



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

Nov 14, 2017 – 01:54 AM EST

PDB ID : 5WLC  
EMDB ID: : EMD-8859  
Title : The complete structure of the small subunit processome  
Authors : Barandun, J.; Chaker-Margot, M.; Hunziker, M.; Klinge, S.  
Deposited on : unknown  
Resolution : 3.80 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.

---

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

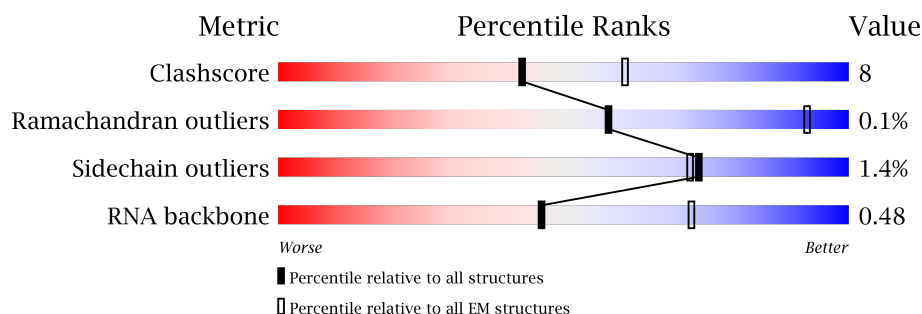
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 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	L0	700	38% 26% 5% 30%
2	L1	1807	30% 21% 6% 43%
3	L2	333	28% 18% • • 49%
4	L3	146	64% 12% • 23%
5	L4	261	63% 23% • 13%
6	L5	225	76% 19% 5%
7	L6	236	36% 11% • 52%
8	L7	190	68% 17% • 13%


























*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LO	923	
24	LP	440	
25	LQ	943	
26	LR	817	
27	LS	594	
28	LT	939	
29	LU	489	
30	LV	707	
31	LW	554	
32	LX	1056	
32	LY	1056	



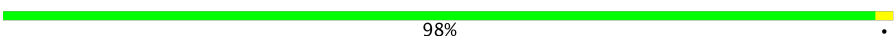







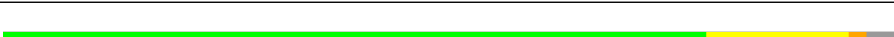

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	LZ	183	
34	NA	593	
35	NB	610	
36	NC	357	
37	ND	214	
38	NE	346	
39	NF	151	
40	NG	137	
41	NH	1237	
42	NI	297	
43	NJ	1729	
44	NK	316	
45	SA	504	
46	SB	511	
47	SC	327	
47	SD	327	
48	SE	126	
48	SF	126	
49	SG	573	
50	SH	367	
51	SI	1184	
52	SJ	252	
52	SK	252	
53	SL	189	
54	SM	290	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
55	SN	274	
56	SO	274	
57	SP	982	
58	SQ	217	
59	SR	145	
60	SS	898	
61	ST	792	
62	SU	552	
63	SV	206	
64	SX	103	
65	SY	250	
66	SZ	483	

## 2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 196921 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 RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	488	Total	C	N	O	P	0	0
			10405	4650	1838	3429	488		

- Molecule 2 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1025	Total	C	N	O	P	0	0
			21866	9773	3905	7163	1025		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	169	Total	C	N	O	P	0	0
			3585	1605	629	1182	169		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L2	200	C	G	conflict	GB 176452

- Molecule 4 is a protein called rpS18\_uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	113	Total	C	N	O	S	0	0
			901	569	168	162	2		

- Molecule 5 is a protein called rpS4\_eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	228	Total	C	N	O	S	0	0
			1810	1158	330	319	3		

- Molecule 6 is a protein called rpS5\_uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	213	Total	C	N	O	S	0	0
			1669	1045	307	314	3		

- Molecule 7 is a protein called rpS6\_eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	113	Total	C	N	O	S	0	0
			888	567	156	163	2		

- Molecule 8 is a protein called rpS7\_eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	165	Total	C	N	O	S	0	0
			1321	854	227	240			

- Molecule 9 is a protein called rpS8\_eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	170	Total	C	N	O	S	0	0
			1349	839	267	241	2		

- Molecule 10 is a protein called rpS9\_uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	175	Total	C	N	O	S	0	0
			1415	895	273	246	1		

- Molecule 11 is a protein called rpS16\_uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	125	Total	C	N	O	S	0	0
			973	625	174	174			

- Molecule 12 is a protein called rpS11\_uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	127	Total	C	N	O	S	0	0
			1027	660	194	170	3		

- Molecule 13 is a protein called rpS22\_uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	127	Total	C	N	O	S	0	0
			1003	640	183	177	3		

- Molecule 14 is a protein called rpS24\_eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	90	Total	C	N	O	S	0	0
			715	458	131	126			

- Molecule 15 is a protein called rpS28\_eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 16 is a protein called Utp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	834	Total	C	N	O	S	0	0
			6633	4215	1121	1278	19		

- Molecule 17 is a protein called Utp8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	487	Total	C	N	O	S	0	0
			2857	1763	529	562	3		

- Molecule 18 is a protein called Utp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	493	Total	C	N	O	S	0	0
			3911	2462	702	735	12		

- Molecule 19 is a protein called Utp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	123	Total	C	N	O	S	0	0
			898	567	166	163	2		

- Molecule 20 is a protein called Utp5.



Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	475	Total	C	N	O	S	0	0
			3772	2400	649	710	13		

- Molecule 21 is a protein called Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	431	Total	C	N	O	S	0	0
			3443	2224	566	641	12		

- Molecule 22 is a protein called Utp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	678	Total	C	N	O	S	0	0
			5344	3384	930	1009	21		

- Molecule 23 is a protein called Utp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 24 is a protein called Utp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	359	Total	C	N	O	S	0	0
			2709	1723	486	488	12		

- Molecule 25 is a protein called Utp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	848	Total	C	N	O	S	0	0
			6640	4244	1116	1253	27		

- Molecule 26 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	729	Total	C	N	O	S	0	0
			4144	2520	797	818	9		

- Molecule 27 is a protein called Utp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LS	481	Total	C	N	O	S	0	0
			3791	2399	668	714	10		

- Molecule 28 is a protein called Utp21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	850	Total	C	N	O	S	0	0
			6697	4253	1154	1269	21		

- Molecule 29 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	457	Total	C	N	O	S	0	0
			3725	2328	679	702	16		

- Molecule 30 is a protein called Enp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	362	Total	C	N	O	S	0	0
			2840	1789	487	555	9		

- Molecule 31 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LW	438	Total	C	N	O	S	0	0
			3428	2163	601	652	12		

- Molecule 32 is a protein called Kre33.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LX	808	Total	C	N	O	S	0	0
			4583	2798	888	890	7		
32	LY	769	Total	C	N	O		0	0
			3823	2285	769	769			

- Molecule 33 is a protein called Imp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 34 is a protein called Mpp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	NA	207	Total	C	N	O	S	0	0
			1667	1034	297	332	4		

- Molecule 35 is a protein called Sas10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	NB	142	Total	C	N	O		0	0
			1098	677	218	203			

- Molecule 36 is a protein called Lcp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NC	136	Total	C	N	O	S	0	0
			1125	674	231	217	3		

- Molecule 37 is a protein called Bud21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	ND	81	Total	C	N	O		0	0
			600	373	122	105			

- Molecule 38 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	NE	158	Total	C	N	O	S	0	0
			1192	731	246	212	3		

- Molecule 39 is a protein called rpS13\_uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	NF	124	Total	C	N	O		0	0
			615	367	124	124			

- Molecule 40 is a protein called rpS14\_uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NG	111	Total	C	N	O		0	0
			543	321	111	111			

- Molecule 41 is a protein called Utp22.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	NH	1082	Total	C	N	O	0	0
			5362	3198	1082	1082		

- Molecule 42 is a protein called Rrp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	NI	169	Total	C	N	O	0	0
			841	503	169	169		

- Molecule 43 is a protein called Rrp5.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	NJ	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 44 is a protein called Krr1.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	NK	175	Total	C	N	O	0	0
			868	518	175	175		

- Molecule 45 is a protein called Nop56.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SA	370	Total	C	N	O	S	0	0
			2854	1815	490	541	8		

- Molecule 46 is a protein called Nop58.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SB	425	Total	C	N	O	S	0	0
			2937	1824	533	572	8		

- Molecule 47 is a protein called Nop1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC	242	Total	C	N	O	S	0	0
			1881	1193	338	340	10		
47	SD	228	Total	C	N	O	S	0	0
			1782	1131	320	321	10		

- Molecule 48 is a protein called Snu13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SE	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
48	SF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 49 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SG	429	Total	C	N	O	S	0	0
			3428	2185	596	637	10		

- Molecule 50 is a protein called Rcl1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SH	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 51 is a protein called Bms1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SI	802	Total	C	N	O	S	0	0
			6412	4108	1142	1133	29		

- Molecule 52 is a protein called Emg1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SJ	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
52	SK	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 53 is a protein called Utp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SL	174	Total	C	N	O	S	0	0
			1395	890	255	240	10		

- Molecule 54 is a protein called Imp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SM	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 55 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SN	247	Total	C	N	O	S	0	0
			2006	1284	356	358	8		

- Molecule 56 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SO	179	Total	C	N	O	S	0	0
			998	606	199	192	1		

- Molecule 57 is a protein called Utp20.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SP	982	Total	C	N	O	0	0
			4910	2946	982	982		

- Molecule 58 is a protein called Fcf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SQ	135	Total	C	N	O	S	0	0
			1137	721	211	201	4		

- Molecule 59 is a protein called rpS23\_uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SR	104	Total	C	N	O	S	0	0
			792	506	145	139	2		

- Molecule 60 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SS	197	Total	C	N	O	S	0	0
			1466	905	282	277	2		

- Molecule 61 is a protein called Nop14.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	ST	599	Total	C	N	O	S	0	0
			4473	2830	809	823	11		

- Molecule 62 is a protein called Noc4.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SU	526	Total	C	N	O	S	0	0
			3781	2422	650	697	12		

- Molecule 63 is a protein called Rrt14.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	SV	63	Total	C	N	O	0	0
			381	234	69	78		

- Molecule 64 is a protein called Unassigned peptides.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	SX	103	Total	C	N	O	0	0
			515	309	103	103		

- Molecule 65 is a protein called Utp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SY	241	Total	C	N	O	S	0	0
			2016	1251	388	370	7		

- Molecule 66 is a protein called Enp1.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	SZ	261	Total	C	N	O	0	0
			1295	773	261	261		

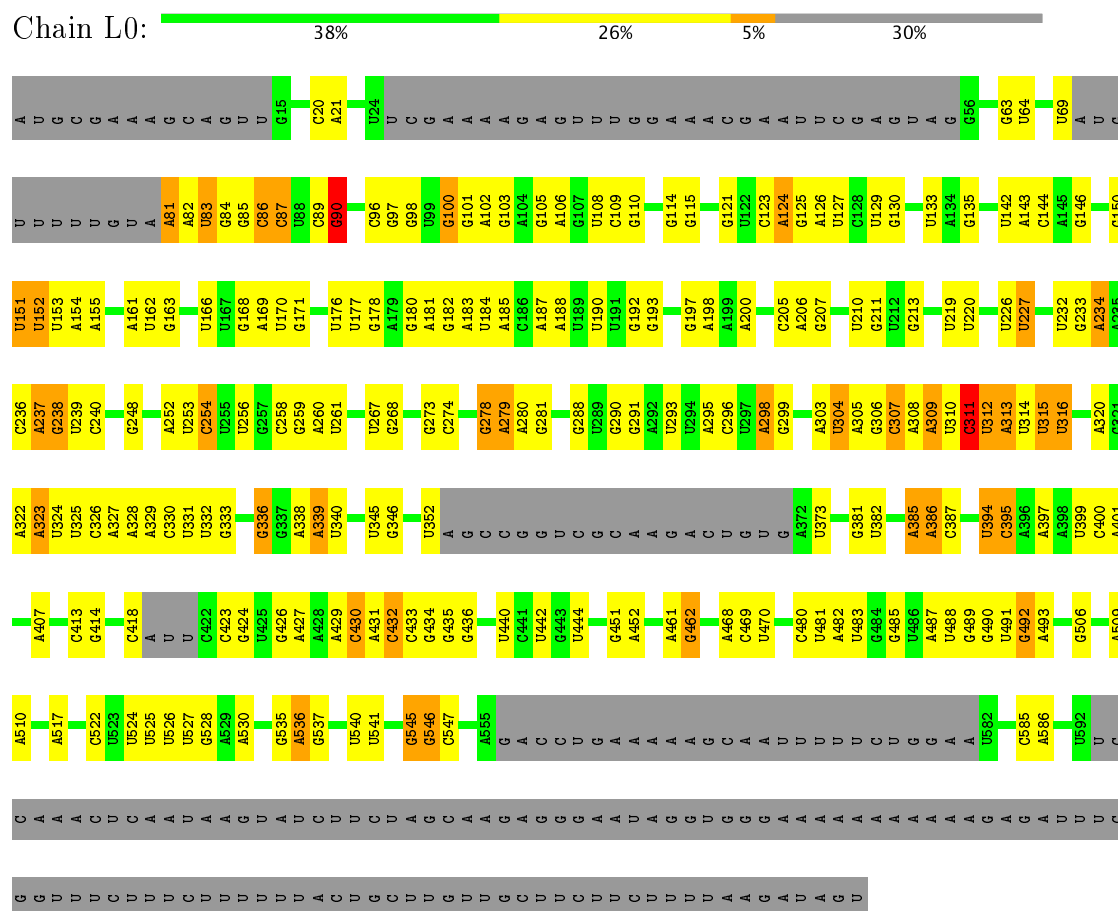
- Molecule 67 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
67	SL	1	Total	Zn	0
			1	1	

