



wwPDB EM Validation Summary Report ⓘ

Mar 31, 2025 – 05:29 PM JST

PDB ID : 5WYJ / pdb_00005wyj
EMDB ID : EMD-6695
Title : Cryo-EM structure of the 90S small subunit pre-ribosome (Dhr1-depleted, Enp1-TAP, state 1)
Authors : Ye, K.; Zhu, X.; Sun, Q.
Deposited on : 2017-01-13
Resolution : 8.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

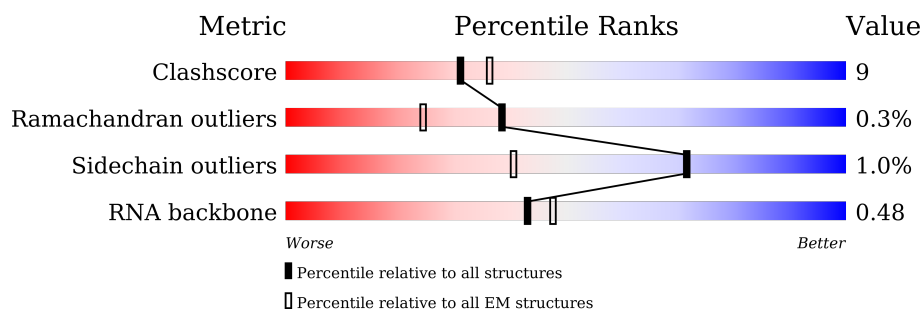
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.70 Å.

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



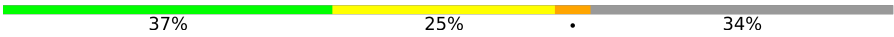







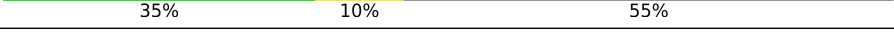

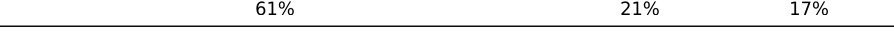
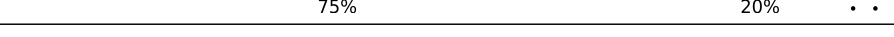

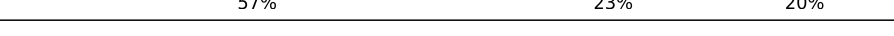


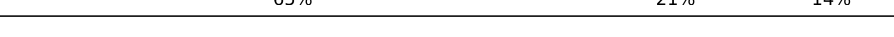

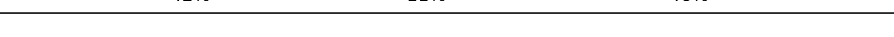






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	3A	333	
2	3B	327	
2	3C	327	
3	3D	504	
4	3E	511	
5	3F	573	
6	3G	126	
6	3H	126	



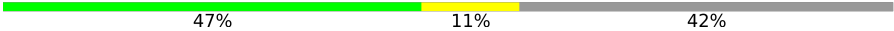








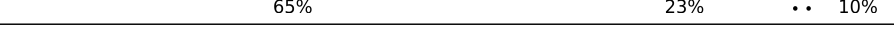







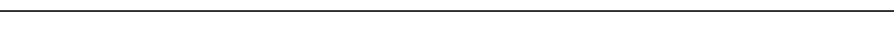

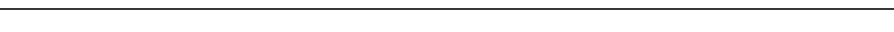
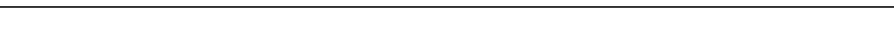


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Mol	Chain	Length	Quality of chain
7	5A	700	
8	AA	776	
9	AB	643	
10	AC	713	
11	AD	575	
12	AE	1769	
13	AF	513	
14	AG	896	
15	B1	1183	
16	BA	923	
17	BB	943	
18	BC	817	
19	BD	594	
20	BE	939	
21	CA	297	
22	CB	1237	
23	E1	252	
23	E2	252	
24	E3	483	
25	E4	707	
26	K1	316	
27	MA	183	
28	MB	290	
29	MC	593	
30	P1	274	

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Mol	Chain	Length	Quality of chain
31	R1	367	
32	R2	1729	
33	S1	489	
34	SA	1812	
35	SC	255	
36	SF	261	
37	SG	225	
38	SH	236	
39	SI	190	
40	SJ	200	
41	SK	197	
42	SM	156	
43	SN	143	
44	SO	151	
45	SP	137	
46	SR	143	
47	SX	130	
48	SY	145	
49	SZ	135	
50	Sc	82	
51	Sd	67	
52	Sf	63	
53	Sg	152	
54	U1	554	
55	U2	250	

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Mol	Chain	Length	Quality of chain
56	U3	2493	 56%44%
57	U4	189	 55%12%33%
58	U5	274	 79%11%9%
59	UA	1615	 21%79%
60	UB	987	 56%44%
61	UC	1033	 62%.36%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 173863 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 U3 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	157	Total	C	N	O	P	0	0
			3327	1488	575	1107	157		

- Molecule 2 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3B	239	Total	C	N	O	S	0	0
			1866	1183	332	341	10		
2	3C	239	Total	C	N	O	S	0	0
			1866	1183	332	341	10		

- Molecule 3 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3D	370	Total	C	N	O	S	0	0
			2915	1843	503	560	9		

- Molecule 4 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3E	382	Total	C	N	O	S	0	0
			2935	1859	498	570	8		

- Molecule 5 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3F	365	Total	C	N	O	S	0	0
			2916	1871	506	529	10		

- Molecule 6 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	3G	122	Total	C	N	O	S	0	0
			924	589	159	172	4		
6	3H	122	Total	C	N	O	S	0	0
			924	589	159	172	4		

- Molecule 7 is a RNA chain called 5ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5A	462	Total	C	N	O	P	0	0
			9867	4406	1749	3250	462		

- Molecule 8 is a protein called Utp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	AA	569	Total	C	N	O	0	0
			2845	1707	569	569		

- Molecule 9 is a protein called Utp5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AB	403	Total	C	N	O	0	0
			2015	1209	403	403		

- Molecule 10 is a protein called Utp8.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	AC	472	Total	C	N	O	0	0
			2360	1416	472	472		

- Molecule 11 is a protein called Utp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	AD	101	Total	C	N	O	0	0
			505	303	101	101		

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 10,Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AE	1536	Total	C	N	O	S	0	0
			9970	6261	1772	1918	19		

- Molecule 13 is a protein called Utp15.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AF	376	Total	C	N	O	0	0
			1880	1128	376	376		

- Molecule 14 is a protein called Utp17.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AG	612	Total	C	N	O	0	0
			3060	1836	612	612		

- Molecule 15 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	B1	536	Total	C	N	O	S	0	0
			4325	2801	758	746	20		

- Molecule 16 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BA	755	Total	C	N	O	S	0	0
			6026	3862	1025	1123	16		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BB	778	Total	C	N	O	S	0	0
			6138	3931	1019	1161	27		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BC	783	Total	C	N	O	S	0	0
			6117	3870	1033	1187	27		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BD	325	Total	C	N	O	S	0	0
			2539	1606	458	466	9		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BE	753	Total	C	N	O	S	0	0
			5936	3769	1020	1126	21		

- Molecule 21 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CA	196	Total	C	N	O	S	0	0
			1582	1016	259	300	7		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CB	1098	Total	C	N	O	S	0	0
			8870	5763	1462	1621	24		

- Molecule 23 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	E1	217	Total	C	N	O	S	0	0
			1689	1073	293	312	11		
23	E2	216	Total	C	N	O	S	0	0
			1695	1078	295	313	9		

- Molecule 24 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	E3	260	Total	C	N	O	S	0	0
			2114	1378	359	374	3		

- Molecule 25 is a protein called Enp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	E4	285	Total	C	N	O	0	0
			1425	855	285	285		

- Molecule 26 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	K1	175	Total	C	N	O	S	0	0
			1410	903	252	245	10		

- Molecule 27 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	MA	133	Total	C	N	O	S	0	0
			1097	692	204	194	7		

- Molecule 28 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	MB	184	Total	C	N	O	S	0	0
			1465	926	273	260	6		

- Molecule 29 is a protein called Mpp10,U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	MC	46	Total	C	N	O	0	0
			307	193	52	62		

- Molecule 30 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	P1	173	Total	C	N	O	S	0	0
			1368	876	245	243	4		

- Molecule 31 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	R1	355	Total	C	N	O	S	0	0
			2742	1756	466	509	11		

- Molecule 32 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R2	272	Total	C	N	O	S	0	0
			2228	1433	374	416	5		

- Molecule 33 is a protein called Sof1.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	S1	285	Total	C	N	O	0	0
			1425	855	285	285		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SA	1115	Total	C	N	O	P	0	0
			23759	10623	4225	7796	1115		

- Molecule 35 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	SC	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 36 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SF	237	Total	C	N	O	S	0	0
			1881	1205	345	328	3		

- Molecule 37 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	SG	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 38 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SH	174	Total	C	N	O	S	0	0
			1369	856	262	248	3		

- Molecule 39 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	SI	165	Total	C	N	O		0	0
			1322	856	227	239			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SJ	170	Total	C	N	O	S	0	0
			1350	839	268	241	2		

- Molecule 41 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SK	175	Total	C	N	O	S	0	0
			1412	892	272	247	1		

- Molecule 42 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SM	141	Total	C	N	O	S	0	0
			1143	733	216	191	3		

- Molecule 43 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SN	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 44 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SO	134	Total	C	N	O	S	0	0
			1087	698	202	186	1		

- Molecule 45 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SP	109	Total	C	N	O	S	0	0
			750	462	147	140	1		

- Molecule 46 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	SR	125	Total	C	N	O	0	0
			973	625	174	174		

- Molecule 47 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SX	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 48 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SY	103	Total	C	N	O	S	0	0
			785	501	144	138	2		

- Molecule 49 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SZ	101	Total	C	N	O		0	0
			801	512	144	145			

- Molecule 50 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Sc	79	Total	C	N	O	S	0	0
			595	371	108	111	5		

- Molecule 51 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 52 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	Sf	30	Total	C	N	O		0
			251	162	50	39		0

- Molecule 53 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Sg	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 54 is a protein called Utp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	U1	285	Total	C	N	O		0
			1425	855	285	285		0

- Molecule 55 is a protein called Utp11.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	U2	73	Total	C	N	O	0	0
			365	219	73	73		

- Molecule 56 is a protein called Utp20.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	U3	1407	Total	C	N	O	0	0
			7035	4221	1407	1407		

- Molecule 57 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	U4	126	Total	C	N	O	S	0	0
			990	633	179	168	10		

- Molecule 58 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	U5	248	Total	C	N	O	S	0	0
			2009	1285	357	359	8		

- Molecule 59 is a protein called Helical domain protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	UA	338	Total	C	N	O	0	0
			1690	1014	338	338		

- Molecule 60 is a protein called Helical domain protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	UB	555	Total	C	N	O	0	0
			2775	1665	555	555		

