



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:24 AM UTC

PDB ID : 7TBL / pdb_00007tbl
EMDB ID : EMD-14322
Title : Composite structure of the human nuclear pore complex (NPC) cytoplasmic face generated with a 12Å cryo-ET map of the purified HeLa cell NPC
Authors : Bley, C.J.; Nie, S.; Mobbs, G.W.; Petrovic, S.; Gres, A.T.; Liu, X.; Mukherjee, S.; Harvey, S.; Huber, F.M.; Lin, D.H.; Brown, B.; Tang, A.W.; Rundlet, E.J.; Correia, A.R.; Chen, S.; Regmi, S.G.; Stevens, T.A.; Jette, C.A.; Dasso, M.; Patke, A.; Palazzo, A.F.; Kossiakoff, A.A.; Hoelz, A.
Deposited on : 2021-12-22
Resolution : 23.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

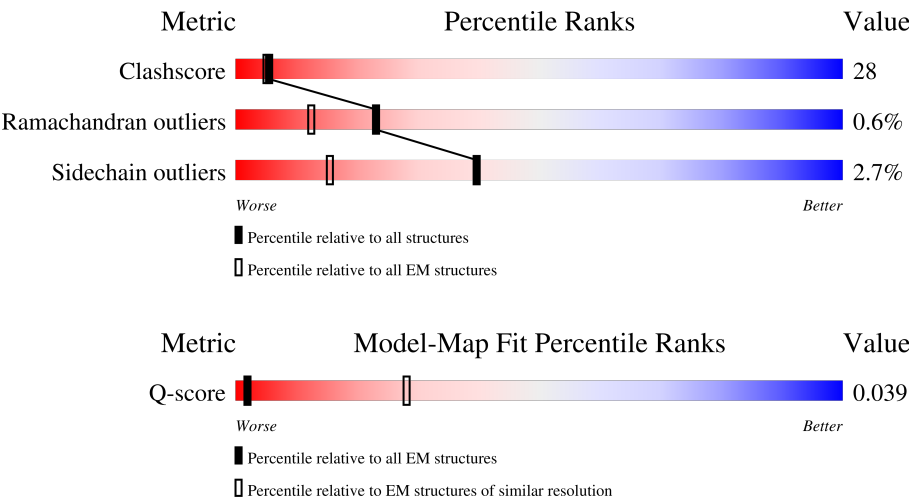
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 23.00 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	-
Q-score	-	25397	93 (11.50 - 12.50)

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	A1	1316	27% 86% 7% 6%
1	A3	1316	30% 87% 7% 6%
2	A2	1328	58% 73% 20% . .

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Mol	Chain	Length	Quality of chain
2	A4	1328	
3	A5	1330	
3	A6	1330	
4	B1	14	
4	B2	14	
4	B3	14	
4	B4	14	
4	B5	14	
4	B6	14	
5	C1	19	
5	C2	19	
5	C3	19	
5	C4	19	
5	C5	19	
5	C6	19	
6	D1	644	
6	D2	644	
6	D3	644	
6	D4	644	
6	D5	644	
6	D6	644	
6	D7	644	
7	E1	8	
7	E2	8	
7	E3	8	

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Mol	Chain	Length	Quality of chain
7	E4	8	62% 75%25%
7	E5	8	75% 75%25%
7	E6	8	25% 75%25%
7	E7	8	100% 75%25%
8	F1	1858	26% 81%7%12%
8	F2	1858	42% 82%6%12%
9	G1	53	40% 68%32%
9	G2	53	55% 85%15%
10	H1	13	62% 100%
10	H2	13	69% 100%
11	I1	1756	30% 67%21%12%
11	I2	1756	31% 67%21%12%
11	I3	1756	21% 78%9%12%
11	I4	1756	39% 79%8%12%
11	I5	1756	25% 78%10%12%
12	J1	63	46% 71%29%
12	J2	63	35% 71%29%
12	J3	63	43% 79%21%
12	J4	63	49% 79%21%
12	J5	63	29% 79%21%
13	K1	9	89% 100%
13	K2	9	89% 100%
13	K3	9	67% 100%
13	K4	9	100%
13	K5	9	78% 100%

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Mol	Chain	Length	Quality of chain
14	L1	2	100%
14	L2	2	100%
14	L3	2	100%
14	L4	2	100%
14	L5	2	50% 100%
15	M1	183	25% 63% 29% 8%
15	M2	183	18% 88% • 8%
15	M3	183	30% 66% 27% 8%
15	M4	183	20% 89% • 8%
16	N1	222	19% 61% 20% 19%
16	N2	222	16% 76% 5% 19%
16	N3	222	23% 60% 21% 19%
16	N4	222	18% 78% • 19%
17	O1	241	27% 68% 30% •
17	O2	241	33% 78% 21% •
17	O3	241	25% 63% 35% •
17	O4	241	36% 81% 18% •
18	P1	116	19% 91% 9%
18	P2	116	17% 92% 8%
18	P3	116	18% 88% 12%
18	P4	116	25% 91% 9%
19	Q1	84	92% 7% •
19	Q2	84	86% 10% 5%
19	Q3	84	• 92% 7% •
19	Q4	84	• 86% 10% 5%

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Mol	Chain	Length	Quality of chain
20	R1	40	
20	R2	40	
20	R3	40	
20	R4	40	
21	S1	1156	
21	S2	1156	
21	S3	1156	
21	S4	1156	
22	T1	258	
22	T2	258	
22	T3	258	
22	T4	258	
23	U1	436	
23	U2	436	
23	U3	436	
23	U4	436	
24	V1	621	
24	V2	621	
24	V3	621	
24	V4	621	
25	W1	286	
25	W2	286	
25	W3	286	
25	W4	286	
26	X1	744	

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Mol	Chain	Length	Quality of chain
26	X2	744	
26	X3	744	
26	X4	744	
27	Y1	349	
27	Y2	349	
27	Y3	349	
27	Y4	349	
28	Z1	1037	
28	Z2	1037	
28	Z3	1037	
28	Z4	1037	
29	a1	380	
29	a2	380	
29	a3	380	
29	a4	380	
30	b1	391	
30	b2	391	
30	b3	391	
30	b4	391	
31	c1	750	
31	c2	750	
31	c3	750	
31	c4	750	
31	c5	750	
32	d1	491	

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Mol	Chain	Length	Quality of chain
32	d2	491	
33	e	316	
34	f	45	
35	g	421	
36	h	232	
37	i	481	
38	j	150	
39	k1	85	
40	k2	37	
41	l1	92	
42	l2	39	
43	m1	88	
44	m2	20	

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 410733 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 protein called NUP155.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	1231	Total	C	N	O	S	1	0
			9730	6152	1707	1843	28		
1	A3	1231	Total	C	N	O	S	1	0
			9730	6152	1707	1843	28		

- Molecule 2 is a protein called NUP155.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	A2	1269	Total	C	N	O	S	Se	0	0
			9946	6277	1745	1890	22	12		
2	A4	1269	Total	C	N	O	S	Se	0	0
			9946	6277	1745	1890	22	12		

- Molecule 3 is a protein called NUP155.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	A5	1276	Total	C	N	O	S	Se	1	0
			10030	6331	1762	1901	24	12		
3	A6	1276	Total	C	N	O	S	Se	1	0
			10030	6331	1762	1901	24	12		

- Molecule 4 is a protein called NUP53 R3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B1	14	Total	C	N	O	S	0	0
			111	73	19	18	1		
4	B2	14	Total	C	N	O	S	0	0
			111	73	19	18	1		
4	B3	14	Total	C	N	O	S	0	0
			111	73	19	18	1		
4	B4	14	Total	C	N	O	S	0	0
			111	73	19	18	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	B5	14	Total	C	N	O	S	0	0
			111	73	19	18	1		
4	B6	14	Total	C	N	O	S	0	0
			111	73	19	18	1		

- Molecule 5 is a protein called NUP98 R3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C1	17	Total	C	N	O	S	0	0
			138	88	24	25	1		
5	C2	19	Total	C	N	O	S	0	0
			157	100	29	27	1		
5	C3	17	Total	C	N	O	S	0	0
			138	88	24	25	1		
5	C4	19	Total	C	N	O	S	0	0
			157	100	29	27	1		
5	C5	17	Total	C	N	O	S	0	0
			138	88	24	25	1		
5	C6	17	Total	C	N	O	S	0	0
			138	88	24	25	1		

- Molecule 6 is a protein called NUP93 SOL.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D1	621	Total	C	N	O	S	0	0
			5034	3200	874	934	26		
6	D2	621	Total	C	N	O	S	0	0
			5034	3200	874	934	26		
6	D3	621	Total	C	N	O	S	0	0
			5034	3200	874	934	26		
6	D4	621	Total	C	N	O	S	0	0
			5034	3200	874	934	26		
6	D5	621	Total	C	N	O	S	0	0
			5034	3200	874	934	26		
6	D6	621	Total	C	N	O	S	0	0
			5034	3200	874	934	26		
6	D7	621	Total	C	N	O	S	0	0
			5034	3200	874	934	26		

- Molecule 7 is a protein called NUP53 R2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	E1	8	Total	C	N	O	0	0
			63	42	11	10		
7	E2	8	Total	C	N	O	0	0
			63	42	11	10		
7	E3	8	Total	C	N	O	0	0
			63	42	11	10		
7	E4	8	Total	C	N	O	0	0
			63	42	11	10		
7	E5	8	Total	C	N	O	0	0
			63	42	11	10		
7	E6	8	Total	C	N	O	0	0
			63	42	11	10		
7	E7	8	Total	C	N	O	0	0
			63	42	11	10		

- Molecule 8 is a protein called NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F1	1641	Total	C	N	O	S	0	0
			12779	8190	2201	2333	55		
8	F2	1641	Total	C	N	O	S	0	0
			12779	8190	2201	2333	55		

- Molecule 9 is a protein called NUP93 R2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G1	53	Total	C	N	O	S	0	0
			438	274	75	88	1		
9	G2	53	Total	C	N	O	S	0	0
			438	274	75	88	1		

- Molecule 10 is a protein called NUP98 R2.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	H1	13	Total	C	N	O	0	0
			94	58	15	21		
10	H2	13	Total	C	N	O	0	0
			94	58	15	21		

- Molecule 11 is a protein called NUP205.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I1	1542	Total	C	N	O	S	0	0
			12307	7880	2084	2278	65		
11	I2	1542	Total	C	N	O	S	0	0
			12307	7880	2084	2278	65		
11	I3	1542	Total	C	N	O	S	0	0
			12307	7880	2084	2278	65		
11	I4	1542	Total	C	N	O	S	0	0
			12307	7880	2084	2278	65		
11	I5	1542	Total	C	N	O	S	0	0
			12307	7880	2084	2278	65		

- Molecule 12 is a protein called NUP93 R2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J1	63	Total	C	N	O	S	0	0
			504	315	86	102	1		
12	J2	63	Total	C	N	O	S	0	0
			504	315	86	102	1		
12	J3	63	Total	C	N	O	S	0	0
			504	315	86	102	1		
12	J4	63	Total	C	N	O	S	0	0
			504	315	86	102	1		
12	J5	63	Total	C	N	O	S	0	0
			504	315	86	102	1		

- Molecule 13 is a protein called NUP98 R1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K1	9	Total	C	N	O	S	0	0
			73	51	10	11	1		
13	K2	9	Total	C	N	O	S	0	0
			73	51	10	11	1		
13	K3	9	Total	C	N	O	S	0	0
			73	51	10	11	1		
13	K4	9	Total	C	N	O	S	0	0
			73	51	10	11	1		
13	K5	9	Total	C	N	O	S	0	0
			73	51	10	11	1		

- Molecule 14 is a protein called NUP53 R1.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L1	2	Total	C	N	O	0	0
			15	11	2	2		
14	L2	2	Total	C	N	O	0	0
			15	11	2	2		
14	L3	2	Total	C	N	O	0	0
			15	11	2	2		
14	L4	2	Total	C	N	O	0	0
			15	11	2	2		
14	L5	2	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 15 is a protein called NUP62.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M1	169	Total	C	N	O	S	0	0
			1372	855	235	276	6		
15	M2	169	Total	C	N	O	S	0	0
			1372	855	235	276	6		
15	M3	169	Total	C	N	O	S	0	0
			1372	855	235	276	6		
15	M4	169	Total	C	N	O	S	0	0
			1372	855	235	276	6		

- Molecule 16 is a protein called NUP58.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N1	180	Total	C	N	O	S	0	0
			1401	876	236	282	7		
16	N2	180	Total	C	N	O	S	0	0
			1401	876	236	282	7		
16	N3	180	Total	C	N	O	S	0	0
			1401	876	236	282	7		
16	N4	180	Total	C	N	O	S	0	0
			1401	876	236	282	7		

- Molecule 17 is a protein called NUP54.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O1	241	Total	C	N	O	S	0	0
			1971	1239	360	368	4		
17	O2	241	Total	C	N	O	S	0	0
			1971	1239	360	368	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	O3	241	Total	C	N	O	S	0	0
			1971	1239	360	368	4		
17	O4	241	Total	C	N	O	S	0	0
			1971	1239	360	368	4		

- Molecule 18 is a protein called NUP54 Ferredoxin-like domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P1	116	Total	C	N	O	S	1	0
			900	560	160	178	2		
18	P2	116	Total	C	N	O	S	1	0
			900	560	160	178	2		
18	P3	116	Total	C	N	O	S	1	0
			900	560	160	178	2		
18	P4	116	Total	C	N	O	S	1	0
			900	560	160	178	2		

- Molecule 19 is a protein called NUP53 RRM.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	Q1	84	Total	C	N	O	S	Se	1	0
			658	421	114	117	1	5		
19	Q2	80	Total	C	N	O	S	Se	1	0
			616	399	103	108	1	5		
19	Q3	84	Total	C	N	O	S	Se	1	0
			658	421	114	117	1	5		
19	Q4	80	Total	C	N	O	S	Se	1	0
			616	399	103	108	1	5		

- Molecule 20 is a protein called NUP93 R1.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	R1	40	Total	C	N	O	0	0
			311	195	59	57		
20	R2	40	Total	C	N	O	0	0
			311	195	59	57		
20	R3	40	Total	C	N	O	0	0
			311	195	59	57		
20	R4	40	Total	C	N	O	0	0
			311	195	59	57		

- Molecule 21 is a protein called NUP133.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S1	902	Total	C	N	O	S	0	0
			6013	3738	1046	1210	19		
21	S2	902	Total	C	N	O	S	0	0
			6013	3738	1046	1210	19		
21	S3	902	Total	C	N	O	S	0	0
			6013	3738	1046	1210	19		
21	S4	902	Total	C	N	O	S	0	0
			6013	3738	1046	1210	19		

- Molecule 22 is a protein called NUP107 CTD.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T1	247	Total	C	N	O	S	0	0
			1993	1282	343	355	13		
22	T2	247	Total	C	N	O	S	0	0
			1993	1282	343	355	13		
22	T3	247	Total	C	N	O	S	0	0
			1993	1282	343	355	13		
22	T4	247	Total	C	N	O	S	0	0
			1993	1282	343	355	13		

- Molecule 23 is a protein called NUP107 NTD.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U1	419	Total	C	N	O	S	0	0
			3404	2178	557	657	12		
23	U2	419	Total	C	N	O	S	0	0
			3404	2178	557	657	12		
23	U3	419	Total	C	N	O	S	0	0
			3404	2178	557	657	12		
23	U4	419	Total	C	N	O	S	0	0
			3404	2178	557	657	12		

- Molecule 24 is a protein called NUP96.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V1	511	Total	C	N	O	S	0	0
			3805	2417	648	730	10		
24	V2	511	Total	C	N	O	S	0	0
			3805	2417	648	730	10		
24	V3	511	Total	C	N	O	S	0	0
			3805	2417	648	730	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
24	V4	511	Total	C	N	O	S	0	0
			3805	2417	648	730	10		

- Molecule 25 is a protein called SEC13.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W1	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		
25	W2	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		
25	W3	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		
25	W4	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		

- Molecule 26 is a protein called NUP75.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X1	620	Total	C	N	O	S	0	0
			4535	2884	753	877	21		
26	X2	620	Total	C	N	O	S	0	0
			4535	2884	753	877	21		
26	X3	620	Total	C	N	O	S	0	0
			4535	2884	753	877	21		
26	X4	620	Total	C	N	O	S	0	0
			4535	2884	753	877	21		

- Molecule 27 is a protein called SEH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y1	307	Total	C	N	O	S	0	0
			2438	1543	422	462	11		
27	Y2	307	Total	C	N	O	S	0	0
			2438	1543	422	462	11		
27	Y3	307	Total	C	N	O	S	0	0
			2438	1543	422	462	11		
27	Y4	307	Total	C	N	O	S	0	0
			2438	1543	422	462	11		

- Molecule 28 is a protein called NUP160.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z1	896	Total	C	N	O	S	0	0
			6622	4232	1099	1275	16		
28	Z2	896	Total	C	N	O	S	0	0
			6622	4232	1099	1275	16		
28	Z3	896	Total	C	N	O	S	0	0
			6622	4232	1099	1275	16		
28	Z4	896	Total	C	N	O	S	0	0
			6622	4232	1099	1275	16		

- Molecule 29 is a protein called NUP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a1	316	Total	C	N	O	S	33	1
			2587	1639	447	488	13		
29	a2	316	Total	C	N	O	S	33	1
			2587	1639	447	488	13		
29	a3	316	Total	C	N	O	S	33	1
			2587	1639	447	488	13		
29	a4	316	Total	C	N	O	S	33	1
			2587	1639	447	488	13		

- Molecule 30 is a protein called NUP37.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b1	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		
30	b2	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		
30	b3	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		
30	b4	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		

- Molecule 31 is a protein called NUP358.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c1	742	Total	C	N	O	S	0	0
			5976	3800	1032	1116	28		
31	c2	742	Total	C	N	O	S	0	0
			5976	3800	1032	1116	28		
31	c3	742	Total	C	N	O	S	0	0
			5976	3800	1032	1116	28		

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Mol	Chain	Residues	Atoms					AltConf	Trace
31	c4	742	Total	C	N	O	S	0	0
			5976	3800	1032	1116	28		
31	c5	742	Total	C	N	O	S	0	0
			5976	3800	1032	1116	28		

- Molecule 32 is a protein called ELYS.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	d1	463	Total	C	N	O	S	Se	7	0
			3629	2304	618	689	14	4		
32	d2	463	Total	C	N	O	S	Se	7	0
			3629	2304	618	689	14	4		

- Molecule 33 is a protein called GLE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	313	Total	C	N	O	S	0	0
			2527	1632	429	451	15		

- Molecule 34 is a protein called NUP42.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	f	45	Total	C	N	O	0	0
			363	239	57	67		

- Molecule 35 is a protein called NUP214 NTD.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	421	Total	C	N	O	S	0	0
			3282	2106	535	619	22		

- Molecule 36 is a protein called DDX19.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	232	Total	C	N	O	S	0	0
			1836	1174	313	338	11		

- Molecule 37 is a protein called NUP88 NTD.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	409	Total	C	N	O	S	13	0
			3280	2134	540	583	23		

- Molecule 38 is a protein called NUP98 APD.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	150	Total	C	N	O	S	1	0
			1197	760	205	228	4		

- Molecule 39 is a protein called NUP62 CCS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k1	85	Total	C	N	O	S	0	0
			719	448	124	145	2		

- Molecule 40 is a protein called NUP62 CCS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k2	37	Total	C	N	O	S	0	0
			308	188	56	63	1		

- Molecule 41 is a protein called NUP214 CCS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	l1	92	Total	C	N	O	0	0
			460	276	92	92		

- Molecule 42 is a protein called NUP214 CCS2.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	l2	39	Total	C	N	O	0	0
			195	117	39	39		

- Molecule 43 is a protein called NUP88 CCS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	m1	88	Total	C	N	O	0	0
			440	264	88	88		

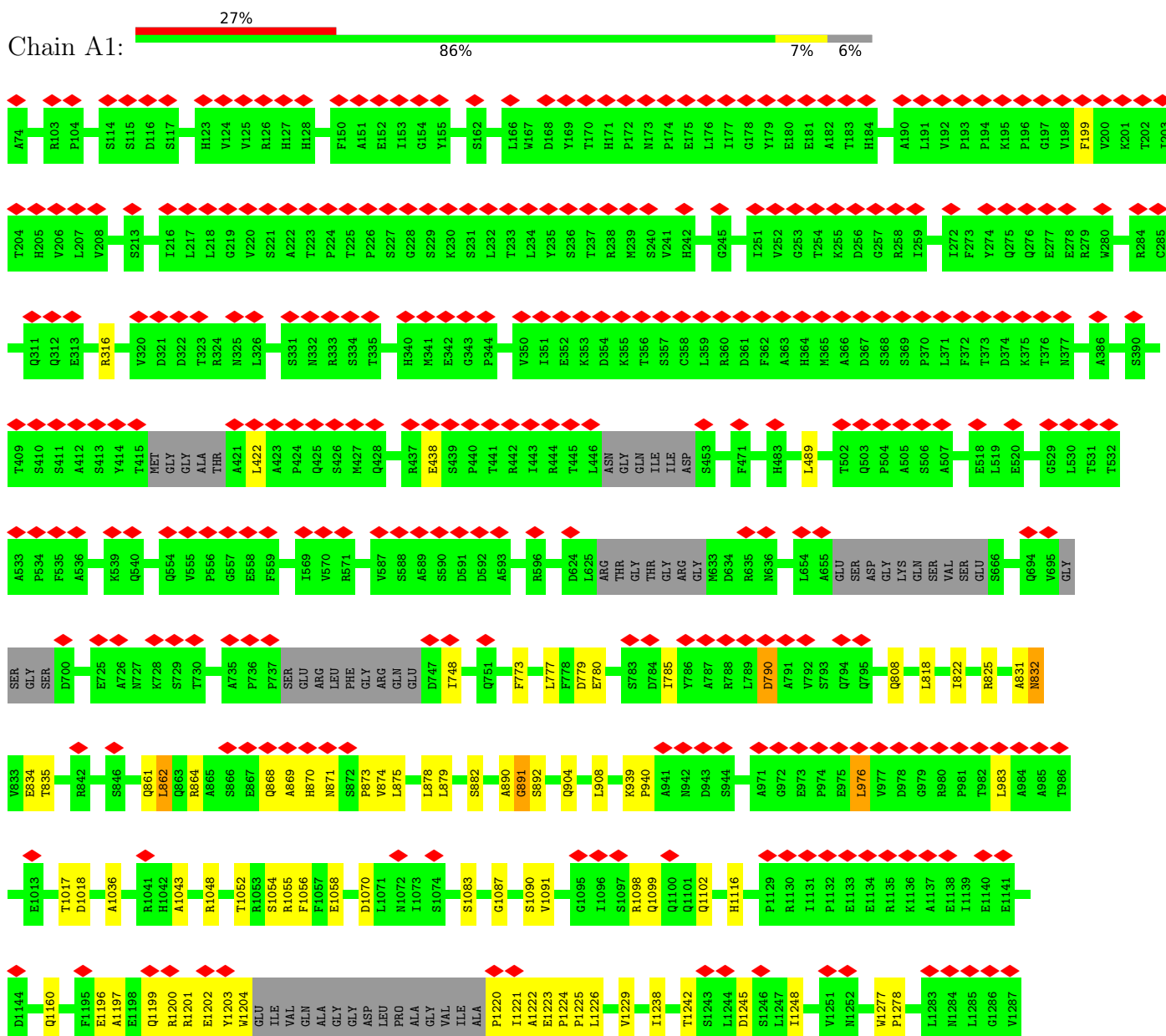
- Molecule 44 is a protein called NUP88 CCS2.

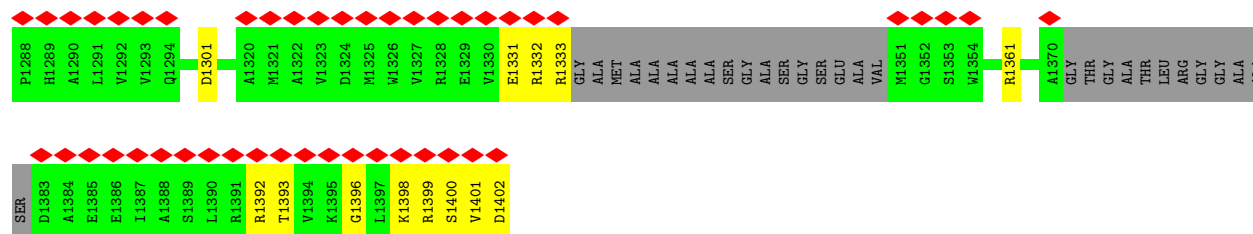
Mol	Chain	Residues	Atoms				AltConf	Trace
44	m2	20	Total	C	N	O	0	0
			100	60	20	20		

3 Residue-property plots

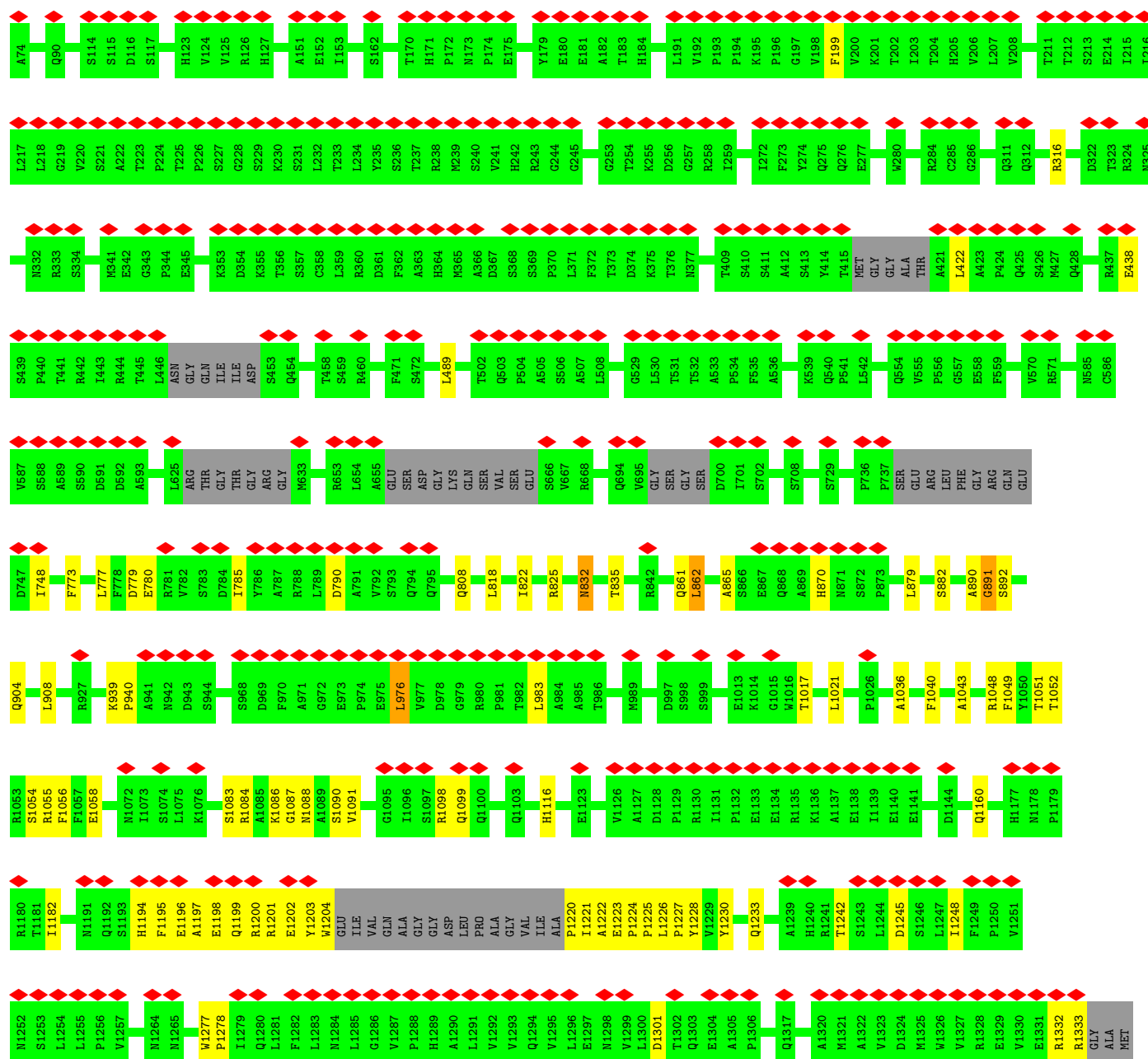
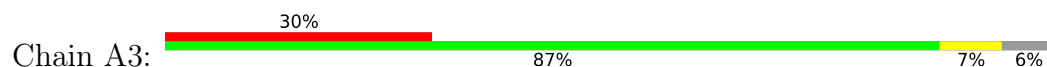
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

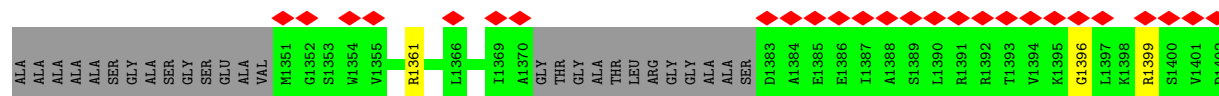
• Molecule 1: NUP155



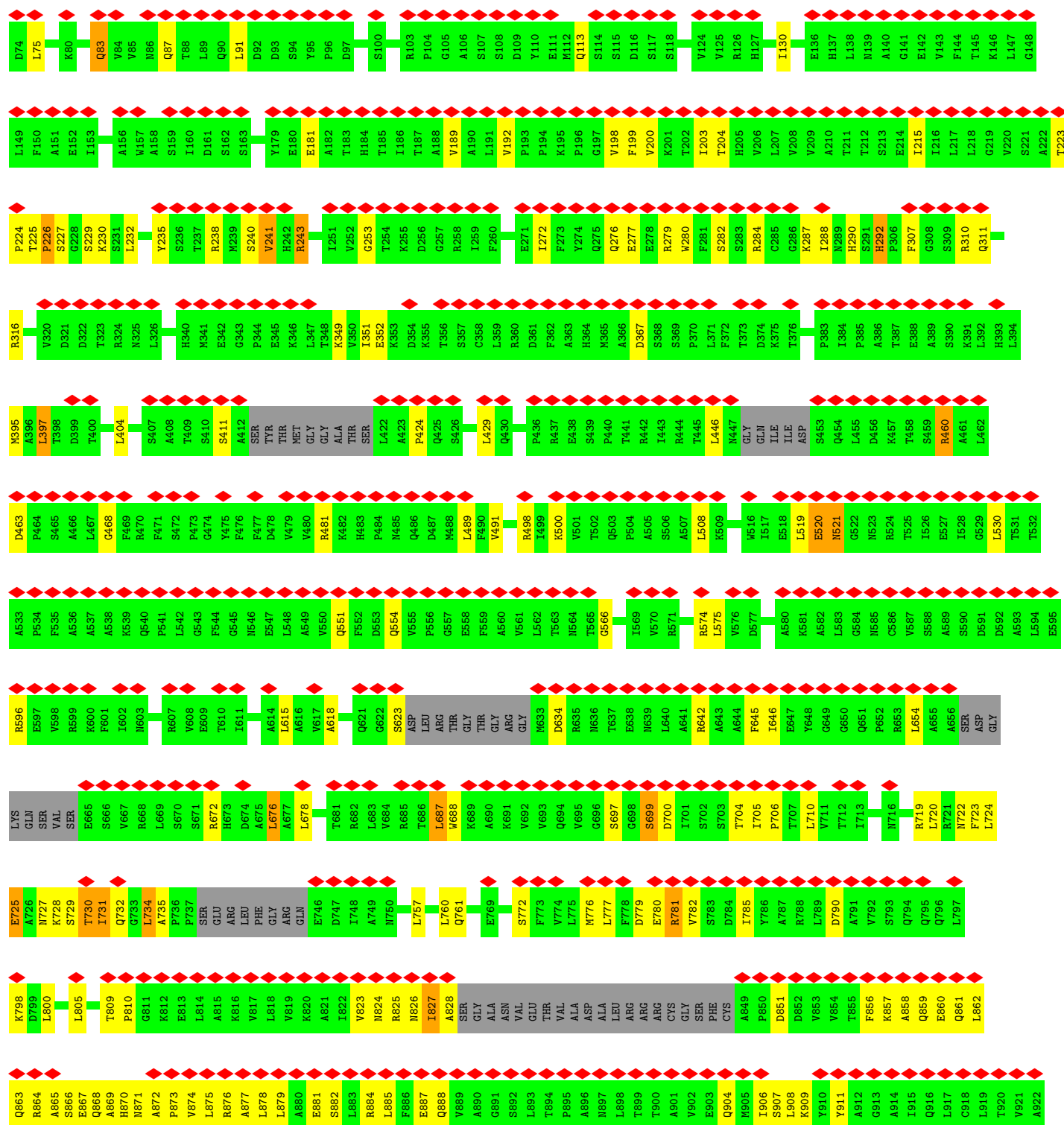
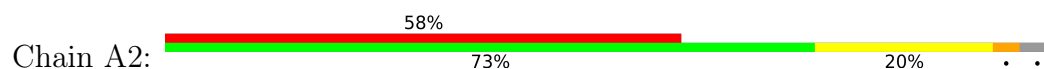


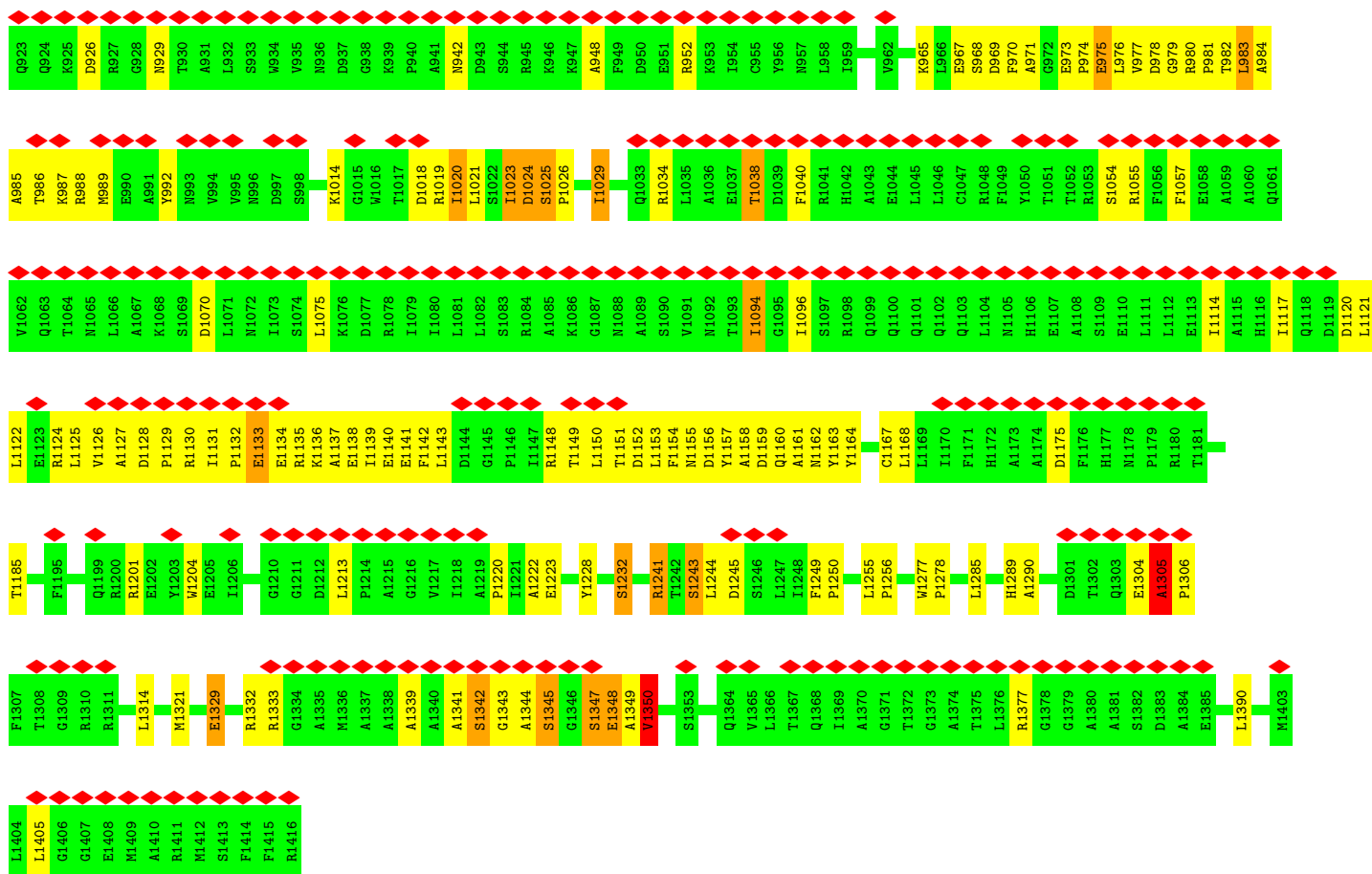
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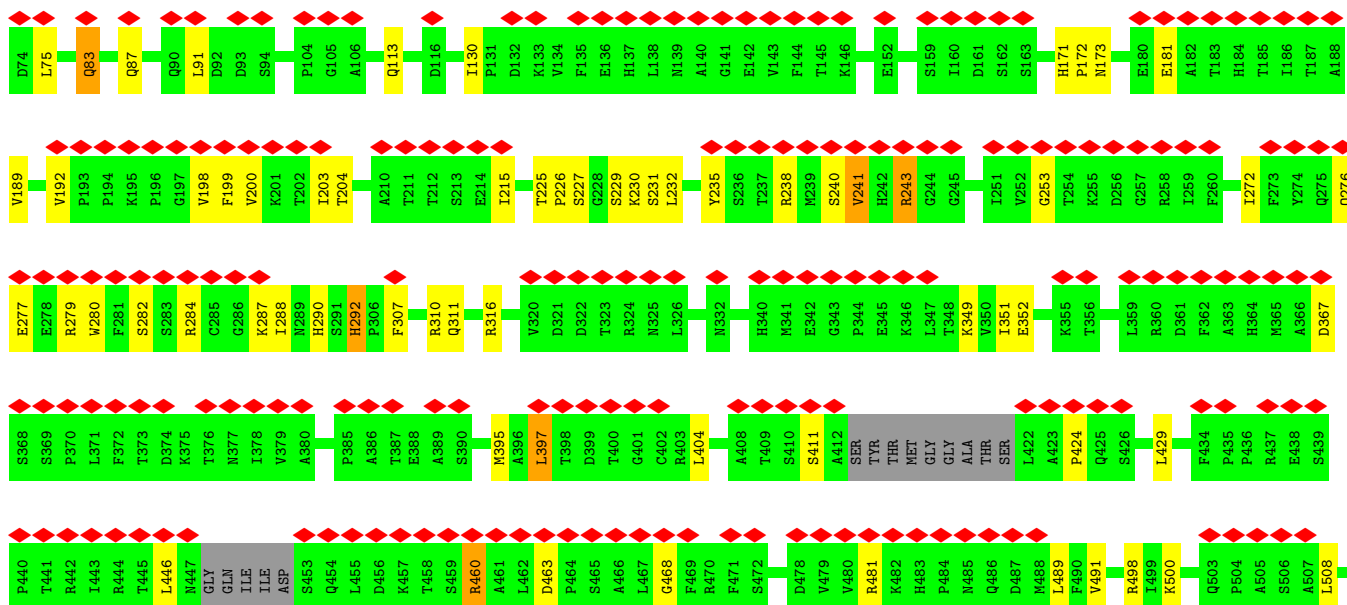
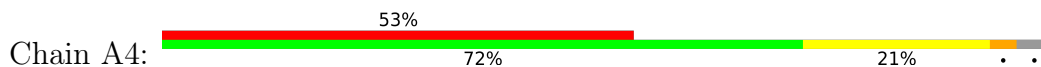


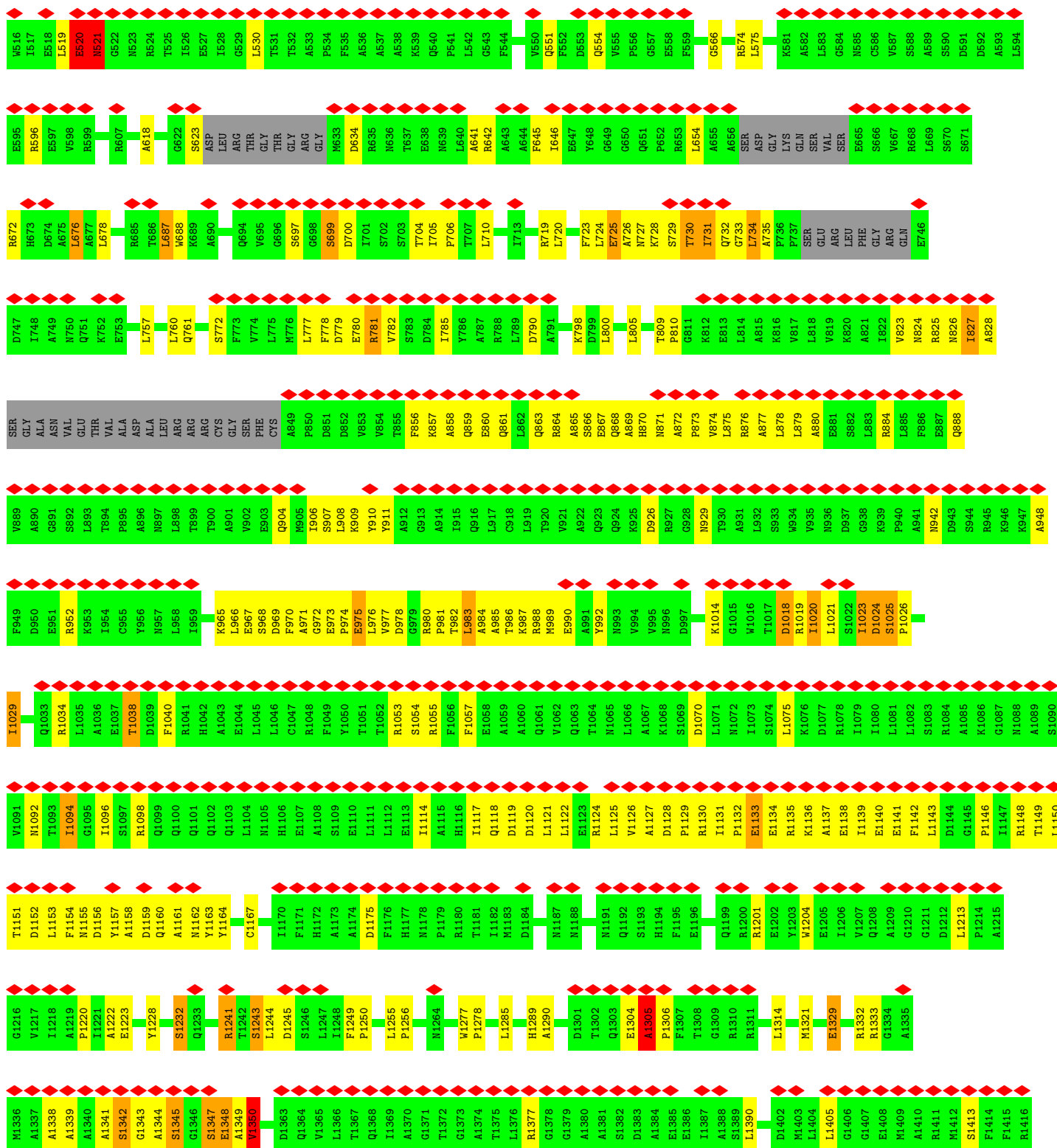
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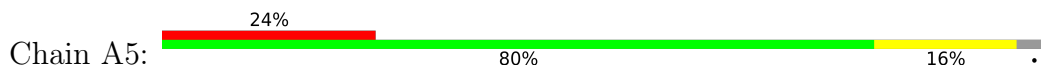


