



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:41 PM UTC

PDB ID : 9N6Y / pdb_00009n6y
EMDB ID : EMD-49078
Title : SSU processome maturation and disassembly, State C
Authors : Buzovetsky, O.; Klinge, S.
Deposited on : 2025-02-05
Resolution : 3.65 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ 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

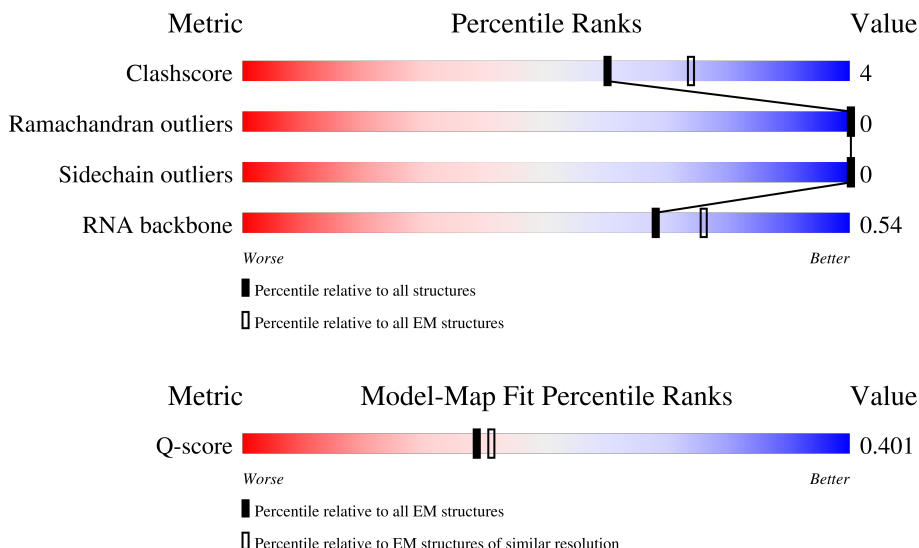
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.65 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	11564 (3.15 - 4.15)

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	L0	700	
2	L1	1808	
3	L2	333	

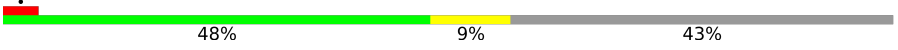
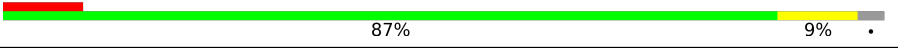
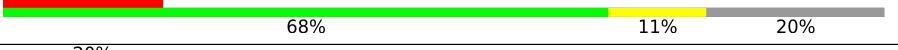
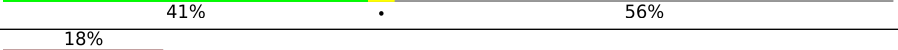
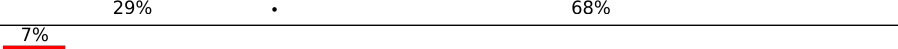
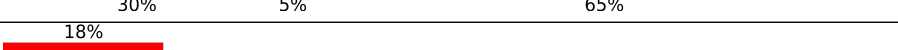
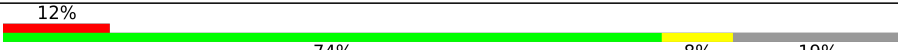
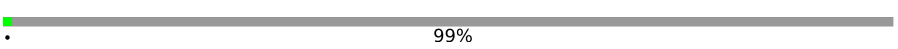
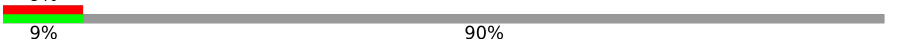
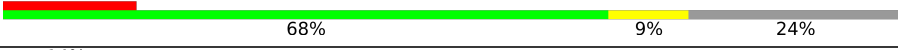
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Mol	Chain	Length	Quality of chain
4	L3	146	
5	L4	261	
6	L5	225	
7	L6	236	
8	L7	190	
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LO	923	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

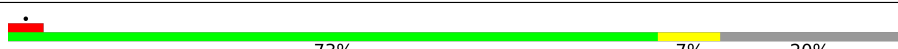
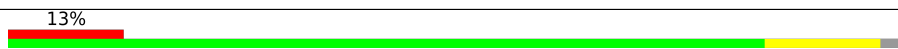
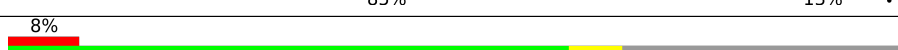
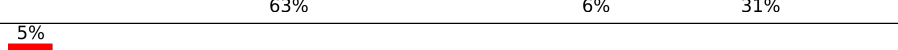
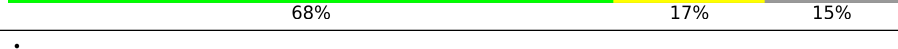
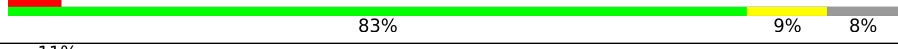
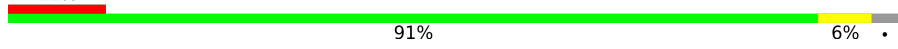
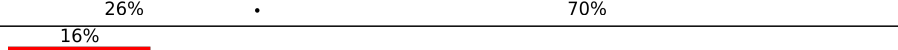
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Mol	Chain	Length	Quality of chain
29	LU	489	
30	LV	707	
31	LW	554	
32	LX	1056	
32	LY	1056	
33	LZ	183	
34	NA	593	
35	NB	610	
36	NC	357	
37	ND	214	
38	NE	346	
39	NF	151	
40	NG	137	
41	NH	1237	
42	NI	297	
43	NK	316	
44	NM	255	
45	NN	534	
46	NQ	82	
47	NV	733	
48	OA	1729	
49	SA	504	
50	SB	511	
51	SC	327	
51	SD	327	

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

2 Entry composition

There are 73 unique types of molecules in this entry. The entry contains 245176 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	445	Total	C	N	O	P	0	0
			9483	4239	1674	3125	445		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1205	Total	C	N	O	P	0	0
			25709	11494	4600	8410	1205		

- 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	244	Total	C	N	O	S	0	0
			1936	1239	359	335	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	170	Total	C	N	O	S	0	0
			1348	836	269	241	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	130	Total	C	N	O		
			1046	662	204	180	0	0

- 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		
			490	302	98	89	1	0	0

- 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		
			6465	4123	1090	1233	19	0	0

- 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		
			3792	2375	679	733	5	0	0

- 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		
			3911	2462	702	735	12	0	0

- 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		
			1068	681	185	199	3	0	0

- 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		
			3982	2522	679	768	13	0	0

- 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	842	Total	C	N	O	S	0	0
			6720	4301	1155	1238	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	115	Total	C	N	O	S	0	0
			777	484	145	145	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
			1930	1212	343	373	2		

- 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 Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	NV	8	Total	C	N	O	0	0
			64	42	12	10		

- Molecule 48 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	OA	171	Total	C	N	O	0	0
			888	539	172	177		

- Molecule 49 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	385	Total	C	N	O	S	0	0
			3035	1926	521	579	9		

- Molecule 50 is a protein called Nucleolar protein 58.

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

- Molecule 51 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

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

- Molecule 52 is a protein called 13 kDa ribonucleoprotein-associated protein.

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

- Molecule 53 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SG	459	Total	C	N	O	S	0	0
			3672	2331	645	686	10		

- Molecule 54 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 55 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI	811	Total	C	N	O	S	0	0
			6577	4219	1156	1173	29		

- Molecule 56 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SJ	213	Total	C	N	O	S	0	0
			1678	1069	292	306	11		
56	SK	229	Total	C	N	O	S	0	0
			1793	1141	312	329	11		

- Molecule 57 is a protein called rRNA-processing protein FCF1.

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

- Molecule 58 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

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

- Molecule 59 is a protein called Ribosome biogenesis protein UTP30.

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

- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SP	2356	Total	C	N	O	S	0	0
			18367	11791	3084	3434	58		

- Molecule 61 is a protein called rRNA-processing protein FCF2.

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

- Molecule 62 is a protein called 40S ribosomal protein S23-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SS	272	Total	C	N	O	S	0	0
			2267	1415	427	415	10		

- Molecule 64 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	ST	582	Total	C	N	O	S	0	0
			4448	2823	802	811	12		

- Molecule 65 is a protein called Nucleolar complex protein 4.

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

- Molecule 66 is a protein called Regulator of rDNA transcription protein 14.

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

- Molecule 67 is a protein called Pre-rRNA-processing protein PNO1.

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

- Molecule 68 is a protein called U3 small nucleolar RNA-associated protein 11.

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

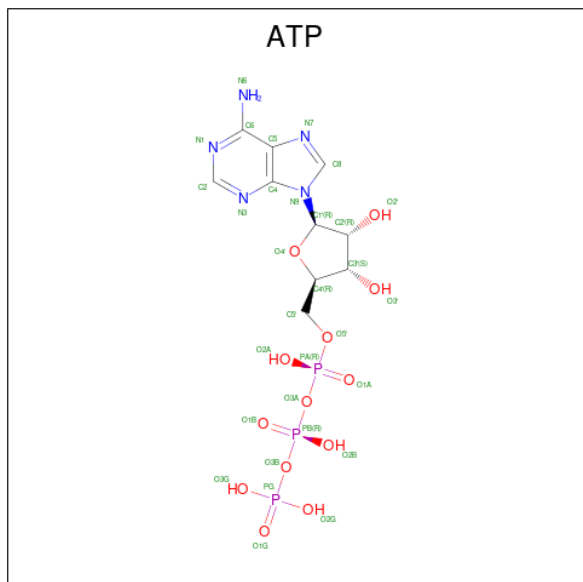
- Molecule 69 is a protein called Essential nuclear protein 1.

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

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

Mol	Chain	Residues	Atoms		AltConf
70	L0	3	Total	Mg	0
			3	3	
70	L1	26	Total	Mg	0
			26	26	
70	L2	2	Total	Mg	0
			2	2	
70	NH	1	Total	Mg	0
			1	1	
70	SI	1	Total	Mg	0
			1	1	
70	SM	1	Total	Mg	0
			1	1	

- Molecule 71 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

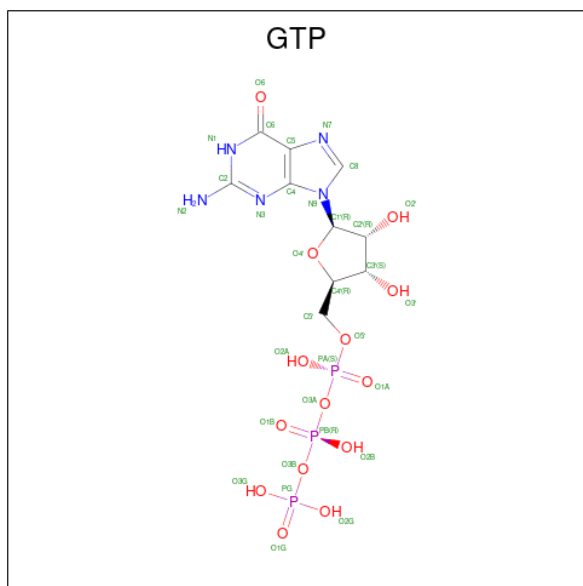


Mol	Chain	Residues	Atoms					AltConf
71	NH	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 72 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 73 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

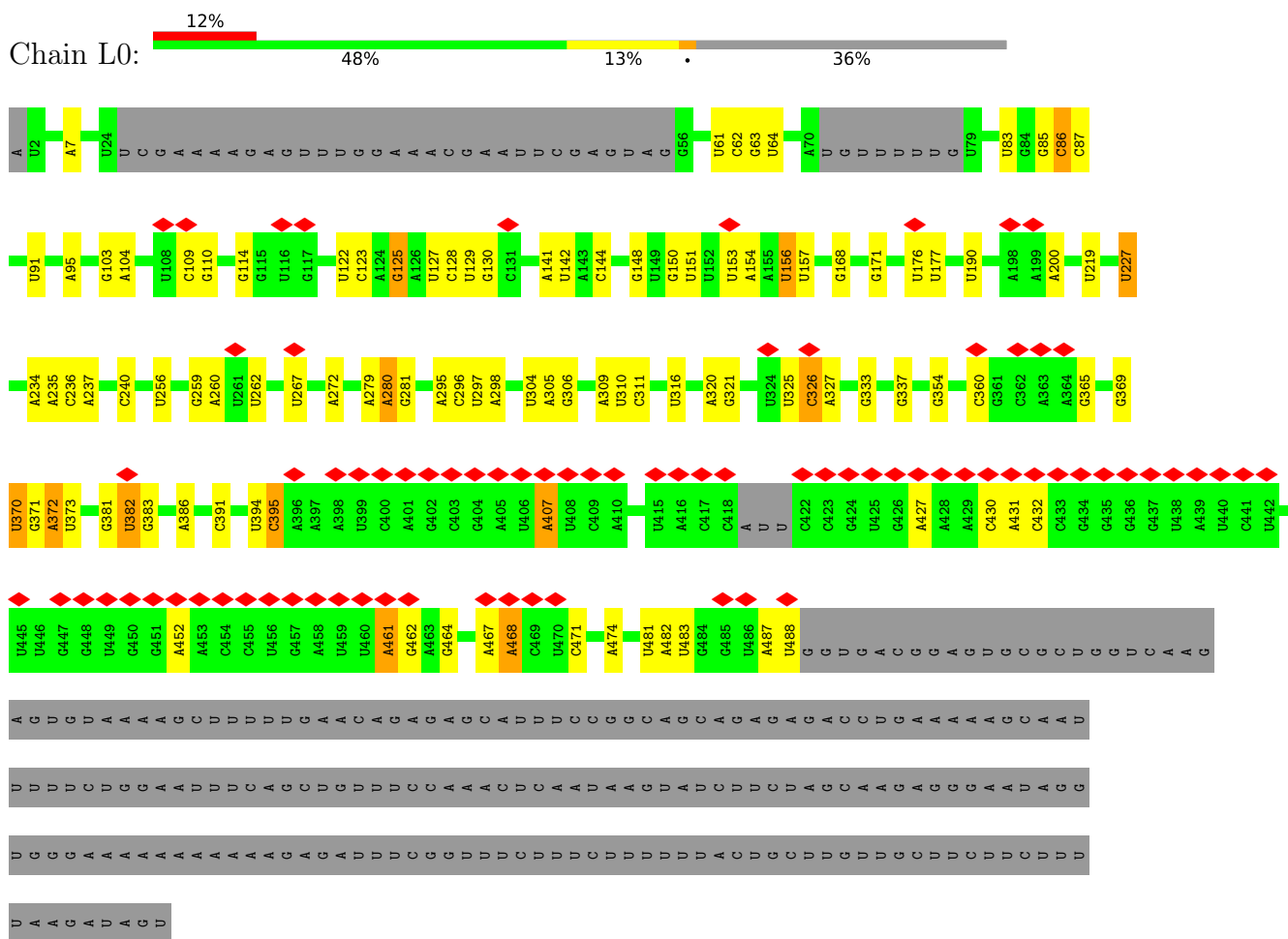


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
73	SI	1	32	10	5	14	3	0

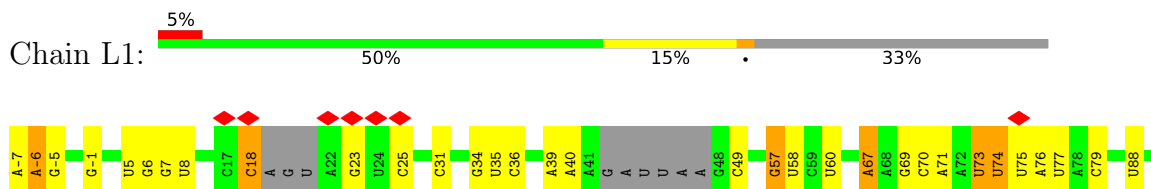
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