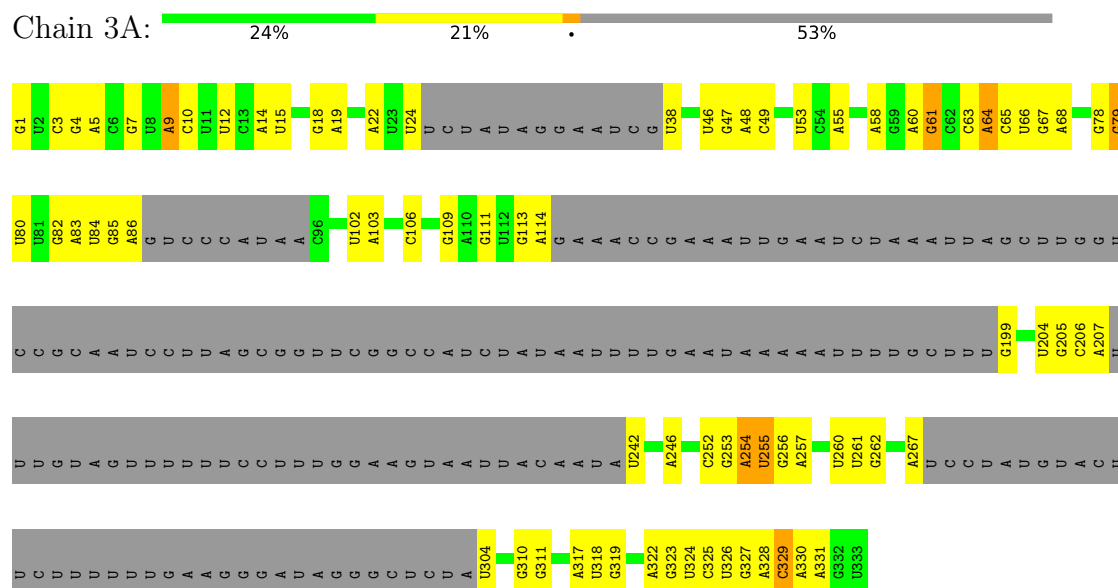
- Molecule 61 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	UC	660	Total	C	N	O	0	0
			3300	1980	660	660		

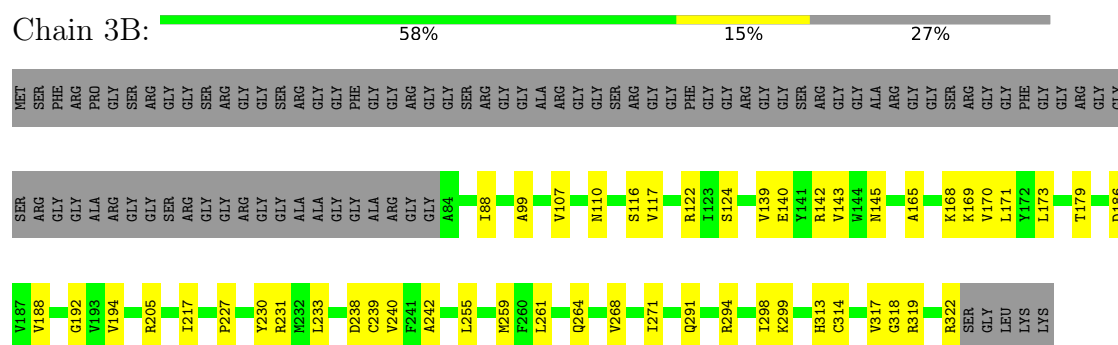
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

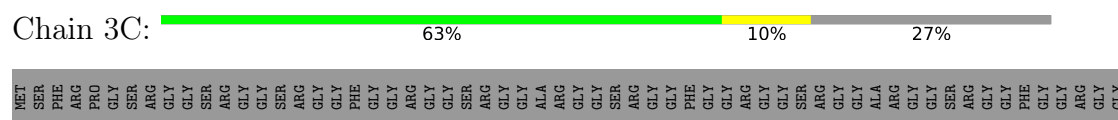
• Molecule 1: U3 RNA



• Molecule 2: rRNA 2'-O-methyltransferase fibrillar

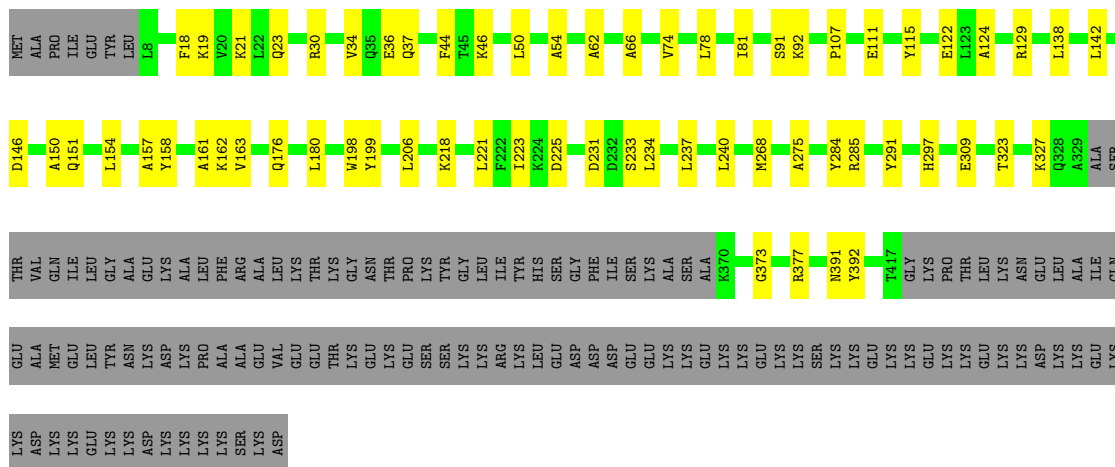


• Molecule 2: rRNA 2'-O-methyltransferase fibrillar



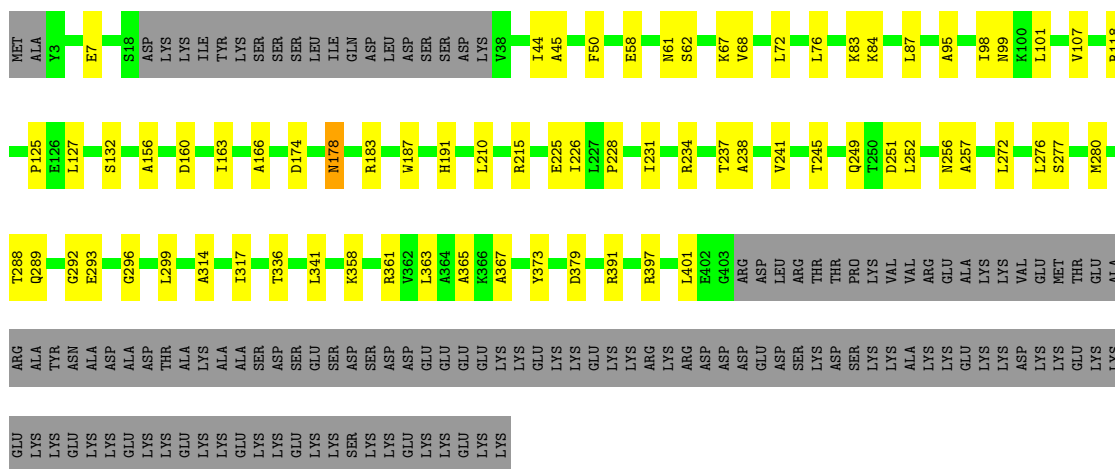
- Molecule 3: Nucleolar protein 56

Chain 3D: 61% 12% 27%



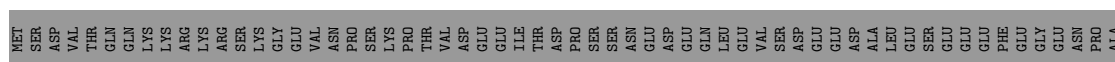
- Molecule 4: Nucleolar protein 58

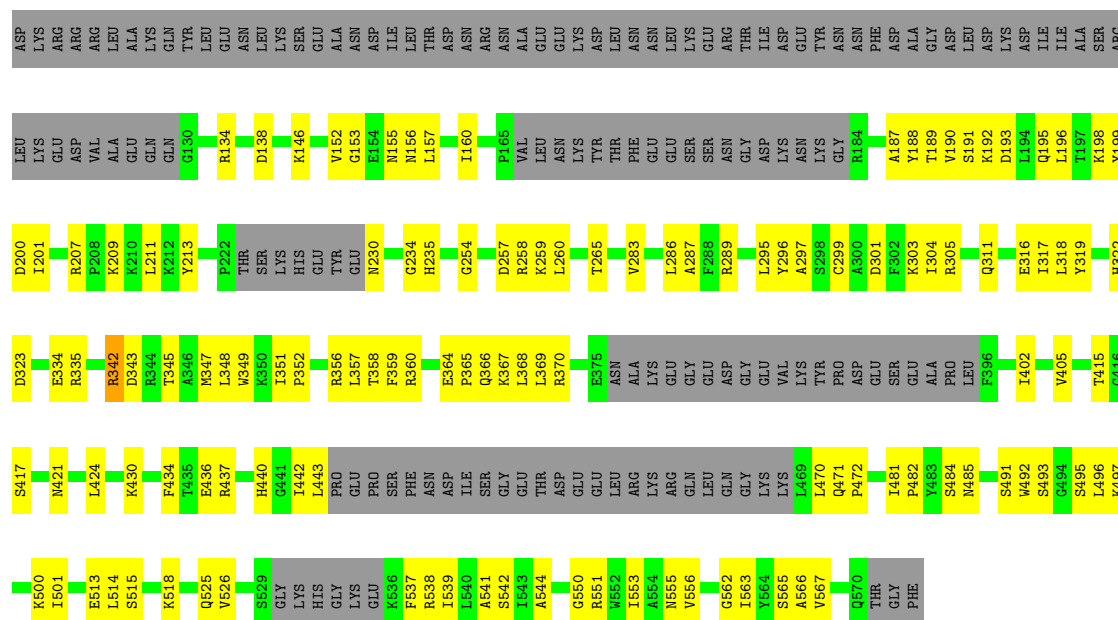
Chain 3E:  61% 14% 25%



- Molecule 5: Ribosomal RNA-processing protein 9

Chain 3F: 42% 22% 36%





- Molecule 6: 13 kDa ribonucleoprotein-associated protein

Chain 3G: 75% 22% .



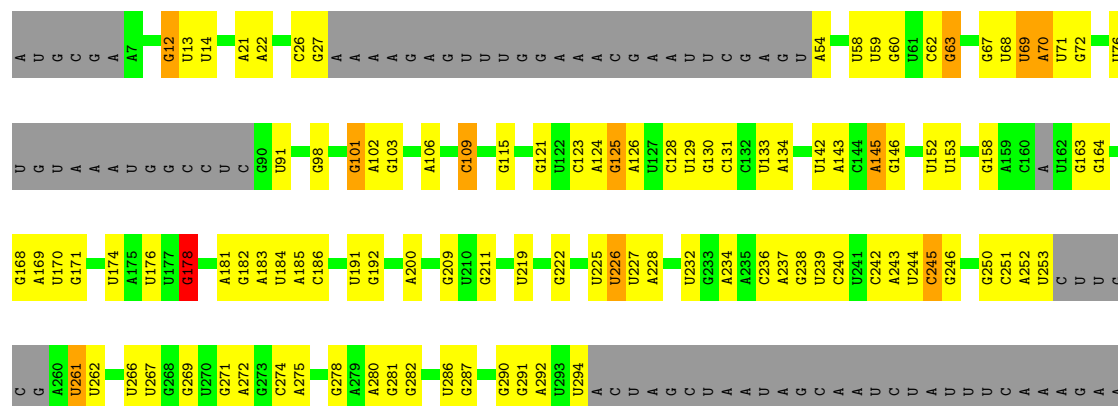
- Molecule 6: 13 kDa ribonucleoprotein-associated protein

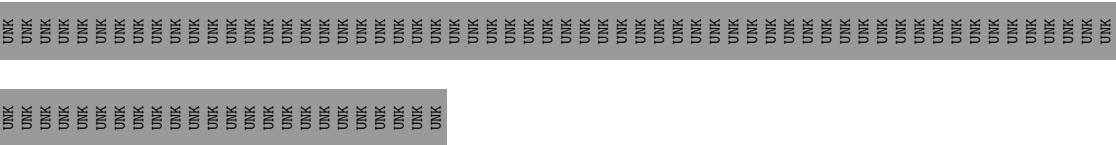
Chain 3H: 79% 17% .



