wwPDB EM Validation Summary Report (i)

May 18, 2024 – 10:24 pm BST

PDB ID	:	6RXZ
EMDB ID	:	EMD-10056
Title	:	Cryo-EM structure of the 90S pre-ribosome (Kre33-Noc4) from Chaetomium thermophilum, state b
Authors	:	Cheng, J.; Kellner, N.; Griesel, S.; Berninghausen, O.; Beckmann, R.; Hurt, E.
Deposited on	:	2019-06-10
Resolution	:	4.40 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

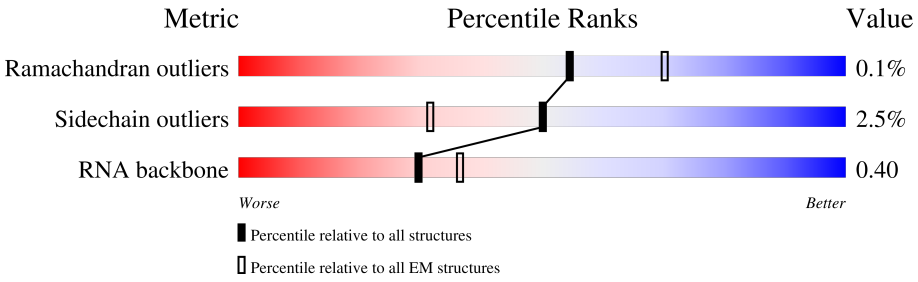
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 4.40 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 <=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	UA	904	91% · 7%
2	UB	907	5% 56% 44%
3	UC	648	11% 89%
4	UD	884	6% 87% 13%
5	UF	414	79% 20%
6	UG	558	6% 84% · 14%
7	UJ	1802	6% 60% · 40%
8	UK	270	78% · 20%

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Mol	Chain	Length	Quality of chain
9	UL	962	7% 81% 18%
10	UM	912	19% 73% 26%
11	UN	938	19% 81%
12	UO	557	90% 10%
13	UQ	960	5% 82% 18%
14	UR	618	72% 28%
15	UU	1049	85% 14%
16	UX	193	95%
17	UZ	391	59% 40%
18	CA	313	76% 23%
18	CB	313	5% 75% 24%
19	CC	523	74% 26%
20	CD	582	72% 28%
21	CE	127	94% 5%
21	CF	127	93% 6%
22	CG	630	66% 34%
23	CH	411	93% 5%
24	CI	1163	69% 29%
25	CJ	183	96%
26	CK	297	97%
27	CL	785	29% 71%
28	CM	446	98%
29	CN	252	6% 90% 10%
29	CO	252	16% 82% 15%
30	CP	322	19% 57% 42%

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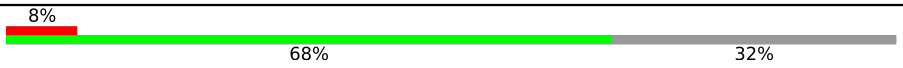
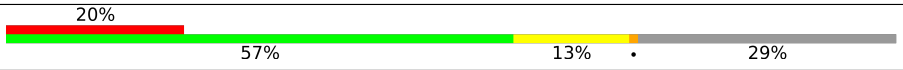
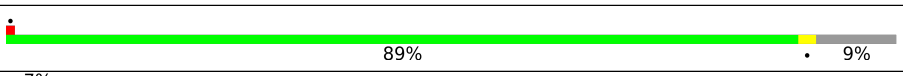
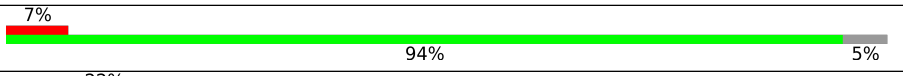
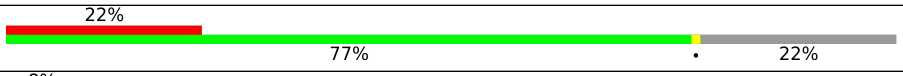
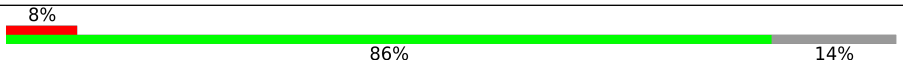
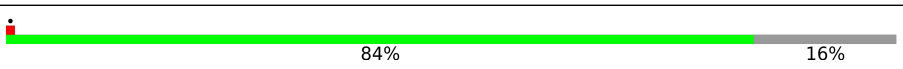
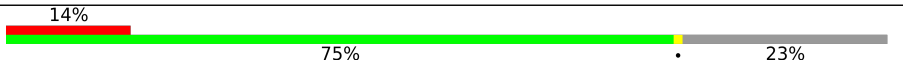
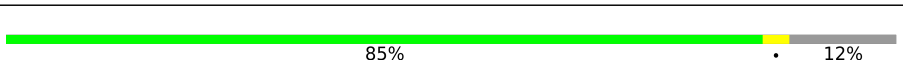
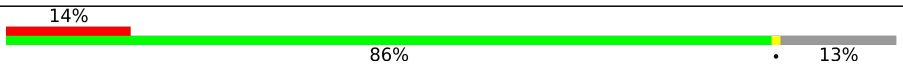
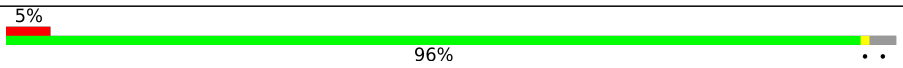
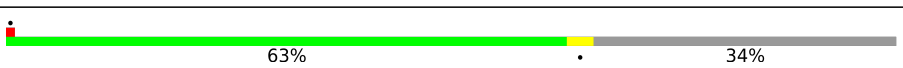
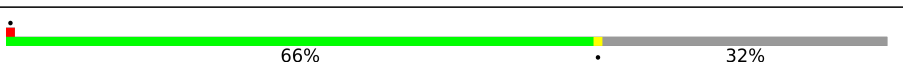
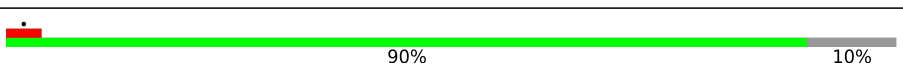
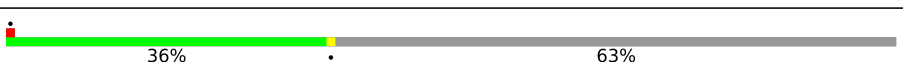
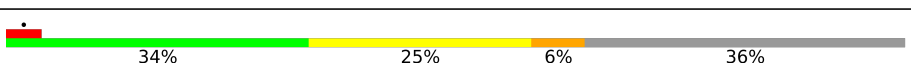
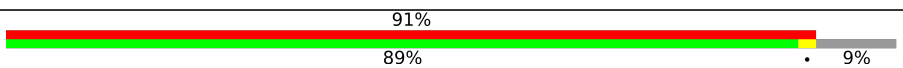
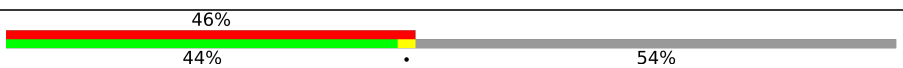
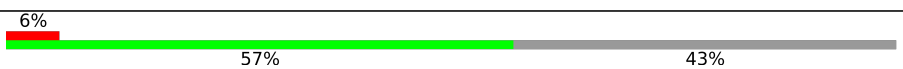
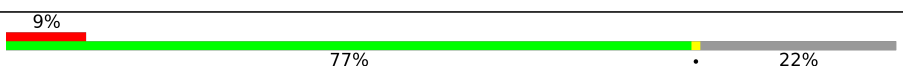
Mol	Chain	Length	Quality of chain
31	CQ	259	
32	CR	1073	
32	CS	1073	
33	CT	203	
34	Cb	264	
35	Cc	212	
36	Cd	239	
37	Ce	203	
38	Cf	202	
39	Cg	190	
40	Ch	151	
41	Ci	150	
42	Cj	143	
43	Ck	161	
44	Cm	130	
45	Cn	145	
46	Co	136	
47	Cp	68	
48	CU	311	
49	C1	2323	
50	C2	230	
51	UV	1171	
52	CV	322	
53	CW	668	
54	UT	2612	

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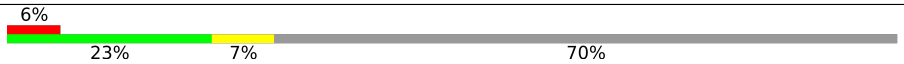
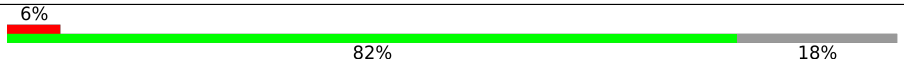
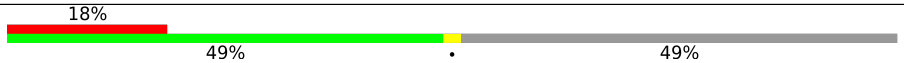
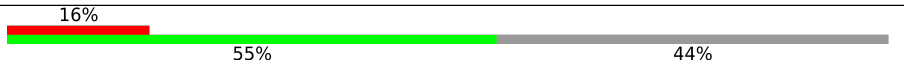
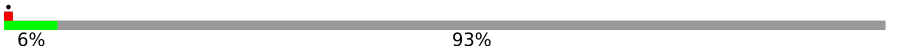
Mol	Chain	Length	Quality of chain
55	UH	930	
56	UE	410	
56	UI	410	
57	US	549	
58	Cl	156	
59	CX	480	
60	CY	381	
61	CZ	609	
62	UP	364	
63	Cz	1796	

2 Entry composition (i)

There are 64 unique types of molecules in this entry. The entry contains 218474 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Periodic tryptophan protein 2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	UA	839	6366	4101	1136	1105	24	0	0

- Molecule 2 is a protein called Utp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	UB	512	4079	2576	781	711	11	0	0

- Molecule 3 is a protein called Utp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	UC	74	588	371	120	97	0	0

- Molecule 4 is a protein called Utp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	UD	772	6071	3851	1093	1103	24	0	0

- Molecule 5 is a protein called Utp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	UF	331	2591	1674	504	399	14	0	0

- Molecule 6 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	UG	479	3717	2369	700	636	12	0	0

- Molecule 7 is a protein called UTP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	UJ	1090	Total	C	N	O	S	0	0
			8416	5408	1452	1525	31		

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	UK	217	Total	C	N	O	S	0	0
			1687	1062	351	269	5		

- Molecule 9 is a protein called Utp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	UL	785	Total	C	N	O	S	0	0
			6175	3940	1088	1130	17		

- Molecule 10 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	UM	679	Total	C	N	O	S	0	0
			5273	3351	924	986	12		

- Molecule 11 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	UN	177	Total	C	N	O	S	0	0
			1401	892	263	239	7		

- Molecule 12 is a protein called Utp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	UO	504	Total	C	N	O	S	0	0
			3819	2422	699	684	14		

- Molecule 13 is a protein called Utp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	UQ	789	Total	C	N	O	S	0	0
			6008	3831	1037	1119	21		

- Molecule 14 is a protein called Utp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UR	447	Total	C	N	O	S	0	0
			3491	2209	656	616	10		

- Molecule 15 is a protein called Putative U3 snoRNP protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	UU	902	Total	C	N	O	S	0	0
			6734	4336	1236	1136	26		

- Molecule 16 is a protein called Utp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	UX	190	Total	C	N	O	S	0	0
			1470	932	282	246	10		

- Molecule 17 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	UZ	235	Total	C	N	O	S	0	0
			1815	1184	330	298	3		

- Molecule 18 is a protein called Nop1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CA	242	Total	C	N	O	S	0	0
			1778	1149	327	293	9		
18	CB	237	Total	C	N	O	S	0	0
			1816	1154	318	335	9		

- Molecule 19 is a protein called Putative nucleolar protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CC	387	Total	C	N	O	S	0	0
			2866	1836	527	492	11		

- Molecule 20 is a protein called Nop58.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CD	420	Total	C	N	O	S	0	0
			3150	2023	560	557	10		

- Molecule 21 is a protein called Snu13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CE	121	Total	C	N	O	S	0	0
			879	557	165	154	3		
21	CF	120	Total	C	N	O	S	0	0
			864	550	161	150	3		

- Molecule 22 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CG	416	Total	C	N	O	S	0	0
			3245	2065	587	580	13		

- Molecule 23 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CH	389	Total	C	N	O	S	0	0
			2888	1827	526	525	10		

- Molecule 24 is a protein called Bms1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CI	822	Total	C	N	O	S	0	0
			6486	4169	1213	1077	27		

- Molecule 25 is a protein called Imp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CJ	179	Total	C	N	O	S	0	0
			1434	918	283	226	7		

- Molecule 26 is a protein called Putative U3 small nucleolar ribonucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	CK	297	Total	C	N	O	S	0	0
			2329	1476	445	400	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	CL	231	Total	C	N	O	S	0	0
			1786	1114	339	327	6		

- Molecule 28 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	CM	445	Total	C	N	O	S	0	0
			3501	2195	672	619	15		

- Molecule 29 is a protein called Emg1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CN	226	Total	C	N	O	S	0	0
			1762	1119	306	327	10		
29	CO	215	Total	C	N	O	S	0	0
			1683	1067	293	313	10		

- Molecule 30 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	CP	187	Total	C	N	O	S	0	0
			1504	961	269	265	9		

- Molecule 31 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	CQ	175	Total	C	N	O	S	0	0
			1361	862	250	242	7		

- Molecule 32 is a protein called Kre33.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	CR	760	Total	C	N	O	S	0	0
			5989	3851	1024	1087	27		
32	CS	760	Total	C	N	O	S	0	0
			5989	3851	1024	1087	27		

- Molecule 33 is a protein called Fcf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	CT	131	Total	C	N	O	S	0	0
			1035	656	197	178	4		

- Molecule 34 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Cb	232	Total	C	N	O	S	0	0
			1851	1179	340	325	7		

- Molecule 35 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Cc	192	Total	C	N	O	S	0	0
			1464	926	278	253	7		

- Molecule 36 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Cd	226	Total	C	N	O	S	0	0
			1819	1138	363	313	5		

- Molecule 37 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	Ce	159	Total	C	N	O	0	0
			1279	810	237	232		

- Molecule 38 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Cf	174	Total	C	N	O	S	0	0
			1398	872	283	242	1		

- Molecule 39 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cg	159	Total	C	N	O	S	0	0
			1242	801	255	184	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
40	Ch	49	Total	C	N	O	0	0
			406	265	79	62		

- Molecule 41 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ci	115	Total	C	N	O	S	0	0
			791	492	154	141	4		

- Molecule 42 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Cj	126	Total	C	N	O	S	0	0
			943	613	177	151	2		

- Molecule 43 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ck	140	Total	C	N	O	S	0	0
			1163	750	224	184	5		

- Molecule 44 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Cm	126	Total	C	N	O	S	0	0
			985	632	184	164	5		

- Molecule 45 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Cn	96	Total	C	N	O	S	0	0
			702	456	134	110	2		

- Molecule 46 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Co	92	Total	C	N	O	S	0	0
			741	474	139	126	2		

- Molecule 47 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Cp	61	Total	C	N	O	0	0
			455	284	97	74		

- Molecule 48 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CU	114	Total	C	N	O	S	0	0
			882	544	178	154	6		

- Molecule 49 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C1	1487	Total 31732	C 14158	N 5691	O 10396	P 1487	0	0

- Molecule 50 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	C2	230	Total 4891	C 2182	N 856	O 1623	P 230	0	0

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	UV	1061	Total 8424	C 5399	N 1480	O 1523	S 22	0	0

- Molecule 52 is a protein called Rrp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CV	148	Total 1145	C 729	N 198	O 216	S 2	0	0

- Molecule 53 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CW	382	Total 2924	C 1857	N 530	O 524	S 13	0	0

- Molecule 54 is a protein called Utp20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	UT	2028	Total 16000	C 10303	N 2813	O 2816	S 68	0	0

- Molecule 55 is a protein called Utp8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	UH	359	Total 2809	C 1773	N 496	O 527	S 13	0	0

- Molecule 56 is a protein called Utp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	UE	125	Total	C	N	O	S	0	0
			972	608	183	175	6		
56	UI	125	Total	C	N	O	S	0	0
			972	608	183	175	6		

- Molecule 57 is a protein called Noc4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	US	451	Total	C	N	O	S	0	0
			3672	2389	608	660	15		

- Molecule 58 is a protein called Rps18.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Cl	80	Total	C	N	O	S	0	0
			633	400	115	117	1		

- Molecule 59 is a protein called Enp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CX	267	Total	C	N	O	S	0	0
			2122	1380	374	358	10		

- Molecule 60 is a protein called U3 small nucleolar ribonucleoprotein protein lcp5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CY	122	Total	C	N	O	S	0	0
			975	590	194	188	3		

- Molecule 61 is a protein called Bfr2.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CZ	42	Total	C	N	O	S	0	0
			354	223	68	62	1		

- Molecule 62 is a protein called Utp16.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	UP	54	Total	C	N	O	0	0
			422	264	88	70		

- Molecule 63 is a protein called Rrp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Cz	275	Total	C	N	O	S	0	0
			2259	1435	401	420	3		

- Molecule 64 is ZINC ION (three-letter code: ZN) (formula: Zn).

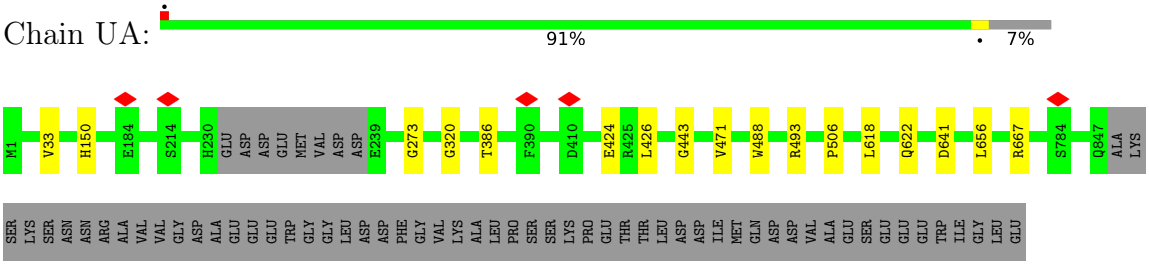
Mol	Chain	Residues	Atoms		AltConf
64	UX	1	Total	Zn	0
			1	1	

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.

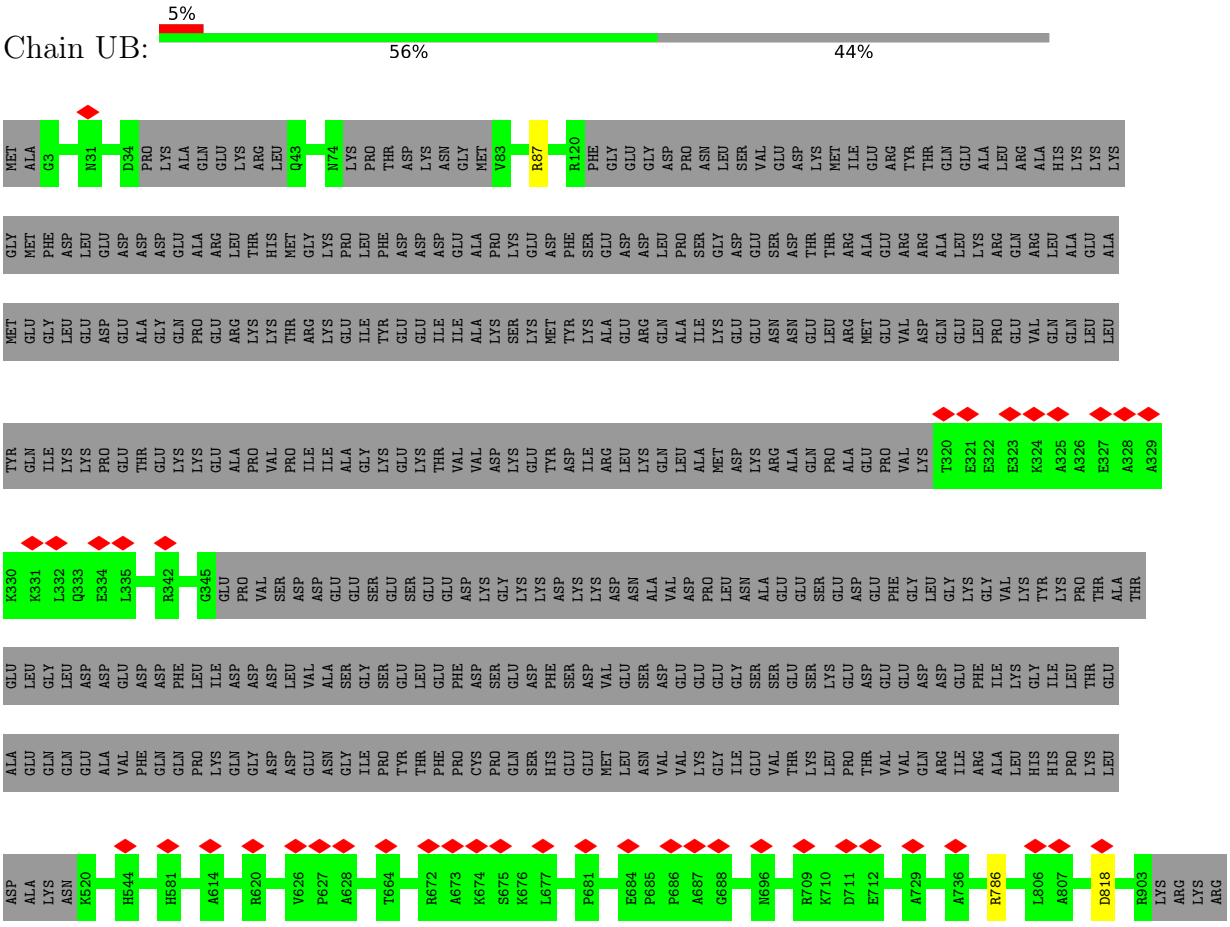
• Molecule 1: Periodic tryptophan protein 2-like protein

Chain UA:



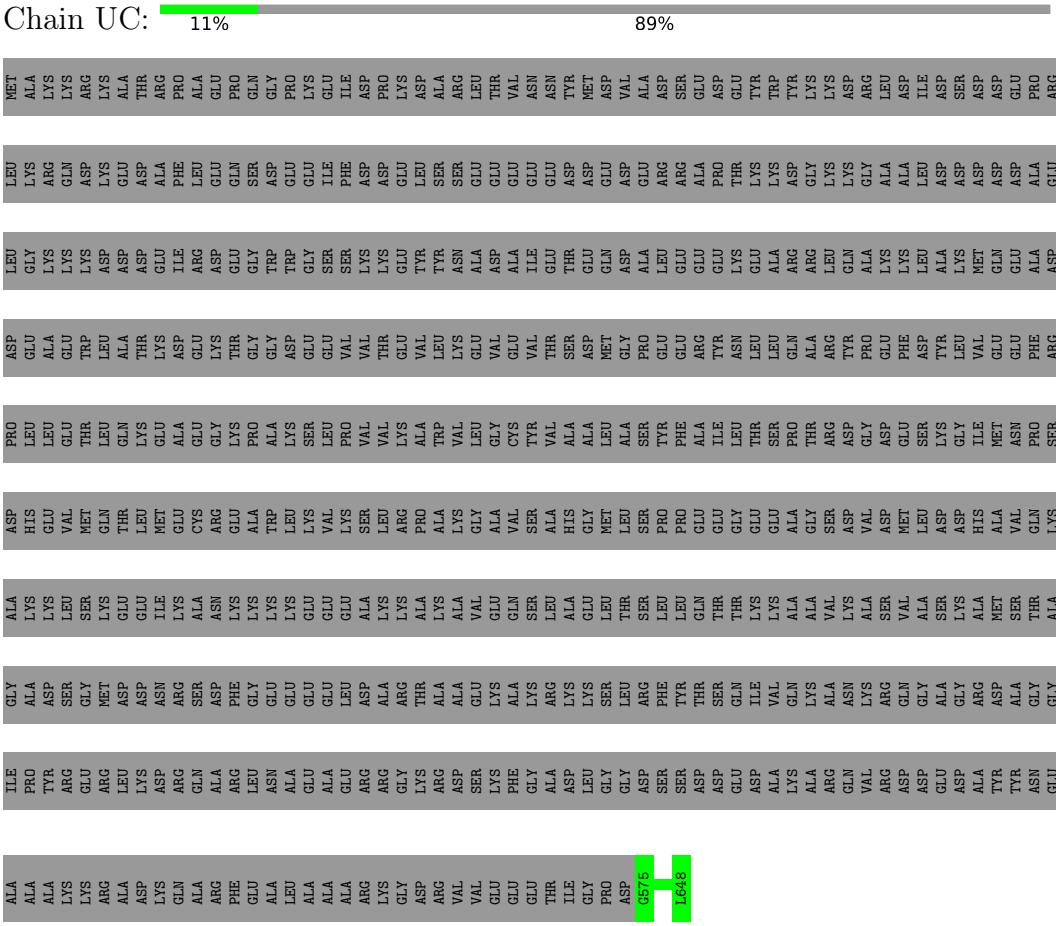
• Molecule 2: Utp2

Chain UB:



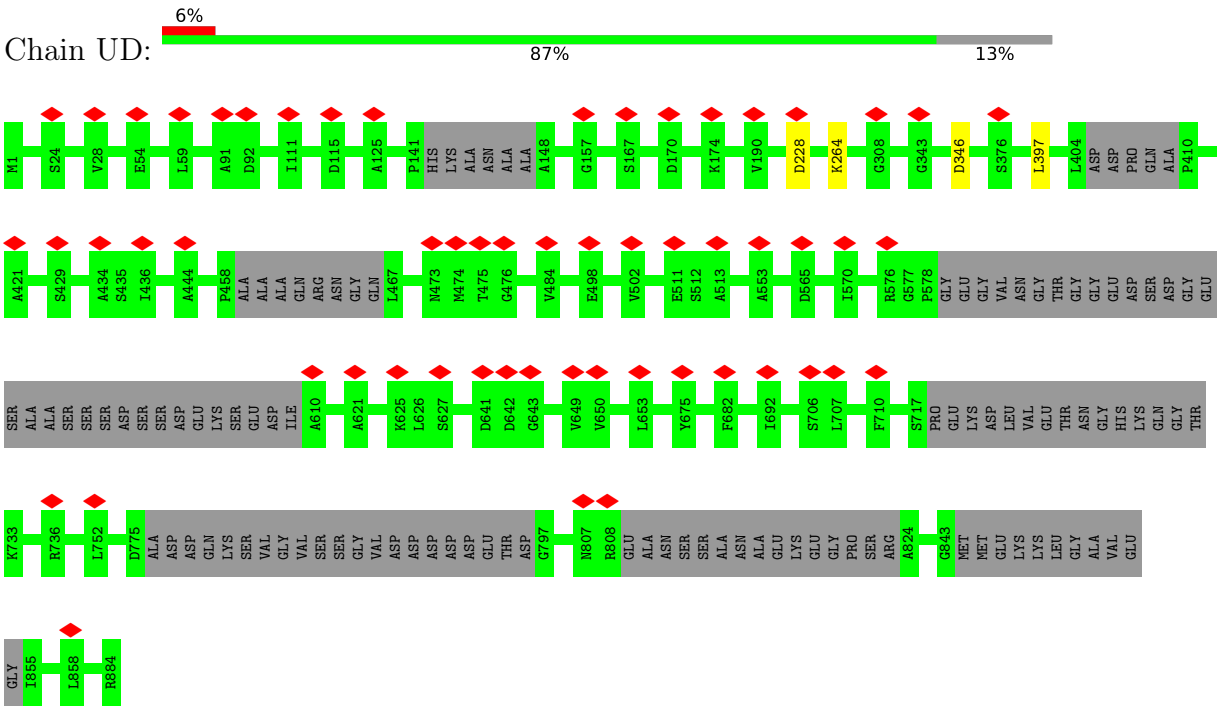
• Molecule 3: Utp3

Chain UC:



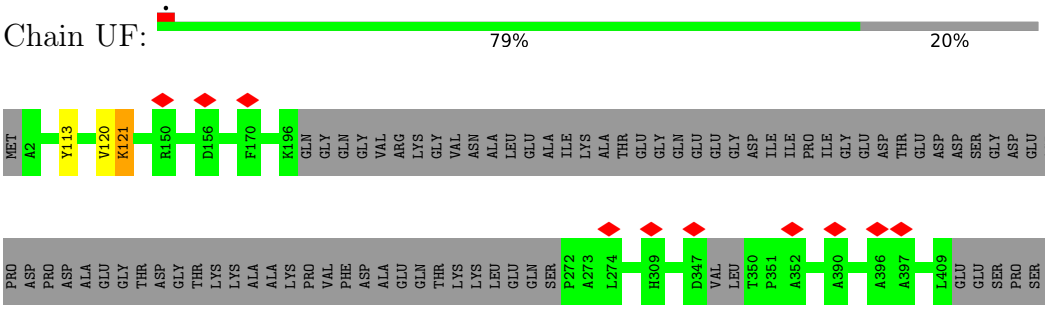
• Molecule 4: Utp4

Chain UD:



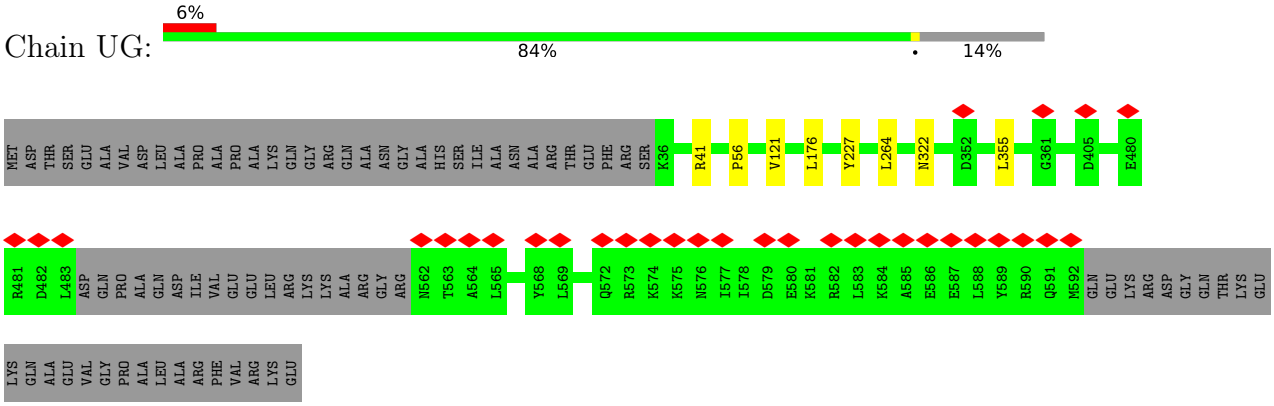
• Molecule 5: Utp6

Chain UF:



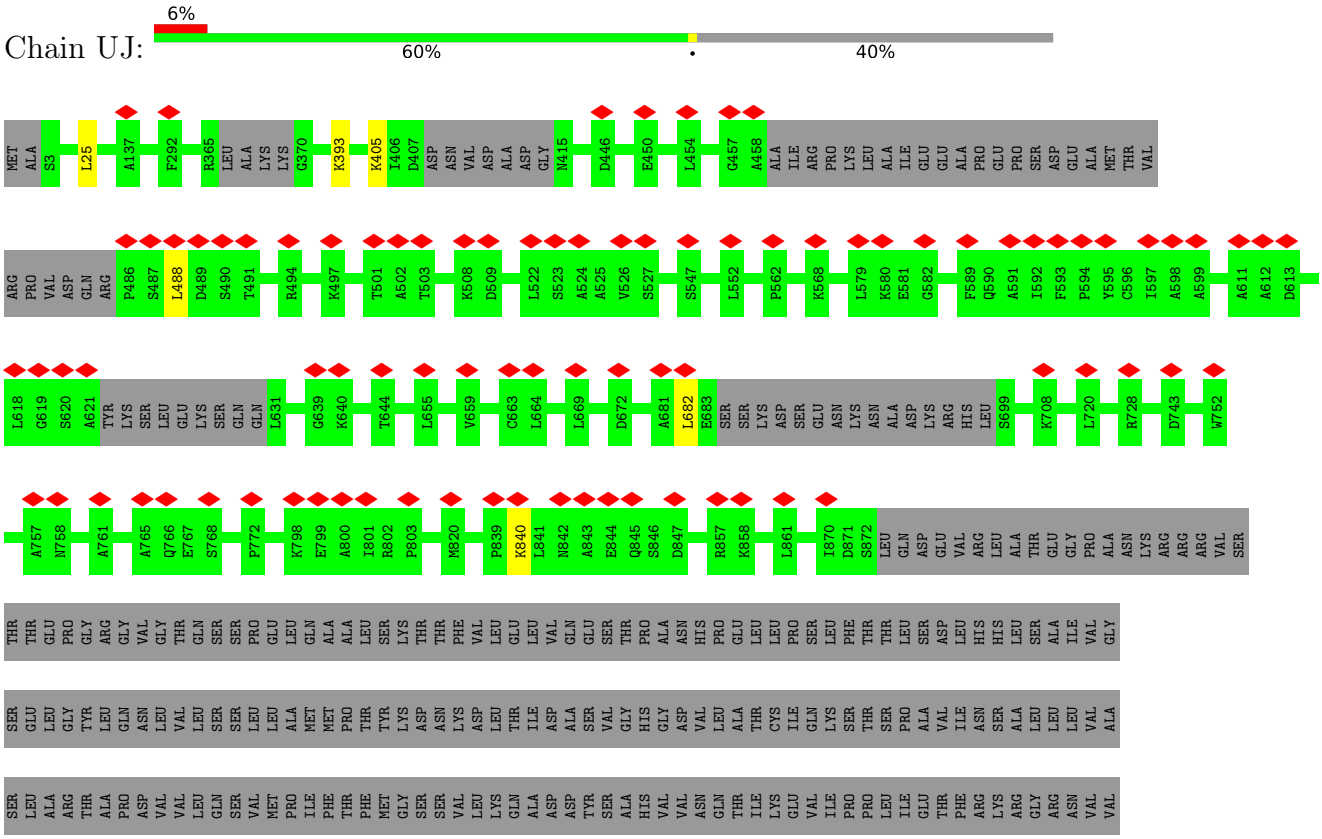
• Molecule 6: Utp7

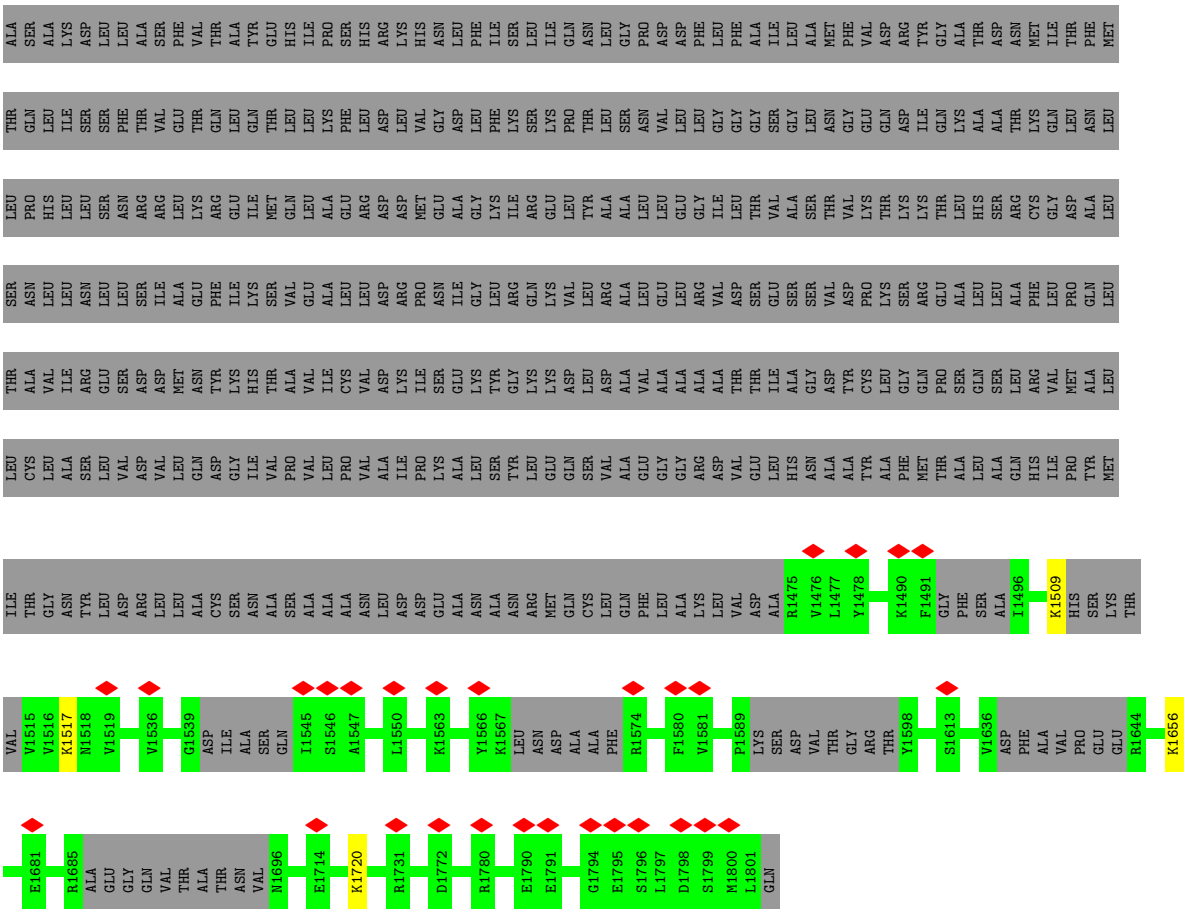
Chain UG:



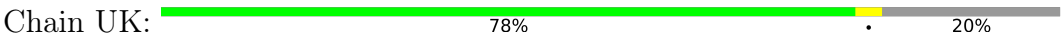
• Molecule 7: UTP10

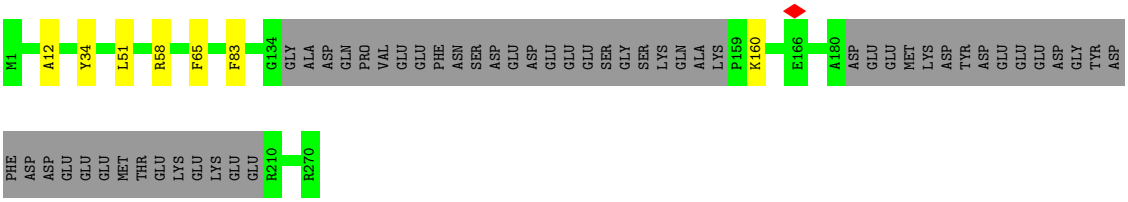
Chain UJ:



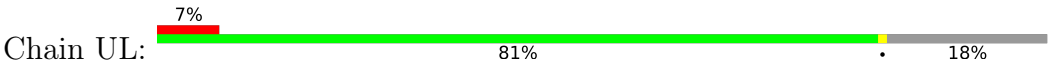


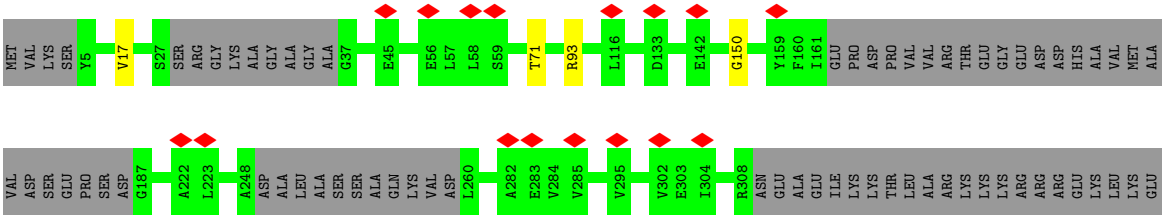
• Molecule 8: U3 small nucleolar RNA-associated protein 11

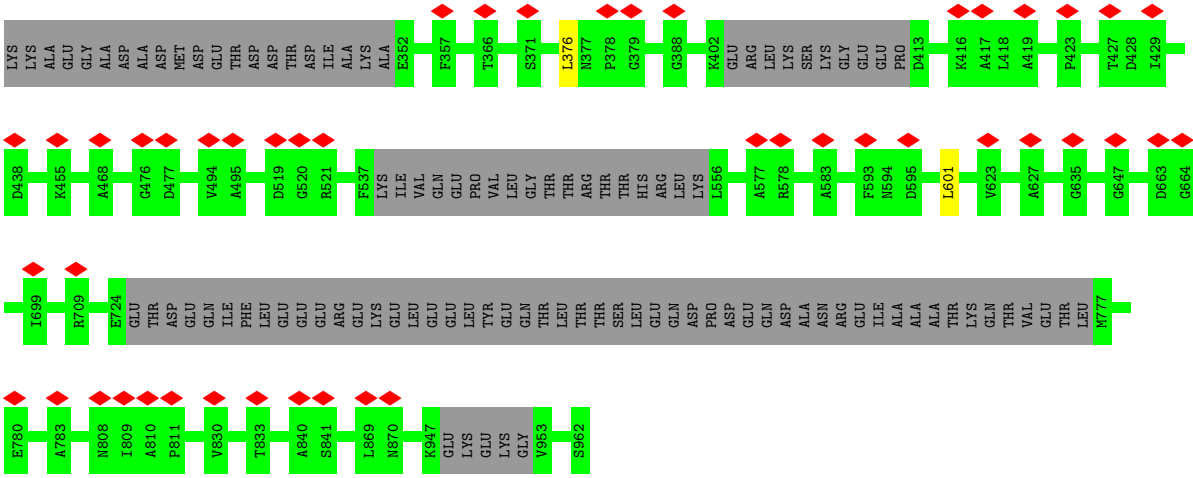




• Molecule 9: Utp12

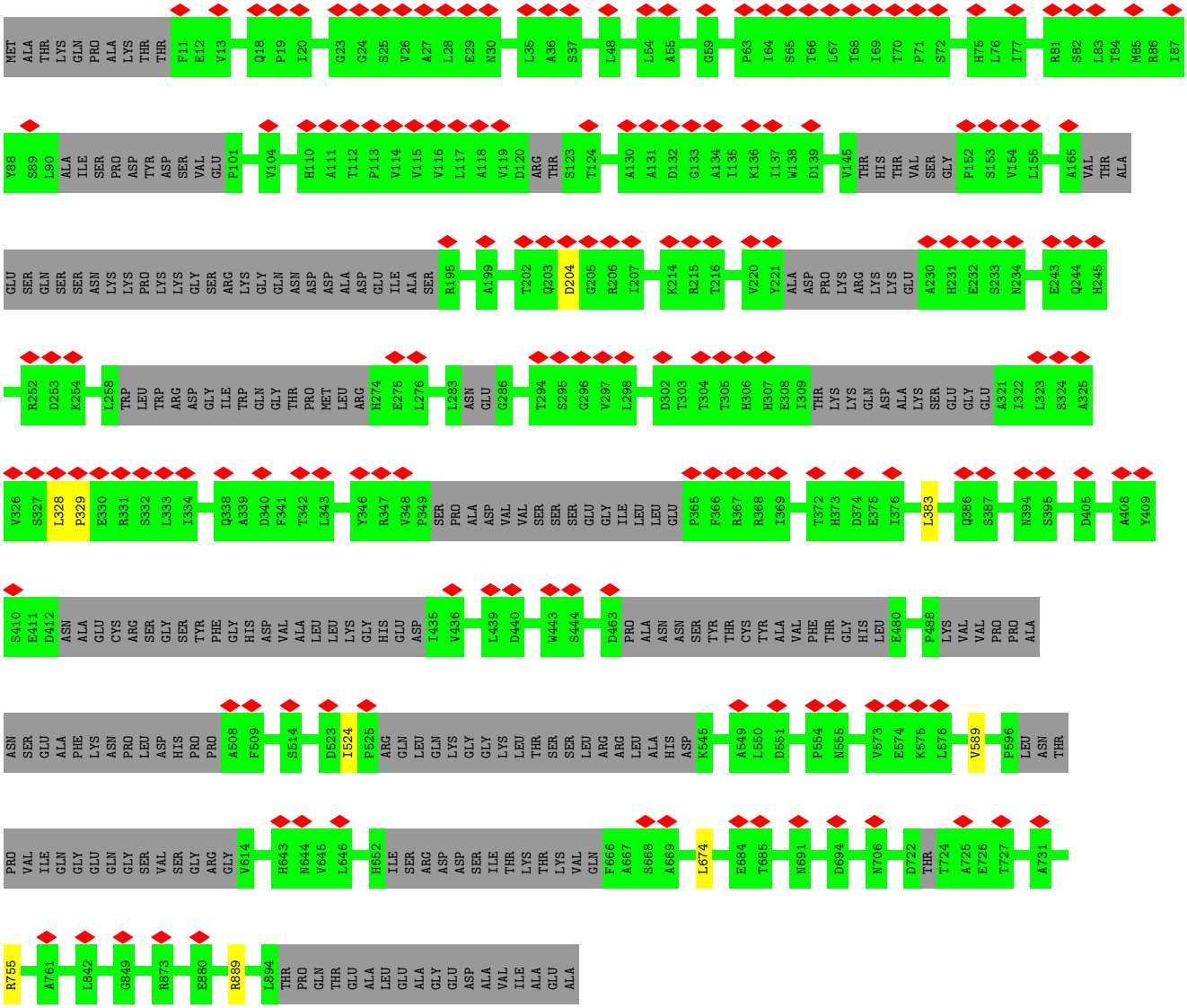






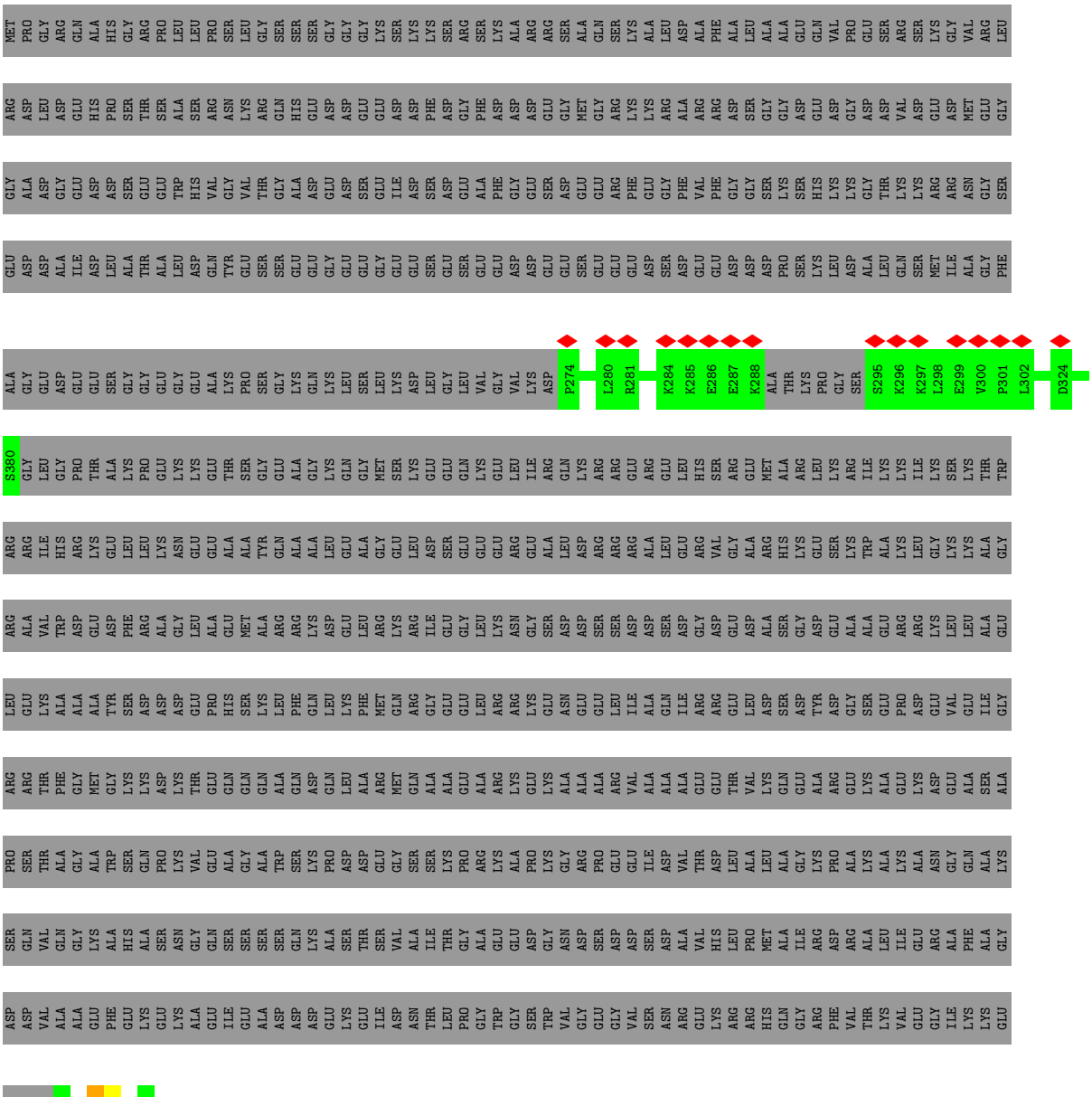
• Molecule 10: Utp13

Chain UM:



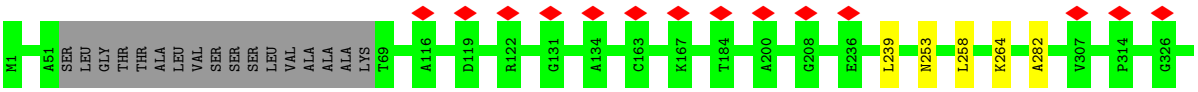
• Molecule 11: Utp14

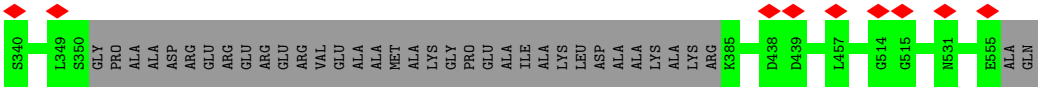
Chain UN:



• Molecule 12: Utp15

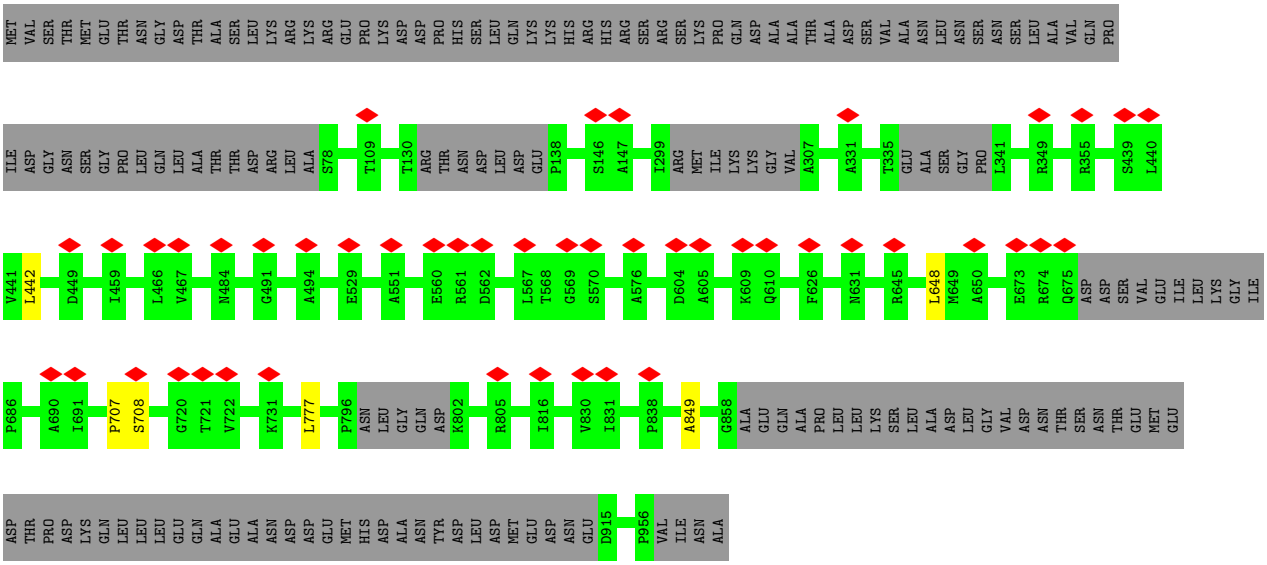
Chain UO:





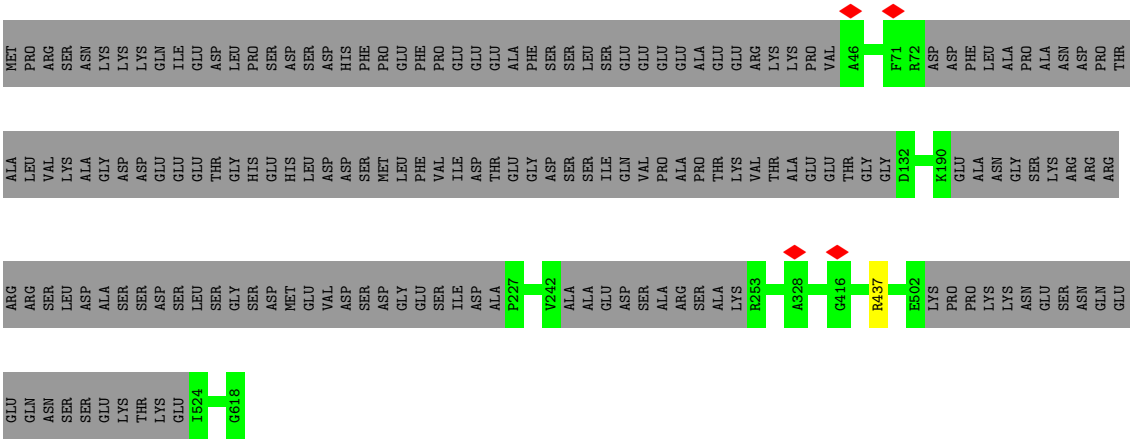
• Molecule 13: Utp17

Chain UQ:



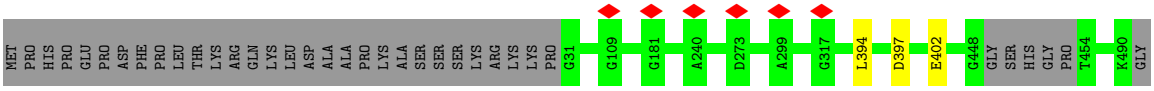
• Molecule 14: Utp18

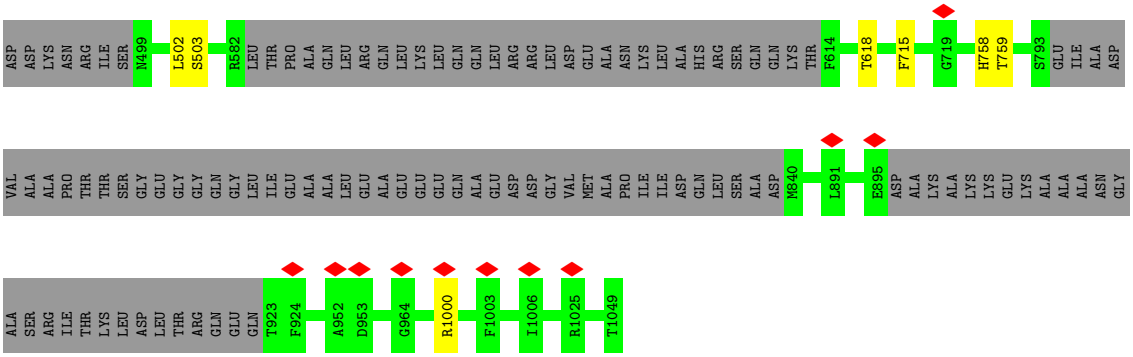
Chain UR:



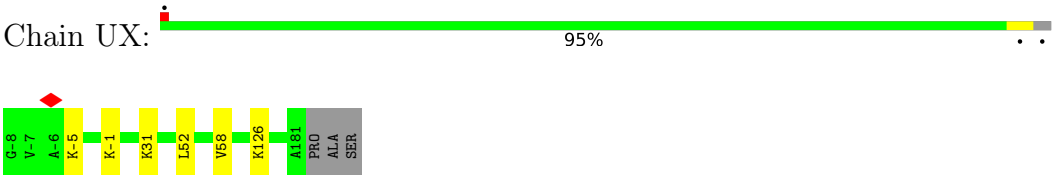
• Molecule 15: Putative U3 snoRNP protein

Chain UU:

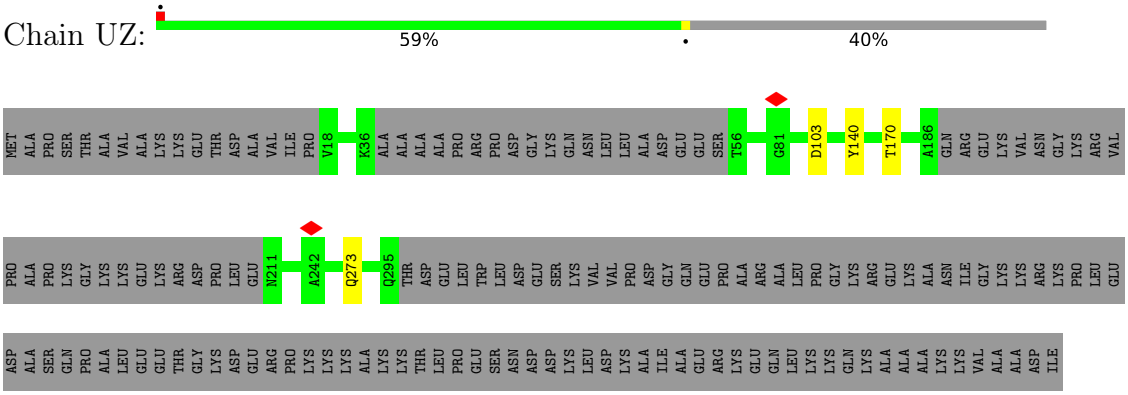




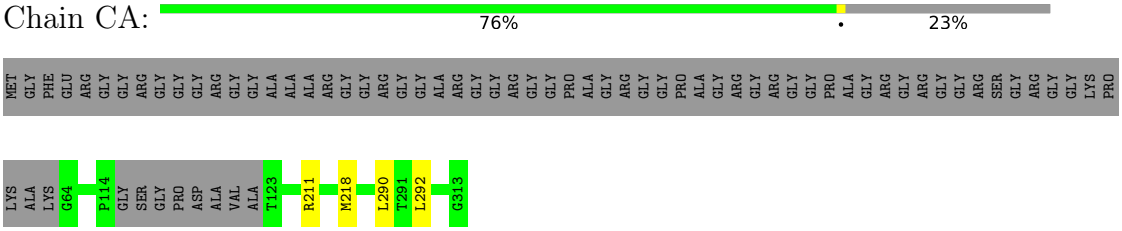
• Molecule 16: Utp24



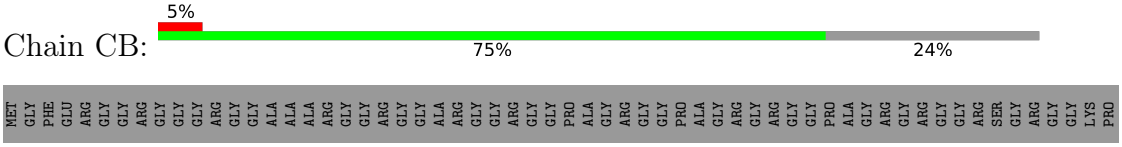
• Molecule 17: Utp30

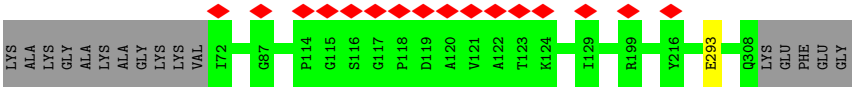


• Molecule 18: Nop1



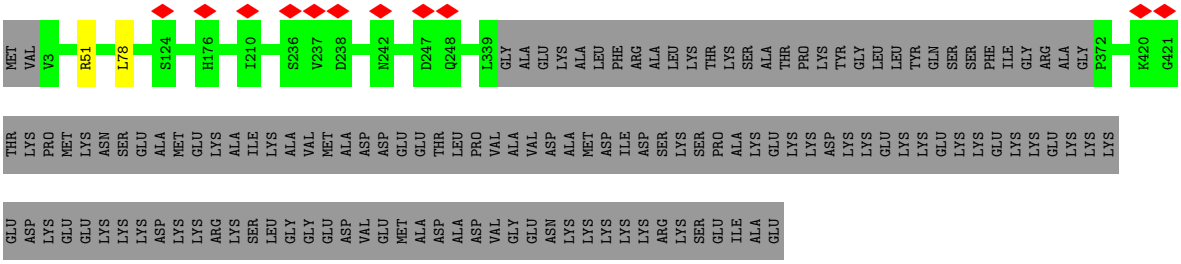
• Molecule 18: Nop1





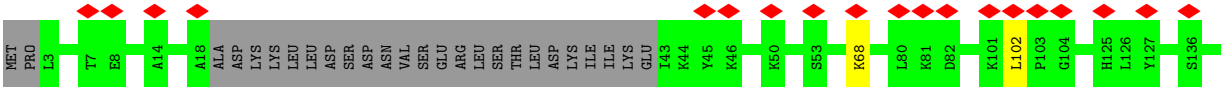
• Molecule 19: Putative nucleolar protein

Chain CC:



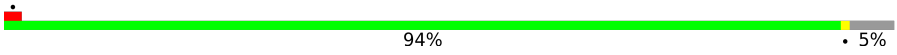
• Molecule 20: Nop58

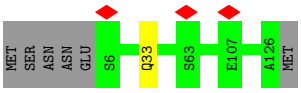
Chain CD:



• Molecule 21: Snu13

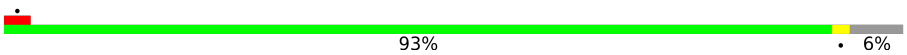
Chain CE:

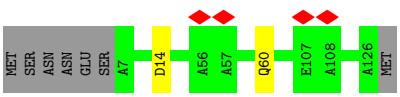




• Molecule 21: Snu13

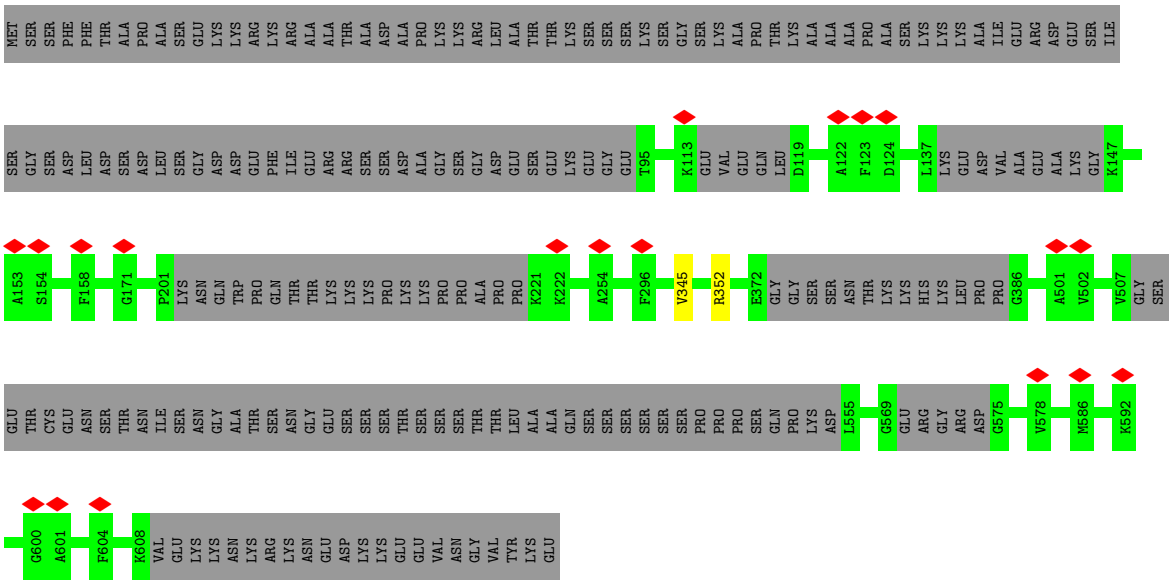
Chain CF:





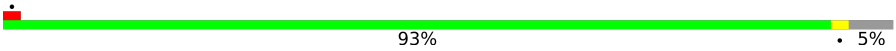
• Molecule 22: Rrp9

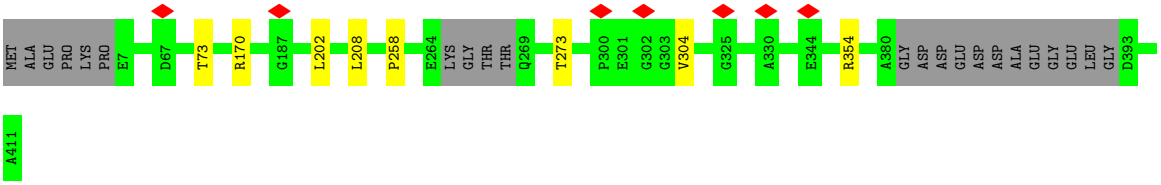
Chain CG:



• Molecule 23: RNA 3'-terminal phosphate cyclase-like protein

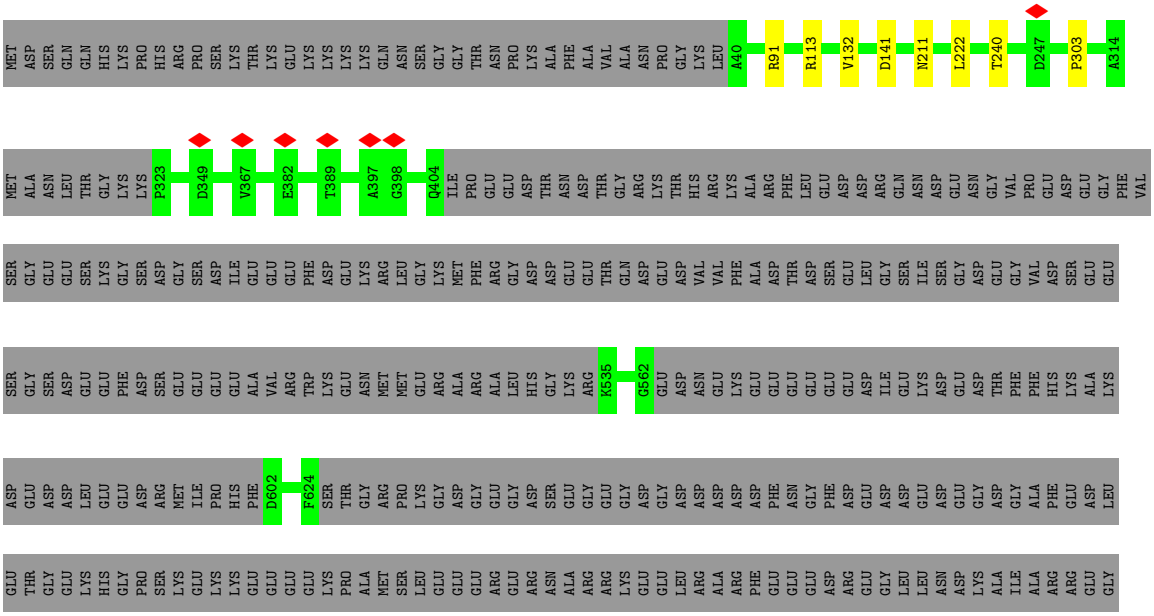
Chain CH:





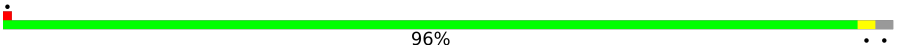
• Molecule 24: Bms1

Chain CI:



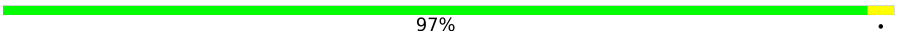
• Molecule 25: Imp3

Chain CJ:



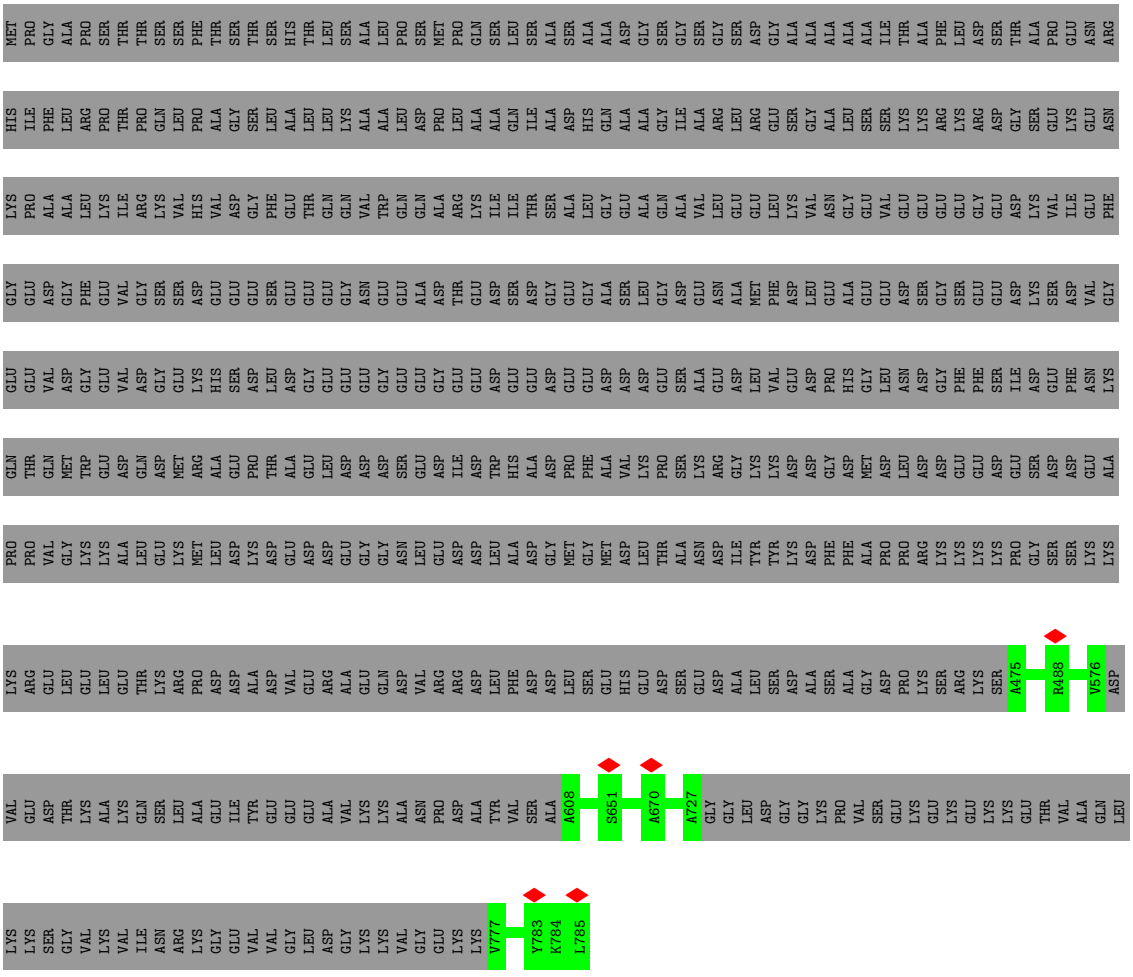
• Molecule 26: Putative U3 small nucleolar ribonucleoprotein

Chain CK:



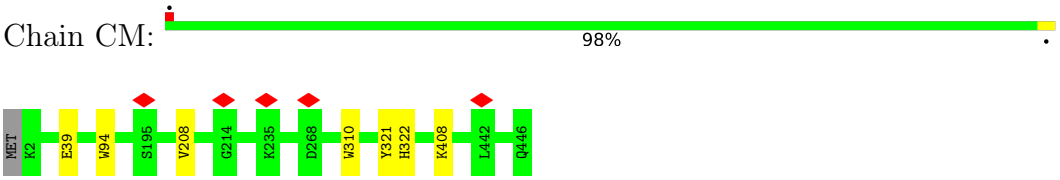
• Molecule 27: Putative U3 small nucleolar ribonucleoprotein protein

Chain CL:



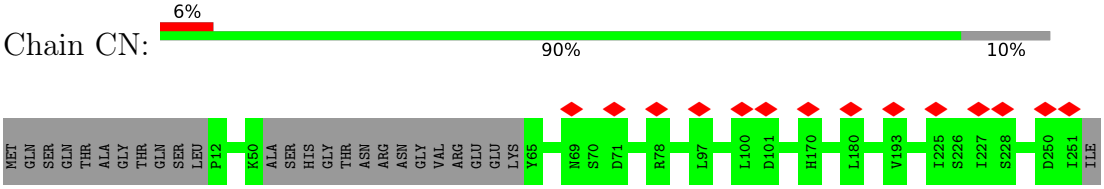
• Molecule 28: Sof1

Chain CM:



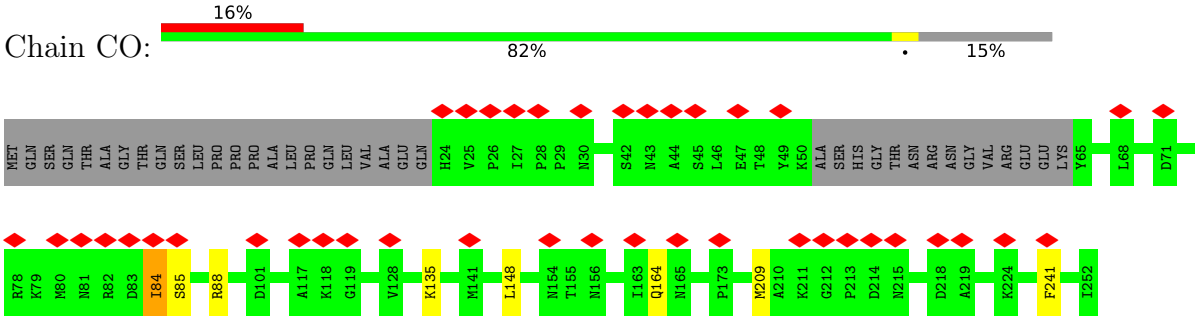
• Molecule 29: Emg1

Chain CN:



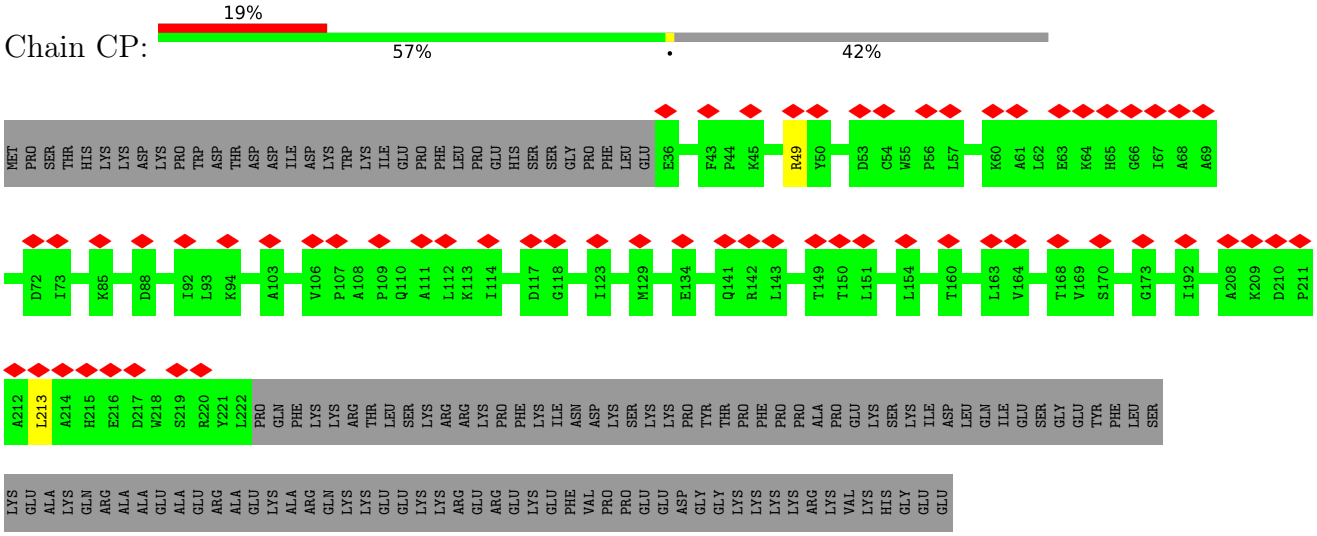
• Molecule 29: Emg1

Chain CO:



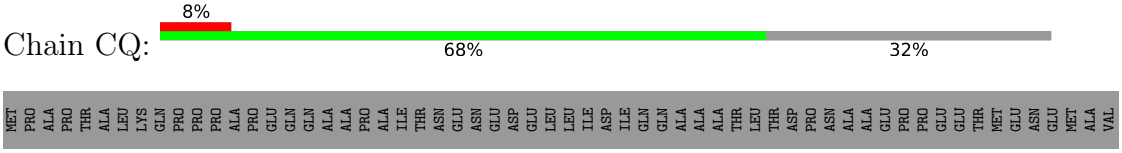
• Molecule 30: KRR1 small subunit processome component

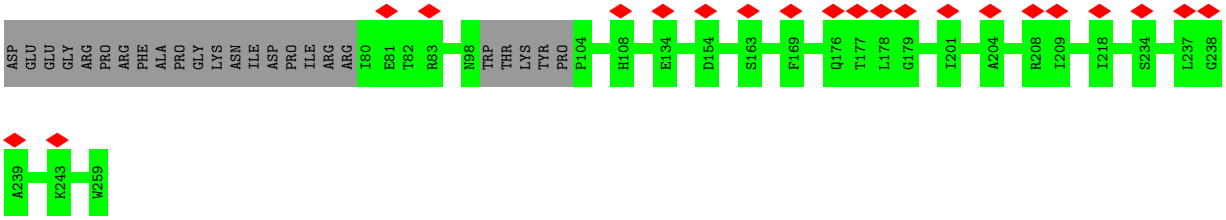
Chain CP:



• Molecule 31: Pre-rRNA-processing protein PNO1

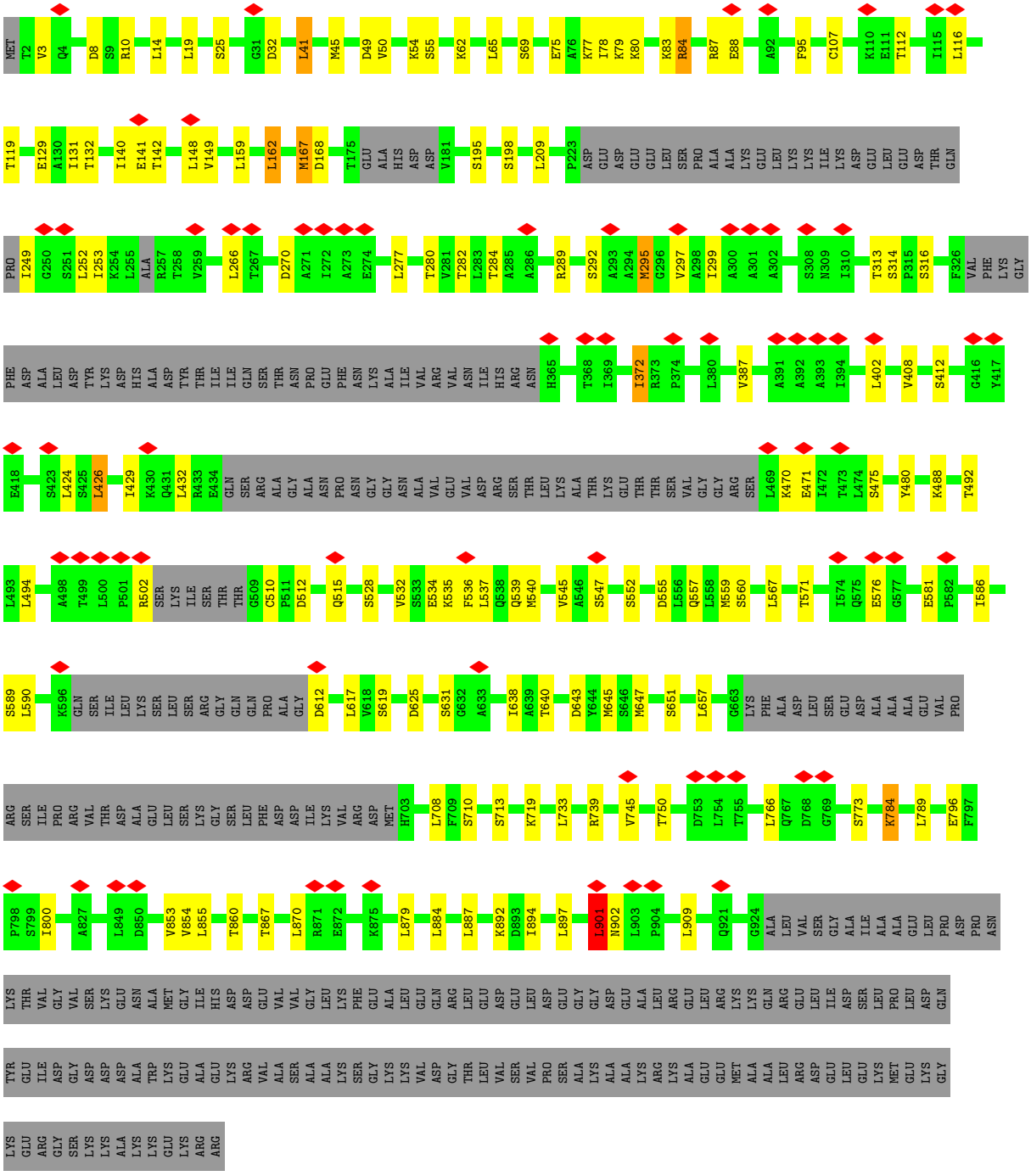
Chain CQ:





• Molecule 32: Kre33

Chain CR:

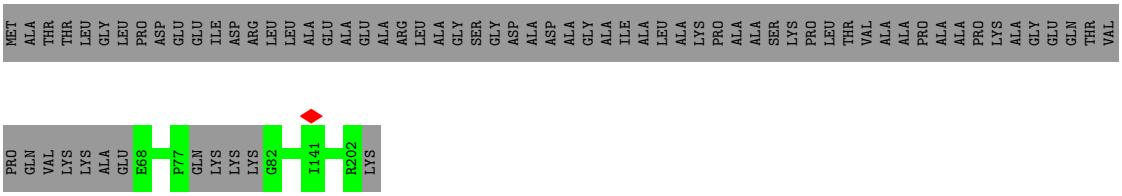


• Molecule 32: Kre33

Chain CS:

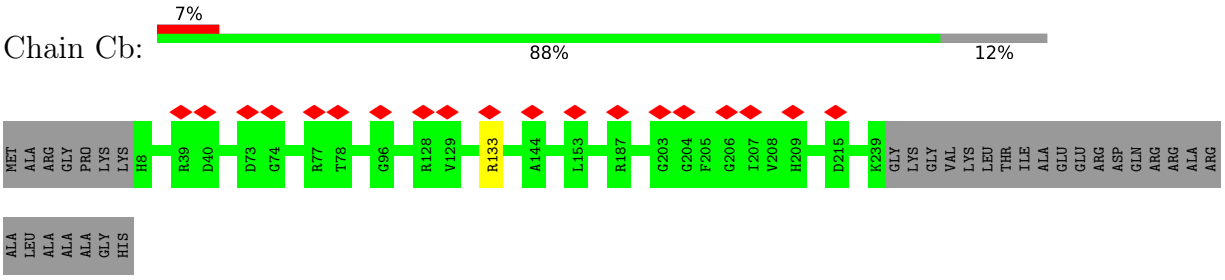
• Molecule 33: Fcf2

Chain CT:



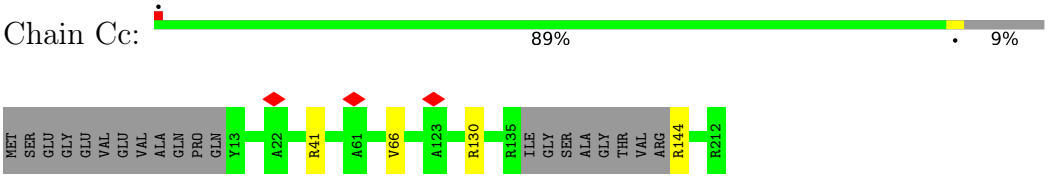
• Molecule 34: 40S ribosomal protein S4

Chain Cb:



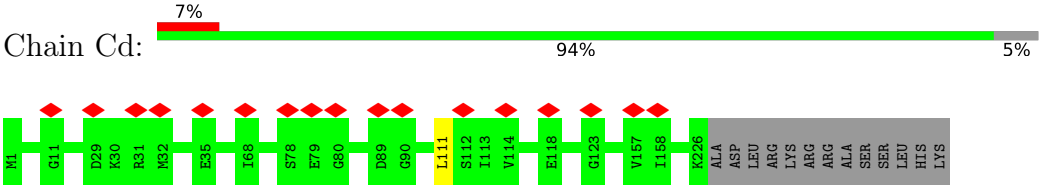
• Molecule 35: 40S ribosomal protein s5-like protein

Chain Cc:



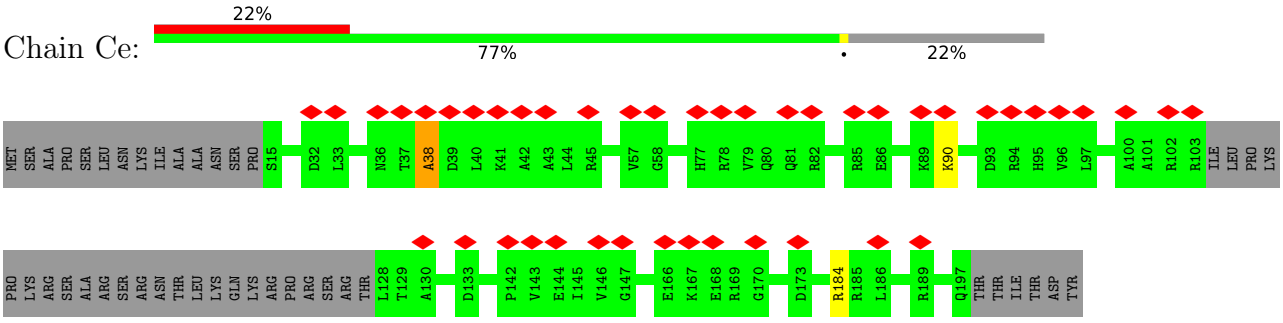
• Molecule 36: 40S ribosomal protein S6

Chain Cd:



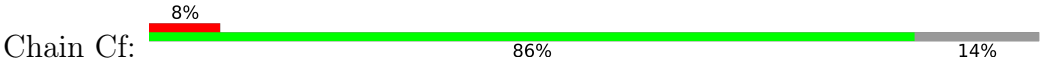
• Molecule 37: 40S ribosomal protein S7

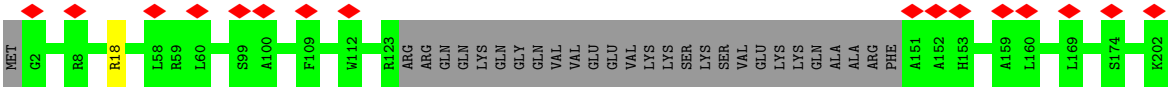
Chain Ce:



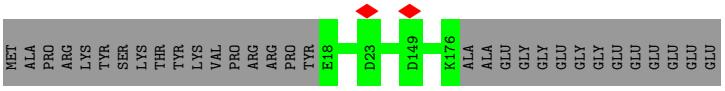
• Molecule 38: 40S ribosomal protein S8

Chain Cf:

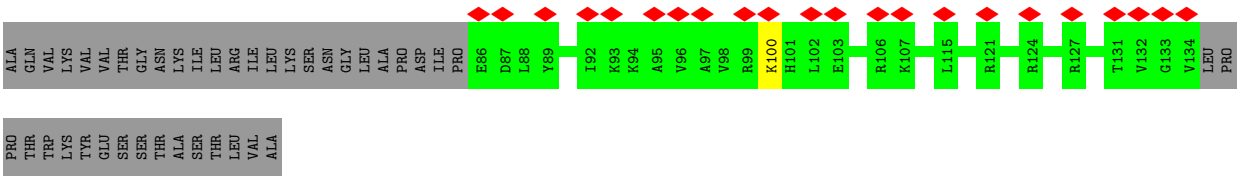




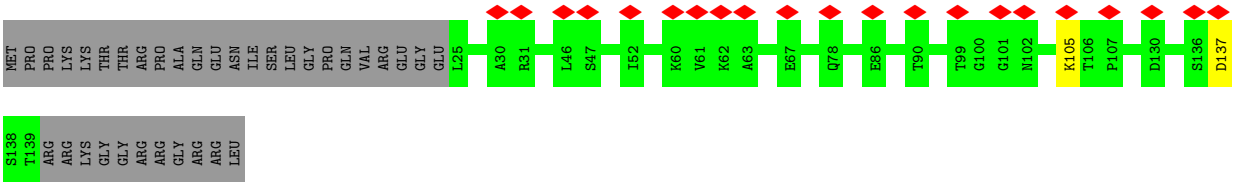
• Molecule 39: 40S ribosomal protein s9-like protein



• Molecule 40: 40S ribosomal protein S13-like protein

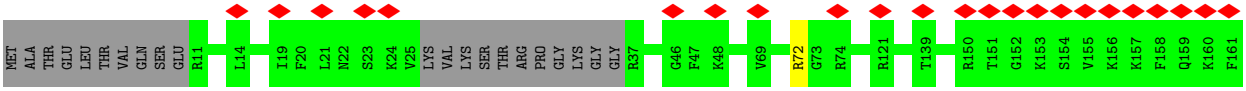


• Molecule 41: 40S ribosomal protein S14-like protein



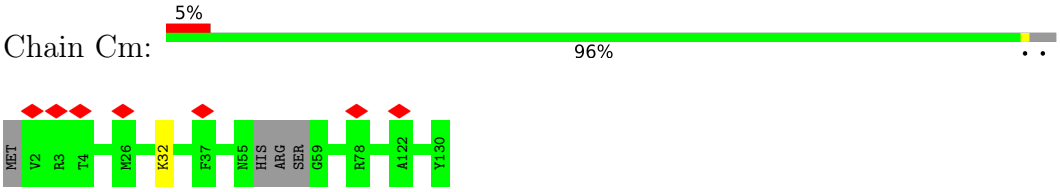
• Molecule 42: 40S ribosomal protein S16-like protein

• Molecule 43: 40S ribosomal protein S11-like protein



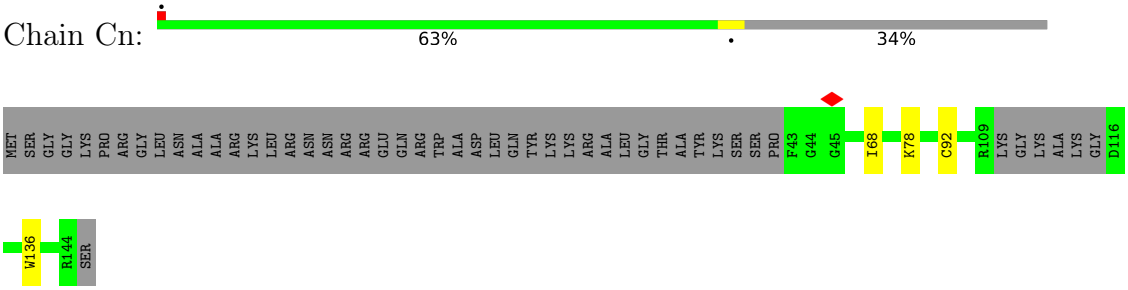
• Molecule 44: 40S ribosomal protein S22-like protein

Chain Cm:



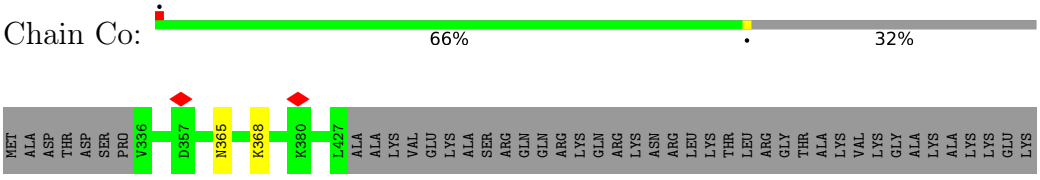
• Molecule 45: 40S ribosomal protein s23-like protein

Chain Cn:



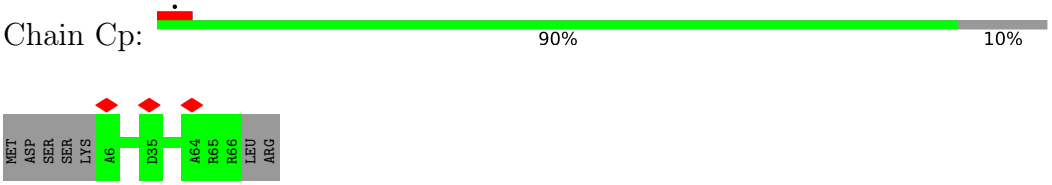
• Molecule 46: 40S ribosomal protein S24

Chain Co:



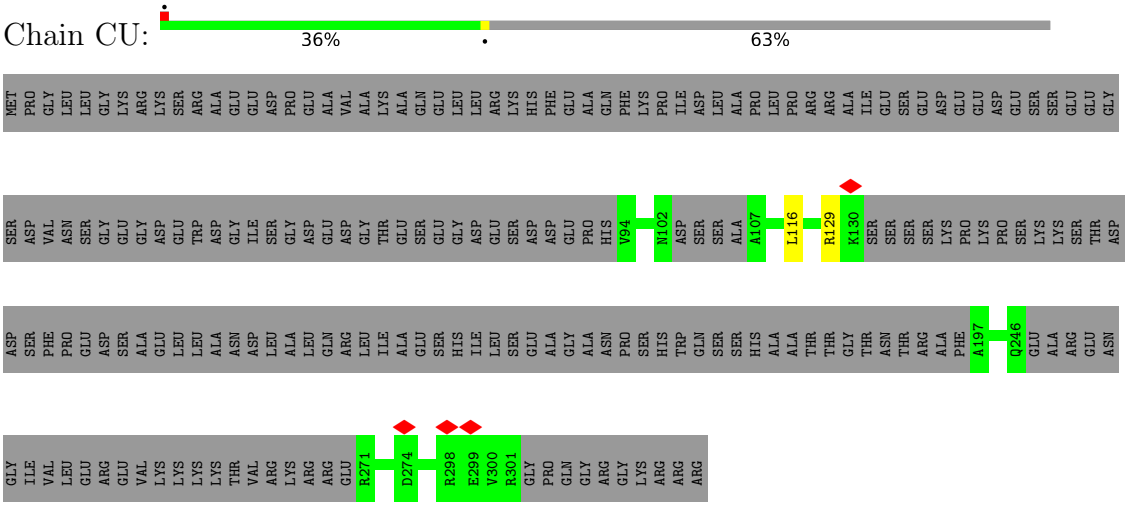
• Molecule 47: 40S ribosomal protein S28-like protein

Chain Cp:



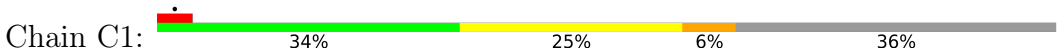
• Molecule 48: Faf1

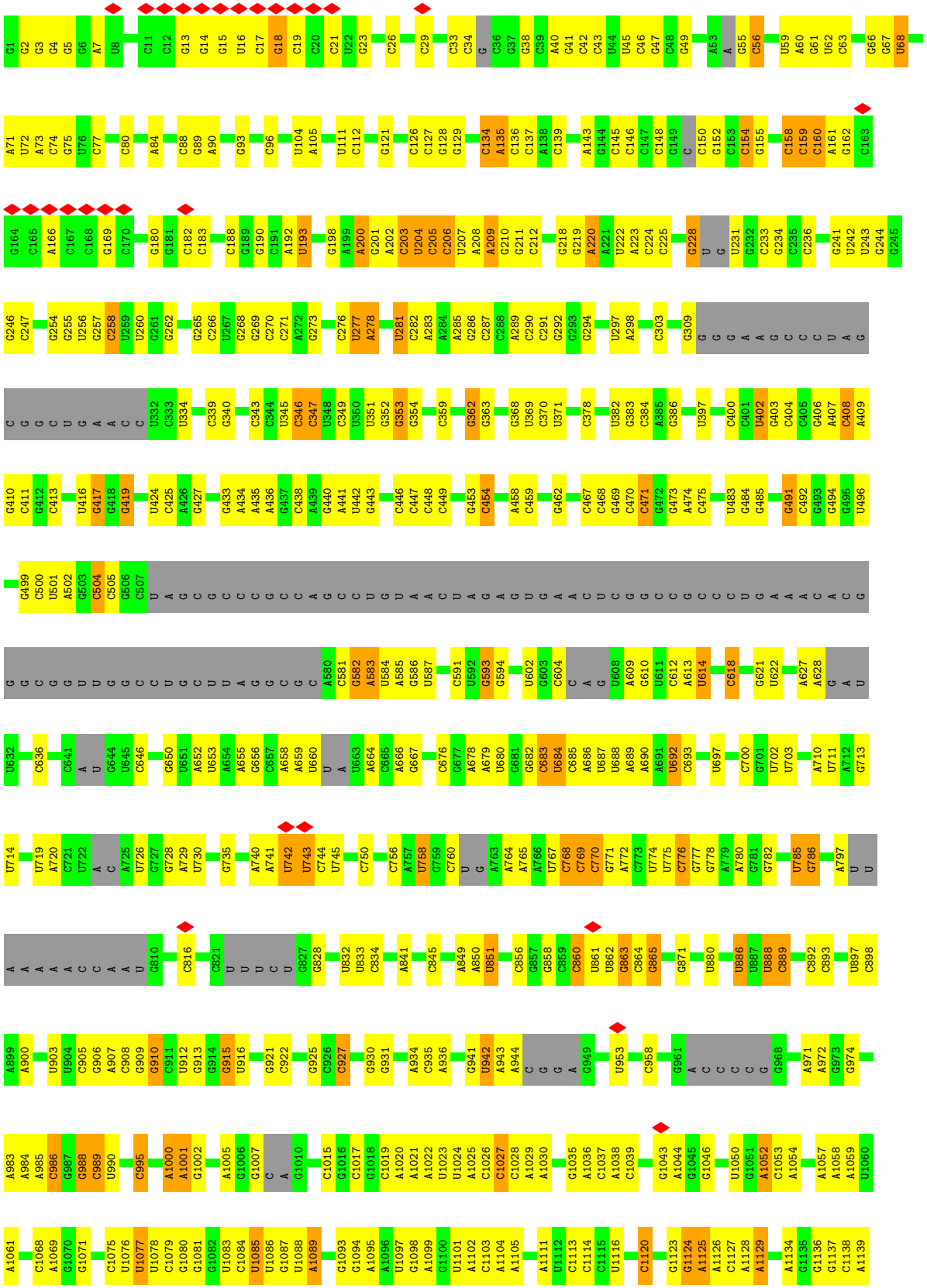
Chain CU:

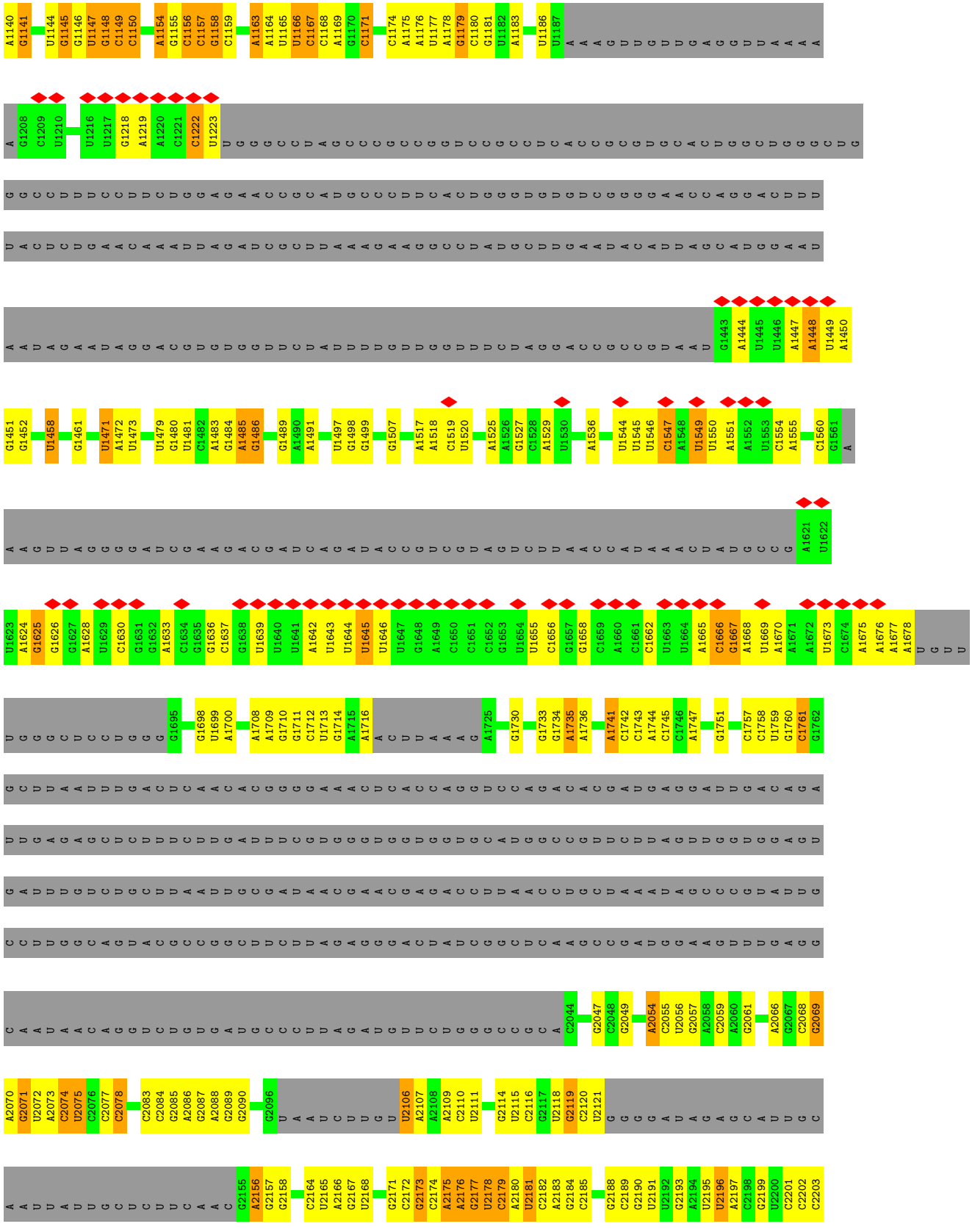


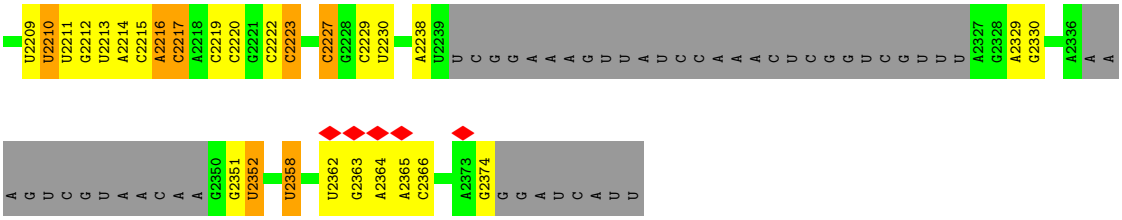
• Molecule 49: 35S ribosomal RNA

Chain C1:



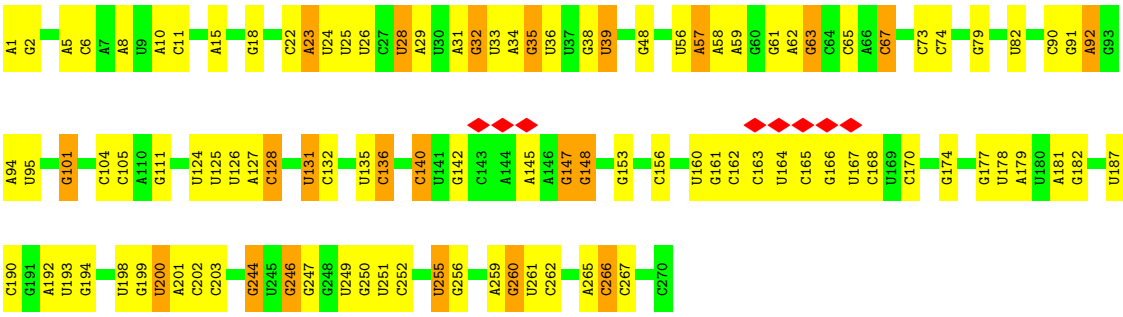






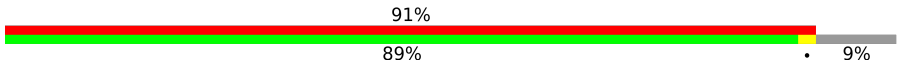
• Molecule 50: U3 snoRNA

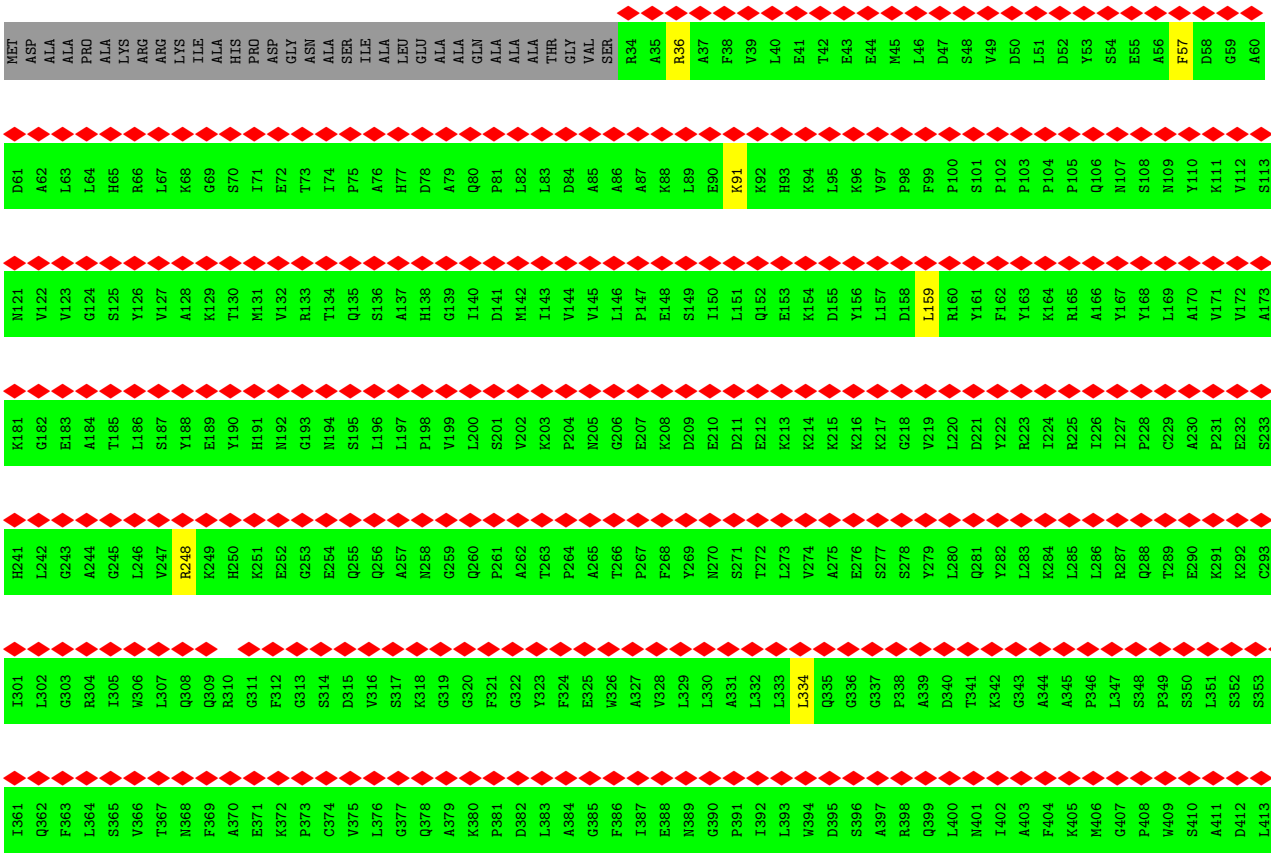
Chain C2:

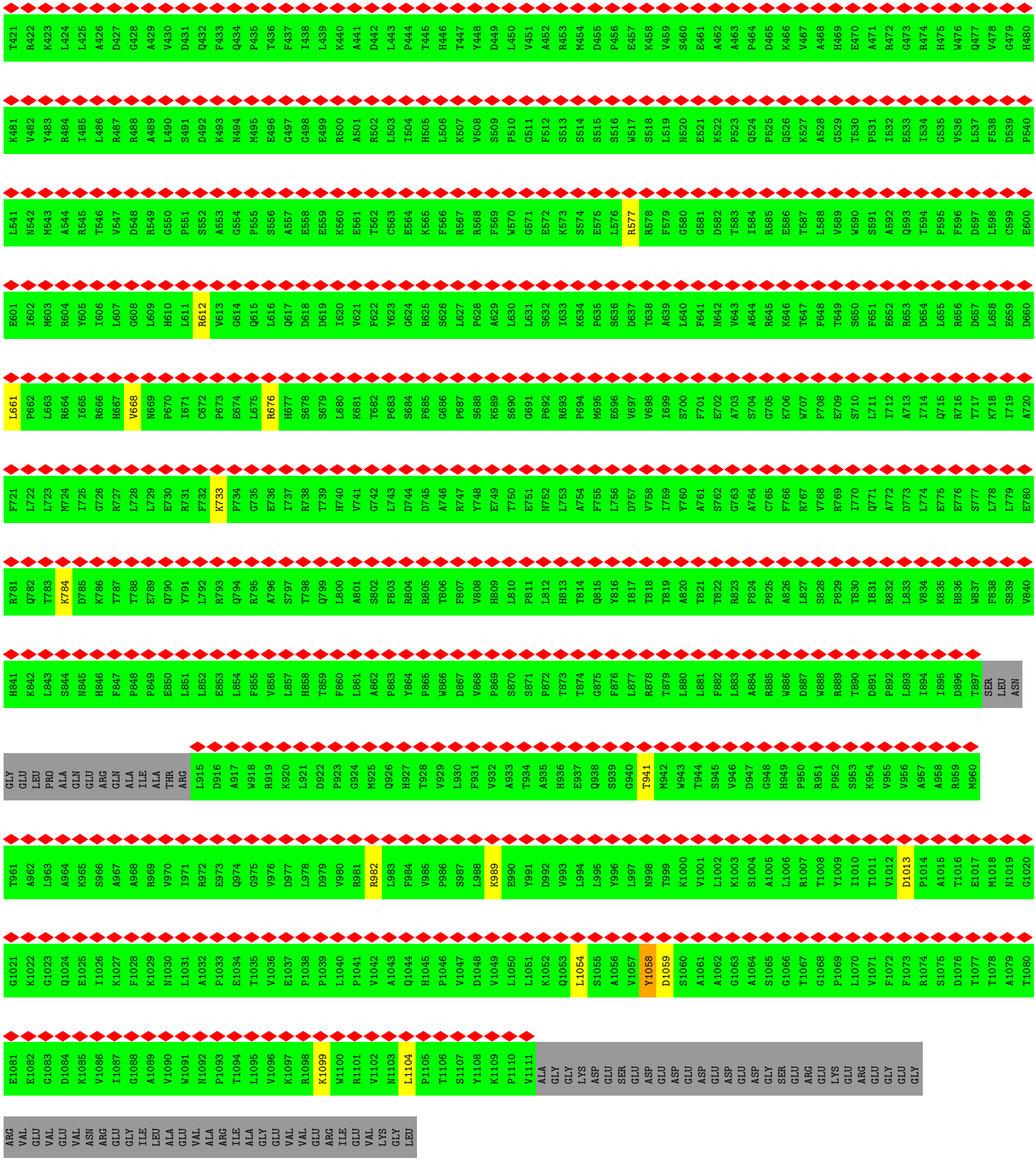


• Molecule 51: U3 small nucleolar RNA-associated protein 22

Chain UV:

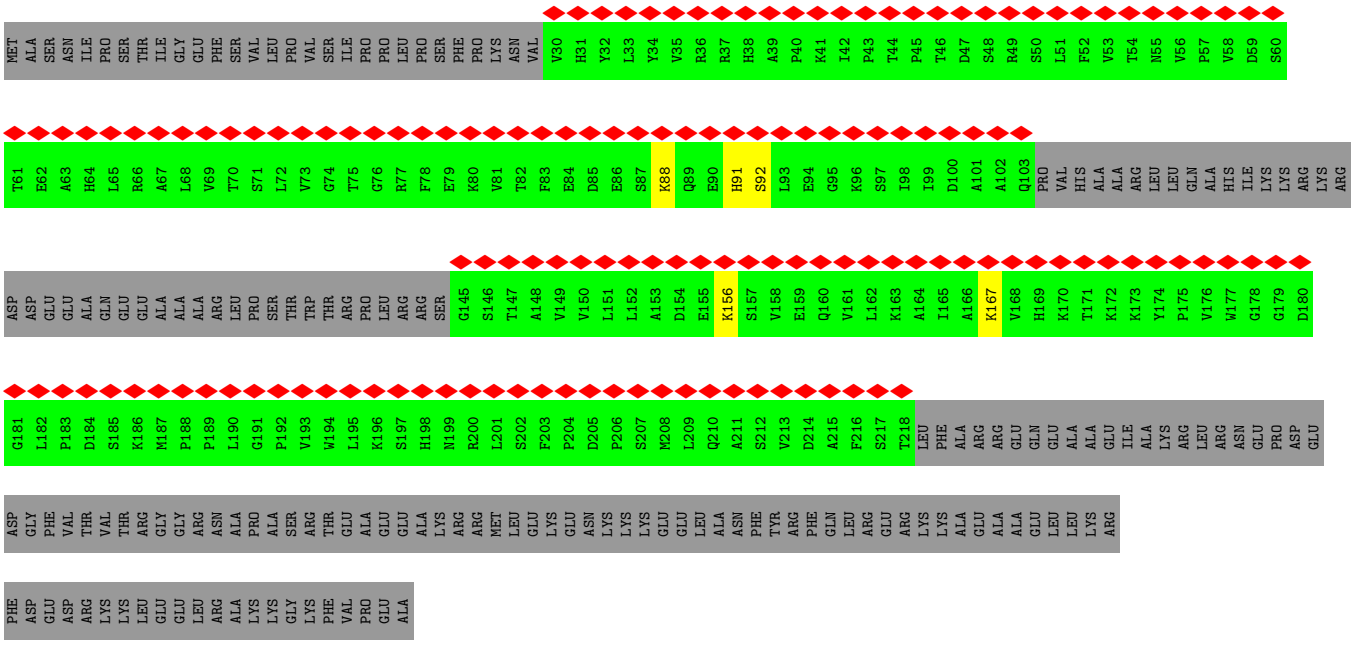






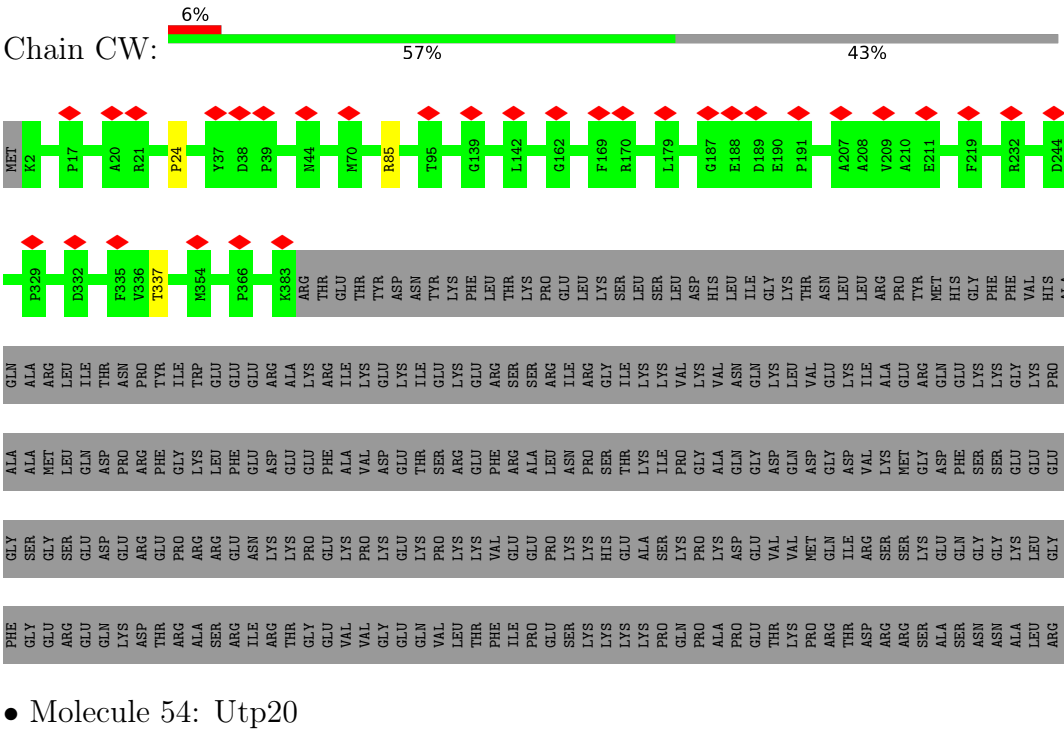
- Molecule 52: Rrp7

Chain CV:



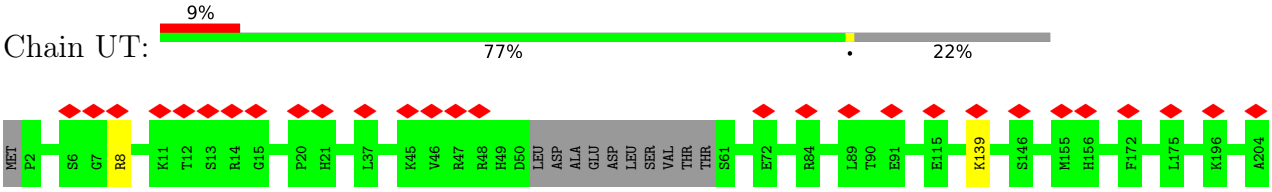
• Molecule 53: Ribosome biogenesis protein ENP2

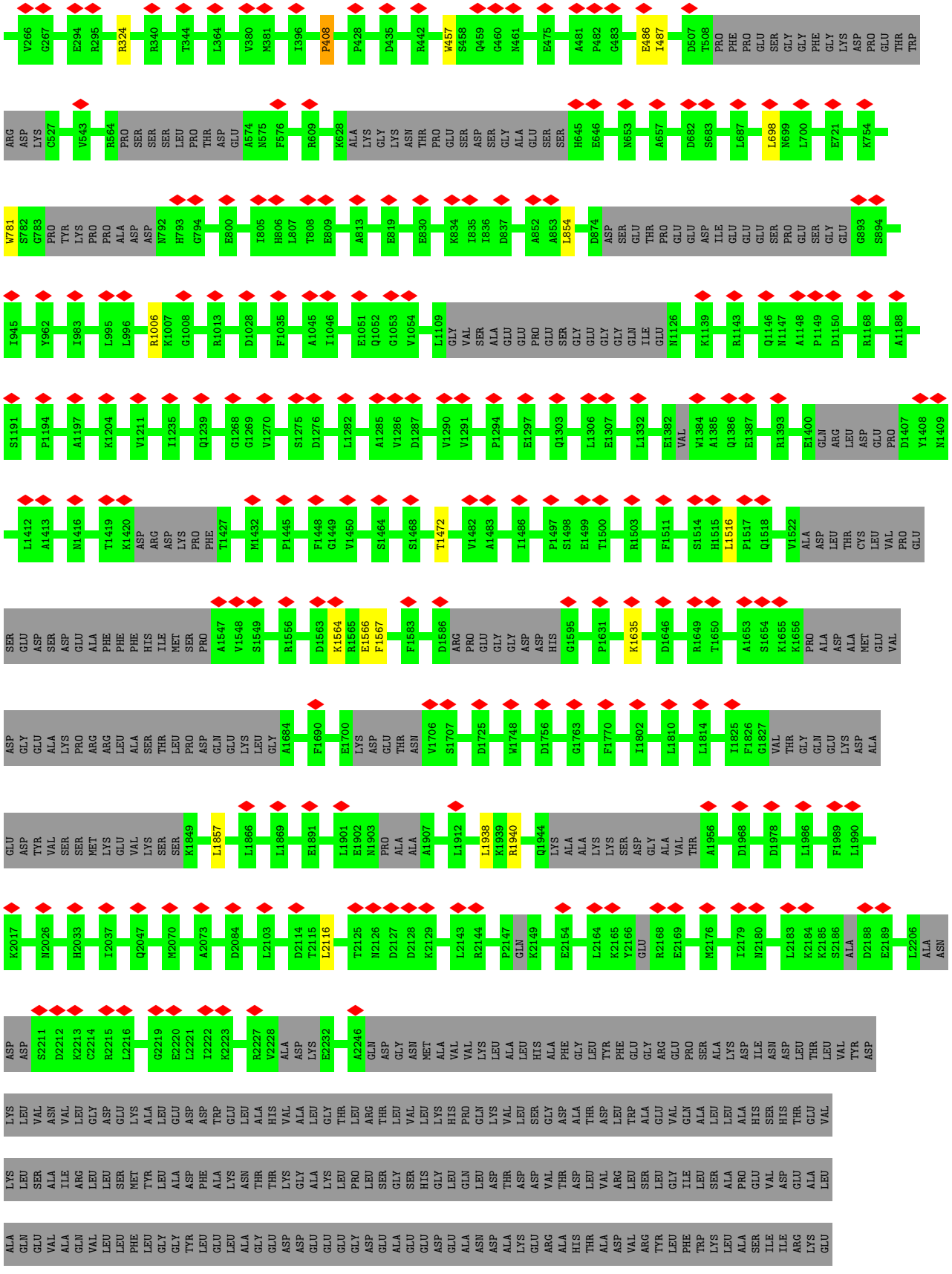
Chain CW:

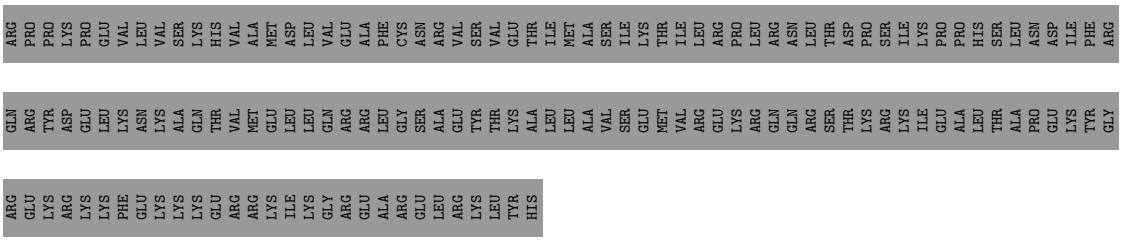


• Molecule 54: Utp20

Chain UT:

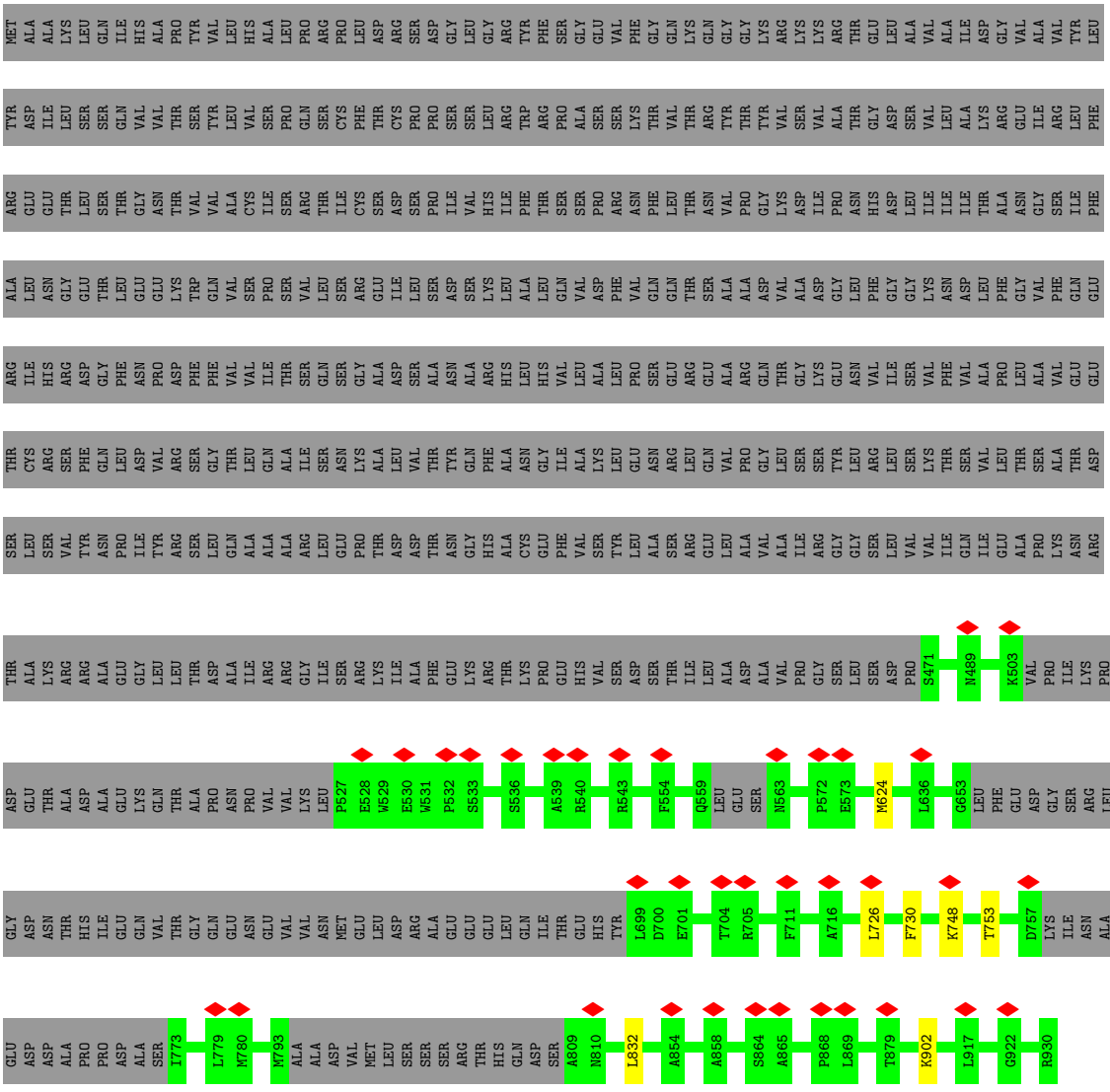



V266 G267 E294 R295 R324 R340 T344 L364 V380 M381 I396 P408 P428 D435 R442 W457 S458 Q459 G460 N461 E475 A481 P482 G483 E486 I487 D507 T508 PRO PHE PRO GLU SER GLY GLY PHE GLY LYS ASP PRO GLU THR TRP
ARG ASP LYS C527 V543 R564 PRO SER SER SER LEU PRO THR ASP GLU A574 N575 F576 R609 K628 ALA LYS GLY LYS ASN THR PRO GLU SER ASP SER GLY ALA GLU SER SER H645 E646 N653 A657 D682 S683 L687 L698 W699 L700 E721 K754
W781 S782 G783 PRO TYR LYS PRO PRO ALA ASP ASP N792 H793 G794 E800 I805 H806 L807 T808 E809 A813 E819 E830 K834 I835 I836 D837 A852 A853 L854 D874 ASP SER GLU THR PRO GLU GLU ASP ILE GLU GLU GLU SER PRO GLU SER GLY GLU G893 S894
I945 Y962 I983 L995 L996 R1006 K1007 G1008 R1013 D1028 F1035 A1045 I1046 E1051 Q1052 G1053 V1054 L1109 GLY VAL SER ALA GLU GLU PRO GLU SER GLY GLU GLY GLY GLN ILE GLU N1126 K1139 R1143 Q1146 N1147 A1148 P1149 D1150 R1168 A1188
S1191 P1194 A1197 K1204 V1211 I1235 Q1239 G1268 G1269 V1270 S1275 D1276 L1282 A1285 V1286 D1287 V1290 V1291 P1294 E1297 Q1303 L1306 E1307 L1332 E1382 VAL W1384 A1385 Q1386 E1387 R1393 E1400 GLN ARG LEU ASP GLU PRO D1407 Y1408 N1409
L1412 A1413 N1416 T1419 K1420 ASP ARG ASP LYS PRO PHE T1427 M1432 P1445 F1448 G1449 V1450 S1464 S1468 T1472 V1482 A1483 I1486 P1497 S1498 E1499 T1500 R1503 F1511 S1514 H1515 L1516 P1517 Q1518 V1522 ALA ASP LEU THR CYS LEU VAL PRO GLU
SER GLU ASP SER ASP GLU ALA PHE PHE PHE HIS ILE MET SER PRO A1547 V1548 S1549 R1556 D1563 K1564 R1565 E1566 F1567 F1583 D1586 ARG PRO GLU GLY GLY ASP ASP HIS G1595 P1631 K1635 D1646 R1649 T1650 A1653 S1654 K1655 K1656 PRO ALA ASP ALA MET GLU VAL
ASP GLY GLU ALA LYS PRO ARG ARG LEU ALA SER THR LEU PRO ASP GLN GLU LYS LEU GLY A1684 F1690 E1700 LYS ASP GLU THR ASN V1706 S1707 D1725 W1748 D1756 G1763 F1770 I1802 L1810 L1814 I1825 F1826 G1827 VAL THR GLY GLN GLU LYS ASP ALA
GLU ASP TYR VAL SER SER MET LYS GLU VAL LYS SER SER K1849 L1857 L1866 L1869 E1891 L1901 E1902 N1903 PRO ALA ALA A1907 L1912 L1938 K1939 R1940 Q1944 LYS ALA ALA LYS LYS SER ASP GLY ALA VAL THR A1956 D1968 D1978 L1986 F1989 L1990
K2017 N2026 H2033 I2037 Q2047 M2070 A2073 D2084 L2103 D2114 T2115 L2116 T2125 N2126 D2127 D2128 K2129 L2143 R2144 P2147 GLN K2149 E2154 L2164 K2165 Y2166 GLU R2168 E2169 M2176 I2179 N2180 L2183 K2184 K2185 S2186 ALA D2188 E2189 L2206 ALA ASN
ASP ASP S2211 D2212 K2213 C2214 R2215 L2216 G2219 E2220 L2221 I2222 K2223 R2227 V2228 ALA ASP LYS E2232 A2246 GLN ASP GLY ASN MET ALA VAL VAL LYS LEU ALA LEU HIS ALA PHE GLY LEU TYR PHE GLU GLY ARG GLU PRO SER ALA LYS ASP ILE ASN ASP LEU THR LEU VAL TYR ASP
LYS LEU VAL ASN VAL LEU GLY ASP GLU LYS ALA LEU GLU ASP ASP TRP GLU LEU ALA HIS VAL ALA LEU GLY THR LEU ARG THR LEU VAL LEU LYS HIS PRO GLN LYS VAL LEU SER GLY ASP ALA THR ASP LEU TRP ALA GLU VAL GLN ALA LEU LEU ALA HIS SER HIS THR GLU VAL
LYS LEU SER ALA ILE ARG LEU LEU SER MET TYR LEU ALA ASP PHE ALA LYS ASN THR THR LYS GLY ALA LYS LEU PRO LEU SER GLY SER HIS GLY LEU GLN LEU ASP THR ASP ASP VAL THR ASP LEU VAL ALA ARG LEU SER LEU GLY ILE LEU SER ALA LEU ALA PRO GLU VAL ASP GLU ALA LEU
ALA GLN GLU VAL ALA GLN VAL LEU LEU LEU PHE LEU GLY GLY TYR LEU GLU LEU ALA GLY GLU ASP ASP GLU GLU GLU GLY ASP GLU ALA GLU GLU ASP GLU ALA ASN ASP ALA LYS GLU ARG ALA HIS THR ALA ASP VAL ARG TYR LEU PHE TRP LYS LEU ALA SER ILE ILE ARG LYS GLU



