/665	0.70	0/891
79	cc	0.52	1/490 (0.2%)	0.72	0/656
8	H	0.41	0/1535	0.66	0/2063
80	dd	0.49	0/470	0.72	0/623
81	ee	0.41	0/447	0.75	0/587
82	ff	0.39	0/567	0.55	0/753
83	gg	0.37	0/2493	0.60	0/3394
84	hh	0.32	0/353	0.74	0/547
85	ii	0.40	0/3345	0.61	0/4492
9	I	0.49	0/1702	0.71	1/2272 (0.0%)
All	All	0.42	14/234908 (0.0%)	0.71	53/344334 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	M	0	1
51	AA	0	1
55	EE	0	1
74	XX	0	1
All	All	0	4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	R	28	GLU	CD-OE2	8.20	1.34	1.25
45	2	20	U	C5'-C4'	7.89	1.60	1.51
18	S	131	GLU	CD-OE2	7.10	1.33	1.25
4	D	238	GLU	CD-OE2	6.30	1.32	1.25
47	5	2411	C	O3'-P	-6.20	1.53	1.61

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	22	ARG	NE-CZ-NH1	8.35	124.47	120.30
50	9	1835	A	C2'-C3'-O3'	7.93	126.95	109.50
50	9	1394	G	C2'-C3'-O3'	7.78	126.61	109.50
19	T	32	ARG	NE-CZ-NH1	7.60	124.10	120.30
47	5	1477	C	C2'-C3'-O3'	7.57	126.16	109.50

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	AA	42	LYS	Peptide
55	EE	155	LYS	Peptide
12	M	67	SER	Peptide
74	XX	61	GLN	Peptide

## 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	A	1898	0	1993	18	0
2	B	3172	0	3310	23	0
3	C	2883	0	3053	25	0
4	D	2391	0	2424	12	0
5	E	1729	0	1887	9	0
6	F	1875	0	1995	9	0
7	G	1879	0	2027	11	0
8	H	1516	0	1597	8	0
9	I	1664	0	1712	2	0
10	J	1362	0	1399	6	0
11	L	1702	0	1820	2	0
12	M	1137	0	1211	14	0
13	N	1701	0	1749	9	0
14	O	1630	0	1778	21	0
15	P	1242	0	1274	5	0
16	Q	1515	0	1634	9	0
17	R	1508	0	1664	7	0
18	S	1462	0	1508	14	0
19	T	1298	0	1366	5	0
20	U	809	0	833	5	0
21	V	979	0	1039	7	0
22	W	860	0	903	4	0
23	X	967	0	1040	3	0
24	Y	1115	0	1205	2	0
25	Z	1107	0	1182	3	0
26	a	1162	0	1209	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	b	848	0	920	0	0
28	c	761	0	794	0	0
29	d	888	0	930	0	0
30	e	1053	0	1147	0	0
31	f	876	0	912	0	0
32	g	906	0	998	0	0
33	h	1013	0	1147	0	0
34	i	830	0	916	0	0
35	j	705	0	737	0	0
36	k	569	0	637	0	0
37	l	447	0	480	0	0
38	m	429	0	466	0	0
39	n	239	0	289	0	0
40	o	851	0	920	0	0
41	p	708	0	758	0	0
42	r	994	0	1051	0	0
43	s	1507	0	1564	0	0
44	t	1160	0	1217	0	0
45	2	1616	0	826	36	0
46	3	1593	0	811	3	0
47	5	75972	0	38391	241	0
48	7	2558	0	1296	4	0
49	8	3208	0	1629	9	0
50	9	36249	0	18324	149	0
51	AA	1710	0	1708	13	0
52	BB	1729	0	1803	8	0
53	CC	1716	0	1806	10	0
54	DD	1768	0	1866	12	0
55	EE	2076	0	2177	18	0
56	FF	1471	0	1522	16	0
57	GG	1923	0	2089	8	0
58	HH	1488	0	1582	8	0
59	II	1686	0	1772	17	0
60	JJ	1525	0	1640	8	0
61	KK	810	0	836	5	0
62	LL	1175	0	1249	9	0
63	MM	908	0	939	4	0
64	NN	1202	0	1289	8	0
65	OO	1016	0	1039	3	0
66	PP	997	0	1045	5	0
67	QQ	1128	0	1195	2	0
68	RR	1068	0	1121	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	SS	1190	0	1249	4	0
70	TT	1097	0	1132	9	0
71	UU	795	0	862	2	0
72	VV	636	0	637	5	0
73	WW	1034	0	1080	9	0
74	XX	1098	0	1167	12	0
75	YY	1011	0	1083	5	0
76	ZZ	598	0	656	6	0
77	aa	814	0	865	0	0
78	bb	651	0	672	0	0
79	cc	488	0	514	0	0
80	dd	459	0	450	0	0
81	ee	443	0	492	0	0
82	ff	555	0	566	0	0
83	gg	2436	0	2393	0	0
84	hh	317	0	161	0	0
85	ii	3295	0	3334	0	0
86	5	169	0	0	0	0
86	7	5	0	0	0	0
86	8	3	0	0	0	0
86	9	71	0	0	0	0
86	B	1	0	0	0	0
86	I	1	0	0	0	0
86	P	1	0	0	0	0
86	Q	1	0	0	0	0
86	V	1	0	0	0	0
86	a	1	0	0	0	0
86	e	1	0	0	0	0
86	g	1	0	0	0	0
86	hh	1	0	0	0	0
86	j	1	0	0	0	0
87	aa	1	0	0	0	0
87	dd	1	0	0	0	0
87	ff	1	0	0	0	0
87	g	1	0	0	0	0
87	j	1	0	0	0	0
87	m	1	0	0	0	0
87	o	1	0	0	0	0
87	p	1	0	0	0	0
All	All	219122	0	163963	772	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 3.

