



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 06:49 PM UTC

PDB ID : 7D5S / pdb_00007d5s
EMDB ID : EMD-30584
Title : Cryo-EM structure of 90S preribosome with inactive Utp24 (state A2)
Authors : Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on : 2020-09-28
Resolution : 4.60 Å (reported)
Based on initial model : 6LQU

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

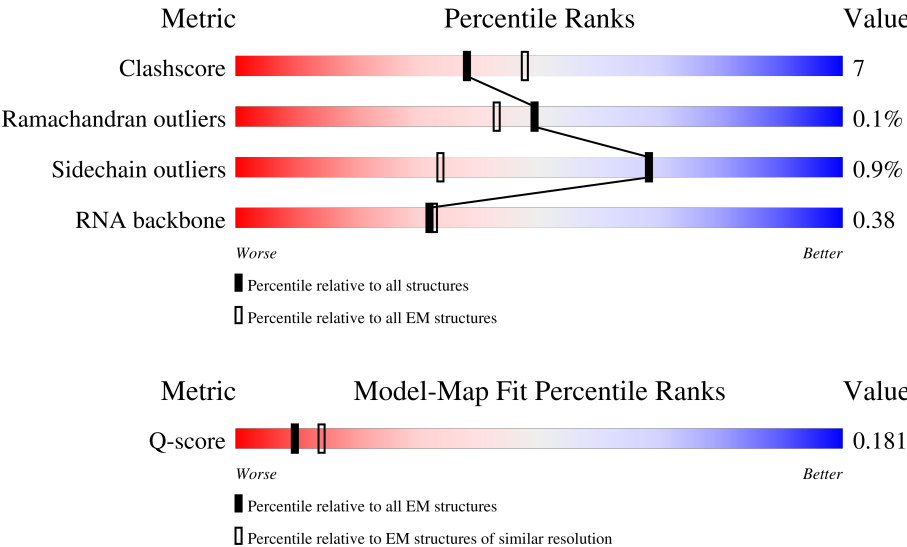
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 Å.

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



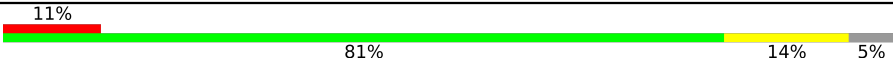
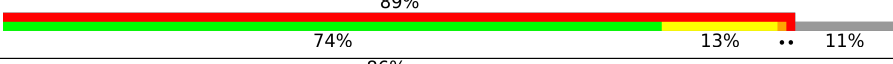
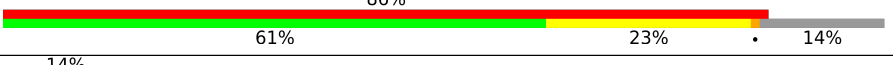
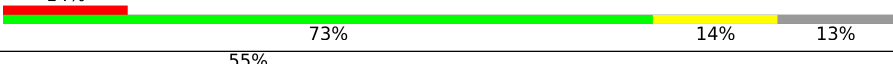
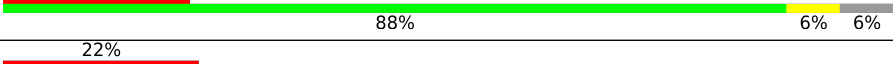
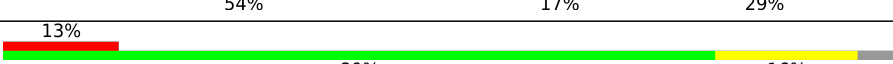
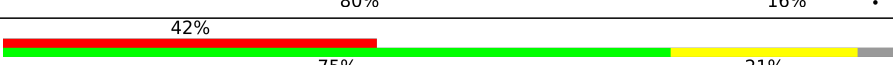
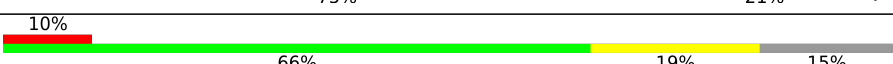
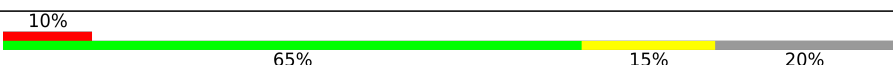
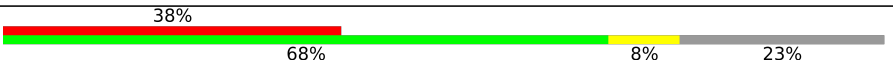
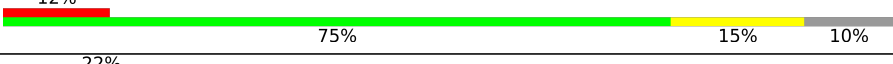
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	1808	

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Mol	Chain	Length	Quality of chain
4	SG	225	
5	SK	197	
6	SN	143	
7	SO	151	
8	SP	137	
9	SR	143	
10	ST	146	
11	SY	145	
12	Sd	67	
13	3B	327	
13	3C	327	
14	3D	504	
15	3E	511	
16	3F	573	
17	3G	126	
17	3H	126	
18	A4	776	
19	A5	643	
20	A8	713	
21	A9	575	
22	AE	1769	
23	AF	513	
24	AG	896	
25	B1	923	
26	B2	943	

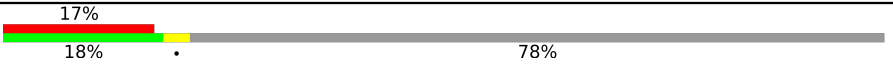
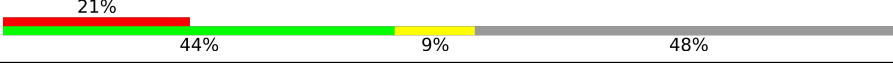
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Mol	Chain	Length	Quality of chain
27	B3	817	
28	B8	594	
29	BE	939	
30	B6	440	
31	5B	214	
32	5C	554	
33	5D	250	
34	5E	593	
35	5F	183	
36	5G	290	
37	5H	610	
38	5I	489	
39	5J	217	
40	5K	189	
41	RC	316	
42	RD	1729	
43	RE	1237	
44	RF	297	
45	RG	252	
45	RH	252	
46	RI	274	
47	RJ	1183	
48	RK	367	
49	RN	810	
50	RO	552	

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Mol	Chain	Length	Quality of chain
51	RQ	899	
52	RS	483	
53	RT	326	
54	RW	206	
55	X1	347	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 179154 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	523	Total	C	N	O	P	0	0
			11163	4988	1984	3668	523		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	859	Total	C	N	O	P	0	0
			18356	8201	3302	5994	859		

- Molecule 4 is a protein called 40S ribosomal protein S5.

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

- Molecule 5 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S12.

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

- Molecule 7 is a protein called 40S ribosomal protein S13.

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

- Molecule 8 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	ST	117	Total	C	N	O	S	0	0
			964	610	184	168	2		

- Molecule 11 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 13 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
13	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 14 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 15 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 16 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3F	406	Total	C	N	O	S	0	0
			3248	2075	566	597	10		

- Molecule 17 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
17	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 4.

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

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 5.

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

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 8.

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

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 9.

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

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AE	649	Total	C	N	O	S	0	0
			5181	3355	849	960	17		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 24 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 25 is a protein called Periodic tryptophan protein 2.

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

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 12.

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

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B3	752	Total	C	N	O	S	0	0
			5882	3746	987	1122	27		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 21.

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

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 31 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	5B	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5C	516	Total	C	N	O	S	0	0
			4084	2561	736	775	12		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 35 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 36 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 37 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	5H	136	Total	C	N	O	S	0	0
			1065	658	211	196			

- Molecule 38 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 39 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 40 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 41 is a protein called KRR1 small subunit processome component.

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

- Molecule 42 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	RD	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 44 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	RF	174	Total	C	N	O	S	0	0
			1404	905	230	261	8		

- Molecule 45 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 46 is a protein called Ribosome biogenesis protein UTP30.

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

- Molecule 47 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	RJ	732	Total	C	N	O	S	0	0
			5953	3829	1057	1041	26		

- Molecule 48 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 49 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RN	607	Total	C	N	O	S	0	0
			4529	2861	820	837	11		

- Molecule 50 is a protein called Nucleolar complex protein 4.

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

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RQ	194	Total	C	N	O	S	0	0
			1436	892	270	272	2		

- Molecule 52 is a protein called Essential nuclear protein 1.

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

- Molecule 53 is a protein called Pno1.

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

- Molecule 54 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	RW	63	Total	C	N	O	0	0
			381	234	69	78		

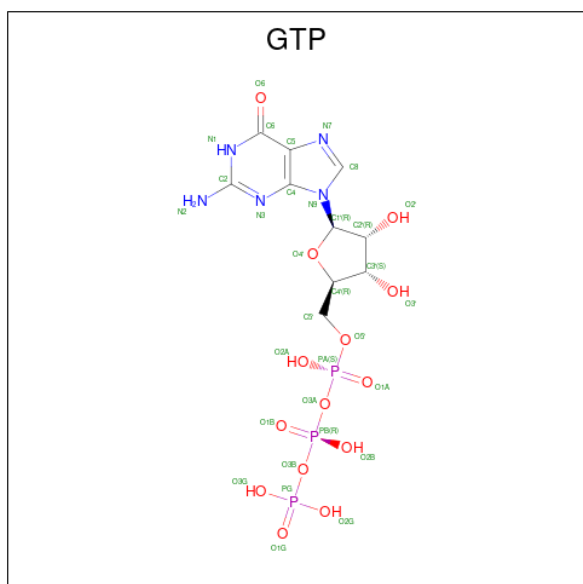
- Molecule 55 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	X1	61	Total	C	N	O	0	0
			305	183	61	61		

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
56	5K	1	Total Zn 1 1	0

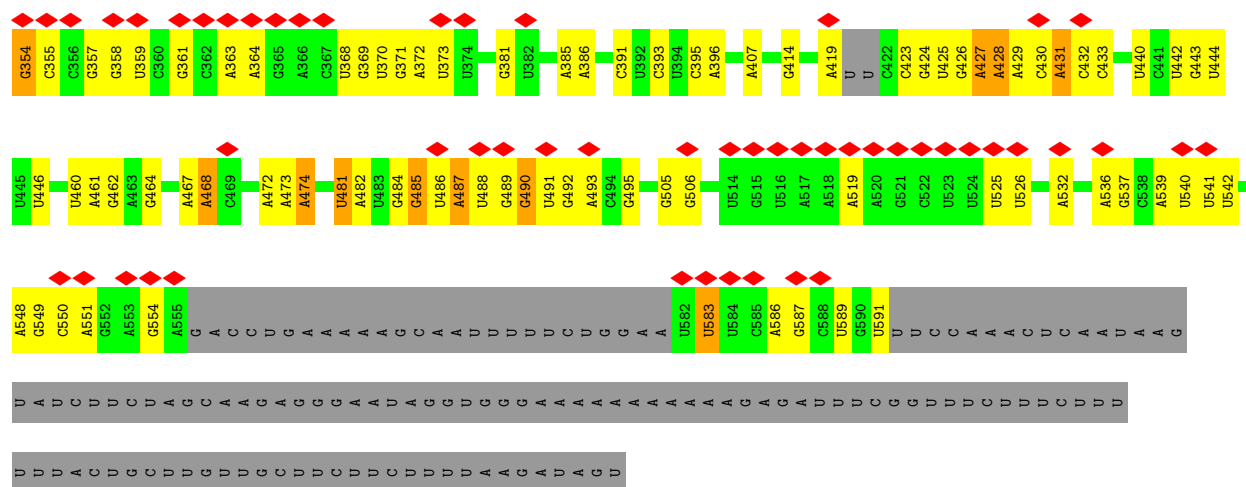
- Molecule 57 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



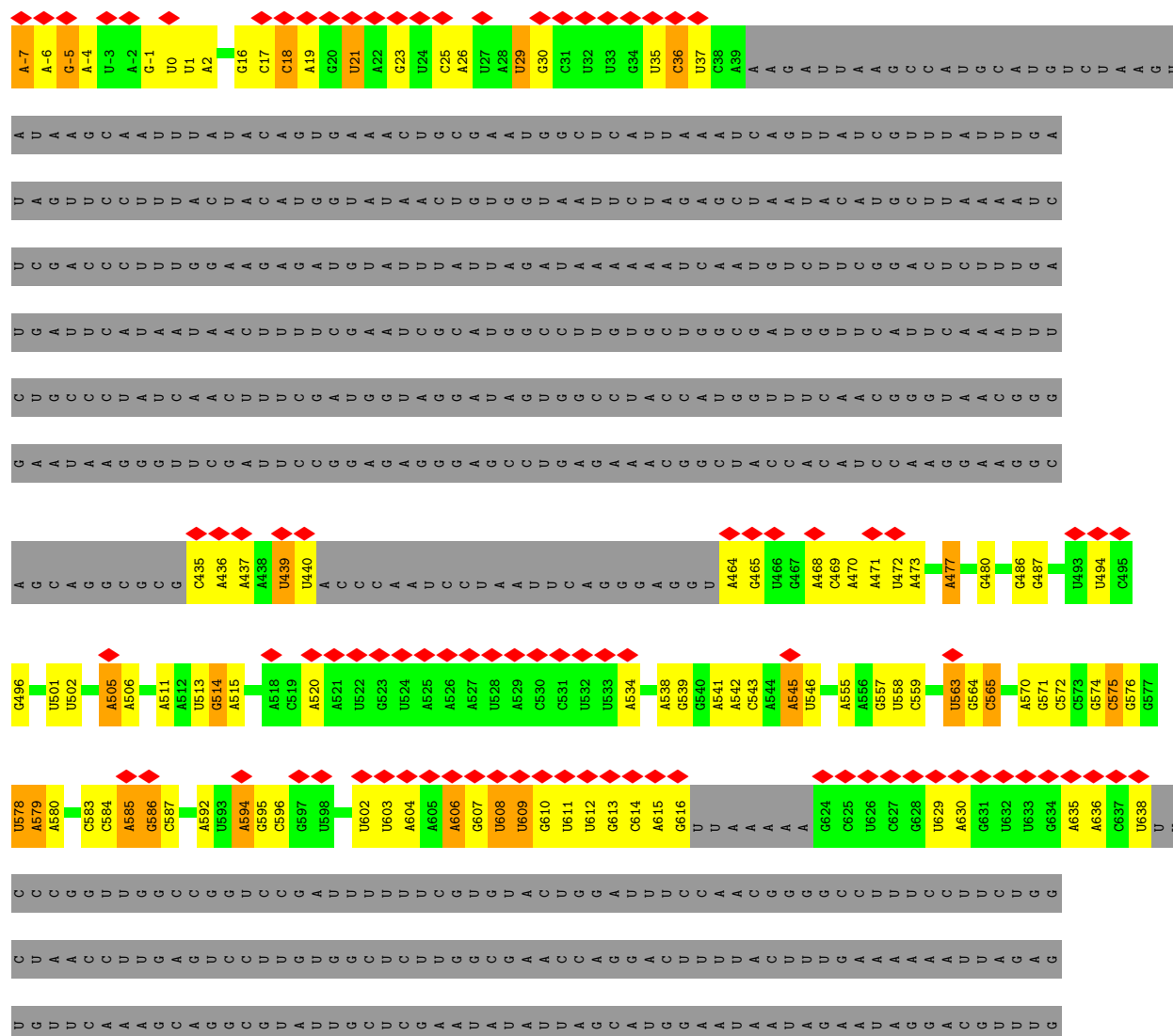
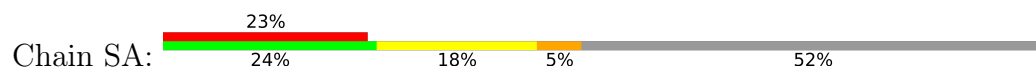
Mol	Chain	Residues	Atoms					AltConf
57	RJ	1	Total 32	C 10	N 5	O 14	P 3	0

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

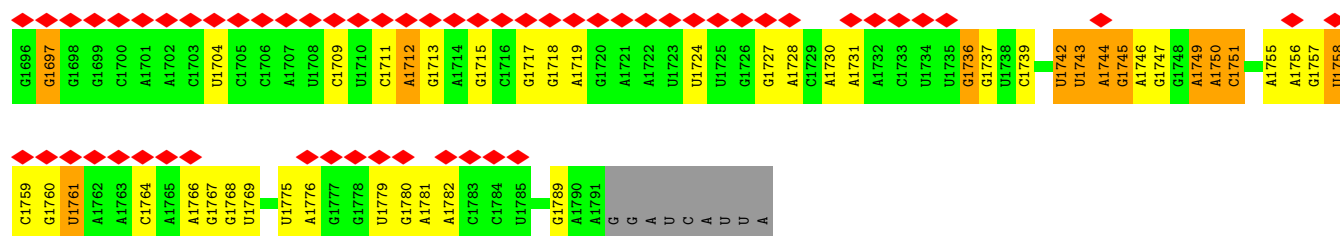
Mol	Chain	Residues	Atoms		AltConf
58	RJ	1	Total	Mg	0
			1	1	



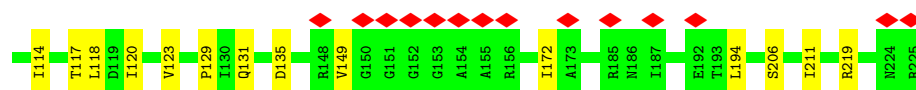
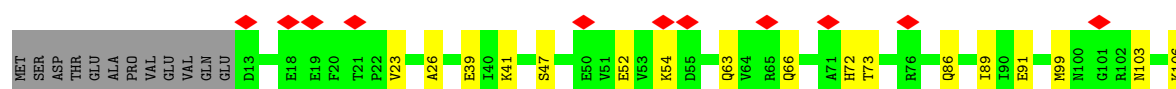
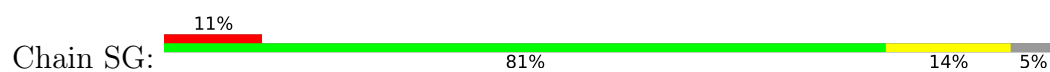
• Molecule 3: 18S rRNA



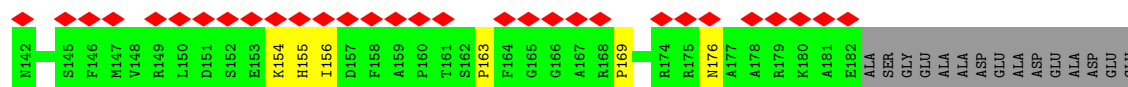
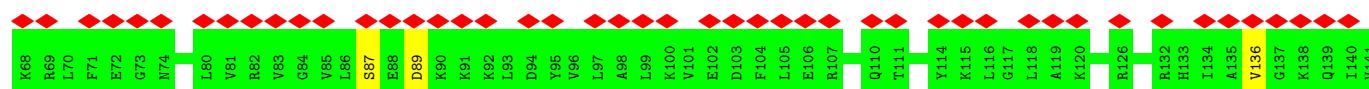
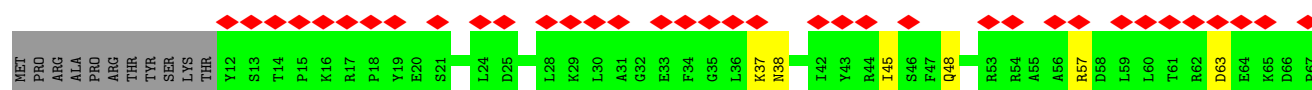
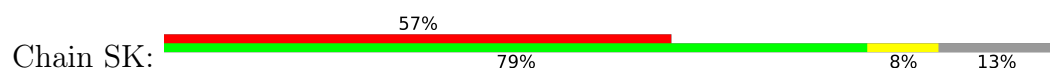




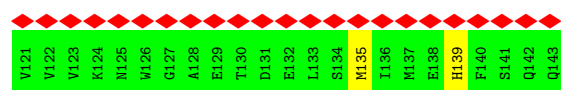
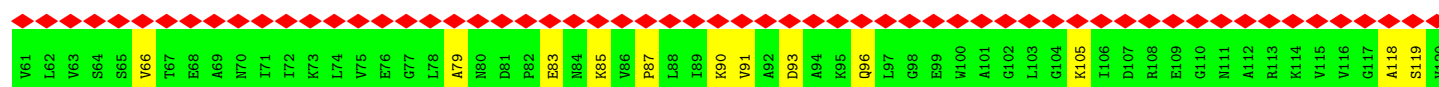
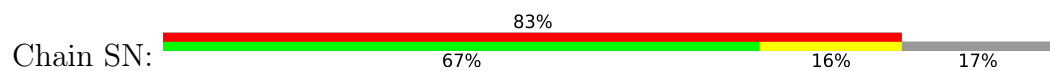
• Molecule 4: 40S ribosomal protein S5



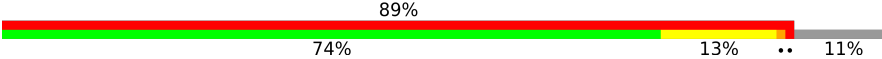
• Molecule 5: 40S ribosomal protein S9-A

