



Full wwPDB EM Validation Report ⓘ

Mar 4, 2026 – 07:32 PM UTC

PDB ID : 9N73 / pdb_00009n73
EMDB ID : EMD-49083
Title : SSU processome maturation and disassembly, State G
Authors : Buzovetsky, O.; Klinge, S.
Deposited on : 2025-02-05
Resolution : 5.96 Å(reported)

This is a Full wwPDB EM Validation 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
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

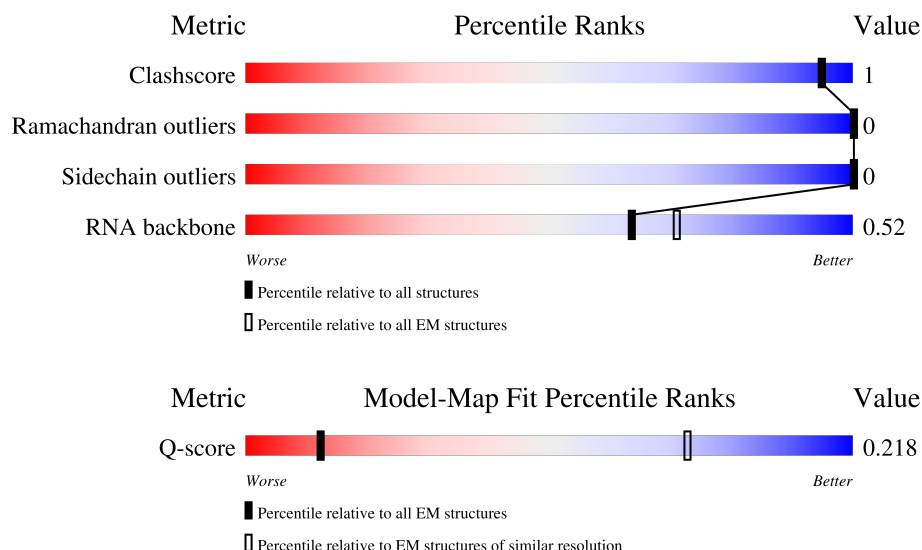
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.96 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	474 (5.47 - 6.46)

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	1810	
3	L2	333	

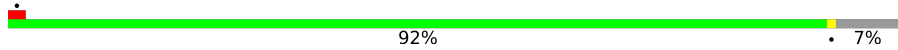
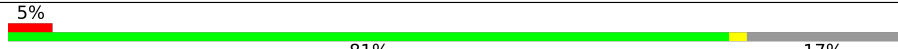
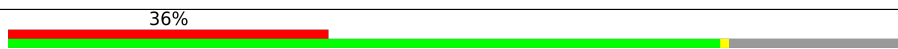
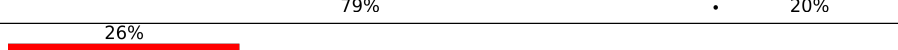
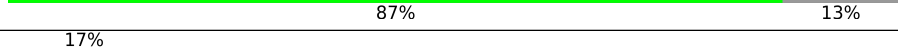
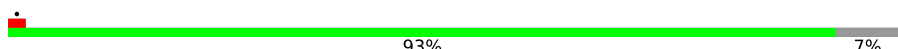
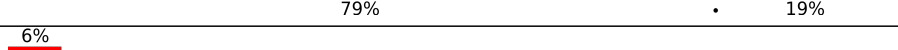
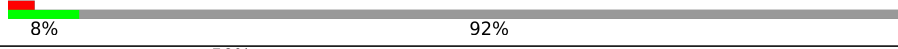
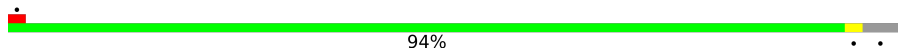
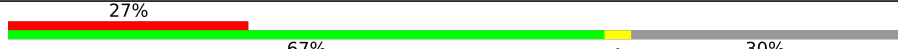
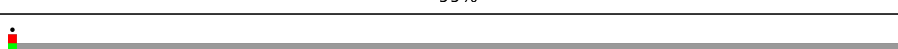
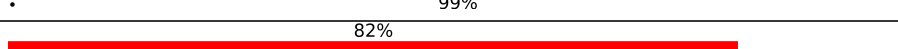
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Mol	Chain	Length	Quality of chain
4	L3	146	
5	L4	261	
6	L5	225	
7	L6	236	
8	L7	190	
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LO	923	
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	NF	151	
39	NG	137	
40	NH	1237	
41	NI	297	
42	NL	318	
43	NM	255	
44	NN	534	
45	NP	144	
46	NQ	82	
47	NS	1267	
48	NV	733	
49	OA	1729	
50	OH	143	
51	OU	152	
52	SA	504	

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Mol	Chain	Length	Quality of chain
53	SB	511	
54	SC	327	
54	SD	327	
55	SE	126	
55	SF	126	
56	SG	573	
57	SH	367	
58	SI	1183	
59	SJ	252	
59	SK	252	
60	SL	189	
61	SM	290	
62	SP	2493	
63	SQ	217	
64	SR	145	
65	SS	899	
66	ST	810	
67	SU	552	
68	SW	274	
69	SY	250	
70	SZ	483	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 163806 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	64	Total	C	N	O	P	0	0
			1370	612	247	447	64		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1266	Total	C	N	O	P	0	0
			27015	12076	4829	8844	1266		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	144	Total	C	N	O	P	0	0
			3064	1369	540	1011	144		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	L3	106	Total	C	N	O	0	0
			529	317	106	106		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
5	L4	234	Total	C	N	O	0	0
			1172	704	234	234		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
6	L5	206	Total	C	N	O	0	0
			1040	628	206	206		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
7	L6	206	Total	C	N	O	0	0
			1029	617	206	206		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	L7	178	Total	C	N	O	0	0
			903	547	178	178		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	L8	171	Total	C	N	O	0	0
			848	506	171	171		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
10	L9	181	Total	C	N	O	0	0
			914	552	181	181		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
11	LC	128	Total	C	N	O	0	0
			642	386	128	128		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
12	LD	137	Total	C	N	O	0	0
			693	419	137	137		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
13	LE	129	Total	C	N	O	0	0
			640	382	129	129		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LF	97	Total	C	N	O	0	0
			484	290	97	97		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
15	LG	62	Total	C	N	O	0	0
			309	185	62	62		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	LH	806	Total	C	N	O	0	0
			4034	2422	806	806		

- 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	0	0
			3027	1827	600	600		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	LJ	476	Total	C	N	O	0	0
			2394	1442	476	476		

- 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	0	0
			664	400	132	132		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	LL	487	Total	C	N	O	0	0
			2440	1466	487	487		

- 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	0	0
			8115	4889	1613	1613		

- 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	0	0
			3315	1989	663	663		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
23	LO	792	Total	C	N	O	0	0
			3958	2374	792	792		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	LP	379	Total	C	N	O	0	0
			1901	1143	379	379		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
25	LQ	815	Total	C	N	O	0	0
			4063	2433	815	815		

- 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	0	0
			3962	2376	793	793		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
27	LS	454	Total	C	N	O	0	0
			2279	1371	454	454		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
28	LT	871	Total	C	N	O	0	0
			4347	2605	871	871		

- Molecule 29 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	LU	454	Total	C	N	O	0	0
			2274	1366	454	454		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
30	LV	357	Total	C	N	O	0	0
			1791	1077	357	357		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
31	LW	459	Total	C	N	O	0	0
			2304	1386	459	459		

- Molecule 32 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	LX	852	Total	C	N	O	0	0
			4302	2598	852	852		
32	LY	846	Total	C	N	O	0	0
			4274	2582	846	846		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
33	LZ	160	Total	C	N	O	0	0
			808	488	160	160		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
34	NA	329	Total	C	N	O	0	0
			1654	996	329	329		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
35	NB	231	Total	C	N	O	0	0
			1159	697	231	231		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
36	NC	135	Total	C	N	O	0	0
			669	399	135	135		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
37	ND	59	Total	C	N	O	0	0
			297	179	59	59		

- Molecule 38 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	NF	141	Total	C	N	O	0	0
			711	429	141	141		

- Molecule 39 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	NG	127	Total	C	N	O	0	0
			630	376	127	127		

- Molecule 40 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	NH	1077	Total	C	N	O	0	0
			5443	3289	1077	1077		

- Molecule 41 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	NI	240	Total	C	N	O	0	0
			1210	730	240	240		

- Molecule 42 is a protein called Dimethyladenosine transferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	NL	285	Total	C	N	O	0	0
			1446	876	285	285		

- Molecule 43 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	NM	237	Total	C	N	O	0	0
			1183	709	237	237		

- Molecule 44 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	NN	43	Total	C	N	O	0	0
			215	129	43	43		

- Molecule 45 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	NP	134	Total	C	N	O	0	0
			666	398	134	134		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
46	NQ	79	Total	C	N	O	0	0
			398	240	79	79		

- Molecule 47 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	NS	891	Total	C	N	O	0	0
			4500	2718	891	891		

- Molecule 48 is a protein called Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	NV	8	Total	C	N	O	0	0
			39	23	8	8		

- Molecule 49 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	OA	14	Total	C	N	O	0	0
			69	41	14	14		

- Molecule 50 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	OH	120	Total	C	N	O	0	0
			594	354	120	120		

- Molecule 51 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	OU	56	Total	C	N	O	0	0
			278	166	56	56		

- Molecule 52 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SA	384	Total	C	N	O	1	0
			1924	1154	385	385		

- Molecule 53 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	SB	433	Total	C	N	O	0	0
			2161	1295	433	433		

- Molecule 54 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	SC	238	Total	C	N	O	0	0
			1198	722	238	238		
54	SD	238	Total	C	N	O	0	0
			1198	722	238	238		

- Molecule 55 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	SE	121	Total	C	N	O	0	0
			615	373	121	121		
55	SF	121	Total	C	N	O	0	0
			615	373	121	121		

- Molecule 56 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SG	453	Total	C	N	O	0	0
			2260	1354	453	453		

- Molecule 57 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SH	360	Total	C	N	O	0	0
			1801	1081	360	360		

- Molecule 58 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	SI	780	Total	C	N	O	0	0
			3939	2379	780	780		

- Molecule 59 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	SJ	213	Total	C	N	O	0	0
			1074	648	213	213		
59	SK	229	Total	C	N	O	0	0
			1160	702	229	229		

- Molecule 60 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	SL	148	Total	C	N	O	0	0
			751	455	148	148		

- Molecule 61 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	SM	247	Total	C	N	O	0	0
			1243	749	247	247		

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	SP	2156	Total	C	N	O	0	0
			10847	6535	2156	2156		

- Molecule 63 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	SQ	117	Total	C	N	O	0	0
			592	358	117	117		

- Molecule 64 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	SR	95	Total	C	N	O	0	0
			476	286	95	95		

- Molecule 65 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	SS	225	Total	C	N	O	1	0
			1145	695	225	225		

- Molecule 66 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	ST	597	Total	C	N	O	0	0
			3010	1816	597	597		

- Molecule 67 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	SU	532	Total	C	N	O	0	0
			2703	1639	532	532		

- Molecule 68 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	SW	219	Total	C	N	O	0	0
			1104	666	219	219		

- Molecule 69 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	SY	122	Total	C	N	O	0	0
			611	367	122	122		

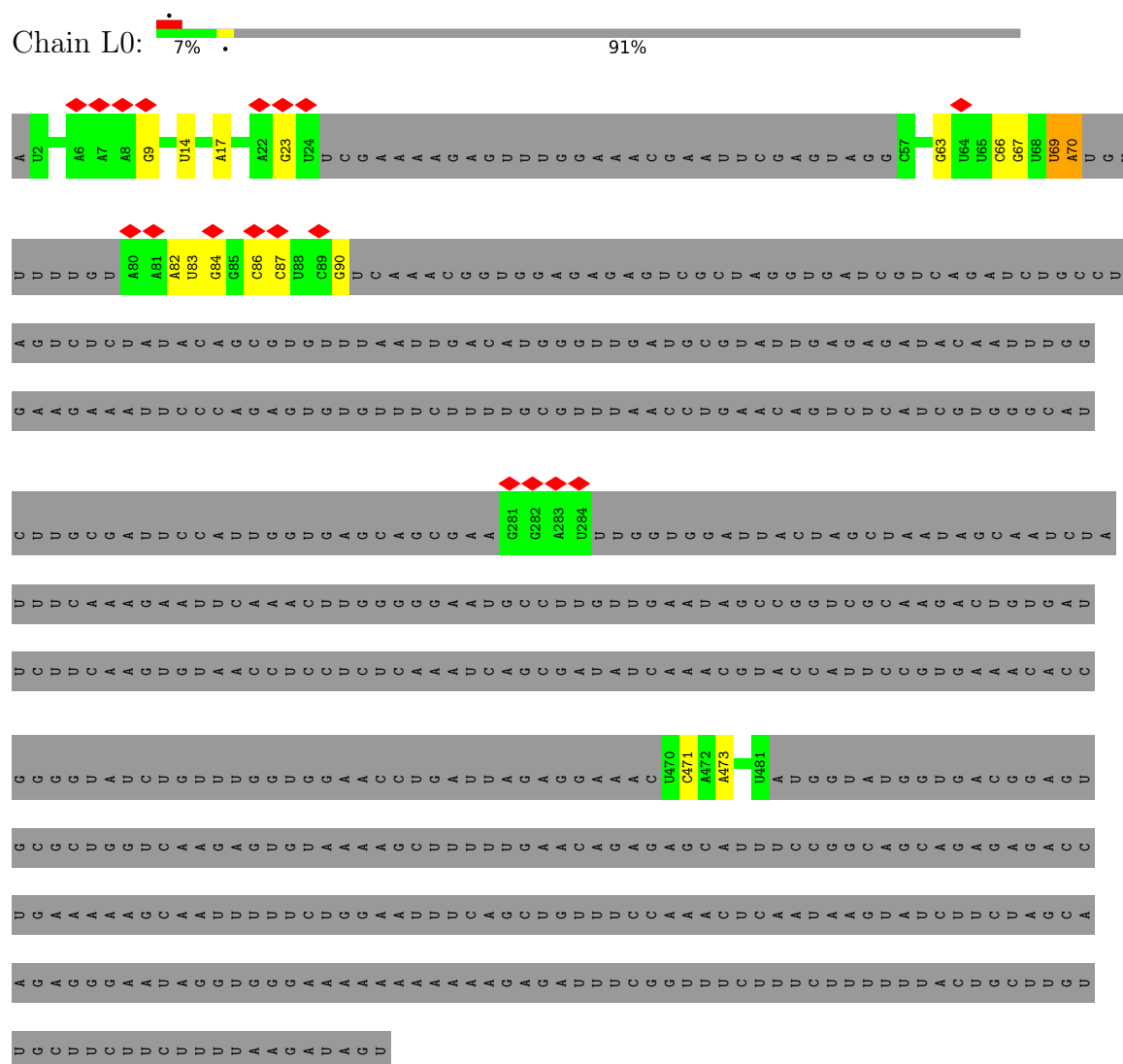
- Molecule 70 is a protein called Essential nuclear protein 1.

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

3 Residue-property plots [i](#)

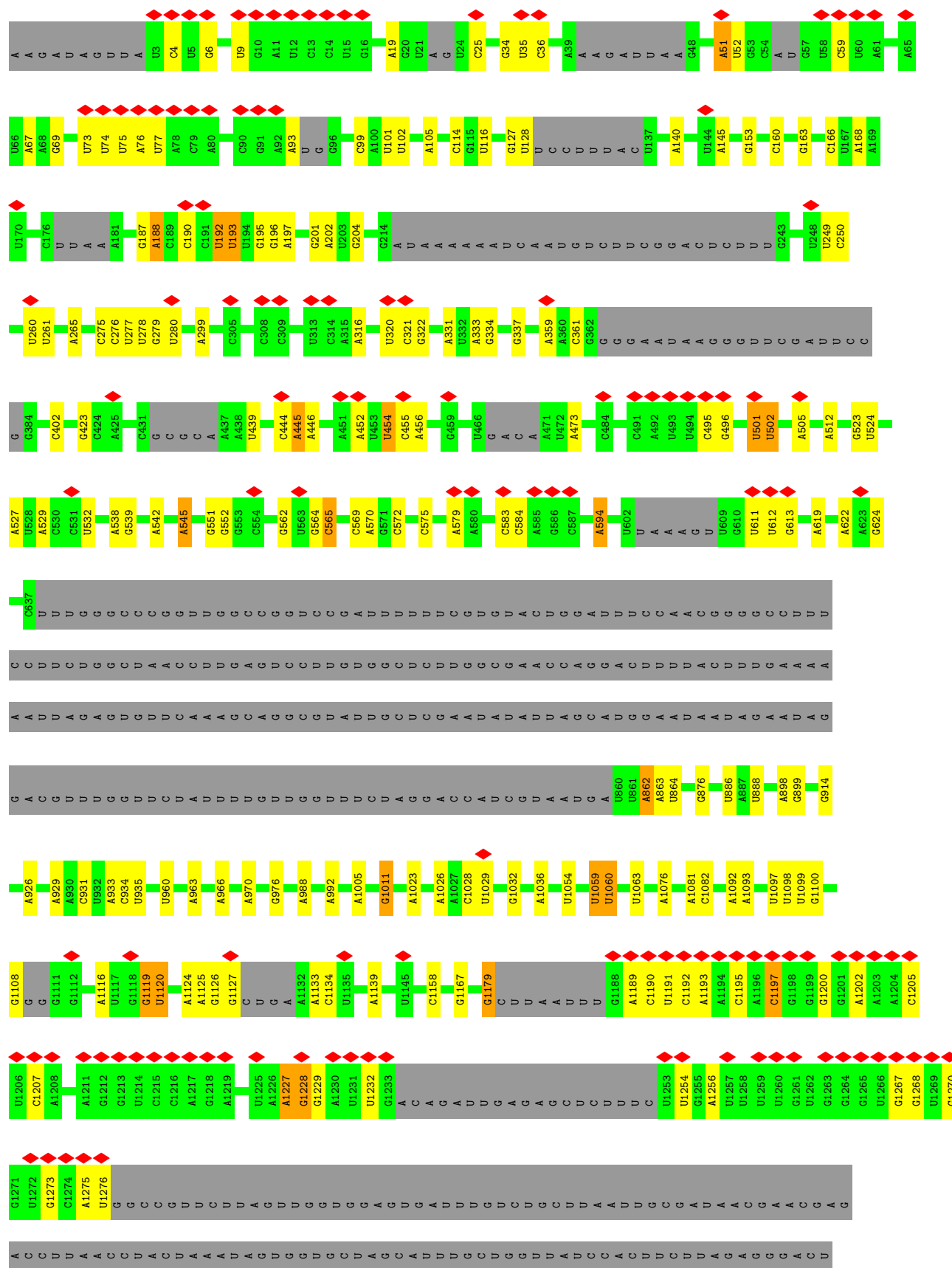
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

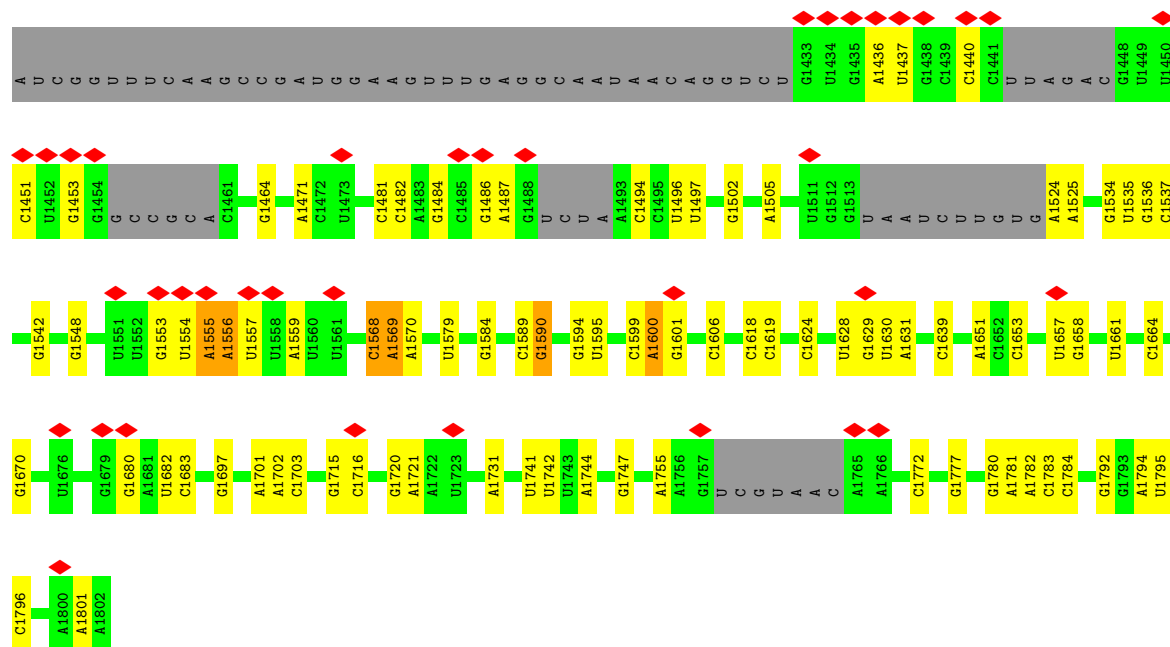
• Molecule 1: 5'ETS rRNA



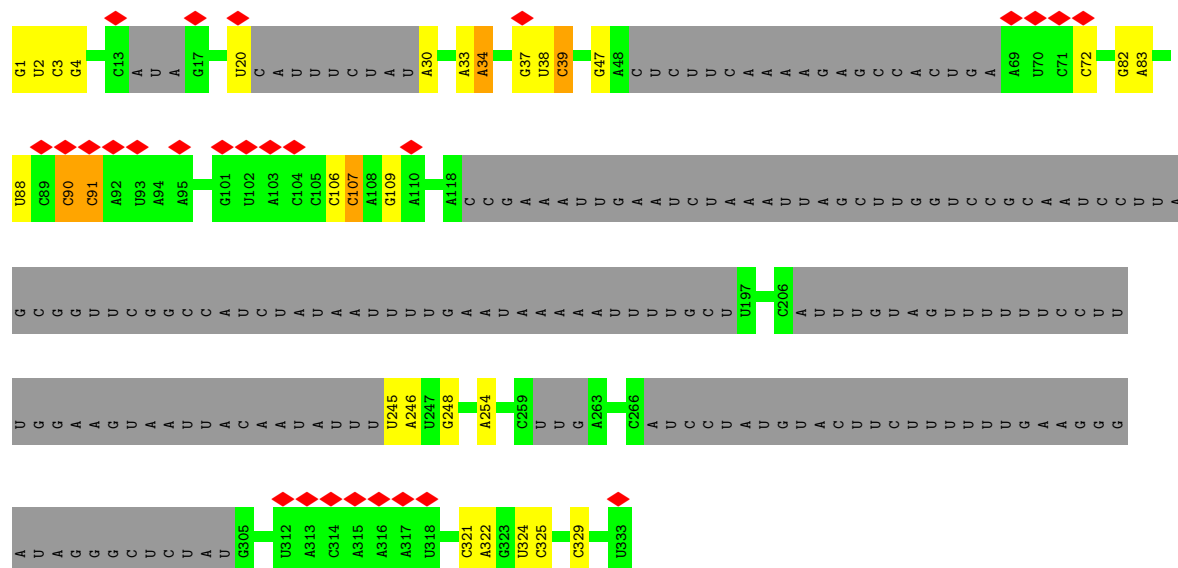
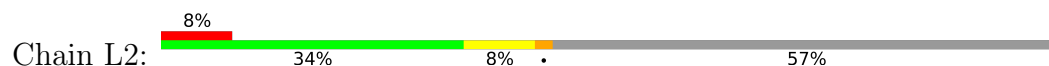
• Molecule 2: 18S rRNA



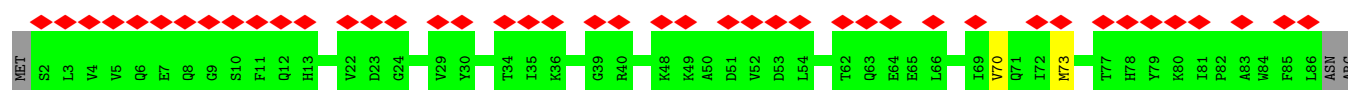
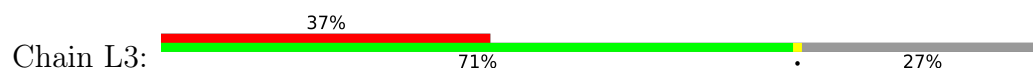


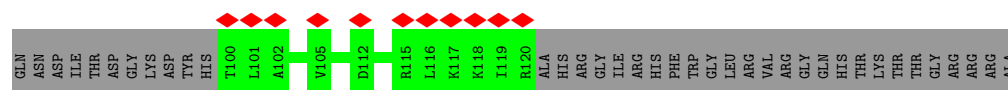


- Molecule 3: U3 snoRNA

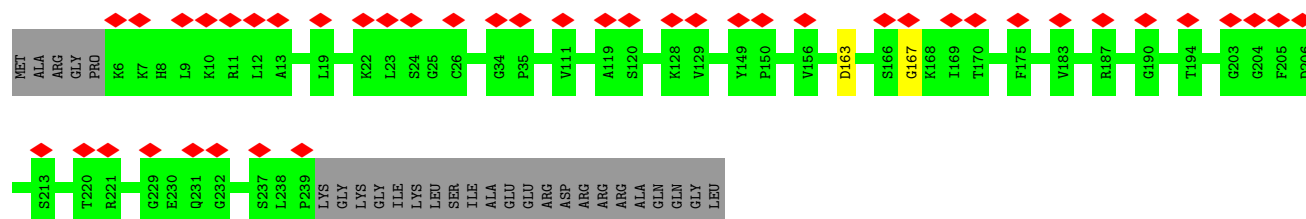
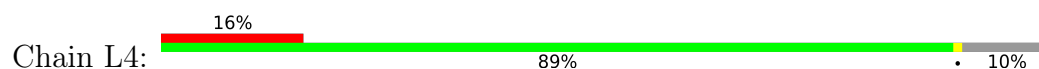


- Molecule 4: 40S ribosomal protein S18-A

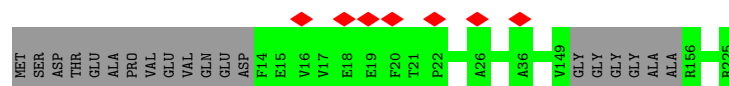




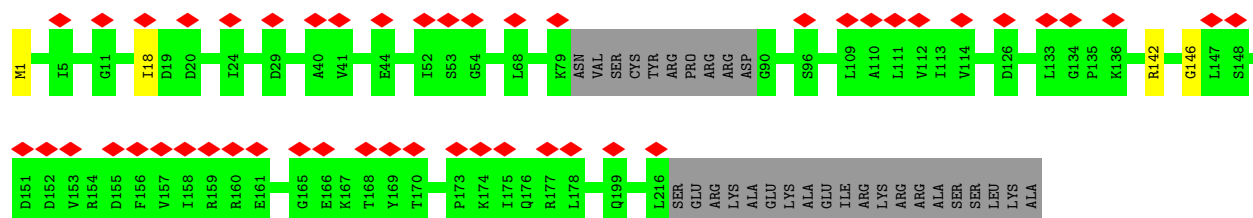
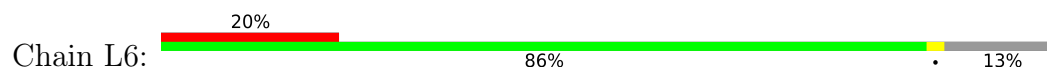
- Molecule 5: 40S ribosomal protein S4-A



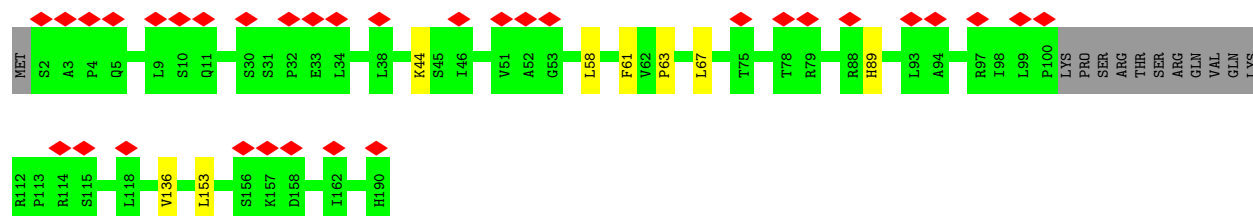
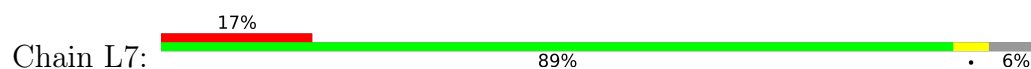
- Molecule 6: 40S ribosomal protein S5



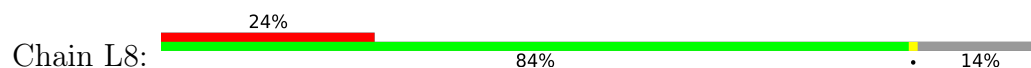
- Molecule 7: 40S ribosomal protein S6-A

