



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:37 AM UTC

PDB ID : 6KE6 / pdb_00006ke6
EMDB ID : EMD-9964
Title : 3.4 angstrom cryo-EM structure of yeast 90S small subunit preribosome
Authors : Du, Y.; Ye, K.; An, W.
Deposited on : 2019-07-03
Resolution : 3.40 Å(reported)
Based on initial models : 5WYJ, 5WLC

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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

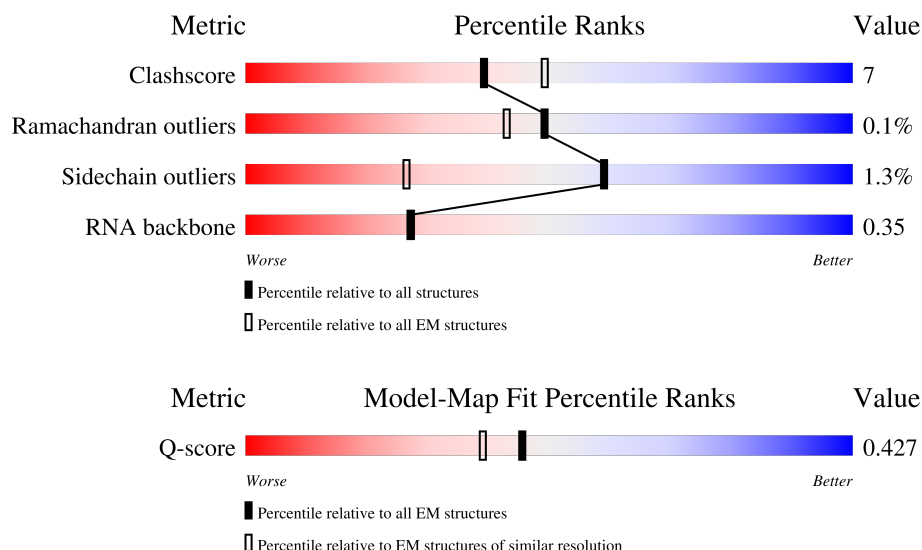
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



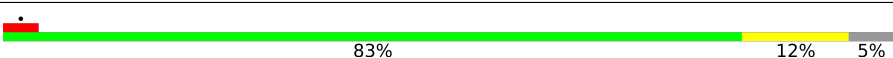
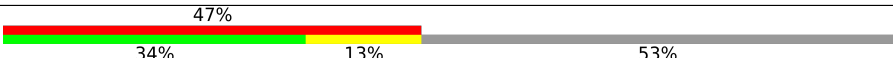
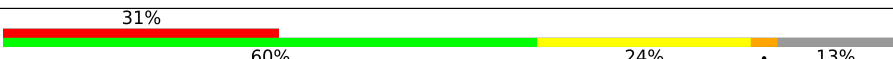
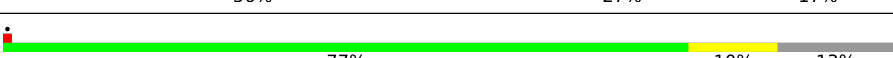
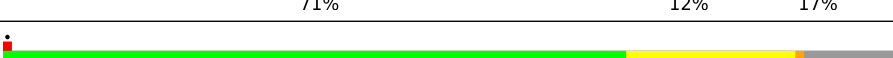
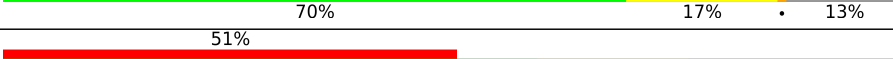
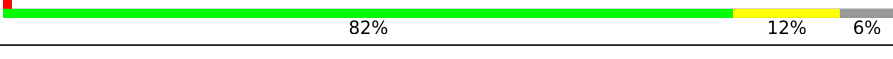
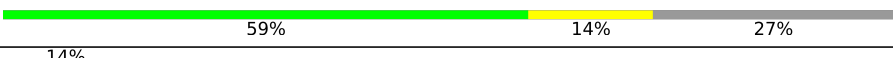
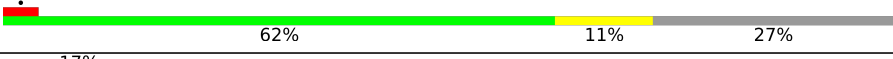
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	3A	333	
2	5A	700	
3	SA	1807	

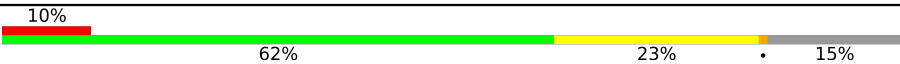
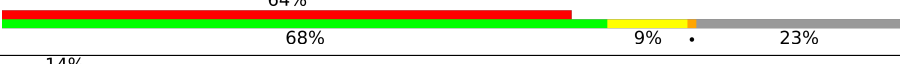
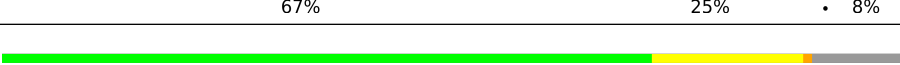
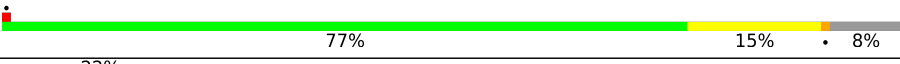
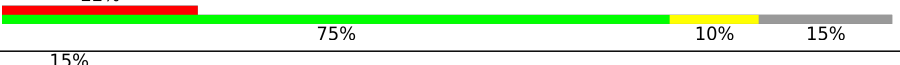
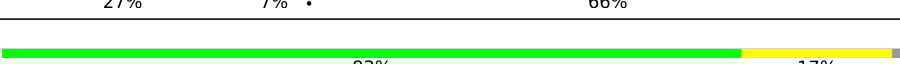
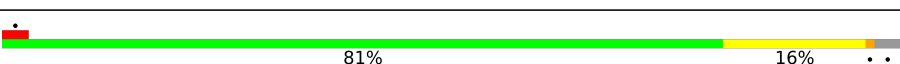
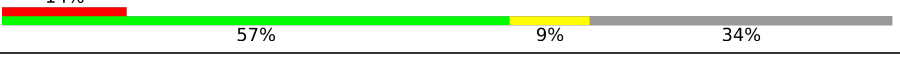
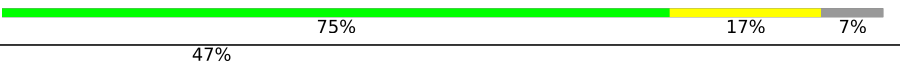
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	
9	SJ	200	
10	SK	197	
11	SM	156	
12	SN	143	
13	SO	151	
14	SP	137	
15	SR	143	
16	ST	146	
17	SX	130	
18	SY	145	
19	SZ	135	
20	Sc	82	
21	Sd	67	
22	3B	327	
22	3C	327	
23	3D	504	
24	3E	511	
25	3F	573	
26	3G	126	
26	3H	126	

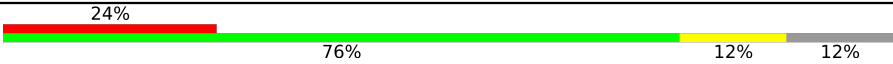
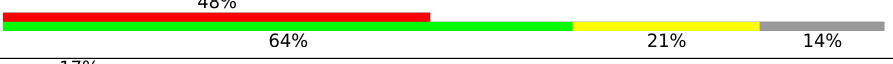
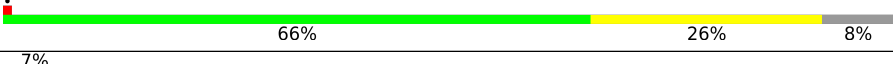
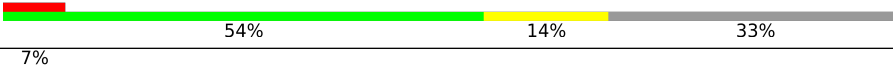
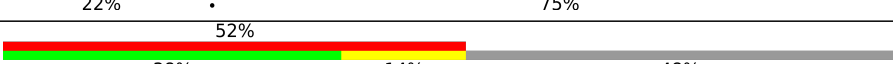
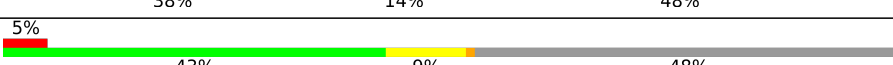
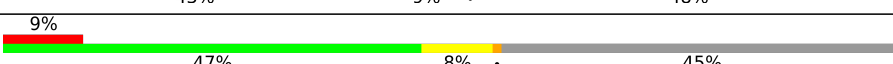
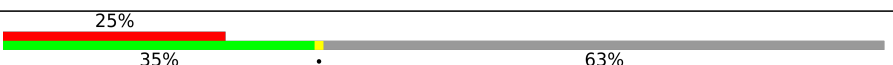
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	
32	AF	513	
33	AG	896	
34	B1	923	
35	B2	943	
36	B3	817	
37	B8	594	
38	BE	939	
39	B6	440	
40	5B	214	
41	5C	554	
42	5D	250	
43	5E	593	
44	5F	183	
45	5G	290	
46	5H	610	
47	5I	489	
48	5J	217	
49	5K	189	
50	RA	707	
51	RB	357	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
52	RC	316	
53	RE	1237	
54	RF	297	
55	RG	252	
55	RH	252	
56	RI	274	
57	RJ	1183	
58	RK	367	
59	RL	1056	
59	RM	1056	
60	RN	810	
61	RO	552	
62	RP	2493	
63	RQ	899	
64	RS	483	
65	RT	326	
66	RV	346	
67	X1	347	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 224791 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 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	175	Total	C	N	O	P	0	0
			3711	1661	648	1227	175		

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	522	Total	C	N	O	P	0	0
			11143	4979	1982	3660	522		

- Molecule 3 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1310	Total	C	N	O	P	0	0
			27940	12487	4981	9162	1310		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	219	Total	C	N	O	S	0	0
			1751	1109	321	317	4		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	229	Total	C	N	O	S	0	0
			1815	1161	331	320	3		

- Molecule 6 is a protein called 40S ribosomal protein S5.

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

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	112	Total	C	N	O	S	0	0
			879	562	155	160	2		

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	165	Total	C	N	O	S	0	0
			1321	853	226	242			

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	166	Total	C	N	O	S	0	0
			1324	824	262	236	2		

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SK	171	Total	C	N	O	S	0	0
			1388	879	268	240	1		

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SM	123	Total	C	N	O	S	0	0
			997	641	189	164	3		

- Molecule 12 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SN	119	Total	C	N	O	S	0	0
			865	545	151	167	2		

- Molecule 13 is a protein called 40S ribosomal protein S13.

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

- Molecule 14 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SP	118	Total	C	N	O	S	0	0
			868	536	164	165	3		

- Molecule 15 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 16 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ST	113	Total	C	N	O	S	0	0
			918	578	174	164	2		

- Molecule 17 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 18 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SY	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

- Molecule 19 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SZ	102	Total	C	N	O		0	0
			809	517	148	144			

- Molecule 20 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sc	80	Total	C	N	O	S	0	0
			603	377	109	112	5		

- Molecule 21 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 22 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
22	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 25 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3F	434	Total	C	N	O	S	0	0
			3473	2211	603	649	10		

- Molecule 26 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
26	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A4	662	Total	C	N	O	S	0	0
			5226	3309	910	986	21		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A5	514	Total	C	N	O	S	0	0
			3976	2520	688	755	13		

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A8	548	Total	C	N	O	S	0	0
			3307	2054	608	642	3		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A9	128	Total	C	N	O	S	0	0
			939	594	173	170	2		

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AE	777	Total	C	N	O	S	0	0
			6197	3998	1014	1166	19		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 33 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AG	826	Total	C	N	O	S	0	0
			6570	4181	1111	1259	19		

- Molecule 34 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B1	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B2	851	Total	C	N	O	S	0	0
			6723	4294	1133	1269	27		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B3	757	Total	C	N	O	S	0	0
			5919	3769	993	1130	27		

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B8	477	Total	C	N	O	S	0	0
			3764	2387	662	705	10		

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	865	Total	C	N	O	S	0	0
			6810	4322	1175	1292	21		

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B6	374	Total	C	N	O	S	0	0
			2800	1782	501	505	12		

- Molecule 40 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	5B	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5C	535	Total	C	N	O	S	0	0
			4237	2656	762	807	12		

- Molecule 42 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 44 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 45 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 46 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5H	136	Total	C	N	O		0	0
			1065	658	211	196			

- Molecule 47 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 48 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	144	Total	C	N	O	S	0	0
			1219	769	230	215	5		

- Molecule 49 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 50 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RA	338	Total	C	N	O	S	0	0
			2709	1713	463	524	9		

- Molecule 51 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RB	134	Total	C	N	O	S	0	0
			1108	664	227	214	3		

- Molecule 52 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RC	278	Total	C	N	O	S	0	0
			2207	1408	391	395	13		

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RE	1079	Total	C	N	O	S	0	0
			8716	5666	1437	1589	24		

- Molecule 54 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RF	241	Total	C	N	O	S	0	0
			1963	1253	335	367	8		

- Molecule 55 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RG	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
55	RH	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 56 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RI	252	Total	C	N	O	S	0	0
			2045	1309	362	366	8		

- Molecule 57 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RJ	796	Total	C	N	O	S	0	0
			6379	4086	1136	1128	29		

- Molecule 58 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 59 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
59	RM	765	Total	C	N	O		0	0
			3774	2244	765	765			

- Molecule 60 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RN	587	Total	C	N	O	S	0	0
			4363	2758	791	803	11		

- Molecule 61 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RO	525	Total	C	N	O	S	0	0
			3766	2412	646	696	12		

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RP	2052	Total	C	N	O		0	0
			10202	6098	2052	2052			

- Molecule 63 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RQ	226	Total	C	N	O	S	0	0
			1651	1023	313	313	2		

- Molecule 64 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RS	251	Total	C	N	O	S	0	0
			2051	1340	349	359	3		

- Molecule 65 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RT	171	Total	C	N	O	S	0	0
			1357	864	249	240	4		

- Molecule 66 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RV	190	Total	C	N	O	S	0	0
			1448	891	290	264	3		

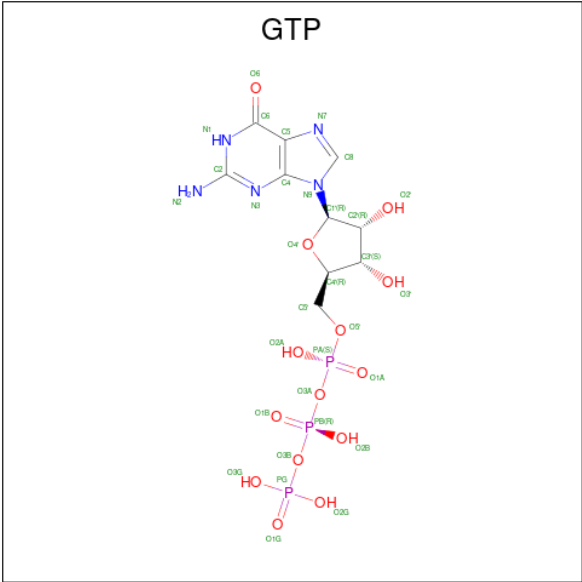
- Molecule 67 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	X1	127	Total	C	N	O	0	0
			635	381	127	127		

- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
68	Sc	1	Total	Zn	0
			1	1	
68	5K	1	Total	Zn	0
			1	1	

- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
69	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

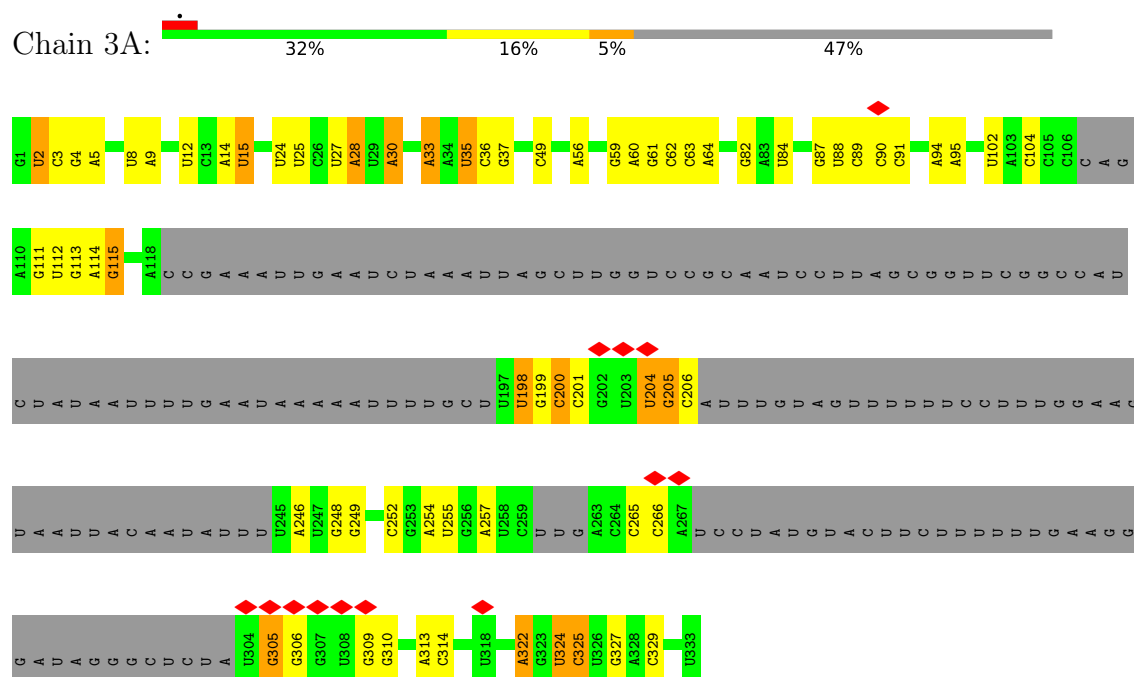
- Molecule 70 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
70	RJ	1	Total	Mg	0
			1	1	

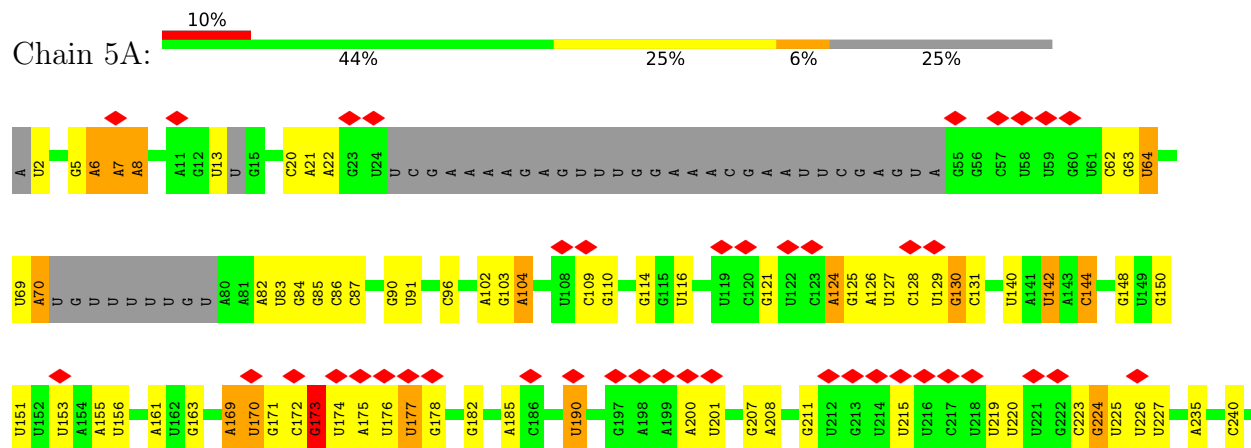
3 Residue-property plots [i](#)

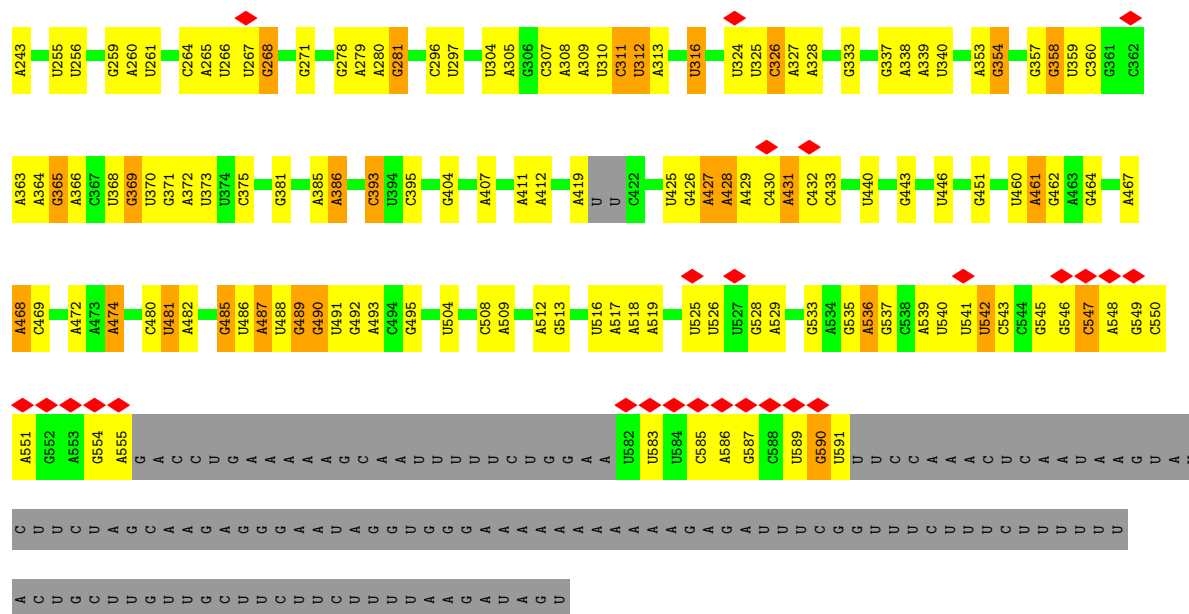
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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 snoRNA

