



## wwPDB EM Map/Model Validation Report ⓘ

Jul 26, 2016 – 05:53 AM EDT

PDB ID : 5JPQ  
EMDB ID: : EMD-8143  
Title : Cryo-EM structure of the 90S pre-ribosome  
Authors : Turk, M.; Cheng, J.; Berninghausen, O.; Kornprobst, M.; Flemming, D.; Kos-Braun, I.C.; Kos, M.; Thoms, M.; Hurt, E.; Beckmann, R.  
Deposited on : 2016-05-04  
Resolution : 7.30 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
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>

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MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027939

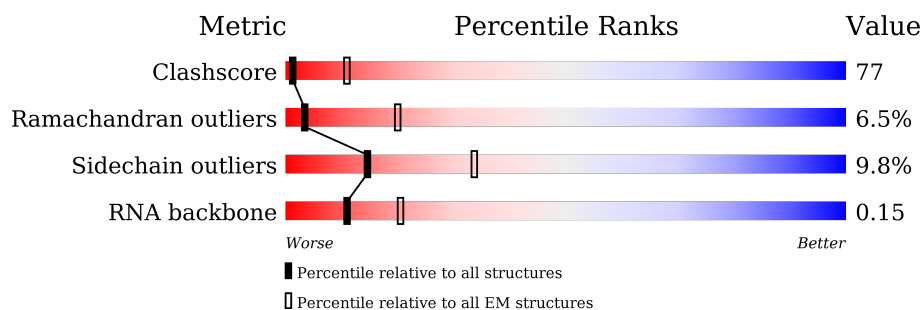
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 7.30 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.
























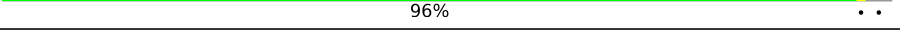
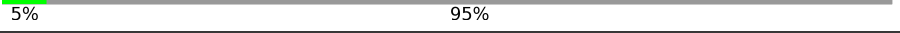


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	A	1290	22% 77%
1	B	1290	21% 77%
1	C	1290	21% 77%
1	D	1290	20% 77%
1	E	1290	20% 77%
1	F	1290	21% 77%
1	J	1290	21% 77%
1	K	1290	21% 77%











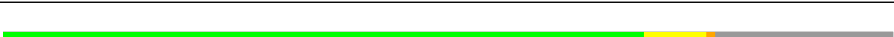


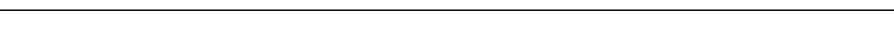
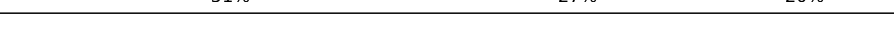
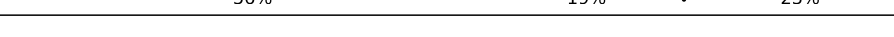

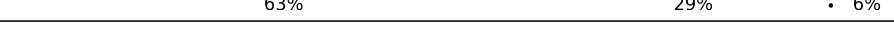

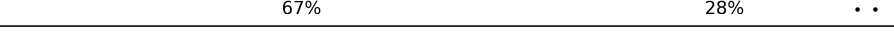
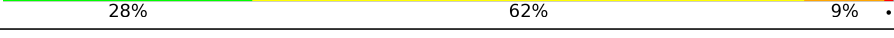
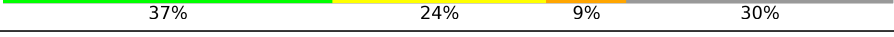

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Mol	Chain	Length	Quality of chain
1	L	1290	 21% . 77%
1	N	1290	 21% . 77%
1	P	1290	 21% . 77%
1	l	1290	 23% 77%
1	n	1290	 23% 77%
2	G	1802	 13% . 84%
3	H	920	 29% 5% . 63%
4	I	939	 67% . 32%
5	M	870	 31% . 64%
5	O	870	 32% . 64%
5	m	870	 36% 64%
6	Q	456	 78% . 18%
7	R	560	 58% . 41%
8	S	412	 85% . 11%
8	T	412	 84% 5% 11%
9	U	130	 82% 12% . 6%
9	V	130	 82% 12% . 6%
10	W	232	 91% 6% .
10	X	232	 91% 6% .
11	Y	573	 63% . 36%
12	Z	367	 96% . .
13	a	1183	 5% 95%
14	b	183	 76% 7% . 16%
15	c	297	 56% 6% . 35%
16	d	184	 52% 15% . 33%

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Mol	Chain	Length	Quality of chain
17	e	252	
17	f	252	
18	g	322	
18	h	322	
19	i	1073	
19	j	1073	
20	k	391	
21	o	265	
22	p	259	
23	q	225	
24	r	293	
25	s	197	
26	t	208	
27	u	197	
28	v	151	
29	w	137	
30	x	143	
31	y	157	
32	z	130	
33	0	149	
34	1	67	
35	2	1800	
36	3	274	

## 2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 95839 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called WD40 domain proteins.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	300	Total	C	N	O	0	0
			1500	900	300	300		
1	B	300	Total	C	N	O	0	0
			1500	900	300	300		
1	C	300	Total	C	N	O	0	0
			1500	900	300	300		
1	D	300	Total	C	N	O	0	0
			1500	900	300	300		
1	E	300	Total	C	N	O	0	0
			1500	900	300	300		
1	F	300	Total	C	N	O	0	0
			1500	900	300	300		
1	J	300	Total	C	N	O	0	0
			1500	900	300	300		
1	K	300	Total	C	N	O	0	0
			1500	900	300	300		
1	L	300	Total	C	N	O	0	0
			1500	900	300	300		
1	N	300	Total	C	N	O	0	0
			1500	900	300	300		
1	P	300	Total	C	N	O	0	0
			1500	900	300	300		
1	l	300	Total	C	N	O	0	0
			1500	900	300	300		
1	n	300	Total	C	N	O	0	0
			1500	900	300	300		

- Molecule 2 is a protein called UTP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	283	Total	C	N	O	0	0
			1402	836	283	283		

- Molecule 3 is a protein called UTP-A oligomerization domain.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	H	343	Total	C	N	O	0	0
			1715	1029	343	343		

- Molecule 4 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	I	634	Total	C	N	O	0	0
			3124	1856	634	634		

- Molecule 5 is a protein called WD40 domain proteins.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	309	Total	C	N	O	0	0
			1545	927	309	309		
5	O	309	Total	C	N	O	0	0
			1545	927	309	309		
5	m	309	Total	C	N	O	0	0
			1545	927	309	309		

- Molecule 6 is a protein called UTP6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	Q	375	Total	C	N	O	0	0
			1875	1125	375	375		

- Molecule 7 is a protein called UTP-B oligomerisation domain.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	R	332	Total	C	N	O	0	0
			1660	996	332	332		

- Molecule 8 is a protein called Pre mRNA splicing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	S	367	Total	C	N	O	0	0
			1815	1081	367	367		
8	T	367	Total	C	N	O	0	0
			1815	1081	367	367		

- Molecule 9 is a protein called Snu13.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	122	Total	C	N	O	0	0
			603	359	122	122		
9	V	122	Total	C	N	O	0	0
			603	359	122	122		

- Molecule 10 is a protein called Nop1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	W	227	Total	C	N	O	0	0
			1124	670	227	227		
10	X	227	Total	C	N	O	0	0
			1124	670	227	227		

- Molecule 11 is a protein called rrp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Y	365	Total	C	N	O	0	0
			1799	1069	365	365		

- Molecule 12 is a protein called Rcl1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Z	355	Total	C	N	O	0	0
			1742	1032	355	355		

- Molecule 13 is a protein called Bms1.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	a	54	Total	C	N	O	0	0
			267	160	54	53		

- Molecule 14 is a protein called Imp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	b	153	Total	C	N	O	0	0
			760	454	153	153		

- Molecule 15 is a protein called Putative U3 small nucleolar ribonucleoprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	c	192	Total	C	N	O	0	0
			951	567	192	192		

- Molecule 16 is a protein called Utp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	d	124	Total	C	N	O	0	0
			616	368	124	124		

- Molecule 17 is a protein called Emg1.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	e	211	Total	C	N	O	0	0
			1047	625	211	211		
17	f	218	Total	C	N	O	0	0
			1081	645	218	218		

- Molecule 18 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	g	174	Total	C	N	O	0	0
			861	513	174	174		
18	h	174	Total	C	N	O	0	0
			861	513	174	174		

- Molecule 19 is a protein called Kre33.

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

- Molecule 20 is a protein called Utp30.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	k	182	Total	C	N	O	0	0
			905	541	182	182		

- Molecule 21 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	o	215	Total	C	N	O	S	0	0
			1724	1090	314	316	4		

- Molecule 22 is a protein called eS4.