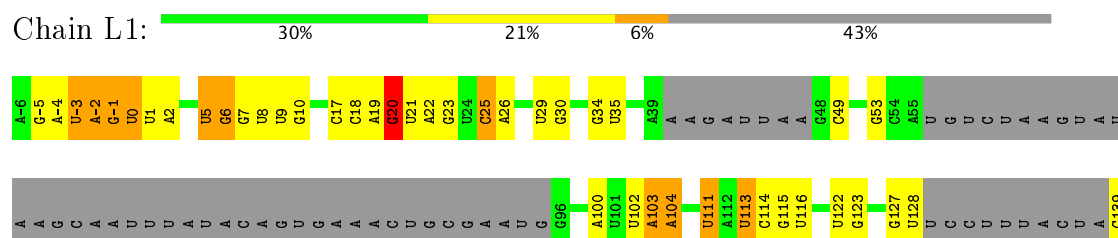
### 3 Residue-property plots [i](#)

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: 5' ETS



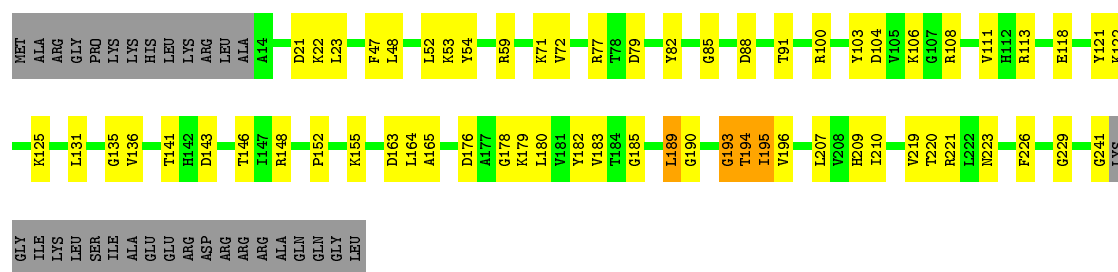
#### • Molecule 2: 18S pre-rRNA





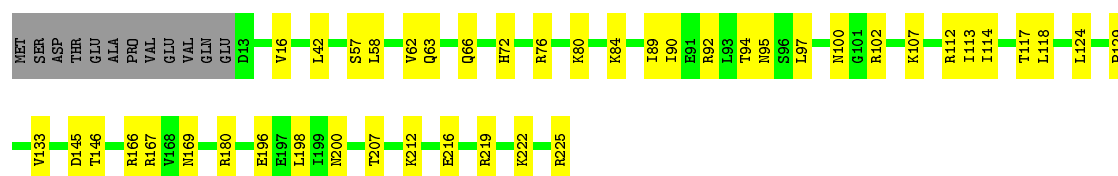




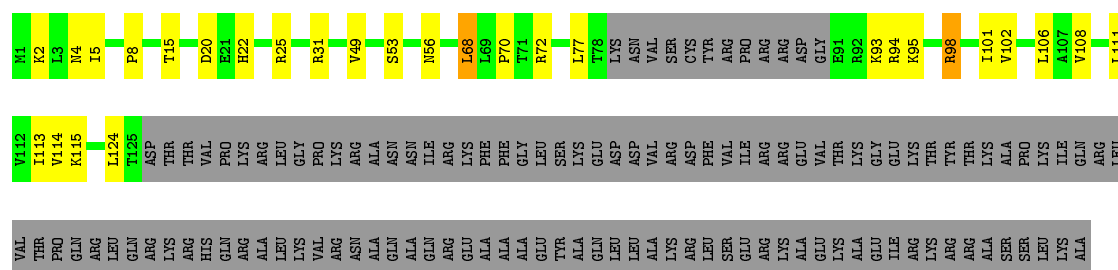
• Molecule 6: rpS5\_uS7

Chain L5: 76% 19% 5%



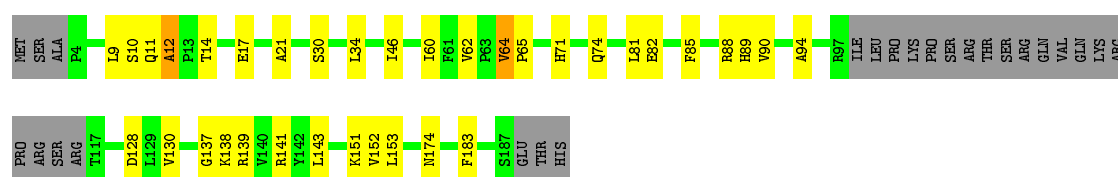
• Molecule 7: rpS6\_eS6

Chain L6: 36% 11% 52%



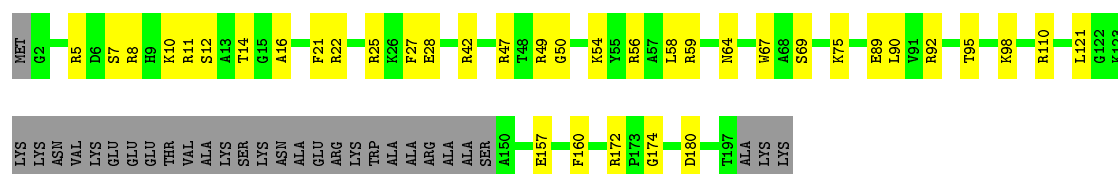
• Molecule 8: rpS7\_eS7

Chain L7: 68% 17% 13%

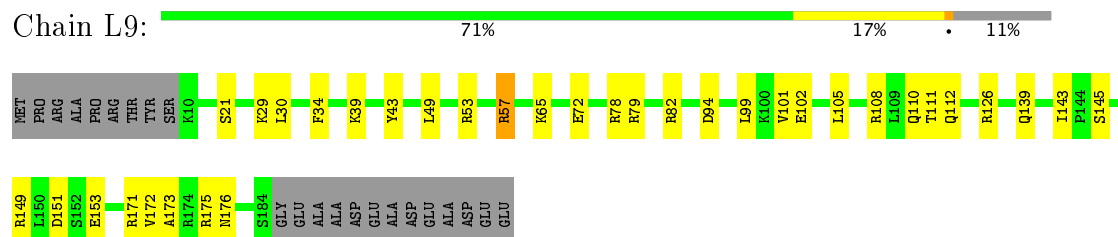


• Molecule 9: rpS8\_eS8

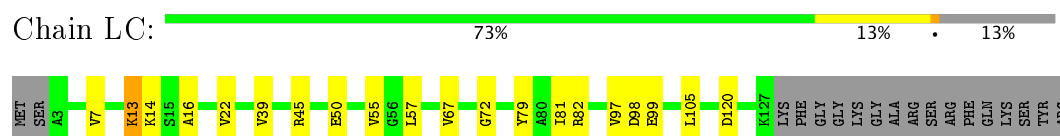
Chain L8: 67% 19% 15%



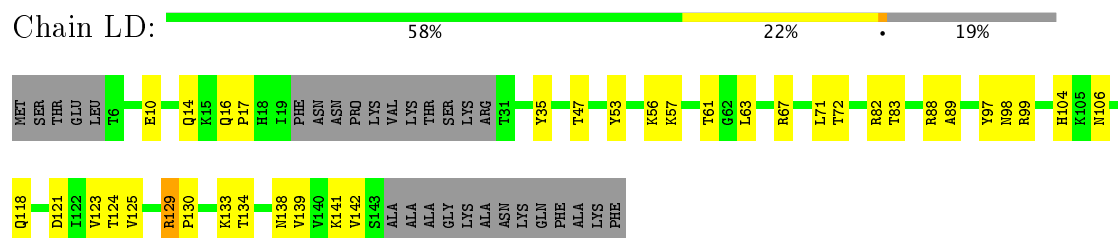
- Molecule 10: rpS9\_uS4



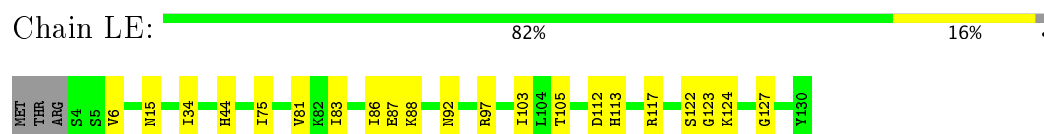
- Molecule 11: rpS16\_uS9



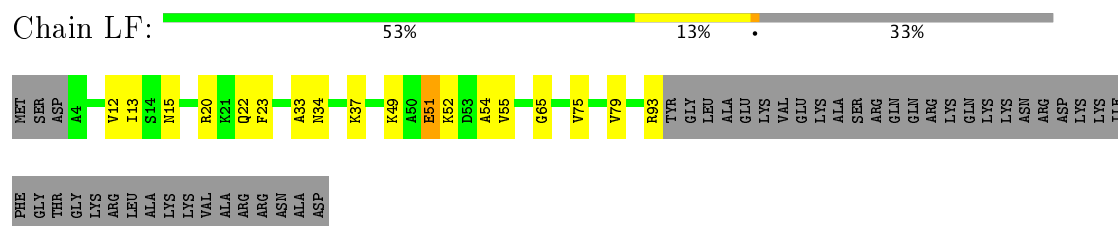
- Molecule 12: rpS11\_uS17



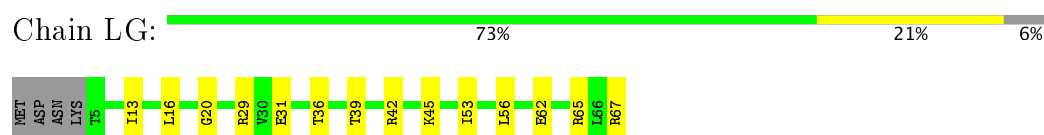
- Molecule 13: rpS22\_uS8



- Molecule 14: rpS24\_eS24

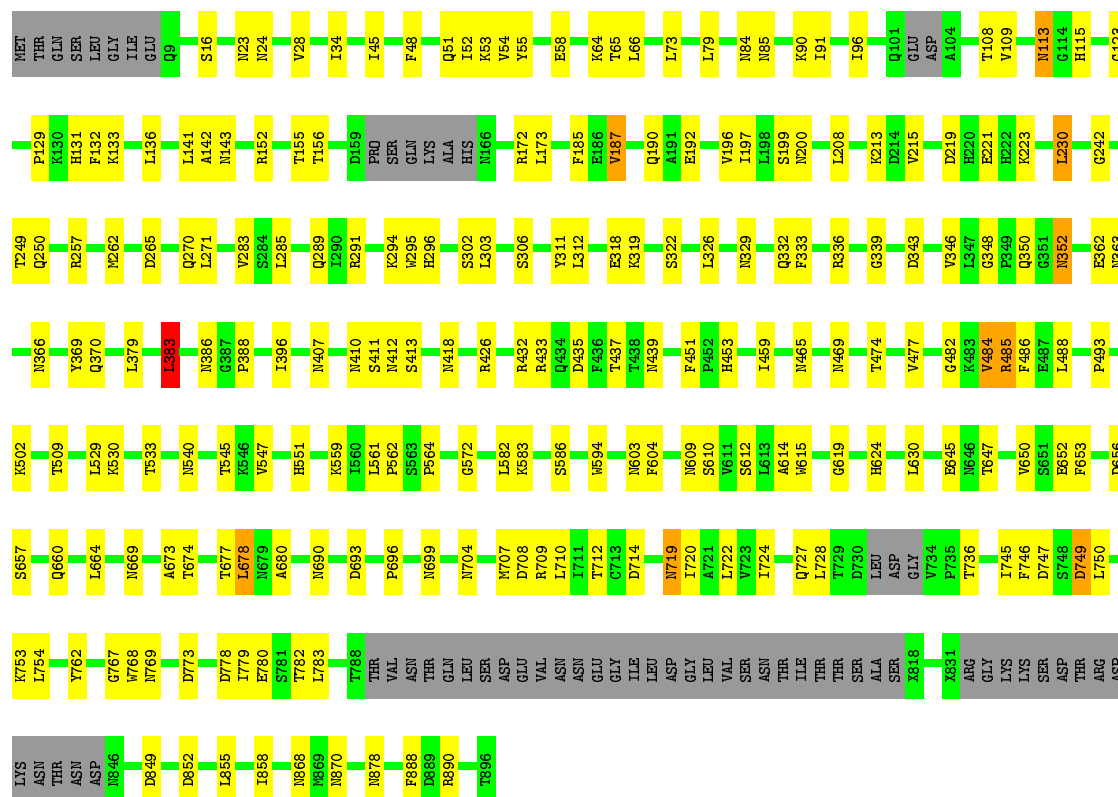
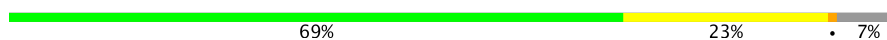