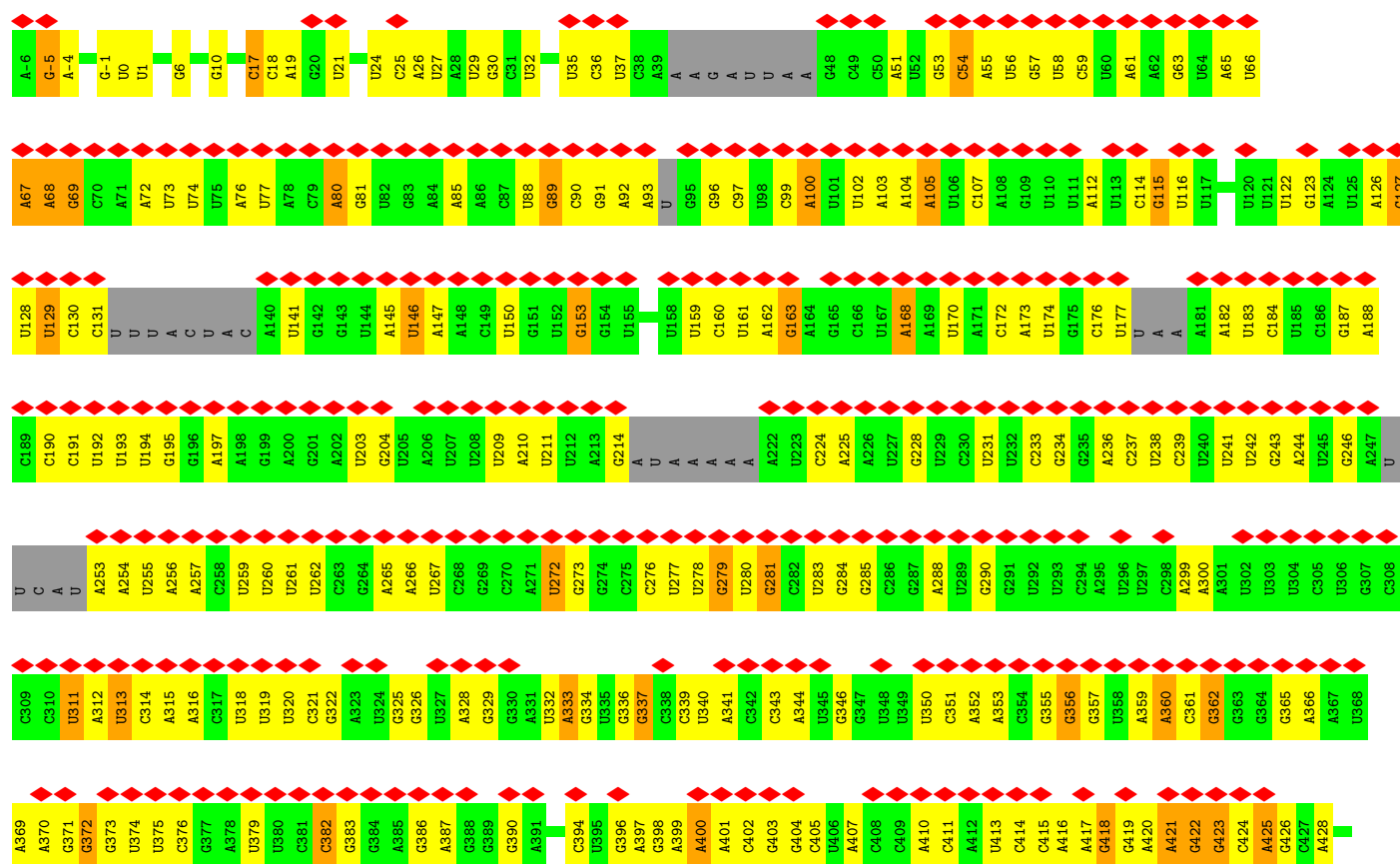


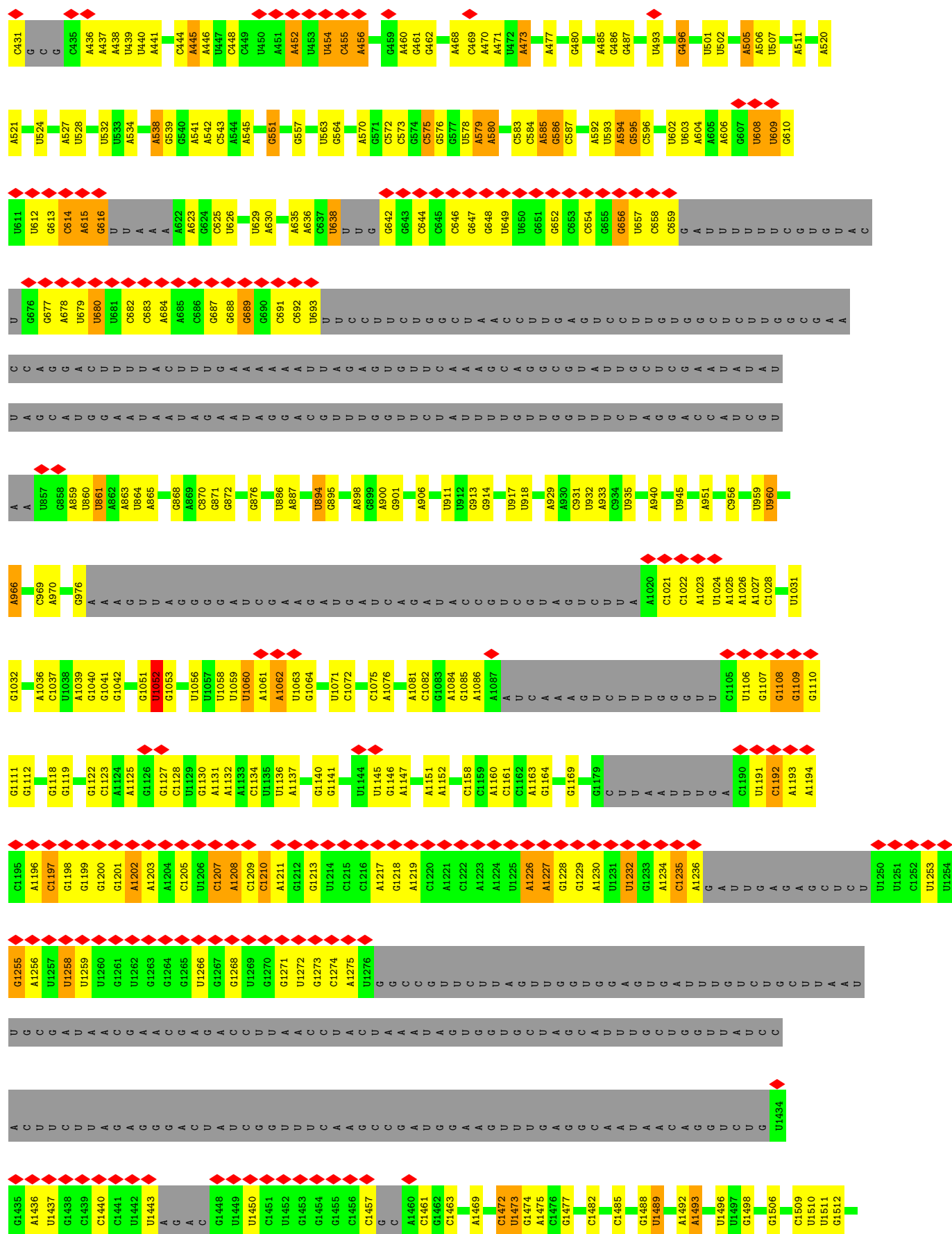
• Molecule 2: 5' ETS





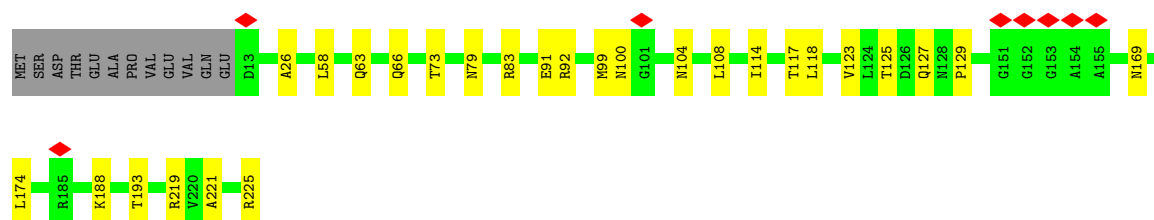
• Molecule 3: 18S rRNA





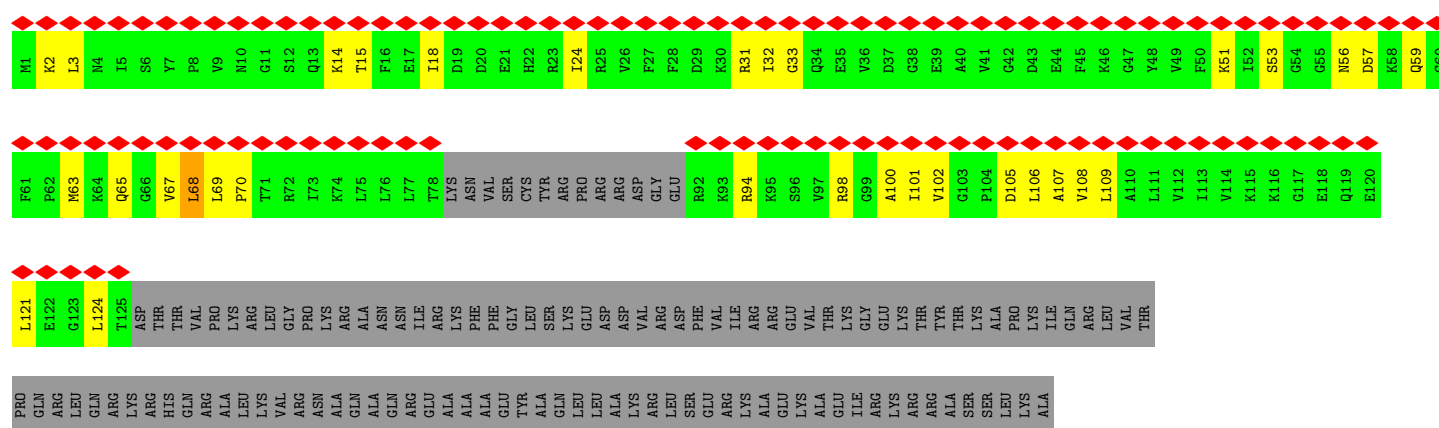
- Molecule 6: 40S ribosomal protein S5

Chain SG: 



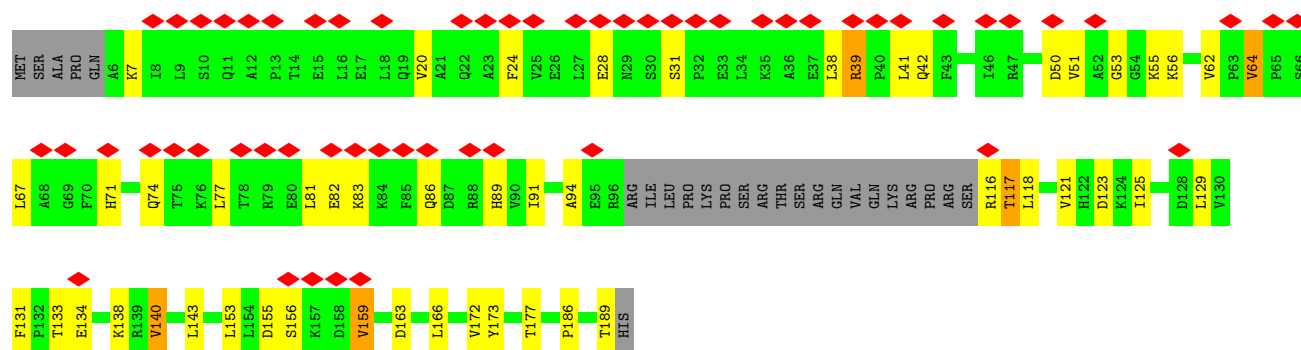
- Molecule 7: 40S ribosomal protein S6-A

Chain SH: 



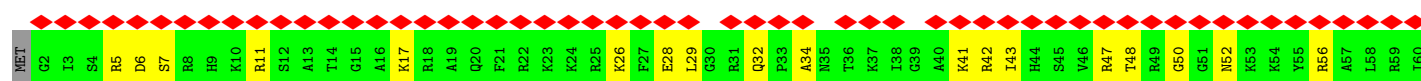
- Molecule 8: 40S ribosomal protein S7-A

Chain SI: 



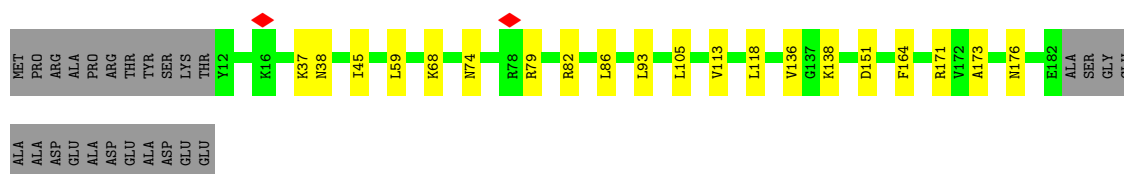
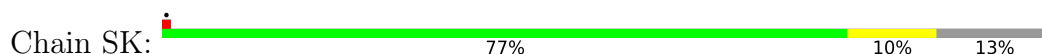
- Molecule 9: 40S ribosomal protein S8-A

Chain SJ: 

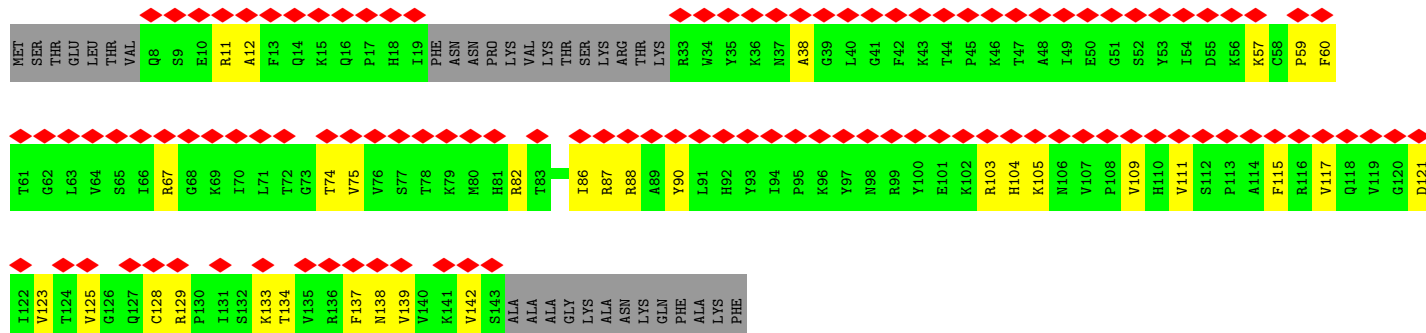
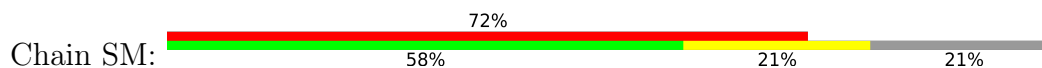




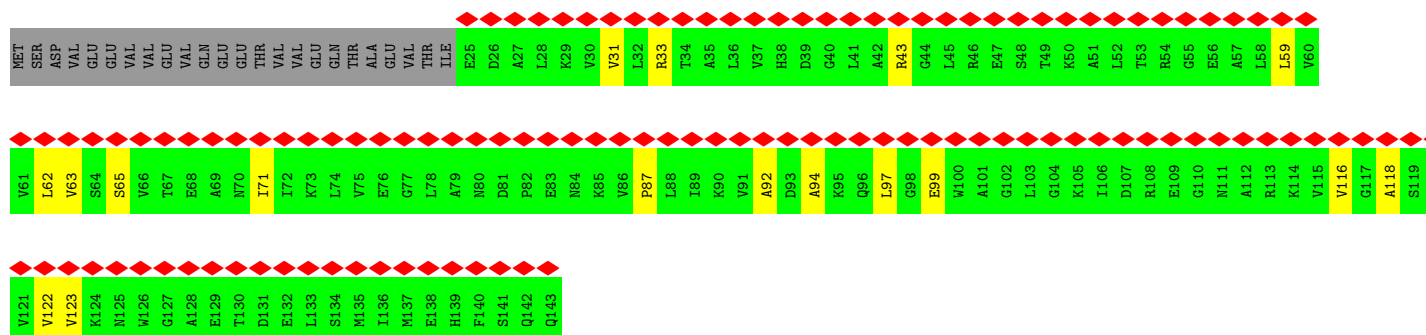
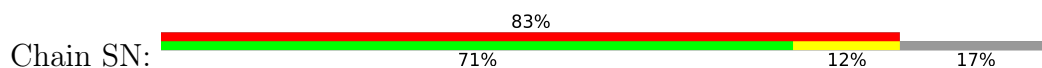
• Molecule 10: 40S ribosomal protein S9-A



• Molecule 11: 40S ribosomal protein S11-A

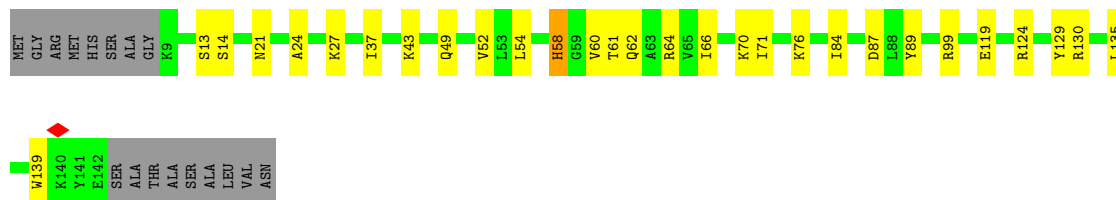


• Molecule 12: 40S ribosomal protein S12



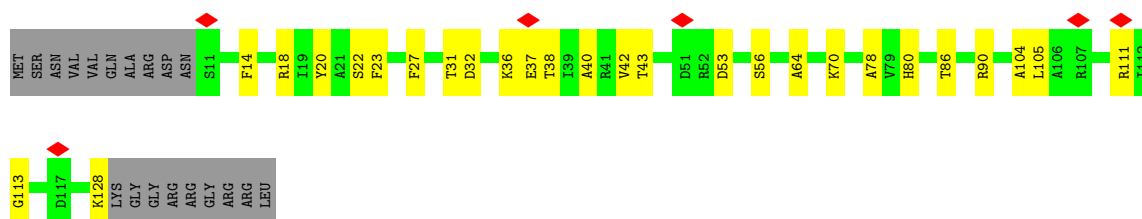
- Molecule 13: 40S ribosomal protein S13

Chain SO: 



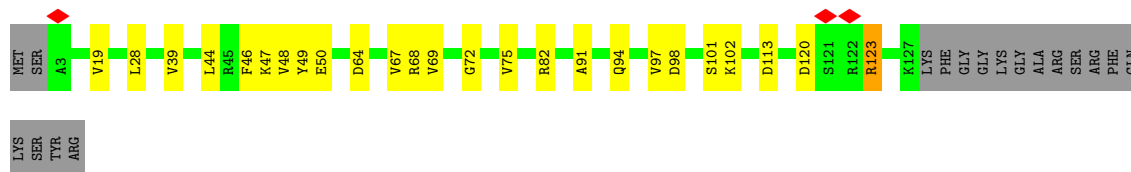
- Molecule 14: 40S ribosomal protein S14-A

Chain SP: 

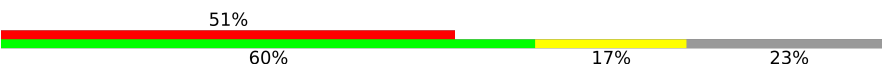


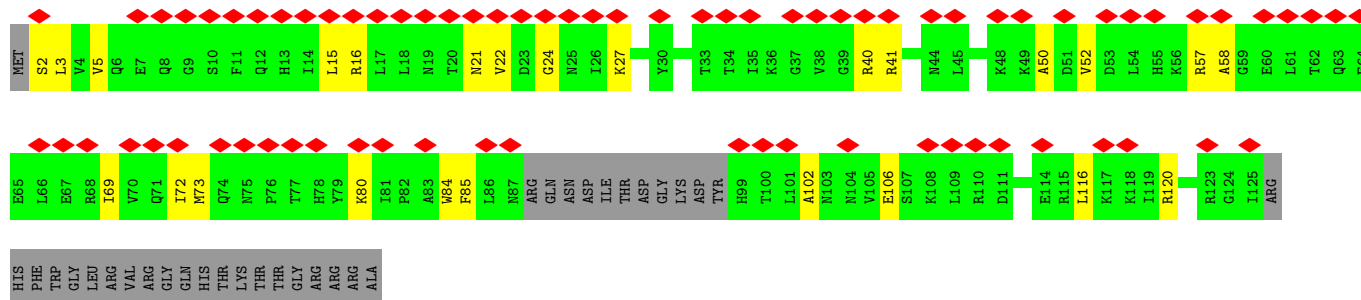
- Molecule 15: 40S ribosomal protein S16-A

Chain SR: 



- Molecule 16: 40S ribosomal protein S18-A

Chain ST: 

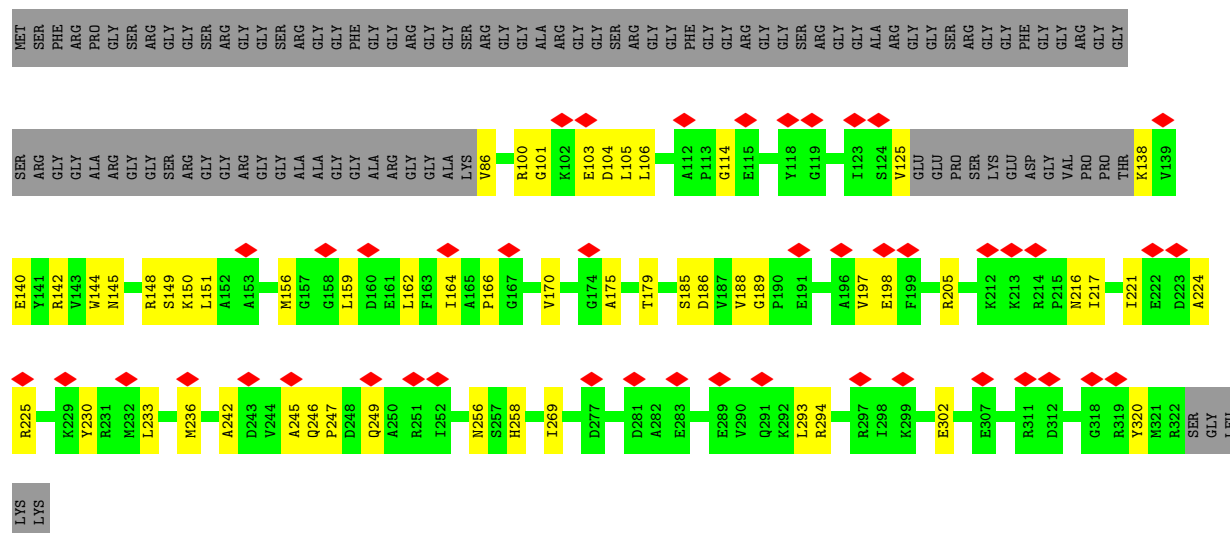


- Molecule 17: 40S ribosomal protein S22-B

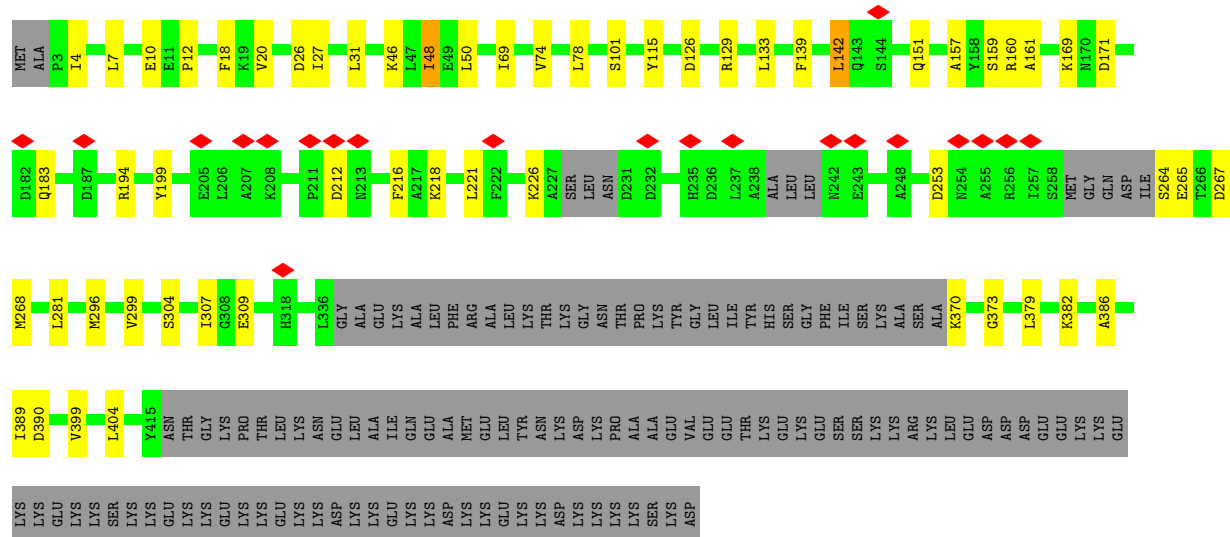
Chain SX: 



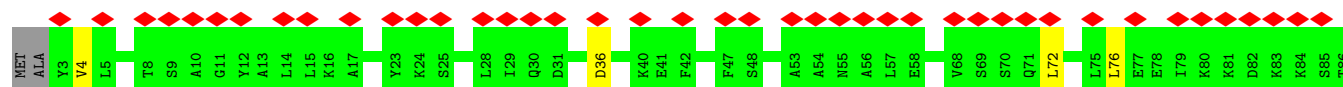
• Molecule 22: rRNA 2'-O-methyltransferase fibrillar