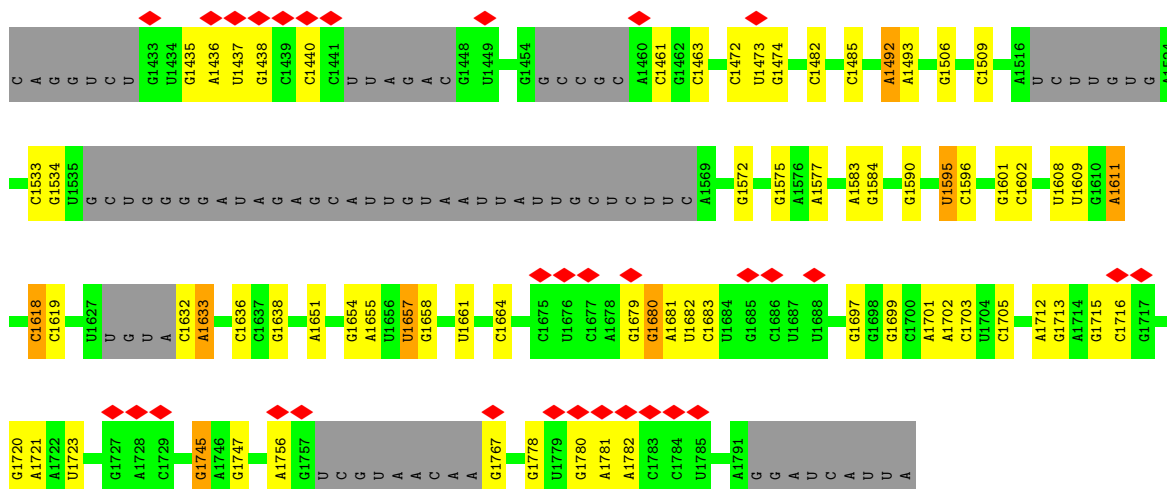
• Molecule 1: 5'ETS rRNA



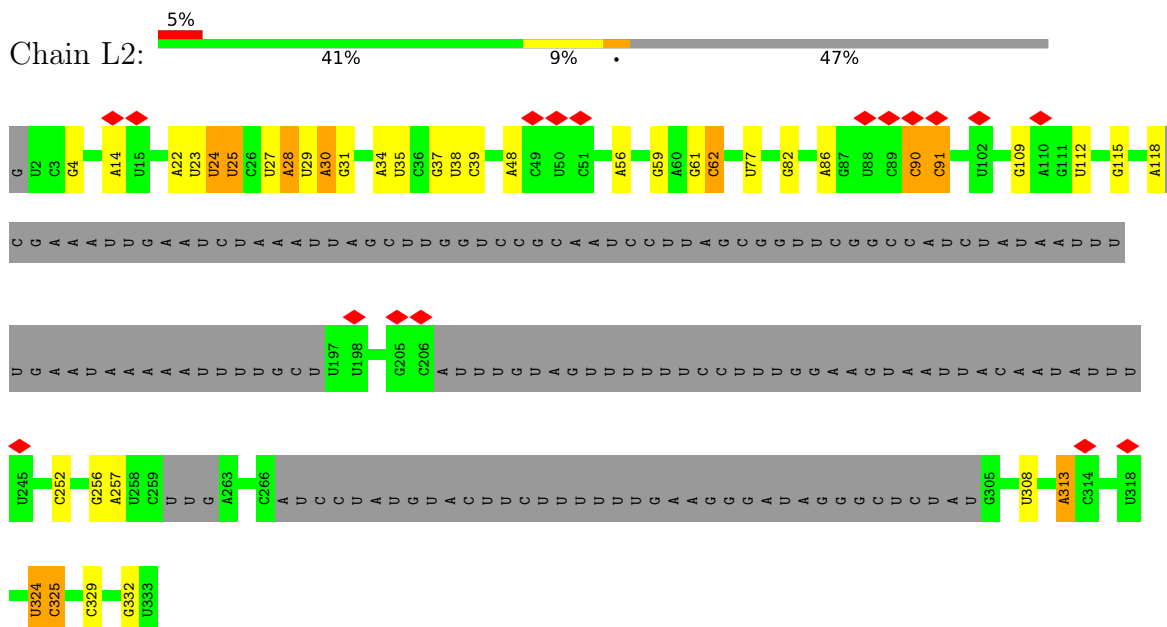
• Molecule 2: 18S rRNA



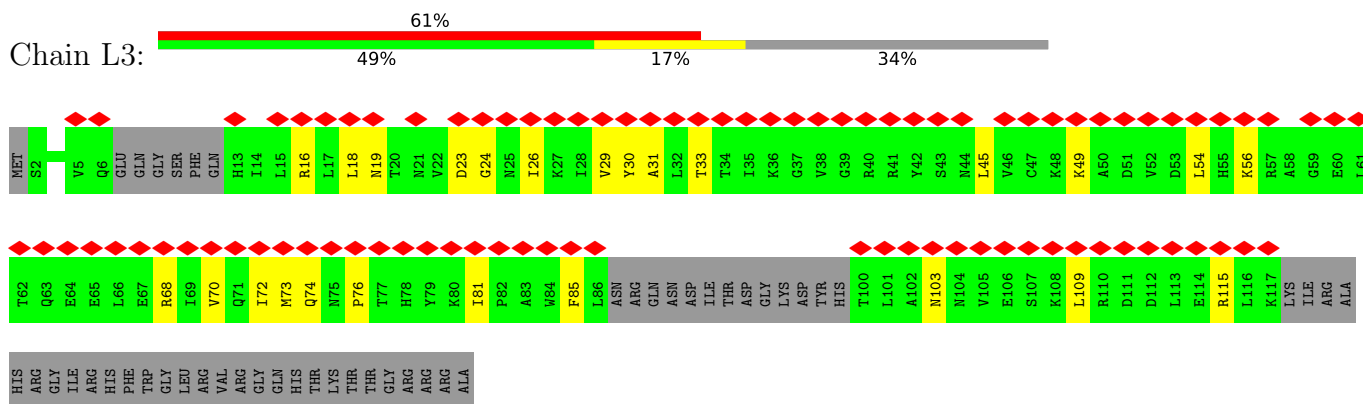




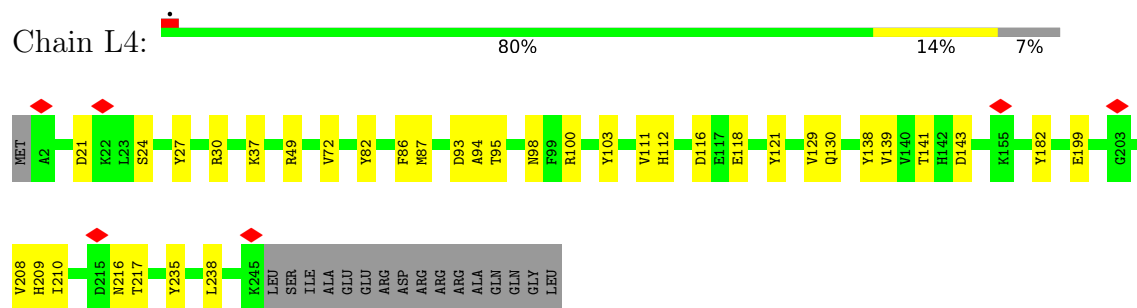
- Molecule 3: TPA: *Saccharomyces cerevisiae* U3a gene for small nucleolar RNA U3a



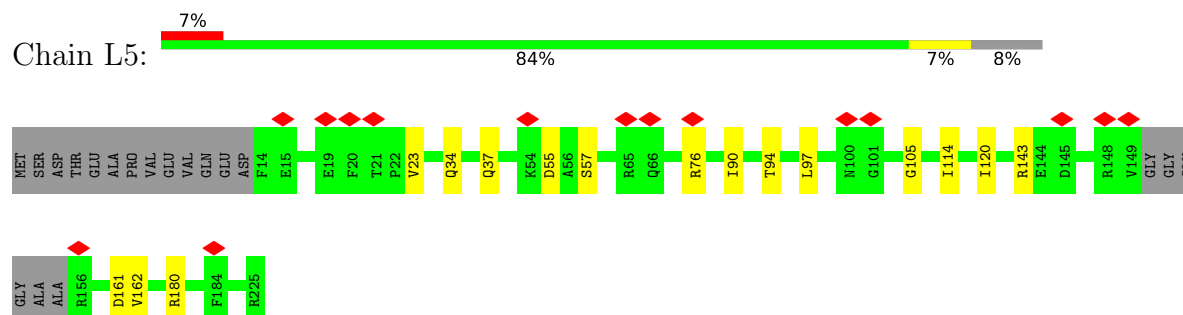
- Molecule 4: 40S ribosomal protein S18-A



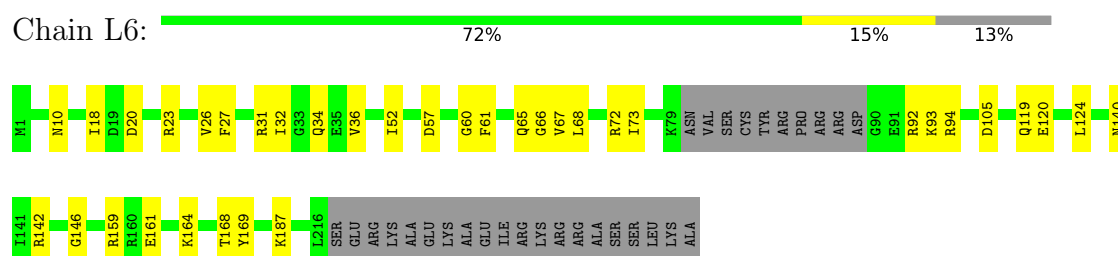
- Molecule 5: 40S ribosomal protein S4-A



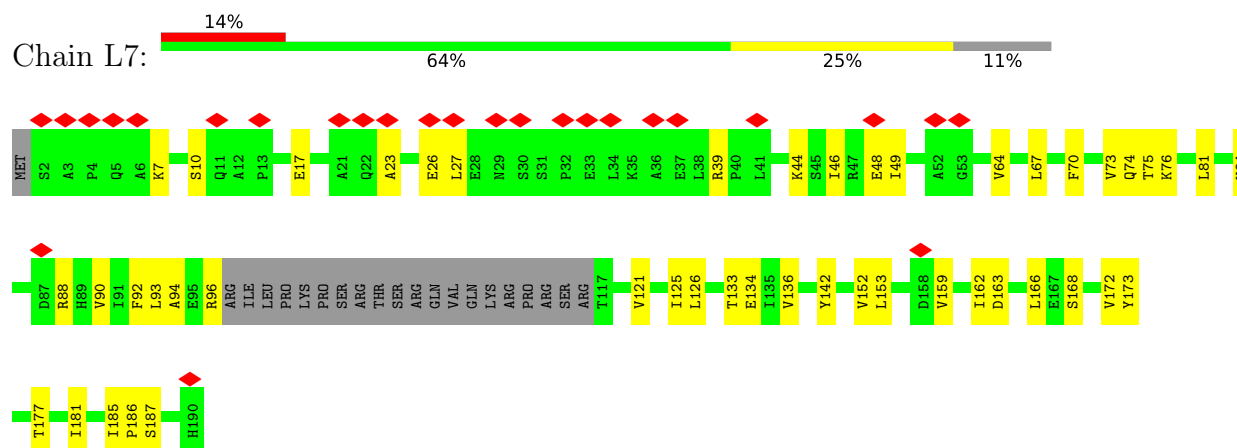
- Molecule 6: 40S ribosomal protein S5



- Molecule 7: 40S ribosomal protein S6-A

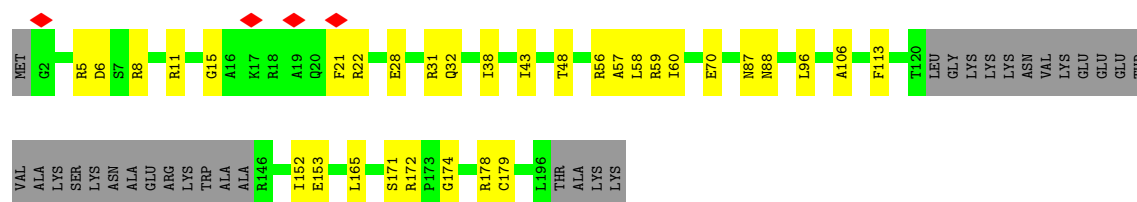


- Molecule 8: 40S ribosomal protein S7-A

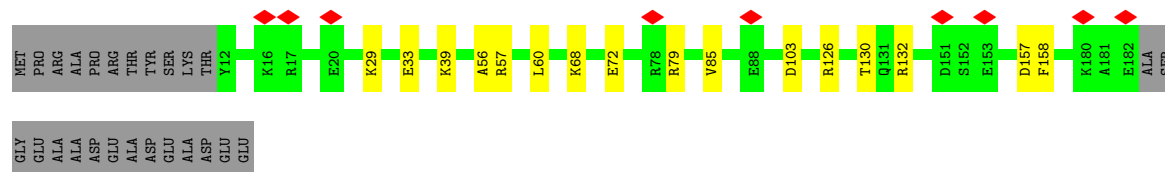
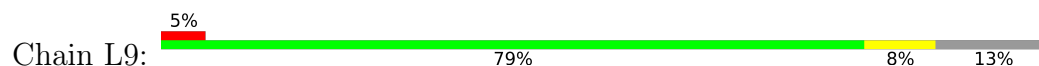


- Molecule 9: 40S ribosomal protein S8-A

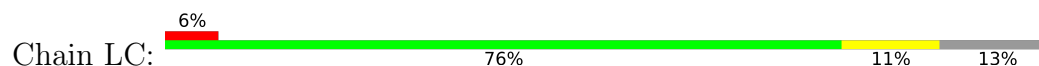




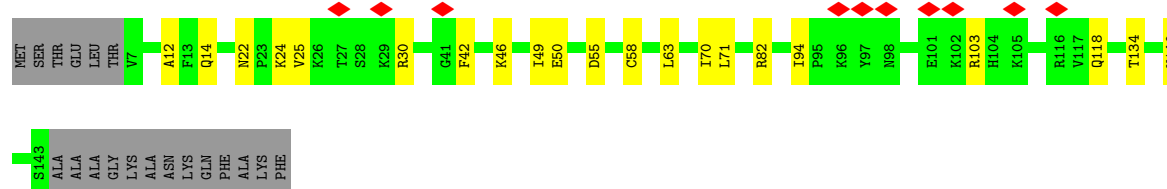
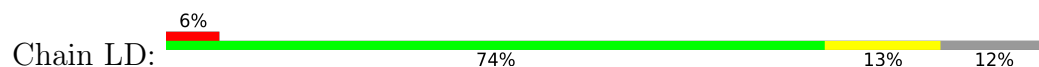
- Molecule 10: 40S ribosomal protein S9-A



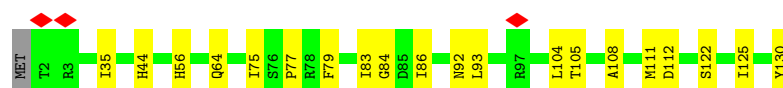
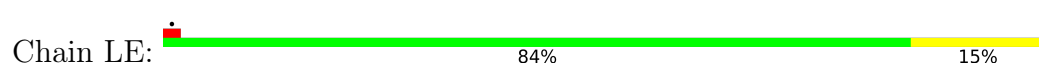
- Molecule 11: 40S ribosomal protein S16-A



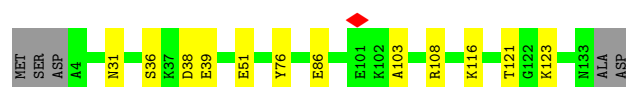
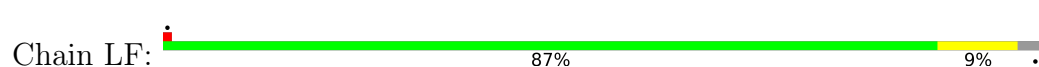
- Molecule 12: 40S ribosomal protein S11-A



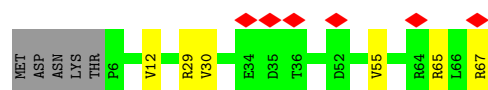
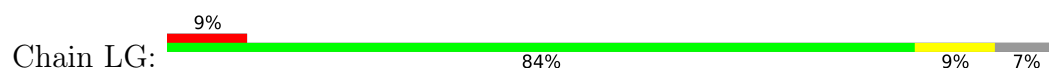
- Molecule 13: 40S ribosomal protein S22-A



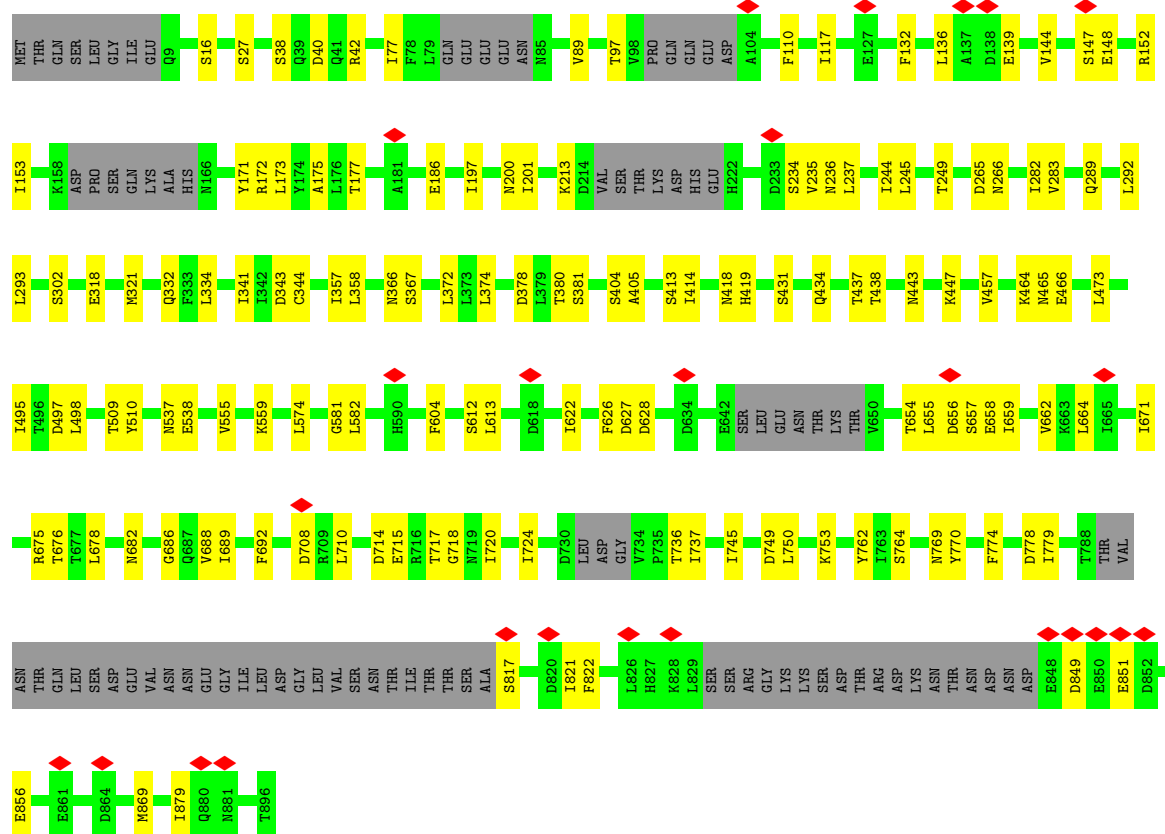
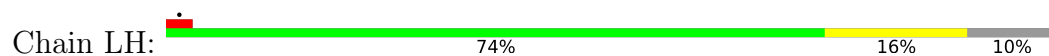
- Molecule 14: 40S ribosomal protein S24-A



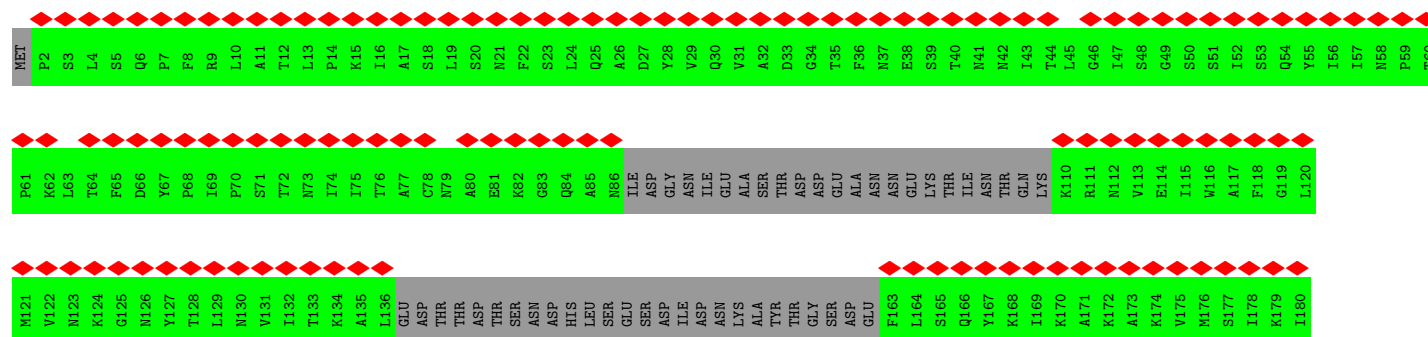
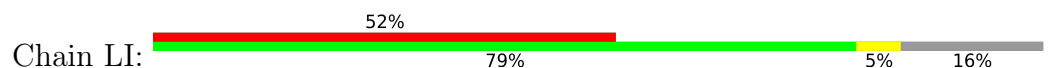
- Molecule 15: 40S ribosomal protein S28-A



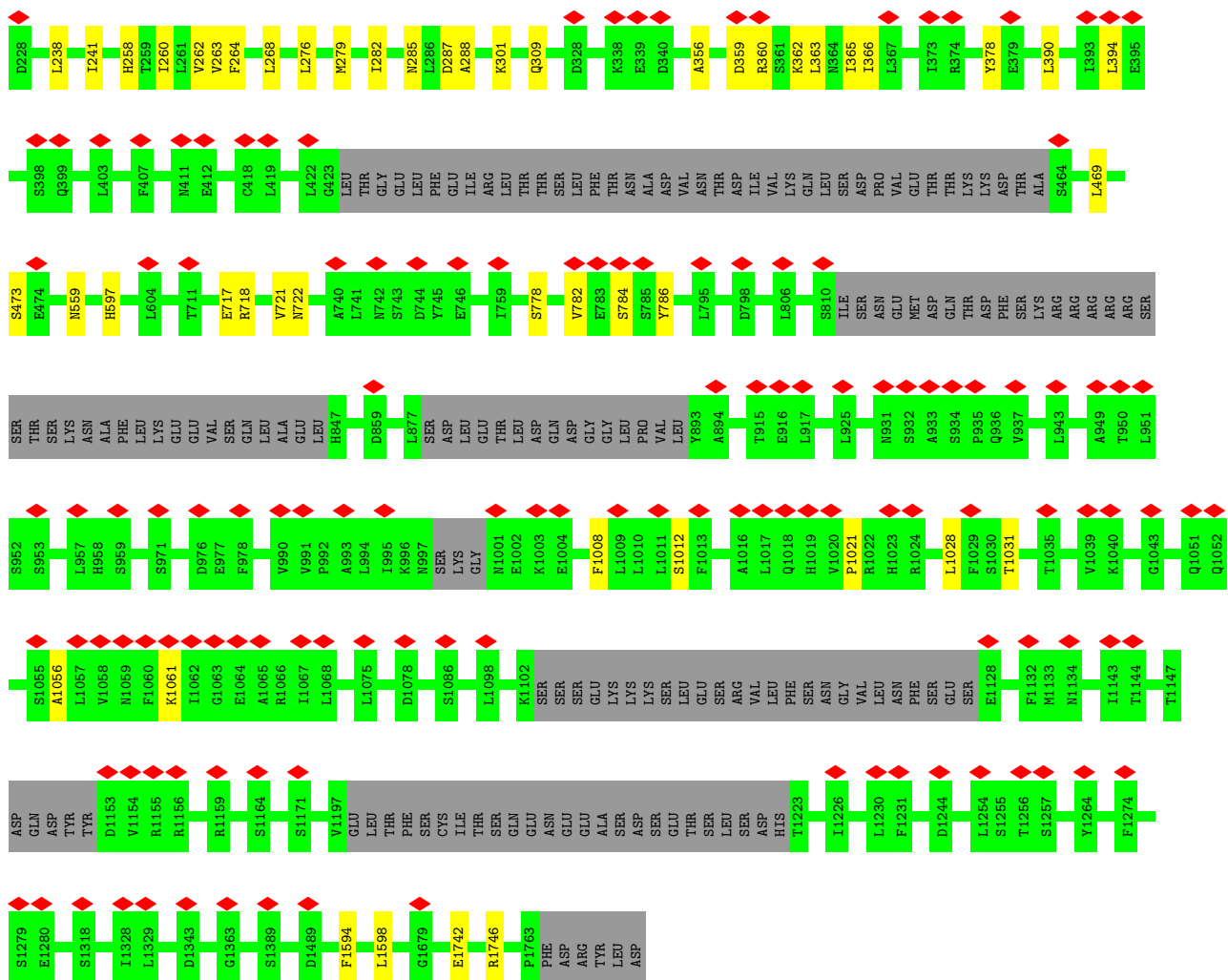
- Molecule 16: NET1-associated nuclear protein 1