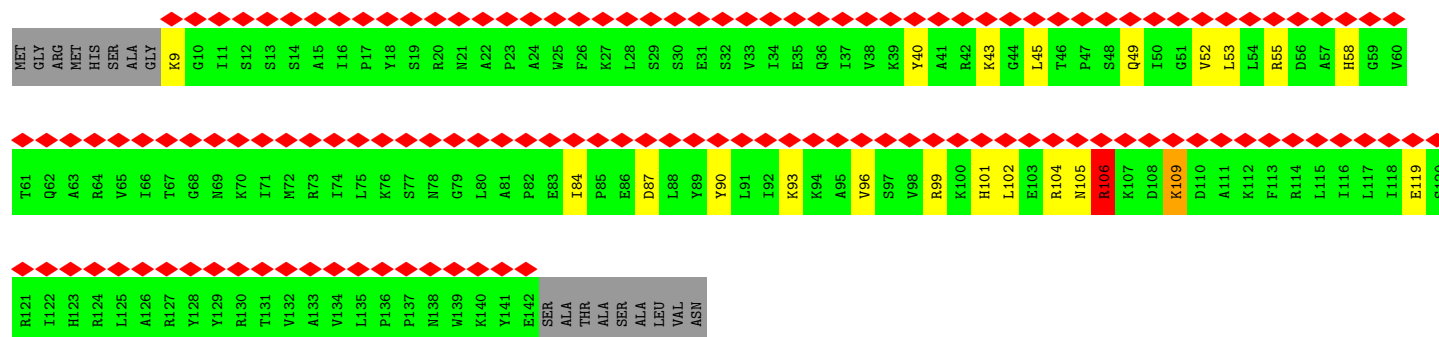


• Molecule 6: 40S ribosomal protein S12



• Molecule 7: 40S ribosomal protein S13

Chain SO: 



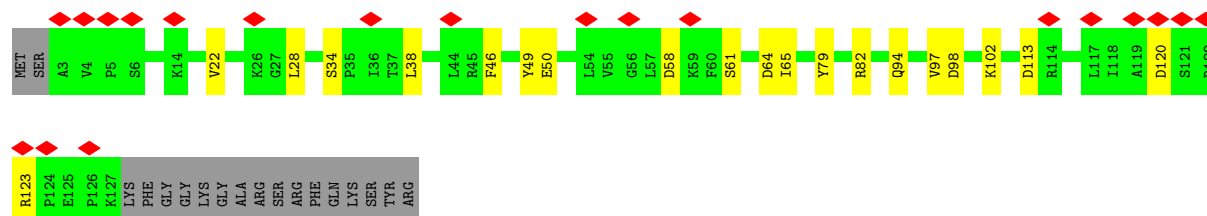
• Molecule 8: 40S ribosomal protein S14-A

Chain SP: 



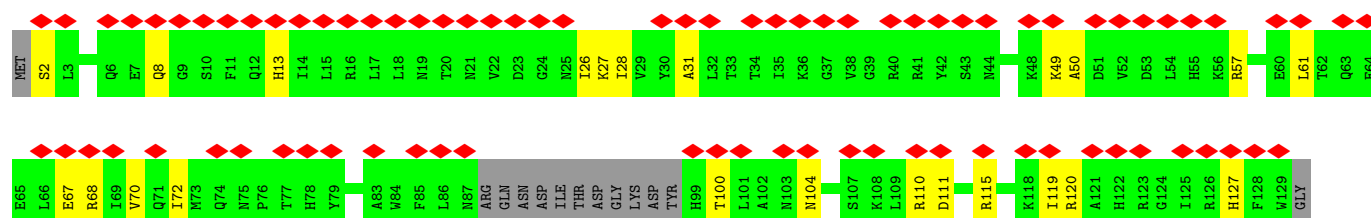
• Molecule 9: 40S ribosomal protein S16-A

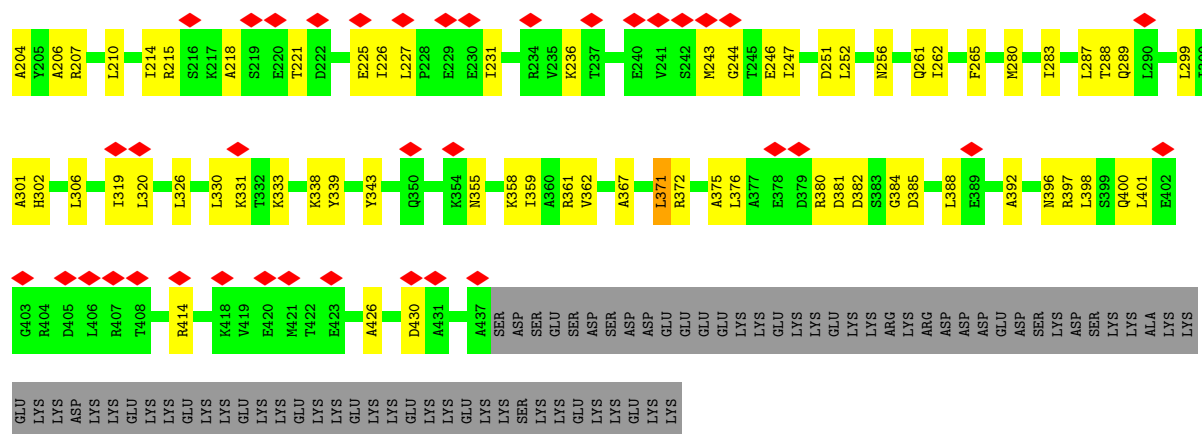
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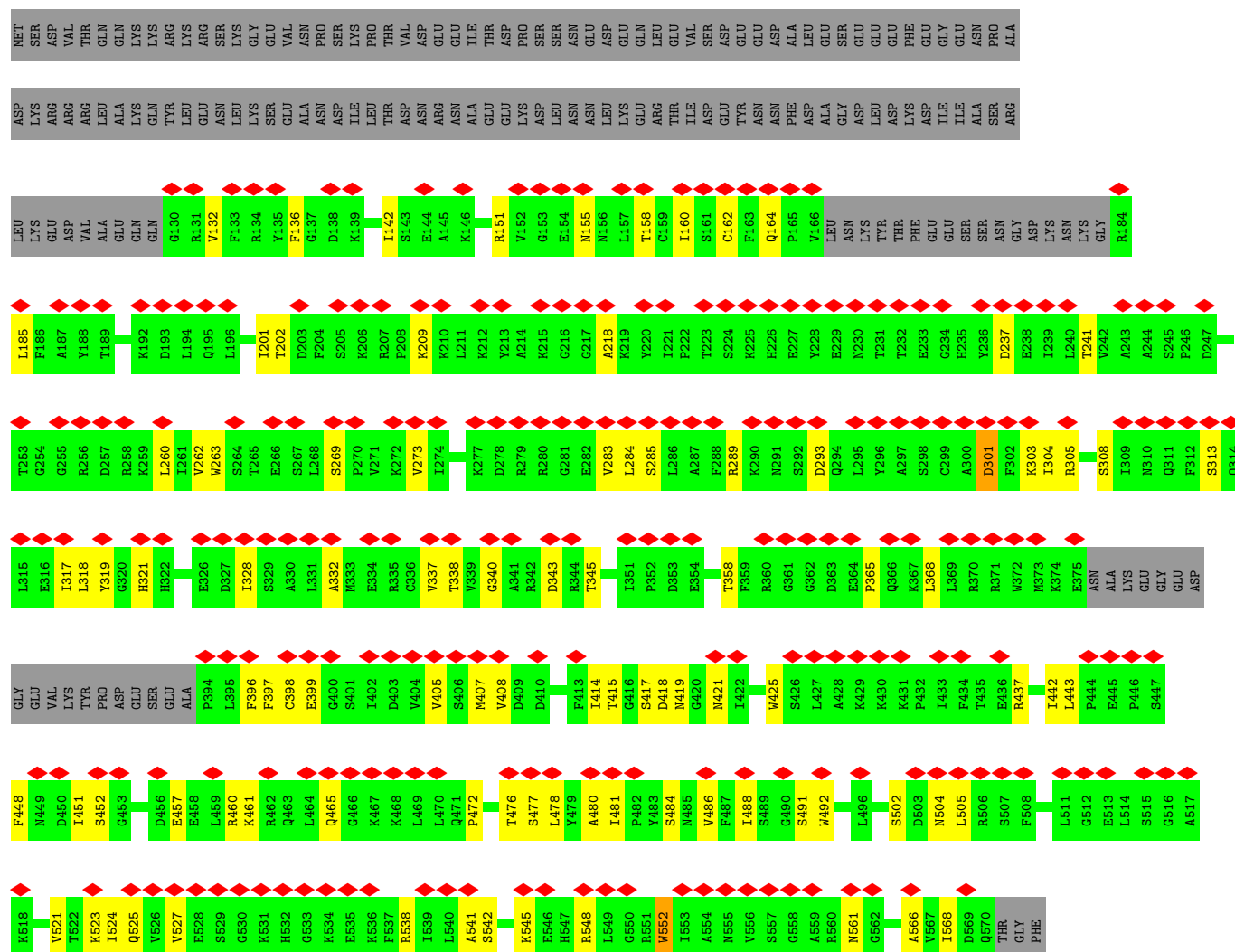
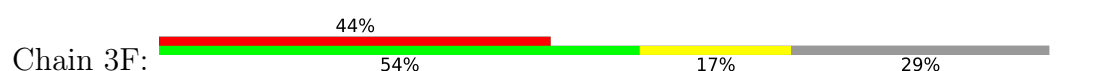
• Molecule 10: 40S ribosomal protein S18-A

Chain ST: 



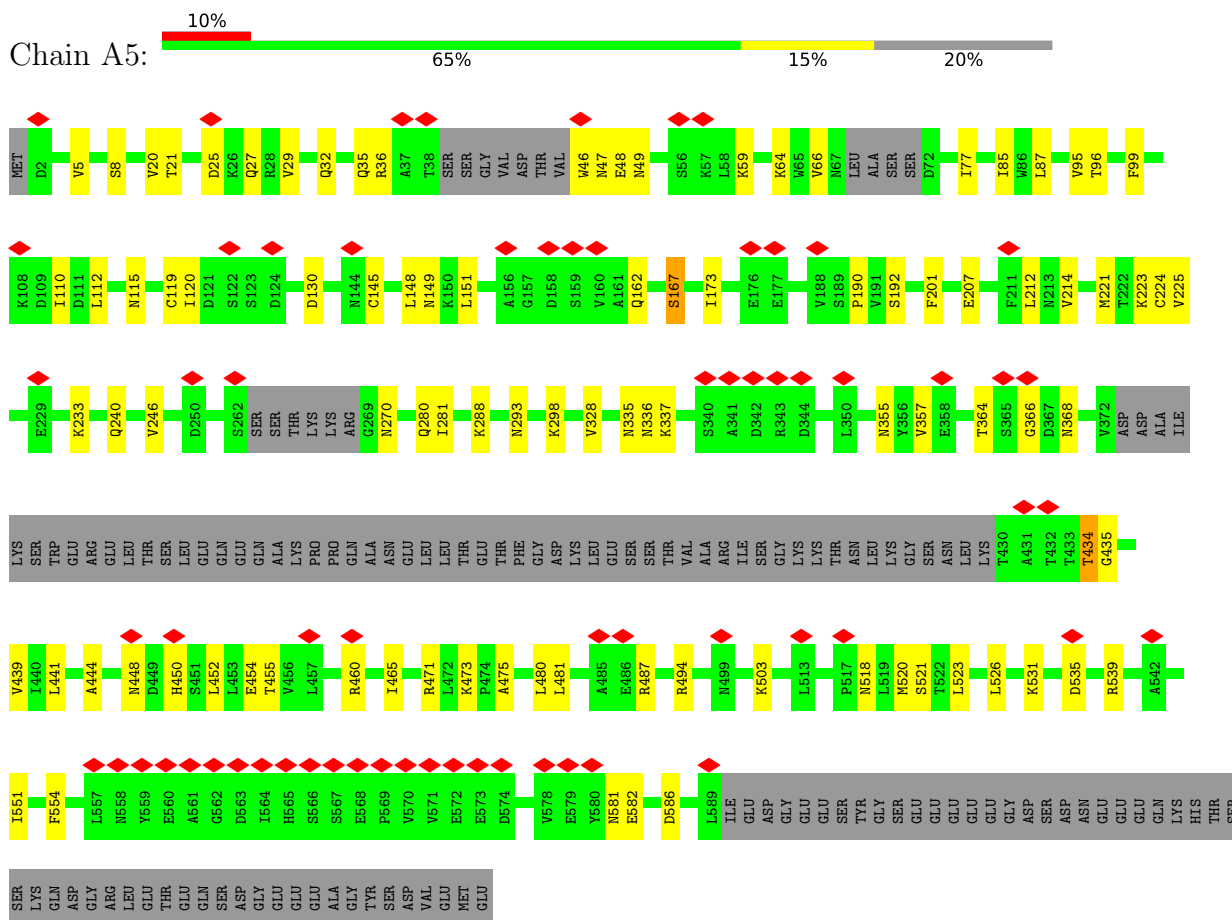


• Molecule 16: Ribosomal RNA-processing protein 9

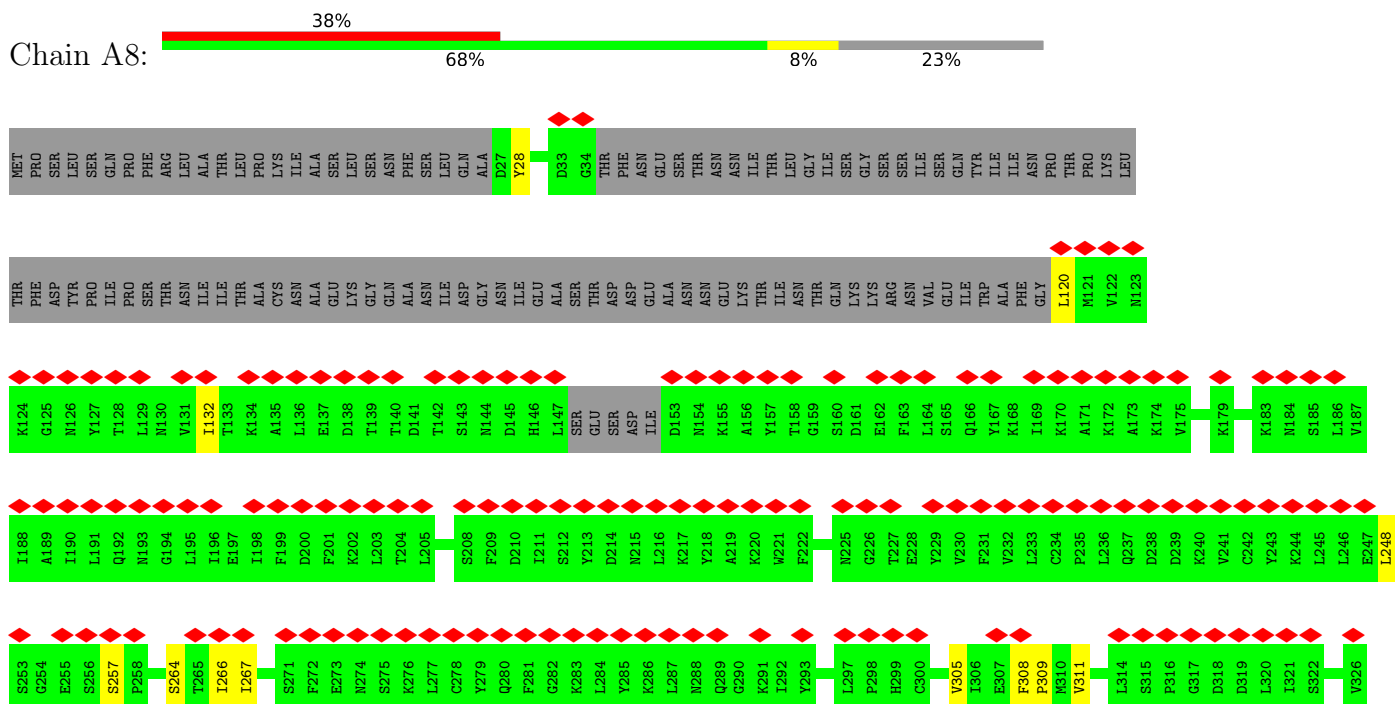


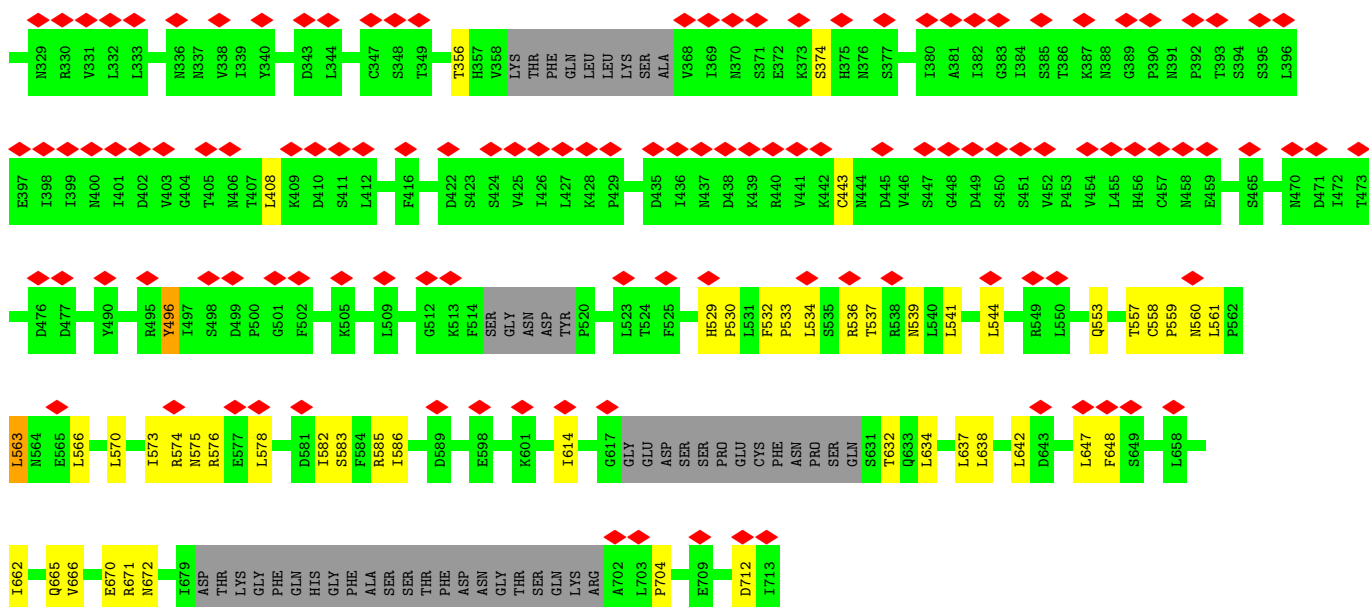
• Molecule 17: 13 kDa ribonucleoprotein-associated protein

Chain A5:

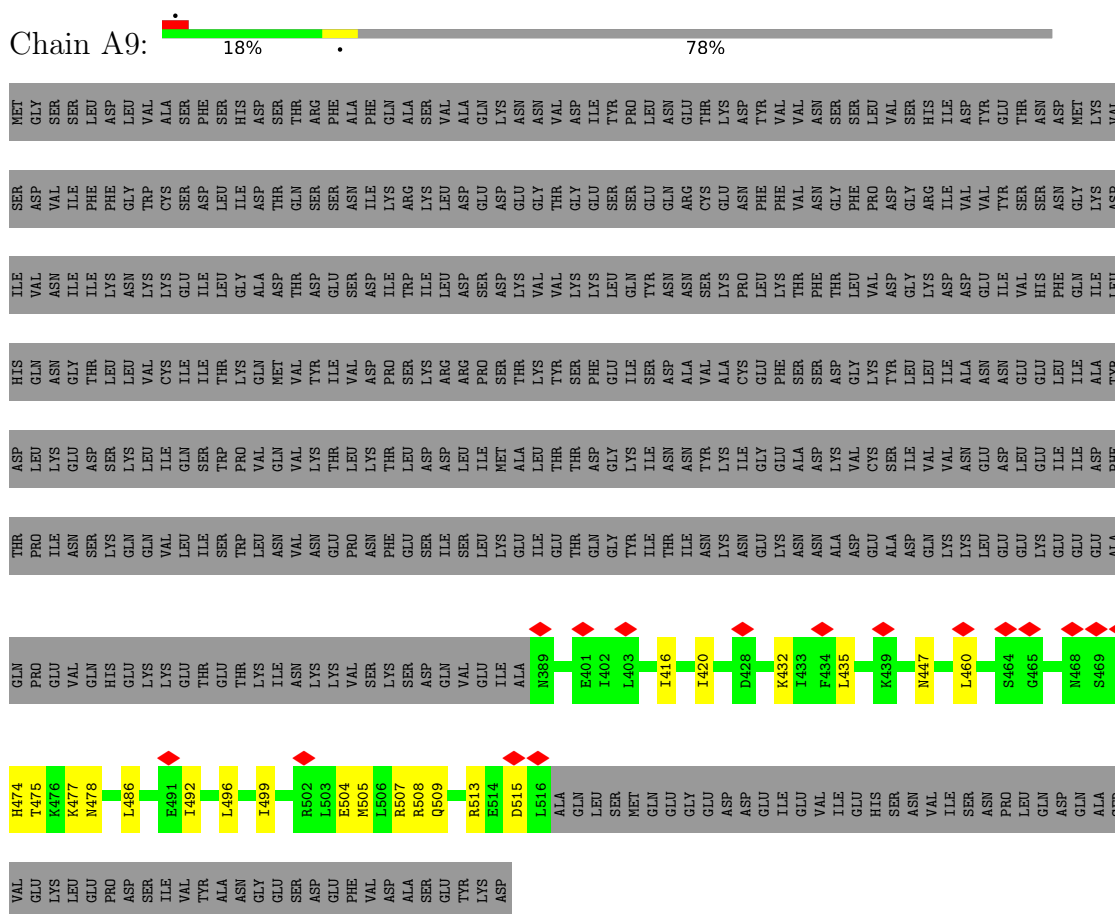


Chain A8:





• Molecule 21: U3 small nucleolar RNA-associated protein 9



• Molecule 22: U3 small nucleolar RNA-associated protein 10



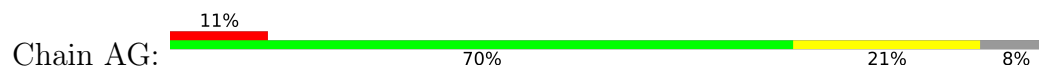


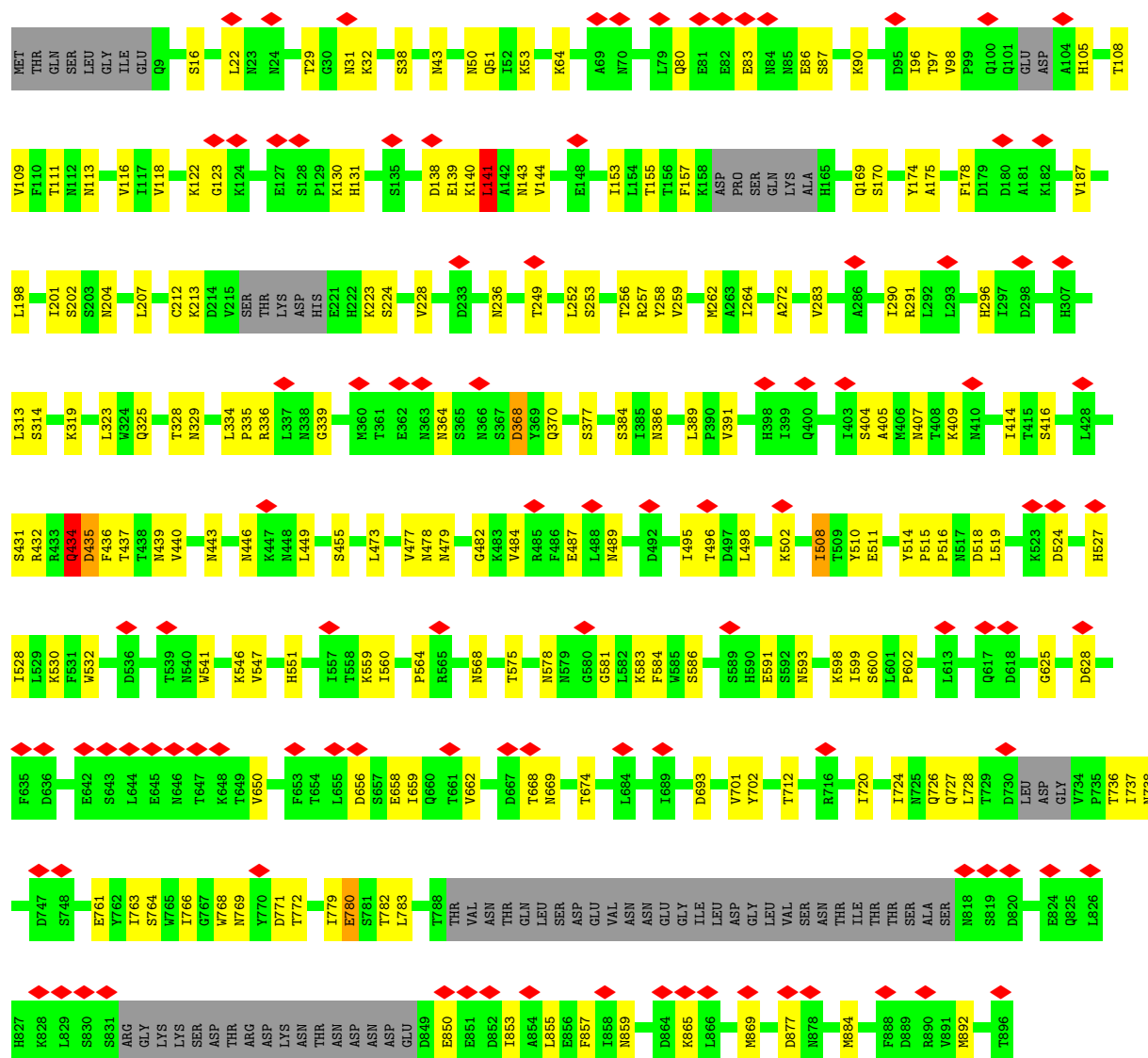


- Molecule 23: U3 small nucleolar RNA-associated protein 15

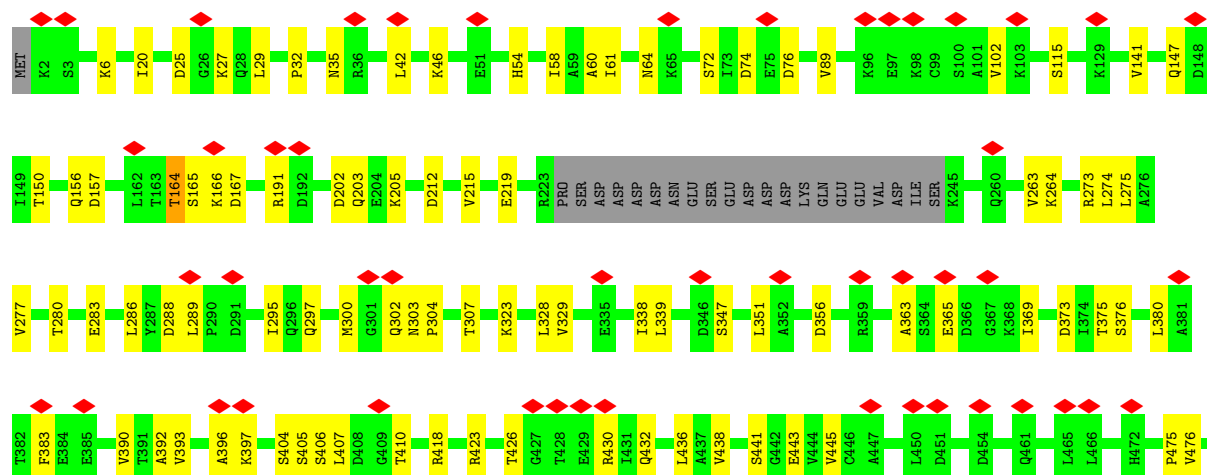
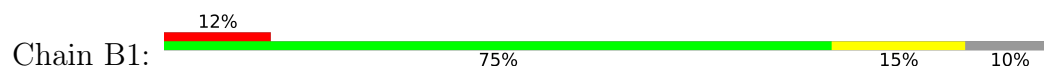


- Molecule 24: NET1-associated nuclear protein 1

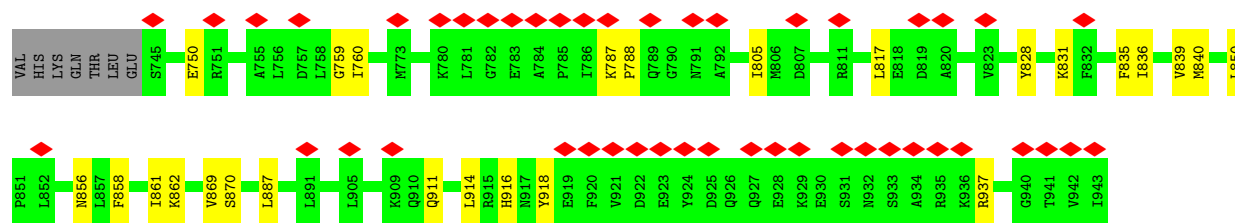




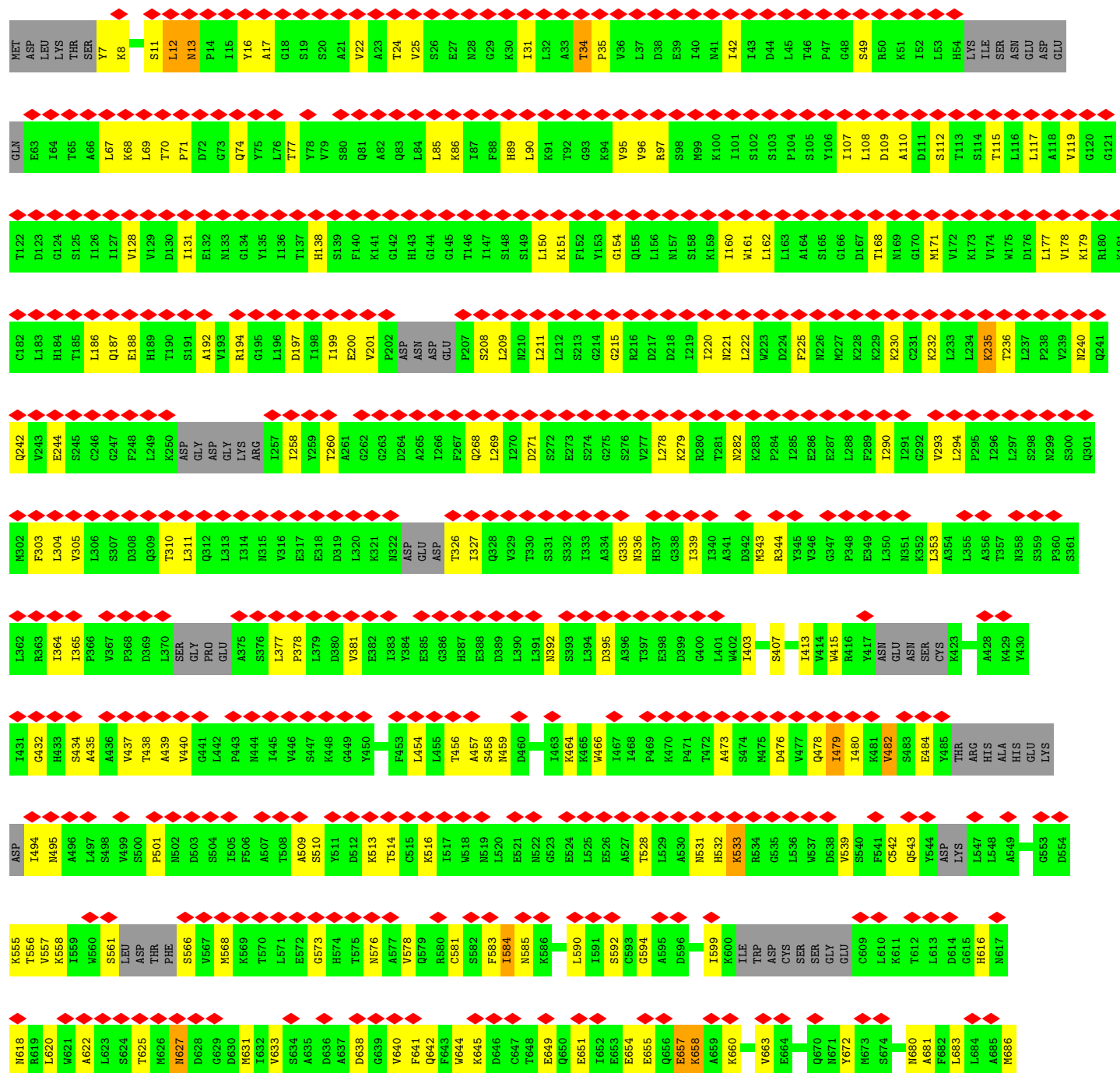
• Molecule 25: Periodic tryptophan protein 2

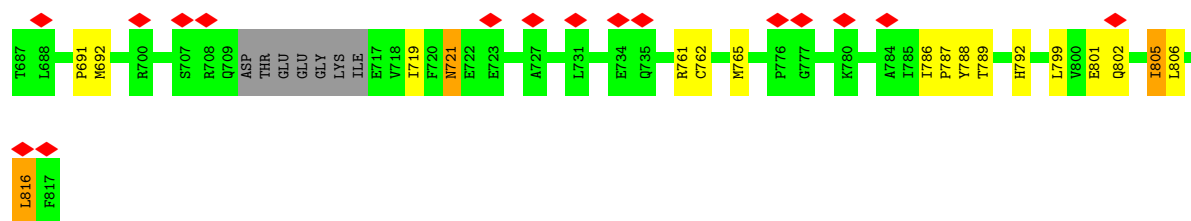




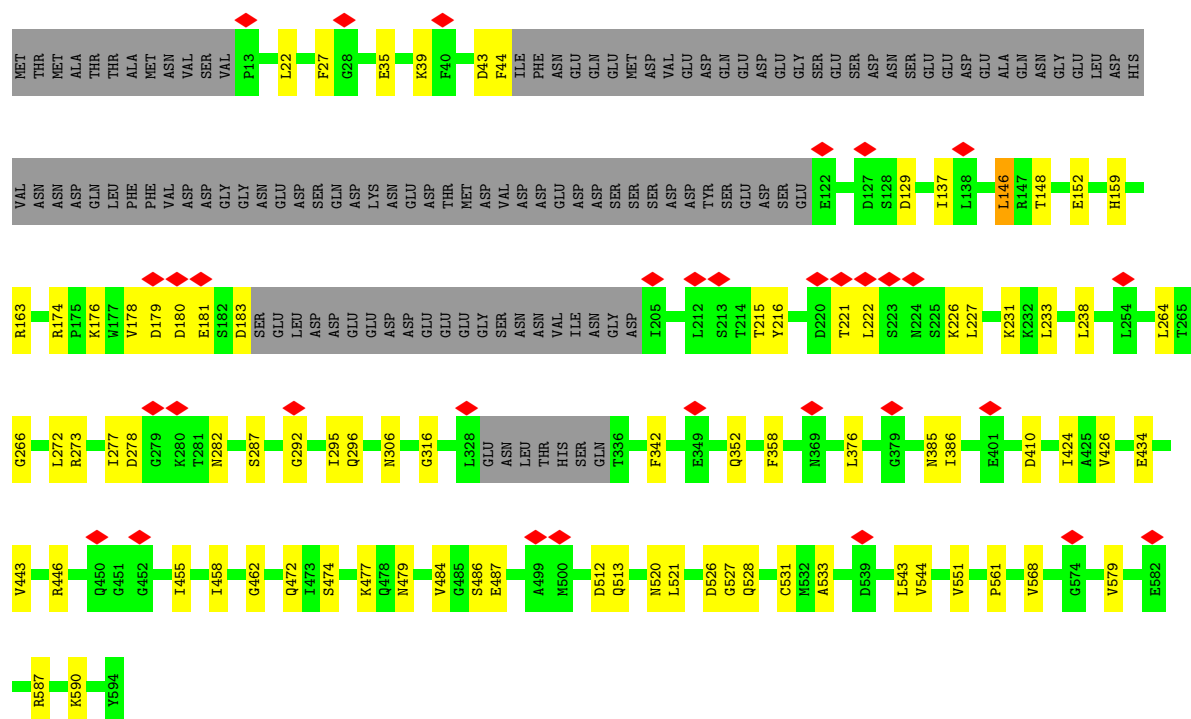


• Molecule 27: U3 small nucleolar RNA-associated protein 13

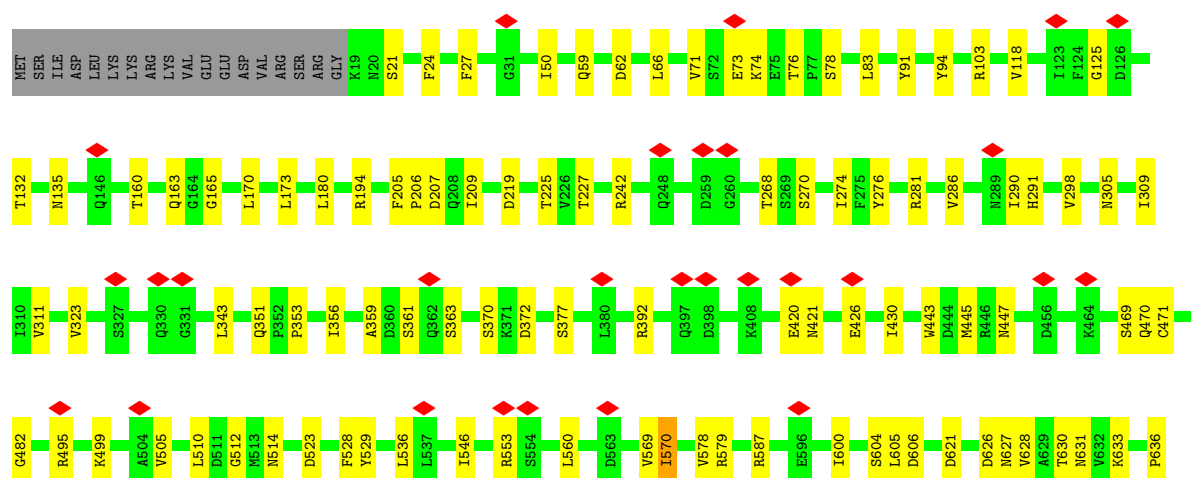
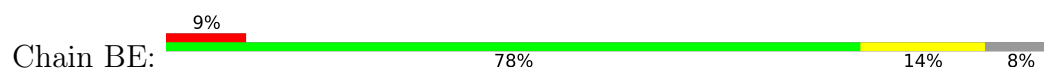


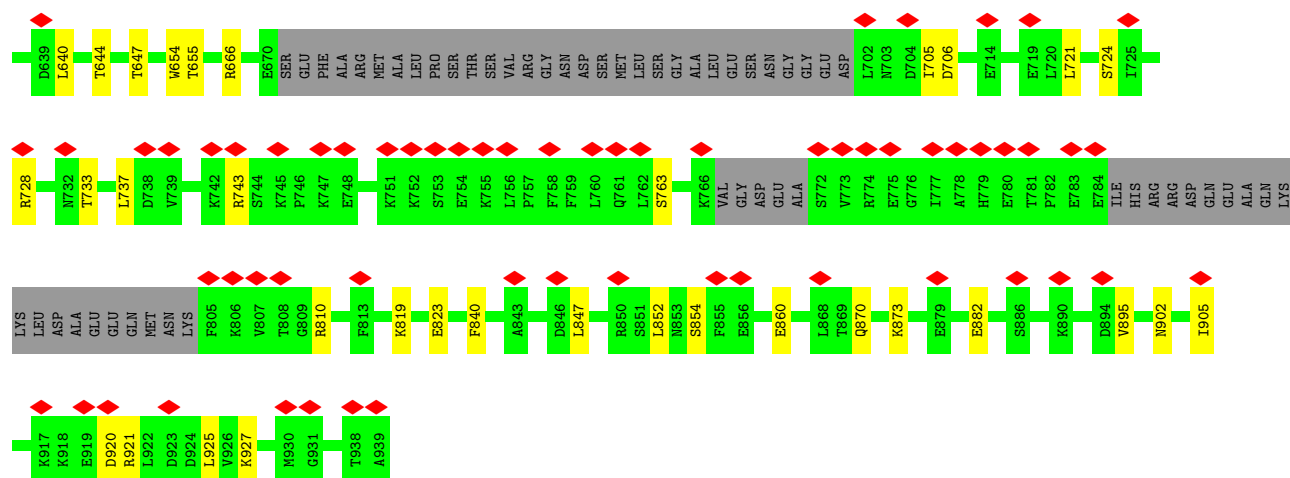


• Molecule 28: U3 small nucleolar RNA-associated protein 18

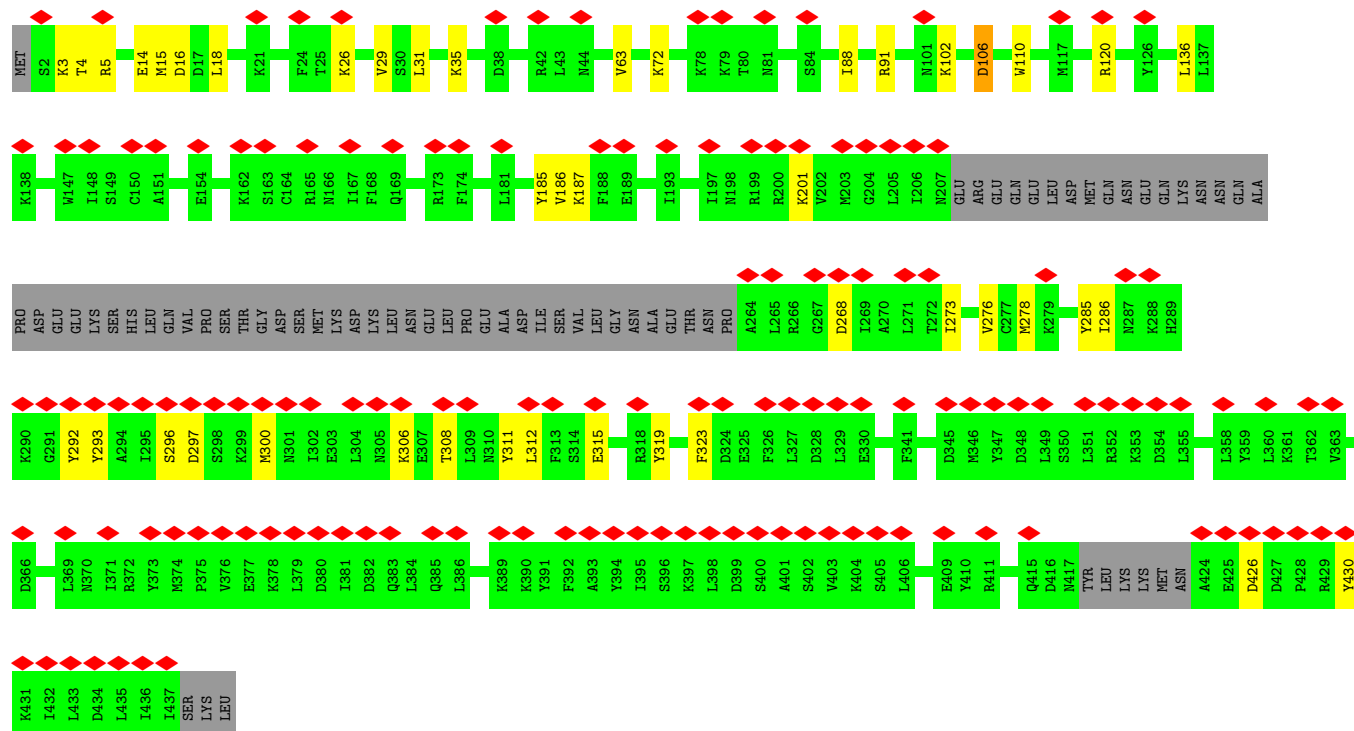
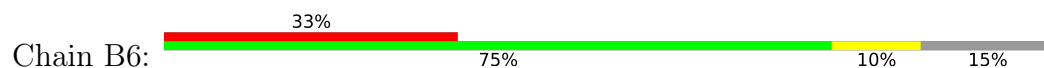