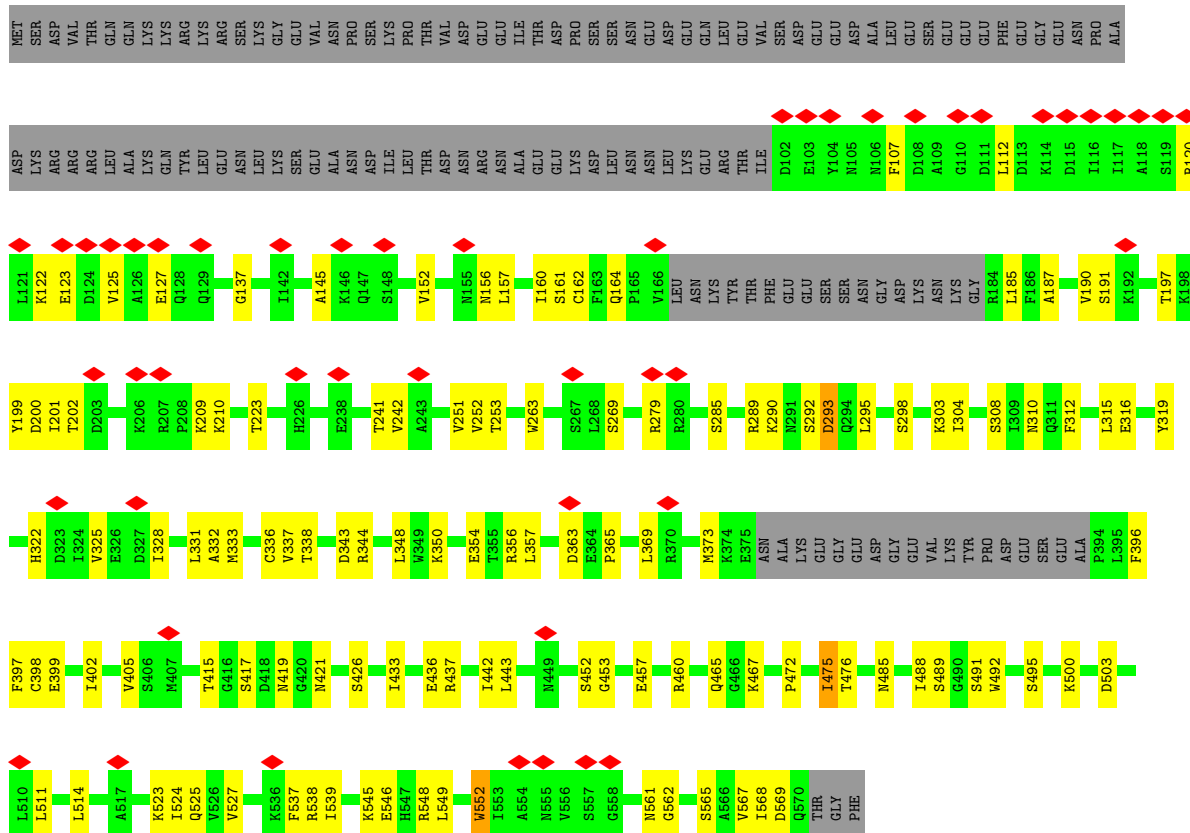
• Molecule 23: Nucleolar protein 56



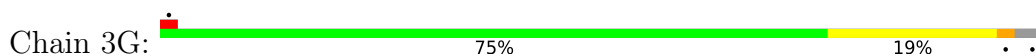
• Molecule 24: Nucleolar protein 58

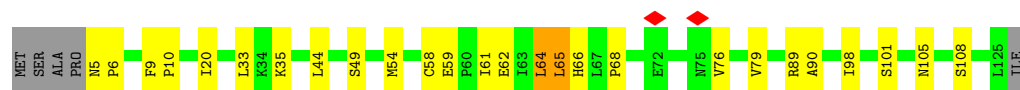


- Molecule 25: Ribosomal RNA-processing protein 9

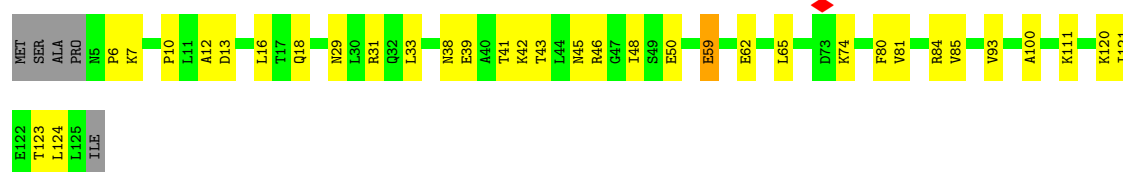


- Molecule 26: 13 kDa ribonucleoprotein-associated protein

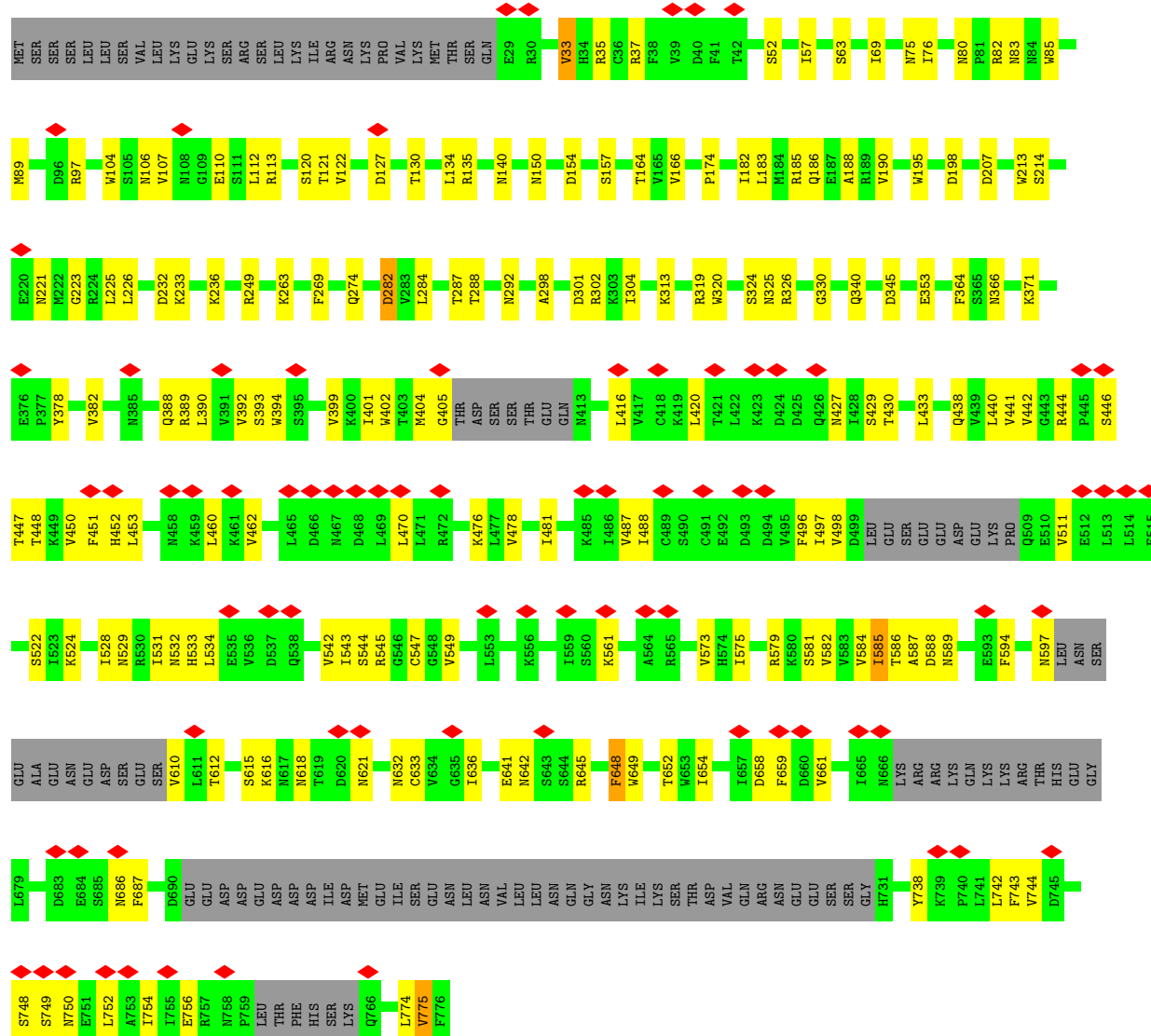




- Molecule 26: 13 kDa ribonucleoprotein-associated protein

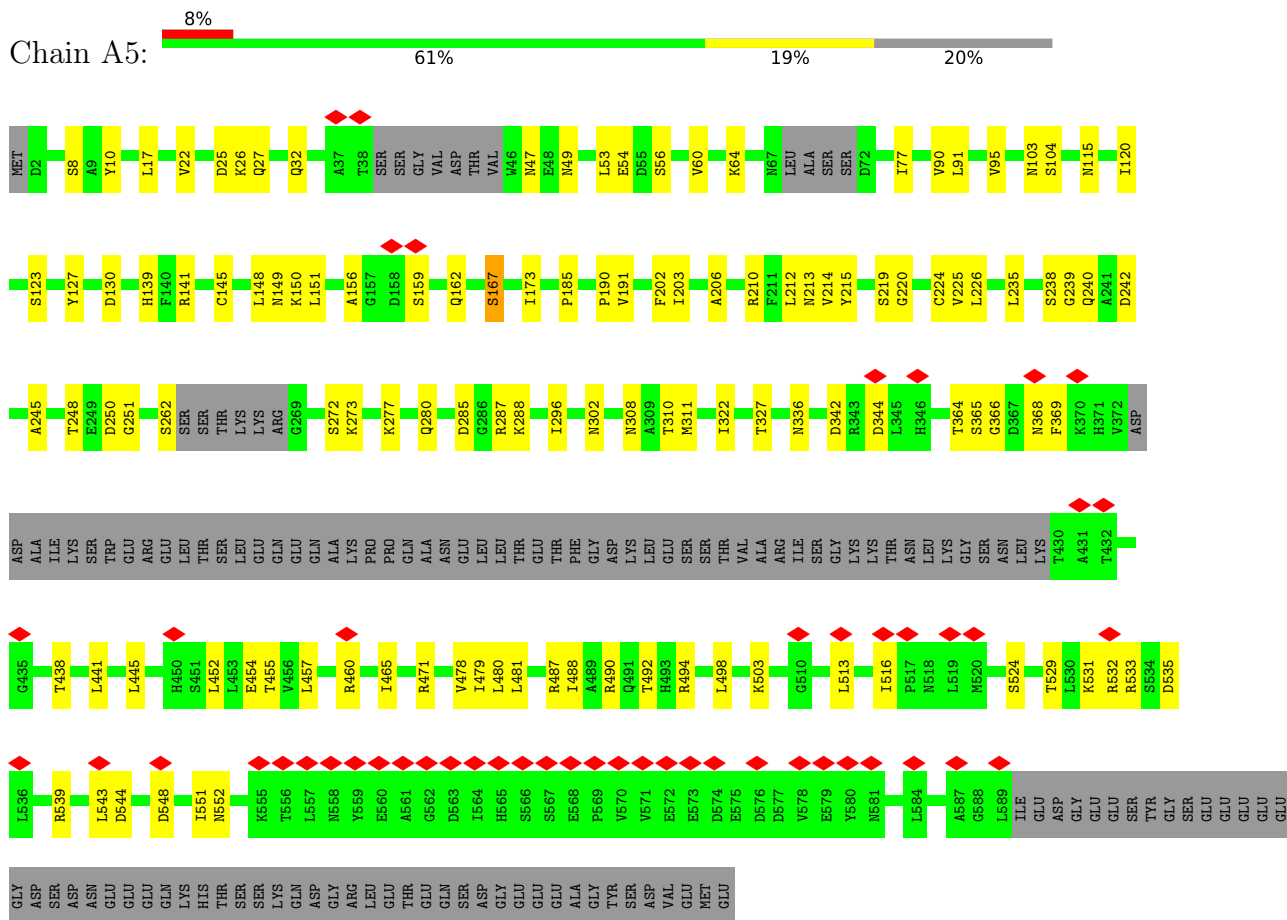


- Molecule 27: U3 small nucleolar RNA-associated protein 4



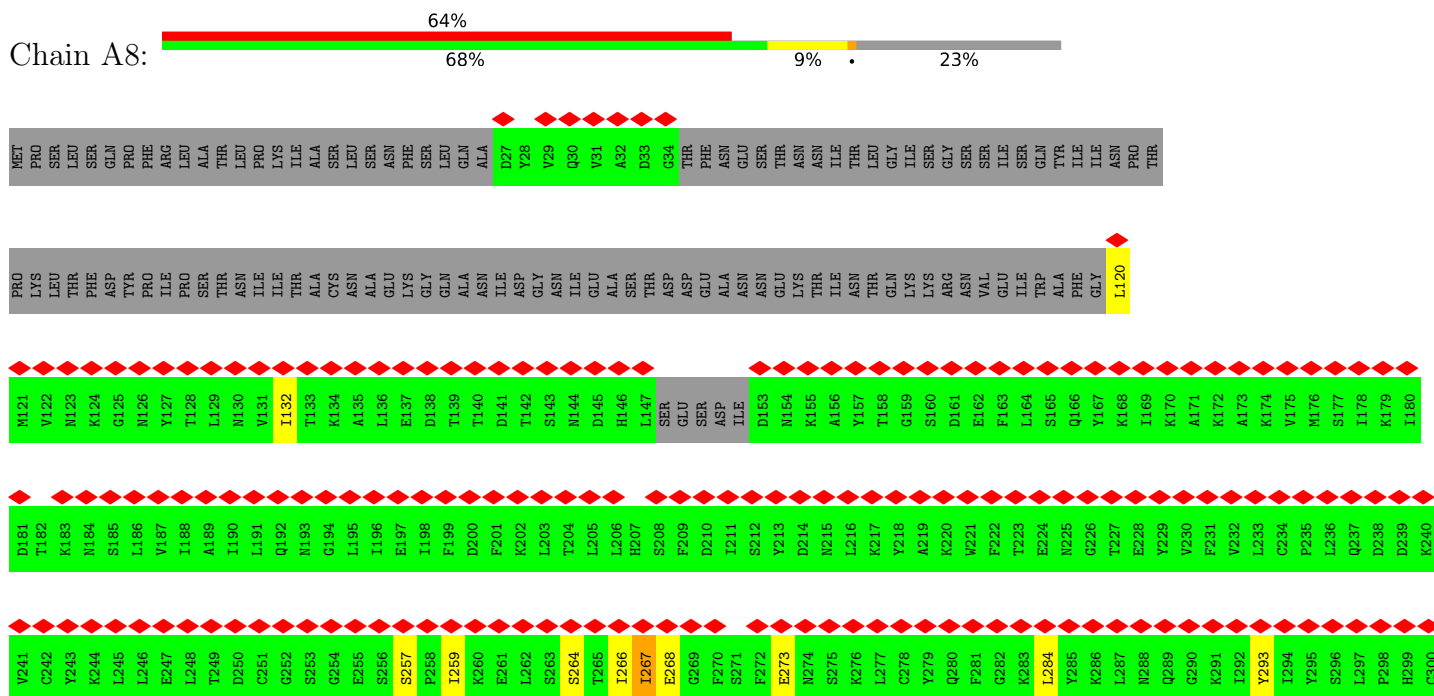
- Molecule 28: U3 small nucleolar RNA-associated protein 5

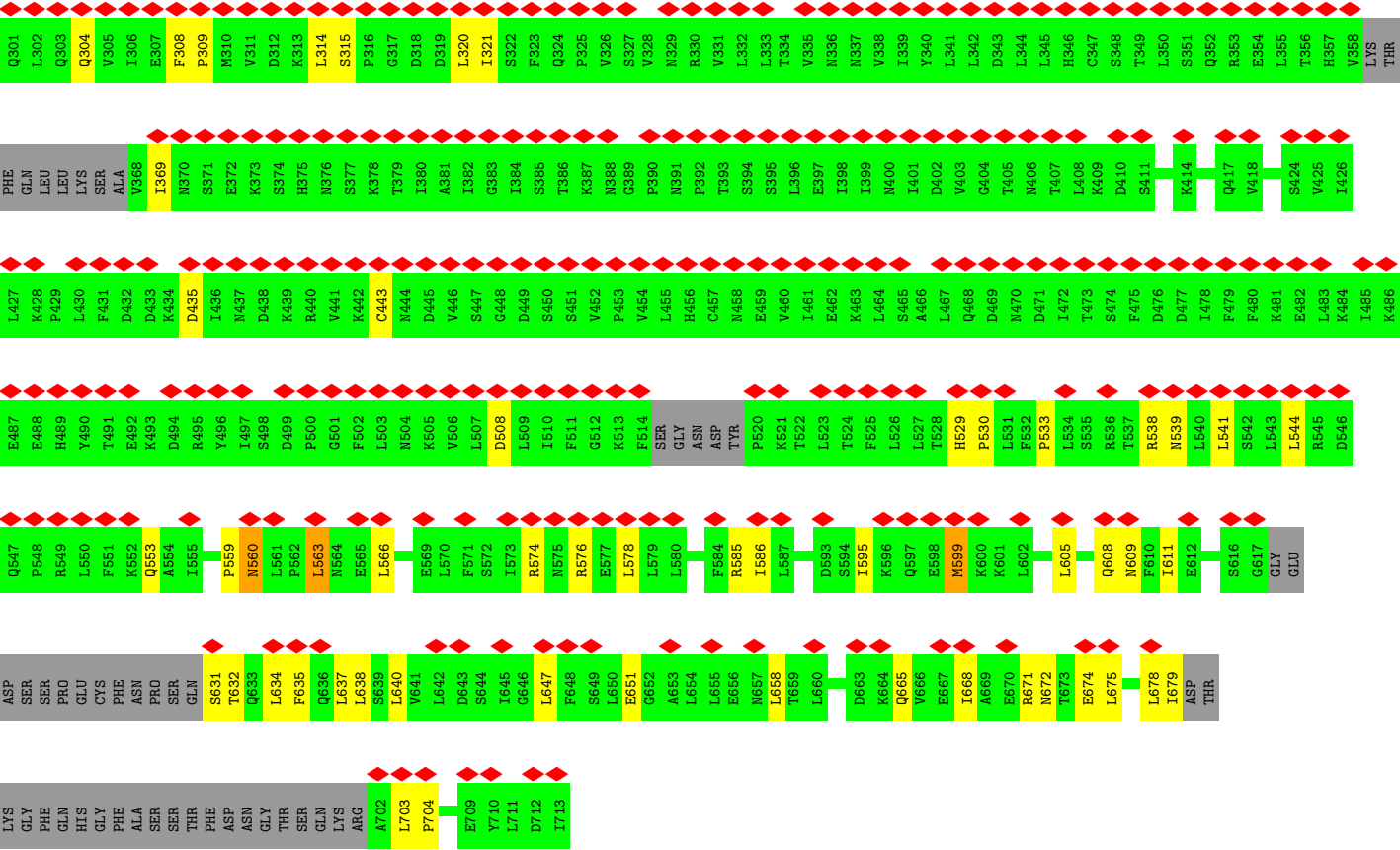
Chain A5:



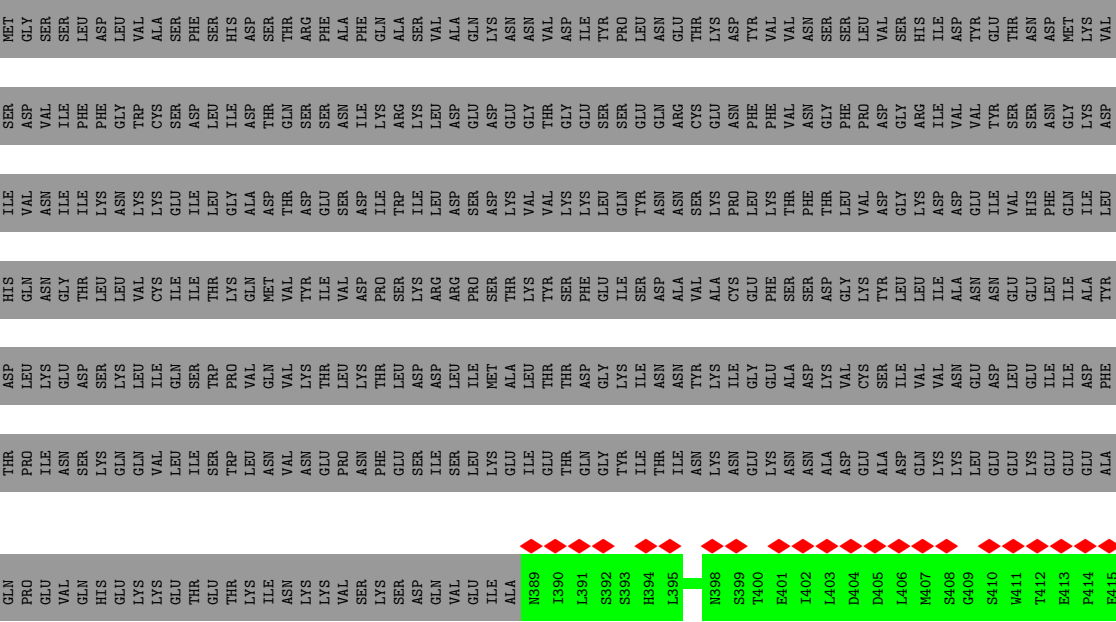
- Molecule 29: U3 small nucleolar RNA-associated protein 8

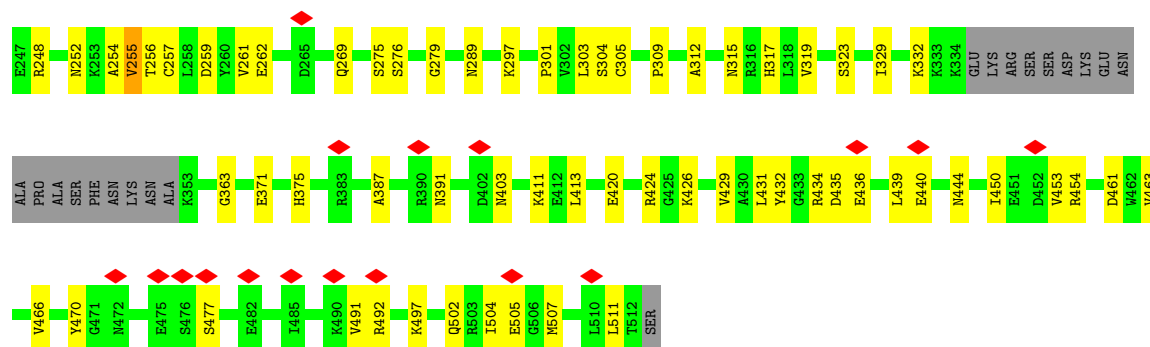
Chain A8:



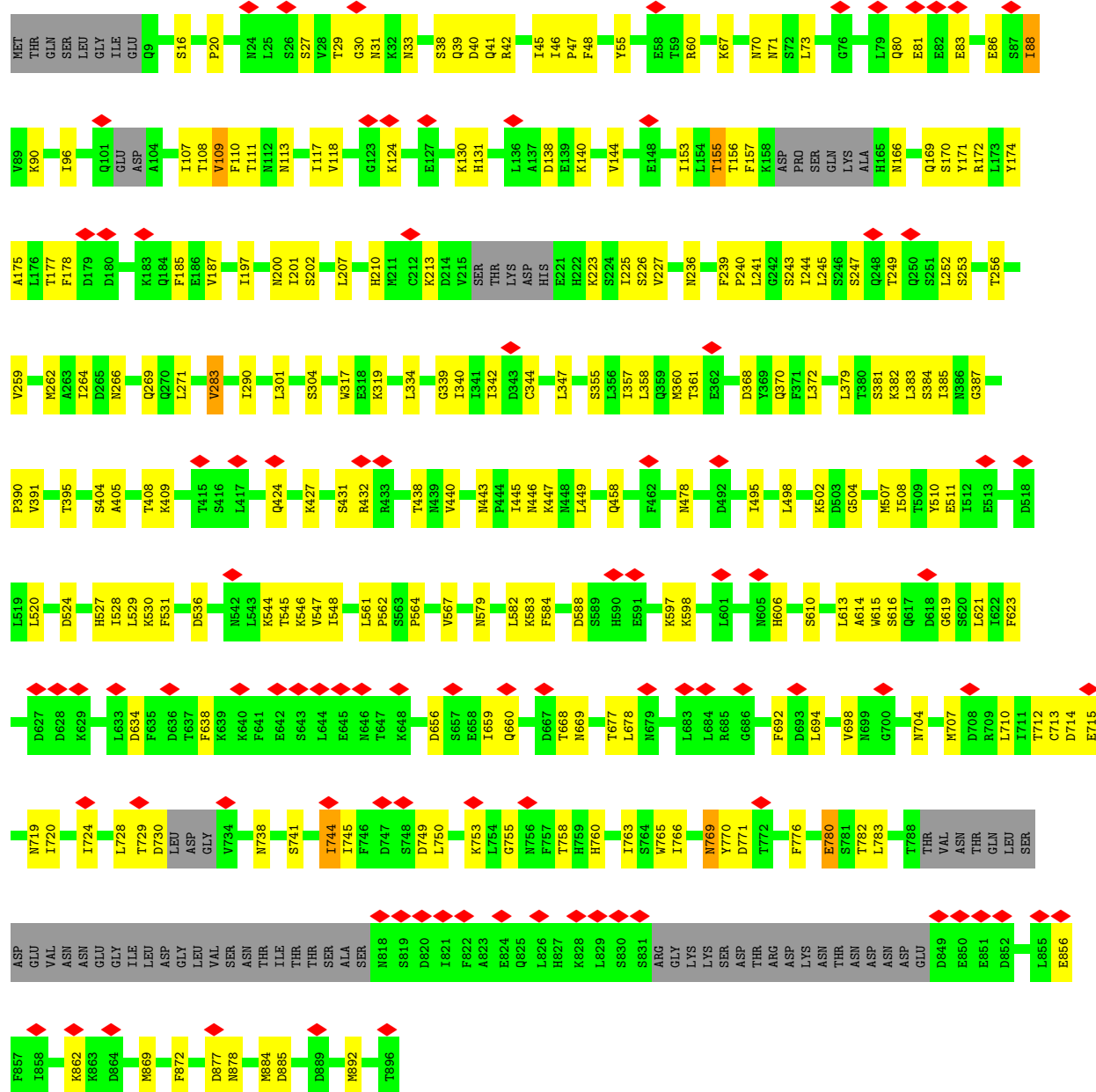


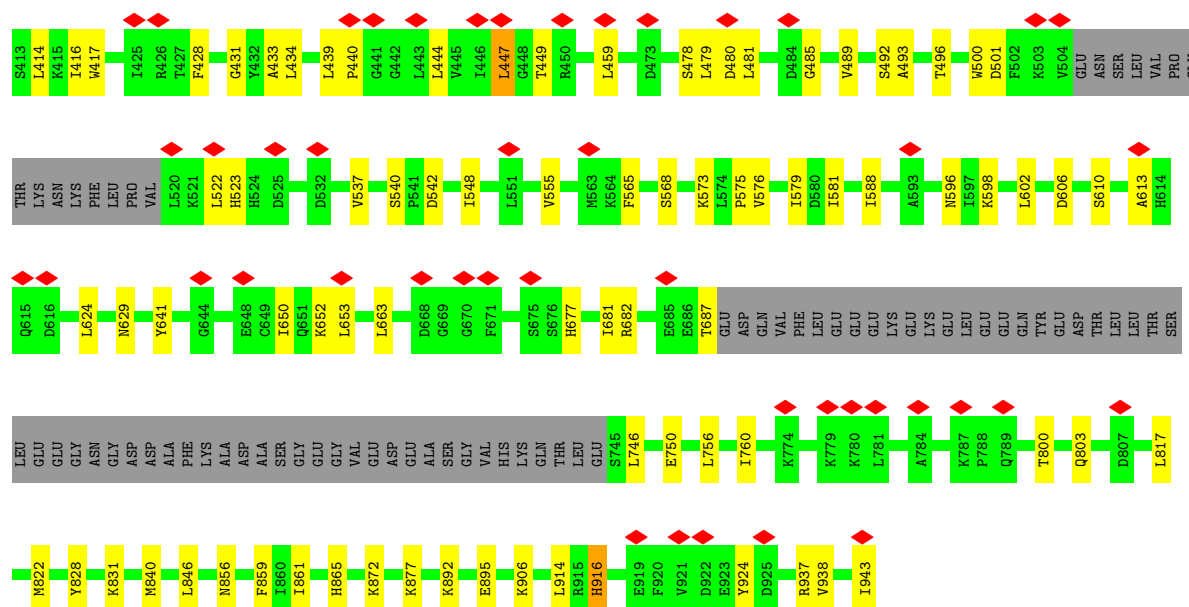
● Molecule 30: U3 small nucleolar RNA-associated protein 9



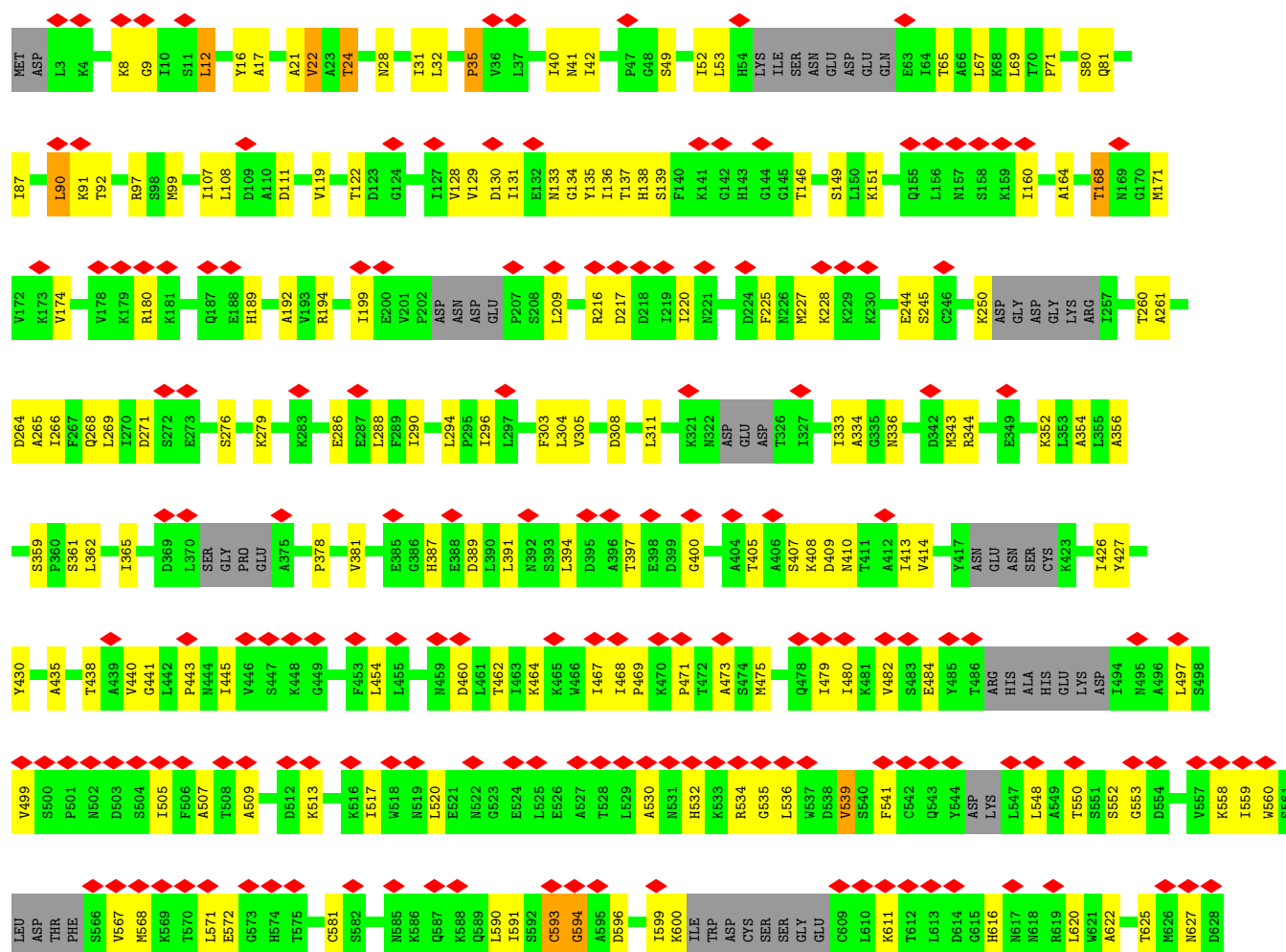


• Molecule 33: NET1-associated nuclear protein 1



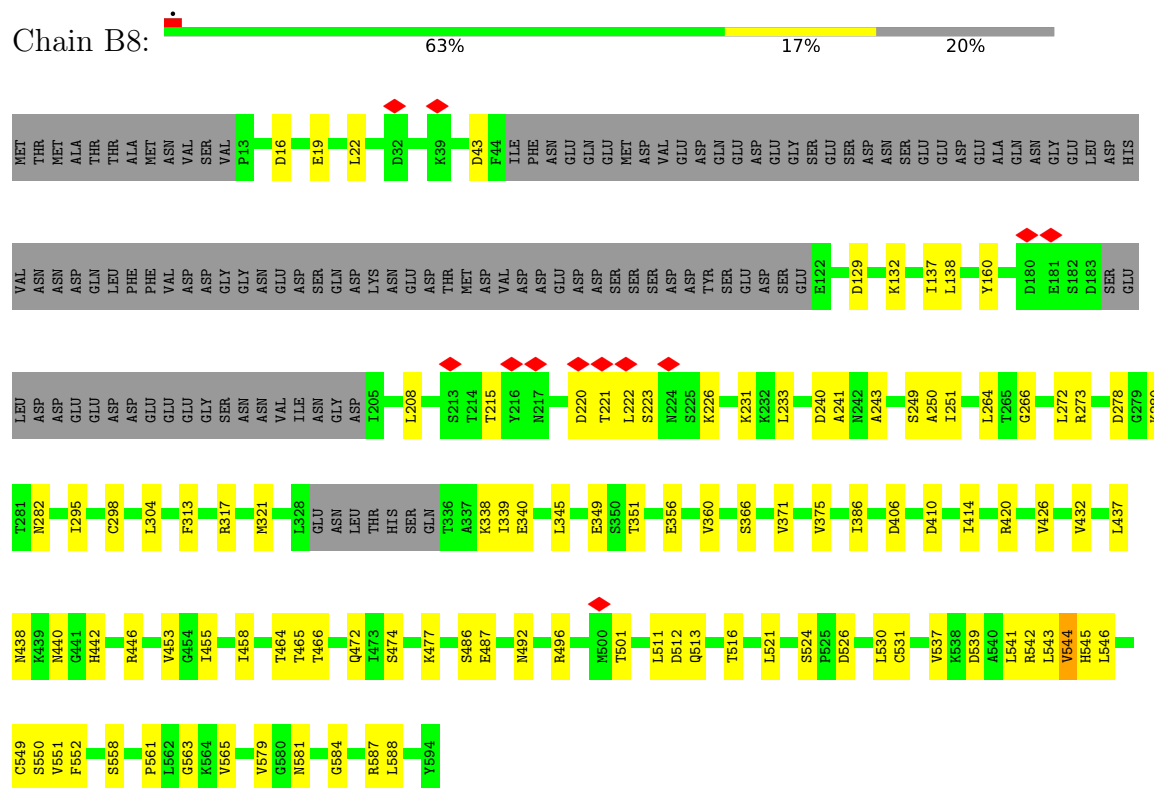


• Molecule 36: U3 small nucleolar RNA-associated protein 13



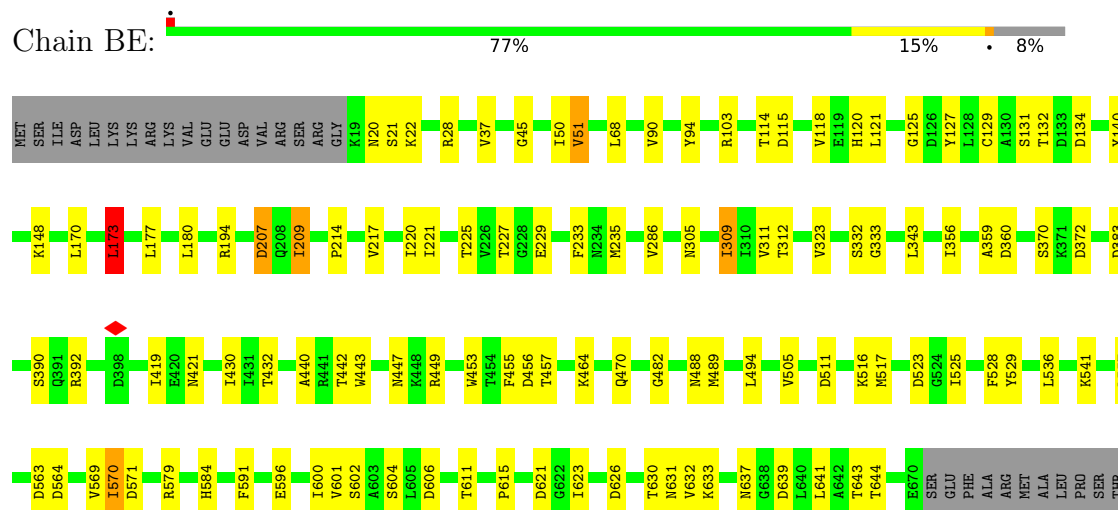
- Molecule 37: U3 small nucleolar RNA-associated protein 18