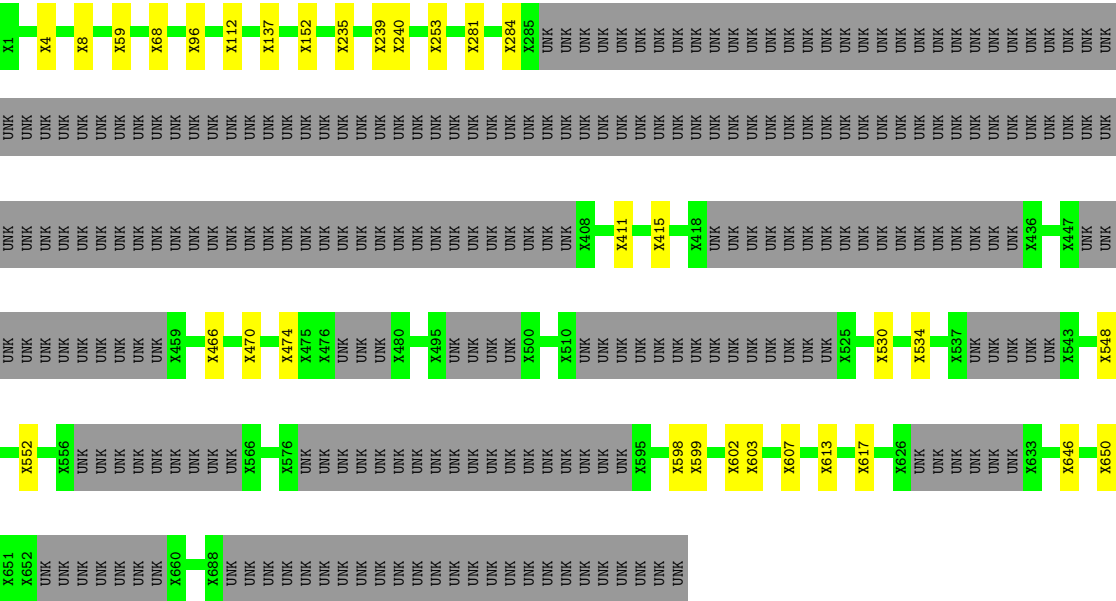
- Molecule 7: 5ETS RNA

Chain 5A: 37% 25% 34% .

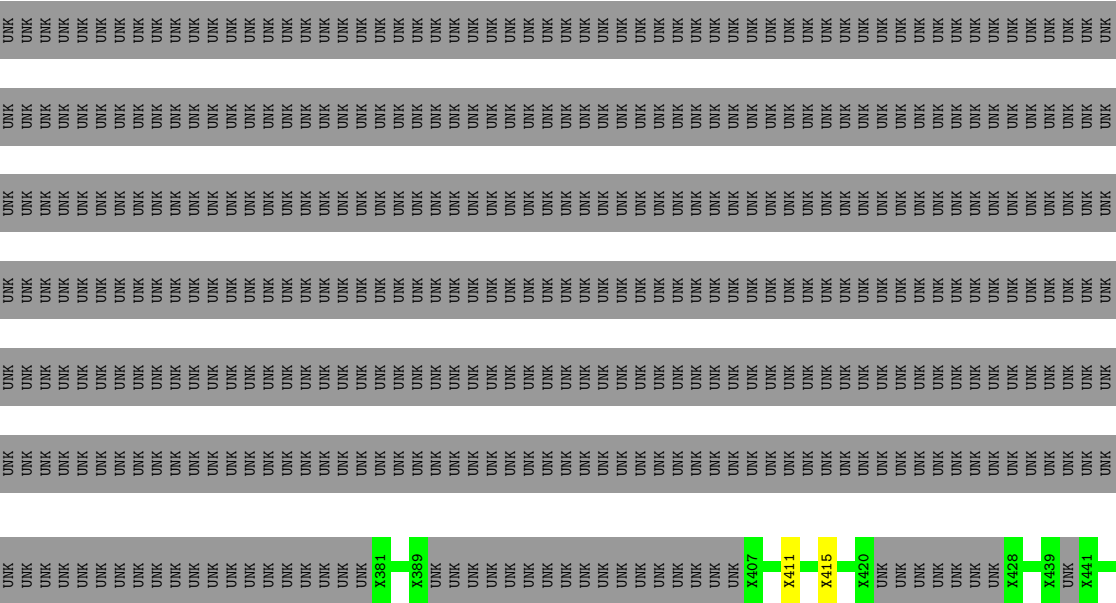


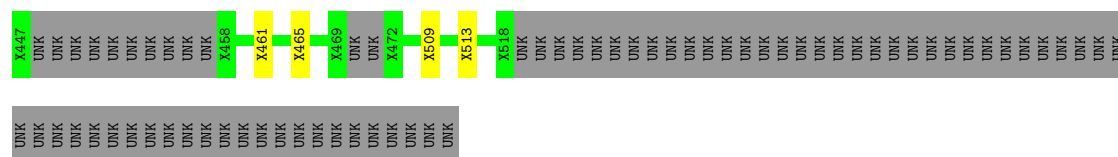


● Molecule 10: Utp8



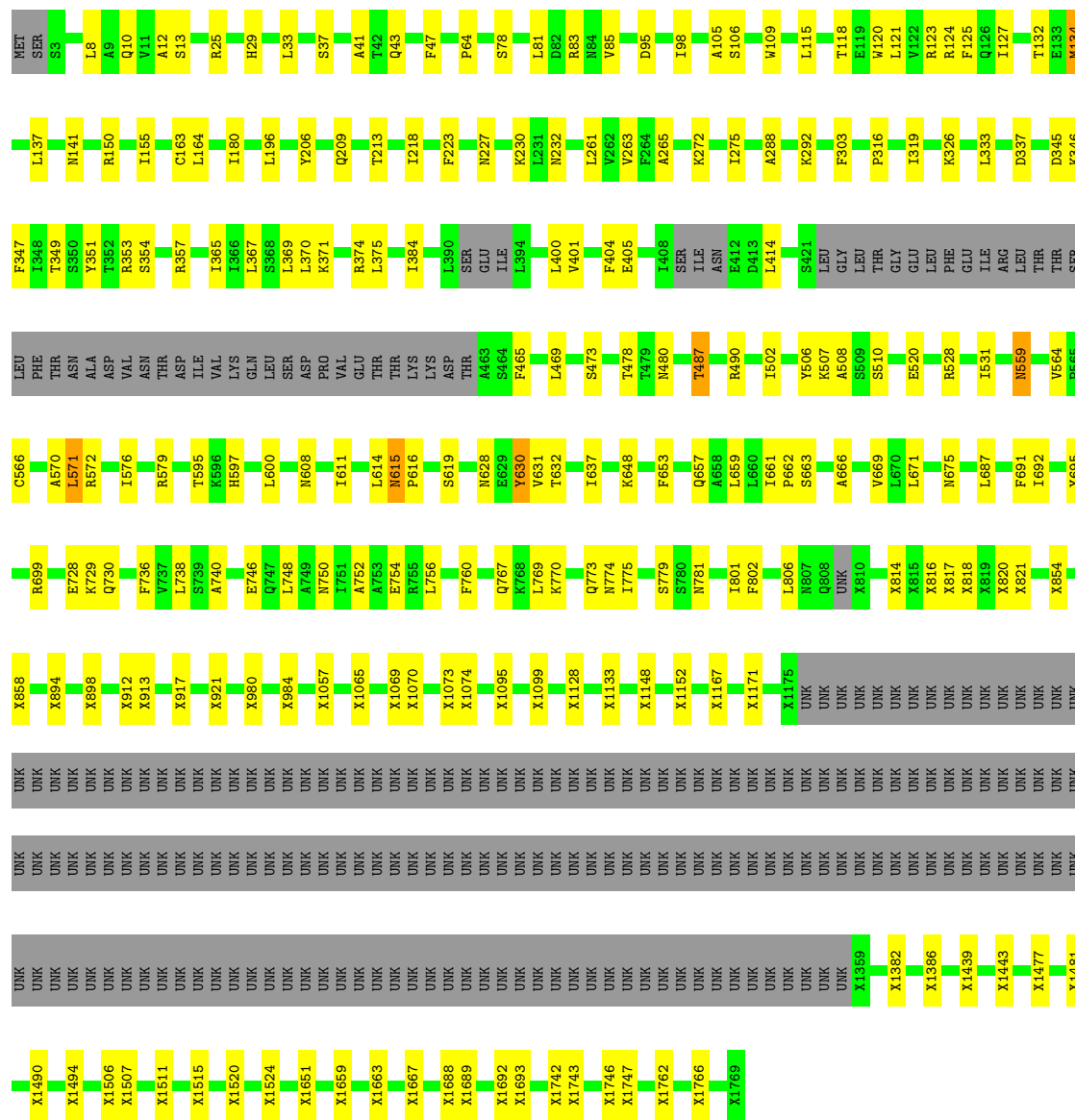
● Molecule 11: Utp9





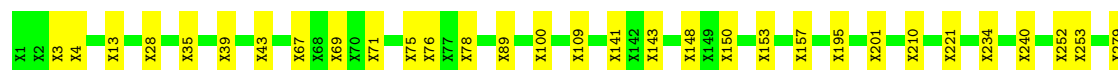
• Molecule 12: U3 small nucleolar RNA-associated protein 10,Utp10

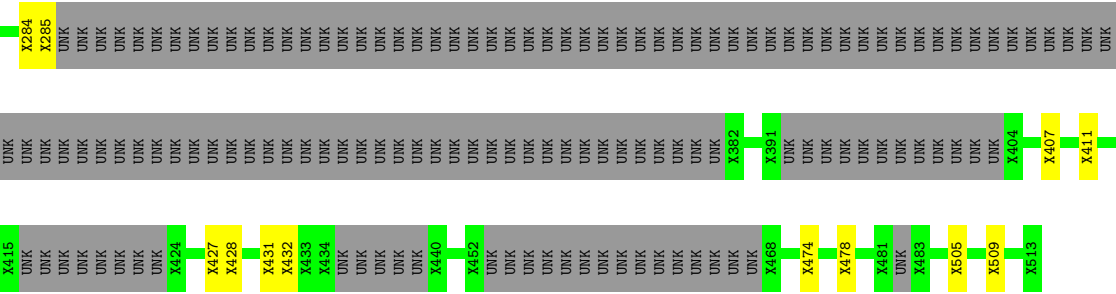
Chain AE:



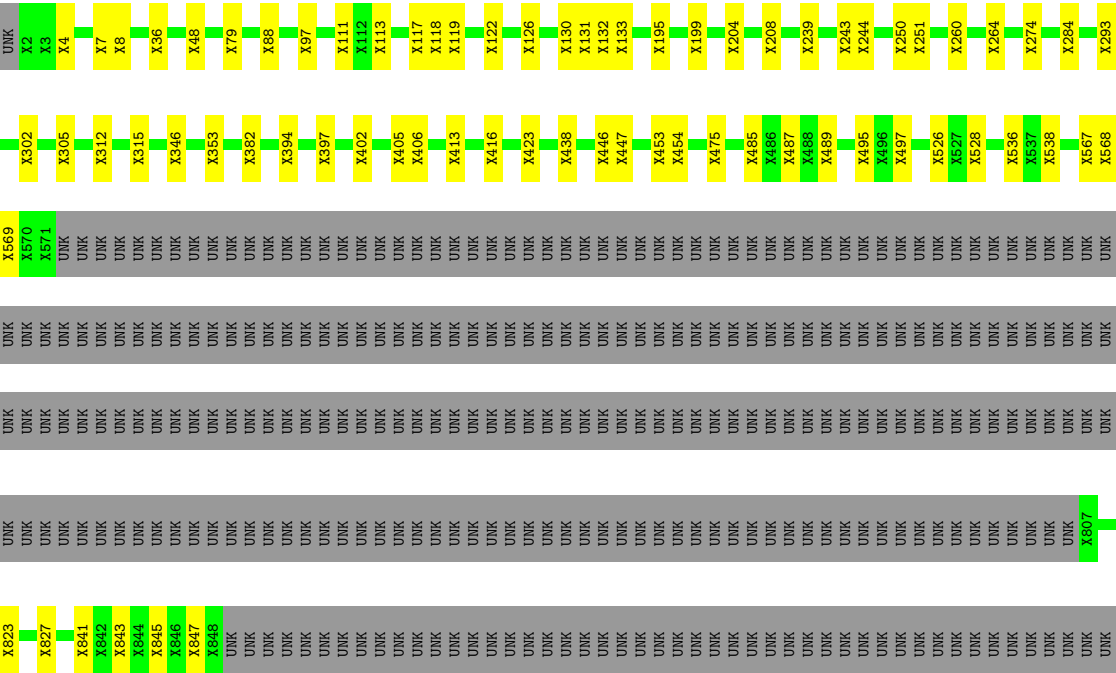
• Molecule 13: Utp15

Chain AF:

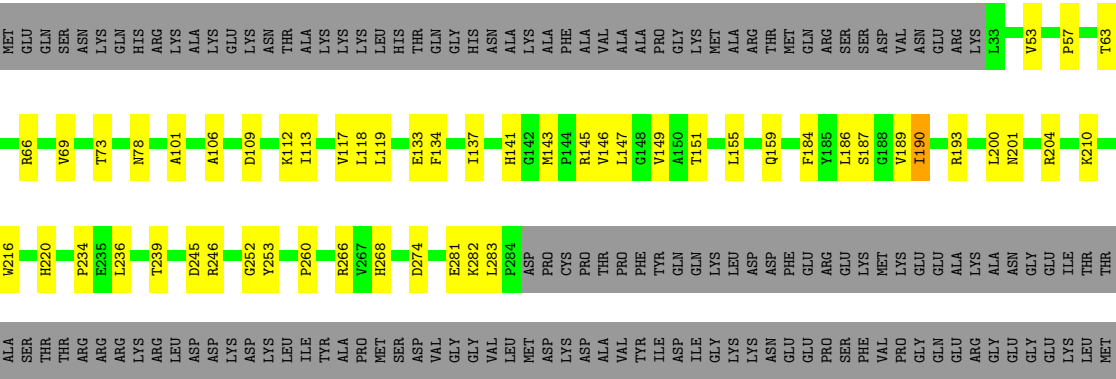
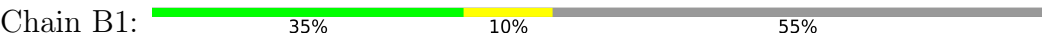




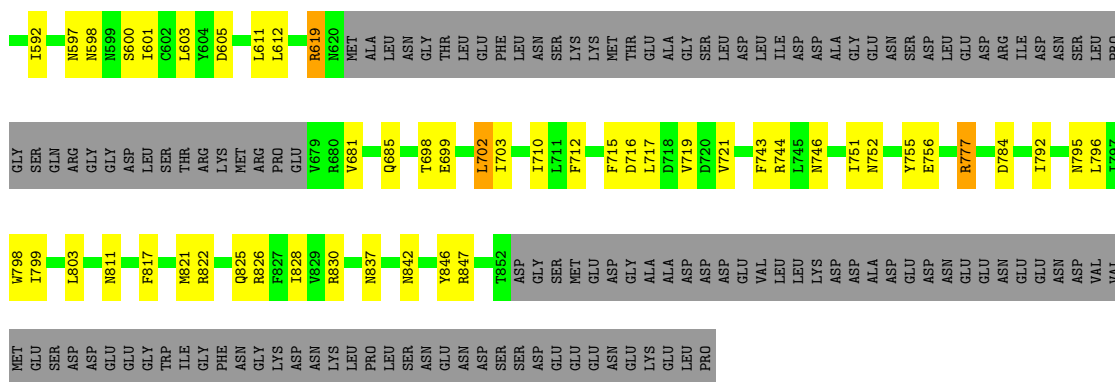
● Molecule 14: Utp17



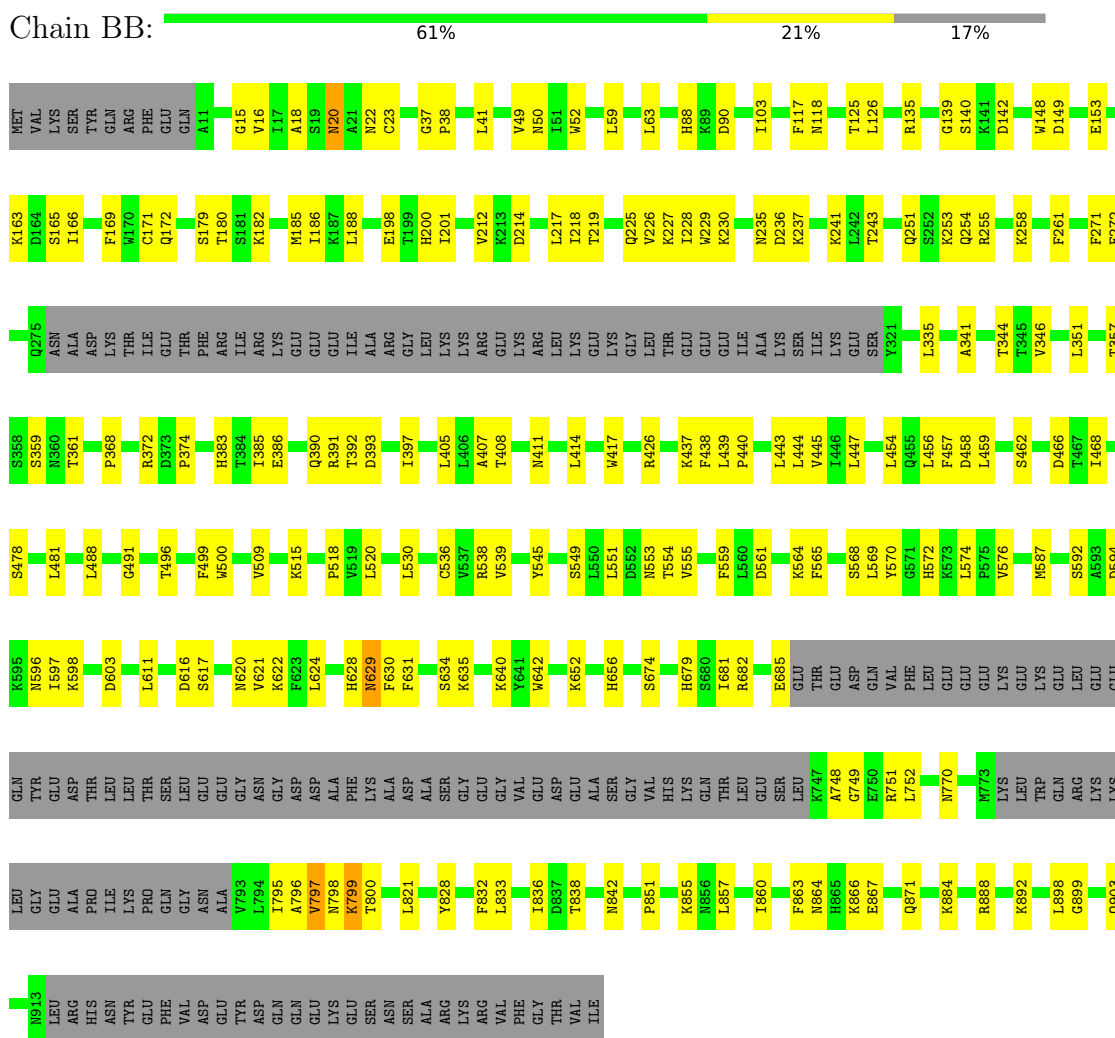
● Molecule 15: Ribosome biogenesis protein BMS1



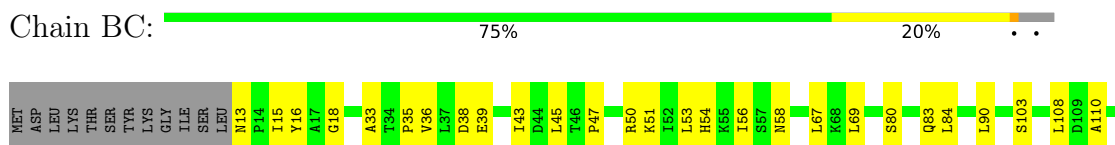
- Molecule 16: Periodic tryptophan protein 2

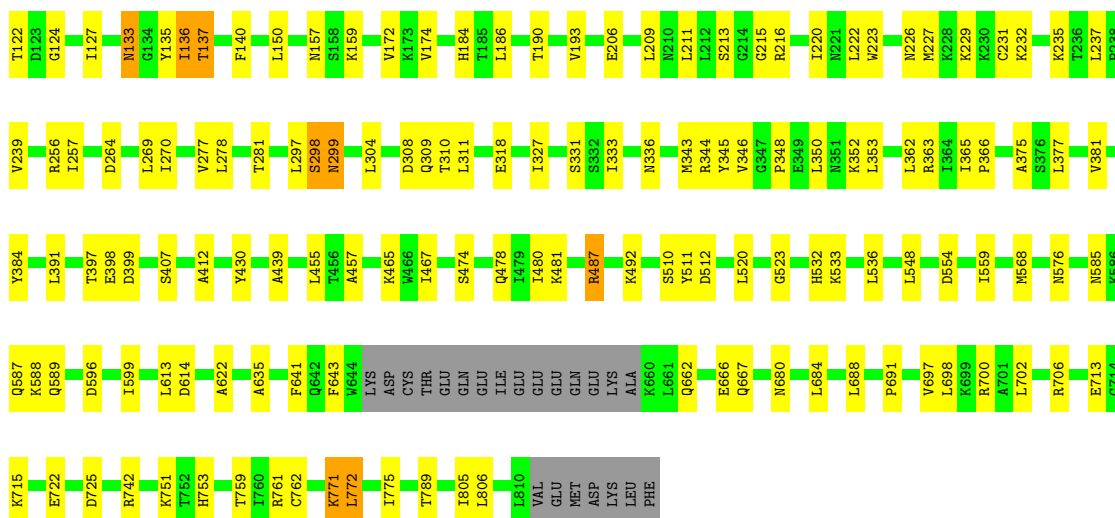


• Molecule 17: U3 small nucleolar RNA-associated protein 12

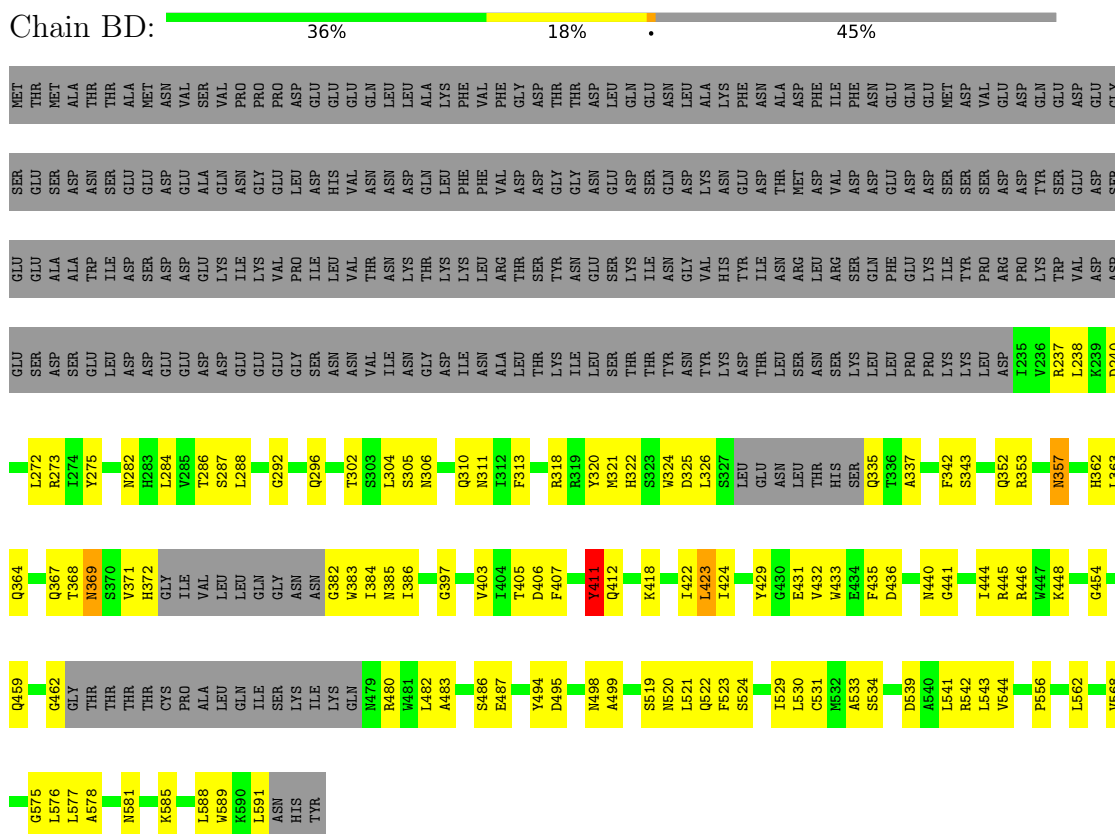


• Molecule 18: U3 small nucleolar RNA-associated protein 13





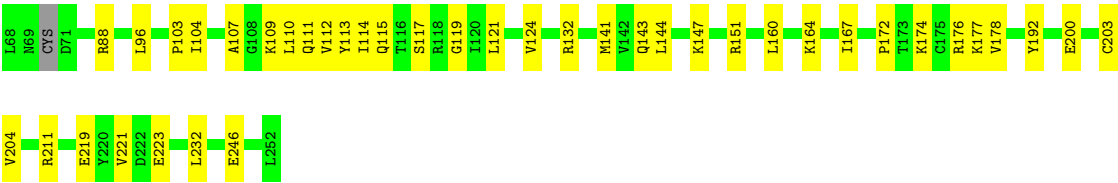
- Molecule 19: U3 small nucleolar RNA-associated protein 18



