



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:53 AM UTC

PDB ID : 7MQ8 / pdb_00007mq8
EMDB ID : EMD-23936
Title : Cryo-EM structure of the human SSU processome, state pre-A1
Authors : Vanden Broeck, A.; Singh, S.; Klinge, S.
Deposited on : 2021-05-05
Resolution : 3.60 Å(reported)
Based on initial models : 6G4S, 6ZOJ, 5FAI, 2IPX, 5WLC, 6ZQD, 2OZB, 6G18, 4JXM

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

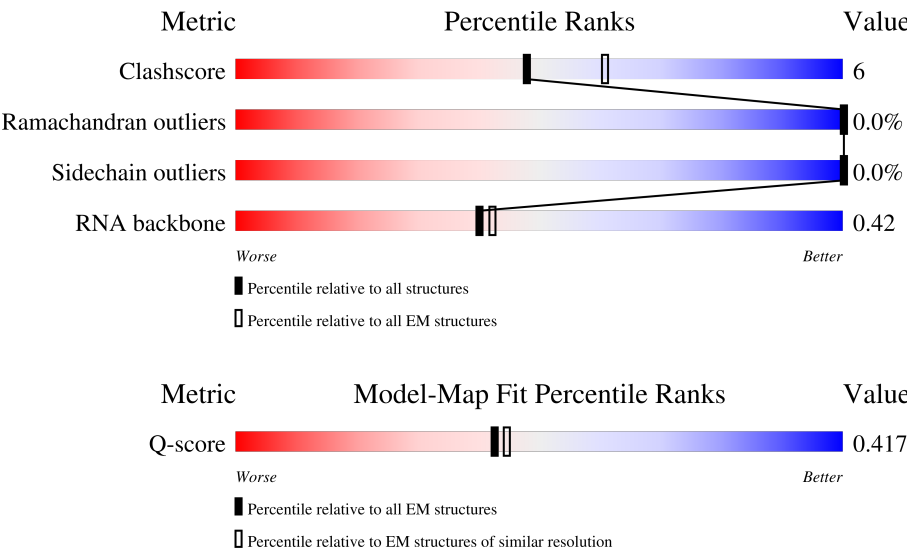
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L0	3617	93%
2	L1	1869	38%
3	L2	217	46%

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Mol	Chain	Length	Quality of chain
4	L3	116	
5	L4	263	
6	L5	204	
7	L6	249	
8	L7	194	
9	L8	208	
10	L9	194	
11	LA	132	
12	LC	146	
13	LD	158	
14	LF	133	
15	LG	69	
16	LH	830	
17	LI	678	
18	LJ	518	
19	LK	677	
19	LL	677	
20	LM	2144	
21	LN	686	
22	LO	919	
23	LP	597	
24	LQ	943	
25	LR	808	
26	LS	556	
27	LT	951	

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Mol	Chain	Length	Quality of chain
28	LU	445	
29	LW	610	
30	LZ	184	
31	N0	22	
32	NA	681	
33	NB	479	
34	NC	315	
35	ND	257	
36	NE	293	
37	NF	151	
38	NG	151	
39	NH	1146	
40	NI	280	
41	NJ	1025	
41	NK	1025	
42	NM	264	
43	NN	560	
44	NO	130	
45	NQ	84	
46	NR	861	
47	NT	156	
48	NU	135	
49	NW	688	
50	NY	381	
51	SA	594	

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Mol	Chain	Length	Quality of chain
52	SB	529	
53	SC	321	
53	SD	321	
54	SE	128	
54	SF	128	
55	SG	475	
56	SH	373	
57	SI	1282	
58	SJ	244	
58	SK	244	
59	SL	198	
60	SM	291	
61	SP	2785	
62	SQ	756	
63	SR	143	
64	SS	771	
65	ST	632	
66	SU	472	
67	SW	252	
68	Sx	38	
69	SX	273	
70	SY	253	
71	SZ	304	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 245114 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	242	Total	C	N	O	P	0	0
			5152	2289	908	1713	242		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1301	Total	C	N	O	P	0	0
			27777	12396	5002	9078	1301		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	215	Total	C	N	O	P	0	0
			4589	2047	809	1518	215		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	115	Total	C	N	O	S	0	0
			854	538	164	151	1		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	190	Total	C	N	O	S	0	0
			1501	939	285	270	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	223	Total	C	N	O	S	0	0
			1811	1133	361	311	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	168	Total	C	N	O	S	0	0
			1346	862	239	244	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	180	Total	C	N	O	S	0	0
			1474	925	294	250	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	171	Total	C	N	O	S	0	0
			1425	908	284	232	1		

- Molecule 11 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LA	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 12 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LC	139	Total	C	N	O	S	0	0
			1098	699	207	189	3		

- Molecule 13 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LD	147	Total	C	N	O	S	0	0
			1204	767	225	206	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	104	Total	C	N	O	S	0	0
			851	543	158	145	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 16 is a protein called WD repeat-containing protein 75.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	746	Total	C	N	O	S	0	0
			5987	3846	1005	1101	35		

- Molecule 17 is a protein called Nucleolar protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	537	Total	C	N	O	S	0	0
			3889	2508	654	706	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	469	Total	C	N	O	S	0	0
			3711	2372	637	688	14		

- Molecule 19 is a protein called WD repeat-containing protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	118	Total	C	N	O	S	0	0
			943	612	163	163	5		
19	LL	510	Total	C	N	O	S	0	0
			3982	2538	686	731	27		

- Molecule 20 is a protein called HEAT repeat-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	2005	Total	C	N	O	S	0	0
			15820	10259	2597	2883	81		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LN	671	Total	C	N	O	S	0	0
			5299	3394	925	956	24		

- Molecule 22 is a protein called Periodic tryptophan protein 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	848	Total	C	N	O	S	0	0
			6676	4258	1151	1234	33		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 6 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LP	567	Total	C	N	O	S	0	0
			4705	3022	808	847	28		

- Molecule 24 is a protein called WD repeat-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LQ	828	Total	C	N	O	S	0	0
			6438	4103	1108	1194	33		

- Molecule 25 is a protein called Transducin beta-like protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	773	Total	C	N	O	S	0	0
			6015	3789	1079	1116	31		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 18 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	453	Total	C	N	O	S	0	0
			3560	2235	631	671	23		

- Molecule 27 is a protein called WD repeat-containing protein 36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	869	Total	C	N	O	S	0	0
			6756	4321	1158	1244	33		

- Molecule 28 is a protein called DDB1- and CUL4-associated factor 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	445	Total	C	N	O	S	0	0
			3611	2282	653	651	25		

- Molecule 29 is a protein called WD repeat-containing protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LW	453	Total	C	N	O	S	0	0
			3519	2221	637	646	15		

- Molecule 30 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LZ	183	Total	C	N	O	S	0	0
			1532	966	292	270	4		

- Molecule 31 is a RNA chain called 5'ETS rRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	N0	22	Total	C	O	P	0	0
			264	110	132	22		

- Molecule 32 is a protein called U3 small nucleolar ribonucleoprotein protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	NA	249	Total	C	N	O	S	0	0
			2055	1299	359	391	6		

- Molecule 33 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	NB	73	Total	C	N	O	0	0
			617	379	140	98		

- Molecule 34 is a protein called Neuroguidin.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	NC	94	Total	C	N	O	S	0	0
			779	469	160	147	3		

- Molecule 35 is a protein called Nucleolar protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	ND	84	Total	C	N	O	S	0	0
			696	438	143	114	1		

- Molecule 36 is a protein called Uncharacterized protein C1orf131.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NE	100	Total	C	N	O	S	0	0
			799	509	143	146	1		

- Molecule 37 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	NF	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 38 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	NG	116	Total	C	N	O	S	0	0
			861	531	159	165	6		

- Molecule 39 is a protein called Nucleolar protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	NH	1066	Total	C	N	O	S	0	0
			8374	5345	1491	1506	32		

- Molecule 40 is a protein called Ribosomal RNA-processing protein 7 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NI	234	Total	C	N	O	S	0	0
			1840	1171	329	336	4		

- Molecule 41 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	NJ	827	Total	C	N	O	S	0	0
			6526	4187	1126	1178	35		
41	NK	815	Total	C	N	O	S	0	0
			6419	4118	1109	1160	32		

- Molecule 42 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	NM	233	Total	C	N	O	S	0	0
			1873	1186	339	334	14		

- Molecule 43 is a protein called Protein AATF.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	NN	42	Total	C	N	O	S	0	0
			340	215	63	60	2		

- Molecule 44 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	NO	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 45 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	NQ	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 46 is a protein called RRP12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	NR	861	Total	C	N	O		0	0
			4305	2583	861	861			

- Molecule 47 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	NT	58	Total	C	N	O	S	0	0
			470	295	89	79	7		

- Molecule 48 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	NU	60	Total	C	N	O	S	0	0
			495	314	98	81	2		

- Molecule 49 is a protein called Nucleolar protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	NW	311	Total	C	N	O	S	0	0
			2498	1599	413	472	14		

- Molecule 50 is a protein called KRR1 small subunit processome component homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NY	274	Total	C	N	O	S	0	0
			2222	1422	391	400	9		

- Molecule 51 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SA	396	Total	C	N	O	S	0	0
			3077	1948	542	575	12		

- Molecule 52 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SB	440	Total	C	N	O	S	0	0
			3439	2179	596	642	22		

- Molecule 53 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SC	229	Total	C	N	O	S	0	0
			1781	1129	322	323	7		
53	SD	237	Total	C	N	O	S	0	0
			1841	1163	337	334	7		

- Molecule 54 is a protein called NHP2-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	125	Total	C	N	O	S	0	0
			968	611	172	180	5		
54	SF	123	Total	C	N	O	S	0	0
			955	604	170	176	5		

- Molecule 55 is a protein called U3 small nucleolar RNA-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG	389	Total	C	N	O	S	1	0
			2884	1809	534	528	13		

- Molecule 56 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SH	368	Total	C	N	O	S	0	0
			2832	1803	495	518	16		

- Molecule 57 is a protein called Ribosome biogenesis protein BMS1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SI	844	Total	C	N	O	S	0	0
			6803	4351	1230	1188	34		

- Molecule 58 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SJ	204	Total	C	N	O	S	0	0
			1579	1012	272	286	9		
58	SK	204	Total	C	N	O	S	0	0
			1579	1012	272	286	9		

- Molecule 59 is a protein called rRNA-processing protein FCF1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SL	192	Total	C	N	O	S	0	0
			1586	1006	290	275	15		

- Molecule 60 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SM	290	Total	C	N	O	S	0	0
			2369	1485	451	424	9		

- Molecule 61 is a protein called Small subunit processome component 20 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SP	1993	Total	C	N	O	S	0	0
			16078	10412	2689	2897	80		

- Molecule 62 is a protein called Deoxynucleotidyltransferase terminal-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SQ	187	Total	C	N	O	S	0	0
			1533	972	278	277	6		

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SR	108	Total	C	N	O	S	0	0
			816	521	153	140	2		

- Molecule 64 is a protein called U3 small nucleolar RNA-associated protein 14 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	197	Total	C	N	O	S	0	0
			1626	1039	301	285	1		

- Molecule 65 is a protein called Nucleolar protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	ST	568	Total	C	N	O	S	0	0
			4170	2634	760	755	21		

- Molecule 66 is a protein called Nucleolar complex protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SU	442	Total	C	N	O	S	0	0
			3154	2030	565	551	8		

- Molecule 67 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SW	180	Total	C	N	O	S	0	0
			1413	906	257	246	4		

- Molecule 68 is a protein called Unassigned peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	Sx	38	Total	C	N	O	0	0
			190	114	38	38		

- Molecule 69 is a protein called Unassigned peptides.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	SX	139	Total	C	N	O	0	0
			695	417	139	139		

- Molecule 70 is a protein called Probable U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY	238	Total	C	N	O	S	0	0
			2024	1280	385	353	6		

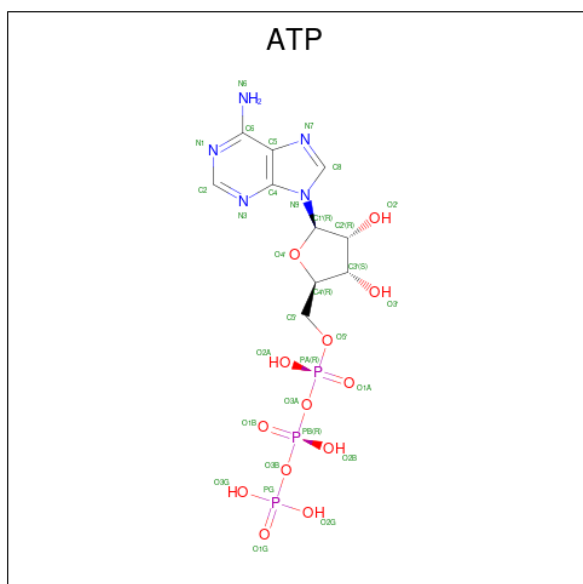
- Molecule 71 is a protein called Bystin.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	290	Total	C	N	O	S	0	0
			2222	1438	392	383	9		

- Molecule 72 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
72	L1	19	Total	Mg	0
			19	19	
72	NH	1	Total	Mg	0
			1	1	
72	SI	1	Total	Mg	0
			1	1	
72	SL	1	Total	Mg	0
			1	1	

- Molecule 73 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



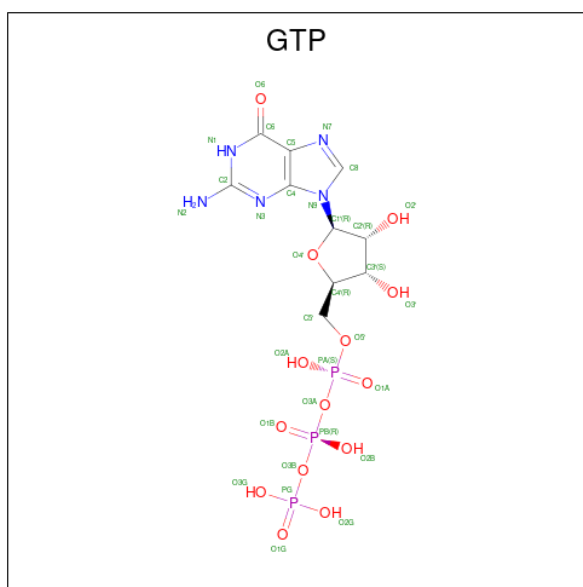
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Mol	Chain	Residues	Atoms					AltConf
73	NK	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 74 is ZINC ION (CCD ID: ZN) (formula: Zn).

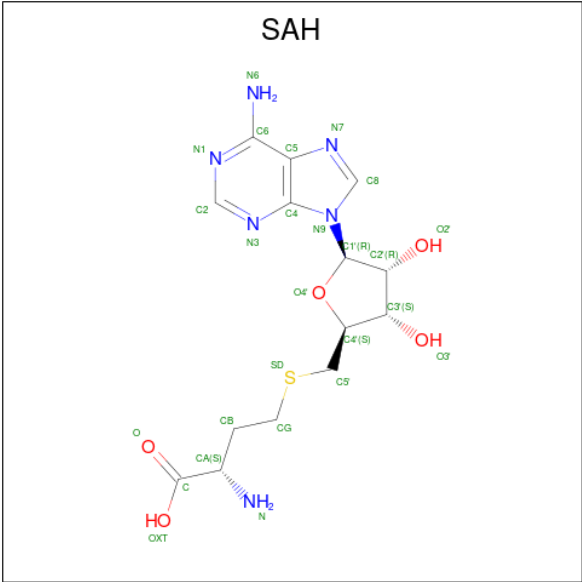
Mol	Chain	Residues	Atoms		AltConf
74	NQ	1	Total	Zn	0
			1	1	
74	NT	1	Total	Zn	0
			1	1	
74	SL	1	Total	Zn	0
			1	1	

- Molecule 75 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 76 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).

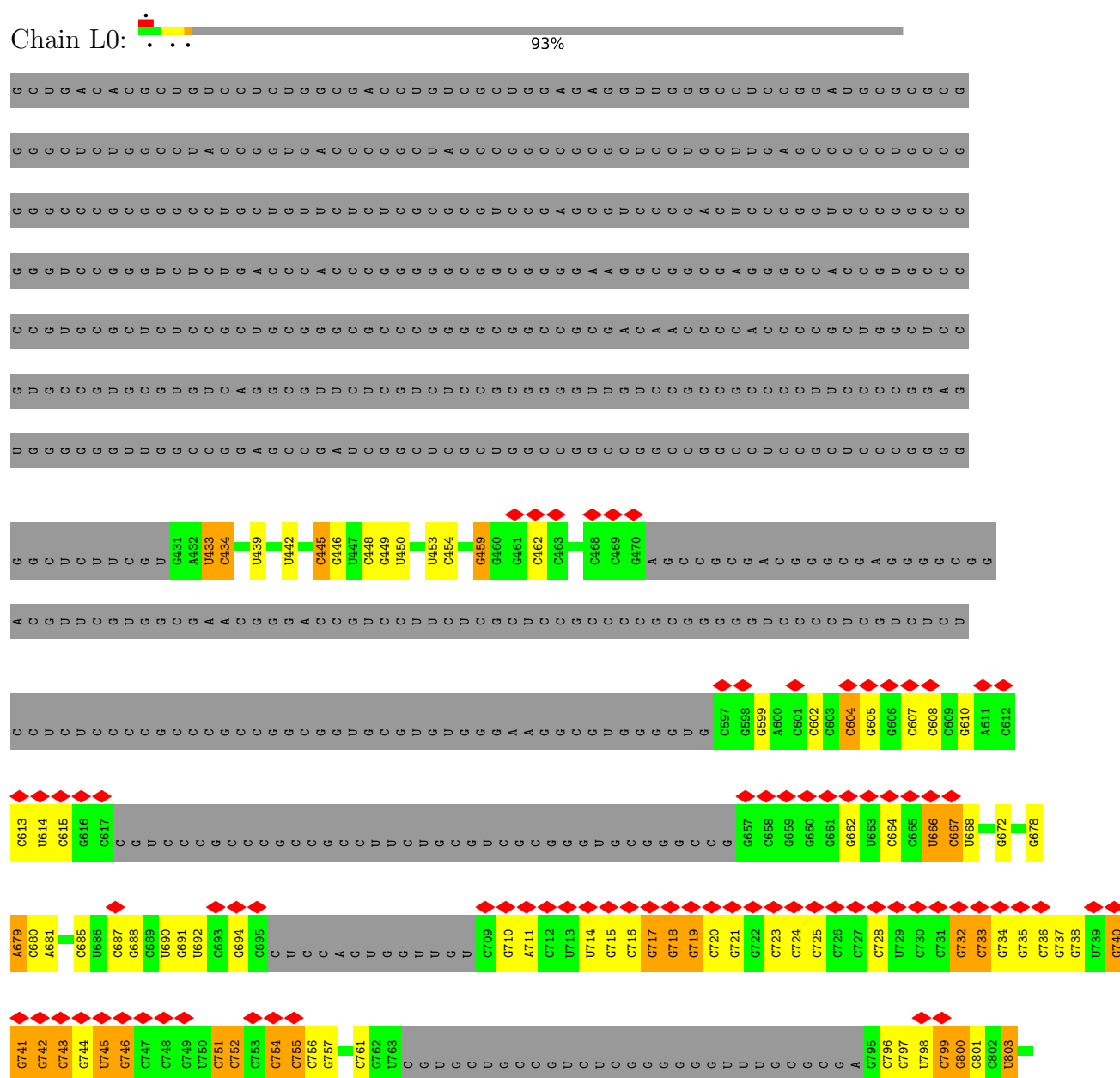


Mol	Chain	Residues	Atoms					AltConf
76	SJ	1	Total	C	N	O	S	0
			26	14	6	5	1	
76	SK	1	Total	C	N	O	S	0
			26	14	6	5	1	