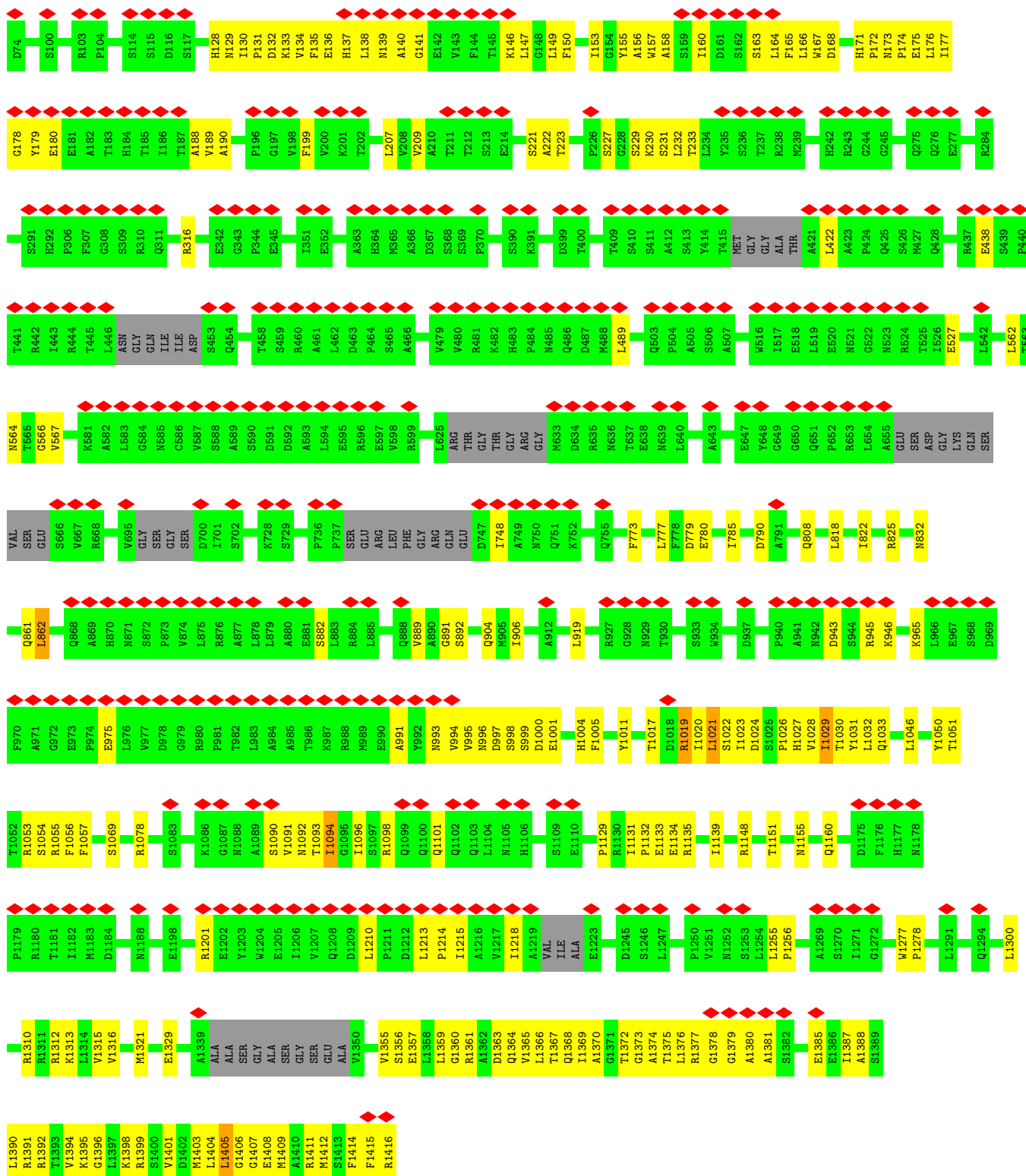
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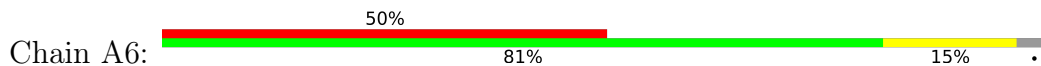


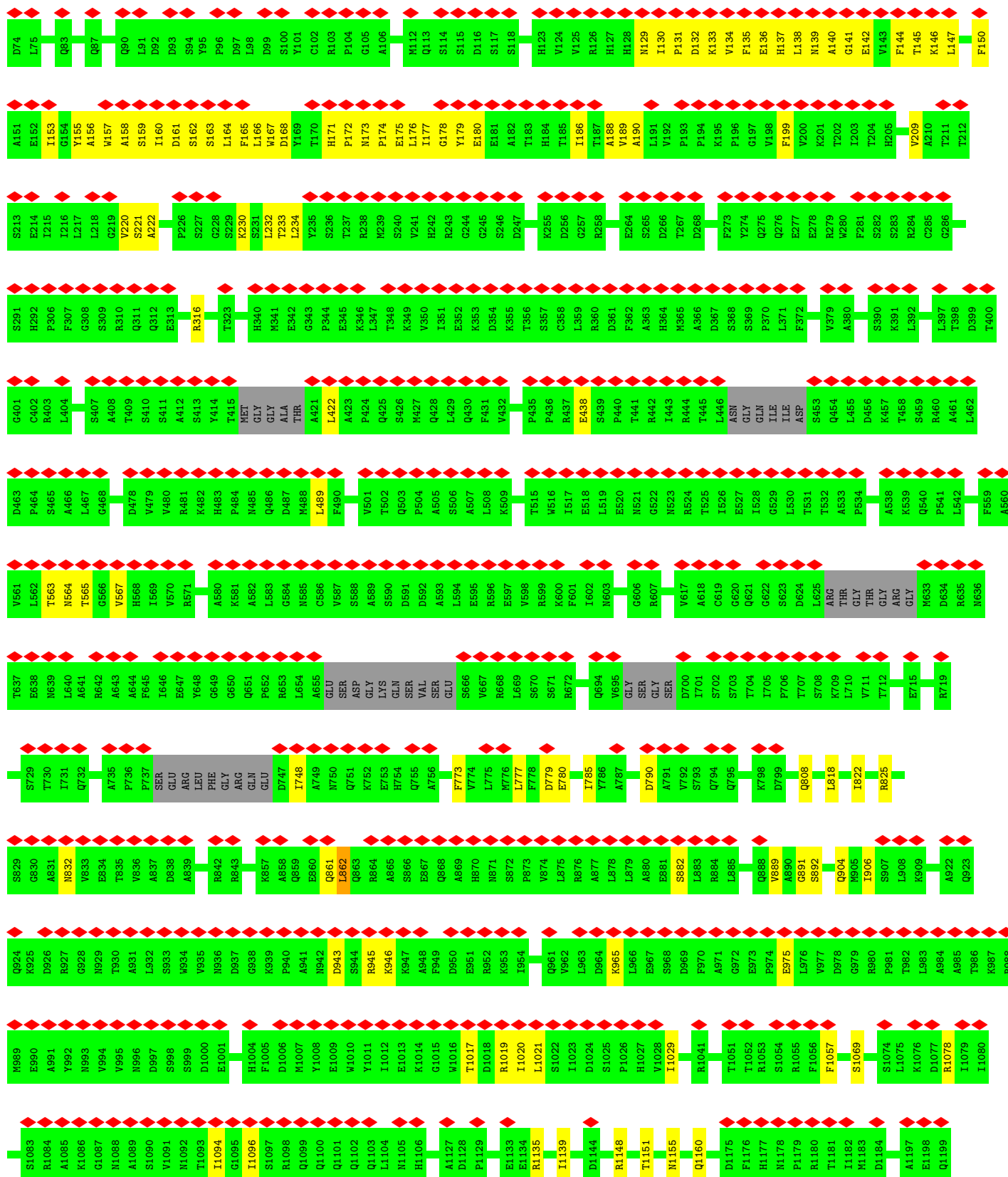
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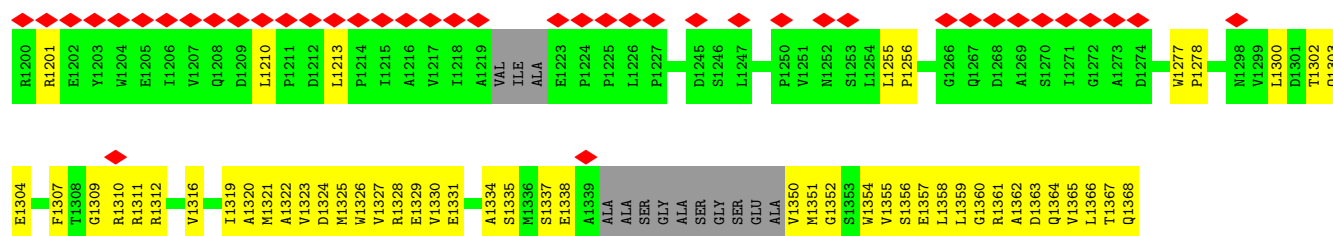




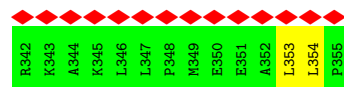
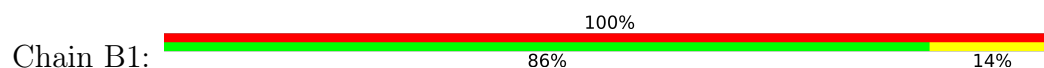
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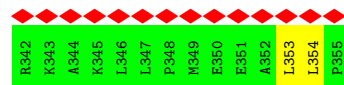
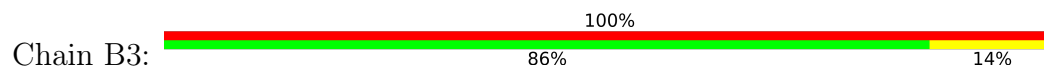
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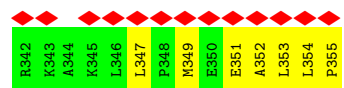
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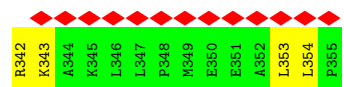
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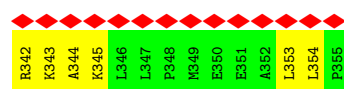
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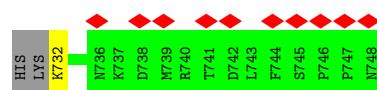
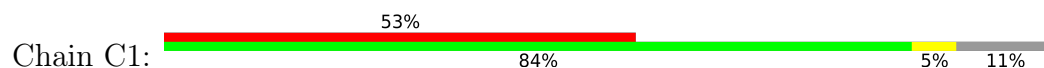
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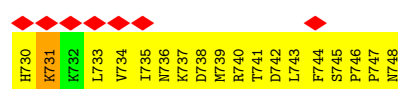
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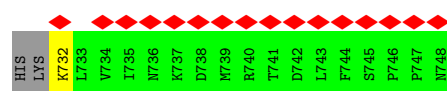
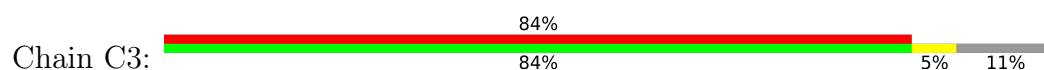
• Molecule 5: NUP98 R3



• Molecule 5: NUP98 R3



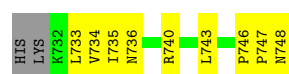
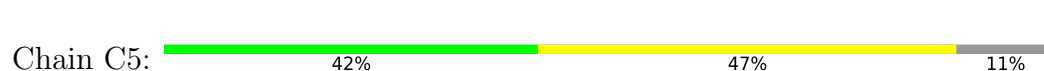
• Molecule 5: NUP98 R3



• Molecule 5: NUP98 R3



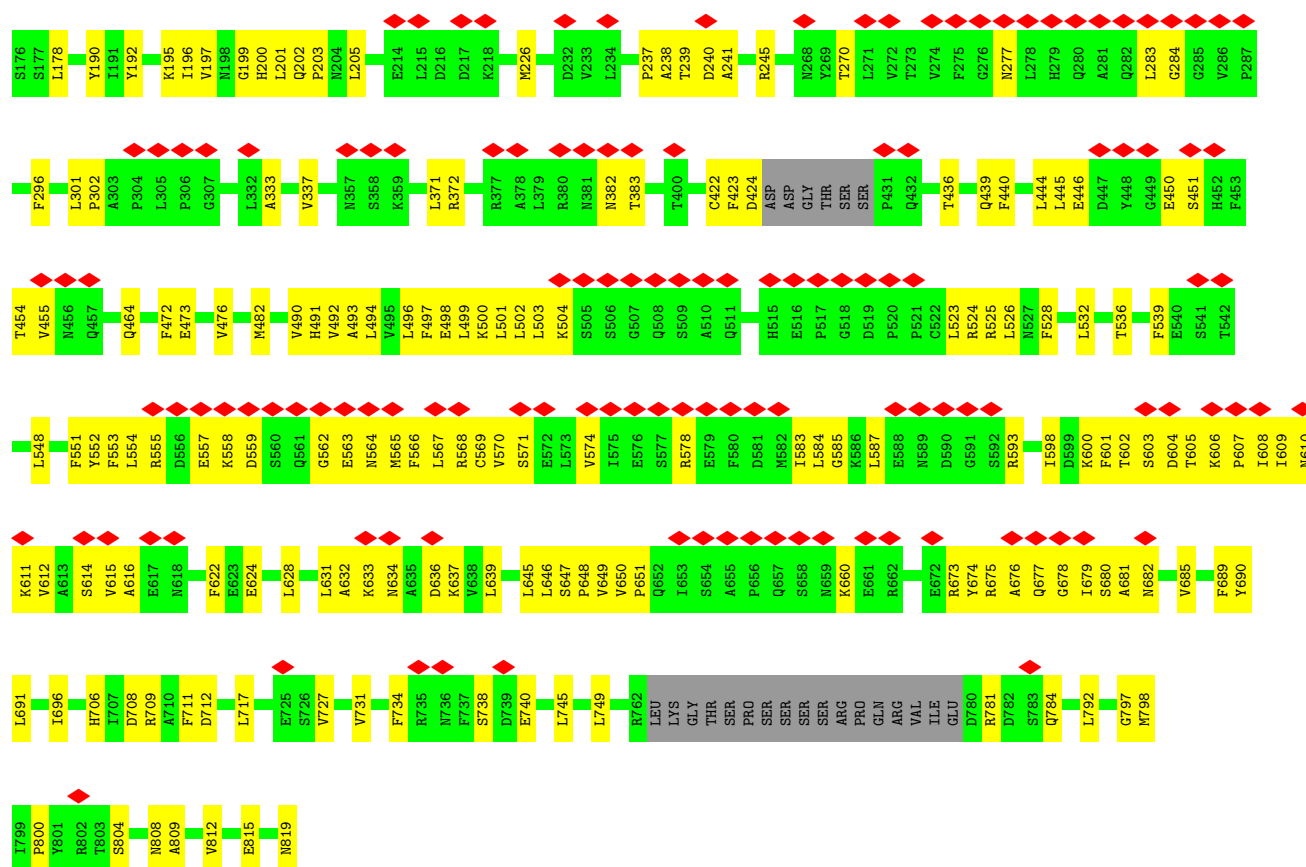
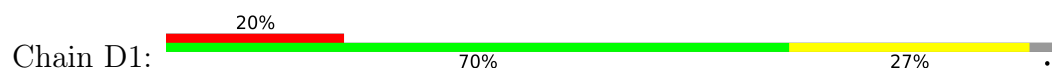
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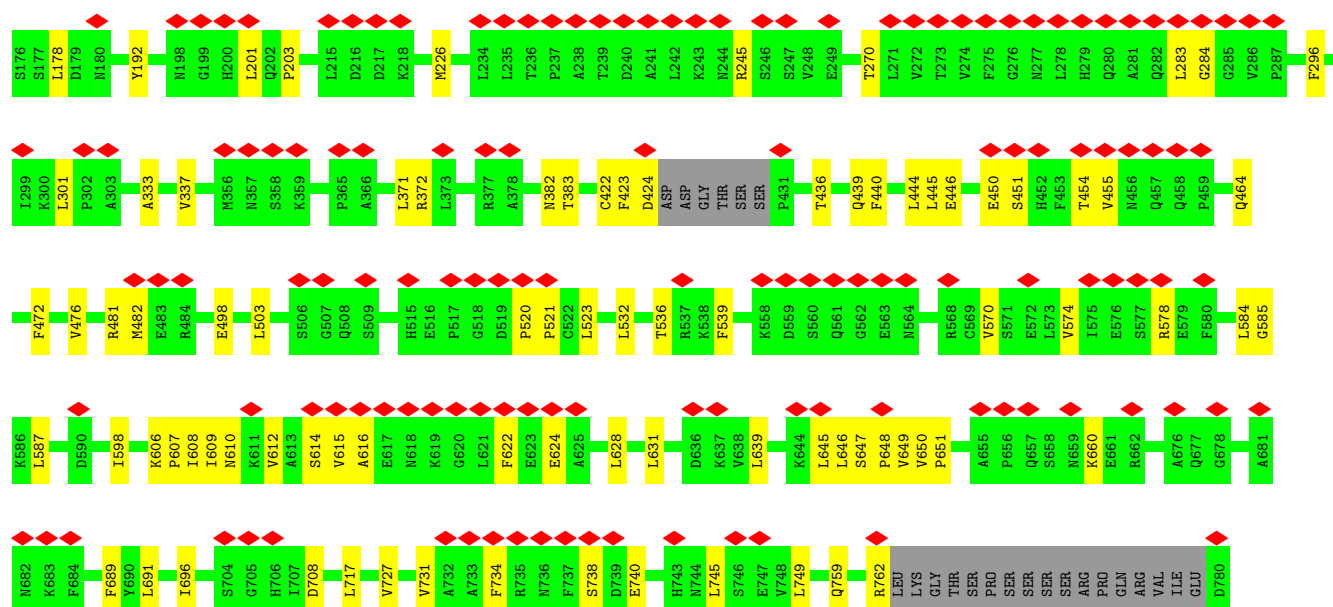
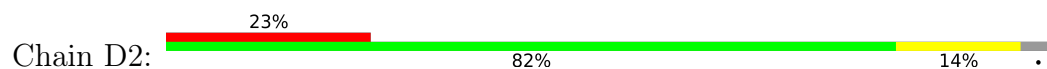
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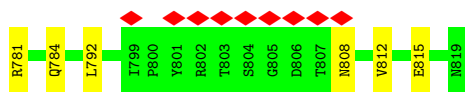


• Molecule 6: NUP93 SOL

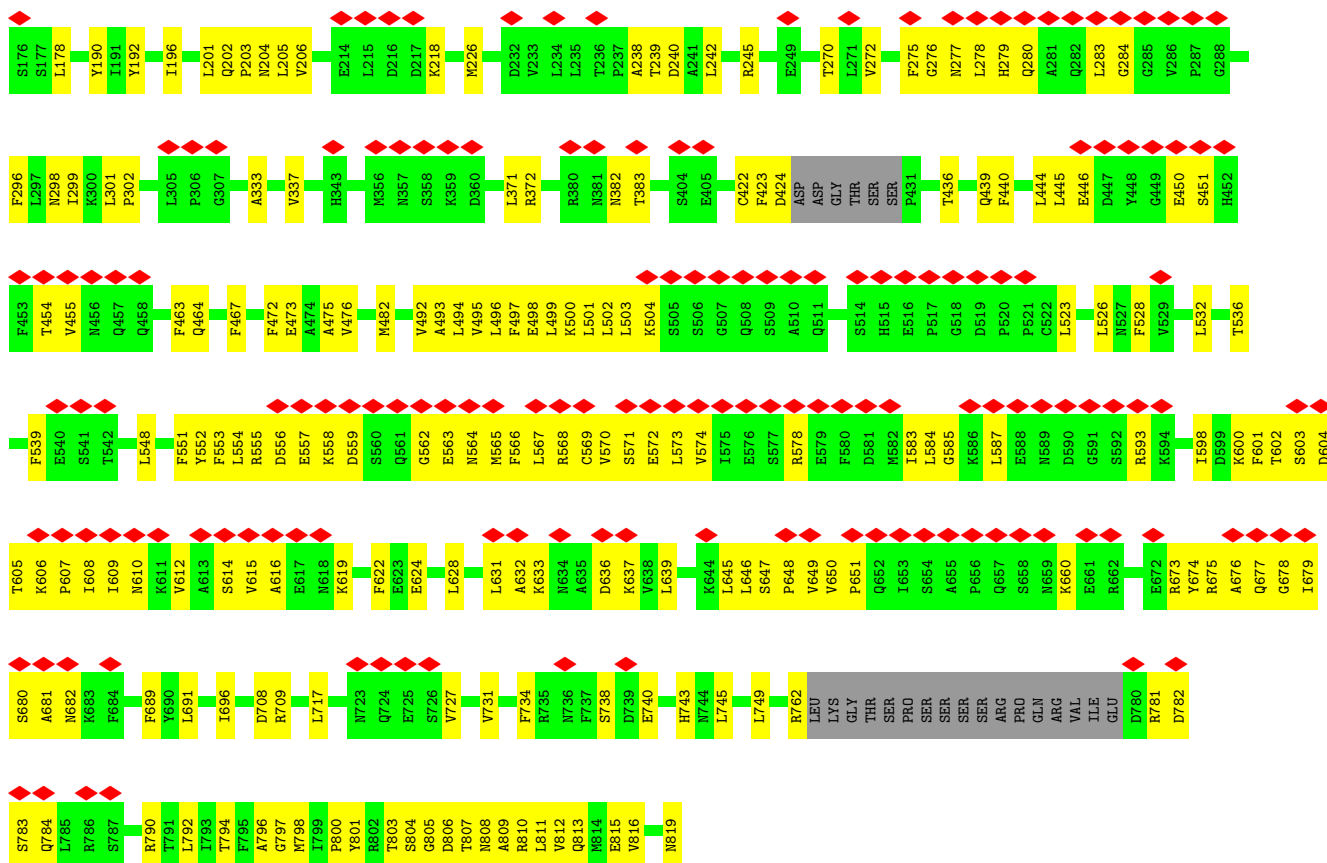


• Molecule 6: NUP93 SOL

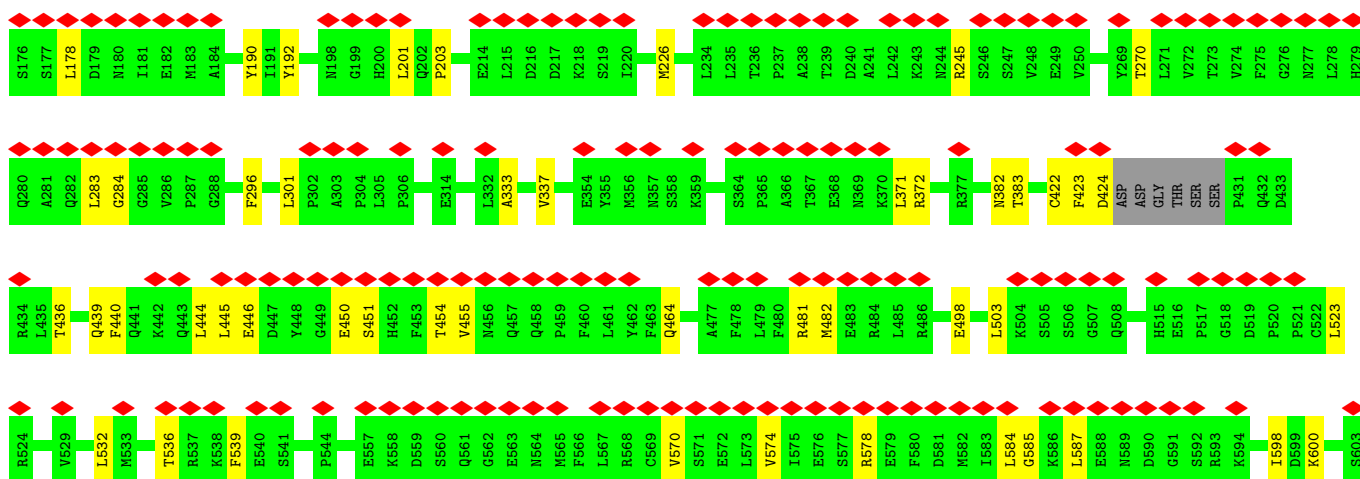
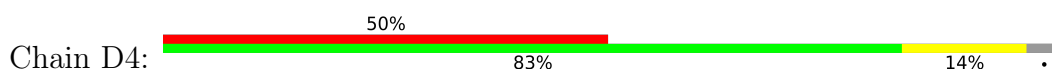


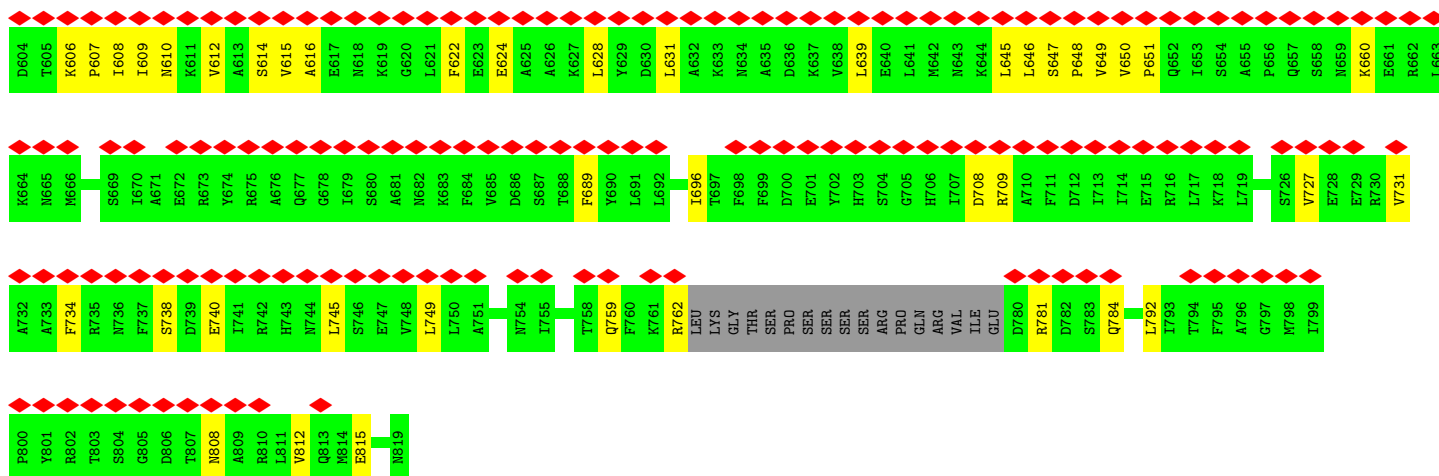


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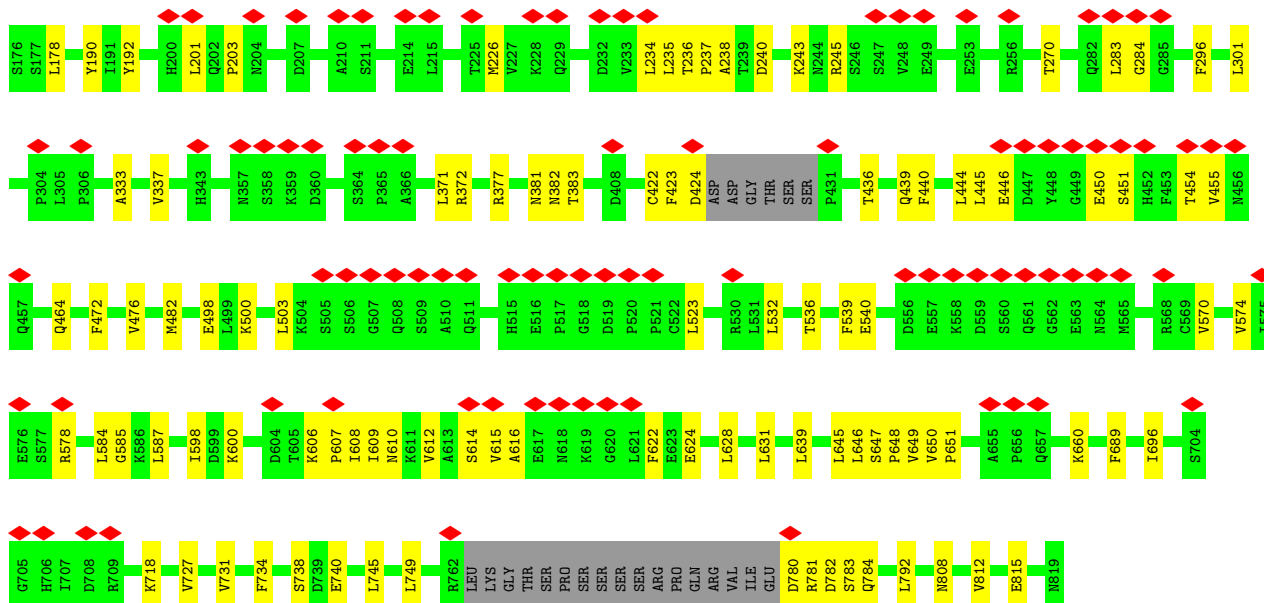
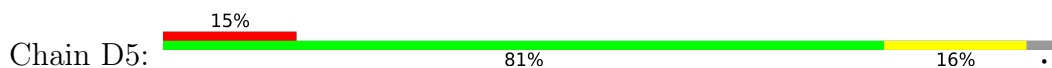


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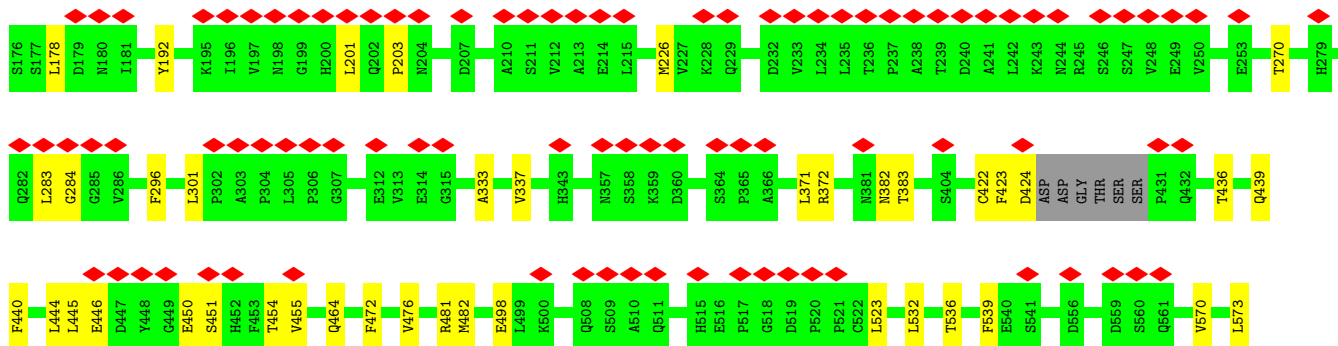
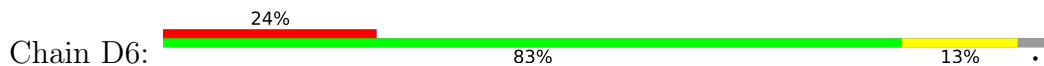


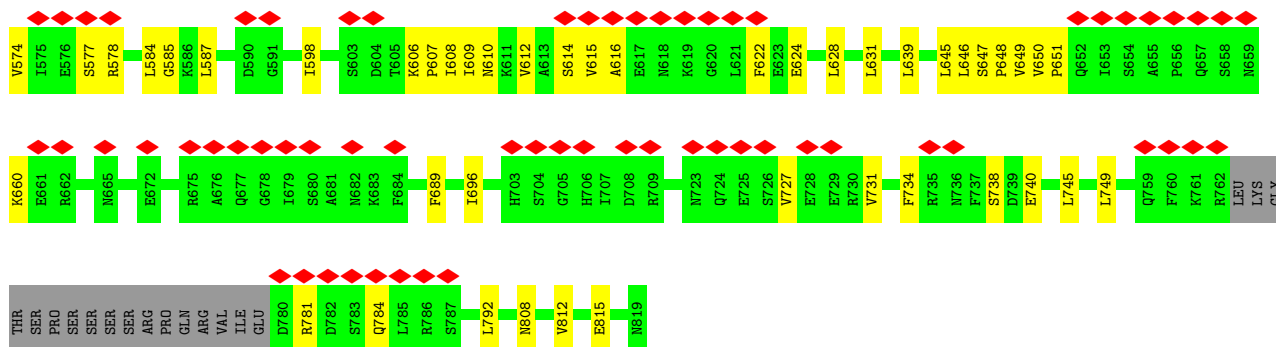


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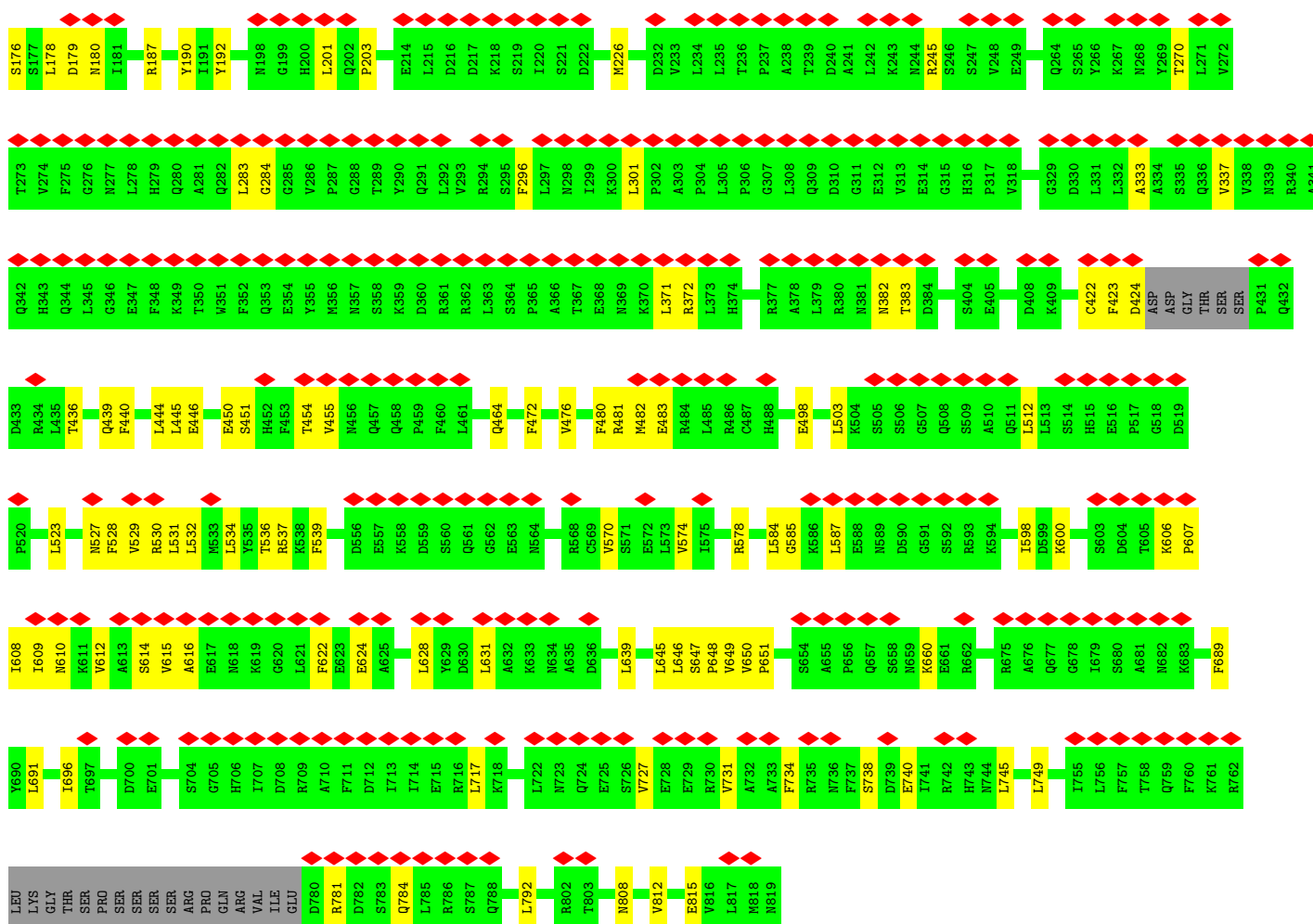


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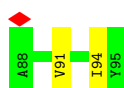
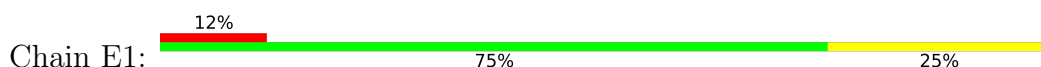




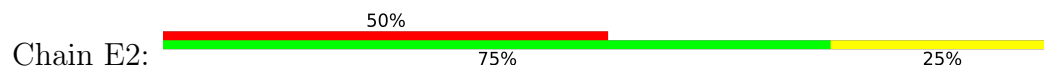
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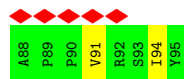
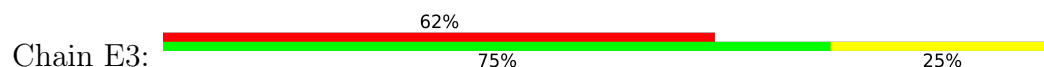
• Molecule 7: NUP53 R2



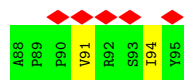
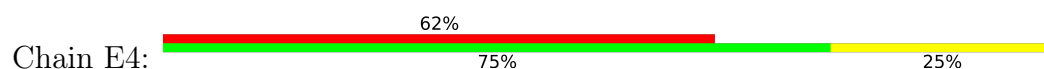
• Molecule 7: NUP53 R2



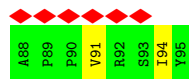
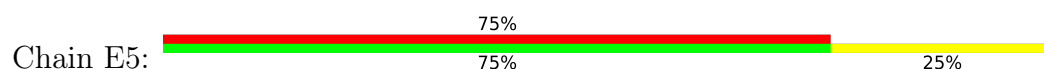
• Molecule 7: NUP53 R2