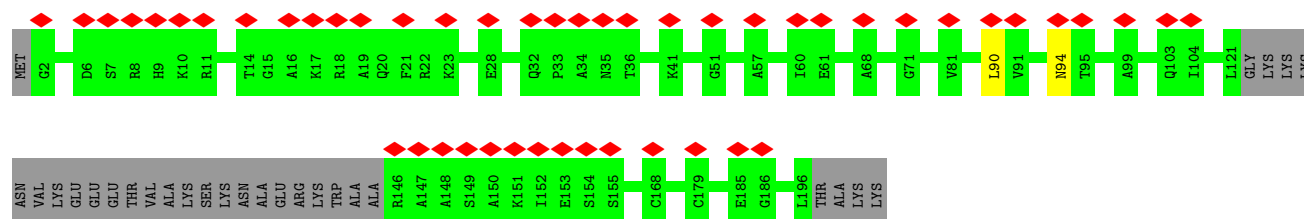


- Molecule 8: 40S ribosomal protein S7-A

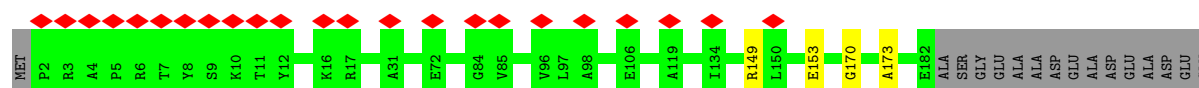


- Molecule 9: 40S ribosomal protein S8-A

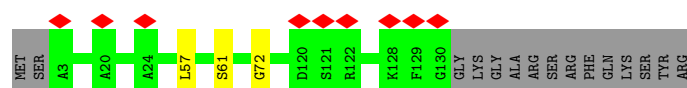
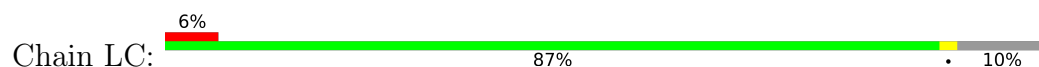




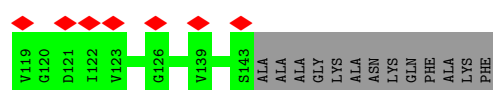
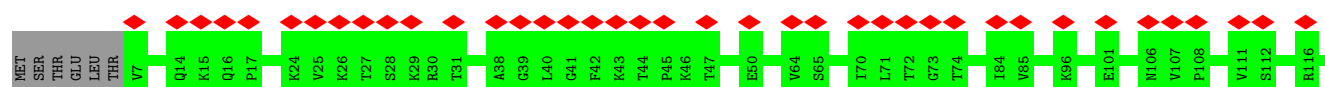
- Molecule 10: 40S ribosomal protein S9-A



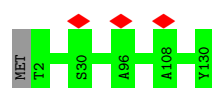
- Molecule 11: 40S ribosomal protein S16-A



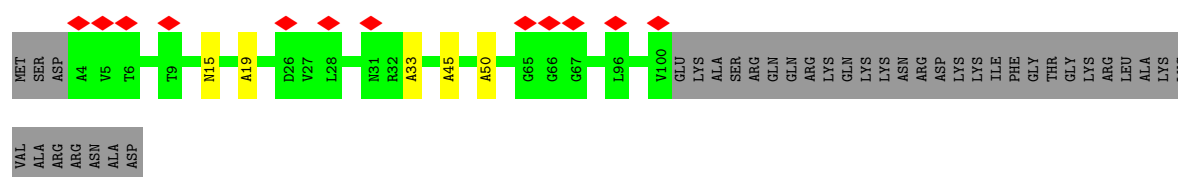
- Molecule 12: 40S ribosomal protein S11-A



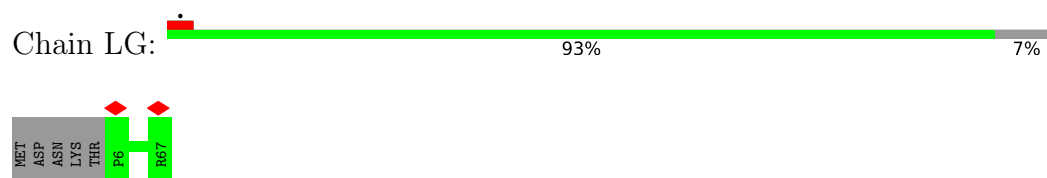
- Molecule 13: 40S ribosomal protein S22-A



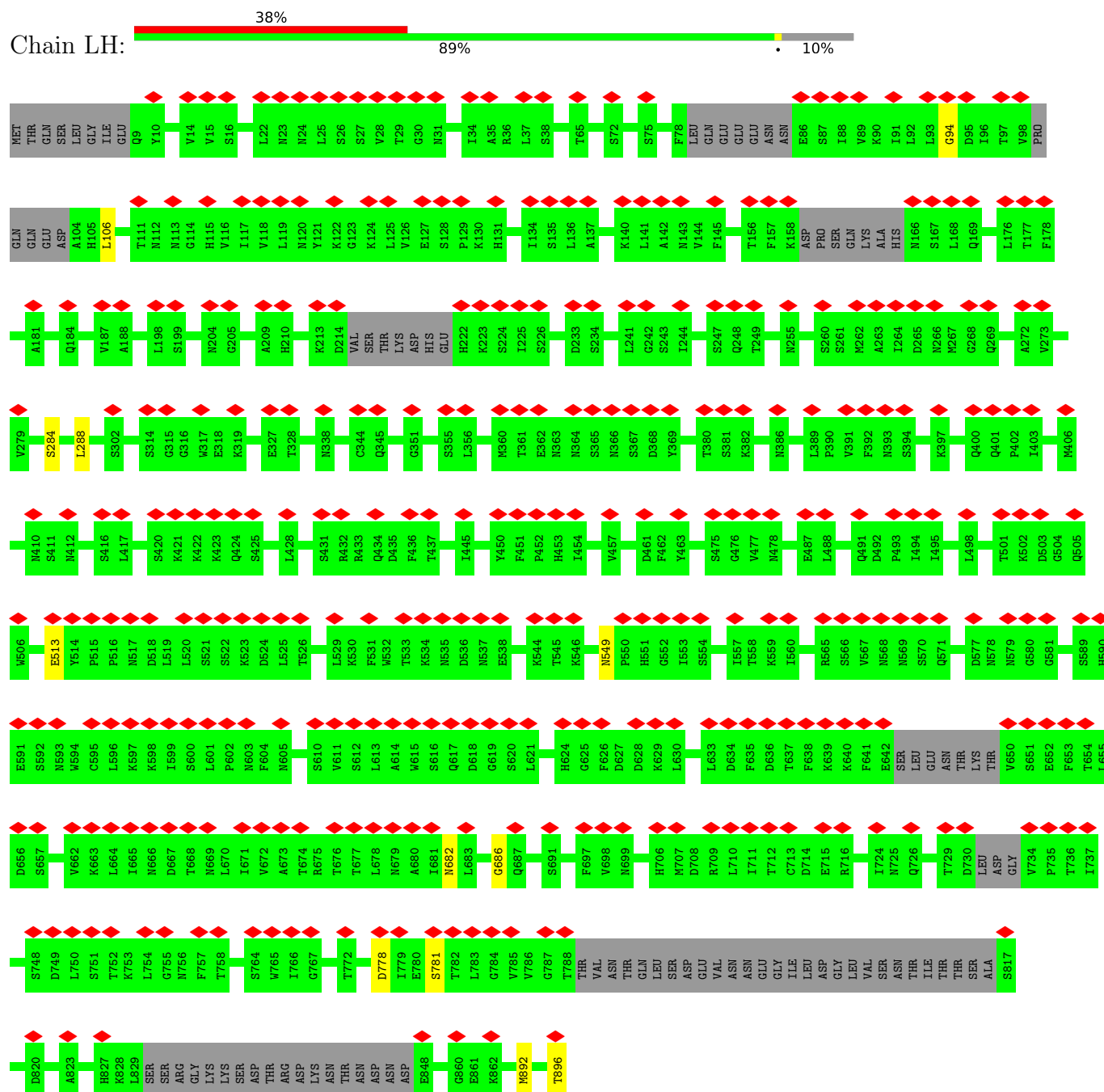
- Molecule 14: 40S ribosomal protein S24-A



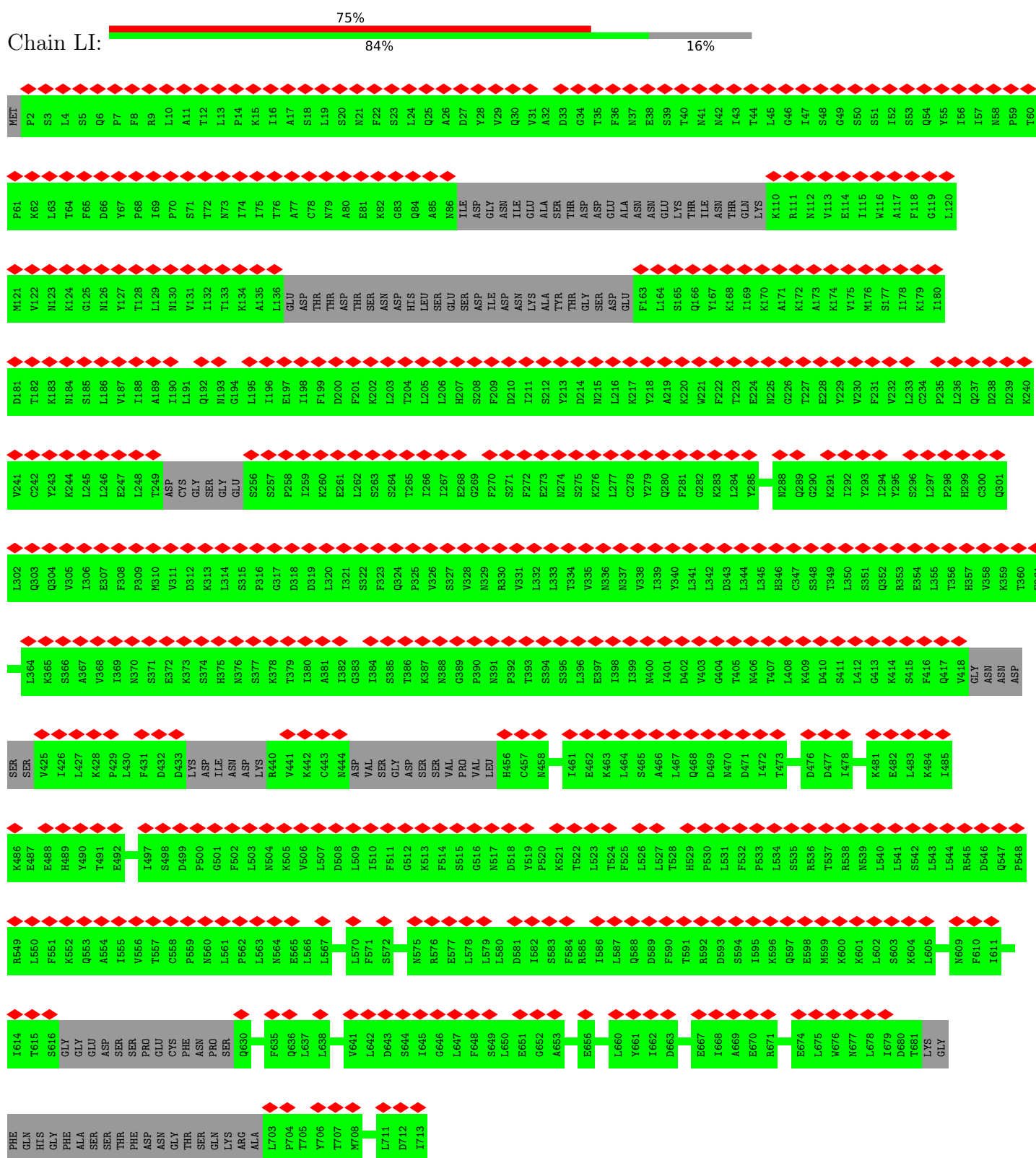
- Molecule 15: 40S ribosomal protein S28-A



- Molecule 16: NET1-associated nuclear protein 1



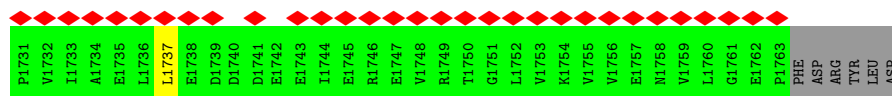
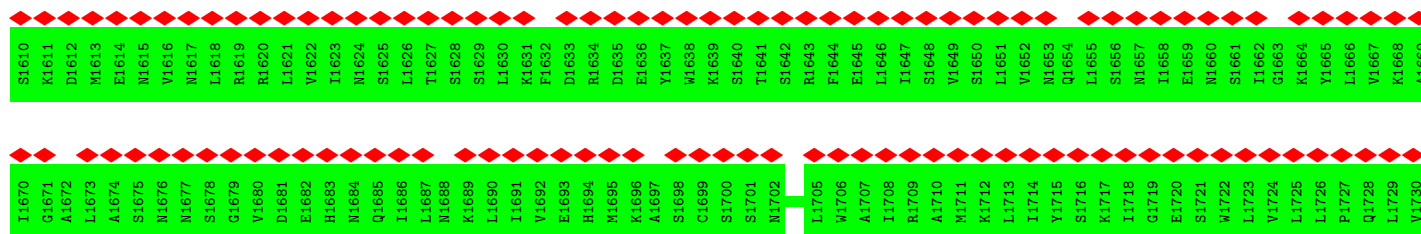
- Molecule 17: U3 small nucleolar RNA-associated protein 8



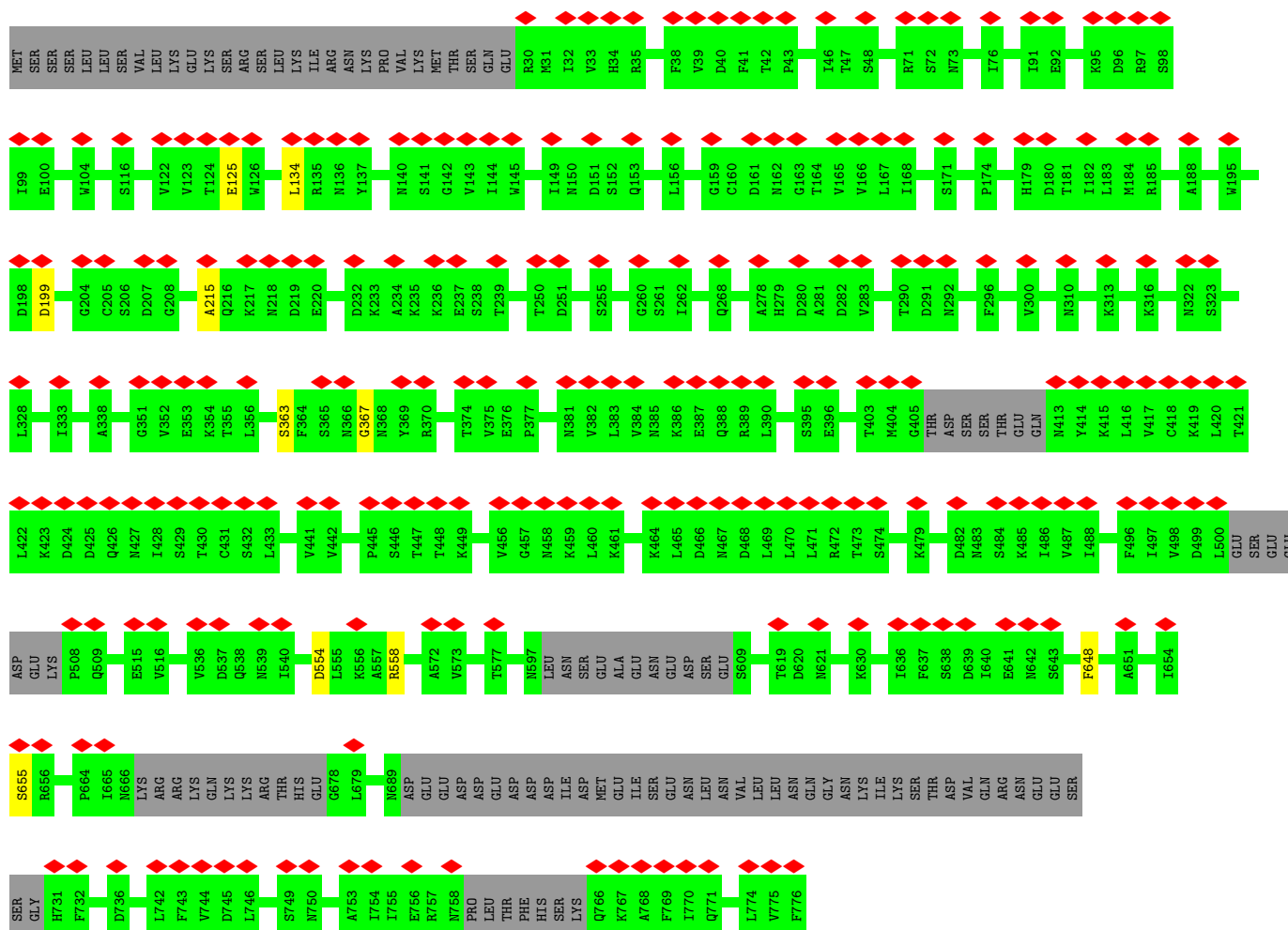
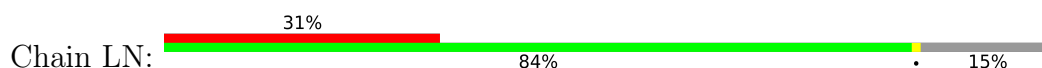
- Molecule 18: U3 small nucleolar RNA-associated protein 15



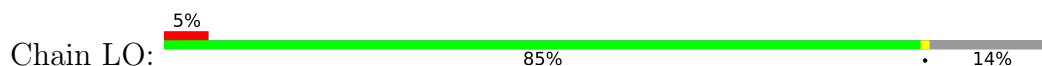
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GLU	THR	LEU	ASP	GLN	ASP	GLY	GLY	LEU	PRO	VAL	LEU	Y893	A894	Q895	E896	T897	L898	I899	L903	N904	T905	I906	K910	E911	H912	G913	C914	T915	E916	L917	T918	N919	V920	R921	A922	D923	I924	T929	R930	E931	S932	A933	S934	P935	Q936	V937	Q938	N939	K940	L941	L942	L943	V944	I945	G946	S947					
ASP	PHE	SER	LYS	ARG	ARG	ARG	ARG	ARG	SER	SER	THR	SER	LYS	ASN	PHE	LEU	LYS	GLU	VAL	SER	GLN	LEU	ALA	GLU	LEU	H847	L848	T852	I853	E856	A857	L858	D859	K860	V861	R862	N863	V864	G865	S866	E867	K868	L869	L870	F871	T872	L873	L874	S875	L876	L877	SER	ASP	LEU							

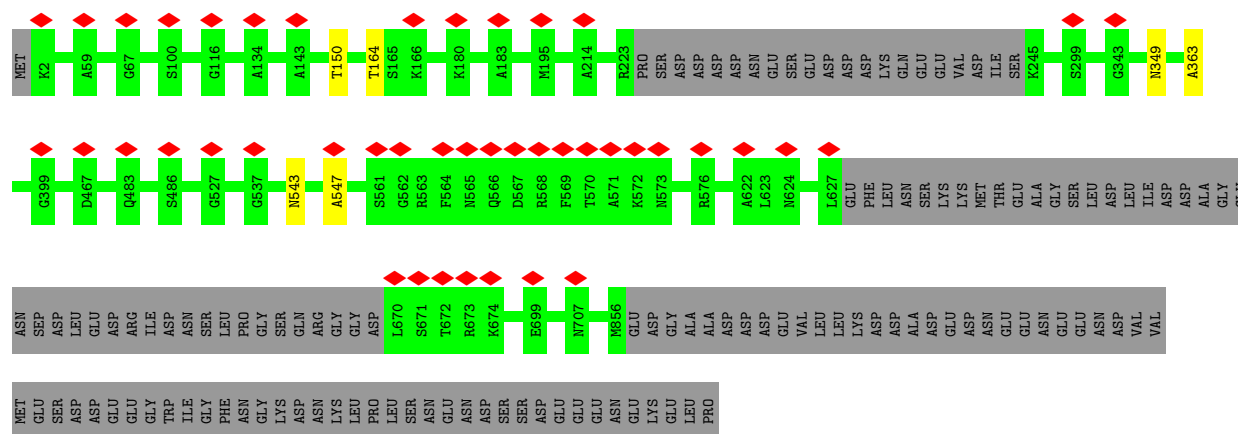


• Molecule 22: U3 small nucleolar RNA-associated protein 4

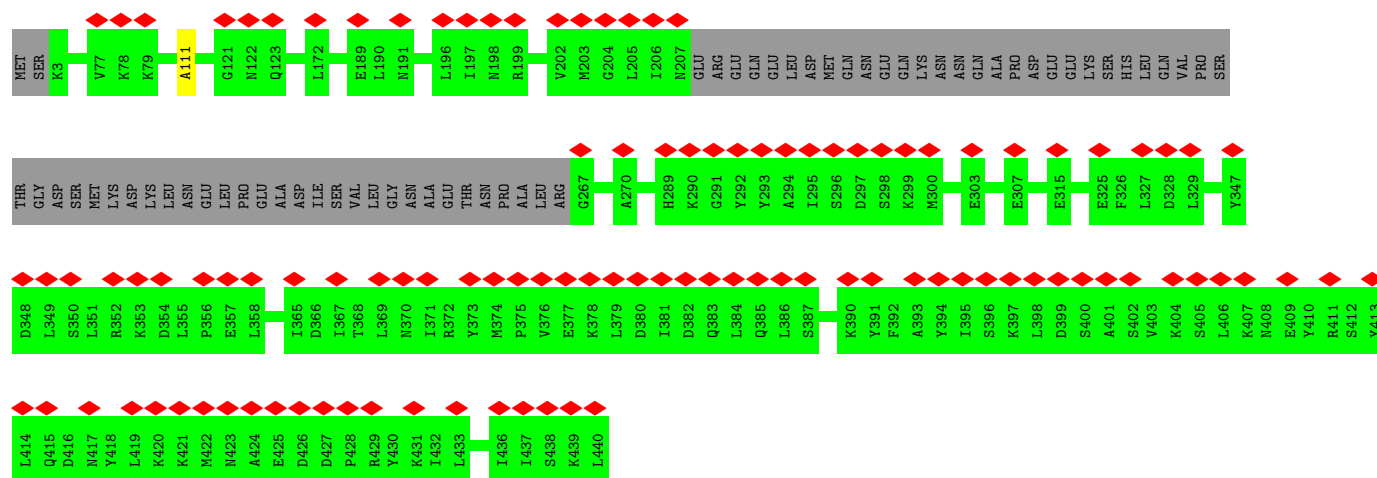
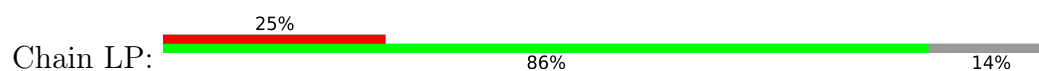


• Molecule 23: Periodic tryptophan protein 2

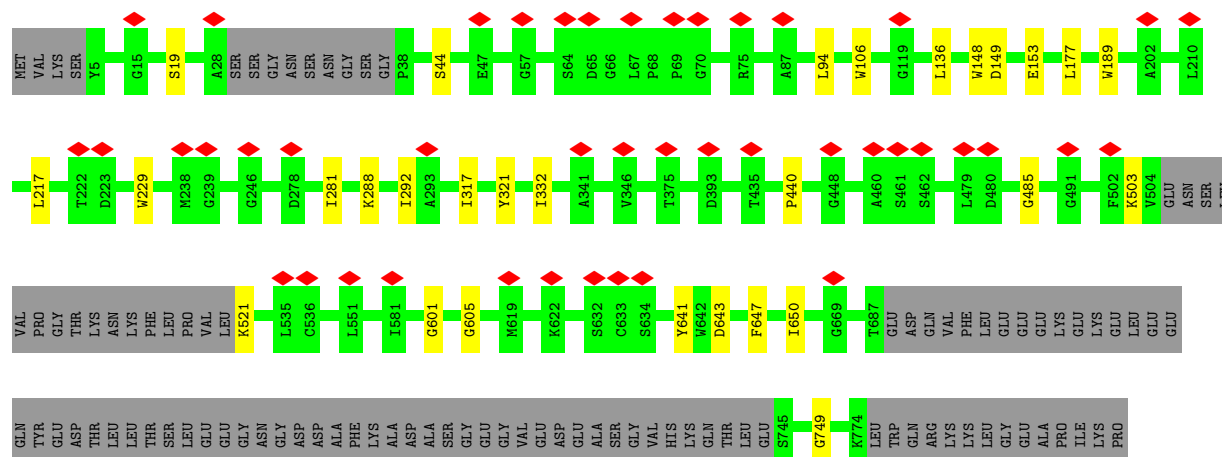
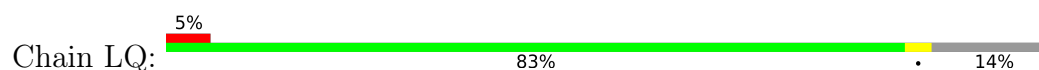


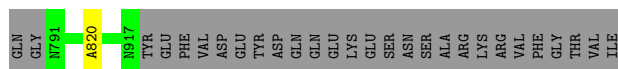


• Molecule 24: U3 small nucleolar RNA-associated protein 6

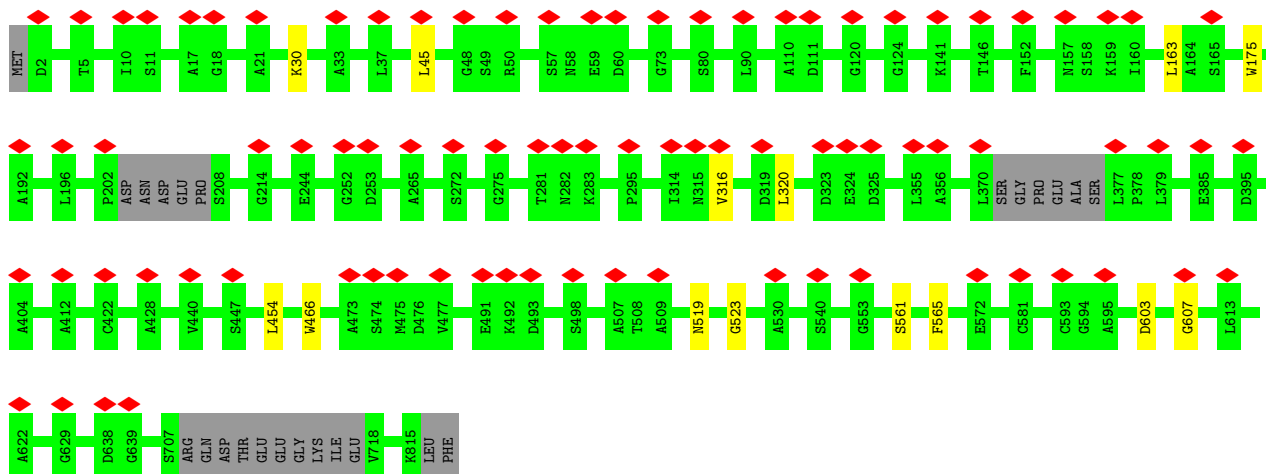


• Molecule 25: U3 small nucleolar RNA-associated protein 12

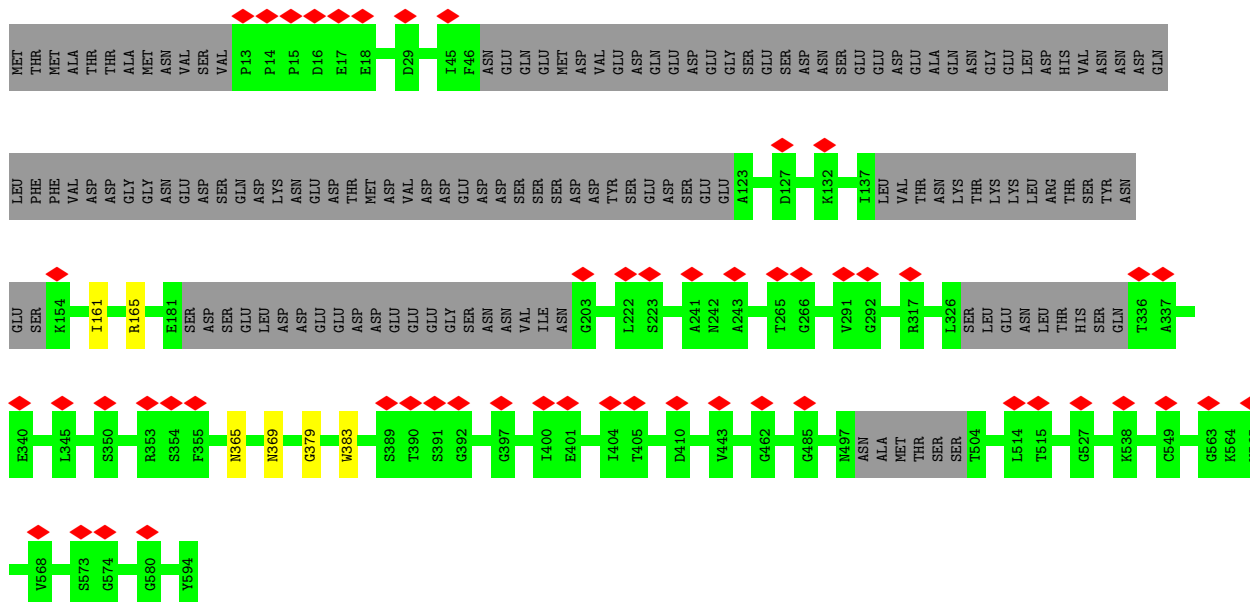
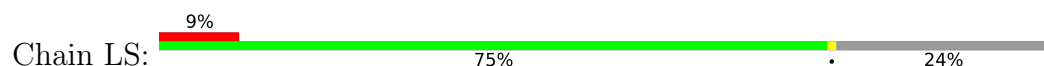