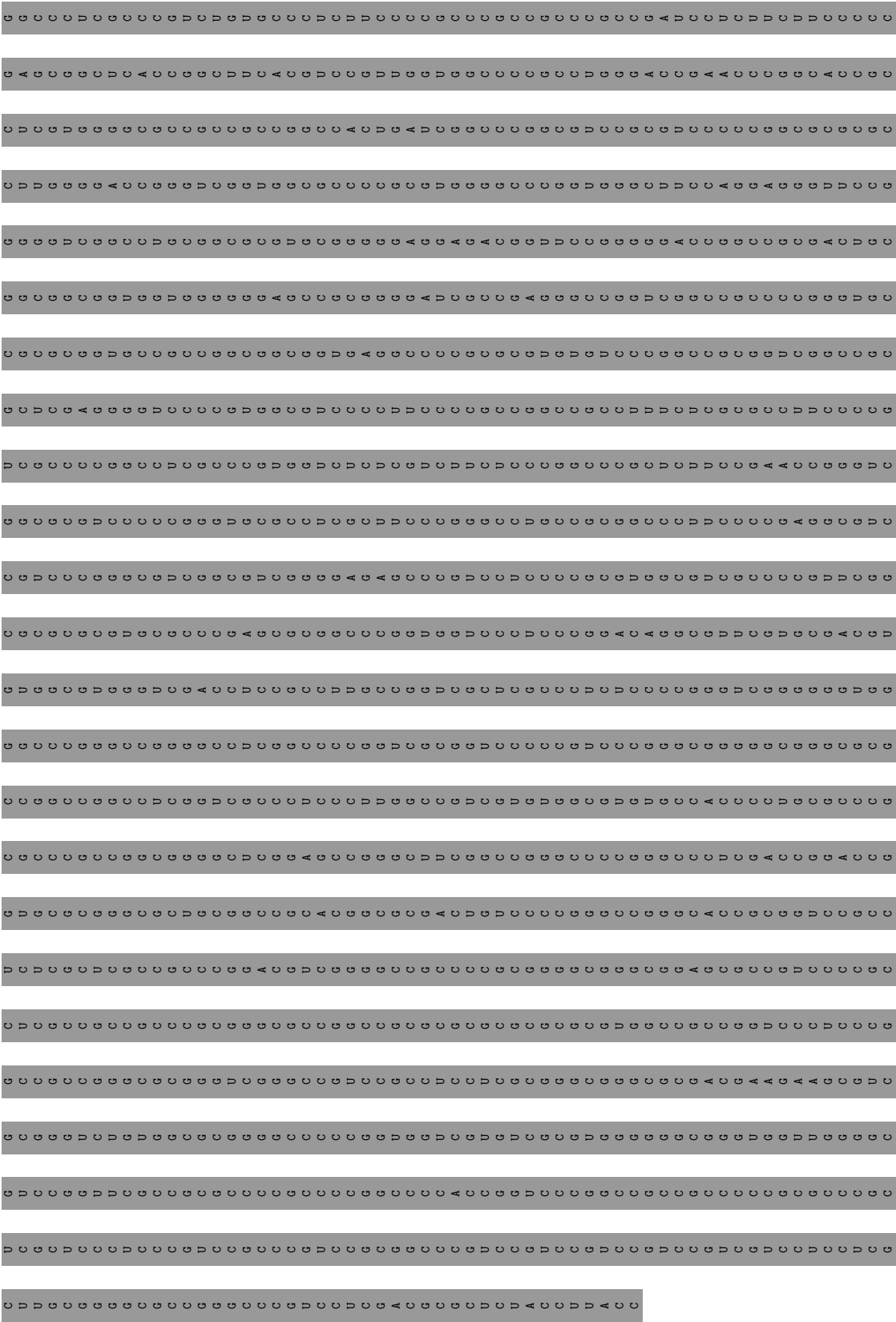
3 Residue-property plots

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

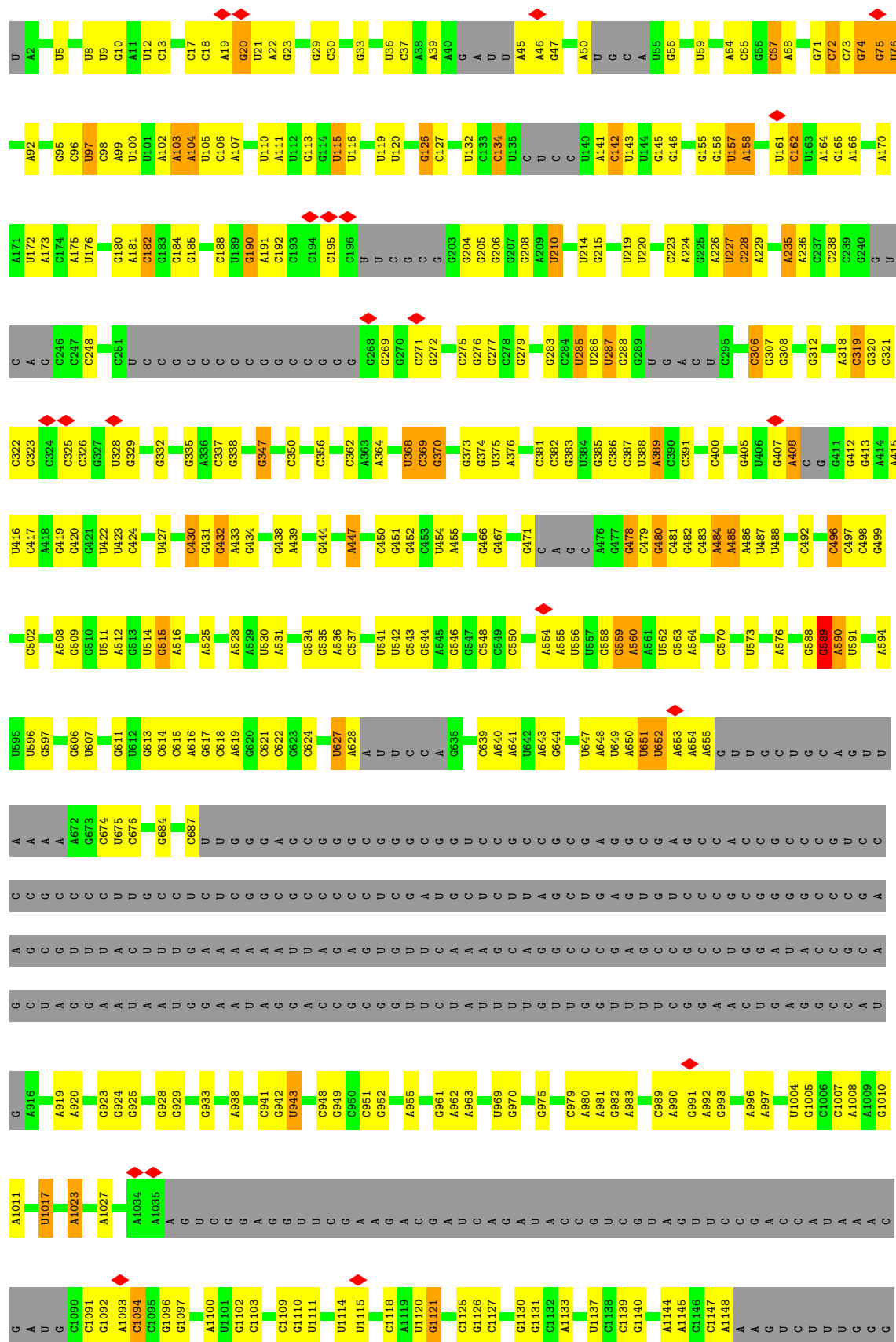


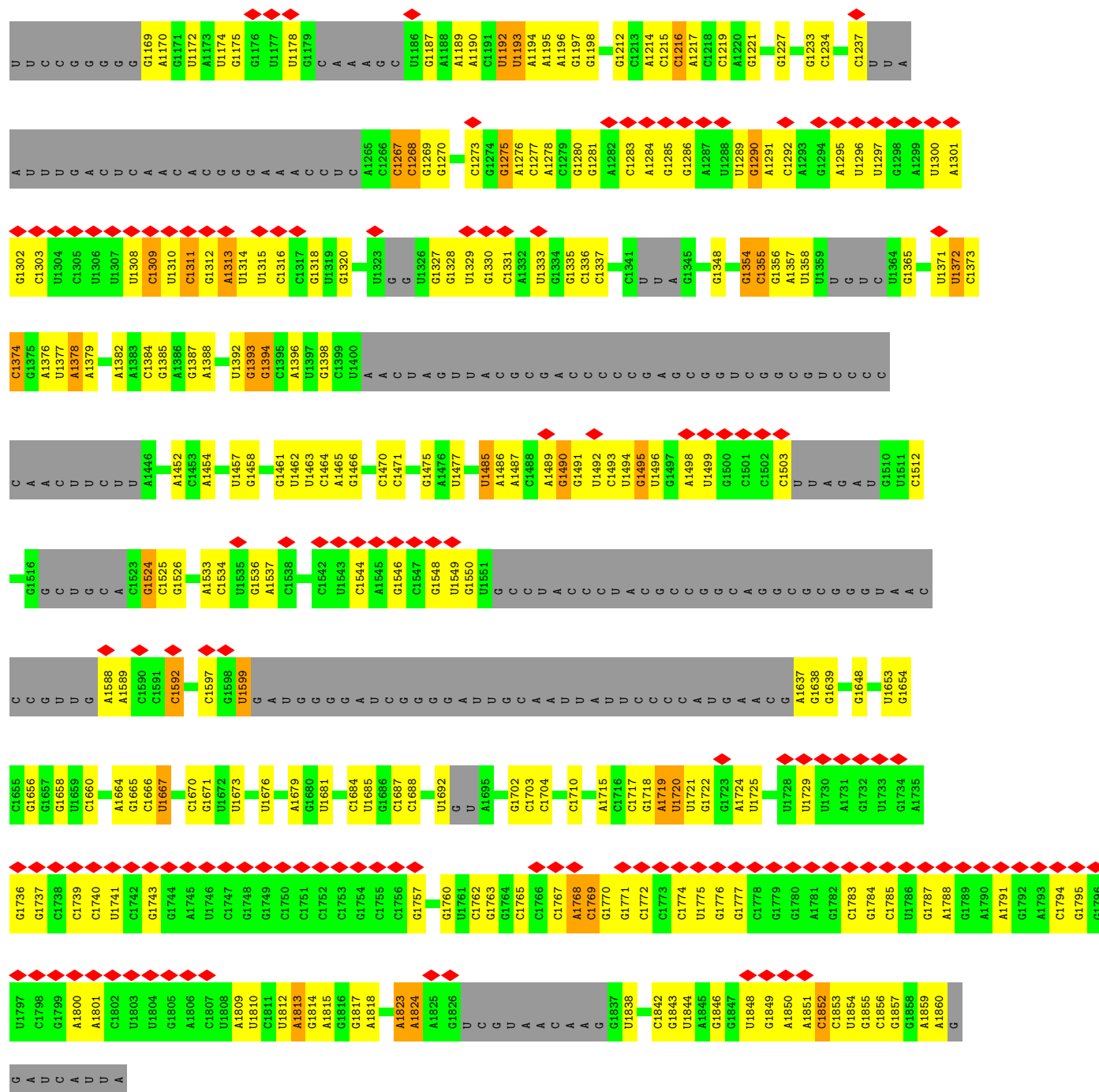




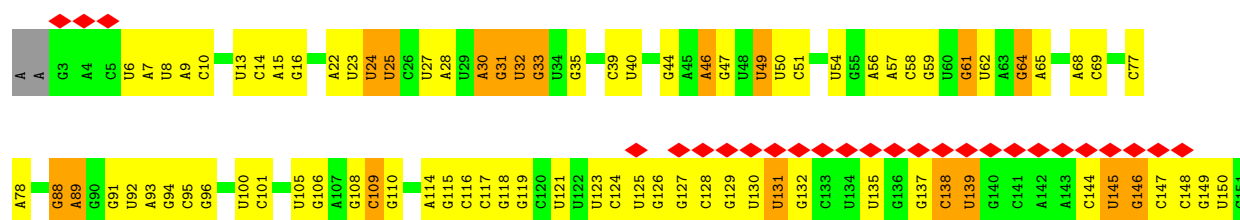
● Molecule 2: 18S rRNA

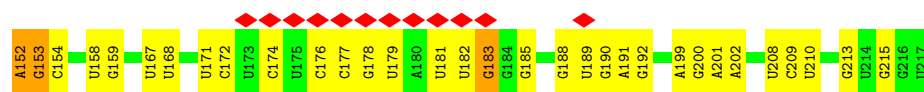




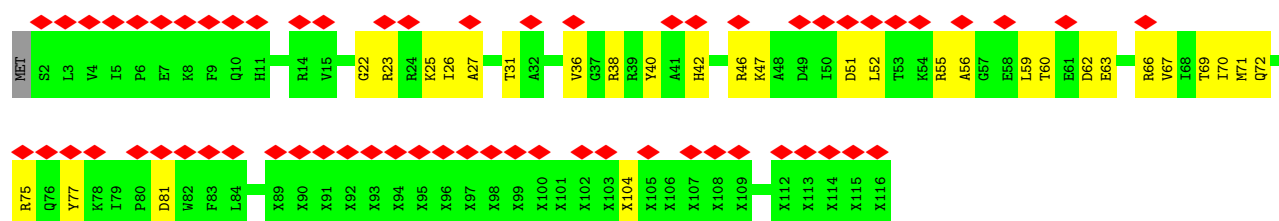
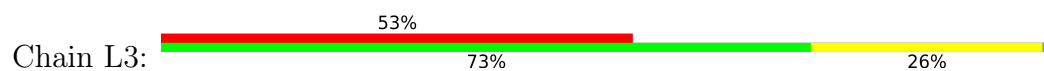


• Molecule 3: U3 snoRNA

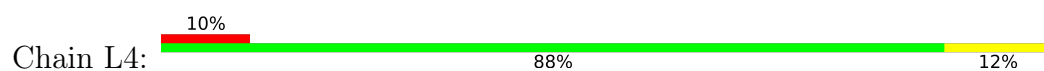




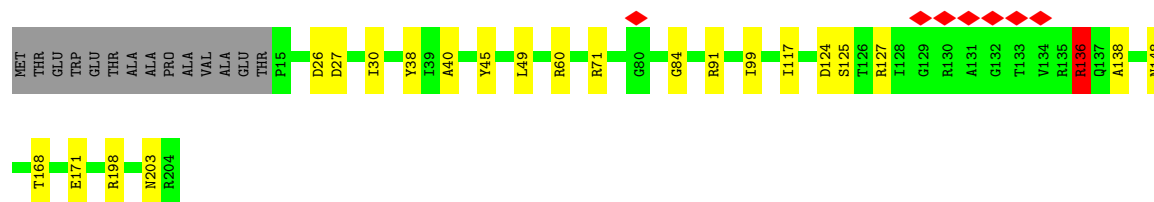
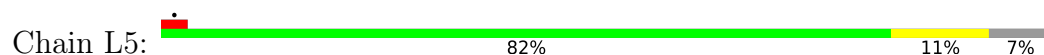
- Molecule 4: 40S ribosomal protein S18



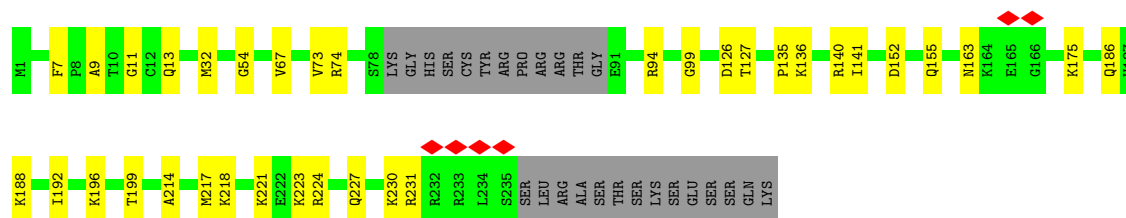
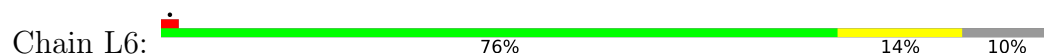
- Molecule 5: 40S ribosomal protein S4, X isoform



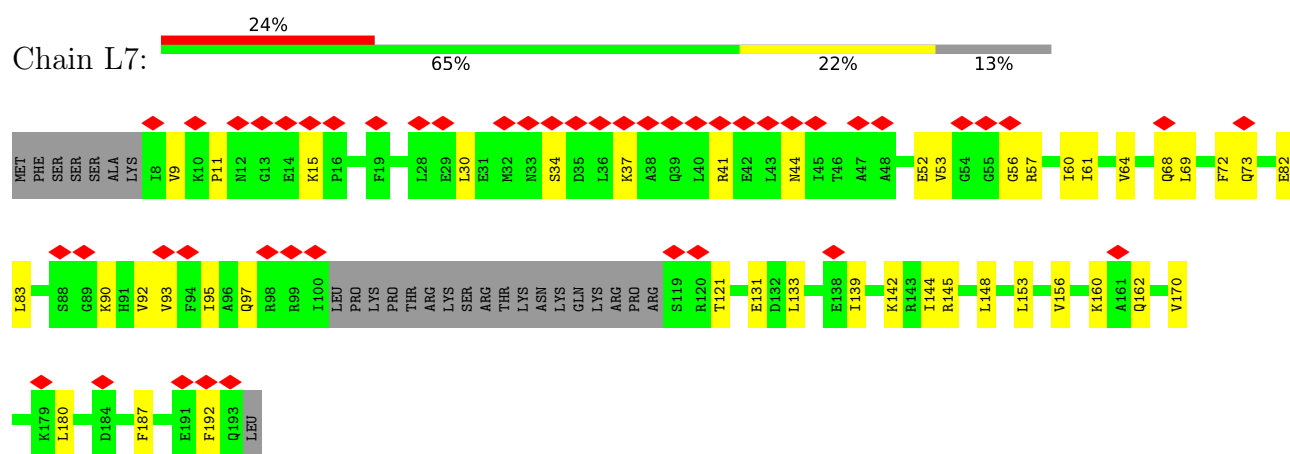
- Molecule 6: 40S ribosomal protein S5



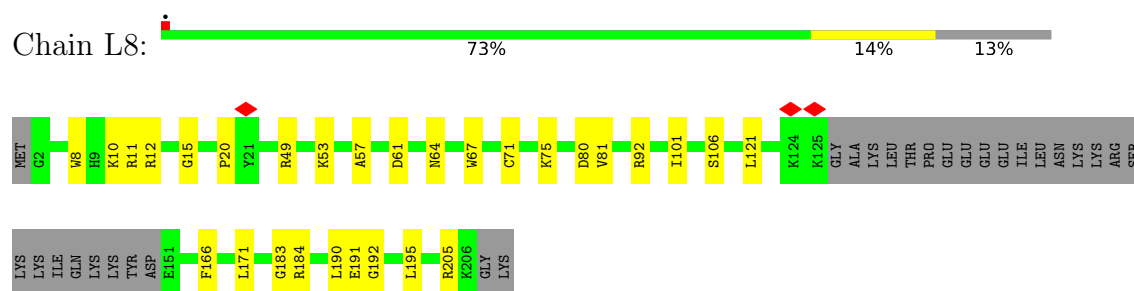
- Molecule 7: 40S ribosomal protein S6



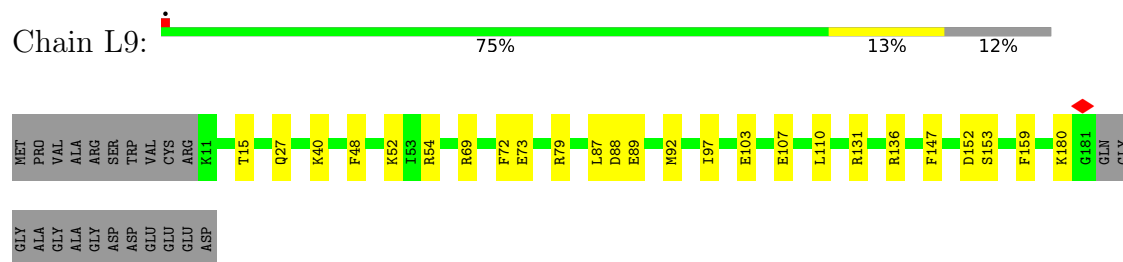
- Molecule 8: 40S ribosomal protein S7



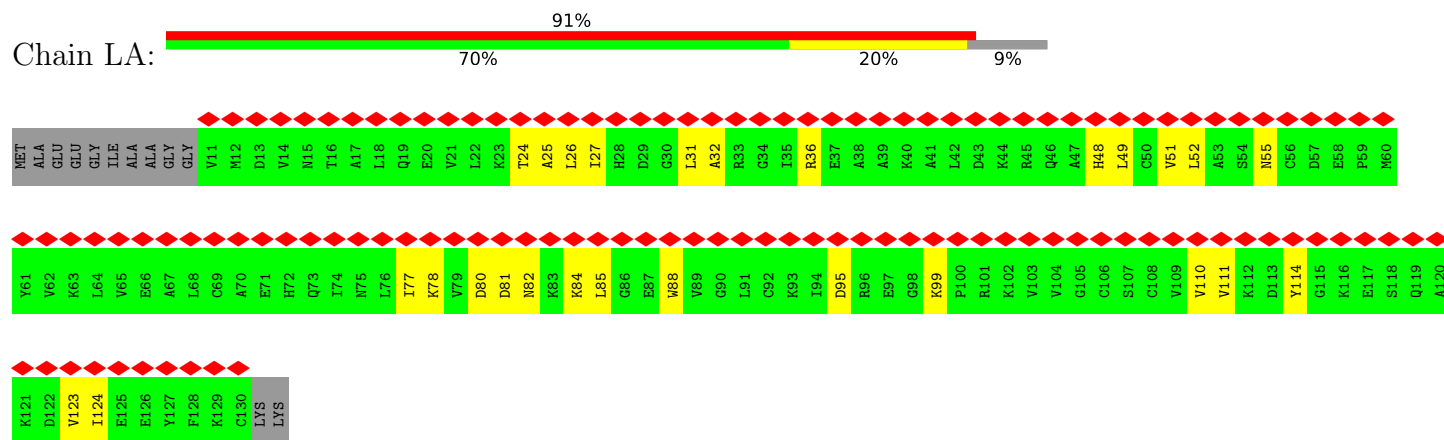
- Molecule 9: 40S ribosomal protein S8



- Molecule 10: 40S ribosomal protein S9

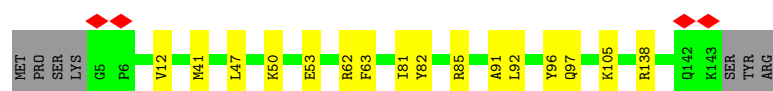


- Molecule 11: 40S ribosomal protein S12



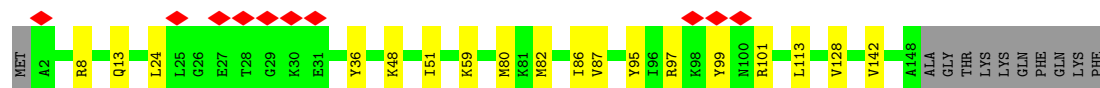
- Molecule 12: 40S ribosomal protein S16

Chain LC: 



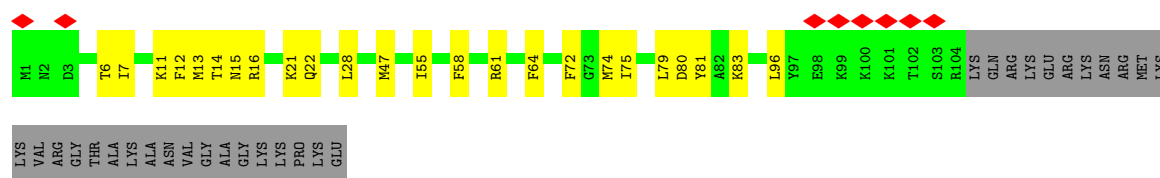
- Molecule 13: 40S ribosomal protein S11

Chain LD: 



- Molecule 14: 40S ribosomal protein S24

Chain LF: 



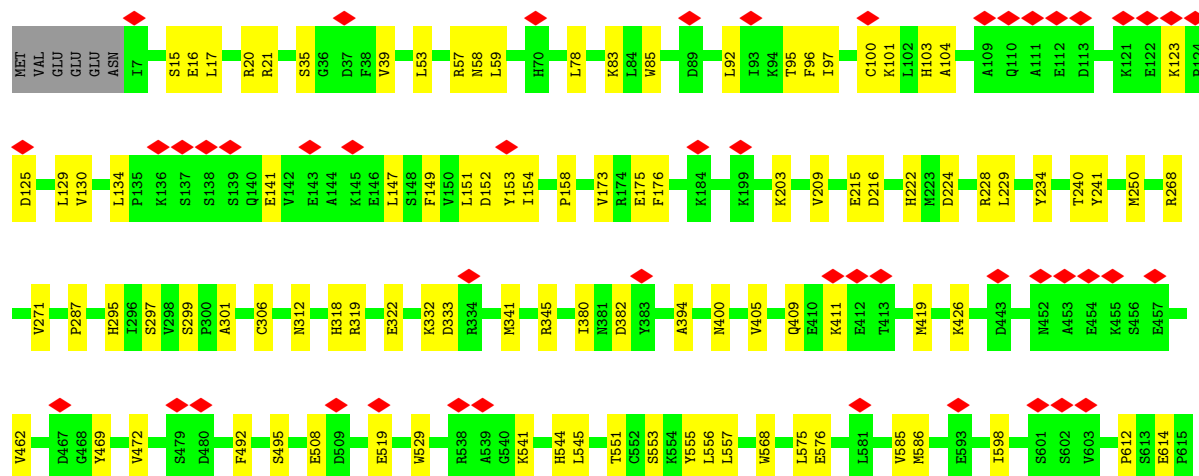
- Molecule 15: 40S ribosomal protein S28

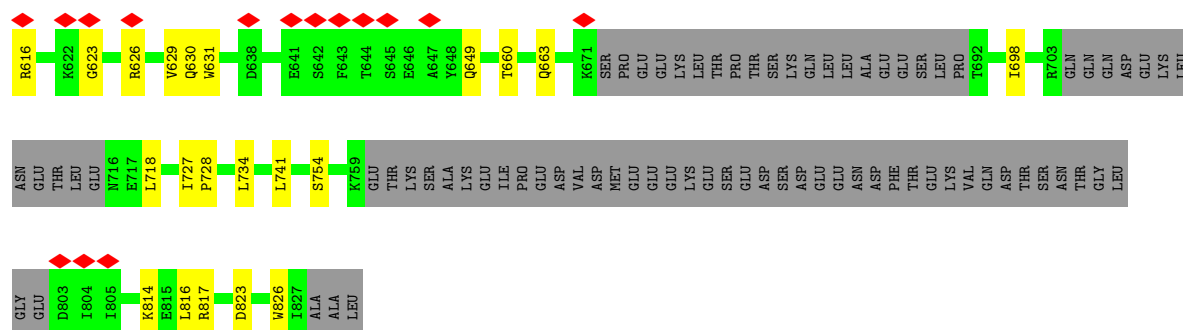
Chain LG: 



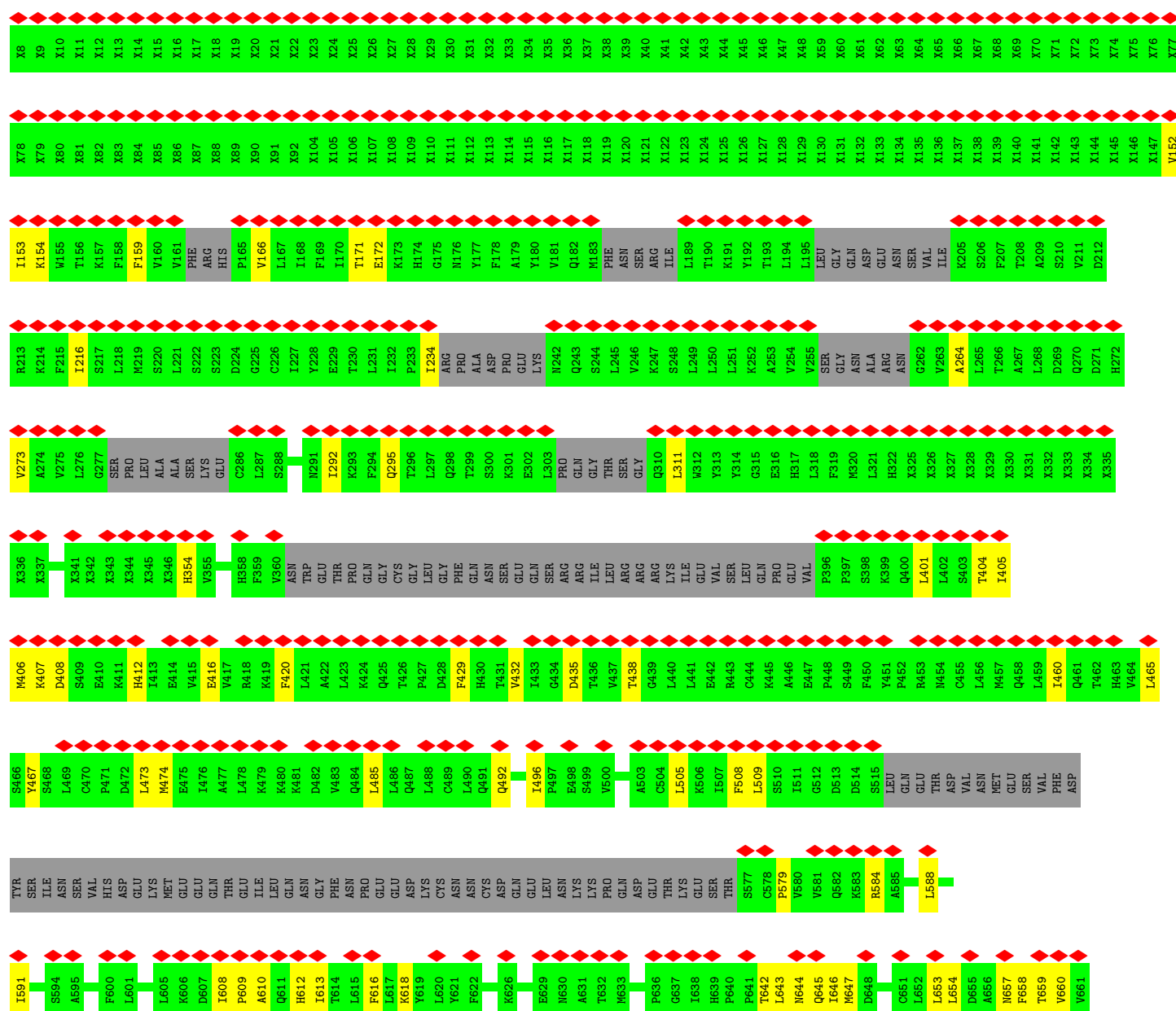
- Molecule 16: WD repeat-containing protein 75

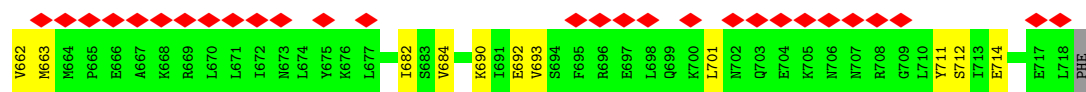
Chain LH: 