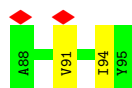
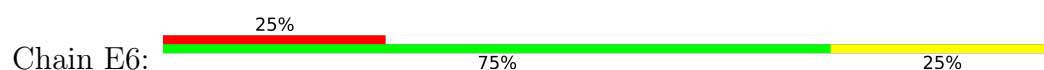
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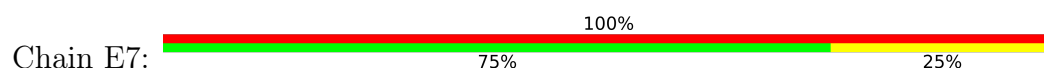
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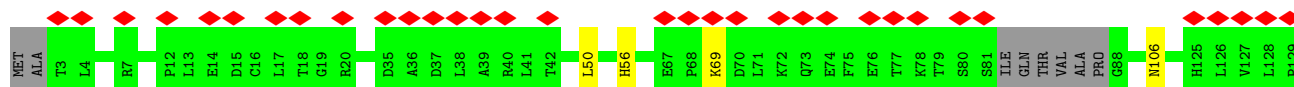
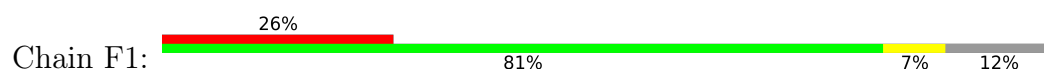
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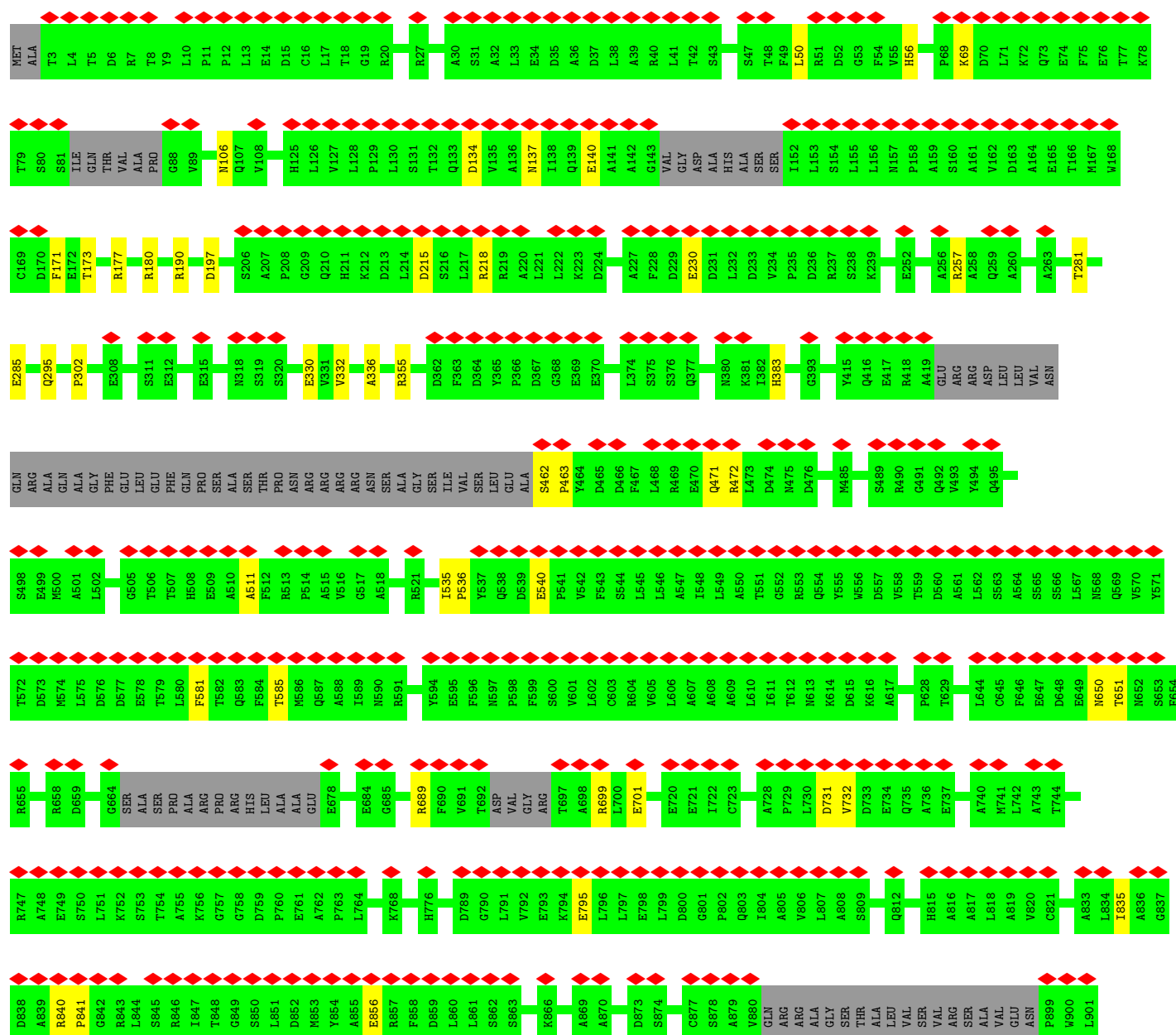
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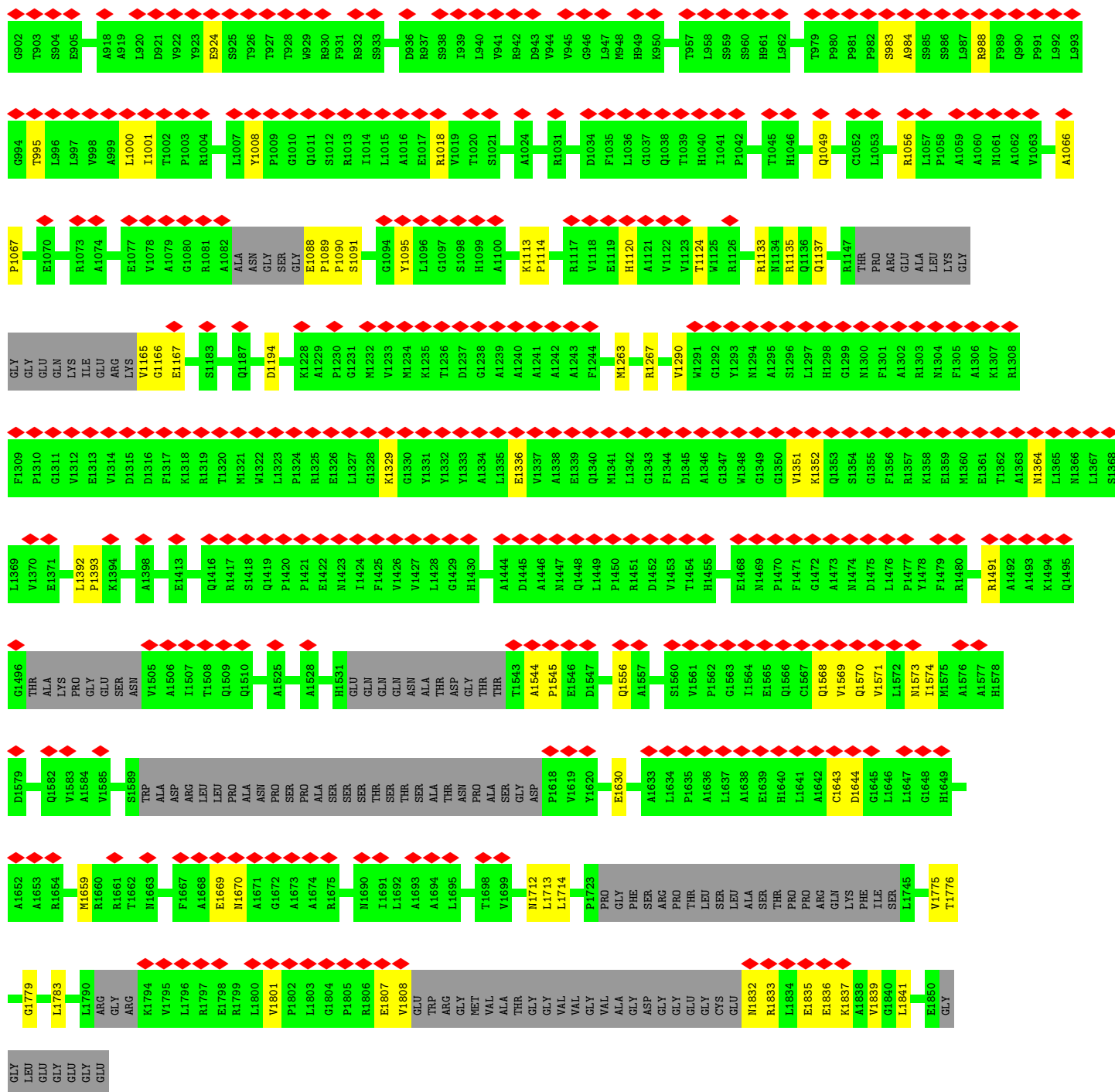


• Molecule 8: NUP188

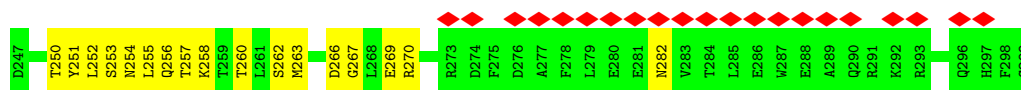
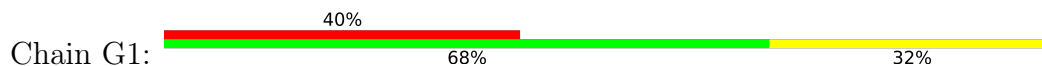


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GLY	GLU	GLN	LYS	ILE	GLU	ARG	LYS	V1165	A1166	E1167	Q1187	D1194	Y1202	W1203	P1204	W1205	R1211	E1215	M1232	V1233	M1234	K1235	T1236	D1237	G1238	A1239	A1240	A1241	A1242	A1243	F1244	M1258	Y1261	H1262	M1263	R1264	Q1265	M1266	R1267	V1290	N1294	A1295	L1296	L1297	H1298	G1299	N1300	F1301	A1302								
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A1363	N1364	L1365	N1366	L1367	S1368	L1369	L1392	P1393	K1394	E1422	N1423	V1426	D1445	A1446	N1447	R1451	F1471	G1472	A1473	N1474	D1475	L1476	P1477	R1491	K1494	Q1495	G1496	THR	ALA	LYS	PRO	GLY	GLU	SER	SER	ASN	THR	V1505	A1506	I1507	H1531	GLU	GLN	GLN	GLN	ASN	ALA	GLY	ASP	P1618	E1630						
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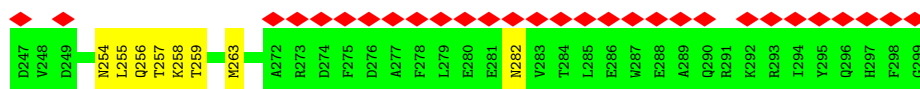
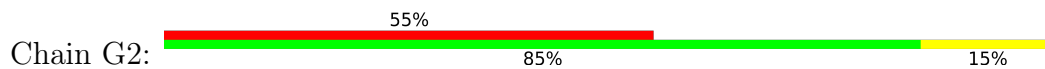




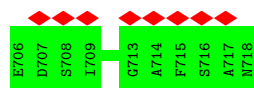
- Molecule 9: NUP93 R2



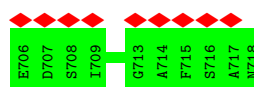
- Molecule 9: NUP93 R2



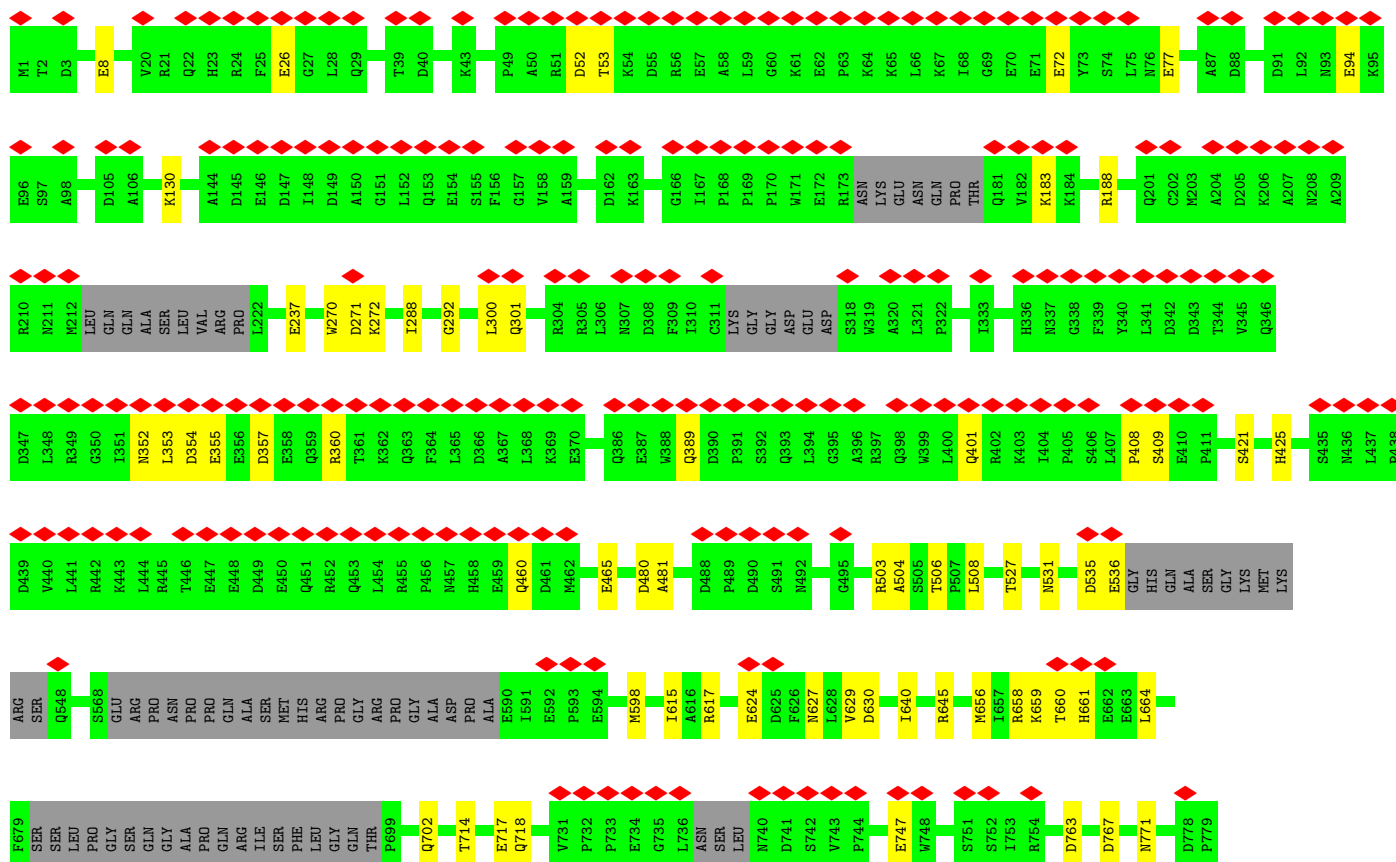
• Molecule 10: NUP98 R2

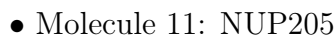


• Molecule 10: NUP98 R2



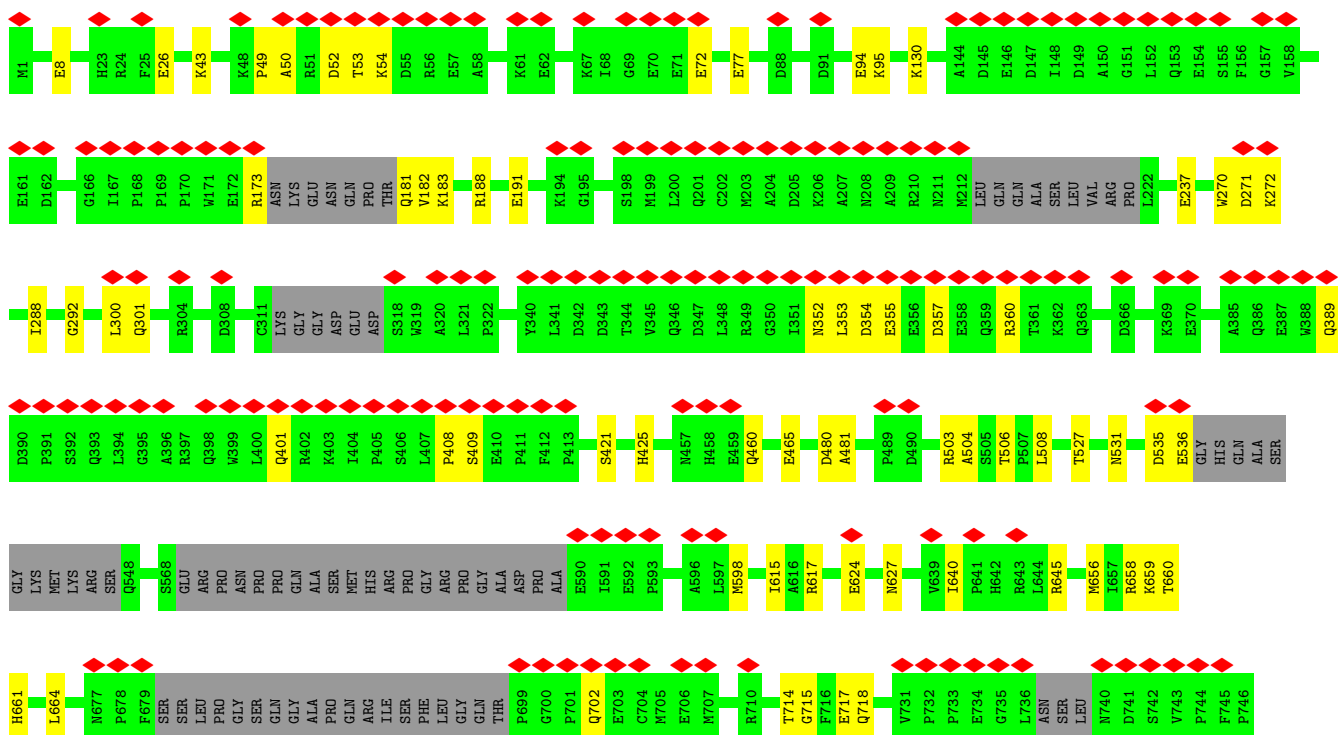
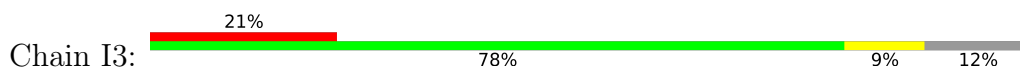
• Molecule 11: NUP205

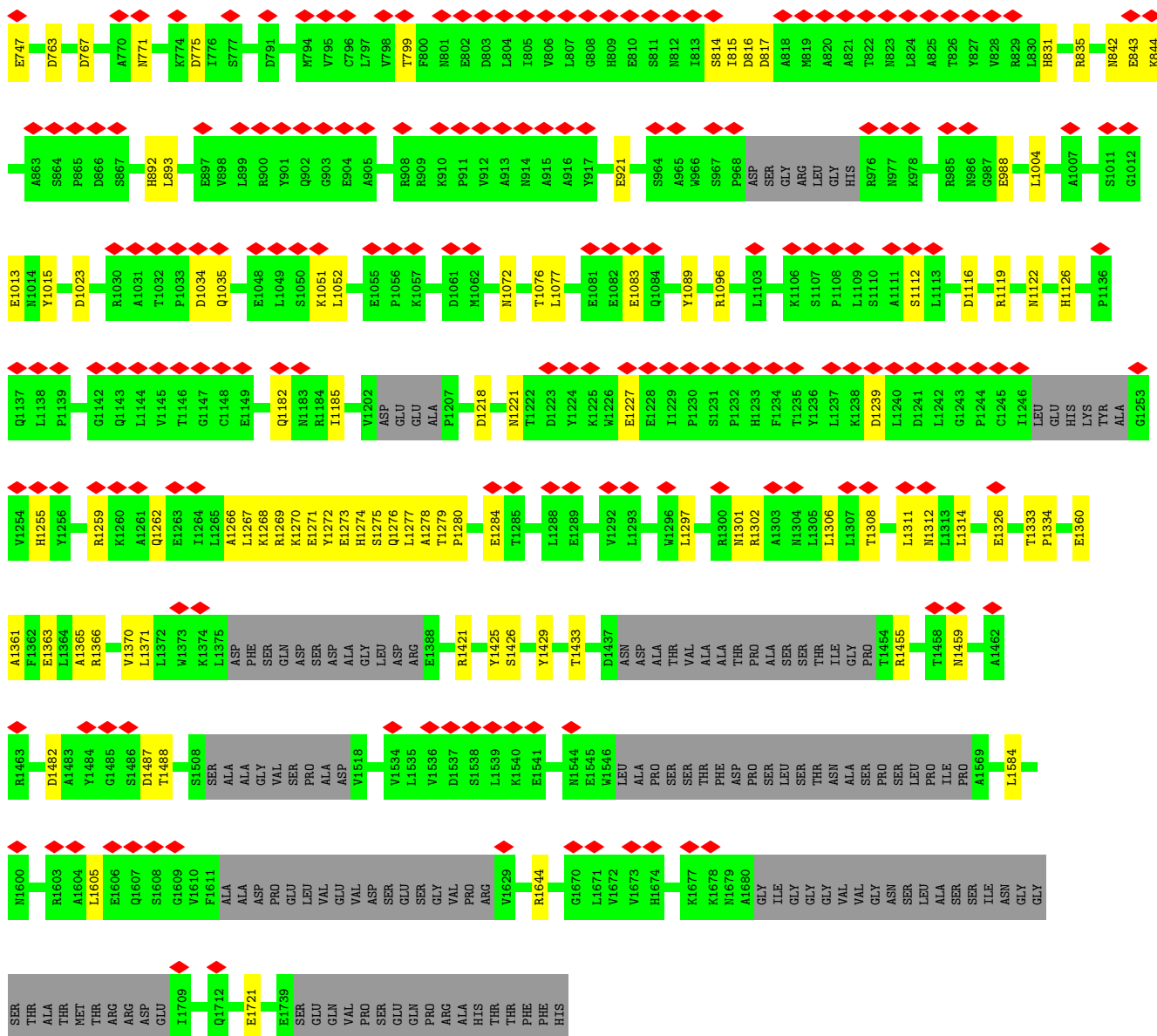




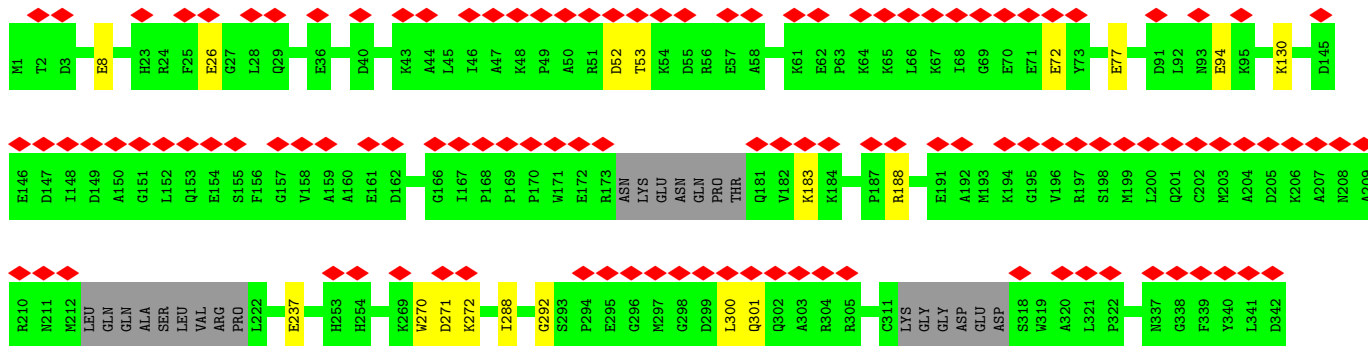
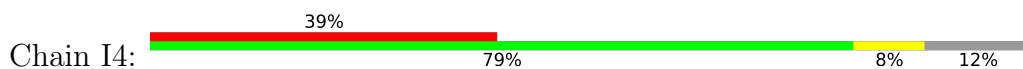


- Molecule 11: NUP205





• Molecule 11: NUP205

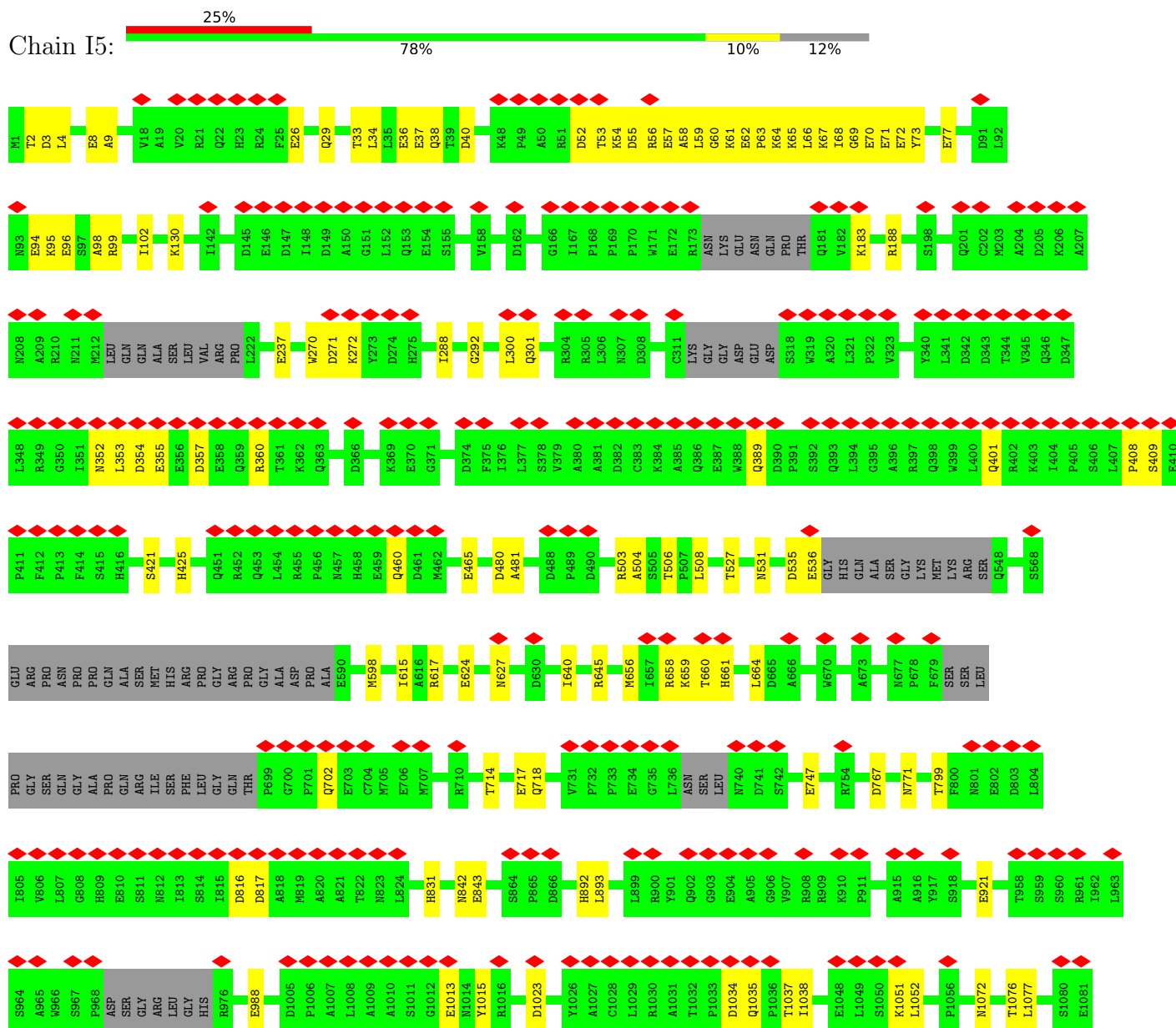


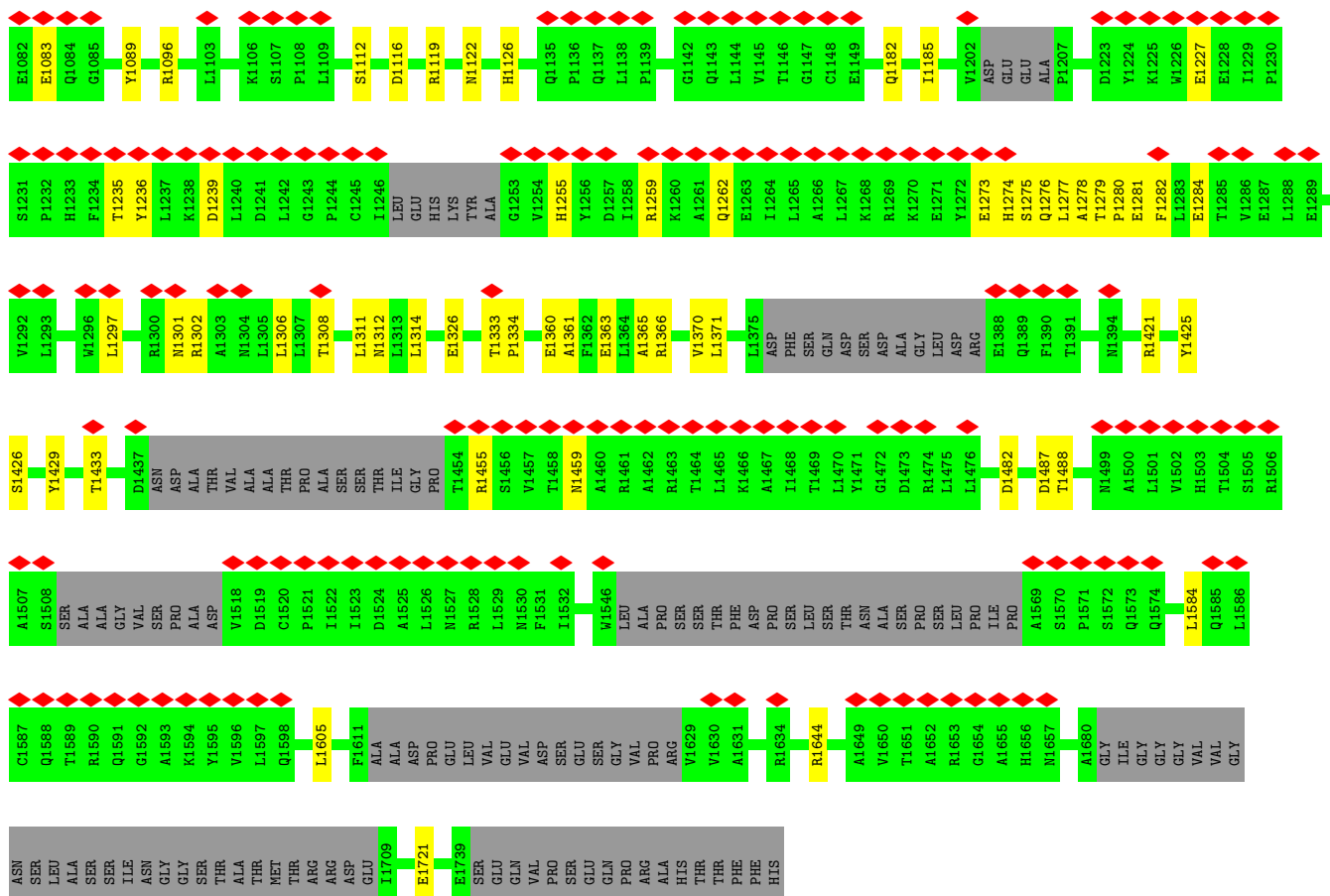
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P413	F414	S421	H425	S435	M436	L437	P438	D439	V440	L441	R442	L443	L444	R445	T446	E447	E448	D449	E450	Q451	R452	Q453	L454	R455	P456	M457	H458	E459	Q460	D461	M462	E465	P479	D480	A481	A482	M483	E487	D488	P489	D490	S491	M492	G495	Q498	R503	A504	T506	P507							
L508	D521	N522	E523	E524	T527	N531	D535	E536	GLY	HIS	GLN	ALA	SER	GLY	LYS	MET	LYS	ARG	Q548	V566	C567	S568	GLU	ARG	PRO	ASN	PRO	GLN	ALA	SER	MET	HIS	ARG	PRO	GLY	ARG	E590	I591	E592	P593	E594	S595	A596	L597	M598	L599										
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LEU	GLY	GLN	THR	P699	Q700	P701	Q702	E703	C704	M705	E706	M707	M708	F709	E710	L711	F712	G713	T714	E717	Q718	T727	T728	L729	L730	V731	P732	P733	E734	G735	L736	ASN	SER	LEU	N740	D741	S742	V743	P744	F745	P746	E747	W748	L749	G750	S751	S752	I753	R754	T755	L756	G757	I758	E759	P760	V762
D763	D767	A770	N771	R772	T773	K774	D775	I776	S777	D778	P779	S780	Q781	D791	M794	V795	C796	L797	V798	T799	F800	N801	E802	D803	L804	I805	V806	L807	G808	H809	N812	I813	S814	T815	D816	D817	A818	M819	A820	A821	T822	N823	L824	A825	T826	R827	V828	R829	L830	H831	N842	E843	K844			
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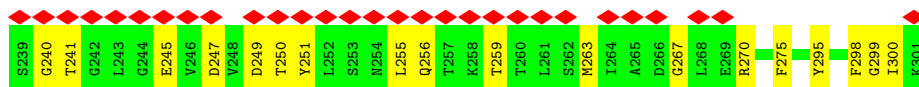
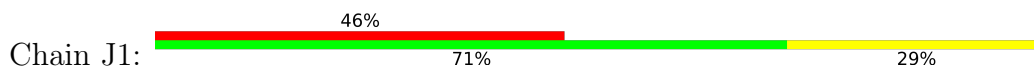
● Molecule 11: NUP205

Chain I5:

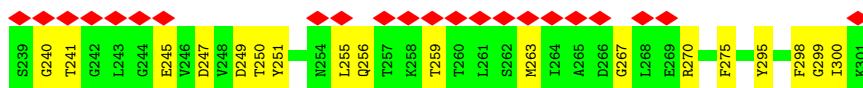




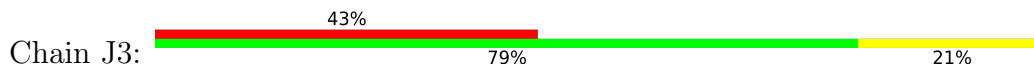
- Molecule 12: NUP93 R2



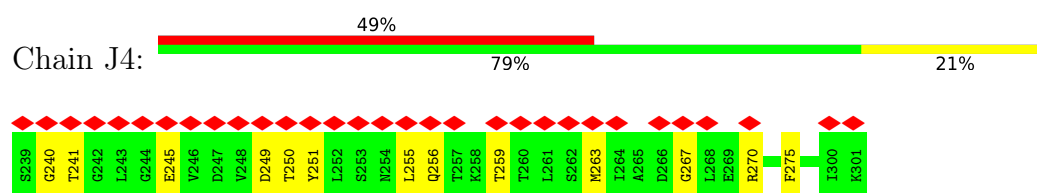
- Molecule 12: NUP93 R2



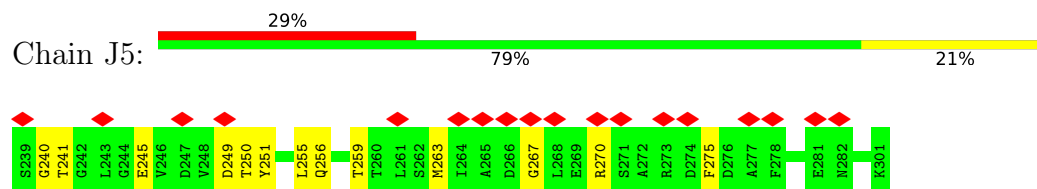
- Molecule 12: NUP93 R2



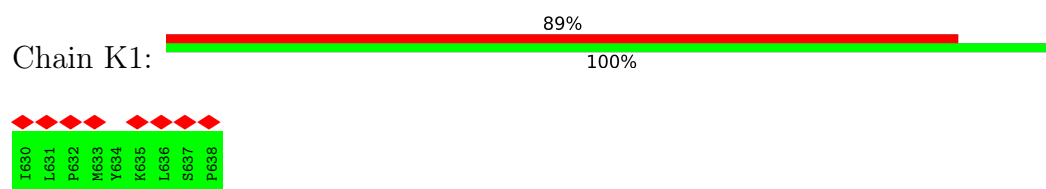
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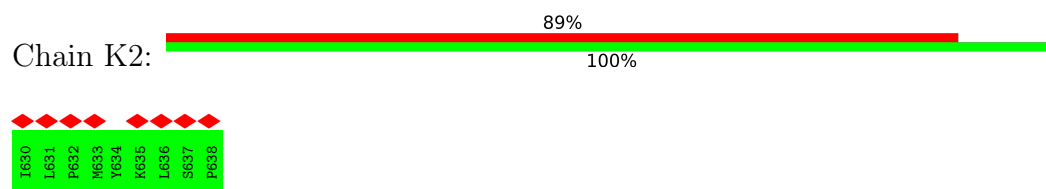
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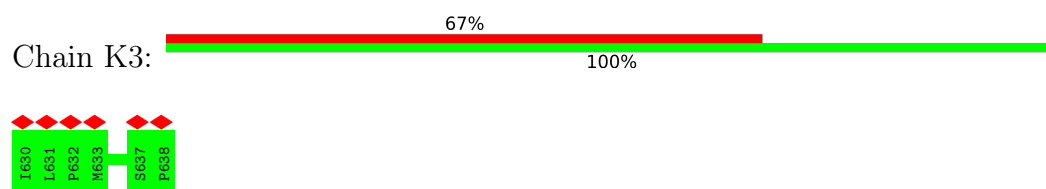
- Molecule 13: NUP98 R1



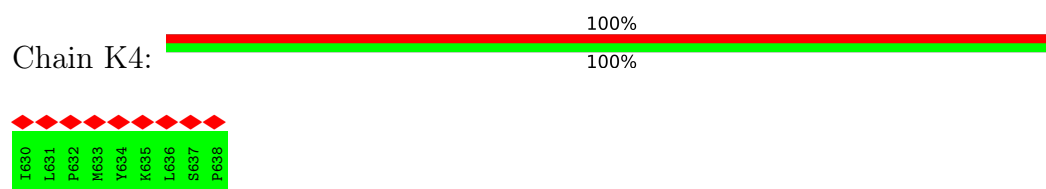
- Molecule 13: NUP98 R1



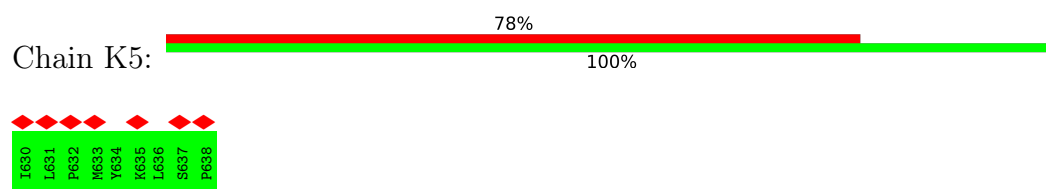
- Molecule 13: NUP98 R1



- Molecule 13: NUP98 R1



- Molecule 13: NUP98 R1

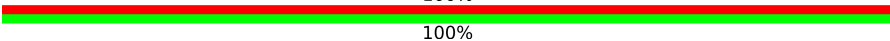


● Molecule 14: NUP53 R1

Chain L1:  100%
100%

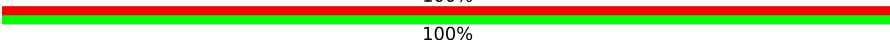


● Molecule 14: NUP53 R1

Chain L2:  100%
100%

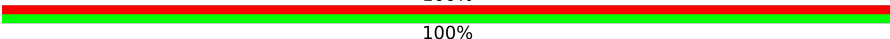


● Molecule 14: NUP53 R1

Chain L3:  100%
100%



● Molecule 14: NUP53 R1

Chain L4:  100%
100%



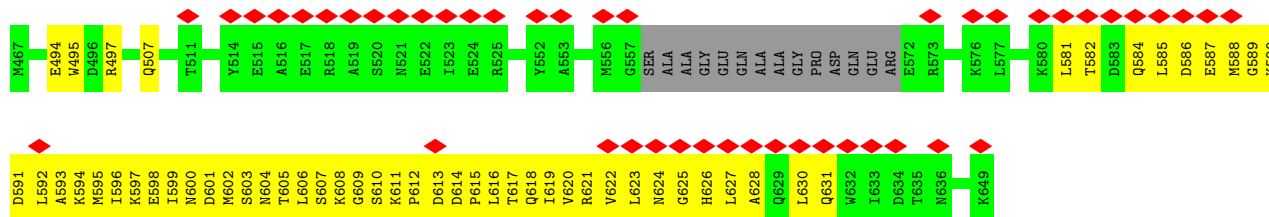
● Molecule 14: NUP53 R1

Chain L5:  50%
100%



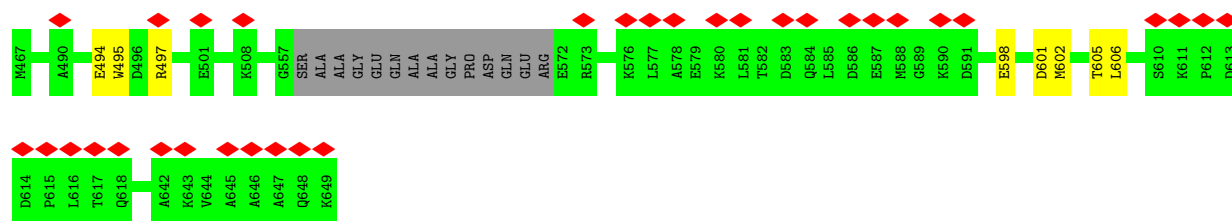
● Molecule 15: NUP62

Chain M1:  25%
63% 29% 8%

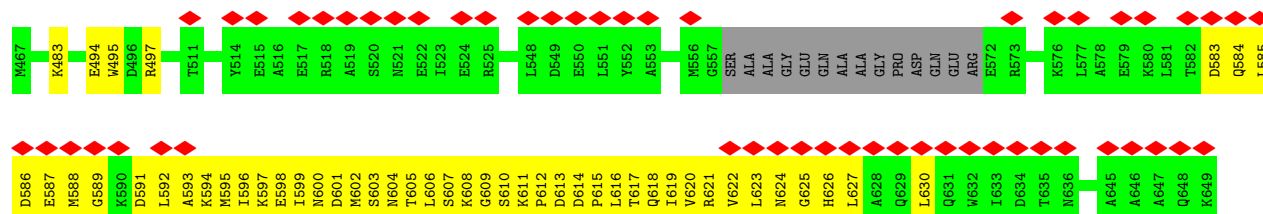


● Molecule 15: NUP62

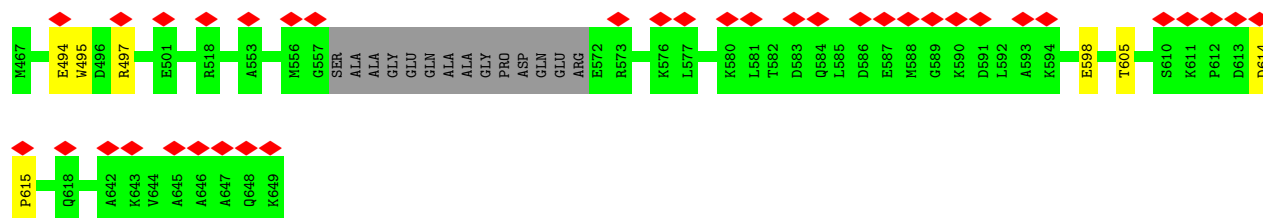
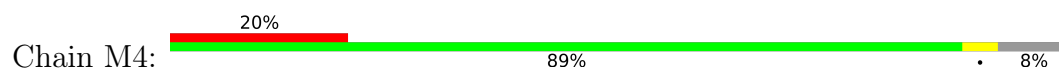
Chain M2:  18%
88% 8%