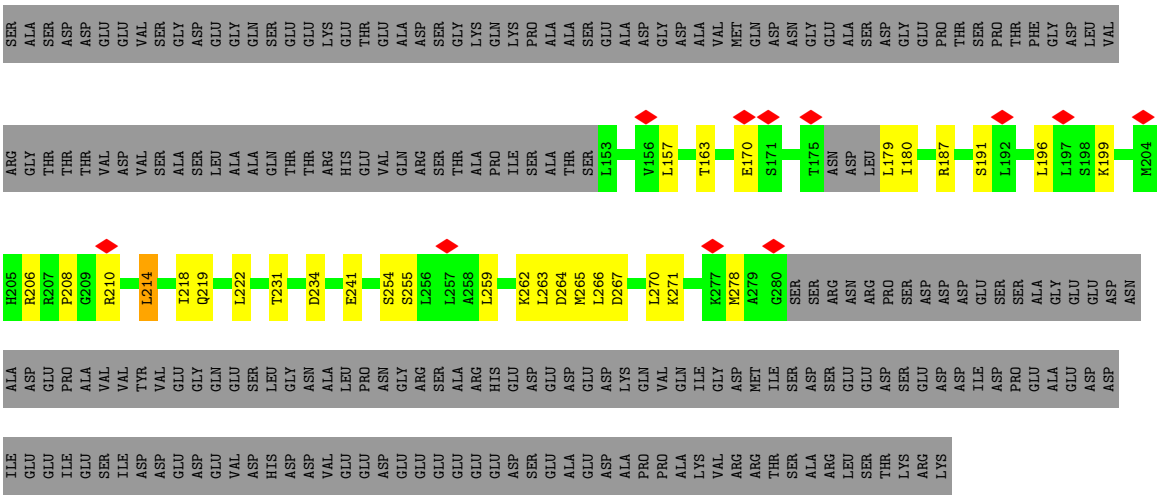
- Molecule 55: Utp8

Chain UH:



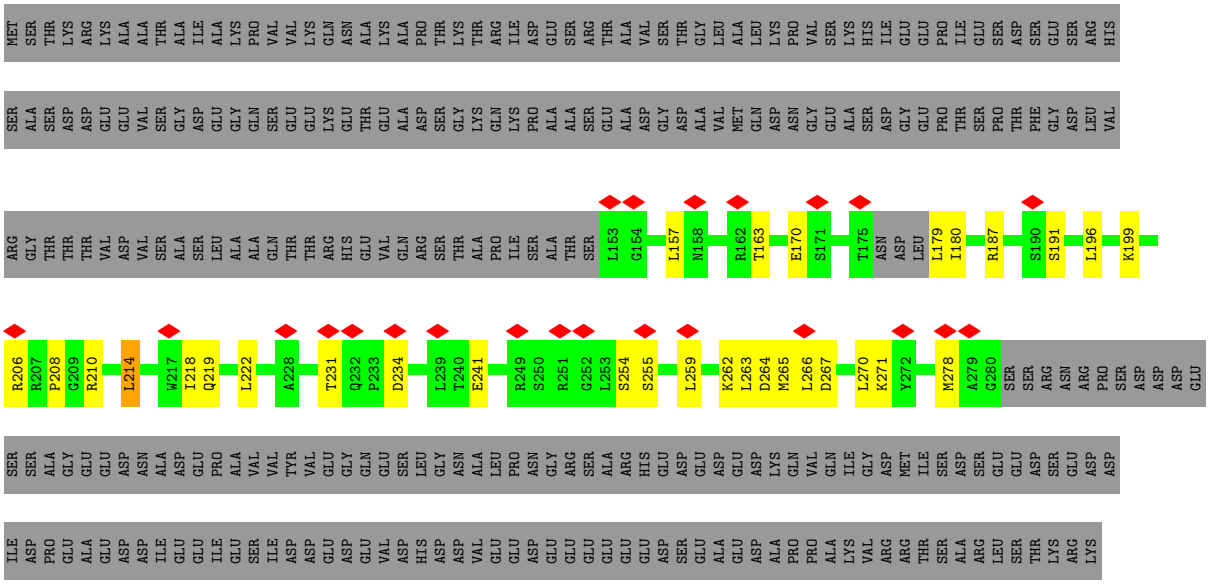
- Molecule 56: Utp5

Chain UE:



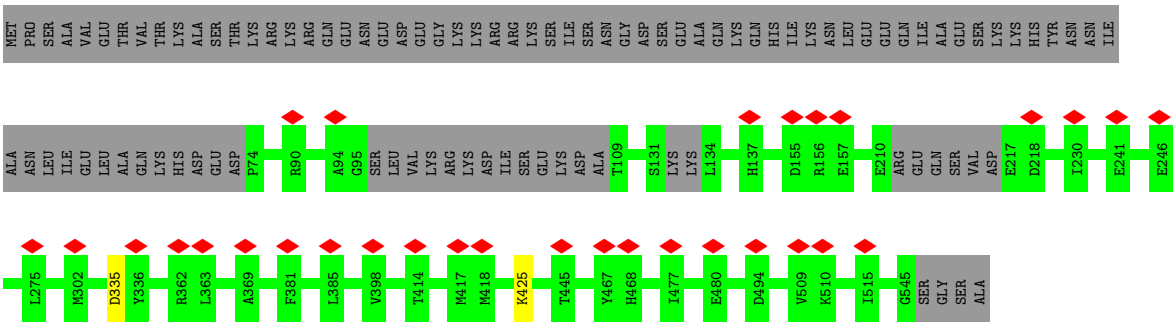
• Molecule 56: Utp5

Chain UI:



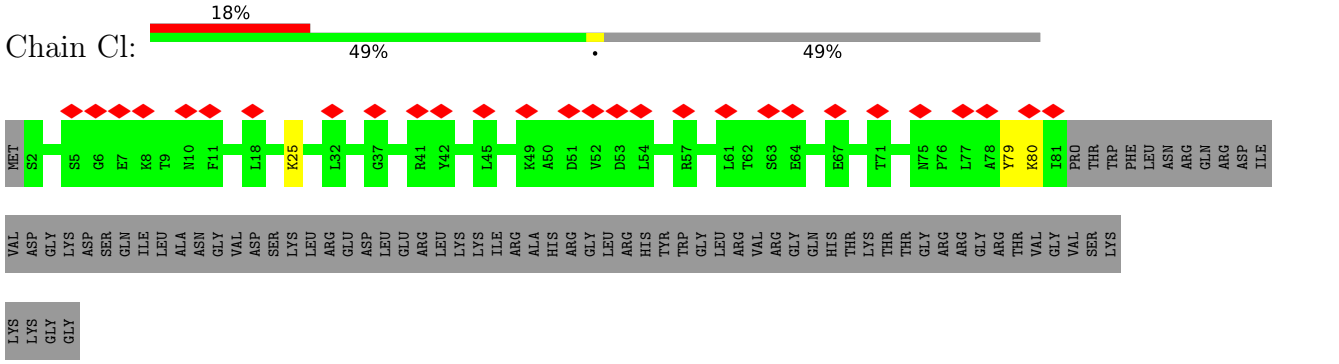
• Molecule 57: Noc4

Chain US:



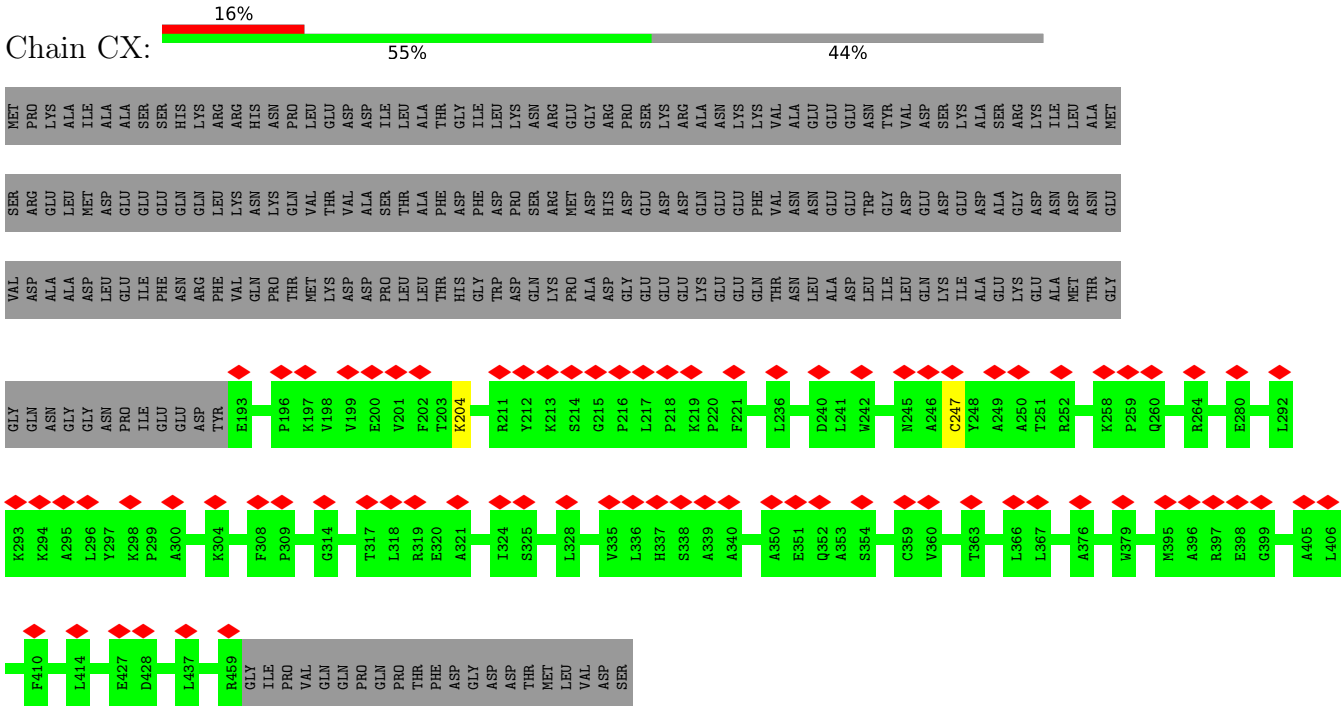
• Molecule 58: Rps18

Chain Cl:



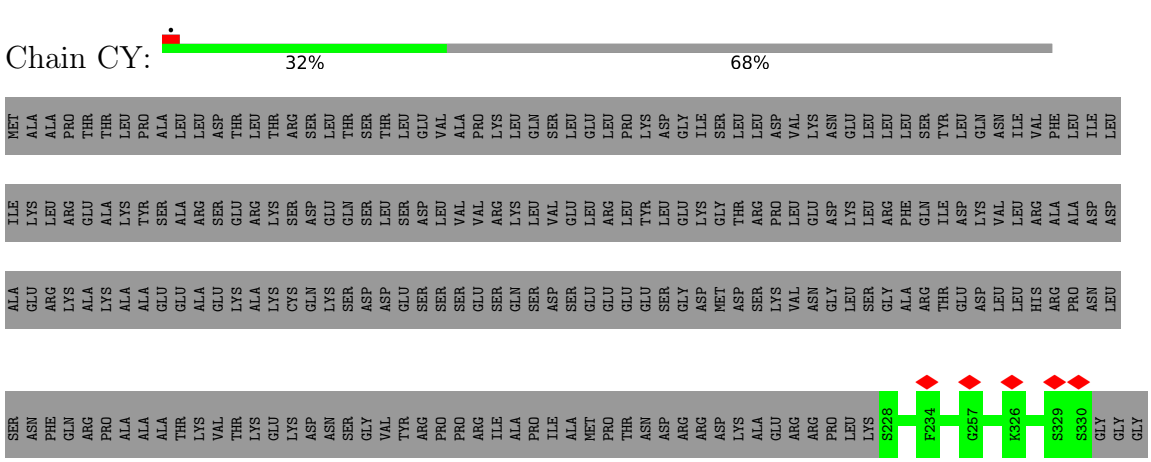
• Molecule 59: Enp1

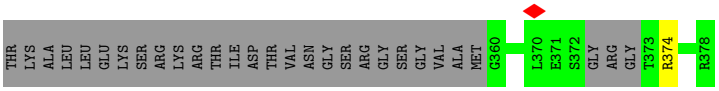
Chain CX:



• Molecule 60: U3 small nucleolar ribonucleoprotein protein lcp5-like protein

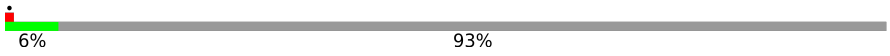
Chain CY:

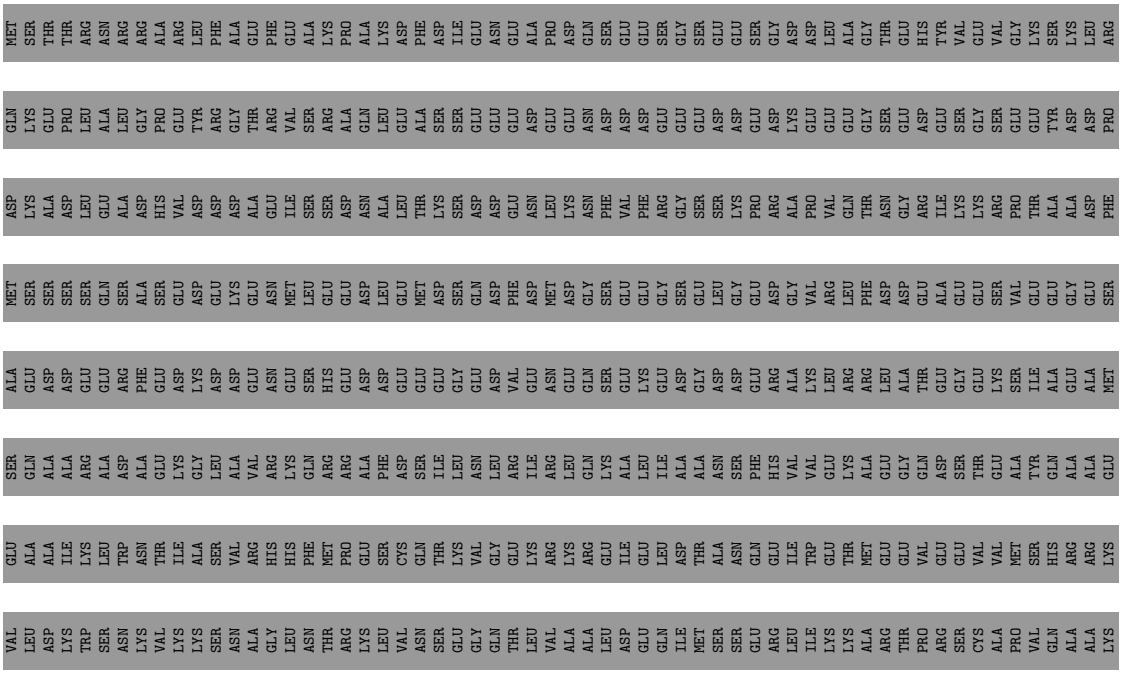




• Molecule 61: Bfr2

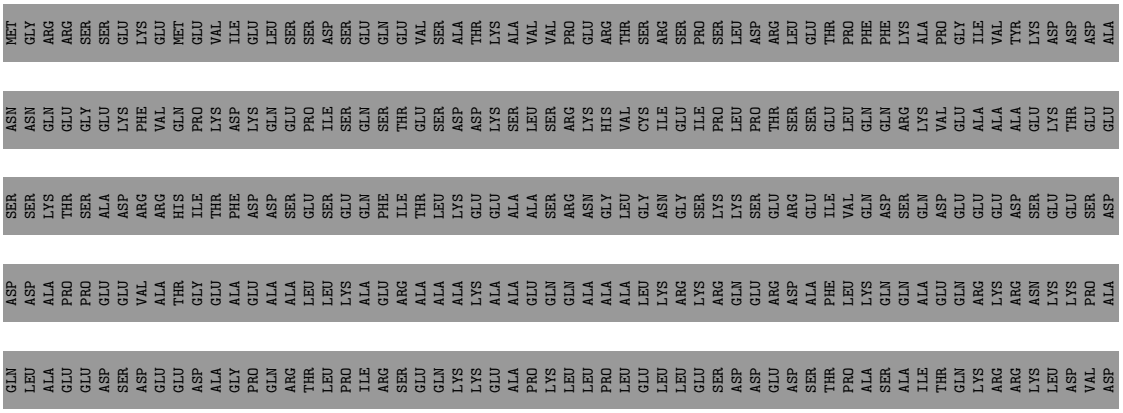
Chain CZ:

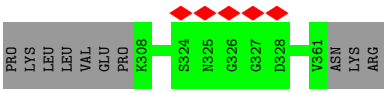




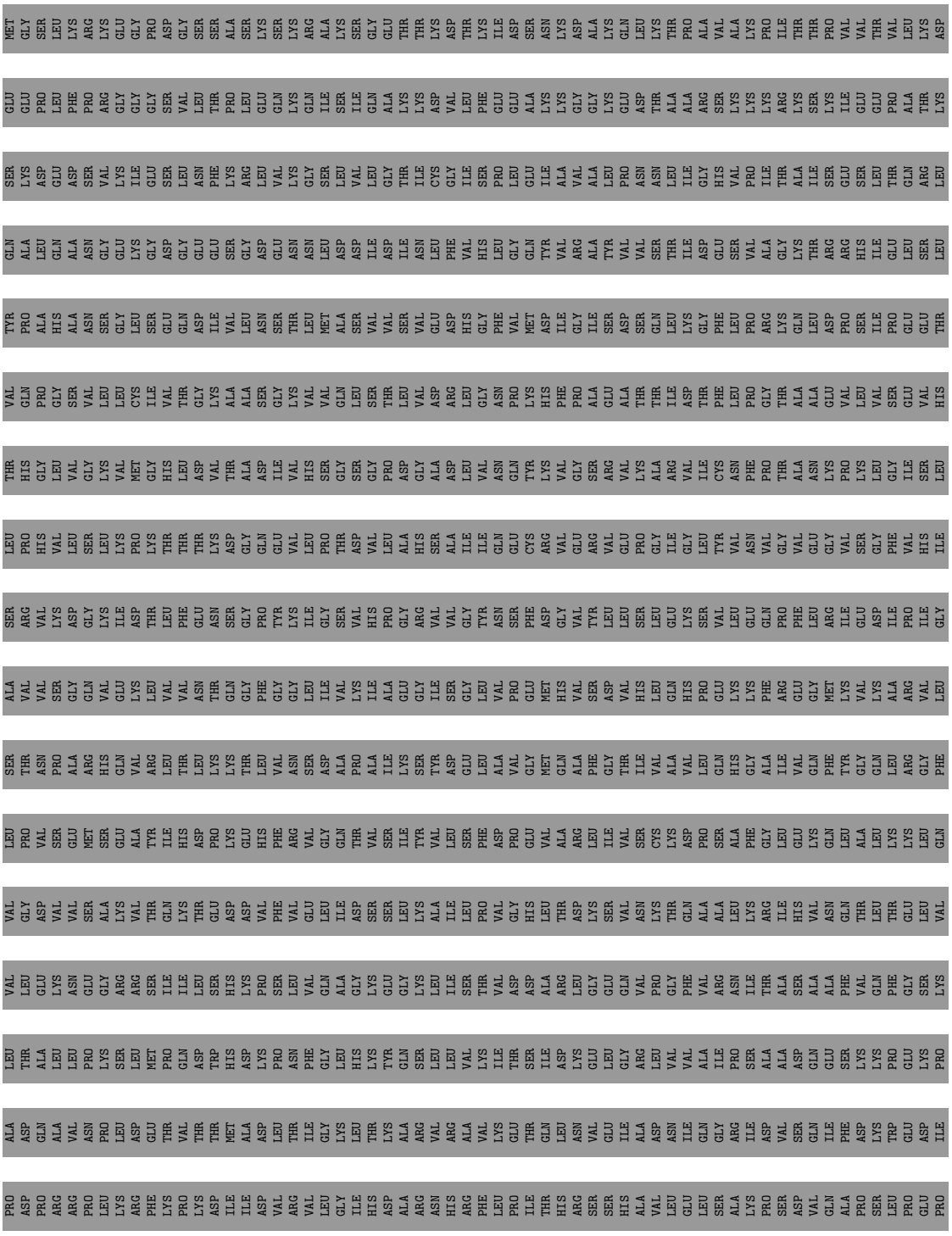
• Molecule 62: Utp16

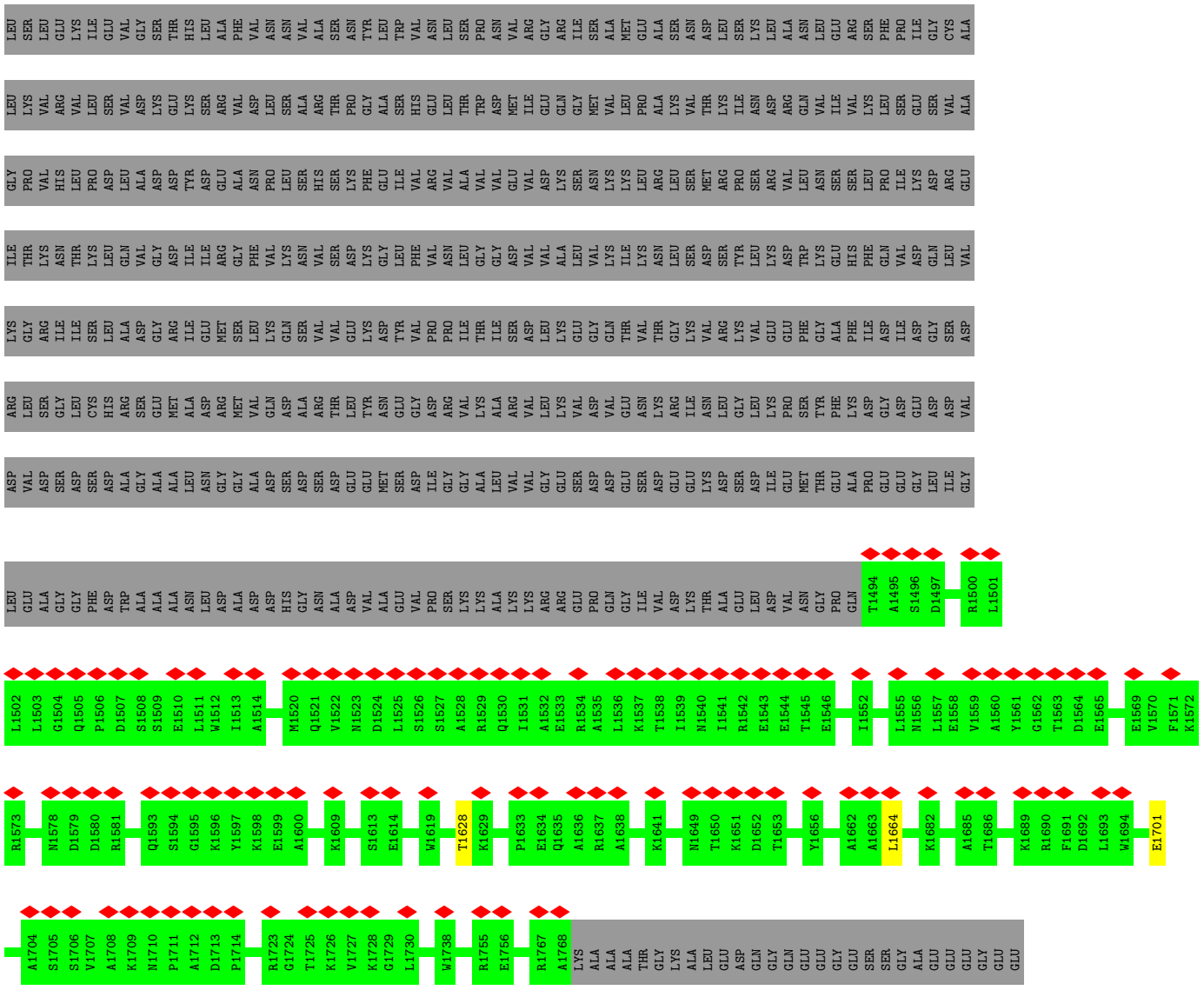
Chain UP:





• Molecule 63: Rrp5




LEU SER LEU GLU LYS ILE GLU VAL GLY SER THR HIS LEU ALA PHE VAL ASN ASN VAL ALA SER ASN TYR LEU TRP VAL ASN LEU SER PRO ASN VAL ARG GLY ARG ILE SER ALA MET GLU ALA SER ASN ASP LEU SER LYS LEU ALA ASN LEU GLU ARG SER PHE PRO ILE GLY CYS ALA
LEU LYS VAL ARG VAL LEU SER VAL ASP LYS GLU LYS SER ARG VAL ASP LEU SER ALA ARG THR PRO GLY ALA SER ILE GLU LEU THR TRP ASP MET ILE GLU GLN GLY MET VAL LEU PRO ALA LYS VAL THR LYS ILE ASN ASP ARG GLN VAL ILE VAL LYS LEU SER GLU SER VAL ALA
GLY PRO VAL HIS LEU PRO ASP LEU ALA ASP ASP TYR ASP GLU ALA ASN PRO LEU SER HIS SER LYS PHE GLU ILE VAL ARG VAL ALA VAL VAL GLU VAL ASP LYS SER ASN LYS LYS LEU ARG LEU SER MET ARG PRO SER ARG VAL LEU ASN ILE SER LEU PRO ILE LYS ASP ARG GLU
ILE THR LYS ASN THR LYS LEU GLN VAL GLY ASP ILE ILE ARG GLY PHE VAL LYS ASN VAL SER ASP LYS GLY LEU PHE VAL ASN LEU GLY GLY ASP VAL VAL ALA LEU VAL LYS ILE LYS ASN LEU SER ASP SER TYR LEU LYS ASP TRP LYS ASP GLN VAL LEU GLU ASP GLN LEU VAL
LYS GLY ARG ILE ILE SER LEU ALA ASP GLY ARG ILE GLU MET SER LEU LYS GLN SER VAL VAL GLU LYS ASP TYR VAL PRO PRO ILE THR ILE SER ASP LEU LYS GLU GLY GLN THR VAL THR GLY LYS VAL ARG LYS LEU VAL GLU GLU PHE GLY ALA PHE ILE ASP ILE ASP GLY GLY SER ASP
ARG LEU SER GLY LEU CYS HIS ARG SER GLU MET ALA ASP ARG MET VAL GLN ASP ALA ARG THR LEU TYR ASN GLU GLY ASP ARG VAL LYS ALA ARG LEU ASP VAL GLU ASN LYS ARG ILE ASN LEU GLY LEU LYS PRO SER TYR PHE LYS ASP GLY ASP GLU ASP ASP VAL
ASP VAL ASP SER ASP SER ASP ALA ALA GLY ALA ALA LEU ASN GLY GLY ALA SER ASP GLU GLU MET SER ASP ILE GLY GLY ALA LEU VAL VAL GLY GLU SER ASP ASP GLU SER ASP GLU GLU LYS ASP SER ASP GLU SER ASP ILE GLU MET THR GLU ALA PRO GLU GLU GLY LEU ILE GLY
LEU GLU ALA GLY GLY PHE ASP TRP ALA ALA ALA ASN LEU ASP ASP HIS GLY ASN ALA ASP VAL ALA GLU VAL PRO SER LYS LYS ALA LYS LYS LYS ARG ARG GLU PRO GLN GLY GLY ILE VAL ASP LYS THR ALA GLU LEU ASP VAL ASN GLY PRO GLN T1494 A1495 S1496 D1497 R1500 L1501
L1502 L1503 G1504 Q1505 P1506 D1507 S1508 S1509 E1510 L1511 W1512 I1513 A1514 M1520 Q1521 V1522 N1523 D1524 L1525 S1526 S1527 A1528 R1529 Q1530 I1531 A1532 E1533 R1534 A1535 L1536 K1537 T1538 I1539 N1540 I1541 R1542 E1543 E1544 T1545 E1546 I1552 L1555 N1556 L1557 E1558 V1559 A1560 Y1561 G1562 T1563 D1564 E1565 E1569 V1570 F1571 K1572
R1573 N1578 D1579 D1580 R1581 Q1593 S1594 G1595 K1596 Y1597 K1598 E1599 A1600 K1609 S1613 E1614 W1619 T1628 K1629 P1633 E1634 Q1635 A1636 R1637 A1638 K1641 N1649 T1650 K1651 D1652 T1653 Y1656 A1662 A1663 L1664 K1682 A1685 T1686 K1689 R1690 F1691 D1692 L1693 W1694 E1701
A1704 S1705 S1706 V1707 A1708 K1709 N1710 P1711 A1712 D1713 P1714 R1723 G1724 T1725 K1726 V1727 K1728 G1729 L1730 W1738 R1755 E1756 R1767 A1768 LYS ALA ALA ALA THR GLY LYS ALA LEU GLU ASP GLN GLY GLN GLU GLU GLY GLU SER SER GLY ALA GLU GLU GLU GLY GLU GLU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24283	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 ($e^-/Å^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.834	Depositor
Minimum map value	-0.505	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	UA	0.55	2/6521 (0.0%)	0.71	2/8867 (0.0%)
2	UB	0.37	0/4154	0.56	1/5583 (0.0%)
3	UC	0.59	0/595	0.65	0/786
4	UD	0.33	0/6211	0.58	1/8408 (0.0%)
5	UF	0.34	0/2657	0.53	0/3596
6	UG	0.49	0/3790	0.65	1/5120 (0.0%)
7	UJ	0.33	0/8567	0.59	2/11619 (0.0%)
8	UK	0.64	2/1701 (0.1%)	0.67	1/2251 (0.0%)
9	UL	0.34	0/6299	0.63	2/8531 (0.0%)
10	UM	0.30	0/5366	0.59	2/7282 (0.0%)
11	UN	0.38	0/1425	0.57	1/1913 (0.1%)
12	UO	0.36	0/3903	0.61	1/5312 (0.0%)
13	UQ	0.32	0/6136	0.59	3/8348 (0.0%)
14	UR	0.40	0/3564	0.61	0/4816
15	UU	0.43	0/6903	0.63	2/9392 (0.0%)
16	UX	0.61	0/1493	0.70	1/2011 (0.0%)
17	UZ	0.40	0/1857	0.62	0/2526
18	CA	0.53	0/1814	0.65	1/2456 (0.0%)
18	CB	0.36	0/1853	0.59	0/2511
19	CC	0.38	0/2911	0.58	1/3937 (0.0%)
20	CD	0.37	0/3205	0.62	1/4338 (0.0%)
21	CE	0.46	0/891	0.60	0/1214
21	CF	0.40	0/876	0.66	0/1195
22	CG	0.34	0/3307	0.60	0/4462
23	CH	0.42	0/2939	0.64	1/3988 (0.0%)
24	CI	0.59	3/6631 (0.0%)	0.70	4/8943 (0.0%)
25	CJ	0.74	1/1462 (0.1%)	0.76	0/1967
26	CK	0.71	1/2376 (0.0%)	0.81	3/3214 (0.1%)
27	CL	0.48	0/1812	0.59	0/2437
28	CM	0.56	3/3573 (0.1%)	0.69	1/4829 (0.0%)
29	CN	0.33	0/1797	0.60	0/2443
29	CO	0.32	0/1714	0.60	2/2325 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
30	CP	0.30	0/1528	0.63	1/2057 (0.0%)
31	CQ	0.29	0/1379	0.57	0/1850
32	CR	0.37	1/6108 (0.0%)	0.74	13/8266 (0.2%)
32	CS	0.37	1/6108 (0.0%)	0.74	13/8266 (0.2%)
33	CT	0.53	0/1053	0.62	0/1413
34	Cb	0.31	0/1890	0.59	0/2548
35	Cc	0.44	0/1485	0.59	0/2008
36	Cd	0.32	0/1850	0.58	0/2474
37	Ce	0.35	0/1298	0.67	1/1750 (0.1%)
38	Cf	0.30	0/1429	0.56	0/1915
39	Cg	0.46	0/1259	0.60	0/1687
40	Ch	0.28	0/412	0.57	0/549
41	Ci	0.31	0/801	0.60	0/1087
42	Cj	0.58	0/958	0.72	0/1293
43	Ck	0.31	0/1190	0.53	0/1592
44	Cm	0.40	0/1001	0.59	0/1345
45	Cn	0.81	2/712 (0.3%)	0.79	0/954
46	Co	0.34	0/754	0.59	0/1011
47	Cp	0.34	0/458	0.65	0/617
48	CU	0.35	0/887	0.61	1/1178 (0.1%)
49	C1	0.83	45/35454 (0.1%)	1.37	556/55209 (1.0%)
50	C2	0.88	3/5459 (0.1%)	1.47	88/8498 (1.0%)
51	UV	0.33	0/8638	0.66	6/11725 (0.1%)
52	CV	0.34	0/1172	0.71	0/1592
53	CW	0.32	0/2996	0.63	1/4075 (0.0%)
54	UT	0.31	0/16314	0.57	4/22075 (0.0%)
55	UH	0.34	0/2852	0.60	3/3846 (0.1%)
56	UE	0.38	0/980	0.78	2/1316 (0.2%)
56	UI	0.38	0/980	0.78	2/1316 (0.2%)
57	US	0.33	0/3765	0.56	1/5100 (0.0%)
58	Cl	0.32	0/638	0.65	0/857
59	CX	0.27	0/2172	0.51	0/2946
60	CY	0.36	0/982	0.61	0/1298
61	CZ	0.33	0/362	0.73	1/483 (0.2%)
62	UP	0.33	0/428	0.57	0/570
63	Cz	0.31	0/2310	0.54	0/3120
All	All	0.51	64/226365 (0.0%)	0.84	727/314506 (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
1	UA	0	10
5	UF	0	1
6	UG	0	2
8	UK	0	2
9	UL	0	2
10	UM	0	4
11	UN	0	1
12	UO	0	1
13	UQ	0	2
15	UU	0	4
16	UX	0	2
17	UZ	0	2
18	CB	0	1
21	CE	0	1
21	CF	0	2
23	CH	0	1
24	CI	0	6
25	CJ	0	2
26	CK	0	1
28	CM	0	1
29	CO	0	2
32	CR	0	1
32	CS	0	1
37	Ce	0	1
41	Ci	0	1
42	Cj	0	3
45	Cn	0	1
46	Co	0	1
51	UV	0	4
52	CV	0	2
54	UT	0	5
55	UH	0	1
58	Cl	0	1
60	CY	0	1
63	Cz	0	1
All	All	0	74

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	UA	488	TRP	CB-CG	-8.05	1.35	1.50
50	C2	57	A	N7-C5	-7.73	1.34	1.39
32	CS	515	GLN	CA-CB	7.33	1.70	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	CR	515	GLN	CA-CB	7.33	1.70	1.53
49	C1	1154	A	N9-C4	-6.99	1.33	1.37

The worst 5 of 727 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
50	C2	2	G	O5'-P-OP1	-32.38	71.84	110.70
50	C2	2	G	OP1-P-OP2	-26.27	80.19	119.60
24	CI	995	VAL	C-N-CA	19.84	171.29	121.70
50	C2	2	G	O5'-P-OP2	17.99	132.29	110.70
49	C1	2074	C	N1-C2-O2	16.01	128.50	118.90

There are no chirality outliers.

5 of 74 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	UA	273	GLY	Peptide
1	UA	320	GLY	Peptide
1	UA	386	THR	Peptide
1	UA	424	GLU	Peptide
1	UA	443	GLY	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	
1	UA	835/904 (92%)	733 (88%)	102 (12%)	0	100	100
2	UB	502/907 (55%)	472 (94%)	30 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	UC	72/648 (11%)	58 (81%)	14 (19%)	0	100	100
4	UD	754/884 (85%)	708 (94%)	46 (6%)	0	100	100
5	UF	325/414 (78%)	303 (93%)	21 (6%)	1 (0%)	41	76
6	UG	475/558 (85%)	433 (91%)	39 (8%)	3 (1%)	25	65
7	UJ	1062/1802 (59%)	1000 (94%)	62 (6%)	0	100	100
8	UK	211/270 (78%)	196 (93%)	15 (7%)	0	100	100
9	UL	767/962 (80%)	704 (92%)	63 (8%)	0	100	100
10	UM	645/912 (71%)	595 (92%)	49 (8%)	1 (0%)	47	81
11	UN	171/938 (18%)	161 (94%)	9 (5%)	1 (1%)	25	65
12	UO	498/557 (89%)	459 (92%)	39 (8%)	0	100	100
13	UQ	775/960 (81%)	703 (91%)	71 (9%)	1 (0%)	51	85
14	UR	437/618 (71%)	400 (92%)	37 (8%)	0	100	100
15	UU	890/1049 (85%)	797 (90%)	93 (10%)	0	100	100
16	UX	188/193 (97%)	172 (92%)	16 (8%)	0	100	100
17	UZ	229/391 (59%)	206 (90%)	23 (10%)	0	100	100
18	CA	238/313 (76%)	218 (92%)	20 (8%)	0	100	100
18	CB	235/313 (75%)	216 (92%)	19 (8%)	0	100	100
19	CC	383/523 (73%)	361 (94%)	22 (6%)	0	100	100
20	CD	416/582 (72%)	384 (92%)	32 (8%)	0	100	100
21	CE	119/127 (94%)	112 (94%)	7 (6%)	0	100	100
21	CF	118/127 (93%)	109 (92%)	9 (8%)	0	100	100
22	CG	402/630 (64%)	366 (91%)	36 (9%)	0	100	100
23	CH	383/411 (93%)	344 (90%)	38 (10%)	1 (0%)	41	76
24	CI	812/1163 (70%)	732 (90%)	80 (10%)	0	100	100
25	CJ	177/183 (97%)	154 (87%)	23 (13%)	0	100	100
26	CK	295/297 (99%)	255 (86%)	40 (14%)	0	100	100
27	CL	225/785 (29%)	205 (91%)	20 (9%)	0	100	100
28	CM	443/446 (99%)	402 (91%)	41 (9%)	0	100	100
29	CN	222/252 (88%)	202 (91%)	20 (9%)	0	100	100
29	CO	211/252 (84%)	196 (93%)	13 (6%)	2 (1%)	17	56
30	CP	185/322 (58%)	181 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	CQ	171/259 (66%)	165 (96%)	6 (4%)	0	100	100
32	CR	746/1073 (70%)	692 (93%)	54 (7%)	0	100	100
32	CS	746/1073 (70%)	692 (93%)	54 (7%)	0	100	100
33	CT	127/203 (63%)	111 (87%)	16 (13%)	0	100	100
34	Cb	230/264 (87%)	211 (92%)	19 (8%)	0	100	100
35	Cc	188/212 (89%)	166 (88%)	22 (12%)	0	100	100
36	Cd	224/239 (94%)	208 (93%)	16 (7%)	0	100	100
37	Ce	155/203 (76%)	145 (94%)	10 (6%)	0	100	100
38	Cf	170/202 (84%)	162 (95%)	8 (5%)	0	100	100
39	Cg	157/190 (83%)	149 (95%)	8 (5%)	0	100	100
40	Ch	47/151 (31%)	47 (100%)	0	0	100	100
41	Ci	113/150 (75%)	100 (88%)	13 (12%)	0	100	100
42	Cj	124/143 (87%)	109 (88%)	15 (12%)	0	100	100
43	Ck	136/161 (84%)	131 (96%)	5 (4%)	0	100	100
44	Cm	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
45	Cn	92/145 (63%)	83 (90%)	9 (10%)	0	100	100
46	Co	90/136 (66%)	82 (91%)	8 (9%)	0	100	100
47	Cp	59/68 (87%)	55 (93%)	4 (7%)	0	100	100
48	CU	106/311 (34%)	99 (93%)	7 (7%)	0	100	100
51	UV	1057/1171 (90%)	948 (90%)	108 (10%)	1 (0%)	51	85
52	CV	144/322 (45%)	129 (90%)	14 (10%)	1 (1%)	22	62
53	CW	380/668 (57%)	349 (92%)	31 (8%)	0	100	100
54	UT	1982/2612 (76%)	1878 (95%)	100 (5%)	4 (0%)	47	81
55	UH	349/930 (38%)	335 (96%)	14 (4%)	0	100	100
56	UE	121/410 (30%)	111 (92%)	9 (7%)	1 (1%)	19	60
56	UI	121/410 (30%)	111 (92%)	9 (7%)	1 (1%)	19	60
57	US	443/549 (81%)	420 (95%)	23 (5%)	0	100	100
58	Cl	78/156 (50%)	74 (95%)	4 (5%)	0	100	100
59	CX	265/480 (55%)	251 (95%)	14 (5%)	0	100	100
60	CY	118/381 (31%)	109 (92%)	9 (8%)	0	100	100
61	CZ	40/609 (7%)	32 (80%)	8 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
62	UP	52/364 (14%)	45 (86%)	7 (14%)	0	100 100
63	Cz	273/1796 (15%)	261 (96%)	12 (4%)	0	100 100
All	All	22926/35864 (64%)	21113 (92%)	1795 (8%)	18 (0%)	54 85

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	UG	176	LEU
29	CO	85	SER
51	UV	1059	ASP
54	UT	487	ILE
5	UF	121	LYS

5.3.2 Protein sidechains (i)

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
1	UA	651/775 (84%)	647 (99%)	4 (1%)	86 92
2	UB	425/788 (54%)	423 (100%)	2 (0%)	88 93
3	UC	61/536 (11%)	61 (100%)	0	100 100
4	UD	653/738 (88%)	650 (100%)	3 (0%)	88 93
5	UF	248/341 (73%)	246 (99%)	2 (1%)	81 89
6	UG	373/474 (79%)	371 (100%)	2 (0%)	88 93
7	UJ	898/1526 (59%)	890 (99%)	8 (1%)	78 88
8	UK	159/227 (70%)	156 (98%)	3 (2%)	57 75
9	UL	667/821 (81%)	665 (100%)	2 (0%)	92 95
10	UM	569/770 (74%)	567 (100%)	2 (0%)	91 94
11	UN	146/765 (19%)	146 (100%)	0	100 100
12	UO	404/456 (89%)	401 (99%)	3 (1%)	84 90
13	UQ	650/817 (80%)	650 (100%)	0	100 100
14	UR	360/524 (69%)	359 (100%)	1 (0%)	92 95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
15	UU	672/863 (78%)	668 (99%)	4 (1%)	86 92
16	UX	150/167 (90%)	147 (98%)	3 (2%)	55 73
17	UZ	186/329 (56%)	184 (99%)	2 (1%)	73 85
18	CA	175/228 (77%)	172 (98%)	3 (2%)	60 78
18	CB	195/228 (86%)	195 (100%)	0	100 100
19	CC	287/435 (66%)	286 (100%)	1 (0%)	92 95
20	CD	319/489 (65%)	318 (100%)	1 (0%)	92 95
21	CE	91/108 (84%)	91 (100%)	0	100 100
21	CF	88/108 (82%)	88 (100%)	0	100 100
22	CG	331/525 (63%)	329 (99%)	2 (1%)	86 92
23	CH	303/320 (95%)	298 (98%)	5 (2%)	60 78
24	CI	661/1009 (66%)	653 (99%)	8 (1%)	71 84
25	CJ	147/169 (87%)	147 (100%)	0	100 100
26	CK	245/266 (92%)	241 (98%)	4 (2%)	62 79
27	CL	181/642 (28%)	181 (100%)	0	100 100
28	CM	364/383 (95%)	361 (99%)	3 (1%)	81 89
29	CN	202/223 (91%)	202 (100%)	0	100 100
29	CO	193/223 (86%)	190 (98%)	3 (2%)	62 79
30	CP	164/287 (57%)	163 (99%)	1 (1%)	86 92
31	CQ	145/215 (67%)	145 (100%)	0	100 100
32	CR	654/916 (71%)	512 (78%)	142 (22%)	1 6
32	CS	654/916 (71%)	512 (78%)	142 (22%)	1 6
33	CT	108/167 (65%)	108 (100%)	0	100 100
34	Cb	199/221 (90%)	198 (100%)	1 (0%)	88 93
35	Cc	149/178 (84%)	145 (97%)	4 (3%)	44 66
36	Cd	192/204 (94%)	191 (100%)	1 (0%)	88 93
37	Ce	137/177 (77%)	135 (98%)	2 (2%)	65 80
38	Cf	139/164 (85%)	138 (99%)	1 (1%)	84 90
39	Cg	122/162 (75%)	122 (100%)	0	100 100
40	Ch	41/130 (32%)	40 (98%)	1 (2%)	49 69
41	Ci	74/117 (63%)	73 (99%)	1 (1%)	67 81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
42	Cj	92/115 (80%)	91 (99%)	1 (1%)	73 85
43	Ck	126/143 (88%)	125 (99%)	1 (1%)	81 89
44	Cm	103/113 (91%)	102 (99%)	1 (1%)	76 86
45	Cn	70/116 (60%)	69 (99%)	1 (1%)	67 81
46	Co	79/115 (69%)	78 (99%)	1 (1%)	69 82
47	Cp	46/61 (75%)	46 (100%)	0	100 100
48	CU	92/260 (35%)	91 (99%)	1 (1%)	73 85
51	UV	908/989 (92%)	895 (99%)	13 (1%)	67 81
52	CV	129/276 (47%)	127 (98%)	2 (2%)	62 79
53	CW	309/587 (53%)	307 (99%)	2 (1%)	86 92
54	UT	1724/2276 (76%)	1715 (100%)	9 (0%)	88 93
55	UH	301/788 (38%)	298 (99%)	3 (1%)	76 86
56	UE	105/346 (30%)	76 (72%)	29 (28%)	0 3
56	UI	105/346 (30%)	76 (72%)	29 (28%)	0 3
57	US	404/493 (82%)	403 (100%)	1 (0%)	93 96
58	Cl	71/135 (53%)	69 (97%)	2 (3%)	43 65
59	CX	225/411 (55%)	223 (99%)	2 (1%)	78 88
60	CY	100/322 (31%)	100 (100%)	0	100 100
61	CZ	36/519 (7%)	34 (94%)	2 (6%)	21 48
62	UP	44/314 (14%)	44 (100%)	0	100 100
63	Cz	235/1533 (15%)	233 (99%)	2 (1%)	78 88
All	All	19136/30385 (63%)	18667 (98%)	469 (2%)	50 68

5 of 469 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	CS	77	LYS
56	UI	191	SER
32	CS	471	GLU
56	UI	157	LEU
55	UH	624	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 279 such sidechains are listed below:

Mol	Chain	Res	Type
54	UT	377	GLN
54	UT	971	ASN
57	US	152	HIS
17	UZ	110	ASN
16	UX	63	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	C1	1461/2323 (62%)	559 (38%)	35 (2%)
50	C2	226/230 (98%)	86 (38%)	6 (2%)
All	All	1687/2553 (66%)	645 (38%)	41 (2%)

5 of 645 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
49	C1	4	G
49	C1	5	G
49	C1	7	A
49	C1	13	G
49	C1	14	G

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	C1	1734	G
50	C2	23	A
49	C1	2054	A
49	C1	2156	A
50	C2	35	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
50	C2	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C2	206:G	O3'	240:C	P	18.94
1	C2	105:C	O3'	110:A	P	15.09
1	C2	119:C	O3'	123:A	P	11.47

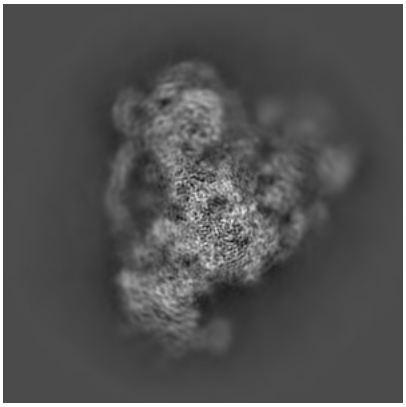
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10056. These allow visual inspection of the internal detail of the map and identification of artifacts.

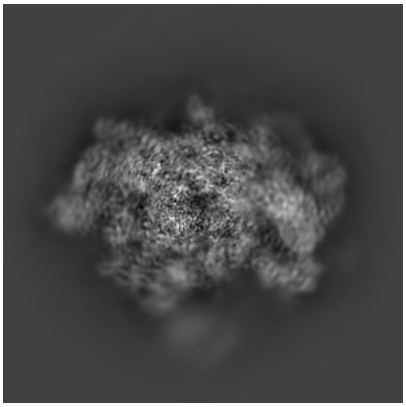
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

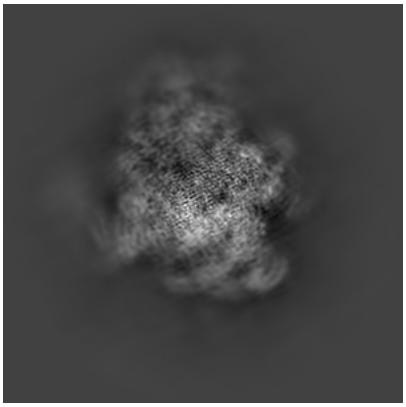
6.1.1 Primary map



X



Y

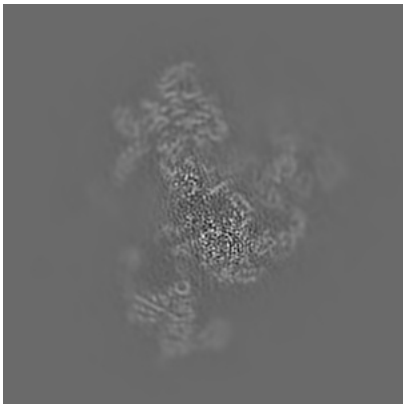


Z

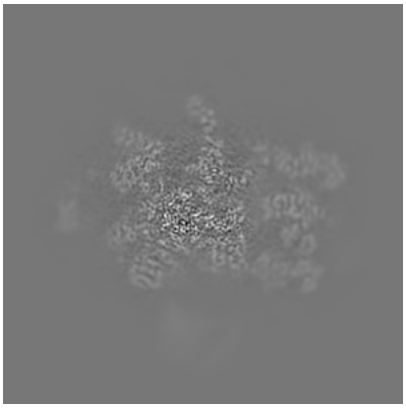
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map



X Index: 240



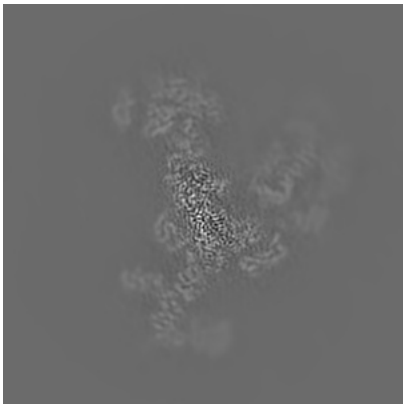
Y Index: 240

Z Index: 240

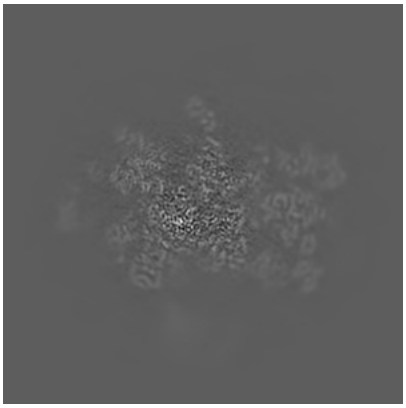
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

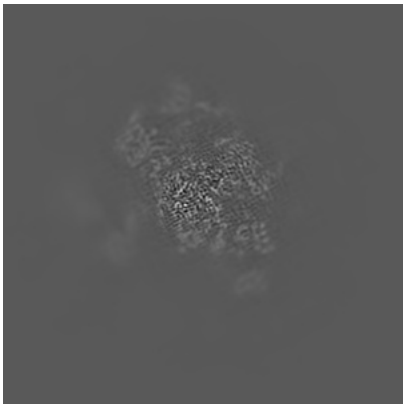
6.3.1 Primary map



X Index: 217



Y Index: 238

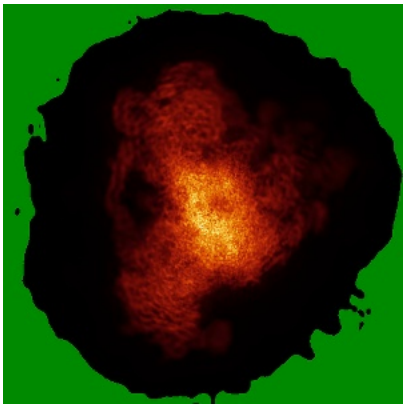


Z Index: 214

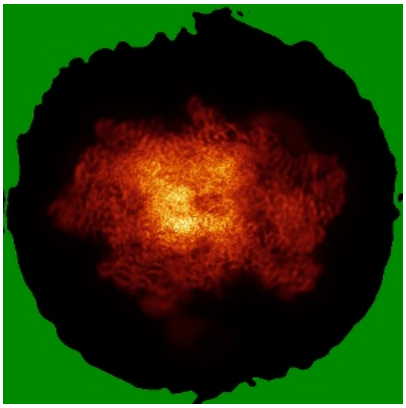
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