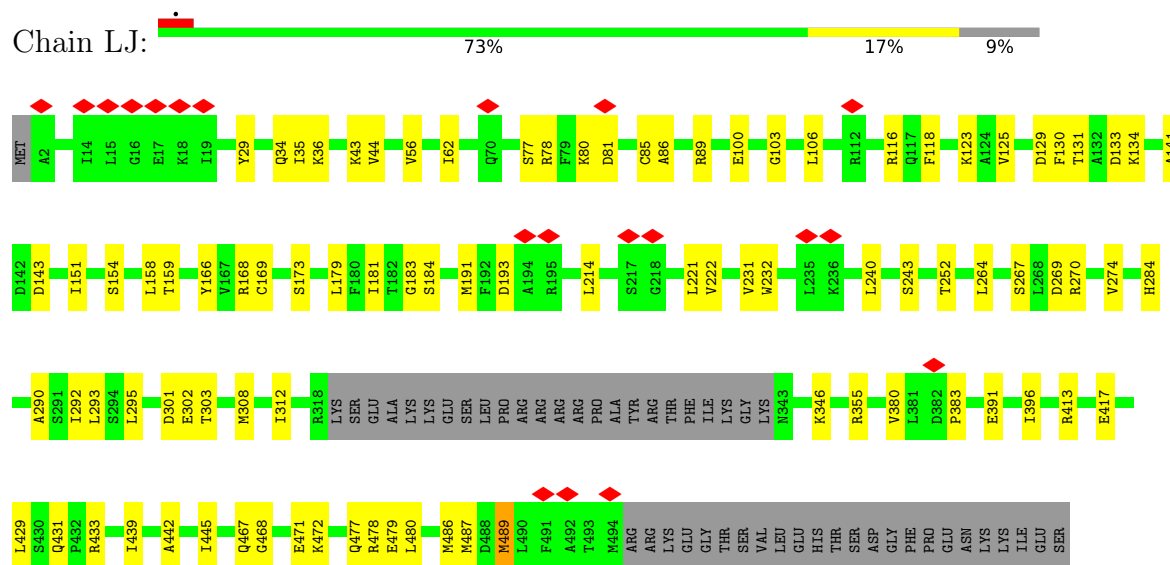


• Molecule 17: Nucleolar protein 11

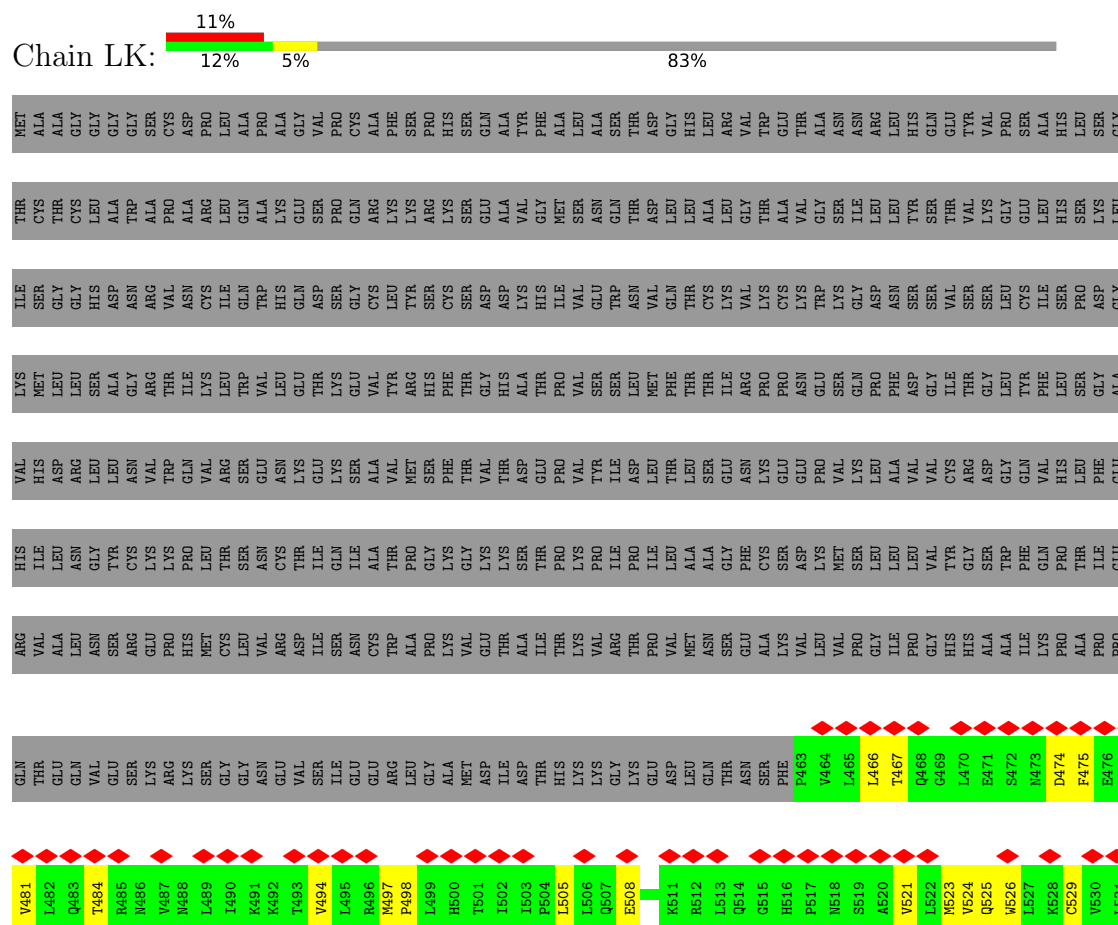


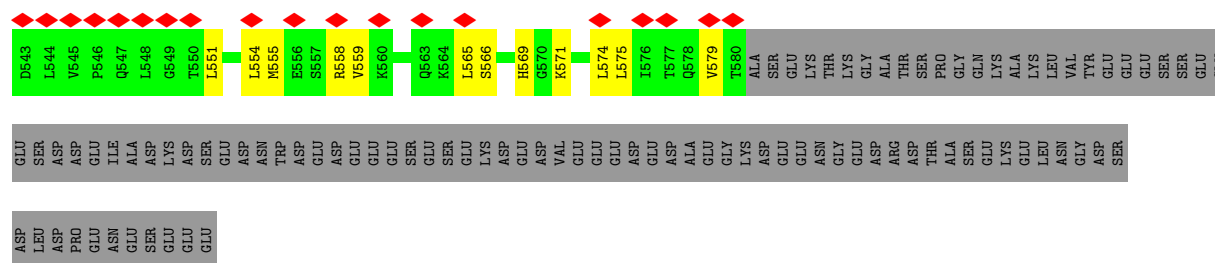


- Molecule 18: U3 small nucleolar RNA-associated protein 15 homolog

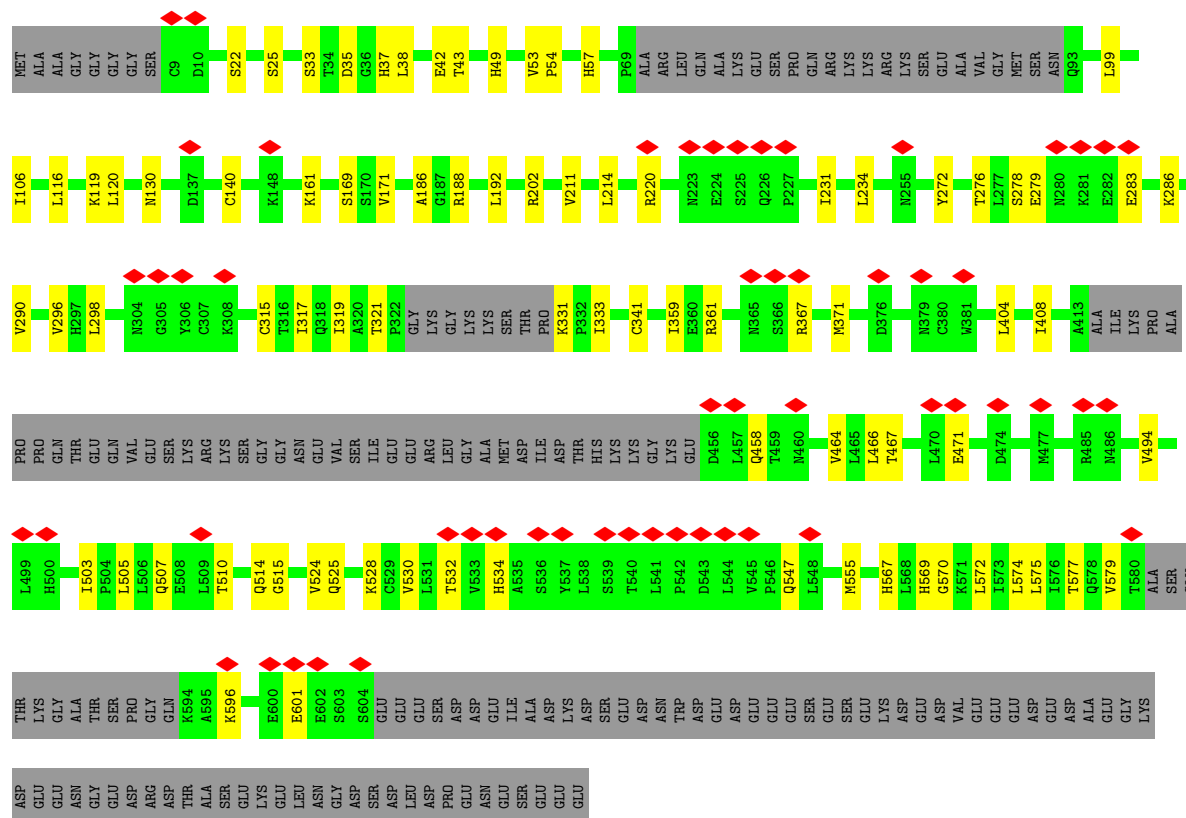


- Molecule 19: WD repeat-containing protein 43

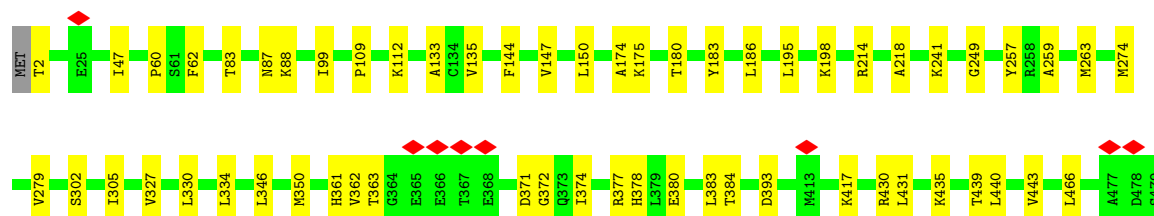
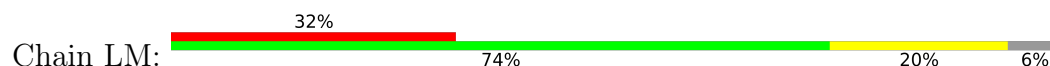




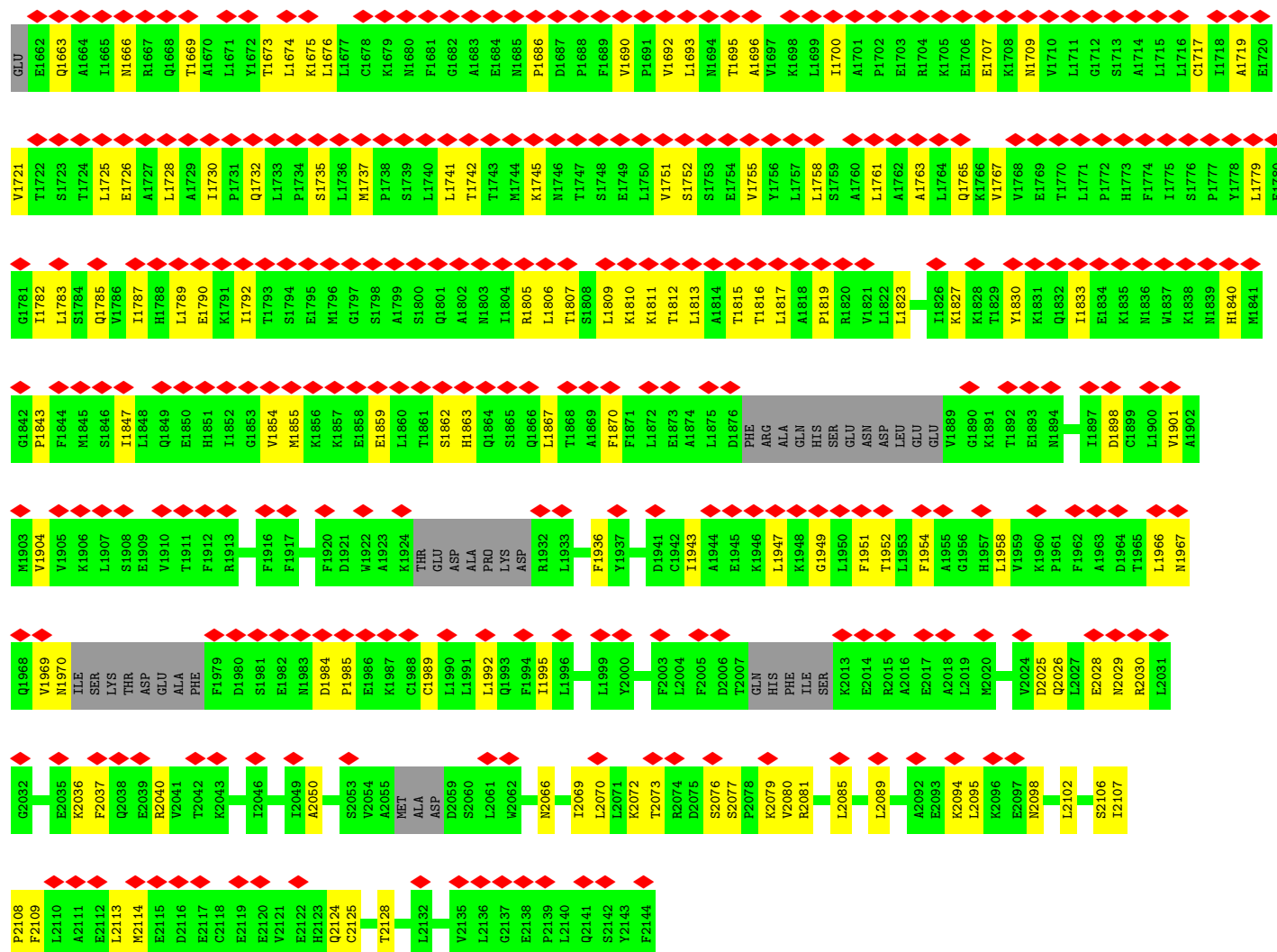
• Molecule 19: WD repeat-containing protein 43



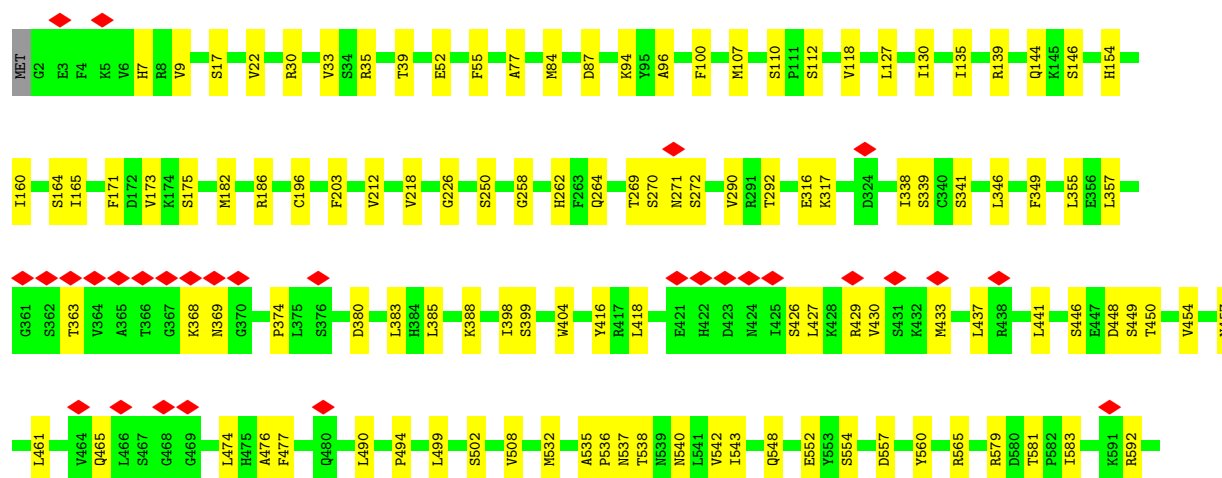
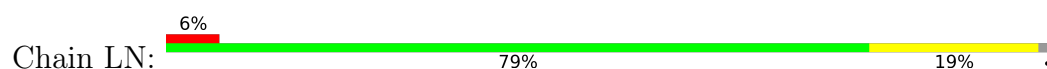
• Molecule 20: HEAT repeat-containing protein 1

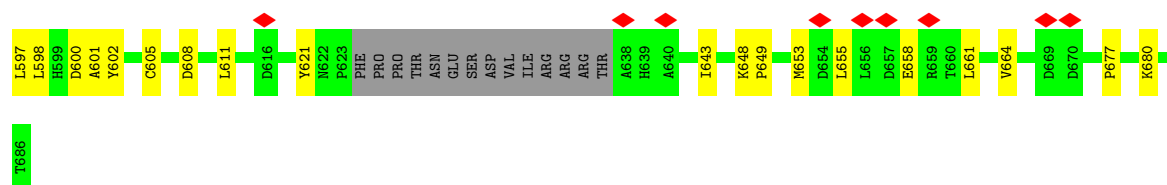




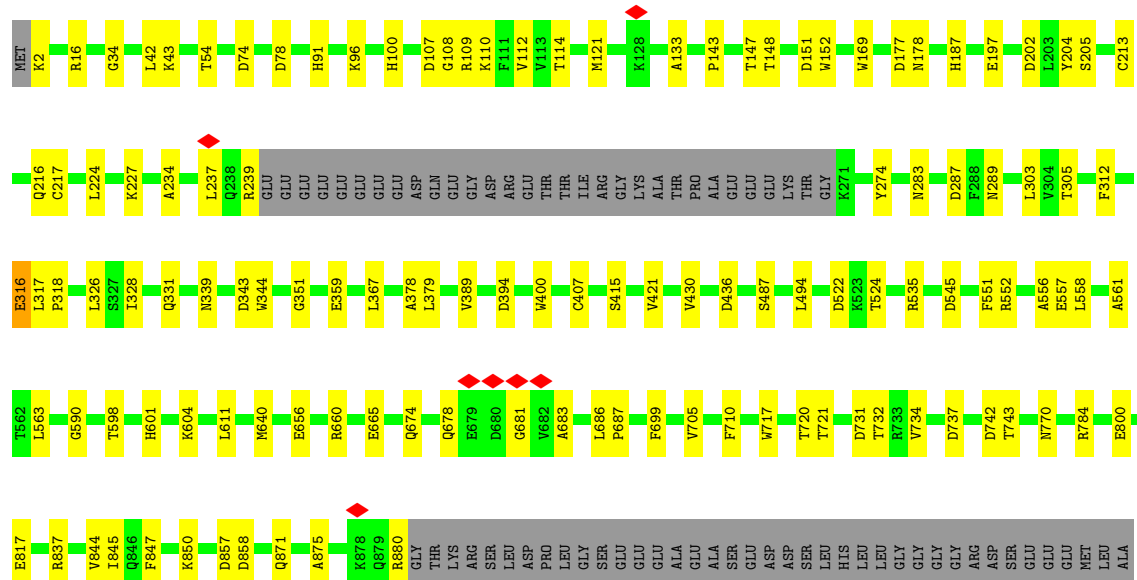
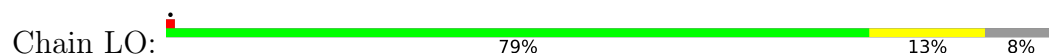


● Molecule 21: U3 small nucleolar RNA-associated protein 4 homolog

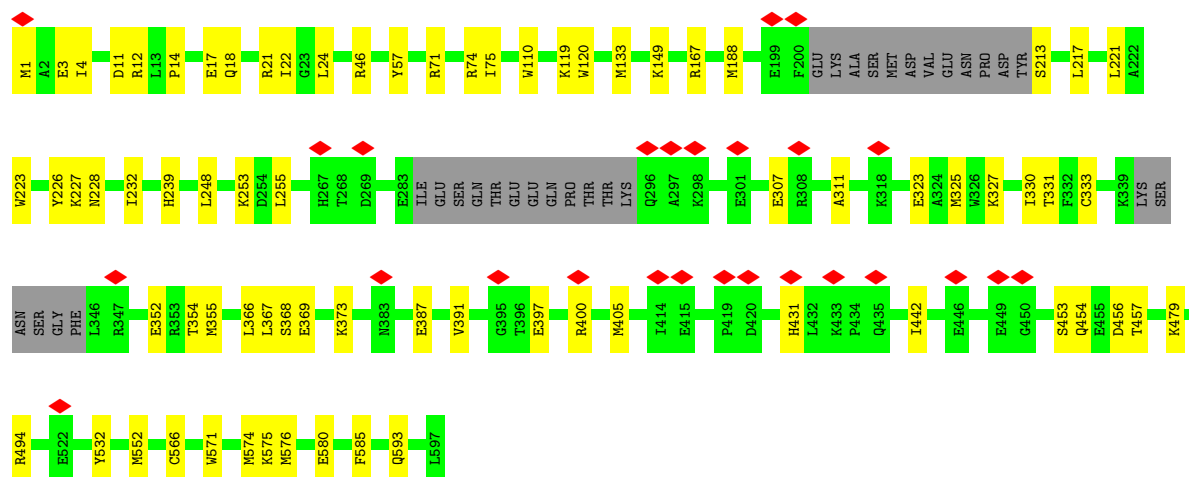
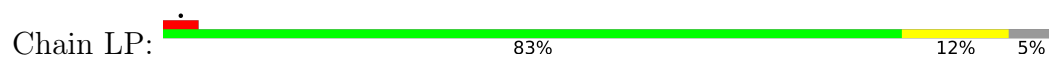




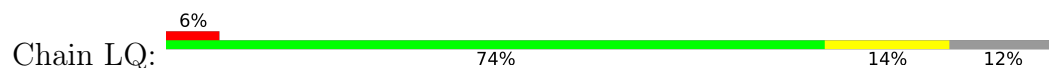
- Molecule 22: Periodic tryptophan protein 2 homolog

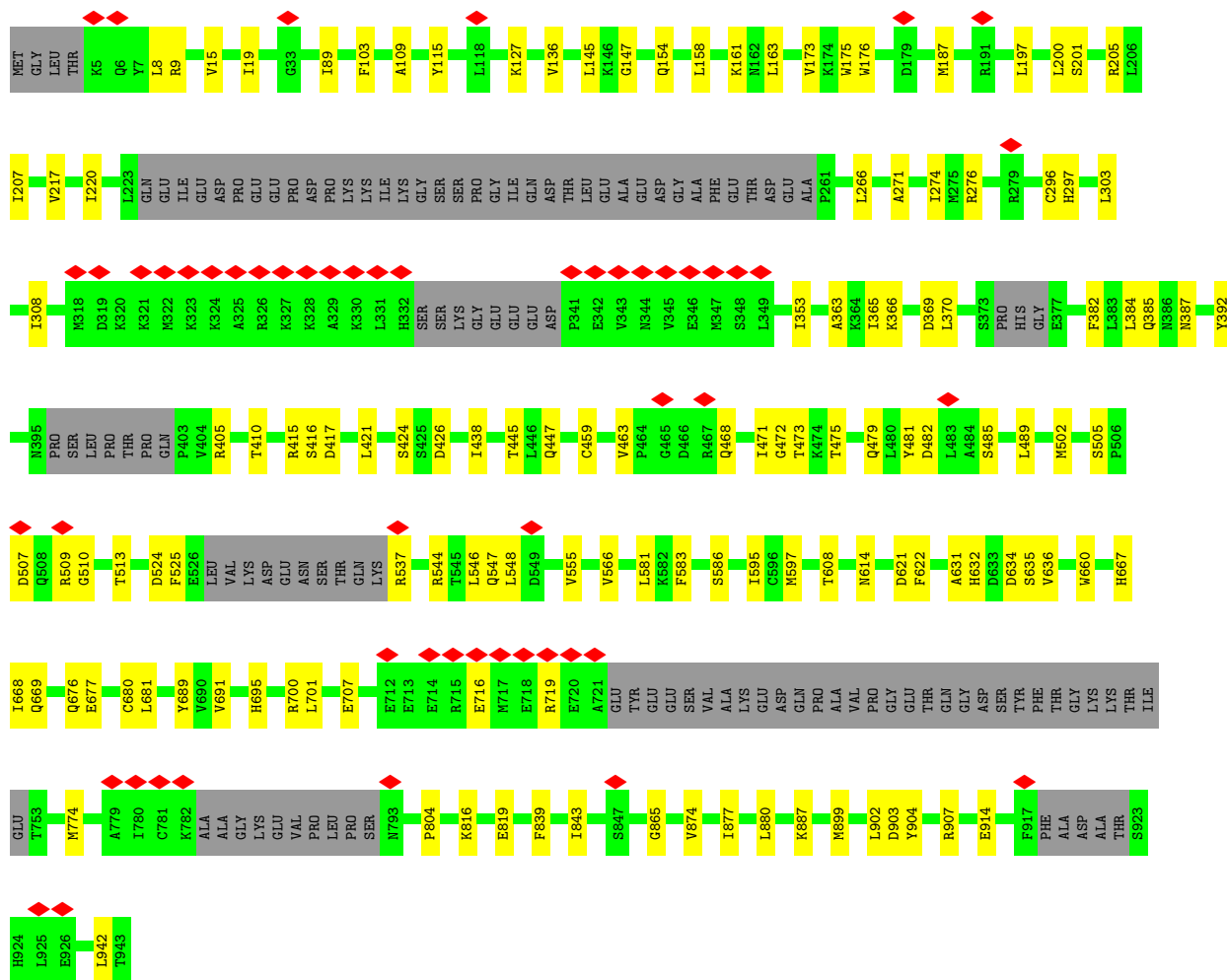


- Molecule 23: U3 small nucleolar RNA-associated protein 6 homolog



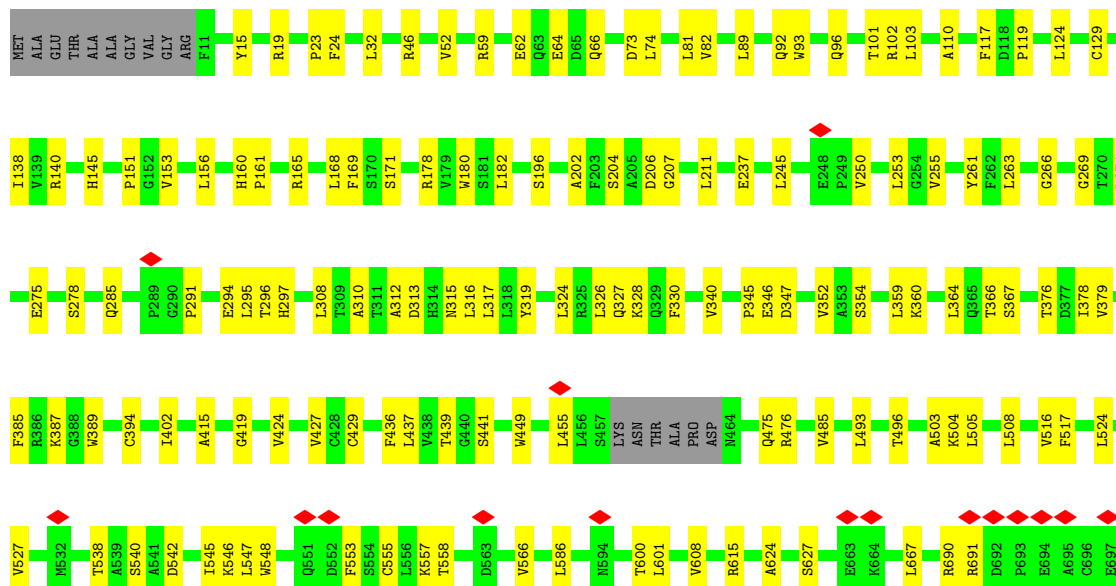
- Molecule 24: WD repeat-containing protein 3





• Molecule 25: Transducin beta-like protein 3

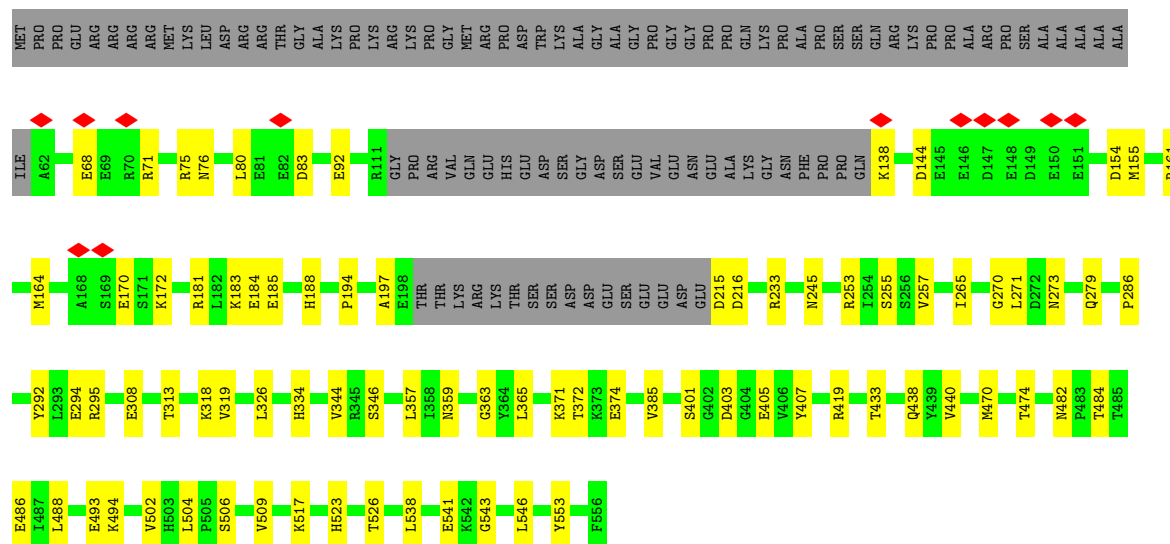
Chain LR:





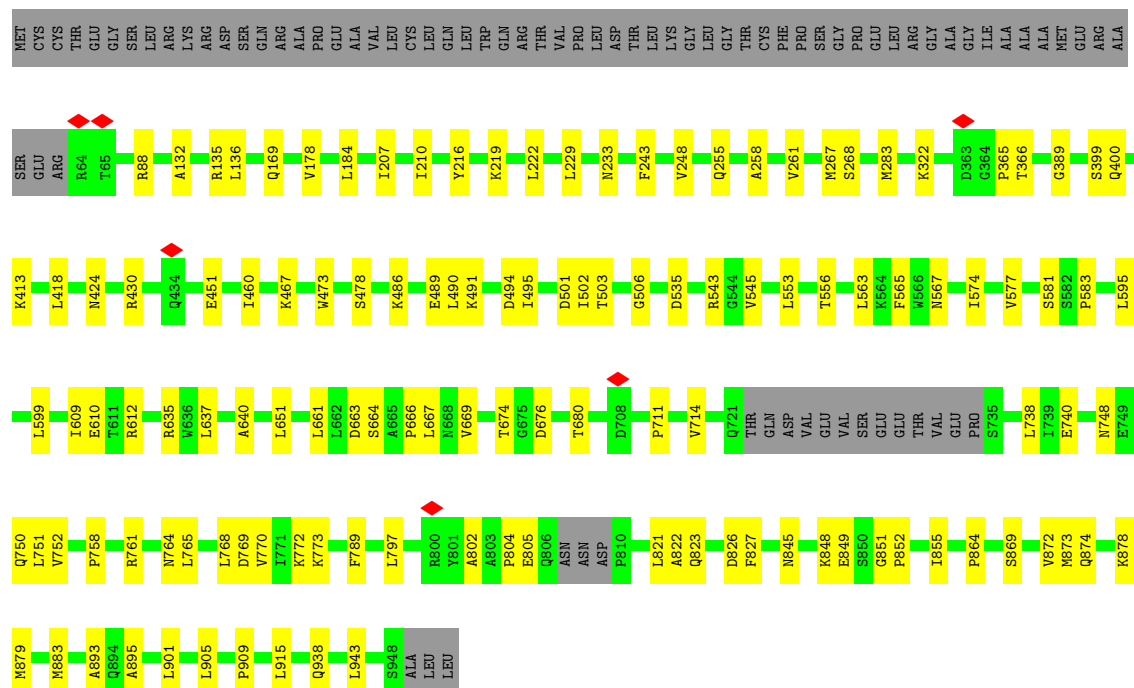
- Molecule 26: U3 small nucleolar RNA-associated protein 18 homolog