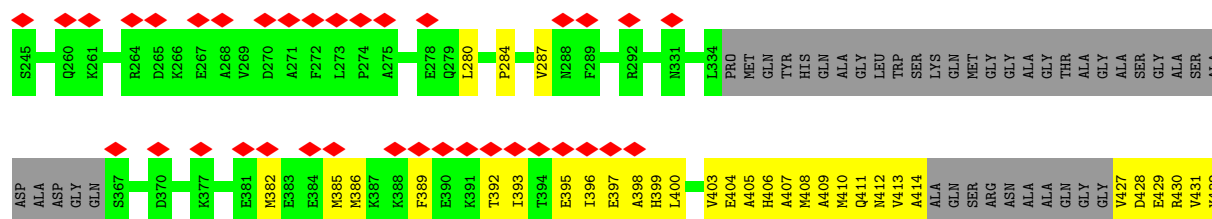
• Molecule 15: NUP62



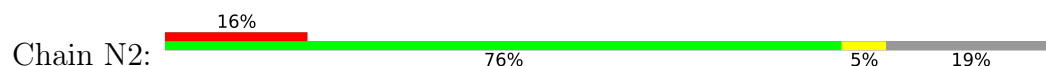
• Molecule 15: NUP62

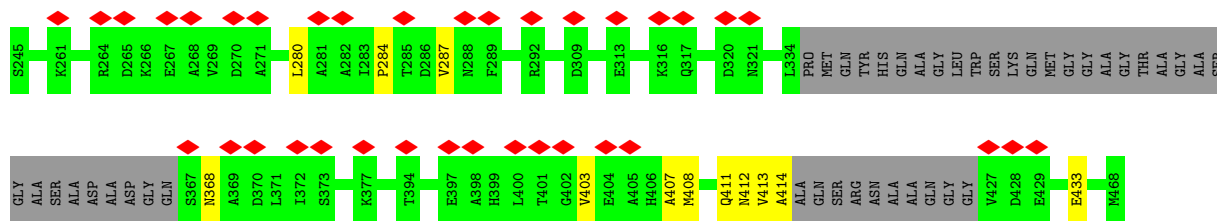


• Molecule 16: NUP58

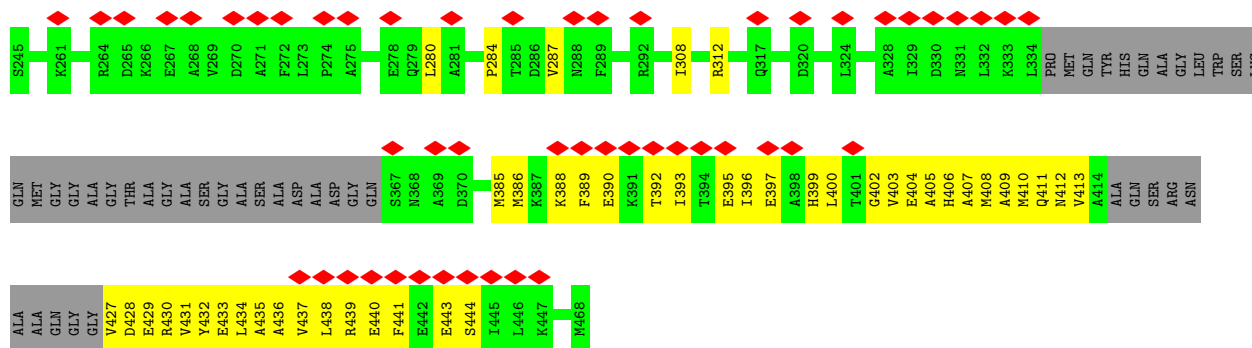


• Molecule 16: NUP58

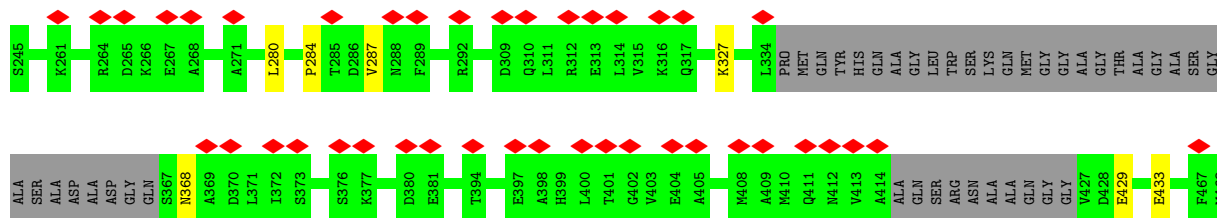
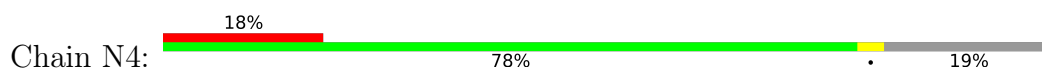




- Molecule 16: NUP58



- Molecule 16: NUP58



- Molecule 17: NUP54



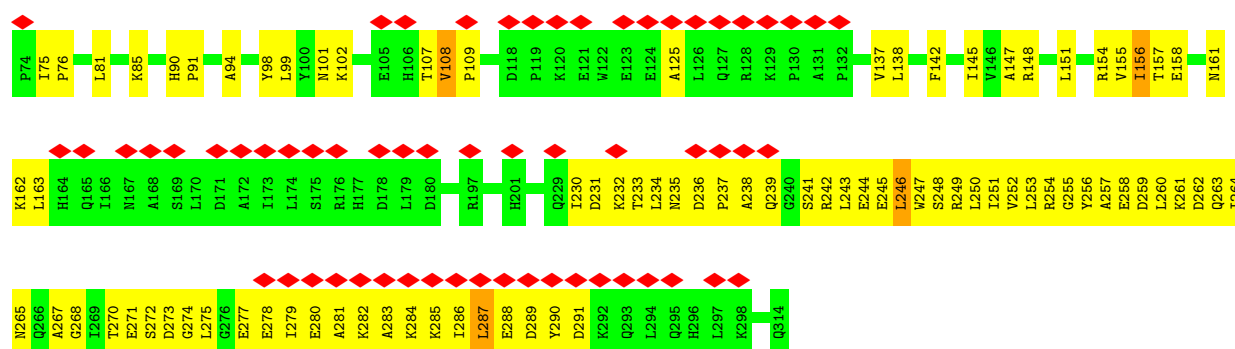
- Molecule 17: NUP54

Chain O2: 



• Molecule 17: NUP54

Chain O3: 

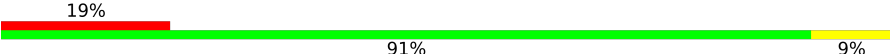


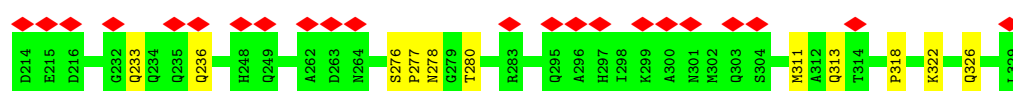
• Molecule 17: NUP54

Chain O4: 

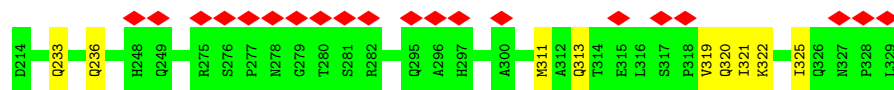


• Molecule 18: NUP54 Ferredoxin-like domain

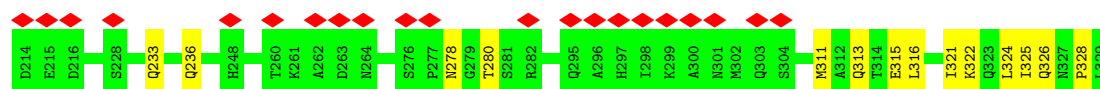
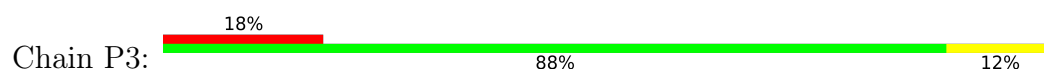
Chain P1: 



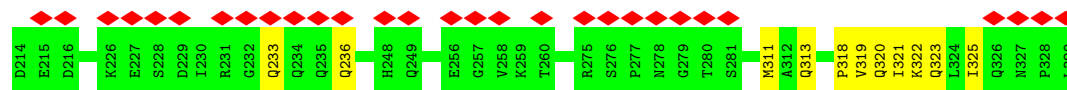
- Molecule 18: NUP54 Ferredoxin-like domain



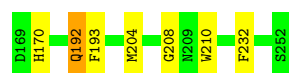
- Molecule 18: NUP54 Ferredoxin-like domain



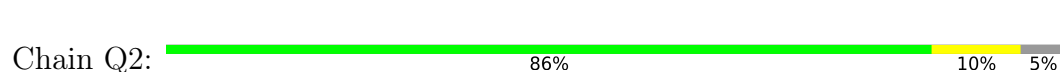
- Molecule 18: NUP54 Ferredoxin-like domain



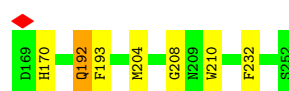
- Molecule 19: NUP53 RRM



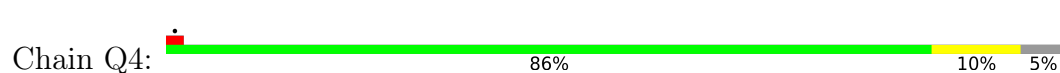
- Molecule 19: NUP53 RRM



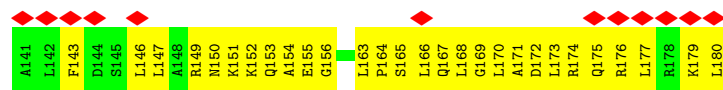
- Molecule 19: NUP53 RRM



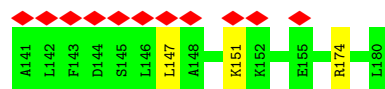
- Molecule 19: NUP53 RRM



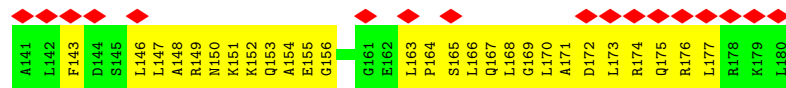
- Molecule 20: NUP93 R1



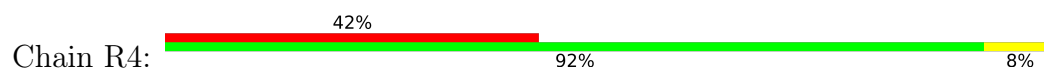
- Molecule 20: NUP93 R1



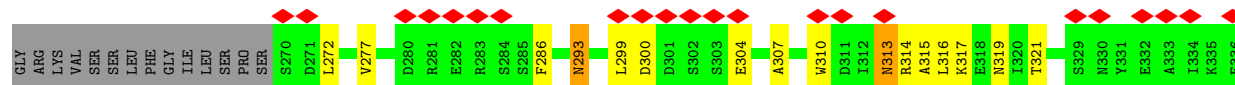
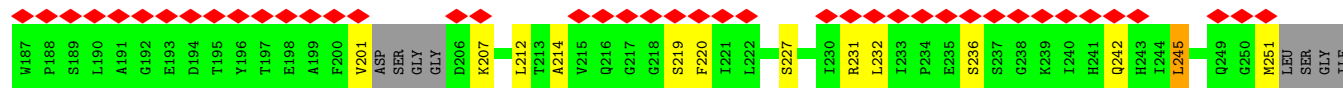
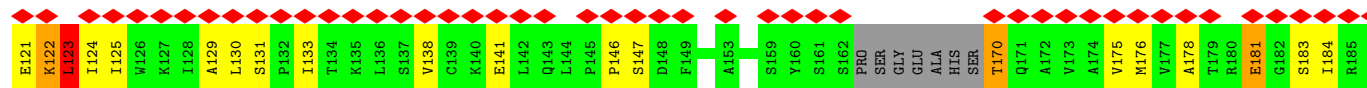
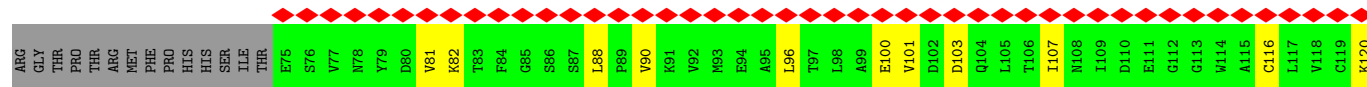
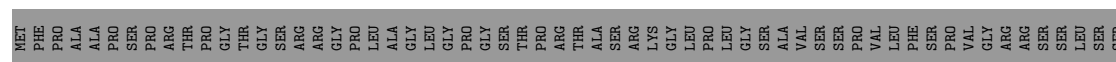
- Molecule 20: NUP93 R1