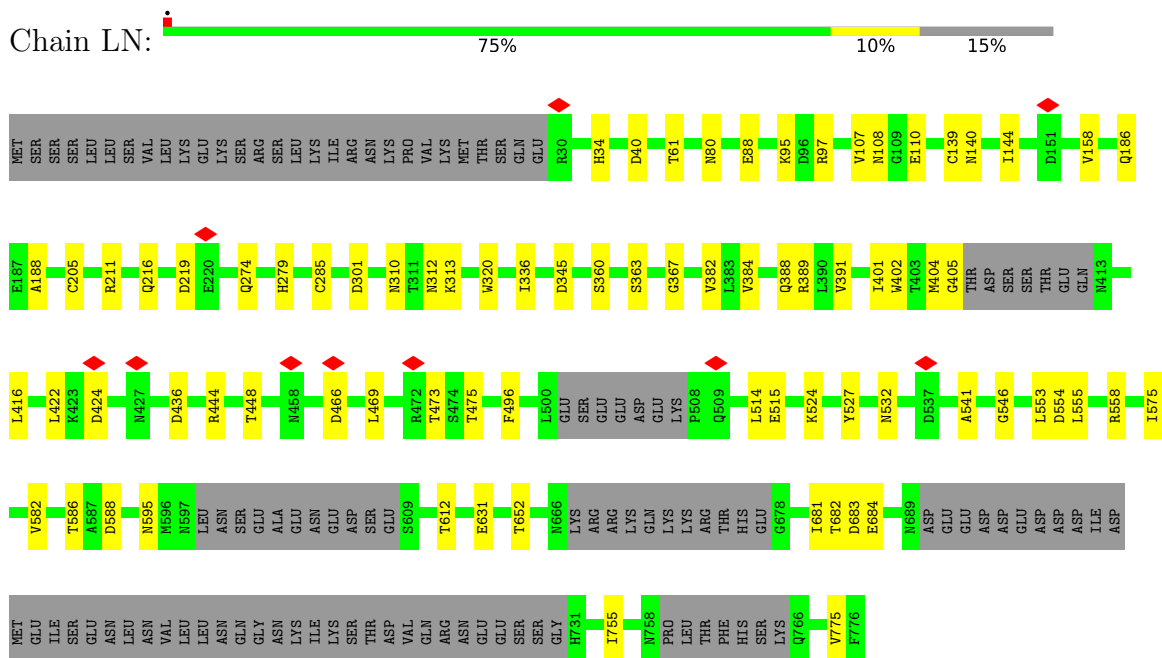
- Molecule 17: U3 small nucleolar RNA-associated protein 8

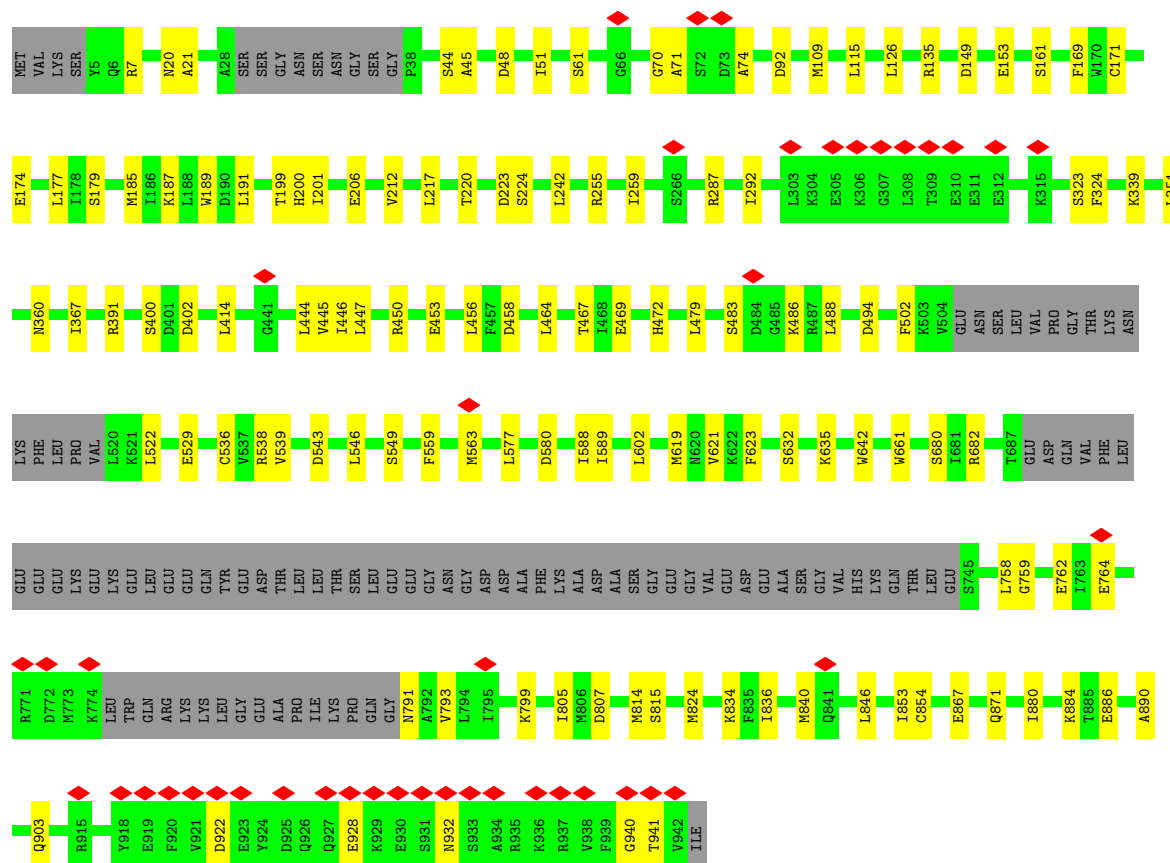




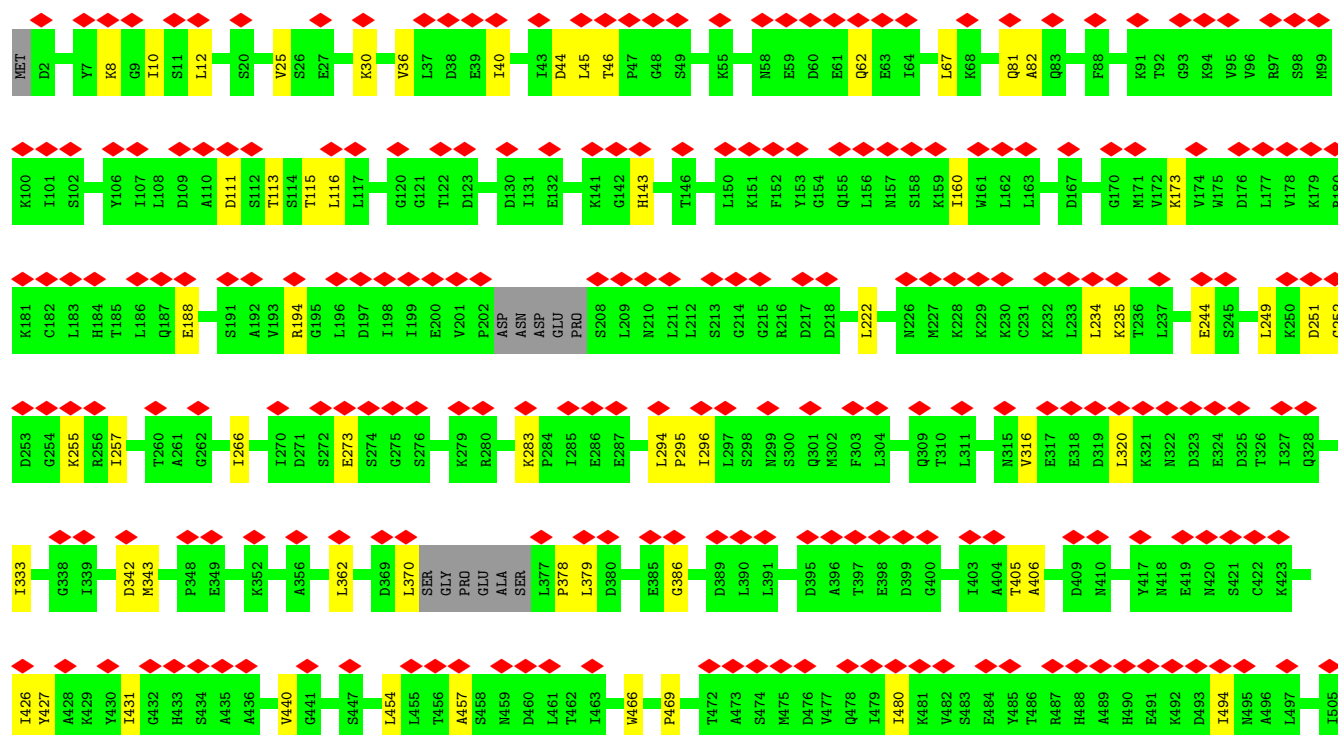
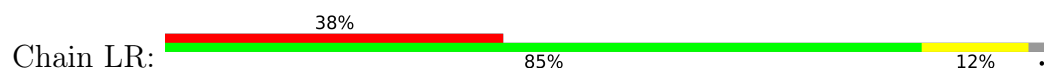


- Molecule 22: U3 small nucleolar RNA-associated protein 4

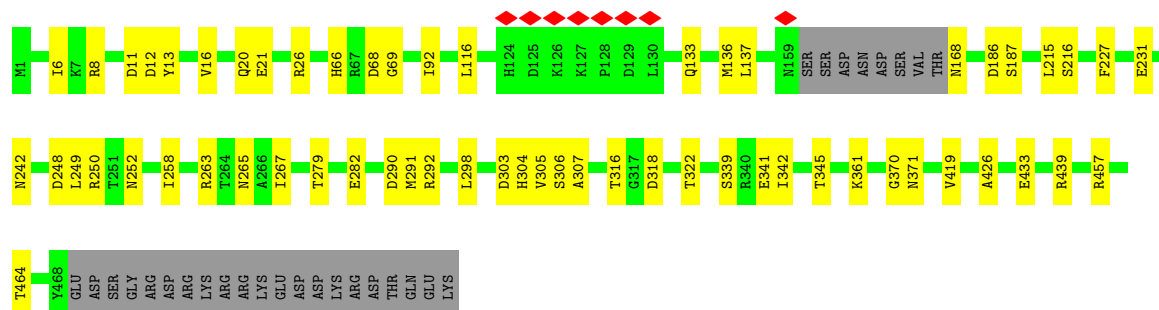
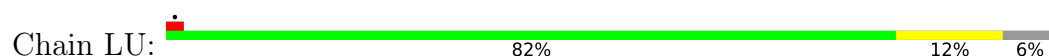




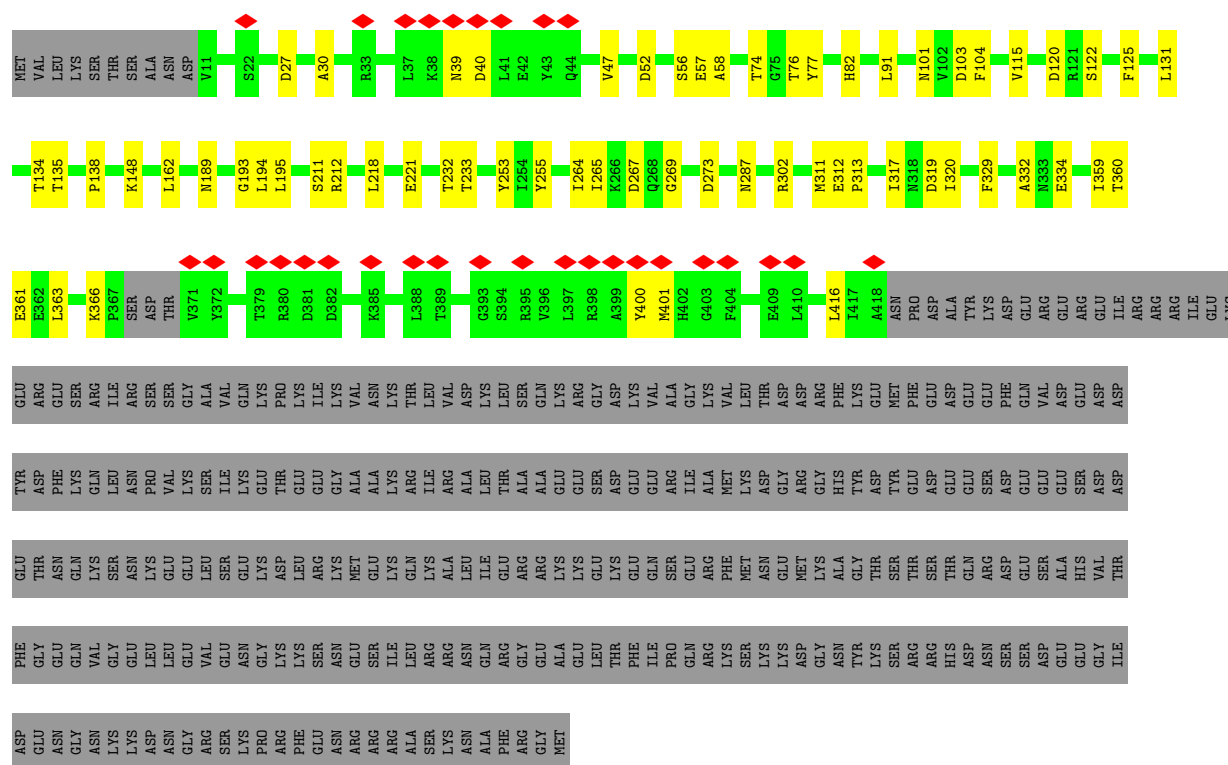
• Molecule 26: U3 small nucleolar RNA-associated protein 13



- Molecule 29: Protein SOF1



- Molecule 30: Ribosome biogenesis protein ENP2

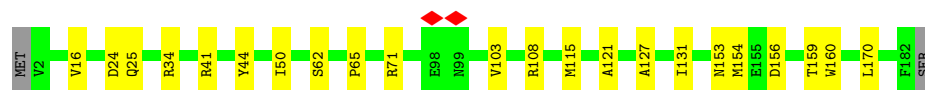


- Molecule 31: U3 small nucleolar RNA-associated protein 7

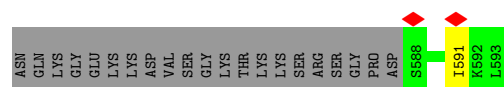
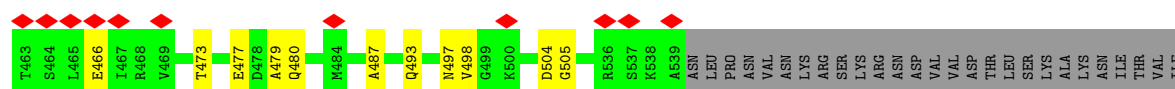
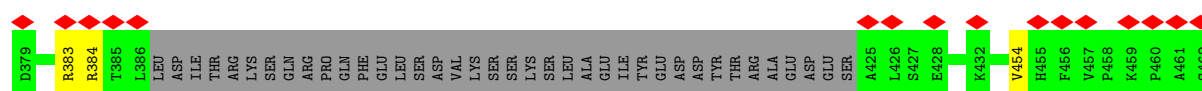
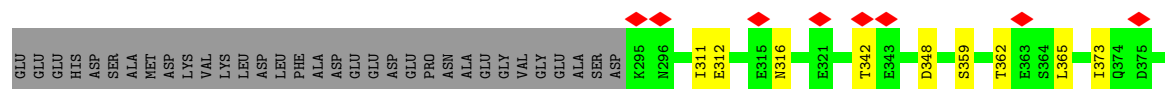
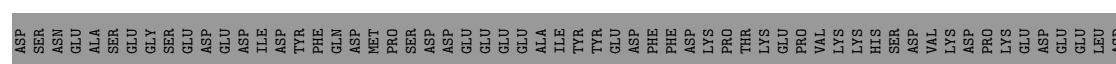
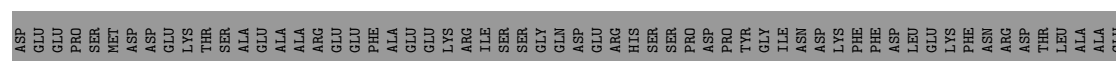
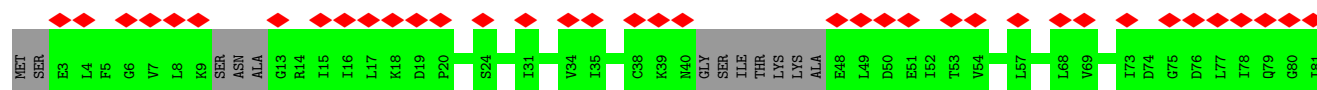


Chain LY:

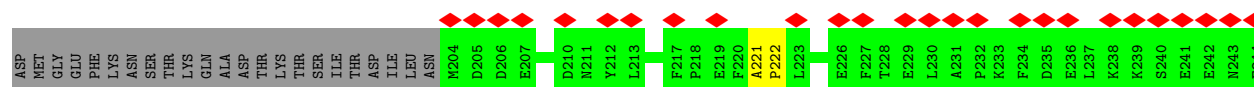
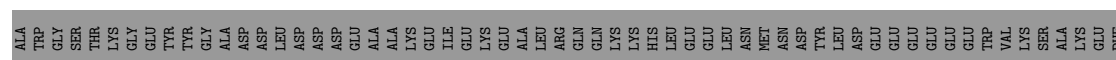
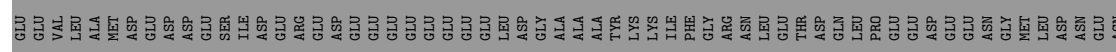
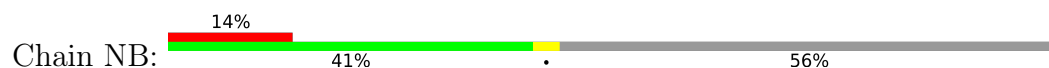