Mol	Chain	Residues	Atoms					AltConf	Trace
22	p	259	Total	C	N	O	S	0	0
			2079	1322	383	370	4		

- Molecule 23 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	q	169	Total	C	N	O		0	0
			836	498	169	169			

- Molecule 24 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	r	235	Total	C	N	O	S	0	0
			1868	1184	347	326	11		

- Molecule 25 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	s	186	Total	C	N	O	S	0	0
			1539	989	271	278	1		

- Molecule 26 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	t	207	Total	C	N	O	S	0	0
			1693	1057	336	296	4		

- Molecule 27 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	u	157	Total	C	N	O		0	0
			777	463	157	157			

- Molecule 28 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	v	117	Total	C	N	O		0	0
			580	346	117	117			

- Molecule 29 is a protein called uS11.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	w	128	Total	C	N	O	0	0
			627	371	128	128		

- Molecule 30 is a protein called uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	x	134	Total	C	N	O	0	0
			658	390	134	134		

- Molecule 31 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	157	Total	C	N	O	S	0	0
			1275	818	235	217	5		

- Molecule 32 is a protein called uS8.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	z	127	Total	C	N	O	0	0
			622	368	127	127		

- Molecule 33 is a protein called eS24.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	0	148	Total	C	N	O	0	0
			1197	763	221	213		

- Molecule 34 is a protein called eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	1	47	Total	C	N	O	0	0
			230	136	47	47		

- Molecule 35 is a RNA chain called 18s RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2	852	Total	C	N	O	P	0	0
			18149	8120	3229	5948	852		

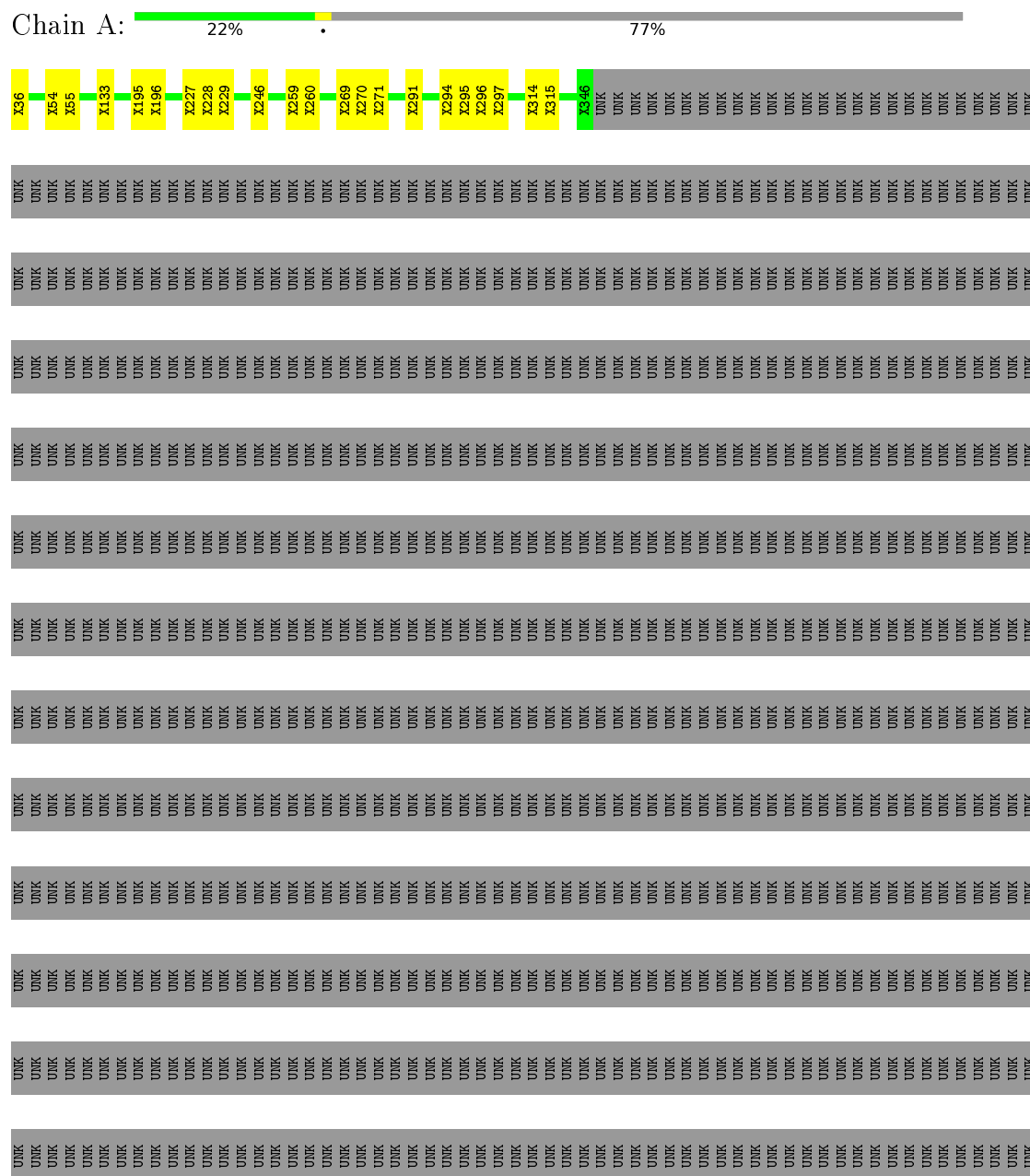
- Molecule 36 is a RNA chain called U3 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	3	164	Total	C	N	O	P	0	0
			3504	1560	626	1154	164		