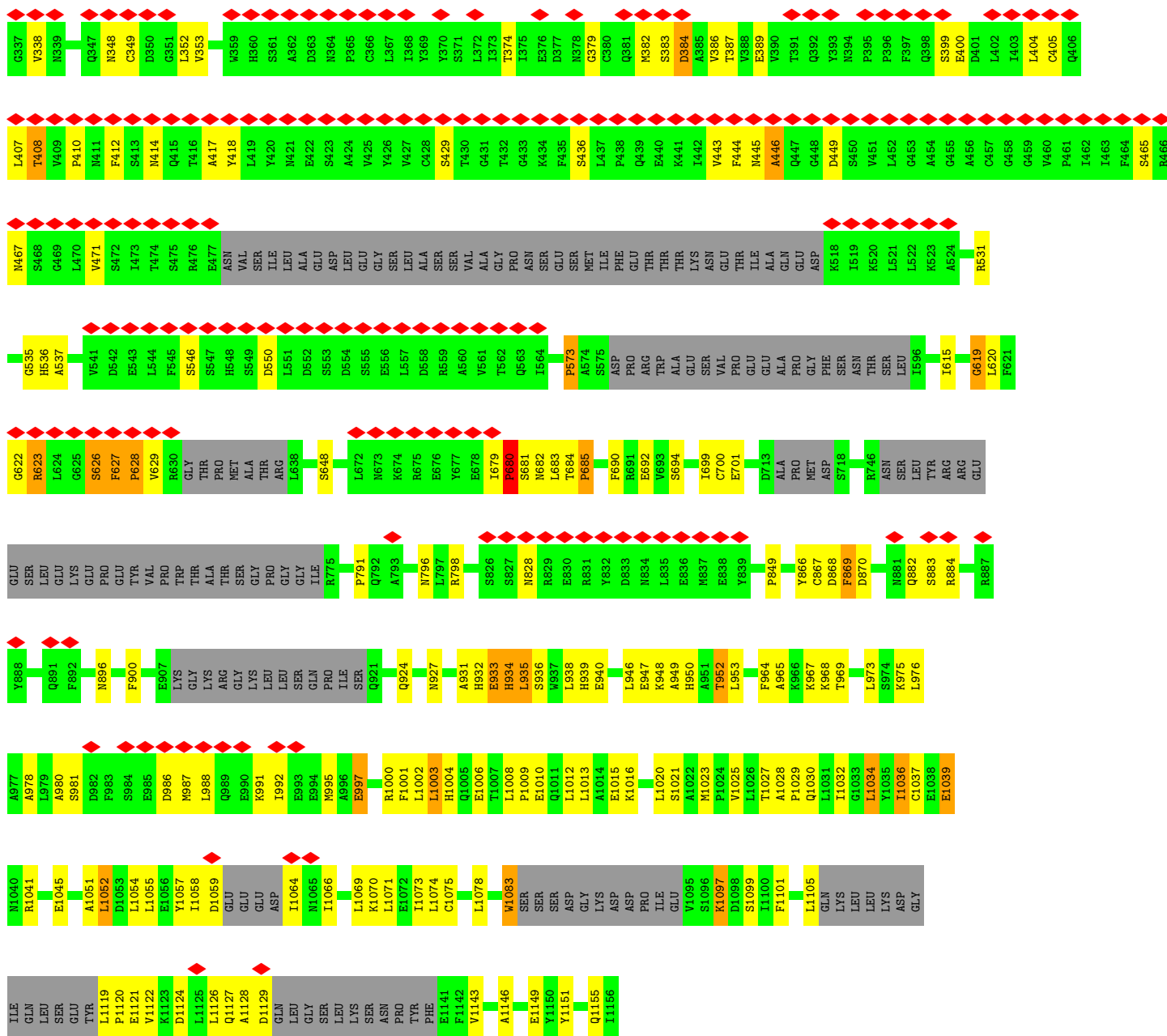


- Molecule 20: NUP93 R1

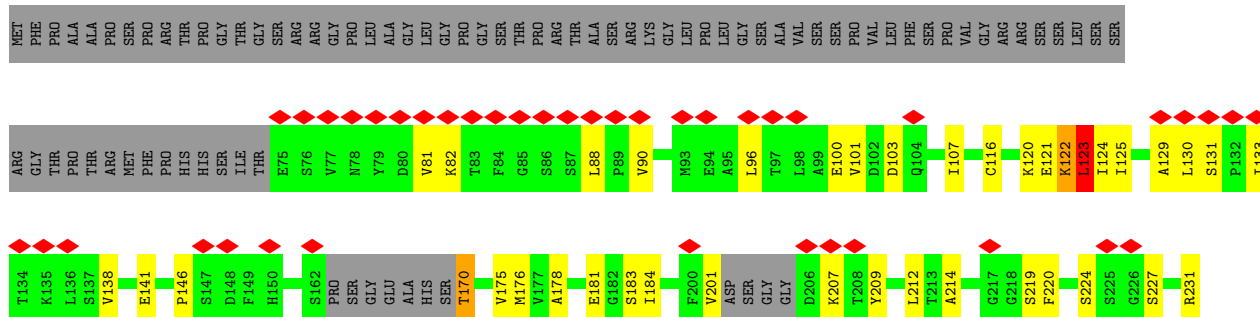


- Molecule 21: NUP133

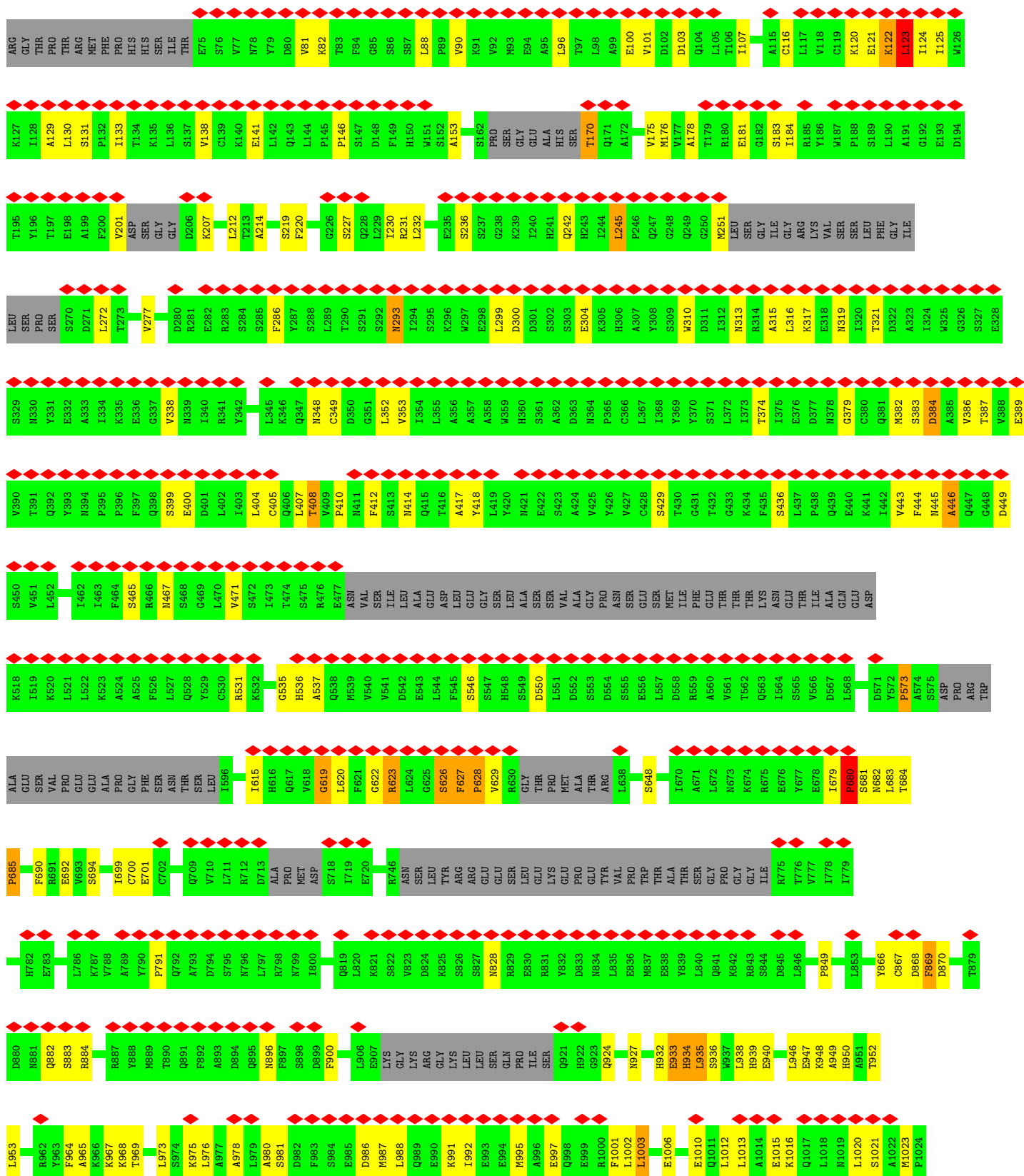


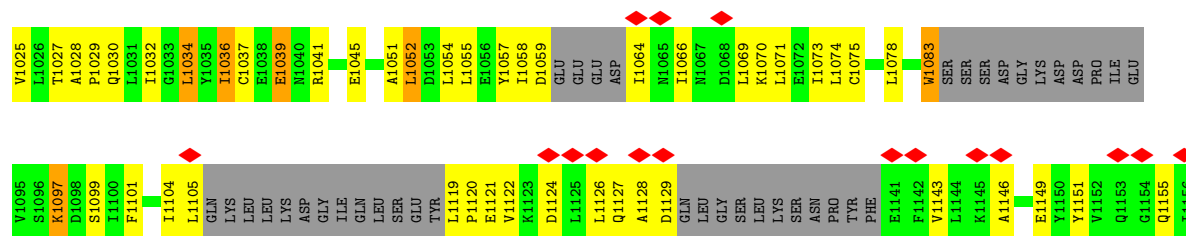


• Molecule 21: NUP133

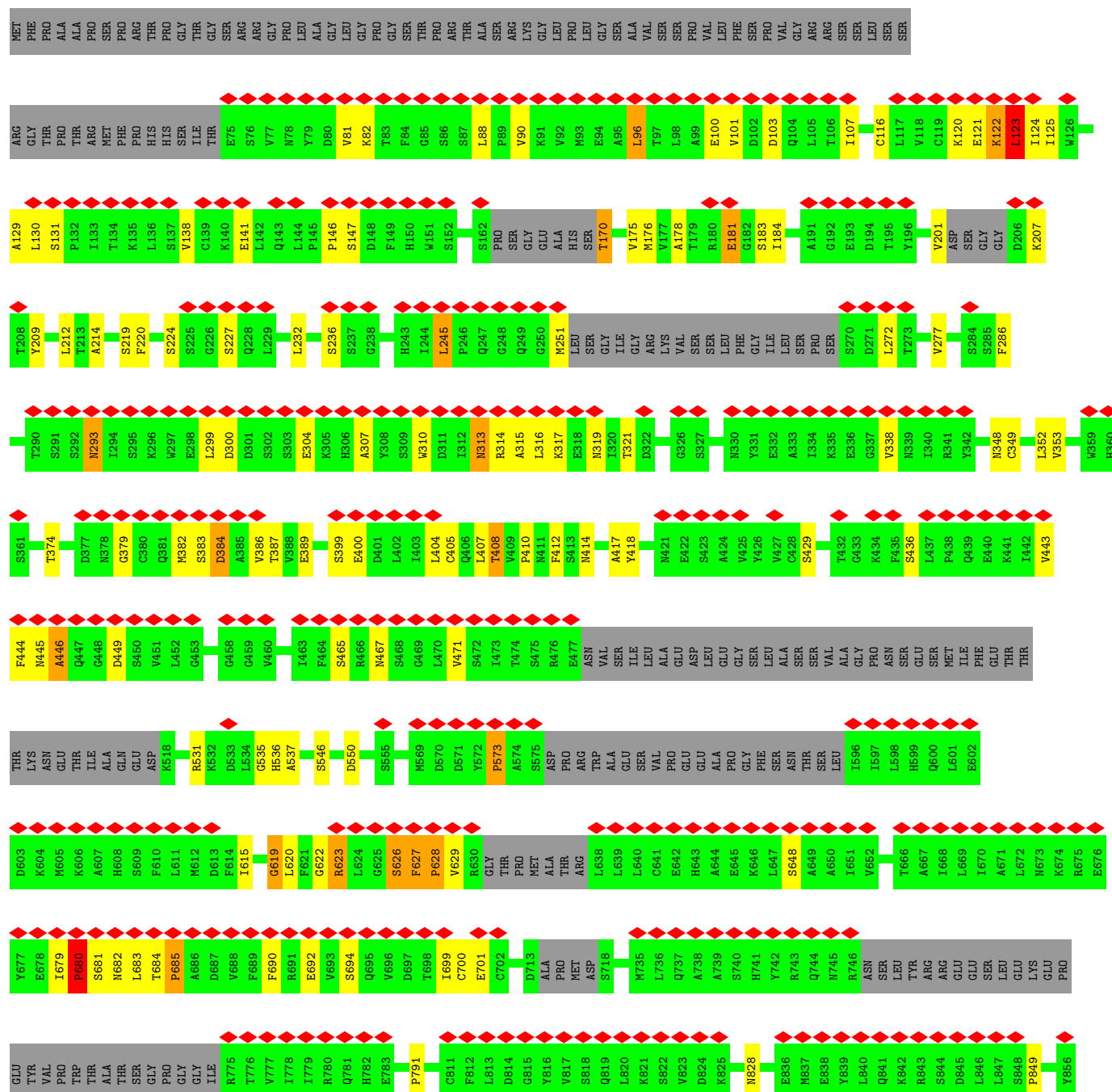


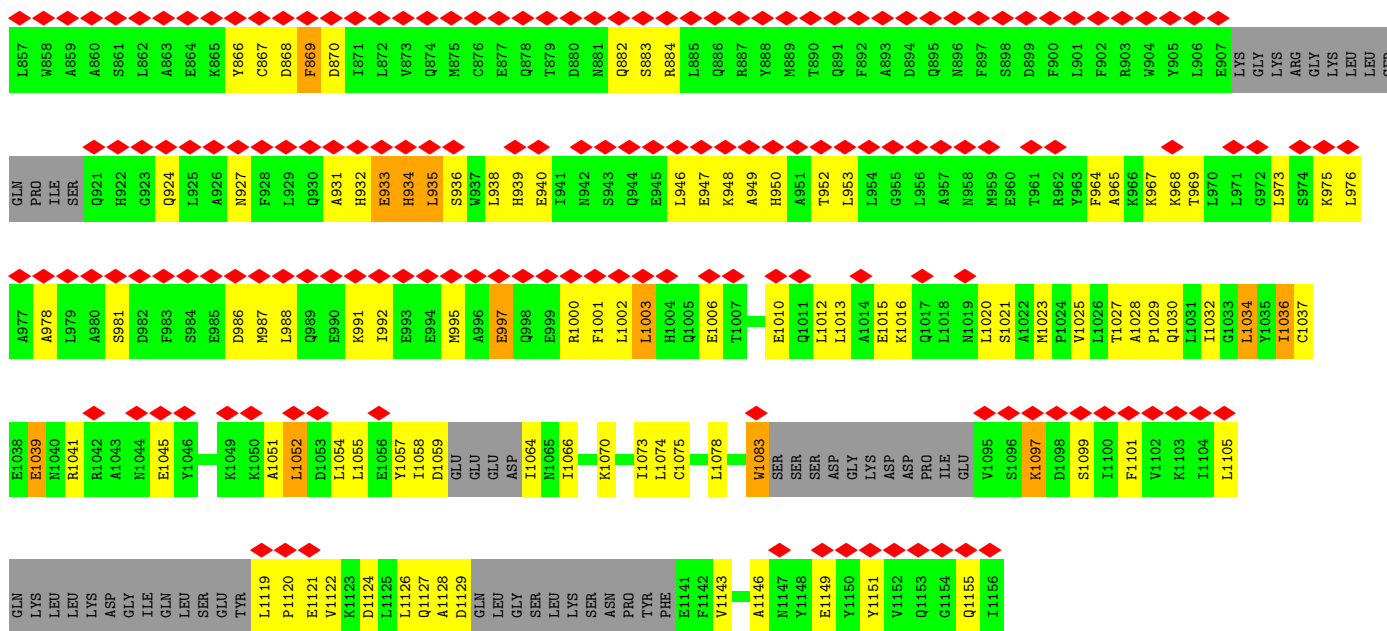




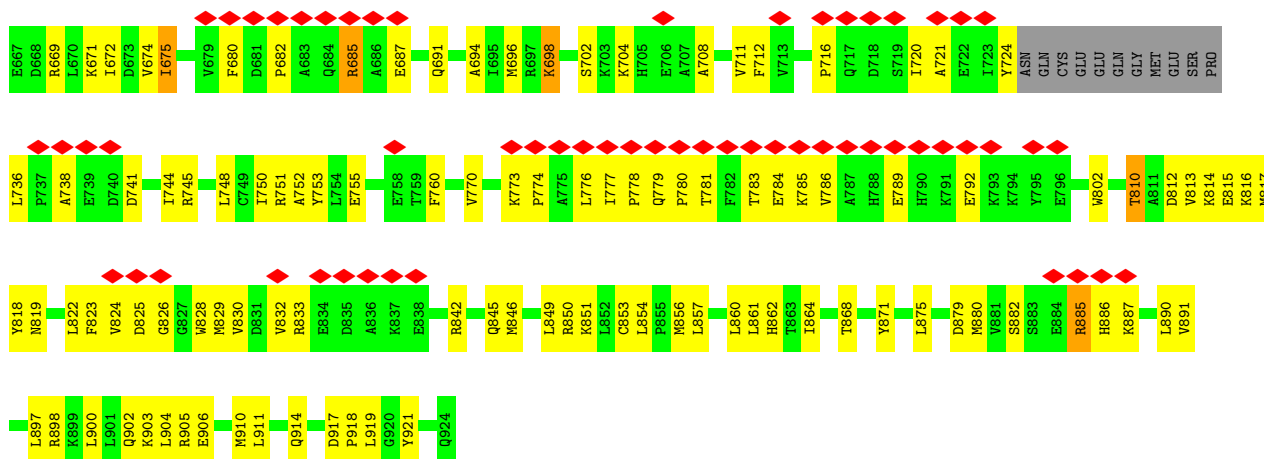


• Molecule 21: NUP133

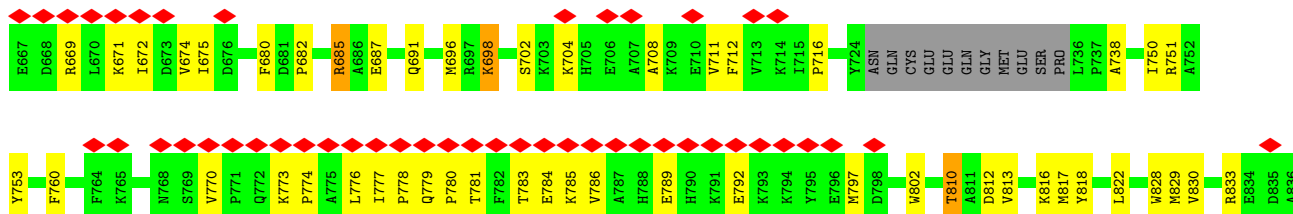


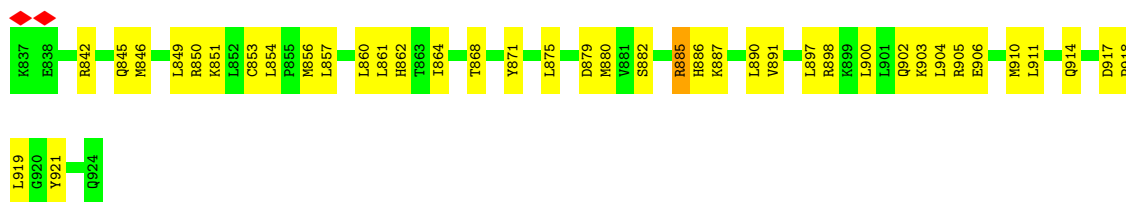


• Molecule 22: NUP107 CTD

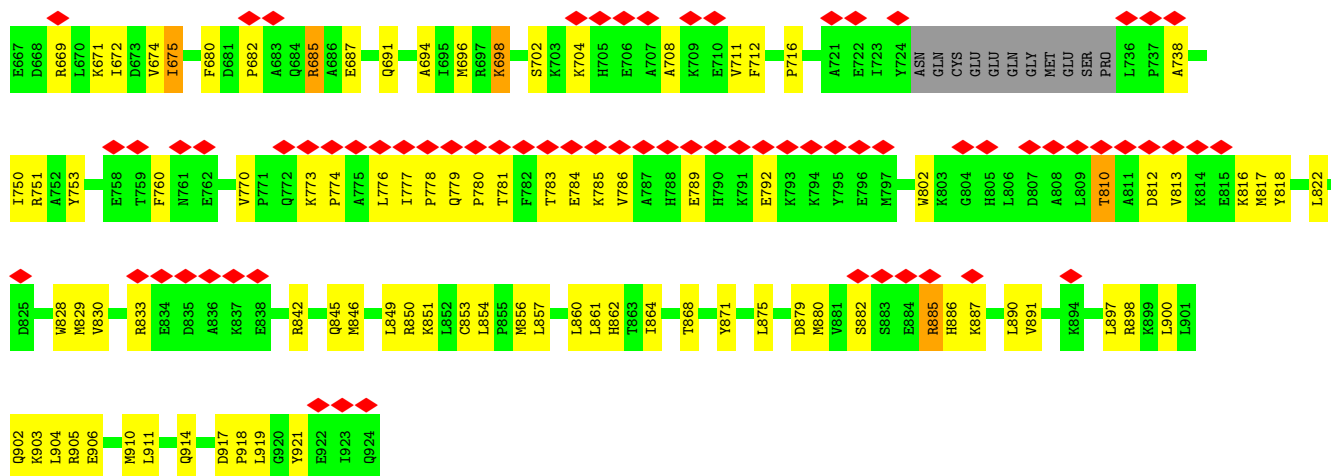


• Molecule 22: NUP107 CTD

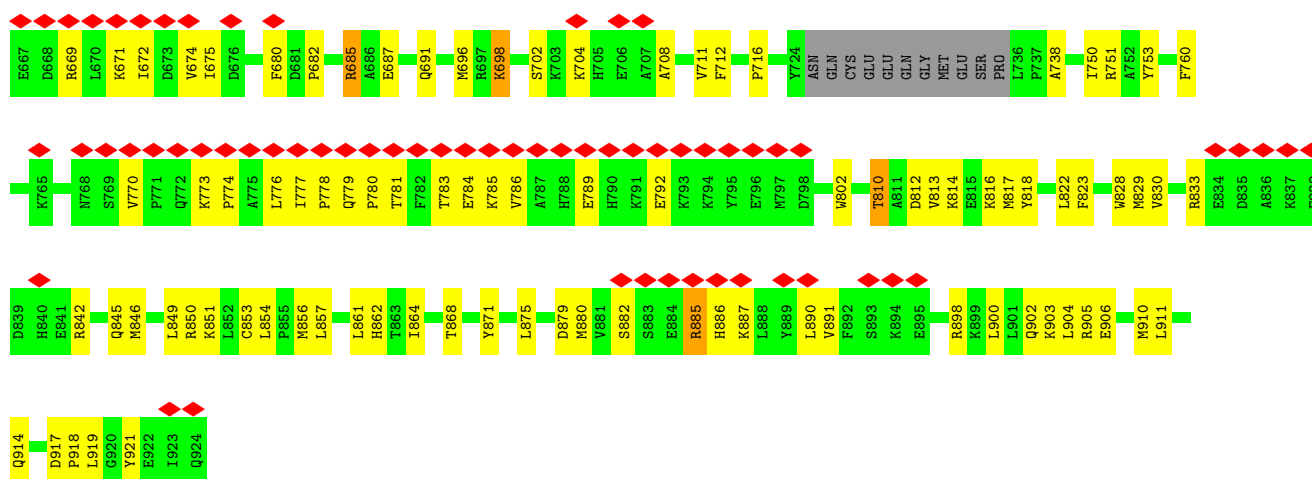




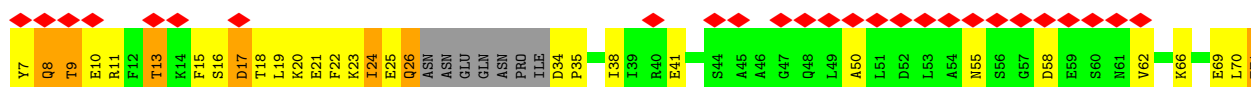
• Molecule 22: NUP107 CTD

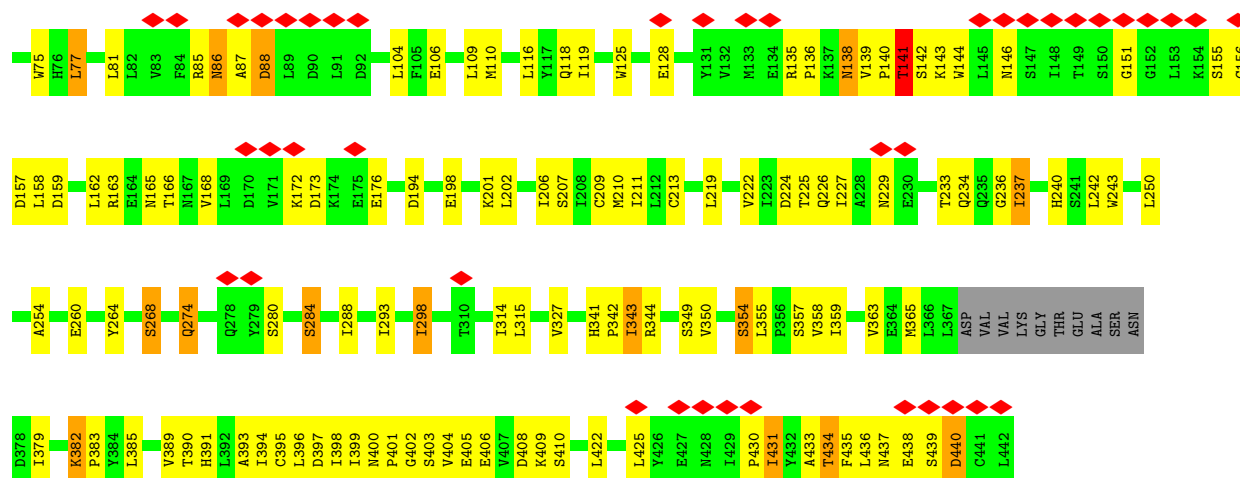


• Molecule 22: NUP107 CTD

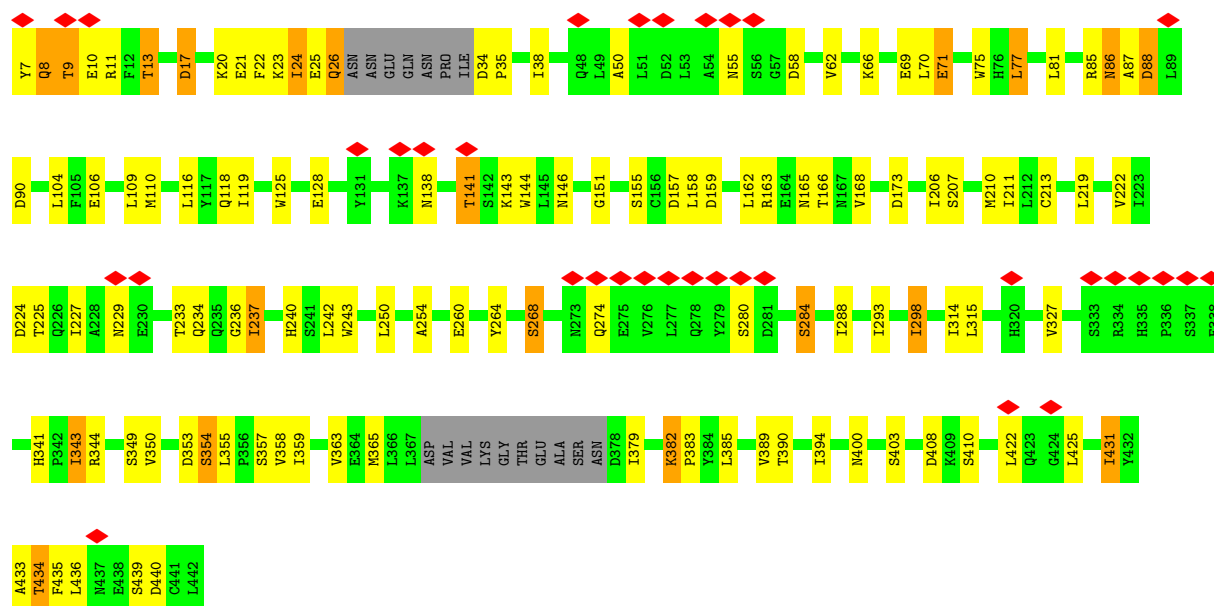


• Molecule 23: NUP107 NTD

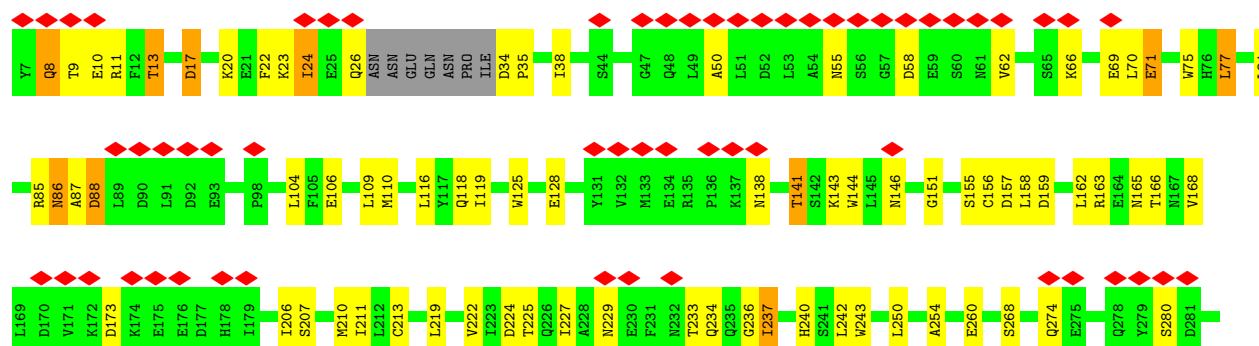


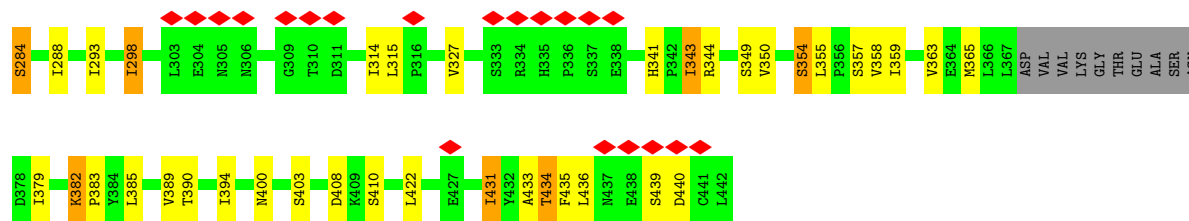


• Molecule 23: NUP107 NTD

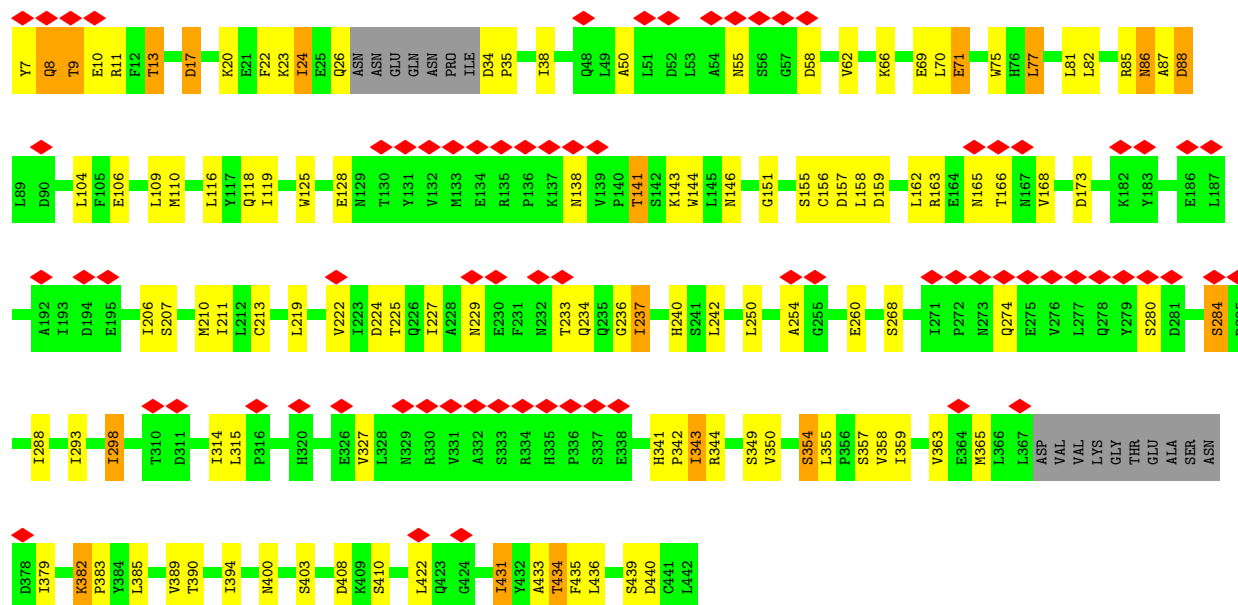


• Molecule 23: NUP107 NTD

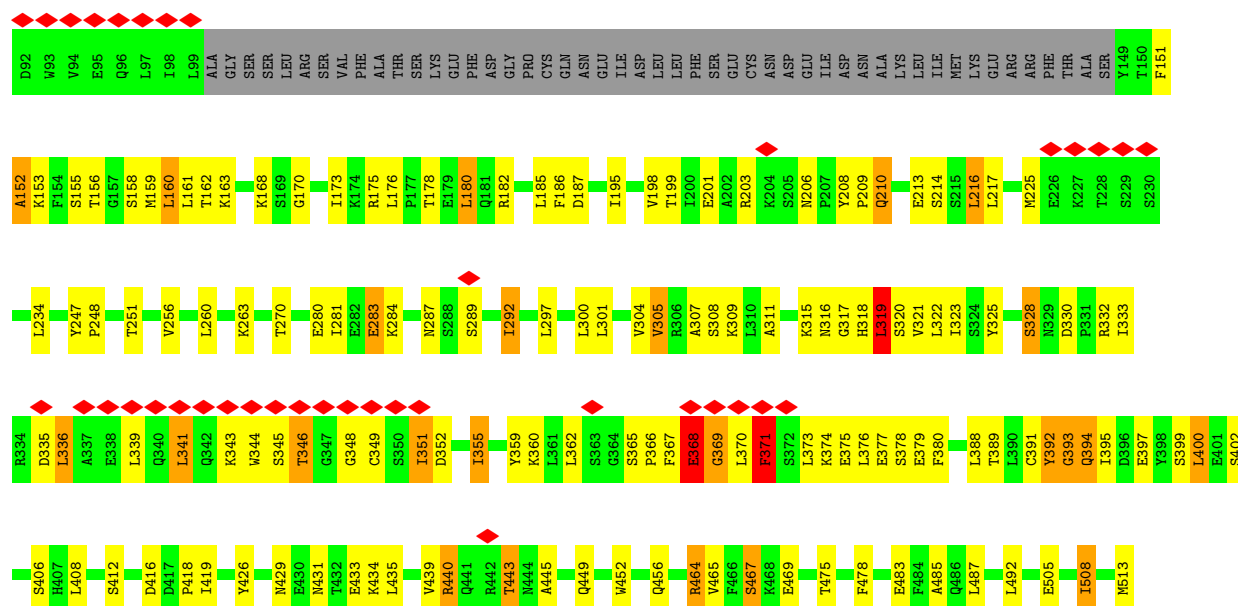


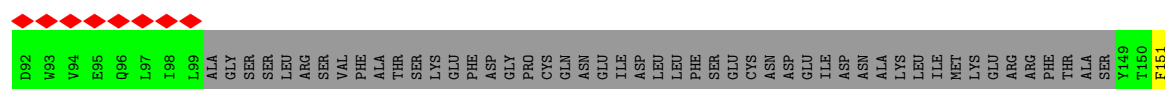


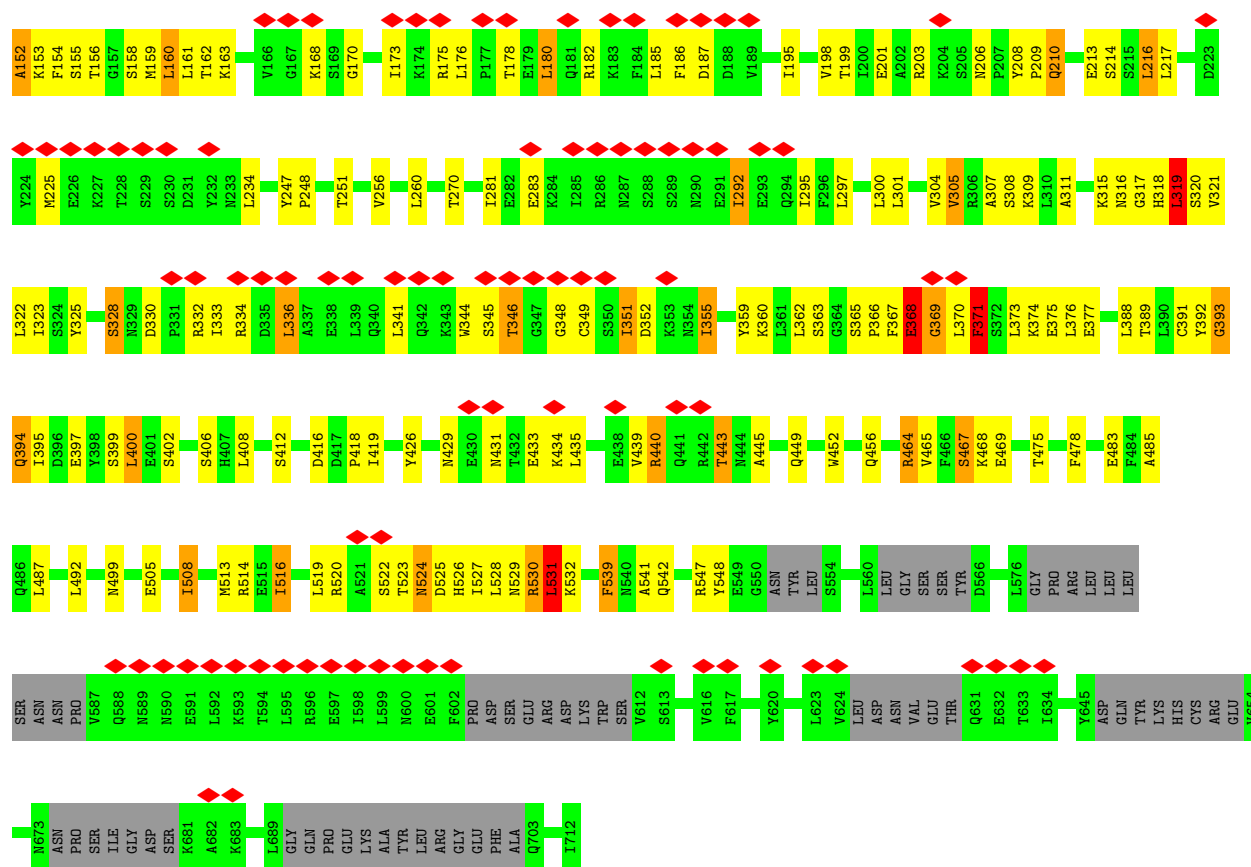
• Molecule 23: NUP107 NTD



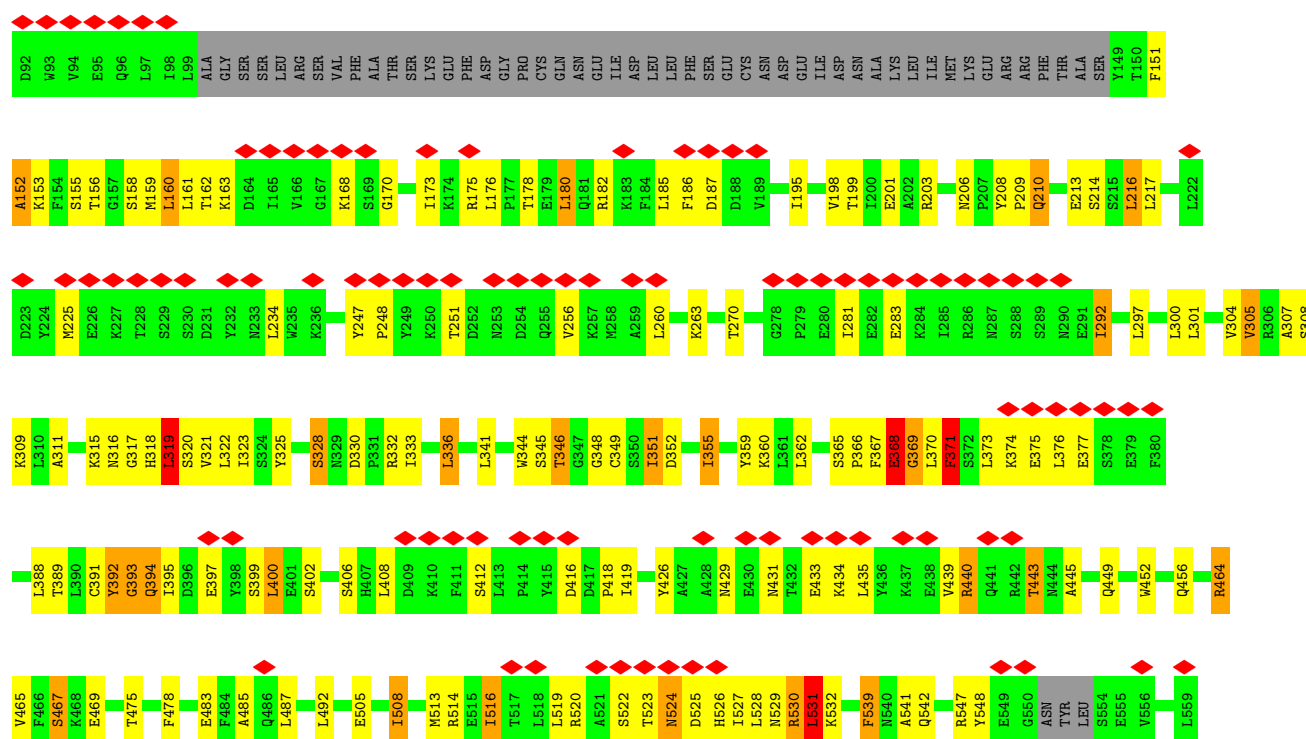
• Molecule 24: NUP96

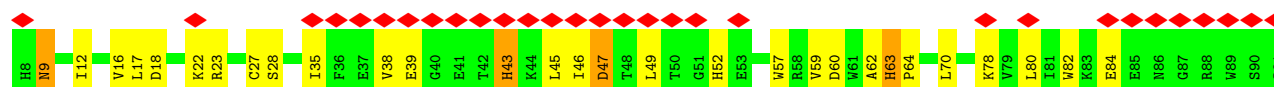


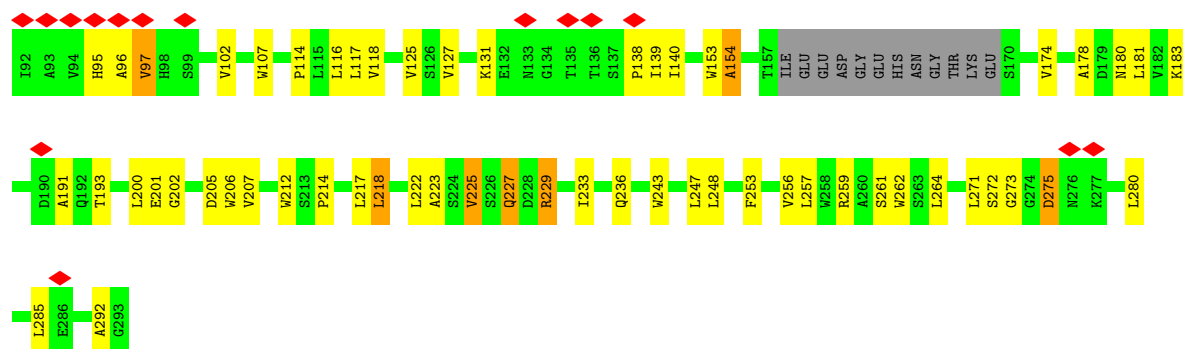




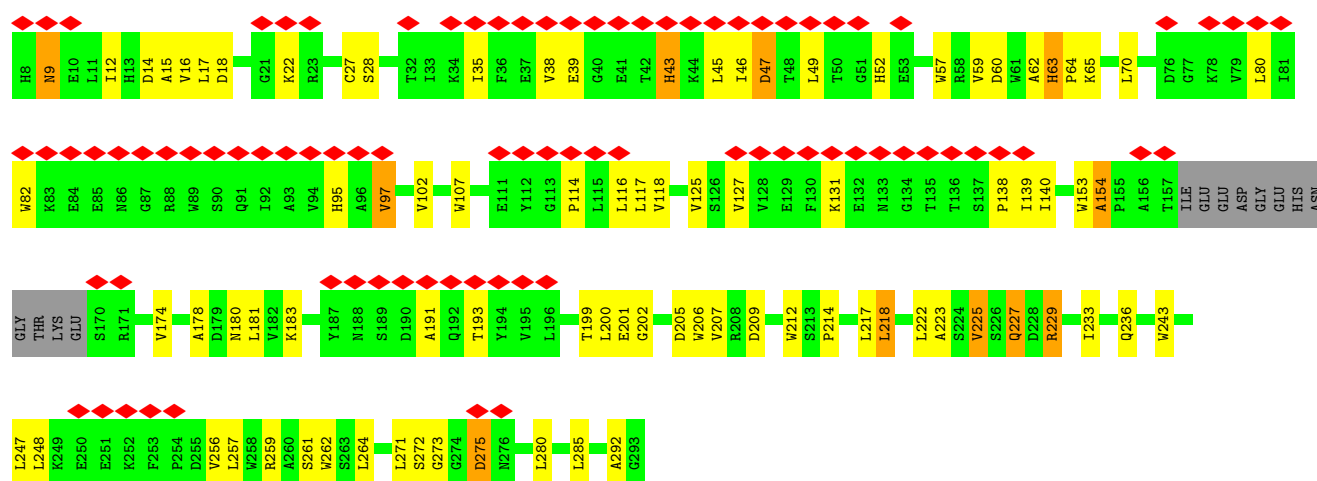
• Molecule 24: NUP96



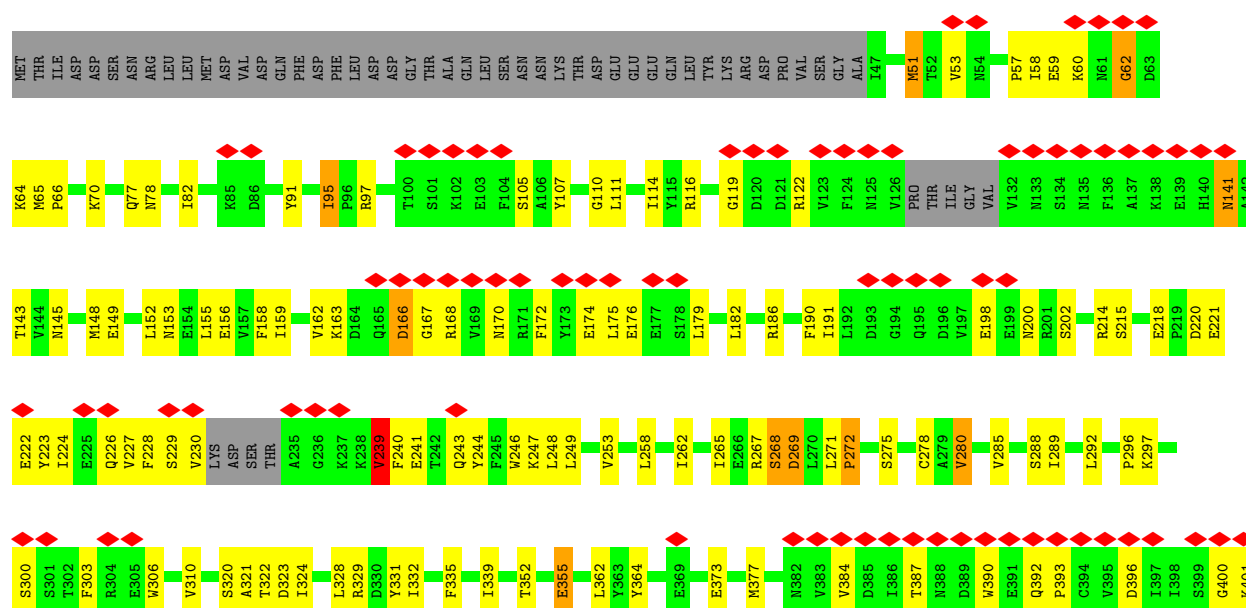




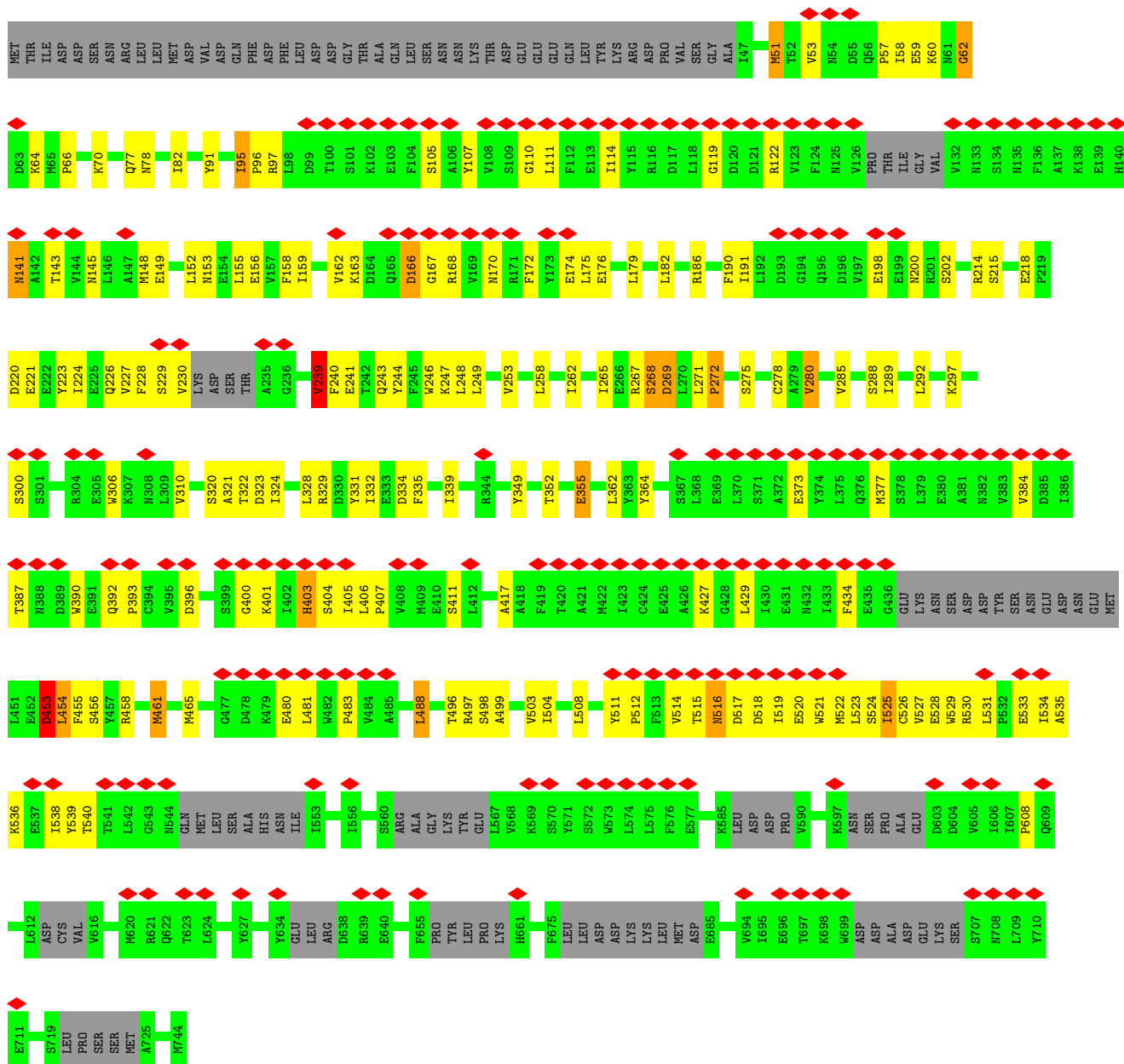
• Molecule 25: SEC13



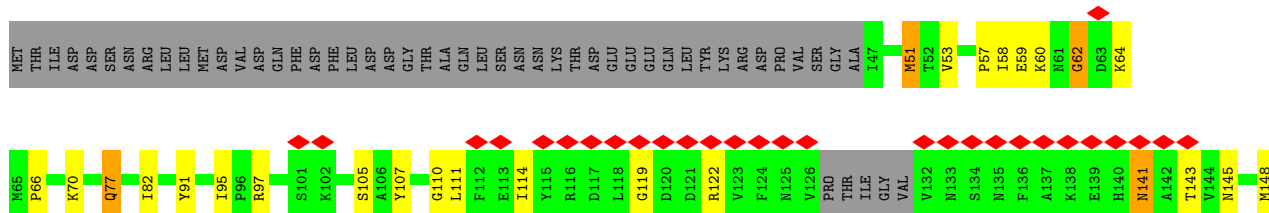
• Molecule 26: NUP75



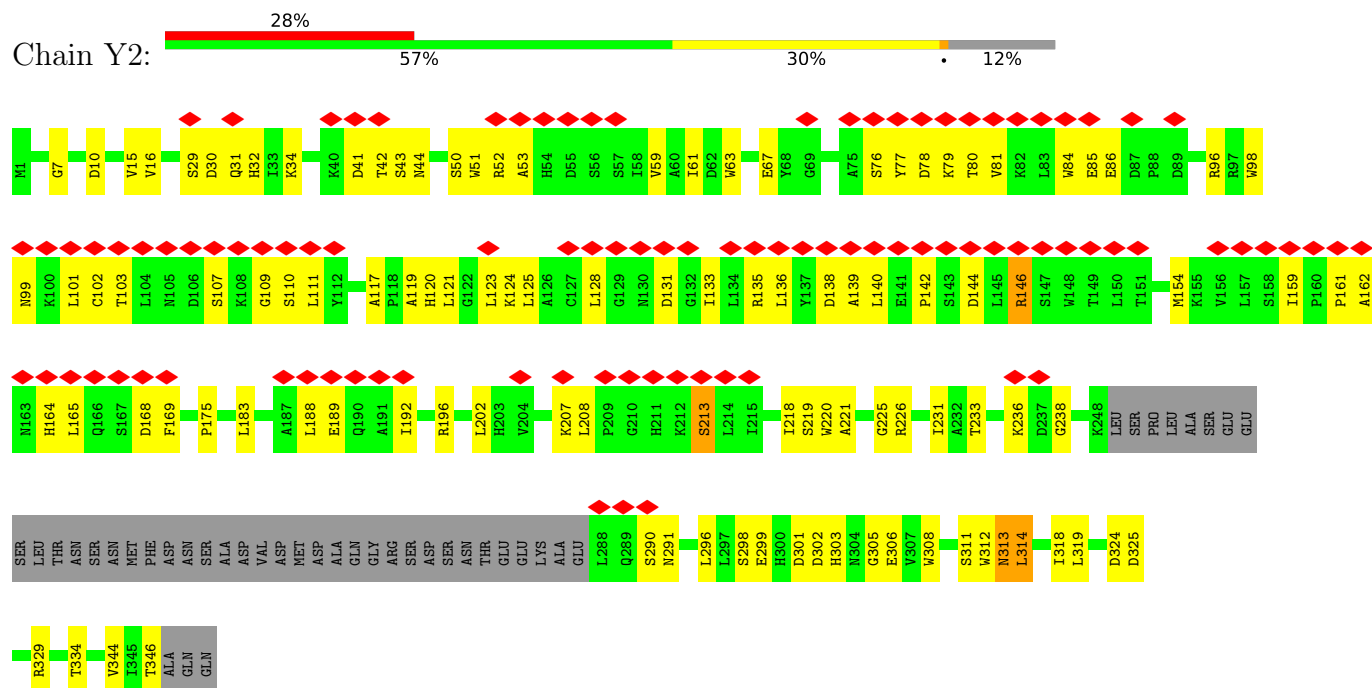