Chain LS: 67% 15% 19%



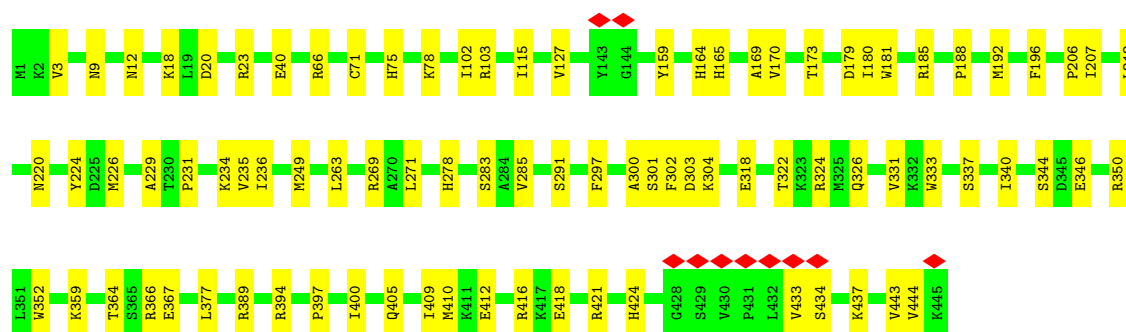
- Molecule 27: WD repeat-containing protein 36

Chain LT: 78% 13% 9%

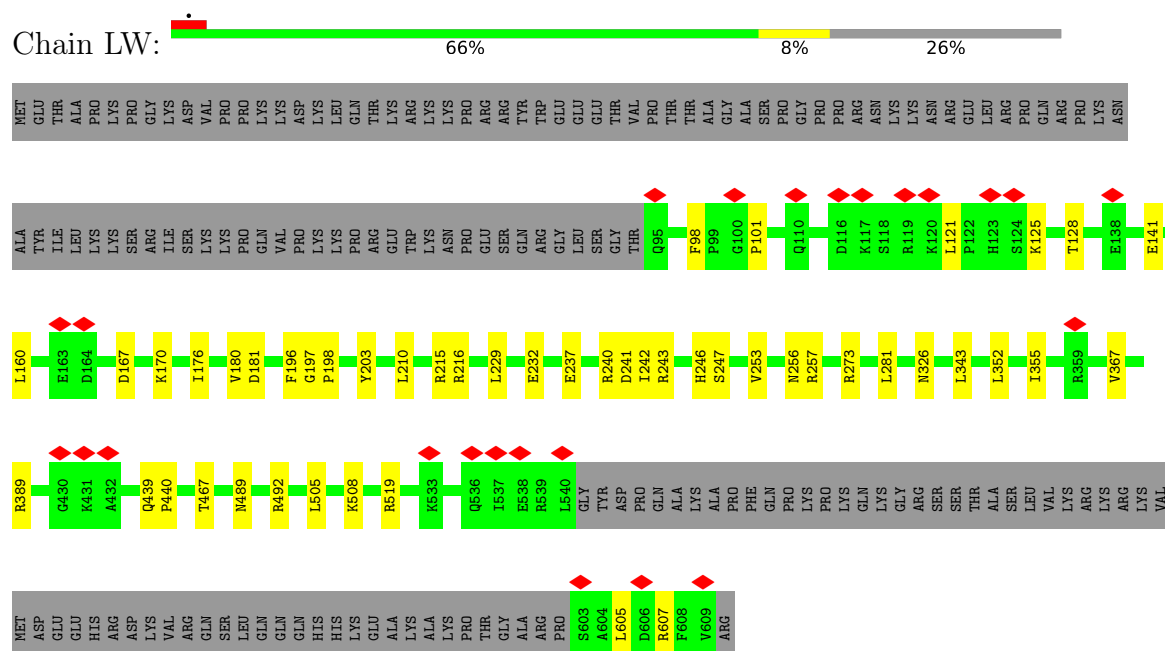


- Molecule 28: DDB1- and CUL4-associated factor 13

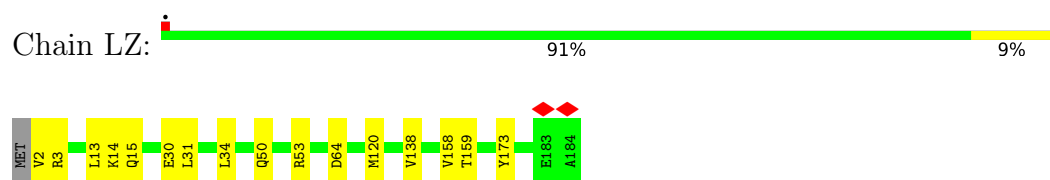
Chain LU: 80% 20%



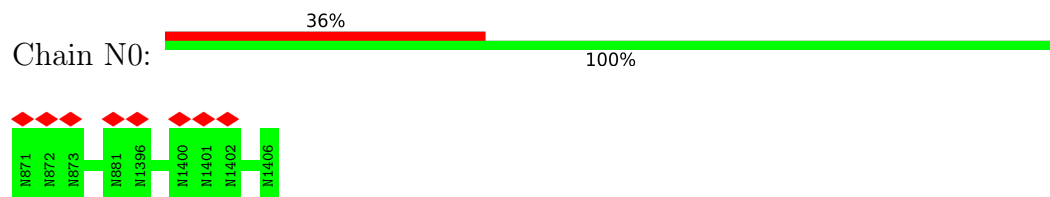
- Molecule 29: WD repeat-containing protein 46



- Molecule 30: U3 small nucleolar ribonucleoprotein protein IMP3



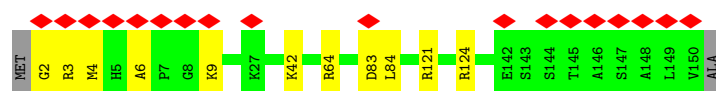
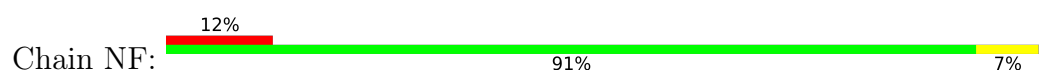
- Molecule 31: 5'ETS rRNA



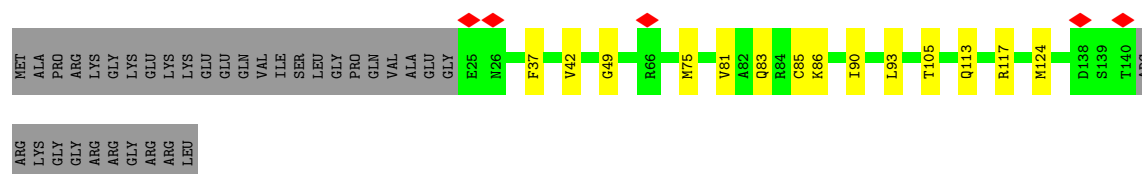
- Molecule 32: U3 small nucleolar ribonucleoprotein protein MPP10



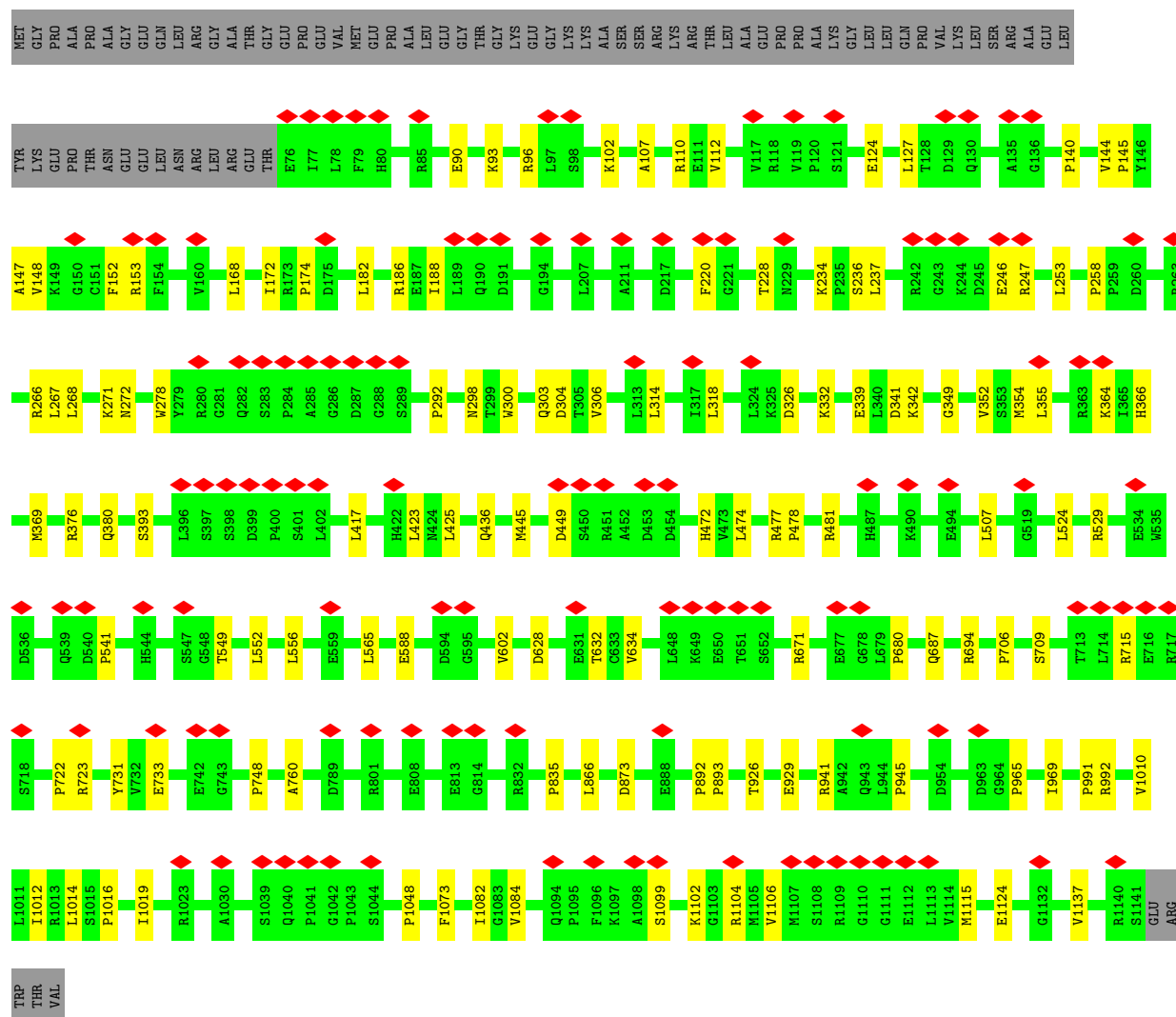
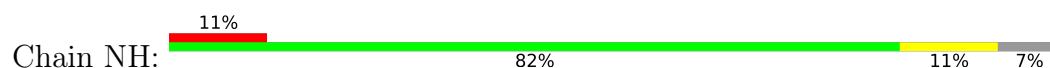




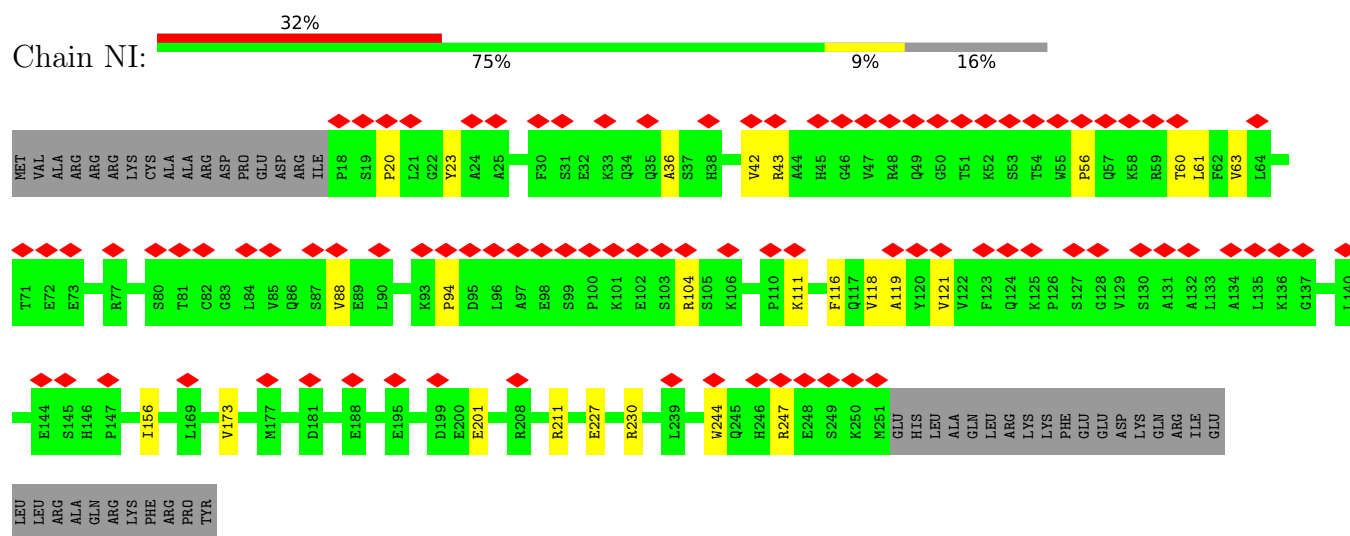
- Molecule 38: 40S ribosomal protein S14



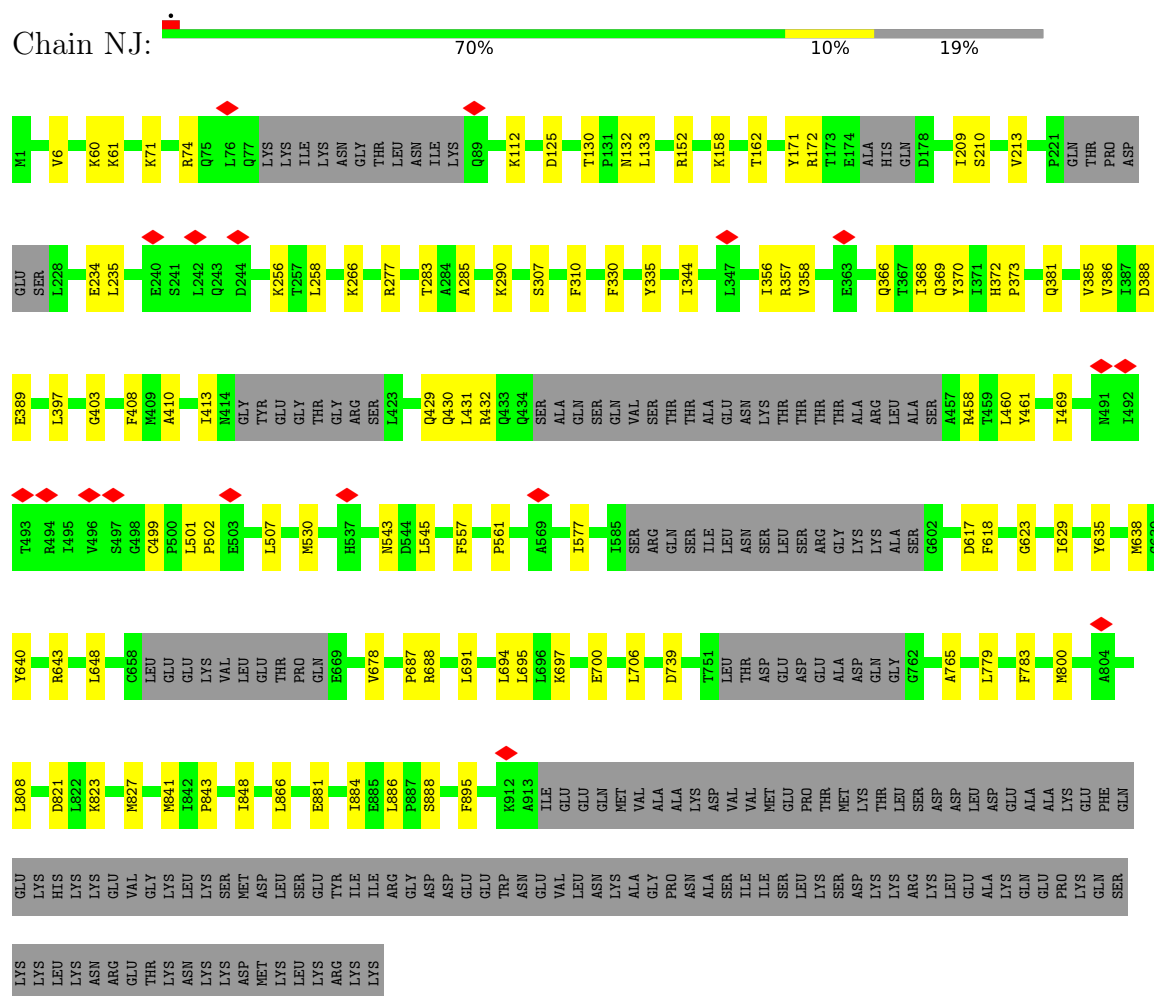
- Molecule 39: Nucleolar protein 6



- Molecule 40: Ribosomal RNA-processing protein 7 homolog A

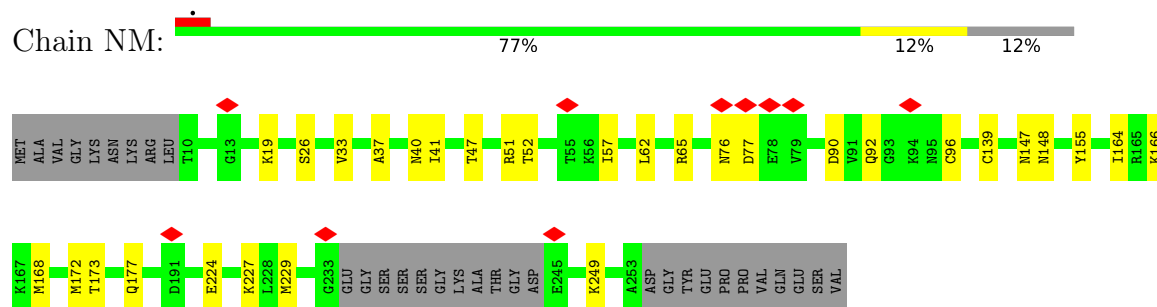


- Molecule 41: RNA cytidine acetyltransferase

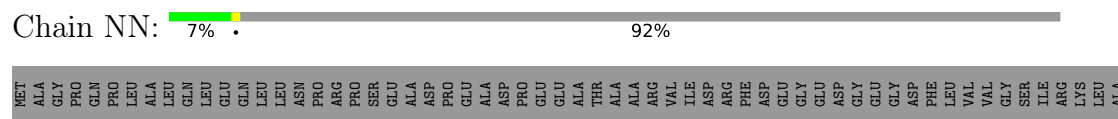


- Molecule 41: RNA cytidine acetyltransferase

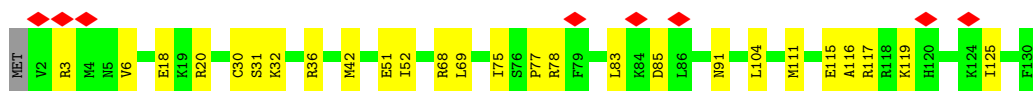
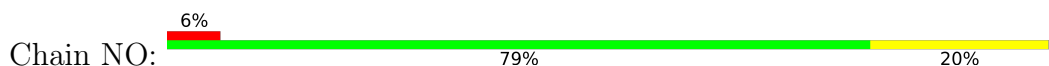
- Molecule 42: 40S ribosomal protein S3a



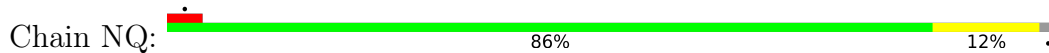
- Molecule 43: Protein AATF



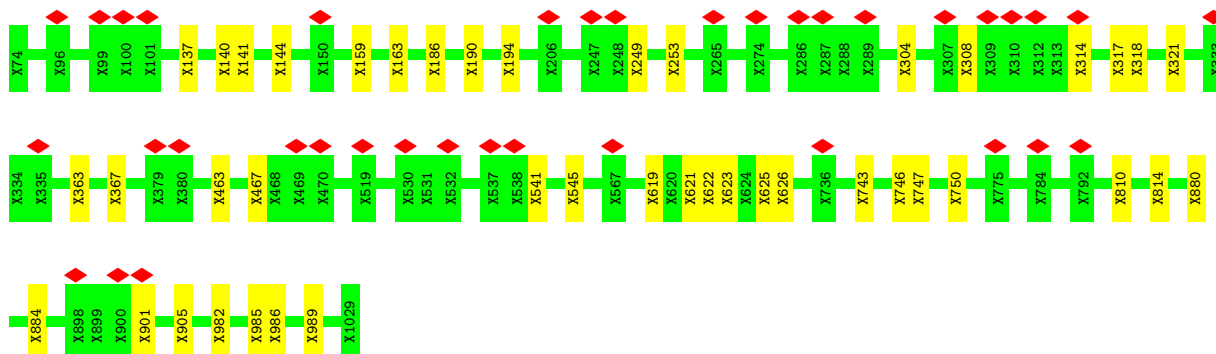
- Molecule 44: 40S ribosomal protein S15a



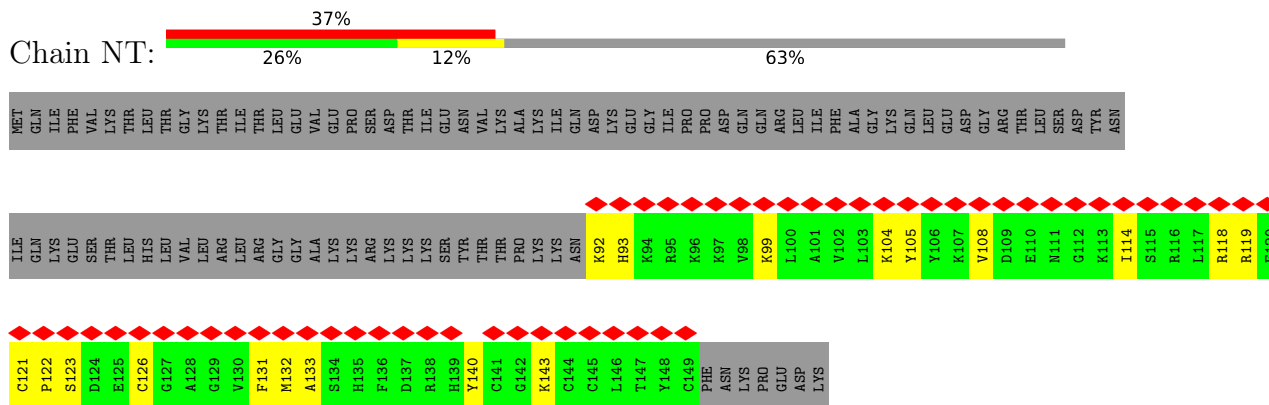
- Molecule 45: 40S ribosomal protein S27



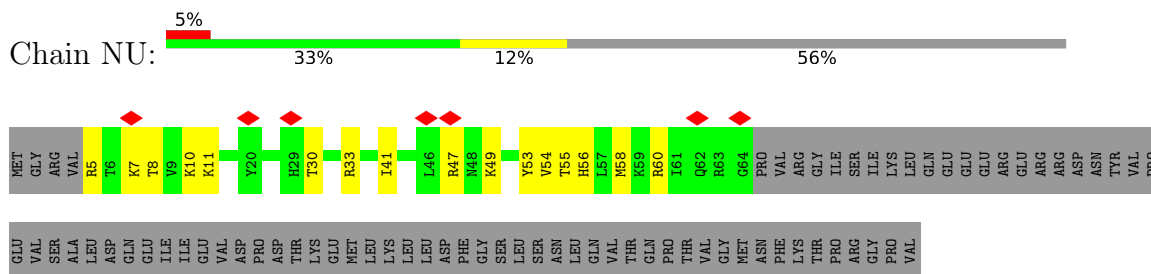
- Molecule 46: RRP12-like protein



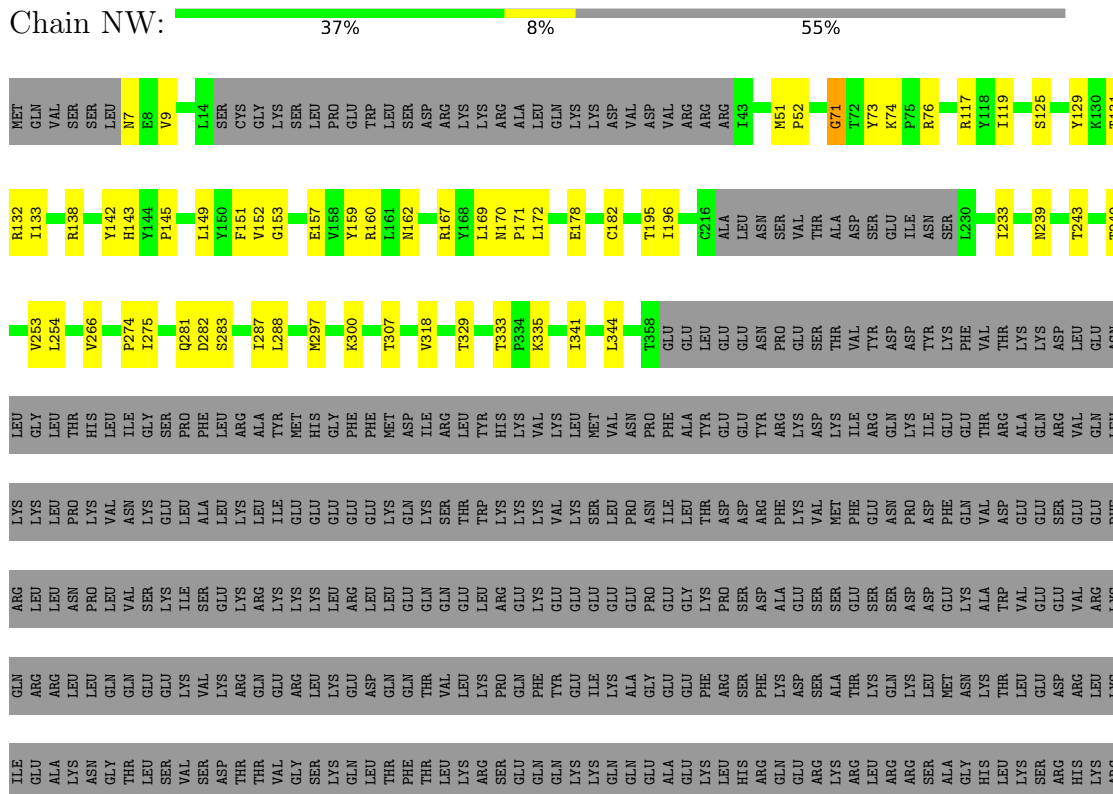
Chain NT:

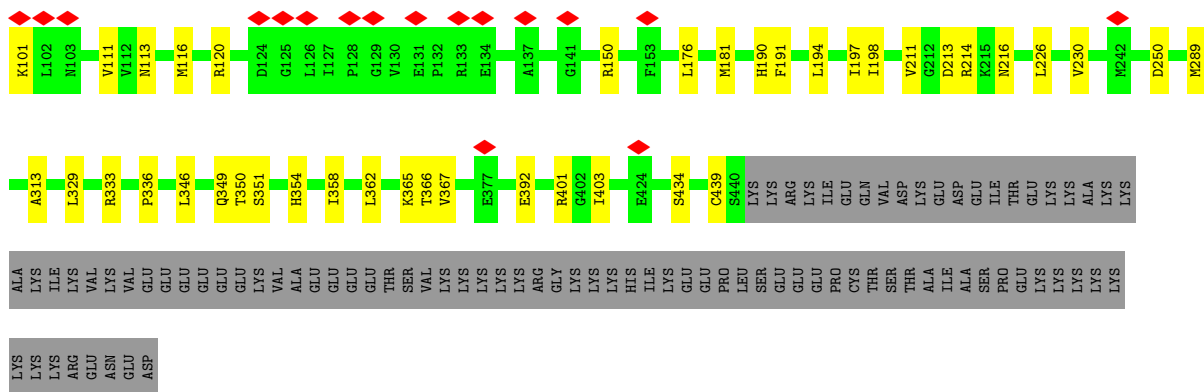


Chain NU:

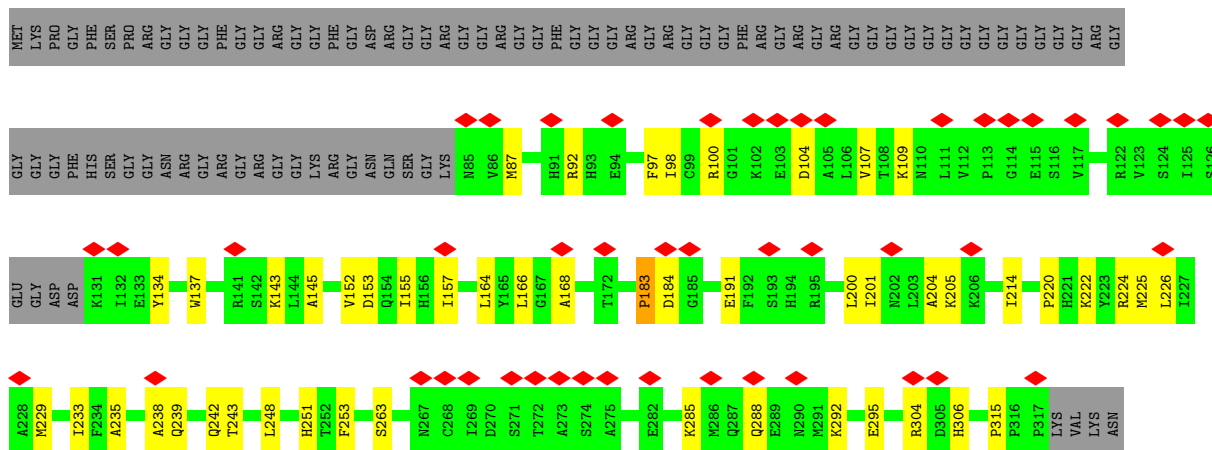


Chain NW:

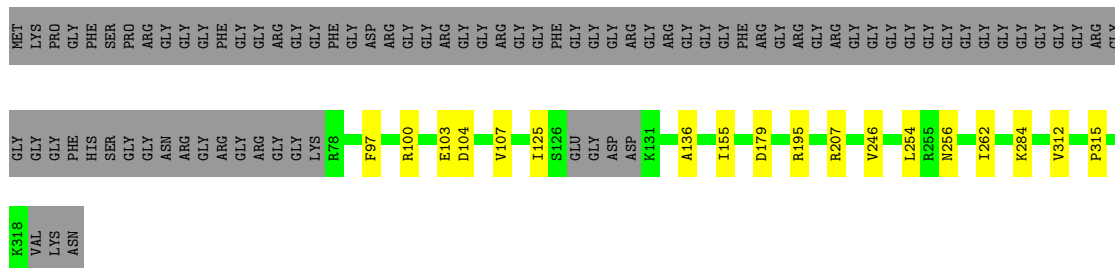




- Molecule 53: rRNA 2'-O-methyltransferase fibrillar



- Molecule 53: rRNA 2'-O-methyltransferase fibrillar

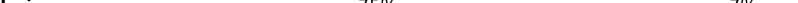


- Molecule 54: NHP2-like protein 1



- Molecule 54: NHP2-like protein 1

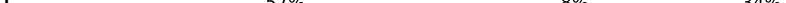
MET
THR
GLU
ALA
ASP
V6
K9
R36
I50
R84
R97
I106
V128

- Chain SG: 

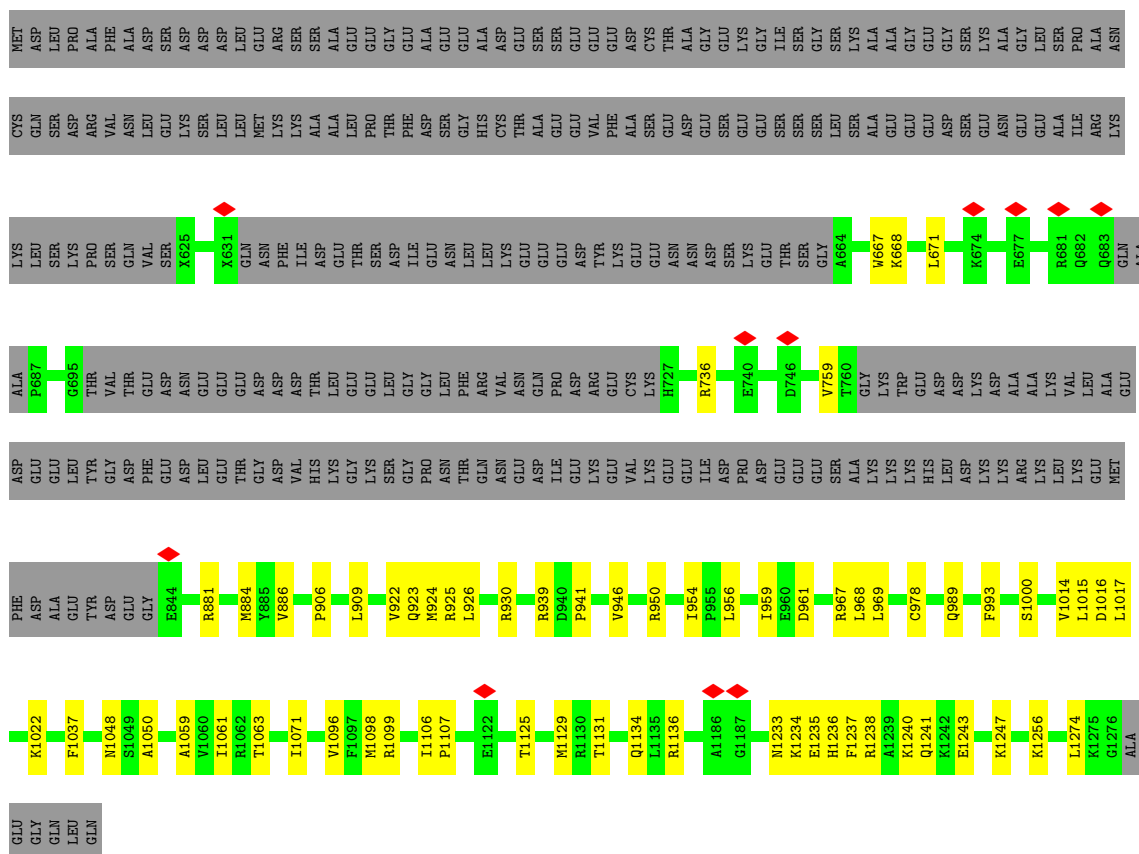
[illegible]

- Chain SH: 86% 13%

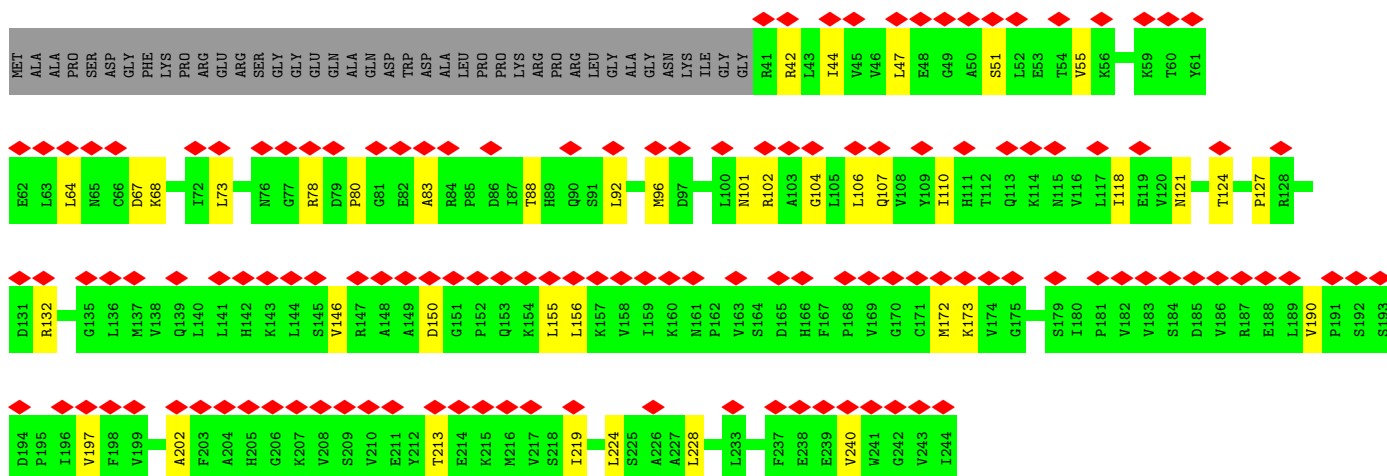
Protein	Residue	Category	Score
Met	ALA	Conserved	0.99
Thr	GLN	Conserved	0.99
ALA	H6	Conserved	0.99
	C13	Conserved	0.99
	I35	Conserved	0.99
	R38	Conserved	0.99
	D39	Conserved	0.99
	D40	Conserved	0.99
	D46	Conserved	0.99
	F47	Conserved	0.99
	K57	Conserved	0.99
	N60	Conserved	0.99
	N67	Conserved	0.99
	T72	Conserved	0.99
	E86	Conserved	0.99
	G94	Conserved	0.99
	V120	Conserved	0.99
	T121	Conserved	0.99
	D123	Conserved	0.99
	Q124	Conserved	0.99
	K133	Conserved	0.99
	A134	Conserved	0.99
	T135	Conserved	0.99
	D146	Conserved	0.99
	L152	Conserved	0.99
	R156	Conserved	0.99
	R157	Conserved	0.99
	G158	Conserved	0.99
	M159	Conserved	0.99
	P160	Conserved	0.99
	G165	Conserved	0.99
	E166	Conserved	0.99
	R174	Conserved	0.99
	K175	Conserved	0.99
	K187	Conserved	0.99
	I191	Conserved	0.99
	Y196	Conserved	0.99
	D210	Conserved	0.99
	S211	Conserved	0.99
	I220	Conserved	0.99
	P221	Conserved	0.99
	D222	Conserved	0.99
	L223	Conserved	0.99
	M230	Conserved	0.99
	S235	Conserved	0.99
	G242	Conserved	0.99
	S256	Conserved	0.99
	A260	Conserved	0.99
	Q266	Conserved	0.99
	E273	Conserved	0.99
	D274	Conserved	0.99
	L275	Conserved	0.99
	L284	Conserved	0.99
	I287	Conserved	0.99
	T306	Conserved	0.99
	S321	Conserved	0.99
	T324	Conserved	0.99
	I337	Conserved	0.99
	G347	Conserved	0.99
	E348	Conserved	0.99
	E349	Conserved	0.99
	L368	Conserved	0.99
	K373	Conserved	0.99

- Chain SI: 

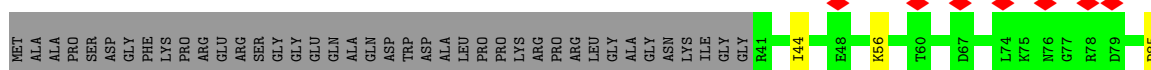
GLU	ASP	D355	I103	GLU	MET
GLU	GLU	LEU	T107	ALA	GLU
SER	GLY	GLY	I108	LYS	ALA
ASP	GLY	GLY	Q109	GLN	LYS
SER	ASP	SER	K110	GLN	ASP
ASP	SER	HIS	L111	LYS	GLN
ASP	VAL	VAL	I114	LYS	LYS
ASP	PHE	GLN	I120	HIS	ARG
GLU	GLN	GLU	I120	LYS	LYS
ASP	GLU	ASP	C133	LYS	ASN
ASP	VAL	VAL	C133	SER	LYS
GLU	GLY	GLY	M138	GLY	GLY
MET	MET	PRO	M138	PRO	PRO
SER	SER	T369	L143	LYS	LYS
GLU	GLY	GLY	L143	LYS	LYS
ASP	ASP	S381	M152	ALA	ALA
ASP	GLY	T382	M152	LYS	LYS
LEU	LEU	A385	M162	LYS	LYS
GLU	GLU	K386	M162	LYS	LYS
ASN	ASN	ASN	L168	ARG	ARG
GLY	GLY	R391	K178	LEU	LEU
SER	SER	V392	I179	GLN	GLN
SER	SER	SER	M180	ASP	ASP
ASP	ASP	G402	M180	GLY	GLY
GLU	GLU	SER	K190	LEU	LEU
GLU	GLU	GLU	H191	GLN	GLN
ALA	ALA	ASP	ILE	LEU	LEU
GLU	GLU	ASP	R205	GLY	GLY
GLU	GLU	ASN	R205	GLU	GLU
GLU	GLU	GLN	T208	ASP	ASP
ASN	ASN	GLY	E209	ALA	ALA
ALA	ALA	LEU	E209	LYS	LYS
GLU	GLU	MET	K215	ARG	ARG
MET	MET	PRO	L216	LYS	LYS
MET	MET	THR	L216	ASN	ASN
THR	THR	ASP	F238	PRO	PRO
ASP	ASP	LYS	F238	LYS	LYS
GLN	GLN	GLU	K243	ASN	ASN
GLN	GLU	GLU	K243	PRO	PRO
TYR	TYR	LYS	R260	LYS	LYS
MET	MET	GLN	R260	ALA	ALA
ALA	ALA	GLN	R260	PHE	PHE
VAL	VAL	MET	L282	ALA	ALA
ASP	ASP	ASP	L282	VAL	VAL
GLY	GLY	LEU	I310	GLN	GLN
ILE	ILE	ASN	I310	S49	S49
LYS	LYS	THR	THR	M88	M88
LYS	ARG	GLY	P320	G89	G89
ARG	ARG	ARG	P320	P90	P90
LYS	LYS	MET	E332	V93	V93
LEU	LEU	ARG	V335	S96	S96
GLU	GLU	ARG	V335	I99	I99
LEU	LEU	LYS	P338		
GLU	GLU	ALA	L339		
GLU	GLU	ILE	L339		
ASP	ASP	PHE	S340		
SER	SER	GLY	S340		
GLU	GLU	ASP			



- Molecule 58: Ribosomal RNA small subunit methyltransferase NEP1



- Molecule 58: Ribosomal RNA small subunit methyltransferase NEP1



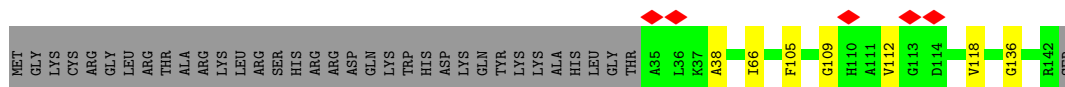


[illegible]

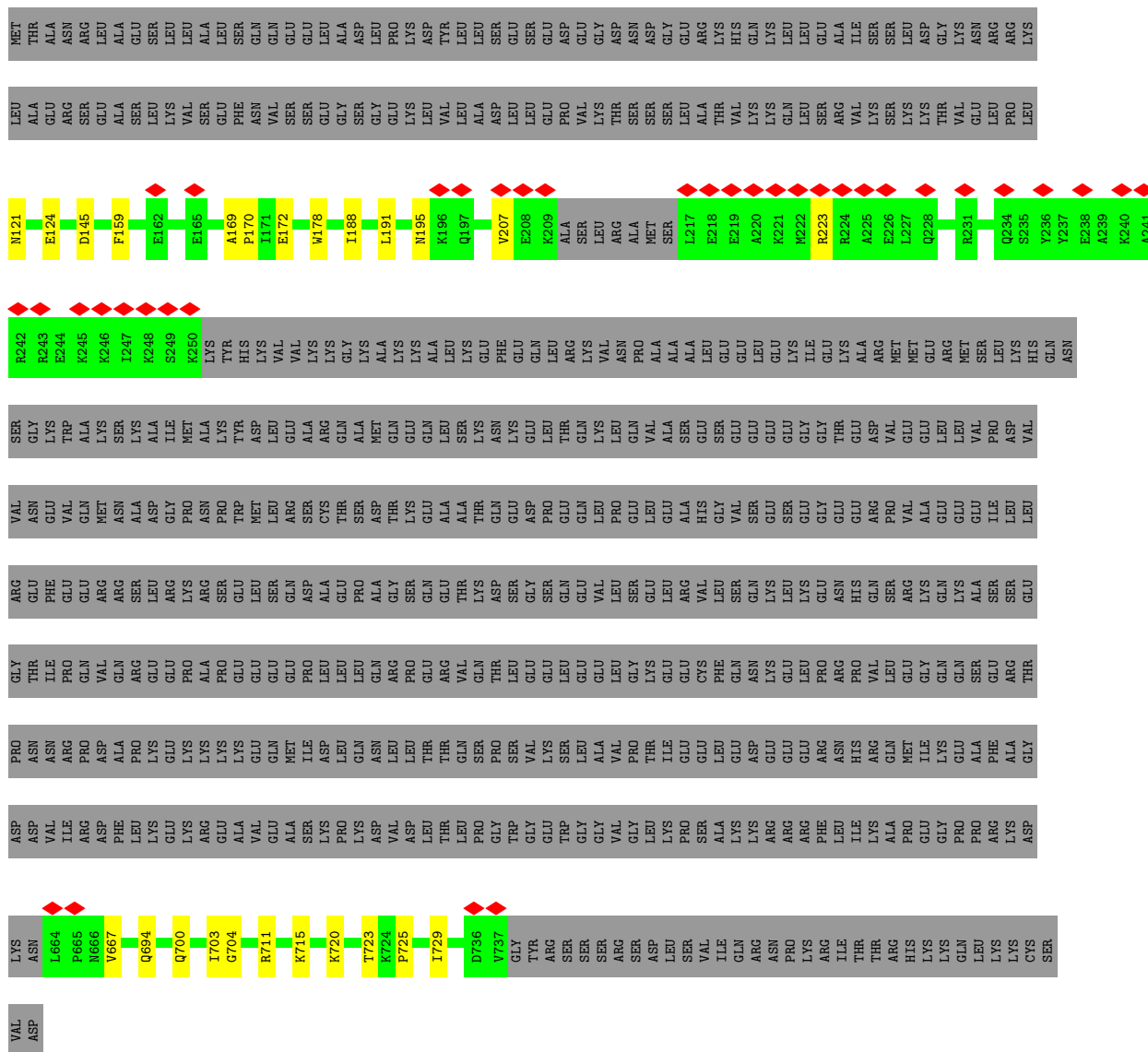
- Molecule 62: Deoxynucleotidyltransferase terminal-interacting protein 2

[illegible]

- Molecule 63: 40S ribosomal protein S23

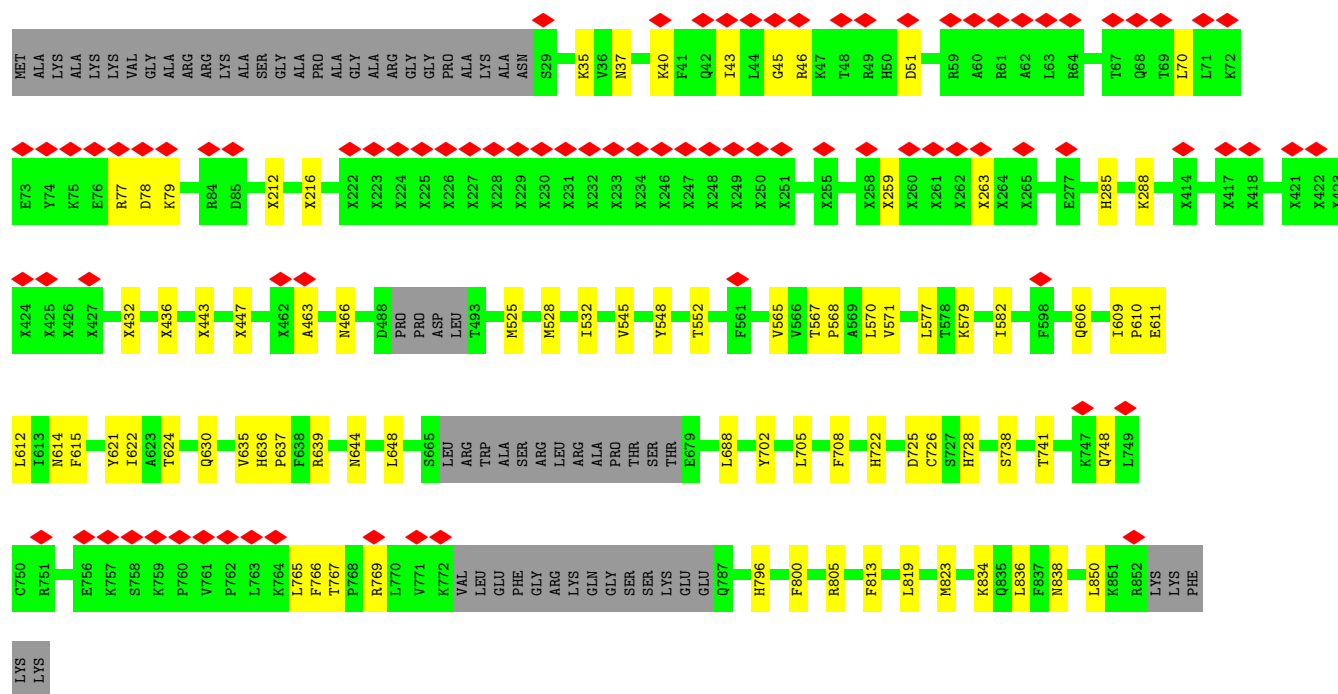


- Molecule 64: U3 small nucleolar RNA-associated protein 14 homolog A



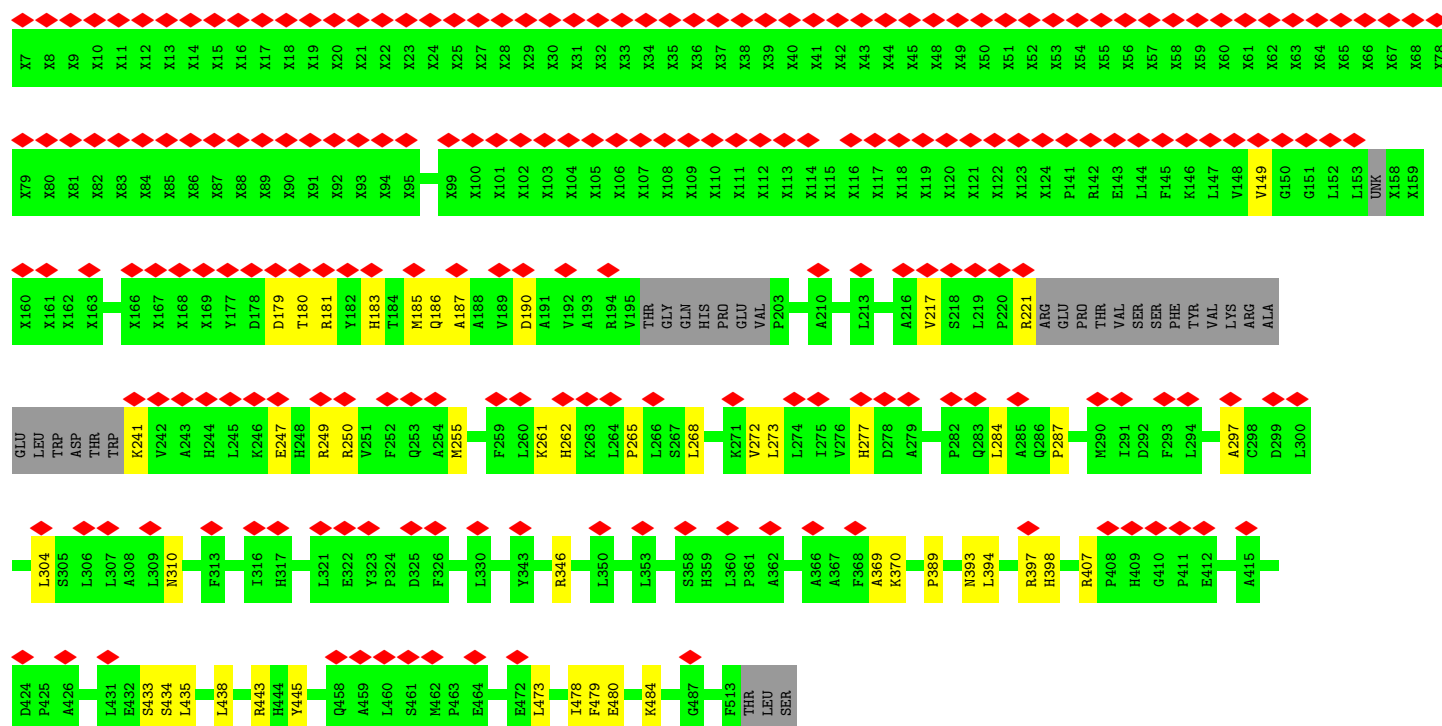
- Molecule 65: Nucleolar protein 14

Chain ST: 

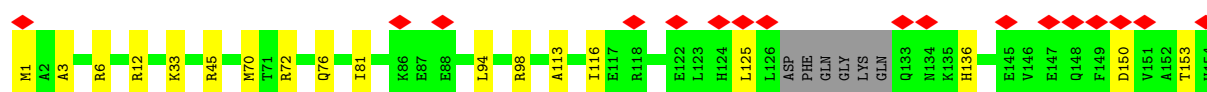
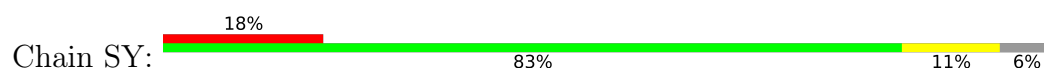


- Molecule 66: Nucleolar complex protein 4 homolog

Chain SU: 

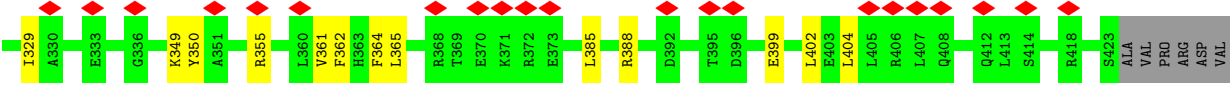
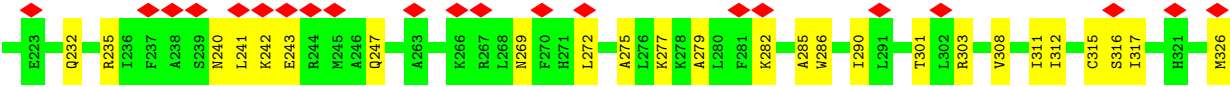
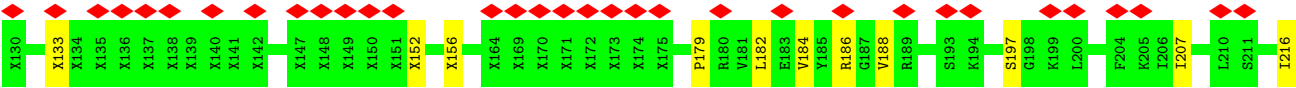
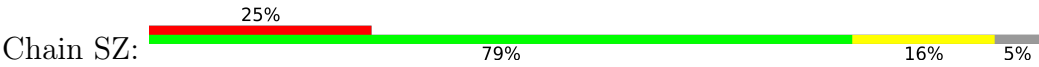