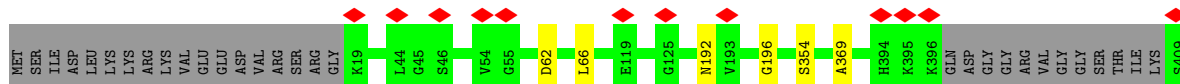
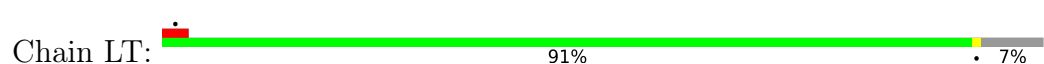
- Molecule 26: U3 small nucleolar RNA-associated protein 13

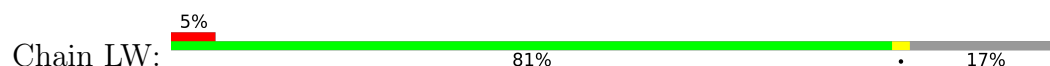


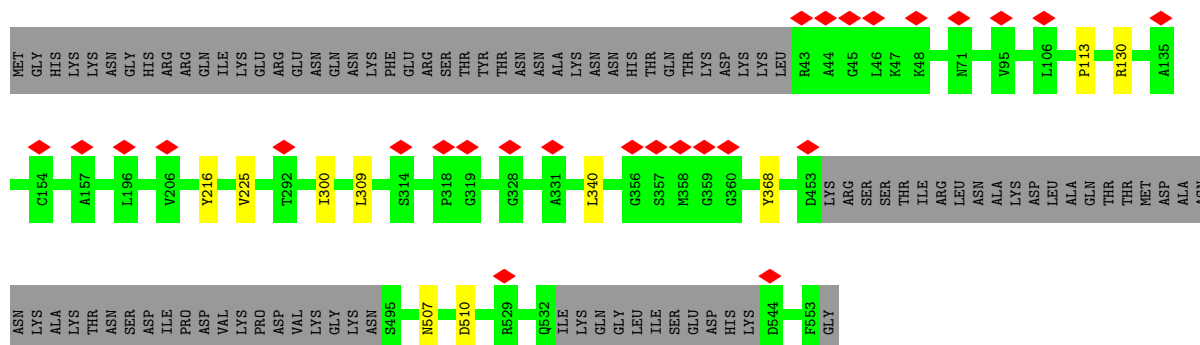
- Molecule 27: U3 small nucleolar RNA-associated protein 18



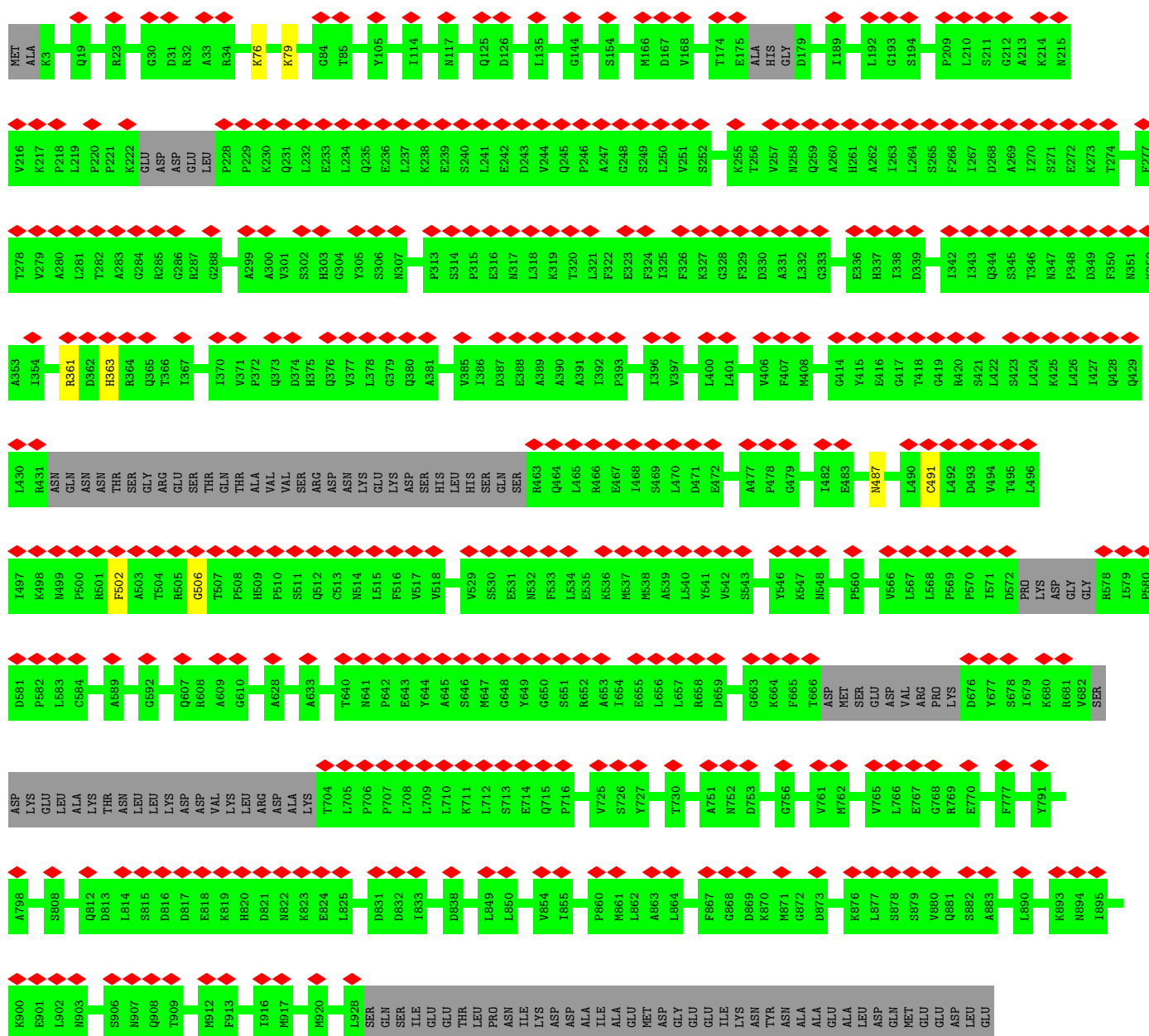
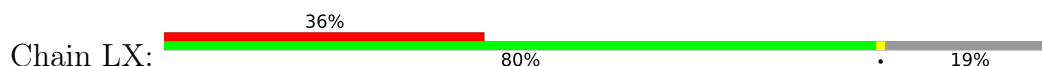
- Molecule 28: U3 small nucleolar RNA-associated protein 21





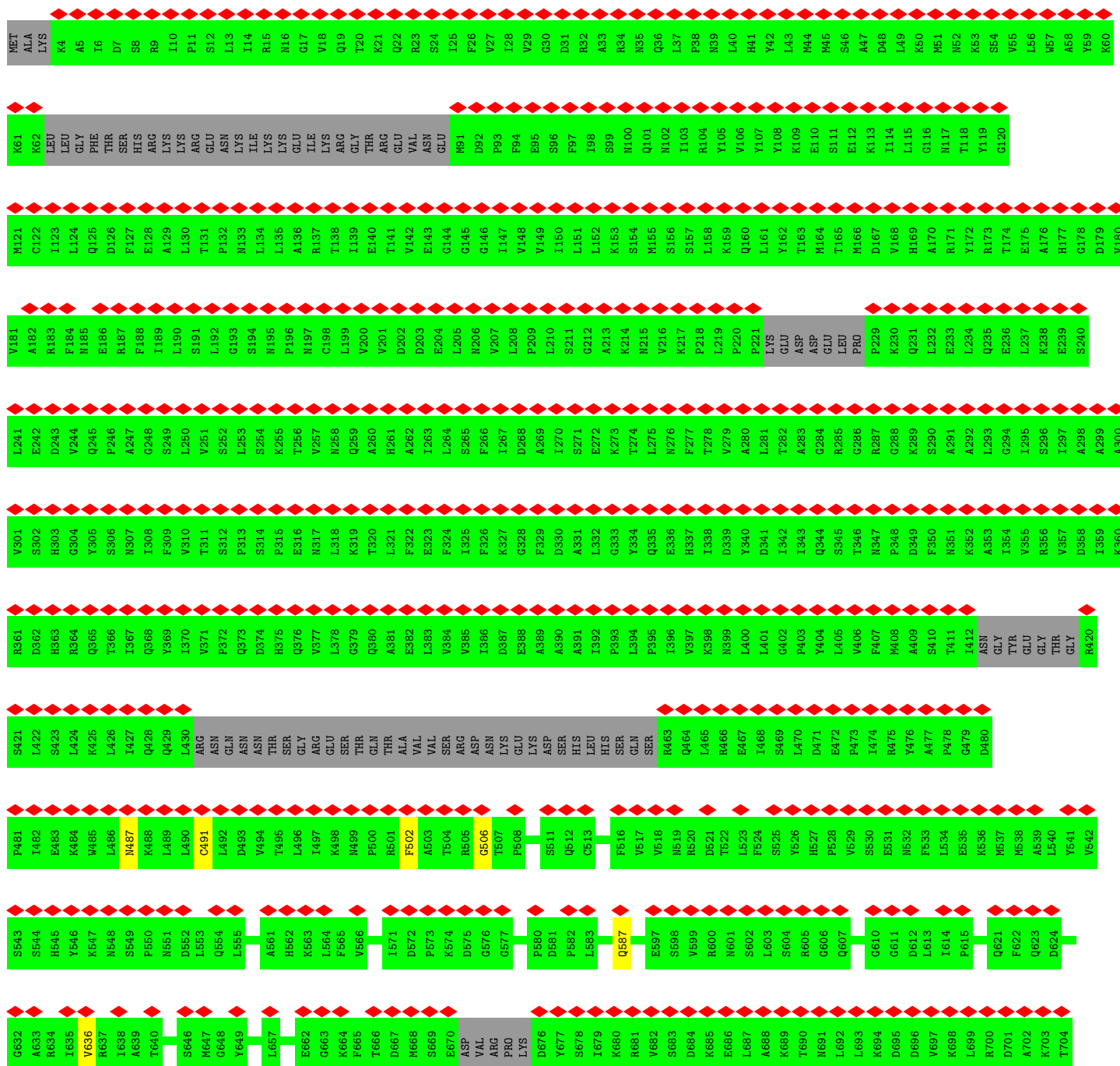
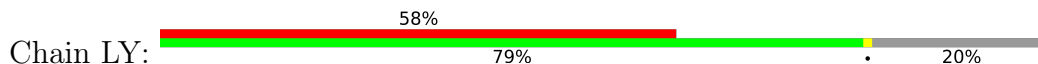


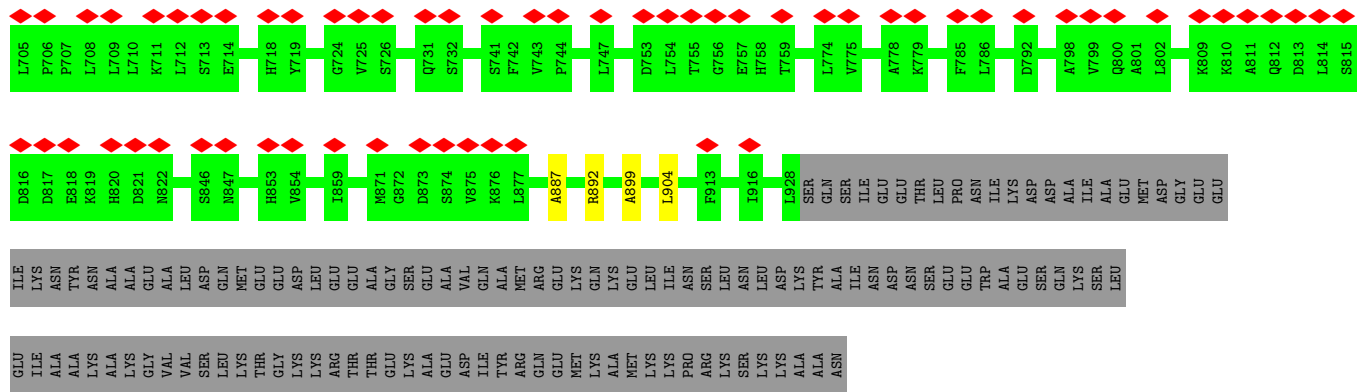
• Molecule 32: RNA cytidine acetyltransferase



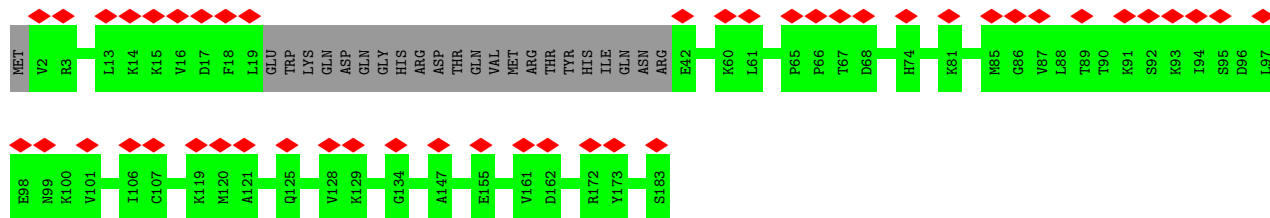
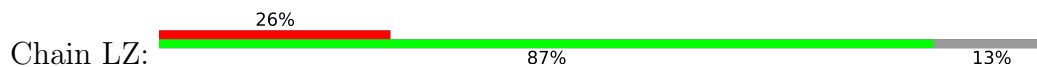
[illegible]

- Molecule 32: RNA cytidine acetyltransferase

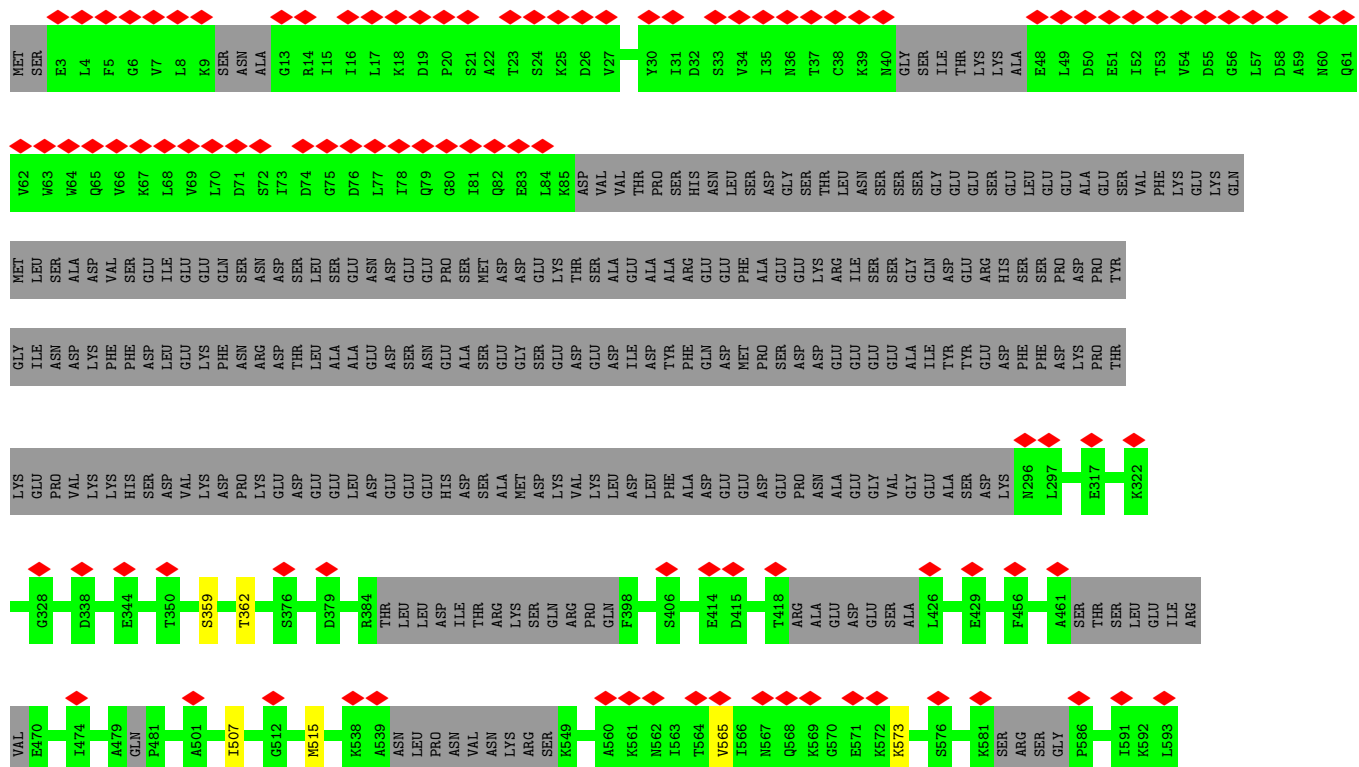




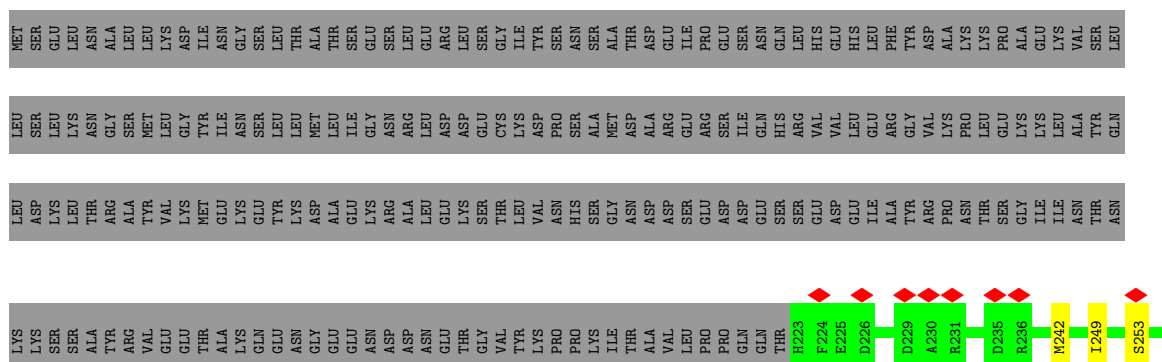
• Molecule 33: U3 small nucleolar ribonucleoprotein protein IMP3



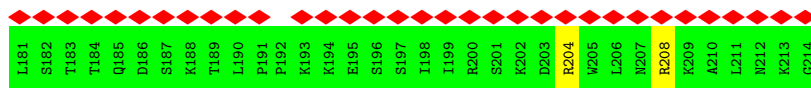
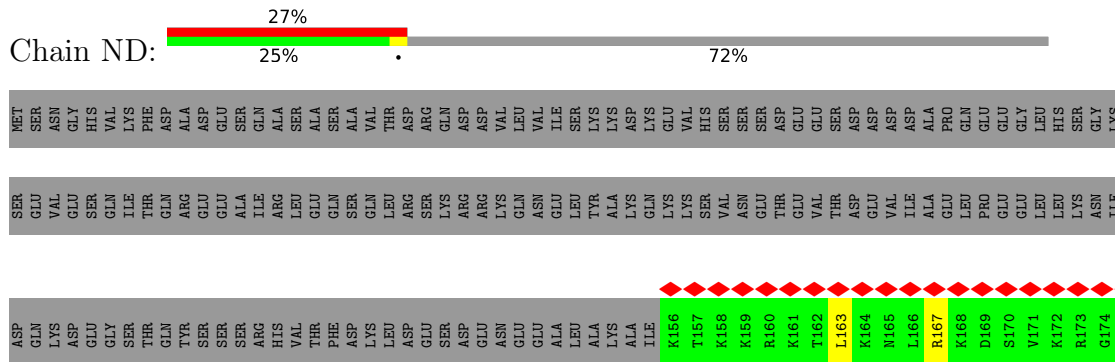
• Molecule 34: U3 small nucleolar RNA-associated protein MPP10



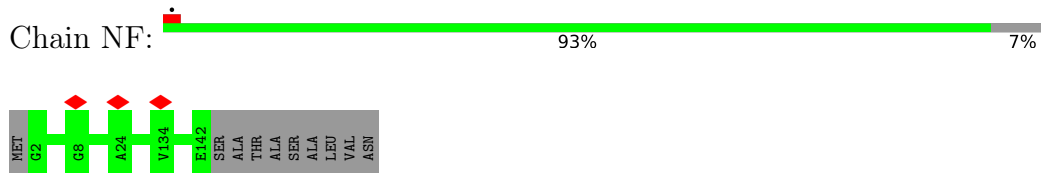
Chain NB:



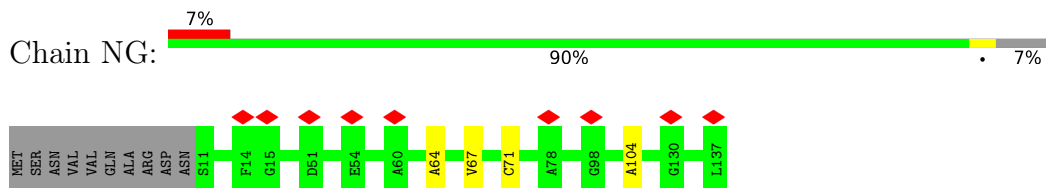
- Molecule 37: Bud site selection protein 21



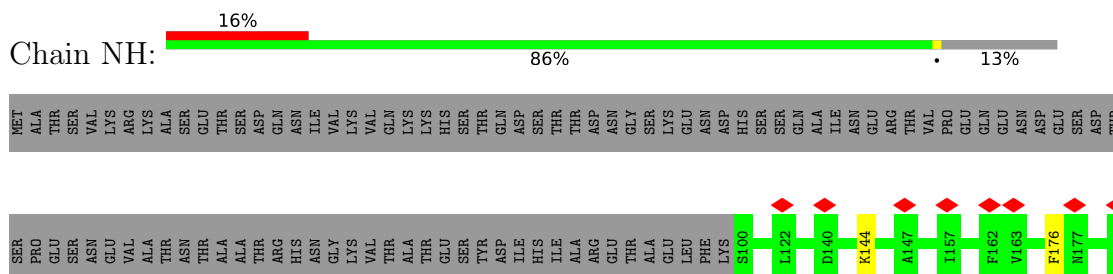
- Molecule 38: 40S ribosomal protein S13

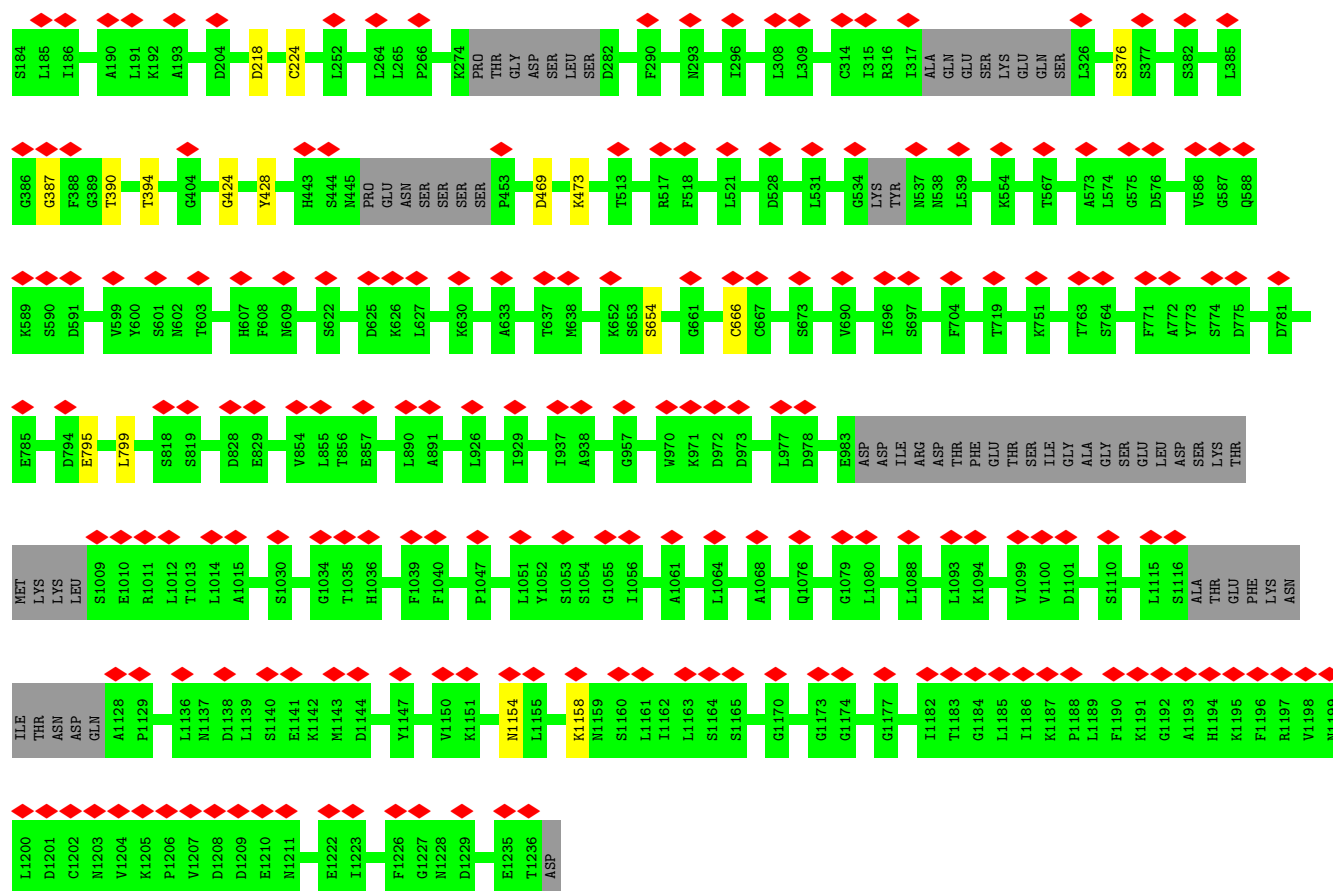


- Molecule 39: 40S ribosomal protein S14-A

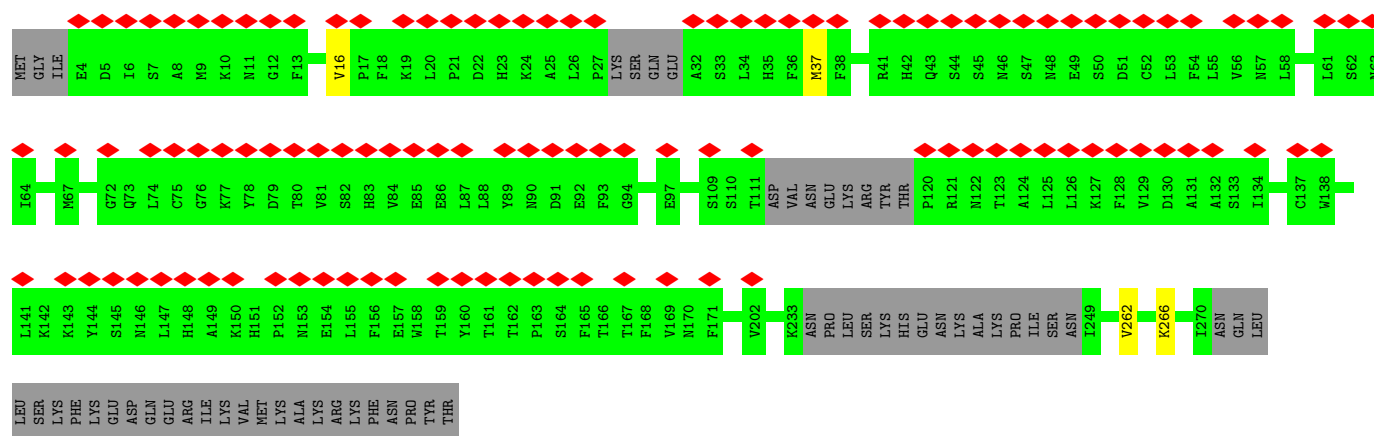
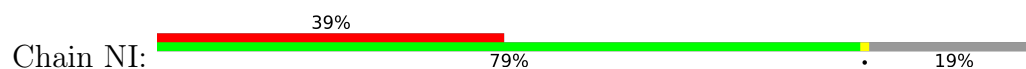