• Molecule 26: NUP75



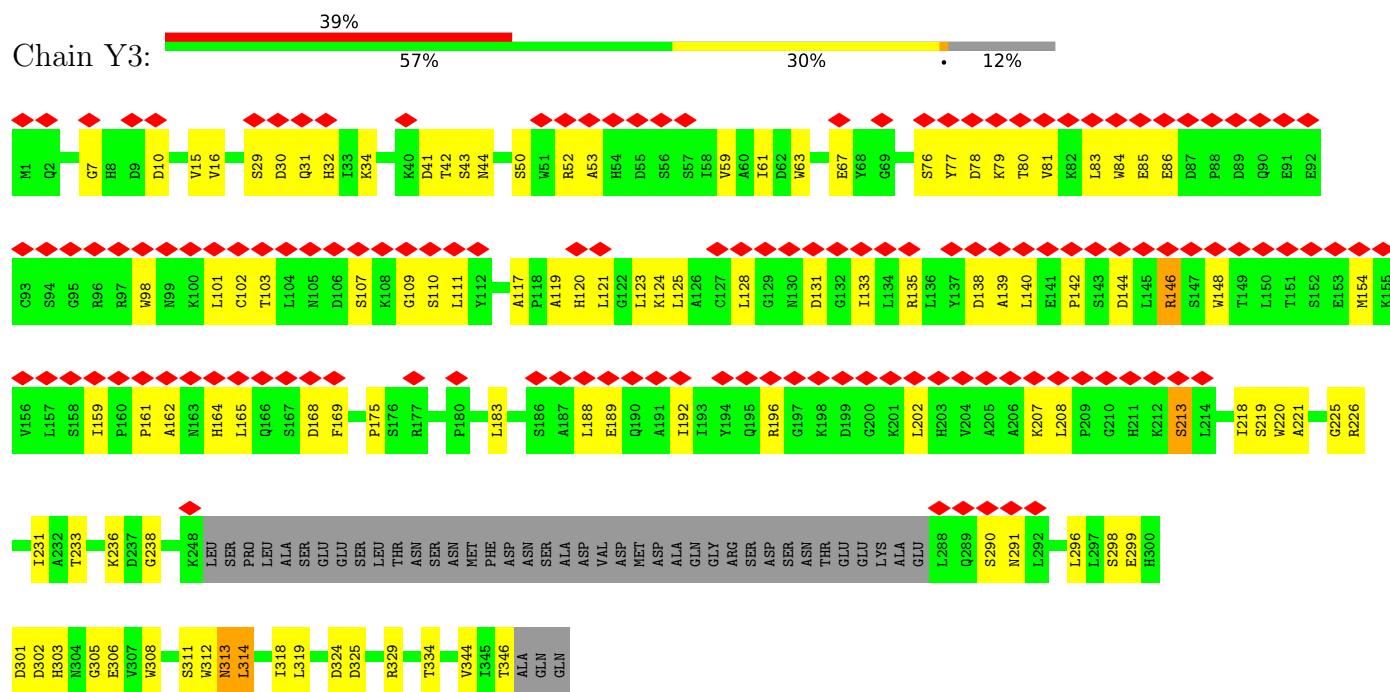
• Molecule 26: NUP75



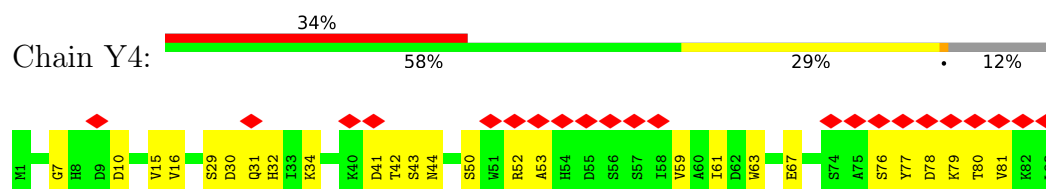
- Molecule 27: SEH1



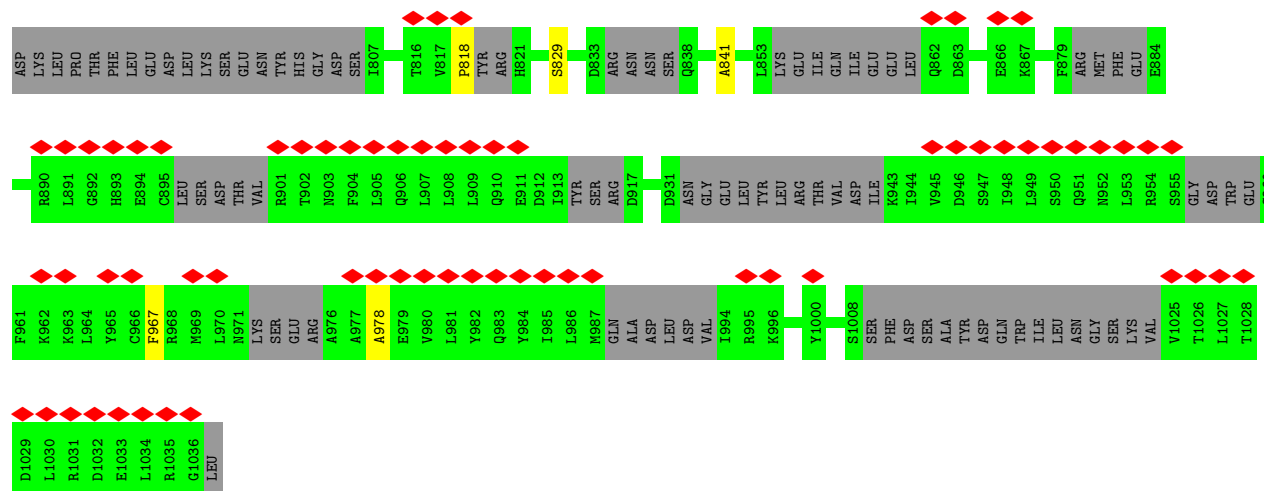
- Molecule 27: SEH1



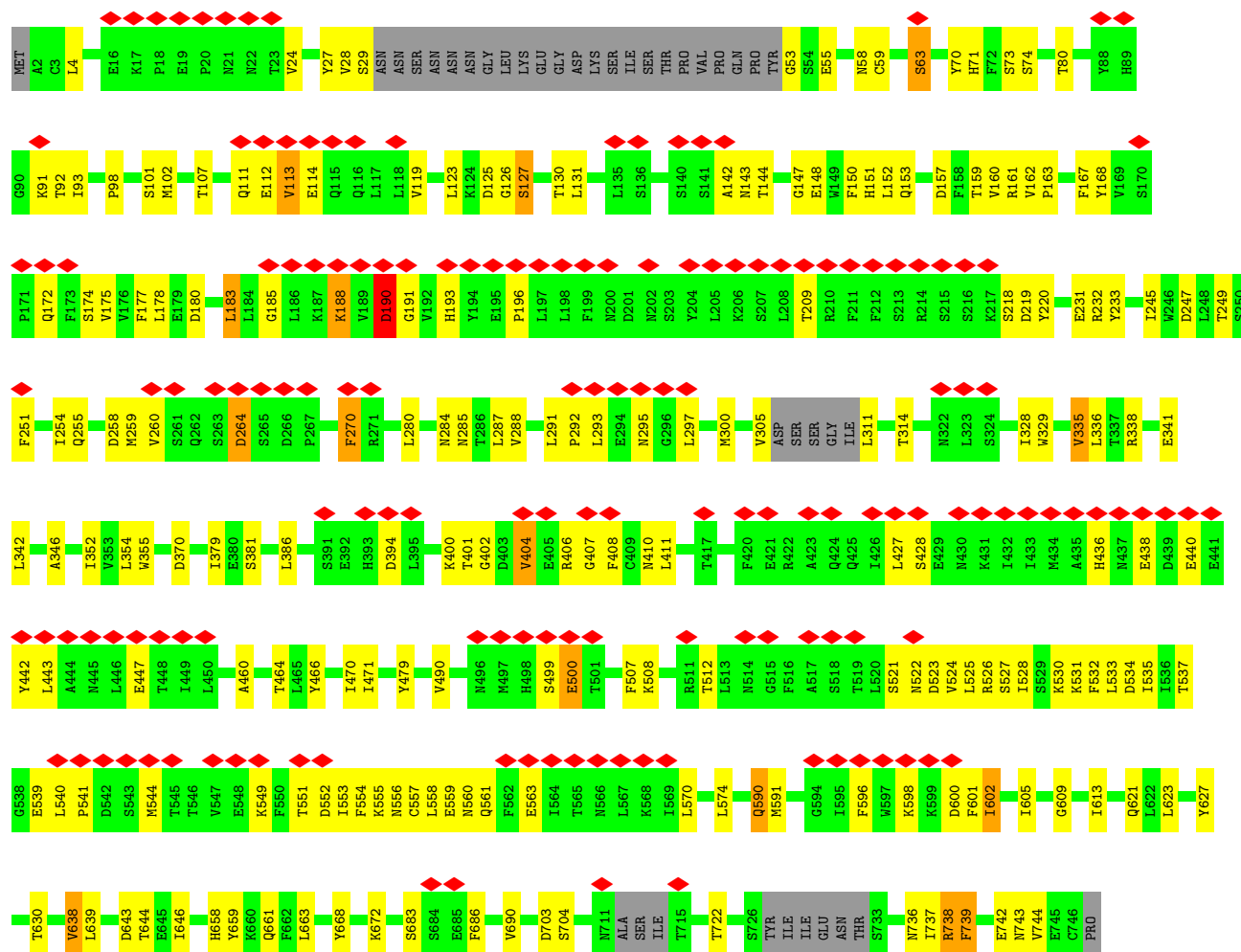
- Molecule 27: SEH1

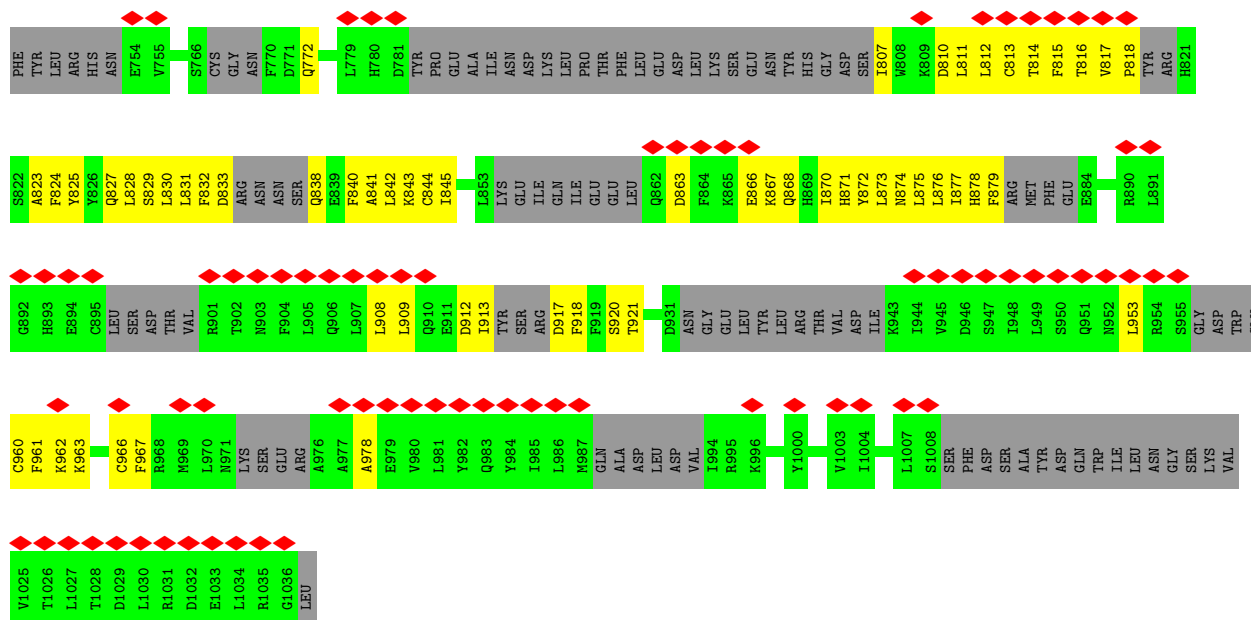




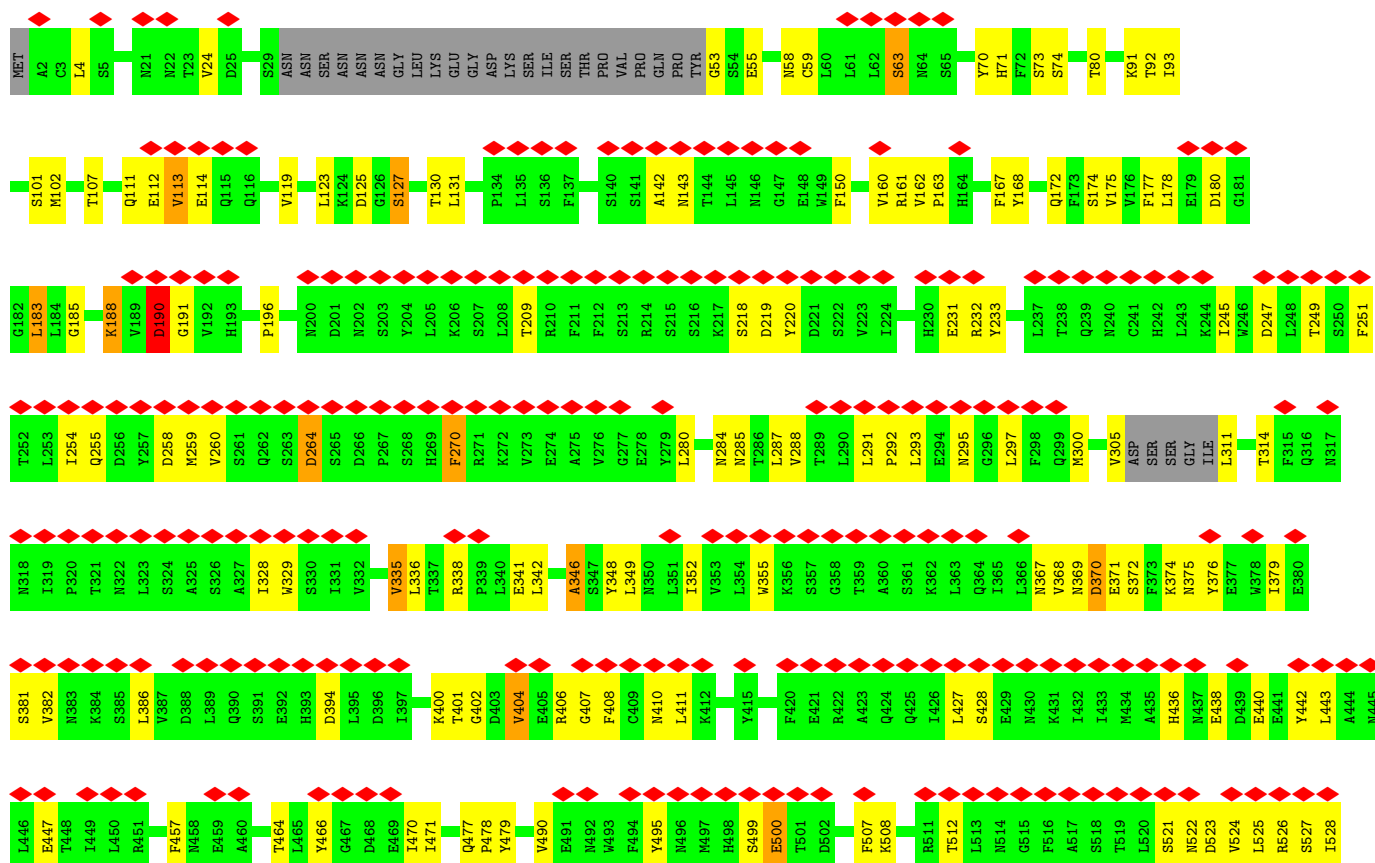


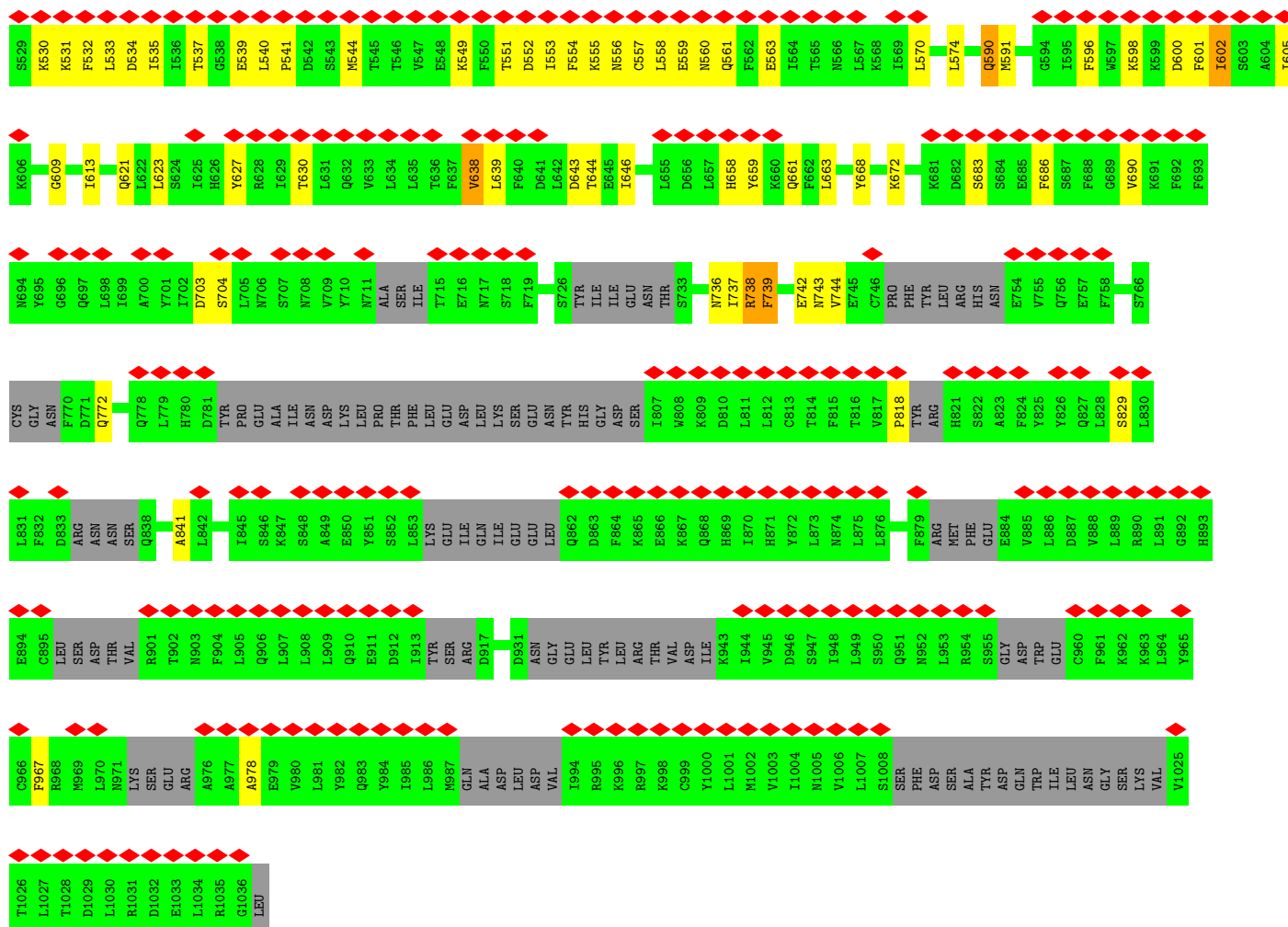
• Molecule 28: NUP160





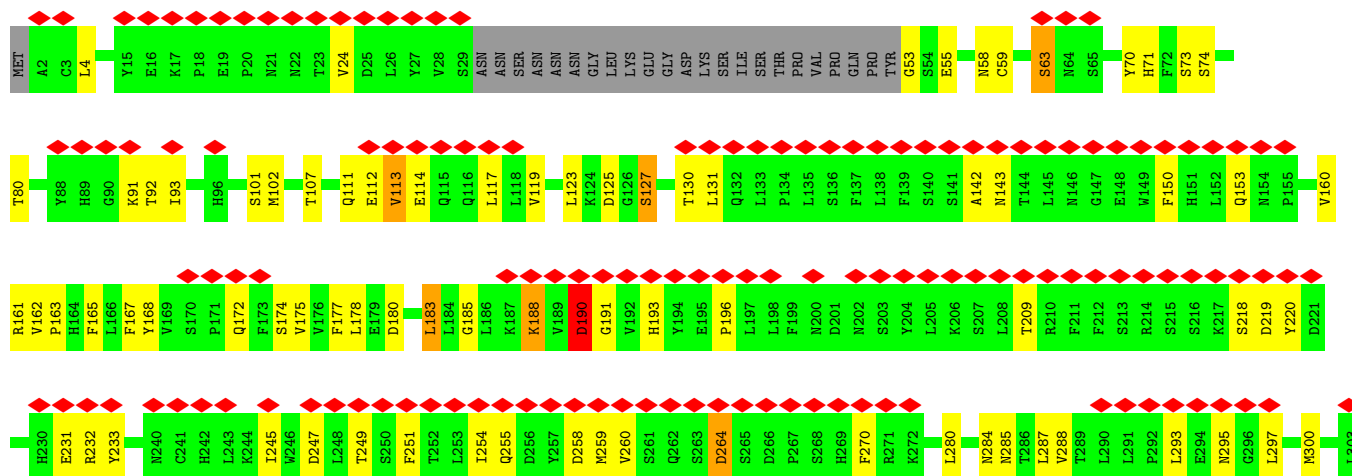
• Molecule 28: NUP160

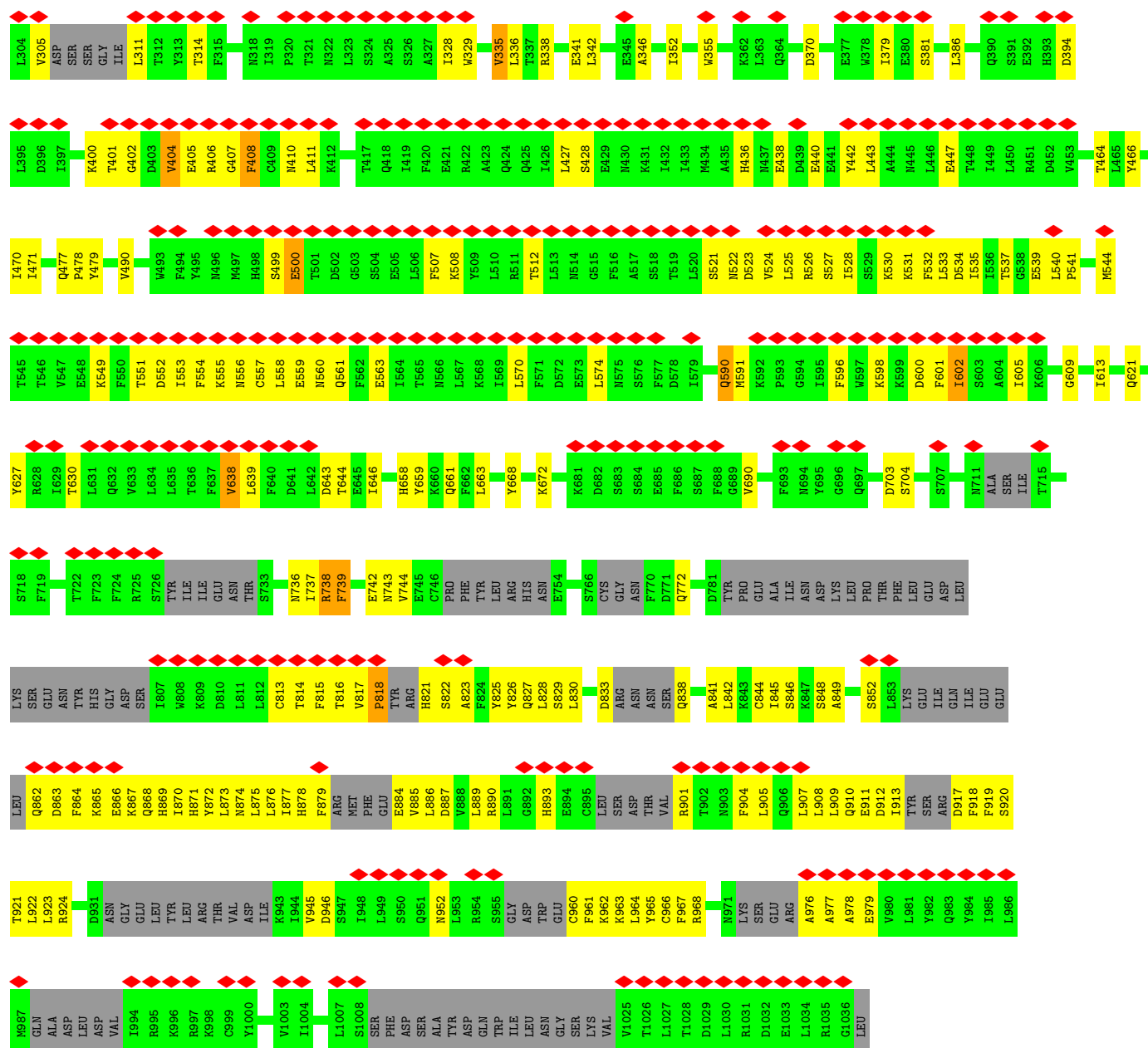




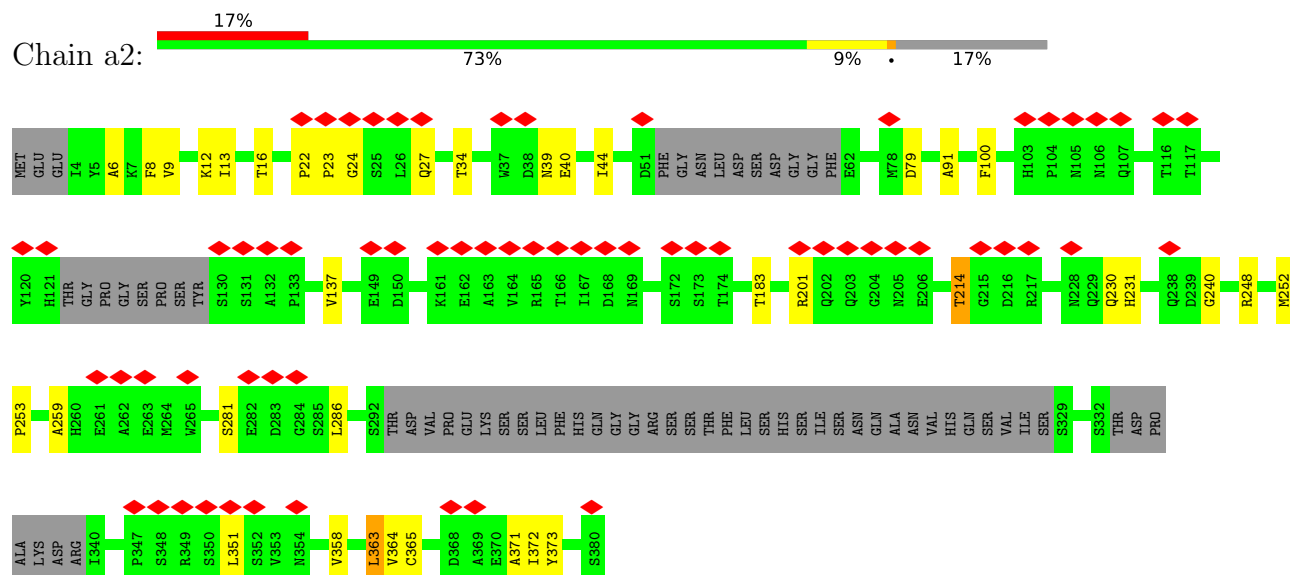
• Molecule 28: NUP160

Chain Z4:

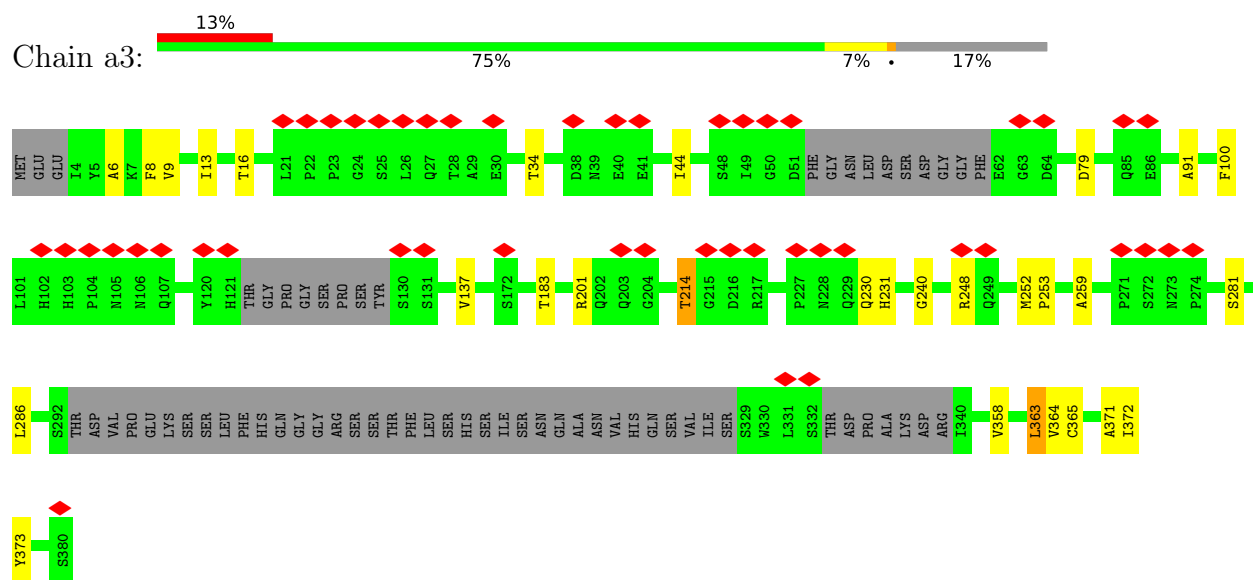




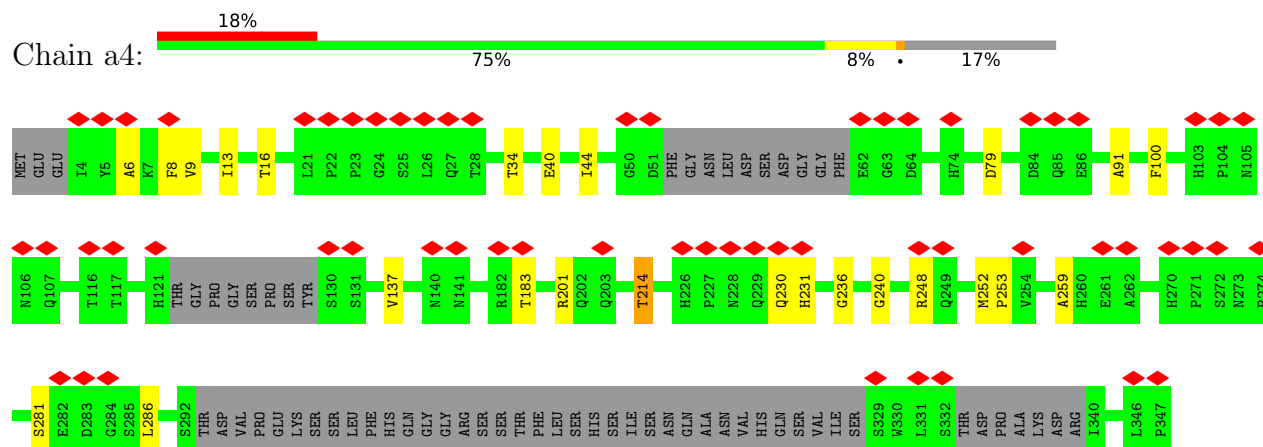
- Molecule 29: NUP43

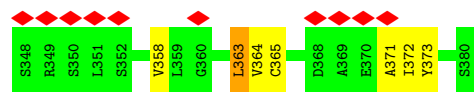


- Molecule 29: NUP43

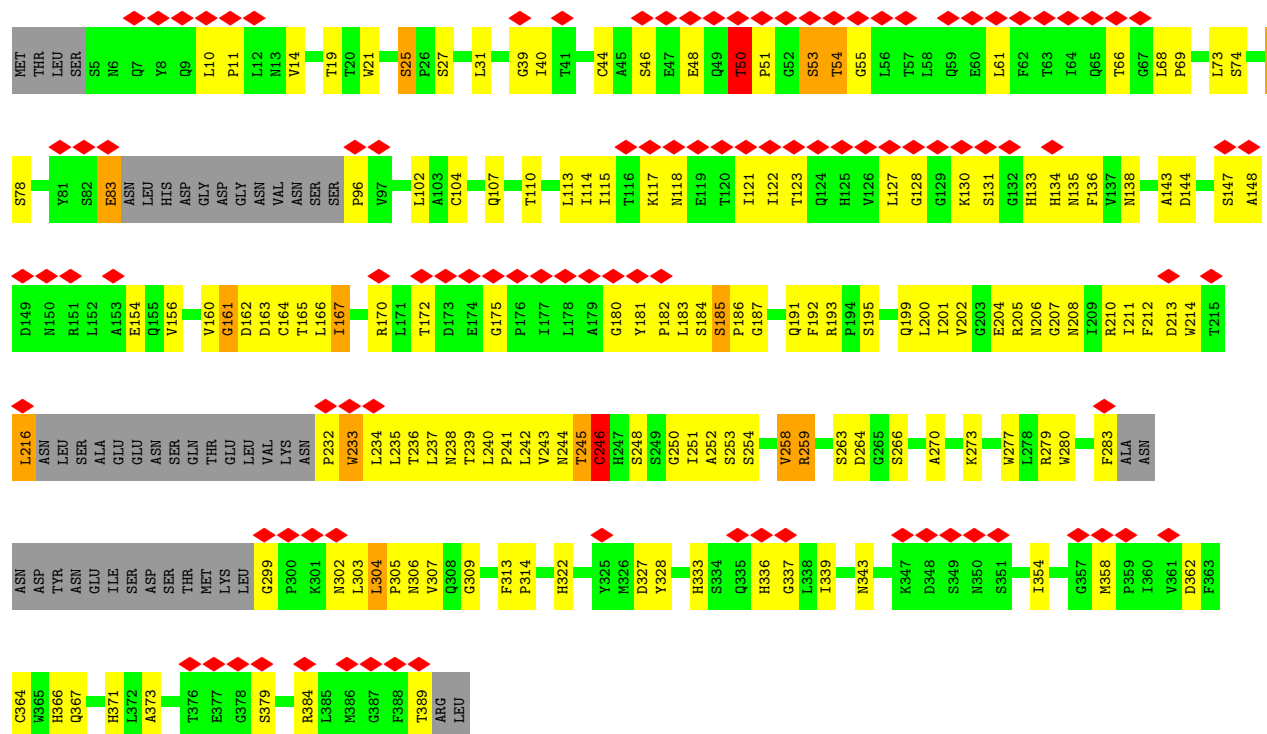


- Molecule 29: NUP43

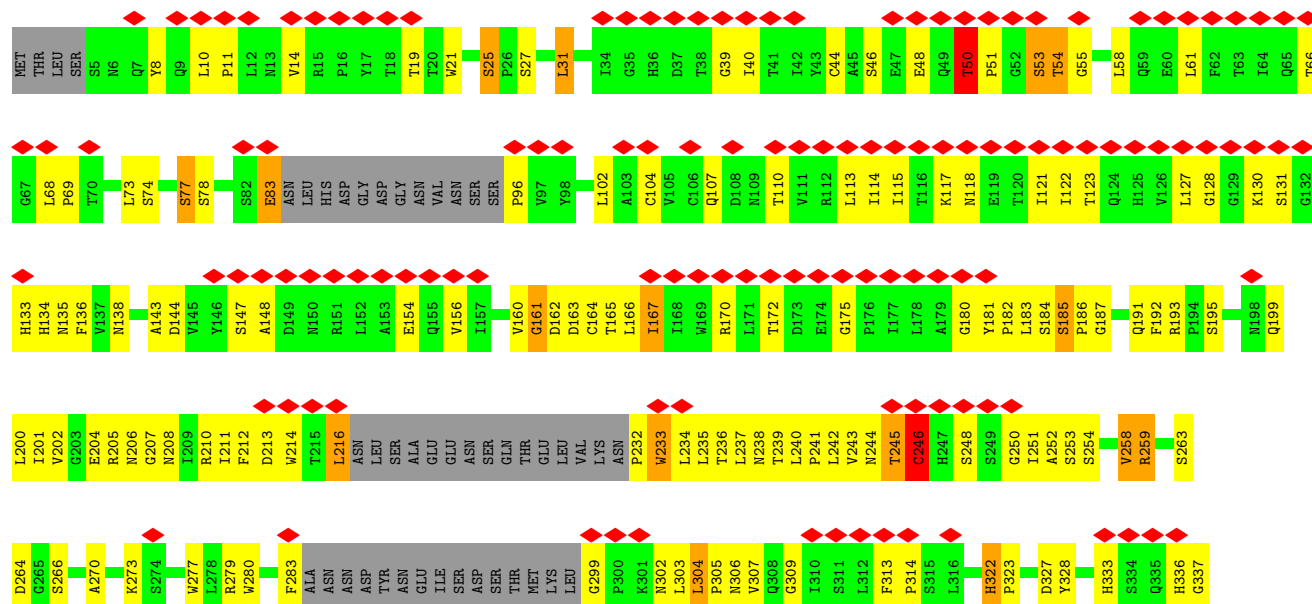
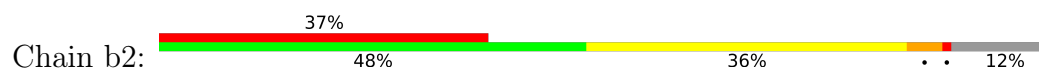




• Molecule 30: NUP37

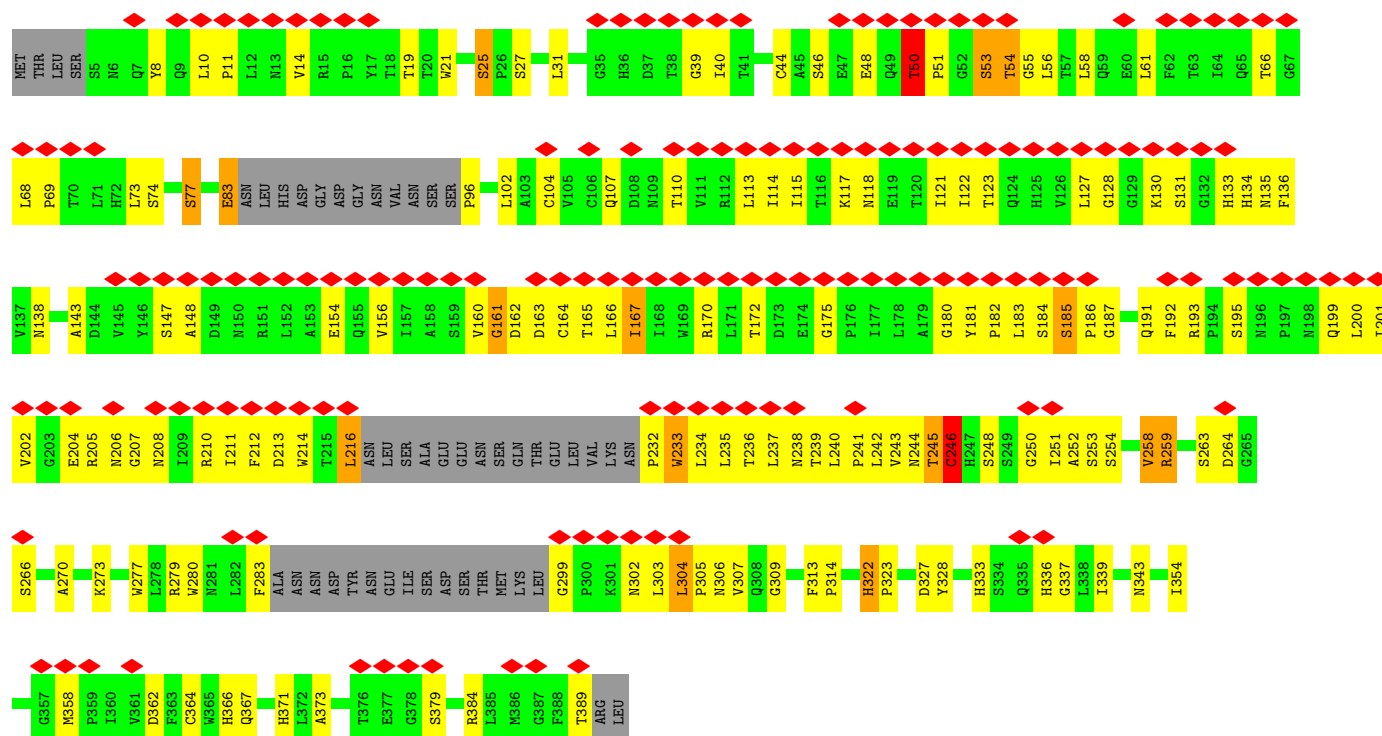
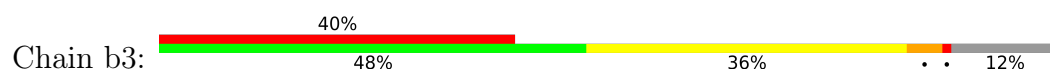


• Molecule 30: NUP37

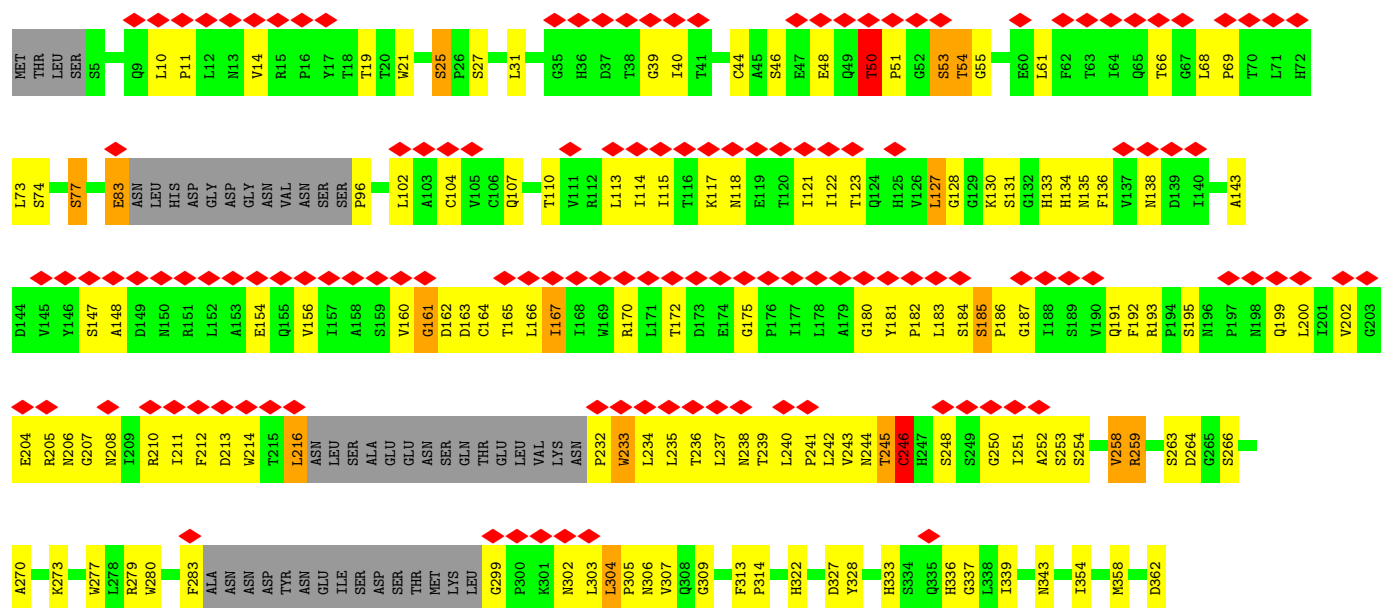




• Molecule 30: NUP37

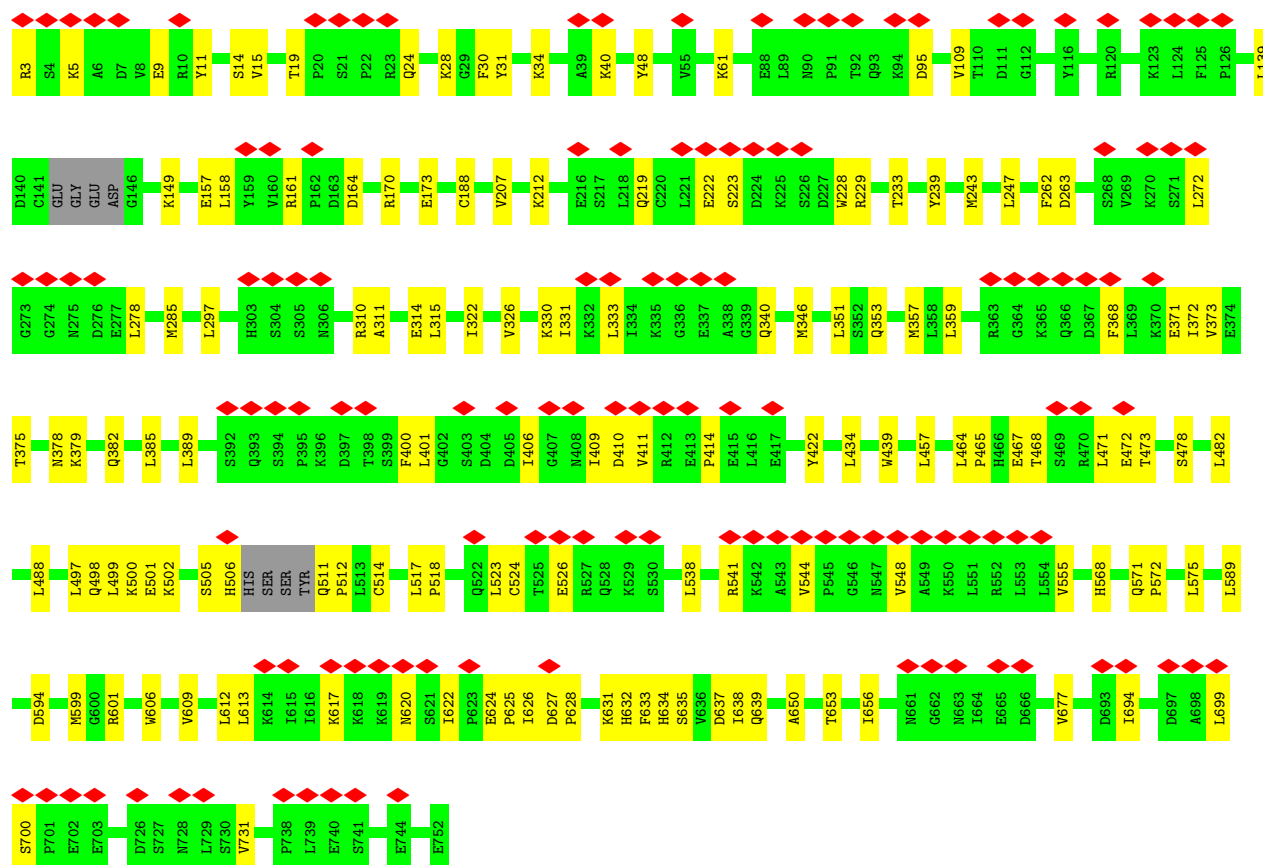
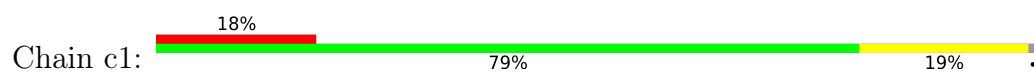


• Molecule 30: NUP37

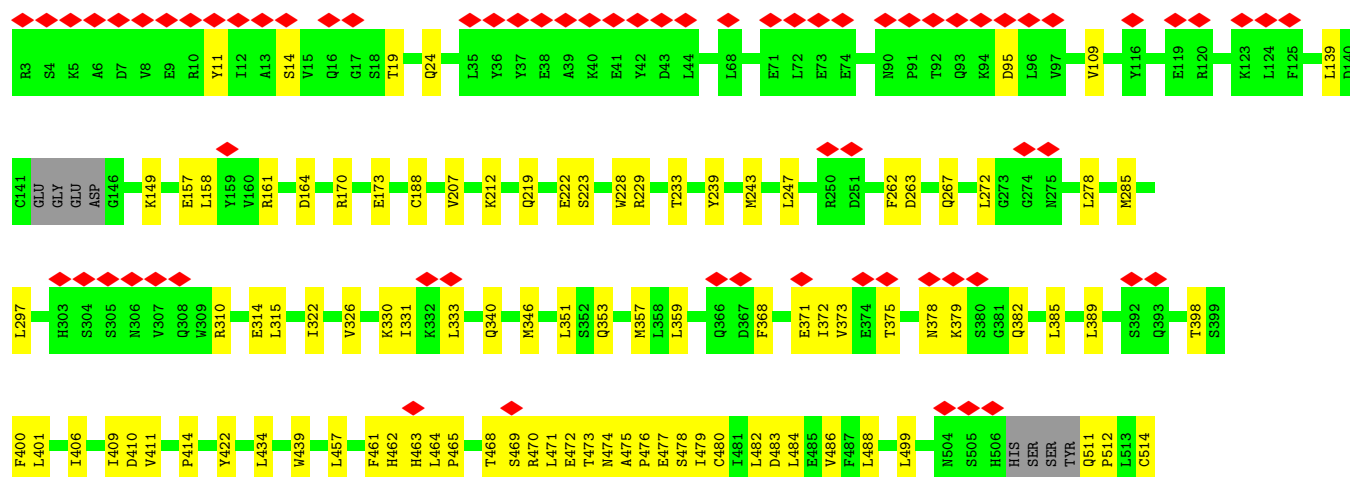
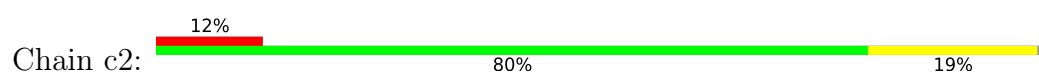


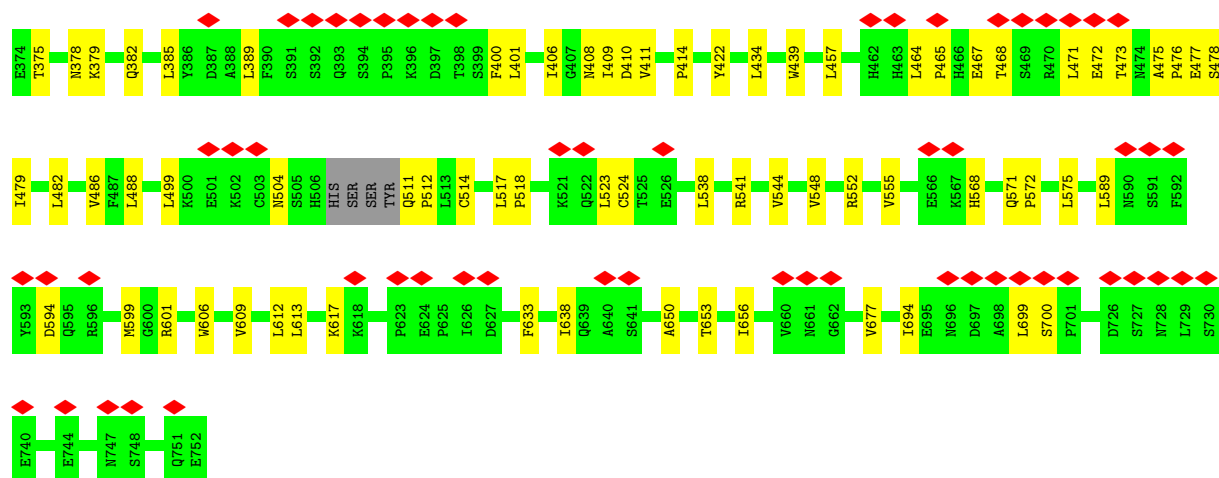


• Molecule 31: NUP358

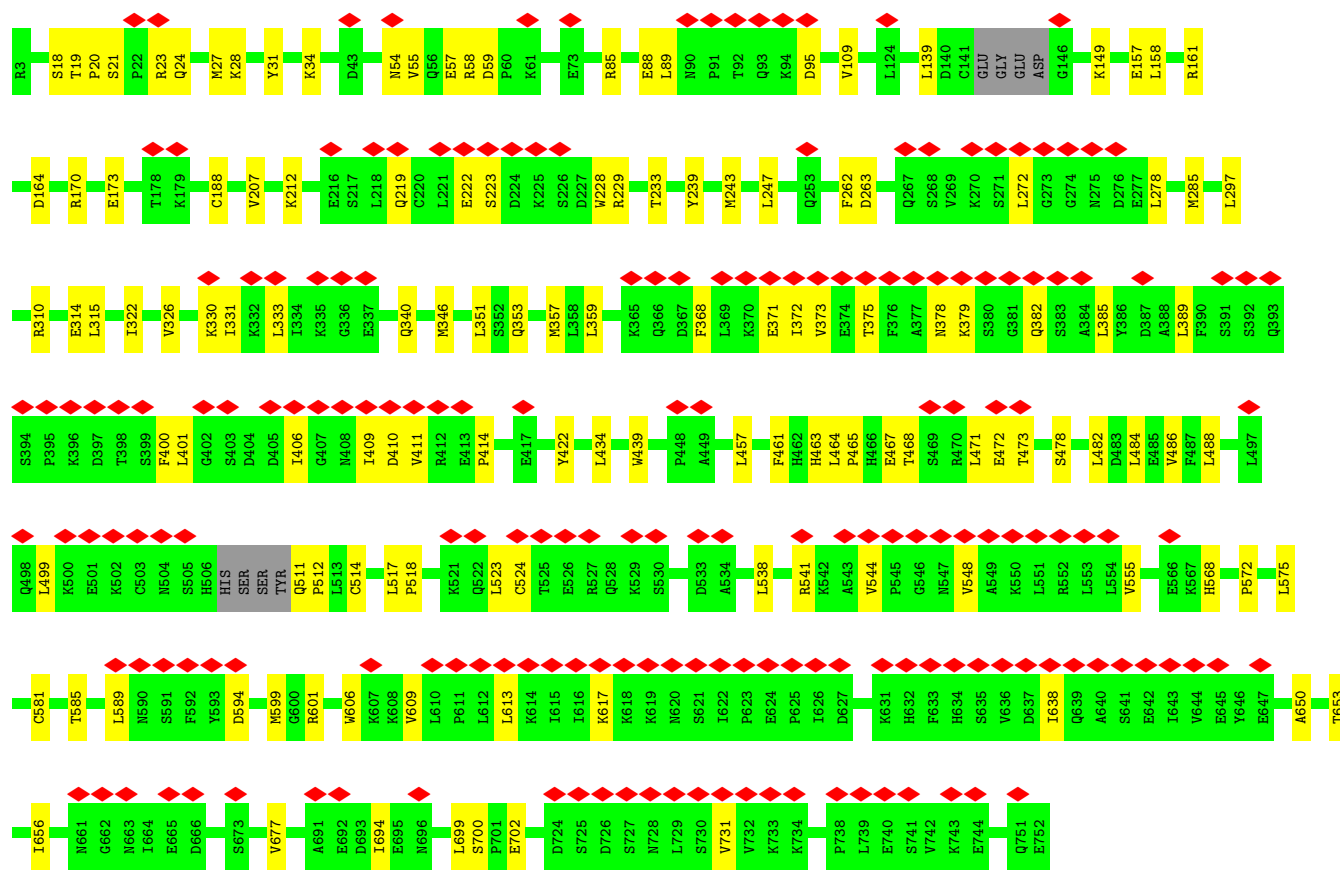
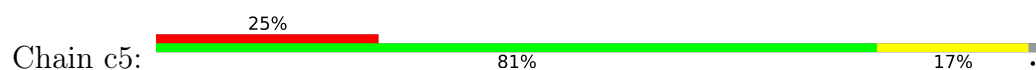


• Molecule 31: NUP358

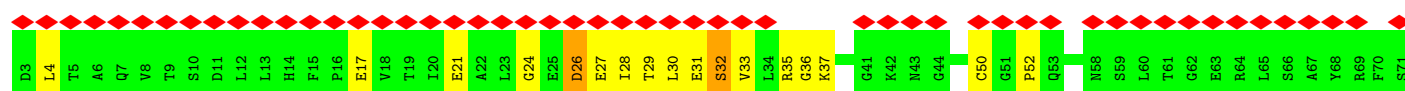
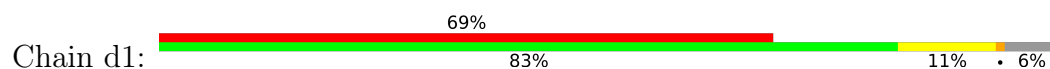