• Molecule 29: U3 small nucleolar RNA-associated protein 21

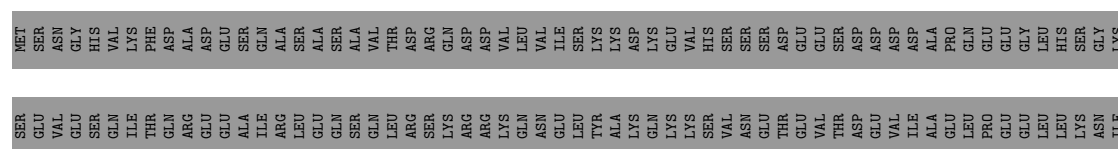


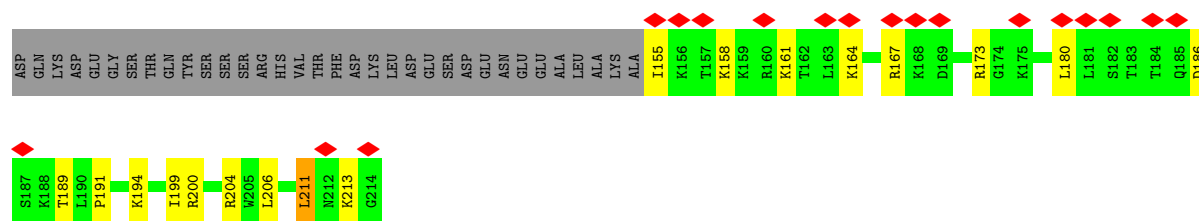


• Molecule 30: U3 small nucleolar RNA-associated protein 6

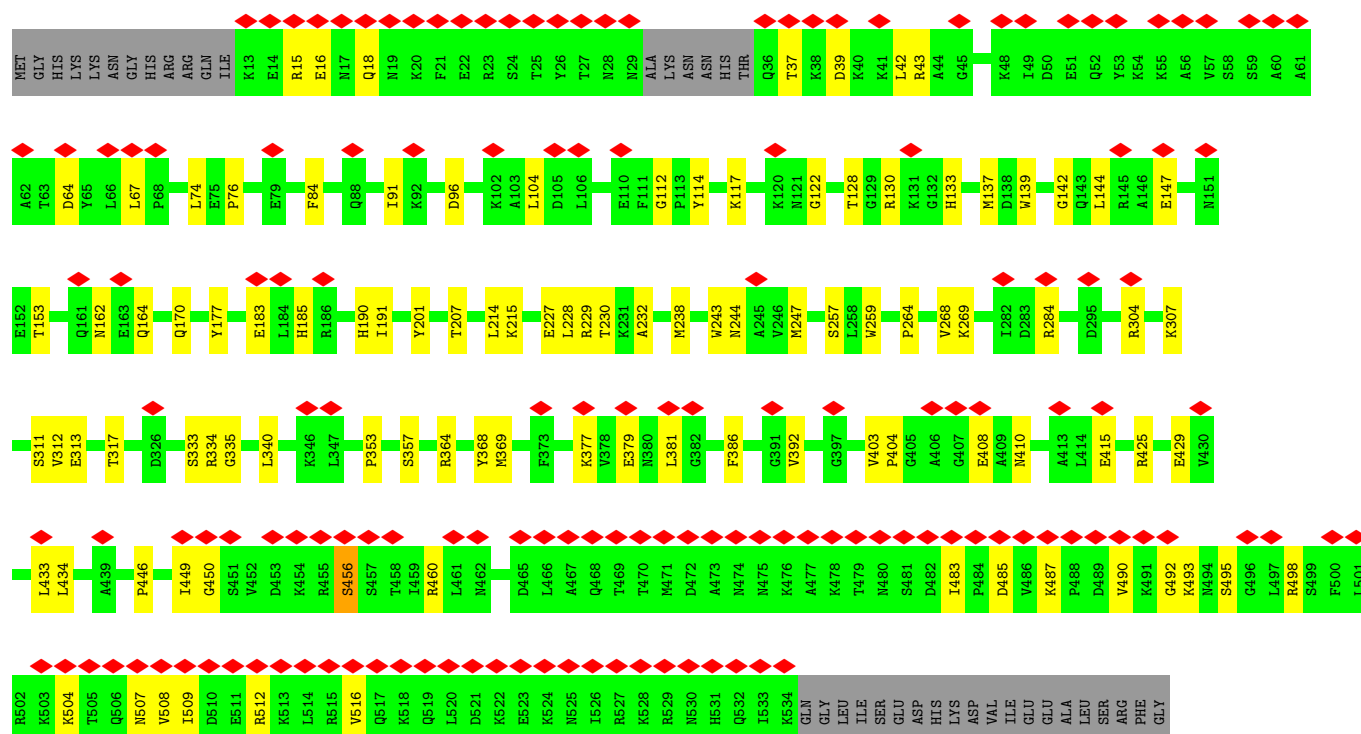
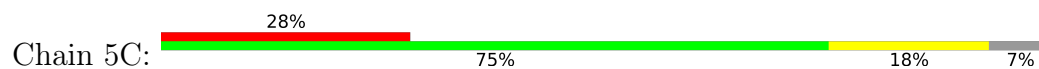


• Molecule 31: Bud site selection protein 21

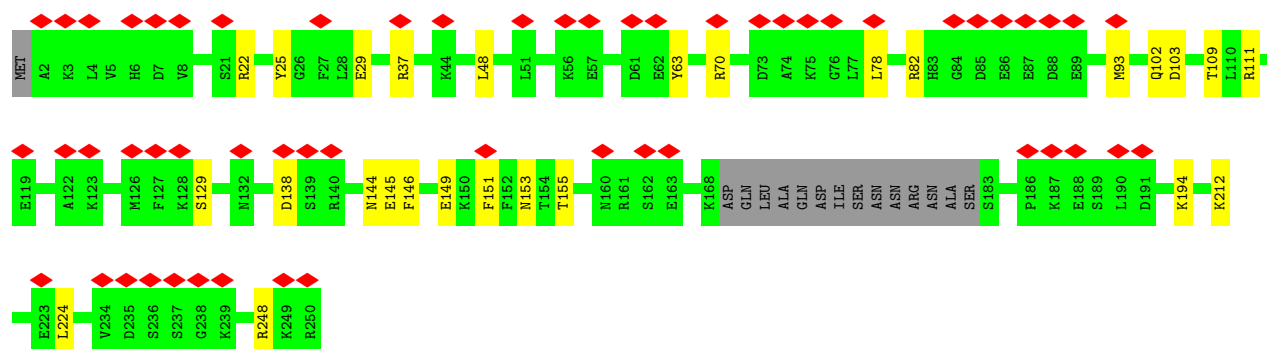
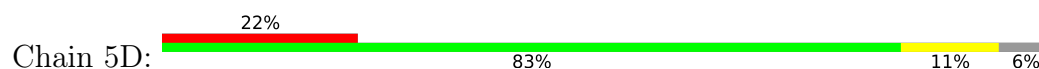




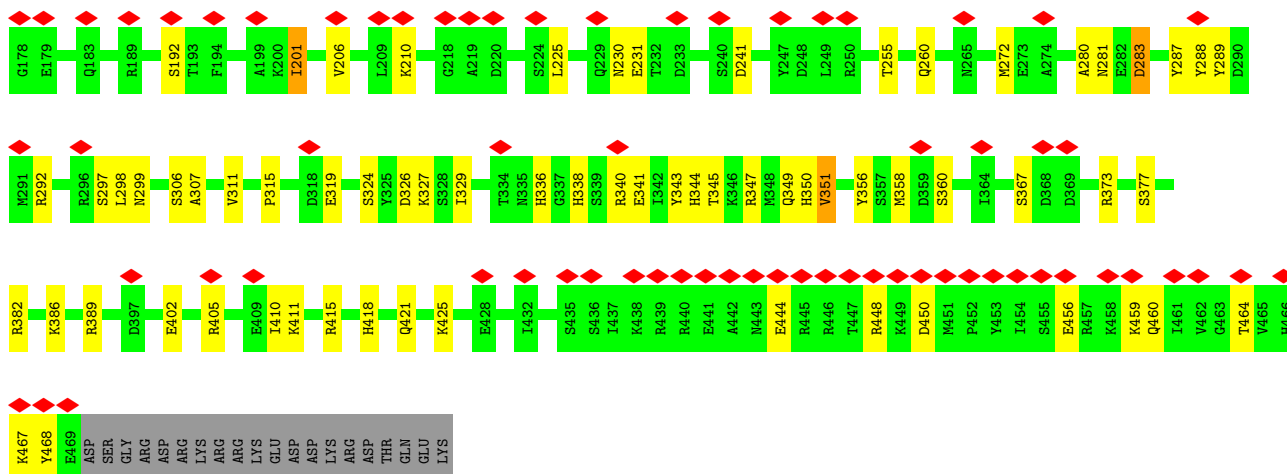
- Molecule 32: U3 small nucleolar RNA-associated protein 7



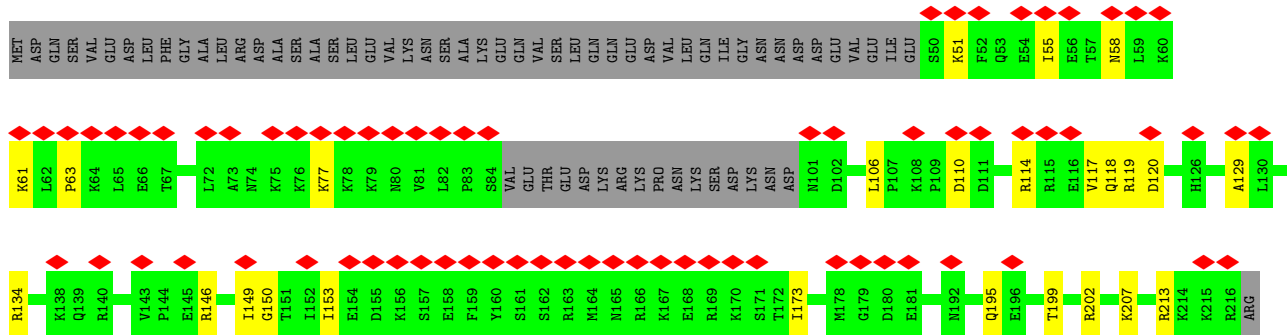
- Molecule 33: U3 small nucleolar RNA-associated protein 11



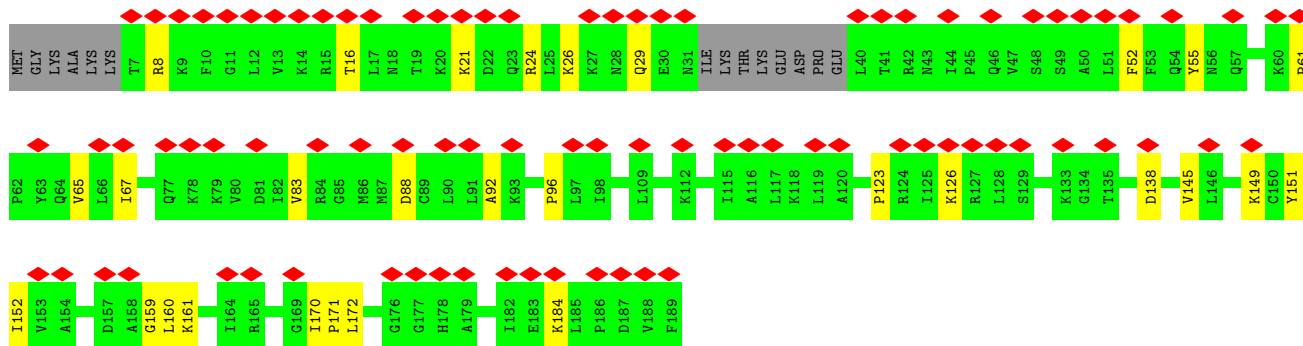
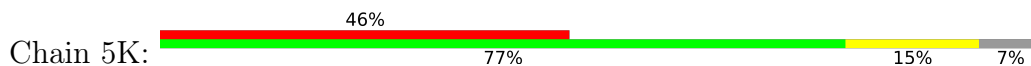
- Molecule 34: U3 small nucleolar RNA-associated protein MPP10



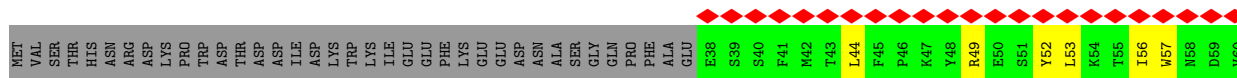
• Molecule 39: rRNA-processing protein FCF2