- Molecule 40: U3 small nucleolar RNA-associated protein 22

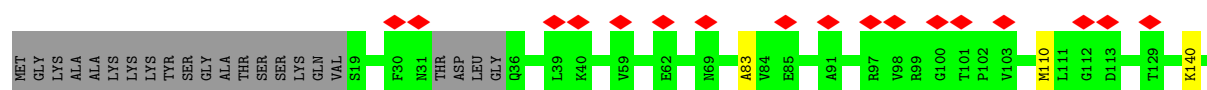
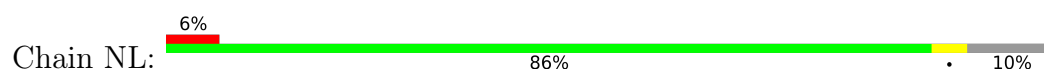


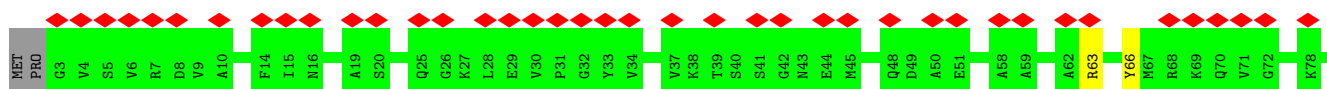


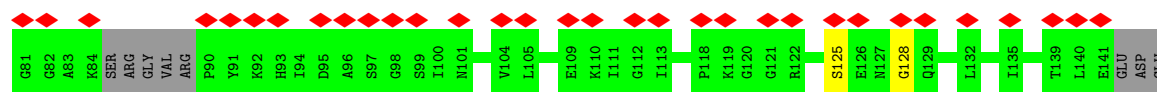
• Molecule 41: Ribosomal RNA-processing protein 7



• Molecule 42: Dimethyladenosine transferase

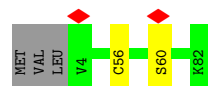






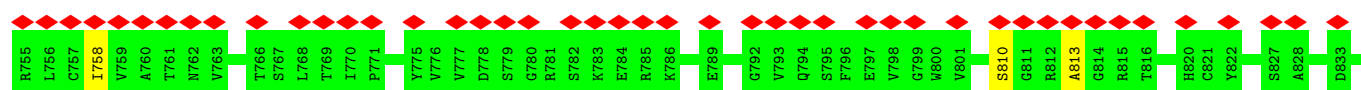
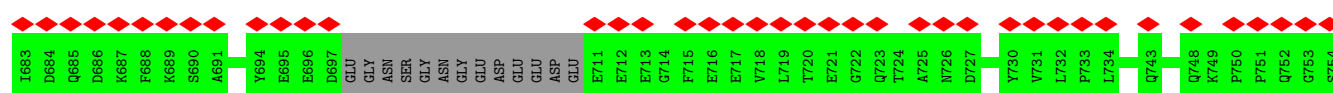
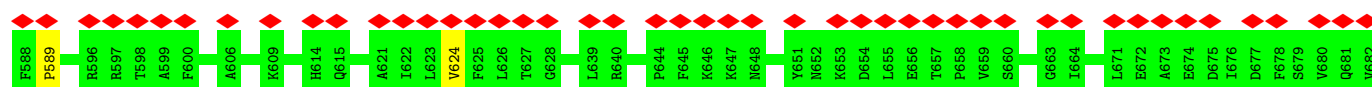
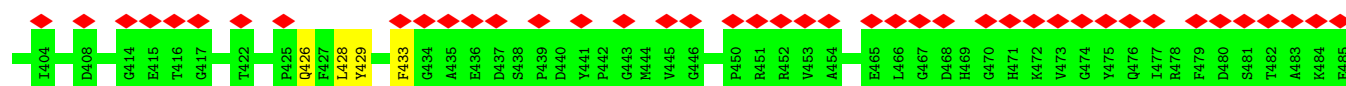
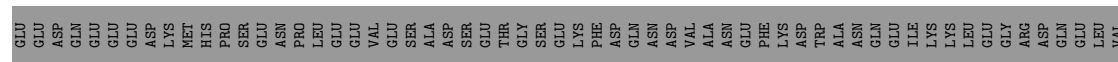
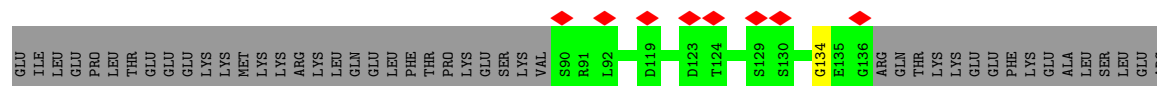
- Molecule 46: 40S ribosomal protein S27-A

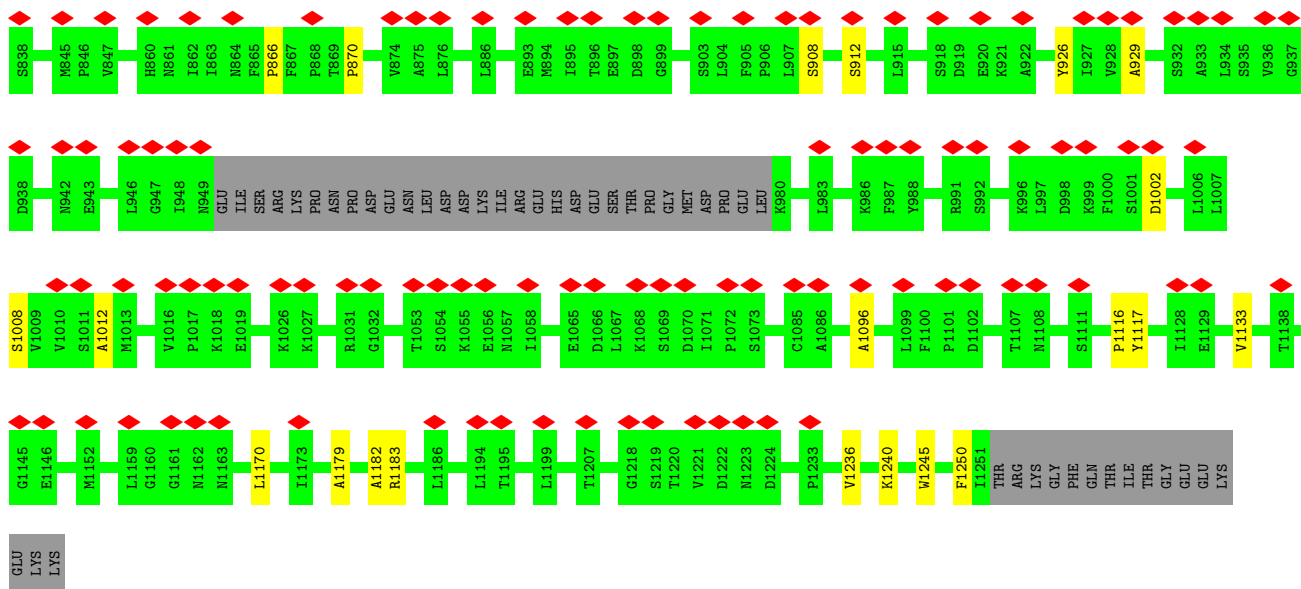
Chain NQ: 94%



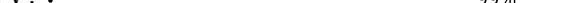
- Molecule 47: Probable ATP-dependent RNA helicase DHR1

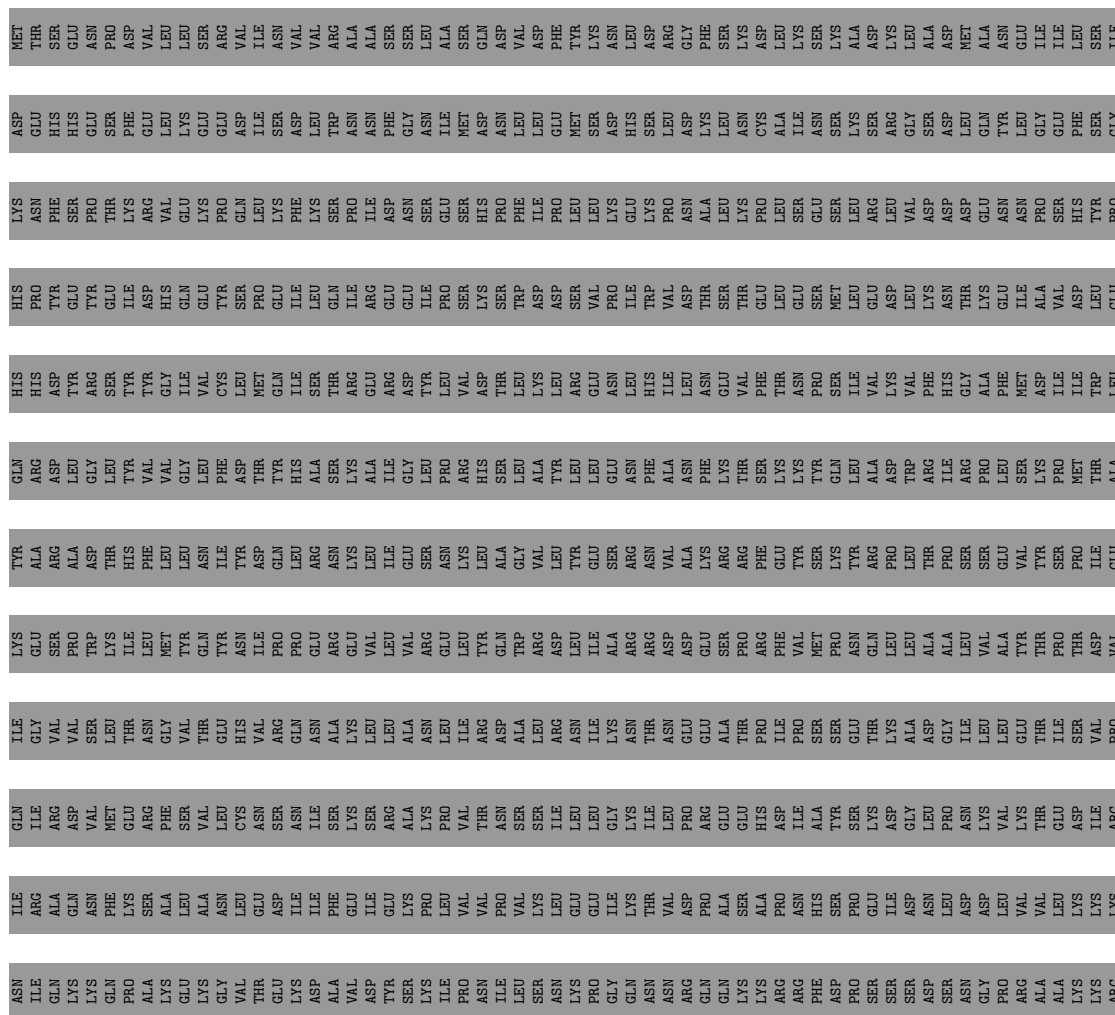
Chain NS: 27% 67% 30%



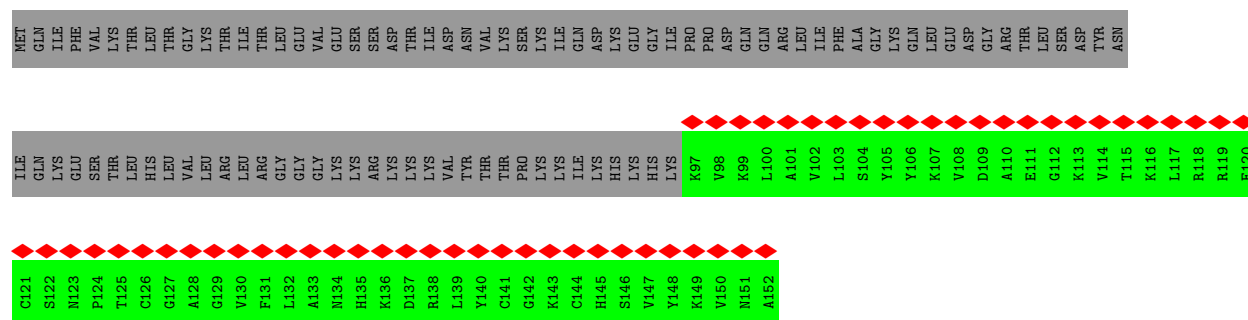


- Molecule 48: Exosome complex exonuclease RRP6

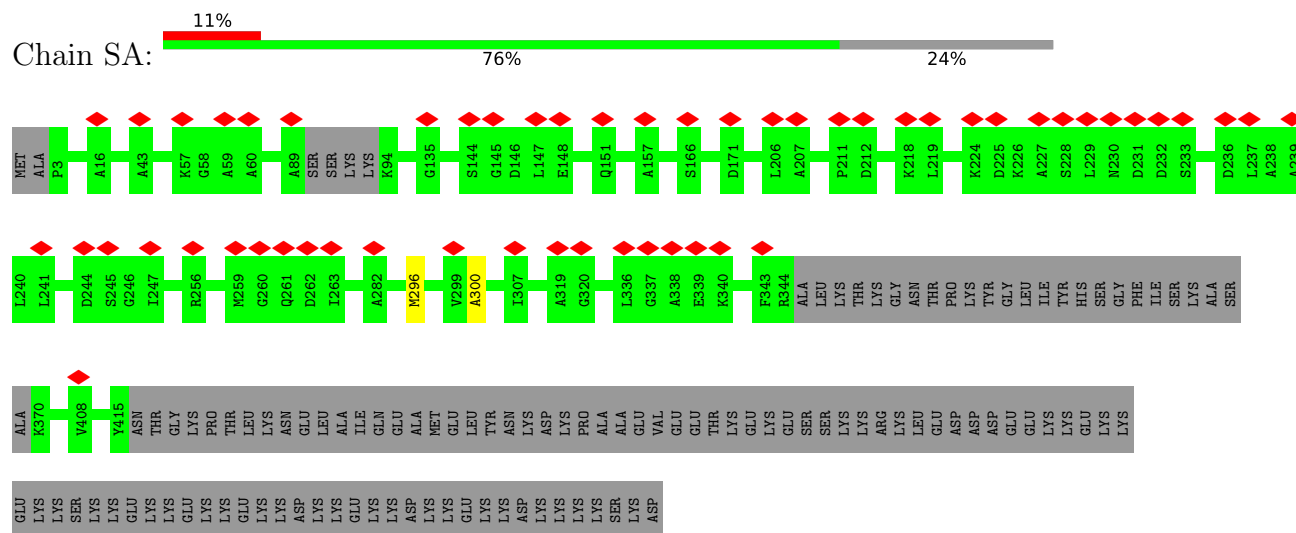
Chain NV:  99%



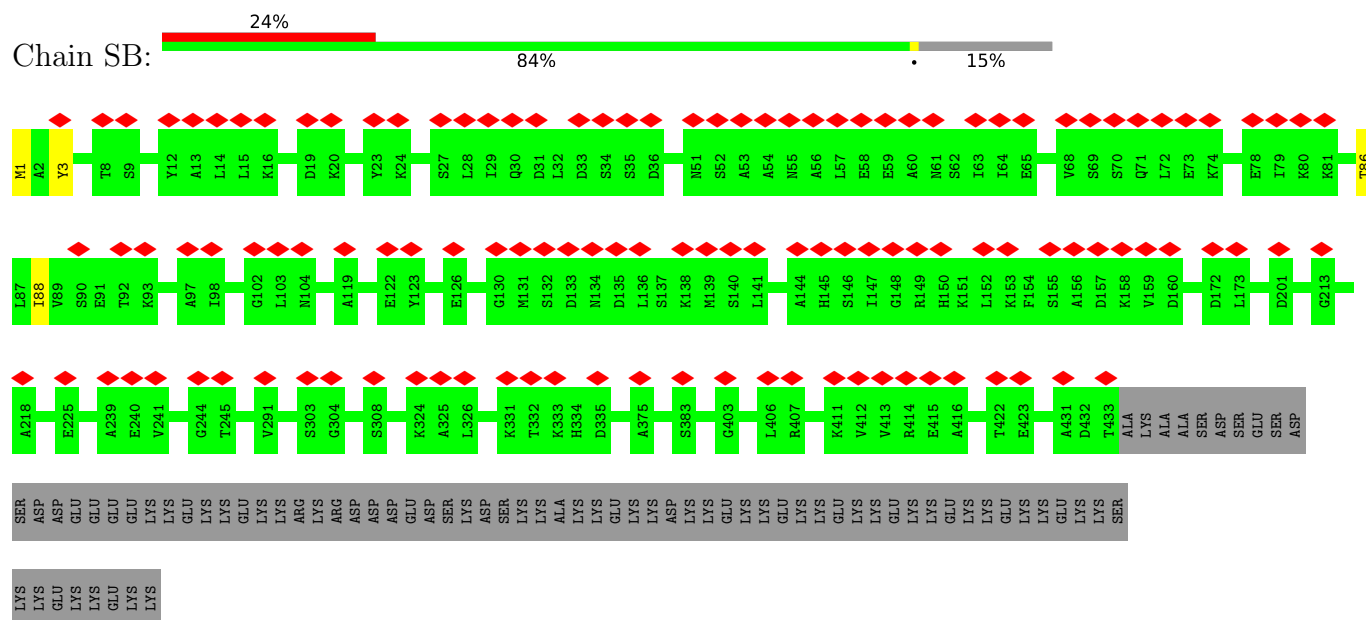




• Molecule 52: Nucleolar protein 56

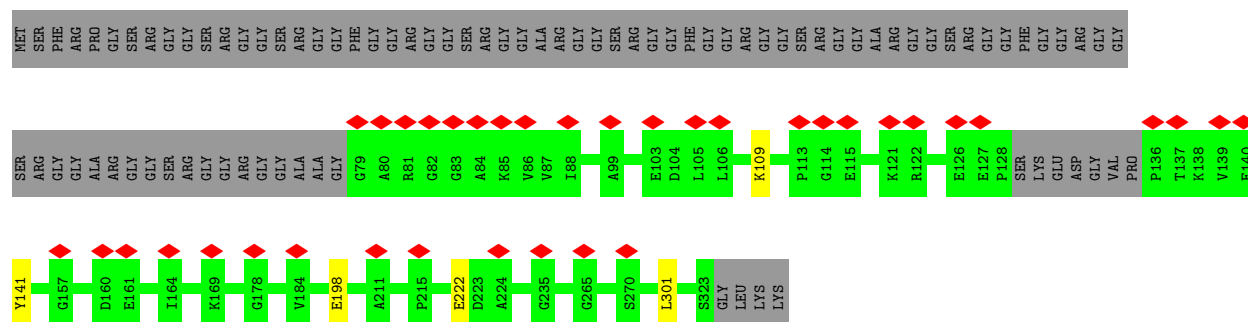


• Molecule 53: Nucleolar protein 58

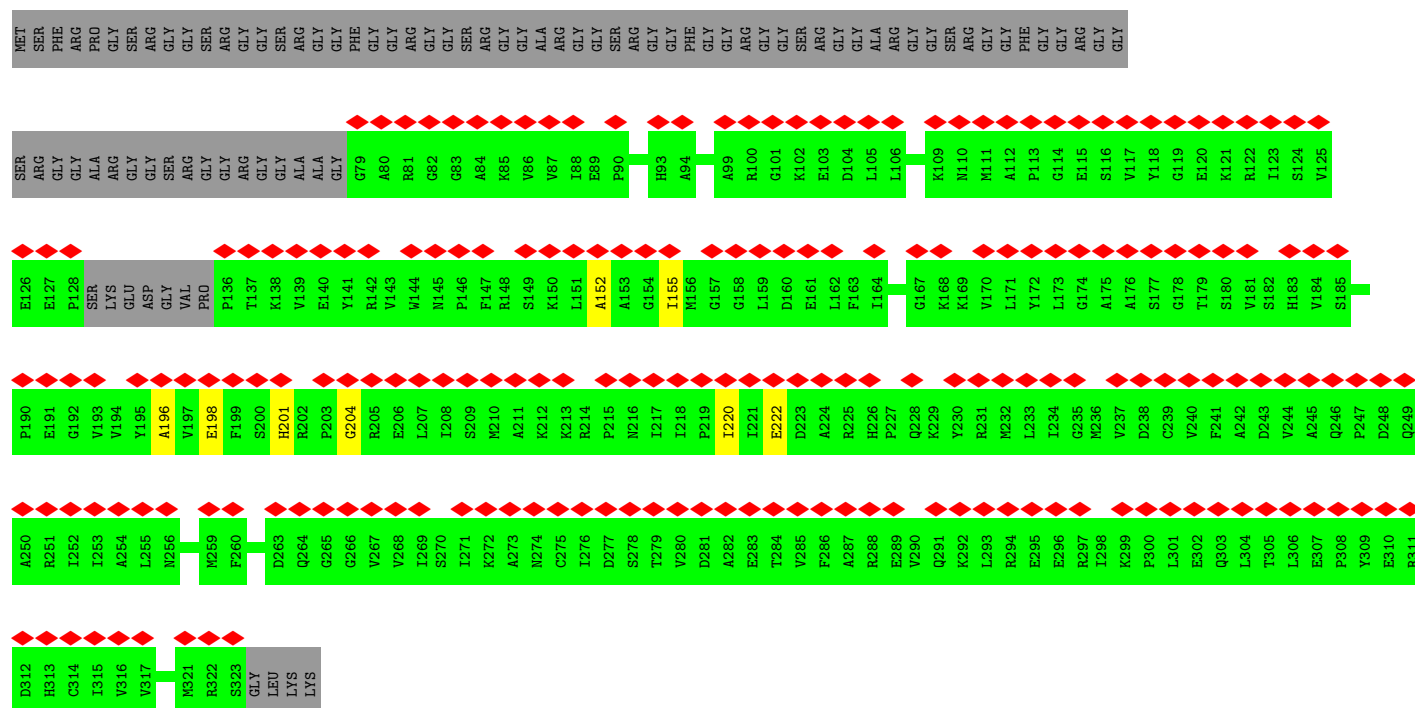
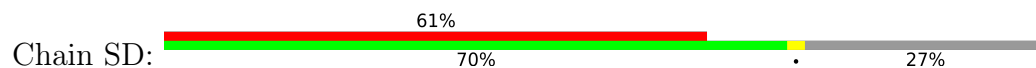


• Molecule 54: rRNA 2'-O-methyltransferase fibrillar

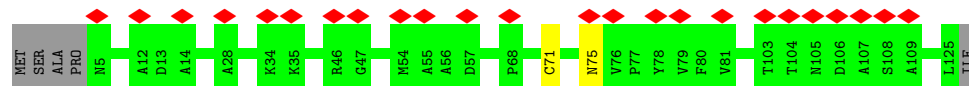




• Molecule 54: rRNA 2'-O-methyltransferase fibrillar



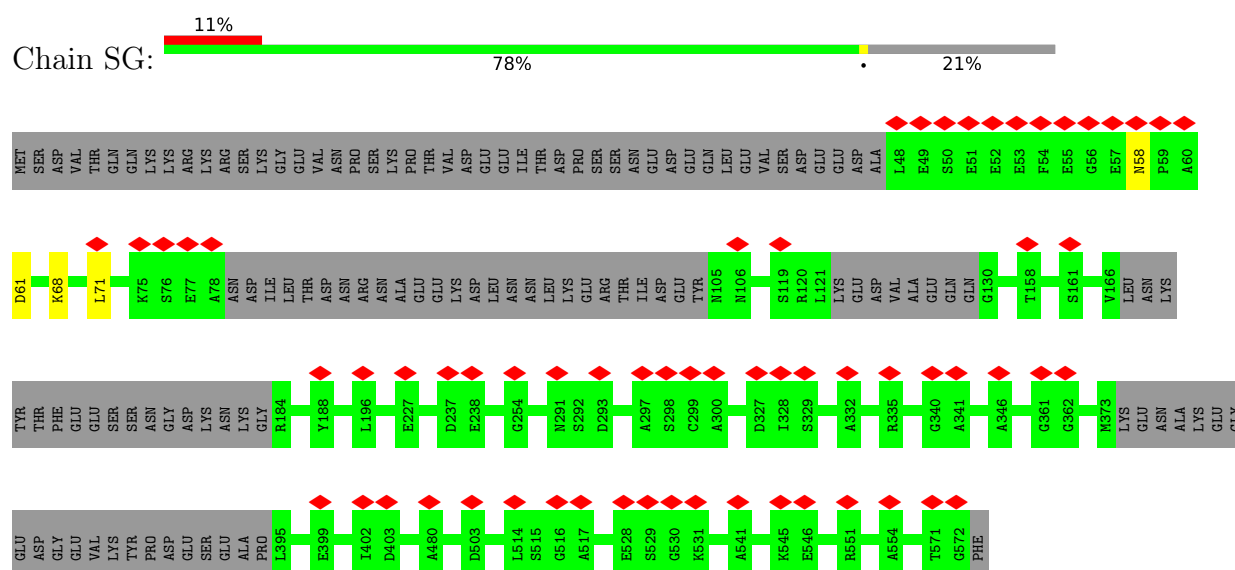
• Molecule 55: 13 kDa ribonucleoprotein-associated protein



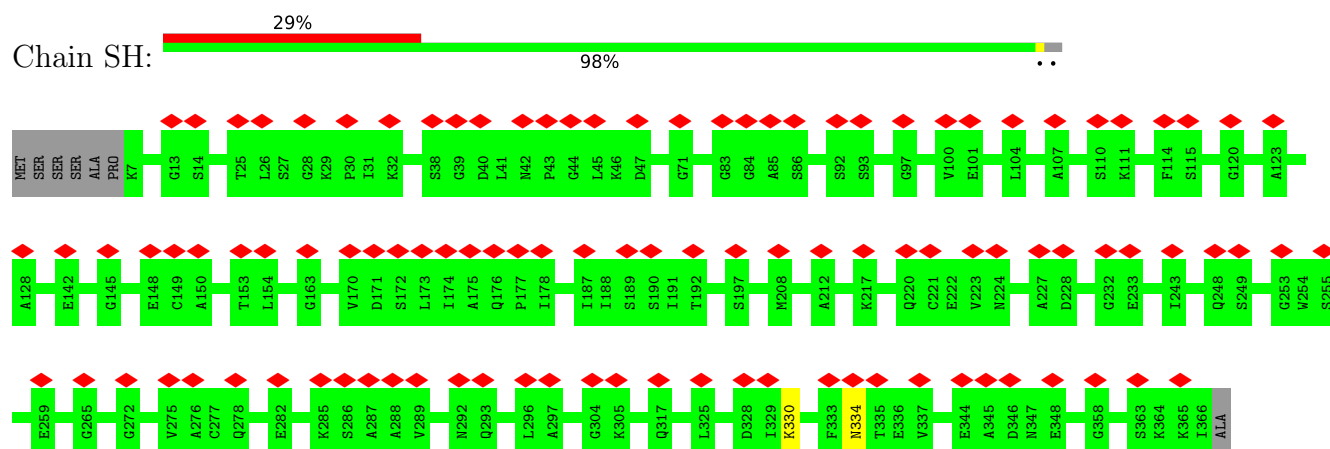
• Molecule 55: 13 kDa ribonucleoprotein-associated protein



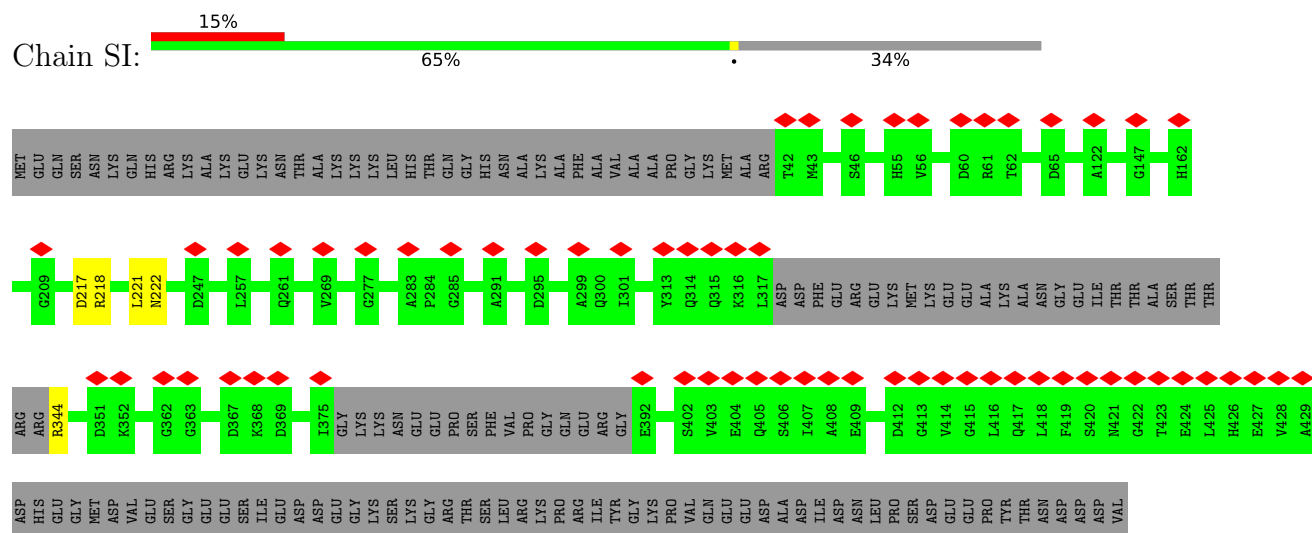
• Molecule 56: Ribosomal RNA-processing protein 9

