



wwPDB EM Validation Summary Report ⓘ

Nov 15, 2022 – 03:11 AM JST

PDB ID : 6KE6
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 : 5WLC, 5WYJ

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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

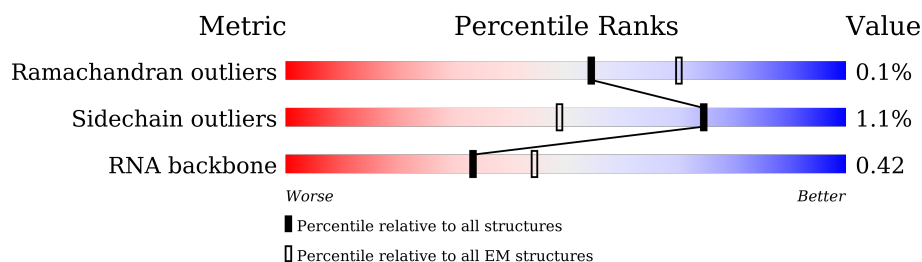
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	

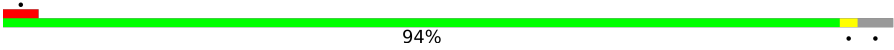
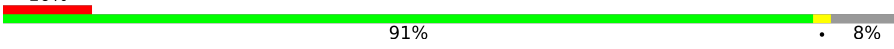


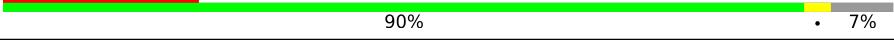

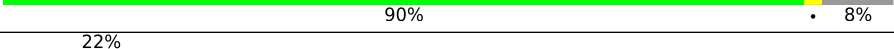
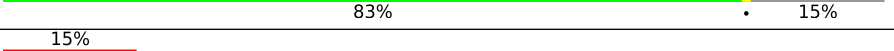
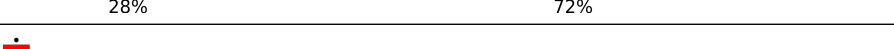
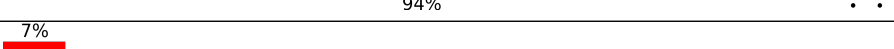
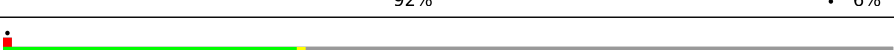

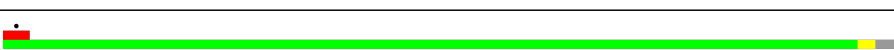

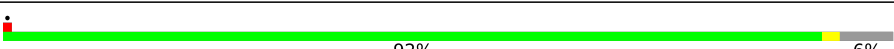





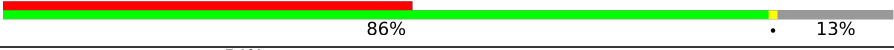




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Mol	Chain	Length	Quality of chain
9	SJ	200	
10	SK	197	
11	SM	156	
12	SN	143	
13	SO	151	
14	SP	137	
15	SR	143	
16	ST	146	
17	SX	130	
18	SY	145	
19	SZ	135	
20	Sc	82	
21	Sd	67	
22	3B	327	
22	3C	327	
23	3D	504	
24	3E	511	
25	3F	573	
26	3G	126	
26	3H	126	
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	



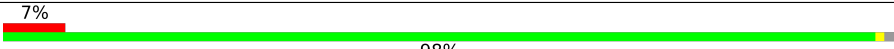



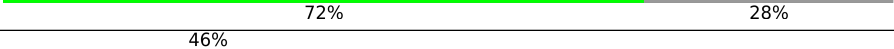
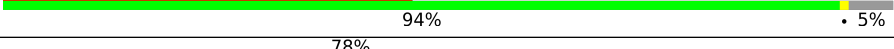





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Mol	Chain	Length	Quality of chain
32	AF	513	
33	AG	896	
34	B1	923	
35	B2	943	
36	B3	817	
37	B8	594	
38	BE	939	
39	B6	440	
40	5B	214	
41	5C	554	
42	5D	250	
43	5E	593	
44	5F	183	
45	5G	290	
46	5H	610	
47	5I	489	
48	5J	217	
49	5K	189	
50	RA	707	
51	RB	357	
52	RC	316	
53	RE	1237	
54	RF	297	
55	RG	252	
55	RH	252	

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Mol	Chain	Length	Quality of chain
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		

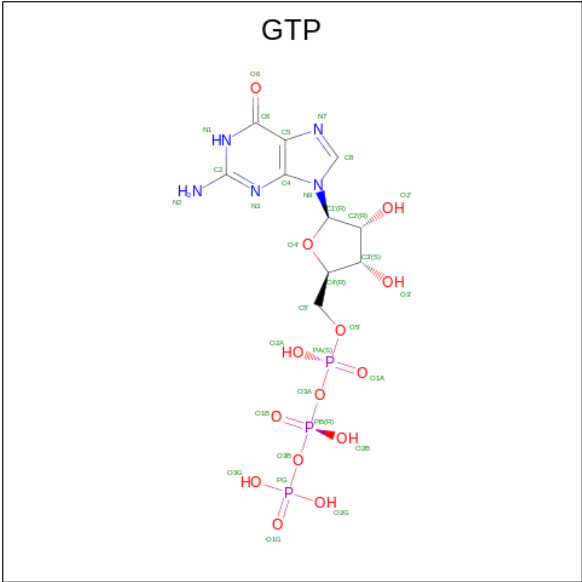
- Molecule 67 is a protein called Unassigned helices.

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

- Molecule 68 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

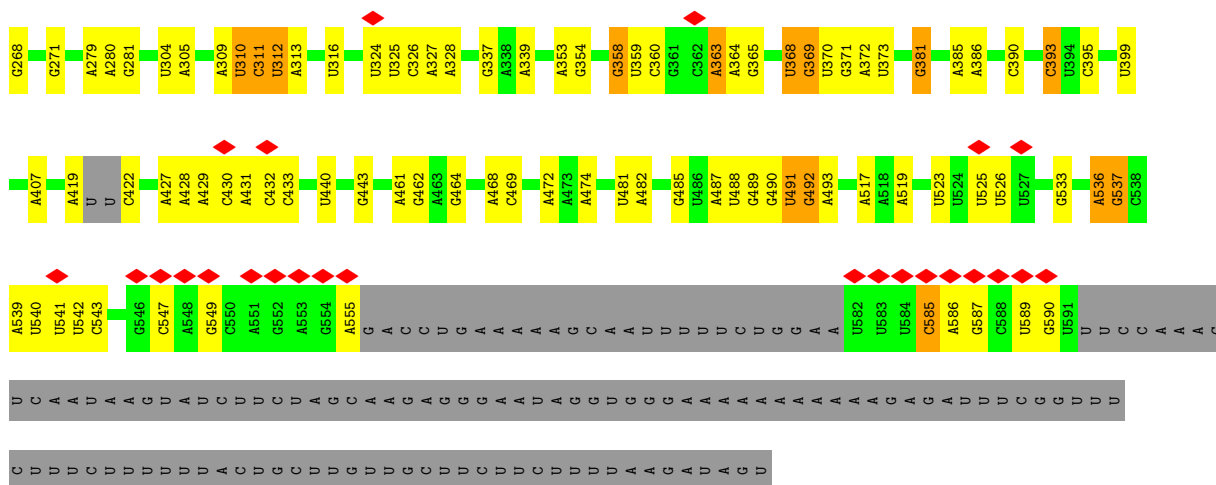
- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



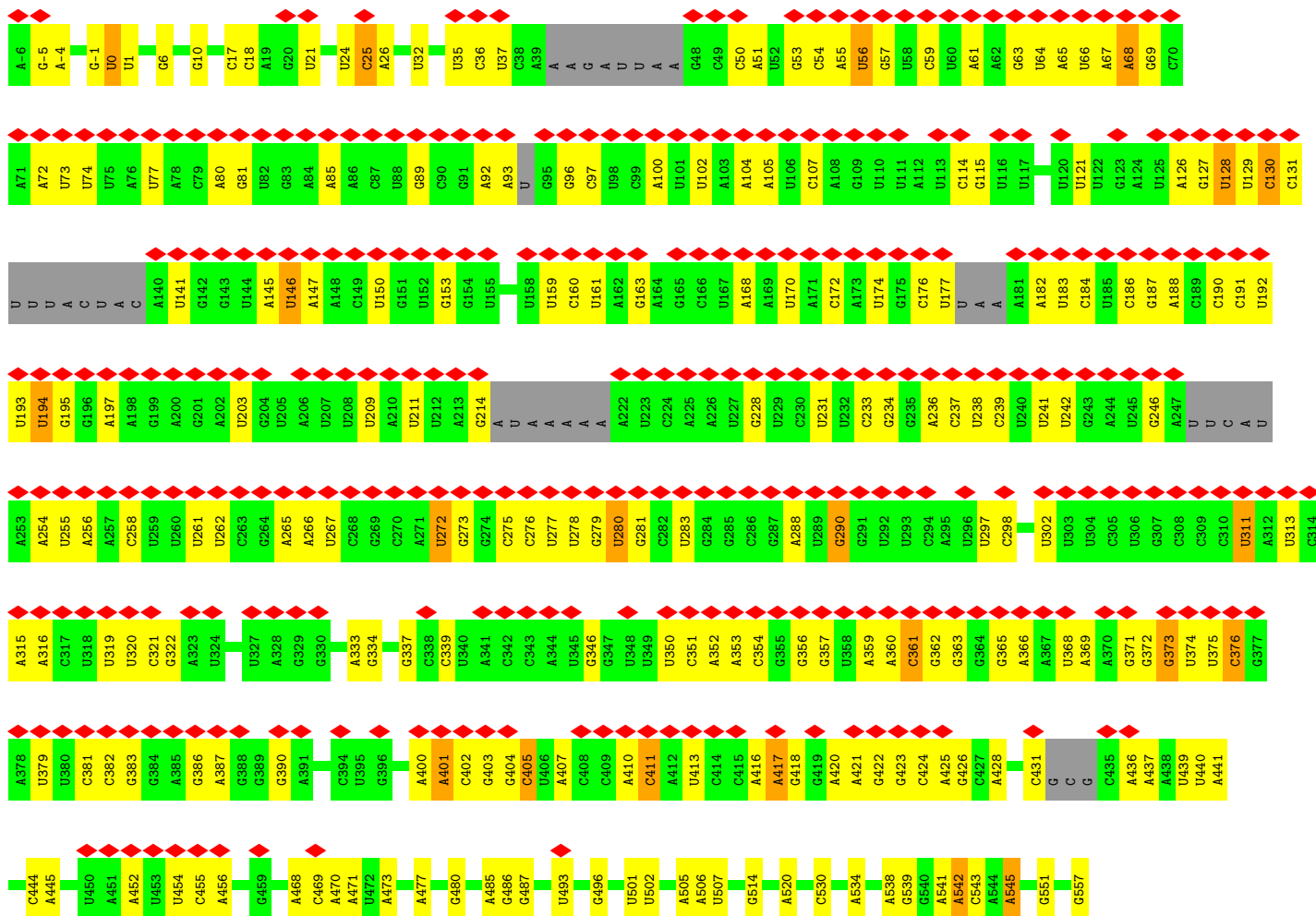
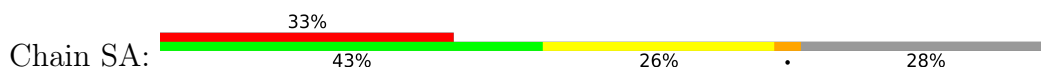
Mol	Chain	Residues	Atoms					AltConf
69	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 70 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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



• Molecule 3: 18S rRNA

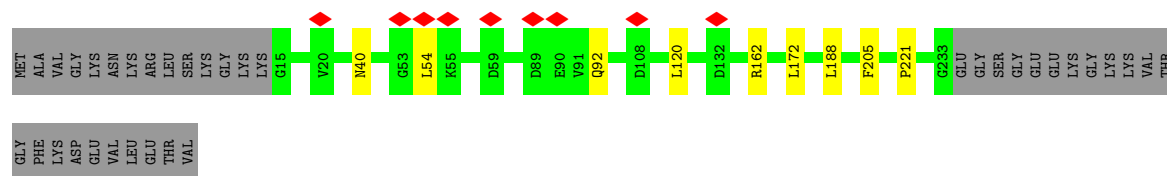






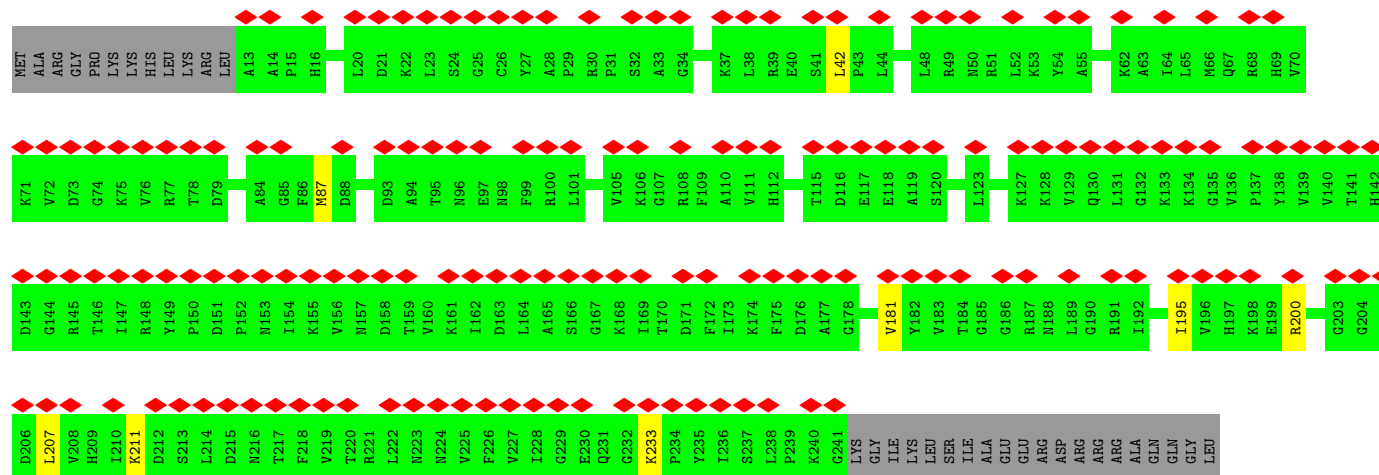
• Molecule 4: 40S ribosomal protein S1-A

Chain SC: 82% 14%



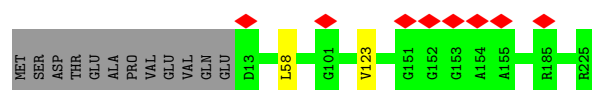
• Molecule 5: 40S ribosomal protein S4-A

Chain SF: 62% 85% 12%

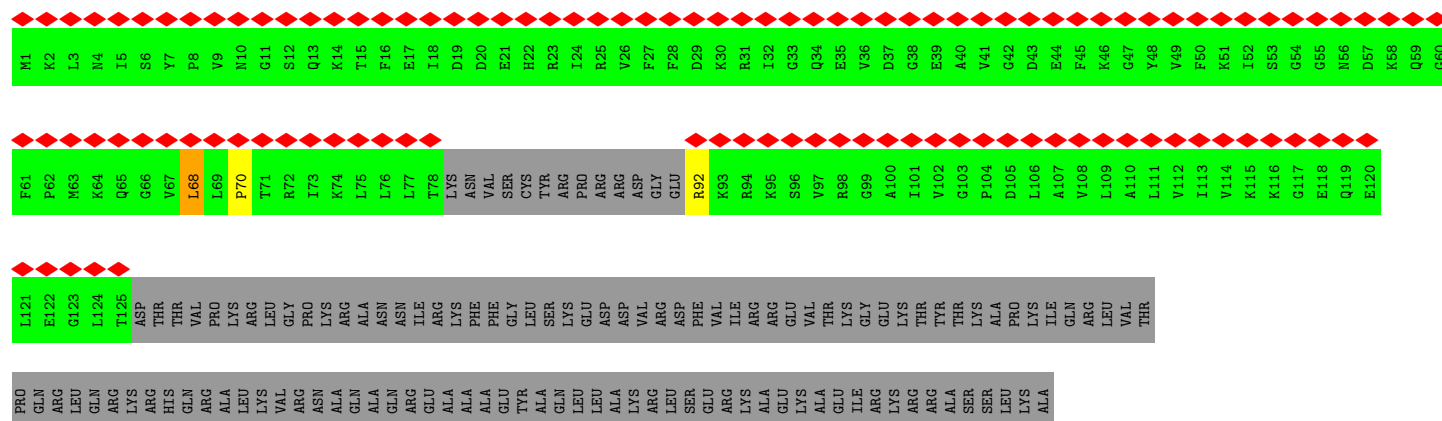


• Molecule 6: 40S ribosomal protein S5

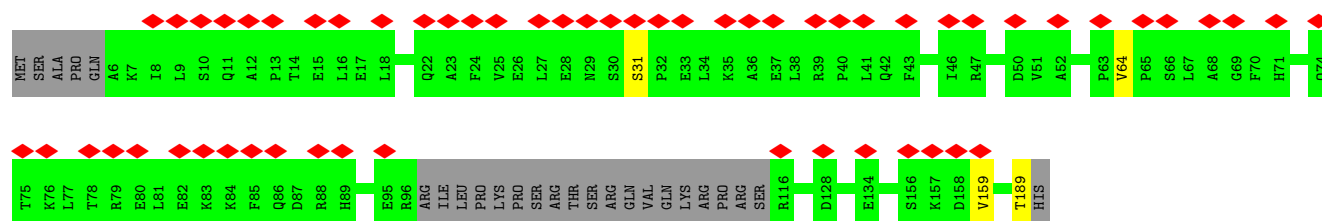
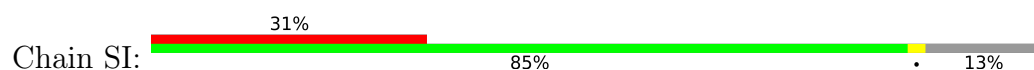
Chain SG: 94% 5%