The worst 5 of 772 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)
45:2:20:U:C1'	45:2:20(A):U:H1'	1.32	1.56
45:2:20:U:C2'	45:2:20(A):U:C1'	1.75	1.55
45:2:20:U:C3'	45:2:20(A):U:C3'	1.77	1.50
45:2:20:U:H2'	45:2:20(A):U:C2'	1.34	1.50
45:2:20:U:C2'	45:2:20(A):U:H1'	1.09	1.39

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	246/257 (96%)	216 (88%)	28 (11%)	2 (1%)	22	65
2	B	392/403 (97%)	364 (93%)	27 (7%)	1 (0%)	44	81
3	C	360/425 (85%)	335 (93%)	24 (7%)	1 (0%)	44	81
4	D	291/297 (98%)	277 (95%)	13 (4%)	1 (0%)	44	81
5	E	208/291 (72%)	194 (93%)	13 (6%)	1 (0%)	32	74
6	F	223/247 (90%)	213 (96%)	9 (4%)	1 (0%)	38	77
7	G	229/319 (72%)	216 (94%)	13 (6%)	0	100	100
8	H	188/192 (98%)	174 (93%)	14 (7%)	0	100	100
9	I	201/214 (94%)	185 (92%)	15 (8%)	1 (0%)	32	74
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
11	L	208/211 (99%)	198 (95%)	8 (4%)	2 (1%)	18	61
12	M	136/218 (62%)	123 (90%)	12 (9%)	1 (1%)	25	68
13	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	32	74
14	O	197/203 (97%)	186 (94%)	8 (4%)	3 (2%)	12	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	P	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
16	Q	185/188 (98%)	172 (93%)	12 (6%)	1 (0%)	32	74
17	R	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
18	S	174/176 (99%)	164 (94%)	9 (5%)	1 (1%)	28	70
19	T	157/160 (98%)	143 (91%)	13 (8%)	1 (1%)	28	70
20	U	97/128 (76%)	88 (91%)	9 (9%)	0	100	100
21	V	129/140 (92%)	114 (88%)	15 (12%)	0	100	100
22	W	102/157 (65%)	97 (95%)	4 (4%)	1 (1%)	18	61
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
25	Z	133/136 (98%)	126 (95%)	4 (3%)	3 (2%)	7	46
26	a	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
27	b	100/245 (41%)	94 (94%)	5 (5%)	1 (1%)	18	61
28	c	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
29	d	105/125 (84%)	92 (88%)	13 (12%)	0	100	100
30	e	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
31	f	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	9	49
32	g	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
33	h	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
34	i	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
35	j	84/97 (87%)	74 (88%)	10 (12%)	0	100	100
36	k	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
38	m	50/102 (49%)	48 (96%)	2 (4%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	99 (97%)	2 (2%)	1 (1%)	18	61
41	p	89/92 (97%)	80 (90%)	7 (8%)	2 (2%)	8	46
42	r	122/137 (89%)	112 (92%)	9 (7%)	1 (1%)	22	65
43	s	194/318 (61%)	177 (91%)	15 (8%)	2 (1%)	18	61
44	t	149/165 (90%)	135 (91%)	13 (9%)	1 (1%)	25	68
51	AA	215/295 (73%)	196 (91%)	18 (8%)	1 (0%)	32	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	BB	211/264 (80%)	202 (96%)	9 (4%)	0	100	100
53	CC	219/293 (75%)	206 (94%)	12 (6%)	1 (0%)	32	74
54	DD	226/243 (93%)	213 (94%)	11 (5%)	2 (1%)	20	63
55	EE	260/263 (99%)	239 (92%)	21 (8%)	0	100	100
56	FF	181/204 (89%)	169 (93%)	11 (6%)	1 (1%)	28	70
57	GG	235/249 (94%)	226 (96%)	8 (3%)	1 (0%)	38	77
58	HH	181/194 (93%)	171 (94%)	10 (6%)	0	100	100
59	II	204/208 (98%)	186 (91%)	17 (8%)	1 (0%)	32	74
60	JJ	183/194 (94%)	175 (96%)	6 (3%)	2 (1%)	17	60
61	KK	94/165 (57%)	88 (94%)	5 (5%)	1 (1%)	17	60
62	LL	139/158 (88%)	126 (91%)	12 (9%)	1 (1%)	25	68
63	MM	115/132 (87%)	105 (91%)	10 (9%)	0	100	100
64	NN	147/151 (97%)	136 (92%)	11 (8%)	0	100	100
65	OO	134/168 (80%)	122 (91%)	10 (8%)	2 (2%)	12	53
66	PP	118/145 (81%)	109 (92%)	9 (8%)	0	100	100
67	QQ	140/146 (96%)	130 (93%)	10 (7%)	0	100	100
68	RR	130/135 (96%)	122 (94%)	8 (6%)	0	100	100
69	SS	142/152 (93%)	135 (95%)	7 (5%)	0	100	100
70	TT	139/145 (96%)	130 (94%)	9 (6%)	0	100	100
71	UU	98/119 (82%)	87 (89%)	11 (11%)	0	100	100
72	VV	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
73	WW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
74	XX	139/143 (97%)	130 (94%)	6 (4%)	3 (2%)	8	46
75	YY	122/130 (94%)	113 (93%)	9 (7%)	0	100	100
76	ZZ	73/125 (58%)	70 (96%)	3 (4%)	0	100	100
77	aa	99/115 (86%)	88 (89%)	11 (11%)	0	100	100
78	bb	81/84 (96%)	73 (90%)	7 (9%)	1 (1%)	15	58
79	cc	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
80	dd	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
81	ee	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
82	ff	66/156 (42%)	60 (91%)	6 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	gg	311/317 (98%)	286 (92%)	25 (8%)	0	100	100
85	ii	410/459 (89%)	394 (96%)	16 (4%)	0	100	100
All	All	11927/13834 (86%)	11108 (93%)	770 (6%)	49 (0%)	42	77