- Molecule 15: rpS28\_eS28



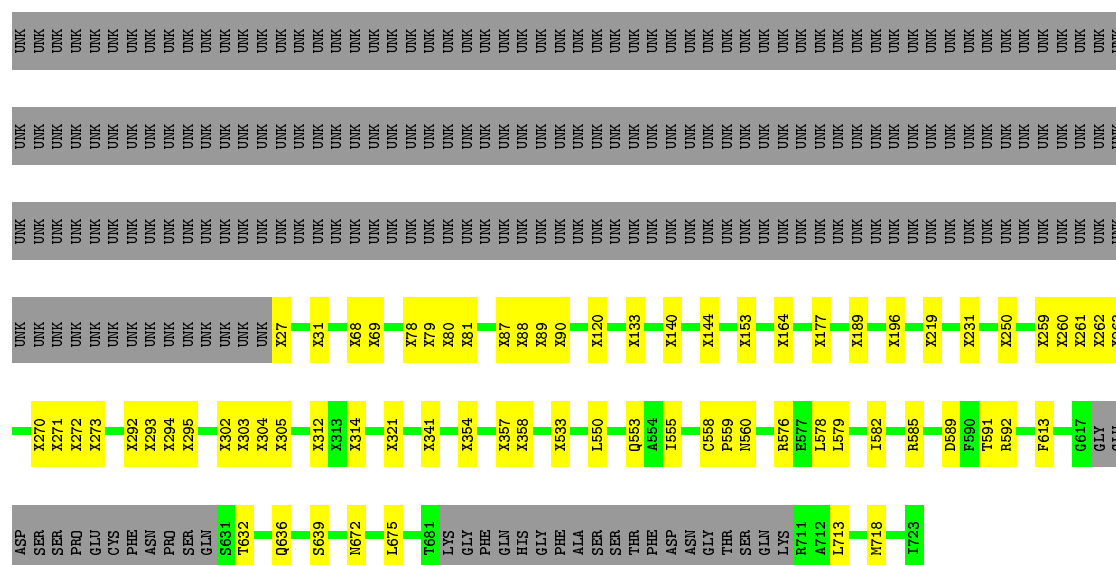
- Molecule 16: Utp17

Chain LH:



- Molecule 17: Utp8

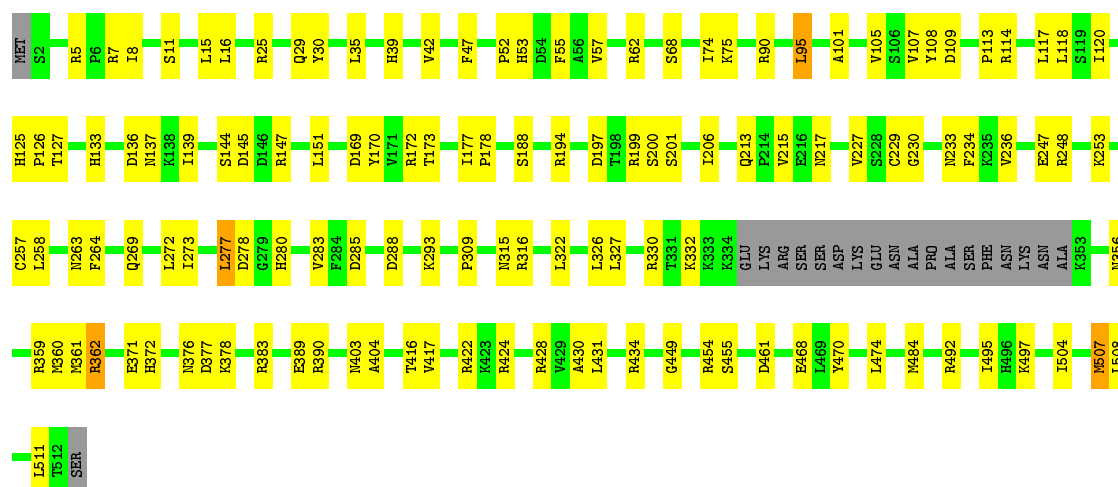
Chain LI:



- Molecule 18: Utp15

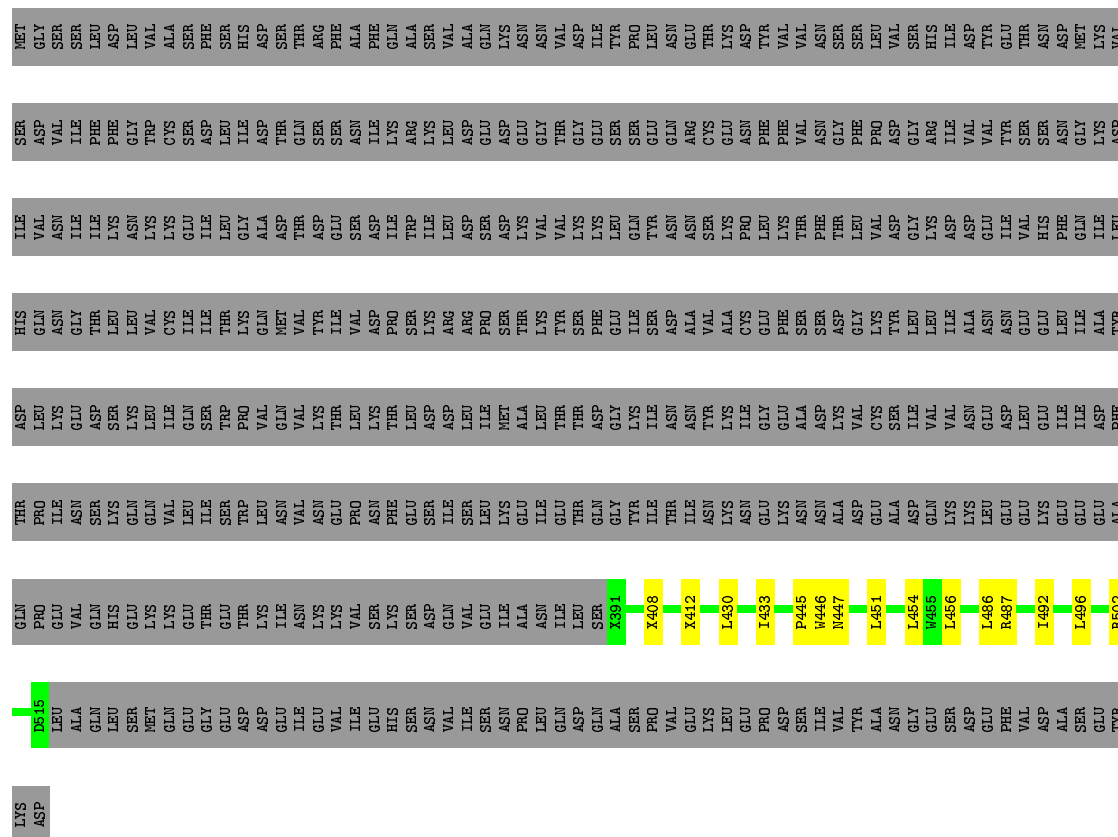
Chain L.J:





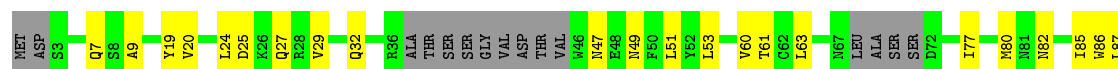
- Molecule 19: Utp9

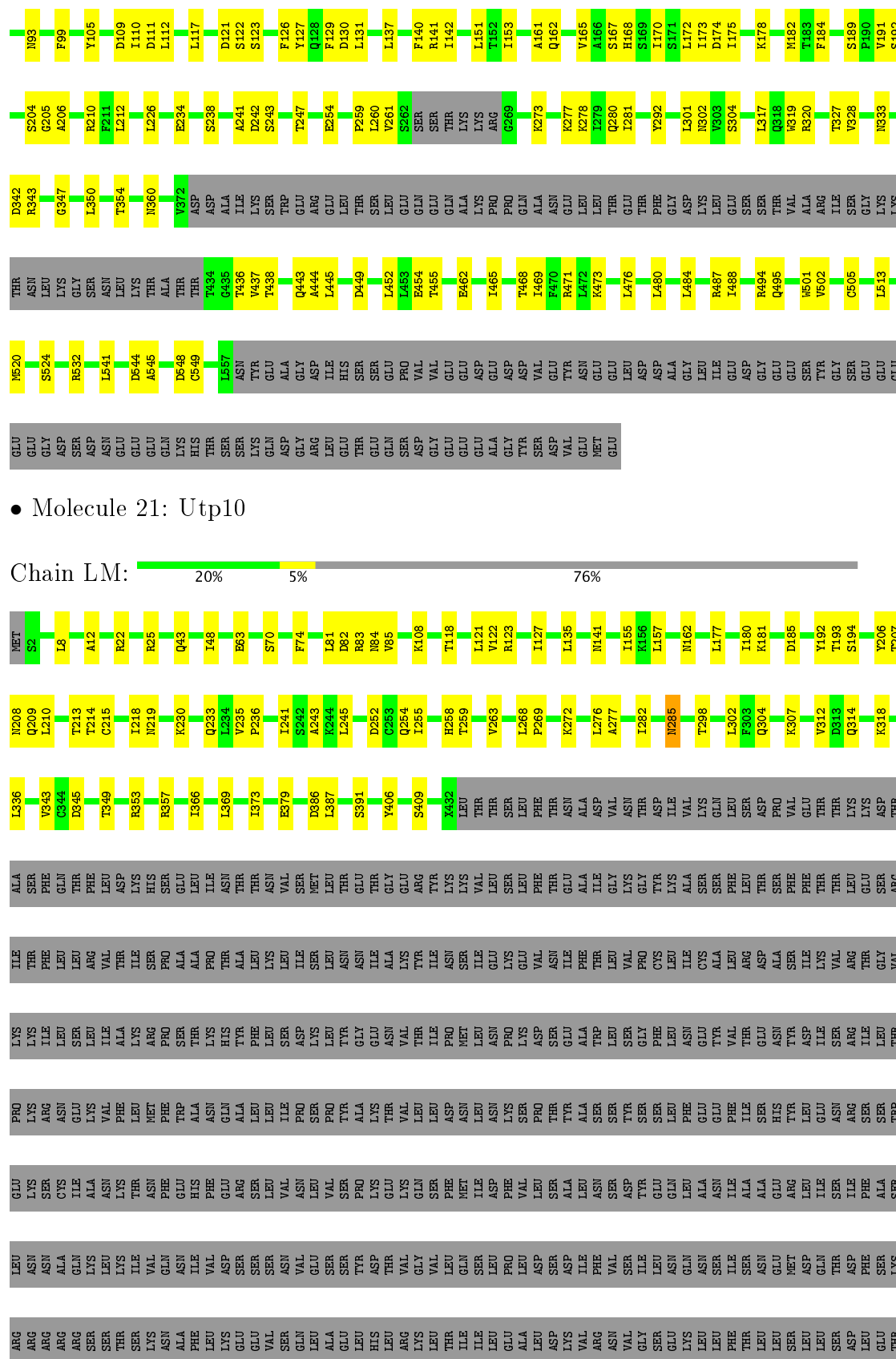
Chain LK:  19% 1% 79%



- Molecule 20: Utp5

Chain LL:  53% 21% 26%

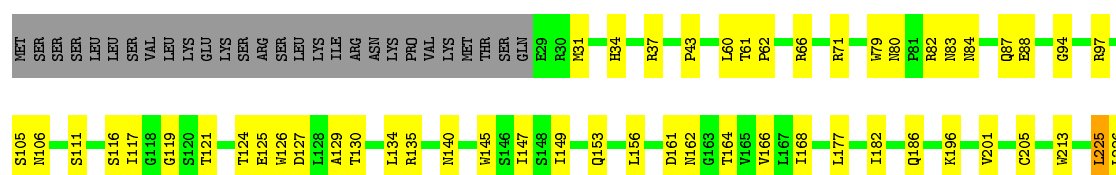




[illegible]