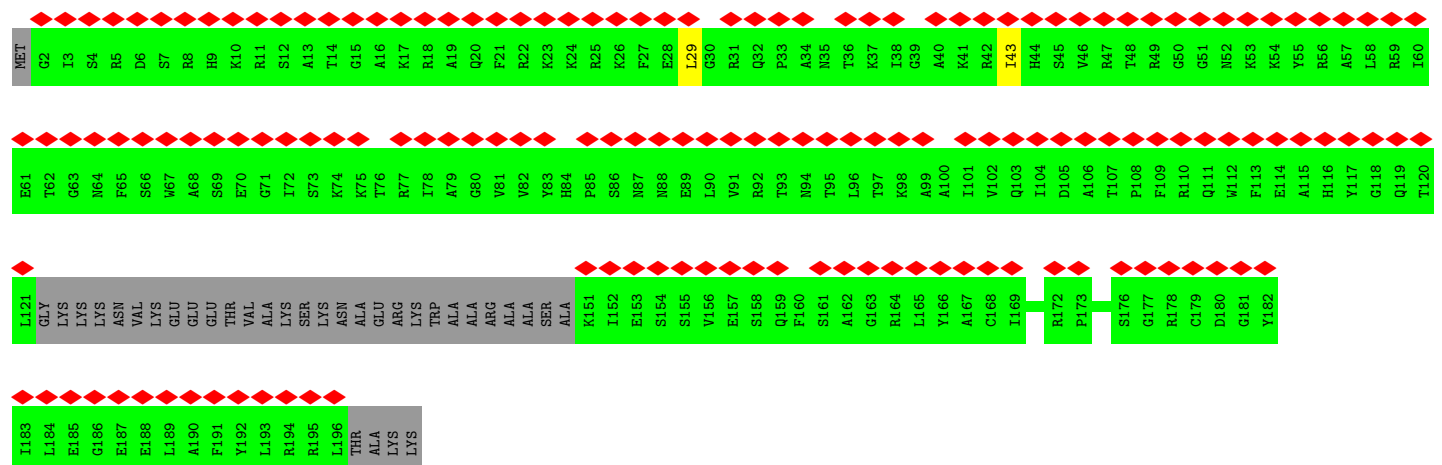
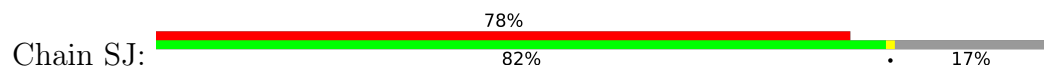
• Molecule 7: 40S ribosomal protein S6-A



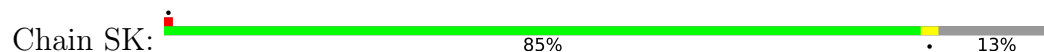
• Molecule 8: 40S ribosomal protein S7-A

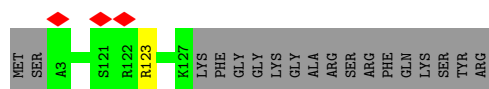
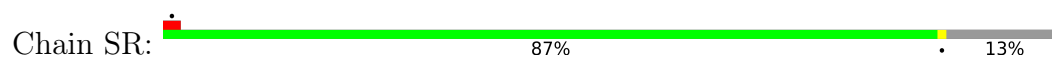


• Molecule 9: 40S ribosomal protein S8-A

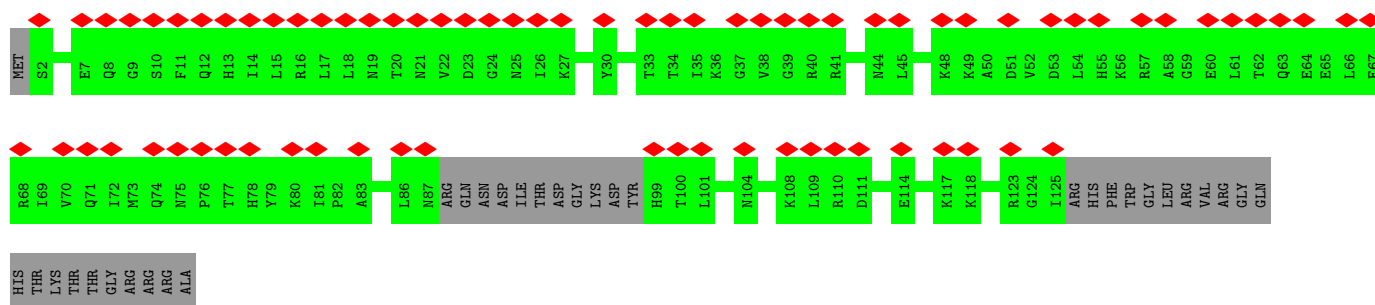
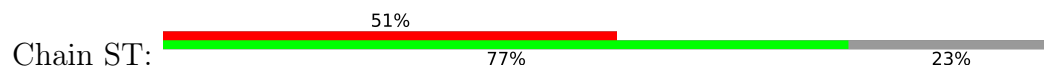


• Molecule 10: 40S ribosomal protein S9-A

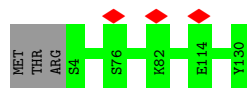




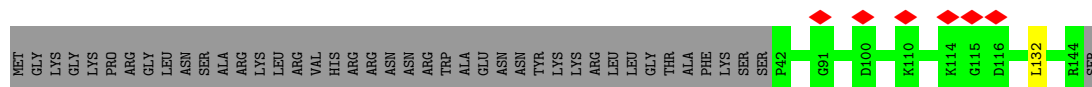
- Molecule 16: 40S ribosomal protein S18-A



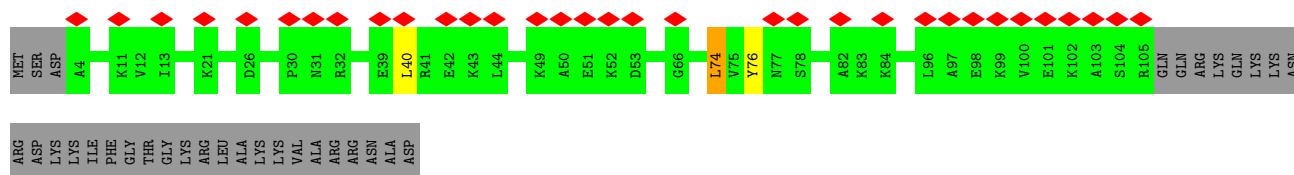
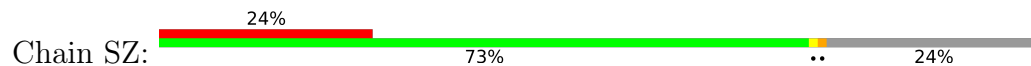
- Molecule 17: 40S ribosomal protein S22-B



- Molecule 18: 40S ribosomal protein S23-A

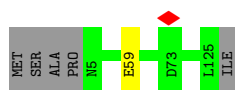


- Molecule 19: 40S ribosomal protein S24-A

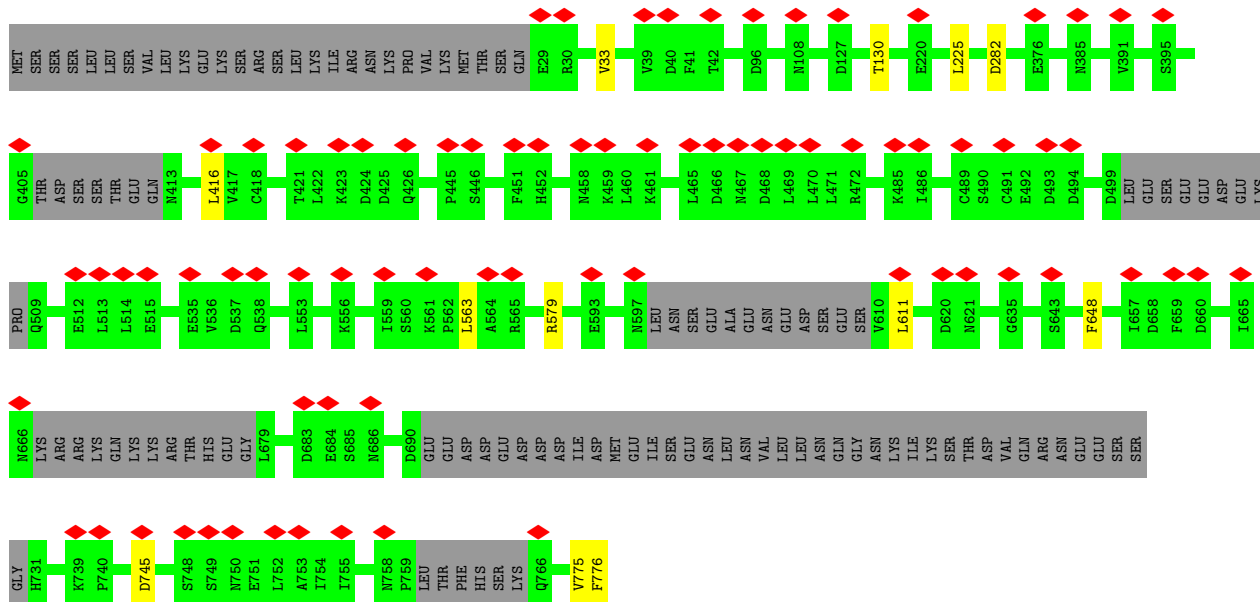
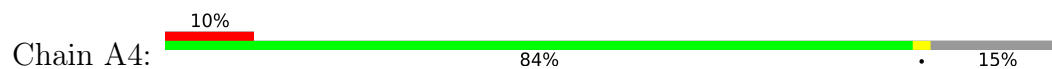


- Molecule 20: 40S ribosomal protein S27-A

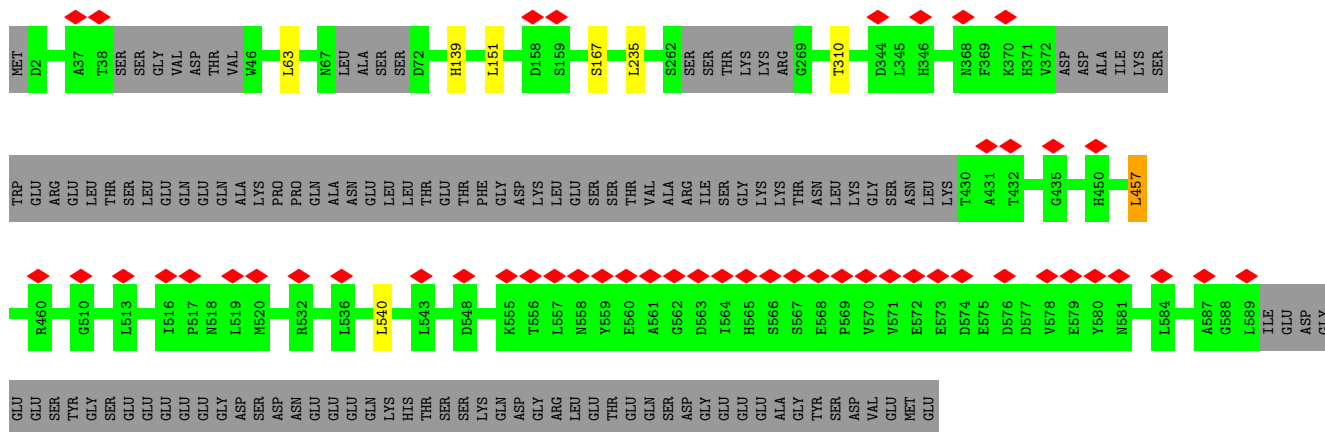
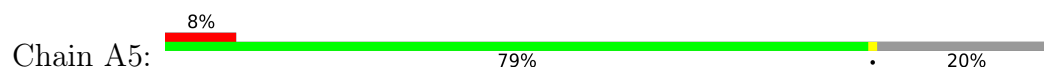




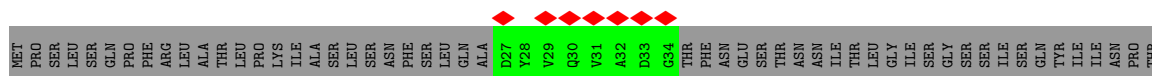
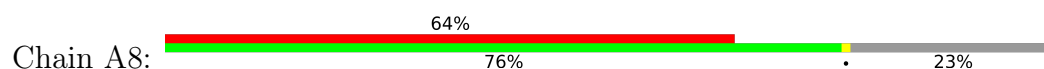
- Molecule 27: U3 small nucleolar RNA-associated protein 4

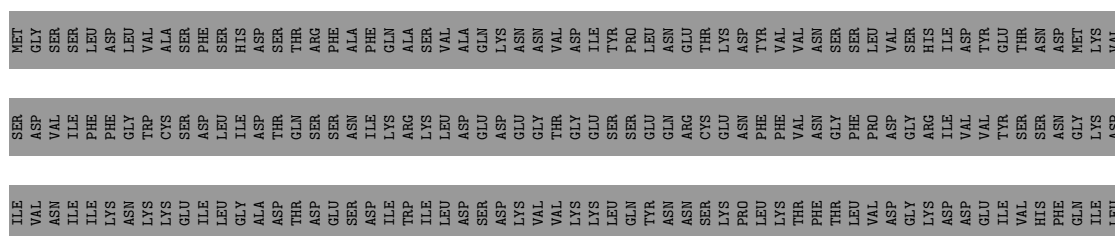


- Molecule 28: U3 small nucleolar RNA-associated protein 5

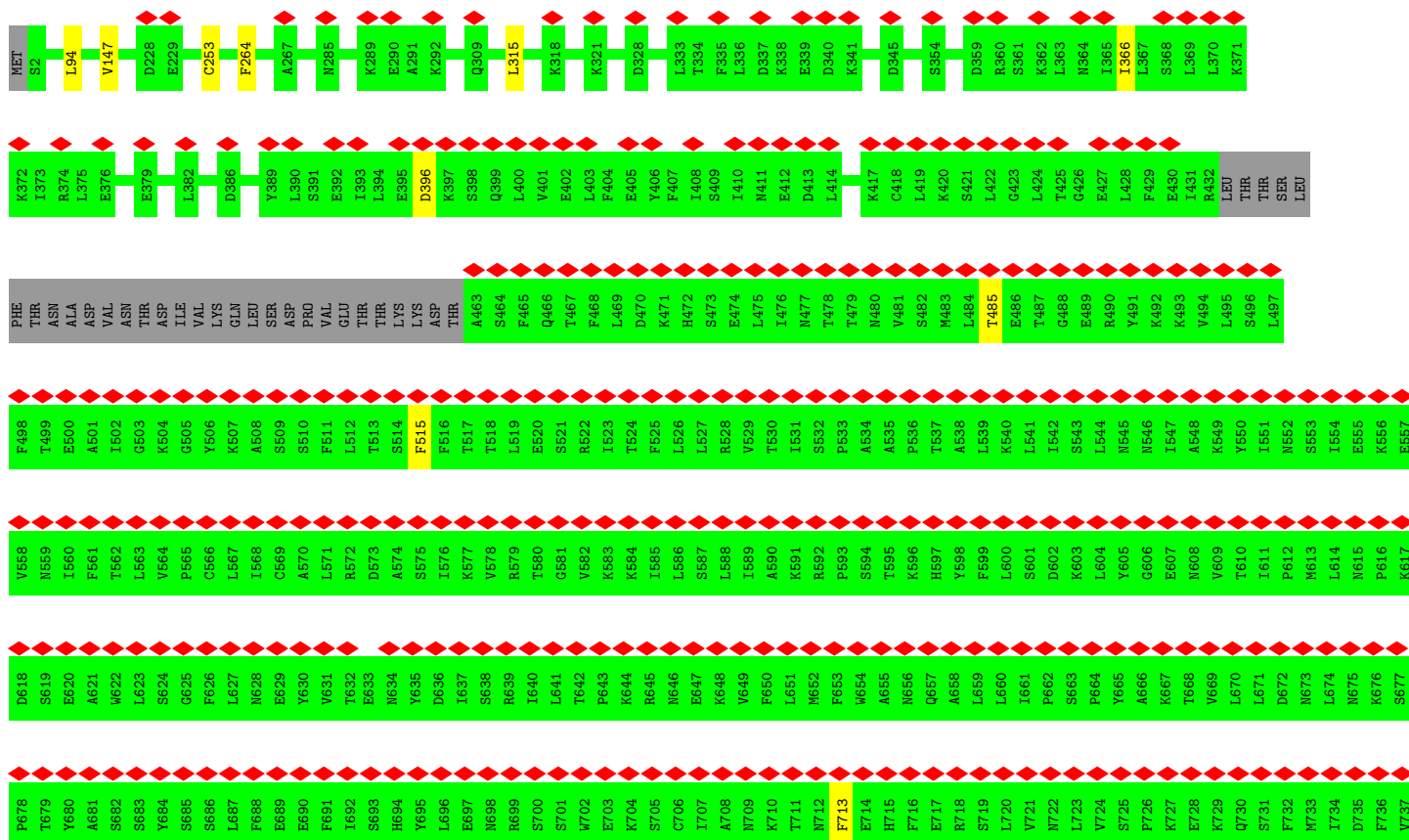


- Molecule 29: U3 small nucleolar RNA-associated protein 8





- Molecule 31: U3 small nucleolar RNA-associated protein 10

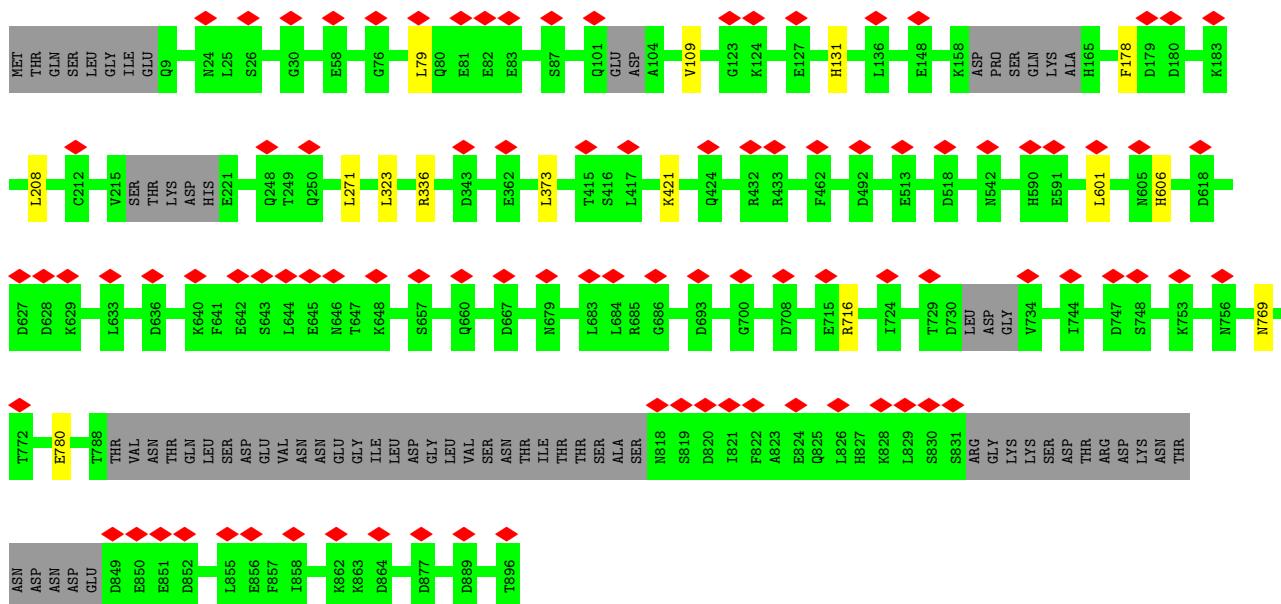
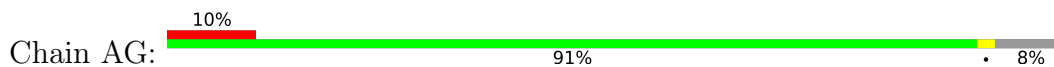


