



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:52 PM UTC

PDB ID : 7TBM / pdb_00007tbm
EMDB ID : EMD-11967
Title : Composite structure of the dilated human nuclear pore complex (NPC) generated with a 37Å in situ cryo-ET map of CD4+ T 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 : 37.00 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

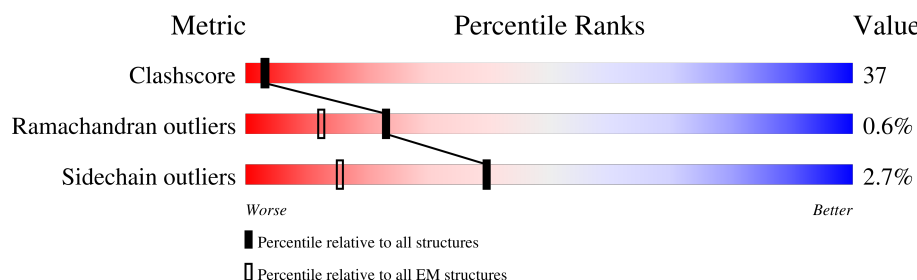
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 37.00 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	36% 86% 7% 6%
1	A3	1316	78% 78% 15% 6%
2	A2	1328	53% 72% 21% . .
2	A4	1328	86% 60% 32% . .
3	A5	1330	50% 80% 15% .
3	A6	1330	85% 60% 35% .
4	B1	14	79% 86% 14%

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Mol	Chain	Length	Quality of chain
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	
7	E4	8	
7	E5	8	
7	E6	8	
7	E7	8	

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Mol	Chain	Length	Quality of chain
8	F1	1858	67% 81% 7% 12%
8	F2	1858	84% 81% 7% 12%
9	G1	53	91% 68% 32%
9	G2	53	100% 85% 15%
10	H1	13	92% 100%
10	H2	13	100%
11	I1	1756	49% 68% 20% 12%
11	I2	1756	73% 67% 21% 12%
11	I3	1756	67% 79% 9% 12%
11	I4	1756	35% 79% 8% 12%
11	I5	1756	88% 77% 11% 12%
12	J1	63	70% 71% 29%
12	J2	63	65% 73% 27%
12	J3	63	46% 78% 22%
12	J4	63	76% 79% 21%
12	J5	63	100% 79% 21%
13	K1	9	100%
13	K2	9	100%
13	K3	9	100%
13	K4	9	100%
13	K5	9	100%
14	L1	2	100%
14	L2	2	100%
14	L3	2	100%
14	L4	2	100%

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Mol	Chain	Length	Quality of chain
14	L5	2	100% 100%
15	M1	183	41% 63% 29% 8%
15	M2	183	56% 86% 6% 8%
15	M3	183	77% 64% 28% 8%
15	M4	183	81% 90% . 8%
16	N1	222	36% 59% 22% 19%
16	N2	222	44% 73% 8% 19%
16	N3	222	55% 61% 20% 19%
16	N4	222	61% 78% . 19%
17	O1	241	54% 67% 32% .
17	O2	241	66% 78% 21% .
17	O3	241	82% 64% 34% .
17	O4	241	98% 80% 19% .
18	P1	116	80% 90% 10%
18	P2	116	100% 92% 8%
18	P3	116	100% 89% 11%
18	P4	116	100% 90% 10%
19	Q1	84	95% 92% 7% .
19	Q2	84	65% 86% 10% 5%
19	Q3	84	50% 92% 7% .
19	Q4	84	21% 86% 10% 5%
20	R1	40	72% 35% 65%
20	R2	40	55% 92% 8%
20	R3	40	60% 30% 70%
20	R4	40	62% 92% 8%

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Mol	Chain	Length	Quality of chain
21	S1	1156	 56% 19% • 22%
21	S2	1156	 57% 18% • 22%
21	S3	1156	 57% 18% • 22%
21	S4	1156	 58% 18% • 22%
22	T1	258	 55% 39% • •
22	T2	258	 59% 35% • •
22	T3	258	 59% 35% • •
22	T4	258	 60% 34% • •
23	U1	436	 60% 31% 5% •
23	U2	436	 55% 35% 6% •
23	U3	436	 68% 24% • •
23	U4	436	 68% 23% • •
24	V1	621	 56% 22% • • 18%
24	V2	621	 56% 21% • • 18%
24	V3	621	 57% 21% • • 18%
24	V4	621	 56% 21% • • 18%
25	W1	286	 65% 27% • •
25	W2	286	 64% 29% • •
25	W3	286	 67% 25% • •
25	W4	286	 61% 31% • •
26	X1	698	 64% 22% • 11%
26	X2	698	 57% 29% • 11%
26	X3	698	 65% 21% • 11%
26	X4	698	 65% 22% • 11%
27	Y1	346	 7% 58% 29% • 11%

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Mol	Chain	Length	Quality of chain
27	Y2	346	
27	Y3	346	
27	Y4	346	
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	385	
30	b2	385	
30	b3	385	
30	b4	385	
31	c1	750	
31	c2	750	
31	c3	750	
31	c4	750	
31	c5	750	
32	g	421	
33	h	232	
34	i	481	
35	j	150	
36	k1	85	

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Mol	Chain	Length	Quality of chain
37	k2	37	
38	l1	92	
39	l2	39	
40	m1	88	
41	m2	20	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 400581 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	418	Total	C	N	O	S	0	0
			3396	2174	555	655	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	743	Total	C	N	O	S	0	0
			5980	3802	1033	1117	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 NUP214 NTD.

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

- Molecule 33 is a protein called DDX19.

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

- Molecule 34 is a protein called NUP88 NTD.

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

- Molecule 35 is a protein called NUP98 APD.

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

- Molecule 36 is a protein called NUP62 CCS1.

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

- Molecule 37 is a protein called NUP62 CCS2.

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

- Molecule 38 is a protein called NUP214 CCS1.

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

- Molecule 39 is a protein called NUP214 CCS2.

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

- Molecule 40 is a protein called NUP88 CCS1.

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

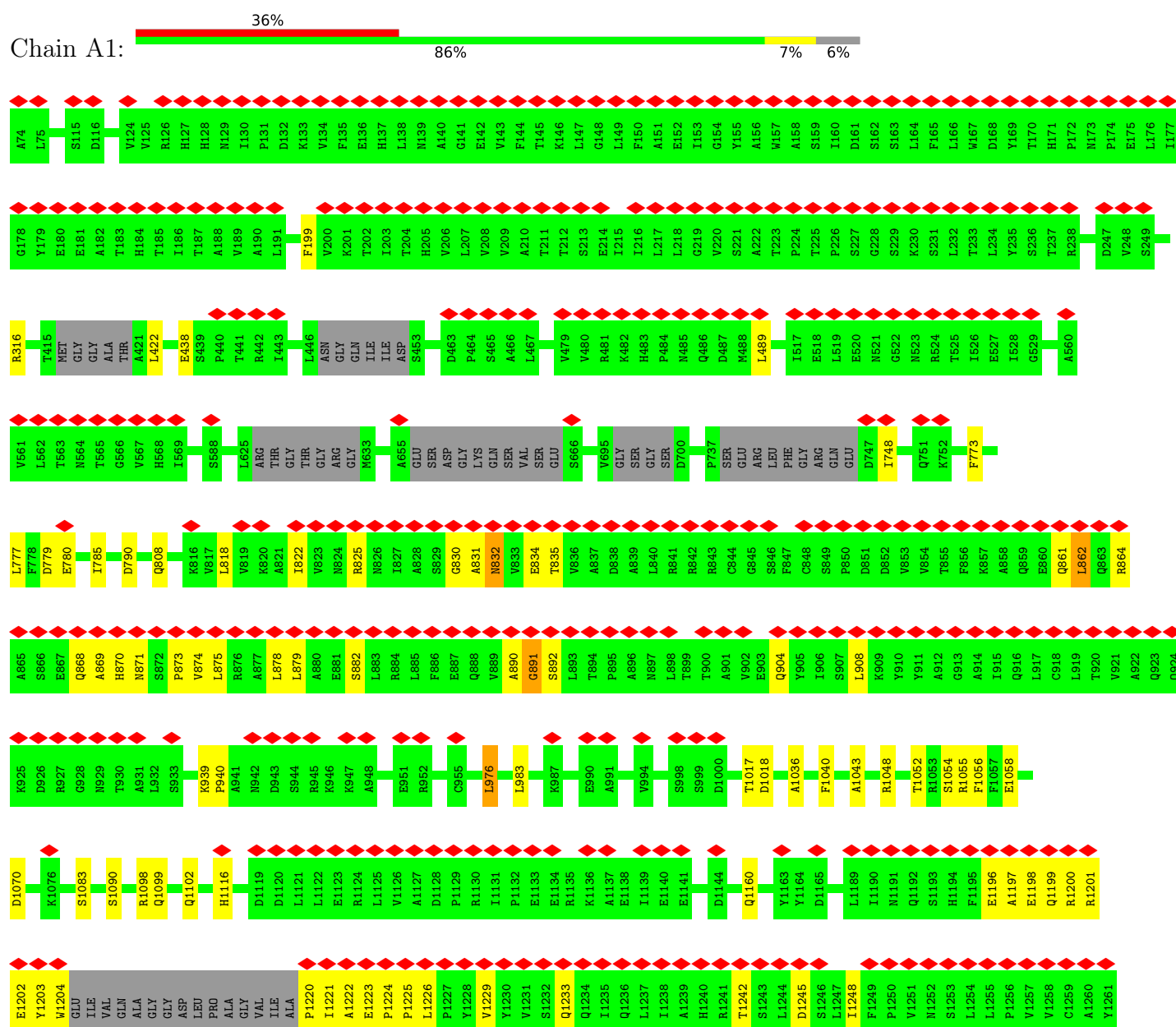
- Molecule 41 is a protein called NUP88 CCS2.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	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

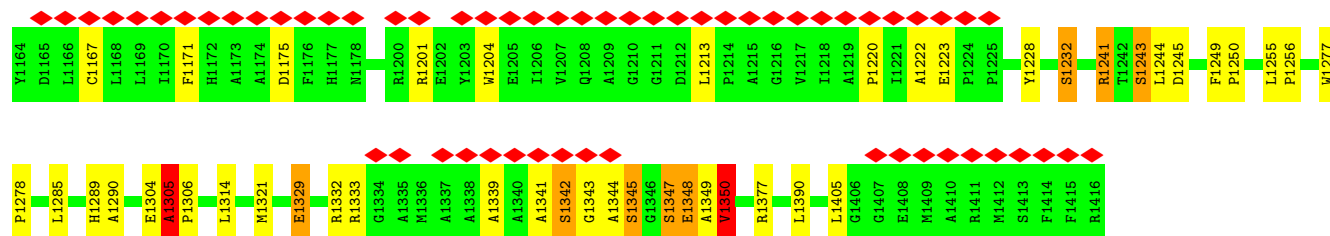




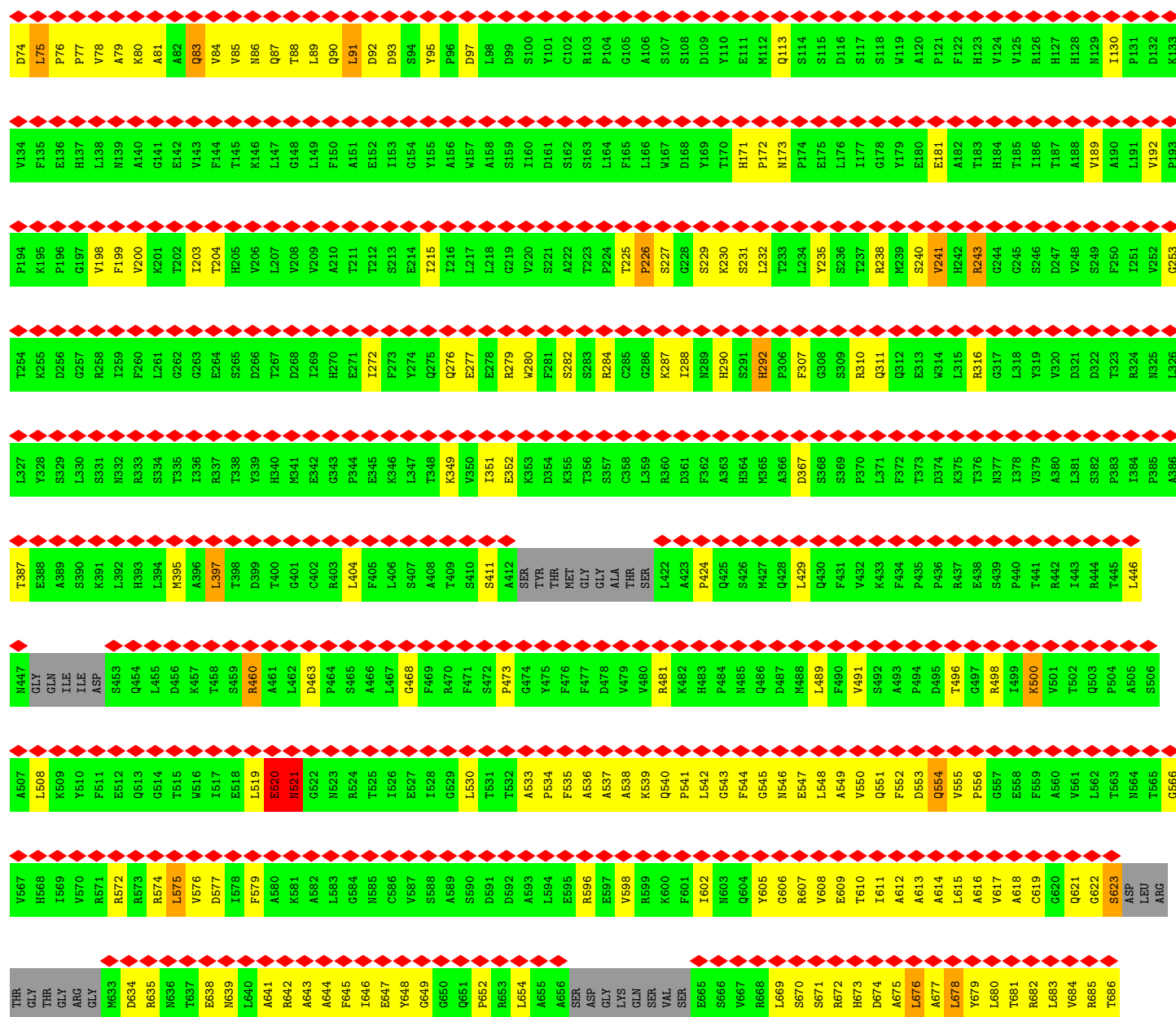
Chain A3:

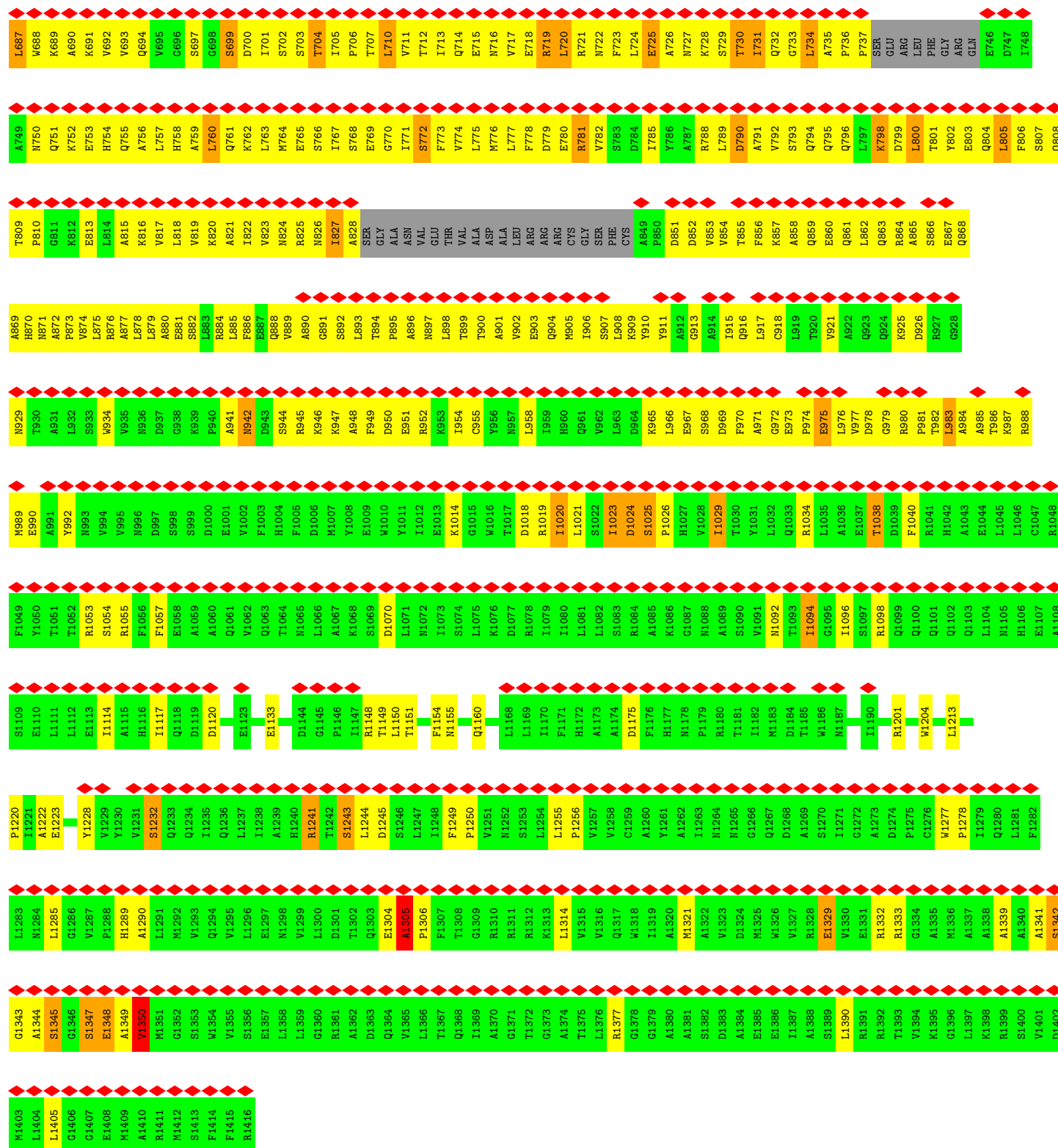


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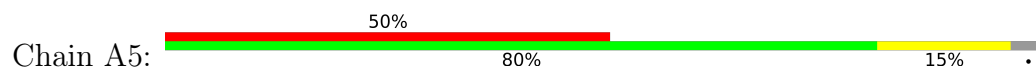


• Molecule 2: NUP155

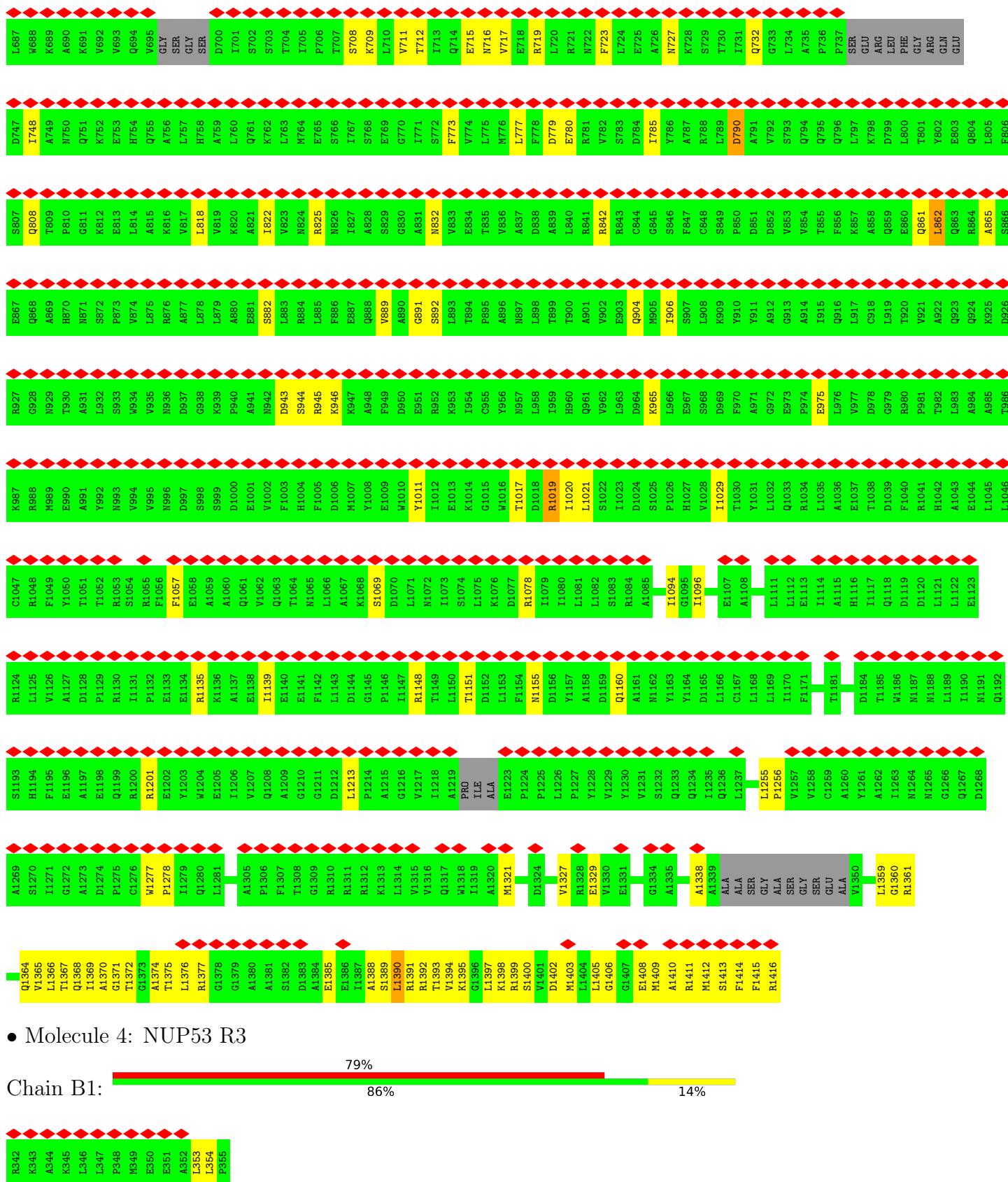




• Molecule 3: NUP155



G1286	V1287	P1288	H1289	A1290	L1291	M1292	V1293	Q1294	L1295	L1296	E1297	N1298	V1299	L1300	D1301	T1302	Q1303	E1304	A1305	F1306	P1307	T1308	G1309	R1310	K1311	R1312	K1313	L1314	V1315	V1316	Q1317	W1318	I1319	A1320	M1321	A1322	V1323	D1324	M1325	W1326	V1327	R1328	E1329	V1330	E1331	R1332	R1333	G1334	A1335	M1336	A1337	A1338	ALA	ALA	SER	GLY	ALA	SER	
L1226	P1227	Y1228	V1229	Y1230	V1231	S1232	Q1233	Q1234	I1235	Q1236	L1237	I1238	A1239	H1240	R1241	T1242	S1243	L1244	D1245	S1246	L1247	I1248	F1249	P1250	V1251	N1252	S1253	L1254	L1255	P1256	V1257	V1258	C1259	A1260	Y1261	A1262	I1263	N1264	N1265	G1266	Q1267	D1268	A1269	S1270	T1271	G1272	A1273	D1274	P1275	C1276	W1277	P1278	T1279	Q1280	L1281	F1282	L1283	N1284	L1285
L1166	C1167	L1168	L1169	I1170	F1171	H1172	A1173	A1174	D1175	F1176	H1177	M1178	P1179	R1180	T1181	I1182	M1183	L1184	T1185	W1186	M1187	L1188	L1189	I1190	M1191	Q1192	S1193	H1194	F1195	E1196	A1197	E1198	Q1199	R1200	R1201	E1202	Y1203	W1204	E1205	I1206	V1207	Q1208	A1209	G1210	G1211	D1212	L1213	P1214	A1215	G1216	V1217	L1218	A1219	PRO	ILE	ALA	E1223	P1224	P1225
S1090	V1091	N1092	T1093	I1094	G1095	I1096	S1097	R1098	Q1099	Q1100	Q1101	Q1102	L1104	N1105	H1106	E1107	A1108	S1109	E1110	L1111	L1112	E1113	I1114	A1115	H1116	I1117	Q1118	D1119	D1120	L1121	L1122	E1123	R1124	P1129	R1130	R1135	I1139	R1148	T1149	L1150	T1151	D1152	L1153	F1154	N1155	A1158	D1159	Q1160	A1161	N1162	Y1163	Y1164	D1165						
S1025	P1026	H1027	V1028	I1029	T1030	Y1031	L1032	Q1033	R1034	L1035	A1036	I1037	T1038	D1039	F1040	H1041	H1042	A1043	E1044	L1045	L1046	C1047	R1048	F1049	Y1050	T1051	T1052	R1053	S1054	R1055	F1056	F1057	E1058	A1059	A1060	Q1061	V1062	Q1063	T1064	M1065	L1066	A1067	K1068	S1069	K1076	D1077	R1078	I1079	I1080	L1081	A1161	S1083	R1084	Y1163	Y1164	K1086	N1088	A1089	
K965	L966	E967	S968	D969	F970	A971	G972	E973	P974	E975	L976	V977	D978	G979	R980	P981	T982	L983	A984	A985	T986	K987	R988	M989	E990	A991	Y992	N993	V994	V995	N996	D997	S998	S999	D1000	E1001	V1002	F1003	H1004	F1005	D1006	M1007	I1008	E1009	W1010	Y1011	I1012	E1013	G1014	G1015	W1016	T1017	L1018	R1019	I1020	L1021	S1022	I1023	D1024
M905	I906	S907	L908	K909	Y910	Y911	A912	G913	A914	I915	Q916	L917	C918	L919	T920	V921	A922	Q923	Q924	N925	D926	R927	G928	N929	T930	A931	L932	S933	W934	V935	N936	D937	G938	K939	P940	A941	N942	D943	S944	R945	K946	R947	A948	F949	E950	E951	R952	K953	I954	C955	Y956	N957	L958	I959	H960	Q961	V962	L963	D964
I827	N832	S849	P850	D851	D852	V853	W854	T855	F856	K857	A858	Q859	E860	Q861	L862	Q863	R864	A865	S866	E867	Q868	A869	H870	N871	S872	P873	W874	L875	A877	L878	L879	A880	E881	S882	L883	R884	L885	F886	E887	Q888	V889	A890	G891	S892	L893	T894	P895	A896	N897	L898	T899	T900	A901	V902	E903	Q904			
ASP	GLY	LYS	GLN	SER	VAL	SER	GLU	S666	S670	S671	R672	H673	D674	A675	L676	V695	GLY	SER	GLY	SER	D700	F737	SER	GLU	ARG	LEU	PHE	GLY	ARG	GLN	D747	I748	A759	L760	F773	L777	F778	D779	E780	I785	D790	Q808	L818	I822	R825	R826													
K581	A582	L583	G584	N585	S588	A589	E595	R596	E597	V598	R599	K600	F601	I602	N603	Q604	Y605	G606	R607	V608	E609	T610	I611	A612	A613	A614	L615	A616	V617	G622	S623	D624	L625	ARG	THR	GLY	THR	GLY	M633	D634	A644	F645	Y648	G649	G650	Q651	P652	R653	L654	A655	GLU	SER							
ASP	S453	Q454	S459	R460	A461	L462	D463	V480	R481	K482	H483	P484	N485	Q486	M488	L489	D495	T496	G497	R498	V501	F511	E512	Q513	G514	T515	W516	I517	E518	L519	E520	N521	G522	N523	R524	L562	T563	N564	T565	G566	V567	H568	I569	R573	R574	L575	V576	R577	I578	F579	A580								
T170	H171	P172	N173	P174	E175	L176	I177	G178	Y179	E180	I186	T187	A188	V189	F199	V220	D487	A222	P226	S227	G228	S229	L232	T233	L234	Y235	R316	T415	MET	GLY	GLY	ALA	THR	A421	L422	P436	R437	E438	S439	P440	T441	R442	I443	R444	T445	L446	ASN	GLY	GLN	ILE	ILE								
D74	D109	Y110	Y111	Y112	Q113	S114	S115	D116	S117	S118	W119	A120	P121	F122	H123	V124	V125	R126	H127	H128	N129	I130	P131	D132	K133	V134	F135	E136	H137	N138	N139	A140	G141	E142	V143	F144	T145	K146	L147	F150	I153	A156	W157	A158	S159	I160	D161	S162	S163	L164	F165	L166	W167	D168	Y169				

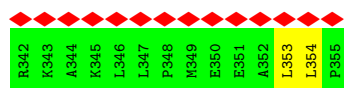


Chain B2:  50% 50%



● Molecule 4: NUP53 R3

Chain B3:  100%
86% 14%



● Molecule 4: NUP53 R3

Chain B4:  100%
50% 50%



● Molecule 4: NUP53 R3

Chain B5:  64% 36%



● Molecule 4: NUP53 R3

Chain B6:  100%
100%



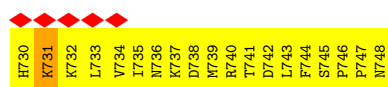
● Molecule 5: NUP98 R3

Chain C1:  84% 5% 11%

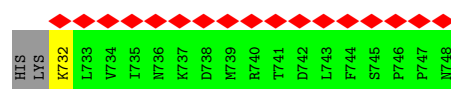
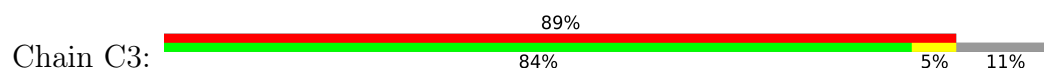


● Molecule 5: NUP98 R3

Chain C2:  26% 95% 5%



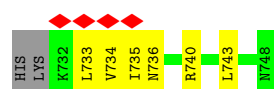
● Molecule 5: NUP98 R3



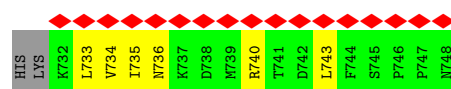
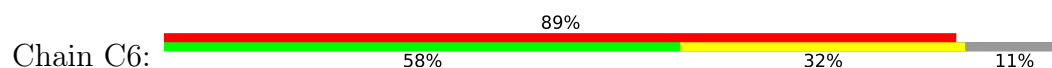
• Molecule 5: NUP98 R3



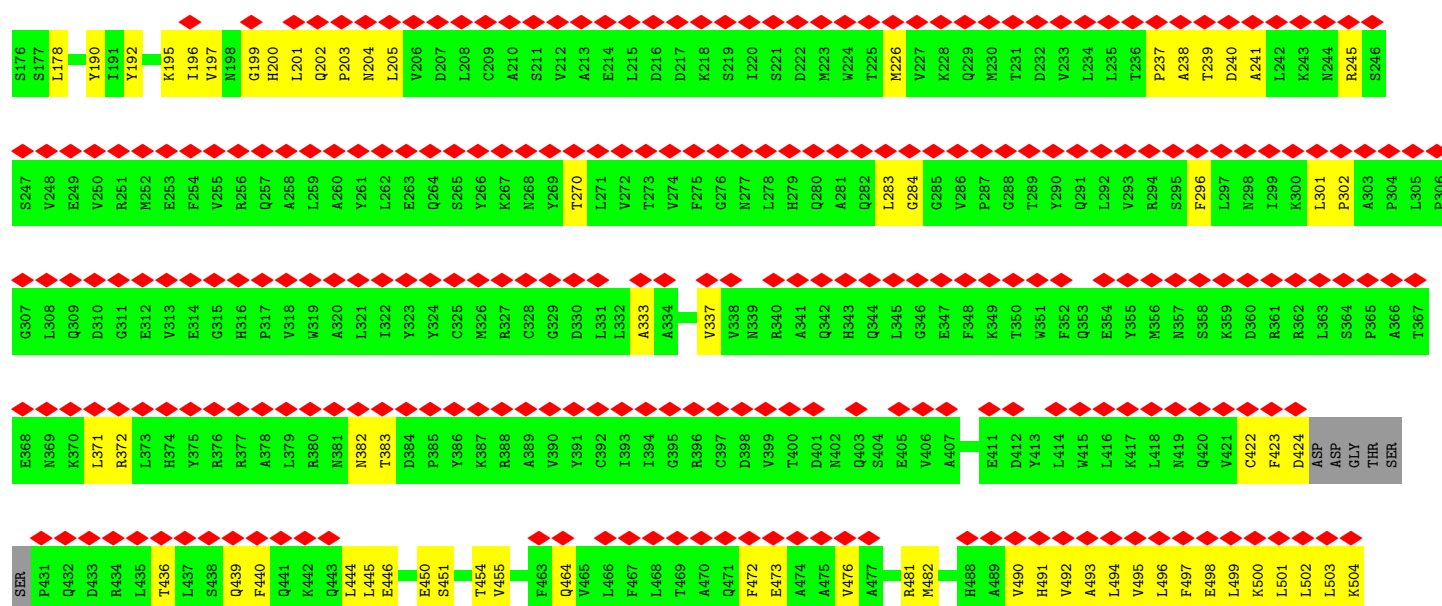
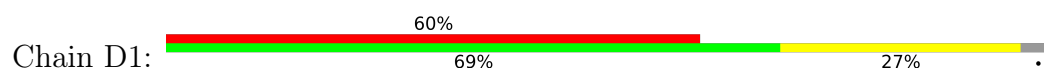
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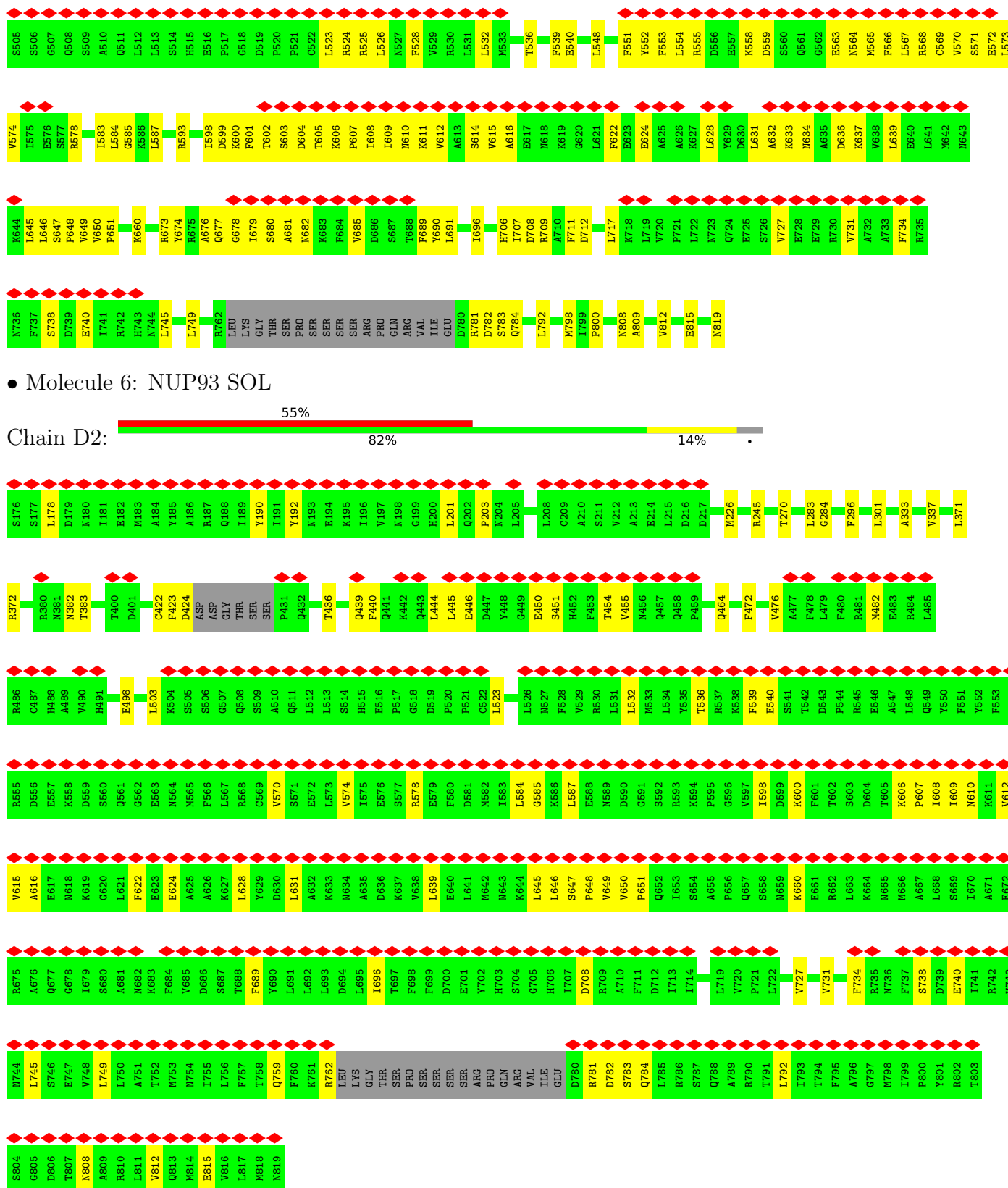