### 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 errors 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.

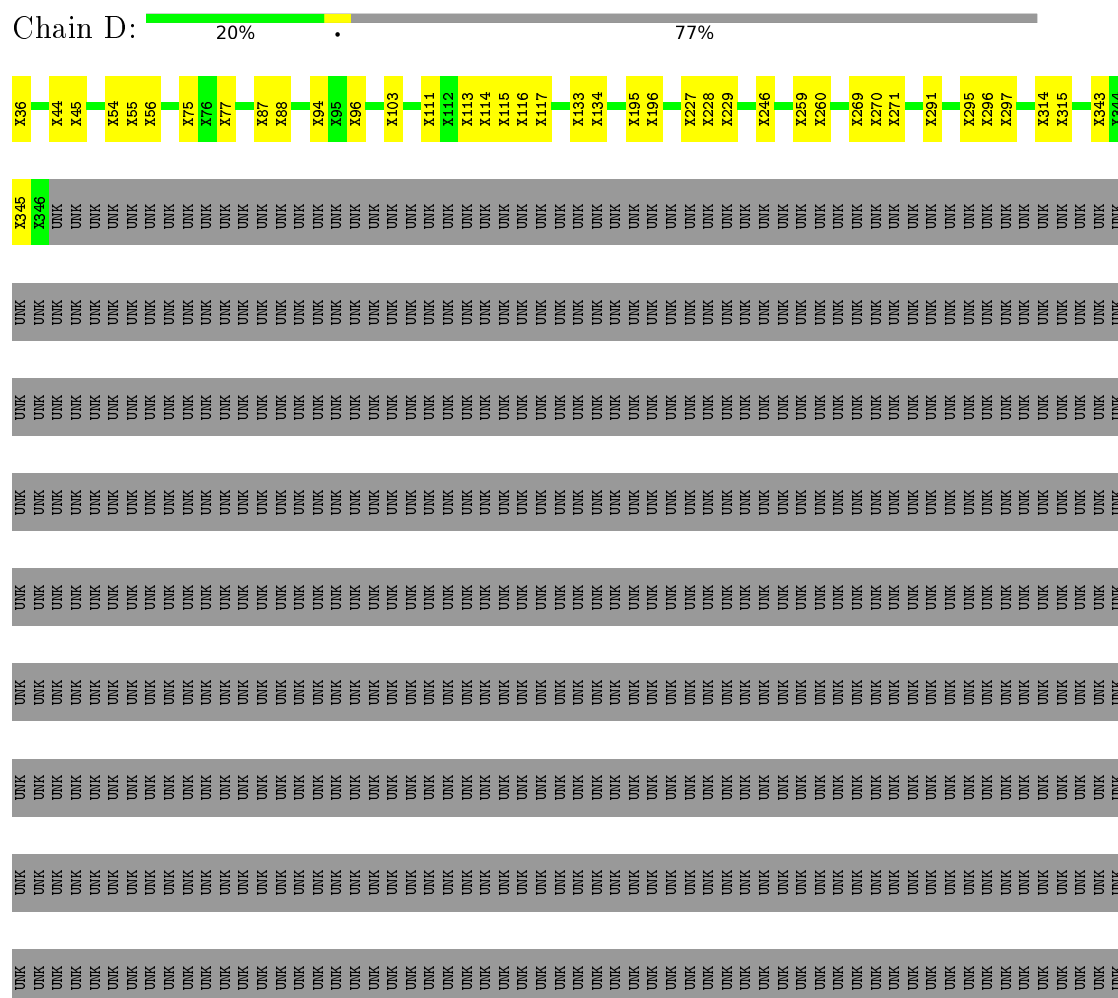
- Molecule 1: WD40 domain proteins





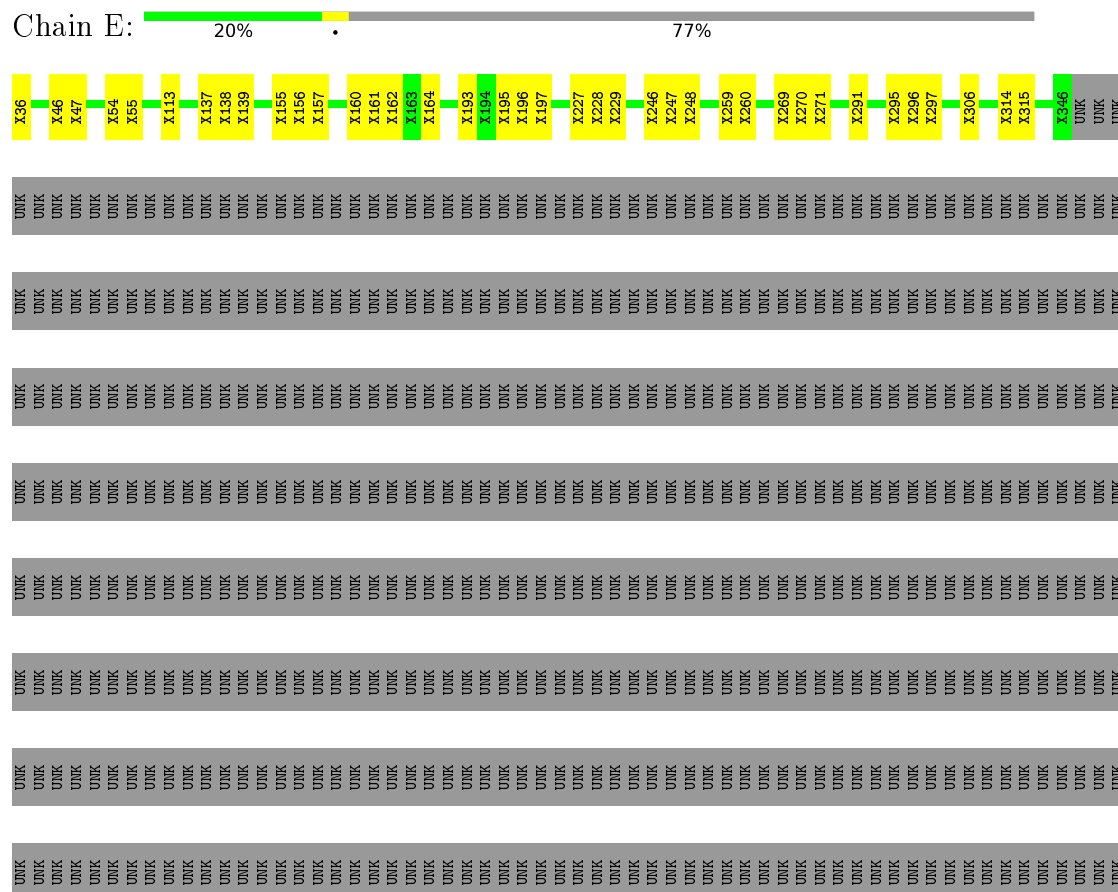


- Molecule 1: WD40 domain proteins

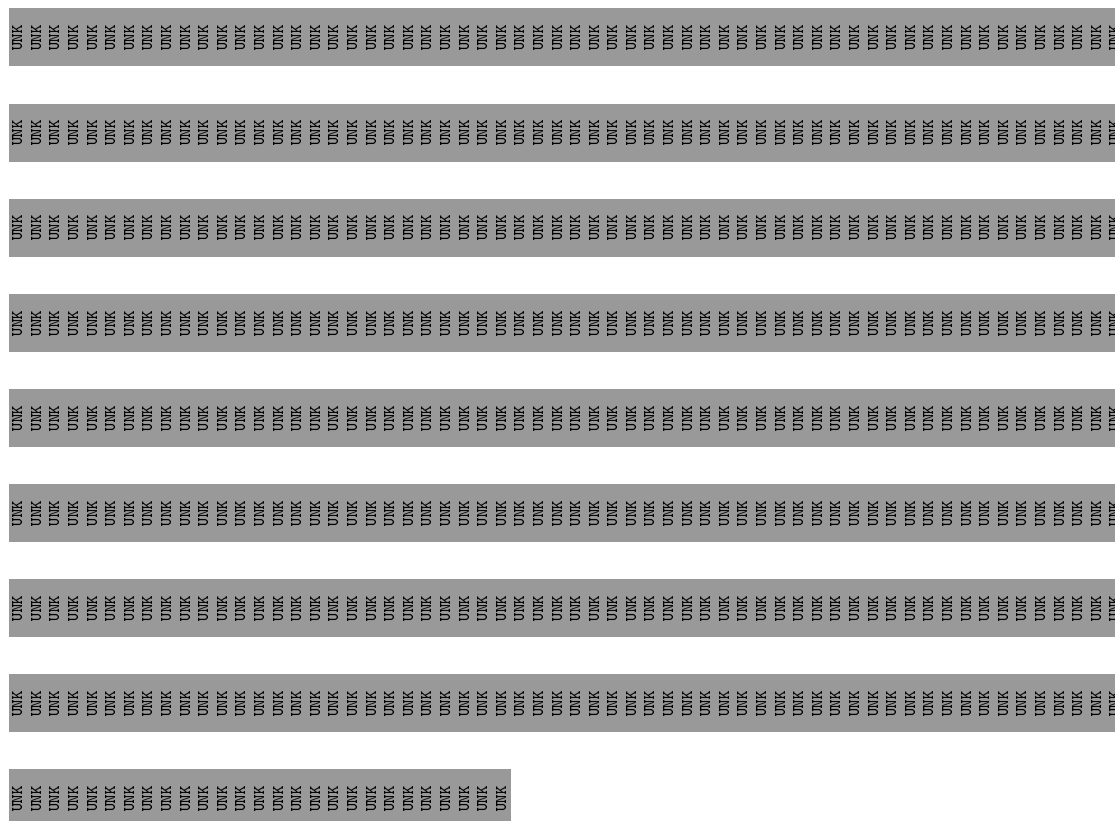


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- Molecule 1: WD40 domain proteins







- Molecule 1: WD40 domain proteins



- Molecule 1: WD40 domain proteins

Chain J:  21% . 77%

[illegible]

[illegible]

- Molecule 1: WD40 domain proteins

Chain K:  21% . 77%

[illegible]

[illegible]

- Molecule 1: WD40 domain proteins

Chain L:  21% • 77%

[illegible]

[illegible]

- Molecule 1: WD40 domain proteins

Chain N:  21% . 77%

[illegible]

[illegible]

- Molecule 1: WD40 domain proteins

Chain P:  21% . 77%

[illegible]














[illegible][illegible]

- Molecule 4: U3 small nucleolar RNA-associated protein 21

Chain I:  67% . 32%

NET	SER	LEU	ASP	LVS	LVS	ARG	VAL	GLU	ASP	VAL	ARG	ARG	GLY	LVS	1020	T227	G228	E229	1246	P326	SER	LEU	SER	GLN	GLY	SER	GLY	ASP	VAL	VAL	VAL	Q338	P332	LEU	HIS	LVS	LVS	GLN	ASP	GLY	GLY	GLY	GLY	THR	LVS	S409
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[illegible]

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

LYS LEU LEU ASP ALA GLU GLN MET LYS PHE PHE VAL THR GLY ARG LEU GLY PHE GLU SER SER HIS PHE THR LYS GLN LEU ARG GLU GLY SER GLN SER SER LYS ASP TYR SER SER LEU LEU LEU THR LEU LEU ASN PHE PHE SER PRO ALA VAL ASP LEU GLU LEU ARG SER ASN SER

PHE GLU PRO PRO PHE ASP PHE GLU LEU VAL TRP PHE PHE LEU ASP ALA LEU THR LEU GLN GLY LEU LYS SER SER ASN LYS ASN PHE PHE GLU LEU TYR THR PHE MET SER SER LEU LEU PHE LYS ALA ALA HIS ASP ASN ASN LYS ASN GLN LEU LEU THR TRP LYS GLU

VAL	HIS	LYS	LYS	GLU	ASP	ARG	LEU	ASP	ASP	LEU	VAL	LYS	PHE	CYS	MET	GLY	VAL	ALA	ALA	PHE	VAL	THR	THR	ALA
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- Molecule 5: WD40 domain proteins

Chain M:  31% 1% 64%

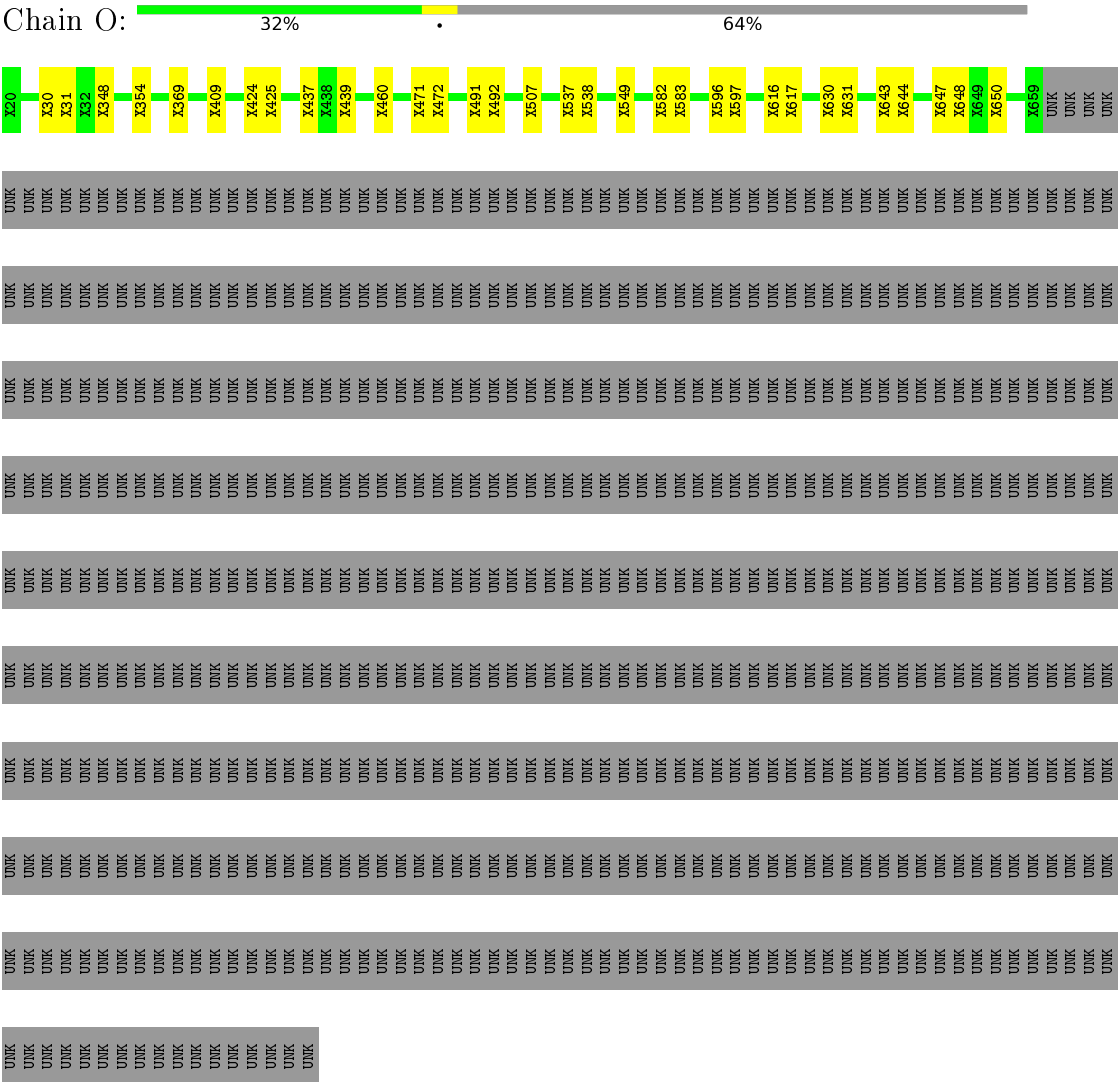
X20	X30	X31	X32	X348	X349	X350	X351	X354	X359	X372	X424	X425	X471	X472	X481	X482	X491	X492	X501	X507	X537	X538	X549	X562	X583	X596	X597	X616	X617	X630	X631	X643	X644	X645	X646	X647	X648	X649	X650	X659
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UNK