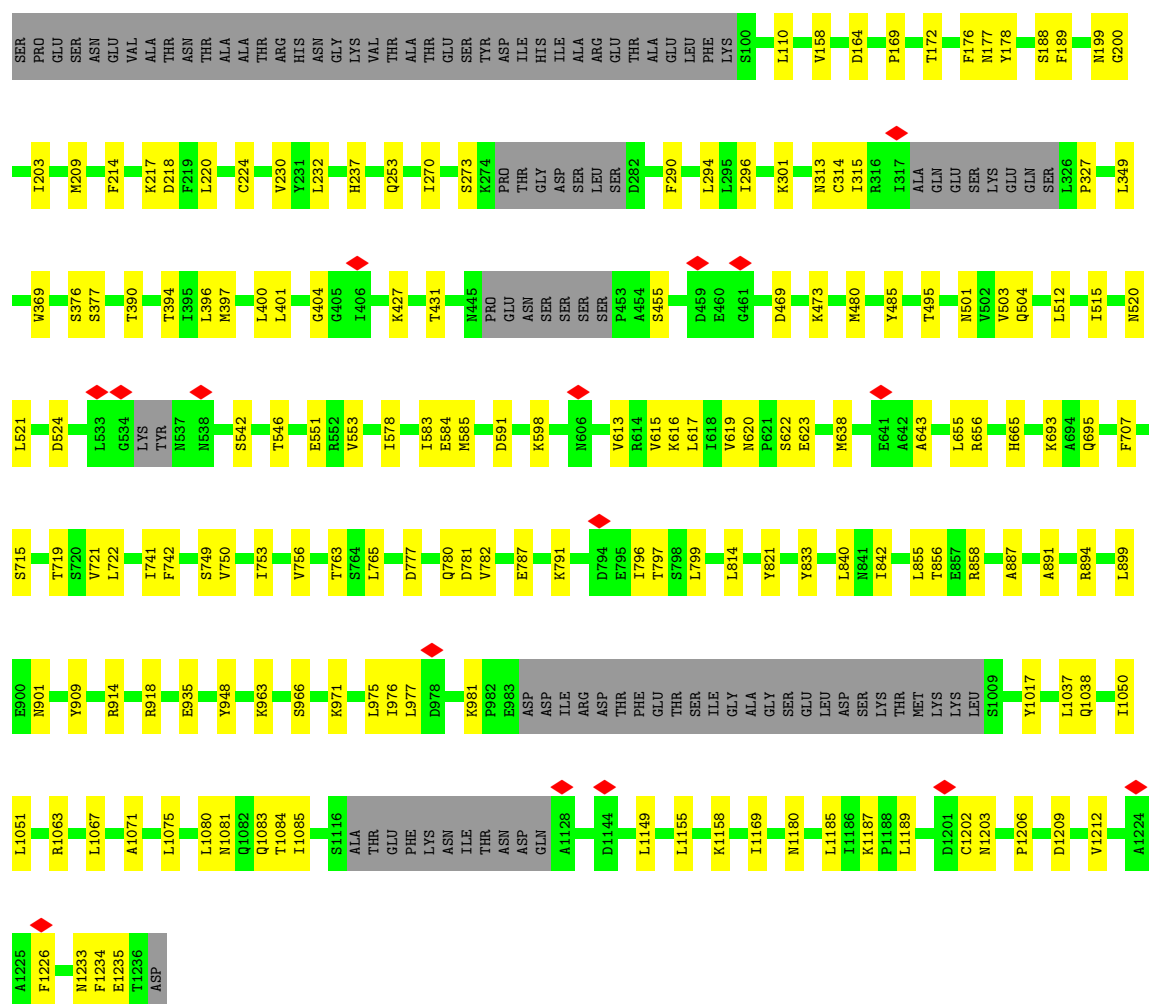
- Molecule 34: U3 small nucleolar RNA-associated protein MPP10



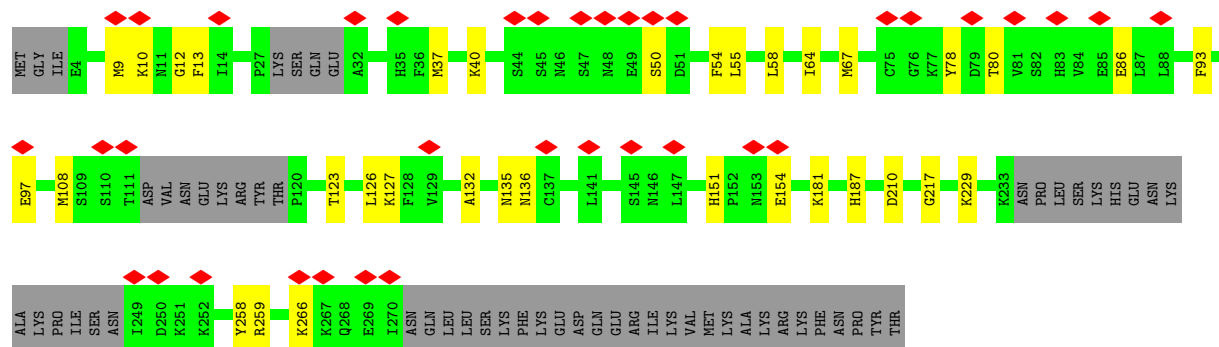
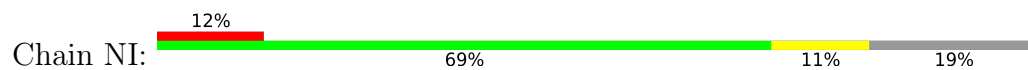
- Molecule 35: Something about silencing protein 10



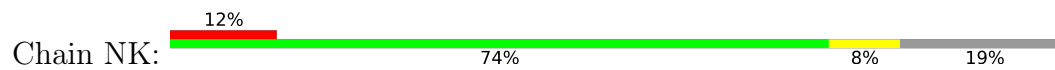




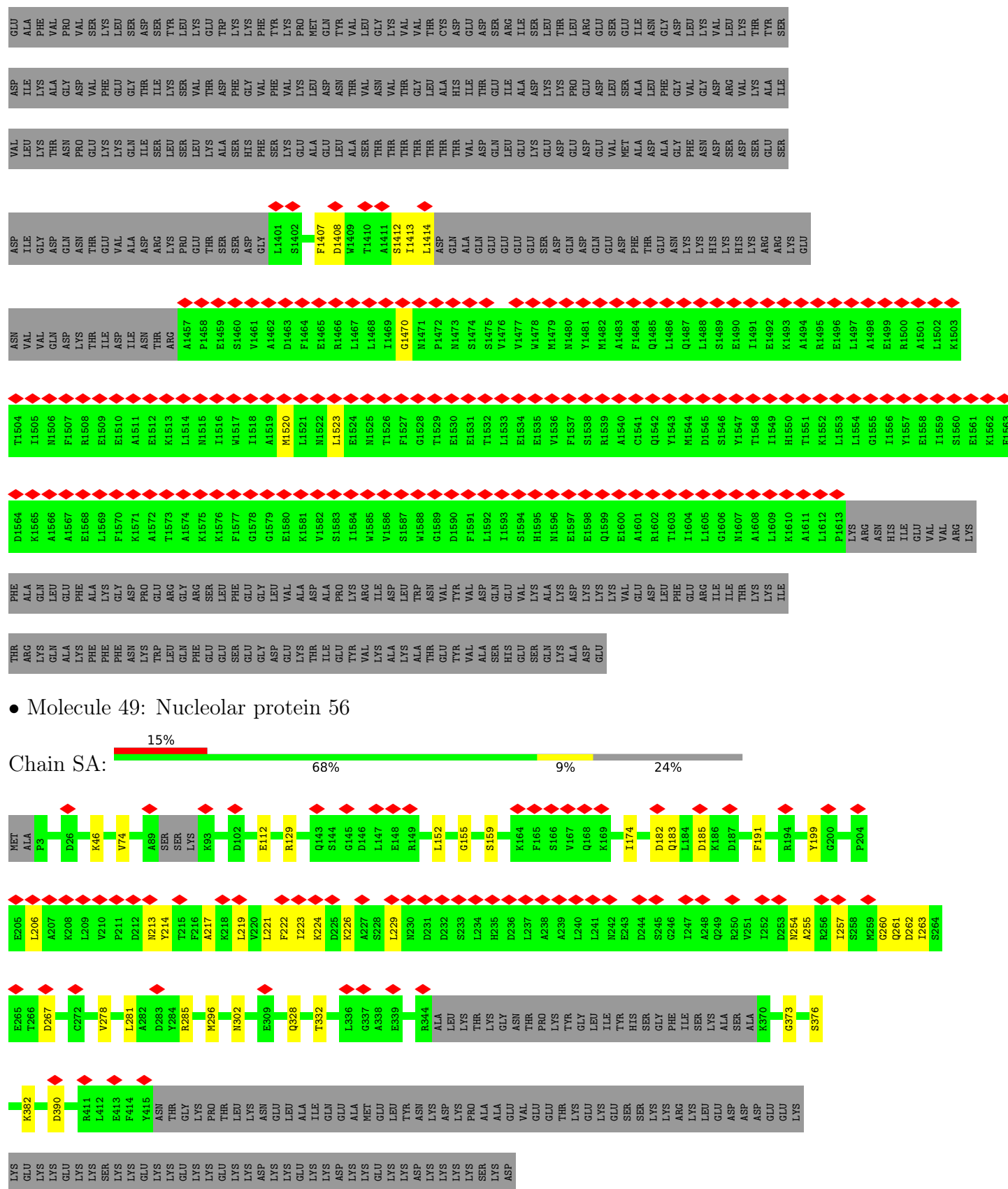
• Molecule 42: Ribosomal RNA-processing protein 7



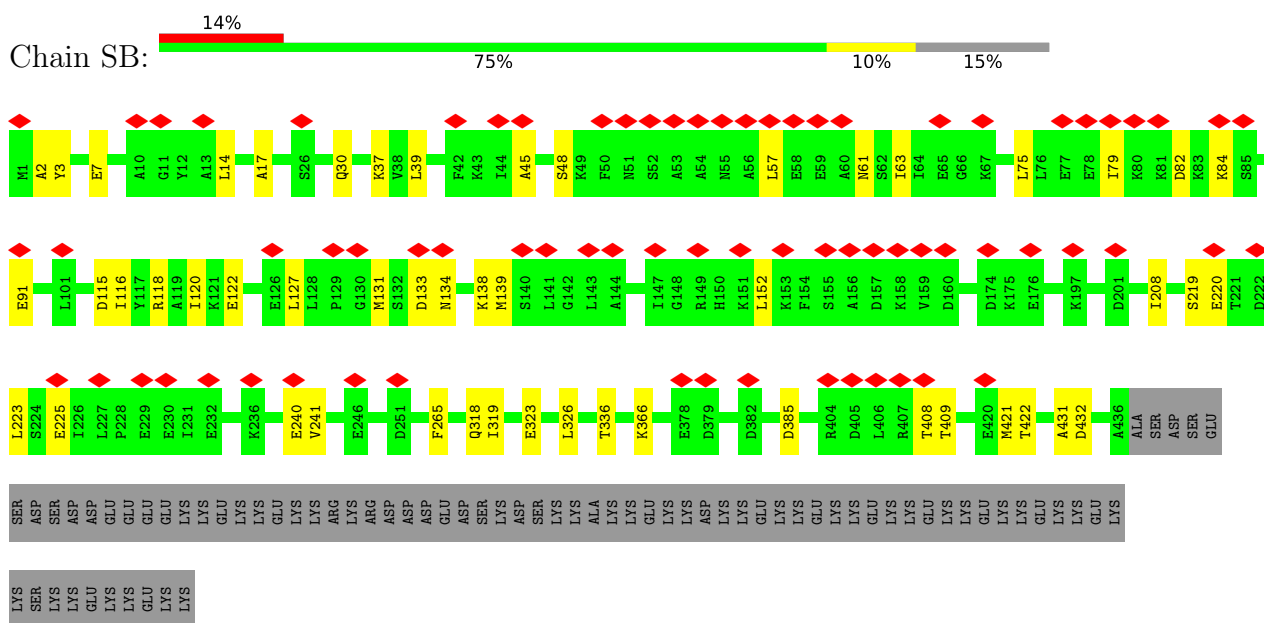
• Molecule 43: KRR1 small subunit processome component



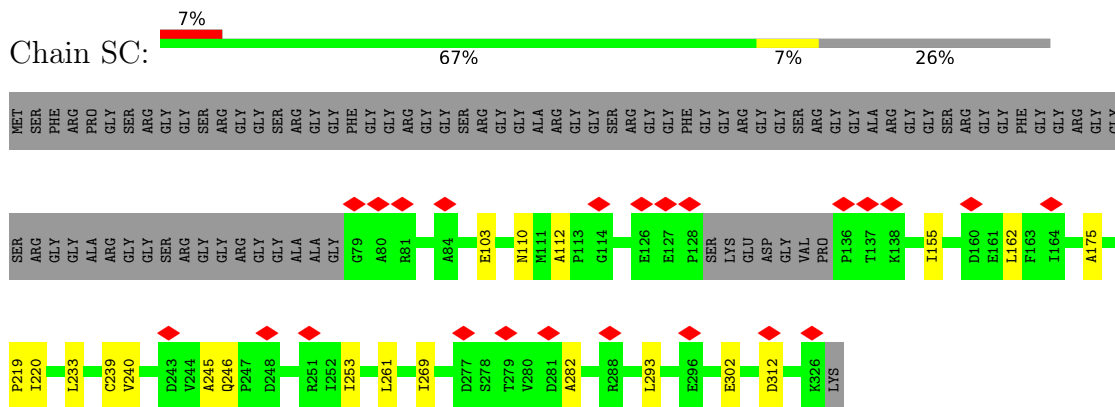
[illegible]



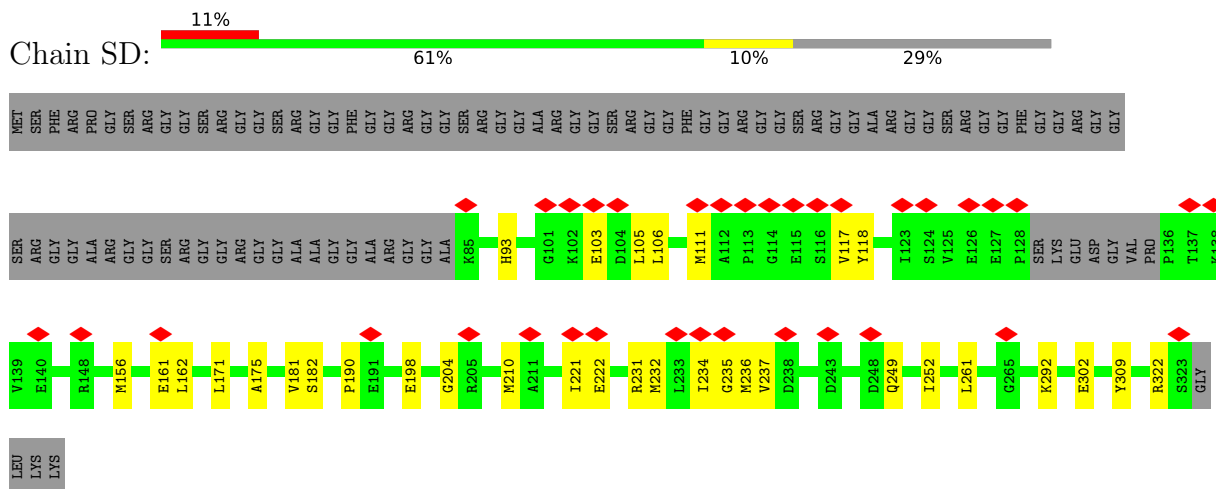
• Molecule 50: Nucleolar protein 58



- Molecule 51: rRNA 2'-O-methyltransferase fibrillar



- Molecule 51: rRNA 2'-O-methyltransferase fibrillar



- Molecule 52: 13 kDa ribonucleoprotein-associated protein

Chain SE:  91% 5%



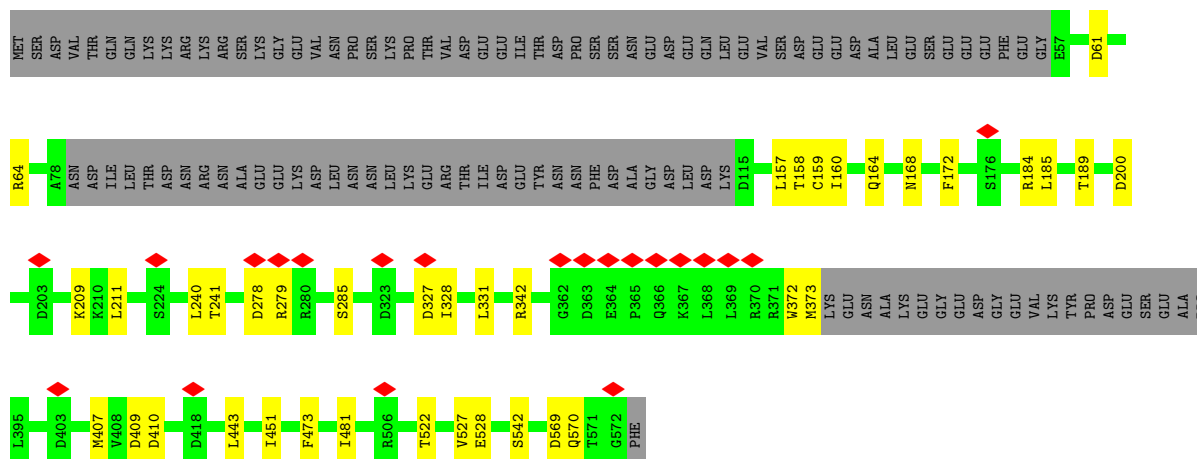
- Molecule 52: 13 kDa ribonucleoprotein-associated protein

Chain SF:  5% 86% 10%



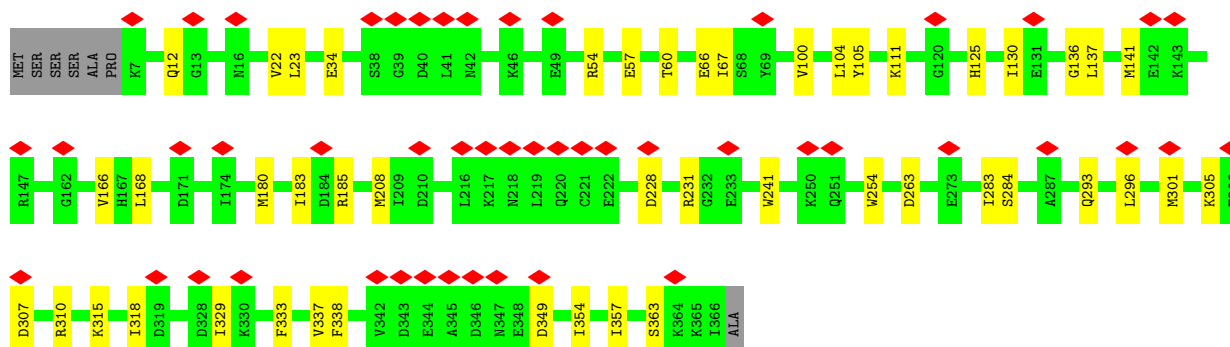
- Molecule 53: Ribosomal RNA-processing protein 9