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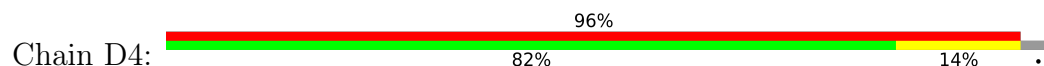
• Molecule 6: NUP93 SOL



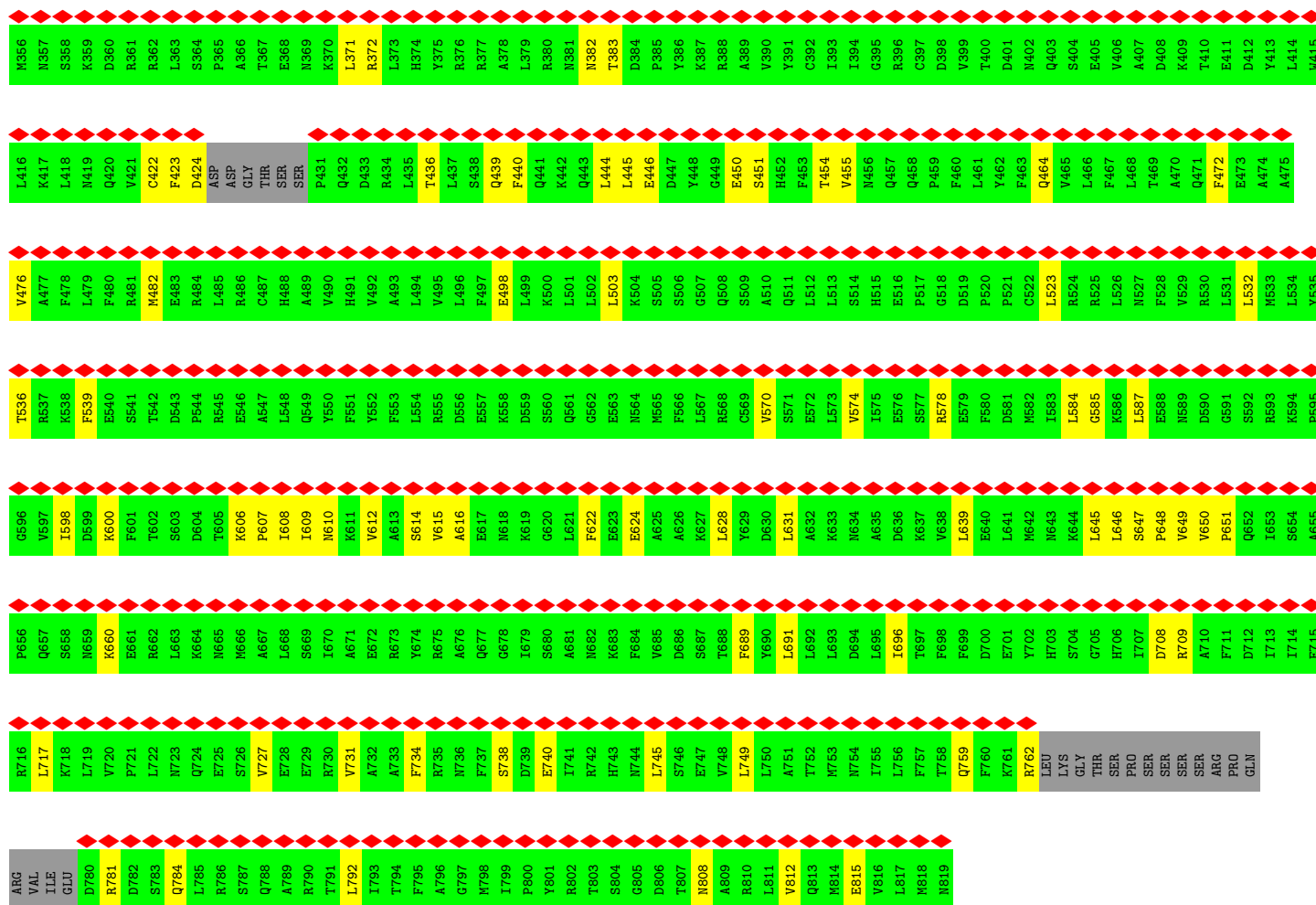


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R716	L717	K718	L719	V720	P721	L722	N723	Q724	E725	S726	V727	E728	R729	R730	V731	A732	A733	F734	R735	N736	F737	G738	S739	E740	I741	R742	H743	N744	L745	S746	E747	V748	L749	L750	A751	T752	M753	N754	I755	L756	F757	T758	Q759	F760	K761	R762	LEU	LYS	GLY	THR	SER	PRO	SER	SER	ARG	ARG	GLN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
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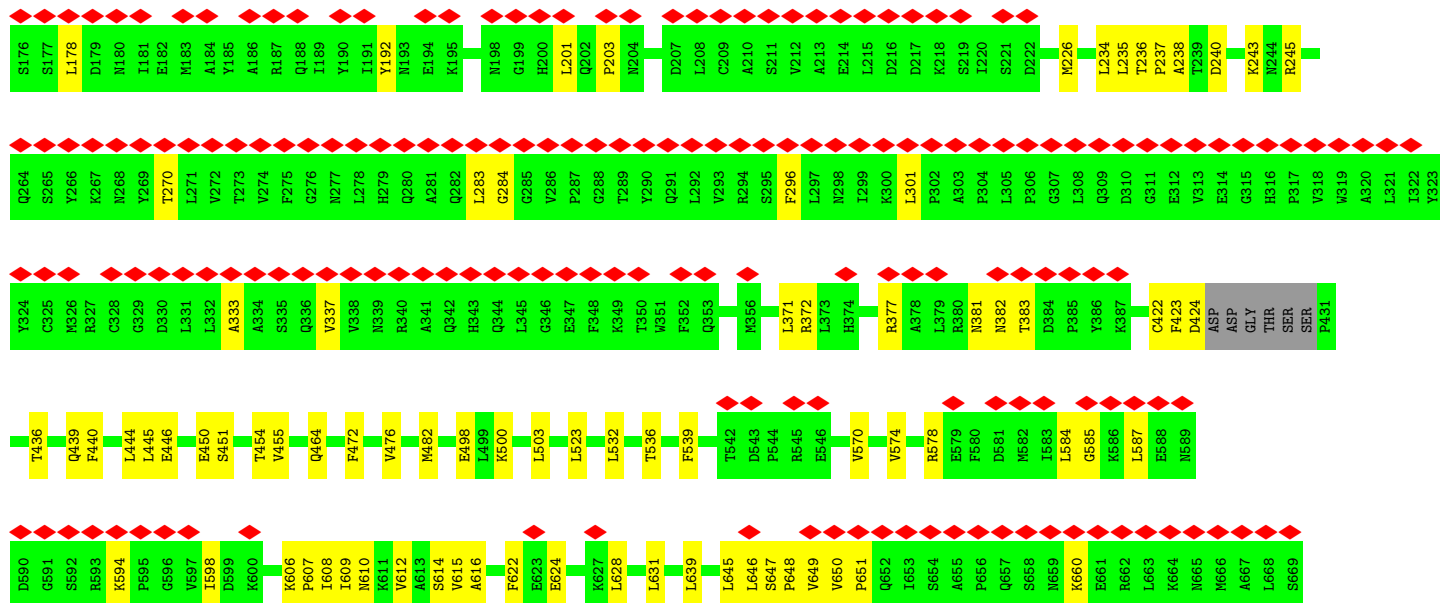
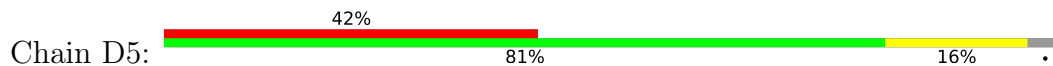
● Molecule 6: NUP93 SOL



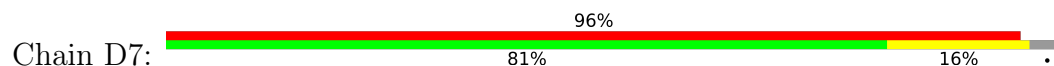
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T236	P237	A238	T239	D240	A241	L242	K243	N244	R245	S246	S247	V248	Q249	V250	R251	M252	E253	F254	V255	R256	Q257	A258	L259	A260	Y261	L262	E263	Q264	S265	Y266	K267	N268	Y269	T270	L271	V272	T273	V274	F275	G276	N277	L278	H279	Q280	A281	S282	L283	G284	C285	V286	P287	G288	T289	Y290	Q291	L292	V293	R294	S295	
S176	S177	L178	D179	N180	I181	E182	M183	A184	Y185	A186	R187	Q188	I189	Y190	I191	Y192	N193	E194	K195	I196	V197	N198	G199	H200	L201	Q202	P203	N204	L205	V206	D207	L208	C209	A210	S211	V212	A213	E214	L215	D216	D217	K218	S219	I220	S221	D222	M223	W224	T225	M226	V227	K228	Q229	M230	T231	D232	L234	L235		



• Molecule 6: NUP93 SOL

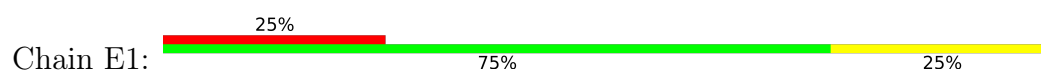


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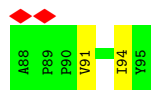
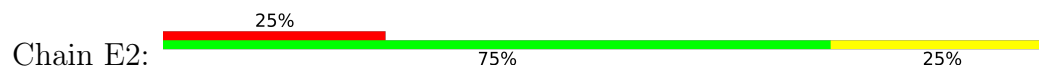
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V720	F721	L722	L663	K664	N665	M666	V727	E728	S669	R730	A671	E672	K673	V674	R735	M736	F737	S738	D739	E740	T741	R742	K683	M744	L745	S746	E747	V748	F689	L749	L750	A751	T752	M753	D694	L695	L696	T697	T758	Q759	F760	K761	R762																														
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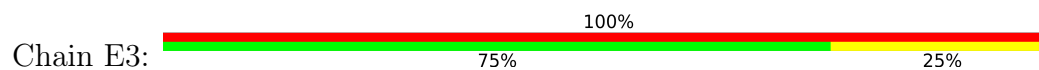


A88	V91	I94	Y95
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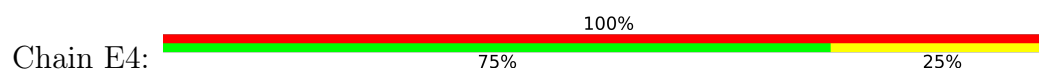
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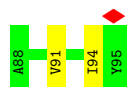
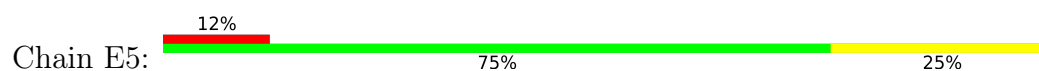
• Molecule 7: NUP53 R2



• Molecule 7: NUP53 R2



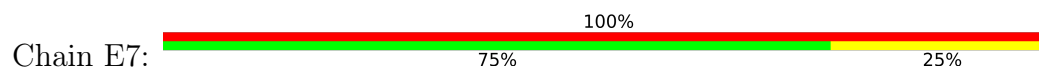
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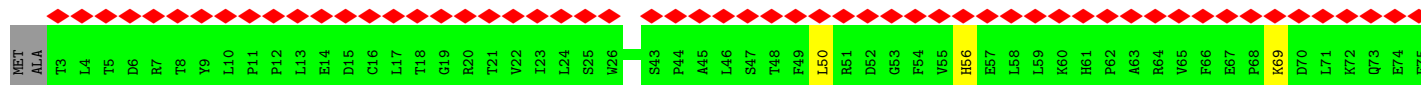
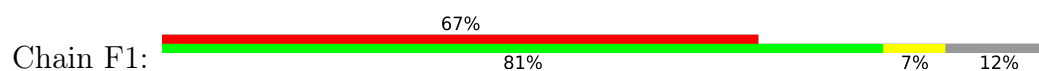
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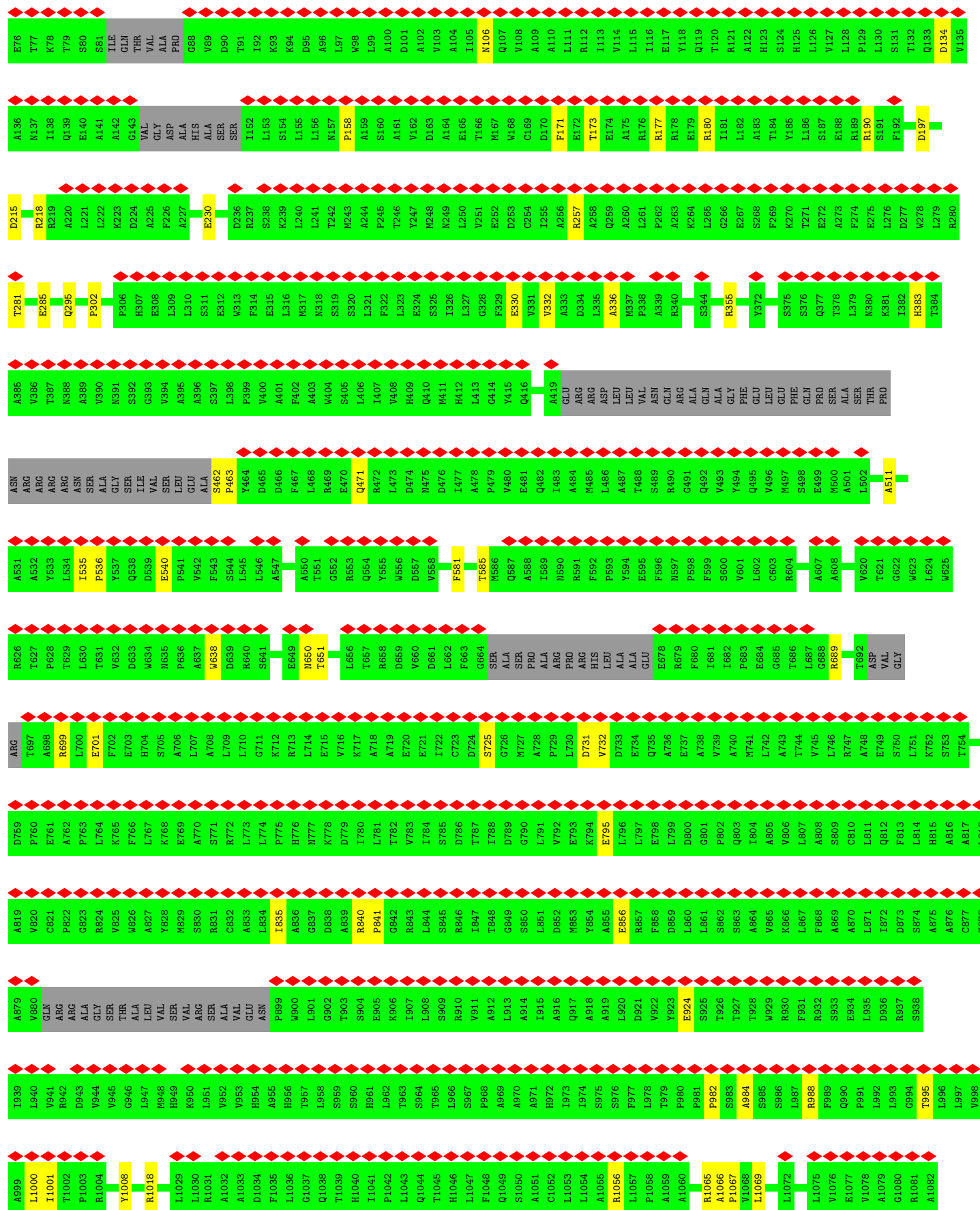


• Molecule 7: NUP53 R2



• Molecule 8: NUP188

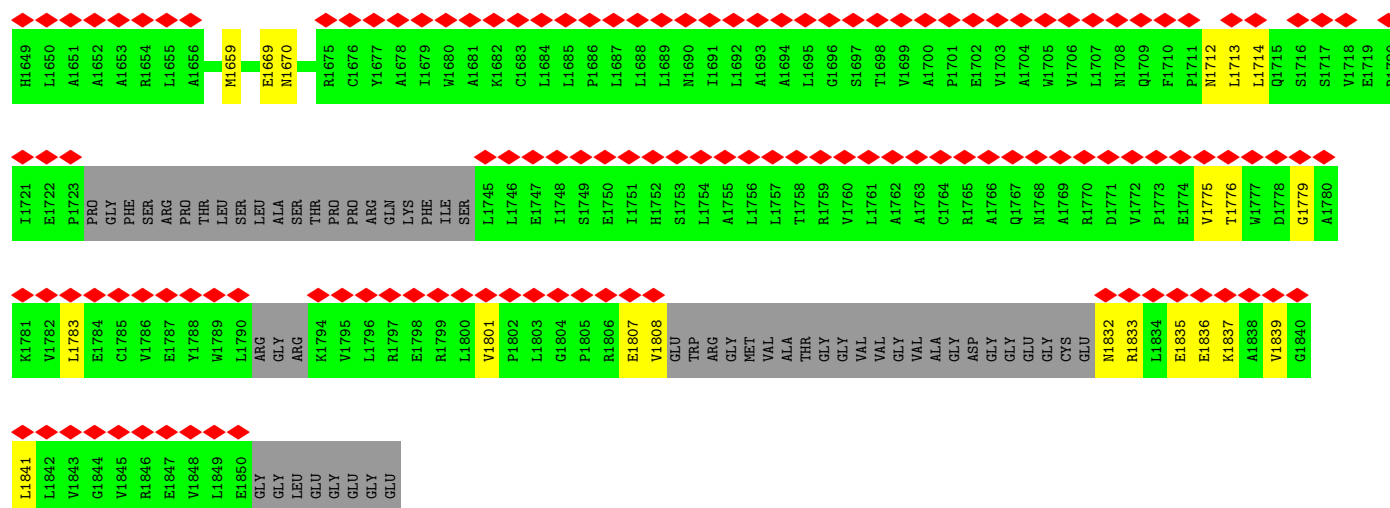




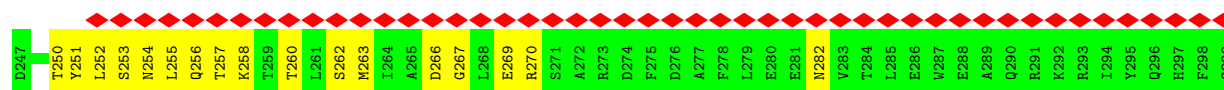


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H61	P62	A63	R64	V65	H66	E67	P68	K69	D70	L71	K72	Q73	E74	F75	E76	T77	K78	T79	S80	S81	I82	GLN	THR	VAL	GLY	ALA	PRO	G88	W89	D90	T91	I92	K93	K94	D95	A96	L97	W98	L99	A100	D101	A102	V103	A104	E105	T106	Q107	V108	A109	A110	L111	R112	I113	V114	L115	T116	E117	Q118	L119	T120
R121	A122	A123	S124	P125	L126	V127	L128	P129	L130	S131	T132	Q133	D134	V135	A136	N137	I138	Q139	E140	A141	A142	G143	VAL	GLY	ASP	ALA	HIS	ALA	SER	SER	I152	L153	S154	L155	L156	N157	P158	A159	S160	A161	V162	D163	E164	E165	T166	M167	Q168	C169	D170	F171	E172	T173	E174	A175	R176	R177	E178	R179	R180	
I181	L182	A183	T184	Y185	L186	L187	E188	R189	R190	S191	F192	T193	A194	A195	V196	D197	A198	L199	V200	T201	F202	L203	L204	H205	S206	A207	P208	G209	Q210	H211	K212	D213	L214	D215	S216	L217	R218	R219	A220	L221	K222	D223	D224	A225	F226	A227	F228	D229	E230	D231	L232	D233	V234	F235	D236	R237	S238	K239	L240	
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T301	P302	Y303	F304	A305	P306	H307	E308	L309	L310	S311	E312	W313	F314	E315	L316	M317	N318	S319	S320	L321	F322	L323	E324	S325	L326	L327	G328	F329	E330	V331	V332	A333	D334	L335	A336	N337	P338	A339	R340	S341	L342	V343	S344	A345	I346	C347	L348	K349	M350	L351	N352	L353	D354	R355	T356	L357	Q358	F359	L360	
H361	D362	L363	D364	Y365	P366	D367	G368	E369	L370	E371	Y372	L373	L374	S375	S376	T377	T378	L379	N380	K381	I382	H383	T384	A385	V386	T387	N388	A389	V390	N391	S392	G393	V394	A395	A396	S397	L398	P399	V400	A401	L402	A403	W404	S405	L406	I407	V408	H409	Q410	M411	H412	L413	G414	Y415	Q416	E417	R418	A419	GLU	
ARG	ARG	ASP	LEU	VAL	ASN	GLN	ALA	GLN	ALA	PHE	GLU	LEU	PHE	GLN	PRO	SER	ALA	THR	PRO	ASN	ARG	ARG	ARG	ASN	SER	ALA	GLY	SER	ILE	VAL	SER	LEU	ALA	S462	P463	Y464	D465	D466	F467	L468	R469	E470	Q471	R472	L473	D474	N475	D476	L477	A478	P479	V480								
E481	Q482	I483	A484	M485	L486	A487	T488	L489	R490	G491	Q492	V493	Y494	Q495	V496	M497	S498	E499	M500	A501	L502	C503	L504	G505	T506	T507	H508	E509	A510	A511	F512	R513	P514	A515	V516	G517	A518	R519	A520	R521	L522	V523	F524	Q525	D526	L527	L528	K529	R530	A531	A532	P533	Y534	I535	P536	Y537	D539	E540		
P541	V542	F543	S544	L545	L546	A547	I548	L549	A550	T551	G552	R553	Q554	Y555	V556	D557	V558	T559	D560	A561	L562	S563	A564	G565	S566	L567	N568	Q569	V570	Y571	T572	D573	M574	L575	D576	D577	E578	T579	L580	F581	T582	Q583	F584	T585	M586	Q587	L588	E589	E590	R591	F592	P593	Y594	E595	F596	N597	P598	F599	S600	
V601	L602	C603	R604	L605	L606	A607	A608	A609	L610	I611	T612	N613	K614	D615	K616	A617	D618	V619	V620	T621	G622	W623	L624	W625	G626	T627	P628	T629	L630	T631	V632	D633	L634	N635	P636	A637	W638	D639	R640	S641	Y642	E643	L644	C645	F646	E647	D648	E649	N650	T651	N652	S653	F654	R655	L656	T657	R658	D659	V660	
D661	L662	F663	G664	SER	ALA	SER	ARG	ARG	PRO	HIS	GLU	ALA	GLU	E678	R679	F680	I681	I682	P683	E684	G685	T686	L687	G688	R689	F690	V691	T692	ASP	VAL	GLY	ARG	T697	A698	R699	L700	E701	F702	E703	H704	S705	A706	L707	A708	L709	L710	G711	K712	R713	L714	L715	V716	K717	A718	A719	E720				
E721	I722	C723	D724	S725	G726	M727	A728	R729	L730	D731	V732	D733	E734	Q735	A736	E737	A738	V739	A740	M741	L742	A743	T744	V745	G688	L746	R747	A748	E749	S750	L751	K752	S753	T754	A755	K756	G757	G758	D759	P760	E761	A762	P763	L764	K765	F766	L767	K768	E769	A770	S771	R772	L773	L774	P775	H776	N777	K778	D779	I780
L781	T782	V783	I784	S785	D786	T787	L788	D789	G790	L791	V792	E793	K794	E795	L796	L797	E798	L799	D800	G801	P802	Q803	I804	A805	V806	L807	A808	S809	C810	L811	Q812	F813	L814	H815	A816	A817	L818	A819	V820	C821	P822	G823	R824	V825	W826	A827	Y828	M829	S830	R831	C832	A833	L834	I835	R840	P841	L844			

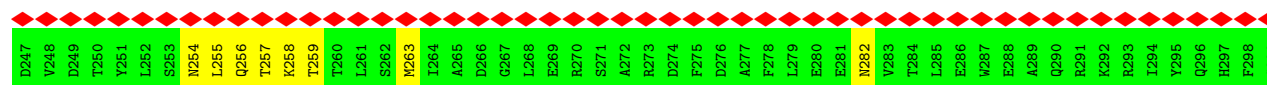
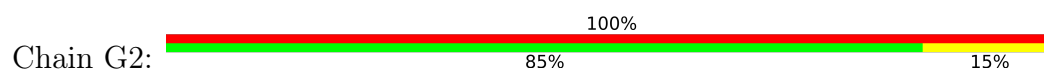
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ARG	H1531	V1351	F1471	V1351	M1291	G1231	L1171	I1111	A1051	A984	S909	S850
LEU	GLU	K1352	G1472	K1352	G1292	M1232	A1172	D1112	C1052		R910	L851
GLN	GLN	Q1353	A1473	Q1353	Y1293	V1233	A1173	K1113	L1053	R989	V911	D852
ASN	GLN	S1354	M1474	S1354	M1294	M1234	A1174	P1114	L1054	Q990	A912	M853
ALA	ASN	G1355	D1475	G1355	A1295	K1235	M1175	F1115	A1055	P991	I915	Y854
ALA	ALA	F1356	L1476	F1356	S1296	T1236	E1176	G1116	R1056	L992	A916	A855
THR	ALA	R1357	P1477	R1357	L1297	D1237	R1177	G1117	L1057	P993	Q917	E856
ASP	THR	K1358	L1478	K1358	H1298	G1238	L1178	V1118	P1058	L994	A918	R857
GLY	THR	E1359	F1479	E1359	G1299	A1239	R1179	E1119	A1059	T995	A919	F858
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		E1361	T1481	E1361	F1301	A1241	V1181	A1121	N1061	L997	V922	L860
		T1362	L1482	T1362	A1302	A1242	K1182	V1122	A1062	Y923	Y923	L861
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		N1364	K1484	N1364	M1304	F1244	L1184	T1124	Y1064	A999	T926	S863
		L1365	L1485	L1365	F1305	Q1245	D1185	M1125	R1065	L1000	T927	A864
		F1426	L1486	F1426	A1306	A1246	V1186	R1126	A1066	I1001	T928	V865
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		G1429	V1488	G1429	F1309	A1249	A1189	A1129	L1069	R1004	F931	F868
		H1430	L1490	H1430	P1310	A1250	V1190	A1130	E1070	A1005	R932	A869
		A1431	R1491	A1431	G1311	Y1251	A1191	V1131	L1071	T1006	S933	A870
		R1432	A1492	R1432	V1312	V1252	M1192	I1132	L1072	L1007	E934	L871
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		L1435	Q1495	L1435	D1315	T1255	F1195	R1135	L1075	G1010	R937	S874
		A1436	G1496	A1436	D1316	F1256	V1196	Q1136	V1076	Q1011	S938	A875
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		L1442	SER	L1442	V1322	H1262	Y1202	C1142	A1082	E1017	V944	ARG
		R1443	ASN	R1443	L1323	M1263	W1203	L1143	ALA	R1018	V945	ARG
		L1443		L1443	L1323	R1264	P1204	L1144	GLY	V1019	G946	ALA
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		D1445		D1445	R1325	M1266	T1206	G1146	GLY	S1021	M948	THR
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		Q1448		Q1448	G1328	A1269	A1209	ARG	GLY	F1025	L951	SER
		L1449		L1449	K1329	A1270	V1210	GLU	Y1091	C1026	V952	VAL
		P1450		P1450	G1330	R1271	R1211	ALA	L1092	T1027	V953	VAL
		A1451		A1451	Y1331	F1272	K1212	LEU	L1093	S1028	H954	ARG
		D1452		D1452	Y1332	A1273	E1213	LYS	G1094	L1029	A955	ALA
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		L1456		L1456	E1336	V1277	D1217	GLN	S1098	I1033	S959	
		L1457		L1457	V1337	A1278	D1218	LYS	H1099	A1034	S960	
		A1458		A1458	E1338	D1279	A1219	ILE	A1100	F1035	H961	
		L1459		L1459	E1339	L1280	L1220	ARG	A1101	L1043	T963	
		V1460		V1460	Q1340	L1281	R1221	LYS	R1102	Q1044	T964	
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		F1462		F1462	L1342	F1283	Y1223	G1166	F1104	H1046	L966	
		A1463		A1463	G1343	L1284	V1224	E1167	I1105	L1047	S967	
		T1464		T1464	F1344	R1285	G1225	G1168	S1106		P968	
		H1465		H1465	D1345	E1286	L1226		L1107			
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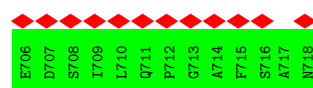
• Molecule 9: NUP93 R2



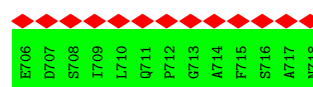
• Molecule 9: NUP93 R2



• Molecule 10: NUP98 R2



• Molecule 10: NUP98 R2



• Molecule 11: NUP205



M1	T2	D3	L4	R5	K6	L7	E8	A9	L10	Q11	A12	L13	H14	A15	E16	L17	V18	A19	V20	R21	Q22	H23	R24	F25	E26	G27	L28	Q29	V30	L31	E32	T33	L34	L35	E36	E37	Q38	T39	D40	A41	F42	K43	A44	L45	I46	A47	K48	P49	A50	R51	D52	T53	K54	D55	R56	E57	A58	K59	
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THR	Q181	V182	K183	F185	I186	P187	R188	C189	M190	E191	A192	M193	K194	W212	LEU	GLN	ALA	ALA	SER	LEU	VAL	ARG	PRO	L222	E237	Q238	H239	E240	C241	L242	A243	S244	I245	L246	H247	A248	A249	F263	I264	K265	L266	L267	R268	K269	W270	D271	K272	Y273	D274	H275	F276	L277	I278	H279	L280				
I281	P282	S283	L284	A285	L288	G292	L300	Q301	T310	C311	LYS	GLY	GLY	ASP	ASP	S318	W319	A320	L321	P322	V323	L324	G325	A326	A327	V328	R329	A330	W331	N352	L353	D354	E355	E356	D357	E358	Q359	R360	T361	K362	Q363	F364	L365	D366	A367	L368	K369	G371	A372	F373	D374	F375							
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T506	P507	L508	T527	N531	D535	E536	GLY	HIS	GLN	ALA	SER	GLY	PRO	MET	LYS	ARG	SER	Q548	S568	GLU	ARG	PRO	ASN	PRO	PRO	GLN	ALA	SER	MET	HIS	ARG	PRO	GLY	ALA	ASP	PRO	ALA	E590	M598	T615	A616	R617	E624	N627	T640	R645													
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D763	D767	N771	K774	S777	D778	P779	L797	V798	T799	F800	G808	N812	I813	S814	I815	D816	D817	A818	N819	A820	H821	T822	N823	L824	E825	T826	Y827	V828	A829	L830	H831	P832	F833	S834	R835	N837	E838	V839	L840	F841	N842	E843	T846	L849	R850	N851	T852	I853											
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E984	R985	N986	G987	E988	G989	E990	T991	S992	S993	A994	S995	L996	K1057	A998	S999	T1000	M1001	A1002	T1003	L1004	D1005	P1006	A1007	L1008	A1009	A1010	S1011	G1012	E1013	N1014	Y1015	R1016	V1017	X1018	L1019	A1020	W1021	L1022	D1023	F1024	L1025	Y1026	A1027	C1028	R1029	R1030	A1031	T1032	P1033	D1034	Q1035	P1036	T1037	I1038	A1039	H1040	L1041	L1042	L1043
G1044	F1045	H1046	C1047	E1048	L1049	S1050	K1051	L1052	G1053	I1054	E1055	P1056	K1057	G1058	P1059	F1060	D1061	M1062	Q1063	K1064	S1065	L1066	F1067	H1068	S1069	L1070	L1071	M1072	V1073	L1074	I1075	L1076	L1077	T1078	V1079	S1080	E1081	E1082	E1083	Q1084	G1085	M1086	R1087	G1088	Y1089	L1090	V1091	T1092	S1093	D1094	A1095	R1096	V1097	L1098	Y1099	I1100	D1101	G1102	L1103
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L1685	A1604	N1544	A1604	L1605	E1546	L1665	Q1667	H1668	R1669	G1670	L1671	Y1738	SER	GLU	GLN	VAL	SER	GLU	GLN	PRO	PRO	GLU	LEU	THR	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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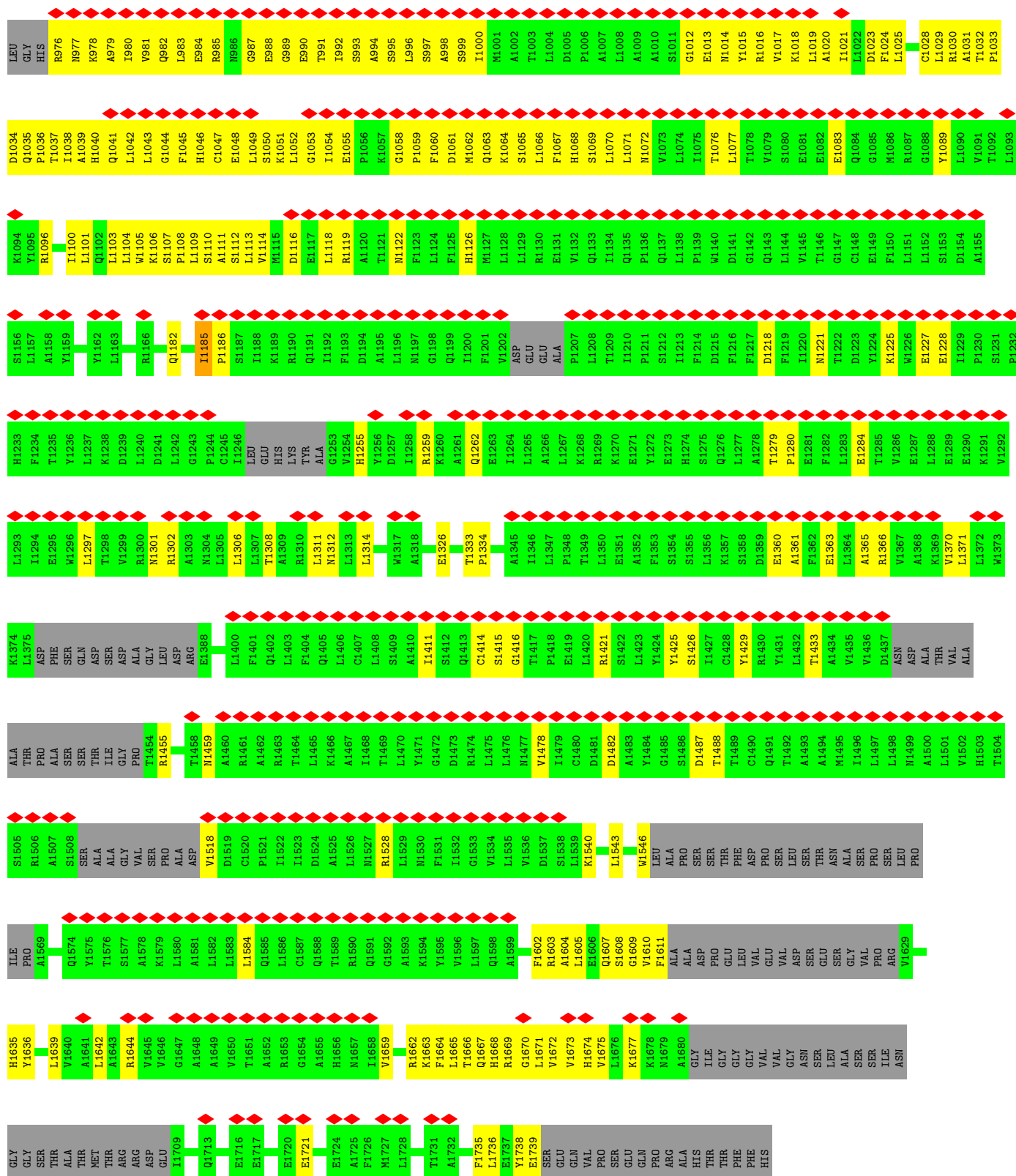
• Molecule 11: NUP205

