



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Nov 8, 2017 – 10:34 PM EST

PDB ID : 5OQL
EMDB ID: : EMD-3847
Title : Cryo-EM structure of the 90S pre-ribosome from *Chaetomium thermophilum*
Authors : Cheng, J.; Kellner, N.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : unknown
Resolution : 3.20 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
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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-20030345

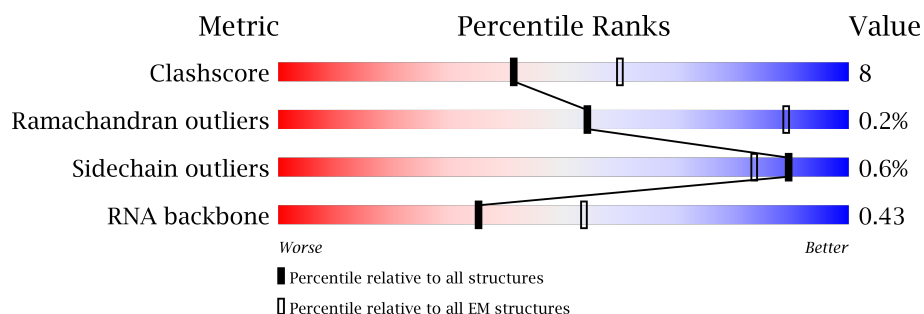
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.





















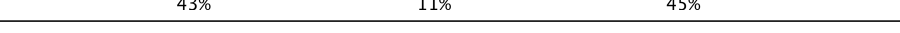
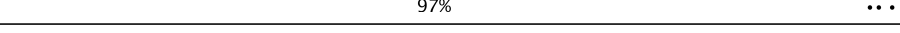
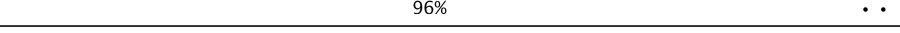

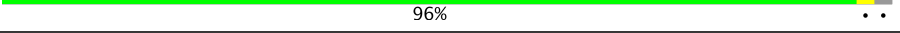


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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 ≥ 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	904	67% 23% • 9%
2	B	907	7% • 92%
3	C	648	10% • 89%
4	D	884	27% 6% 67%
5	E	414	68% 12% 20%
6	F	558	60% 15% • 23%
7	G	1802	17% • 80%
8	H	270	59% 11% 30%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	962	
10	J	912	
11	K	938	
12	L	557	
13	M	960	
14	N	618	
15	O	1049	
16	P	194	
17	Q	391	
18	R	313	
18	S	313	
19	T	523	
20	U	582	
21	V	127	
21	W	127	
22	X	630	
23	Y	411	
24	Z	1163	
25	a	183	
26	b	297	
27	c	785	
28	d	446	
29	e	252	
29	f	252	
30	g	322	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
31	h	259	
32	i	1073	
32	j	1073	
33	k	203	
34	l	255	
35	m	264	
36	n	212	
37	o	239	
38	p	203	
39	q	202	
40	r	190	
41	s	151	
42	t	150	
43	u	143	
44	v	161	
45	w	130	
46	x	145	
47	y	136	
48	z	68	
49	0	311	
50	1	2568	
51	2	274	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 135120 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 Periodic tryptophan protein 2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	827	Total	C	N	O	S	0	0
			6242	4029	1114	1077	22		

- Molecule 2 is a protein called Utp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	69	Total	C	N	O	0	0
			537	338	121	78		

- Molecule 3 is a protein called Utp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	74	Total	C	N	O	0	0
			588	371	120	97		

- Molecule 4 is a protein called Utp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	292	Total	C	N	O	S	0	0
			2170	1383	403	373	11		

- Molecule 5 is a protein called Utp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	331	Total	C	N	O	S	0	0
			2591	1674	504	399	14		

- Molecule 6 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	429	Total	C	N	O	S	0	0
			3282	2103	611	557	11		

- Molecule 7 is a protein called Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	363	Total	C	N	O	S	0	0
			2772	1784	501	473	14		

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1456	915	306	230	5		

- Molecule 9 is a protein called Utp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	155	Total	C	N	O	S	0	0
			1230	788	222	214	6		

- Molecule 10 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	151	Total	C	N	O	S	0	0
			1201	765	214	222			

- Molecule 11 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	147	Total	C	N	O	S	0	0
			1139	725	215	194	5		

- Molecule 12 is a protein called Utp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	280	Total	C	N	O	S	0	0
			2070	1320	379	363	8		

- Molecule 13 is a protein called Utp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	284	Total	C	N	O	S	0	0
			2134	1386	364	378	6		

- Molecule 14 is a protein called Utp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	443	Total	C	N	O	S	0	0
			3435	2181	646	598	10		

- Molecule 15 is a protein called Putative U3 snoRNP protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	864	Total	C	N	O	S	0	0
			6446	4152	1189	1079	26		

- Molecule 16 is a protein called Utp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	190	Total	C	N	O	S	0	0
			1460	928	281	241	10		

- Molecule 17 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	182	Total	C	N	O		0	0
			905	541	182	182			

- Molecule 18 is a protein called Nop1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	242	Total	C	N	O	S	0	0
			1778	1149	327	293	9		
18	S	237	Total	C	N	O	S	0	0
			1816	1154	318	335	9		

- Molecule 19 is a protein called Putative nucleolar protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	387	Total	C	N	O	S	0	0
			2866	1836	527	492	11		

- Molecule 20 is a protein called Nop58.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	405	Total	C	N	O	S	0	0
			3035	1954	539	532	10		

- Molecule 21 is a protein called Snu13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	121	Total	C	N	O	S	0	0
			879	557	165	154	3		
21	W	120	Total	C	N	O	S	0	0
			864	550	161	150	3		

- Molecule 22 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	347	Total	C	N	O	S	0	0
			2686	1707	486	481	12		

- Molecule 23 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	345	Total	C	N	O	S	0	0
			2594	1648	465	472	9		

- Molecule 24 is a protein called Bms1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	639	Total	C	N	O	S	0	0
			4848	3145	903	782	18		

- Molecule 25 is a protein called Imp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	179	Total	C	N	O	S	0	0
			1434	918	283	226	7		

- Molecule 26 is a protein called Putative U3 small nucleolar ribonucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	291	Total	C	N	O	S	0	0
			2279	1445	437	389	8		

- Molecule 27 is a protein called Putative U3 small nucleolar ribonucleoprotein protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	175	Total	C	N	O	S	0	0
			1387	869	269	244	5		

- Molecule 28 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	439	Total	C	N	O	S	0	0
			3436	2158	663	600	15		

- Molecule 29 is a protein called Emg1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	215	Total	C	N	O	S	0	0
			1683	1067	293	313	10		
29	f	215	Total	C	N	O	S	0	0
			1683	1067	293	313	10		

- Molecule 30 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	174	Total	C	N	O	S	0	0
			1393	890	250	244	9		

- Molecule 31 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	167	Total	C	N	O	S	0	0
			1288	817	234	231	6		

- Molecule 32 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	659	Total	C	N	O		0	0
			3254	1936	659	659			
32	j	677	Total	C	N	O		0	0
			3342	1988	677	677			

- Molecule 33 is a protein called Fcf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	k	117	Total	C	N	O	S	0	0
			930	589	179	158	4		

- Molecule 34 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	l	214	Total	C	N	O	S	0	0
			1735	1105	322	303	5		

- Molecule 35 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	m	258	Total	C	N	O	S	0	0
			2057	1305	386	359	7		

- Molecule 36 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	192	Total	C	N	O	S	0	0
			1447	918	277	245	7		

- Molecule 37 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	237	Total	C	N	O	S	0	0
			1911	1192	384	330	5		

- Molecule 38 is a protein called 40S ribosomal protein S7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	p	159	Total	C	N	O		0	0
			1279	810	237	232			

- Molecule 39 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	q	201	Total	C	N	O	S	0	0
			1622	1009	330	282	1		

- Molecule 40 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	r	159	Total	C	N	O	S	0	0
			1242	801	255	184	2		

- Molecule 41 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	s	49	Total	C	N	O	0	0
			416	270	82	64		

- Molecule 42 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	t	115	Total	C	N	O	S	0	0
			791	492	154	141	4		

- Molecule 43 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	126	Total	C	N	O	S	0	0
			943	613	177	151	2		

- Molecule 44 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	v	157	Total	C	N	O	S	0	0
			1286	825	248	208	5		

- Molecule 45 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	w	126	Total	C	N	O	S	0	0
			985	632	184	164	5		

- Molecule 46 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	x	94	Total	C	N	O	S	0	0
			684	445	129	108	2		

- Molecule 47 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	93	Total	C	N	O	S	0	0
			752	481	140	129	2		

- Molecule 48 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	z	61	Total	C	N	O	0	0
			455	284	97	74		

- Molecule 49 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	0	92	Total	C	N	O	S	0	0
			694	426	144	120	4		

- Molecule 50 is a RNA chain called 35S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	1350	Total	C	N	O	P	0	0
			28796	12851	5157	9440	1348		

- Molecule 51 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2	230	Total	C	N	O	P	0	0
			4891	2182	856	1623	230		

- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	P	1	Total	Zn	0
			1	1	

A883 N887 R891 R903
LYS ARG LYS ARG

Chain C: 10% . 89%

ALA	ALA	ILE	GLY	ALA	ASP
ALA	ALA	PRO	ALA	LYS	HIS
LYS	ALA	TYR	ASP	LYS	GLU
ARG	LYS	ARG	SER	LEU	VAL
ARG	LYS	GLU	GLY	SER	MET
ALA	ARG	ARG	MET	LYS	GLN
ASP	ALA	LEU	ASP	GLU	THR
LYS	ASP	LYS	ASP	GLU	LEU
GLN	ASP	ASP	ASN	ILE	MET
ALA	ARG	ARG	ARG	LYS	GLU
ARG	ALA	GLN	SER	ALA	CYS
ARG	ALA	ARG	ASP	ASN	ARG
PHE	ARG	ARG	PHE	LYS	GLU
GLU	LEU	ARG	GLY	LYS	ALA
ALA	ALA	ASN	GLU	LYS	TRP
LEU	LEU	ALA	GLU	LYS	LYS
ALA	ALA	GLU	GLU	GLU	LYS
ALA	ALA	ALA	GLU	GLU	VAL
ALA	GLU	GLU	LEU	GLU	LYS
ARG	ARG	ARG	ASP	ALA	SER
LYS	LYS	ARG	ALA	LYS	LEU
GLY	GLY	GLY	ARG	LYS	ARG
ASP	ASP	LYS	THR	ALA	PRO
ARG	ARG	ARG	ALA	LYS	ALA
VAL	VAL	ASP	ALA	LYS	LYS
VAL	GLU	SER	GLU	VAL	GLY
GLU	GLU	PHE	ALA	GLN	VAL
GLU	GLU	GLY	LYS	SER	SER
THR	THR	ALA	ARG	LEU	ALA
ILE	ILE	ASP	LYS	ALA	HIS
GLY	LEU	LEU	LYS	GLU	GLY
PRO	PRO	GLY	SER	LEU	MET
ASP	ASP	GLY	LEU	THR	LEU
G575	G575	ASP	ARG	SER	SER
I579	I579	SER	PHE	LEU	PRO
I583	I583	SER	TYR	LEU	PRO
I583	I583	ASP	THR	GLN	GLU
K587	K587	GLU	SER	THR	GLY
K587	K587	ASP	ILE	LYS	GLU
R598	R598	ALA	VAL	LYS	GLU
R598	R598	LYS	GLN	LYS	GLU
W602	W602	ALA	LYS	ALA	ALA
W602	W602	ARG	ALA	VAL	GLY
K644	K644	GLN	ASN	SER	SER
K644	K644	VAL	LYS	LYS	VAL
L648	L648	ARG	ARG	ALA	ASP
L648	L648	ASP	GLN	SER	ASP
L648	L648	GLY	GLY	VAL	MET
L648	L648	GLU	ALA	ALA	LEU
L648	L648	ASP	ALA	SER	ASP
L648	L648	GLU	GLY	LYS	HIS
L648	L648	ALA	ARG	ALA	ALA
L648	L648	TYR	ASP	MET	VAL
L648	L648	TYR	ALA	SER	GLN
L648	L648	ASN	GLY	THR	LYS
L648	L648	GLU	GLY	ALA	LYS
L648	L648	VAL	ASP	ALA	PRO
L648	L648	VAL	MET	THR	LYS
L648	L648	GLN	ASP	SER	LYS

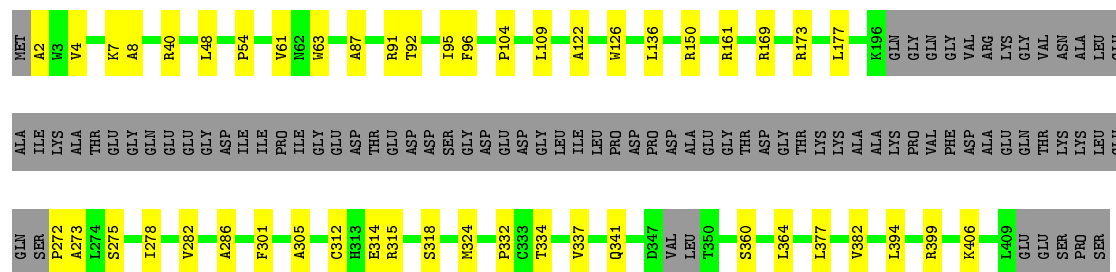
- Molecule 4: Utp4

Chain D:  27% 6% 67%

[illegible]

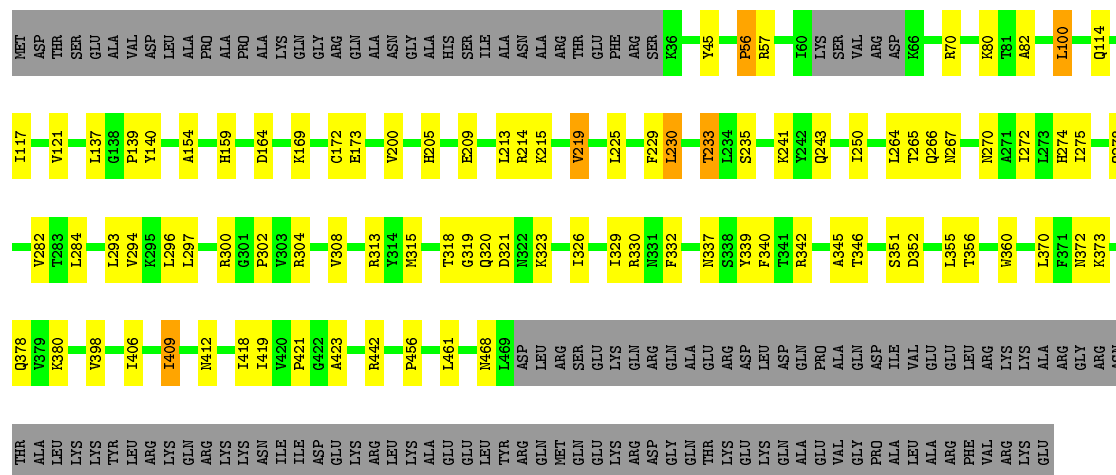
- Molecule 5: Utp6

Chain E:  68% 12% 20%



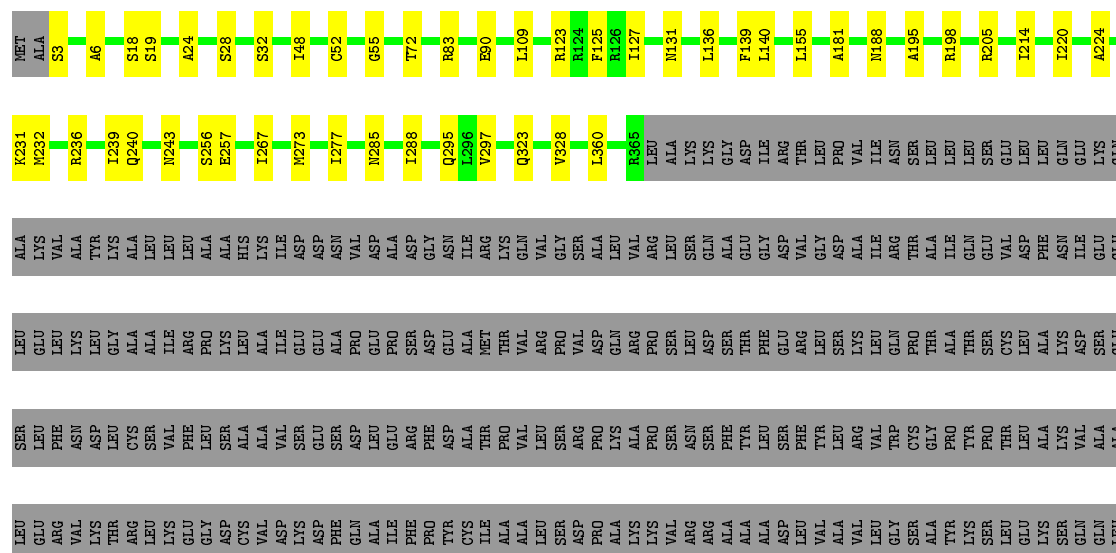
- Molecule 6: Utp7

Chain F:  60% 15% 23%



- Molecule 7: Utp10

Chain G:  17% 80%

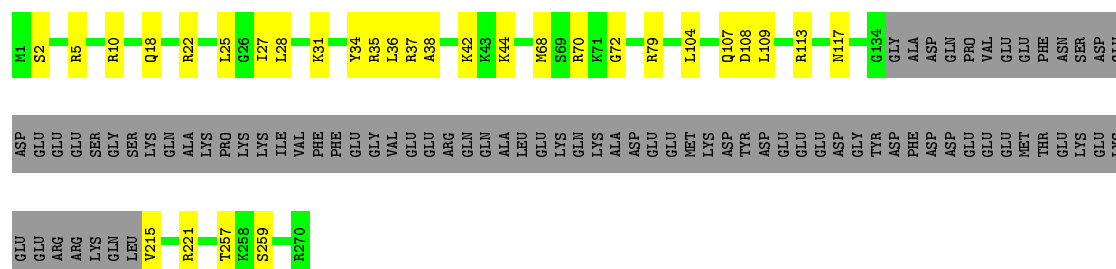





ASP ASP ASP ASP GLU VAL VAL GLU ARG GLU ASN ARG ARG TRP ILE VAL GLY ILE GLU GLU LYS LEU GLY GLU SER SER LEU ASP SER MET LEU GLN

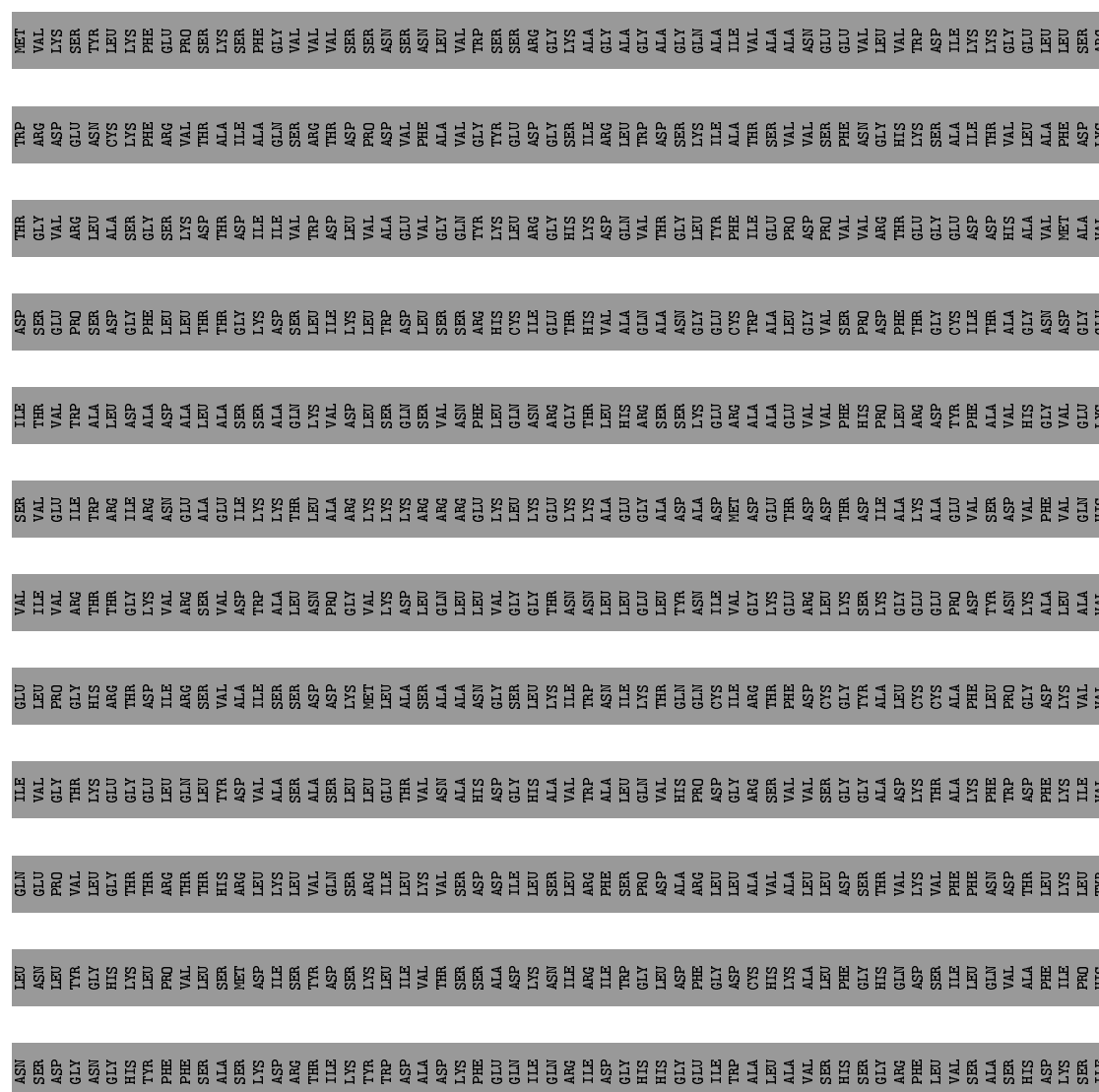
- Molecule 8: U3 small nucleolar RNA-associated protein 11