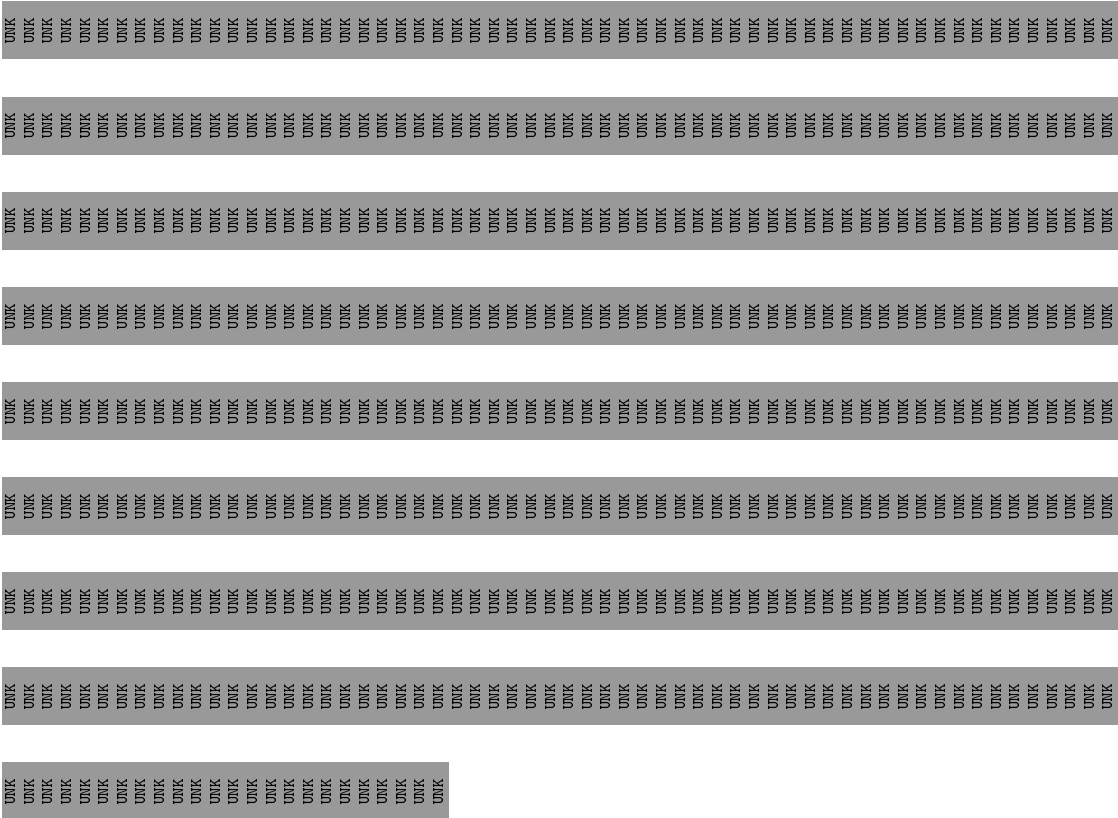


● Molecule 5: WD40 domain proteins

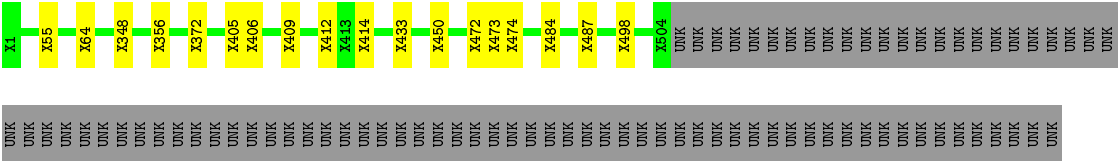
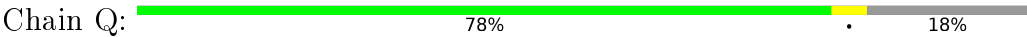