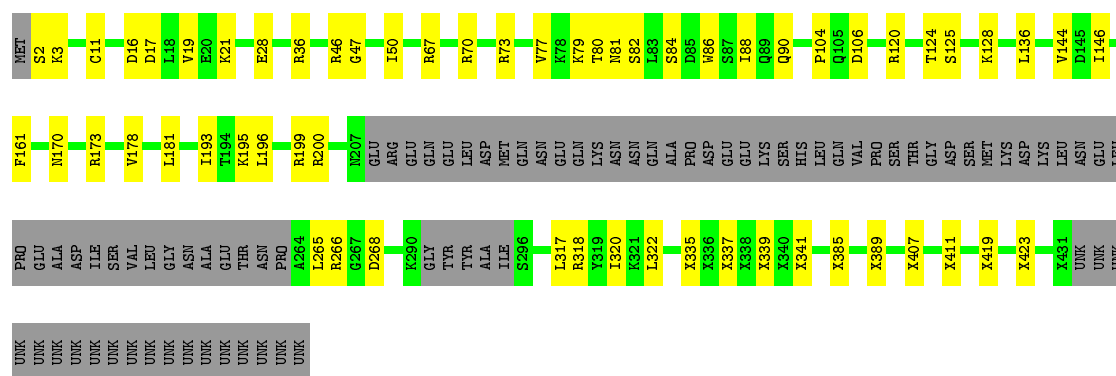
- Molecule 22: Utp4

Chain LN: 64% 23% 13%



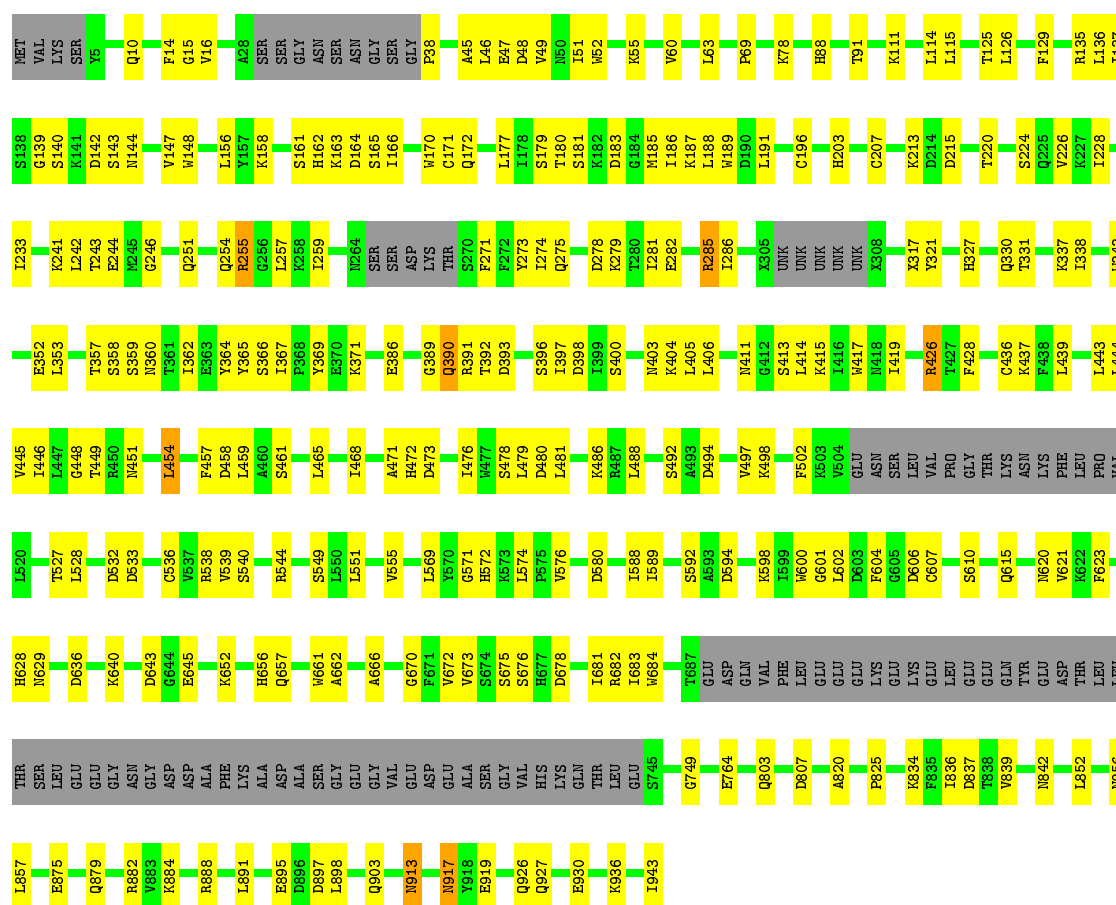






### • Molecule 25: Utp12

Chain LQ: 63% 26% 10%

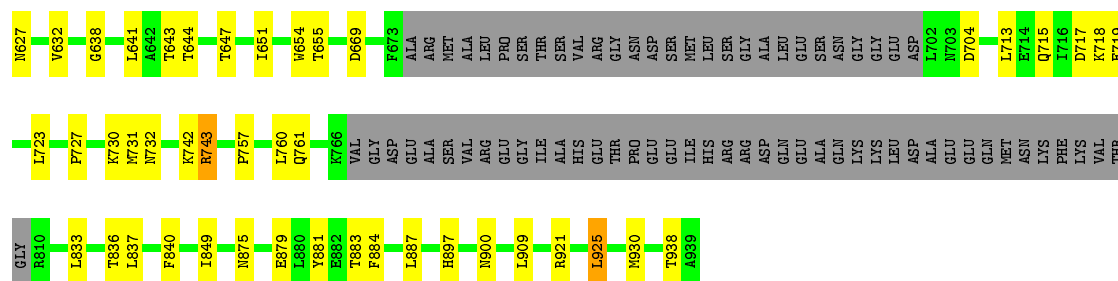


### • Molecule 26: Utp13

Chain LR: 79% 11% 11%

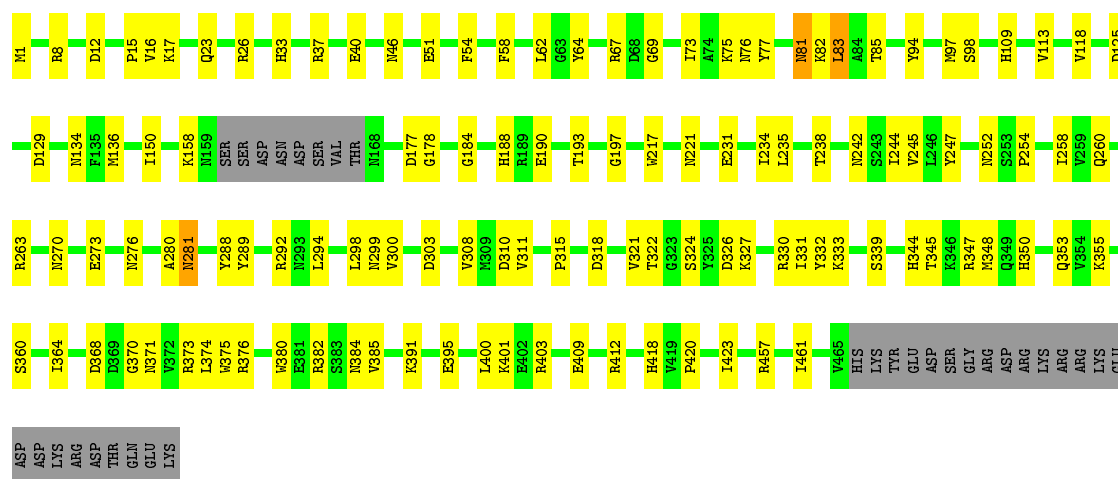






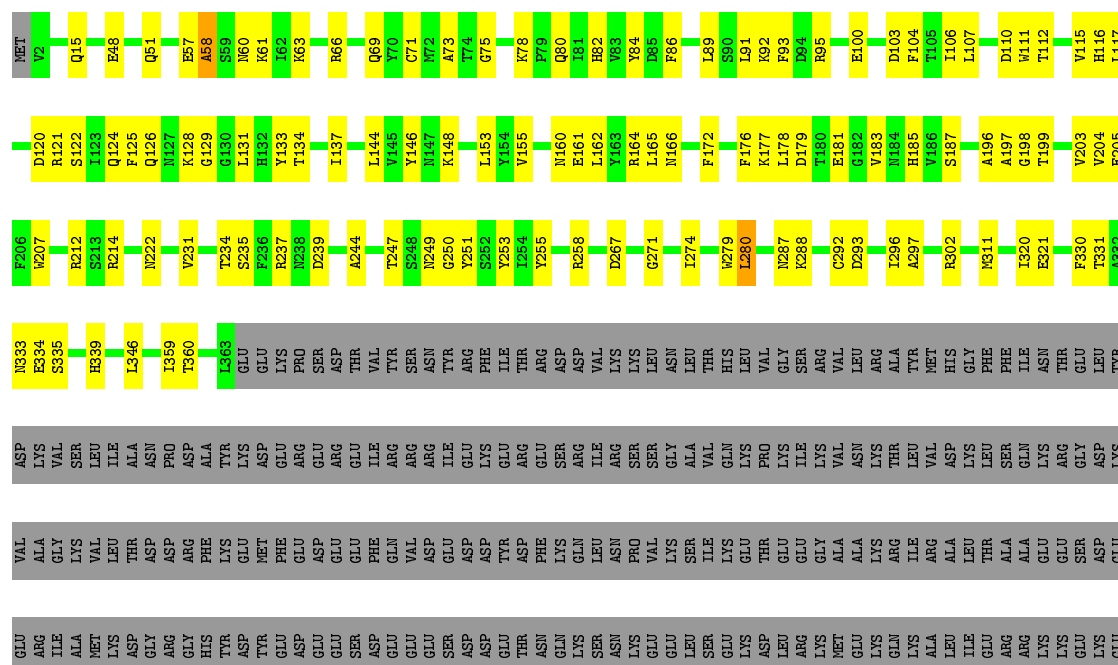
• Molecule 29: Sof1

Chain LU: 69% 24% 7%



• Molecule 30: Enp2

Chain LV: 35% 16% 49%

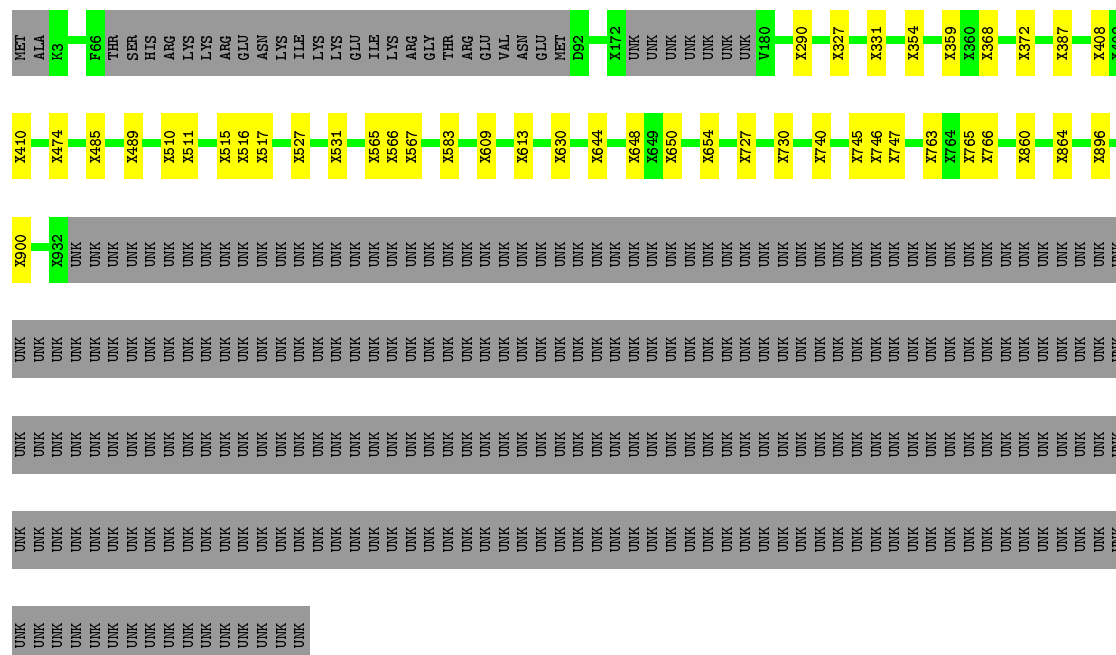




UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK

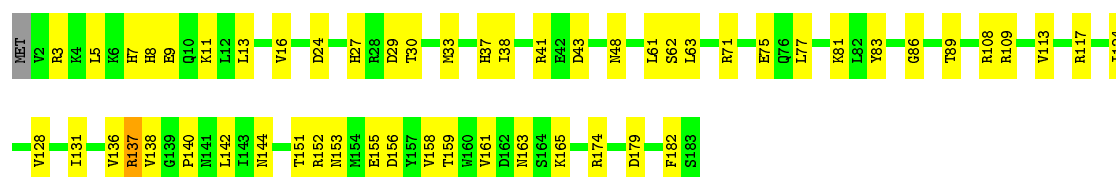
- Molecule 32: Kre33

Chain LY:  69% 0 27%



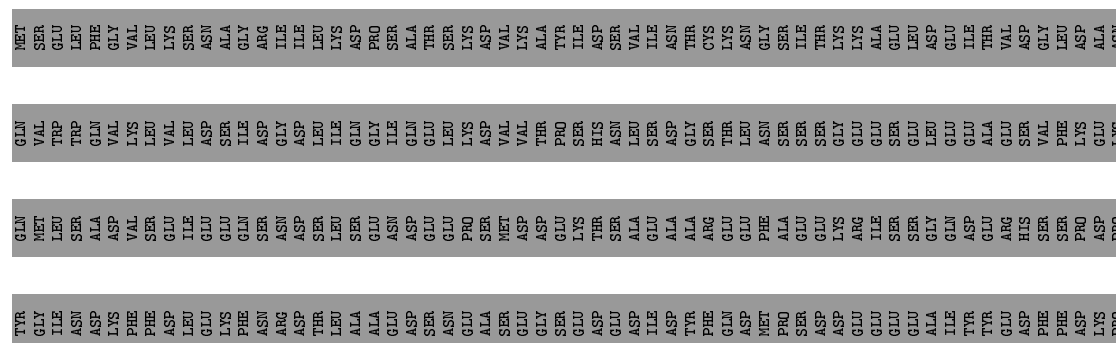
- Molecule 33: Imp3

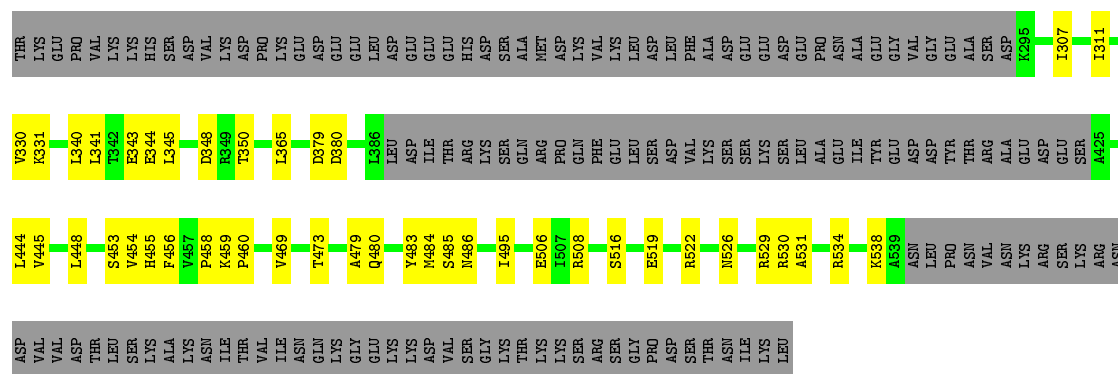
Chain LZ:  70% 29%



- Molecule 34: Mpp10

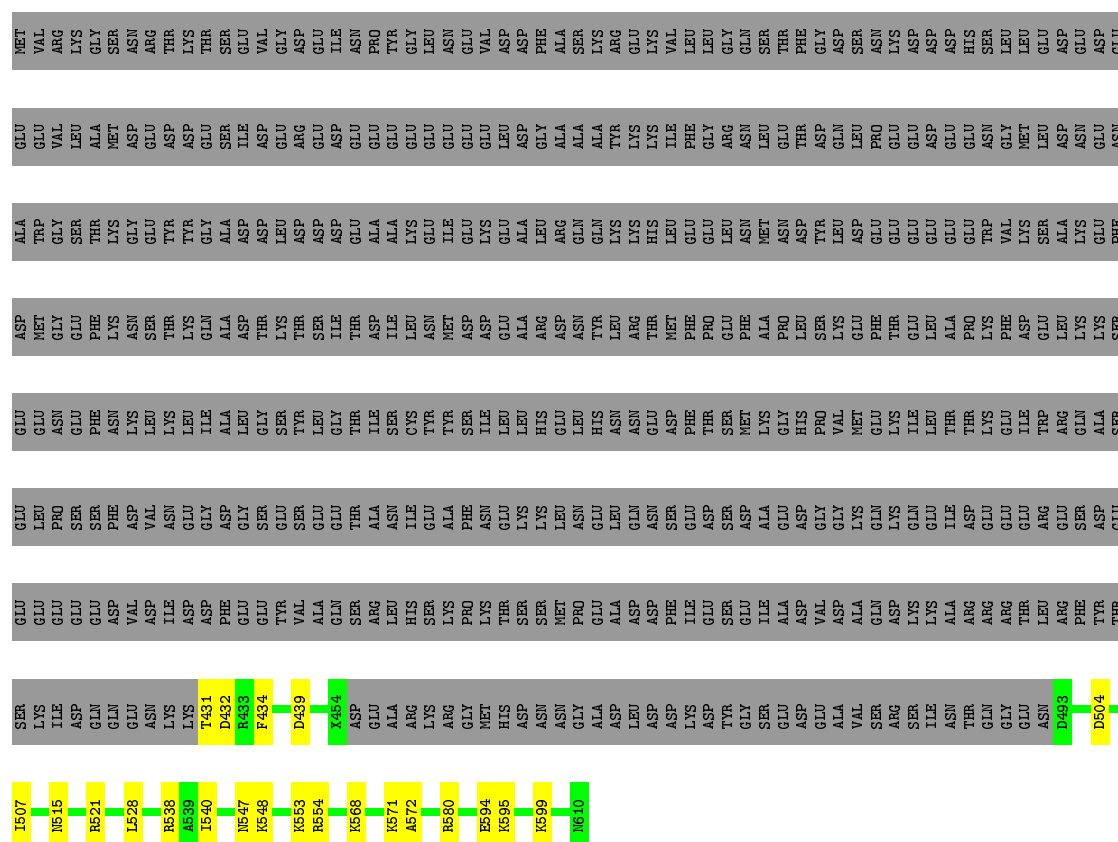