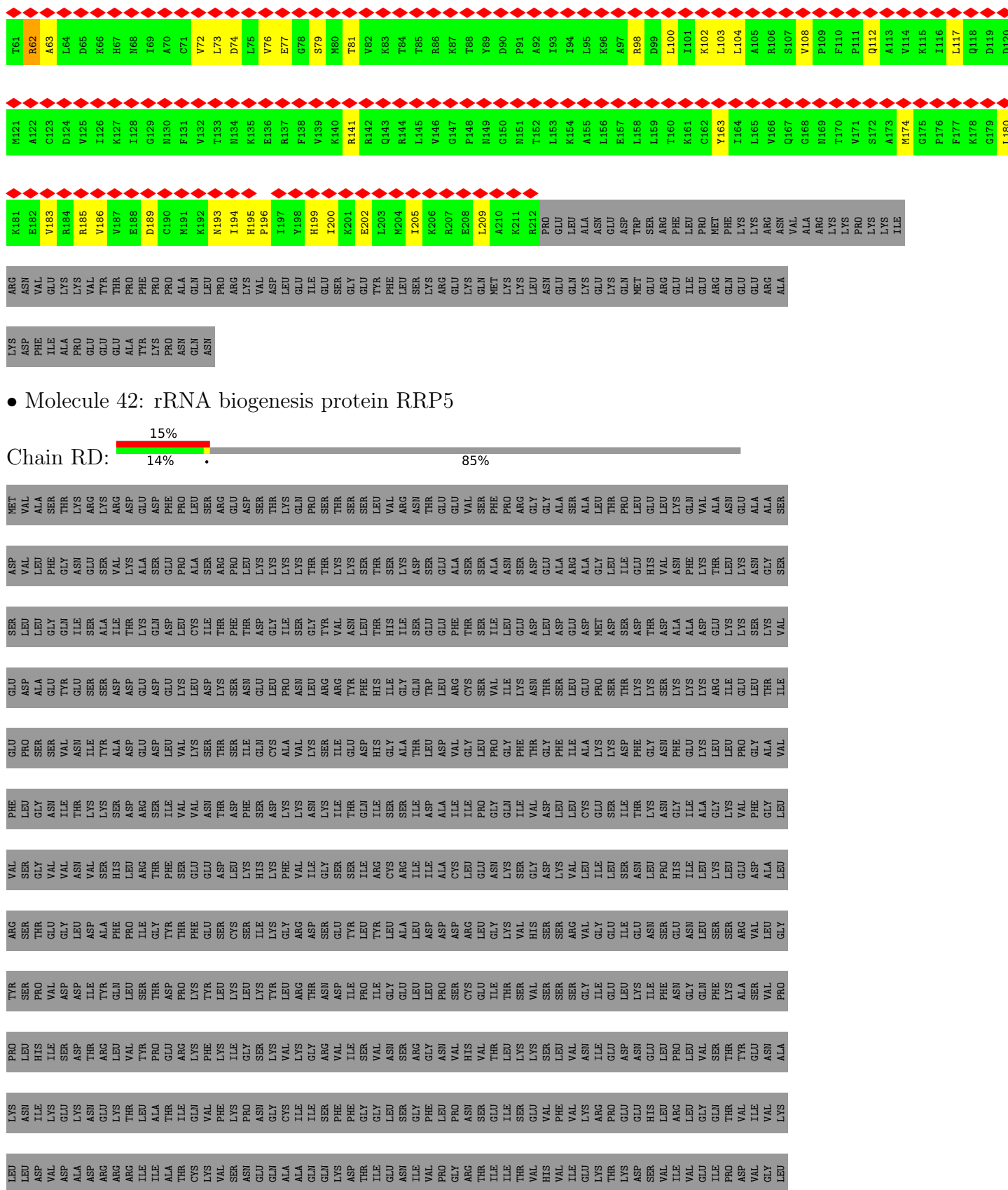


• Molecule 40: rRNA-processing protein FCF1

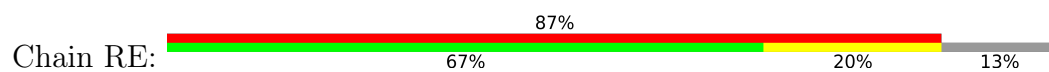


• Molecule 41: KRR1 small subunit processome component



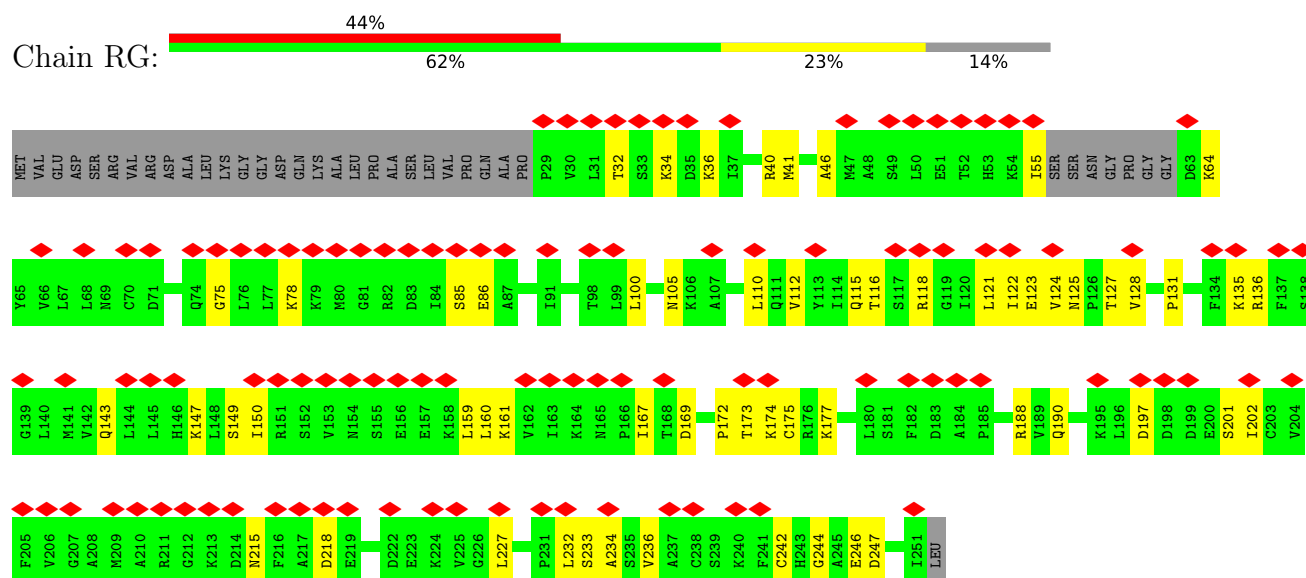


- Molecule 43: U3 small nucleolar RNA-associated protein 22

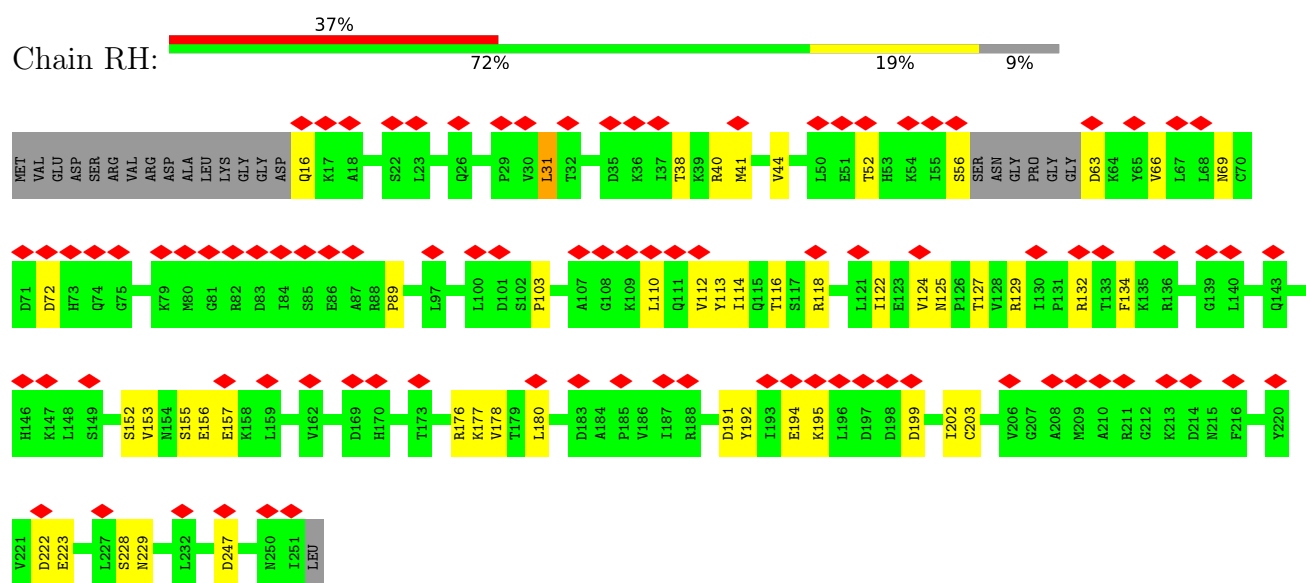


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SER	PRO	GLU	SER	ASN	GLU	VAL	ALA	THR	ASN	THR	ALA	ALA	THR	THR	THR	ARG	ASN	HIS	ASN	GLY	VAL	THR	ALA	LYS	THR	GLU	THR	THR	ASP	ALA	ARG	THR	ALA	LEU	PHE	LYS	S100	N101	I102	F103	K104	L105	Q106	I107	D108	E109	L110	L111	E112	Q113	V114	K115	L116	K117	Q118	K119	H120			
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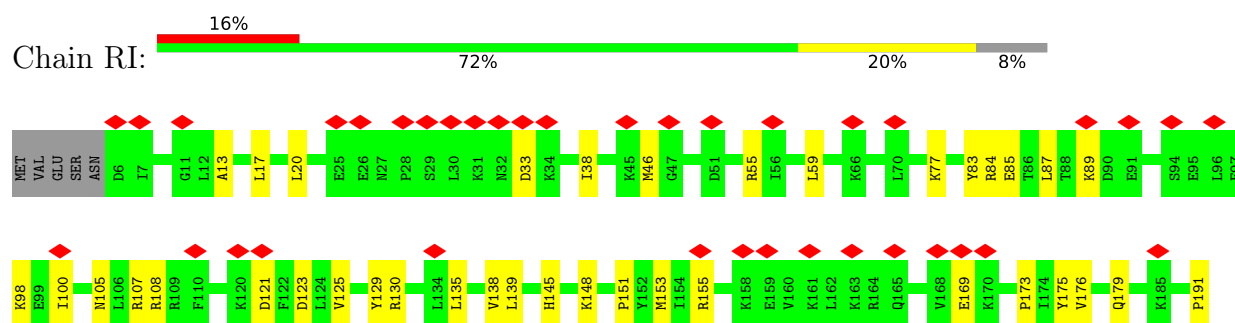
- Molecule 45: Ribosomal RNA small subunit methyltransferase NEP1

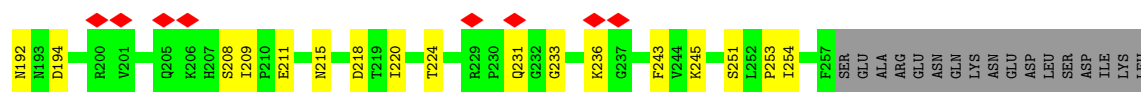


- Molecule 45: Ribosomal RNA small subunit methyltransferase NEP1

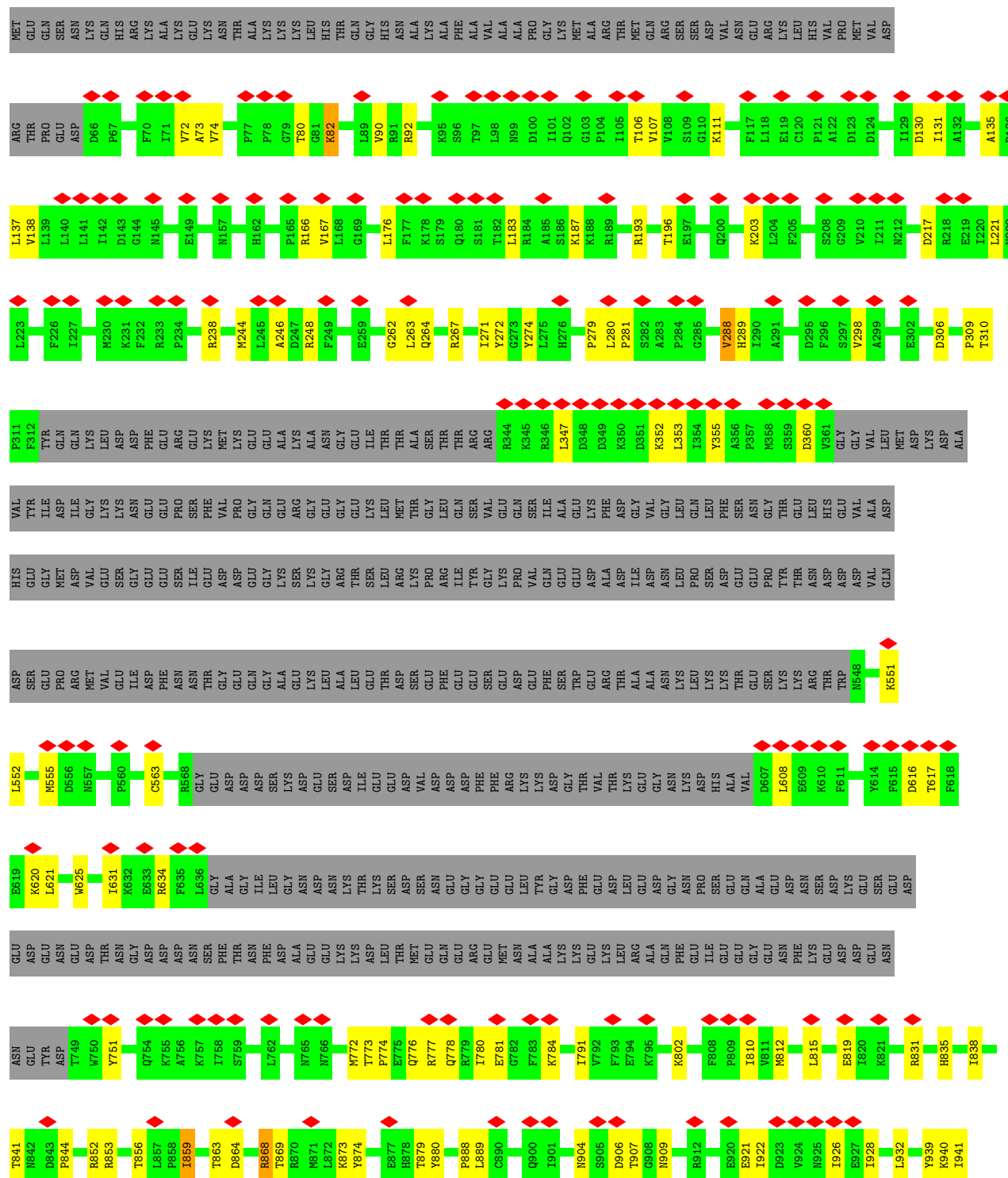


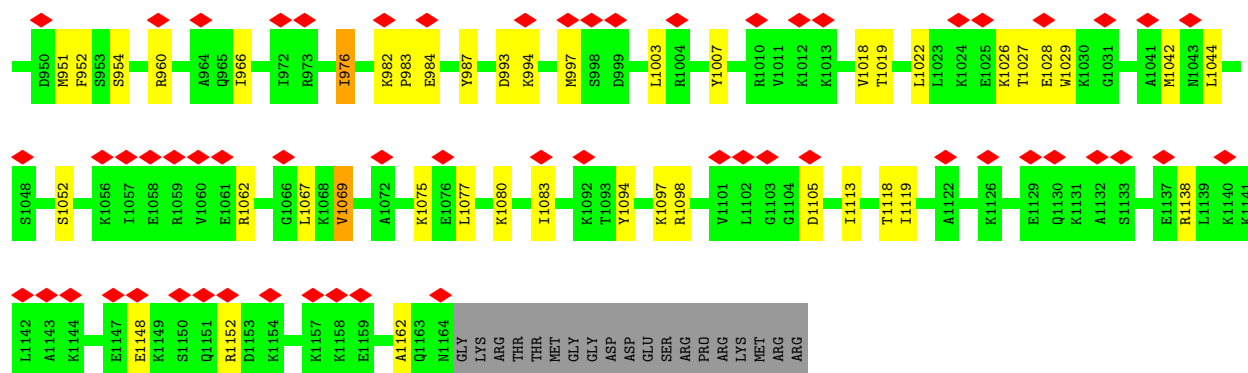
- Molecule 46: Ribosome biogenesis protein UTP30



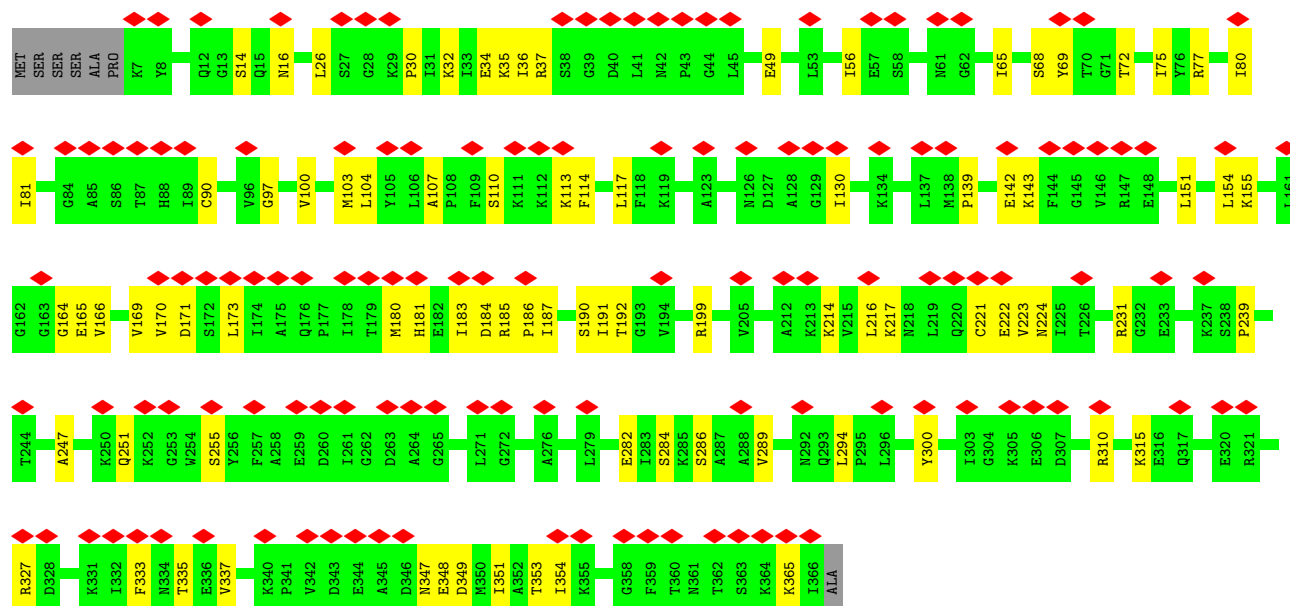
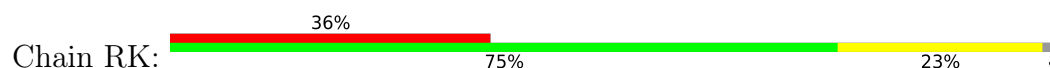


• Molecule 47: Ribosome biogenesis protein BMS1

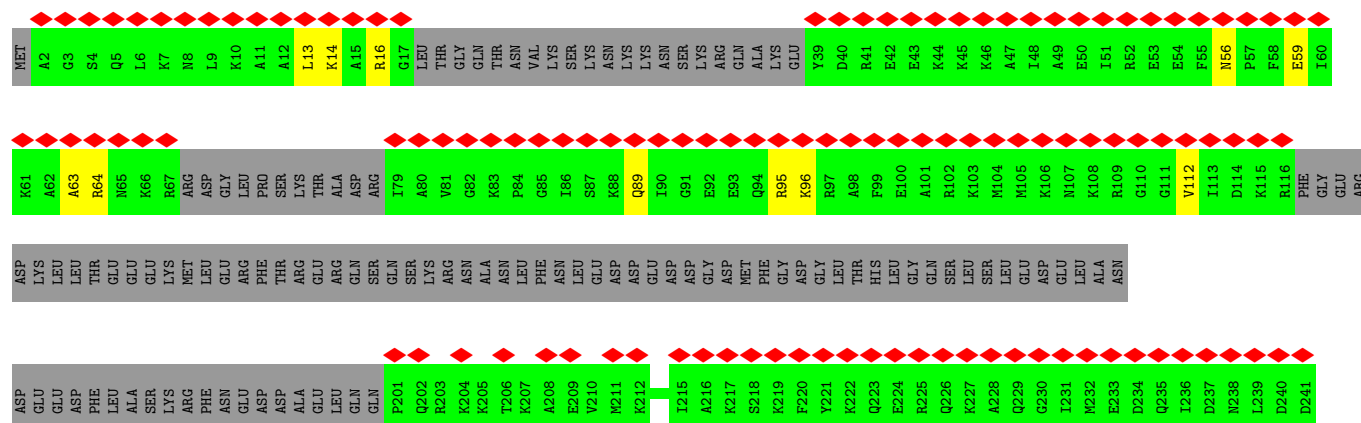
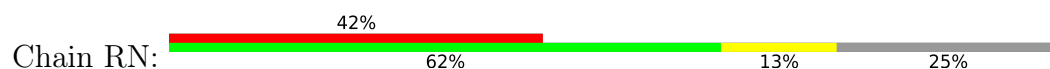


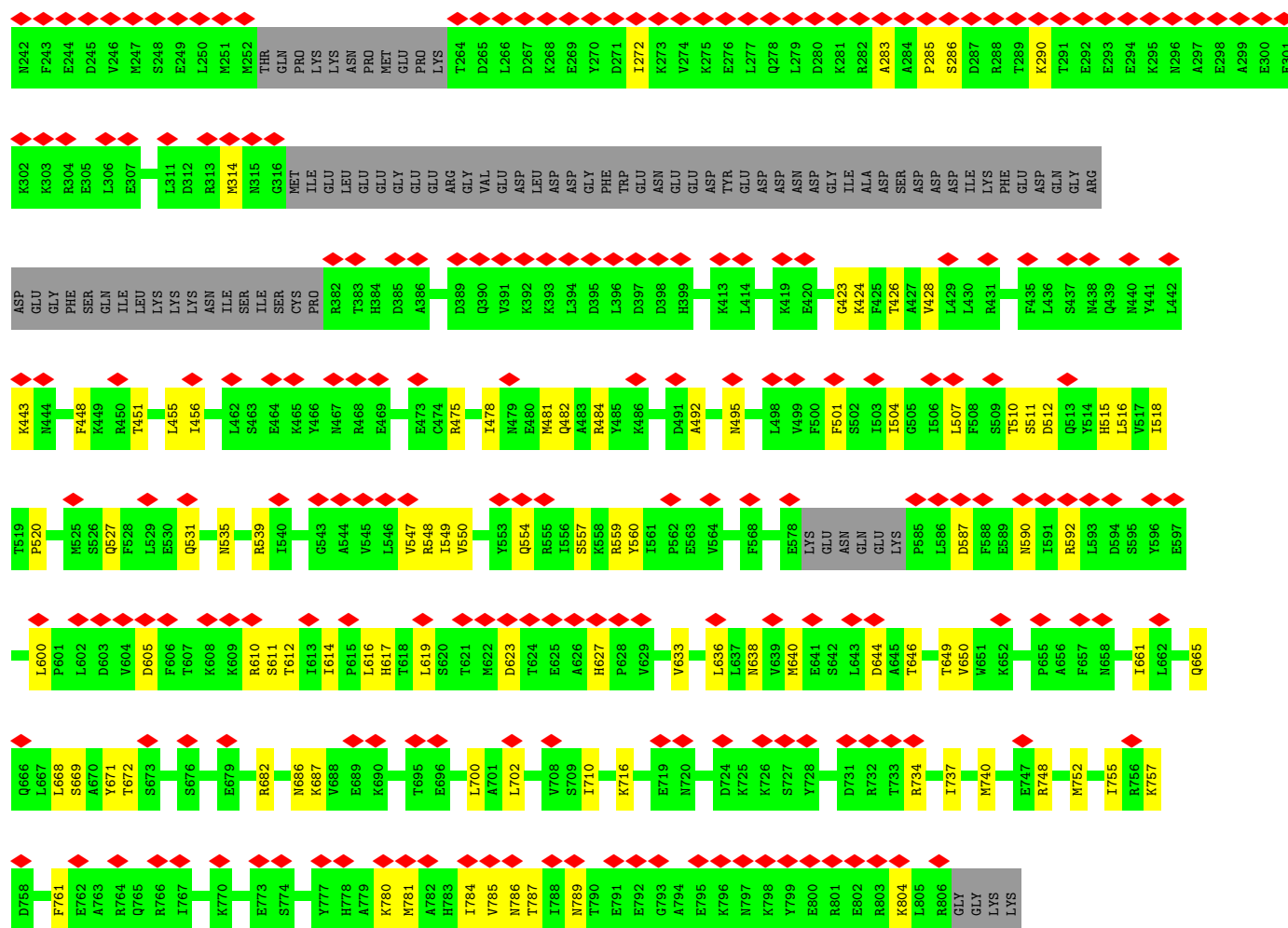


• Molecule 48: RNA 3'-terminal phosphate cyclase-like protein

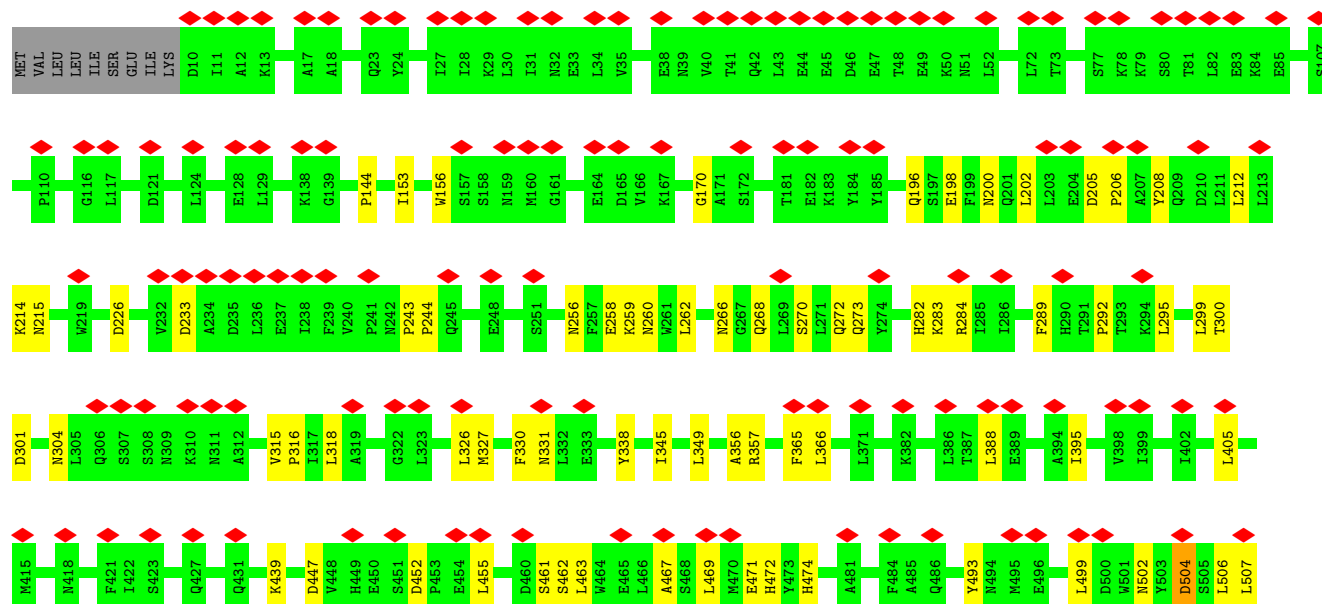
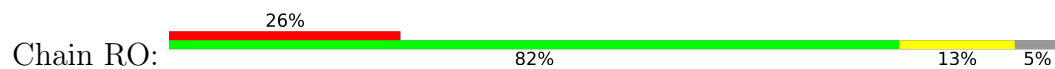