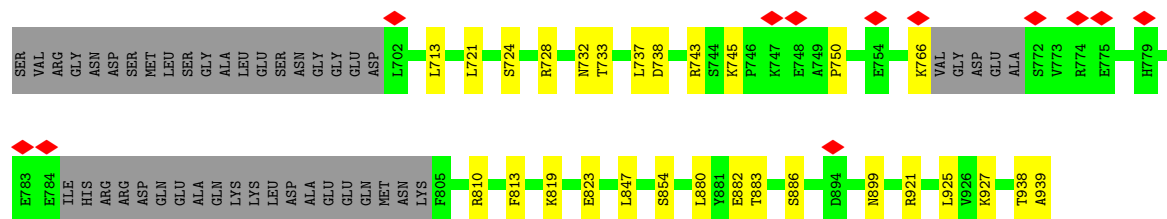
Chain B8:



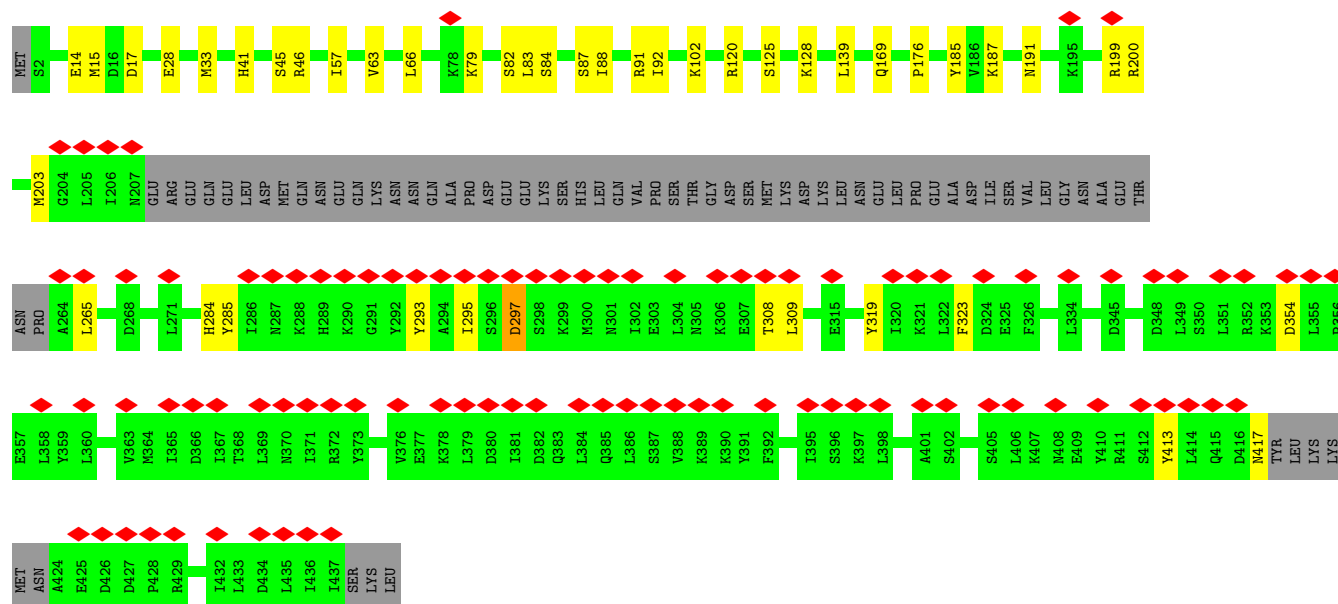
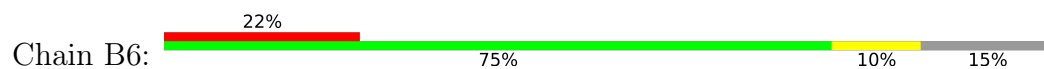
- Molecule 38: U3 small nucleolar RNA-associated protein 21

Chain BE:

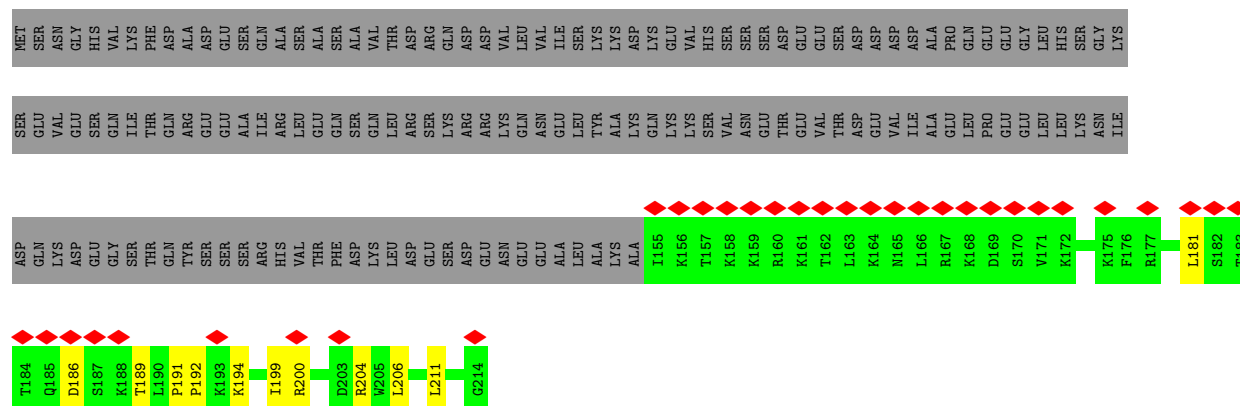




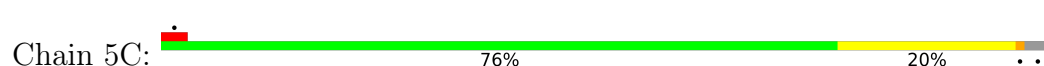
• Molecule 39: U3 small nucleolar RNA-associated protein 6



• Molecule 40: Bud site selection protein 21



• Molecule 41: U3 small nucleolar RNA-associated protein 7



- Molecule 44: U3 small nucleolar ribonucleoprotein protein IMP3

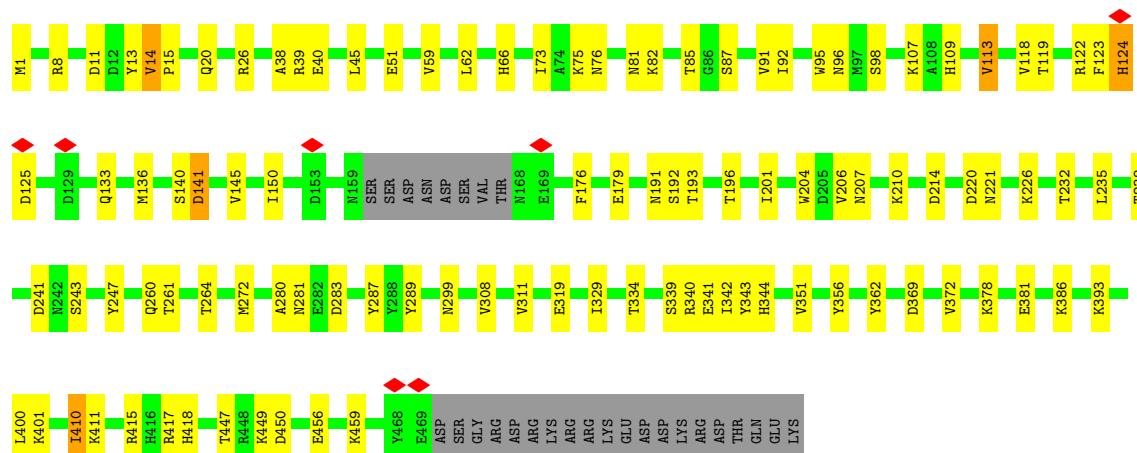
- Molecule 45: U3 small nucleolar ribonucleoprotein protein IMP4

- Molecule 46: Something about silencing protein 10



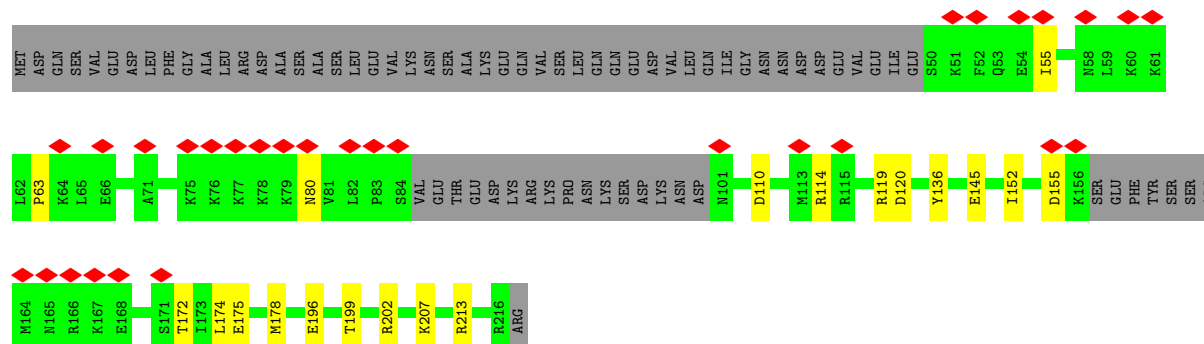
• Molecule 47: Protein SOF1

Chain 5I: 73% 21% 6%



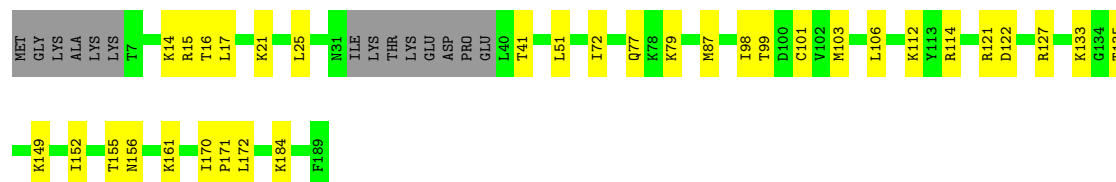
• Molecule 48: rRNA-processing protein FCF2

Chain 5J: 14% 57% 9% 34%



• Molecule 49: rRNA-processing protein FCF1

Chain 5K: 75% 17% 7%



• Molecule 50: Ribosome biogenesis protein ENP2

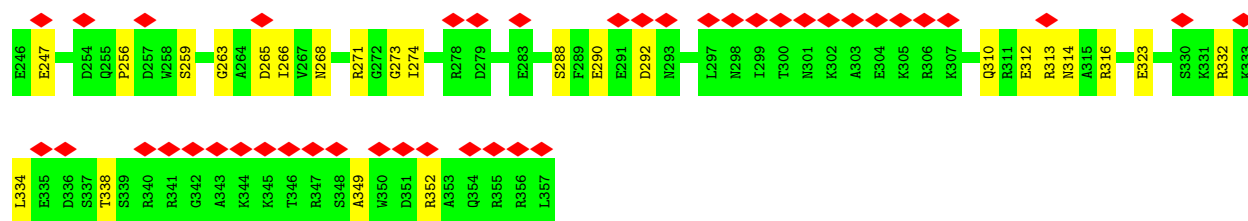
Chain RA: 47% 32% 15% 52%

MET	V2	L3	K4	S5	T6	S7	A8	N9	D10	V11	S12	V13	V14	Q15	V16	S17	G18	T19	Q20	V21	SER	ARG	SER	LEU	PRO	ASP	TRP	ILE	ALA	LYS	ARG	LYS	GLN	LEU	ASN	ASP	L41	E42	Y43	Q44	N45	R46	V47	E48	L49	I50	Q51	D52	F53	E54	F55	S56	E57	A58	S59	N60			
K61	I62	K63	V64	S65	R66	D67	G68	Q69	V70	C71	W72	A73	T74	G75	T76	Y77	K78	P79	Q80	T81	H82	V83	T84	D85	F86	A87	N88	L89	S90	L91	K92	F93	D94	R95	H96	T97	D98	A99	E100	N101	V102	D103	F104	T105	I106	L107	S108	ASP	ASP	W111	T112	K113	S114	V115	H116	L117	Q118	N119	D120
R121	S122	I123	Q124	F125	Q126	N127	K128	G129	E130	L131	H132	Y133	T134	T135	R136	I137	P138	K139	F140	T141	R142	S143	L144	V145	Y146	M147	K148	V149	M150	C151	D152	L153	Y154	V155	G156	A157	S158	G159	N160	E161	L162	Y163	R164	L165	N166	L167	E168	K169	G170	R171	F172	L173	M174	P175	F176	K177	L178	D179	T180
E181	G182	V183	N184	H185	V186	S187	I188	N189	E190	V191	N192	G193	L194	L195	A196	A197	G198	T199	E200	T201	N202	V203	V204	E205	F206	W207	D208	P209	R210	S211	R212	S213	R214	V215	S216	K217	L218	Y219	L220	E221	N222	N223	T224	D225	N226	R227	F228	F229	Q230	V231	T232	T233	T234	S235	F236	R237	N238	D239	G240
L241	T242	F243	A244	C245	G246	T247	S248	N249	G250	Y251	S252	Y253	T254	Y255	D256	L257	R258	T259	E260	E261	P262	S263	T264	I265	K266	D267	Q268	G269	Y270	G271	F272	D273	T274	K275	K276	T277	T278	W279	D281	N282	V283	G284	T285	E286	N287	K288	T289	V290	T291	C292	D293	K294	R295	T296	A297	K298	T299	W300	
D301	R302	L303	D304	G305	K306	A307	Y308	A309	S310	N311	E312	F313	S314	V315	D316	T317	N318	D319	I320	E321	H322	V323	P324	G325	T326	G327	N328	F329	F330	T331	A332	N333	E334	S335	I336	P337	N338	H339	T340	Y341	Y342	I343	P344	S345	L346	G347	P348	S349	P350	R351	W352	C353	S354	F355	L356	D357	S358	I359	T360
GLU	GLU	LEU	GLU	GLU	LYS	PRO	SER	ASP	GLU	ASP	GLU	THR	VAL	GLU	THR	ASP	GLU	LYS	LEU	GLU	ASN	THR	LEU	VAL	GLY	SER	GLY	LYS	ARG	VAL	ASN	GLY	PHE	PHE	ILE	ASN	GLY	THR	GLY	ASP	LEU	TYR	ASP	VAL	LYS	VAL	GLY	VAL	LYS	SER	LEU	ILE	ALA	ASN	PRO				
ASP	ALA	TYR	LYS	GLU	GLU	ARG	GLU	ARG	GLU	ASP	GLU	THR	VAL	GLU	THR	ASP	GLU	LYS	PRO	VAL	LYS	GLY	THR	LEU	VAL	GLY	GLY	LYS	ARG	VAL	ASN	GLY	PHE	PHE	ILE	ASN	GLY	THR	GLY	ASP	LEU	TYR	ASP	VAL	LYS	VAL	GLY	VAL	LYS	SER	LEU	ILE	ALA	ASN	PRO				
ARG	PHE	GLY	LYS	MET	PHE	GLU	ASP	GLU	ASP	GLU	THR	PHE	GLU	THR	ASP	GLU	LYS	PRO	VAL	LYS	GLY	THR	LEU	VAL	GLY	GLY	LYS	ARG	VAL	ASN	GLY	PHE	PHE	ILE	ASN	GLY	THR	GLY	ASP	LEU	TYR	ASP	VAL	LYS	VAL	GLY	VAL	LYS	SER	LEU	ILE	ALA	ASN	PRO					
GLY	HIS	TYR	ASP	TYR	GLU	ASP	GLU	GLU	ASP	GLU	SER	ASP	GLU	THR	ASN	GLY	LYS	ASN	GLY	GLU	GLY	THR	LEU	VAL	GLY	GLY	LYS	ASN	ILE	LEU	ARG	ASN	ASN	GLN	ARG	GLY	GLY	ARG	LEU	GLY	THR	PHE	THR	LYS	PRO	GLY	VAL	LYS	PRO	GLY	VAL	LYS	SER	LEU					
LYS	ALA	GLY	THR	SER	THR	SER	GLN	ARG	ASP	GLU	ASP	GLU	PHE	GLY	GLU	GLN	GLY	GLU	LEU	LEU	GLU	VAL	GLY	GLY	GLY	LYS	ASN	ILE	LEU	ARG	ASN	ASN	ALA	PHE	ARG	GLY	GLY	ALA	GLY	THR	PHE	THR	LYS	PRO	GLY	VAL	LYS	PRO	GLY	VAL	LYS	SER	LEU						
GLY	ASN	TYR	LYS	LYS	ARG	ARG	HIS	ASP	ASP	GLU	GLY	GLY	ILE	ASP	GLU	ASN	GLY	LYS	ASP	ASN	ARG	PHE	GLU	GLY	GLY	ASN	ASN	ARG	ALA	LYS	ASN	ASN	ALA	PHE	ARG	GLY	GLY	MET																					
MET	SER	LEU	ASN	ALA	LEU	LEU	LYS	LEU	ILE	ASN	GLY	THR	THR	GLU	GLU	SER	GLY	ASP	ARG	LEU	SER	ALA	SER	MET	ALA	THR	ASP	GLU	ILE	PRO	GLU	SER	GLN	ASN	HIS	ARG	LEU	GLU	HIS	PHE	THR	ASP	ALA	PRO	LYS	PRO	GLY	VAL	LYS	PRO	GLY	VAL	LYS	SER	LEU				
LEU	SER	LEU	LYS	ASN	GLY	SER	MET	GLY	TYR	ILE	GLY	THR	THR	ILE	GLY	ASN	GLY	ASP	ARG	LEU	SER	ALA	SER	MET	ALA	THR	ASP	GLU	ILE	PRO	GLU	SER	GLN	ASN	HIS	ARG	LEU	GLU	HIS	PHE	THR	ASP	ALA	PRO	LYS	PRO	GLY	VAL	LYS	PRO	GLY	VAL	LYS	SER	LEU				
LEU	ASP	LEU	THR	ARG	ALA	TYR	VAL	VAL	LYS	GLY	ASP	ASP	ALA	GLY	GLY	LYS	ASN	GLY	ASP	ARG	LEU	SER	ALA	SER	MET	ALA	THR	ASP	GLU	ILE	PRO	GLU	SER	GLN	ASN	HIS	ARG	LEU	GLU	HIS	PHE	THR	ASP	ALA	PRO	LYS	PRO	GLY	VAL	LYS	PRO	GLY	VAL	LYS	SER	LEU			
LYS	LYS	SER	ALA	ARG	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL			

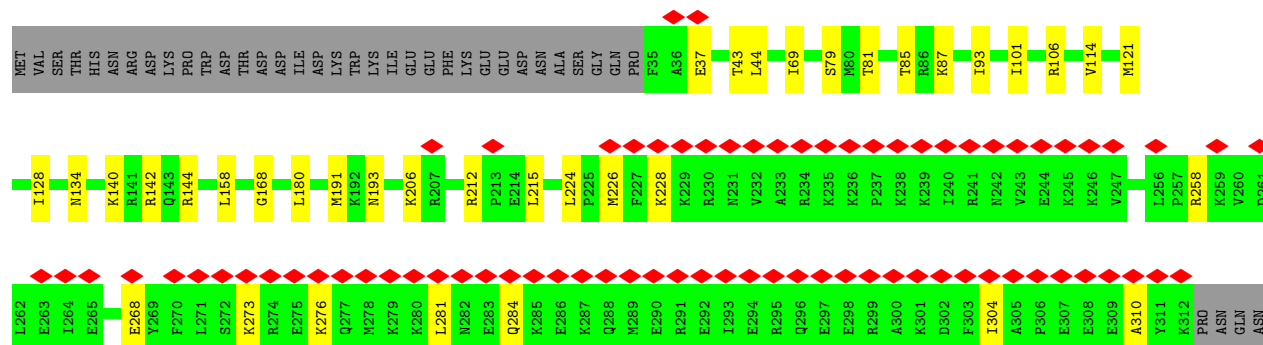
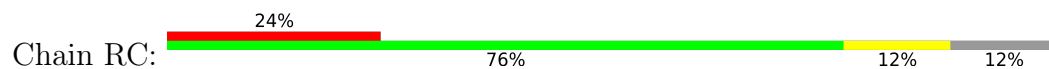
<

● Molecule 51: U3 small nucleolar ribonucleoprotein protein LCP5

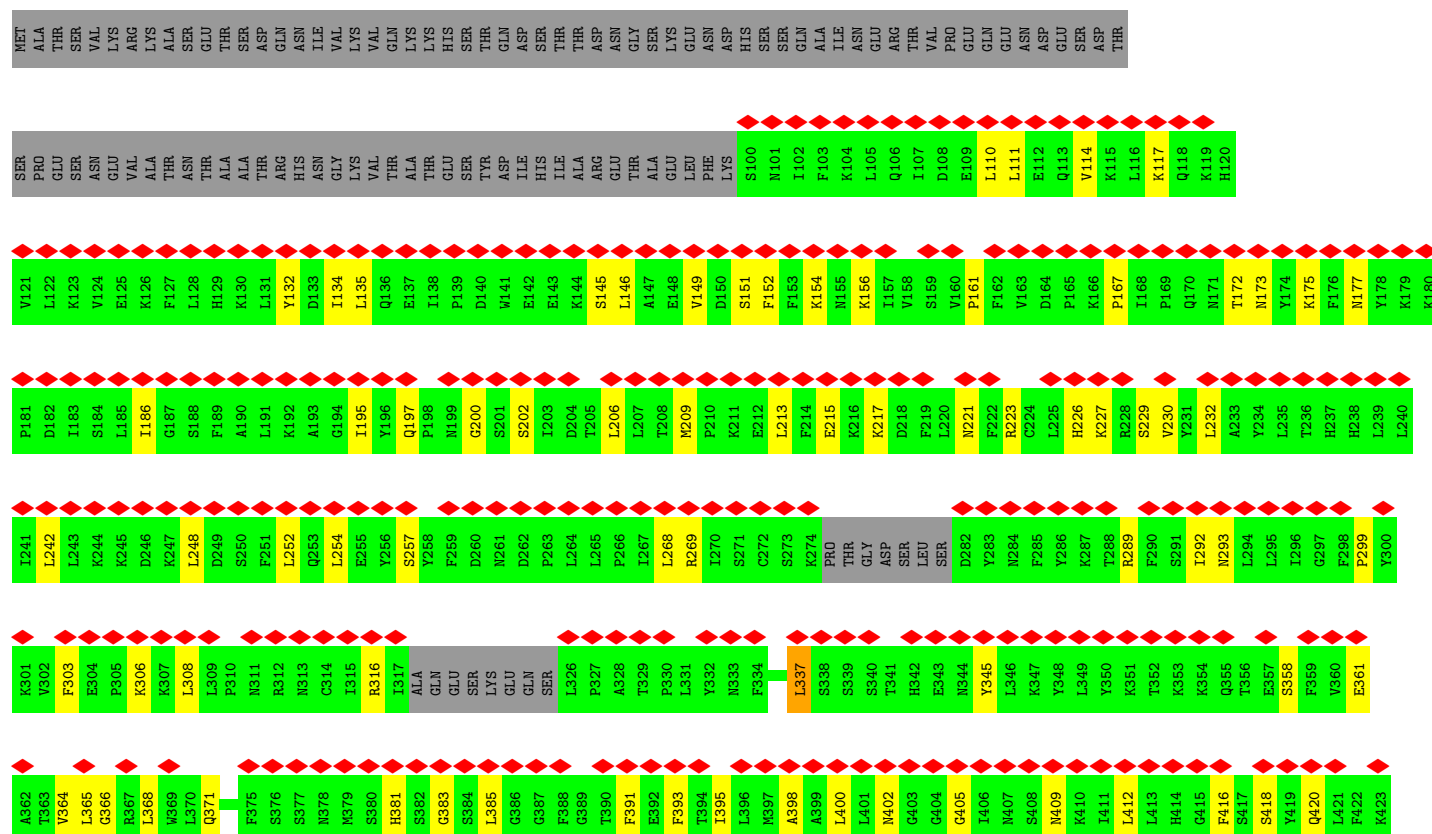
Chain RB: 

