wwPDB EM Validation Summary Report (i)

Jul 10, 2024 – 01:32 pm BST

PDB ID	:	7R5J
EMDB ID	:	EMD-14321
Title	:	Human nuclear pore complex (dilated)
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	:	50.00 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:

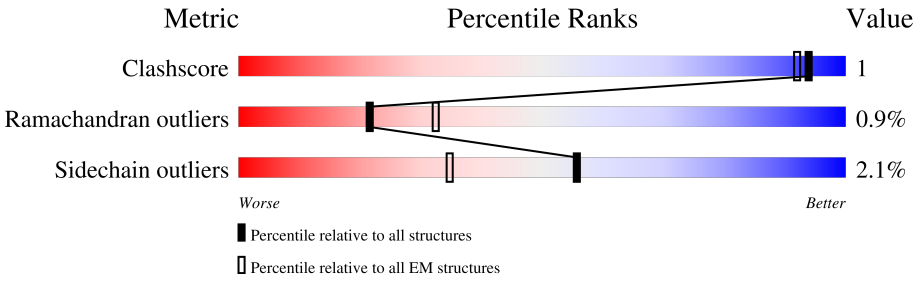
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 50.00 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	7% 21% 77%
1	01	3224	22% 77%
1	02	3224	22% 77%
1	03	3224	6% 22% 77%
1	04	3224	22% 77%
2	10	1887	73% 92%
2	11	1887	49% 93%
2	12	1887	31% 93%

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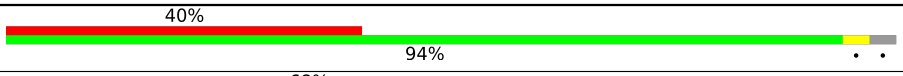
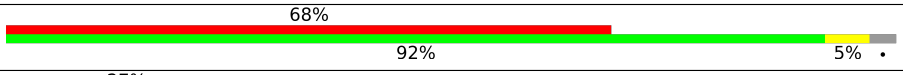
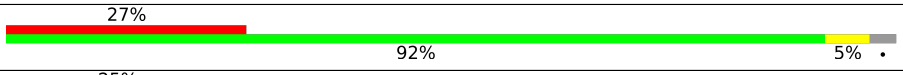
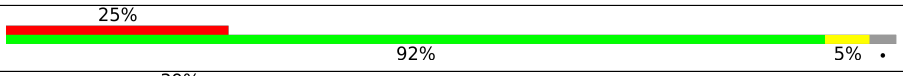
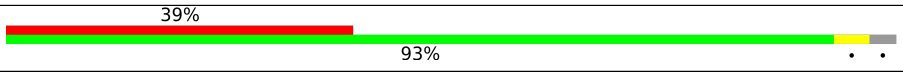
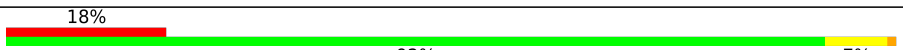
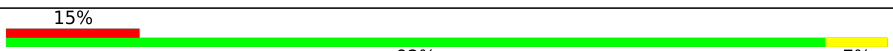
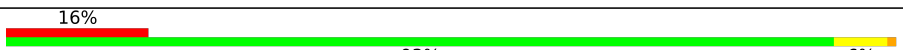
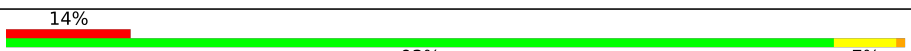
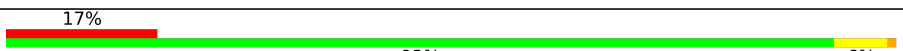
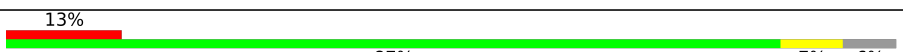
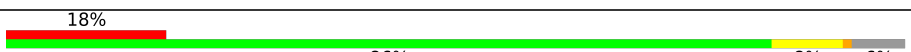
Mol	Chain	Length	Quality of chain
2	13	1887	
2	14	1887	
2	15	1887	
2	16	1887	
2	17	1887	
3	40	546	
3	41	546	
4	A0	819	
4	A1	819	
4	A2	819	
4	A3	819	
4	A4	819	
4	A5	819	
4	A6	819	
5	B0	1749	
5	B1	1749	
6	C0	2012	
6	C1	2012	
6	C2	2012	
6	C3	2012	
6	C4	2012	
7	D0	1391	
7	D1	1391	
7	D2	1391	
7	D3	1391	