Chain I2:

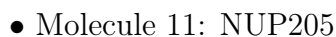


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K61	E62	P63	K64	K65	L66	K67	F68	G69	E70	E71	E72	Y73	L74	L75	N76	E77	D78	F79	V80	N81	D82	C83	L84	K85	L86	A87	D88	E89	L90	D91	L92	N93	E94	K95	E96	S97	A98	A99	I100	A41	L101	I102	D103	C104	D105	A106	E107	G108	P409	V110	E111	T112	Q113	K114	R115	P116	L117	A118	E119	L120

A913	N914	A915	A916	Y917	S918	A919	F920	S921	D922	G923	I924	L925	S926	H927	L928	S929	L930	V931	V932	D933	L934	G935	K936	Y937	C938	N939	L940	G941	H942	A943	E944	L945	T946	L947	A948	C949	L950	K951	L952	L953	E954	K955	L956	S957	T958	S959	S960	R961	L962	L963	S964	A965	W966	S967	R968	ASP	SER	GLY	ARG	
T852	I853	H854	Q855	D856	P857	L858	S859	L860	G861	S862	A863	S864	P865	D866	S867	P868	L869	V870	S871	S872	L873	L874	R875	A876	L877	Q878	V879	M880	T881	K882	A883	L884	E885	L886	Q887	T889	V890	L891	H892	L893	L894	R895	P896	E897	S898	L899	R900	Y901	Q902	A905	G906	V907	R908	S909	E910	P911	V912			
Q781	L782	R783	L784	L785	R786	L787	S788	C789	L790	D791	A792	F793	W794	V795	C796	L797	V798	T799	F800	H801	L804	D816	D817	A818	H819	A820	A821	T822	H823	L824	A825	L826	T827	V828	R829	L830	H831	F832	F833	S834	R835	V836	M837	E838	H839	L840	F841	N842	E843	K844	T845	I846	T847	L848	I849	I850	H851			
A721	F722	I723	Q724	L725	L726	T727	T728	L729	L730	V731	P732	P733	E734	G735	L736	ASN	SER	LEU	W740	D741	S742	F743	P744	F745	P746	E747	W748	L749	G750	S751	S752	L753	R754	T755	L756	G757	I758	E759	P760	Y761	W762	D763	F764	W765	F766	D767	V768	F769	A770	W771	R772	T773	K774	D775	T776	S777	D778	P779	S780	
H661	E662	E663	L664	D665	A666	M667	W668	R669	W670	V671	E672	A673	W674	M675	T676	M677	P678	F679	SER	SER	PRO	GLY	SER	GLN	GLY	ALA	PRO	GLN	ARG	ILE	SER	PHE	LEU	GLY	GLN	THR	P699	G700	P701	Q702	E703	C704	W705	E706	W707	W708	F709	R710	E711	F712	G713	T714	G715	F716	E717	Q718	S719	W720		
C601	Y602	L603	R604	L605	L606	A607	K608	L609	A610	T611	E612	S613	E614	L615	A616	R617	K618	R619	L620	M621	M622	D623	E624	D625	F626	N627	L628	V629	D630	T631	L632	L633	K634	L635	S636	V637	G638	V639	T640	P641	H642	R643	L644	R645	A646	C647	T648	F649	V650	V651	L652	K653	A654	L655	M656	T657	R658	K659	T660	
SER	GLY	LYS	MET	LYS	ARG	SER	Q548	S549	L550	T551	S552	S553	Q554	I555	F556	K557	E558	L559	E560	Y561	F562	T563	T564	K565	V566	C567	S568	GLU	ARG	PRO	ASN	ASN	PRO	PRO	GLN	ALA	SER	MET	HIS	ARG	GLY	PRO	GLY	ARG	PRO	GLY	ALA	ASP	ALA	E590	E591	E592	P593	E594	S595	A596	L597	M598	L599	E600
A481	A482	M483	S484	F485	V486	E487	D488	P489	D490	S491	N492	L493	A494	G495	F496	L497	Q498	W499	A500	S501	R502	R503	A504	S505	T506	P507	L508	V509	S510	A511	P512	C513	E514	M515	L516	R517	C518	L519	A520	D521	N522	E523	E524	C525	A526	T527	A528	A529	H530	N531	F532	L533	L534	D535	E536	GLY	HIS	GLN	ALA	
S421	L422	M423	V424	H425	L426	E427	G428	F429	V430	D431	A432	T433	A434	S435	N436	L437	A438	D439	V440	L441	R442	K443	L444	R445	T446	E447	E448	D449	E450	Q451	R452	Q453	L454	R455	P456	M457	H458	E459	Q460	D461	M462	D463	L464	E465	R466	F467	L468	L469	I470	I471	S472	Y473	A474	Y475	E476	G477	R478	P479	D480	
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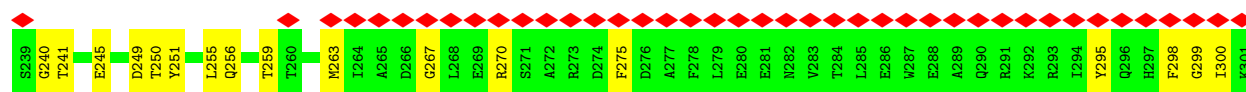




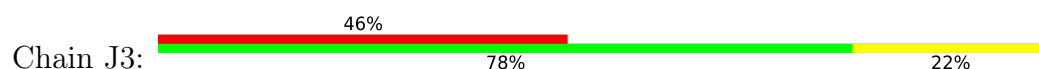
Chain I4: 



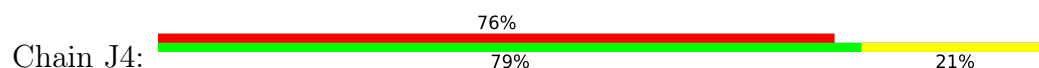
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Q1143	E1083	D1023	L963	G903	E943	R783	I723	E663	L603	LYS	M423
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V1145	G1085	L1025	A965	A905	V845	L785	L725	D665	L605	ARG	H425
T1146	G1086	Y1026	V966	G906	L846	R786	L726	A666	I606	SER	L426
G1147	R1087	A1027	S967	V907	T847	L787	L727	M667	A607	Q548	E427
C1148	G1088	C1028	P968	R908	S848	S788	L728	V668	K608	S549	G428
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F1150	L1090	R1030	SER	K910	T850	L790	L730	V670	A610	T551	V430
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L1152	T1092	T1032	ARG	V912	T852	F792	P732	E672	E612	Q554	A432
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D1154	K1094	D1034	HIS	N914	H854	M794	E734	V674	E614	F556	I434
A1155	Y1095	Q1035	R976	A915	Q855	V795	G735	M675	I615	K557	S435
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I1160	I1100	H1040	Q982	F920	L860	T799	N740	SER	L620	Y561	V440
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Y1162	T1102	L1042	L983	D922	S862	E802	S742	PRG	M622	T563	R442
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S1165	V1105	F1045	N986	L925	P865	I805	F745	GLN	D625	V566	R445
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Y1172	S1112	L1052	S993	V932	V671	N812	S752	LEU	I632	PRG	R452
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K1175	M1115	E1055	L996	G935	R875	I815	L755	P699	L635	MET	R455
E1176	D1116	P1056	S997	K936	A876	D816	G757	G700	S636	HIS	P456
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S1181	T1121	D1061	A1002	G941	I881	A821	V762	E706	P641	ASP	D461
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I1185	F1125	S1065	P1006	L945	E885	A825	F766	F709	R645	E590	E465
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Q1191	E1131	L1071	G1012	K951	Y891	L831	N771	G715	V651	L597	I471
I1192	V1132	N1072	E1013	L952	H892	H832	R772	F716	L652	M598	S472
F1193	Q1133	V1073	N1014	L953	L893	P832	T773	E717	K653	F532	Y473
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A1195	Q1135	I1075	R1016	K955	R895	S834	D775	S719	L655	E600	Y475
L1196	P1136	T1076	V1017	L956	P896	V836	L776	M720	M656	E536	E476
M1197	Q1137	L1077	K1018	L957	E897	M637	S777		I657	GLY	G477
G1198	L1138	T1078	L1019	T958	E898	E838	D778		R658	HIS	R478
Q1199	P1139	V1079	A1020	S959	L899	V839	S780		K659	GLN	P479
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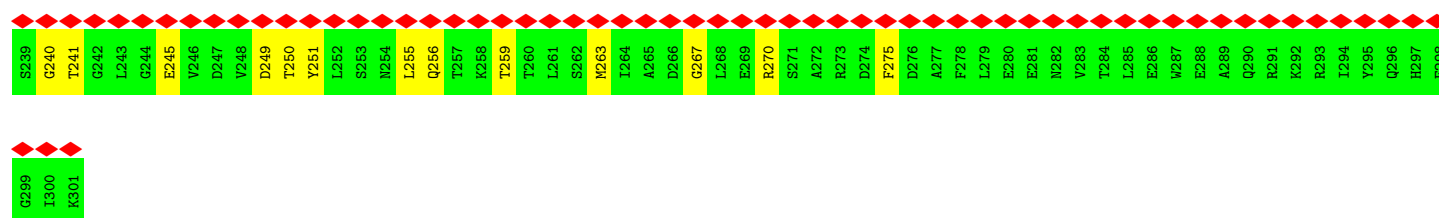
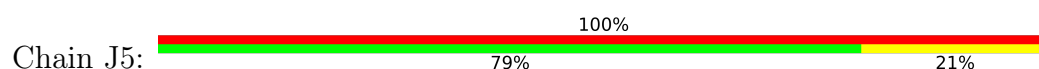
- Molecule 12: NUP93 R2



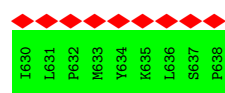
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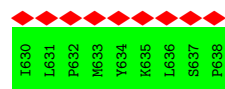
- Molecule 12: NUP93 R2



- Molecule 13: NUP98 R1

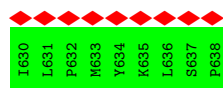


- Molecule 13: NUP98 R1



- Molecule 13: NUP98 R1





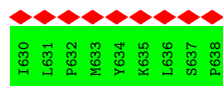
- Molecule 13: NUP98 R1

Chain K4:  100%

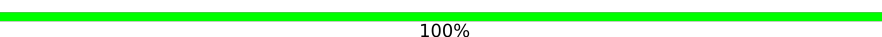
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- Molecule 13: NUP98 R1

Chain K5:  100%
100%

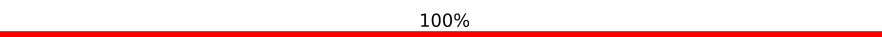


- Molecule 14: NUP53 R1

Chain L1:  100%

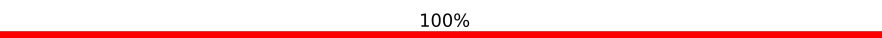
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- Molecule 14: NUP53 R1

Chain L2:  100%
100%

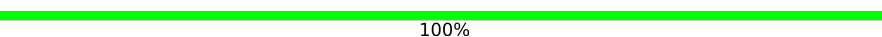


- Molecule 14: NUP53 R1

Chain L3:  100%
100%

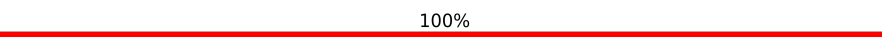


- Molecule 14: NUP53 R1

Chain L4:  100%

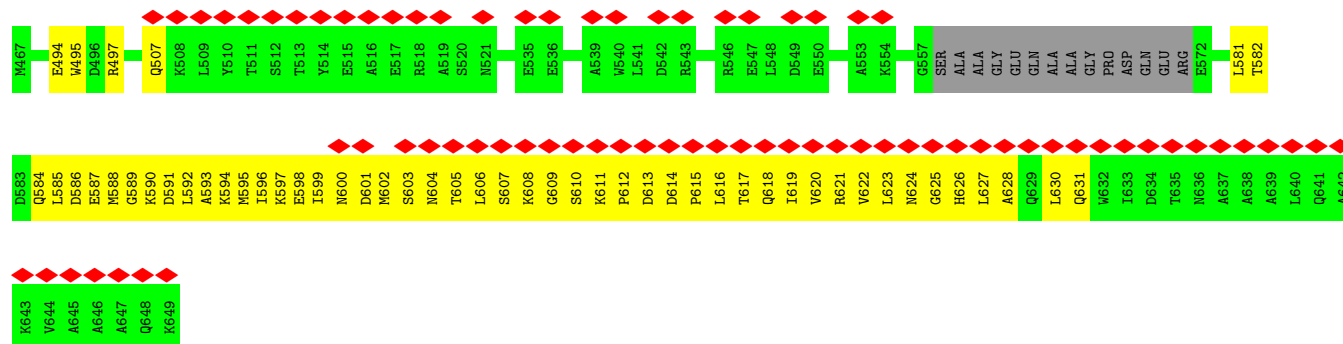
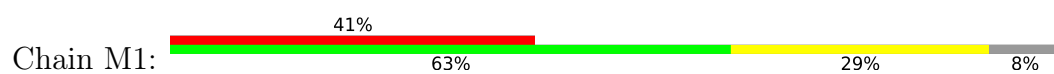
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- Molecule 14: NUP53 R1

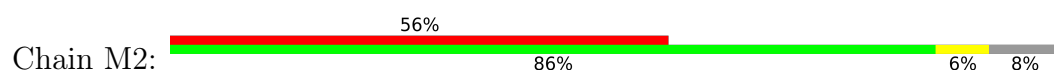
Chain L5:  100%
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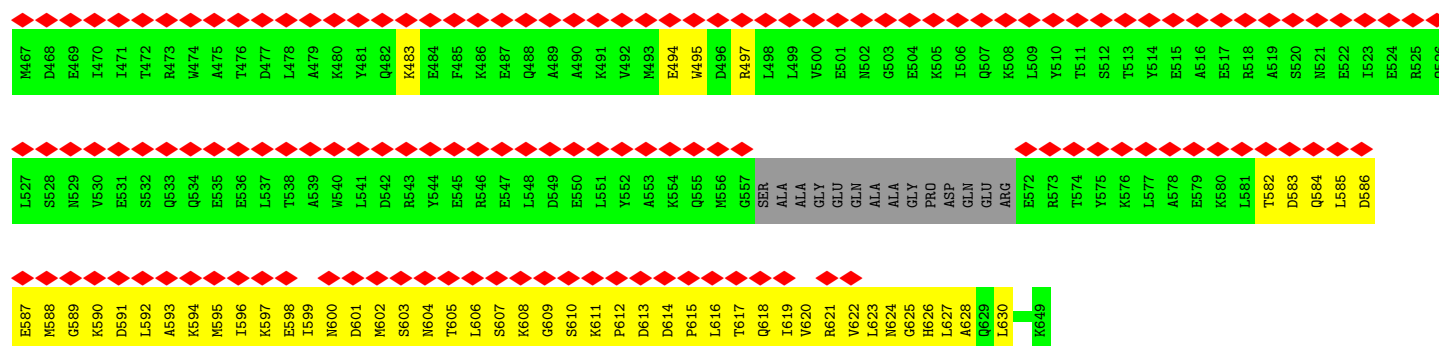
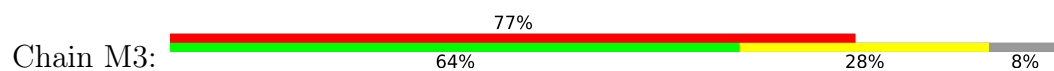
- Molecule 15: NUP62



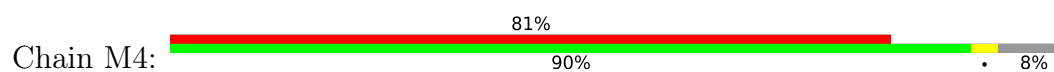
• Molecule 15: NUP62

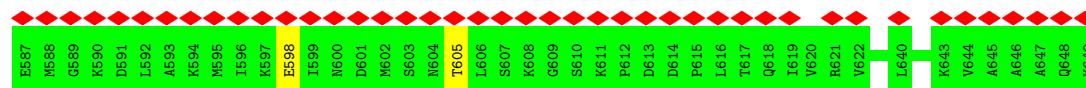
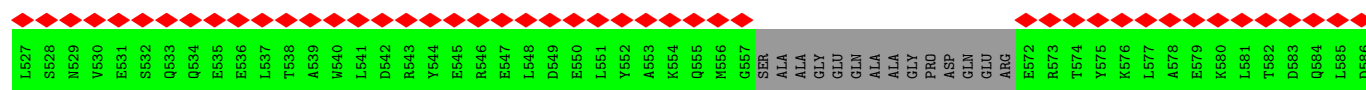


• Molecule 15: NUP62

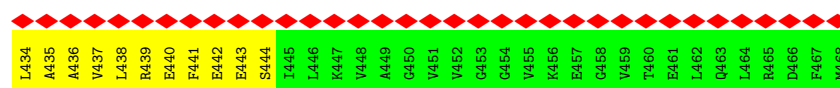
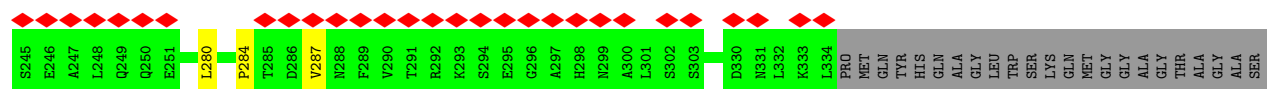


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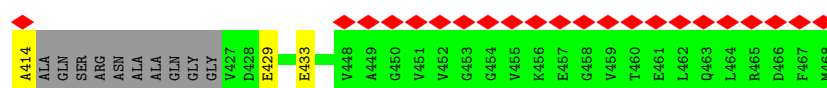
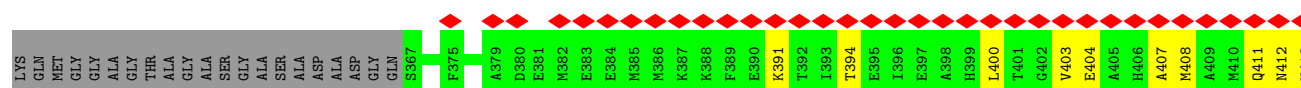
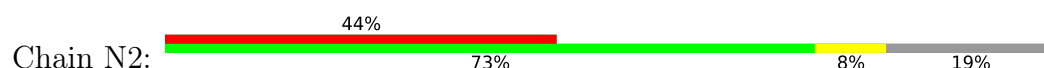




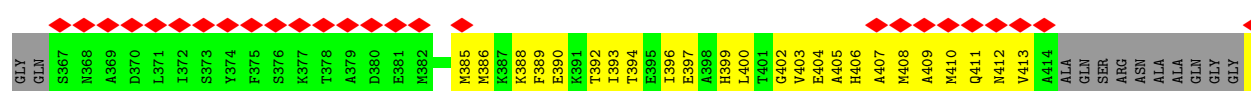
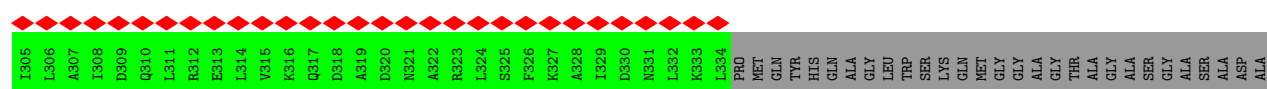
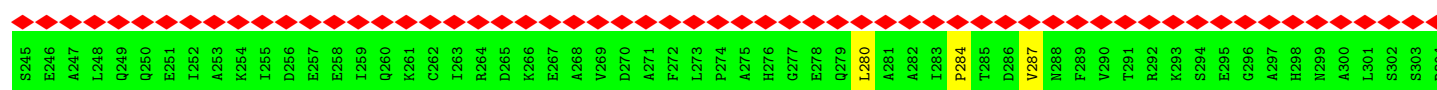
• Molecule 16: NUP58

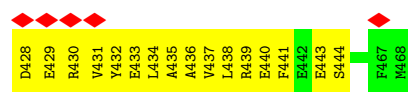


• Molecule 16: NUP58

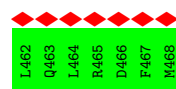
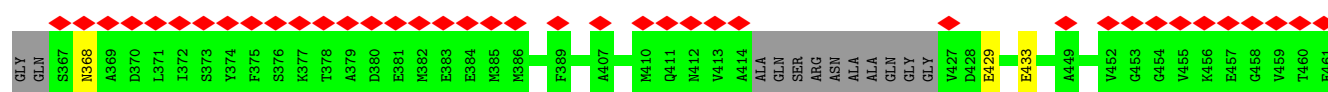
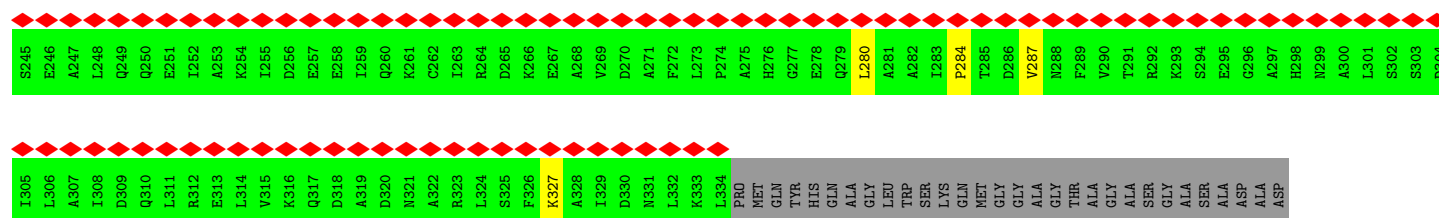
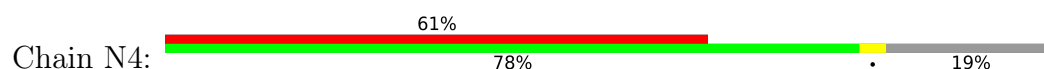


• Molecule 16: NUP58

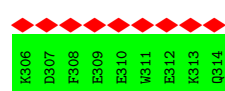
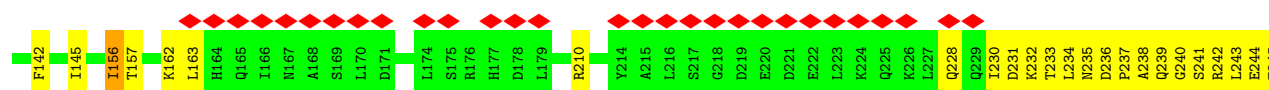
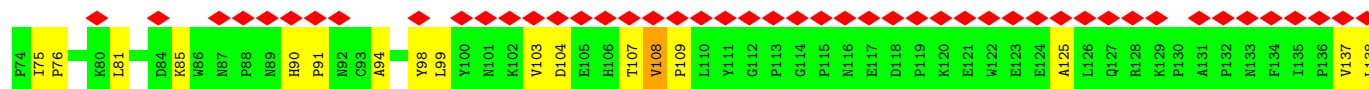




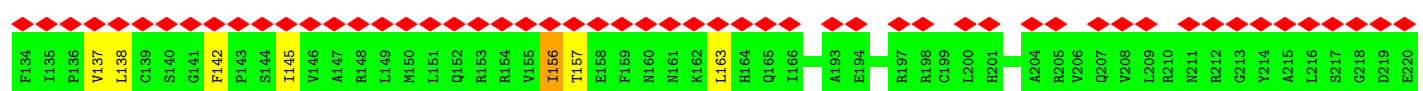
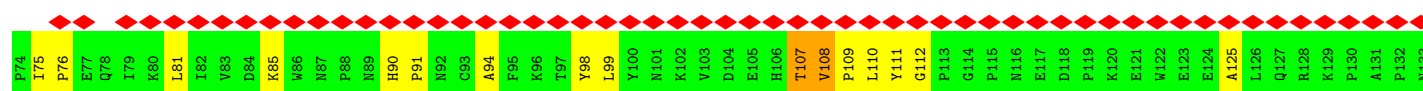
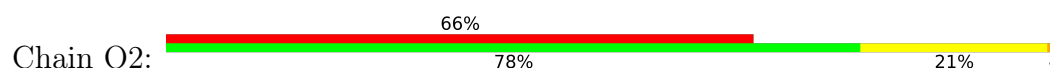
• Molecule 16: NUP58

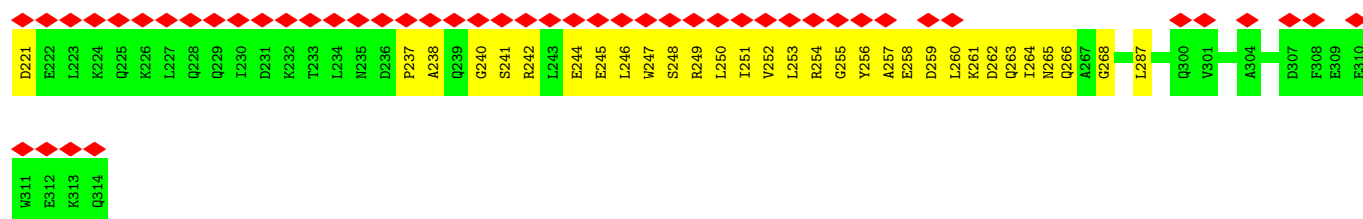


• Molecule 17: NUP54

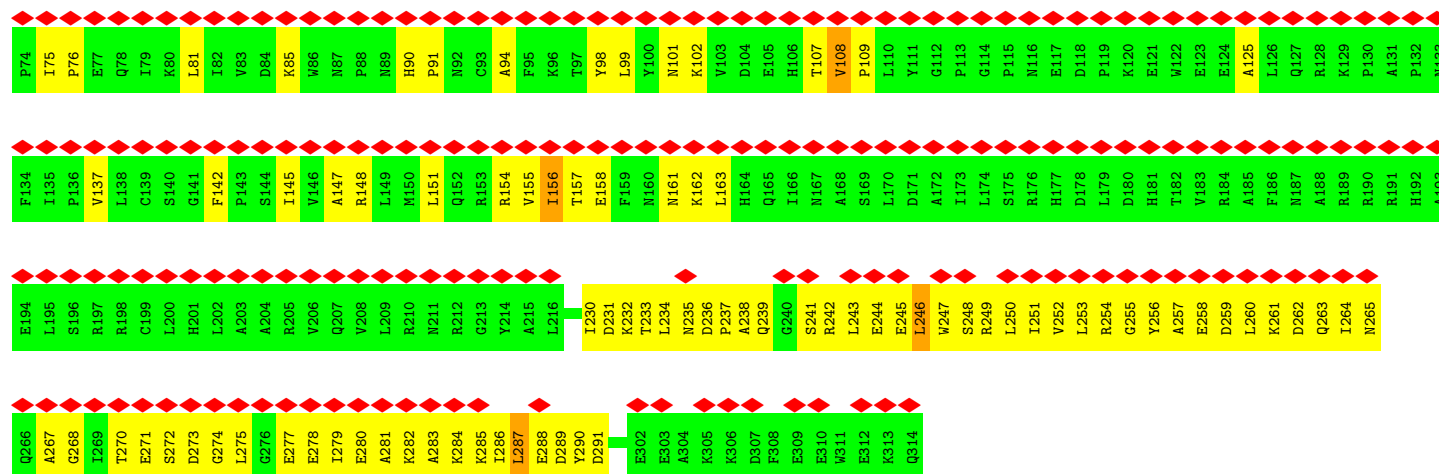
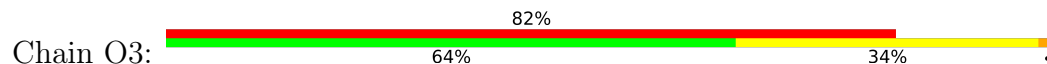


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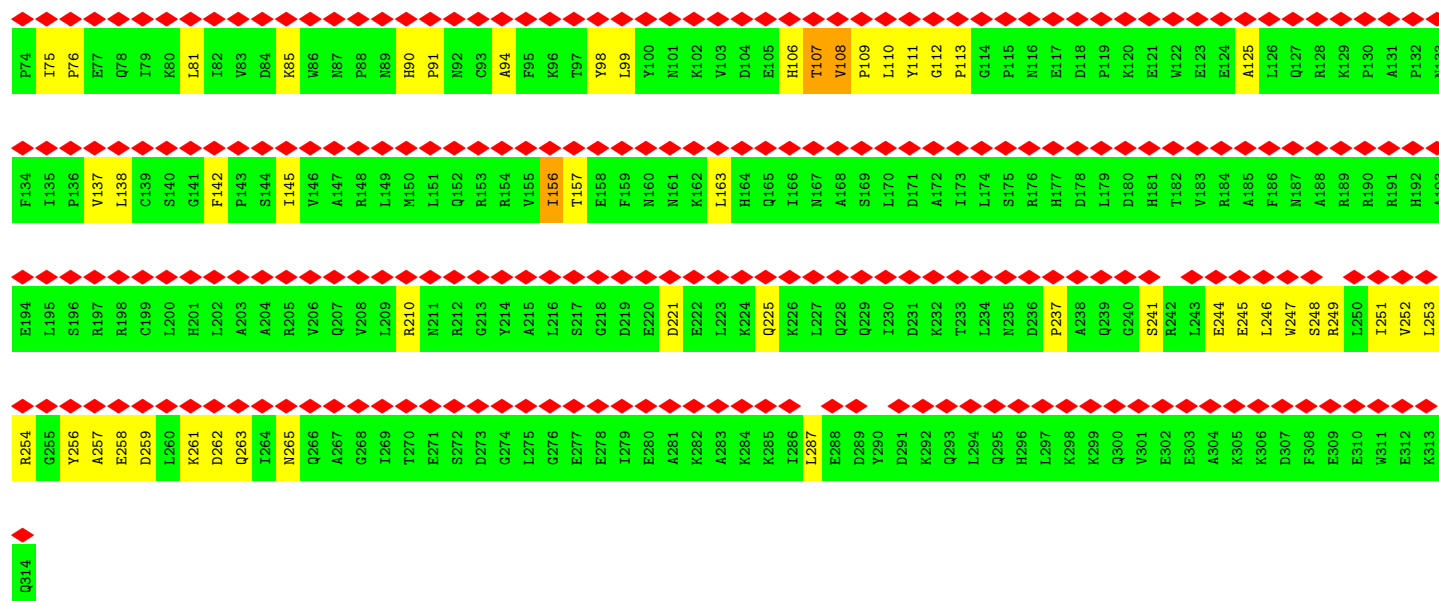
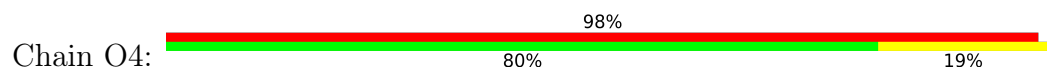




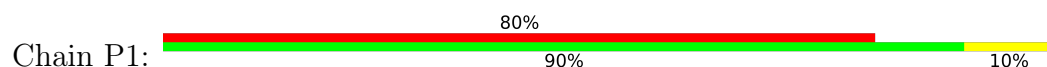
• Molecule 17: NUP54

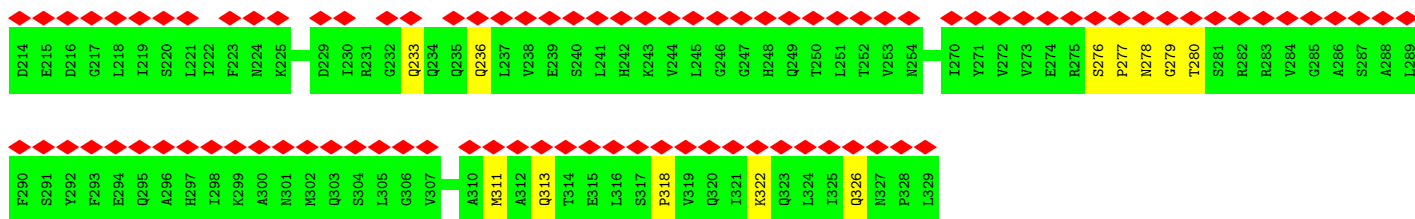


• Molecule 17: NUP54

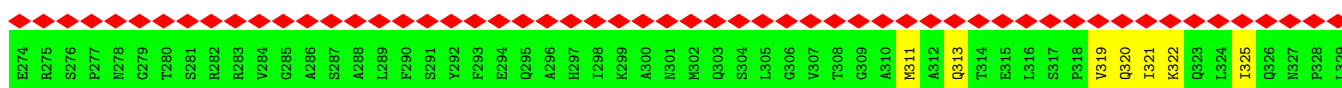
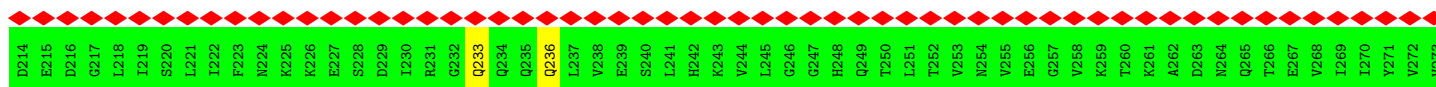


• Molecule 18: NUP54 Ferredoxin-like domain

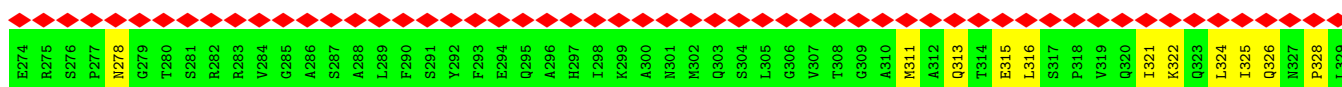
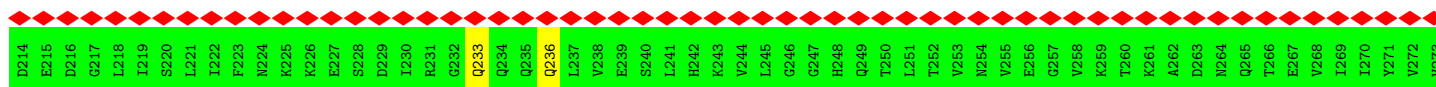




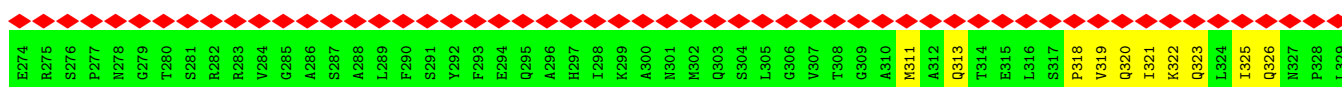
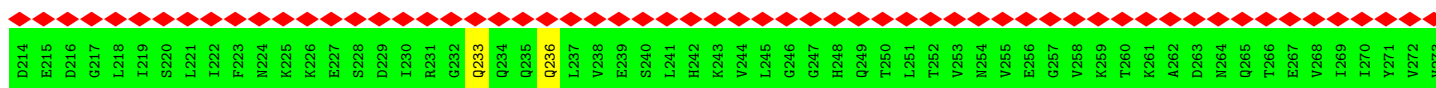
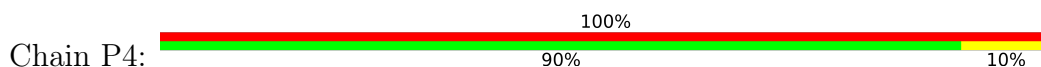
- Molecule 18: NUP54 Ferredoxin-like domain



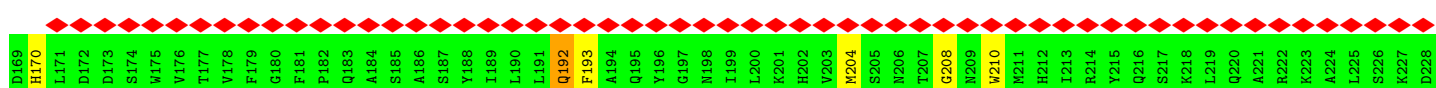
- Molecule 18: NUP54 Ferredoxin-like domain

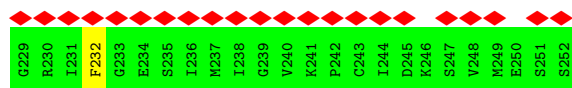


- Molecule 18: NUP54 Ferredoxin-like domain

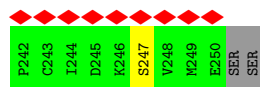
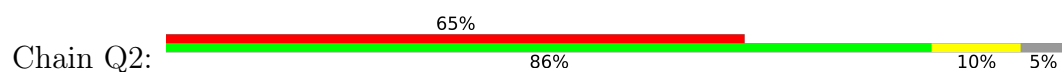


