



## wwPDB EM Validation Summary Report ⓘ

Nov 3, 2025 – 05:07 PM EST

PDB ID : 9N6W / pdb\_00009n6w  
EMDB ID : EMD-49076  
Title : SSU processome maturation and disassembly, State A\*  
Authors : Buzovetsky, O.; Klinge, S.  
Deposited on : 2025-02-05  
Resolution : 3.05 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](mailto: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>.

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

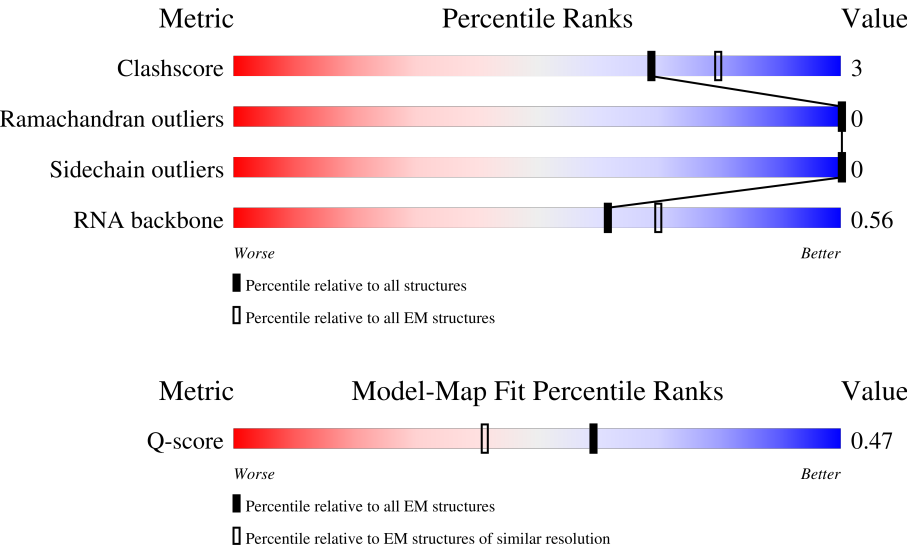
EMDB validation analysis : 0.0.1.dev129  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
EM percentile statistics : 202505.v01 (Using data in the EMDB 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) : 2.46

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.05 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	13971 ( 2.55 - 3.55 )

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  $\geq 3$ , 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	L0	700	<div> <div>5%</div> <div>58%</div> <div>14%</div> <div>25%</div> </div>
2	L1	1808	<div> <div>6%</div> <div>49%</div> <div>13%</div> <div>36%</div> </div>
3	L2	333	<div> <div>42%</div> <div>9%</div> <div>47%</div> </div>

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Mol	Chain	Length	Quality of chain
4	L3	146	
5	L4	261	
6	L5	225	
7	L6	236	
8	L7	190	
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LO	923	
24	LP	440	
25	LQ	943	
26	LR	817	
27	LS	594	
28	LT	939	

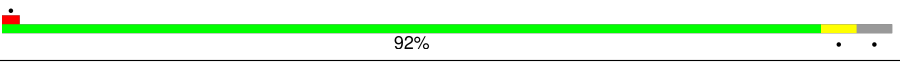

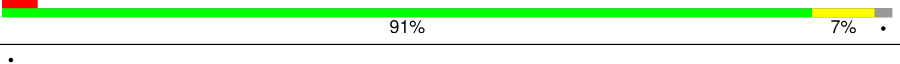


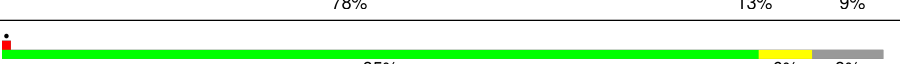
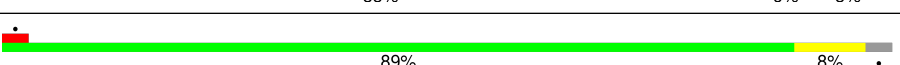
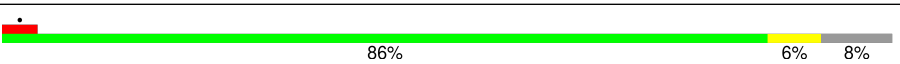


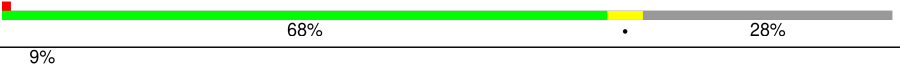

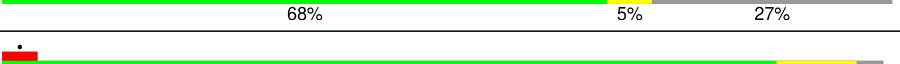
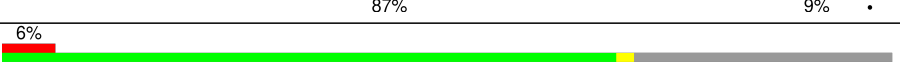
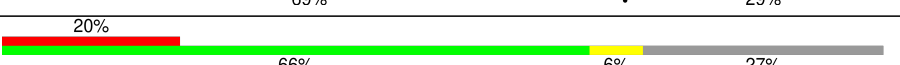

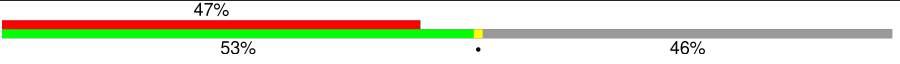


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Mol	Chain	Length	Quality of chain
29	LU	489	
30	LV	707	
31	LW	554	
32	LX	1056	
32	LY	1056	
33	LZ	183	
34	NA	593	
35	NB	610	
36	NC	357	
37	ND	214	
38	NE	346	
39	NF	151	
40	NG	137	
41	NH	1237	
42	NI	297	
43	NK	316	
44	NM	255	
45	NN	534	
46	NQ	82	
47	OA	1729	
48	SA	504	
49	SB	511	
50	SC	327	
50	SD	327	
51	SE	126	

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Mol	Chain	Length	Quality of chain
51	SF	126	
52	SG	573	
53	SH	367	
54	SI	1183	
55	SJ	252	
55	SK	252	
56	SL	189	
57	SM	290	
58	SN	274	
59	SP	2493	
60	SQ	217	
61	SR	145	
62	SS	899	
63	ST	810	
64	SU	552	
65	SV	206	
66	SW	274	
67	SY	250	
68	SZ	483	

## 2 Entry composition

There are 72 unique types of molecules in this entry. The entry contains 243904 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 5'ETS rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	523	Total	C	N	O	P	0	0
			11158	4986	1978	3671	523		

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1149	Total	C	N	O	P	0	0
			24510	10958	4383	8020	1149		

- Molecule 3 is a RNA chain called TPA: *Saccharomyces cerevisiae* U3a gene for small nucleolar RNA U3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	175	Total	C	N	O	P	0	0
			3712	1661	649	1227	175		

- Molecule 4 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	97	Total	C	N	O	S	0	0
			786	498	144	142	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	234	Total	C	N	O	S	0	0
			1866	1195	343	325	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	206	Total	C	N	O	S	0	0
			1635	1027	300	305	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	206	Total	C	N	O	S	0	0
			1653	1043	315	293	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	169	Total	C	N	O	S	0	0
			1347	869	230	248			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	171	Total	C	N	O	S	0	0
			1356	842	270	242	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	171	Total	C	N	O	S	0	0
			1388	879	268	240	1		

- Molecule 11 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	125	Total	C	N	O	S	0	0
			973	625	174	174			

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	137	Total	C	N	O	S	0	0
			1112	714	212	183	3		

- Molecule 13 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	129	Total	C	N	O	S	0	0
			1022	650	188	181	3		

- Molecule 14 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LF	95	Total	C	N	O	0	0
			753	483	136	134		

- Molecule 15 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	62	Total	C	N	O	S	0	0
			490	302	98	89	1		

- Molecule 16 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	808	Total	C	N	O	S	0	0
			6465	4123	1090	1233	19		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	600	Total	C	N	O	S	0	0
			3792	2375	679	733	5		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	132	Total	C	N	O	S	0	0
			1068	681	185	199	3		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	504	Total	C	N	O	S	0	0
			3982	2522	679	768	13		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 10.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	1613	Total	C	N	O	S	0	0
			9380	5798	1748	1822	12		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	663	Total	C	N	O	S	0	0
			5263	3333	913	995	22		

- Molecule 23 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	LO	834	Total	C	N	O	P	S	0	0
			6639	4223	1140	1256	1	19		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	380	Total	C	N	O	S	0	0
			3220	2081	545	578	16		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	841	Total	C	N	O	S	0	0
			6707	4284	1125	1271	27		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	793	Total	C	N	O	S	0	0
			6207	3931	1044	1203	29		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	LS	480	Total	C	N	O	P	S	0	0
			3793	2402	666	715	1	9		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	873	Total	C	N	O	S	0	0
			6876	4363	1188	1303	22		

- Molecule 29 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	460	Total	C	N	O	S	0	0
			3756	2349	685	706	16		

- Molecule 30 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	405	Total	C	N	O	S	0	0
			3286	2083	567	626	10		

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 7.

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

- Molecule 32 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LX	852	Total	C	N	O	S	0	0
			6803	4350	1173	1254	26		
32	LY	846	Total	C	N	O	S	0	0
			6179	3918	1079	1165	17		

- Molecule 33 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	181	Total	C	N	O	S	0	0
			1524	964	286	267	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	NA	286	Total	C	N	O	S	0	0
			2075	1279	378	414	4		

- Molecule 35 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	NB	267	Total	C	N	O	S	0	0
			1873	1156	360	356	1		

- Molecule 36 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NC	250	Total	C	N	O	S	0	0
			1693	1015	345	330	3		

- Molecule 37 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	ND	74	Total	C	N	O	0	0
			609	380	119	110		

- Molecule 38 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	NE	215	Total	C	N	O	S	0	0
			1649	1021	327	298	3		

- Molecule 39 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	NF	141	Total	C	N	O	S	0	0
			1135	725	214	194	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NG	119	Total	C	N	O	S	0	0
			875	541	166	165	3		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	NH	1077	Total	C	N	O	S	0	0
			8693	5650	1434	1585	24		

- Molecule 42 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	NI	240	Total	C	N	O	S	0	0
			1953	1248	331	366	8		

- Molecule 43 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	NK	257	Total	C	N	O	S	0	0
			2107	1344	369	381	13		

- Molecule 44 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	NM	230	Total	C	N	O	S	0	0
			1838	1163	337	334	4		

- Molecule 45 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	NN	267	Total	C	N	O	S	0	0
			1481	909	280	292			

- Molecule 46 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	NQ	79	Total	C	N	O	S	0	0
			595	371	108	111	5		

- Molecule 47 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	OA	13	Total	C	N	O	S	0	0
			96	63	14	19			

- Molecule 48 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	388	Total	C	N	O	S	0	0
			3056	1938	525	584	9		

- Molecule 49 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SB	436	Total	C	N	O	S	0	0
			3357	2116	574	657	10		

- Molecule 50 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	241	Total	C	N	O	S	0	0
			1871	1185	337	339	10		
50	SD	232	Total	C	N	O	S	0	0
			1817	1153	324	330	10		

- Molecule 51 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
51	SF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 52 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	SG	453	Total	C	N	O	P	S	0	0
			3627	2302	633	681	1	10		

- Molecule 53 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 54 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	815	Total	C	N	O	S	0	0
			6616	4243	1167	1177	29		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SJ	213	Total	C	N	O	S	0	0
			1678	1069	292	306	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
55	SK	229	Total	C	N	O	S	0	0
			1793	1141	312	329	11		

- Molecule 56 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	173	Total	C	N	O	S	0	0
			1384	881	254	239	10		

- Molecule 57 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 58 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SN	253	Total	C	N	O	S	0	0
			2053	1313	364	368	8		

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	2156	Total	C	N	O	S	0	0
			17548	11328	2906	3254	60		

- Molecule 60 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	135	Total	C	N	O	S	0	0
			1137	721	211	201	4		

- Molecule 61 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	104	Total	C	N	O	S	0	0
			792	506	145	139	2		

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SS	253	Total	C	N	O	S	0	0
			2102	1314	389	391	8		

- Molecule 63 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	ST	588	Total	C	N	O	S	0	0
			4482	2845	808	817	12		

- Molecule 64 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SU	534	Total	C	N	O	S	0	0
			4370	2845	709	802	14		

- Molecule 65 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SV	147	Total	C	N	O		0	0
			869	529	160	180			

- Molecule 66 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SW	199	Total	C	N	O	S	0	0
			1565	998	284	279	4		

- Molecule 67 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SY	233	Total	C	N	O	S	0	0
			1953	1218	379	349	7		

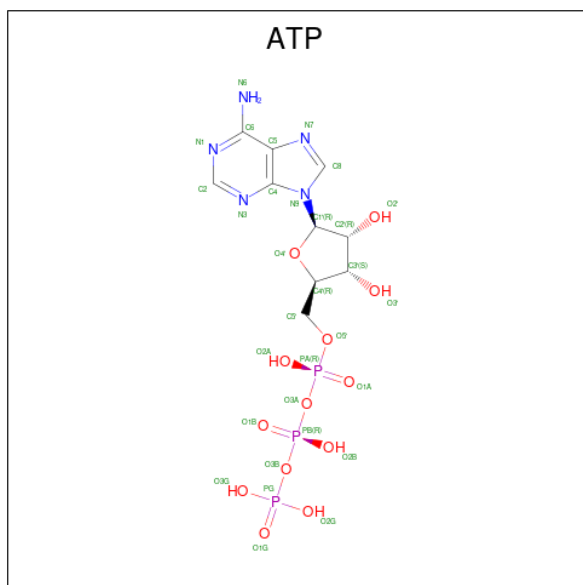
- Molecule 68 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SZ	259	Total	C	N	O		0	0
			1314	796	259	259			

- Molecule 69 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
69	L1	22	Total	Mg	0
			22	22	
69	L2	1	Total	Mg	0
			1	1	
69	NH	1	Total	Mg	0
			1	1	
69	SI	1	Total	Mg	0
			1	1	

- Molecule 70 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



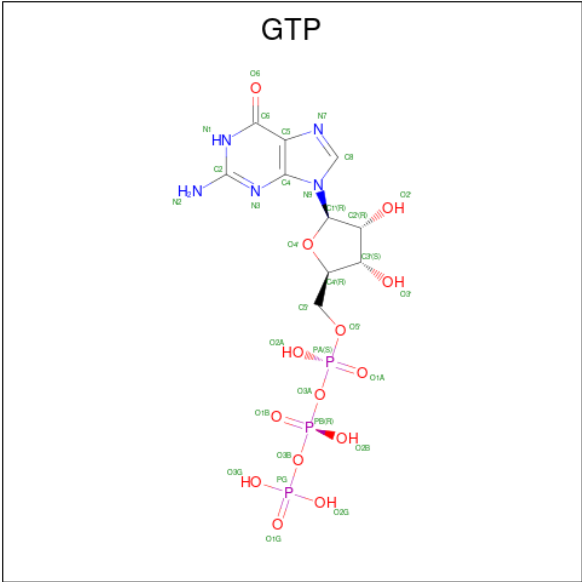
Mol	Chain	Residues	Atoms					AltConf
70	NH	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 71 is ZINC ION (CCD ID: ZN) (formula:  $Zn$ ).

Mol	Chain	Residues	Atoms		AltConf
71	NQ	1	Total	Zn	0
			1	1	
71	SL	1	Total	Zn	0
			1	1	

- Molecule 72 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).

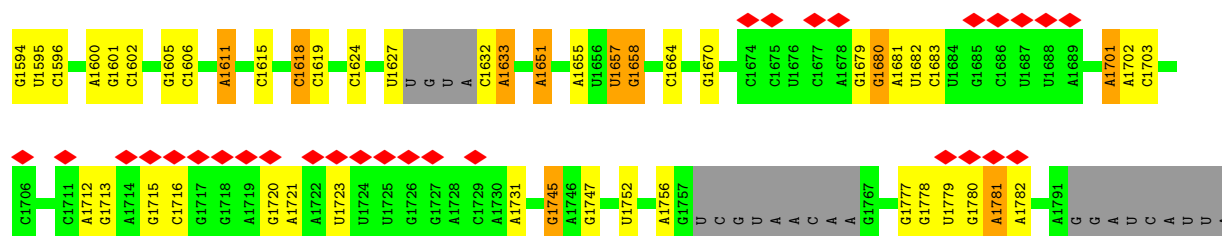




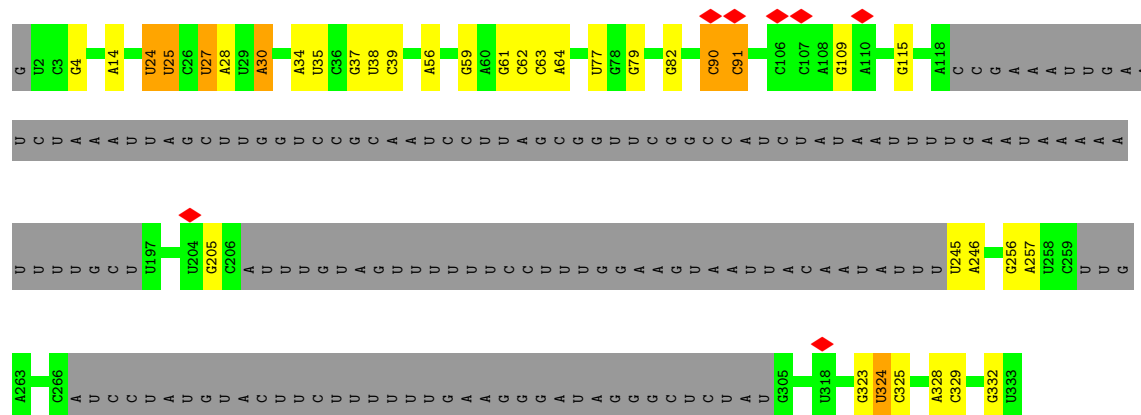
Mol	Chain	Residues	Atoms					AltConf
72	SI	1	Total	C	N	O	P	0
			32	10	5	14	3	



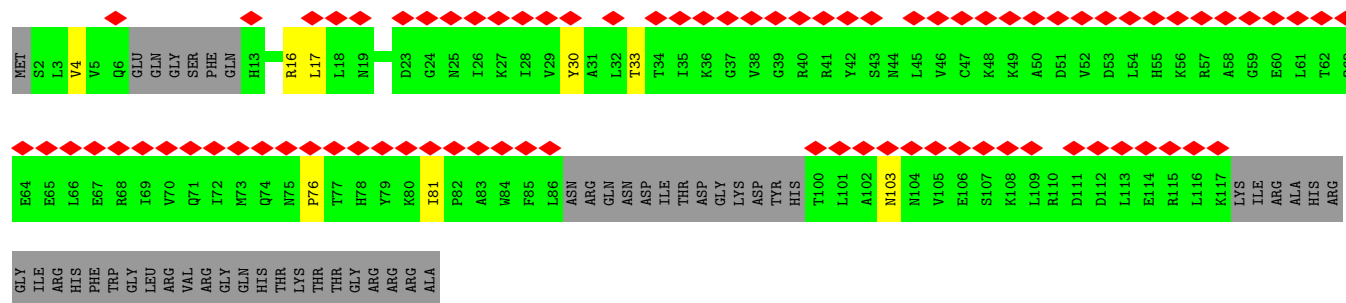




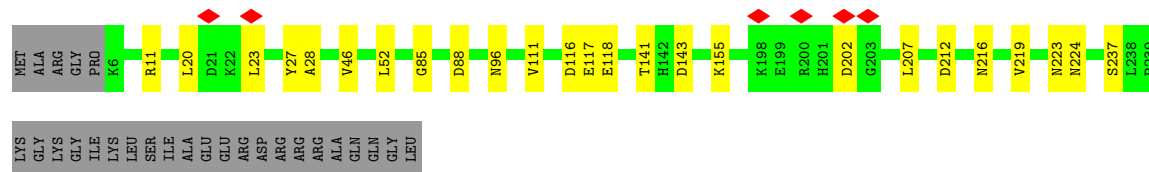
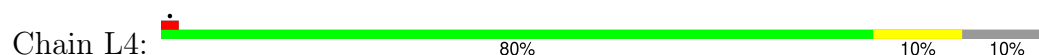
- Molecule 3: TPA: *Saccharomyces cerevisiae* U3a gene for small nucleolar RNA U3a