5 of 49 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	r	11	ARG
74	XX	61	GLN
74	XX	62	PRO
11	L	17	ASP
18	S	155	PRO

### 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	A	190/199 (96%)	173 (91%)	17 (9%)	11	45
2	B	342/348 (98%)	324 (95%)	18 (5%)	26	63
3	C	302/347 (87%)	287 (95%)	15 (5%)	28	65
4	D	247/250 (99%)	235 (95%)	12 (5%)	29	65
5	E	190/251 (76%)	179 (94%)	11 (6%)	23	61
6	F	196/215 (91%)	184 (94%)	12 (6%)	22	59
7	G	200/272 (74%)	185 (92%)	15 (8%)	16	52
8	H	169/171 (99%)	154 (91%)	15 (9%)	11	45
9	I	175/181 (97%)	164 (94%)	11 (6%)	21	58
10	J	143/149 (96%)	138 (96%)	5 (4%)	41	73
11	L	175/176 (99%)	167 (95%)	8 (5%)	31	67
12	M	117/161 (73%)	109 (93%)	8 (7%)	18	56
13	N	171/172 (99%)	163 (95%)	8 (5%)	30	66
14	O	171/173 (99%)	160 (94%)	11 (6%)	20	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	134/163 (82%)	125 (93%)	9 (7%)	19	56
16	Q	164/165 (99%)	154 (94%)	10 (6%)	22	59
17	R	159/175 (91%)	144 (91%)	15 (9%)	10	42
18	S	157/157 (100%)	143 (91%)	14 (9%)	11	45
19	T	139/140 (99%)	130 (94%)	9 (6%)	20	57
20	U	89/114 (78%)	88 (99%)	1 (1%)	78	89
21	V	101/107 (94%)	94 (93%)	7 (7%)	18	55
22	W	86/126 (68%)	85 (99%)	1 (1%)	75	89
23	X	106/134 (79%)	100 (94%)	6 (6%)	24	61
24	Y	124/135 (92%)	119 (96%)	5 (4%)	36	69
25	Z	117/118 (99%)	115 (98%)	2 (2%)	66	86
26	a	119/120 (99%)	115 (97%)	4 (3%)	42	73
27	b	84/184 (46%)	82 (98%)	2 (2%)	54	79
28	c	84/98 (86%)	82 (98%)	2 (2%)	54	79
29	d	98/110 (89%)	90 (92%)	8 (8%)	13	48
30	e	114/121 (94%)	106 (93%)	8 (7%)	18	55
31	f	88/89 (99%)	82 (93%)	6 (7%)	18	56
32	g	98/100 (98%)	93 (95%)	5 (5%)	28	64
33	h	109/110 (99%)	105 (96%)	4 (4%)	39	71
34	i	86/89 (97%)	83 (96%)	3 (4%)	41	73
35	j	73/80 (91%)	67 (92%)	6 (8%)	13	48
36	k	64/65 (98%)	62 (97%)	2 (3%)	45	75
37	l	47/48 (98%)	47 (100%)	0	100	100
38	m	48/90 (53%)	45 (94%)	3 (6%)	21	58
39	n	24/24 (100%)	22 (92%)	2 (8%)	13	48