- Molecule 19: NUP53 RRM

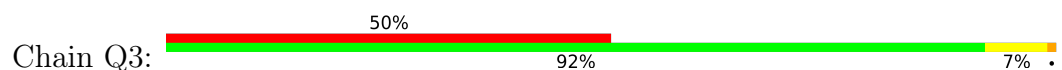




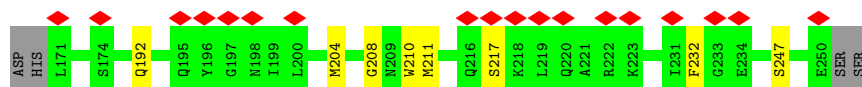
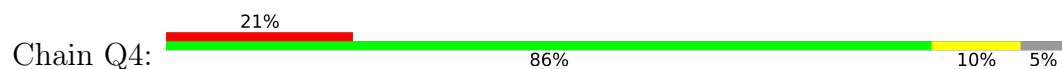
- Molecule 19: NUP53 RRM



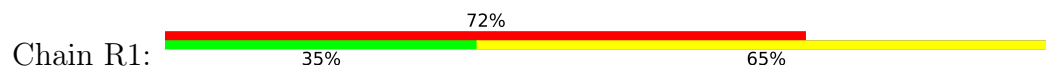
- Molecule 19: NUP53 RRM



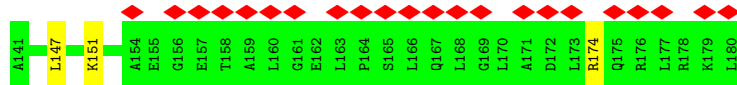
- Molecule 19: NUP53 RRM



- Molecule 20: NUP93 R1

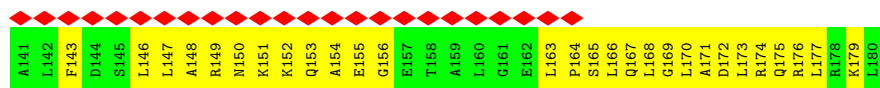


- Molecule 20: NUP93 R1

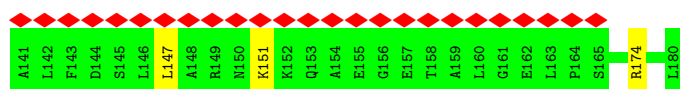


- Molecule 20: NUP93 R1

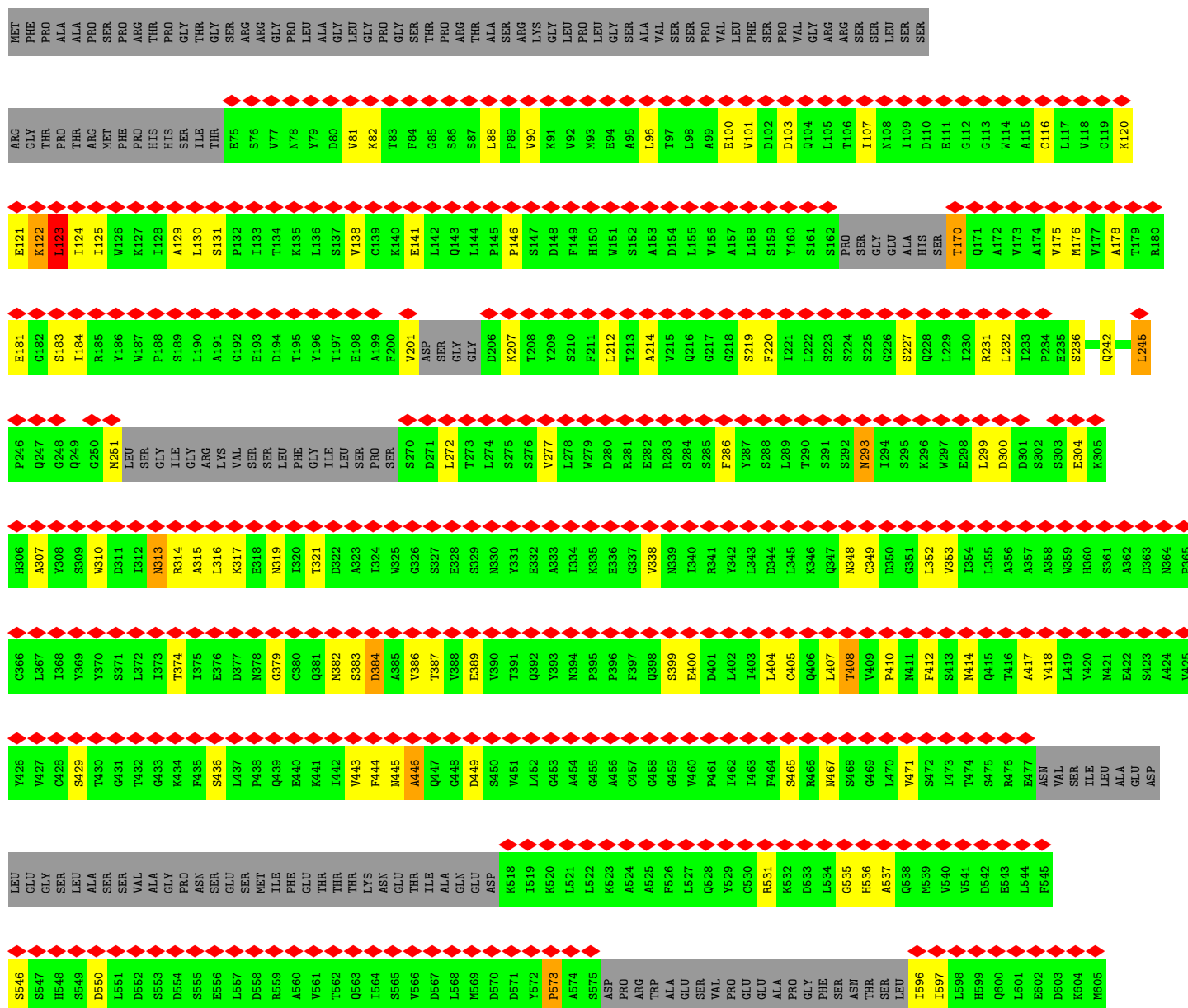
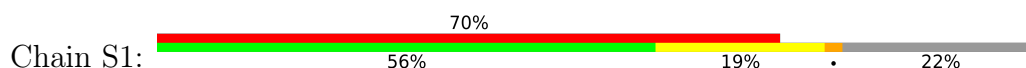


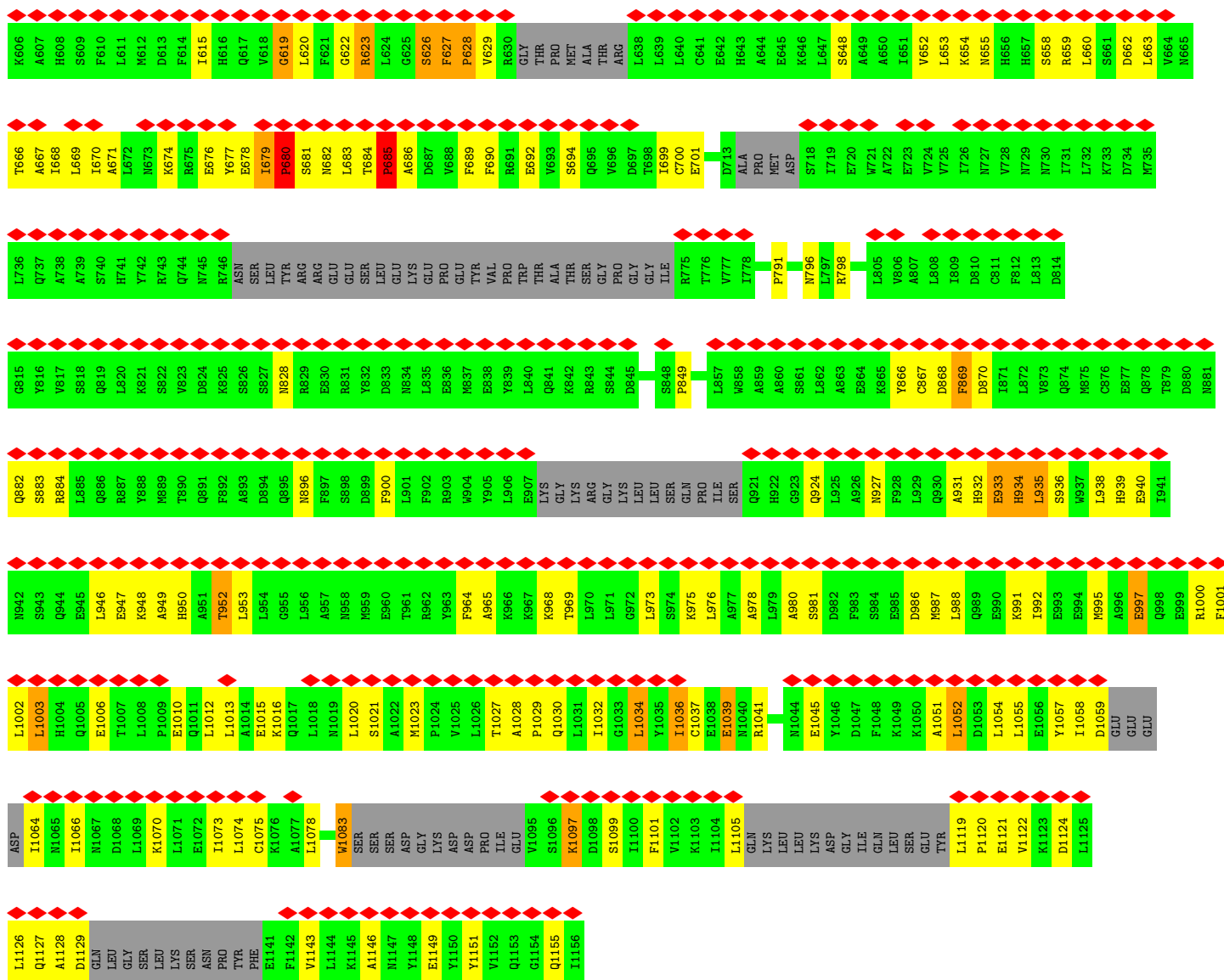


• Molecule 20: NUP93 R1

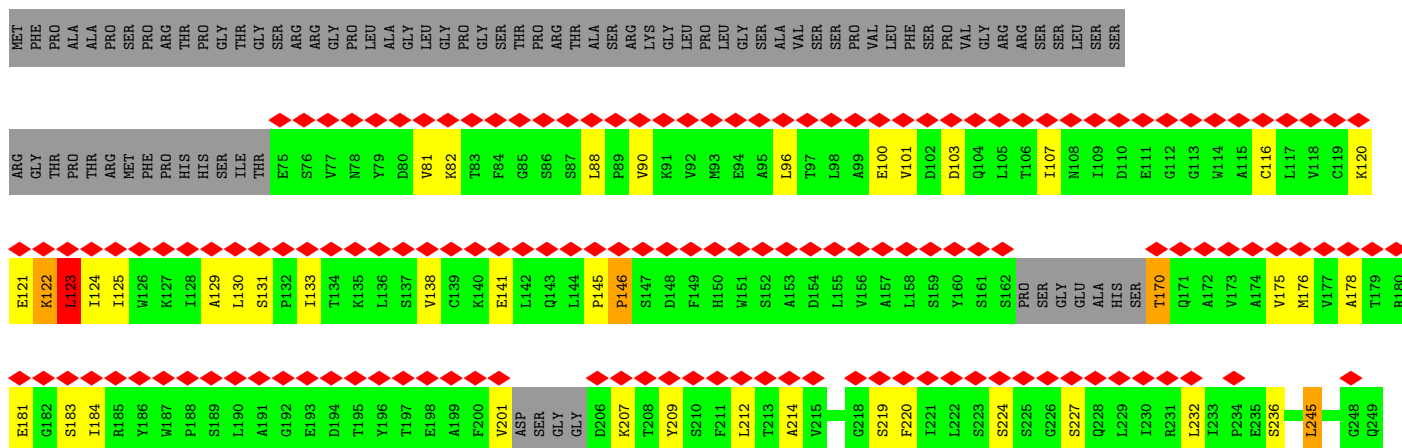


• Molecule 21: NUP133





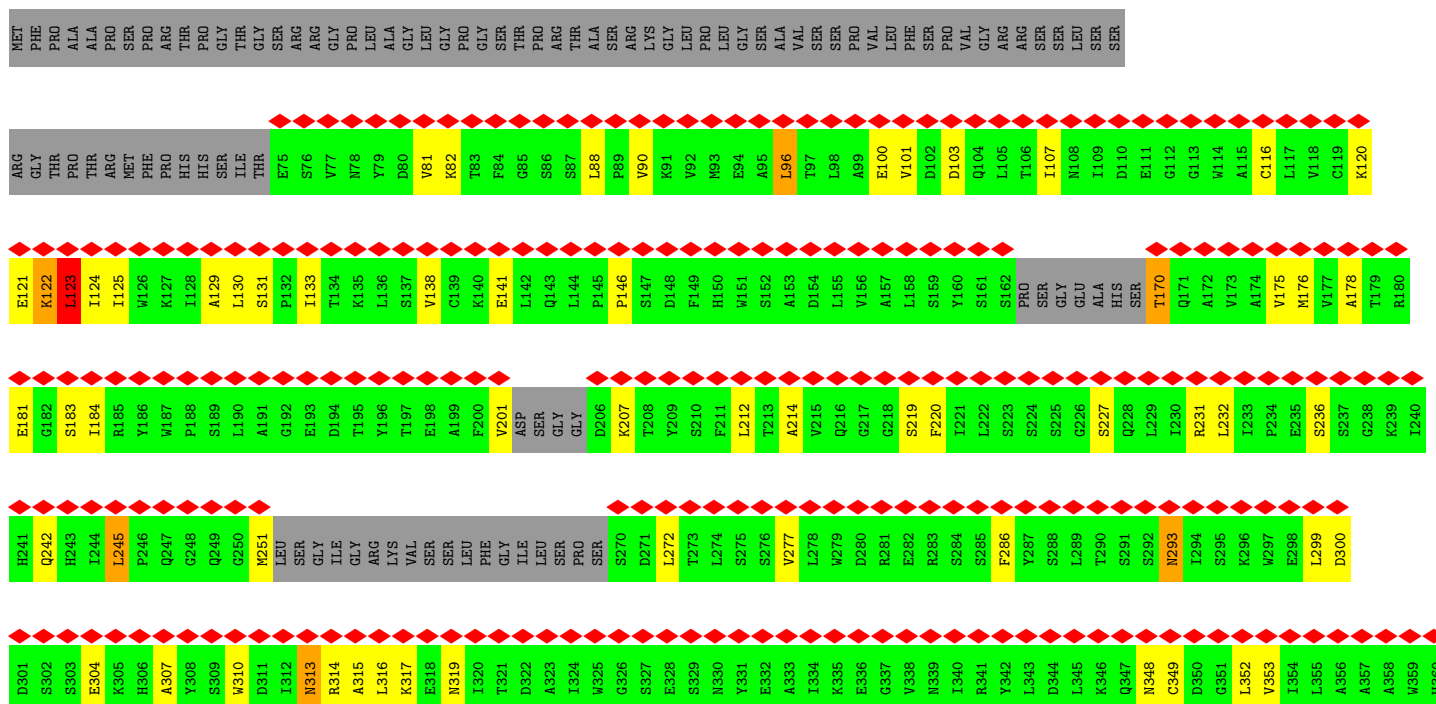
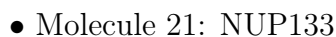
• Molecule 21: NUP133





Chain S3:

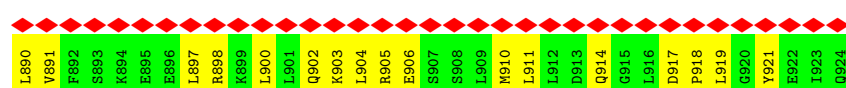
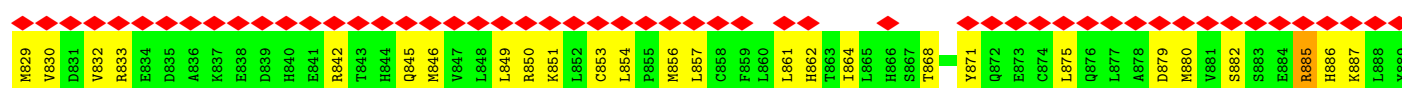
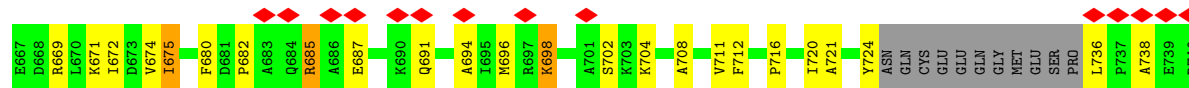




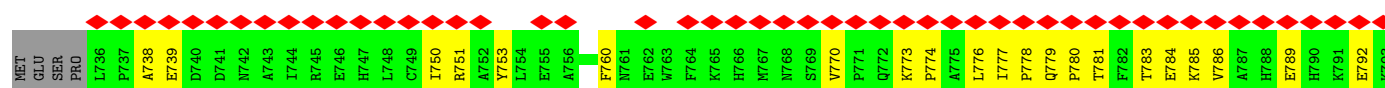
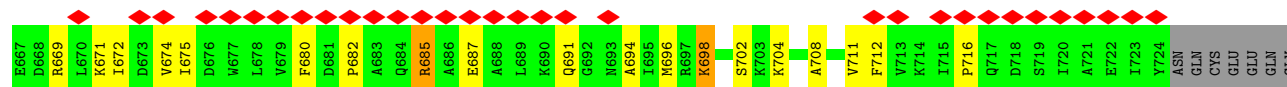




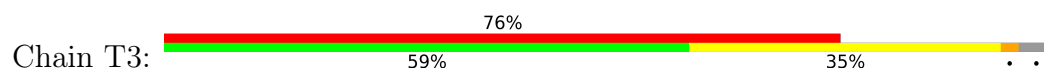
● Molecule 22: NUP107 CTD

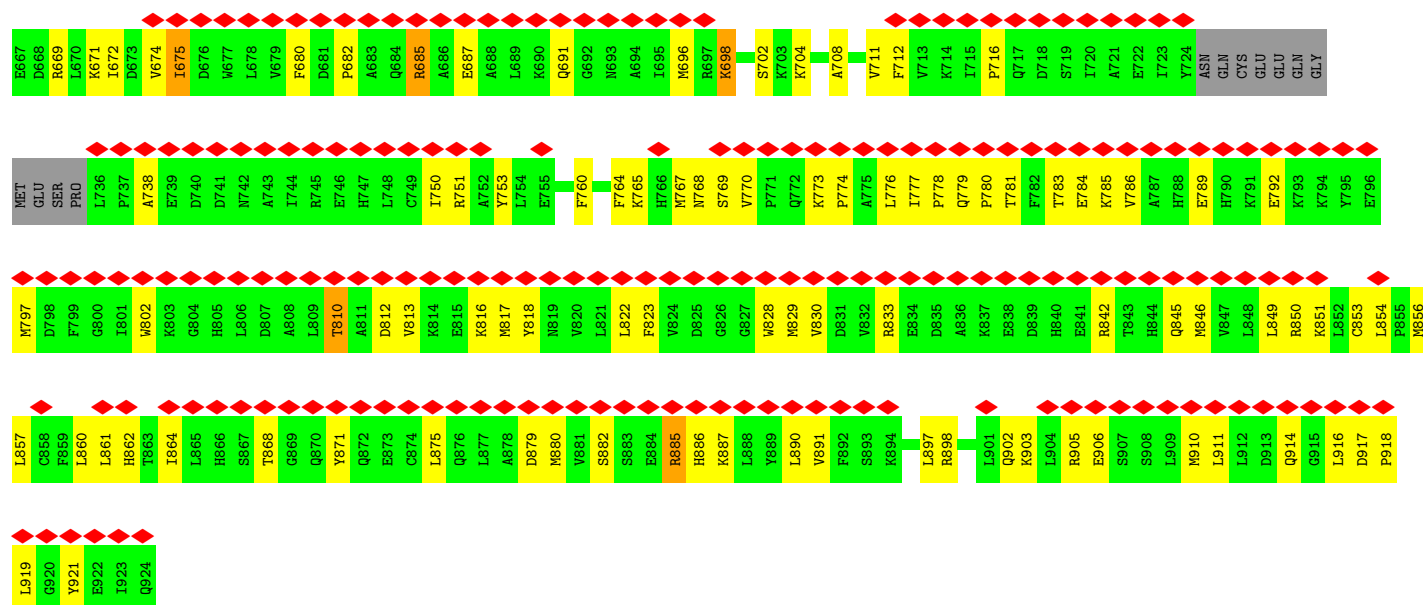


● Molecule 22: NUP107 CTD

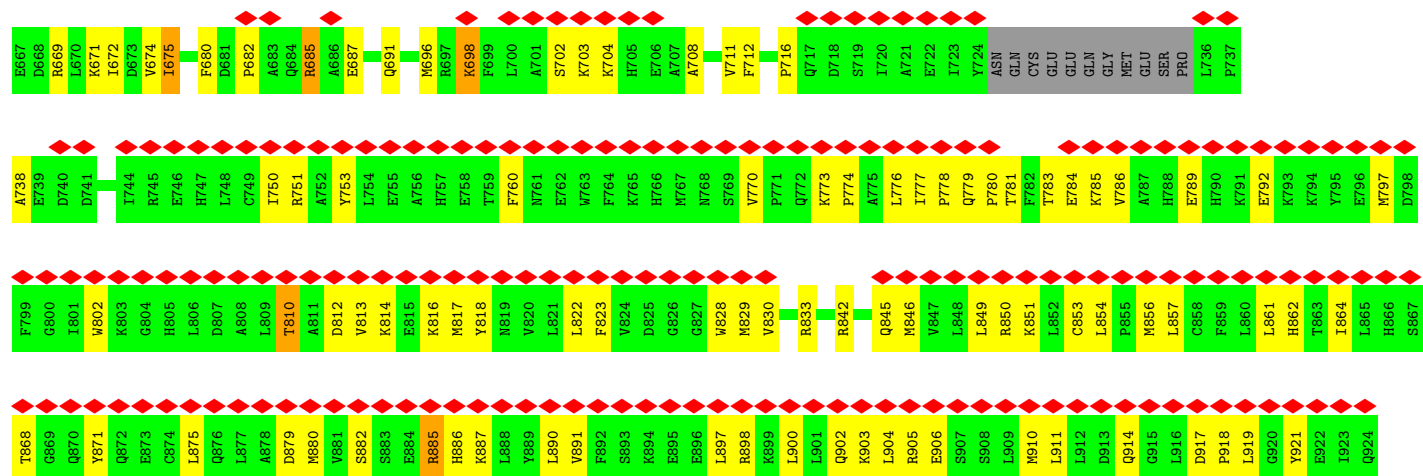
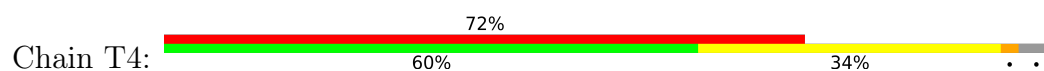


● Molecule 22: NUP107 CTD

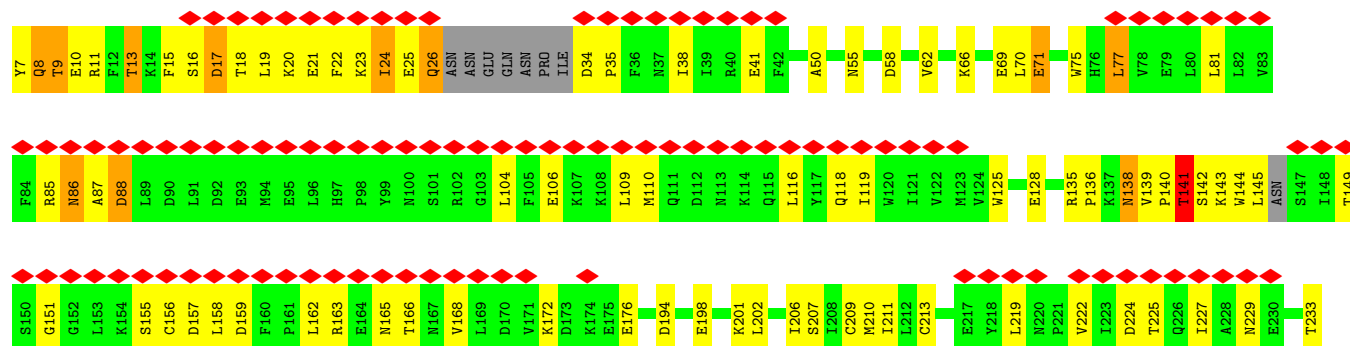


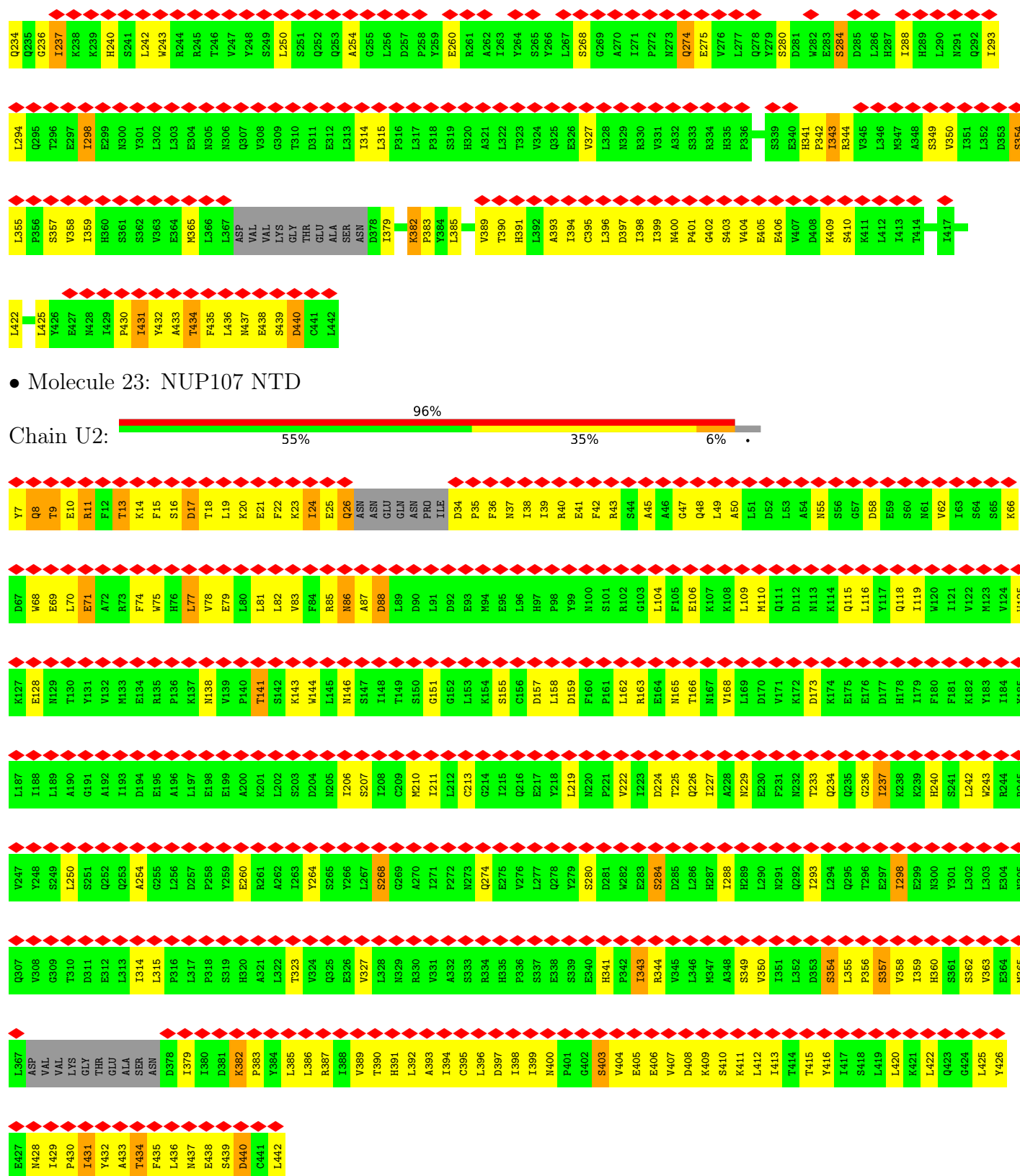


• Molecule 22: NUP107 CTD



• Molecule 23: NUP107 NTD





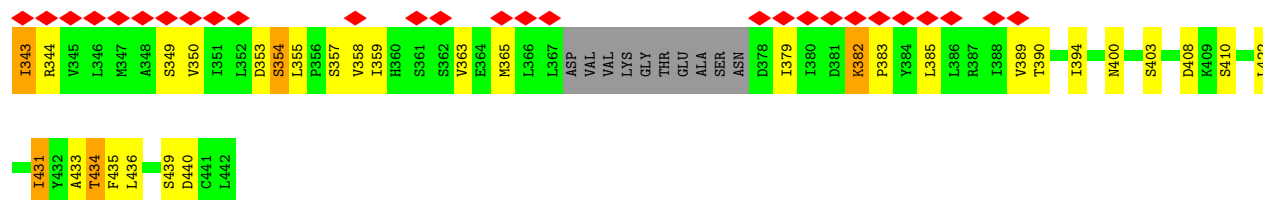
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Q307	V308	G309	T310	D311	E312	L313	I314	L315	P316	L317	P318	S319	H320	A321	L322	Y323	V324	Q325	E326	V327	L328	N329	R330	V331	A332	S333	R334	H335	P336	S337	E338	N400	P401	G402	S403	V404	E405	E406	V407	D408	K409	S410	K411	L412	I413	T414	T415	Y416	I417	L418	L419	K421	L422	Q423	G424	L425	Y426		
V247	Y248	S249	L250	S251	Q252	Q253	A254	G255	L256	D257	P258	Y259	E260	R261	A262	I263	Y264	S265	Y266	L267	S268	G269	A270	I271	P272	N273	Q274	E275	V276	L277	Q278	Y279	S280	D281	W282	E283	S284	D285	L286	H287	I288	H289	L290	N291	Q292	I293	L294	Q295	T296	E297	I298	E299	N300	Y301	L302	L303	E304	N305	N306
L187	I188	L189	A190	G191	A192	I193	D194	E195	A196	L197	E198	E199	A200	K201	L202	S203	D204	W205	I206	S207	L208	C209	M210	I211	L212	C213	G214	I215	Q216	E217	V218	L219	W220	P221	V222	L223	D224	T225	Q226	I227	N228	N229	E230	F231	D232	T233	Q234	Q235	C236	I237	K238	D239	S241	L242	W243	R244	R245	T246	
K127	E128	M129	T130	V131	V132	M133	E134	R135	P136	K137	N138	V139	P140	T141	S142	K143	V144	L145	N146	S147	I148	T149	S150	G151	G152	L153	K154	S155	G156	D157	L158	D159	F160	P161	L162	R163	E164	N165	T166	N167	V168	L169	D170	V171	K172	D173	K174	E175	E176	D177	H178	I179	F180	F181	K182	V183	T184	Y185	E186
D67	W68	E69	L70	E71	A72	R73	F74	W75	H76	L77	V78	E79	L80	L81	L82	W83	F84	R85	N86	A87	D88	L89	D90	L91	D92	E93	W94	E95	L96	H97	P98	Y99	N100	S101	R102	G103	L104	F105	E106	K107	K108	L109	M110	Q111	D112	N113	K114	Q115	L116	Y117	Q118	L119	W120	T121	V122	W123	V124	W125	L126
Y7	Q8	T9	E10	R11	F12	T13	K14	F15	S16	D17	T18	L19	K20	E21	F22	K23	T24	E25	Q26	ASN	ASN	GLU	GLN	ASN	ASN	PRO	TLE	D34	P35	F36	N37	I38	I39	R40	E41	R43	S44	A45	A46	G47	Q48	L49	A50	L51	D52	L53	A54	N55	S56	G57	D58	E59	S60	N61	V62	T63	S64	S65	K66

● Molecule 23: NUP107 NTD

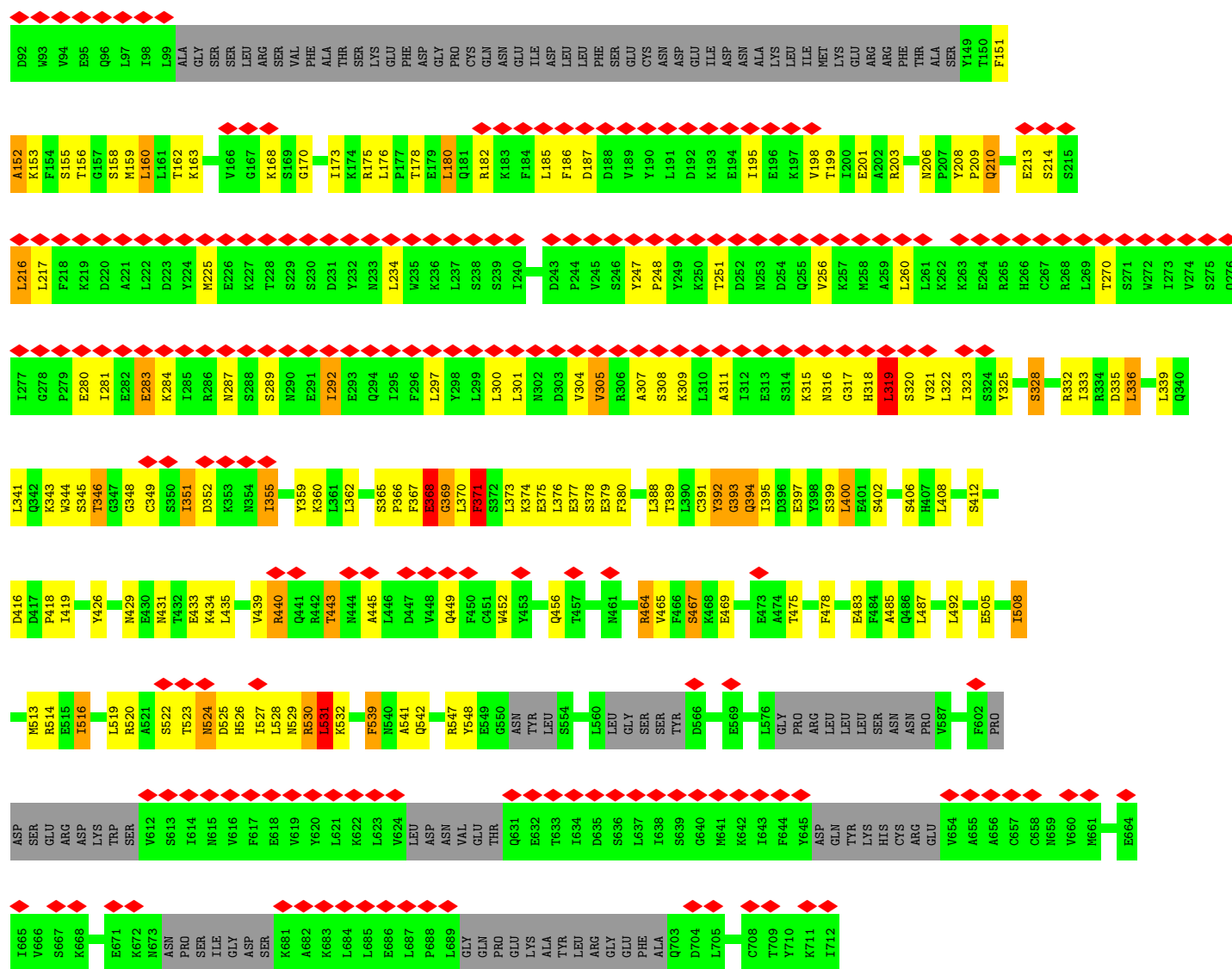
Chain U4:



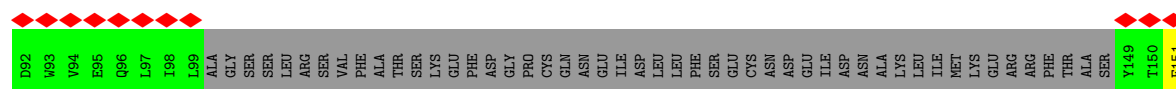
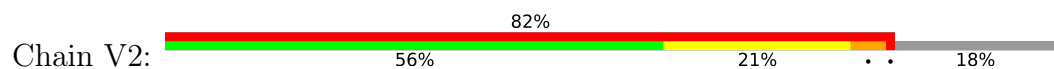
L267	S268	G269	A270	I271	N272	N273	Q274	E275	V276	L277	Q278	Y279	S280	D281	W282	E283	S284	D285	L286	H287	I288	E289	L290	N291	Q292	I293	L294	Q295	T296	E297	I298	E299	I314	L315	P316	L317	P318	L322	T323	V324	V327	N328	R329	R330	R331	A332	S333	R334	H335	P336	S337	E338	S339	E340	H341	P342			
S203	D204	N205	I206	S207	I208	C209	M210	I211	L212	C213	G214	I215	L219	V222	I223	D224	T225	Q226	I227	A228	N229	E230	F231	N232	T233	Q234	Q235	G236	I237	H240	S241	L242	W243	R244	R245	T246	V247	Y248	S249	L250	S251	Q252	Q253	A254	Q255	L256	D257	P258	Y259	E260	R261	A262	I263	Y264	S265	Y266			
K143	W144	L145	N146	S147	I148	T149	S150	G151	G152	L153	K154	S155	C156	D157	L158	D159	F160	P161	L162	R163	E164	N165	T166	N167	V168	L169	D170	V171	K172	S241	L242	W243	R244	R245	T246	V247	Y248	S249	L250	S251	Q252	Q253	A254	Q255	L256	D257	P258	Y259	E260	R261	A262	I263	Y264	S265	Y266				
D67	W68	E69	L70	E71	A72	R73	F74	W75	H76	L77	V78	E79	L80	L81	L82	R85	N86	A87	D88	D92	E93	L104	F105	E106	L109	M110	L116	Y117	Q118	I119	W120	I121	V122	M123	V124	W125	L126	K127	E128	M129	T130	Y131	V132	M133	E134	R135	P136	K137	N138	V139	P140	T141	S142						
Y7	Q8	T9	E10	R11	F12	T13	K14	F15	S16	D17	T18	L19	K20	E21	F22	K23	T24	E25	Q26	ASN	ASN	GLU	GLN	ASN	PRO	TLE	D34	P35	F36	N37	I38	I39	R40	E41	F42	R43	S44	A45	A46	G47	Q48	L49	A50	L51	D52	L53	A54	N55	S56	G57	D58	E59	S60	N61	V62	T63	S64	S65	K66

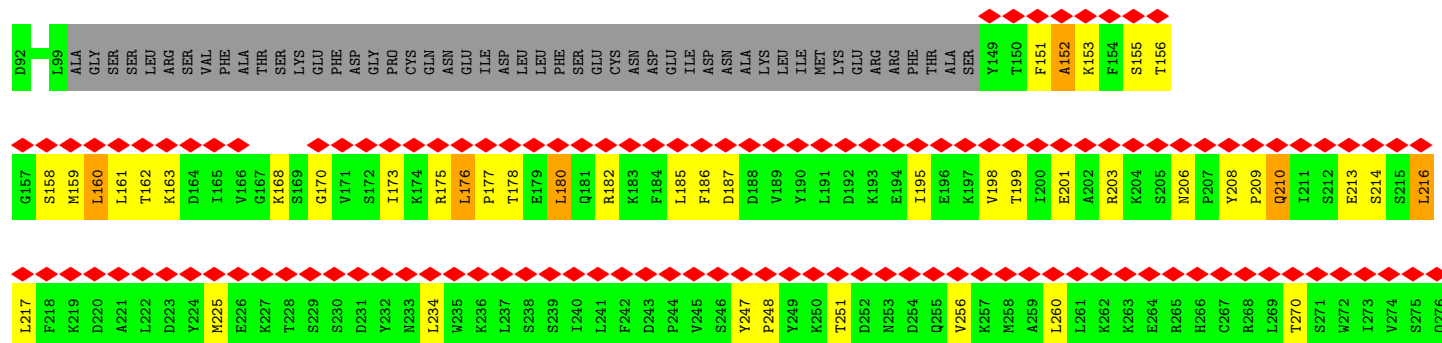
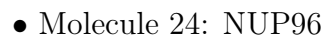


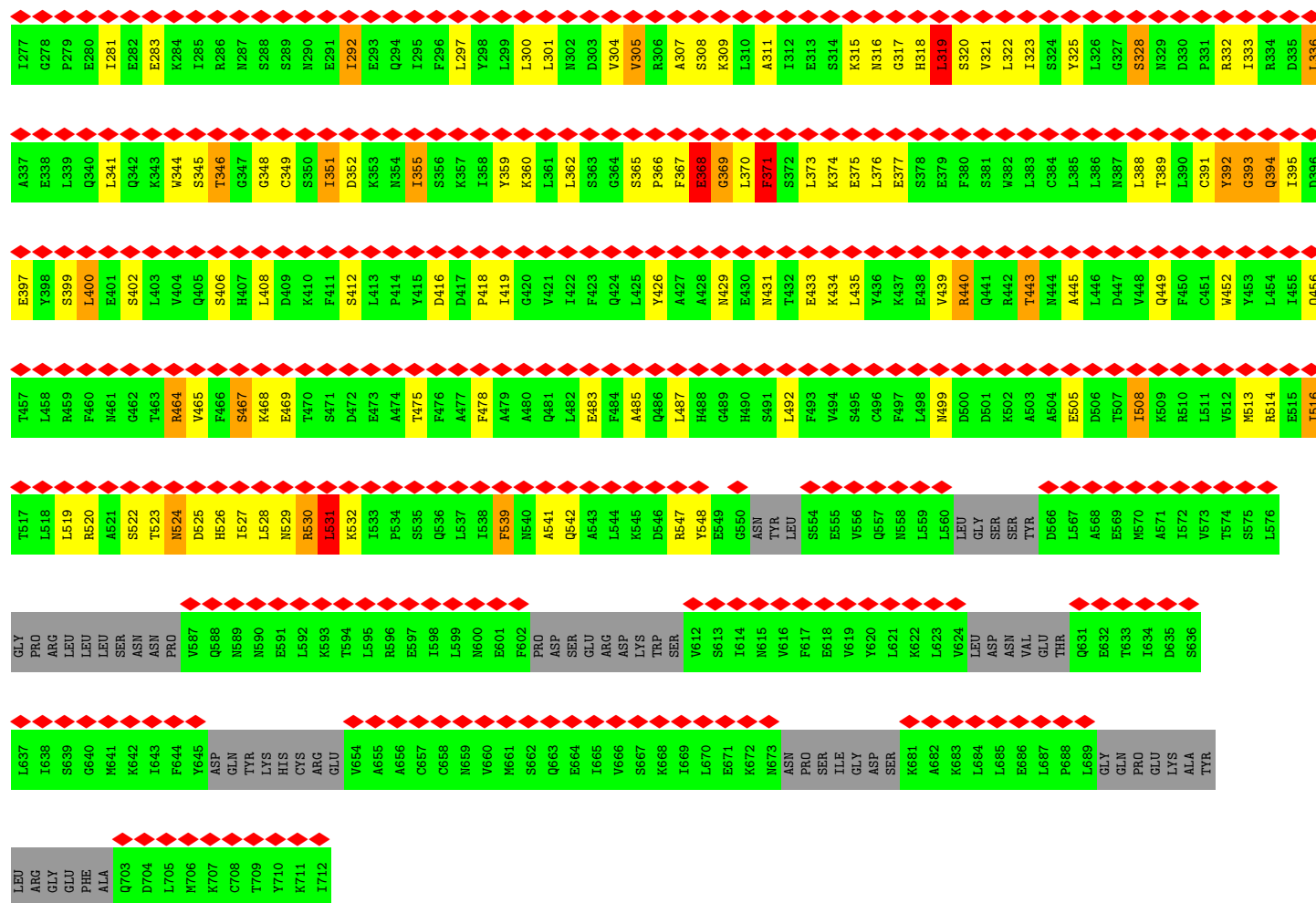
• Molecule 24: NUP96



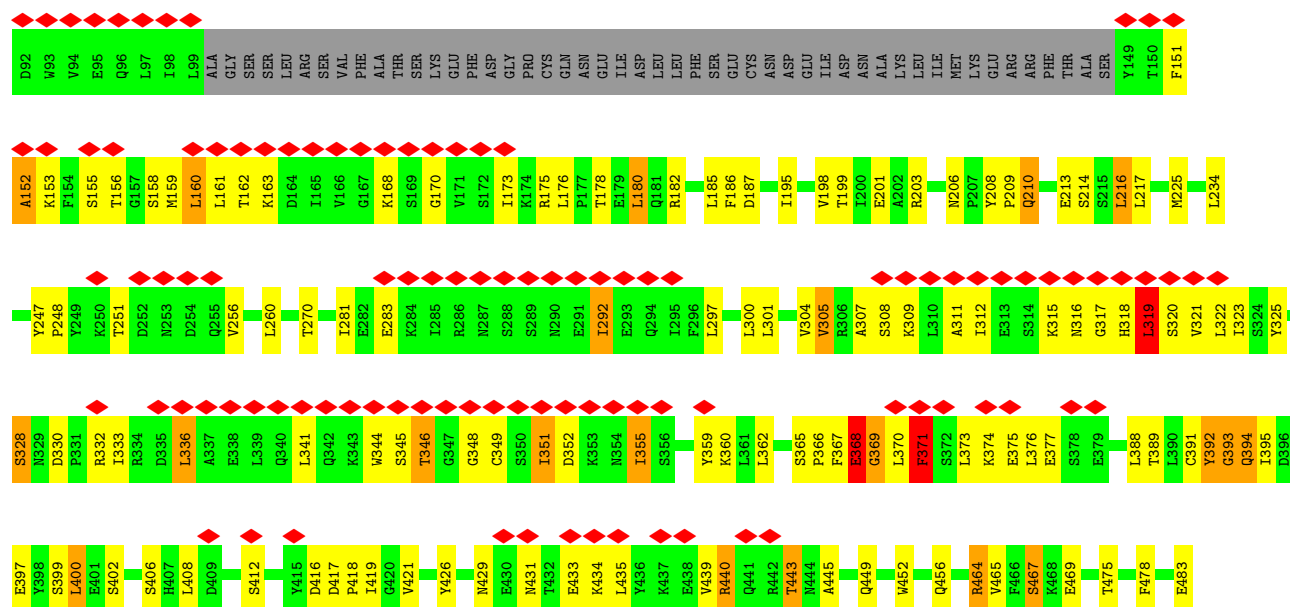
• Molecule 24: NUP96



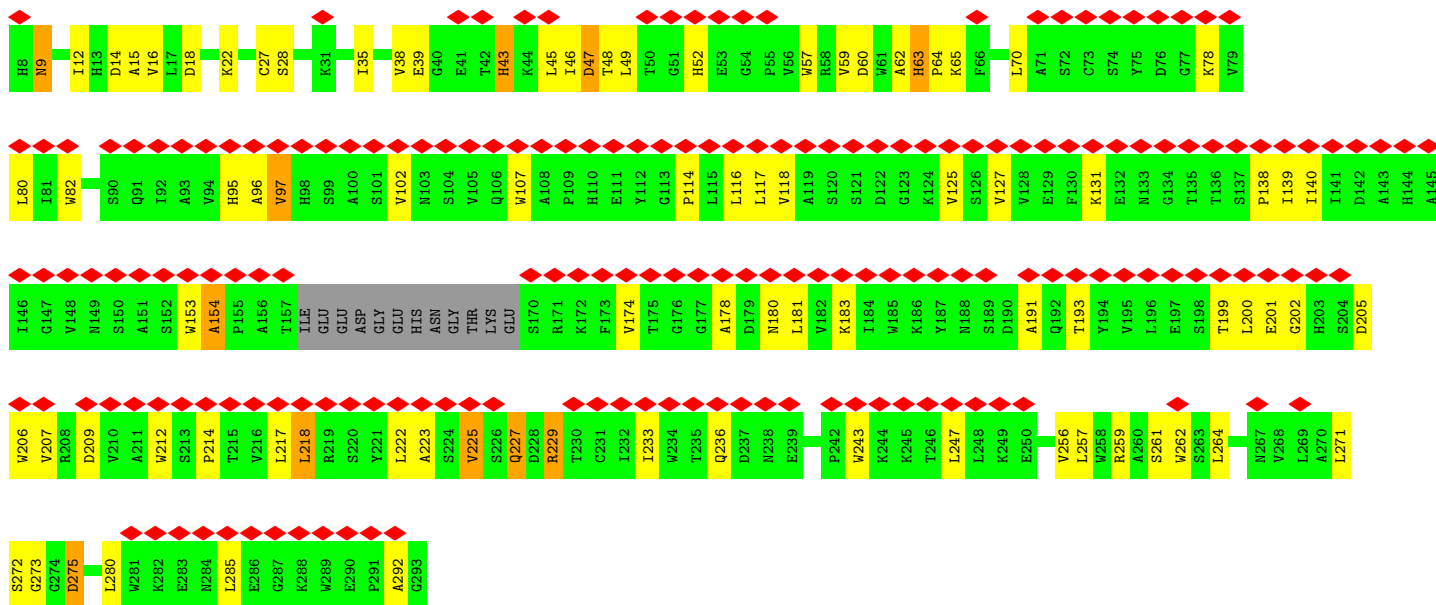




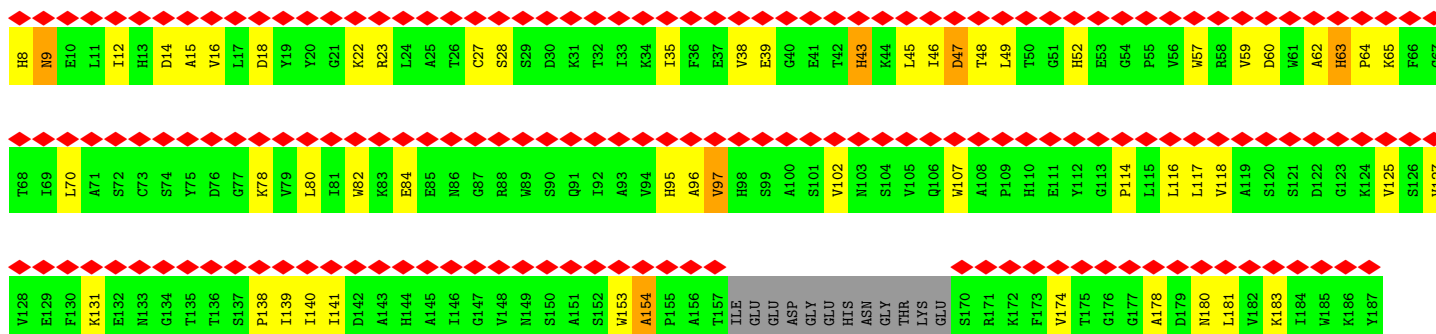
• Molecule 24: NUP96



- Molecule 25: SEC13

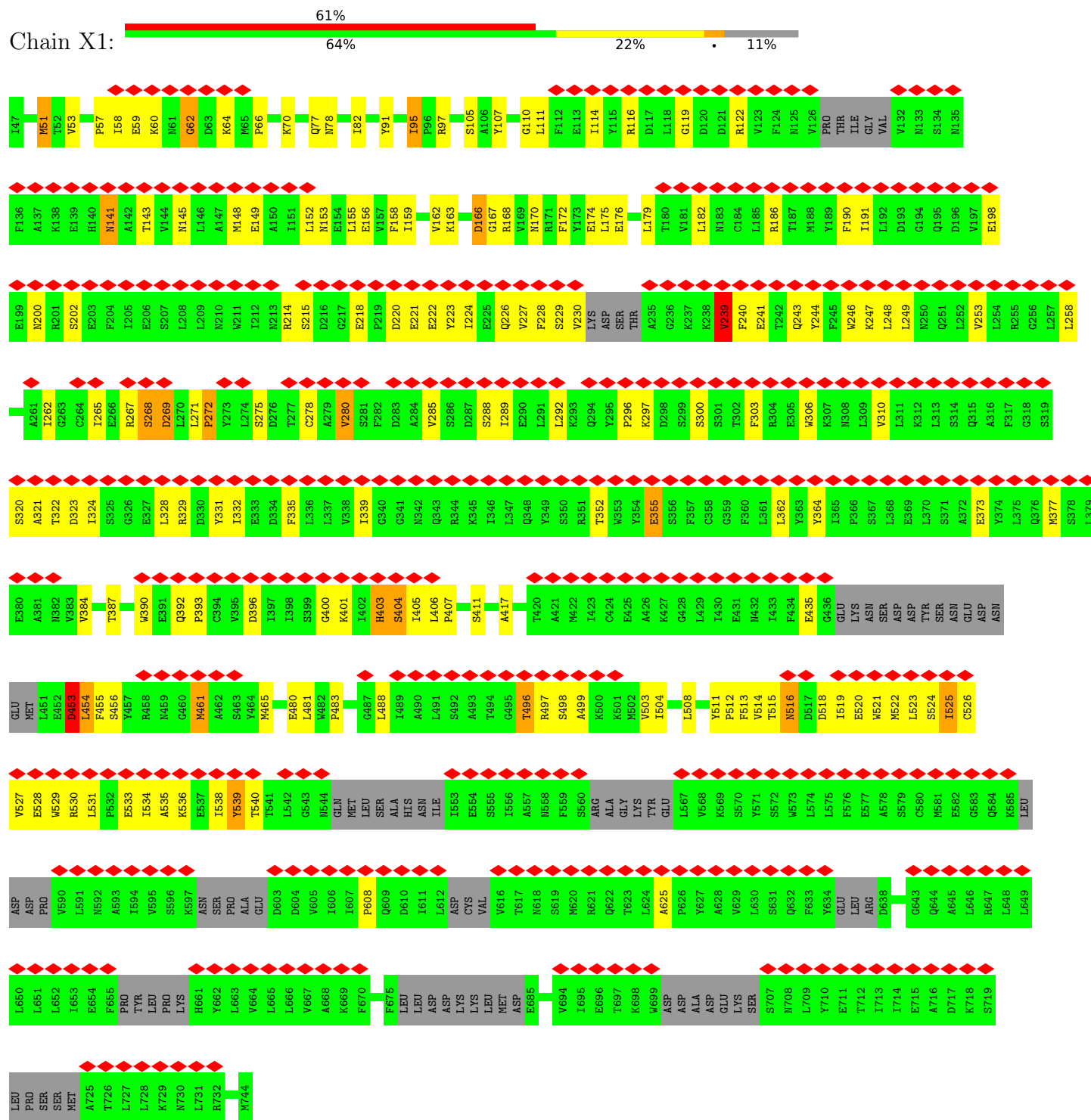


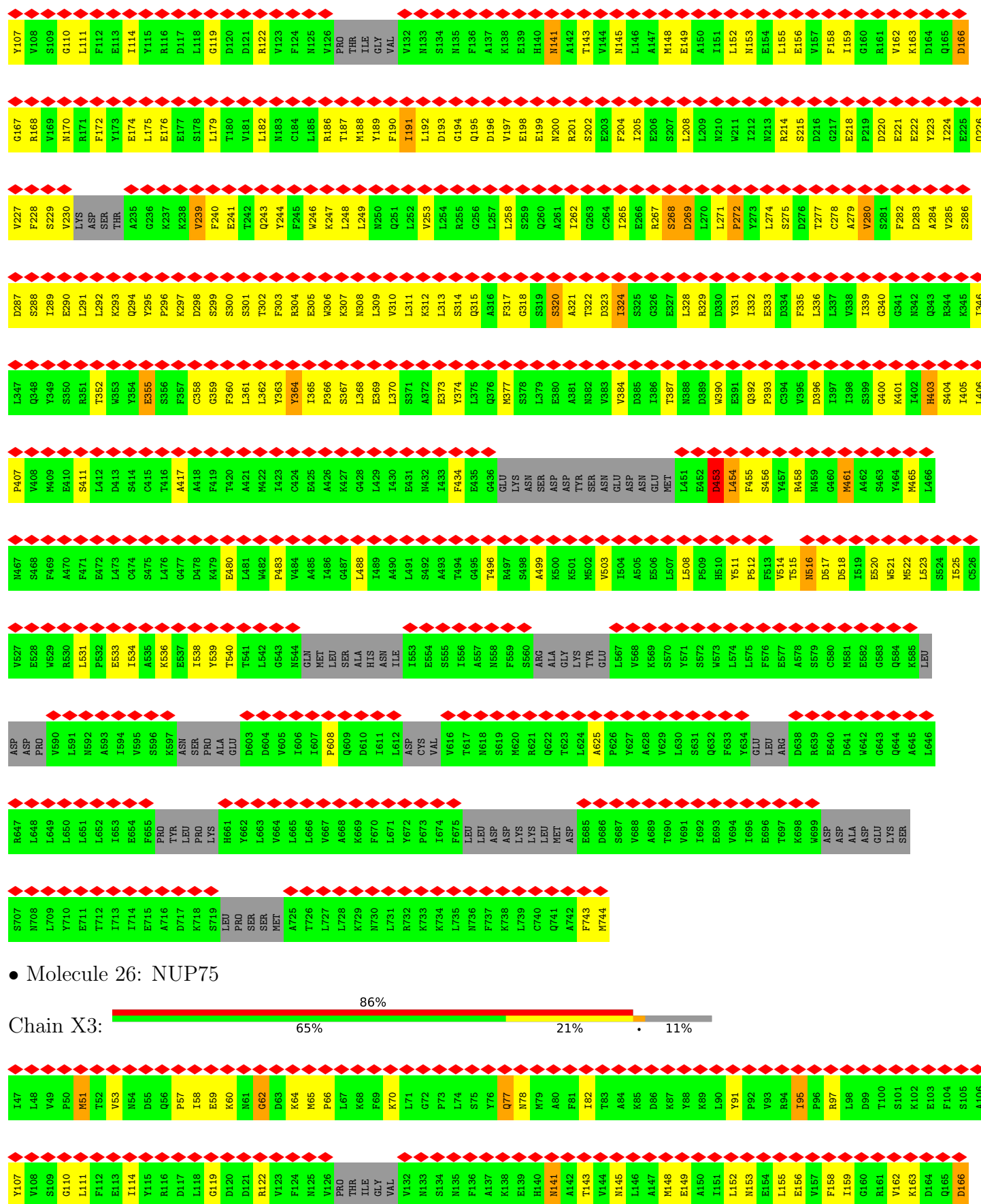
- Molecule 25: SEC13



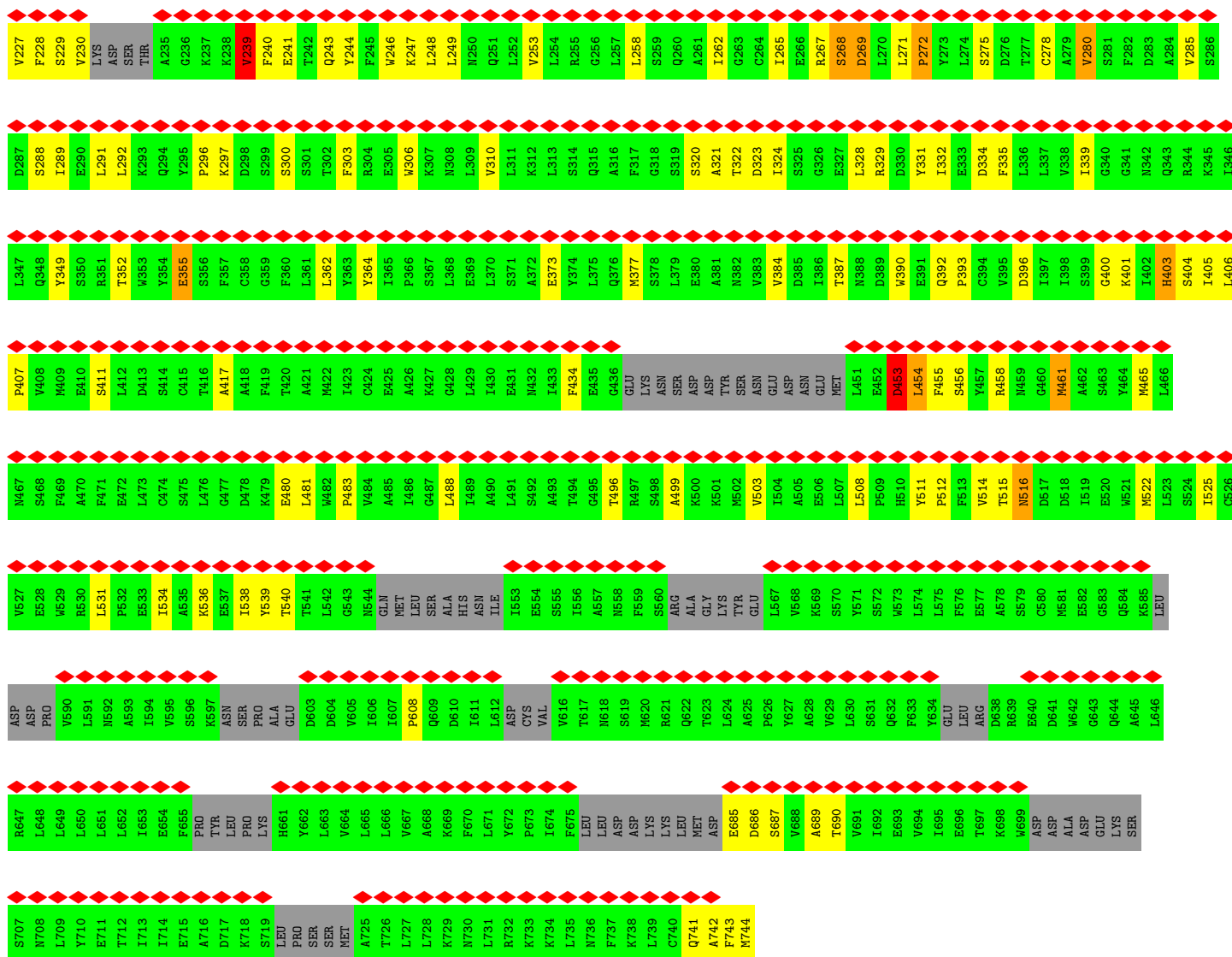
• Molecule 26: NUP75

Chain X1:

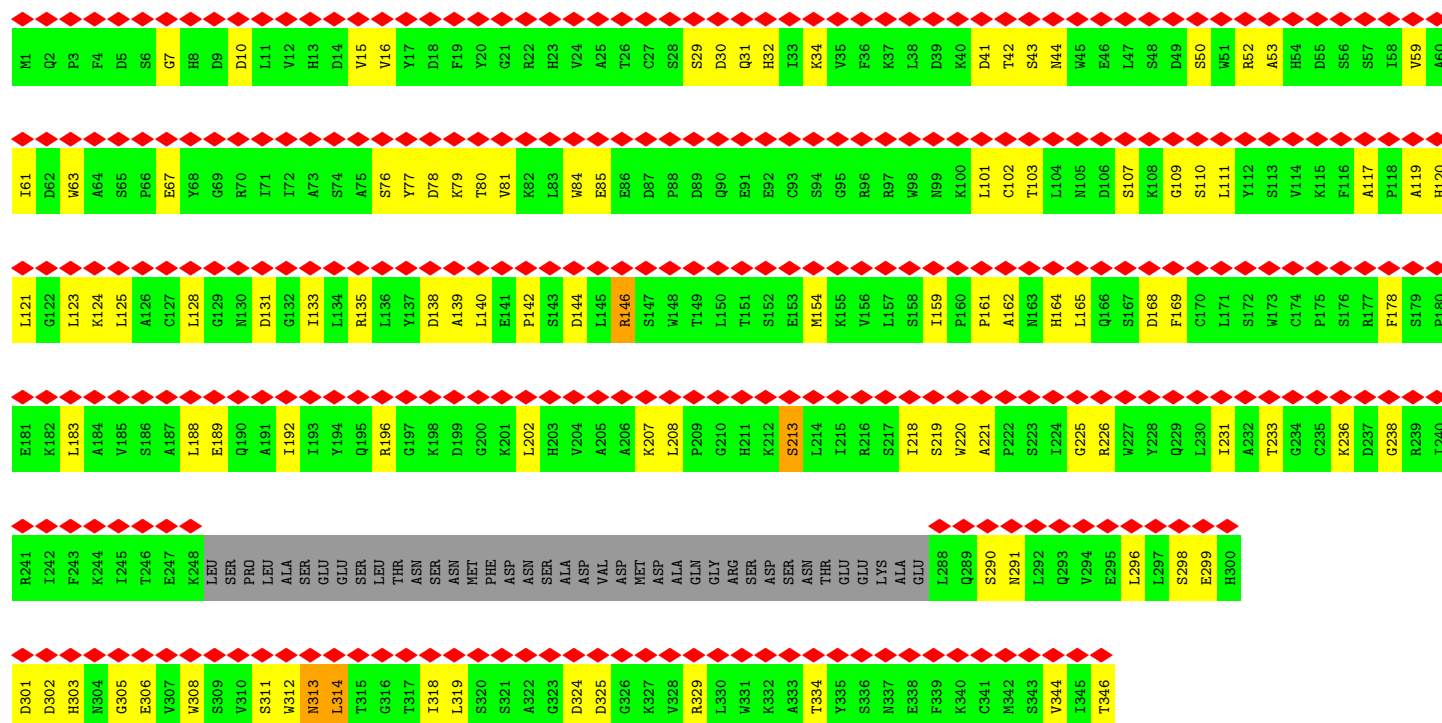




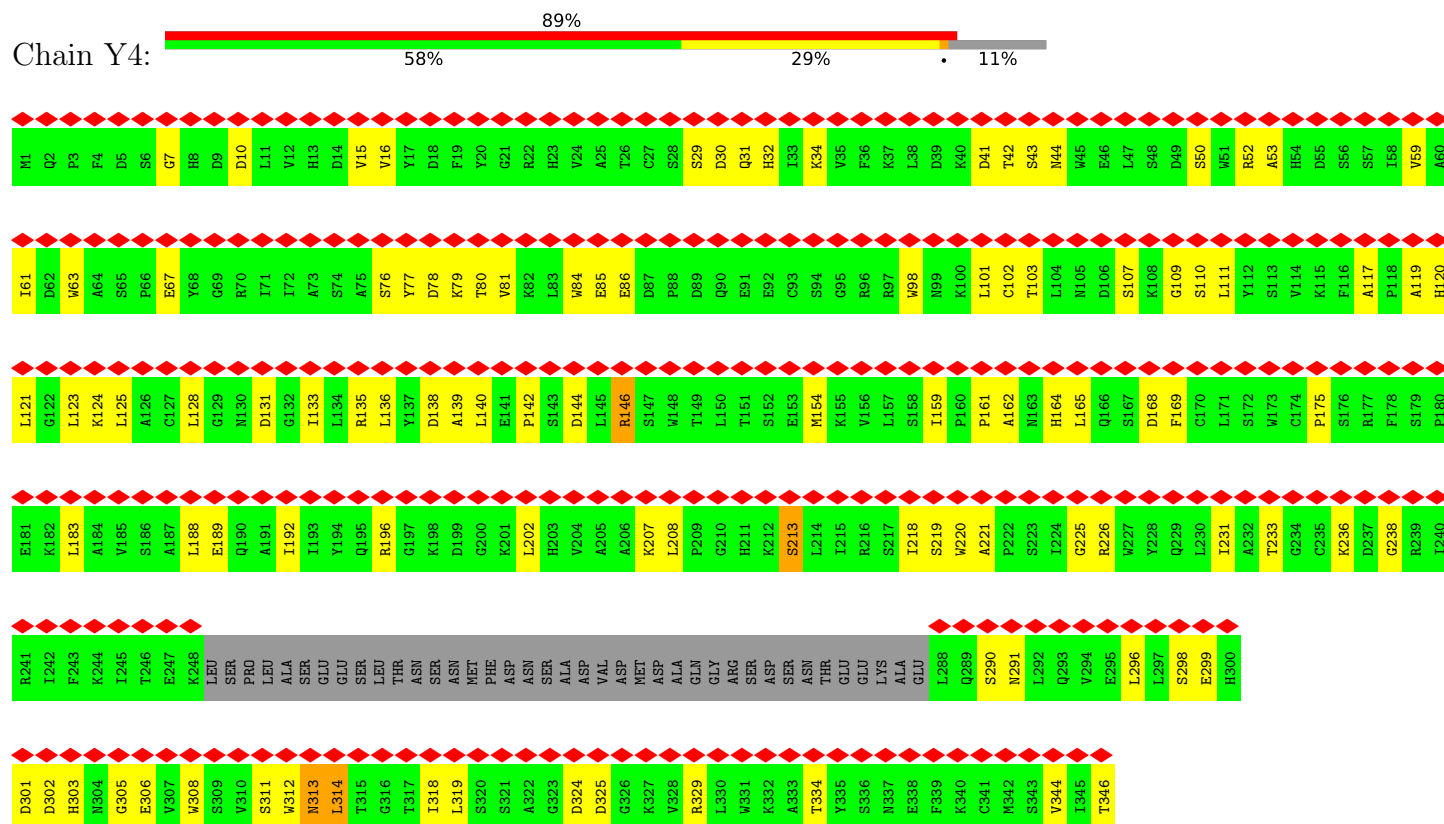
• Molecule 26: NUP75



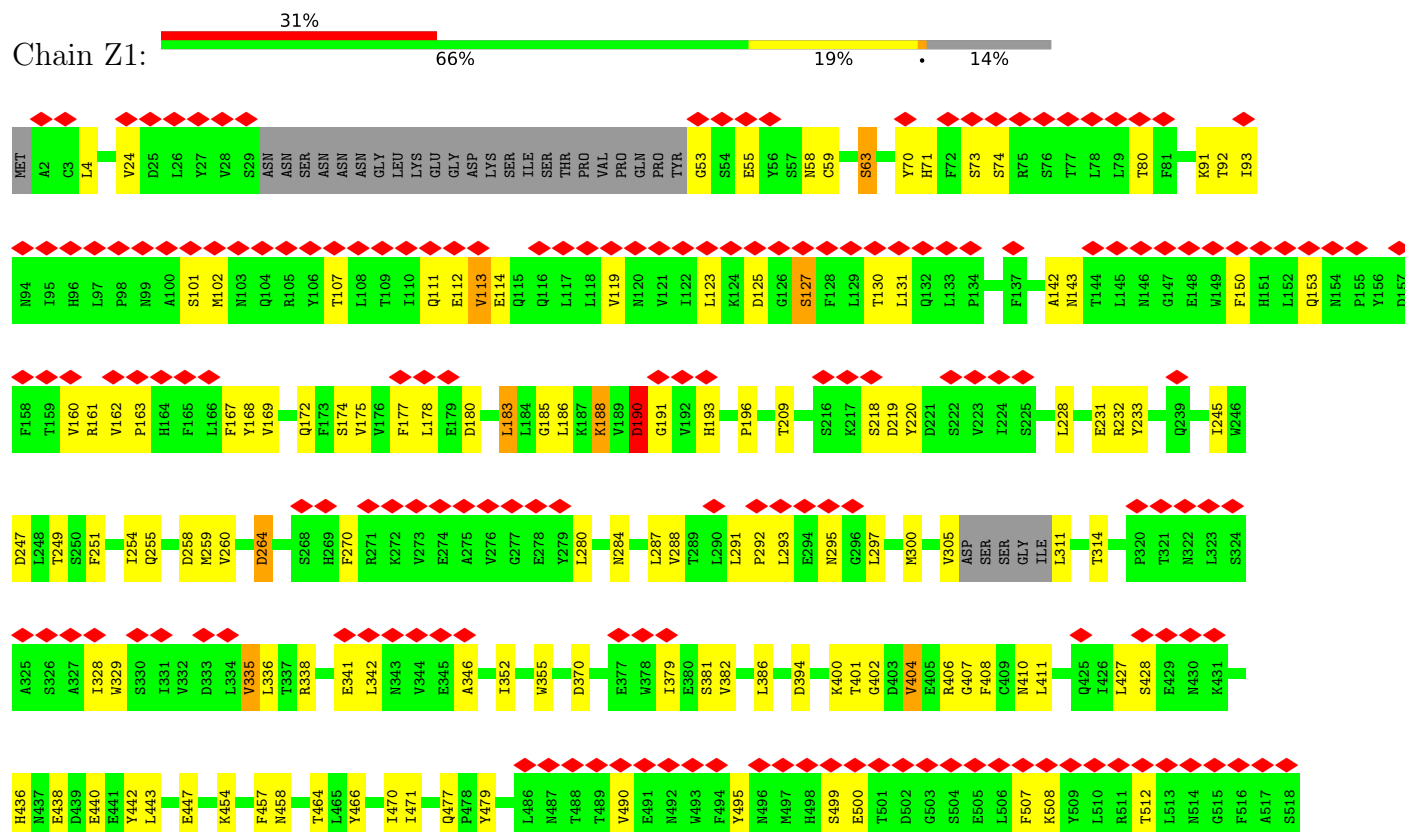
Chain Y2: 80% 59% 29% 11%

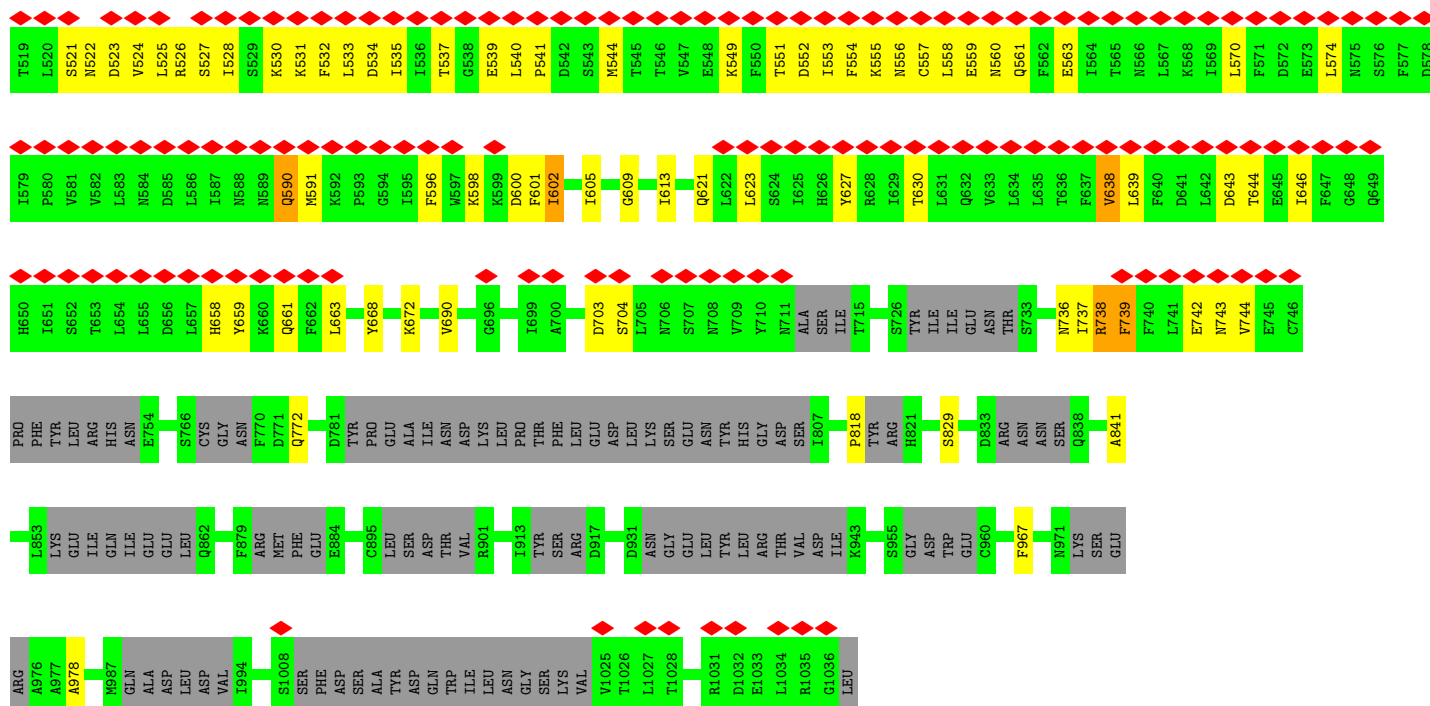


- Molecule 27: SEH1

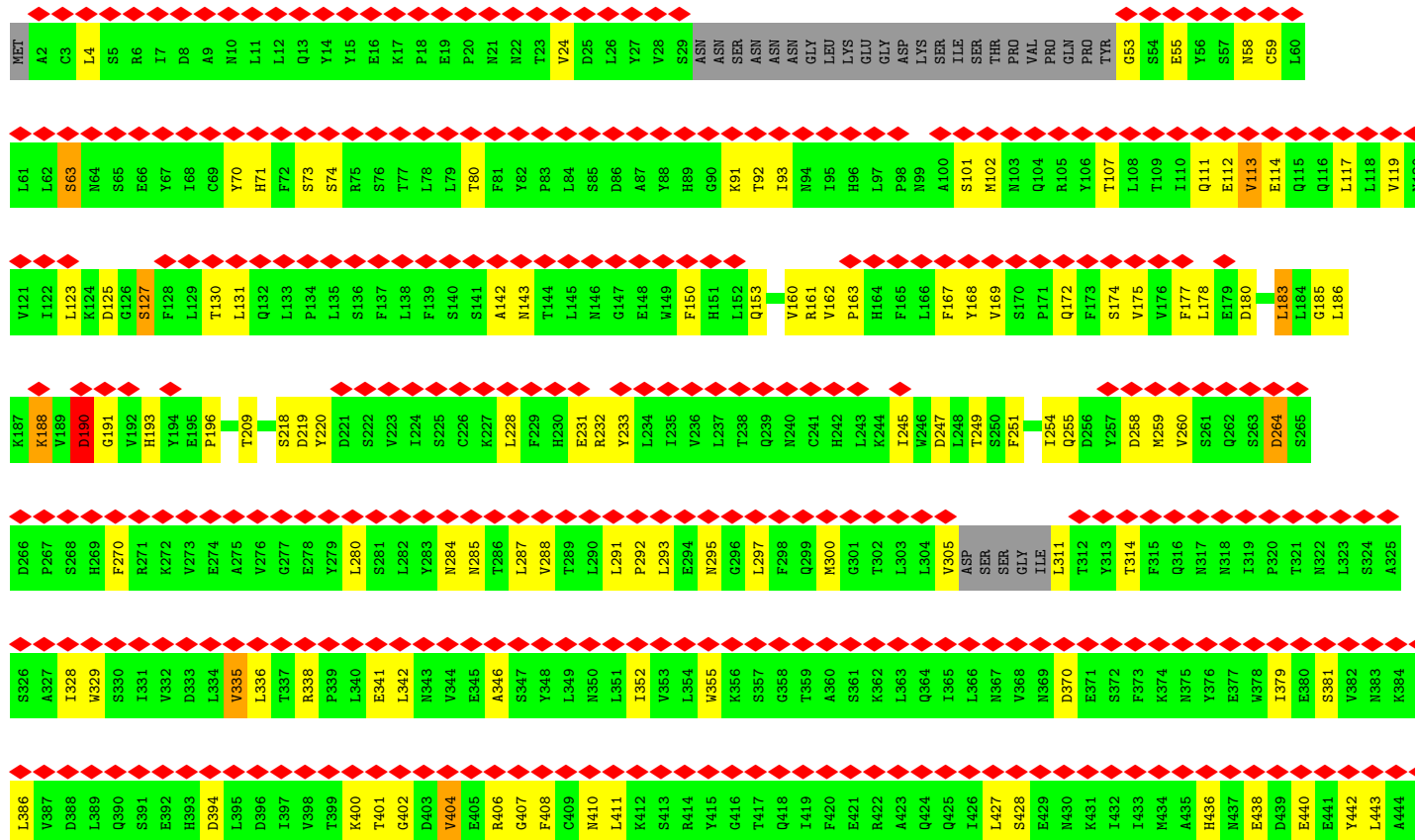
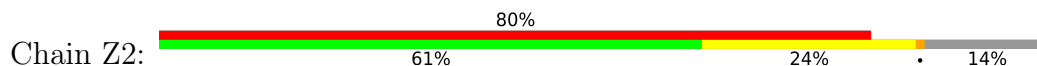


- Molecule 28: NUP160

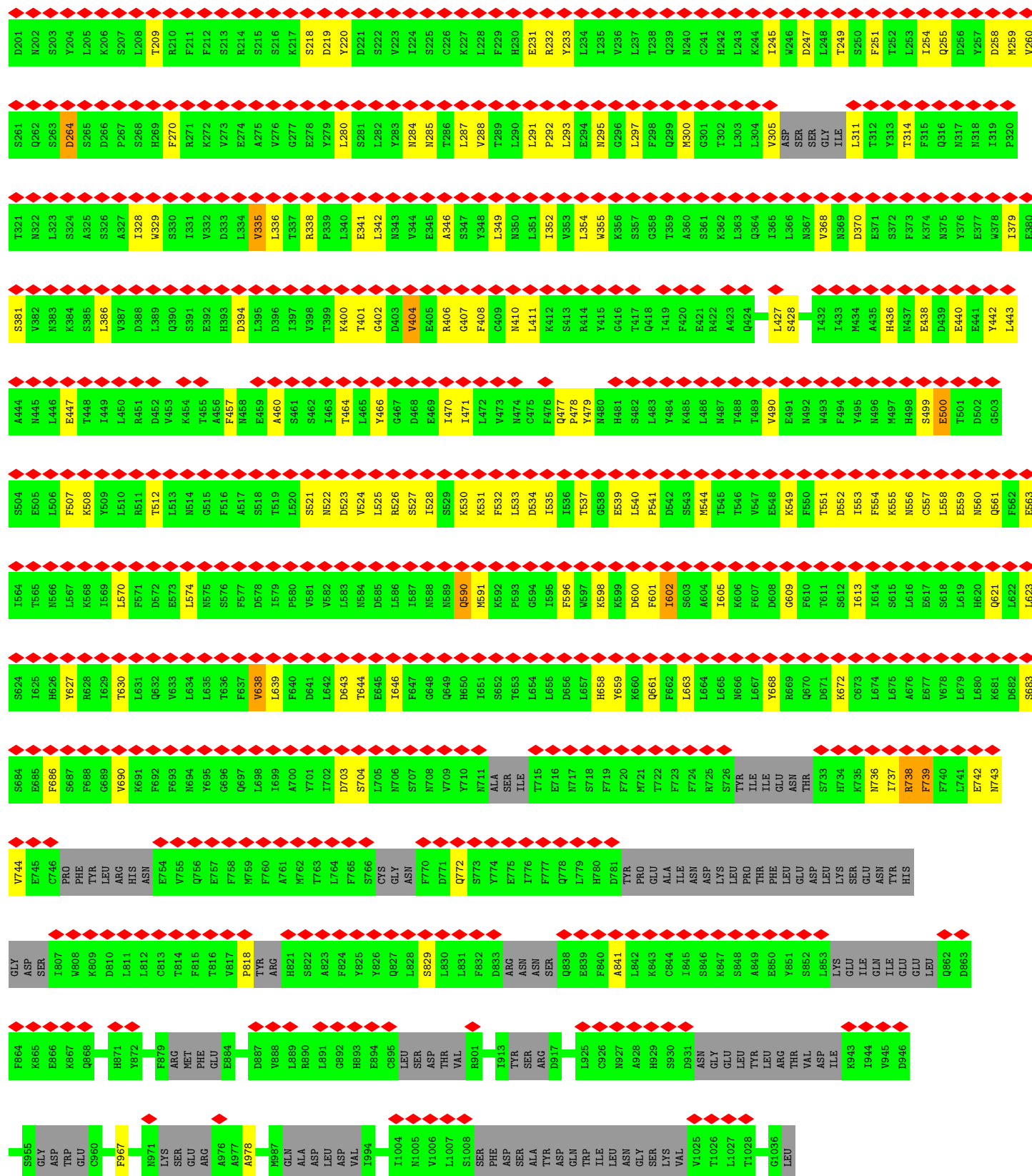




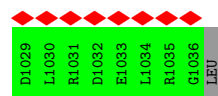
• Molecule 28: NUP160



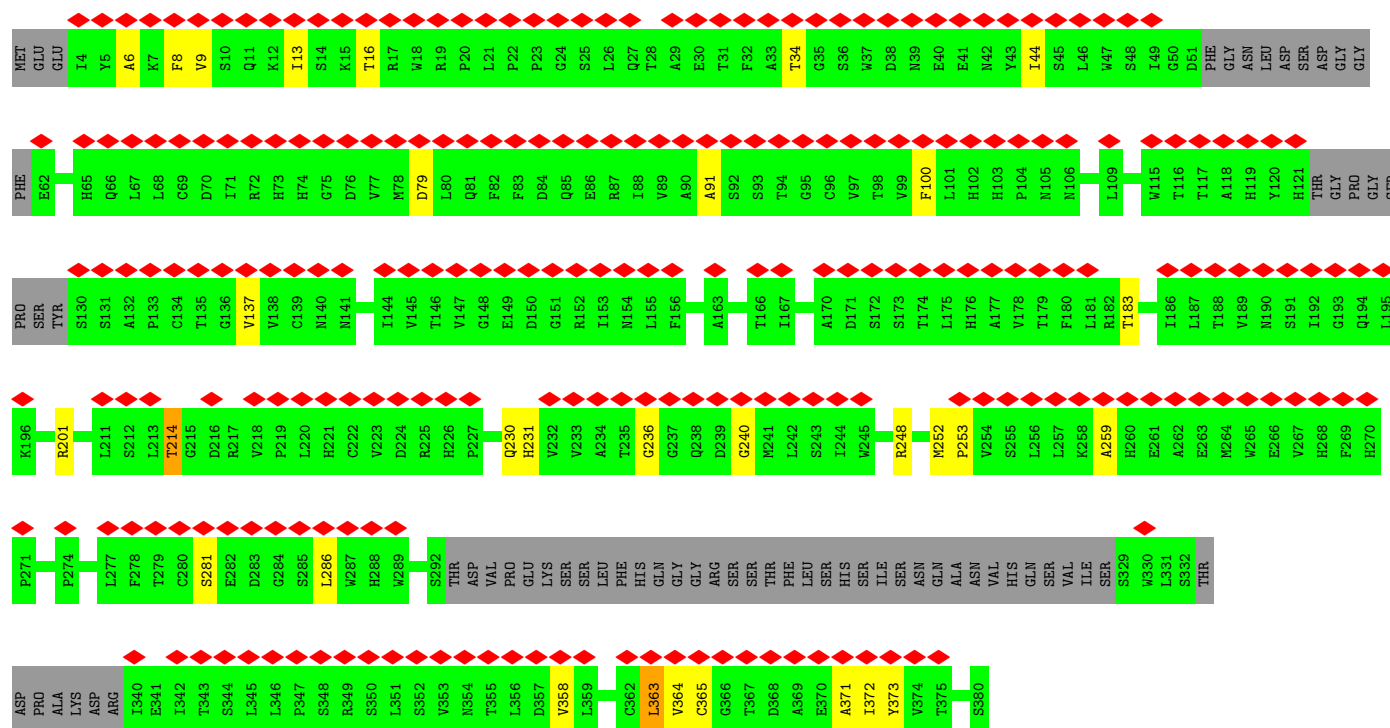
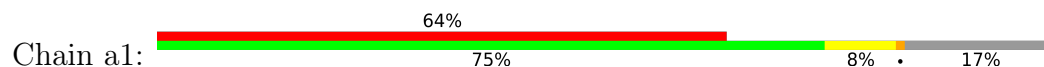




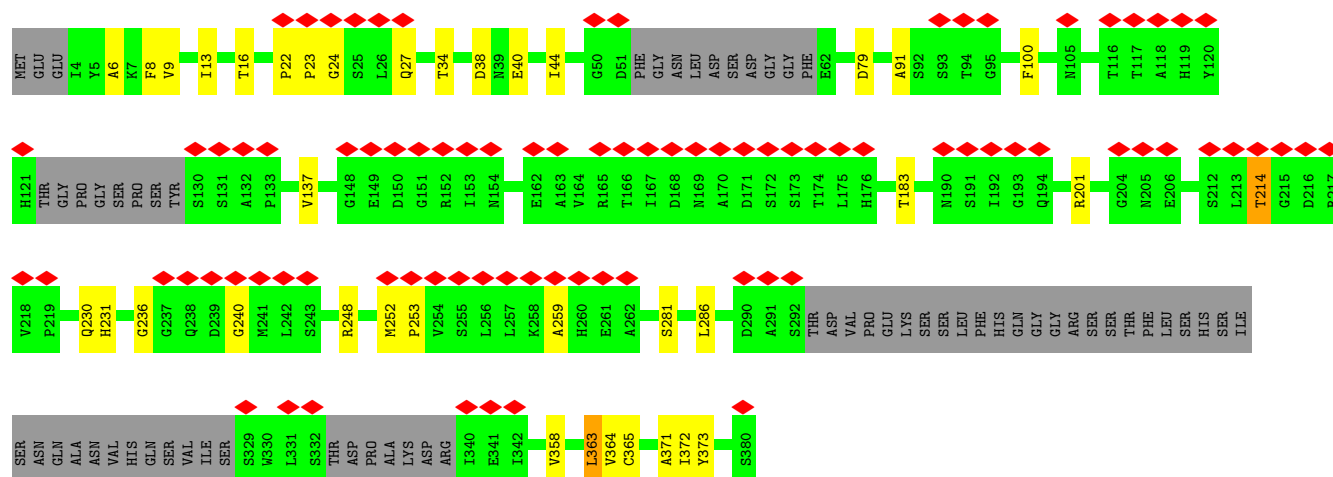
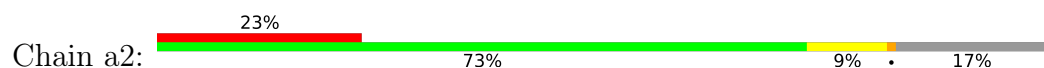




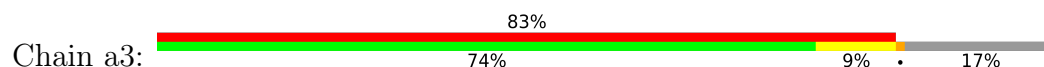
• Molecule 29: NUP43

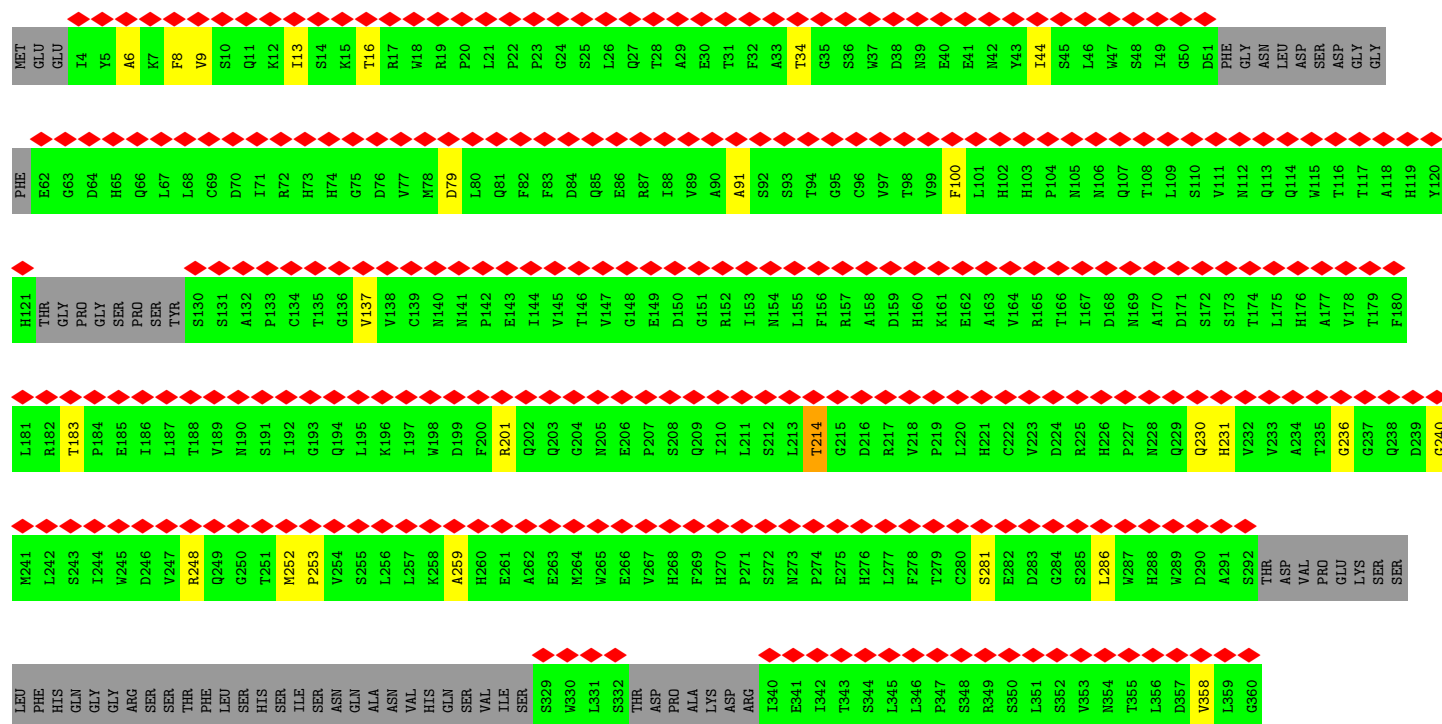
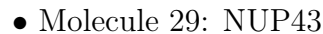


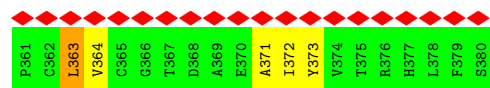
• Molecule 29: NUP43



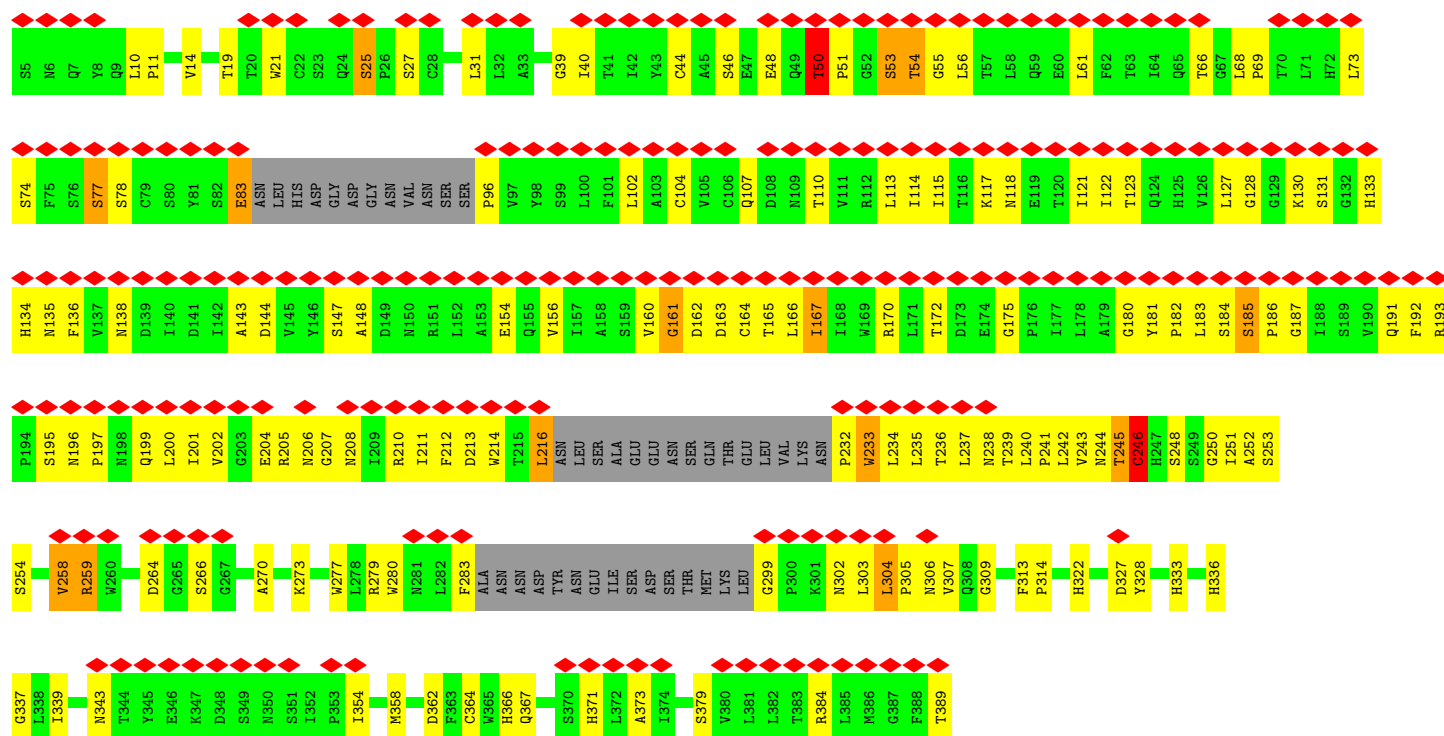
• Molecule 29: NUP43



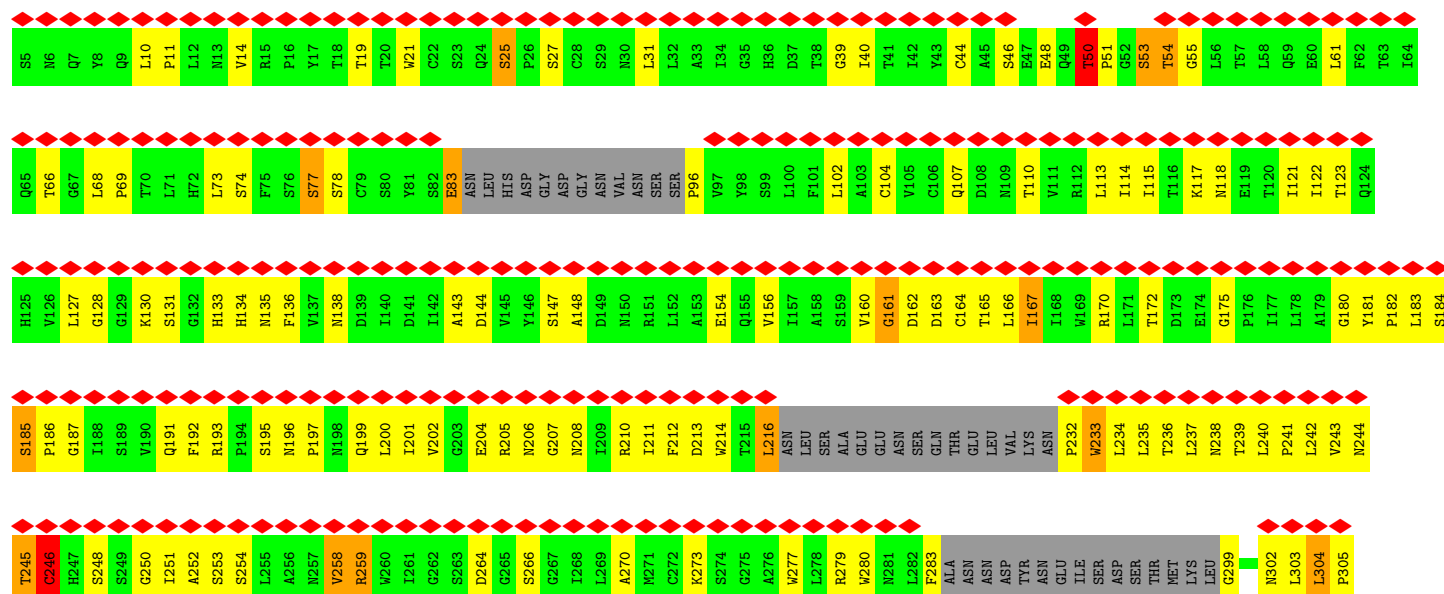
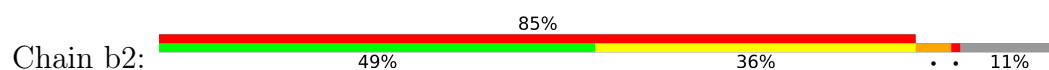


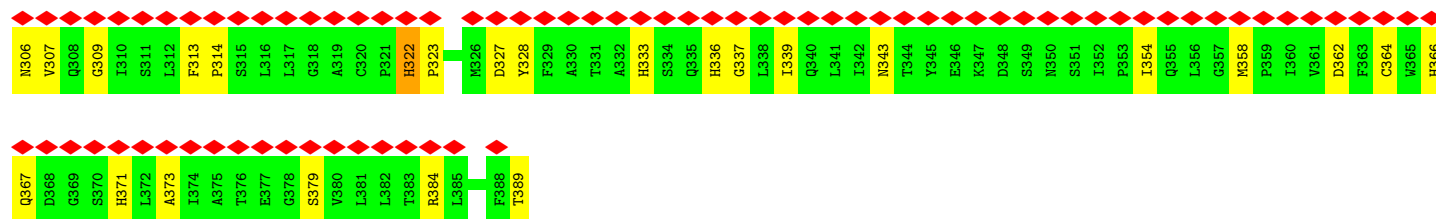


• Molecule 30: NUP37

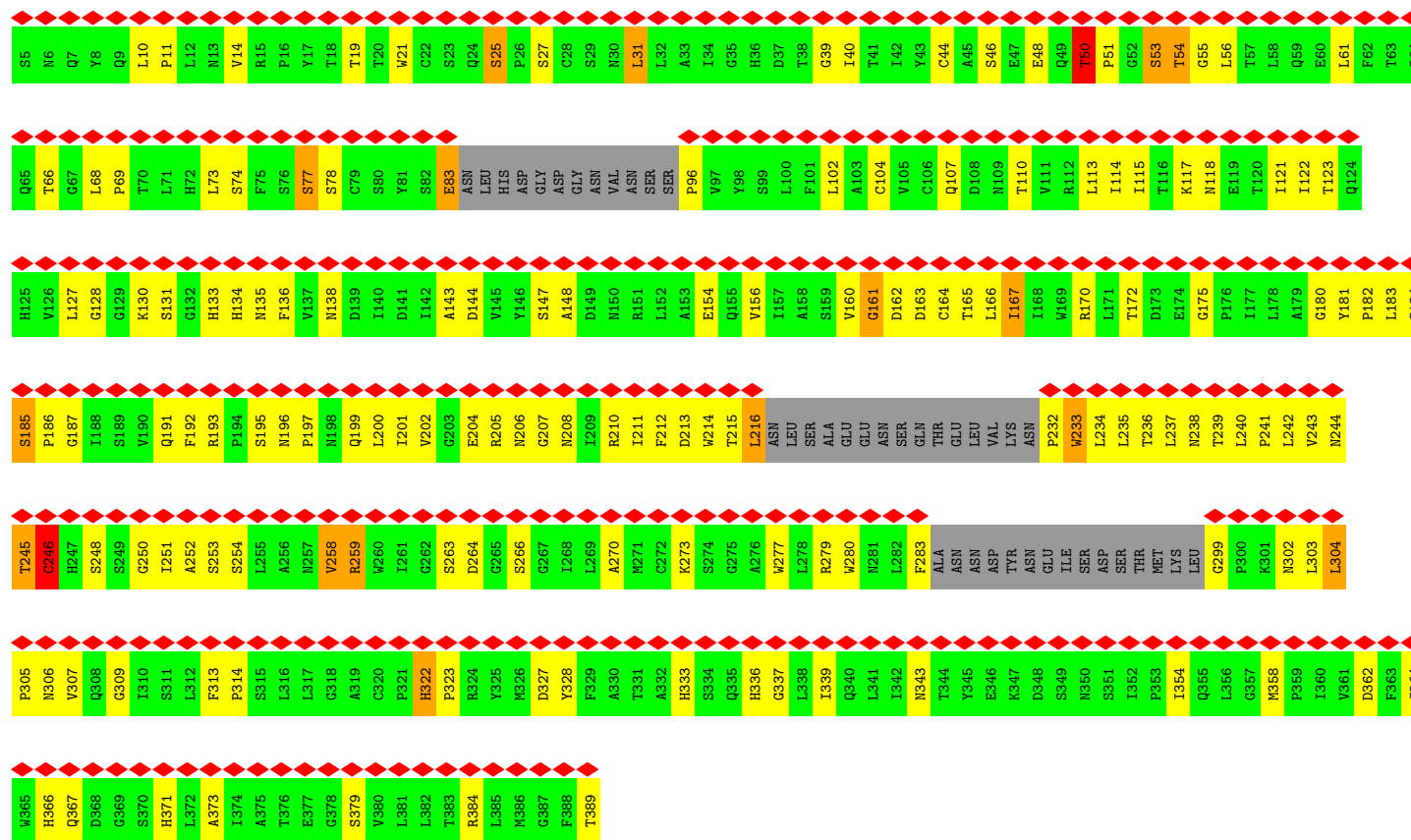
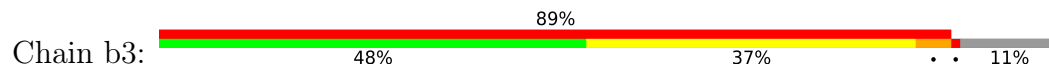