Chain NA:  27% 7% 65%





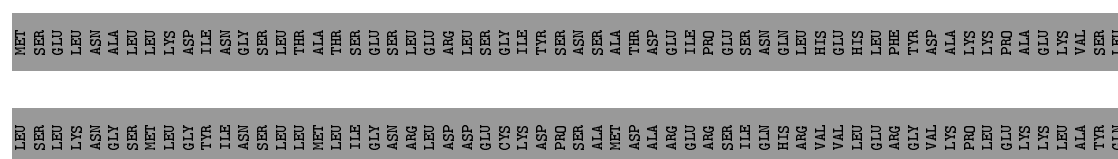
- Molecule 35: Sas10

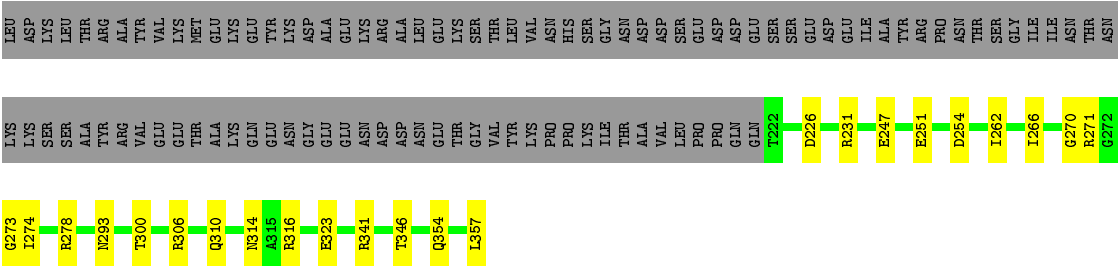
Chain NB:  20% 3% 77%



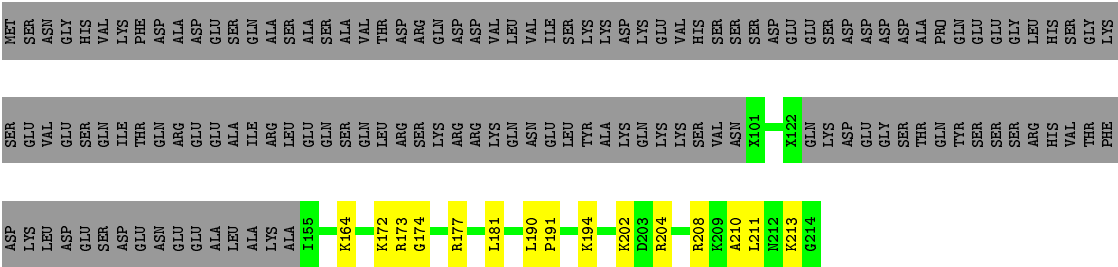
- Molecule 36: Lcp5

Chain NC:  32% 6% 62%

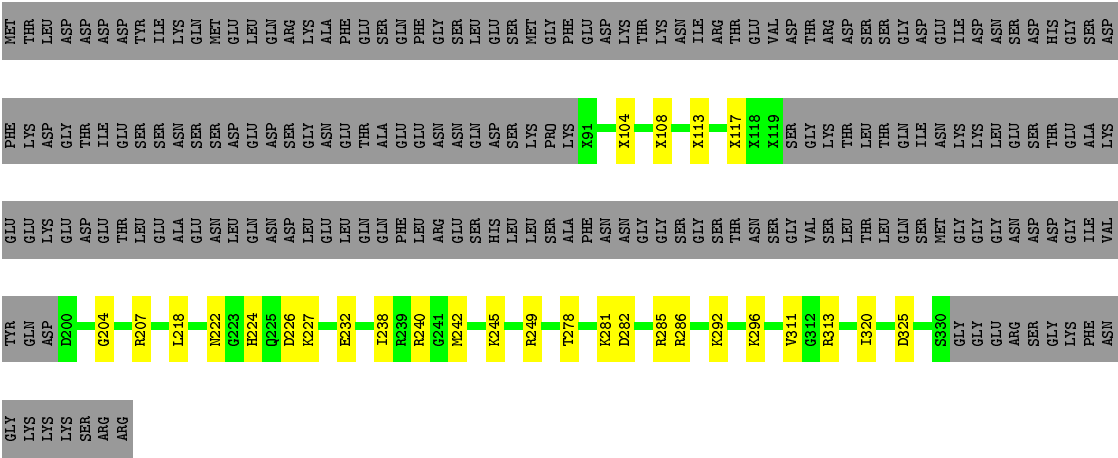
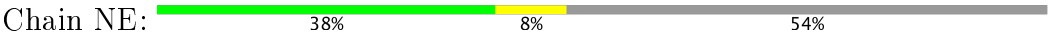




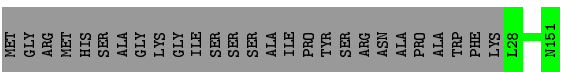
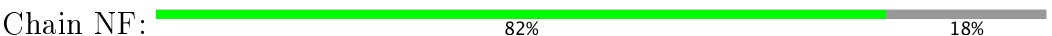
• Molecule 37: Bud21



• Molecule 38: Faf1



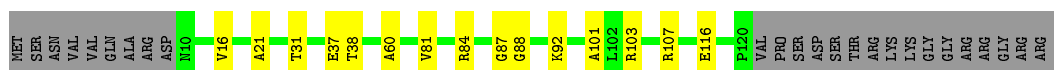
• Molecule 39: rpS13\_uS15



• Molecule 40: rpS14\_uS11

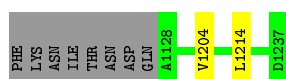
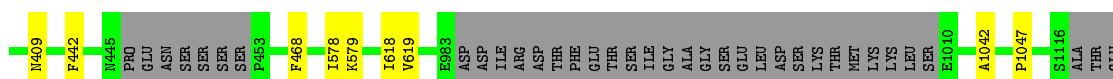
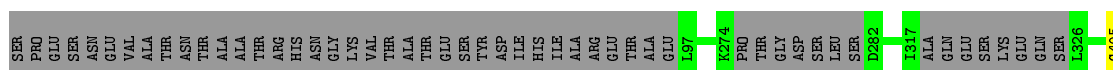
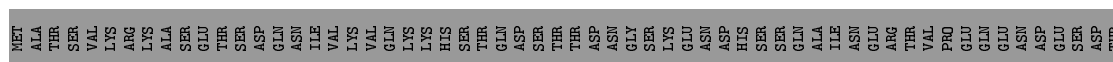






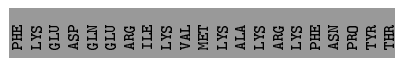
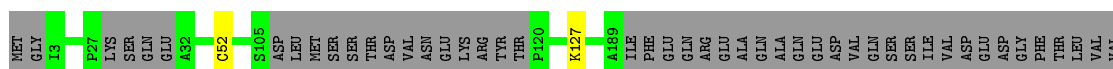
- Molecule 41: Utp22