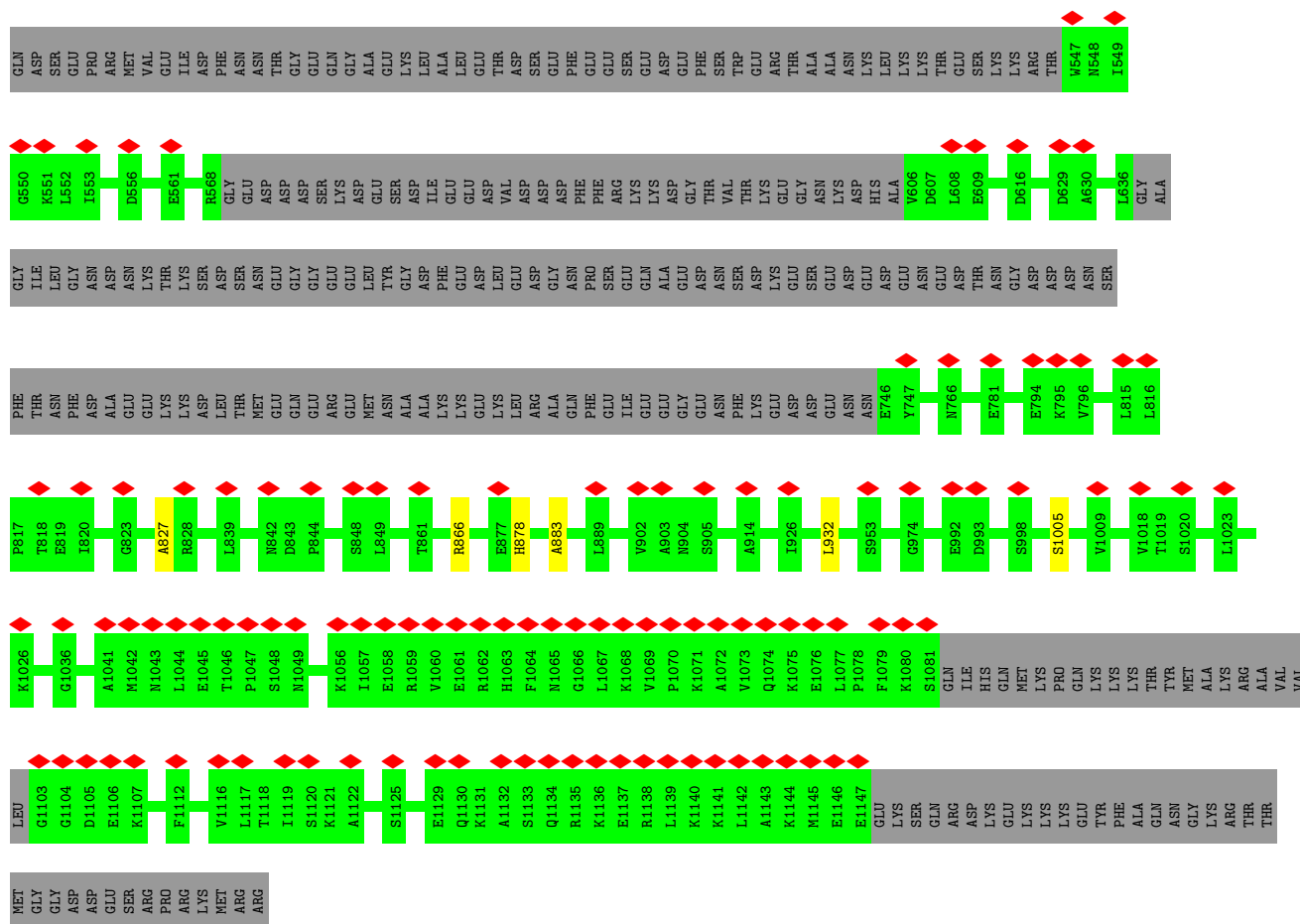


- Molecule 57: RNA 3'-terminal phosphate cyclase-like protein.

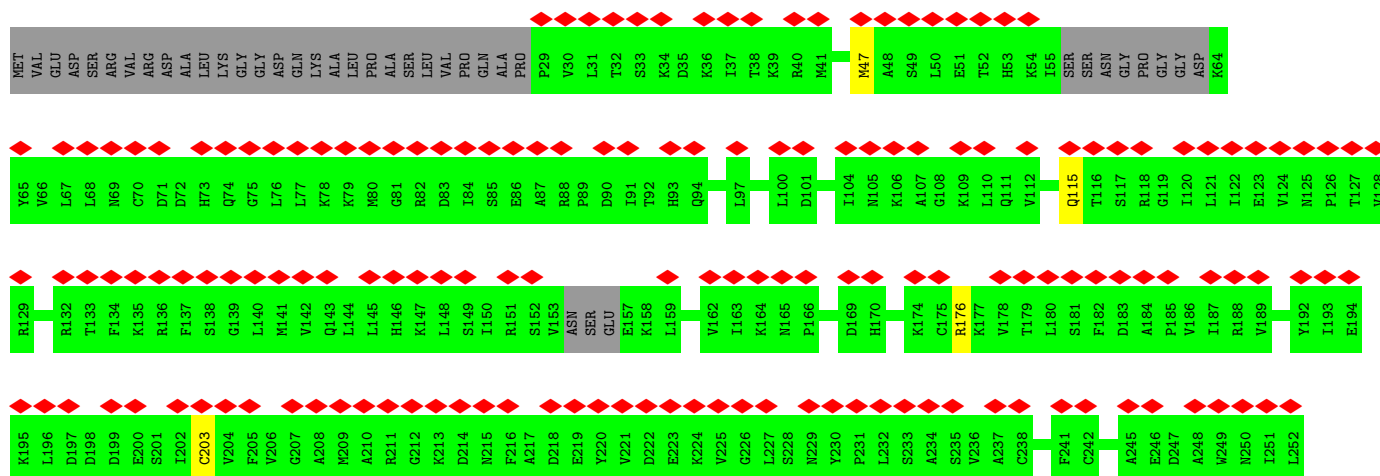
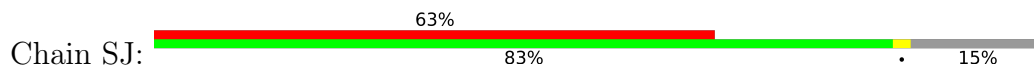


- Molecule 58: Ribosome biogenesis protein BMS1

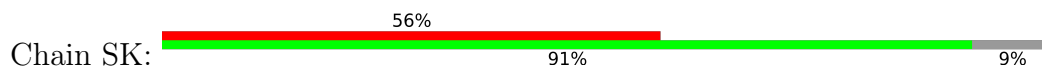


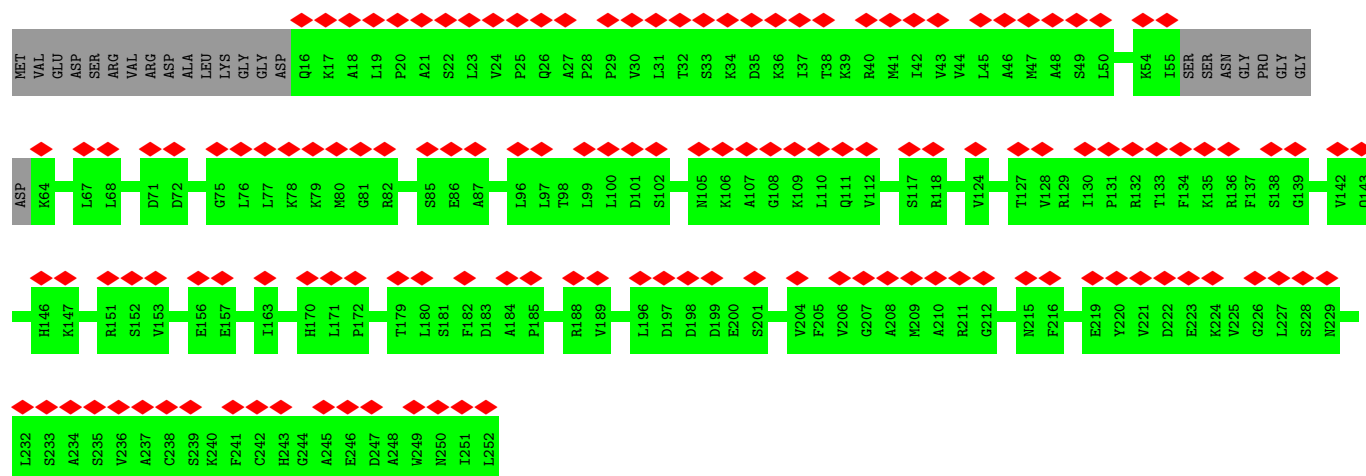


• Molecule 59: Ribosomal RNA small subunit methyltransferase NEP1



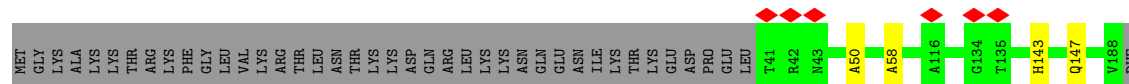
• Molecule 59: Ribosomal RNA small subunit methyltransferase NEP1





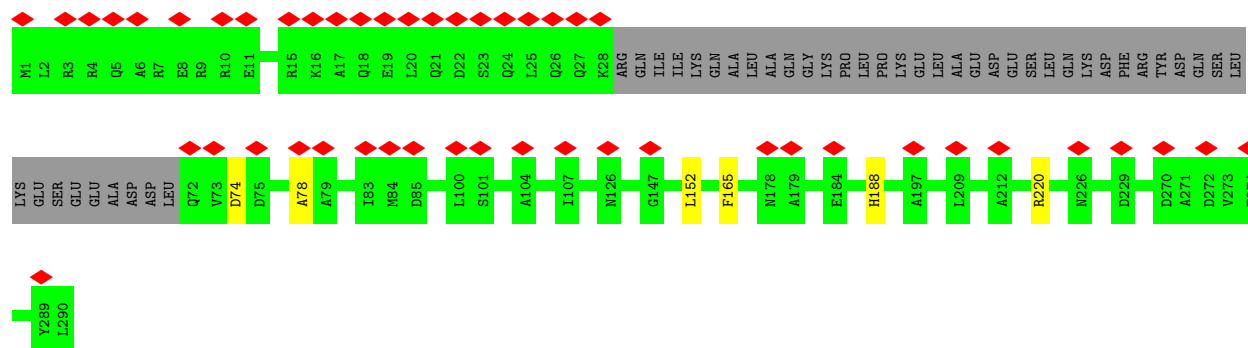
- Molecule 60: rRNA-processing protein FCF1

Chain SL: 76% 22%



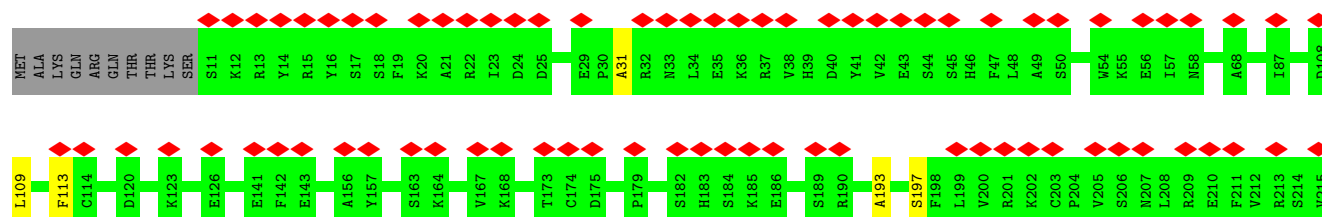
- Molecule 61: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM: 17% 83% 15%



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

Chain SP: 42% 86% 14%

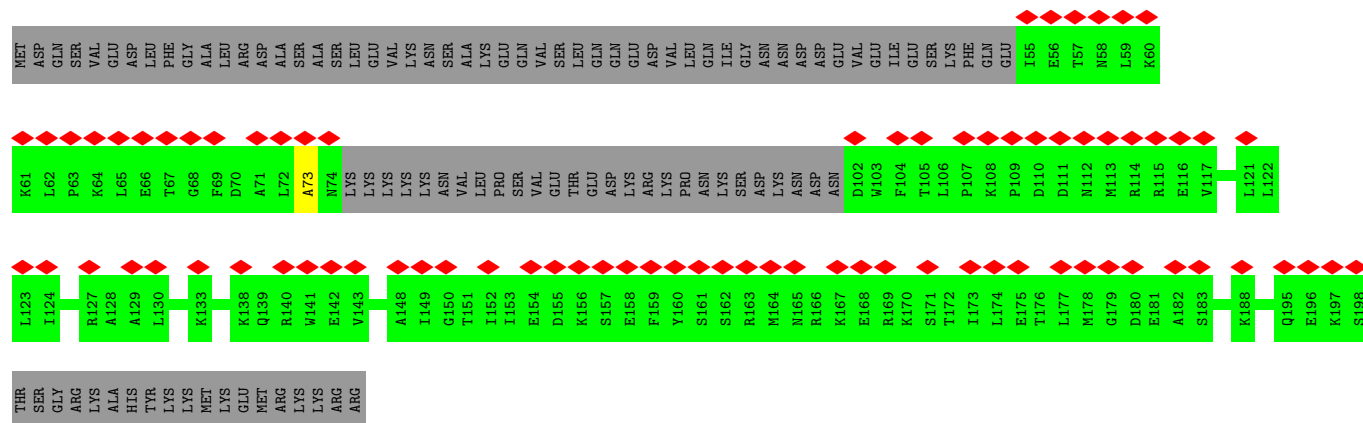




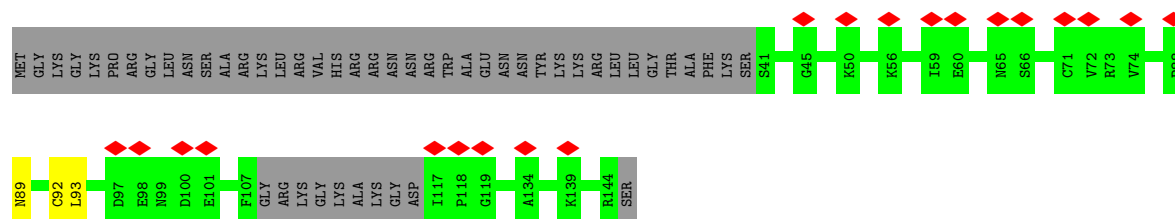
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HIS	ARG	MET	ASP	SER	PHE	MET	ASN	SER	LYS	ILE	GLU	LYS	GLN	VAL	CYS	ILE	LEU	GLN	VAL	THR	VAL	GLN	GLY	THR	LEU	ASP	LEU	VAL	GLU	GLY	GLU	PRO	LYS	THR	ILE	GLN	VAL	LEU	THR	VAL	GLN	THR	LEU	GLY	THR	ARG	ASP	GLU	THR	ALA						
H2226	G2227	F2228	K2229	L2230	T2231	W2232	D2233	G2234	T2235	L2236	T2237	C2238	L2239	L2240	Y2241	W2245	Q2248	S2249	A2250	A2251	L2252	V2254	H2255	Q2256	L2257	T2258	A2259	N2260	LYS	ASP	LYS	LEU	GLU	ILE	ASP	LEU	GLN	HIS	THR	ARG	LEU	GLY	PRO	SER												
K2150	D2153	N2154	A2155	N2159	L2160	T2164	V2167	Y2168	L2169	K2170	G2173	F2174	E2175	H2176	T2177	I2178	E2179	L2180	L2183	A2184	R2187	I2188	I2191	L2192	S2193	D2194	T2195	S2196	V2197	A2198	S2199	E2200	H2201	Q2202	W2203	D2204	N2211	T2212	F2213	S2214	N2217	E2218	A2219	T2220	E2221	S2222	Y2224	K2225								
E2049	Y2050	D2051	Q2052	S2053	K2054	G2055	Q2060	F2061	K2062	E2073	S2074	G2075	V2079	T2088	K2089	A2090	N2091	L2094	L2095	S2096	K2097	L2098	S2101	F2102	V2107	N2112	D2113	D2114	A2115	P2116	R2117	C2118	R2119	E2120	S2127	T2128	K2132	L2133	E2134	D2137	L2138	E2139	I2140	Y2144	I2145	L2149										
V1947	S1948	P1949	S1950	T1951	S1952	Q1957	N1958	F1962	A1965	F1966	I1967	D1971	S1972	T1973	L1974	K1975	D1976	T1977	S1980	P1988	D1989	L1990	M1991	E1992	P1993	S1994	R1995	Q1996	G1997	L1998	A1999	S2008	K2009	H2010	T2011	M2012	L2016	T2019	A2020	E2025	V2028	T2029	V2038	Y2043	H2048											
ASN	LEU	GLU	SER	LYS	THR	THR	N1868	S1869	N1880	D1874	L1875	V1879	R1882	F1886	L1887	T1888	L1892	E1893	G1894	F1895	I1896	P1897	F1898	L1899	L1903	L1904	E1906	N1907	I1912	S1913	T1914	L1915	I1922	R1923	L1924	E1929	S1930	F1934	K1940	V1941	L1942	N1943	I1944	I1945	K1946											
SER	GLU	ASN	TYR	HIS	THR	LYS	V1742	K1743	E1744	I1745	K1746	I1756	N1760	I1761	M1778	R1795	Y1796	S1806	E1807	S1808	E1809	S1810	I1811	Q1817	L1818	F1819	MET	SER	ASN	SER	PRO	GLN	ILE	PRO	LYS	LYS	VAL	ASP	GLN	VAL	ASP	GLU	LYS	GLU	ASP	PHE	LEU	VAL								
G1622	L1623	T1624	N1625	D1626	D1627	F1631	N1638	R1644	S1645	K1646	S1647	D1652	A1653	L1665	G1666	A1667	L1670	V1671	E1676	L1677	R1683	G1684	S1685	Q1686	V1689	L1690	G1703	V1704	H1707	S1708	D1709	L1710	S1713	S1714	I1721	M1722	I1725	F1728	ALA	GLY	GLU	GLU	LYS	ASP												
L1551	S1552	L1555	R1556	E1557	T1558	L1559	V1562	R1563	ASP	GLY	ALA	GLU	SER	LYS	LEU	T1571	L1572	S1573	K1574	F1575	P1576	S1577	N1578	L1579	D1580	E1581	P1582	S1583	Q1588	E1589	L1590	T1593	L1594	S1595	K1596	I1597	D1602	D1603	E1604	T1605	I1606	I1607	P1611	I1612	A1613	E1614	A1615	L1616	V1620	L1621						
R1468	L1469	G1470	E1471	H1472	H1473	H1474	Q1475	N1479	S1482	H1483	Y1484	M1488	I1489	E1490	H1491	D1496	D1497	E1498	R1499	Y1500	I1503	G1504	N1505	E1506	T1507	Q1508	I1511	G1512	G1513	L1514	A1515	M1518	N1521	Q1522	Y1523	K1524	A1525	R1528	I1531	K1535	T1536	K1537	P1538	N1539	Q1540	M1541	L1547									
P1400	N1401	T1402	R1403	L1404	G1405	L1406	R1407	D1408	S1409	L1410	E1411	E1412	V1413	Q1414	Y1417	V1420	L1421	V1425	K1426	R1427	T1428	K1429	Y1430	F1431	T1432	D1433	F1434	E1435	D1436	M1437	A1438	L1439	L1440	L1441	Y1442	N1443	G1444	D1445	E1446	E1447	A1448	D1449	F1450	F1451	T1452	N1453	V1454	N1455	P1456	N1457	Q1458	R1464	L1465	L1466	K1467	
Y1336	K1337	S1340	E1341	L1342	E1343	W1344	L1345	P1346	L1347	L1348	F1349	T1350	F1351	L1352	H1353	F1354	T1355	N1356	N1357	K1358	E1359	E1360	L1361	A1362	L1363	L1364	T1365	N1366	A1367	S1368	H1372	I1375	D1376	F1377	I1378	N1379	E1380	K1381	P1382	N1383	L1384	N1385	E1386	A1387	S1388	K1389	T1390	T1391	S1392	M1393	L1394	K1395	D1396	T1397	L1398	L1399

ARG
SER
GLN
ARG
GLU
SER
LYS
VAL
GLU
ASP
GLY
LYS
HIS
LEU
PHE
GLY
LYS
ASP
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GLN
ARG
SER
ASN
LYS
LYS
ARG
LYS
ALA

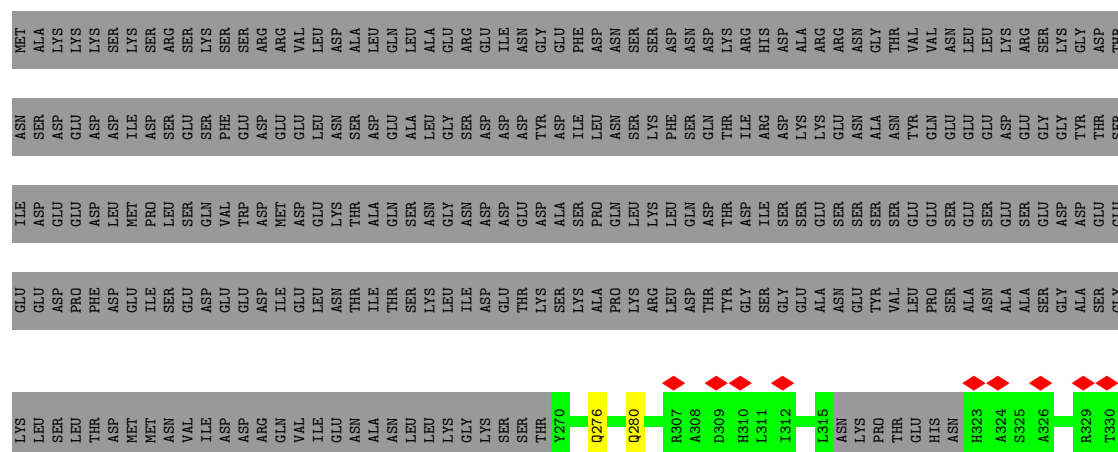
• Molecule 63: rRNA-processing protein FCF2

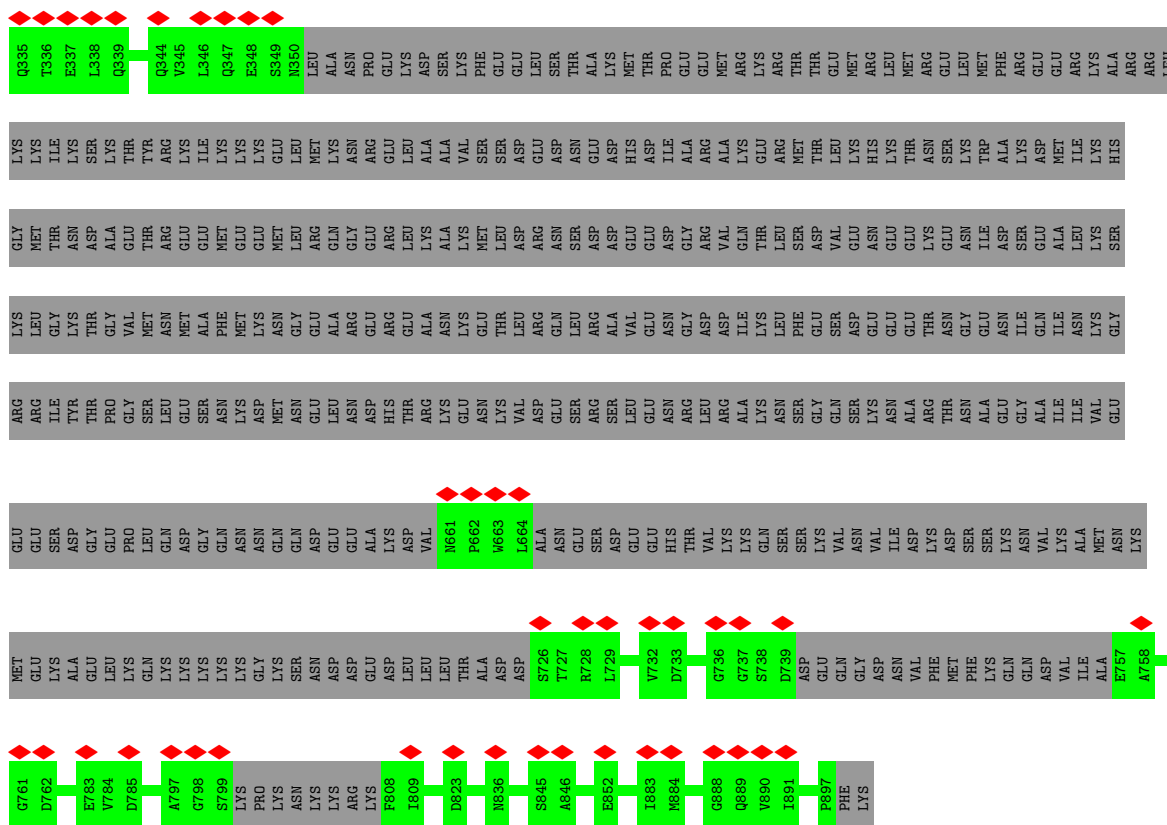


• Molecule 64: 40S ribosomal protein S23-A

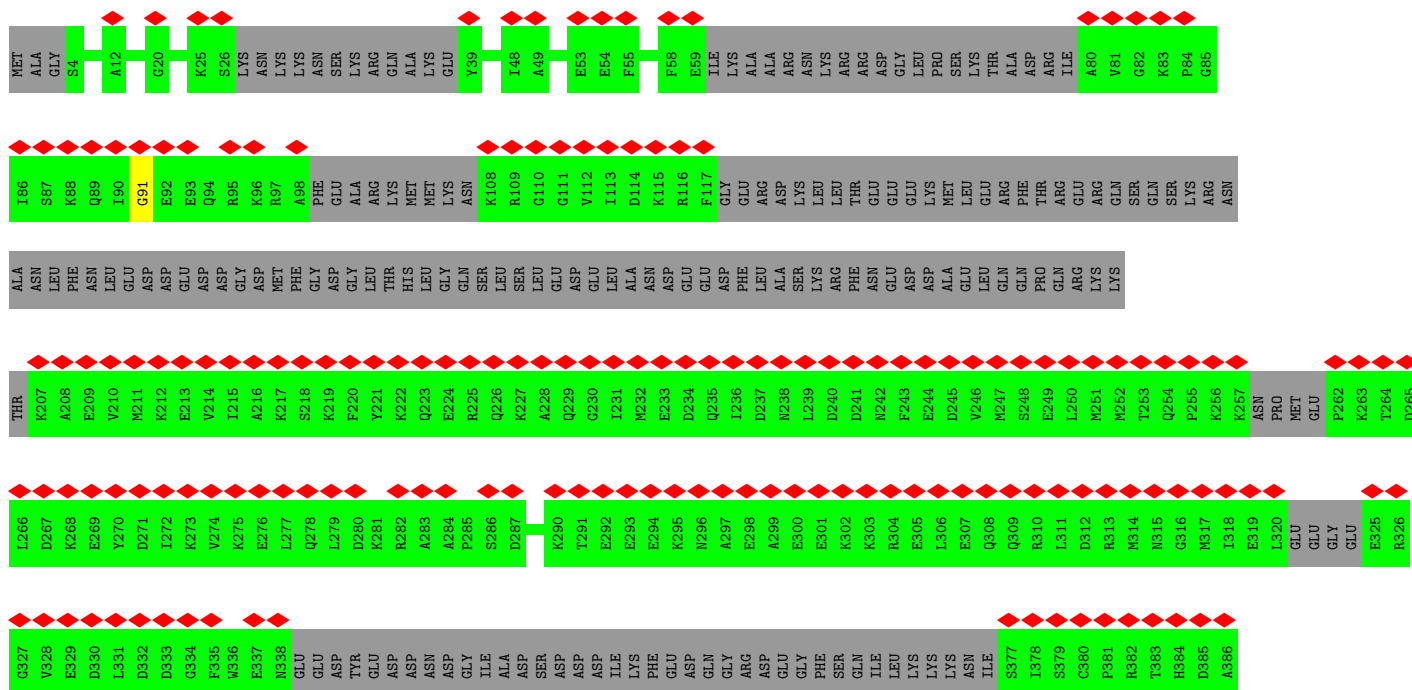
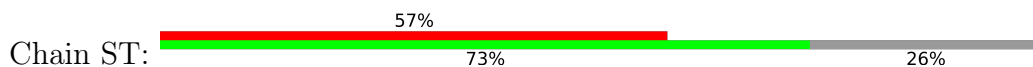