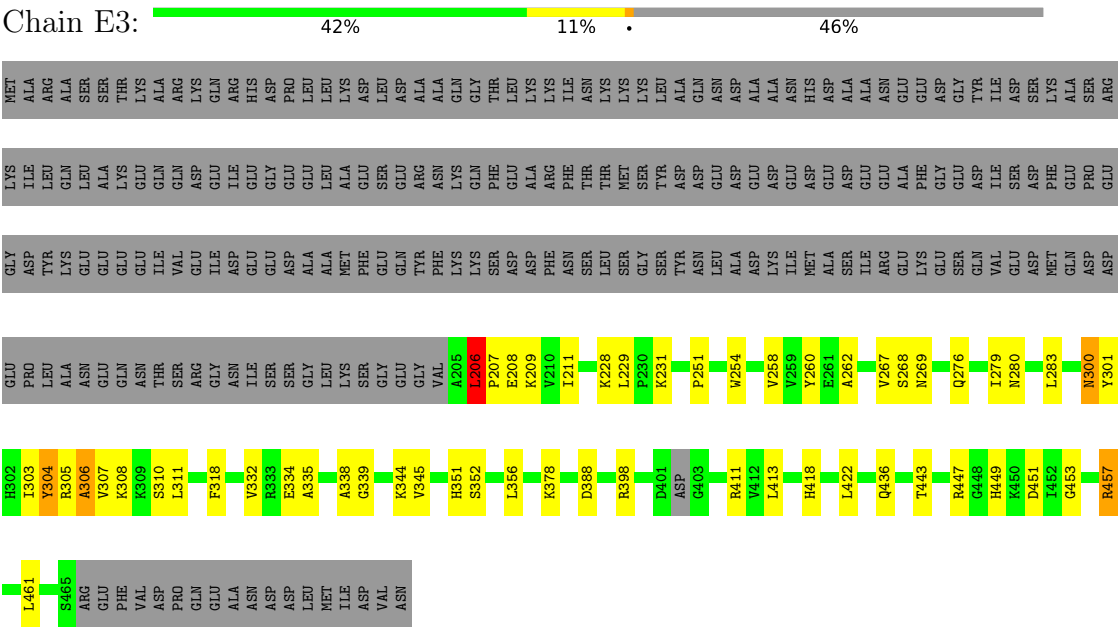
- Molecule 20: U3 small nucleolar RNA-associated protein 21



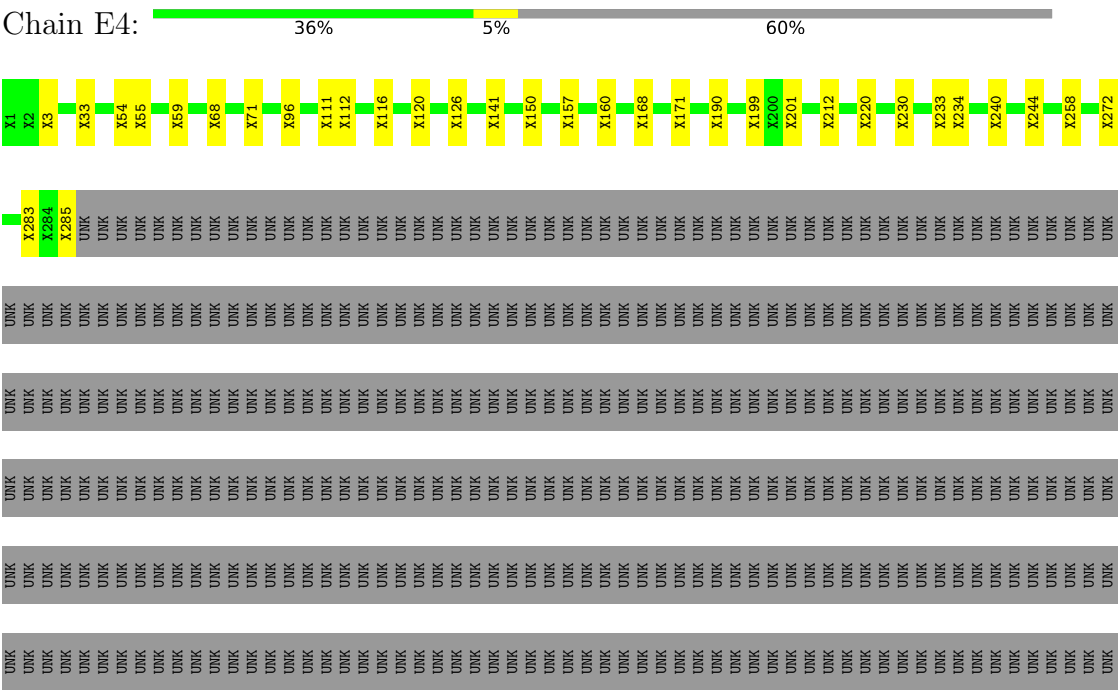




● Molecule 24: Essential nuclear protein 1



● Molecule 25: Enp2

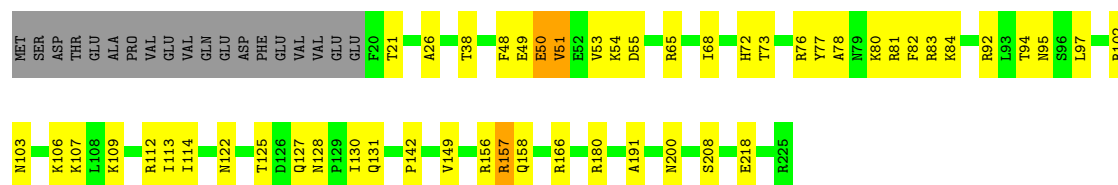


Chain R2: 14% . 84%

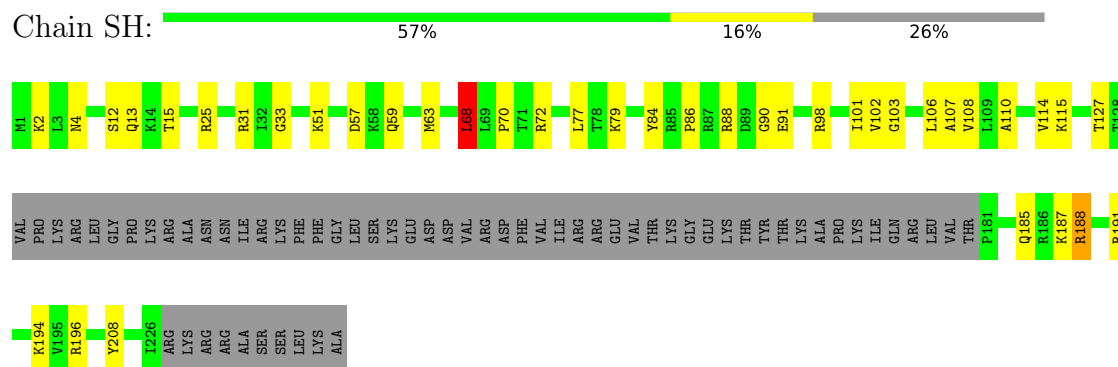




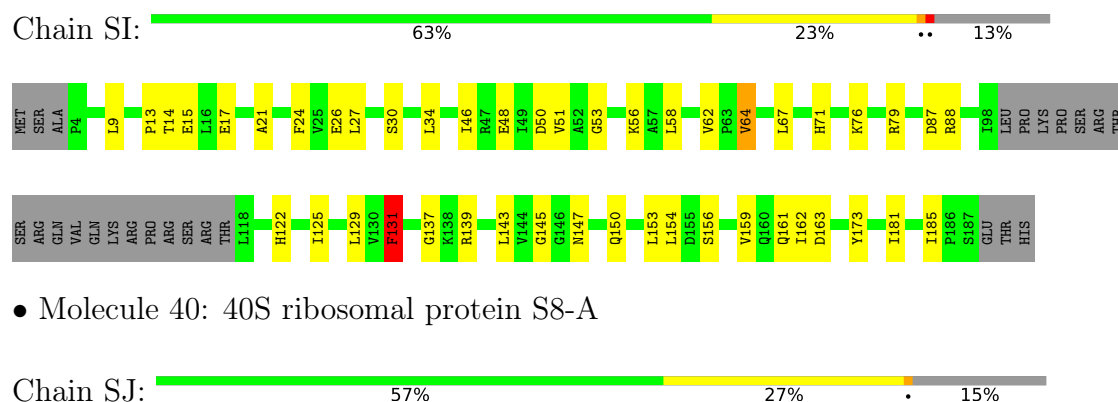




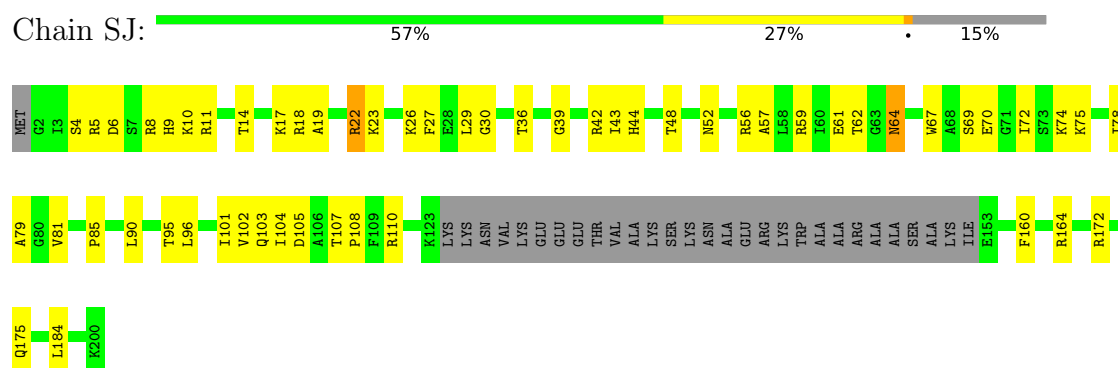
- Molecule 38: 40S ribosomal protein S6-A



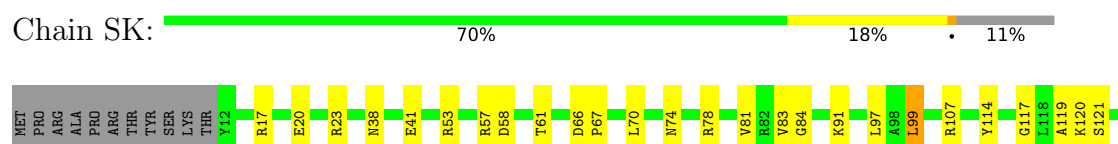
- Molecule 39: 40S ribosomal protein S7-A