Chain NH:  86% . 13%



- Molecule 42: Rrp7

Chain NI:  56% 43%

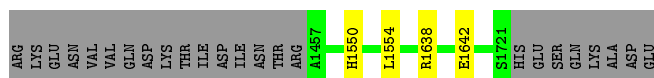


- Molecule 43: Rrp5

Chain NJ:  15% 85%

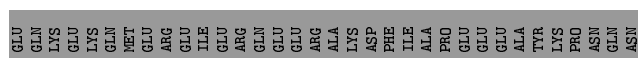
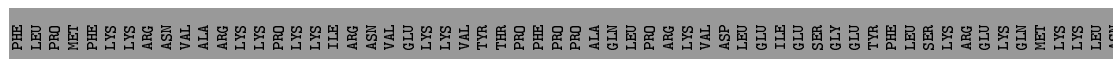
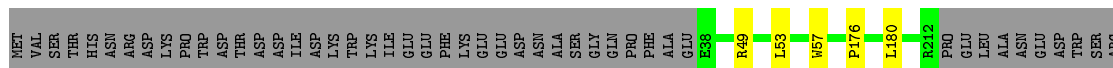




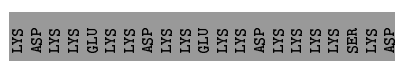
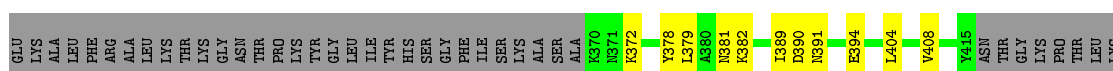
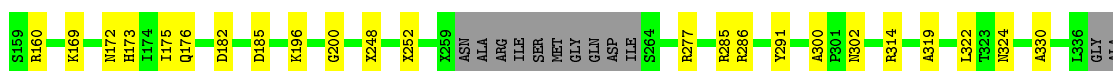
- Molecule 44: Krr1

Chain NK:



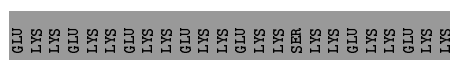
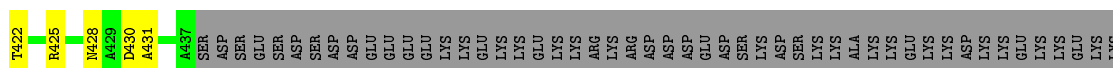
- Molecule 45: Nop56

Chain SA:



- Molecule 46: Nop58

Chain SB:



- Molecule 47: Nop1

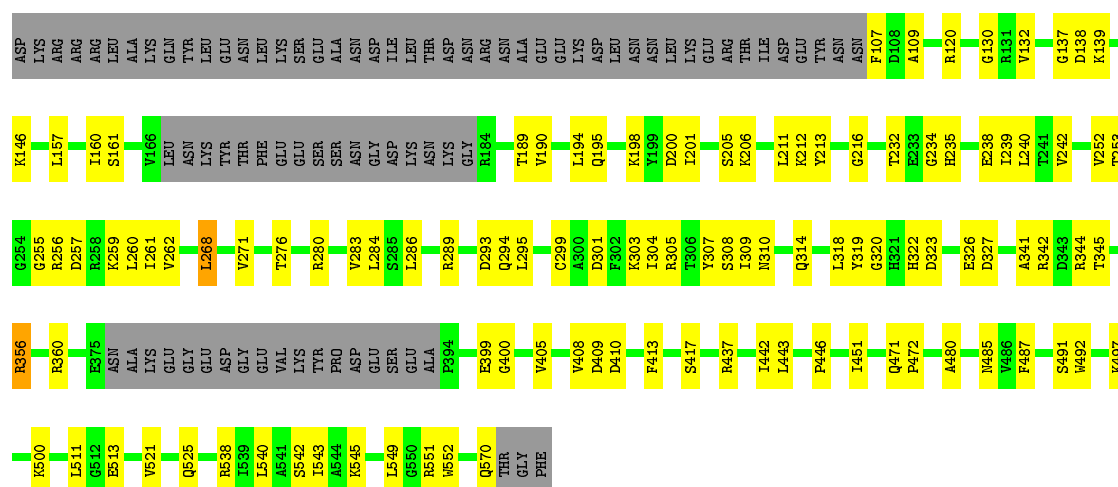
26%

## 30%


## 14%

## 20%

## 25%



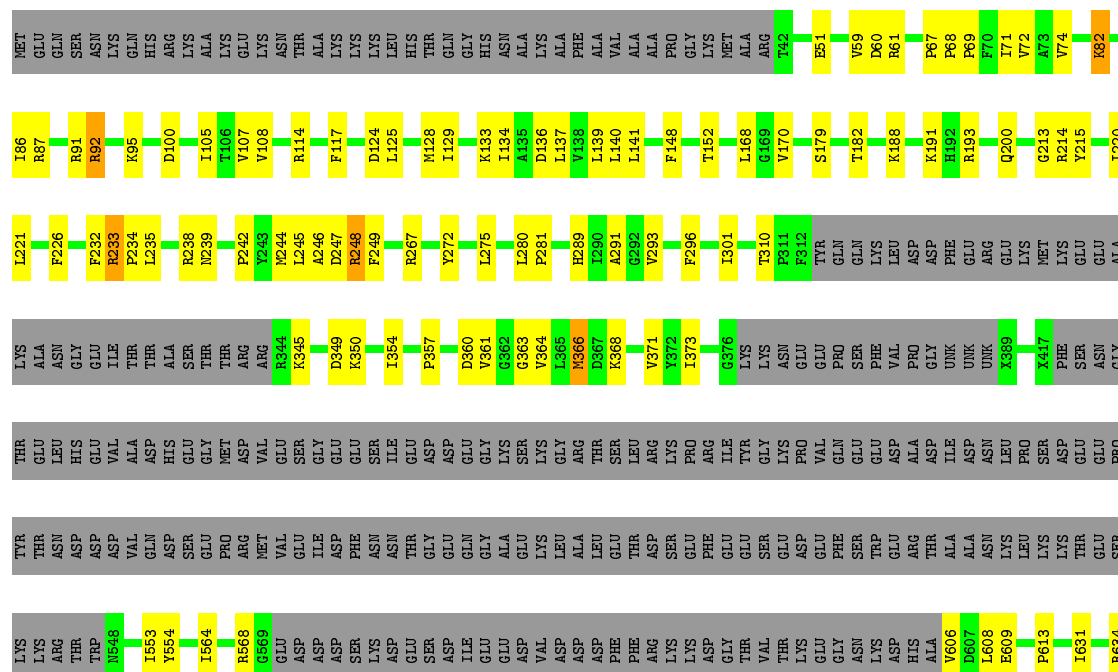
- Molecule 50: Rcl1

Chain SH:  77% 21%



- Molecule 51: Bms1

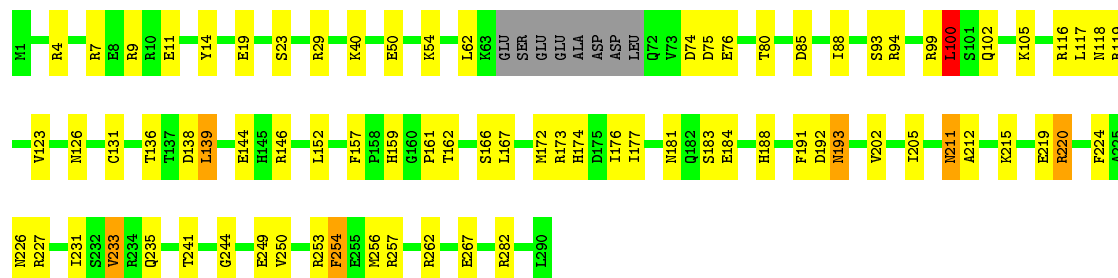
Chain SI: 50% 17% 32%





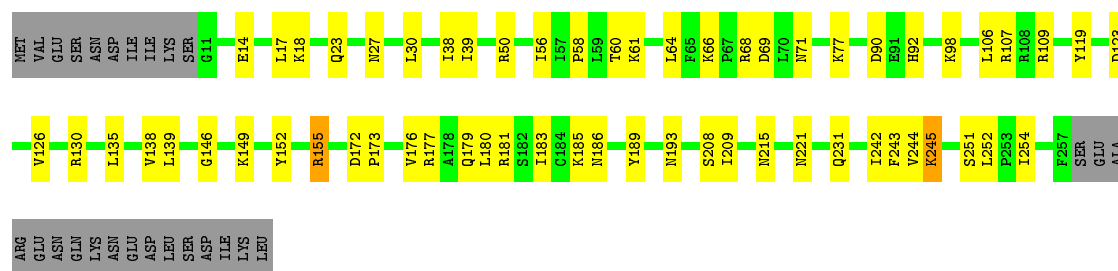
- Molecule 54: Imp4

Chain SM: 



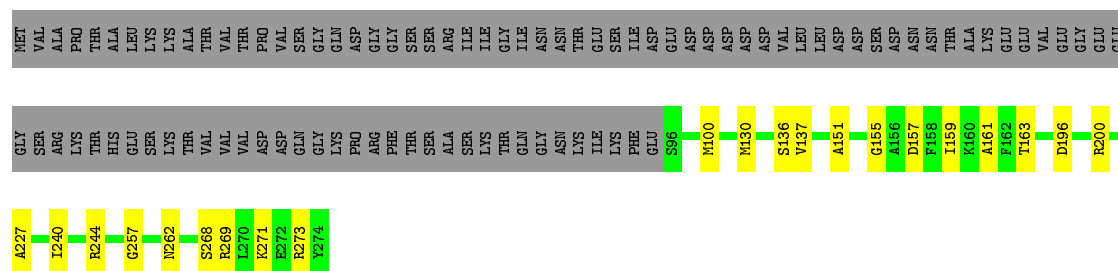
- Molecule 55: Utp30

Chain SN:  68% 21% 10%



- Molecule 56: Pno1

Chain SO: 



