wwPDB EM Validation Summary Report (i)

Jul 10, 2024 – 08:10 pm BST

PDB ID	:	7R5K
EMDB ID	:	EMD-14322
Title	:	Human nuclear pore complex (constricted)
Authors	:	Mosalaganti, S.; Obarska-Kosinska, A.; Siggel, M.; Taniguchi, R.; Turonova, B.; Zimmerli, C.E.; Buczak, K.; Schmidt, F.H.; Margiotta, E.; Mackmull, M.T.; Hagen, W.J.H.; Hummer, G.; Kosinski, J.; Beck, M.
Deposited on	:	2022-02-10
Resolution	:	12.00 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 (i) 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 (i)) were used in the production of this report:

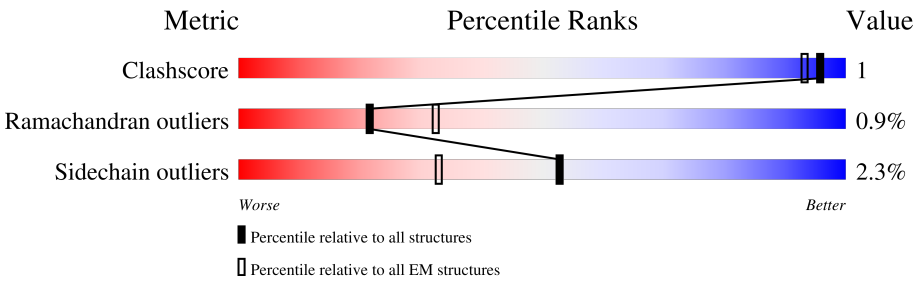
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 12.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	00	3224	5% 21% • 77%
1	01	3224	• 22% • 77%
1	02	3224	6% 22% • 77%
1	03	3224	• 22% • 77%
1	04	3224	5% 22% • 77%
2	10	1887	96% 92% 5% •
2	11	1887	96% 91% 5% •
2	12	1887	96% 91% 6% •

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Mol	Chain	Length	Quality of chain
2	13	1887	96% 92% 5%
2	14	1887	97% 92% 5%
2	15	1887	97% 92% 5%
2	16	1887	96% 92% 5%
2	17	1887	96% 92% 5%
3	40	546	25% 65% 5% 30%
3	41	546	17% 65% 5% 30%
4	A0	819	31% 89% 9%
4	A1	819	27% 90% 9%
4	A2	819	31% 90% 9%
4	A3	819	54% 91% 8%
4	A4	819	44% 80% 8% 11%
4	A5	819	24% 81% 7% 11%
4	A6	819	36% 81% 7% 11%
5	B0	1749	26% 94% 6%
5	B1	1749	44% 94% 6%
6	C0	2012	33% 93% 7%
6	C1	2012	35% 93% 7%
6	C2	2012	20% 93% 6%
6	C3	2012	19% 91% 8%
6	C4	2012	39% 93% 6%
7	D0	1391	36% 87% 7% 6%
7	D1	1391	65% 85% 8% 6%
7	D2	1391	38% 87% 7% 6%
7	D3	1391	64% 86% 7% 6%

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Mol	Chain	Length	Quality of chain
7	D4	1391	34% 87% 7% 6%
7	D5	1391	56% 86% 8% 6%
8	E0	674	50% 77% 19%
8	E1	674	38% 78% 19%
9	F0	326	44% 58% 14% 26%
9	F1	326	35% 65% 8% 26%
9	F2	326	42% 61% 10% 26%
9	F3	326	41% 63% 9% 26%
10	H0	507	25% 70% 6% 24%
10	H1	507	24% 70% 5% 24%
10	H2	507	21% 71% 5% 24%
10	H3	507	22% 70% 6% 24%
11	I0	599	10% 27% 71%
11	I1	599	28% 71%
11	I2	599	10% 28% 71%
11	I3	599	28% 71%
12	J0	522	6% 31% 67%
12	J1	522	10% 31% 67%
12	J2	522	6% 31% 67%
12	J3	522	11% 31% 67%
12	J4	522	19% 31% 67%
13	K0	1156	31% 86% 8% 6%
13	K1	1156	32% 87% 7% 6%
13	K2	1156	51% 87% 7% 6%
13	K3	1156	48% 86% 7% 6%

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Mol	Chain	Length	Quality of chain
14	L0	925	10% 78% 6% 15%
14	L1	925	18% 77% 7% • 15%
14	L2	925	25% 78% 6% 15%
14	L3	925	23% 78% 5% • 15%
15	M0	937	10% 65% 6% • 28%
15	M1	937	9% 65% 6% • 28%
15	M2	937	17% 65% 6% • 28%
15	M3	937	15% 66% 6% • 28%
16	N0	322	14% 87% 7% 7%
16	N1	322	6% 88% 5% 7%
16	N2	322	30% 89% 5% 7%
16	N3	322	13% 88% 6% 7%
17	O0	360	• 84% 6% • 10%
17	O1	360	17% 84% 5% 10%
17	O2	360	18% 83% 6% 10%
17	O3	360	27% 82% 7% 10%
18	P0	656	16% 91% 8%
18	P1	656	21% 91% 8% •
18	P2	656	27% 92% 7% •
18	P3	656	32% 92% 7% •
19	Q0	380	15% 87% • 9%
19	Q1	380	8% 88% • 9%
19	Q2	380	27% 86% • 9%
19	Q3	380	16% 88% • 9%
20	R0	1436	16% 89% 8% •

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Mol	Chain	Length	Quality of chain
20	R1	1436	22% 89% 7%
20	R2	1436	37% 89% 8%
20	R3	1436	44% 90% 7%
21	S0	326	40% 93% 6%
21	S1	326	22% 93% 5%
21	S2	326	41% 93% 5%
21	S3	326	36% 92% 6%
22	T0	2266	25% 41% 56%
22	T1	2266	35% 42% 56%
23	U0	880	14% 15% 83%
23	U1	880	98%
23	U2	880	98%
23	U3	880	98%
23	U4	880	98%
23	U5	880	98%
23	U6	880	98%
24	V0	2090	8% 12% 87%
25	W0	741	46% 91% 8%

2 Entry composition (i)

There are 25 unique types of molecules in this entry. The entry contains 617133 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 E3 SUMO-protein ligase RanBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	00	756	6085	3866	1045	1147	27	0	0
1	01	756	6085	3866	1045	1147	27	0	0
1	02	756	6085	3866	1045	1147	27	0	0
1	03	756	6085	3866	1045	1147	27	0	0
1	04	756	6085	3866	1045	1147	27	0	0

- Molecule 2 is a protein called Nuclear pore membrane glycoprotein 210.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	10	1831	14046	8947	2406	2644	49	0	0
2	11	1831	14046	8947	2406	2644	49	0	0
2	12	1831	14046	8947	2406	2644	49	0	0
2	13	1831	14046	8947	2406	2644	49	0	0
2	14	1831	14046	8947	2406	2644	49	0	0
2	15	1831	14046	8947	2406	2644	49	0	0
2	16	1831	14046	8947	2406	2644	49	0	0
2	17	1831	14046	8947	2406	2644	49	0	0

- Molecule 3 is a protein called Aladin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	40	383	2922	1864	509	533	16	0	0
3	41	383	2922	1864	509	533	16	0	0

- Molecule 4 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A0	818	6568	4136	1145	1259	28	0	0
4	A1	818	6568	4136	1145	1259	28	0	0
4	A2	818	6568	4136	1145	1259	28	0	0
4	A3	818	6568	4136	1145	1259	28	0	0
4	A4	726	5860	3705	1018	1109	28	0	0
4	A5	726	5860	3705	1018	1109	28	0	0
4	A6	726	5860	3705	1018	1109	28	0	0

- Molecule 5 is a protein called Nucleoporin NUP188 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B0	1748	13746	8743	2353	2559	91	0	0
5	B1	1748	13746	8743	2353	2559	91	0	0

- Molecule 6 is a protein called Nuclear pore complex protein Nup205.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C0	2011	16013	10208	2753	2965	87	0	0
6	C1	2011	16013	10208	2753	2965	87	0	0
6	C2	2011	16013	10208	2753	2965	87	0	0
6	C3	2011	16013	10208	2753	2965	87	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C4	2011	16013	10208	2753	2965	87	0	0

- Molecule 7 is a protein called Nuclear pore complex protein Nup155.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	D0	1312	10363	6569	1786	1949	59	0	0
7	D1	1312	10363	6569	1786	1949	59	0	0
7	D2	1312	10363	6569	1786	1949	59	0	0
7	D3	1312	10363	6569	1786	1949	59	0	0
7	D4	1312	10363	6569	1786	1949	59	0	0
7	D5	1312	10363	6569	1786	1949	59	0	0

- Molecule 8 is a protein called Nucleoporin NDC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	E0	548	4432	2923	729	758	22	0	0
8	E1	548	4432	2923	729	758	22	0	0

- Molecule 9 is a protein called Nucleoporin NUP35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F0	241	1837	1154	313	359	11	0	0
9	F1	241	1837	1154	313	359	11	0	0
9	F2	241	1837	1154	313	359	11	0	0
9	F3	241	1837	1154	313	359	11	0	0

- Molecule 10 is a protein called Nucleoporin p54.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	H0	383	3066	1921	544	592	9	0	0
10	H1	383	3066	1921	544	592	9	0	0
10	H2	383	3066	1921	544	592	9	0	0
10	H3	383	3066	1921	544	592	9	0	0

- Molecule 11 is a protein called Nucleoporin p58/p45.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	I0	173	1398	881	245	267	5	0	0
11	I1	173	1398	881	245	267	5	0	0
11	I2	173	1398	881	245	267	5	0	0
11	I3	173	1398	881	245	267	5	0	0

- Molecule 12 is a protein called Nuclear pore glycoprotein p62.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	J0	171	1403	872	243	285	3	0	0
12	J1	171	1403	872	243	285	3	0	0
12	J2	171	1403	872	243	285	3	0	0
12	J3	171	1403	872	243	285	3	0	0
12	J4	171	1403	872	243	285	3	0	0

- Molecule 13 is a protein called Nuclear pore complex protein Nup133.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	K0	1086	8574	5420	1425	1692	37	0	0
13	K1	1086	8574	5420	1425	1692	37	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	K2	1086	8574	5420	1425	1692	37	0	0
13	K3	1086	8574	5420	1425	1692	37	0	0

- Molecule 14 is a protein called Nuclear pore complex protein Nup107.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	L0	782	6383	4064	1079	1208	32	0	0
14	L1	782	6383	4064	1079	1208	32	0	0
14	L2	782	6383	4064	1079	1208	32	0	0
14	L3	782	6383	4064	1079	1208	32	0	0

- Molecule 15 is a protein called Nuclear pore complex protein Nup96.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	M0	673	5461	3467	964	1004	26	0	0
15	M1	673	5461	3467	964	1004	26	0	0
15	M2	673	5461	3467	964	1004	26	0	0
15	M3	673	5461	3467	964	1004	26	0	0

- Molecule 16 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	N0	301	2352	1479	409	452	12	0	0
16	N1	301	2352	1479	409	452	12	0	0
16	N2	301	2352	1479	409	452	12	0	0
16	N3	301	2352	1479	409	452	12	0	0

- Molecule 17 is a protein called Nucleoporin SEH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	O0	323	2528	1584	452	475	17	0	0
17	O1	323	2528	1584	452	475	17	0	0
17	O2	323	2528	1584	452	475	17	0	0
17	O3	323	2528	1584	452	475	17	0	0

- Molecule 18 is a protein called Nuclear pore complex protein Nup85.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	P0	655	5257	3341	898	982	36	0	0
18	P1	655	5257	3341	898	982	36	0	0
18	P2	655	5257	3341	898	982	36	0	0
18	P3	655	5257	3341	898	982	36	0	0

- Molecule 19 is a protein called Nucleoporin Nup43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	Q0	345	2703	1690	474	527	12	0	0
19	Q1	345	2703	1690	474	527	12	0	0
19	Q2	345	2703	1690	474	527	12	0	0
19	Q3	345	2703	1690	474	527	12	0	0

- Molecule 20 is a protein called Nuclear pore complex protein Nup160.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	R0	1399	11132	7093	1878	2088	73	0	0
20	R1	1399	11132	7093	1878	2088	73	0	0
20	R2	1399	11132	7093	1878	2088	73	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	R3	1399	11132	7093	1878	2088	73	0	0

- Molecule 21 is a protein called Nucleoporin Nup37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	S0	322	2552	1626	436	475	15	0	0
21	S1	322	2552	1626	436	475	15	0	0
21	S2	322	2552	1626	436	475	15	0	0
21	S3	322	2552	1626	436	475	15	0	0

- Molecule 22 is a protein called Protein ELYS.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	T0	1004	7960	5069	1359	1490	42	0	0
22	T1	1004	7960	5069	1359	1490	42	0	0

- Molecule 23 is a protein called Nuclear pore complex protein Nup98.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	U0	150	1193	756	205	229	3	0	0
23	U1	19	Total	C	N	O		0	0
			151	98	27	26			
23	U2	19	Total	C	N	O		0	0
			151	98	27	26			
23	U3	19	Total	C	N	O		0	0
			151	98	27	26			
23	U4	19	Total	C	N	O		0	0
			151	98	27	26			
23	U5	19	Total	C	N	O		0	0
			151	98	27	26			
23	U6	19	Total	C	N	O		0	0
			151	98	27	26			

- Molecule 24 is a protein called Nuclear pore complex protein Nup214.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	V0	273	2203	1376	398	423	6	0	0

- Molecule 25 is a protein called Nuclear pore complex protein Nup88.

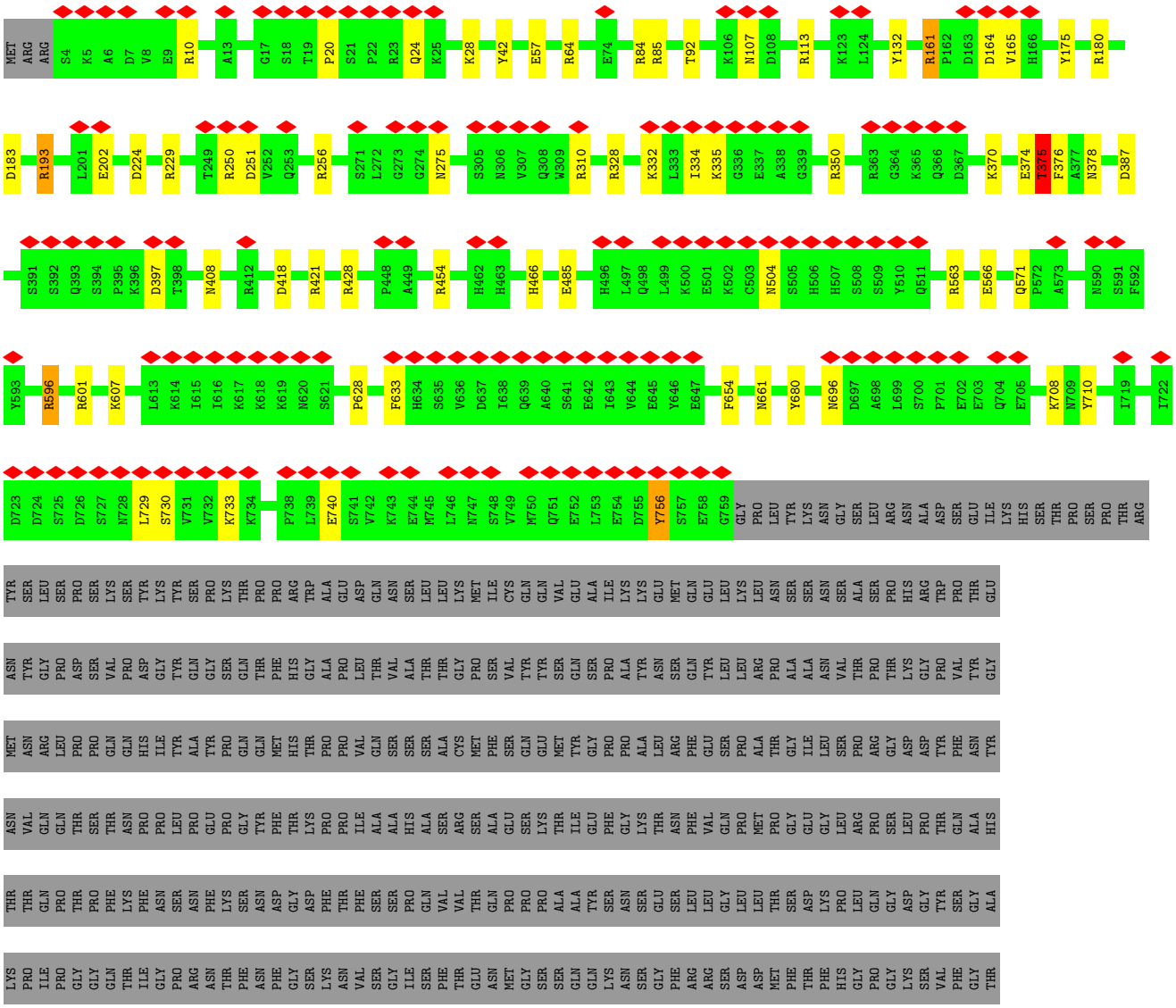
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	W0	735	5836	3714	988	1103	31	0	0

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: E3 SUMO-protein ligase RanBP2

Chain 00:



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R454 H466 E485 N504 A543 A549 L553 R563 E566 Q571 Y593 R596 R601 K607 K619 I626 D627 P628 F633 Q639 A640 S641 F654 N661 K675 Y680 H688 N696 K708 N709 Y710 L711 R712 R715 D716
I719 K720 I721 I722 D723 D724 S725 D726 S727 N728 L729 S730 V731 V732 K733 K734 L735 P736 V737 F738 L739 E740 S741 V742 K743 E744 N745 L746 N747 M750 Q751 E752 L753 E754 D755 Y756 S757 E758 G759
GLY PRO LEU TYR LYS ASN GLY SER LEU ARG ASN ALA ASP SER GLU ILE LYS HIS SER
THR PRO SER PRO THR ARG TYR SER LEU SER PRO SER LYS SER TYR LYS TYR SER PRO LYS THR PRO PRO ARG TRP ALA GLU ASP GLN ASN SER LEU LEU LYS MET ILE CYS GLN GLN VAL GLU ALA ILE LYS LYS GLU MET GLN GLU LEU LYS LEU ASN SER SER ALA ALA SER PRO
HIS ARG TRP PRO THR GLU ASN TYR GLY PRO ASP SER VAL PRO ASP GLY TYR GLN GLY SER GLN THR PHE HIS GLY ALA PRO LEU THR VAL ALA THR THR LYS SER GLN TYR TYR SER GLN SER PRO ALA TYR ASN SER GLN TYR LEU LEU ARG PRO ALA ALA ASN VAL THR PRO THR
LYS GLY PRO VAL TYR GLY MET ASN ARG LEU PRO PRO PRO GLN HIS ILE TYR ALA TYR PRO PRO GLN GLN MET HIS THR PRO PRO VAL GLN SER SER SER ALA CYS MET PHE SER GLN GLU MET TYR GLY PRO PRO ALA LEU ARG PHE GLU SER PRO ALA THR GLY ILE LEU SER PRO ARG GLY
ASP ASP TYR PHE ASN TYR ASN VAL GLN GLN THR SER THR ASN PRO PRO LEU PRO GLU PRO GLY TYR PHE THR LYS PRO PRO ILE ALA ALA HIS SER ARG SER ALA GLU SER LYS THR ILE ALA GLU PHE GLY LYS THR ASN PHE VAL GLN SER SER ALA LEU PRO GLU GLY LEU ARG PRO SER
LEU PRO THR GLN ALA HIS THR THR GLN PRO THR PRO PHE LYS PHE ASN SER ASN PHE LYS SER ASN ASP GLY ASP PHE THR PHE SER SER PRO GLN VAL VAL THR GLN PRO PRO PRO ALA ALA TYR SER ASN SER GLU SER LEU LEU GLY LEU LEU THR SER ASP LYS PRO LEU GLN GLY
ASP GLY TYR SER GLY ALA LYS PRO ILE PRO GLY GLY GLN THR ILE GLY PRO ARG ASN THR PHE ASN PHE GLY SER LYS ASN VAL SER GLY ILE SER PHE THR GLU ASN MET GLY SER SER GLN GLN LYS ASN SER GLY PHE ARG ARG SER ASP ASP MET PHE THR PHE HIS GLY PRO GLY
LYS SER VAL PHE GLY THR PRO THR LEU GLU THR ALA ASN LYS ASN HIS GLU THR ASP GLY GLY SER ALA HIS GLY ASP ASP ASP ASP ASP GLY PRO HIS PHE GLU PRO VAL PRO LEU PRO PRO ASP LYS ILE ILE GLU VAL LYS THR GLY GLU GLU ASP GLU GLU THR ASN ARG
ALA LYS LEU PHE ARG PHE ASP VAL GLU SER LYS GLU TRP LYS GLU ARG GLY ILE GLY ASN VAL LYS ILE LEU ARG HIS LYS THR SER GLY LYS ILE ARG LEU LEU MET ARG ARG GLU GLN VAL LEU LYS ILE CYS ALA ASN HIS TYR ILE SER PRO ASP MET LYS LEU THR PRO ASN ALA
GLY SER ASP ARG SER PHE VAL TRP HIS ALA LEU ASP TYR ALA ASP GLU LEU PRO LYS PRO GLU GLN LEU ALA ILE ARG PHE LYS THR PRO GLU GLU GLU ALA ALA LEU PHE LYS CYS LYS PHE GLU GLU ALA GLN SER ILE LEU LYS ALA ALA THR GLY GLU ASN VAL ALA ALA THR ASN ASN GLN
ALA VAL ARG ILE VAL LYS GLU PRO THR SER HIS ASP ASN LYS ASP ILE CYS LYS SER ASP ALA GLY ASN LEU ASN PHE GLU PHE GLN VAL ALA LYS LYS GLU GLU GLY SER TRP TRP HIS CYS ASN SER CYS SER LEU LYS ASN ALA SER THR ALA LYS LYS CYS VAL SER CYS ASN GLN LEU
ASN PRO SER ASN LYS GLU LEU VAL GLY PRO PRO LEU ALA GLU THR VAL PHE THR PRO LYS THR SER PRO GLU ASN VAL GLN ASP ARG PHE ALA LEU VAL THR PRO LYS LYS GLU GLY HIS TRP ASP CYS SER ILE CYS LEU VAL ARG ASN GLU PRO THR VAL SER ARG CYS ILE ALA CYS
GLN ASN THR LYS SER ALA ASN LYS SER GLY GLN GLY GLY ASP LEU PRO LYS SER ASN ILE ASN SER SER SER PHE LYS PHE GLY GLN GLY GLU GLY GLN TRP ASP CYS SER ALA ASN ASP LEU LYS SER THR LYS SER SER LEU VAL LYS ASN SER ALA LEU CYS ASP LYS SER SER LYS
CYS ALA ALA CYS GLN ASN PRO ARG LYS GLN SER LEU PRO ALA ALA THR SER ILE PRO THR PRO ALA SER PHE LYS PHE GLY THR SER GLU THR SER LYS THR LEU LYS SER GLY PHE GLU ASP MET PHE ALA LYS LYS GLU GLY GLN TRP ASP CYS SER SER CYS LEU VAL ARG ASN GLU ALA
ASN ALA THR ARG CYS VAL ALA CYS GLN ASN PRO ASP LYS PRO SER PRO SER ALA PRO ALA SER PHE LYS PHE GLY THR SER GLU THR SER LYS ALA PRO LYS SER GLY PHE GLU GLY MET PHE THR LYS LYS GLU GLY GLN TRP ASP CYS SER VAL SER VAL CYS ARG
ASN GLU ALA SER ALA THR LYS CYS ILE ALA CYS GLN ASN PRO GLY LYS LYS GLN ASN GLN THR THR SER ALA ALA VAL SER THR PRO ALA SER SER GLU THR SER LYS ALA PRO LYS SER GLY PHE GLU GLY MET PHE THR LYS LYS GLU GLY GLN TRP ASP CYS SER VAL VAL CYS LEU VAL ARG ASN
GLU ALA SER ALA THR LYS CYS ILE ALA CYS GLN CYS PRO SER LYS GLN ASN GLN THR THR SER ALA ALA VAL SER THR PRO ALA SER SER GLU THR SER LYS ALA PRO LYS SER GLY PHE GLU GLY MET PHE THR LYS LYS GLU GLY GLN TRP ASP CYS SER VAL CYS LEU VAL ARG ASN GLU
ALA SER ALA THR LYS CYS PRO PRO THR HIS LYS GLY PHE GLN GLN GLY SER SER GLU ILE SER LYS ALA PRO LYS SER SER GLY PHE GLU GLY MET PHE ILE ARG LYS GLY GLN TRP ASP CYS SER VAL CYS SER GLU GLN GLY SER ASN PHE SER GLU LYS ALA SER LYS PHE GLY ASN THR GLY PHE LYS SER ASN GLU MET LYS LEU HIS ASP SER SER GLY GLN VAL GLY THR GLY PHE GLU GLN GLN GLU GLU GLU GLN GLN LYS ASN SER GLY PHE ARG ARG SER ASP ASP MET PHE THR PHE HIS GLY PRO GLY

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SER LYS GLU THR ASN PRO VAL VAL PHE PHE ASP VAL CYS ALA ASP GLY GLU PRO LEU GLY ARG ILE THR MET GLU LEU PHE SER ASN ILE VAL PRO ARG THR ALA GLU ASN PHE ARG ALA LEU CYS THR GLY GLU LYS GLY PHE GLY PHE LYS ASN SER ILE PHE HIS ARG VAL ILE PRO

ASP PHE VAL CYS GLN GLY GLY ASP ILE THR LYS HIS ASP GLY THR GLY GLY GLN SER ILE TYR GLY ASP LYS PHE GLU ASP GLU ASN PHE ASP VAL LYS HIS THR GLY PRO GLY LEU LEU SER MET ALA ASN GLN GLY GLN ASN THR ASN ASN SER GLN PHE VAL ILE THR LEU LYS LYS

ALA GLU HIS LEU ASP PHE LYS HIS VAL VAL PHE GLY PHE VAL LYS ASP GLY MET ASP THR VAL LYS LYS ILE GLU SER PHE GLY SER PRO LYS GLY SER VAL CYS ARG ARG ILE THR ILE THR GLU CYS GLY GLN ILE

- Molecule 1: E3 SUMO-protein ligase RanBP2

Chain 02: 6% 22% 77%

MET ARG ARG S4 K5 A6 R10 A13 S14 V15 Q16 G17 S18 T19 P20 S21 P22 R23 K40 E41 Y42 R58 R64 D77 R85 E88 L89 N90 P91 T92 Q93 K94 D95 E102 N107 T110 D111 G112 R113 Y116 K123 L124 F125 P126 G127 S128 P129

Y132 E144 D145 Y159 V160 R161 P162 D163 D164 V165 R170 R180 D183 E190 R193 N194 I195 A196 E202 Q219 C220 L221 E222 S223 D224 K225 S226 R229 R250 D251 R256 S271 L272 G273 G274 N275 D276 E277 L278 S279 S305 N306 R310

R328 P329 K330 I331 K332 L333 I334 K335 G336 E337 A338 G339 Q340 N341 R350 G364 K365 Q366 D367 K370 E374 N378 K379 S380 S392 Q393 S394 P395 K396 D397 T398 S403 D404 D405 I406 G407 N408 I409 D410 V411 R412 E415 L416 E417 D418 R421 R428 L447 P448

A449 R454 H466 S469 R470 E485 N504 S505 H506 C520 E526 R527 Q528 K529 S530 D533 T537 K542 A543 V544 P545 G546 N547 V548 A549 K550 L551 L554 R563 E566 K567 R601 K607 L610 L613 K614 I615 I616 K617 K618 K619 N620 S621

I622 P623 I626 D627 S635 V636 D637 I638 Q639 A640 S641 E642 I643 V644 E645 Y646 E647 E648 D649 F654 N663 D666 S673 I674 K675 S676 V677 Y680 D697 S700 P701 E702 K708 N709 Y710 I722 D723 D724 S725 D726 S727 N728 L729 S730 V731 V732 K733 K734 L735

P738 L739 E740 Y756 S757 E758 G759 GLY PRO LEU TYR LYS ASN GLY SER LEU ARG ASN ALA ASP SER GLU ILE LYS HIS SER THR PRO SER PRO THR ARG TRP TYR SER LEU SER PRO SER LYS SER TYR LYS TYR SER PRO LYS THR PRO PRO ARG TRP ALA GLU ASP GLN ASN SER LEU

LEU LYS MET ILE CYS GLN GLN VAL GLU ALA ILE LYS LYS GLU MET GLN GLU LEU LYS LEU ASN SER SER ASN SER ALA SER PRO HIS ARG TRP PRO THR GLU ASN TYR GLY PRO ASP SER VAL PRO ASP GLY TYR GLN GLY SER GLN THR PHE HIS GLY ALA PRO LEU THR VAL ALA THR

THR GLY PRO SER VAL TYR TYR SER GLN SER PRO ALA TYR ASN SER GLN TYR LEU LEU ARG PRO ALA ARG THR PRO THR LYS GLY PRO VAL TYR GLY MET ASN ARG LEU PRO PRO GLN GLN HIS ILE TYR ALA TYR PRO GLN GLN MET HIS THR PRO PRO VAL GLN SER SER SER

ALA CYS MET PHE SER GLN GLU MET TYR GLY PRO PRO ALA LEU ARG PHE GLU SER PRO ALA THR GLY ILE LEU SER PRO ARG GLY ASP ASP TYR PHE ASN TYR ASN VAL GLN GLN THR SER THR ASN PRO PRO LEU PRO GLU PRO GLY TYR PHE THR LYS PRO PRO ILE ALA ALA HIS ALA

SER ARG SER ALA GLU SER LYS THR ILE GLU PHE GLY LYS THR ASN PHE VAL GLN PRO MET PRO GLY GLU GLY LEU ARG PRO SER LEU PRO THR GLN ALA HIS THR THR GLN PRO THR PRO PHE LYS PHE ASN SER ASN PHE LYS SER ASN ASP PHE THR PHE SER GLY ASP PHE THR PRO VAL GLN

VAL VAL THR GLN PRO PRO PRO ALA ALA TYR SER ASN SER GLU SER LEU LEU GLY LEU LEU THR SER ASP LYS PRO LEU GLN GLY ASP GLY TYR SER ASN GLY TYR SER GLY ALA LYS PRO ILE PRO GLY GLY GLN THR ILE GLY PRO ARG ASN THR PHE ASN PHE GLY SER LYS ASN VAL SER GLY ILE SER

PHE THR GLU ASN MET GLY SER SER GLN GLN LYS ASN SER GLY GLY ASP HIS GLY PRO GLY LYS SER VAL PHE GLY THR PRO THR LEU GLU THR ALA ASN LYS ASN HIS GLU THR ASP GLY GLY SER ALA HIS GLY ASP PHE THR PHE ASP ASP ASP ASP GLY ILE PRO

HIS PHE GLU PRO VAL VAL PRO LEU PRO ASP LYS ILE GLU VAL LYS THR GLY GLU GLU ASP GLU GLU GLU PHE PHE CYS ASN ARG ALA LYS LEU PHE ARG PHE ASP VAL GLU SER LYS GLU TRP LYS GLU ARG GLY ILE GLY ASN VAL LYS ILE ARG HIS LYS THR SER GLY LYS ILE

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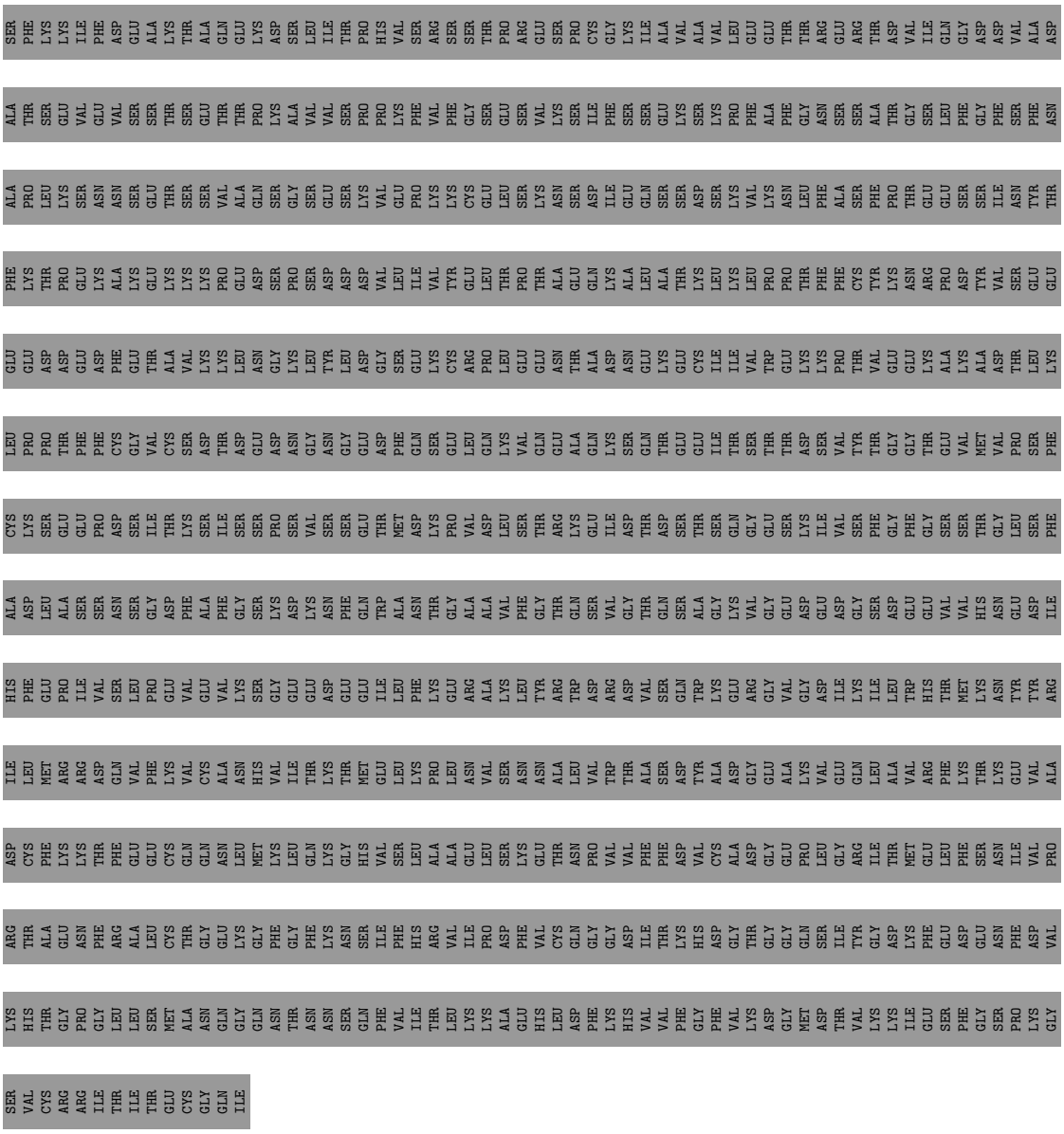
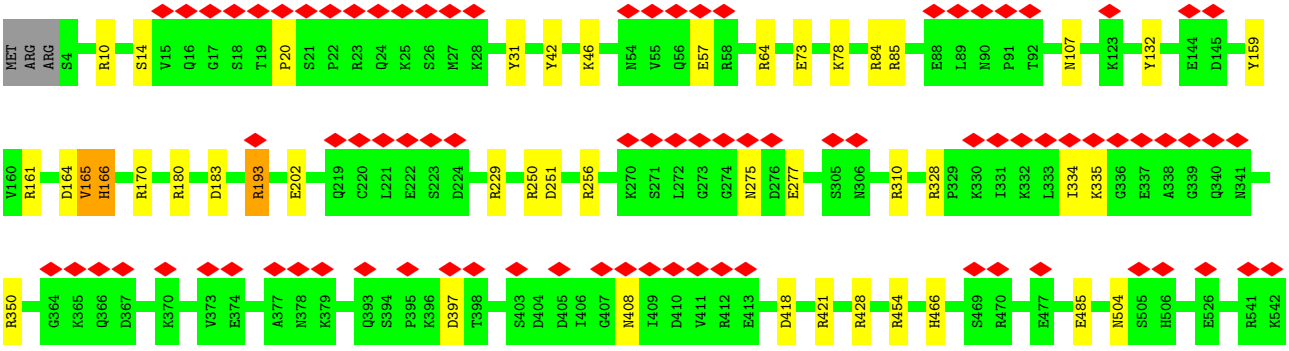
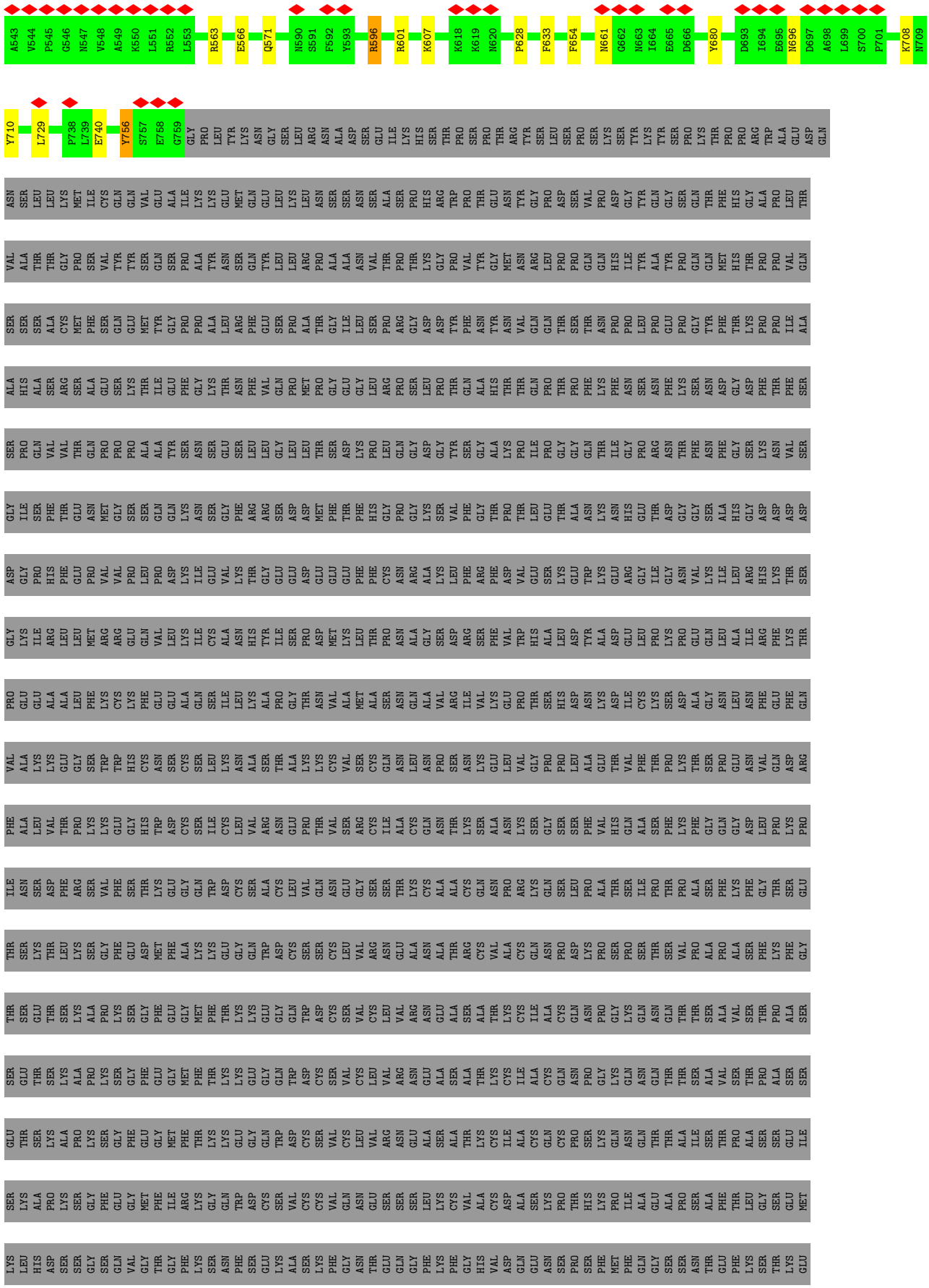


- Molecule 1: E3 SUMO-protein ligase RanBP2

Chain 03:




A543 V544 P545 G546 N547 V548 A549 K550 L551 R552 L553 R563 E566 Q571 N590 S591 F592 Y593 R596 R601 K607 K618 K619 N620 P628 F633 F654 N661 G662 N663 I664 E665 D666 Y680 D693 I694 E695 N696 D697 A698 L699 S700 P701 K708 N709
Y710 L729 P738 L739 E740 Y756 S757 E758 G759 GLY PRO LEU TYR LYS ASN GLY SER LEU ARG ASN ALA ASP SER GLU ILE LYS HIS SER THR PRO SER PRO THR ARG TYR SER LEU SER PRO SER LYS SER TYR LYS TYR SER PRO LYS THR PRO PRO ARG LYS HIS GLY ALA TRP ALA GLU ASP GLN
ASN SER LEU LEU LYS MET ILE CYS GLN GLN VAL GLU ALA ILE LYS LYS GLU MET GLN GLU LEU LYS LEU ASN SER SER ASN SER ALA SER PRO HIS ARG TRP PRO THR GLU ASN TYR GLY PRO ASP SER VAL PRO ASP GLY TYR GLN GLY SER GLN THR PHE HIS GLY ALA PRO LEU THR
VAL ALA THR THR GLY PRO SER VAL TYR TYR SER GLN SER PRO ALA TYR ASN SER GLN TYR LEU LEU ARG PRO ALA ASN VAL THR PRO THR LYS GLY PRO VAL TYR GLY MET ASN ARG LEU PRO PRO GLN GLN HIS ILE TYR ALA TYR PRO GLN GLN MET HIS THR PRO PRO VAL GLN
SER SER SER ALA CYS MET PHE SER GLN GLU MET TYR GLY PRO PRO ALA LEU ARG PHE GLU SER PRO ALA THR GLY ILE LEU SER PRO ARG GLY ASP ASP TYR PHE ASN TYR ASN VAL GLN GLN GLN THR SER THR ASN PRO PRO LEU PRO GLU PRO GLY TYR PHE THR LYS PRO PRO ILE ALA
ALA HIS ALA SER ARG SER ALA GLU SER LYS THR ALA GLU PHE GLY LYS THR ASN PHE VAL GLN PRO MET PRO GLY GLU GLY LEU ARG PRO SER LEU PRO THR GLN GLN ALA HIS THR THR GLN PRO THR PRO PHE LYS PHE ASN SER ASN PHE LYS SER ASP ASP GLY ASP PHE THR PHE SER
SER PRO GLN VAL VAL THR GLN PRO PRO PRO ALA ALA TYR SER ASN SER GLU SER LEU LEU GLY LEU LEU THR SER ASP LYS PRO LEU GLN GLY ASP GLY TYR SER GLY ALA ALA LYS PRO ILE PRO GLY GLY GLN THR ILE GLY PRO ARG ASN THR PHE ASN PHE GLY LYS SER ASN VAL SER
GLY ILE SER PHE THR GLU ASN MET GLY SER SER GLN GLN LYS ASN SER GLY PHE ARG ARG SER ASP ASP MET PHE THR PHE HIS GLY PRO GLY LYS SER VAL PHE GLY THR PRO THR LEU GLU THR ALA ASN LYS ASN HIS GLU THR ASP GLY GLY SER ALA HIS GLY ASP ASP ASP
ASP GLY PRO HIS PHE GLU PRO VAL VAL PRO LEU PRO ASP LYS ILE GLU VAL LYS THR GLY GLU GLU ASP GLU GLU GLU PHE PHE CYS ASN ARG ALA LYS LEU PHE ARG PHE ASP VAL GLU SER LYS GLU TRP LYS GLU ARG GLY ILE GLY ASN VAL LYS ILE LEU ARG HIS LYS THR SER
GLY LYS ILE ARG LEU LEU MET ARG ARG GLU GLN VAL LEU LYS ILE CYS ALA ASN HIS TYR ILE SER PRO ASP MET LYS LEU THR PRO ASN ALA GLY SER ASP ARG ARG SER PHE VAL TRP HIS ALA LEU ASP TYR ALA ASP ASP GLU LEU PRO LYS PRO GLU GLN LEU ALA ILE ARG PHE LYS THR
PRO GLU GLU ALA ALA LEU PHE LYS CYS LYS PHE GLU GLU ALA GLN SER ILE LEU LYS ALA ALA PRO GLY THR ASN VAL ALA MET ALA SER ASN GLN ALA VAL PRO THR SER HIS ASP ASN LYS ASP ILE CYS LYS PRO GLU GLN ASN ASN GLN ALA GLU GLU PHE GLU GLU PHE
VAL ALA LYS LYS GLU GLY SER TRP HIS CYS ASN SER CYS SER THR ALA LYS LYS CYS VAL ALA SER CYS GLN ASN LEU ASN PRO SER ASP GLN LEU VAL GLY PRO PRO LEU ALA GLU THR VAL PHE THR PRO LYS THR SER PRO GLU ASN VAL GLN ASP ARG
PHE ALA LEU VAL THR PRO LYS LYS GLU GLY HIS TRP ASP CYS SER ILE CYS LEU VAL ARG ASN GLU PRO THR VAL SER ARG CYS ILE ALA CYS GLN ASN THR LYS SER ALA ASN LYS SER GLY SER SER PHE VAL HIS GLN ALA SER PHE LYS PHE GLY GLN GLY ASP LEU PRO PRO PHE
ILE ASN SER ASP PHE ARG SER VAL PHE SER THR LYS GLU GLY GLN TRP ASP CYS SER ALA CYS LEU VAL GLN ASN GLU GLY SER SER THR ALA CYS GLN ASN PRO ARG LYS GLN GLN SER LEU PRO ALA THR SER ILE PRO THR PRO ALA GLY PHE LYS PHE GLY THR SER GLU
THR SER LYS THR LEU LYS SER GLY PHE GLU ASP MET PHE ALA LYS LYS GLU GLY GLN TRP ASP CYS SER SER CYS LEU VAL ARG ASN GLU ALA ASN ALA THR ARG CYS VAL ALA CYS GLN ASN PRO ASP LYS PRO SER PRO SER THR SER VAL PRO ALA PRO ALA SER PHE
THR SER GLU THR SER LYS ALA PRO LYS SER GLY PHE GLU THR LYS LYS GLU GLY GLN TRP ASP CYS SER VAL CYS LEU VAL ARG ASN GLU ALA ASN GLU ALA ALA SER ALA THR LYS CYS VAL ALA CYS GLN ASN PRO GLY LYS GLN GLN THR THR SER ALA ALA VAL SER THR PRO ALA SER
SER GLU THR SER LYS ALA PRO LYS SER GLY PHE GLU THR LYS LYS GLU GLY GLN TRP ASP CYS SER VAL CYS LEU VAL ARG ASN GLU ALA SER ALA THR LYS CYS ILE ALA CYS GLN ASN PRO GLY LYS GLN ASN GLN THR THR SER ALA VAL SER THR PRO SER ALA SER
GLU THR SER LYS ALA PRO LYS SER GLY PHE GLU GLY MET PHE THR LYS LYS GLU GLY GLN TRP ASP CYS SER VAL CYS LEU VAL ARG ASN GLU ALA ASN GLU ALA SER ALA THR LYS CYS ILE ALA CYS GLN GLN THR THR ALA ILE SER ALA PRO ALA SER ALA
SER LYS ALA PRO LYS SER GLY PHE GLU GLY MET PHE ILE ARG LYS GLY GLN TRP ASP CYS SER VAL CYS SER GLU SER SER LEU LYS CYS PHE GLY HIS GLY ALA SER VAL CYS GLN ASN GLU GLU SER ALA THR LYS VAL ALA PRO THR PHE ALA ALA SER GLU MET
LYS LEU HIS ASP SER SER GLN VAL GLY THR GLY PHE LYS SER GLN GLY PHE GLY ASN THR GLU GLN GLY PHE LYS PHE GLY HIS VAL ASP GLN GLU ASN SER PHE MET PHE GLN GLY SER SER ASN THR GLU PHE LYS SER THR LYS GLU
WORLDWIDE PDB PROTEIN DATA BANK

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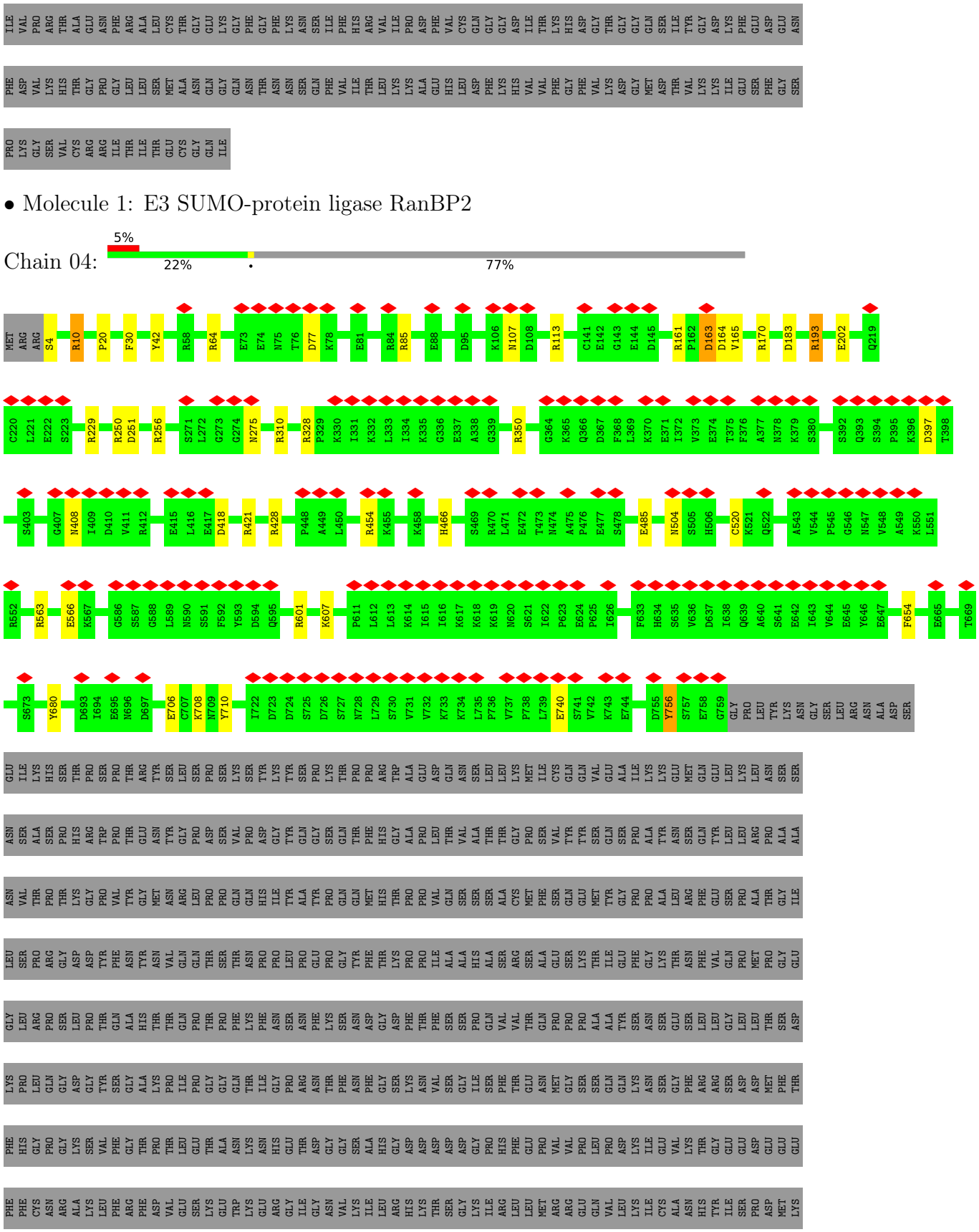
ILE VAL PRO ARG THR ALA GLU ASN PHE ARG ALA LEU CYS THR GLY GLU LYS GLY PHE GLY PHE LYS ASN SER ILE PHE HIS ARG VAL ILE PRO ASP PHE VAL CYS GLN GLY GLY ASP ILE THR LYS HIS ASP GLY THR GLY GLY GLN SER ILE TYR GLY ASP LYS PHE GLU ASP GLU ASN
PHE ASP VAL LYS HIS THR GLY PRO GLY LEU LEU SER MET ALA ASN GLN GLY GLN ASN THR ASN ASN SER GLN PHE VAL ILE THR LEU LYS LYS ALA GLU HIS LEU LEU ASP PHE LYS HIS VAL VAL PHE GLY PHE VAL LYS ASP GLY MET ASP THR VAL LYS LYS ILE GLU SER PHE GLY SER
PRO LYS GLY SER VAL CYS ARG ARG ILE THR ILE THR GLU CYS GLY GLN ILE
5%
Chain 04:
22%
77%
MET ARG ARG S4 R10 P20 F30 Y42 R58 R64 E73 E74 N75 T76 D77 K78 E81 R84 R85 E88 D95 K106 N107 D108 R113 C141 E142 G143 E144 D145 R161 P162 D163 D164 V165 R170 D183 R193 E202 Q219
C220 L221 E222 S223 R229 R250 D251 R256 S271 L272 G273 G274 N275 R310 R328 P329 K330 I331 K332 L333 I334 K335 G336 E337 A338 G339 R350 G364 K365 Q366 D367 F368 L369 K370 E371 I372 V373 E374 T375 F376 A377 N378 K379 S380 S392 Q393 S394 P395 K396 D397 T398
S403 G407 N408 I409 D410 V411 R412 E415 L416 E417 D418 R421 R428 P448 A449 L450 R454 K455 K458 H466 S469 R470 L471 E472 T473 N474 A475 P476 E477 S478 E485 N504 S505 H506 C520 K521 Q522 A543 V544 P545 G546 N547 V548 A549 K550 L551
R552 R563 E566 K567 G586 S587 G588 L589 N590 S591 F592 Y593 D594 Q595 R601 K607 P611 L612 L613 K614 I615 I616 K617 K618 K619 N620 S621 I622 P623 E624 P625 I626 F633 H634 S635 V636 D637 I638 Q639 A640 S641 E642 I643 V644 E645 Y646 E647 F654 E665 T669
S673 Y680 D693 I694 E695 N696 D697 E706 G707 K708 N709 Y710 I722 D723 D724 S725 D726 S727 N728 L729 S730 V731 V732 K733 K734 L735 P736 V737 P738 L739 E740 S741 V742 K743 E744 D755 Y756 S757 E758 G759 GLY PRO LEU TYR LYS ASN GLY SER LEU ARG ASN ALA ASP SER
GLU ILE LYS HIS SER THR PRO SER PRO THR ARG TYR SER LEU SER PRO SER LYS SER TYR LYS TYR SER PRO LYS THR PRO PRO ARG TRP ALA GLU ASP GLN ASN SER LEU LEU LYS MET ILE CYS GLN GLN VAL GLU ALA ILE LYS LYS GLU MET GLN GLU LEU LYS LEU ASN SER SER
ASN SER ALA SER PRO HIS ARG TRP PRO THR GLU ASN TYR SER GLY PRO ASP SER VAL PRO ASP GLY TYR GLN GLY SER GLN THR PHE HIS GLY ALA PRO LEU THR VAL ALA THR THR GLY PRO SER VAL TYR TYR SER GLN SER PRO ALA TYR ASN SER GLN TYR LEU LEU ARG PRO ALA ALA
ASN VAL THR PRO THR LYS GLY PRO VAL TYR GLY MET ASN ARG LEU PRO PRO GLN GLN HIS ILE TYR ALA TYR PRO GLN GLN MET HIS THR PRO PRO VAL GLN SER SER SER ALA CYS MET PHE SER GLN GLU MET TYR GLY PRO PRO ALA LEU ARG PHE GLU SER PRO ALA THR GLY ILE
LEU SER PRO ARG GLY ASP ASP TYR PHE ASN TYR ASN VAL GLN GLN THR SER THR ASN PRO PRO LEU PRO GLU PRO GLY TYR PHE THR LYS PRO PRO ILE ALA ALA HIS ALA SER ARG SER ALA GLU SER LYS THR ILE GLU PHE GLY LYS THR ASN PHE VAL GLN PRO MET PRO GLY GLU
GLY LEU ARG PRO SER LEU PRO THR PRO GLN ALA HIS THR THR GLN PRO THR PRO PHE LYS PHE ASN SER ASN PHE LYS SER ASN ASP GLY ASP PHE THR PHE SER SER PRO GLN VAL VAL THR GLN PRO PRO PRO ALA ALA TYR SER ASN SER GLU SER LEU LEU GLY LEU LEU THR SER ASP
LYS PRO LEU GLN GLY ASP GLY TYR SER GLY ALA LYS PRO ILE PRO GLY GLN THR ILE GLY PRO ARG ASN THR PHE ASN PHE GLY GLY SER LYS ASN VAL SER GLY ILE SER PHE THR GLU ASN MET GLY SER SER GLN GLN LYS ASN SER GLY PHE ARG ARG SER ASP ASP MET PHE THR
PHE HIS GLY PRO GLY LYS SER VAL PHE GLY THR PRO THR LEU GLU THR ALA ASN LYS ASN HIS GLU THR ASP GLY GLY SER ALA HIS GLY ASP ASP ASP ASP ASP GLY PRO HIS PHE GLU PRO VAL VAL PRO LEU PRO ASP LYS ILE GLU VAL LYS THR GLY GLU GLU ASP GLU GLU GLU
PHE PHE CYS ASN ARG ALA LYS LEU PHE ARG PHE ASP VAL GLU SER LYS GLU TRP LYS GLU ARG GLY ILE GLY ASN VAL LYS ILE LEU ARG HIS LYS THR SER GLY LYS ILE ARG LEU LEU MET ARG ARG GLU GLN VAL LEU LYS ILE CYS ALA ASN HIS TYR ILE SER PRO ASP MET LYS

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E241 N242 I243 L244 L245 N246 P247 A248 Y249 D250 V251 Y252 L253 M254 V255 G256 T257 S258 I259 H260 Y261 K262 V263 Q264 K265 I266 R267 Q268 G269 K270 I271 T272 E273 L274 S275 M276 P277 S278 D279 Q280 Y281 E282 L283 Q284 L285 Q286 N287 S288 I289 P290 G291 P292 E293 G294 D295 P296 A297 R298 P299 V300

A301 V302 L303 A304 Q305 D306 T307 S308 M309 V310 T311 A312 L313 Q314 L315 G316 Q317 S318 S319 L320 V321 L322 G323 H324 R325 S326 I327 R328 M329 Q330 G331 A332 S333 R334 L335 P336 N337 S338 T339 I340 Y341 V342 V343 E344 P345 G346 Y347 L348 G349 F350 T351 V352 H353 P354 G355 D356 R357 W358 V359 L360

E361 T362 G363 R364 L365 Y366 E367 I368 T369 I370 E371 V372 F373 D374 K375 F376 S377 N378 K379 V380 Y381 V382 S383 D384 N385 I386 R387 I388 E389 T390 V391 L392 P393 A394 E395 F396 F397 E398 V399 L400 S401 S402 S403 Q404 N405 G406 S407 Y408 H409 R410 I411 R412 A413 L414 K415 R416 G417 Q418 T419 A420

I421 D422 A423 A424 L425 T426 S427 V428 V429 D430 Q431 D432 G433 G434 V435 H436 I437 L438 Q439 V440 P441 V442 W443 N444 Q445 Q446 E447 V448 E449 I450 H451 I452 P453 I454 T455 L456 Y457 P458 S459 I460 L461 T462 F463 P464 W465 Q466 P467 K468 T469 G470 A471 Y472 Q473 Y474 T475 I476 R477 A478 H479 G480

G481 S482 G483 N484 F485 S486 W487 S488 S489 S490 S491 H492 L493 V494 A495 T496 V497 T498 V499 K500 G501 V502 M503 T504 T505 G506 S507 D508 I509 G510 F511 S512 V513 I514 Q515 A516 H517 D518 V519 Q520 N521 P522 L523 H524 F525 G526 E527 M528 K529 V530 Y531 V532 I533 E534 P535 H536 S537 M538 E539 F540

A541 P542 C543 Q544 V545 E546 A547 R548 V549 G550 Q551 A552 L553 E554 L555 P556 L557 R558 I559 S560 G561 L562 M563 P564 G565 G566 A567 S568 E569 V570 V571 T572 L573 S574 D575 C576 S577 H578 F579 D580 L581 A582 V583 E584 V585 E586 N587 Q588 G589 V590 F591 Q592 P593 L594 P595 G596 R597 L598 P599 P600

G601 S602 E603 H604 C605 S606 G607 I608 R609 V610 K611 A612 E613 A614 Q615 G616 S617 T618 T619 L620 L621 V622 S623 Y624 R625 H626 G627 H628 V629 H630 L631 S632 A633 K634 I635 T636 I637 A638 A639 Y640 L641 P642 L643 K644 A645 V646 D647 P648 S649 S650 V651 A652 L653 V654 T655 L656 G657 S658 S659 K660

E661 M662 L663 F664 E665 G666 G667 P668 R669 P670 W671 I672 L673 E674 P675 S676 K677 F678 F679 Q680 N681 V682 T683 A684 E685 D686 T687 D688 S689 I690 G691 L692 A693 L694 F695 A696 P697 H698 S699 S700 R701 N702 Y703 Q704 Q705 H706 W707 I708 L709 V710 T711 C712 Q713 A714 L715 G716 E717 Q718 V719 I720