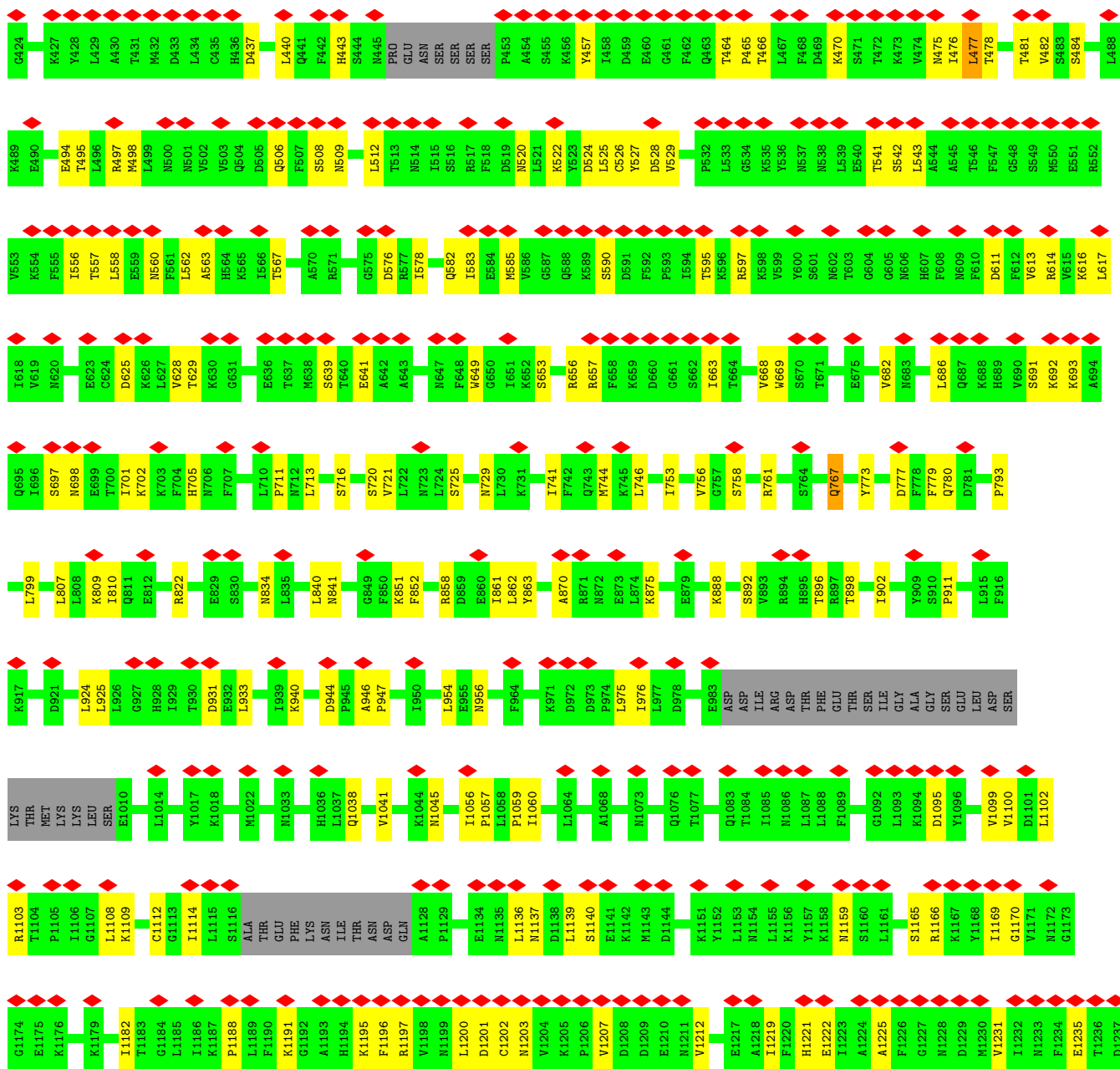


• Molecule 52: KRR1 small subunit processome component

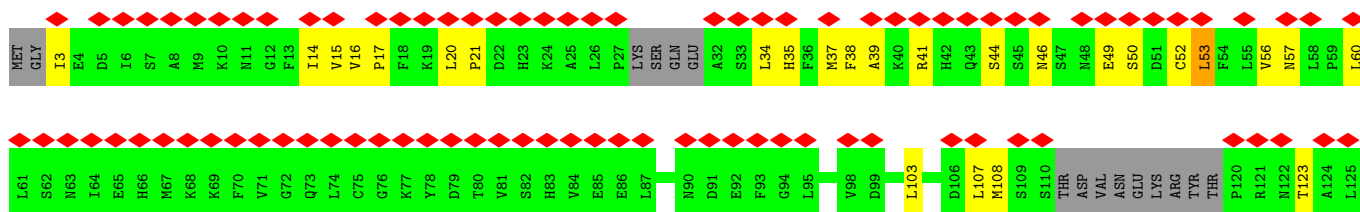


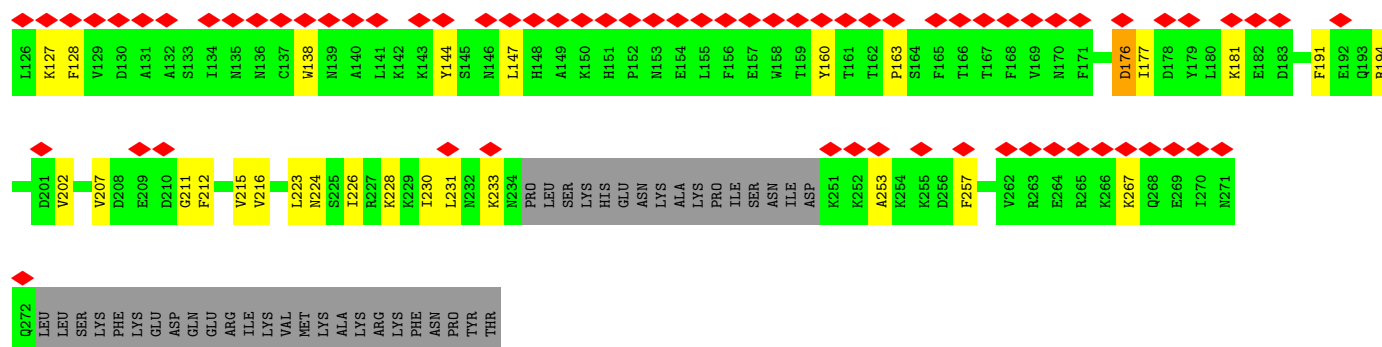
• Molecule 53: U3 small nucleolar RNA-associated protein 22



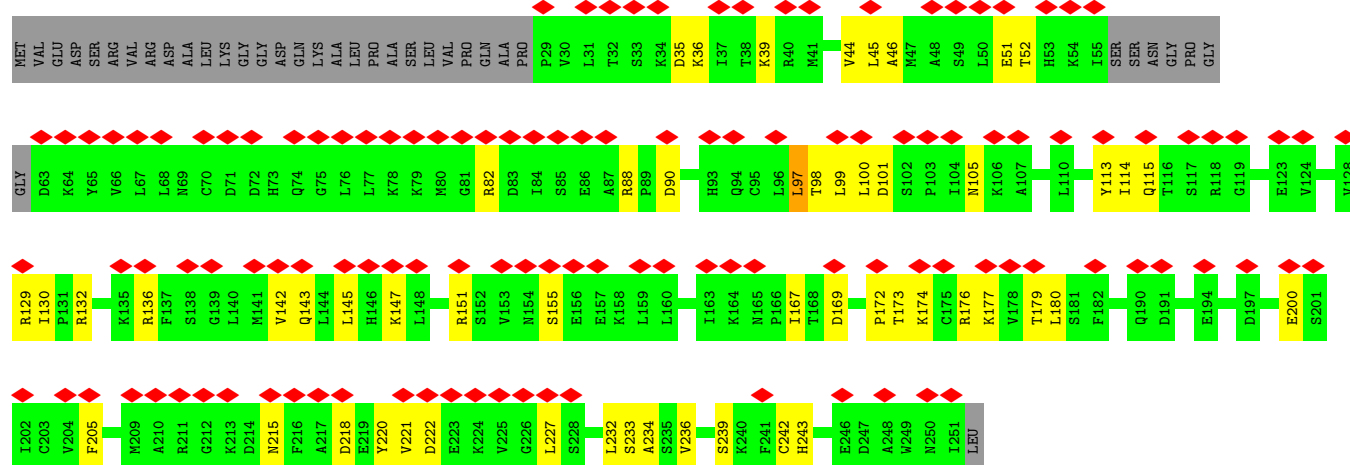


• Molecule 54: Ribosomal RNA-processing protein 7

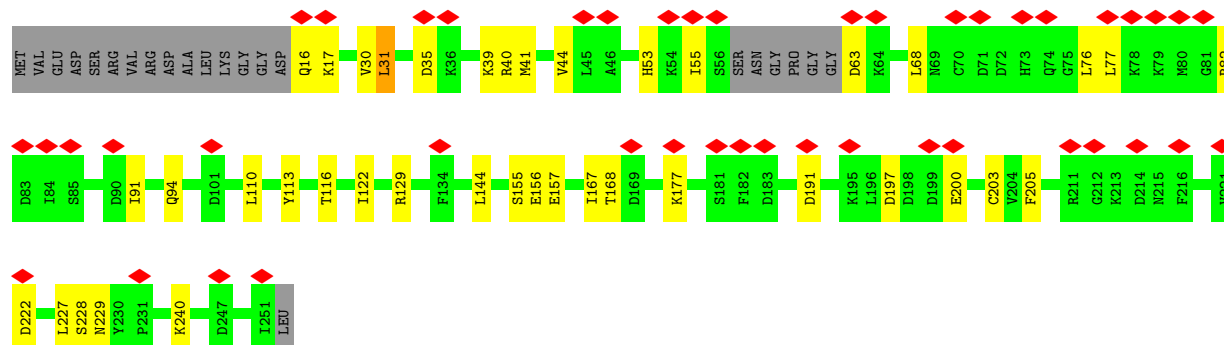
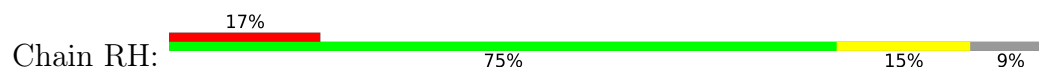




- Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1

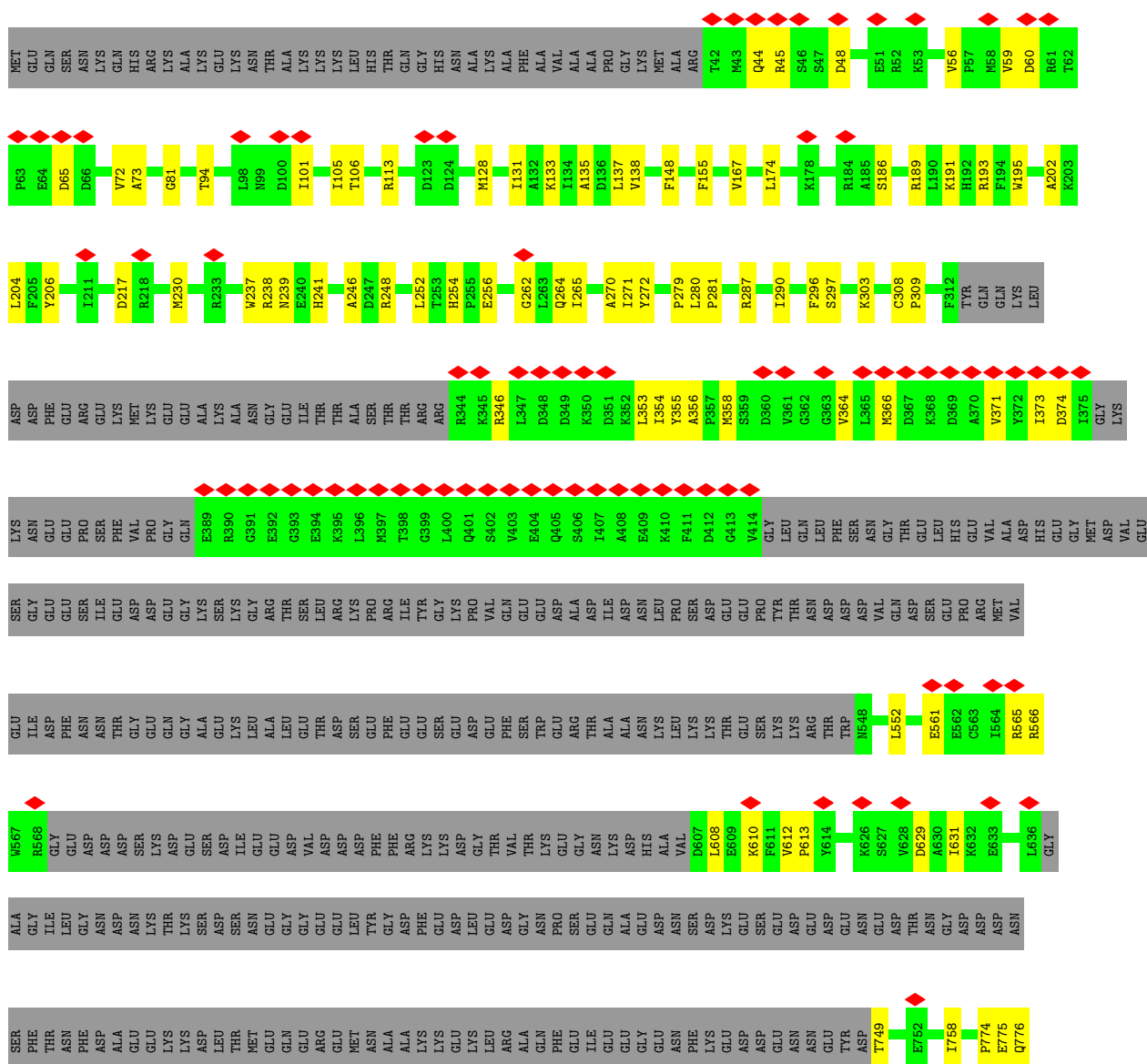


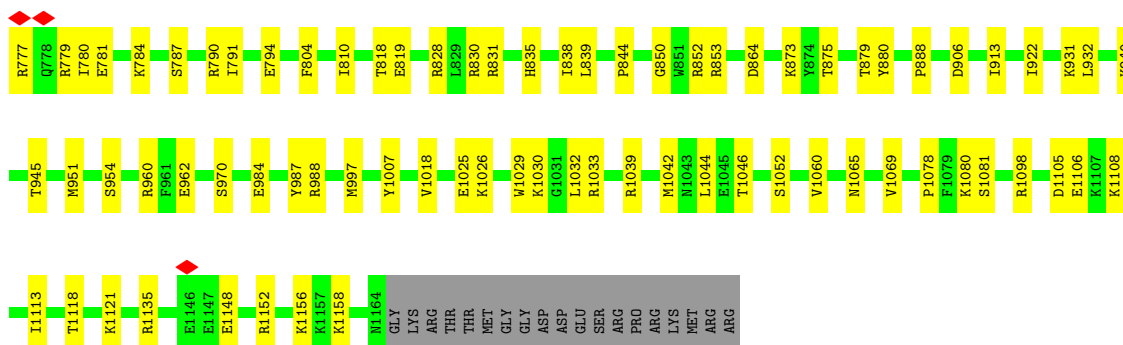
- Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1



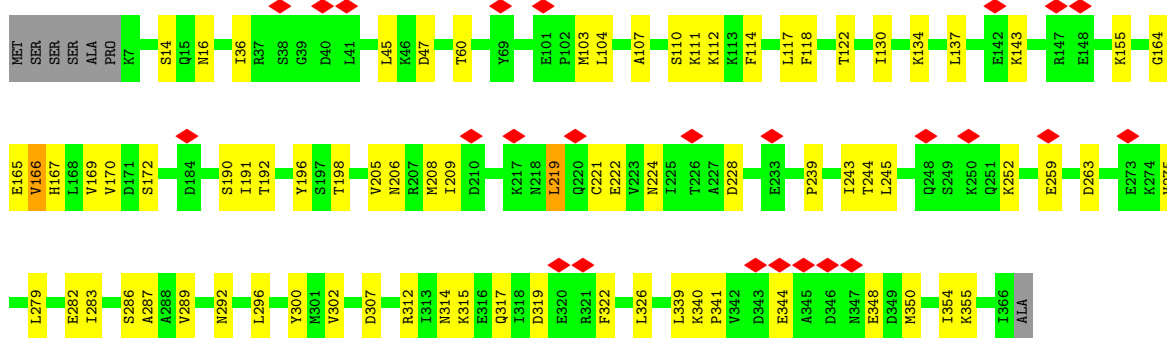
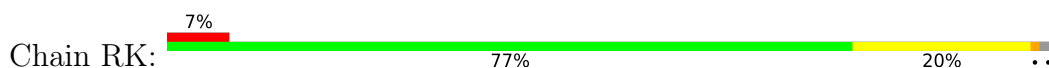
- Molecule 56: Ribosome biogenesis protein UTP30



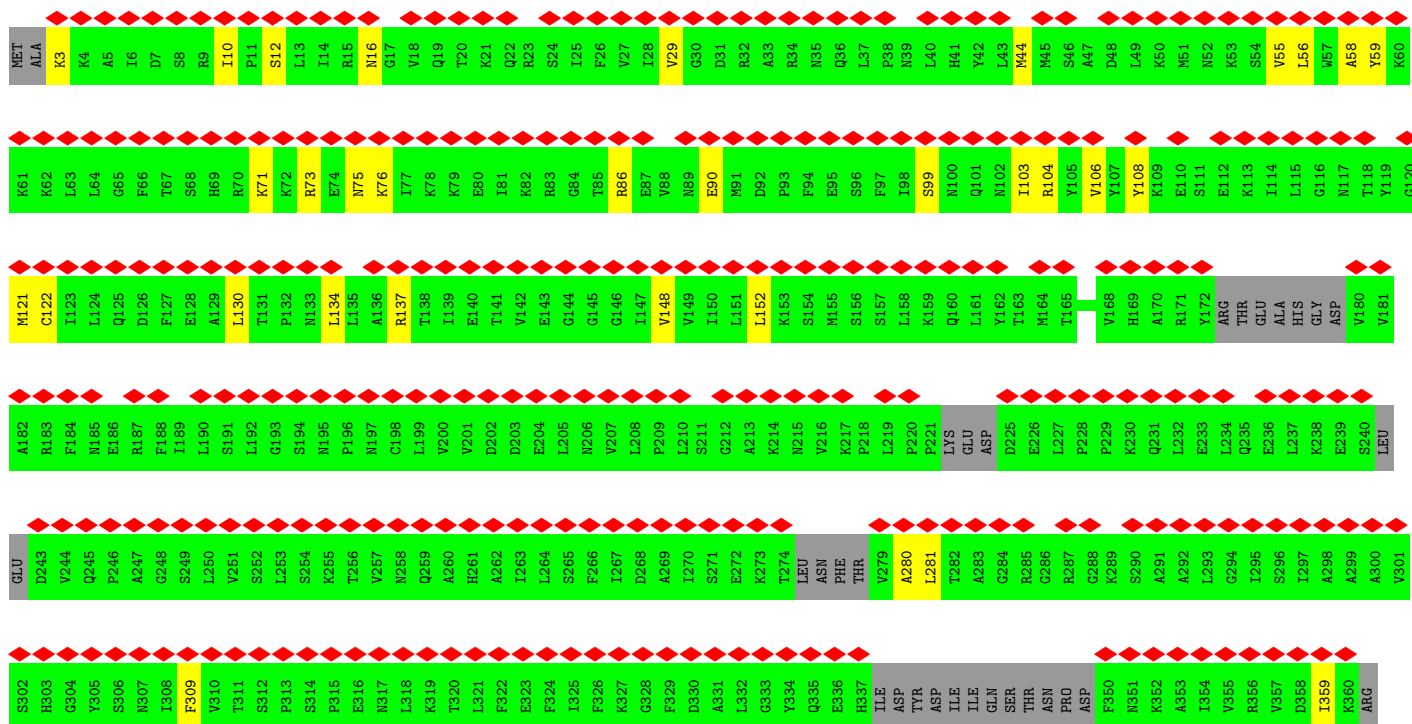
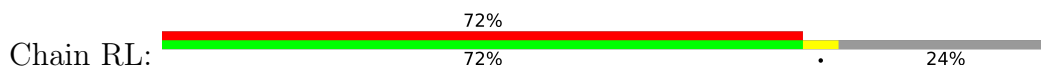