- Molecule 40: 40S ribosomal protein S8-A

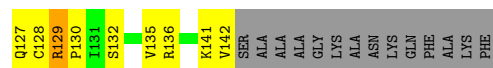


- Molecule 41: 40S ribosomal protein S9-A



- Molecule 42: 40S ribosomal protein S11-A

Chain SM:  65% 23% .. 10%



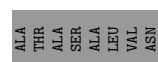
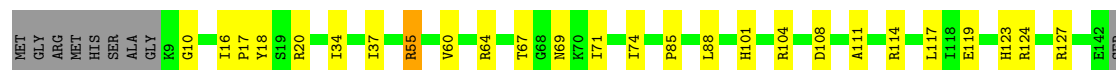
- Molecule 43: 40S ribosomal protein S12

Chain SN: 



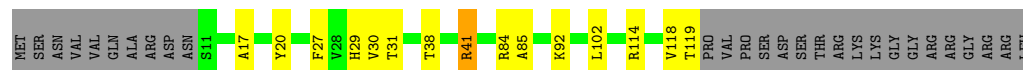
- Molecule 44: 40S ribosomal protein S13

Chain SO:  72% 17% 11%



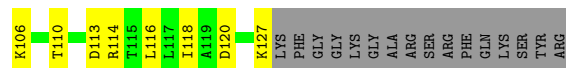
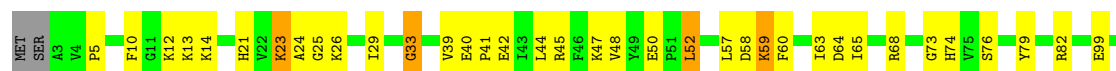
- Molecule 45: 40S ribosomal protein S14-A

Chain SP:  69% 10% 20%

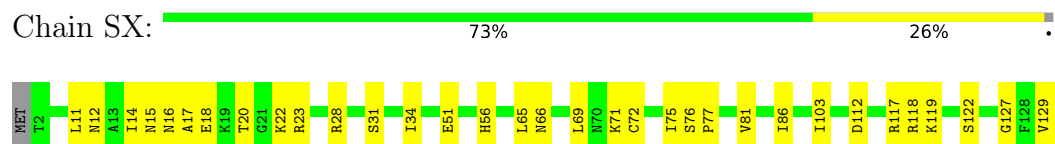


- Molecule 46: 40S ribosomal protein S16-A

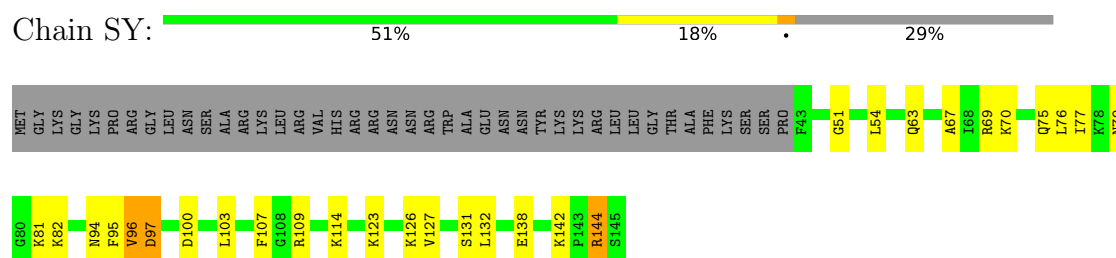
Chain SR:  57% 28% 0 13%



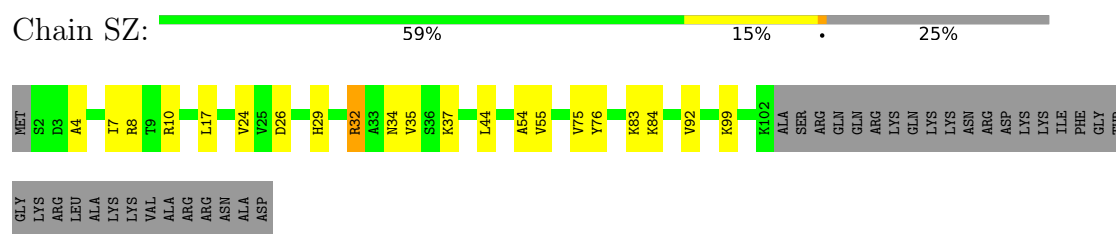
- Molecule 47: 40S ribosomal protein S22-A



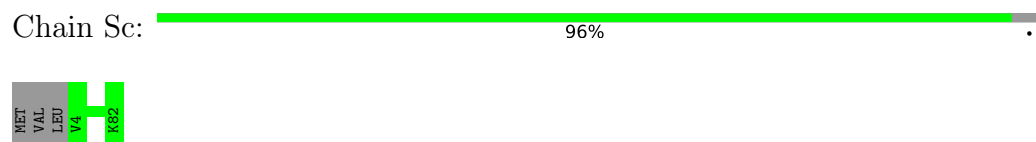
- Molecule 48: 40S ribosomal protein S23-A



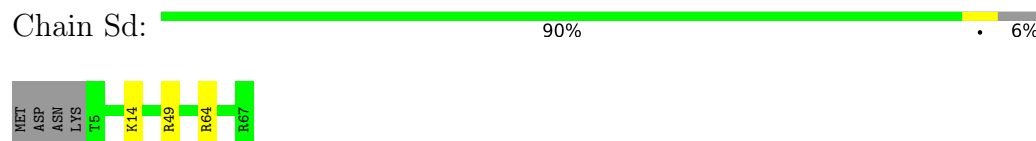
- Molecule 49: 40S ribosomal protein S24-A



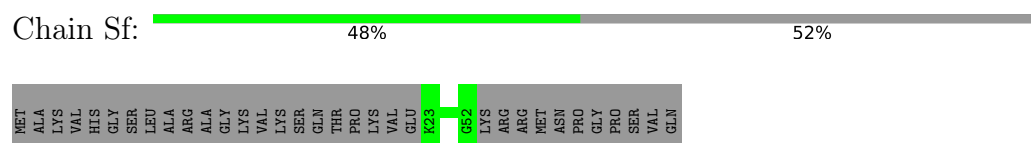
- Molecule 50: 40S ribosomal protein S27-A



- Molecule 51: 40S ribosomal protein S28-A



- Molecule 52: 40S ribosomal protein S30-A



- Molecule 53: Ubiquitin-40S ribosomal protein S31

ILE GLN GLY LYS SER THR LEU HIS VAL ARG LEU ARG GLY GLY LYS LYS ARG LYS LYS VAL TYR THR THR PRO LYS LYS ILE LYS HIS LYS LYS VAL LYS LEU ALA

- Molecule 54: Utp7

[illegible]

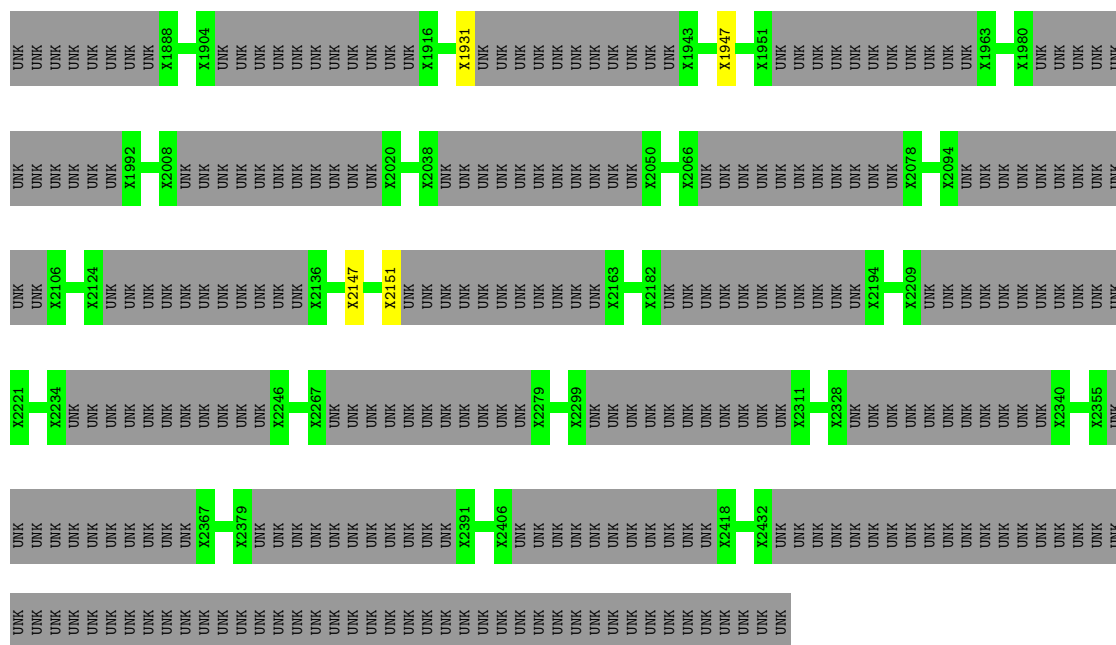
- Molecule 55: Utp11

[illegible]

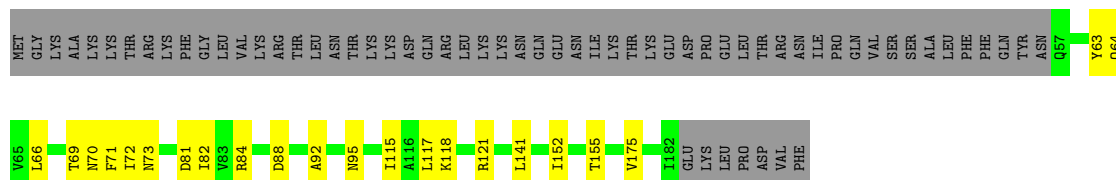
- Molecule 56: Utp20

[illegible]

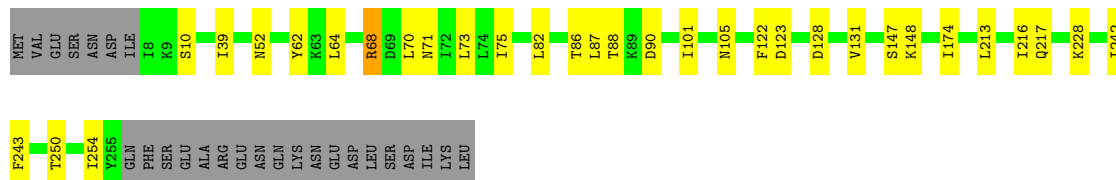
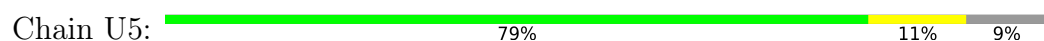




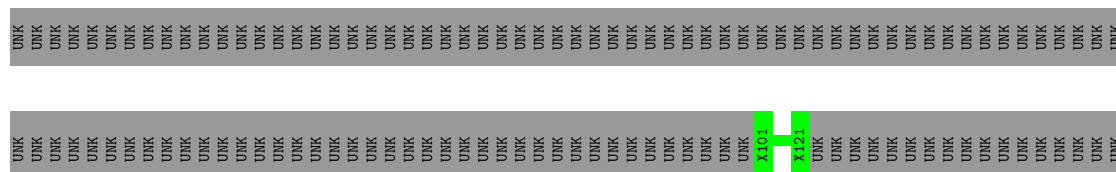
- Molecule 57: rRNA-processing protein FCF1