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Mol	Chain	Length	Quality of chain
7	D4	1391	10% 85% 8% 6%
7	D5	1391	16% 87% 7% 6%
8	E0	674	75% 5% 19%
8	E1	674	77% 19%
9	F0	326	9% 64% 10% 26%
9	F1	326	21% 64% 9% 26%
9	F2	326	17% 66% 7% 26%
9	F3	326	25% 68% 6% 26%
10	H0	507	17% 72% 24%
10	H1	507	17% 71% 24%
10	H2	507	20% 72% 24%
10	H3	507	12% 72% 24%
11	I0	599	12% 28% 71%
11	I1	599	9% 28% 71%
11	I2	599	8% 27% 71%
11	I3	599	9% 27% 71%
12	J0	522	10% 32% 67%
12	J1	522	14% 32% 67%
12	J2	522	6% 32% 67%
12	J3	522	13% 32% 67%
12	J4	522	5% 31% 67%
13	K0	1156	19% 87% 7% 6%
13	K1	1156	15% 87% 6% 6%
13	K2	1156	25% 86% 8% 6%
13	K3	1156	22% 87% 7% 6%

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Mol	Chain	Length	Quality of chain
14	L0	925	7% 77% 7% 15%
14	L1	925	24% 78% 6% 15%
14	L2	925	20% 78% 6% 15%
14	L3	925	9% 78% 6% 15%
15	M0	937	65% 6% 28%
15	M1	937	17% 65% 6% 28%
15	M2	937	66% 6% 28%
15	M3	937	13% 66% 6% 28%
16	N0	322	17% 86% 7% 7%
16	N1	322	7% 88% 6% 7%
16	N2	322	88% 5% 7%
16	N3	322	7% 88% 5% 7%
17	O0	360	15% 83% 7% 10%
17	O1	360	83% 6% 10%
17	O2	360	9% 83% 6% 10%
17	O3	360	6% 84% 6% 10%
18	P0	656	21% 91% 9%
18	P1	656	9% 93% 6%
18	P2	656	8% 92% 6%
18	P3	656	11% 92% 7%
19	Q0	380	19% 86% 5% 9%
19	Q1	380	14% 87% 9%
19	Q2	380	9% 84% 6% 9%
19	Q3	380	87% 9%
20	R0	1436	11% 89% 7%

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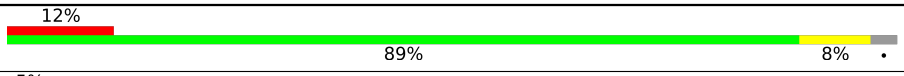
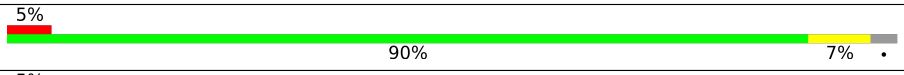
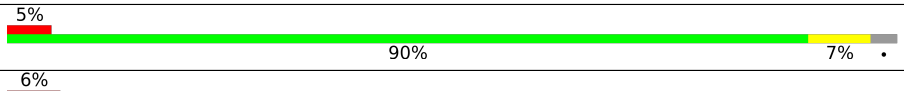
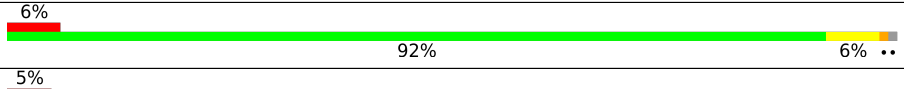
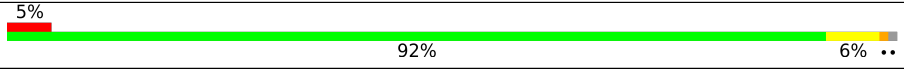
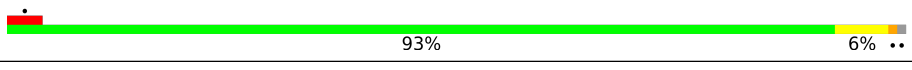
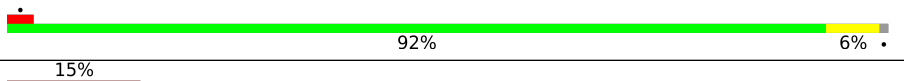
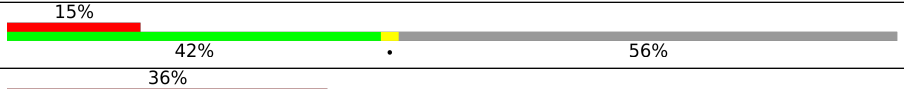
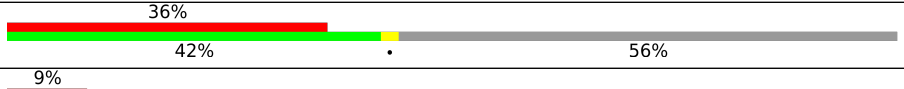
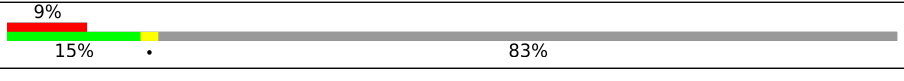
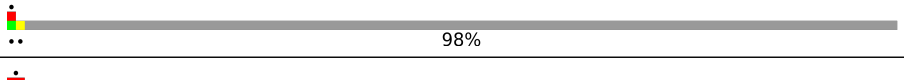
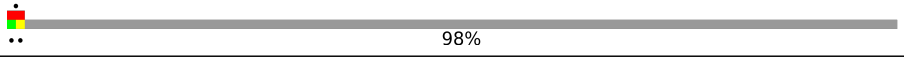
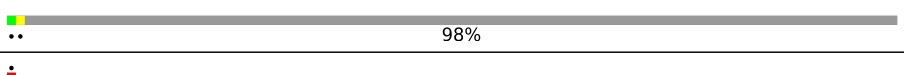
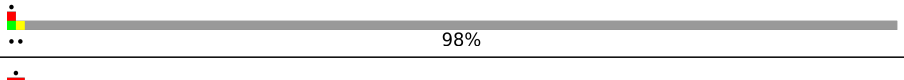
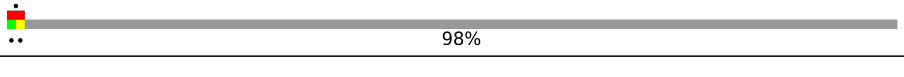
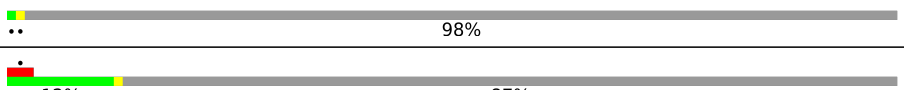
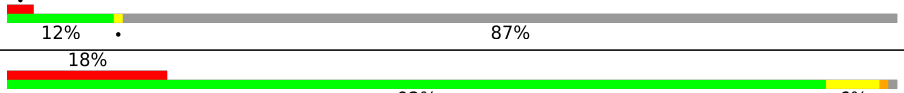
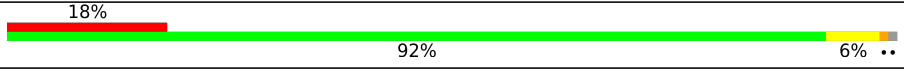
Mol	Chain	Length	Quality of chain
20	R1	1436	
20	R2	1436	
20	R3	1436	
21	S0	326	
21	S1	326	
21	S2	326	
21	S3	326	
22	T0	2266	
22	T1	2266	
23	U0	880	
23	U1	880	
23	U2	880	
23	U3	880	
23	U4	880	
23	U5	880	
23	U6	880	
24	V0	2090	
25	W0	741	