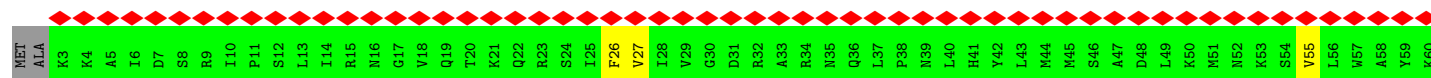


• Molecule 58: RNA 3'-terminal phosphate cyclase-like protein

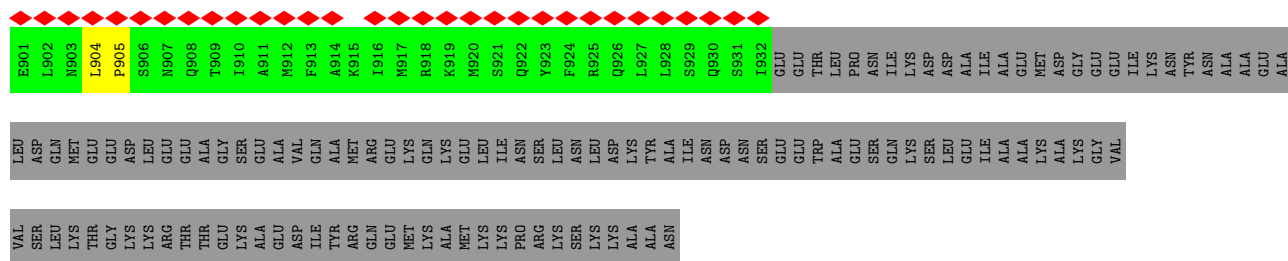


• Molecule 59: RNA cytidine acetyltransferase

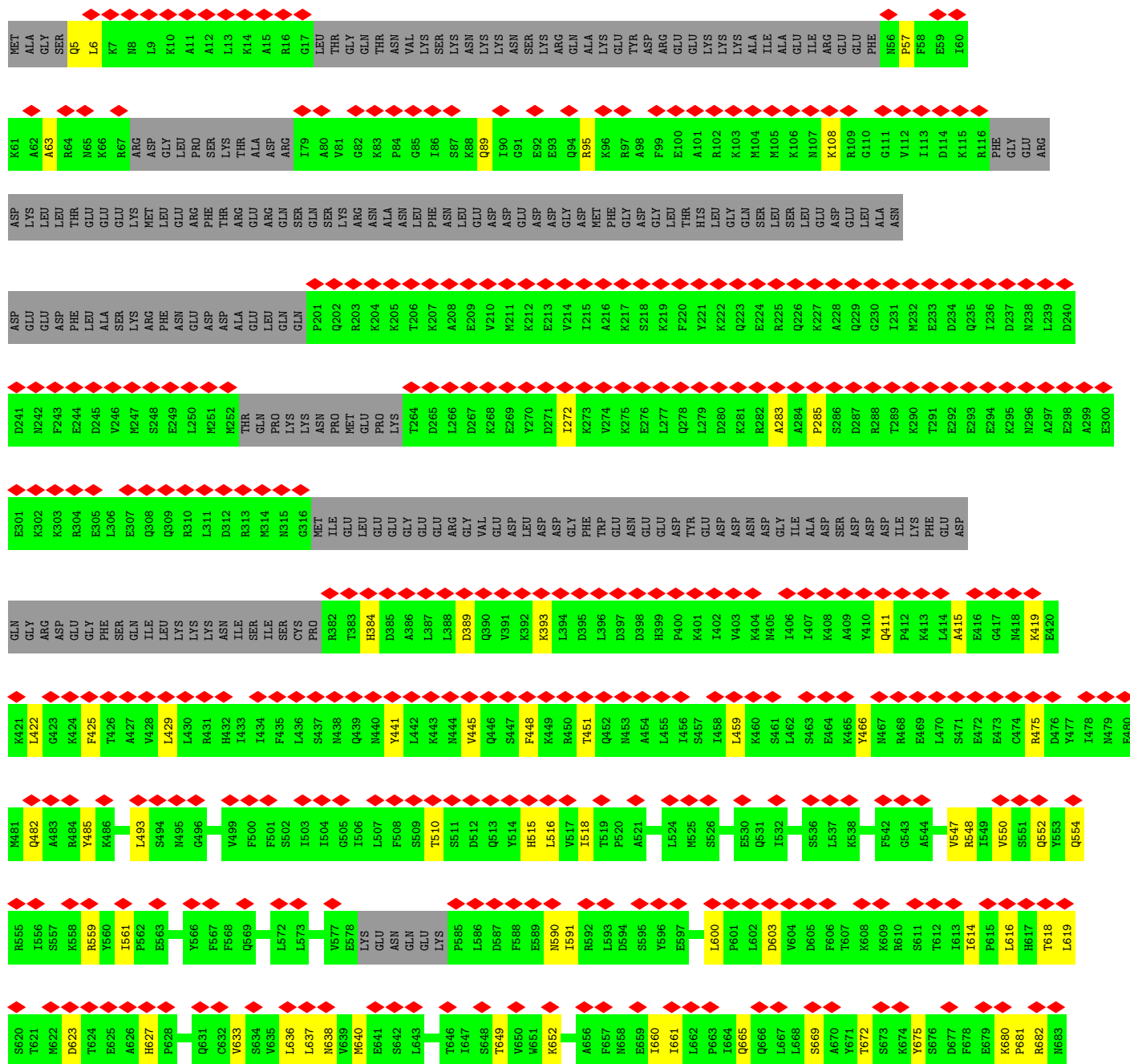


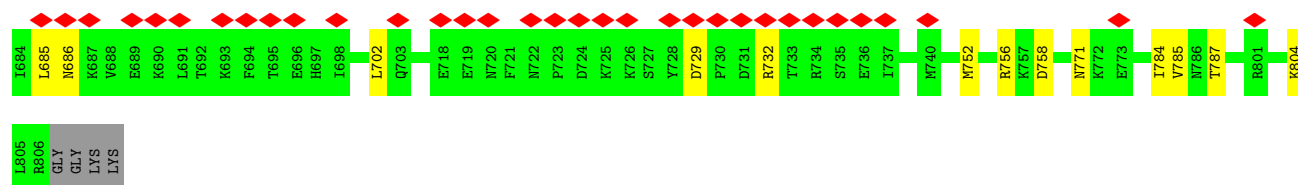


R841	L842	D843	S844	R845	S846	S847	L788	L789	S790	Y791	D792	F793	H794	K795	G796	T797	A798	V799	Q800	A801	L802	S803	V804	L805	E806	S807	S808	K809	K810	A811	Q812	D813	L814	S815	D816	D817	S878	S879	V880	S881	S882	A883	L884	E885	L886	A887	I888	G889	L890	Q891	R892	K893	L894	I895	D896	T897	I898	K900													
H721	Y722	L723	G724	Y725	S726	Y727	G728	L729	S730	Q731	S732	L733	H734	K735	F736	W737	K738	N739	H740	S741	F742	V743	P744	Y745	Y746	L747	R748	Q749	D869	T750	A751	N752	D753	L754	T755	G756	E757	H758	T759	G760	V761	M762	L763	N764	V765	L766	E767	G768	R769	E770	S771	N772	W773	L774	V775	E776	F777	A778	K779	D780											
F781	R782	K783	R784	F785	L786	S787	L788	L789	S790	Y791	D792	F793	H794	K795	G796	T797	A798	V799	Q800	A801	L802	S803	V804	L805	E806	S807	S808	K809	K810	A811	Q812	D813	L814	S815	D816	D817	S878	S879	V880	S881	S882	A883	L884	E885	L886	A887	I888	G889	L890	Q891	R892	K893	L894	I895	D896	T897	I898	K900													
F661	GLY	LYS	PHE	THR	ASP	MET	SER	GLU	ASP	VAL	ARG	PRO	LYS	ASP	TYR	SER	ILE	LYS	ARG	VAL	SER	ASP	LYS	GLU	LEU	LEU	LYS	ASP	ASP	VAL	LYS	LEU	ARG	ASP	ALA	LYS	THR	LEU	PRO	PRO	L708	L709	L710	K711	L712	S713	E714	Q715	P716	P717	H718	Y719	L720																		
N601	S602	L603	S604	R605	G606	Q607	R608	A609	G610	M611	D612	L613	T614	P615	V616	L617	I618	S619	Q620	R621	F622	Q623	D624	E625	E626	F627	A628	S629	L630	S631	G632	A633	R634	L635	V636	R637	T638	A639	T640	N641	P642	E643	Y644	A645	S646	M647	G648	Y649	G650	S651	R652	A653	T654	E655	L656	L657	R658	D659	Y660												
Y541	V542	S543	S544	H545	Y546	K547	N548	S549	P550	N551	D552	L553	Q554	L555	M556	S557	D558	A559	P560	A561	H562	K563	L564	F565	V566	L567	L568	P569	S570	P571	D572	P573	K574	D575	G576	G577	R578	L579	P580	D581	P582	L583	C584	V585	L586	Q587	L588	A589	LEU	G592	E593	L594	S595	K596	E597	S598	V599	R600													
P481	I482	E483	K484	W485	L486	N487	K488	L489	L490	C491	L492	D493	V494	L495	L496	S497	I497	K498	N499	P500	R501	F502	A503	T504	R505	G506	T507	P508	H509	P510	S511	Q512	C513	N514	L515	F516	V517	V518	N519	R520	D521	T522	L523	F524	S525	S526	H527	P528	V529	E531	N532	F533	L534	E535	K536	M537	M538	A539	L540												
SER	L422	S423	L424	K425	L426	L427	Q428	Q429	L430	R431	M432	Q433	ASN	ASN	THR	SER	GLY	ARG	GLU	SER	THR	GLN	THR	ALA	VAL	SER	ASP	ASN	LYS	LYS	ASP	HIS	LEU	HIS	SER	GLN	SER	ARG	GLN	LEU	ARG	E467	I468	S469	L470	D471	E472	P473	R474	R475	Y476	A477	P478	G479	D480																
ARG	ASP	HIS	ARG	GLN	THR	ILE	Q368	Y369	I370	V371	P372	Q373	D374	H375	Q376	V377	L378	G379	Q380	A381	E382	L383	V384	V385	I386	D387	E388	A389	A390	A391	I392	PRO	LEU	PRO	I396	V397	K398	N399	L400	L401	G402	P403	Y404	L405	V406	F407	M408	A409	S410	T411	I412	M413	G414	T415	GLU	GLY	THR	GLY	ARG												
V301	S302	H303	G304	Y305	S306	N307	I308	F309	V310	T311	S312	P313	S314	P315	E316	N317	L318	K319	T320	L321	F322	E323	F324	I325	F326	K327	G328	F329	D330	A331	L332	G333	Y334	Q335	E336	H337	ILE	ASP	TYR	ASP	ILE	GLN	SER	THR	ASN	PRO	PHE	THR	V279	A280	L281	T282	A283	G284	SER	R285	G286	R287	G288	K289	S290	A291	A292	L293	G294	I295	S296	I297	A298	A299	A300
LEU	D243	V244	Q245	P246	A247	G248	S249	L250	V251	S252	L253	S254	K255	T256	V257	N258	Q259	H260	A261	A262	I263	L264	S265	F266	I267	D268	A269	I270	S271	E272	K273	T274	LEU	ASN	PHE	THR	V279	A280	L281	T282	A283	G284	SER	R285	G286	R287	G288	K289	S290	A291	A292	L293	G294	I295	S296	I297	A298	A299	A300												
V181	A182	R183	F184	E185	E186	R187	F188	I189	L190	S191	L192	G193	S194	N195	P196	N197	G198	L199	V200	V201	D202	D203	E204	L205	N206	V207	L208	P209	L210	S211	G212	A213	K214	N215	V216	K217	PRO	LEU	PRO	PRO	LYS	GLU	D224	D225	E226	L227	P228	P229	K230	Q231	L232	E233	L234	Q235	E236	L237	K238	E239	SER												
M121	C122	I123	L124	Q125	D126	F127	E128	A129	L130	Y131	P132	L133	L134	L135	A136	R137	T138	I139	E140	T141	V142	E143	G144	G145	G146	I147	V148	V149	I150	L151	L152	K153	S154	M155	S156	S157	L158	K159	Q160	L161	Y162	T163	M164	T165	M166	D167	V168	H169	Q231	L232	E233	L234	Q235	E236	L237	K238	E239	V180													
K61	K62	L63	L64	G65	F66	THR	SER	HIS	HIS	ARG	LYS	LYS	ARG	GLU	ASN	LYS	ILE	LYS	LYS	GLU	ILE	LYS	ARG	THR	ARG	GLY	THR	GLU	VAL	ASN	GLU	MET	D92	P93	F94	E95	S96	F97	I98	S99	N100	Q101	N102	I103	R104	Y105	V106	Y107	Y108	K109	E110	S111	E112	K113	I114	L115	G116	N117	T118	Y119	G120										

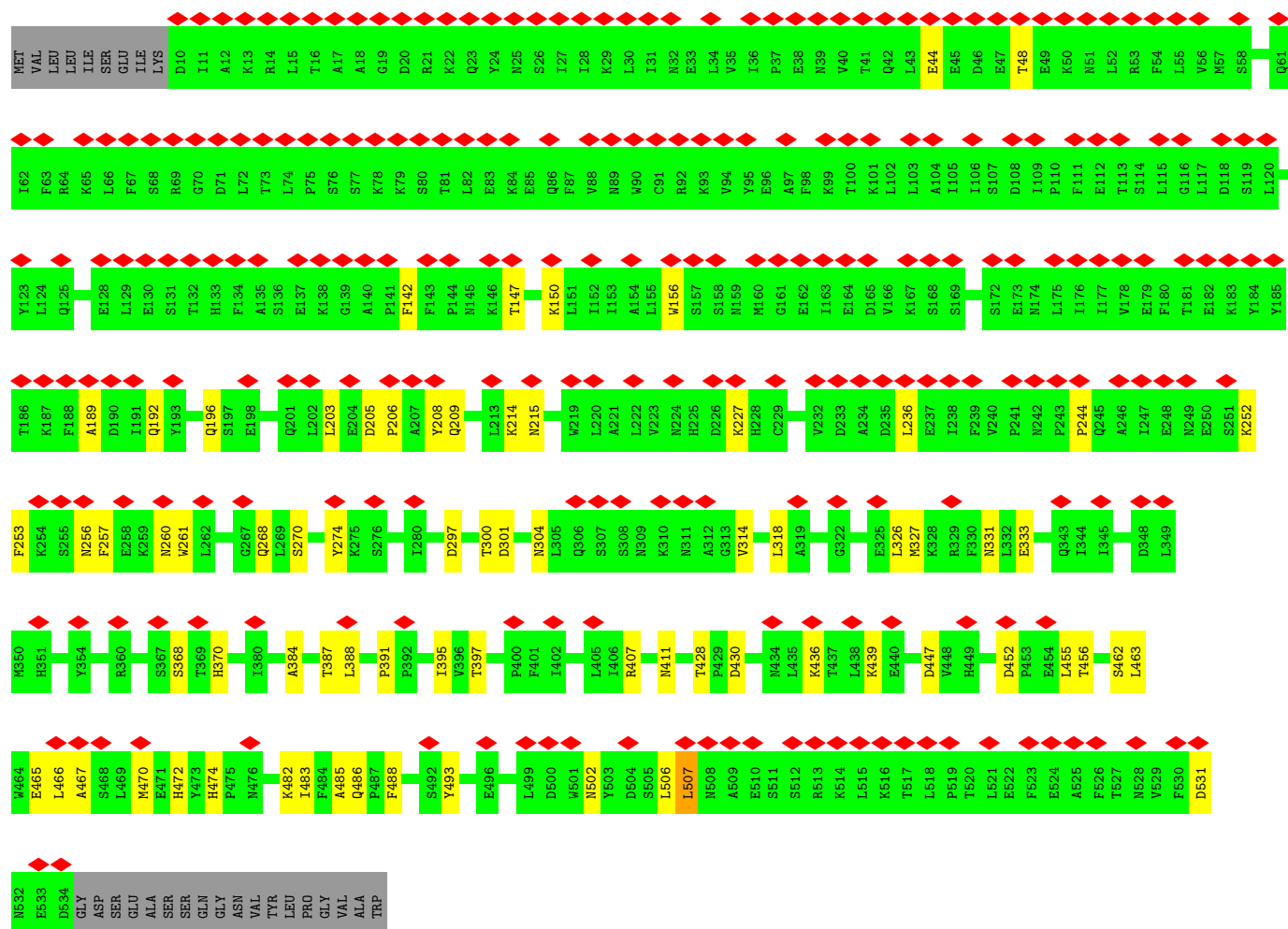
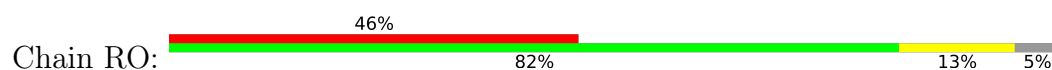


• Molecule 60: Nucleolar complex protein 14

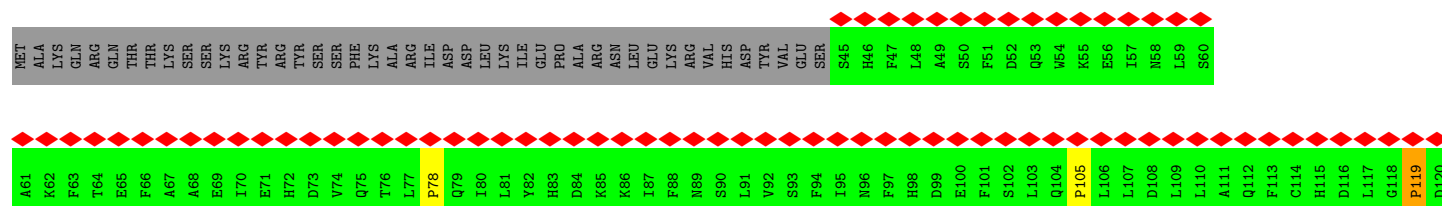
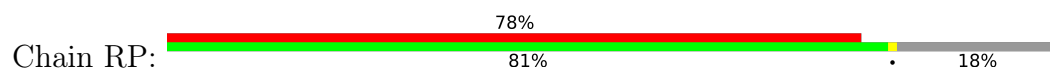




• Molecule 61: Nucleolar complex protein 4



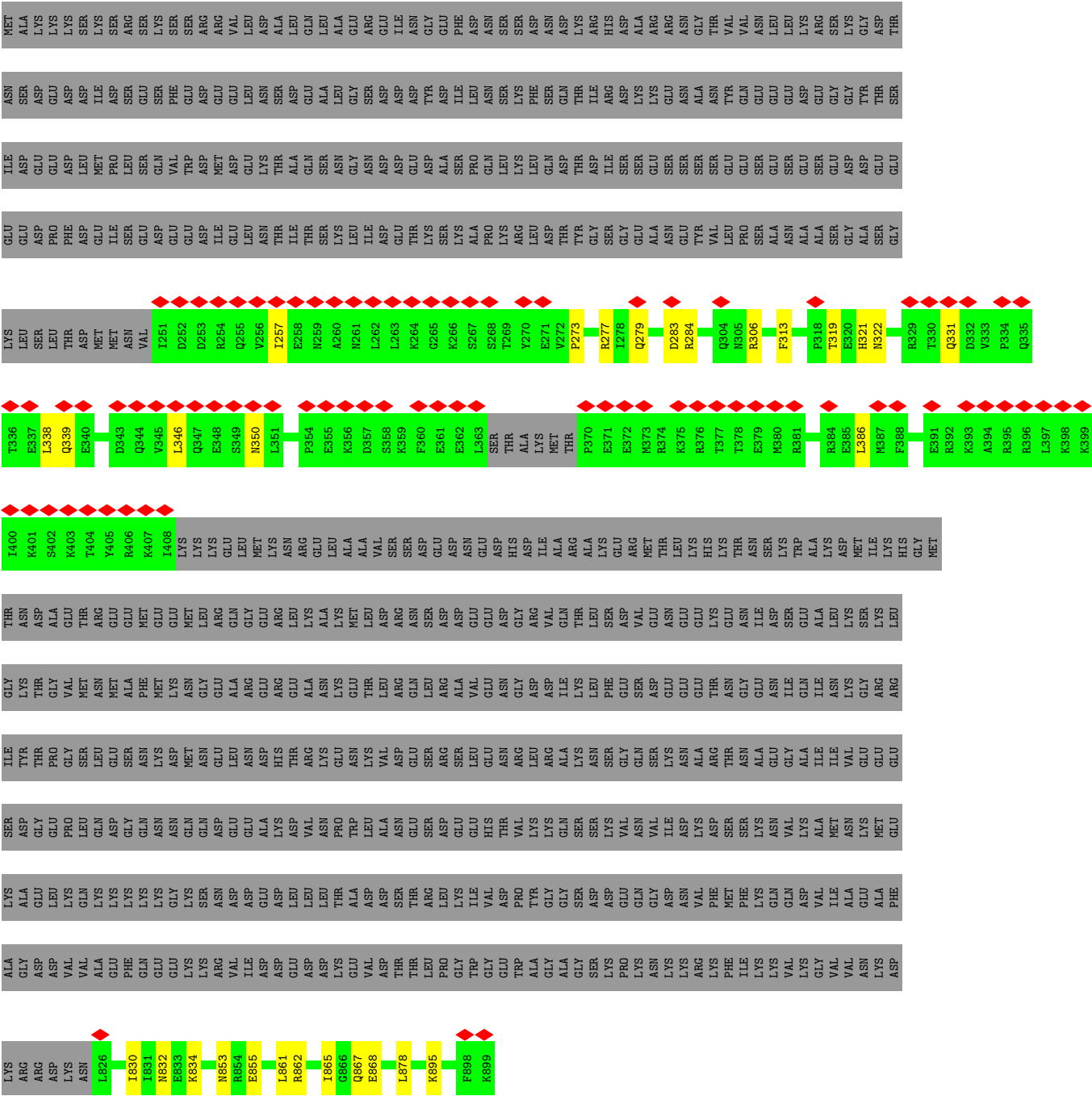
• Molecule 62: U3 small nucleolar RNA-associated protein 20



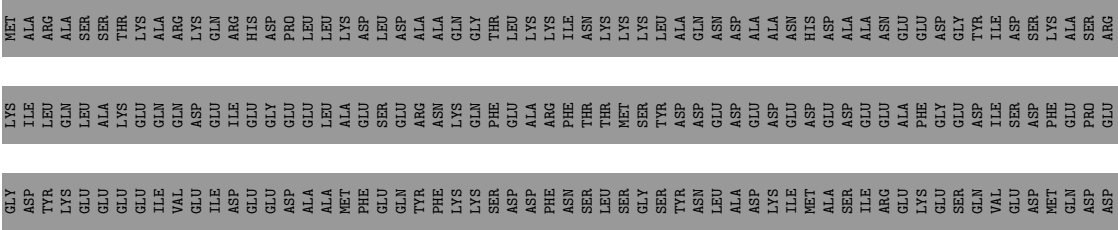
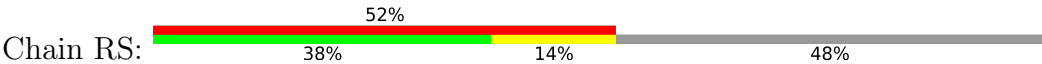
F121	L181	T241	D301	L361	L421	TRP	I541	F661	E721	V781	I841	I901
L122	S182	S242	F302	F362	K422	ARG	L542	F662	D722	H782	K842	T902
K123	H183	T243	N303	A363	K423	ALA	D543	L663	G723	L783	N843	T903
F124	S184	Q244	D304	L364	N424	ILE	N544	K664	A724	S784	V844	F904
Y125	K185	E245	S305	F365	N425	I485	Y545	L665	M725	T785	Y845	L905
E126	E186	T246	LEU	I366	Q426	F486	E546	L666	K726	T786	S846	T906
E127	Y187	L247	ASP	R367	S427	K487	N547	F667	V727	Q787	A847	E907
A128	L188	H248	ALA	N368	Q428	Y488	Y548	G668	L728	V788	T848	N908
I129	S189	T249	THR	S369	Q429	S489	K549	L669	W729	A789	E849	G909
K130	R190	K250	ASN	D370	K430	K490	E550	L670	L730	E790	L850	S910
T131	F191	A251	ILE	D371	K431	L491	S551	T671	S731	M791	H851	Q911
L132	S192	K252	ASP	V371	I432	Q492	L552	V672	S732	H792	D852	S912
I133	A193	E253	R313	K372	I433	N493	ASN	R673	V733	F793	H853	I913
N134	E194	I254	I314	T373	A434	T494	PHE	F674	V734	V794	L854	K914
L135	A195	M255	L315	L374	L435	E495	LEU	S675	R735	D795	M855	A915
L136	L196	S256	K316	T375	F436	L496	ARG	P676	L736	T796	V856	E916
D137	S197	V257	V317	L376	I437	L497	G557	V677	R737	A797	L857	D917
A138	F198	L258	T319	F377	E438	ILE	W558	V678	D738	T798	L858	E918
A139	L199	L259	T320	H378	E439	PRO	N559	W679	T739	F799	G859	K919
I140	V200	H260	I321	Q379	V439	LEU	K560	S680	I740	W800	S860	V920
E141	R201	E261	V322	L381	D440	E502	L561	V681	D741	Y801	R861	V921
F142	K202	A262	F323	F382	K441	R503	V562	F682	T742	N802	N862	M922
E143	C203	L263	S324	N383	P443	I504	S563	D683	F743	D803	T863	P923
S144	P204	T264	E325	Y384	E444	F505	N564	T684	S744	F804	D864	Y924
S145	V205	K265	SER	A385	L445	S506	L565	L685	H745	K805	V865	V925
N146	S206	S266	GLY	L386	Q446	T507	H566	E686	I746	T806	Q866	L926
V147	N207	S267	ARG	T387	K447	F508	P567	V687	W747	Y807	K867	R927
F148	L208	P268	LYS	N388	V448	A509	S568	W688	S748	K808	L868	I928
E149	R209	E269	P331	I389	R449	S510	E569	Y689	K749	D809	A869	F929
W150	E210	R270	D332	S390	E450	P511	S570	T690	V750	E810	L870	P930
G151	F211	S271	W333	D391	V451	D512	L571	K691	S751	E811	D871	Q931
F152	V212	V272	N334	C392	N452	N513	K572	D692	Q752	D812	A872	R932
N153	R213	S273	K335	F393	F453	F514	L574	E693	Q753	M813	L873	A933
C154	S214	L274	I336	L394	P454	T515	M575	A694	N754	E814	L874	Q934
L155	V215	L275	T337	E395	E455	K516	S576	L695	T755	N815	A875	V935
A156	F216	S276	I338	F396	E456	ASP	S577	V696	S756	E816	Y876	P936
Y157	E217	D277	L339	F397	F457	MET	H578	W697	I757	R817	K877	P937
I158	K218	I278	I340	Q398	I458	VAL	V579	K698	L758	V818	N878	S938
F159	L219	W279	E341	F399	L459	T521	S580	L699	S759	I819	T879	S939
K160	E220	M280	R342	A400	S460	L522	L581	V700	T760	T820	K881	Q940
Y161	GLY	N281	I343	L401	I461	L523	L582	R641	T761	G821	L881	Q941
S162	ASP	I282	N344	R402	E462	K524	L583	I642	I762	S822	N882	K942
S163	ASP	S283	SER	L403	D463	I525	S584	ASN	E763	W823	K883	R943
K164	GLN	K284	SER	S404	F464	V526	L585	VAL	R764	T824	Y884	S944
F165	THR	Y285	GLU	Y405	F465	R527	T586	ALA	K765	E825	R885	R945
L166	ASN	A286	ASN	E406	V466	K528	V587	GLU	L766	W826	D886	K946
V167	CYS	S287	CYS	R407	T467	E529	N588	PHE	P707	D827	N887	I947
K168	ALA	I288	ALA	V408	A468	D530	V589	GLY	D708	R828	L888	A948
E230	Y229	E289	SER	F409	E469	D531	M590	LVS	E709	W829	K889	V949
K169	E231	E290	L353	S410	I470	A532	L591	T652	W710	V830	N890	I950
L170	Q231	S290	Q355	F411	N471	S533	P592	K653	Q711	F831	L891	S951
V171	L232	L291	D356	GLY	D472	ASN	D593	T654	N712	L832	L892	V952
L172	L233	L292	K357	LEU	S473	ASN	G594	D655	L713	K833	D893	L953
T173	L234	P293	L358	LVS	N474	LEU	K595	K656	D714	T834	D894	P954
C174	L235	V294	V358	PHE	D475	L538	T596	L657	W715	L835	T895	N955
D175	F236	Y295	A359	LEU	L476	K539	R597	V658	Y716	S836	L896	P956
L176	T237	E296	F360	GLN	F477	T540	Y598	S659	Q717	K837	F897	K957
L177	E238	V297		L419	E478		GLU	T660	P718	F838	L898	P958
I178	S239	M298		F420	I479		THR	S660	L719	K839	D899	P959
P179	M240	Y299									E900	V960
L180												



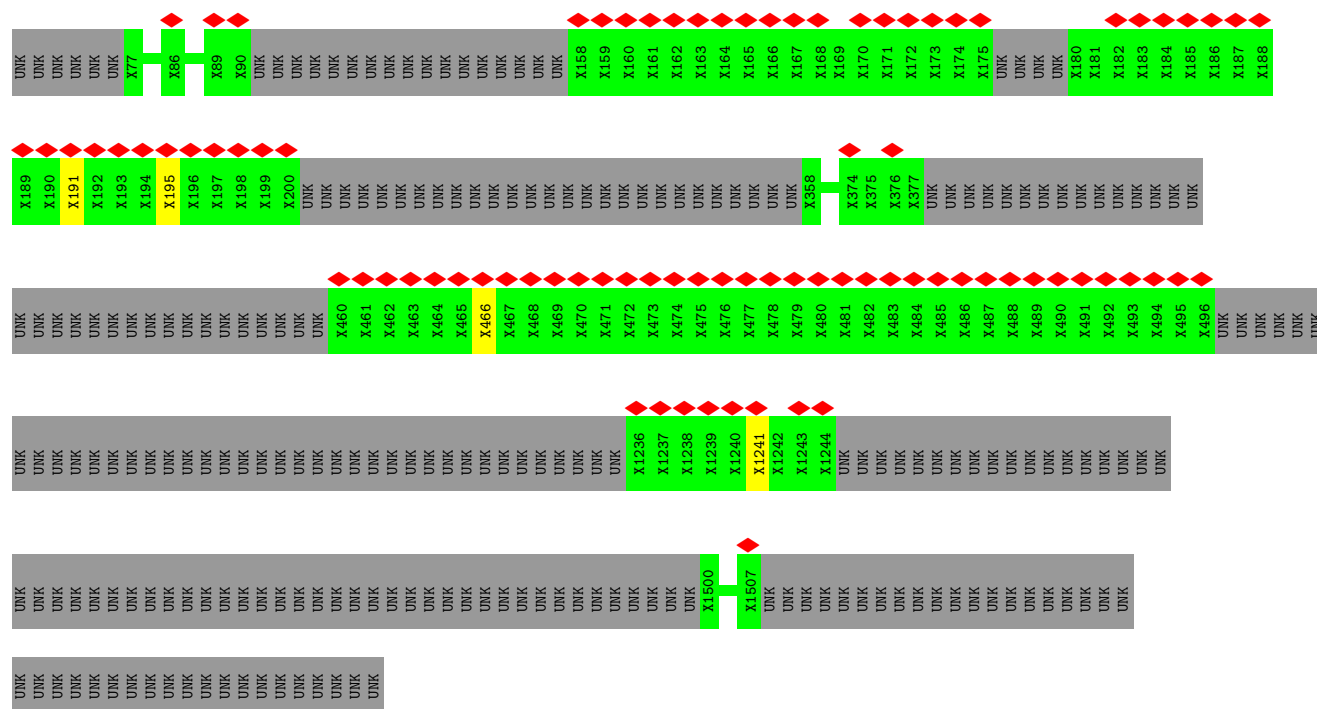




● Molecule 64: Essential nuclear protein 1







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	121139	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	25000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	-0.073	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3A	0.61	0/4141	0.54	0/6433
2	5A	0.55	0/12462	0.53	5/19411 (0.0%)
3	SA	0.42	0/31237	0.50	5/48637 (0.0%)
4	SC	0.54	0/1777	0.82	5/2388 (0.2%)
5	SF	0.31	0/1854	0.75	0/2504
6	SG	0.66	0/1690	0.71	0/2285
7	SH	0.31	0/890	0.72	0/1189
8	SI	0.42	1/1341 (0.1%)	0.79	2/1806 (0.1%)
9	SJ	0.28	0/1347	0.65	0/1801
10	SK	0.58	0/1410	0.70	0/1888
11	SM	0.34	0/1020	0.73	0/1374
12	SN	0.27	0/873	0.71	0/1185
13	SO	0.46	0/1109	0.70	0/1495
14	SP	0.51	0/879	0.77	0/1186
15	SR	0.78	0/990	0.90	3/1335 (0.2%)
16	ST	0.32	0/930	0.67	0/1251
17	SX	0.59	0/1020	0.72	0/1371
18	SY	0.60	0/798	0.77	0/1065
19	SZ	0.36	0/822	0.74	0/1103
20	Sc	0.50	0/613	0.72	0/828
21	Sd	0.66	0/499	0.82	0/670
22	3B	0.74	0/1901	0.78	0/2567
22	3C	0.40	0/1796	0.70	0/2424
23	3D	0.52	0/2891	0.69	0/3895
24	3E	0.49	0/3059	0.69	0/4153
25	3F	0.42	0/3544	0.74	0/4775
26	3G	0.70	0/928	0.79	1/1262 (0.1%)
26	3H	0.54	0/928	0.75	0/1262
27	A4	0.46	0/5321	0.72	2/7207 (0.0%)
28	A5	0.55	0/4044	0.75	0/5493
29	A8	0.28	0/3328	0.74	3/4565 (0.1%)
30	A9	0.30	0/951	0.65	0/1287

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.45	0/6308	0.71	0/8543
32	AF	0.50	0/3993	0.73	0/5413
33	AG	0.43	0/6699	0.71	0/9077
34	B1	0.82	0/6780	0.81	2/9175 (0.0%)
35	B2	0.42	0/6853	0.76	7/9256 (0.1%)
36	B3	0.42	0/6014	0.78	4/8137 (0.0%)
37	B8	0.70	0/3848	0.75	0/5218
38	BE	0.72	0/6948	0.74	3/9391 (0.0%)
39	B6	0.47	0/2849	0.68	0/3853
40	5B	0.35	0/499	0.74	0/659
41	5C	0.76	0/4321	0.78	0/5832
42	5D	0.63	0/1998	0.78	0/2644
43	5E	0.55	0/1665	0.71	1/2233 (0.0%)
44	5F	0.92	0/1559	0.86	1/2097 (0.0%)
45	5G	0.68	0/2337	0.78	3/3148 (0.1%)
46	5H	0.56	0/1074	0.65	0/1422
47	5I	0.74	0/3844	0.81	0/5174
48	5J	0.54	0/1238	0.69	0/1641
49	5K	0.73	0/1426	0.79	1/1917 (0.1%)
50	RA	0.32	0/2769	0.73	4/3753 (0.1%)
51	RB	0.38	0/1121	0.79	0/1487
52	RC	0.51	0/2245	0.67	1/3021 (0.0%)
53	RE	0.33	0/8924	0.67	4/12070 (0.0%)
54	RF	0.31	0/2004	0.70	1/2697 (0.0%)
55	RG	0.33	0/1727	0.75	0/2329
55	RH	0.40	0/1828	0.67	0/2470
56	RI	0.51	0/2080	0.72	0/2797
57	RJ	0.55	0/6514	0.69	0/8768
58	RK	0.41	0/2832	0.67	0/3825
59	RL	0.25	0/4549	0.60	2/6241 (0.0%)
59	RM	0.21	0/3760	0.53	1/5211 (0.0%)
60	RN	0.32	0/4423	0.68	3/5965 (0.1%)
61	RO	0.34	0/3849	0.68	0/5261
62	RP	0.23	0/10172	0.61	11/14158 (0.1%)
63	RQ	0.48	0/1678	0.68	1/2282 (0.0%)
64	RS	0.32	0/2104	0.76	0/2854
65	RT	0.41	0/1379	0.70	0/1853
66	RV	0.59	0/1456	0.72	1/1937 (0.1%)
All	All	0.50	1/232060 (0.0%)	0.68	77/323904 (0.0%)

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

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	1
6	SG	0	1
7	SH	0	1
8	SI	0	2
11	SM	0	1
12	SN	0	1
13	SO	0	1
14	SP	0	1
19	SZ	0	1
20	Sc	0	1
22	3B	0	1
23	3D	0	1
24	3E	0	2
26	3G	0	3
26	3H	0	1
28	A5	0	2
29	A8	0	4
33	AG	0	3
34	B1	0	3
35	B2	0	9
36	B3	0	8
37	B8	0	3
38	BE	0	3
39	B6	0	1
41	5C	0	3
42	5D	0	1
43	5E	0	1
44	5F	0	1
47	5I	0	1
49	5K	0	2
51	RB	0	1
53	RE	0	1
54	RF	0	1
56	RI	0	1
57	RJ	0	2
59	RL	0	1
59	RM	0	1
62	RP	0	1
63	RQ	0	1
66	RV	0	1
All	All	0	76

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	SI	39	ARG	C-N	6.54	1.38	1.33

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	RP	1897	PRO	N-CA-CB	10.22	109.66	102.81
35	B2	343	TRP	N-CA-C	7.40	117.78	108.45
15	SR	123	ARG	C-N-CD	-7.33	104.48	120.60
62	RP	2071	PRO	N-CA-CB	7.18	110.16	103.41
62	RP	1949	PRO	N-CA-CB	7.12	110.98	102.72

There are no chirality outliers.