A721 L722 S723 V724 G725 N726 K727 P728 S729 L730 T731 N732 P733 F734 P735 A736 V737 E738 P739 A740 V741 V742 K743 F744 V745 C746 A747 P748 P749 S750 R751 L752 T753 L754 A755 P756 V757 Y758 T759 S760 P761 Q762 L763 D764 M765 S766 C767 P768 L769 L770 Q771 Q772 N773 K774 Q775 V776 V777 P778 V779 S780

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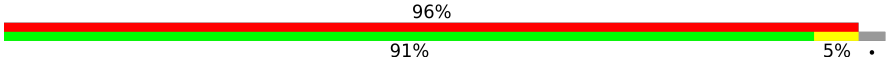
ALA TYR ALA SER HIS

- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 11:



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F1811 F1812 T1813 L1814 F1815 A1816 L1817 L1818 A1819 G1820 T1821 A1822 G1832 THR PRO ARG ASP LEU ALA VAL PRO ALA ALA LEU THR PRO ARG ALA SER PRO GLY HIS SER PRO HIS TYR PHE ALA ALA SER SER PRO THR SER PRO ASN ALA LEU PRO PRO ALA ARG LYS ALA SER PRO PRO SER GLY

LEU TRP SER PRO ALA TYR ALA SER HIS

- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 12: 96% 91% 6%

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E241 N242 I243 L244 L245 N246 P247 A248 Y249 D250 V251 Y252 L253 M254 V255 G256 T257 S258 I259 H260 Y261 K262 V263 Q264 K265 I266 R267 Q268 G269 K270 I271 T272 E273 L274 S275 M276 P277 S278 D279 Q280 Y281 E282 L283 Q284 L285 Q286 N287 S288 I289 P290 G291 P292 E293 G294 D295 P296 A297 R298 P299 V300

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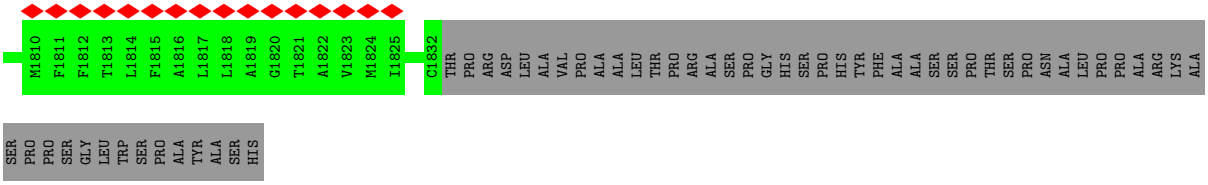
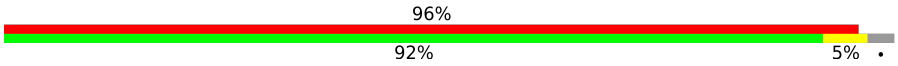
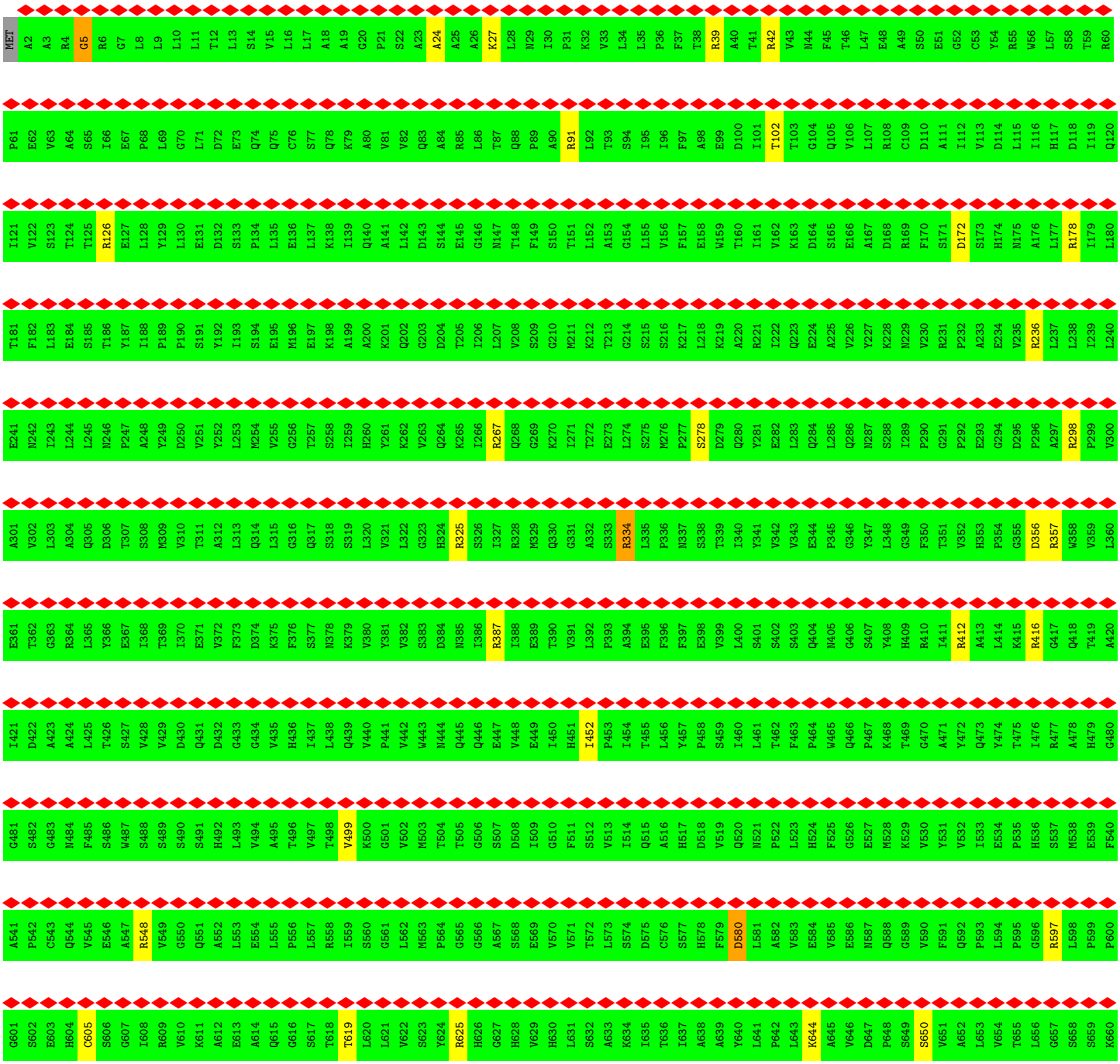


- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 13:





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ALA ARG LYS ALA SER PRO PRO SER GLY LEU TRP SER PRO ALA TYR ALA SER HIS

- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 14: 97% 92% 5% •

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T181 F182 L183 E184 S185 T186 Y187 I188 P189 P190 S191 Y192 I193 S194 E195 M196 E197 K198 A199 A200 K201 Q202 G203 D204 T205 I206 L207 V208 S209 G210 M211 K212 T213 G214 S215 S216 K217 L218 K219 A220 R221 I222 Q223 E224 A225 V226 Y227 K228 N229 V230 R231 P232 A233 E234 V235 R236 L237 L238 I239 L240

E241 N242 I243 L244 L245 N246 P247 A248 Y249 D250 V251 Y252 L253 M254 V255 G256 T257 S258 I259 H260 Y261 K262 V263 Q264 K265 I266 R267 Q268 G269 K270 I271 T272 E273 L274 S275 M276 P277 S278 D279 Q280 Y281 E282 L283 Q284 L285 Q286 N287 S288 I289 P290 G291 P292 E293 G294 D295 P296 A297 R298 P299 V300

A301 V302 L303 A304 Q305 D306 T307 S308 M309 V310 T311 A312 L313 Q314 L315 G316 Q317 S318 S319 L320 V321 L322 G323 H324 R325 S326 I327 R328 M329 Q330 G331 A332 S333 R334 L335 P336 N337 S338 T339 I340 Y341 V342 V343 E344 P345 G346 Y347 L348 G349 F350 T351 V352 H353 P354 G355 D356 R357 W358 V359 L360

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G601 S602 E603 H604 C605 S606 G607 I608 R609 V610 K611 A612 E613 A614 Q615 G616 S617 T618 T619 L620 L621 V622 S623 Y624 R625 H626 G627 H628 V629 H630 L631 S632 A633 K634 I635 T636 I637 A638 A639 Y640 L641 P642 L643 K644 A645 V646 D647 P648 S649 S650 V651 A652 L653 V654 T655 L656 G657 S658 S659 K660

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S781 H782 R783 N784 P785 R786 L787 D788 L789 A790 A791 Y792 D793 Q794 E795 G796 R797 R798 F799 D800 N801 F802 S803 S804 L805 S806 I807 Q808 W809 E810 S811 T812 R813 P814 V815 L816 A817 S818 I819 E820 P821 E822 L823 P824 M825 Q826 L827 V828 S829 Q830 D831 D832 E833 S834 G835 Q836 K837 K838 L839 H840

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W1741 P1742 S1743 F1744 I1745 T1746 Y1747 T1748 V1749 G1750 V1751 L1752 D1753 P1754 A1755 A1756 G1757 S1758 Q1759 G1760 P1761 L1762 S1763 T1764 T1765 L1766 T1767 F1768 S1769 S1770 P1771 V1772 T1773 N1774 Q1775 A1776 I1777 A1778 I1779 P1780 V1781 T1782 V1783 A1784 F1785 V1786 V1787 D1788 R1789 R1790 G1791 P1792 G1793 P1794 Y1795 G1796 A1797 S1798 L1799 F1800

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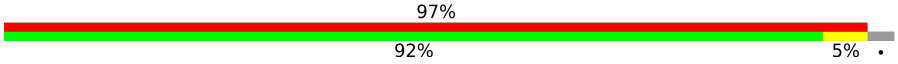
PRO THR SER PRO ASN ALA LEU PRO PRO ALA ARG LYS ALA SER PRO PRO SER GLY LEU TRP SER PRO ALA TYR ALA SER HIS

- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 15:



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P61 E62 V63 A64 S65 I66 E67 P68 L69 G70 L71 D72 E73 Q74 Q75 C76 S77 Q78 K79 A80 V81 V82 Q83 A84 R85 L86 T87 Q88 P89 A90 R91 L92 T93 S94 I95 I96 F97 A98 E99 D100 I101 T102 T103 G104 Q105 V106 L107 R108 C109 D110 A111 I112 V113 D114 L115 I116 H117 D118 I119 Q120

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T181 F182 L183 E184 S185 T186 Y187 I188 P189 P190 S191 Y192 I193 S194 E195 M196 E197 K198 A199 A200 K201 Q202 G203 D204 T205 I206 L207 V208 S209 G210 M211 K212 T213 G214 S215 S216 K217 L218 K219 A220 R221 I222 Q223 E224 A225 V226 Y227 K228 N229 V230 R231 P232 A233 E234 V235 R236 L237 L238 I239 L240

E241 N242 I243 L244 L245 N246 P247 A248 Y249 D250 V251 Y252 L253 M254 V255 G256 T257 S258 I259 H260 Y261 K262 V263 Q264 K265 I266 R267 Q268 G269 K270 I271 T272 E273 L274 S275 M276 P277 S278 D279 Q280 Y281 E282 L283 Q284 L285 Q286 N287 S288 I289 P290 G291 P292 E293 G294 D295 P296 A297 R298 P299 V300

A301 V302 L303 A304 Q305 D306 T307 S308 M309 V310 T311 A312 L313 Q314 L315 G316 Q317 S318 S319 L320 V321 L322 G323 H324 R325 S326 I327 R328 M329 Q330 G331 A332 S333 R334 L335 P336 N337 S338 T339 I340 Y341 V342 V343 E344 P345 G346 Y347 L348 G349 F350 T351 V352 H353 P354 G355 D356 R357 W358 V359 L360

E361 T362 G363 R364 L365 Y366 E367 I368 T369 I370 E371 V372 F373 D374 K375 F376 S377 N378 K379 V380 Y381 V382 S383 D384 N385 I386 R387 I388 E389 T390 V391 L392 P393 A394 E395 F396 F397 E398 Y399 L400 S401 S402 S403 Q404 N405 Q406 S407 Y408 H409 R410 I411 R412 A413 L414 K415 R416 G417 Q418 T419 A420

I421 D422 A423 A424 L425 T426 S427 V428 V429 D430 Q431 D432 G433 G434 V435 H436 I437 L438 Q439 V440 P441 V442 W443 N444 Q445 Q446 E447 V448 E449 I450 H451 I452 P453 I454 T455 L456 Y457 P458 S459 I460 L461 T462 F463 P464 W465 Q466 P467 K468 T469 G470 A471 Y472 Q473 Y474 T475 I476 R477 A478 H479 G480

G481 S482 G483 N484 F485 S486 W487 S488 S489 S490 S491 H492 L493 V494 A495 T496 V497 T498 V499 K500 G501 V502 M503 T504 T505 G506 S507 D508 I509 G510 F511 S512 V513 I514 Q515 A516 H517 D518 V519 Q520 N521 P522 L523 H524 F525 G526 E527 M528 K529 V530 V531 V532 I533 E534 P535 H536 S537 M538 E539 F540

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G601 S602 E603 H604 C605 S606 G607 I608 R609 V610 K611 A612 E613 A614 Q615 G616 S617 T618 T619 L620 L621 V622 S623 Y624 R625 H626 G627 H628 V629 H630 L631 S632 A633 K634 I635 T636 I637 A638 A639 Y640 L641 P642 L643 K644 A645 V646 D647 P648 S649 S650 V651 A652 L653 V654 T655 L656 G657 S658 S659 K660

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S781 H782 R783 N784 P785 R786 L787 D788 L789 A790 A791 Y792 D793 Q794 E795 G796 R797 R798 F799 D800 N801 F802 S803 S804 L805 S806 I807 Q808 W809 E810 S811 T812 R813 P814 V815 L816 A817 S818 I819 E820 P821 E822 L823 P824 M825 Q826 L827 V828 S829 Q830 D831 D832 E833 S834 G835 Q836 K837 K838 L839 H840

G841 L842 Q843 A844 I845 L846 V847 H848 E849 A850 S851 G852 T853 T854 A855 I856 T857 A858 T859 A860 T861 G862 Y863 Q864 E865 S866 H867 L868 S869 S870 A871 R872 T873 K874 Q875 P876 H877 D878 P879 L880 V881 P882 L883 S884 A885 S886 I887 E888 L889 I890 L891 V892 E893 D894 V895 R896 V897 S898 P899 E900

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L1804 D1805 S1806 Y1807 Q1808 V1809 M1810 F1811 F1812 T1813 L1814 F1815 A1816 L1817 L1818 A1819 G1820 T1821 A1822 V1823 M1824 I1825 I1826 A1827 Y1828 H1829 T1830 V1831 C1832 THR PRO ARG ASP LEU ALA VAL PRO ALA ALA LEU THR PRO ARG ALA SER PRO GLY HIS SER PRO HIS TYR PHE ALA ALA SER SER PRO THR SER

PRO ASN ALA LEU PRO PRO ALA ARG LYS ALA SER PRO PRO SER GLY LEU TRP SER PRO ALA TYR ALA SER HIS

- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 16: 96% 92% 5%

MET A2 A3 R4 G5 R6 G7 L8 L9 L10 L11 T12 L13 S14 V15 L16 L17 A18 A19 G20 P21 S22 A23 A24 A25 A26 K27 L28 N29 I30 P31 K32 V33 L34 L35 P36 F37 T38 R39 A40 T41 R42 V43 N44 F45 T46 L47 E48 A49 S50 E51 G52 C53 Y54 R55 W56 L57 S58 T59 R60

P61 E62 V63 A64 S65 I66 E67 P68 L69 G70 L71 D72 E73 Q74 Q75 C76 S77 Q78 K79 A80 V81 V82 Q83 A84 R85 L86 T87 Q88 P89 A90 R91 L92 T93 S94 I95 I96 F97 A98 E99 D100 I101 T102 T103 G104 Q105 V106 L107 R108 C109 D110 A111 I112 V113 D114 L115 I116 H117 D118 I119 Q120

I121 V122 S123 T124 T125 R126 E127 L128 Y129 L130 E131 D132 S133 P134 L135 E136 L137 K138 I139 Q140 A141 L142 D143 S144 E145 G146 N147 T148 F149 S150 T151 L152 A153 G154 L155 V156 F157 E158 W159 T160 I161 V162 K163 D164 S165 E166 A167 D168 R169 F170 S171 D172 S173 H174 N175 A176 L177 R178 I179 L180

T181 F182 L183 E184 S185 T186 Y187 I188 P189 P190 S191 Y192 I193 S194 E195 M196 E197 K198 A199 A200 K201 Q202 G203 D204 T205 I206 L207 V208 S209 G210 M211 K212 T213 G214 S215 S216 K217 L218 K219 A220 R221 I222 Q223 E224 A225 V226 Y227 K228 N229 V230 R231 P232 A233 E234 V235 R236 L237 L238 I239 L240

E241 N242 I243 L244 L245 N246 P247 A248 Y249 D250 V251 Y252 L253 M254 V255 G256 T257 S258 I259 H260 Y261 K262 V263 Q264 K265 I266 R267 Q268 G269 K270 I271 T272 E273 L274 S275 M276 P277 S278 D279 Q280 Y281 E282 L283 Q284 L285 Q286 N287 S288 I289 P290 G291 P292 E293 G294 D295 P296 A297 R298 P299 V300

A301 V302 L303 A304 Q305 D306 T307 S308 M309 V310 T311 A312 L313 Q314 L315 G316 Q317 S318 S319 L320 V321 L322 G323 H324 R325 S326 I327 R328 M329 Q330 G331 A332 S333 R334 L335 P336 N337 S338 T339 I340 Y341 V342 V343 E344 P345 G346 Y347 L348 G349 F350 T351 V352 H353 P354 G355 D356 R357 W358 V359 L360

E361 T362 G363 R364 L365 Y366 E367 I368 T369 I370 E371 V372 F373 D374 K375 F376 S377 N378 K379 V380 Y381 V382 S383 D384 N385 I386 R387 I388 E389 T390 V391 L392 P393 A394 E395 F396 F397 E398 V399 L400 S401 S402 S403 Q404 N405 G406 S407 Y408 H409 R410 I411 R412 A413 L414 K415 R416 G417 Q418 T419 A420

I421 D422 A423 A424 L425 T426 S427 V428 V429 D430 Q431 D432 G433 G434 V435 H436 I437 L438 Q439 V440 P441 V442 W443 N444 Q445 Q446 E447 V448 E449 I450 H451 I452 P453 I454 T455 L456 Y457 P458 S459 I460 L461 T462 F463 P464 W465 Q466 P467 K468 T469 G470 A471 Y472 Q473 Y474 T475 I476 R477 A478 H479 G480

G481 S482 G483 N484 F485 S486 W487 S488 S489 S490 S491 H492 L493 V494 A495 T496 V497 T498 V499 K500 G501 V502 M503 T504 T505 G506 S507 D508 I509 G510 F511 S512 V513 I514 Q515 A516 H517 D518 V519 Q520 N521 P522 L523 H524 F525 G526 E527 M528 K529 V530 Y531 V532 I533 E534 P535 H536 S537 M538 E539 F540

A541 P542 C543 Q544 V545 E546 A547 R548 V549 G550 Q551 A552 L553 E554 L555 P556 L557 R558 I559 S560 G561 L562 M563 P564 G565 G566 A567 S568 E569 V570 V571 T572 L573 S574 D575 C576 S577 H578 F579 D580 L581 A582 V583 E584 V585 E586 N587 Q588 G589 V590 F591 Q592 P593 L594 P595 G596 R597 L598 P599 P600

G601 S602 E603 H604 C605 S606 G607 I608 R609 V610 K611 A612 E613 A614 Q615 G616 S617 T618 T619 L620 L621 V622 S623 Y624 R625 H626 G627 H628 V629 H630 L631 S632 A633 K634 I635 T636 I637 A638 A639 Y640 L641 P642 L643 K644 A645 V646 D647 P648 S649 S650 V651 A652 L653 V654 T655 L656 G657 S658 S659 K660

E661 M662 L663 F664 E665 G666 G667 P668 R669 P670 W671 I672 L673 E674 P675 S676 K677 F678 F679 Q680 N681 V682 T683 A684 E685 D686 T687 D688 S689 I690 G691 L692 A693 L694 F695 A696 P697 H698 S699 S700 R701 N702 Y703 Q704 Q705 H706 W707 I708 L709 V710 T711 C712 Q713 A714 L715 G716 E717 Q718 V719 I720

A721 L722 S723 V724 G725 N726 K727 P728 S729 L730 T731 N732 P733 F734 P735 A736 V737 E738 P739 A740 V741 V742 K743 F744 V745 C746 A747 P748 P749 S750 R751 L752 T753 L754 A755 P756 V757 Y758 T759 S760 P761 Q762 L763 D764 M765 S766 C767 P768 L769 L770 Q771 Q772 N773 K774 Q775 V776 V777 P778 V779 S780

S781 H782 R783 N784 P785 R786 L787 D788 L789 A790 A791 Y792 D793 Q794 E795 G796 R797 R798 F799 D800 N801 F802 S803 S804 L805 S806 I807 Q808 W809 E810 S811 T812 R813 P814 V815 L816 A817 S818 I819 E820 P821 E822 L823 P824 M825 Q826 L827 V828 S829 Q830 D831 D832 E833 S834 G835 Q836 K837 K838 L839 H840

G841 L842 Q843 A844 I845 L846 V847 H848 E849 A850 S851 G852 T853 T854 A855 I856 T857 A858 T859 A860 T861 G862 Y863 Q864 E865 S866 H867 L868 S869 S870 A871 R872 T873 K874 Q875 P876 H877 D878 P879 L880 V881 P882 L883 S884 A885 S886 I887 E888 L889 I890 L891 V892 E893 D894 V895 R896 V897 S898 P899 E900

E901 V902 T903 I904 Y905 N906 H907 P908 G909 I910 Q911 A912 E913 L914 R915 I916 R917 E918 G919 S920 G921 Y922 F923 F924 L925 N926 T927 S928 T929 A930 D931 V932 V933 K934 V935 A936 Y937 Q938 E939 A940 R941 G942 V943 A944 M945 V946 H947 P948 I949 L950 P951 G952 S953 S954 T955 I956 M957 I958 H959 D960

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L1021 R1022 A1023 A1024 S1025 P1026 I1027 I1028 T1029 L1030 V1031 A1032 L1033 D1034 E1035 A1036 L1037 D1038 N1039 Y1040 T1041 I1042 T1043 F1044 L1045 I1046 R1047 G1048 V1049 A1050 I1051 G1052 Q1053 T1054 S1055 L1056 T1057 A1058 S1059 V1060 T1061 N1062 K1063 A1064 G1065 Q1066 R1067 I1068 N1069 S1070 A1071 P1072 Q1073 Q1074 I1075 E1076 V1077 F1078 P1079 P1080

F1081 R1082 L1083 M1084 P1085 R1086 K1087 V1088 T1089 L1090 L1091 I1092 G1093 A1094 T1095 M1096 Q1097 V1098 T1099 S1100 E1101 G1102 G1103 P1104 Q1105 P1106 Q1107 S1108 N1109 I1110 L1111 F1112 S1113 I1114 S1115 N1116 E1117 S1118 V1119 A1120 L1121 V1122 S1123 A1124 A1125 G1126 L1127 V1128 Q1129 G1130 L1131 A1132 I1133 G1134 N1135 G1136 T1137 V1138 S1139 G1140

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F1201 G1202 N1203 A1204 V1205 P1206 G1207 L1208 T1209 F1210 H1211 W1212 S1213 V1214 T1215 K1216 R1217 D1218 V1219 L1220 D1221 L1222 R1223 G1224 R1225 H1226 H1227 E1228 A1229 S1230 I1231 R1232 L1233 P1234 S1235 Q1236 Y1237 N1238 F1239 A1240 M1241 N1242 V1243 L1244 G1245 R1246 V1247 K1248 G1249 R1250 T1251 G1252 L1253 R1254 V1255 V1256 V1257 K1258 A1259 V1260

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V1681 G1682 A1683 E1684 V1685 P1686 F1687 S1688 P1689 G1690 L1691 F1692 A1693 D1694 Q1695 A1696 E1697 I1698 L1699 L1700 S1701 N1702 H1703 Y1704 T1705 S1706 S1707 E1708 I1709 R1710 V1711 F1712 G1713 A1714 P1715 E1716 V1717 L1718 E1719 N1720 L1721 E1722 V1723 K1724 S1725 G1726 S1727 P1728 A1729 V1730 L1731 A1732 F1733 A1734 K1735 E1736 K1737 S1738 F1739 G1740

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M1810 F1811 F1812 T1813 L1814 F1815 A1816 L1817 L1818 A1819 I1826 A1827 Y1828 H1829 T1830 V1831 C1832 THR PRO ARG ASP LEU ALA VAL PRO ALA ALA LEU THR PRO ARG ALA SER PRO GLY HIS SER PRO HIS TYR PHE ALA ALA SER SER PRO THR SER PRO ASN ALA LEU PRO PRO ALA ARG LYS ALA SER

PRO PRO SER GLY LEU TRP SER PRO ALA TYR ALA SER HIS

- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 17: 96% 92% 5%

MET A2 A3 R4 G5 R6 G7 L8 L9 L10 L11 T12 L13 S14 V15 L16 L17 A18 A19 G20 P21 S22 A23 A24 A25 A26 K27 L28 N29 I30 P31 K32 V33 L34 L35 P36 F37 T38 R39 A40 T41 R42 V43 N44 F45 T46 L47 E48 A49 S50 E51 G52 C53 Y54 R55 W56 L57 S58 T59 R60

P61 E62 V63 A64 S65 I66 E67 P68 L69 G70 L71 D72 E73 Q74 Q75 C76 S77 Q78 K79 A80 V81 V82 Q83 A84 R85 L86 T87 Q88 P89 A90 R91 L92 T93 S94 I95 I96 F97 A98 E99 D100 I101 T102 T103 G104 Q105 V106 L107 R108 C109 D110 A111 I112 V113 D114 L115 I116 H117 D118 I119 Q120

I121 V122 S123 T124 T125 R126 E127 L128 Y129 L130 E131 D132 S133 P134 L135 E136 L137 K138 I139 Q140 A141 L142 D143 S144 E145 G146 N147 T148 F149 S150 T151 L152 A153 G154 L155 V156 F157 E158 W159 T160 I161 V162 K163 D164 S165 E166 A167 D168 R169 F170 S171 D172 S173 H174 N175 A176 L177 R178 I179 L180

T181 F182 L183 E184 S185 T186 Y187 I188 P189 P190 S191 Y192 I193 S194 E195 M196 E197 K198 A199 A200 K201 Q202 G203 D204 T205 I206 L207 V208 S209 G210 M211 K212 T213 G214 S215 S216 K217 L218 K219 A220 R221 I222 Q223 E224 A225 V226 Y227 K228 N229 V230 R231 P232 A233 E234 V235 R236 L237 L238 I239 L240

E241 N242 I243 L244 L245 N246 P247 A248 Y249 D250 V251 Y252 L253 M254 V255 G256 T257 S258 I259 H260 Y261 K262 V263 Q264 K265 I266 R267 Q268 G269 K270 I271 T272 E273 L274 S275 M276 P277 S278 D279 Q280 Y281 E282 L283 Q284 L285 Q286 N287 S288 I289 P290 G291 P292 E293 G294 D295 P296 A297 R298 P299 V300

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E361 T362 G363 R364 L365 Y366 E367 I368 T369 I370 E371 V372 F373 D374 K375 F376 S377 N378 K379 V380 Y381 V382 S383 D384 N385 I386 R387 I388 E389 T390 V391 L392 P393 A394 E395 F396 F397 E398 Y399 L400 S401 S402 S403 Q404 N405 G406 S407 Y408 H409 R410 I411 R412 A413 L414 K415 R416 G417 Q418 T419 A420

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GLY LEU TRP SER PRO ALA TYR ALA SER HIS

- Molecule 3: Aladin

Chain 40: 25% 65% 5% 30%

MET C2 S3 L4 G5 L6 Y19 E20 H21 N22 N23 E24 S29 S30 Y31 GLU SER PRO PRO PRO ASP PHE ARG GLY GLN TRP ILE ASN LEU PRO VAL LEU GLN LEU THR LYS ASP PRO LEU LYS THR PRO GLY ARG LEU ASP HIS GLY THR ARG THR ALA PHE ILE HIS HIS ARG GLU

GLN VAL TRP LYS ARG CYS ILE ASN ILE TRP ARG ASP VAL GLY LEU PHE GLY VAL LEU ASN GLU ILE ALA ASN SER GLU GLU GLU VAL PHE GLU TRP VAL LYS THR ALA SER GLY TRP ALA LEU ALA LEU CYS ARG TRP ALA SER SER LEU HIS GLY SER LEU PHE PRO HIS LEU SER L134

R135 S136 E137 D138 F143 R155 A158 N164 K165 D173 N179 A180 S181 S182 T183 I184 K189 H190 R191 L192 Q193 R194 N195 L199 S205 A206 Q214 S215 C216 I217 L218 I219 W220 T221 L222 D223 P224 T225 S226 L227 S228 S232 S233 G234 C235 A236 Q237 V238 L239

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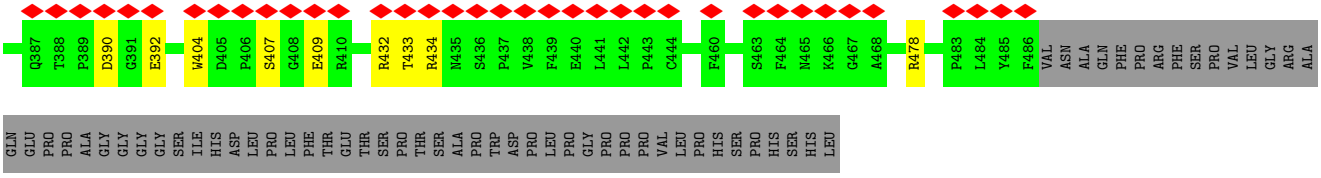

- Molecule 3: Aladin

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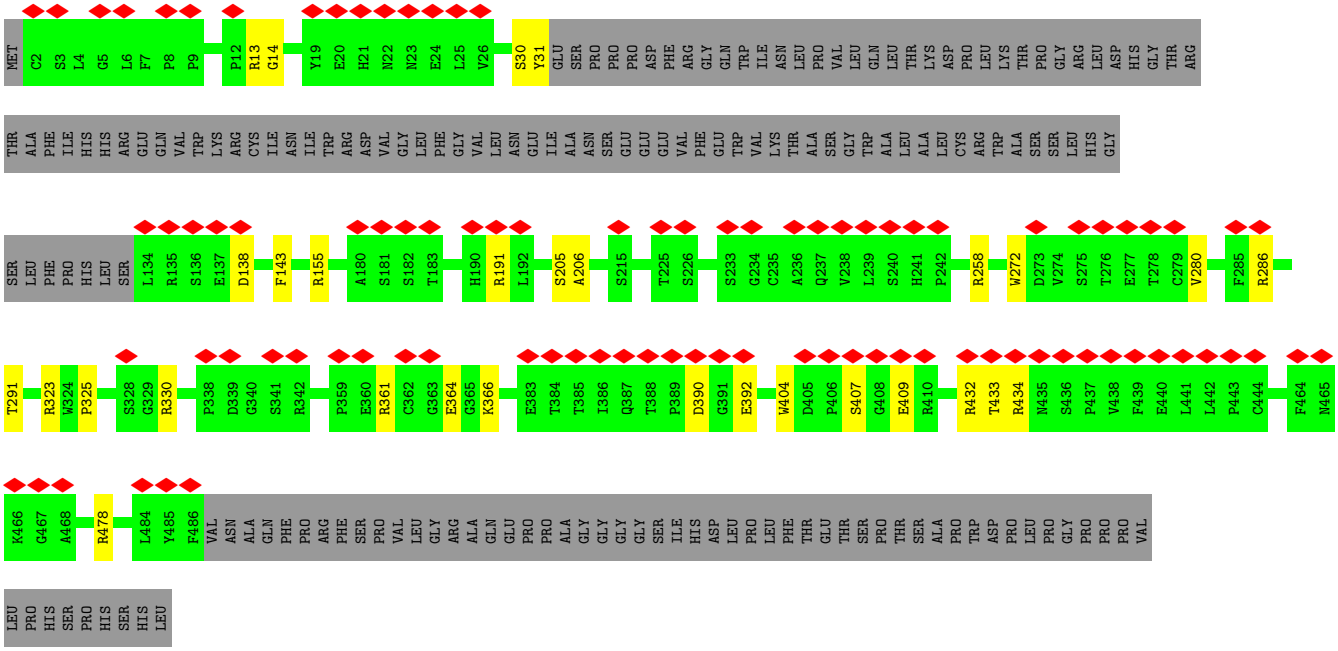
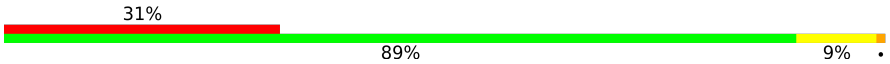
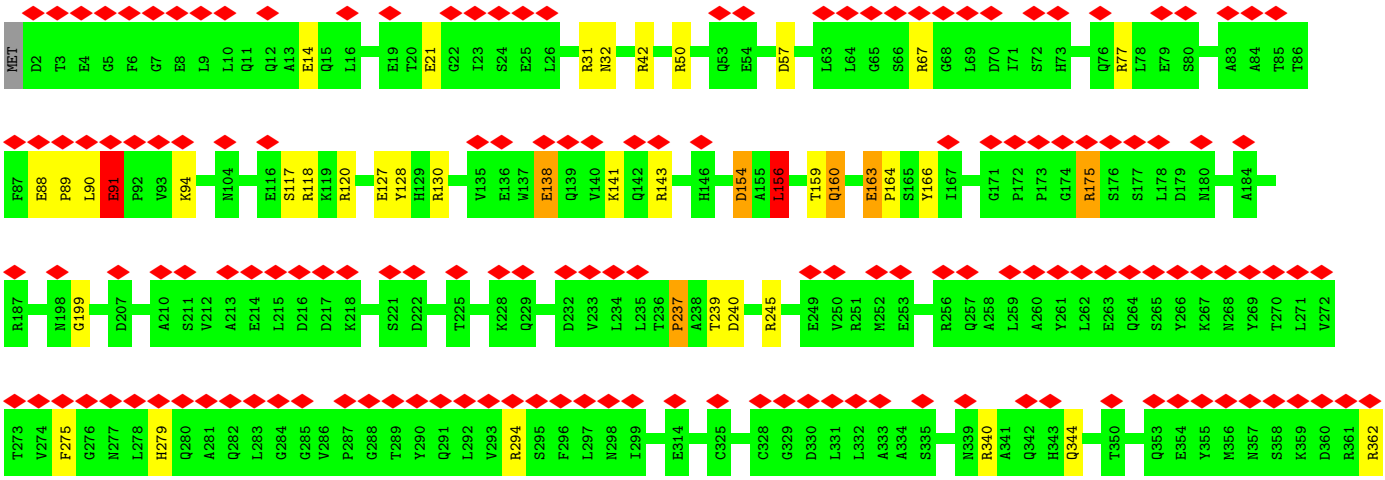
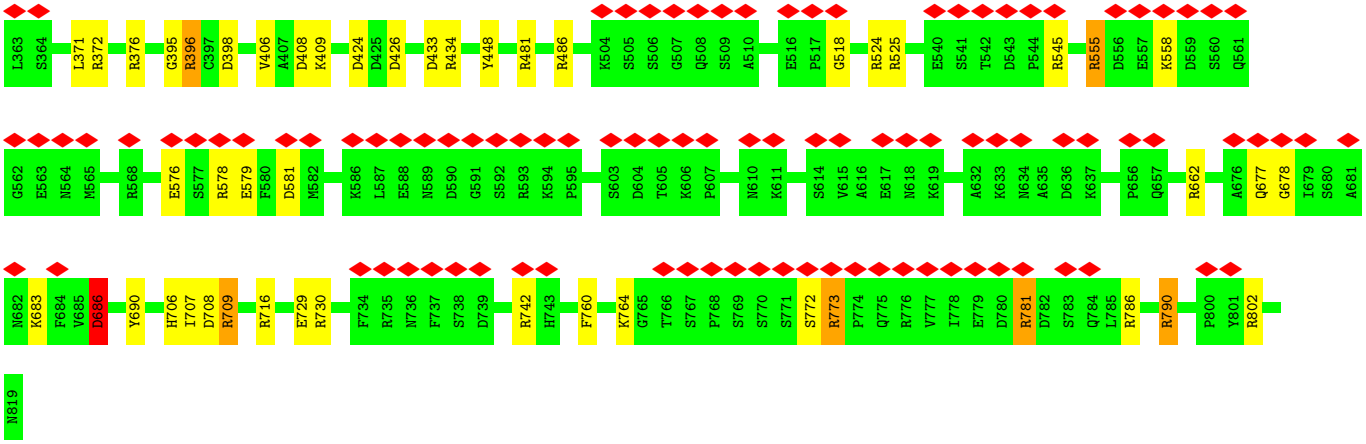


- Molecule 4: Nuclear pore complex protein Nup93

Chain A0:







• Molecule 4: Nuclear pore complex protein Nup93

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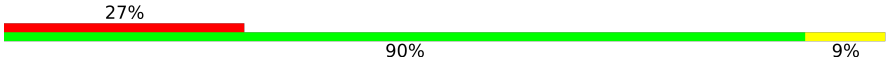

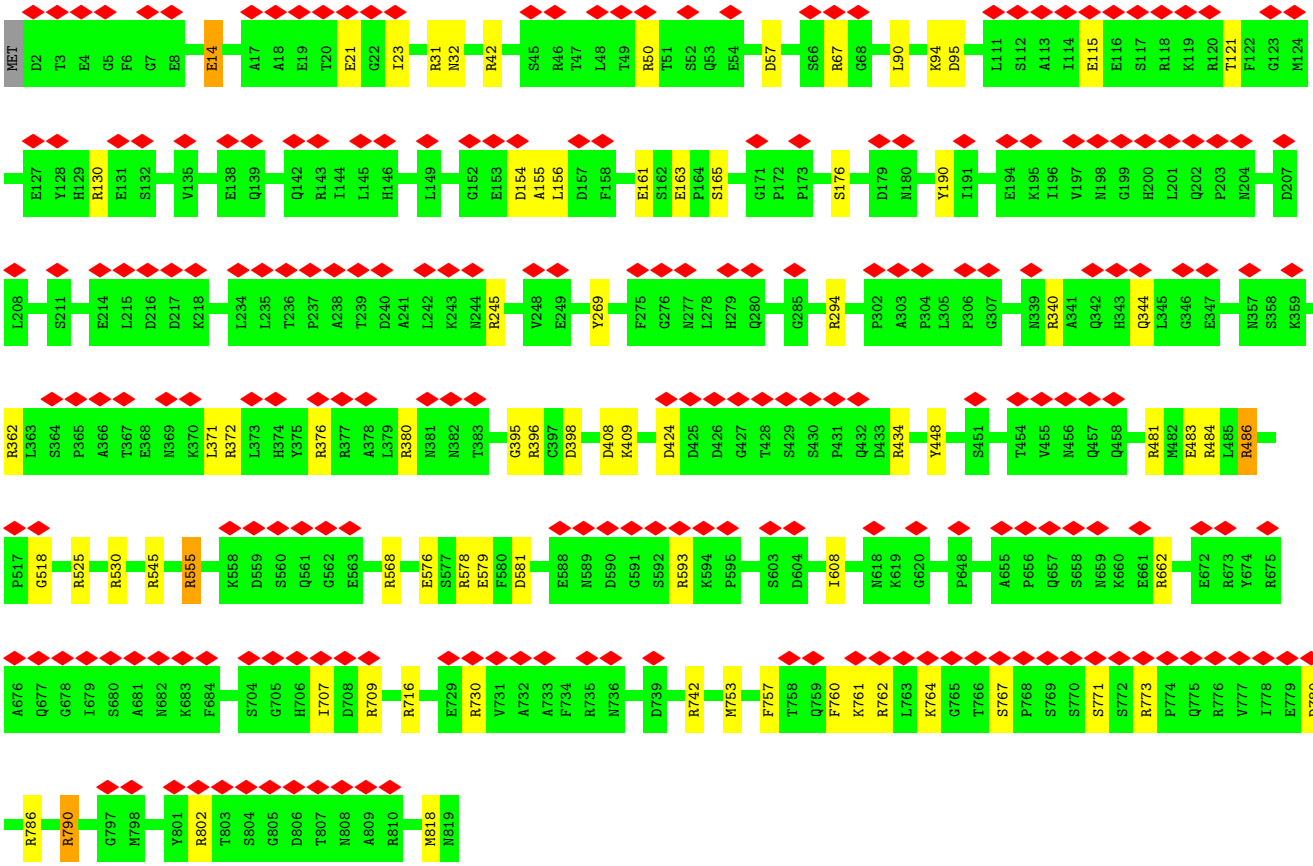

• Molecule 4: Nuclear pore complex protein Nup93

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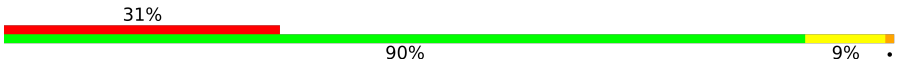
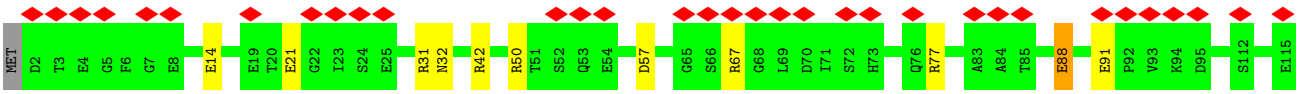
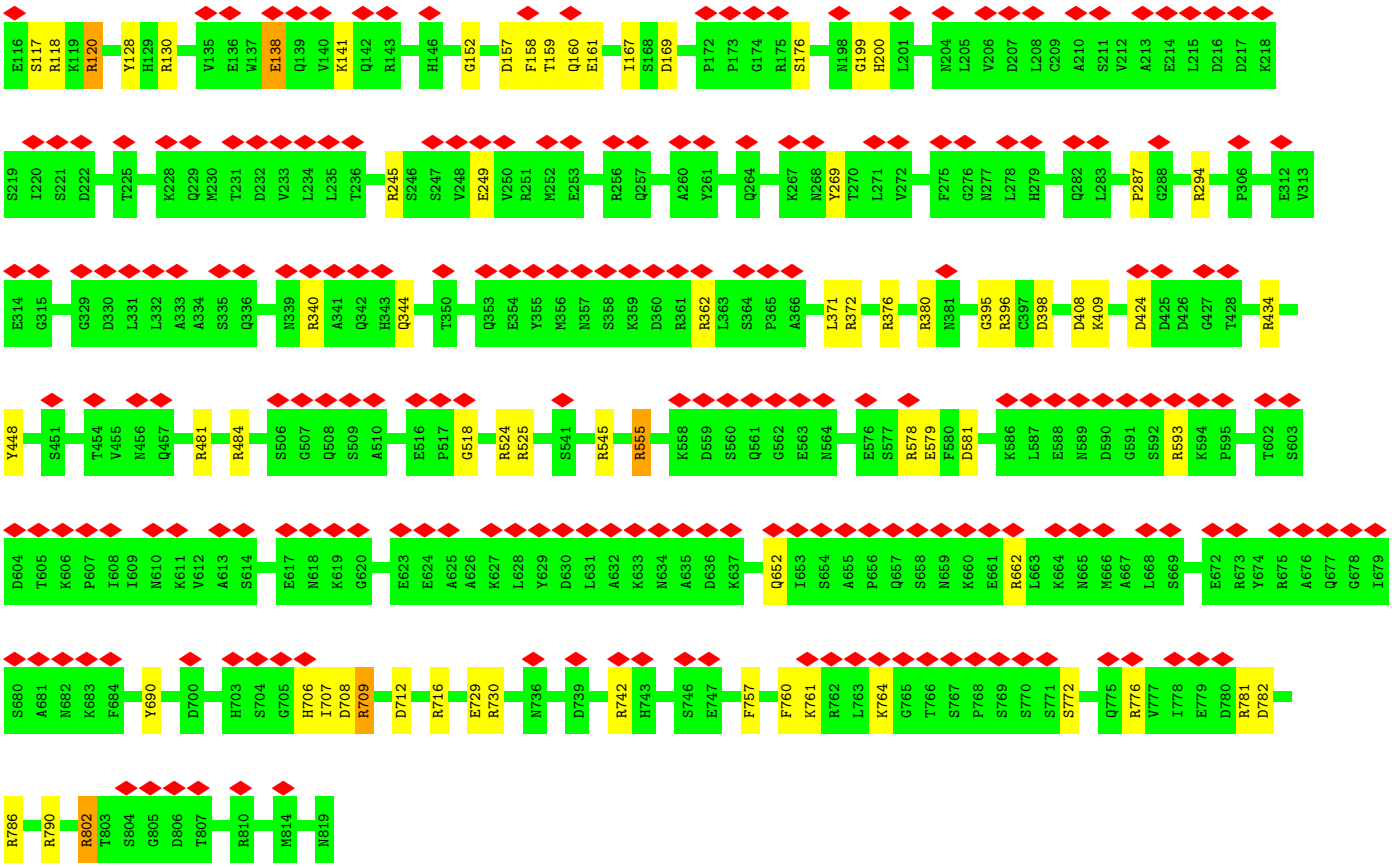
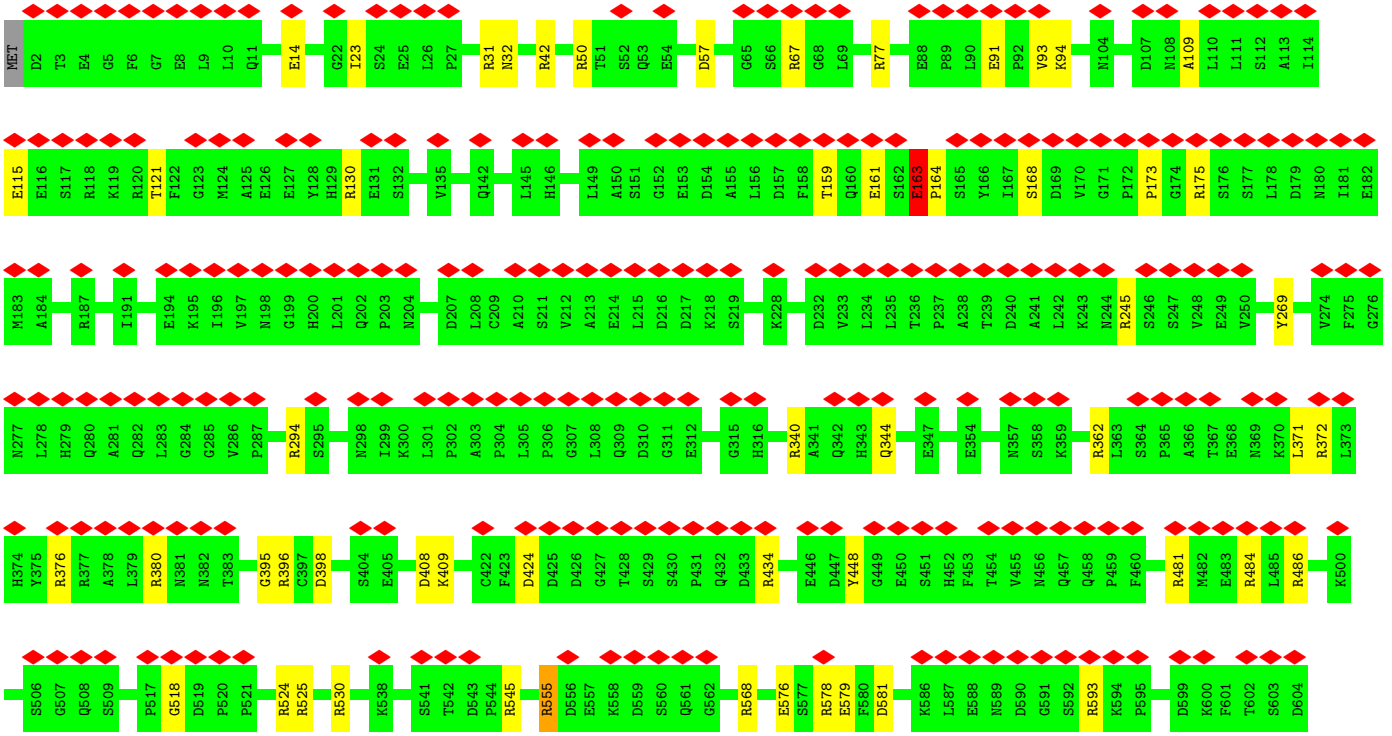


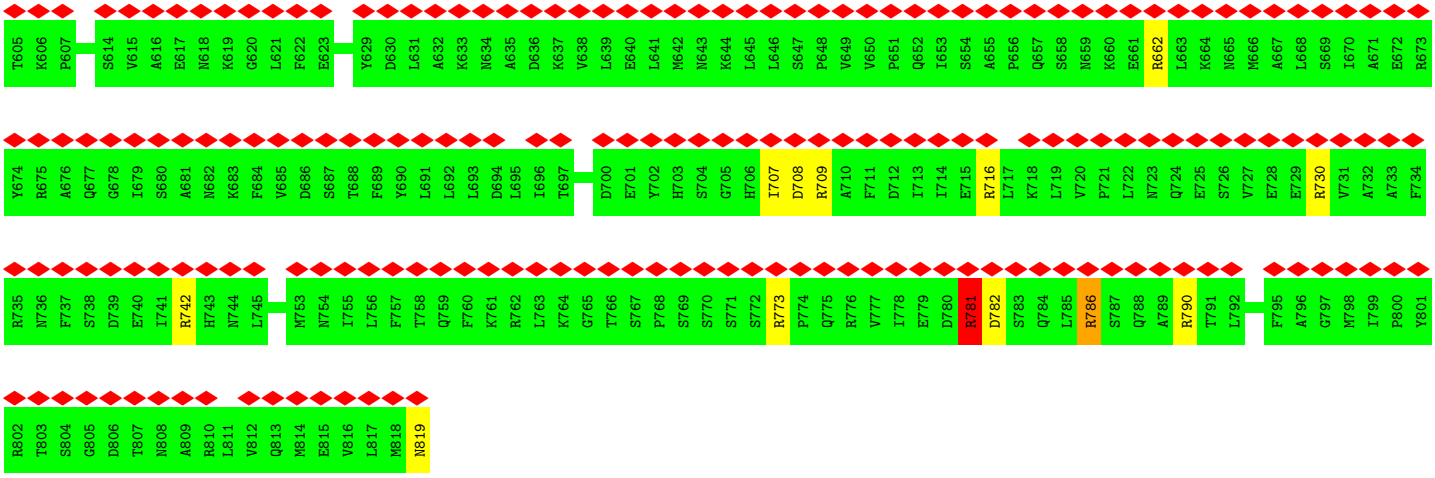




- Molecule 4: Nuclear pore complex protein Nup93

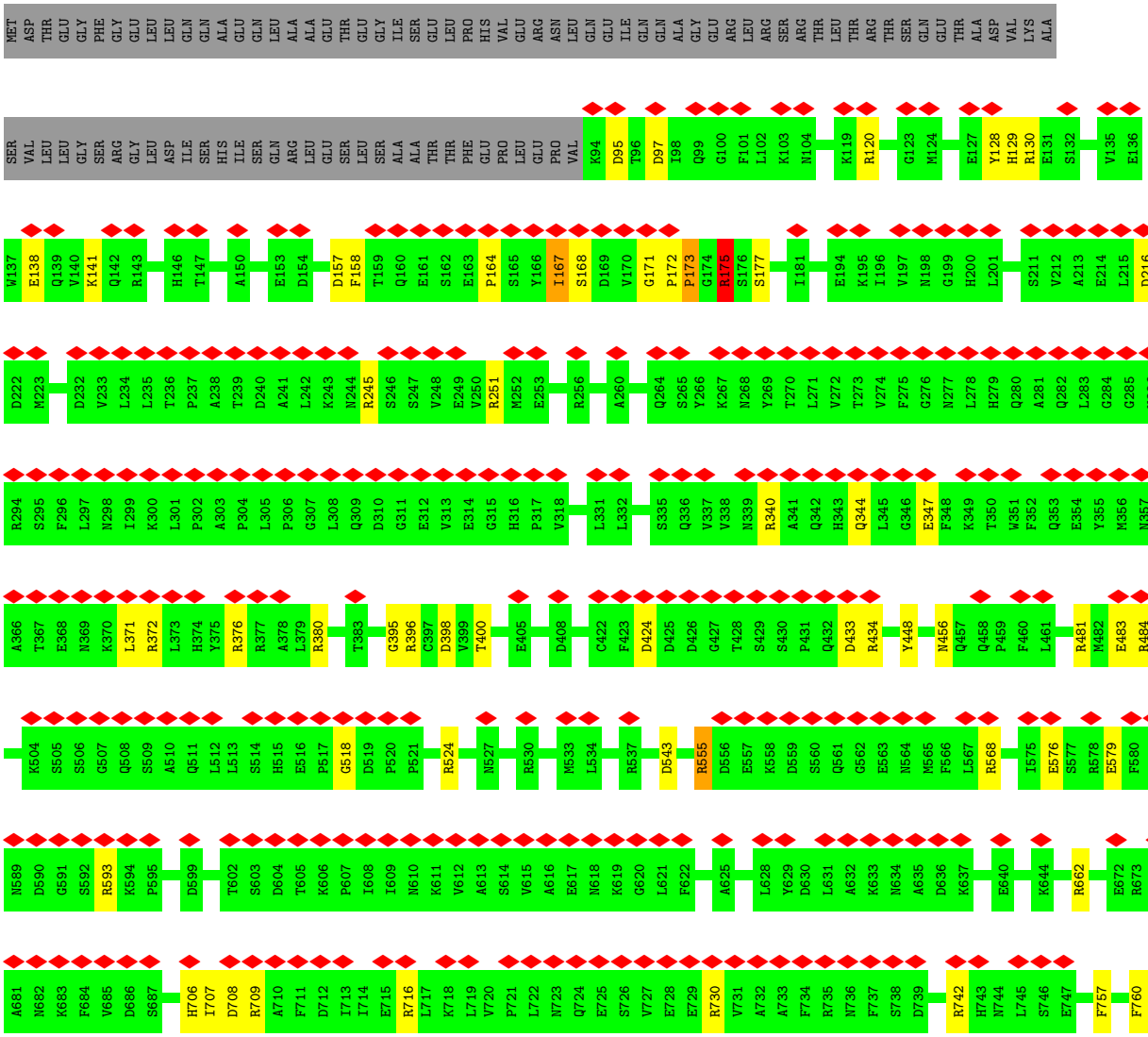
Chain A3: 54% 91% 8%

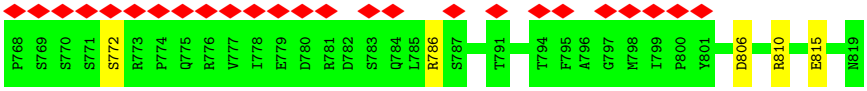




- Molecule 4: Nuclear pore complex protein Nup93

Chain A4:





• Molecule 4: Nuclear pore complex protein Nup93

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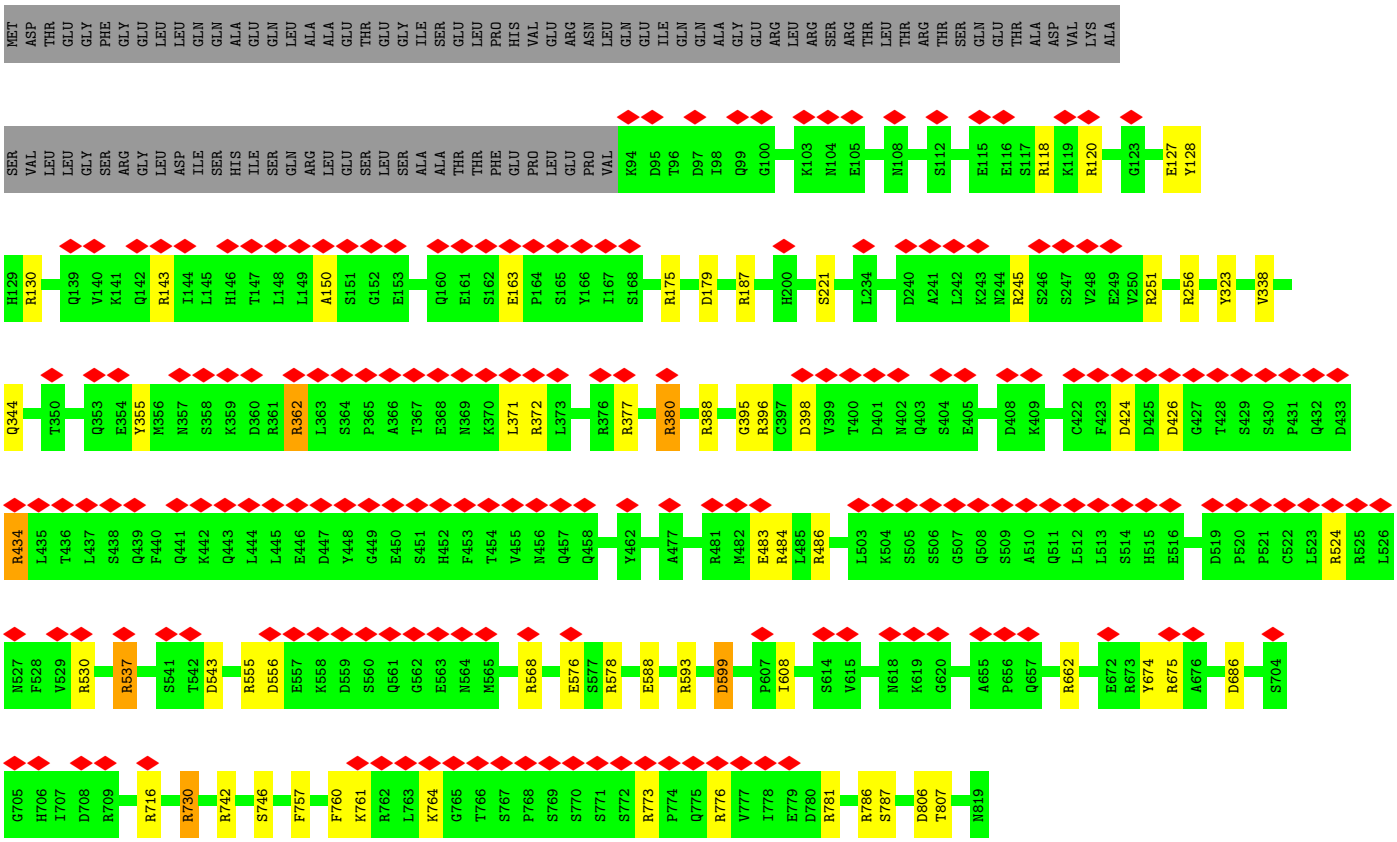
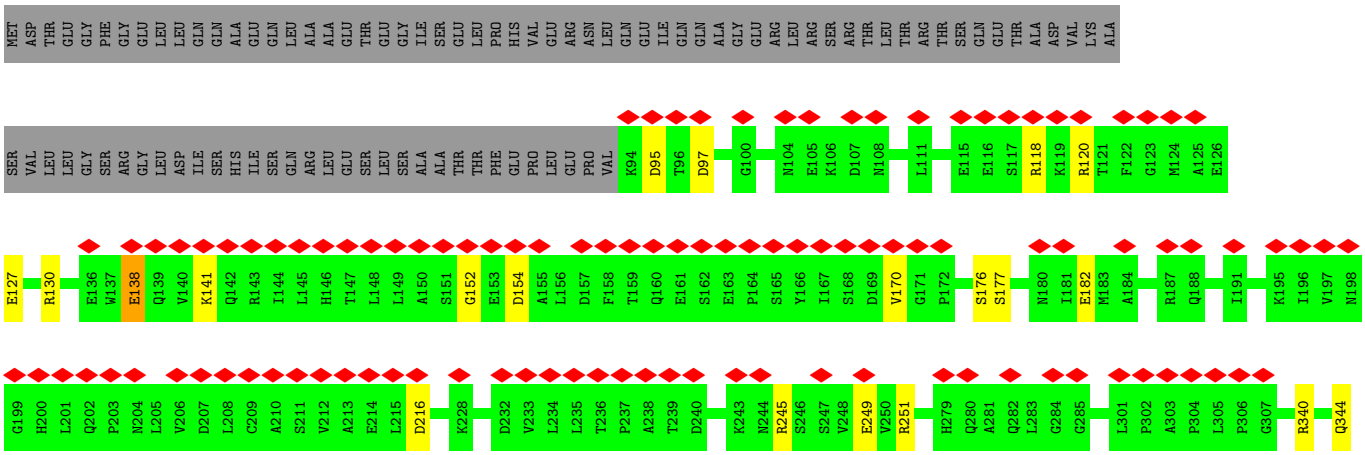
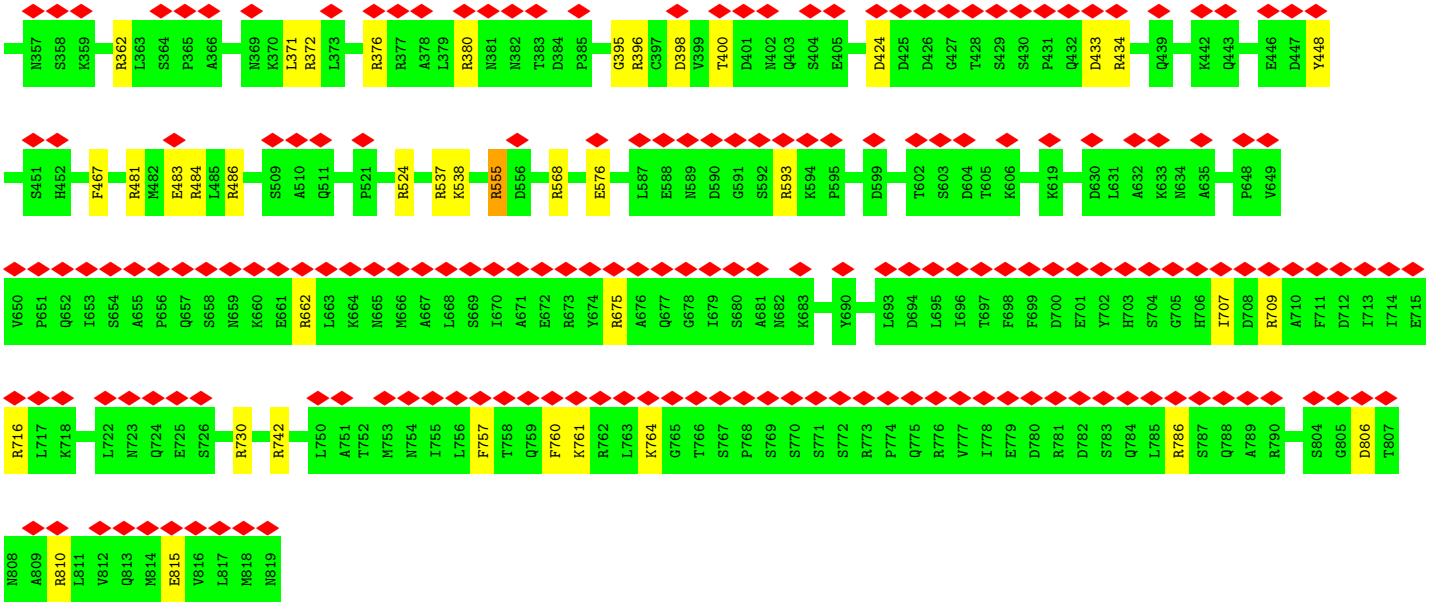