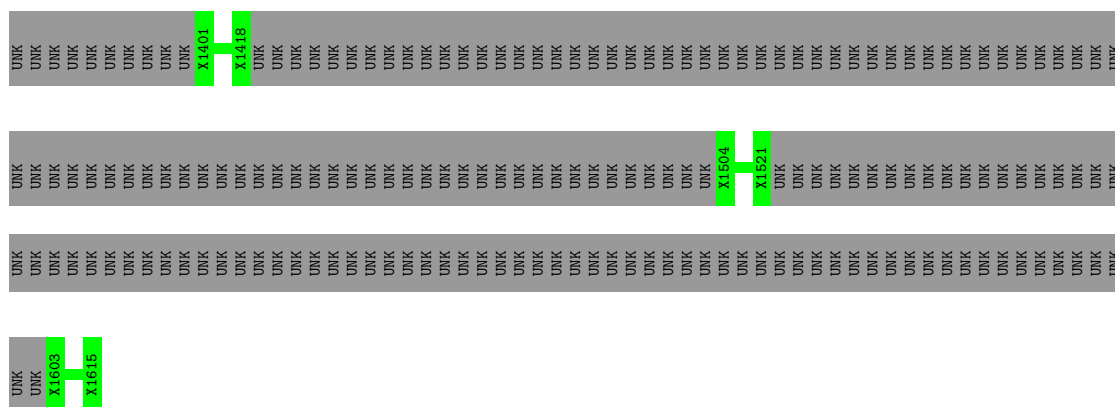
- Molecule 58: Ribosome biogenesis protein UTP30



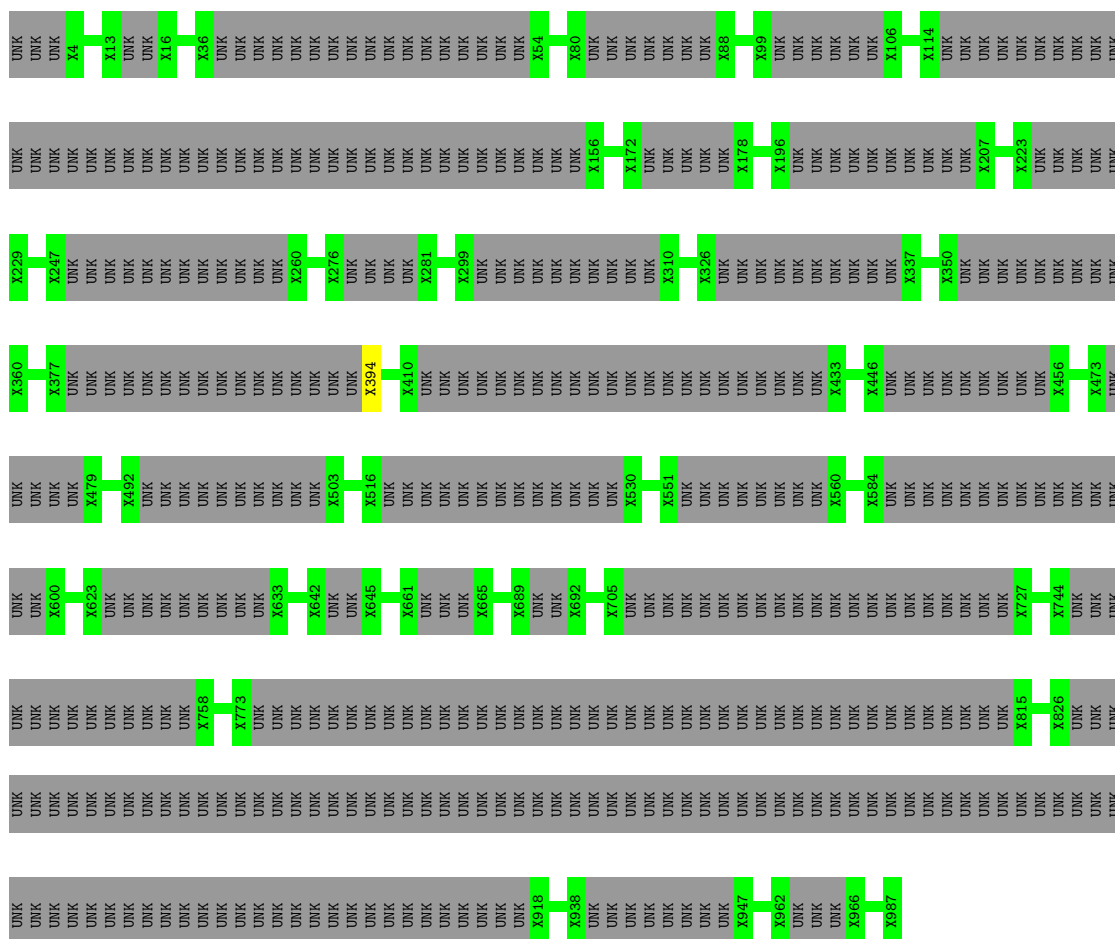
- Molecule 59: Helical domain protein



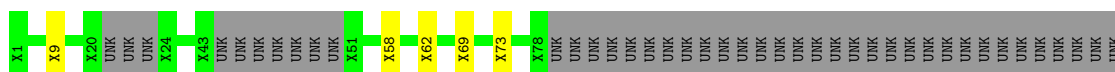


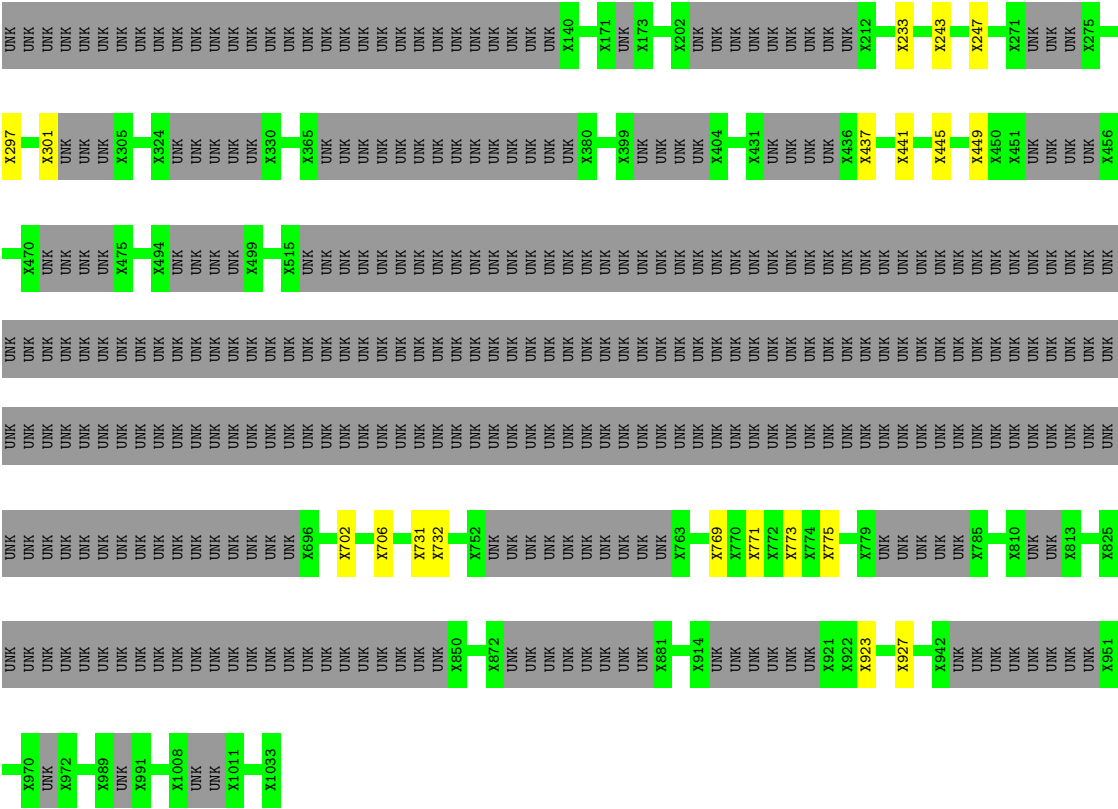


- Molecule 60: Helical domain protein



- Molecule 61: Unassigned helices





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30995	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	79545	Depositor
Image detector	OTHER	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	3A	0.34	0/3710	1.04	6/5763 (0.1%)
2	3B	0.31	0/1903	0.53	0/2572
2	3C	0.28	0/1903	0.52	1/2572 (0.0%)
3	3D	0.30	0/2960	0.52	0/3987
4	3E	0.27	0/2970	0.46	0/4004
5	3F	0.30	0/2975	0.56	0/4008
6	3G	0.28	0/936	0.51	0/1273
6	3H	0.27	0/936	0.50	0/1273
7	5A	0.31	0/11029	1.07	51/17170 (0.3%)
12	AE	0.41	1/6194 (0.0%)	0.58	5/8384 (0.1%)
15	B1	0.30	0/4431	0.56	0/5988
16	BA	0.31	0/6164	0.58	4/8349 (0.0%)
17	BB	0.29	0/6264	0.59	0/8473
18	BC	0.29	0/6226	0.60	2/8442 (0.0%)
19	BD	0.46	4/2597 (0.2%)	0.64	4/3520 (0.1%)
20	BE	0.30	0/6056	0.56	0/8189
21	CA	0.27	0/1621	0.45	0/2196
22	CB	0.28	0/9081	0.47	0/12283
23	E1	0.25	0/1716	0.47	0/2319
23	E2	0.26	0/1721	0.48	0/2323
24	E3	0.29	0/2168	0.51	1/2942 (0.0%)
26	K1	0.29	0/1432	0.53	1/1926 (0.1%)
27	MA	0.27	0/1117	0.47	0/1509
28	MB	0.30	0/1496	0.53	0/2025
29	MC	0.26	0/209	0.50	0/282
30	P1	0.27	0/1394	0.51	0/1881
31	R1	0.28	0/2793	0.49	0/3774
32	R2	0.26	0/2271	0.44	0/3054
34	SA	0.70	9/26553 (0.0%)	1.17	165/41320 (0.4%)
35	SC	0.31	0/1735	0.72	1/2335 (0.0%)
36	SF	0.30	0/1920	0.64	3/2589 (0.1%)
37	SG	0.34	0/1629	0.62	0/2202
38	SH	0.28	0/1385	0.58	1/1851 (0.1%)
39	SI	0.33	0/1343	0.64	1/1808 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
40	SJ	0.28	0/1373	0.60	1/1834 (0.1%)
41	SK	0.29	0/1434	0.62	1/1920 (0.1%)
42	SM	0.35	0/1169	0.57	0/1576
43	SN	0.31	0/898	0.79	1/1220 (0.1%)
44	SO	0.28	0/1109	0.54	0/1495
45	SP	0.28	0/758	0.58	0/1028
46	SR	0.31	0/990	0.66	0/1335
47	SX	0.28	0/1038	0.58	0/1395
48	SY	0.30	0/796	0.67	0/1062
49	SZ	0.31	0/814	0.53	0/1093
50	Sc	0.28	0/605	0.56	0/817
51	Sd	0.26	0/499	0.55	0/670
52	Sf	0.29	0/255	0.54	0/339
53	Sg	0.29	0/404	0.56	0/542
57	U4	0.28	0/1007	0.54	0/1357
58	U5	0.27	0/2043	0.52	0/2747
All	All	0.41	14/144030 (0.0%)	0.78	249/203016 (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
3	3D	0	2
5	3F	0	2
12	AE	0	1
15	B1	0	3
16	BA	0	2
17	BB	0	7
18	BC	0	6
19	BD	0	3
20	BE	0	4
21	CA	0	1
22	CB	0	1
34	SA	0	1
35	SC	0	2
36	SF	0	2
37	SG	0	7
38	SH	0	1
39	SI	0	3
41	SK	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
42	SM	0	1
43	SN	0	4
45	SP	0	1
46	SR	0	3
48	SY	0	1
53	Sg	0	1
58	U5	0	1
61	UC	0	2
All	All	0	65

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	SA	283	U	C2-N3	53.18	1.75	1.37
34	SA	283	U	N3-C4	40.53	1.75	1.38
34	SA	283	U	N1-C2	39.84	1.74	1.38
34	SA	283	U	N1-C6	36.49	1.70	1.38
34	SA	283	U	C4-C5	32.43	1.72	1.43

The worst 5 of 249 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	SA	487	G	C5-C6-O6	38.33	151.60	128.60
34	SA	487	G	N1-C6-O6	-33.63	99.72	119.90
34	SA	493	U	C5-C4-O4	25.11	140.96	125.90
34	SA	493	U	N3-C4-O4	-20.41	105.11	119.40
34	SA	487	G	C4-C5-N7	-19.97	102.81	110.80

There are no chirality outliers.