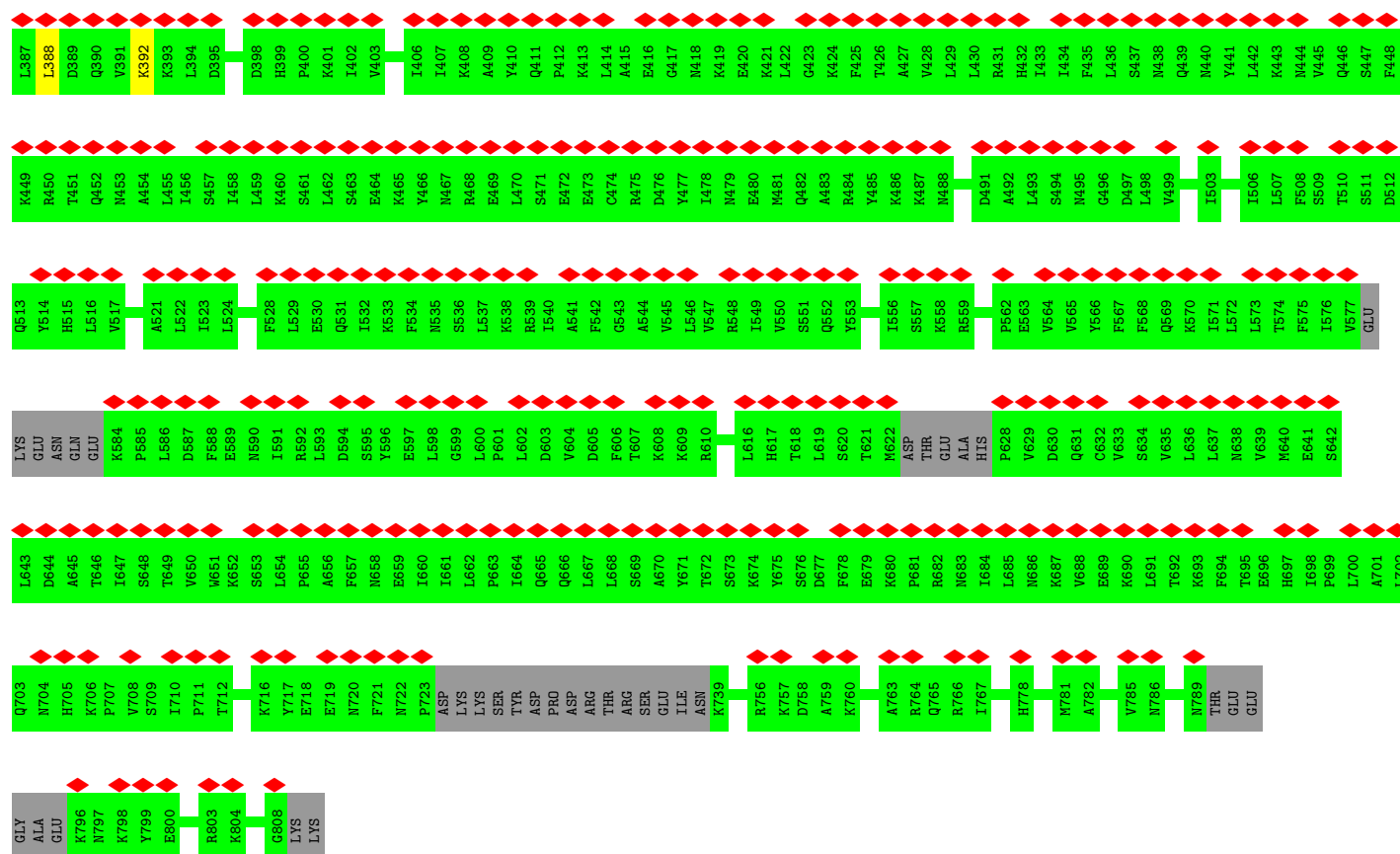
• Molecule 65: U3 small nucleolar RNA-associated protein 14





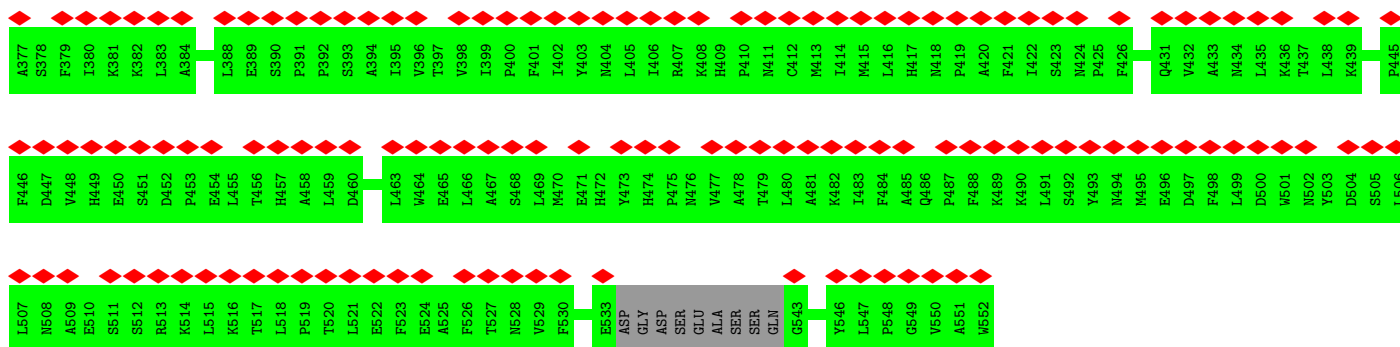
- Molecule 66: Nucleolar complex protein 14



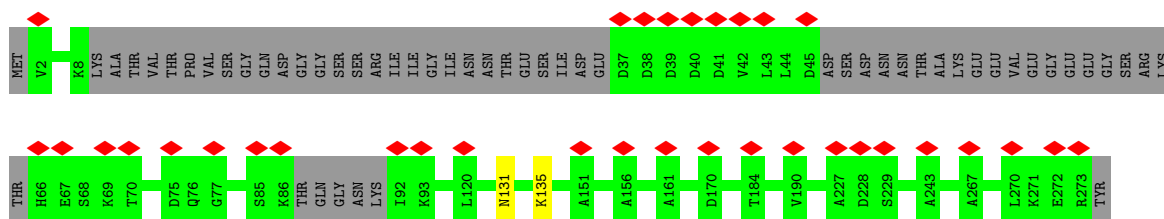
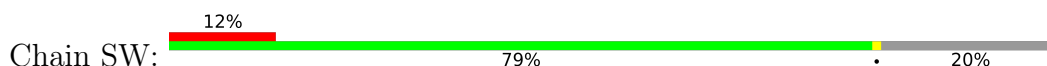


• Molecule 67: Nucleolar complex protein 4

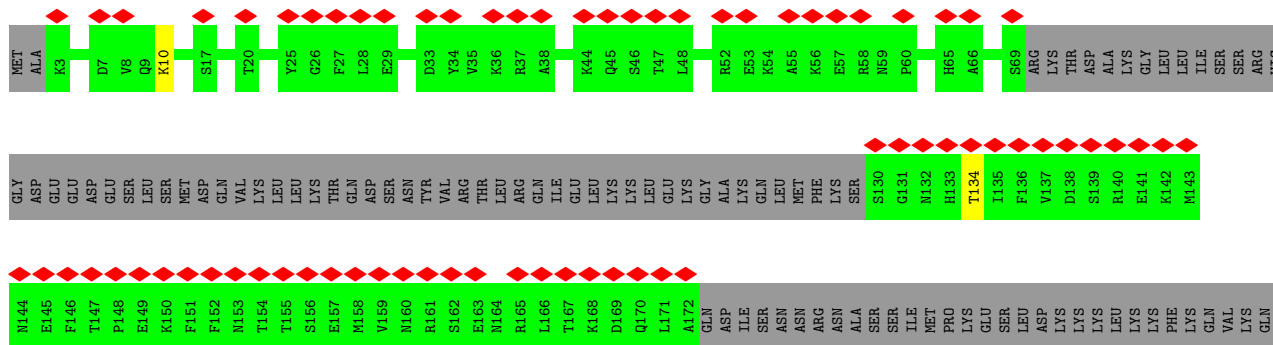




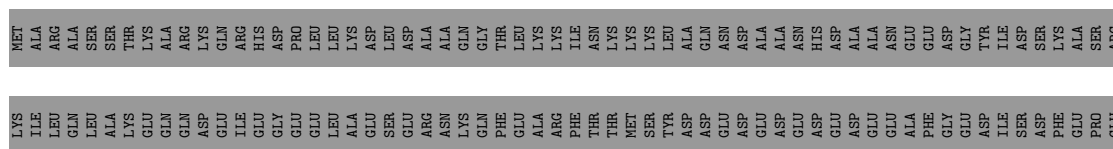
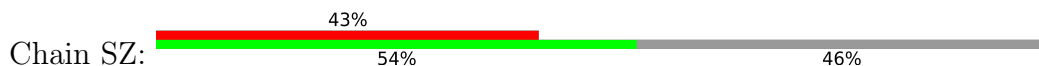
- Molecule 68: Pre-rRNA-processing protein PNO1



- Molecule 69: U3 small nucleolar RNA-associated protein 11



- Molecule 70: Essential nuclear protein 1



D438	F439	L440	L441	E442	T443	V444	R447	G448	H449	K450	D451	I452	G453	P454	E455	I456	R457	R458	E459	L460	L461	A462	G463	A464	S465	R466	GLU	PHE	VAL	ASP	PRO	GLN	GLU	ALA	ASN	ASP	ASP	LEU	MET	ILE	ASP	VAL	ASN															
V370	F371	I372	K373	I374	L375	L376	D377	Y380	A381	L382	Q385	T386	V387	D388	D389	C390	V391	Y392	Y393	F394	M395	R396	I399	L400	ASP	ASP	GLY	S404	N405	G406	E407	D408	A409	T410	R411	V412	L413	P414	V415	I416	A420	F421	F424	A425	Y428	K429	N430	D431	Q434	D435	Q436	R437						
Y304	R305	A306	K309	S310	L311	Y312	P314	S315	A316	F317	F318	K319	G320	F321	L322	F323	P324	L325	V326	E327	T328	N331	V332	R333	E334	A335	A338	G339	S340	V341	L342	A343	K344	V345	S346	V347	P348	A349	L350	H351	S352	S353	A354	A355	L356	L359	L360	R361	L362	P363	F364	T368	T369					
N241	W242	Q243	D244	V245	I246	Y247	V248	T249	N250	P251	E252	E253	W254	S255	P256	H257	V258	V259	Y260	E261	A262	T263	K264	L265	F266	V267	S268	N269	L270	T271	A272	K273	E274	S275	Q276	K277	F278	I279	N280	L281	T282	L283	L284	E285	R286	F287	R288	D289	N290	I291	E292	T293	S294	E295	S298	H302	I303	
GLU	PRO	LEU	ALA	ASN	GLU	GLN	ASN	THR	SER	ARG	GLY	ASN	ILE	ASP	SER	SER	GLY	GLN	GLY	VAL	A205	L206	P207	ASP	E208	K209	V210	I211	K212	A213	Y214	T215	T216	V217	G218	S219	I220	L221	K222	T223	W224	T225	H226	G227	K228	L229	P230	K231	L232	F233	K234	V235	I236	P237	S238	L239	R240	
GLY	ASP	TYR	LYS	GLU	GLU	ILE	VAL	GLU	ILE	ASP	GLU	GLU	ASP	ALA	ALA	MET	PHE	GLU	GLN	TYR	PHE	LYS	LYS	SER	SER	ASP	PHE	ASN	SER	LEU	SER	GLY	SER	TYR	ASN	LEU	ALA	ASP	LYS	ILE	MET	ALA	SER	SER	ILE	ARG	GLU	LYS	GLU	SER	GLN	VAL	GLU	ASP	MET	GLN	ASP	ASP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4987	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	4.783	Depositor
Minimum map value	0.000	Depositor
Average map value	0.116	Depositor
Map value standard deviation	0.209	Depositor
Recommended contour level	1	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: SEP

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	0.11	0/1529	0.29	0/2372
2	L1	0.09	0/30206	0.26	0/47024
3	L2	0.09	0/3417	0.26	0/5305
4	L3	0.16	0/529	0.39	0/736
5	L4	0.15	0/1182	0.39	0/1650
6	L5	0.17	0/1046	0.42	0/1464
7	L6	0.17	0/1035	0.36	0/1442
8	L7	0.22	0/911	0.55	0/1276
9	L8	0.17	0/850	0.39	0/1181
10	L9	0.19	0/922	0.54	0/1290
11	LC	0.18	0/647	0.47	0/903
12	LD	0.15	0/700	0.36	0/980
13	LE	0.22	0/642	0.58	0/893
14	LF	0.20	0/486	0.54	0/677
15	LG	0.15	0/310	0.39	0/430
16	LH	0.19	1/4046 (0.0%)	0.41	2/5644 (0.0%)
17	LI	0.15	0/3042	0.38	0/4250
18	LJ	0.14	0/2410	0.37	0/3370
19	LK	0.59	2/667 (0.3%)	0.84	5/933 (0.5%)
20	LL	0.14	0/2448	0.36	0/3415
21	LM	0.12	0/8150	0.30	0/11410
22	LN	0.14	0/3326	0.36	0/4637
23	LO	0.14	0/3976	0.35	0/5552
24	LP	0.12	0/1907	0.34	0/2667
25	LQ	0.17	0/4075	0.43	0/5682
26	LR	0.14	0/3980	0.36	0/5555
27	LS	0.18	0/2288	0.38	0/3188
28	LT	0.13	0/4367	0.34	0/6091
29	LU	0.15	0/2284	0.42	0/3190
30	LV	0.15	0/1804	0.41	0/2522
31	LW	0.17	0/2322	0.42	0/3243
32	LX	0.14	0/4337	0.36	0/6068

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LY	0.12	0/4310	0.32	0/6033
33	LZ	0.17	0/812	0.41	0/1136
34	NA	0.13	0/1654	0.34	0/2299
35	NB	0.14	0/1162	0.37	0/1618
36	NC	0.18	0/669	0.49	0/931
37	ND	0.13	0/298	0.37	0/416
38	NF	0.16	0/717	0.40	0/1003
39	NG	0.16	0/634	0.40	0/881
40	NH	0.13	0/5489	0.34	0/7686
41	NI	0.13	0/1214	0.34	0/1695
42	NL	0.19	0/1460	0.45	0/2045
43	NM	0.13	0/1185	0.34	0/1651
44	NN	0.12	0/216	0.35	0/300
45	NP	0.15	0/669	0.39	0/928
46	NQ	0.15	0/401	0.38	0/560
47	NS	0.18	0/4540	0.43	1/6357 (0.0%)
48	NV	0.21	0/38	0.48	0/51
49	OA	0.11	0/68	0.35	0/93
50	OH	0.09	0/595	0.25	0/827
51	OU	0.10	0/278	0.30	0/386
52	SA	0.13	0/1931	0.34	0/2693
53	SB	0.13	0/2168	0.35	0/3028
54	SC	0.17	0/1210	0.46	0/1689
54	SD	0.15	0/1210	0.42	0/1689
55	SE	0.18	0/621	0.43	0/871
55	SF	0.19	0/621	0.43	0/871
56	SG	0.14	0/2263	0.37	0/3150
57	SH	0.16	0/1817	0.42	0/2536
58	SI	0.16	0/3975	0.39	0/5560
59	SJ	0.13	0/1080	0.32	0/1508
59	SK	0.13	0/1170	0.31	0/1639
60	SL	0.17	0/759	0.41	0/1064
61	SM	0.16	0/1251	0.42	0/1749
62	SP	0.14	0/10900	0.35	0/15259
63	SQ	0.17	0/595	0.43	0/832
64	SR	0.18	0/479	0.45	0/666
65	SS	0.18	0/1150	0.42	0/1604
66	ST	0.12	0/3020	0.30	0/4213
67	SU	0.12	0/2726	0.33	0/3825
68	SW	0.17	0/1111	0.45	0/1550
69	SY	0.16	0/609	0.46	0/846
70	SZ	0.11	0/1326	0.30	0/1859
All	All	0.14	3/168242 (0.0%)	0.36	8/240637 (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
36	NC	0	1
47	NS	0	1
58	SI	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	LK	414	PRO	CG-CD	-11.24	1.12	1.50
16	LH	549	ASN	C-O	7.61	1.27	1.23
19	LK	494	PRO	CG-CD	-7.40	1.25	1.50

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	LK	414	PRO	N-CD-CG	-13.45	83.02	103.20
19	LK	414	PRO	CA-N-CD	-9.27	99.03	112.00
19	LK	494	PRO	CA-N-CD	-9.16	99.17	112.00
19	LK	494	PRO	N-CD-CG	-8.99	89.72	103.20
19	LK	414	PRO	CA-CB-CG	-6.99	91.22	104.50
16	LH	513	GLU	CA-C-N	5.34	130.16	121.83
16	LH	513	GLU	C-N-CA	5.34	130.16	121.83
47	NS	589	PRO	CA-N-CD	-5.21	104.70	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	NC	242	MET	Peptide
47	NS	870	PRO	Peptide
58	SI	866	ARG	Peptide

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	1370	0	692	1	0
2	L1	27015	0	13616	51	0
3	L2	3064	0	1554	8	0
4	L3	529	0	240	1	0
5	L4	1172	0	578	1	0
6	L5	1040	0	519	0	0
7	L6	1029	0	512	2	0
8	L7	903	0	450	4	0
9	L8	848	0	429	1	0
10	L9	914	0	464	4	0
11	LC	642	0	328	2	0
12	LD	693	0	336	0	0
13	LE	640	0	307	0	0
14	LF	484	0	242	3	0
15	LG	309	0	145	0	0
16	LH	4034	0	1821	5	0
17	LI	3027	0	1390	0	0
18	LJ	2394	0	1161	3	0
19	LK	664	0	299	2	0
20	LL	2440	0	1139	2	0
21	LM	8115	0	3739	9	0
22	LN	3315	0	1518	5	0
23	LO	3958	0	1889	3	0
24	LP	1901	0	836	1	0
25	LQ	4063	0	1898	17	0
26	LR	3962	0	1883	7	0
27	LS	2279	0	1110	3	0
28	LT	4347	0	2073	7	0
29	LU	2274	0	1064	3	0
30	LV	1791	0	844	3	0
31	LW	2304	0	1146	5	0
32	LX	4302	0	2100	4	0
32	LY	4274	0	2096	5	0
33	LZ	808	0	370	0	0
34	NA	1654	0	771	3	0
35	NB	1159	0	548	4	0
36	NC	669	0	309	6	0
37	ND	297	0	132	3	0
38	NF	711	0	360	0	0
39	NG	630	0	341	2	0
40	NH	5443	0	2602	9	0
41	NI	1210	0	565	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	NL	1446	0	710	6	0
43	NM	1183	0	553	5	0
44	NN	215	0	111	0	0
45	NP	666	0	345	2	0
46	NQ	398	0	200	1	0
47	NS	4500	0	2179	19	0
48	NV	39	0	16	0	0
49	OA	69	0	34	0	0
50	OH	594	0	298	1	0
51	OU	278	0	135	0	0
52	SA	1924	0	946	1	0
53	SB	2161	0	1090	2	0
54	SC	1198	0	625	3	0
54	SD	1198	0	625	4	0
55	SE	615	0	331	1	0
55	SF	615	0	331	1	0
56	SG	2260	0	1085	2	0
57	SH	1801	0	897	1	0
58	SI	3939	0	1944	6	0
59	SJ	1074	0	514	2	0
59	SK	1160	0	570	0	0
60	SL	751	0	377	2	0
61	SM	1243	0	602	3	0
62	SP	10847	0	4961	8	0
63	SQ	592	0	278	1	0
64	SR	476	0	237	2	0
65	SS	1145	0	565	1	0
66	ST	3010	0	1415	2	0
67	SU	2703	0	1302	0	0
68	SW	1104	0	544	1	0
69	SY	611	0	265	3	0
70	SZ	1314	0	649	0	0
All	All	163806	0	79150	253	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 1.