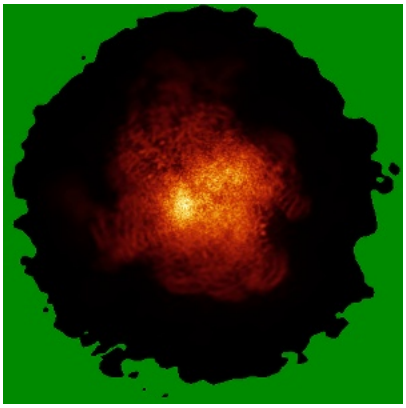
6.4.1 Primary map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

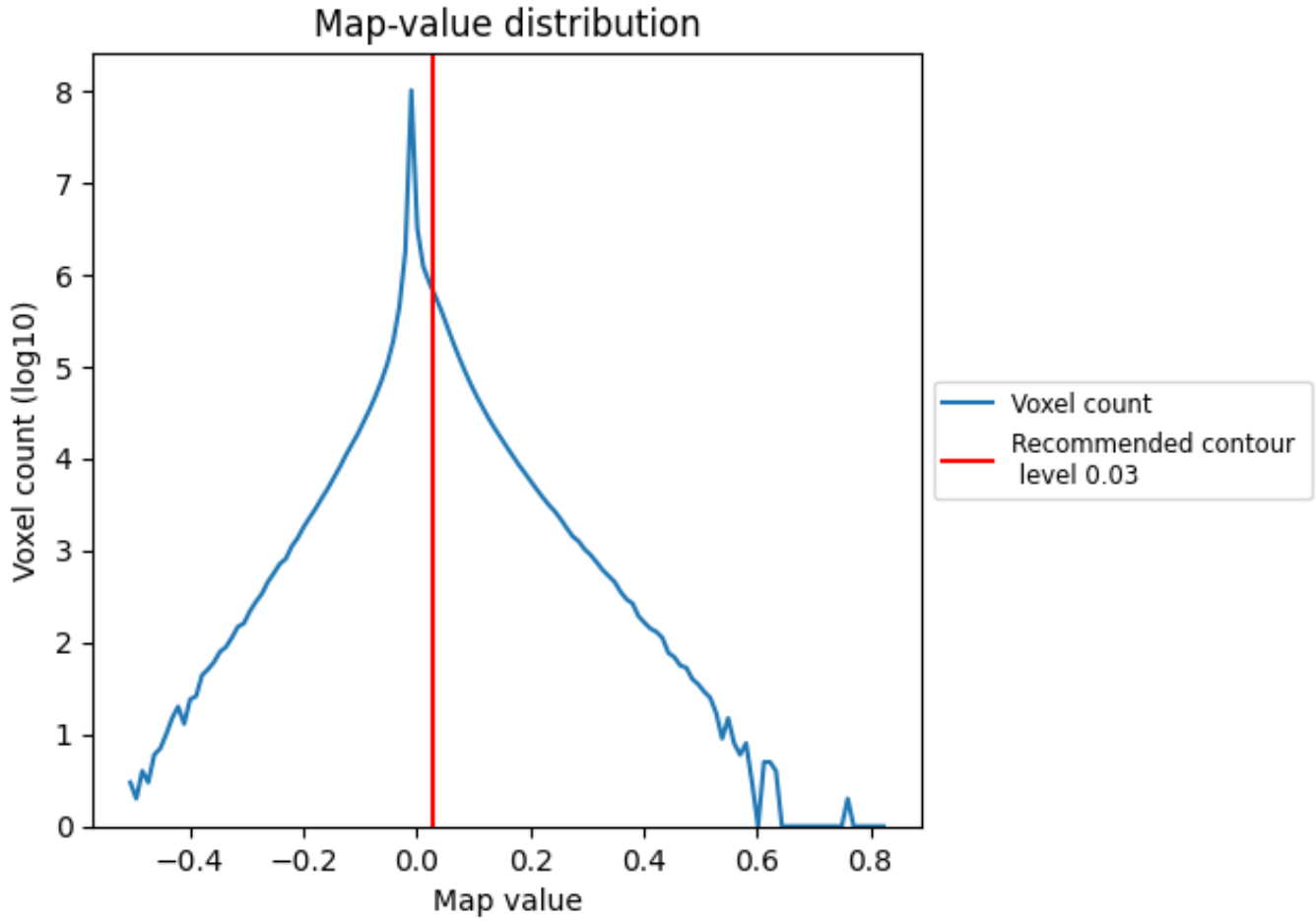
6.6 Mask visualisation (i)

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

7 Map analysis

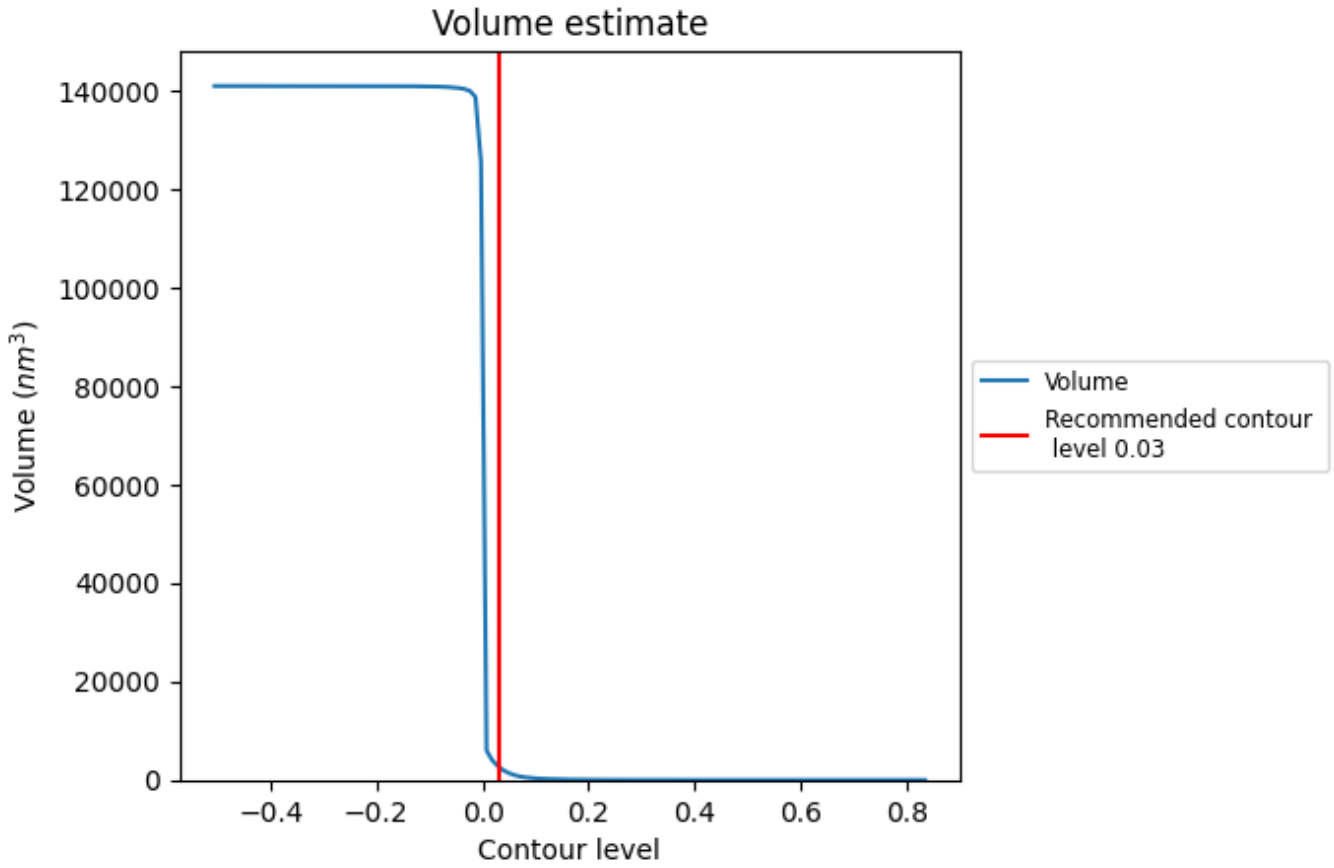
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

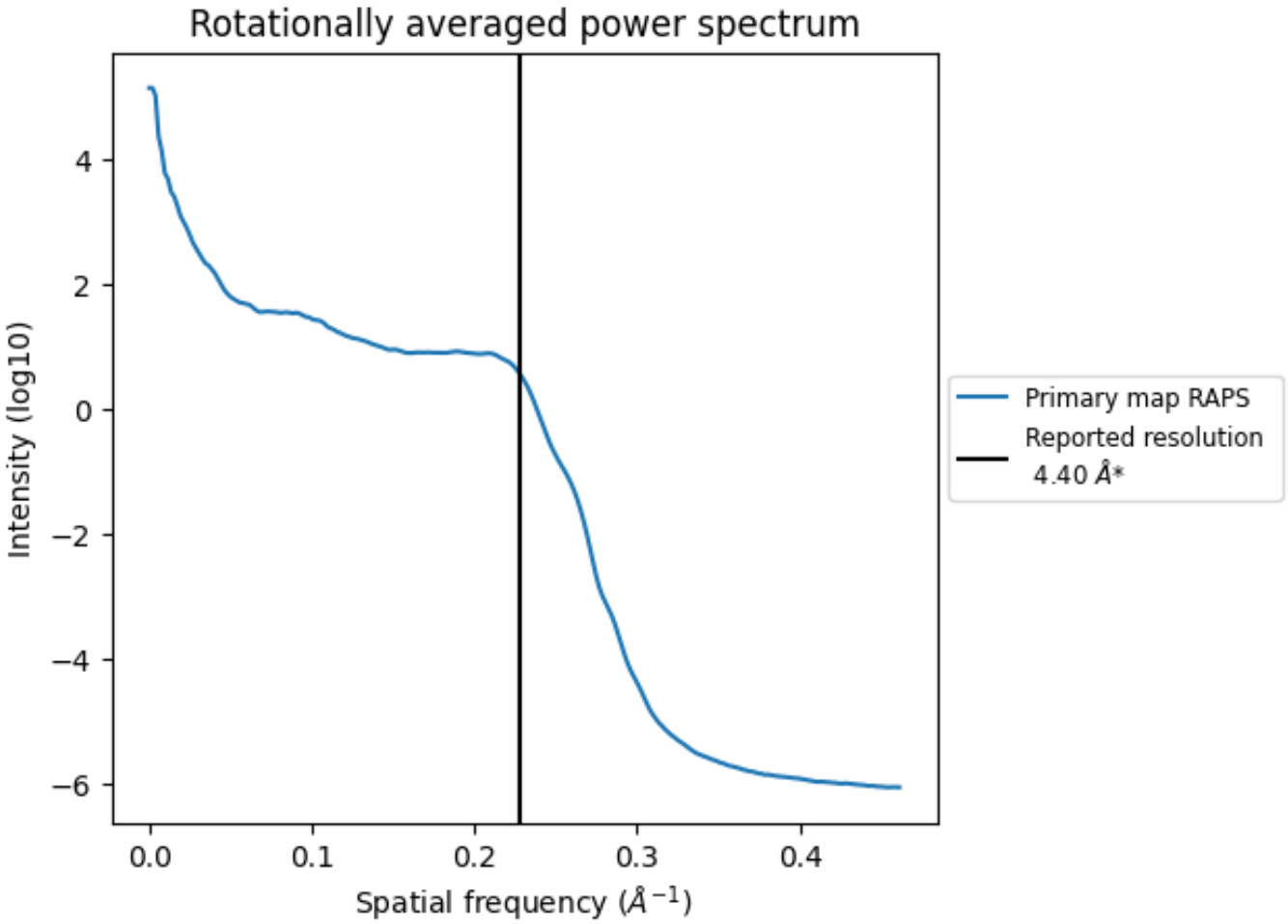
7.2 Volume estimate (i)



The volume at the recommended contour level is 2721 nm^3; this corresponds to an approximate mass of 2458 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 (i)

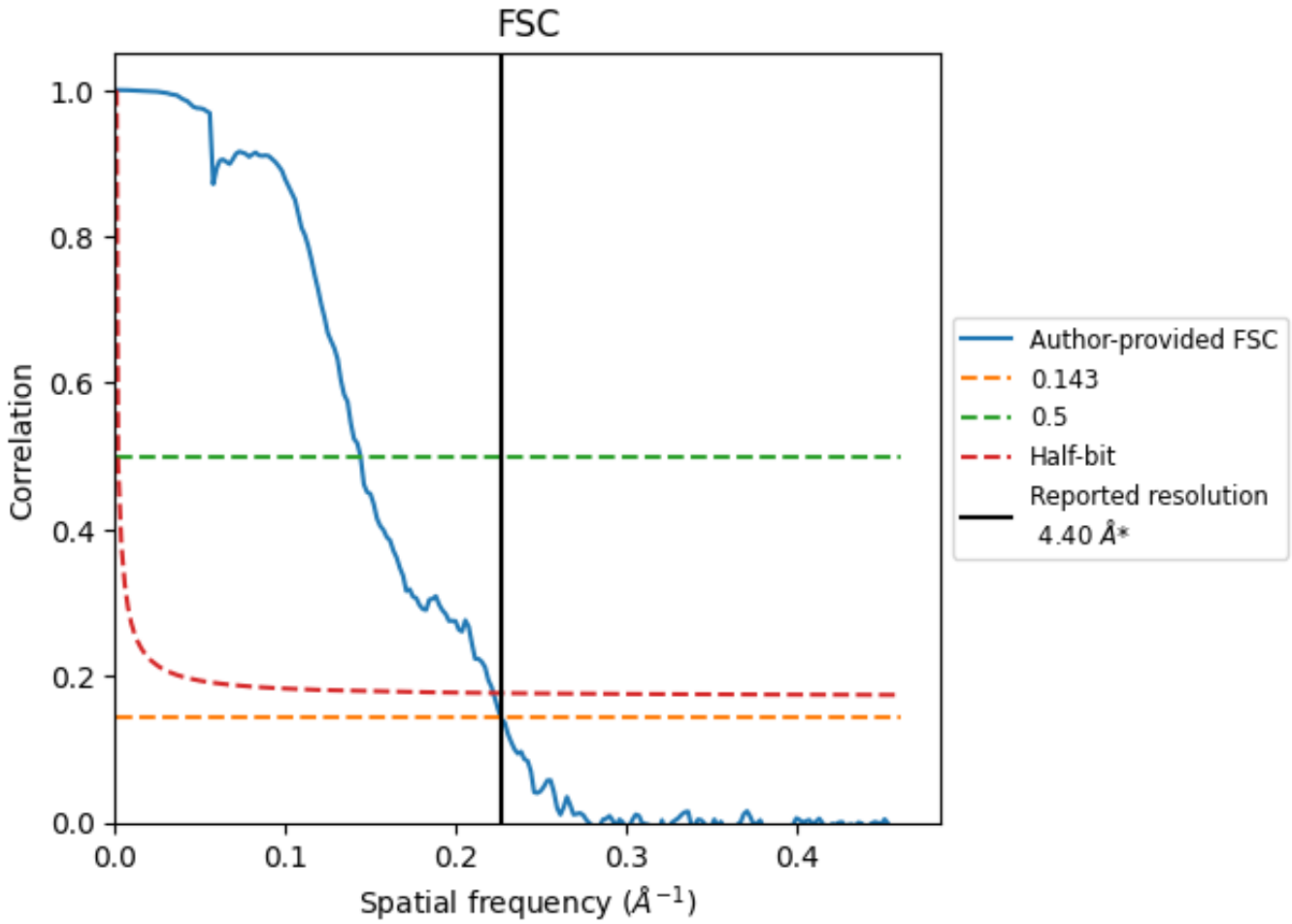


*Reported resolution corresponds to spatial frequency of 0.227 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.227 Å^{-1}

8.2 Resolution estimates (i)

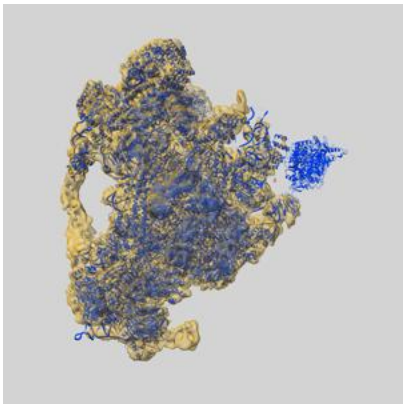
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.42	6.93	4.50
Unmasked-calculated*	-	-	-

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

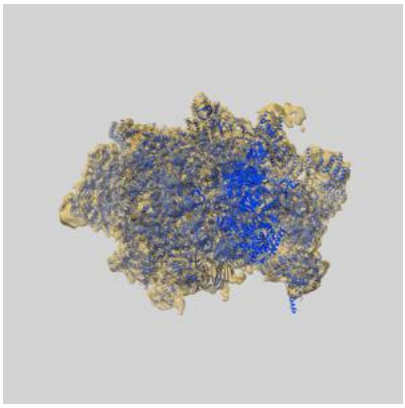
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10056 and PDB model 6RXZ. Per-residue inclusion information can be found in section 3 on page 16.

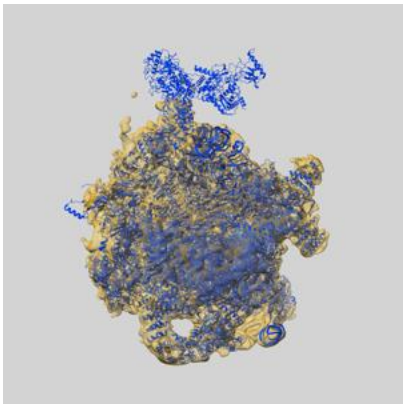
9.1 Map-model overlay



X



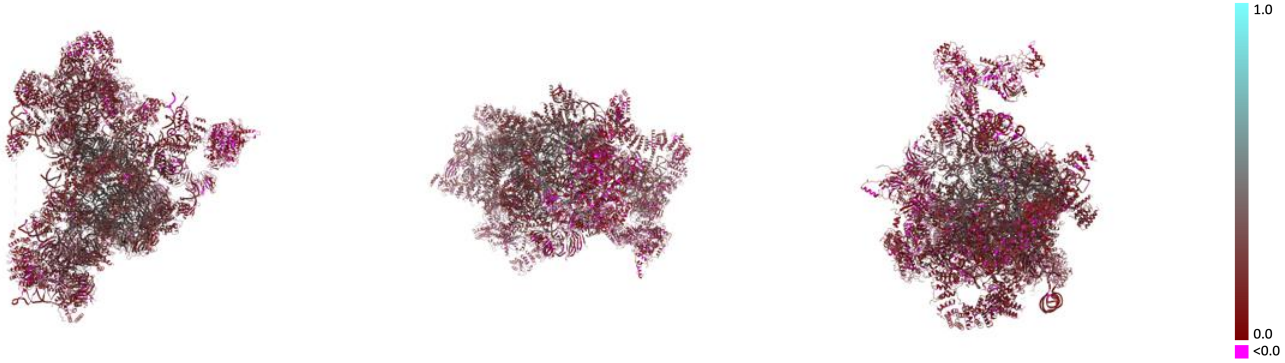
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03 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.

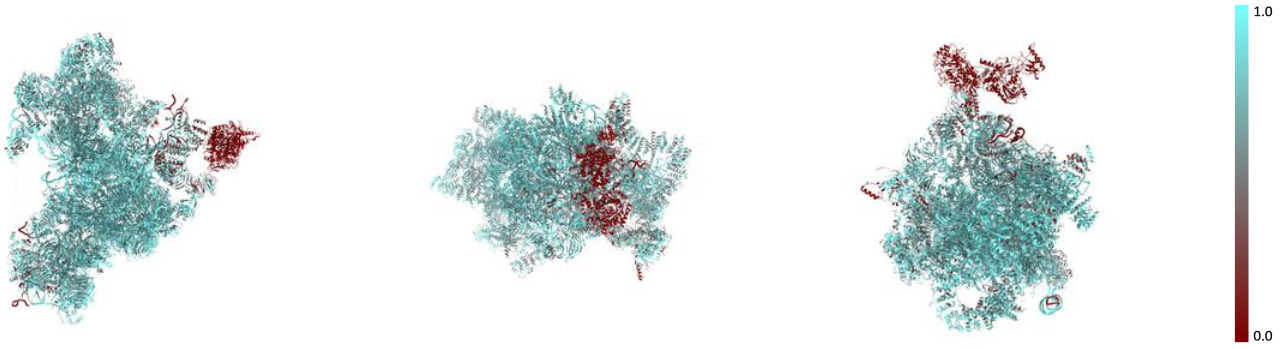
9.2 Q-score mapped to coordinate model



X Y Z

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.

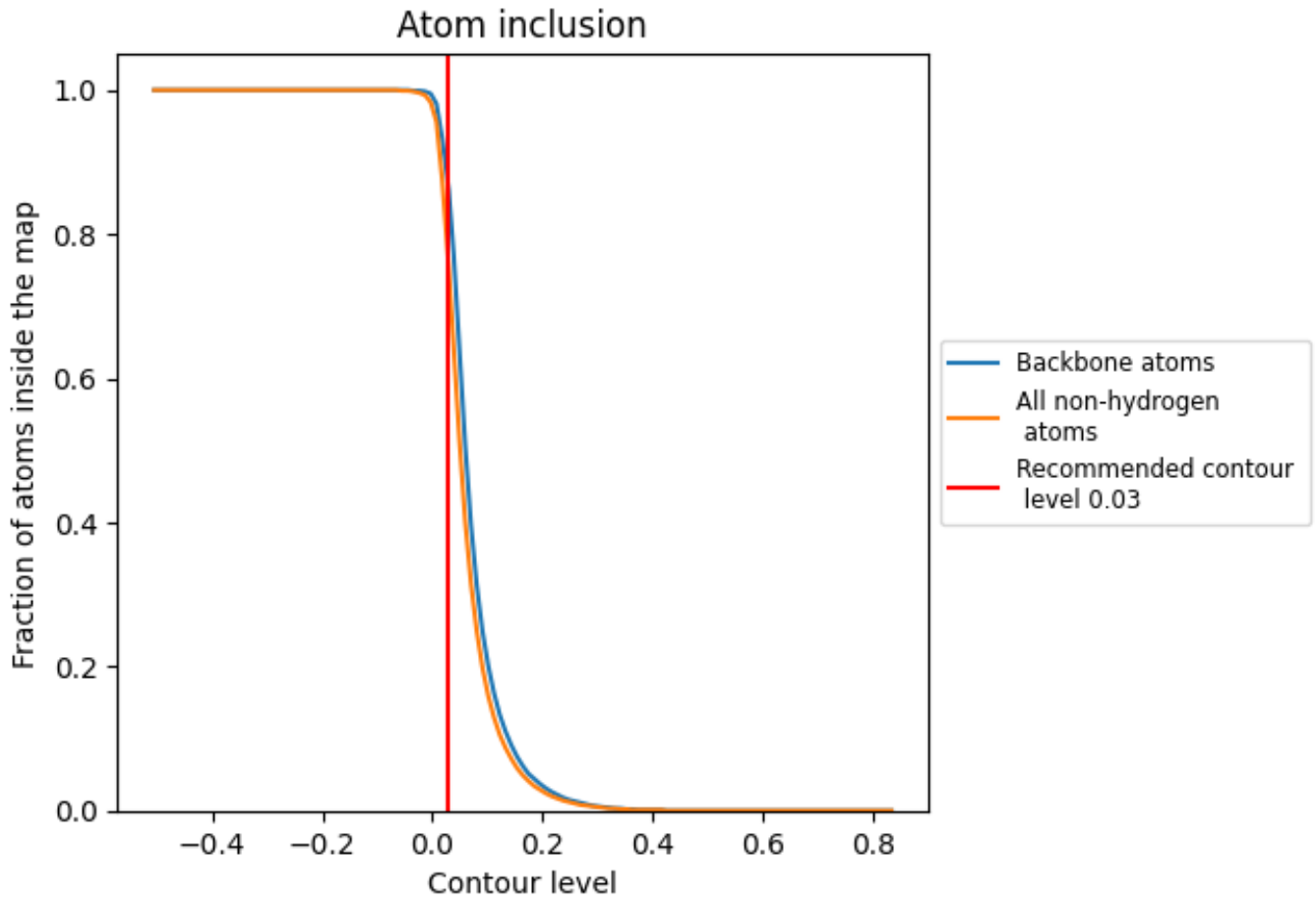
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.03).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 75% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7520	0.2270
C1	0.8700	0.2580
C2	0.9050	0.2760
CA	0.8720	0.3590
CB	0.7420	0.2130
CC	0.8130	0.2470
CD	0.7940	0.2420
CE	0.8610	0.3370
CF	0.8180	0.2680
CG	0.7830	0.2070
CH	0.8130	0.2770
CI	0.8790	0.3550
CJ	0.9150	0.4170
CK	0.8980	0.4110
CL	0.8390	0.3190
CM	0.8580	0.3350
CN	0.7370	0.2190
CO	0.6650	0.1760
CP	0.5340	0.1610
CQ	0.7250	0.1670
CR	0.7260	0.1710
CS	0.6120	0.1210
CT	0.8940	0.3680
CU	0.7960	0.2810
CV	0.0000	0.0660
CW	0.7380	0.1660
CX	0.6190	0.1010
CY	0.7510	0.2410
CZ	0.6960	0.1540
Cb	0.7140	0.1810
Cc	0.8230	0.2950
Cd	0.7370	0.1700
Ce	0.5820	0.1730
Cf	0.7440	0.1410
Cg	0.8540	0.3460

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Chain	Atom inclusion	Q-score
Ch	0.5340	0.1030
Ci	0.6460	0.1590
Cj	0.8910	0.4000
Ck	0.6730	0.1430
Cl	0.5030	0.2250
Cm	0.7760	0.2740
Cn	0.9170	0.4400
Co	0.7560	0.2010
Cp	0.8020	0.2540
Cz	0.4380	0.1550
UA	0.8580	0.3350
UB	0.7750	0.2200
UC	0.8880	0.3970
UD	0.7720	0.2150
UE	0.7200	0.1650
UF	0.8260	0.2180
UG	0.8040	0.3170
UH	0.7480	0.1680
UI	0.6510	0.1390
UJ	0.7460	0.2010
UK	0.8760	0.3630
UL	0.7580	0.1780
UM	0.6520	0.1240
UN	0.7670	0.2770
UO	0.7730	0.2240
UP	0.7540	0.2410
UQ	0.7900	0.2070
UR	0.8520	0.3000
US	0.7560	0.1660
UT	0.7440	0.1570
UU	0.8530	0.2850
UV	0.0030	0.0740
UX	0.8960	0.4090
UZ	0.8150	0.2630