Chain H: 59% 11% 30%



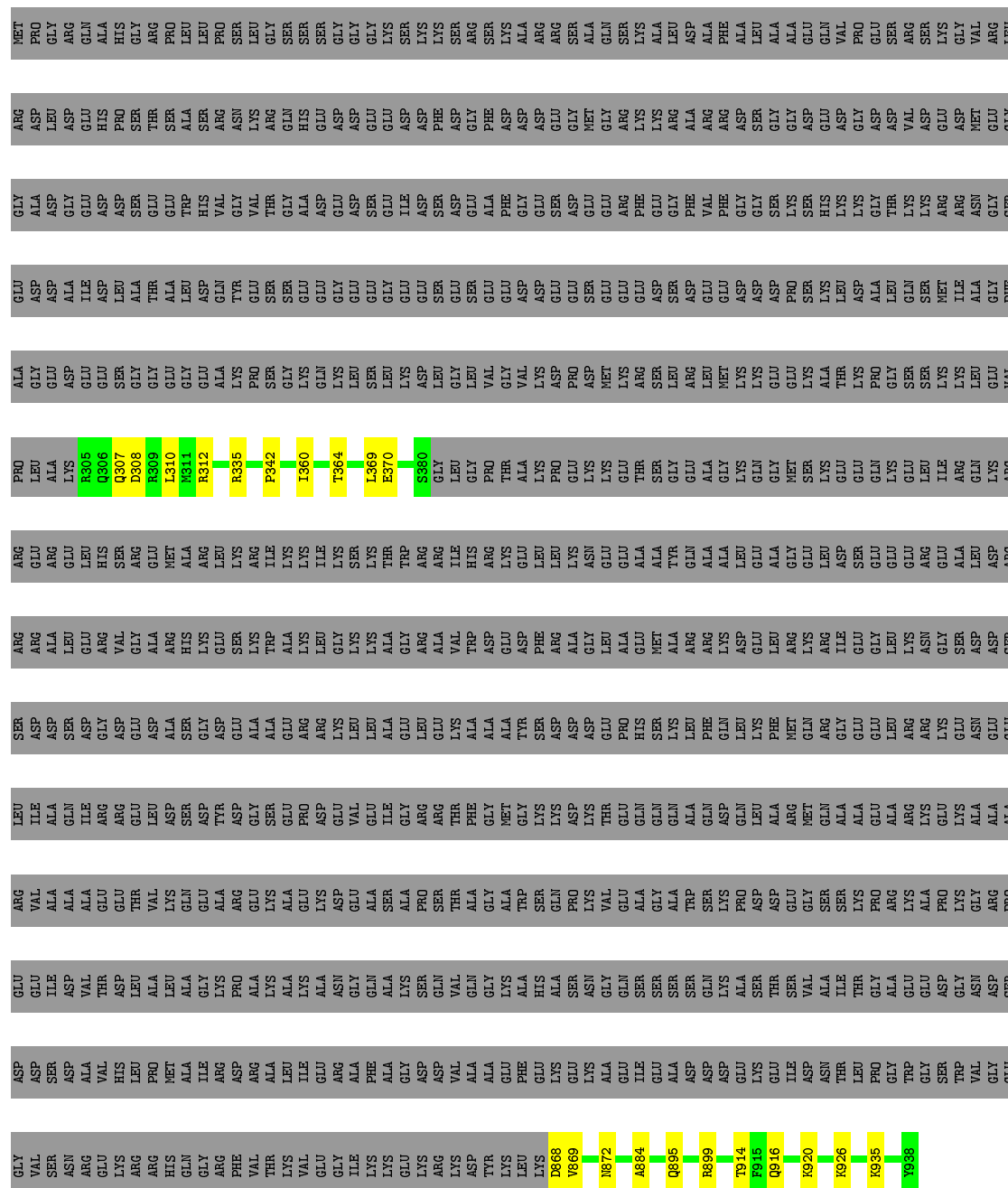
- Molecule 9: Utp12

Chain I:  12% 4% 84%

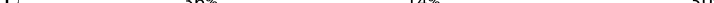


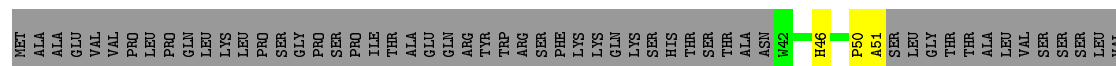
- Molecule 11: Utp14

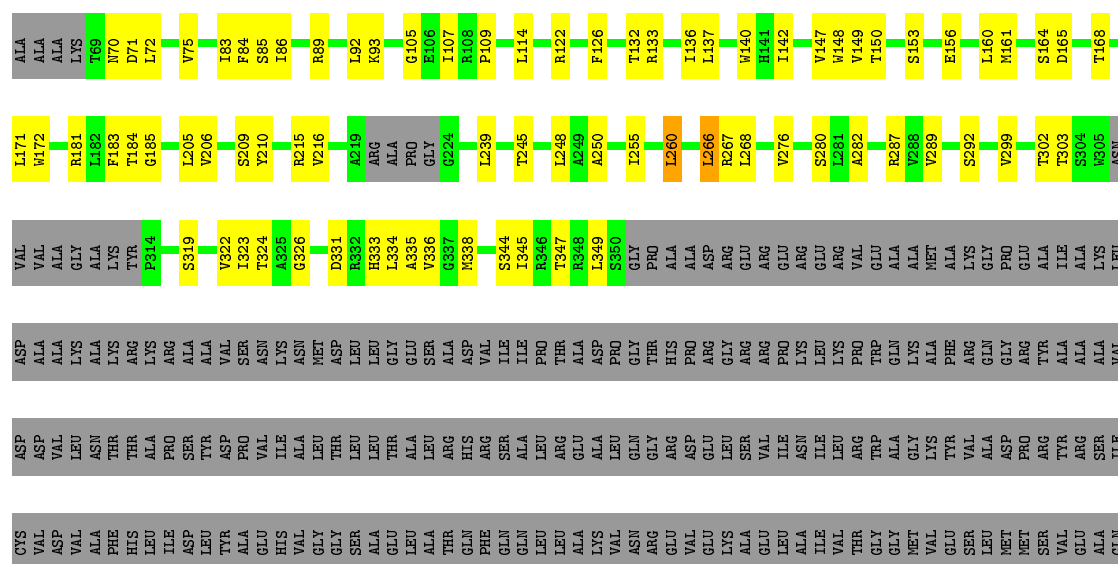
Chain K:  13% . 84%



- Molecule 12: Utp15

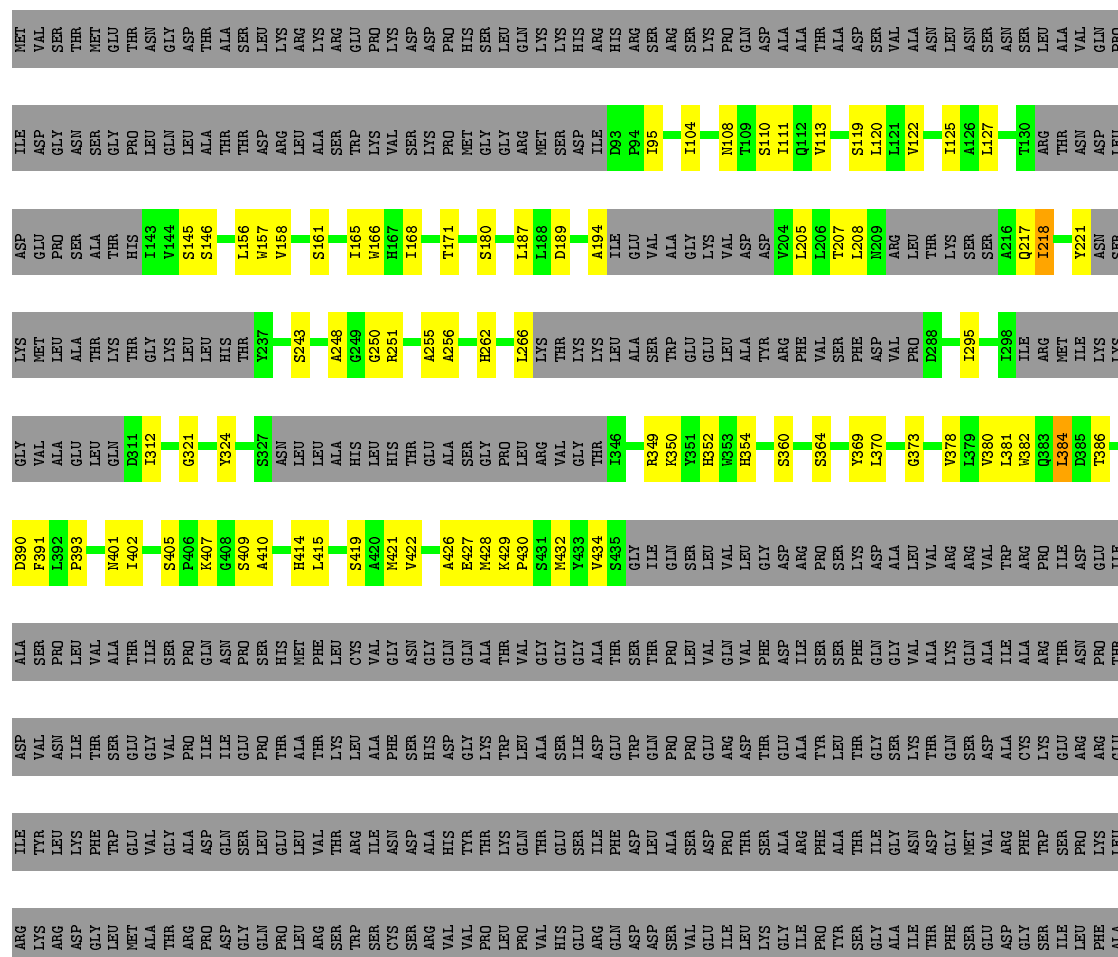
Chain L:  36% 14% 50%

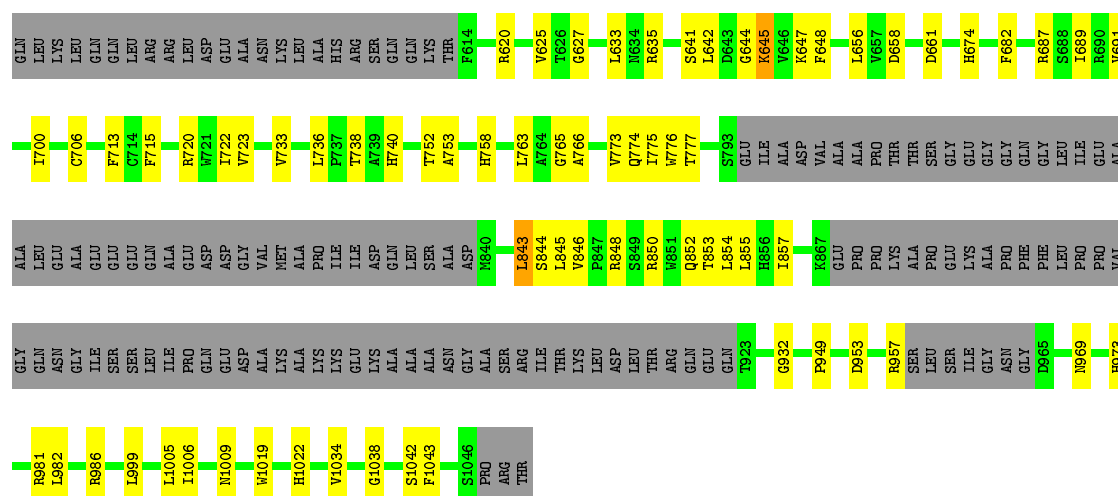




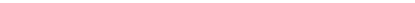
- Molecule 13: Utp17