All (253) 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)
2:L1:1108:G:OP2	2:L1:1108:G:N2	2.12	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LP:111:ALA:HB1	63:SQ:73:ALA:HB2	1.62	0.81
3:L2:39:C:O2'	29:LU:18:SER:O	1.98	0.80
16:LH:892:MET:O	16:LH:896:THR:N	2.15	0.79
2:L1:562:G:N2	2:L1:564:G:OP1	2.16	0.78
25:LQ:503:LYS:O	25:LQ:521:LYS:N	2.18	0.77
2:L1:545:A:O2'	2:L1:594:A:N6	2.19	0.75
40:NH:376:SER:O	40:NH:387:GLY:N	2.21	0.73
2:L1:51:A:N3	58:SI:344:ARG:N	2.39	0.70
54:SC:198:GLU:O	54:SC:222:GLU:N	2.26	0.69
31:LW:340:LEU:O	31:LW:368:TYR:N	2.26	0.68
58:SI:827:ALA:O	58:SI:883:ALA:N	2.25	0.68
47:NS:926:TYR:O	47:NS:929:ALA:N	2.27	0.67
25:LQ:317:ILE:O	25:LQ:321:TYR:N	2.27	0.67
62:SP:389:ILE:O	62:SP:393:PHE:N	2.28	0.66
2:L1:1524:A:N3	2:L1:1590:G:O2'	2.26	0.66
37:ND:204:ARG:O	37:ND:208:ARG:N	2.28	0.66
2:L1:584:C:N4	69:SY:10:LYS:O	2.29	0.66
36:NC:309:LYS:O	36:NC:313:ARG:N	2.29	0.65
2:L1:1179:G:OP1	66:ST:91:GLY:N	2.29	0.65
47:NS:1096:ALA:HB3	47:NS:1116:PRO:HG2	1.80	0.64
21:LM:778:SER:O	21:LM:782:VAL:N	2.31	0.64
32:LX:487:ASN:O	32:LX:491:CYS:N	2.30	0.64
2:L1:1555:A:O2'	2:L1:1556:A:O5'	2.16	0.63
2:L1:59:C:O4'	2:L1:452:A:O2'	2.16	0.63
40:NH:144:LYS:O	40:NH:176:PHE:N	2.31	0.63
2:L1:1594:G:O2'	2:L1:1600:A:N1	2.32	0.62
43:NM:138:PHE:O	43:NM:213:ARG:N	2.30	0.62
21:LM:1594:PHE:O	21:LM:1598:LEU:N	2.33	0.62
36:NC:249:ILE:O	36:NC:253:SER:N	2.33	0.62
2:L1:1228:G:OP2	50:OH:45:LEU:N	2.33	0.61
31:LW:507:ASN:O	31:LW:510:ASP:N	2.34	0.60
47:NS:1179:ALA:O	47:NS:1183:ARG:N	2.34	0.60
2:L1:192:U:H3	2:L1:193:U:HO2'	1.50	0.60
2:L1:1502:G:N2	2:L1:1505:A:OP2	2.30	0.60
25:LQ:641:TYR:O	25:LQ:650:ILE:N	2.33	0.60
16:LH:778:ASP:O	16:LH:781:SER:N	2.34	0.60
32:LY:887:ALA:O	32:LY:892:ARG:N	2.34	0.59
47:NS:1179:ALA:HA	47:NS:1182:ALA:HB3	1.84	0.59
3:L2:321:C:OP2	3:L2:322:A:O2'	2.18	0.59
23:LO:349:ASN:N	23:LO:363:ALA:O	2.36	0.59
40:NH:424:GLY:O	40:NH:428:TYR:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LO:543:ASN:O	23:LO:547:ALA:N	2.35	0.59
26:LR:561:SER:O	26:LR:565:PHE:N	2.36	0.59
47:NS:522:ASN:O	47:NS:526:ASP:N	2.35	0.58
47:NS:1117:TYR:N	47:NS:1133:VAL:O	2.36	0.58
31:LW:300:ILE:O	31:LW:309:LEU:N	2.35	0.58
2:L1:1482:C:O2'	11:LC:72:GLY:O	2.09	0.58
39:NG:67:VAL:O	39:NG:71:CYS:N	2.33	0.57
25:LQ:19:SER:N	25:LQ:44:SER:O	2.37	0.57
58:SI:217:ASP:O	58:SI:221:LEU:N	2.37	0.57
18:LJ:303:LEU:N	18:LJ:321:GLY:O	2.37	0.57
54:SD:198:GLU:O	54:SD:222:GLU:N	2.38	0.57
31:LW:113:PRO:O	31:LW:130:ARG:N	2.38	0.56
47:NS:428:LEU:O	47:NS:433:PHE:N	2.39	0.56
20:LL:61:THR:N	20:LL:79:GLY:O	2.36	0.56
2:L1:512:A:OP1	10:L9:170:GLY:N	2.37	0.55
2:L1:1555:A:O2'	2:L1:1556:A:O4'	2.23	0.55
2:L1:1534:G:O2'	2:L1:1536:G:O6	2.23	0.55
25:LQ:149:ASP:O	25:LQ:153:GLU:N	2.37	0.55
56:SG:68:LYS:O	56:SG:71:LEU:N	2.39	0.55
32:LX:76:LYS:O	32:LX:79:LYS:N	2.40	0.55
66:ST:388:LEU:O	66:ST:392:LYS:N	2.39	0.55
19:LK:499:ILE:O	19:LK:502:ARG:N	2.39	0.55
2:L1:1011:G:O2'	47:NS:134:GLY:O	2.24	0.55
3:L2:245:U:O4	3:L2:246:A:N6	2.41	0.54
60:SL:143:HIS:O	60:SL:147:GLN:N	2.39	0.54
2:L1:512:A:OP2	10:L9:173:ALA:N	2.40	0.54
43:NM:30:PHE:N	43:NM:46:THR:O	2.36	0.54
30:LV:79:PRO:O	30:LV:97:THR:N	2.36	0.54
2:L1:1484:G:H21	2:L1:1606:C:H1'	1.72	0.54
11:LC:57:LEU:O	11:LC:61:SER:N	2.38	0.53
31:LW:216:TYR:O	31:LW:225:VAL:N	2.38	0.53
25:LQ:217:LEU:N	25:LQ:229:TRP:O	2.39	0.53
27:LS:379:GLY:N	27:LS:383:TRP:O	2.36	0.53
40:NH:795:GLU:O	40:NH:799:LEU:N	2.42	0.53
42:NL:283:THR:O	42:NL:286:LYS:N	2.41	0.53
45:NP:63:ARG:O	45:NP:66:TYR:N	2.42	0.53
54:SD:196:ALA:O	54:SD:220:ILE:N	2.42	0.53
14:LF:15:ASN:O	14:LF:19:ALA:N	2.41	0.52
32:LY:502:PHE:O	32:LY:506:GLY:N	2.40	0.52
10:L9:149:ARG:O	10:L9:153:GLU:N	2.39	0.52
29:LU:288:TYR:O	29:LU:298:LEU:N	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LX:502:PHE:O	32:LX:506:GLY:N	2.41	0.52
36:NC:314:ASN:O	36:NC:318:ASN:N	2.35	0.52
28:LT:354:SER:N	28:LT:369:ALA:O	2.40	0.52
2:L1:524:U:O2'	2:L1:527:A:N6	2.36	0.52
30:LV:123:ILE:N	30:LV:135:THR:O	2.38	0.52
21:LM:390:LEU:O	21:LM:394:LEU:N	2.41	0.52
52:SA:296:MET:O	52:SA:300:ALA:N	2.39	0.52
65:SS:276:GLN:O	65:SS:280:GLN:N	2.36	0.52
60:SL:50:ALA:HB1	60:SL:58:ALA:HB2	1.91	0.51
2:L1:163:G:OP2	2:L1:163:G:N2	2.37	0.51
55:SF:48:ILE:O	55:SF:104:THR:N	2.36	0.51
23:LO:150:THR:N	23:LO:164:THR:O	2.43	0.51
2:L1:612:U:OP2	2:L1:613:G:O2'	2.12	0.51
47:NS:1008:SER:O	47:NS:1012:ALA:HB2	2.11	0.51
32:LY:487:ASN:O	32:LY:491:CYS:N	2.43	0.51
9:L8:90:LEU:O	9:L8:94:ASN:N	2.44	0.51
34:NA:507:ILE:O	34:NA:515:MET:N	2.43	0.50
22:LN:199:ASP:O	22:LN:215:ALA:N	2.41	0.50
34:NA:359:SER:O	34:NA:362:THR:N	2.44	0.50
2:L1:1525:A:N3	2:L1:1589:C:O2'	2.37	0.50
22:LN:125:GLU:O	22:LN:134:LEU:N	2.45	0.50
25:LQ:288:LYS:O	25:LQ:292:ILE:N	2.41	0.50
42:NL:239:SER:O	42:NL:243:LYS:N	2.44	0.50
2:L1:1133:A:OP2	2:L1:1134:C:N4	2.45	0.50
2:L1:188:A:N6	2:L1:197:A:O2'	2.45	0.49
2:L1:976:G:N1	2:L1:1023:A:O2'	2.43	0.49
35:NB:217:PHE:O	35:NB:219:GLU:N	2.45	0.49
21:LM:56:LEU:O	21:LM:60:SER:N	2.42	0.49
55:SE:71:CYS:O	55:SE:75:ASN:N	2.46	0.49
53:SB:1:MET:O	53:SB:86:THR:N	2.43	0.49
8:L7:44:LYS:N	8:L7:61:PHE:O	2.45	0.49
28:LT:515:ARG:O	28:LT:531:PHE:N	2.42	0.48
40:NH:218:ASP:O	40:NH:224:CYS:N	2.45	0.48
25:LQ:177:LEU:O	25:LQ:189:TRP:N	2.38	0.48
62:SP:1962:PHE:O	62:SP:1966:PHE:N	2.40	0.48
54:SC:109:LYS:HA	54:SC:141:TYR:HA	1.94	0.48
47:NS:908:SER:O	47:NS:912:SER:N	2.40	0.48
62:SP:1384:LEU:O	62:SP:1388:SER:N	2.41	0.48
25:LQ:281:ILE:O	25:LQ:332:ILE:N	2.46	0.48
26:LR:30:LYS:O	26:LR:45:LEU:N	2.43	0.48
2:L1:1670:G:O2'	2:L1:1731:A:N6	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LR:316:VAL:O	26:LR:320:LEU:N	2.38	0.48
47:NS:426:GLN:O	47:NS:429:TYR:N	2.44	0.48
2:L1:501:U:O2'	2:L1:502:U:OP2	2.26	0.47
2:L1:1119:G:O2'	2:L1:1120:U:OP1	2.29	0.47
28:LT:530:ASP:O	28:LT:534:SER:N	2.42	0.47
53:SB:3:TYR:O	53:SB:88:ILE:N	2.40	0.47
30:LV:80:GLN:HA	30:LV:96:HIS:HA	1.96	0.47
7:L6:142:ARG:O	7:L6:146:GLY:N	2.46	0.47
28:LT:192:ASN:O	28:LT:196:GLY:N	2.44	0.47
2:L1:572:C:N4	58:SI:878:HIS:O	2.46	0.47
21:LM:180:ILE:O	21:LM:184:ASN:N	2.46	0.47
40:NH:469:ASP:O	40:NH:473:LYS:N	2.46	0.47
8:L7:63:PRO:O	8:L7:67:LEU:N	2.45	0.47
4:L3:70:VAL:O	4:L3:73:MET:N	2.48	0.47
25:LQ:177:LEU:N	25:LQ:189:TRP:O	2.45	0.47
43:NM:180:THR:O	43:NM:184:LEU:N	2.43	0.46
42:NL:83:ALA:O	42:NL:110:MET:N	2.42	0.46
58:SI:218:ARG:O	58:SI:222:ASN:N	2.45	0.46
62:SP:109:LEU:O	62:SP:113:PHE:N	2.43	0.46
2:L1:569:C:H2'	2:L1:570:A:O4'	2.16	0.46
36:NC:286:VAL:O	36:NC:290:GLU:N	2.45	0.46
42:NL:156:GLN:HA	42:NL:204:SER:HA	1.98	0.46
25:LQ:440:PRO:HG3	25:LQ:485:GLY:HA3	1.98	0.46
32:LX:361:ARG:O	32:LX:363:HIS:N	2.49	0.46
2:L1:1190:C:N4	2:L1:1197:C:O2	2.48	0.46
3:L2:33:A:O2'	3:L2:34:A:OP2	2.27	0.46
18:LJ:435:ASP:O	18:LJ:439:LEU:N	2.49	0.46
41:NI:262:VAL:O	41:NI:266:LYS:N	2.40	0.46
22:LN:648:PHE:O	22:LN:655:SER:N	2.43	0.46
45:NP:125:SER:O	45:NP:128:GLY:N	2.49	0.46
18:LJ:491:VAL:O	18:LJ:495:ILE:N	2.47	0.46
27:LS:365:ASN:O	27:LS:369:ASN:N	2.48	0.46
47:NS:1236:VAL:HA	47:NS:1250:PHE:HA	1.98	0.45
62:SP:1331:LEU:O	62:SP:1336:TYR:N	2.42	0.45
2:L1:931:C:O2'	43:NM:118:GLN:O	2.30	0.45
3:L2:30:A:N6	29:LU:342:ILE:O	2.36	0.45
25:LQ:643:ASP:O	25:LQ:647:PHE:N	2.49	0.45
2:L1:1568:C:O2'	2:L1:1569:A:O5'	2.31	0.45
2:L1:1227:A:N6	2:L1:1256:A:O2'	2.48	0.45
25:LQ:136:LEU:O	25:LQ:148:TRP:N	2.46	0.45
69:SY:231:LYS:N	69:SY:243:LYS:O	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:45:ALA:HB1	14:LF:50:ALA:O	2.17	0.45
2:L1:1059:U:O2'	2:L1:1060:U:H4'	2.16	0.45
16:LH:94:GLY:N	16:LH:106:LEU:O	2.47	0.45
21:LM:1737:LEU:CB	62:SP:31:ALA:HB1	2.47	0.44
26:LR:603:ASP:O	26:LR:607:GLY:N	2.44	0.44
40:NH:654:SER:O	40:NH:666:CYS:N	2.40	0.44
47:NS:247:ASN:O	47:NS:251:ARG:N	2.46	0.44
47:NS:624:VAL:N	47:NS:758:ILE:O	2.48	0.44
57:SH:330:LYS:O	57:SH:334:ASN:N	2.44	0.44
64:SR:89:ASN:O	64:SR:92:CYS:N	2.51	0.44
64:SR:89:ASN:O	64:SR:93:LEU:N	2.44	0.44
1:L0:69:U:H5'	1:L0:70:A:OP2	2.18	0.44
26:LR:519:ASN:O	26:LR:523:GLY:N	2.47	0.44
47:NS:810:SER:O	47:NS:813:ALA:HB3	2.18	0.44
2:L1:532:U:O2'	14:LF:33:ALA:O	2.34	0.44
25:LQ:94:LEU:O	25:LQ:106:TRP:N	2.48	0.44
42:NL:140:LYS:O	42:NL:144:GLN:N	2.51	0.44
40:NH:390:THR:O	40:NH:394:THR:N	2.38	0.44
2:L1:67:A:O2'	2:L1:69:G:OP1	2.35	0.44
22:LN:554:ASP:O	22:LN:558:ARG:N	2.47	0.43
22:LN:363:SER:O	22:LN:367:GLY:N	2.46	0.43
32:LY:587:GLN:O	32:LY:636:VAL:N	2.52	0.43
35:NB:608:PHE:N	54:SC:301:LEU:O	2.38	0.43
8:L7:136:VAL:N	8:L7:153:LEU:O	2.49	0.43
26:LR:163:LEU:O	26:LR:175:TRP:N	2.51	0.43
61:SM:152:LEU:O	61:SM:165:PHE:N	2.43	0.43
62:SP:482:ARG:O	62:SP:486:PHE:N	2.47	0.43
32:LY:899:ALA:HB1	32:LY:904:LEU:O	2.19	0.43
21:LM:199:CYS:O	21:LM:203:ASN:N	2.52	0.43
47:NS:1117:TYR:O	47:NS:1133:VAL:N	2.42	0.43
3:L2:82:G:O2'	3:L2:83:A:OP2	2.28	0.43
54:SD:201:HIS:O	54:SD:204:GLY:N	2.51	0.43
21:LM:404:PHE:O	21:LM:408:ILE:N	2.49	0.43
61:SM:188:HIS:N	61:SM:220:ARG:O	2.45	0.43
5:L4:163:ASP:O	5:L4:167:GLY:N	2.46	0.43
7:L6:1:MET:N	7:L6:18:ILE:O	2.51	0.43
19:LK:505:MET:O	19:LK:508:ARG:N	2.52	0.43
28:LT:62:ASP:O	28:LT:66:LEU:N	2.45	0.43
59:SJ:47:MET:N	59:SJ:115:GLN:O	2.52	0.43
2:L1:192:U:N3	2:L1:193:U:O2'	2.46	0.42
27:LS:161:ILE:O	27:LS:165:ARG:N	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:NQ:56:CYS:O	46:NQ:60:SER:N	2.47	0.42
2:L1:454:U:OP1	2:L1:455:C:N4	2.52	0.42
2:L1:445:A:O2'	2:L1:446:A:O5'	2.38	0.42
61:SM:74:ASP:O	61:SM:78:ALA:N	2.52	0.42
2:L1:929:A:OP2	2:L1:931:C:N4	2.52	0.42
16:LH:284:SER:O	16:LH:288:LEU:N	2.49	0.42
36:NC:315:ALA:O	36:NC:319:VAL:N	2.53	0.42
2:L1:1682:U:O2	2:L1:1720:G:N2	2.53	0.42
2:L1:512:A:P	10:L9:173:ALA:HB2	2.60	0.42
2:L1:523:G:H1'	2:L1:529:A:H61	1.84	0.42
2:L1:1568:C:HO2'	2:L1:1569:A:P	2.42	0.42
3:L2:106:C:H3'	3:L2:107:C:C5'	2.49	0.42
62:SP:193:ALA:O	62:SP:197:SER:N	2.49	0.42
40:NH:1154:ASN:O	40:NH:1158:LYS:N	2.53	0.42
16:LH:682:ASN:O	16:LH:686:GLY:N	2.52	0.42
36:NC:309:LYS:O	36:NC:312:GLU:N	2.52	0.42
41:NI:16:VAL:N	41:NI:37:MET:O	2.52	0.42
8:L7:58:LEU:N	8:L7:89:HIS:O	2.42	0.41
25:LQ:601:GLY:O	25:LQ:605:GLY:N	2.53	0.41
28:LT:488:ASN:O	28:LT:492:GLY:N	2.53	0.41
34:NA:565:VAL:N	34:NA:573:LYS:O	2.35	0.41
47:NS:1002:ASP:N	47:NS:1170:LEU:O	2.52	0.41
47:NS:1240:LYS:HA	47:NS:1245:TRP:HA	2.02	0.41
56:SG:58:ASN:O	56:SG:61:ASP:N	2.53	0.41
3:L2:90:C:O2'	3:L2:91:C:OP1	2.31	0.41
59:SJ:176:ARG:O	59:SJ:203:CYS:N	2.44	0.41
37:ND:177:ARG:O	69:SY:134:THR:HA	2.20	0.41
68:SW:131:ASN:O	68:SW:135:LYS:N	2.53	0.41
21:LM:91:ILE:O	21:LM:95:ASP:N	2.45	0.41
47:NS:530:GLY:HA3	47:NS:866:PRO:O	2.21	0.41
20:LL:231:ASP:O	20:LL:249:GLU:N	2.47	0.41
26:LR:454:LEU:N	26:LR:466:TRP:O	2.54	0.41
37:ND:163:LEU:O	37:ND:167:ARG:N	2.48	0.41
2:L1:564:G:H21	2:L1:565:C:H2'	1.86	0.41
2:L1:888:U:O2	2:L1:988:A:O2'	2.39	0.41
28:LT:587:ARG:O	28:LT:605:LEU:N	2.49	0.41
25:LQ:217:LEU:O	25:LQ:229:TRP:N	2.38	0.41
43:NM:85:LYS:O	43:NM:101:HIS:N	2.50	0.41
54:SD:152:ALA:O	54:SD:155:ILE:N	2.54	0.41
2:L1:862:A:O2'	2:L1:963:A:N1	2.50	0.41
58:SI:932:LEU:N	58:SI:1005:SER:O	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:NB:231:ALA:HB3	35:NB:232:PRO:HD3	2.03	0.40
42:NL:221:ASN:O	42:NL:225:GLY:N	2.52	0.40
39:NG:64:ALA:HB3	39:NG:104:ALA:HB3	2.02	0.40
2:L1:6:G:O6	2:L1:19:A:N6	2.54	0.40
25:LQ:749:GLY:HA2	25:LQ:820:ALA:HB1	2.03	0.40
35:NB:221:ALA:HB3	35:NB:222:PRO:HD3	2.03	0.40

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	102/146 (70%)	100 (98%)	2 (2%)	0	100	100
5	L4	232/261 (89%)	230 (99%)	2 (1%)	0	100	100
6	L5	202/225 (90%)	199 (98%)	3 (2%)	0	100	100
7	L6	202/236 (86%)	199 (98%)	3 (2%)	0	100	100
8	L7	174/190 (92%)	170 (98%)	4 (2%)	0	100	100
9	L8	167/200 (84%)	164 (98%)	3 (2%)	0	100	100
10	L9	179/197 (91%)	175 (98%)	4 (2%)	0	100	100
11	LC	126/143 (88%)	122 (97%)	4 (3%)	0	100	100
12	LD	135/156 (86%)	131 (97%)	4 (3%)	0	100	100
13	LE	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
14	LF	95/135 (70%)	90 (95%)	5 (5%)	0	100	100
15	LG	60/67 (90%)	60 (100%)	0	0	100	100
16	LH	788/896 (88%)	766 (97%)	22 (3%)	0	100	100
17	LI	582/713 (82%)	574 (99%)	8 (1%)	0	100	100
18	LJ	470/513 (92%)	458 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	LK	130/575 (23%)	130 (100%)	0	0	100	100
20	LL	475/643 (74%)	463 (98%)	12 (2%)	0	100	100
21	LM	1597/1769 (90%)	1575 (99%)	22 (1%)	0	100	100
22	LN	649/776 (84%)	637 (98%)	12 (2%)	0	100	100
23	LO	786/923 (85%)	769 (98%)	17 (2%)	0	100	100
24	LP	375/440 (85%)	373 (100%)	2 (0%)	0	100	100
25	LQ	805/943 (85%)	791 (98%)	14 (2%)	0	100	100
26	LR	785/817 (96%)	768 (98%)	17 (2%)	0	100	100
27	LS	441/594 (74%)	431 (98%)	10 (2%)	0	100	100
28	LT	861/939 (92%)	841 (98%)	20 (2%)	0	100	100
29	LU	448/489 (92%)	441 (98%)	7 (2%)	0	100	100
30	LV	355/707 (50%)	345 (97%)	10 (3%)	0	100	100
31	LW	453/554 (82%)	439 (97%)	14 (3%)	0	100	100
32	LX	838/1056 (79%)	821 (98%)	17 (2%)	0	100	100
32	LY	834/1056 (79%)	824 (99%)	10 (1%)	0	100	100
33	LZ	156/183 (85%)	155 (99%)	1 (1%)	0	100	100
34	NA	309/593 (52%)	305 (99%)	4 (1%)	0	100	100
35	NB	221/610 (36%)	218 (99%)	3 (1%)	0	100	100
36	NC	133/357 (37%)	125 (94%)	8 (6%)	0	100	100
37	ND	57/214 (27%)	57 (100%)	0	0	100	100
38	NF	139/151 (92%)	138 (99%)	1 (1%)	0	100	100
39	NG	125/137 (91%)	122 (98%)	3 (2%)	0	100	100
40	NH	1063/1237 (86%)	1056 (99%)	7 (1%)	0	100	100
41	NI	232/297 (78%)	225 (97%)	7 (3%)	0	100	100
42	NL	279/318 (88%)	276 (99%)	3 (1%)	0	100	100
43	NM	231/255 (91%)	228 (99%)	3 (1%)	0	100	100
44	NN	41/534 (8%)	41 (100%)	0	0	100	100
45	NP	130/144 (90%)	128 (98%)	2 (2%)	0	100	100
46	NQ	77/82 (94%)	75 (97%)	2 (3%)	0	100	100
47	NS	881/1267 (70%)	862 (98%)	19 (2%)	0	100	100
48	NV	6/733 (1%)	6 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	OA	12/1729 (1%)	12 (100%)	0	0	100	100
50	OH	118/143 (82%)	118 (100%)	0	0	100	100
51	OU	54/152 (36%)	54 (100%)	0	0	100	100
52	SA	379/504 (75%)	372 (98%)	7 (2%)	0	100	100
53	SB	431/511 (84%)	424 (98%)	7 (2%)	0	100	100
54	SC	234/327 (72%)	227 (97%)	7 (3%)	0	100	100
54	SD	234/327 (72%)	228 (97%)	6 (3%)	0	100	100
55	SE	119/126 (94%)	116 (98%)	3 (2%)	0	100	100
55	SF	119/126 (94%)	115 (97%)	4 (3%)	0	100	100
56	SG	442/573 (77%)	434 (98%)	8 (2%)	0	100	100
57	SH	358/367 (98%)	349 (98%)	9 (2%)	0	100	100
58	SI	766/1183 (65%)	748 (98%)	18 (2%)	0	100	100
59	SJ	207/252 (82%)	206 (100%)	1 (0%)	0	100	100
59	SK	225/252 (89%)	224 (100%)	1 (0%)	0	100	100
60	SL	146/189 (77%)	139 (95%)	7 (5%)	0	100	100
61	SM	243/290 (84%)	237 (98%)	6 (2%)	0	100	100
62	SP	2136/2493 (86%)	2102 (98%)	34 (2%)	0	100	100
63	SQ	113/217 (52%)	112 (99%)	1 (1%)	0	100	100
64	SR	91/145 (63%)	89 (98%)	2 (2%)	0	100	100
65	SS	213/899 (24%)	210 (99%)	3 (1%)	0	100	100
66	ST	573/810 (71%)	561 (98%)	12 (2%)	0	100	100
67	SU	524/552 (95%)	518 (99%)	6 (1%)	0	100	100
68	SW	211/274 (77%)	204 (97%)	7 (3%)	0	100	100
69	SY	114/250 (46%)	111 (97%)	3 (3%)	0	100	100
70	SZ	255/483 (53%)	249 (98%)	6 (2%)	0	100	100
All	All	25870/36775 (70%)	25385 (98%)	485 (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	2/129 (2%)	2 (100%)	0	100	100
5	L4	11/222 (5%)	11 (100%)	0	100	100
6	L5	8/191 (4%)	8 (100%)	0	100	100
7	L6	8/201 (4%)	8 (100%)	0	100	100
8	L7	10/170 (6%)	10 (100%)	0	100	100
9	L8	4/161 (2%)	4 (100%)	0	100	100
10	L9	9/166 (5%)	9 (100%)	0	100	100
11	LC	6/119 (5%)	6 (100%)	0	100	100
12	LD	8/137 (6%)	8 (100%)	0	100	100
13	LE	3/111 (3%)	3 (100%)	0	100	100
14	LF	3/113 (3%)	3 (100%)	0	100	100
15	LG	2/60 (3%)	2 (100%)	0	100	100
16	LH	21/826 (2%)	21 (100%)	0	100	100
17	LI	24/657 (4%)	24 (100%)	0	100	100
18	LJ	19/454 (4%)	19 (100%)	0	100	100
19	LK	4/533 (1%)	4 (100%)	0	100	100
20	LL	14/574 (2%)	14 (100%)	0	100	100
21	LM	43/1633 (3%)	43 (100%)	0	100	100
22	LN	18/713 (2%)	18 (100%)	0	100	100
23	LO	21/811 (3%)	21 (100%)	0	100	100
24	LP	8/414 (2%)	8 (100%)	0	100	100
25	LQ	17/832 (2%)	17 (100%)	0	100	100
26	LR	22/719 (3%)	22 (100%)	0	100	100
27	LS	21/528 (4%)	21 (100%)	0	100	100
28	LT	25/819 (3%)	25 (100%)	0	100	100
29	LU	13/443 (3%)	13 (100%)	0	100	100
30	LV	14/636 (2%)	14 (100%)	0	100	100
31	LW	21/480 (4%)	21 (100%)	0	100	100
32	LX	42/934 (4%)	42 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	LY	42/934 (4%)	42 (100%)	0	100	100
33	LZ	6/172 (4%)	6 (100%)	0	100	100
34	NA	10/535 (2%)	10 (100%)	0	100	100
35	NB	8/538 (2%)	8 (100%)	0	100	100
36	NC	1/315 (0%)	1 (100%)	0	100	100
37	ND	2/196 (1%)	2 (100%)	0	100	100
38	NF	7/128 (6%)	7 (100%)	0	100	100
39	NG	5/105 (5%)	5 (100%)	0	100	100
40	NH	53/1125 (5%)	53 (100%)	0	100	100
41	NI	8/274 (3%)	8 (100%)	0	100	100
42	NL	17/283 (6%)	17 (100%)	0	100	100
43	NM	5/224 (2%)	5 (100%)	0	100	100
44	NN	2/482 (0%)	2 (100%)	0	100	100
45	NP	5/116 (4%)	5 (100%)	0	100	100
46	NQ	4/71 (6%)	4 (100%)	0	100	100
47	NS	45/1140 (4%)	45 (100%)	0	100	100
50	OH	2/119 (2%)	2 (100%)	0	100	100
51	OU	1/135 (1%)	1 (100%)	0	100	100
52	SA	10/435 (2%)	10 (100%)	0	100	100
53	SB	8/433 (2%)	8 (100%)	0	100	100
54	SC	14/240 (6%)	14 (100%)	0	100	100
54	SD	14/240 (6%)	14 (100%)	0	100	100
55	SE	7/104 (7%)	7 (100%)	0	100	100
55	SF	7/104 (7%)	7 (100%)	0	100	100
56	SG	14/502 (3%)	14 (100%)	0	100	100
57	SH	17/312 (5%)	17 (100%)	0	100	100
58	SI	43/1039 (4%)	43 (100%)	0	100	100
59	SJ	9/222 (4%)	9 (100%)	0	100	100
59	SK	12/222 (5%)	12 (100%)	0	100	100
60	SL	9/169 (5%)	9 (100%)	0	100	100
61	SM	10/258 (4%)	10 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	SP	63/2307 (3%)	63 (100%)	0	100	100
63	SQ	5/200 (2%)	5 (100%)	0	100	100
64	SR	5/120 (4%)	5 (100%)	0	100	100
65	SS	14/807 (2%)	14 (100%)	0	100	100
66	ST	22/732 (3%)	22 (100%)	0	100	100
67	SU	27/506 (5%)	27 (100%)	0	100	100
68	SW	11/238 (5%)	11 (100%)	0	100	100
69	SY	2/234 (1%)	2 (100%)	0	100	100
70	SZ	14/424 (3%)	14 (100%)	0	100	100
All	All	981/30526 (3%)	981 (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. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	59/700 (8%)	17 (28%)	1 (1%)
2	L1	1243/1810 (68%)	228 (18%)	4 (0%)
3	L2	137/333 (41%)	20 (14%)	1 (0%)
All	All	1439/2843 (50%)	265 (18%)	6 (0%)

All (265) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	9	G
1	L0	14	U
1	L0	17	A
1	L0	23	G
1	L0	63	G
1	L0	66	C
1	L0	67	G
1	L0	69	U
1	L0	70	A
1	L0	82	A
1	L0	83	U

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Mol	Chain	Res	Type
1	L0	84	G
1	L0	86	C
1	L0	87	C
1	L0	90	G
1	L0	471	C
1	L0	473	A
2	L1	4	C
2	L1	9	U
2	L1	25	C
2	L1	34	G
2	L1	35	U
2	L1	36	C
2	L1	51	A
2	L1	52	U
2	L1	73	U
2	L1	74	U
2	L1	75	U
2	L1	76	A
2	L1	77	U
2	L1	93	A
2	L1	99	C
2	L1	101	U
2	L1	102	U
2	L1	105	A
2	L1	114	C
2	L1	116	U
2	L1	127	G
2	L1	128	U
2	L1	140	A
2	L1	145	A
2	L1	153	G
2	L1	160	C
2	L1	166	C
2	L1	168	A
2	L1	187	G
2	L1	188	A
2	L1	190	C
2	L1	192	U
2	L1	193	U
2	L1	195	G
2	L1	196	G
2	L1	201	G

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Mol	Chain	Res	Type
2	L1	202	A
2	L1	204	G
2	L1	249	U
2	L1	250	C
2	L1	260	U
2	L1	261	U
2	L1	265	A
2	L1	275	C
2	L1	276	C
2	L1	277	U
2	L1	278	U
2	L1	279	G
2	L1	280	U
2	L1	299	A
2	L1	316	A
2	L1	320	U
2	L1	321	C
2	L1	322	G
2	L1	331	A
2	L1	333	A
2	L1	334	G
2	L1	337	G
2	L1	359	A
2	L1	361	C
2	L1	402	C
2	L1	423	G
2	L1	439	U
2	L1	444	C
2	L1	445	A
2	L1	454	U
2	L1	456	A
2	L1	473	A
2	L1	495	C
2	L1	496	G
2	L1	501	U
2	L1	502	U
2	L1	505	A
2	L1	538	A
2	L1	539	G
2	L1	542	A
2	L1	545	A
2	L1	551	G

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Mol	Chain	Res	Type
2	L1	552	G
2	L1	565	C
2	L1	575	C
2	L1	579	A
2	L1	583	C
2	L1	594	A
2	L1	611	U
2	L1	619	A
2	L1	622	A
2	L1	624	G
2	L1	862	A
2	L1	863	A
2	L1	864	U
2	L1	876	G
2	L1	886	U
2	L1	898	A
2	L1	899	G
2	L1	914	G
2	L1	926	A
2	L1	933	A
2	L1	934	C
2	L1	935	U
2	L1	960	U
2	L1	966	A
2	L1	970	A
2	L1	992	A
2	L1	1005	A
2	L1	1011	G
2	L1	1026	A
2	L1	1028	C
2	L1	1029	U
2	L1	1032	G
2	L1	1036	A
2	L1	1054	U
2	L1	1059	U
2	L1	1060	U
2	L1	1063	U
2	L1	1076	A
2	L1	1081	A
2	L1	1082	C
2	L1	1092	A
2	L1	1093	A

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Mol	Chain	Res	Type
2	L1	1097	U
2	L1	1098	U
2	L1	1099	U
2	L1	1100	G
2	L1	1116	A
2	L1	1119	G
2	L1	1120	U
2	L1	1124	A
2	L1	1125	A
2	L1	1126	G
2	L1	1127	G
2	L1	1139	A
2	L1	1158	C
2	L1	1167	G
2	L1	1179	G
2	L1	1189	A
2	L1	1191	U
2	L1	1192	C
2	L1	1193	A
2	L1	1195	C
2	L1	1197	C
2	L1	1200	G
2	L1	1202	A
2	L1	1205	C
2	L1	1207	C
2	L1	1227	A
2	L1	1228	G
2	L1	1229	G
2	L1	1232	U
2	L1	1254	U
2	L1	1267	G
2	L1	1268	G
2	L1	1270	G
2	L1	1273	G
2	L1	1275	A
2	L1	1276	U
2	L1	1436	A
2	L1	1437	U
2	L1	1440	C
2	L1	1451	C
2	L1	1453	G
2	L1	1464	G

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Mol	Chain	Res	Type
2	L1	1471	A
2	L1	1481	C
2	L1	1486	G
2	L1	1487	A
2	L1	1494	C
2	L1	1496	U
2	L1	1497	U
2	L1	1535	U
2	L1	1537	C
2	L1	1542	G
2	L1	1548	G
2	L1	1553	G
2	L1	1554	U
2	L1	1555	A
2	L1	1556	A
2	L1	1557	U
2	L1	1559	A
2	L1	1569	A
2	L1	1570	A
2	L1	1579	U
2	L1	1584	G
2	L1	1590	G
2	L1	1595	U
2	L1	1599	C
2	L1	1600	A
2	L1	1601	G
2	L1	1618	C
2	L1	1619	C
2	L1	1624	C
2	L1	1628	U
2	L1	1629	G
2	L1	1630	U
2	L1	1631	A
2	L1	1639	C
2	L1	1651	A
2	L1	1653	C
2	L1	1657	U
2	L1	1658	G
2	L1	1661	U
2	L1	1664	C
2	L1	1680	G
2	L1	1683	C

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Mol	Chain	Res	Type
2	L1	1697	G
2	L1	1701	A
2	L1	1702	A
2	L1	1703	C
2	L1	1715	G
2	L1	1716	C
2	L1	1721	A
2	L1	1741	U
2	L1	1742	U
2	L1	1744	A
2	L1	1747	G
2	L1	1755	A
2	L1	1772	C
2	L1	1777	G
2	L1	1780	G
2	L1	1781	A
2	L1	1782	A
2	L1	1783	C
2	L1	1784	C
2	L1	1792	G
2	L1	1794	A
2	L1	1795	U
2	L1	1796	C
2	L1	1801	A
3	L2	2	U
3	L2	3	C
3	L2	4	G
3	L2	20	U
3	L2	34	A
3	L2	37	G
3	L2	38	U
3	L2	39	C
3	L2	47	G
3	L2	72	C
3	L2	88	U
3	L2	90	C
3	L2	91	C
3	L2	107	C
3	L2	109	G
3	L2	248	G
3	L2	254	A
3	L2	324	U

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Mol	Chain	Res	Type
3	L2	325	C
3	L2	329	C

All (6) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L0	69	U
2	L1	320	U
2	L1	1119	G
2	L1	1555	A
2	L1	1568	C
3	L2	1	G

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	$\# Z > 2$
65	SEP	SS	738	65	3,4,10	0.71	0	2,4,14	0.74	0
56	SEP	SG	50	56	3,4,10	0.62	0	2,4,14	0.90	0
27	SEP	LS	128	27	3,4,10	0.69	0	2,4,14	0.77	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
65	SEP	SS	738	65	-	0/1/2/10	-
56	SEP	SG	50	56	-	0/1/2/10	-
27	SEP	LS	128	27	-	1/1/2/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
27	LS	128	SEP	O-C-CA-CB

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](#)

There are no ligands in this entry.