Chain SG:  73% 7% 20%



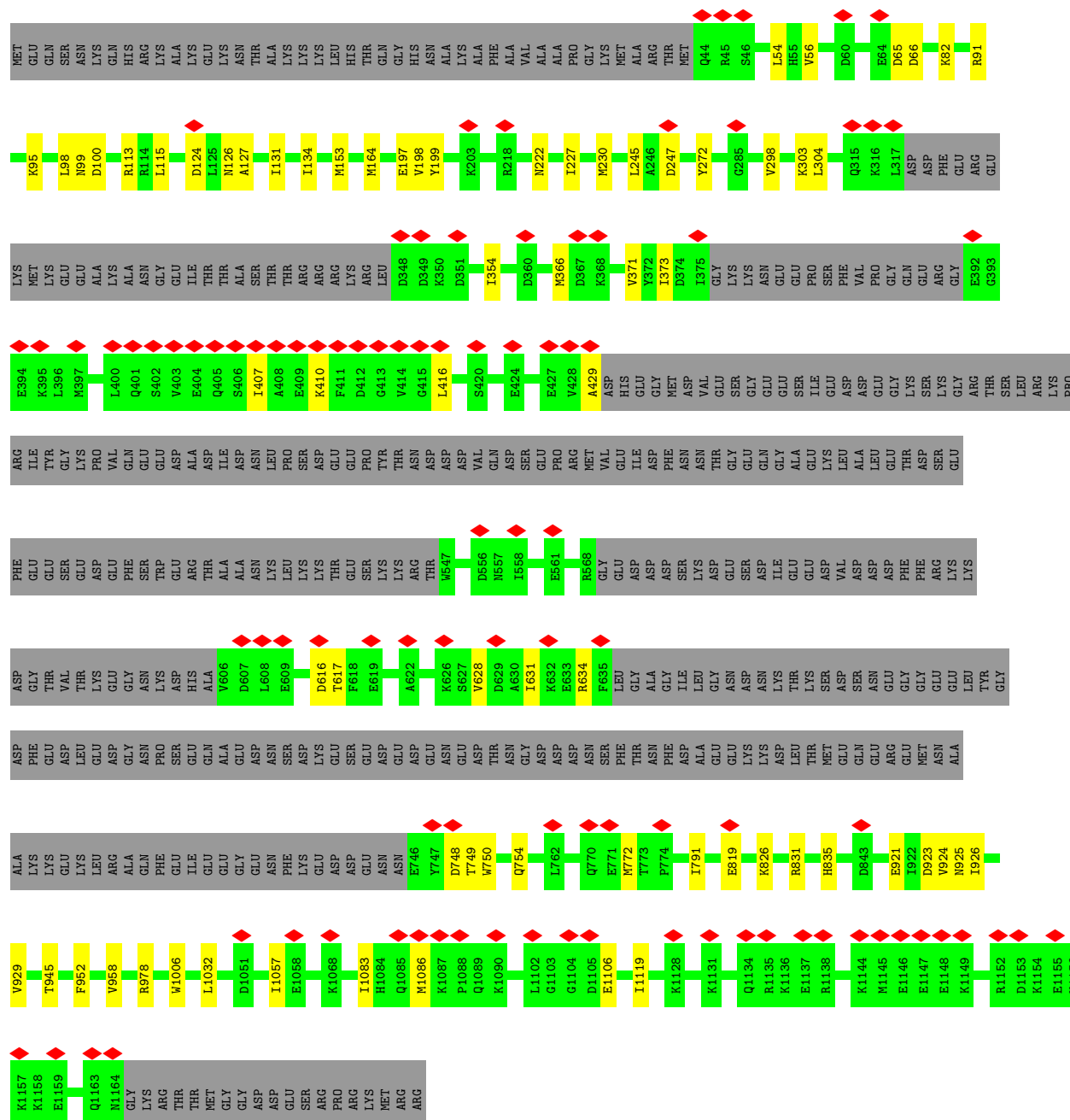
- Molecule 54: RNA 3'-terminal phosphate cyclase-like protein

Chain SH:  13% 85% 13%

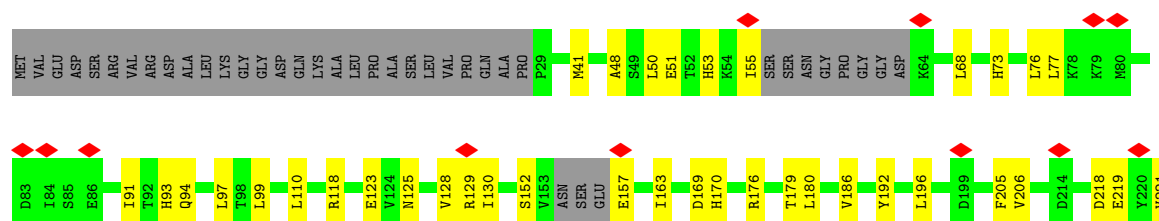


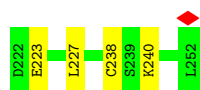
- Molecule 55: Ribosome biogenesis protein BMS1

Chain SI:  8% 63% 6% 31%



• Molecule 56: Ribosomal RNA small subunit methyltransferase NEP1





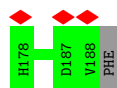
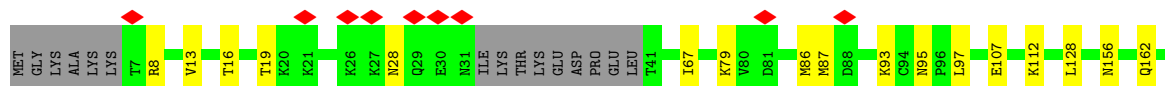
- Molecule 56: Ribosomal RNA small subunit methyltransferase NEP1

Chain SK: 74% 17% 9%



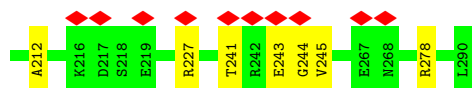
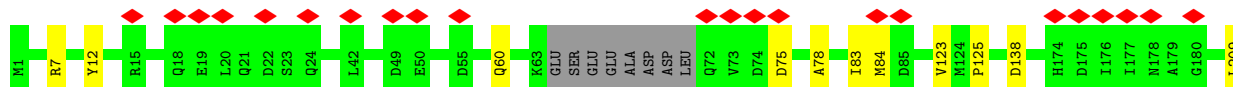
- Molecule 57: rRNA-processing protein FCF1

Chain SL: 6% 83% 9% 8%



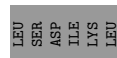
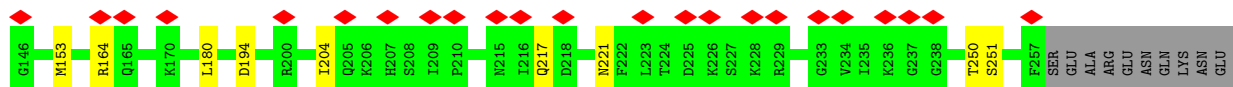
- Molecule 58: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM: 11% 91% 6% 2%

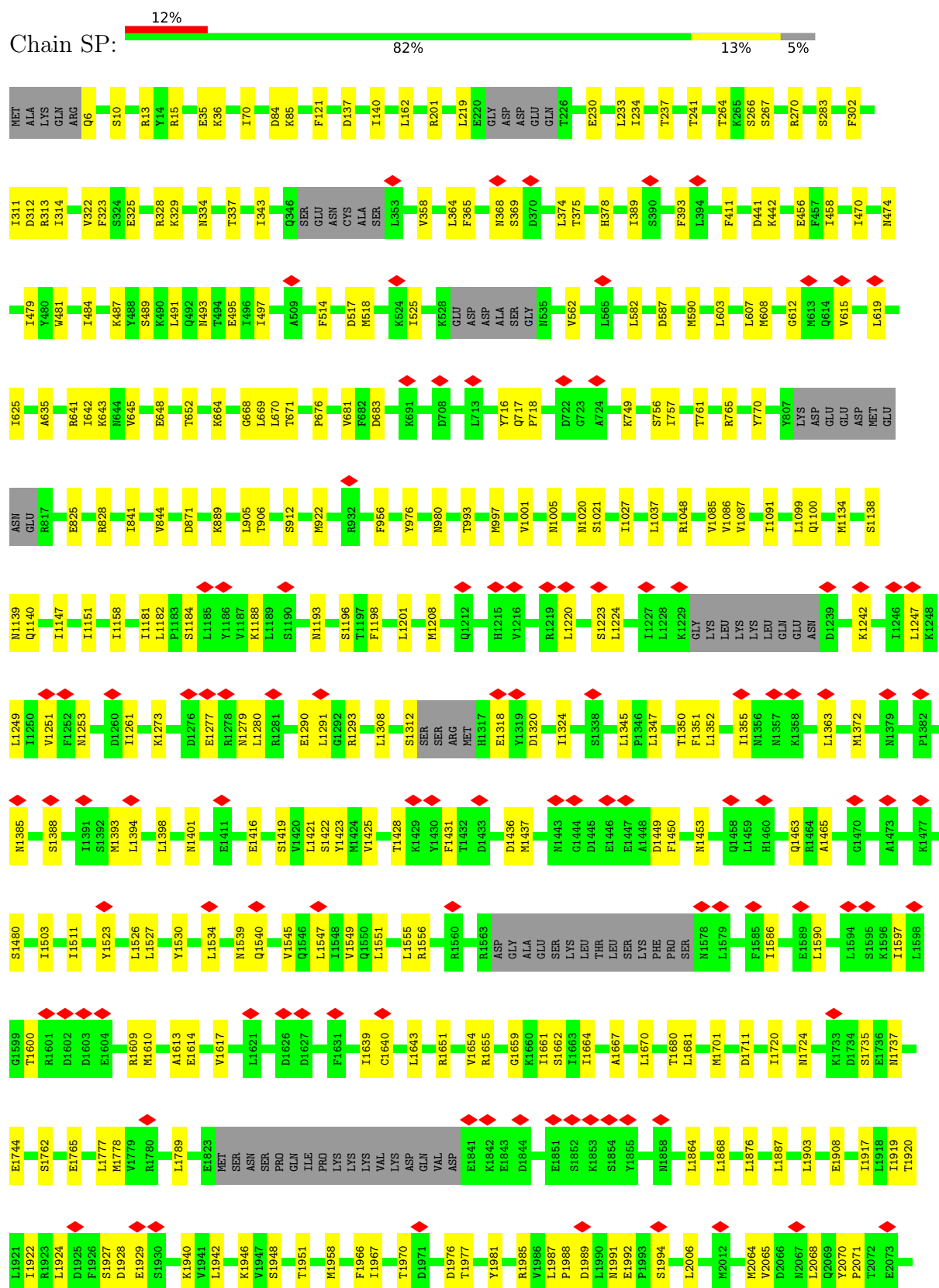


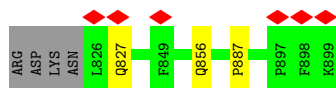
- Molecule 59: Ribosome biogenesis protein UTP30

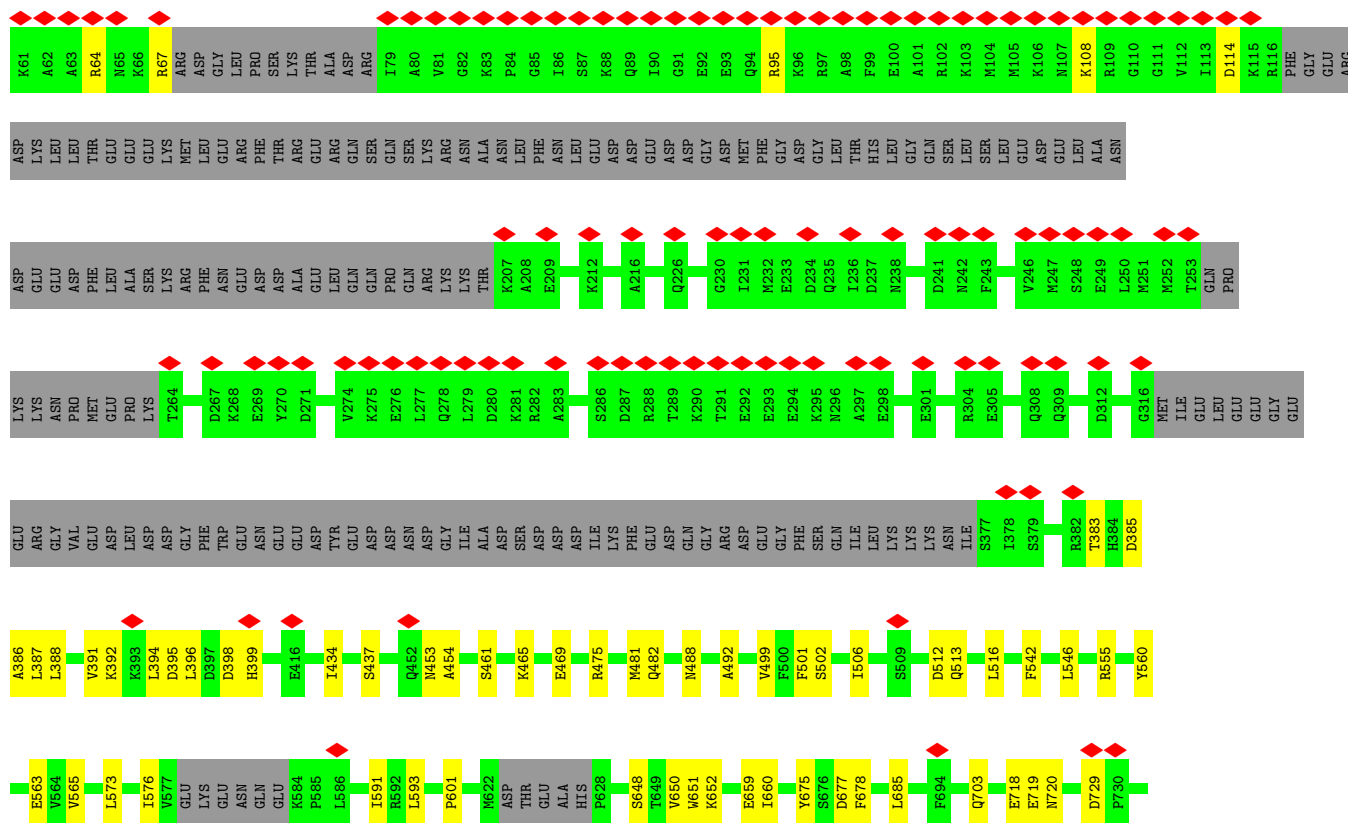
Chain SN: 19% 87% 5% 8%



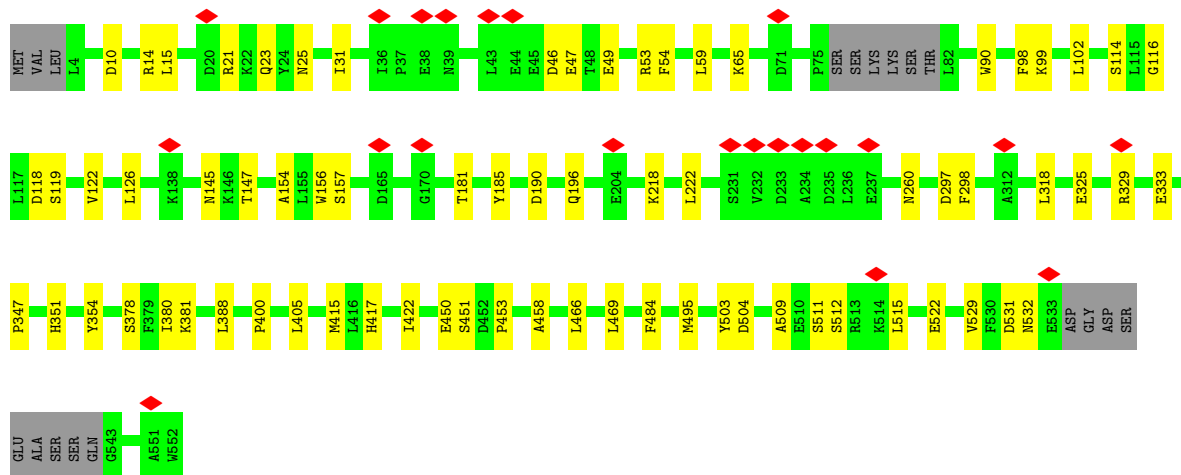
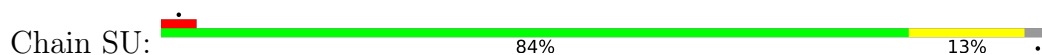
• Molecule 60: U3 small nucleolar RNA-associated protein 20



[illegible]

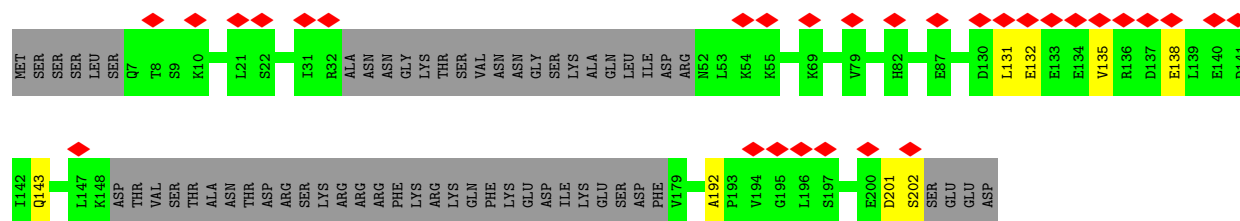


• Molecule 65: Nucleolar complex protein 4

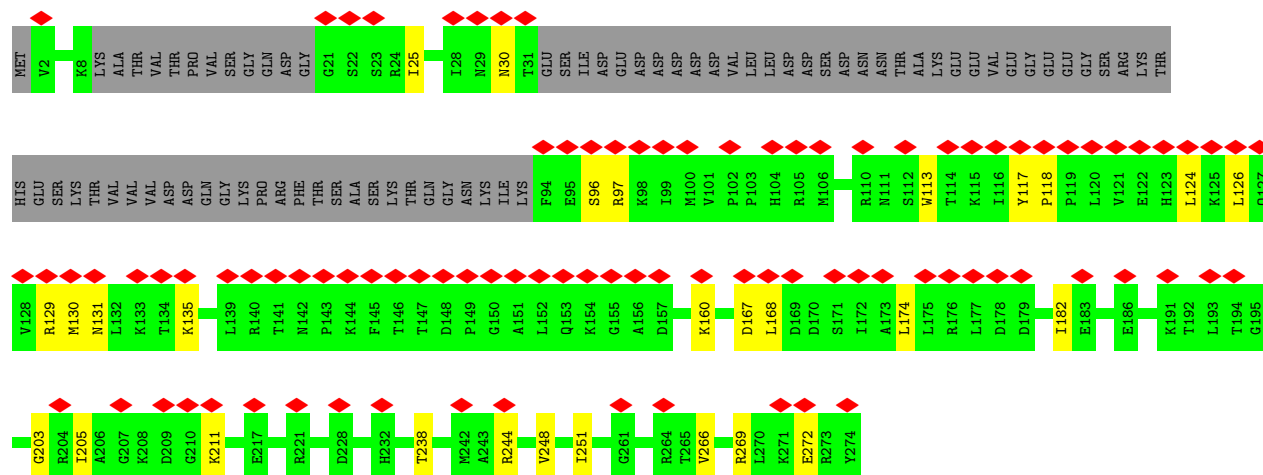


• Molecule 66: Regulator of rDNA transcription protein 14

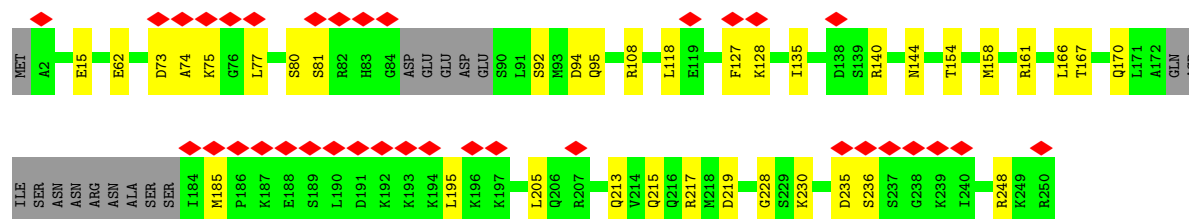
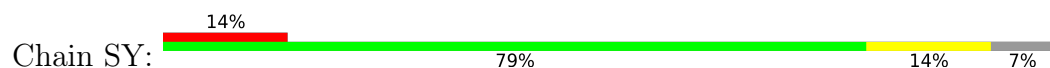