● Molecule 5: WD40 domain proteins

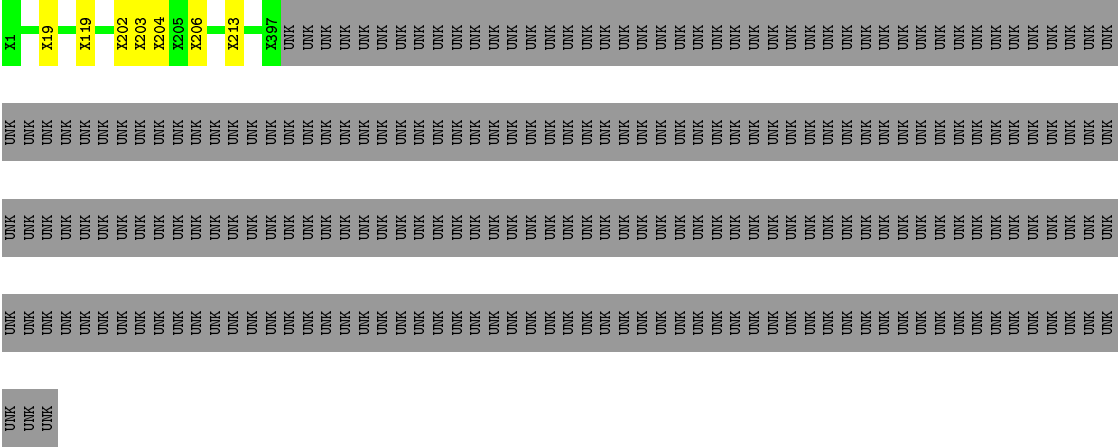





● Molecule 6: UTP6

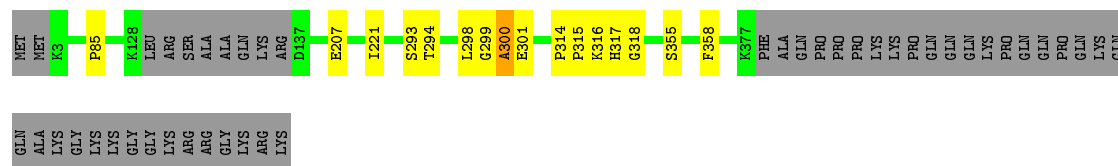


● Molecule 7: UTP-B oligomerisation domain




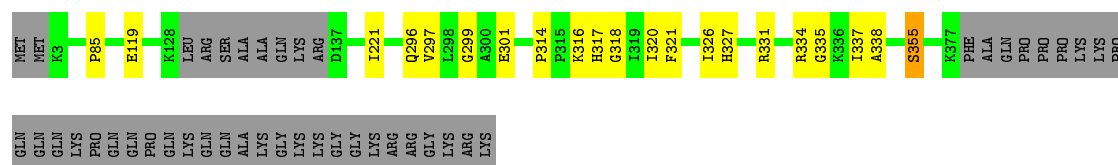
- Molecule 8: Pre mRNA splicing protein

Chain S:  85% 11%




- Molecule 8: Pre mRNA splicing protein

Chain T:  84% 5% 11%




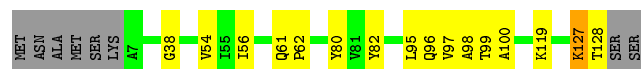
- Molecule 9: Snul3

Chain U:  82% 12% 6%



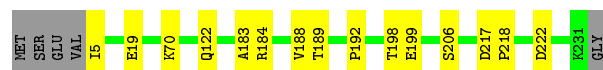
- Molecule 9: Snul3

Chain V:  82% 12% 6%



- Molecule 10: Nop1

Chain W:  91% 6%



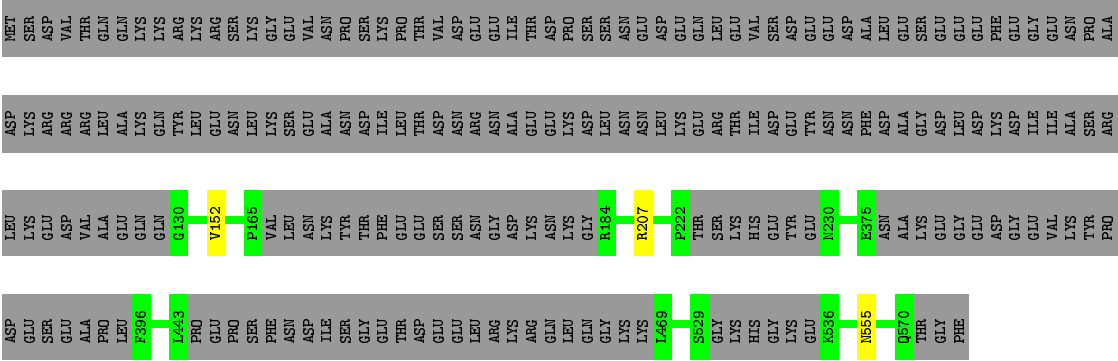
- Molecule 10: Nop1

Chain X:  91% 6%



- Molecule 11: rrp9

Chain Y:  63% 36%



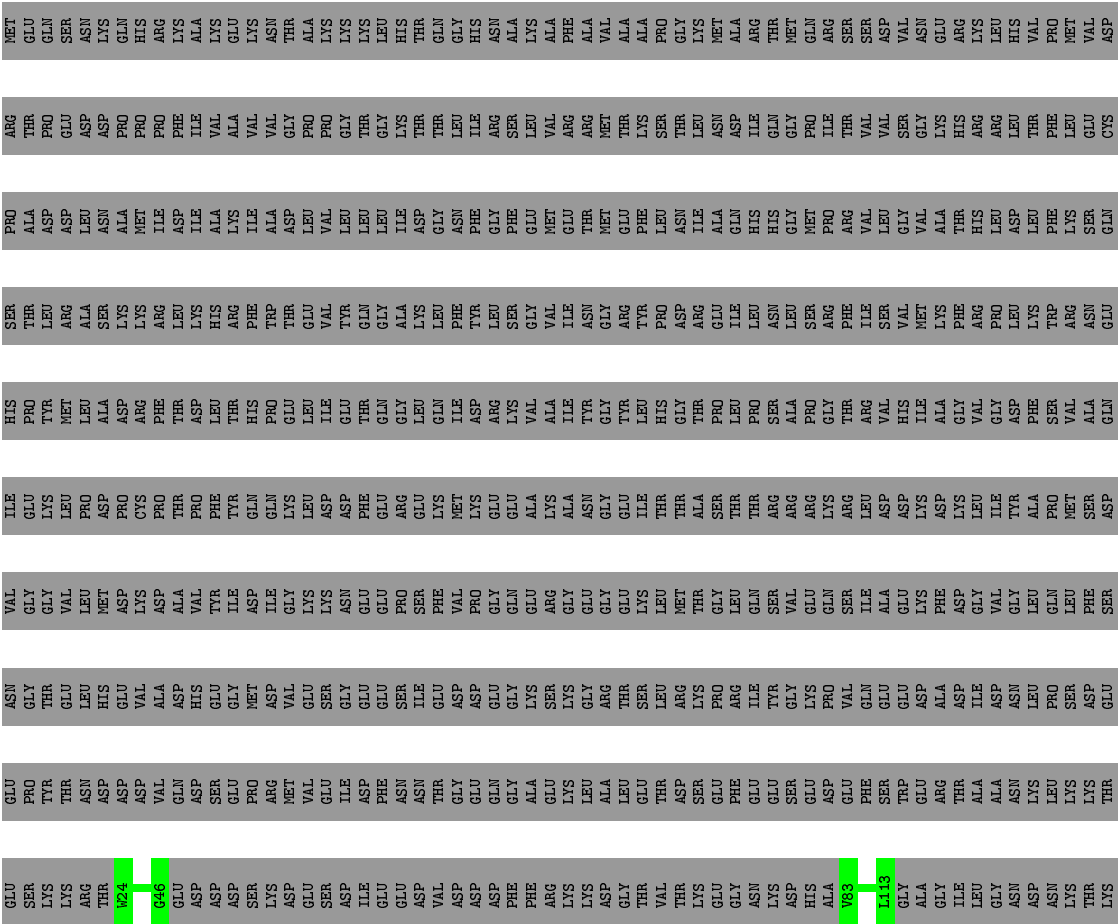
● Molecule 12: Rcl1

Chain Z: 96%



● Molecule 13: Bms1

Chain a: 5%





[illegible]

- Molecule 14: Imp3

Chain b:  76% 7% • 16%

MET	VAL	ARG	LYS	LEU	LYS	THR	HIS	GLU	GLN	LYS	LEU	LYS	LEU	LYS	LEU	LYS	GLN	ASN	ILE	MET	LYS	THR	ARG	ASP	LYS	LEU	LYS	ASP	ASP	PHE	GLU	LEU
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- Molecule 15: Putative U3 small nucleolar ribonucleoprotein

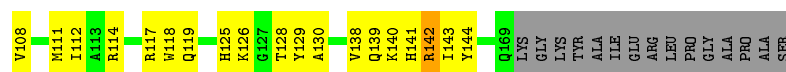
Chain c:  56% 6% 35%

[illegible]

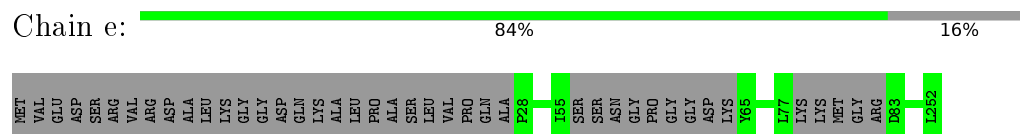
- Molecule 16: Utp24

Chain d:  52% 15% 33%

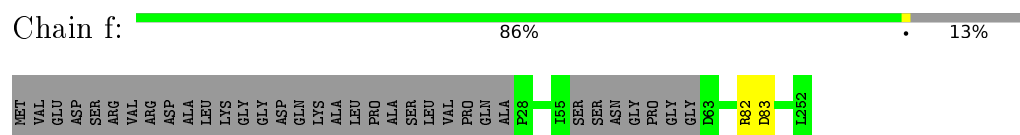
MET	GLY	VAL	LYS	ARG	ILE	LEU	GLY	GLN	ASP	GLU	ARG	ARG	ARG	LYS	ALA	ALA	ALA	ILE	ARG	GLU	VAL	LYS	LYS	LYS	GLU	GLU	GLU	GLN	ALA	ALA	ALA	ILE	ARG	GLU	VAL	PHE	F46	E47	H48	N49	E50			P74	K101	L102	P103	P104	R105	I106	P107	P108	P109	P110	P111	P112	P113	P114	P115	P116	P117	P118	P119	P120	P121	P122	P123	P124	P125	P126	P127	P128	P129	P130	P131	P132	P133	P134	P135	P136	P137	P138	P139	P140	P141	P142	P143	P144	P145	P146	P147	P148	P149	P150	P151	P152	P153	P154	P155	P156	P157	P158	P159	P160	P161	P162	P163	P164	P165	P166	P167	P168	P169	P170	P171	P172	P173	P174	P175	P176	P177	P178	P179	P180	P181	P182	P183	P184	P185	P186	P187	P188	P189	P190	P191	P192	P193	P194	P195	P196	P197	P198	P199	P200	P201	P202	P203	P204	P205	P206	P207	P208	P209	P210	P211	P212	P213	P214	P215	P216	P217	P218	P219	P220	P221	P222	P223	P224	P225	P226	P227	P228	P229	P230	P231	P232	P233	P234	P235	P236	P237	P238	P239	P240	P241	P242	P243	P244	P245	P246	P247	P248	P249	P250	P251	P252	P253	P254	P255	P256	P257	P258	P259	P260	P261	P262	P263	P264	P265	P266	P267	P268	P269	P270	P271	P272	P273	P274	P275	P276	P277	P278	P279	P280	P281	P282	P283	P284	P285	P286	P287	P288	P289	P290	P291	P292	P293	P294	P295	P296	P297	P298	P299	P300	P301	P302	P303	P304	P305	P306	P307	P308	P309	P310	P311	P312	P313	P314	P315	P316	P317	P318	P319	P320	P321	P322	P323	P324	P325	P326	P327	P328	P329	P330	P331	P332	P333	P334	P335	P336	P337	P338	P339	P340	P341	P342	P343	P344	P345	P346	P347	P348	P349	P350	P351	P352	P353	P354	P355	P356	P357	P358	P359	P360	P361	P362	P363	P364	P365	P366	P367	P368	P369	P370	P371	P372	P373	P374	P375	P376	P377	P378	P379	P380	P381	P382	P383	P384	P385	P386	P387	P388	P389	P390	P391	P392	P393	P394	P395	P396	P397	P398	P399	P400	P401	P402	P403	P404	P405	P406	P407	P408	P409	P410	P411	P412	P413	P414	P415	P416	P417	P418	P419	P420	P421	P422	P423	P424	P425	P426	P427	P428	P429	P430	P431	P432	P433	P434	P435	P436	P437	P438	P439	P440	P441	P442	P443	P444	P445	P446	P447	P448	P449	P450	P451	P452	P453	P454	P455	P456	P457	P458	P459	P460	P461	P462	P463	P464	P465	P466	P467	P468	P469	P470	P471	P472	P473	P474	P475	P476	P477	P478	P479	P480	P481	P482	P483	P484	P485	P486	P487	P488	P489	P490	P491	P492	P493	P494	P495	P496	P497	P498	P499	P500	P501	P502	P503	P504	P505	P506	P507	P508	P509	P510	P511	P512	P513	P514	P515	P516	P517	P518	P519	P520	P521	P522	P523	P524	P525	P526	P527	P528	P529	P530	P531	P532	P533	P534	P535	P536	P537	P538	P539	P540	P541	P542	P543	P544	P545	P546	P547	P548	P549	P550	P551	P552	P553	P554	P555	P556	P557	P558	P559	P560	P561	P562	P563	P564	P565	P566	P567	P568	P569	P570	P571	P572	P573	P574	P575	P576	P577	P578	P579	P580	P581	P582	P583	P584	P585	P586	P587	P588	P589	P590	P591	P592	P593	P594	P595	P596	P597	P598	P599	P600	P601	P602	P603	P604	P605	P606	P607	P608	P609	P610	P611	P612	P613	P614	P615	P616	P617	P618	P619	P620	P621	P622	P623	P624	P625	P626	P627	P628	P629	P630	P631	P632	P633	P634	P635	P636	P637	P638	P639	P640	P641	P642	P643	P644	P645	P646	P647	P648	P649	P650	P651	P652	P653	P654	P655	P656	P657	P658	P659	P660	P661	P662	P663	P664	P665	P666	P667	P668	P669	P670	P671	P672	P673	P674	P675	P676	P677	P678	P679	P680	P681	P682	P683	P684	P685	P686	P687	P688	P689	P690	P691	P692	P693	P694	P695	P696	P697	P698	P699	P700	P701	P702	P703	P704	P705	P706	P707	P708	P709	P710	P711	P712	P713	P714	P715	P716	P717	P718	P719	P720	P721	P722	P723	P724	P725	P726	P727	P728	P729	P730	P731	P732	P733	P734	P735	P736	P737	P738	P739	P740	P741	P742	P743	P744	P745	P746	P747	P748	P749	P750	P751	P752	P753	P754	P755	P756	P757	P758	P759	P760	P761	P762	P763	P764	P765	P766	P767	P768	P769	P770	P771	P772	P773	P774	P775	P776	P777	P778	P779	P780	P781	P782	P783	P784	P785	P786	P787	P788	P789	P790	P791	P792	P793	P794	P795	P796	P797	P798	P799	P800	P801	P802	P803	P804	P805	P806	P807	P808	P809	P810	P811	P812	P813	P814	P815	P816	P817	P818	P819	P820	P821	P822	P823	P824	P825	P826	P827	P828	P829	P830	P831	P832	P833	P834	P835	P836	P837	P838	P839	P840	P841	P842	P843	P844	P845	P846	P847	P848	P849	P850	P851	P852	P853	P854	P855	P856	P857	P858	P859	P860	P861	P862	P863	P864	P865	P866	P867	P868	P869	P870	P871	P872	P873	P874	P875	P876	P877	P878	P879	P880	P881	P882	P883	P884	P885	P886	P887	P888	P889	P890	P891	P892	P893	P894	P895	P896	P897	P898	P899	P900	P901	P902	P903	P904	P905	P906	P907	P908	P909	P910	P911	P912	P913	P914	P915	P916	P917	P918	P919	P920	P921	P922	P923	P924	P925	P926	P927	P928	P929	P930	P931	P932	P933	P934	P935	P936	P937	P938	P939	P940	P941	P942	P943	P944	P945	P946	P947	P948	P949	P950	P951	P952	P953	P954	P955	P956	P957	P958	P959	P960	P961	P962	P963	P964	P965	P966	P967	P968	P969	P970	P971	P972	P973	P974	P975	P976	P977	P978	P979	P980	P981	P982	P983	P984	P985	P986	P987	P988	P989	P990	P991	P992	P993	P994	P995	P996	P997	P998	P999	P1000
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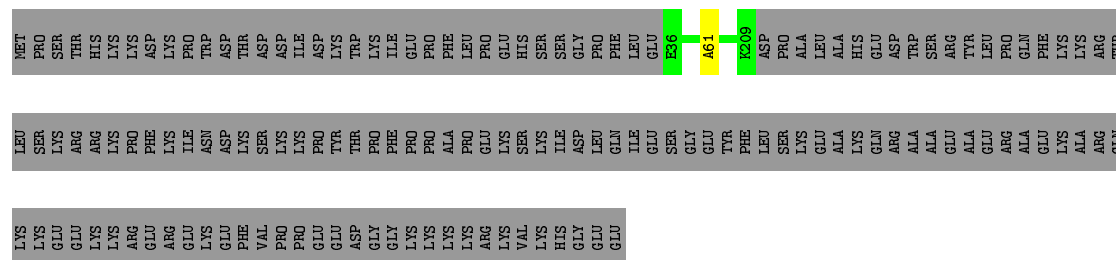
- Molecule 17: Emg1