ASN	VAL	ASN	VAL	ASN	GLY	TRP	ASN	GLY	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
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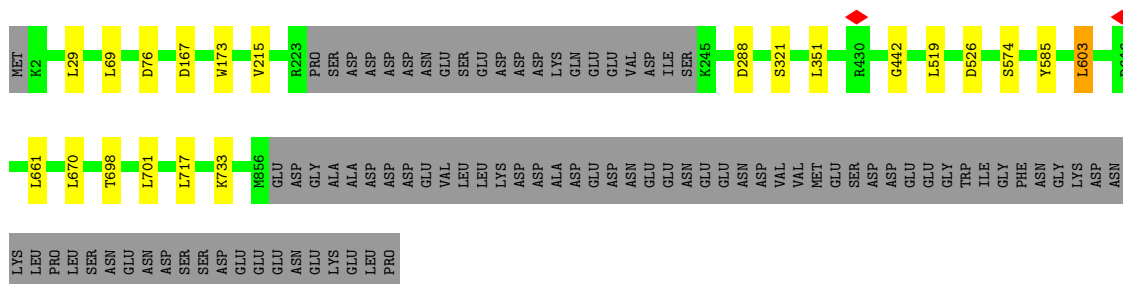
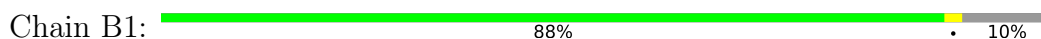
● Molecule 32: U3 small nucleolar RNA-associated protein 15



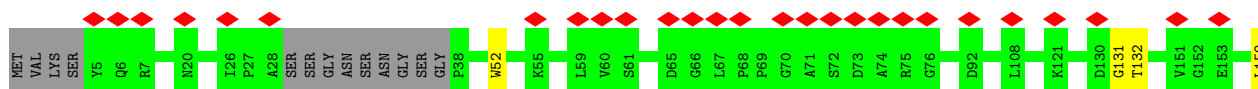
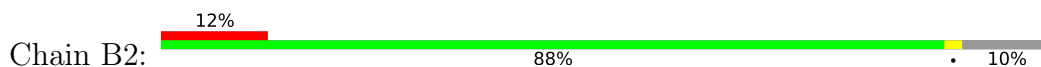
- Molecule 33: NET1-associated nuclear protein 1

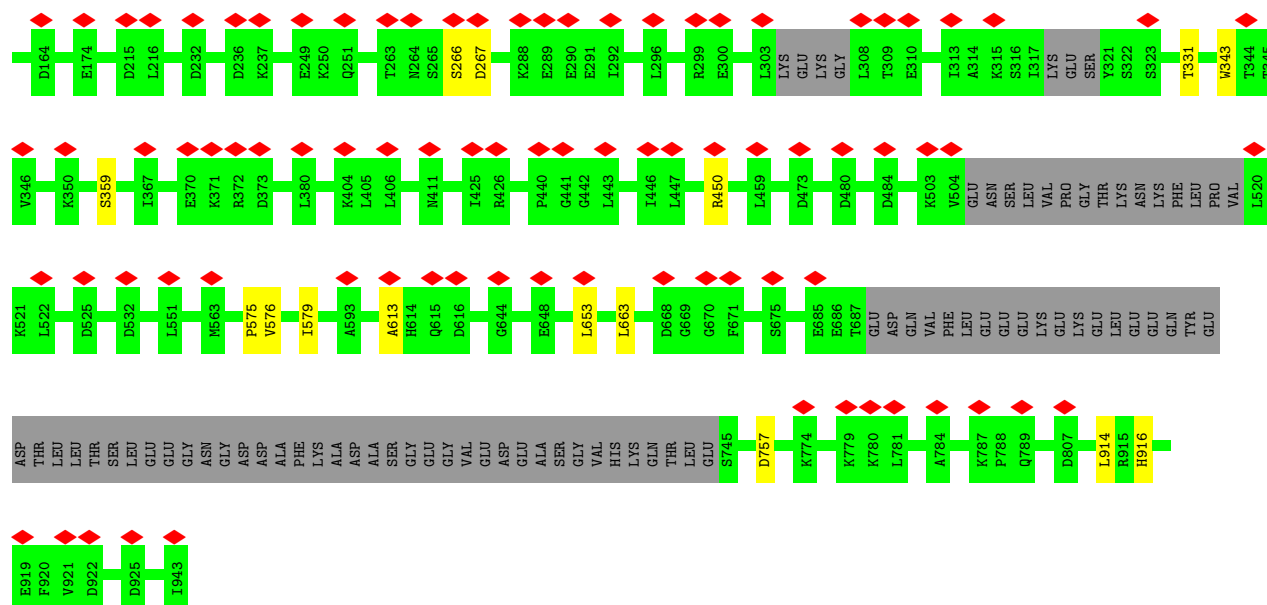


- Molecule 34: Periodic tryptophan protein 2



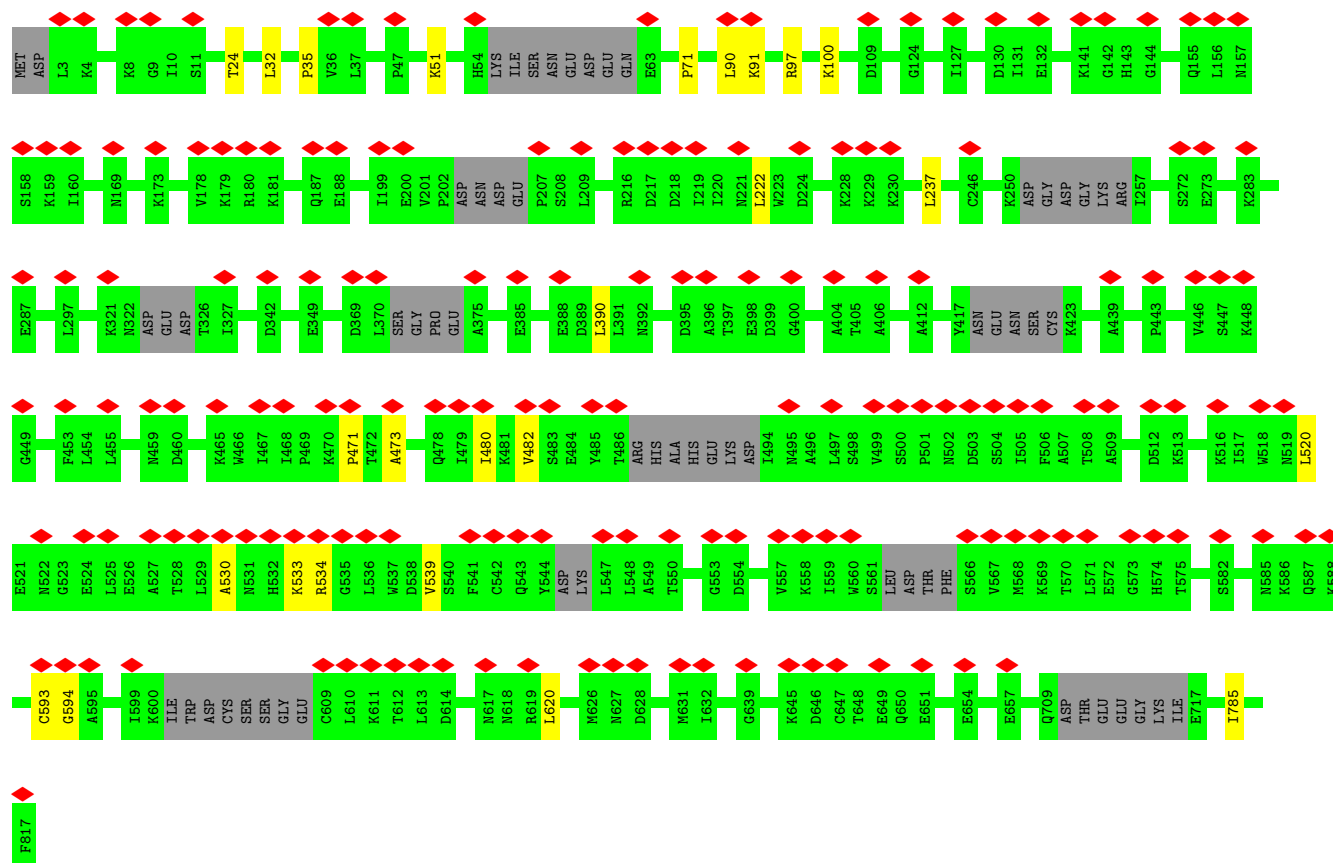
- Molecule 35: U3 small nucleolar RNA-associated protein 12



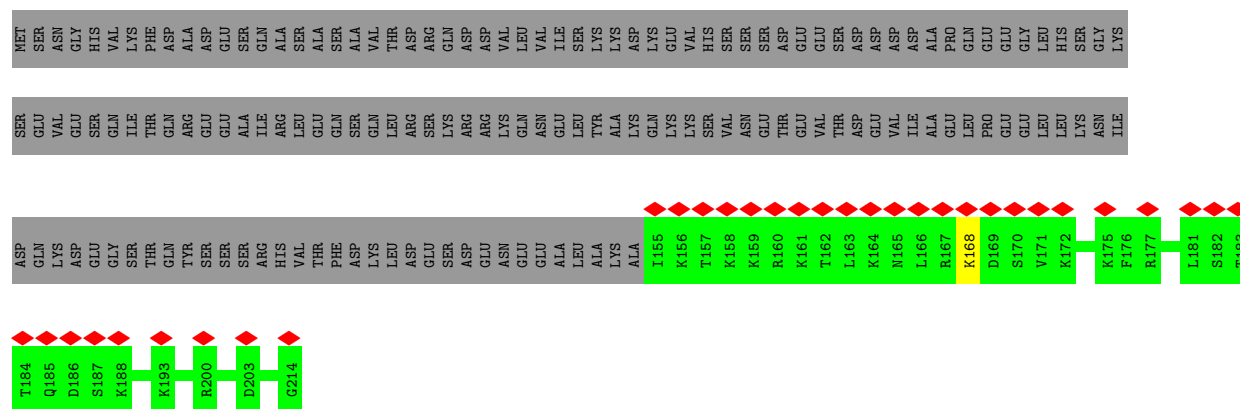


- Molecule 36: U3 small nucleolar RNA-associated protein 13

Chain B3: 22% 90% 7%

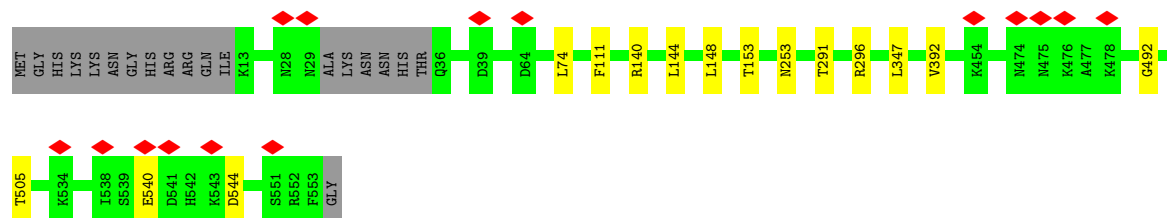


- Molecule 37: U3 small nucleolar RNA-associated protein 18



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

Chain 5C: 94%



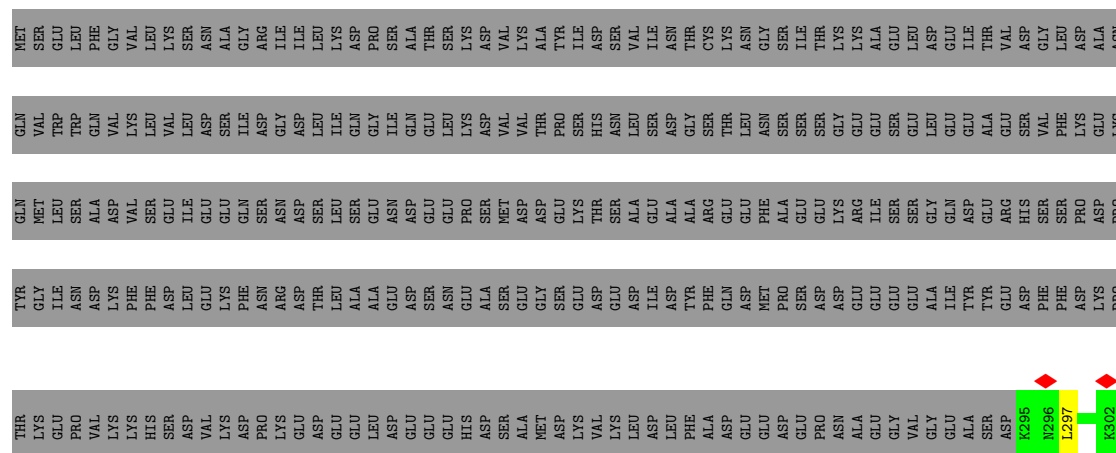
- Molecule 42: U3 small nucleolar RNA-associated protein 11

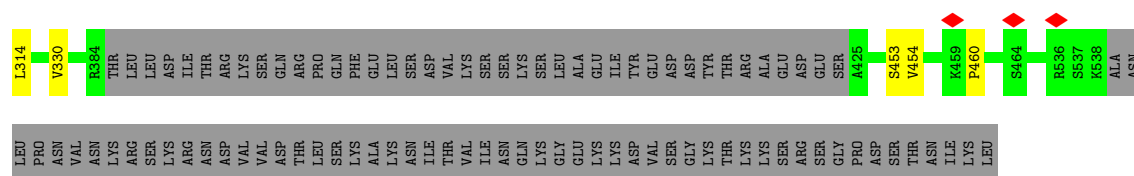
Chain 5D: 7% 92% 6%



- Molecule 43: U3 small nucleolar RNA-associated protein MPP10

Chain 5E: 33% 66%





- Molecule 44: U3 small nucleolar ribonucleoprotein protein IMP3

Chain 5F: 97%



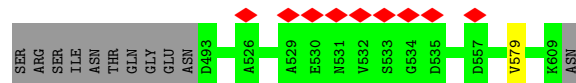
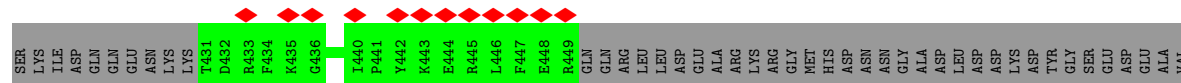
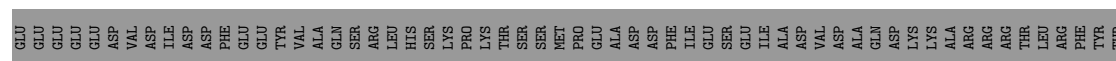
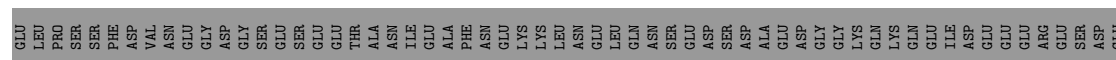
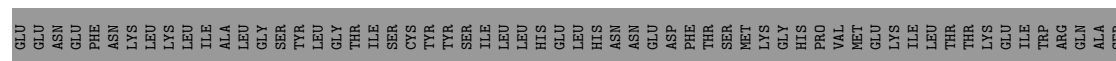
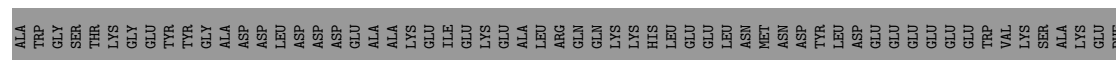
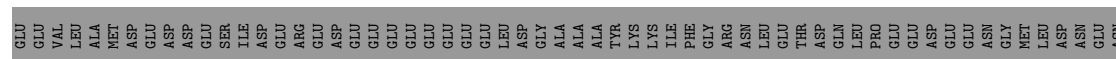
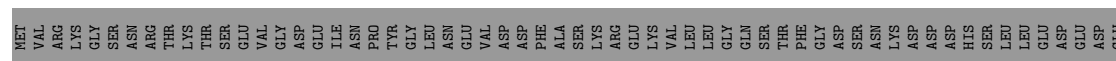
- Molecule 45: U3 small nucleolar ribonucleoprotein protein IMP4

Chain 5G: 96%




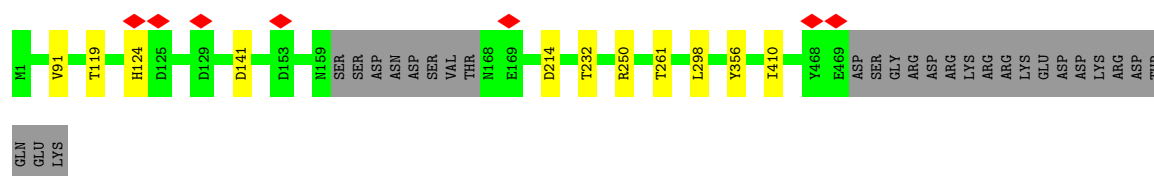
- Molecule 46: Something about silencing protein 10

Chain 5H: 22% 78%



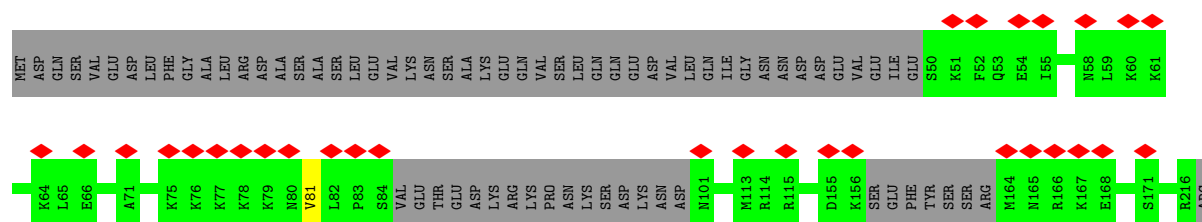
- Molecule 47: Protein SOF1

Chain 5I:  92% 6%



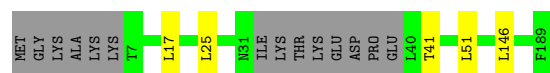
- Molecule 48: rRNA-processing protein FCF2