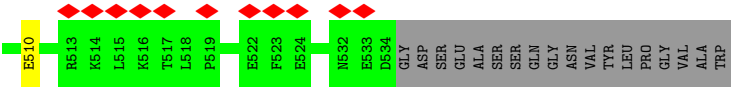
• Molecule 49: Nucleolar complex protein 14



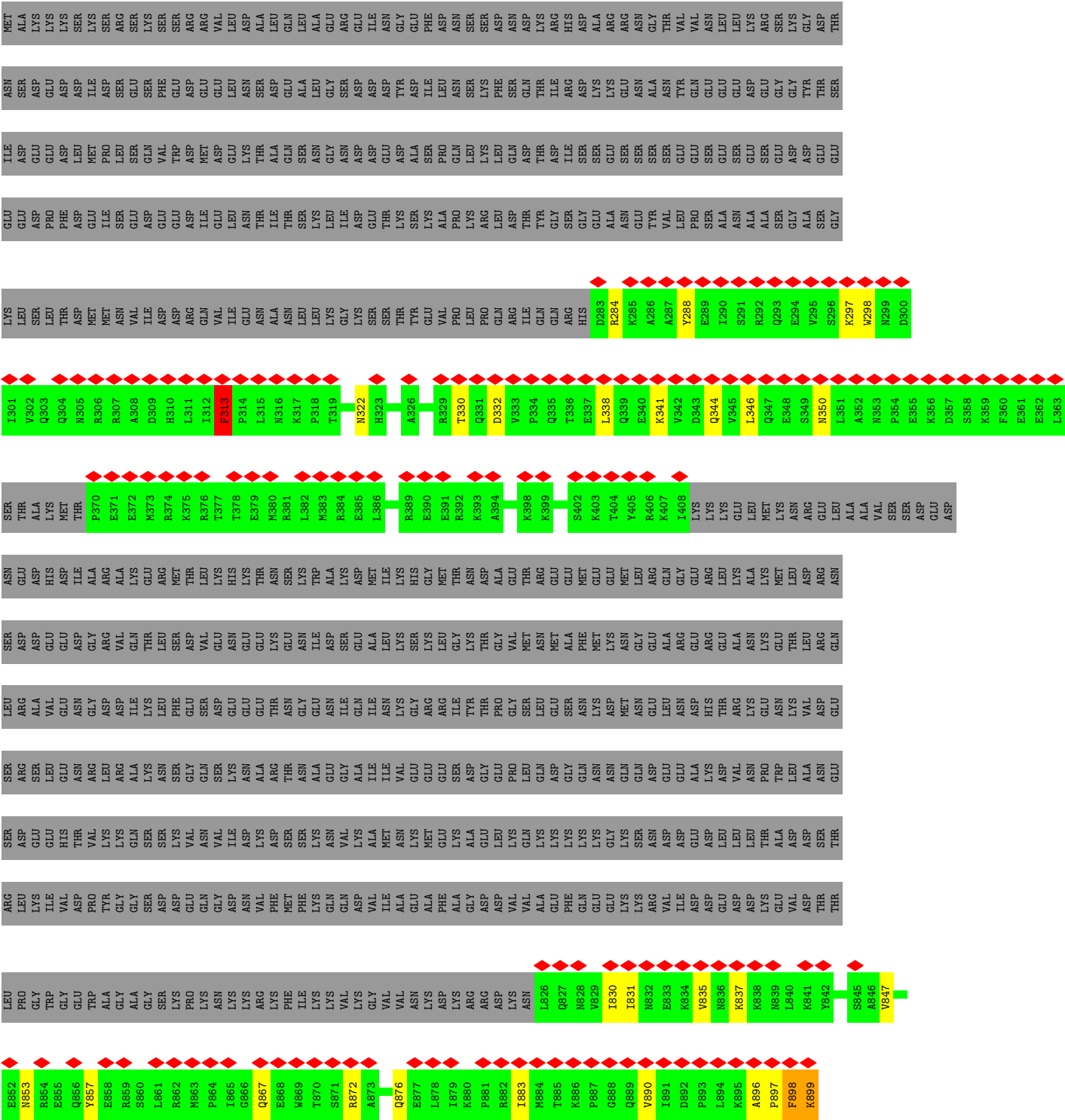


• Molecule 50: Nucleolar complex protein 4

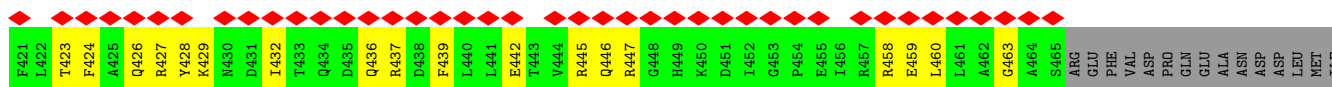
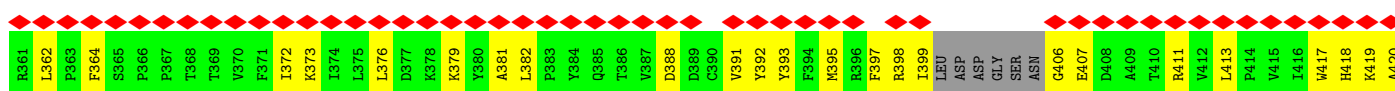
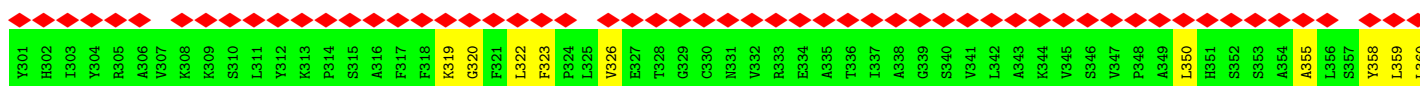
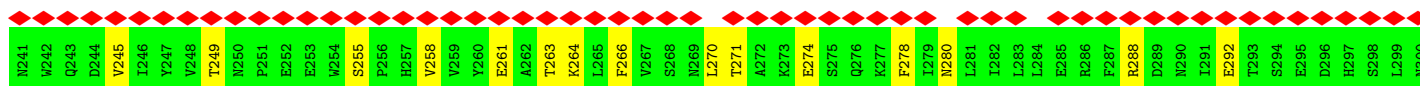
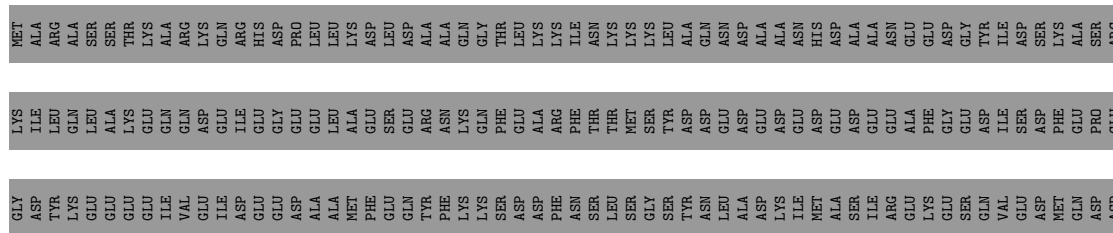
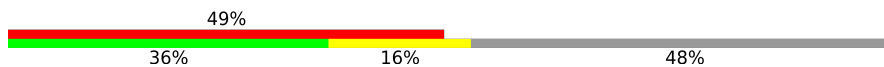




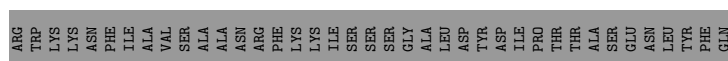
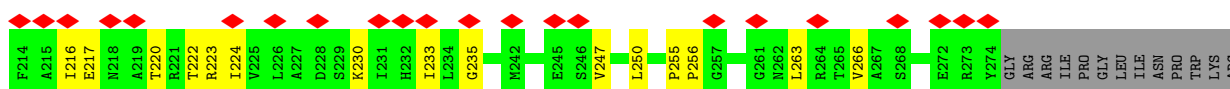
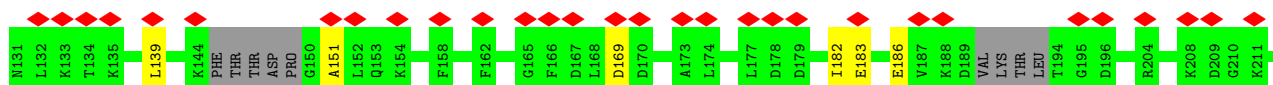
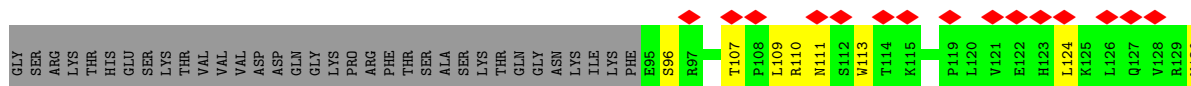
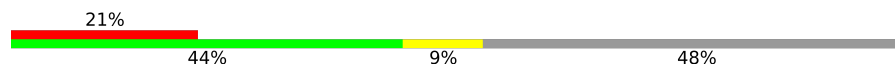
• Molecule 51: U3 small nucleolar RNA-associated protein 14



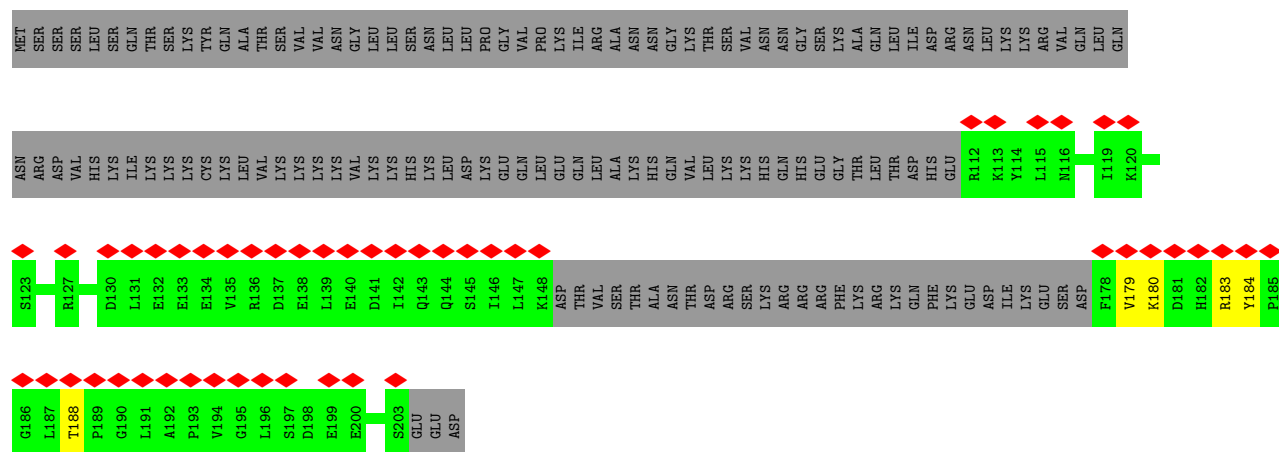
Chain RS:



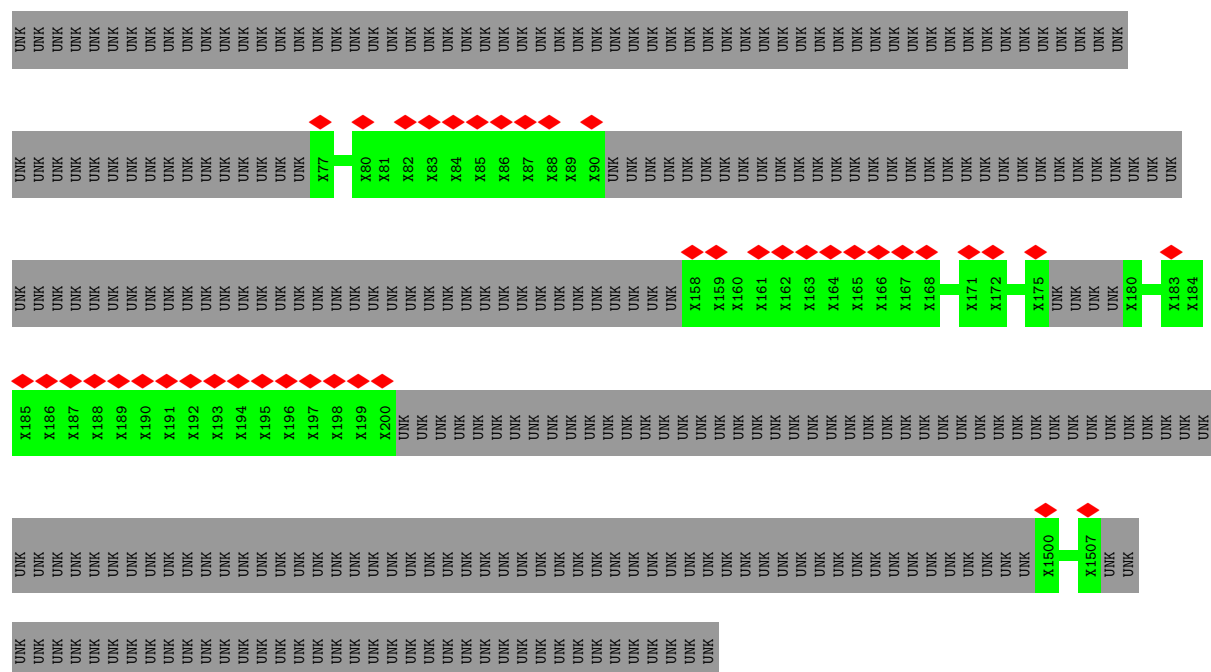
Chain RT:



Chain RW:



Chain X1:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40111	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	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	531.19995, 531.19995, 531.19995	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3279998, 1.3279998, 1.3279998	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	0.45	0/4141	0.48	0/6433
2	5A	0.41	0/12485	0.47	2/19449 (0.0%)
3	SA	0.36	0/20532	0.53	18/31980 (0.1%)
4	SG	0.49	0/1690	0.67	2/2285 (0.1%)
5	SK	0.44	0/1410	0.63	0/1888
6	SN	0.29	0/873	0.79	0/1185
7	SO	0.35	0/1109	0.74	2/1495 (0.1%)
8	SP	0.38	0/879	0.85	3/1186 (0.3%)
9	SR	0.52	0/990	0.77	3/1335 (0.2%)
10	ST	0.31	0/980	0.65	0/1319
11	SY	0.48	0/798	0.65	0/1065
12	Sd	0.50	0/499	0.72	2/670 (0.3%)
13	3B	0.51	0/1901	0.66	1/2567 (0.0%)
13	3C	0.37	0/1796	0.66	0/2424
14	3D	0.40	0/2891	0.62	0/3895
15	3E	0.38	0/3059	0.62	0/4153
16	3F	0.37	0/3317	0.65	0/4469
17	3G	0.51	0/928	0.72	1/1262 (0.1%)
17	3H	0.46	0/928	0.70	0/1262
18	A4	0.43	0/5321	0.66	0/7207
19	A5	0.44	0/4044	0.65	0/5493
20	A8	0.24	0/3328	0.62	0/4565
21	A9	0.28	0/951	0.60	0/1287
22	AE	0.41	1/5274 (0.0%)	0.64	0/7142
23	AF	0.48	0/3993	0.68	0/5413
24	AG	0.42	0/6699	0.64	3/9077 (0.0%)
25	B1	0.58	0/6780	0.69	0/9175
26	B2	0.39	0/6853	0.69	2/9256 (0.0%)
27	B3	0.33	0/5977	0.78	4/8087 (0.0%)
28	B8	0.55	0/3848	0.63	0/5218
29	BE	0.53	0/6948	0.64	2/9391 (0.0%)
30	B6	0.37	0/2849	0.60	0/3853

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	5B	0.32	0/499	0.62	0/659
32	5C	0.56	0/4166	0.66	2/5624 (0.0%)
33	5D	0.46	0/1998	0.70	0/2644
34	5E	0.44	0/1665	0.66	2/2233 (0.1%)
35	5F	0.64	0/1559	0.72	1/2097 (0.0%)
36	5G	0.52	0/2337	0.67	2/3148 (0.1%)
37	5H	0.40	0/1074	0.57	0/1422
38	5I	0.56	0/3844	0.68	0/5174
39	5J	0.36	0/1302	0.58	0/1728
40	5K	0.52	0/1426	0.66	0/1917
41	RC	0.34	0/1432	0.66	0/1926
42	RD	0.26	0/1313	0.60	1/1830 (0.1%)
43	RE	0.25	0/8924	0.67	2/12070 (0.0%)
44	RF	0.26	0/1441	0.69	0/1951
45	RG	0.32	0/1727	0.70	0/2329
45	RH	0.37	0/1828	0.59	0/2470
46	RI	0.41	0/2080	0.65	0/2797
47	RJ	0.45	0/6085	0.62	0/8186
48	RK	0.39	0/2832	0.64	0/3825
49	RN	0.31	0/4591	0.63	1/6187 (0.0%)
50	RO	0.32	0/3849	0.63	0/5261
51	RQ	0.43	0/1459	0.62	1/1981 (0.1%)
52	RS	0.30	0/2104	0.70	0/2854
53	RT	0.38	0/1379	0.68	0/1853
54	RW	0.26	0/385	0.49	0/529
All	All	0.42	1/185370 (0.0%)	0.63	57/258181 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	SO	0	1
10	ST	0	1
14	3D	0	3
15	3E	0	1
16	3F	0	1
17	3G	0	2
17	3H	0	1
18	A4	0	2
19	A5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
20	A8	0	4
24	AG	0	2
25	B1	0	3
26	B2	0	9
27	B3	0	7
29	BE	0	1
33	5D	0	1
34	5E	0	1
35	5F	0	1
36	5G	0	1
38	5I	0	2
43	RE	0	2
47	RJ	0	2
48	RK	0	1
49	RN	0	1
50	RO	0	1
51	RQ	0	1
All	All	0	53

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	AE	564	VAL	C-N	5.35	1.40	1.34

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SA	1746	A	C4'-C3'-O3'	8.88	126.33	113.00
3	SA	1147	A	C1'-C2'-O2'	-8.62	95.48	108.40
3	SA	915	A	C4'-C3'-O3'	8.19	125.29	113.00
3	SA	1746	A	C1'-C2'-O2'	-7.76	96.76	108.40
3	SA	1147	A	C4'-C3'-O3'	7.24	123.85	113.00

There are no chirality outliers.