5 of 65 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3D	392	TYR	Peptide
3	3D	91	SER	Peptide
5	3F	342	ARG	Peptide
5	3F	437	ARG	Peptide
12	AE	64	PRO	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	3A	3327	0	1687	58	0
2	3B	1866	0	1904	30	0
2	3C	1866	0	1904	20	0
3	3D	2915	0	2930	43	0
4	3E	2935	0	3033	48	0
5	3F	2916	0	2947	82	0
6	3G	924	0	975	20	0
6	3H	924	0	975	17	0
7	5A	9867	0	4954	82	0
8	AA	2845	0	658	47	0
9	AB	2015	0	454	19	0
10	AC	2360	0	534	17	0
11	AD	505	0	116	3	0
12	AE	9970	0	7056	161	0
13	AF	1880	0	425	23	0
14	AG	3060	0	707	36	0
15	B1	4325	0	4434	83	0
16	BA	6026	0	5940	129	0
17	BB	6138	0	6163	116	0
18	BC	6117	0	6141	98	0
19	BD	2539	0	2520	69	0
20	BE	5936	0	5882	137	0
21	CA	1582	0	1528	35	0
22	CB	8870	0	8975	149	0
23	E1	1689	0	1738	34	0
23	E2	1695	0	1757	38	0
24	E3	2114	0	2154	55	0
25	E4	1425	0	322	18	0
26	K1	1410	0	1503	27	0
27	MA	1097	0	1130	7	0
28	MB	1465	0	1486	31	0
29	MC	307	0	231	2	0
30	P1	1368	0	1436	9	0
31	R1	2742	0	2829	40	0
32	R2	2228	0	2228	15	0
33	S1	1425	0	334	35	0
34	SA	23759	0	11991	338	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	SC	1709	0	1784	47	0
36	SF	1881	0	1958	50	0
37	SG	1609	0	1675	41	0
38	SH	1369	0	1414	69	0
39	SI	1322	0	1394	29	0
40	SJ	1350	0	1374	41	0
41	SK	1412	0	1486	22	0
42	SM	1143	0	1210	26	0
43	SN	890	0	887	12	0
44	SO	1087	0	1152	16	0
45	SP	750	0	728	9	0
46	SR	973	0	1029	37	0
47	SX	1021	0	1060	27	0
48	SY	785	0	840	20	0
49	SZ	801	0	828	13	0
50	Sc	595	0	613	0	0
51	Sd	497	0	535	0	0
52	Sf	251	0	277	0	0
53	Sg	397	0	399	0	0
54	U1	1425	0	329	23	0
55	U2	365	0	75	0	0
56	U3	7035	0	1590	5	0
57	U4	990	0	1054	13	0
58	U5	2009	0	2130	16	0
59	UA	1690	0	370	0	0
60	UB	2775	0	620	1	0
61	UC	3300	0	727	12	0
All	All	173863	0	129519	2467	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 9.

The worst 5 of 2467 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)
12:AE:630:TYR:CE1	12:AE:637:ILE:CD1	1.86	1.56
34:SA:283:U:N3	34:SA:283:U:C2	1.75	1.54
34:SA:283:U:N1	34:SA:283:U:C6	1.70	1.54
34:SA:283:U:N3	34:SA:283:U:C4	1.74	1.53
34:SA:283:U:C2	34:SA:283:U:N1	1.74	1.52

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	
2	3B	237/327 (72%)	227 (96%)	10 (4%)	0	100	100
2	3C	237/327 (72%)	216 (91%)	21 (9%)	0	100	100
3	3D	366/504 (73%)	343 (94%)	23 (6%)	0	100	100
4	3E	378/511 (74%)	358 (95%)	20 (5%)	0	100	100
5	3F	353/573 (62%)	334 (95%)	19 (5%)	0	100	100
6	3G	120/126 (95%)	114 (95%)	6 (5%)	0	100	100
6	3H	120/126 (95%)	118 (98%)	2 (2%)	0	100	100
12	AE	751/1769 (42%)	703 (94%)	48 (6%)	0	100	100
15	B1	528/1183 (45%)	481 (91%)	47 (9%)	0	100	100
16	BA	747/923 (81%)	669 (90%)	76 (10%)	2 (0%)	37	73
17	BB	770/943 (82%)	682 (89%)	86 (11%)	2 (0%)	37	73
18	BC	779/817 (95%)	678 (87%)	96 (12%)	5 (1%)	22	60
19	BD	317/594 (53%)	278 (88%)	39 (12%)	0	100	100
20	BE	741/939 (79%)	699 (94%)	42 (6%)	0	100	100
21	CA	190/297 (64%)	180 (95%)	10 (5%)	0	100	100
22	CB	1086/1237 (88%)	1059 (98%)	27 (2%)	0	100	100
23	E1	213/252 (84%)	209 (98%)	4 (2%)	0	100	100
23	E2	210/252 (83%)	204 (97%)	6 (3%)	0	100	100
24	E3	256/483 (53%)	242 (94%)	12 (5%)	2 (1%)	16	55
26	K1	173/316 (55%)	167 (96%)	6 (4%)	0	100	100
27	MA	131/183 (72%)	128 (98%)	3 (2%)	0	100	100
28	MB	182/290 (63%)	168 (92%)	14 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	MC	24/593 (4%)	24 (100%)	0	0	100	100
30	P1	171/274 (62%)	161 (94%)	10 (6%)	0	100	100
31	R1	353/367 (96%)	348 (99%)	5 (1%)	0	100	100
32	R2	266/1729 (15%)	262 (98%)	4 (2%)	0	100	100
35	SC	212/255 (83%)	170 (80%)	37 (18%)	5 (2%)	5	27
36	SF	235/261 (90%)	210 (89%)	24 (10%)	1 (0%)	30	68
37	SG	204/225 (91%)	181 (89%)	21 (10%)	2 (1%)	13	49
38	SH	170/236 (72%)	159 (94%)	11 (6%)	0	100	100
39	SI	161/190 (85%)	142 (88%)	18 (11%)	1 (1%)	22	60
40	SJ	166/200 (83%)	146 (88%)	19 (11%)	1 (1%)	22	60
41	SK	173/197 (88%)	157 (91%)	15 (9%)	1 (1%)	22	60
42	SM	139/156 (89%)	124 (89%)	13 (9%)	2 (1%)	9	41
43	SN	122/143 (85%)	83 (68%)	35 (29%)	4 (3%)	3	21
44	SO	132/151 (87%)	129 (98%)	3 (2%)	0	100	100
45	SP	107/137 (78%)	95 (89%)	12 (11%)	0	100	100
46	SR	123/143 (86%)	113 (92%)	8 (6%)	2 (2%)	8	38
47	SX	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
48	SY	101/145 (70%)	82 (81%)	16 (16%)	3 (3%)	3	23
49	SZ	99/135 (73%)	88 (89%)	11 (11%)	0	100	100
50	Sc	77/82 (94%)	67 (87%)	10 (13%)	0	100	100
51	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
52	Sf	28/63 (44%)	28 (100%)	0	0	100	100
53	Sg	49/152 (32%)	37 (76%)	12 (24%)	0	100	100
57	U4	124/189 (66%)	115 (93%)	8 (6%)	1 (1%)	16	55
58	U5	246/274 (90%)	229 (93%)	17 (7%)	0	100	100
All	All	12555/19466 (64%)	11579 (92%)	942 (8%)	34 (0%)	38	73

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	BC	298	SER
24	E3	306	ALA
35	SC	207	LEU

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Mol	Chain	Res	Type
35	SC	209	ASN
37	SG	50	GLU

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	
2	3B	202/240 (84%)	200 (99%)	2 (1%)	73	82
2	3C	202/240 (84%)	202 (100%)	0	100	100
3	3D	317/435 (73%)	315 (99%)	2 (1%)	84	88
4	3E	314/433 (72%)	312 (99%)	2 (1%)	84	88
5	3F	317/503 (63%)	316 (100%)	1 (0%)	91	92
6	3G	101/104 (97%)	100 (99%)	1 (1%)	73	82
6	3H	101/104 (97%)	100 (99%)	1 (1%)	73	82
12	AE	698/744 (94%)	688 (99%)	10 (1%)	62	75
15	B1	471/1039 (45%)	466 (99%)	5 (1%)	70	80
16	BA	663/812 (82%)	653 (98%)	10 (2%)	60	75
17	BB	687/832 (83%)	676 (98%)	11 (2%)	58	73
18	BC	687/719 (96%)	683 (99%)	4 (1%)	84	88
19	BD	281/529 (53%)	277 (99%)	4 (1%)	62	75
20	BE	657/819 (80%)	654 (100%)	3 (0%)	86	89
21	CA	178/274 (65%)	177 (99%)	1 (1%)	84	88
22	CB	1000/1125 (89%)	994 (99%)	6 (1%)	84	88
23	E1	191/222 (86%)	191 (100%)	0	100	100
23	E2	193/222 (87%)	193 (100%)	0	100	100
24	E3	232/424 (55%)	228 (98%)	4 (2%)	56	72
26	K1	158/289 (55%)	158 (100%)	0	100	100
27	MA	123/172 (72%)	121 (98%)	2 (2%)	58	73
28	MB	164/258 (64%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	MC	24/148 (16%)	24 (100%)	0	100	100
30	P1	151/238 (63%)	150 (99%)	1 (1%)	81	87
31	R1	302/312 (97%)	301 (100%)	1 (0%)	91	92
32	R2	235/1544 (15%)	233 (99%)	2 (1%)	75	83
35	SC	191/224 (85%)	191 (100%)	0	100	100
36	SF	203/222 (91%)	199 (98%)	4 (2%)	50	68
37	SG	173/191 (91%)	171 (99%)	2 (1%)	67	78
38	SH	141/201 (70%)	138 (98%)	3 (2%)	48	66
39	SI	146/170 (86%)	146 (100%)	0	100	100
40	SJ	138/161 (86%)	137 (99%)	1 (1%)	81	87
41	SK	149/166 (90%)	145 (97%)	4 (3%)	40	58
42	SM	128/137 (93%)	123 (96%)	5 (4%)	27	48
43	SN	88/119 (74%)	85 (97%)	3 (3%)	32	51
44	SO	117/128 (91%)	115 (98%)	2 (2%)	56	72
45	SP	66/105 (63%)	66 (100%)	0	100	100
46	SR	105/119 (88%)	103 (98%)	2 (2%)	52	69
47	SX	110/111 (99%)	110 (100%)	0	100	100
48	SY	85/120 (71%)	84 (99%)	1 (1%)	67	78
49	SZ	85/113 (75%)	83 (98%)	2 (2%)	44	62
50	Sc	68/71 (96%)	68 (100%)	0	100	100
51	Sd	56/60 (93%)	53 (95%)	3 (5%)	18	40
52	Sf	27/54 (50%)	27 (100%)	0	100	100
53	Sg	43/135 (32%)	42 (98%)	1 (2%)	45	64
57	U4	110/169 (65%)	110 (100%)	0	100	100
58	U5	231/256 (90%)	229 (99%)	2 (1%)	75	83
All	All	11109/15813 (70%)	11001 (99%)	108 (1%)	71	82

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	CB	155	ASN
32	R2	1466	ARG
48	SY	144	ARG

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Mol	Chain	Res	Type
22	CB	216	LYS
24	E3	304	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 149 such sidechains are listed below:

Mol	Chain	Res	Type
32	R2	1661	GLN
57	U4	57	GLN
35	SC	146	GLN
39	SI	147	ASN
17	BB	20	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	151/333 (45%)	31 (20%)	1 (0%)
34	SA	1091/1812 (60%)	268 (24%)	22 (2%)
7	5A	452/700 (64%)	102 (22%)	4 (0%)
All	All	1694/2845 (59%)	401 (23%)	27 (1%)

5 of 401 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	9	A
1	3A	14	A
1	3A	15	U
1	3A	22	A
1	3A	24	U

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	SA	503	G
34	SA	929	A
34	SA	1441	C
34	SA	913	G
34	SA	1083	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6695. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.