Chain SW:





• Molecule 71: Bystin



GLU
ASP
VAL
PRO
ILE
THR
VAL
GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	42142	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	20.935	Depositor
Minimum map value	-14.456	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.682	Depositor
Recommended contour level	2.68	Depositor
Map size (Å)	604.80005, 604.80005, 604.80005	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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

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	0/5739	0.32	0/8931
2	L1	0.11	0/31039	0.31	1/48327 (0.0%)
3	L2	0.10	0/5130	0.29	0/7996
4	L3	0.17	0/720	0.42	0/970
5	L4	0.12	0/2118	0.36	0/2849
6	L5	0.16	0/1523	0.40	2/2048 (0.1%)
7	L6	0.16	0/1830	0.39	0/2434
8	L7	0.19	0/1365	0.44	0/1830
9	L8	0.13	0/1500	0.33	0/2002
10	L9	0.12	0/1447	0.31	0/1930
11	LA	0.19	0/941	0.45	0/1264
12	LC	0.14	0/1115	0.34	0/1494
13	LD	0.14	0/1225	0.39	0/1640
14	LF	0.12	0/868	0.32	0/1159
15	LG	0.10	0/490	0.31	0/656
16	LH	0.13	0/6127	0.36	0/8292
17	LI	0.15	0/3245	0.37	0/4386
18	LJ	0.16	0/3788	0.43	1/5128 (0.0%)
19	LK	0.21	0/959	0.55	1/1302 (0.1%)
19	LL	0.14	0/4072	0.38	0/5539
20	LM	0.17	0/16110	0.41	0/21817
21	LN	0.13	0/5438	0.36	0/7377
22	LO	0.14	0/6835	0.40	0/9256
23	LP	0.12	0/4806	0.32	0/6455
24	LQ	0.12	0/6548	0.34	0/8839
25	LR	0.13	0/6141	0.36	0/8348
26	LS	0.11	0/3621	0.32	0/4876
27	LT	0.12	0/6907	0.34	0/9359
28	LU	0.12	0/3695	0.35	0/4986
29	LW	0.19	1/3594 (0.0%)	0.39	3/4867 (0.1%)
30	LZ	0.13	0/1560	0.34	0/2104
32	NA	0.13	0/2084	0.35	0/2789

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	NB	0.12	0/622	0.32	0/816
34	NC	0.13	0/788	0.34	0/1049
35	ND	0.13	0/708	0.32	0/947
36	NE	0.11	0/807	0.29	0/1069
37	NF	0.11	0/1226	0.28	0/1649
38	NG	0.11	0/873	0.31	0/1177
39	NH	0.13	0/8580	0.32	0/11685
40	NI	0.12	0/1887	0.32	0/2558
41	NJ	0.14	0/6652	0.37	0/9006
41	NK	0.15	0/6545	0.38	1/8867 (0.0%)
42	NM	0.10	0/1899	0.30	0/2533
43	NN	0.13	0/346	0.38	0/462
44	NO	0.16	0/1051	0.44	0/1406
45	NQ	0.10	0/653	0.29	0/876
47	NT	0.18	0/479	0.53	1/635 (0.2%)
48	NU	0.15	0/501	0.38	0/667
49	NW	0.14	0/2556	0.43	2/3469 (0.1%)
50	NY	0.13	0/2265	0.32	0/3045
51	SA	0.10	0/3122	0.27	0/4208
52	SB	0.12	0/3491	0.33	0/4695
53	SC	0.19	0/1818	0.41	2/2463 (0.1%)
53	SD	0.10	0/1878	0.30	1/2540 (0.0%)
54	SE	0.12	0/980	0.33	0/1323
54	SF	0.13	0/967	0.34	0/1305
55	SG	0.11	0/2941	0.31	0/3988
56	SH	0.10	0/2882	0.30	0/3887
57	SI	0.12	0/6917	0.32	0/9297
58	SJ	0.14	0/1609	0.39	0/2181
58	SK	0.13	0/1609	0.38	0/2181
59	SL	0.13	0/1619	0.34	0/2174
60	SM	0.12	0/2420	0.34	0/3264
61	SP	0.14	0/16393	0.36	0/22173
62	SQ	0.11	0/1561	0.29	0/2083
63	SR	0.13	0/828	0.36	0/1110
64	SS	0.13	0/1663	0.34	0/2250
65	ST	0.18	0/3597	0.37	0/4836
66	SU	0.14	0/2634	0.36	0/3581
67	SW	0.19	0/1436	0.43	0/1936
70	SY	0.10	0/2051	0.29	0/2723
71	SZ	0.14	0/2043	0.40	0/2763
All	All	0.13	1/245477 (0.0%)	0.35	15/340127 (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
6	L5	0	1
22	LO	0	1
67	SW	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	LW	101	PRO	CG-CD	-7.69	1.24	1.50

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	LW	101	PRO	N-CD-CG	-10.97	86.75	103.20
53	SC	183	PRO	CA-N-CD	-7.84	101.03	112.00
53	SC	183	PRO	N-CD-CG	-7.76	91.56	103.20
6	L5	136	ARG	CB-CG-CD	7.24	127.95	111.30
19	LK	542	PRO	CA-N-CD	-7.23	101.88	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	L5	136	ARG	Sidechain
22	LO	316	GLU	Peptide
67	SW	247	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	5152	0	2630	52	0
2	L1	27777	0	14063	253	0
3	L2	4589	0	2306	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L3	854	0	774	25	0
5	L4	2076	0	2177	18	0
6	L5	1501	0	1557	16	0
7	L6	1811	0	1974	23	0
8	L7	1346	0	1410	31	0
9	L8	1474	0	1542	19	0
10	L9	1425	0	1541	17	0
11	LA	931	0	961	17	0
12	LC	1098	0	1168	11	0
13	LD	1204	0	1274	11	0
14	LF	851	0	894	18	0
15	LG	488	0	514	4	0
16	LH	5987	0	5953	77	0
17	LI	3889	0	3464	55	0
18	LJ	3711	0	3758	69	0
19	LK	943	0	1023	28	0
19	LL	3982	0	4031	55	0
20	LM	15820	0	16318	290	0
21	LN	5299	0	5269	80	0
22	LO	6676	0	6579	76	0
23	LP	4705	0	4720	57	0
24	LQ	6438	0	6400	78	0
25	LR	6015	0	5981	90	0
26	LS	3560	0	3570	56	0
27	LT	6756	0	6768	87	0
28	LU	3611	0	3618	64	0
29	LW	3519	0	3518	34	0
30	LZ	1532	0	1553	12	0
31	N0	264	0	178	0	0
32	NA	2055	0	2135	21	0
33	NB	617	0	685	8	0
34	NC	779	0	788	11	0
35	ND	696	0	729	10	0
36	NE	799	0	854	11	0
37	NF	1202	0	1289	10	0
38	NG	861	0	871	10	0
39	NH	8374	0	8456	80	0
40	NI	1840	0	1812	19	0
41	NJ	6526	0	6599	60	0
41	NK	6419	0	6480	91	0
42	NM	1873	0	1968	20	0
43	NN	340	0	345	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	NO	1034	0	1080	20	0
45	NQ	640	0	661	8	0
46	NR	4305	0	945	22	0
47	NT	470	0	474	14	0
48	NU	495	0	541	9	0
49	NW	2498	0	2456	34	0
50	NY	2222	0	2310	18	0
51	SA	3077	0	3139	32	0
52	SB	3439	0	3559	45	0
53	SC	1781	0	1803	37	0
53	SD	1841	0	1867	14	0
54	SE	968	0	1017	7	0
54	SF	955	0	1008	5	0
55	SG	2884	0	2751	17	0
56	SH	2832	0	2937	29	0
57	SI	6803	0	6966	68	0
58	SJ	1579	0	1646	29	0
58	SK	1579	0	1646	24	0
59	SL	1586	0	1641	31	0
60	SM	2369	0	2376	18	0
61	SP	16078	0	16633	216	0
62	SQ	1533	0	1579	9	0
63	SR	816	0	871	5	0
64	SS	1626	0	1677	20	0
65	ST	4170	0	3804	60	0
66	SU	3154	0	2736	35	0
67	SW	1413	0	1489	29	0
68	Sx	190	0	41	2	0
69	SX	695	0	151	0	0
70	SY	2024	0	2148	20	0
71	SZ	2222	0	2142	31	0
72	L1	19	0	0	0	0
72	NH	1	0	0	0	0
72	SI	1	0	0	0	0
72	SL	1	0	0	0	0
73	NH	31	0	12	2	0
73	NK	31	0	12	1	0
74	NQ	1	0	0	0	0
74	NT	1	0	0	0	0
74	SL	1	0	0	0	0
75	SI	32	0	12	0	0
76	SJ	26	0	19	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	SK	26	0	19	0	0
All	All	245114	0	224665	2688	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 6.

The worst 5 of 2688 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)
20:LM:1457:GLN:HE21	20:LM:1457:GLN:N	1.53	1.06
28:LU:66:ARG:HH12	59:SL:127:PRO:HD3	1.40	0.84
27:LT:748:ASN:HB3	27:LT:751:LEU:HD23	1.60	0.83
21:LN:461:LEU:HB2	21:LN:477:PHE:HB2	1.63	0.81
61:SP:1430:VAL:HG12	61:SP:1477:ASN:HD21	1.45	0.80

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	85/116 (73%)	84 (99%)	1 (1%)	0	100	100
5	L4	260/263 (99%)	259 (100%)	1 (0%)	0	100	100
6	L5	188/204 (92%)	182 (97%)	6 (3%)	0	100	100
7	L6	219/249 (88%)	218 (100%)	1 (0%)	0	100	100
8	L7	164/194 (84%)	160 (98%)	4 (2%)	0	100	100
9	L8	176/208 (85%)	174 (99%)	2 (1%)	0	100	100
10	L9	169/194 (87%)	168 (99%)	1 (1%)	0	100	100
11	LA	118/132 (89%)	111 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	LC	137/146 (94%)	136 (99%)	1 (1%)	0	100	100
13	LD	145/158 (92%)	141 (97%)	4 (3%)	0	100	100
14	LF	102/133 (77%)	102 (100%)	0	0	100	100
15	LG	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
16	LH	738/830 (89%)	721 (98%)	17 (2%)	0	100	100
17	LI	374/678 (55%)	370 (99%)	4 (1%)	0	100	100
18	LJ	465/518 (90%)	448 (96%)	17 (4%)	0	100	100
19	LK	116/677 (17%)	113 (97%)	3 (3%)	0	100	100
19	LL	500/677 (74%)	483 (97%)	17 (3%)	0	100	100
20	LM	1977/2144 (92%)	1933 (98%)	44 (2%)	0	100	100
21	LN	667/686 (97%)	647 (97%)	19 (3%)	1 (0%)	48	79
22	LO	844/919 (92%)	826 (98%)	18 (2%)	0	100	100
23	LP	559/597 (94%)	556 (100%)	3 (0%)	0	100	100
24	LQ	810/943 (86%)	792 (98%)	18 (2%)	0	100	100
25	LR	769/808 (95%)	748 (97%)	21 (3%)	0	100	100
26	LS	447/556 (80%)	440 (98%)	7 (2%)	0	100	100
27	LT	863/951 (91%)	847 (98%)	16 (2%)	0	100	100
28	LU	443/445 (100%)	435 (98%)	8 (2%)	0	100	100
29	LW	449/610 (74%)	436 (97%)	13 (3%)	0	100	100
30	LZ	181/184 (98%)	179 (99%)	2 (1%)	0	100	100
32	NA	243/681 (36%)	242 (100%)	1 (0%)	0	100	100
33	NB	71/479 (15%)	69 (97%)	2 (3%)	0	100	100
34	NC	92/315 (29%)	90 (98%)	2 (2%)	0	100	100
35	ND	82/257 (32%)	81 (99%)	1 (1%)	0	100	100
36	NE	94/293 (32%)	94 (100%)	0	0	100	100
37	NF	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
38	NG	114/151 (76%)	113 (99%)	1 (1%)	0	100	100
39	NH	1064/1146 (93%)	1044 (98%)	20 (2%)	0	100	100
40	NI	232/280 (83%)	229 (99%)	3 (1%)	0	100	100
41	NJ	809/1025 (79%)	783 (97%)	26 (3%)	0	100	100
41	NK	801/1025 (78%)	782 (98%)	19 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	NM	229/264 (87%)	226 (99%)	3 (1%)	0	100	100
43	NN	40/560 (7%)	39 (98%)	1 (2%)	0	100	100
44	NO	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
45	NQ	80/84 (95%)	79 (99%)	1 (1%)	0	100	100
47	NT	56/156 (36%)	55 (98%)	1 (2%)	0	100	100
48	NU	58/135 (43%)	57 (98%)	1 (2%)	0	100	100
49	NW	305/688 (44%)	293 (96%)	12 (4%)	0	100	100
50	NY	270/381 (71%)	270 (100%)	0	0	100	100
51	SA	390/594 (66%)	388 (100%)	2 (0%)	0	100	100
52	SB	438/529 (83%)	437 (100%)	1 (0%)	0	100	100
53	SC	225/321 (70%)	219 (97%)	6 (3%)	0	100	100
53	SD	233/321 (73%)	227 (97%)	6 (3%)	0	100	100
54	SE	123/128 (96%)	122 (99%)	1 (1%)	0	100	100
54	SF	121/128 (94%)	119 (98%)	2 (2%)	0	100	100
55	SG	383/475 (81%)	374 (98%)	9 (2%)	0	100	100
56	SH	366/373 (98%)	362 (99%)	4 (1%)	0	100	100
57	SI	825/1282 (64%)	812 (98%)	13 (2%)	0	100	100
58	SJ	202/244 (83%)	200 (99%)	2 (1%)	0	100	100
58	SK	202/244 (83%)	200 (99%)	2 (1%)	0	100	100
59	SL	190/198 (96%)	186 (98%)	4 (2%)	0	100	100
60	SM	288/291 (99%)	280 (97%)	8 (3%)	0	100	100
61	SP	1967/2785 (71%)	1933 (98%)	34 (2%)	0	100	100
62	SQ	183/756 (24%)	182 (100%)	1 (0%)	0	100	100
63	SR	106/143 (74%)	104 (98%)	2 (2%)	0	100	100
64	SS	191/771 (25%)	187 (98%)	4 (2%)	0	100	100
65	ST	432/632 (68%)	424 (98%)	8 (2%)	0	100	100
66	SU	316/472 (67%)	311 (98%)	5 (2%)	0	100	100
67	SW	178/252 (71%)	175 (98%)	3 (2%)	0	100	100
70	SY	232/253 (92%)	230 (99%)	2 (1%)	0	100	100
71	SZ	244/304 (80%)	237 (97%)	7 (3%)	0	100	100
All	All	24774/33986 (73%)	24292 (98%)	481 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	LN	175	SER

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	76/77 (99%)	76 (100%)	0	100	100
5	L4	224/225 (100%)	224 (100%)	0	100	100
6	L5	160/170 (94%)	160 (100%)	0	100	100
7	L6	195/218 (89%)	195 (100%)	0	100	100
8	L7	149/174 (86%)	149 (100%)	0	100	100
9	L8	155/180 (86%)	155 (100%)	0	100	100
10	L9	152/168 (90%)	152 (100%)	0	100	100
11	LA	102/108 (94%)	102 (100%)	0	100	100
12	LC	114/121 (94%)	114 (100%)	0	100	100
13	LD	133/142 (94%)	133 (100%)	0	100	100
14	LF	92/115 (80%)	92 (100%)	0	100	100
15	LG	55/62 (89%)	55 (100%)	0	100	100
16	LH	670/748 (90%)	669 (100%)	1 (0%)	88	87
17	LI	368/497 (74%)	368 (100%)	0	100	100
18	LJ	412/456 (90%)	412 (100%)	0	100	100
19	LK	112/594 (19%)	112 (100%)	0	100	100
19	LL	456/594 (77%)	456 (100%)	0	100	100
20	LM	1783/1943 (92%)	1782 (100%)	1 (0%)	88	87
21	LN	582/597 (98%)	582 (100%)	0	100	100
22	LO	726/783 (93%)	726 (100%)	0	100	100
23	LP	499/527 (95%)	499 (100%)	0	100	100
24	LQ	690/828 (83%)	690 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	LR	648/672 (96%)	648 (100%)	0	100	100
26	LS	393/476 (83%)	393 (100%)	0	100	100
27	LT	744/823 (90%)	744 (100%)	0	100	100
28	LU	399/399 (100%)	399 (100%)	0	100	100
29	LW	373/512 (73%)	373 (100%)	0	100	100
30	LZ	166/167 (99%)	166 (100%)	0	100	100
32	NA	229/626 (37%)	229 (100%)	0	100	100
33	NB	63/413 (15%)	63 (100%)	0	100	100
34	NC	87/282 (31%)	87 (100%)	0	100	100
35	ND	72/222 (32%)	72 (100%)	0	100	100
36	NE	86/253 (34%)	86 (100%)	0	100	100
37	NF	130/131 (99%)	130 (100%)	0	100	100
38	NG	92/119 (77%)	92 (100%)	0	100	100
39	NH	917/984 (93%)	917 (100%)	0	100	100
40	NI	193/246 (78%)	193 (100%)	0	100	100
41	NJ	707/899 (79%)	706 (100%)	1 (0%)	88	87
41	NK	692/899 (77%)	692 (100%)	0	100	100
42	NM	207/231 (90%)	207 (100%)	0	100	100
43	NN	37/484 (8%)	37 (100%)	0	100	100
44	NO	112/113 (99%)	112 (100%)	0	100	100
45	NQ	74/76 (97%)	74 (100%)	0	100	100
47	NT	51/140 (36%)	51 (100%)	0	100	100
48	NU	53/122 (43%)	53 (100%)	0	100	100
49	NW	282/635 (44%)	281 (100%)	1 (0%)	84	81
50	NY	245/340 (72%)	245 (100%)	0	100	100
51	SA	334/511 (65%)	334 (100%)	0	100	100
52	SB	372/455 (82%)	372 (100%)	0	100	100
53	SC	192/234 (82%)	192 (100%)	0	100	100
53	SD	198/234 (85%)	198 (100%)	0	100	100
54	SE	108/111 (97%)	108 (100%)	0	100	100
54	SF	107/111 (96%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	SG	287/382 (75%)	287 (100%)	0	100	100
56	SH	315/318 (99%)	315 (100%)	0	100	100
57	SI	738/1114 (66%)	738 (100%)	0	100	100
58	SJ	181/209 (87%)	181 (100%)	0	100	100
58	SK	181/209 (87%)	181 (100%)	0	100	100
59	SL	177/182 (97%)	177 (100%)	0	100	100
60	SM	253/254 (100%)	253 (100%)	0	100	100
61	SP	1822/2522 (72%)	1822 (100%)	0	100	100
62	SQ	165/676 (24%)	165 (100%)	0	100	100
63	SR	85/115 (74%)	85 (100%)	0	100	100
64	SS	177/686 (26%)	177 (100%)	0	100	100
65	ST	389/439 (89%)	389 (100%)	0	100	100
66	SU	269/303 (89%)	269 (100%)	0	100	100
67	SW	152/208 (73%)	152 (100%)	0	100	100
70	SY	219/232 (94%)	219 (100%)	0	100	100
71	SZ	214/227 (94%)	214 (100%)	0	100	100
All	All	21892/29323 (75%)	21888 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	LH	649	GLN
20	LM	1457	GLN
41	NJ	430	GLN
49	NW	7	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 210 such sidechains are listed below:

Mol	Chain	Res	Type
41	NK	359	ASN
53	SC	259	HIS
64	SS	680	HIS
41	NK	543	ASN
49	NW	170	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	234/3617 (6%)	101 (43%)	6 (2%)
2	L1	1275/1869 (68%)	346 (27%)	23 (1%)
3	L2	214/217 (98%)	80 (37%)	4 (1%)
31	N0	0/22	-	-
All	All	1723/5725 (30%)	527 (30%)	33 (1%)

5 of 527 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	434	C
1	L0	439	U
1	L0	442	U
1	L0	445	C
1	L0	446	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	1823	A
3	L2	14	C
3	L2	188	G
2	L1	423	U
2	L1	369	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 25 are monoatomic - leaving 5 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	ATP	NK	1101	-	32,33,33	0.27	0	48,52,52	0.28	0
75	GTP	SI	2001	72	33,34,34	0.97	1 (3%)	50,54,54	1.64	9 (18%)
76	SAH	SK	301	-	27,28,28	1.09	4 (14%)	36,40,40	2.02	9 (25%)
76	SAH	SJ	301	-	27,28,28	1.09	4 (14%)	36,40,40	2.02	10 (27%)
73	ATP	NH	3000	72	32,33,33	0.28	0	48,52,52	0.36	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	ATP	NK	1101	-	-	9/22/38/38	0/3/3/3
75	GTP	SI	2001	72	-	7/22/38/38	0/3/3/3
76	SAH	SK	301	-	-	9/15/31/31	0/3/3/3
76	SAH	SJ	301	-	-	2/15/31/31	0/3/3/3
73	ATP	NH	3000	72	-	7/22/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	SK	301	SAH	C2-N1	2.57	1.38	1.33
76	SJ	301	SAH	C2-N1	2.55	1.38	1.33
76	SJ	301	SAH	C2-N3	2.53	1.38	1.33
76	SK	301	SAH	C2-N3	2.47	1.38	1.33
76	SK	301	SAH	OXT-C	-2.21	1.23	1.30

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	SK	301	SAH	N3-C2-N1	-5.51	120.25	128.58
76	SJ	301	SAH	N3-C2-N1	-5.50	120.25	128.58
75	SI	2001	GTP	C5-C4-N3	-5.48	119.66	128.39
75	SI	2001	GTP	C2-N3-C4	4.91	120.76	112.30
76	SJ	301	SAH	C5-C4-N3	-4.58	120.41	126.72

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
73	NH	3000	ATP	C5'-O5'-PA-O1A
73	NH	3000	ATP	C5'-O5'-PA-O3A
73	NK	1101	ATP	C5'-O5'-PA-O1A
73	NK	1101	ATP	C5'-O5'-PA-O3A
75	SI	2001	GTP	C5'-O5'-PA-O3A

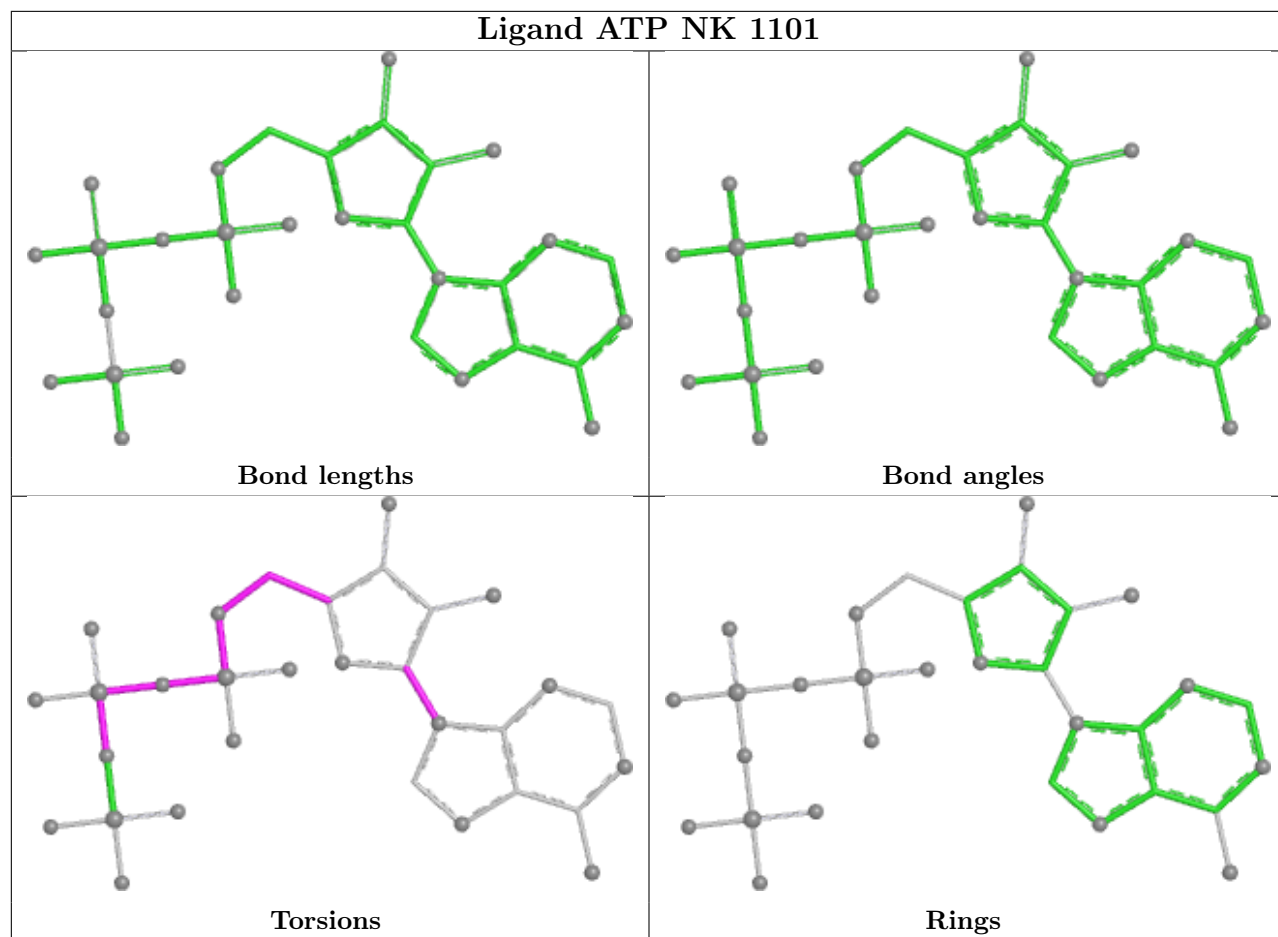
There are no ring outliers.