5 of 53 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	3D	142	LEU	Peptide
14	3D	202	HIS	Peptide
14	3D	286	ARG	Peptide
7	SO	58	HIS	Peptide

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Mol	Chain	Res	Type	Group
10	ST	13	HIS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3711	0	1882	21	0
2	5A	11163	0	5611	81	0
3	SA	18356	0	9246	205	0
4	SG	1669	0	1724	18	0
5	SK	1388	0	1467	12	0
6	SN	865	0	874	15	0
7	SO	1087	0	1152	24	0
8	SP	868	0	894	26	0
9	SR	973	0	1029	13	0
10	ST	964	0	991	17	0
11	SY	786	0	843	7	0
12	Sd	497	0	535	3	0
13	3B	1865	0	1910	30	0
13	3C	1763	0	1805	36	0
14	3D	2848	0	2815	42	0
15	3E	3028	0	2813	63	0
16	3F	3248	0	3274	58	0
17	3G	916	0	964	11	0
17	3H	916	0	964	25	0
18	A4	5226	0	5199	93	0
19	A5	3976	0	3919	58	0
20	A8	3307	0	2316	40	0
21	A9	939	0	898	18	0
22	AE	5181	0	5373	87	0
23	AF	3911	0	3906	73	0
24	AG	6570	0	6473	129	0
25	B1	6635	0	6525	99	0
26	B2	6723	0	6698	132	0
27	B3	5882	0	5964	148	0
28	B8	3764	0	3757	57	0
29	BE	6810	0	6787	89	0
30	B6	2800	0	2517	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	5B	495	0	561	14	0
32	5C	4084	0	4092	77	0
33	5D	1972	0	2054	26	0
34	5E	1647	0	1678	33	0
35	5F	1530	0	1572	27	0
36	5G	2296	0	2325	39	0
37	5H	1065	0	1097	16	0
38	5I	3765	0	3714	72	0
39	5J	1280	0	1331	21	0
40	5K	1403	0	1484	20	0
41	RC	1410	0	1503	43	0
42	RD	1314	0	610	22	0
43	RE	8716	0	8828	160	0
44	RF	1404	0	1364	25	0
45	RG	1701	0	1767	39	0
45	RH	1799	0	1872	33	0
46	RI	2045	0	2162	37	0
47	RJ	5953	0	6152	105	0
48	RK	2781	0	2878	54	0
49	RN	4529	0	4262	68	0
50	RO	3766	0	3269	49	0
51	RQ	1436	0	1280	28	0
52	RS	2051	0	2096	53	0
53	RT	1357	0	1426	17	0
54	RW	381	0	255	4	0
55	X1	305	0	73	0	0
56	5K	1	0	0	0	0
57	RJ	32	0	12	2	0
58	RJ	1	0	0	0	0
All	All	179154	0	160842	2493	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2493 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:RD:1487:GLN:O	43:RE:411:ILE:HG23	1.40	1.18
27:B3:12:LEU:HD23	27:B3:377:LEU:HB2	1.23	1.17
8:SP:42:VAL:HG12	8:SP:67:VAL:HG23	1.31	1.12
8:SP:42:VAL:CG1	8:SP:67:VAL:HG23	1.82	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:12:LEU:CB	27:B3:377:LEU:HD12	1.84	1.07

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
5	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
6	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
7	SO	132/151 (87%)	121 (92%)	10 (8%)	1 (1%)	16	53
8	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	14	49
9	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
10	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
11	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
12	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
13	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
13	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
14	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
15	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
16	3F	400/573 (70%)	362 (90%)	37 (9%)	1 (0%)	36	71
17	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	53
17	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
18	A4	648/776 (84%)	591 (91%)	57 (9%)	0	100	100
19	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
20	A8	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	30	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
22	AE	645/1769 (36%)	595 (92%)	50 (8%)	0	100	100
23	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
24	AG	812/896 (91%)	732 (90%)	79 (10%)	1 (0%)	48	83
25	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
26	B2	839/943 (89%)	748 (89%)	89 (11%)	2 (0%)	43	77
27	B3	728/817 (89%)	595 (82%)	131 (18%)	2 (0%)	36	71
28	B8	469/594 (79%)	438 (93%)	31 (7%)	0	100	100
29	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100	100
30	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
31	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
32	5C	512/554 (92%)	474 (93%)	37 (7%)	1 (0%)	43	77
33	5D	231/250 (92%)	205 (89%)	26 (11%)	0	100	100
34	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	24	63
35	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100	100
36	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100	100
37	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100	100
38	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
39	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
40	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
41	RC	173/316 (55%)	169 (98%)	4 (2%)	0	100	100
42	RD	263/1729 (15%)	254 (97%)	9 (3%)	0	100	100
43	RE	1067/1237 (86%)	998 (94%)	69 (6%)	0	100	100
44	RF	168/297 (57%)	145 (86%)	23 (14%)	0	100	100
45	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
45	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
46	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100	100
47	RJ	722/1183 (61%)	670 (93%)	51 (7%)	1 (0%)	48	83
48	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
49	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	43	77
50	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	RQ	188/899 (21%)	177 (94%)	11 (6%)	0	100	100
52	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
53	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
54	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
All	All	18453/27161 (68%)	16810 (91%)	1628 (9%)	15 (0%)	49	83

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	5E	454	VAL
7	SO	106	ARG
8	SP	45	GLY
47	RJ	82	LYS
20	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	SG	180/191 (94%)	179 (99%)	1 (1%)	78	80
5	SK	147/166 (89%)	147 (100%)	0	100	100
6	SN	88/119 (74%)	87 (99%)	1 (1%)	65	74
7	SO	117/128 (91%)	115 (98%)	2 (2%)	53	67
8	SP	90/105 (86%)	89 (99%)	1 (1%)	65	74
9	SR	105/119 (88%)	105 (100%)	0	100	100
10	ST	105/129 (81%)	105 (100%)	0	100	100
11	SY	85/120 (71%)	83 (98%)	2 (2%)	43	63
12	Sd	56/60 (93%)	56 (100%)	0	100	100
13	3B	201/240 (84%)	201 (100%)	0	100	100
13	3C	190/240 (79%)	188 (99%)	2 (1%)	65	74
14	3D	296/435 (68%)	295 (100%)	1 (0%)	86	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	3E	262/433 (60%)	261 (100%)	1 (0%)	84	82
16	3F	354/503 (70%)	350 (99%)	4 (1%)	65	74
17	3G	100/104 (96%)	100 (100%)	0	100	100
17	3H	100/104 (96%)	100 (100%)	0	100	100
18	A4	591/713 (83%)	584 (99%)	7 (1%)	63	73
19	A5	433/574 (75%)	429 (99%)	4 (1%)	70	76
20	A8	174/657 (26%)	173 (99%)	1 (1%)	78	80
21	A9	89/533 (17%)	89 (100%)	0	100	100
22	AE	589/1633 (36%)	587 (100%)	2 (0%)	86	84
23	AF	437/454 (96%)	431 (99%)	6 (1%)	59	71
24	AG	750/826 (91%)	739 (98%)	11 (2%)	57	70
25	B1	730/812 (90%)	720 (99%)	10 (1%)	59	71
26	B2	736/832 (88%)	729 (99%)	7 (1%)	68	76
27	B3	660/719 (92%)	644 (98%)	16 (2%)	43	63
28	B8	421/529 (80%)	417 (99%)	4 (1%)	68	76
29	BE	757/819 (92%)	752 (99%)	5 (1%)	76	79
30	B6	251/414 (61%)	249 (99%)	2 (1%)	73	77
31	5B	57/196 (29%)	56 (98%)	1 (2%)	51	67
32	5C	448/480 (93%)	445 (99%)	3 (1%)	76	79
33	5D	221/234 (94%)	221 (100%)	0	100	100
34	5E	185/535 (35%)	185 (100%)	0	100	100
35	5F	171/172 (99%)	168 (98%)	3 (2%)	51	67
36	5G	251/258 (97%)	246 (98%)	5 (2%)	48	65
37	5H	107/538 (20%)	107 (100%)	0	100	100
38	5I	416/443 (94%)	412 (99%)	4 (1%)	68	76
39	5J	140/200 (70%)	140 (100%)	0	100	100
40	5K	157/169 (93%)	157 (100%)	0	100	100
41	RC	158/289 (55%)	156 (99%)	2 (1%)	61	72
43	RE	984/1125 (88%)	972 (99%)	12 (1%)	63	73
44	RF	159/274 (58%)	157 (99%)	2 (1%)	61	72
45	RG	195/222 (88%)	193 (99%)	2 (1%)	68	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	RH	206/222 (93%)	205 (100%)	1 (0%)	81	81
46	RI	235/256 (92%)	234 (100%)	1 (0%)	84	82
47	RJ	648/1039 (62%)	643 (99%)	5 (1%)	73	77
48	RK	307/312 (98%)	304 (99%)	3 (1%)	68	76
49	RN	422/732 (58%)	422 (100%)	0	100	100
50	RO	329/506 (65%)	326 (99%)	3 (1%)	70	76
51	RQ	132/808 (16%)	129 (98%)	3 (2%)	44	63
52	RS	225/424 (53%)	224 (100%)	1 (0%)	84	82
53	RT	148/282 (52%)	148 (100%)	0	100	100
54	RW	22/192 (12%)	21 (96%)	1 (4%)	24	46
All	All	15417/22619 (68%)	15275 (99%)	142 (1%)	68	76

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	RE	400	LEU
43	RE	1087	LEU
47	RJ	1069	VAL
25	B1	164	THR
25	B1	141	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 364 such sidechains are listed below:

Mol	Chain	Res	Type
32	5C	468	GLN
43	RE	634	HIS
34	5E	316	ASN
38	5I	281	ASN
44	RF	63	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)
3	SA	848/1808 (46%)	301 (35%)	20 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	1535/2841 (54%)	506 (32%)	33 (2%)

5 of 506 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	1632	C
3	SA	1654	G
3	SA	1749	A
2	5A	536	A
2	5A	492	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 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
57	GTP	RJ	1201	58	33,34,34	0.56	0	50,54,54	0.72	1 (2%)

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
57	GTP	RJ	1201	58	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	RJ	1201	GTP	C4'-O4'-C1'	-2.14	104.73	109.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	RJ	1201	GTP	O4'-C4'-C5'-O5'
57	RJ	1201	GTP	C3'-C4'-C5'-O5'
57	RJ	1201	GTP	C4'-C5'-O5'-PA

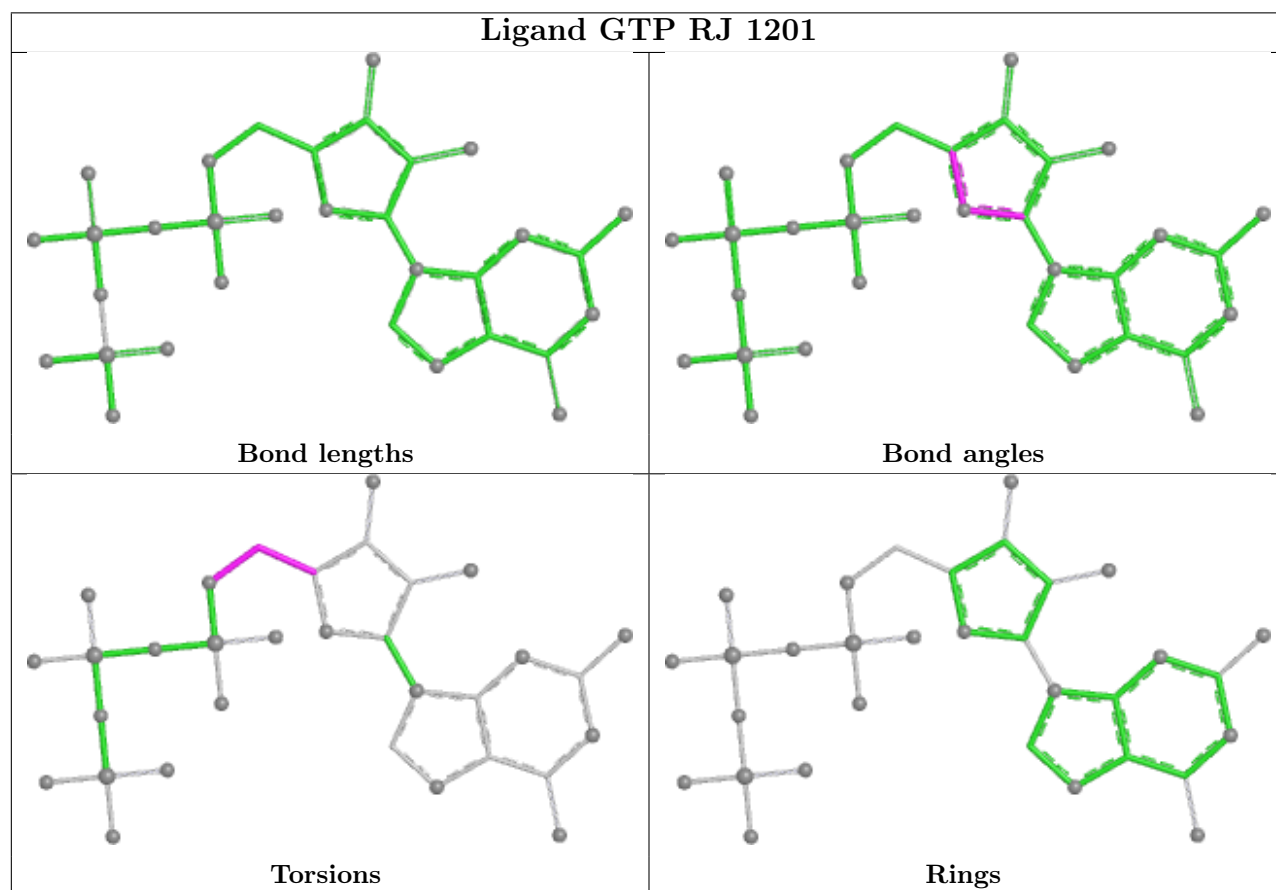
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	RJ	1201	GTP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

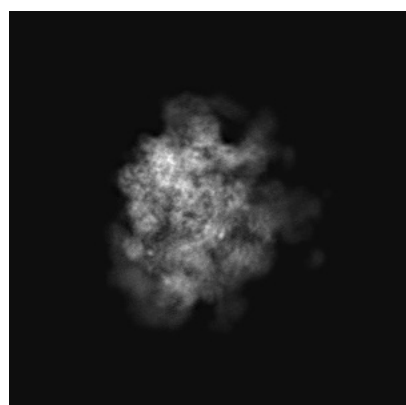
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30584. These allow visual inspection of the internal detail of the map and identification of artifacts.

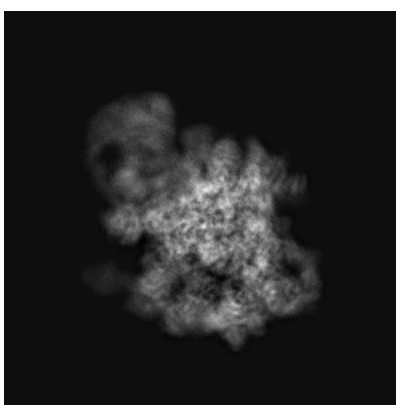
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

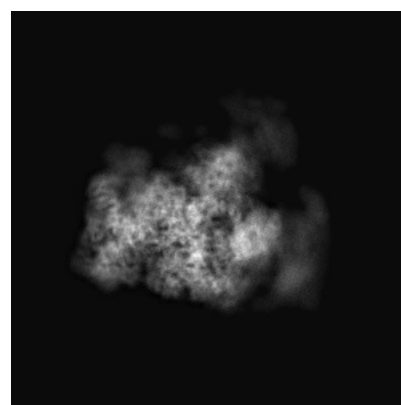
6.1.1 Primary map



X



Y

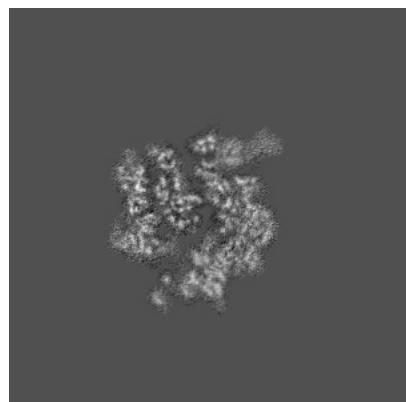


Z

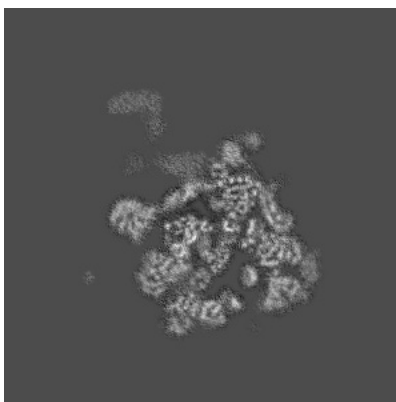
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

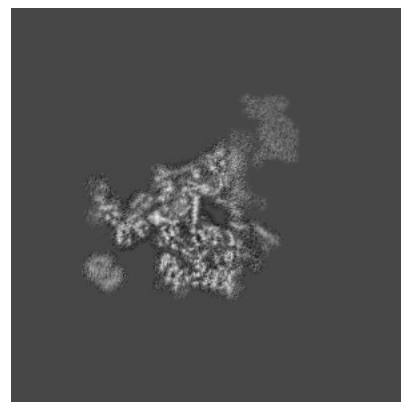
6.2.1 Primary map



X Index: 200



Y Index: 200

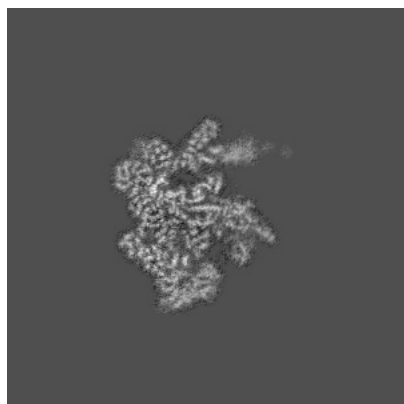


Z Index: 200

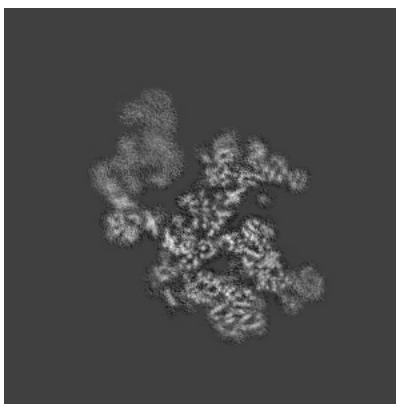
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

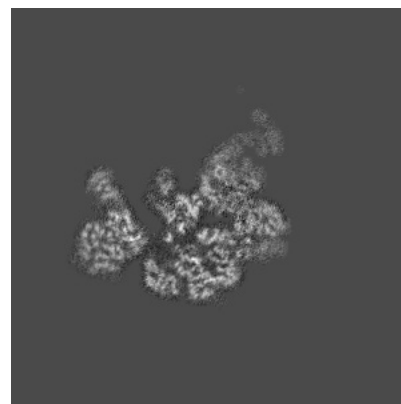
6.3.1 Primary map



X Index: 184



Y Index: 177

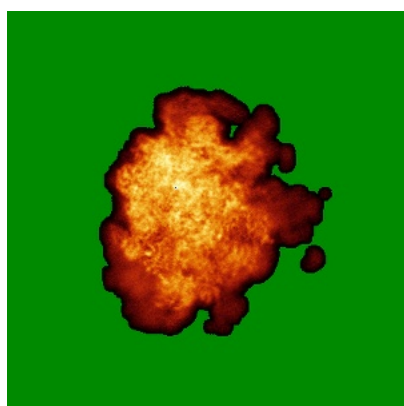


Z Index: 222

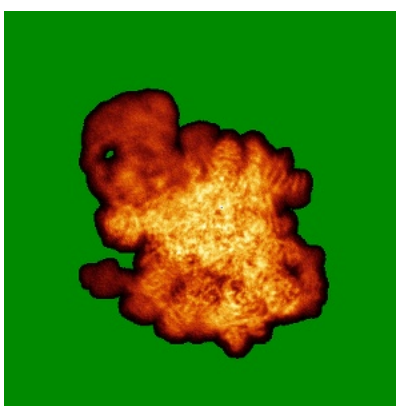
The images above show the largest variance slices of the map in three orthogonal directions.

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

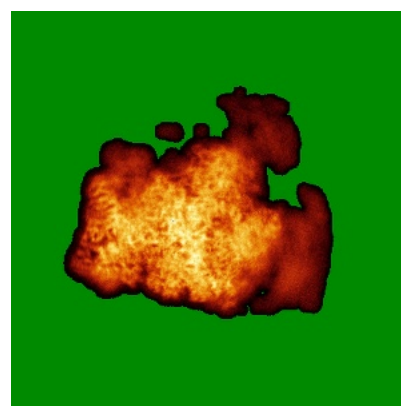
6.4.1 Primary map



X



Y

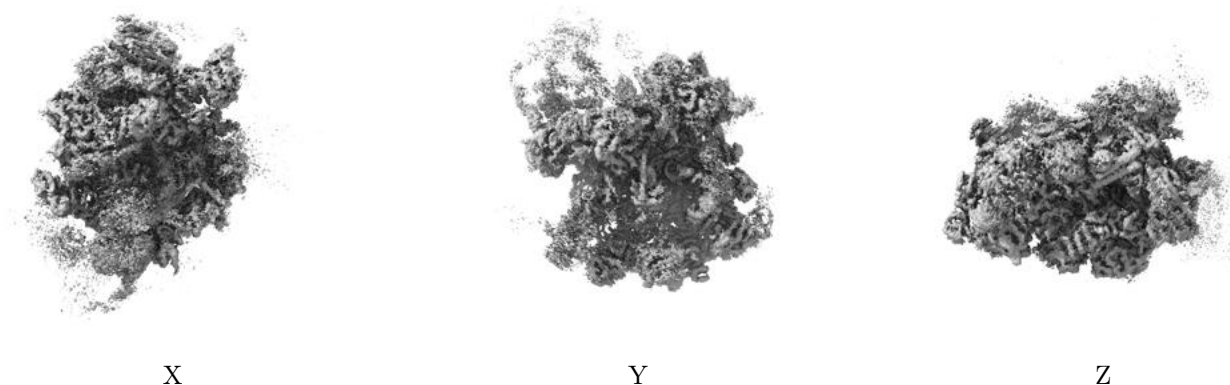


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

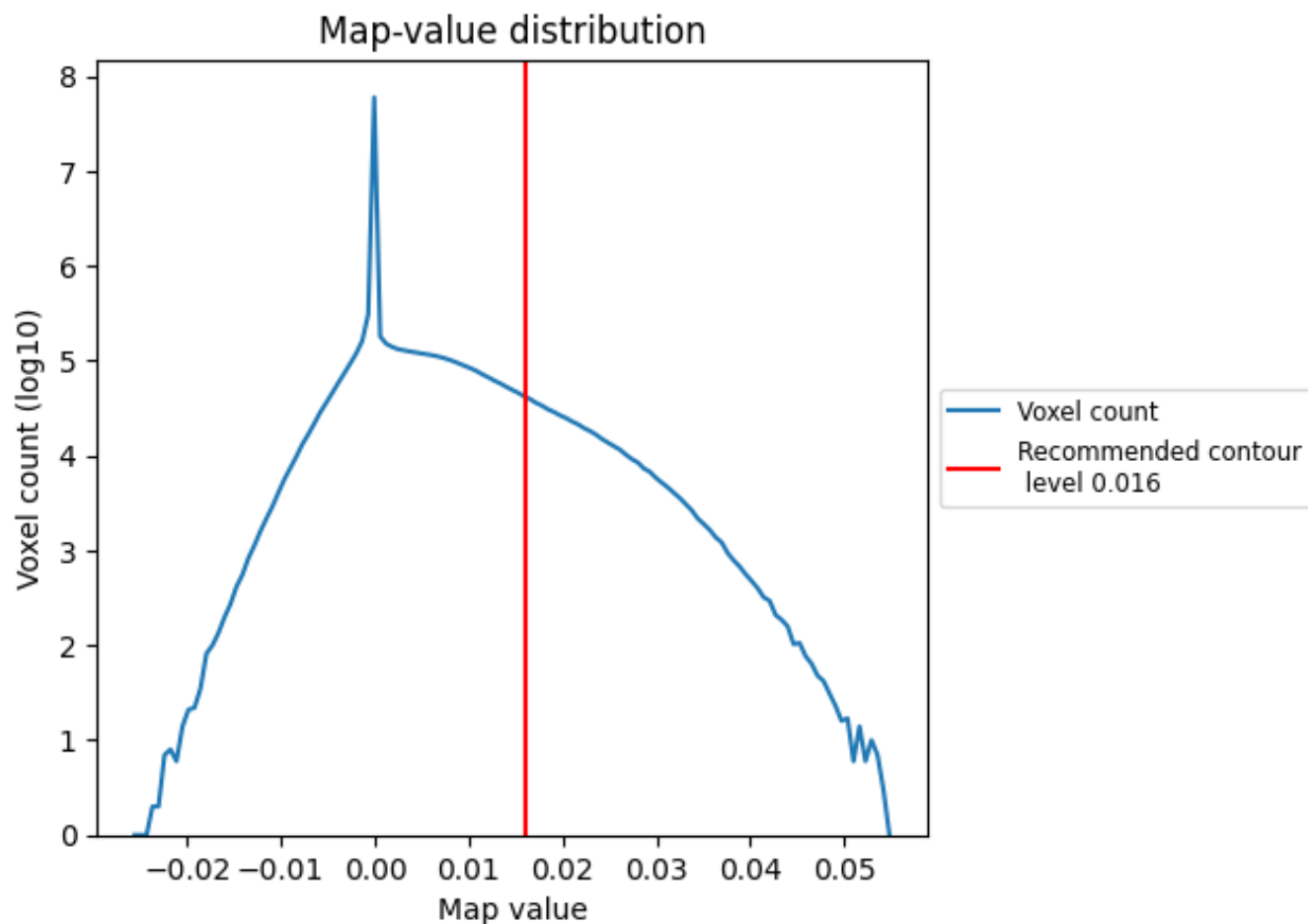
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

