wwPDB EM Validation Summary Report

Mar 6, 2026 – 06:38 AM UTC

PDB ID	:	7TBJ / pdb_00007tbj
EMDB ID	:	EMD-14322
Title	:	Composite structure of the human nuclear pore complex (NPC) symmetric core generated with a 12A cryo-ET map of the purified HeLa cell NPC
Authors	:	Petrovic, S.; Samanta, D.; Perriches, T.; Bley, C.J.; Thierbach, K.; Brown, B.; Nie, S.; Mobbs, G.W.; Stevens, T.A.; Liu, X.; Tomaleri, G.P.; Schaus, L.; Hoelz, A.
Deposited on	:	2021-12-22
Resolution	:	23.00 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

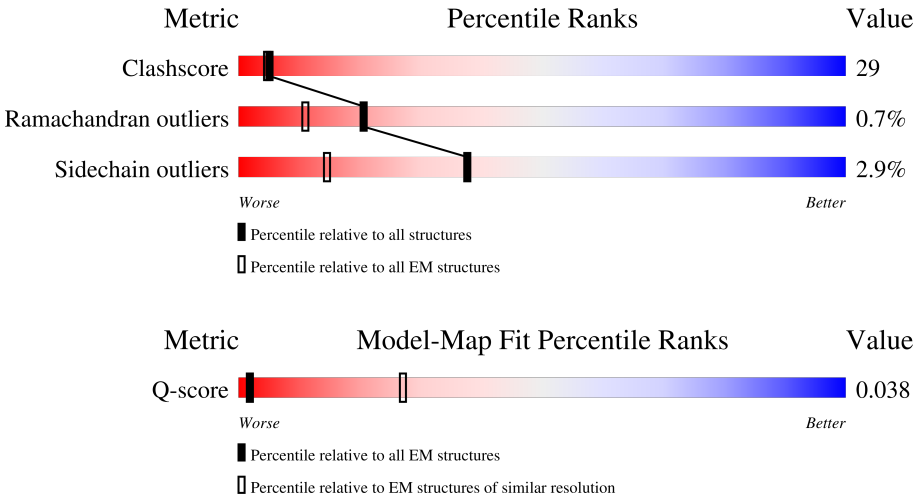
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 23.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	93 (11.50 - 12.50)

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

Mol	Chain	Length	Quality of chain
1	A1	1316	27% 86% 7% 6%
1	A3	1316	30% 87% 7% 6%
2	A2	1328	58% 73% 20%
2	A4	1328	53% 72% 21%

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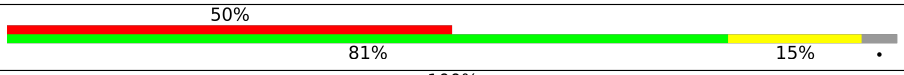
Mol	Chain	Length	Quality of chain
3	A5	1330	
3	A6	1330	
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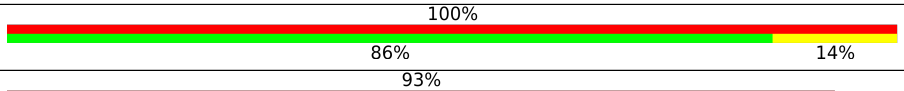
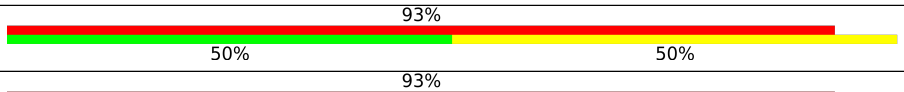
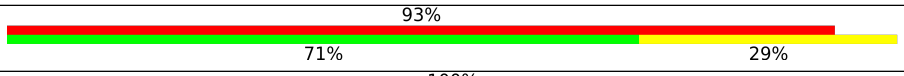
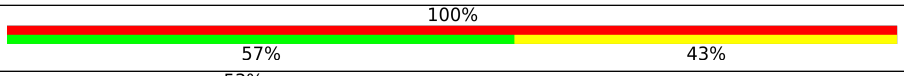
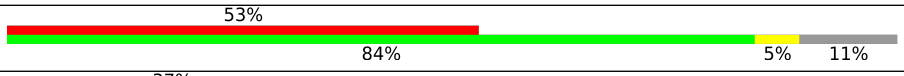
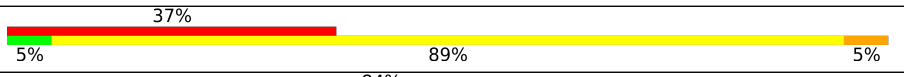
4	B2	14	
4	B3	14	
4	B4	14	
4	B5	14	
4	B6	14	
5	C1	19	
5	C2	19	
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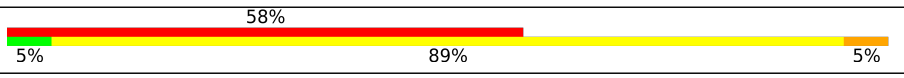
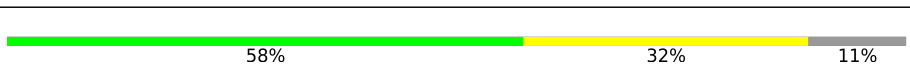
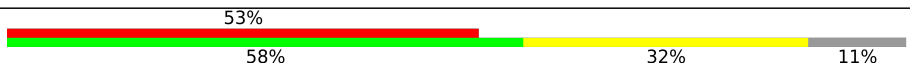
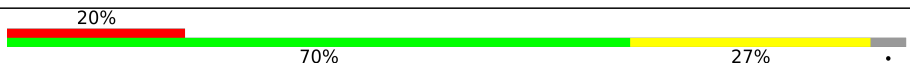
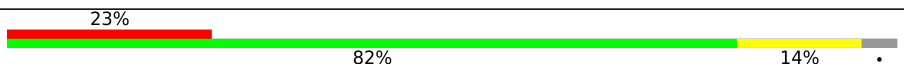
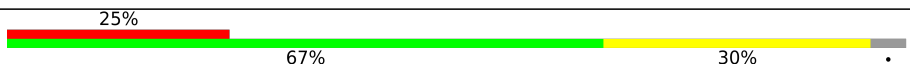
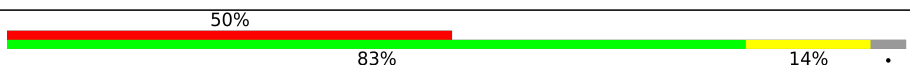
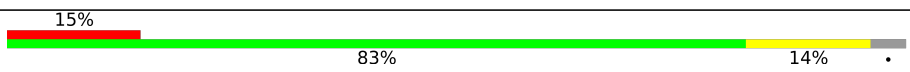
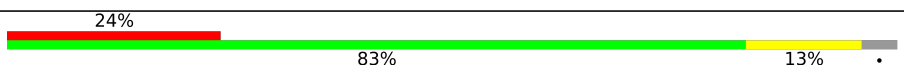
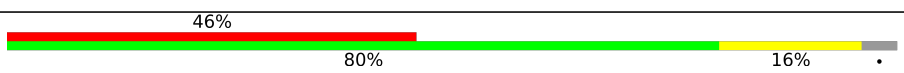
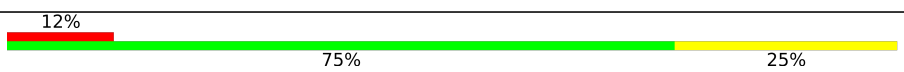
5	C4	19	
5	C5	19	
5	C6	19	
6	D1	644	
6	D2	644	
6	D3	644	
6	D4	644	
6	D5	644	
6	D6	644	
6	D7	644	
7	E1	8	
7	E2	8	
7	E3	8	
7	E4	8	

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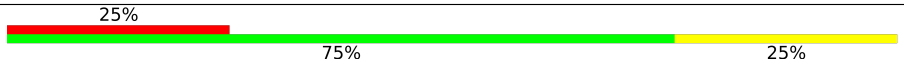
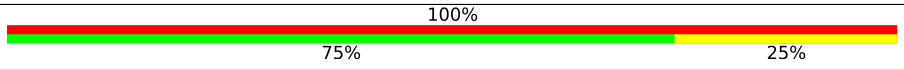
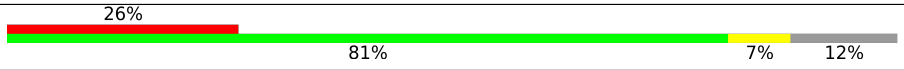
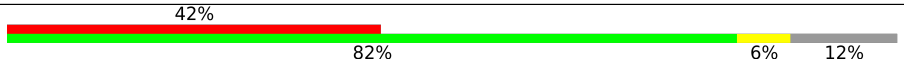
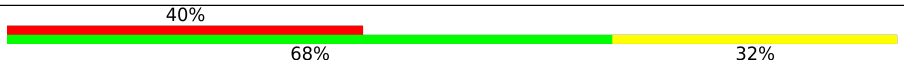
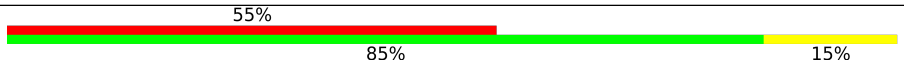
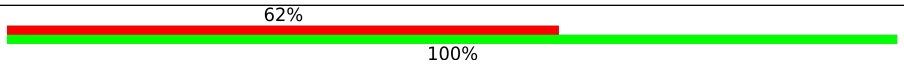
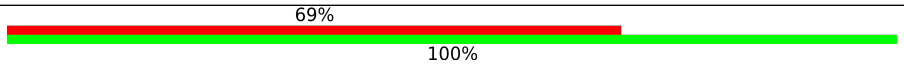
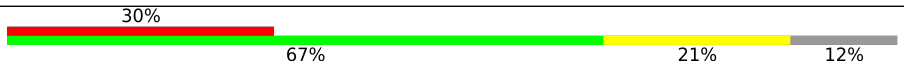
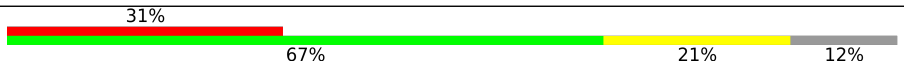
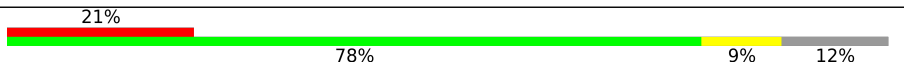
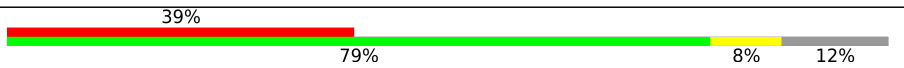
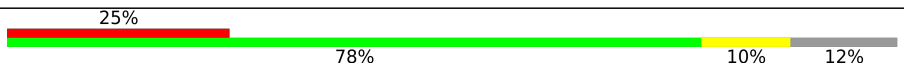
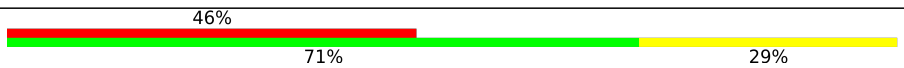
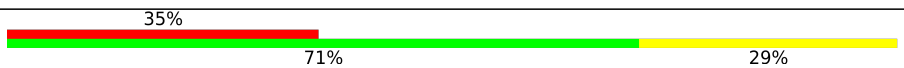
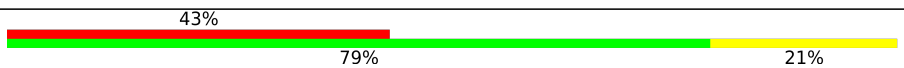
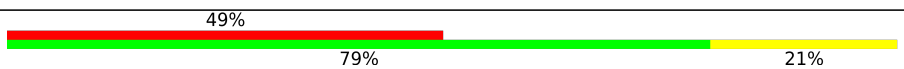
Mol	Chain	Length	Quality of chain
7	E5	8	
7	E6	8	
7	E7	8	
8	F1	1858	
8	F2	1858	
9	G1	53	
9	G2	53	
10	H1	13	
10	H2	13	
11	I1	1756	
11	I2	1756	
11	I3	1756	
11	I4	1756	
11	I5	1756	
12	J1	63	
12	J2	63	
12	J3	63	
12	J4	63	
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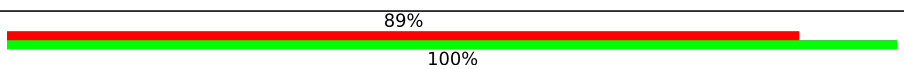
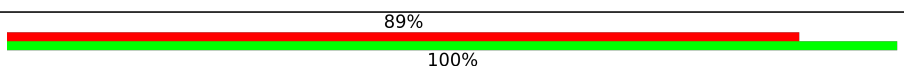
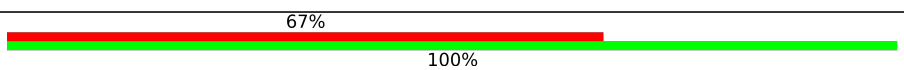
13	K1	9	
13	K2	9	
13	K3	9	
13	K4	9	
13	K5	9	
14	L1	2	

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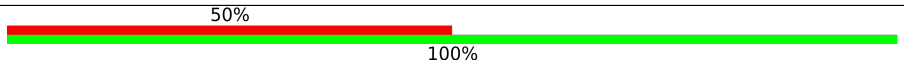
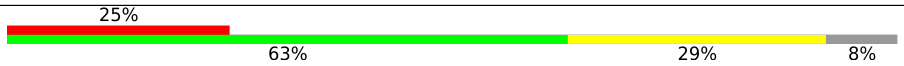
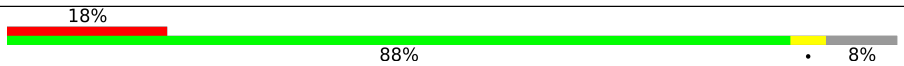
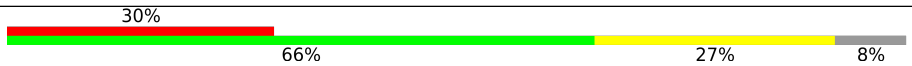
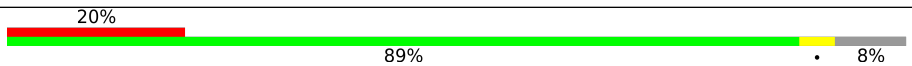
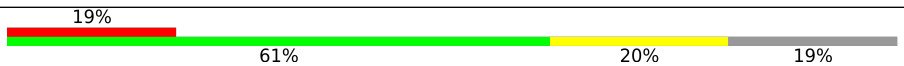
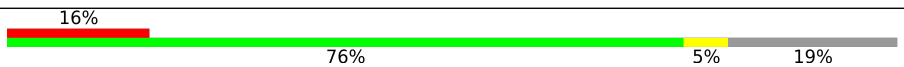
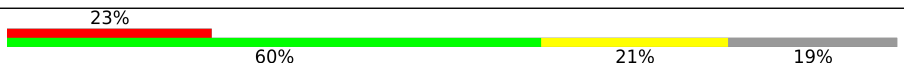
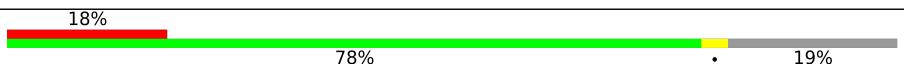
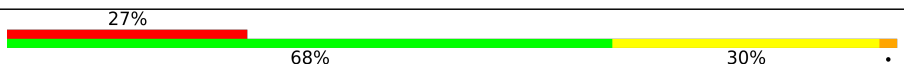
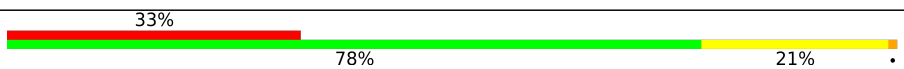
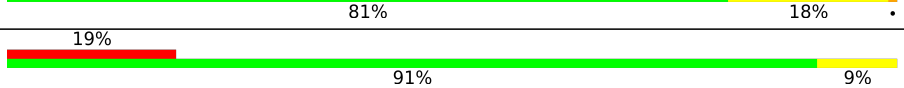
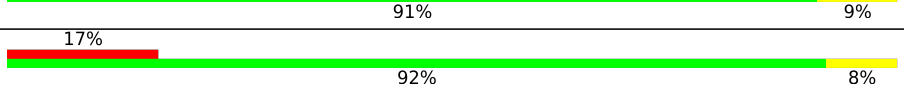
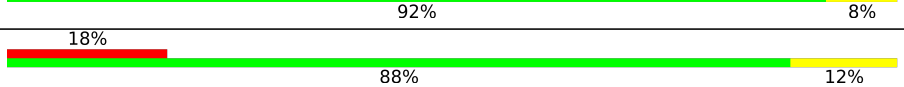
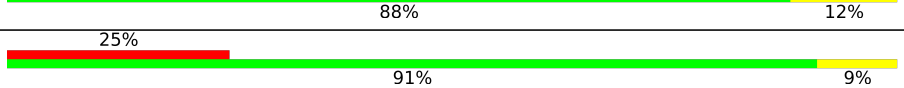
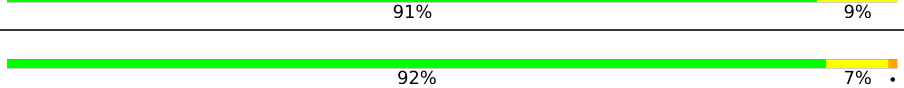
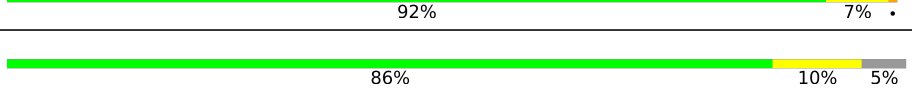
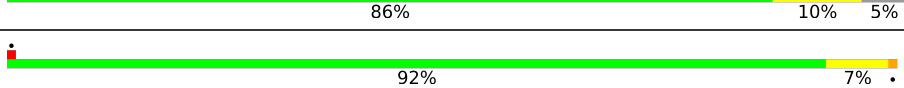
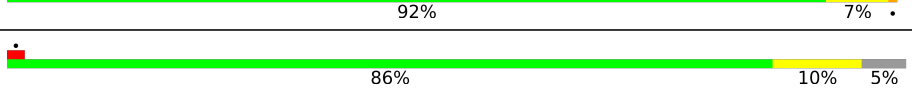
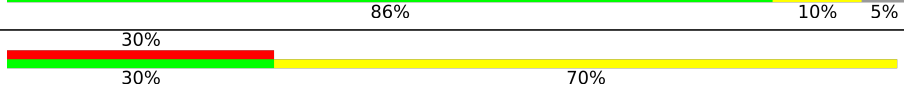
Mol	Chain	Length	Quality of chain
14	L2	2	
14	L3	2	
14	L4	2	
14	L5	2	
15	M1	183	
15	M2	183	
15	M3	183	
15	M4	183	
16	N1	222	
16	N2	222	
16	N3	222	
16	N4	222	
17	O1	241	
17	O2	241	
17	O3	241	
17	O4	241	
18	P1	116	
18	P2	116	
18	P3	116	
18	P4	116	
19	Q1	84	
19	Q2	84	
19	Q3	84	
19	Q4	84	
20	R1	40	

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Mol	Chain	Length	Quality of chain
20	R2	40	28% 92% 8%
20	R3	40	42% 32% 68%
20	R4	40	42% 92% 8%
21	S1	1156	31% 58% 18% 22%
21	S2	1156	31% 58% 18% 22%
21	S3	1156	43% 58% 18% 22%
21	S4	1156	44% 58% 17% 22%
22	T1	258	23% 60% 34%
22	T2	258	19% 60% 34%
22	T3	258	28% 60% 33%
22	T4	258	25% 61% 33%
23	U1	436	16% 68% 23% 5%
23	U2	436	8% 69% 23%
23	U3	436	18% 69% 23%
23	U4	436	17% 69% 23%
24	V1	621	8% 57% 20% 18%
24	V2	621	11% 57% 21% 18%
24	V3	621	16% 56% 22% 18%
24	V4	621	19% 57% 21% 18%
25	W1	286	12% 64% 28%
25	W2	286	19% 63% 29%
25	W3	286	16% 65% 27%
25	W4	286	30% 65% 27%
26	X1	698	16% 64% 22% 11%
26	X2	698	14% 65% 22% 11%

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Mol	Chain	Length	Quality of chain
26	X3	698	27% 63% 23% • 11%
26	X4	698	37% 65% 22% • 11%
27	Y1	346	33% 59% 29% • 11%
27	Y2	346	28% 58% 29% • 11%
27	Y3	346	39% 58% 30% • 11%
27	Y4	346	35% 59% 29% • 11%
28	Z1	1035	29% 67% 18% • 13%
28	Z2	1035	23% 62% 23% • 13%
28	Z3	1035	47% 66% 19% • 13%
28	Z4	1035	40% 59% 26% • 13%
29	a1	380	5% 75% 8% • 17%
29	a2	380	17% 73% 9% • 17%
29	a3	380	13% 75% 7% • 17%
29	a4	380	18% 75% 8% • 17%
30	b1	385	27% 49% 36% • • 11%
30	b2	385	38% 48% 36% • • 11%
30	b3	385	41% 49% 36% • • 11%
30	b4	385	36% 50% 35% • • 11%

2 Entry composition (i)

There are 30 unique types of molecules in this entry. The entry contains 358888 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 1971	C 1239	N 360	O 368	S 4	0	0
17	O4	241	Total 1971	C 1239	N 360	O 368	S 4	0	0

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

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

- Molecule 19 is a protein called NUP53 RRM.

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

- Molecule 20 is a protein called NUP93 R1.

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

- Molecule 21 is a protein called NUP133.

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

- Molecule 22 is a protein called NUP107 CTD.

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

- Molecule 23 is a protein called NUP107 NTD.

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

- Molecule 24 is a protein called NUP96.

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

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

- Molecule 25 is a protein called SEC13.

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

- Molecule 26 is a protein called NUP75.

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

- Molecule 27 is a protein called SEH1.

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

- Molecule 28 is a protein called NUP160.

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

- Molecule 29 is a protein called NUP43.

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

- Molecule 30 is a protein called NUP37.

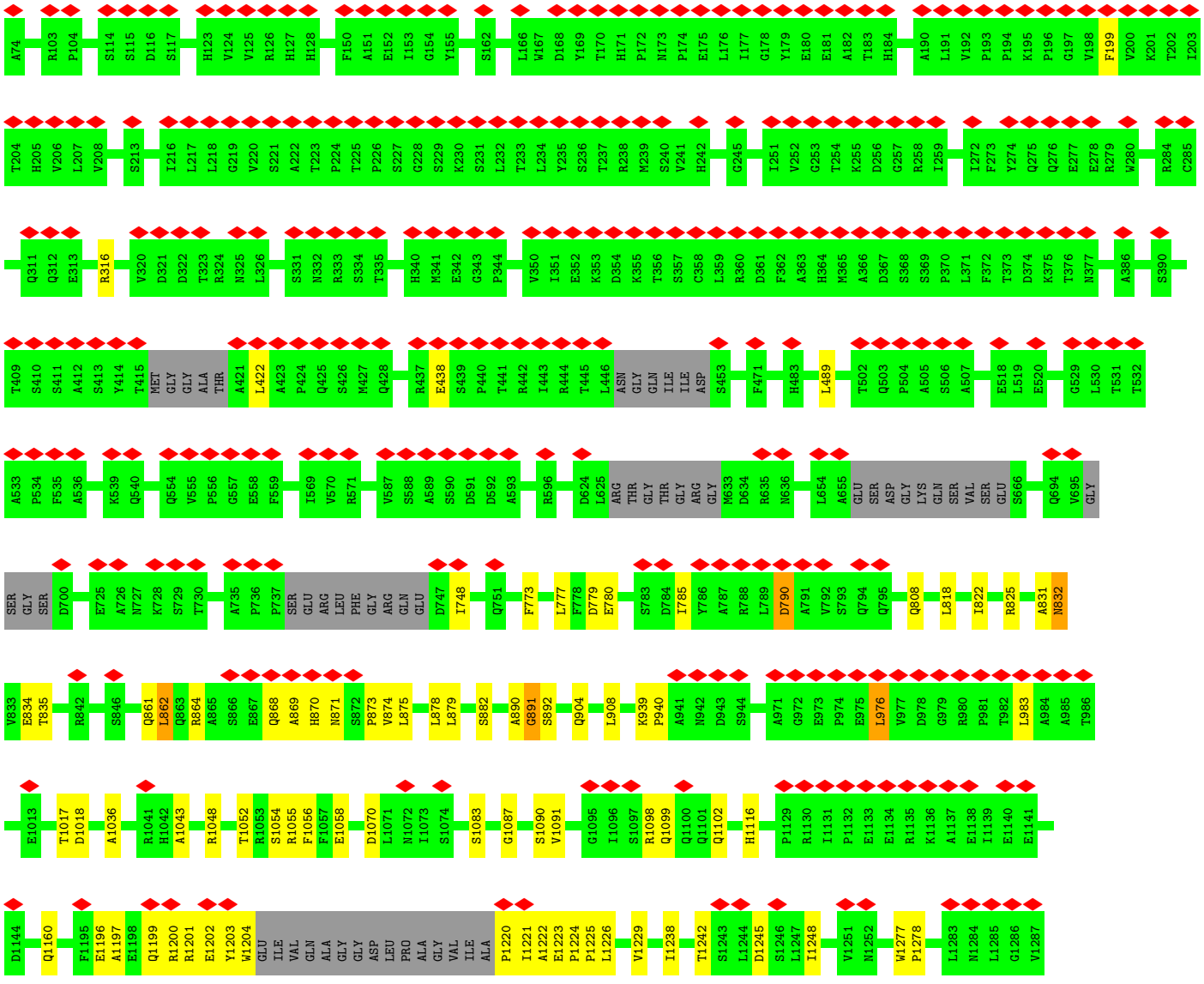
Mol	Chain	Residues	Atoms					AltConf	Trace
30	b1	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		
30	b2	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		
30	b3	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		
30	b4	343	Total	C	N	O	S	0	0
			2638	1676	447	500	15		

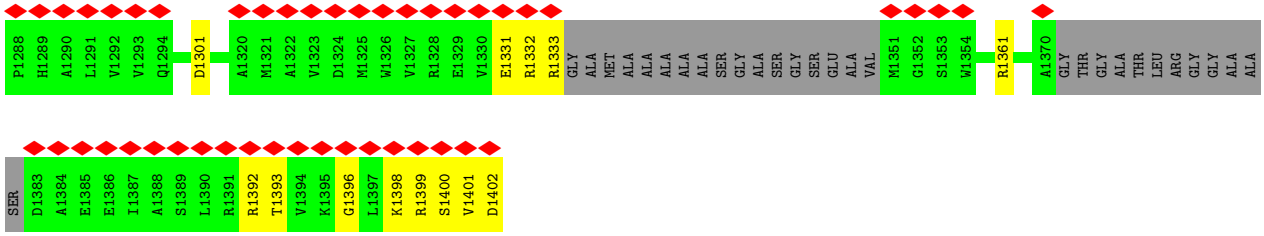
3 Residue-property plots (i)

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

- Molecule 1: NUP155

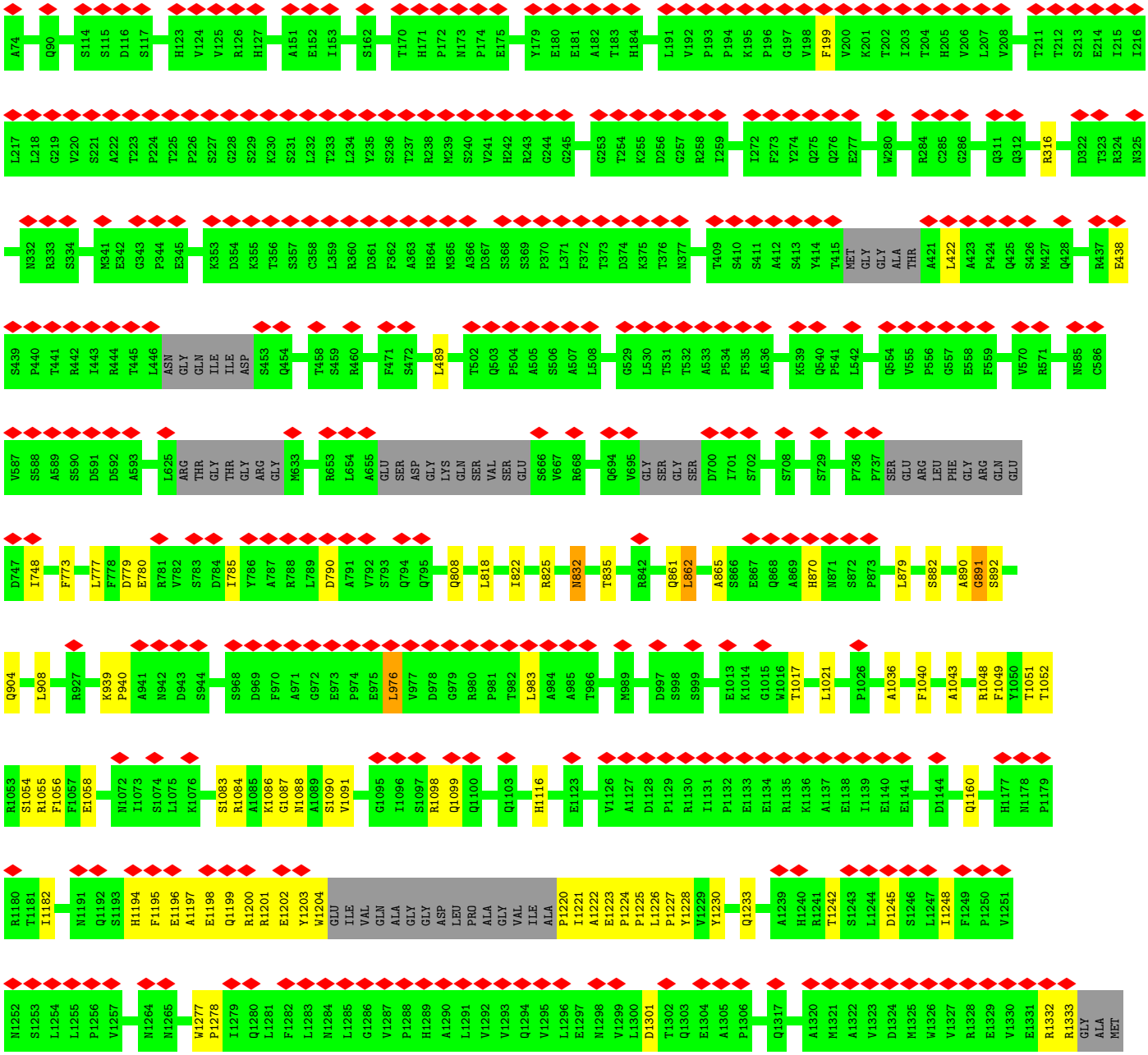
Chain A1:

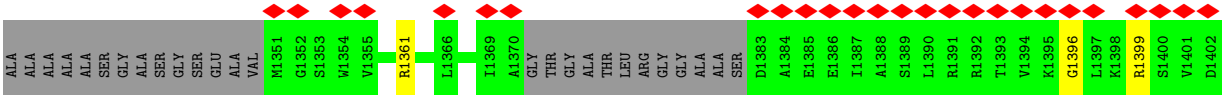




• Molecule 1: NUP155

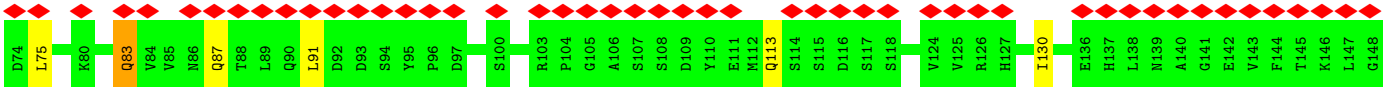
Chain A3:

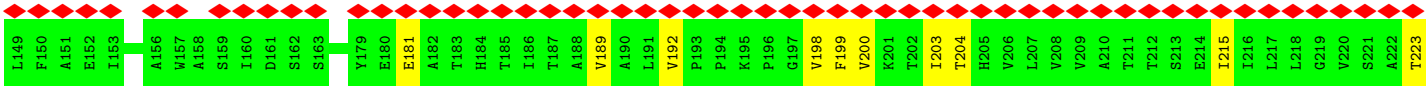


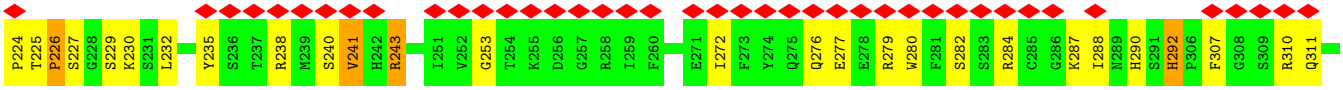


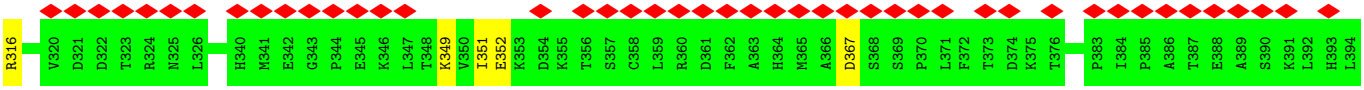
• Molecule 2: NUP155

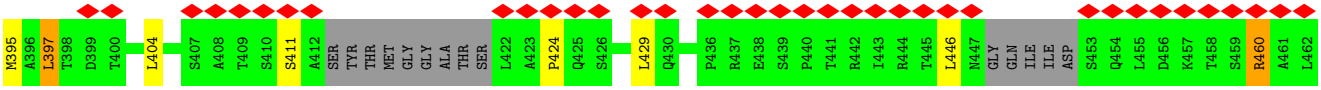
Chain A2:

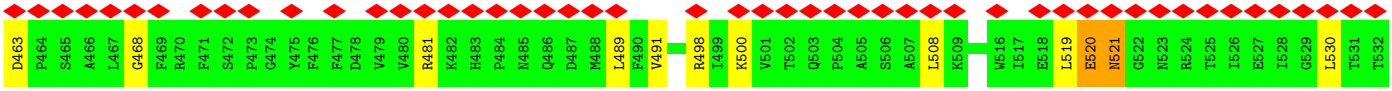


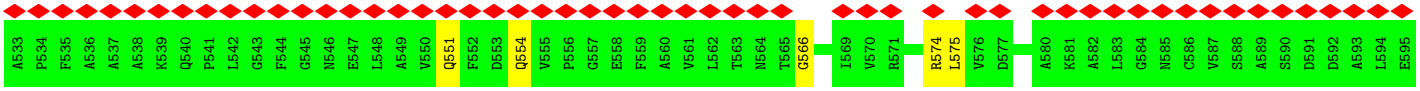


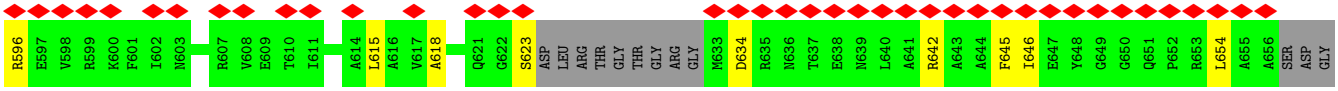


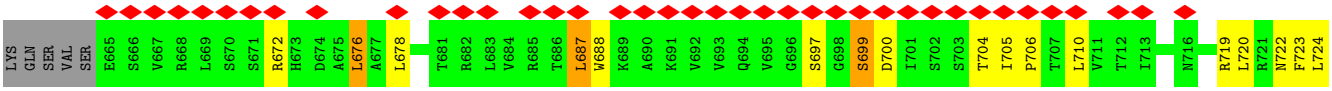


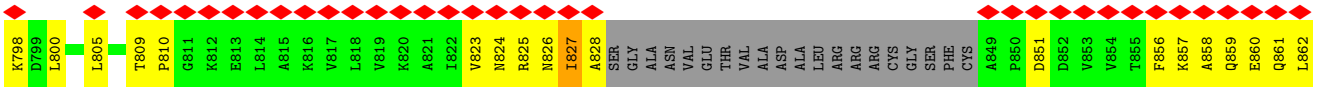


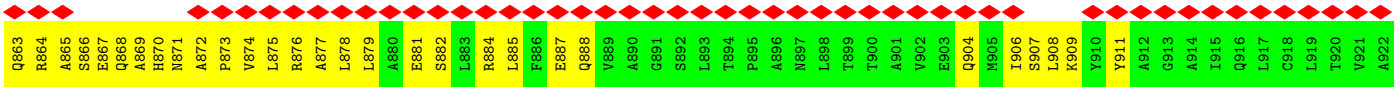


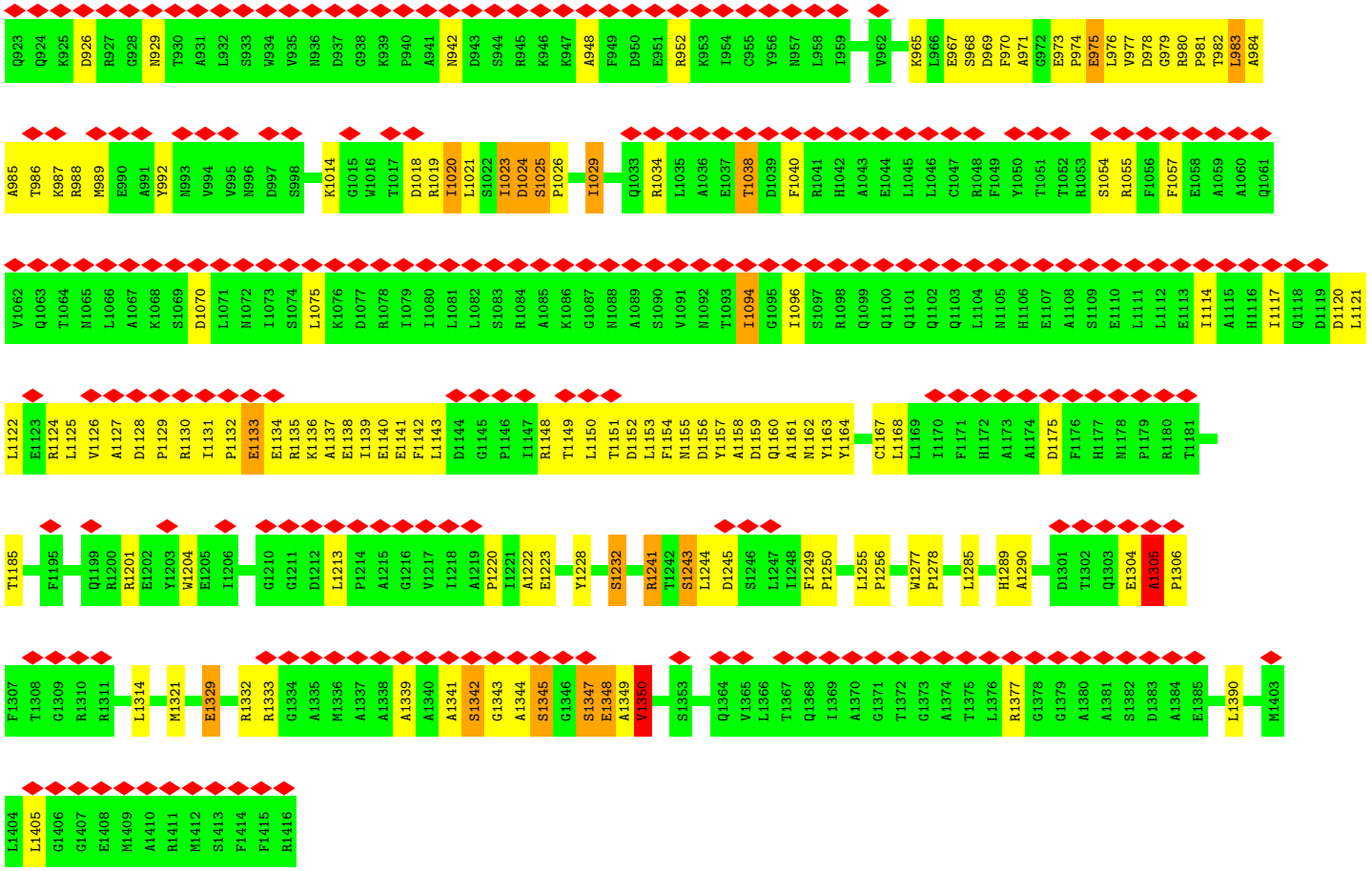






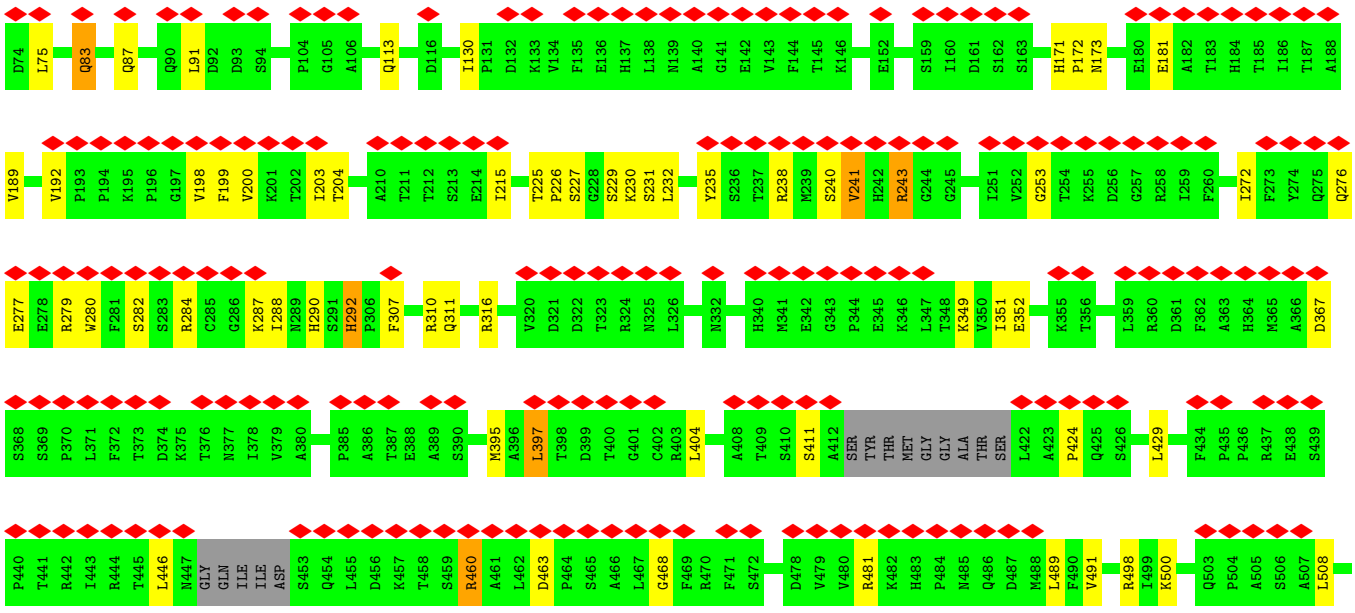


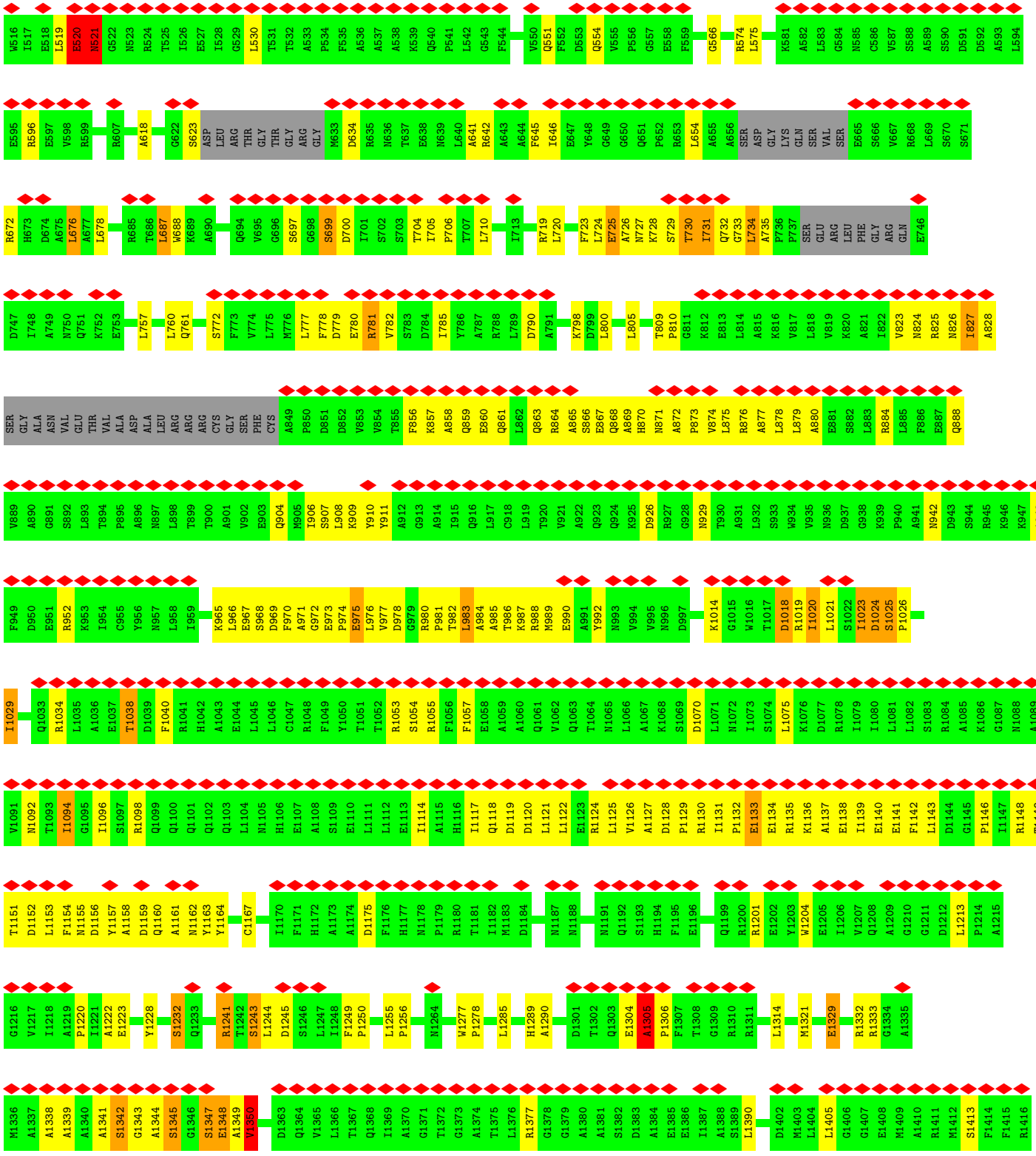




• Molecule 2: NUP155

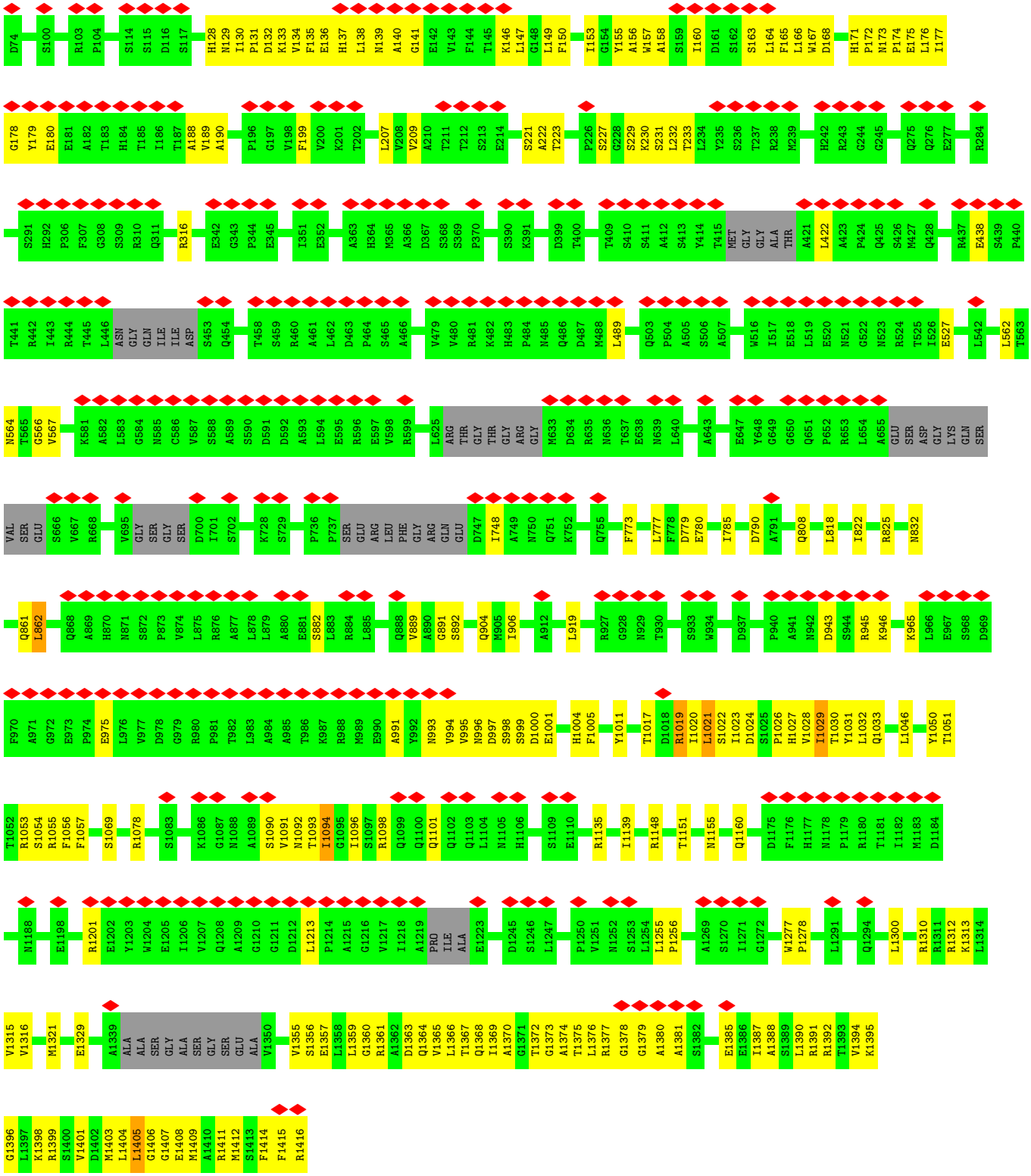
Chain A4:





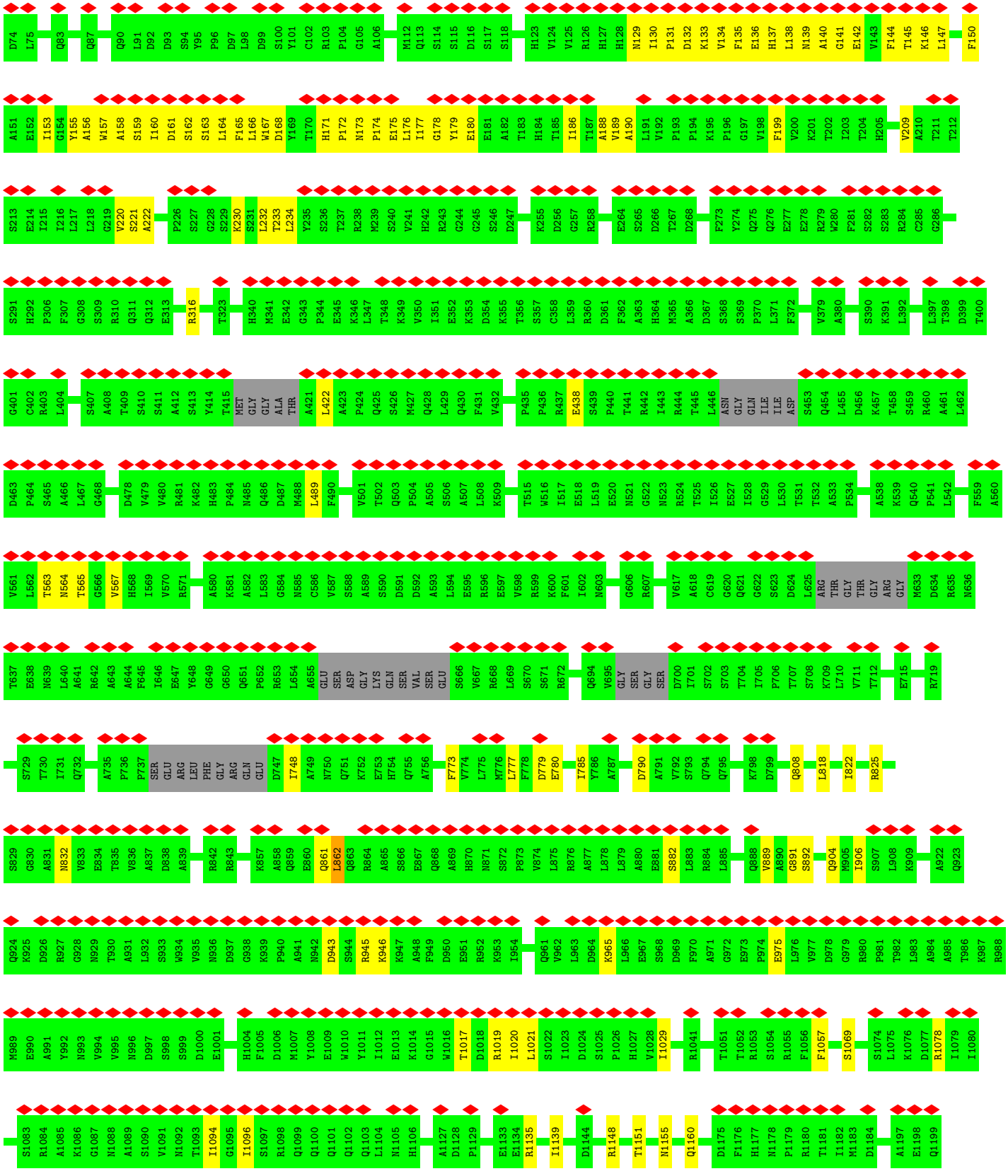
- Molecule 3: NUP155

Chain A5:



- Molecule 3: NUP155

Chain A6: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A151 E152 I153 G154 Y155 A156 W157 A158 S159 I160 D161 S162 S163 L164 F165 L166 W167 D168 Y169 T170 H171 P172 N173 P174 E175 L176 I177 G178 Y179 E180 E181 A182 T183 H184 T185 I186 T187 A188 V189 A190 L191 V192 P193 P194 K195 P196 G197 V198 F199 V200 K201 T202 I203 T204 H205 V209 K210 T211 T212
S213 E214 I215 I216 L217 L218 G219 V220 S221 A222 P226 S227 G228 S229 K230 S231 L232 T233 L234 Y235 S236 T237 R238 M239 S240 V241 H242 R243 G244 G245 S246 D247 K255 D256 G257 R258 E264 S265 D266 T267 D268 F273 Y274 Q275 Q276 E277 E278 R279 W280 F281 S282 S283 R284 C285 G286
S291 H292 P306 F307 G308 S309 R310 Q311 Q312 E313 R316 T323 H340 M341 E342 G343 P344 E345 K346 L347 T348 K349 V350 I351 E352 K353 D354 K355 T356 S357 C358 L359 R360 D361 F362 A363 H364 M365 A366 D367 S368 S369 P370 L371 F372 V379 A380 S390 K391 L392 L397 T398 D399 T400
G401 C402 R403 L404 S407 A408 T409 S410 S411 A412 S413 Y414 T415 MET GLY GLY ALA THR A421 L422 A423 P424 Q425 S426 M427 Q428 L429 Q430 F431 V432 P435 P436 R437 E438 S439 P440 T441 R442 I443 R444 T445 L446 ASN GLY GLN ILE ILE ASP S453 Q454 L455 D456 K457 T458 S459 R460 A461 L462
D463 P464 S465 A466 L467 G468 D478 V479 V480 R481 K482 H483 P484 N485 Q486 D487 M488 L489 F490 V501 T502 Q503 P504 A505 S506 A507 L508 K509 T515 W516 I517 E518 L519 E520 N521 G522 N523 R524 T525 I526 E527 I528 G529 L530 T531 T532 A533 P534 A538 K539 Q540 P541 L542 F559 A560
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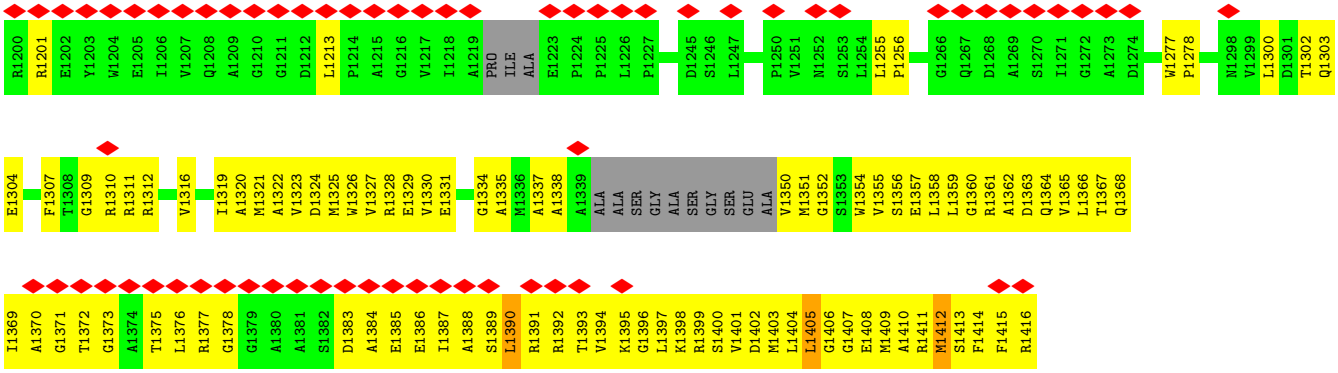
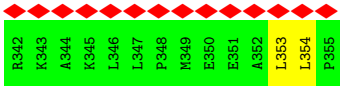
T637 E638 N639 L640 A641 R642 A643 A644 F645 I646 E647 Y648 G649 G650 Q651 P652 R653 L654 A655 GLU SER ASP GLY LYS GLN SER VAL SER GLU S666 V667 R668 L669 S670 S671 R672 Q694 V695 GLY SER GLY SER D700 I701 S702 S703 T704 I705 P706 T707 S708 K709 L710 V711 T712 E715 R719
S729 T730 I731 Q732 A735 P736 P737 SER GLU ARG LEU PHE GLY ARG GLN GLU D747 I748 A749 N750 Q751 K752 E753 H754 Q755 A756 F773 V774 L775 M776 L777 F778 D779 E780 I785 Y786 A787 D790 A791 V792 S793 Q794 Q795 K798 D799 Q808 L818 I822 R825
S829 G830 A831 N832 V833 E834 T835 V836 A837 D838 A839 R842 R843 K857 A858 Q859 E860 Q861 L862 Q863 R864 A865 S866 E867 Q868 A869 H870 N871 S872 P873 V874 L875 R876 A877 L878 L879 A880 E881 S882 L883 R884 L885 Q888 V889 A890 G891 S892 Q904 M905 I906 S907 L908 K909 A922 Q923
Q924 K925 D926 R927 G928 N929 T930 A931 L932 S933 W934 V935 N936 D937 G938 K939 P940 A941 N942 D943 S944 R945 K946 K947 A948 F949 D950 E951 R952 K953 I954 Q961 V962 L963 D964 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 H1004 F1005 D1006 M1007 Y1008 E1009 W1010 Y1011 I1012 E1013 K1014 G1015 W1016 T1017 D1018 R1019 I1020 L1021 S1022 I1023 D1024 S1025 P1026 H1027 V1028 I1029 R1041 T1051 T1052 R1053 S1054 R1055 F1056 F1057 S1069 S1074 L1075 K1076 D1077 R1078 I1079 I1080
S1083 R1084 A1085 K1086 G1087 N1088 A1089 S1090 V1091 N1092 T1093 I1094 G1095 I1096 S1097 R1098 Q1099 Q1100 Q1101 Q1102 Q1103 L1104 N1105 H1106 A1127 D1128 P1129 E1133 E1134 R1135 I1139 D1144 R1148 T1151 N1155 Q1160 D1175 F1176 H1177 N1178 P1179 R1180 T1181 I1182 M1183 D1184 A1197 E1198 Q1199



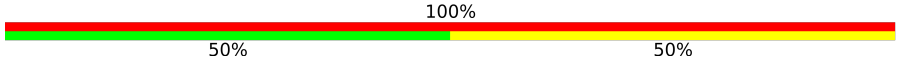
• Molecule 4: NUP53 R3

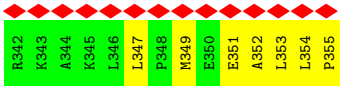
Chain B1:



• Molecule 4: NUP53 R3

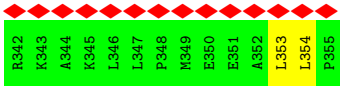
Chain B2:





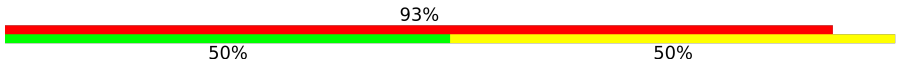
• Molecule 4: NUP53 R3

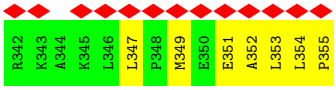
Chain B3:



• Molecule 4: NUP53 R3

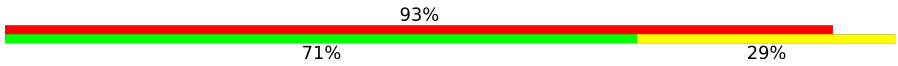
Chain B4:

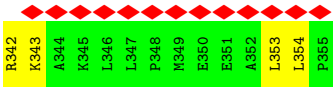




• Molecule 4: NUP53 R3

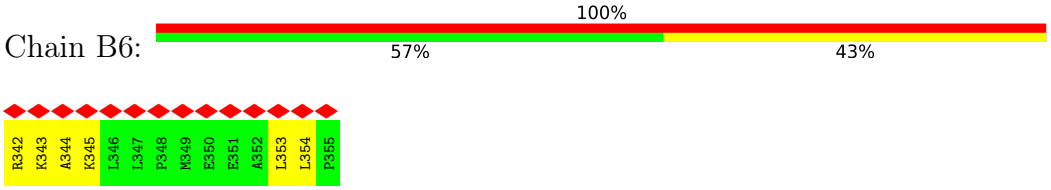
Chain B5:





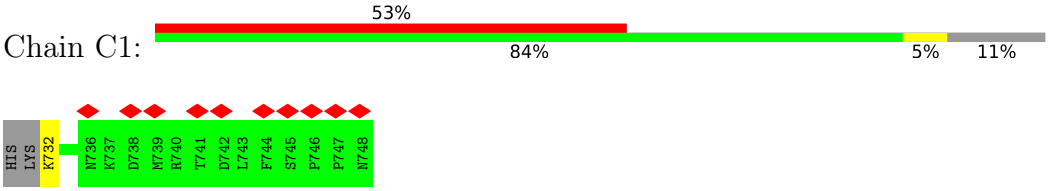
• Molecule 4: NUP53 R3

Chain B6:



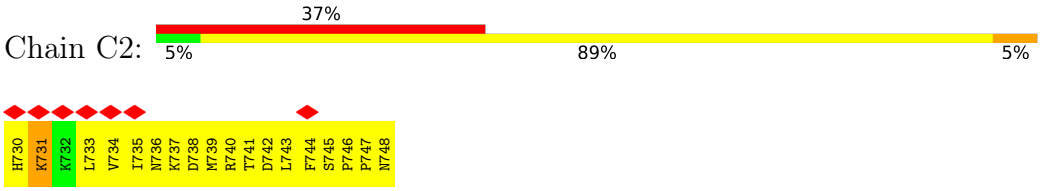
• Molecule 5: NUP98 R3

Chain C1:



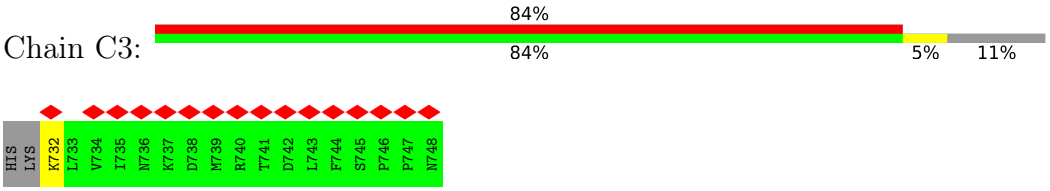
• Molecule 5: NUP98 R3

Chain C2:



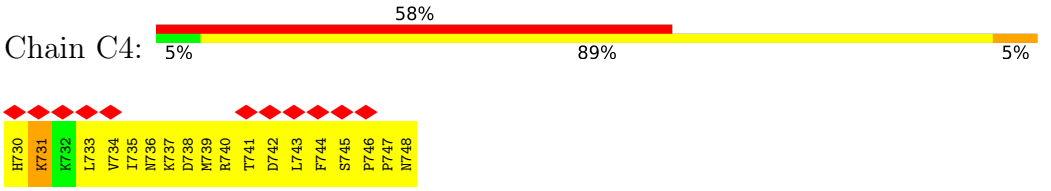
• Molecule 5: NUP98 R3

Chain C3:



• Molecule 5: NUP98 R3

Chain C4:

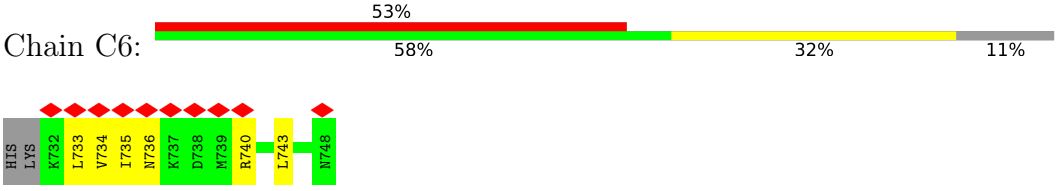


• Molecule 5: NUP98 R3

Chain C5:

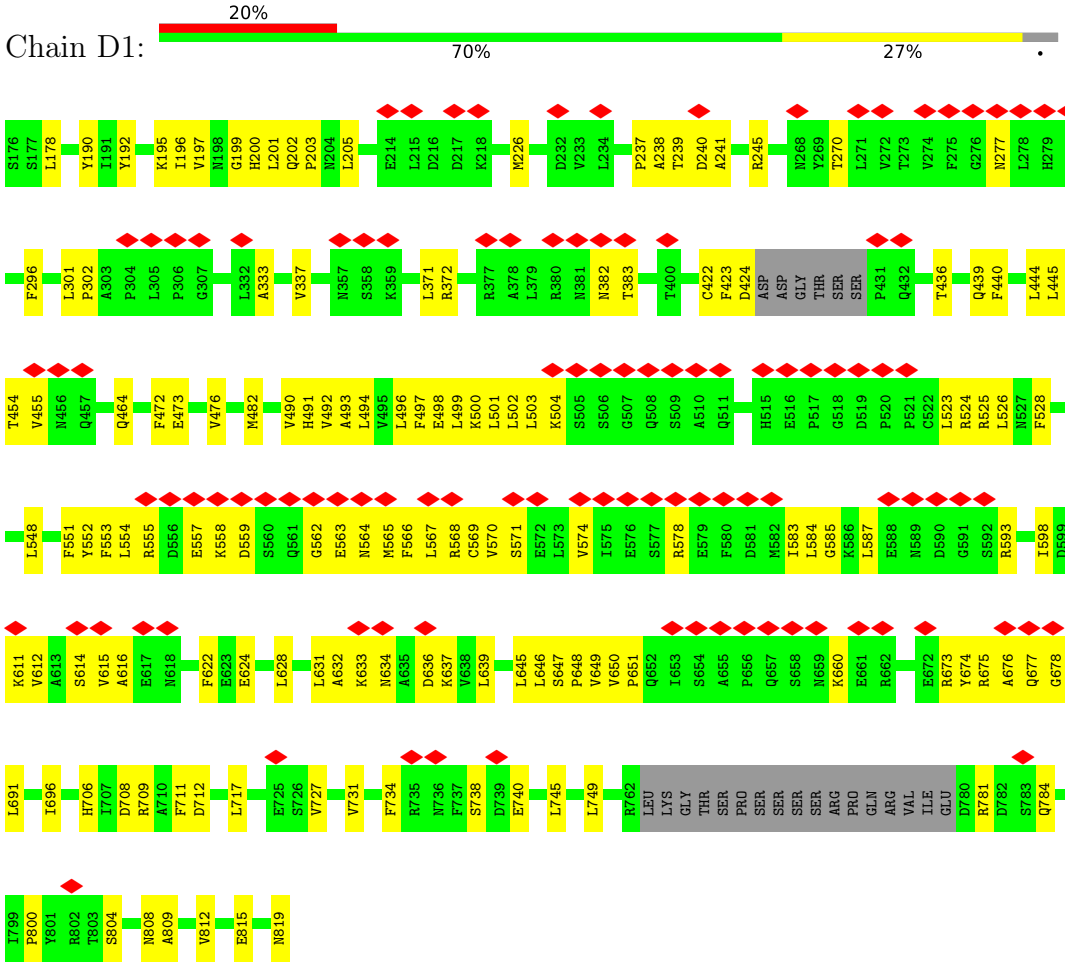
• Molecule 5: NUP98 R3

Chain C6:



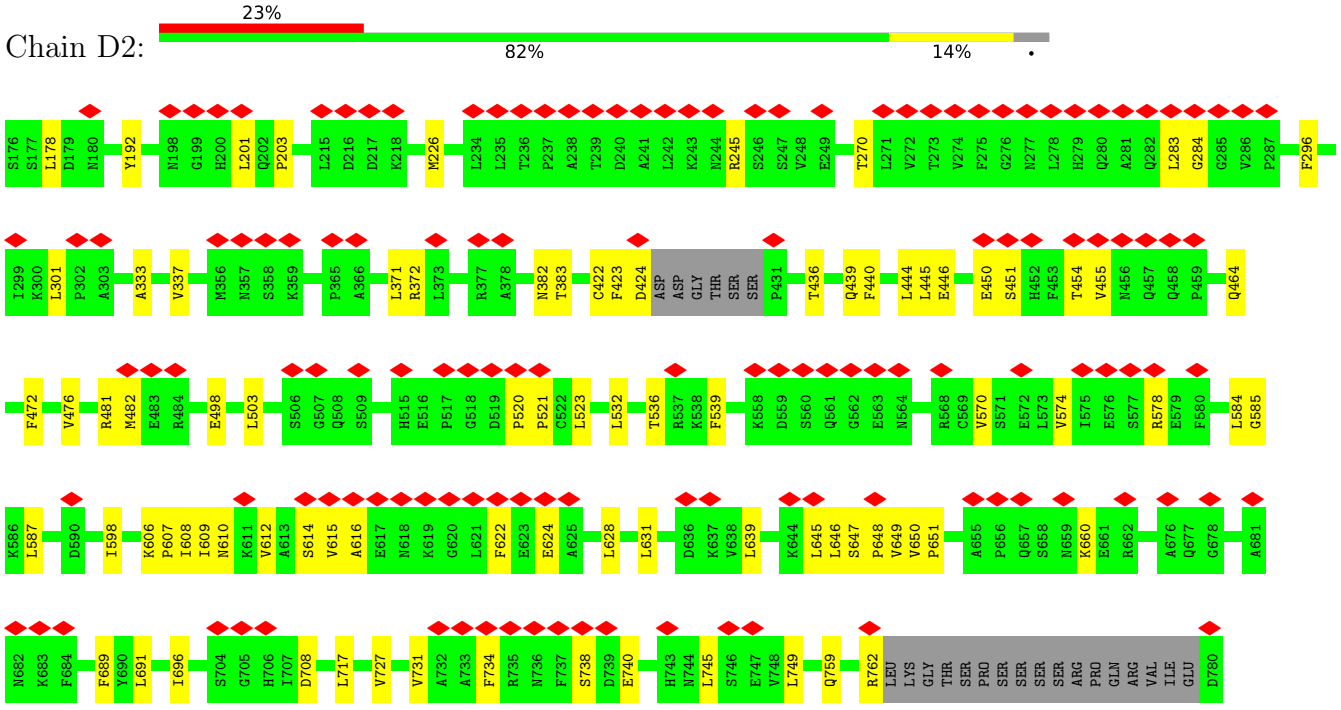
• Molecule 6: NUP93 SOL

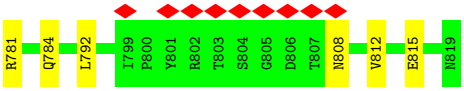
Chain D1:



• Molecule 6: NUP93 SOL

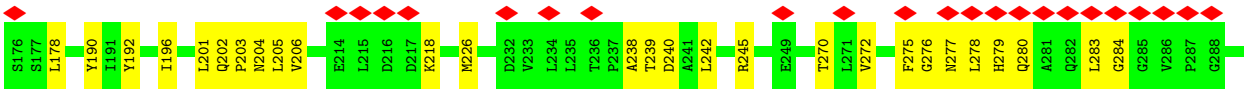
Chain D2:

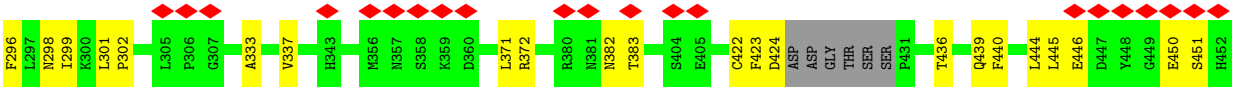


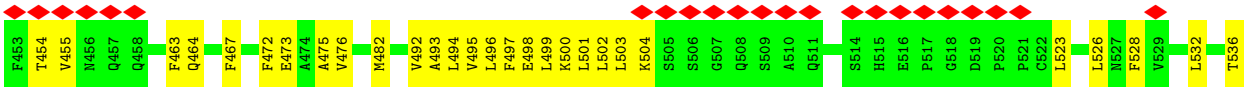


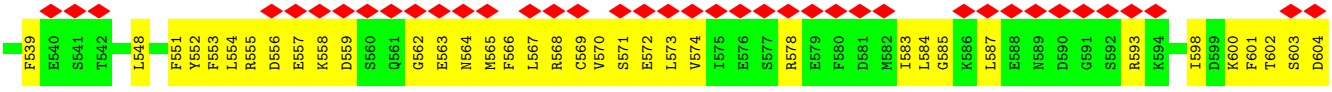
• Molecule 6: NUP93 SOL

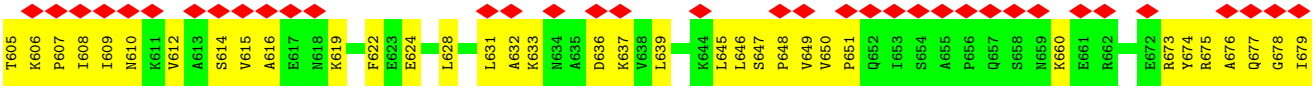
Chain D3:

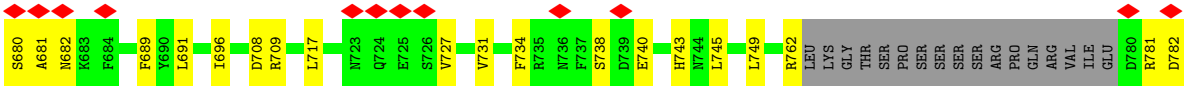


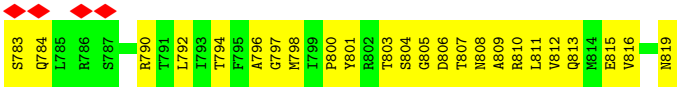






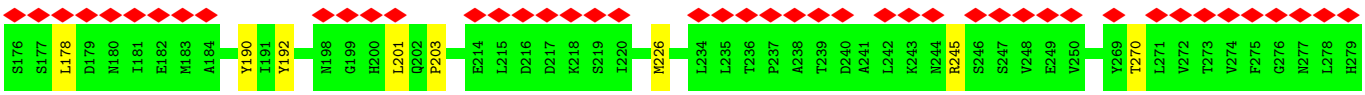


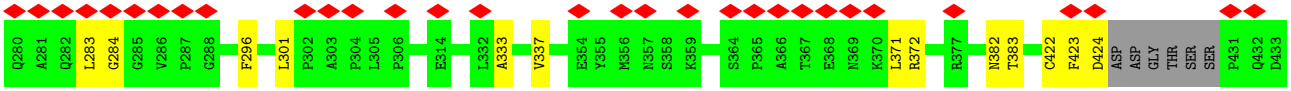


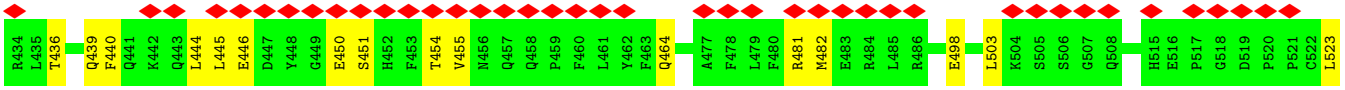


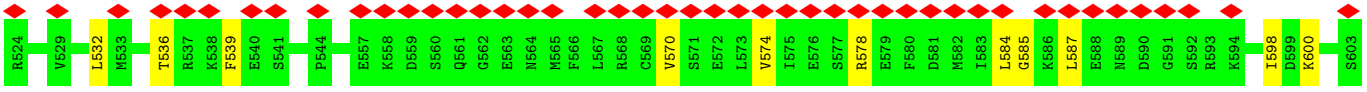
• Molecule 6: NUP93 SOL

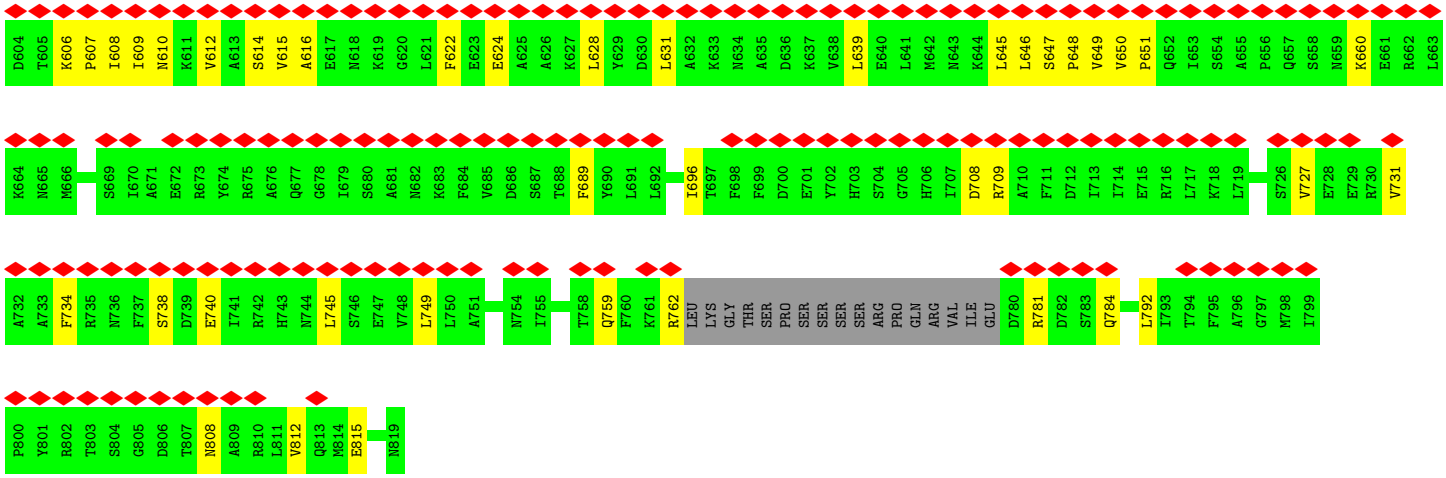
Chain D4:





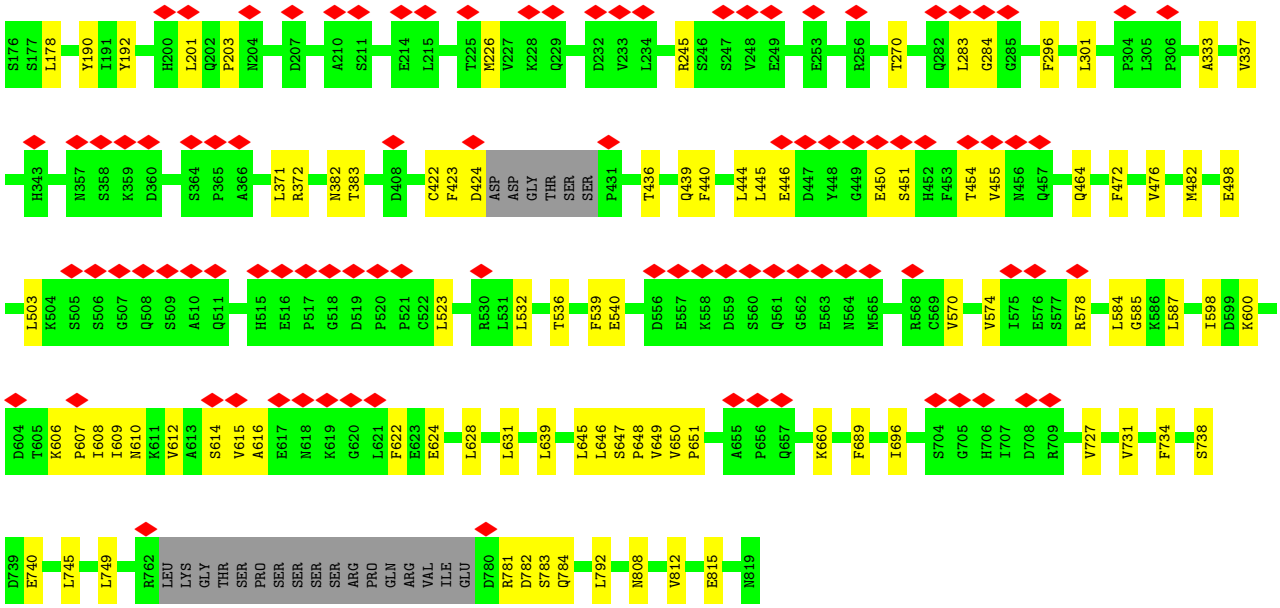






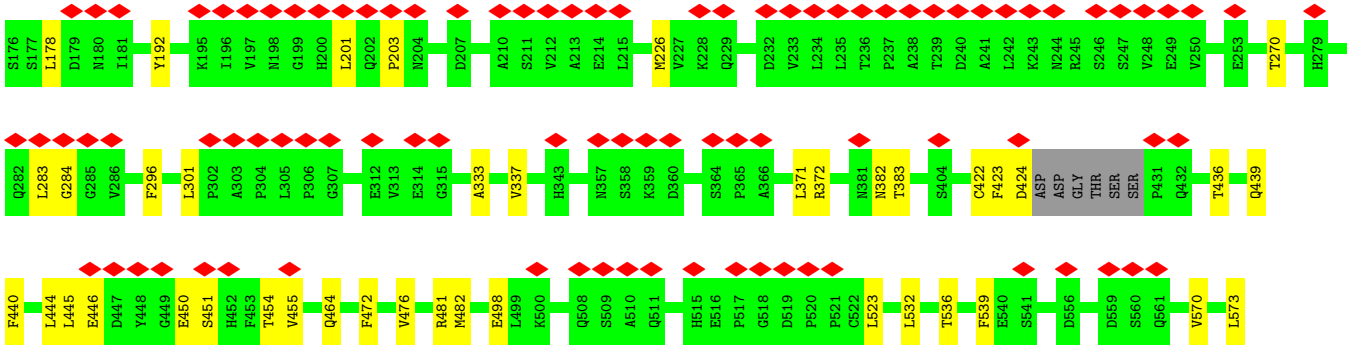
• Molecule 6: NUP93 SOL

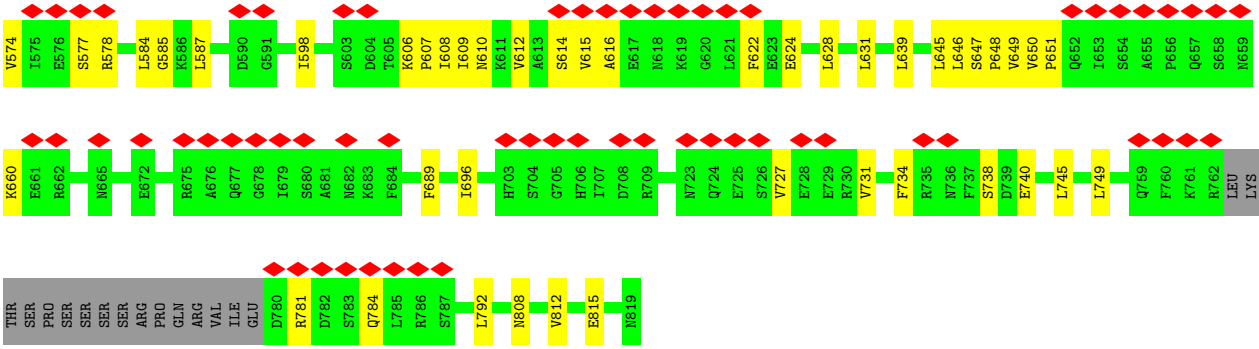
Chain D5:



• Molecule 6: NUP93 SOL

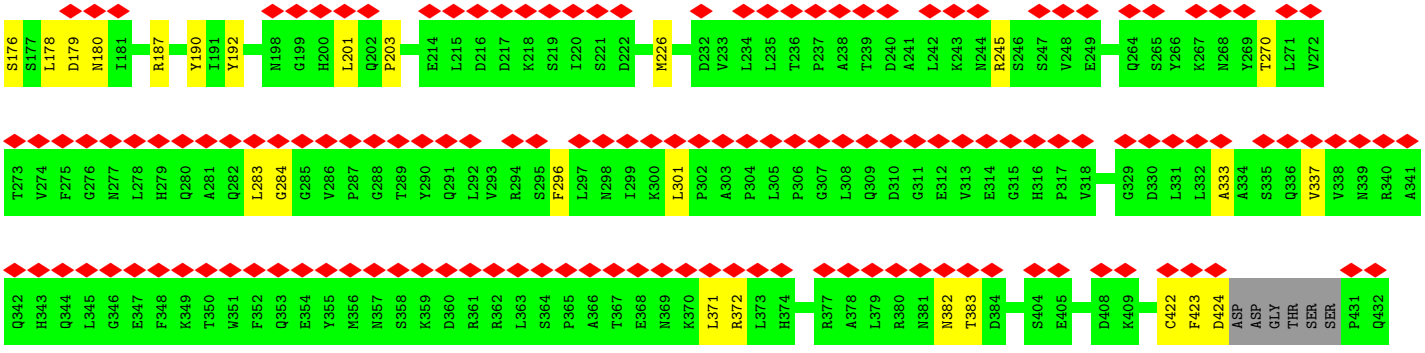
Chain D6:





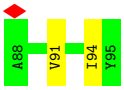
• Molecule 6: NUP93 SOL

Chain D7:



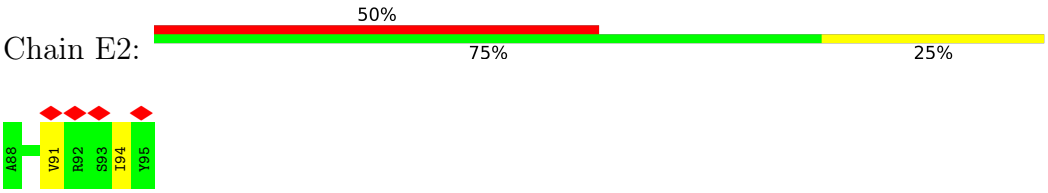
• Molecule 7: NUP53 R2

Chain E1:



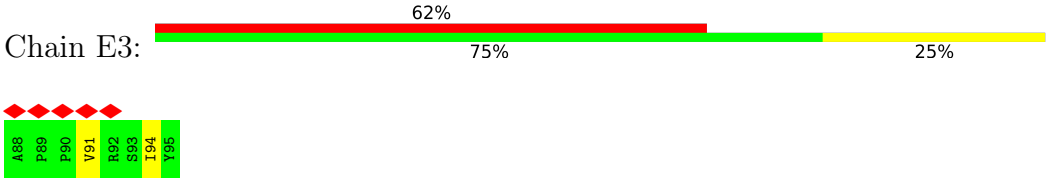
• Molecule 7: NUP53 R2

Chain E2:



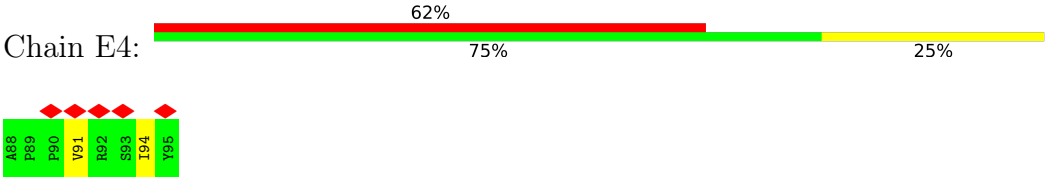
• Molecule 7: NUP53 R2

Chain E3:



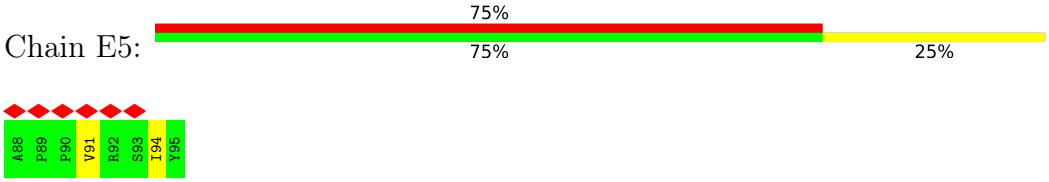
• Molecule 7: NUP53 R2

Chain E4:



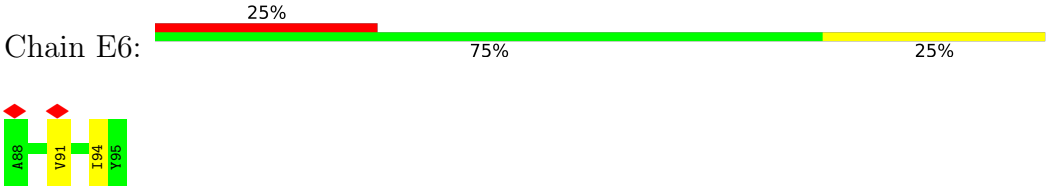
• Molecule 7: NUP53 R2

Chain E5:



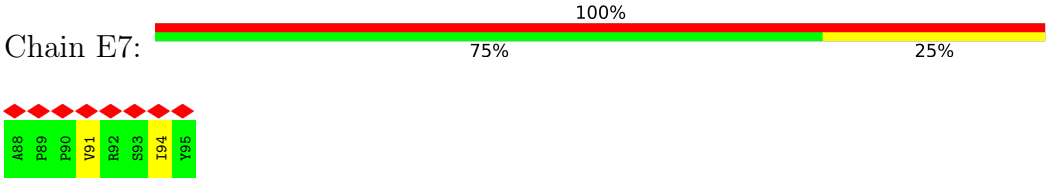
• Molecule 7: NUP53 R2

Chain E6:



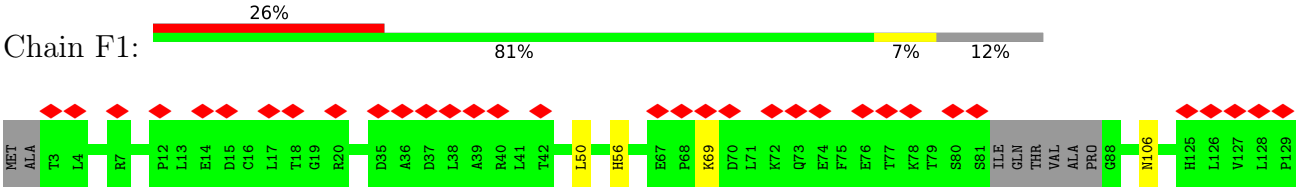
• Molecule 7: NUP53 R2

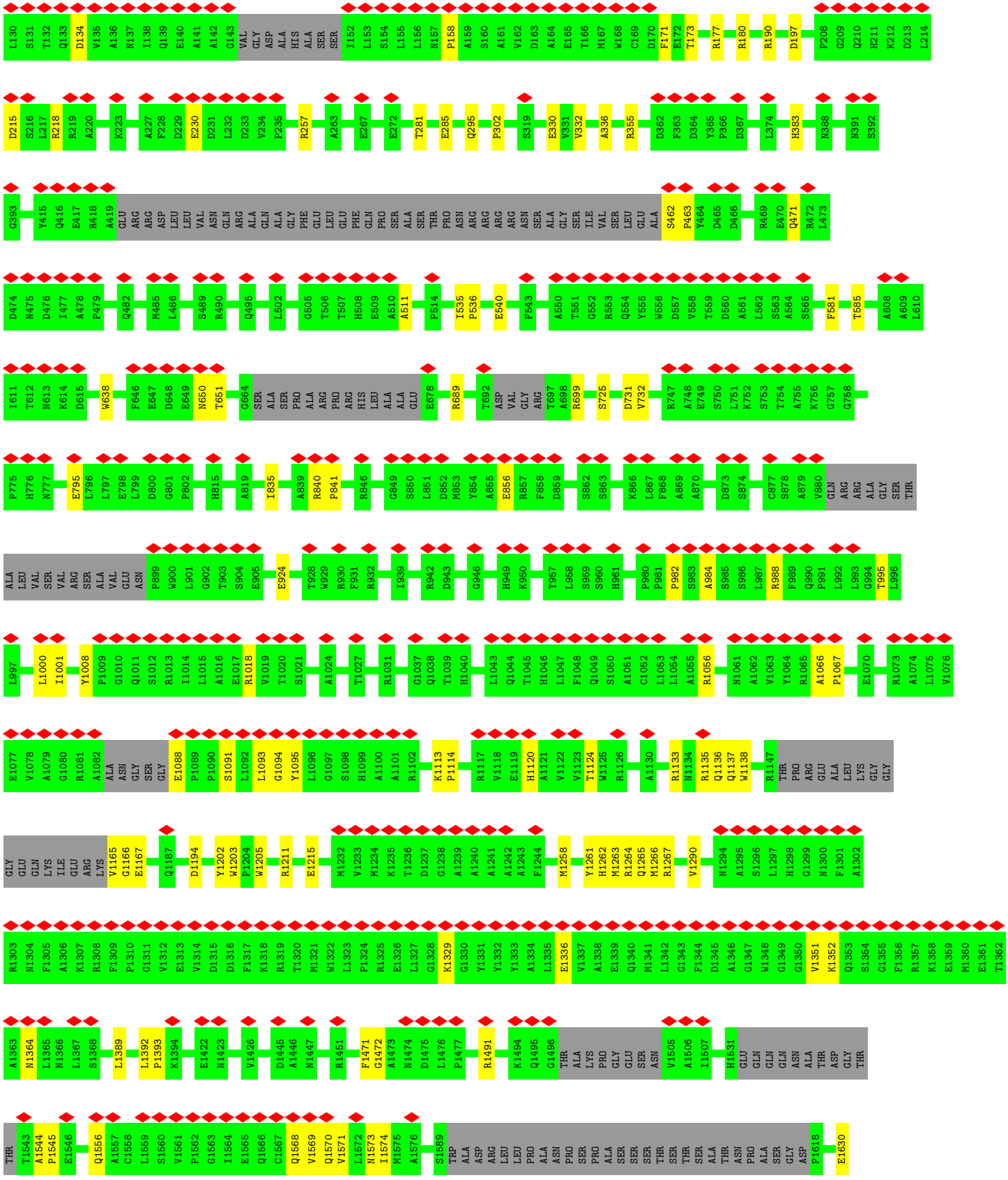
Chain E7:



• Molecule 8: NUP188

Chain F1:

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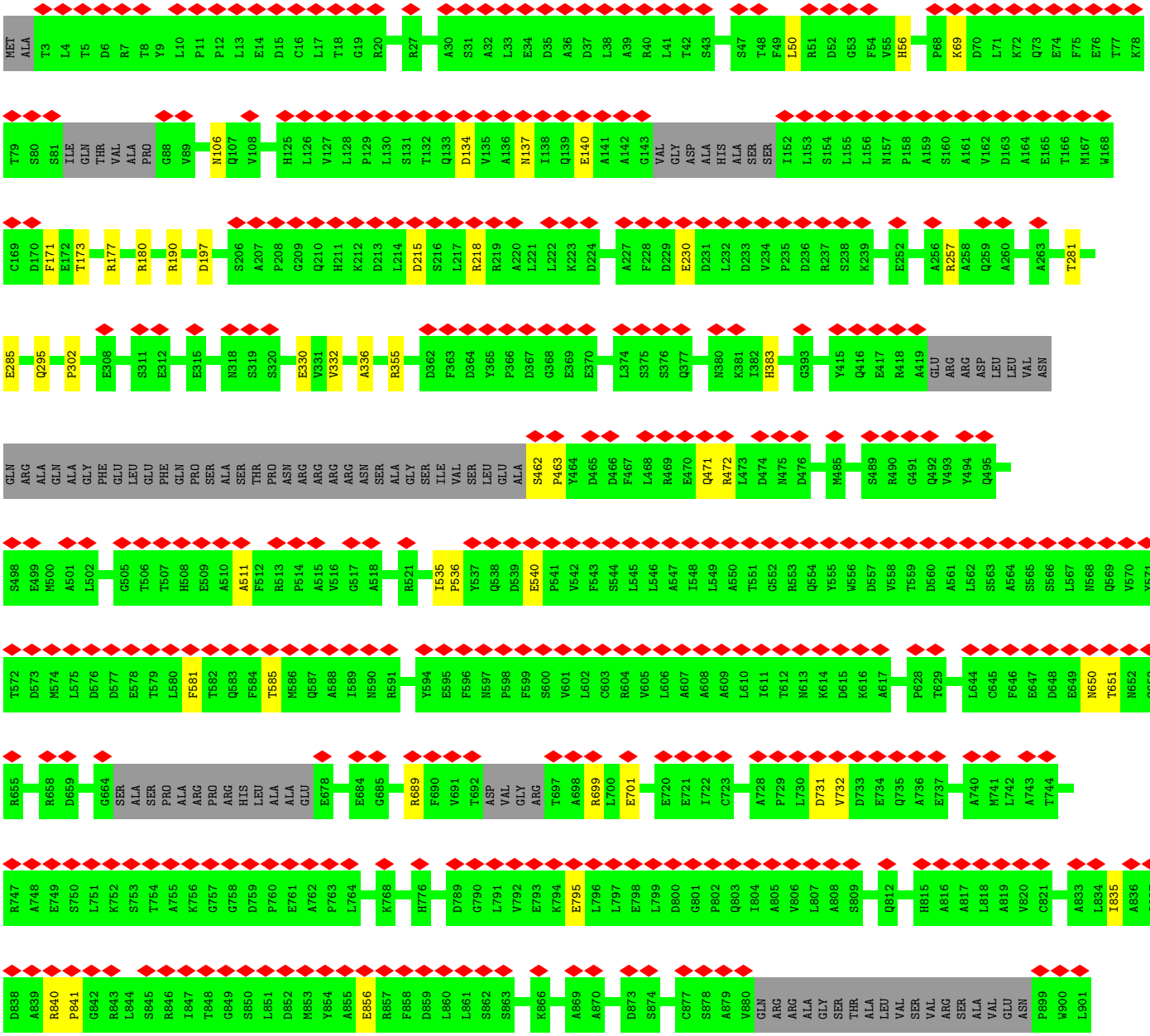
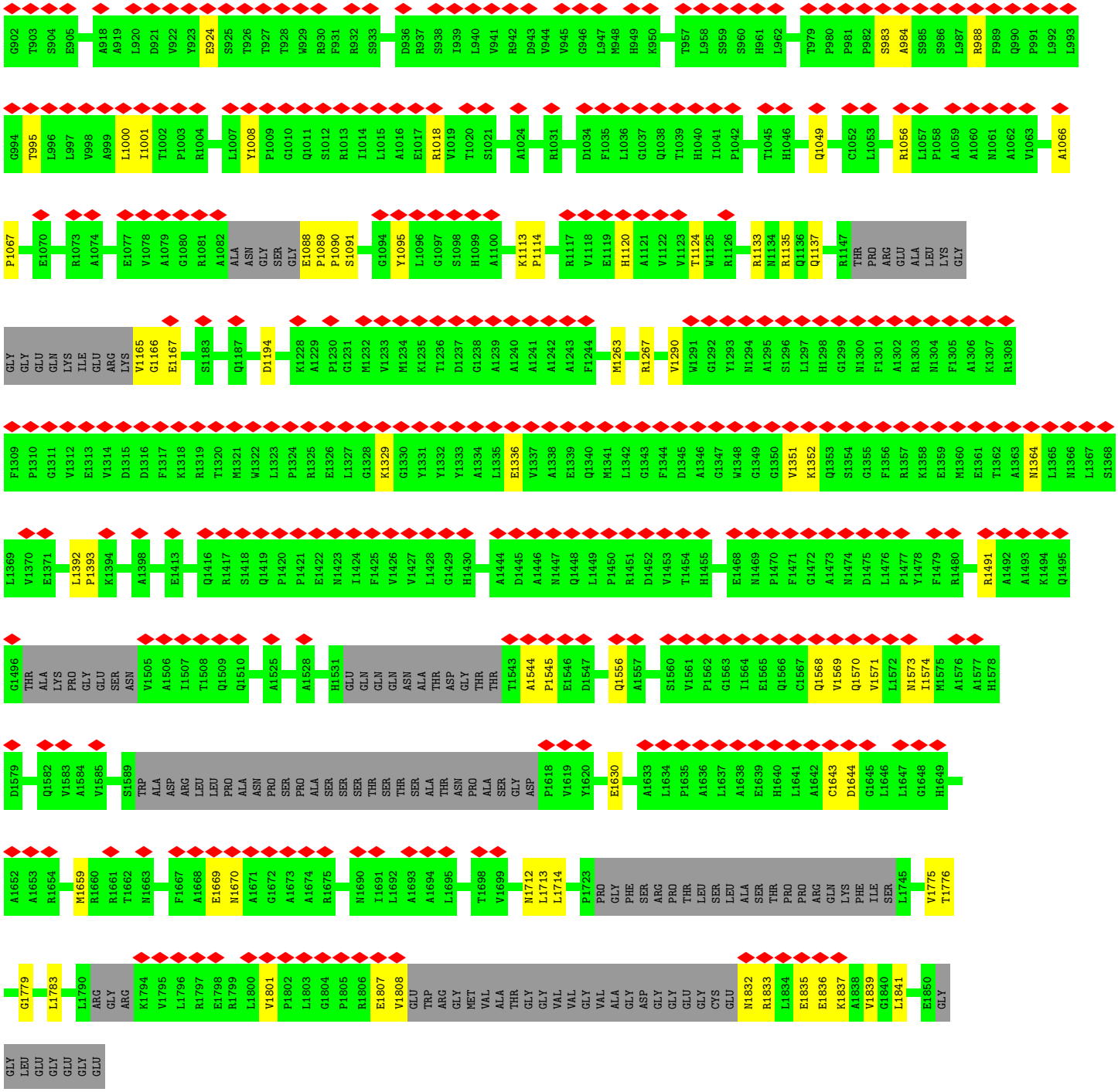
D215 S216 L217 R218 R219 A220 K223 A227 F228 D229 E230 D231 L232 D233 V234 P235 R257 A263 E267 E272 T281 E285 Q295 P302 S319 E330 V331 V332 A336 R355 D362 F363 D364 Y365 P366 D367 L374 H383 N388 N391 S392
G393 Y415 Q416 E417 R418 A419 GLU ARG ARG ASP LEU LEU VAL ASN GLN ARG ALA GLN ALA GLY PHE GLU LEU GLU PHE GLN PRO SER ALA SER THR PRO ASN ARG ARG ARG ASN SER ALA GLY SER ILE VAL SER LEU GLU ALA S462 P463 Y464 D465 D466 R469 E470 Q471 R472 L473
D474 N475 D476 I477 A478 P479 Q482 M485 L486 S489 R490 Q495 L502 G505 T506 T507 H508 E509 A510 A511 P514 I535 P536 E540 F543 A550 T551 G552 R553 Q554 Y555 W556 D557 V558 T559 D560 A561 L562 S563 A564 S565 F581 T585 A608 A609 L610
I611 T612 N613 K614 D615 W638 F646 E647 D648 E649 N650 T651 G664 SER ALA SER PRO ALA ARG PRO ARG HIS LEU ALA ALA GLU E678 R689 T692 ASP VAL GLY ARG T697 A698 R699 S725 D731 V732 R747 A748 E749 S750 L751 K752 S753 T754 A755 K756 G757 G758
P775 H776 N777 E795 L796 L797 E798 L799 D800 G801 P802 H815 A819 I835 A839 R840 P841 R846 G849 S850 L851 D852 M853 Y854 A855 E856 R857 F858 D859 S862 S863 K866 L867 F868 A869 A870 D873 S874 C877 S878 A879 V880 GLN ARG ARG ALA GLY SER THR
ALA LEU VAL SER VAL ARG SER ALA VAL GLU ASN P899 W900 L901 G902 T903 S904 E905 E924 T928 W929 R930 F931 R932 I939 R942 D943 G946 H949 K950 T957 L958 S959 S960 H961 P980 P981 P982 S983 A984 S985 S986 L987 R988 F989 Q990 P991 L992 L993 G994 T995 L996
L997 L1000 I1001 Y1008 P1009 G1010 Q1011 S1012 R1013 I1014 L1015 A1016 E1017 R1018 V1019 T1020 S1021 A1024 T1027 R1031 G1037 Q1038 T1039 H1040 L1043 Q1044 T1045 H1046 L1047 F1048 Q1049 S1050 A1051 C1052 L1053 L1054 A1055 R1056 N1061 A1062 V1063 Y1064 R1065 A1066 P1067 E1070 R1073 A1074 L1075 V1076
E1077 V1078 A1079 G1080 R1081 A1082 ALA ASN GLY SER GLY E1088 P1089 P1090 S1091 L1092 L1093 G1094 Y1095 L1096 G1097 S1098 H1099 A1100 A1101 R1102 K1113 P1114 R1117 V1118 E1119 H1120 A1121 V1122 V1123 T1124 W1125 R1126 A1130 R1133 N1134 R1135 Q1136 Q1137 W1138 R1147 THR PRO ARG GLU ALA LEU LYS GLY GLY
GLY GLU GLN LYS ILE GLU ARG LYS V1165 G1166 E1167 Q1187 D1194 Y1202 W1203 P1204 W1205 R1211 E1215 M1232 V1233 M1234 K1235 T1236 D1237 G1238 A1239 A1240 A1241 A1242 A1243 F1244 M1258 Y1261 H1262 M1263 R1264 Q1265 M1266 R1267 V1290 N1294 A1295 S1296 L1297 H1298 G1299 N1300 F1301 A1302
R1303 N1304 F1305 A1306 K1307 R1308 F1309 P1310 G1311 V1312 E1313 V1314 D1315 D1316 F1317 K1318 R1319 T1320 M1321 W1322 L1323 P1324 R1325 E1326 L1327 G1328 K1329 G1330 Y1331 Y1332 Y1333 A1334 L1335 E1336 V1337 A1338 E1339 Q1340 M1341 L1342 G1343 F1344 D1345 A1346 G1347 W1348 G1349 G1350 V1351 K1352 Q1353 S1354 G1355 F1356 R1357 K1358 E1359 M1360 E1361 T1362
A1363 N1364 L1365 N1366 L1367 S1368 L1389 L1392 P1393 K1394 E1422 N1423 V1426 D1445 A1446 N1447 R1451 F1471 G1472 A1473 N1474 D1475 L1476 P1477 R1491 K1494 Q1495 G1496 THR ALA LYS PRO GLY GLU SER ASN V1505 A1506 I1507 H1531 GLU GLN GLN GLN ASN ALA THR ASP GLY THR
THR T1543 A1544 P1545 E1546 Q1556 A1557 C1558 L1559 S1560 V1561 P1562 G1563 I1564 E1565 Q1566 C1567 Q1568 V1569 Q1570 V1571 L1572 N1573 I1574 M1575 A1576 S1589 TRP ALA ASP ARG LEU LEU PRO ALA ASN PRO SER PRO ALA SER SER SER THR SER THR SER ALA THR ASN PRO ALA SER GLY ASP P1618 E1630

• Molecule 8: NUP188

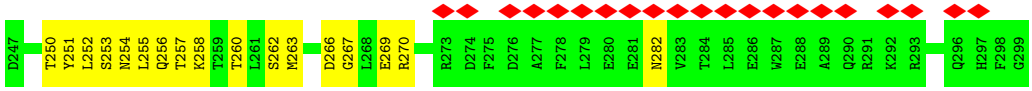
Chain F2:





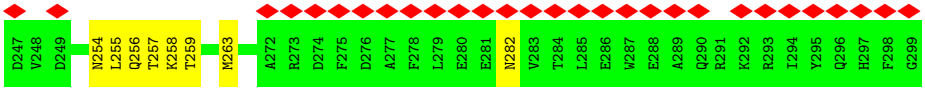
• Molecule 9: NUP93 R2

Chain G1:



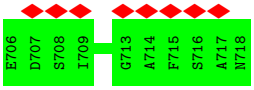
• Molecule 9: NUP93 R2

Chain G2:



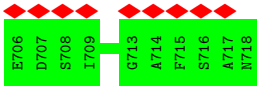
• Molecule 10: NUP98 R2

Chain H1:



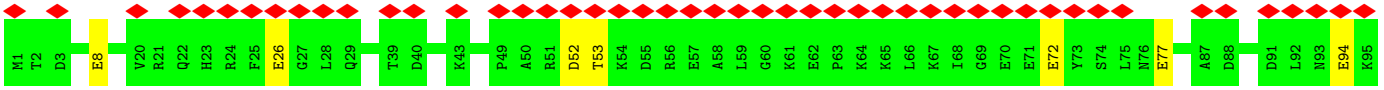
• Molecule 10: NUP98 R2

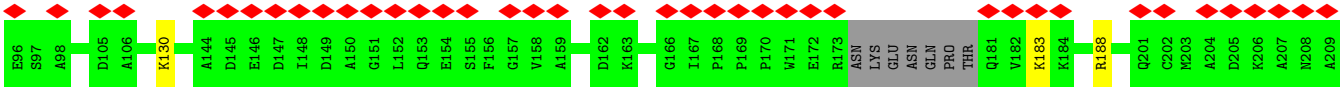
Chain H2:

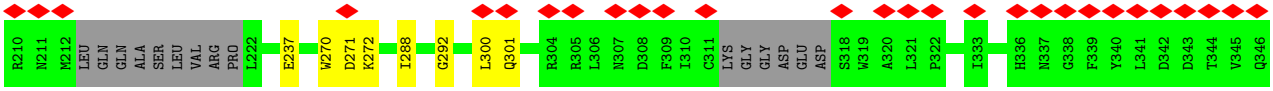


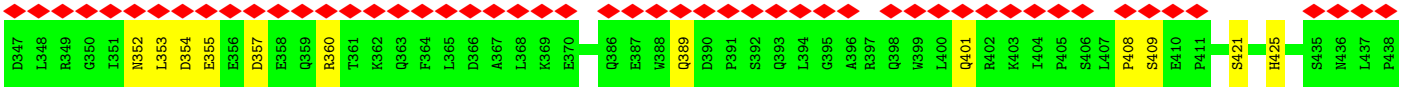
• Molecule 11: NUP205

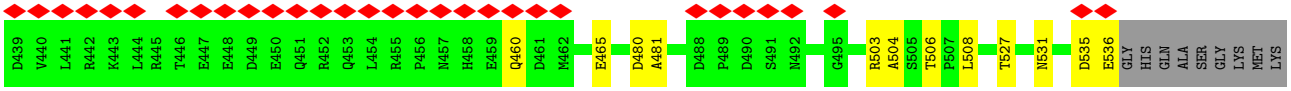
Chain I1:

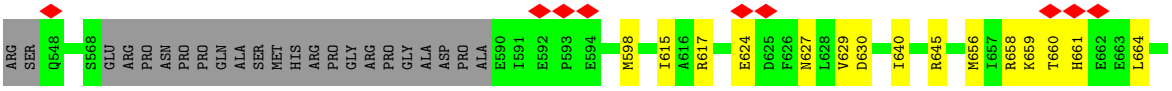


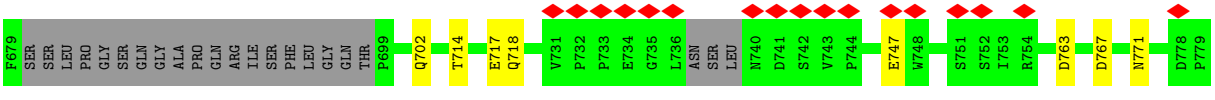


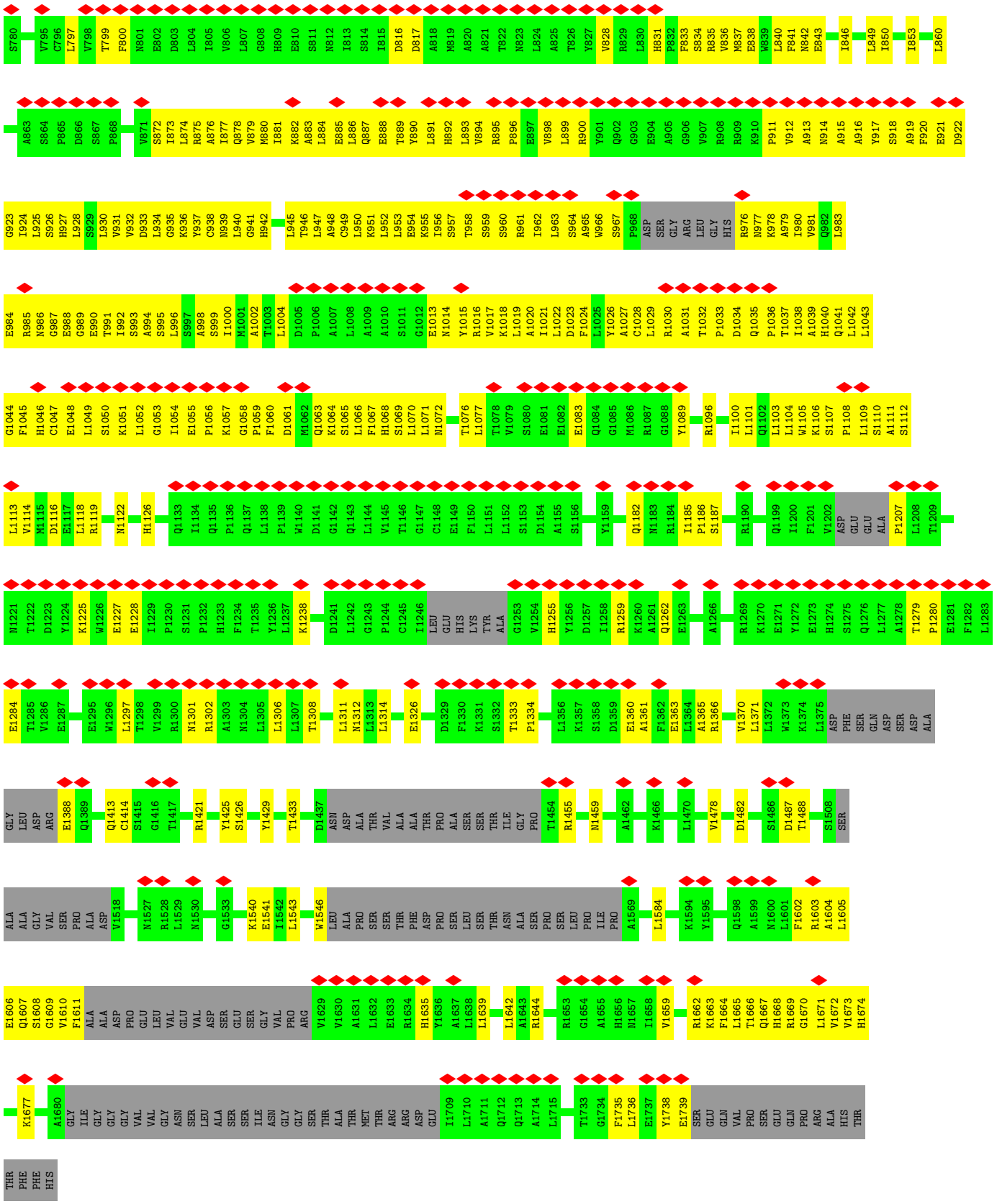








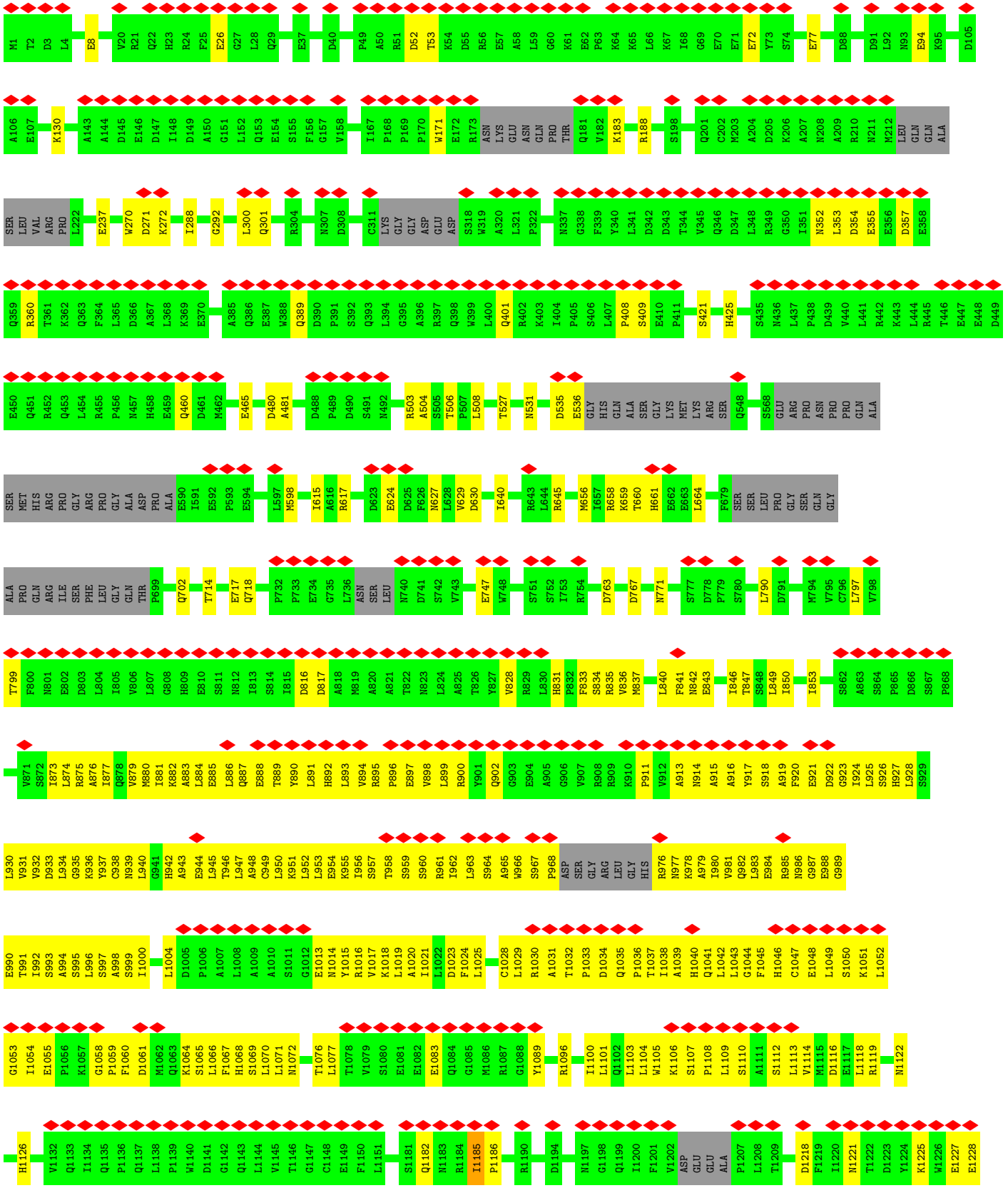




• Molecule 11: NUP205

Chain I2:

31%
67%
21%
12%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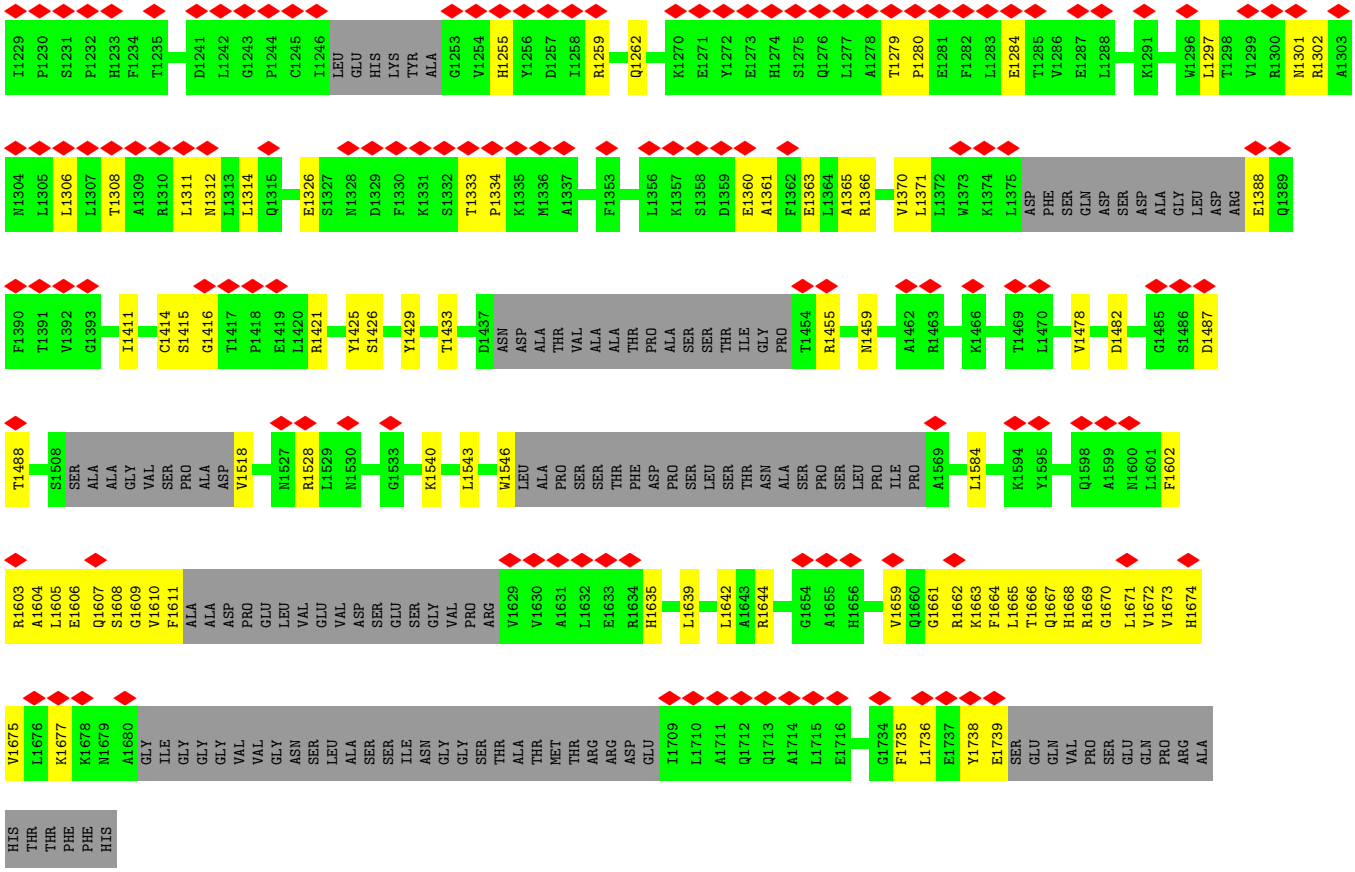
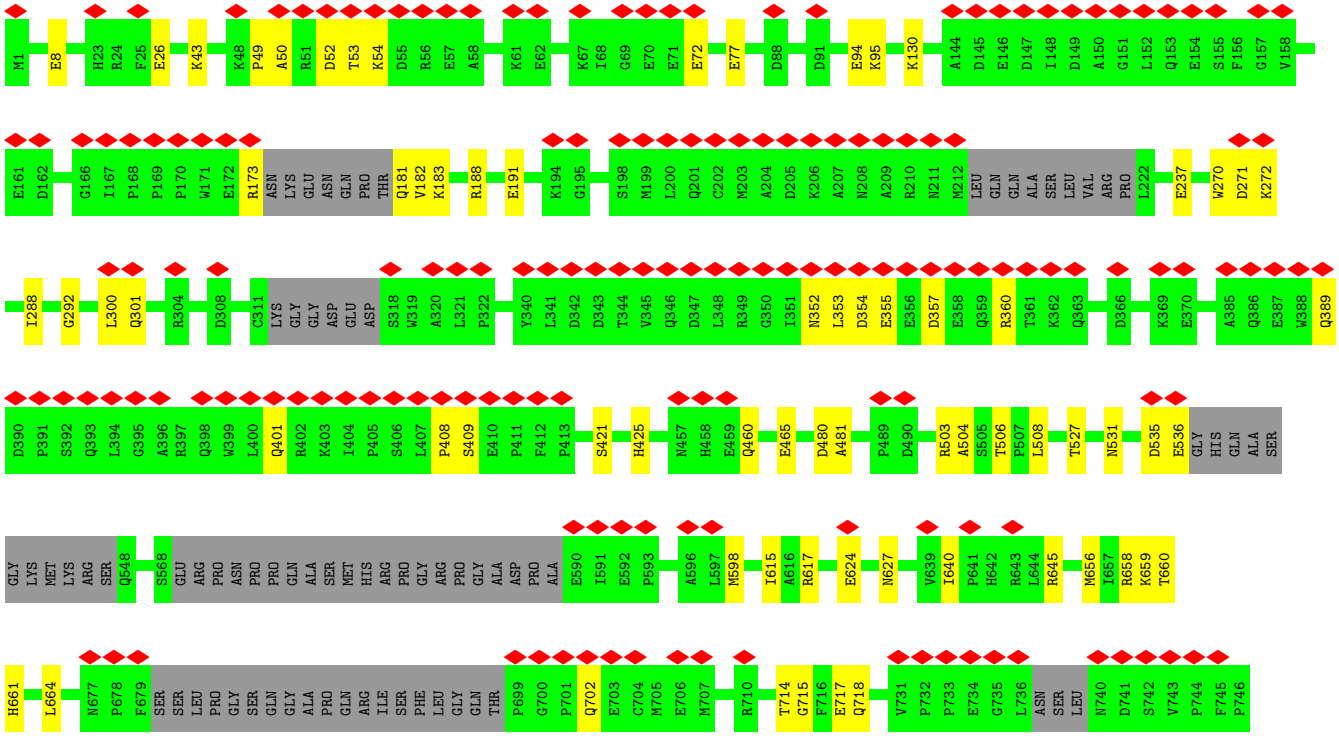
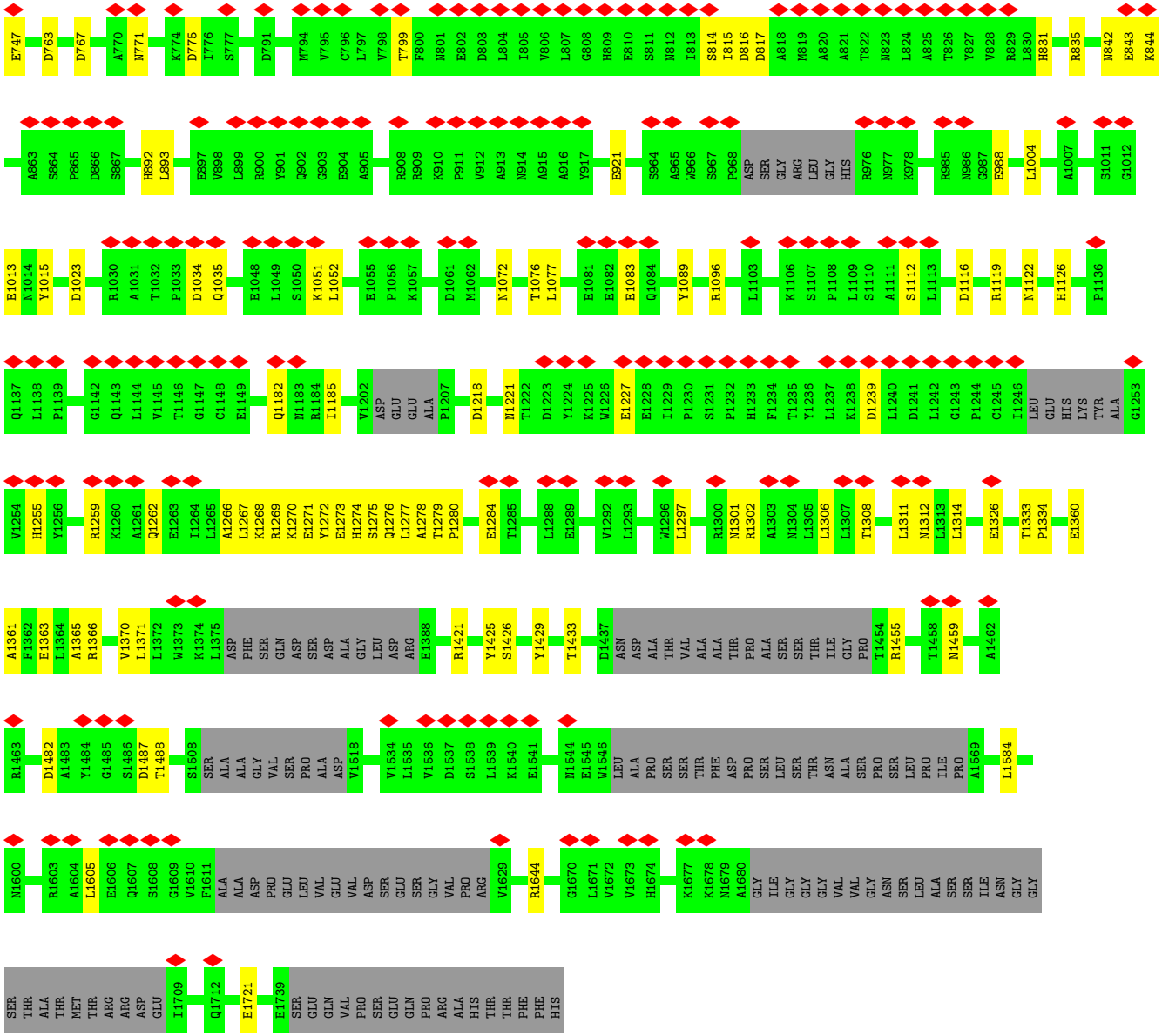
A106 E107 K130 A143 A144 D145 E146 D147 I148 D149 A150 G151 L152 Q153 E154 S155 F156 G157 V158 I167 P168 P169 P170 W171 E172 R173 ASN LYS GLU ASN GLN PRO THR Q181 V182 K183 R188 S198 Q201 C202 M203 A204 D205 K206 A207 N208 A209 R210 N211 M212 LEU GLN GLN ALA
SER LEU VAL ARG PRO L222 E237 W270 D271 K272 I288 G292 L300 Q301 R304 N307 D308 C311 LYS GLY GLY ASP GLU ASP S318 W319 A320 L321 P322 N337 G338 F339 Y340 L341 D342 D343 T344 V345 Q346 D347 L348 R349 G350 I351 N352 L353 D354 E355 E356 D357 E358
Q359 R360 T361 K362 Q363 F364 L365 D366 A367 L368 K369 E370 A385 Q386 E387 W388 Q389 D390 P391 S392 Q393 L394 G395 A396 R397 Q398 W399 L400 Q401 R402 K403 I404 P405 S406 L407 P408 S409 E410 P411 S421 H425 S435 N436 L437 P438 D439 V440 L441 R442 K443 L444 R445 T446 E447 E448 D449
E450 Q451 R452 Q453 L454 R455 P456 N457 H458 E459 Q460 D461 M462 E465 D480 A481 D488 P489 D490 S491 N492 R503 A504 S505 T506 P507 L508 T527 N531 D535 E536 GLY HIS GLN ALA SER GLY LYS MET LYS ARG SER Q548 S568 GLU ARG PRO ASN PRO PRO GLN ALA
SER MET HIS ARG PRO GLY ARG PRO GLY ALA ASP PRO ALA E590 I591 E592 P593 E594 L597 M598 I615 A616 R617 D623 E624 D625 F626 N627 L628 V629 D630 I640 R643 L644 R645 M656 I657 R658 K659 T660 H661 E662 E663 L664 F679 SER SER LEU PRO GLY SER GLN GLY
ALA PRO GLN ARG ILE SER PHE LEU GLY GLN THR P699 Q702 T714 E717 Q718 P732 P733 E734 G735 L736 ASN SER LEU N740 D741 S742 V743 E747 W748 S751 S752 I753 R754 D763 D767 N771 S777 D778 P779 S780 L790 D791 M794 V795 C796 L797 V798
T799 F800 N801 E802 D803 L804 I805 V806 L807 G808 H809 E810 S811 N812 I813 S814 I815 D816 D817 A818 M819 A820 A821 T822 N823 L824 A825 T826 Y827 V828 R829 L830 H831 P832 F833 S834 R835 V836 M837 L840 F841 N842 E843 I846 T847 S848 L849 I850 I853 S862 A863 S864 P865 D866 S867 P868
V871 S872 I873 L874 R875 A876 I877 Q878 V879 M880 I881 K882 A883 L884 E885 L886 Q887 E888 T889 Y890 L891 H892 L893 V894 R895 P896 E897 V898 L899 R900 Y901 Q902 G903 E904 A905 G906 V907 R908 R909 K910 P911 V912 A913 N914 A915 A916 Y917 S918 A919 F920 E921 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 I956 S957 T958 S959 S960 R961 I962 L963 S964 A965 W966 S967 P968 ASP SER GLY ARG LEU GLY HIS R976 N977 K978 A979 I980 V981 Q982 L983 E984 R985 N986 G987 E988 G989
E990 T991 I992 S993 A994 S995 L996 S997 A998 S999 I1000 L1004 D1005 P1006 A1007 L1008 A1009 A1010 S1011 G1012 E1013 N1014 Y1015 R1016 V1017 K1018 L1019 A1020 I1021 L1022 D1023 F1024 L1025 C1028 L1029 R1030 A1031 T1032 P1033 D1034 Q1035 P1036 T1037 I1038 A1039 H1040 Q1041 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 N1072 T1076 L1077 T1078 V1079 S1080 E1081 E1082 E1083 Q1084 G1085 M1086 R1087 G1088 Y1089 R1096 I1100 L1101 Q1102 L1103 L1104 W1105 K1106 S1107 P1108 L1109 S1110 A1111 S1112 L1113 V1114 M1115 D1116 E1117 L1118 R1119 N1122
H1126 V1132 Q1133 I1134 Q1135 P1136 Q1137 L1138 P1139 W1140 D1141 G1142 Q1143 L1144 V1145 T1146 G1147 C1148 E1149 F1150 L1151 S1181 Q1182 N1183 R1184 I1185 P1186 R1190 D1194 N1197 G1198 Q1199 I1200 F1201 V1202 ASP GLU GLU ALA P1207 L1208 T1209 D1218 F1219 I1220 N1221 T1222 D1223 Y1224 K1225 W1226 E1227 E1228



• Molecule 11: NUP205

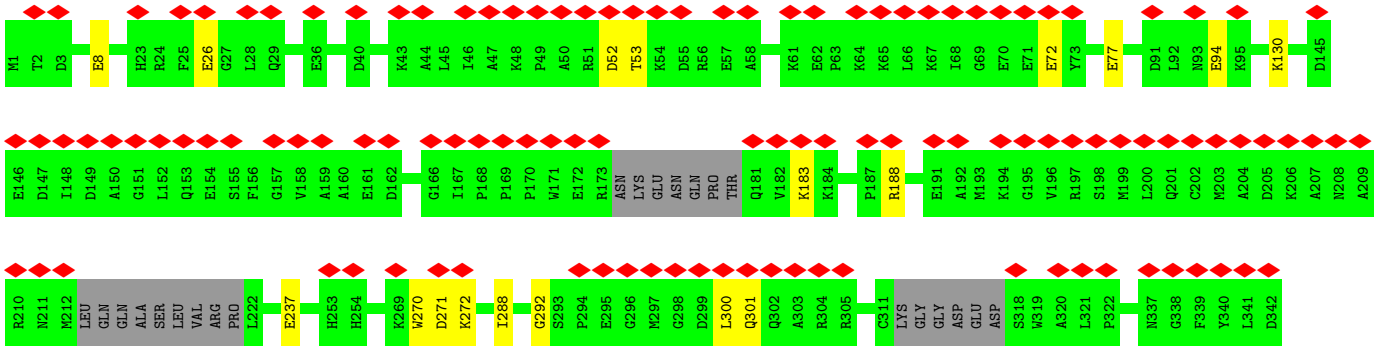
Chain I3:

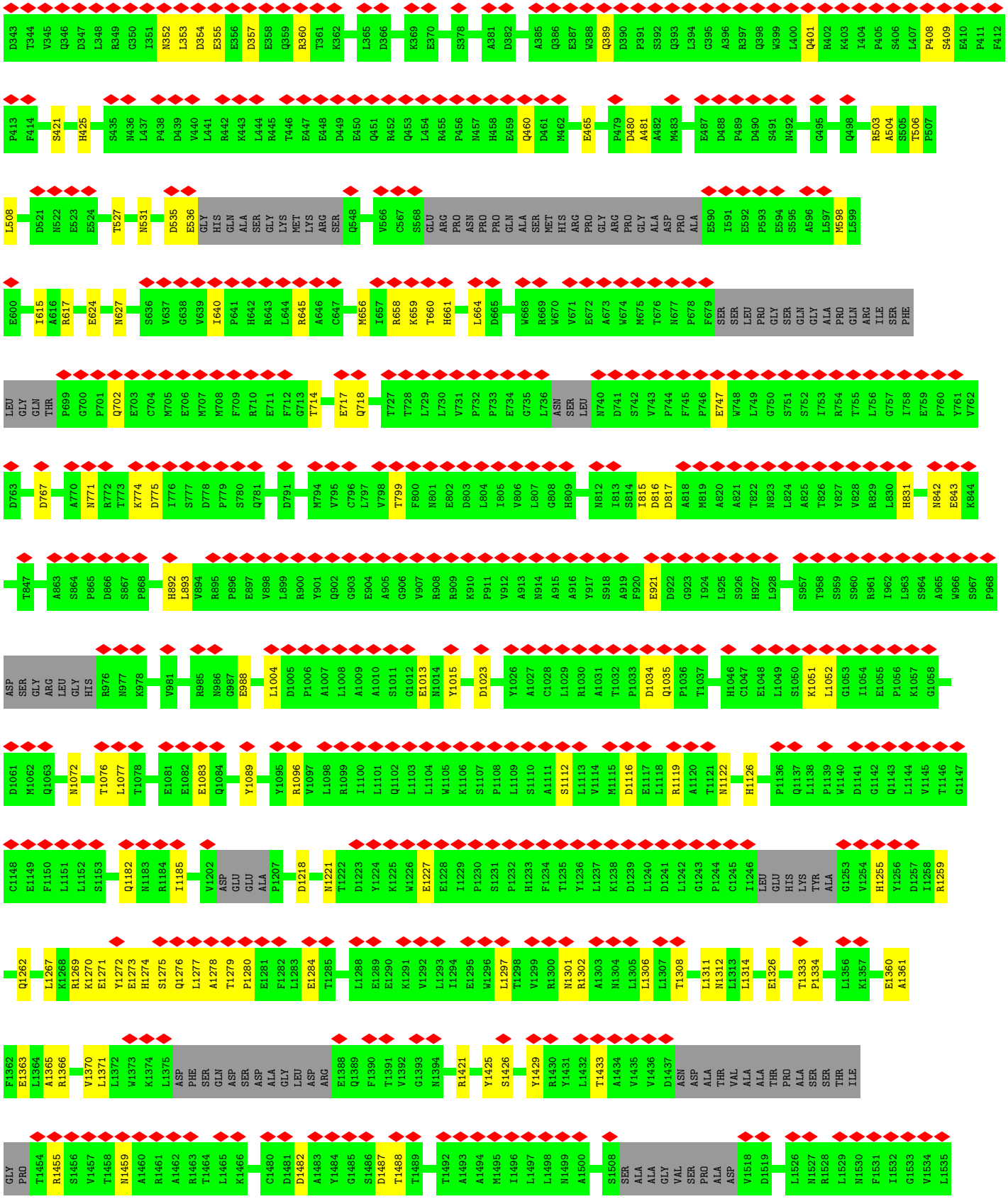




• Molecule 11: NUP205

Chain I4:

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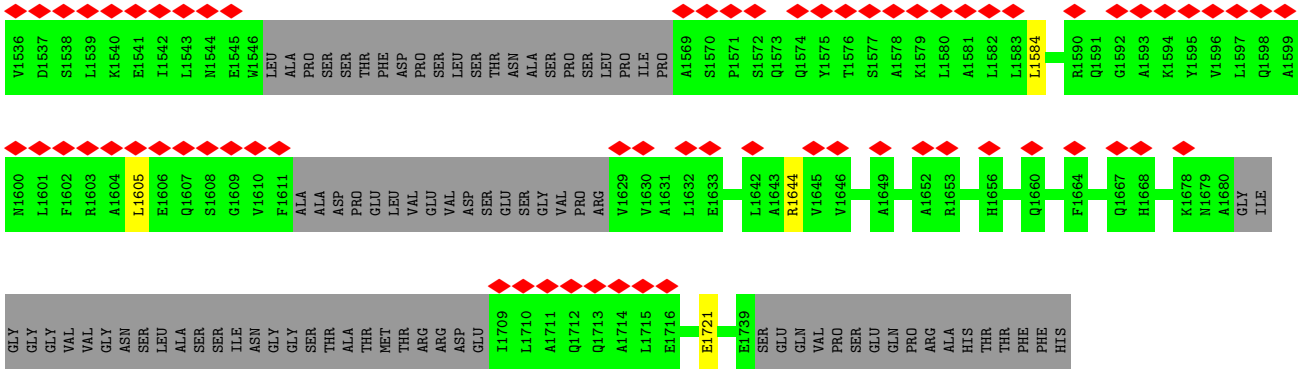
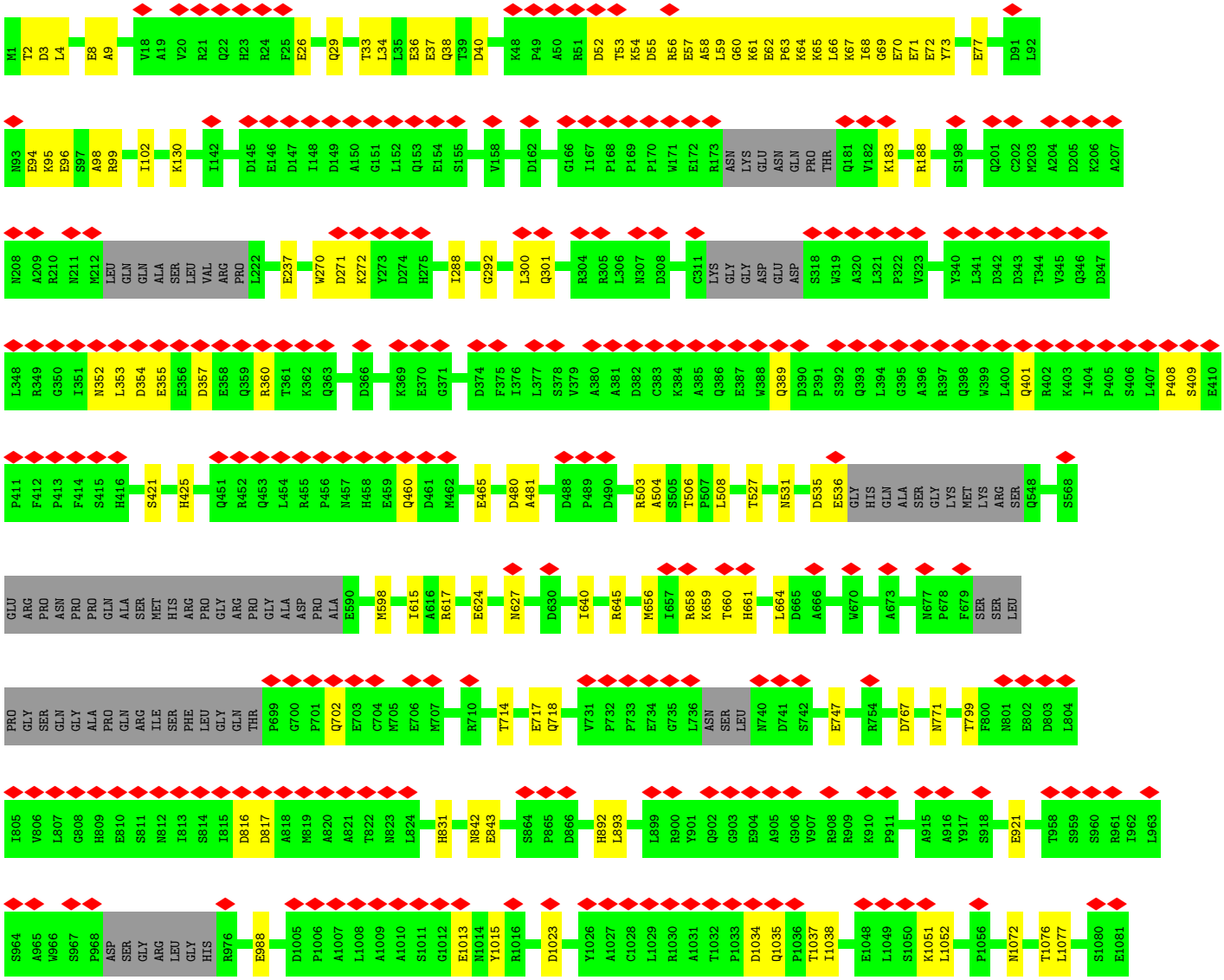
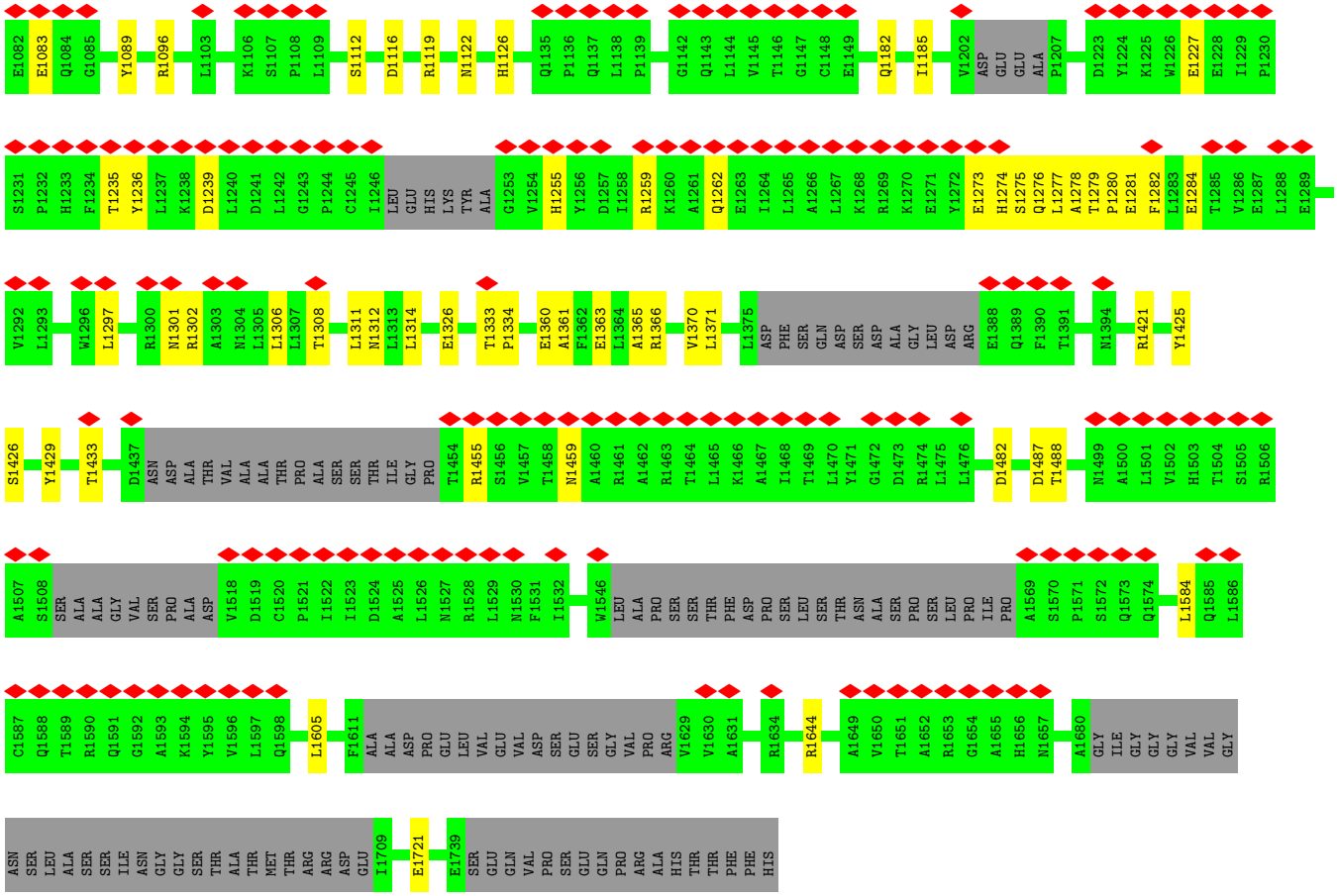
P413 F414 S421 H425 S435 N436 L437 P438 D439 V440 L441 R442 K443 L444 R445 T446 E447 E448 D449 E450 Q451 R452 Q453 L454 R455 P456 N457 H458 E459 Q460 D461 M462 E465 P479 D480 A481 A482 M483 E487 D488 P489 D490 S491 N492 G495 Q498 R503 A504 S505 T506 P507
L508 D521 N522 E523 E524 T527 N531 D535 E536 GLY HIS GLN ALA SER GLY LYS MET LYS ARG SER Q548 V566 C567 S568 GLU ARG PRO ASN PRO PRO GLN ALA ALA SER MET HIS ARG PRO GLY ARG PRO GLY ALA ASP PRO ALA E590 I591 E592 P593 E594 S595 A596 L597 M598 L599
E600 I615 A616 R617 E624 N627 S636 V637 G638 V639 I640 P641 H642 R643 L644 R645 A646 C647 M656 I657 R658 K659 T660 H661 L664 D665 W668 R669 W670 V671 E672 A673 W674 M675 T676 N677 P678 F679 SER SER LEU PRO GLY SER GLN GLY ALA PRO GLN ARG ILE SER PHE
LEU GLY GLN THR P699 G700 P701 Q702 E703 C704 M705 E706 M707 M708 F709 R710 E711 F712 G713 T714 E717 Q718 T727 T728 L729 L730 V731 P732 P733 E734 G735 L736 ASN SER LEU N740 D741 S742 V743 P744 F745 P746 E747 W748 L749 G750 S751 S752 I753 R754 T755 L756 G757 I758 E759 P760 Y761 V762
D763 D767 A770 N771 R772 T773 K774 D775 I776 S777 D778 P779 S780 Q781 D791 M794 V795 C796 L797 V798 T799 F800 N801 E802 D803 L804 I805 V806 L807 G808 H809 N812 I813 S814 I815 D816 D817 A818 M819 A820 A821 T822 N823 L824 A825 T826 Y827 V828 R829 L830 H831 N842 E843 K844
T847 A863 S864 P865 D866 S867 P868 H892 L893 V894 R895 P896 E897 V898 L899 R900 Y901 Q902 G903 E904 A905 G906 V907 R908 R909 K910 P911 V912 A913 N914 A915 A916 Y917 S918 A919 F920 E921 D922 G923 I924 L925 S926 H927 L928 S957 T958 S959 S960 R961 I962 L963 S964 A965 W966 S967 P968
ASP SER GLY ARG LEU GLY HIS R976 N977 K978 V981 R985 N986 G987 E988 L1004 D1005 P1006 A1007 L1008 A1009 A1010 S1011 G1012 E1013 N1014 Y1015 D1023 Y1026 A1027 C1028 L1029 R1030 A1031 T1032 P1033 D1034 Q1035 P1036 T1037 H1046 C1047 E1048 L1049 S1050 K1051 L1052 G1053 I1054 E1055 P1056 K1057 G1058
D1061 M1062 Q1063 N1072 T1076 L1077 T1078 E1081 E1082 E1083 Q1084 Y1089 Y1095 R1096 V1097 L1098 R1099 I1100 L1101 Q1102 L1103 L1104 W1105 K1106 S1107 P1108 L1109 S1110 A1111 S1112 L1113 V1114 M1115 D1116 E1117 L1118 R1119 A1120 T1121 N1122 H1126 P1136 Q1137 L1138 P1139 W1140 D1141 G1142 Q1143 L1144 V1145 T1146 G1147
C1148 E1149 F1150 L1151 L1152 S1153 Q1182 N1183 R1184 I1185 V1202 ASP GLU GLU ALA P1207 D1218 N1221 T1222 D1223 Y1224 K1225 W1226 E1227 E1228 I1229 P1230 S1231 P1232 H1233 F1234 T1235 Y1236 L1237 K1238 D1239 L1240 D1241 L1242 G1243 P1244 C1245 I1246 LEU GLU HIS LYS TYR ALA G1253 V1254 H1255 Y1256 D1257 I1258 R1259
Q1262 L1267 K1268 R1269 K1270 E1271 Y1272 E1273 H1274 S1275 Q1276 L1277 A1278 T1279 P1280 E1281 F1282 L1283 E1284 T1285 L1288 E1289 E1290 K1291 V1292 L1293 I1294 E1295 W1296 L1297 T1298 V1299 R1300 N1301 R1302 A1303 N1304 L1305 L1306 L1307 T1308 L1311 N1312 L1313 L1314 E1326 T1333 P1334 L1356 K1357 E1360 A1361
F1362 E1363 L1364 A1365 R1366 V1370 L1371 L1372 W1373 K1374 L1375 ASP PHE SER GLN ASP SER ASP ALA GLY LEU ASP ARG E1388 Q1389 F1390 T1391 V1392 G1393 N1394 R1421 Y1425 S1426 Y1429 R1430 Y1431 L1432 T1433 A1434 V1435 V1436 D1437 ASN ASP ALA THR VAL ALA ALA THR PRO ALA SER SER THR ILE
GLY PRO T1454 R1455 S1456 V1457 T1458 N1459 A1460 R1461 A1462 R1463 T1464 L1465 K1466 C1480 D1481 D1482 A1483 Y1484 G1485 S1486 D1487 T1488 T1489 T1492 A1493 A1494 M1495 I1496 L1497 L1498 N1499 A1500 S1508 SER ALA ALA GLY VAL SER PRO ALA ASP V1518 D1519 L1526 N1527 R1528 L1529 N1530 F1531 I1532 G1533 V1534 L1535



• Molecule 11: NUP205

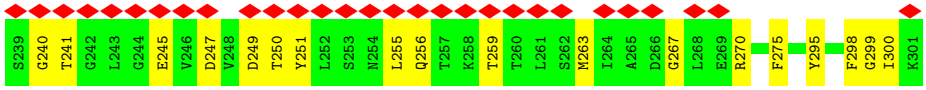
Chain I5:





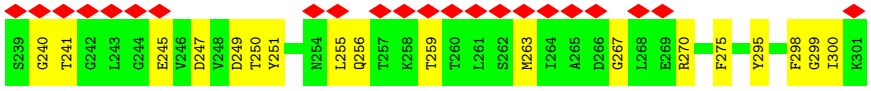
- Molecule 12: NUP93 R2

Chain J1:



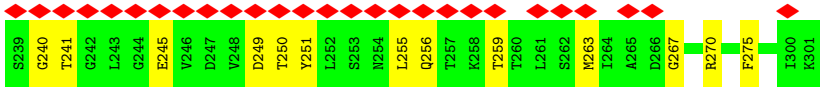
- Molecule 12: NUP93 R2

Chain J2:



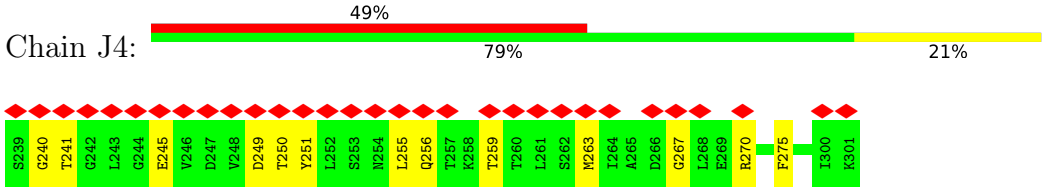
- Molecule 12: NUP93 R2

Chain J3:



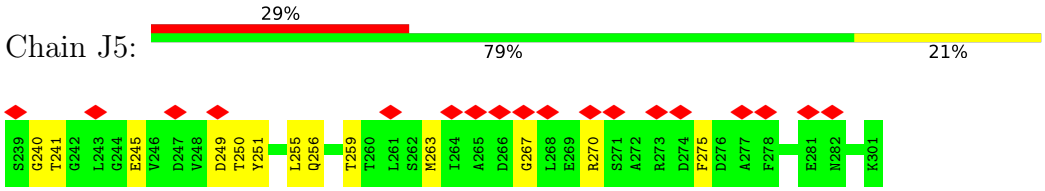
- Molecule 12: NUP93 R2

Chain J4:



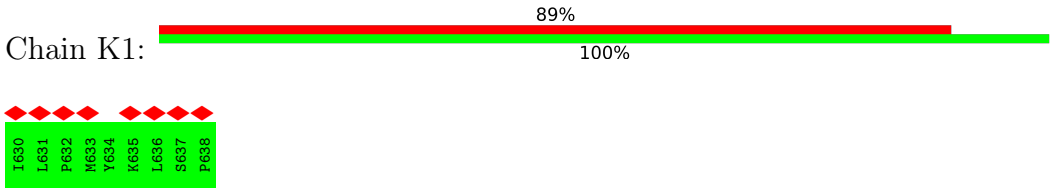
• Molecule 12: NUP93 R2

Chain J5:



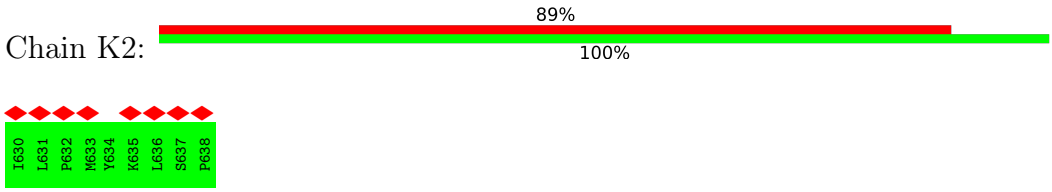
• Molecule 13: NUP98 R1

Chain K1:



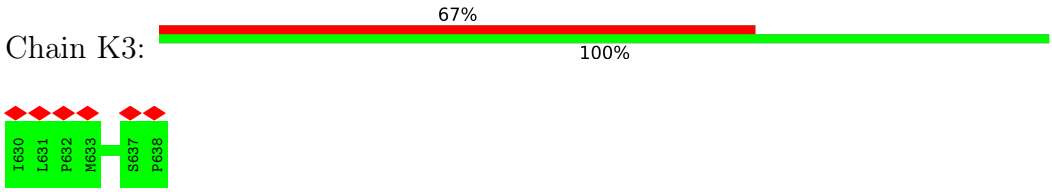
• Molecule 13: NUP98 R1

Chain K2:



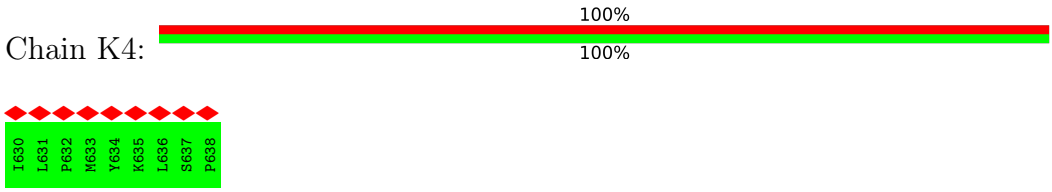
• Molecule 13: NUP98 R1

Chain K3:



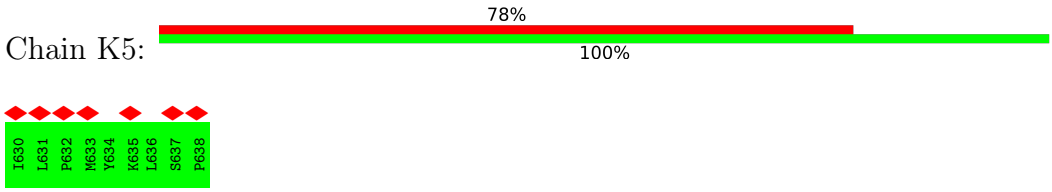
• Molecule 13: NUP98 R1

Chain K4:



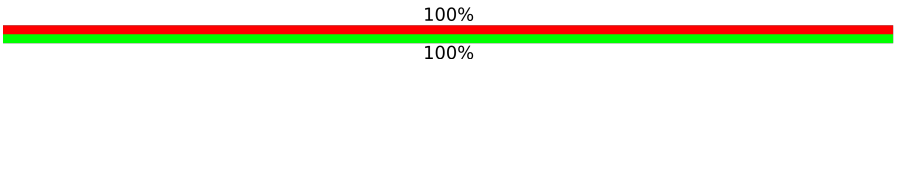
• Molecule 13: NUP98 R1

Chain K5:



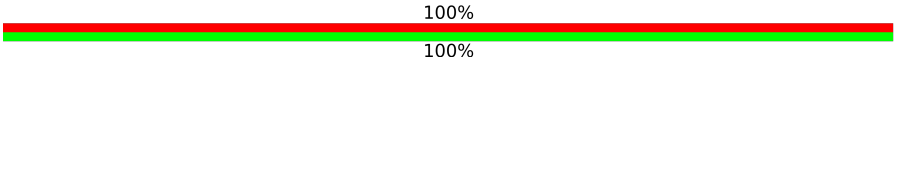
• Molecule 14: NUP53 R1

Chain L1:



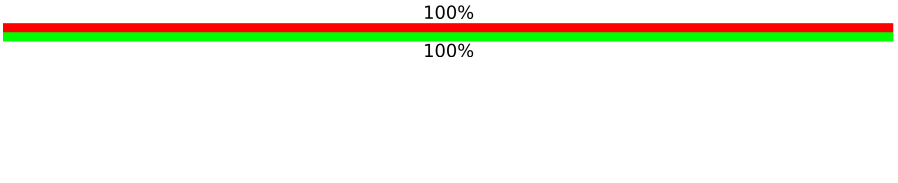
• Molecule 14: NUP53 R1

Chain L2:



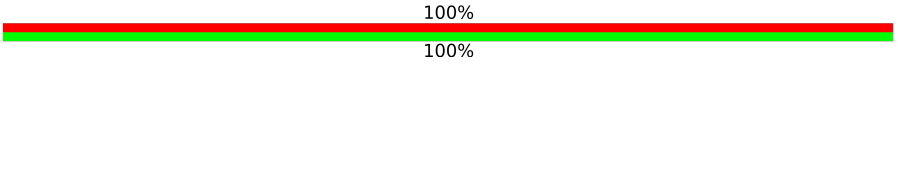
• Molecule 14: NUP53 R1

Chain L3:



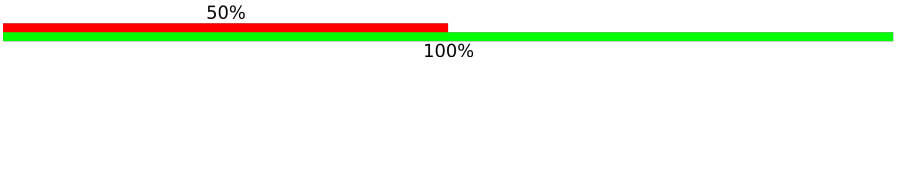
• Molecule 14: NUP53 R1

Chain L4:



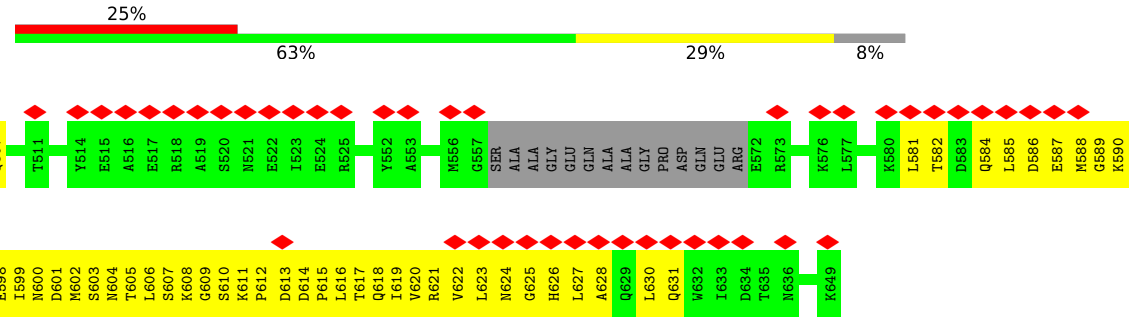
• Molecule 14: NUP53 R1

Chain L5:



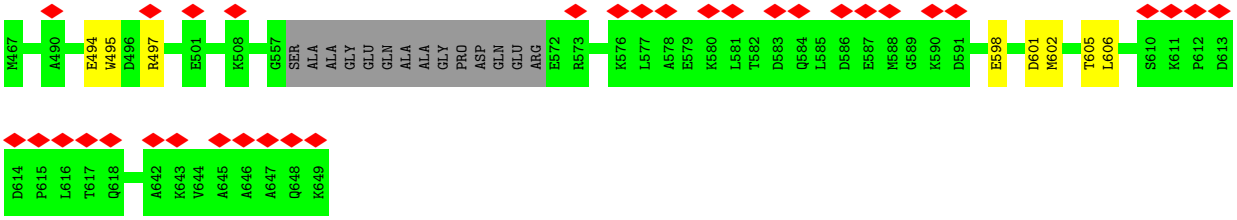
• Molecule 15: NUP62

Chain M1:



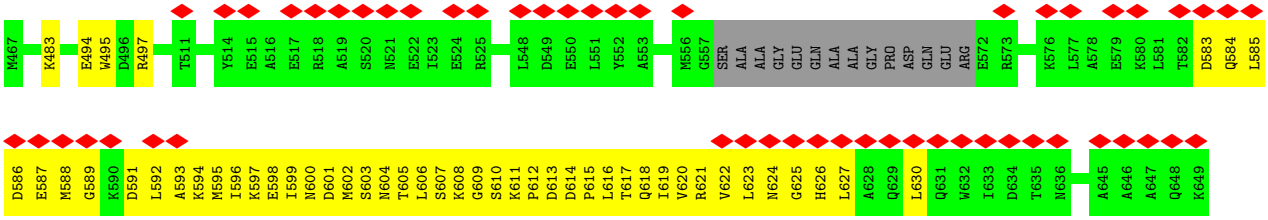
• Molecule 15: NUP62

Chain M2:



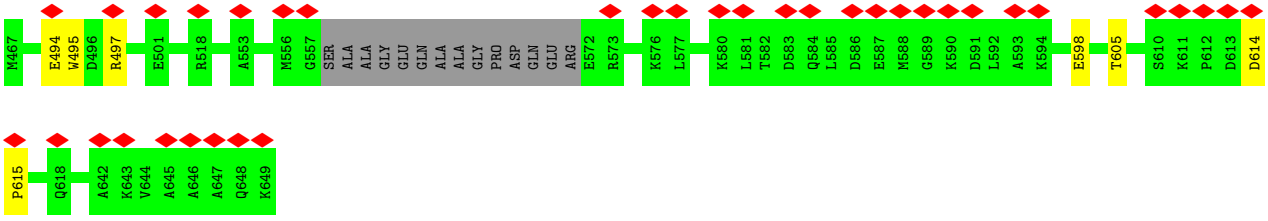
• Molecule 15: NUP62

Chain M3:



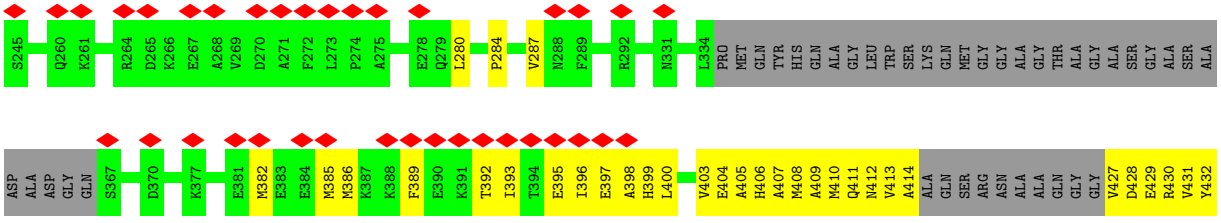
• Molecule 15: NUP62

Chain M4:



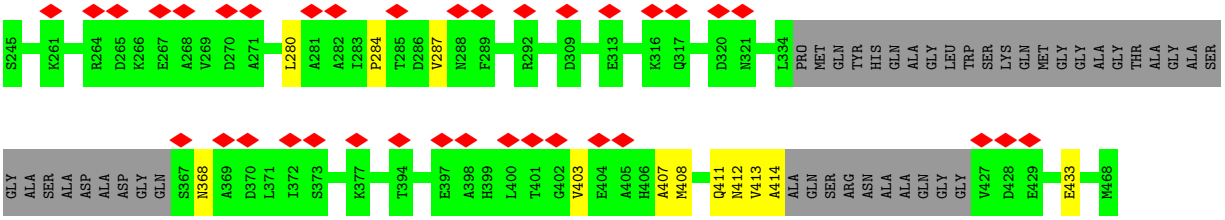
• Molecule 16: NUP58

Chain N1:



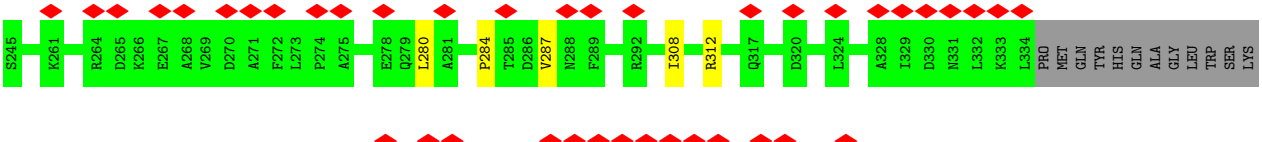
• Molecule 16: NUP58

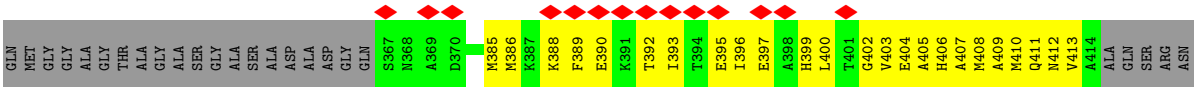
Chain N2:

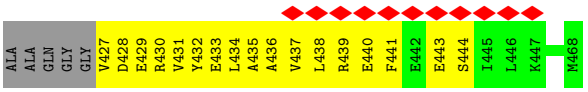


• Molecule 16: NUP58

Chain N3:

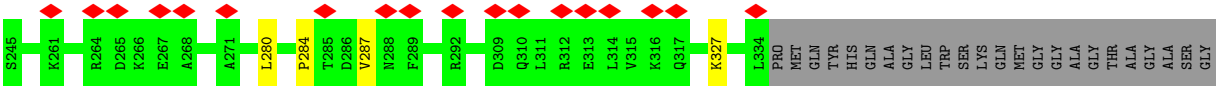


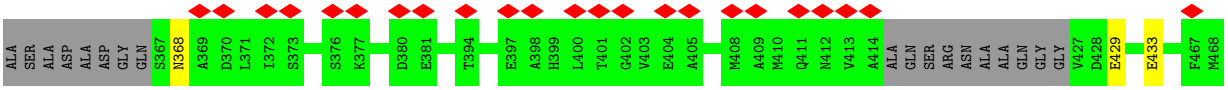




• Molecule 16: NUP58

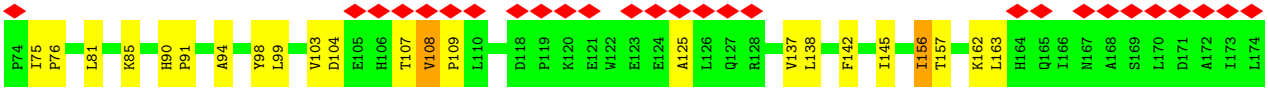
Chain N4:

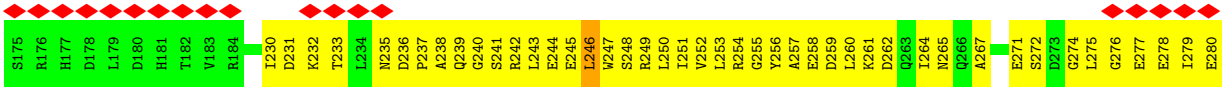


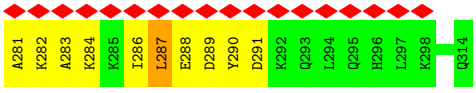


• Molecule 17: NUP54

Chain O1:

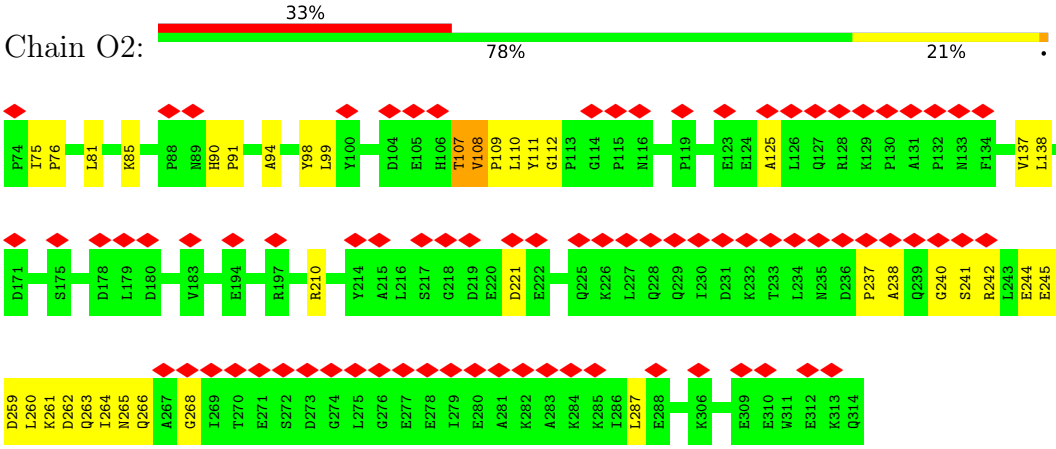






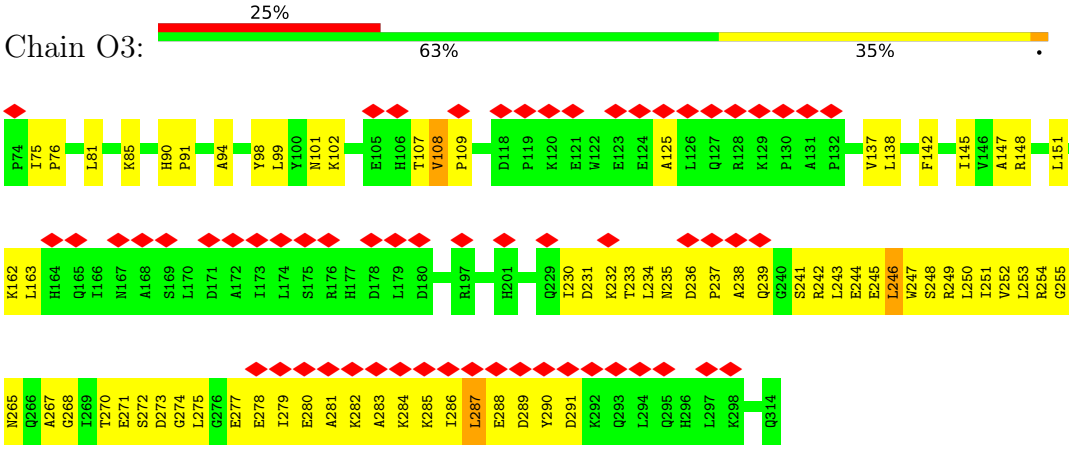
• Molecule 17: NUP54

Chain O2:



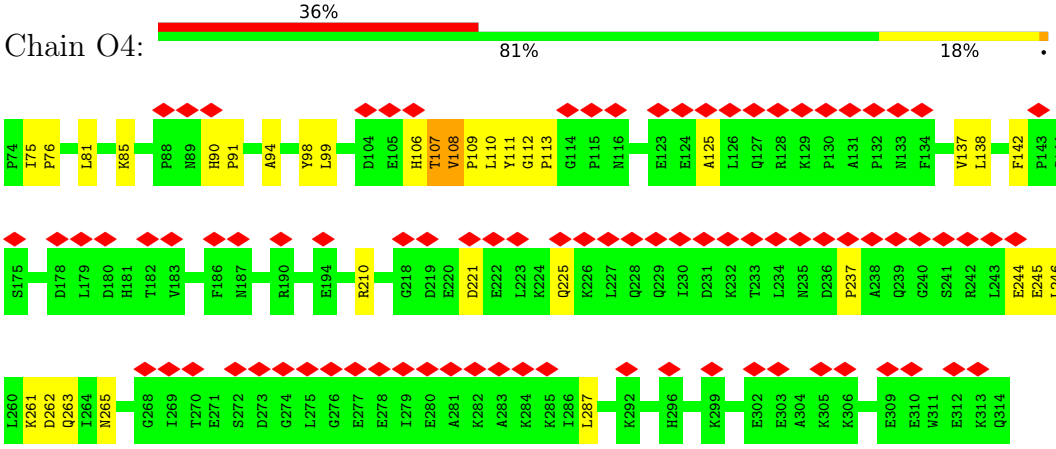
• Molecule 17: NUP54

Chain O3:



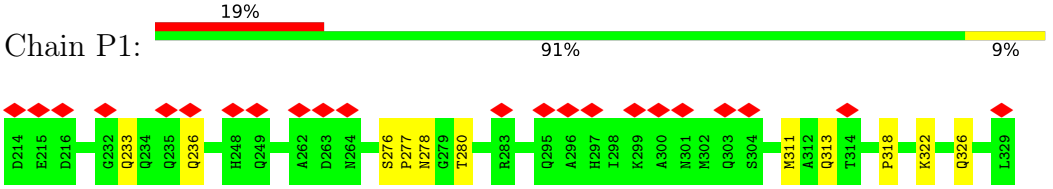
• Molecule 17: NUP54

Chain O4:



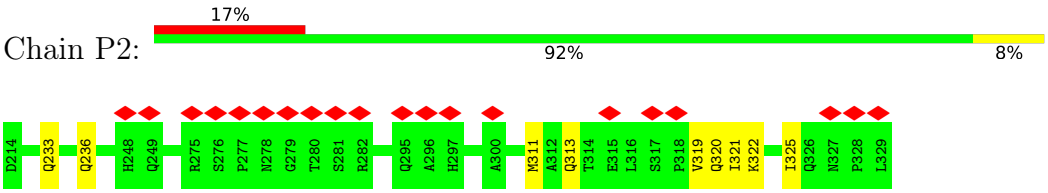
• Molecule 18: NUP54 Ferrodoxin-like domain

Chain P1:



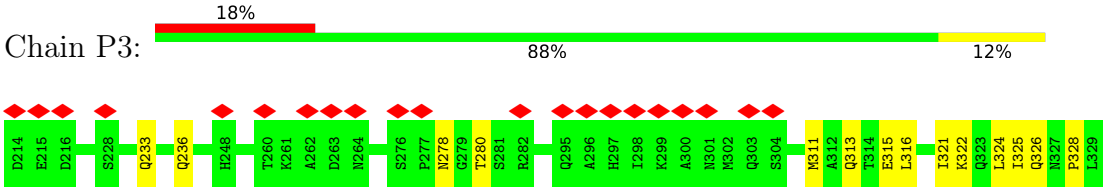
• Molecule 18: NUP54 Ferrodoxin-like domain

Chain P2:



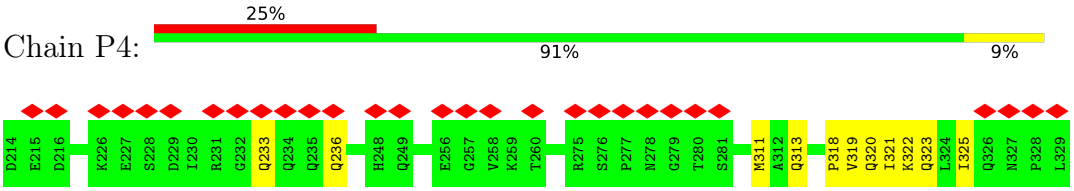
• Molecule 18: NUP54 Ferrodoxin-like domain

Chain P3:



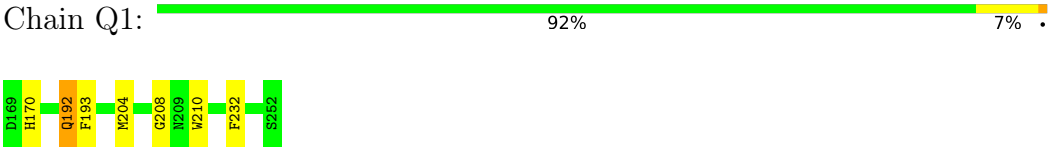
• Molecule 18: NUP54 Ferrodoxin-like domain

Chain P4:



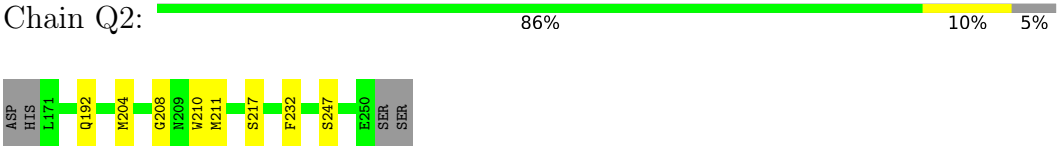
• Molecule 19: NUP53 RRM

Chain Q1:



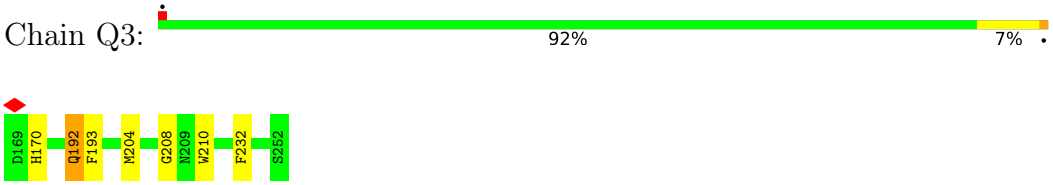
• Molecule 19: NUP53 RRM

Chain Q2:



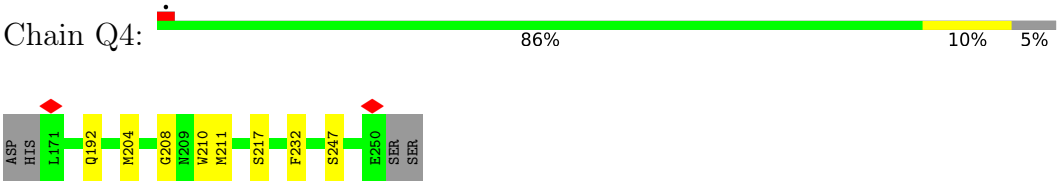
• Molecule 19: NUP53 RRM

Chain Q3:



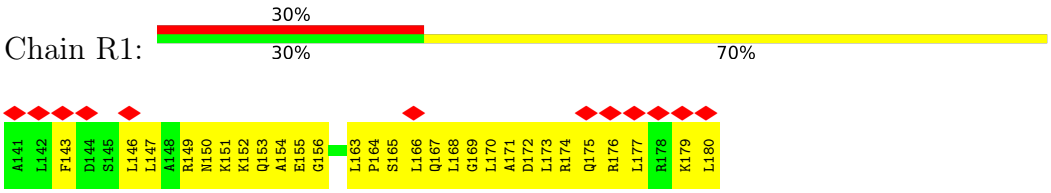
• Molecule 19: NUP53 RRM

Chain Q4:



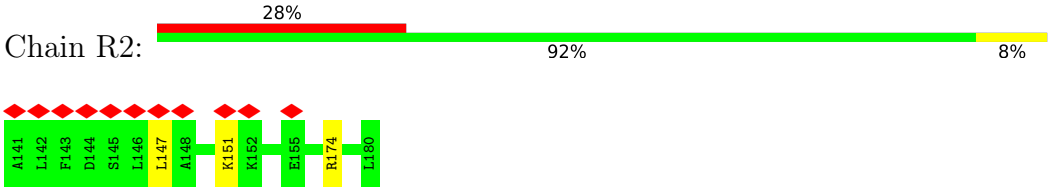
• Molecule 20: NUP93 R1

Chain R1:



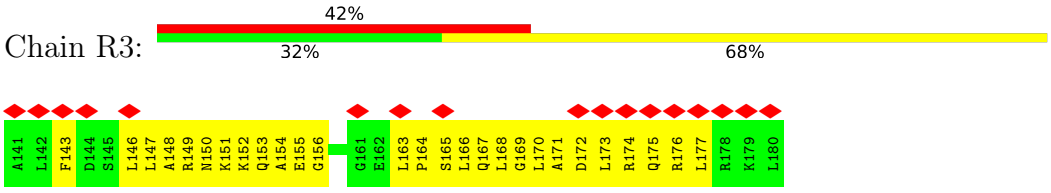
• Molecule 20: NUP93 R1

Chain R2:



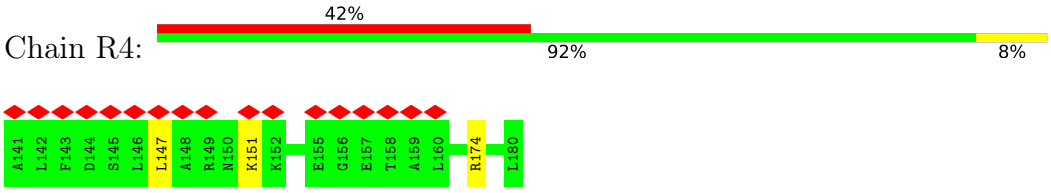
• Molecule 20: NUP93 R1

Chain R3:



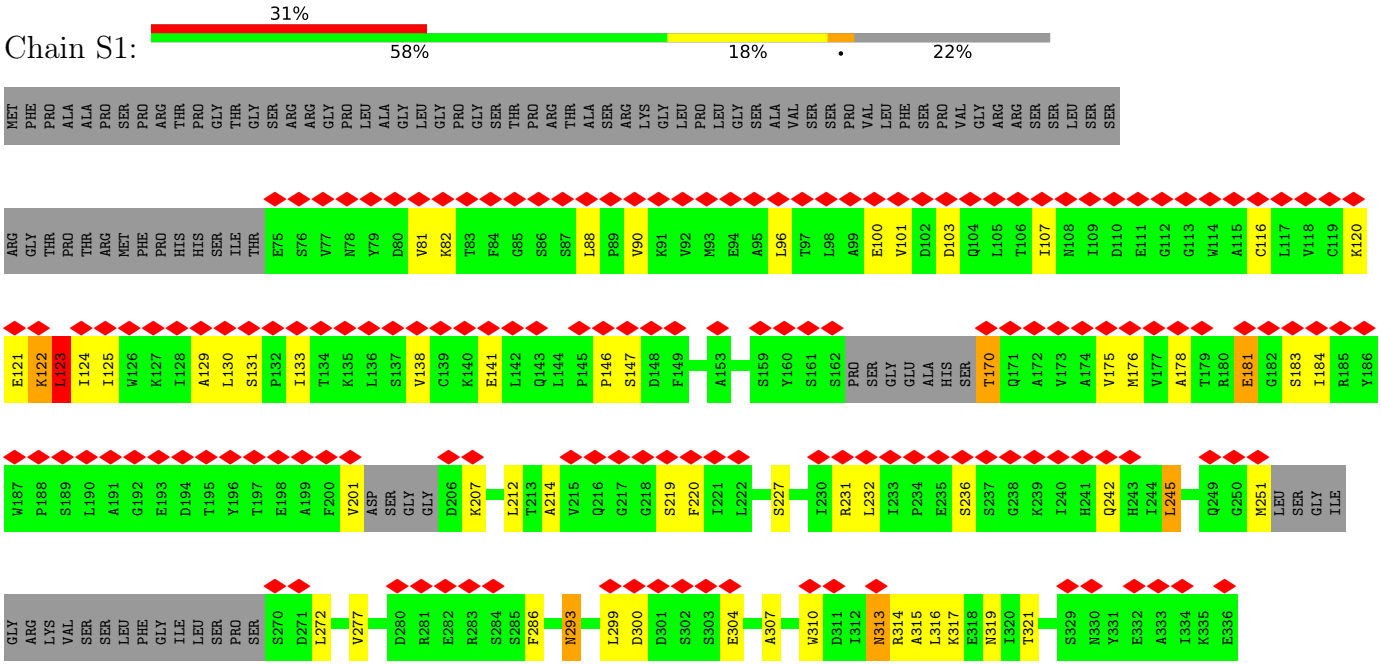
• Molecule 20: NUP93 R1

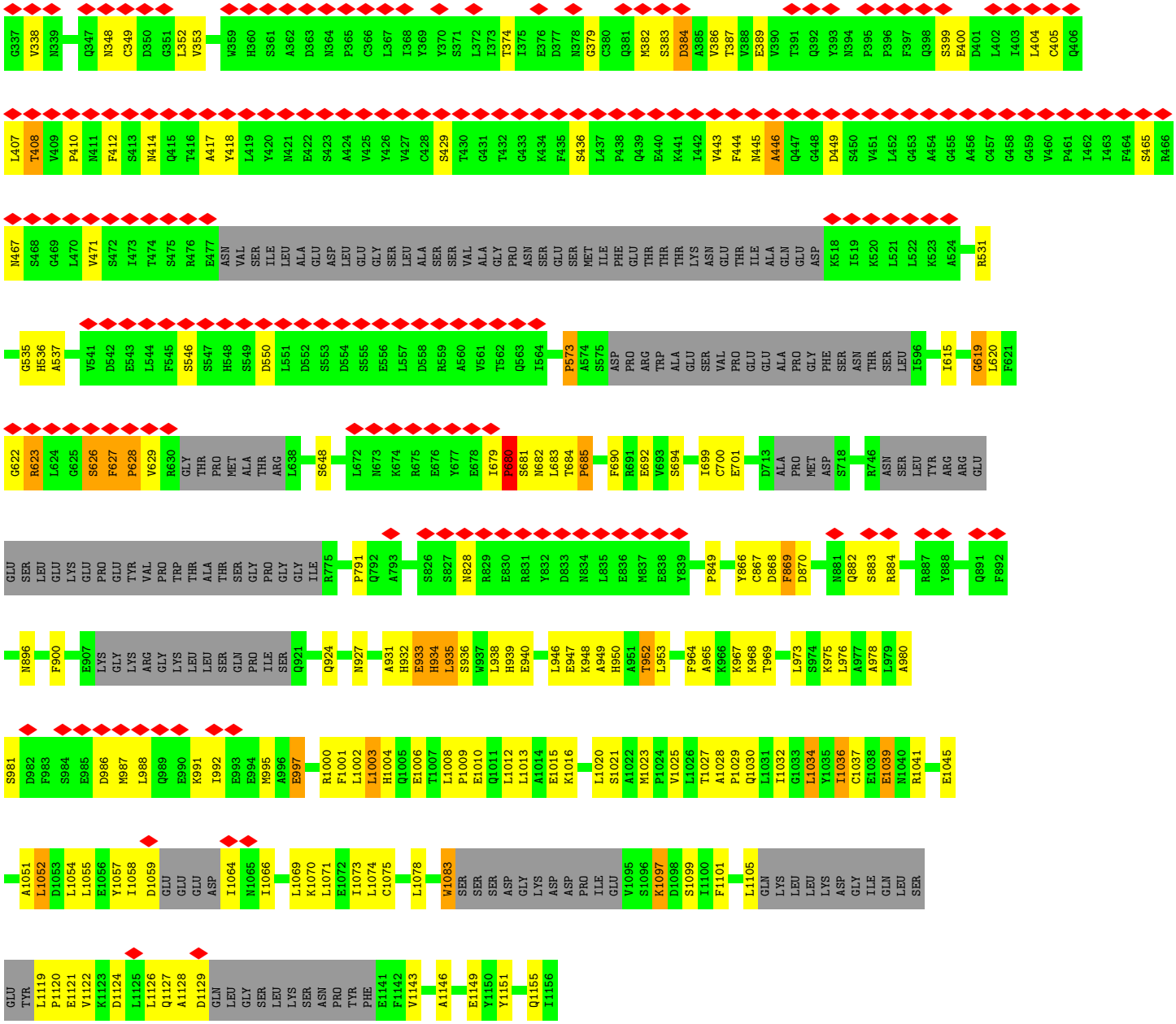
Chain R4:



• Molecule 21: NUP133

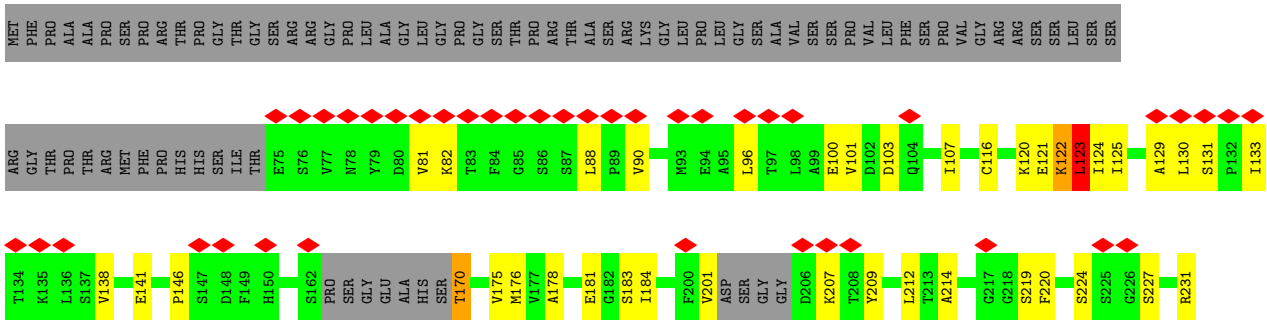
Chain S1:

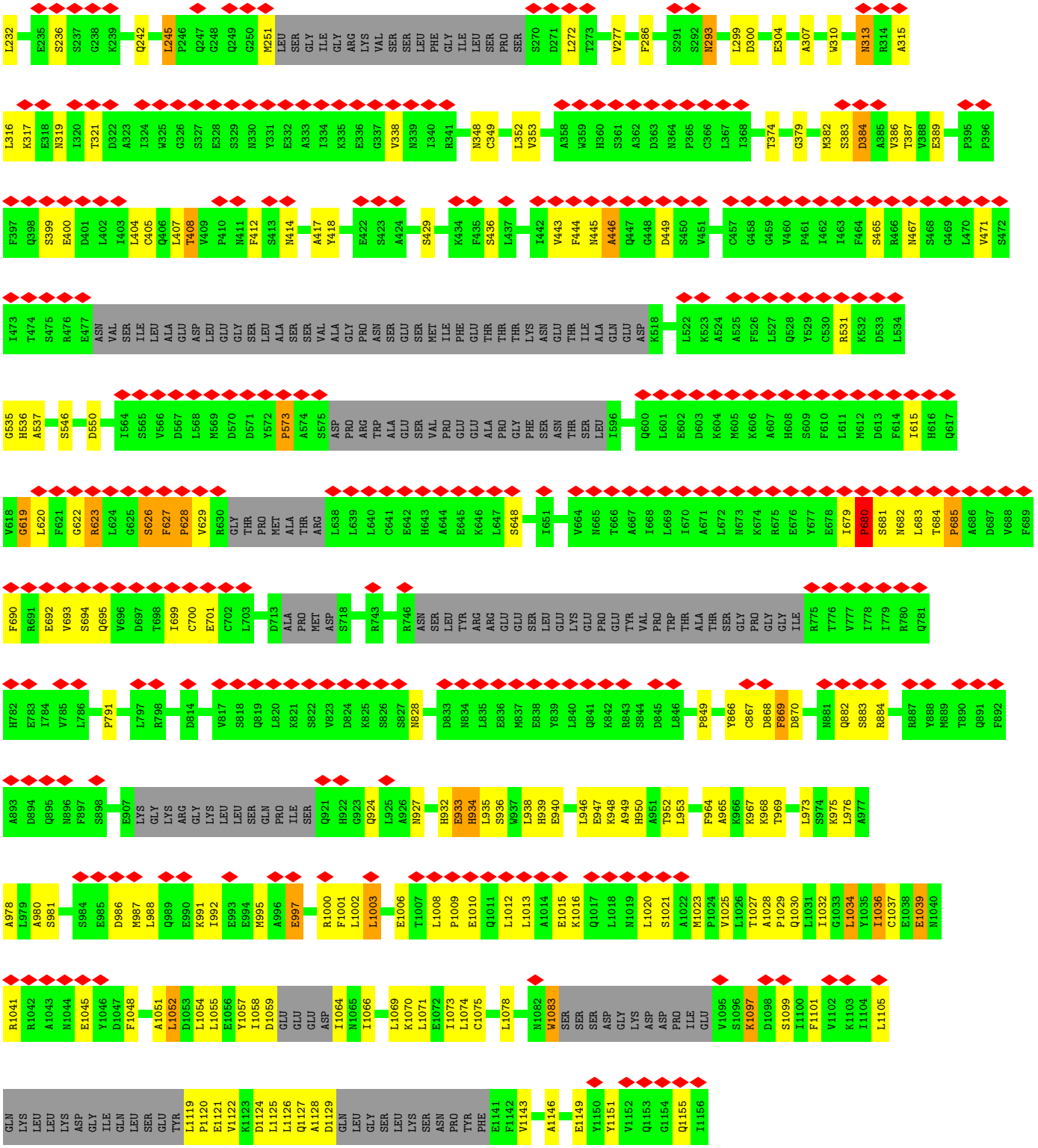




• Molecule 21: NUP133

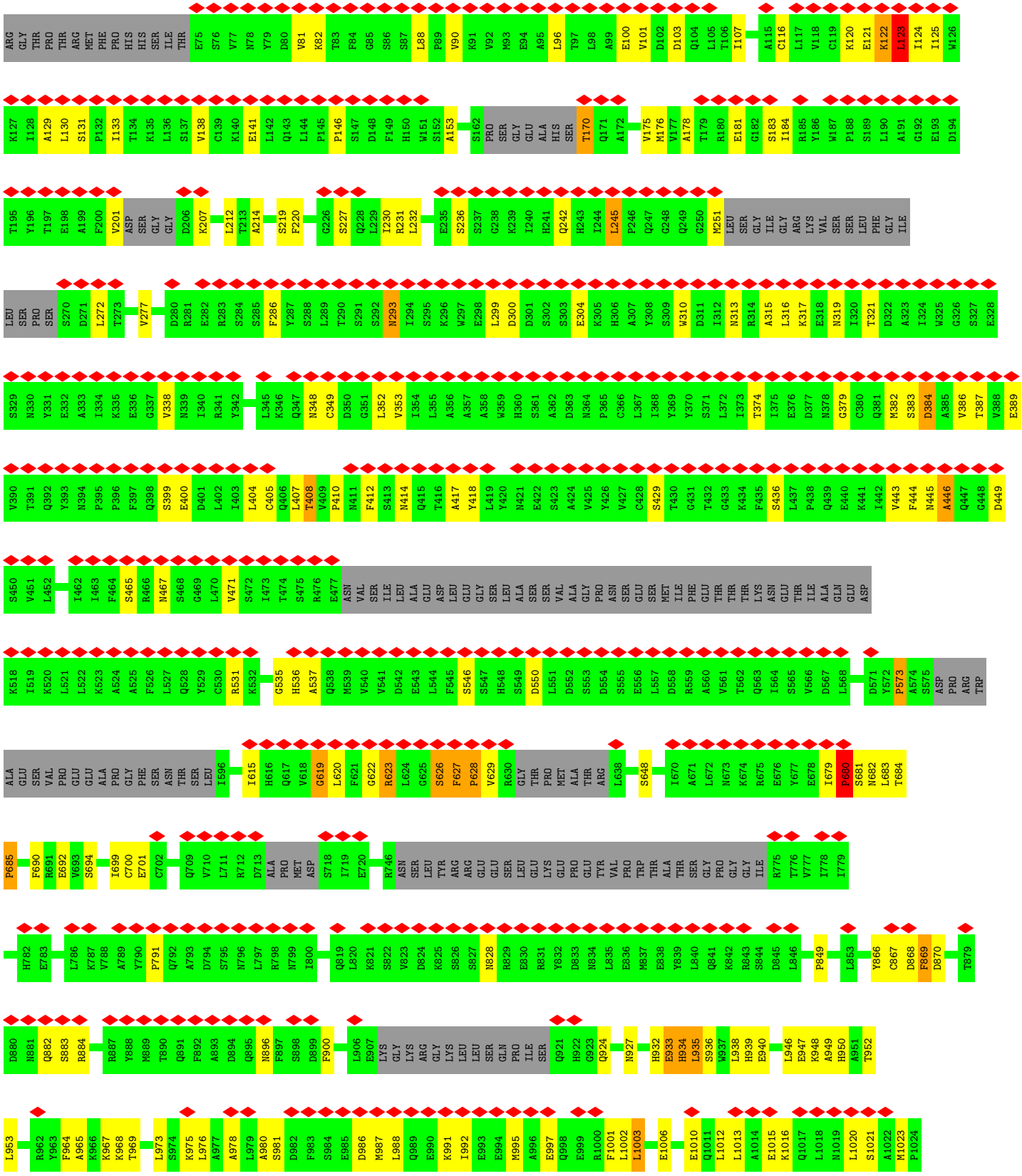
Chain S2:

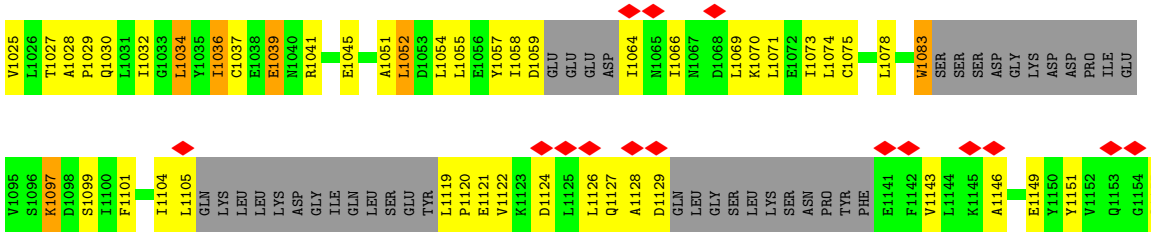




• Molecule 21: NUP133

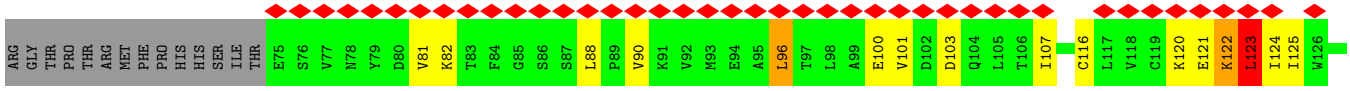
Chain S3:

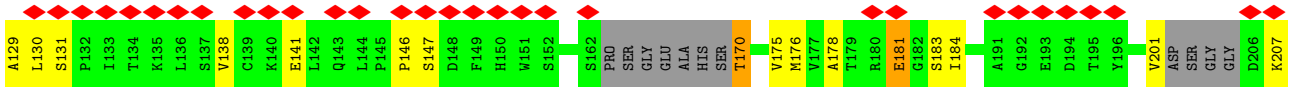

ARG GLY THR PRO THR ARG MET PHE PRO HIS HIS SER ILE THR E75 S76 V77 N78 Y79 D80 V81 K82 T83 F84 G85 S86 S87 L88 P89 V90 K91 V92 M93 E94 A95 L96 T97 L98 A99 E100 V101 D102 D103 Q104 L105 T106 I107 A115 C116 L117 V118 C119 K120 E121 K122 L123 I124 I125 W126
K127 I128 A129 L130 S131 P132 I133 T134 K135 L136 S137 V138 C139 K140 E141 L142 Q143 L144 P145 P146 S147 D148 F149 H150 W151 S152 A153 S162 PRO SER GLY GLU ALA HIS SER T170 Q171 A172 V175 M176 V177 A178 T179 R180 E181 G182 S183 I184 R185 Y186 W187 P188 S189 L190 A191 G192 E193 D194
T195 Y196 T197 E198 A199 F200 V201 ASP SER GLY GLY D206 K207 L212 T213 A214 S219 F220 G226 S227 Q228 L229 I230 R231 L232 E235 S236 S237 G238 K239 I240 H241 Q242 H243 I244 L245 P246 Q247 G248 Q249 G250 M251 LEU SER GLY ILE GLY ARG LYS VAL SER SER LEU PHE GLY ILE
LEU SER PRO SER S270 D271 L272 T273 V277 D280 R281 E282 R283 S284 S285 F286 Y287 S288 L289 T290 S291 S292 N293 I294 S295 K296 W297 E298 L299 D300 D301 S302 S303 E304 K305 H306 A307 Y308 S309 W310 D311 I312 N313 R314 A315 L316 K317 E318 N319 I320 T321 D322 A323 I324 W325 G326 S327 E328
S329 N330 Y331 E332 A333 I334 K335 E336 G337 V338 N339 I340 R341 Y342 L345 K346 Q347 N348 C349 D350 G351 L352 V353 I354 L355 A356 A357 A358 W359 H360 S361 A362 D363 N364 P365 C366 L367 I368 Y369 Y370 S371 L372 I373 T374 I375 E376 D377 N378 G379 C380 Q381 M382 S383 D384 A385 V386 T387 V388 E389
V390 T391 Q392 Y393 N394 P395 P396 F397 Q398 S399 E400 D401 L402 I403 L404 C405 Q406 L407 T408 V409 P410 N411 F412 S413 N414 Q415 T416 A417 Y418 L419 Y420 N421 E422 S423 A424 V425 Y426 V427 C428 S429 T430 G431 T432 G433 K434 F435 S436 L437 P438 Q439 E440 K441 I442 V443 F444 N445 A446 Q447 G448 D449
S450 V451 L452 T462 I463 F464 S465 R466 N467 S468 G469 L470 V471 S472 I473 T474 S475 R476 E477 ASN VAL SER ILE LEU ALA GLU ASP LEU GLU GLY SER LEU ALA SER SER VAL ALA GLY PRO ASN SER GLU SER MET ILE PHE GLU THR THR THR LYS ASN GLU THR ILE ALA GLN GLU ASP
K518 I519 K520 L521 L522 K523 A524 A525 F526 L527 Q528 Y529 C530 R531 K532 G535 H536 A537 Q538 M539 V540 V541 D542 E543 L544 P545 S546 S547 H548 S549 D550 L551 D552 S553 D554 S555 E556 L557 D558 R559 A560 V561 T562 Q563 I564 S565 V566 D567 L568 D571 Y572 P573 A574 S575 ASP PRO ARG TRP
ALA GLU SER VAL PRO GLU GLU ALA PRO GLY PHE SER ASN THR SER LEU I596 I615 H616 Q617 V618 G619 L620 F621 G622 R623 L624 G625 S626 F627 P628 V629 R630 GLY THR PRO MET ALA THR ARG L638 S643 I670 A671 L672 N673 K674 R675 E676 Y677 E678 I679 P680 S681 N682 L683 T684
P685 F690 R691 E692 V693 S694 I699 C700 E701 C702 Q709 V710 L711 R712 D713 ALA PRO MET ASP S718 I719 E720 R746 ASN SER LEU TYR ARG ARG GLU GLU SER LEU GLU LYS GLU PRO GLU TYR VAL PRO TRP THR ALA THR SER GLY PRO GLY GLY ILE R775 T776 V777 I778 I779
H782 E783 L786 K787 V788 A789 Y790 P791 Q792 A793 D794 S795 N796 L797 R798 N799 I800 Q819 L820 K821 S822 V823 D824 K825 S826 S827 N828 R829 E830 R831 Y832 D833 N834 L835 E836 M837 E838 Y839 L840 Q841 K842 R843 S844 D845 L846 P849 L853 Y866 C867 D868 F869 D870 T879
D880 N881 Q882 S883 R884 R887 Y888 M889 T890 Q891 F892 A893 D894 Q895 N896 F897 S898 D899 F900 L906 E907 LYS GLY LYS ARG GLY LYS LEU LEU SER GLN PRO ILE SER Q921 H922 G923 Q924 N927 H932 E933 H934 L935 S936 W937 L938 H939 E940 L946 E947 K948 A949 H950 A951 T952
L953 R962 Y963 F964 A965 K966 K967 K968 T969 L973 S974 K975 L976 A977 A978 L979 A980 S981 D982 F983 S984 E985 D986 M987 L988 Q989 E990 K991 I992 E993 E994 W995 A996 E997 Q998 E999 R1000 F1001 L1002 L1003 E1006 E1010 Q1011 L1012 L1013 A1014 E1015 K1016 Q1017 L1018 N1019 L1020 S1021 A1022 M1023 P1024

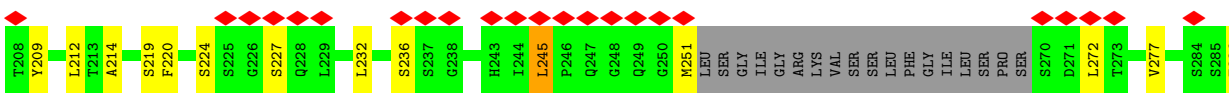


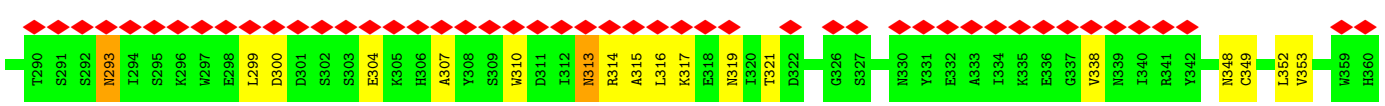
• Molecule 21: NUP133

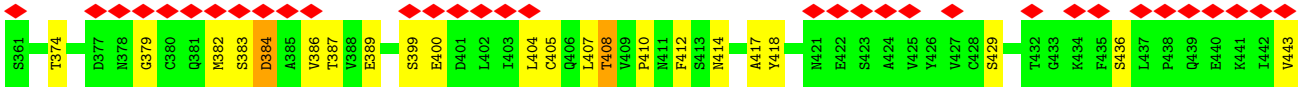
Chain S4:

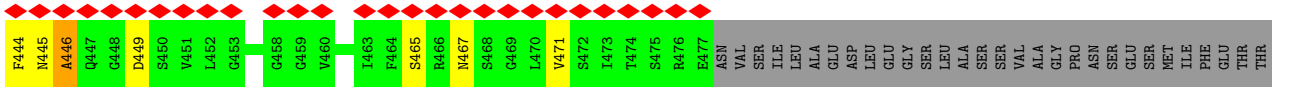


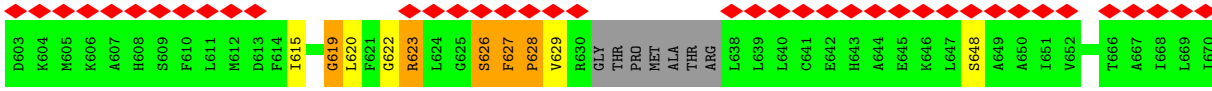


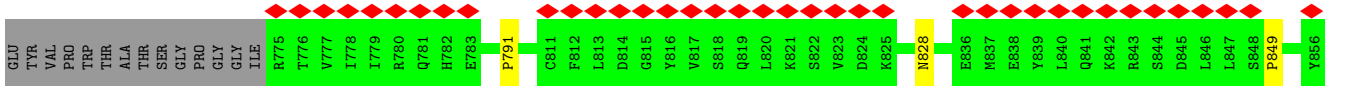


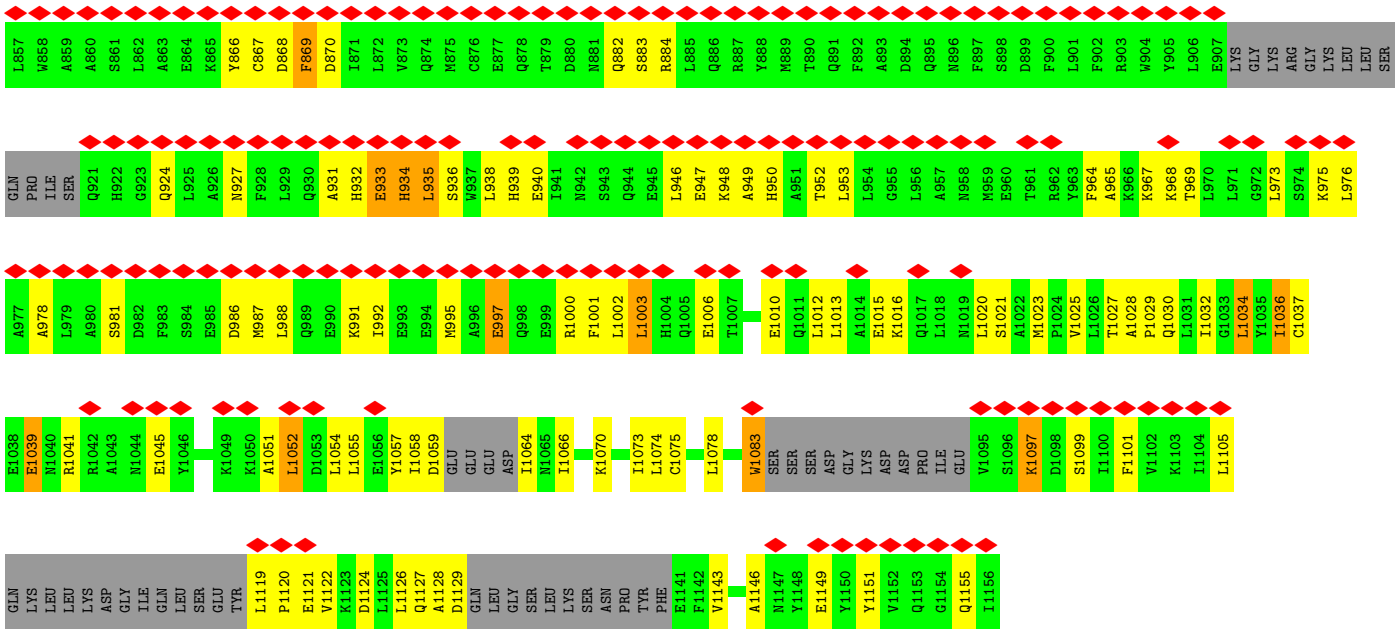






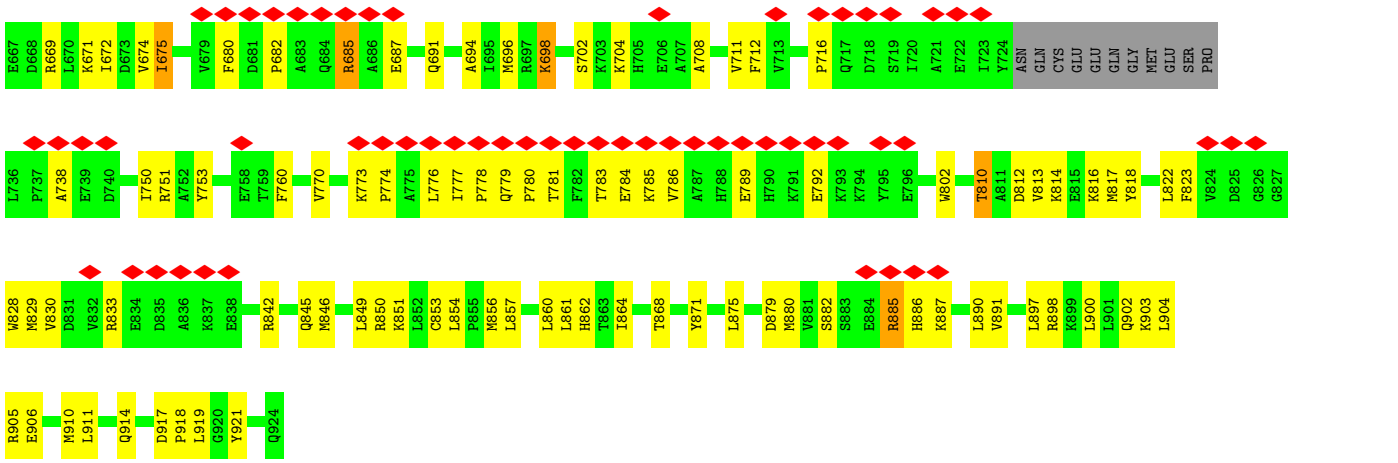






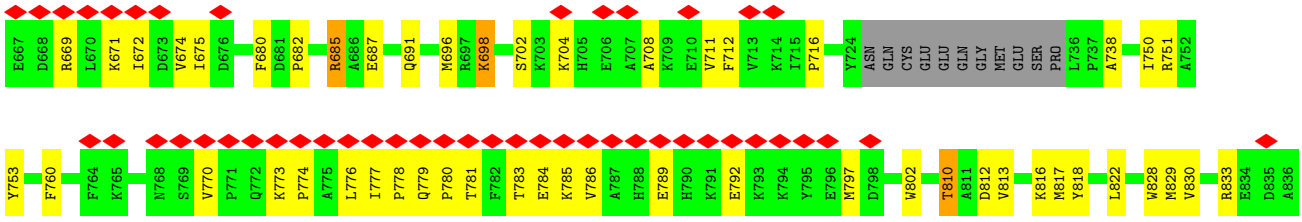
• Molecule 22: NUP107 CTD

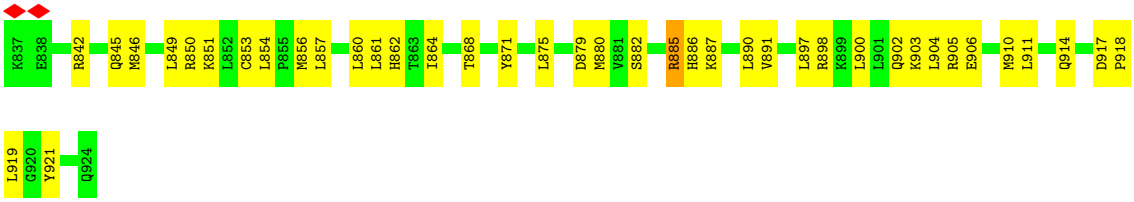
Chain T1:



• Molecule 22: NUP107 CTD

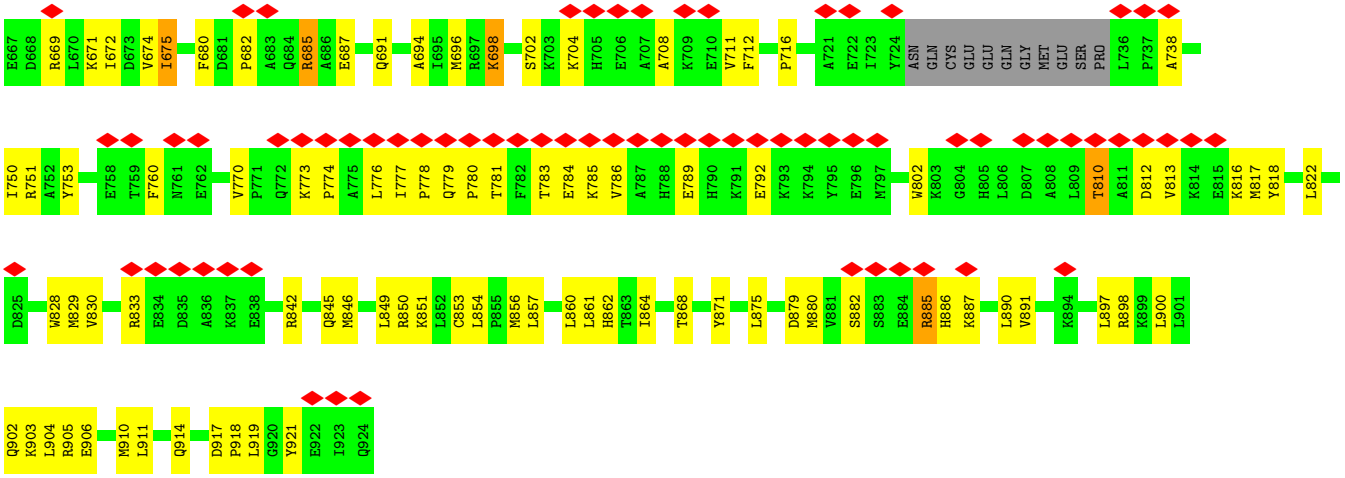
Chain T2:





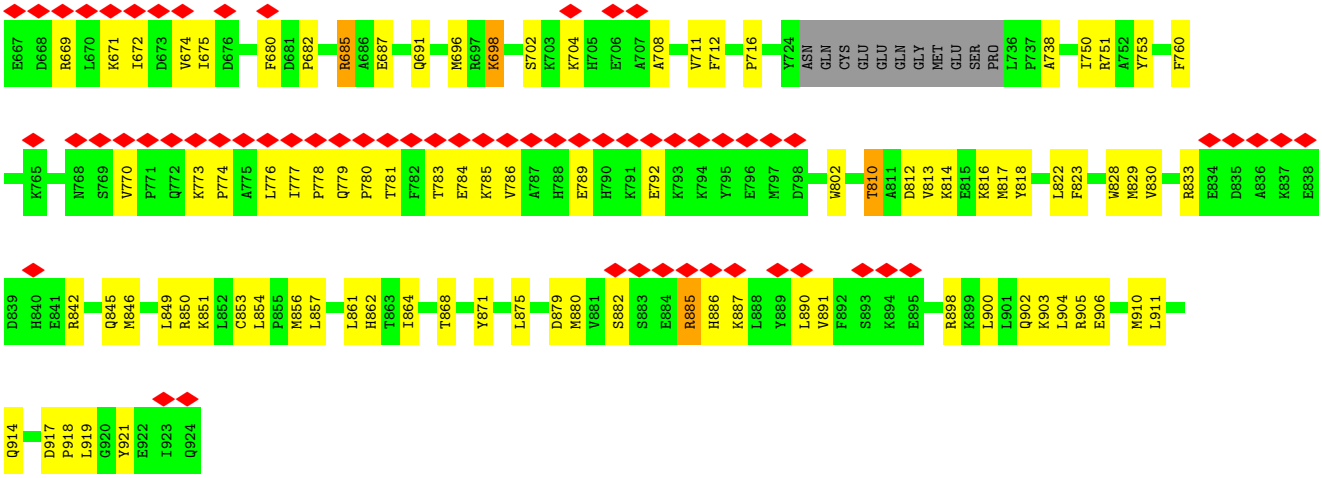
• Molecule 22: NUP107 CTD

Chain T3:



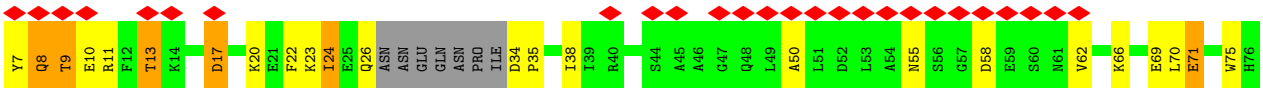
• Molecule 22: NUP107 CTD

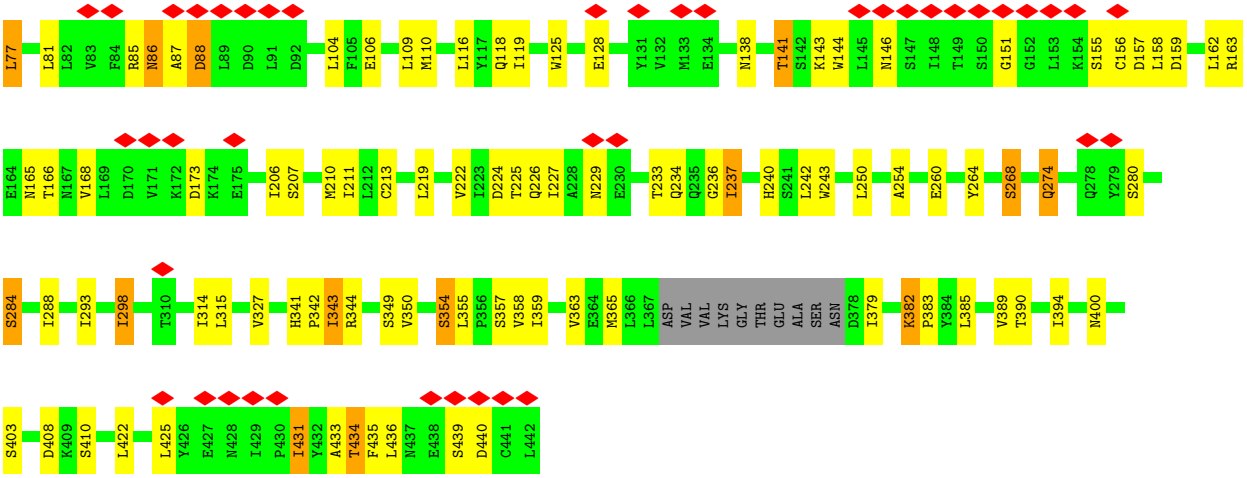
Chain T4:



• Molecule 23: NUP107 NTD

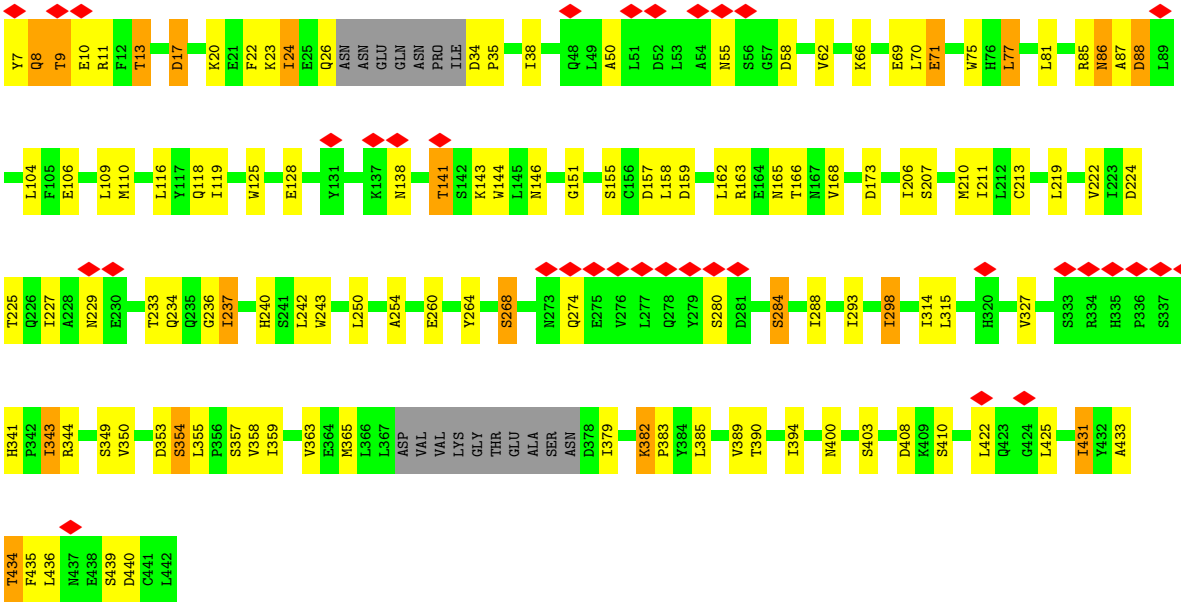
Chain U1:





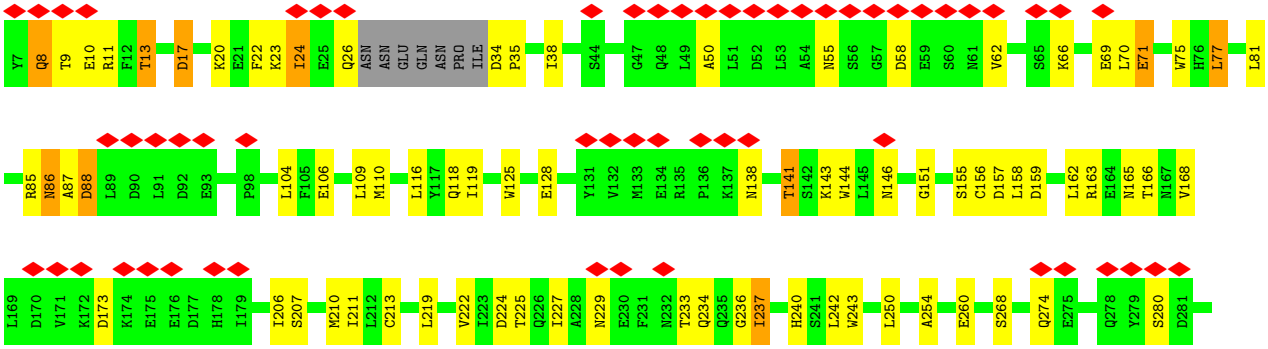
• Molecule 23: NUP107 NTD

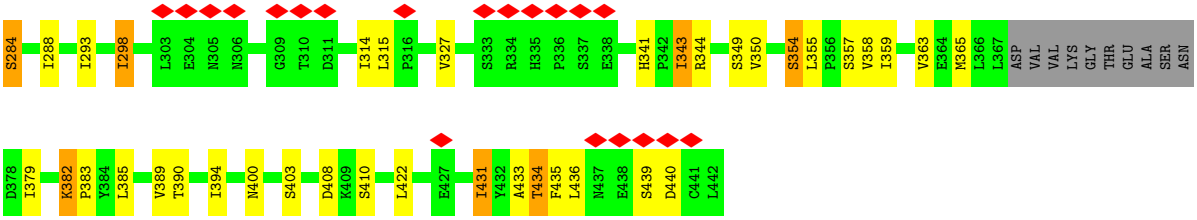
Chain U2:



• Molecule 23: NUP107 NTD

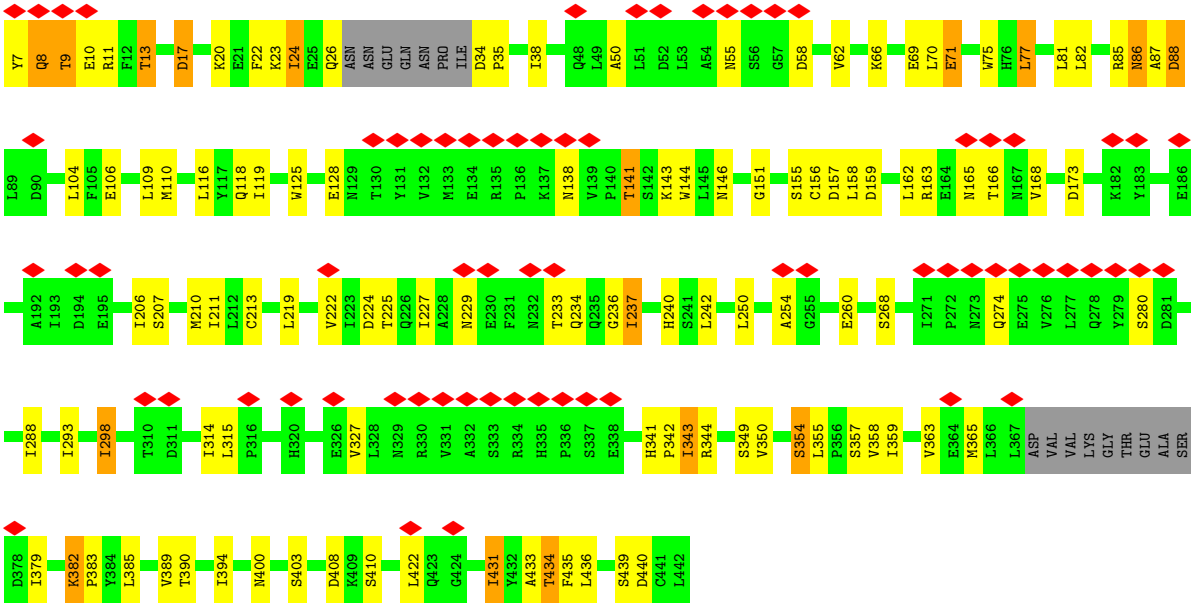
Chain U3:





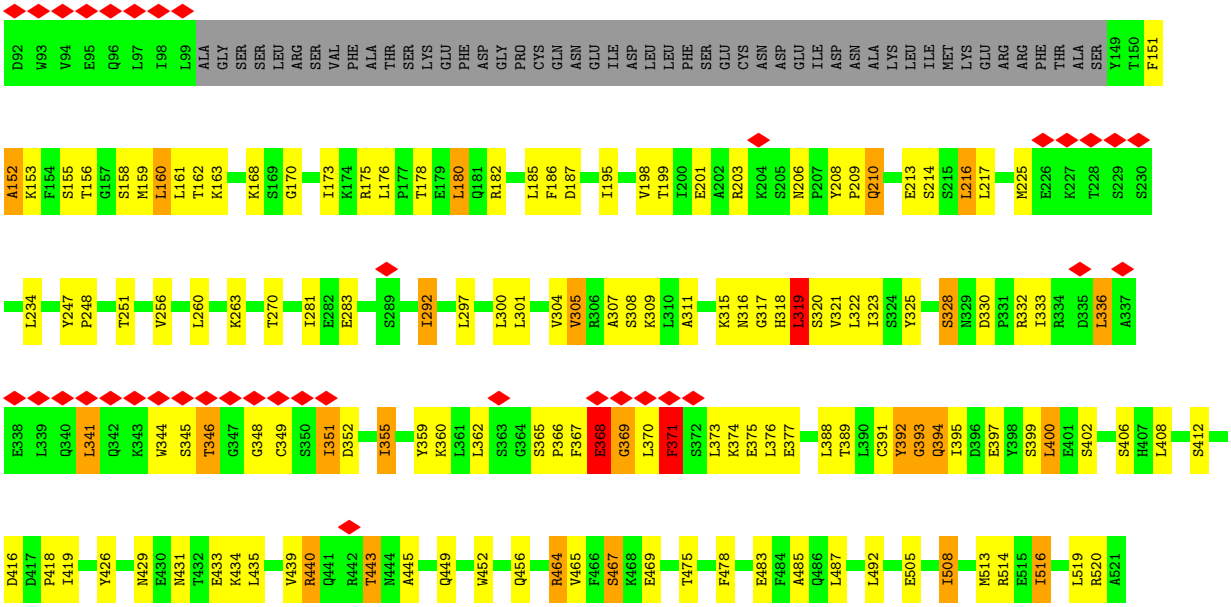
• Molecule 23: NUP107 NTD

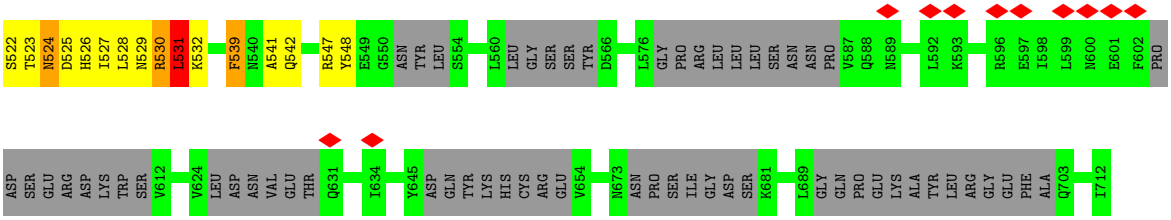
Chain U4:



• Molecule 24: NUP96

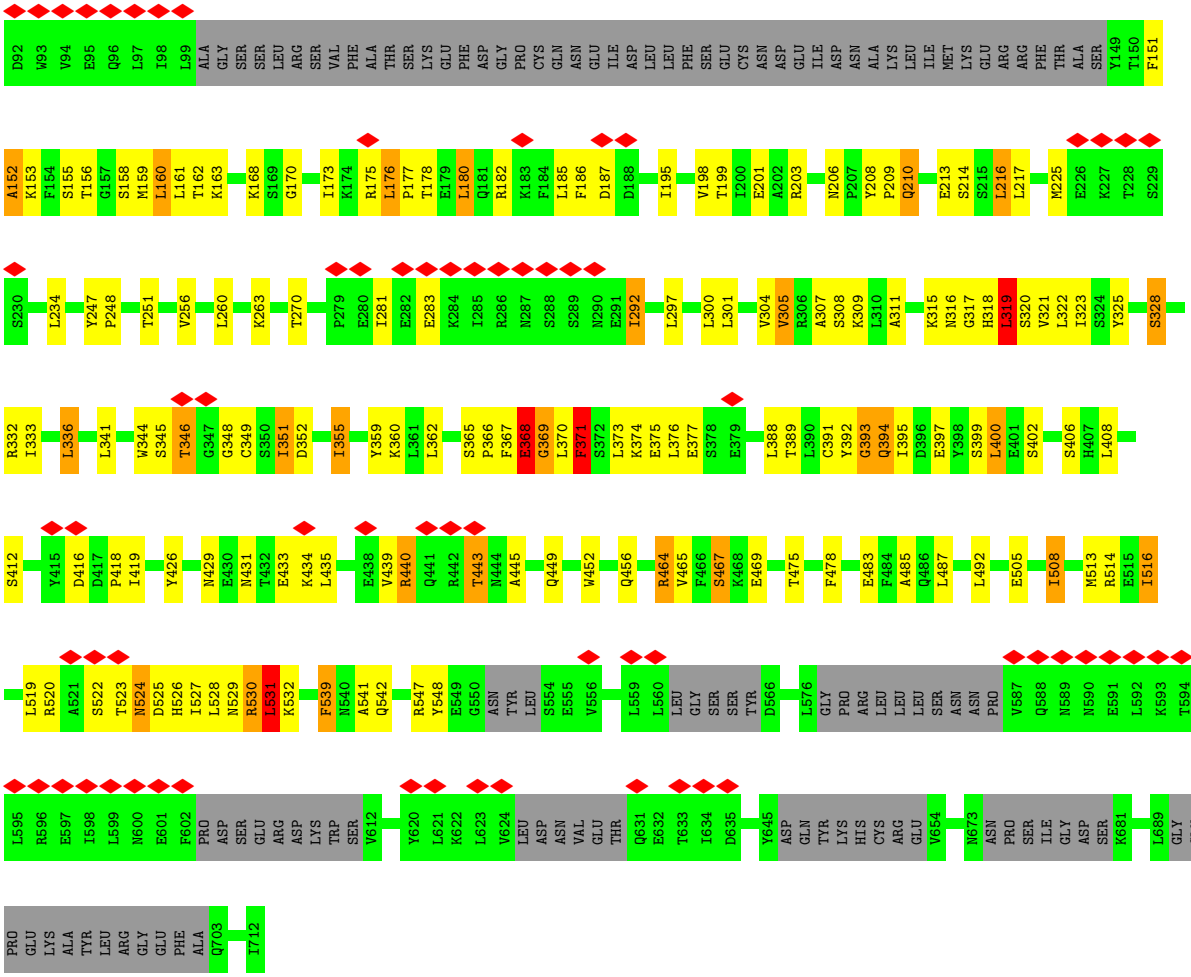
Chain V1:





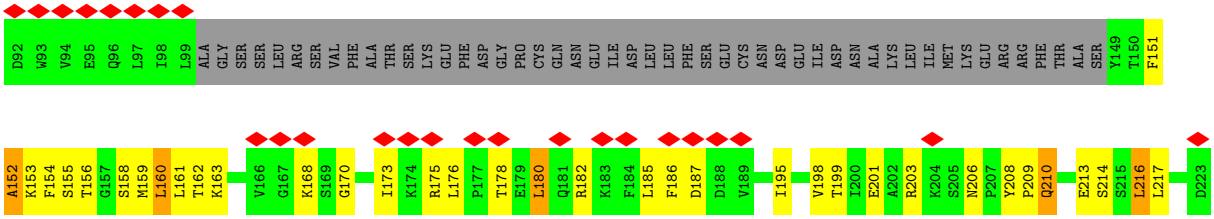
• Molecule 24: NUP96

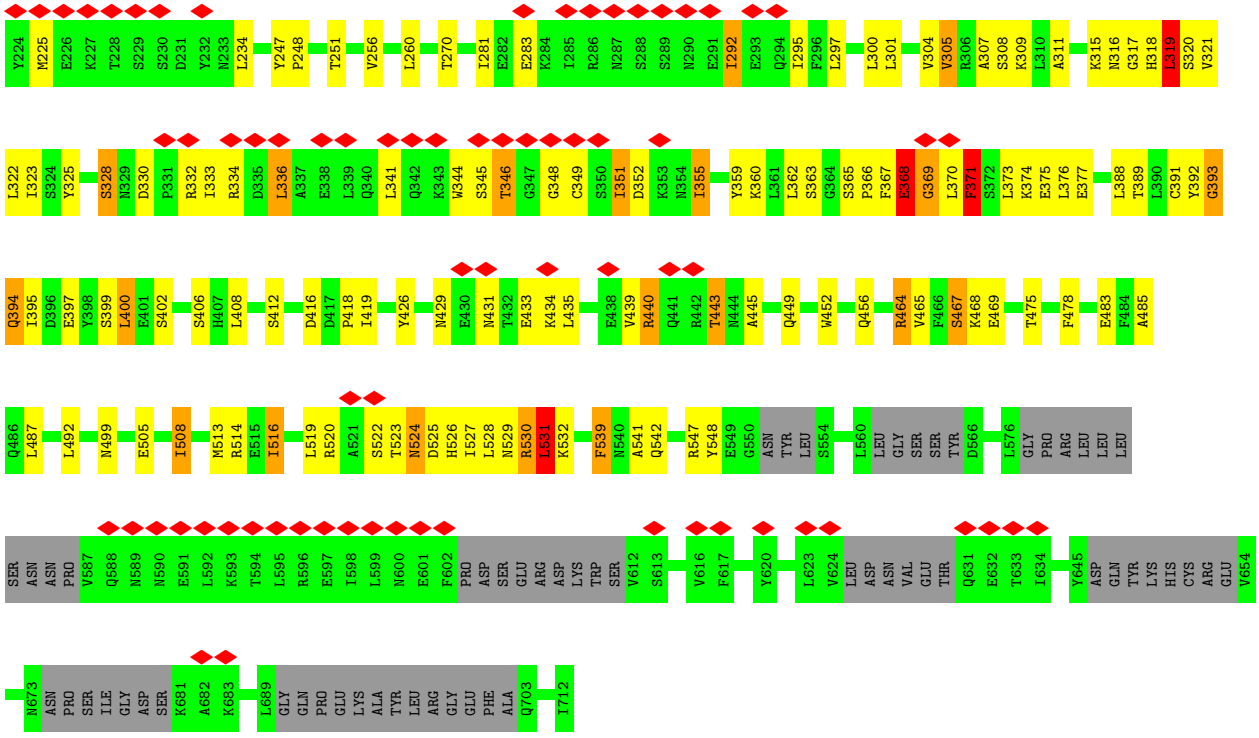
Chain V2:



• Molecule 24: NUP96

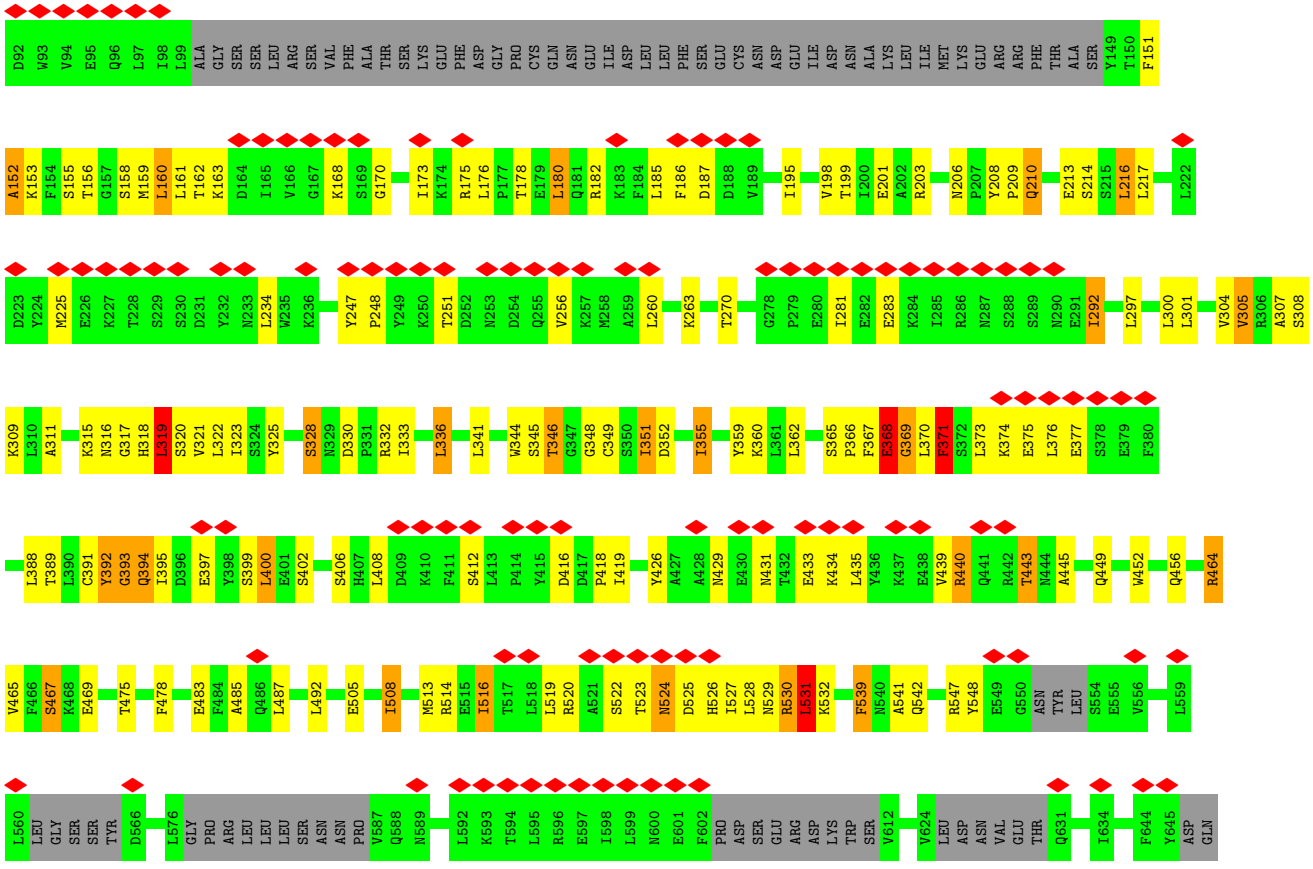
Chain V3:

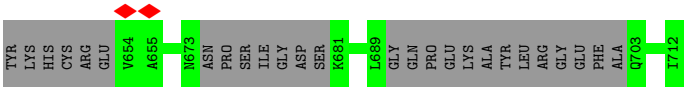




• Molecule 24: NUP96

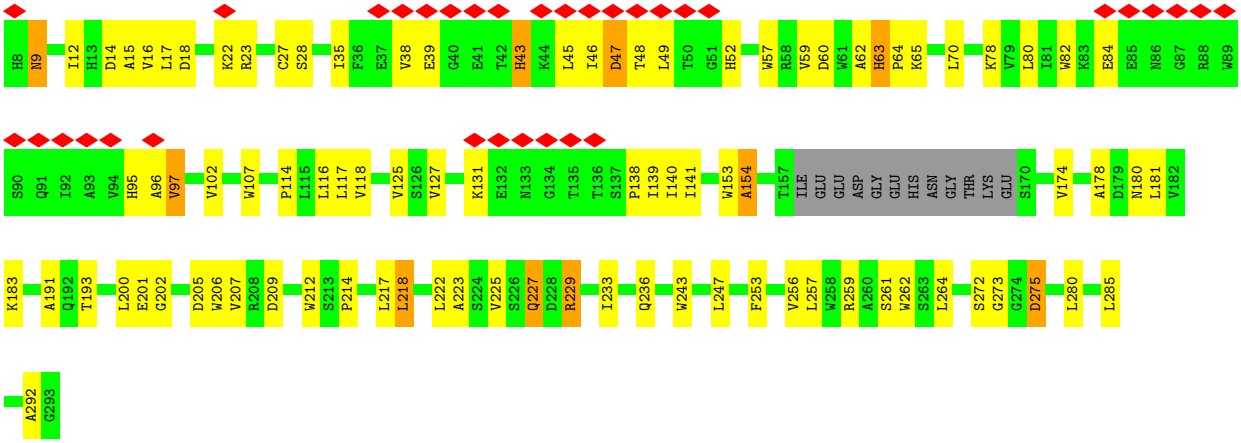
Chain V4:





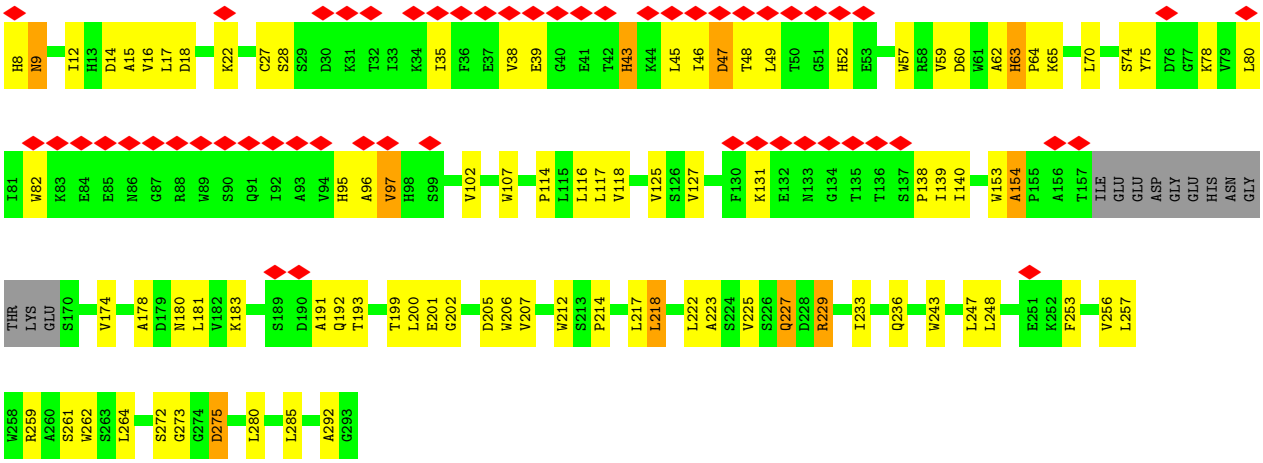
• Molecule 25: SEC13

Chain W1:



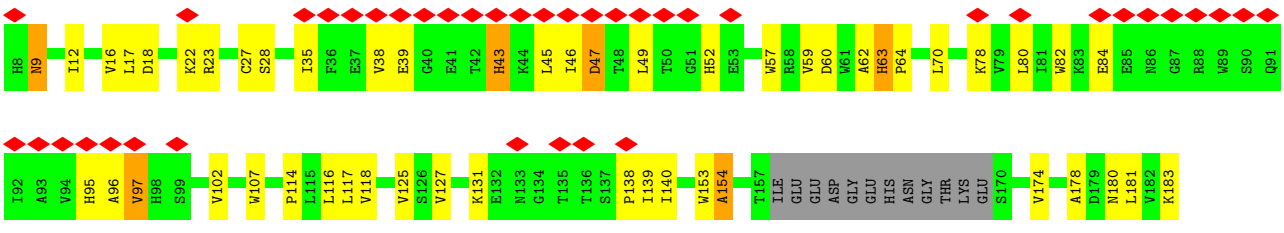
• Molecule 25: SEC13

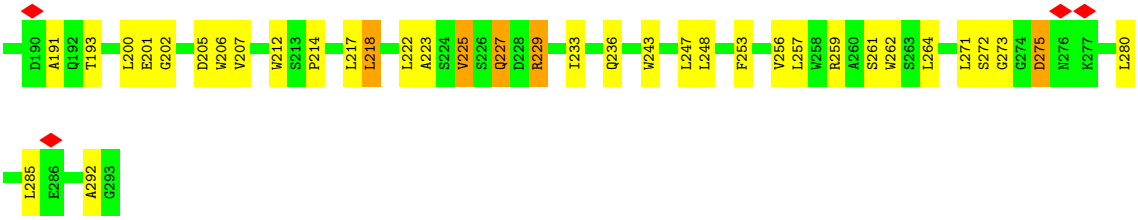
Chain W2:



• Molecule 25: SEC13

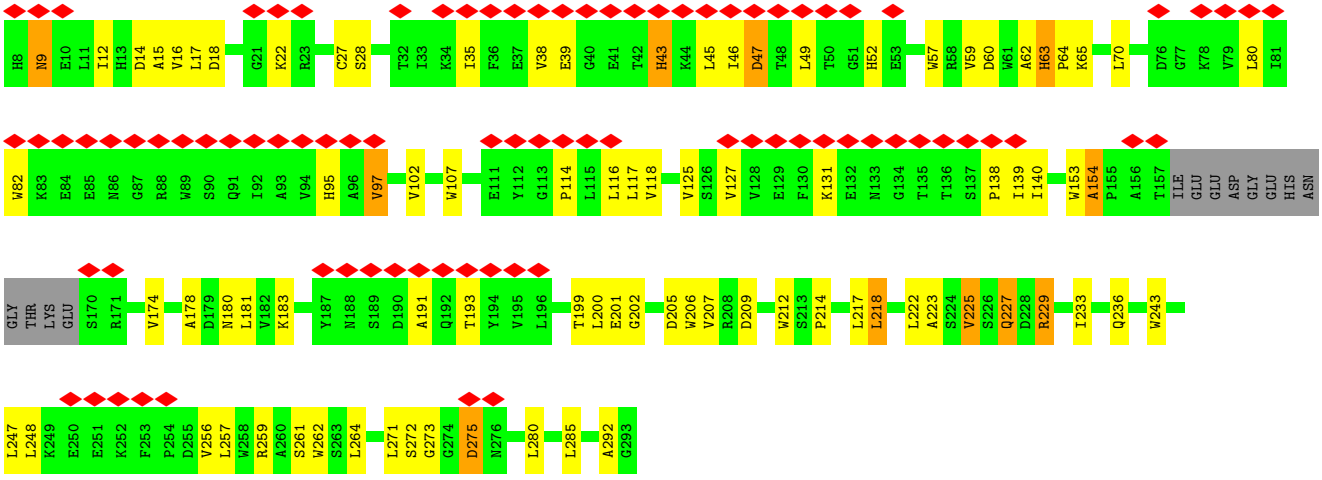
Chain W3:





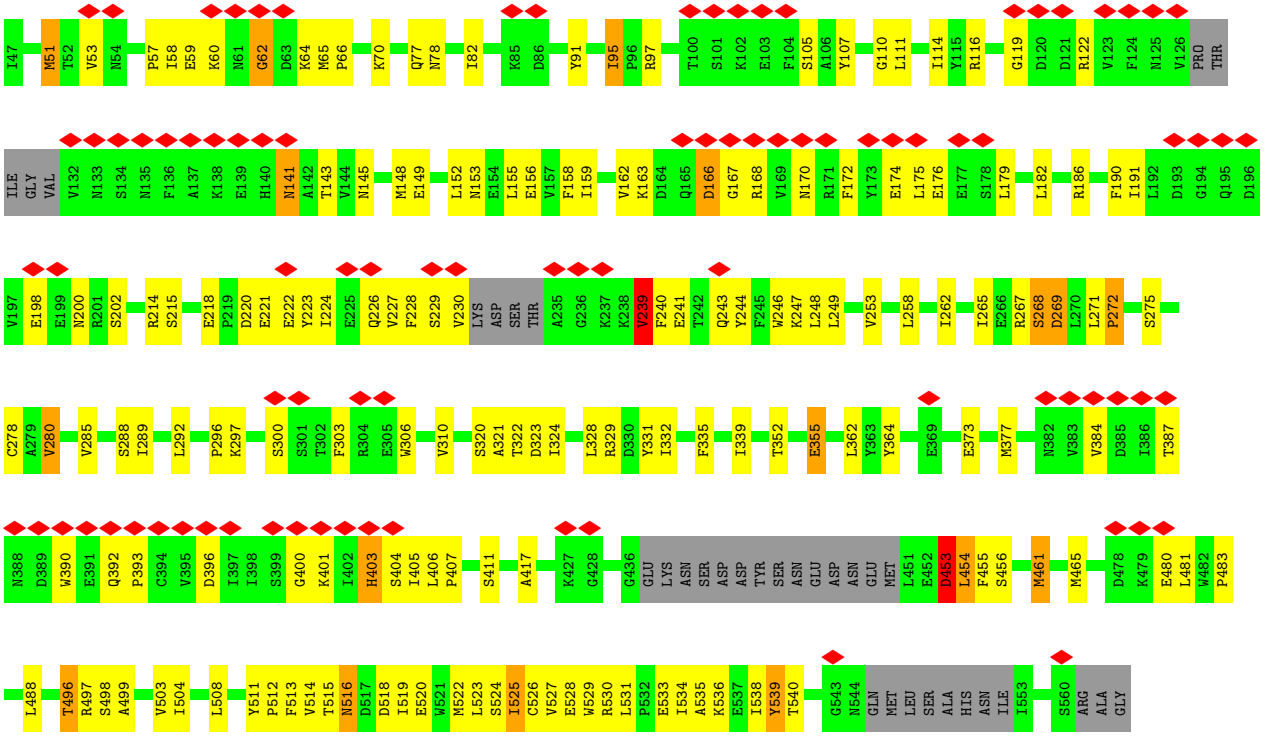
• Molecule 25: SEC13

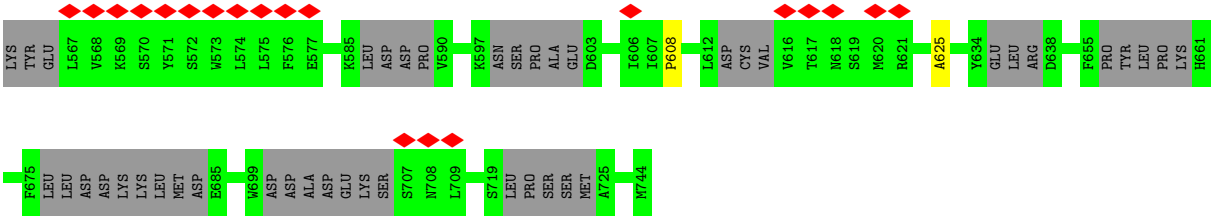
Chain W4:



• Molecule 26: NUP75

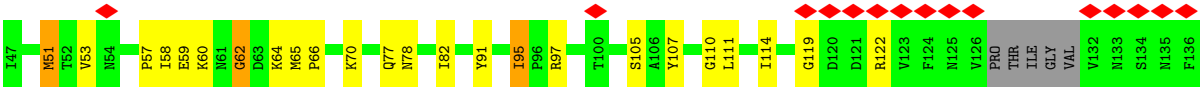
Chain X1:

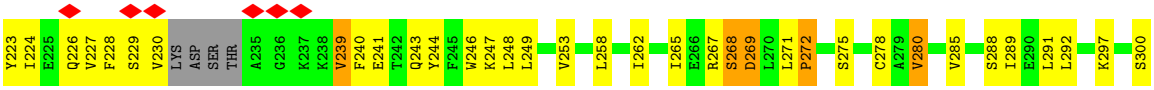


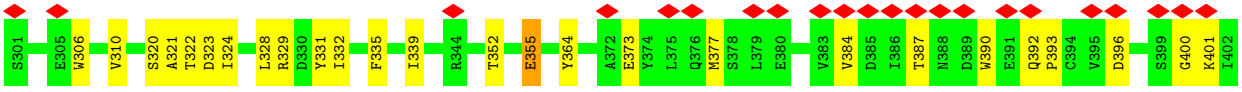


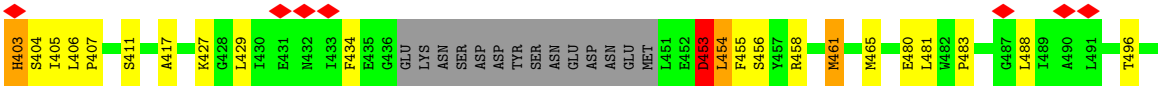
• Molecule 26: NUP75

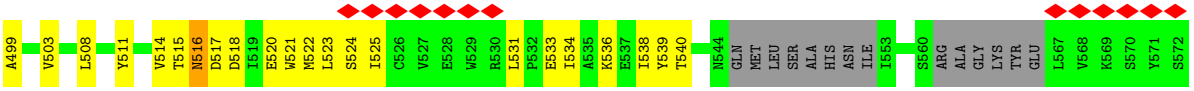
Chain X2:

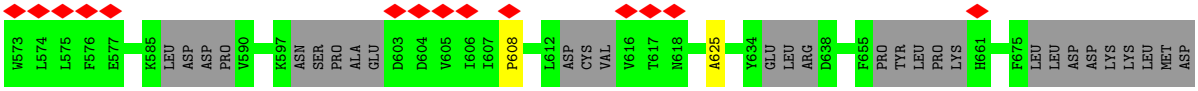


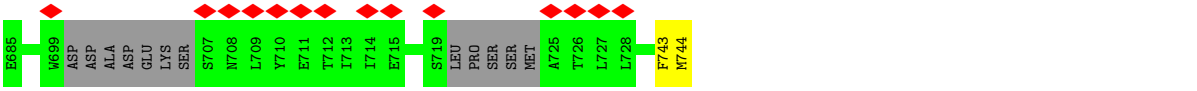


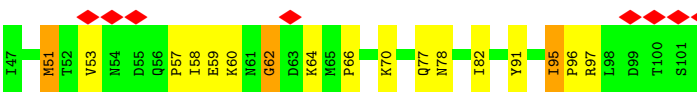






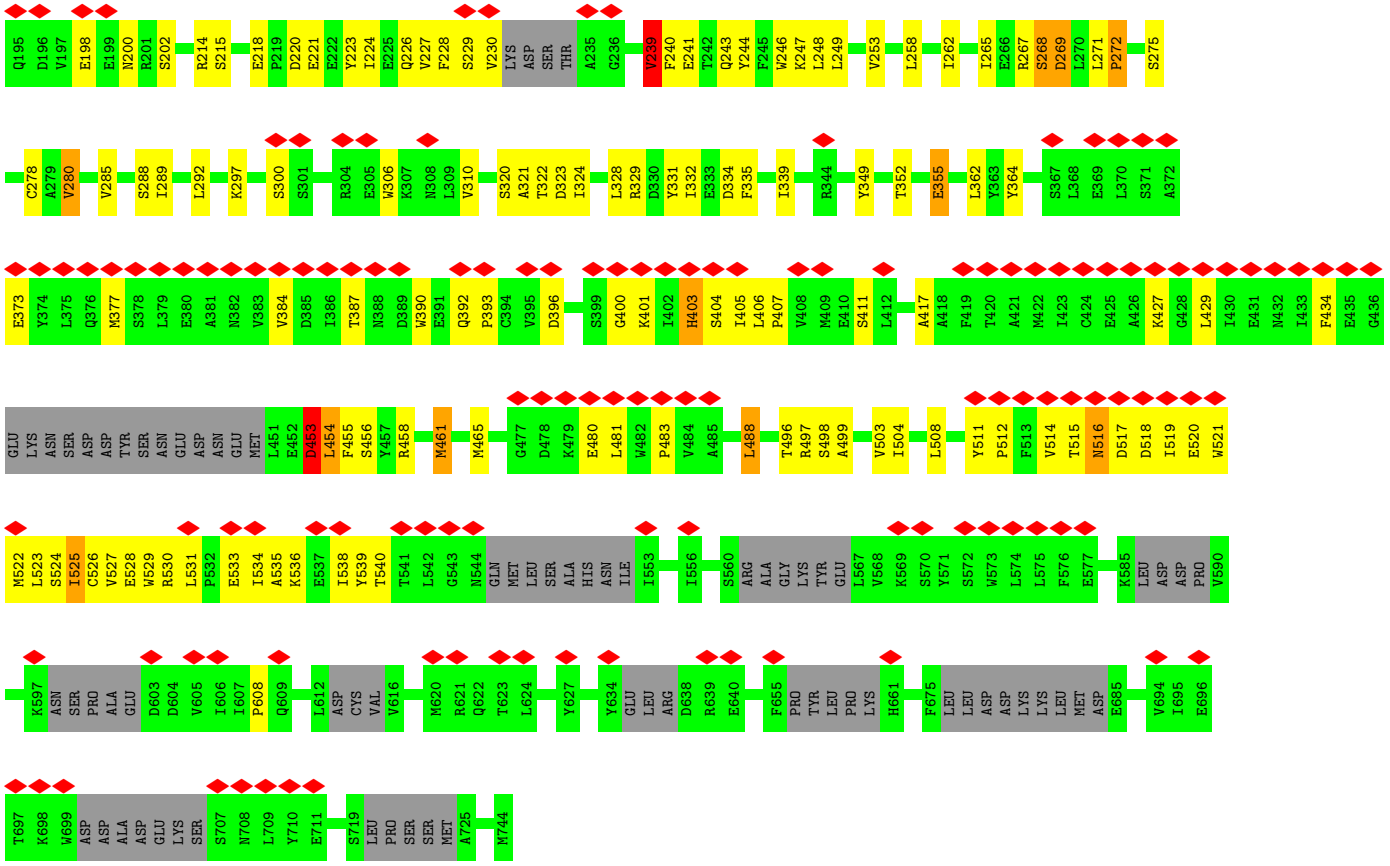






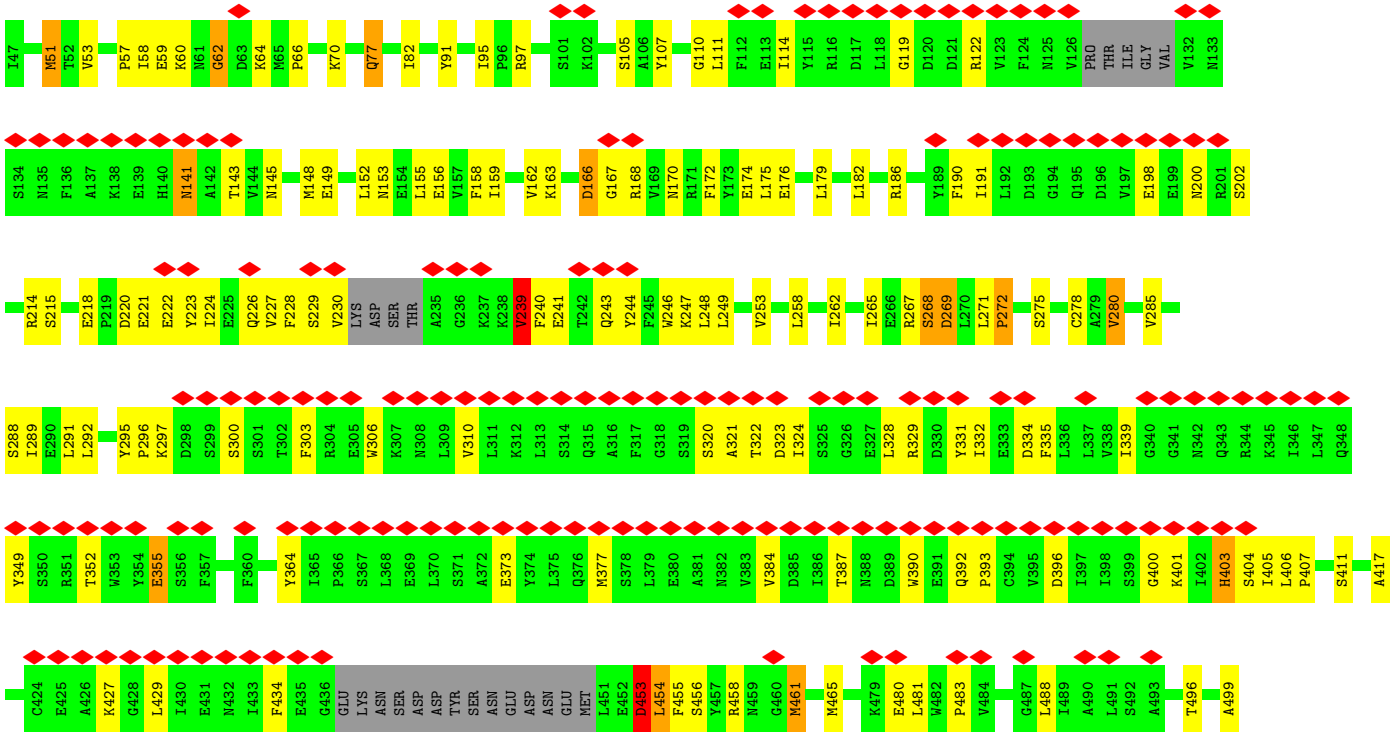
• Molecule 26: NUP75

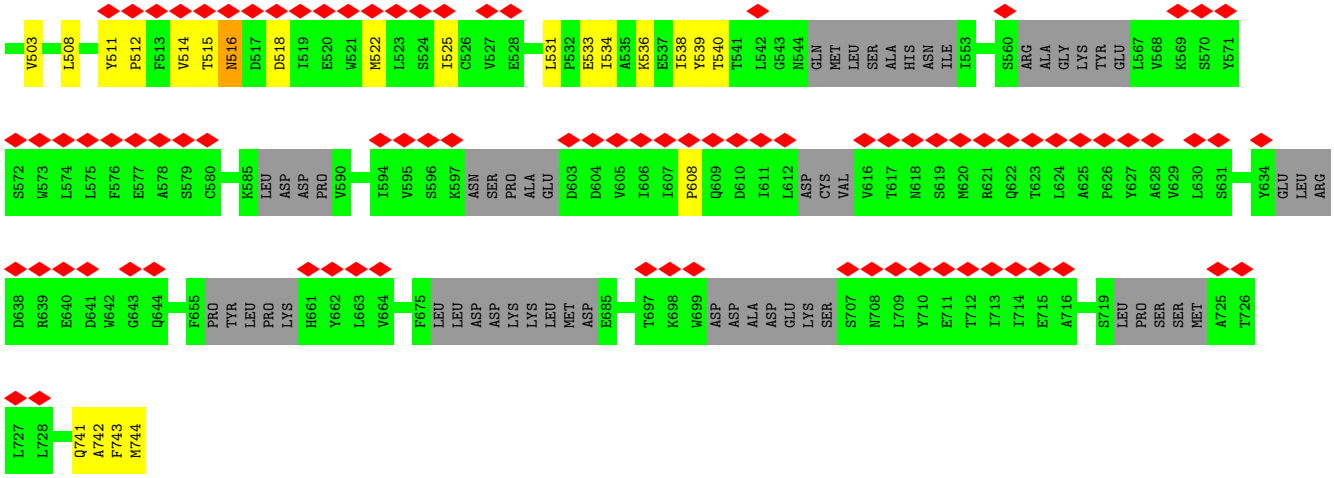
Chain X3:



• Molecule 26: NUP75

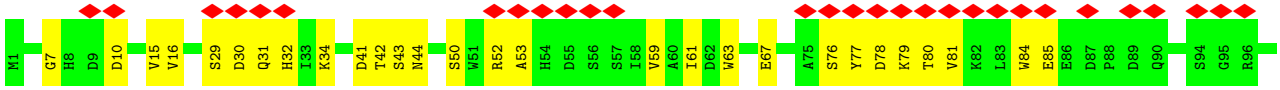
Chain X4:

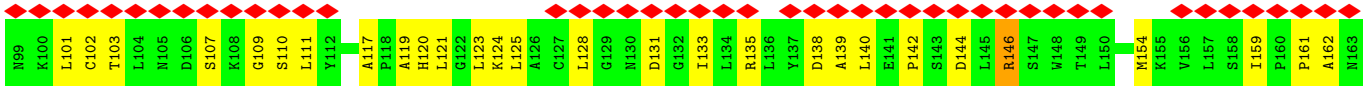


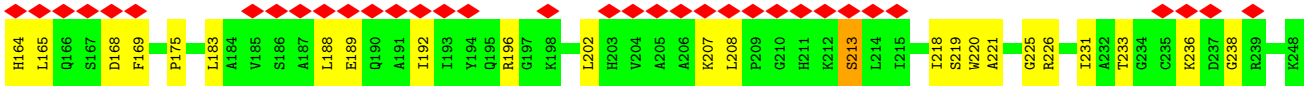


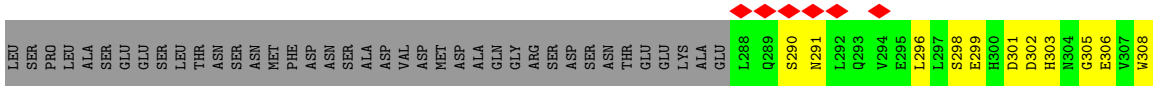
- Molecule 27: SEH1

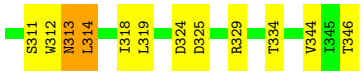
Chain Y1:





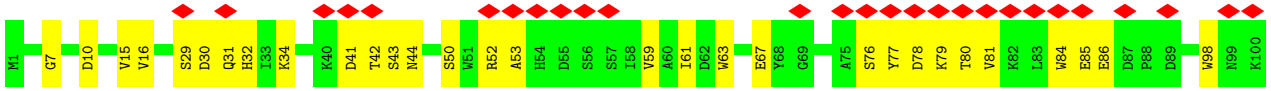


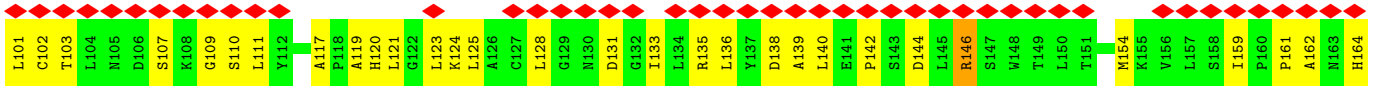


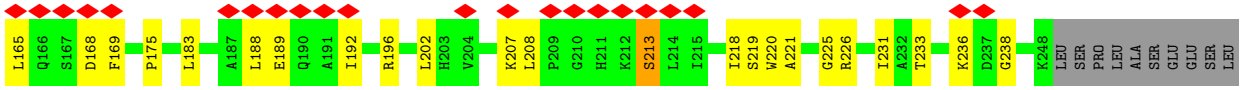


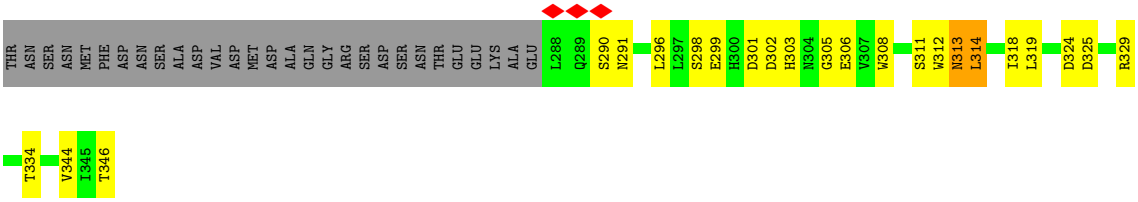
- Molecule 27: SEH1

Chain Y2:



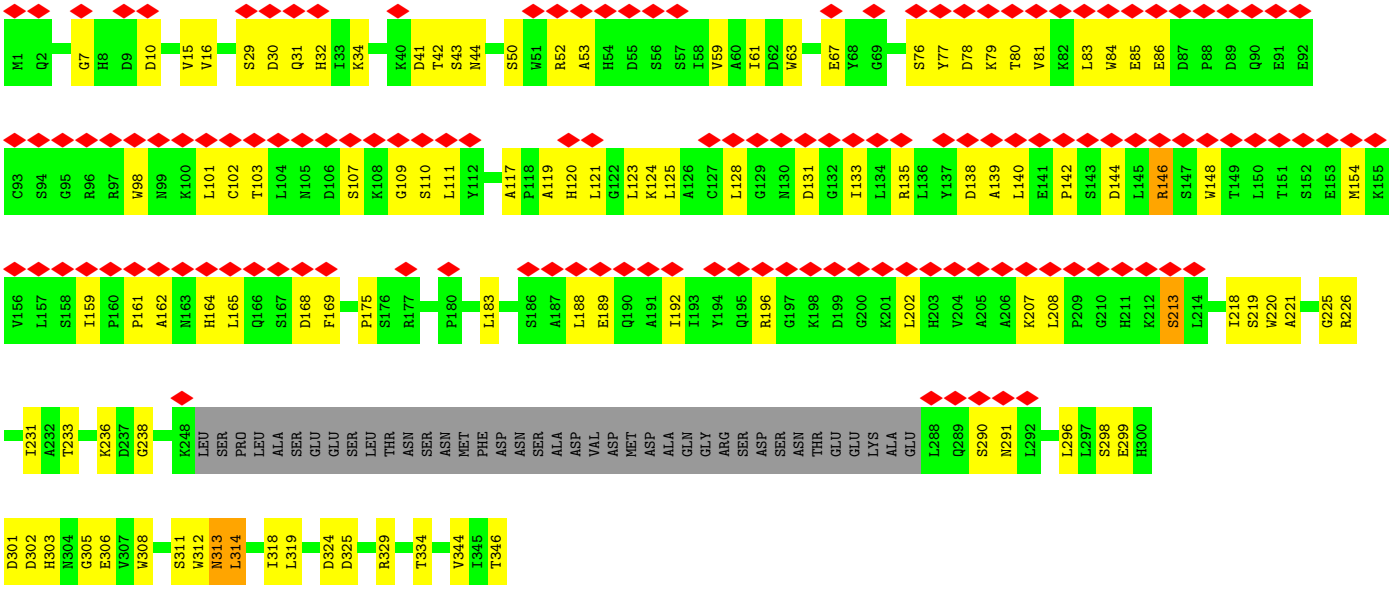






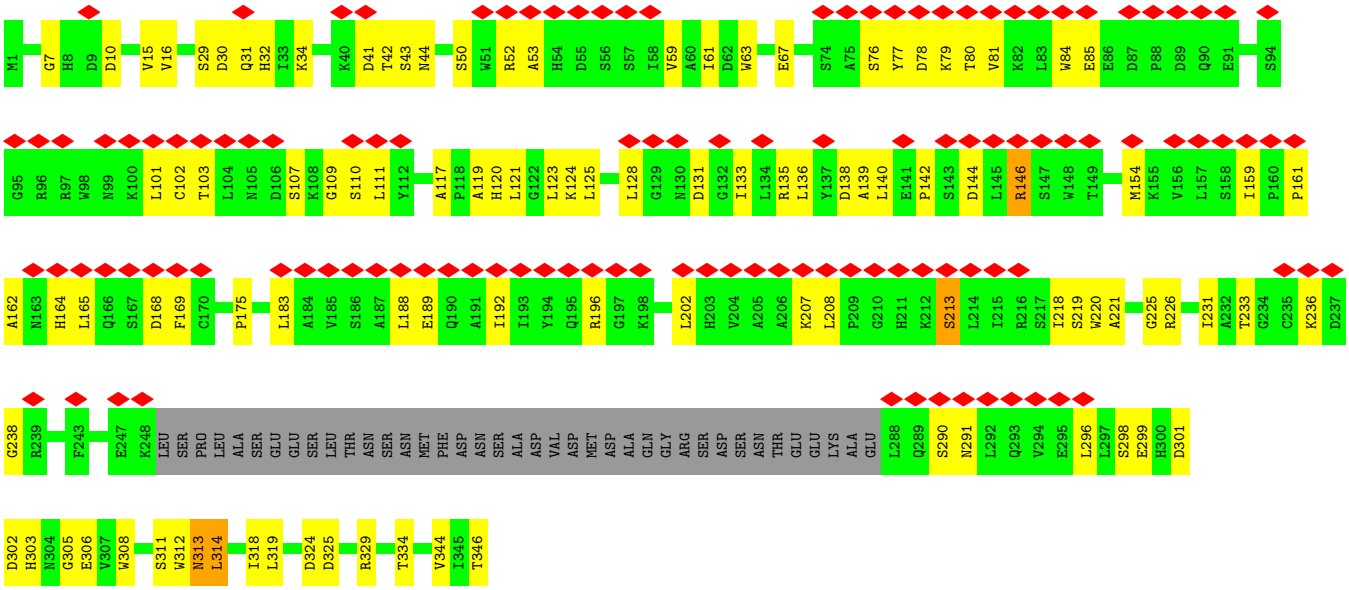
• Molecule 27: SEH1

Chain Y3:



• Molecule 27: SEH1

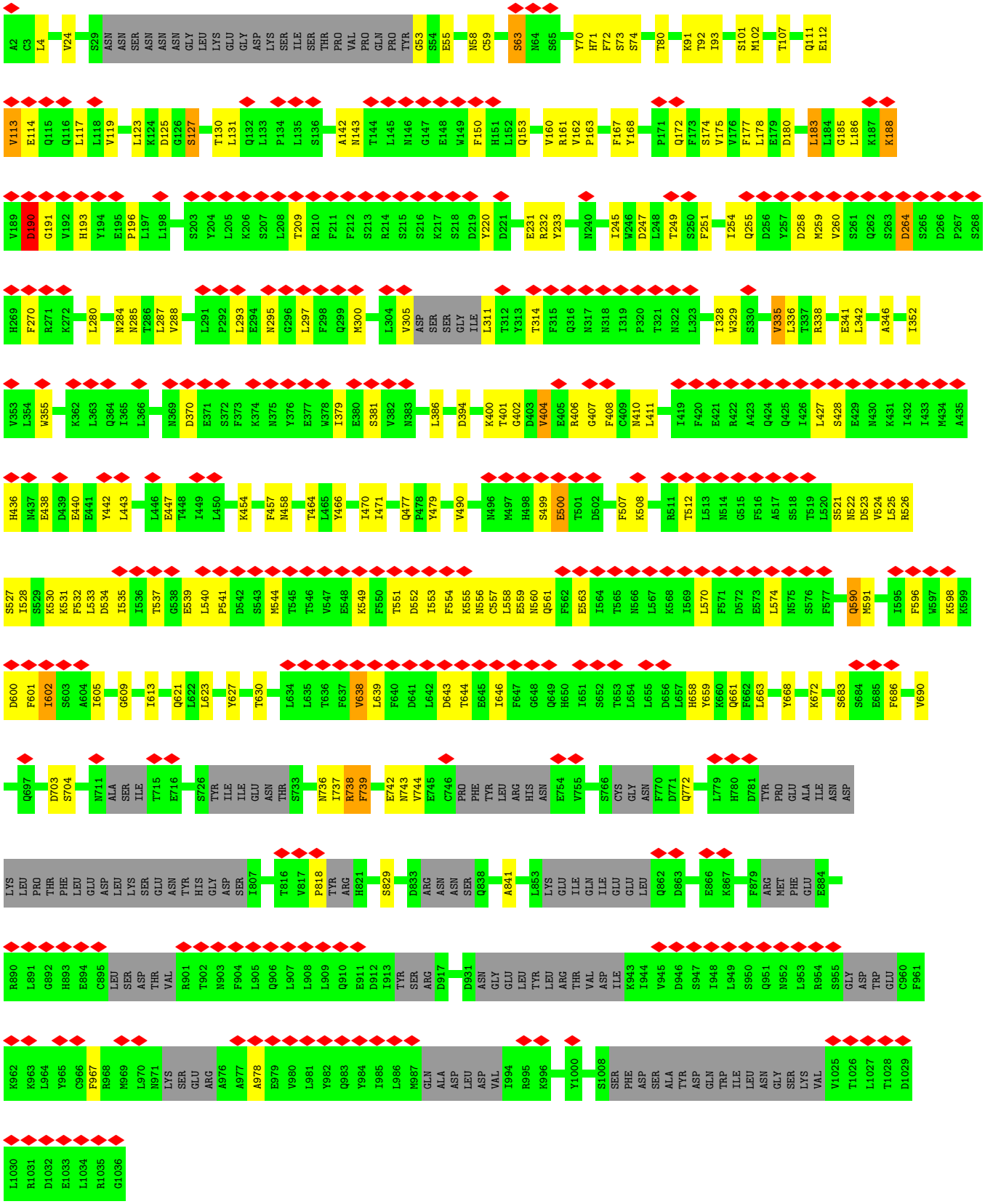
Chain Y4:



• Molecule 28: NUP160

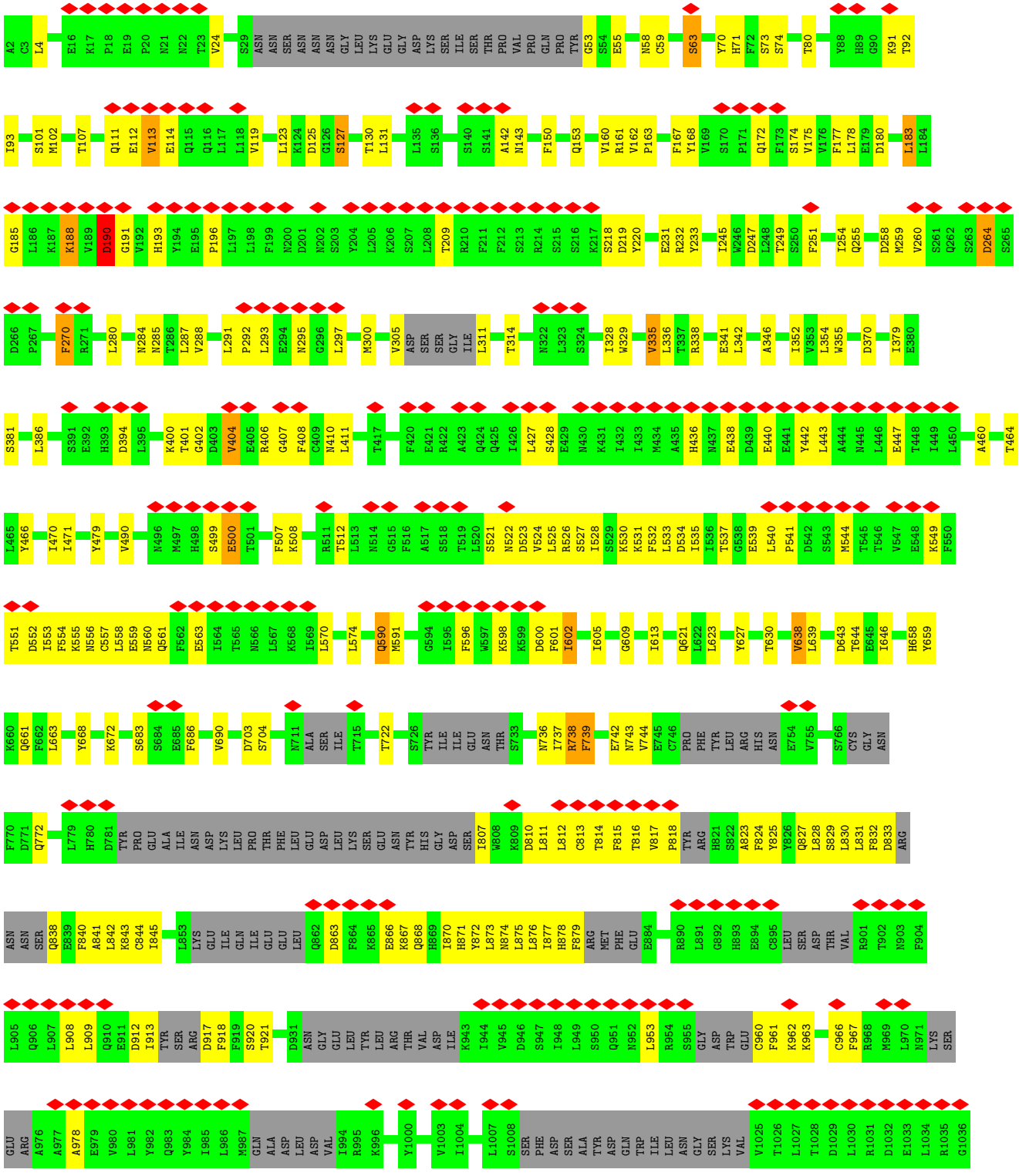
Chain Z1:

29%
67%
18%
13%


A2 C3 L4 V24 S29 ASN ASN SER ASN ASN ASN GLY LEU LYS GLU GLY ASP LYS SER ILE SER THR PRO VAL PRO GLN PRO TYR G53 S54 E55 N58 C59 S63 N64 S65 Y70 H71 F72 S73 S74 T80 K91 T92 I93 S101 M102 T107 Q111 E112
V113 E114 Q115 Q116 L117 L118 V119 L123 K124 D125 G126 S127 T130 L131 Q132 L133 P134 L135 S136 A142 N143 T144 L145 N146 G147 E148 W149 F150 H151 L152 Q153 V160 R161 V162 P163 F167 Y168 P171 Q172 F173 S174 V175 V176 F177 L178 E179 D180 L183 L184 G185 L186 K187 K188
V189 D190 G191 V192 H193 Y194 E195 P196 L197 L198 S203 Y204 L205 K206 S207 L208 T209 R210 F211 F212 S213 R214 S215 S216 K217 S218 D219 Y220 D221 E231 R232 Y233 N240 I245 W246 D247 L248 T249 S250 F251 I254 Q255 D256 Y257 D258 M259 V260 S261 Q262 S263 D264 S265 D266 P267 S268
H269 F270 R271 K272 L280 N284 N285 T286 L287 V288 L291 P292 L293 E294 N295 G296 L297 F298 Q299 M300 L304 V305 ASP SER SER GLY ILE L311 T312 Y313 T314 F315 Q316 N317 N318 I319 P320 T321 N322 L323 I328 W329 S330 V335 L336 T337 R338 E341 L342 A346 I352
V353 L354 W355 K362 L363 Q364 I365 L366 N369 D370 E371 S372 F373 K374 N375 Y376 E377 W378 I379 E380 S381 V382 N383 L386 D394 K400 T401 G402 D403 V404 E405 R406 G407 F408 C409 N410 L411 I419 F420 E421 R422 A423 Q424 Q425 I426 L427 S428 E429 N430 K431 I432 I433 M434 A435
H436 N437 E438 D439 E440 E441 Y442 L443 L446 E447 T448 I449 L450 K454 F457 N458 T464 L465 Y466 I470 I471 Q477 P478 Y479 V490 N496 M497 H498 S499 E500 T501 D502 F507 K508 R511 T512 L513 N514 G515 F516 A517 S518 T519 L520 S521 N522 D523 V524 L525 R526
S527 I528 S529 K530 K531 F532 L533 D534 I535 T536 T537 G538 E539 L540 P541 D542 S543 M544 T545 T546 V547 E548 K549 F550 T551 D552 I553 F554 K555 N556 C557 L558 E559 N560 Q561 F562 E563 I564 T565 N566 L567 K568 I569 L570 F571 D572 E573 L574 N575 S576 F577 Q590 M591 I595 F596 W597 K598 K599
D600 F601 I602 S603 A604 I605 G609 I613 Q621 L622 L623 Y627 T630 L634 L635 T636 F637 V638 L639 F640 D641 L642 D643 T644 E645 I646 F647 G648 Q649 H650 I651 S652 T653 L654 L655 D656 L657 H658 Y659 K660 Q661 F662 L663 Y668 K672 S683 S684 E685 F686 V690
Q697 D703 S704 W711 ALA SER ILE T715 E716 S726 TYR ILE ILE GLU ASN THR S733 N736 I737 R738 F739 E742 N743 V744 E745 C746 PRO PHE TYR LEU ARG HIS ASN E754 V755 S766 CYS GLY ASN F770 D771 Q772 L779 H780 D781 TYR PRO GLU ALA ILE ASN ASP
LYS LEU PRO THR PHE LEU GLU ASP LEU LYS SER GLU ASN TYR HIS GLY ASP SER I807 T816 V817 P818 TYR ARG H821 S829 D833 ARG ASN ASN SER Q838 A841 L853 LYS GLU ILE GLN ILE GLU GLU LEU Q862 D863 E866 K867 F879 ARG MET PHE GLU E884
R890 L891 G892 H893 E894 C895 LEU SER ASP THR VAL R901 T902 N903 F904 L905 Q906 L907 L908 L909 Q910 E911 D912 I913 TYR SER ARG D917 D931 ASN GLY GLU LEU TYR LEU ARG THR VAL ASP ILE K943 I944 V945 D946 S947 I948 L949 S950 Q951 N952 L953 R954 S955 GLY ASP TRP GLU C960 F961
K962 K963 L964 Y965 C966 F967 R968 M969 L970 N971 LYS SER GLU ARG A976 A977 A978 E979 V980 L981 Y982 Q983 Y984 I985 L986 M987 GLN ALA ASP LEU ASP VAL I994 R995 K996 Y1000 S1008 SER PHE ASP SER ALA TYR ASP GLN TRP ILE LEU ASN GLY SER LYS VAL V1025 T1026 L1027 T1028 D1029
L1030 R1031 D1032 E1033 L1034 R1035 G1036

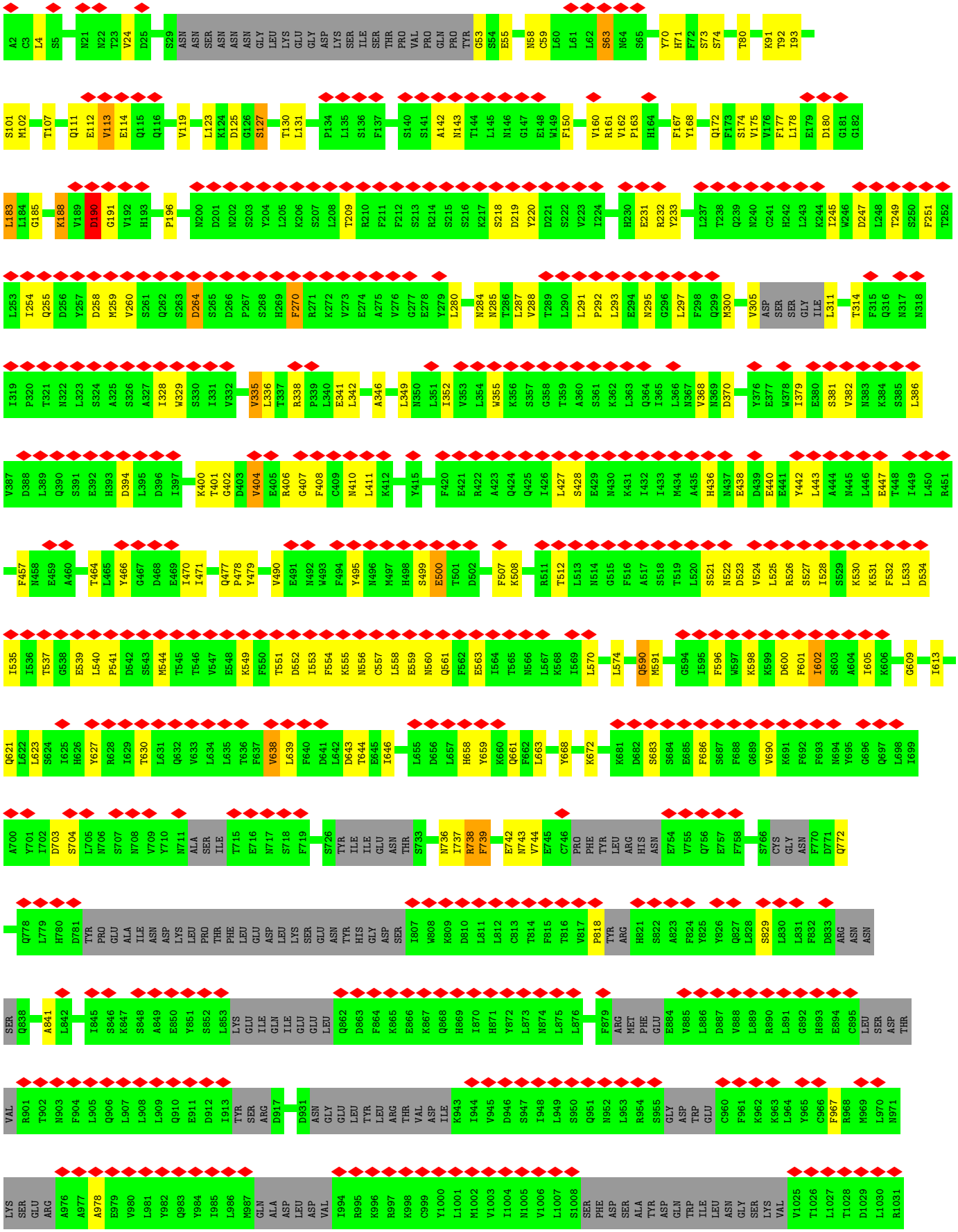
• Molecule 28: NUP160

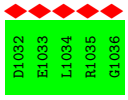
Chain Z2:



• Molecule 28: NUP160

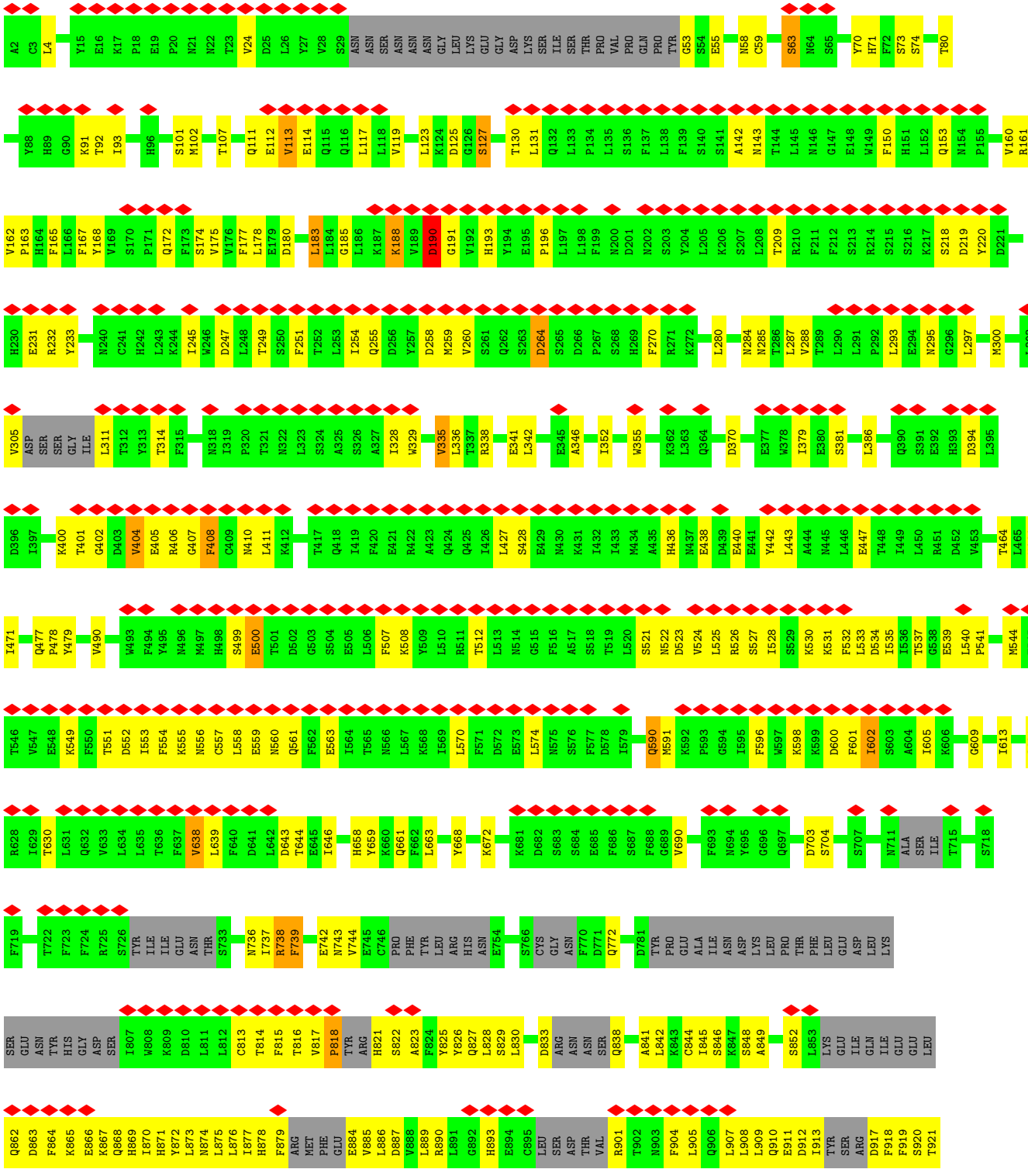
Chain Z3:

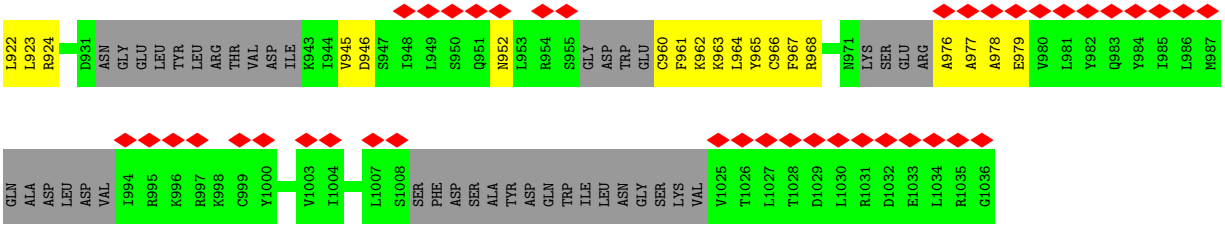

A2 C3 L4 S5 N21 N22 T23 V24 D25 S29 ASN ASN SER ASN ASN ASN GLY LEU LYS GLU GLY ASP LYS SER ILE SER THR PRO VAL PRO GLN PRO TYR G53 S54 E55 N58 C59 L60 L61 L62 S63 N64 S65 Y70 H71 F72 S73 S74 T80 K91 T92 I93
S101 M102 T107 Q111 E112 V113 E114 Q115 Q116 V119 L123 K124 D125 G126 S127 T130 L131 P134 L135 S136 F137 S140 S141 A142 N143 T144 L145 N146 G147 E148 W149 F150 V160 R161 V162 P163 H164 F167 Y168 Q172 F173 S174 V175 V176 F177 L178 E179 D180 G181 G182
L183 L184 G185 K188 V189 D190 G191 V192 H193 P196 N200 D201 N202 S203 Y204 L205 K206 S207 L208 T209 R210 F211 F212 S213 R214 S215 S216 K217 S218 D219 Y220 D221 S222 V223 I224 H230 E231 R232 Y233 L237 T238 Q239 N240 C241 H242 L243 K244 I245 W246 D247 L248 T249 S250 F251 T252
L253 I254 Q255 D256 Y257 D258 M259 V260 S261 Q262 S263 D264 S265 D266 P267 S268 H269 F270 R271 K272 V273 E274 A275 V276 G277 E278 Y279 L280 N284 N285 T286 L287 V288 T289 L290 L291 P292 L293 E294 N295 G296 L297 F298 Q299 M300 V305 ASP SER SER GLY ILE L311 T314 F315 Q316 N317 N318
I319 P320 T321 N322 L323 S324 A325 S326 A327 I328 W329 S330 I331 V332 V335 L336 T337 R338 P339 L340 E341 L342 A346 L349 N350 L351 I352 V353 L354 W355 K356 S357 G358 T359 A360 S361 K362 L363 Q364 I365 L366 N367 V368 N369 D370 Y376 E377 W378 I379 E380 S381 V382 N383 K384 S385 L386
V387 D388 L389 Q390 S391 E392 H393 D394 L395 D396 I397 K400 T401 G402 D403 V404 E405 R406 G407 F408 C409 N410 L411 K412 Y415 F420 E421 R422 A423 Q424 Q425 I426 L427 S428 E429 N430 K431 I432 I433 M434 A435 H436 N437 E438 D439 E440 E441 Y442 L443 A444 N445 L446 E447 T448 I449 L450 R451
F457 N458 E459 A460 T464 L465 Y466 G467 D468 E469 I470 I471 Q477 P478 Y479 V490 E491 N492 W493 F494 Y495 N496 M497 H498 S499 E500 T501 D502 F507 K508 R511 T512 L513 N514 G515 F516 A517 S518 T519 L520 S521 N522 D523 V524 L525 R526 S527 I528 S529 K530 K531 F532 L533 D534
I535 I536 T537 G538 E539 L540 P541 D542 S543 M544 T545 T546 V547 E548 K549 F550 T551 D552 I553 F554 K555 N556 C557 L558 E559 N560 Q561 F562 E563 I564 T565 N566 L567 K568 I569 L570 L574 Q590 M591 G594 I595 F596 W597 K598 K599 D600 F601 I602 S603 A604 I605 K606 G609 I613
Q621 L622 L623 S624 I625 H626 Y627 R628 I629 T630 L631 Q632 V633 L634 L635 T636 F637 V638 L639 F640 D641 L642 D643 T644 E645 I646 L655 D656 L657 H658 Y659 K660 Q661 F662 L663 Y668 K672 K681 D682 S683 S684 E685 F686 S687 F688 G689 V690 K691 F692 F693 N694 Y695 G696 Q697 L698 I699
A700 Y701 I702 D703 S704 L705 N706 S707 N708 V709 Y710 N711 ALA SER ILE T715 E716 N717 S718 F719 S726 TYR ILE ILE GLU ASN THR S733 N736 I737 R738 F739 E742 N743 V744 E745 C746 PRO PHE TYR LEU ARG HIS ASN E754 V755 Q756 E757 F758 S766 CYS GLY ASN F770 D771 Q772
Q778 L779 H780 D781 TYR PRO GLU ALA ILE ASN ASP LYS LEU PRO THR PHE LEU GLU ASP LEU LYS SER GLU ASN TYR HIS GLY ASP SER I807 W808 K809 D810 L811 L812 C813 T814 F815 T816 V817 P818 TYR ARG H821 S822 A823 F824 Y825 Y826 Q827 L828 S829 L830 L831 F832 D833 ARG ASN ASN
SER Q838 A841 L842 I845 S846 K847 S848 A849 E850 Y851 S852 L853 LYS GLU ILE GLN ILE GLU GLU LEU Q862 D863 F864 K865 E866 K867 Q868 H869 I870 H871 Y872 L873 N874 L875 L876 F879 ARG MET PHE GLU E884 V885 L886 D887 V888 L889 R890 L891 G892 H893 E894 C895 LEU SER ASP THR
VAL R901 T902 N903 F904 L905 Q906 L907 L908 L909 Q910 E911 D912 I913 TYR SER ARG D917 D931 ASN GLY GLU LEU TYR LEU ARG THR VAL ASP ILE K943 I944 V945 D946 S947 I948 L949 S950 Q951 N952 L953 R954 S955 GLY ASP TRP GLU C960 F961 K962 K963 L964 Y965 C966 F967 R968 M969 L970 N971
LYS SER GLU ARG A976 A977 A978 E979 V980 L981 Y982 Q983 Y984 I985 L986 M987 GLN ALA ASP LEU ASP VAL I994 R995 K996 R997 K998 C999 Y1000 L1001 M1002 V1003 I1004 N1005 V1006 L1007 S1008 SER PHE ASP SER ALA TYR ASP GLN TRP ILE LEU ASN GLY SER LYS VAL V1025 T1026 L1027 T1028 D1029 L1030 R1031



• Molecule 28: NUP160

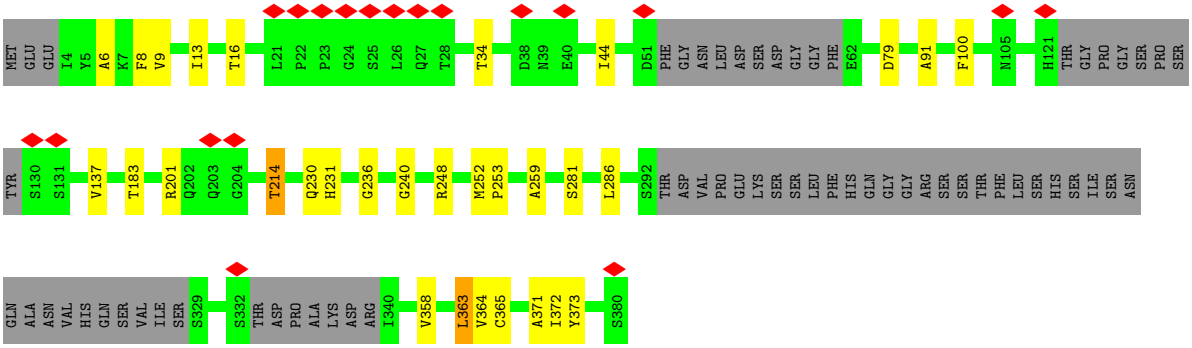
Chain Z4:





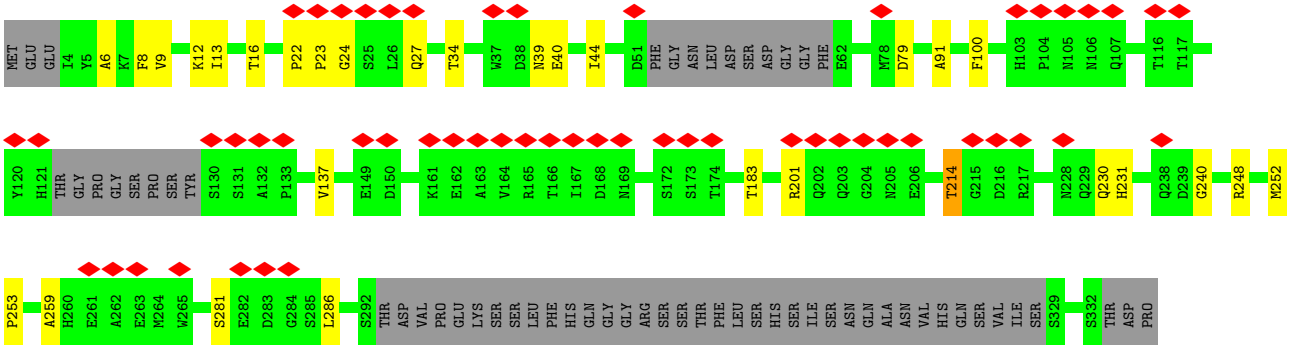
• Molecule 29: NUP43

Chain a1:



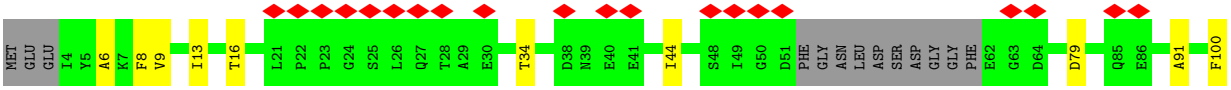
• Molecule 29: NUP43

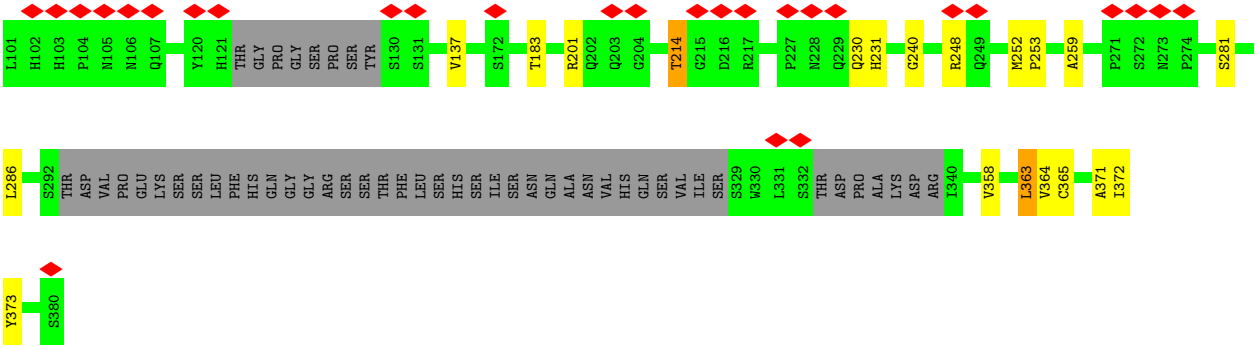
Chain a2:



• Molecule 29: NUP43

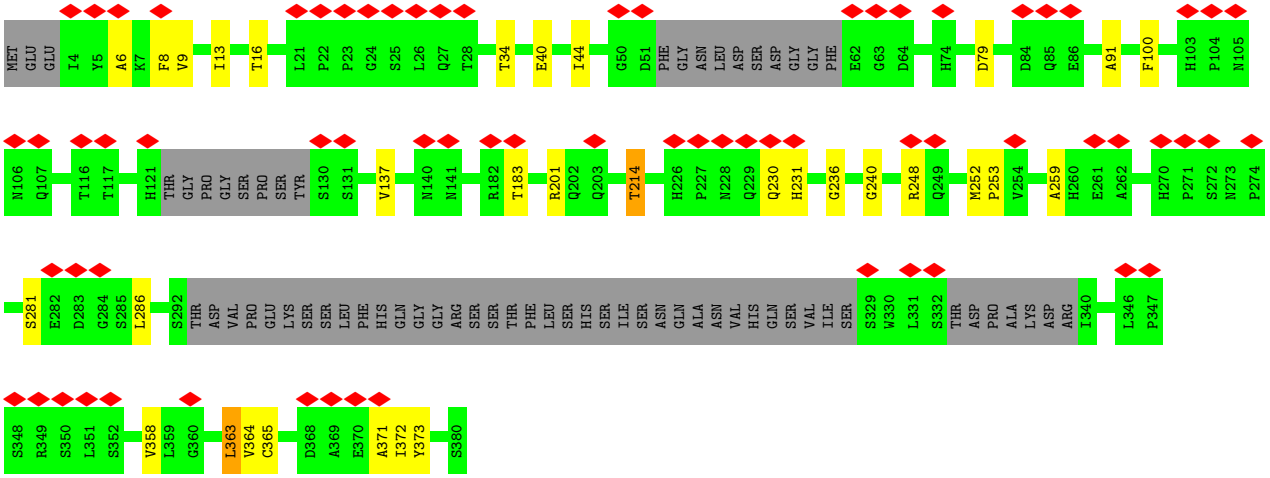
Chain a3:





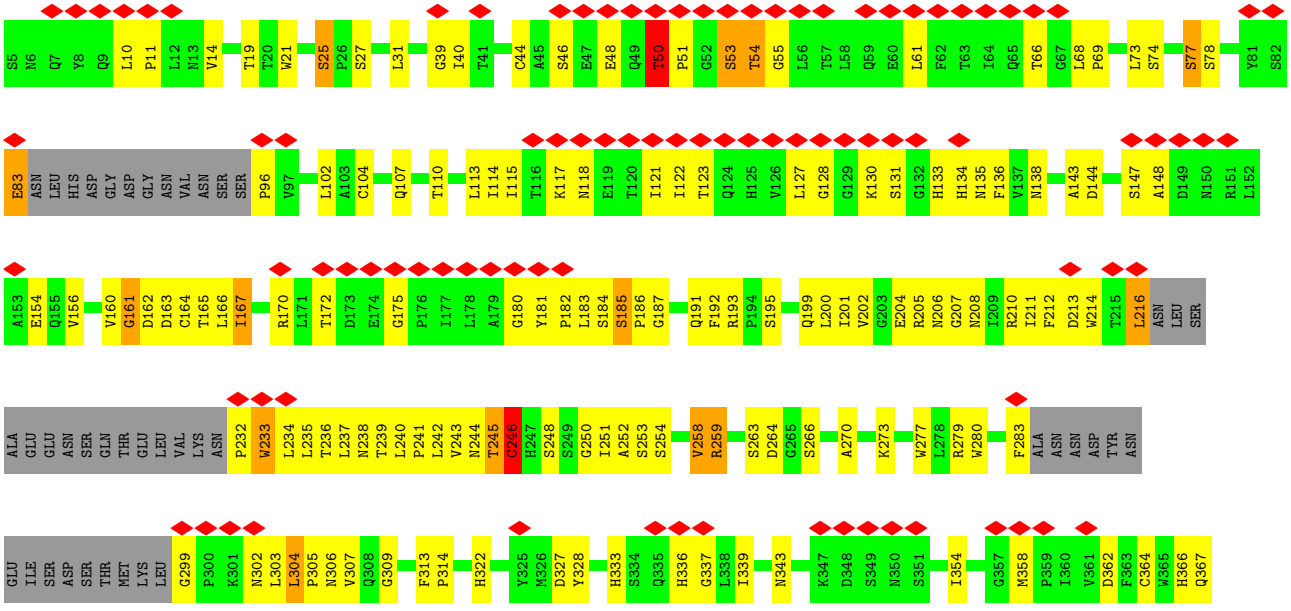
• Molecule 29: NUP43

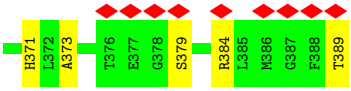
Chain a4:



• Molecule 30: NUP37

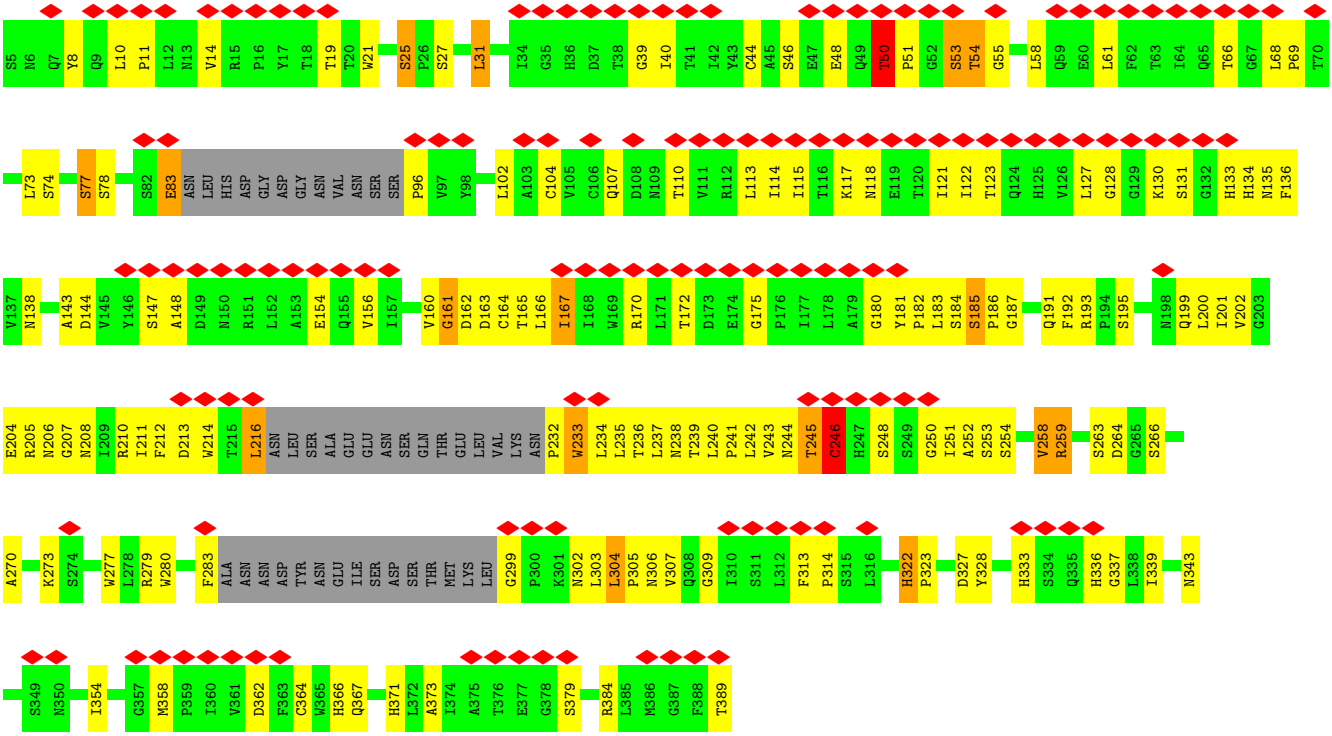
Chain b1:





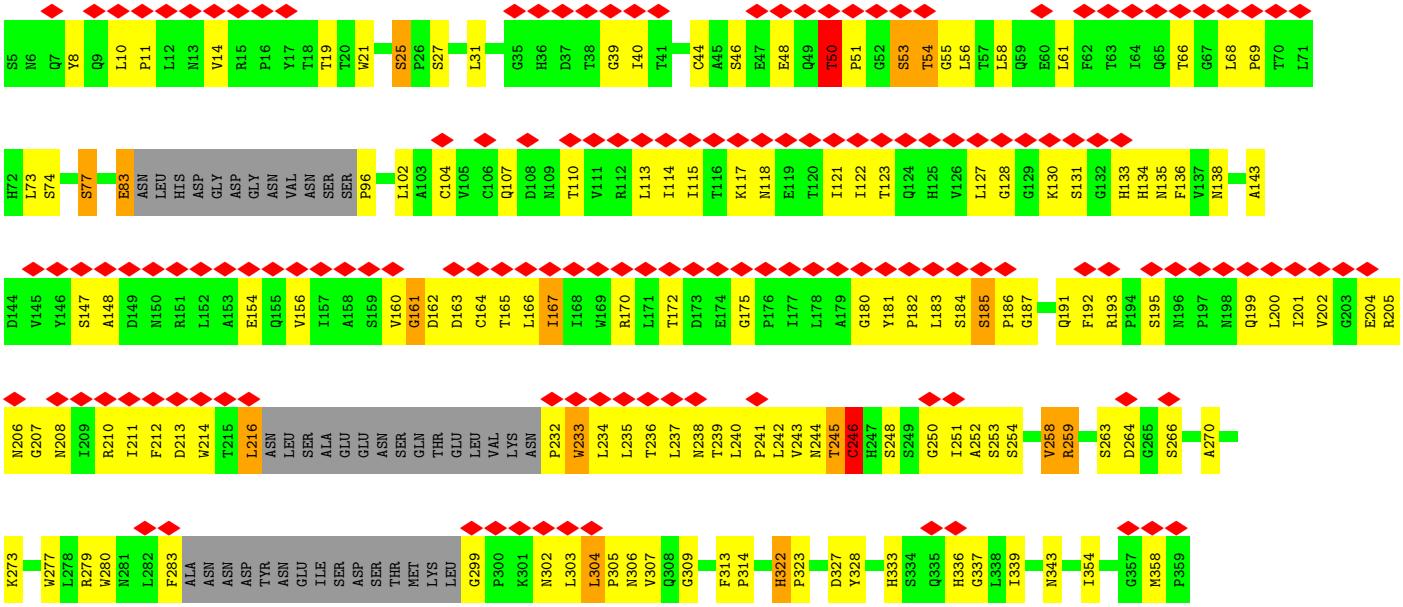
• Molecule 30: NUP37

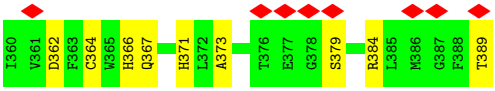
Chain b2:



• Molecule 30: NUP37

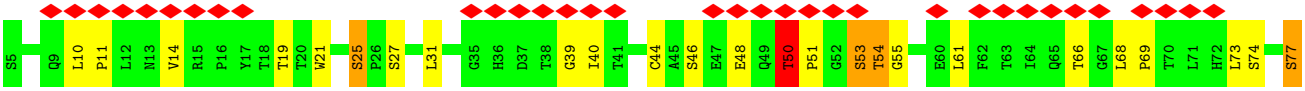
Chain b3:

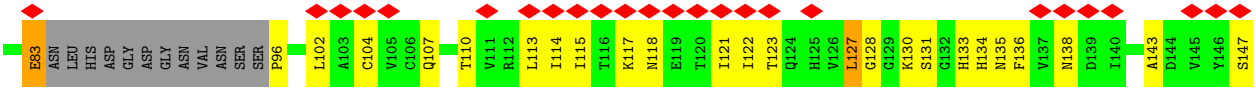


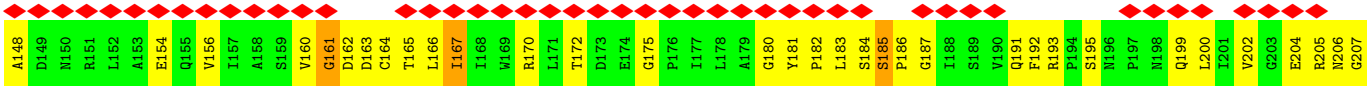


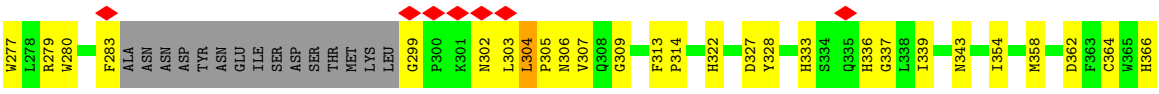
• Molecule 30: NUP37

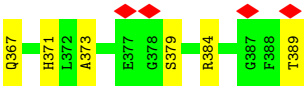
Chain b4:











4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	17368	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	110	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	82.185	Depositor
Minimum map value	-69.686	Depositor
Average map value	0.077	Depositor
Map value standard deviation	0.791	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	1941.1199, 1941.1199, 1941.1199	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.37, 3.37, 3.37	Depositor

5 Model quality

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

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
30	b3	0.46	0/2702	1.01	13/3689 (0.4%)
30	b4	0.46	0/2702	1.01	13/3689 (0.4%)
All	All	0.42	59/365761 (0.0%)	0.70	390/495950 (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 59 bond length outliers are listed below:

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

The worst 5 of 390 bond angle outliers are listed below:

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

There are no chirality outliers.