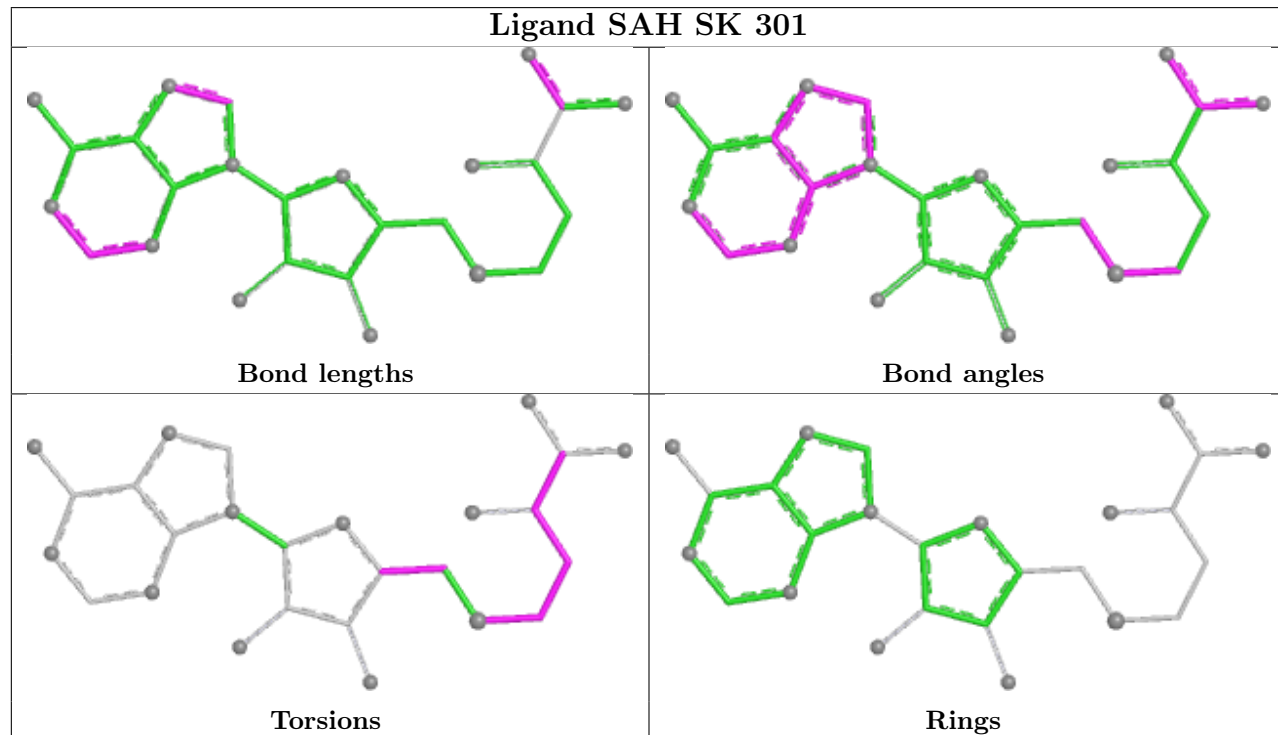
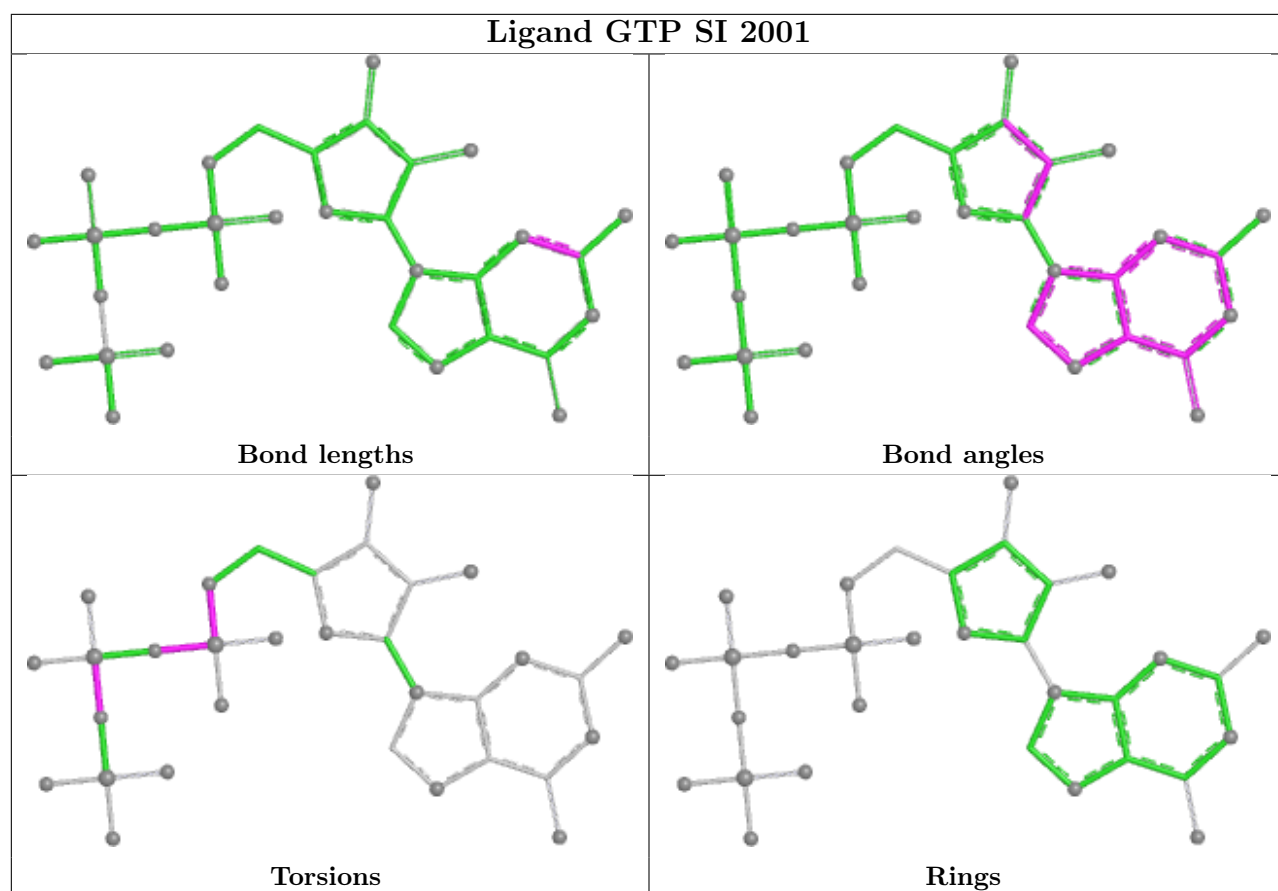
3 monomers are involved in 6 short contacts:

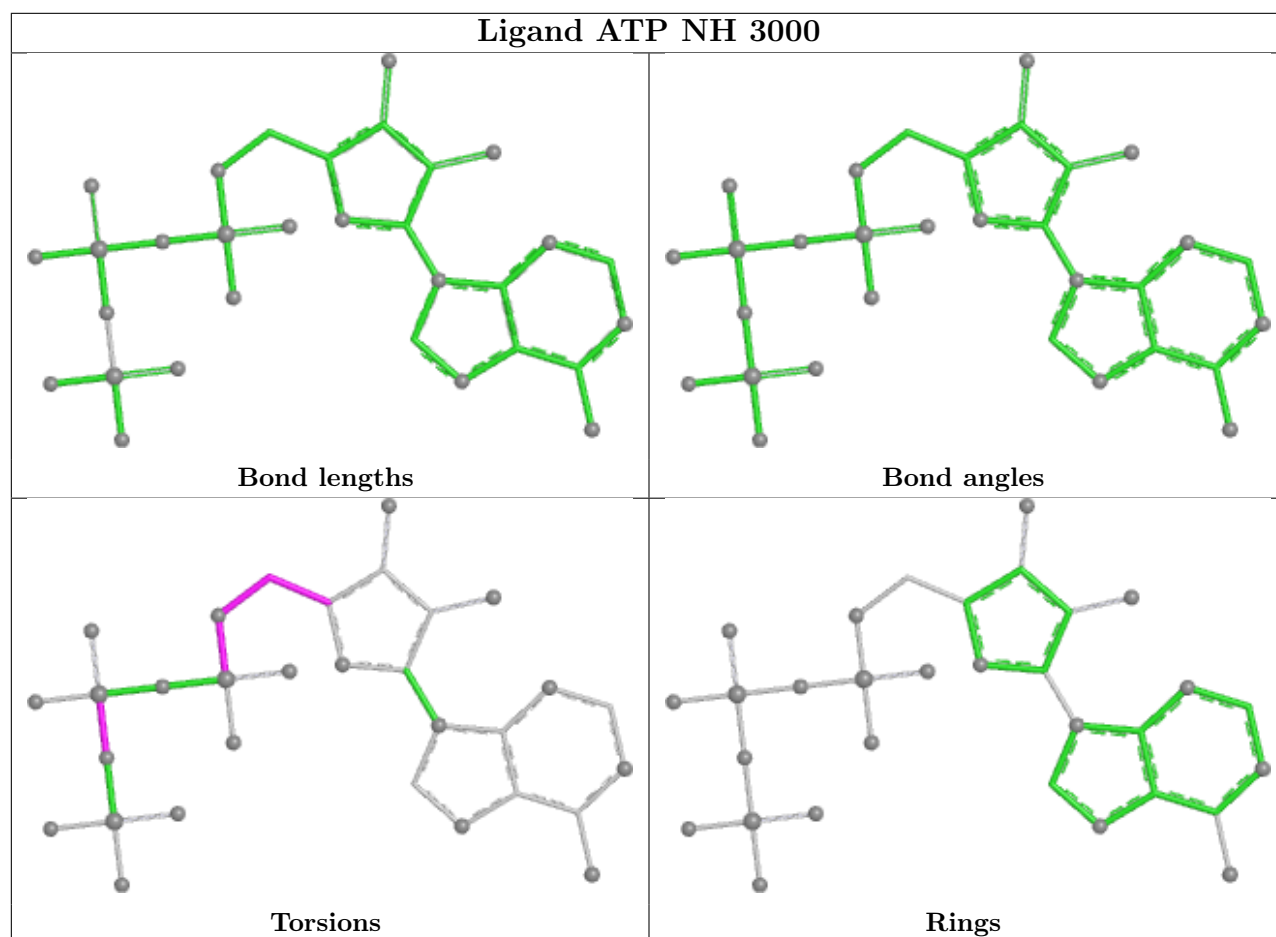
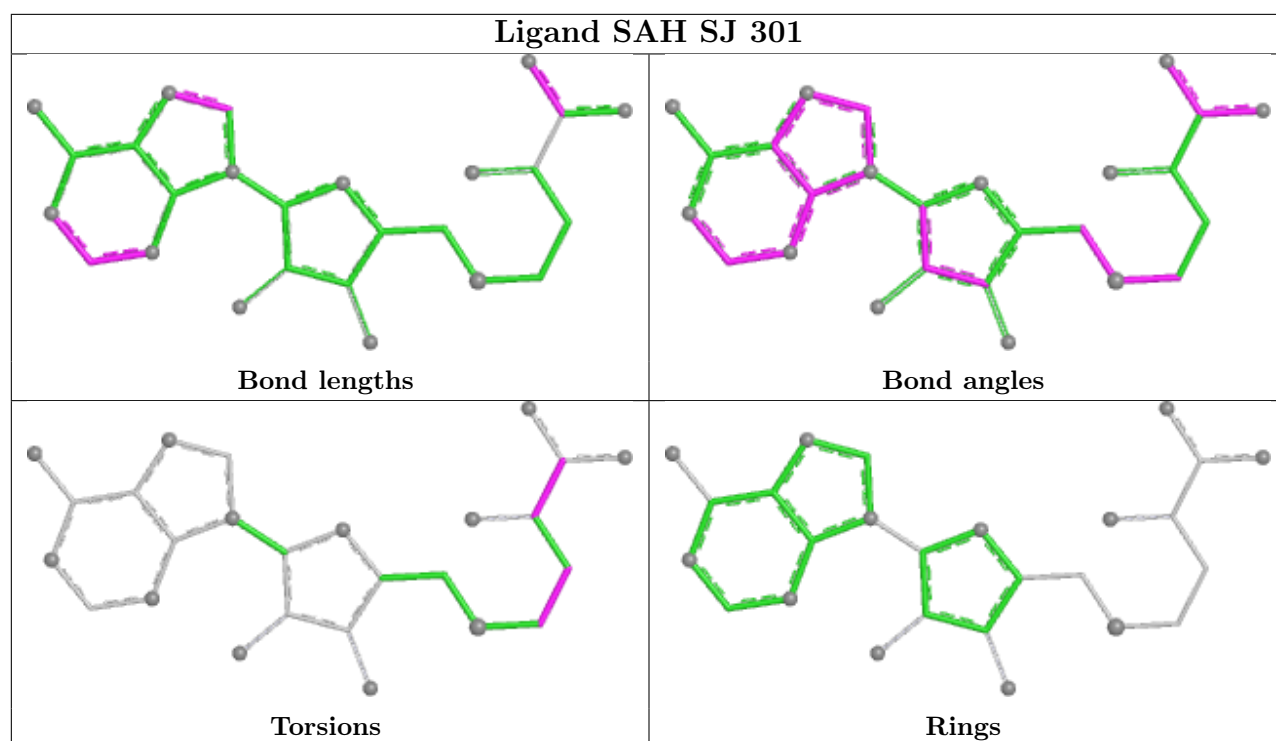
Mol	Chain	Res	Type	Clashes	Symm-Clashes
73	NK	1101	ATP	1	0
76	SJ	301	SAH	3	0
73	NH	3000	ATP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ATP NK 1101







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	NR	41
17	LI	5
66	SU	5
65	ST	3
31	N0	1
71	SZ	1

The worst 5 of 56 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	ST	298:LEU	C	414:UNK	N	52.49
1	ST	86:LYS	C	186:UNK	N	37.14
1	LI	48:UNK	C	59:UNK	N	26.45
1	ST	234:UNK	C	246:UNK	N	22.17
1	LI	92:UNK	C	104:UNK	N	18.16

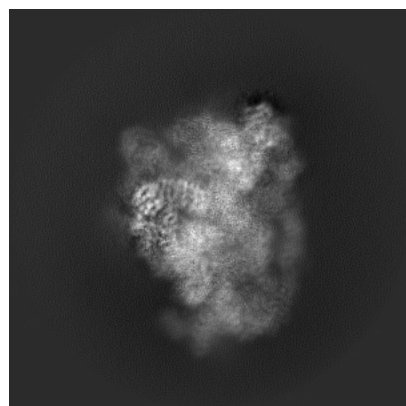
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23936. These allow visual inspection of the internal detail of the map and identification of artifacts.

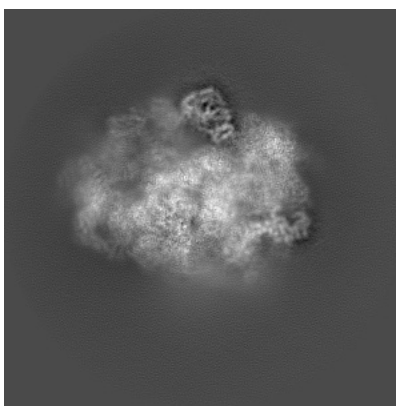
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

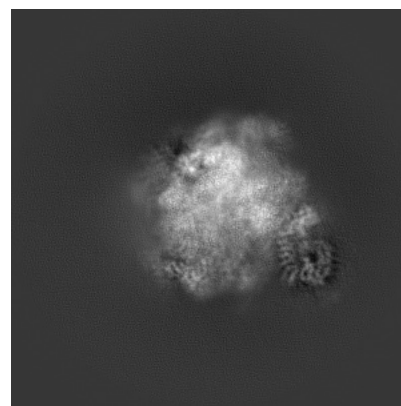
6.1.1 Primary map



X

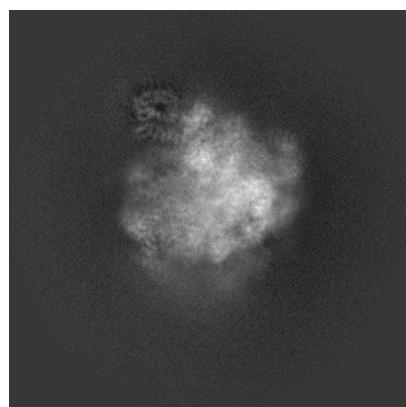


Y

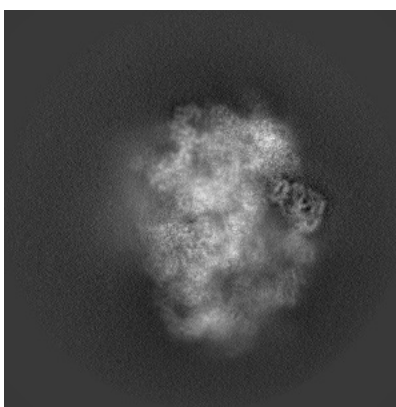


Z

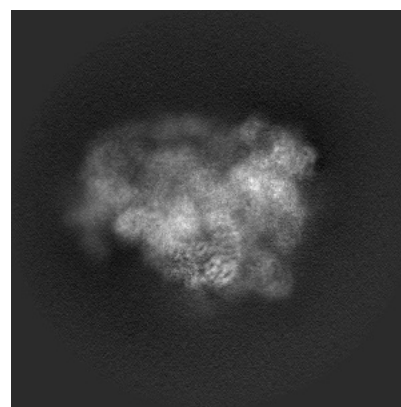
6.1.2 Raw map



X



Y

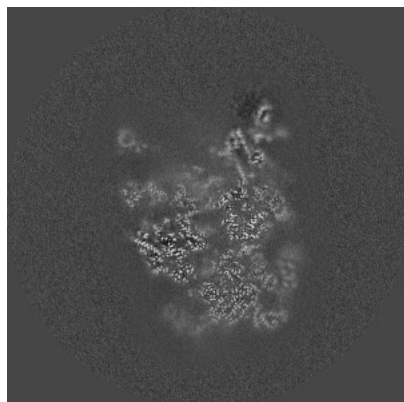


Z

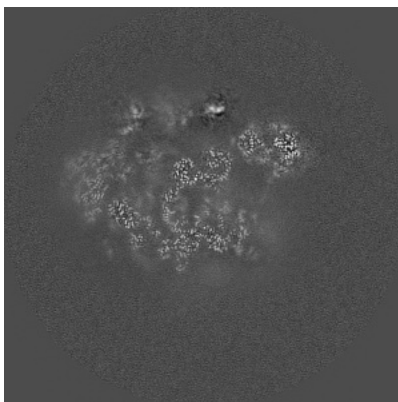
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

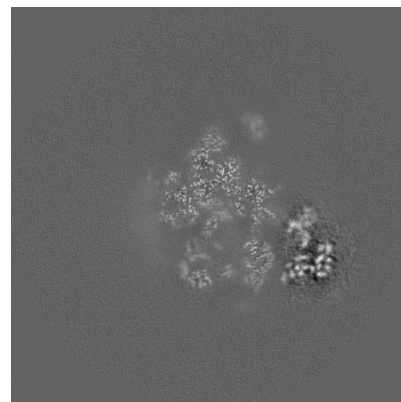
6.2.1 Primary map



X Index: 280

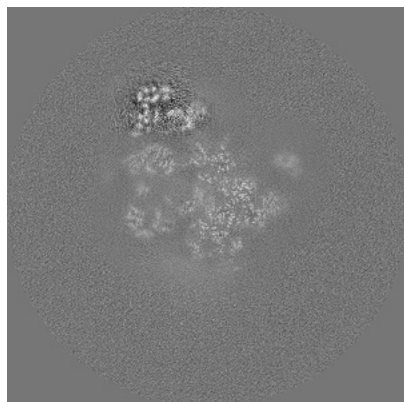


Y Index: 280

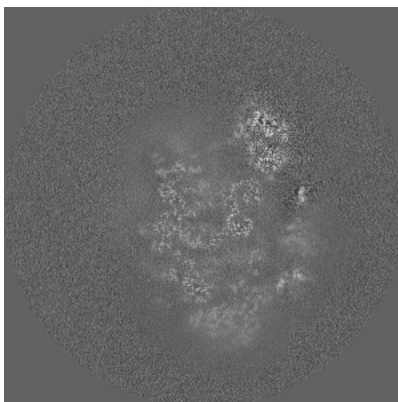


Z Index: 280

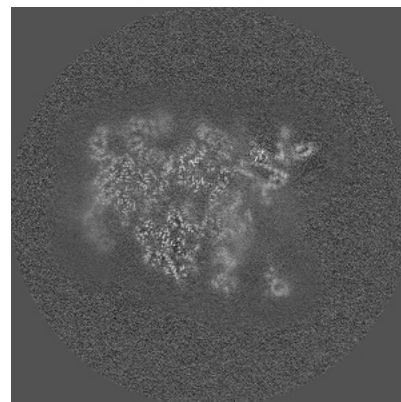
6.2.2 Raw map



X Index: 280



Y Index: 280

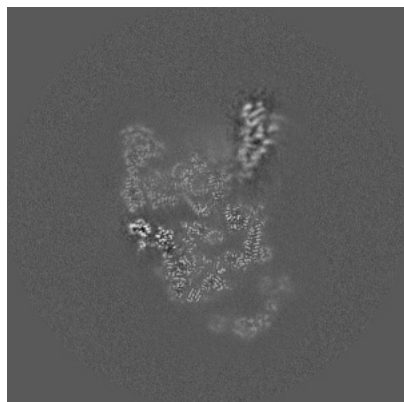


Z Index: 280

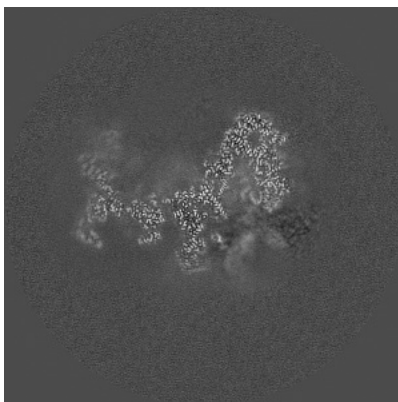
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

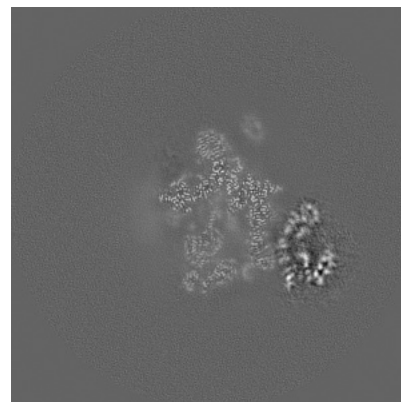
6.3.1 Primary map



X Index: 254

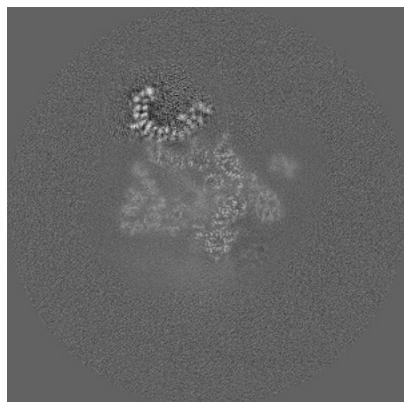


Y Index: 318

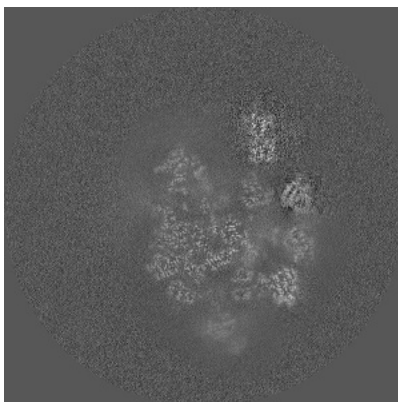


Z Index: 291

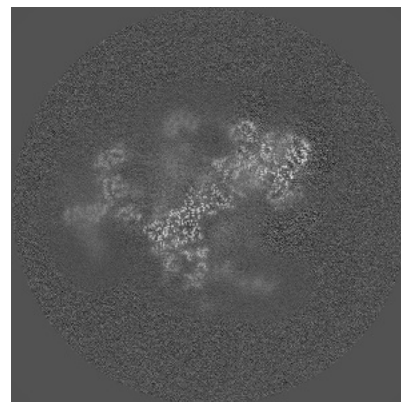
6.3.2 Raw map



X Index: 298



Y Index: 261

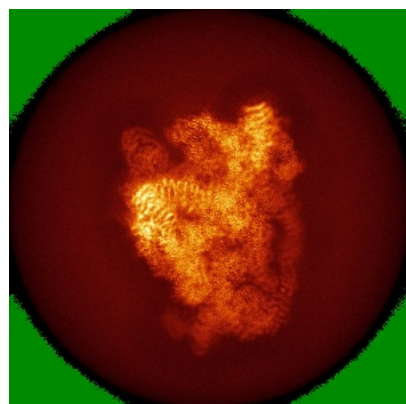


Z Index: 320

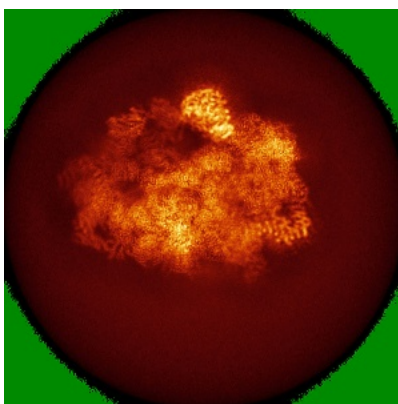
The images above show the largest variance slices of the map in three orthogonal directions.

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

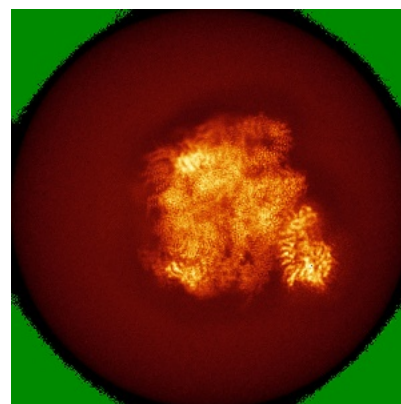
6.4.1 Primary map



X

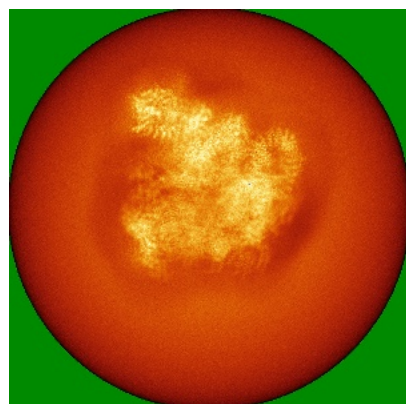


Y

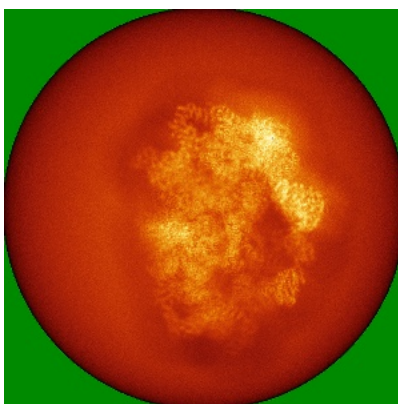


Z

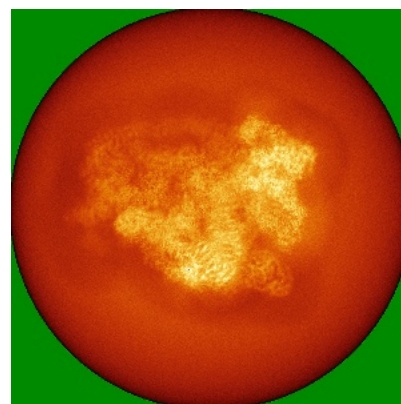
6.4.2 Raw map



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](#)

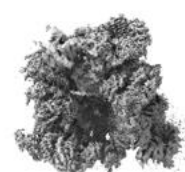
6.5.1 Primary map



X



Y



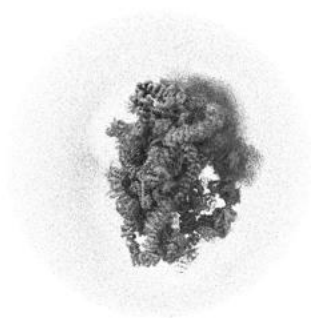
Z

The images above show the 3D surface view of the map at the recommended contour level 2.68. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

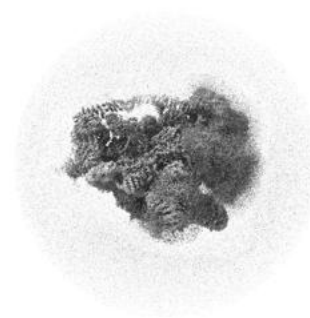
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

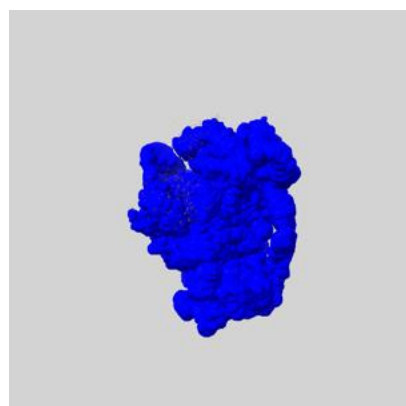
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

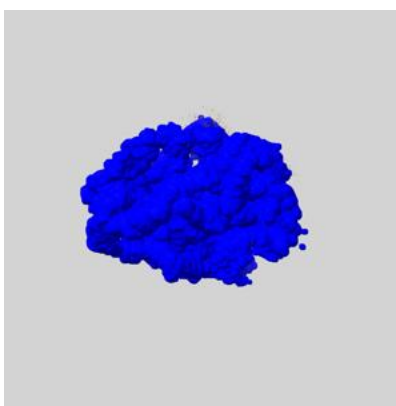
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