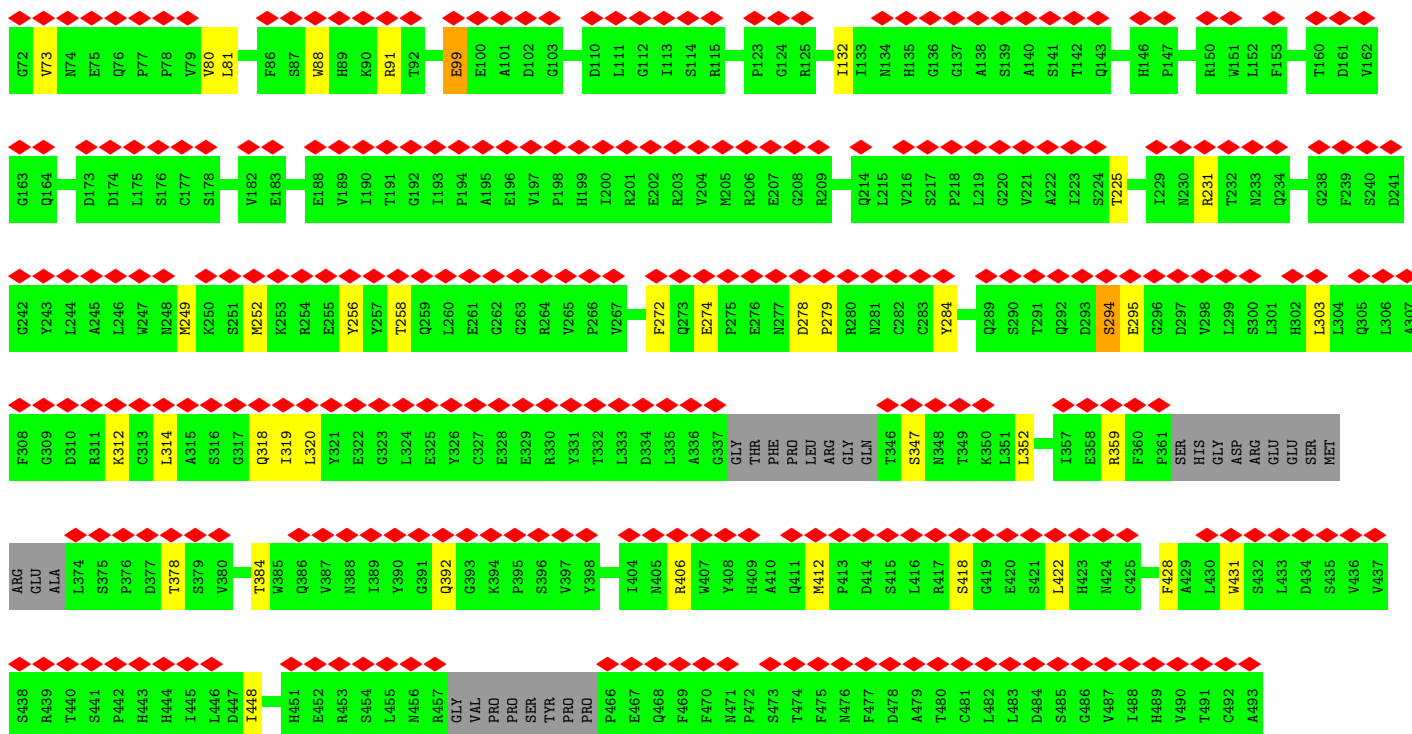


• Molecule 31: NUP358

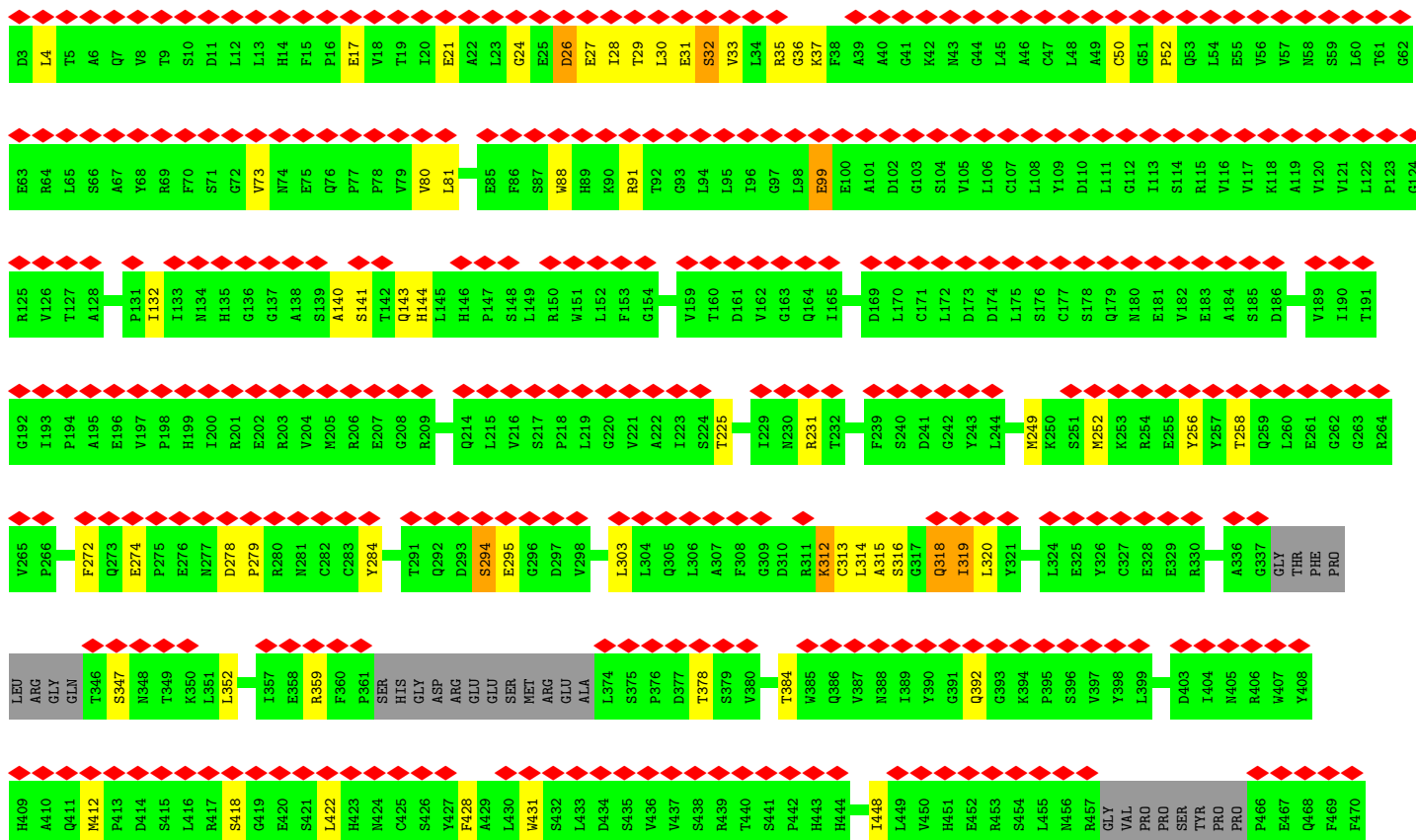
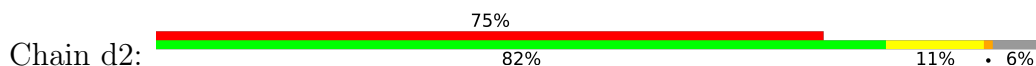


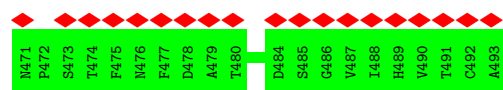
• Molecule 32: ELYS



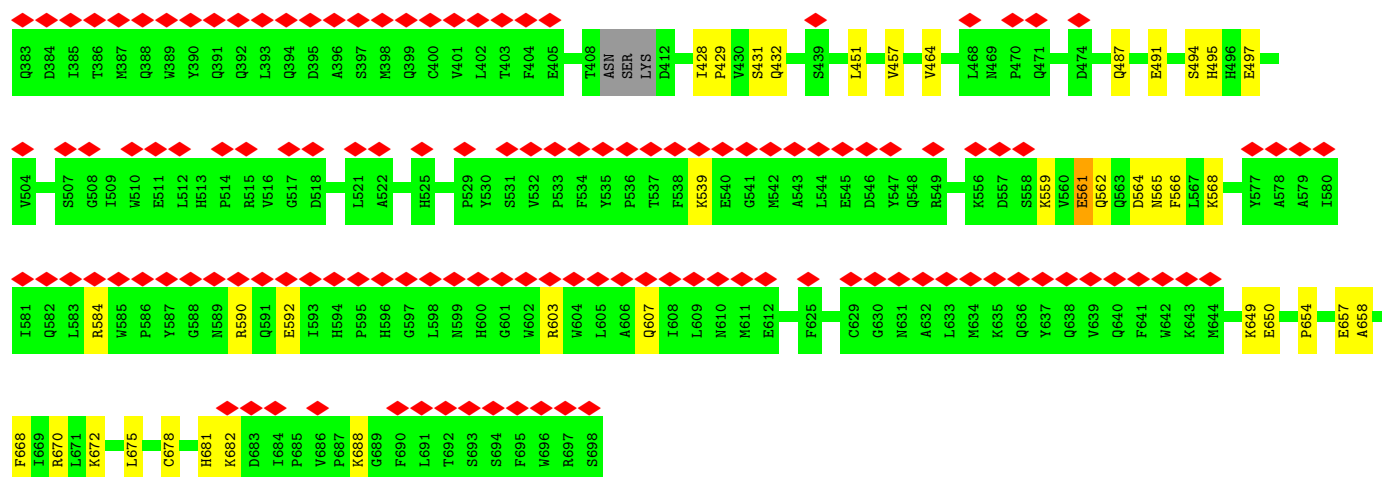
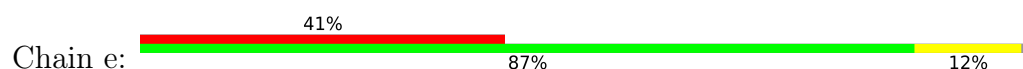


• Molecule 32: ELYS

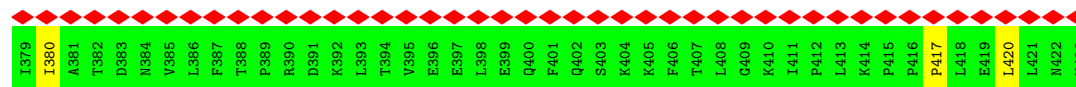
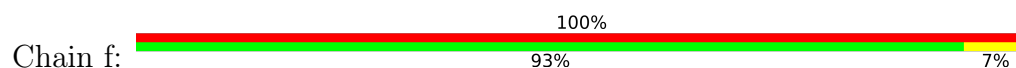




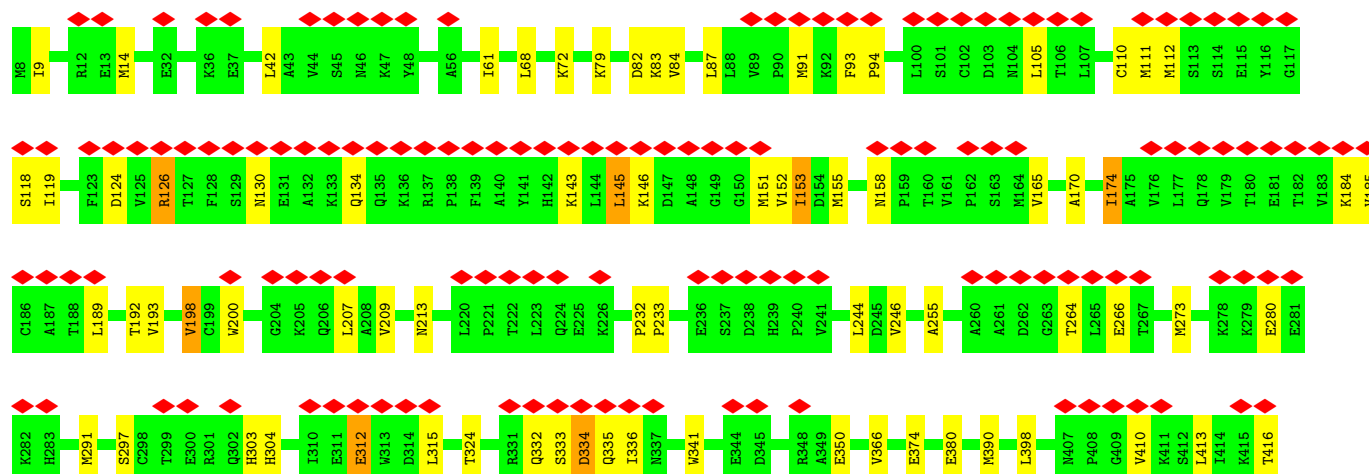
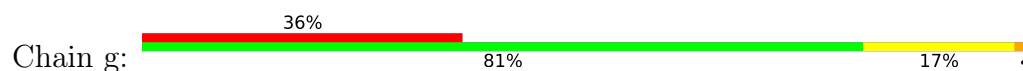
• Molecule 33: GLE1



• Molecule 34: NUP42

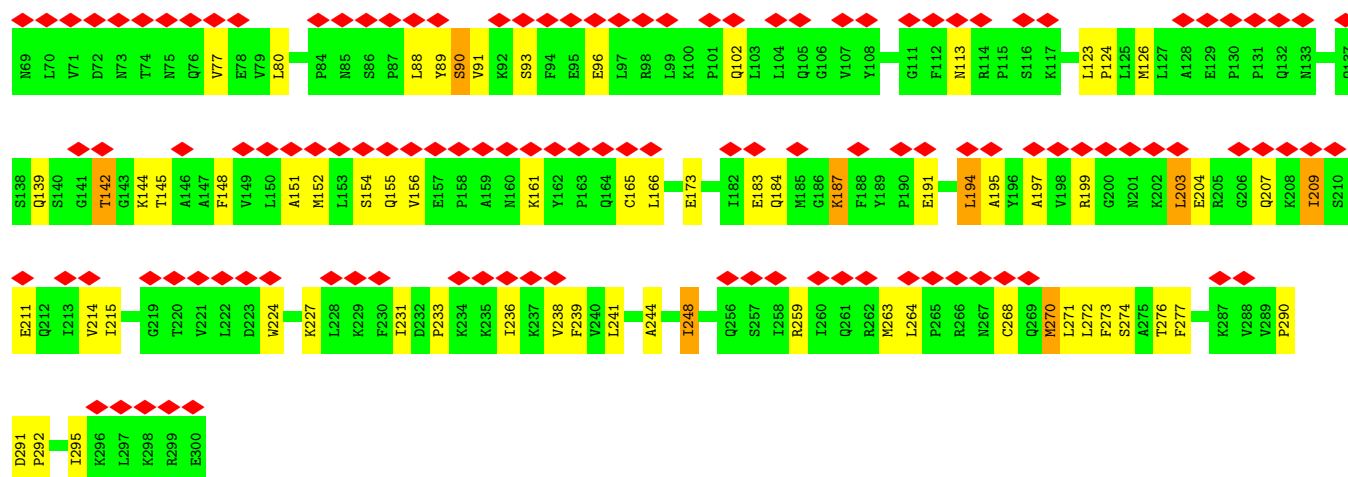
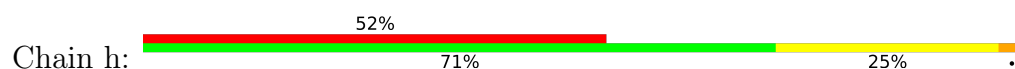


• Molecule 35: NUP214 NTD

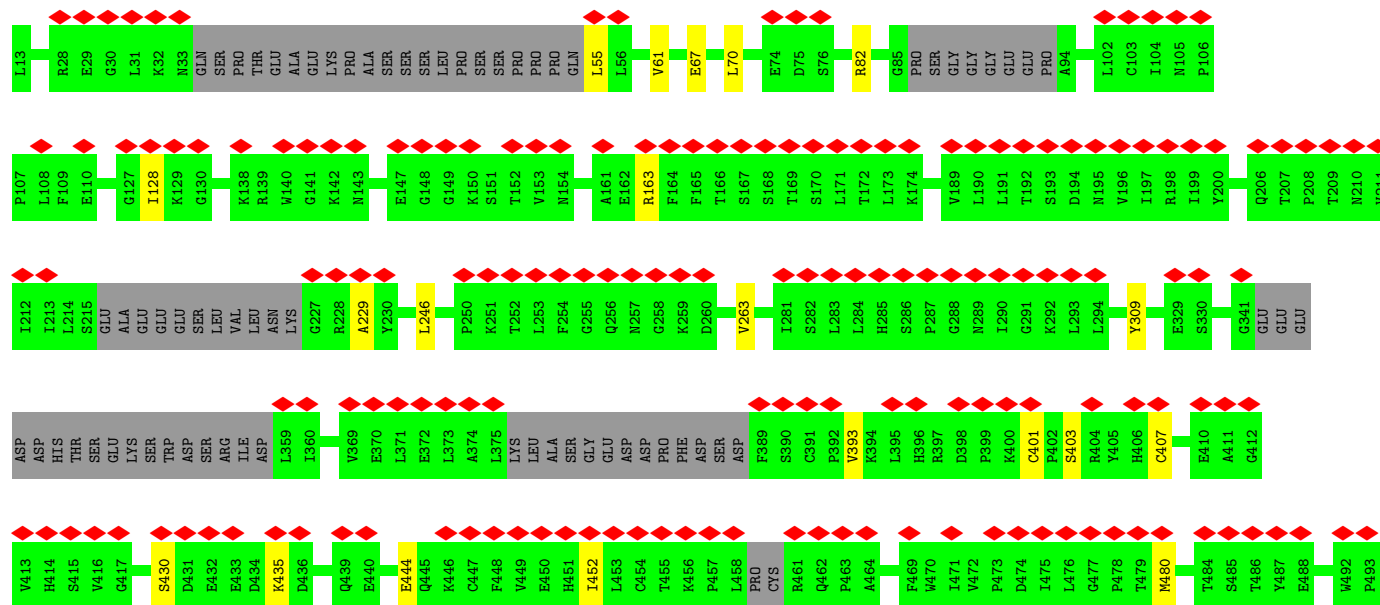
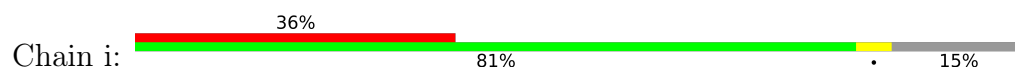




• Molecule 36: DDX19

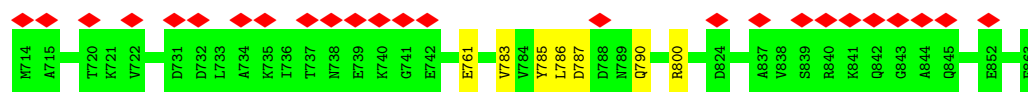


• Molecule 37: NUP88 NTD



• Molecule 38: NUP98 APD





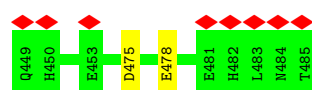
• Molecule 39: NUP62 CCS1

Chain k1: 81% 18%



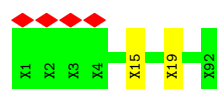
• Molecule 40: NUP62 CCS2

Chain k2: 22% 95% 5%



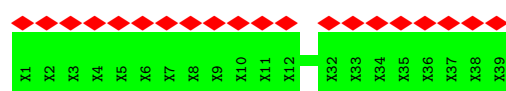
• Molecule 41: NUP214 CCS1

Chain l1: 98%



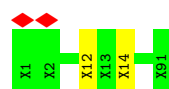
• Molecule 42: NUP214 CCS2

Chain l2: 51% 100%



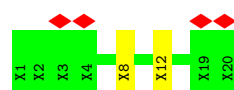
• Molecule 43: NUP88 CCS1

Chain m1: 98%



• Molecule 44: NUP88 CCS2

Chain m2: 20% 90% 10%



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	17368	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 ($e^-/\text{\AA}^2$)	110	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	82.185	Depositor
Minimum map value	-69.686	Depositor
Average map value	0.077	Depositor
Map value standard deviation	0.791	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	1941.1199, 1941.1199, 1941.1199	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.37, 3.37, 3.37	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	A1	0.21	2/9926 (0.0%)	0.36	0/13474
1	A3	0.21	2/9926 (0.0%)	0.36	0/13474
2	A2	0.34	0/10133	0.67	3/13731 (0.0%)
2	A4	0.34	0/10133	0.67	3/13731 (0.0%)
3	A5	0.18	2/10216 (0.0%)	0.33	0/13838
3	A6	0.19	2/10216 (0.0%)	0.33	0/13838
4	B1	0.18	0/112	0.52	0/149
4	B2	0.18	0/112	0.52	0/149
4	B3	0.18	0/112	0.51	0/149
4	B4	0.18	0/112	0.51	0/149
4	B5	0.19	0/112	0.51	0/149
4	B6	0.18	0/112	0.52	0/149
5	C1	0.28	0/140	0.40	0/188
5	C2	0.23	0/160	0.48	0/214
5	C3	0.28	0/140	0.40	0/188
5	C4	0.24	0/160	0.48	0/214
5	C5	0.28	0/140	0.40	0/188
5	C6	0.28	0/140	0.40	0/188
6	D1	0.17	0/5130	0.34	0/6930
6	D2	0.17	0/5130	0.34	0/6930
6	D3	0.17	0/5130	0.34	0/6930
6	D4	0.17	0/5130	0.35	0/6930
6	D5	0.16	0/5130	0.34	0/6930
6	D6	0.17	0/5130	0.35	0/6930
6	D7	0.17	0/5130	0.34	0/6930
7	E1	0.17	0/65	0.41	0/89
7	E2	0.19	0/65	0.41	0/89
7	E3	0.19	0/65	0.41	0/89
7	E4	0.17	0/65	0.41	0/89
7	E5	0.18	0/65	0.41	0/89
7	E6	0.18	0/65	0.41	0/89
7	E7	0.18	0/65	0.41	0/89
8	F1	0.10	0/13031	0.25	0/17717
8	F2	0.10	0/13031	0.25	0/17717

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	G1	0.11	0/445	0.33	0/600
9	G2	0.11	0/445	0.32	0/600
10	H1	0.12	0/95	0.23	0/128
10	H2	0.12	0/95	0.23	0/128
11	I1	0.08	0/12541	0.20	0/16980
11	I2	0.08	0/12541	0.20	0/16980
11	I3	0.08	0/12541	0.20	0/16980
11	I4	0.09	0/12541	0.20	0/16980
11	I5	0.08	0/12541	0.20	0/16980
12	J1	0.09	0/511	0.18	0/688
12	J2	0.09	0/511	0.18	0/688
12	J3	0.09	0/511	0.18	0/688
12	J4	0.09	0/511	0.18	0/688
12	J5	0.09	0/511	0.18	0/688
13	K1	0.08	0/75	0.23	0/101
13	K2	0.08	0/75	0.23	0/101
13	K3	0.08	0/75	0.23	0/101
13	K4	0.08	0/75	0.23	0/101
13	K5	0.08	0/75	0.23	0/101
14	L1	0.04	0/15	0.06	0/18
14	L2	0.04	0/15	0.07	0/18
14	L3	0.04	0/15	0.07	0/18
14	L4	0.04	0/15	0.07	0/18
14	L5	0.04	0/15	0.07	0/18
15	M1	0.30	0/1388	0.66	0/1866
15	M2	0.31	0/1388	0.66	0/1866
15	M3	0.30	0/1388	0.66	0/1866
15	M4	0.31	0/1388	0.66	0/1866
16	N1	0.31	0/1413	0.67	0/1898
16	N2	0.30	0/1413	0.67	0/1898
16	N3	0.31	0/1413	0.67	0/1898
16	N4	0.31	0/1413	0.67	0/1898
17	O1	0.34	0/2011	0.68	1/2715 (0.0%)
17	O2	0.34	0/2011	0.68	1/2715 (0.0%)
17	O3	0.34	0/2011	0.68	1/2715 (0.0%)
17	O4	0.34	0/2011	0.68	1/2715 (0.0%)
18	P1	0.49	0/910	0.62	0/1228
18	P2	0.49	0/910	0.62	0/1228
18	P3	0.49	0/910	0.62	0/1228
18	P4	0.49	0/910	0.62	0/1228
19	Q1	0.84	0/672	1.13	1/898 (0.1%)
19	Q2	0.82	0/629	1.17	2/842 (0.2%)
19	Q3	0.84	0/672	1.13	1/898 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	Q4	0.82	0/629	1.16	2/842 (0.2%)
20	R1	0.30	0/312	0.62	0/416
20	R2	0.30	0/312	0.63	0/416
20	R3	0.29	0/312	0.63	0/416
20	R4	0.29	0/312	0.63	0/416
21	S1	1.00	11/6081 (0.2%)	1.17	30/8304 (0.4%)
21	S2	1.00	10/6081 (0.2%)	1.17	30/8304 (0.4%)
21	S3	1.00	9/6081 (0.1%)	1.17	30/8304 (0.4%)
21	S4	1.00	11/6081 (0.2%)	1.17	30/8304 (0.4%)
22	T1	0.30	0/2037	0.71	0/2749
22	T2	0.30	0/2037	0.71	0/2749
22	T3	0.30	0/2037	0.71	0/2749
22	T4	0.31	0/2037	0.71	0/2749
23	U1	0.48	0/3472	0.99	5/4714 (0.1%)
23	U2	0.48	0/3472	0.99	5/4714 (0.1%)
23	U3	0.49	0/3472	0.99	5/4714 (0.1%)
23	U4	0.49	0/3472	0.99	5/4714 (0.1%)
24	V1	0.49	0/3860	1.01	15/5224 (0.3%)
24	V2	0.49	0/3860	1.01	15/5224 (0.3%)
24	V3	0.49	0/3860	1.01	15/5224 (0.3%)
24	V4	0.49	0/3860	1.01	15/5224 (0.3%)
25	W1	0.41	0/2220	0.90	4/3028 (0.1%)
25	W2	0.41	0/2220	0.90	4/3028 (0.1%)
25	W3	0.41	0/2220	0.90	4/3028 (0.1%)
25	W4	0.41	0/2220	0.89	4/3028 (0.1%)
26	X1	0.42	0/4602	0.99	17/6246 (0.3%)
26	X2	0.42	0/4602	0.99	16/6246 (0.3%)
26	X3	0.42	0/4602	1.00	15/6246 (0.2%)
26	X4	0.42	0/4602	0.99	14/6246 (0.2%)
27	Y1	0.35	0/2499	0.95	7/3388 (0.2%)
27	Y2	0.35	0/2499	0.95	7/3388 (0.2%)
27	Y3	0.35	0/2499	0.95	7/3388 (0.2%)
27	Y4	0.35	0/2499	0.95	7/3388 (0.2%)
28	Z1	0.41	0/6730	0.86	3/9158 (0.0%)
28	Z2	0.41	0/6730	0.86	3/9158 (0.0%)
28	Z3	0.41	0/6730	0.86	3/9158 (0.0%)
28	Z4	0.41	0/6730	0.86	3/9158 (0.0%)
29	a1	0.98	3/2723 (0.1%)	0.84	1/3715 (0.0%)
29	a2	0.98	2/2723 (0.1%)	0.84	1/3715 (0.0%)
29	a3	0.98	2/2723 (0.1%)	0.84	1/3715 (0.0%)
29	a4	0.98	3/2723 (0.1%)	0.84	1/3715 (0.0%)
30	b1	0.46	0/2702	1.01	13/3689 (0.4%)
30	b2	0.46	0/2702	1.01	13/3689 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	b3	0.46	0/2702	1.01	13/3689 (0.4%)
30	b4	0.46	0/2702	1.01	13/3689 (0.4%)
31	c1	0.12	0/6098	0.29	0/8246
31	c2	0.13	0/6098	0.29	0/8246
31	c3	0.12	0/6098	0.29	0/8246
31	c4	0.12	0/6098	0.29	0/8246
31	c5	0.13	0/6098	0.29	0/8246
32	d1	0.72	2/3722 (0.1%)	0.88	1/5056 (0.0%)
32	d2	0.72	2/3722 (0.1%)	0.88	1/5056 (0.0%)
33	e	0.14	0/2589	0.33	0/3493
34	f	0.18	0/370	0.44	0/501
35	g	0.85	0/3359	0.91	1/4572 (0.0%)
36	h	0.86	0/1871	0.99	2/2530 (0.1%)
37	i	0.13	0/3398	0.29	0/4629
38	j	0.11	0/1223	0.24	0/1653
39	k1	0.48	0/727	0.78	0/977
40	k2	0.42	0/310	0.70	0/414
All	All	0.42	63/417542 (0.0%)	0.68	395/566061 (0.1%)

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
1	A1	0	2
1	A3	0	2
2	A2	0	1
2	A4	0	1
23	U1	0	1
23	U2	0	1
23	U3	0	1
23	U4	0	1
24	V1	0	2
24	V2	0	2
24	V3	0	2
24	V4	0	2
28	Z1	0	2
28	Z2	0	2
28	Z3	0	2
28	Z4	0	2
30	b1	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
30	b2	0	3
30	b3	0	3
30	b4	0	3
All	All	0	38

The worst 5 of 63 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A1	891	GLY	C-N	9.04	1.50	1.34
1	A3	891	GLY	C-N	8.99	1.50	1.34
3	A6	891	GLY	C-N	8.42	1.47	1.33
3	A5	891	GLY	C-N	8.38	1.47	1.33
21	S4	214	ALA	C-O	-7.41	1.15	1.24

The worst 5 of 395 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	S2	131	SER	CA-C-N	10.39	130.68	119.87
21	S2	131	SER	C-N-CA	10.39	130.68	119.87
21	S4	131	SER	CA-C-N	10.39	130.68	119.87
21	S4	131	SER	C-N-CA	10.39	130.68	119.87
21	S3	131	SER	CA-C-N	10.33	130.62	119.87

There are no chirality outliers.

5 of 38 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	891	GLY	Mainchain
1	A1	976	LEU	Peptide
2	A2	699	SER	Peptide
1	A3	891	GLY	Mainchain
1	A3	976	LEU	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	A1	9730	0	9632	537	0
1	A3	9730	0	9631	480	0
2	A2	9946	0	9773	1900	0
2	A4	9946	0	9778	1962	0
3	A5	10030	0	9871	1562	0
3	A6	10030	0	9890	1569	0
4	B1	111	0	127	2	0
4	B2	111	0	127	25	0
4	B3	111	0	127	2	0
4	B4	111	0	127	25	0
4	B5	111	0	126	46	0
4	B6	111	0	124	60	0
5	C1	138	0	144	32	0
5	C2	157	0	158	272	0
5	C3	138	0	144	10	0
5	C4	157	0	155	374	0
5	C5	138	0	144	39	0
5	C6	138	0	144	23	0
6	D1	5034	0	5006	1053	0
6	D2	5034	0	5030	87	0
6	D3	5034	0	4979	1467	0
6	D4	5034	0	5030	94	0
6	D5	5034	0	5024	136	0
6	D6	5034	0	5030	57	0
6	D7	5034	0	5026	130	0
7	E1	63	0	65	2	0
7	E2	63	0	65	2	0
7	E3	63	0	65	2	0
7	E4	63	0	65	2	0
7	E5	63	0	65	2	0
7	E6	63	0	65	2	0
7	E7	63	0	65	2	0
8	F1	12779	0	12914	341	0
8	F2	12779	0	12917	119	0
9	G1	438	0	411	211	0
9	G2	438	0	412	68	0
10	H1	94	0	84	0	0
10	H2	94	0	84	0	0
11	I1	12307	0	12275	3132	0
11	I2	12307	0	12283	3065	0
11	I3	12307	0	12352	481	0
11	I4	12307	0	12359	367	0
11	I5	12307	0	12350	535	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	J1	504	0	486	52	0
12	J2	504	0	485	52	0
12	J3	504	0	487	30	0
12	J4	504	0	487	30	0
12	J5	504	0	487	30	0
13	K1	73	0	82	0	0
13	K2	73	0	82	0	0
13	K3	73	0	82	0	0
13	K4	73	0	82	0	0
13	K5	73	0	82	0	0
14	L1	15	0	11	0	0
14	L2	15	0	11	0	0
14	L3	15	0	11	0	0
14	L4	15	0	11	0	0
14	L5	15	0	11	0	0
15	M1	1372	0	1330	700	0
15	M2	1372	0	1361	56	0
15	M3	1372	0	1333	579	0
15	M4	1372	0	1363	5	0
16	N1	1401	0	1376	733	0
16	N2	1401	0	1398	63	0
16	N3	1401	0	1384	612	0
16	N4	1401	0	1398	10	0
17	O1	1971	0	1944	839	0
17	O2	1971	0	1961	388	0
17	O3	1971	0	1937	1111	0
17	O4	1971	0	1963	230	0
18	P1	900	0	910	52	0
18	P2	900	0	910	43	0
18	P3	900	0	908	148	0
18	P4	900	0	907	109	0
19	Q1	658	0	645	3	0
19	Q2	616	0	600	3	0
19	Q3	658	0	645	3	0
19	Q4	616	0	600	3	0
20	R1	311	0	314	406	0
20	R2	311	0	334	2	0
20	R3	311	0	314	436	0
20	R4	311	0	334	2	0
21	S1	6013	0	4982	184	0
21	S2	6013	0	4984	177	0
21	S3	6013	0	4984	177	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	S4	6013	0	4984	177	0
22	T1	1993	0	1976	271	0
22	T2	1993	0	1981	73	0
22	T3	1993	0	1981	75	0
22	T4	1993	0	1981	71	0
23	U1	3404	0	3360	639	0
23	U2	3404	0	3376	101	0
23	U3	3404	0	3378	79	0
23	U4	3404	0	3378	82	0
24	V1	3805	0	3499	216	0
24	V2	3805	0	3498	109	0
24	V3	3805	0	3499	114	0
24	V4	3805	0	3499	110	0
25	W1	2160	0	2096	66	0
25	W2	2160	0	2096	74	0
25	W3	2160	0	2096	63	0
25	W4	2160	0	2096	66	0
26	X1	4535	0	4064	390	0
26	X2	4535	0	4071	167	0
26	X3	4535	0	4063	357	0
26	X4	4535	0	4073	146	0
27	Y1	2438	0	2378	74	0
27	Y2	2438	0	2378	95	0
27	Y3	2438	0	2378	76	0
27	Y4	2438	0	2378	75	0
28	Z1	6622	0	5893	624	0
28	Z2	6622	0	5880	1133	0
28	Z3	6622	0	5888	739	0
28	Z4	6622	0	5872	1347	0
29	a1	2587	0	2488	38	0
29	a2	2587	0	2488	73	0
29	a3	2587	0	2488	36	0
29	a4	2587	0	2488	51	0
30	b1	2638	0	2573	610	0
30	b2	2638	0	2573	602	0
30	b3	2638	0	2573	609	0
30	b4	2638	0	2573	610	0
31	c1	5976	0	5991	349	0
31	c2	5976	0	5982	493	0
31	c3	5976	0	5996	133	0
31	c4	5976	0	5992	122	0
31	c5	5976	0	5996	272	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	d1	3629	0	3591	43	0
32	d2	3629	0	3577	152	0
33	e	2527	0	2537	198	0
34	f	363	0	388	2	0
35	g	3282	0	3310	76	0
36	h	1836	0	1893	52	0
37	i	3280	0	3320	34	0
38	j	1197	0	1198	12	0
39	k1	719	0	713	2	0
40	k2	308	0	302	0	0
41	l1	460	0	94	1	0
42	l2	195	0	41	0	0
43	m1	440	0	93	1	0
44	m2	100	0	22	1	0
All	All	410733	0	397629	22366	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 28.

The worst 5 of 22366 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)
27:Y2:41:ASP:HB3	29:a2:231[B]:HIS:CE1	1.17	1.69
28:Z1:524:VAL:HG13	30:b1:236:THR:CB	1.22	1.68
11:I3:1267:LEU:HD22	26:X1:497:ARG:CZ	1.20	1.68
22:T1:720:ILE:HG22	31:c5:31:TYR:CE2	1.29	1.67
3:A6:1369:ILE:HA	28:Z4:826:TYR:CB	1.23	1.67

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	
1	A1	1211/1316 (92%)	1172 (97%)	39 (3%)	0	100	100
1	A3	1211/1316 (92%)	1172 (97%)	39 (3%)	0	100	100
2	A2	1255/1328 (94%)	1183 (94%)	54 (4%)	18 (1%)	9	40
2	A4	1255/1328 (94%)	1182 (94%)	55 (4%)	18 (1%)	9	40
3	A5	1258/1330 (95%)	1221 (97%)	36 (3%)	1 (0%)	48	83
3	A6	1258/1330 (95%)	1221 (97%)	36 (3%)	1 (0%)	48	83
4	B1	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
4	B2	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
4	B3	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
4	B4	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
4	B5	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
4	B6	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
5	C1	15/19 (79%)	11 (73%)	4 (27%)	0	100	100
5	C2	17/19 (90%)	12 (71%)	5 (29%)	0	100	100
5	C3	15/19 (79%)	11 (73%)	4 (27%)	0	100	100
5	C4	17/19 (90%)	12 (71%)	5 (29%)	0	100	100
5	C5	15/19 (79%)	11 (73%)	4 (27%)	0	100	100
5	C6	15/19 (79%)	11 (73%)	4 (27%)	0	100	100
6	D1	615/644 (96%)	604 (98%)	11 (2%)	0	100	100
6	D2	615/644 (96%)	604 (98%)	11 (2%)	0	100	100
6	D3	615/644 (96%)	604 (98%)	11 (2%)	0	100	100
6	D4	615/644 (96%)	604 (98%)	11 (2%)	0	100	100
6	D5	615/644 (96%)	604 (98%)	11 (2%)	0	100	100
6	D6	615/644 (96%)	604 (98%)	11 (2%)	0	100	100
6	D7	615/644 (96%)	604 (98%)	11 (2%)	0	100	100
7	E1	6/8 (75%)	6 (100%)	0	0	100	100
7	E2	6/8 (75%)	6 (100%)	0	0	100	100
7	E3	6/8 (75%)	6 (100%)	0	0	100	100
7	E4	6/8 (75%)	6 (100%)	0	0	100	100
7	E5	6/8 (75%)	6 (100%)	0	0	100	100
7	E6	6/8 (75%)	6 (100%)	0	0	100	100
7	E7	6/8 (75%)	6 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	F1	1611/1858 (87%)	1589 (99%)	22 (1%)	0	100	100
8	F2	1611/1858 (87%)	1589 (99%)	22 (1%)	0	100	100
9	G1	51/53 (96%)	51 (100%)	0	0	100	100
9	G2	51/53 (96%)	51 (100%)	0	0	100	100
10	H1	11/13 (85%)	7 (64%)	4 (36%)	0	100	100
10	H2	11/13 (85%)	7 (64%)	4 (36%)	0	100	100
11	I1	1508/1756 (86%)	1491 (99%)	17 (1%)	0	100	100
11	I2	1508/1756 (86%)	1491 (99%)	17 (1%)	0	100	100
11	I3	1508/1756 (86%)	1491 (99%)	17 (1%)	0	100	100
11	I4	1508/1756 (86%)	1491 (99%)	17 (1%)	0	100	100
11	I5	1508/1756 (86%)	1491 (99%)	17 (1%)	0	100	100
12	J1	61/63 (97%)	61 (100%)	0	0	100	100
12	J2	61/63 (97%)	61 (100%)	0	0	100	100
12	J3	61/63 (97%)	61 (100%)	0	0	100	100
12	J4	61/63 (97%)	61 (100%)	0	0	100	100
12	J5	61/63 (97%)	61 (100%)	0	0	100	100
13	K1	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
13	K2	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
13	K3	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
13	K4	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
13	K5	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
15	M1	165/183 (90%)	158 (96%)	7 (4%)	0	100	100
15	M2	165/183 (90%)	158 (96%)	7 (4%)	0	100	100
15	M3	165/183 (90%)	158 (96%)	7 (4%)	0	100	100
15	M4	165/183 (90%)	158 (96%)	7 (4%)	0	100	100
16	N1	174/222 (78%)	172 (99%)	2 (1%)	0	100	100
16	N2	174/222 (78%)	172 (99%)	2 (1%)	0	100	100
16	N3	174/222 (78%)	172 (99%)	2 (1%)	0	100	100
16	N4	174/222 (78%)	172 (99%)	2 (1%)	0	100	100
17	O1	239/241 (99%)	213 (89%)	26 (11%)	0	100	100
17	O2	239/241 (99%)	212 (89%)	27 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	O3	239/241 (99%)	213 (89%)	26 (11%)	0	100	100
17	O4	239/241 (99%)	213 (89%)	26 (11%)	0	100	100
18	P1	115/116 (99%)	114 (99%)	1 (1%)	0	100	100
18	P2	115/116 (99%)	114 (99%)	1 (1%)	0	100	100
18	P3	115/116 (99%)	114 (99%)	1 (1%)	0	100	100
18	P4	115/116 (99%)	114 (99%)	1 (1%)	0	100	100
19	Q1	83/84 (99%)	81 (98%)	2 (2%)	0	100	100
19	Q2	79/84 (94%)	77 (98%)	2 (2%)	0	100	100
19	Q3	83/84 (99%)	81 (98%)	2 (2%)	0	100	100
19	Q4	79/84 (94%)	77 (98%)	2 (2%)	0	100	100
20	R1	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
20	R2	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
20	R3	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
20	R4	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
21	S1	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
21	S2	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
21	S3	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
21	S4	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
22	T1	243/258 (94%)	235 (97%)	8 (3%)	0	100	100
22	T2	243/258 (94%)	234 (96%)	9 (4%)	0	100	100
22	T3	243/258 (94%)	234 (96%)	9 (4%)	0	100	100
22	T4	243/258 (94%)	234 (96%)	9 (4%)	0	100	100
23	U1	413/436 (95%)	368 (89%)	34 (8%)	11 (3%)	4	25
23	U2	413/436 (95%)	367 (89%)	35 (8%)	11 (3%)	4	25
23	U3	413/436 (95%)	368 (89%)	34 (8%)	11 (3%)	4	25
23	U4	413/436 (95%)	368 (89%)	34 (8%)	11 (3%)	4	25
24	V1	491/621 (79%)	451 (92%)	30 (6%)	10 (2%)	6	31
24	V2	491/621 (79%)	451 (92%)	30 (6%)	10 (2%)	6	31
24	V3	491/621 (79%)	451 (92%)	30 (6%)	10 (2%)	6	31
24	V4	491/621 (79%)	451 (92%)	30 (6%)	10 (2%)	6	31
25	W1	270/286 (94%)	228 (84%)	36 (13%)	6 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	W2	270/286 (94%)	228 (84%)	36 (13%)	6 (2%)	5	29
25	W3	270/286 (94%)	228 (84%)	36 (13%)	6 (2%)	5	29
25	W4	270/286 (94%)	228 (84%)	36 (13%)	6 (2%)	5	29
26	X1	592/744 (80%)	531 (90%)	51 (9%)	10 (2%)	7	36
26	X2	592/744 (80%)	531 (90%)	51 (9%)	10 (2%)	7	36
26	X3	592/744 (80%)	532 (90%)	50 (8%)	10 (2%)	7	36
26	X4	592/744 (80%)	532 (90%)	50 (8%)	10 (2%)	7	36
27	Y1	303/349 (87%)	266 (88%)	31 (10%)	6 (2%)	6	31
27	Y2	303/349 (87%)	266 (88%)	31 (10%)	6 (2%)	6	31
27	Y3	303/349 (87%)	266 (88%)	31 (10%)	6 (2%)	6	31
27	Y4	303/349 (87%)	266 (88%)	31 (10%)	6 (2%)	6	31
28	Z1	858/1037 (83%)	798 (93%)	49 (6%)	11 (1%)	9	42
28	Z2	858/1037 (83%)	798 (93%)	49 (6%)	11 (1%)	9	42
28	Z3	858/1037 (83%)	798 (93%)	49 (6%)	11 (1%)	9	42
28	Z4	858/1037 (83%)	798 (93%)	49 (6%)	11 (1%)	9	42
29	a1	334/380 (88%)	325 (97%)	9 (3%)	0	100	100
29	a2	334/380 (88%)	325 (97%)	9 (3%)	0	100	100
29	a3	334/380 (88%)	325 (97%)	9 (3%)	0	100	100
29	a4	334/380 (88%)	325 (97%)	9 (3%)	0	100	100
30	b1	335/391 (86%)	315 (94%)	19 (6%)	1 (0%)	36	72
30	b2	335/391 (86%)	315 (94%)	19 (6%)	1 (0%)	36	72
30	b3	335/391 (86%)	315 (94%)	19 (6%)	1 (0%)	36	72
30	b4	335/391 (86%)	315 (94%)	19 (6%)	1 (0%)	36	72
31	c1	736/750 (98%)	727 (99%)	9 (1%)	0	100	100
31	c2	736/750 (98%)	727 (99%)	9 (1%)	0	100	100
31	c3	736/750 (98%)	727 (99%)	9 (1%)	0	100	100
31	c4	736/750 (98%)	727 (99%)	9 (1%)	0	100	100
31	c5	736/750 (98%)	727 (99%)	9 (1%)	0	100	100
32	d1	462/491 (94%)	446 (96%)	16 (4%)	0	100	100
32	d2	462/491 (94%)	446 (96%)	16 (4%)	0	100	100
33	e	309/316 (98%)	295 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	f	43/45 (96%)	41 (95%)	2 (5%)	0	100	100
35	g	419/421 (100%)	404 (96%)	14 (3%)	1 (0%)	43	78
36	h	230/232 (99%)	217 (94%)	10 (4%)	3 (1%)	9	42
37	i	408/481 (85%)	401 (98%)	7 (2%)	0	100	100
38	j	149/150 (99%)	144 (97%)	4 (3%)	1 (1%)	18	56
39	k1	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
40	k2	35/37 (95%)	35 (100%)	0	0	100	100
All	All	51567/58373 (88%)	49046 (95%)	2194 (4%)	327 (1%)	23	59