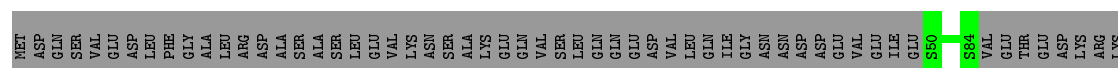
- Molecule 57: Utp20

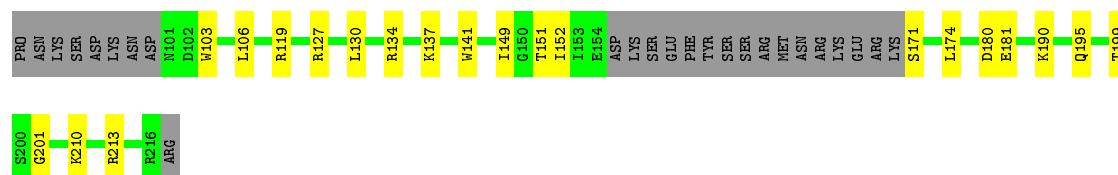
Chain SP:  98%



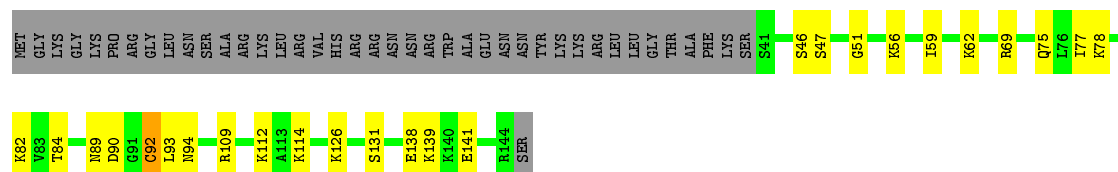
- Molecule 58: Fcf2

Chain SQ:  53% 10% 38%

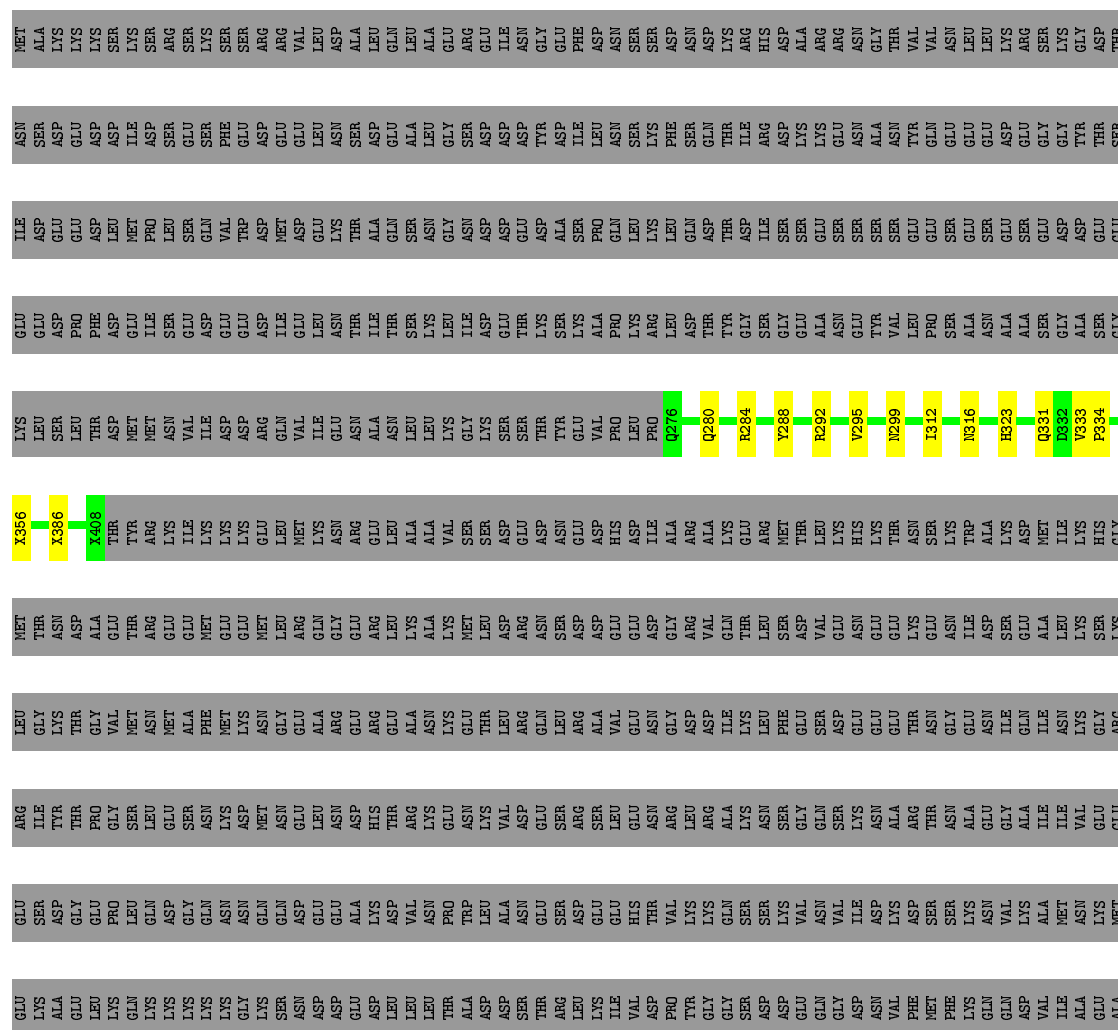




- Molecule 59: rpS23 uS12



- Molecule 60: Utp14

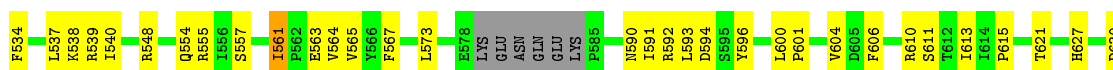
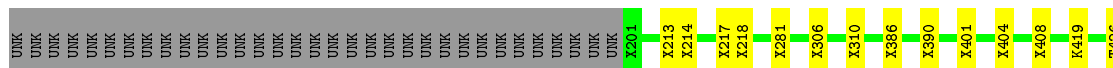
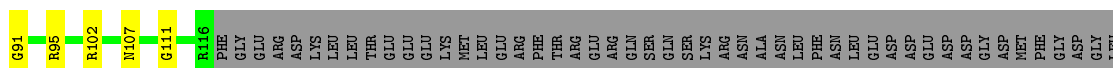
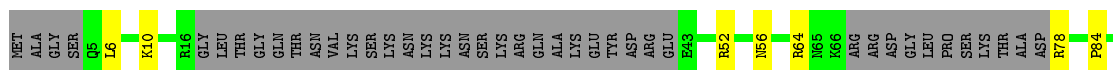







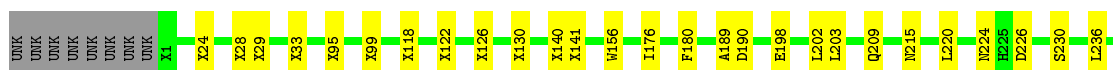
- Molecule 61: Nop14

Chain ST: 



- Molecule 62: Noc4

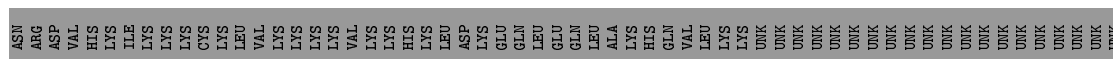
Chain SU:  78% 17% • 5%



- Molecule 63: Rrt14

Chain SV:  27% 0 69%

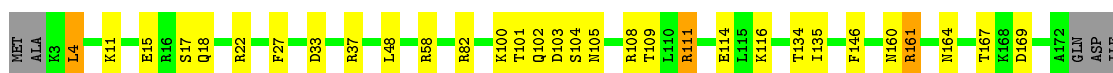
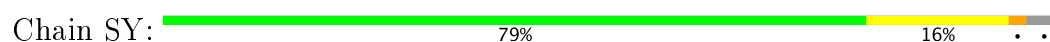




- Molecule 64: Unassigned peptides



- Molecule 65: Utp11



- Molecule 66: Enp1



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	284213	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 ( $e^-/\text{\AA}^2$ )	1.56	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section:  
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	L0	0.72	0/11634	1.03	32/18120 (0.2%)
10	L9	0.43	0/1437	0.63	0/1924
11	LC	0.60	0/990	0.72	1/1335 (0.1%)
12	LD	0.31	0/1050	0.57	0/1415
13	LE	0.31	0/1020	0.54	0/1371
14	LF	0.36	0/727	0.70	0/977
15	LG	0.44	0/499	0.62	0/670
16	LH	0.38	0/6694	0.63	5/9070 (0.1%)
17	LI	0.28	0/1105	0.53	0/1491
18	LJ	0.44	0/3993	0.63	2/5413 (0.0%)
19	LK	0.27	0/735	0.51	0/987
2	L1	0.54	0/24442	1.01	70/38042 (0.2%)
20	LL	0.40	0/3840	0.62	0/5208
21	LM	0.44	0/3470	0.61	2/4694 (0.0%)
22	LN	0.39	0/5369	0.63	4/7272 (0.1%)
23	LO	0.54	0/6780	0.68	3/9175 (0.0%)
24	LP	0.39	0/2281	0.53	0/3059
25	LQ	0.34	0/6574	0.61	2/8881 (0.0%)
26	LR	0.39	0/1336	0.55	1/1800 (0.1%)
27	LS	0.50	0/3875	0.64	1/5254 (0.0%)
28	LT	0.47	0/6834	0.60	0/9238
29	LU	0.48	0/3802	0.63	2/5118 (0.0%)
3	L2	0.74	0/4001	1.03	11/6215 (0.2%)
30	LV	0.33	0/2902	0.64	2/3941 (0.1%)
31	LW	0.55	0/3505	0.69	4/4748 (0.1%)
32	LX	0.32	0/1481	0.57	0/1987
32	LY	0.22	0/768	0.40	0/1065
33	LZ	0.57	0/1559	0.71	0/2097
34	NA	0.39	0/1685	0.61	0/2261
35	NB	0.40	0/1042	0.53	0/1377
36	NC	0.33	0/1139	0.61	1/1512 (0.1%)
37	ND	0.31	0/499	0.58	0/659

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
38	NE	0.27	0/1063	0.56	0/1402
39	NF	0.23	0/614	0.42	0/855
4	L3	0.30	0/871	0.53	0/1171
40	NG	0.26	0/542	0.53	0/750
41	NH	0.23	0/5356	0.42	0/7460
42	NI	0.23	0/838	0.41	0/1166
43	NJ	0.23	0/1313	0.37	0/1830
44	NK	0.24	0/867	0.42	0/1208
45	SA	0.39	0/2769	0.54	1/3728 (0.0%)
46	SB	0.40	0/2344	0.59	0/3160
47	SC	0.54	0/1917	0.66	1/2588 (0.0%)
47	SD	0.35	0/1815	0.57	0/2448
48	SE	0.44	0/928	0.60	0/1262
48	SF	0.39	0/928	0.61	0/1262
49	SG	0.36	0/3498	0.58	0/4712
5	L4	0.31	0/1849	0.65	1/2497 (0.0%)
50	SH	0.36	0/2832	0.54	0/3825
51	SI	0.45	0/6403	0.63	1/8616 (0.0%)
52	SJ	0.30	0/1727	0.51	0/2329
52	SK	0.35	0/1828	0.55	0/2470
53	SL	0.49	0/1418	0.64	0/1906
54	SM	0.51	0/2337	0.72	5/3148 (0.2%)
55	SN	0.40	0/2041	0.64	0/2745
56	SO	0.28	0/1003	0.47	0/1381
58	SQ	0.39	0/1156	0.56	0/1536
59	SR	0.44	0/804	0.67	1/1074 (0.1%)
6	L5	0.44	0/1690	0.61	0/2285
60	SS	0.34	0/1230	0.54	0/1660
61	ST	0.32	0/3826	0.52	1/5125 (0.0%)
62	SU	0.36	0/3064	0.57	0/4163
63	SV	0.36	0/201	0.56	0/273
65	SY	0.44	0/2042	0.62	0/2704
66	SZ	0.24	0/1294	0.39	0/1804
7	L6	0.29	0/899	0.58	0/1201
8	L7	0.30	0/1342	0.62	0/1807
9	L8	0.28	0/1372	0.53	0/1834
All	All	0.46	0/183089	0.72	154/255761 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	LC	0	1
12	LD	0	1
14	LF	0	1
16	LH	0	2
22	LN	0	2
23	LO	0	2
25	LQ	0	2
28	LT	0	1
29	LU	0	1
30	LV	0	3
31	LW	0	2
34	NA	0	1
36	NC	0	2
4	L3	0	1
46	SB	0	1
48	SE	0	1
49	SG	0	1
5	L4	0	2
54	SM	0	3
56	SO	0	1
58	SQ	0	2
8	L7	0	4
All	All	0	37

There are no bond length outliers.

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L1	965	U	N1-C2-O2	11.23	130.66	122.80
1	L0	430	C	N1-C2-O2	11.16	125.59	118.90
2	L1	374	U	N1-C2-O2	11.06	130.54	122.80
2	L1	965	U	C2-N1-C1'	11.06	130.97	117.70
2	L1	374	U	C2-N1-C1'	10.92	130.80	117.70

There are no chirality outliers.

5 of 37 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	L3	13	HIS	Peptide
5	L4	193	GLY	Peptide
5	L4	194	THR	Peptide
8	L7	10	SER	Peptide

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
8	L7	12	ALA	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	L0	10405	0	5231	112	0
2	L1	21866	0	11031	252	0
3	L2	3585	0	1819	43	0
4	L3	901	0	904	15	0
5	L4	1810	0	1865	52	0
6	L5	1669	0	1724	35	0
7	L6	888	0	928	20	0
8	L7	1321	0	1390	18	0
9	L8	1349	0	1372	38	0
10	L9	1415	0	1497	31	0
11	LC	973	0	1029	16	0
12	LD	1027	0	1084	24	0
13	LE	1003	0	1040	12	0
14	LF	715	0	744	11	0
15	LG	497	0	535	12	0
16	LH	6633	0	6509	125	0
17	LI	2857	0	1520	46	0
18	LJ	3911	0	3906	93	0
19	LK	898	0	809	11	0
20	LL	3772	0	3806	90	0
21	LM	3443	0	3558	56	0
22	LN	5344	0	5303	116	0
23	LO	6635	0	6525	136	0
24	LP	2709	0	2363	45	0
25	LQ	6640	0	6501	172	0
26	LR	4144	0	1952	53	0
27	LS	3791	0	3772	105	0
28	LT	6697	0	6676	136	0
29	LU	3725	0	3679	94	0
30	LV	2840	0	2685	78	0
31	LW	3428	0	3407	81	0
32	LX	4583	0	2198	62	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	LY	3823	0	983	25	0
33	LZ	1530	0	1572	40	0
34	NA	1667	0	1701	43	0
35	NB	1098	0	1100	23	0
36	NC	1125	0	1101	18	0
37	ND	600	0	586	18	0
38	NE	1192	0	1184	22	0
39	NF	615	0	280	0	0
40	NG	543	0	277	9	0
41	NH	5362	0	2295	6	0
42	NI	841	0	365	1	0
43	NJ	1314	0	610	2	0
44	NK	868	0	379	3	0
45	SA	2854	0	2787	50	0
46	SB	2937	0	2512	43	0
47	SC	1881	0	1928	42	0
47	SD	1782	0	1826	43	0
48	SE	916	0	964	15	0
48	SF	916	0	964	19	0
49	SG	3428	0	3446	76	0
50	SH	2781	0	2878	57	0
51	SI	6412	0	6497	160	0
52	SJ	1701	0	1767	25	0
52	SK	1799	0	1872	40	0
53	SL	1395	0	1473	35	0
54	SM	2296	0	2325	61	0
55	SN	2006	0	2118	45	0
56	SO	998	0	631	11	0
57	SP	4910	0	1107	10	0
58	SQ	1137	0	1188	16	0
59	SR	792	0	847	26	0
60	SS	1466	0	1253	24	0
61	ST	4473	0	4053	73	0
62	SU	3781	0	3106	62	0
63	SV	381	0	224	7	0
64	SX	515	0	118	4	0
65	SY	2016	0	2093	38	0
66	SZ	1295	0	571	4	0
67	SL	1	0	0	0	0
All	All	196921	0	158343	2804	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 2804 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)
2:L1:547:U:OP2	35:NB:554:ARG:NH1	1.81	1.12
1:L0:90:G:OP1	18:LJ:378:LYS:NZ	1.84	1.10
3:L2:253:G:OP2	48:SF:95:ARG:NH1	1.93	1.00
51:SI:1059:ARG:NH1	65:SY:33:ASP:OD2	1.95	0.99
29:LU:292:ARG:HH12	60:SS:299:ASN:HB2	1.28	0.98