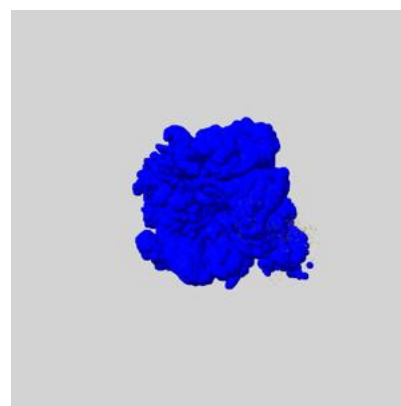
6.6.1 emd_23936_msk_1.map [i](#)



X



Y

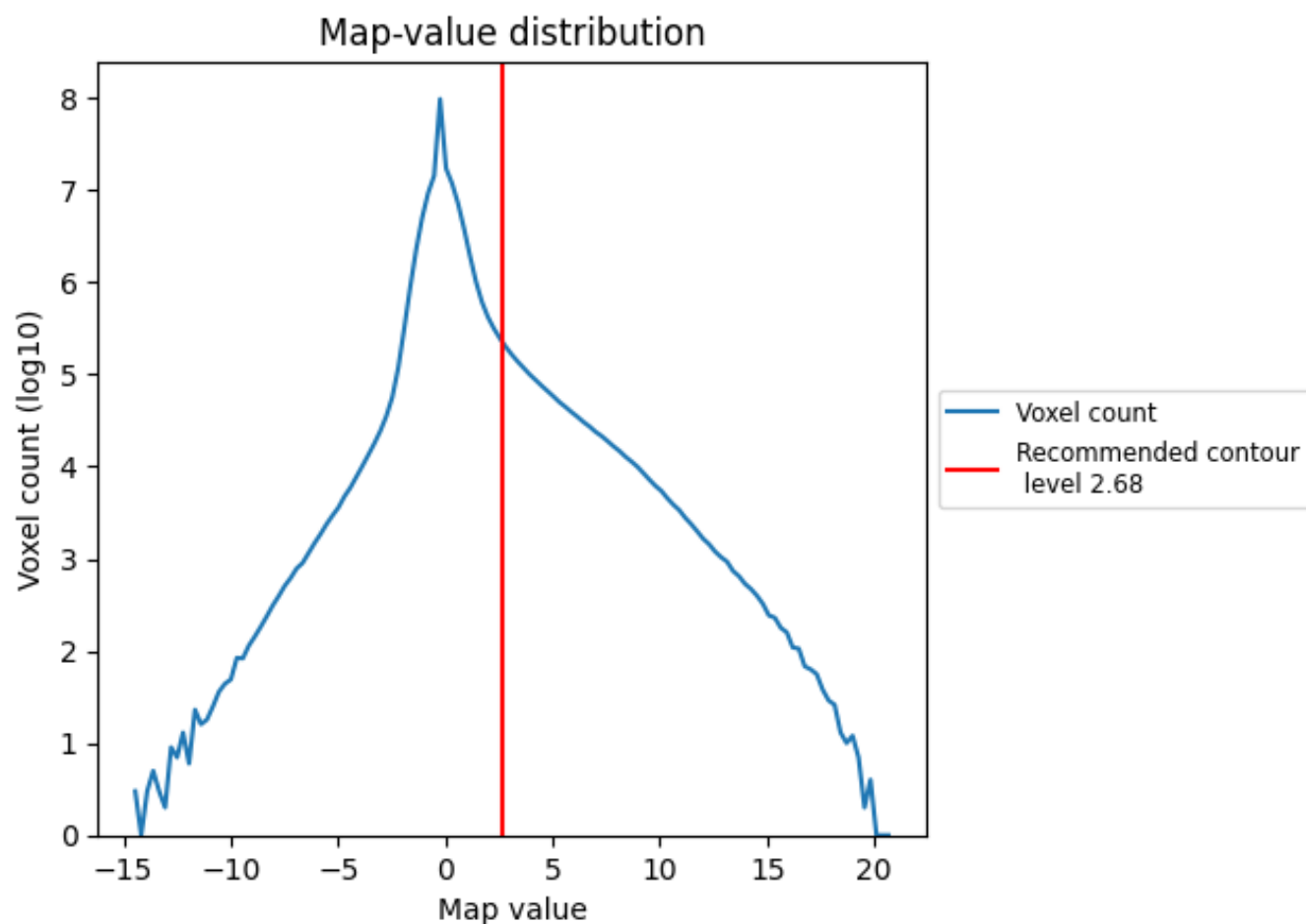


Z

7 Map analysis [i](#)

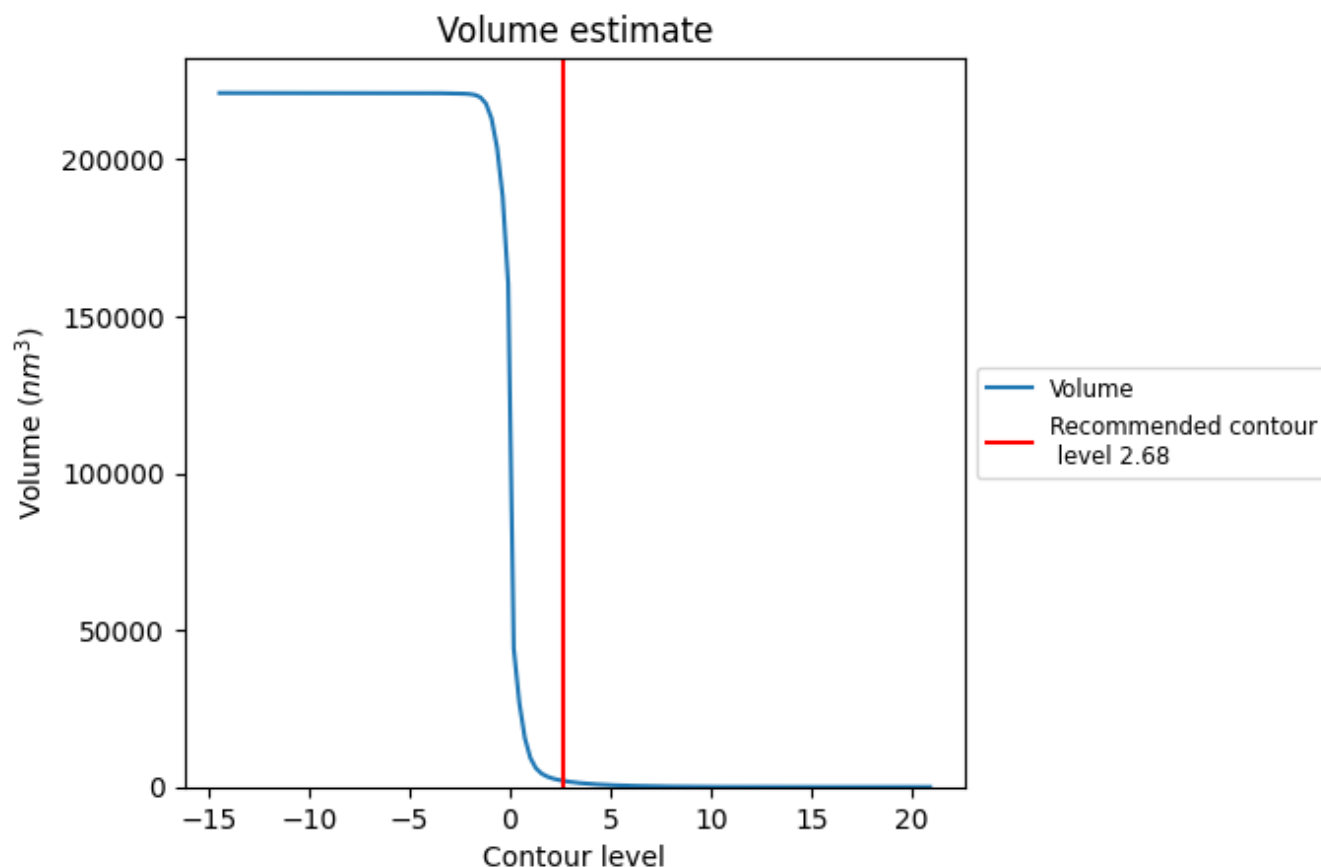
This section contains the results of statistical analysis of the map.

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.

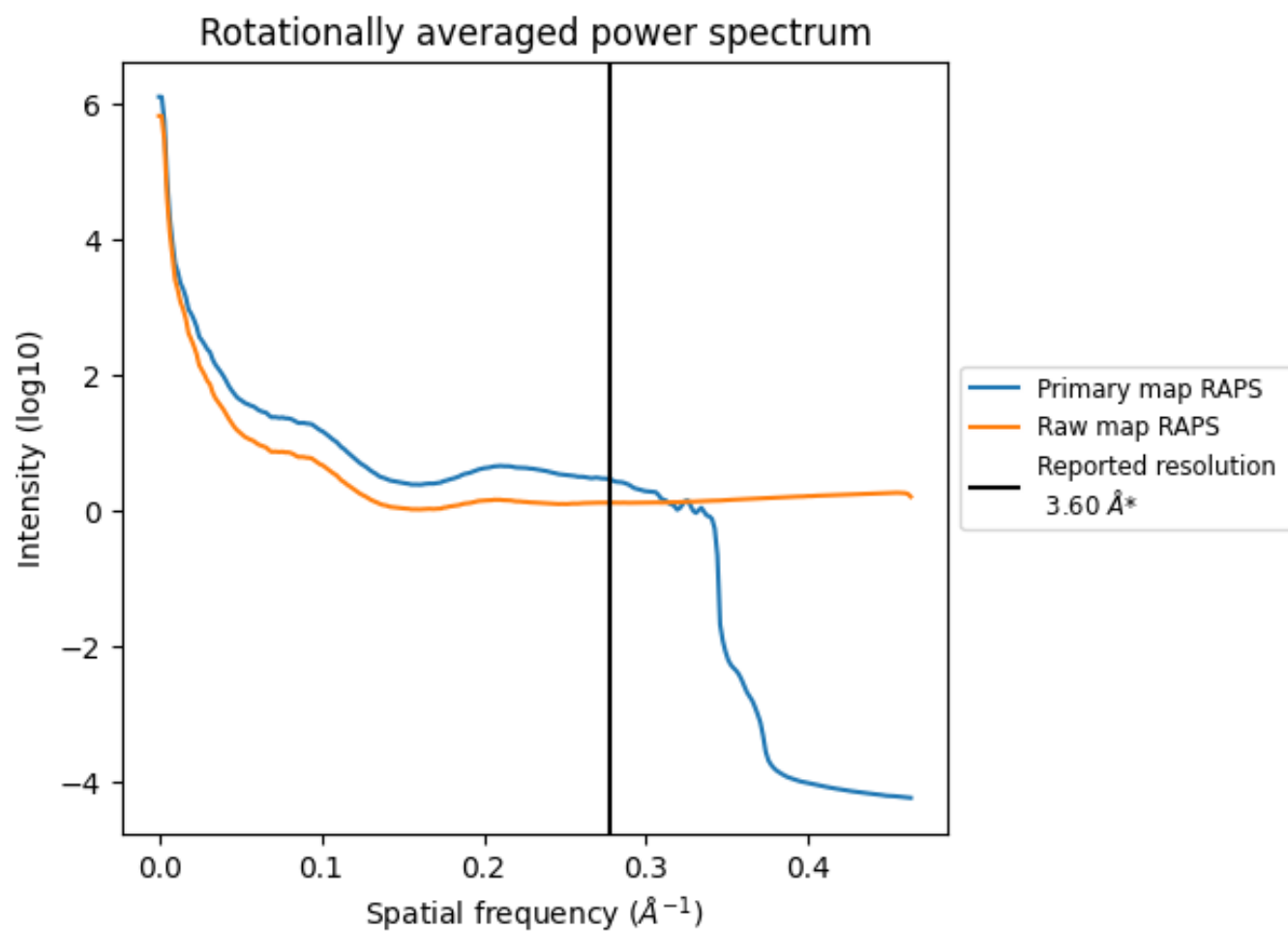
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1931 nm^3 ; this corresponds to an approximate mass of 1744 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 ⓘ

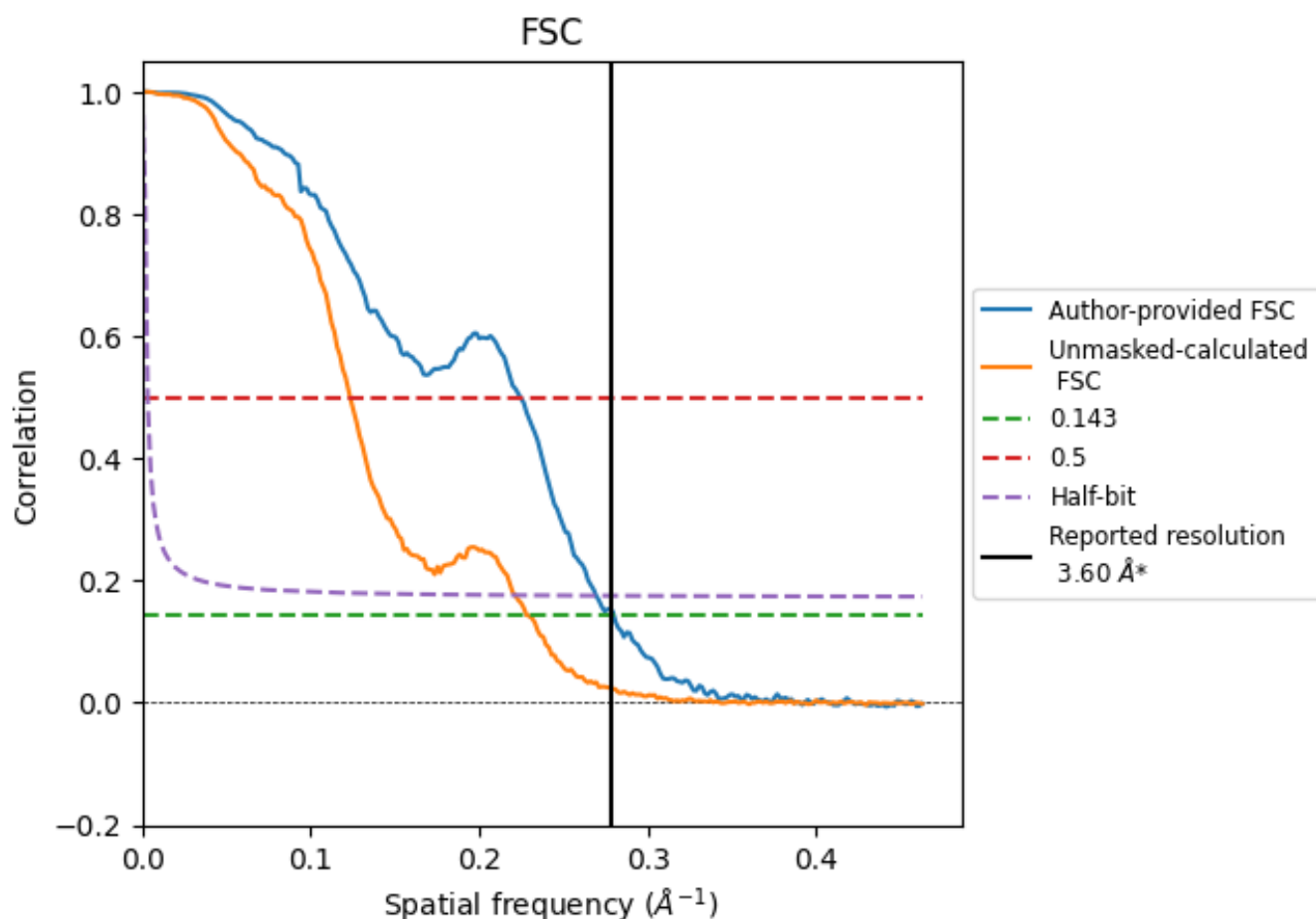


*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

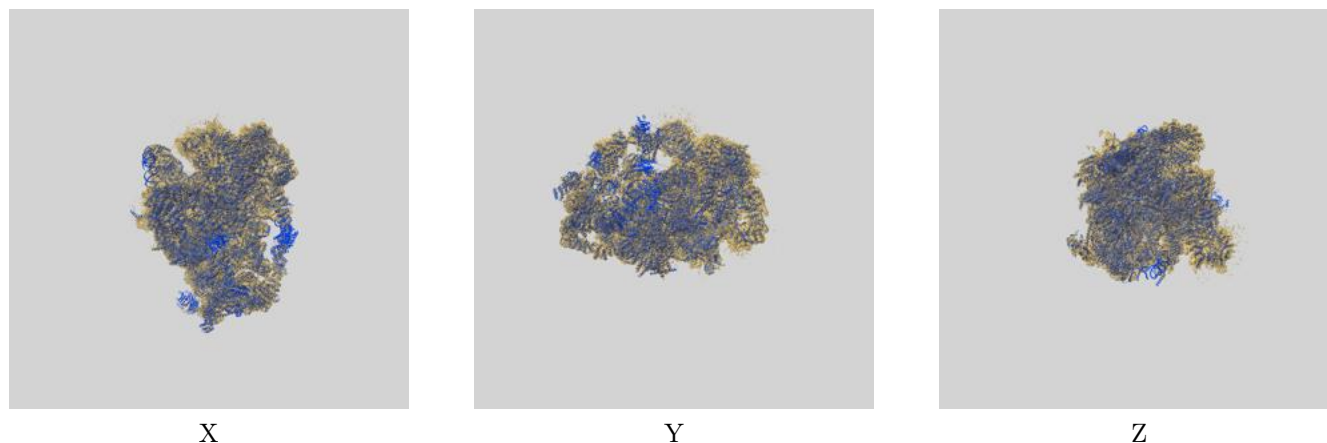
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.57	4.46	3.71
Unmasked-calculated*	4.38	8.10	4.52

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.38 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

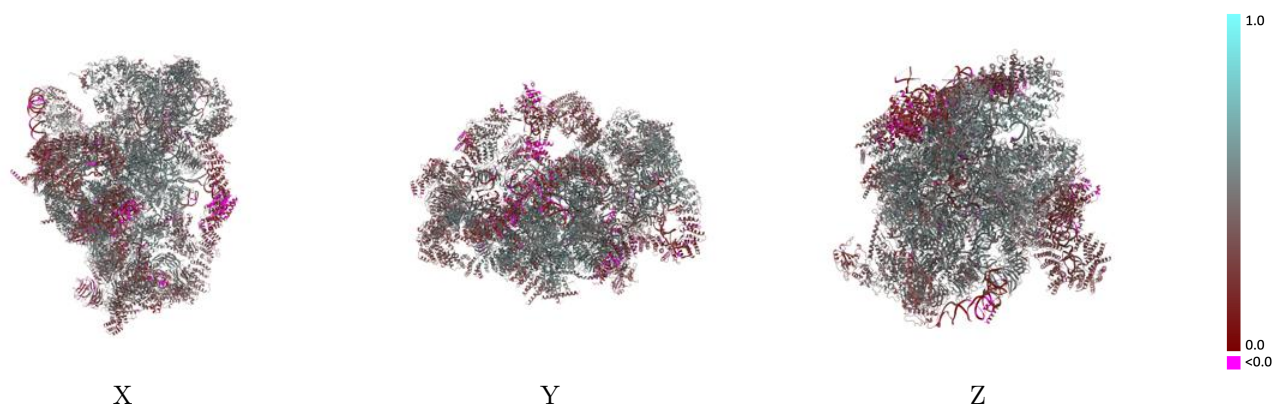
This section contains information regarding the fit between EMDB map EMD-23936 and PDB model 7MQ8. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



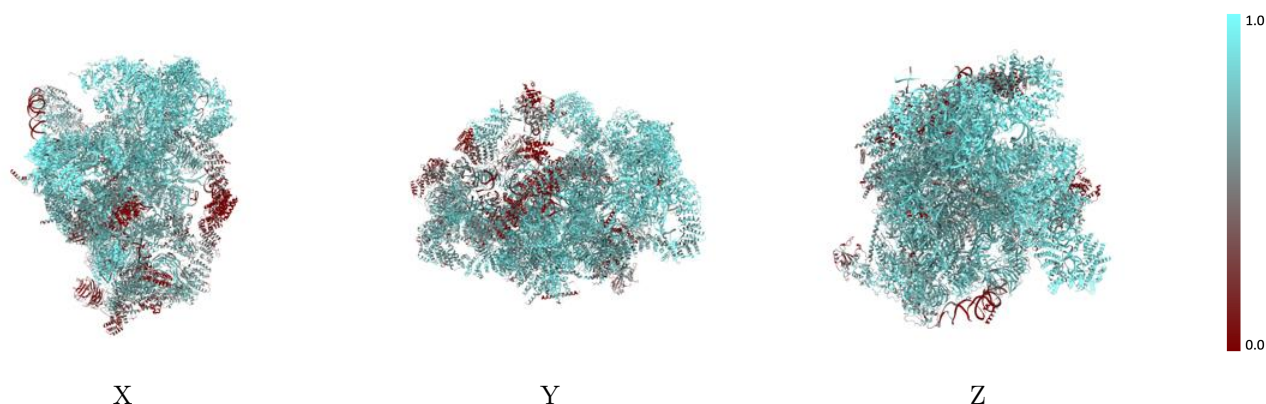
The images above show the 3D surface view of the map at the recommended contour level 2.68 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



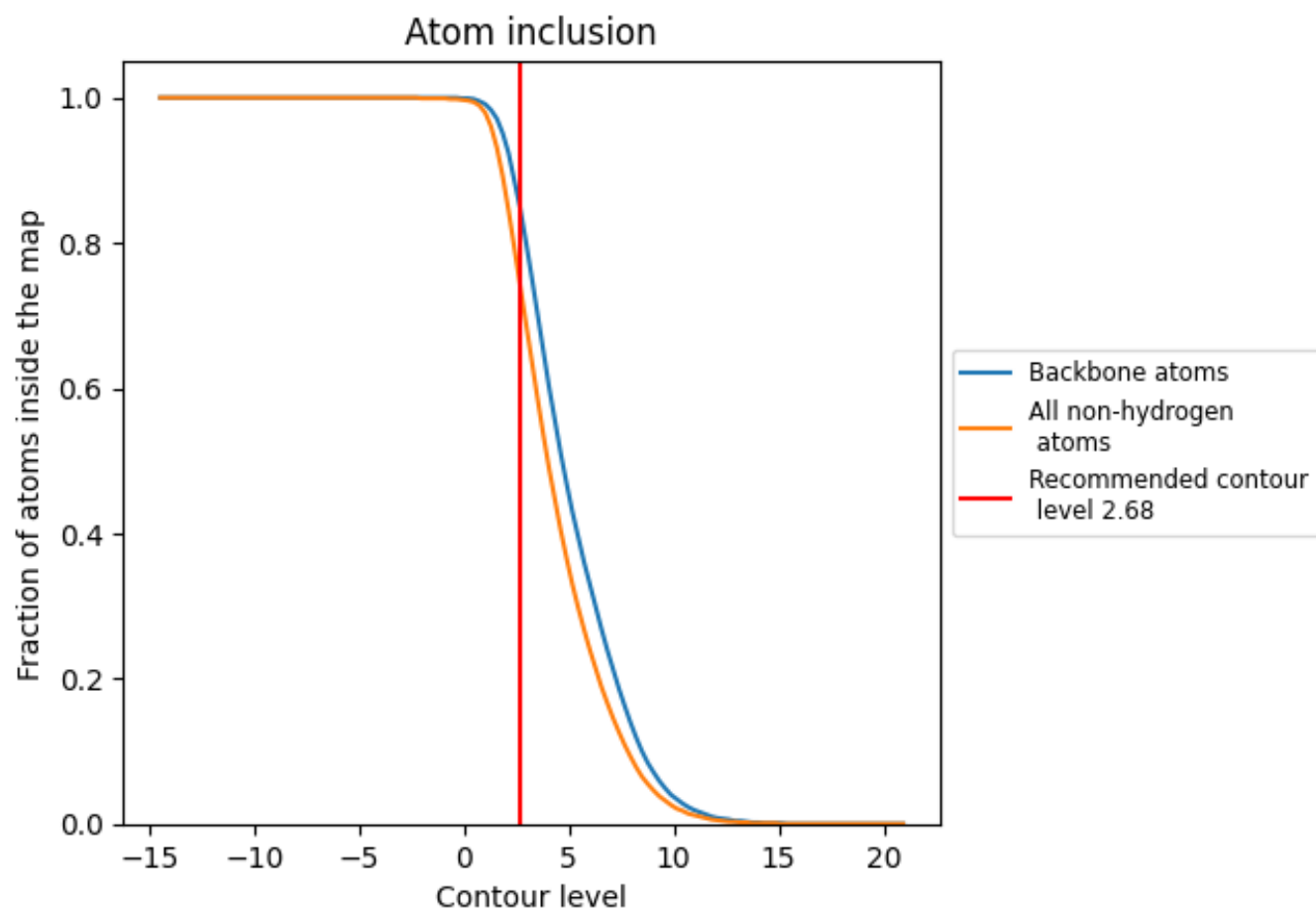
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.68).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 74% 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 (2.68) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7440	 0.4170
L0	 0.5930	 0.3800
L1	 0.8240	 0.3850
L2	 0.7870	 0.4060
L3	 0.3730	 0.3330
L4	 0.8270	 0.4270
L5	 0.8640	 0.5070
L6	 0.8730	 0.4700
L7	 0.5340	 0.3320
L8	 0.9090	 0.4960
L9	 0.9010	 0.5360
LA	 0.0020	 0.0770
LC	 0.8590	 0.5180
LD	 0.8340	 0.4070
LF	 0.8150	 0.4490
LG	 0.8570	 0.5030
LH	 0.7380	 0.4450
LI	 0.1930	 0.2410
LJ	 0.7520	 0.4570
LK	 0.3240	 0.3190
LL	 0.7280	 0.4550
LM	 0.5090	 0.2910
LN	 0.7620	 0.4500
LO	 0.8740	 0.5190
LP	 0.7730	 0.4530
LQ	 0.7590	 0.4540
LR	 0.7840	 0.4430
LS	 0.8280	 0.5170
LT	 0.8670	 0.5220
LU	 0.8530	 0.5120
LW	 0.8220	 0.5080
LZ	 0.8780	 0.5340
N0	 0.5300	 0.3920
NA	 0.7890	 0.4960
NB	 0.9140	 0.5630



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Chain	Atom inclusion	Q-score
NC	 0.7540	 0.4330
ND	 0.6010	 0.4040
NE	 0.6560	 0.4580
NF	 0.6800	 0.4240
NG	 0.7670	 0.4680
NH	 0.6650	 0.3730
NI	 0.4700	 0.3110
NJ	 0.8630	 0.4660
NK	 0.8890	 0.4630
NM	 0.7030	 0.4550
NN	 0.8550	 0.4880
NO	 0.7100	 0.4780
NQ	 0.7710	 0.5090
NR	 0.9110	 0.2750
NT	 0.0350	 0.1220
NU	 0.7070	 0.2240
NW	 0.8850	 0.4900
NY	 0.6540	 0.4250
SA	 0.8380	 0.4900
SB	 0.7290	 0.4540
SC	 0.6170	 0.3780
SD	 0.9280	 0.5620
SE	 0.8620	 0.5220
SF	 0.8800	 0.5270
SG	 0.7850	 0.4290
SH	 0.8560	 0.5200
SI	 0.8630	 0.5100
SJ	 0.3440	 0.2800
SK	 0.5870	 0.4270
SL	 0.8710	 0.5300
SM	 0.8860	 0.5350
SP	 0.7810	 0.3450
SQ	 0.7580	 0.4580
SR	 0.8750	 0.5290
SS	 0.6780	 0.4560
ST	 0.7310	 0.3820
SU	 0.4610	 0.3320
SW	 0.8380	 0.3510
SX	 0.0010	 0.0460
SY	 0.6790	 0.4100
SZ	 0.5930	 0.2680
Sx	 0.3740	 0.2470