• Molecule 30: NUP37

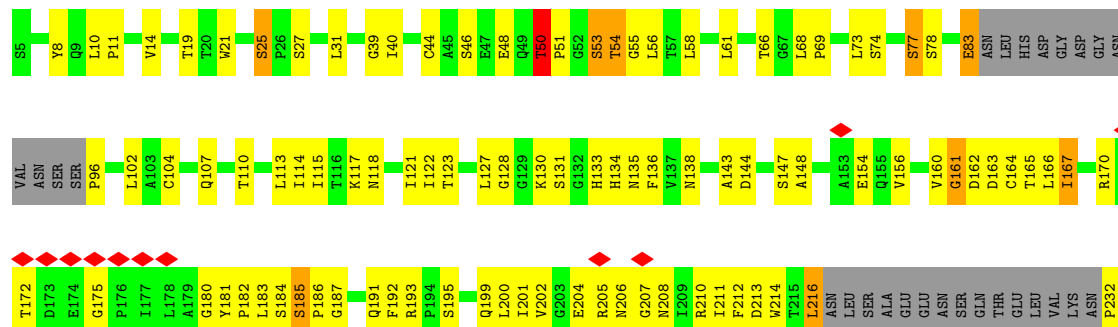


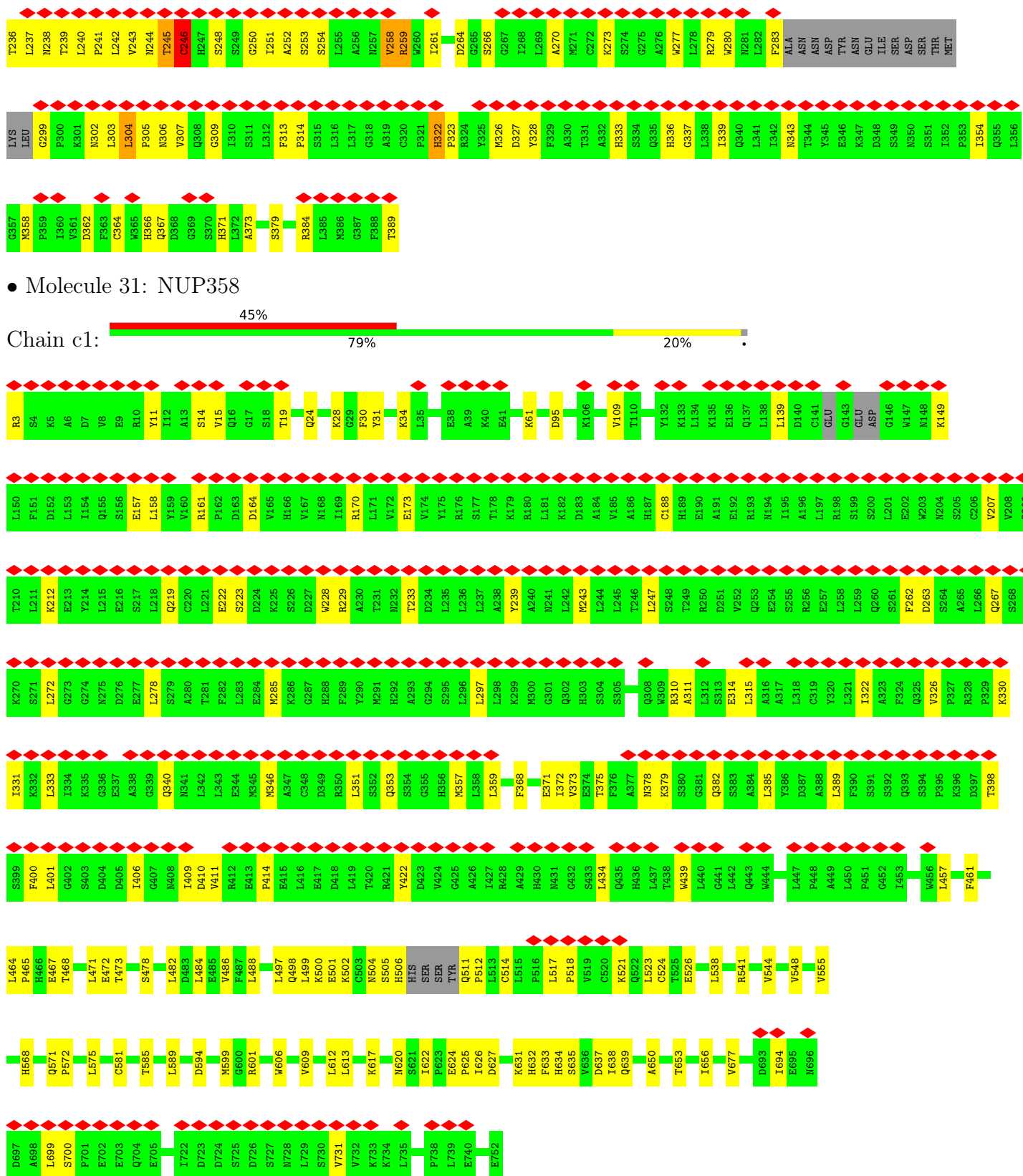


• Molecule 30: NUP37



• Molecule 30: NUP37



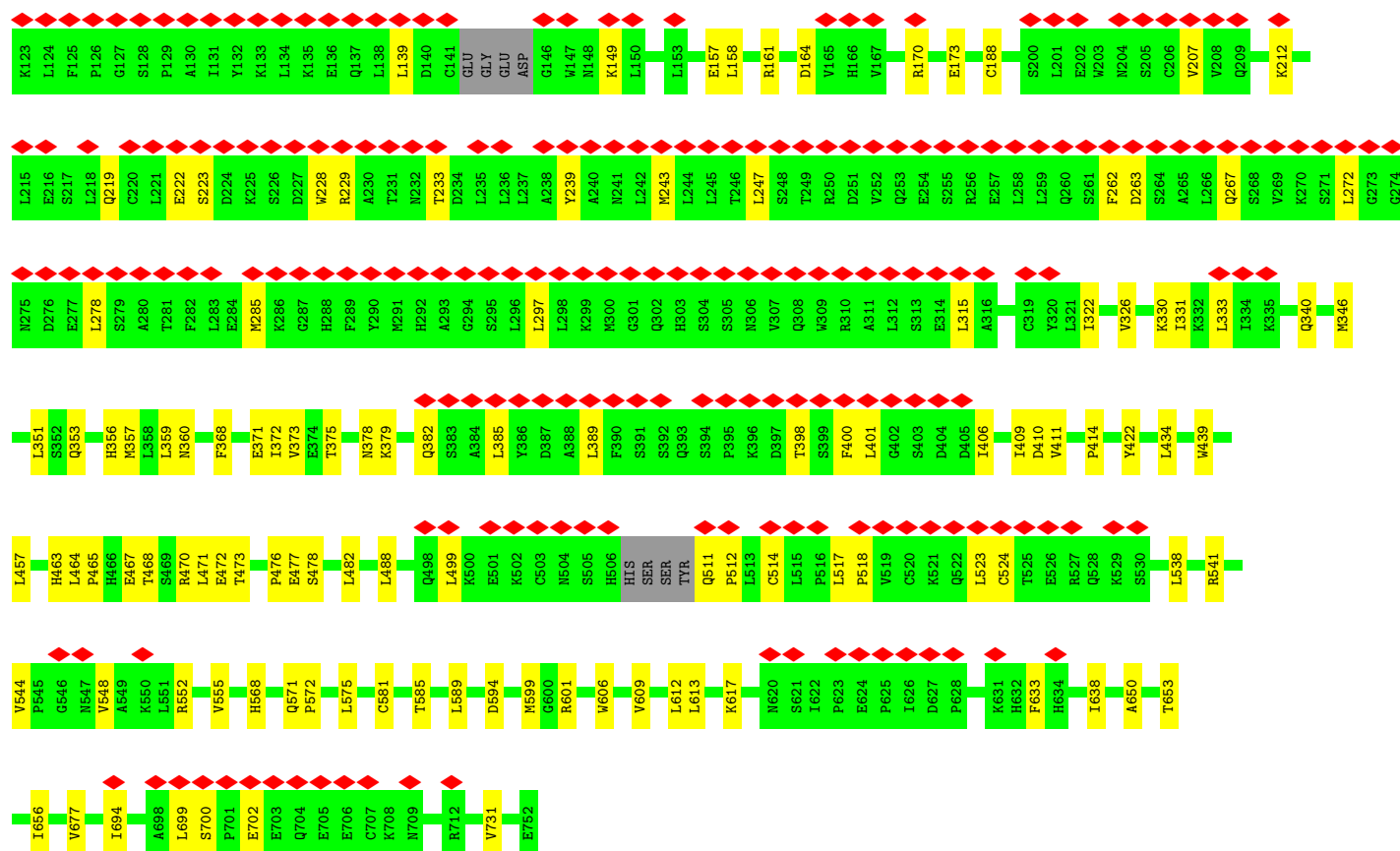


V603	A543	D483	D423	R363	H303	M243	D183	K123	H63	R3
H604	V544	L484	V424	G364	S304	L244	A184	L124	R64	S4
Y605	P545	E485	G425	K365	S305	L245	V185	F125	F65	K5
W606	G546	V486	A426	Q366	N306	T246	A186	P126	L66	A6
K607	N547	F487	I427	D367	V307	L247	H187	G127	Q67	D7
R608	V548	L488	R428	F368	Q308	S248	C188	S128	L68	V8
V609	A549	L489	A429	L369	W309	T249	H189	P129	L69	E9
L610	K550	H430	H430	K370	R310	R250	E190	A130	Y70	R10
P611	L551	V491	M431	E371	A311	D251	A191	I131	E71	Y11
L612	R552	V492	G432	L372	L312	V252	E192	Y132	L72	I12
L613	L553	Y493	S433	V373	S313	Q253	R193	K133	E73	A13
K614	L554	T494	L434	E374	E314	E254	H194	L134	E74	S14
I615	V555	S495	Q435	T375	L315	S255	I195	K135	M75	V15
I616	Q556	H496	H436	F376	A316	R256	A196	E136	T76	Q16
K617	H557	L497	L437	A377	L317	E257	L197	Q137	D77	G17
K618	E558	Q498	T438	N378	L318	L258	R198	L138	K78	S18
K619	I559	W439	W439	K379	C319	L259	S199	L139	A79	T19
N620	N560	K500	L440	S380	Y320	Q260	S200	D140	V80	P20
S621	T561	E501	G441	G381	L321	S261	L201	C141	E81	S21
I622	L562	K502	L442	Q382	I322	F262	E202	GLU	C82	P22
P623	R563	C503	Q443	S383	A323	D263	W203	GLU	X83	R23
E624	A564	N504	W444	A384	F324	S264	W204	ASP	R84	Q24
P625	Q565	S505	M445	L385	Q325	A265	S205	G146	R85	K25
I626	E566	H506	S446	Y386	V326	L266	C206	W147	S86	S26
D627	K567	HIS	L447	D387	P327	Q267	V207	N148	V87	M27
P628	H568	SER	P448	A388	R328	S268	W208	K149	E88	K28
L629	G569	SER	A449	L389	P329	V269	Q209	L150	L89	G29
F630	L570	Q511	L450	F390	K330	K270	T210	F151	N90	F30
K631	Q571	P512	P451	S391	I331	S271	L211	D152	P91	V31
H632	P572	L513	Q452	S392	K332	L272	K212	L153	T92	F32
F633	A573	C514	I453	Q393	L333	G273	E213	I154	Q93	A33
H634	L574	L515	R454	S394	I334	G274	Y214	Q155	K94	K34
S635	L575	P516	K455	P395	K335	N275	L215	S156	D95	L35
V636	V576	L517	W456	K396	G336	D276	E216	E157	L96	V36
D637	H577	P518	L457	D397	E337	E277	L217	L158	V97	V37
I638	V578	V519	K459	T398	A338	L278	L218	Y159	L98	E38
Q639	A579	C520	Q459	S399	G339	S279	Q219	V160	K99	A39
A640	E580	K521	L460	F400	Q340	A280	C220	R161	I100	K40
S641	C581	Q522	F461	L401	N341	T281	L221	P162	A101	E41
E642	L582	L523	H462	G402	L342	F282	E222	D163	E102	Y42
I643	Q583	C524	H463	S403	L343	L283	S223	D164	L103	D43
K584	K584	T525	L464	D404	E344	E284	D224	V165	L104	L44
Y646	T585	E526	P465	D405	E344	M285	D224	C105	C106	A45
	G586	R527	H466	I406	M345	K286	S226	V167	K106	K46
A650	S587	Q528	E467	G407	A347	G287	D227	N107	N107	K47
T653	G588	K529	T468	N408	C348	H288	W228	I169	D108	Y48
	L589	Y589	S469	I409	D349	F289	R229	R170	V109	I49
I656	N590	W531	R470	D410	R350	Y290	A230	L171	T110	C50
V677	S591	W532	L471	V411	L351	M291	T231	V172	D111	T51
I694	F592	D533	E472	R412	S352	H292	W232	E173	G112	V62
	Y593	A534	T473	E413	Q353	A293	T233	V174	R113	I53
L699	D594	N474	M474	P414	S354	Q294	D234	V175	A114	N54
S700	Q595	A475	A475	E415	G355	S295	L235	R176	K115	V55
Y731	R596	C536	P476	L416	H356	L296	L236	S177	Y116	O56
	E597	T537	P476	L416	H356	L296	L236	S177	Y116	O56
V731	L538	E477	E417	R412	M357	L297	L237	T178	W117	E57
E752	Y598	L539	S478	D418	L358	L298	A238	K179	L118	R58
	M599	I539	I479	L419	L359	K299	Y239	R180	E119	D59
G600	G600	H540	I479	L419	L359	K299	Y239	R180	E119	D59
R601	R601	R541	C480	T420	N360	M300	A240	L181	R120	P60
S602	S602	K542	I481	R421	L361	G301	A121	K182	A121	K61
			L482	Y422	S362	O302	T242		A122	A62

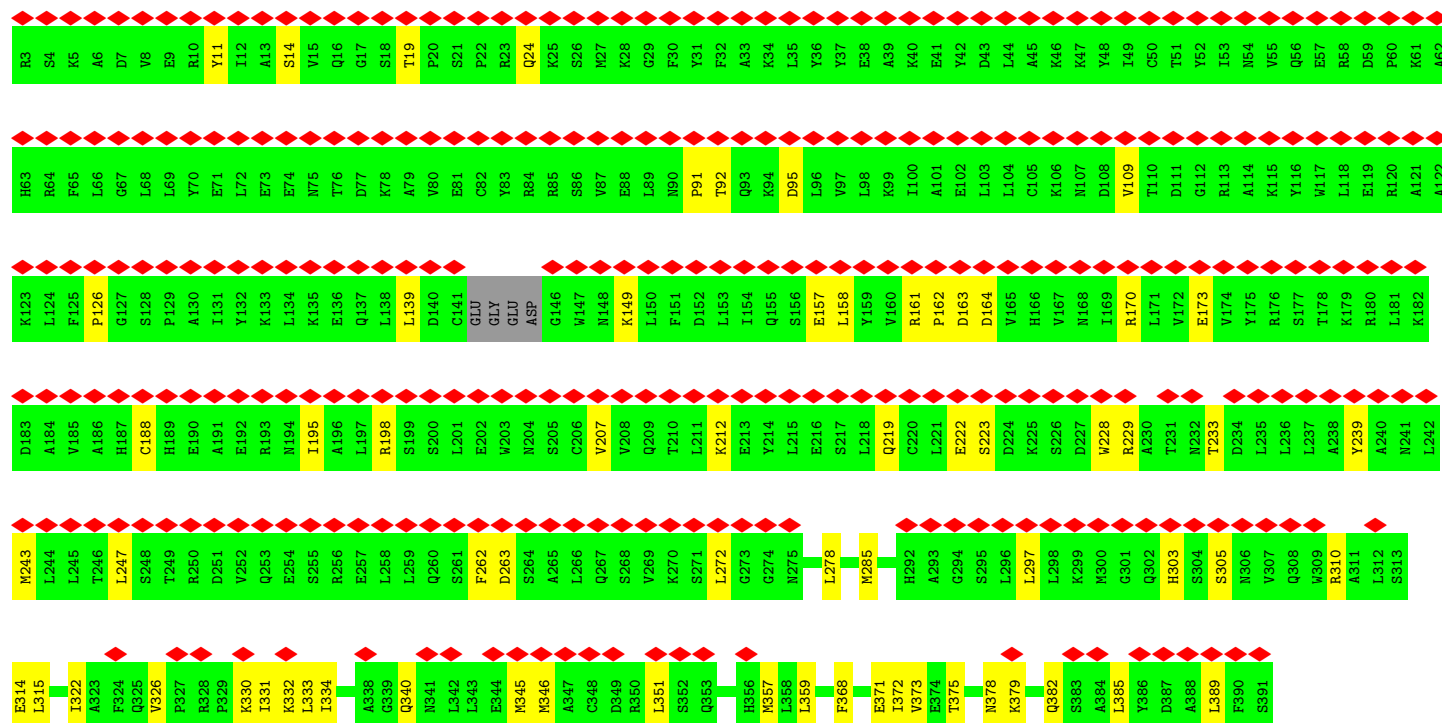
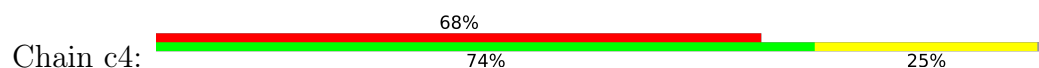
• Molecule 31: NUP358

Chain c3: 

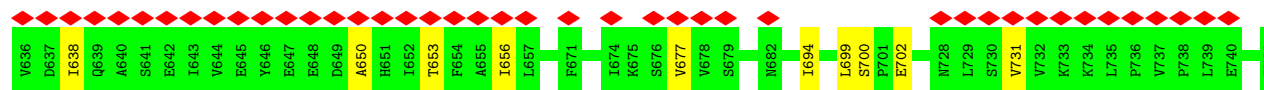
R3	S4	K5	A6	D7	V8	E9	R10	Y11	I12	A13	S14	V15	Q16	G17	S18	T19	P20	S21	P22	R23	Q24	K25	S26	M27	K28	G29	F30	Y31	F32	A33	K34	L35	Y36	Y37	E38	A39	K40	E41	Y42	D43	L44	A45	K46	K47	Y48	I49	C50	T51	Y52	I53	N54	V55	O56	E57	R58	D59	P60	K61	A62
H63	R64	F65	L66	G67	L68	L69	Y70	E71	L72	E73	E74	M75	T76	D77	K78	A79	V80	E81	C82	Y83	R84	R85	S86	V87	E88	L89	N90	P91	T92	Q93	K94	D95	L96	V97	L98	K99	I100	A101	E102	L103	L104	C105	K106	M107	N108	V109	T110	D111	G112	R113	A114	K115	Y116	W117	L118	E119	R120	A121	A122



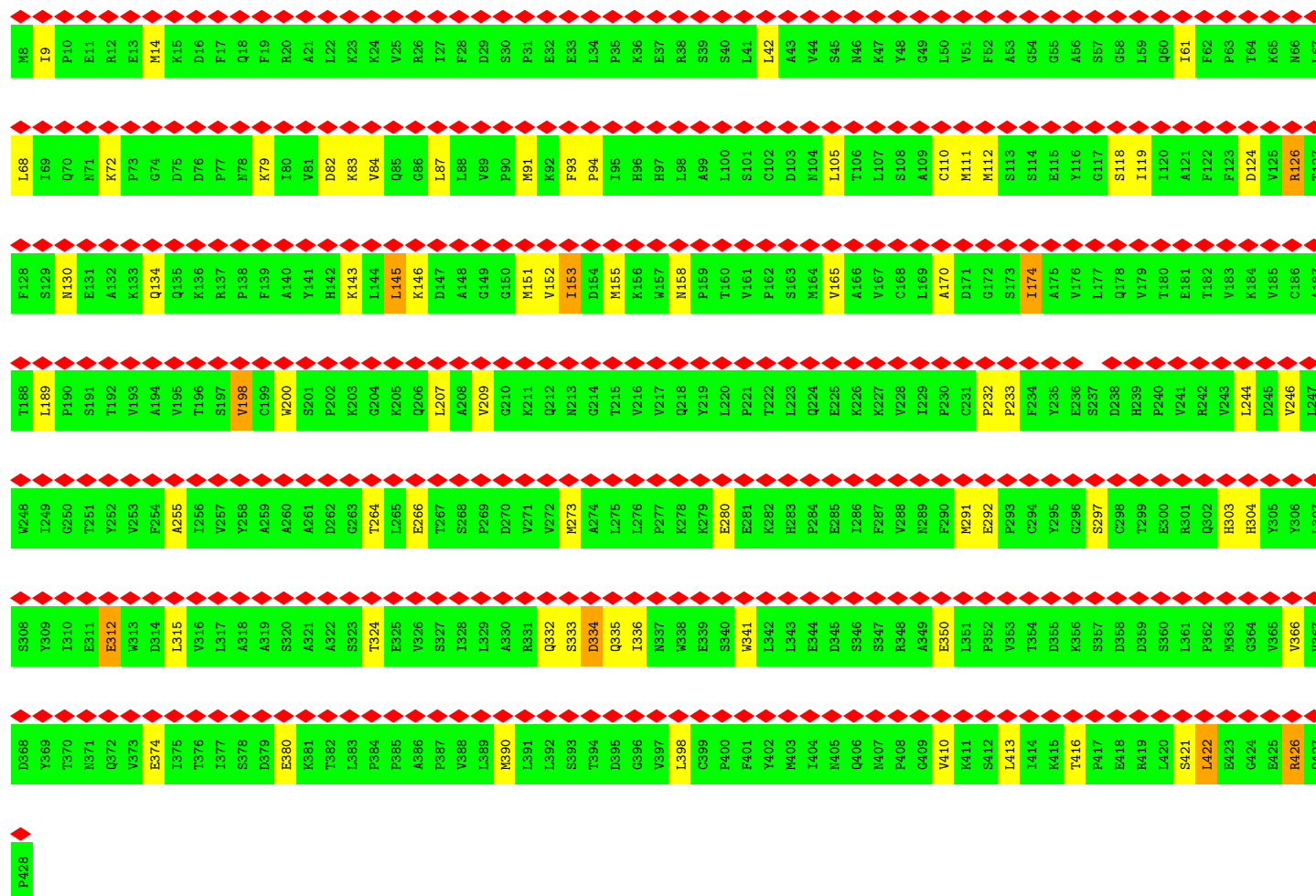
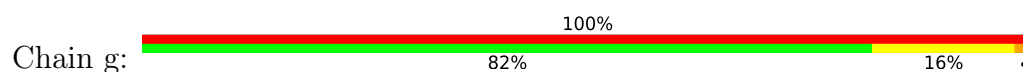
• Molecule 31: NUP358



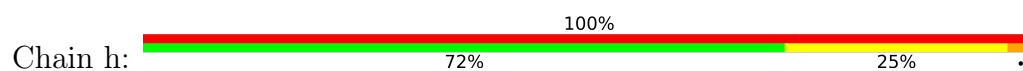




• Molecule 32: NUP214 NTD

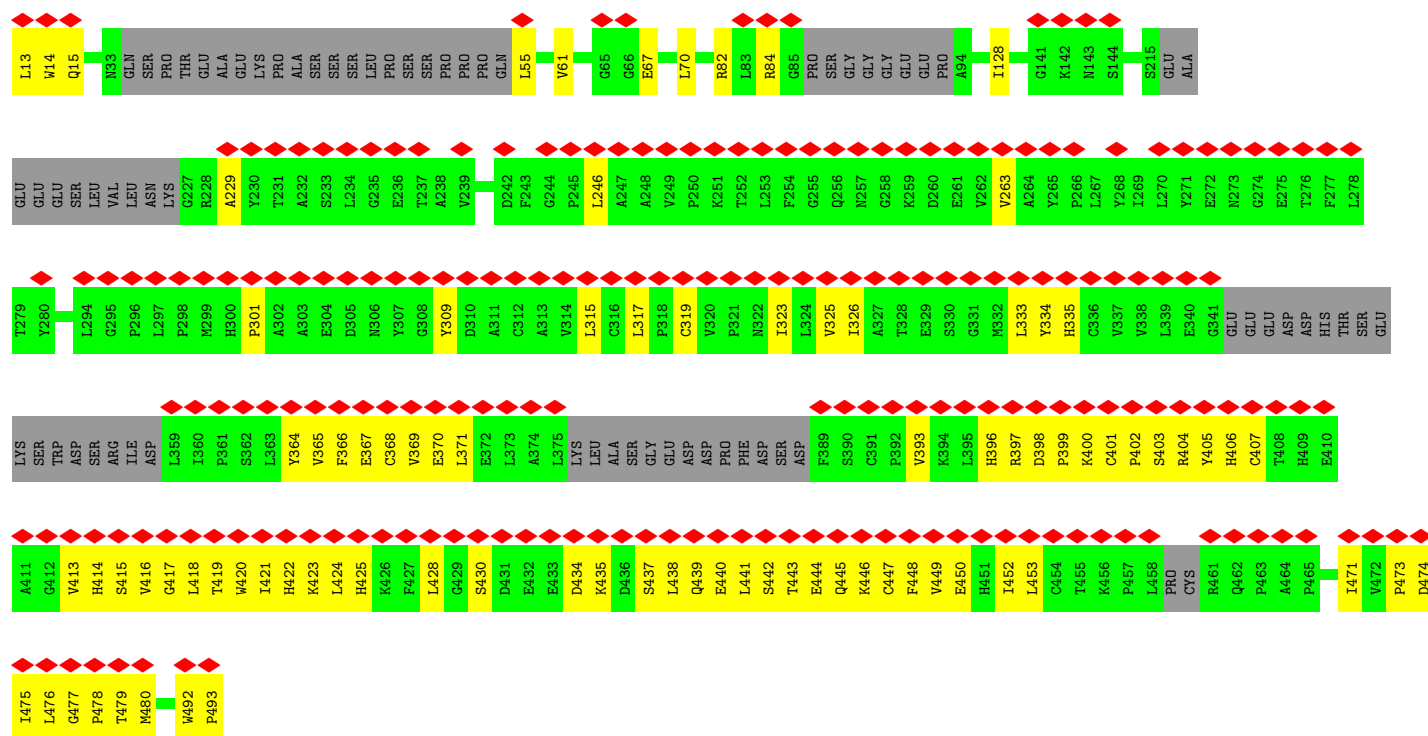
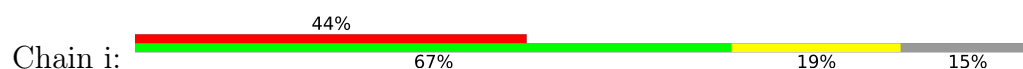


• Molecule 33: DDX19

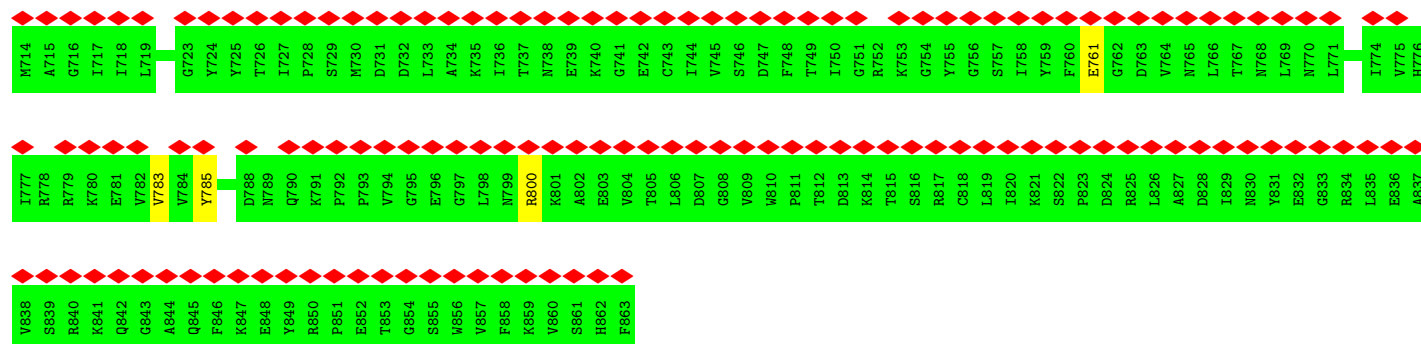
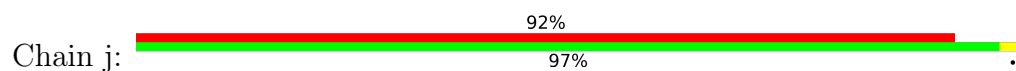




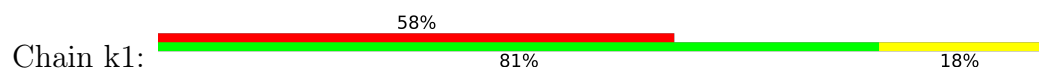
• Molecule 34: NUP88 NTD

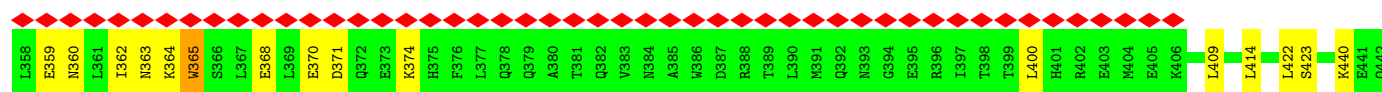


• Molecule 35: NUP98 APD

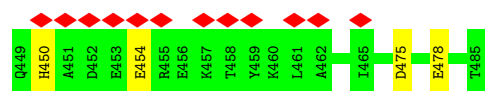
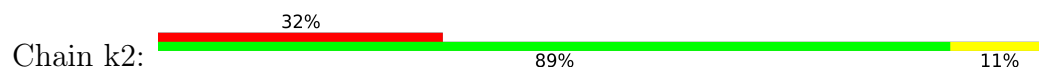


• Molecule 36: NUP62 CCS1

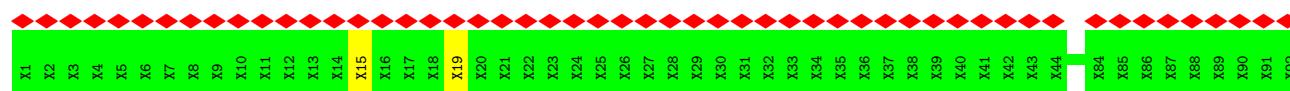




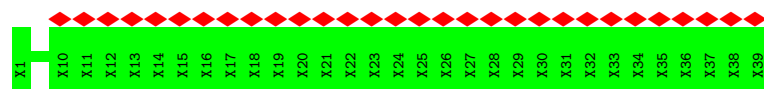
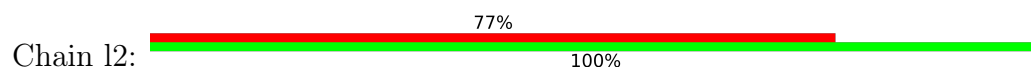
• Molecule 37: NUP62 CCS2



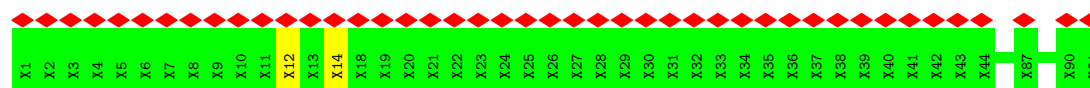
• Molecule 38: NUP214 CCS1



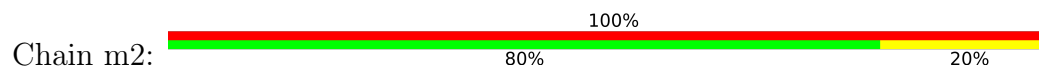
• Molecule 39: NUP214 CCS2



• Molecule 40: NUP88 CCS1



• Molecule 41: NUP88 CCS2



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	792	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 ($e^-/\text{\AA}^2$)	140	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.524	Depositor
Minimum map value	-0.301	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	1987.2001, 1987.2001, 1987.2001	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	13.8, 13.8, 13.8	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.19	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	0.19	0/112	0.52	0/149
5	C1	0.28	0/140	0.40	0/188
5	C2	0.24	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	0.35	0/6930
6	D3	0.17	0/5130	0.35	0/6930
6	D4	0.17	0/5130	0.35	0/6930
6	D5	0.17	0/5130	0.34	0/6930
6	D6	0.18	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	0.20	0/65	0.41	0/89
7	E4	0.18	0/65	0.41	0/89
7	E5	0.18	0/65	0.41	0/89
7	E6	0.18	0/65	0.40	0/89
7	E7	0.19	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	0.12	0/445	0.33	0/600
9	G2	0.12	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	0.09	0/12541	0.20	0/16980
11	I2	0.09	0/12541	0.20	0/16980
11	I3	0.09	0/12541	0.20	0/16980
11	I4	0.09	0/12541	0.20	0/16980
11	I5	0.09	0/12541	0.20	0/16980
12	J1	0.10	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	0.10	0/511	0.18	0/688
12	J5	0.10	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	0.09	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	0.05	0/15	0.07	0/18
14	L4	0.04	0/15	0.07	0/18
14	L5	0.04	0/15	0.06	0/18
15	M1	0.31	0/1388	0.66	0/1866
15	M2	0.31	0/1388	0.66	0/1866
15	M3	0.31	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	1.16	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	0.63	0/416
20	R2	0.30	0/312	0.63	0/416
20	R3	0.29	0/312	0.63	0/416
20	R4	0.30	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	0.31	0/2037	0.72	0/2749
22	T3	0.31	0/2037	0.71	0/2749
22	T4	0.31	0/2037	0.71	0/2749
23	U1	0.49	0/3463	0.99	5/4700 (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	1.00	17/6246 (0.3%)
26	X2	0.42	0/4602	1.00	16/6246 (0.3%)
26	X3	0.42	0/4602	1.00	15/6246 (0.2%)
26	X4	0.42	0/4602	1.00	15/6246 (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	3/2723 (0.1%)	0.84	1/3715 (0.0%)
29	a3	0.98	3/2723 (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	0.13	0/6101	0.29	0/8248
31	c2	0.13	0/6098	0.29	0/8246
31	c3	0.13	0/6098	0.29	0/8246
31	c4	0.13	0/6098	0.29	0/8246
31	c5	0.13	0/6098	0.29	0/8246
32	g	0.85	0/3359	0.91	1/4572 (0.0%)
33	h	0.86	0/1871	0.99	2/2530 (0.1%)
34	i	0.13	0/3398	0.29	0/4629
35	j	0.11	0/1223	0.25	0/1653
36	k1	0.48	0/727	0.78	0/977
37	k2	0.42	0/310	0.70	0/414
All	All	0.42	61/407133 (0.0%)	0.67	394/551943 (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
30	b2	0	3
30	b3	0	3
30	b4	0	3
All	All	0	38

The worst 5 of 61 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	8.45	1.47	1.33
3	A5	891	GLY	C-N	8.42	1.47	1.33
21	S3	214	ALA	C-O	-7.43	1.15	1.24

The worst 5 of 394 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	S4	131	SER	CA-C-N	10.39	130.67	119.87
21	S4	131	SER	C-N-CA	10.39	130.67	119.87
21	S2	131	SER	CA-C-N	10.34	130.62	119.87
21	S2	131	SER	C-N-CA	10.34	130.62	119.87
21	S1	131	SER	CA-C-N	10.31	130.59	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	9629	542	0
1	A3	9730	0	9573	2342	0
2	A2	9946	0	9774	1876	0
2	A4	9946	0	9656	5076	0
3	A5	10030	0	9892	1575	0
3	A6	10030	0	9732	6093	0
4	B1	111	0	127	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B2	111	0	127	26	0
4	B3	111	0	127	2	0
4	B4	111	0	127	27	0
4	B5	111	0	122	39	0
4	B6	111	0	118	191	0
5	C1	138	0	144	27	0
5	C2	157	0	157	354	0
5	C3	138	0	144	8	0
5	C4	157	0	164	63	0
5	C5	138	0	144	23	0
5	C6	138	0	144	22	0
6	D1	5034	0	4999	1044	0
6	D2	5034	0	5029	85	0
6	D3	5034	0	4965	1798	0
6	D4	5034	0	5030	96	0
6	D5	5034	0	5024	136	0
6	D6	5034	0	5027	88	0
6	D7	5034	0	5027	131	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	12916	382	0
8	F2	12779	0	12917	133	0
9	G1	438	0	404	212	0
9	G2	438	0	412	74	0
10	H1	94	0	84	0	0
10	H2	94	0	84	0	0
11	I1	12307	0	12271	3218	0
11	I2	12307	0	12280	3272	0
11	I3	12307	0	12354	477	0
11	I4	12307	0	12360	283	0
11	I5	12307	0	12347	554	0
12	J1	504	0	485	55	0
12	J2	504	0	485	54	0
12	J3	504	0	487	32	0
12	J4	504	0	487	30	0
12	J5	504	0	487	31	0
13	K1	73	0	82	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	1333	733	0
15	M2	1372	0	1361	52	0
15	M3	1372	0	1333	577	0
15	M4	1372	0	1363	4	0
16	N1	1401	0	1375	720	0
16	N2	1401	0	1397	77	0
16	N3	1401	0	1383	617	0
16	N4	1401	0	1398	10	0
17	O1	1971	0	1943	923	0
17	O2	1971	0	1962	421	0
17	O3	1971	0	1935	1245	0
17	O4	1971	0	1961	237	0
18	P1	900	0	910	61	0
18	P2	900	0	910	43	0
18	P3	900	0	908	150	0
18	P4	900	0	907	120	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	315	351	0
20	R2	311	0	334	2	0
20	R3	311	0	313	469	0
20	R4	311	0	334	2	0
21	S1	6013	0	4977	337	0
21	S2	6013	0	4980	341	0
21	S3	6013	0	4983	251	0
21	S4	6013	0	4979	247	0
22	T1	1993	0	1975	291	0
22	T2	1993	0	1981	88	0
22	T3	1993	0	1981	106	0
22	T4	1993	0	1981	75	0
23	U1	3396	0	3352	661	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	U2	3404	0	3326	1240	0
23	U3	3404	0	3377	140	0
23	U4	3404	0	3378	83	0
24	V1	3805	0	3499	207	0
24	V2	3805	0	3499	138	0
24	V3	3805	0	3499	110	0
24	V4	3805	0	3499	115	0
25	W1	2160	0	2096	65	0
25	W2	2160	0	2096	76	0
25	W3	2160	0	2096	62	0
25	W4	2160	0	2096	129	0
26	X1	4535	0	4064	407	0
26	X2	4535	0	4032	1286	0
26	X3	4535	0	4068	239	0
26	X4	4535	0	4071	154	0
27	Y1	2438	0	2378	75	0
27	Y2	2438	0	2378	73	0
27	Y3	2438	0	2378	82	0
27	Y4	2438	0	2378	74	0
28	Z1	6622	0	5893	609	0
28	Z2	6622	0	5883	1038	0
28	Z3	6622	0	5893	616	0
28	Z4	6622	0	5885	853	0
29	a1	2587	0	2488	38	0
29	a2	2587	0	2488	85	0
29	a3	2587	0	2486	74	0
29	a4	2587	0	2488	38	0
30	b1	2638	0	2573	597	0
30	b2	2638	0	2573	606	0
30	b3	2638	0	2573	604	0
30	b4	2638	0	2573	612	0
31	c1	5980	0	5992	322	0
31	c2	5976	0	5981	540	0
31	c3	5976	0	5996	138	0
31	c4	5976	0	5949	1266	0
31	c5	5976	0	5997	305	0
32	g	3282	0	3310	45	0
33	h	1836	0	1893	50	0
34	i	3280	0	3277	1134	0
35	j	1197	0	1198	2	0
36	k1	719	0	713	2	0
37	k2	308	0	302	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	l1	460	0	94	1	0
39	l2	195	0	41	0	0
40	m1	440	0	93	1	0
41	m2	100	0	21	3	0
All	All	400581	0	386997	29463	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 37.