5 of 76 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	40	ASN	Peptide
5	SF	195	ILE	Peptide
6	SG	58	LEU	Peptide
7	SH	68	LEU	Peptide
8	SI	31	SER	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	3711	0	1882	32	0
2	5A	11143	0	5602	93	0
3	SA	27940	0	14087	248	0
4	SC	1751	0	1834	25	0
5	SF	1815	0	1870	45	0
6	SG	1669	0	1724	17	0
7	SH	879	0	922	22	0
8	SI	1321	0	1387	34	0
9	SJ	1324	0	1344	40	0
10	SK	1388	0	1467	15	0
11	SM	997	0	1048	21	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	SN	865	0	874	11	0
13	SO	1087	0	1152	17	0
14	SP	868	0	894	18	0
15	SR	973	0	1029	20	0
16	ST	918	0	952	19	0
17	SX	1003	0	1040	18	0
18	SY	786	0	843	13	0
19	SZ	809	0	842	16	0
20	Sc	603	0	623	8	0
21	Sd	497	0	535	4	0
22	3B	1865	0	1910	33	0
22	3C	1763	0	1805	36	0
23	3D	2848	0	2815	40	0
24	3E	3028	0	2813	61	0
25	3F	3473	0	3477	82	0
26	3G	916	0	964	16	0
26	3H	916	0	964	26	0
27	A4	5226	0	5199	113	0
28	A5	3976	0	3919	80	0
29	A8	3307	0	2316	39	0
30	A9	939	0	898	16	0
31	AE	6197	0	6365	92	0
32	AF	3911	0	3906	94	0
33	AG	6570	0	6473	156	0
34	B1	6635	0	6525	107	0
35	B2	6723	0	6698	140	0
36	B3	5919	0	6007	145	0
37	B8	3764	0	3757	71	0
38	BE	6810	0	6787	99	0
39	B6	2800	0	2517	35	0
40	5B	495	0	561	10	0
41	5C	4237	0	4239	81	0
42	5D	1972	0	2054	30	0
43	5E	1647	0	1678	42	0
44	5F	1530	0	1572	25	0
45	5G	2296	0	2325	31	0
46	5H	1065	0	1097	16	0
47	5I	3765	0	3714	74	0
48	5J	1219	0	1278	17	0
49	5K	1403	0	1484	24	0
50	RA	2709	0	2622	75	0
51	RB	1108	0	1087	23	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	RC	2207	0	2229	25	0
53	RE	8716	0	8828	155	0
54	RF	1963	0	1942	37	0
55	RG	1701	0	1767	34	0
55	RH	1799	0	1872	25	0
56	RI	2045	0	2162	46	0
57	RJ	6379	0	6506	109	0
58	RK	2781	0	2878	46	0
59	RL	4539	0	2874	24	0
59	RM	3774	0	1649	16	0
60	RN	4363	0	4100	51	0
61	RO	3766	0	3269	44	0
62	RP	10202	0	4350	14	0
63	RQ	1651	0	1450	22	0
64	RS	2051	0	2096	39	0
65	RT	1357	0	1426	20	0
66	RV	1448	0	1435	22	0
67	X1	635	0	147	3	0
68	5K	1	0	0	0	0
68	Sc	1	0	0	0	0
69	RJ	32	0	12	0	0
70	RJ	1	0	0	0	0
All	All	224791	0	192769	2979	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 7.

The worst 5 of 2979 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)
3:SA:356:G:N2	3:SA:357:G:H22	1.43	1.16
3:SA:356:G:N2	3:SA:357:G:N2	1.95	1.14
3:SA:1663:G:H1	3:SA:1738:U:H3	1.06	0.92
3:SA:1775:U:H3	3:SA:1786:G:H1	1.15	0.90
39:B6:319:TYR:O	39:B6:323:PHE:HB2	1.70	0.90

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	
4	SC	217/255 (85%)	186 (86%)	30 (14%)	1 (0%)	24	54
5	SF	227/261 (87%)	192 (85%)	35 (15%)	0	100	100
6	SG	211/225 (94%)	197 (93%)	14 (7%)	0	100	100
7	SH	108/236 (46%)	98 (91%)	9 (8%)	1 (1%)	14	42
8	SI	161/190 (85%)	139 (86%)	22 (14%)	0	100	100
9	SJ	162/200 (81%)	141 (87%)	21 (13%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/156 (76%)	99 (83%)	20 (17%)	0	100	100
12	SN	117/143 (82%)	96 (82%)	21 (18%)	0	100	100
13	SO	132/151 (87%)	125 (95%)	7 (5%)	0	100	100
14	SP	116/137 (85%)	102 (88%)	14 (12%)	0	100	100
15	SR	123/143 (86%)	113 (92%)	10 (8%)	0	100	100
16	ST	109/146 (75%)	100 (92%)	9 (8%)	0	100	100
17	SX	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
18	SY	101/145 (70%)	91 (90%)	10 (10%)	0	100	100
19	SZ	100/135 (74%)	86 (86%)	14 (14%)	0	100	100
20	Sc	78/82 (95%)	68 (87%)	10 (13%)	0	100	100
21	Sd	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
22	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
22	3C	221/327 (68%)	203 (92%)	18 (8%)	0	100	100
23	3D	359/504 (71%)	344 (96%)	15 (4%)	0	100	100
24	3E	427/511 (84%)	394 (92%)	33 (8%)	0	100	100
25	3F	428/573 (75%)	384 (90%)	43 (10%)	1 (0%)	43	71
26	3G	119/126 (94%)	109 (92%)	9 (8%)	1 (1%)	16	44
26	3H	119/126 (94%)	110 (92%)	9 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	A4	648/776 (84%)	576 (89%)	72 (11%)	0	100	100
28	A5	504/643 (78%)	460 (91%)	44 (9%)	0	100	100
29	A8	534/713 (75%)	407 (76%)	124 (23%)	3 (1%)	21	50
30	A9	126/575 (22%)	119 (94%)	7 (6%)	0	100	100
31	AE	773/1769 (44%)	710 (92%)	63 (8%)	0	100	100
32	AF	489/513 (95%)	437 (89%)	51 (10%)	1 (0%)	43	71
33	AG	812/896 (91%)	730 (90%)	82 (10%)	0	100	100
34	B1	830/923 (90%)	752 (91%)	76 (9%)	2 (0%)	43	71
35	B2	839/943 (89%)	750 (89%)	88 (10%)	1 (0%)	48	78
36	B3	733/817 (90%)	599 (82%)	132 (18%)	2 (0%)	36	65
37	B8	469/594 (79%)	423 (90%)	46 (10%)	0	100	100
38	BE	857/939 (91%)	792 (92%)	65 (8%)	0	100	100
39	B6	368/440 (84%)	337 (92%)	31 (8%)	0	100	100
40	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
41	5C	531/554 (96%)	472 (89%)	58 (11%)	1 (0%)	43	71
42	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100	100
43	5E	200/593 (34%)	187 (94%)	11 (6%)	2 (1%)	12	40
44	5F	180/183 (98%)	169 (94%)	11 (6%)	0	100	100
45	5G	278/290 (96%)	249 (90%)	29 (10%)	0	100	100
46	5H	132/610 (22%)	121 (92%)	11 (8%)	0	100	100
47	5I	457/489 (94%)	420 (92%)	37 (8%)	0	100	100
48	5J	138/217 (64%)	129 (94%)	9 (6%)	0	100	100
49	5K	171/189 (90%)	160 (94%)	11 (6%)	0	100	100
50	RA	332/707 (47%)	287 (86%)	45 (14%)	0	100	100
51	RB	132/357 (37%)	116 (88%)	16 (12%)	0	100	100
52	RC	276/316 (87%)	260 (94%)	16 (6%)	0	100	100
53	RE	1067/1237 (86%)	984 (92%)	83 (8%)	0	100	100
54	RF	233/297 (78%)	214 (92%)	19 (8%)	0	100	100
55	RG	212/252 (84%)	186 (88%)	26 (12%)	0	100	100
55	RH	226/252 (90%)	212 (94%)	14 (6%)	0	100	100
56	RI	250/274 (91%)	228 (91%)	22 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	RJ	784/1183 (66%)	723 (92%)	61 (8%)	0	100	100
58	RK	358/367 (98%)	335 (94%)	23 (6%)	0	100	100
59	RL	781/1056 (74%)	670 (86%)	109 (14%)	2 (0%)	36	65
59	RM	737/1056 (70%)	640 (87%)	93 (13%)	4 (0%)	24	54
60	RN	573/810 (71%)	524 (91%)	48 (8%)	1 (0%)	43	71
61	RO	523/552 (95%)	457 (87%)	66 (13%)	0	100	100
62	RP	1992/2493 (80%)	1801 (90%)	189 (10%)	2 (0%)	48	78
63	RQ	220/899 (24%)	197 (90%)	23 (10%)	0	100	100
64	RS	247/483 (51%)	223 (90%)	23 (9%)	1 (0%)	30	59
65	RT	165/326 (51%)	151 (92%)	14 (8%)	0	100	100
66	RV	184/346 (53%)	168 (91%)	16 (9%)	0	100	100
All	All	23995/32886 (73%)	21566 (90%)	2403 (10%)	26 (0%)	49	78

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	5E	454	VAL
59	RL	744	PRO
59	RM	744	PRO
62	RP	119	PRO
29	A8	309	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	
4	SC	195/224 (87%)	192 (98%)	3 (2%)	57	69
5	SF	196/222 (88%)	191 (97%)	5 (3%)	40	61
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	80
7	SH	95/201 (47%)	95 (100%)	0	100	100
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	64

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	SJ	136/161 (84%)	135 (99%)	1 (1%)	76	78
10	SK	147/166 (89%)	145 (99%)	2 (1%)	59	70
11	SM	110/137 (80%)	110 (100%)	0	100	100
12	SN	88/119 (74%)	88 (100%)	0	100	100
13	SO	117/128 (91%)	114 (97%)	3 (3%)	40	61
14	SP	90/105 (86%)	88 (98%)	2 (2%)	45	63
15	SR	105/119 (88%)	103 (98%)	2 (2%)	50	66
16	ST	101/129 (78%)	101 (100%)	0	100	100
17	SX	108/111 (97%)	106 (98%)	2 (2%)	50	66
18	SY	85/120 (71%)	83 (98%)	2 (2%)	43	62
19	SZ	85/113 (75%)	83 (98%)	2 (2%)	43	62
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	54 (96%)	2 (4%)	31	56
22	3B	201/240 (84%)	200 (100%)	1 (0%)	81	81
22	3C	190/240 (79%)	189 (100%)	1 (0%)	81	81
23	3D	296/435 (68%)	293 (99%)	3 (1%)	68	75
24	3E	262/433 (60%)	259 (99%)	3 (1%)	65	74
25	3F	378/503 (75%)	374 (99%)	4 (1%)	65	74
26	3G	100/104 (96%)	100 (100%)	0	100	100
26	3H	100/104 (96%)	99 (99%)	1 (1%)	68	75
27	A4	591/713 (83%)	583 (99%)	8 (1%)	59	70
28	A5	433/574 (75%)	428 (99%)	5 (1%)	63	72
29	A8	174/657 (26%)	173 (99%)	1 (1%)	78	80
30	A9	89/533 (17%)	89 (100%)	0	100	100
31	AE	708/1633 (43%)	704 (99%)	4 (1%)	78	80
32	AF	437/454 (96%)	429 (98%)	8 (2%)	51	67
33	AG	750/826 (91%)	738 (98%)	12 (2%)	55	68
34	B1	730/812 (90%)	715 (98%)	15 (2%)	47	64
35	B2	736/832 (88%)	721 (98%)	15 (2%)	48	65
36	B3	665/719 (92%)	656 (99%)	9 (1%)	59	70
37	B8	421/529 (80%)	419 (100%)	2 (0%)	81	81

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	BE	757/819 (92%)	744 (98%)	13 (2%)	53	67
39	B6	251/414 (61%)	250 (100%)	1 (0%)	84	83
40	5B	57/196 (29%)	56 (98%)	1 (2%)	51	67
41	5C	465/480 (97%)	454 (98%)	11 (2%)	43	62
42	5D	221/234 (94%)	219 (99%)	2 (1%)	70	76
43	5E	185/535 (35%)	182 (98%)	3 (2%)	55	68
44	5F	171/172 (99%)	171 (100%)	0	100	100
45	5G	251/258 (97%)	247 (98%)	4 (2%)	55	68
46	5H	107/538 (20%)	105 (98%)	2 (2%)	50	66
47	5I	416/443 (94%)	404 (97%)	12 (3%)	37	60
48	5J	133/200 (66%)	132 (99%)	1 (1%)	73	77
49	5K	157/169 (93%)	155 (99%)	2 (1%)	61	71
50	RA	303/636 (48%)	301 (99%)	2 (1%)	76	78
51	RB	117/315 (37%)	117 (100%)	0	100	100
52	RC	231/289 (80%)	230 (100%)	1 (0%)	84	83
53	RE	984/1125 (88%)	977 (99%)	7 (1%)	76	78
54	RF	221/274 (81%)	217 (98%)	4 (2%)	51	67
55	RG	195/222 (88%)	194 (100%)	1 (0%)	81	81
55	RH	206/222 (93%)	201 (98%)	5 (2%)	43	62
56	RI	235/256 (92%)	233 (99%)	2 (1%)	70	76
57	RJ	683/1039 (66%)	679 (99%)	4 (1%)	78	80
58	RK	307/312 (98%)	305 (99%)	2 (1%)	76	78
59	RL	164/934 (18%)	162 (99%)	2 (1%)	63	72
60	RN	406/732 (56%)	404 (100%)	2 (0%)	81	81
61	RO	329/506 (65%)	324 (98%)	5 (2%)	57	69
63	RQ	148/808 (18%)	145 (98%)	3 (2%)	48	65
64	RS	225/424 (53%)	222 (99%)	3 (1%)	61	71
65	RT	148/282 (52%)	146 (99%)	2 (1%)	59	70
66	RV	141/304 (46%)	138 (98%)	3 (2%)	47	64
All	All	17584/26026 (68%)	17362 (99%)	222 (1%)	59	71

5 of 222 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	B3	168	THR
66	RV	315	THR
41	5C	291	THR
66	RV	164	LEU
57	RJ	1069	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 400 such sidechains are listed below:

Mol	Chain	Res	Type
41	5C	133	HIS
50	RA	166	ASN
66	RV	271	GLN
41	5C	410	ASN
45	5G	156	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	46 (27%)	2 (1%)
2	5A	516/700 (73%)	146 (28%)	10 (1%)
3	SA	1290/1807 (71%)	461 (35%)	16 (1%)
All	All	1975/2840 (69%)	653 (33%)	28 (1%)

5 of 653 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	5	A
1	3A	14	A
1	3A	15	U
1	3A	24	U

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	68	A
3	SA	1594	G
3	SA	401	A
3	SA	1052	U
3	SA	372	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](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
69	GTP	RJ	1201	70	33,34,34	0.89	0	50,54,54	1.62	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GTP	RJ	1201	70	-	2/22/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	RJ	1201	GTP	C5-C4-N3	-4.86	120.66	128.39
69	RJ	1201	GTP	C2-N3-C4	4.49	120.03	112.30
69	RJ	1201	GTP	C2-N1-C6	-3.12	119.46	125.11
69	RJ	1201	GTP	N9-C4-N3	2.94	131.83	125.95
69	RJ	1201	GTP	N9-C8-N7	-2.85	108.12	113.40

There are no chirality outliers.

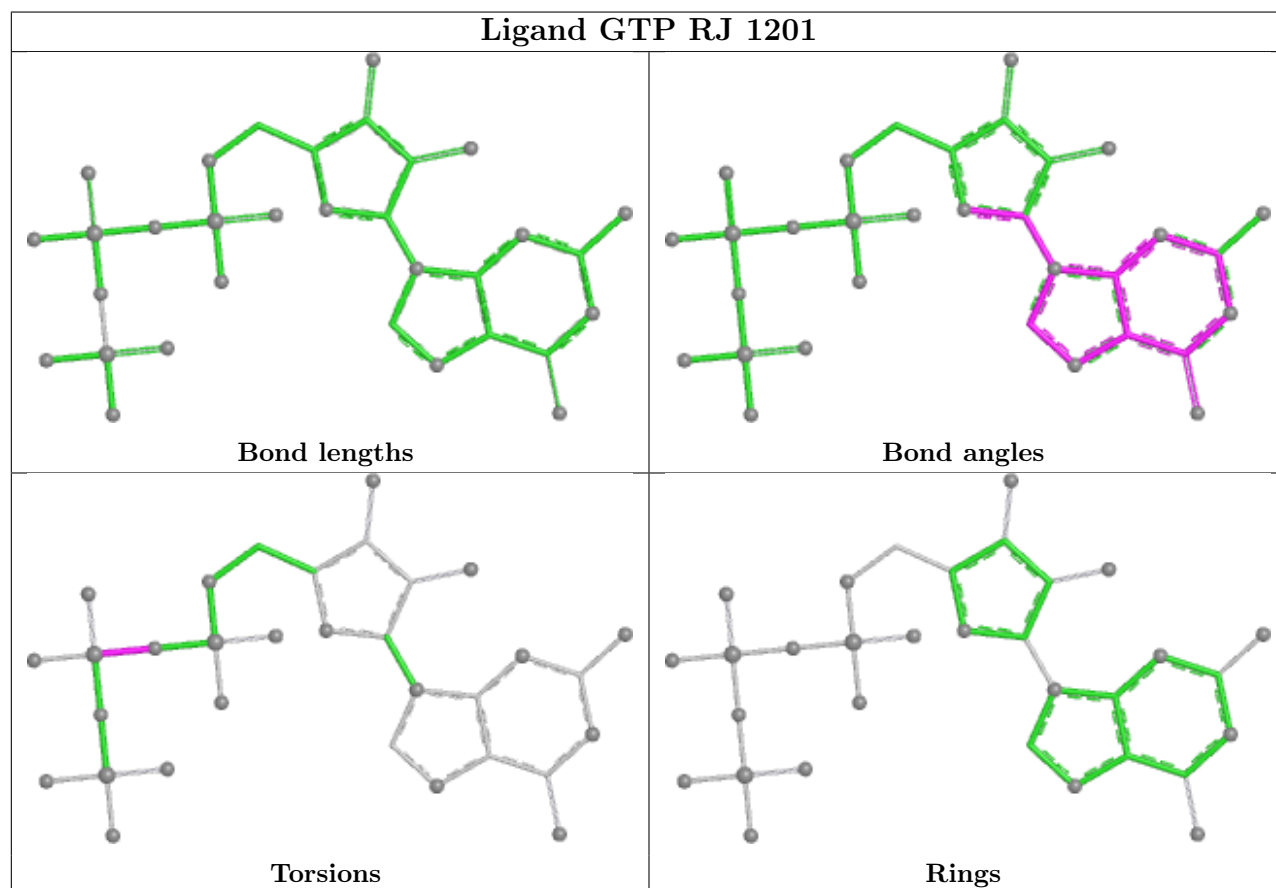
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
69	RJ	1201	GTP	PA-O3A-PB-O2B
69	RJ	1201	GTP	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

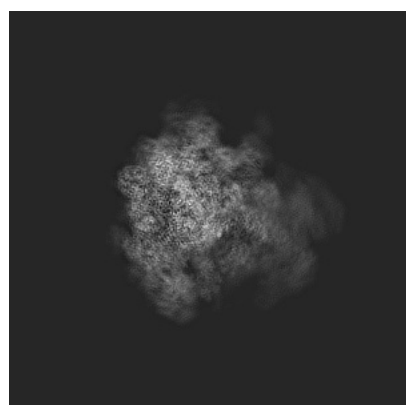
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9964. These allow visual inspection of the internal detail of the map and identification of artifacts.

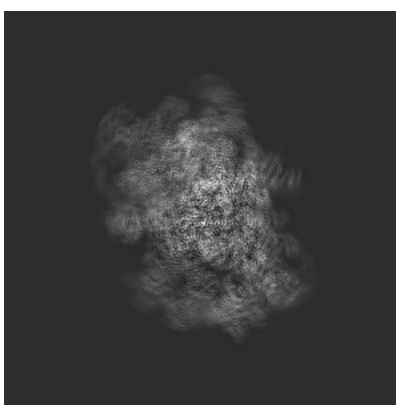
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

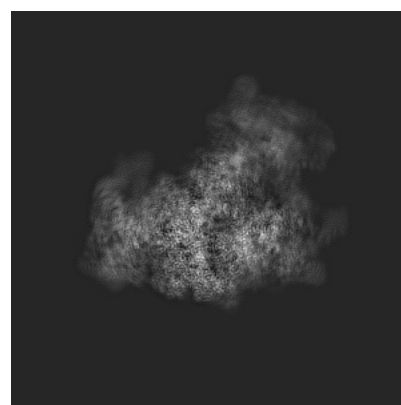
6.1.1 Primary map



X



Y



Z

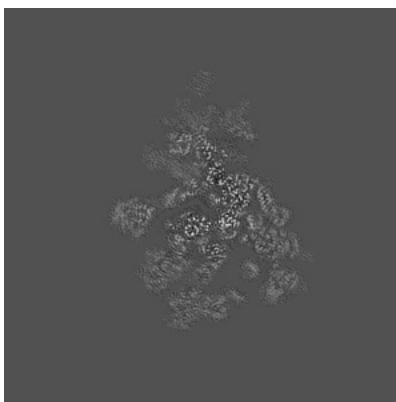
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

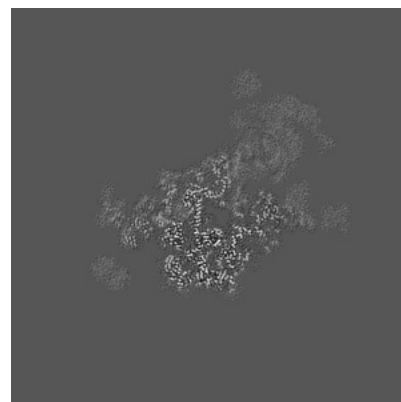
6.2.1 Primary map



X Index: 256



Y Index: 256

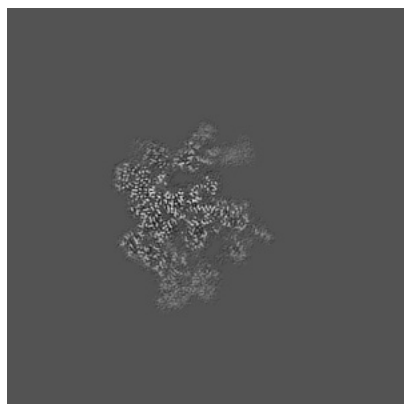


Z Index: 256

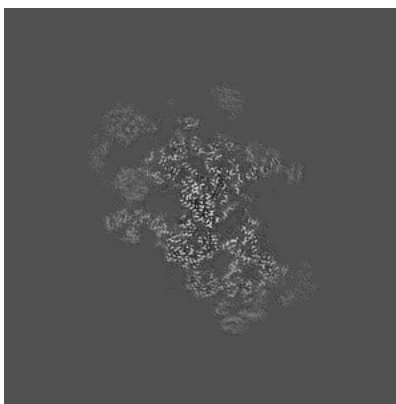
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

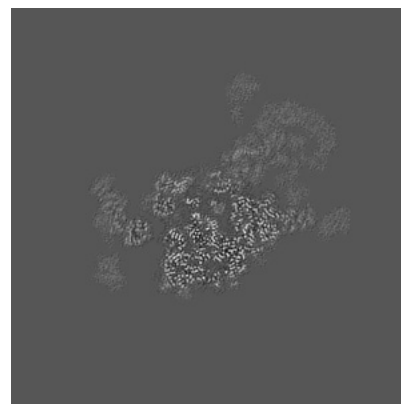
6.3.1 Primary map



X Index: 240



Y Index: 216

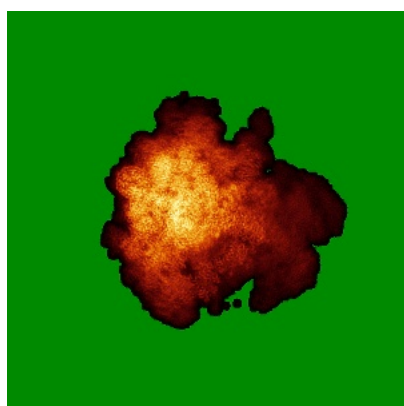


Z Index: 267

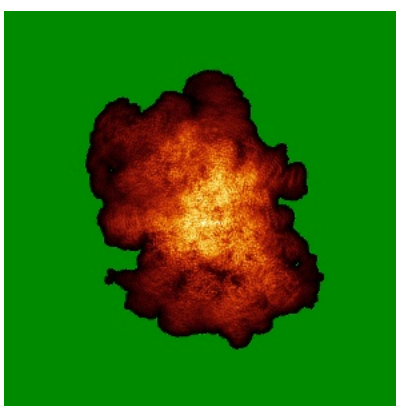
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