Chain 5J:  14% 66% 34%



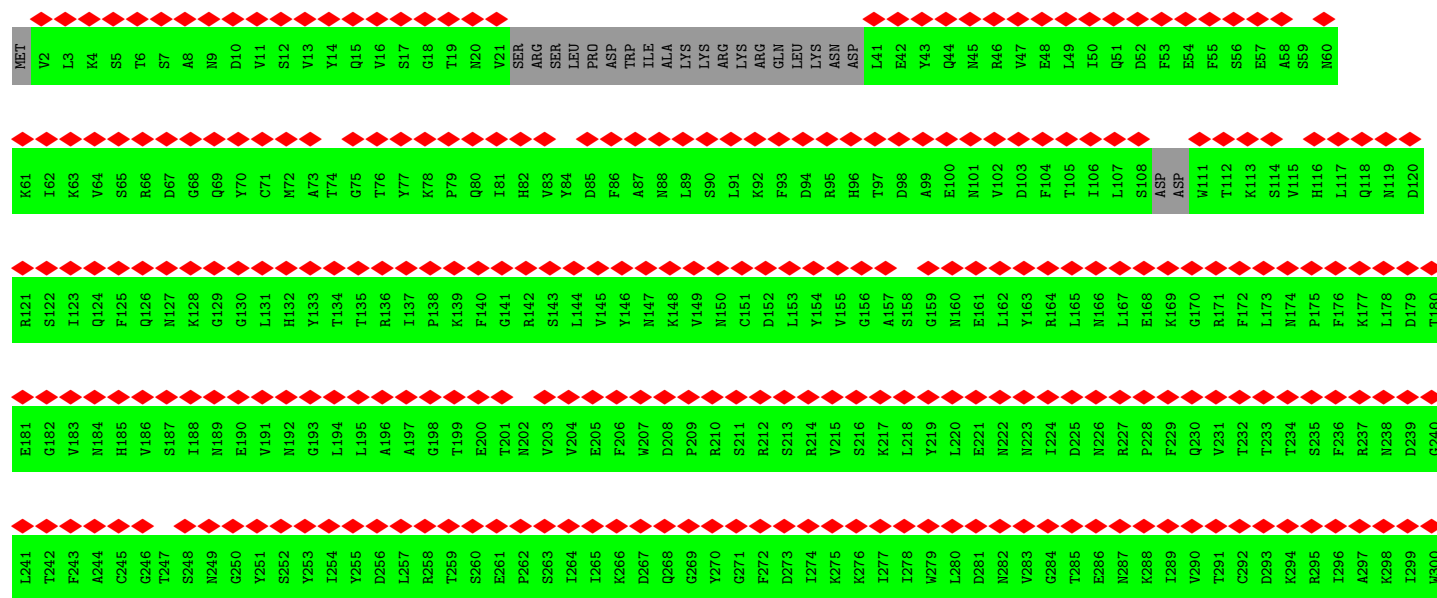
- Molecule 49: rRNA-processing protein FCF1

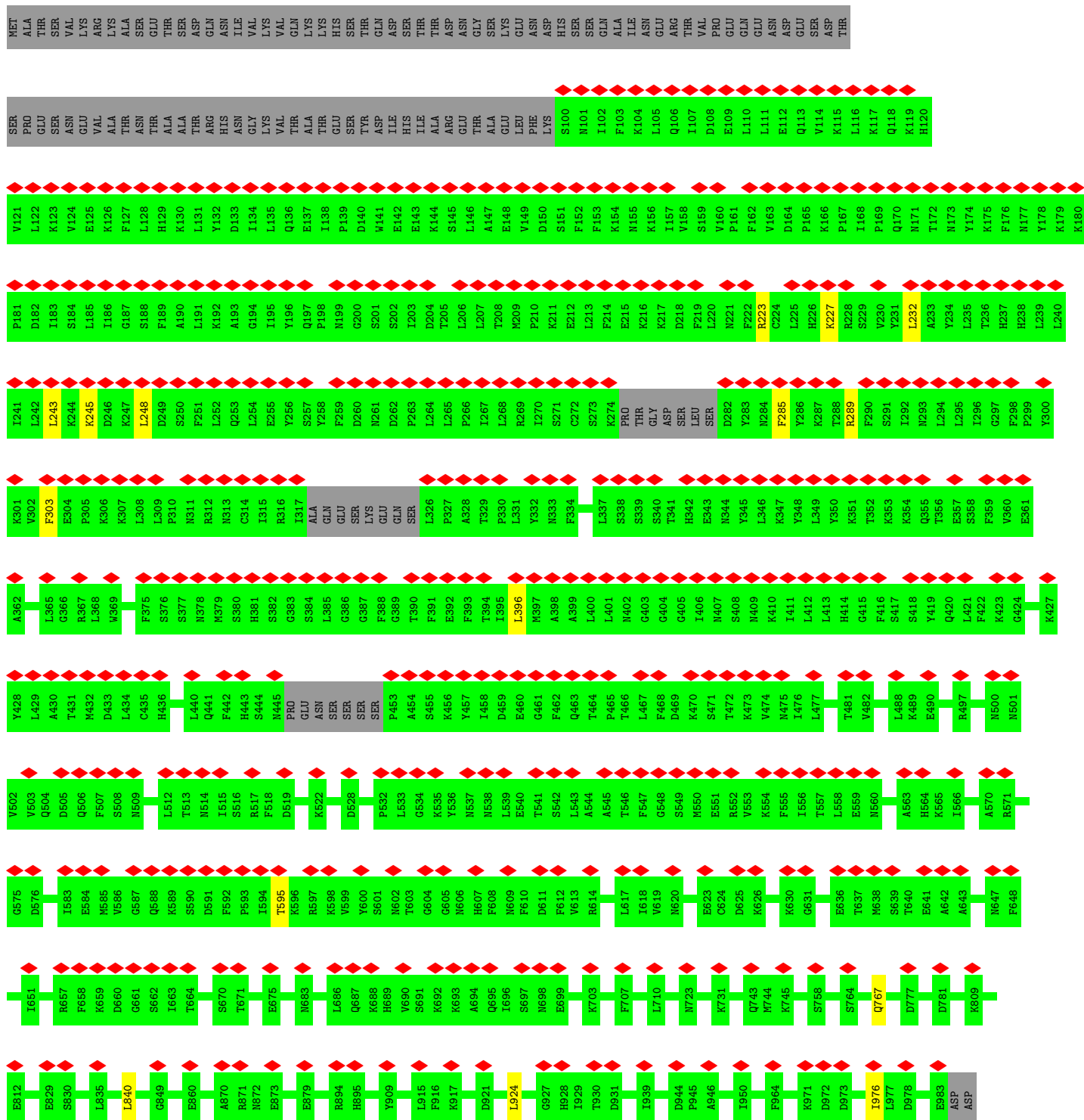
Chain 5K:  90% 7%

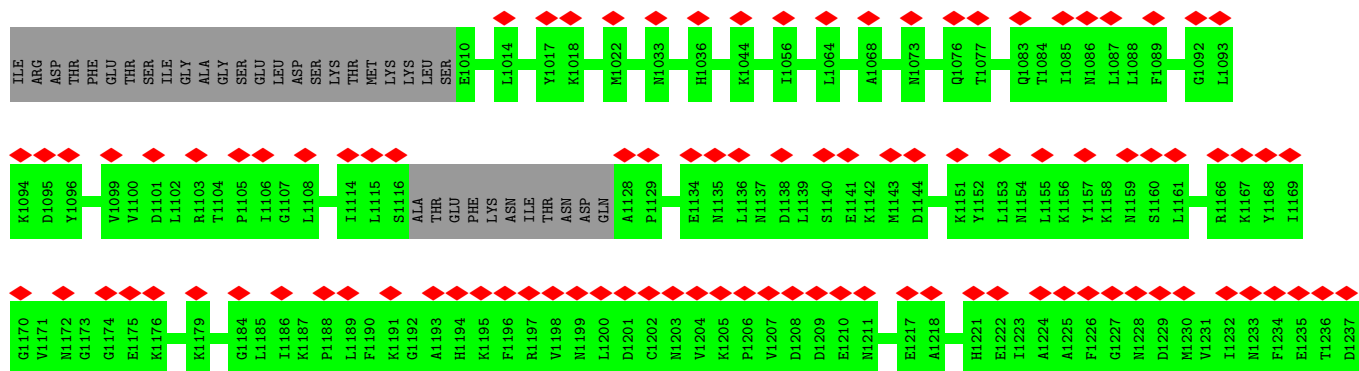


- Molecule 50: Ribosome biogenesis protein ENP2

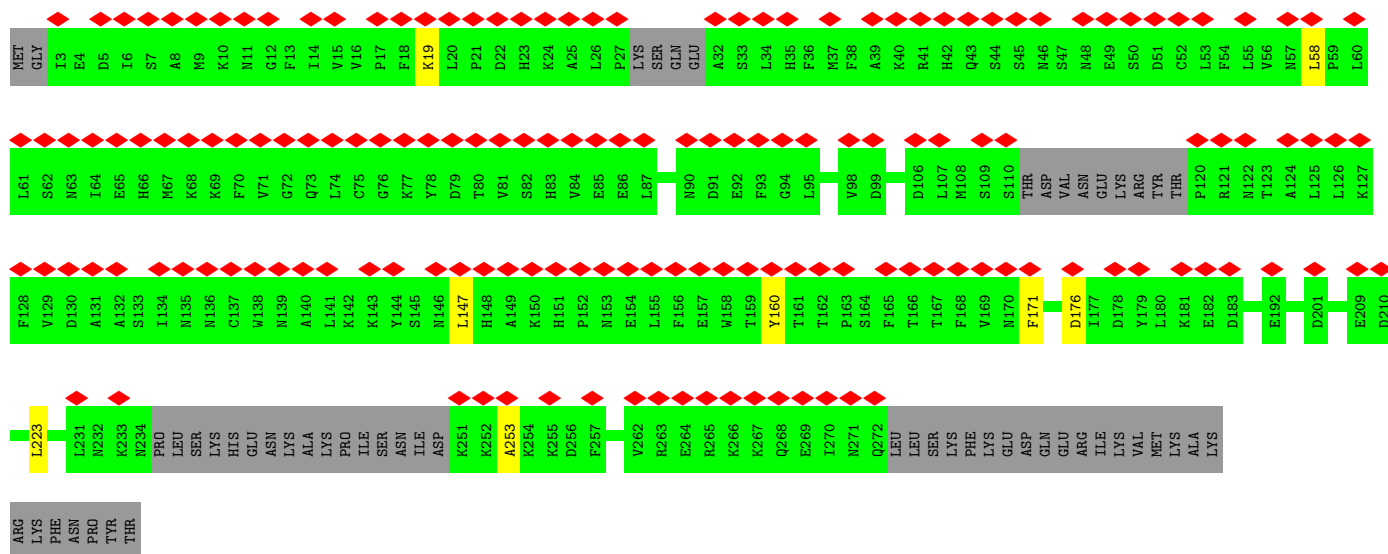
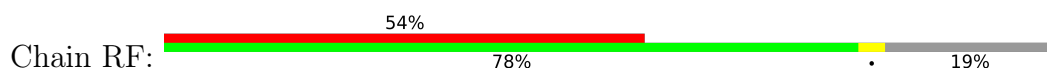
Chain RA:  47% 48% 52%



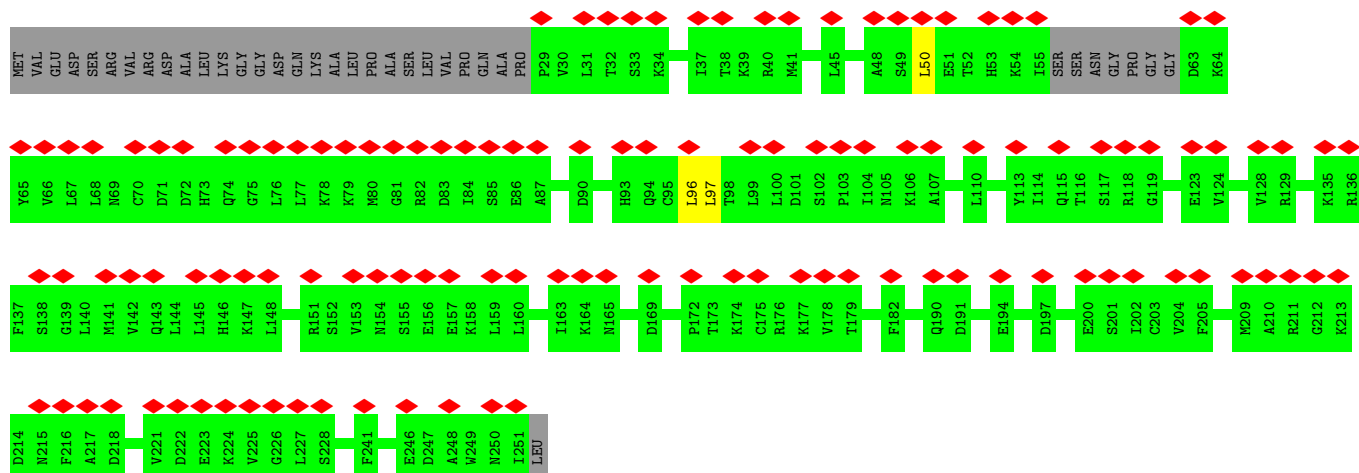
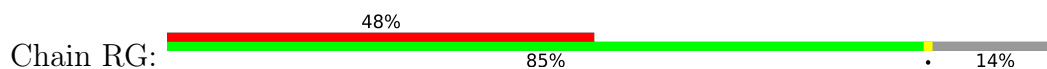




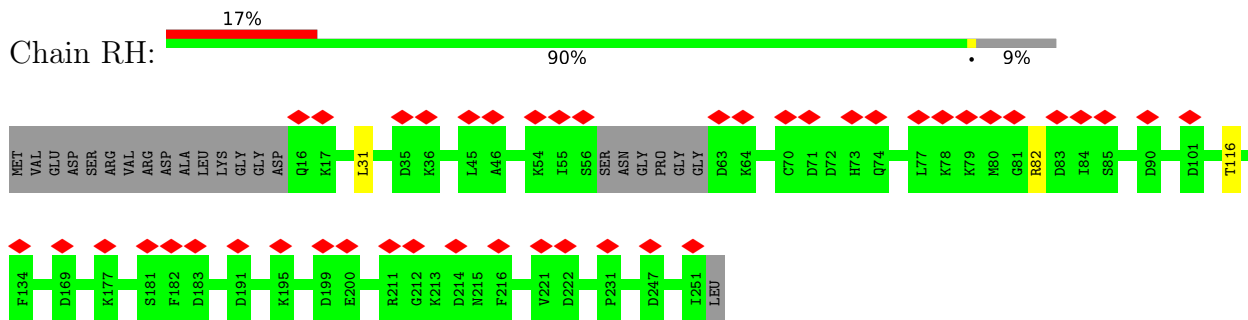
• Molecule 54: Ribosomal RNA-processing protein 7



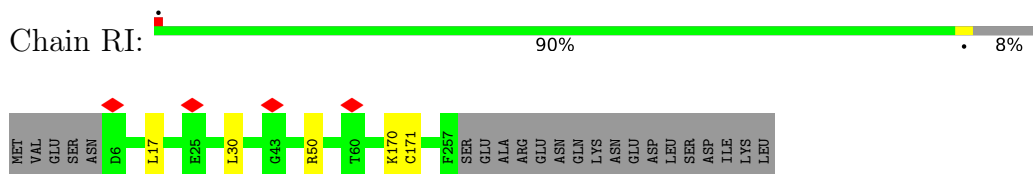
• Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1



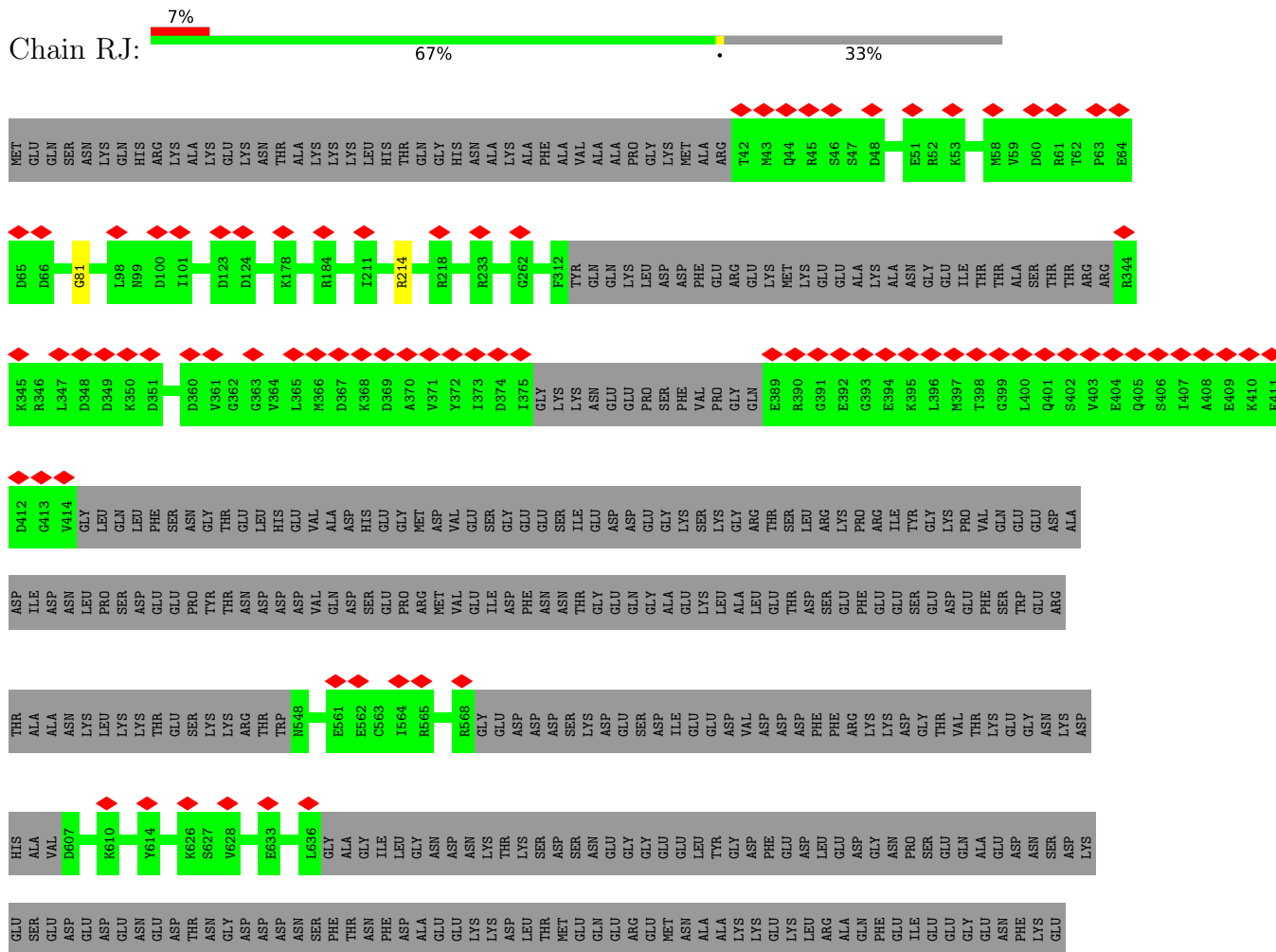
- Chain RH:



- Chain RI:



- Chain RJ:

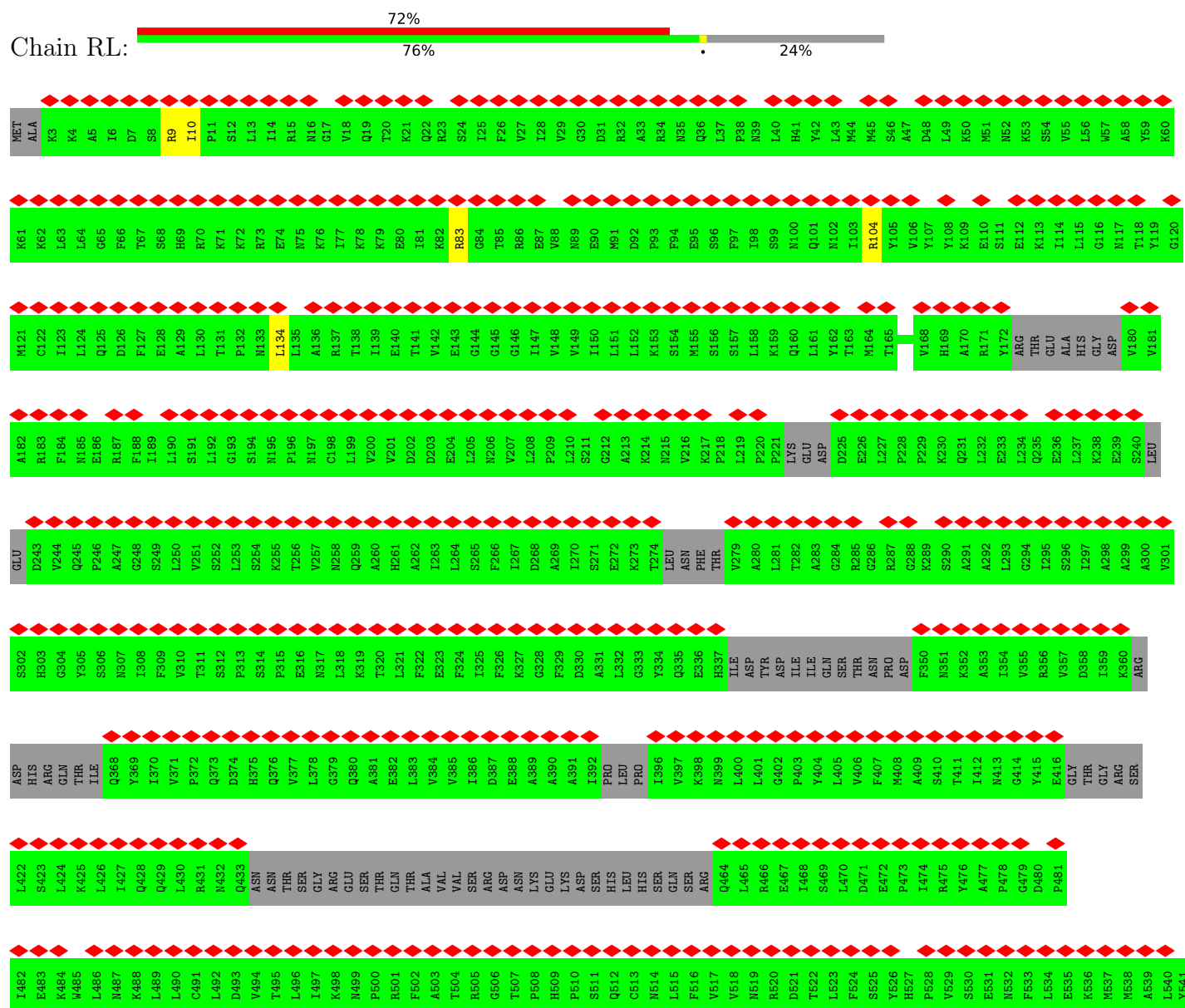




- Molecule 58: RNA 3'-terminal phosphate cyclase-like protein

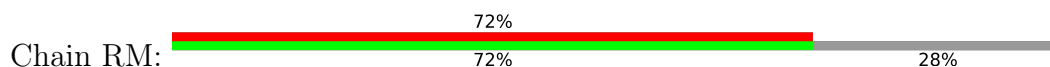


- Molecule 59: RNA cytidine acetyltransferase



V542	S642	L603	S602	R782	L842	L902	ASP	SER	MET	K61	M121	V181
S543	L603	S603	S602	K783	D843	N903	GLN	LEU	ALA	K62	C122	A182
S544	L603	S604	S603	K784	S844	N904	MET	THR	THR	K63	C123	A183
H545	R605	S605	R605	F785	Y845	P905	GLY	GLY	GLY	L64	L124	F184
Y546	G606	G606	G606	L786	S846	S906	ASP	LYS	LYS	G65	Q125	M185
K547	Q607	Q607	Q607	S787	N847	N907	LEU	ARG	ARG	P66	Q126	E186
N548	R608	R608	R608	L788	N848	Q908	GLU	THR	THR	THR	F127	R187
S549	A609	A609	A609	L789	L849	T909	ALA	GLU	GLU	SER	E128	F188
P550	G610	G610	G610	S790	L850	I910	LYS	LYS	LYS	ARG	A129	I189
N551	G611	G611	G611	Y791	D851	A911	ALA	ALA	ALA	LYS	L130	L190
D552	D612	D612	D612	D792	Y852	M912	VAL	GLU	GLU	ASP	T131	S191
L553	L613	L613	L613	F793	H853	F913	ILE	ILE	ILE	GLU	P132	L192
Q554	I614	I614	I614	H794	V854	A914	ALA	ALA	ALA	ASN	M133	G193
M555	P615	P615	P615	K795	I855	K915	MET	ARG	ARG	LYS	L134	S194
M556	W616	W616	W616	F796	G856	I916	GLN	GLN	GLN	LYS	L135	M195
S557	I617	I617	I617	T797	D857	M917	GLU	GLU	GLU	LYS	A136	P196
D558	I618	I618	I618	A798	N858	K918	LYS	LYS	LYS	GLU	T137	M197
A559	S619	S619	S619	V799	L859	K919	ALA	ALA	ALA	LYS	T138	C198
P560	Q620	Q620	Q620	Q800	P860	M920	LYS	LYS	LYS	GLY	I139	L199
A561	Q621	Q621	Q621	A801	M861	S921	ILE	ILE	ILE	ARG	E140	V200
H562	F622	F622	F622	L802	L862	Q922	ASN	ASN	ASN	THR	T141	V201
L564	D624	D624	D624	V804	L864	Y923	SER	SER	SER	ARG	V142	D202
F565	E625	E625	E625	I805	L865	F924	ASN	ASN	ASN	VAL	E143	D203
V566	E626	E626	E626	S806	Y866	R925	LEU	LEU	LEU	ASN	G144	E204
L567	F627	F627	F627	S807	F867	Q926	ASP	ASP	ASP	MET	G145	L205
L568	A628	A628	A628	S808	G868	L928	TYR	TYR	TYR	D92	I147	V207
P569	S629	S629	S629	K809	D869	S929	ALA	ALA	ALA	P93	V148	L208
P570	L630	L630	L630	K910	K870	Q930	ILE	ILE	ILE	E95	V149	P209
I571	S631	S631	S631	A811	M871	Q931	ASN	ASN	ASN	S96	I150	L210
D572	G632	G632	G632	Q812	GLY	I932	ASP	ASP	ASP	F97	L151	S211
P573	A633	A633	A633	D813	ASP	T932	SER	SER	SER	S98	L152	G212
K574	R634	R634	R634	L814	VAL	L928	GLU	GLU	GLU	A33	K153	L213
D575	I635	I635	I635	S815	LYS	S929	TRP	TRP	TRP	S99	S154	A214
G576	V636	V636	V636	D816	LEU	Q930	ALA	ALA	ALA	M100	M155	K215
G577	R637	R637	R637	D817	LEU	Q931	GLU	GLU	GLU	Q101	S157	V216
R578	I638	I638	I638	S818	S878	I932	SER	SER	SER	I103	L158	K217
I579	A639	A639	A639	E819	S879	T932	GLN	GLN	GLN	R104	K159	PRO
P580	T640	T640	T640	K819	V880	L928	LYS	LYS	LYS	N39	Q160	PRO
D581	N641	N641	N641	H820	Q881	S929	ASP	ASP	ASP	Y105	L161	PRO
P582	P642	P642	P642	D821	A883	Q931	LEU	LEU	LEU	V106	Y162	LYS
L583	E643	E643	E643	N822	I884	L928	GLU	GLU	GLU	Y107	T163	GLU
C584	G644	G644	G644	K823	L885	M920	ALA	ALA	ALA	Y108	M164	D224
V585	E645	E645	E645	E824	L886	D926	LYS	LYS	LYS	K109	T165	D225
I586	S646	S646	S646	L825	A887	T927	ASP	ASP	ASP	E110	M166	E226
Q587	M647	M647	M647	T826	I888	L928	GLY	GLY	GLY	S111	L227	L227
I588	G648	G648	G648	R827	G889	L928	GLU	GLU	GLU	A47	M168	P228
A589	Y649	Y649	Y649	T828	L890	L928	ILE	ILE	ILE	D48	H169	P229
L590	G650	G650	G650	H829	Q891	T929	LYS	LYS	LYS	K113	A170	K230
E591	S651	S651	S651	L830	R892	K923	ASN	ASN	ASN	L114	G171	Q231
G592	R652	R652	R652	D831	K893	N924	TYR	TYR	TYR	X50	Y172	L232
E593	A653	A653	A653	D832	N894	I895	ALA	ALA	ALA	M51	ARG	L233
I594	I654	I654	I654	I833	I895	D896	GLU	GLU	GLU	N52	THR	L234
S595	E655	E655	E655	F834	D896	T897	ALA	ALA	ALA	K53	GLU	Q235
K596	L656	L656	L656	S835	I898	T897	LYS	LYS	LYS	S54	ALA	E236
E597	L657	L657	L657	P836	I899	A899	GLY	GLY	GLY	V55	HIS	L237
S598	R658	R658	R658	F837	K900	E901	ASP	ASP	ASP	M57	GLY	K238
V599	D659	D659	D659	D838	K900	E901	ASN	ASN	ASN	A58	ASP	E239
R600	Y660	Y660	Y660	L839	E901	E901	LEU	LEU	LEU	Y59	V180	SER
N601	F661	F661	F661	K940	E901	E901	LEU	LEU	LEU	X60		

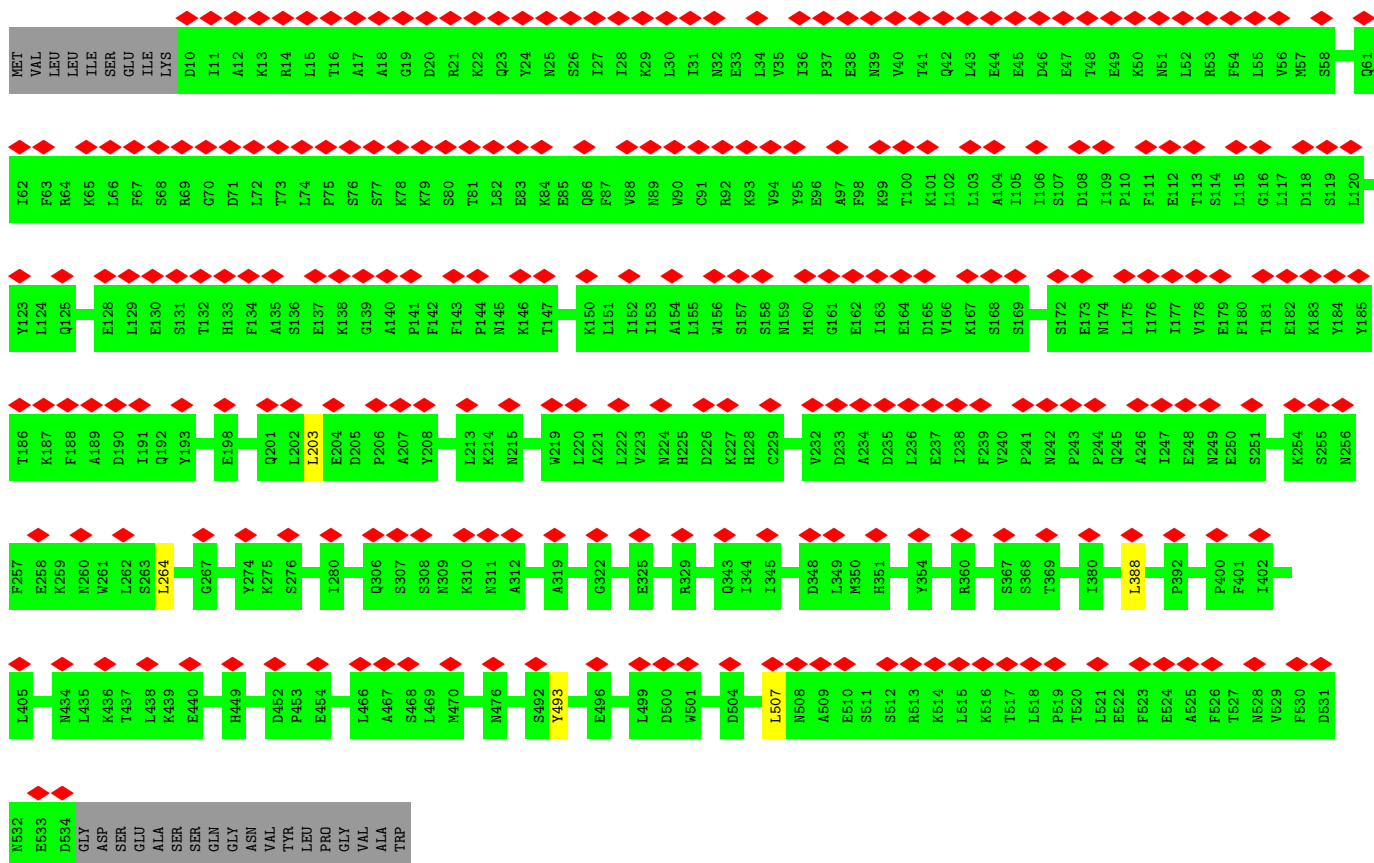
• Molecule 59: RNA cytidine acetyltransferase



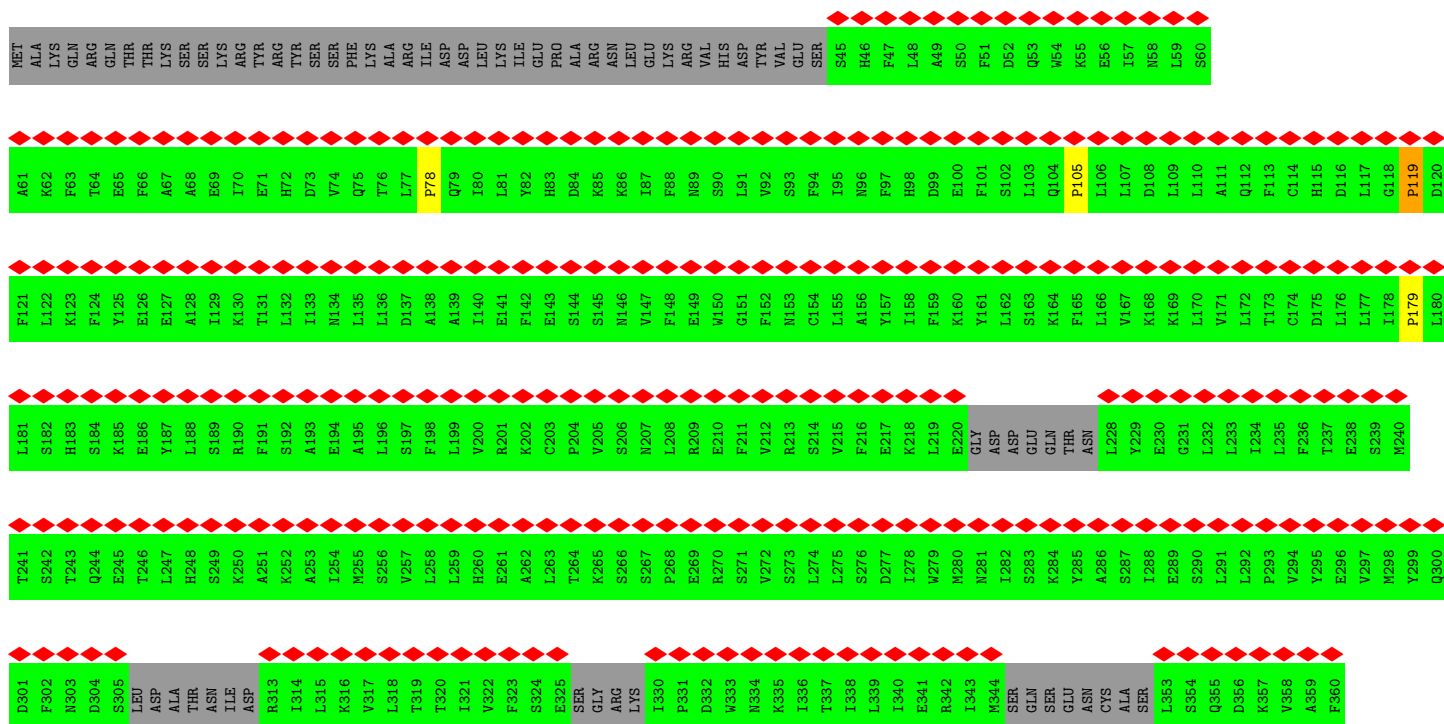
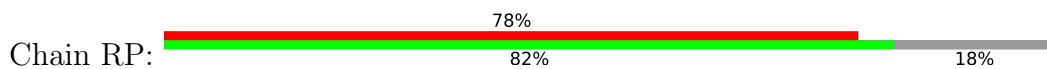
[illegible]

- Molecule 60: Nucleolar complex protein 14



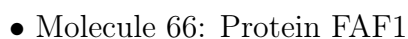
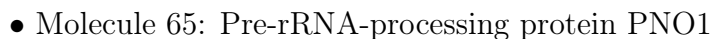


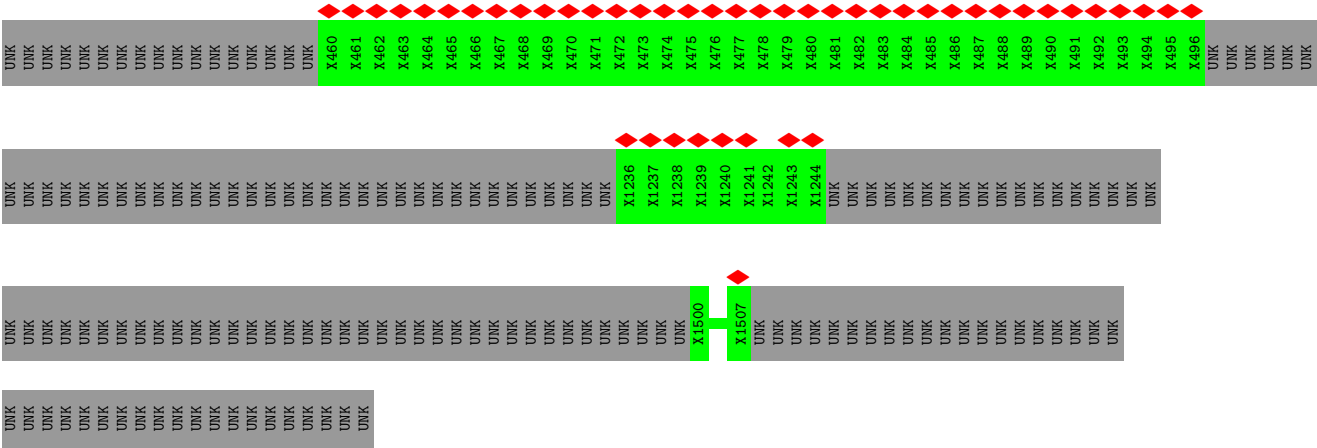
• Molecule 62: U3 small nucleolar RNA-associated protein 20