• Molecule 4: Nuclear pore complex protein Nup93

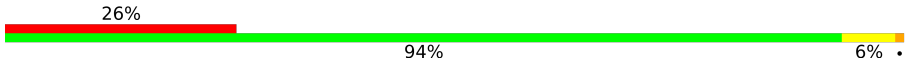
Chain A6:

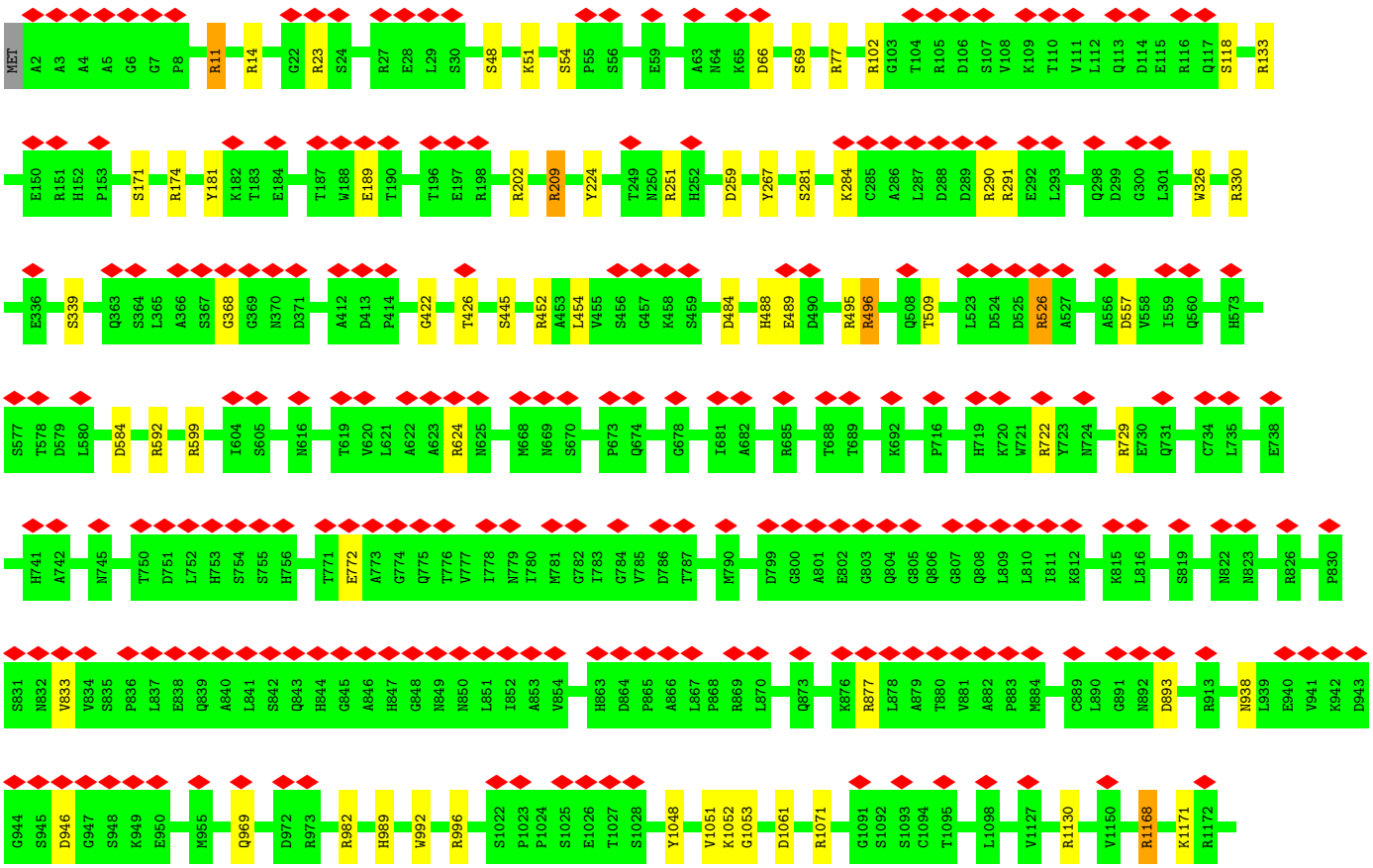


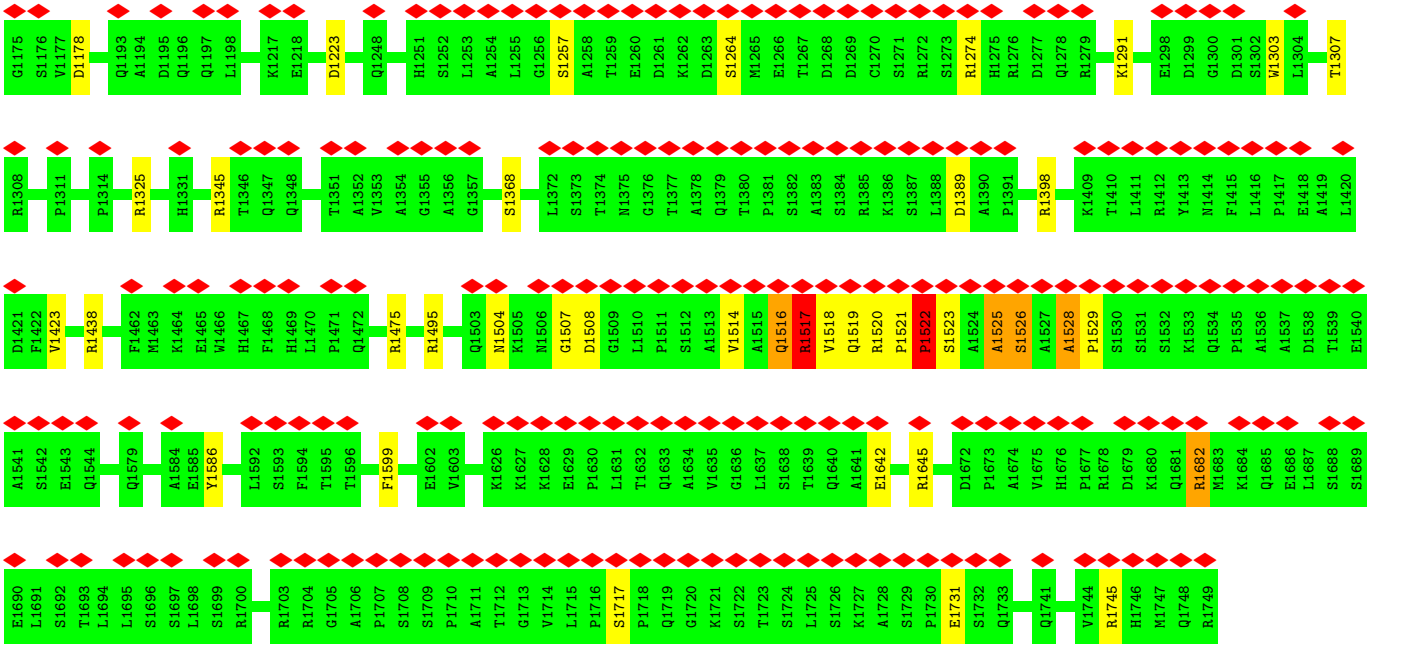


- Molecule 5: Nucleoporin NUP188 homolog

Chain B0:







- Molecule 5: Nucleoporin NUP188 homolog

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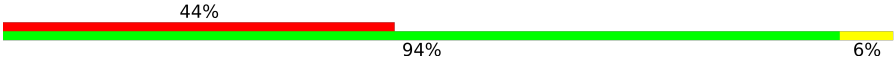

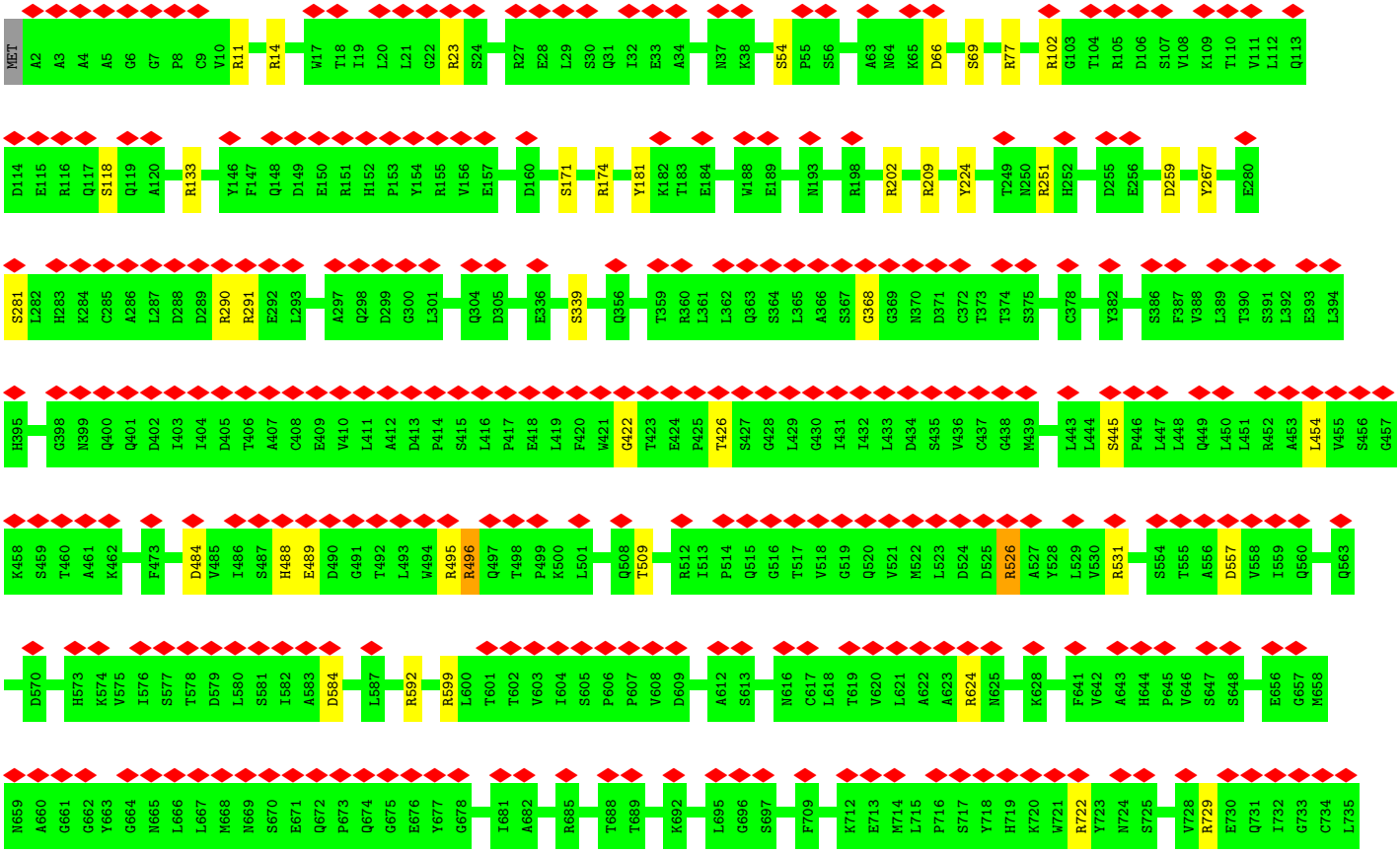

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- Molecule 6: Nuclear pore complex protein Nup205

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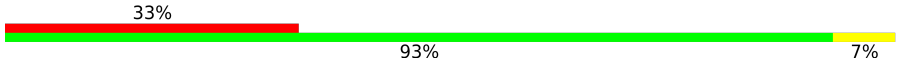

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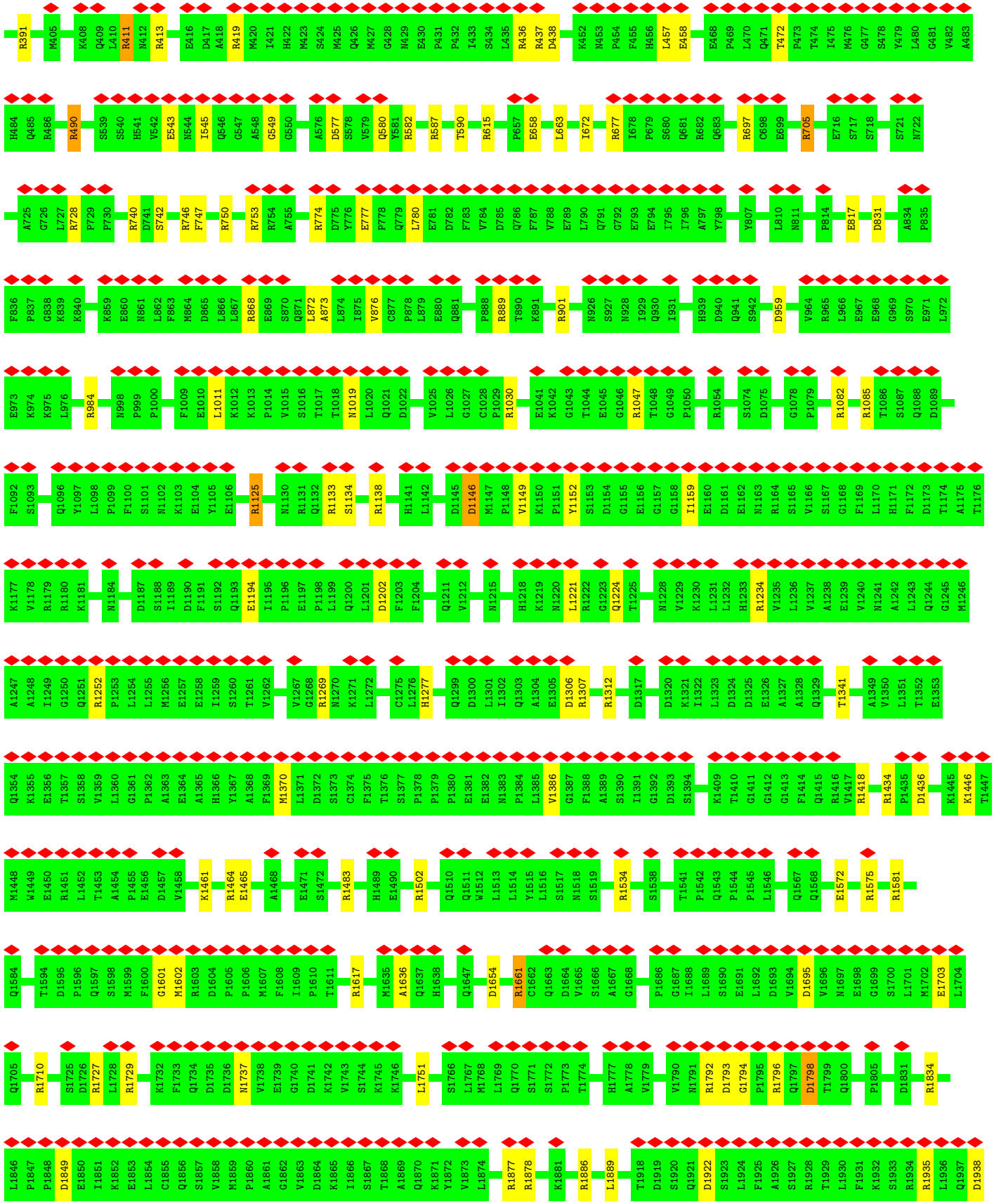
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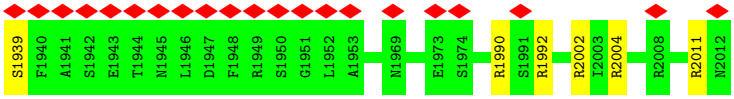

- Molecule 6: Nuclear pore complex protein Nup205

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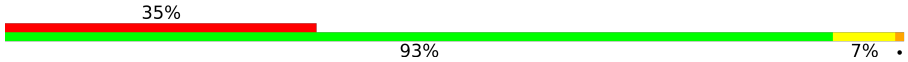

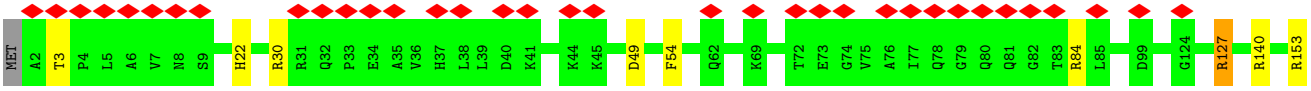

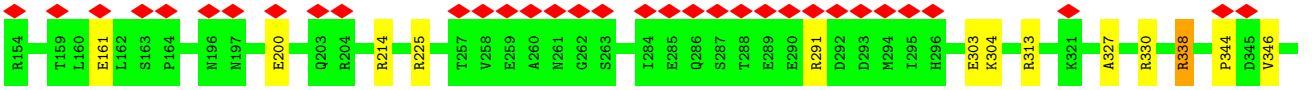

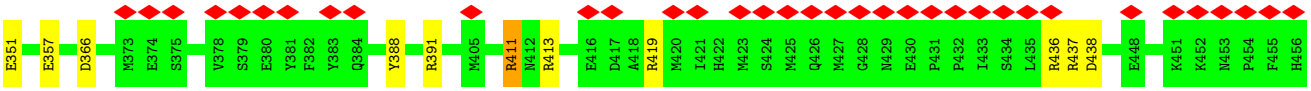

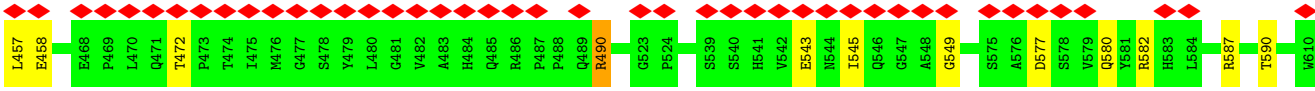

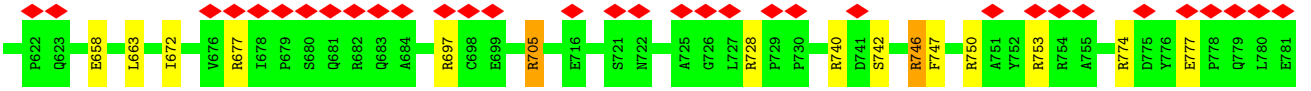

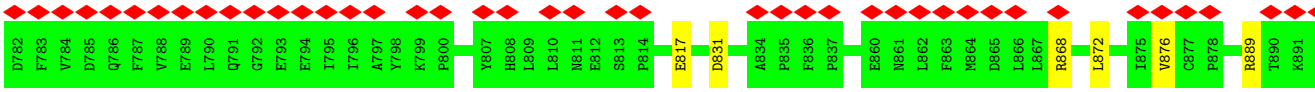

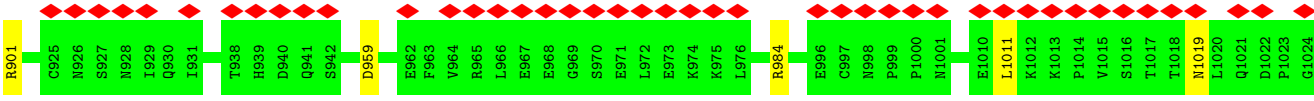

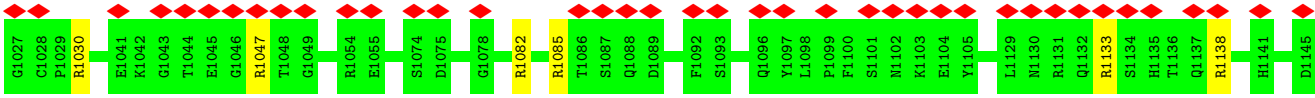

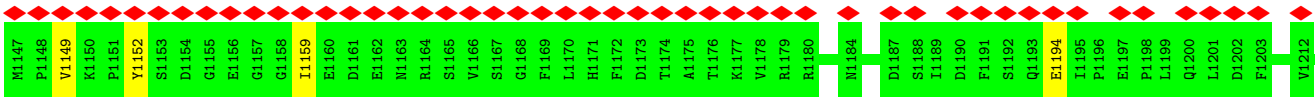

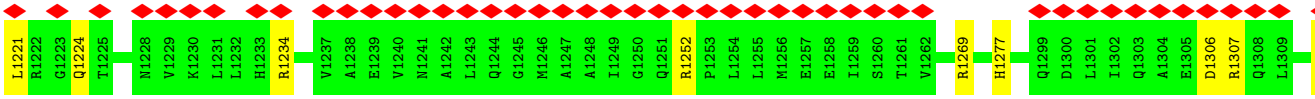

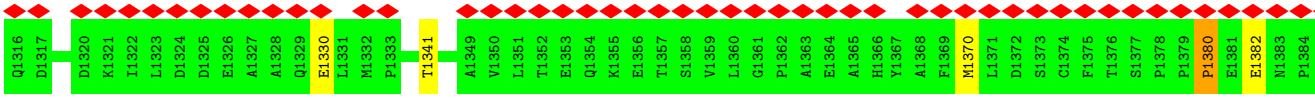

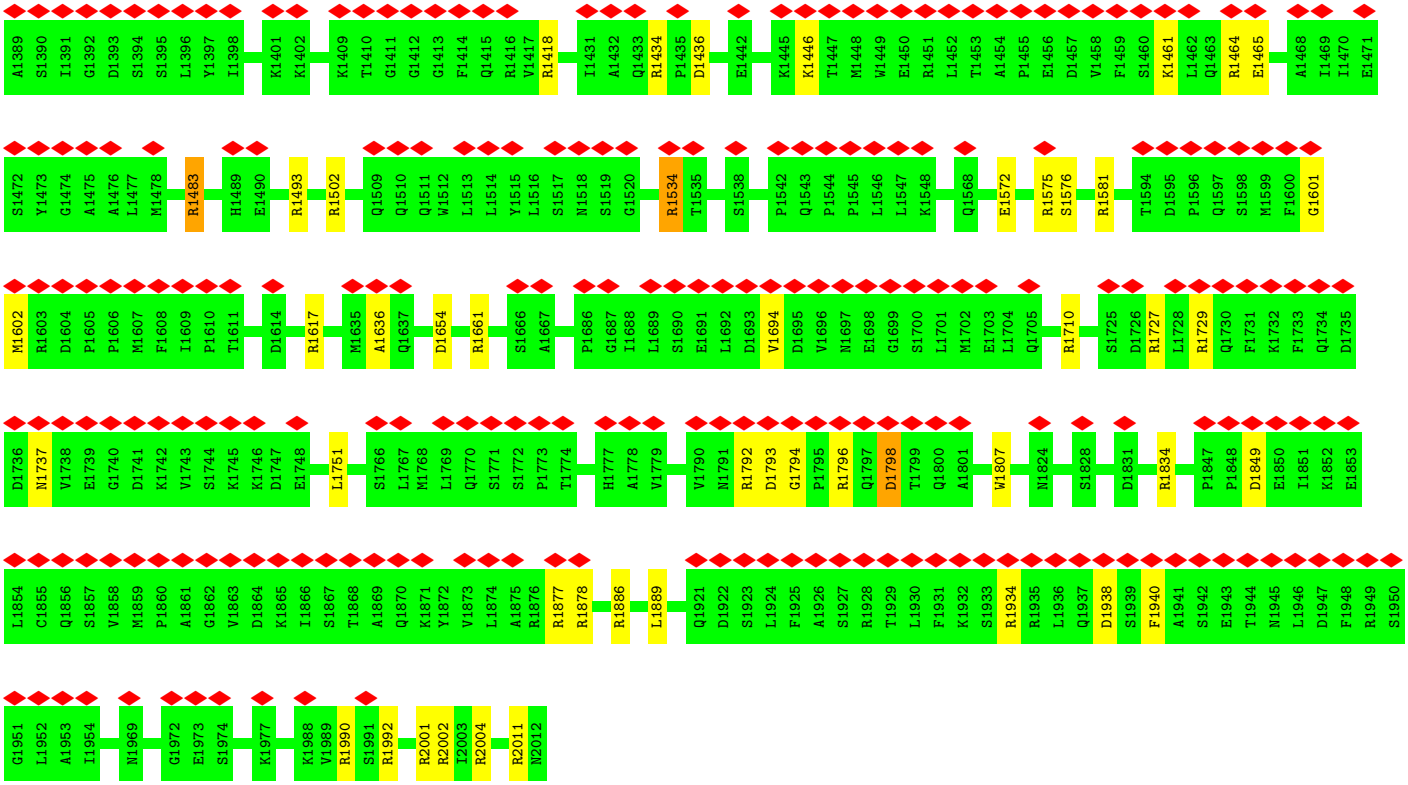

- Molecule 6: Nuclear pore complex protein Nup205

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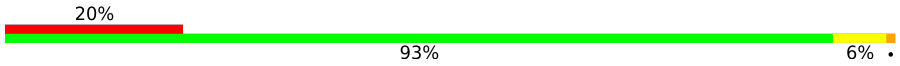

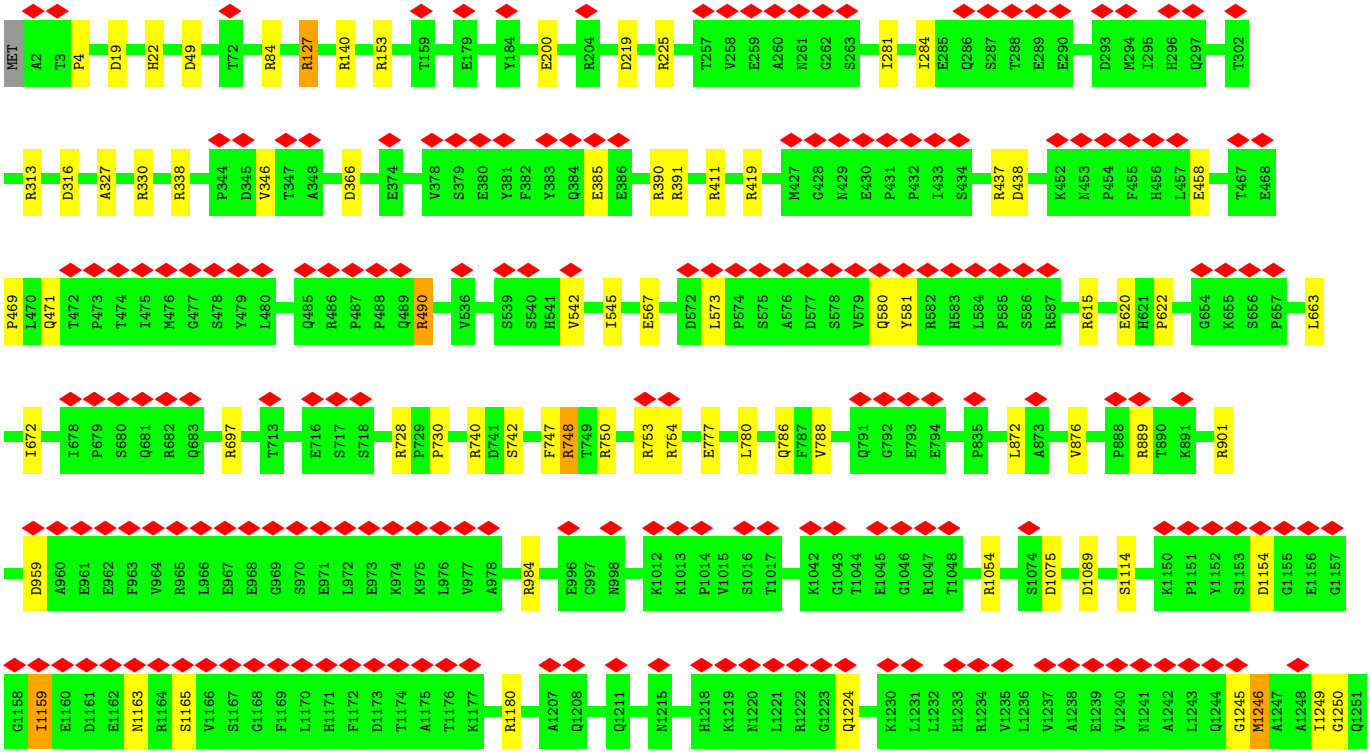

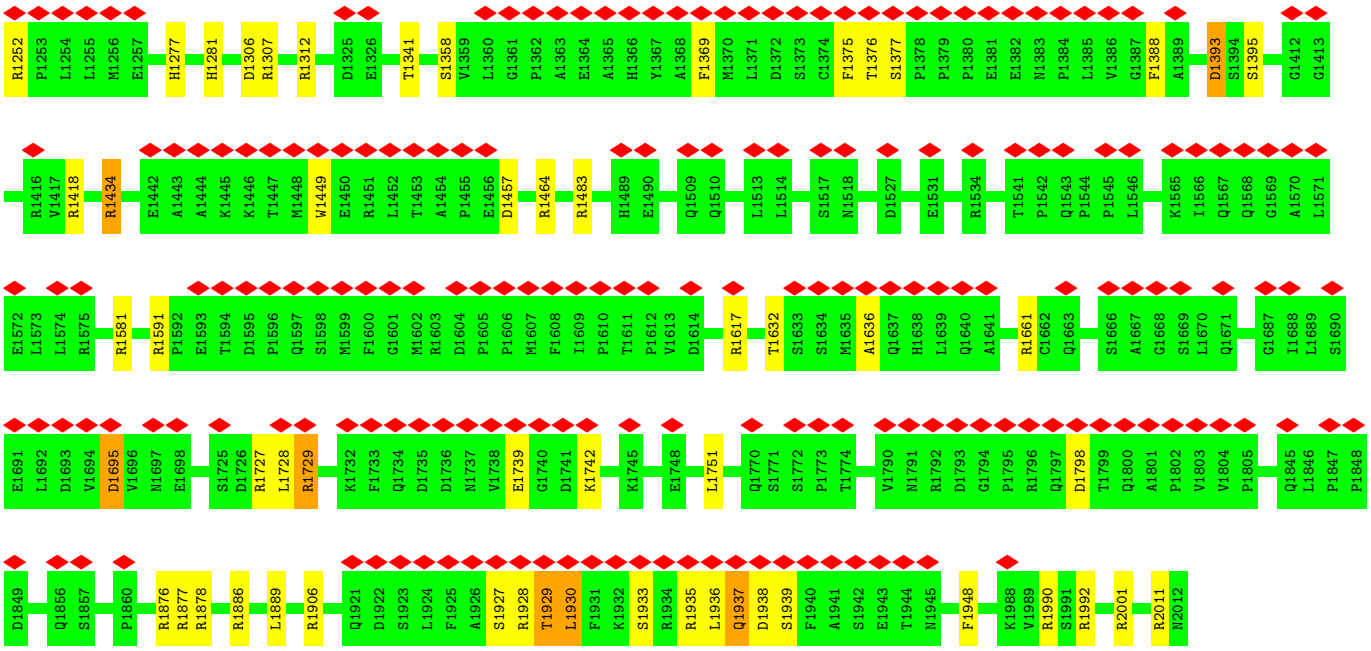

- Molecule 6: Nuclear pore complex protein Nup205

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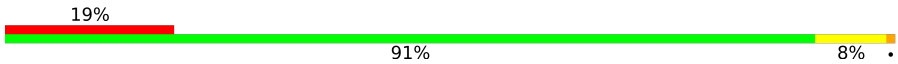

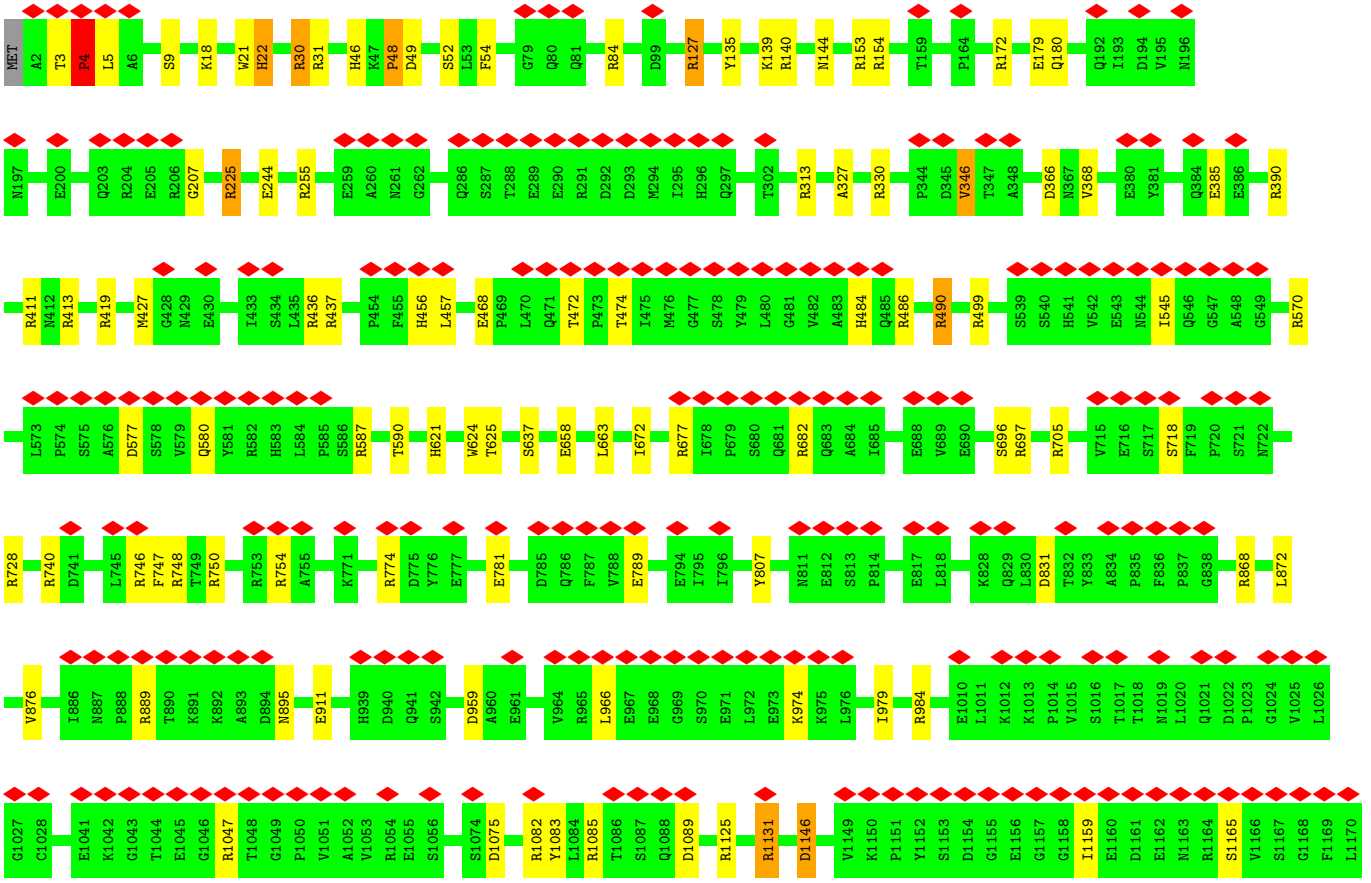

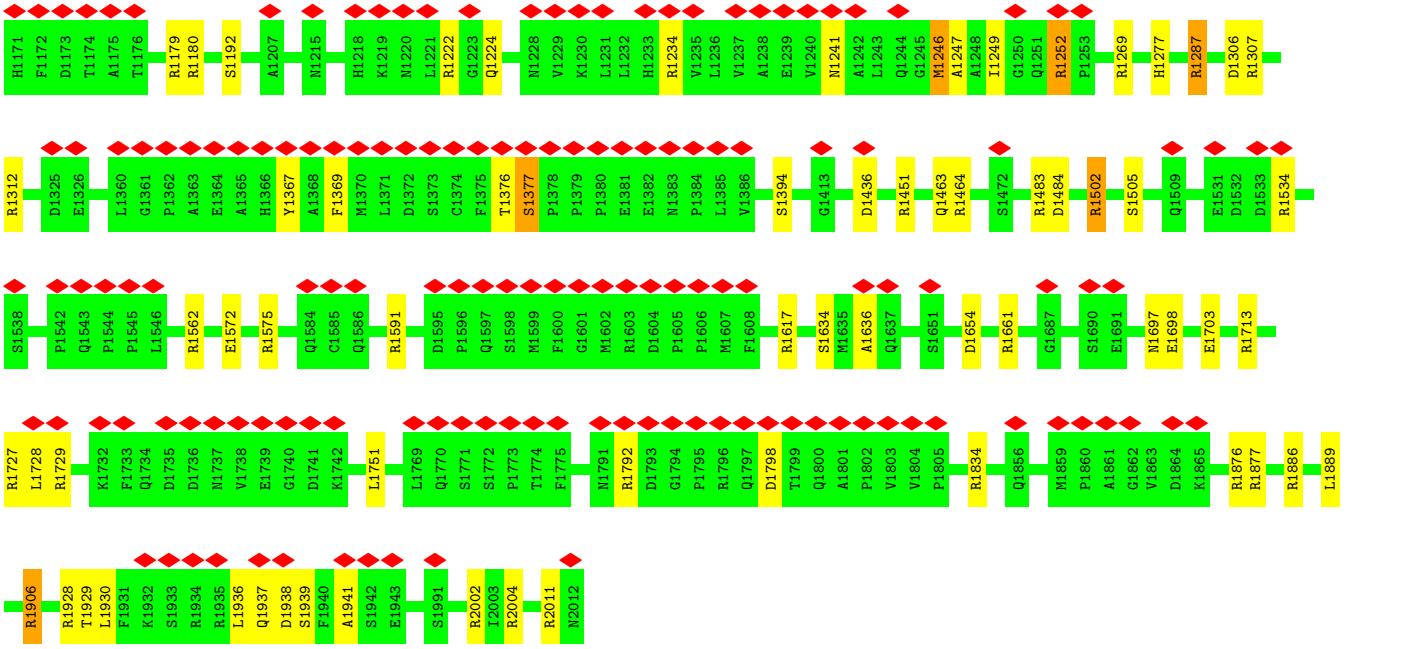

- Molecule 6: Nuclear pore complex protein Nup205

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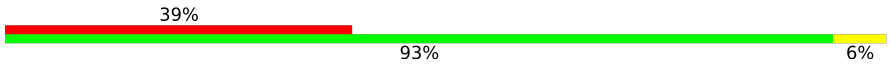

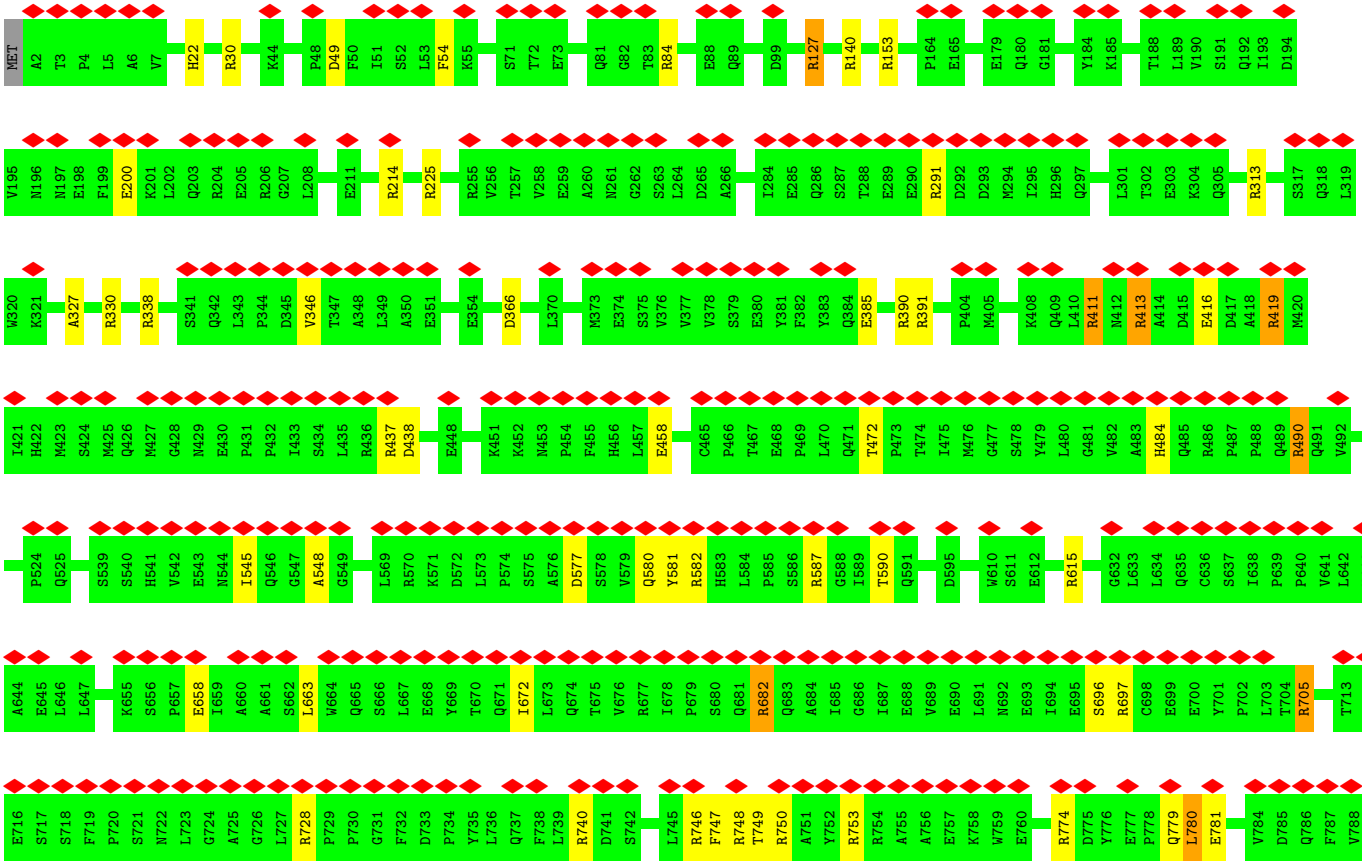

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- Molecule 7: Nuclear pore complex protein Nup155

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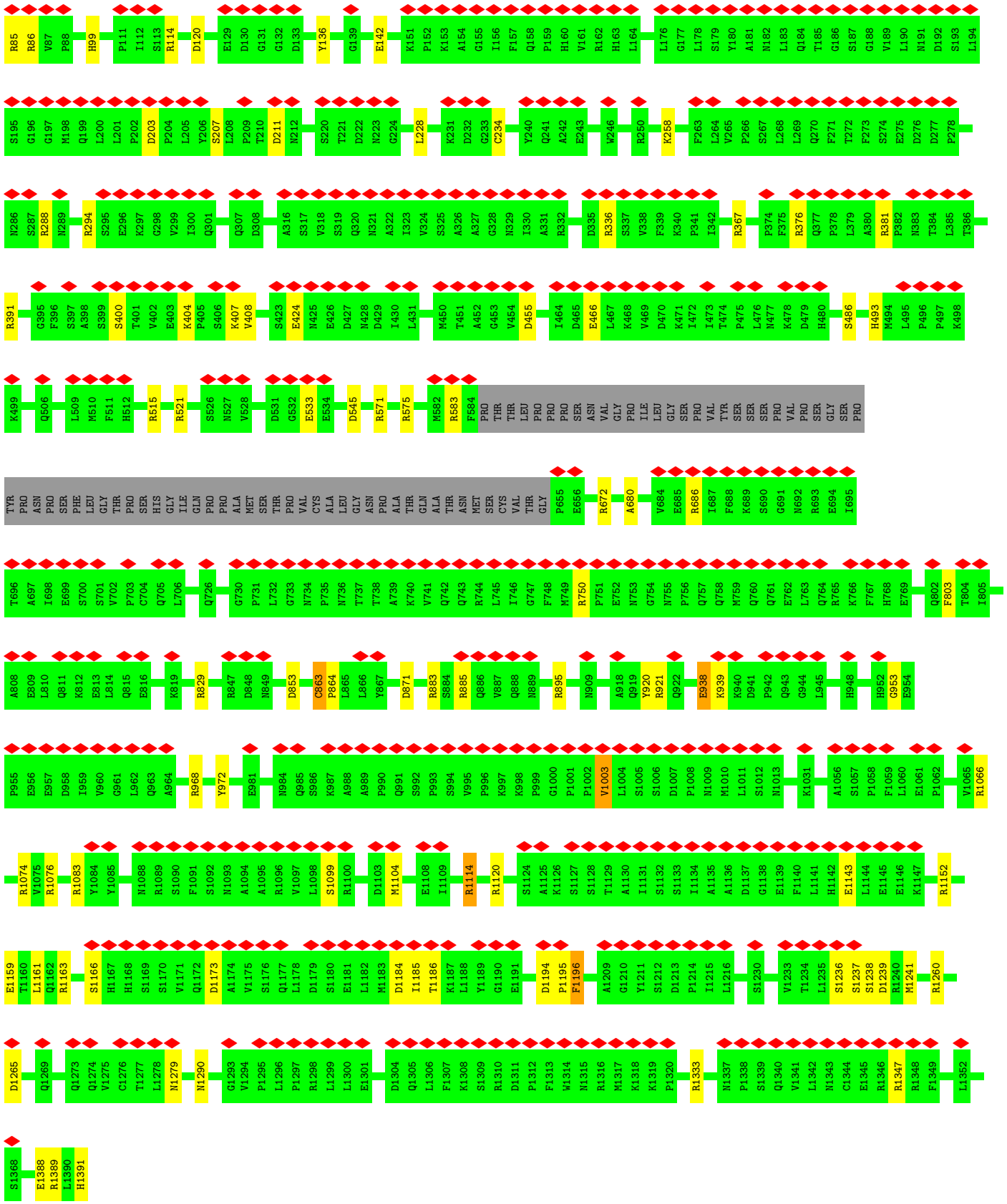

- Molecule 7: Nuclear pore complex protein Nup155

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S61 D62 M63 D64 L67 Q68 G69 P70 G71 L72 L73 S74 V75 P76 N77 L78 P79 E80 I81 S82 S83 I84 R85 R86 V87 E92 E95 Q96 F97 G98 H99 M100 Q101 C102 N103 C104 M105 M106 G107 V108 F109 P110 P111 I112 S113 R114 A115 W116 L117 T118 I119 D120 S121 D122 I123 L134

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A452 G453 V454 D455 G456 H457 S458 W459 A460 L461 S462 A463 I464 D465 E466 L467 K468 V469 D470 K471 I472 I473 T474 P475 L476 N477 K478 D479 H480 I481 P482 I483 T484 D485 S486 P487 V488 V489 V490 Q491 Q492 H493 M494 L495 P496 P497 K498 K499 F500 V501 L502 L503 S504 A505 Q506 G507 S508 L509 M510 F511

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R750 P751 E752 N753 G754 N755 P756 Q757 Q758 M759 E762 L772 I776 Q779 A780 I781 Q782 Q783 R786 Y789 L792 A793 L794 W795 K796 L797 L798 C799 E800 H801 Q802 F803 T804 I805 I806 V807 A808 E809 L810 Q811 K812 E813 L814 Q815 E816 Q817 L818 K819 I820 I821 T822 F823 K824

D825 L826 V827 I828 R829 D830 K831 E832 L833 T834 G835 A836 L837 I838 A839 S840 L841 I842 N843 C844 Y845 I846 R847 D848 N849 A850 A851 V852 D853 G854 I855 S856 L857 H858 L859 Q860 D861 I862 C863 P864 L865 L866 Y867 S868 T869 D870 D871 A872 I873 C874 S875 K876 A877 N878 E879 L880 L881 Q882 R883 S884

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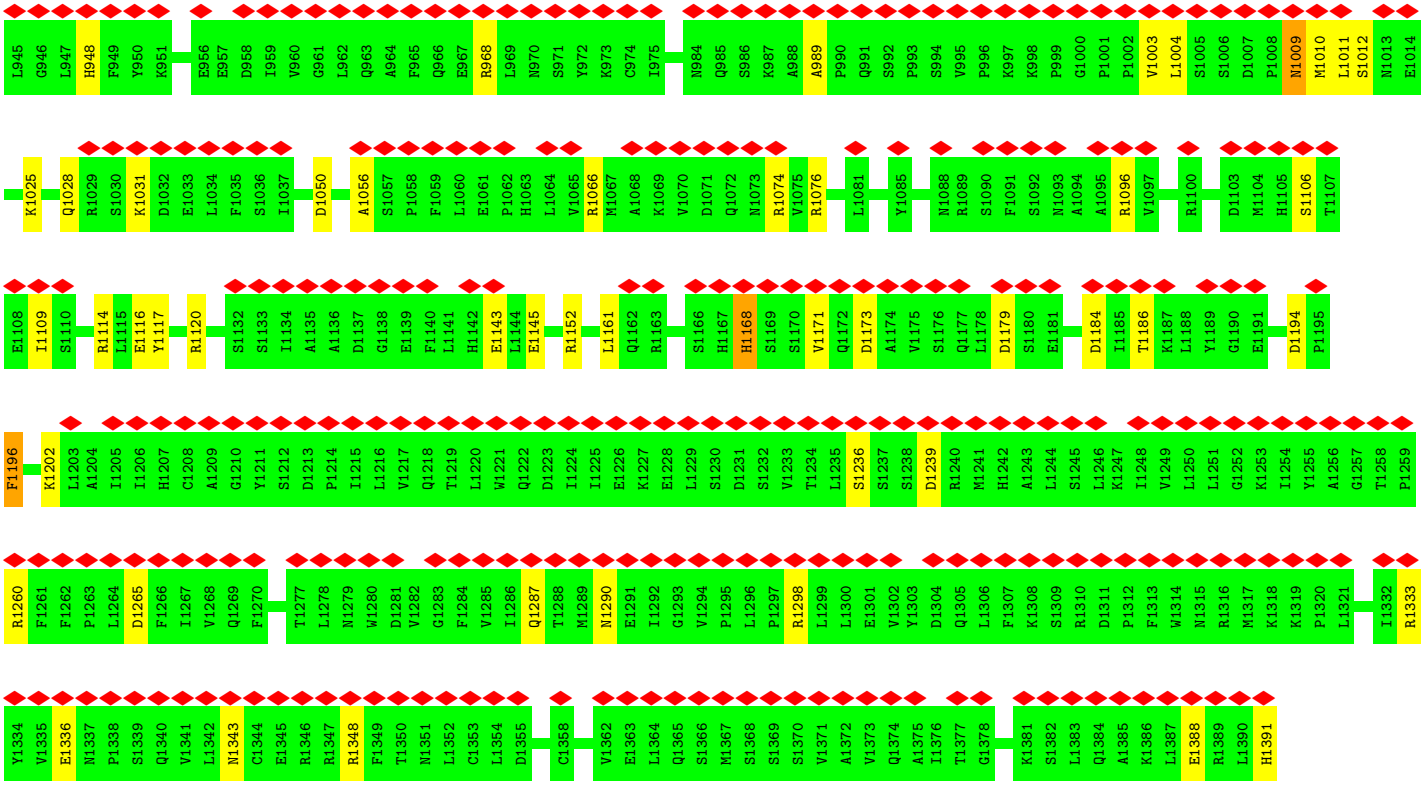

- Molecule 7: Nuclear pore complex protein Nup155

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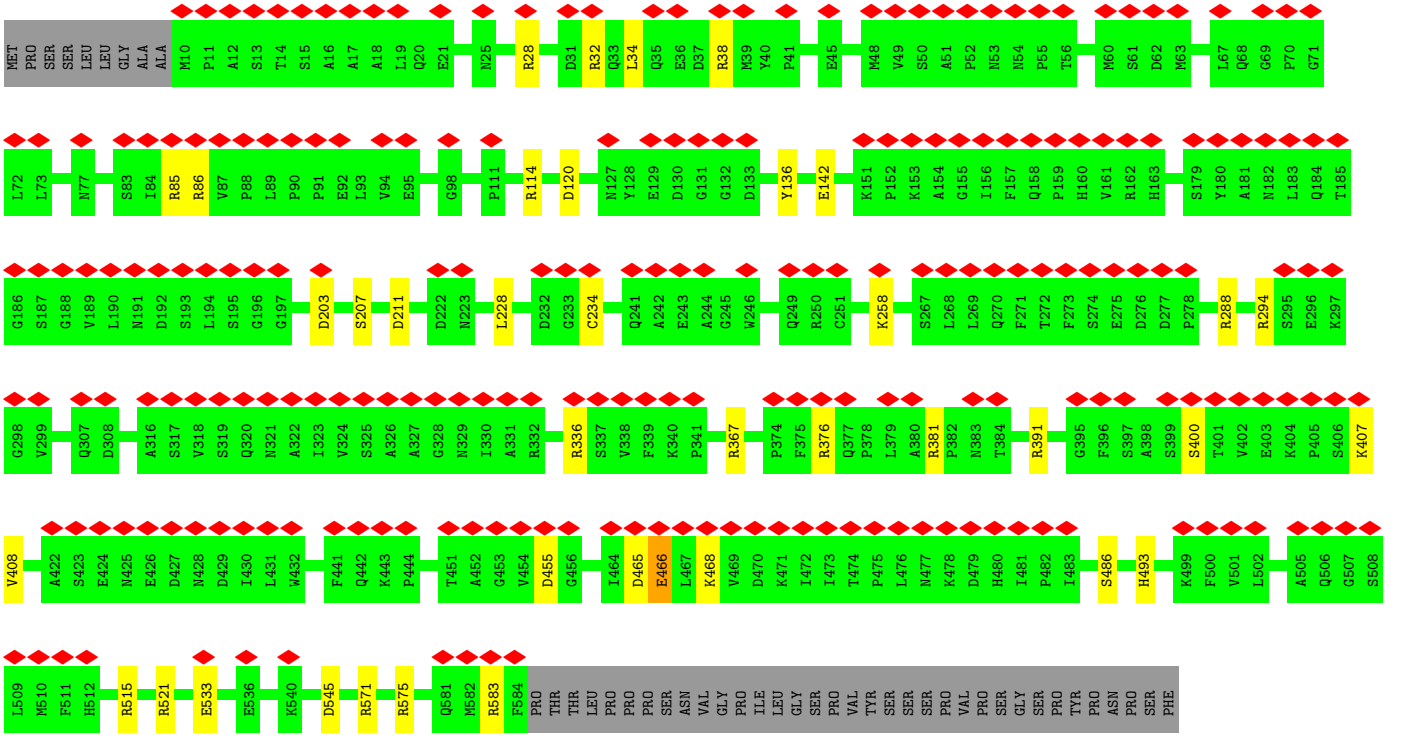

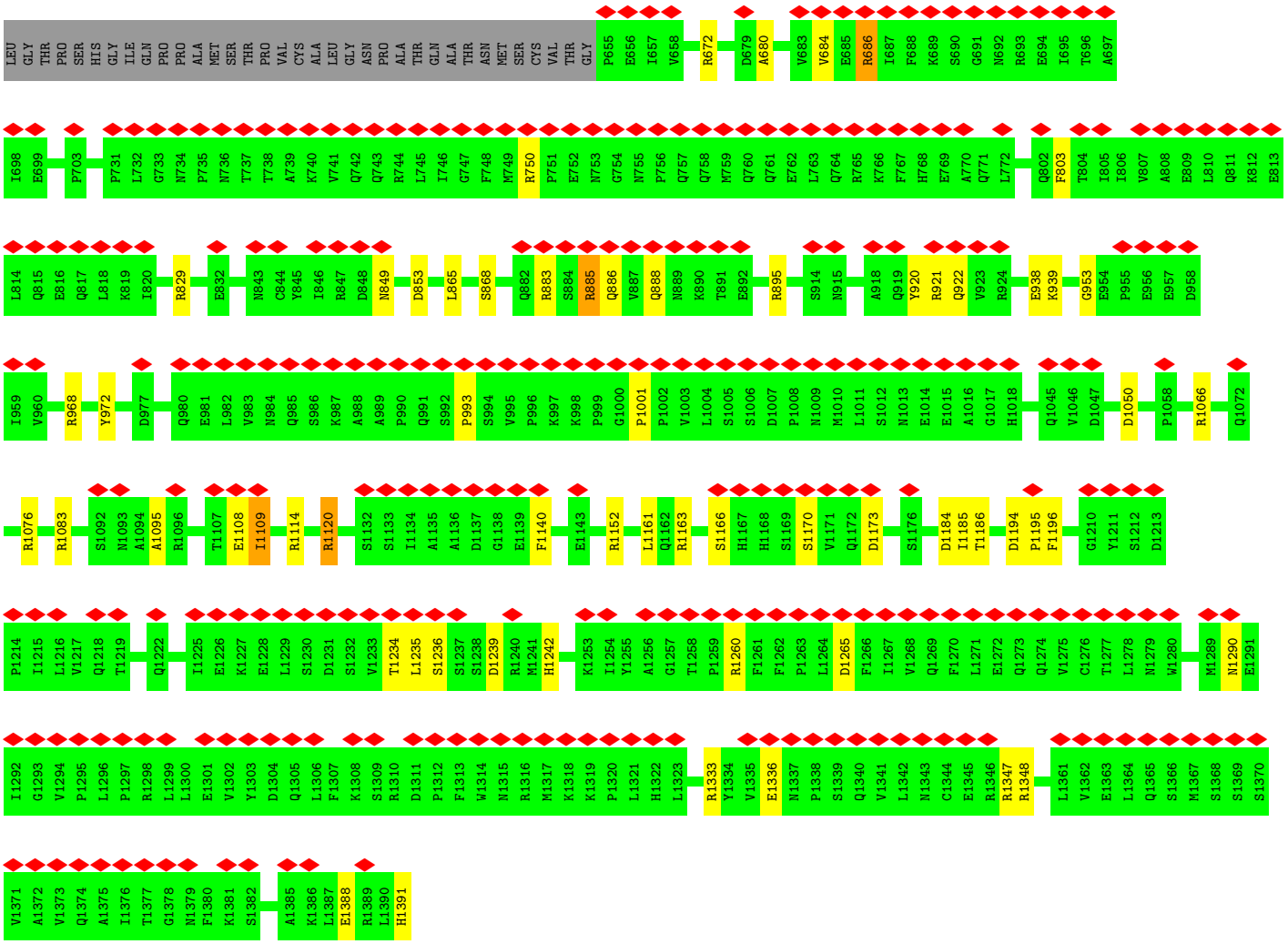

- Molecule 7: Nuclear pore complex protein Nup155

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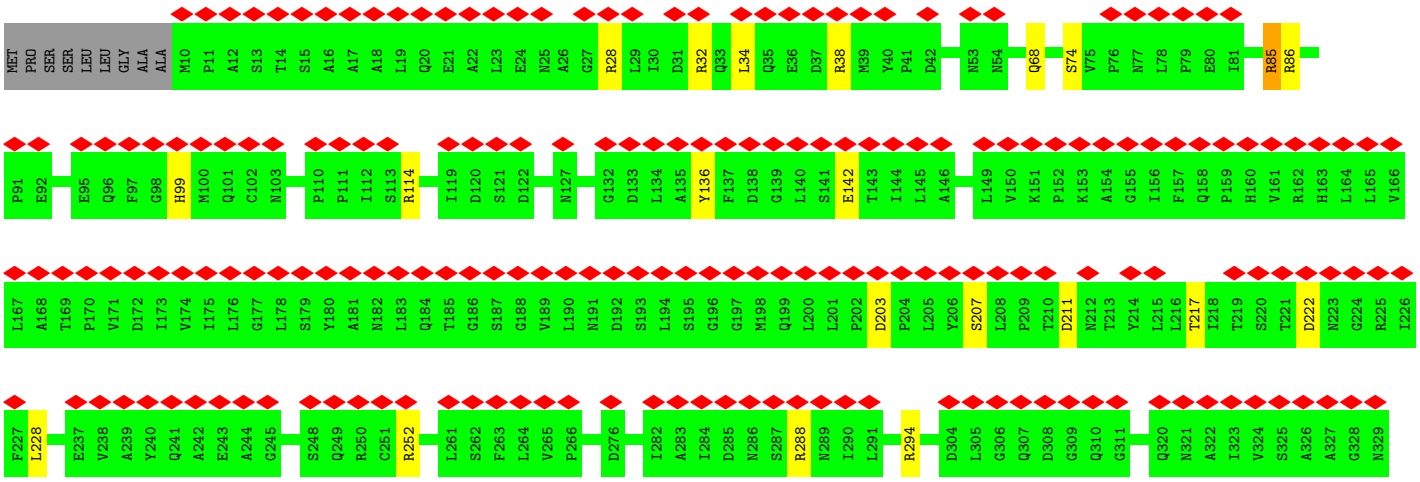