- Molecule 4: 40S ribosomal protein S18-A

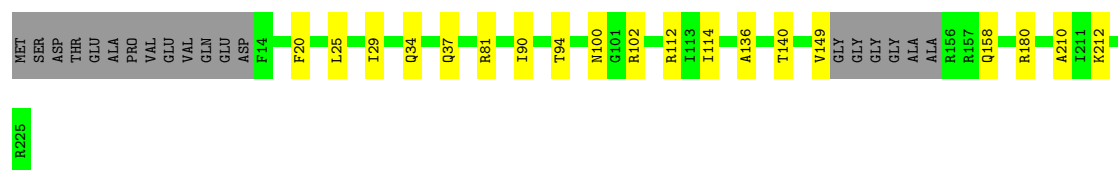


- Molecule 5: 40S ribosomal protein S4-A




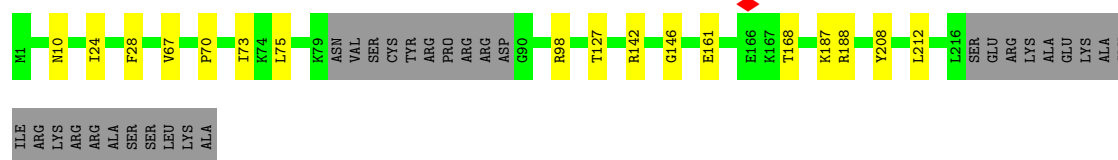
- Molecule 6: 40S ribosomal protein S5

Chain L5: 




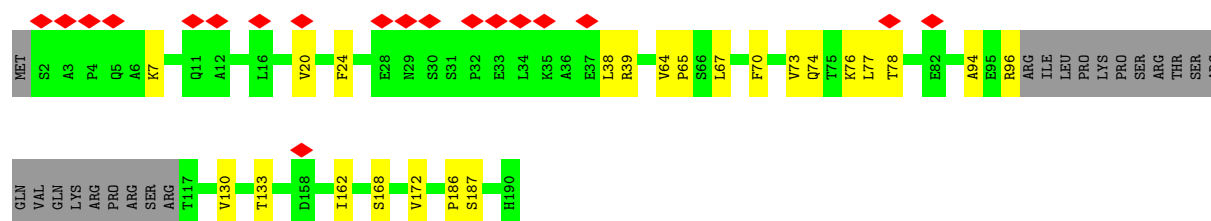
- Molecule 7: 40S ribosomal protein S6-A

Chain L6: 




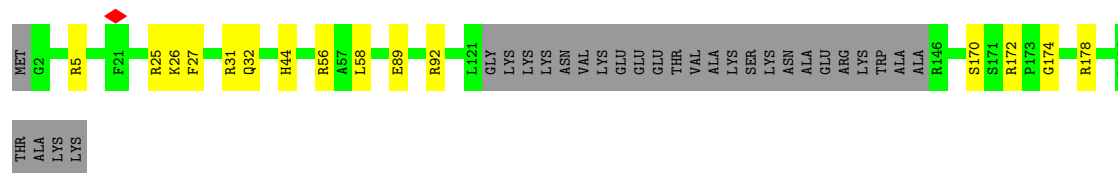
- Molecule 8: 40S ribosomal protein S7-A

Chain L7: 




- Molecule 9: 40S ribosomal protein S8-A

Chain L8: 




- Molecule 10: 40S ribosomal protein S9-A

Chain L9: 

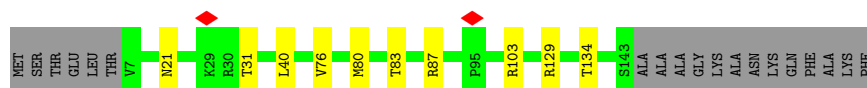
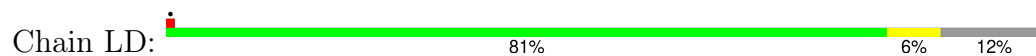


- Molecule 11: 40S ribosomal protein S16-A

Chain LC: 



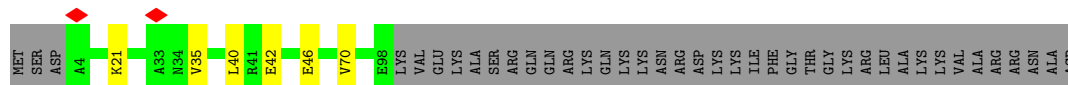
- Molecule 12: 40S ribosomal protein S11-A



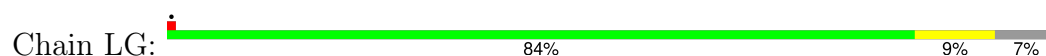
- Molecule 13: 40S ribosomal protein S22-A



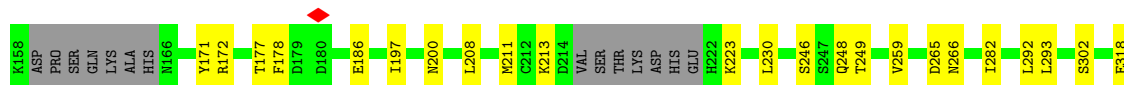
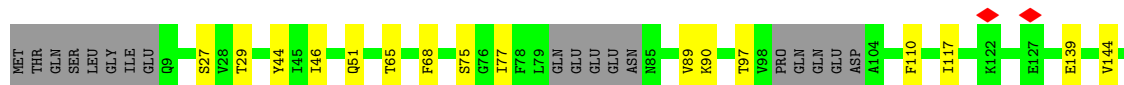
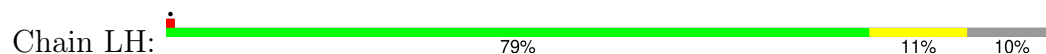
- Molecule 14: 40S ribosomal protein S24-A

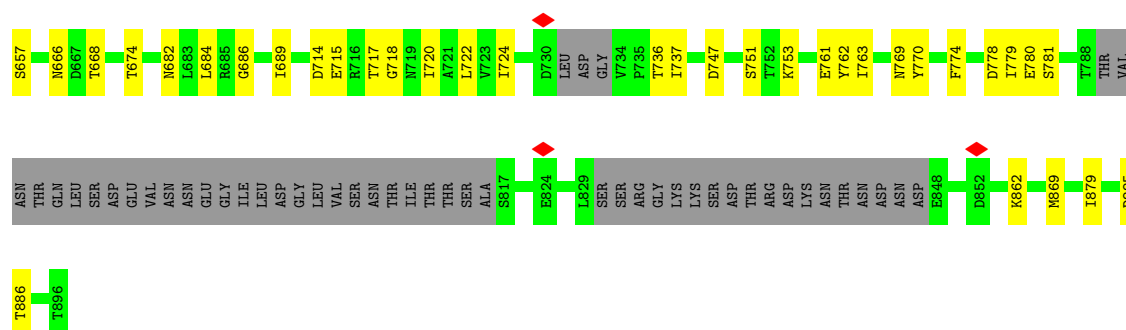


- Molecule 15: 40S ribosomal protein S28-A

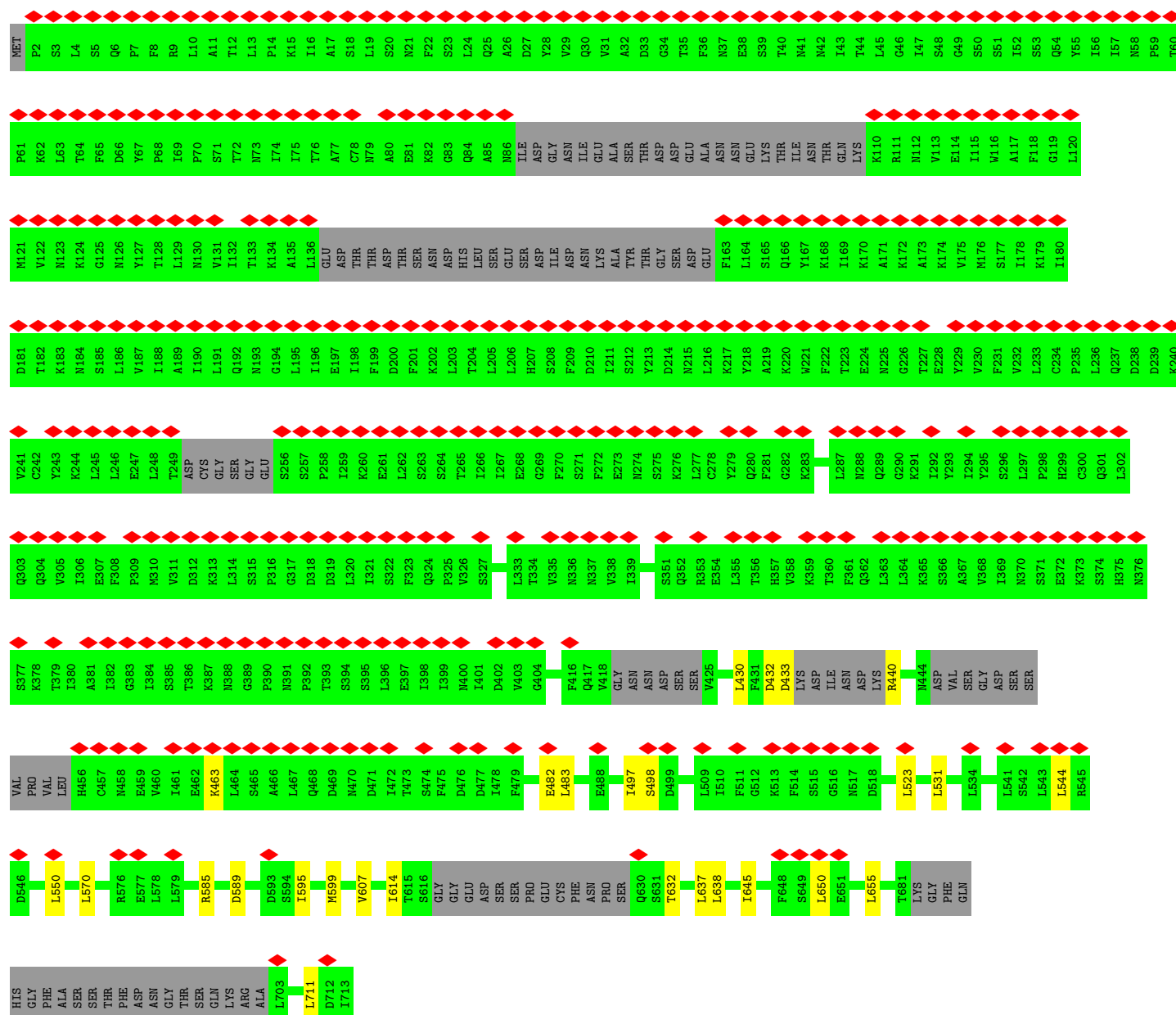
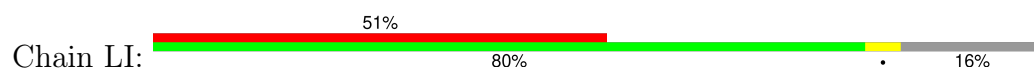


- Molecule 16: NET1-associated nuclear protein 1




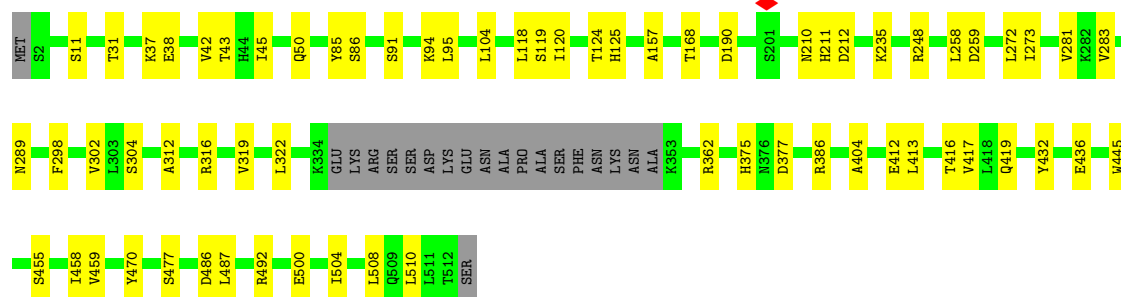


• Molecule 17: U3 small nucleolar RNA-associated protein 8



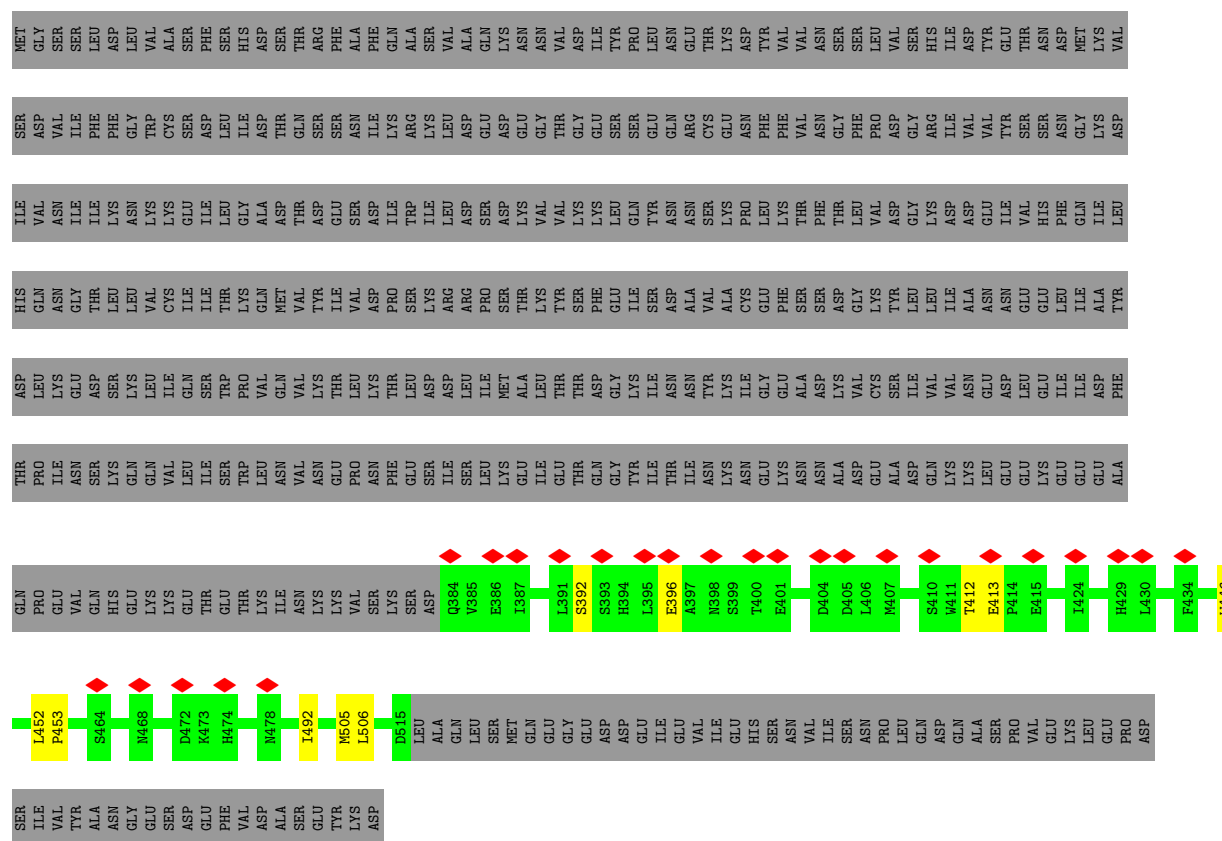
- Molecule 18: U3 small nucleolar RNA-associated protein 15

Chain LJ:  83% 13%



- Molecule 19: U3 small nucleolar RNA-associated protein 9

Chain LK:  21% 77%



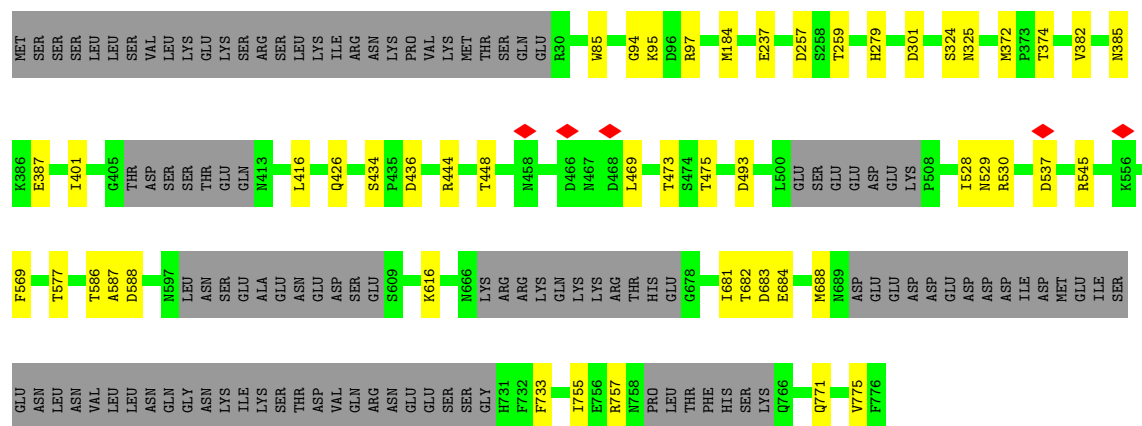
- Molecule 20: U3 small nucleolar RNA-associated protein 5

Chain LL:  70% 8% 22%

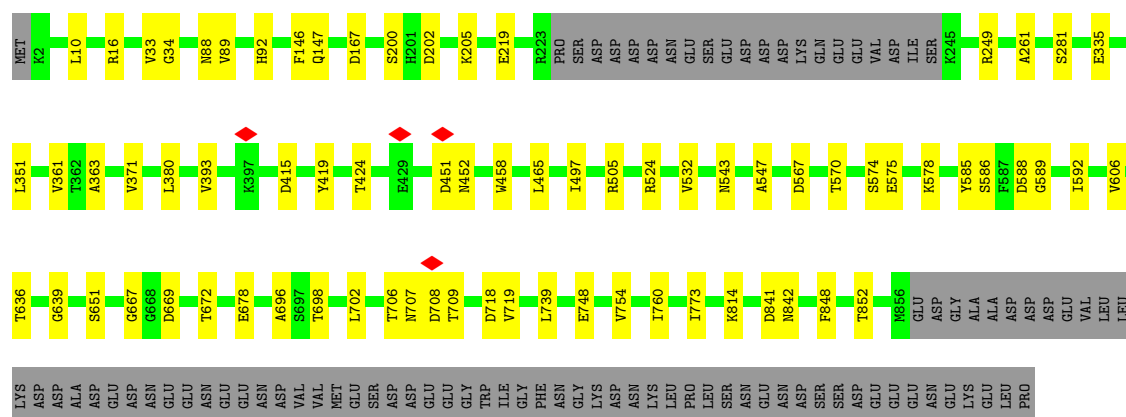
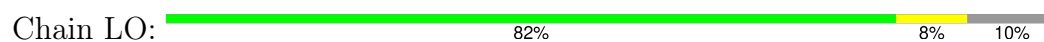




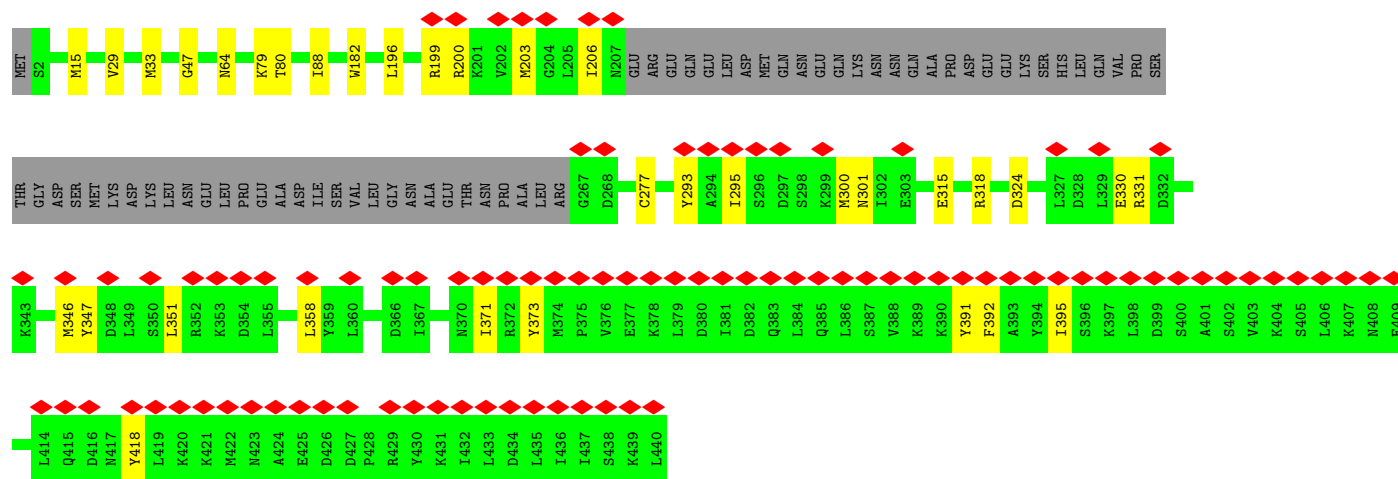
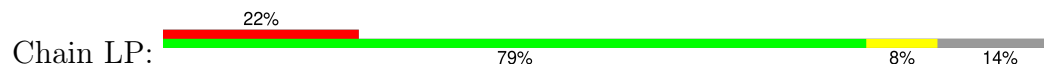