• Molecule 67: Pre-rRNA-processing protein PNO1



• Molecule 68: U3 small nucleolar RNA-associated protein 11



• Molecule 69: Essential nuclear protein 1



VAL	ASN	GLU	PRO	LEU	ALA	ASN	GLU	GLN	ASN	THR	SER	ARG	GLY	GLY	ASN	ILE	SER	SER	GLY	LEU	LYS	SER	GLY	GLU	GLY	VAL	A205	L206	P207	E208	K209	V210	I211	K212	A213	Y214	S219	I220	L221	K222	T223	G227	K228	L229	P230	K231	L232	F233	T236	W241	D242	Q243	D244	V245	I246	T247	V248	T249																																																
		N250			E253		W254			H257		V258		V259		A262		T263		K264		L265		F266		V267		S268		M269		L270		T271		A272		K273		E274		S275		F278		L279		M280		L281		T282		L283		D289		S294		E295		D296		H297		S298		L299		Y304		R305		A306		K309		S310		L311		Y312		ASP		K313		P314		F317		F321		L322		L325		V326		E327		T328				
		G329		C330		N331		V332		T336		I337		A338		V341		L342		A343		K344				P348		S353		A354		A355		L360		R361		F364		S365		P366		P367		T368		T369		V370		R371		I372		K378		A381		T386		D389		C390		H395		R396		F397		R398		I399		L400		ASP		ASP		GLY		S404		N405		A406		E407		D408		A409		I410		R411		V412						
		L413		P414		V415		W417		H418		K419		A420		F421		L422		T423		F424		A425		K429		N430		D431		I432		T433		Q434		D435		Q436		L440		T443		V444		R445		Q446		R447		G448		D451		I452		G453		P454		E459		L460		L461		A462		G463		A464		S465		R466		GLU		PHE		VAL		ASP		PRO		GLN		GLU		ALA		ASN		ASP		LJU		MET		ILE		ASP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23899	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	4.462	Depositor
Minimum map value	0.000	Depositor
Average map value	0.110	Depositor
Map value standard deviation	0.179	Depositor
Recommended contour level	0.77	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 [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L0	0.12	0/10603	0.25	0/16514
2	L1	0.14	0/28743	0.28	0/44737
3	L2	0.12	0/4143	0.24	0/6440
4	L3	0.17	0/794	0.43	0/1069
5	L4	0.15	0/1977	0.35	0/2664
6	L5	0.15	0/1655	0.33	0/2237
7	L6	0.16	0/1674	0.36	0/2236
8	L7	0.19	0/1369	0.41	0/1846
9	L8	0.16	0/1371	0.37	0/1833
10	L9	0.15	0/1410	0.35	0/1888
11	LC	0.36	1/990 (0.1%)	0.56	3/1335 (0.2%)
12	LD	0.17	0/1138	0.38	0/1533
13	LE	0.17	0/1039	0.37	0/1395
14	LF	0.16	0/1060	0.35	0/1412
15	LG	0.13	0/492	0.31	0/659
16	LH	0.17	0/6592	0.39	0/8924
17	LI	0.14	0/3835	0.35	0/5263
18	LJ	0.16	0/3993	0.34	0/5413
19	LK	0.15	0/1085	0.32	0/1463
20	LL	0.13	0/4052	0.30	0/5501
21	LM	0.13	0/9462	0.32	1/13078 (0.0%)
22	LN	0.15	0/5359	0.31	0/7255
23	LO	0.16	0/6773	0.32	0/9164
24	LP	0.13	0/3288	0.29	0/4419
25	LQ	0.16	1/6837 (0.0%)	0.32	0/9227
26	LR	0.13	0/6313	0.31	0/8551
27	LS	0.16	0/3866	0.30	1/5239 (0.0%)
28	LT	0.15	0/7015	0.32	0/9479
29	LU	0.16	0/3835	0.32	0/5162
30	LV	0.18	0/3360	0.37	0/4549
31	LW	0.15	0/4321	0.32	0/5832
32	LX	0.15	0/6852	0.34	0/9258

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LY	0.14	0/6292	0.33	0/8556
33	LZ	0.14	0/1553	0.31	0/2089
34	NA	0.14	0/2090	0.34	0/2817
35	NB	0.13	0/1891	0.32	0/2541
36	NC	0.14	0/783	0.35	0/1056
37	ND	0.13	0/613	0.33	0/811
38	NE	0.12	0/1662	0.32	0/2212
39	NF	0.13	0/1158	0.32	0/1559
40	NG	0.15	0/886	0.33	0/1194
41	NH	0.15	0/8899	0.32	0/12035
42	NI	0.17	0/1994	0.37	0/2684
43	NK	0.14	0/2144	0.34	0/2880
44	NM	0.14	0/1862	0.31	0/2494
45	NN	0.11	0/1953	0.29	0/2646
46	NQ	0.15	0/605	0.33	0/817
47	NV	0.22	0/64	0.39	0/81
48	OA	0.10	0/892	0.27	0/1241
49	SA	0.12	0/3082	0.28	0/4151
50	SB	0.15	0/3396	0.33	0/4576
51	SC	0.15	0/1906	0.31	0/2570
51	SD	0.18	0/1852	0.37	0/2500
52	SE	0.15	0/928	0.31	0/1262
52	SF	0.14	0/928	0.34	0/1262
53	SG	0.14	0/3744	0.31	0/5040
54	SH	0.15	0/2832	0.36	0/3825
55	SI	0.15	0/6719	0.33	0/9043
56	SJ	0.15	0/1703	0.35	0/2295
56	SK	0.16	0/1822	0.37	0/2462
57	SL	0.15	0/1406	0.33	0/1890
58	SM	0.15	0/2337	0.33	0/3148
59	SN	0.14	0/2088	0.34	0/2808
60	SP	0.13	0/18707	0.31	0/25354
61	SQ	0.14	0/1302	0.31	0/1728
62	SR	0.16	0/804	0.34	0/1074
63	SS	0.16	0/2307	0.43	2/3091 (0.1%)
64	ST	0.14	0/4513	0.31	0/6075
65	SU	0.14	0/4480	0.31	0/6073
66	SV	0.15	0/875	0.36	0/1206
67	SW	0.15	0/1591	0.34	0/2143
68	SY	0.14	0/1978	0.36	0/2616
69	SZ	0.13	0/1326	0.33	0/1859
All	All	0.15	2/253263 (0.0%)	0.32	7/351339 (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
27	LS	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	LC	126	PRO	CG-CD	-8.60	1.21	1.50
25	LQ	255	ARG	C-N	6.61	1.36	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	LC	126	PRO	N-CD-CG	-10.40	87.60	103.20
11	LC	126	PRO	CA-N-CD	-9.81	98.26	112.00
21	LM	1021	PRO	CA-N-CD	-9.05	99.33	112.00
11	LC	126	PRO	CA-CB-CG	-5.87	93.35	104.50
63	SS	313	PHE	CA-C-N	-5.45	113.03	119.84

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
27	LS	535	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	9483	0	4770	32	0
2	L1	25709	0	12967	140	0
3	L2	3712	0	1882	18	0
4	L3	786	0	823	24	0
5	L4	1936	0	2019	23	0
6	L5	1635	0	1697	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	L6	1653	0	1750	26	0
8	L7	1347	0	1406	32	0
9	L8	1348	0	1366	25	0
10	L9	1388	0	1467	11	0
11	LC	973	0	1029	12	0
12	LD	1112	0	1179	16	0
13	LE	1022	0	1060	18	0
14	LF	1046	0	1114	9	0
15	LG	490	0	529	4	0
16	LH	6465	0	6415	97	0
17	LI	3792	0	2859	33	0
18	LJ	3911	0	3906	46	0
19	LK	1068	0	1120	14	0
20	LL	3982	0	3983	58	0
21	LM	9380	0	6279	49	0
22	LN	5263	0	5270	53	0
23	LO	6639	0	6524	64	0
24	LP	3220	0	3272	30	0
25	LQ	6707	0	6738	80	0
26	LR	6207	0	6247	62	0
27	LS	3793	0	3770	37	0
28	LT	6876	0	6853	60	0
29	LU	3756	0	3708	47	0
30	LV	3286	0	3208	44	0
31	LW	4237	0	4239	38	0
32	LX	6720	0	6840	86	0
32	LY	6179	0	5745	58	0
33	LZ	1524	0	1567	18	0
34	NA	2075	0	1915	22	0
35	NB	1873	0	1638	15	0
36	NC	777	0	684	12	0
37	ND	609	0	671	11	0
38	NE	1649	0	1669	27	0
39	NF	1135	0	1197	8	0
40	NG	875	0	905	11	0
41	NH	8693	0	8806	100	0
42	NI	1953	0	1933	27	0
43	NK	2107	0	2184	18	0
44	NM	1838	0	1933	22	0
45	NN	1930	0	1738	15	0
46	NQ	595	0	609	5	0
47	NV	64	0	72	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	OA	888	0	484	6	0
49	SA	3035	0	3059	31	0
50	SB	3357	0	3471	47	0
51	SC	1871	0	1916	18	0
51	SD	1817	0	1857	24	0
52	SE	916	0	964	4	0
52	SF	916	0	964	10	0
53	SG	3672	0	3690	24	0
54	SH	2781	0	2878	35	0
55	SI	6577	0	6743	64	0
56	SJ	1678	0	1756	30	0
56	SK	1793	0	1874	31	0
57	SL	1384	0	1465	14	0
58	SM	2296	0	2325	14	0
59	SN	2053	0	2168	11	0
60	SP	18367	0	17934	211	0
61	SQ	1280	0	1331	22	0
62	SR	792	0	847	10	0
63	SS	2267	0	2300	47	0
64	ST	4448	0	4337	53	0
65	SU	4370	0	4365	55	0
66	SV	869	0	554	7	0
67	SW	1565	0	1647	20	0
68	SY	1953	0	2050	29	0
69	SZ	1314	0	649	1	0
70	L0	3	0	0	0	0
70	L1	26	0	0	0	0
70	L2	2	0	0	0	0
70	NH	1	0	0	0	0
70	SI	1	0	0	0	0
70	SM	1	0	0	0	0
71	NH	31	0	12	1	0
72	NQ	1	0	0	0	0
72	SL	1	0	0	0	0
73	SI	32	0	12	1	0
All	All	245176	0	221207	2066	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 4.

The worst 5 of 2066 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)
31:LW:433:LEU:HD21	33:LZ:16:VAL:HG21	1.38	1.04
8:L7:67:LEU:HD22	8:L7:94:ALA:HB2	1.39	1.01
2:L1:384:G:O2'	9:L8:22:ARG:NH2	2.01	0.93
36:NC:68:MET:HE1	45:NN:190:ILE:HD13	1.52	0.91
60:SP:2065:VAL:HG21	63:SS:262:LEU:HD13	1.50	0.91

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%)	89 (98%)	2 (2%)	0	100	100
5	L4	242/261 (93%)	240 (99%)	2 (1%)	0	100	100
6	L5	202/225 (90%)	200 (99%)	2 (1%)	0	100	100
7	L6	202/236 (86%)	201 (100%)	1 (0%)	0	100	100
8	L7	165/190 (87%)	161 (98%)	4 (2%)	0	100	100
9	L8	166/200 (83%)	165 (99%)	1 (1%)	0	100	100
10	L9	169/197 (86%)	169 (100%)	0	0	100	100
11	LC	123/143 (86%)	122 (99%)	1 (1%)	0	100	100
12	LD	135/156 (86%)	132 (98%)	3 (2%)	0	100	100
13	LE	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
14	LF	128/135 (95%)	126 (98%)	2 (2%)	0	100	100
15	LG	60/67 (90%)	60 (100%)	0	0	100	100
16	LH	790/896 (88%)	774 (98%)	16 (2%)	0	100	100
17	LI	582/713 (82%)	574 (99%)	8 (1%)	0	100	100
18	LJ	489/513 (95%)	473 (97%)	16 (3%)	0	100	100
19	LK	130/575 (23%)	130 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	LL	496/643 (77%)	486 (98%)	10 (2%)	0	100	100
21	LM	1597/1769 (90%)	1567 (98%)	30 (2%)	0	100	100
22	LN	649/776 (84%)	639 (98%)	10 (2%)	0	100	100
23	LO	829/923 (90%)	819 (99%)	10 (1%)	0	100	100
24	LP	376/440 (86%)	372 (99%)	4 (1%)	0	100	100
25	LQ	831/943 (88%)	813 (98%)	18 (2%)	0	100	100
26	LR	785/817 (96%)	767 (98%)	18 (2%)	0	100	100
27	LS	469/594 (79%)	457 (97%)	12 (3%)	0	100	100
28	LT	865/939 (92%)	844 (98%)	21 (2%)	0	100	100
29	LU	456/489 (93%)	448 (98%)	8 (2%)	0	100	100
30	LV	401/707 (57%)	388 (97%)	13 (3%)	0	100	100
31	LW	531/554 (96%)	522 (98%)	9 (2%)	0	100	100
32	LX	826/1056 (78%)	812 (98%)	14 (2%)	0	100	100
32	LY	834/1056 (79%)	822 (99%)	12 (1%)	0	100	100
33	LZ	179/183 (98%)	178 (99%)	1 (1%)	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	111/357 (31%)	109 (98%)	2 (2%)	0	100	100
37	ND	70/214 (33%)	70 (100%)	0	0	100	100
38	NE	207/346 (60%)	206 (100%)	1 (0%)	0	100	100
39	NF	139/151 (92%)	138 (99%)	1 (1%)	0	100	100
40	NG	117/137 (85%)	114 (97%)	3 (3%)	0	100	100
41	NH	1063/1237 (86%)	1044 (98%)	19 (2%)	0	100	100
42	NI	232/297 (78%)	224 (97%)	8 (3%)	0	100	100
43	NK	253/316 (80%)	251 (99%)	2 (1%)	0	100	100
44	NM	224/255 (88%)	222 (99%)	2 (1%)	0	100	100
45	NN	257/534 (48%)	257 (100%)	0	0	100	100
46	NQ	77/82 (94%)	76 (99%)	1 (1%)	0	100	100
47	NV	6/733 (1%)	6 (100%)	0	0	100	100
48	OA	167/1729 (10%)	166 (99%)	1 (1%)	0	100	100
49	SA	379/504 (75%)	376 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	SB	434/511 (85%)	427 (98%)	7 (2%)	0	100	100
51	SC	237/327 (72%)	233 (98%)	4 (2%)	0	100	100
51	SD	228/327 (70%)	223 (98%)	5 (2%)	0	100	100
52	SE	119/126 (94%)	115 (97%)	4 (3%)	0	100	100
52	SF	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
53	SG	453/573 (79%)	444 (98%)	9 (2%)	0	100	100
54	SH	358/367 (98%)	349 (98%)	9 (2%)	0	100	100
55	SI	799/1183 (68%)	785 (98%)	14 (2%)	0	100	100
56	SJ	207/252 (82%)	206 (100%)	1 (0%)	0	100	100
56	SK	225/252 (89%)	219 (97%)	6 (3%)	0	100	100
57	SL	169/189 (89%)	164 (97%)	5 (3%)	0	100	100
58	SM	278/290 (96%)	276 (99%)	2 (1%)	0	100	100
59	SN	251/274 (92%)	249 (99%)	2 (1%)	0	100	100
60	SP	2334/2493 (94%)	2303 (99%)	31 (1%)	0	100	100
61	SQ	147/217 (68%)	139 (95%)	8 (5%)	0	100	100
62	SR	102/145 (70%)	101 (99%)	1 (1%)	0	100	100
63	SS	262/899 (29%)	255 (97%)	7 (3%)	0	100	100
64	ST	566/810 (70%)	560 (99%)	6 (1%)	0	100	100
65	SU	528/552 (96%)	523 (99%)	5 (1%)	0	100	100
66	SV	141/206 (68%)	140 (99%)	1 (1%)	0	100	100
67	SW	193/274 (70%)	188 (97%)	5 (3%)	0	100	100
68	SY	227/250 (91%)	226 (100%)	1 (0%)	0	100	100
69	SZ	255/483 (53%)	252 (99%)	3 (1%)	0	100	100
All	All	26388/35893 (74%)	25947 (98%)	441 (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	208/222 (94%)	208 (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
9	L8	137/161 (85%)	137 (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	109/113 (96%)	109 (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	751/934 (80%)	751 (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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	NB	149/538 (28%)	149 (100%)	0	100	100
36	NC	59/315 (19%)	59 (100%)	0	100	100
37	ND	70/196 (36%)	70 (100%)	0	100	100
38	NE	166/304 (55%)	166 (100%)	0	100	100
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	175/482 (36%)	175 (100%)	0	100	100
46	NQ	68/71 (96%)	68 (100%)	0	100	100
47	NV	7/671 (1%)	7 (100%)	0	100	100
48	OA	14/1544 (1%)	14 (100%)	0	100	100
49	SA	328/435 (75%)	328 (100%)	0	100	100
50	SB	360/433 (83%)	360 (100%)	0	100	100
51	SC	200/240 (83%)	200 (100%)	0	100	100
51	SD	197/240 (82%)	197 (100%)	0	100	100
52	SE	100/104 (96%)	100 (100%)	0	100	100
52	SF	100/104 (96%)	100 (100%)	0	100	100
53	SG	399/503 (79%)	399 (100%)	0	100	100
54	SH	307/312 (98%)	307 (100%)	0	100	100
55	SI	718/1039 (69%)	718 (100%)	0	100	100
56	SJ	192/222 (86%)	192 (100%)	0	100	100
56	SK	205/222 (92%)	205 (100%)	0	100	100
57	SL	155/169 (92%)	155 (100%)	0	100	100
58	SM	251/258 (97%)	251 (100%)	0	100	100
59	SN	236/256 (92%)	236 (100%)	0	100	100
60	SP	1956/2307 (85%)	1956 (100%)	0	100	100
61	SQ	140/200 (70%)	140 (100%)	0	100	100
62	SR	86/120 (72%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	SS	251/808 (31%)	251 (100%)	0	100	100
64	ST	441/732 (60%)	441 (100%)	0	100	100
65	SU	490/506 (97%)	490 (100%)	0	100	100
66	SV	42/192 (22%)	42 (100%)	0	100	100
67	SW	172/238 (72%)	172 (100%)	0	100	100
68	SY	218/234 (93%)	218 (100%)	0	100	100
69	SZ	14/424 (3%)	14 (100%)	0	100	100
All	All	21401/31991 (67%)	21401 (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 174 such sidechains are listed below:

Mol	Chain	Res	Type
50	SB	334	HIS
59	SN	248	ASN
52	SF	113	GLN
55	SI	761	GLN
60	SP	1483	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	442/700 (63%)	82 (18%)	1 (0%)
2	L1	1180/1808 (65%)	197 (16%)	1 (0%)
3	L2	170/333 (51%)	27 (15%)	0
All	All	1792/2841 (63%)	306 (17%)	2 (0%)

5 of 306 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	7	A
1	L0	61	U
1	L0	62	C
1	L0	63	G
1	L0	64	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L0	381	G
2	L1	248	U

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

2 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	$\# Z > 2$
27	SEP	LS	128	27	8,9,10	1.60	1 (12%)	7,12,14	1.28	1 (14%)
23	SEP	LO	651	23	8,9,10	1.58	1 (12%)	7,12,14	1.35	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
27	SEP	LS	128	27	-	0/6/8/10	-
23	SEP	LO	651	23	-	1/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	LS	128	SEP	P-O1P	3.49	1.61	1.50
23	LO	651	SEP	P-O1P	3.45	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	LO	651	SEP	OG-CB-CA	2.90	110.97	108.14
27	LS	128	SEP	OG-CB-CA	2.71	110.78	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 38 ligands modelled in this entry, 36 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	$\# Z > 2$
73	GTP	SI	2001	70	33,34,34	1.82	4 (12%)	50,54,54	1.47	7 (14%)
71	ATP	NH	1300	70	32,33,33	0.31	0	48,52,52	0.69	0

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
73	GTP	SI	2001	70	-	6/22/38/38	0/3/3/3
71	ATP	NH	1300	70	-	3/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	SI	2001	GTP	C5-N7	6.62	1.52	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	SI	2001	GTP	C8-N9	-4.29	1.27	1.37
73	SI	2001	GTP	C4-N9	-3.86	1.28	1.38
73	SI	2001	GTP	C4-N3	2.27	1.39	1.34

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	SI	2001	GTP	C8-N9-C4	7.19	119.51	106.03
73	SI	2001	GTP	N9-C4-N3	2.71	131.38	125.95
73	SI	2001	GTP	C6-C5-N7	2.52	134.88	130.29
73	SI	2001	GTP	C1'-N9-C8	-2.26	120.32	126.73
73	SI	2001	GTP	C1'-N9-C4	-2.14	120.17	126.49