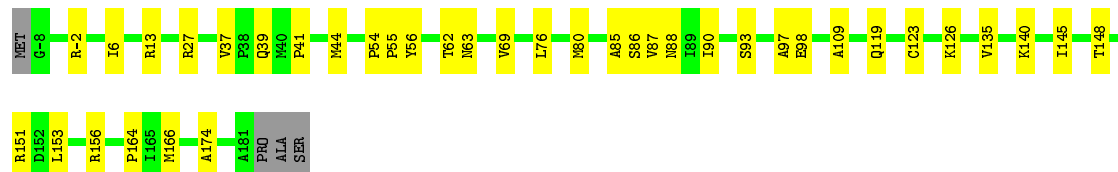
Chain M:  21% 8% 70%





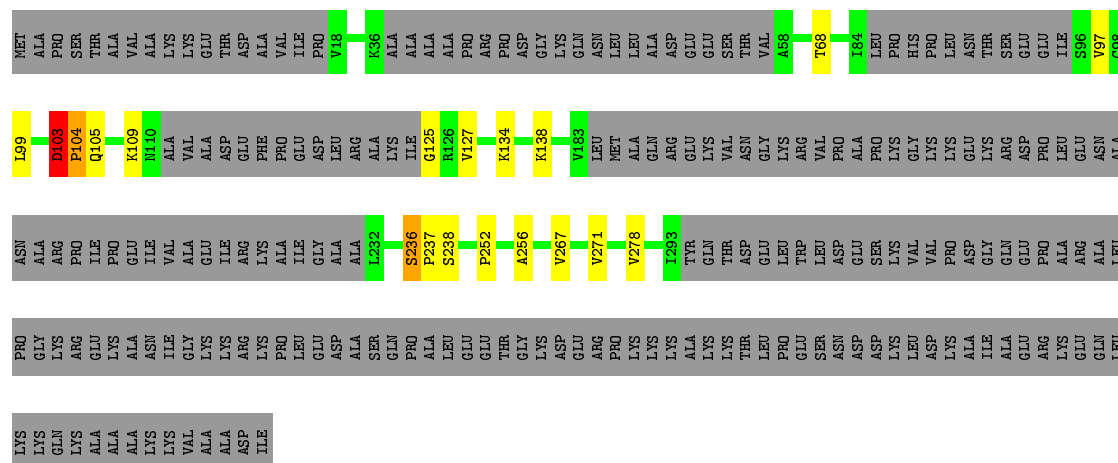
- Molecule 16: Utp24

Chain P:  78% 20% .



- Molecule 17: Utp30

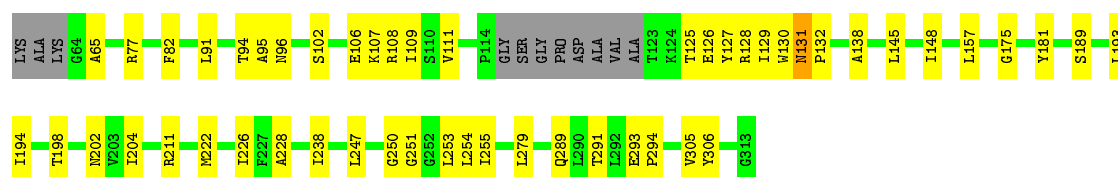
Chain Q: 42% . . 53%



- Molecule 18: Nop1

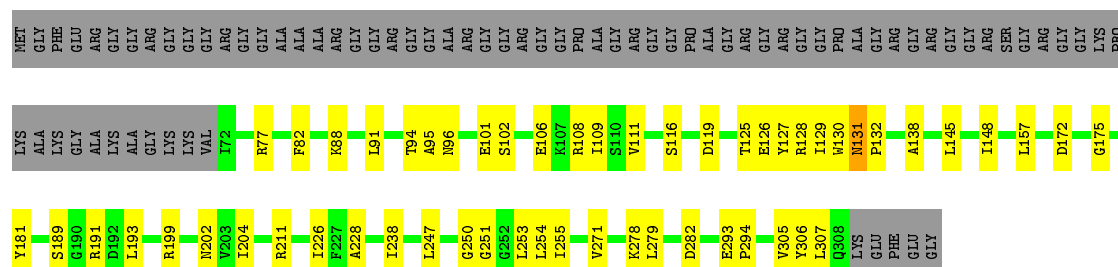
Chain R:  61% 16% 23%





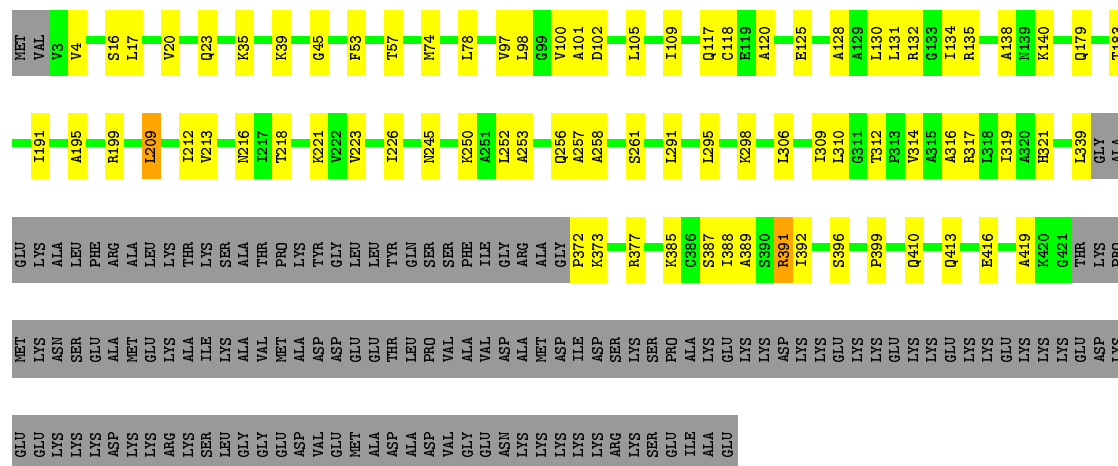
- Molecule 18: Nop1

Chain S:  58% 17% 24%



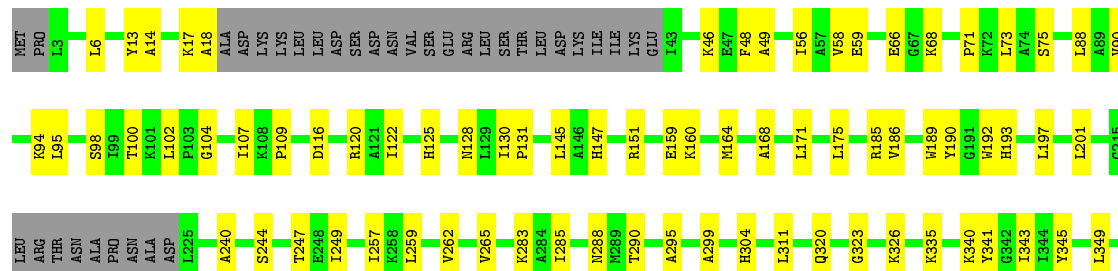
- Molecule 19: Putative nucleolar protein