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
1	00	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	01	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	02	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	03	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	04	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		

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

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

- Molecule 3 is a protein called Aladin.

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

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

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

- Molecule 5 is a protein called Nucleoporin NUP188 homolog.

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

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

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

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

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

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

- Molecule 8 is a protein called Nucleoporin NDC1.

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

- Molecule 9 is a protein called Nucleoporin NUP35.

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

- Molecule 10 is a protein called Nucleoporin p54.

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 16 is a protein called Protein SEC13 homolog.

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

- Molecule 17 is a protein called Nucleoporin SEH1.

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

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

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

- Molecule 19 is a protein called Nucleoporin Nup43.

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

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

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

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

- Molecule 21 is a protein called Nucleoporin Nup37.

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

- Molecule 22 is a protein called Protein ELYS.

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

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

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

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

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

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

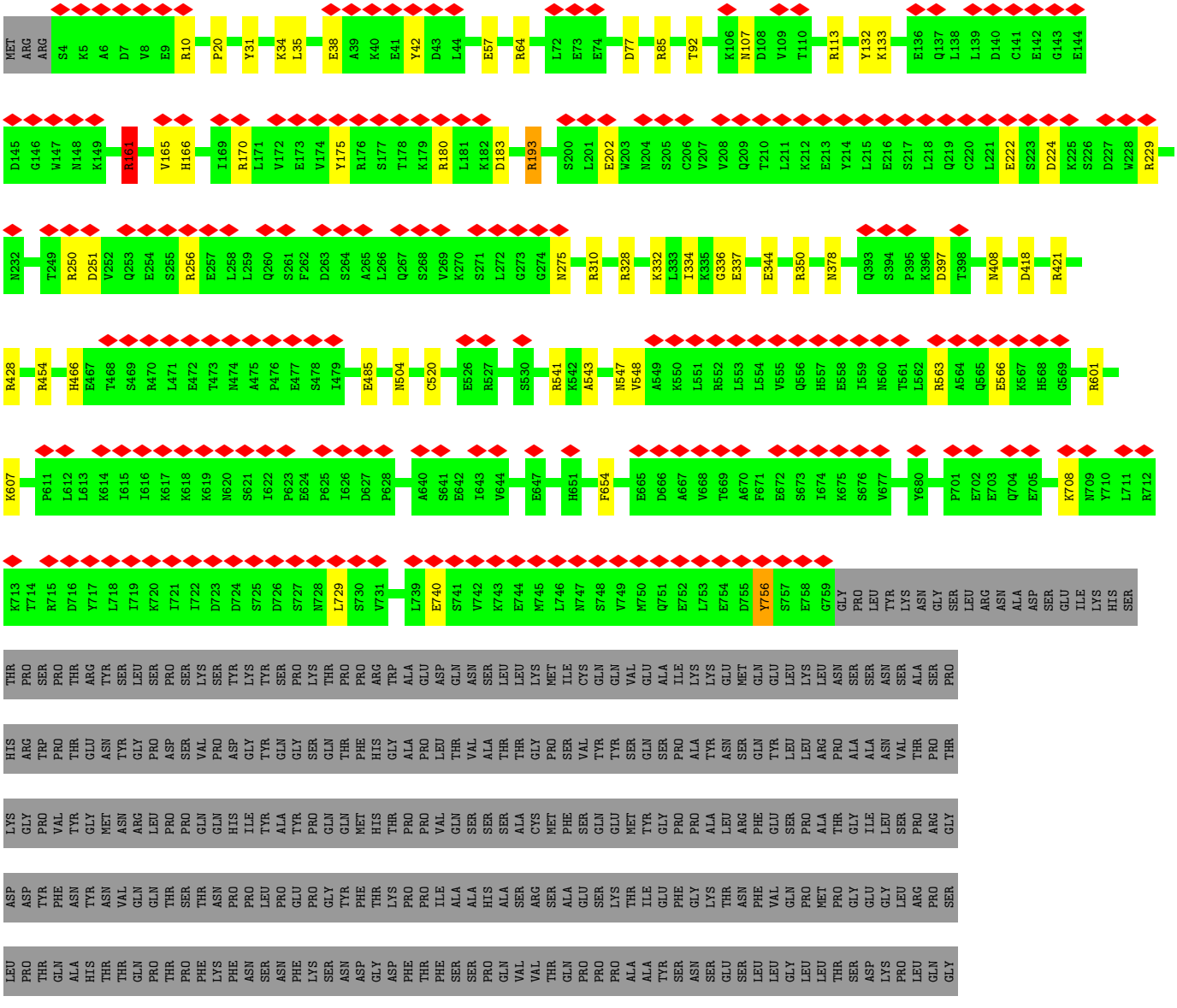
Mol	Chain	Residues	Atoms					AltConf	Trace
25	W0	735	Total	C	N	O	S	0	0
			5836	3714	988	1103	31		

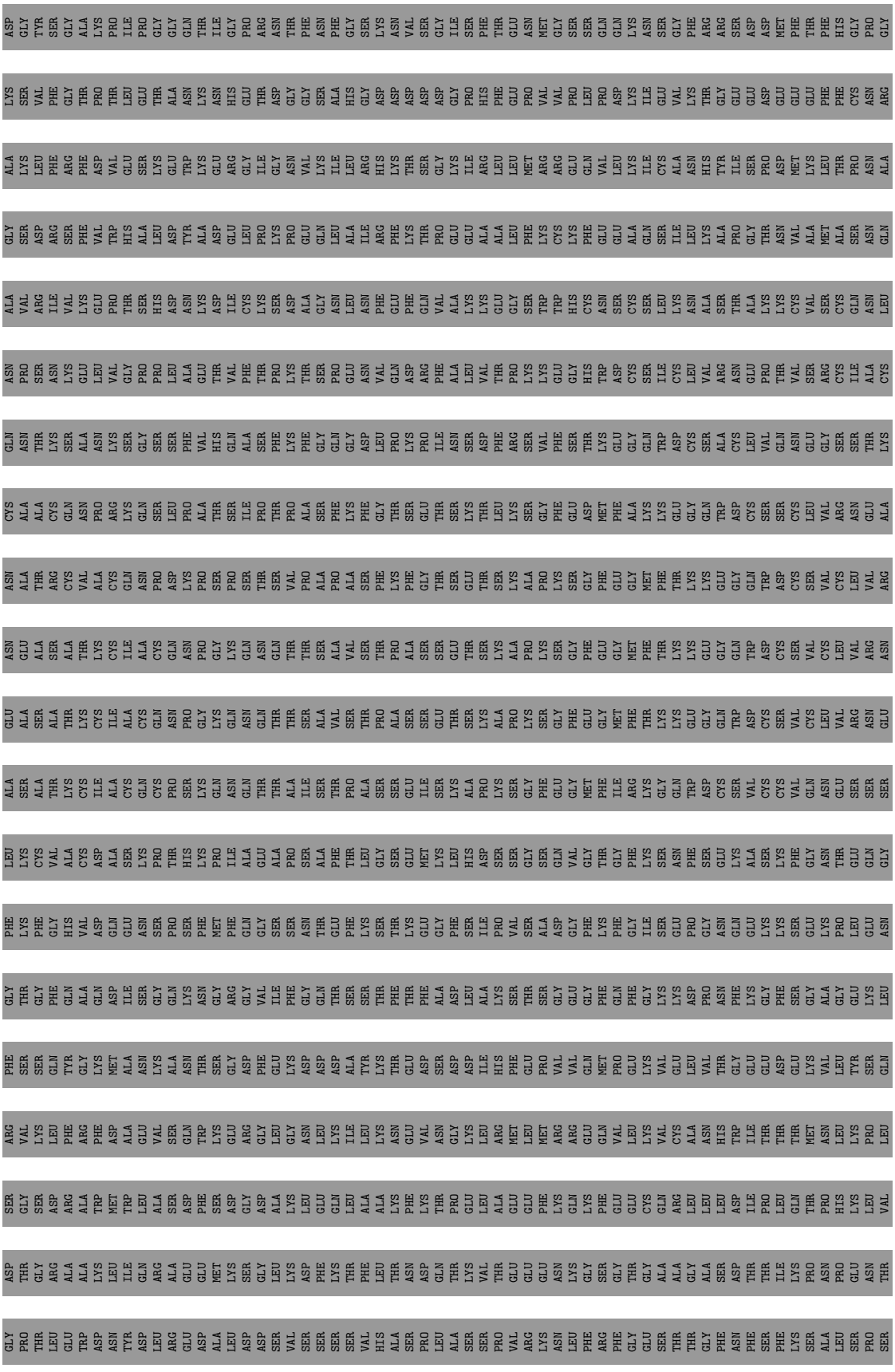
3 Residue-property plots (i)