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.

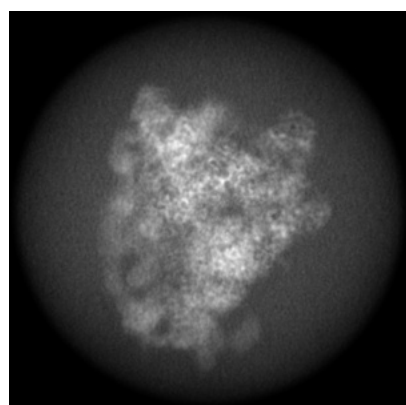
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49083. These allow visual inspection of the internal detail of the map and identification of artifacts.

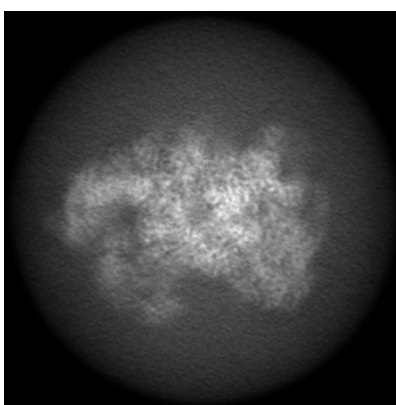
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

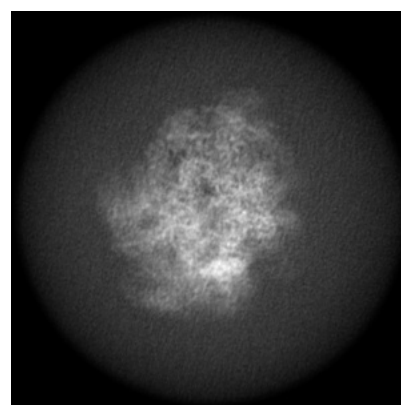
6.1.1 Primary map



X



Y

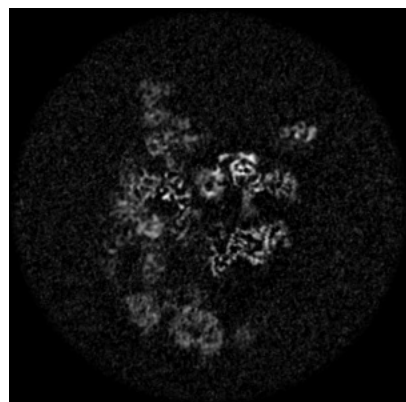


Z

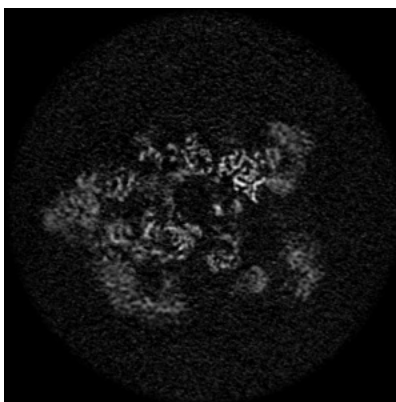
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

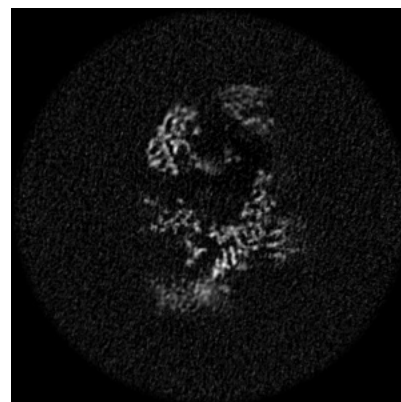
6.2.1 Primary map



X Index: 252



Y Index: 252

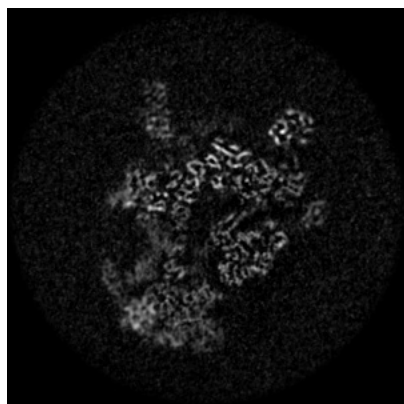


Z Index: 252

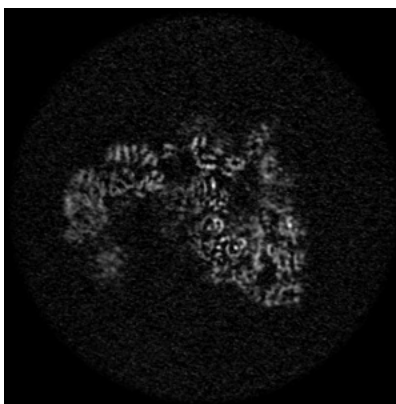
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

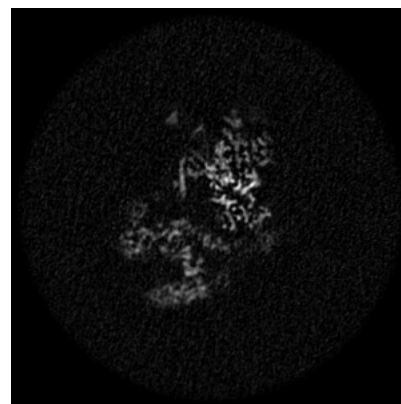
6.3.1 Primary map



X Index: 269



Y Index: 222

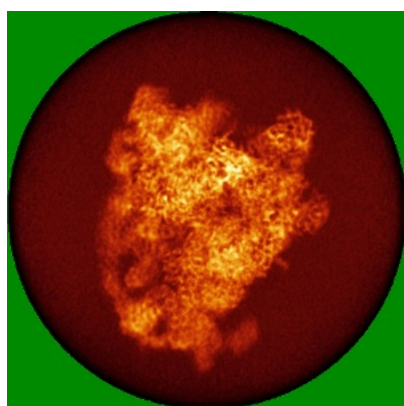


Z Index: 304

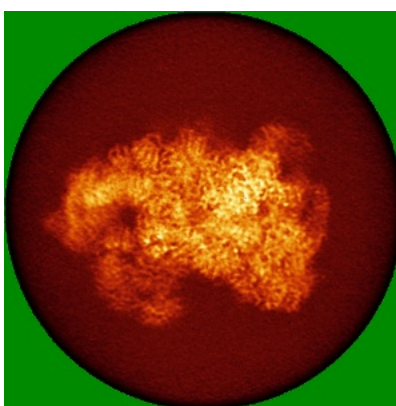
The images above show the largest variance slices of the map in three orthogonal directions.

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

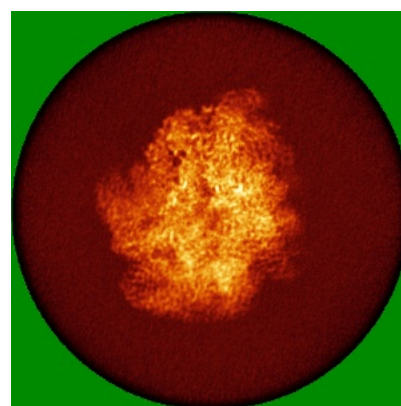
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

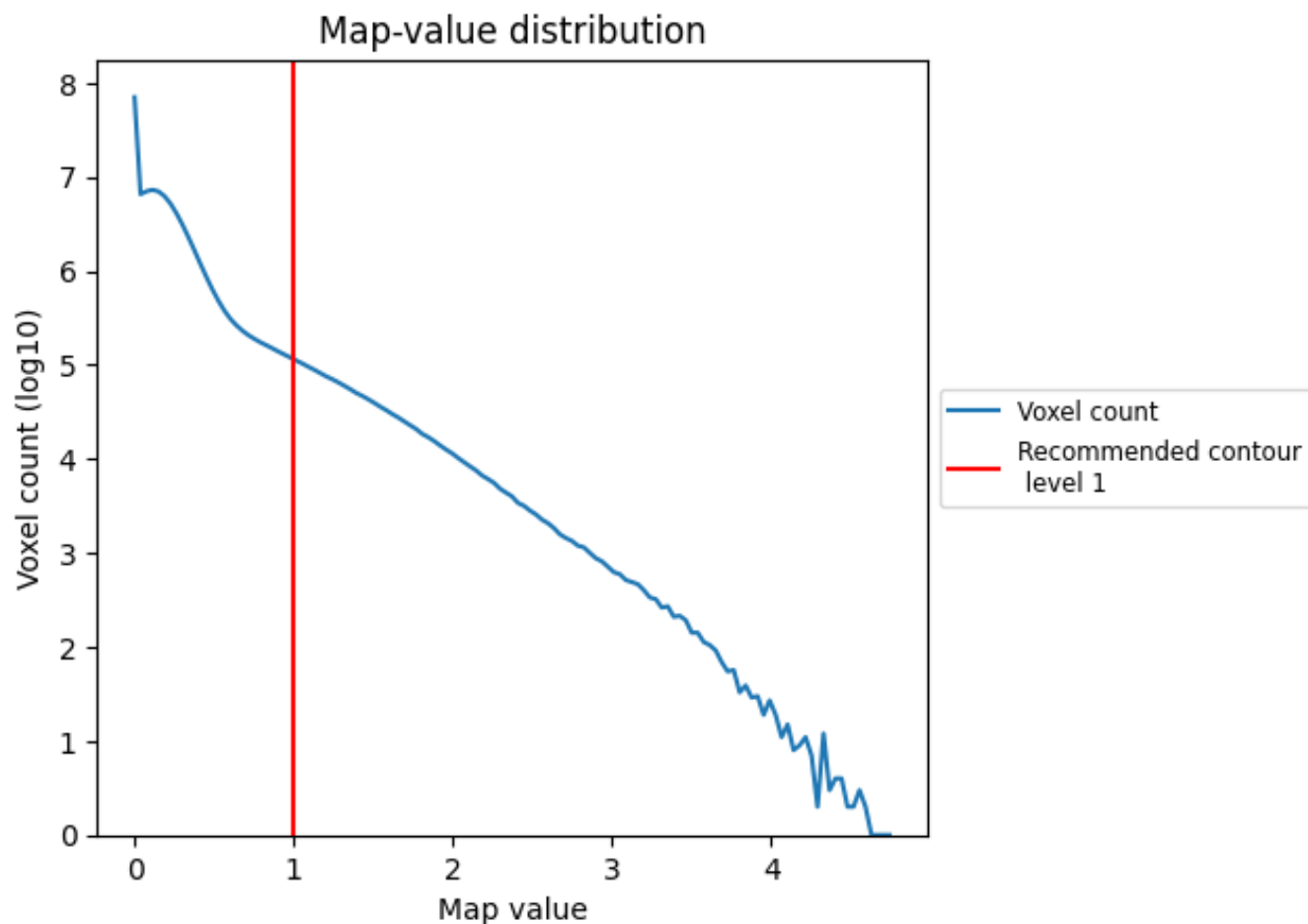
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

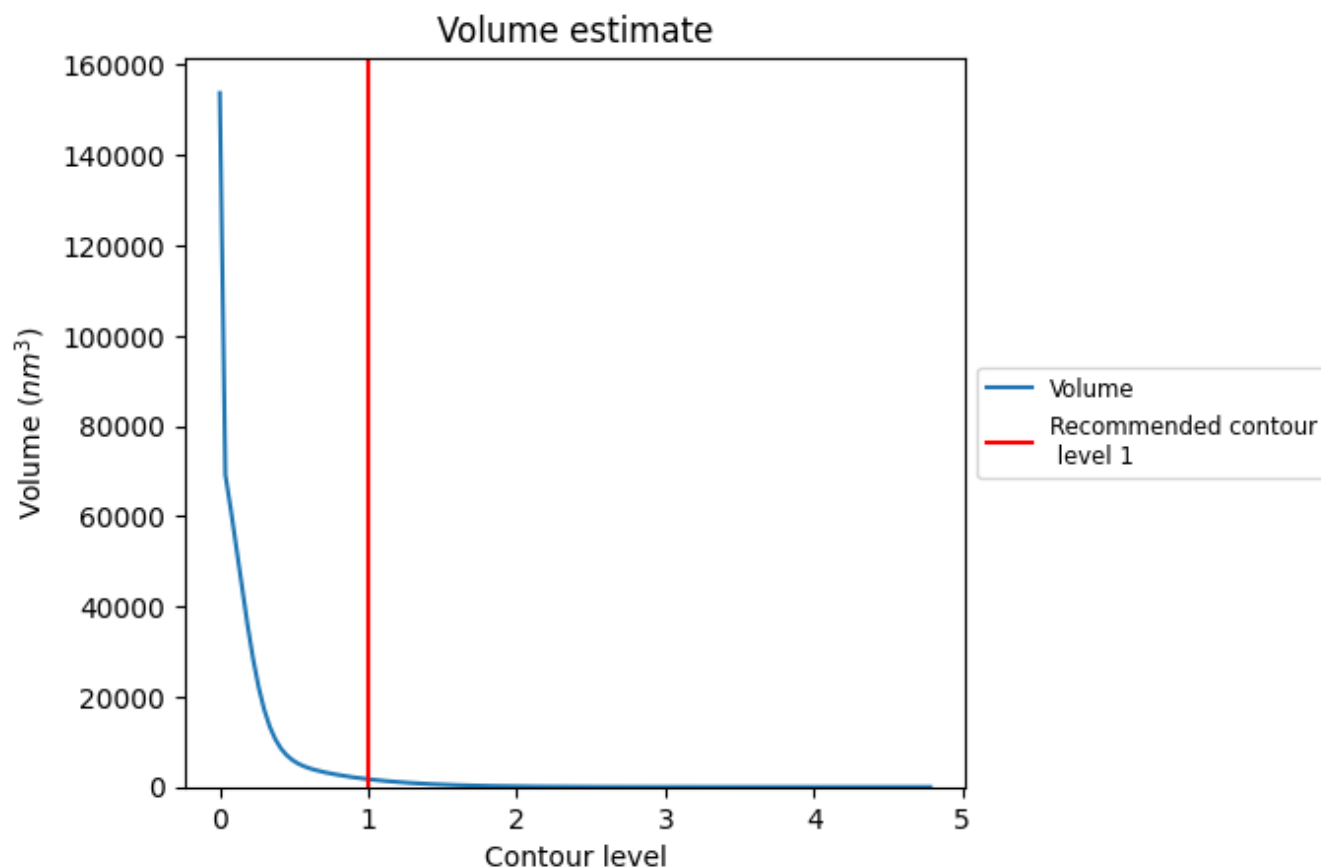
This section contains the results of statistical analysis of the map.

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.

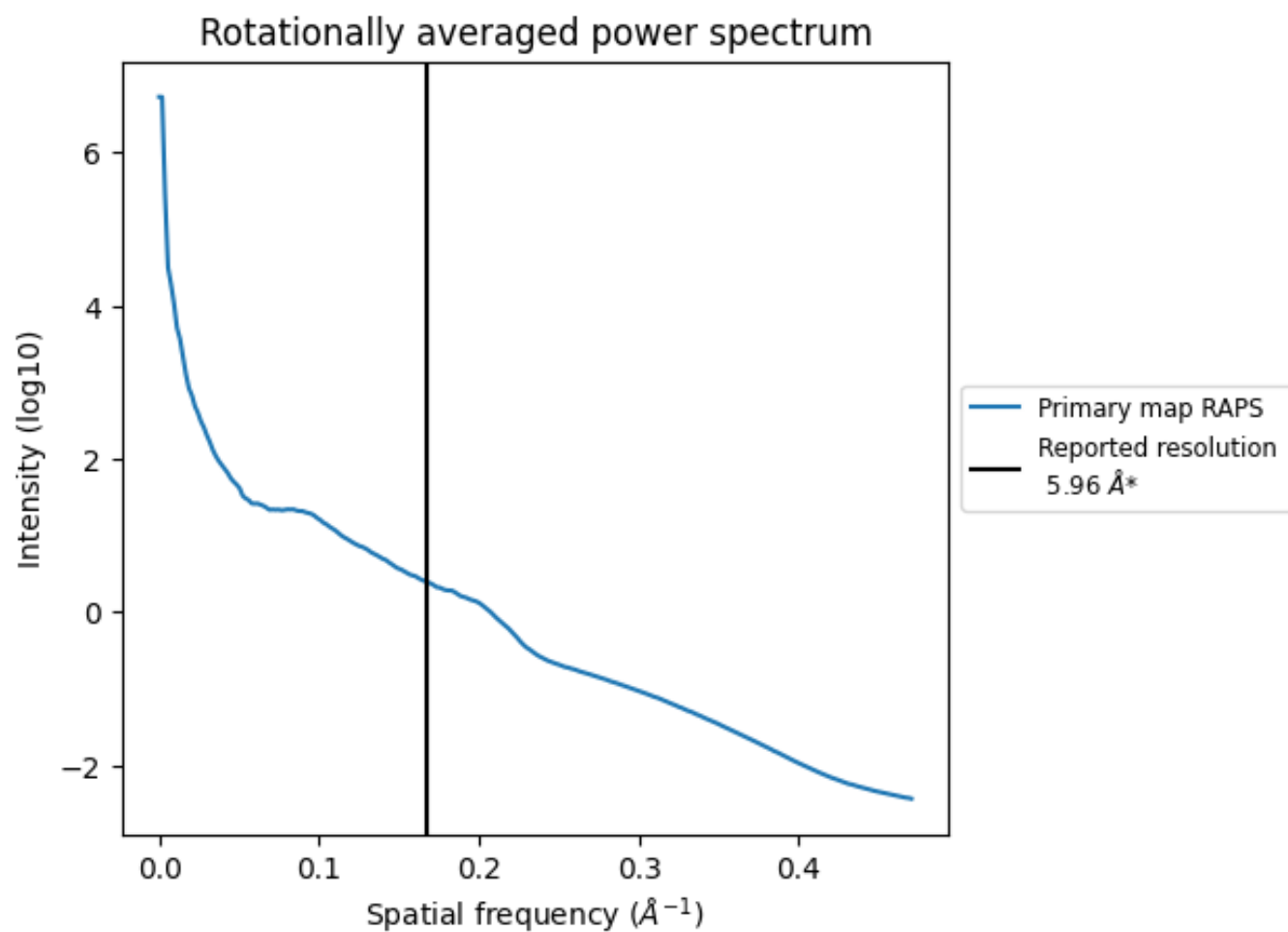
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1717 nm^3 ; this corresponds to an approximate mass of 1551 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 0.168 Å⁻¹

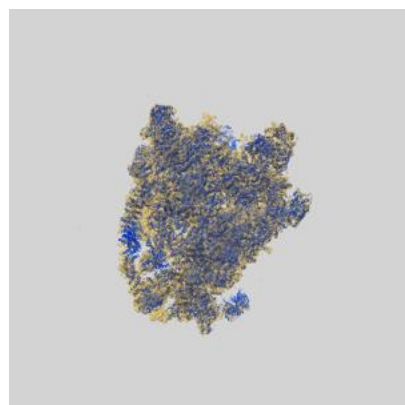
8 Fourier-Shell correlation ⓘ

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

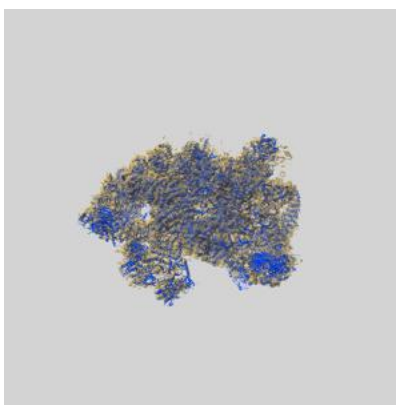
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49083 and PDB model 9N73. Per-residue inclusion information can be found in section [3](#) on page [17](#).

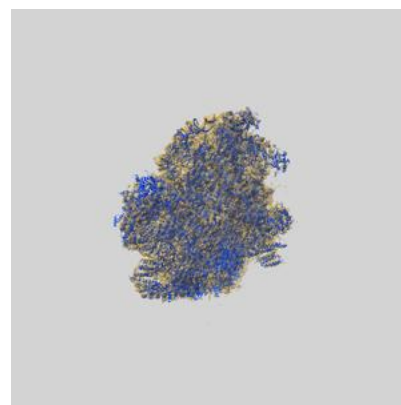
9.1 Map-model overlay [i](#)



X



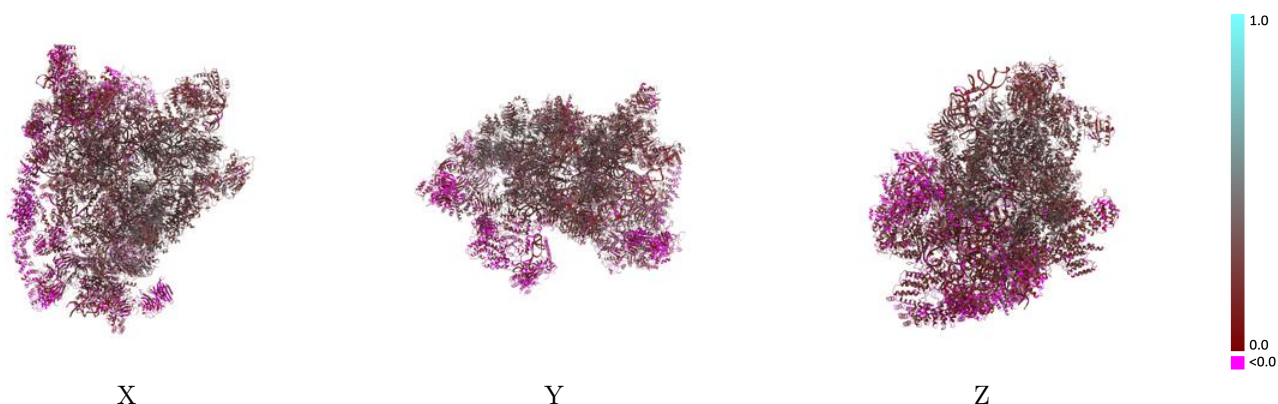
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0 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](#)

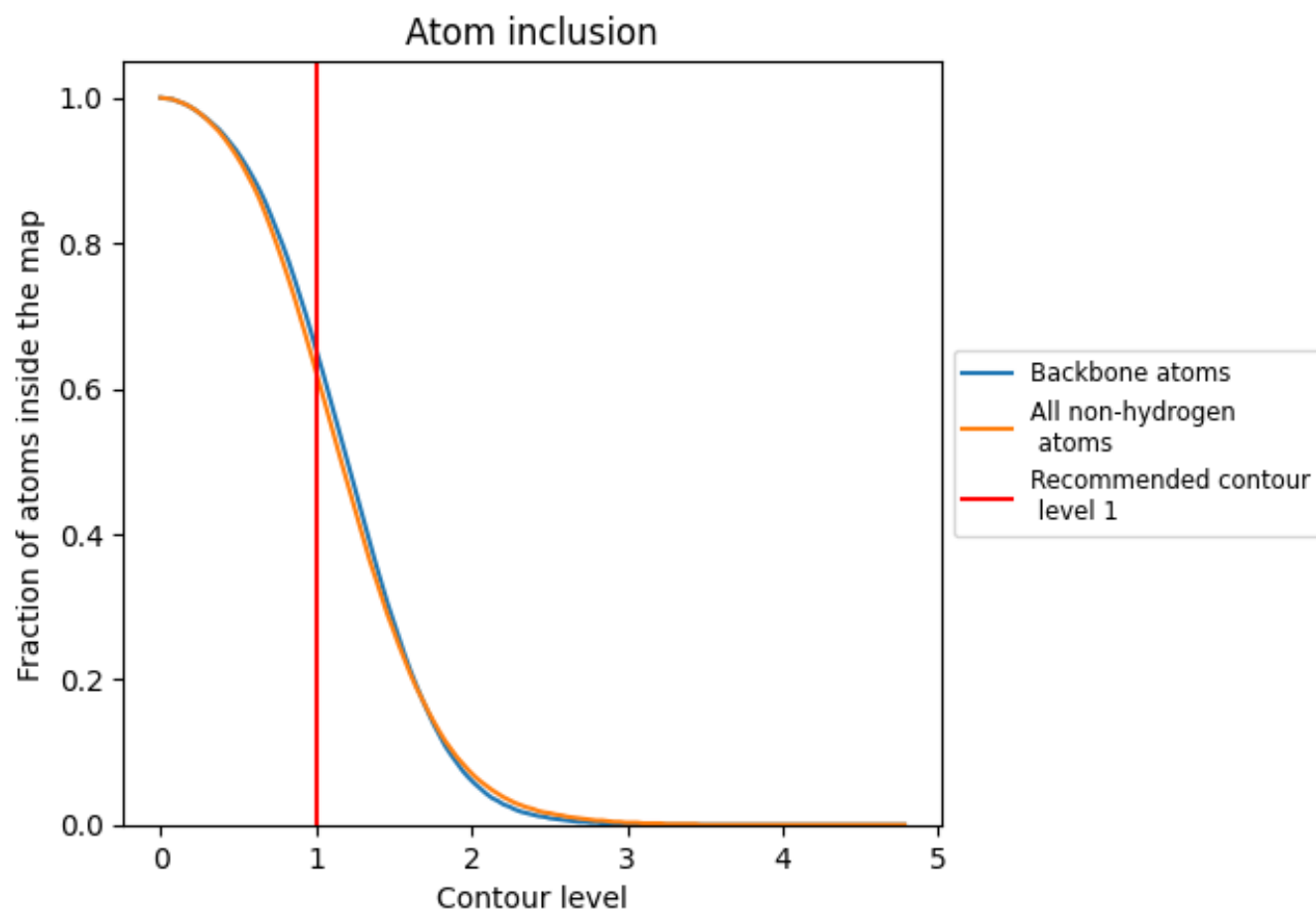


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 65% of all backbone atoms, 62% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6230	 0.2180
L0	 0.5670	 0.1330
L1	 0.7520	 0.2040
L2	 0.7080	 0.1850
L3	 0.4900	 0.2050
L4	 0.7510	 0.2000
L5	 0.8860	 0.3320
L6	 0.7150	 0.1840
L7	 0.7520	 0.2450
L8	 0.6890	 0.1740
L9	 0.7670	 0.2580
LC	 0.8260	 0.3350
LD	 0.6090	 0.1530
LE	 0.8870	 0.3140
LF	 0.8450	 0.2340
LG	 0.8670	 0.3760
LH	 0.5320	 0.2020
LI	 0.1290	 0.0540
LJ	 0.6410	 0.2070
LK	 0.3300	 0.1660
LL	 0.6750	 0.2850
LM	 0.3650	 0.0900
LN	 0.6110	 0.1710
LO	 0.8590	 0.3770
LP	 0.6520	 0.2460
LQ	 0.8730	 0.2880
LR	 0.7970	 0.3290
LS	 0.7810	 0.3450
LT	 0.8660	 0.3590
LU	 0.8940	 0.3320
LV	 0.6520	 0.1720
LW	 0.8330	 0.3660
LX	 0.5210	 0.1760
LY	 0.2610	 0.0770
LZ	 0.6440	 0.2790



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Chain	Atom inclusion	Q-score
NA	 0.6240	 0.2480
NB	 0.3300	 0.1320
NC	 0.5850	 0.2320
ND	 0.0370	 0.1550
NF	 0.9040	 0.2930
NG	 0.7940	 0.3670
NH	 0.7220	 0.2770
NI	 0.4840	 0.2510
NL	 0.7780	 0.3300
NM	 0.8040	 0.3560
NN	 0.5720	 0.1700
NP	 0.4640	 0.2650
NQ	 0.8790	 0.2940
NS	 0.5570	 0.2790
NV	 0.0000	 -0.1640
OA	 0.0000	 0.0600
OH	 0.0180	 -0.0470
OU	 0.0000	 -0.0180
SA	 0.7750	 0.2810
SB	 0.6660	 0.2320
SC	 0.7520	 0.3030
SD	 0.2070	 0.0690
SE	 0.7040	 0.2590
SF	 0.8420	 0.2790
SG	 0.7900	 0.2400
SH	 0.6450	 0.2660
SI	 0.6820	 0.2860
SJ	 0.2720	 0.0980
SK	 0.3840	 0.1110
SL	 0.8630	 0.3200
SM	 0.7000	 0.3150
SP	 0.5010	 0.1450
SQ	 0.3350	 0.2640
SR	 0.7120	 0.2860
SS	 0.6600	 0.3130
ST	 0.2300	 0.0910
SU	 0.1910	 0.0770
SW	 0.7460	 0.3600
SY	 0.2900	 0.1990
SZ	 0.2040	 0.0580