5 of 327 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A2	521	ASN
2	A2	1024	ASP
2	A2	1305	ALA
2	A2	1342	SER
2	A2	1345	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	
1	A1	1061/1111 (96%)	1048 (99%)	13 (1%)	63	75
1	A3	1061/1111 (96%)	1048 (99%)	13 (1%)	63	75
2	A2	1073/1107 (97%)	978 (91%)	95 (9%)	9	28
2	A4	1073/1107 (97%)	978 (91%)	95 (9%)	9	28
3	A5	1087/1118 (97%)	1064 (98%)	23 (2%)	47	65
3	A6	1087/1118 (97%)	1064 (98%)	23 (2%)	47	65
4	B1	12/12 (100%)	12 (100%)	0	100	100
4	B2	12/12 (100%)	12 (100%)	0	100	100
4	B3	12/12 (100%)	12 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B4	12/12 (100%)	12 (100%)	0	100	100
4	B5	12/12 (100%)	12 (100%)	0	100	100
4	B6	12/12 (100%)	12 (100%)	0	100	100
5	C1	17/19 (90%)	17 (100%)	0	100	100
5	C2	19/19 (100%)	18 (95%)	1 (5%)	20	41
5	C3	17/19 (90%)	17 (100%)	0	100	100
5	C4	19/19 (100%)	18 (95%)	1 (5%)	20	41
5	C5	17/19 (90%)	17 (100%)	0	100	100
5	C6	17/19 (90%)	17 (100%)	0	100	100
6	D1	554/575 (96%)	554 (100%)	0	100	100
6	D2	554/575 (96%)	554 (100%)	0	100	100
6	D3	554/575 (96%)	554 (100%)	0	100	100
6	D4	554/575 (96%)	554 (100%)	0	100	100
6	D5	554/575 (96%)	554 (100%)	0	100	100
6	D6	554/575 (96%)	554 (100%)	0	100	100
6	D7	554/575 (96%)	554 (100%)	0	100	100
7	E1	7/7 (100%)	7 (100%)	0	100	100
7	E2	7/7 (100%)	7 (100%)	0	100	100
7	E3	7/7 (100%)	7 (100%)	0	100	100
7	E4	7/7 (100%)	7 (100%)	0	100	100
7	E5	7/7 (100%)	7 (100%)	0	100	100
7	E6	7/7 (100%)	7 (100%)	0	100	100
7	E7	7/7 (100%)	7 (100%)	0	100	100
8	F1	1350/1512 (89%)	1350 (100%)	0	100	100
8	F2	1350/1512 (89%)	1350 (100%)	0	100	100
9	G1	47/47 (100%)	47 (100%)	0	100	100
9	G2	47/47 (100%)	47 (100%)	0	100	100
10	H1	10/10 (100%)	10 (100%)	0	100	100
10	H2	10/10 (100%)	10 (100%)	0	100	100
11	I1	1340/1509 (89%)	1339 (100%)	1 (0%)	88	89
11	I2	1340/1509 (89%)	1339 (100%)	1 (0%)	88	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	I3	1340/1509 (89%)	1339 (100%)	1 (0%)	88	89
11	I4	1340/1509 (89%)	1339 (100%)	1 (0%)	88	89
11	I5	1340/1509 (89%)	1339 (100%)	1 (0%)	88	89
12	J1	54/54 (100%)	54 (100%)	0	100	100
12	J2	54/54 (100%)	54 (100%)	0	100	100
12	J3	54/54 (100%)	54 (100%)	0	100	100
12	J4	54/54 (100%)	54 (100%)	0	100	100
12	J5	54/54 (100%)	54 (100%)	0	100	100
13	K1	9/9 (100%)	9 (100%)	0	100	100
13	K2	9/9 (100%)	9 (100%)	0	100	100
13	K3	9/9 (100%)	9 (100%)	0	100	100
13	K4	9/9 (100%)	9 (100%)	0	100	100
13	K5	9/9 (100%)	9 (100%)	0	100	100
14	L1	1/1 (100%)	1 (100%)	0	100	100
14	L2	1/1 (100%)	1 (100%)	0	100	100
14	L3	1/1 (100%)	1 (100%)	0	100	100
14	L4	1/1 (100%)	1 (100%)	0	100	100
14	L5	1/1 (100%)	1 (100%)	0	100	100
15	M1	146/154 (95%)	146 (100%)	0	100	100
15	M2	146/154 (95%)	146 (100%)	0	100	100
15	M3	146/154 (95%)	146 (100%)	0	100	100
15	M4	146/154 (95%)	146 (100%)	0	100	100
16	N1	150/173 (87%)	150 (100%)	0	100	100
16	N2	150/173 (87%)	150 (100%)	0	100	100
16	N3	150/173 (87%)	150 (100%)	0	100	100
16	N4	150/173 (87%)	150 (100%)	0	100	100
17	O1	213/213 (100%)	208 (98%)	5 (2%)	44	64
17	O2	213/213 (100%)	208 (98%)	5 (2%)	44	64
17	O3	213/213 (100%)	208 (98%)	5 (2%)	44	64
17	O4	213/213 (100%)	208 (98%)	5 (2%)	44	64
18	P1	101/100 (101%)	101 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	P2	101/100 (101%)	101 (100%)	0	100	100
18	P3	101/100 (101%)	101 (100%)	0	100	100
18	P4	101/100 (101%)	101 (100%)	0	100	100
19	Q1	70/69 (101%)	66 (94%)	4 (6%)	18	40
19	Q2	63/69 (91%)	62 (98%)	1 (2%)	55	70
19	Q3	70/69 (101%)	66 (94%)	4 (6%)	18	40
19	Q4	63/69 (91%)	62 (98%)	1 (2%)	55	70
20	R1	32/32 (100%)	32 (100%)	0	100	100
20	R2	32/32 (100%)	32 (100%)	0	100	100
20	R3	32/32 (100%)	32 (100%)	0	100	100
20	R4	32/32 (100%)	32 (100%)	0	100	100
21	S1	488/1013 (48%)	457 (94%)	31 (6%)	16	37
21	S2	488/1013 (48%)	457 (94%)	31 (6%)	16	37
21	S3	488/1013 (48%)	457 (94%)	31 (6%)	16	37
21	S4	488/1013 (48%)	457 (94%)	31 (6%)	16	37
22	T1	211/231 (91%)	205 (97%)	6 (3%)	38	60
22	T2	211/231 (91%)	205 (97%)	6 (3%)	38	60
22	T3	211/231 (91%)	205 (97%)	6 (3%)	38	60
22	T4	211/231 (91%)	205 (97%)	6 (3%)	38	60
23	U1	387/402 (96%)	363 (94%)	24 (6%)	16	38
23	U2	387/402 (96%)	363 (94%)	24 (6%)	16	38
23	U3	387/402 (96%)	363 (94%)	24 (6%)	16	38
23	U4	387/402 (96%)	363 (94%)	24 (6%)	16	38
24	V1	367/567 (65%)	321 (88%)	46 (12%)	4	16
24	V2	367/567 (65%)	321 (88%)	46 (12%)	4	16
24	V3	367/567 (65%)	321 (88%)	46 (12%)	4	16
24	V4	367/567 (65%)	321 (88%)	46 (12%)	4	16
25	W1	233/243 (96%)	223 (96%)	10 (4%)	26	47
25	W2	233/243 (96%)	223 (96%)	10 (4%)	26	47
25	W3	233/243 (96%)	223 (96%)	10 (4%)	26	47
25	W4	233/243 (96%)	223 (96%)	10 (4%)	26	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	X1	424/670 (63%)	408 (96%)	16 (4%)	29	50
26	X2	424/670 (63%)	408 (96%)	16 (4%)	29	50
26	X3	424/670 (63%)	408 (96%)	16 (4%)	29	50
26	X4	424/670 (63%)	408 (96%)	16 (4%)	29	50
27	Y1	269/305 (88%)	258 (96%)	11 (4%)	27	49
27	Y2	269/305 (88%)	258 (96%)	11 (4%)	27	49
27	Y3	269/305 (88%)	258 (96%)	11 (4%)	27	49
27	Y4	269/305 (88%)	258 (96%)	11 (4%)	27	49
28	Z1	639/972 (66%)	611 (96%)	28 (4%)	25	47
28	Z2	639/972 (66%)	611 (96%)	28 (4%)	25	47
28	Z3	639/972 (66%)	611 (96%)	28 (4%)	25	47
28	Z4	639/972 (66%)	611 (96%)	28 (4%)	25	47
29	a1	293/335 (88%)	289 (99%)	4 (1%)	59	72
29	a2	293/335 (88%)	289 (99%)	4 (1%)	59	72
29	a3	293/335 (88%)	289 (99%)	4 (1%)	59	72
29	a4	293/335 (88%)	289 (99%)	4 (1%)	59	72
30	b1	299/343 (87%)	278 (93%)	21 (7%)	14	35
30	b2	299/343 (87%)	278 (93%)	21 (7%)	14	35
30	b3	299/343 (87%)	278 (93%)	21 (7%)	14	35
30	b4	299/343 (87%)	278 (93%)	21 (7%)	14	35
31	c1	663/670 (99%)	663 (100%)	0	100	100
31	c2	663/670 (99%)	663 (100%)	0	100	100
31	c3	663/670 (99%)	663 (100%)	0	100	100
31	c4	663/670 (99%)	663 (100%)	0	100	100
31	c5	663/670 (99%)	663 (100%)	0	100	100
32	d1	406/418 (97%)	395 (97%)	11 (3%)	39	61
32	d2	406/418 (97%)	395 (97%)	11 (3%)	39	61
33	e	275/278 (99%)	271 (98%)	4 (2%)	57	72
34	f	43/43 (100%)	43 (100%)	0	100	100
35	g	373/373 (100%)	350 (94%)	23 (6%)	16	38
36	h	206/206 (100%)	190 (92%)	16 (8%)	11	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	i	372/425 (88%)	371 (100%)	1 (0%)	86	86
38	j	132/131 (101%)	132 (100%)	0	100	100
39	k1	82/82 (100%)	69 (84%)	13 (16%)	2	11
40	k2	33/33 (100%)	31 (94%)	2 (6%)	17	38
All	All	43298/50980 (85%)	42130 (97%)	1168 (3%)	40	61

5 of 1168 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	Z2	638	VAL
36	h	194	LEU
28	Z3	605	ILE
28	Z2	605	ILE
30	b2	258	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 620 such sidechains are listed below:

Mol	Chain	Res	Type
28	Z1	393	HIS
31	c3	303	HIS
28	Z2	410	ASN
28	Z1	350	ASN
29	a3	105	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
43	m1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	m1	14:UNK	C	18:UNK	N	8.65

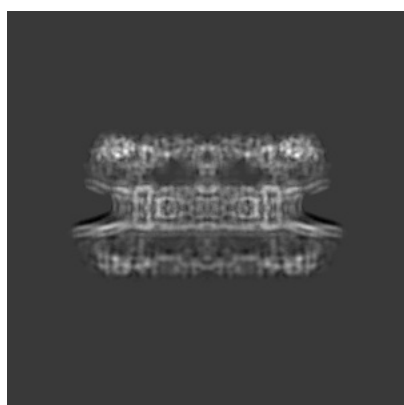
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14322. These allow visual inspection of the internal detail of the map and identification of artifacts.

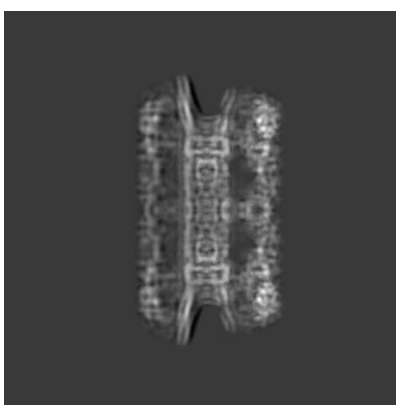
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

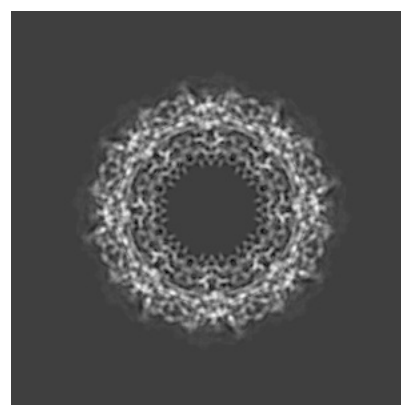
6.1.1 Primary map



X



Y

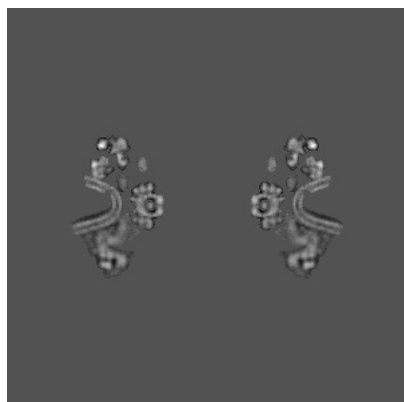


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 288



Y Index: 288



Z Index: 288

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

6.3 Largest variance slices [i](#)

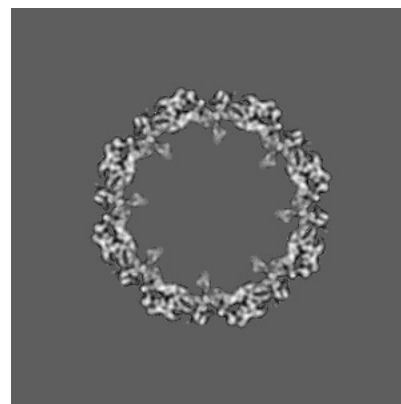
6.3.1 Primary map



X Index: 404



Y Index: 172

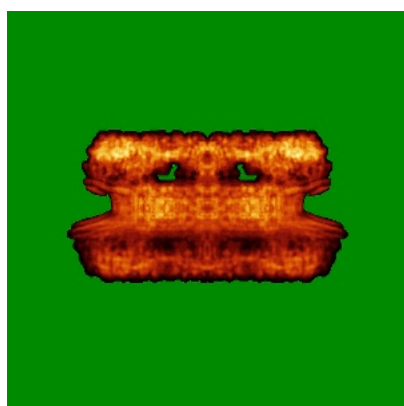


Z Index: 370

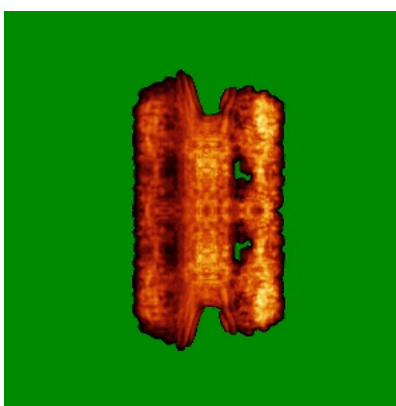
The images above show the largest variance slices of the map in three orthogonal directions.

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

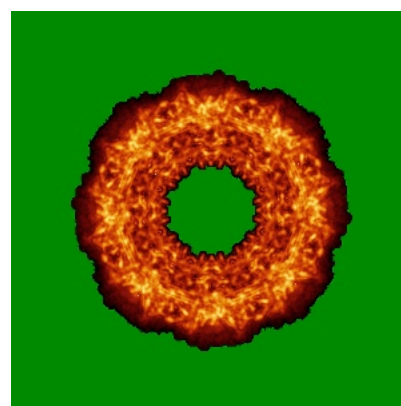
6.4.1 Primary map



X



Y

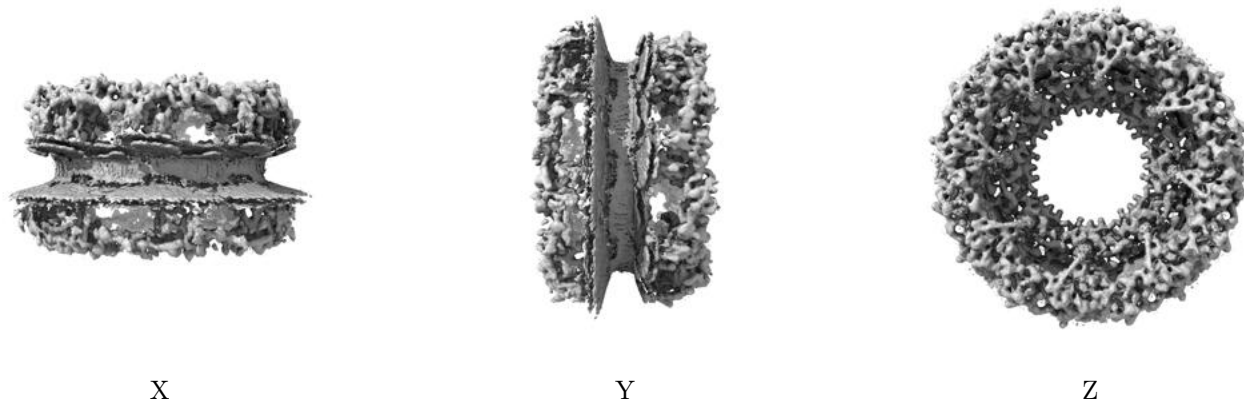


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

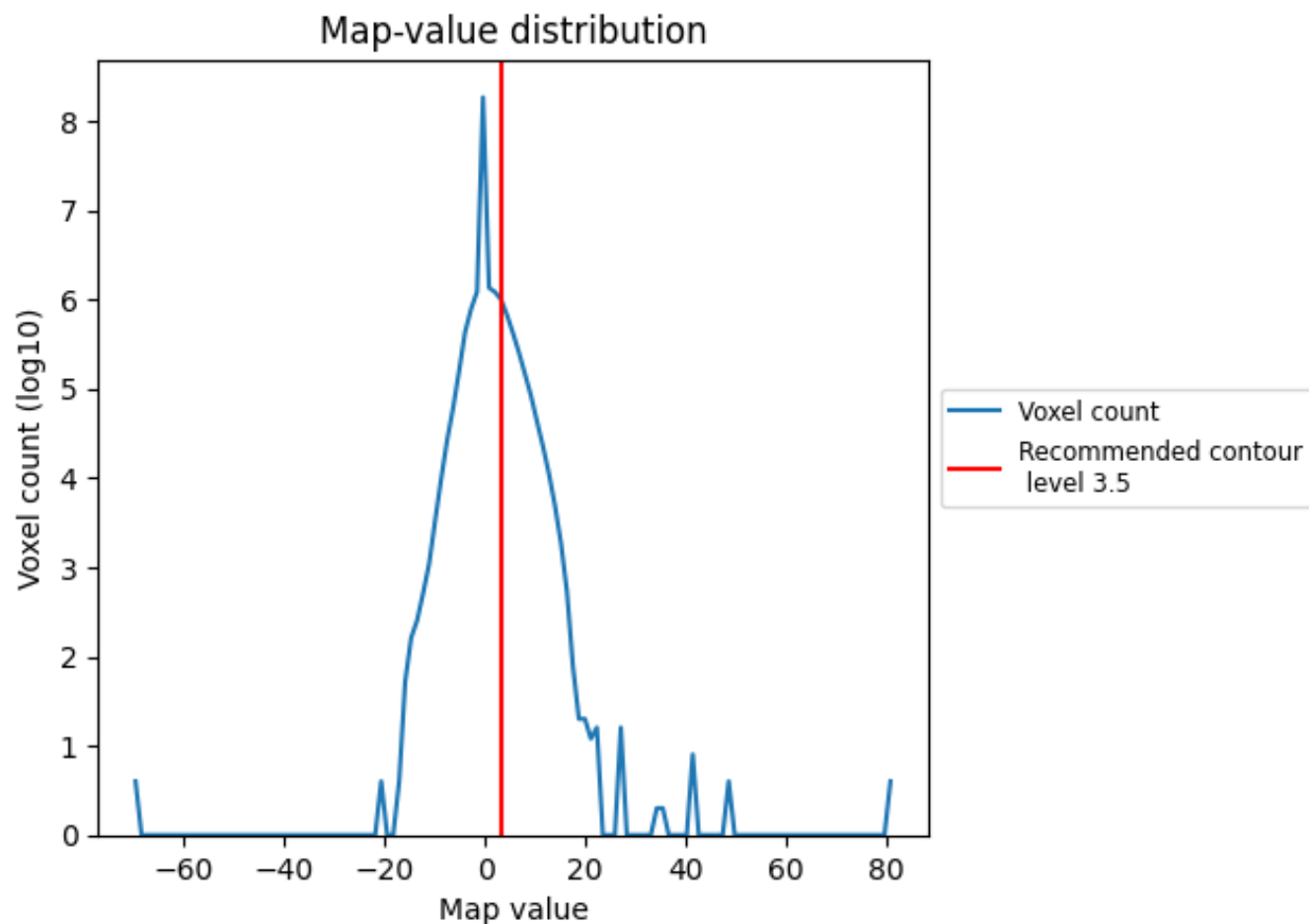
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

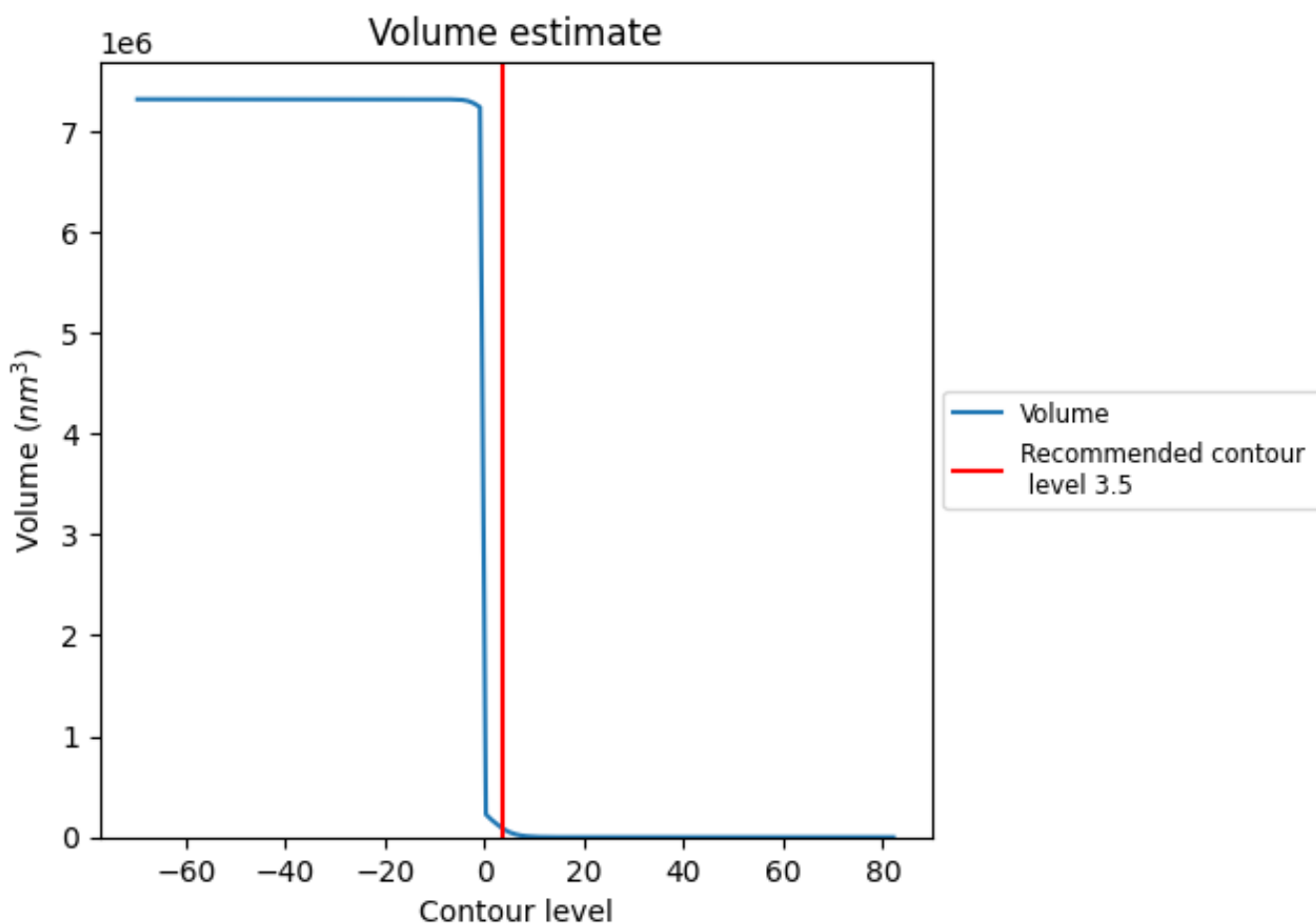
This section contains the results of statistical analysis of the map.

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.

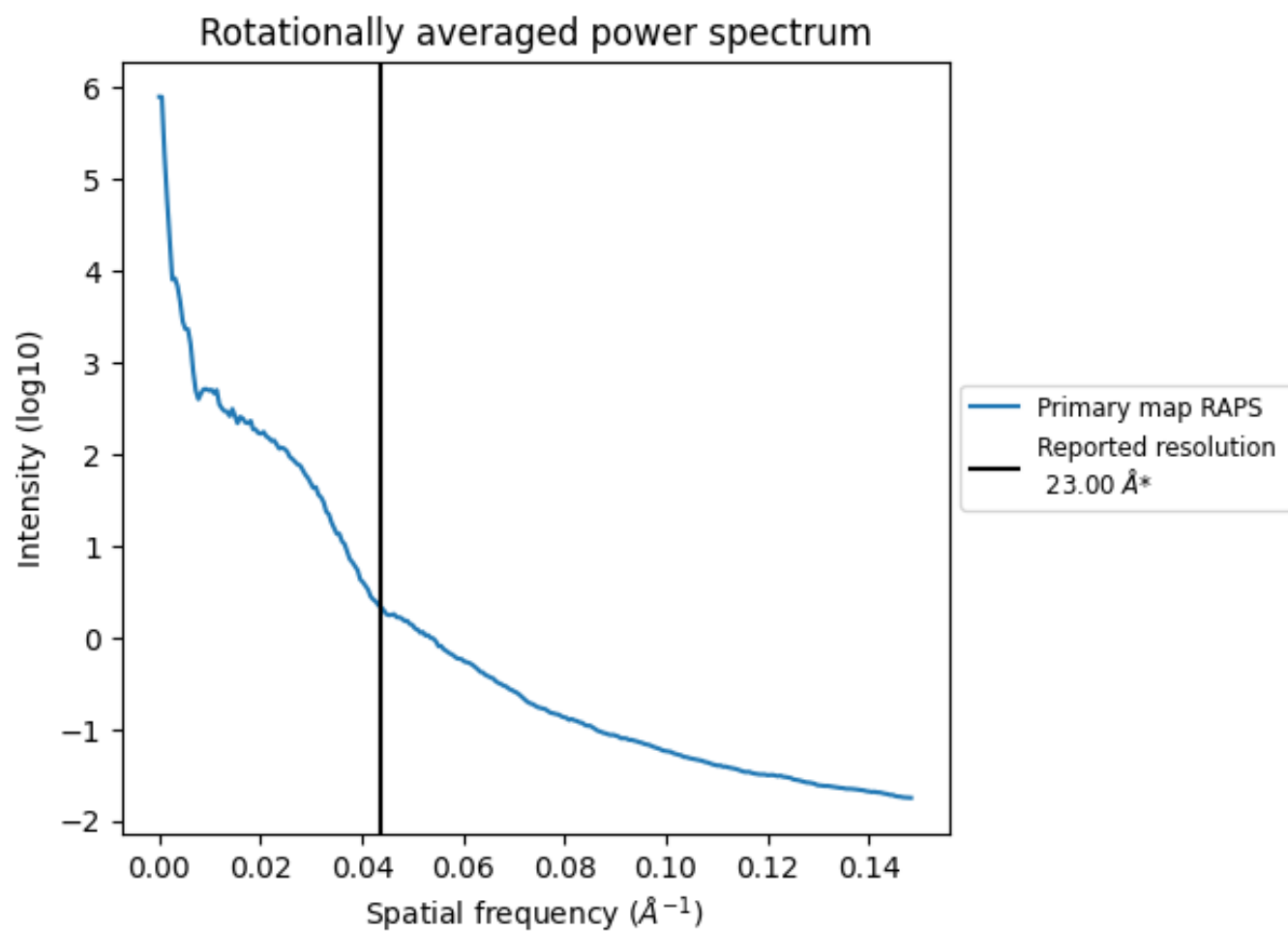
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 93549 nm^3 ; this corresponds to an approximate mass of 84505 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 0.043 Å⁻¹

8 Fourier-Shell correlation

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

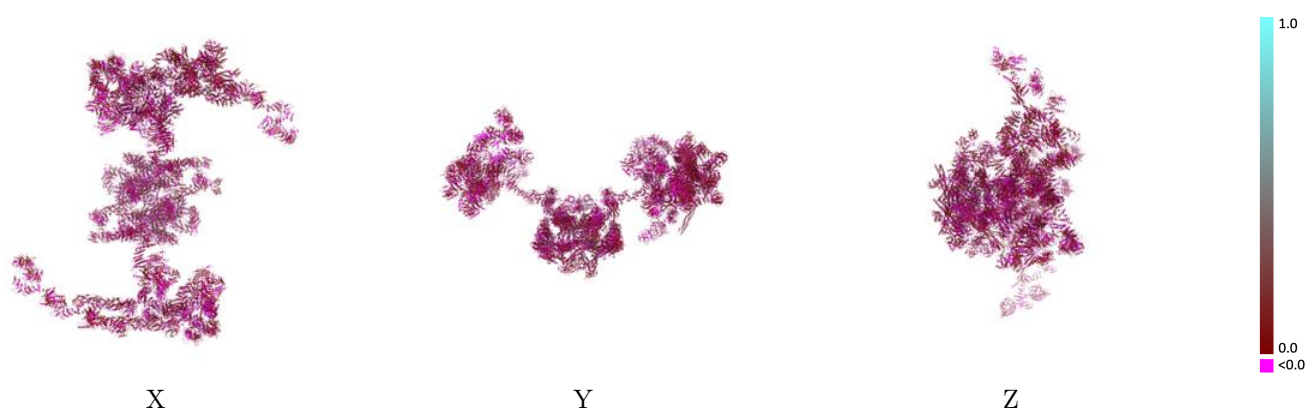
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14322 and PDB model 7TBL. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

This section was not generated.

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

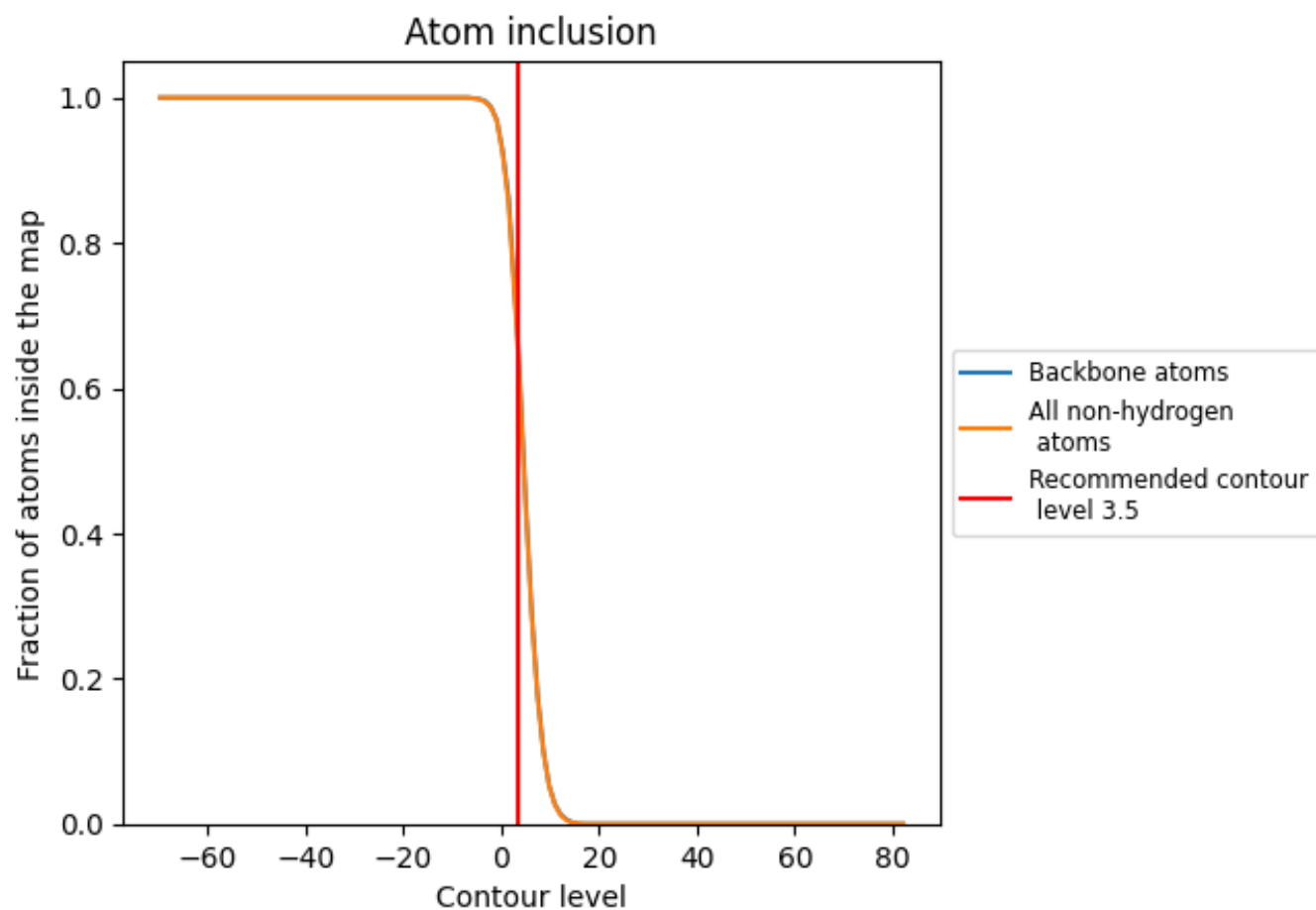


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 65% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6480	 0.0390
A1	 0.6920	 0.0430
A2	 0.3830	 0.0190
A3	 0.6640	 0.0450
A4	 0.4330	 0.0280
A5	 0.7310	 0.0460
A6	 0.4680	 0.0430
B1	 0.0000	 -0.0460
B2	 0.0090	 -0.0370
B3	 0.0000	 0.0070
B4	 0.0920	 0.0130
B5	 0.0830	 -0.0330
B6	 0.0090	 -0.0100
C1	 0.3530	 0.0440
C2	 0.5870	 0.0120
C3	 0.1180	 0.0320
C4	 0.3160	 0.0530
C5	 0.9560	 0.0560
C6	 0.4040	 0.0310
D1	 0.7760	 0.0550
D2	 0.7520	 0.0520
D3	 0.7200	 0.0420
D4	 0.4600	 0.0450
D5	 0.8300	 0.0650
D6	 0.7240	 0.0560
D7	 0.5020	 0.0260
E1	 0.6830	 0.0250
E2	 0.5000	 -0.0320
E3	 0.4000	 0.0590
E4	 0.2330	 0.0450
E5	 0.2830	 -0.0510
E6	 0.6500	 -0.0050
E7	 0.0170	 -0.0360
F1	 0.6830	 0.0410
F2	 0.5170	 0.0400



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Chain	Atom inclusion	Q-score
G1	 0.5250	 -0.0020
G2	 0.4170	 0.0080
H1	 0.4790	 0.0300
H2	 0.3080	 0.0530
I1	 0.6300	 0.0290
I2	 0.6240	 0.0350
I3	 0.7450	 0.0450
I4	 0.5340	 0.0360
I5	 0.7090	 0.0330
J1	 0.5580	 0.0060
J2	 0.6690	 0.0090
J3	 0.5800	 -0.0120
J4	 0.5440	 0.0240
J5	 0.7060	 0.0110
K1	 0.1250	 -0.0050
K2	 0.1250	 -0.0300
K3	 0.3750	 0.0010
K4	 0.0140	 -0.0060
K5	 0.3610	 -0.0030
L1	 0.0000	 -0.0780
L2	 0.0000	 -0.0120
L3	 0.2670	 -0.0820
L4	 0.0000	 -0.0270
L5	 0.8000	 0.0520
M1	 0.7070	 0.0410
M2	 0.7550	 0.0580
M3	 0.6620	 0.0360
M4	 0.7620	 0.0690
N1	 0.7250	 0.0480
N2	 0.7650	 0.0650
N3	 0.6890	 0.0400
N4	 0.7230	 0.0560
O1	 0.7140	 0.0490
O2	 0.6490	 0.0480
O3	 0.7230	 0.0560
O4	 0.6280	 0.0490
P1	 0.7620	 0.0680
P2	 0.7860	 0.0620
P3	 0.8120	 0.0670
P4	 0.7250	 0.0540
Q1	 0.9920	 0.0740
Q2	 0.9880	 0.0710

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Chain	Atom inclusion	Q-score
Q3	 0.9690	 0.0810
Q4	 0.9570	 0.0660
R1	 0.5880	 0.0100
R2	 0.6930	 0.0350
R3	 0.4690	 0.0400
R4	 0.5640	 0.0110
S1	 0.5780	 0.0370
S2	 0.6120	 0.0320
S3	 0.4210	 0.0320
S4	 0.4220	 0.0280
T1	 0.7540	 0.0460
T2	 0.7920	 0.0580
T3	 0.6970	 0.0410
T4	 0.7120	 0.0520
U1	 0.8160	 0.0490
U2	 0.8910	 0.0620
U3	 0.7920	 0.0490
U4	 0.7940	 0.0550
V1	 0.8960	 0.0590
V2	 0.8700	 0.0560
V3	 0.8050	 0.0570
V4	 0.7490	 0.0440
W1	 0.8670	 0.0440
W2	 0.7860	 0.0340
W3	 0.8110	 0.0500
W4	 0.6560	 0.0230
X1	 0.7950	 0.0330
X2	 0.8330	 0.0380
X3	 0.6600	 0.0310
X4	 0.5720	 0.0220
Y1	 0.6240	 0.0280
Y2	 0.6590	 0.0230
Y3	 0.5470	 0.0220
Y4	 0.5650	 0.0250
Z1	 0.6390	 0.0160
Z2	 0.7330	 0.0240
Z3	 0.4490	 0.0190
Z4	 0.5050	 0.0200
a1	 0.9260	 0.0530
a2	 0.7790	 0.0430
a3	 0.8270	 0.0500
a4	 0.7590	 0.0490

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Chain	Atom inclusion	Q-score
b1	 0.6780	 0.0320
b2	 0.5550	 0.0240
b3	 0.5230	 0.0100
b4	 0.5680	 0.0180
c1	 0.7960	 0.0590
c2	 0.8550	 0.0550
c3	 0.7240	 0.0480
c4	 0.7900	 0.0500
c5	 0.7210	 0.0480
d1	 0.2660	 0.0360
d2	 0.1980	 0.0310
e	 0.5520	 0.0290
f	 0.0000	 0.0190
g	 0.6070	 0.0380
h	 0.4410	 0.0230
i	 0.5580	 0.0190
j	 0.7870	 0.0570
k1	 0.9580	 0.0830
k2	 0.7060	 0.0520
l1	 0.9570	 0.1010
l2	 0.4970	 0.0670
m1	 0.9750	 0.0850
m2	 0.8100	 0.0940