40	o	92/94 (98%)	86 (94%)	6 (6%)	20	57
41	p	74/75 (99%)	71 (96%)	3 (4%)	35	69
42	r	108/121 (89%)	101 (94%)	7 (6%)	20	57
43	s	164/258 (64%)	158 (96%)	6 (4%)	39	71
44	t	126/137 (92%)	122 (97%)	4 (3%)	44	74
51	AA	180/245 (74%)	162 (90%)	18 (10%)	9	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	BB	194/231 (84%)	174 (90%)	20 (10%)	8	38
53	CC	187/225 (83%)	172 (92%)	15 (8%)	14	50
54	DD	190/202 (94%)	174 (92%)	16 (8%)	13	48
55	EE	224/225 (100%)	207 (92%)	17 (8%)	15	52
56	FF	158/170 (93%)	143 (90%)	15 (10%)	10	41
57	GG	207/218 (95%)	189 (91%)	18 (9%)	12	46
58	HH	165/174 (95%)	153 (93%)	12 (7%)	16	53
59	II	178/180 (99%)	167 (94%)	11 (6%)	21	59
60	JJ	161/168 (96%)	147 (91%)	14 (9%)	12	46
61	KK	87/136 (64%)	80 (92%)	7 (8%)	14	50
62	LL	130/142 (92%)	116 (89%)	14 (11%)	7	36
63	MM	99/108 (92%)	83 (84%)	16 (16%)	3	19
64	NN	130/131 (99%)	115 (88%)	15 (12%)	6	33
65	OO	106/130 (82%)	91 (86%)	15 (14%)	4	25
66	PP	109/130 (84%)	97 (89%)	12 (11%)	7	35
67	QQ	117/121 (97%)	108 (92%)	9 (8%)	15	51
68	RR	119/121 (98%)	107 (90%)	12 (10%)	9	38
69	SS	125/132 (95%)	112 (90%)	13 (10%)	8	37
70	TT	111/115 (96%)	101 (91%)	10 (9%)	11	44
71	UU	92/107 (86%)	84 (91%)	8 (9%)	12	46
72	VV	67/67 (100%)	66 (98%)	1 (2%)	70	87
73	WW	112/113 (99%)	104 (93%)	8 (7%)	17	54
74	XX	113/115 (98%)	107 (95%)	6 (5%)	26	63
75	YY	107/112 (96%)	95 (89%)	12 (11%)	7	35
76	ZZ	66/103 (64%)	61 (92%)	5 (8%)	15	52
77	aa	88/98 (90%)	79 (90%)	9 (10%)	8	38
78	bb	75/76 (99%)	68 (91%)	7 (9%)	10	43
79	cc	55/62 (89%)	49 (89%)	6 (11%)	7	36
80	dd	48/49 (98%)	46 (96%)	2 (4%)	34	68
81	ee	46/106 (43%)	41 (89%)	5 (11%)	7	36
82	ff	61/140 (44%)	52 (85%)	9 (15%)	3	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	gg	272/275 (99%)	258 (95%)	14 (5%)	28	64
85	ii	360/394 (91%)	339 (94%)	21 (6%)	23	61
All	All	10403/11733 (89%)	9685 (93%)	718 (7%)	23	55