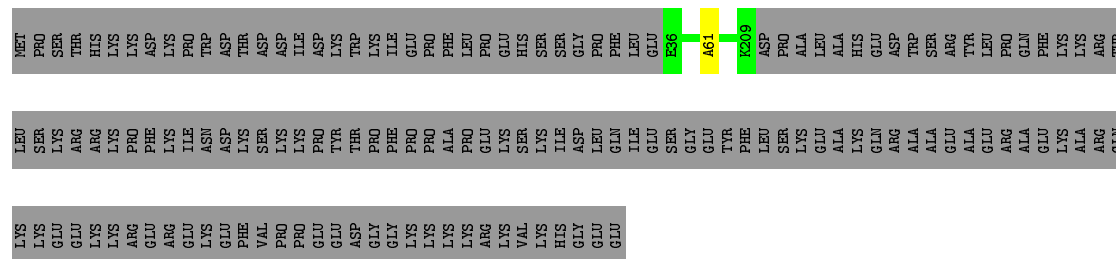
- Molecule 17: Emg1



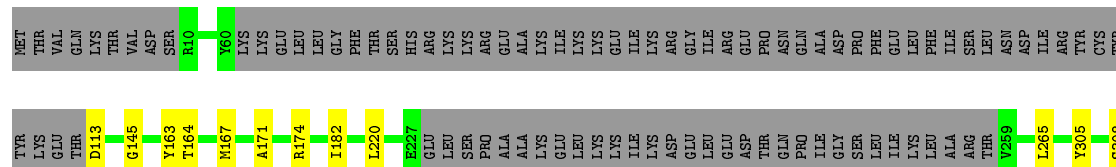
- Molecule 18: KRR1 small subunit processome component



- Molecule 18: KRR1 small subunit processome component



- Molecule 19: Kre33

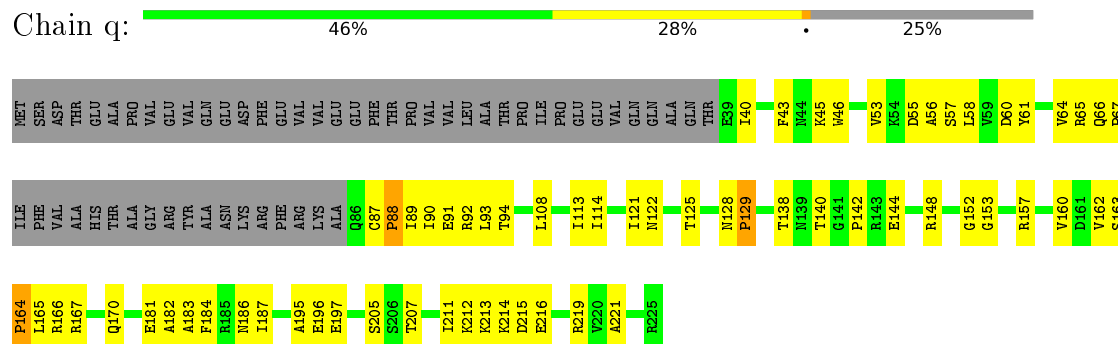




- Molecule 21: eS1

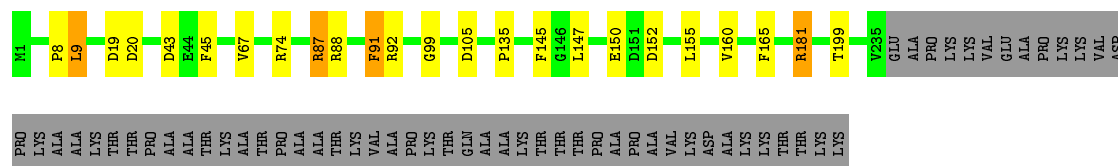
- Molecule 22: eS4

- Molecule 23: uS7



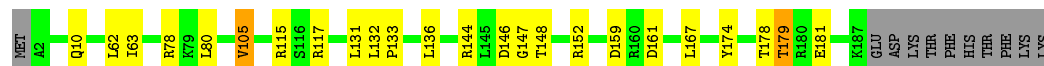
- Molecule 24: eS6

Chain r:  72% 7% • 20%



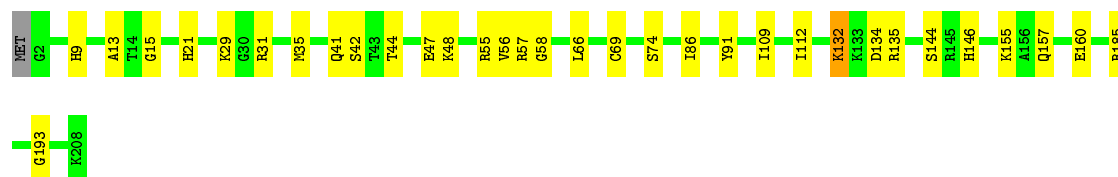
- Molecule 25: eS7

Chain s:  82% 11% • 6%



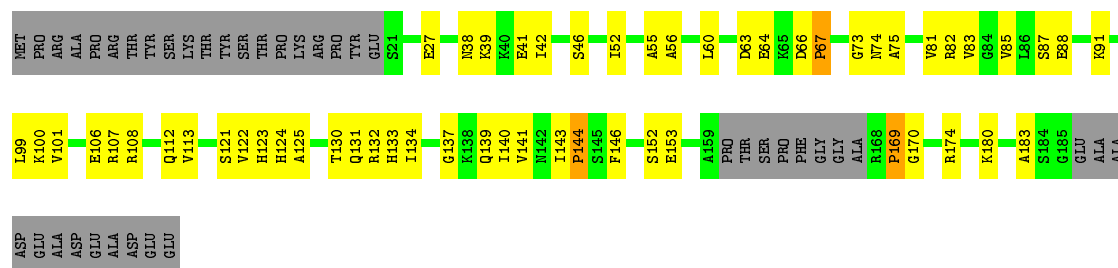
- Molecule 26: eS8

Chain t:  84% 15%



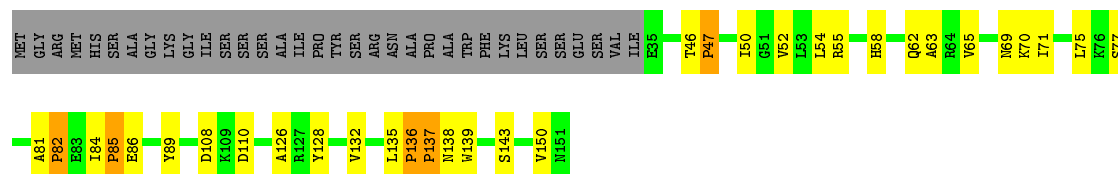
- Molecule 27: uS4

Chain u: 