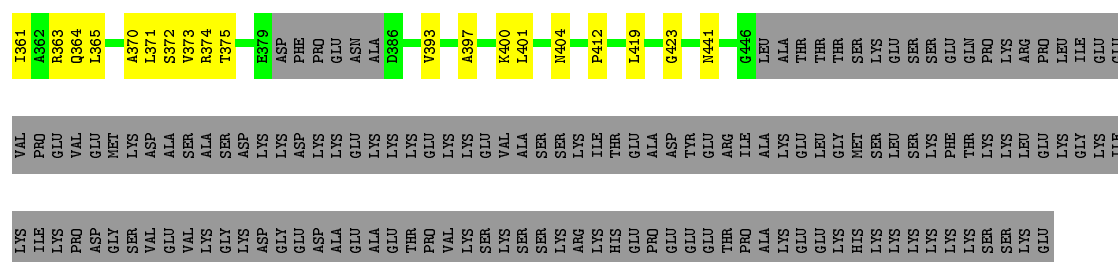
Chain T:  59% 15% 26%



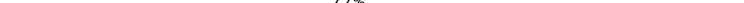
- Molecule 20: Nop58

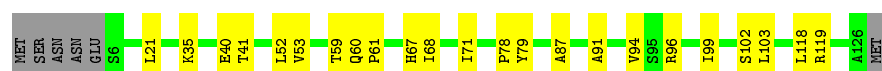
Chain U: 53% 16% 30%





- Molecule 21: Snu13

Chain V:  77% 18% 5%



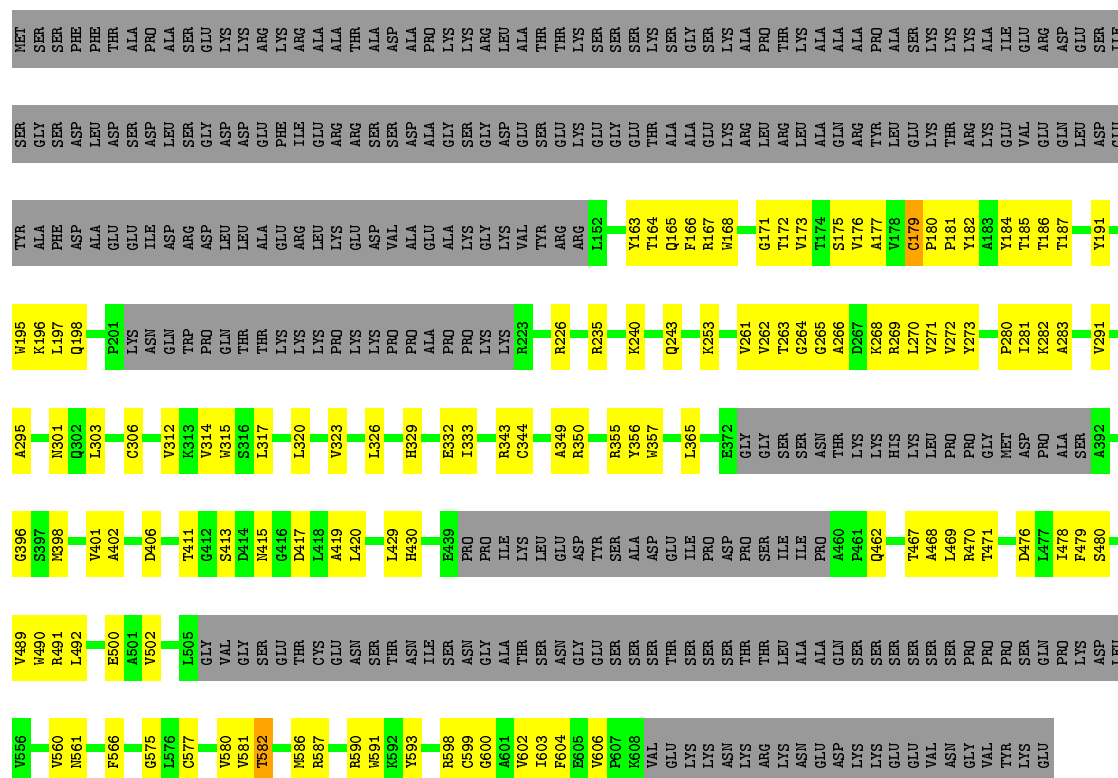
- Molecule 21: Snu13

Chain W:  72% 23% 6%



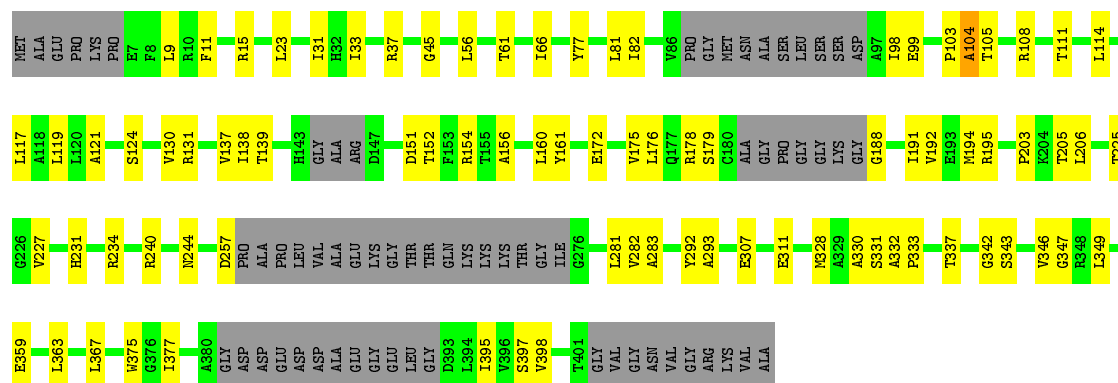
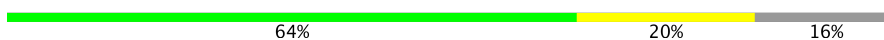
- Molecule 22: Rrp9

Chain X: 36% 18% 45%



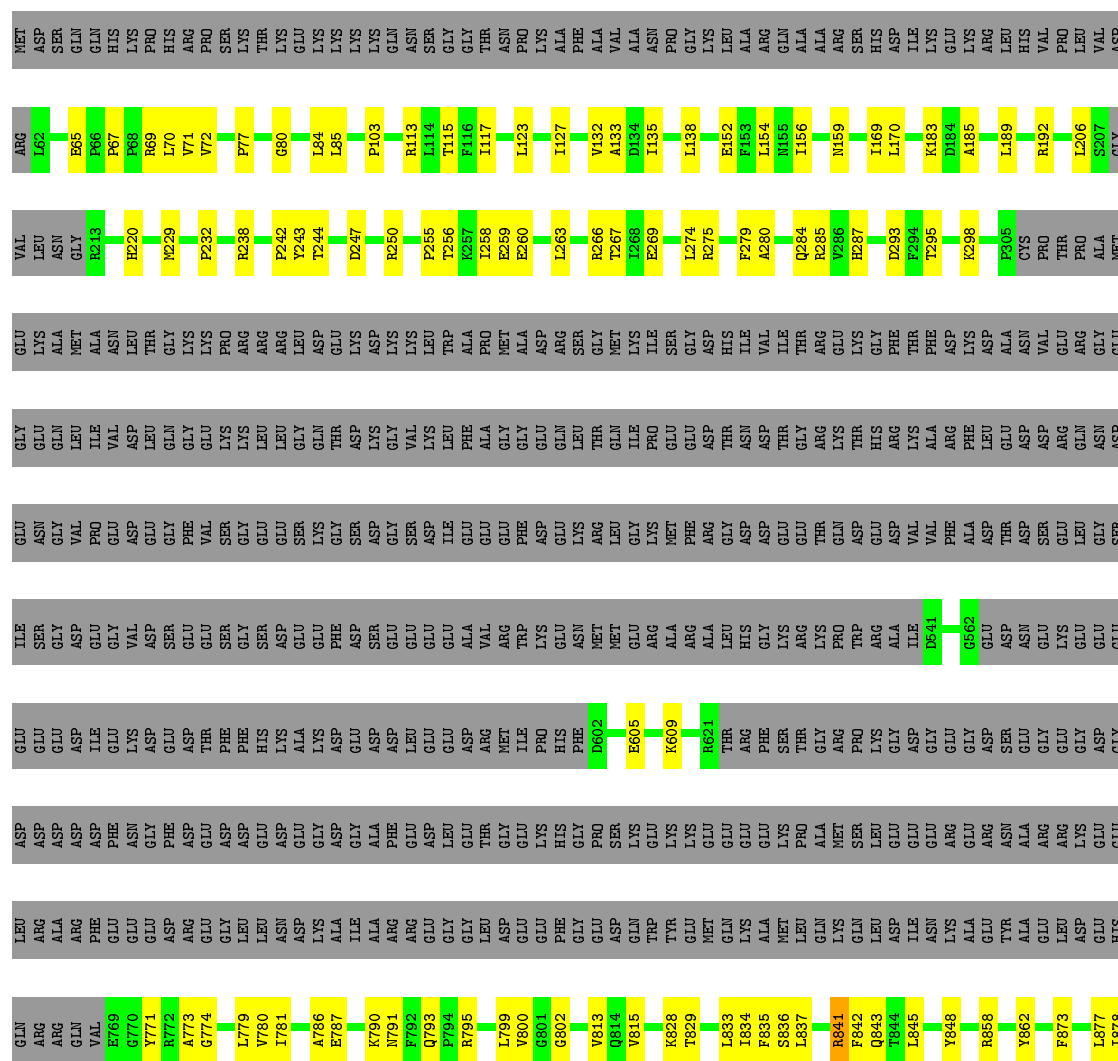
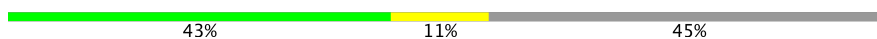
- Molecule 23: RNA 3'-terminal phosphate cyclase-like protein

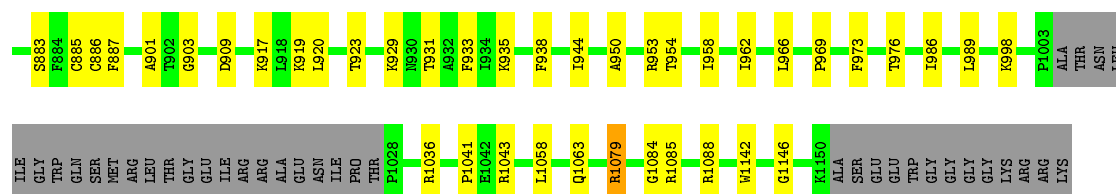
Chain Y:



- Molecule 24: Bms1

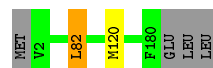
Chain Z:





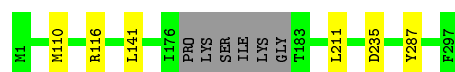
- Molecule 25: Imp3

Chain a: 97%



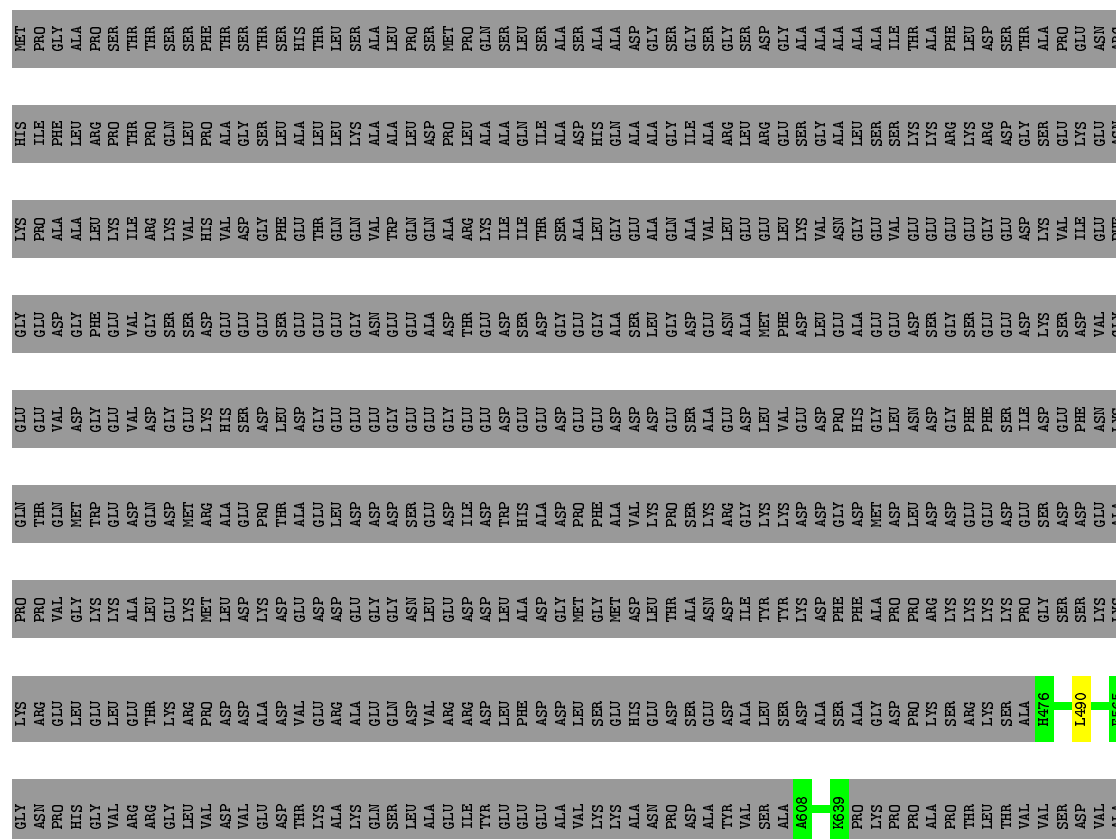
- Molecule 26: Putative U3 small nucleolar ribonucleoprotein

Chain b: 96%



- Molecule 27: Putative U3 small nucleolar ribonucleoprotein protein

Chain c: 22% 78%

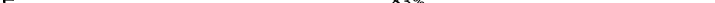


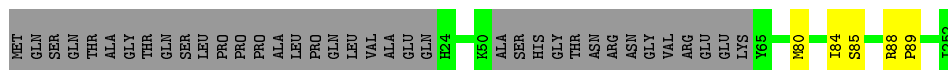
- Molecule 28: Sof1

Chain d:  96%



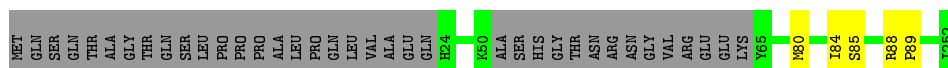
- Molecule 29: Emg1

Chain e:  83% • 15%



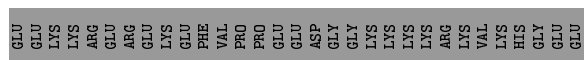
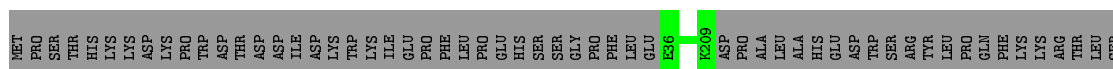
- Molecule 29: Emg1

Chain f: 83% • 15%



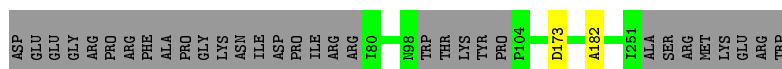
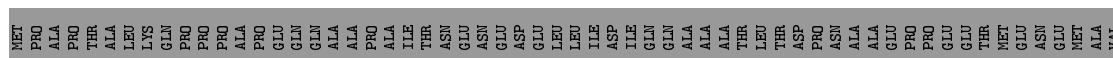
- Molecule 30: KRR1 small subunit processome component

Chain g:  54% 46%



- Molecule 31: Pre-rRNA-processing protein PNO1

Chain h: 64% 36%



- Molecule 32: RNA cytidine acetyltransferase

Chain i:

61%

39%

GLU	LYS	MET	GLU	GLY	LYS	LYS	GLU	ARG	GLY	SER	LYS	LYS	LYS	LYS	LYS	TRP	ALA	ALA	GLU	GLY	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 32: RNA cytidine acetyltransferase

Chain j:

63%

37%

ARG	GLU	ASP	VAL	ALA	SER	GLY	LYS	LYS	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----


- Molecule 33: Fcf2

Chain k:  58% 42%

MET ALA THR LEU GLY LEU PRO ASP GLU ASP ILE ARG LEU LEU ALA GLU ALA GLU ARG ALA GLY SER ASP ASP ALA GLY ILE ILE LEU ALA LYS PRO PRO ALA SER LYS PRO LEU THR VAL ALA ALA PRO ALA ALA LYS GLY GLN THR VAL

PRO GLN VAL LYS ALA GLU LEU SER VAL ARG VAL PRO GLN LEU PRO GLN LYS LYS GLY ALA PRO ASP T86 R202 LYS

- Molecule 34: 40S ribosomal protein S1

Chain l:  80% 16%

MET ALA VAL GLY LYS ASN LYS ARG LEU SER LYS GLY LYS LYS LYS LYS LYS LYS K19 V20 Q21 K33 L47 L61 K62 I65 L110 L135 R166 T180 I212 H232 GLY GLU SER SER GLU GLU ALA GLY GLN LYS VAL VAL ARG GLU PHE ARG GLN


VAL LEU GLU SER VAL

- Molecule 35: 40S ribosomal protein S4

Chain m:  97%

MET A2 R87 L164 E231 L259 ALA ALA GLY HIS

- Molecule 36: 40S ribosomal protein s5-like protein

Chain n:  89% 9%


MET SER GLY GLY VAL GLU VAL ALA ALA GIN PRO GIN Y13 D14 V15 N91 M126 R135 ILE GLY SER ALA GLY THR VAL ARG R144 R212

- Molecule 37: 40S ribosomal protein S6

Chain o:  97%

H1 Q59 L147 S148 K149 P176 R177 L237 HIS LYS

- Molecule 38: 40S ribosomal protein S7-like protein

Chain p:  78% 22%

MET SER ALA PRO SER LEU ASN LYS ILE ALA ALA ASN SER PRO S15 A38 R103 ILE LEU PRO LYS PRO LYS ARG SER ALA ARG SER ARG ASN THR LEU LYS GIN LYS ARG PRO ARG SER ARG THR L128 Q197 THR THR ILE THR ASP TYR

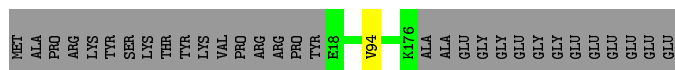
- Molecule 39: 40S ribosomal protein S8

Chain q:  99%



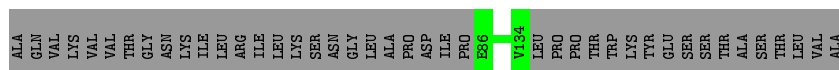
- Molecule 40: 40S ribosomal protein s9-like protein

Chain r: 83% 16%



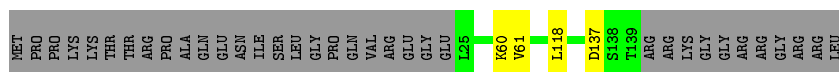
- Molecule 41: 40S ribosomal protein S13-like protein

Chain s: 32% 68%



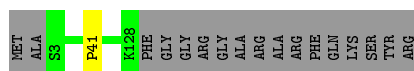
- Molecule 42: 40S ribosomal protein S14-like protein

Chain t: 74% 23%



- Molecule 43: 40S ribosomal protein S16-like protein

Chain u: 87% 12%



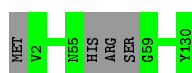
- Molecule 44: 40S ribosomal protein S11-like protein

Chain v: 96% 2%



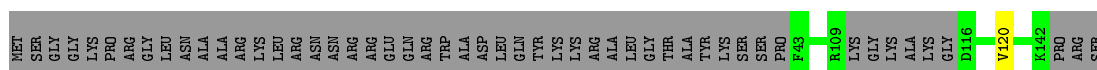
- Molecule 45: 40S ribosomal protein S22-like protein

Chain w: 97% 2%

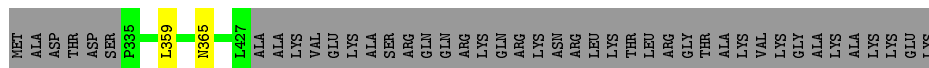


- Molecule 46: 40S ribosomal protein s23-like protein

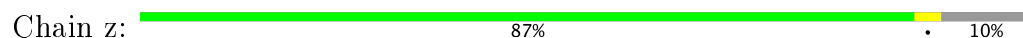
Chain x: 64% 35%



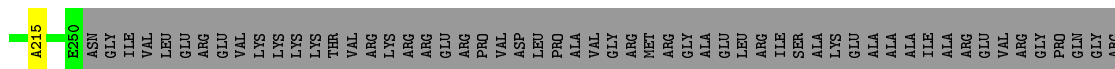
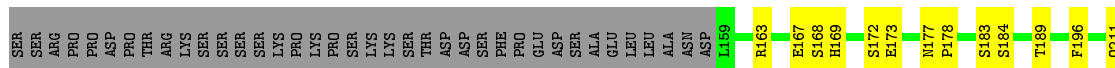
- Molecule 47: 40S ribosomal protein S24



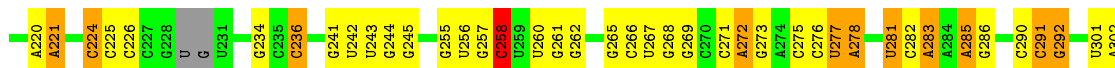
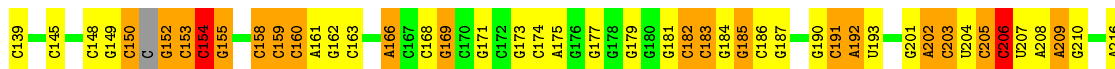
- Molecule 48: 40S ribosomal protein S28-like protein