The worst 5 of 29463 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)
11:I2:950:LEU:HD11	16:N3:410:MET:SD	1.20	1.72
3:A6:444:ARG:HG2	6:D3:737:PHE:CZ	1.21	1.69
23:U2:391:HIS:CD2	31:c4:477:GLU:HA	1.23	1.69
27:Y1:41:ASP:HB3	29:a1:231[B]:HIS:CE1	1.17	1.69
23:U2:432:TYR:CE1	31:c4:464:LEU:HD12	1.18	1.68

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	1224 (97%)	34 (3%)	0	100	100
3	A6	1258/1330 (95%)	1224 (97%)	34 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	410/436 (94%)	365 (89%)	34 (8%)	11 (3%)	4	25
23	U2	413/436 (95%)	368 (89%)	34 (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
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	592/698 (85%)	531 (90%)	51 (9%)	10 (2%)	7	36
26	X2	592/698 (85%)	531 (90%)	51 (9%)	10 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	X3	592/698 (85%)	532 (90%)	50 (8%)	10 (2%)	7	36
26	X4	592/698 (85%)	532 (90%)	50 (8%)	10 (2%)	7	36
27	Y1	303/346 (88%)	266 (88%)	31 (10%)	6 (2%)	6	31
27	Y2	303/346 (88%)	266 (88%)	31 (10%)	6 (2%)	6	31
27	Y3	303/346 (88%)	266 (88%)	31 (10%)	6 (2%)	6	31
27	Y4	303/346 (88%)	266 (88%)	31 (10%)	6 (2%)	6	31
28	Z1	858/1037 (83%)	798 (93%)	50 (6%)	10 (1%)	10	44
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	335/385 (87%)	315 (94%)	19 (6%)	1 (0%)	36	72
30	b2	335/385 (87%)	315 (94%)	19 (6%)	1 (0%)	36	72
30	b3	335/385 (87%)	315 (94%)	19 (6%)	1 (0%)	36	72
30	b4	335/385 (87%)	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	g	419/421 (100%)	404 (96%)	14 (3%)	1 (0%)	43	78
33	h	230/232 (99%)	217 (94%)	10 (4%)	3 (1%)	9	42
34	i	408/481 (85%)	401 (98%)	7 (2%)	0	100	100
35	j	149/150 (99%)	144 (97%)	4 (3%)	1 (1%)	18	56
36	k1	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
37	k2	35/37 (95%)	35 (100%)	0	0	100	100
All	All	50288/56810 (88%)	47822 (95%)	2142 (4%)	324 (1%)	23	59

5 of 324 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	1087/1111 (98%)	1064 (98%)	23 (2%)	47	65
3	A6	1087/1111 (98%)	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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	386/402 (96%)	362 (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
26	X1	424/628 (68%)	408 (96%)	16 (4%)	29	50
26	X2	424/628 (68%)	408 (96%)	16 (4%)	29	50
26	X3	424/628 (68%)	408 (96%)	16 (4%)	29	50
26	X4	424/628 (68%)	408 (96%)	16 (4%)	29	50
27	Y1	269/303 (89%)	258 (96%)	11 (4%)	27	49
27	Y2	269/303 (89%)	258 (96%)	11 (4%)	27	49
27	Y3	269/303 (89%)	258 (96%)	11 (4%)	27	49
27	Y4	269/303 (89%)	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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	299/337 (89%)	278 (93%)	21 (7%)	14	35
30	b2	299/337 (89%)	278 (93%)	21 (7%)	14	35
30	b3	299/337 (89%)	278 (93%)	21 (7%)	14	35
30	b4	299/337 (89%)	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	g	373/373 (100%)	350 (94%)	23 (6%)	16	38
33	h	206/206 (100%)	190 (92%)	16 (8%)	11	32
34	i	372/425 (88%)	371 (100%)	1 (0%)	86	86
35	j	132/131 (101%)	132 (100%)	0	100	100
36	k1	82/82 (100%)	69 (84%)	13 (16%)	2	11
37	k2	33/33 (100%)	31 (94%)	2 (6%)	17	38
All	All	42167/49609 (85%)	41025 (97%)	1142 (3%)	40	61

5 of 1142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	Z2	638	VAL
28	Z3	605	ILE
28	Z2	605	ILE
30	b2	258	VAL
21	S3	1066	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 612 such sidechains are listed below:

Mol	Chain	Res	Type
28	Z1	10	ASN
31	c2	466	HIS
28	Z2	116	GLN
27	Y4	99	ASN
29	a2	105	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
40	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

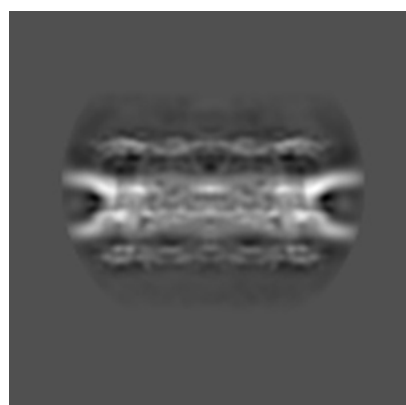
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11967. These allow visual inspection of the internal detail of the map and identification of artifacts.

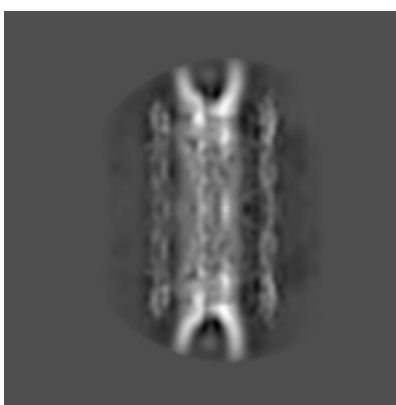
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

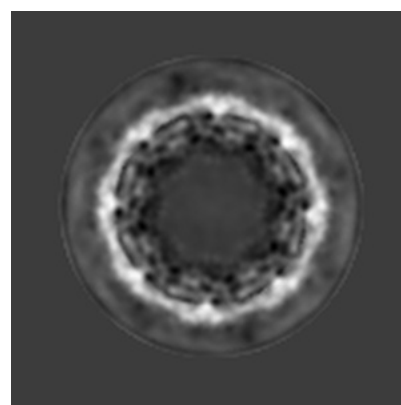
6.1.1 Primary map



X



Y



Z

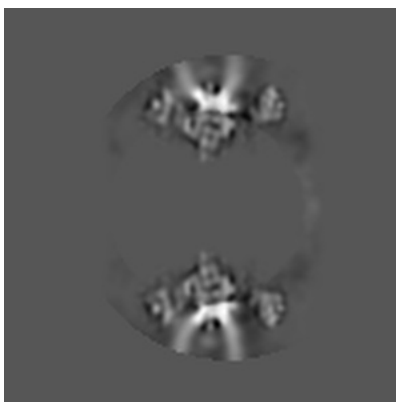
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

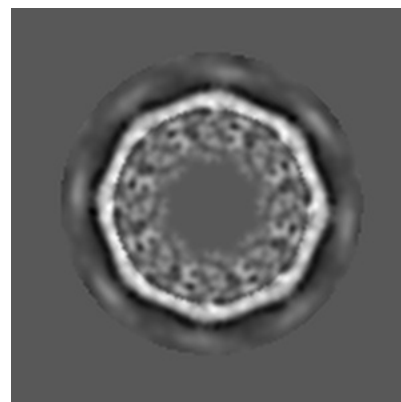
6.2.1 Primary map



X Index: 72



Y Index: 72



Z Index: 72

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

6.3 Largest variance slices [i](#)

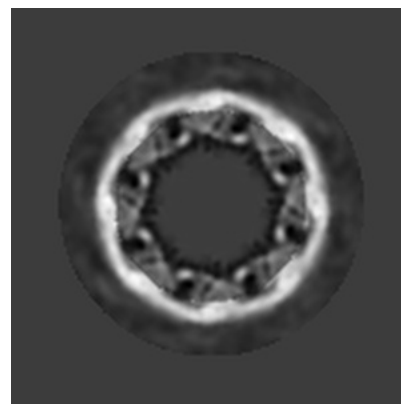
6.3.1 Primary map



X Index: 36



Y Index: 108

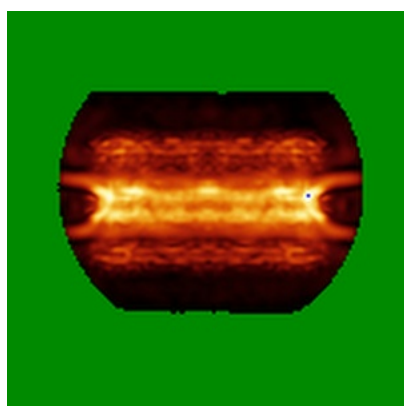


Z Index: 78

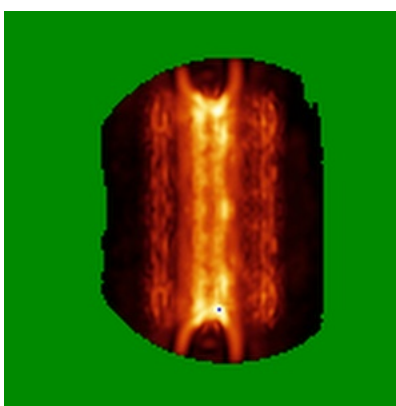
The images above show the largest variance slices of the map in three orthogonal directions.

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

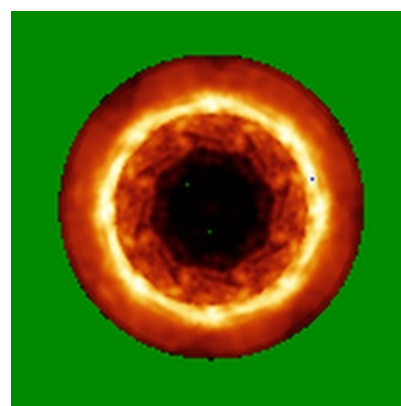
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

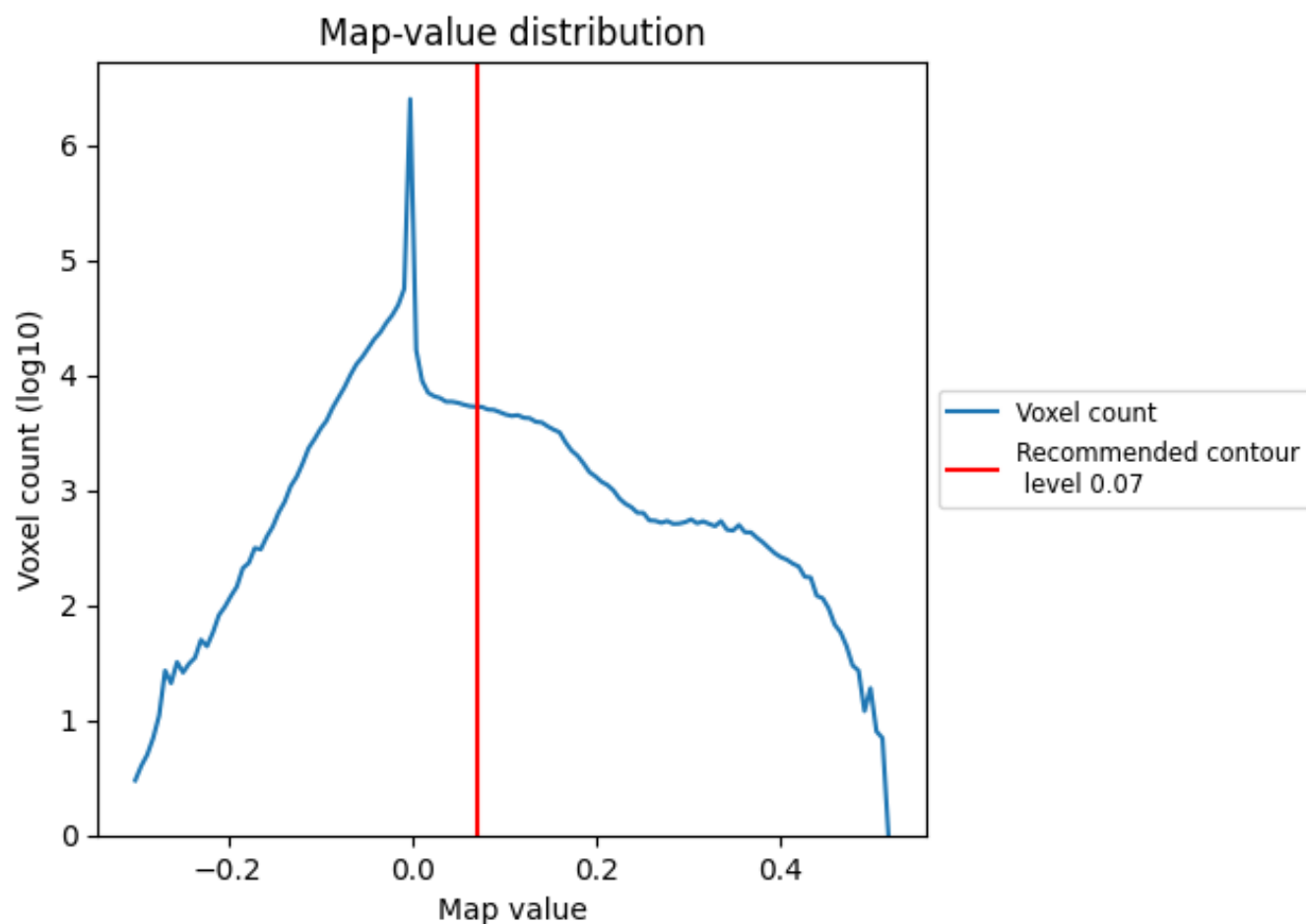
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

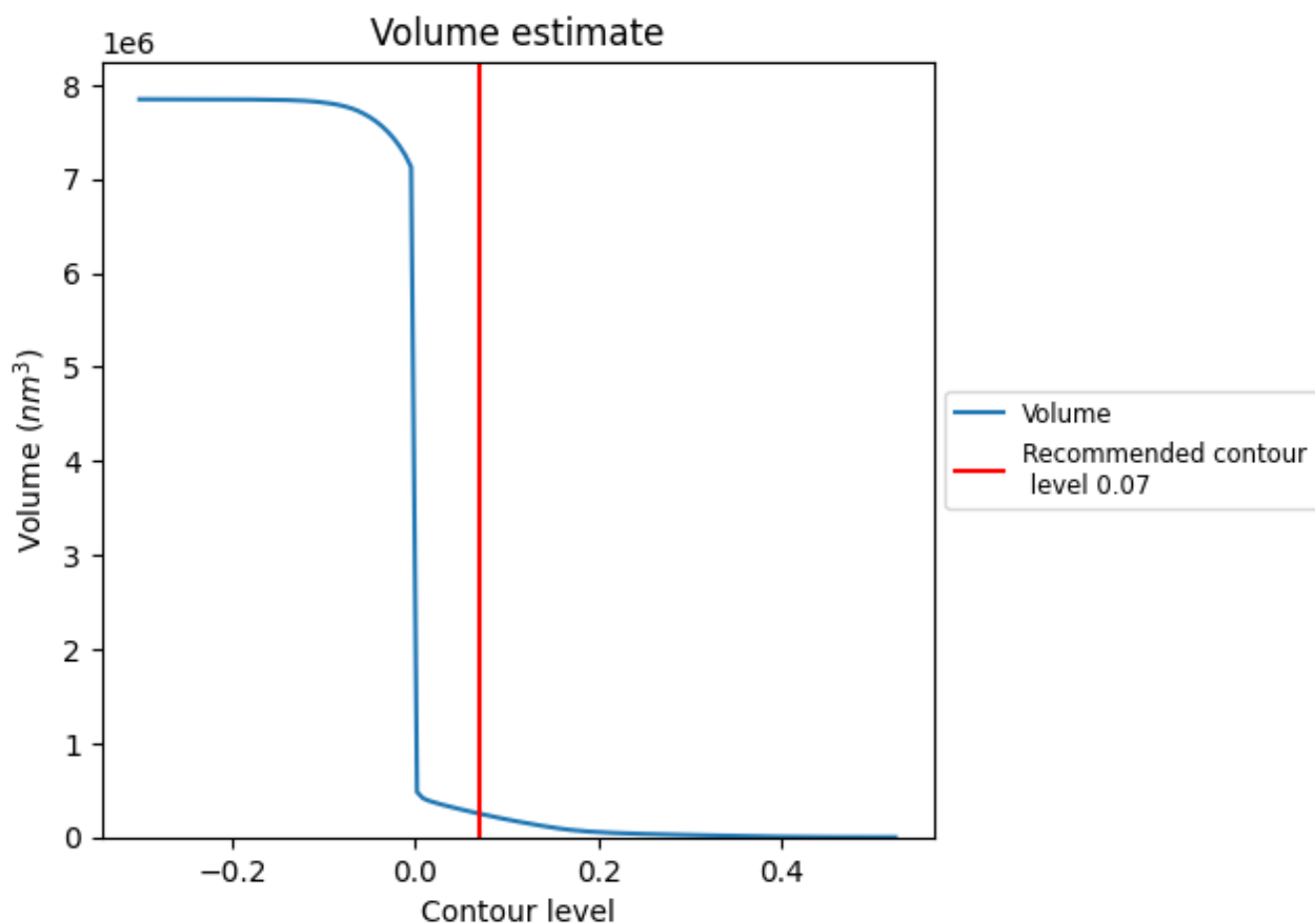
This section contains the results of statistical analysis of the map.

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.

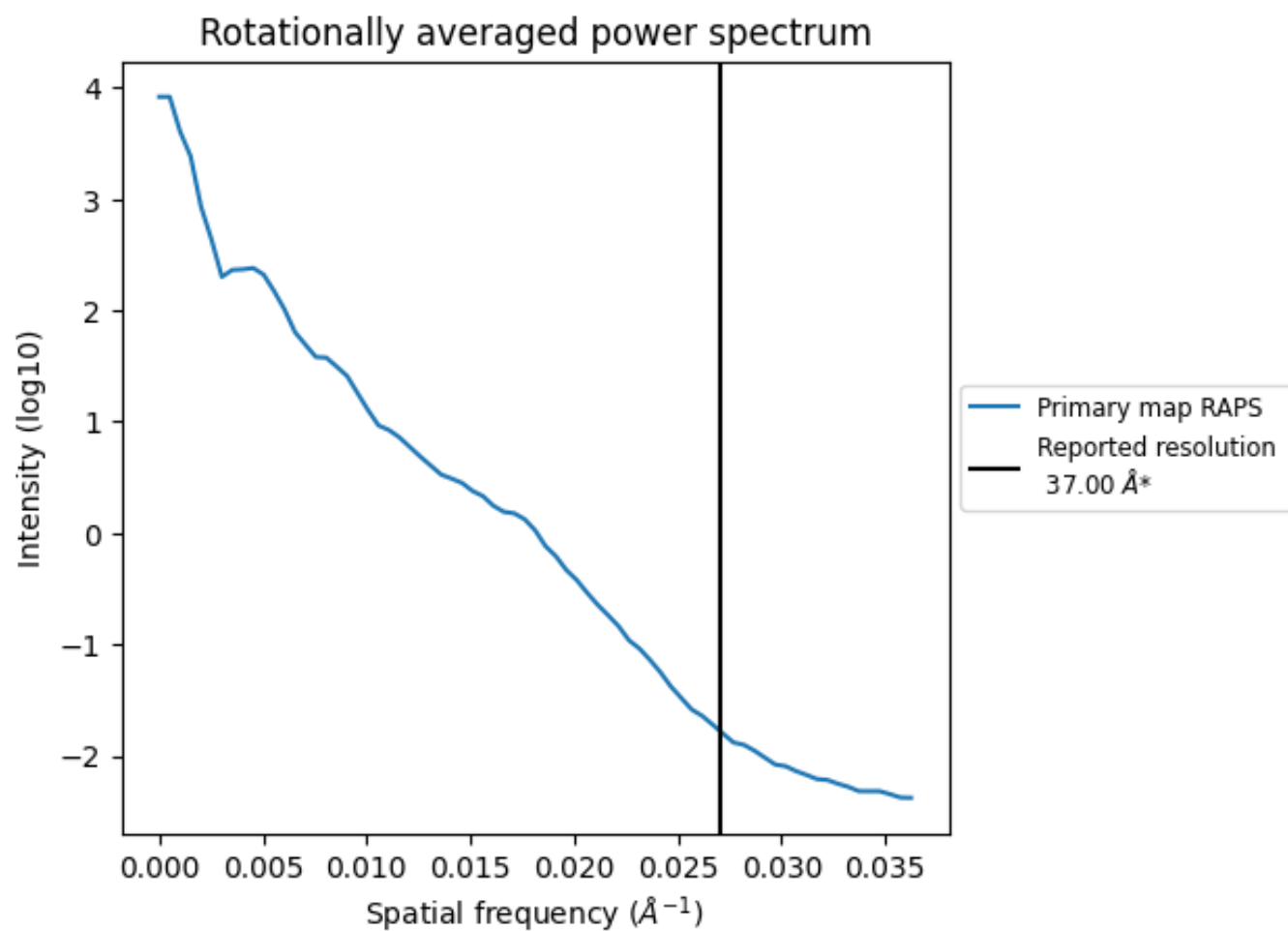
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 250411 nm³; this corresponds to an approximate mass of 226203 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 0.027 Å⁻¹

8 Fourier-Shell correlation

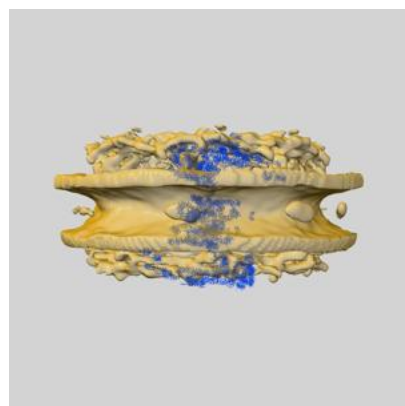
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

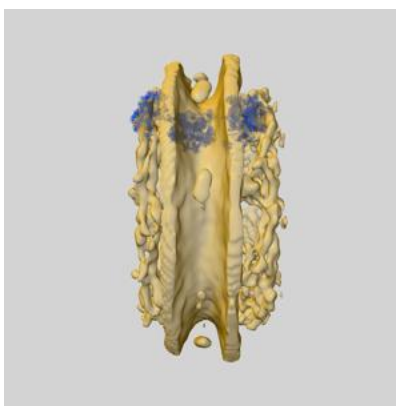
This section contains information regarding the fit between EMDB map EMD-11967 and PDB model 7TBM. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlays

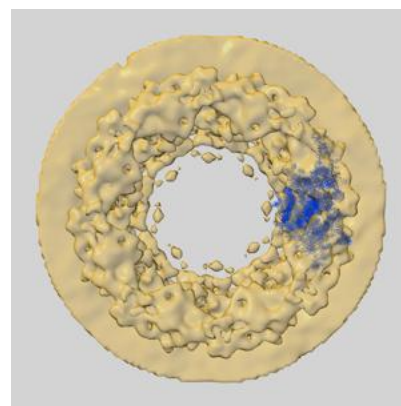
9.1.1 Map-model overlay [i](#)



X

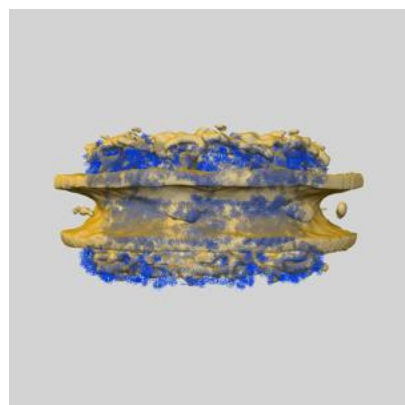


Y

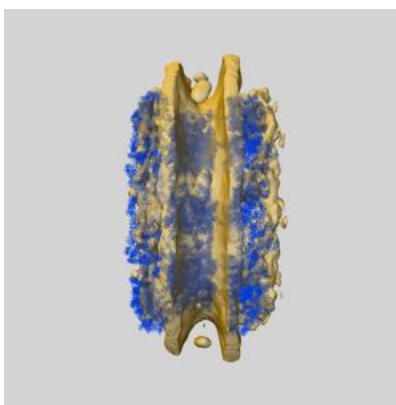


Z

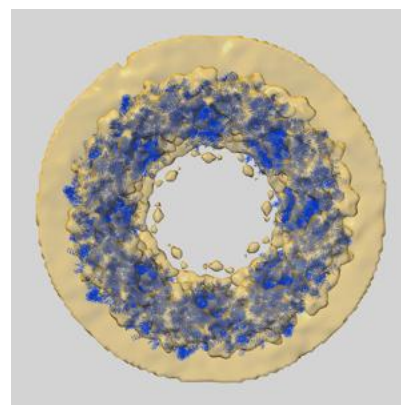
9.1.2 Map-model assembly overlay [i](#)



X



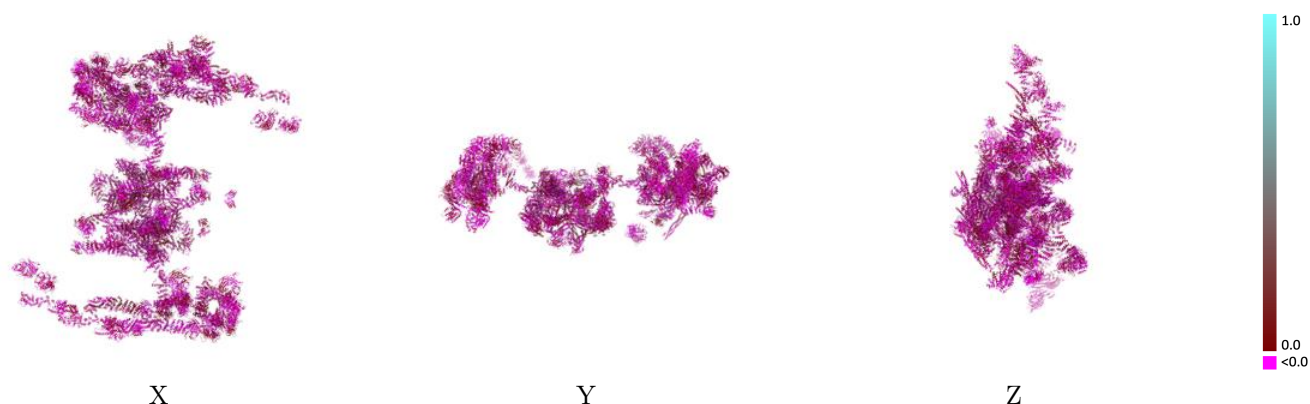
Y



Z

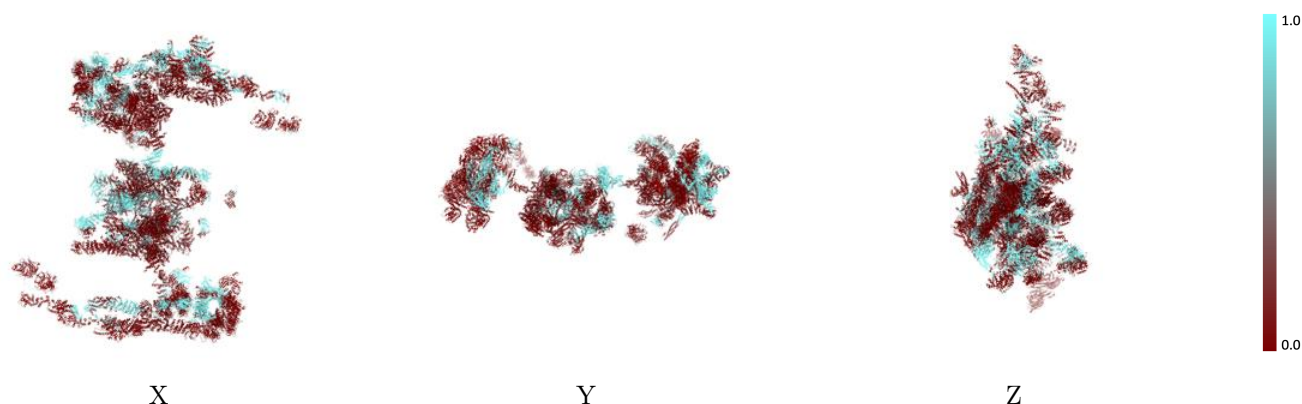
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



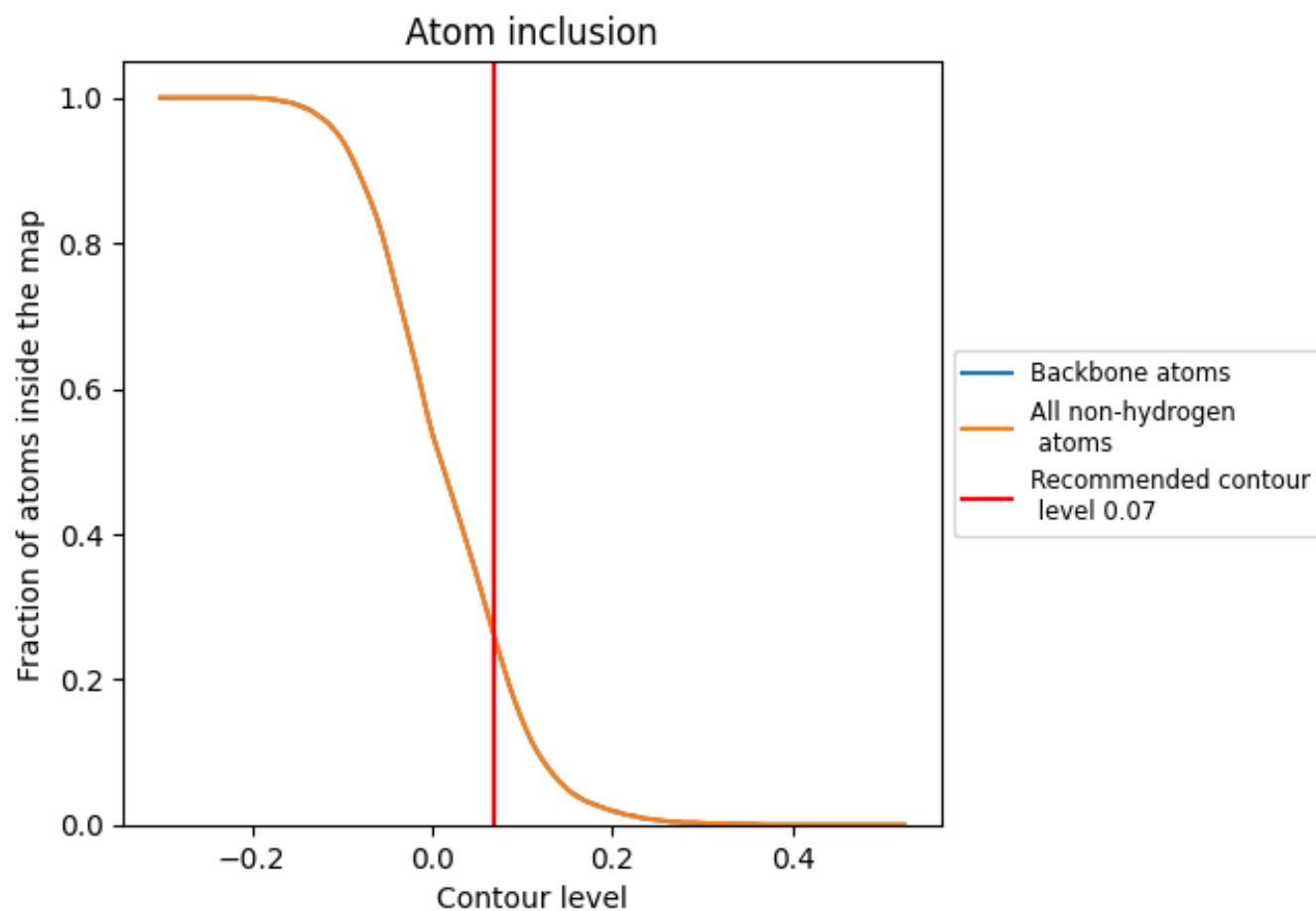
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 26% of all backbone atoms, 26% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2560	 -0.0040
A1	 0.6040	 0.0060
A2	 0.4360	 -0.0060
A3	 0.1580	 -0.0070
A4	 0.0940	 -0.0080
A5	 0.4660	 -0.0130
A6	 0.1090	 0.0020
B1	 0.2110	 -0.0340
B2	 1.0000	 0.0600
B3	 0.0000	 -0.0480
B4	 0.0000	 -0.0250
B5	 0.9820	 0.0030
B6	 0.0000	 0.0230
C1	 1.0000	 0.0130
C2	 0.7230	 -0.0560
C3	 0.0000	 0.0310
C4	 0.8260	 0.0830
C5	 0.7350	 0.0160
C6	 0.0000	 -0.0060
D1	 0.3740	 0.0130
D2	 0.4240	 0.0040
D3	 0.2120	 -0.0180
D4	 0.0000	 0.0010
D5	 0.5660	 0.0120
D6	 0.1530	 -0.0060
D7	 0.0090	 -0.0410
E1	 0.7500	 0.0310
E2	 0.7000	 0.0010
E3	 0.0000	 -0.0090
E4	 0.0000	 0.0130
E5	 0.8170	 0.0230
E6	 0.0000	 -0.0450
E7	 0.0000	 -0.0300
F1	 0.2340	 -0.0000
F2	 0.0390	 -0.0200



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Chain	Atom inclusion	Q-score
G1	 0.1100	 -0.0010
G2	 0.0000	 -0.0520
H1	 0.0640	 -0.0260
H2	 0.0000	 -0.0020
I1	 0.4410	 0.0030
I2	 0.1600	 0.0050
I3	 0.2320	 -0.0020
I4	 0.6060	 0.0080
I5	 0.0000	 -0.0090
J1	 0.3230	 -0.0120
J2	 0.3210	 -0.0080
J3	 0.5030	 0.0220
J4	 0.2210	 -0.0060
J5	 0.0000	 0.0420
K1	 0.0000	 -0.0460
K2	 0.0000	 -0.0150
K3	 0.0420	 -0.0040
K4	 1.0000	 0.0160
K5	 0.0000	 -0.0190
L1	 1.0000	 -0.0560
L2	 0.0000	 -0.0040
L3	 0.0000	 0.0010
L4	 1.0000	 0.0020
L5	 0.0000	 -0.0120
M1	 0.5520	 0.0270
M2	 0.3890	 0.0090
M3	 0.1730	 -0.0070
M4	 0.0970	 -0.0020
N1	 0.5490	 0.0300
N2	 0.4510	 -0.0000
N3	 0.3240	 -0.0000
N4	 0.2380	 0.0000
O1	 0.4370	 0.0200
O2	 0.3110	 -0.0040
O3	 0.1660	 -0.0060
O4	 0.0170	 -0.0250
P1	 0.2000	 -0.0060
P2	 0.0030	 -0.0140
P3	 0.0000	 -0.0070
P4	 0.0000	 -0.0010
Q1	 0.0340	 -0.0260
Q2	 0.3240	 -0.0100

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Chain	Atom inclusion	Q-score
Q3	 0.4780	 0.0110
Q4	 0.7610	 0.0450
R1	 0.2410	 -0.0060
R2	 0.4420	 -0.0130
R3	 0.4120	 0.0460
R4	 0.3860	 0.0200
S1	 0.1020	 -0.0130
S2	 0.2030	 -0.0010
S3	 0.1140	 -0.0060
S4	 0.0030	 -0.0200
T1	 0.5170	 0.0010
T2	 0.2740	 0.0140
T3	 0.2010	 -0.0070
T4	 0.2240	 -0.0020
U1	 0.3660	 0.0010
U2	 0.0000	 -0.0210
U3	 0.0000	 -0.0270
U4	 0.3640	 0.0110
V1	 0.5810	 0.0200
V2	 0.0000	 -0.0260
V3	 0.0190	 -0.0340
V4	 0.6610	 0.0360
W1	 0.3290	 -0.0120
W2	 0.0000	 -0.0310
W3	 0.0890	 -0.0130
W4	 0.0650	 -0.0150
X1	 0.3160	 -0.0060
X2	 0.0030	 -0.0210
X3	 0.0190	 -0.0090
X4	 0.0070	 -0.0370
Y1	 0.9160	 0.0300
Y2	 0.1020	 0.0060
Y3	 0.0000	 0.0010
Y4	 0.0000	 0.0210
Z1	 0.5980	 0.0080
Z2	 0.0750	 -0.0150
Z3	 0.1360	 -0.0090
Z4	 0.4500	 0.0080
a1	 0.2030	 -0.0150
a2	 0.7300	 0.0350
a3	 0.0000	 -0.0130
a4	 0.0020	 -0.0330

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Chain	Atom inclusion	Q-score
b1	 0.3270	 0.0130
b2	 0.0480	 -0.0230
b3	 0.0000	 -0.0360
b4	 0.6490	 0.0080
c1	 0.5430	 0.0160
c2	 0.1450	 -0.0160
c3	 0.5340	 -0.0050
c4	 0.3000	 0.0130
c5	 0.4420	 0.0000
g	 0.0020	 -0.0240
h	 0.0000	 -0.0410
i	 0.4800	 0.0200
j	 0.0750	 0.0010
k1	 0.4190	 -0.0100
k2	 0.6340	 -0.0110
l1	 0.4260	 -0.0100
l2	 0.2310	 -0.0210
m1	 0.4930	 0.0010
m2	 0.0000	 -0.0370