### • Molecule 23: Periodic tryptophan protein 2

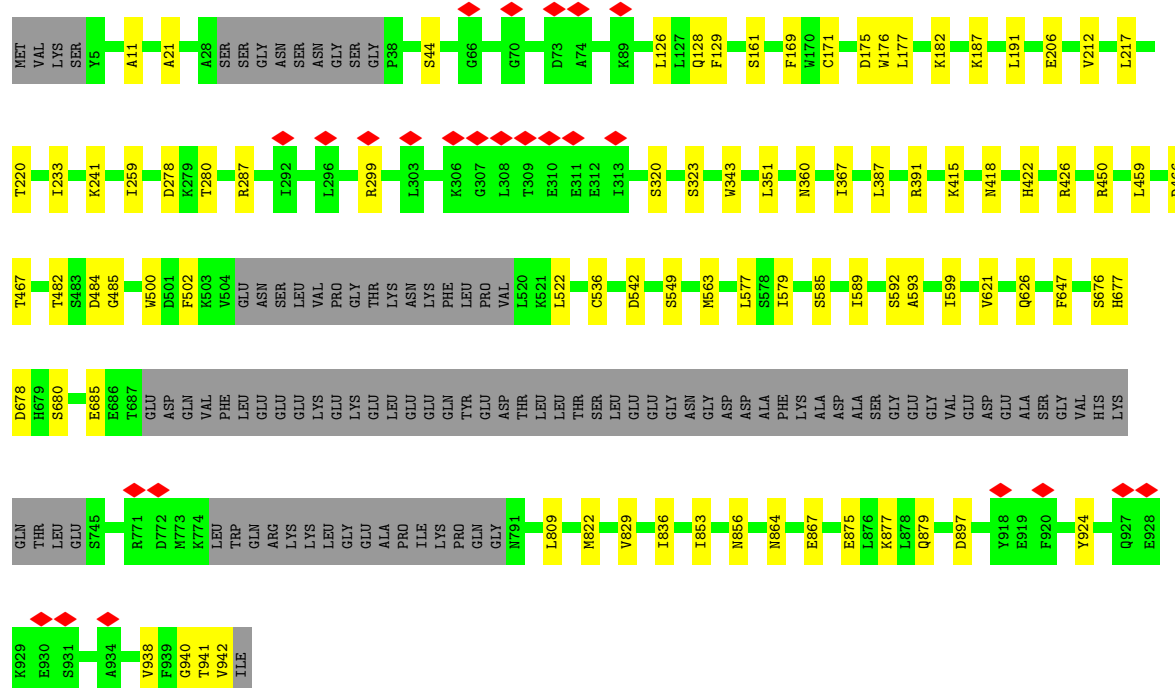


### • Molecule 24: U3 small nucleolar RNA-associated protein 6




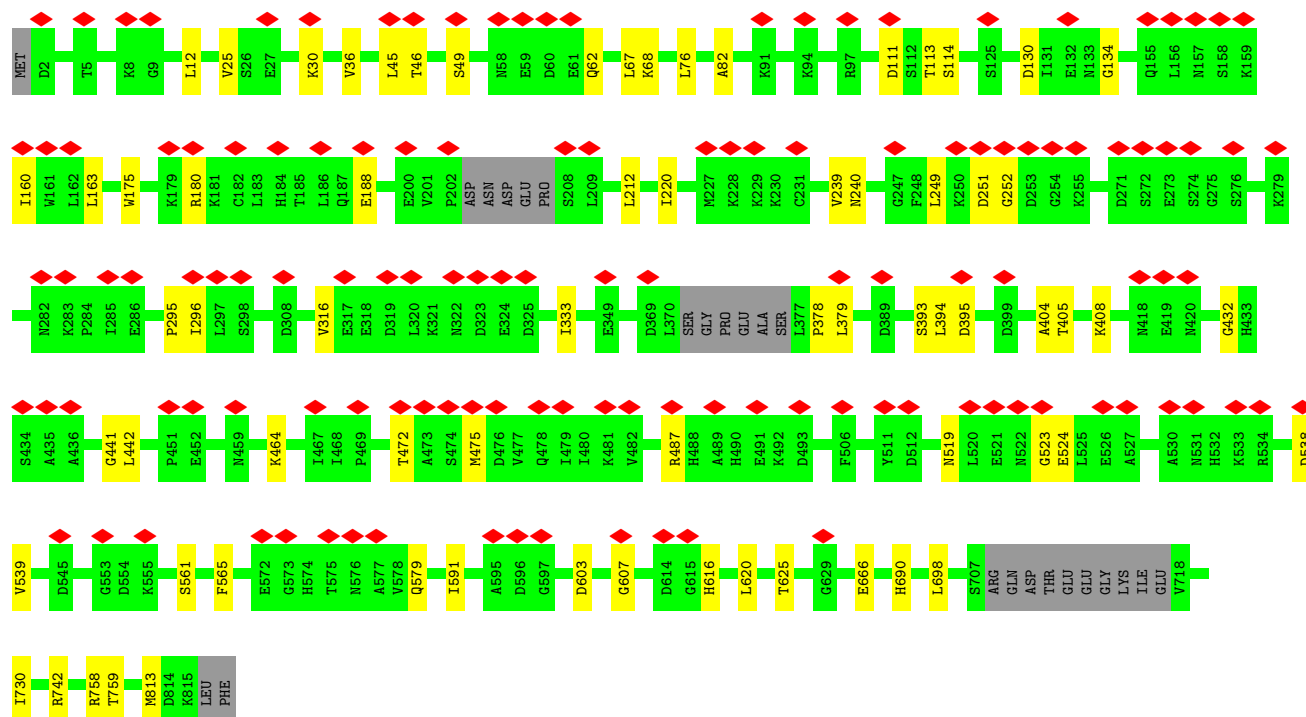
### • Molecule 25: U3 small nucleolar RNA-associated protein 12

Chain LQ: 



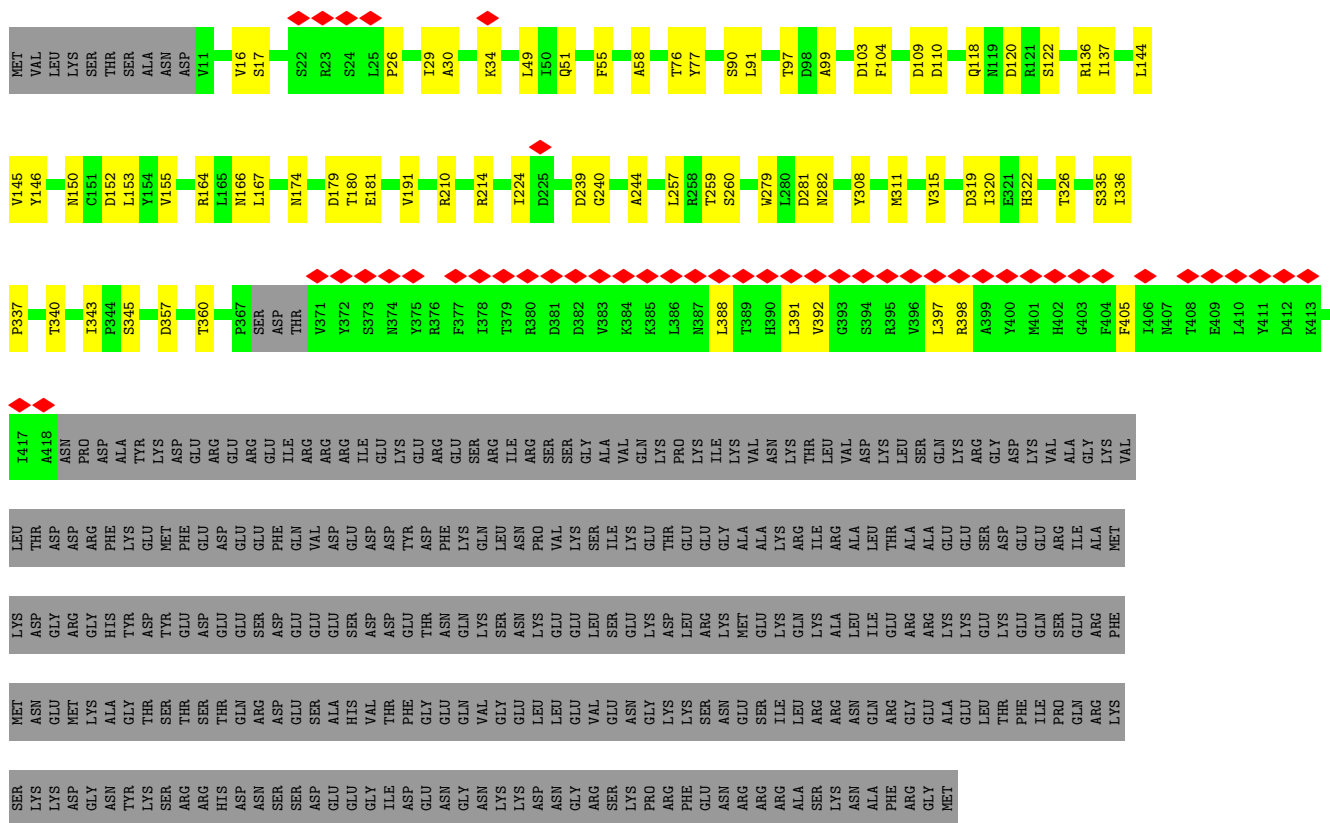
- Molecule 26: U3 small nucleolar RNA-associated protein 13

Chain LR: 

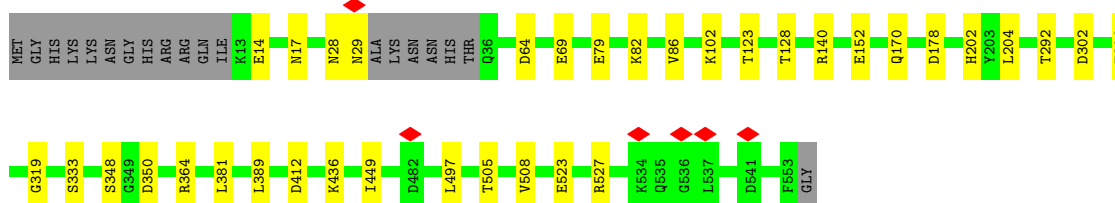


- Molecule 27: U3 small nucleolar RNA-associated protein 18

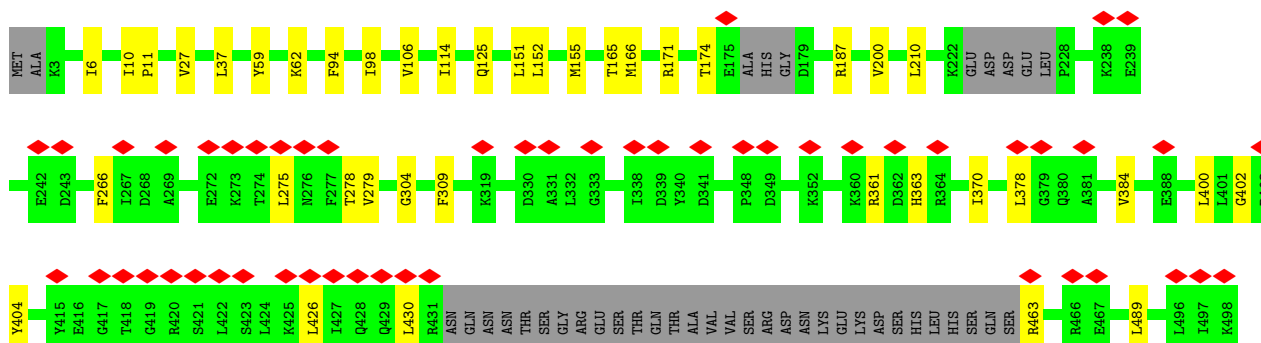
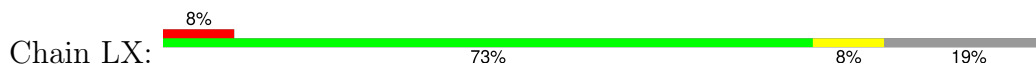




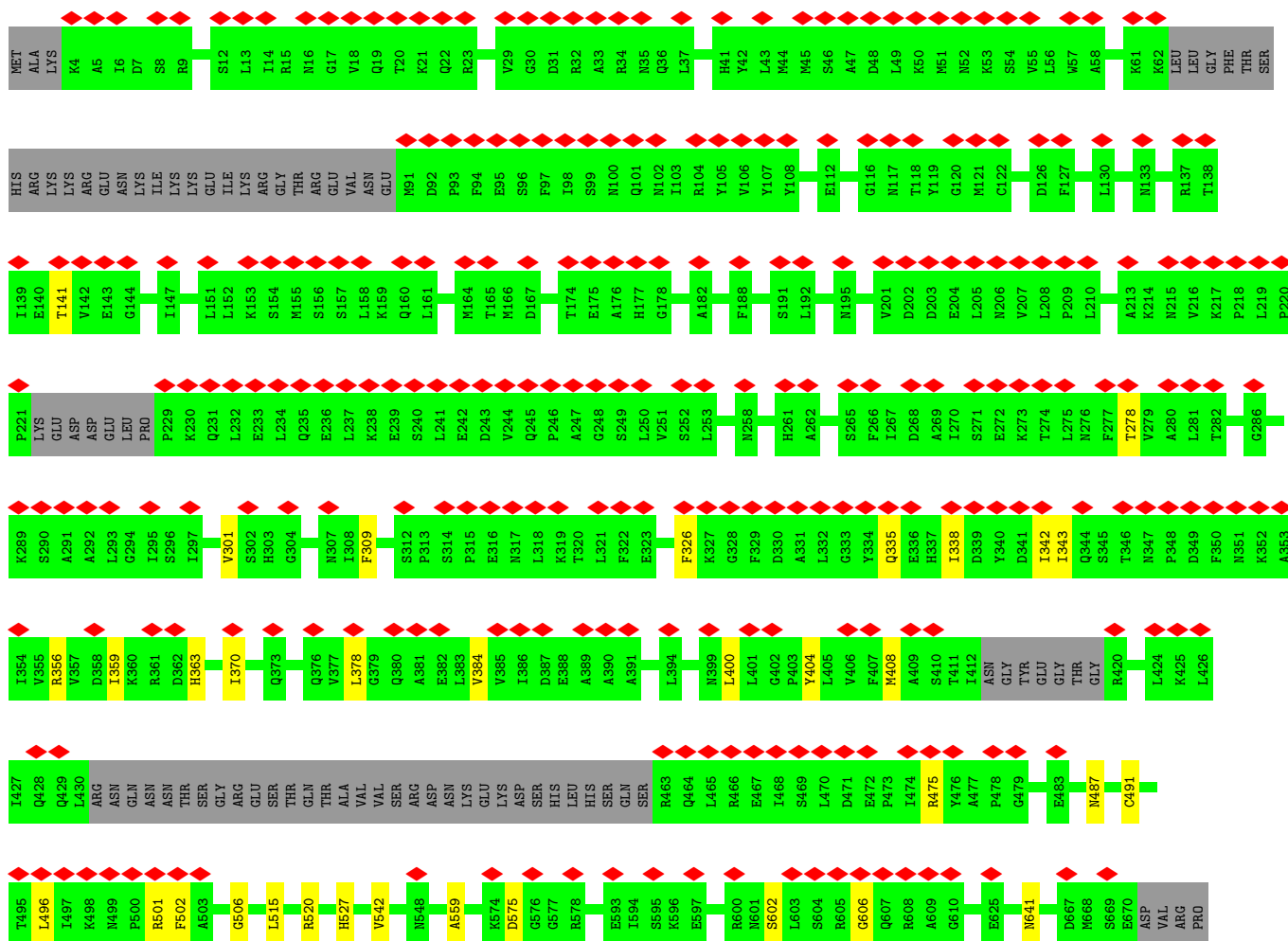
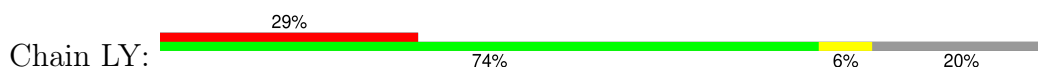
- Molecule 31: U3 small nucleolar RNA-associated protein 7