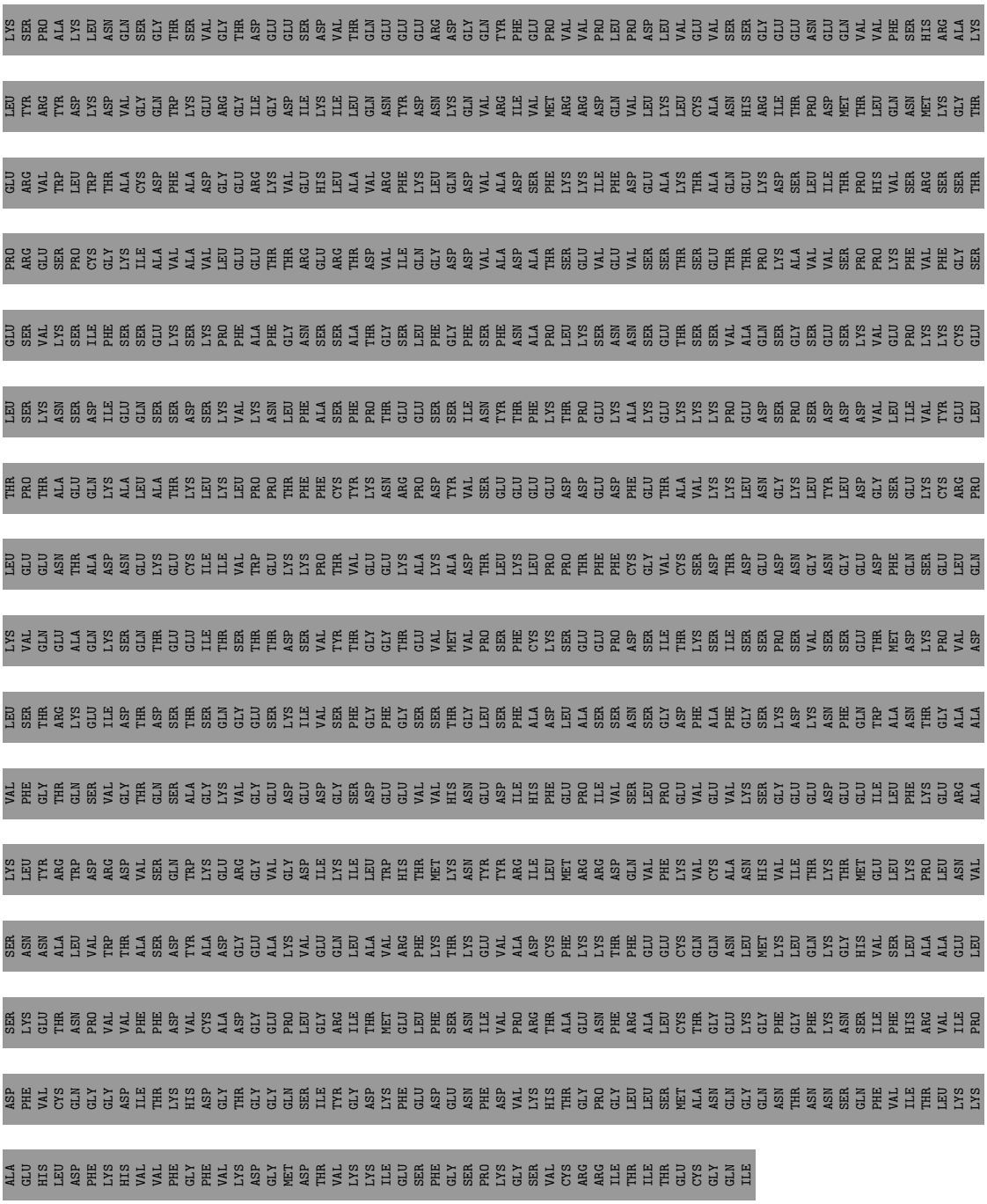
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