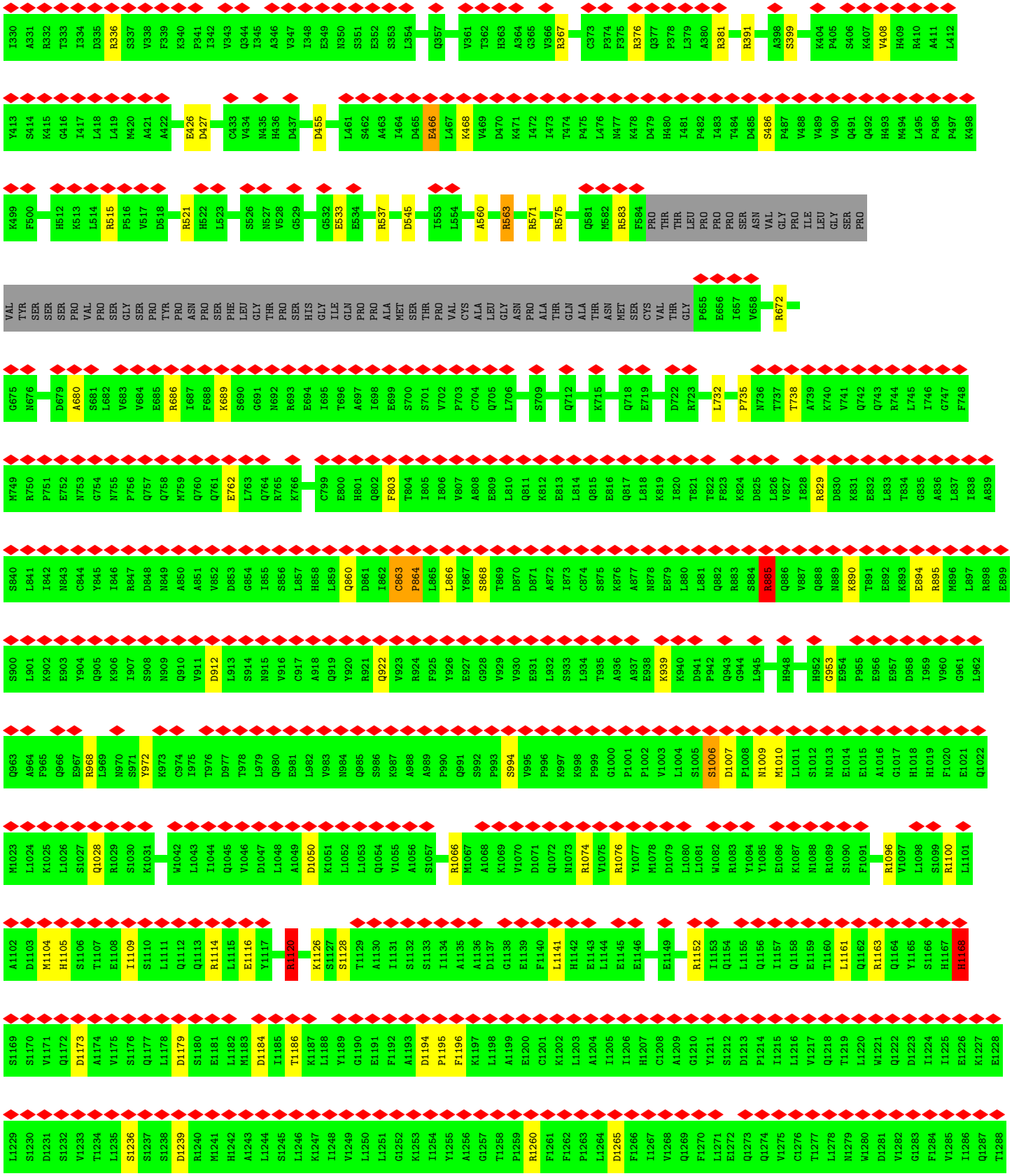
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VAL TYR SER SER SER PRO VAL PRO SER GLY SER PRO TYR PRO ASN PRO SER PHE LEU GLY THR PRO SER HIS GLY ILE GLN PRO PRO ALA MET SER THR PRO VAL CYS ALA LEU GLY ASN PRO ALA THR GLN ALA THR ASN MET SER CYS VAL THR GLY P655 E656 I657 V658 R672
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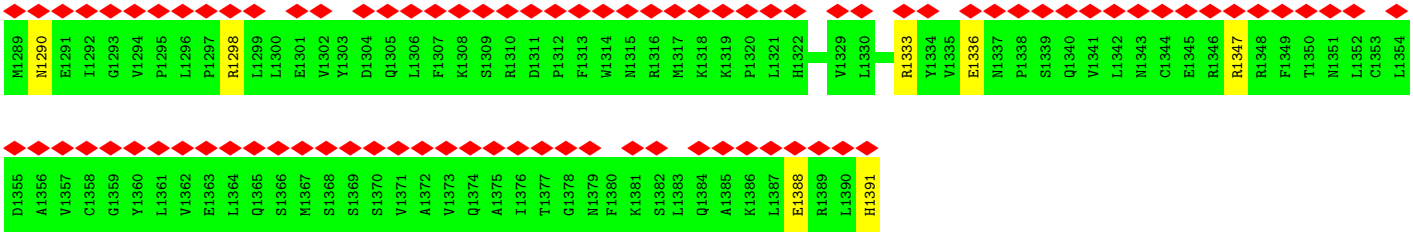

- Molecule 7: Nuclear pore complex protein Nup155

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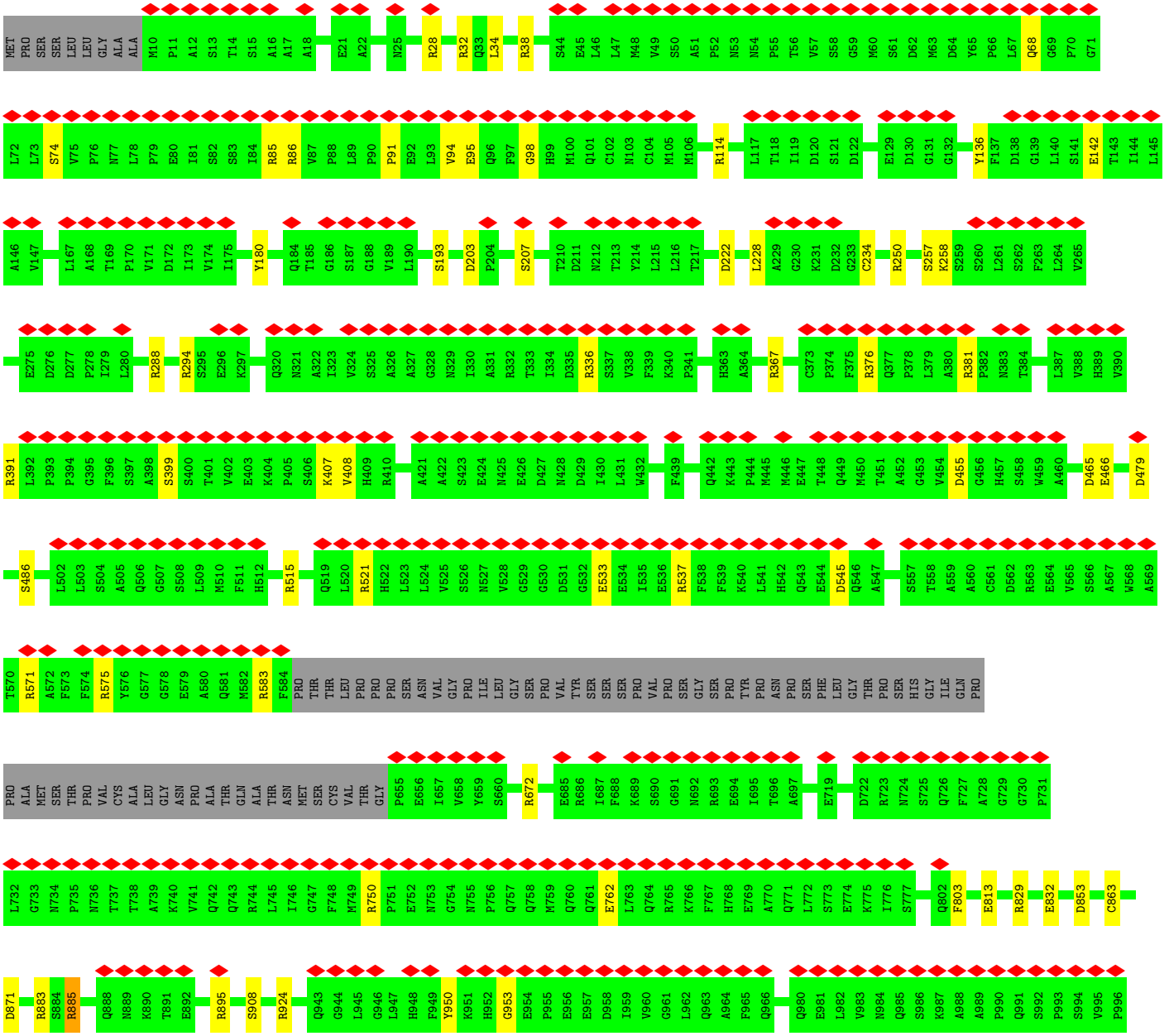

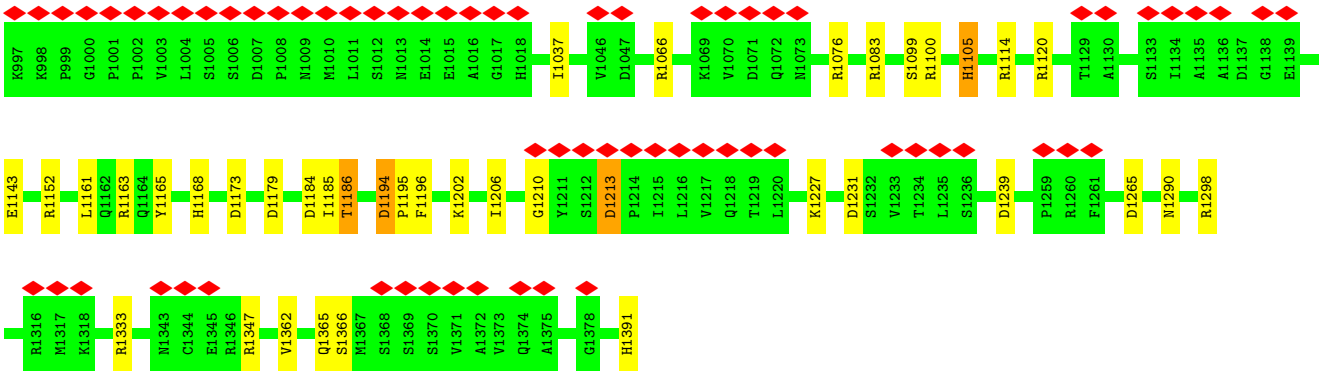

- Molecule 7: Nuclear pore complex protein Nup155

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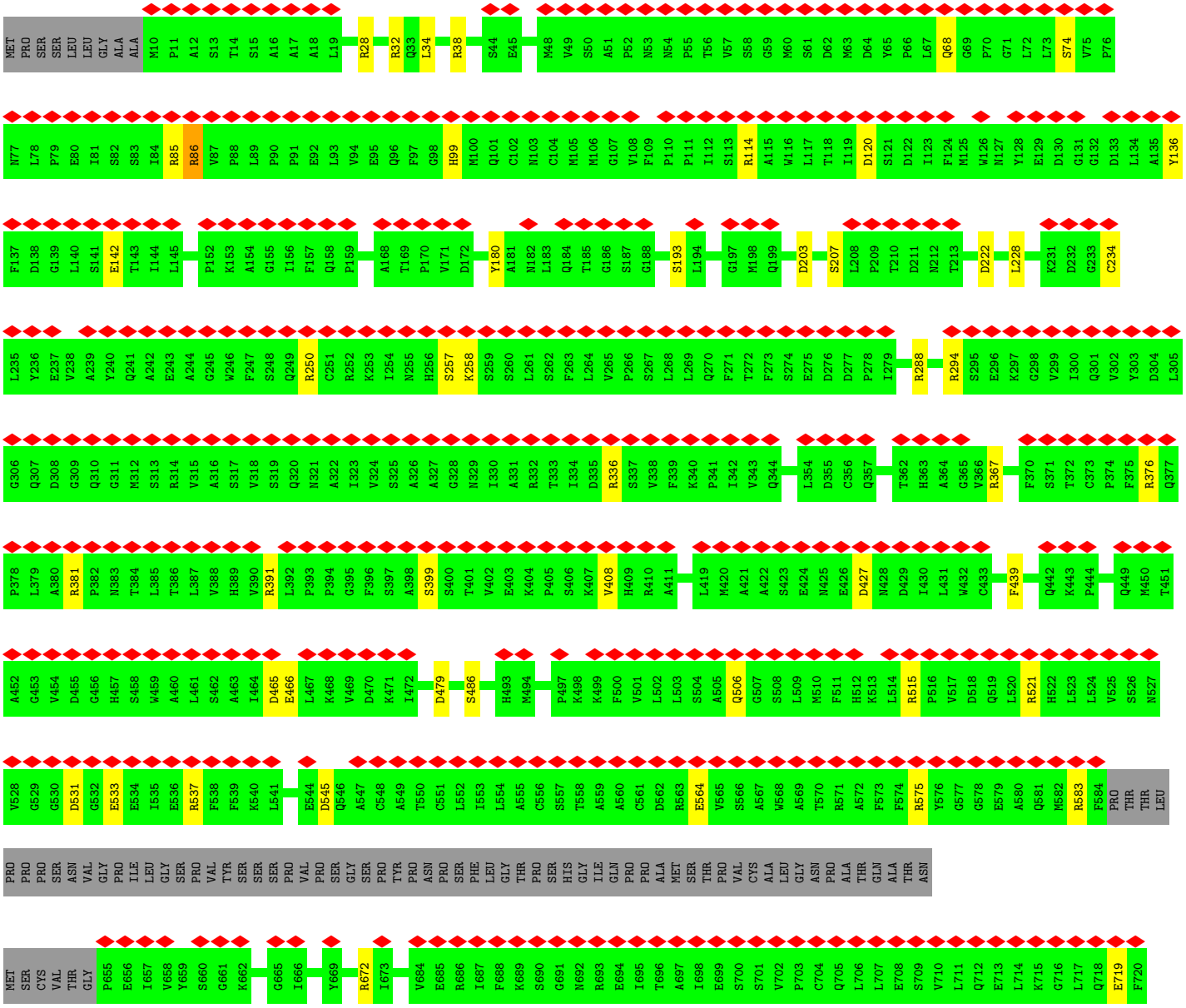

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- Molecule 8: Nucleoporin NDC1

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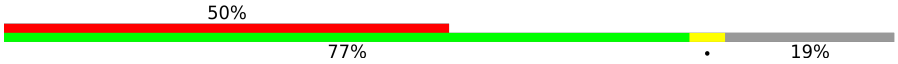

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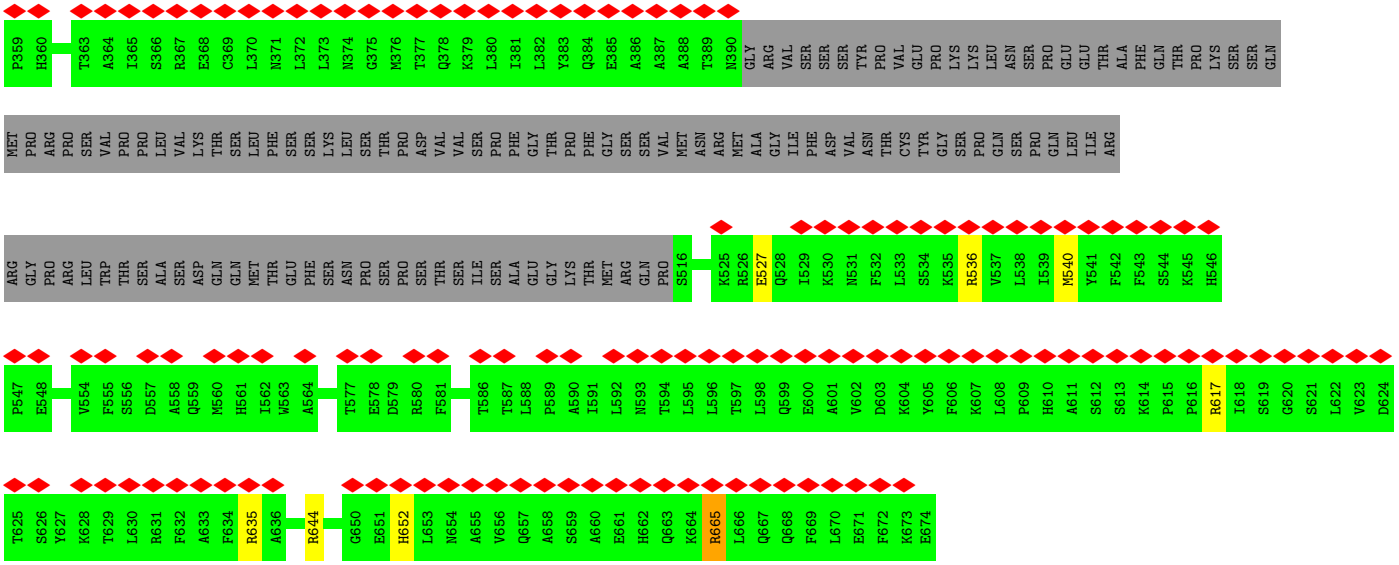

- Molecule 8: Nucleoporin NDC1

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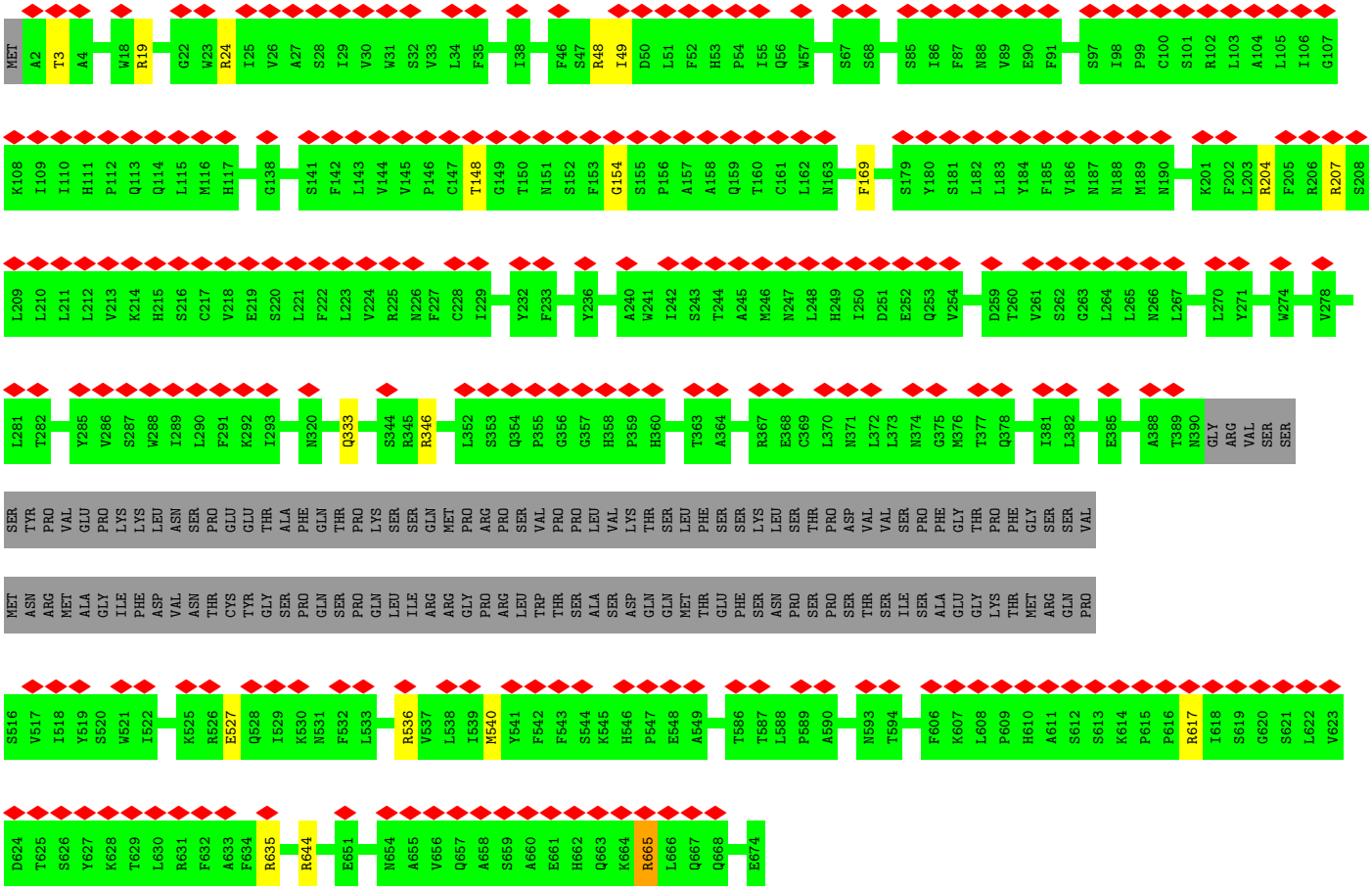

- Molecule 9: Nucleoporin NUP35

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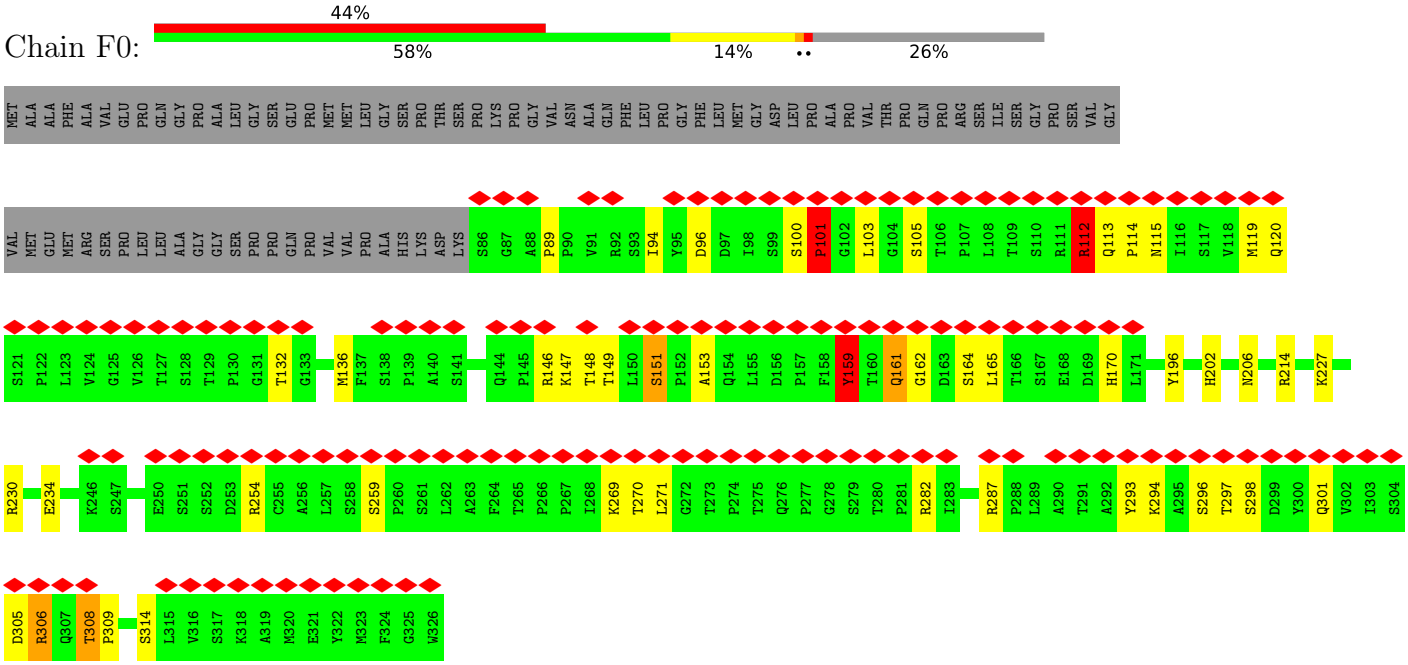
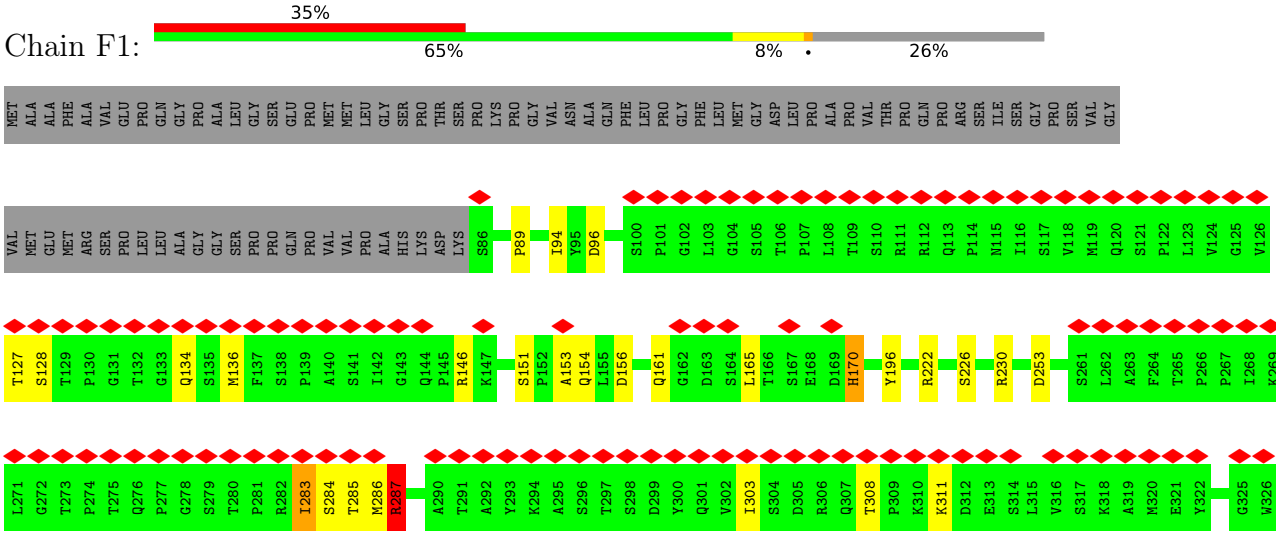


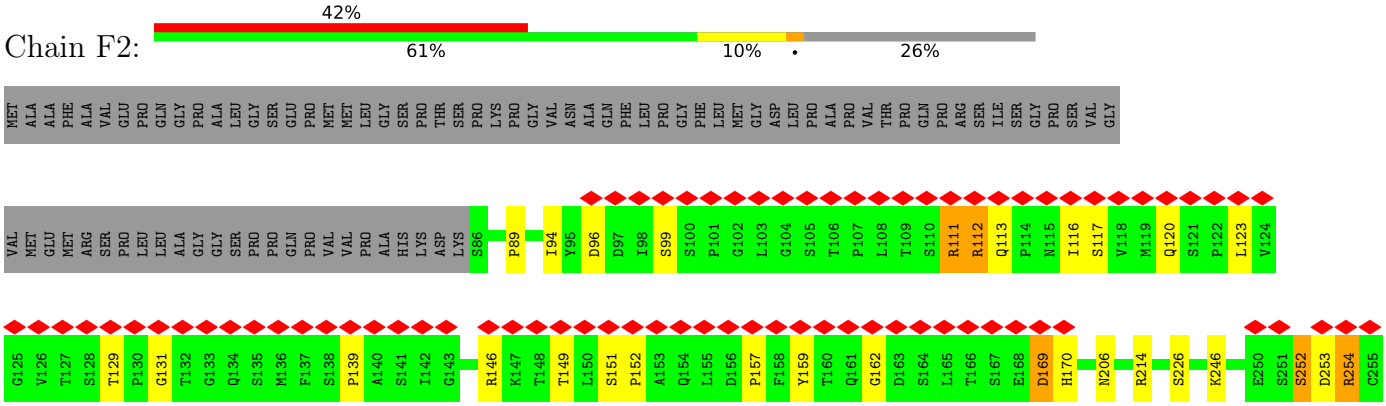
• Molecule 9: Nucleoporin NUP35

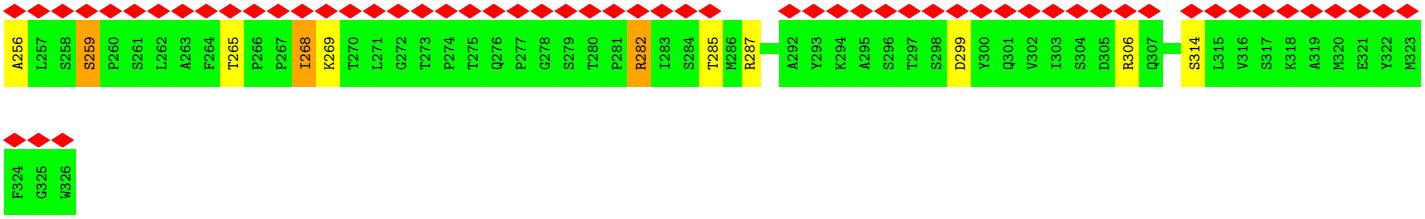
Chain F1:



• Molecule 9: Nucleoporin NUP35

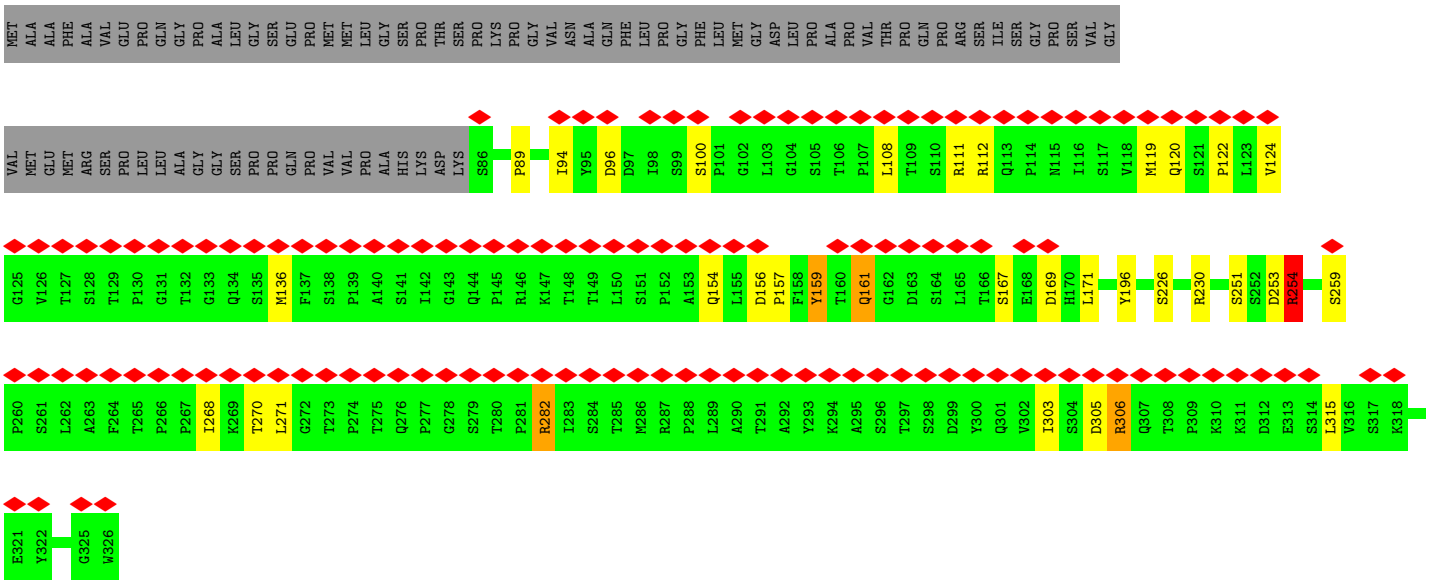
Chain F2:





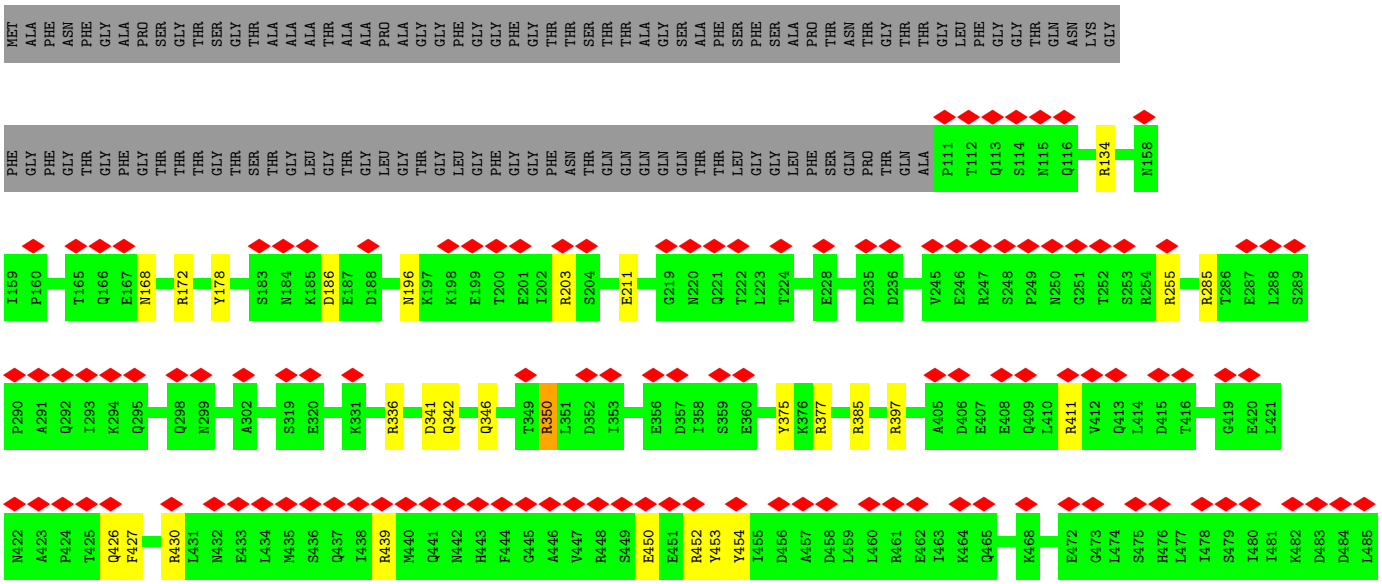
• Molecule 9: Nucleoporin NUP35

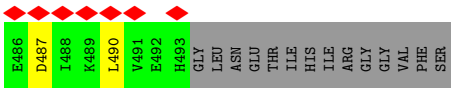
Chain F3:



• Molecule 10: Nucleoporin p54

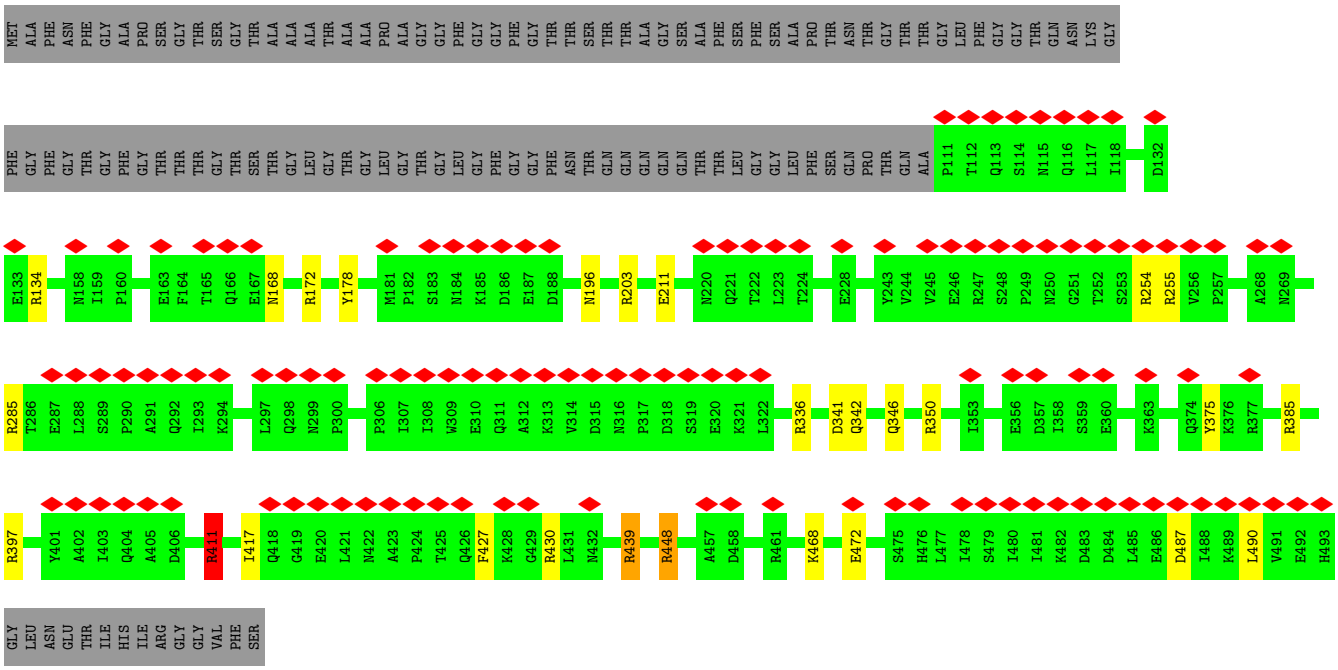
Chain H0:





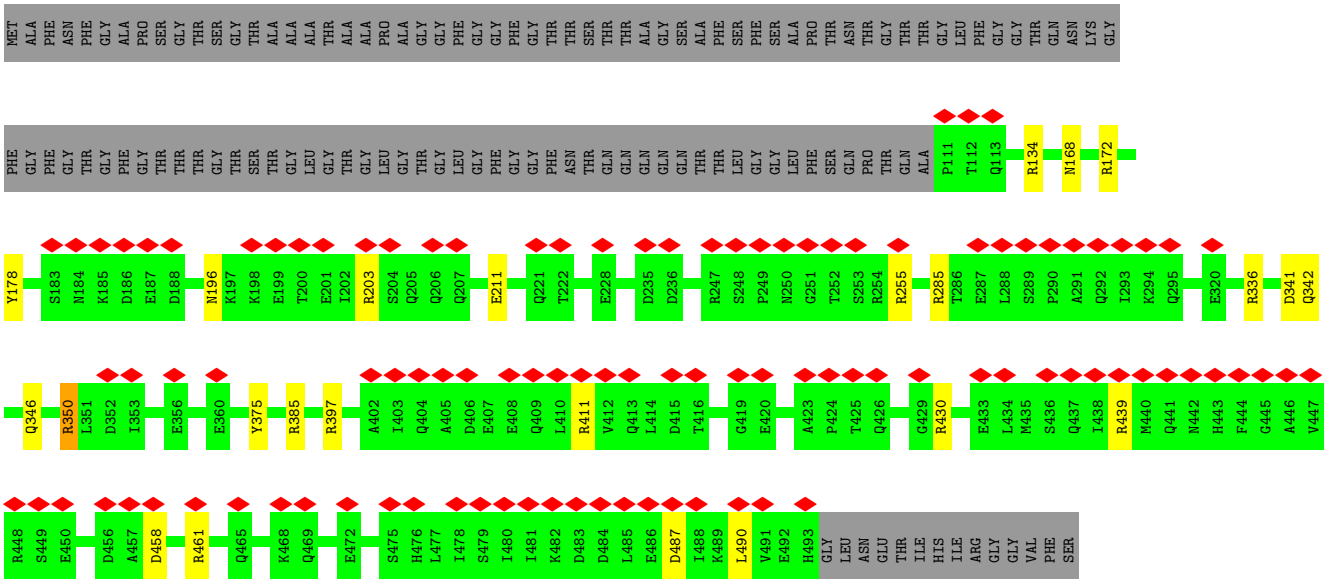
• Molecule 10: Nucleoporin p54

Chain H1:



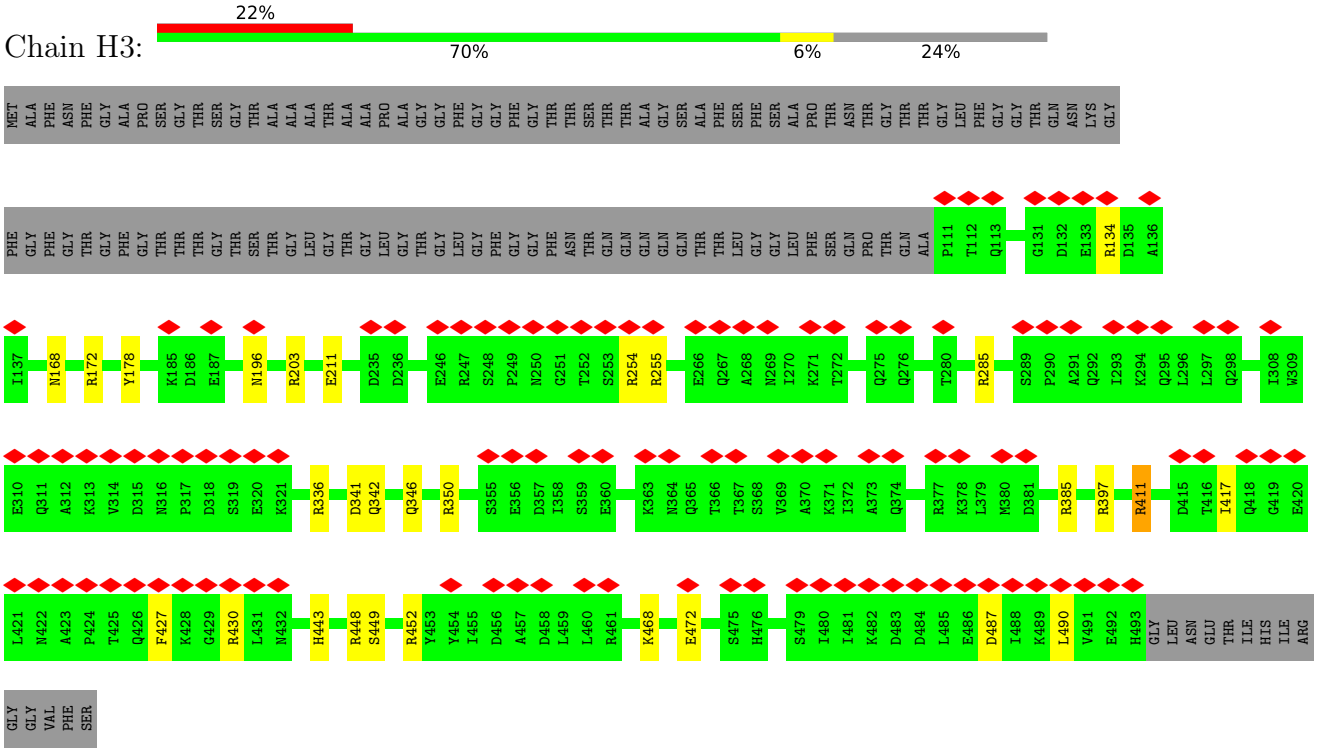
• Molecule 10: Nucleoporin p54

Chain H2:



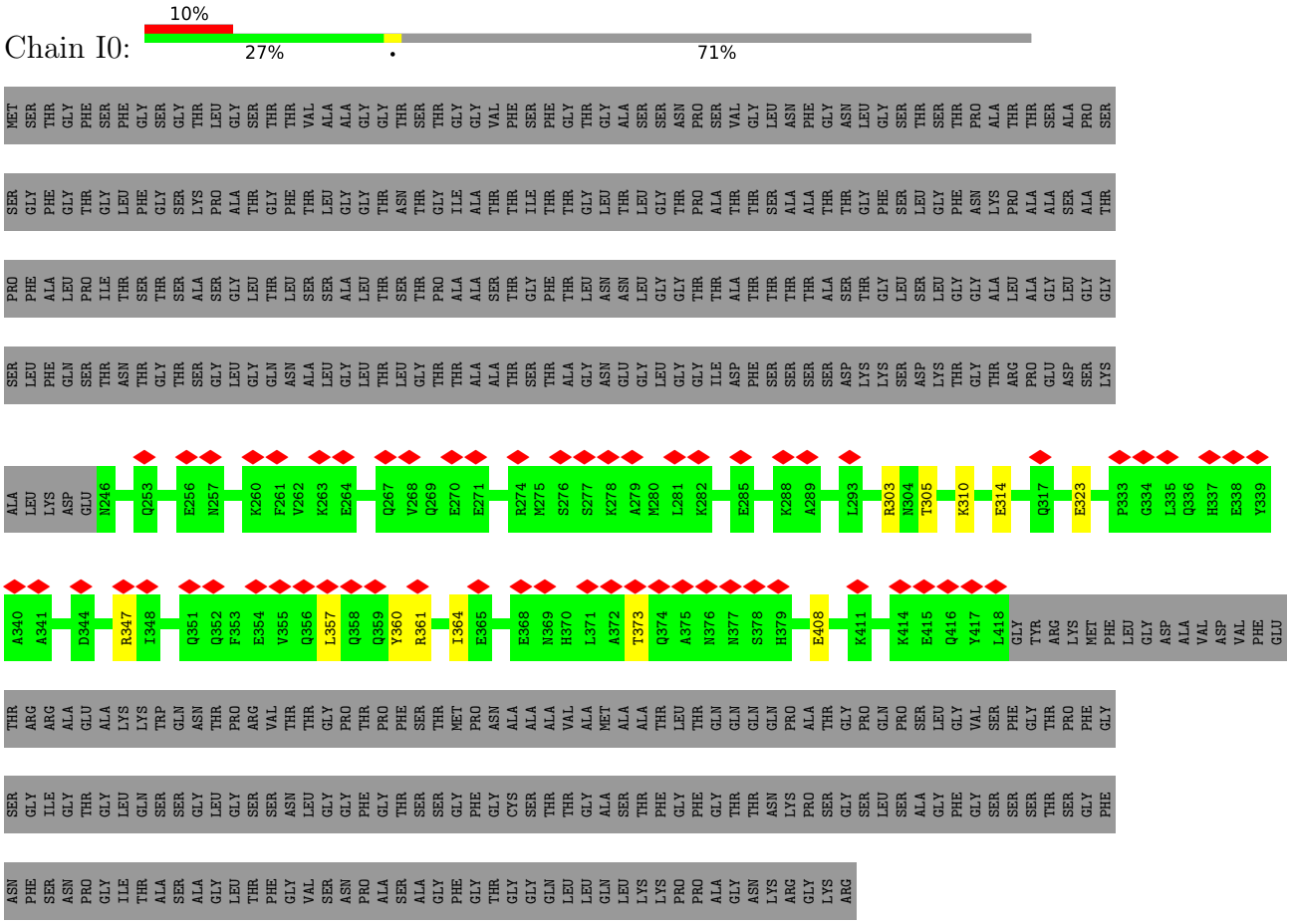
• Molecule 10: Nucleoporin p54

Chain H3:



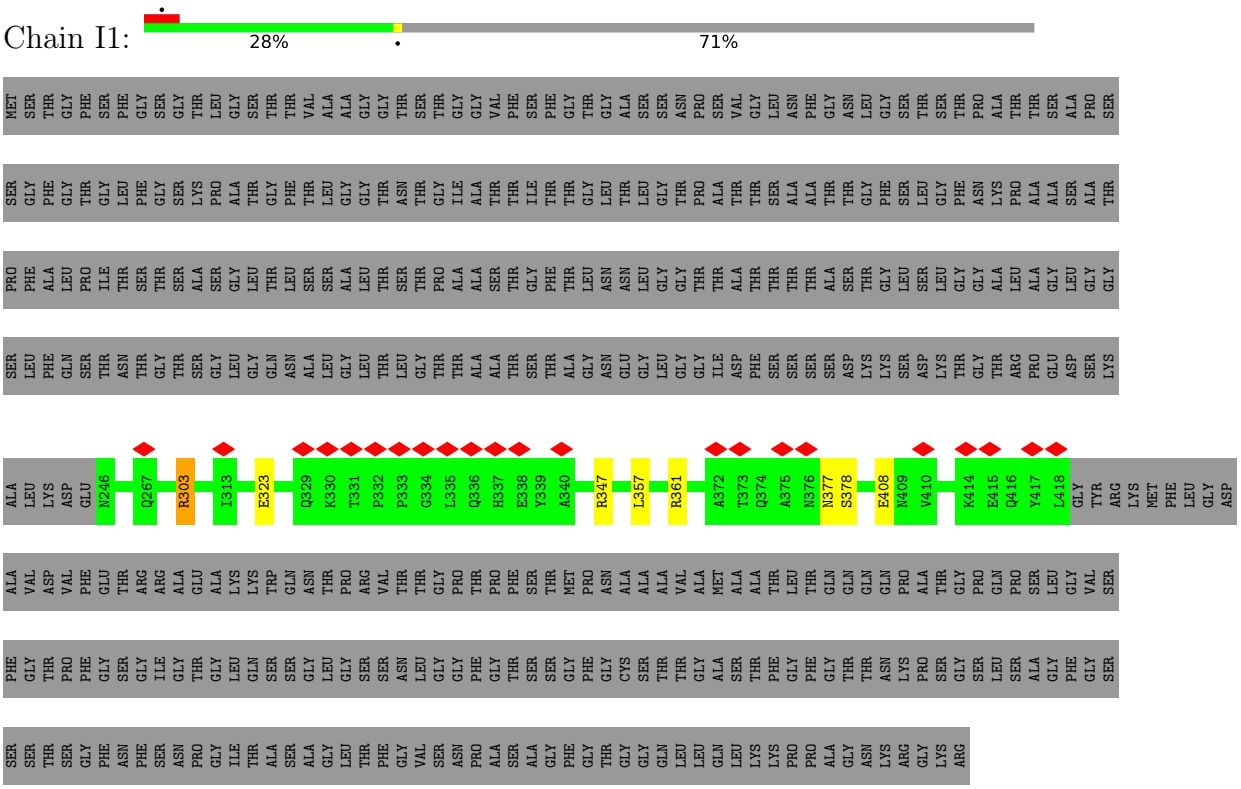
- Molecule 11: Nucleoporin p58/p45

Chain I0:



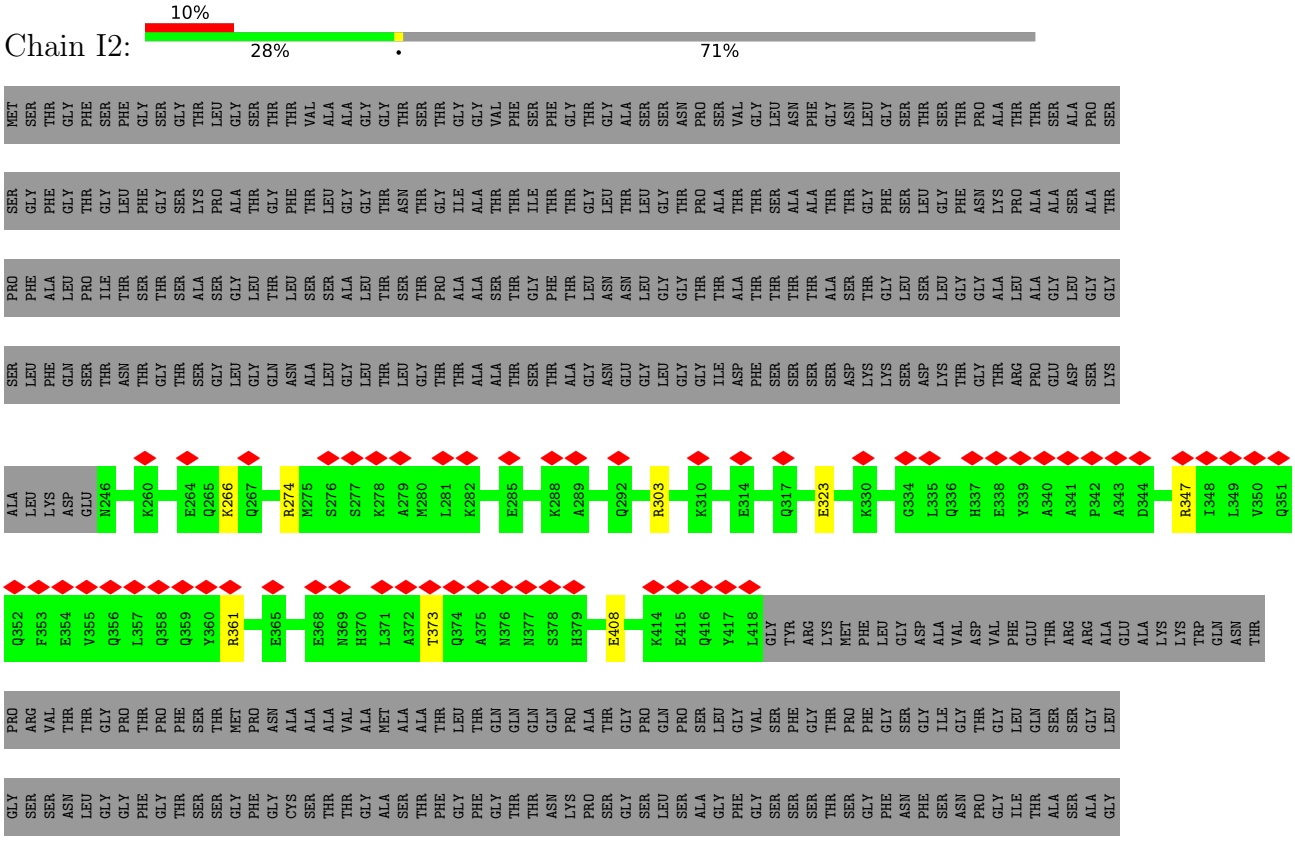
- Molecule 11: Nucleoporin p58/p45

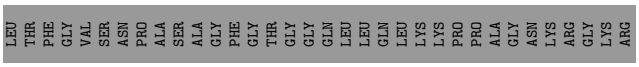
Chain I1:



- Molecule 11: Nucleoporin p58/p45

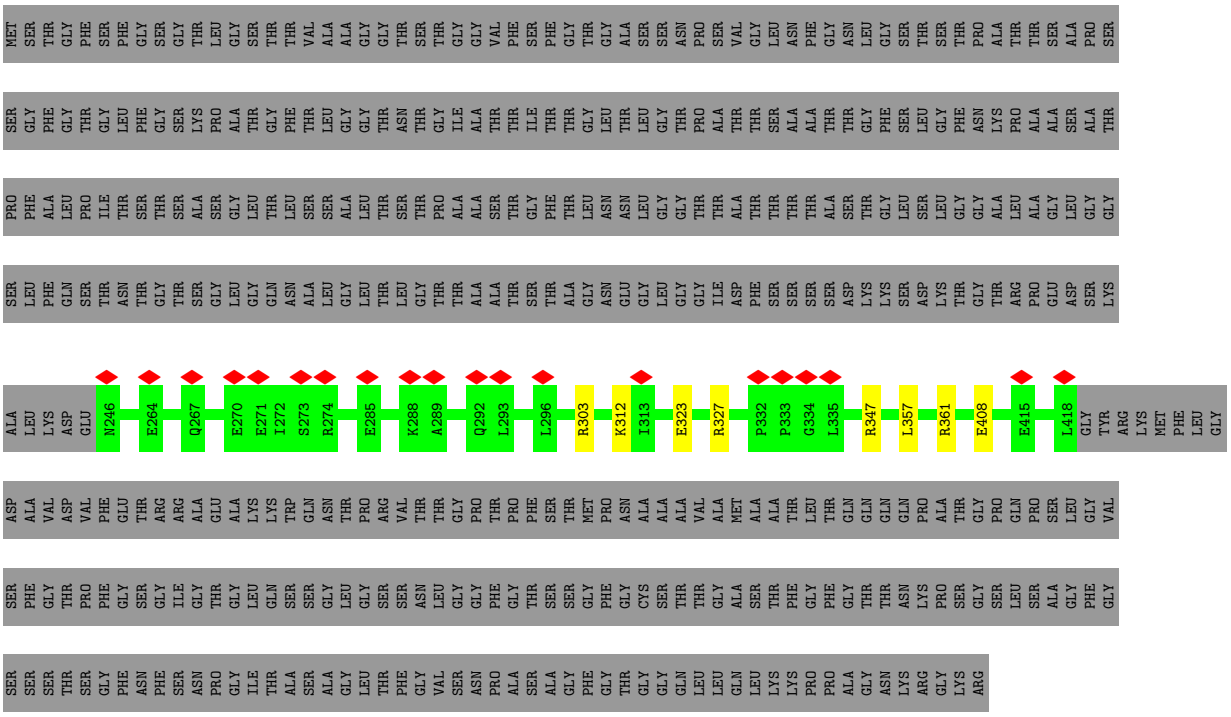
Chain I2:





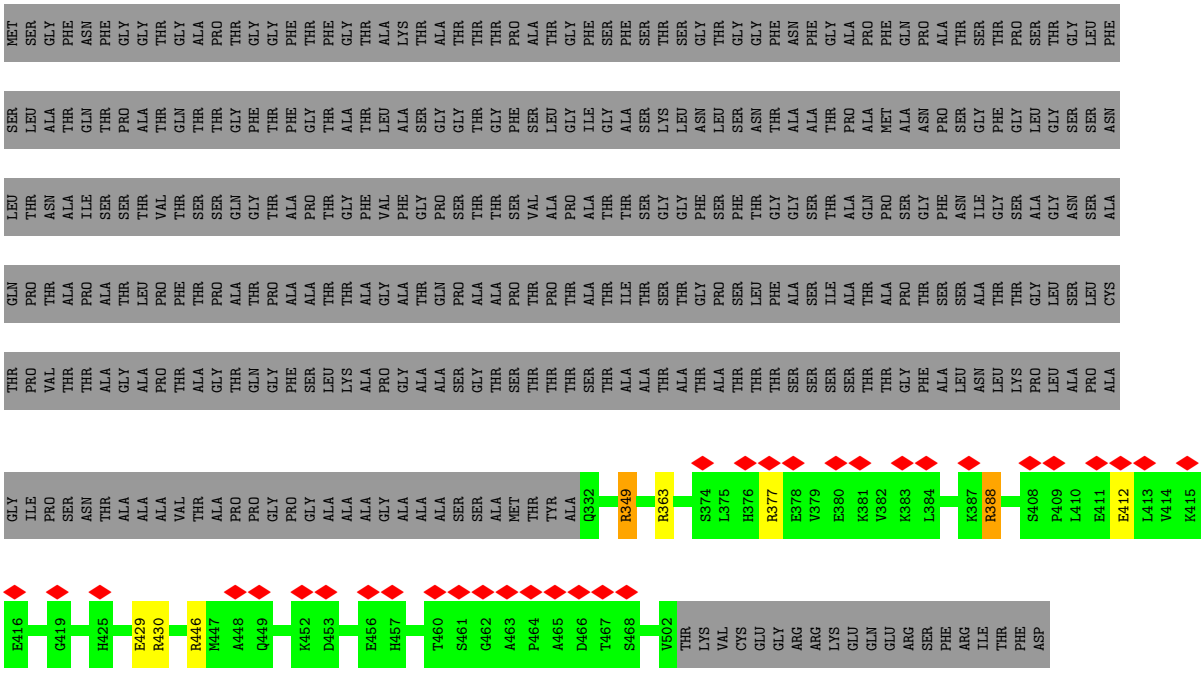
• Molecule 11: Nucleoporin p58/p45

Chain I3:



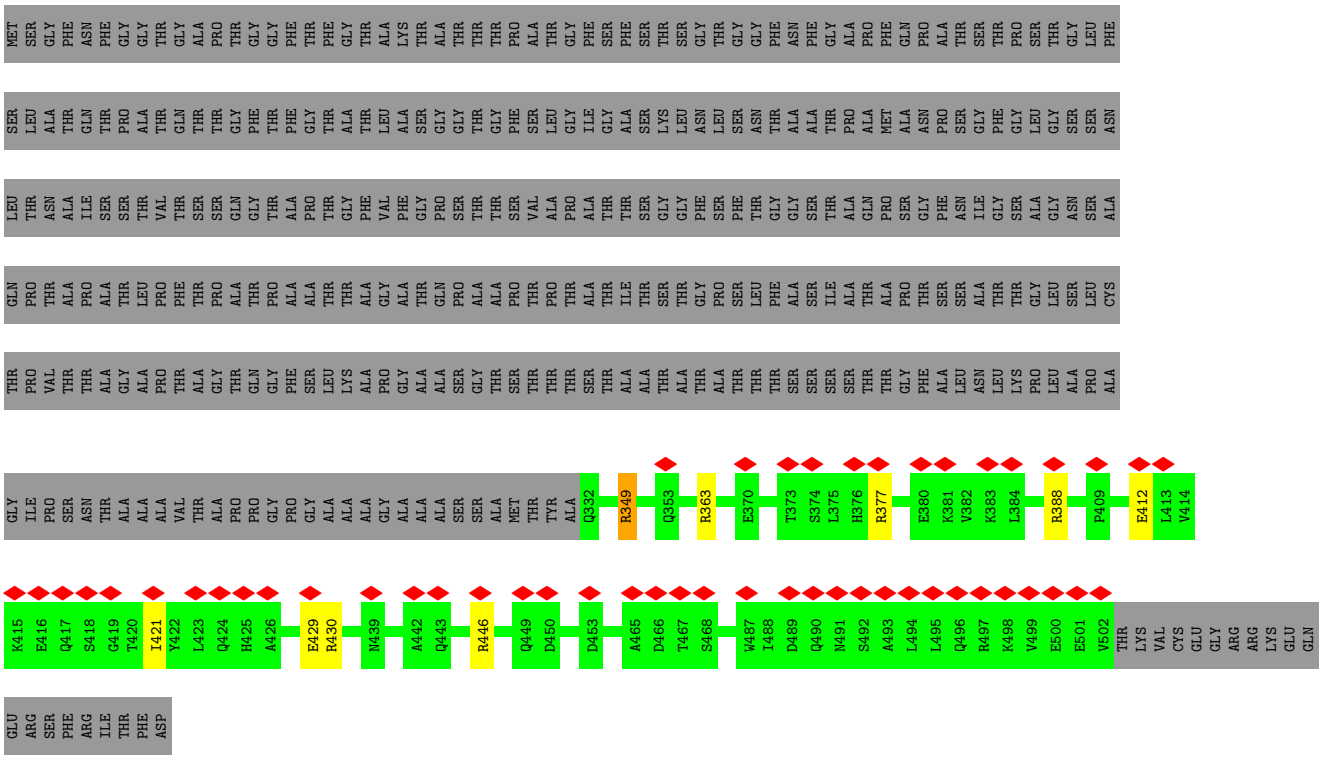
• Molecule 12: Nuclear pore glycoprotein p62

Chain J0:



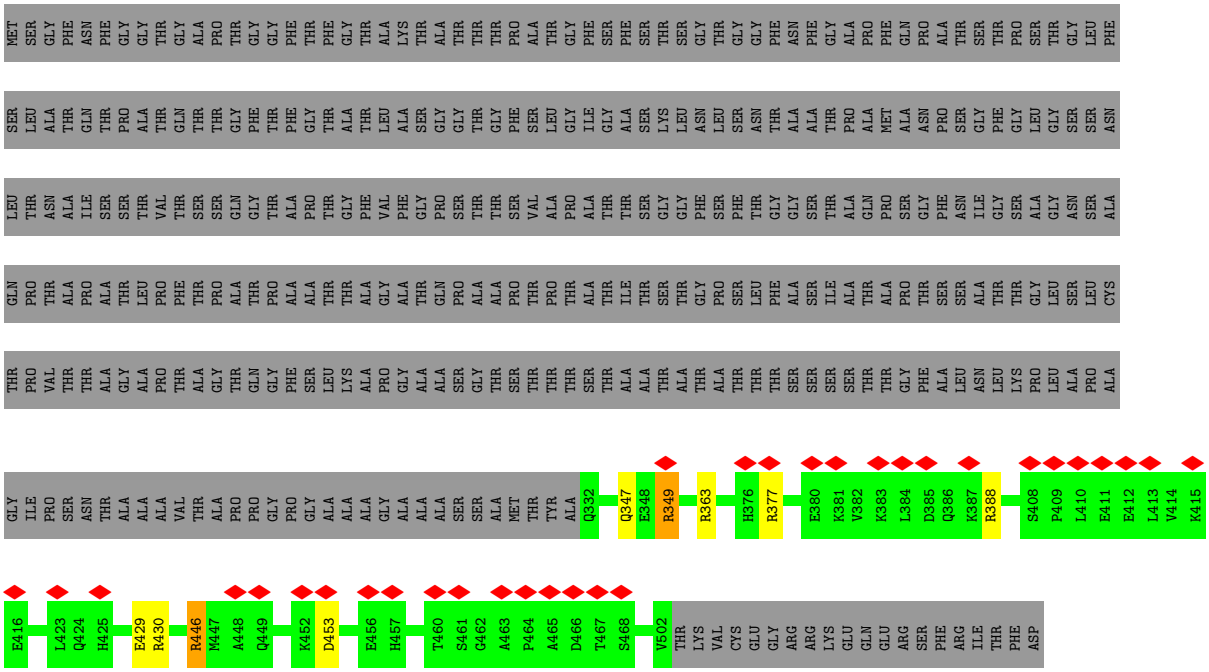
- Molecule 12: Nuclear pore glycoprotein p62

Chain J1:



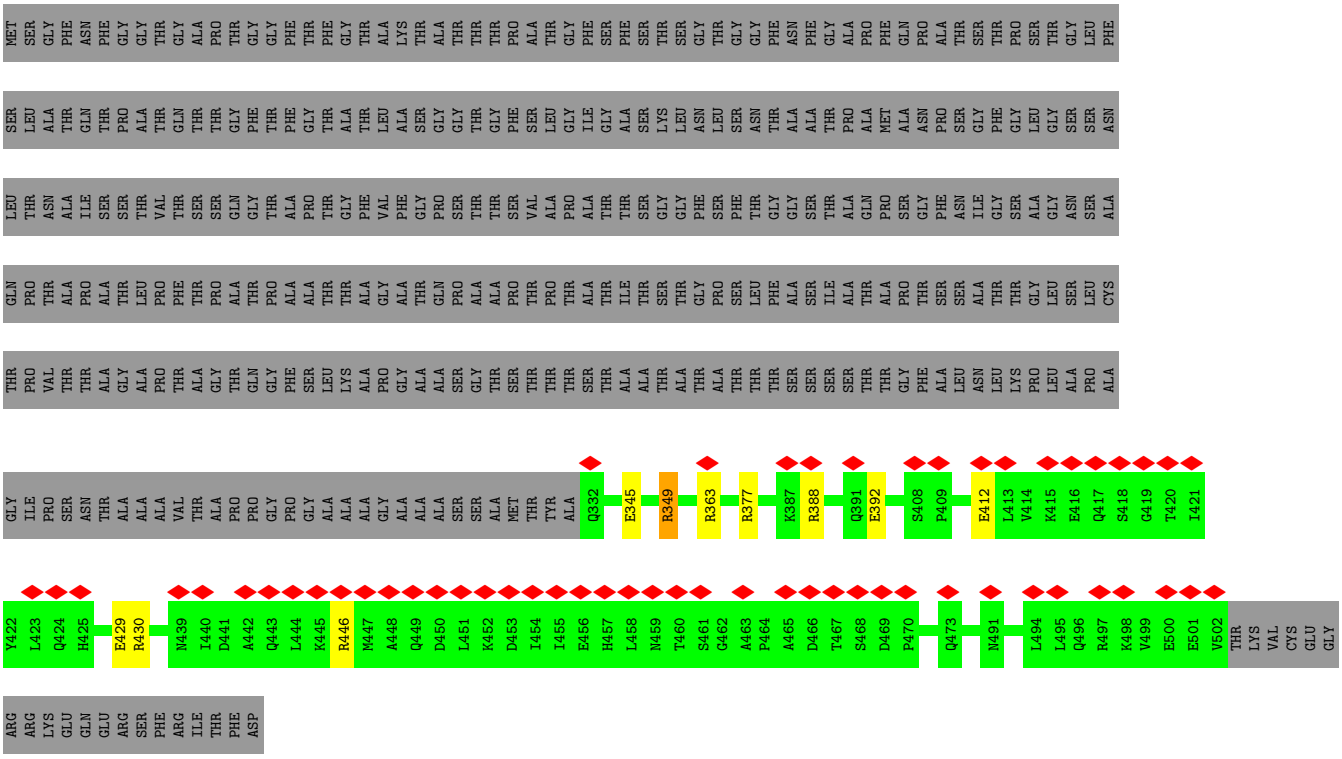
- Molecule 12: Nuclear pore glycoprotein p62

Chain J2:



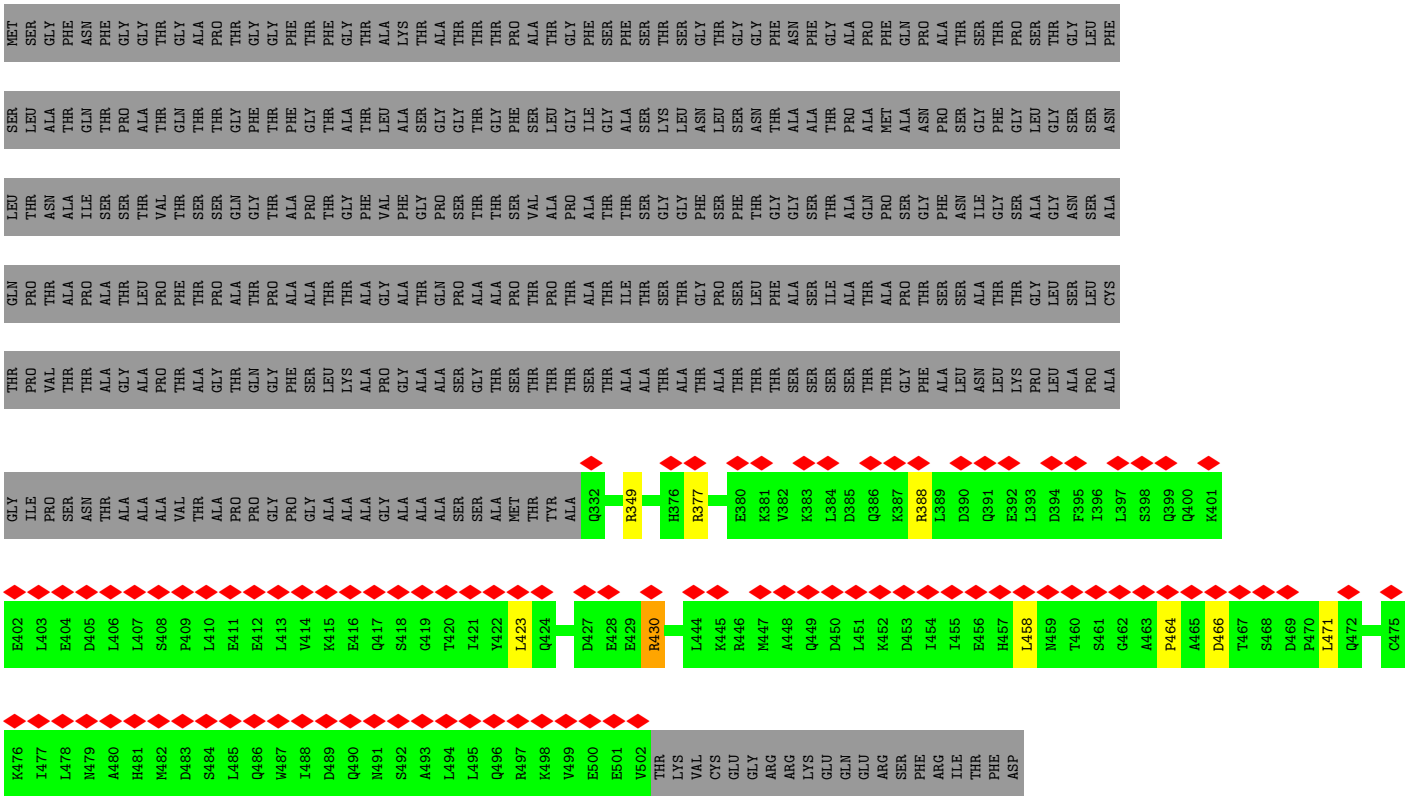
- Molecule 12: Nuclear pore glycoprotein p62

Chain J3:



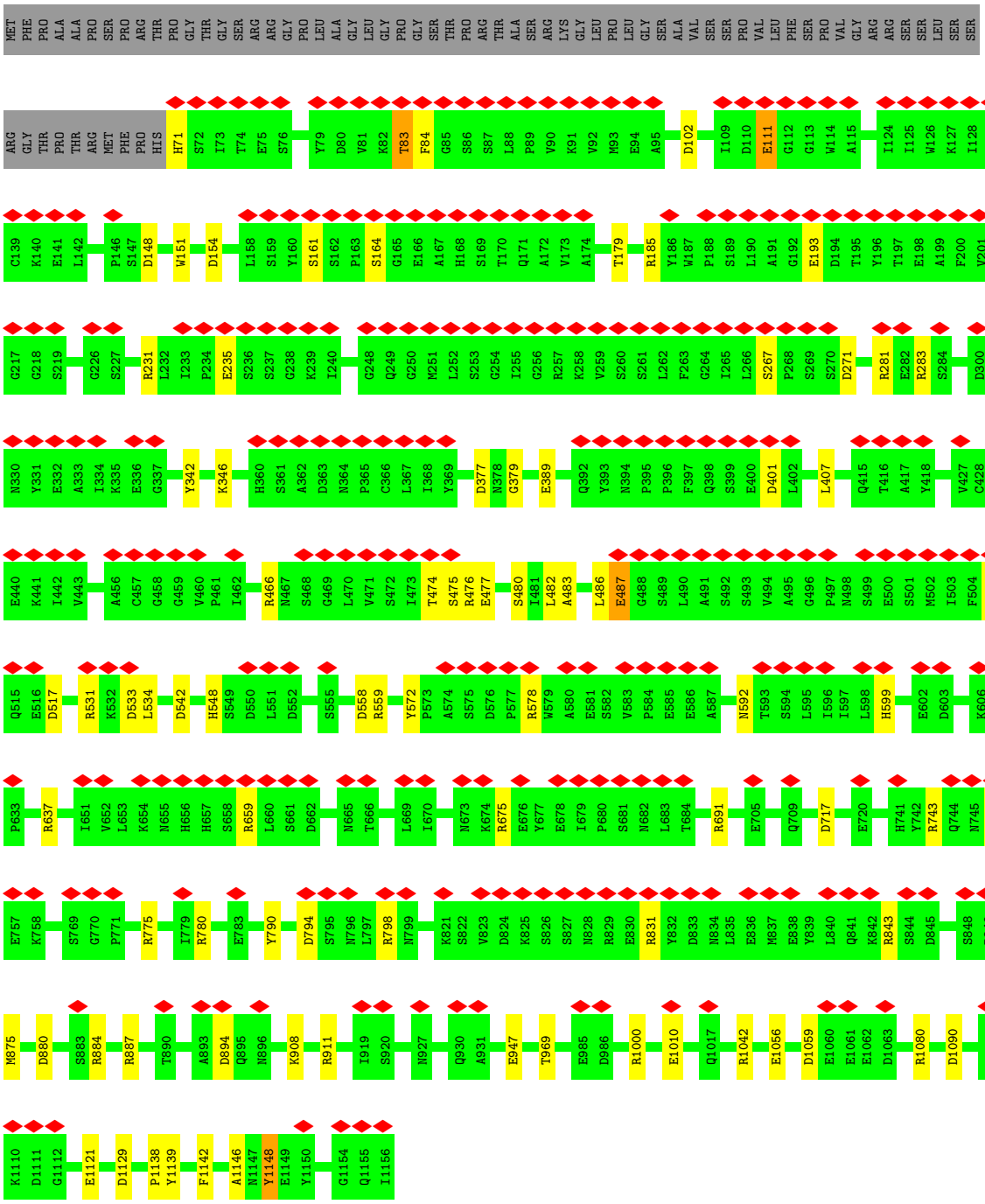
- Molecule 12: Nuclear pore glycoprotein p62

Chain J4:



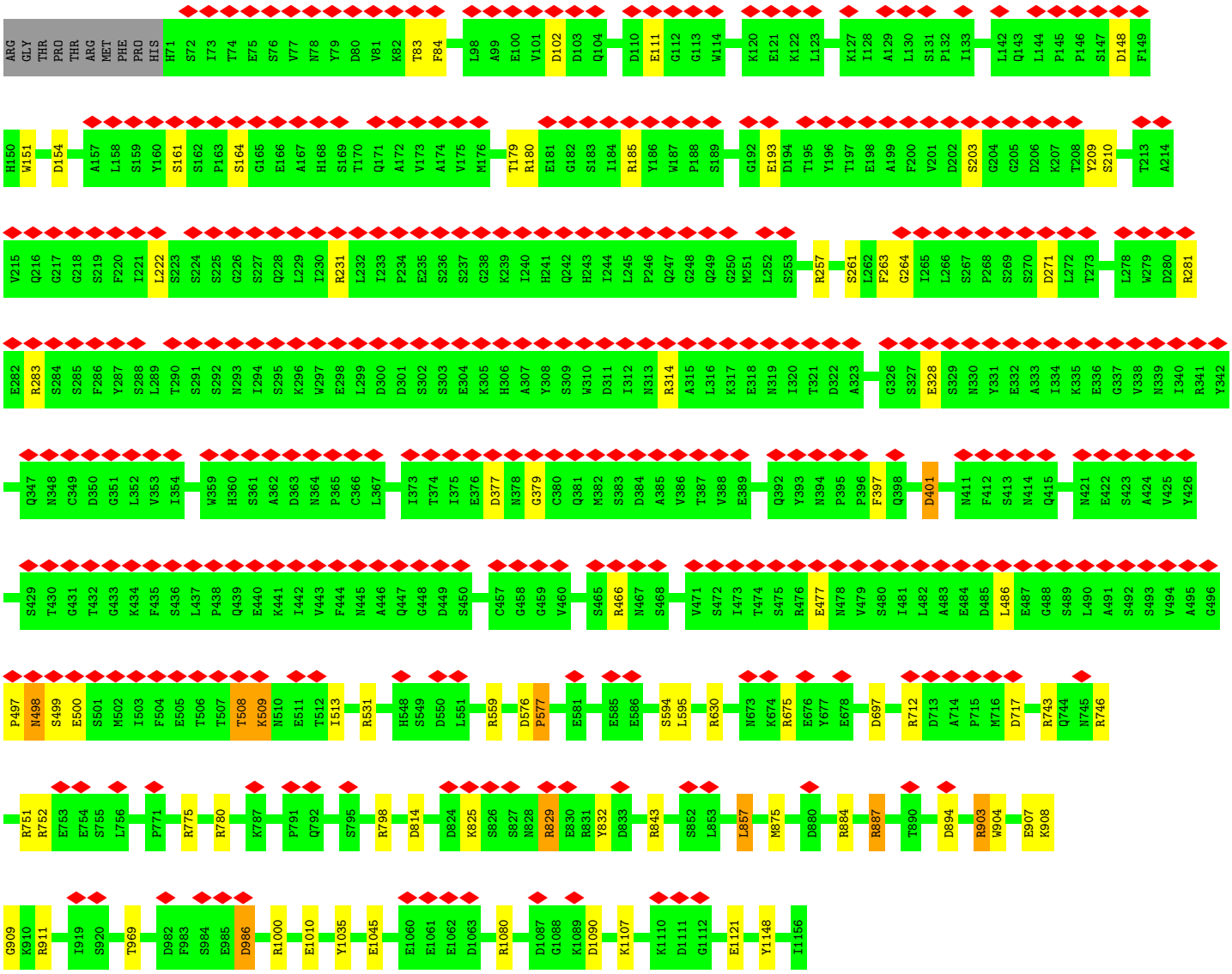
- Molecule 13: Nuclear pore complex protein Nup133

Chain K0:



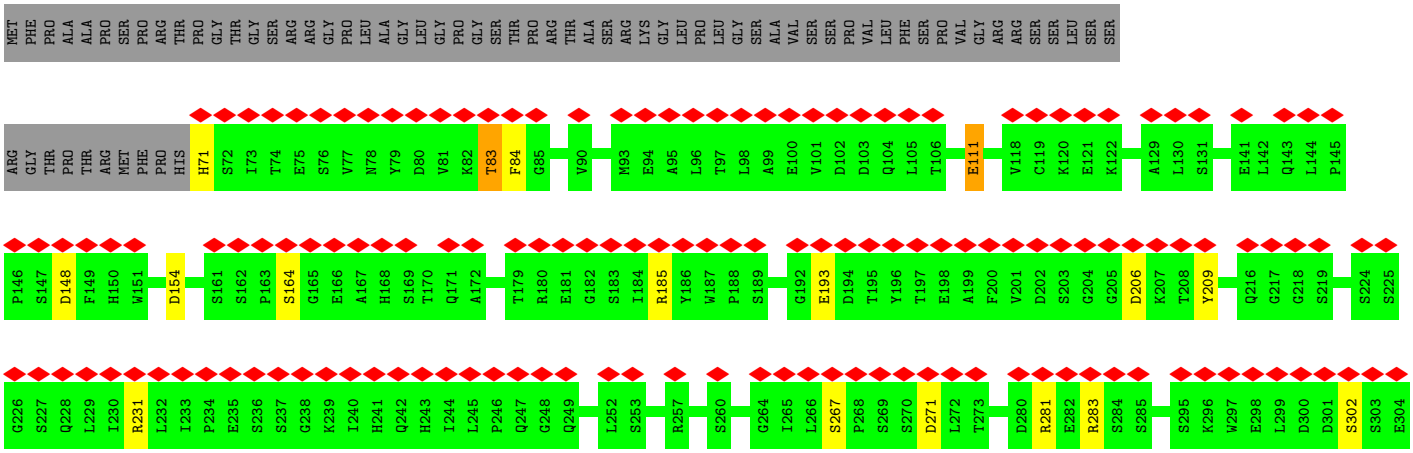
- Molecule 13: Nuclear pore complex protein Nup133

Chain K1:



- Molecule 13: Nuclear pore complex protein Nup133

Chain K2:



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E993 E994 M995 A996 E997 Q998 E999 R1000 L1003 E1010 Q1017 L1018 N1019 A1022 R1042 E1045 Y1046 E1060 E1061 E1062 D1063 I1064 N1065 R1080 S1084 S1085 S1086 D1087 G1088 K1089 D1090 E1094 V1095 S1096 K1097 D1098 K1103 Q1106 K1107 L1108 L1109 K1110 D1111 G1112 I1113 Q1114 L1115 S1116

E1117 E1121 V1122 K1123 D1124 L1125 L1126 Q1127 A1128 D1129 G1132 S1133 L1134 K1135 S1136 N1137 P1138 Y1148 E1149 Q1153 G1154 Q1155 T1156

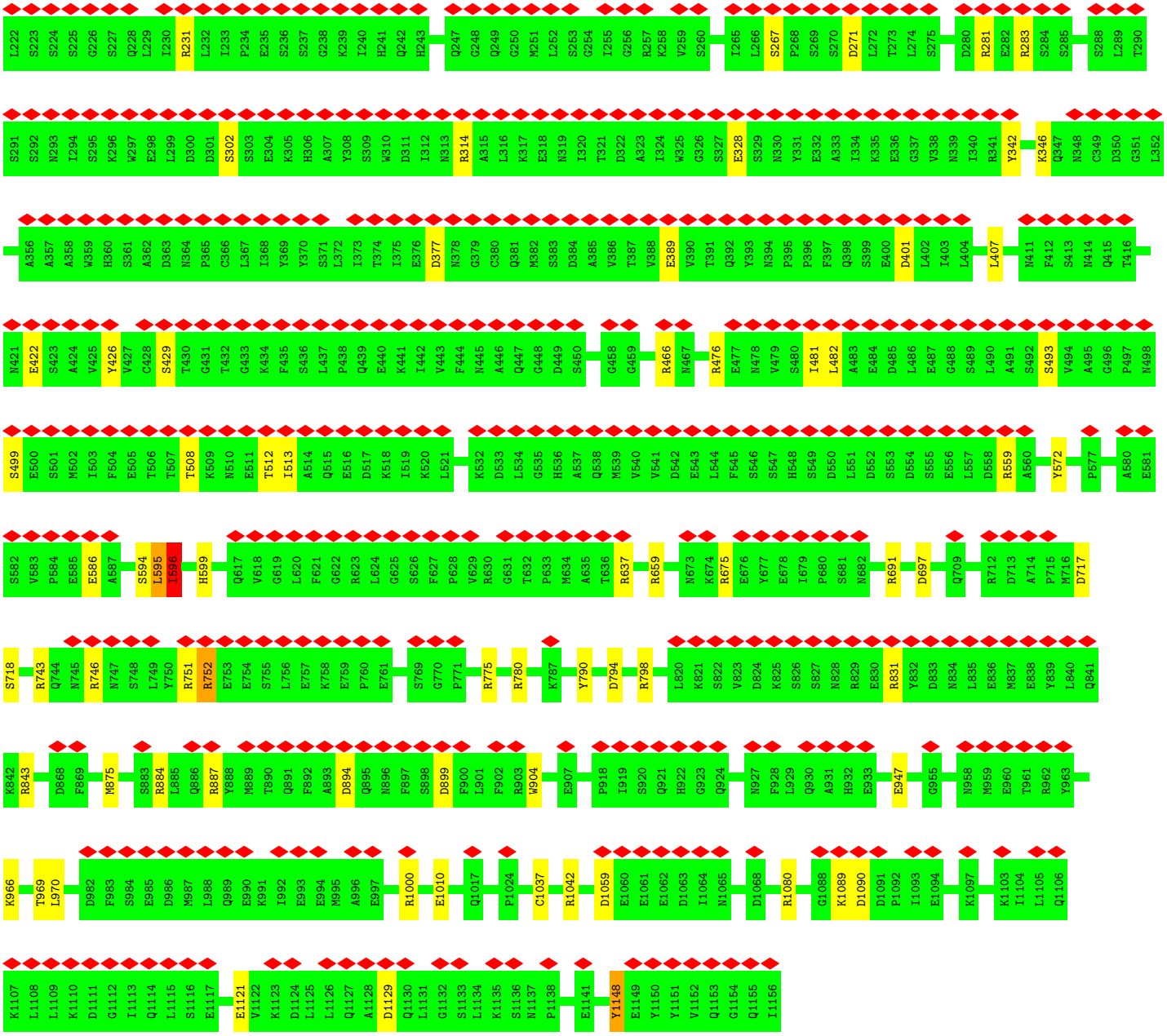
- Molecule 13: Nuclear pore complex protein Nup133

Chain K3:

MET PHE PRO ALA ALA PRO SER PRO ARG THR PRO GLY THR GLY SER ARG ARG GLY PRO LEU ALA GLY LEU GLY PRO GLY SER THR PRO ARG THR ALA SER ARG LYS GLY LEU PRO LEU GLY SER ALA VAL SER SER PRO VAL LEU PHE SER PRO VAL GLY ARG ARG SER SER LEU SER SER

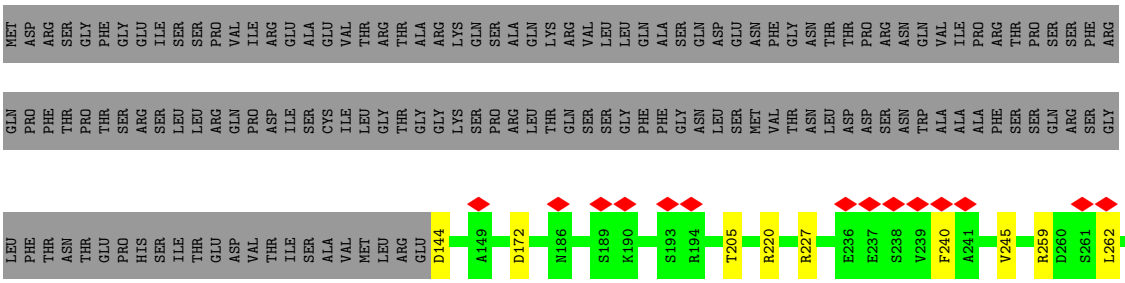
ARG GLY THR PRO THR ARG MET PHE PRO HIS H71 V77 T83 F84 V90 K91 V92 M93 E94 A95 L96 T97 L98 A99 E100 V101 D102 D103 Q104 L105 E111 G112 V118 C119 K120 E121 K122 K140 E141 L142 Q143 L144 P145 P146 S147 D148 F149 H150 W151 S152 A153 D154 S159

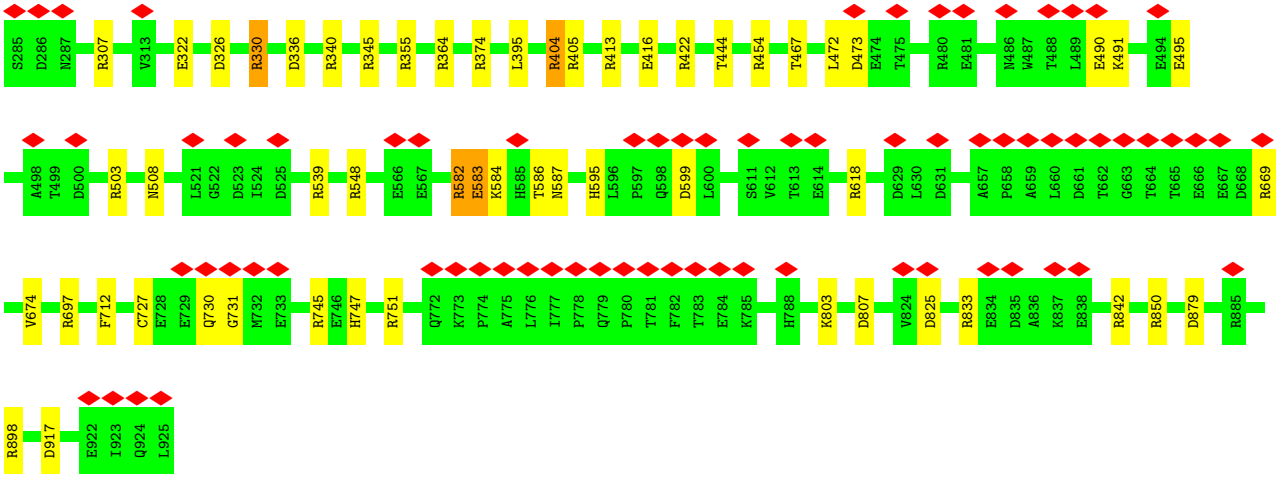
Y160 S161 S162 P163 S164 G165 E166 A167 H168 S169 T170 Q171 A172 V173 A174 V175 M176 V177 A178 T179 R180 E181 G182 S183 I184 R185 Y186 W187 P188 S189 L190 A191 G192 E193 D194 T195 Y196 T197 E198 A199 P200 V201 D202 S203 G204 G205 D206 K207 T208 Y209 S210 F211 V215 Q216 G217 G218 S219 F220 I221



• Molecule 14: Nuclear pore complex protein Nup107

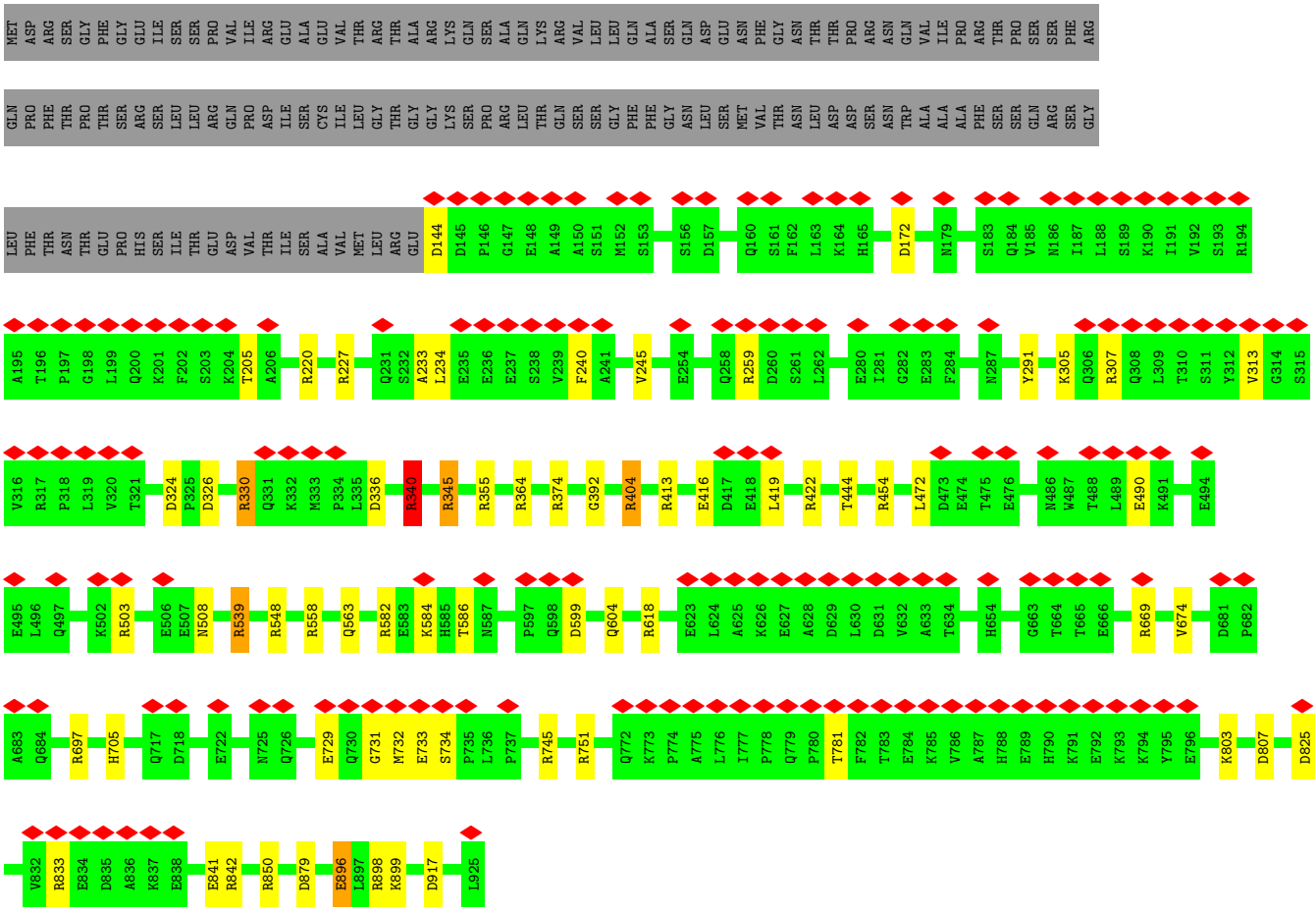
Chain L0:





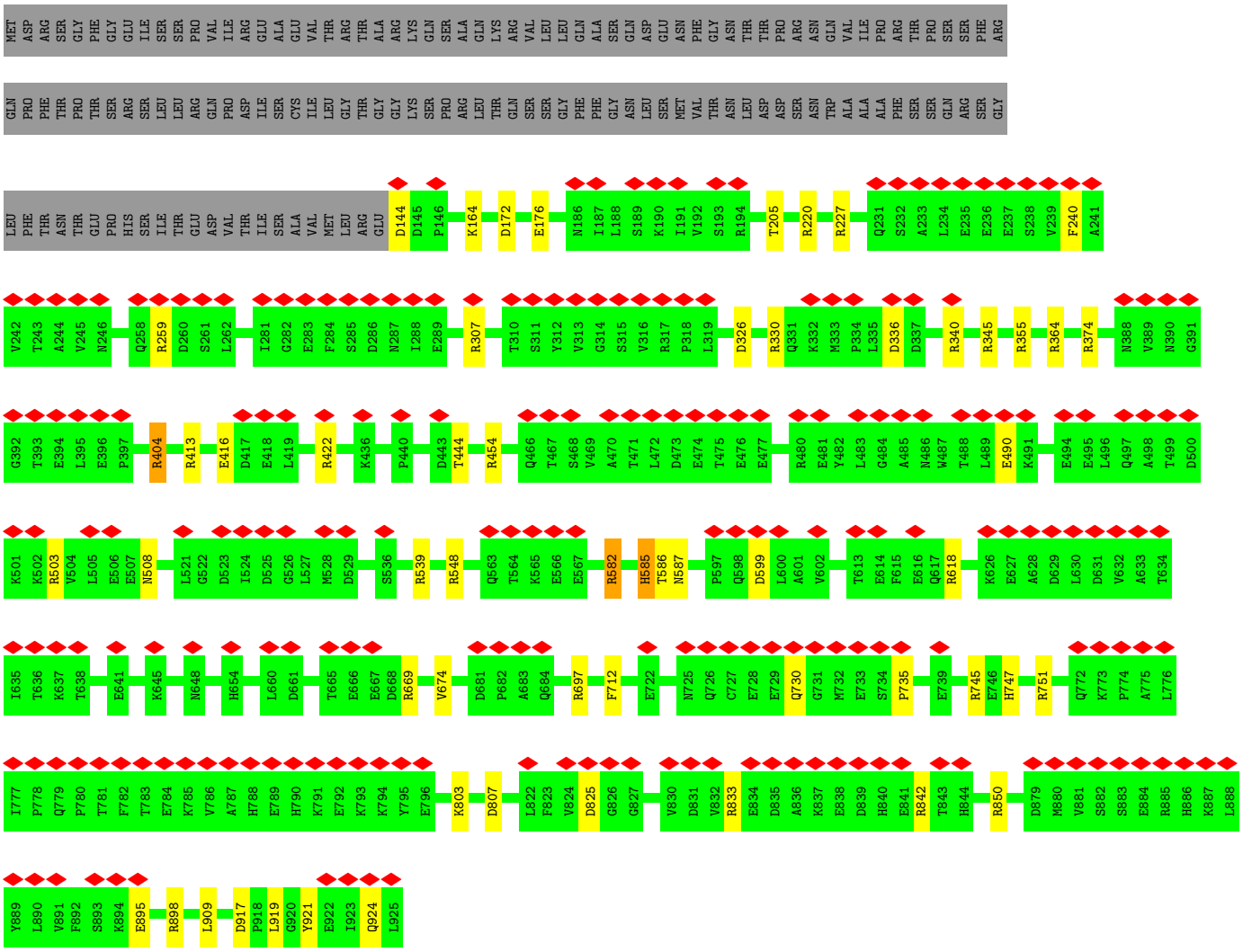
- Molecule 14: Nuclear pore complex protein Nup107

Chain L1:



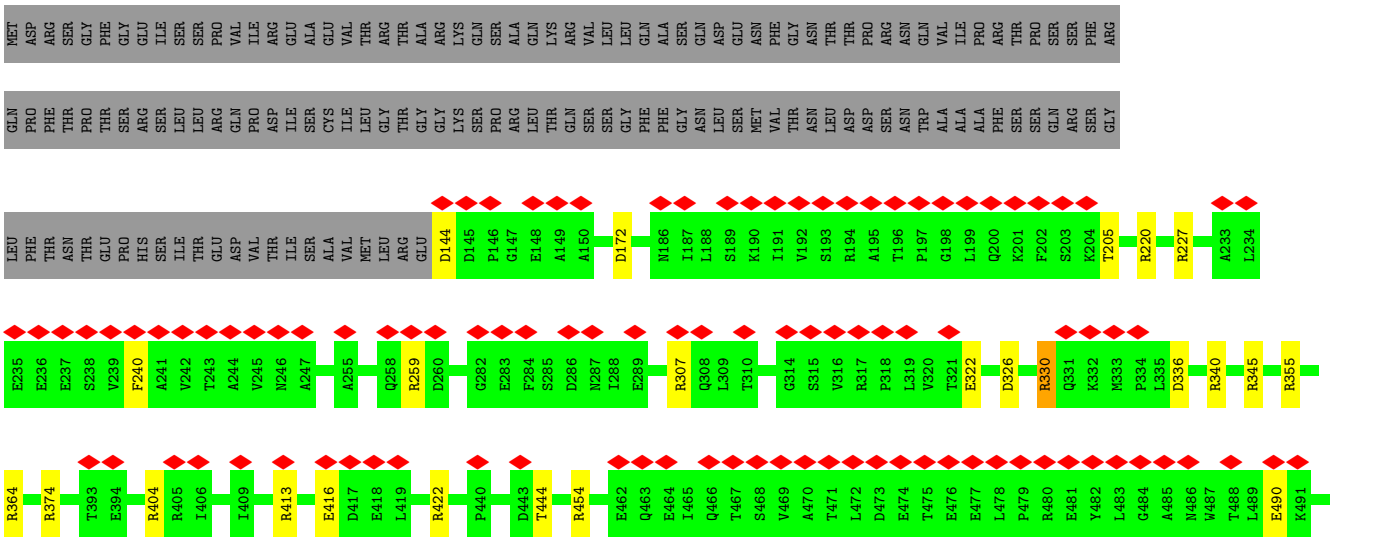
- Molecule 14: Nuclear pore complex protein Nup107

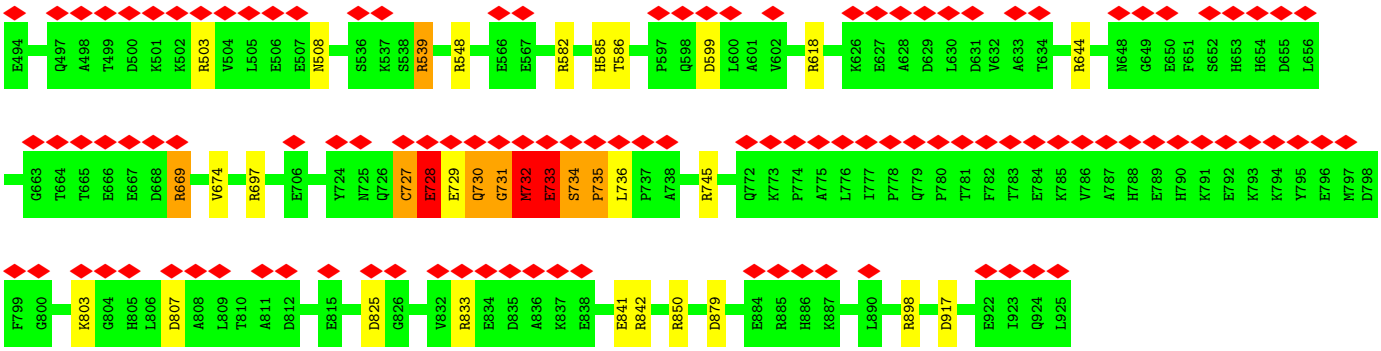
Chain L2:



• Molecule 14: Nuclear pore complex protein Nup107

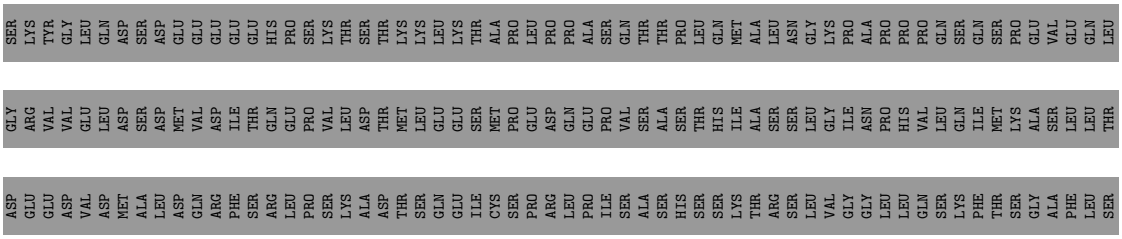
Chain L3:





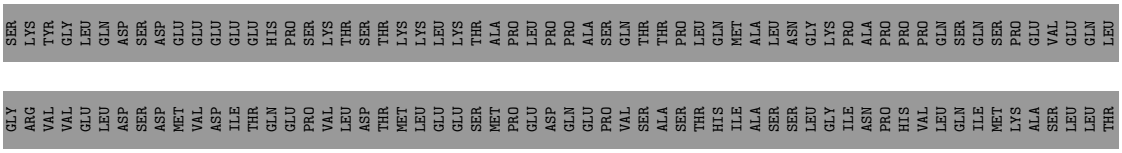
• Molecule 15: Nuclear pore complex protein Nup96

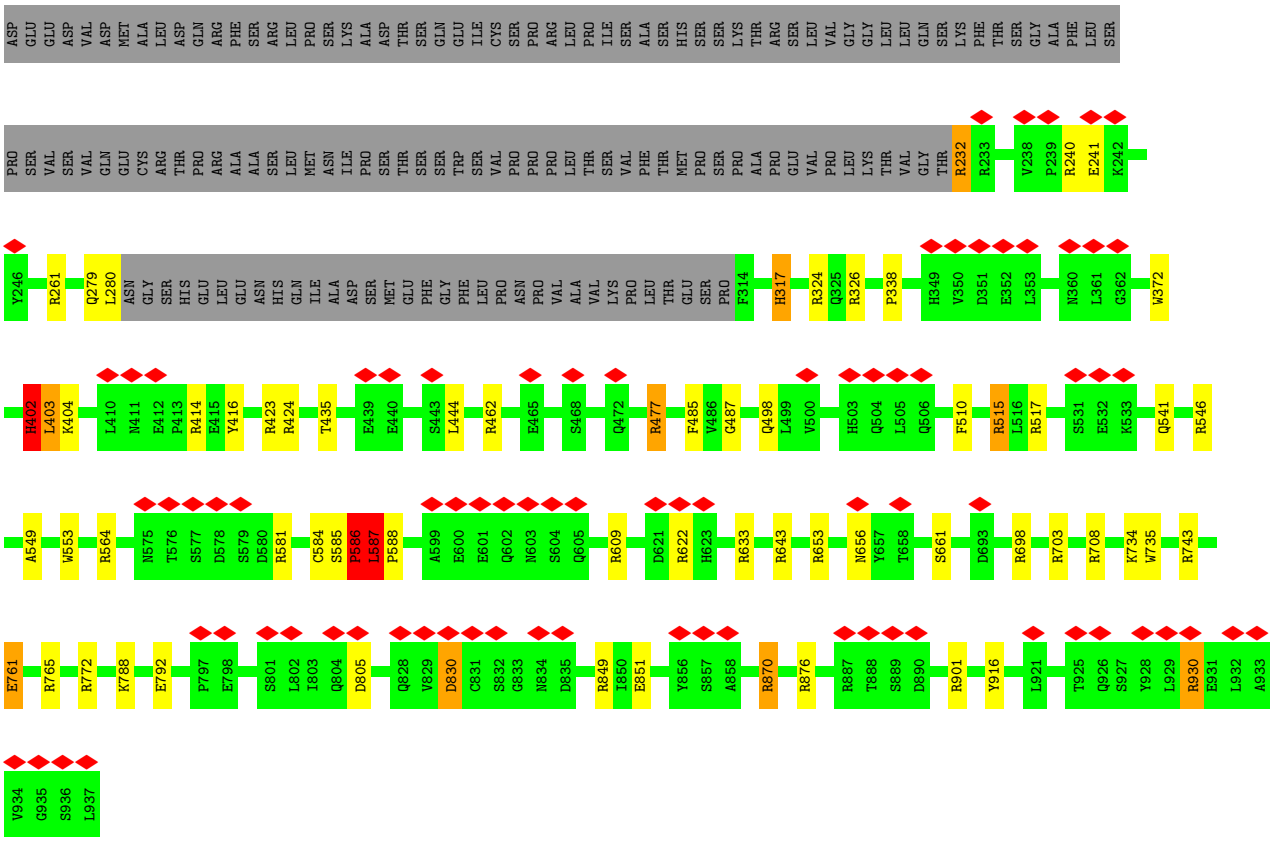
Chain M0:



• Molecule 15: Nuclear pore complex protein Nup96

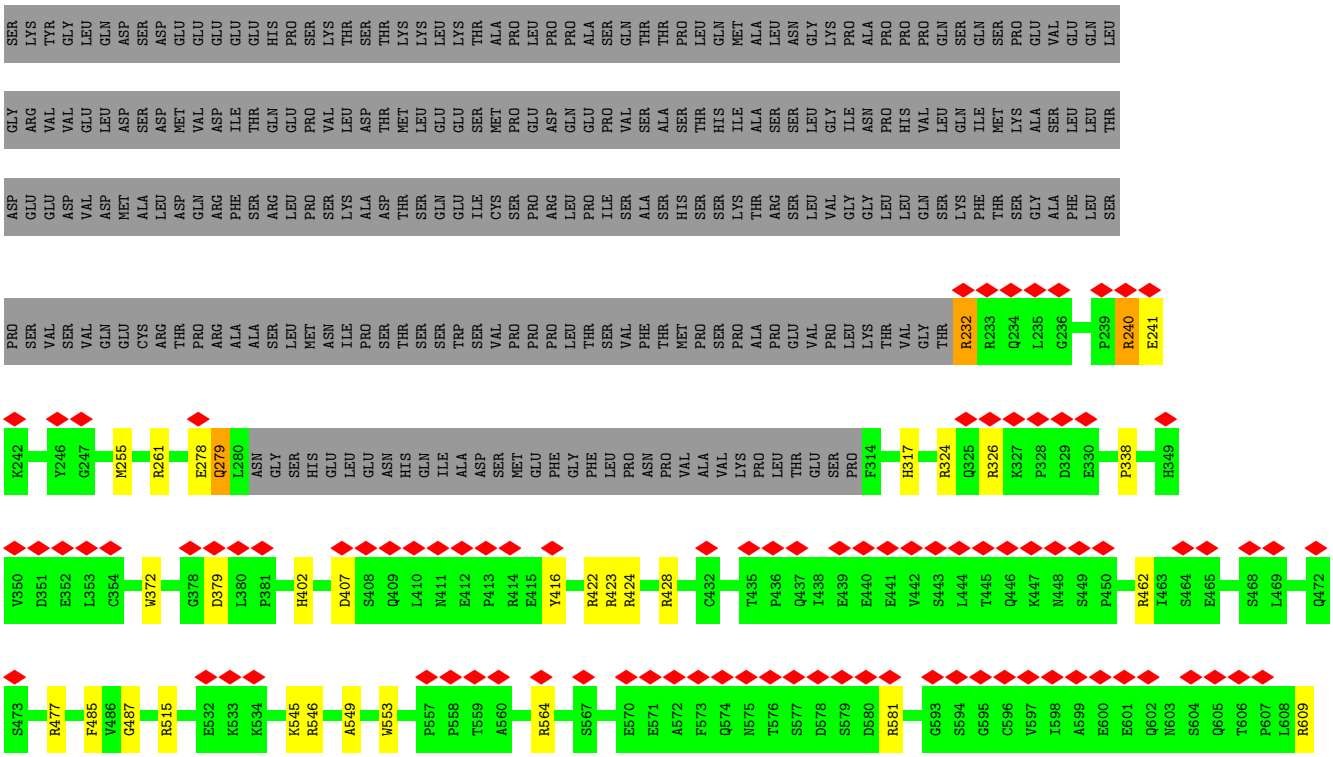
Chain M1:

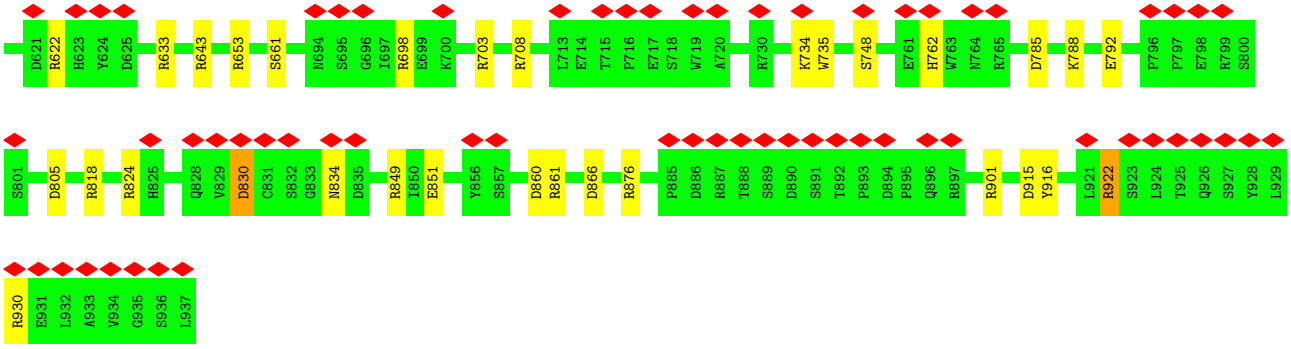




- Molecule 15: Nuclear pore complex protein Nup96

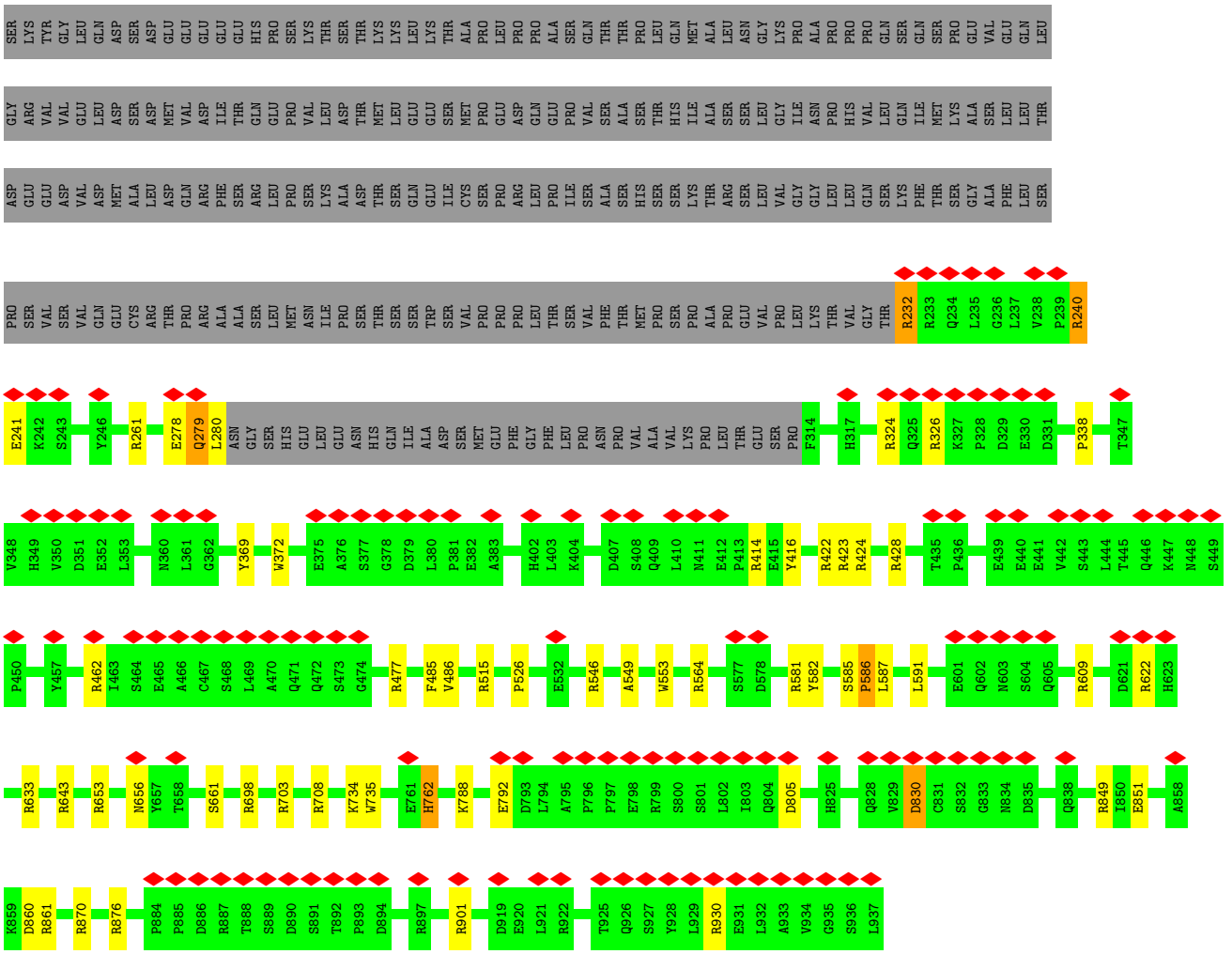
Chain M2:





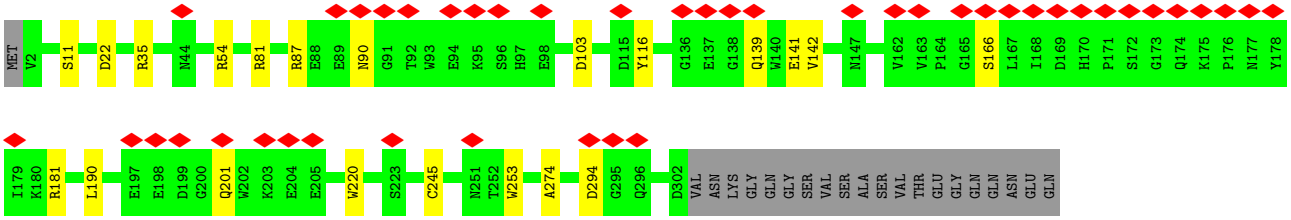
• Molecule 15: Nuclear pore complex protein Nup96

Chain M3:



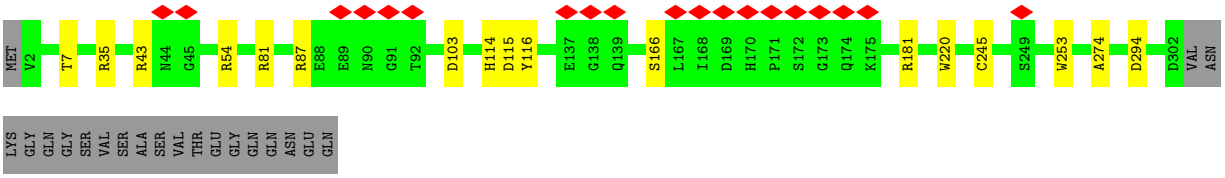
• Molecule 16: Protein SEC13 homolog

Chain N0:



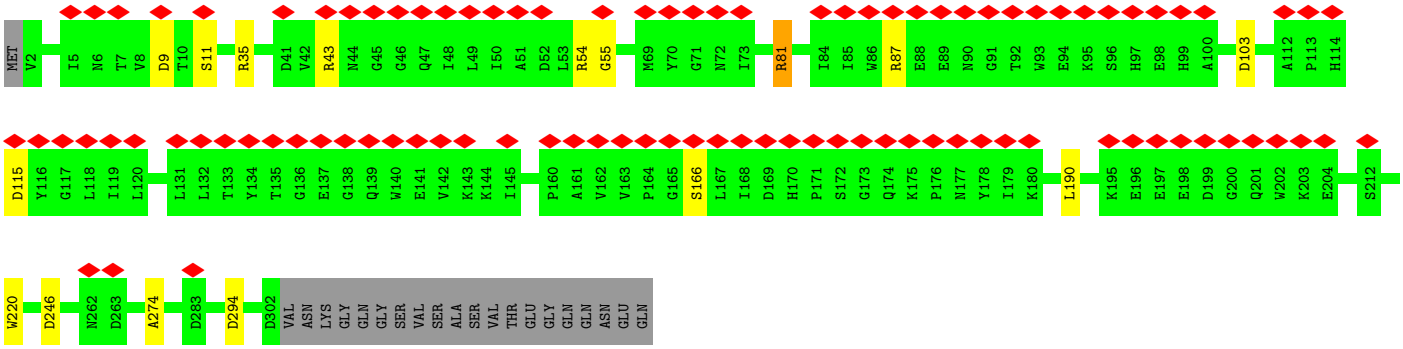
- Molecule 16: Protein SEC13 homolog

Chain N1:



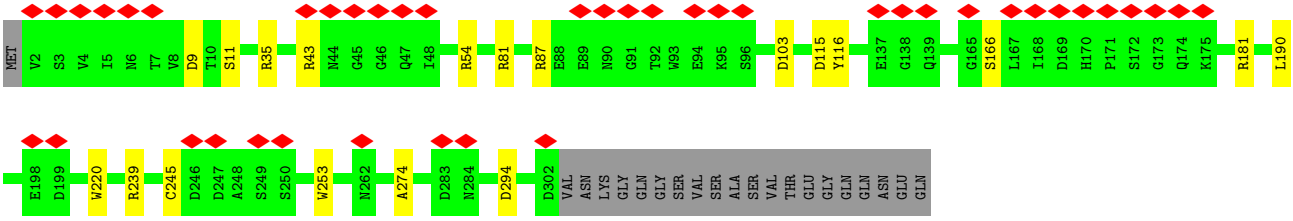
- Molecule 16: Protein SEC13 homolog

Chain N2:



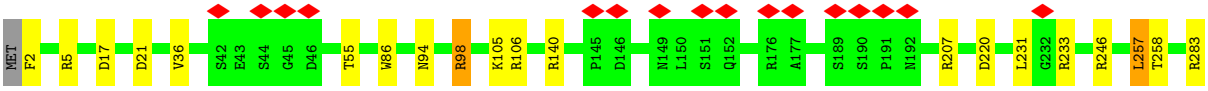
- Molecule 16: Protein SEC13 homolog

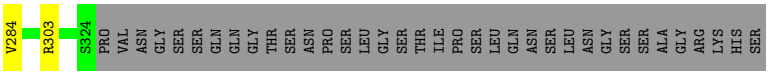
Chain N3:



- Molecule 17: Nucleoporin SEH1

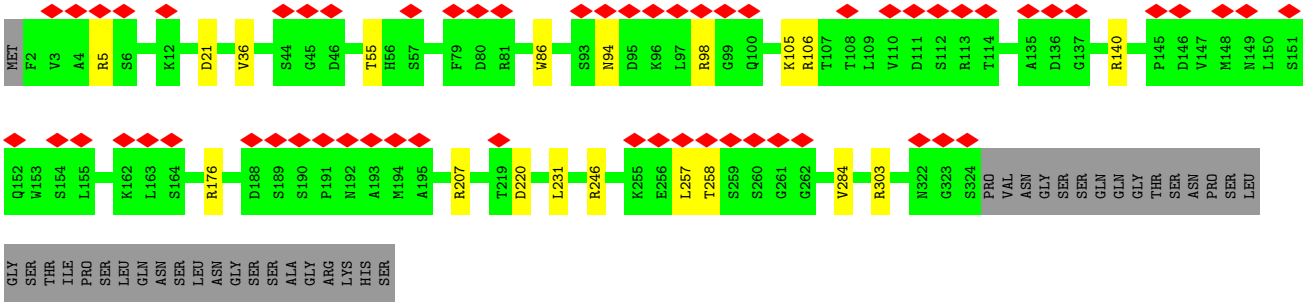
Chain O0:





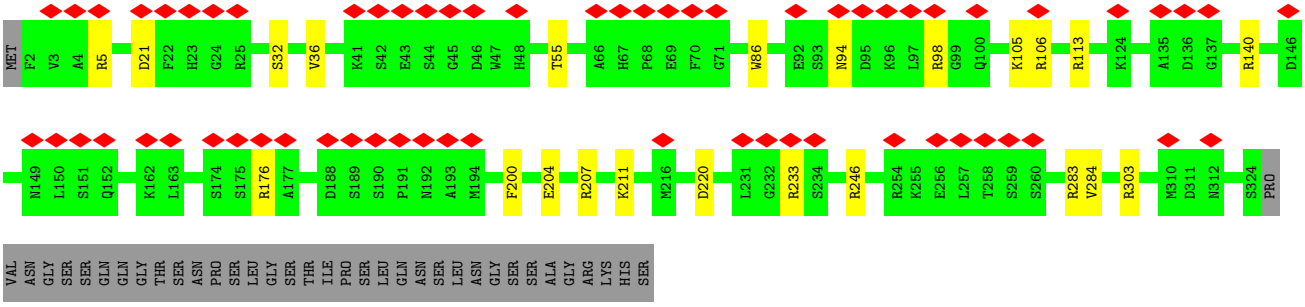
- Molecule 17: Nucleoporin SEH1

Chain O1:



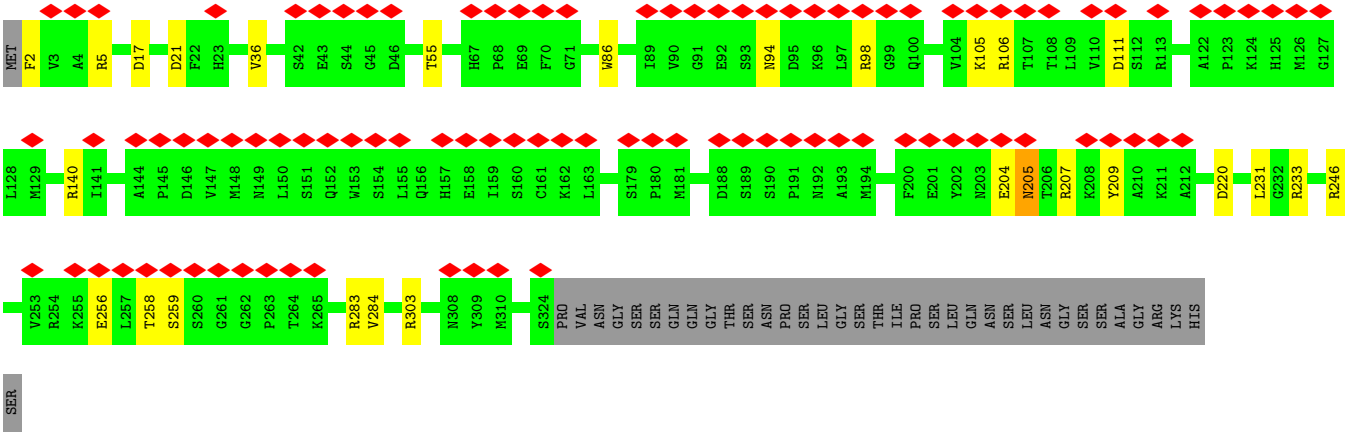
- Molecule 17: Nucleoporin SEH1

Chain O2:



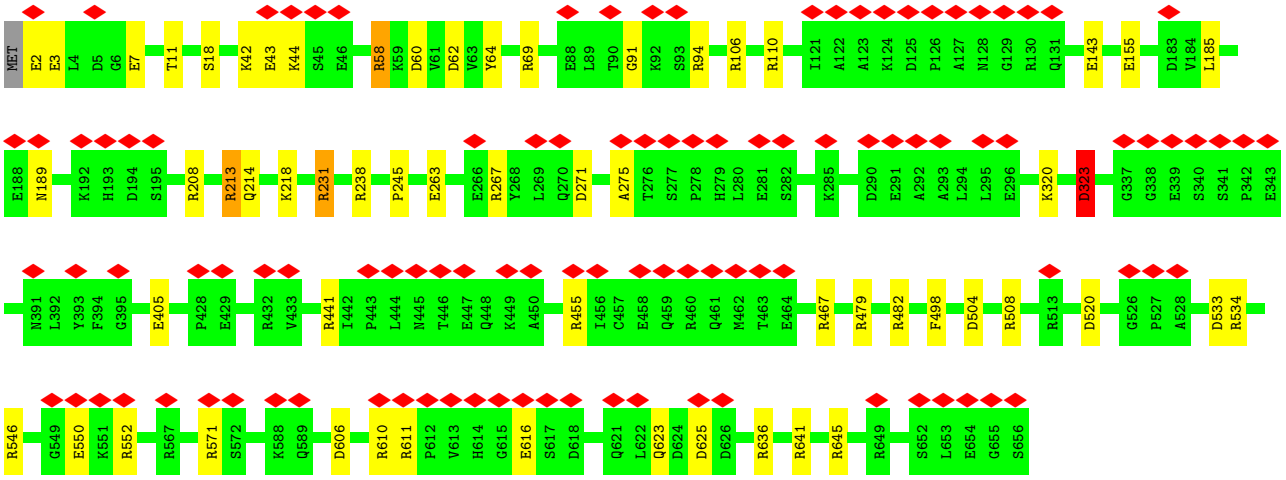
- Molecule 17: Nucleoporin SEH1

Chain O3:



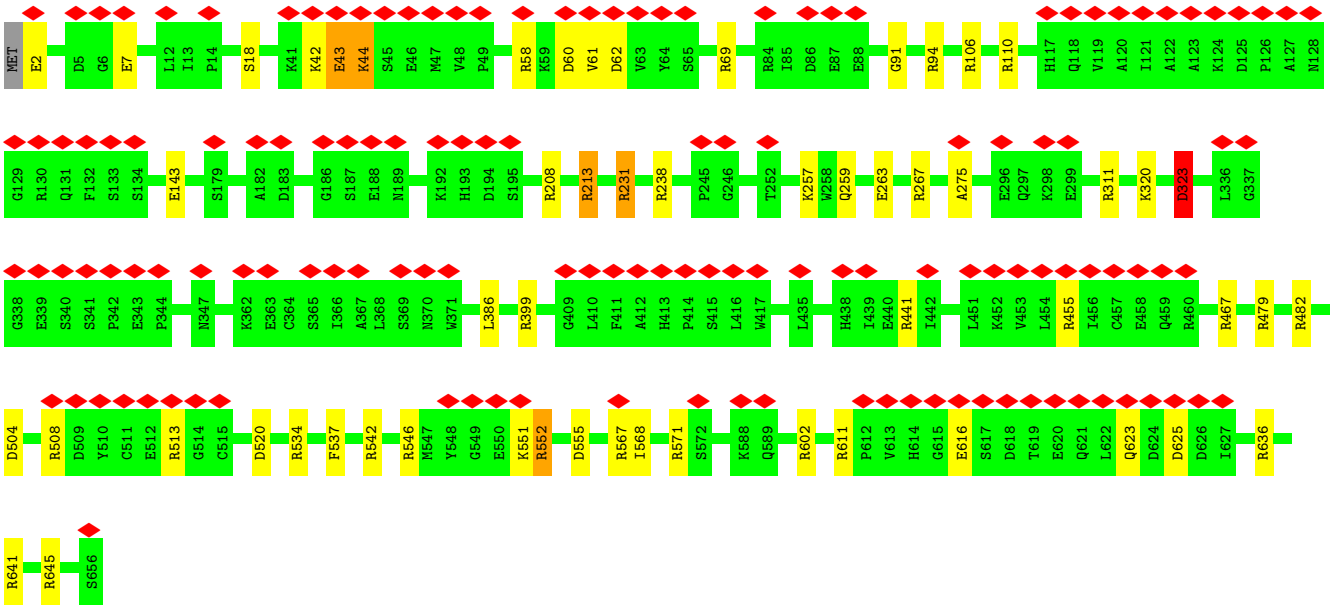
- Molecule 18: Nuclear pore complex protein Nup85

Chain P0: 16% 91% 8%



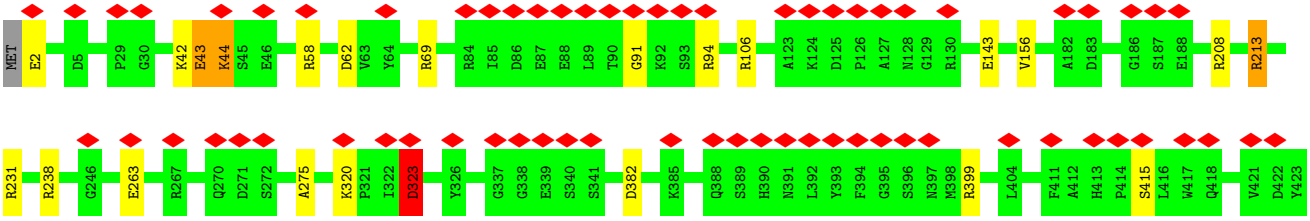
- Molecule 18: Nuclear pore complex protein Nup85

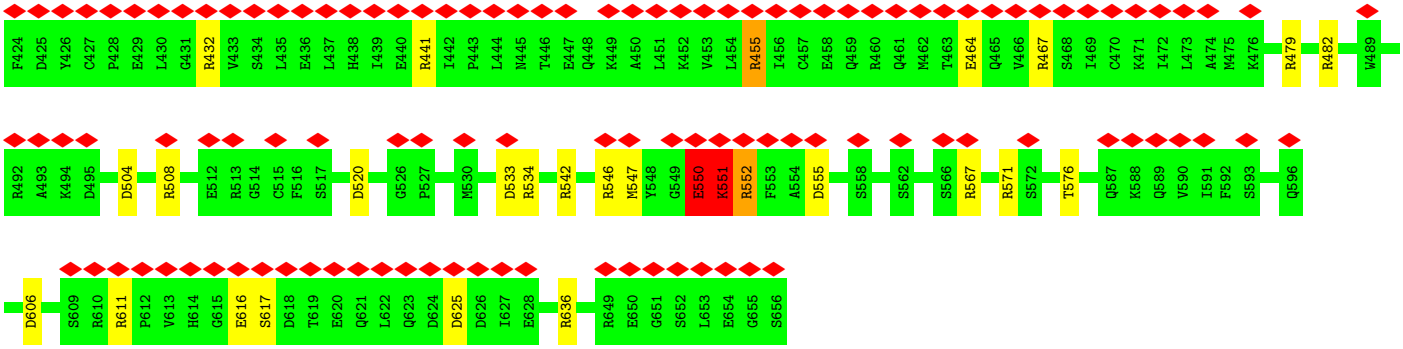
Chain P1: 21% 91% 8%



- Molecule 18: Nuclear pore complex protein Nup85

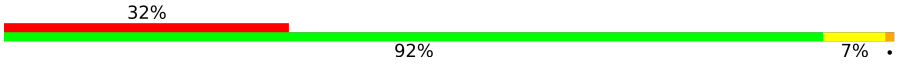
Chain P2: 27% 92% 7%

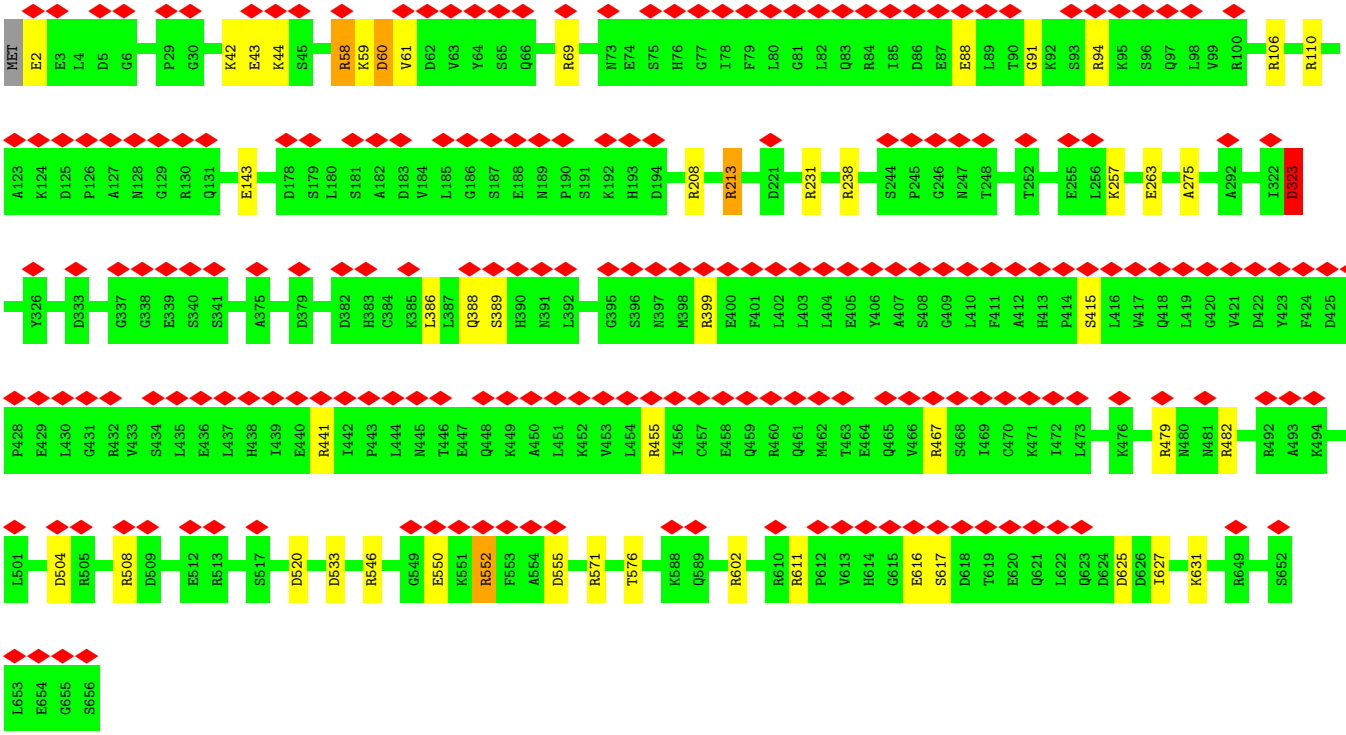




- Molecule 18: Nuclear pore complex protein Nup85

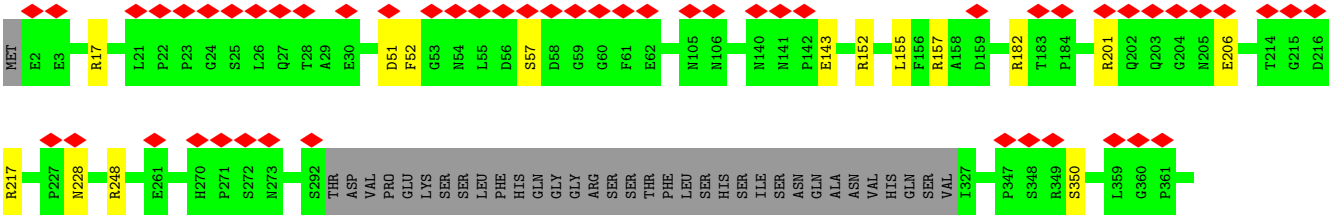
Chain P3:

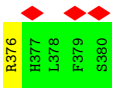




- Molecule 19: Nucleoporin Nup43

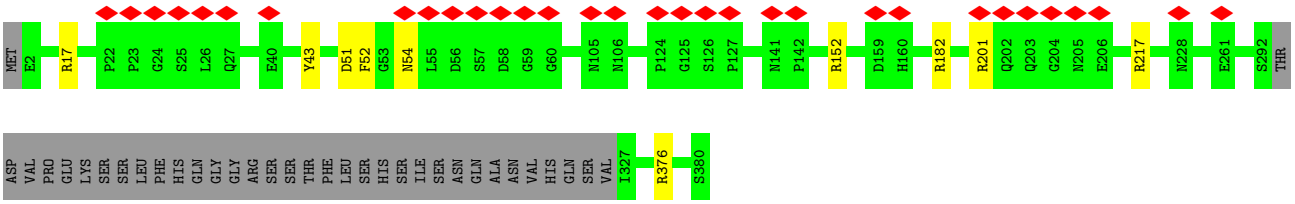
Chain Q0:





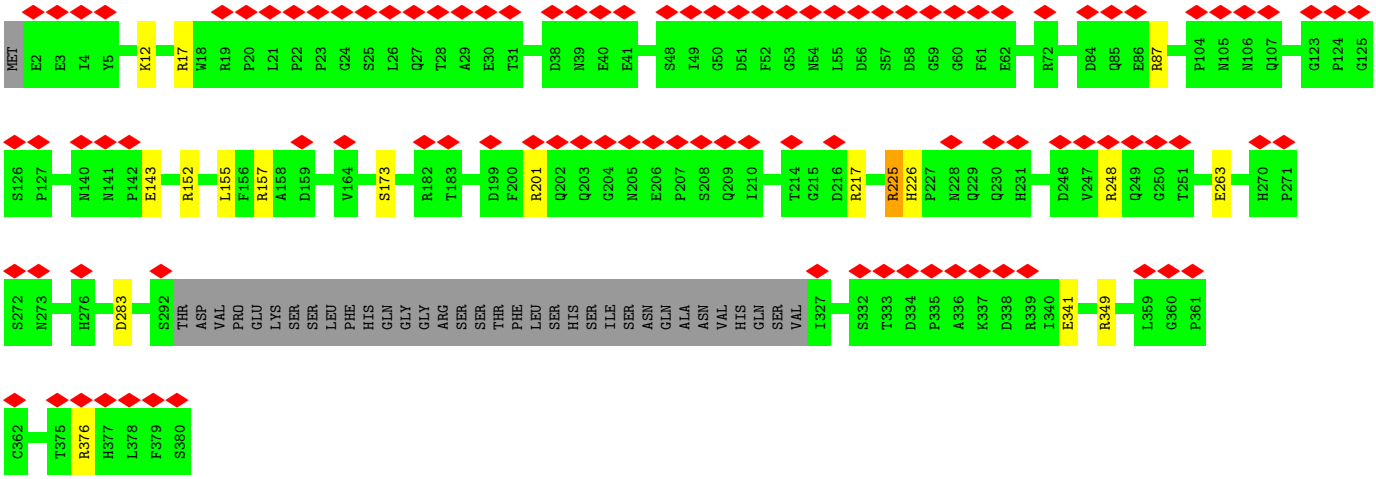
• Molecule 19: Nucleoporin Nup43

Chain Q1:



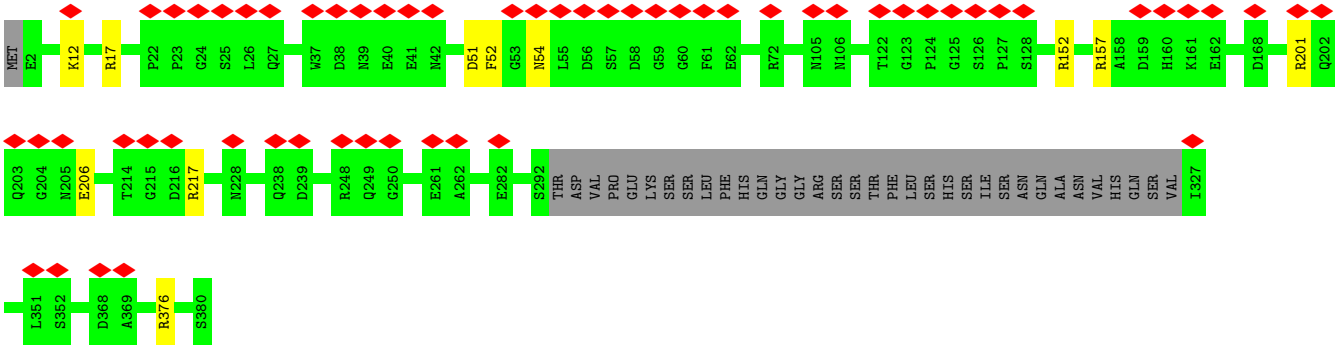
• Molecule 19: Nucleoporin Nup43

Chain Q2:



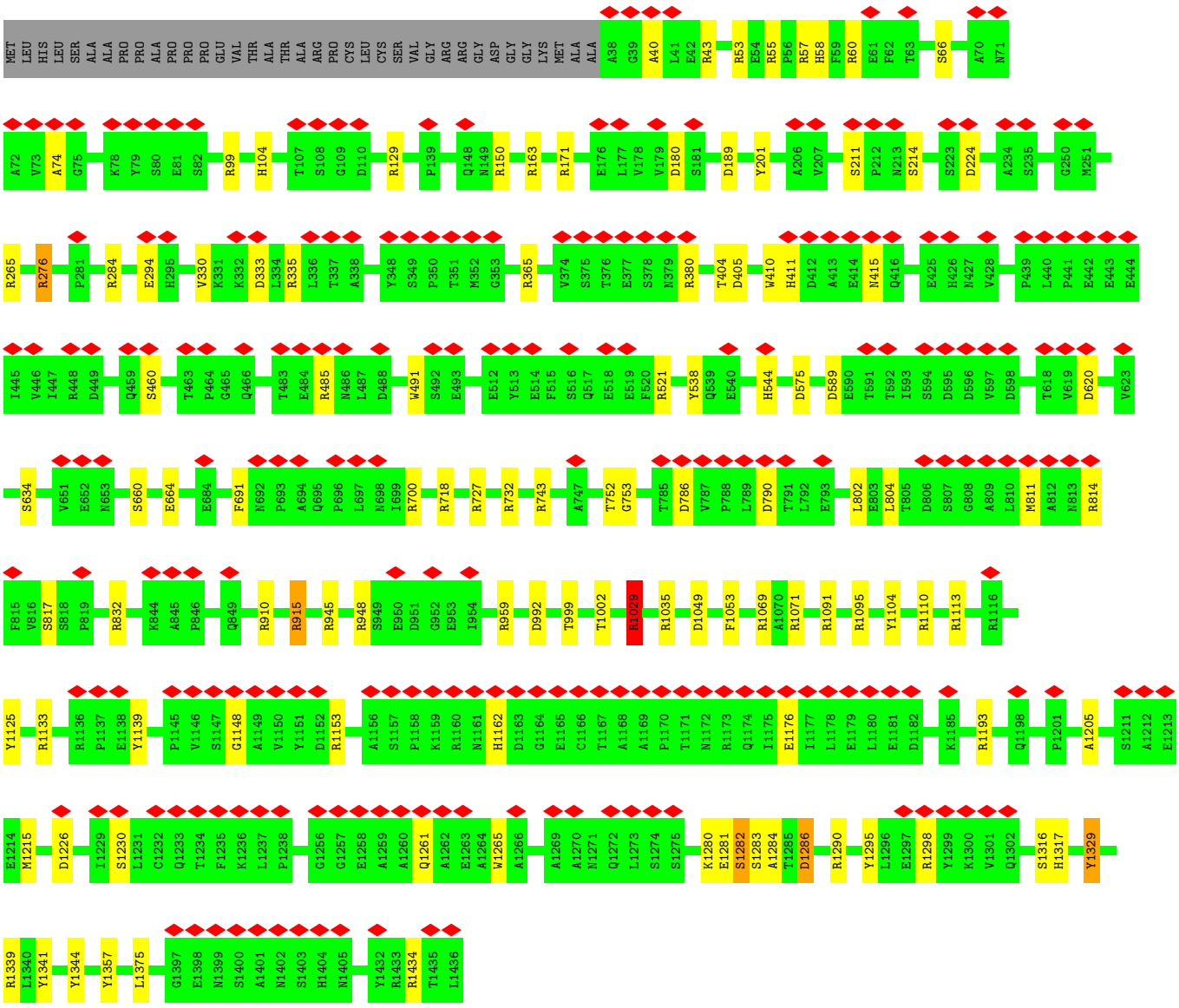
• Molecule 19: Nucleoporin Nup43

Chain Q3:



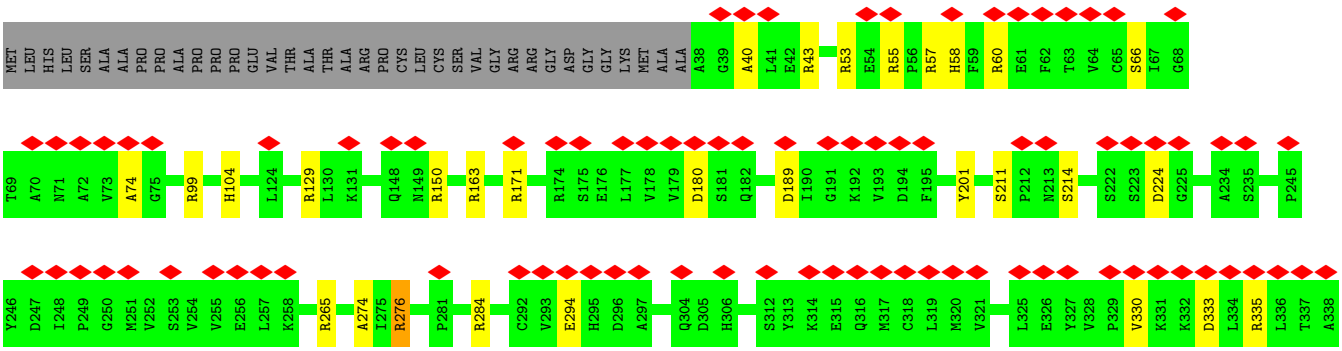
• Molecule 20: Nuclear pore complex protein Nup160

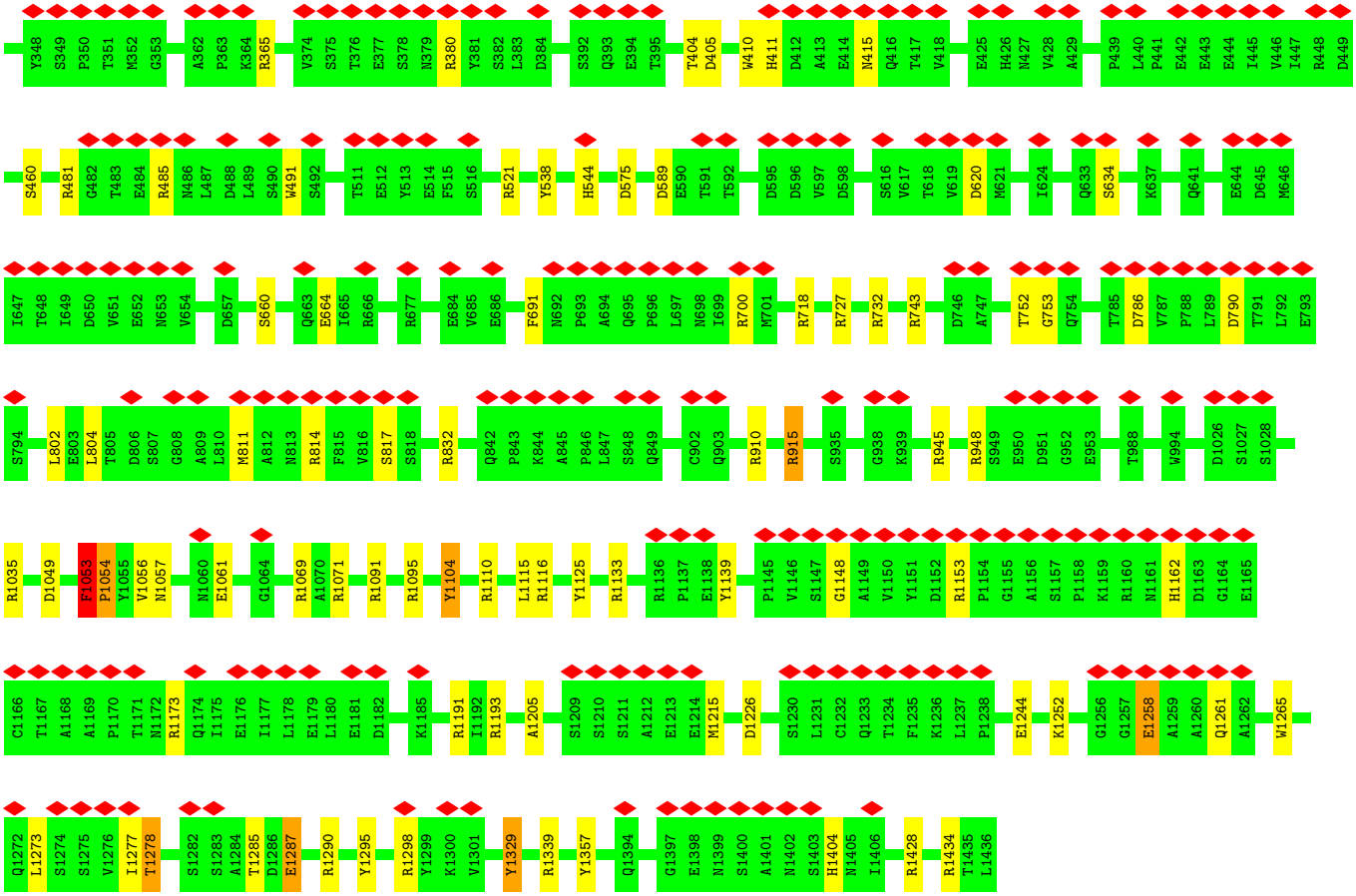
Chain R0:



• Molecule 20: Nuclear pore complex protein Nup160

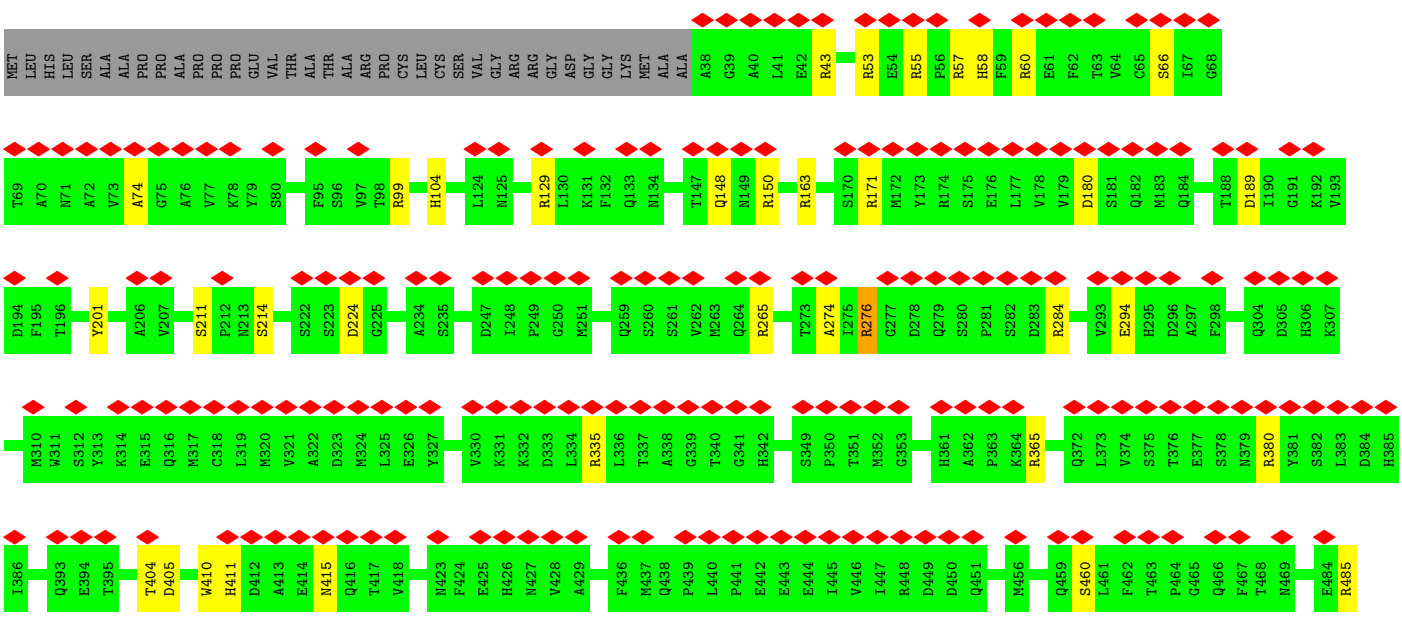
Chain R1:

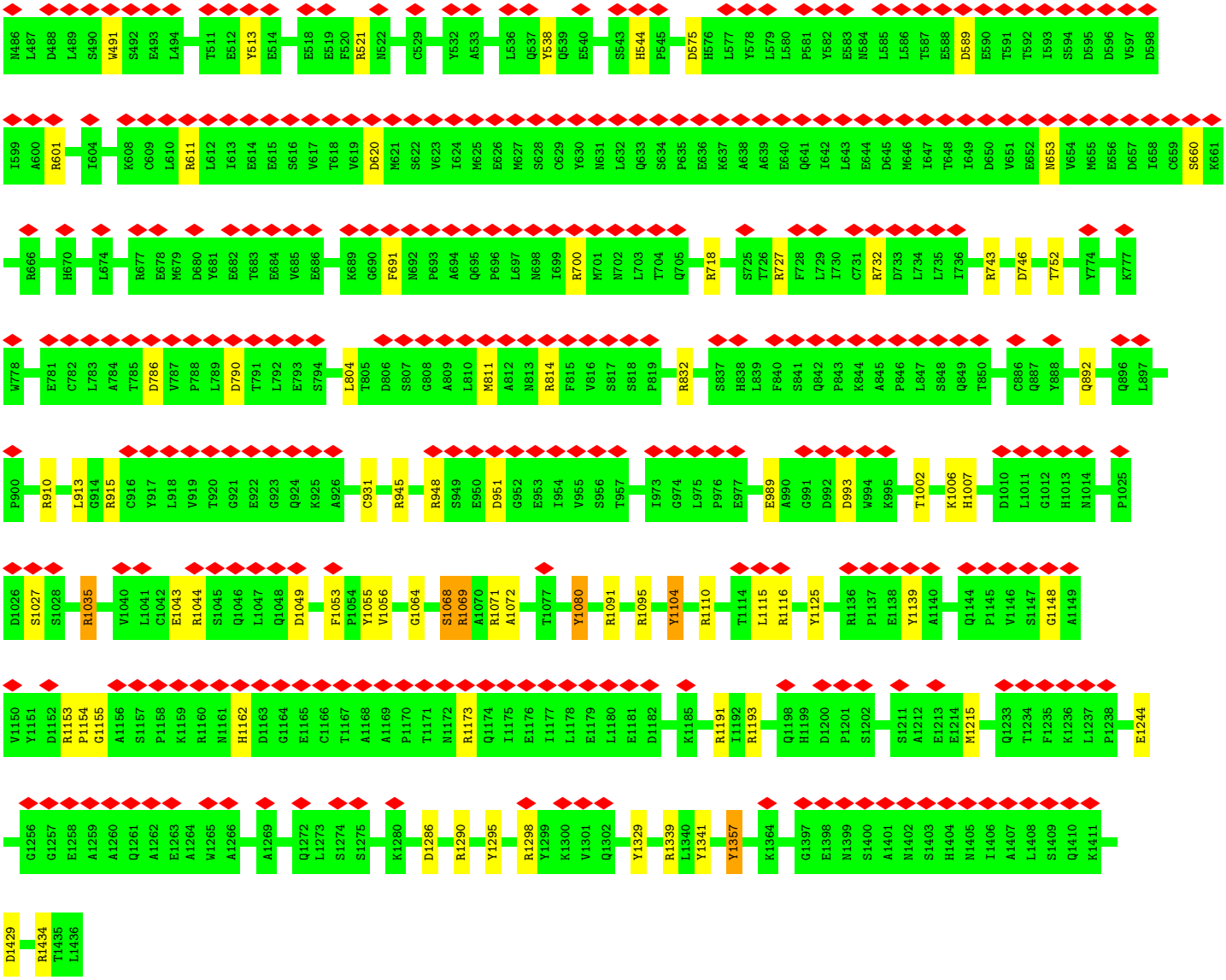




- Molecule 20: Nuclear pore complex protein Nup160

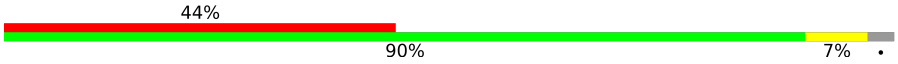
Chain R2:

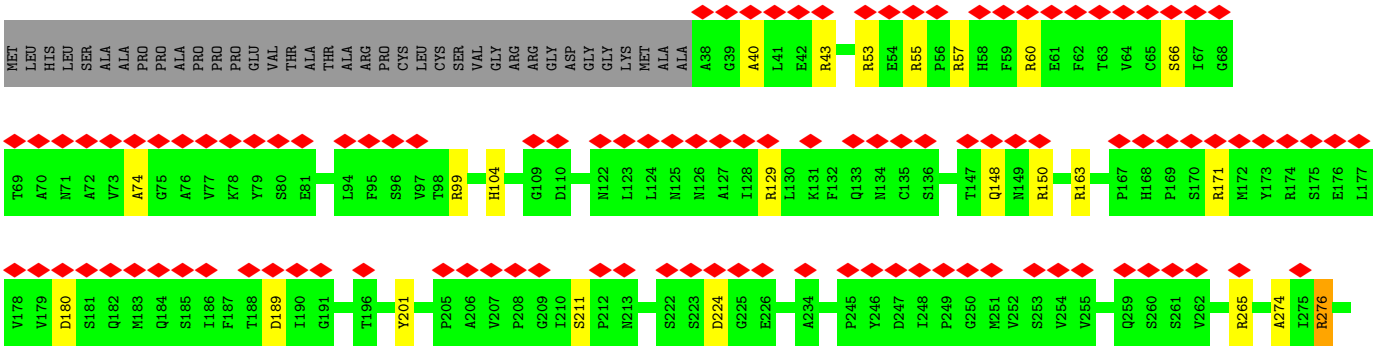




- Molecule 20: Nuclear pore complex protein Nup160

Chain R3:





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F371 Q372 L373 V374 S375 T376 E377 S378 N379 R380 Y381 S382 L383 D384 H385 I386 S387 S392 Q393 E394 T395 L396 I397 T402 S403 T404 D405 W410 H411 D412 A413 E414 N415 Q416 T417 V418 F424 E425 H426 N427 V428 M437 Q438 P439 L440 P441 E442 E443 E444 I445 V446 I447 R448 D449 D450

Q459 S460 T463 P464 G465 Q466 F467 R481 G482 T483 E484 R485 N486 L487 D488 L489 S490 W491 S492 E493 Y513 E514 F515 S516 Q517 E518 R521 L536 Q537 Y538 Q539 E540 A541 L542 S543 H544 P545 K562 D575 E588 D589 E590 T591 T592 I593 S594 D595 D596 V597 D598 I599

A600 R601 D602 V603 L612 I613 E614 E615 S616 V617 T618 V619 D620 M621 S622 V623 I624 M625 E626 M627 S628 C629 Y630 N631 L632 Q633 S634 P635 E636 K637 A638 A639 E640 Q641 I642 D645 M646 I647 T648 I649 D650 V651 E652 N653 V654 M655 E656 D657 S660 Q663 E664 I665 R666 N667 P668 I669

H670 A671 L674 R677 D680 Y681 E682 T683 E684 V685 E686 K689 G690 F691 N692 P693 A694 Q695 P696 L697 N698 I699 R700 M701 N702 R718 S725 T726 R727 F728 L729 I730 C731 R732 D733 R743 D746 I749 W750 G751 T752 A767 P768 L769 L770 L771 Y774 E781

C782 L783 A784 T785 D786 V787 P788 L789 D790 T791 L792 E793 S794 N795 L796 Q797 H798 L799 S800 E803 L804 T805 D806 S807 G808 A809 L810 M811 A812 N813 R814 F815 V816 S817 S818 P819 Q820 T821 R832 H838 L839 F840 S841 Q842 P843 K844 A845 P846 L847 S848 Q849 T850 G851 E856 Q892

H899 P900 W901 C902 Q903 V904 R910 L913 G914 R915 G921 G938 K939 D944 R945 R948 S949 E950 D951 G952 E953 I954 V955 S956 T957 P958 G974 L975 P976 E977 L978 V979 I980 Q981 T984 I987 T988 E989 A990 G991 D992 D993 W994 K995 S996 Q997 A998 T999 L1000 R1001

T1002 C1003 I1004 F1005 K1006 H1007 H1008 L1009 D1010 L1011 G1012 H1013 N1014 S1015 Q1016 A1017 Y1018 E1019 A1020 L1021 T1022 Q1023 I1024 P1025 D1026 S1027 S1028 R1029 Q1030 L1031 D1032 C1033 L1034 R1035 E1043 R1044 Q1048 D1049 E1052 F1053 P1054 Y1055 V1056 N1057 L1058 R1069 A1070 R1071 R1091 Y1104 G1105 M1106 G1109

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E1186 C1187 S1188 L1189 R1193 A1197 Q1198 H1199 D1200 P1201 S1202 A1203 V1204 A1205 V1206 A1207 G1208 S1209 S1210 S1211 A1212 E1213 E1214 M1215 D1226 I1229 S1230 L1231 C1232 Q1233 T1234 F1235 K1236 L1237 P1238 Q1254 F1255 G1256 G1257 E1258 A1259 A1260 Q1261 A1262 E1263 A1264 W1265 Q1272 E1281 S1282 S1283 A1284 T1285

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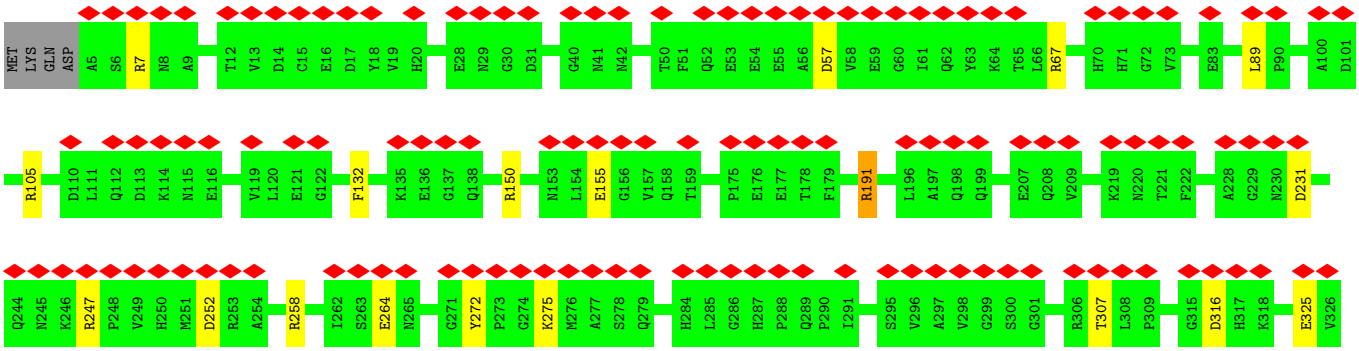
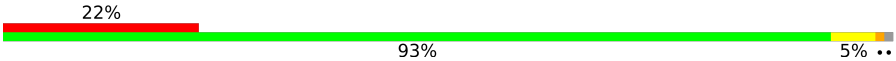
- Molecule 21: Nucleoporin Nup37

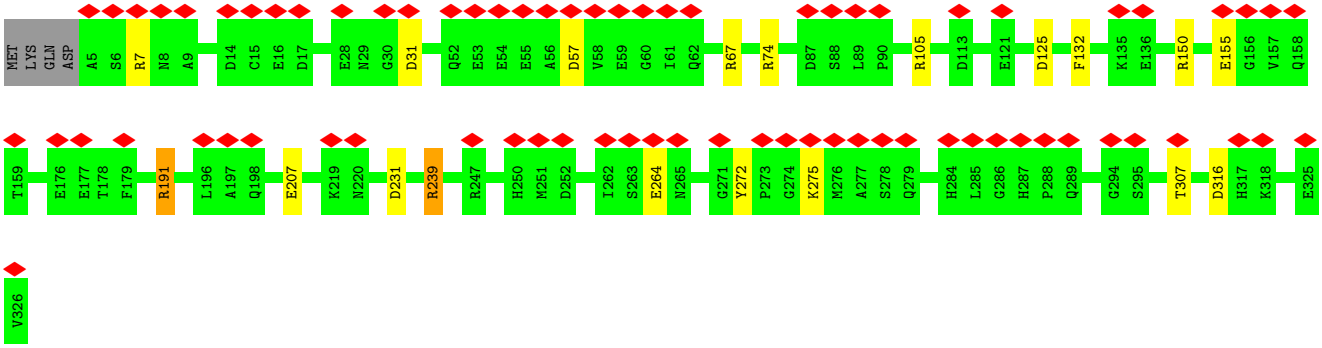
Chain S0: 40% 93% 6%



• Molecule 21: Nucleoporin Nup37

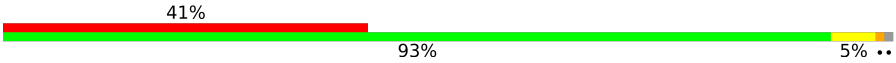
Chain S1:

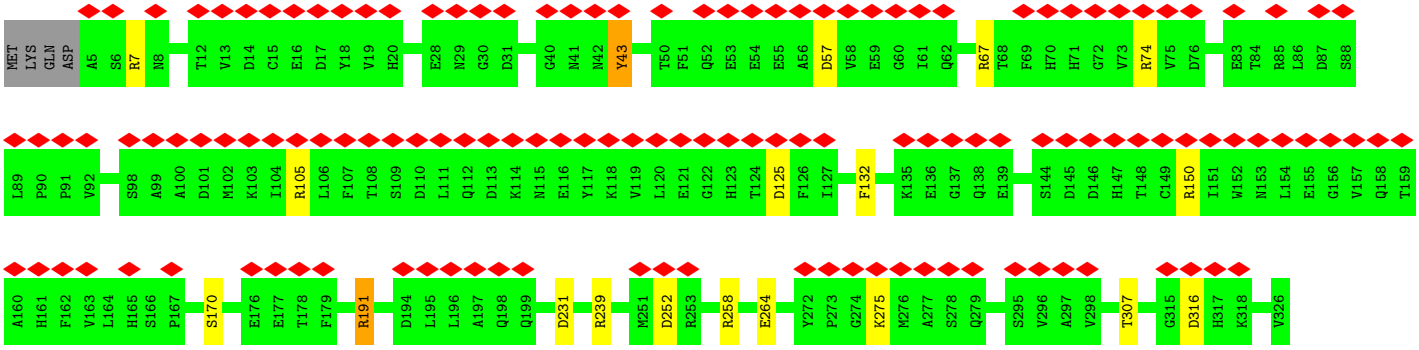




• Molecule 21: Nucleoporin Nup37

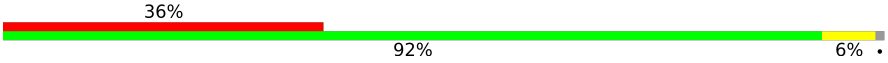
Chain S2:

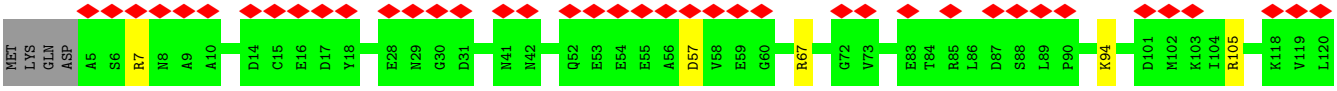




• Molecule 21: Nucleoporin Nup37

Chain S3:





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D252 R253 R258 T262 S263 E264 N265 G271 Y272 P273 G274 K275 M276 A277 S278 Q279 G286 H287 P288 Q289 M293 G294 S295 V296 A297 V298 G299 T307 L308 G315 D316 H317 K318 E325 V326

- Molecule 22: Protein ELYS

Chain T0: 25% 41% • 56%

MET R2 D3 L4 R5 A6 Q7 V8 T9 S10 G11 L12 L13 Q21 A22 L23 G24 E25 D26 E27 I28 T29 L30 E31 S32 V33 L34 R35 G36 K37 F38 A39 A40 G41 K42 N43 G44 L45 A46 C47 L48 A49 C50 G51 P52 Q53 L54 N58 S59 I60 T61 Y68 R69 F70 S71 G72 V73

N74 E75 Q76 P77 P78 V79 V80 L81 A82 V83 K84 E85 F86 S87 W88 Q89 K90 R91 T92 G93 L94 L95 I96 G97 L98 E99 E100 T101 E102 G103 S104 V105 L106 C107 L108 Y109 D110 L111 G112 I113 S114 K115 V116 V117 K118 A119 V120 V121 L122 P123 G124 R125 V126 T127 A128 I129 E130 P131 I132 I133

N134 H135 G136 G137 A138 S139 A140 S141 T142 Q143 H144 L145 H146 P147 S148 L149 R150 W151 L152 F153 A157 V158 V159 T160 D161 V162 G163 Q164 I165 L166 L167 V168 C171 L172 D173 D174 L175 S176 C177 N178 Q179 N180 E181 V182 E183 A184 S185 D186 L187 E188 V189 L190 T191 G192 I193 P194 A195 E196

V197 P198 H199 I200 R201 E202 S203 V204 M205 R206 Q207 G208 R209 H210 L211 C212 F213 Q214 L215 V216 S217 P218 T219 G220 T221 A222 V223 S224 F239 S240 D241 G242 Y243 K250 S251 M252 K253 R254 Y257 I258 Q259 L260 E261 S262 G263 Q264 V265 P266 V267 E276 N277 D278 P279 R280 N281

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E372 A373 L374 S375 P376 D377 T378 Q386 V387 N388 I389 Y390 G391 Q392 G393 K394 P395 R406 H409 R417 S418 H423 N424 S432 L433 E434 S435 V436 V437 S438 R439 T440 S441 P442 H443 G444 I445 L446 D447 I448 L449 V450 H451 E452 R453 S454 L455 N456 R457 G458 V459 P460 P461 S462

Y463 P464 P465 P466 E467 Q468 F469 F470 N471 P472 S473 T474 Y475 N476 F477 D478 A479 T480 C481 L482 L483 N484 S485 G486 V487 V488 H489 L490 T491 C492 T493 G494 F495 Q496 K497 E498 T499 L500 T501 F502 L503 K504 K505 S506 G507 P508 S509 L510 N511 E512 L513 I514 P515 D516 G517 Y518 N519 R520 C521 L522

V523 A524 G525 L526 L527 S528 P529 R530 F531 V532 D533 V534 Q535 P536 S537 S538 L539 S540 Q541 E542 E543 Q544 L545 E546 A547 I548 L549 S550 A551 A552 I553 Q554 T555 S556 S557 L558 G559 L560 G563 Y564 I565 R566 R567 W568 I569 T570 E571 E572 Q573 P574 N575 S576 A577 T578 M579 F582 N589

V592 L593 E596 E597 F598 D599 R600 L601 C602 V603 P604 D607 G608 S609 C610 H611 D614 P615 Q616 T617 I618 Q619 S620 S640 E641 A642 R643 E644 I645 T646 E647 R648 I683 D684 D685 S686 V687 Q688 L689 S690 R706 R707 Q708 E711 R712 L713 S714 R715 G716 K717 W718 N719

G727 S730 Q731 L732 G733 E734 R735 I736 E737 K738 K741 R742 D743 E744 G745 G746 T747 G748 K749 L764 D765 G766 V767 T768 Y778 N789 T800 H820 N821 D822 Y823 E824 S825 H832 A836 K837 P838 L839 S840 W841 G854 R857 R861 Q864 K867

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R993 N994 S995 I996 L997 D998 Q999 Y1000 G1001 K1002 I1003 L1004 P1005 ARG VAL HIS ARG LYS LEU ALA ILE GLU ARG ALA LYS PRO TYR HIS LEU SER THR SER SER VAL PHE ARG LEU VAL SER ARG PRO LYS PRO LEU SER ALA VAL PRO LYS GLN VAL VAL THR GLY THR VAL LEU THR ARG SER

VAL PHE ILE ASN ASN VAL LEU SER LYS ILE GLY GLU VAL TRP ALA SER SER LYS GLU PRO ILE ASN SER THR THR PRO PHE ASN SER SER LYS ILE GLU VAL TYR SER LEU PRO GLU ALA PRO GLU LEU PRO GLU ALA PHE PHE GLY THR PRO ILE SER LYS SER GLN

LYS ILE SER ARG LEU LEU ASP LEU VAL VAL GLN PRO VAL PRO ARG PRO SER GLN CYS SER GLU PHE ILE GLN GLN SER SER MET LYS SER PRO LEU TYR LEU PRO SER SER SER SER GLN LEU LYS GLY SER PRO GLN ALA ILE SER ARG ALA SER GLU LEU HIS LEU

LEU GLU THR PRO LEU VAL VAL LYS LYS ALA LYS SER LEU ALA MET SER VAL THR THR SER GLY PHE SER GLU PHE THR PRO GLN SER ILE LEU ARG SER THR PRO LEU ALA SER PRO SER PRO GLN ARG LEU LYS GLU THR ARG ILE SER

PHE VAL GLU GLU ASP VAL HIS PRO LYS TRP ILE PRO GLY ALA ALA ASP ASP SER LYS LEU GLU VAL PHE THR THR PRO LYS LYS CYS ALA VAL PRO VAL GLU THR GLU TRP LEU LYS SER LYS ASP ARG THR THR SER PHE PHE LEU ASN SER PRO GLU GLU LYS GLU HIS GLN GLU MET ASP

GLU GLY SER GLN SER LEU GLU LYS LEU ASP SER SER SER VAL SER ILE THR SER ASP GLU THR THR PRO LEU GLU TYR GLN ASP ALA PRO SER GLU ASP LEU GLU GLU THR VAL PHE THR ALA SER LYS PRO LYS SER SER SER PHE THR THR ASN ASN VAL THR

GLU GLN THR GLU LYS ASP GLY ASP LYS ASP VAL PHE ALA SER GLU VAL THR PRO SER ASP LEU LEU ASP LEU GLN LYS GLN MET GLY ASN LEU GLU ASP ALA GLU THR GLN GLY GLU GLU LEU GLU GLU VAL ALA PHE SER GLU LEU HIS GLY ASN GLY GLY ASP GLY ALA ILE ARG GLN ALA ALA ASN ASP ASN LYS SER MET ALA ASP VAL LEU GLY GLY ASP GLY GLY ASN SER SER ILE HIS LEU SER PRO VAL GLN GLY THR GLU ALA SER GLU LEU CYS

VAL SER GLU ARG ARG LEU ASN GLN GLU VAL ALA ALA LEU ASN LEU LYS VAL ASP HIS GLU VAL GLU VAL GLY VAL LEU LYS GLU SER VAL ASP LEU PRO GLU GLU LYS VAL ASP PRO ALA ILE ARG ALA ASN ASP ASN LYS SER SER MET ALA ASP VAL LEU GLY GLY ASP GLY GLY ASN SER SER GLU GLN GLU ILE HIS VAL ILE GLU GLU GLN GLU LYS LEU SER GLU GLN GLN ASP

SER GLY GLU GLU ALA ARG ASN LEU SER PHE ASN GLU LEU TYR PRO SER GLY THR LEU LYS LEU GLN TYR ASN PHE ASP THR ILE ASP GLN GLN PHE CYS ASP LEU ALA ASN ASP ASN LYS ASP THR ALA GLU VAL ASP GLY ILE ILE ALA GLU CYS ASP ILE ALA ASN HIS GLY GLN ILE GLU VAL ASP GLY ALA ALA PHE PHE LEU ASN SER GLN PHE

THR LEU ILE LEU GLU GLY GLU GLU GLY GLU VAL GLU PRO GLY ASP PHE ALA SER SER ASP VAL LEU PRO LYS ALA ALA ASN THR ALA THR GLU GLU LYS LEU VAL CYS SER GLY GLU ASN ASP ASN HIS GLY GLN ILE ALA ALA ASN LEU PRO SER ALA VAL THR SER ASP GLN LYS SER GLN

LYS VAL ASP THR LEU PRO TYR VAL PRO GLU PRO ILE LYS VAL ALA ILE ALA GLU ASN LEU LEU ASP VAL ALA ILE LYS ASP THR ARG SER LYS GLU ILE THR SER ASP THR MET GLU GLN SER ILE HIS GLU THR ILE PRO LEU VAL SER GLN ASN ILE MET CYS PRO THR LYS LEU VAL LYS

SER ALA PHE LYS THR ALA GLN GLU THR SER THR MET THR MET ASN VAL SER GLN VAL ASP ASP VAL VAL SER SER LYS THR ARG ARG THR ARG GLY GLN ARG ILE ALA GLN GLN GLU ALA SER ALA ASP VAL ALA THR PRO VAL SER LYS SER GLN

ARG LYS LYS THR ARG LYS ALA LYS GLU ILE SER GLU ASN ILE TYR SER ASP VAL ARG GLY LEU SER SER LYS GLN ASN GLN ILE PRO GLN ASN GLN ILE SER SER VAL THR PRO ARG ARG GLY ARG ARG ARG ILE LYS LYS GLU VAL ASN GLN ASP ILE LEU GLU ASN VAL SER GLN ASN ILE MET CYS PRO THR LYS LEU VAL LYS

LEU GLN ILE THR THR GLY ARG GLU LYS SER SER GLN LEU LEU GLU PRO ALA VAL GLU GLU GLU THR THR LYS LYS GLU VAL SER VAL THR LYS ARG THR PRO ARG ARG ARG ILE LYS ARG SER VAL GLU ASN ILE ILE ASN ASP LEU LYS

VAL SER THR VAL THR SER PRO SER ARG MET ILE ARG LYS SER ARG ALA SER GLU ASN THR GLY ASN LYS GLN ASP ASP LYS GLN GLN ASP VAL ARG ARG VAL ARG ARG VAL ARG GLY ARG GLU GLU VAL SER ILE LYS HIS VAL ARG ARG LYS ILE LYS ARG SER VAL ARG GLU ASN GLN ASP ILE LEU GLU ASN GLN GLU VAL SER PRO SER ASP VAL ARG GLU GLN GLU

ASN LEU GLU SER SER GLN LEU THR VAL GLN ALA GLU PHE ASP MET SER ALA ILE PRO ARG LYS ARG GLY ARG PRO ARG ILE SER LYS ILE ASN PRO SER GLU ASP VAL ALA VAL LYS GLU GLU ARG SER PRO LYS LYS ARG LYS LYS GLU ARG ARG GLU ARG GLU ARG GLU ARG ARG ARG ARG SER THR ARG ASN

THR PRO ALA LYS SER GLU ASN VAL ASP VAL GLY LYS SER ILE ILE ASP PRO ASN GLU GLU LEU SER MET VAL MET SER SER GLU SER LYS LYS THR GLU GLU SER GLN SER GLN LYS ARG SER LEU HIS SER VAL SER GLU LEU ARG GLU ARG THR ASP GLU MET

THR HIS LYS GLU THR ASN GLU GLN GLU GLU ARG LEU LEU ALA THR ALA SER PHE THR LYS SER SER ARG THR ARG SER SER LYS ALA ILE LEU LEU PRO ASP LEU SER GLU PRO ASN SER SER SER ARG GLU GLU PRO LEU PHE SER PRO ALA SER PRO GLU VAL ILE ARG ARG SER THR ASP ALA LYS

LYS ILE GLU VAL PRO ALA GLN LEU LYS GLU LEU VAL SER ASP THR SER GLN PHE VAL ILE SER PRO PRO ALA LEU LYS ASP ASP ALA GLN SER VAL THR LEU GLY LYS PRO LYS ALA LYS ARG

ILE ARG THR SER LYS THR LYS GLN ALA SER LYS ASN THR GLU LYS GLU SER ALA TRP SER PRO PRO PRO ILE GLU ILE ARG LEU ILE SER PRO LEU ALA SER PRO ALA ASP GLY VAL LYS SER LYS PRO ARG LYS THR THR GLU VAL THR GLY THR GLY LEU GLY ARG ASN ARG LYS LYS

LEU SER SER TYR PRO LYS GLN ILE LEU ARG ARG LYS MET LEU

- Molecule 22: Protein ELYS

Chain T1: 35% 42% • 56%

MET R2 D3 L4 R5 A6 Q7 V8 T9 S10 G11 L12 L13 P14 E17 L20 Q21 A22 L23 G24 E25 D26 E27 I28 T29 L30 E31 S32 V33 L34 R35 A39 A40 G41 K42 N43 G44 L45 A49 C50 G51 P52 Q53 L54 Y68 R69 F70 S71 G72 V73 N74 E75 Q76 P77 P78