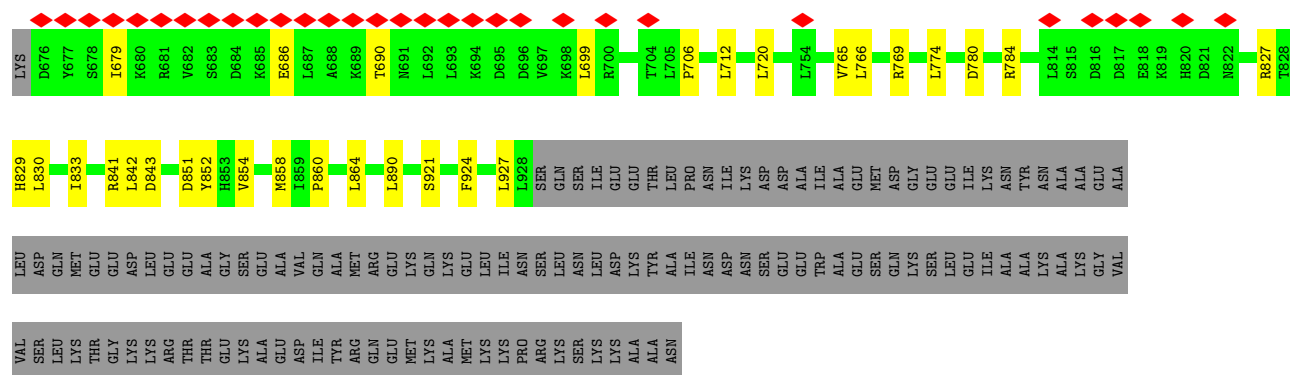


- Molecule 32: RNA cytidine acetyltransferase



- Molecule 32: RNA cytidine acetyltransferase

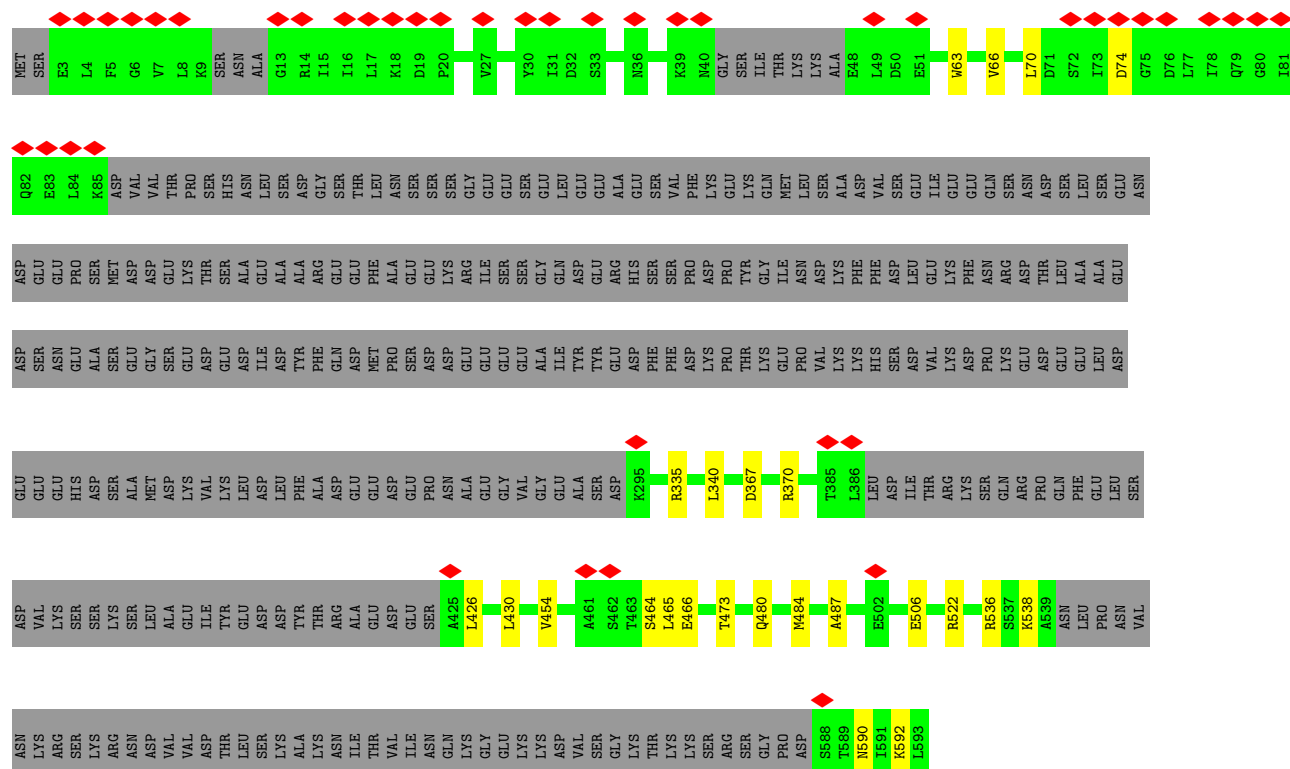




- Molecule 33: U3 small nucleolar ribonucleoprotein protein IMP3

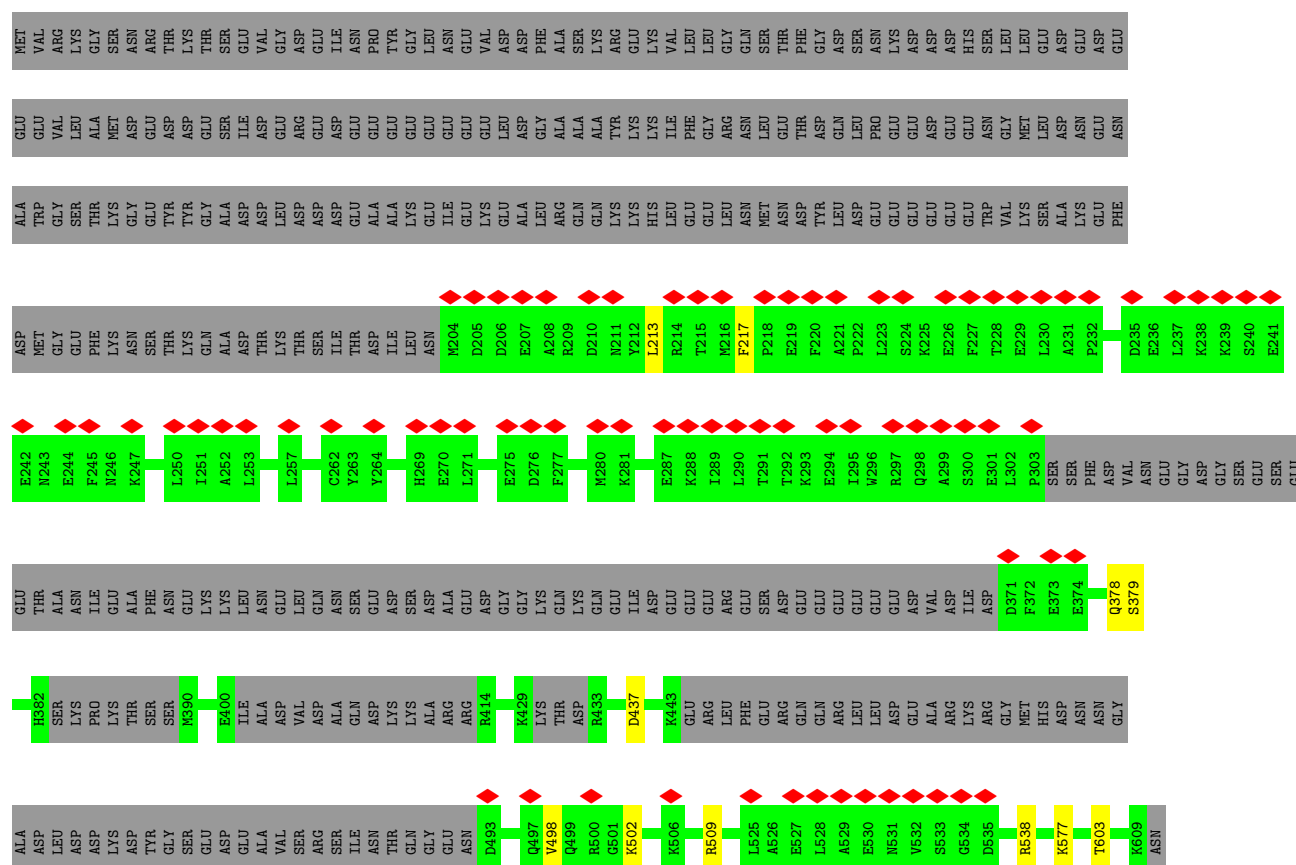


- Molecule 34: U3 small nucleolar RNA-associated protein MPP10

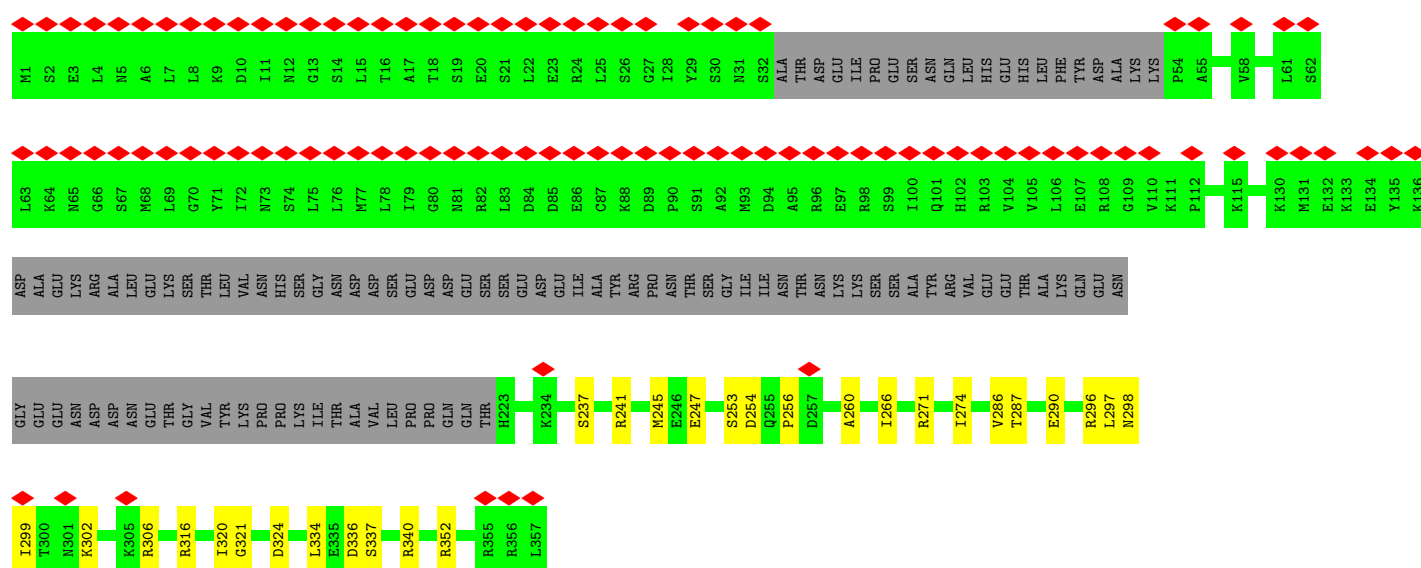


- Molecule 35: Something about silencing protein 10





• Molecule 36: U3 small nucleolar ribonucleoprotein protein LCP5

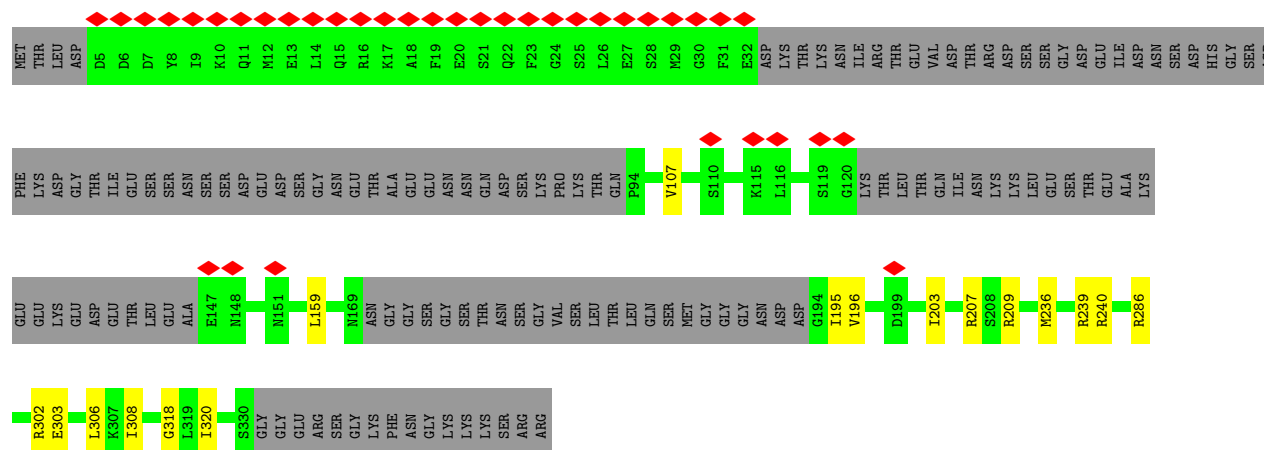


• Molecule 37: Bud site selection protein 21

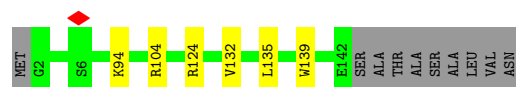
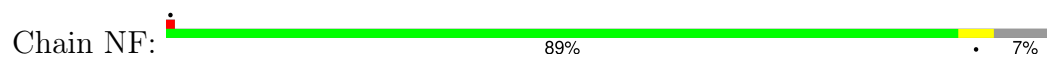




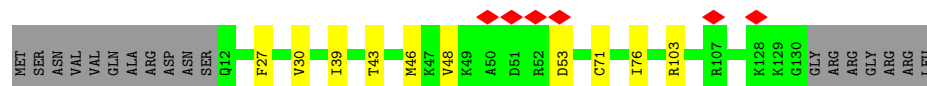
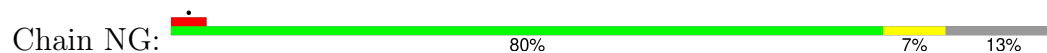
- Molecule 38: Protein FAF1



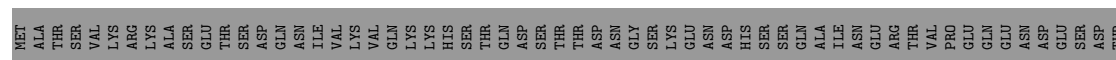
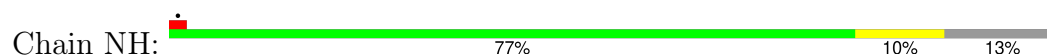
- Molecule 39: 40S ribosomal protein S13

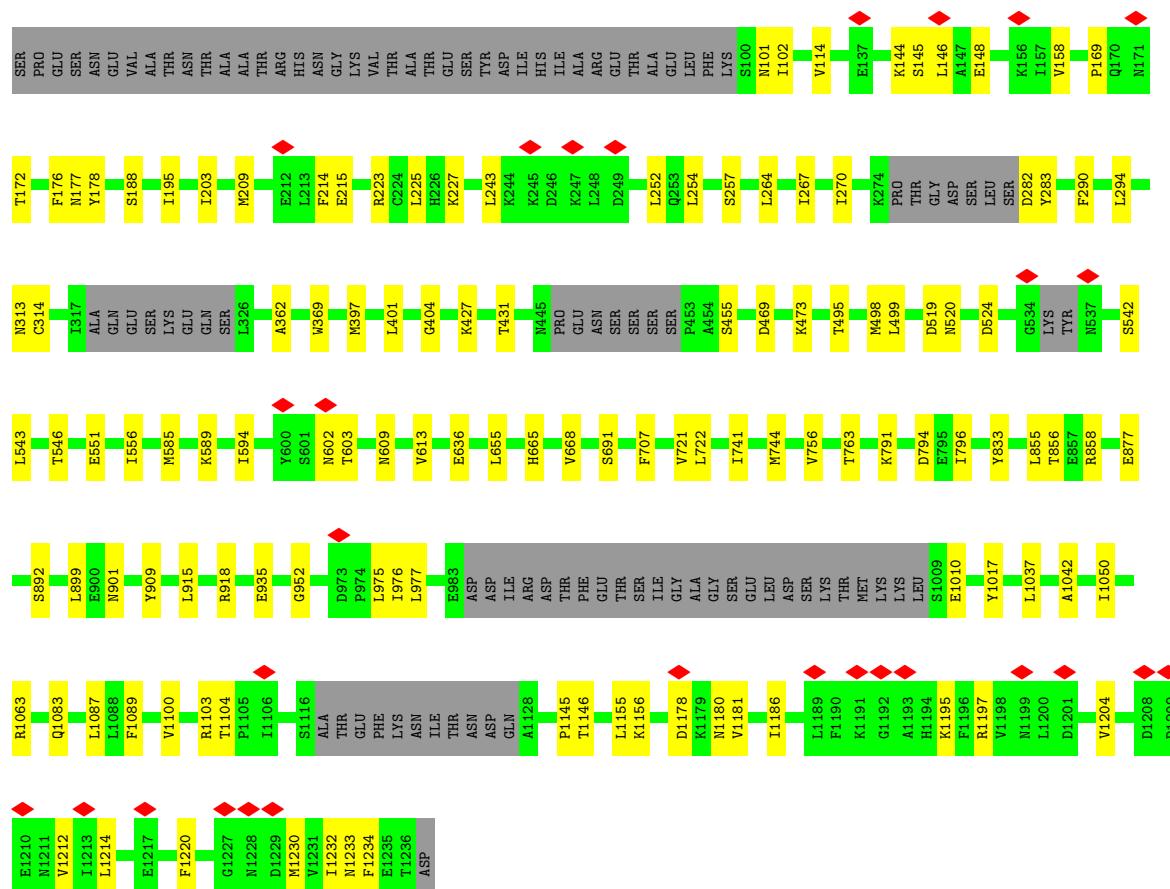


- Molecule 40: 40S ribosomal protein S14-A

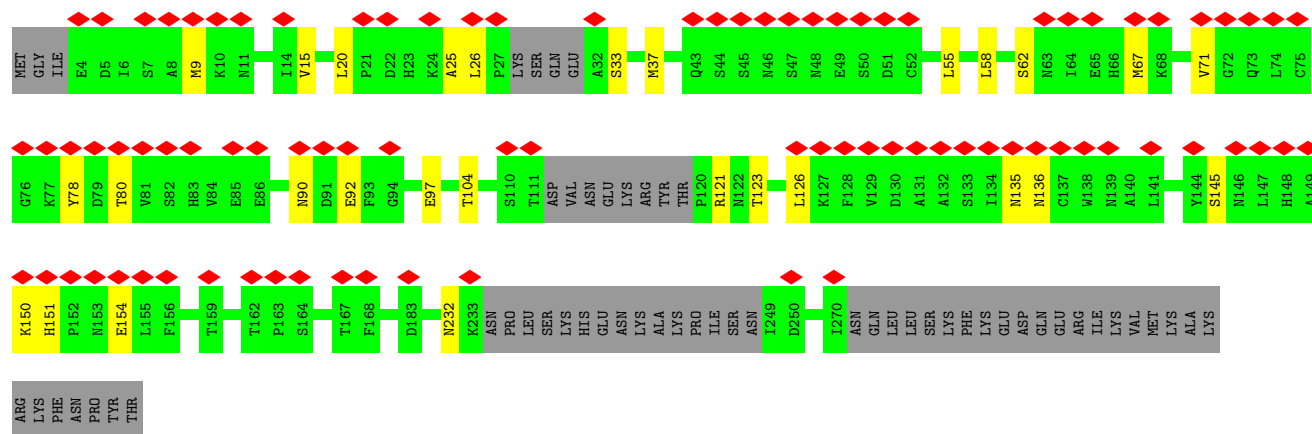
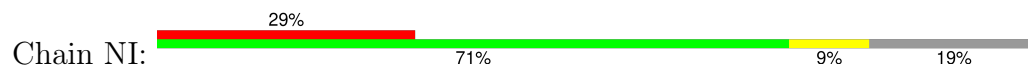


- Molecule 41: U3 small nucleolar RNA-associated protein 22

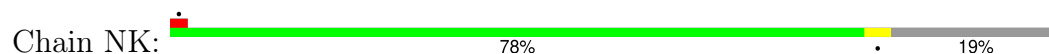




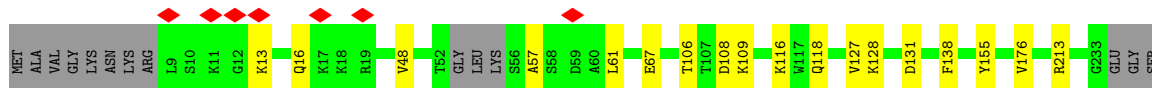
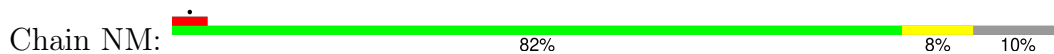
• Molecule 42: Ribosomal RNA-processing protein 7



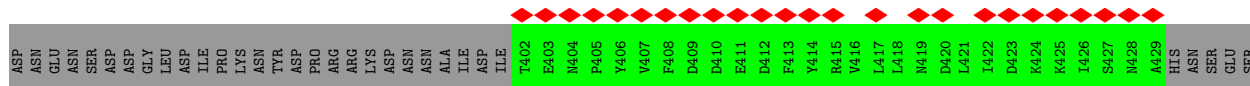
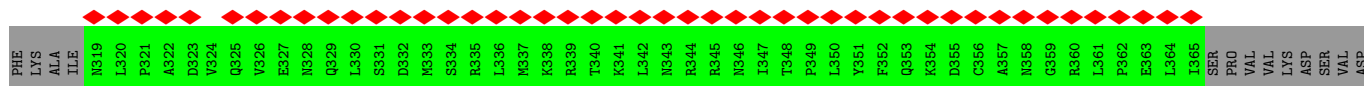
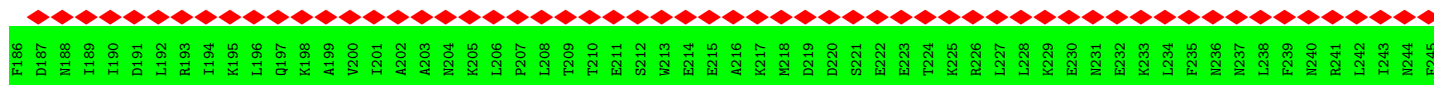
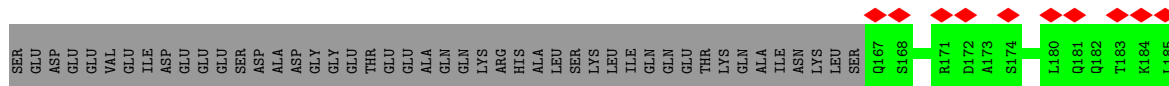
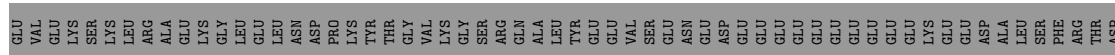
• Molecule 43: KRR1 small subunit processome component



- Molecule 44: Small ribosomal subunit protein eS1A



- Molecule 45: Protein BFR2



- Molecule 46: 40S ribosomal protein S27-A

MET	VAL	LEU
V4	K20	P38
T55	C59	S60
T61	I62	T77
K82		

Chain OA: 99%

[illegible]

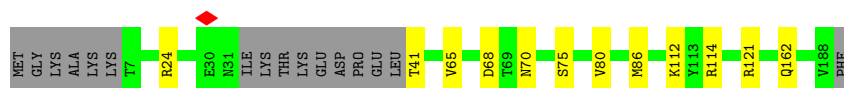




- [illegible]