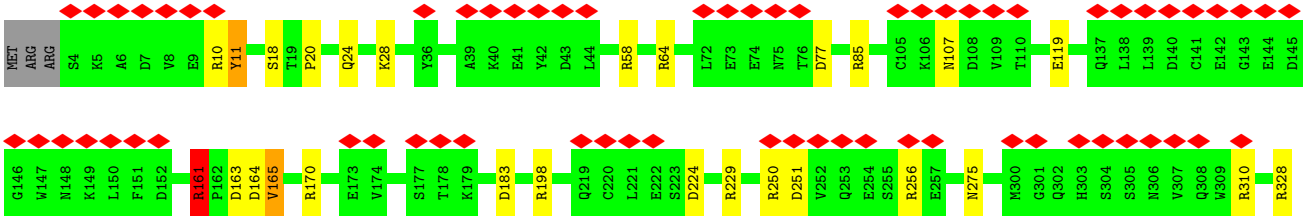


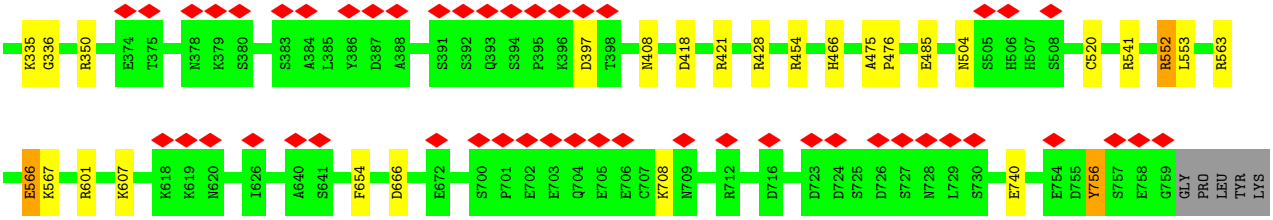




• Molecule 1: E3 SUMO-protein ligase RanBP2

Chain 01:

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Q393
S394
P395
K396
D397
T398
N408
D418
R421
R428
R454
H466
A475
P476
E485
N504
S505
H506
H507
S508
C520
R541
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L553
R563
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K567
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S725
D726
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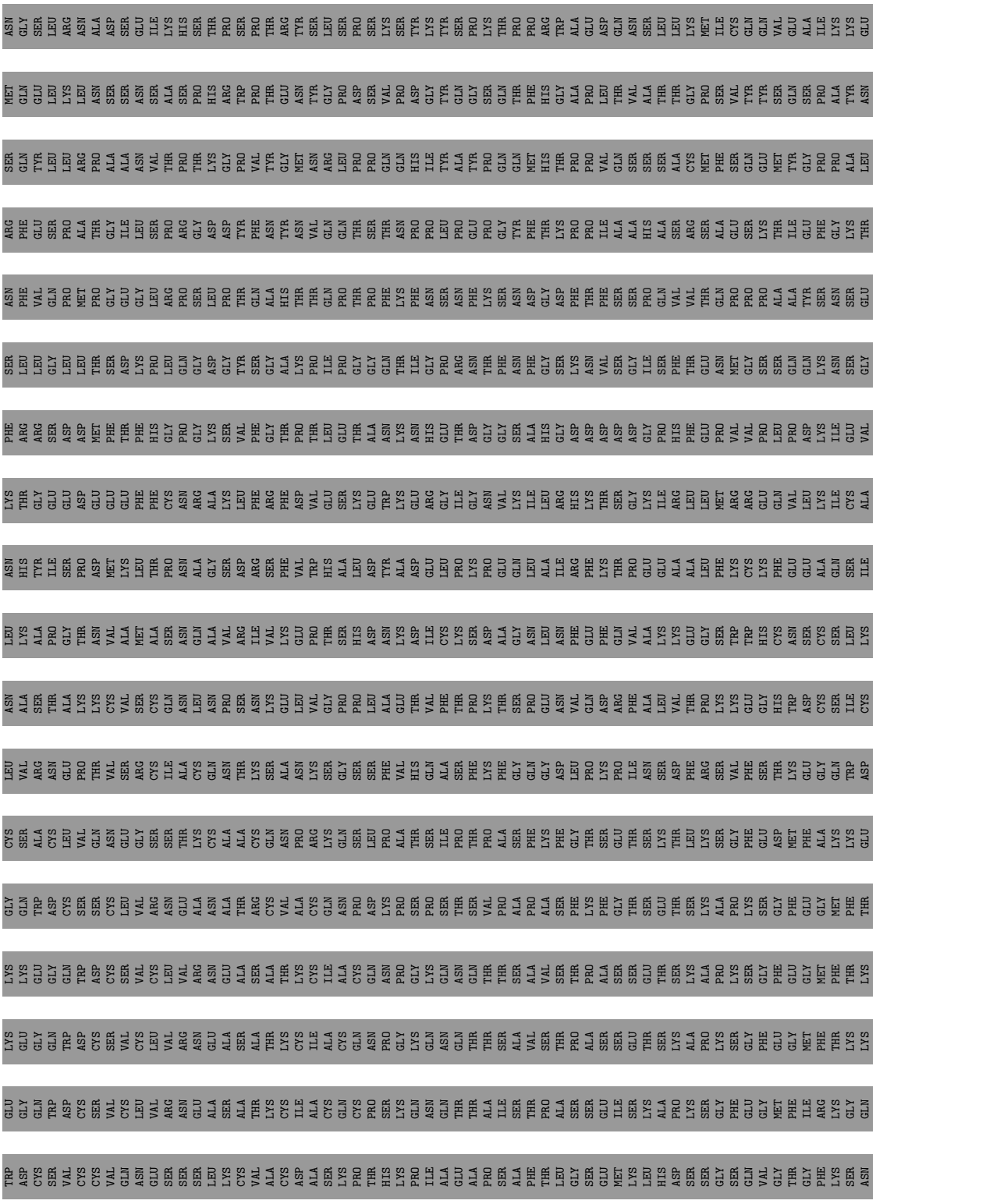

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PRO GLY ASN GLN GLU LYS LYS SER GLU LYS PRO LEU GLU ASN GLY THR GLY PHE GLN ALA GLN ASP ILE SER GLY GLN LYS ASN GLY ARG GLY VAL ILE PHE GLY GLN THR SER SER THR PHE THR PHE ALA ASP LEU ALA LYS SER THR SER GLY GLU GLY PHE GLN PHE GLY LYS LYS

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

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

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

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

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

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

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

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

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

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

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

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

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

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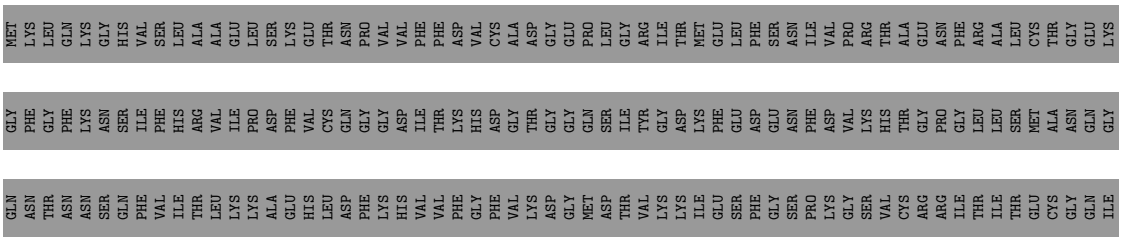
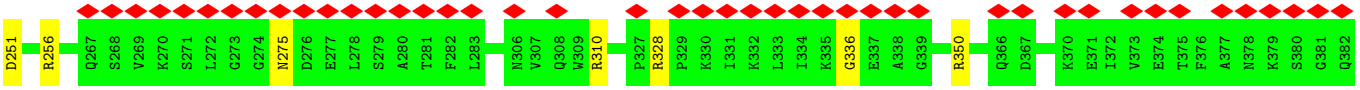
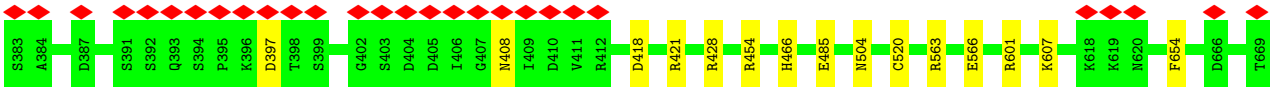
HIS VAL ILE THR LYS THR MET GLU LEU LYS PRO LEU ASN VAL SER ASN ASN ALA LEU VAL TRP THR ALA SER ASP TYR ALA ASP GLY GLU ALA LYS VAL GLU GLN LEU ALA VAL ARG PHE LYS THR LYS GLU VAL ALA ASP CYS PHE LYS LYS THR PHE GLU GLU CYS GLN GLN ASN LEU