D1081	I1082	Y1083	A1084	V1085	V1086	V1087	K1088	S1029	R1089	I1090	A1031	M1032	A1033	Y1034	Y1035	V1036	L1037	D1038	T1039	E1040	S1041	T1042	E1043	S1104	S1105	L1106	R1107	L1108	F1109	L1110	Y1111	W1112	A1113	H1114	N1115	P1116	S1117	L1118	Y1119	Q1120	F1121	L1122	Y1123	Y1124	E1125	D1126	F1127	A1128	T1129	I1130	T1131	A1132	L1133	N1134	D1135	T1136	I1137	S1138	N1139	Q1140	
S1021	V1022	L1023	Q1024	P1025	L1026	I1027	Y1028	S1029	I1030	A1031	M1032	A1033	Y1034	Y1035	V1036	L1037	D1038	T1039	E1040	S1041	T1042	E1043	E1044	V1045	H1046	L1047	R1048	K1049	M1050	A1051	S1052	M1053	L1054	R1055	Q1056	Q1057	G1058	L1059	Q1060	C1061	L1062	S1063	S1064	V1065	F1066	E1067	F1068	V1069	G1070	M1071	T1072	F1073	D1074	W1075	S1076	T1077	S1078	M1079	E1080		
I961	N962	D963	F964	L965	S966	L967	A968	S969	G969	E970	R971	D972	D973	Y974	N975	Y976	F977	G978	G979	N980	S981	Q982	Q983	Y924	N985	S986	S987	K988	A989	T990	L991	K992	T993	L994	R995	R996	M997	T998	G999	F1000	V1001	N1002	I1003	V1004	N1005	S1006	T1007	L1008	S1009	V1010	L1011	R1012	T1013	N1014	F1015	P1016	L1017	H1018	T1019	N1020	
I781	M782	L783	S784	I785	P786	Q787	V788	A789	E790	N791	F792	F793	V794	D795	I796	A797	P798	F799	V800	Y801	N802	D803	F804	K805	T806	Y807	K808	D809	E810	E811	D812	M813	E814	N815	E816	R817	V818	I819	T820	G821	S822	M823	T824	E825	V826	D827	R828	N829	N890	L891	D892	D893	D894	T895	L896	F897	K898	D899	E900		
I841	K842	N843	V844	Y845	S846	A847	T848	E849	L850	H851	D852	H853	L854	M855	V856	L857	L858	G859	S860	R861	N862	T863	D864	V865	K866	K867	L868	A869	L870	D871	A872	L873	L874	A875	Y876	K877	N878	P879	T880	L881	N882	K883	Y884	R885	D886	N887	L888	K889	N890	L891	D892	D893	D894	T895	L896	F897	K898	D899	E900		
T901	T902	T903	F904	L905	T906	E907	N908	G909	S910	Q911	S912	I913	K914	A915	E916	D917	E918	K919	V920	Y921	N922	P923	Y924	V925	L926	R927	I928	F929	F930	G931	R932	A933	Q934	V935	P936	P937	T938	S939	Q940	Q941	K942	R943	S944	R945	K946	I947	A948	S1009	V1010	L1011	R1012	T1013	N1014	F1015	P1016	L1017	H1018	T1019	N1020		
L421	K422	K423	N424	W425	Q426	S427	Q428	G429	K430	K431	I432	A433	L434	F435	F436	L437	E438	V439	D440	D441	K442	P443	E444	L445	Q446	K447	V448	R449	E450	V451	N452	F453	P454	E455	E456	F457	I458	L459	S460	I461	R462	D463	F464	F465	V466	T467	A468	E469	I470	N471	D472	S473	N474	D475	L476	F477	E478	I479	TYR		
TRP	ARG	ALA	ILE	I485	F486	K487	Y488	S489	K490	L491	Q492	N493	T494	E495	I496	I497	ILE	PRO	LEU	E502	R503	I504	F505	S506	T507	F508	A509	S510	P511	D512	N513	F514	F515	K516	ASP	MET	VAL	G520	T521	L522	L523	K524	I525	Y526	R527	K528	E529	D530	D531	A532	S533	GLY	ASN	ASN	LEU	L538	K539	T540			
I541	L542	D543	N544	Y545	E546	N547	Y548	K549	L550	E550	S551	ASN	PHE	LEU	ARG	G557	W558	N559	K560	L561	V562	S563	N564	L565	H566	P567	S568	E569	S570	L571	K572	G573	L574	M575	S576	H577	Y578	P579	S580	L581	L582	L583	S584	L585	T586	D587	N588	F589	M590	L591	P592	D593	G594	K595	I596	R597	Y598	GLU	THR		
LEU	GLU	LEU	MET	K605	T606	L607	M608	I609	L610	Q611	G612	M613	Q614	V615	P616	D617	L618	L619	S620	S621	C622	M623	V624	I625	E626	E627	I628	P629	L630	T631	L632	Q633	N634	A635	R636	D637	L638	T639	I640	R641	I642	K643	ASN	VAL	GLY	ALA	GLU	PHE	GLY	LYS	T652	K653	T654	D655	K656	L657	V658	S659	S660		
F662	L663	K664	Y665	L666	F667	G668	L669	L670	Q671	T672	V673	R674	S675	P676	V677	W678	T679	G680	V681	F682	D683	L684	I685	P686	N687	V688	Y689	T690	K691	D692	E693	A694	L695	V696	W697	K698	L699	V700	L701	S702	F703	I704	R705	L706	P707	D708	E709	N710	Q711	N712	L713	D714	Y715	Y716	Q717	P718	L719	L720			
E721	D722	G723	A724	M725	K726	V727	L728	M729	D730	S731	S732	F733	V734	R735	L736	D737	D738	T739	I740	D741	T742	F743	S744	H745	I746	W747	S748	K749	V750	S751	T752	E753	M754	T755	S756	I757	L758	S759	T760	T761	I762	E763	R764	R765	G766	M767	T768	T769	V770	P771	I772	L773	L774	R775	N776	Q777	A778	L779	K780		
V781	M782	L783	S784	I785	P786	Q787	V788	A789	E790	N791	F792	F793	V794	D795	I796	A797	P798	F799	V800	Y801	N802	D803	F804	K805	T806	Y807	K808	D809	E810	E811	D812	M813	E814	N815	E816	R817	V818	I819	T820	G821	S822	M823	T824	E825	V826	D827	R828	N829	N890	L891	D892	D893	D894	T895	L896	F897	K898	D899	E900		
I841	K842	N843	V844	Y845	S846	A847	T848	E849	L850	H851	D852	H853	L854	M855	V856	L857	L858	G859	S860	R861	N862	T863	D864	V865	K866	K867	L868	A869	L870	D871	A872	L873	L874	A875	Y876	K877	N878	P879	T880	L881	N882	K883	Y884	R885	D886	N887	L888	K889	N890	L891	D892	D893	D894	T895	L896	F897	K898	D899	E900		
T901	T902	T903	F904	L905	T906	E907	N908	G909	S910	Q911	S912	I913	K914	A915	E916	D917	E918	K919	V920	Y921	N922	P923	Y924	V925	L926	R927	I928	F929	F930	G931	R932	A933	Q934	V935	P936	P937	T938	S939	Q940	Q941	K942	R943	S944	R945	K946	I947	A948	S1009	V1010	L1011	R1012	T1013	N1014	F1015	P1016	L1017	H1018	T1019	N1020		







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 (\AA)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	1.23	0/4141	1.27	34/6433 (0.5%)
2	5A	1.10	0/12462	1.20	78/19411 (0.4%)
3	SA	0.85	0/31237	1.22	263/48637 (0.5%)
4	SC	0.56	0/1777	0.77	4/2388 (0.2%)
5	SF	0.35	0/1854	0.69	2/2504 (0.1%)
6	SG	0.67	0/1690	0.65	0/2285
7	SH	0.36	0/890	0.67	1/1189 (0.1%)
8	SI	0.43	0/1341	0.70	0/1806
9	SJ	0.33	0/1347	0.59	1/1801 (0.1%)
10	SK	0.62	0/1410	0.66	1/1888 (0.1%)
11	SM	0.36	0/1020	0.63	0/1374
12	SN	0.29	0/873	0.66	0/1185
13	SO	0.50	0/1109	0.65	0/1495
14	SP	0.55	0/879	0.66	0/1186
15	SR	0.84	0/990	0.79	2/1335 (0.1%)
16	ST	0.37	0/930	0.64	0/1251
17	SX	0.63	0/1020	0.69	0/1371
18	SY	0.65	0/798	0.74	1/1065 (0.1%)
19	SZ	0.42	0/822	0.69	2/1103 (0.2%)
20	Sc	0.51	0/613	0.68	0/828
21	Sd	0.71	0/499	0.71	0/670
22	3B	0.81	0/1901	0.74	1/2567 (0.0%)
22	3C	0.46	0/1796	0.64	1/2424 (0.0%)
23	3D	0.55	0/2891	0.67	5/3895 (0.1%)
24	3E	0.50	0/3059	0.65	2/4153 (0.0%)
25	3F	0.47	0/3544	0.68	2/4775 (0.0%)
26	3G	0.67	0/928	0.77	2/1262 (0.2%)
26	3H	0.56	0/928	0.71	0/1262
27	A4	0.49	0/5321	0.68	4/7207 (0.1%)
28	A5	0.57	0/4044	0.70	4/5493 (0.1%)
29	A8	0.30	0/3328	0.64	1/4565 (0.0%)
30	A9	0.32	0/951	0.61	0/1287

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.48	0/6308	0.67	3/8543 (0.0%)
32	AF	0.54	0/3993	0.68	3/5413 (0.1%)
33	AG	0.46	0/6699	0.66	5/9077 (0.1%)
34	B1	0.87	0/6780	0.75	6/9175 (0.1%)
35	B2	0.45	0/6853	0.69	2/9256 (0.0%)
36	B3	0.45	0/6014	0.72	5/8137 (0.1%)
37	B8	0.72	0/3848	0.71	4/5218 (0.1%)
38	BE	0.75	0/6948	0.70	7/9391 (0.1%)
39	B6	0.53	0/2849	0.60	2/3853 (0.1%)
40	5B	0.36	0/499	0.66	0/659
41	5C	0.79	0/4321	0.72	3/5832 (0.1%)
42	5D	0.67	0/1998	0.71	2/2644 (0.1%)
43	5E	0.58	0/1665	0.66	1/2233 (0.0%)
44	5F	0.96	0/1559	0.85	3/2097 (0.1%)
45	5G	0.72	0/2337	0.71	3/3148 (0.1%)
46	5H	0.57	0/1074	0.58	0/1422
47	5I	0.80	0/3844	0.72	1/5174 (0.0%)
48	5J	0.58	0/1238	0.62	1/1641 (0.1%)
49	5K	0.76	0/1426	0.74	1/1917 (0.1%)
50	RA	0.35	0/2769	0.66	0/3753
51	RB	0.40	0/1121	0.65	0/1487
52	RC	0.55	0/2245	0.63	0/3021
53	RE	0.39	0/8924	0.64	5/12070 (0.0%)
54	RF	0.37	0/2004	0.66	3/2697 (0.1%)
55	RG	0.36	0/1727	0.71	2/2329 (0.1%)
55	RH	0.43	0/1828	0.64	0/2470
56	RI	0.54	0/2080	0.67	0/2797
57	RJ	0.60	0/6514	0.63	2/8768 (0.0%)
58	RK	0.45	0/2832	0.65	0/3825
59	RL	0.29	0/4549	0.52	0/6241
59	RM	0.25	0/3760	0.47	0/5211
60	RN	0.37	0/4423	0.61	2/5965 (0.0%)
61	RO	0.38	0/3849	0.62	2/5261 (0.0%)
62	RP	0.25	0/10172	0.46	11/14158 (0.1%)
63	RQ	0.52	0/1678	0.61	0/2282
64	RS	0.34	0/2104	0.69	1/2854 (0.0%)
65	RT	0.42	0/1379	0.62	1/1853 (0.1%)
66	RV	0.60	0/1456	0.69	2/1937 (0.1%)
All	All	0.65	0/232060	0.82	494/323904 (0.2%)

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

There are no bond length outliers.

The worst 5 of 494 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	5F	13	LEU	CA-CB-CG	10.94	140.47	115.30
3	SA	1034	C	C5-C6-N1	10.38	126.19	121.00
3	SA	1254	U	C2-N1-C1'	10.13	129.85	117.70
2	5A	312	U	O4'-C1'-N1	9.96	116.17	108.20
2	5A	310	U	N3-C2-O2	-9.45	115.59	122.20

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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	217/255 (85%)	186 (86%)	30 (14%)	1 (0%)	29	61
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%)	17	49
8	SI	161/190 (85%)	139 (86%)	22 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	47	78
26	3G	119/126 (94%)	109 (92%)	9 (8%)	1 (1%)	19	51
26	3H	119/126 (94%)	110 (92%)	9 (8%)	0	100	100
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%)	25	57
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%)	47	78
33	AG	812/896 (91%)	730 (90%)	82 (10%)	0	100	100
34	B1	830/923 (90%)	752 (91%)	76 (9%)	2 (0%)	47	78
35	B2	839/943 (89%)	750 (89%)	88 (10%)	1 (0%)	51	82
36	B3	733/817 (90%)	599 (82%)	132 (18%)	2 (0%)	41	72
37	B8	469/594 (79%)	423 (90%)	46 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	47	78
42	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100	100
43	5E	200/593 (34%)	187 (94%)	11 (6%)	2 (1%)	15	46
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
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%)	41	72
59	RM	737/1056 (70%)	640 (87%)	93 (13%)	4 (0%)	29	61
60	RN	573/810 (71%)	524 (91%)	48 (8%)	1 (0%)	47	78
61	RO	523/552 (95%)	457 (87%)	66 (13%)	0	100	100
62	RP	1992/2493 (80%)	1801 (90%)	189 (10%)	2 (0%)	51	82
63	RQ	220/899 (24%)	197 (90%)	23 (10%)	0	100	100
64	RS	247/483 (51%)	223 (90%)	23 (9%)	1 (0%)	34	67
65	RT	165/326 (51%)	151 (92%)	14 (8%)	0	100	100
66	RV	184/346 (53%)	168 (91%)	16 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	23995/32886 (73%)	21566 (90%)	2403 (10%)	26 (0%)	54	82

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%)	65	82
5	SF	196/222 (88%)	191 (97%)	5 (3%)	46	72
6	SG	180/191 (94%)	179 (99%)	1 (1%)	86	94
7	SH	95/201 (47%)	94 (99%)	1 (1%)	73	86
8	SI	146/170 (86%)	144 (99%)	2 (1%)	67	83
9	SJ	136/161 (84%)	135 (99%)	1 (1%)	84	92
10	SK	147/166 (89%)	144 (98%)	3 (2%)	55	77
11	SM	110/137 (80%)	109 (99%)	1 (1%)	78	90
12	SN	88/119 (74%)	88 (100%)	0	100	100
13	SO	117/128 (91%)	115 (98%)	2 (2%)	60	80
14	SP	90/105 (86%)	88 (98%)	2 (2%)	52	75
15	SR	105/119 (88%)	105 (100%)	0	100	100
16	ST	101/129 (78%)	101 (100%)	0	100	100
17	SX	108/111 (97%)	108 (100%)	0	100	100
18	SY	85/120 (71%)	85 (100%)	0	100	100
19	SZ	85/113 (75%)	84 (99%)	1 (1%)	71	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	56 (100%)	0	100	100
22	3B	201/240 (84%)	200 (100%)	1 (0%)	88	94
22	3C	190/240 (79%)	190 (100%)	0	100	100
23	3D	296/435 (68%)	292 (99%)	4 (1%)	67	83
24	3E	262/433 (60%)	260 (99%)	2 (1%)	81	91
25	3F	378/503 (75%)	373 (99%)	5 (1%)	69	84
26	3G	100/104 (96%)	99 (99%)	1 (1%)	76	88
26	3H	100/104 (96%)	100 (100%)	0	100	100
27	A4	591/713 (83%)	583 (99%)	8 (1%)	67	83
28	A5	433/574 (75%)	430 (99%)	3 (1%)	84	92
29	A8	174/657 (26%)	173 (99%)	1 (1%)	86	94
30	A9	89/533 (17%)	89 (100%)	0	100	100
31	AE	708/1633 (43%)	700 (99%)	8 (1%)	73	86
32	AF	437/454 (96%)	432 (99%)	5 (1%)	73	86
33	AG	750/826 (91%)	743 (99%)	7 (1%)	78	90
34	B1	730/812 (90%)	719 (98%)	11 (2%)	65	82
35	B2	736/832 (88%)	729 (99%)	7 (1%)	76	88
36	B3	665/719 (92%)	654 (98%)	11 (2%)	60	80
37	B8	421/529 (80%)	417 (99%)	4 (1%)	76	88
38	BE	757/819 (92%)	748 (99%)	9 (1%)	71	85
39	B6	251/414 (61%)	246 (98%)	5 (2%)	55	77
40	5B	57/196 (29%)	56 (98%)	1 (2%)	59	79
41	5C	465/480 (97%)	457 (98%)	8 (2%)	60	80
42	5D	221/234 (94%)	219 (99%)	2 (1%)	78	90
43	5E	185/535 (35%)	183 (99%)	2 (1%)	73	86
44	5F	171/172 (99%)	171 (100%)	0	100	100
45	5G	251/258 (97%)	249 (99%)	2 (1%)	81	91
46	5H	107/538 (20%)	106 (99%)	1 (1%)	78	90
47	5I	416/443 (94%)	407 (98%)	9 (2%)	52	75
48	5J	133/200 (66%)	133 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	5K	157/169 (93%)	155 (99%)	2 (1%)	69	84
50	RA	303/636 (48%)	303 (100%)	0	100	100
51	RB	117/315 (37%)	115 (98%)	2 (2%)	60	80
52	RC	231/289 (80%)	230 (100%)	1 (0%)	91	95
53	RE	984/1125 (88%)	975 (99%)	9 (1%)	78	90
54	RF	221/274 (81%)	217 (98%)	4 (2%)	59	79
55	RG	195/222 (88%)	194 (100%)	1 (0%)	88	94
55	RH	206/222 (93%)	203 (98%)	3 (2%)	65	82
56	RI	235/256 (92%)	231 (98%)	4 (2%)	60	80
57	RJ	683/1039 (66%)	679 (99%)	4 (1%)	86	94
58	RK	307/312 (98%)	305 (99%)	2 (1%)	84	92
59	RL	164/934 (18%)	159 (97%)	5 (3%)	41	68
60	RN	406/732 (56%)	406 (100%)	0	100	100
61	RO	329/506 (65%)	326 (99%)	3 (1%)	78	90
63	RQ	148/808 (18%)	147 (99%)	1 (1%)	84	92
64	RS	225/424 (53%)	221 (98%)	4 (2%)	59	79
65	RT	148/282 (52%)	145 (98%)	3 (2%)	55	77
66	RV	141/304 (46%)	140 (99%)	1 (1%)	84	92
All	All	17584/26026 (68%)	17396 (99%)	188 (1%)	74	86

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	5C	153	THR
52	RC	62	ARG
41	5C	347	LEU
47	5I	91	VAL
53	RE	595	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 285 such sidechains are listed below:

Mol	Chain	Res	Type
55	RG	105	ASN
56	RI	186	ASN
60	RN	771	ASN

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Mol	Chain	Res	Type
32	AF	250	ASN
32	AF	72	GLN

5.3.3 RNA ⓘ

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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

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	26,34,34	1.23	1 (3%)	32,54,54	1.65	6 (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	-	2/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	RJ	1201	GTP	C5-C6	-4.38	1.38	1.47

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	RJ	1201	GTP	PA-O3A-PB	-4.27	118.18	132.83
69	RJ	1201	GTP	PB-O3B-PG	-3.72	120.06	132.83
69	RJ	1201	GTP	C5-C6-N1	3.41	119.98	113.95
69	RJ	1201	GTP	C8-N7-C5	3.09	108.88	102.99
69	RJ	1201	GTP	C2-N1-C6	-3.06	119.46	125.10

There are no chirality outliers.