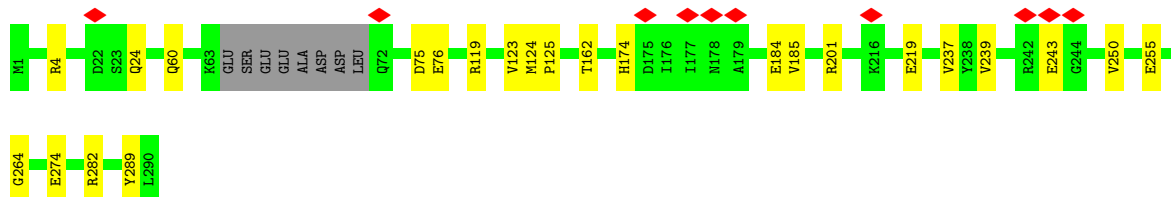






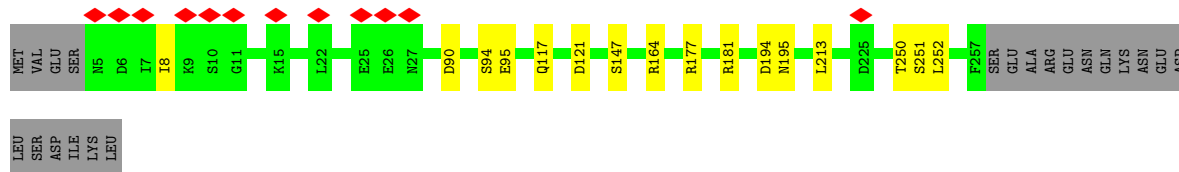
- Molecule 57: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM: 89% 8%



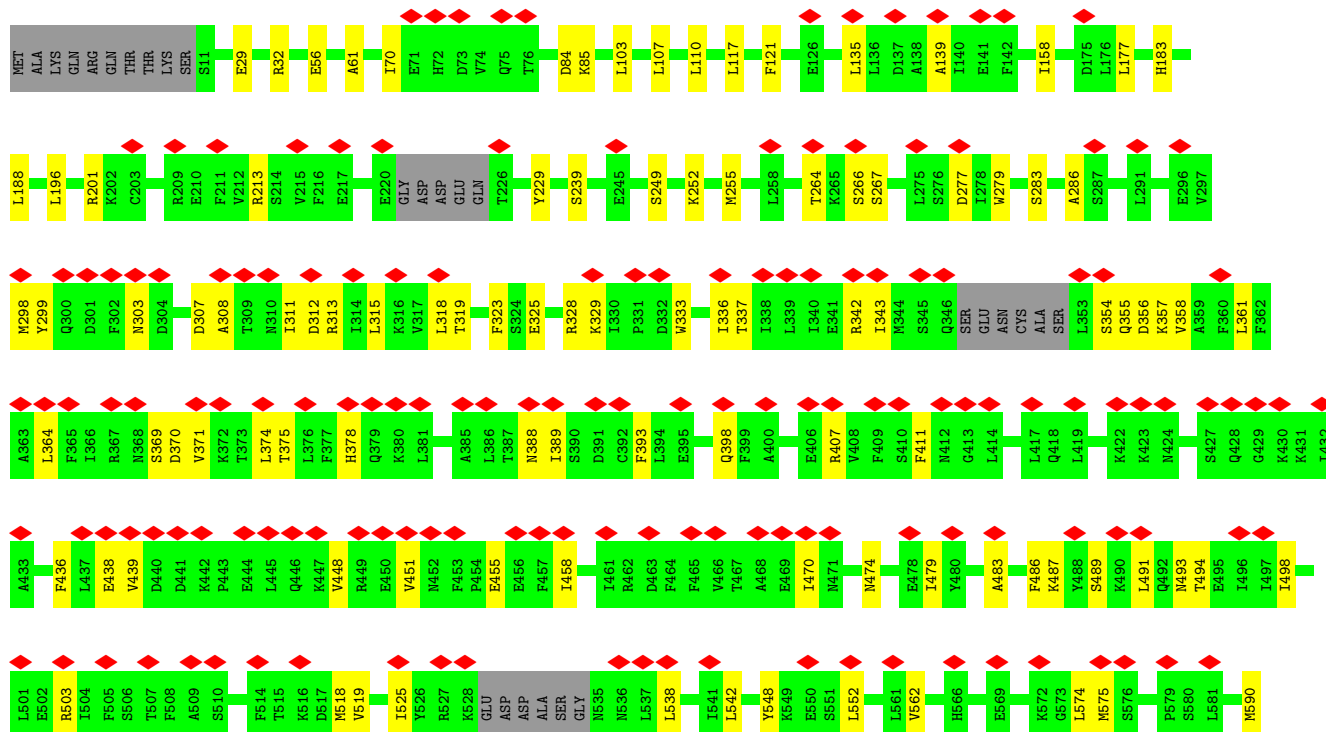
- Molecule 58: Ribosome biogenesis protein UTP30

Chain SN: 86% 6% 8%

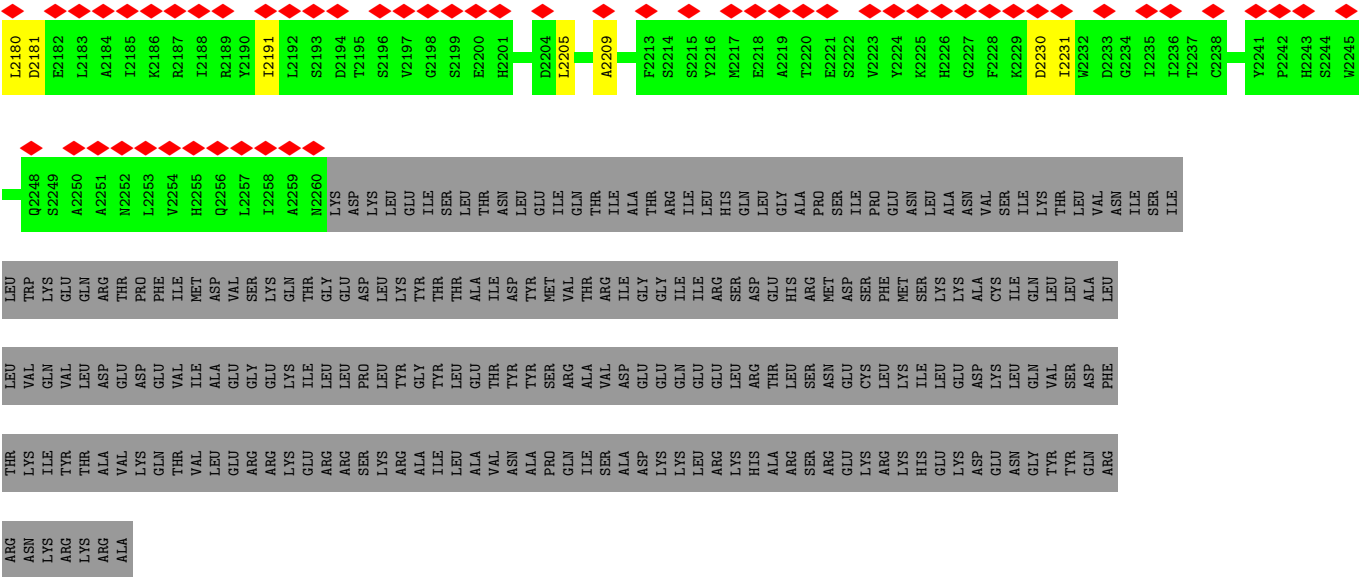


- Molecule 59: U3 small nucleolar RNA-associated protein 20

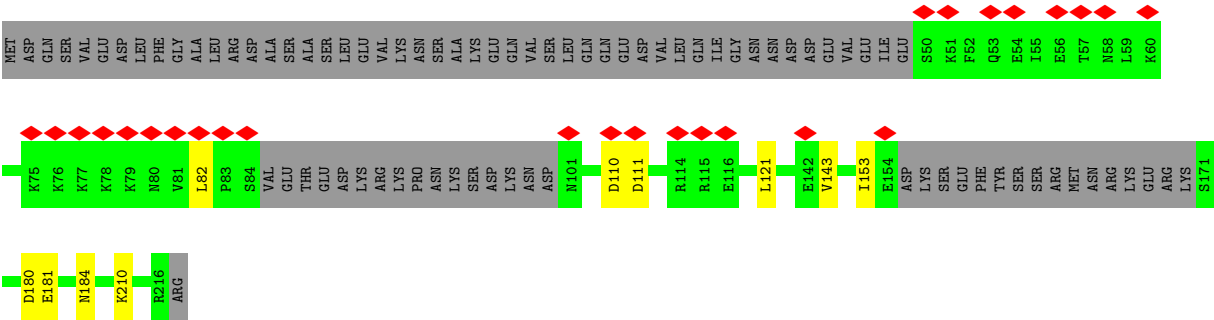
Chain SP: 18% 72% 14% 14%







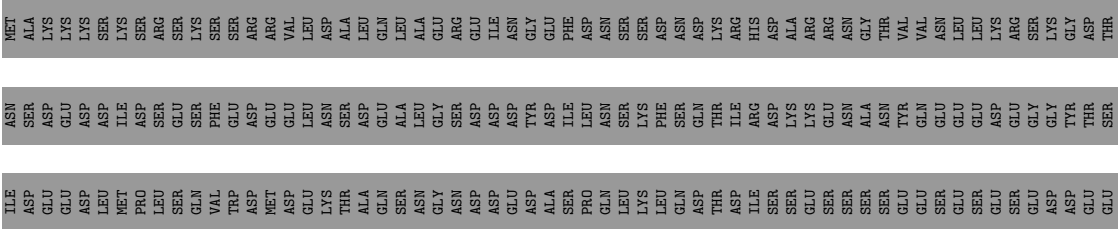
• Molecule 60: rRNA-processing protein FCF2



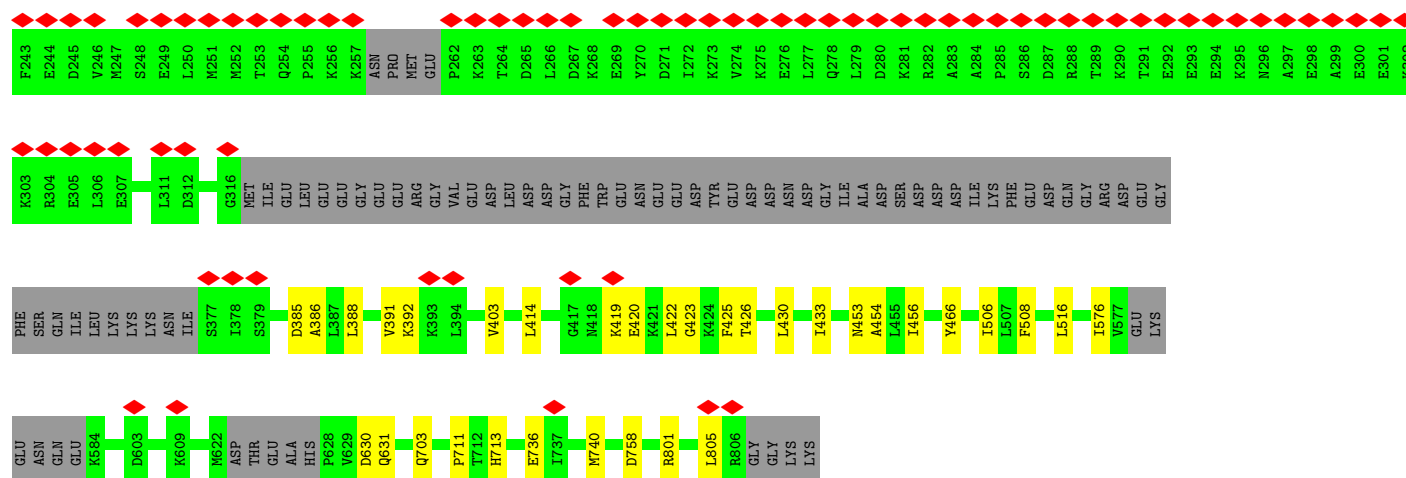
• Molecule 61: 40S ribosomal protein S23-A



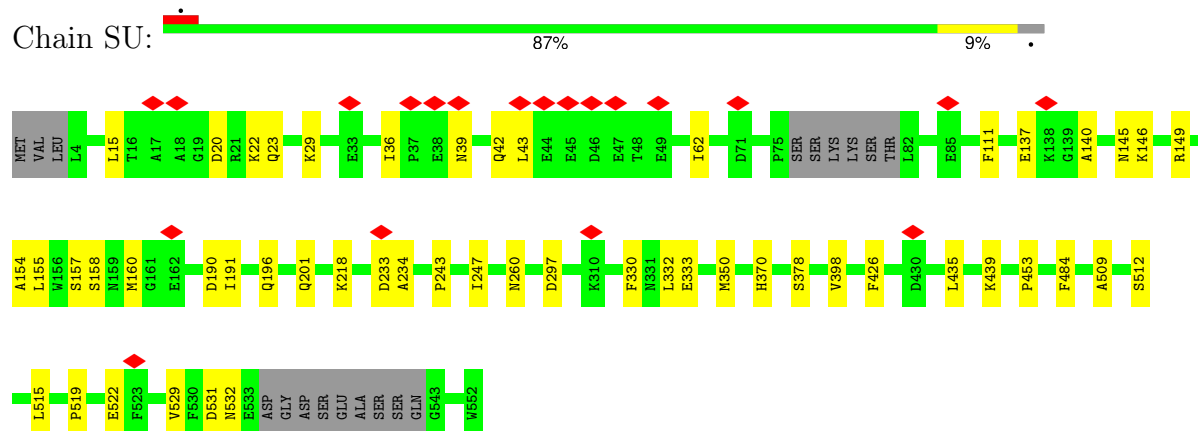
• Molecule 62: U3 small nucleolar RNA-associated protein 14



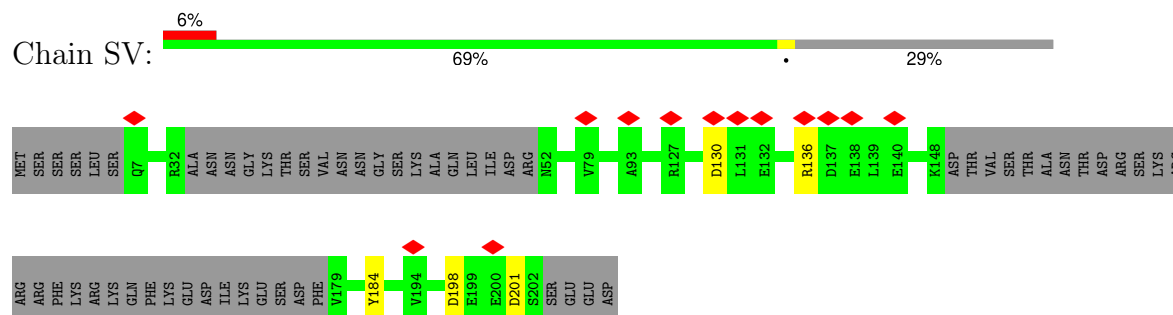




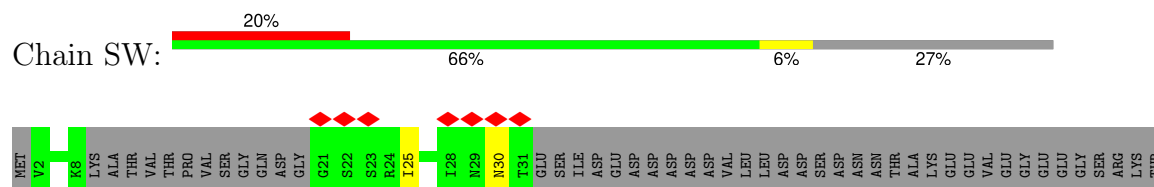
• Molecule 64: Nucleolar complex protein 4

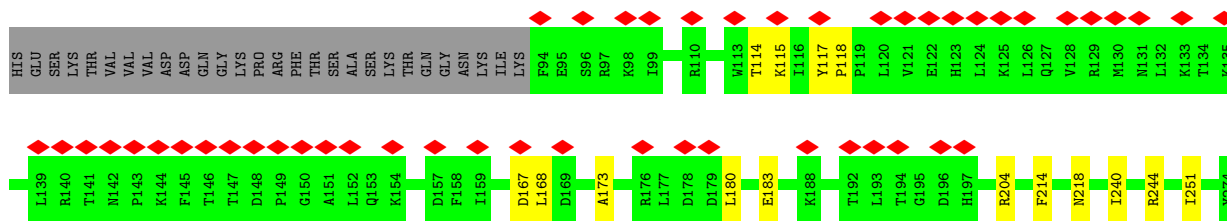


• Molecule 65: Regulator of rDNA transcription protein 14



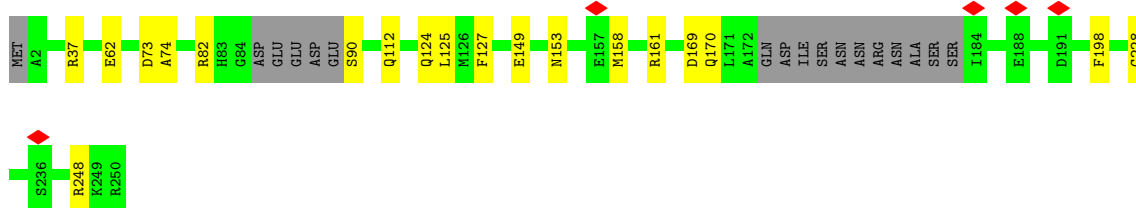
• Molecule 66: Pre-rRNA-processing protein PNO1





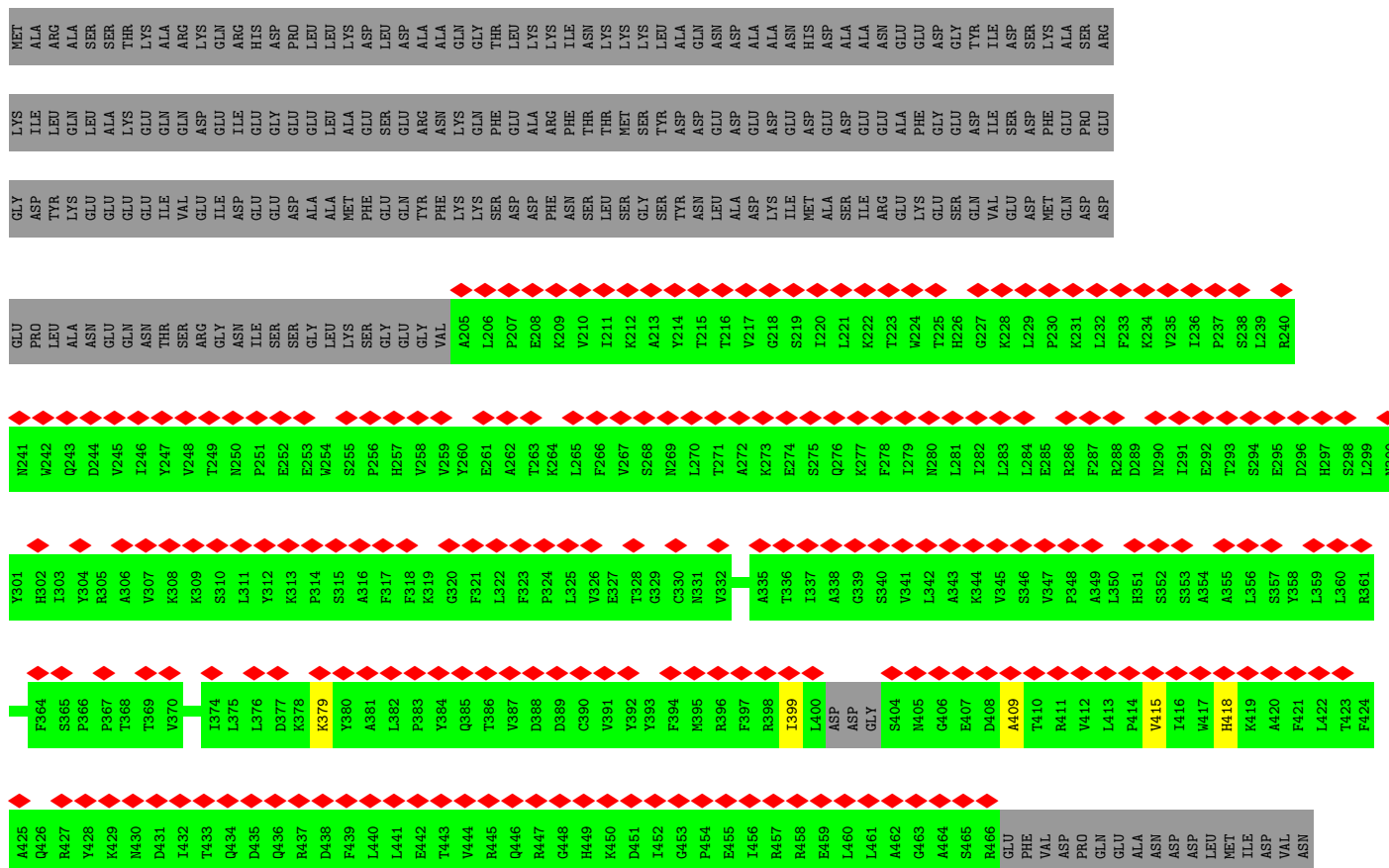
- Molecule 67: U3 small nucleolar RNA-associated protein 11