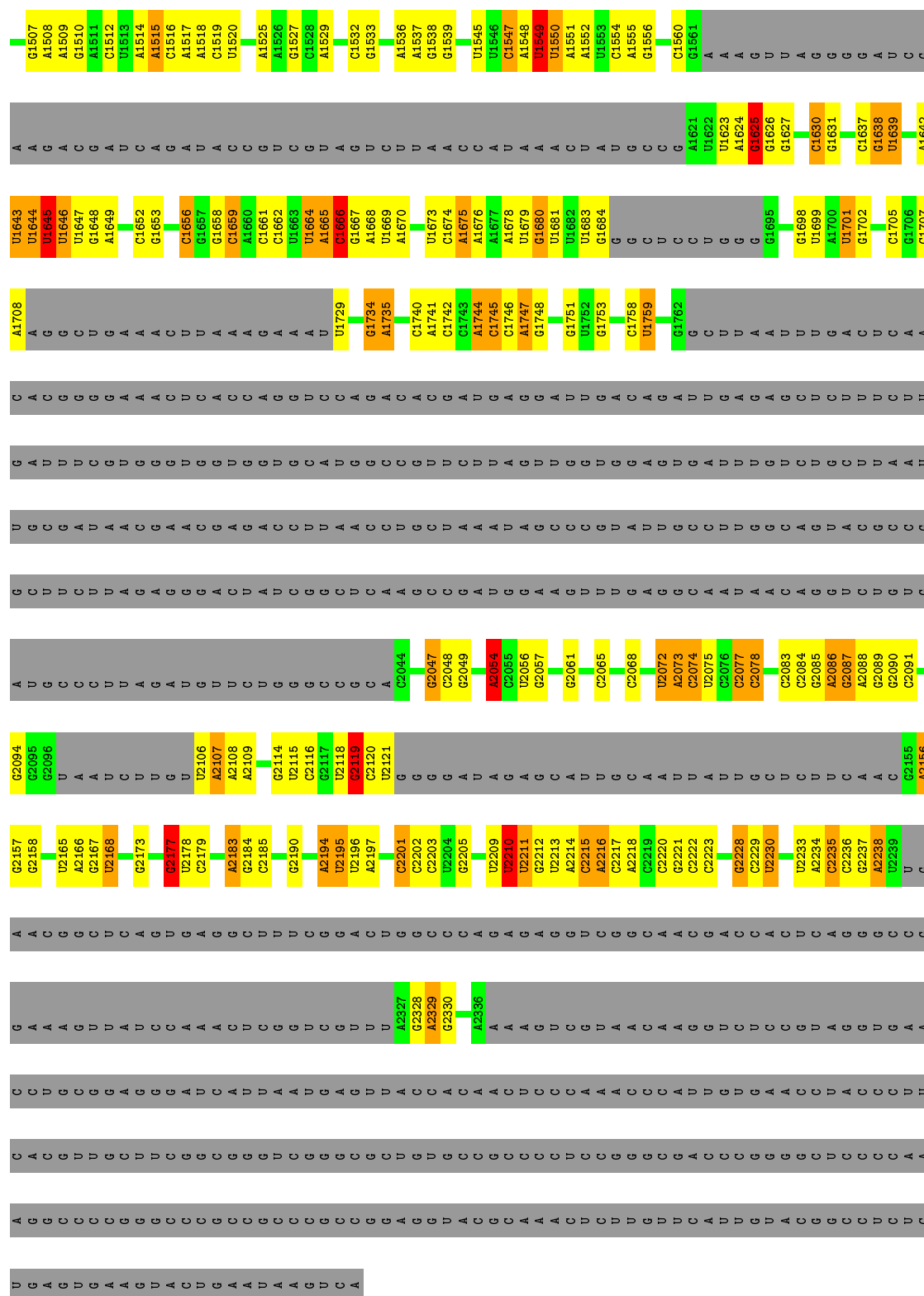
- Molecule 49: Faf1



- Molecule 50: 35S rRNA

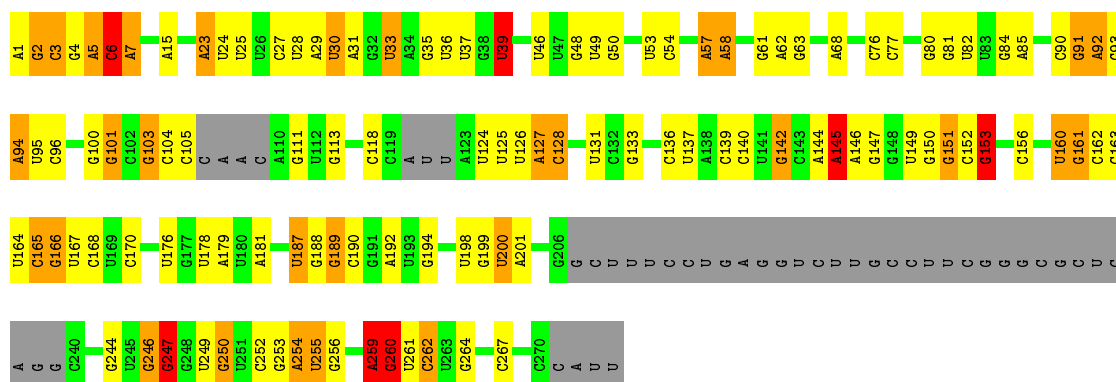






- Molecule 51: U3 snoRNA





4 Experimental information ⓘ

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	231121	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.4	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	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

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	0.50	0/6395	0.75	10/8703 (0.1%)
10	J	0.38	0/1221	0.65	0/1662
11	K	0.39	0/1161	0.64	1/1570 (0.1%)
12	L	0.33	0/2117	0.69	3/2887 (0.1%)
13	M	0.37	0/2179	0.72	2/2972 (0.1%)
14	N	0.42	0/3508	0.64	2/4742 (0.0%)
15	O	0.45	0/6604	0.76	10/8981 (0.1%)
16	P	0.43	0/1483	0.70	0/1998
17	Q	0.25	0/900	0.49	0/1249
18	R	0.39	0/1814	0.59	0/2456
18	S	0.40	0/1853	0.59	0/2511
19	T	0.36	0/2911	0.66	1/3937 (0.0%)
2	B	0.33	0/541	0.46	0/713
20	U	0.35	0/3085	0.65	1/4169 (0.0%)
21	V	0.38	0/891	0.67	1/1214 (0.1%)
21	W	0.38	0/876	0.67	1/1195 (0.1%)
22	X	0.36	0/2739	0.69	1/3699 (0.0%)
23	Y	0.33	0/2638	0.63	1/3580 (0.0%)
24	Z	0.39	0/4960	0.66	4/6710 (0.1%)
25	a	0.49	0/1462	0.71	2/1967 (0.1%)
26	b	0.48	0/2324	0.73	4/3144 (0.1%)
27	c	0.36	0/1405	0.59	1/1879 (0.1%)
28	d	0.50	0/3506	0.72	3/4739 (0.1%)
29	e	0.28	0/1714	0.53	0/2325
29	f	0.28	0/1714	0.53	0/2325
3	C	0.38	0/595	0.56	0/786
30	g	0.32	0/1412	0.61	0/1897
31	h	0.28	0/1304	0.61	0/1751
32	i	0.25	0/3246	0.45	0/4507
32	j	0.24	0/3335	0.45	0/4632
33	k	0.41	0/945	0.60	0/1264
34	l	0.31	0/1764	0.73	4/2377 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
35	m	0.29	0/2097	0.63	1/2821 (0.0%)
36	n	0.41	0/1468	0.63	0/1987
37	o	0.32	0/1942	0.67	1/2595 (0.0%)
38	p	0.34	0/1298	0.69	1/1750 (0.1%)
39	q	0.28	0/1655	0.57	0/2213
4	D	0.37	0/2209	0.66	0/2986
40	r	0.38	0/1259	0.63	0/1687
41	s	0.26	0/422	0.48	0/561
42	t	0.31	0/801	0.62	1/1087 (0.1%)
43	u	0.48	0/958	0.70	0/1293
44	v	0.31	0/1315	0.59	0/1760
45	w	0.36	0/1001	0.63	0/1345
46	x	0.42	0/693	0.59	0/928
47	y	0.28	0/766	0.65	1/1027 (0.1%)
48	z	0.42	0/458	0.67	0/617
49	0	0.32	0/702	0.58	0/939
5	E	0.37	0/2657	0.55	1/3596 (0.0%)
50	1	0.54	2/32166 (0.0%)	1.31	444/50073 (0.9%)
51	2	0.62	0/5459	1.45	76/8498 (0.9%)
6	F	0.51	0/3353	0.73	1/4544 (0.0%)
7	G	0.41	0/2828	0.65	1/3841 (0.0%)
8	H	0.42	0/1468	0.60	0/1946
9	I	0.34	0/1251	0.62	0/1696
All	All	0.44	2/140828 (0.0%)	0.91	580/198331 (0.3%)

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
1	A	0	4
12	L	0	1
13	M	0	4
14	N	0	1
15	O	0	5
17	Q	0	3
18	R	0	1
18	S	0	1
21	V	0	1
21	W	0	1
22	X	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
23	Y	0	2
24	Z	0	3
26	b	0	1
28	d	0	1
29	e	0	3
29	f	0	3
31	h	0	2
32	i	0	1
32	j	0	1
34	l	0	5
35	m	0	2
37	o	0	2
38	p	0	1
39	q	0	1
4	D	0	1
42	t	0	1
43	u	0	1
44	v	0	2
46	x	0	1
47	y	0	1
6	F	0	3
All	All	0	64

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	1	435	A	N9-C4	-5.50	1.34	1.37
50	1	2194	A	C2-N3	-5.21	1.28	1.33

The worst 5 of 580 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	2	2	G	O5'-P-OP1	-32.85	71.28	110.70
51	2	2	G	OP1-P-OP2	-26.67	79.59	119.60
50	1	18	G	N1-C6-O6	-19.83	108.00	119.90
51	2	2	G	O5'-P-OP2	19.02	133.53	110.70
50	1	18	G	C5-C6-O6	16.50	138.50	128.60