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	
4	L3	100/146 (68%)	93 (93%)	6 (6%)	1 (1%)	18	61
5	L4	226/261 (87%)	206 (91%)	19 (8%)	1 (0%)	38	77
6	L5	211/225 (94%)	198 (94%)	13 (6%)	0	100	100
7	L6	109/236 (46%)	100 (92%)	8 (7%)	1 (1%)	20	62
8	L7	161/190 (85%)	149 (92%)	10 (6%)	2 (1%)	15	58
9	L8	166/200 (83%)	155 (93%)	11 (7%)	0	100	100
10	L9	173/197 (88%)	165 (95%)	8 (5%)	0	100	100
11	LC	123/143 (86%)	111 (90%)	12 (10%)	0	100	100
12	LD	123/156 (79%)	109 (89%)	13 (11%)	1 (1%)	22	65
13	LE	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
14	LF	88/135 (65%)	73 (83%)	12 (14%)	3 (3%)	4	38
15	LG	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
16	LH	810/896 (90%)	760 (94%)	50 (6%)	0	100	100
17	LI	128/713 (18%)	121 (94%)	7 (6%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LJ	489/513 (95%)	459 (94%)	30 (6%)	0	100	100
19	LK	86/575 (15%)	83 (96%)	3 (4%)	0	100	100
20	LL	465/643 (72%)	437 (94%)	28 (6%)	0	100	100
21	LM	424/1769 (24%)	407 (96%)	17 (4%)	0	100	100
22	LN	654/776 (84%)	600 (92%)	54 (8%)	0	100	100
23	LO	830/923 (90%)	762 (92%)	68 (8%)	0	100	100
24	LP	259/440 (59%)	253 (98%)	6 (2%)	0	100	100
25	LQ	798/943 (85%)	747 (94%)	51 (6%)	0	100	100
26	LR	156/817 (19%)	152 (97%)	4 (3%)	0	100	100
27	LS	473/594 (80%)	442 (93%)	31 (7%)	0	100	100
28	LT	844/939 (90%)	800 (95%)	44 (5%)	0	100	100
29	LU	453/489 (93%)	431 (95%)	22 (5%)	0	100	100
30	LV	360/707 (51%)	319 (89%)	40 (11%)	1 (0%)	44	81
31	LW	436/554 (79%)	405 (93%)	31 (7%)	0	100	100
32	LX	179/1056 (17%)	170 (95%)	9 (5%)	0	100	100
32	LY	152/1056 (14%)	139 (91%)	13 (9%)	0	100	100
33	LZ	180/183 (98%)	168 (93%)	11 (6%)	1 (1%)	28	70
34	NA	203/593 (34%)	188 (93%)	13 (6%)	2 (1%)	18	61
35	NB	126/610 (21%)	119 (94%)	7 (6%)	0	100	100
36	NC	134/357 (38%)	118 (88%)	16 (12%)	0	100	100
37	ND	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
38	NE	129/346 (37%)	124 (96%)	5 (4%)	0	100	100
39	NF	122/151 (81%)	116 (95%)	6 (5%)	0	100	100
40	NG	109/137 (80%)	94 (86%)	15 (14%)	0	100	100
41	NH	1070/1237 (86%)	1019 (95%)	51 (5%)	0	100	100
42	NI	163/297 (55%)	159 (98%)	4 (2%)	0	100	100
43	NJ	263/1729 (15%)	256 (97%)	7 (3%)	0	100	100
44	NK	173/316 (55%)	164 (95%)	9 (5%)	0	100	100
45	SA	338/504 (67%)	326 (96%)	12 (4%)	0	100	100
46	SB	297/511 (58%)	283 (95%)	14 (5%)	0	100	100
47	SC	238/327 (73%)	220 (92%)	18 (8%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	SD	224/327 (68%)	216 (96%)	8 (4%)	0	100	100
48	SE	119/126 (94%)	114 (96%)	4 (3%)	1 (1%)	22	65
48	SF	119/126 (94%)	117 (98%)	2 (2%)	0	100	100
49	SG	423/573 (74%)	395 (93%)	28 (7%)	0	100	100
50	SH	358/367 (98%)	343 (96%)	15 (4%)	0	100	100
51	SI	763/1184 (64%)	721 (94%)	41 (5%)	1 (0%)	55	88
52	SJ	212/252 (84%)	208 (98%)	4 (2%)	0	100	100
52	SK	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
53	SL	170/189 (90%)	157 (92%)	13 (8%)	0	100	100
54	SM	278/290 (96%)	252 (91%)	26 (9%)	0	100	100
55	SN	245/274 (89%)	230 (94%)	15 (6%)	0	100	100
56	SO	177/274 (65%)	167 (94%)	10 (6%)	0	100	100
58	SQ	129/217 (59%)	121 (94%)	8 (6%)	0	100	100
59	SR	102/145 (70%)	88 (86%)	13 (13%)	1 (1%)	18	61
60	SS	142/898 (16%)	134 (94%)	8 (6%)	0	100	100
61	ST	448/792 (57%)	432 (96%)	16 (4%)	0	100	100
62	SU	366/552 (66%)	349 (95%)	17 (5%)	0	100	100
63	SV	24/206 (12%)	20 (83%)	4 (17%)	0	100	100
65	SY	237/250 (95%)	218 (92%)	18 (8%)	1 (0%)	38	77
66	SZ	259/483 (54%)	245 (95%)	14 (5%)	0	100	100
All	All	18286/31778 (58%)	17177 (94%)	1092 (6%)	17 (0%)	58	88

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	L4	195	ILE
34	NA	454	VAL
59	SR	90	ASP
14	LF	52	LYS
30	LV	58	ALA

### 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	
4	L3	96/123 (78%)	95 (99%)	1 (1%)	80	90
5	L4	196/222 (88%)	194 (99%)	2 (1%)	80	90
6	L5	180/191 (94%)	180 (100%)	0	100	100
7	L6	96/201 (48%)	94 (98%)	2 (2%)	59	82
8	L7	146/170 (86%)	145 (99%)	1 (1%)	87	94
9	L8	138/161 (86%)	137 (99%)	1 (1%)	87	94
10	L9	150/166 (90%)	149 (99%)	1 (1%)	87	94
11	LC	105/119 (88%)	105 (100%)	0	100	100
12	LD	114/137 (83%)	112 (98%)	2 (2%)	64	85
13	LE	108/111 (97%)	107 (99%)	1 (1%)	82	92
14	LF	76/113 (67%)	74 (97%)	2 (3%)	51	78
15	LG	56/60 (93%)	56 (100%)	0	100	100
16	LH	758/813 (93%)	737 (97%)	21 (3%)	49	76
17	LI	126/153 (82%)	124 (98%)	2 (2%)	68	86
18	LJ	437/454 (96%)	430 (98%)	7 (2%)	68	86
19	LK	83/500 (17%)	81 (98%)	2 (2%)	54	80
20	LL	428/574 (75%)	426 (100%)	2 (0%)	91	96
21	LM	391/1627 (24%)	386 (99%)	5 (1%)	73	88
22	LN	604/699 (86%)	595 (98%)	9 (2%)	70	87
23	LO	730/812 (90%)	723 (99%)	7 (1%)	80	90
24	LP	248/303 (82%)	247 (100%)	1 (0%)	93	97
25	LQ	717/794 (90%)	709 (99%)	8 (1%)	78	89
26	LR	147/155 (95%)	146 (99%)	1 (1%)	87	94
27	LS	424/529 (80%)	420 (99%)	4 (1%)	82	92
28	LT	745/819 (91%)	737 (99%)	8 (1%)	78	89
29	LU	412/443 (93%)	407 (99%)	5 (1%)	75	88
30	LV	307/636 (48%)	305 (99%)	2 (1%)	87	94
31	LW	373/480 (78%)	372 (100%)	1 (0%)	94	97
32	LX	164/165 (99%)	159 (97%)	5 (3%)	46	75

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	LZ	171/172 (99%)	165 (96%)	6 (4%)	41	73
34	NA	187/535 (35%)	184 (98%)	3 (2%)	68	86
35	NB	108/525 (21%)	107 (99%)	1 (1%)	82	92
36	NC	119/315 (38%)	118 (99%)	1 (1%)	85	93
37	ND	57/176 (32%)	57 (100%)	0	100	100
38	NE	114/278 (41%)	113 (99%)	1 (1%)	82	92
45	SA	296/413 (72%)	293 (99%)	3 (1%)	80	90
46	SB	243/319 (76%)	238 (98%)	5 (2%)	59	82
47	SC	202/240 (84%)	198 (98%)	4 (2%)	60	83
47	SD	192/240 (80%)	189 (98%)	3 (2%)	68	86
48	SE	100/104 (96%)	98 (98%)	2 (2%)	60	83
48	SF	100/104 (96%)	100 (100%)	0	100	100
49	SG	373/503 (74%)	371 (100%)	2 (0%)	91	96
50	SH	307/312 (98%)	307 (100%)	0	100	100
51	SI	684/1014 (68%)	670 (98%)	14 (2%)	60	83
52	SJ	195/222 (88%)	190 (97%)	5 (3%)	51	78
52	SK	206/222 (93%)	201 (98%)	5 (2%)	54	80
53	SL	156/169 (92%)	154 (99%)	2 (1%)	73	88
54	SM	251/258 (97%)	244 (97%)	7 (3%)	49	76
55	SN	230/256 (90%)	226 (98%)	4 (2%)	66	85
56	SO	33/238 (14%)	32 (97%)	1 (3%)	46	75
58	SQ	124/200 (62%)	124 (100%)	0	100	100
59	SR	86/120 (72%)	84 (98%)	2 (2%)	56	80
60	SS	135/758 (18%)	135 (100%)	0	100	100
61	ST	417/534 (78%)	412 (99%)	5 (1%)	75	88
62	SU	330/338 (98%)	323 (98%)	7 (2%)	59	82
63	SV	22/117 (19%)	22 (100%)	0	100	100
65	SY	226/234 (97%)	220 (97%)	6 (3%)	50	77
All	All	14219/20646 (69%)	14027 (99%)	192 (1%)	74	87

5 of 192 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	LT	283	ARG
33	LZ	137	ARG
61	ST	704	ASN
28	LT	925	LEU
31	LW	199	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 259 such sidechains are listed below:

Mol	Chain	Res	Type
25	LQ	916	HIS
29	LU	252	ASN
61	ST	482	GLN
26	LR	690	HIS
28	LT	135	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	484/700 (69%)	122 (25%)	7 (1%)
2	L1	1004/1807 (55%)	282 (28%)	19 (1%)
3	L2	163/333 (48%)	45 (27%)	0
All	All	1651/2840 (58%)	449 (27%)	26 (1%)

5 of 449 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	63	G
1	L0	64	U
1	L0	82	A
1	L0	83	U
1	L0	85	G

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	103	A
2	L1	272	U
2	L1	1620	C
2	L1	139	C
2	L1	187	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
57	SP	61
26	LR	14
32	LY	11
32	LX	11
17	LI	9
64	SX	3
19	LK	2
24	LP	2
45	SA	2
61	ST	2
46	SB	2
60	SS	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Number of breaks
22	LN	1
25	LQ	1
62	SU	1
38	NE	1
63	SV	1
37	ND	1

The worst 5 of 126 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	SX	2034:UNK	C	3098:UNK	N	257.52
1	SX	1058:UNK	C	2000:UNK	N	68.50
1	SX	3115:UNK	C	3218:UNK	N	49.43
1	LI	358:UNK	C	457:UNK	N	41.95
1	LR	323:UNK	C	329:UNK	N	40.86