Chain SY: 86% 8% 7%



- Molecule 68: Essential nuclear protein 1

Chain SZ: 47% 53% 46%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	56168	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	6.919	Depositor
Minimum map value	-0.132	Depositor
Average map value	0.136	Depositor
Map value standard deviation	0.216	Depositor
Recommended contour level	0.8	Depositor
Map size (Å)	535.75195, 535.75195, 535.75195	wwPDB
Map dimensions	504, 504, 504	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.063, 1.063, 1.063	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, MG, GTP, SEP, ATP

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	L0	0.17	0/12478	0.26	0/19437
2	L1	0.17	0/27400	0.27	0/42643
3	L2	0.18	0/4143	0.24	0/6440
4	L3	0.12	0/794	0.27	0/1069
5	L4	0.17	0/1906	0.34	0/2572
6	L5	0.18	0/1655	0.32	0/2237
7	L6	0.18	0/1674	0.33	0/2236
8	L7	0.17	0/1369	0.36	0/1846
9	L8	0.19	0/1379	0.31	0/1844
10	L9	0.17	0/1410	0.31	0/1888
11	LC	0.21	0/990	0.35	0/1335
12	LD	0.17	0/1138	0.34	0/1533
13	LE	0.21	0/1039	0.37	0/1395
14	LF	0.19	0/766	0.39	0/1030
15	LG	0.18	0/492	0.34	0/659
16	LH	0.21	0/6592	0.38	0/8924
17	LI	0.13	0/3835	0.31	0/5263
18	LJ	0.19	0/3993	0.35	0/5413
19	LK	0.14	0/1085	0.31	0/1463
20	LL	0.18	0/4052	0.32	0/5501
21	LM	0.18	0/9462	0.35	0/13078
22	LN	0.20	0/5359	0.31	0/7255
23	LO	0.21	0/6773	0.33	0/9164
24	LP	0.15	0/3288	0.28	0/4419
25	LQ	0.15	0/6837	0.30	0/9227
26	LR	0.13	0/6313	0.29	0/8551
27	LS	0.23	0/3866	0.33	0/5239
28	LT	0.19	0/7015	0.31	0/9479
29	LU	0.21	0/3835	0.32	0/5162
30	LV	0.21	0/3360	0.37	0/4549
31	LW	0.20	0/4321	0.32	0/5832
32	LX	0.16	0/6936	0.32	1/9371 (0.0%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	LY	0.14	0/6292	0.31	0/8556
33	LZ	0.20	0/1553	0.31	0/2089
34	NA	0.14	0/2090	0.29	0/2817
35	NB	0.15	0/1891	0.30	0/2541
36	NC	0.15	0/1708	0.35	0/2303
37	ND	0.17	0/613	0.32	0/811
38	NE	0.14	0/1662	0.29	0/2212
39	NF	0.15	0/1158	0.32	0/1559
40	NG	0.16	0/886	0.31	0/1194
41	NH	0.16	0/8899	0.29	0/12035
42	NI	0.14	0/1994	0.32	0/2684
43	NK	0.16	0/2144	0.33	0/2880
44	NM	0.15	0/1862	0.30	0/2494
45	NN	0.12	0/1491	0.27	0/2063
46	NQ	0.16	0/605	0.32	0/817
47	OA	0.13	0/98	0.30	0/133
48	SA	0.14	0/3104	0.27	0/4181
49	SB	0.15	0/3396	0.30	0/4576
50	SC	0.18	0/1906	0.33	0/2570
50	SD	0.16	0/1852	0.32	0/2500
51	SE	0.20	0/928	0.31	0/1262
51	SF	0.16	0/928	0.33	0/1262
52	SG	0.15	0/3686	0.31	0/4959
53	SH	0.17	0/2832	0.32	0/3825
54	SI	0.18	0/6758	0.33	0/9093
55	SJ	0.19	0/1703	0.36	0/2295
55	SK	0.22	0/1822	0.34	0/2462
56	SL	0.19	0/1406	0.31	0/1890
57	SM	0.18	0/2337	0.31	0/3148
58	SN	0.15	0/2088	0.32	0/2808
59	SP	0.14	0/17901	0.32	0/24216
60	SQ	0.16	0/1156	0.34	0/1536
61	SR	0.18	0/804	0.34	0/1074
62	SS	0.18	0/2139	0.42	2/2872 (0.1%)
63	ST	0.15	0/4549	0.30	0/6126
64	SU	0.16	0/4480	0.32	0/6073
65	SV	0.13	0/875	0.31	0/1206
66	SW	0.15	0/1591	0.32	0/2143
67	SY	0.17	0/1978	0.31	0/2616
68	SZ	0.13	0/1326	0.33	0/1859
All	All	0.17	0/252046	0.31	3/349794 (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
21	LM	0	1
48	SA	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	SS	313	PHE	CA-C-N	-5.75	112.66	119.84
62	SS	313	PHE	C-N-CA	-5.75	112.66	119.84
32	LX	848	ASN	N-CA-C	-5.52	106.50	113.23

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	LM	1545	ARG	Peptide
48	SA	160	ARG	Sidechain

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L0	11158	0	5609	36	0
2	L1	24510	0	12366	118	0
3	L2	3712	0	1882	18	0
4	L3	786	0	823	5	0
5	L4	1866	0	1935	15	0
6	L5	1635	0	1697	15	0
7	L6	1653	0	1750	11	0
8	L7	1347	0	1406	15	0
9	L8	1356	0	1377	14	0
10	L9	1388	0	1467	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	LC	973	0	1029	8	0
12	LD	1112	0	1179	8	0
13	LE	1022	0	1060	10	0
14	LF	753	0	778	4	0
15	LG	490	0	529	6	0
16	LH	6465	0	6415	68	0
17	LI	3792	0	2859	21	0
18	LJ	3911	0	3906	46	0
19	LK	1068	0	1120	10	0
20	LL	3982	0	3983	35	0
21	LM	9380	0	6279	52	0
22	LN	5263	0	5270	31	0
23	LO	6639	0	6524	53	0
24	LP	3220	0	3272	25	0
25	LQ	6707	0	6738	56	0
26	LR	6207	0	6247	49	0
27	LS	3793	0	3770	38	0
28	LT	6876	0	6853	50	0
29	LU	3756	0	3708	25	0
30	LV	3286	0	3208	50	0
31	LW	4237	0	4239	25	0
32	LX	6803	0	6928	57	0
32	LY	6179	0	5745	40	0
33	LZ	1524	0	1567	9	0
34	NA	2075	0	1915	22	0
35	NB	1873	0	1638	10	0
36	NC	1693	0	1368	22	0
37	ND	609	0	671	6	0
38	NE	1649	0	1669	15	0
39	NF	1135	0	1197	5	0
40	NG	875	0	905	7	0
41	NH	8693	0	8806	88	0
42	NI	1953	0	1933	20	0
43	NK	2107	0	2184	10	0
44	NM	1838	0	1933	17	0
45	NN	1481	0	866	5	0
46	NQ	595	0	609	4	0
47	OA	96	0	90	4	0
48	SA	3056	0	3083	21	0
49	SB	3357	0	3471	26	0
50	SC	1871	0	1916	16	0
50	SD	1817	0	1857	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	SE	916	0	964	3	0
51	SF	916	0	964	3	0
52	SG	3627	0	3626	24	0
53	SH	2781	0	2878	20	0
54	SI	6616	0	6793	48	0
55	SJ	1678	0	1756	21	0
55	SK	1793	0	1874	24	0
56	SL	1384	0	1464	10	0
57	SM	2296	0	2325	21	0
58	SN	2053	0	2168	13	0
59	SP	17548	0	17805	236	0
60	SQ	1137	0	1188	9	0
61	SR	792	0	847	4	0
62	SS	2102	0	2120	21	0
63	ST	4482	0	4360	33	0
64	SU	4370	0	4365	36	0
65	SV	869	0	554	5	0
66	SW	1565	0	1647	11	0
67	SY	1953	0	2050	16	0
68	SZ	1314	0	649	3	0
69	L1	22	0	0	0	0
69	L2	1	0	0	0	0
69	NH	1	0	0	0	0
69	SI	1	0	0	0	0
70	NH	31	0	12	1	0
71	NQ	1	0	0	0	0
71	SL	1	0	0	0	0
72	SI	32	0	12	0	0
All	All	243904	0	220050	1609	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 3.

The worst 5 of 1609 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)
8:L7:67:LEU:HD22	8:L7:94:ALA:HB2	1.50	0.94
59:SP:1610:MET:HE3	59:SP:1653:ALA:HB1	1.54	0.89
18:LJ:258:LEU:HD21	18:LJ:272:LEU:HD11	1.56	0.86
11:LC:98:ASP:OD1	28:LT:488:ASN:ND2	2.10	0.85
21:LM:628:ASN:O	22:LN:616:LYS:NZ	2.10	0.85

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L3	91/146 (62%)	90 (99%)	1 (1%)	0	100	100
5	L4	232/261 (89%)	231 (100%)	1 (0%)	0	100	100
6	L5	202/225 (90%)	199 (98%)	3 (2%)	0	100	100
7	L6	202/236 (86%)	201 (100%)	1 (0%)	0	100	100
8	L7	165/190 (87%)	164 (99%)	1 (1%)	0	100	100
9	L8	167/200 (84%)	164 (98%)	3 (2%)	0	100	100
10	L9	169/197 (86%)	167 (99%)	2 (1%)	0	100	100
11	LC	123/143 (86%)	122 (99%)	1 (1%)	0	100	100
12	LD	135/156 (86%)	131 (97%)	4 (3%)	0	100	100
13	LE	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
14	LF	93/135 (69%)	91 (98%)	2 (2%)	0	100	100
15	LG	60/67 (90%)	59 (98%)	1 (2%)	0	100	100
16	LH	790/896 (88%)	768 (97%)	22 (3%)	0	100	100
17	LI	582/713 (82%)	574 (99%)	8 (1%)	0	100	100
18	LJ	489/513 (95%)	474 (97%)	15 (3%)	0	100	100
19	LK	130/575 (23%)	130 (100%)	0	0	100	100
20	LL	496/643 (77%)	487 (98%)	9 (2%)	0	100	100
21	LM	1597/1769 (90%)	1565 (98%)	32 (2%)	0	100	100
22	LN	649/776 (84%)	638 (98%)	11 (2%)	0	100	100
23	LO	829/923 (90%)	820 (99%)	9 (1%)	0	100	100
24	LP	376/440 (86%)	371 (99%)	5 (1%)	0	100	100
25	LQ	831/943 (88%)	807 (97%)	24 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	LR	785/817 (96%)	774 (99%)	11 (1%)	0	100	100
27	LS	469/594 (79%)	458 (98%)	11 (2%)	0	100	100
28	LT	865/939 (92%)	852 (98%)	13 (2%)	0	100	100
29	LU	456/489 (93%)	449 (98%)	7 (2%)	0	100	100
30	LV	401/707 (57%)	387 (96%)	14 (4%)	0	100	100
31	LW	531/554 (96%)	519 (98%)	12 (2%)	0	100	100
32	LX	838/1056 (79%)	827 (99%)	11 (1%)	0	100	100
32	LY	834/1056 (79%)	822 (99%)	12 (1%)	0	100	100
33	LZ	179/183 (98%)	179 (100%)	0	0	100	100
34	NA	274/593 (46%)	270 (98%)	4 (2%)	0	100	100
35	NB	255/610 (42%)	253 (99%)	2 (1%)	0	100	100
36	NC	244/357 (68%)	239 (98%)	5 (2%)	0	100	100
37	ND	70/214 (33%)	70 (100%)	0	0	100	100
38	NE	207/346 (60%)	204 (99%)	3 (1%)	0	100	100
39	NF	139/151 (92%)	139 (100%)	0	0	100	100
40	NG	117/137 (85%)	114 (97%)	3 (3%)	0	100	100
41	NH	1063/1237 (86%)	1050 (99%)	13 (1%)	0	100	100
42	NI	232/297 (78%)	228 (98%)	4 (2%)	0	100	100
43	NK	253/316 (80%)	250 (99%)	3 (1%)	0	100	100
44	NM	224/255 (88%)	223 (100%)	1 (0%)	0	100	100
45	NN	257/534 (48%)	256 (100%)	1 (0%)	0	100	100
46	NQ	77/82 (94%)	76 (99%)	1 (1%)	0	100	100
47	OA	11/1729 (1%)	11 (100%)	0	0	100	100
48	SA	384/504 (76%)	381 (99%)	3 (1%)	0	100	100
49	SB	434/511 (85%)	431 (99%)	3 (1%)	0	100	100
50	SC	237/327 (72%)	235 (99%)	2 (1%)	0	100	100
50	SD	228/327 (70%)	227 (100%)	1 (0%)	0	100	100
51	SE	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
51	SF	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
52	SG	442/573 (77%)	431 (98%)	11 (2%)	0	100	100
53	SH	358/367 (98%)	352 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	SI	803/1183 (68%)	786 (98%)	17 (2%)	0	100	100
55	SJ	207/252 (82%)	204 (99%)	3 (1%)	0	100	100
55	SK	225/252 (89%)	221 (98%)	4 (2%)	0	100	100
56	SL	169/189 (89%)	163 (96%)	6 (4%)	0	100	100
57	SM	278/290 (96%)	275 (99%)	3 (1%)	0	100	100
58	SN	251/274 (92%)	250 (100%)	1 (0%)	0	100	100
59	SP	2136/2493 (86%)	2106 (99%)	30 (1%)	0	100	100
60	SQ	129/217 (59%)	123 (95%)	6 (5%)	0	100	100
61	SR	102/145 (70%)	101 (99%)	1 (1%)	0	100	100
62	SS	243/899 (27%)	240 (99%)	3 (1%)	0	100	100
63	ST	572/810 (71%)	566 (99%)	6 (1%)	0	100	100
64	SU	528/552 (96%)	524 (99%)	4 (1%)	0	100	100
65	SV	141/206 (68%)	138 (98%)	3 (2%)	0	100	100
66	SW	193/274 (70%)	191 (99%)	2 (1%)	0	100	100
67	SY	227/250 (91%)	227 (100%)	0	0	100	100
68	SZ	255/483 (53%)	250 (98%)	5 (2%)	0	100	100
All	All	26096/35160 (74%)	25687 (98%)	409 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	L3	88/129 (68%)	88 (100%)	0	100	100
5	L4	202/222 (91%)	202 (100%)	0	100	100
6	L5	179/191 (94%)	179 (100%)	0	100	100
7	L6	175/201 (87%)	175 (100%)	0	100	100
8	L7	149/170 (88%)	149 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	L8	138/161 (86%)	138 (100%)	0	100	100
10	L9	147/166 (89%)	147 (100%)	0	100	100
11	LC	105/119 (88%)	105 (100%)	0	100	100
12	LD	124/137 (90%)	124 (100%)	0	100	100
13	LE	110/111 (99%)	110 (100%)	0	100	100
14	LF	79/113 (70%)	79 (100%)	0	100	100
15	LG	55/60 (92%)	55 (100%)	0	100	100
16	LH	745/826 (90%)	745 (100%)	0	100	100
17	LI	244/657 (37%)	244 (100%)	0	100	100
18	LJ	437/454 (96%)	437 (100%)	0	100	100
19	LK	124/533 (23%)	124 (100%)	0	100	100
20	LL	452/574 (79%)	452 (100%)	0	100	100
21	LM	421/1633 (26%)	421 (100%)	0	100	100
22	LN	603/713 (85%)	603 (100%)	0	100	100
23	LO	729/811 (90%)	729 (100%)	0	100	100
24	LP	360/414 (87%)	360 (100%)	0	100	100
25	LQ	746/832 (90%)	746 (100%)	0	100	100
26	LR	698/719 (97%)	698 (100%)	0	100	100
27	LS	423/528 (80%)	423 (100%)	0	100	100
28	LT	763/819 (93%)	763 (100%)	0	100	100
29	LU	415/443 (94%)	415 (100%)	0	100	100
30	LV	366/636 (58%)	366 (100%)	0	100	100
31	LW	465/480 (97%)	465 (100%)	0	100	100
32	LX	760/934 (81%)	760 (100%)	0	100	100
32	LY	592/934 (63%)	592 (100%)	0	100	100
33	LZ	170/172 (99%)	170 (100%)	0	100	100
34	NA	194/535 (36%)	194 (100%)	0	100	100
35	NB	149/538 (28%)	149 (100%)	0	100	100
36	NC	121/315 (38%)	121 (100%)	0	100	100
37	ND	70/196 (36%)	70 (100%)	0	100	100
38	NE	166/304 (55%)	166 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	NF	121/128 (94%)	121 (100%)	0	100	100
40	NG	90/105 (86%)	90 (100%)	0	100	100
41	NH	982/1125 (87%)	982 (100%)	0	100	100
42	NI	220/274 (80%)	220 (100%)	0	100	100
43	NK	233/289 (81%)	233 (100%)	0	100	100
44	NM	205/224 (92%)	205 (100%)	0	100	100
45	NN	44/482 (9%)	44 (100%)	0	100	100
46	NQ	68/71 (96%)	68 (100%)	0	100	100
47	OA	10/1544 (1%)	10 (100%)	0	100	100
48	SA	331/435 (76%)	331 (100%)	0	100	100
49	SB	360/433 (83%)	360 (100%)	0	100	100
50	SC	200/240 (83%)	200 (100%)	0	100	100
50	SD	197/240 (82%)	197 (100%)	0	100	100
51	SE	100/104 (96%)	100 (100%)	0	100	100
51	SF	100/104 (96%)	100 (100%)	0	100	100
52	SG	392/502 (78%)	392 (100%)	0	100	100
53	SH	307/312 (98%)	307 (100%)	0	100	100
54	SI	722/1039 (70%)	722 (100%)	0	100	100
55	SJ	192/222 (86%)	192 (100%)	0	100	100
55	SK	205/222 (92%)	205 (100%)	0	100	100
56	SL	155/169 (92%)	155 (100%)	0	100	100
57	SM	251/258 (97%)	251 (100%)	0	100	100
58	SN	236/256 (92%)	236 (100%)	0	100	100
59	SP	2002/2307 (87%)	2002 (100%)	0	100	100
60	SQ	124/200 (62%)	124 (100%)	0	100	100
61	SR	86/120 (72%)	86 (100%)	0	100	100
62	SS	234/808 (29%)	234 (100%)	0	100	100
63	ST	443/732 (60%)	443 (100%)	0	100	100
64	SU	490/506 (97%)	490 (100%)	0	100	100
65	SV	42/192 (22%)	42 (100%)	0	100	100
66	SW	172/238 (72%)	172 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	SY	218/234 (93%)	218 (100%)	0	100	100
68	SZ	14/424 (3%)	14 (100%)	0	100	100
All	All	21310/31319 (68%)	21310 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 182 such sidechains are listed below:

Mol	Chain	Res	Type
42	NI	219	ASN
56	SL	77	GLN
48	SA	23	GLN
50	SD	201	HIS
59	SP	115	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	519/700 (74%)	91 (17%)	0
2	L1	1124/1808 (62%)	171 (15%)	1 (0%)
3	L2	170/333 (51%)	24 (14%)	0
All	All	1813/2841 (63%)	286 (15%)	1 (0%)

5 of 286 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	7	A
1	L0	63	G
1	L0	64	U
1	L0	83	U
1	L0	85	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	320	U

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues are modelled in this entry.