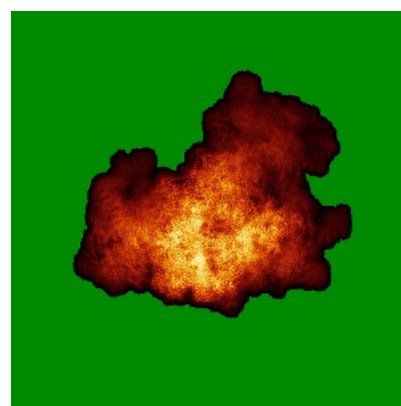
6.4.1 Primary map



X



Y

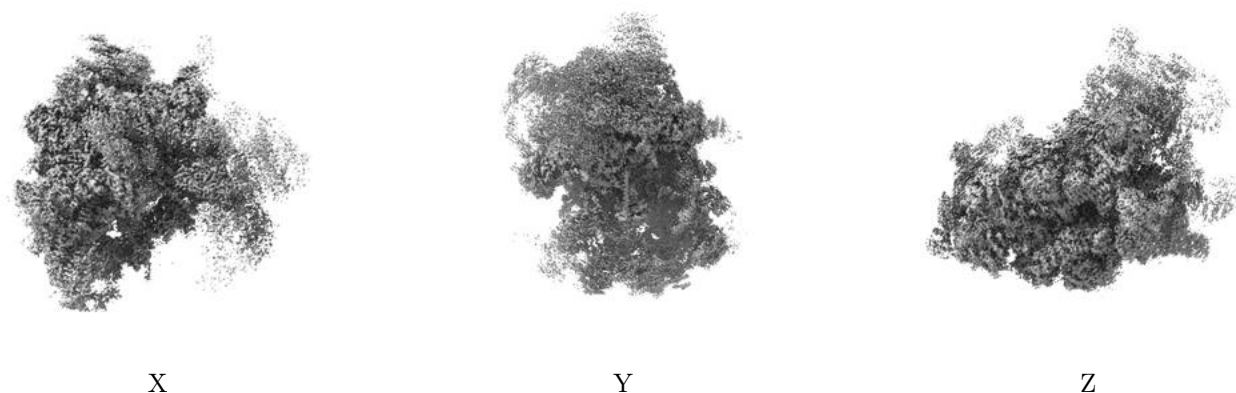


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

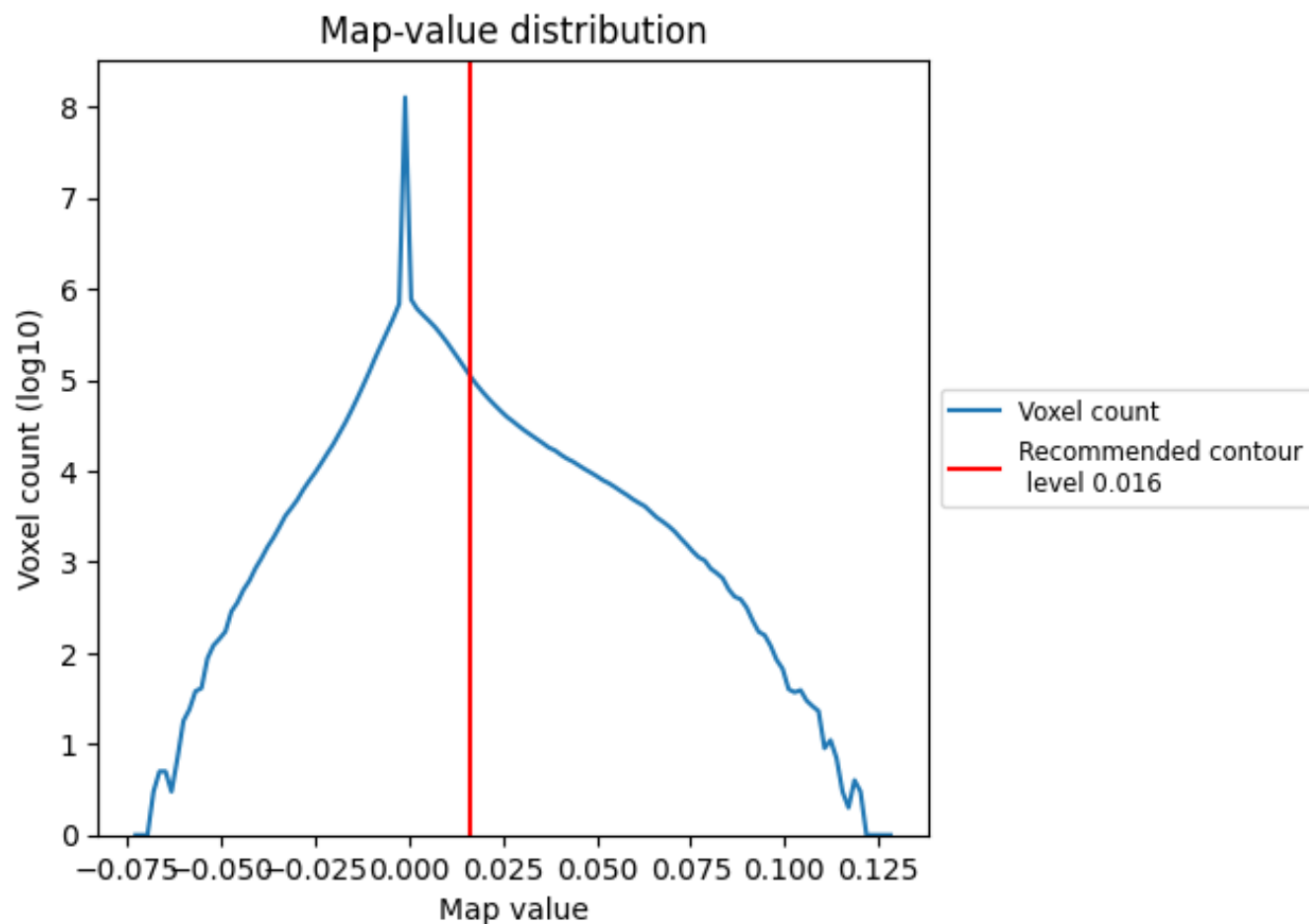
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

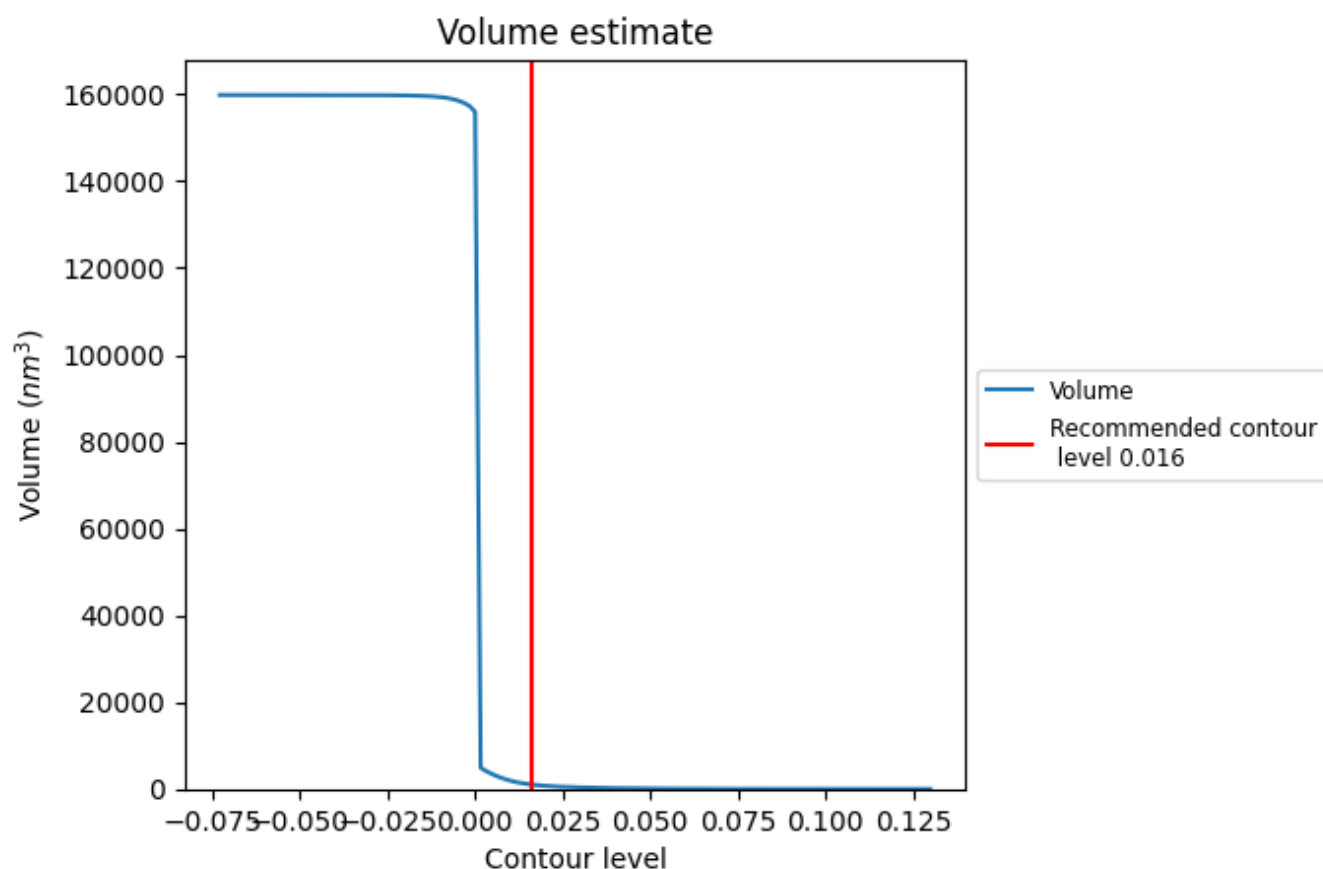
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

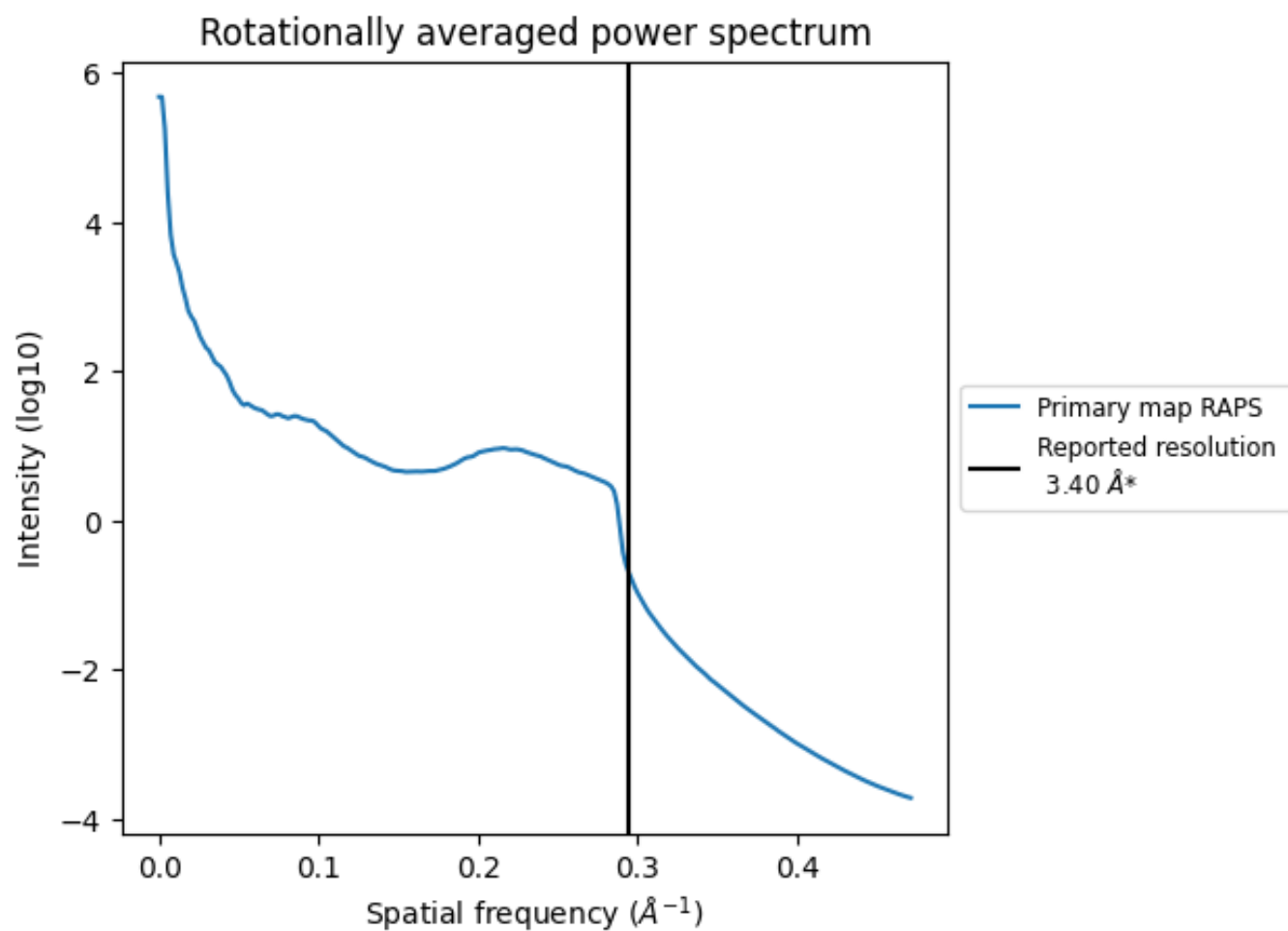
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1022 nm³; this corresponds to an approximate mass of 923 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

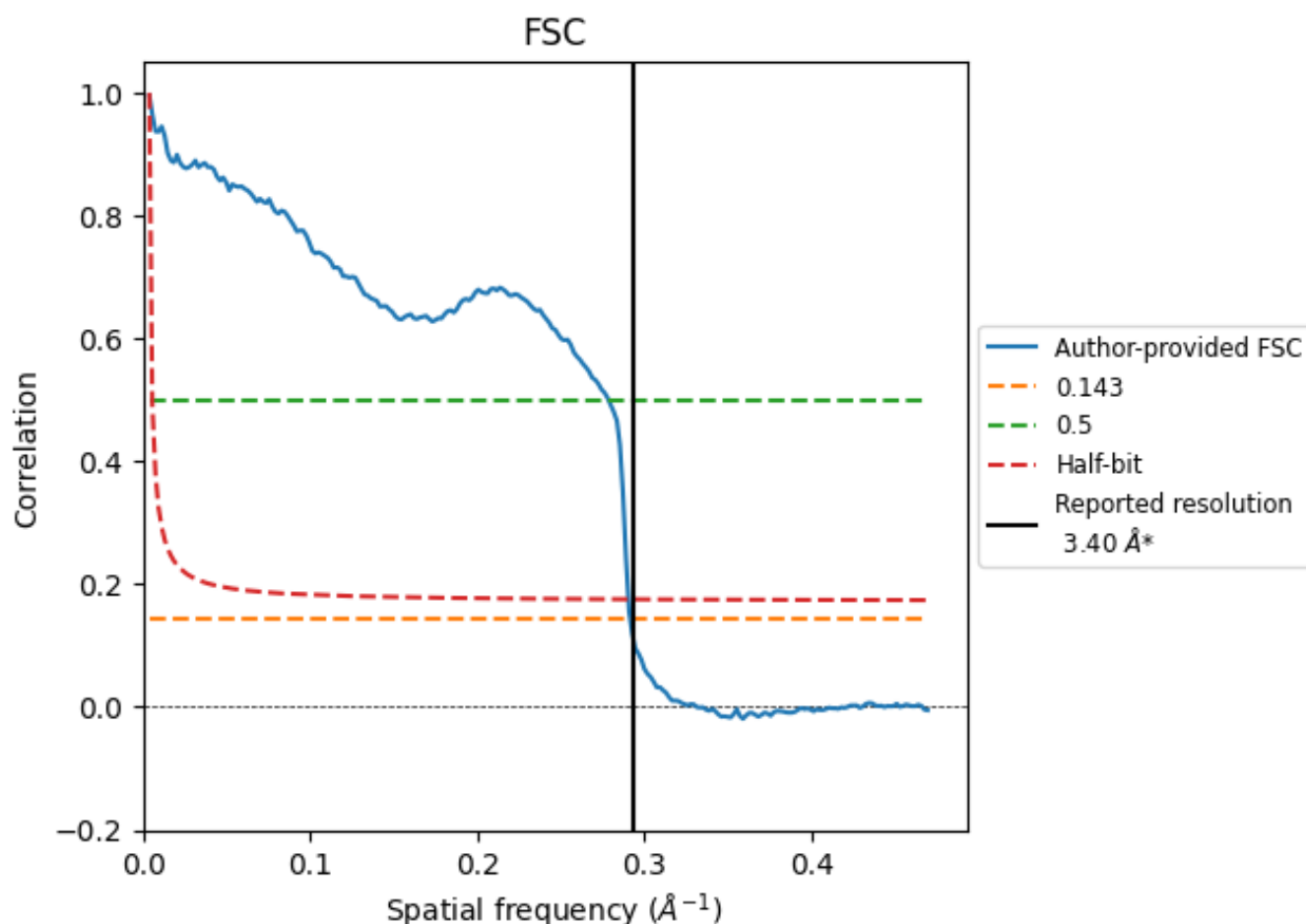


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

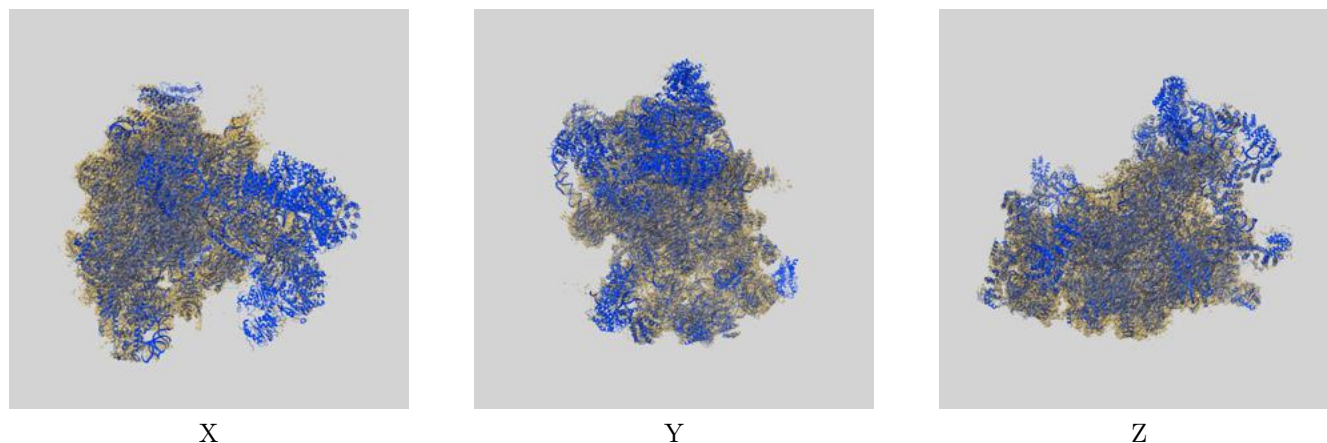
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.43	3.59	3.44
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

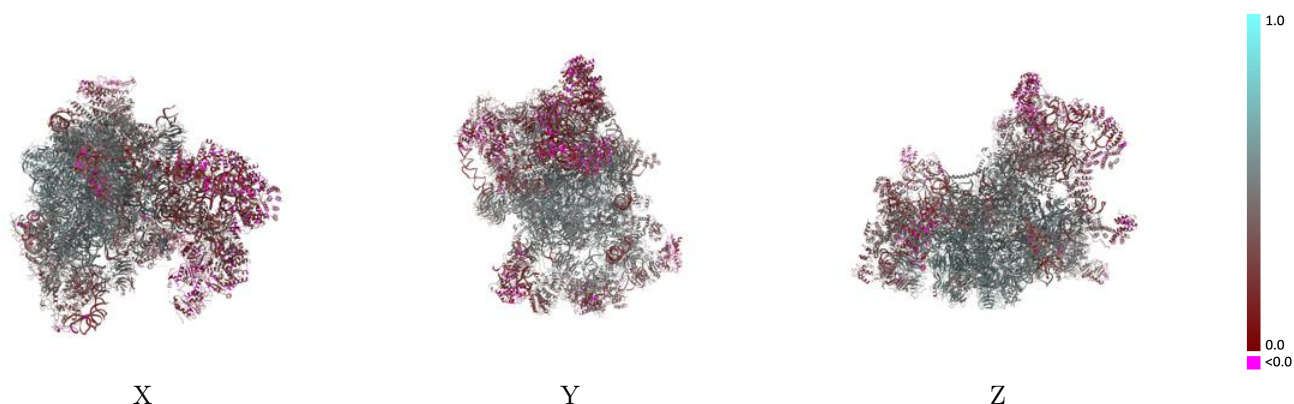
This section contains information regarding the fit between EMDB map EMD-9964 and PDB model 6KE6. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



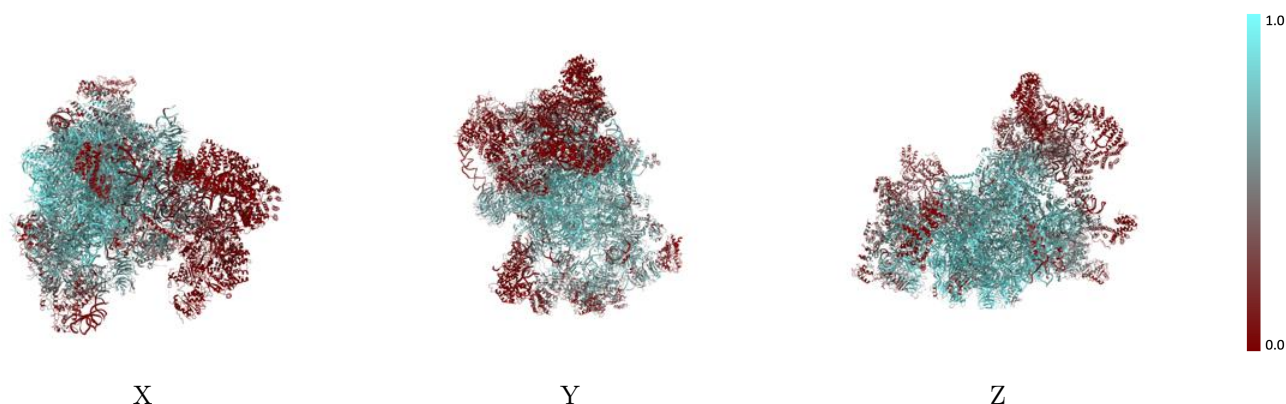
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



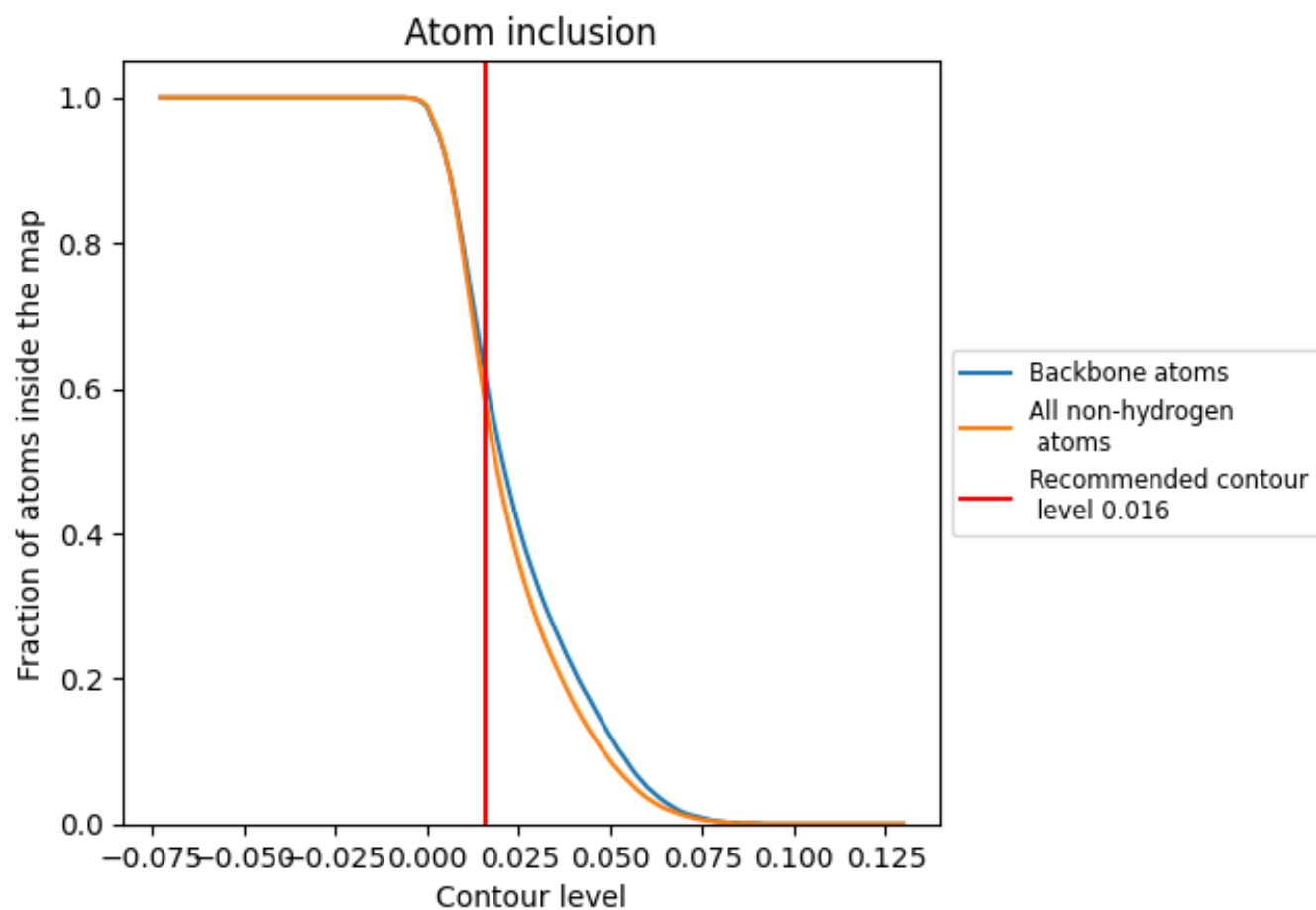
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 57% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5740	 0.4270
3A	 0.8270	 0.4550
3B	 0.8620	 0.5570
3C	 0.5800	 0.4410
3D	 0.7370	 0.4890
3E	 0.6830	 0.4590
3F	 0.6610	 0.4530
3G	 0.8340	 0.5450
3H	 0.7580	 0.5110
5A	 0.7640	 0.4290
5B	 0.4040	 0.3970
5C	 0.8460	 0.5510
5D	 0.7550	 0.5110
5E	 0.7530	 0.5240
5F	 0.8870	 0.5690
5G	 0.8110	 0.5500
5H	 0.7230	 0.5000
5I	 0.8630	 0.5500
5J	 0.6630	 0.4970
5K	 0.8570	 0.5580
A4	 0.6830	 0.4510
A5	 0.7530	 0.4910
A8	 0.2280	 0.3060
A9	 0.3970	 0.3630
AE	 0.3780	 0.3480
AF	 0.7590	 0.5060
AG	 0.6910	 0.4690
B1	 0.8810	 0.5590
B2	 0.6660	 0.4520
B3	 0.5920	 0.4230
B6	 0.6690	 0.4400
B8	 0.8480	 0.5430
BE	 0.8700	 0.5550
RA	 0.0960	 0.2760
RB	 0.4640	 0.4280



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
RC	 0.6170	 0.4820
RE	 0.3870	 0.4000
RF	 0.2960	 0.3630
RG	 0.3630	 0.3870
RH	 0.5720	 0.4780
RI	 0.7660	 0.4930
RJ	 0.7420	 0.5030
RK	 0.6830	 0.4860
RL	 0.1200	 0.3130
RM	 0.0190	 0.1970
RN	 0.3310	 0.3780
RO	 0.4480	 0.3860
RP	 0.0910	 0.2260
RQ	 0.5790	 0.4680
RS	 0.0370	 0.2090
RT	 0.6790	 0.4800
RV	 0.7190	 0.5180
SA	 0.5130	 0.3620
SC	 0.7480	 0.5170
SF	 0.2900	 0.3660
SG	 0.8170	 0.5350
SH	 0.0940	 0.3450
SI	 0.5210	 0.4250
SJ	 0.1430	 0.2790
SK	 0.8060	 0.5300
SM	 0.1530	 0.2840
SN	 0.0050	 0.1060
SO	 0.7580	 0.5080
SP	 0.7590	 0.5120
SR	 0.8490	 0.5530
ST	 0.3320	 0.4150
SX	 0.7840	 0.5300
SY	 0.7750	 0.5270
SZ	 0.4900	 0.4280
Sc	 0.7680	 0.5200
Sd	 0.8410	 0.5500
X1	 0.3290	 0.3770