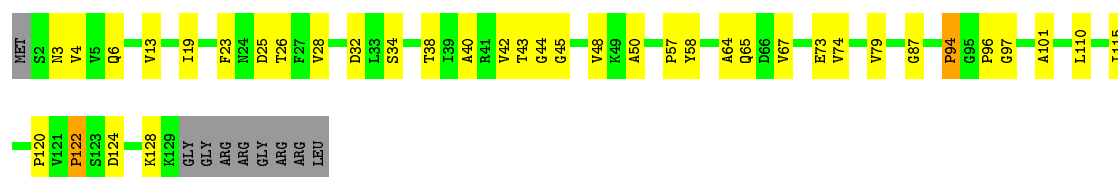
- Molecule 28: uS15

Chain v:  56% 19% . 23%



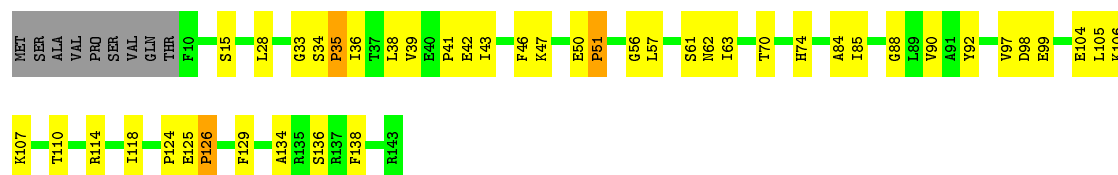
- Molecule 29: uS11

Chain w:  66% 26% 7%



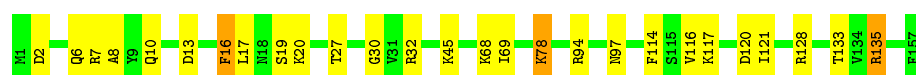
• Molecule 30: uS9

Chain x: 63% 29% 6%



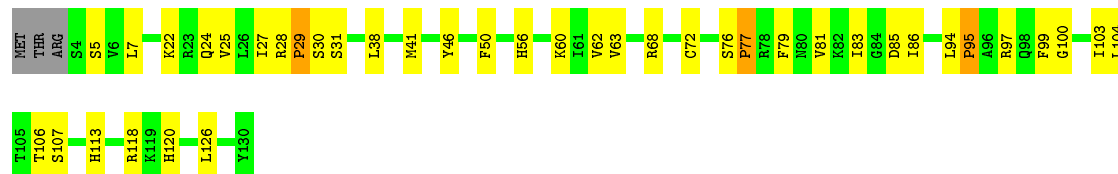
• Molecule 31: uS17

Chain y: 83% 15% 2%



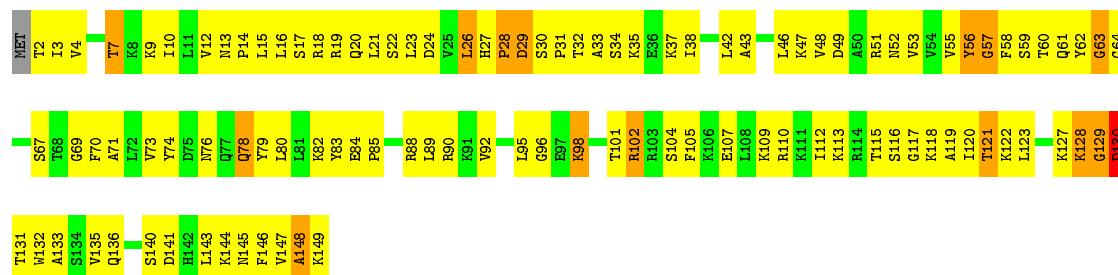
• Molecule 32: uS8

Chain z: 67% 28% 5%



• Molecule 33: eS24

Chain 0: 28% 62% 9%



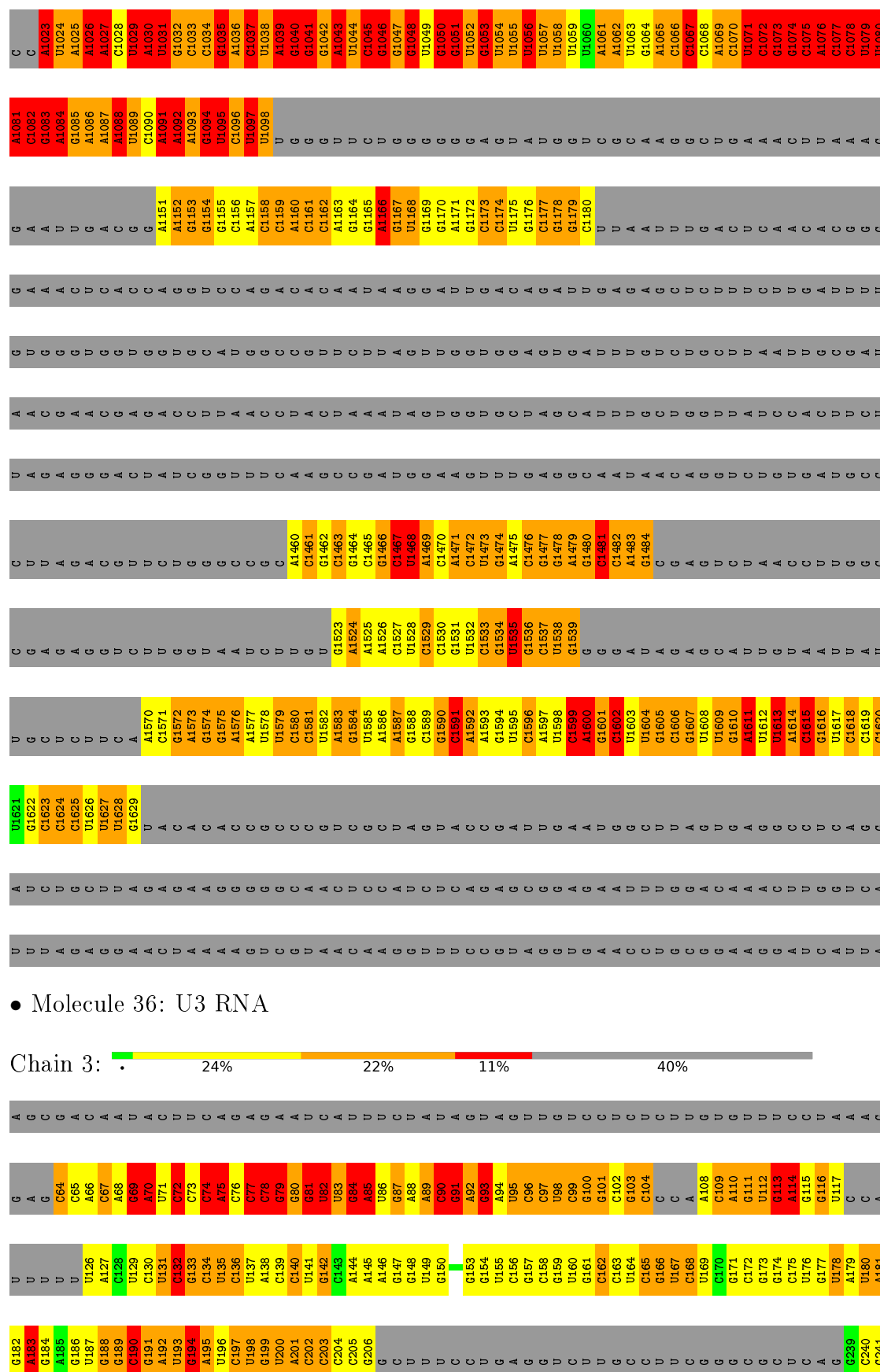
• Molecule 34: eS28

Chain 1: 37% 24% 9% 30%



Chain 2: 5% 16% 26% 53%







G242	G243	G244	U245	G246	G247	G248	U249	G250	U251	G252	G253	A254	U255	G256	G257	A258	A259	G260	U261	G262	U263	G264	A265	G266	G267	G268	G269	G270	C	A	U	U
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## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	43000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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  >2	RMSZ	# Z  >2
10	W	0.40	0/1123	0.62	0/1564
10	X	0.35	0/1123	0.57	0/1564
11	Y	0.23	0/1793	0.52	0/2485
12	Z	0.45	0/1741	0.70	0/2416
13	a	0.48	0/265	0.70	0/367
14	b	0.72	0/759	1.01	2/1058 (0.2%)
15	c	0.74	3/950 (0.3%)	1.32	15/1323 (1.1%)
16	d	0.55	1/615 (0.2%)	2.34	41/857 (4.8%)
17	e	0.35	0/1044	0.61	0/1452
17	f	0.39	0/1079	0.58	0/1502
18	g	0.53	0/860	0.73	1/1197 (0.1%)
18	h	0.53	0/860	0.74	1/1197 (0.1%)
19	i	1.00	5/3246 (0.2%)	1.37	27/4507 (0.6%)
19	j	1.01	5/3335 (0.1%)	1.40	31/4632 (0.7%)
2	G	0.99	0/1393	1.23	7/1928 (0.4%)
20	k	0.88	0/900	2.02	18/1249 (1.4%)
21	o	0.40	0/1748	0.71	1/2340 (0.0%)
22	p	0.42	0/2119	0.74	0/2849
23	q	0.45	0/834	0.71	5/1159 (0.4%)
24	r	0.38	0/1895	0.67	0/2523
25	s	0.41	0/1563	0.71	0/2100
26	t	0.38	0/1717	0.70	1/2288 (0.0%)
27	u	0.54	0/775	0.73	3/1077 (0.3%)
28	v	0.52	0/579	0.79	5/806 (0.6%)
29	w	0.44	0/626	0.72	4/867 (0.5%)
30	x	0.49	0/657	0.78	5/911 (0.5%)
31	y	0.46	0/1298	0.74	0/1741
32	z	0.56	0/621	0.85	3/860 (0.3%)
33	0	0.41	0/1215	0.70	0/1626
34	1	0.40	0/229	0.64	1/316 (0.3%)
35	2	2.02	729/20292 (3.6%)	2.64	2257/31586 (7.1%)
36	3	1.06	8/3912 (0.2%)	1.68	94/6092 (1.5%)
4	I	0.23	0/3120	0.49	0/4334
8	S	0.36	0/1813	0.53	0/2523