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
52	SEP	SG	50	52	8,9,10	1.58	1 (12%)	7,12,14	1.35	1 (14%)
23	SEP	LO	651	23	8,9,10	1.55	1 (12%)	7,12,14	1.33	1 (14%)
27	SEP	LS	128	27	8,9,10	1.58	1 (12%)	7,12,14	1.21	1 (14%)

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
52	SEP	SG	50	52	-	0/6/8/10	-
23	SEP	LO	651	23	-	1/6/8/10	-
27	SEP	LS	128	27	-	0/6/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	SG	50	SEP	P-O1P	3.48	1.61	1.50
27	LS	128	SEP	P-O1P	3.46	1.61	1.50
23	LO	651	SEP	P-O1P	3.38	1.61	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	SG	50	SEP	OG-CB-CA	2.97	111.03	108.14
23	LO	651	SEP	OG-CB-CA	2.83	110.90	108.14
27	LS	128	SEP	OG-CB-CA	2.54	110.61	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	LO	651	SEP	CA-CB-OG-P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 29 ligands modelled in this entry, 27 are monoatomic - leaving 2 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	$\# Z  > 2$
72	GTP	SI	2001	69	29,34,34	0.91	0	35,54,54	0.76	0
70	ATP	NH	1300	69	28,33,33	0.69	0	34,52,52	0.92	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
72	GTP	SI	2001	69	-	1/18/38/38	0/3/3/3
70	ATP	NH	1300	69	-	1/18/38/38	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( $^{\circ}$ )	Ideal( $^{\circ}$ )
70	NH	1300	ATP	C5-C6-N6	2.34	123.87	120.31

There are no chirality outliers.

All (2) torsion outliers are listed below:

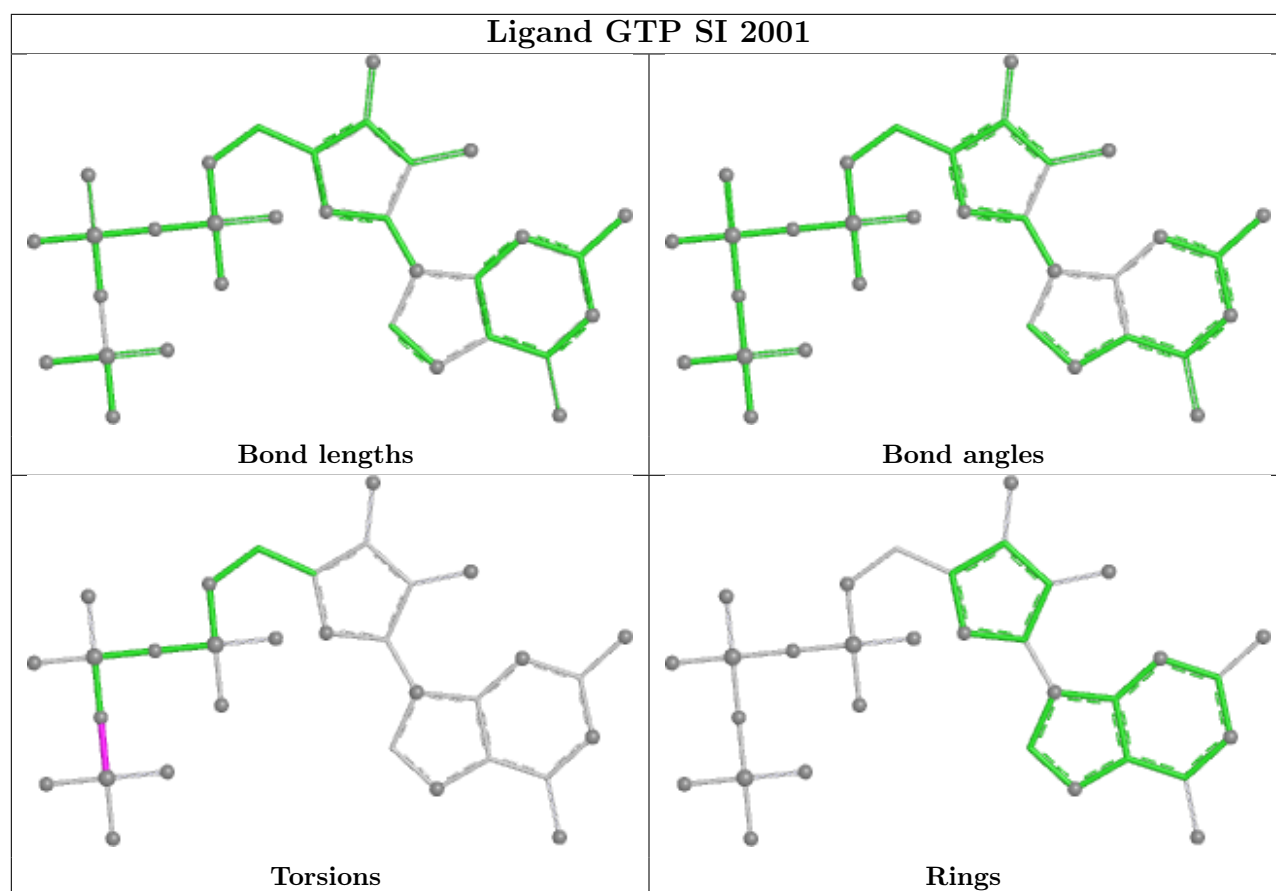
Mol	Chain	Res	Type	Atoms
72	SI	2001	GTP	PB-O3B-PG-O2G
70	NH	1300	ATP	PA-O3A-PB-O2B

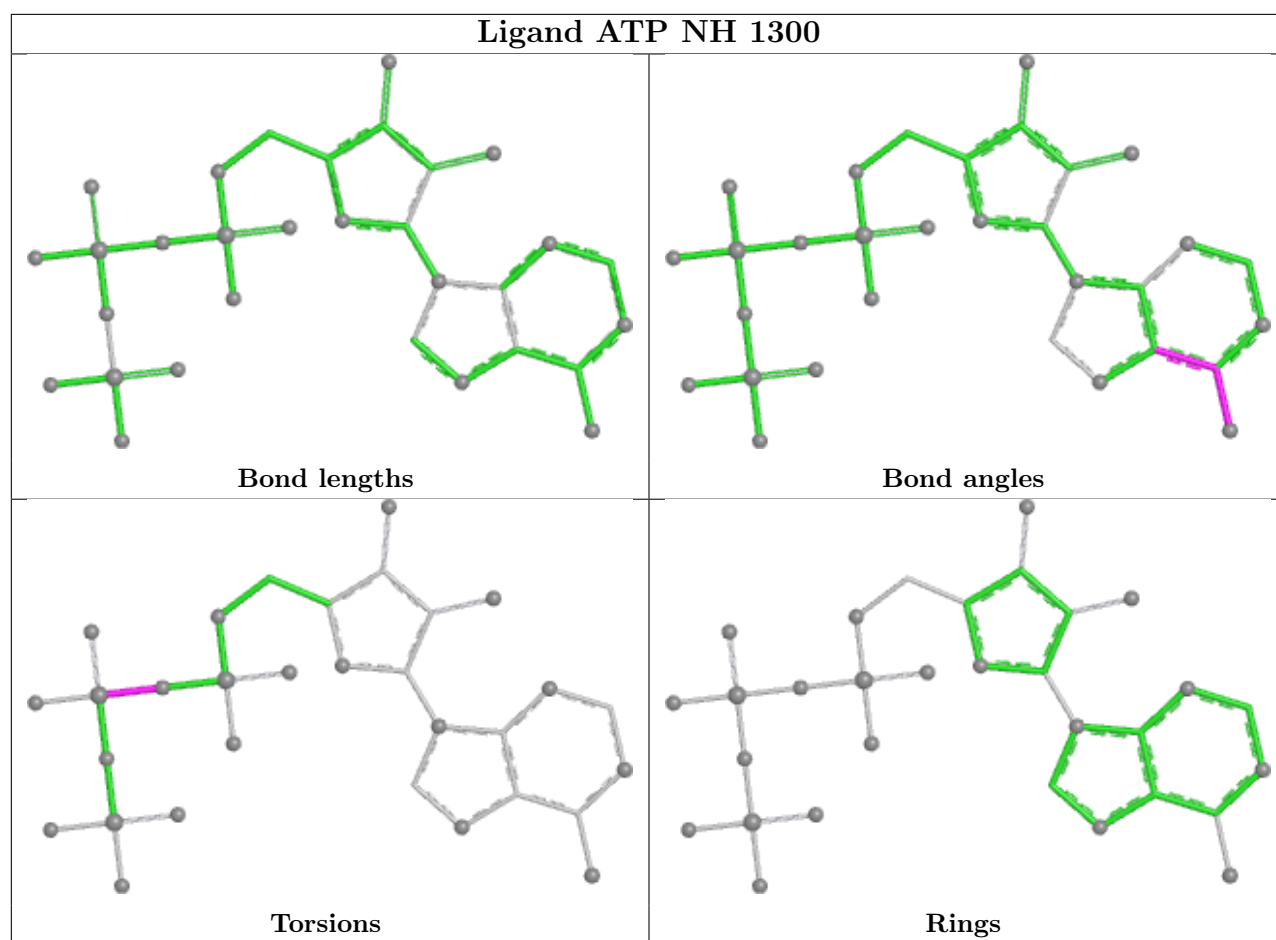
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
70	NH	1300	ATP	1	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.

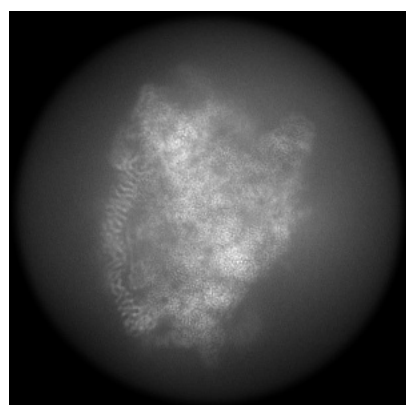
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49076. These allow visual inspection of the internal detail of the map and identification of artifacts.

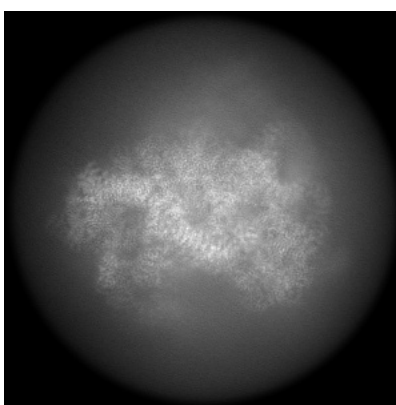
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

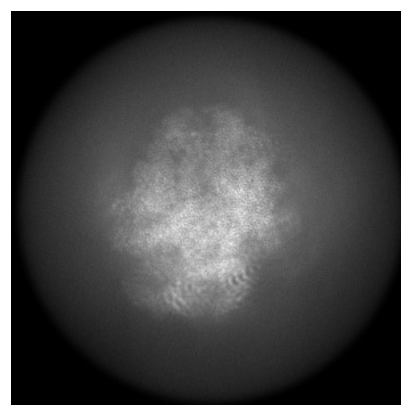
#### 6.1.1 Primary map



X



Y

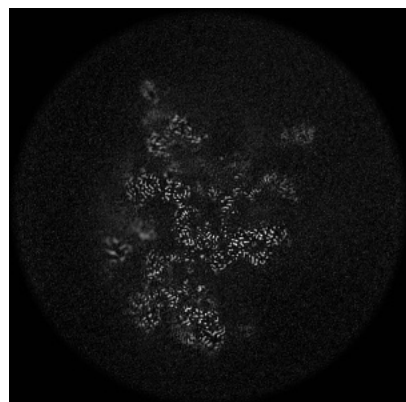


Z

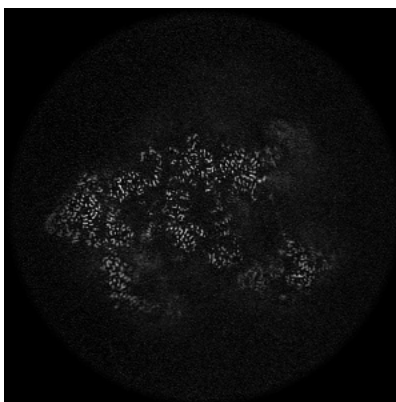
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

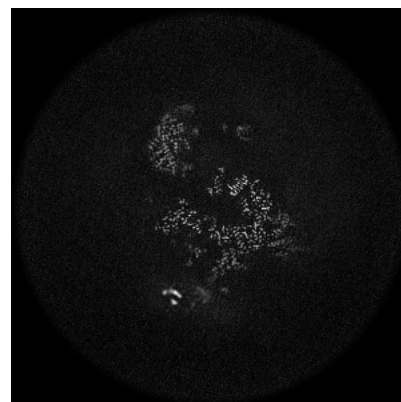
#### 6.2.1 Primary map



X Index: 252



Y Index: 252



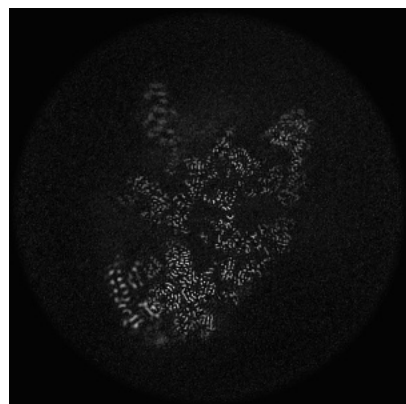
Z Index: 252



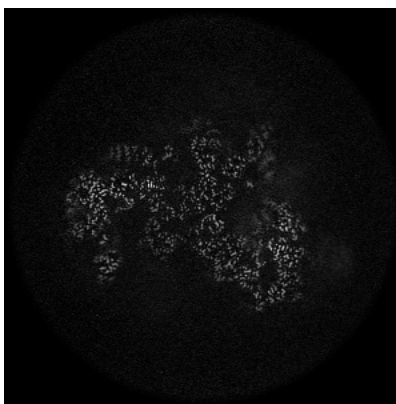
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

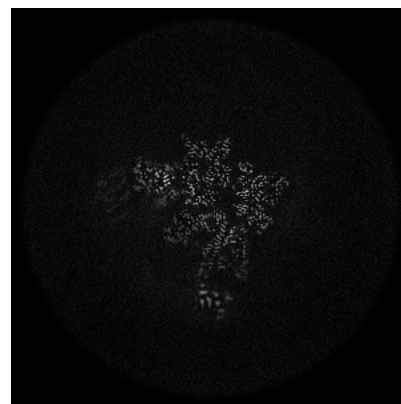
### 6.3.1 Primary map



X Index: 278



Y Index: 223

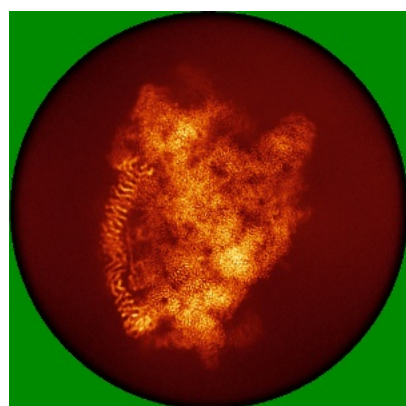


Z Index: 192

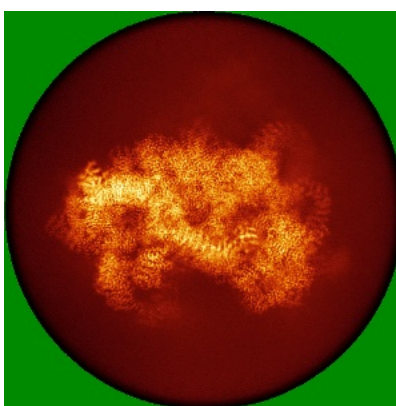
The images above show the largest variance slices of the map in three orthogonal directions.

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

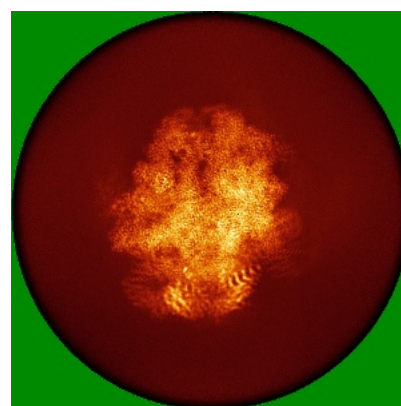
### 6.4.1 Primary map



X



Y

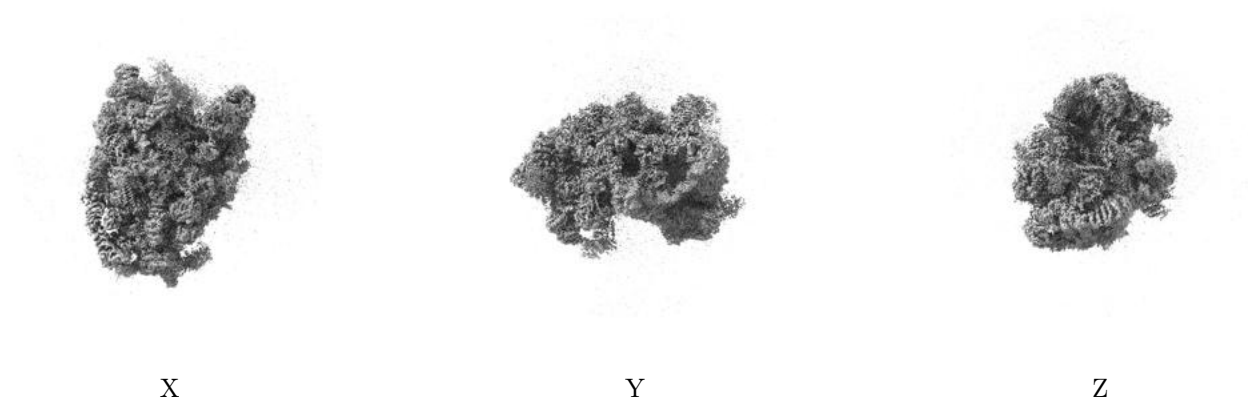


Z

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 0.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

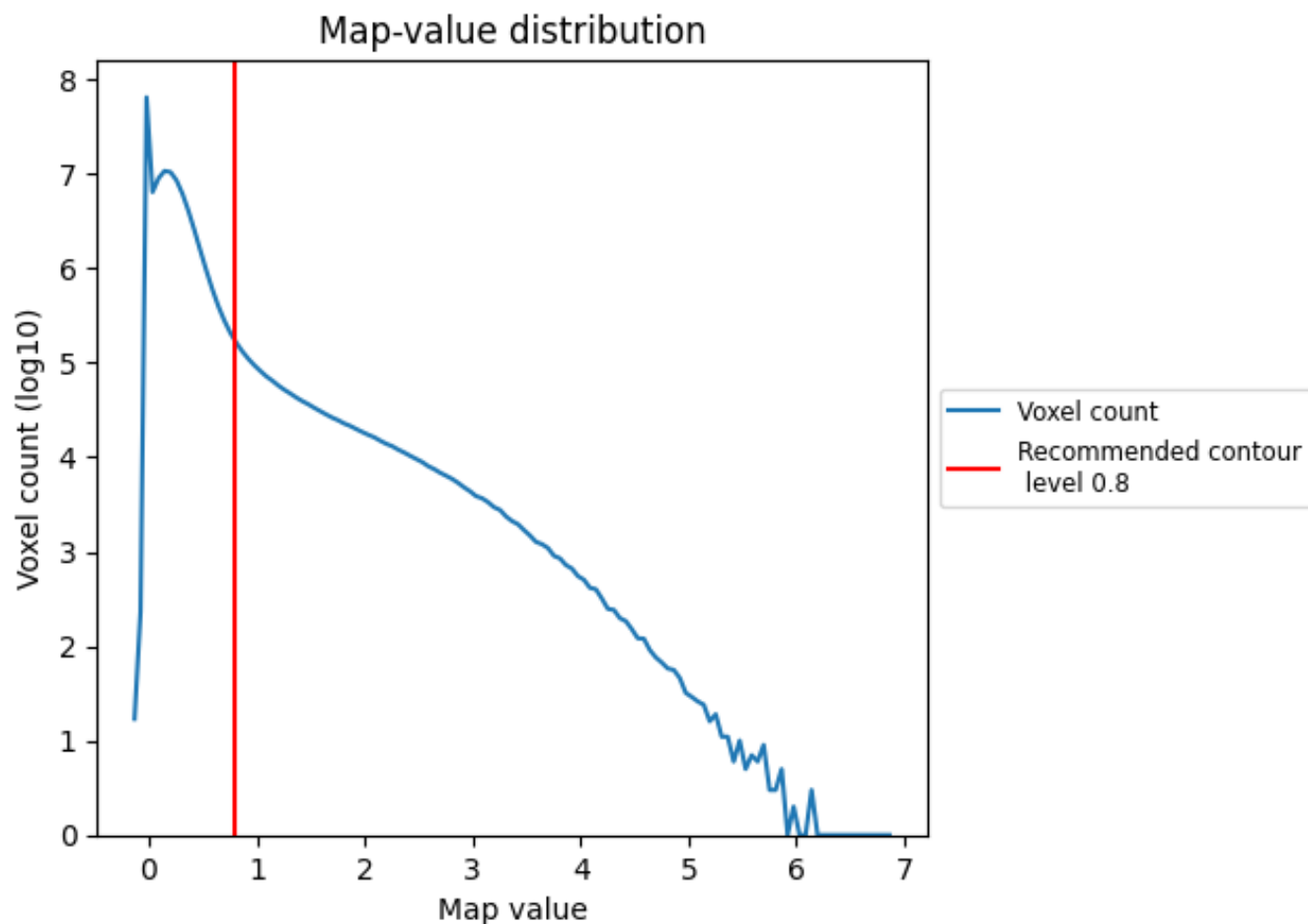
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