5 of 38 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	891	GLY	Mainchain
1	A1	976	LEU	Peptide
2	A2	699	SER	Peptide
1	A3	891	GLY	Mainchain
1	A3	976	LEU	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	9730	0	9632	537	0
1	A3	9730	0	9631	480	0
2	A2	9946	0	9773	1900	0
2	A4	9946	0	9778	1962	0
3	A5	10030	0	9896	1498	0
3	A6	10030	0	9914	1574	0
4	B1	111	0	127	2	0
4	B2	111	0	127	25	0
4	B3	111	0	127	2	0
4	B4	111	0	127	25	0
4	B5	111	0	126	46	0
4	B6	111	0	124	60	0
5	C1	138	0	144	32	0
5	C2	157	0	158	272	0
5	C3	138	0	144	10	0
5	C4	157	0	155	374	0
5	C5	138	0	144	23	0
5	C6	138	0	144	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D1	5034	0	5006	1053	0
6	D2	5034	0	5030	87	0
6	D3	5034	0	4979	1467	0
6	D4	5034	0	5030	94	0
6	D5	5034	0	5030	57	0
6	D6	5034	0	5030	57	0
6	D7	5034	0	5026	130	0
7	E1	63	0	65	2	0
7	E2	63	0	65	2	0
7	E3	63	0	65	2	0
7	E4	63	0	65	2	0
7	E5	63	0	65	2	0
7	E6	63	0	65	2	0
7	E7	63	0	65	2	0
8	F1	12779	0	12914	341	0
8	F2	12779	0	12917	119	0
9	G1	438	0	411	211	0
9	G2	438	0	412	68	0
10	H1	94	0	84	0	0
10	H2	94	0	84	0	0
11	I1	12307	0	12275	3132	0
11	I2	12307	0	12283	3065	0
11	I3	12307	0	12352	481	0
11	I4	12307	0	12359	367	0
11	I5	12307	0	12350	535	0
12	J1	504	0	486	52	0
12	J2	504	0	485	52	0
12	J3	504	0	487	30	0
12	J4	504	0	487	30	0
12	J5	504	0	487	30	0
13	K1	73	0	82	0	0
13	K2	73	0	82	0	0
13	K3	73	0	82	0	0
13	K4	73	0	82	0	0
13	K5	73	0	82	0	0
14	L1	15	0	11	0	0
14	L2	15	0	11	0	0
14	L3	15	0	11	0	0
14	L4	15	0	11	0	0
14	L5	15	0	11	0	0
15	M1	1372	0	1330	700	0
15	M2	1372	0	1361	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	M3	1372	0	1333	579	0
15	M4	1372	0	1363	5	0
16	N1	1401	0	1376	733	0
16	N2	1401	0	1398	63	0
16	N3	1401	0	1384	612	0
16	N4	1401	0	1398	10	0
17	O1	1971	0	1944	839	0
17	O2	1971	0	1961	388	0
17	O3	1971	0	1937	1111	0
17	O4	1971	0	1963	230	0
18	P1	900	0	910	52	0
18	P2	900	0	910	43	0
18	P3	900	0	908	148	0
18	P4	900	0	907	109	0
19	Q1	658	0	645	3	0
19	Q2	616	0	600	3	0
19	Q3	658	0	645	3	0
19	Q4	616	0	600	3	0
20	R1	311	0	314	406	0
20	R2	311	0	334	2	0
20	R3	311	0	314	436	0
20	R4	311	0	334	2	0
21	S1	6013	0	4984	178	0
21	S2	6013	0	4984	177	0
21	S3	6013	0	4984	177	0
21	S4	6013	0	4984	177	0
22	T1	1993	0	1981	79	0
22	T2	1993	0	1981	73	0
22	T3	1993	0	1981	75	0
22	T4	1993	0	1981	71	0
23	U1	3404	0	3378	84	0
23	U2	3404	0	3378	83	0
23	U3	3404	0	3378	79	0
23	U4	3404	0	3378	82	0
24	V1	3805	0	3499	111	0
24	V2	3805	0	3499	108	0
24	V3	3805	0	3499	114	0
24	V4	3805	0	3499	110	0
25	W1	2160	0	2096	66	0
25	W2	2160	0	2096	74	0
25	W3	2160	0	2096	63	0
25	W4	2160	0	2096	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	X1	4535	0	4064	390	0
26	X2	4535	0	4071	166	0
26	X3	4535	0	4063	357	0
26	X4	4535	0	4073	146	0
27	Y1	2438	0	2378	74	0
27	Y2	2438	0	2378	75	0
27	Y3	2438	0	2378	76	0
27	Y4	2438	0	2378	75	0
28	Z1	6622	0	5893	624	0
28	Z2	6622	0	5882	1025	0
28	Z3	6622	0	5893	621	0
28	Z4	6622	0	5872	1352	0
29	a1	2587	0	2488	38	0
29	a2	2587	0	2488	73	0
29	a3	2587	0	2488	36	0
29	a4	2587	0	2488	51	0
30	b1	2638	0	2573	610	0
30	b2	2638	0	2573	602	0
30	b3	2638	0	2573	609	0
30	b4	2638	0	2573	610	0
All	All	358888	0	346683	20457	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 29.

The worst 5 of 20457 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y2:41:ASP:HB3	29:a2:231[B]:HIS:CE1	1.17	1.69
28:Z1:524:VAL:HG13	30:b1:236:THR:CB	1.22	1.68
11:I3:1267:LEU:HD22	26:X1:497:ARG:CZ	1.20	1.68
3:A6:1369:ILE:HA	28:Z4:826:TYR:CB	1.23	1.67
8:F1:1262:HIS:CE1	17:O2:259:ASP:HB2	1.26	1.67

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	1211/1316 (92%)	1172 (97%)	39 (3%)	0	100	100
1	A3	1211/1316 (92%)	1172 (97%)	39 (3%)	0	100	100
2	A2	1255/1328 (94%)	1183 (94%)	54 (4%)	18 (1%)	9	40
2	A4	1255/1328 (94%)	1182 (94%)	55 (4%)	18 (1%)	9	40
3	A5	1258/1330 (95%)	1224 (97%)	34 (3%)	0	100	100
3	A6	1258/1330 (95%)	1224 (97%)	34 (3%)	0	100	100
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
18	P4	115/116 (99%)	114 (99%)	1 (1%)	0	100	100
19	Q1	83/84 (99%)	81 (98%)	2 (2%)	0	100	100
19	Q2	79/84 (94%)	77 (98%)	2 (2%)	0	100	100
19	Q3	83/84 (99%)	81 (98%)	2 (2%)	0	100	100
19	Q4	79/84 (94%)	77 (98%)	2 (2%)	0	100	100
20	R1	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
20	R2	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
20	R3	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
20	R4	38/40 (95%)	31 (82%)	7 (18%)	0	100	100
21	S1	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
21	S2	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
21	S3	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
21	S4	874/1156 (76%)	784 (90%)	74 (8%)	16 (2%)	6	34
22	T1	243/258 (94%)	235 (97%)	8 (3%)	0	100	100
22	T2	243/258 (94%)	234 (96%)	9 (4%)	0	100	100
22	T3	243/258 (94%)	234 (96%)	9 (4%)	0	100	100
22	T4	243/258 (94%)	234 (96%)	9 (4%)	0	100	100
23	U1	413/436 (95%)	368 (89%)	34 (8%)	11 (3%)	4	25
23	U2	413/436 (95%)	367 (89%)	35 (8%)	11 (3%)	4	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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	858/1035 (83%)	798 (93%)	49 (6%)	11 (1%)	9	42
28	Z2	858/1035 (83%)	798 (93%)	49 (6%)	11 (1%)	9	42
28	Z3	858/1035 (83%)	798 (93%)	49 (6%)	11 (1%)	9	42
28	Z4	858/1035 (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
All	All	45287/51646 (88%)	42909 (95%)	2058 (4%)	320 (1%)	20	56

5 of 320 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 (i)

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	D2	554/575 (96%)	554 (100%)	0	100	100
6	D3	554/575 (96%)	554 (100%)	0	100	100
6	D4	554/575 (96%)	554 (100%)	0	100	100
6	D5	554/575 (96%)	554 (100%)	0	100	100
6	D6	554/575 (96%)	554 (100%)	0	100	100
6	D7	554/575 (96%)	554 (100%)	0	100	100
7	E1	7/7 (100%)	7 (100%)	0	100	100
7	E2	7/7 (100%)	7 (100%)	0	100	100
7	E3	7/7 (100%)	7 (100%)	0	100	100
7	E4	7/7 (100%)	7 (100%)	0	100	100
7	E5	7/7 (100%)	7 (100%)	0	100	100
7	E6	7/7 (100%)	7 (100%)	0	100	100
7	E7	7/7 (100%)	7 (100%)	0	100	100
8	F1	1350/1512 (89%)	1350 (100%)	0	100	100
8	F2	1350/1512 (89%)	1350 (100%)	0	100	100
9	G1	47/47 (100%)	47 (100%)	0	100	100
9	G2	47/47 (100%)	47 (100%)	0	100	100
10	H1	10/10 (100%)	10 (100%)	0	100	100
10	H2	10/10 (100%)	10 (100%)	0	100	100
11	I1	1340/1509 (89%)	1339 (100%)	1 (0%)	88	89
11	I2	1340/1509 (89%)	1339 (100%)	1 (0%)	88	89
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	K3	9/9 (100%)	9 (100%)	0	100	100
13	K4	9/9 (100%)	9 (100%)	0	100	100
13	K5	9/9 (100%)	9 (100%)	0	100	100
14	L1	1/1 (100%)	1 (100%)	0	100	100
14	L2	1/1 (100%)	1 (100%)	0	100	100
14	L3	1/1 (100%)	1 (100%)	0	100	100
14	L4	1/1 (100%)	1 (100%)	0	100	100
14	L5	1/1 (100%)	1 (100%)	0	100	100
15	M1	146/154 (95%)	146 (100%)	0	100	100
15	M2	146/154 (95%)	146 (100%)	0	100	100
15	M3	146/154 (95%)	146 (100%)	0	100	100
15	M4	146/154 (95%)	146 (100%)	0	100	100
16	N1	150/173 (87%)	150 (100%)	0	100	100
16	N2	150/173 (87%)	150 (100%)	0	100	100
16	N3	150/173 (87%)	150 (100%)	0	100	100
16	N4	150/173 (87%)	150 (100%)	0	100	100
17	O1	213/213 (100%)	208 (98%)	5 (2%)	44	64
17	O2	213/213 (100%)	208 (98%)	5 (2%)	44	64
17	O3	213/213 (100%)	208 (98%)	5 (2%)	44	64
17	O4	213/213 (100%)	208 (98%)	5 (2%)	44	64
18	P1	101/100 (101%)	101 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	R4	32/32 (100%)	32 (100%)	0	100	100
21	S1	488/1013 (48%)	457 (94%)	31 (6%)	16	37
21	S2	488/1013 (48%)	457 (94%)	31 (6%)	16	37
21	S3	488/1013 (48%)	457 (94%)	31 (6%)	16	37
21	S4	488/1013 (48%)	457 (94%)	31 (6%)	16	37
22	T1	211/231 (91%)	205 (97%)	6 (3%)	38	60
22	T2	211/231 (91%)	205 (97%)	6 (3%)	38	60
22	T3	211/231 (91%)	205 (97%)	6 (3%)	38	60
22	T4	211/231 (91%)	205 (97%)	6 (3%)	38	60
23	U1	387/402 (96%)	363 (94%)	24 (6%)	16	38
23	U2	387/402 (96%)	363 (94%)	24 (6%)	16	38
23	U3	387/402 (96%)	363 (94%)	24 (6%)	16	38
23	U4	387/402 (96%)	363 (94%)	24 (6%)	16	38
24	V1	367/567 (65%)	321 (88%)	46 (12%)	4	16
24	V2	367/567 (65%)	321 (88%)	46 (12%)	4	16
24	V3	367/567 (65%)	321 (88%)	46 (12%)	4	16
24	V4	367/567 (65%)	321 (88%)	46 (12%)	4	16
25	W1	233/243 (96%)	223 (96%)	10 (4%)	26	47
25	W2	233/243 (96%)	223 (96%)	10 (4%)	26	47
25	W3	233/243 (96%)	223 (96%)	10 (4%)	26	47
25	W4	233/243 (96%)	223 (96%)	10 (4%)	26	47
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	639/970 (66%)	611 (96%)	28 (4%)	25	47
28	Z2	639/970 (66%)	611 (96%)	28 (4%)	25	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	Z3	639/970 (66%)	611 (96%)	28 (4%)	25	47
28	Z4	639/970 (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
All	All	37655/45001 (84%)	36568 (97%)	1087 (3%)	38	58

5 of 1087 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 553 such sidechains are listed below:

Mol	Chain	Res	Type
28	Z1	575	ASN
28	Z2	575	ASN
28	Z1	560	ASN
29	a3	229	GLN
11	I1	1635	HIS

5.3.3 RNA

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)

There are no chain breaks in this entry.

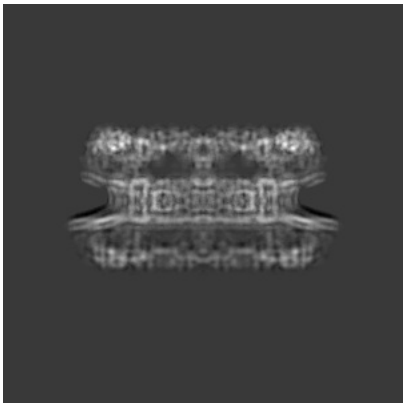
6 Map visualisation

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

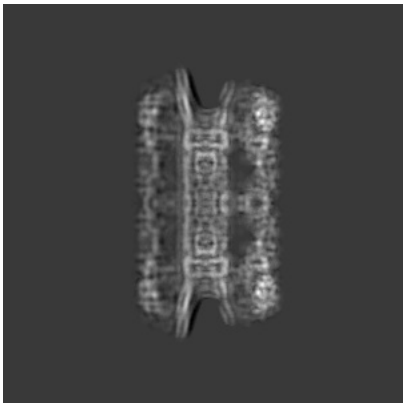
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

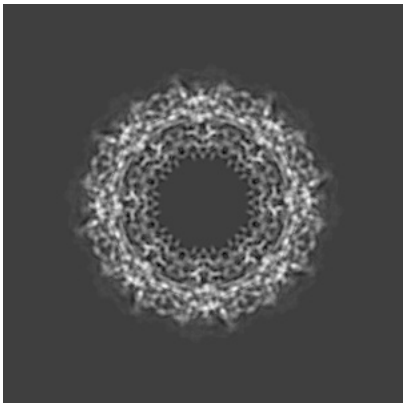
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices

6.2.1 Primary map

X Index: 288

Y Index: 288

Z Index: 288

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

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 404

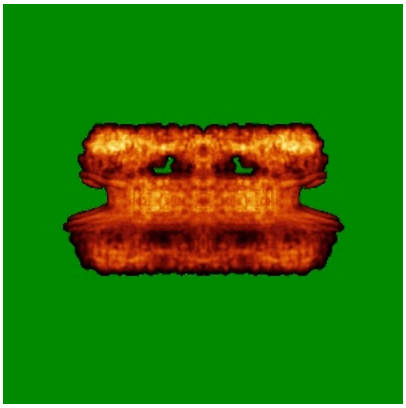
Y Index: 172

Z Index: 370

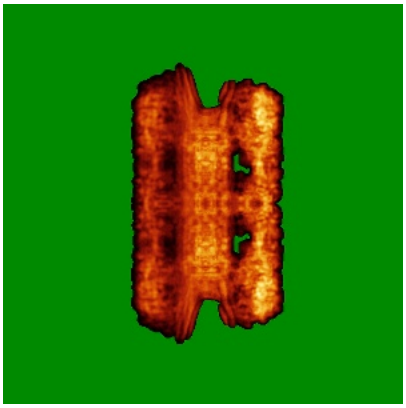
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

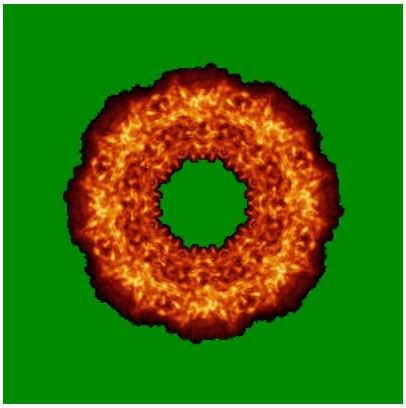
6.4.1 Primary map



X



Y

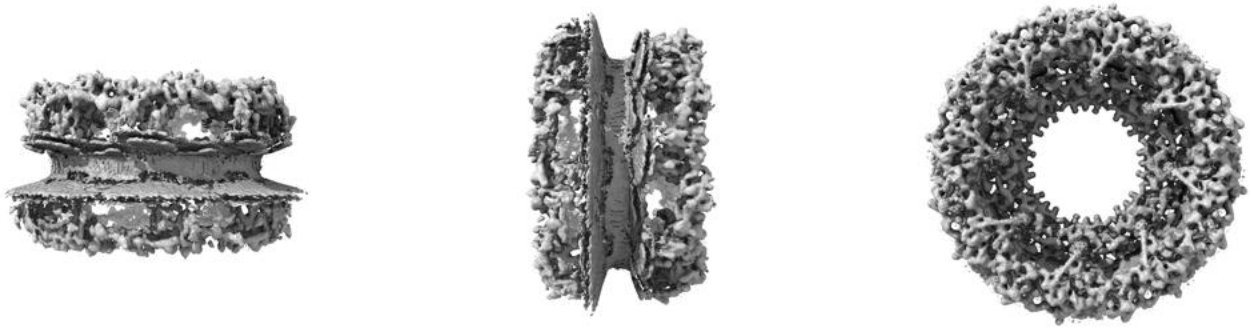


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

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

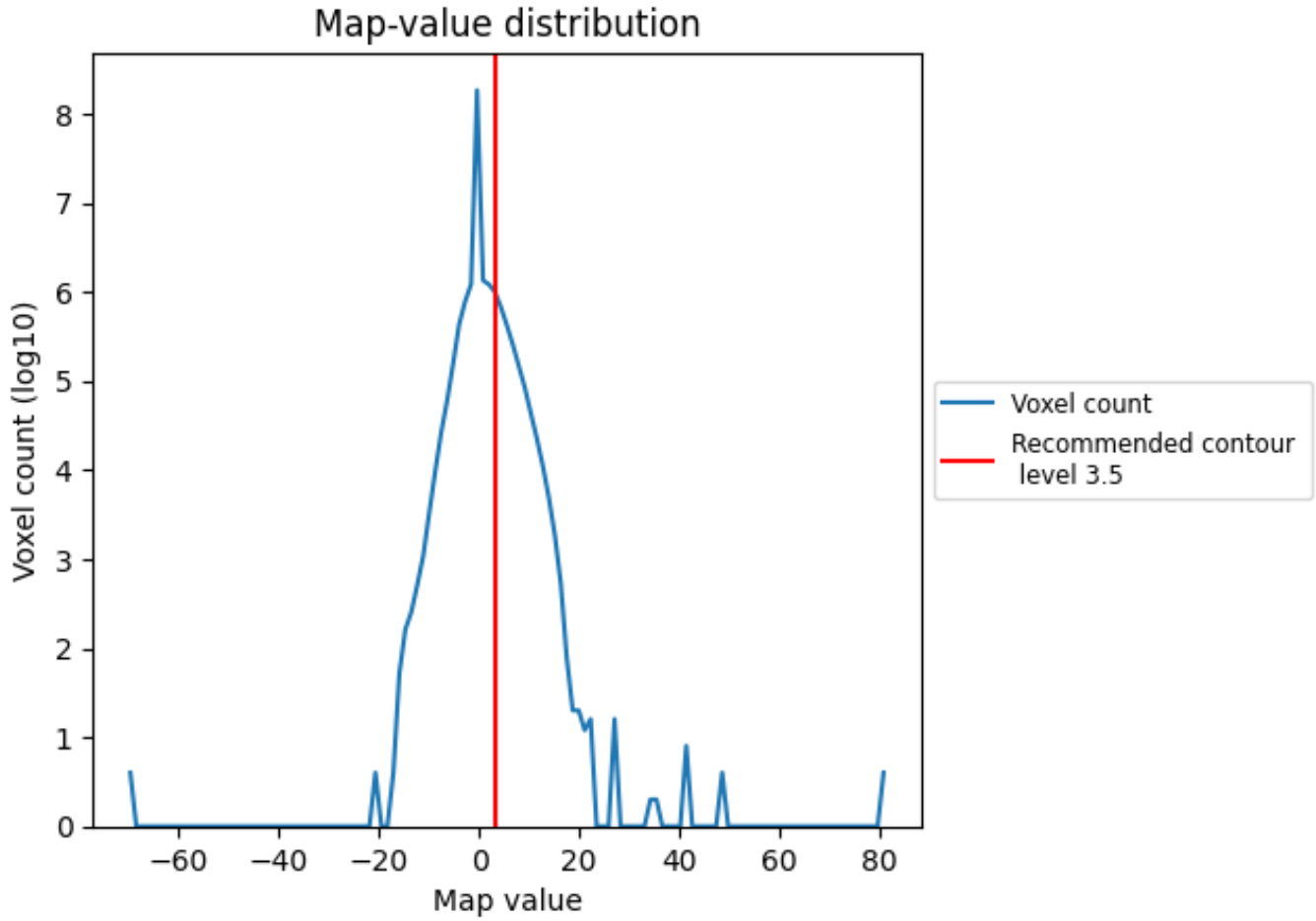
6.6 Mask visualisation (i)

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

7 Map analysis

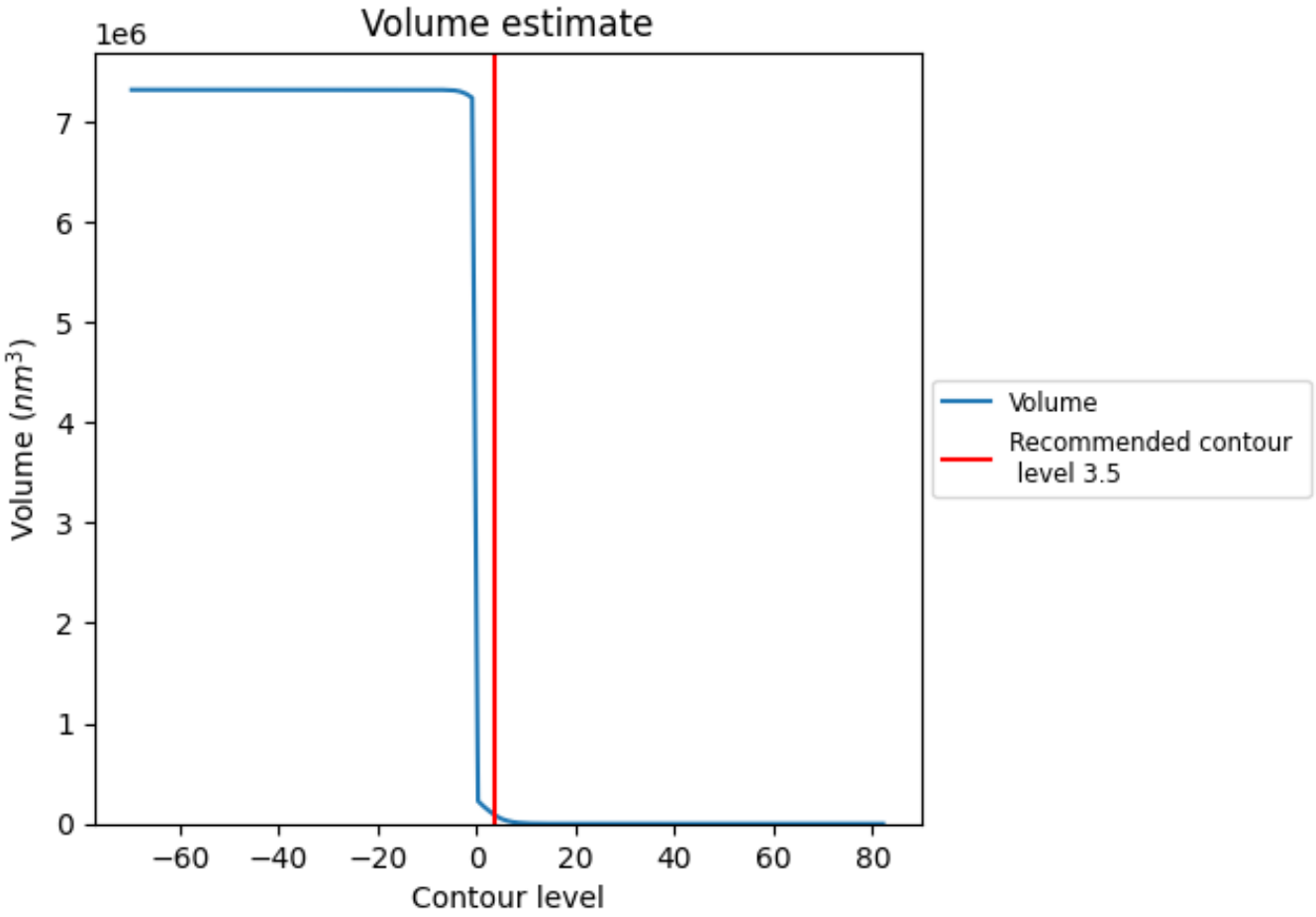
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

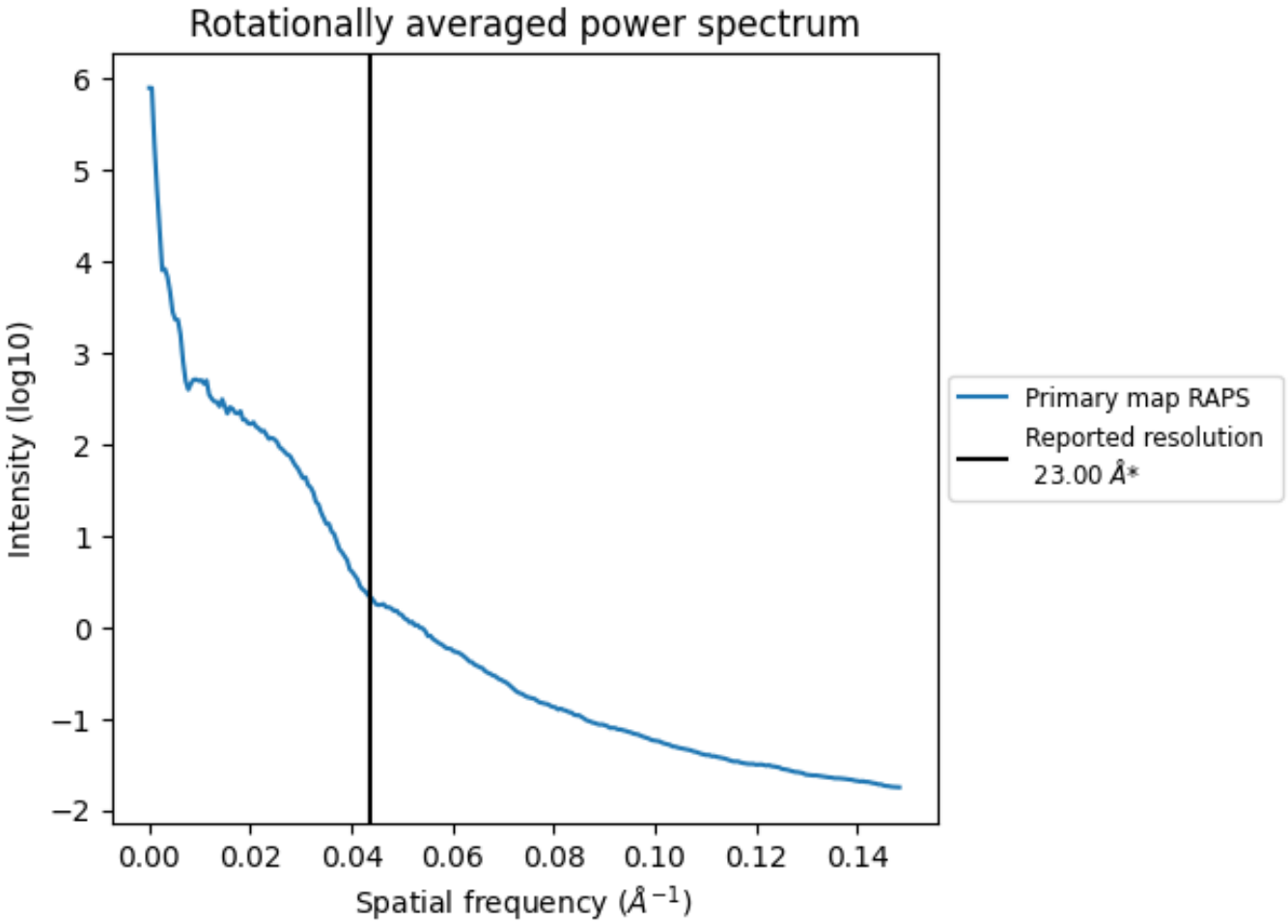
7.2 Volume estimate (i)



The volume at the recommended contour level is 93549 nm^3; this corresponds to an approximate mass of 84505 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.043 Å^{-1}

8 Fourier-Shell correlation

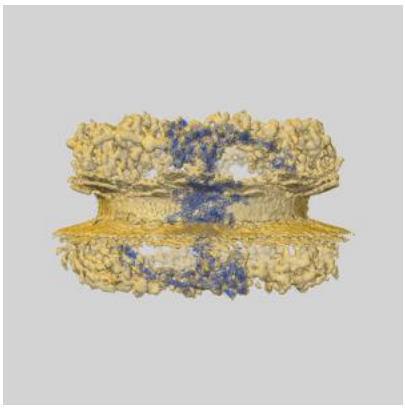
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

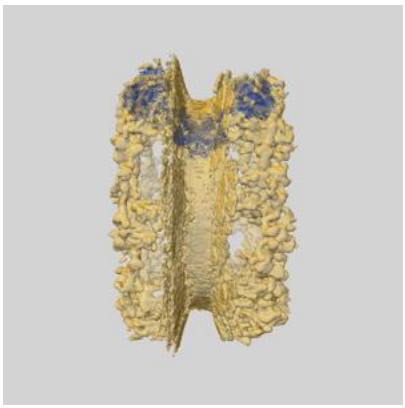
This section contains information regarding the fit between EMDB map EMD-14322 and PDB model 7TBJ. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlays

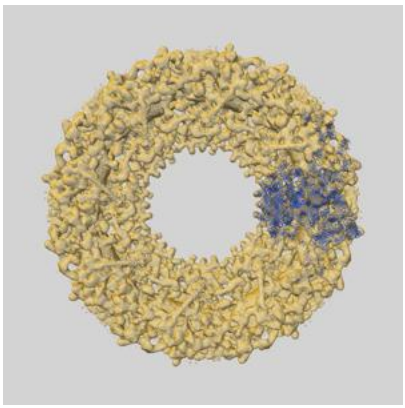
9.1.1 Map-model overlay



X

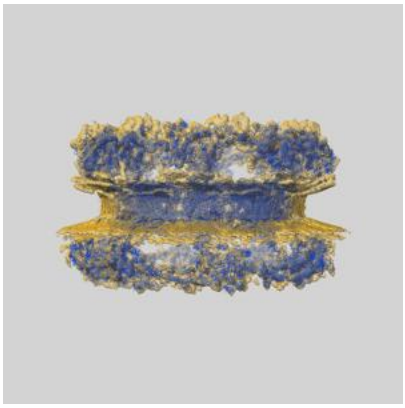


Y

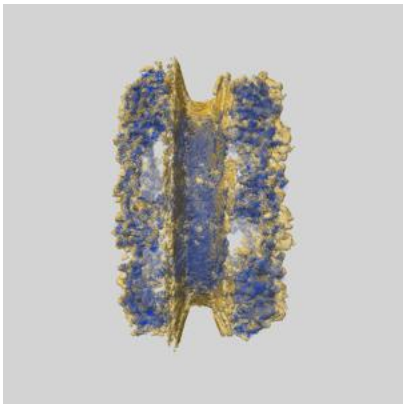


Z

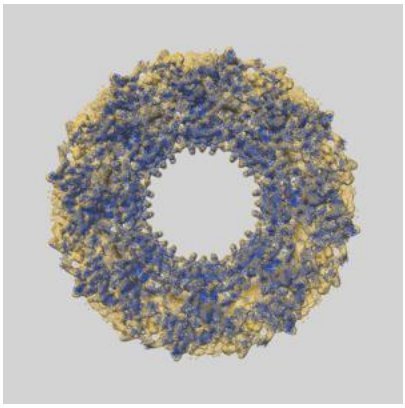
9.1.2 Map-model assembly overlay



X



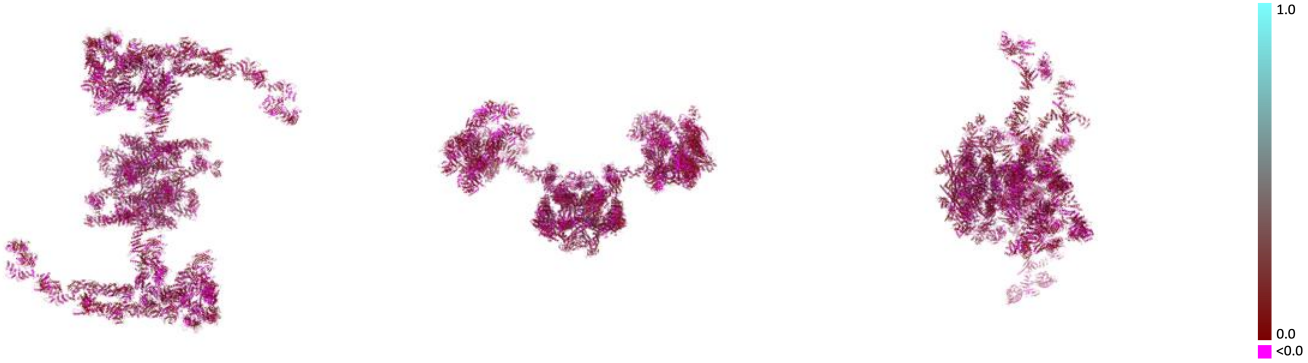
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.5 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.

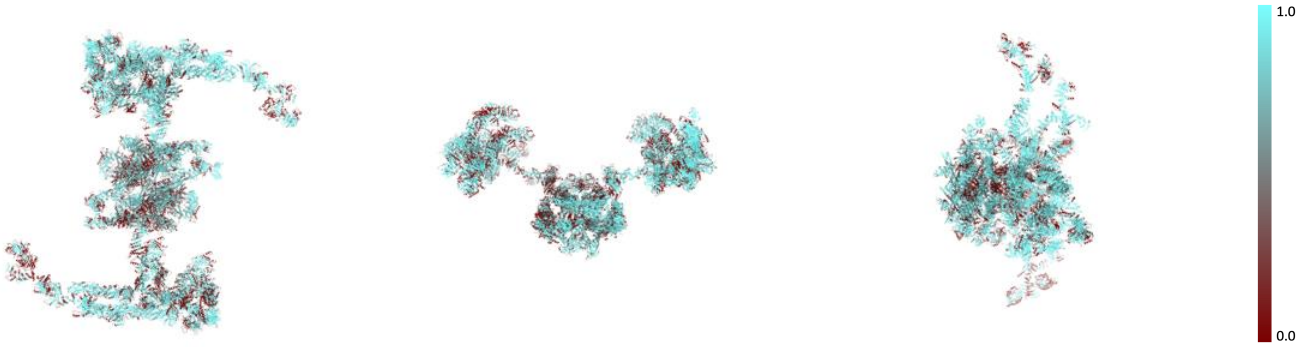
9.2 Q-score mapped to coordinate model



X Y Z

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.

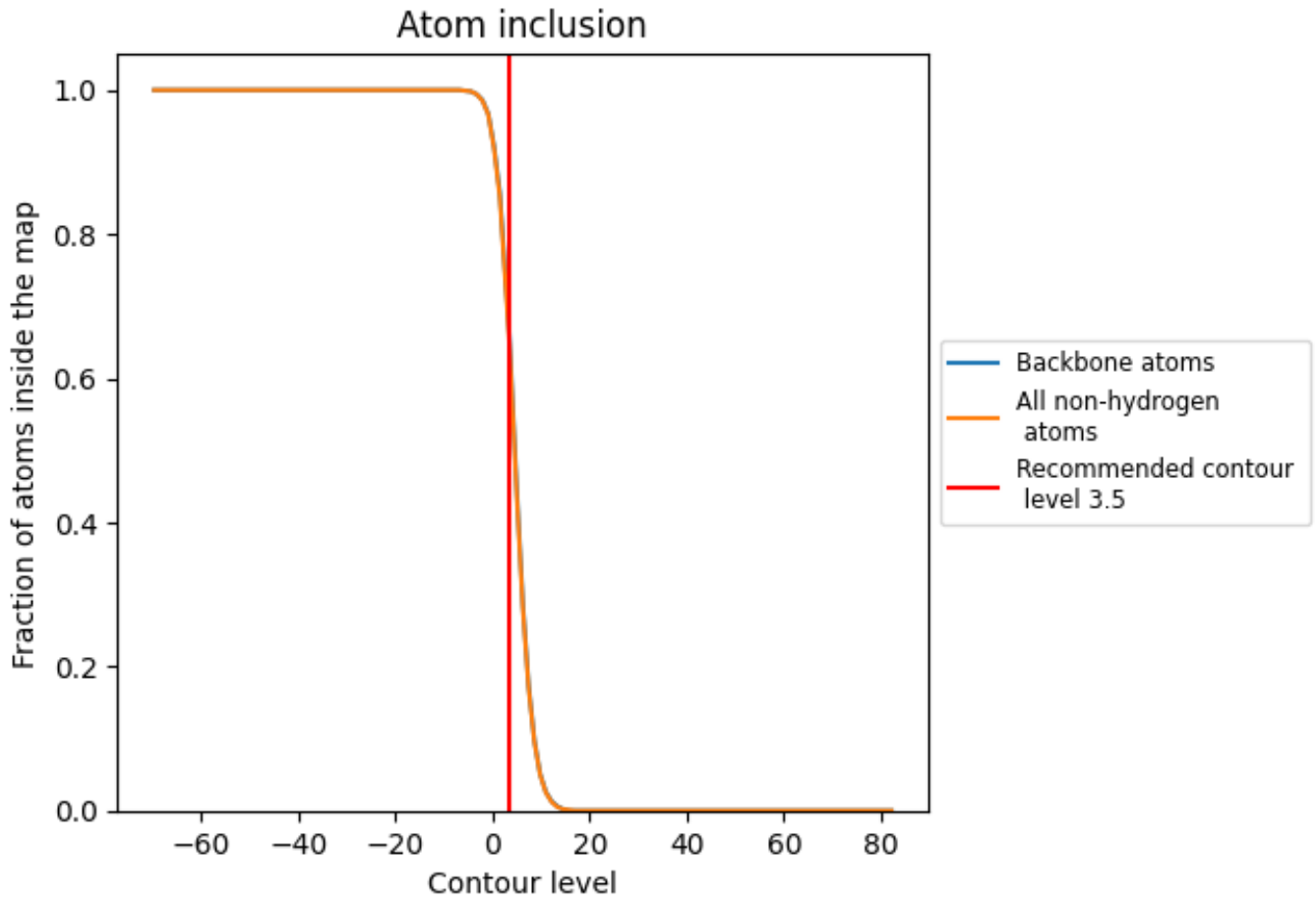
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (3.5).

9.4 Atom inclusion (i)



At the recommended contour level, 66% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6470	0.0380
A1	0.6920	0.0430
A2	0.3830	0.0190
A3	0.6640	0.0450
A4	0.4330	0.0280
A5	0.7310	0.0460
A6	0.4680	0.0430
B1	0.0000	-0.0460
B2	0.0090	-0.0370
B3	0.0000	0.0070
B4	0.0920	0.0130
B5	0.0830	-0.0330
B6	0.0090	-0.0100
C1	0.3530	0.0440
C2	0.5870	0.0120
C3	0.1180	0.0320
C4	0.3160	0.0530
C5	0.9560	0.0590
C6	0.4040	0.0310
D1	0.7760	0.0550
D2	0.7520	0.0520
D3	0.7200	0.0420
D4	0.4600	0.0450
D5	0.8300	0.0650
D6	0.7240	0.0560
D7	0.5020	0.0260
E1	0.6830	0.0250
E2	0.5000	-0.0320
E3	0.4000	0.0590
E4	0.2330	0.0450
E5	0.2830	-0.0510
E6	0.6500	-0.0050
E7	0.0170	-0.0360
F1	0.6830	0.0410
F2	0.5170	0.0400

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

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Chain	Atom inclusion	Q-score
Q3	0.9690	0.0810
Q4	0.9570	0.0660
R1	0.5880	0.0100
R2	0.6930	0.0350
R3	0.4690	0.0400
R4	0.5640	0.0110
S1	0.5780	0.0370
S2	0.6120	0.0320
S3	0.4210	0.0320
S4	0.4220	0.0280
T1	0.7540	0.0460
T2	0.7920	0.0580
T3	0.6970	0.0410
T4	0.7120	0.0520
U1	0.8160	0.0450
U2	0.8910	0.0620
U3	0.7920	0.0490
U4	0.7940	0.0550
V1	0.8960	0.0590
V2	0.8700	0.0560
V3	0.8050	0.0570
V4	0.7490	0.0440
W1	0.8670	0.0440
W2	0.7860	0.0340
W3	0.8110	0.0500
W4	0.6560	0.0230
X1	0.7950	0.0330
X2	0.8330	0.0380
X3	0.6600	0.0310
X4	0.5720	0.0220
Y1	0.6240	0.0280
Y2	0.6590	0.0230
Y3	0.5470	0.0220
Y4	0.5650	0.0250
Z1	0.6390	0.0160
Z2	0.7330	0.0240
Z3	0.4490	0.0190
Z4	0.5050	0.0200
a1	0.9260	0.0530
a2	0.7790	0.0430
a3	0.8270	0.0500
a4	0.7590	0.0490

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Chain	Atom inclusion	Q-score
b1	0.6780	0.0320
b2	0.5550	0.0240
b3	0.5230	0.0100
b4	0.5680	0.0180