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

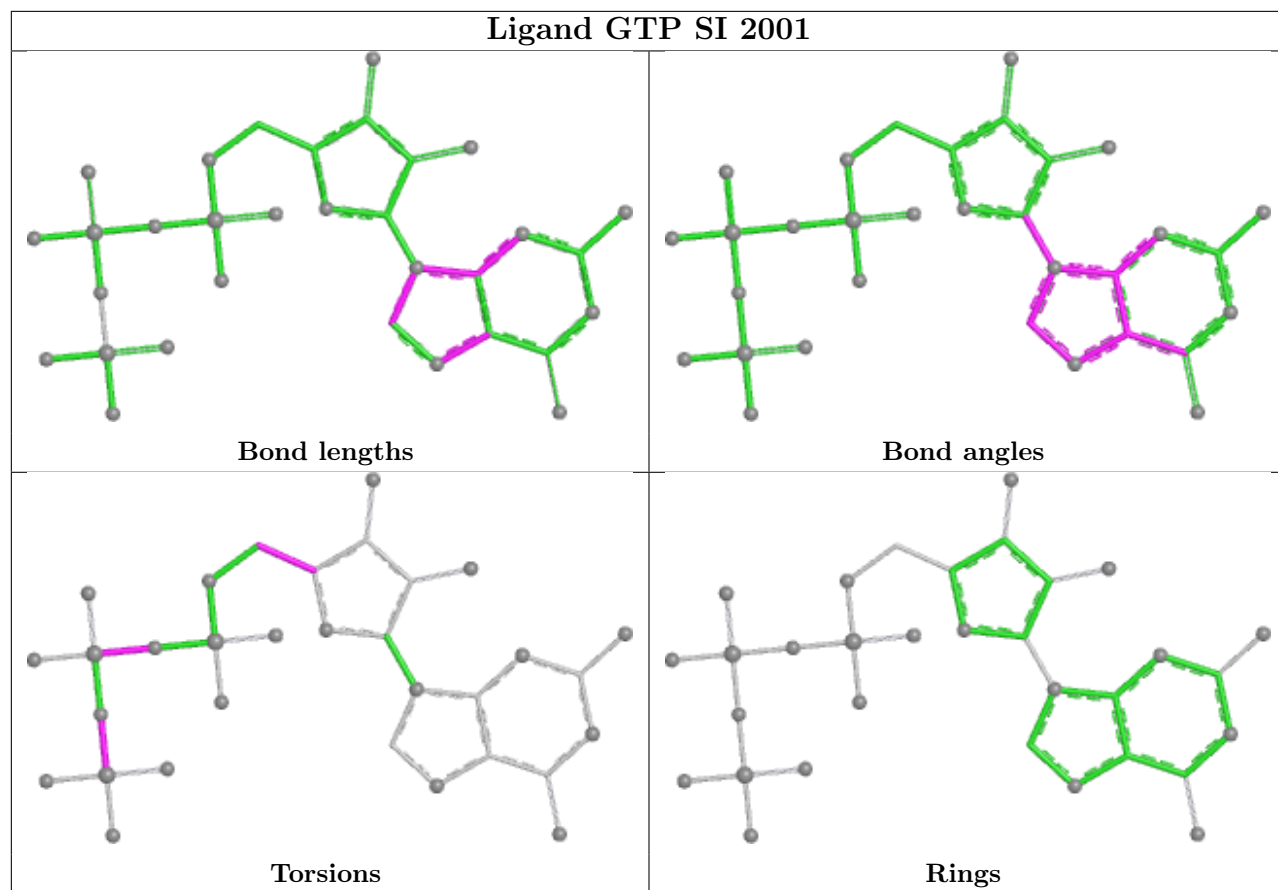
Mol	Chain	Res	Type	Atoms
71	NH	1300	ATP	PB-O3B-PG-O2G
71	NH	1300	ATP	PB-O3B-PG-O3G
73	SI	2001	GTP	PB-O3B-PG-O3G
73	SI	2001	GTP	O4'-C4'-C5'-O5'
73	SI	2001	GTP	C3'-C4'-C5'-O5'

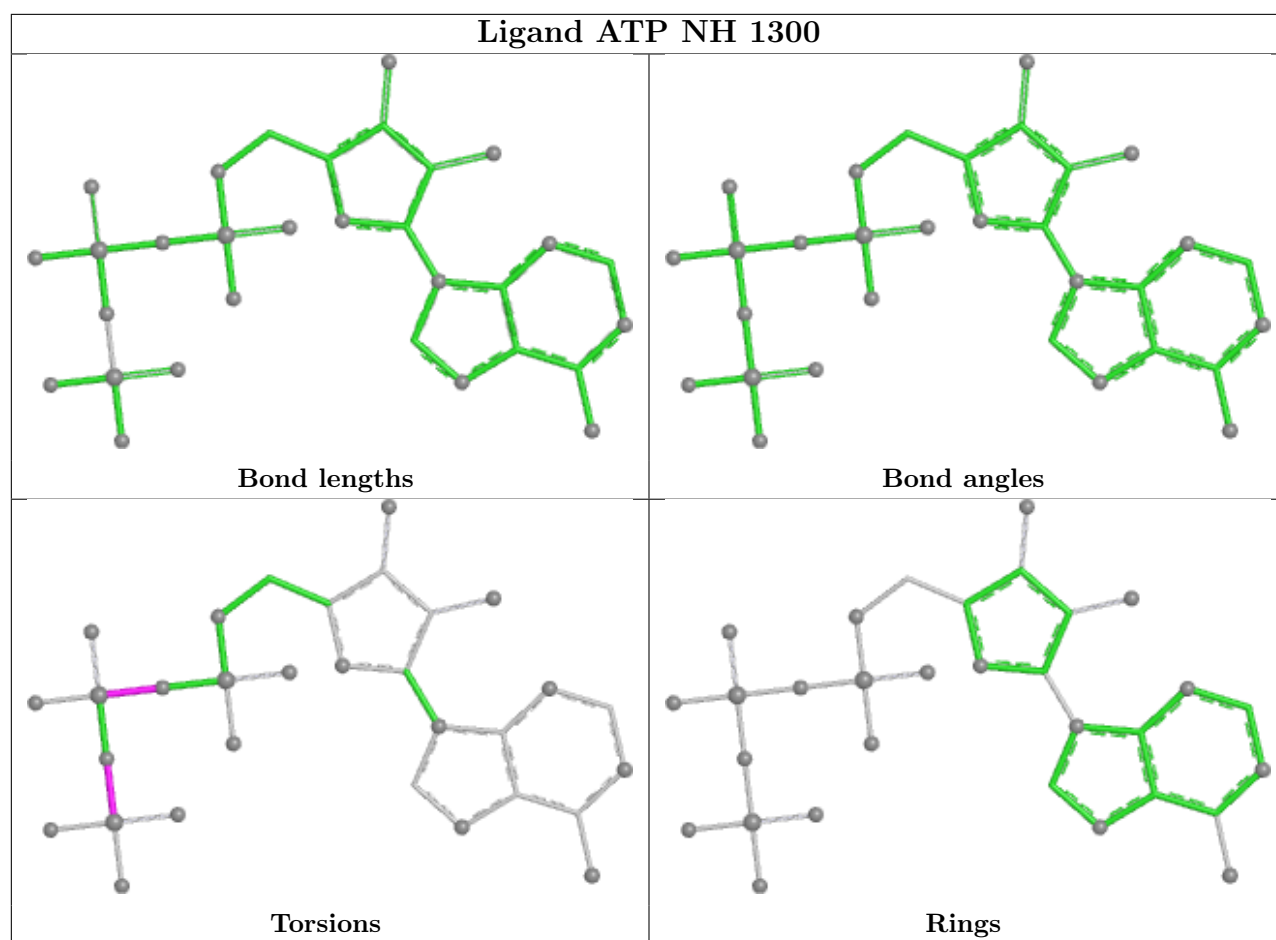
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
73	SI	2001	GTP	1	0
71	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.

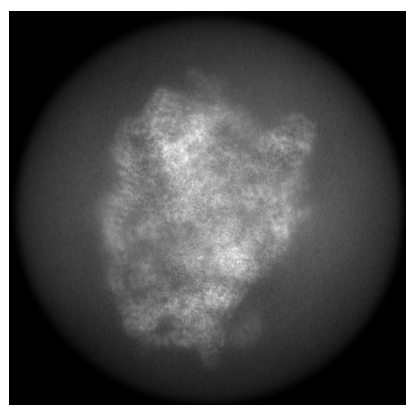
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49078. These allow visual inspection of the internal detail of the map and identification of artifacts.

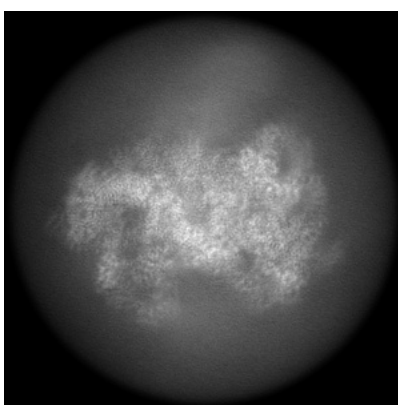
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

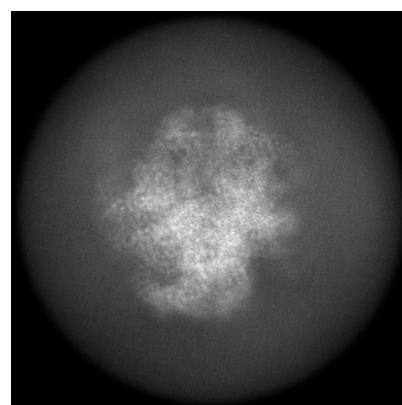
6.1.1 Primary map



X



Y

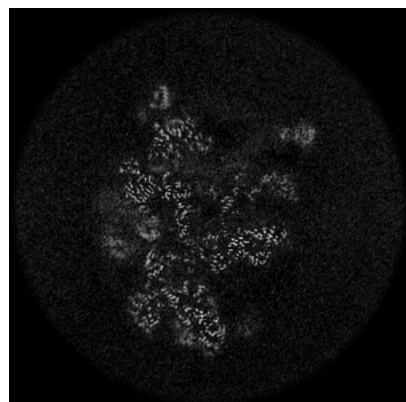


Z

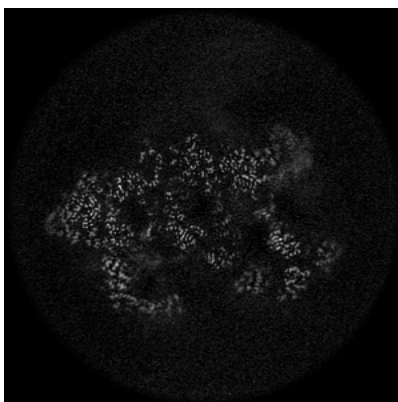
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

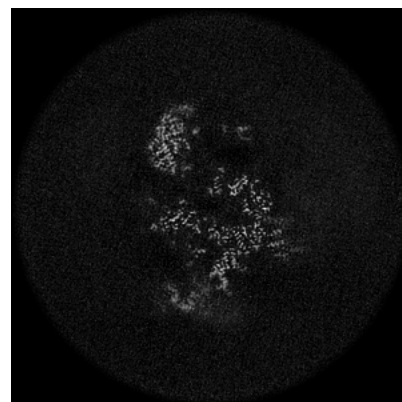
6.2.1 Primary map



X Index: 252



Y Index: 252

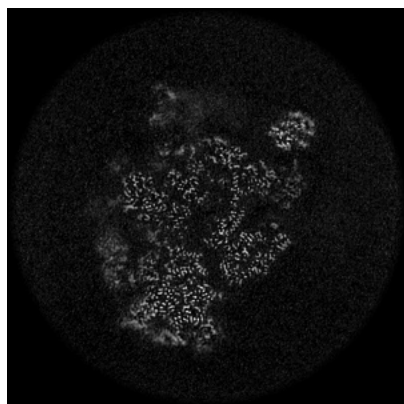


Z Index: 252

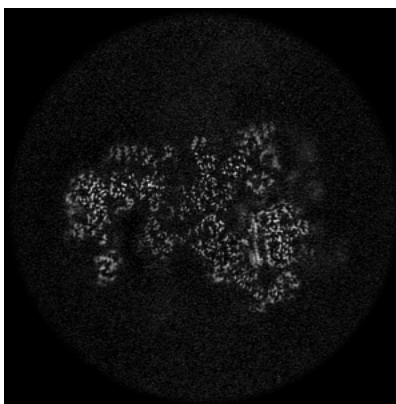
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

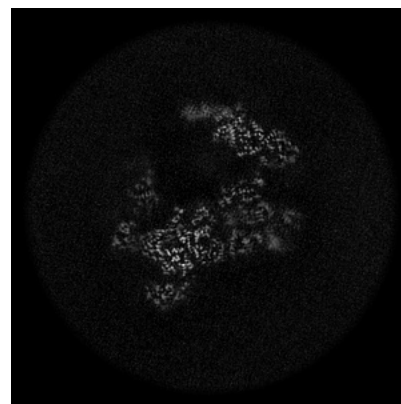
6.3.1 Primary map



X Index: 268



Y Index: 223

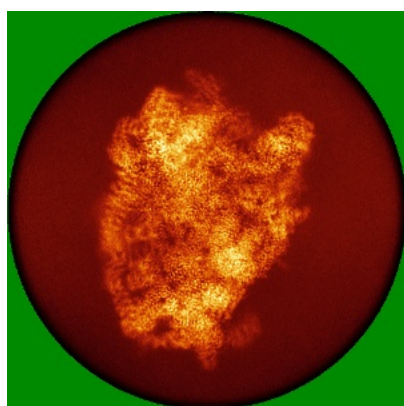


Z Index: 333

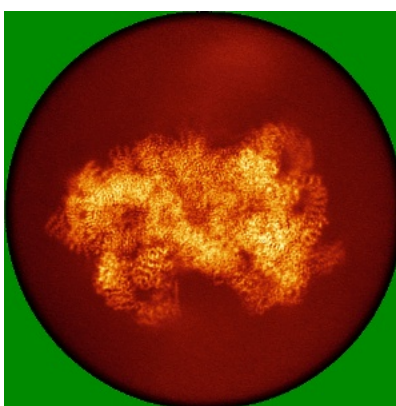
The images above show the largest variance slices of the map in three orthogonal directions.

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

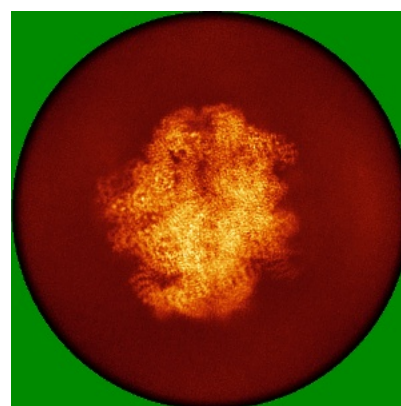
6.4.1 Primary map



X



Y

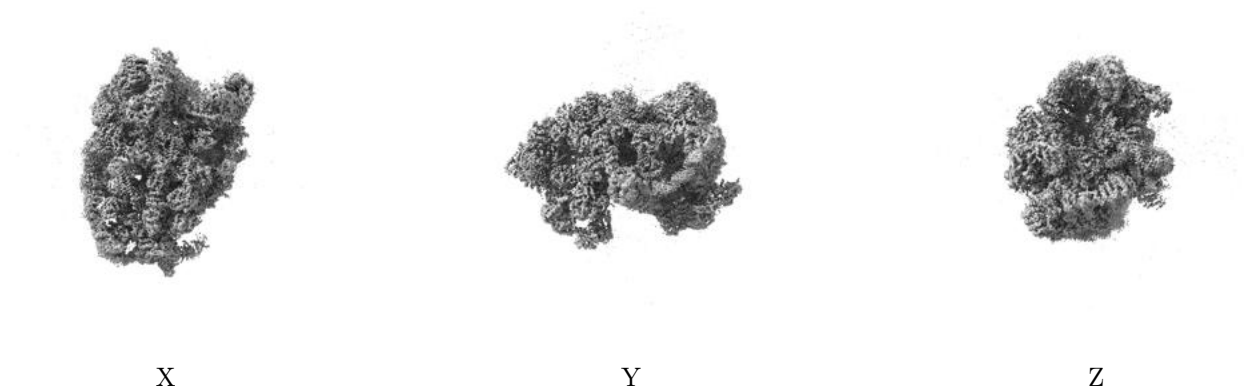


Z

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

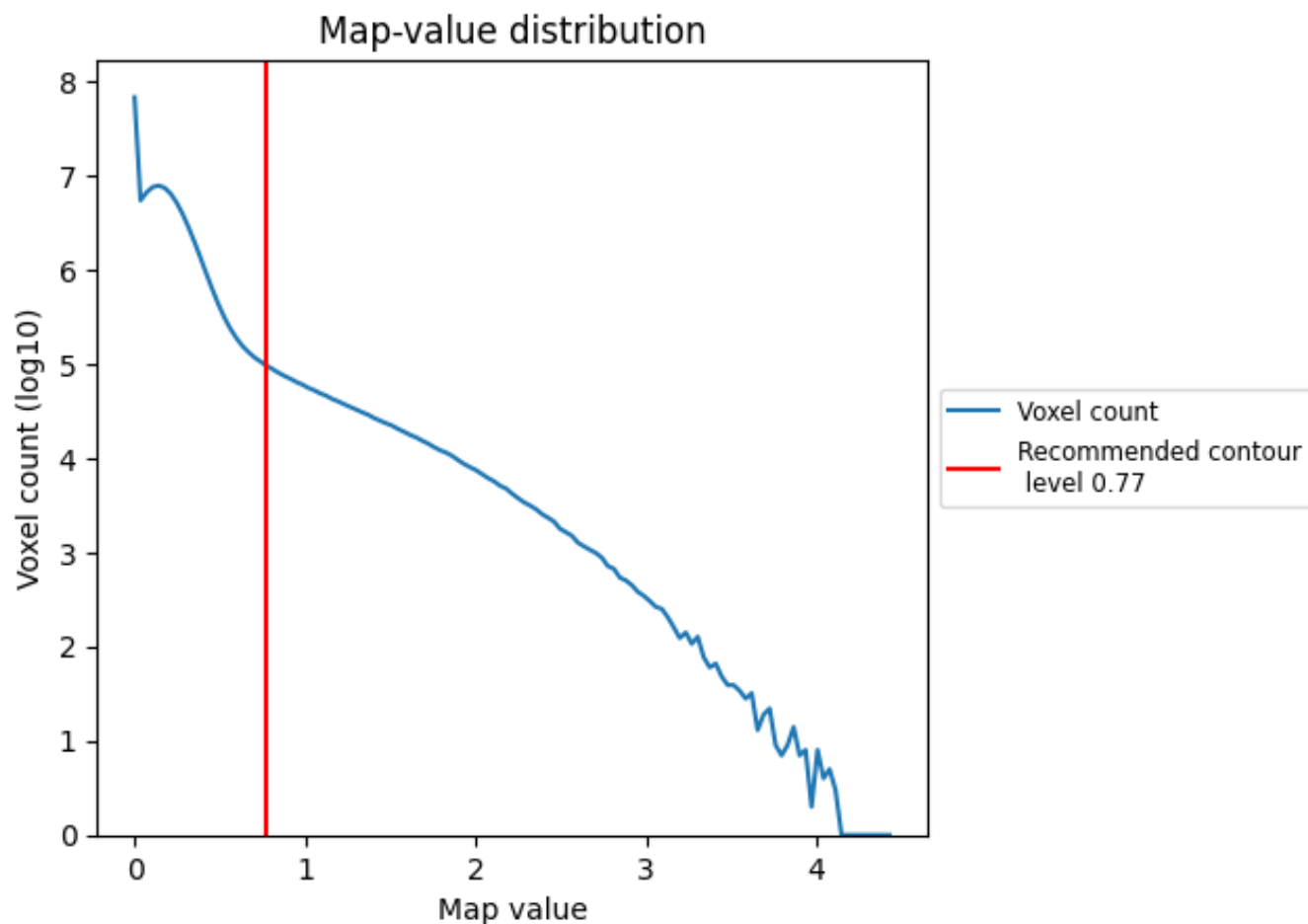
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