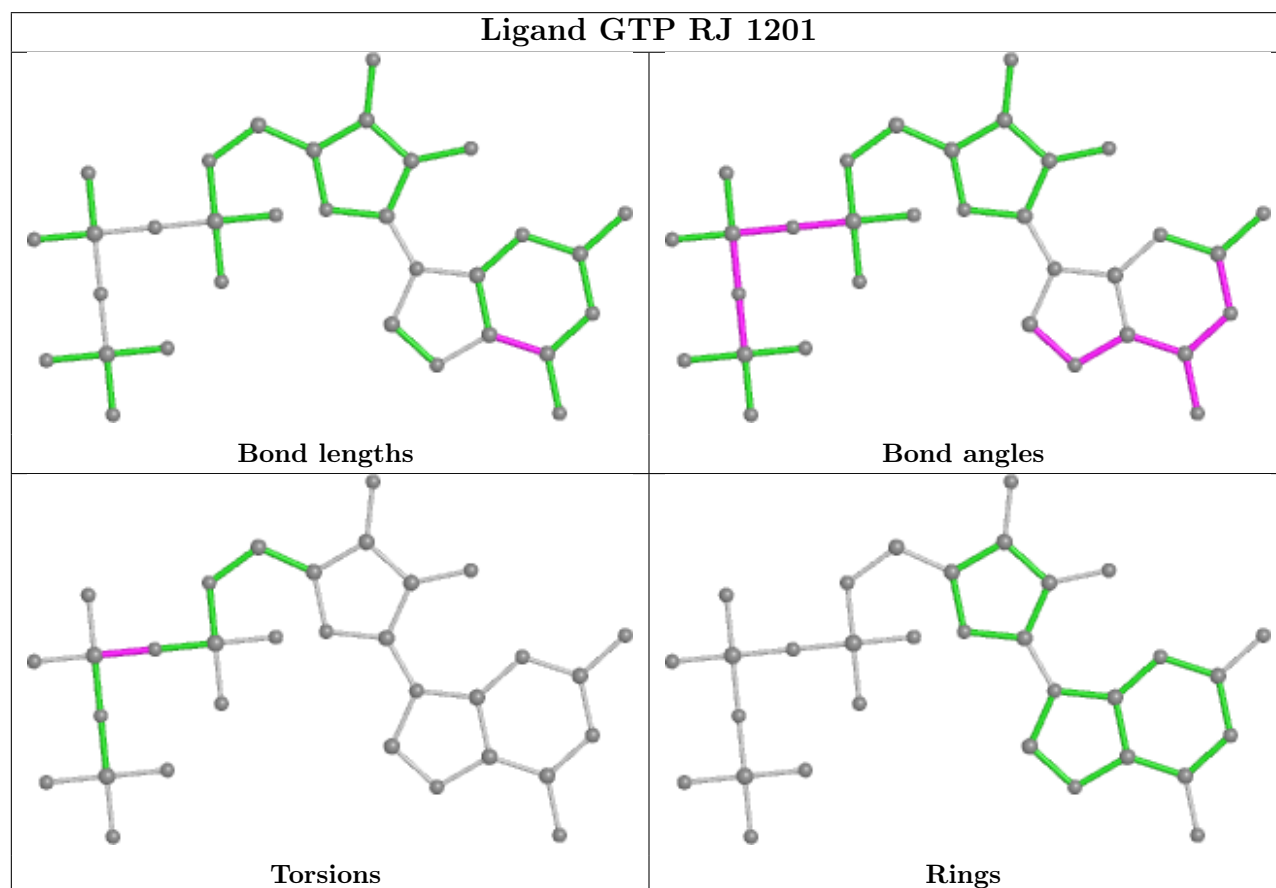
All (2) torsion outliers are listed below:

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 ⓘ

There are no chain breaks in this entry.

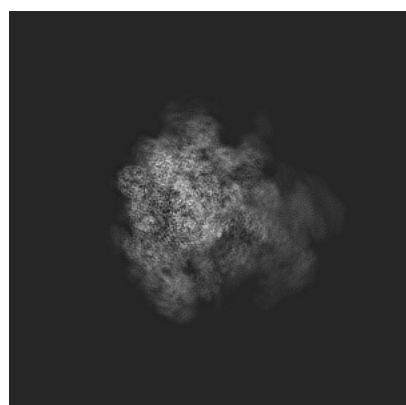
6 Map visualisation [i](#)

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.

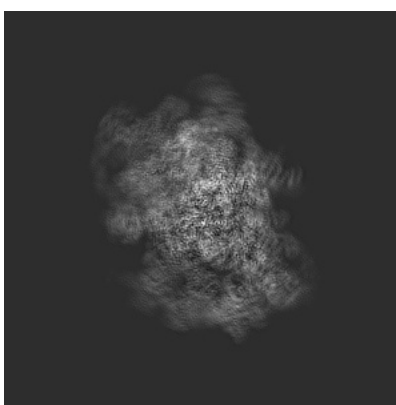
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

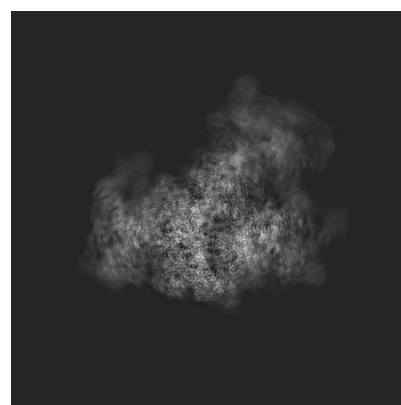
6.1.1 Primary map



X



Y



Z

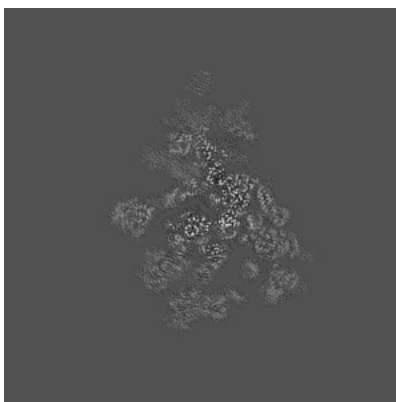
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

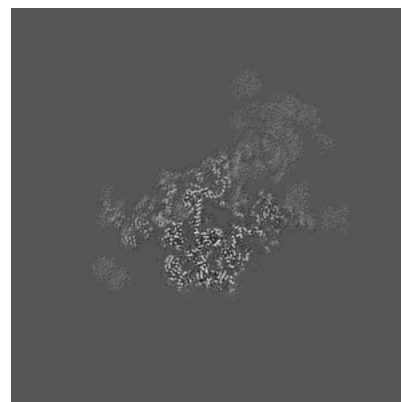
6.2.1 Primary map



X Index: 256



Y Index: 256

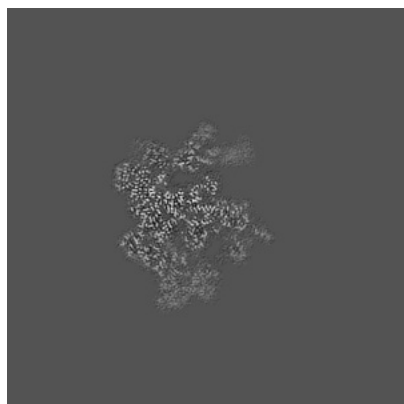


Z Index: 256

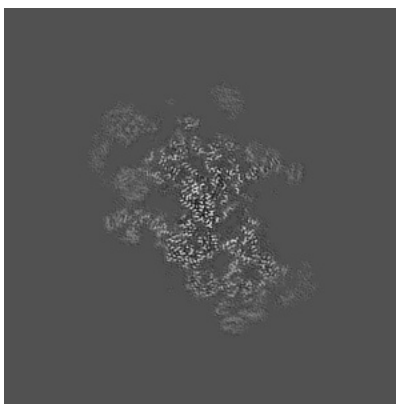
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

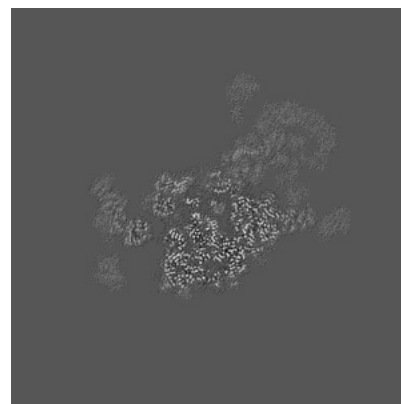
6.3.1 Primary map



X Index: 240



Y Index: 216



Z Index: 267

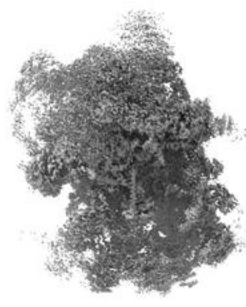
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

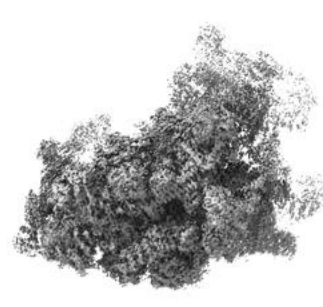
6.4.1 Primary map



X



Y



Z

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.

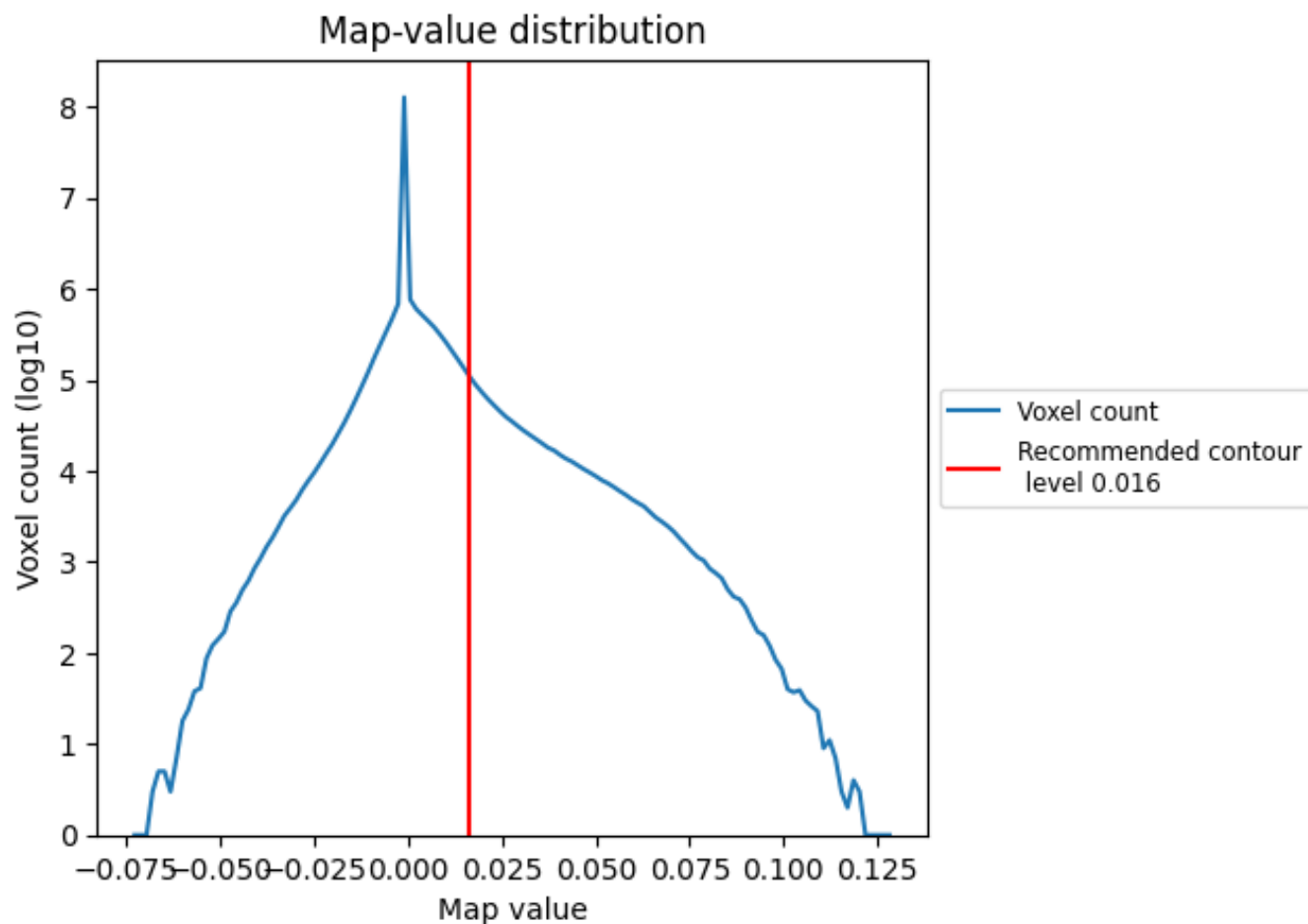
6.5 Mask visualisation

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

7 Map analysis [i](#)

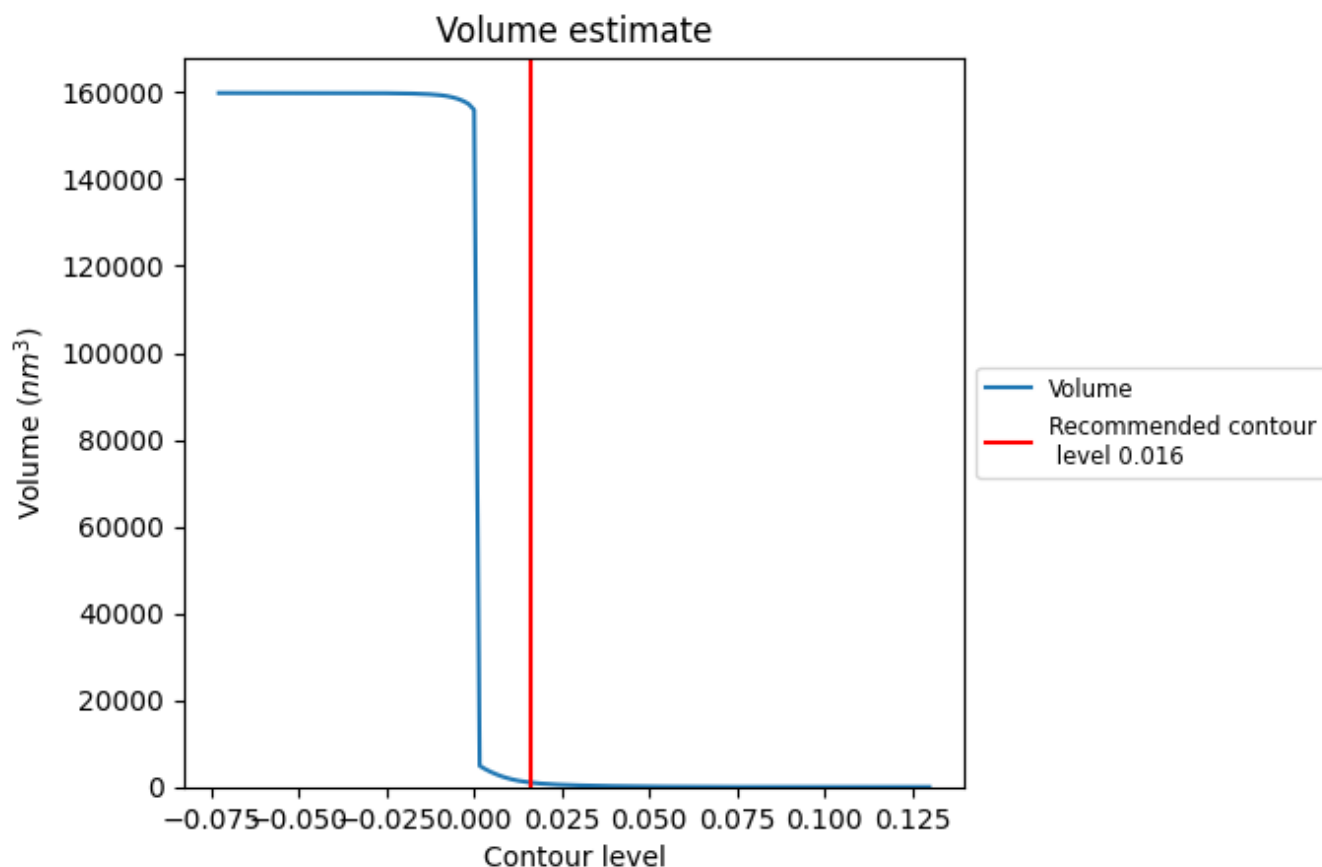
This section contains the results of statistical analysis of the map.

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.