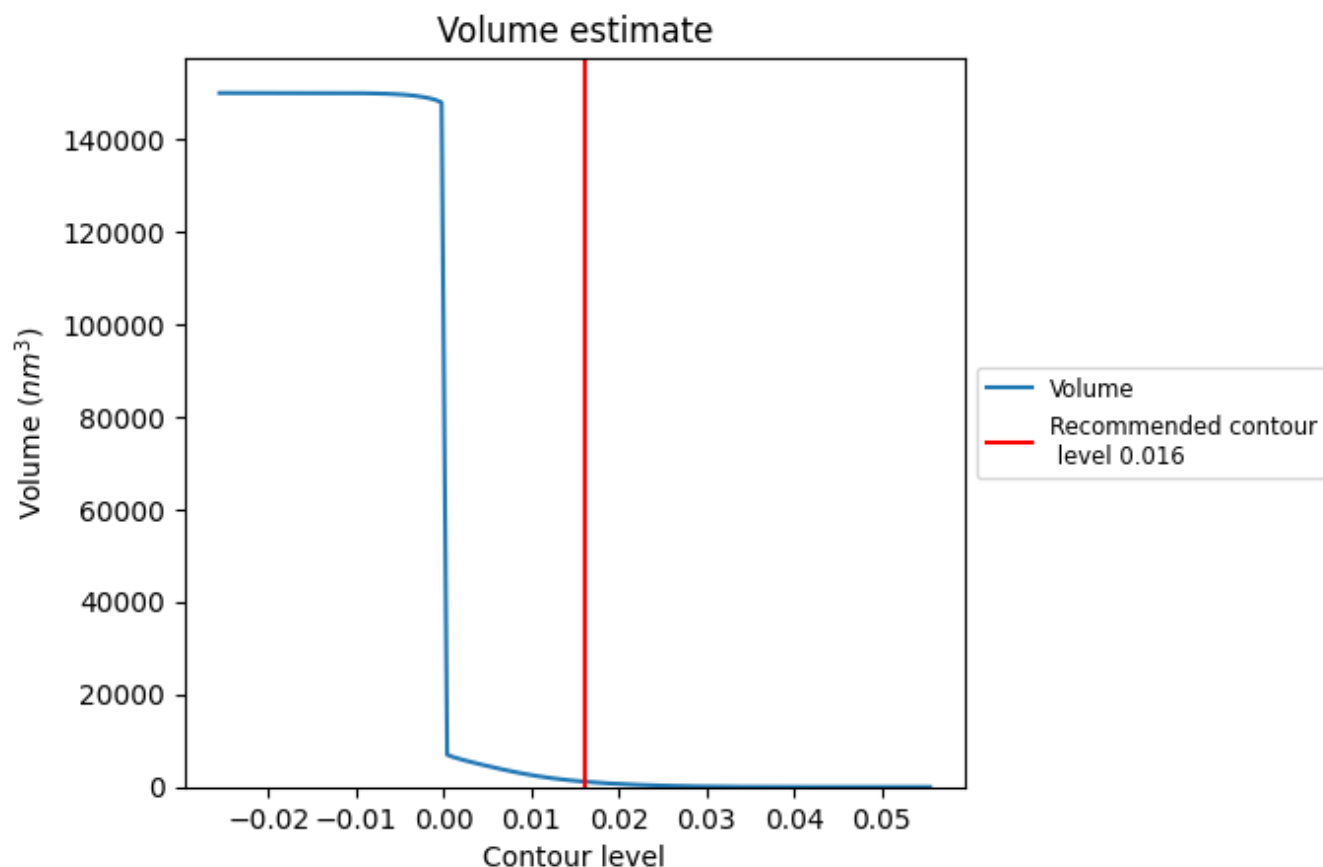
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

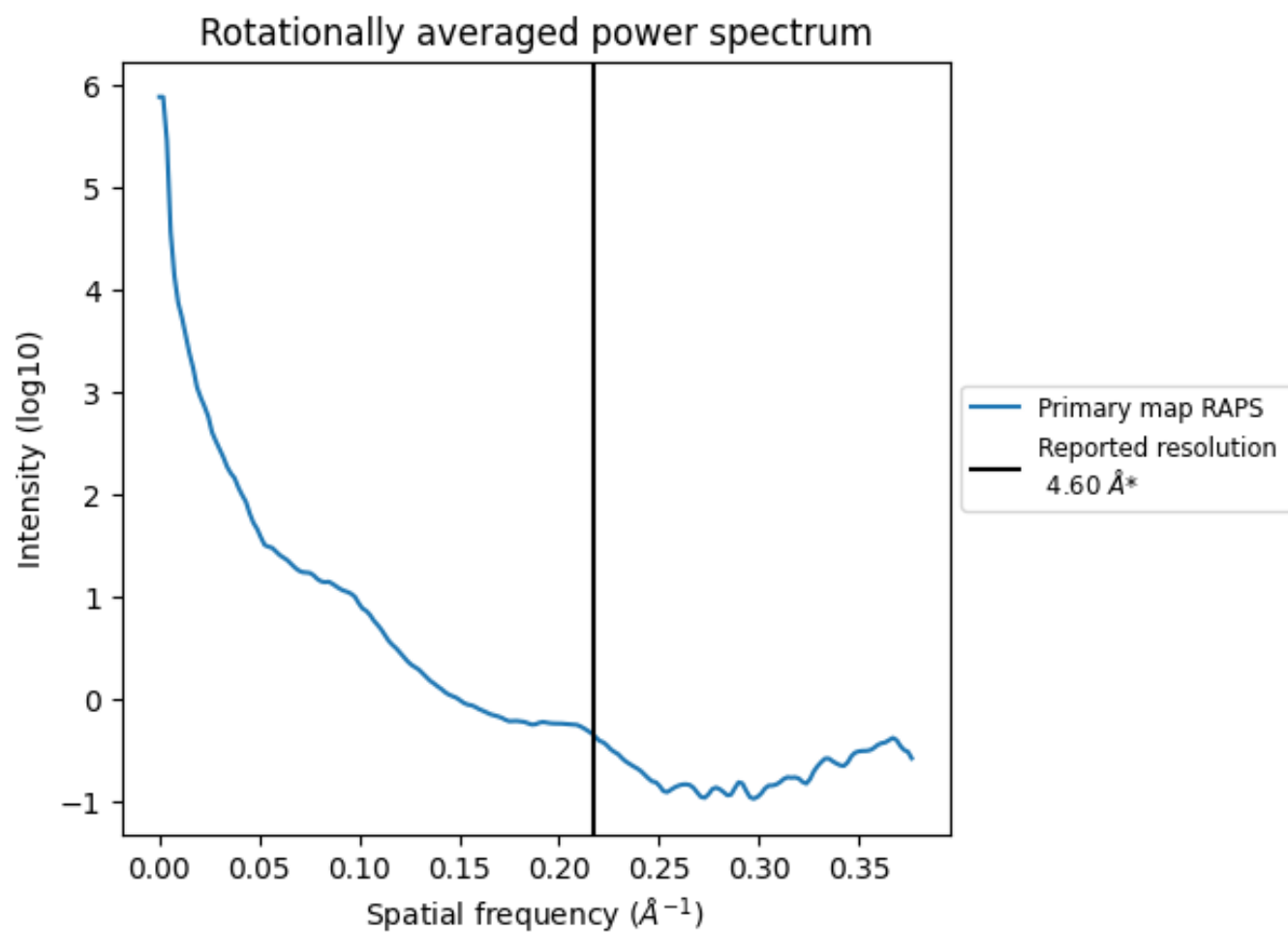
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1155 nm^3 ; this corresponds to an approximate mass of 1044 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 0.217 Å⁻¹

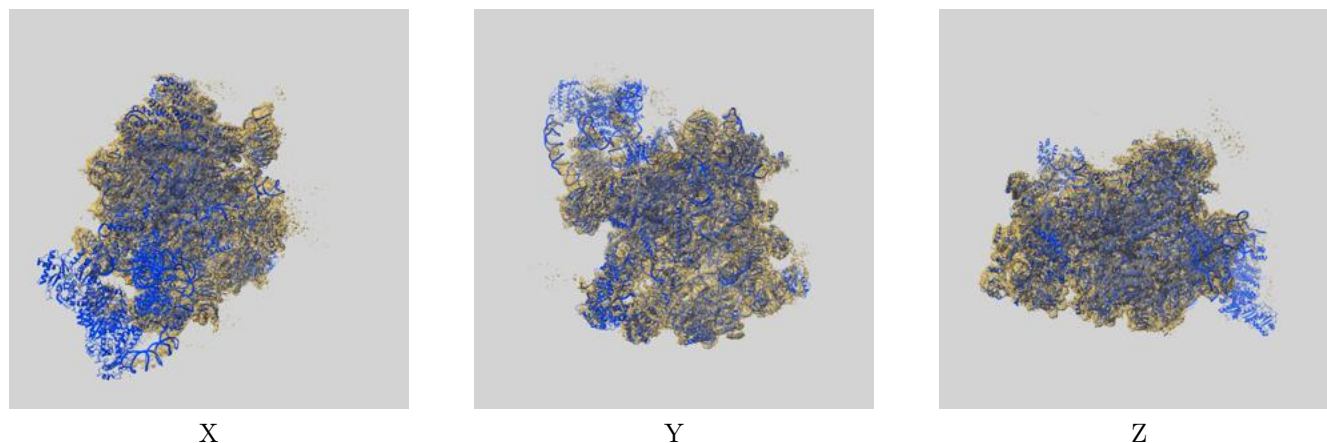
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

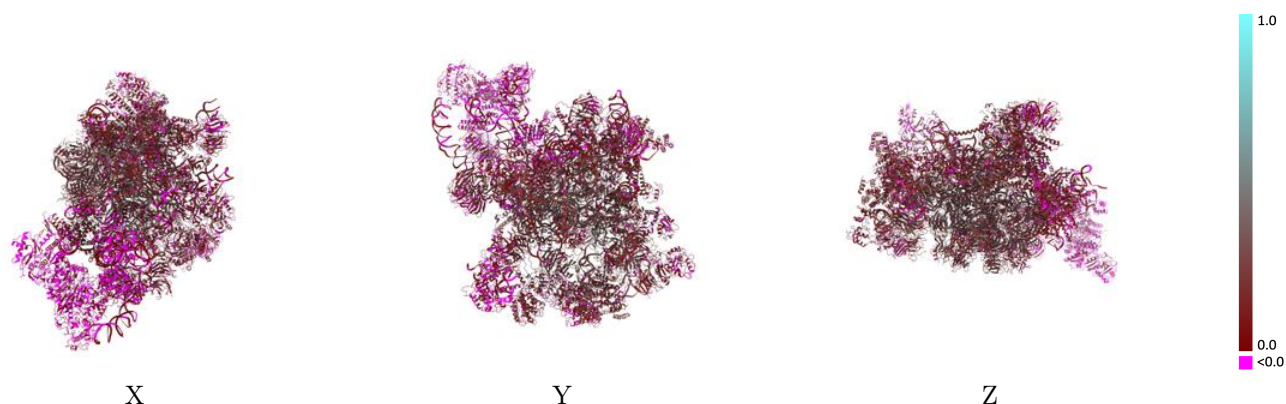
This section contains information regarding the fit between EMDB map EMD-30584 and PDB model 7D5S. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



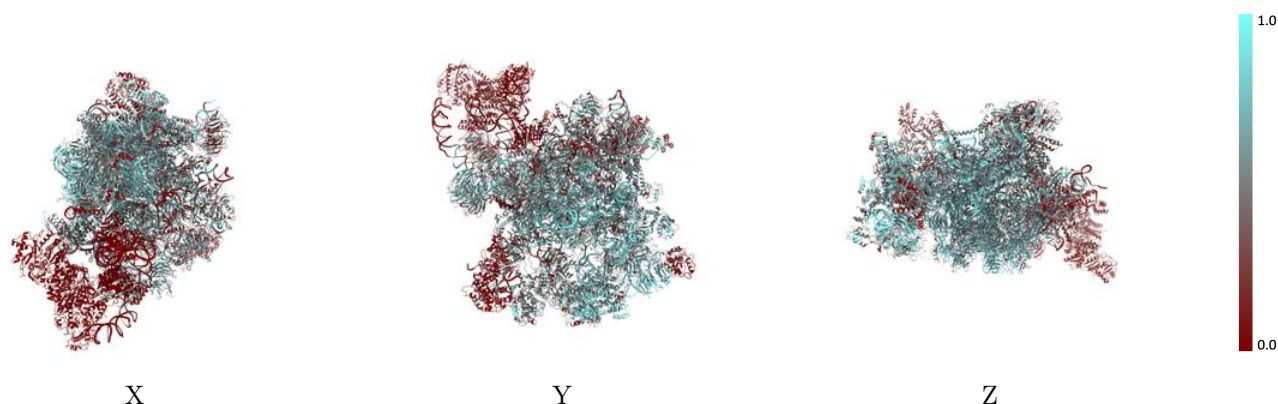
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



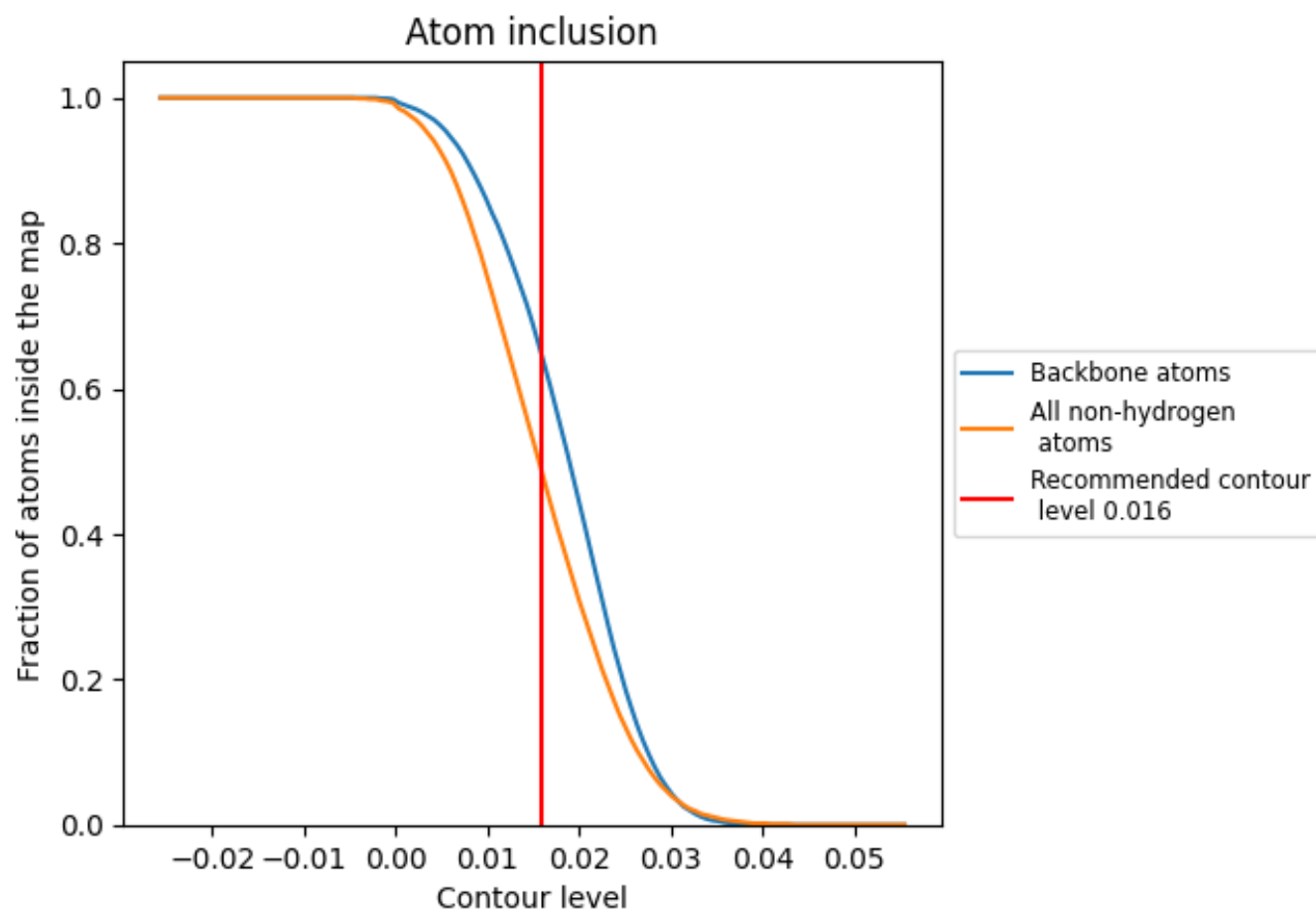
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 64% of all backbone atoms, 48% 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	 0.4820	 0.1810
3A	 0.7750	 0.2400
3B	 0.5190	 0.2300
3C	 0.5630	 0.2000
3D	 0.5420	 0.1850
3E	 0.5950	 0.2150
3F	 0.3600	 0.1270
3G	 0.6170	 0.2850
3H	 0.4440	 0.2030
5A	 0.7380	 0.2250
5B	 0.5020	 0.1960
5C	 0.5190	 0.2300
5D	 0.5620	 0.2480
5E	 0.4920	 0.2040
5F	 0.5780	 0.2600
5G	 0.4710	 0.2230
5H	 0.4360	 0.1930
5I	 0.5640	 0.1830
5J	 0.3770	 0.1950
5K	 0.4330	 0.1940
A4	 0.6490	 0.2330
A5	 0.6400	 0.2520
A8	 0.4600	 0.1310
A9	 0.6130	 0.2000
AE	 0.3960	 0.1900
AF	 0.6420	 0.2690
AG	 0.6370	 0.2400
B1	 0.6170	 0.2730
B2	 0.5790	 0.1620
B3	 0.2620	 0.0760
B6	 0.4860	 0.1650
B8	 0.6630	 0.2900
BE	 0.6510	 0.2670
RC	 0.0180	 0.0130
RD	 0.0380	 0.0320



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Chain	Atom inclusion	Q-score
RE	 0.0030	 0.0090
RF	 0.0000	 -0.0230
RG	 0.3780	 0.1680
RH	 0.4420	 0.2090
RI	 0.5760	 0.2190
RJ	 0.5170	 0.1940
RK	 0.4680	 0.1600
RN	 0.3660	 0.1580
RO	 0.5490	 0.1940
RQ	 0.2300	 0.1500
RS	 0.1150	 0.0550
RT	 0.4890	 0.1240
RW	 0.2090	 0.1480
SA	 0.4460	 0.1350
SG	 0.5980	 0.2850
SK	 0.3330	 0.1550
SN	 0.0090	 0.0370
SO	 0.0060	 -0.0110
SP	 0.0110	 0.0160
SR	 0.5680	 0.3000
ST	 0.2810	 0.1720
SY	 0.2990	 0.1390
Sd	 0.5740	 0.2920
X1	 0.3110	 0.1720