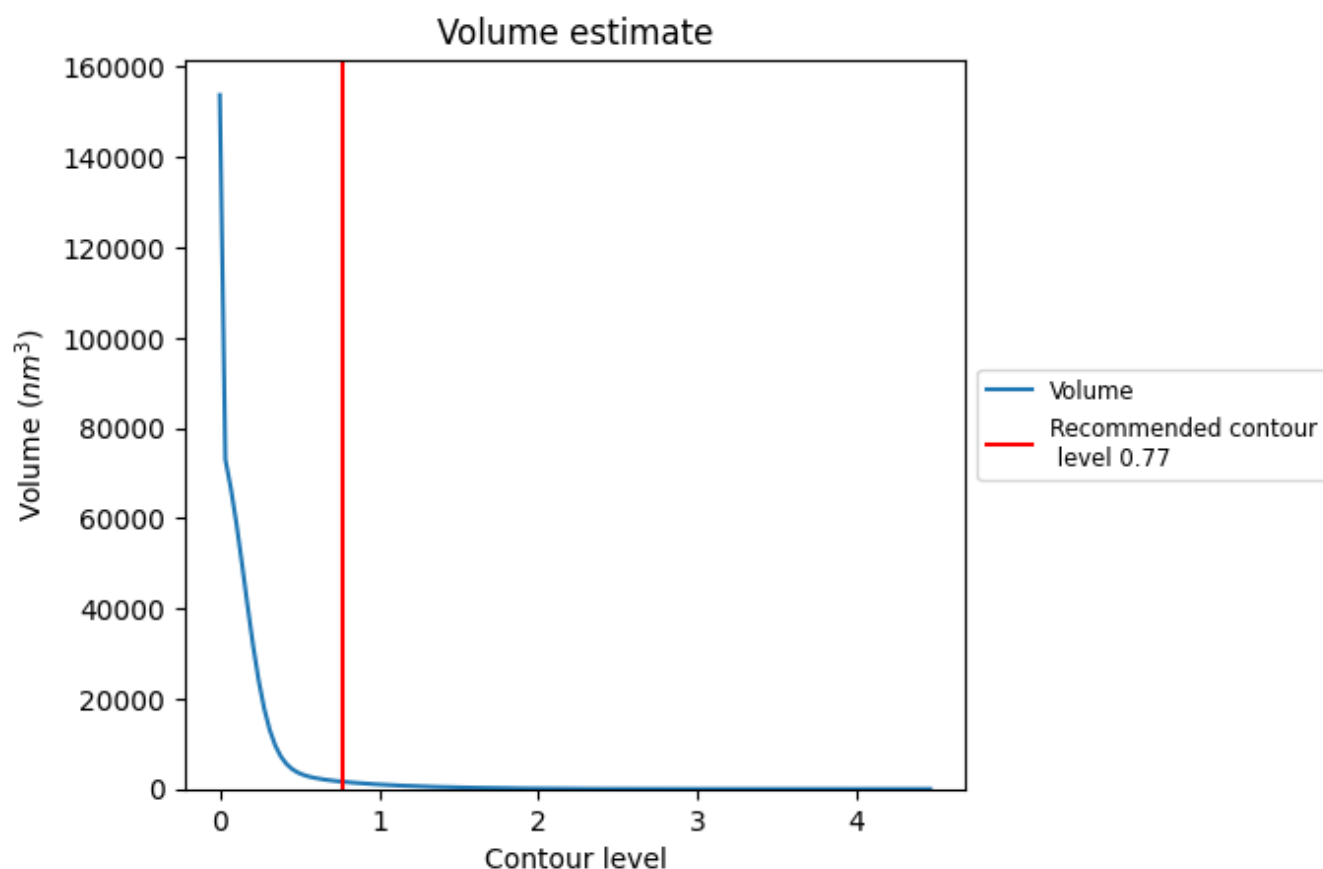
This section contains the results of statistical analysis of the map.

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.

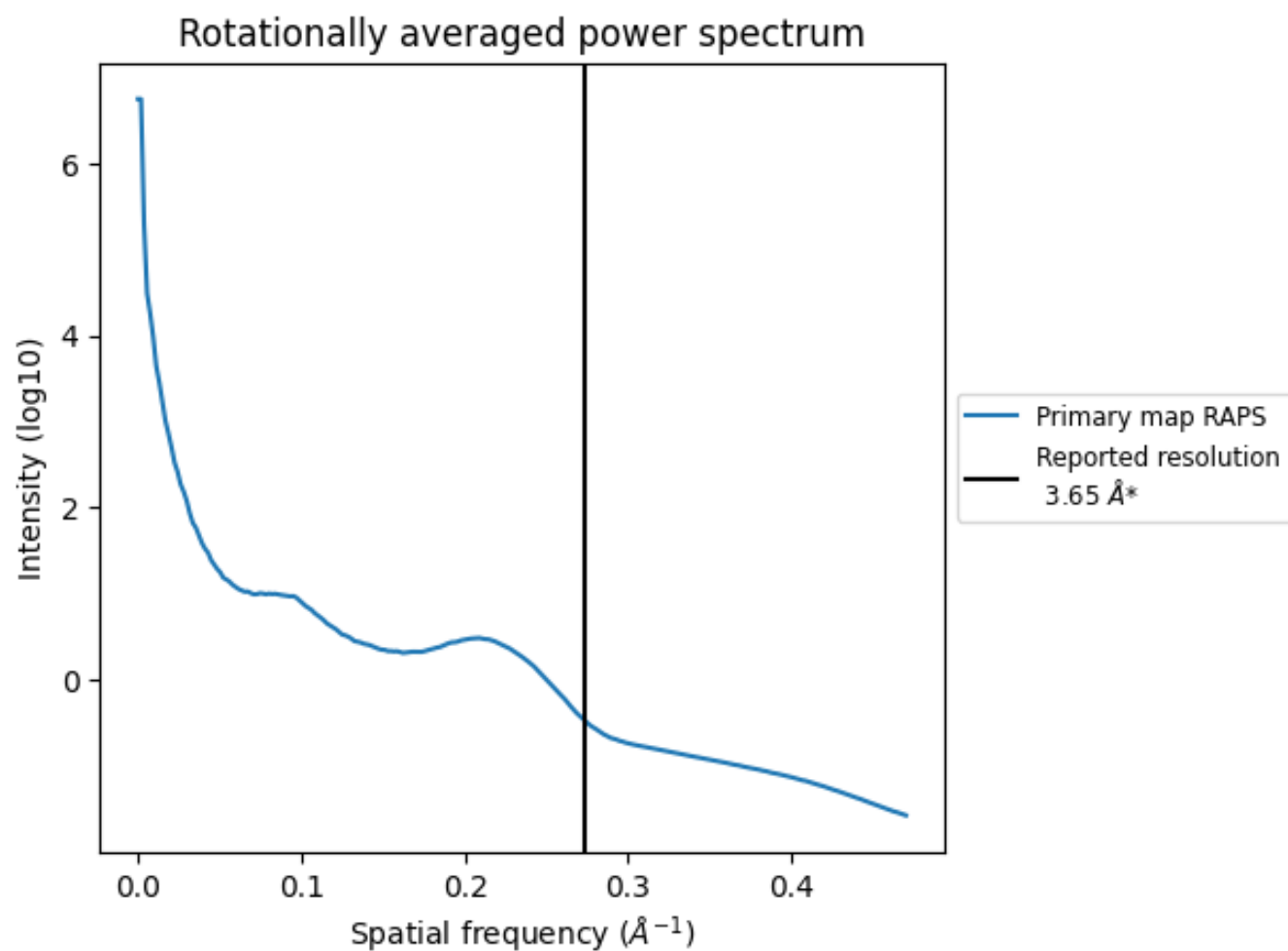
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1608 nm^3 ; this corresponds to an approximate mass of 1453 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 0.274 Å⁻¹

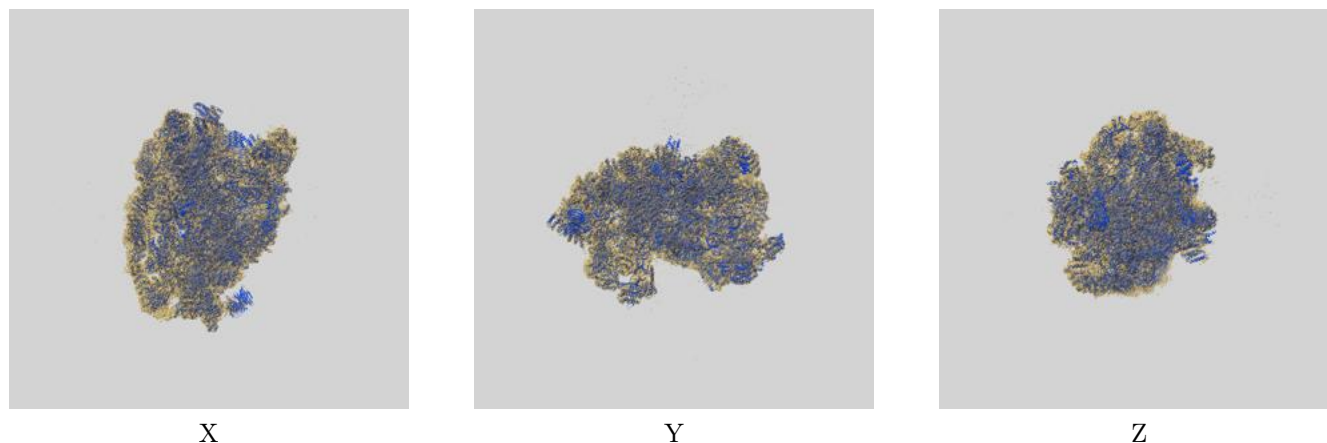
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

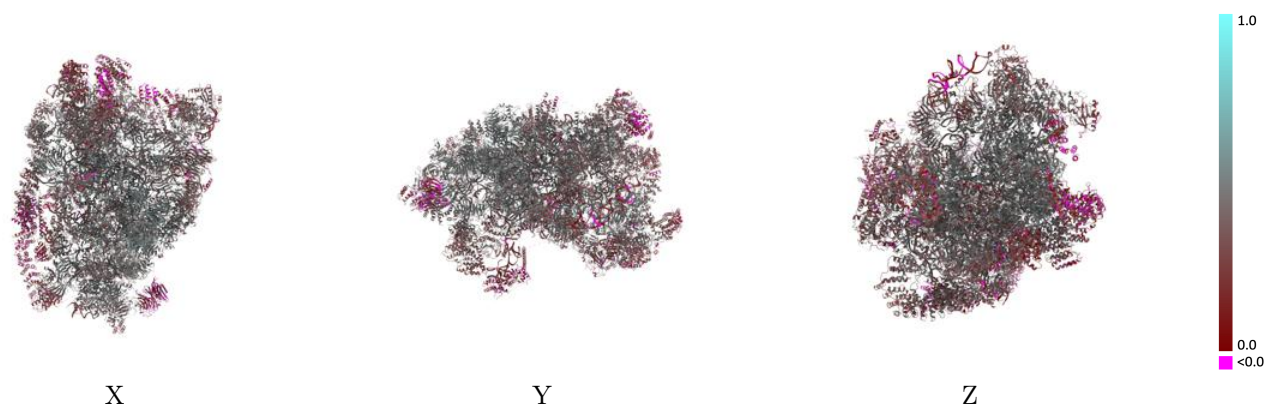
This section contains information regarding the fit between EMDB map EMD-49078 and PDB model 9N6Y. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



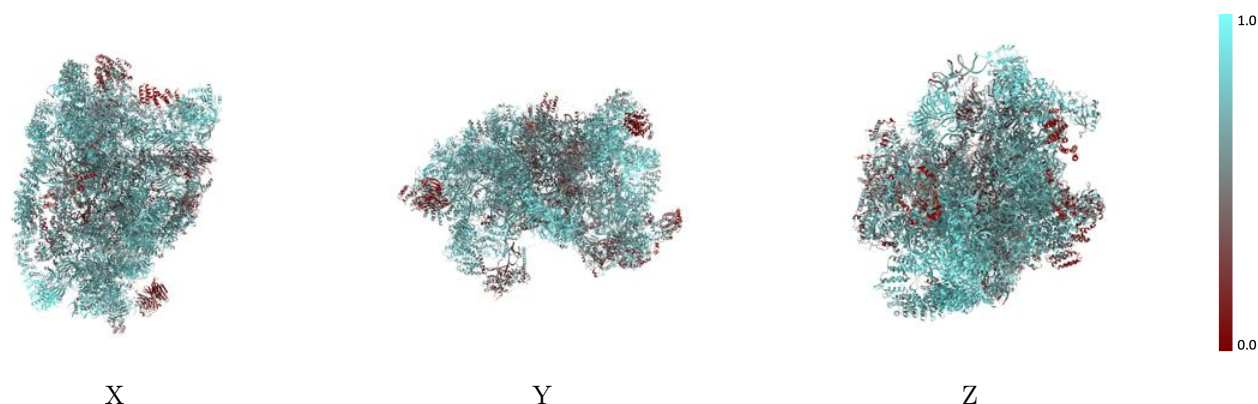
The images above show the 3D surface view of the map at the recommended contour level 0.77 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



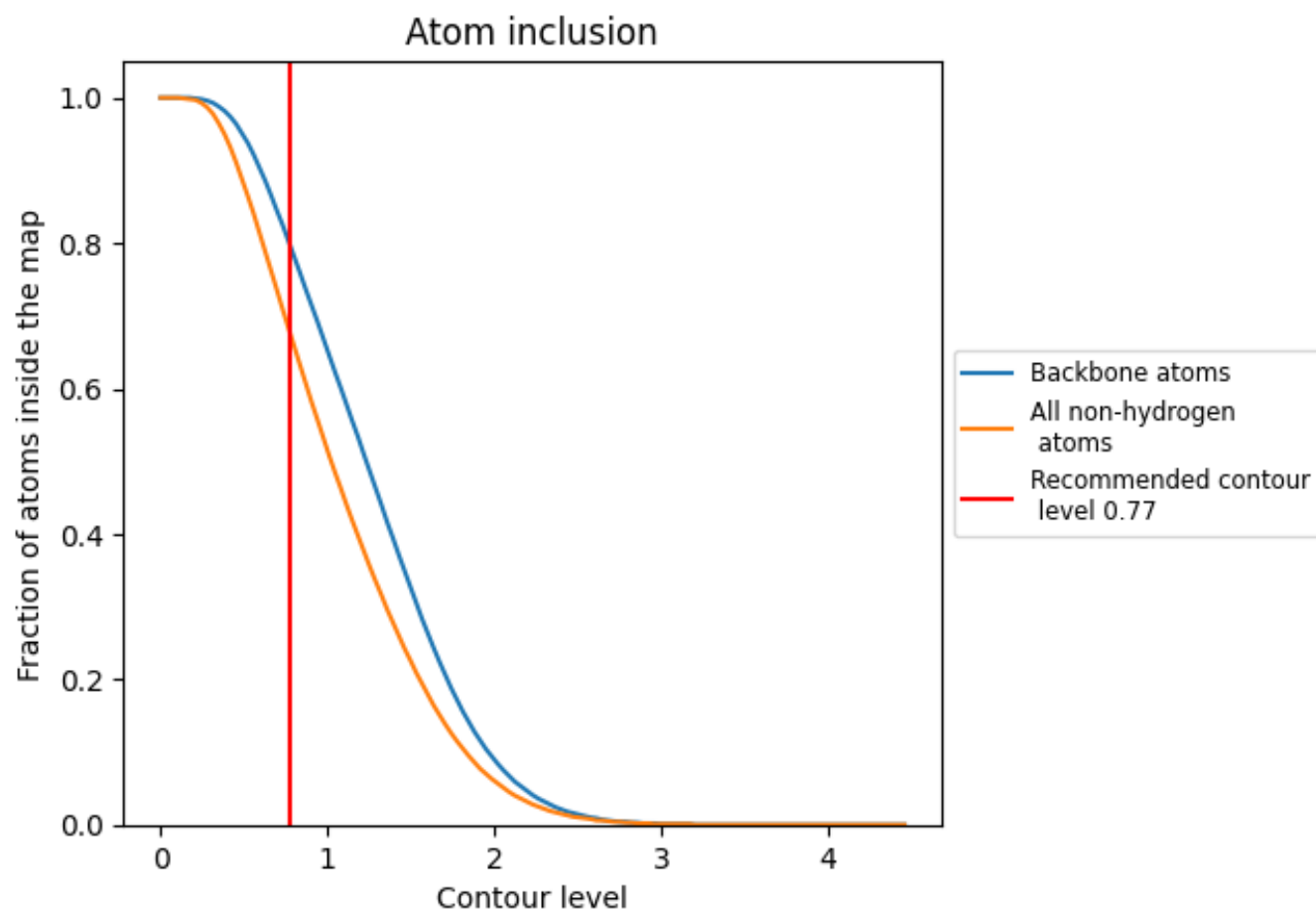
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.77).

9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 68% 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 (0.77) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6810	 0.4010
L0	 0.6940	 0.3980
L1	 0.8000	 0.3920
L2	 0.7530	 0.4080
L3	 0.0910	 0.2740
L4	 0.7840	 0.4640
L5	 0.6940	 0.4680
L6	 0.8190	 0.4260
L7	 0.6260	 0.3410
L8	 0.8280	 0.4520
L9	 0.6910	 0.4680
LC	 0.6830	 0.4820
LD	 0.7200	 0.4140
LE	 0.7600	 0.4650
LF	 0.8420	 0.4770
LG	 0.6700	 0.4950
LH	 0.7580	 0.4560
LI	 0.3630	 0.2570
LJ	 0.7600	 0.4590
LK	 0.5930	 0.3480
LL	 0.7320	 0.4500
LM	 0.7660	 0.3260
LN	 0.7760	 0.4410
LO	 0.7290	 0.4960
LP	 0.5210	 0.3740
LQ	 0.7750	 0.3980
LR	 0.4890	 0.3680
LS	 0.7410	 0.4780
LT	 0.7040	 0.4830
LU	 0.7650	 0.4930
LV	 0.7650	 0.4400
LW	 0.6730	 0.4870
LX	 0.5620	 0.3450
LY	 0.5860	 0.3440
LZ	 0.7160	 0.5090



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Chain	Atom inclusion	Q-score
NA	 0.5650	 0.3930
NB	 0.5600	 0.3300
NC	 0.3920	 0.2840
ND	 0.6200	 0.3780
NE	 0.5310	 0.4260
NF	 0.7320	 0.4500
NG	 0.5610	 0.4580
NH	 0.8150	 0.4070
NI	 0.6390	 0.3410
NK	 0.5730	 0.4290
NM	 0.6390	 0.4630
NN	 0.4300	 0.2800
NQ	 0.7720	 0.4610
NV	 0.4220	 0.4460
OA	 0.0790	 0.1320
SA	 0.5890	 0.4170
SB	 0.5980	 0.3780
SC	 0.6580	 0.4860
SD	 0.6180	 0.4130
SE	 0.7550	 0.4720
SF	 0.6680	 0.4760
SG	 0.6990	 0.4540
SH	 0.6040	 0.4320
SI	 0.6500	 0.4430
SJ	 0.7400	 0.3440
SK	 0.8000	 0.3900
SL	 0.6600	 0.4920
SM	 0.6340	 0.4770
SN	 0.5540	 0.4290
SP	 0.6980	 0.3340
SQ	 0.4680	 0.4280
SR	 0.6440	 0.4840
SS	 0.4140	 0.3320
ST	 0.6100	 0.3270
SU	 0.7340	 0.3430
SV	 0.6590	 0.3260
SW	 0.4020	 0.3890
SY	 0.6270	 0.4440
SZ	 0.4440	 0.2110