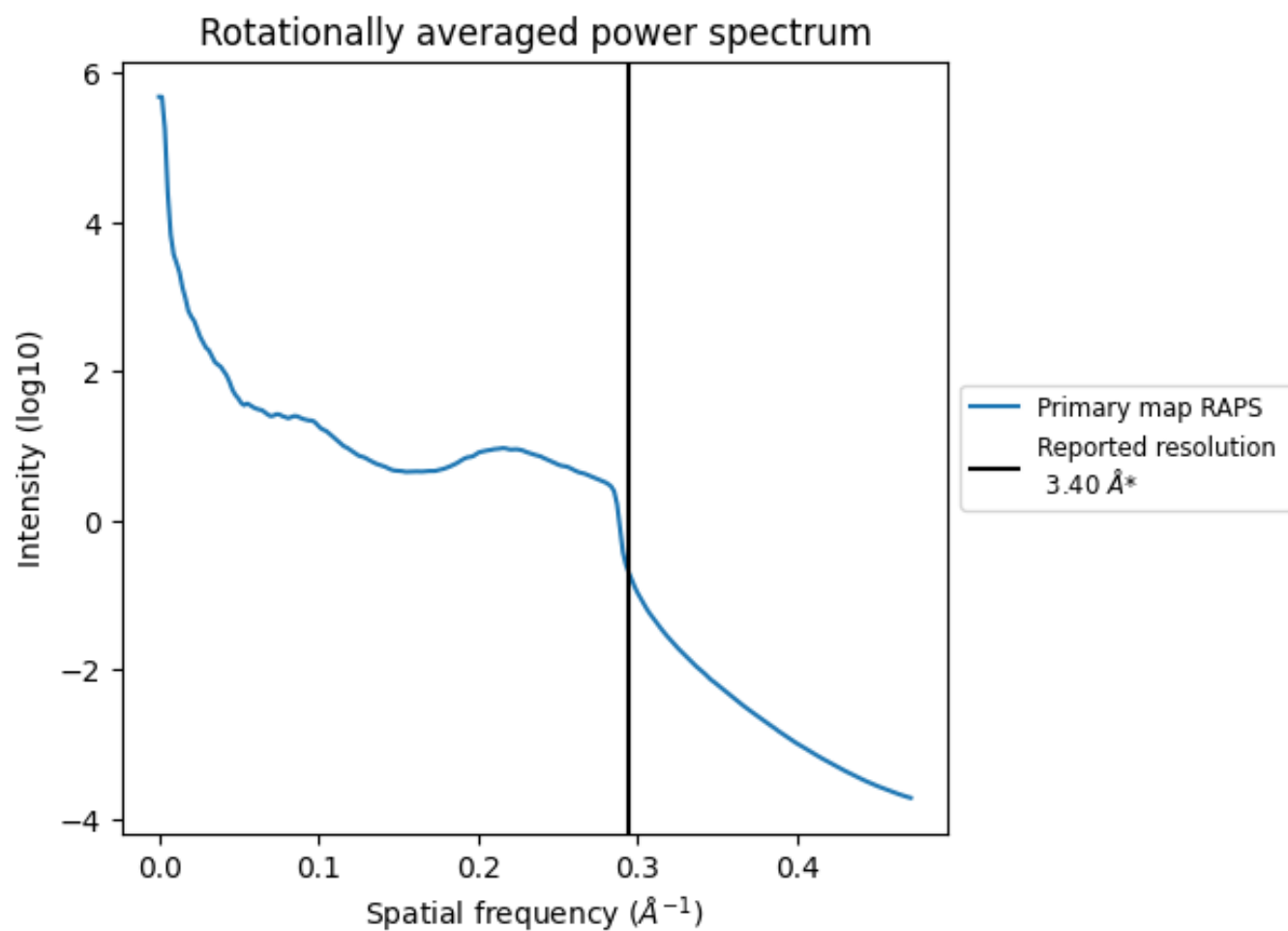
7.2 Volume estimate [i](#)



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 ⓘ

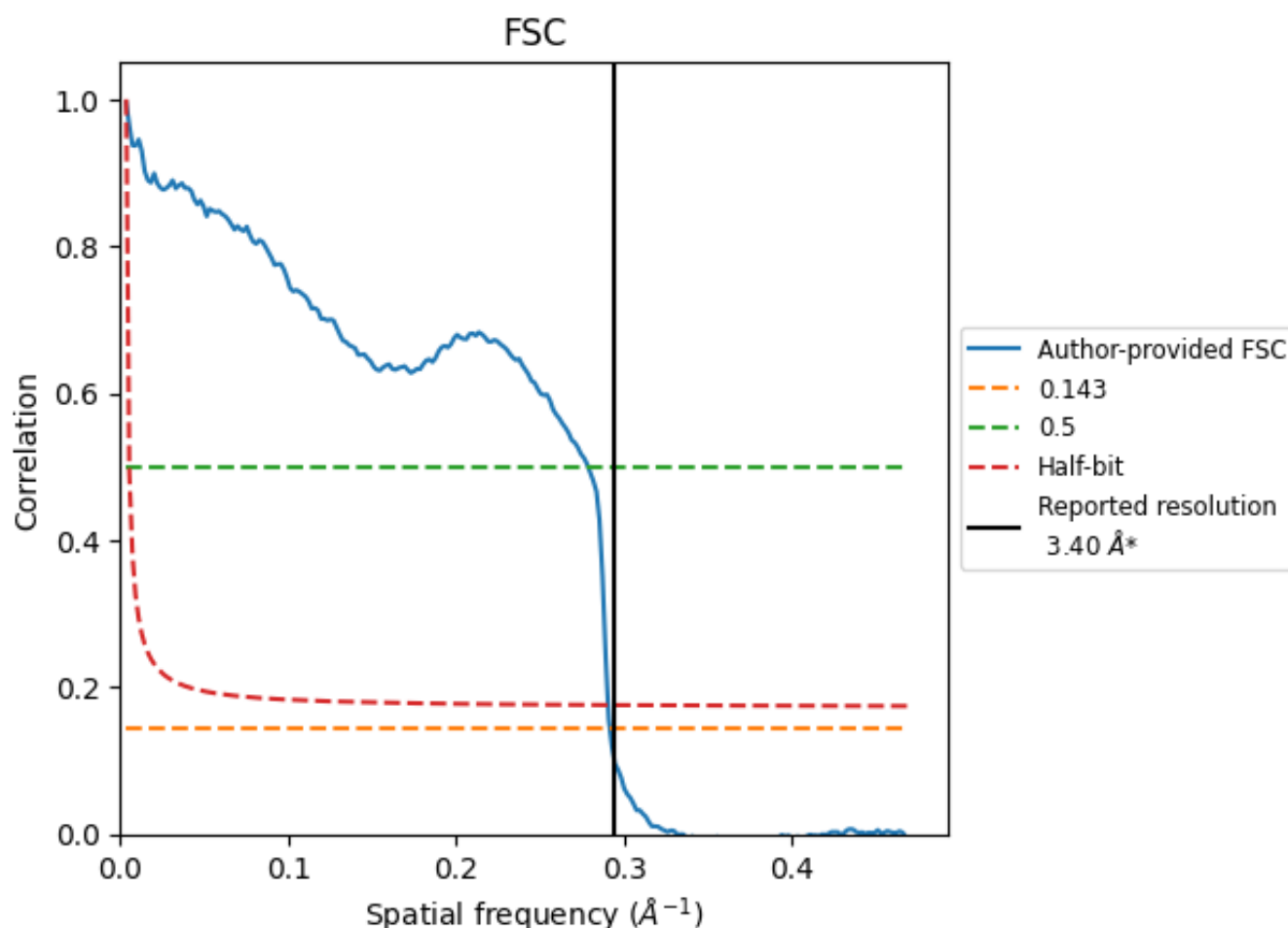


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

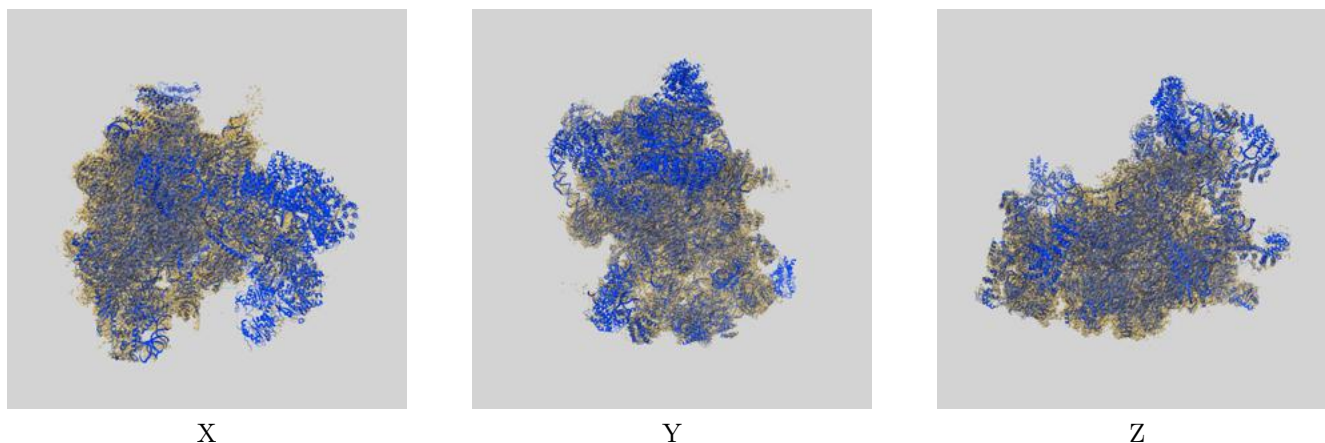
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.43	3.59	3.44
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

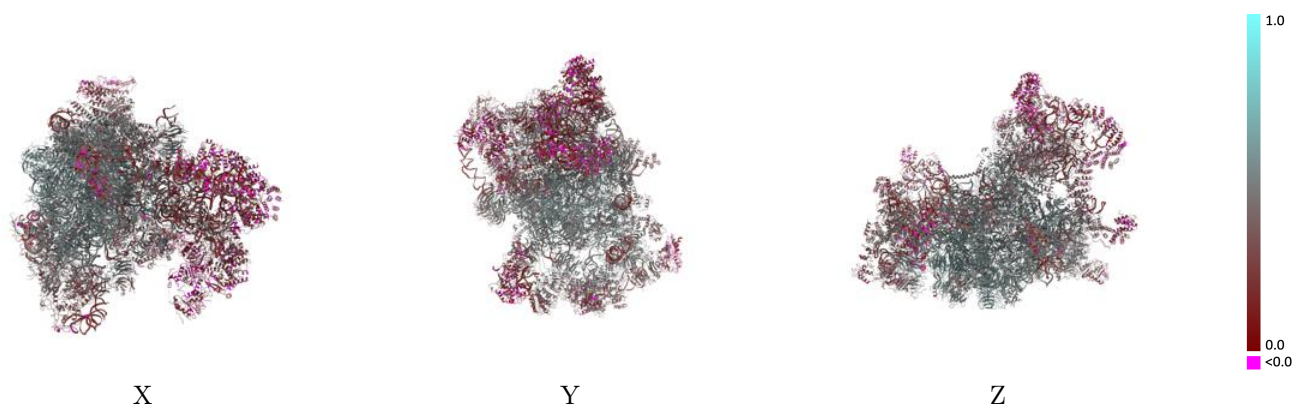
This section contains information regarding the fit between EMDB map EMD-9964 and PDB model 6KE6. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



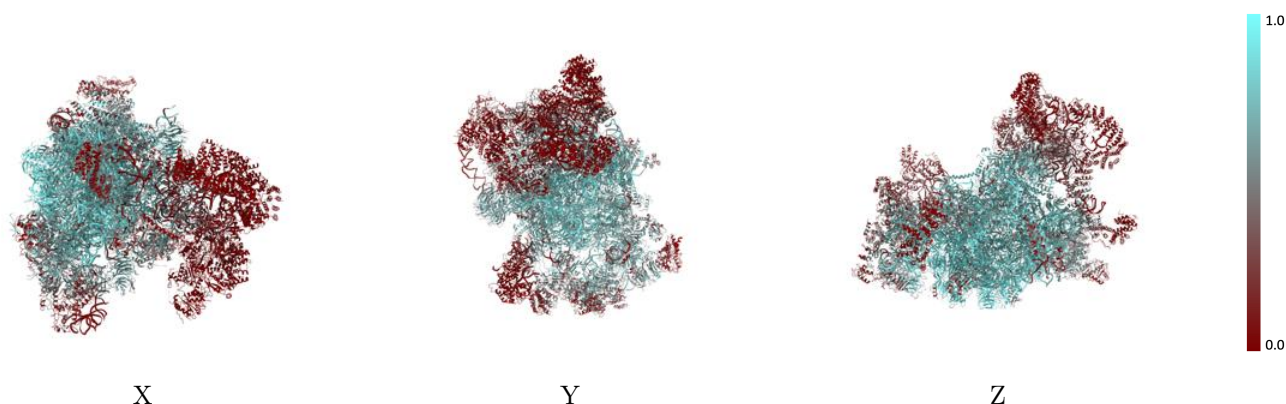
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



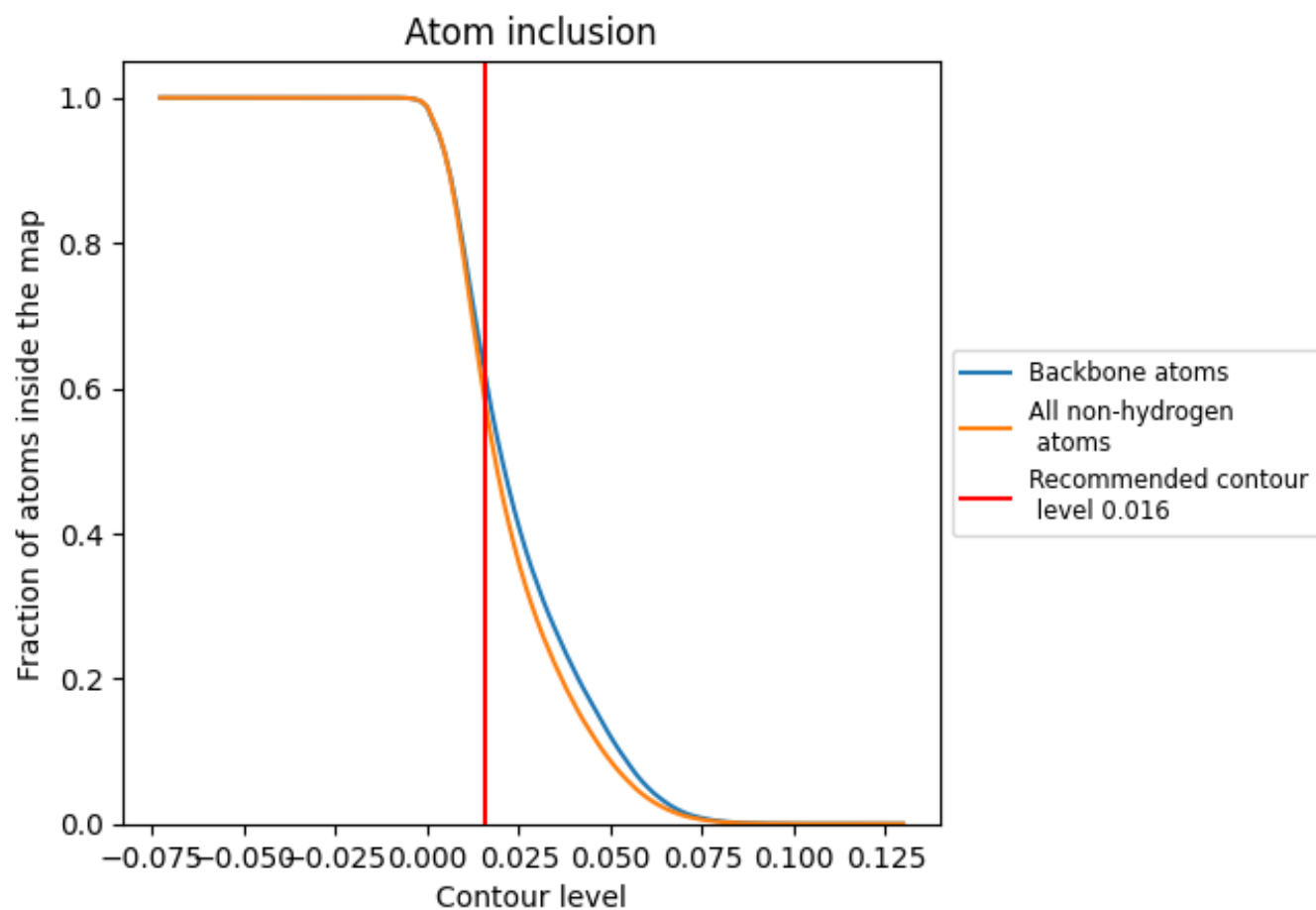
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.5738	 0.4270
3A	 0.8273	 0.4550
3B	 0.8617	 0.5570
3C	 0.5797	 0.4410
3D	 0.7370	 0.4890
3E	 0.6832	 0.4590
3F	 0.6611	 0.4530
3G	 0.8341	 0.5450
3H	 0.7577	 0.5110
5A	 0.7638	 0.4290
5B	 0.4042	 0.3970
5C	 0.8457	 0.5510
5D	 0.7549	 0.5110
5E	 0.7528	 0.5240
5F	 0.8870	 0.5690
5G	 0.8111	 0.5500
5H	 0.7232	 0.5000
5I	 0.8633	 0.5500
5J	 0.6630	 0.4970
5K	 0.8566	 0.5580
A4	 0.6835	 0.4510
A5	 0.7526	 0.4910
A8	 0.2282	 0.3060
A9	 0.3974	 0.3630
AE	 0.3779	 0.3480
AF	 0.7595	 0.5060
AG	 0.6906	 0.4690
B1	 0.8807	 0.5590
B2	 0.6662	 0.4520
B3	 0.5917	 0.4230
B6	 0.6692	 0.4400
B8	 0.8478	 0.5430
BE	 0.8703	 0.5550
RA	 0.0961	 0.2760
RB	 0.4638	 0.4280



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Chain	Atom inclusion	Q-score
RC	 0.6171	 0.4820
RE	 0.3869	 0.4000
RF	 0.2959	 0.3630
RG	 0.3634	 0.3870
RH	 0.5720	 0.4780
RI	 0.7656	 0.4930
RJ	 0.7419	 0.5030
RK	 0.6827	 0.4860
RL	 0.1198	 0.3130
RM	 0.0188	 0.1970
RN	 0.3311	 0.3780
RO	 0.4476	 0.3860
RP	 0.0911	 0.2260
RQ	 0.5787	 0.4680
RS	 0.0369	 0.2090
RT	 0.6793	 0.4800
RV	 0.7186	 0.5180
SA	 0.5135	 0.3620
SC	 0.7475	 0.5170
SF	 0.2899	 0.3660
SG	 0.8173	 0.5350
SH	 0.0939	 0.3450
SI	 0.5207	 0.4250
SJ	 0.1434	 0.2790
SK	 0.8061	 0.5300
SM	 0.1529	 0.2840
SN	 0.0047	 0.1060
SO	 0.7576	 0.5080
SP	 0.7589	 0.5120
SR	 0.8491	 0.5530
ST	 0.3315	 0.4150
SX	 0.7841	 0.5300
SY	 0.7755	 0.5270
SZ	 0.4905	 0.4280
Sc	 0.7681	 0.5200
Sd	 0.8407	 0.5500
X1	 0.3291	 0.3770