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
8	T	0.38	0/1813	0.55	0/2523
9	U	0.35	0/602	0.57	0/837
9	V	0.39	0/602	0.59	0/837
All	All	1.22	751/69116 (1.1%)	1.71	2522/99493 (2.5%)

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
10	W	0	1
10	X	0	1
14	b	0	5
15	c	0	7
16	d	0	2
19	i	0	3
19	j	0	3
20	k	0	1
3	H	0	33
8	T	0	1
9	U	0	1
9	V	0	1
All	All	0	59

The worst 5 of 751 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	2	407	A	N9-C4	-12.24	1.30	1.37
35	2	485	A	N9-C4	-12.21	1.30	1.37
35	2	328	A	N9-C4	-12.18	1.30	1.37
35	2	432	G	N7-C5	-12.13	1.31	1.39
35	2	503	G	N9-C4	-11.40	1.28	1.38

The worst 5 of 2522 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	k	272	PRO	N-CA-CB	37.92	148.80	103.30
16	d	104	PRO	N-CA-CB	37.74	148.58	103.30
20	k	82	LYS	O-C-N	-24.01	84.28	122.70
16	d	128	THR	N-CA-CB	23.81	155.54	110.30
35	2	381	C	N3-C4-N4	-22.05	102.57	118.00

There are no chirality outliers.

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	21	UNK	Mainchain
3	H	22	UNK	Mainchain
3	H	23	UNK	Mainchain
3	H	24	UNK	Mainchain
3	H	25	UNK	Mainchain

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1500	0	326	24	0
1	B	1500	0	326	35	0
1	C	1500	0	326	28	0
1	D	1500	0	321	84	0
1	E	1500	0	321	85	0
1	F	1500	0	326	26	0
1	J	1500	0	323	30	0
1	K	1500	0	326	22	0
1	L	1500	0	325	47	0
1	N	1500	0	324	28	0
1	P	1500	0	326	22	0
1	l	1500	0	325	0	0
1	n	1500	0	325	0	0
2	G	1402	0	649	75	0
3	H	1715	0	364	121	0
4	I	3124	0	1397	6	0
5	M	1545	0	333	45	0
5	O	1545	0	331	20	0
5	m	1545	0	334	0	0
6	Q	1875	0	432	18	0
7	R	1660	0	362	13	0
8	S	1815	0	842	37	0
8	T	1815	0	841	69	0
9	U	603	0	287	52	0
9	V	603	0	288	37	0
10	W	1124	0	497	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	X	1124	0	497	19	0
11	Y	1799	0	805	3	0
12	Z	1742	0	785	5	0
13	a	267	0	112	0	0
14	b	760	0	331	0	0
15	c	951	0	392	0	0
16	d	616	0	270	0	0
17	e	1047	0	454	0	0
17	f	1081	0	469	0	0
18	g	861	0	385	0	0
18	h	861	0	386	0	0
19	i	3254	0	1481	0	0
19	j	3342	0	1522	0	0
20	k	905	0	399	0	0
21	o	1724	0	1793	0	0
22	p	2079	0	2150	0	0
23	q	836	0	390	0	0
24	r	1868	0	1985	0	0
25	s	1539	0	1620	0	0
26	t	1693	0	1793	0	0
27	u	777	0	360	0	0
28	v	580	0	266	0	0
29	w	627	0	307	0	0
30	x	658	0	304	0	0
31	y	1275	0	1353	0	0
32	z	622	0	283	0	0
33	0	1197	0	1281	274	0
34	1	230	0	100	9	0
35	2	18149	0	9087	5871	0
36	3	3504	0	1769	650	0
All	All	95839	0	44306	7269	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 77.

The worst 5 of 7269 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)
1:E:248:UNK:CB	3:H:312:UNK:CA	1.75	1.64
3:H:1:UNK:CB	3:H:173:UNK:CA	1.77	1.62
2:G:3230:GLU:CB	33:0:148:ALA:HB2	1.29	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:UNK:CA	1:E:139:UNK:CB	1.80	1.55
3:H:268:UNK:CB	3:H:307:UNK:CB	1.86	1.53

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	
2	G	265/1802 (15%)	245 (92%)	11 (4%)	9 (3%)	5	40
4	I	626/939 (67%)	609 (97%)	17 (3%)	0	100	100
8	S	363/412 (88%)	344 (95%)	14 (4%)	5 (1%)	14	58
8	T	363/412 (88%)	341 (94%)	20 (6%)	2 (1%)	30	74
9	U	120/130 (92%)	111 (92%)	7 (6%)	2 (2%)	11	55
9	V	120/130 (92%)	112 (93%)	6 (5%)	2 (2%)	11	55
10	W	225/232 (97%)	206 (92%)	16 (7%)	3 (1%)	15	60
10	X	225/232 (97%)	204 (91%)	17 (8%)	4 (2%)	11	53
11	Y	353/573 (62%)	341 (97%)	11 (3%)	1 (0%)	46	83
12	Z	353/367 (96%)	347 (98%)	6 (2%)	0	100	100
13	a	50/1183 (4%)	49 (98%)	1 (2%)	0	100	100
14	b	151/183 (82%)	128 (85%)	14 (9%)	9 (6%)	2	26
15	c	190/297 (64%)	163 (86%)	12 (6%)	15 (8%)	1	19
16	d	122/184 (66%)	110 (90%)	8 (7%)	4 (3%)	5	40
17	e	205/252 (81%)	190 (93%)	15 (7%)	0	100	100
17	f	214/252 (85%)	201 (94%)	11 (5%)	2 (1%)	21	67
18	g	172/322 (53%)	163 (95%)	9 (5%)	0	100	100
18	h	172/322 (53%)	163 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	i	643/1073 (60%)	577 (90%)	38 (6%)	28 (4%)	3	33
19	j	663/1073 (62%)	591 (89%)	43 (6%)	29 (4%)	3	33
20	k	172/391 (44%)	151 (88%)	12 (7%)	9 (5%)	2	30
21	o	213/265 (80%)	161 (76%)	33 (16%)	19 (9%)	1	17
22	p	257/259 (99%)	193 (75%)	40 (16%)	24 (9%)	1	16
23	q	165/225 (73%)	55 (33%)	46 (28%)	64 (39%)	0	0
24	r	233/293 (80%)	188 (81%)	31 (13%)	14 (6%)	2	26
25	s	184/197 (93%)	151 (82%)	23 (12%)	10 (5%)	2	29
26	t	205/208 (99%)	147 (72%)	38 (18%)	20 (10%)	1	14
27	u	153/197 (78%)	48 (31%)	49 (32%)	56 (37%)	0	0
28	v	115/151 (76%)	49 (43%)	33 (29%)	33 (29%)	0	0
29	w	126/137 (92%)	51 (40%)	39 (31%)	36 (29%)	0	0
30	x	132/143 (92%)	57 (43%)	33 (25%)	42 (32%)	0	0
31	y	155/157 (99%)	115 (74%)	26 (17%)	14 (9%)	1	17
32	z	125/130 (96%)	50 (40%)	35 (28%)	40 (32%)	0	0
33	0	146/149 (98%)	115 (79%)	20 (14%)	11 (8%)	1	21
34	1	45/67 (67%)	17 (38%)	12 (27%)	16 (36%)	0	0
All	All	8021/13339 (60%)	6743 (84%)	755 (9%)	523 (6%)	3	25

5 of 523 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	2992	ASN
2	G	3194	ASP
8	T	355	SER
9	U	62	PRO
9	V	62	PRO

### 5.3.2 Protein sidechains ⓘ

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

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



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	o	191/225 (85%)	166 (87%)	25 (13%)	5	28
22	p	226/226 (100%)	197 (87%)	29 (13%)	5	29
24	r	201/244 (82%)	187 (93%)	14 (7%)	19	56
25	s	172/183 (94%)	156 (91%)	16 (9%)	11	42
26	t	184/185 (100%)	171 (93%)	13 (7%)	18	55
31	y	141/141 (100%)	125 (89%)	16 (11%)	7	33
33	0	133/134 (99%)	124 (93%)	9 (7%)	20	57
All	All	1248/1338 (93%)	1126 (90%)	122 (10%)	14	39

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	r	19	ASP
25	s	62	LEU
31	y	135	ARG
24	r	20	ASP
24	r	105	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
25	s	28	ASN
25	s	154	GLN
33	0	20	GLN
25	s	44	GLN
25	s	49	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	2	842/1800 (46%)	640 (76%)	124 (14%)
36	3	160/274 (58%)	80 (50%)	11 (6%)
All	All	1002/2074 (48%)	720 (71%)	135 (13%)

5 of 720 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	2	21	U

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Mol	Chain	Res	Type
35	2	22	A
35	2	23	G
35	2	24	U
35	2	25	C

5 of 135 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	2	398	G
35	2	477	A
36	3	78	C
35	2	400	A
35	2	455	C

## 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](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	Q	30
7	R	15
3	H	13

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Mol	Chain	Number of breaks
5	O	2
5	M	2
5	m	2
1	P	1
1	J	1
1	D	1
1	K	1
1	E	1
1	l	1
1	B	1
1	C	1
1	n	1
1	A	1
1	N	1
1	L	1
1	F	1

The worst 5 of 77 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Q	171:UNK	C	301:UNK	N	88.70
1	R	41:UNK	C	51:UNK	N	66.84
1	R	141:UNK	C	151:UNK	N	66.84
1	R	241:UNK	C	251:UNK	N	66.84
1	R	341:UNK	C	351:UNK	N	66.84