5 of 718 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	t	133	LEU
55	EE	66	MET
79	cc	31	ARG
51	AA	60	LEU
53	CC	78	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
16	Q	57	ASN
34	i	20	ASN
85	ii	185	GLN
19	T	69	GLN
40	o	19	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	2	73/76 (96%)	15 (20%)	1 (1%)
46	3	72/75 (96%)	25 (34%)	2 (2%)
47	5	3515/3543 (99%)	893 (25%)	175 (4%)
48	7	119/120 (99%)	17 (14%)	2 (1%)
49	8	150/156 (96%)	36 (24%)	8 (5%)
50	9	1671/1869 (89%)	436 (26%)	70 (4%)
84	hh	14/15 (93%)	8 (57%)	0
All	All	5614/5854 (95%)	1430 (25%)	258 (4%)

5 of 1430 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	2	8	U
45	2	9	A

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Mol	Chain	Res	Type
45	2	13	U
45	2	16	C
45	2	19	G

5 of 258 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	5	2394	G
47	5	4076	G
50	9	1476	A
47	5	2428	A
47	5	2724	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 266 ligands modelled in this entry, 266 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	5	29
50	9	15
85	ii	3
45	2	2
46	3	2
44	t	1

The worst 5 of 52 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.35
1	5	1252:C	O3'	1271:G	P	35.75
1	5	1219:G	O3'	1233:G	P	22.89
1	5	3948:C	O3'	4065:G	P	19.77
1	5	1406(C):G	O3'	1411:C	P	18.60