V79 V80 L81 A82 V83 K84 E85 F86 S87 W88 Q89 K90 R91 T92 G93 L94 L95 I96 G97 L98 E99 E100 T101 E102 G103 S104 V105 L106 C107 L108 Y109 D110 L111 G112 I113 S114 K115 V116 V117 K118 A119 V120 V121 L122 P123 G124 R125 V126 T127 A128 I129 E130 P131 I132 I133 N134 H135 G136 G137 A138

S139 A140 S141 T142 Q143 H146 P147 S148 L149 R150 W151 L152 F153 G154 V155 A156 A157 V158 V159 T160 D161 V162 G163 Q164 I165 L166 L167 V168 D169 L170 C171 L172 D173 D174 L175 S176 C177 N178 Q179 N180 E181 V182 E183 A184 S185 D186 L187 E188 V189 L190 T191 G192 I193 P194 A195 E196 V197 P198 H199

I200 R201 E202 S203 V204 M205 R206 Q207 G208 R209 H210 L211 C212 F213 Q214 L215 V216 S217 P218 T219 G220 T221 A222 V223 S224 T225 R231 G238 F239 S240 D241 G242 Y243 K250 S251 M252 K253 R254 E255 Y256 Y257 I258 Q259 L260 E261 S262 G263 Q264 V265 P266 V267 Y268 E276 N277 D278 P279

R280 V288 Q289 S290 T291 Q292 D293 S294 E295 G296 D297 V298 L299 S300 L301 H302 L303 L304 Q305 L306 A307 F308 G309 N310 R311 K312 C313 L314 A315 S316 G317 Q318 I319 L320 Y321 E322 G323 L324 E325 Y326 C327 E328 E329 R330 Y331 T332 L333 D334 L335 T336 G337 G338 M339 F340 P341 L342 R343 G344 Q345

T346 S347 N348 T349 K350 I357 E358 K359 F360 R361 S362 H363 G364 D365 R366 E367 E368 G369 V370 N371 E372 A373 L374 S375 P376 D377 T378 Q386 V387 N388 I389 Y390 G391 Q392 G393 K394 P395 S396 N405 R406 W407 Y408 H409 A410 Q411 M412 P413 D414 S415 L416 R417 S418 G419 E420 Y421 L422 H423

N424 C425 S426 Y427 F428 A429 L430 W431 S435 V436 V437 S438 R439 T440 S441 P442 H443 G444 I445 L446 L449 V450 H451 E452 R453 S454 L455 N456 R457 G458 V459 P460 P461 S462 Y463 P464 P465 P466 E467 Q468 F469 F470 N471 P472 S473 T474 Y475 N476 F477 D478 A479 L483 N484 S485 V488 H489

L490 T491 C492 T493 G494 F495 Q496 K497 E498 T499 L500 T501 F502 L503 K504 K505 S506 G507 P508 S509 L510 N511 E512 L513 I514 P515 D516 G517 Y518 N519 R520 C521 L522 V523 A524 G525 L526 L527 S528 P529 R530 F531 V532 D533 V534 Q535 P536 S537 S538 L539 S540 Q541 E542 E543 Q544 L545 E546 A547 T548 L549

S550 A551 A552 I553 Q554 T555 S556 G559 L560 L561 T562 G563 Y564 I565 R566 R567 W568 I569 T570 E571 E572 Q573 P574 N575 S576 A577 T578 N579 L580 R581 F582 V583 L584 E585 W586 T587 W588 N589 K590 V591 V592 L593 T594 K595 E596 E597 F598 D599 R600 L601 C602 V603 P604 L605 F606 D607 G608 S609 C610

H611 F612 M613 D614 P615 Q616 T617 I618 Q619 S620 I621 Q622 Q623 C624 S640 E641 A642 R643 E644 I645 T646 E647 R648 G649 L650 I651 S654 N655 V658 P680 E681 G682 I683 D684 D685 S686 V687 Q688 L689 S690 R691 L692 C693 Y694 N695 Y696 P697 V698 I699 Q700 N701 Y702 S705 R706 R707

R712 L713 S714 R715 G716 K717 W718 M724 G727 L728 V729 S730 Q731 L732 G733 E734 R735 T736 E737 K738 L739 W740 K741 R742 D743 E744 G745 G746 T747 G748 A753 S754 L755 H756 M761 L764 D765 G766 V767 T768 E769 A770 A771 K772 H773 S774 Y778 Y785 S786 F787 P788 N789

K790 T791 D792 T793 I804 S805 W806 G807 Q808 V809 K810 L811 I812 Q813 G814 F815 W816 L817 I818 D819 H820 N821 D822 Y823 E824 S825 G826 L827 D828 L829 L830 F831 H832 P833 A834 T835 A836 K837 P838 L839 S840 W841 Q842 H843 S844 K845 I846 I847 Q848 A849 F850 M851 S852 Q853 G854 E855 H856 R857 Q858
A859 L860 R861 Y862 I863 Q864 T865 M866 K867 P868 T869 V870 S871 S872 G873 N874 D875 V876 I877 L878 H879 L880 T881 V882 L883 L884 F885 N886 R887 C888 M889 V890 E891 A892 W893 N894 F895 L896 R897 Q898 H899 C900 N901 R902 L903 N904 I905 E906 E907 L908 L909 K910 H911 M912 Y913 E914 V915 C916 Q917 E918
M919 G920 L921 M922 E923 D924 L925 L926 K927 L928 P929 F930 T931 D932 T933 E934 Q935 E936 C937 L938 V939 K940 F941 L942 Q943 S944 S945 A946 S947 V948 Q949 N950 H951 E952 F953 L954 L955 V956 H957 H958 L959 Q960 R961 A962 N963 Y964 V965 P966 A967 L968 K969 L970 N971 Q972 T973 L974 K975 I976 N977 V978
M979 N980 D981 R982 D983 P984 R985 L986 R987 E988 R989 S990 L991 A992 R993 N994 S995 I996 L997 D998 Q999 Y1000 G1001 K1002 I1003 L1004 P1005 ARG VAL HIS ARG LYS LEU ALA ILE GLU ARG ALA LYS PRO TYR HIS LEU SER THR SER SER VAL PHE ARG LEU VAL SER ARG PRO LYS PRO LEU SER ALA
VAL PRO LYS GLN VAL VAL THR GLY THR VAL LEU THR ARG SER VAL PHE ILE ASN ASN VAL LEU SER LYS ILE GLY GLU VAL TRP ALA SER LYS GLU PRO ILE ASN SER THR THR PRO PHE ASN SER SER LYS ILE GLU GLU PRO SER PRO ILE VAL TYR SER LEU PRO ALA PRO GLU LEU
PRO GLU ALA PHE PHE GLY THR PRO ILE SER LYS ALA SER GLN LYS ILE SER ARG LEU LEU ASP LEU VAL VAL GLN PRO VAL PRO ARG PRO SER GLN CYS SER GLU PHE ILE GLN GLN SER SER MET LYS SER PRO LEU TYR LEU VAL SER ARG SER LEU PRO SER SER SER GLN LEU LYS
GLY SER PRO GLN ALA ILE SER ARG ALA SER GLU LEU HIS LEU LEU GLU THR PRO LEU VAL VAL LYS LYS ALA LYS SER LEU ALA MET SER VAL THR THR SER GLY PHE SER GLU PHE THR PRO GLN SER ILE LEU ARG SER THR LEU ARG SER THR PRO LEU ALA SER PRO SER PRO SER
PRO GLY ARG SER PRO GLN ARG LEU LYS GLU THR ARG ILE SER PHE VAL GLU GLU ASP VAL HIS PRO LYS TRP ILE PRO GLY ALA ALA ASP ASP SER LYS LEU GLU VAL PHE THR THR PRO LYS LYS CYS ALA VAL PRO VAL GLU THR GLU TRP LEU LYS SER LYS ASP ARG THR THR SER
PHE PHE LEU ASN SER PRO GLU LYS GLU HIS HIS GLN GLU MET ASP GLU GLY SER GLN SER LEU GLU LYS LEU ASP VAL SER SER VAL SER LYS GLY ASN SER SER VAL SER ILE THR SER ASP GLU THR THR LEU GLU TYR GLN ASP ALA PRO SER PRO GLU ASP LEU LEU GLU GLU THR VAL PHE THR ALA SER
LYS PRO LYS SER SER SER THR ALA LEU THR THR ASN VAL THR GLU GLN THR GLU LYS ASP GLY ASP LYS LYS ASP VAL PHE ALA SER GLU VAL THR PRO SER LYS ASP LEU GLN LYS GLN MET GLY ASN LEU GLU ASP ALA GLU THR LYS ASP LEU LEU VAL ALA ALA GLU ALA PHE SER GLU LEU
ASN HIS LEU SER PRO VAL GLN GLY THR GLU ALA SER LEU CYS ALA PRO SER VAL TYR GLU GLY LYS ILE PHE THR GLN LYS SER GLY VAL LYS VAL PRO VAL LEU ASP GLU GLY LEU THR SER VAL GLU THR TYR THR PRO ALA ILE ARG ALA ASN ASP ASN LYS SER MET ALA ASP VAL LEU GLY
ASP GLY GLY ASN SER SER LEU THR ILE SER GLU GLY PRO ILE VAL ARG LEU ASN GLN GLU VAL ALA LEU ASN LEU LYS GLU ASP HIS GLU VAL GLU ARG ARG LEU ASN GLU GLU GLY VAL GLY VAL LEU LYS GLU SER VAL ASP LEU PRO GLU GLU LYS LEU ILE SER ASP GLU VAL GLU LYS ILE GLU
GLU ILE HIS VAL ILE GLU GLN GLU LYS LEU GLU ALA GLN ASP SER GLY GLU GLU ALA ARG ASN LEU SER PHE ASN GLU GLU LEU TYR PRO SER GLY THR LEU LYS LEU LYS LEU GLN TYR ASN PHE ASP THR ILE ASP GLN GLN PHE CYS ASP LEU ALA ASP ASN LYS ASP THR LYS ILE
ALA GLU VAL ASP GLY GLU LEU PHE VAL ALA GLN SER ASN PHE THR LEU ILE LEU GLU GLY GLU GLU GLY GLU VAL GLU PRO GLY ASP PHE ALA SER SER ASP VAL LEU PRO LYS ALA ALA ASN THR ALA THR GLU GLU LYS LEU VAL CYS SER GLY GLU ASN ASP SER PRO ILE GLN ILE
ALA ASN LEU PRO SER ALA VAL THR SER ASP GLN LYS SER GLN LYS VAL ASP THR LEU PRO TYR VAL PRO GLU PRO ILE LYS VAL ALA ILE ALA GLU LEU LYS LEU VAL ASP VAL ILE LYS ASP THR ARG SER LYS GLU ILE THR SER ASP THR MET GLU GLN SER ILE HIS GLU THR ILE PRO
LEU VAL SER GLN LEU LYS LEU VAL LYS SER ALA ALA PHE LYS THR ALA GLN GLU THR SER THR MET THR MET ASN VAL SER GLN VAL ASP ASP VAL LEU ASP VAL ILE LYS SER SER LYS THR THR ARG THR ARG GLY GLN ARG ILE GLN ASN VAL ASN VAL LYS SER ILE HIS GLU GLN GLN ALA
SER ALA ASP VAL ALA THR PRO LYS MET PRO GLY GLN SER VAL LYS LYS THR ARG LYS ALA LYS GLU ILE SER GLU ASN GLU ALA SER GLU ASN ILE TYR SER ASP VAL ARG GLY LEU SER GLN GLN GLN ILE PRO GLN ASN SER VAL THR PRO ARG ARG GLY ARG ARG LYS LYS GLU VAL
ASN GLN ASP ILE LEU GLU ASN THR SER SER GLN ILE LEU LEU GLU PRO ALA VAL GLU THR THR GLY ARG GLU GLU SER LYS SER SER GLN LEU LEU GLU PRO VAL ASP VAL LYS LYS GLU VAL LYS VAL SER SER VAL THR LYS ARG THR PRO ARG ARG ILE LYS ARG SER

VAL GLU ASN GLN GLU SER VAL GLU ILE ILE ASN ASP LEU LYS VAL SER THR VAL THR SER PRO SER ARG MET ILE ARG LYS LEU ARG SER THR ASN LEU ASP ALA SER GLU ASN THR GLY ASN LYS GLN ASP ASP LYS SER SER ASP LYS GLN LEU ARG ILE LYS HIS VAL ARG ARG VAL

ARG GLY ARG GLU VAL SER PRO SER ASP VAL ARG GLU ASP SER ASN LEU GLU SER SER GLN LEU THR VAL GLN ALA GLU PHE ASP MET SER ALA ILE PRO ARG LYS ARG GLY ARG PRO ARG LYS ILE ASN PRO SER GLU ASP VAL GLY LYS SER LYS ALA VAL LYS GLU GLU ARG SER PRO LYS

LYS LYS GLU ALA PRO SER ILE ARG ARG ARG ARG SER THR ARG ASN THR PRO ALA LYS SER GLU ASN VAL ASP VAL GLY LYS PRO ALA LEU GLY LYS SER ILE LEU VAL PRO ASN GLU GLU LEU SER MET VAL MET SER SER SER LYS LYS LYS LEU THR LYS LYS THR GLU SER GLN SER PRO GLN LYS

ARG SER LEU HIS SER VAL SER LYS GLU GLU ARG THR ASP GLU MET THR HIS LYS GLU THR ASN GLU GLN GLU GLU ARG LEU ARG THR ALA SER PHE THR LYS SER SER ARG SER SER ARG THR ARG SER LYS ALA ILE LEU LEU PRO ASP LEU SER GLU PRO ASN ASN GLU GLU PRO ALA ALA LEU LEU ALA LEU LEU LEU LEU LEU LEU

PHE SER PRO ALA SER GLU VAL PRO ARG LYS ALA ALA LYS ALA LYS LYS ILE GLU VAL PRO ALA GLN LEU LYS GLU LEU VAL SER ASP LEU SER SER GLN PHE VAL ILE SER PRO PRO ALA LEU ARG SER ARG GLN LYS ASN THR SER ASN LYS ASN LYS LYS LEU GLU ASP GLU LEU LYS ASP ASP

ALA GLN SER VAL GLU THR LEU GLY LYS PRO LYS ALA LYS ARG ILE ARG THR SER LYS THR LYS GLN ALA SER LYS ASN THR GLU LYS GLU SER ALA TRP SER PRO PRO PRO ILE GLU ILE ARG LEU ILE SER PRO LEU ALA SER PRO ALA ASP GLY VAL LYS SER LYS PRO ARG LYS THR

THR GLU VAL THR GLY THR GLY LEU GLY ARG ASN ARG LYS LYS LEU SER SER TYR PRO LYS GLN ILE LEU ARG ARG LYS MET LEU

- Molecule 23: Nuclear pore complex protein Nup98

Chain U0: 14% 15% 83%

MET PHE ASN LYS SER PHE GLY THR PRO PHE GLY GLY GLY THR GLY GLY PHE GLY THR THR SER THR PHE GLY GLN ASN THR GLY PHE GLY THR THR SER GLY GLY ALA PHE GLY THR SER ALA PHE GLY SER SER ASN ASN THR GLY GLY LEU PHE GLY ASN SER GLN THR LYS PRO GLY

GLY LEU PHE GLY THR SER SER PHE SER GLN PRO ALA THR SER THR SER THR GLY PHE GLY THR SER THR GLY THR ALA ASN THR LEU PHE GLY THR ALA SER THR GLY THR SER LEU PHE SER SER GLN ASN ASN ALA PHE ALA GLN ASN LYS PRO THR GLY PHE GLY ASN PHE

GLY THR SER THR SER SER GLY LEU PHE GLY THR THR SER GLY SER LEU PHE GLY PRO SER SER PHE THR ALA ALA PRO THR GLY THR THR ILE LYS PHE ASN PRO PRO THR GLY THR ASP THR MET VAL LYS ALA GLY VAL SER THR

ASN ILE SER THR LYS HIS GLN CYS ILE THR ALA MET LYS GLU TYR GLU SER LYS SER LEU GLU ASP TYR GLN ALA ASN ARG LYS GLY PRO GLN ASN GLN VAL GLY ALA GLY THR THR THR GLY SER SER PRO ALA THR SER SER ALA THR GLY GLU

PHE SER SER SER THR ASN SER GLY PHE ALA TYR GLY GLN ASN LYS THR ALA PHE GLY GLY THR SER THR THR GLY PHE GLY THR ASN PRO GLY GLY LEU PHE GLY GLN GLN THR THR SER LEU PHE SER LYS PRO PHE GLY GLN ALA THR THR THR THR GLN ASN THR GLY PHE

SER PHE GLY ASN THR SER THR ILE GLY GLN PRO SER THR ASN THR MET GLY LEU PHE GLY VAL THR GLN ALA SER GLN PRO GLY GLY LEU PHE GLY THR ALA THR ASN THR SER SER THR GLY THR ALA PHE GLY THR GLY TYR THR ASN THR ASN GLY LEU PHE GLY GLN THR ASN THR GLY PHE

GLY SER THR LEU PHE GLY ASN ASN LYS LEU THR THR PHE GLY SER GLY THR THR SER GLY GLY LEU PHE GLY ASN LYS PRO THR LEU THR GLY THR ASN THR SER ASN PHE GLY PHE GLY THR ASN THR GLY ASN SER GLY PHE

GLY SER LYS PRO ALA PRO GLY THR GLY LEU GLY ALA PHE GLY THR ALA LEU GLY GLY ALA GLN SER LEU PHE GLY ASN ASN GLN PRO LYS ILE GLY GLY PRO LEU GLY GLY THR THR GLY ALA PHE GLY ALA PRO GLY PHE ASN THR THR THR GLY PHE PHE

ALA PRO GLN ALA PRO VAL ALA LEU THR ASP PRO ASN ALA SER ALA ALA GLN GLN ALA VAL LEU GLN GLN GLN HIS ILE ASN SER LEU THR TYR SER PRO PHE GLY ASP SER PRO LEU PHE ARG ASN PRO MET SER ASP PRO LYS LYS LYS GLU GLU ARG LEU LYS PRO THR ASN PRO ALA ALA

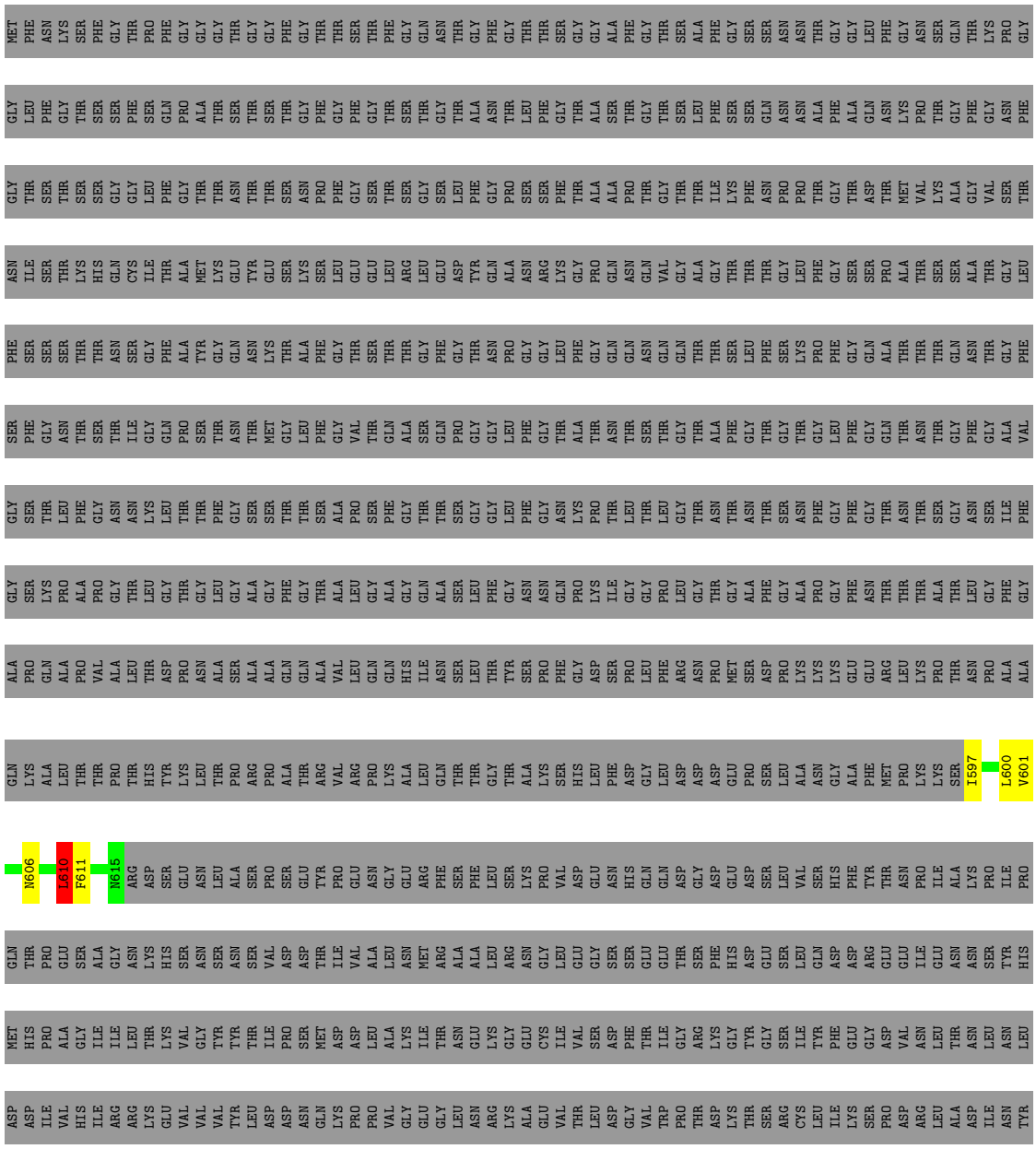
GLN LYS ALA LEU THR THR PRO THR HIS TYR LYS LEU THR PRO ARG PRO ALA THR ARG VAL ARG PRO LYS ALA LEU GLN THR THR GLY THR ALA LYS SER HIS LEU PHE ASP GLY LEU ASP ASP GLU PRO SER LEU ALA ASN GLY ALA PHE MET PRO LYS LYS SER ILE LYS LYS LEU

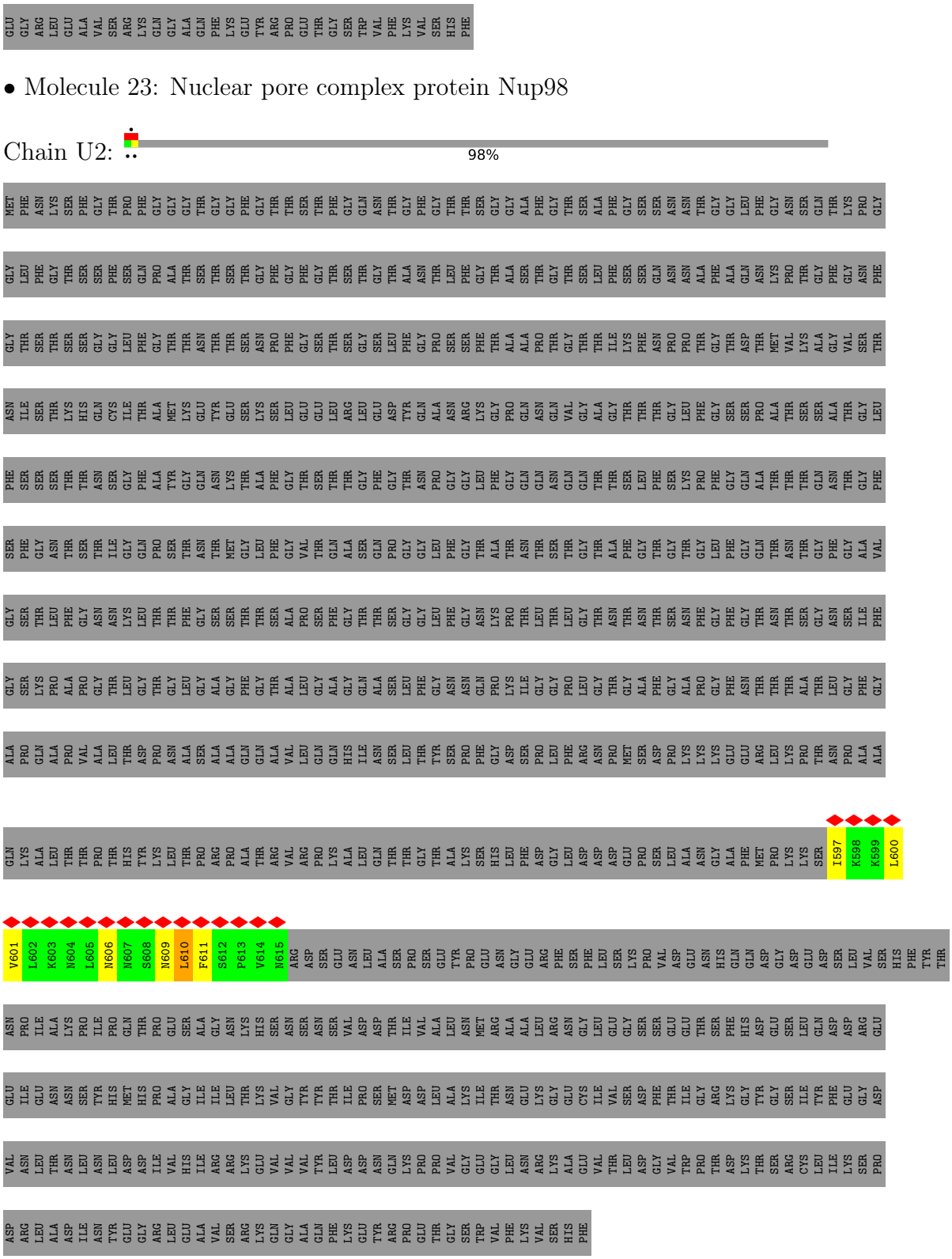
VAL LEU LYS ASN LEU ASN ASN SER ASN PHE SER ASN PRO VAL ARG ASP SER GLU GLU ASN ARG PHE SER PHE LEU SER LYS PRO VAL ASP GLU ASN HIS GLN GLN ASP GLY ASP SER LEU VAL SER HIS PHE TYR THR

ASN PRO ILE ALA LYS PRO ILE PRO CLN THR PRO GLU SER ALA GLY ASN LYS HIS SER ASN SER ASN SER VAL ASP ASP THR ILE VAL ALA LEU ASN MET ARG ALA ALA LEU ARG ASN GLY LEU GLU GLY SER GLU GLU THR SER PHE HIS ASP GLU SER LEU GLN ASP ASP ARG GLU

- Molecule 23: Nuclear pore complex protein Nup98

Chain U1: 98%



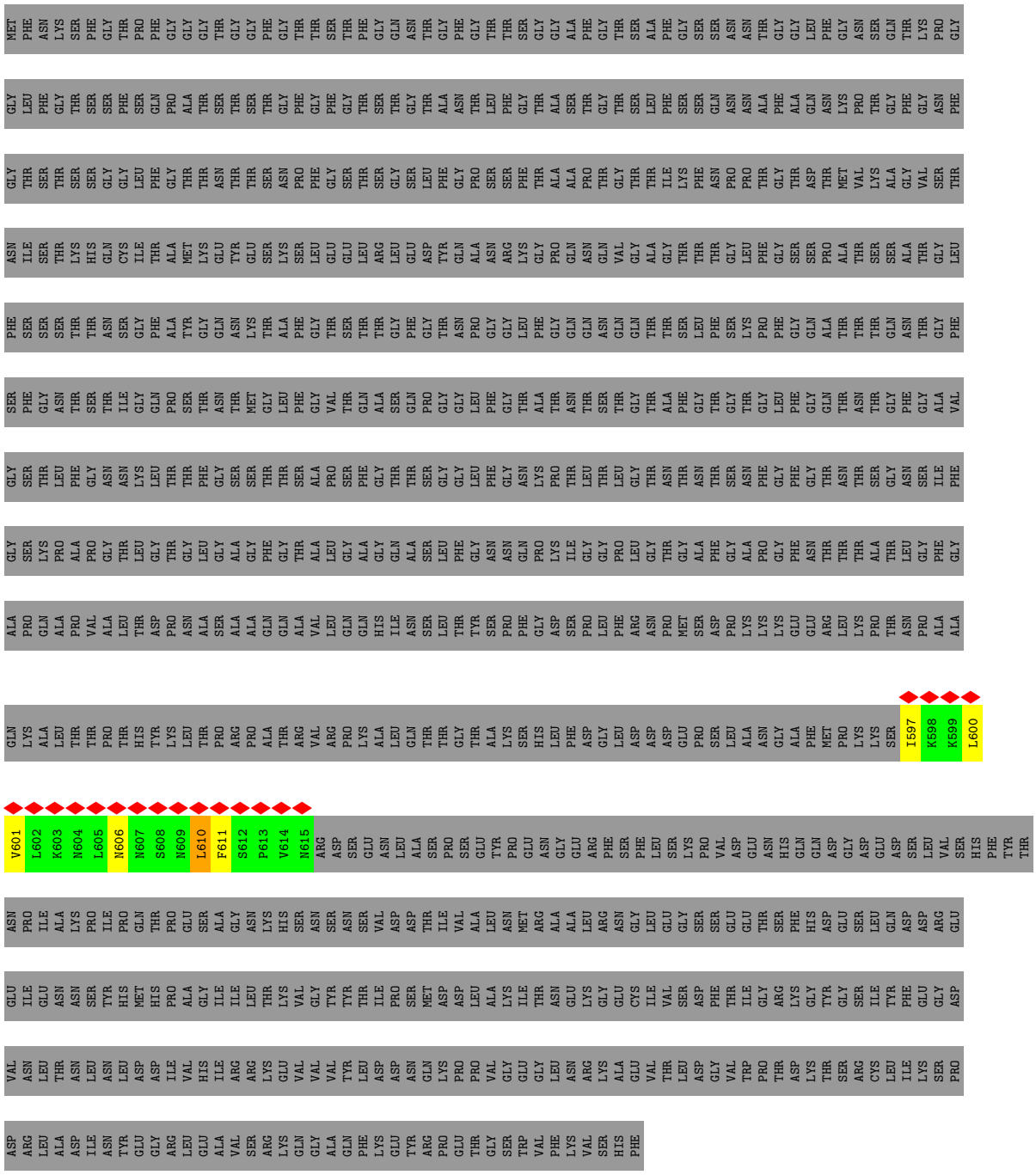


• Molecule 23: Nuclear pore complex protein Nup98

Chain U2:

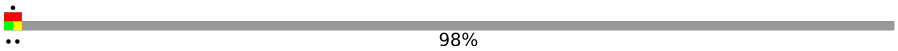
• Molecule 23: Nuclear pore complex protein Nup98

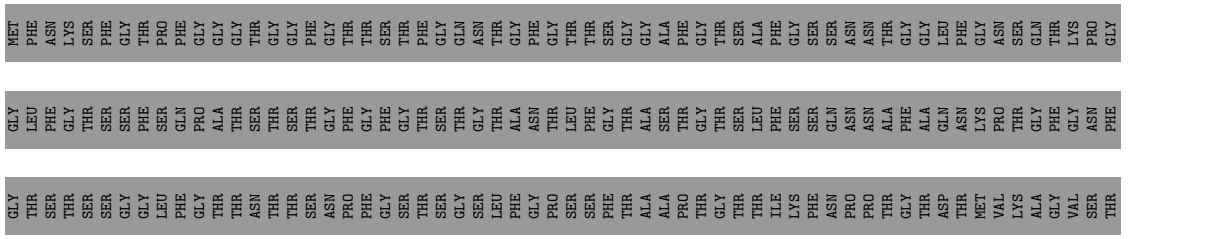
Chain U3:

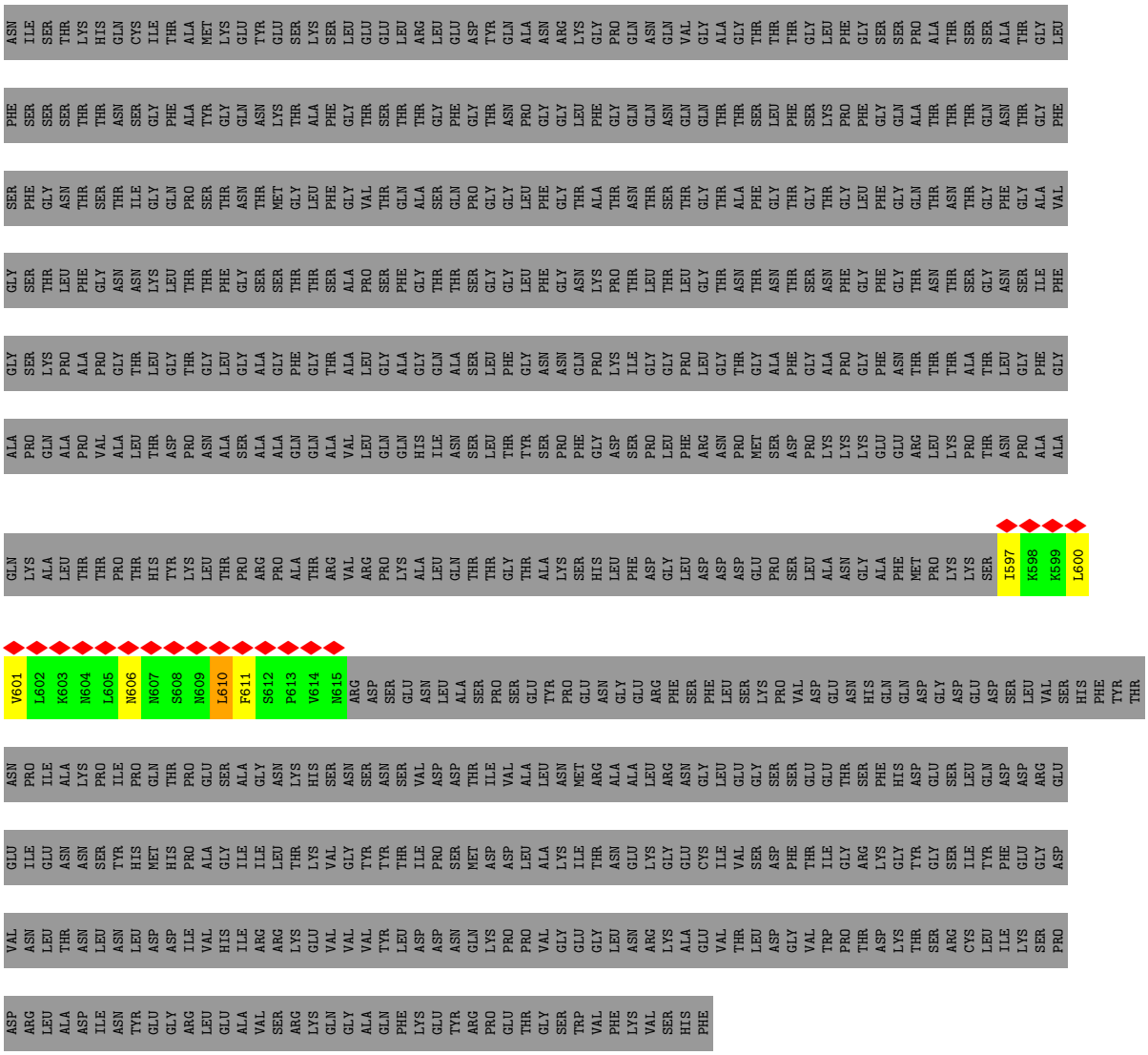


• Molecule 23: Nuclear pore complex protein Nup98

Chain U4:

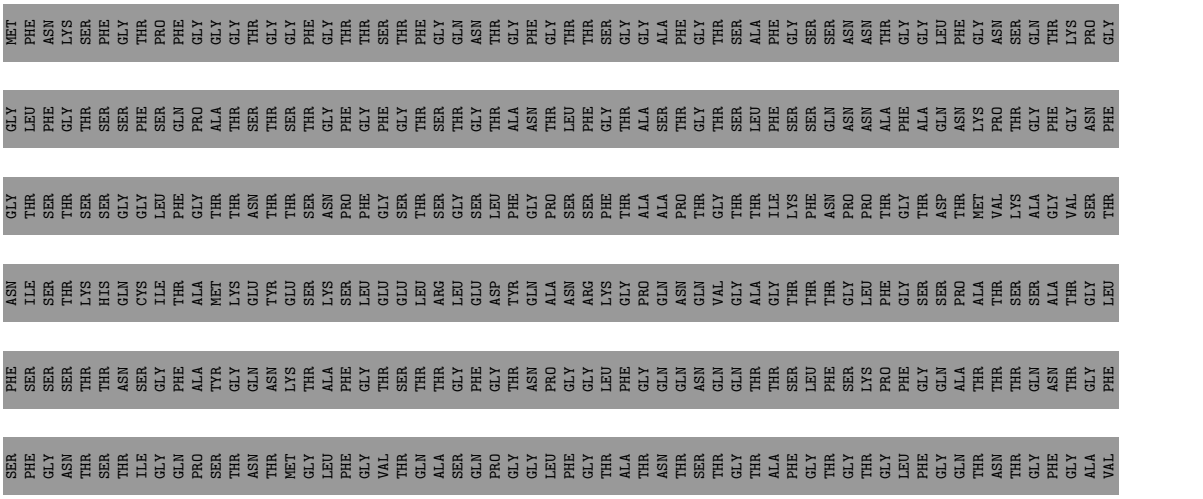


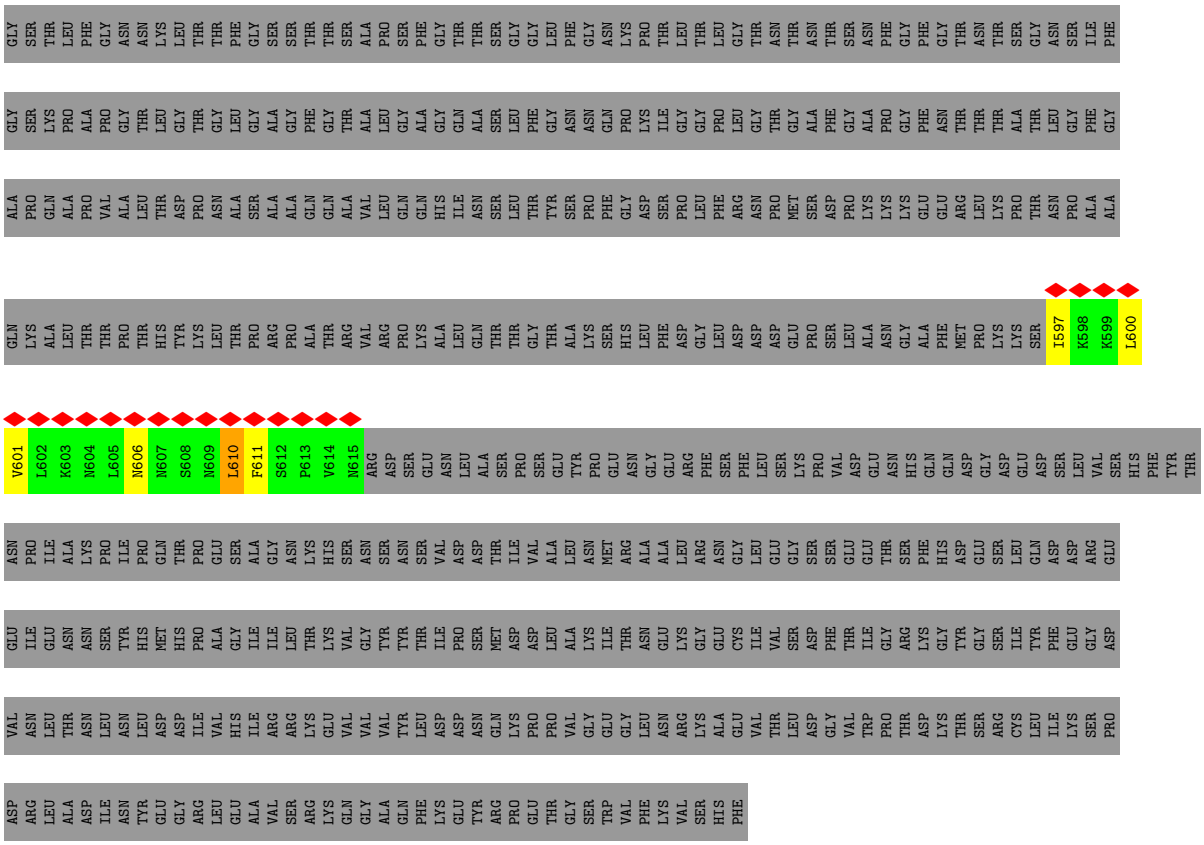




• Molecule 23: Nuclear pore complex protein Nup98

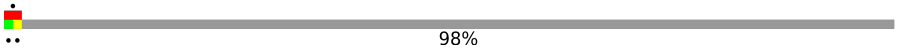
Chain U5: 98%

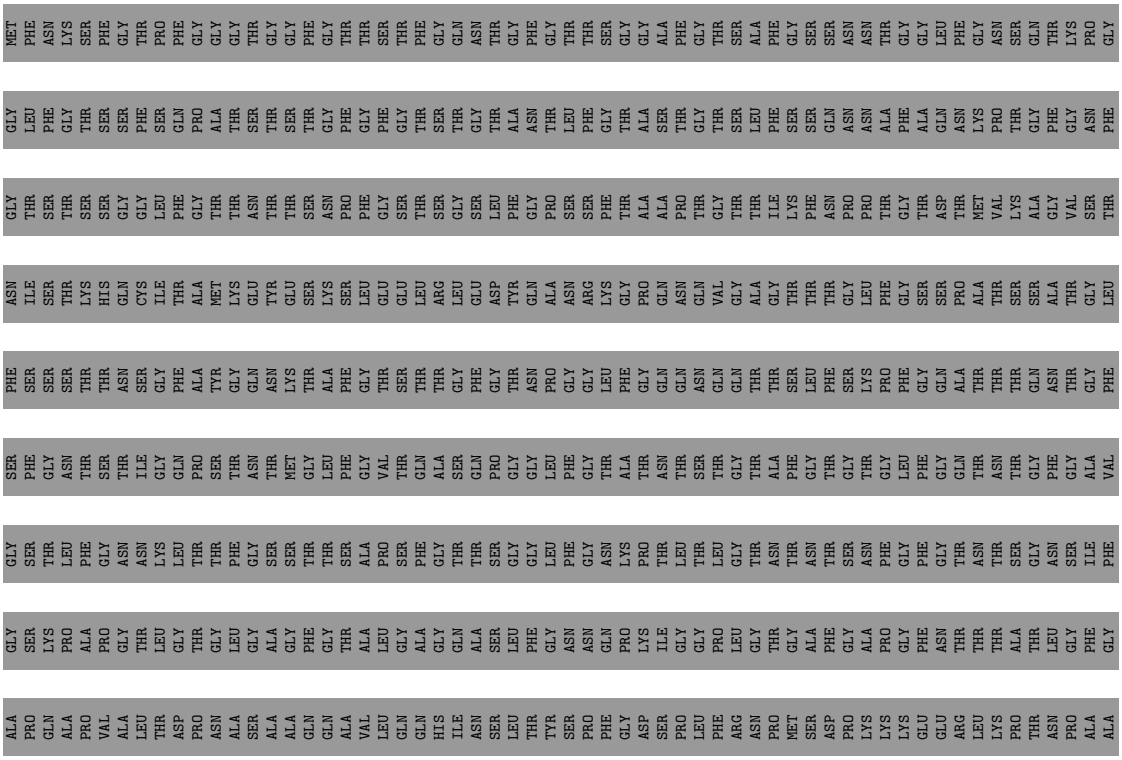




• Molecule 23: Nuclear pore complex protein Nup98

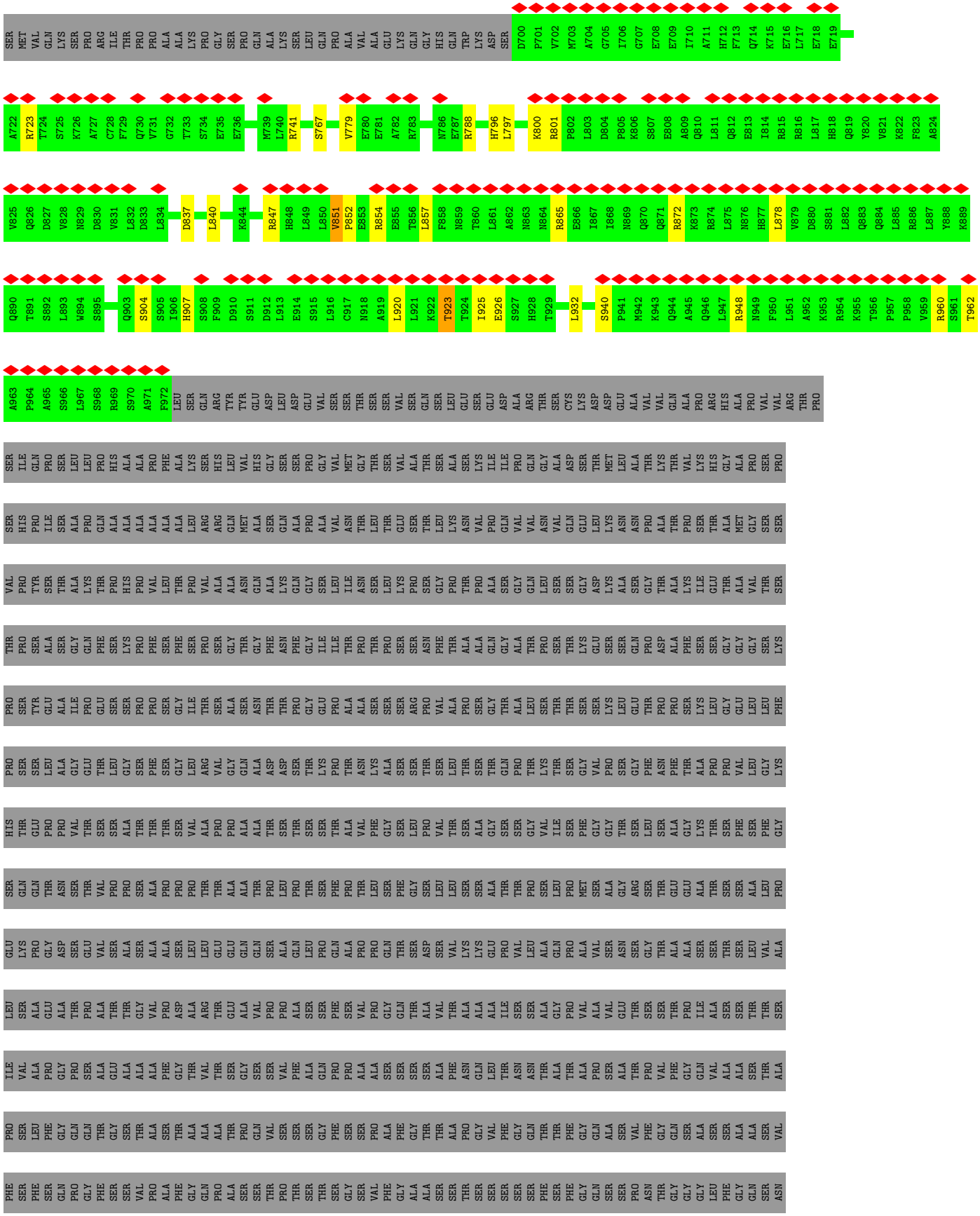
Chain U6:





• Molecule 24: Nuclear pore complex protein Nup214

Chain V0:


SER MET VAL GLN LYS SER PRO ARG ILE THR PRO PRO ALA ALA LYS PRO GLY SER PRO GLN ALA LYS SER LEU GLN PRO ALA VAL ALA GLU LYS GLN GLY HIS GLN TRP LYS ASP SER
D700 P701 V702 M703 A704 G705 I706 G707 E708 E709 I710 A711 H712 F713 Q714 K715 E716 L717 E718 E719
A722 R723 T724 S725 K726 A727 C728 F729 Q730 V731 G732 T733 S734 E735 E736 M739 L740 R741 S767 V779 E780 E781 A782 R783 N786 E787 R788 H796 L797 K800 R801 P802 L803 D804 P805 K806 S807 E808 A809 Q810 L811 Q812 E813 I814 R815 R816 L817 H818 Q819 Y820 V821 K822 F823 A824
V825 Q826 D827 V828 N829 D830 V831 L832 D833 L834 D837 L840 K844 R847 H848 L849 L850 V851 P852 E853 R854 E855 T856 L857 F858 N859 T860 L861 A862 N863 N864 R865 E866 I867 I868 N869 Q870 Q871 R872 K873 R874 L875 N876 H877 L878 V879 D880 S881 L882 Q883 Q884 L885 R886 L887 Y888 K889
Q890 T891 S892 L893 W894 S895 Q903 S904 S905 I906 H907 S908 F909 D910 S911 D912 L913 E914 S915 L916 C917 N918 A919 L920 L921 K922 T923 T924 I925 E926 S927 H928 T929 L932 S940 P941 M942 K943 Q944 A945 Q946 L947 R948 N949 F950 L951 A952 K953 R954 K955 T956 P957 P958 V959 R960 S961 T962
A963 P964 A965 S966 L967 S968 R969 S970 A971 F972 LEU SER GLN ARG TYR TYR GLU ASP LEU ASP GLU VAL SER SER THR SER SER VAL SER GLN SER LEU GLU SER GLU ASP ALA ARG THR SER CYS LYS ASP ASP GLU ALA VAL VAL GLN ALA PRO ARG HIS ALA PRO VAL VAL ARG THR PRO
SER ILE GLN PRO SER LEU LEU PRO HIS ALA ALA PRO PHE ALA LYS SER HIS LEU VAL HIS GLY SER SER PRO GLY VAL MET GLY THR SER VAL ALA THR SER ALA SER LYS ILE ILE PRO GLN GLY ALA ASP SER THR MET LEU ALA THR LYS THR VAL LYS HIS GLY ALA PRO SER PRO
SER HIS PRO ILE SER ALA PRO GLN ALA ALA ALA ALA ALA LEU ARG ARG GLN MET ALA SER GLN ALA PRO ALA VAL ASN THR LEU THR GLU SER THR LEU LYS ASN VAL PRO GLN VAL VAL ASN VAL GLN GLU LEU LEU LYS ASN ASN PRO ALA THR PRO VAL LYS HIS GLY ALA PRO SER SER
VAL PRO TYR SER THR ALA LYS THR PRO HIS PRO VAL LEU THR PRO VAL ALA ALA ASN GLN ALA LYS GLN GLY SER LEU ILE ASN SER LEU LYS PRO SER GLY PRO THR PRO ALA SER GLY GLN LEU SER SER GLY ASP LYS ALA SER GLY THR PRO SER SER
THR PRO SER ALA SER GLY GLN PHE SER LYS PRO PHE SER PHE SER PRO SER GLY THR GLY PHE ASN PHE GLY ILE ILE THR PRO THR PRO SER SER ASN PHE THR ALA ALA GLN GLY ALA THR PRO SER THR LYS GLU SER SER GLN PRO ASP ALA PHE SER SER GLY GLY GLY SER LYS
PRO SER TYR GLU ALA ILE PRO GLU SER SER PRO PRO SER GLY ILE THR SER ALA SER ASN THR THR PRO GLY GLU PRO ALA ALA SER SER SER ARG PRO VAL ALA PRO SER GLY THR ALA LEU SER SER THR THR SER SER LYS LYS LEU GLU THR PRO PRO SER SER
PRO SER SER LEU ALA GLY GLU THR LEU GLY SER PHE SER GLY LEU ARG VAL GLY GLN ALA ASP ASP SER THR LYS PRO THR ASN LYS ALA SER SER THR SER LEU SER LEU LEU THR SER THR THR GLN PRO THR THR LYS THR SER GLY VAL PRO SER GLY PHE ASN PHE THR ALA PRO PRO VAL LEU GLY LYS
HIS THR GLU PRO PRO VAL THR SER ALA THR THR THR SER VAL ALA PRO PRO ALA ALA THR SER THR SER SER THR SER ALA VAL PHE GLY SER LEU PRO VAL THR SER ALA GLY SER SER GLY VAL ILE SER PHE GLY GLY THR SER LEU SER ALA GLY LYS THR SER PHE SER PHE GLY
SER GLN GLN THR ASN SER THR VAL PRO PRO SER PHE ALA ALA PRO PRO PRO THR THR ALA THR PRO LEU PRO THR SER PHE PRO THR LEU LEU SER PHE GLY SER LEU LEU SER SER ALA THR THR PRO THR SER LEU PRO MET SER ALA GLY ARG SER THR GLU GLU ALA THR SER SER SER ALA LEU PRO
GLU LYS PRO GLY ASP SER GLU VAL SER ALA ALA ALA SER LEU LEU GLU GLU VAL ALA GLN LEU PRO GLN ALA PRO PRO GLN THR SER ASP SER VAL LYS LYS GLU PRO VAL LEU ALA GLN PRO ALA VAL SER ASN SER GLY THR ALA ALA GLY SER THR SER LEU VAL ALA
LEU SER ALA GLU ALA THR PRO ALA THR GLY VAL ALA THR GLU ALA VAL PRO PRO ALA ALA SER SER PHE SER VAL PRO GLY GLN THR ALA VAL THR ALA ALA ILE SER SER ALA GLY PRO VAL ALA ALA GLU THR SER SER THR PRO ILE ALA SER SER THR THR SER
ILE VAL ALA PRO GLY PRO SER ALA GLU ALA ALA ALA PHE GLY THR VAL THR SER GLY SER SER SER ALA PHE ASN GLN LEU THR ASN ASN THR ALA THR ALA PRO SER ALA THR PRO VAL PHE GLY GLN VAL ALA ALA SER THR
PRO SER LEU PHE GLY GLN GLN THR GLY SER SER THR ALA SER PHE GLY GLN GLN ALA THR PRO GLY VAL PHE SER SER PRO ALA PHE GLY THR THR ALA PRO GLY VAL PHE GLY GLN GLN ALA SER VAL PHE GLY GLN SER SER ALA GLY GLY SER
PHE SER PHE SER GLN PRO GLY PHE SER SER VAL PRO ALA PHE GLY GLN PRO ALA SER SER THR PRO THR SER THR SER GLY SER PHE ALA PHE GLY GLY PHE GLY ALA ALA THR SER SER SER PRO ASN THR GLY GLY GLY LEU PHE GLY GLN SER ASN

ALA PRO ALA PHE GLY GLN SER PRO GLY PHE GLY GLN GLY GLY SER VAL PHE GLY GLY THR SER ALA ALA THR THR THR ALA ALA THR SER GLY PHE SER PHE CYS GLN ALA SER GLY PHE GLY SER SER ASN THR GLY SER VAL PHE GLY GLN ALA ALA SER THR GLY GLY ILE VAL PHE

GLY GLN GLN SER SER SER SER SER SER GLY SER VAL PHE GLY SER SER GLY ASN THR GLY ARG GLY GLY GLY GLY PHE PHE SER GLY LEU GLY GLY LYS PRO SER GLN ASP ALA ALA ASN LYS ASN PRO PHE SER SER GLN GLY GLY SER PHE GLY GLY THR GLN ALA SER THR ASN THR SER ASN LEU PHE

GLY ASN SER GLY ALA LYS THR PHE GLY GLY PHE ALA SER SER SER PHE GLY GLU GLN LYS PRO THR GLY GLY THR PHE SER SER GLY GLY GLY SER VAL ALA SER GLN GLY PHE GLY PHE SER SER PRO ASN LYS THR GLY GLY PHE GLY ALA ALA PRO VAL PHE GLY SER PRO PRO THR PHE

GLY GLY SER PRO GLY PHE GLY GLY VAL PRO ALA PHE GLY SER ALA PRO ALA PHE THR SER PRO LEU GLY SER THR GLY GLY LYS VAL PHE GLY GLU GLY THR ALA ALA ALA SER ALA GLY GLY PHE GLY PHE GLY SER SER SER ASN THR THR SER PHE GLY THR LEU ALA SER GLN ASN

ALA PRO THR PHE GLY SER LEU SER GLN GLN THR SER GLY PHE GLY THR GLN SER SER GLY PHE SER GLY PHE GLY SER THR GLY GLY PHE GLY SER GLY THR GLY GLY PHE SER PHE GLY SER ASN ASN SER SER VAL GLN GLY PHE GLY GLY TRP ARG SER

- Molecule 25: Nuclear pore complex protein Nup88

Chain W0: 46% 91% 8%

MET ALA ALA ALA GLU GLY P7 V8 G9 D10 G11 E12 L13 W14 Q15 T16 N20 L25 R26 L27 R28 E29 G30 L31 K32 N33 Q34 S35 P36 T37 E38 A39 E40 K41 P42 A43 S44 S45 S46 L47 P48 S49 S50 P51 P52 L55 R58 G65 R82 N105 P106 P107 L108

F109 E110 T119 Q120 G127 I128 K129 G130 L131 M132 R139 P159 V160 A161 E162 R163 F164 F165 T166 S167 S168 T169 S170 L171 T172 E182 S193 D194 N195 V196 I197 R198 I199 Y200 S201 L202 R203 E204 P205 Q206 T207 P208 T209 N210 V211 I212 I213 L214 S215 E216 A217 E218 E219 E220

S221 L222 V223 L224 N225 K226 G227 R228 A229 Y230 T231 A232 S233 L234 V249 P250 K251 T252 L253 F254 G255 Q256 N257 G258 K259 D260 N273 G274 E275 T276 F277 S286 P287 G288 N289 I290 G291 K292 L293 L294 G295 P296 L297 P298 M299 H300 P301 A302 A303 E304 D305 N306 Y307 G308 Y309 D310 A311

I326 A327 T328 E329 S330 G331 M332 L333 Y334 H335 C336 V337 V338 L339 E340 G341 E342 E343 E344 D345 D346 H347 T348 S349 E350 K351 S352 W353 D354 S355 R356 I357 D358 L359 I360 P361 S362 L363 Y364 V365 F366 E367 C368 V369 E370 G380 E381 D382 D383 P384 F385 D386 R404 L418 T419 W420

I421 H422 K423 L424 H425 K426 F427 L428 G429 S430 D431 E432 E433 D434 K435 D436 S437 L438 Q439 E440 L441 S442 T443 E444 Q445 K446 C447 F448 R461 V472 P473 D474 I475 L476 G477 P478 Y487 S496 P500 A501 S502 P503 P504 L505 L506 C507 T508 R509 E510 D511 V512 E513 V514 A515 E516

S517 P518 L519 R520 V521 D527 R534 R539 E551 A555 P556 P557 P558 E559 L562 R567 R573 E574 R589 R590 V591 K592 L593 L594 C595 D596 K599 K600 Q601 L602 E603 D604 L605 S606 Y607 C608 R609 E610 E611 R612 K613 S614 E617 M618 R621 R639 M640

K641 K642 L643 L644 H645 S646 F647 H648 S649 E650 L651 P652 V653 L654 S655 D656 S657 E658 R659 D660 M661 K662 K663 E664 L665 Q666 L667 I668 P669 D670 Q671 L672 R673 H674 L675 A678 E694 K695 V696 L697 S698 L699 P700 K701 P702 T703 I704 T705 A708 Y709 Q710 R711 S716 E721 G722