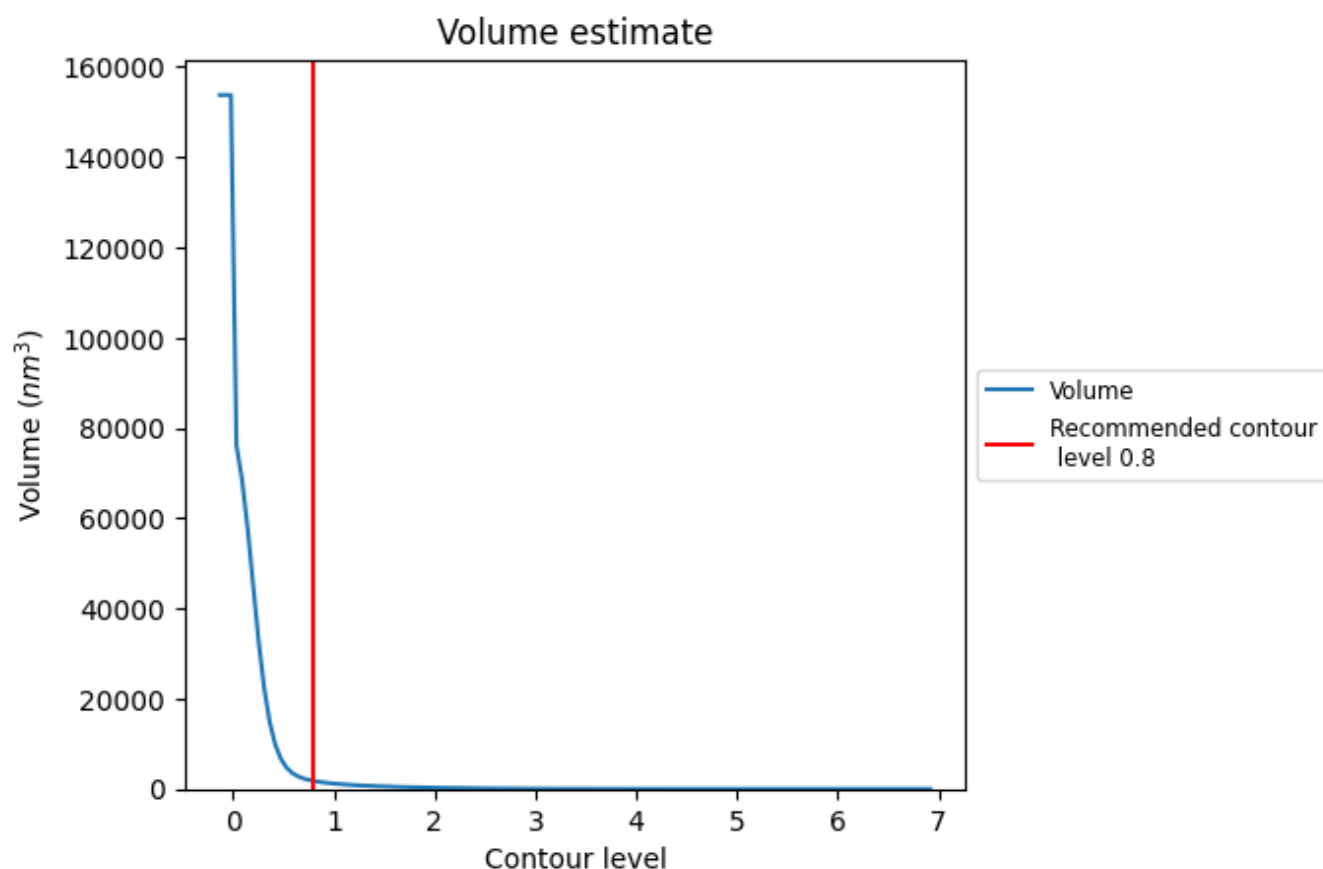
This section contains the results of statistical analysis of the map.

### 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.

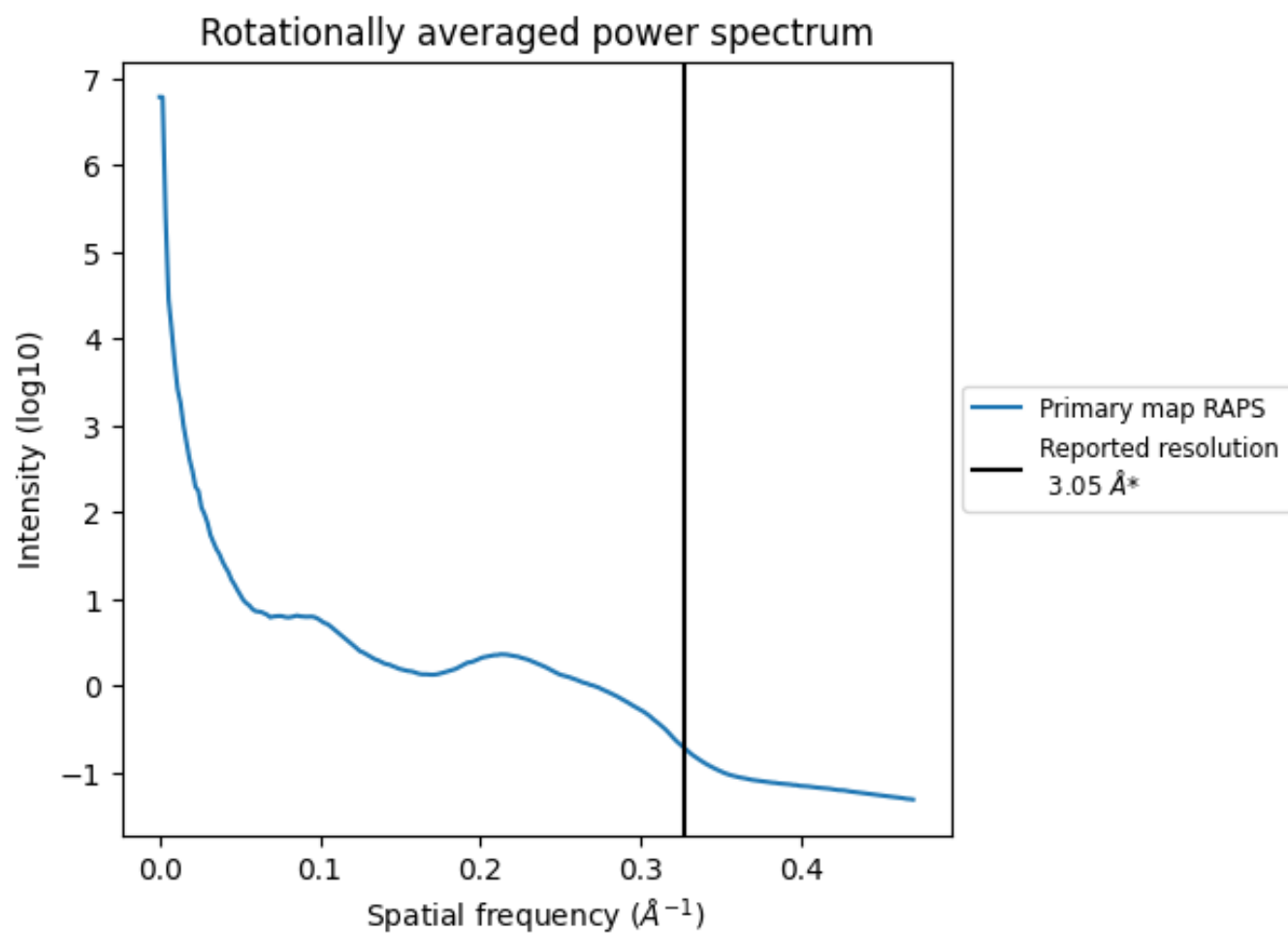
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1771  $\text{nm}^3$ ; this corresponds to an approximate mass of 1600 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 0.328 Å<sup>-1</sup>

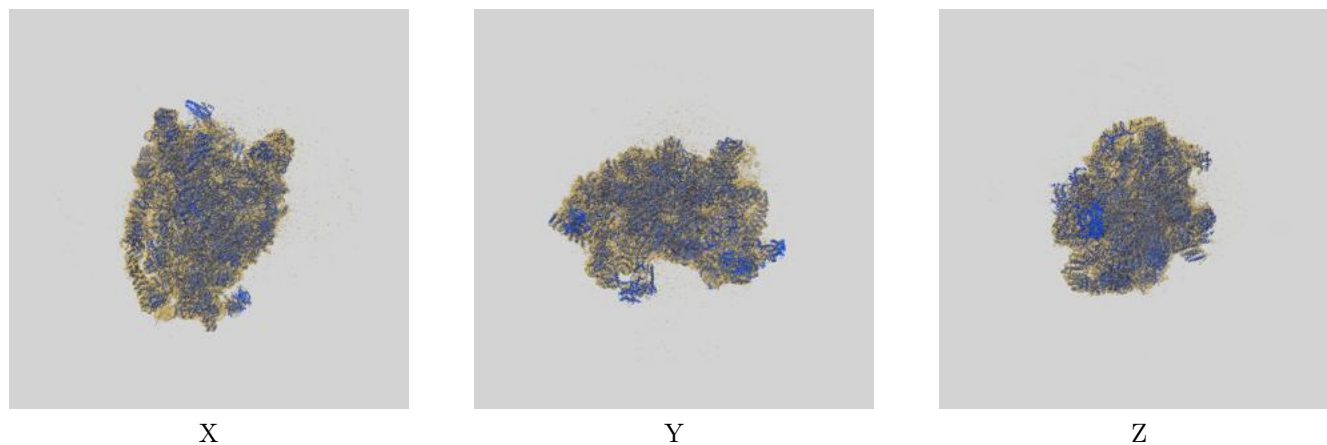
## 8 Fourier-Shell correlation ⓘ

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

## 9 Map-model fit [i](#)

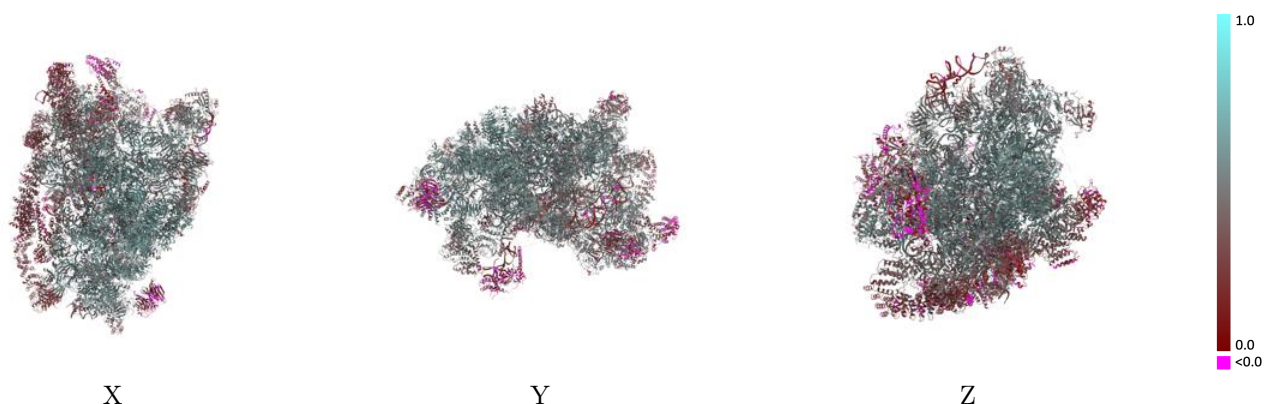
This section contains information regarding the fit between EMDB map EMD-49076 and PDB model 9N6W. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

### 9.1 Map-model overlay [i](#)



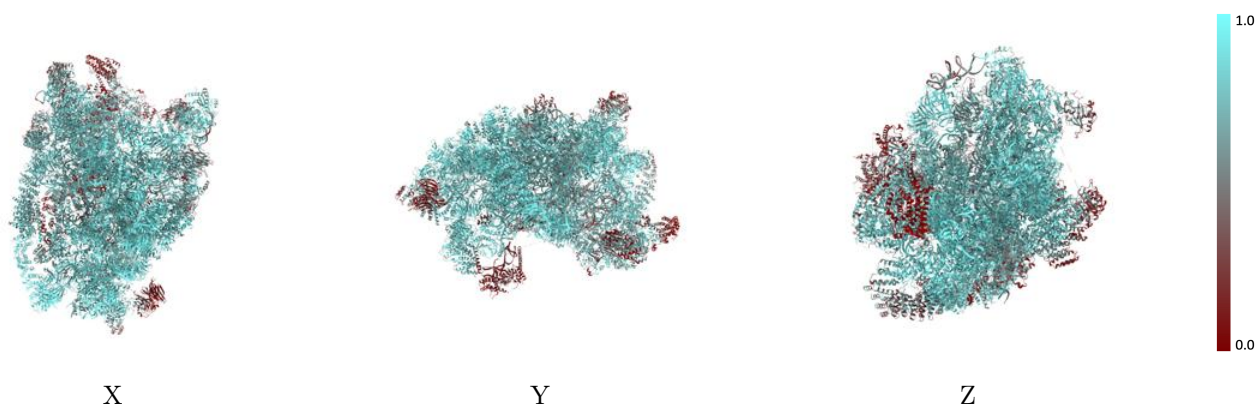
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

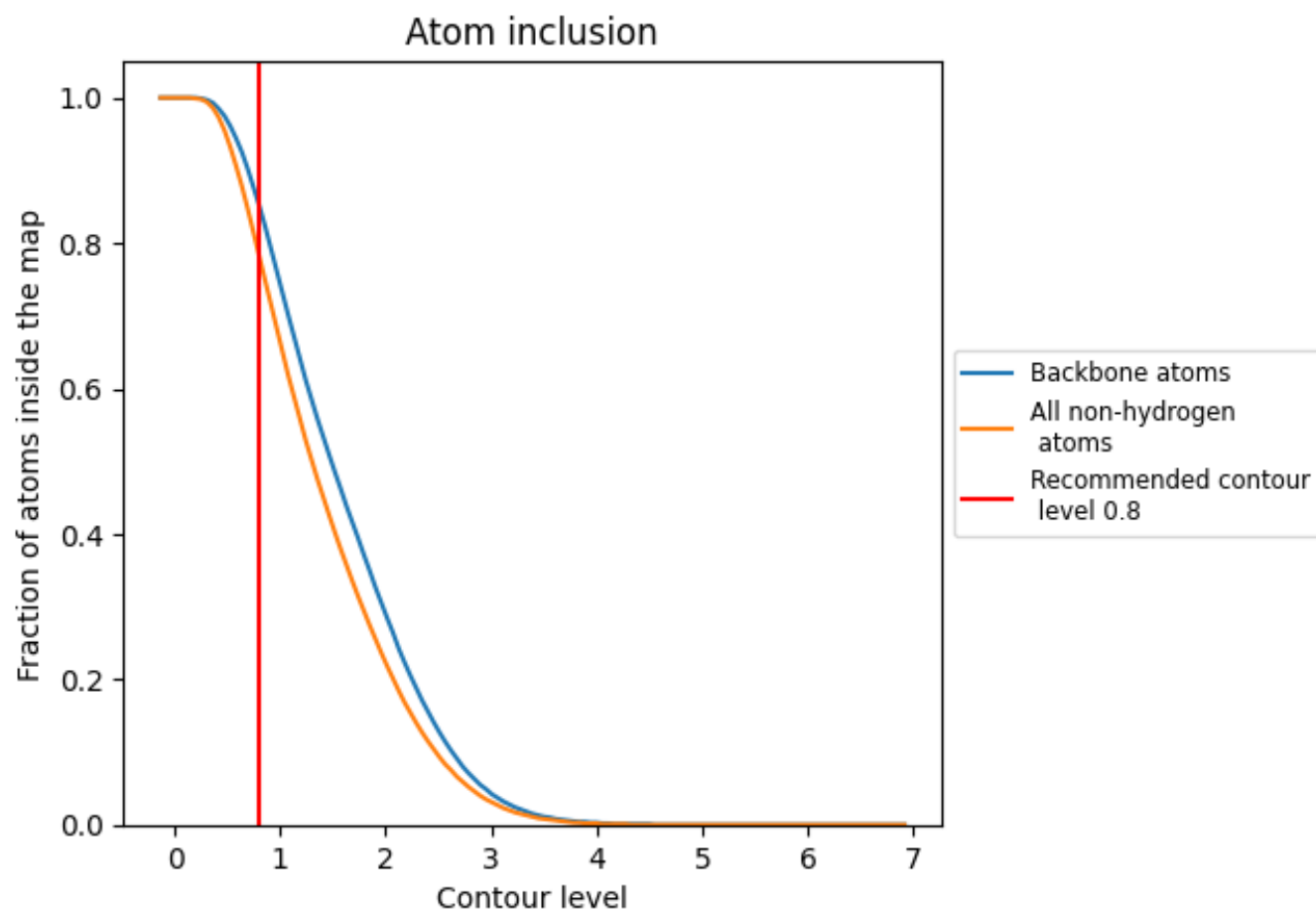
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.8).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 78% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.4700
L0	 0.8550	 0.5070
L1	 0.8510	 0.4660
L2	 0.8760	 0.5030
L3	 0.1730	 0.2540
L4	 0.8460	 0.4500
L5	 0.8740	 0.5600
L6	 0.8800	 0.4680
L7	 0.7380	 0.4060
L8	 0.9370	 0.5320
L9	 0.8670	 0.5560
LC	 0.8990	 0.5840
LD	 0.8720	 0.4770
LE	 0.9230	 0.5550
LF	 0.8850	 0.4010
LG	 0.8600	 0.5630
LH	 0.8840	 0.5440
LI	 0.4030	 0.2720
LJ	 0.9190	 0.5620
LK	 0.6250	 0.3880
LL	 0.8890	 0.5500
LM	 0.8540	 0.3530
LN	 0.9040	 0.5190
LO	 0.9110	 0.5930
LP	 0.6370	 0.4210
LQ	 0.8420	 0.4730
LR	 0.6430	 0.4350
LS	 0.9080	 0.5830
LT	 0.8850	 0.5820
LU	 0.9310	 0.5850
LV	 0.8120	 0.4840
LW	 0.8850	 0.5900
LX	 0.7450	 0.4610
LY	 0.5630	 0.3750
LZ	 0.9400	 0.6180



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Chain	Atom inclusion	Q-score
NA	 0.7300	 0.4730
NB	 0.6570	 0.3830
NC	 0.5470	 0.3340
ND	 0.6750	 0.4220
NE	 0.7220	 0.4830
NF	 0.8930	 0.5520
NG	 0.8050	 0.5440
NH	 0.8160	 0.4860
NI	 0.5320	 0.4130
NK	 0.8110	 0.5390
NM	 0.7880	 0.5360
NN	 0.3150	 0.2130
NQ	 0.9230	 0.5670
OA	 0.4000	 0.4180
SA	 0.6990	 0.4460
SB	 0.7150	 0.4270
SC	 0.8780	 0.5800
SD	 0.7880	 0.5140
SE	 0.9440	 0.5930
SF	 0.8290	 0.5510
SG	 0.8000	 0.5060
SH	 0.7990	 0.5390
SI	 0.8450	 0.5490
SJ	 0.8090	 0.4500
SK	 0.9060	 0.4920
SL	 0.9020	 0.5880
SM	 0.8520	 0.5640
SN	 0.7280	 0.5130
SP	 0.6190	 0.3040
SQ	 0.7110	 0.5080
SR	 0.8940	 0.5780
SS	 0.6180	 0.4330
ST	 0.6480	 0.3960
SU	 0.8290	 0.4430
SV	 0.7450	 0.3290
SW	 0.5870	 0.4470
SY	 0.8510	 0.5610
SZ	 0.1830	 0.1570