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	192	SER	Peptide
1	A	284	MET	Peptide
1	A	556	GLY	Peptide
1	A	686	SER	Peptide
4	D	169	GLU	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	6242	0	6135	134	0
2	B	537	0	569	3	0
3	C	588	0	647	7	0
4	D	2170	0	2191	32	0
5	E	2591	0	2642	31	0
6	F	3282	0	3289	64	0
7	G	2772	0	2847	28	0
8	H	1456	0	1571	27	0
9	I	1230	0	1297	29	0
10	J	1201	0	1218	30	0
11	K	1139	0	1151	19	0
12	L	2070	0	2073	51	0
13	M	2134	0	2117	46	0
14	N	3435	0	3455	47	0
15	O	6446	0	6452	124	0
16	P	1460	0	1522	24	0
17	Q	905	0	400	10	0
18	R	1778	0	1830	32	0
18	S	1816	0	1847	33	0
19	T	2866	0	2960	55	0
20	U	3035	0	3159	69	0
21	V	879	0	918	14	0
21	W	864	0	900	21	0
22	X	2686	0	2676	80	0
23	Y	2594	0	2660	49	0
24	Z	4848	0	4850	84	0
25	a	1434	0	1482	0	0
26	b	2279	0	2314	0	0
27	c	1387	0	1424	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	d	3436	0	3437	0	0
29	e	1683	0	1726	0	0
29	f	1683	0	1726	0	0
30	g	1393	0	1499	0	0
31	h	1288	0	1357	0	0
32	i	3254	0	1481	0	0
32	j	3342	0	1522	0	0
33	k	930	0	957	0	0
34	l	1735	0	1825	0	0
35	m	2057	0	2140	0	0
36	n	1447	0	1483	0	0
37	o	1911	0	2022	0	0
38	p	1279	0	1322	0	0
39	q	1622	0	1645	0	0
40	r	1242	0	1354	0	0
41	s	416	0	451	0	0
42	t	791	0	795	0	0
43	u	943	0	1002	0	0
44	v	1286	0	1366	0	0
45	w	985	0	1021	0	0
46	x	684	0	730	0	0
47	y	752	0	797	0	0
48	z	455	0	482	0	0
49	0	694	0	717	9	0
50	1	28796	0	14588	240	0
51	2	4891	0	2476	57	0
52	P	1	0	0	0	0
All	All	135120	0	116517	1312	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 1312 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)
50:1:152:G:O2'	50:1:153:C:H6	1.28	1.17
4:D:83:VAL:O	4:D:100:SER:HA	1.57	1.03
10:J:748:TYR:CD2	10:J:757:ALA:HB2	1.93	1.03
50:1:2237:G:H1	50:1:2329:A:N6	1.56	1.02
50:1:149:G:O2'	50:1:150:C:H5'	1.65	0.97

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	A	823/904 (91%)	739 (90%)	83 (10%)	1 (0%)	55	89
2	B	67/907 (7%)	66 (98%)	1 (2%)	0	100	100
3	C	72/648 (11%)	64 (89%)	8 (11%)	0	100	100
4	D	280/884 (32%)	256 (91%)	23 (8%)	1 (0%)	38	77
5	E	325/414 (78%)	312 (96%)	13 (4%)	0	100	100
6	F	425/558 (76%)	390 (92%)	34 (8%)	1 (0%)	51	86
7	G	361/1802 (20%)	340 (94%)	21 (6%)	0	100	100
8	H	186/270 (69%)	178 (96%)	8 (4%)	0	100	100
9	I	153/962 (16%)	141 (92%)	12 (8%)	0	100	100
10	J	147/912 (16%)	139 (95%)	8 (5%)	0	100	100
11	K	143/938 (15%)	130 (91%)	13 (9%)	0	100	100
12	L	272/557 (49%)	237 (87%)	35 (13%)	0	100	100
13	M	266/960 (28%)	222 (84%)	43 (16%)	1 (0%)	38	77
14	N	433/618 (70%)	404 (93%)	29 (7%)	0	100	100
15	O	850/1049 (81%)	768 (90%)	82 (10%)	0	100	100
16	P	188/194 (97%)	173 (92%)	15 (8%)	0	100	100
17	Q	172/391 (44%)	146 (85%)	23 (13%)	3 (2%)	11	48
18	R	238/313 (76%)	222 (93%)	15 (6%)	1 (0%)	38	77
18	S	235/313 (75%)	221 (94%)	13 (6%)	1 (0%)	38	77
19	T	383/523 (73%)	352 (92%)	31 (8%)	0	100	100
20	U	397/582 (68%)	375 (94%)	22 (6%)	0	100	100
21	V	119/127 (94%)	105 (88%)	13 (11%)	1 (1%)	22	65

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	W	118/127 (93%)	104 (88%)	13 (11%)	1 (1%)	22	65
22	X	337/630 (54%)	294 (87%)	42 (12%)	1 (0%)	44	81
23	Y	333/411 (81%)	300 (90%)	30 (9%)	3 (1%)	20	64
24	Z	627/1163 (54%)	582 (93%)	44 (7%)	1 (0%)	51	86
25	a	177/183 (97%)	162 (92%)	15 (8%)	0	100	100
26	b	287/297 (97%)	263 (92%)	24 (8%)	0	100	100
27	c	169/785 (22%)	160 (95%)	9 (5%)	0	100	100
28	d	435/446 (98%)	390 (90%)	45 (10%)	0	100	100
29	e	211/252 (84%)	199 (94%)	10 (5%)	2 (1%)	20	64
29	f	211/252 (84%)	199 (94%)	10 (5%)	2 (1%)	20	64
30	g	172/322 (53%)	164 (95%)	8 (5%)	0	100	100
31	h	163/259 (63%)	154 (94%)	9 (6%)	0	100	100
32	i	643/1073 (60%)	569 (88%)	74 (12%)	0	100	100
32	j	663/1073 (62%)	588 (89%)	75 (11%)	0	100	100
33	k	115/203 (57%)	101 (88%)	14 (12%)	0	100	100
34	l	212/255 (83%)	184 (87%)	27 (13%)	1 (0%)	32	74
35	m	256/264 (97%)	219 (86%)	37 (14%)	0	100	100
36	n	188/212 (89%)	170 (90%)	17 (9%)	1 (0%)	32	74
37	o	235/239 (98%)	202 (86%)	31 (13%)	2 (1%)	20	64
38	p	155/203 (76%)	137 (88%)	18 (12%)	0	100	100
39	q	199/202 (98%)	187 (94%)	12 (6%)	0	100	100
40	r	157/190 (83%)	152 (97%)	5 (3%)	0	100	100
41	s	47/151 (31%)	45 (96%)	2 (4%)	0	100	100
42	t	113/150 (75%)	95 (84%)	16 (14%)	2 (2%)	10	47
43	u	124/143 (87%)	113 (91%)	11 (9%)	0	100	100
44	v	155/161 (96%)	134 (86%)	21 (14%)	0	100	100
45	w	122/130 (94%)	113 (93%)	9 (7%)	0	100	100
46	x	90/145 (62%)	79 (88%)	11 (12%)	0	100	100
47	y	91/136 (67%)	82 (90%)	9 (10%)	0	100	100
48	z	59/68 (87%)	51 (86%)	8 (14%)	0	100	100
49	0	90/311 (29%)	82 (91%)	8 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	13489/25262 (53%)	12254 (91%)	1209 (9%)	26 (0%)	54 86

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	e	85	SER
29	f	85	SER
34	l	62	LYS
23	Y	105	THR
36	n	91	ASN

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	633/775 (82%)	628 (99%)	5 (1%)	85 95
2	B	43/788 (6%)	43 (100%)	0	100 100
3	C	61/536 (11%)	60 (98%)	1 (2%)	68 89
4	D	222/738 (30%)	222 (100%)	0	100 100
5	E	248/341 (73%)	248 (100%)	0	100 100
6	F	326/474 (69%)	322 (99%)	4 (1%)	75 91
7	G	289/1526 (19%)	289 (100%)	0	100 100
8	H	135/227 (60%)	134 (99%)	1 (1%)	87 96
9	I	134/821 (16%)	134 (100%)	0	100 100
10	J	129/770 (17%)	127 (98%)	2 (2%)	68 89
11	K	115/765 (15%)	115 (100%)	0	100 100
12	L	218/456 (48%)	217 (100%)	1 (0%)	91 97
13	M	219/817 (27%)	217 (99%)	2 (1%)	82 94
14	N	351/524 (67%)	349 (99%)	2 (1%)	89 96
15	O	638/863 (74%)	633 (99%)	5 (1%)	85 95
16	P	147/168 (88%)	146 (99%)	1 (1%)	87 96

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	R	175/228 (77%)	172 (98%)	3 (2%)	66	88
18	S	195/228 (86%)	192 (98%)	3 (2%)	70	90
19	T	287/435 (66%)	284 (99%)	3 (1%)	80	93
20	U	307/489 (63%)	307 (100%)	0	100	100
21	V	91/108 (84%)	91 (100%)	0	100	100
21	W	88/108 (82%)	88 (100%)	0	100	100
22	X	273/525 (52%)	273 (100%)	0	100	100
23	Y	275/320 (86%)	274 (100%)	1 (0%)	93	97
24	Z	466/1009 (46%)	461 (99%)	5 (1%)	78	92
25	a	147/169 (87%)	146 (99%)	1 (1%)	87	96
26	b	238/266 (90%)	237 (100%)	1 (0%)	93	97
27	c	138/642 (22%)	138 (100%)	0	100	100
28	d	354/383 (92%)	348 (98%)	6 (2%)	66	88
29	e	193/223 (86%)	193 (100%)	0	100	100
29	f	193/223 (86%)	193 (100%)	0	100	100
30	g	153/287 (53%)	153 (100%)	0	100	100
31	h	138/215 (64%)	138 (100%)	0	100	100
33	k	95/167 (57%)	95 (100%)	0	100	100
34	l	189/223 (85%)	188 (100%)	1 (0%)	91	97
35	m	219/221 (99%)	219 (100%)	0	100	100
36	n	144/178 (81%)	142 (99%)	2 (1%)	71	90
37	o	202/204 (99%)	201 (100%)	1 (0%)	91	97
38	p	137/177 (77%)	137 (100%)	0	100	100
39	q	163/164 (99%)	162 (99%)	1 (1%)	89	96
40	r	122/162 (75%)	121 (99%)	1 (1%)	85	95
41	s	43/130 (33%)	43 (100%)	0	100	100
42	t	74/117 (63%)	74 (100%)	0	100	100
43	u	92/115 (80%)	92 (100%)	0	100	100
44	v	140/143 (98%)	140 (100%)	0	100	100
45	w	103/113 (91%)	103 (100%)	0	100	100
46	x	68/116 (59%)	68 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	y	81/115 (70%)	81 (100%)	0	100	100
48	z	46/61 (75%)	44 (96%)	2 (4%)	33	71
49	0	68/260 (26%)	68 (100%)	0	100	100
All	All	9605/19113 (50%)	9550 (99%)	55 (1%)	89	96

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	R	96	ASN
19	T	209	LEU
37	o	177	ARG
18	R	131	ASN
18	S	96	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
18	R	308	GLN
20	U	404	ASN
43	u	15	ASN
18	S	96	ASN
19	T	176	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	1	1319/2568 (51%)	478 (36%)	27 (2%)
51	2	226/274 (82%)	76 (33%)	5 (2%)
All	All	1545/2842 (54%)	554 (35%)	32 (2%)

5 of 554 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	1	3	G
50	1	5	G
50	1	6	G
50	1	7	A
50	1	8	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	1	742	U
50	1	1085	U
51	2	35	G
50	1	1068	C
50	1	1087	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.