E723 H724 I725 R726 E727 M728 V729 K730 Q731 I732 N733 D734 I735 R736 N737 H738 V739 N740 F741

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	7711	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	120	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	82.185	Depositor
Minimum map value	-69.686	Depositor
Average map value	0.077	Depositor
Map value standard deviation	0.791	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	1941.1199, 1941.1199, 1941.1199	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.37, 3.37, 3.37	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	00	0.69	0/6212	1.06	25/8405 (0.3%)
1	01	0.69	0/6212	1.05	23/8405 (0.3%)
1	02	0.69	0/6212	1.04	24/8405 (0.3%)
1	03	0.69	0/6212	1.05	23/8405 (0.3%)
1	04	0.69	0/6212	1.04	20/8405 (0.2%)
2	10	0.66	0/14350	1.04	51/19560 (0.3%)
2	11	0.66	0/14350	1.04	52/19560 (0.3%)
2	12	0.66	0/14350	1.04	49/19560 (0.3%)
2	13	0.66	0/14350	1.04	51/19560 (0.3%)
2	14	0.66	0/14350	1.03	51/19560 (0.3%)
2	15	0.66	0/14350	1.03	50/19560 (0.3%)
2	16	0.66	0/14350	1.03	50/19560 (0.3%)
2	17	0.66	0/14350	1.03	51/19560 (0.3%)
3	40	0.68	0/3007	1.07	8/4114 (0.2%)
3	41	0.68	0/3007	1.06	10/4114 (0.2%)
4	A0	0.72	0/6687	1.10	34/9036 (0.4%)
4	A1	0.71	0/6687	1.07	31/9036 (0.3%)
4	A2	0.72	0/6687	1.09	34/9036 (0.4%)
4	A3	0.71	0/6687	1.06	30/9036 (0.3%)
4	A4	0.71	0/5972	1.08	31/8068 (0.4%)
4	A5	0.71	0/5972	1.09	39/8068 (0.5%)
4	A6	0.71	0/5972	1.04	25/8068 (0.3%)
5	B0	0.68	0/14018	1.02	39/19022 (0.2%)
5	B1	0.68	0/14018	1.03	36/19022 (0.2%)
6	C0	0.69	0/16330	1.04	75/22131 (0.3%)
6	C1	0.69	0/16330	1.04	73/22131 (0.3%)
6	C2	0.68	0/16330	1.00	50/22131 (0.2%)
6	C3	0.68	1/16330 (0.0%)	1.06	80/22131 (0.4%)
6	C4	0.69	0/16330	1.02	63/22131 (0.3%)
7	D0	0.67	0/10568	1.02	40/14320 (0.3%)
7	D1	0.68	0/10568	1.02	39/14320 (0.3%)
7	D2	0.67	0/10568	1.02	39/14320 (0.3%)
7	D3	0.68	0/10568	1.03	41/14320 (0.3%)
7	D4	0.67	0/10568	1.01	38/14320 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
7	D5	0.68	0/10568	1.03	43/14320 (0.3%)
8	E0	0.73	0/4563	1.00	11/6214 (0.2%)
8	E1	0.73	0/4563	0.98	10/6214 (0.2%)
9	F0	0.72	0/1882	1.12	6/2556 (0.2%)
9	F1	0.70	0/1882	1.05	4/2556 (0.2%)
9	F2	0.72	0/1882	1.17	11/2556 (0.4%)
9	F3	0.70	0/1882	1.08	9/2556 (0.4%)
10	H0	0.65	0/3114	1.04	14/4211 (0.3%)
10	H1	0.65	0/3114	1.03	16/4211 (0.4%)
10	H2	0.64	0/3114	1.03	14/4211 (0.3%)
10	H3	0.64	0/3114	1.02	15/4211 (0.4%)
11	I0	0.65	0/1416	0.97	3/1911 (0.2%)
11	I1	0.65	0/1416	0.99	3/1911 (0.2%)
11	I2	0.65	0/1416	0.98	3/1911 (0.2%)
11	I3	0.65	0/1416	0.98	3/1911 (0.2%)
12	J0	0.62	0/1420	1.00	6/1915 (0.3%)
12	J1	0.62	0/1420	1.01	6/1915 (0.3%)
12	J2	0.62	0/1420	1.00	6/1915 (0.3%)
12	J3	0.62	0/1420	1.02	6/1915 (0.3%)
12	J4	0.63	0/1420	1.00	4/1915 (0.2%)
13	K0	0.69	0/8740	1.04	27/11848 (0.2%)
13	K1	0.69	1/8740 (0.0%)	1.22	37/11848 (0.3%)
13	K2	0.68	0/8740	1.02	28/11848 (0.2%)
13	K3	0.68	0/8740	1.02	27/11848 (0.2%)
14	L0	0.71	0/6518	1.07	35/8819 (0.4%)
14	L1	0.71	0/6518	1.07	32/8819 (0.4%)
14	L2	0.70	0/6518	1.06	29/8819 (0.3%)
14	L3	0.72	2/6518 (0.0%)	1.10	41/8819 (0.5%)
15	M0	0.70	0/5588	1.13	30/7581 (0.4%)
15	M1	0.70	0/5588	1.13	35/7581 (0.5%)
15	M2	0.70	0/5588	1.11	35/7581 (0.5%)
15	M3	0.69	0/5588	1.11	35/7581 (0.5%)
16	N0	0.67	0/2419	1.05	5/3301 (0.2%)
16	N1	0.67	0/2419	1.04	7/3301 (0.2%)
16	N2	0.67	0/2419	1.04	5/3301 (0.2%)
16	N3	0.67	0/2419	1.04	7/3301 (0.2%)
17	O0	0.67	0/2593	1.04	7/3520 (0.2%)
17	O1	0.66	0/2593	1.03	7/3520 (0.2%)
17	O2	0.67	0/2593	1.05	10/3520 (0.3%)
17	O3	0.66	0/2593	1.06	8/3520 (0.2%)
18	P0	0.70	0/5365	1.05	25/7257 (0.3%)
18	P1	0.70	0/5365	1.05	31/7257 (0.4%)
18	P2	0.70	0/5365	1.05	26/7257 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	P3	0.70	0/5365	1.04	23/7257 (0.3%)
19	Q0	0.67	0/2775	1.05	9/3786 (0.2%)
19	Q1	0.67	0/2775	1.02	7/3786 (0.2%)
19	Q2	0.67	0/2775	1.05	10/3786 (0.3%)
19	Q3	0.66	0/2775	1.04	7/3786 (0.2%)
20	R0	0.71	0/11371	1.05	48/15446 (0.3%)
20	R1	0.70	0/11371	1.06	55/15446 (0.4%)
20	R2	0.71	0/11371	1.06	57/15446 (0.4%)
20	R3	0.70	0/11371	1.05	49/15446 (0.3%)
21	S0	0.70	0/2623	1.03	8/3568 (0.2%)
21	S1	0.69	0/2623	1.02	7/3568 (0.2%)
21	S2	0.69	0/2623	1.04	6/3568 (0.2%)
21	S3	0.70	0/2623	1.03	7/3568 (0.2%)
22	T0	0.70	0/8141	1.03	27/11065 (0.2%)
22	T1	0.69	0/8141	1.02	22/11065 (0.2%)
23	U0	0.72	0/1217	1.04	4/1644 (0.2%)
23	U1	0.67	0/152	1.32	1/204 (0.5%)
23	U2	0.77	0/152	1.53	4/204 (2.0%)
23	U3	0.82	0/152	1.58	4/204 (2.0%)
23	U4	0.83	0/152	1.64	4/204 (2.0%)
23	U5	0.79	0/152	1.39	3/204 (1.5%)
23	U6	0.66	0/152	1.28	1/204 (0.5%)
24	V0	0.67	0/2240	1.07	11/3019 (0.4%)
25	W0	0.67	0/5972	1.04	26/8105 (0.3%)
All	All	0.68	4/630097 (0.0%)	1.05	2497/855041 (0.3%)

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	00	0	6
1	01	0	3
1	02	0	4
1	03	0	5
1	04	0	4
2	10	0	11
2	11	0	13
2	12	0	10
2	13	0	13
2	14	0	11

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	15	0	13
2	16	0	10
2	17	0	13
3	40	0	4
3	41	0	6
4	A0	1	23
4	A1	0	16
4	A2	0	17
4	A3	0	14
4	A4	0	9
4	A5	0	9
4	A6	0	6
5	B0	0	28
5	B1	0	26
6	C0	1	15
6	C1	1	16
6	C2	1	18
6	C3	1	23
6	C4	1	15
7	D0	0	7
7	D1	0	14
7	D2	0	12
7	D3	0	14
7	D4	0	7
7	D5	0	16
8	E0	0	2
8	E1	0	2
9	F0	0	6
9	F1	0	3
9	F2	0	3
9	F3	0	2
10	H0	0	6
10	H1	0	3
10	H2	0	3
10	H3	0	4
12	J0	0	2
12	J1	0	1
12	J2	0	2
12	J3	0	1
12	J4	0	1
13	K0	0	12
13	K1	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	K2	0	13
13	K3	0	10
14	L0	0	6
14	L1	0	6
14	L2	0	7
14	L3	0	5
15	M0	0	9
15	M1	0	9
15	M2	0	7
15	M3	0	6
16	N0	0	2
16	N1	0	2
16	N2	0	2
16	N3	0	2
17	O3	0	1
18	P0	0	7
18	P1	1	9
18	P2	0	8
18	P3	0	8
19	Q0	0	1
19	Q1	0	2
19	Q2	0	2
19	Q3	0	1
20	R0	0	14
20	R1	0	13
20	R2	0	17
20	R3	0	18
21	S0	0	4
21	S1	0	5
21	S2	0	6
21	S3	0	5
22	T0	2	11
22	T1	2	9
23	U0	0	1
24	V0	0	1
25	W0	0	10
All	All	11	728

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	L3	731	GLY	CA-C	6.62	1.62	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	L3	731	GLY	N-CA	6.34	1.55	1.46
6	C3	4	PRO	N-CD	-5.29	1.40	1.47
13	K1	577	PRO	N-CD	-5.17	1.40	1.47

The worst 5 of 2497 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	K1	986	ASP	CB-CG-OD1	50.04	163.34	118.30
13	K1	986	ASP	CB-CG-OD2	-37.67	84.40	118.30
2	15	5	GLY	O-C-N	-27.80	78.22	122.70
2	10	5	GLY	O-C-N	-27.48	78.72	122.70
2	13	5	GLY	O-C-N	-27.47	78.75	122.70

5 of 11 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A0	156	LEU	CA
6	C0	174	THR	CB
6	C1	174	THR	CB
6	C2	174	THR	CB
6	C3	174	THR	CB

5 of 728 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	00	132	TYR	Sidechain
1	00	175	TYR	Sidechain
1	00	193	ARG	Sidechain
1	00	375	THR	Peptide,Mainchain
1	00	710	TYR	Sidechain

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	00	6085	0	6080	38	0
1	01	6085	0	6080	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	02	6085	0	6080	8	0
1	03	6085	0	6080	37	0
1	04	6085	0	6080	12	0
2	10	14046	0	14194	20	0
2	11	14046	0	14194	26	0
2	12	14046	0	14194	33	0
2	13	14046	0	14194	22	0
2	14	14046	0	14194	25	0
2	15	14046	0	14194	14	0
2	16	14046	0	14194	10	0
2	17	14046	0	14194	10	0
3	40	2922	0	2899	4	0
3	41	2922	0	2899	2	0
4	A0	6568	0	6527	68	0
4	A1	6568	0	6527	8	0
4	A2	6568	0	6527	22	0
4	A3	6568	0	6527	7	0
4	A4	5860	0	5828	22	0
4	A5	5860	0	5828	4	0
4	A6	5860	0	5828	7	0
5	B0	13746	0	13949	4	0
5	B1	13746	0	13949	7	0
6	C0	16013	0	16224	13	0
6	C1	16013	0	16224	14	0
6	C2	16013	0	16224	86	0
6	C3	16013	0	16224	69	0
6	C4	16013	0	16224	58	0
7	D0	10363	0	10400	47	0
7	D1	10363	0	10400	115	0
7	D2	10363	0	10400	55	0
7	D3	10363	0	10400	65	0
7	D4	10363	0	10400	56	0
7	D5	10363	0	10400	57	0
8	E0	4432	0	4472	13	0
8	E1	4432	0	4472	1	0
9	F0	1837	0	1825	13	0
9	F1	1837	0	1825	4	0
9	F2	1837	0	1825	3	0
9	F3	1837	0	1825	10	0
10	H0	3066	0	3103	26	0
10	H1	3066	0	3103	5	0
10	H2	3066	0	3103	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	H3	3066	0	3103	3	0
11	I0	1398	0	1431	26	0
11	I1	1398	0	1431	3	0
11	I2	1398	0	1431	3	0
11	I3	1398	0	1431	4	0
12	J0	1403	0	1391	2	0
12	J1	1403	0	1391	2	0
12	J2	1403	0	1391	1	0
12	J3	1403	0	1391	1	0
12	J4	1403	0	1391	0	0
13	K0	8574	0	8438	14	0
13	K1	8574	0	8438	17	0
13	K2	8574	0	8438	21	0
13	K3	8574	0	8438	21	0
14	L0	6383	0	6313	24	0
14	L1	6383	0	6313	34	0
14	L2	6383	0	6313	13	0
14	L3	6383	0	6313	12	0
15	M0	5461	0	5443	9	0
15	M1	5461	0	5443	11	0
15	M2	5461	0	5443	4	0
15	M3	5461	0	5443	6	0
16	N0	2352	0	2220	17	0
16	N1	2352	0	2220	2	0
16	N2	2352	0	2220	0	0
16	N3	2352	0	2220	1	0
17	O0	2528	0	2444	44	0
17	O1	2528	0	2444	6	0
17	O2	2528	0	2444	6	0
17	O3	2528	0	2444	19	0
18	P0	5257	0	5249	10	0
18	P1	5257	0	5249	8	0
18	P2	5257	0	5249	3	0
18	P3	5257	0	5249	11	0
19	Q0	2703	0	2555	16	0
19	Q1	2703	0	2555	0	0
19	Q2	2703	0	2555	5	0
19	Q3	2703	0	2555	1	0
20	R0	11132	0	11066	72	0
20	R1	11132	0	11066	19	0
20	R2	11132	0	11066	23	0
20	R3	11132	0	11066	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	S0	2552	0	2452	4	0
21	S1	2552	0	2452	0	0
21	S2	2552	0	2452	0	0
21	S3	2552	0	2452	1	0
22	T0	7960	0	7896	3	0
22	T1	7960	0	7896	3	0
23	U0	1193	0	1188	7	0
23	U1	151	0	167	25	0
23	U2	151	0	167	25	0
23	U3	151	0	167	20	0
23	U4	151	0	167	25	0
23	U5	151	0	167	24	0
23	U6	151	0	167	25	0
24	V0	2203	0	2226	19	0
25	W0	5836	0	5850	14	0
All	All	617133	0	616873	1129	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 1129 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)
6:C2:1249:ILE:HG21	20:R0:1284:ALA:CB	1.29	1.54
6:C2:622:PRO:HB3	20:R0:1316:SER:CB	1.44	1.47
6:C2:788:VAL:CG2	17:O0:258:THR:HG21	1.53	1.39
6:C2:1249:ILE:CG2	20:R0:1284:ALA:HB2	1.58	1.33
6:C2:622:PRO:CB	20:R0:1316:SER:HB3	1.56	1.33

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	00	754/3224 (23%)	703 (93%)	43 (6%)	8 (1%)	14	52
1	01	754/3224 (23%)	706 (94%)	42 (6%)	6 (1%)	19	60
1	02	754/3224 (23%)	707 (94%)	44 (6%)	3 (0%)	34	72
1	03	754/3224 (23%)	700 (93%)	45 (6%)	9 (1%)	13	50
1	04	754/3224 (23%)	702 (93%)	49 (6%)	3 (0%)	34	72
2	10	1829/1887 (97%)	1726 (94%)	94 (5%)	9 (0%)	29	69
2	11	1829/1887 (97%)	1725 (94%)	93 (5%)	11 (1%)	25	66
2	12	1829/1887 (97%)	1724 (94%)	95 (5%)	10 (0%)	29	69
2	13	1829/1887 (97%)	1711 (94%)	107 (6%)	11 (1%)	25	66
2	14	1829/1887 (97%)	1731 (95%)	90 (5%)	8 (0%)	34	72
2	15	1829/1887 (97%)	1733 (95%)	87 (5%)	9 (0%)	29	69
2	16	1829/1887 (97%)	1734 (95%)	86 (5%)	9 (0%)	29	69
2	17	1829/1887 (97%)	1724 (94%)	95 (5%)	10 (0%)	29	69
3	40	379/546 (69%)	350 (92%)	28 (7%)	1 (0%)	41	77
3	41	379/546 (69%)	348 (92%)	29 (8%)	2 (0%)	29	69
4	A0	816/819 (100%)	741 (91%)	65 (8%)	10 (1%)	13	50
4	A1	816/819 (100%)	753 (92%)	54 (7%)	9 (1%)	14	52
4	A2	816/819 (100%)	756 (93%)	50 (6%)	10 (1%)	13	50
4	A3	816/819 (100%)	755 (92%)	55 (7%)	6 (1%)	22	63
4	A4	724/819 (88%)	680 (94%)	40 (6%)	4 (1%)	25	66
4	A5	724/819 (88%)	688 (95%)	31 (4%)	5 (1%)	22	63
4	A6	724/819 (88%)	674 (93%)	47 (6%)	3 (0%)	34	72
5	B0	1746/1749 (100%)	1634 (94%)	93 (5%)	19 (1%)	14	52
5	B1	1746/1749 (100%)	1626 (93%)	103 (6%)	17 (1%)	15	55
6	C0	2009/2012 (100%)	1878 (94%)	111 (6%)	20 (1%)	15	55
6	C1	2009/2012 (100%)	1879 (94%)	109 (5%)	21 (1%)	15	55
6	C2	2009/2012 (100%)	1886 (94%)	106 (5%)	17 (1%)	19	60
6	C3	2009/2012 (100%)	1876 (93%)	118 (6%)	15 (1%)	22	63
6	C4	2009/2012 (100%)	1873 (93%)	123 (6%)	13 (1%)	25	66
7	D0	1308/1391 (94%)	1207 (92%)	89 (7%)	12 (1%)	17	57
7	D1	1308/1391 (94%)	1209 (92%)	88 (7%)	11 (1%)	19	60
7	D2	1308/1391 (94%)	1218 (93%)	81 (6%)	9 (1%)	22	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	D3	1308/1391 (94%)	1210 (92%)	85 (6%)	13 (1%)	15	55
7	D4	1308/1391 (94%)	1221 (93%)	77 (6%)	10 (1%)	19	60
7	D5	1308/1391 (94%)	1233 (94%)	65 (5%)	10 (1%)	19	60
8	E0	544/674 (81%)	516 (95%)	26 (5%)	2 (0%)	34	72
8	E1	544/674 (81%)	514 (94%)	29 (5%)	1 (0%)	47	81
9	F0	239/326 (73%)	189 (79%)	33 (14%)	17 (7%)	1	14
9	F1	239/326 (73%)	192 (80%)	33 (14%)	14 (6%)	1	17
9	F2	239/326 (73%)	177 (74%)	45 (19%)	17 (7%)	1	14
9	F3	239/326 (73%)	188 (79%)	39 (16%)	12 (5%)	2	20
10	H0	381/507 (75%)	365 (96%)	16 (4%)	0	100	100
10	H1	381/507 (75%)	364 (96%)	16 (4%)	1 (0%)	41	77
10	H2	381/507 (75%)	366 (96%)	15 (4%)	0	100	100
10	H3	381/507 (75%)	363 (95%)	16 (4%)	2 (0%)	29	69
11	I0	171/599 (28%)	168 (98%)	3 (2%)	0	100	100
11	I1	171/599 (28%)	167 (98%)	3 (2%)	1 (1%)	25	66
11	I2	171/599 (28%)	167 (98%)	4 (2%)	0	100	100
11	I3	171/599 (28%)	167 (98%)	4 (2%)	0	100	100
12	J0	169/522 (32%)	166 (98%)	3 (2%)	0	100	100
12	J1	169/522 (32%)	168 (99%)	1 (1%)	0	100	100
12	J2	169/522 (32%)	167 (99%)	2 (1%)	0	100	100
12	J3	169/522 (32%)	166 (98%)	2 (1%)	1 (1%)	25	66
12	J4	169/522 (32%)	168 (99%)	1 (1%)	0	100	100
13	K0	1084/1156 (94%)	985 (91%)	85 (8%)	14 (1%)	12	48
13	K1	1084/1156 (94%)	990 (91%)	78 (7%)	16 (2%)	10	46
13	K2	1084/1156 (94%)	992 (92%)	82 (8%)	10 (1%)	17	57
13	K3	1084/1156 (94%)	1001 (92%)	70 (6%)	13 (1%)	13	50
14	L0	780/925 (84%)	734 (94%)	42 (5%)	4 (0%)	29	69
14	L1	780/925 (84%)	734 (94%)	38 (5%)	8 (1%)	15	55
14	L2	780/925 (84%)	732 (94%)	45 (6%)	3 (0%)	34	72
14	L3	780/925 (84%)	731 (94%)	43 (6%)	6 (1%)	19	60
15	M0	669/937 (71%)	609 (91%)	50 (8%)	10 (2%)	10	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	M1	669/937 (71%)	613 (92%)	48 (7%)	8 (1%)	13	50
15	M2	669/937 (71%)	618 (92%)	45 (7%)	6 (1%)	17	57
15	M3	669/937 (71%)	612 (92%)	50 (8%)	7 (1%)	15	55
16	N0	299/322 (93%)	277 (93%)	19 (6%)	3 (1%)	15	55
16	N1	299/322 (93%)	277 (93%)	20 (7%)	2 (1%)	22	63
16	N2	299/322 (93%)	277 (93%)	19 (6%)	3 (1%)	15	55
16	N3	299/322 (93%)	278 (93%)	18 (6%)	3 (1%)	15	55
17	O0	321/360 (89%)	304 (95%)	14 (4%)	3 (1%)	17	57
17	O1	321/360 (89%)	302 (94%)	15 (5%)	4 (1%)	13	50
17	O2	321/360 (89%)	302 (94%)	18 (6%)	1 (0%)	41	77
17	O3	321/360 (89%)	299 (93%)	19 (6%)	3 (1%)	17	57
18	P0	653/656 (100%)	607 (93%)	40 (6%)	6 (1%)	17	57
18	P1	653/656 (100%)	612 (94%)	35 (5%)	6 (1%)	17	57
18	P2	653/656 (100%)	610 (93%)	36 (6%)	7 (1%)	14	52
18	P3	653/656 (100%)	611 (94%)	35 (5%)	7 (1%)	14	52
19	Q0	341/380 (90%)	320 (94%)	20 (6%)	1 (0%)	41	77
19	Q1	341/380 (90%)	322 (94%)	18 (5%)	1 (0%)	41	77
19	Q2	341/380 (90%)	320 (94%)	20 (6%)	1 (0%)	41	77
19	Q3	341/380 (90%)	323 (95%)	17 (5%)	1 (0%)	41	77
20	R0	1397/1436 (97%)	1288 (92%)	93 (7%)	16 (1%)	14	52
20	R1	1397/1436 (97%)	1285 (92%)	94 (7%)	18 (1%)	12	48
20	R2	1397/1436 (97%)	1298 (93%)	87 (6%)	12 (1%)	17	57
20	R3	1397/1436 (97%)	1294 (93%)	93 (7%)	10 (1%)	22	63
21	S0	320/326 (98%)	292 (91%)	26 (8%)	2 (1%)	25	66
21	S1	320/326 (98%)	293 (92%)	24 (8%)	3 (1%)	17	57
21	S2	320/326 (98%)	290 (91%)	28 (9%)	2 (1%)	25	66
21	S3	320/326 (98%)	292 (91%)	25 (8%)	3 (1%)	17	57
22	T0	1002/2266 (44%)	927 (92%)	62 (6%)	13 (1%)	12	48
22	T1	1002/2266 (44%)	931 (93%)	58 (6%)	13 (1%)	12	48
23	U0	148/880 (17%)	140 (95%)	8 (5%)	0	100	100
23	U1	17/880 (2%)	16 (94%)	1 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	U2	17/880 (2%)	15 (88%)	2 (12%)	0	100	100
23	U3	17/880 (2%)	15 (88%)	1 (6%)	1 (6%)	1	17
23	U4	17/880 (2%)	15 (88%)	2 (12%)	0	100	100
23	U5	17/880 (2%)	14 (82%)	2 (12%)	1 (6%)	1	17
23	U6	17/880 (2%)	16 (94%)	1 (6%)	0	100	100
24	V0	271/2090 (13%)	255 (94%)	12 (4%)	4 (2%)	10	46
25	W0	733/741 (99%)	688 (94%)	40 (6%)	5 (1%)	22	63
All	All	77792/109146 (71%)	72515 (93%)	4606 (6%)	671 (1%)	21	57

5 of 671 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	02	165	VAL
4	A1	90	LEU
4	A1	95	ASP
4	A2	88	GLU
4	A2	167	ILE

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	00	675/2818 (24%)	662 (98%)	13 (2%)	57	75
1	01	675/2818 (24%)	663 (98%)	12 (2%)	59	77
1	02	675/2818 (24%)	659 (98%)	16 (2%)	49	69
1	03	675/2818 (24%)	662 (98%)	13 (2%)	57	75
1	04	675/2818 (24%)	658 (98%)	17 (2%)	47	68
2	10	1565/1608 (97%)	1536 (98%)	29 (2%)	57	75
2	11	1565/1608 (97%)	1537 (98%)	28 (2%)	59	77
2	12	1565/1608 (97%)	1535 (98%)	30 (2%)	57	75
2	13	1565/1608 (97%)	1534 (98%)	31 (2%)	55	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	14	1565/1608 (97%)	1538 (98%)	27 (2%)	60	78
2	15	1565/1608 (97%)	1538 (98%)	27 (2%)	60	78
2	16	1565/1608 (97%)	1539 (98%)	26 (2%)	60	78
2	17	1565/1608 (97%)	1540 (98%)	25 (2%)	62	79
3	40	323/463 (70%)	314 (97%)	9 (3%)	43	65
3	41	323/463 (70%)	313 (97%)	10 (3%)	40	62
4	A0	725/726 (100%)	702 (97%)	23 (3%)	39	61
4	A1	725/726 (100%)	705 (97%)	20 (3%)	43	65
4	A2	725/726 (100%)	708 (98%)	17 (2%)	50	70
4	A3	725/726 (100%)	707 (98%)	18 (2%)	47	68
4	A4	647/726 (89%)	629 (97%)	18 (3%)	43	65
4	A5	647/726 (89%)	631 (98%)	16 (2%)	47	68
4	A6	647/726 (89%)	629 (97%)	18 (3%)	43	65
5	B0	1540/1541 (100%)	1504 (98%)	36 (2%)	50	70
5	B1	1540/1541 (100%)	1505 (98%)	35 (2%)	50	70
6	C0	1776/1777 (100%)	1740 (98%)	36 (2%)	55	74
6	C1	1776/1777 (100%)	1743 (98%)	33 (2%)	57	75
6	C2	1776/1777 (100%)	1742 (98%)	34 (2%)	57	75
6	C3	1776/1777 (100%)	1740 (98%)	36 (2%)	55	74
6	C4	1776/1777 (100%)	1741 (98%)	35 (2%)	55	74
7	D0	1157/1222 (95%)	1129 (98%)	28 (2%)	49	69
7	D1	1157/1222 (95%)	1123 (97%)	34 (3%)	42	64
7	D2	1157/1222 (95%)	1133 (98%)	24 (2%)	53	72
7	D3	1157/1222 (95%)	1119 (97%)	38 (3%)	38	61
7	D4	1157/1222 (95%)	1126 (97%)	31 (3%)	44	65
7	D5	1157/1222 (95%)	1121 (97%)	36 (3%)	40	62
8	E0	489/604 (81%)	482 (99%)	7 (1%)	67	80
8	E1	489/604 (81%)	483 (99%)	6 (1%)	71	83
9	F0	210/277 (76%)	191 (91%)	19 (9%)	9	30
9	F1	210/277 (76%)	201 (96%)	9 (4%)	29	53
9	F2	210/277 (76%)	193 (92%)	17 (8%)	11	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	F3	210/277 (76%)	196 (93%)	14 (7%)	16	41
10	H0	345/425 (81%)	338 (98%)	7 (2%)	55	74
10	H1	345/425 (81%)	339 (98%)	6 (2%)	60	78
10	H2	345/425 (81%)	338 (98%)	7 (2%)	55	74
10	H3	345/425 (81%)	339 (98%)	6 (2%)	60	78
11	I0	155/459 (34%)	152 (98%)	3 (2%)	57	75
11	I1	155/459 (34%)	153 (99%)	2 (1%)	69	81
11	I2	155/459 (34%)	151 (97%)	4 (3%)	46	66
11	I3	155/459 (34%)	153 (99%)	2 (1%)	69	81
12	J0	158/401 (39%)	156 (99%)	2 (1%)	69	81
12	J1	158/401 (39%)	156 (99%)	2 (1%)	69	81
12	J2	158/401 (39%)	156 (99%)	2 (1%)	69	81
12	J3	158/401 (39%)	156 (99%)	2 (1%)	69	81
12	J4	158/401 (39%)	153 (97%)	5 (3%)	39	61
13	K0	958/1013 (95%)	921 (96%)	37 (4%)	32	56
13	K1	958/1013 (95%)	934 (98%)	24 (2%)	47	68
13	K2	958/1013 (95%)	927 (97%)	31 (3%)	39	61
13	K3	958/1013 (95%)	927 (97%)	31 (3%)	39	61
14	L0	701/827 (85%)	686 (98%)	15 (2%)	53	72
14	L1	701/827 (85%)	681 (97%)	20 (3%)	42	64
14	L2	701/827 (85%)	687 (98%)	14 (2%)	55	74
14	L3	701/827 (85%)	685 (98%)	16 (2%)	50	70
15	M0	602/840 (72%)	587 (98%)	15 (2%)	47	68
15	M1	602/840 (72%)	584 (97%)	18 (3%)	41	63
15	M2	602/840 (72%)	583 (97%)	19 (3%)	39	61
15	M3	602/840 (72%)	592 (98%)	10 (2%)	60	78
16	N0	255/272 (94%)	250 (98%)	5 (2%)	55	74
16	N1	255/272 (94%)	251 (98%)	4 (2%)	62	79
16	N2	255/272 (94%)	248 (97%)	7 (3%)	44	65
16	N3	255/272 (94%)	250 (98%)	5 (2%)	55	74
17	O0	279/310 (90%)	274 (98%)	5 (2%)	59	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	O1	279/310 (90%)	275 (99%)	4 (1%)	67	80
17	O2	279/310 (90%)	274 (98%)	5 (2%)	59	77
17	O3	279/310 (90%)	273 (98%)	6 (2%)	52	71
18	P0	584/585 (100%)	564 (97%)	20 (3%)	37	60
18	P1	584/585 (100%)	571 (98%)	13 (2%)	52	71
18	P2	584/585 (100%)	566 (97%)	18 (3%)	40	62
18	P3	584/585 (100%)	567 (97%)	17 (3%)	42	64
19	Q0	303/335 (90%)	301 (99%)	2 (1%)	84	90
19	Q1	303/335 (90%)	302 (100%)	1 (0%)	92	95
19	Q2	303/335 (90%)	301 (99%)	2 (1%)	84	90
19	Q3	303/335 (90%)	301 (99%)	2 (1%)	84	90
20	R0	1233/1259 (98%)	1202 (98%)	31 (2%)	47	68
20	R1	1233/1259 (98%)	1203 (98%)	30 (2%)	49	69
20	R2	1233/1259 (98%)	1202 (98%)	31 (2%)	47	68
20	R3	1233/1259 (98%)	1207 (98%)	26 (2%)	53	72
21	S0	278/282 (99%)	272 (98%)	6 (2%)	52	71
21	S1	278/282 (99%)	272 (98%)	6 (2%)	52	71
21	S2	278/282 (99%)	271 (98%)	7 (2%)	47	68
21	S3	278/282 (99%)	273 (98%)	5 (2%)	59	77
22	T0	891/2037 (44%)	874 (98%)	17 (2%)	57	75
22	T1	891/2037 (44%)	875 (98%)	16 (2%)	59	77
23	U0	131/703 (19%)	125 (95%)	6 (5%)	27	52
23	U1	19/703 (3%)	17 (90%)	2 (10%)	7	24
23	U2	19/703 (3%)	18 (95%)	1 (5%)	22	47
23	U3	19/703 (3%)	18 (95%)	1 (5%)	22	47
23	U4	19/703 (3%)	18 (95%)	1 (5%)	22	47
23	U5	19/703 (3%)	18 (95%)	1 (5%)	22	47
23	U6	19/703 (3%)	17 (90%)	2 (10%)	7	24
24	V0	249/1685 (15%)	238 (96%)	11 (4%)	28	53
25	W0	661/663 (100%)	645 (98%)	16 (2%)	49	69
All	All	68601/94353 (73%)	67018 (98%)	1583 (2%)	53	70

5 of 1583 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	F2	151	SER
14	L1	340	ARG
10	H0	196	ASN
9	F2	123	LEU
13	K1	102	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
17	O1	125	HIS
18	P0	621	GLN
20	R1	759	GLN
6	C2	854	ASN
6	C2	786	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

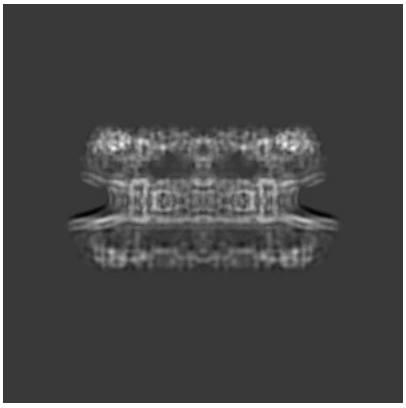
6 Map visualisation (i)

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

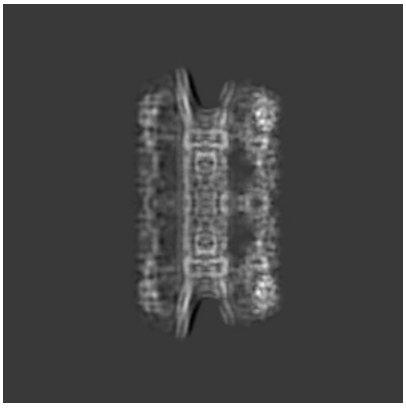
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

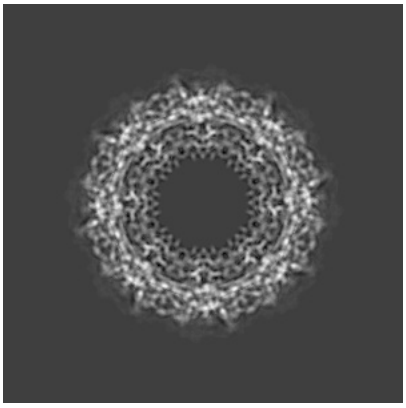
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices (i)

6.2.1 Primary map

X Index: 288

Y Index: 288

Z Index: 288

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

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 404

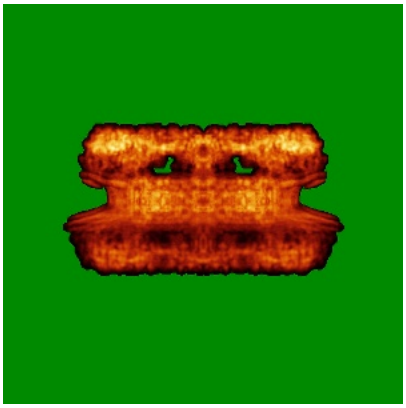
Y Index: 172

Z Index: 370

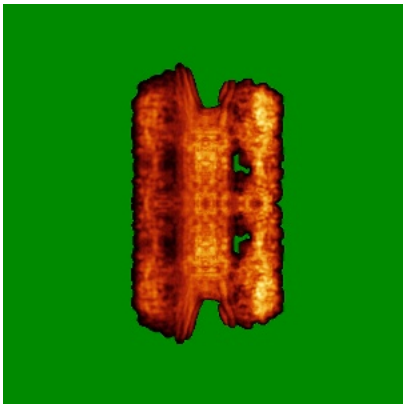
The images above show the largest variance slices of the map in three orthogonal directions.

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

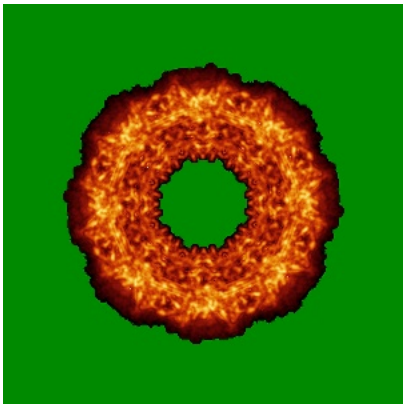
6.4.1 Primary map



X



Y

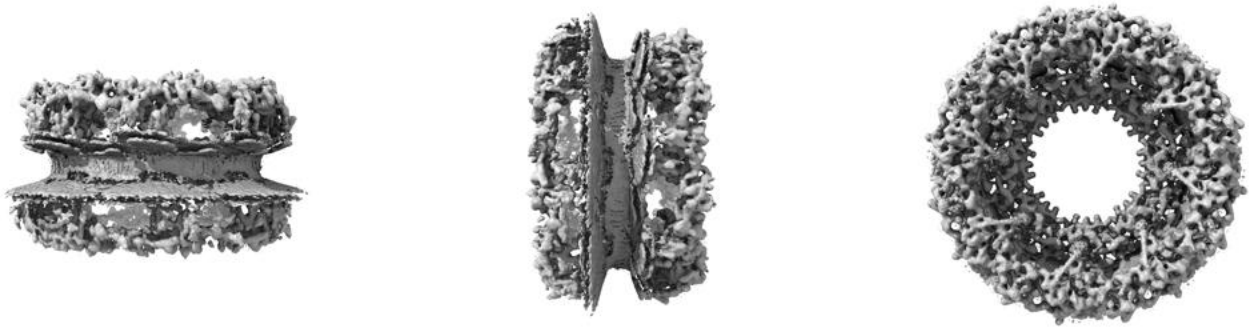


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



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.

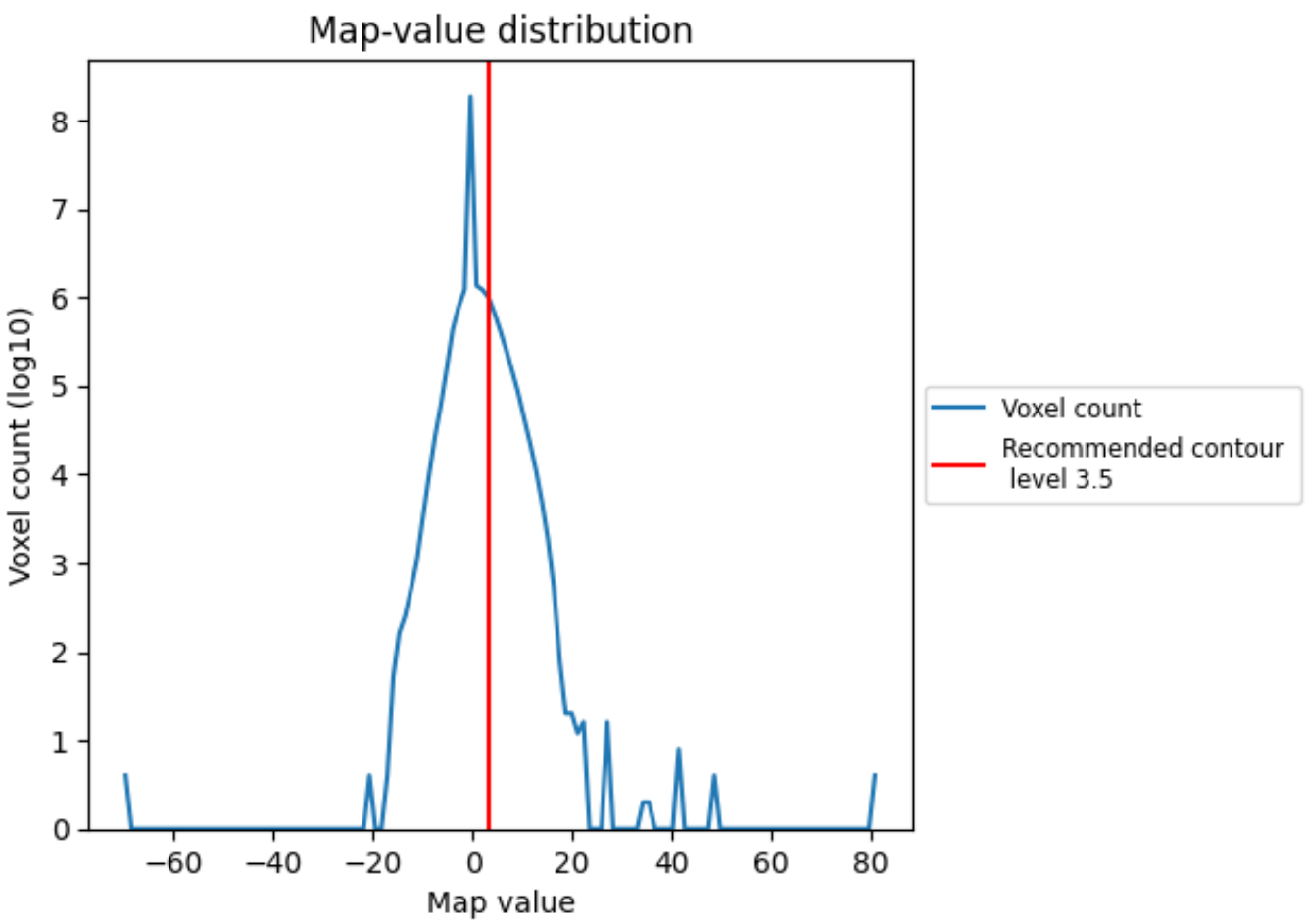
6.6 Mask visualisation (i)

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

7 Map analysis (i)

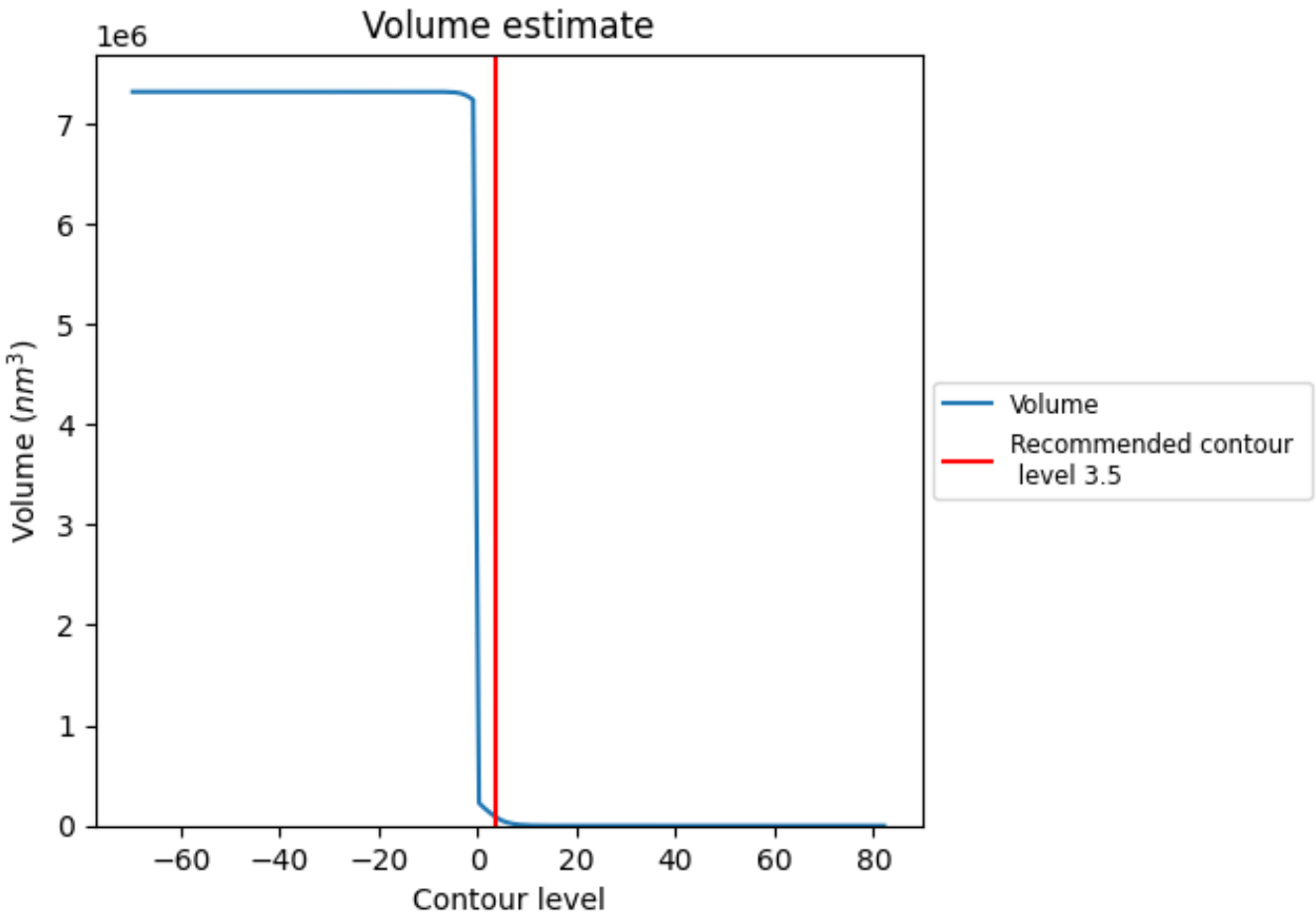
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

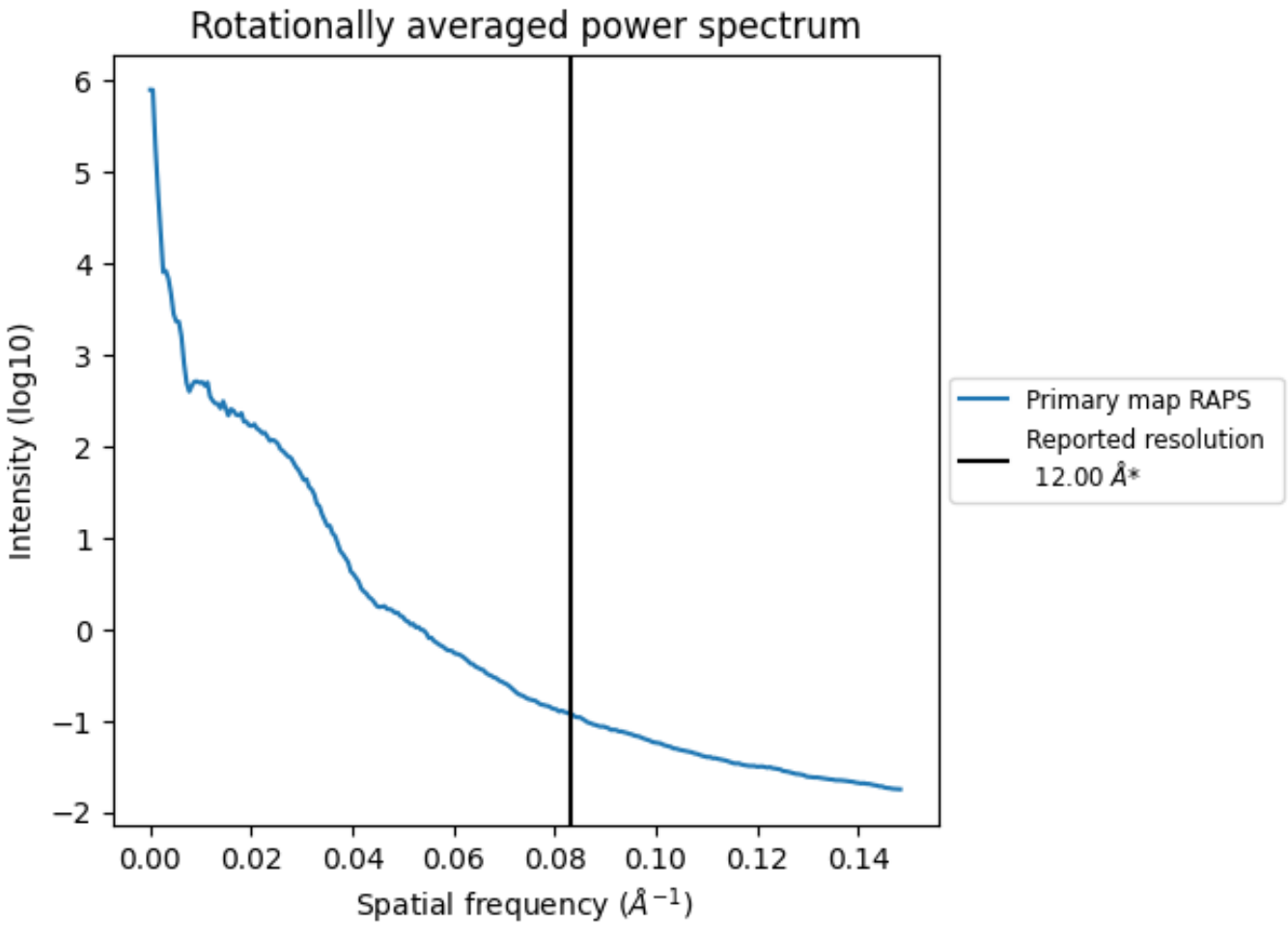
7.2 Volume estimate (i)



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

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.083 Å^{-1}

8 Fourier-Shell correlation (i)

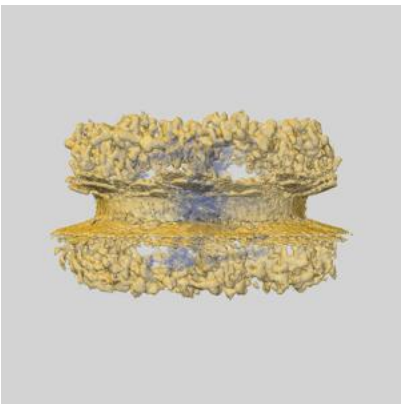
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit (i)

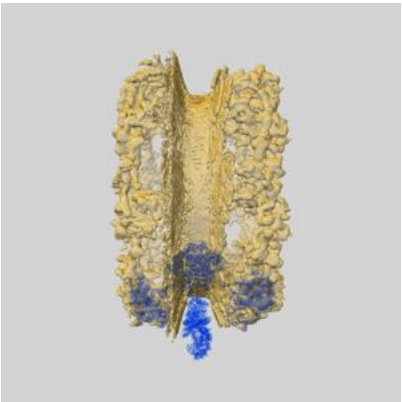
This section contains information regarding the fit between EMDB map EMD-14322 and PDB model 7R5K. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlays

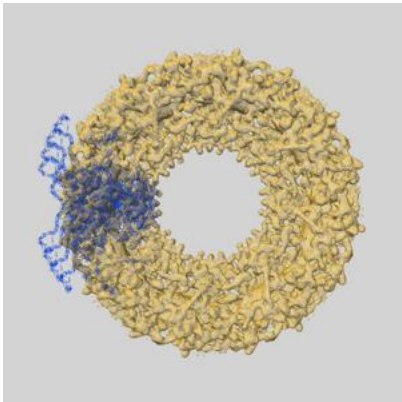
9.1.1 Map-model overlay (i)



X

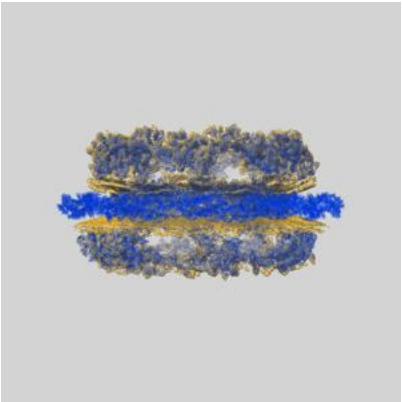


Y

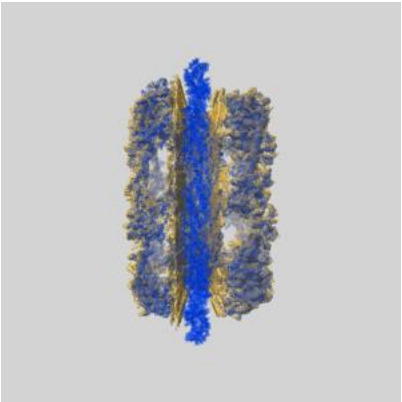


Z

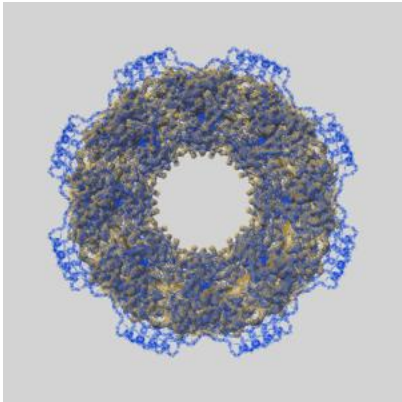
9.1.2 Map-model assembly overlay (i)



X



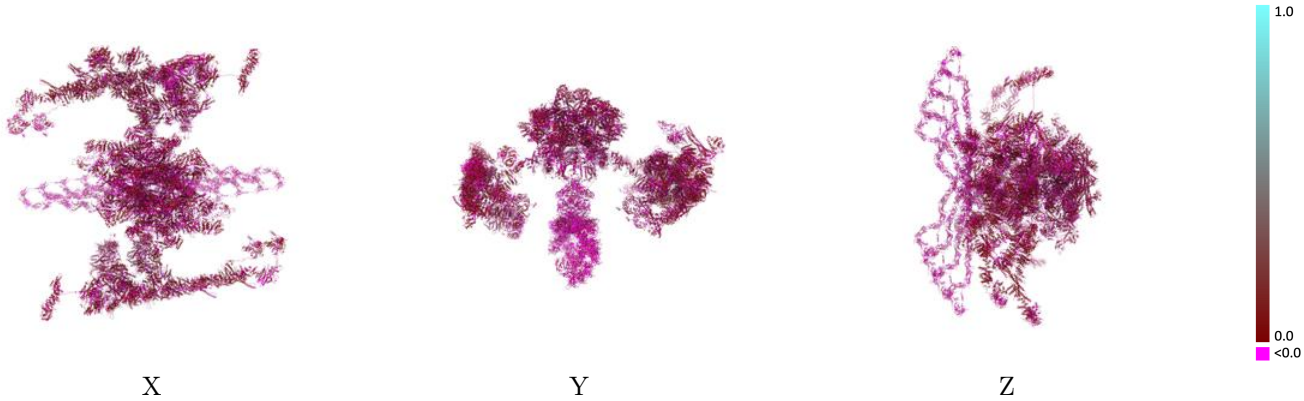
Y



Z

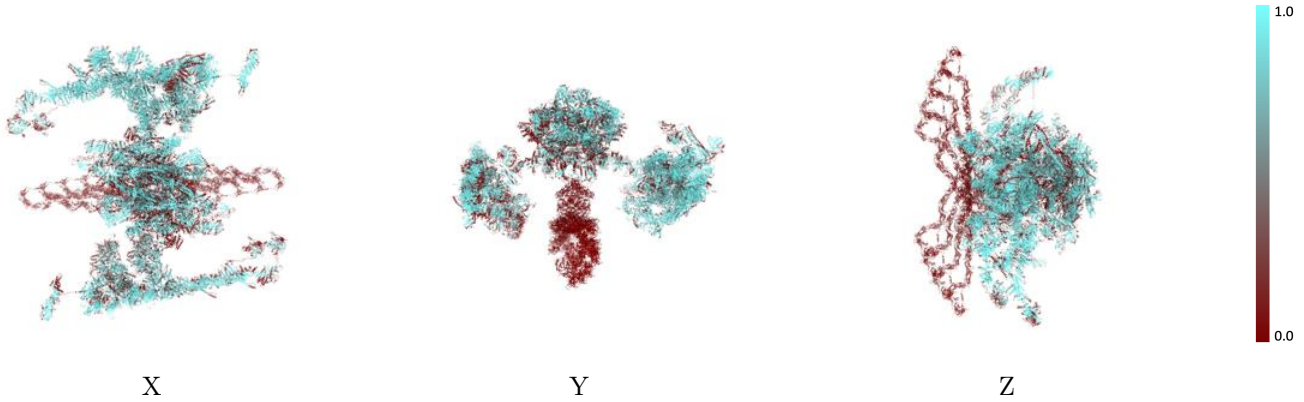
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



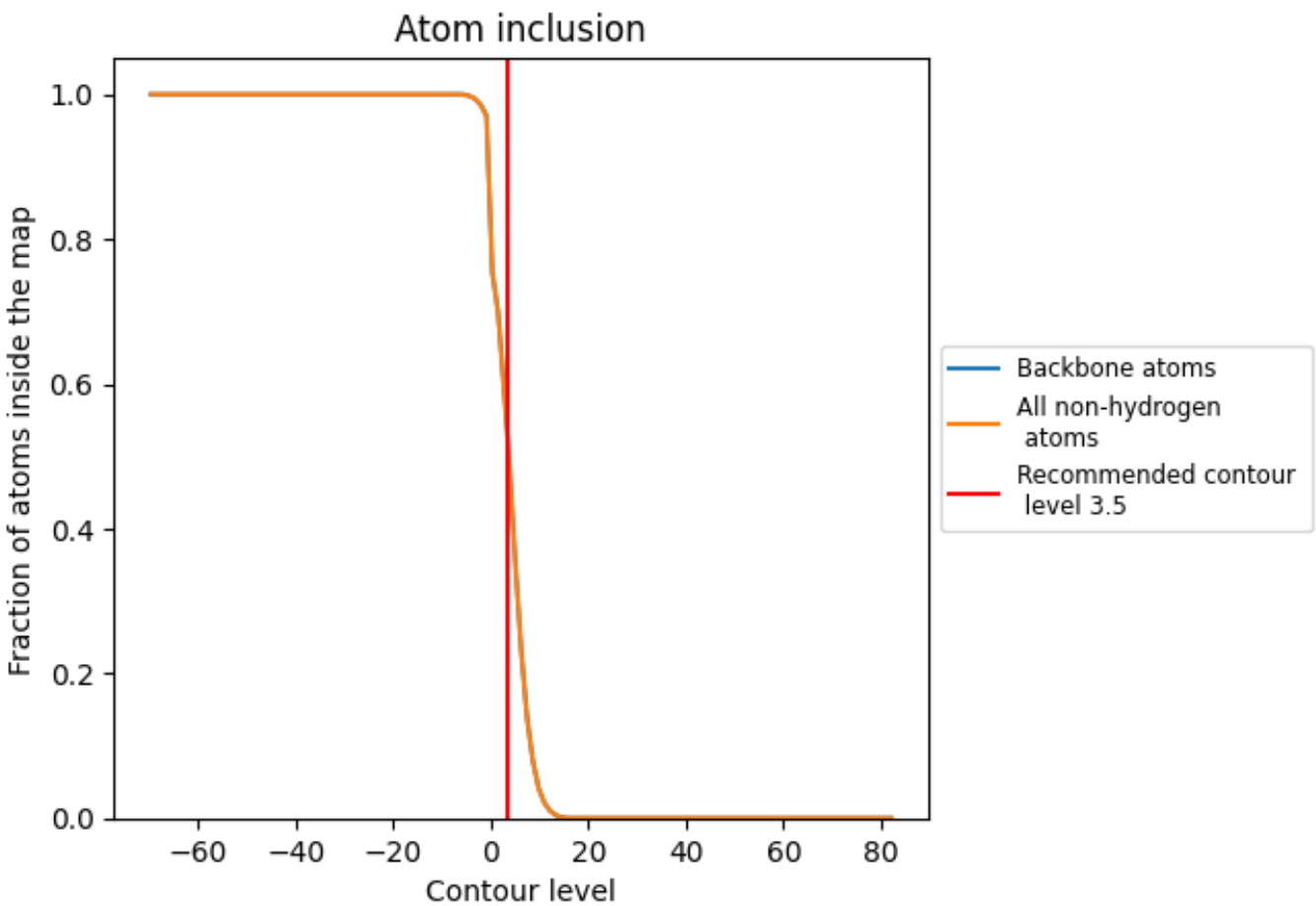
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.5).

9.4 Atom inclusion (i)



At the recommended contour level, 52% of all backbone atoms, 52% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

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	0.5200	0.0340
00	0.7710	0.0570
01	0.8680	0.0670
02	0.7430	0.0510
03	0.8230	0.0600
04	0.7590	0.0550
10	0.0120	-0.0060
11	0.0120	-0.0040
12	0.0110	0.0040
13	0.0050	-0.0000
14	0.0010	-0.0020
15	0.0020	0.0020
16	0.0080	0.0020
17	0.0090	0.0010
40	0.6160	0.0330
41	0.7430	0.0250
A0	0.6740	0.0430
A1	0.7070	0.0470
A2	0.6610	0.0350
A3	0.4500	0.0420
A4	0.4880	0.0200
A5	0.7030	0.0440
A6	0.5810	0.0430
B0	0.7170	0.0430
B1	0.5480	0.0460
C0	0.6490	0.0390
C1	0.6230	0.0380
C2	0.7760	0.0500
C3	0.7830	0.0510
C4	0.5730	0.0360
D0	0.5970	0.0340
D1	0.3000	0.0200
D2	0.5780	0.0340
D3	0.2990	0.0260
D4	0.6280	0.0360

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Chain	Atom inclusion	Q-score
D5	0.3960	0.0340
E0	0.3660	0.0300
E1	0.4950	0.0300
F0	0.4030	0.0140
F1	0.5440	0.0380
F2	0.4320	0.0080
F3	0.4360	0.0200
H0	0.6290	0.0510
H1	0.6440	0.0450
H2	0.6890	0.0530
H3	0.6760	0.0500
I0	0.6100	0.0360
I1	0.8110	0.0740
I2	0.5930	0.0350
I3	0.8400	0.0700
J0	0.7640	0.0770
J1	0.6620	0.0480
J2	0.7830	0.0580
J3	0.6210	0.0270
J4	0.3930	0.0100
K0	0.6410	0.0440
K1	0.6500	0.0460
K2	0.4360	0.0320
K3	0.4760	0.0500
L0	0.8650	0.0640
L1	0.7600	0.0530
L2	0.6900	0.0530
L3	0.7000	0.0500
M0	0.8390	0.0520
M1	0.8520	0.0520
M2	0.7400	0.0460
M3	0.7740	0.0560
N0	0.8210	0.0420
N1	0.9280	0.0520
N2	0.6600	0.0300
N3	0.8470	0.0500
O0	0.9370	0.0600
O1	0.8100	0.0420
O2	0.7760	0.0430
O3	0.6630	0.0300
P0	0.8220	0.0440
P1	0.7660	0.0420

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Chain	Atom inclusion	Q-score
P2	0.7050	0.0450
P3	0.6510	0.0390
Q0	0.8020	0.0550
Q1	0.8860	0.0590
Q2	0.6720	0.0420
Q3	0.7960	0.0480
R0	0.8160	0.0500
R1	0.7570	0.0390
R2	0.6000	0.0360
R3	0.5240	0.0350
S0	0.5650	0.0350
S1	0.7370	0.0430
S2	0.5650	0.0290
S3	0.6200	0.0350
T0	0.4250	0.0380
T1	0.1950	0.0270
U0	0.1440	-0.0000
U1	1.0000	0.0840
U2	0.0000	-0.0540
U3	0.0000	-0.0440
U4	0.0070	-0.0040
U5	0.0000	-0.0250
U6	0.2720	0.0500
V0	0.3540	0.0120
W0	0.5130	0.0120