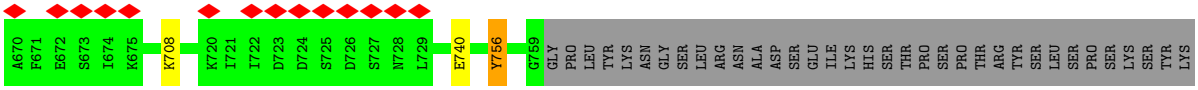


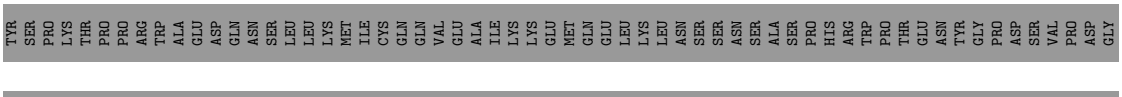
• Molecule 1: E3 SUMO-protein ligase RanBP2

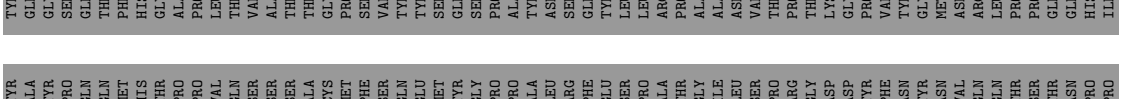
Chain 02:

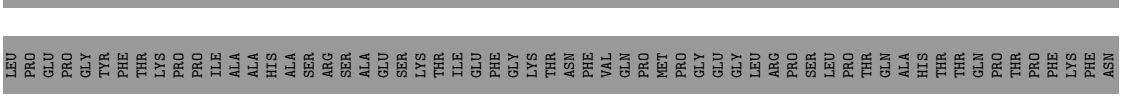


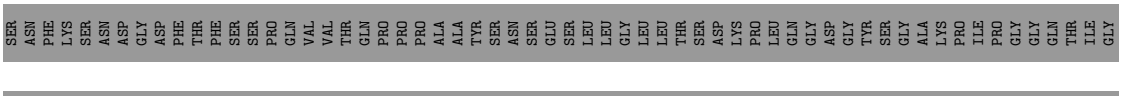


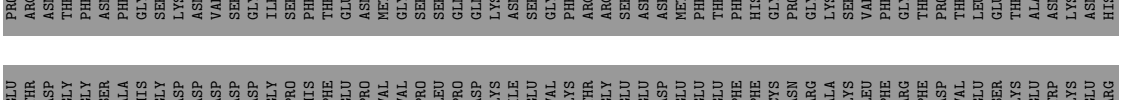


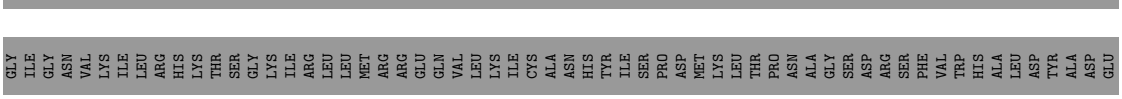


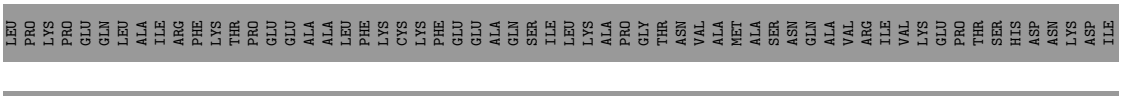


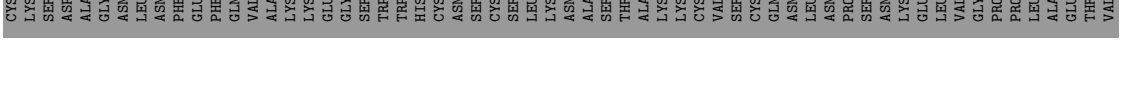












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ALA SER PHE LYS PHE GLY GLN GLY ASP LEU PRO LYS PRO ILE ASN SER ASP PHE ARG SER VAL PHE SER THR LYS GLU GLY GLN TRP ASP CYS SER ALA CYS LEU VAL GLN ASN GLU GLY SER SER THR LYS CYS ALA ALA CYS GLN ASN PRO ARG LYS GLN SER LEU PRO ALA THR SER

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

ASN GLN THR THR SER 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 ILE ALA CYS GLN CYS PRO SER LYS GLN ASN

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

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

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

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

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

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

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

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

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

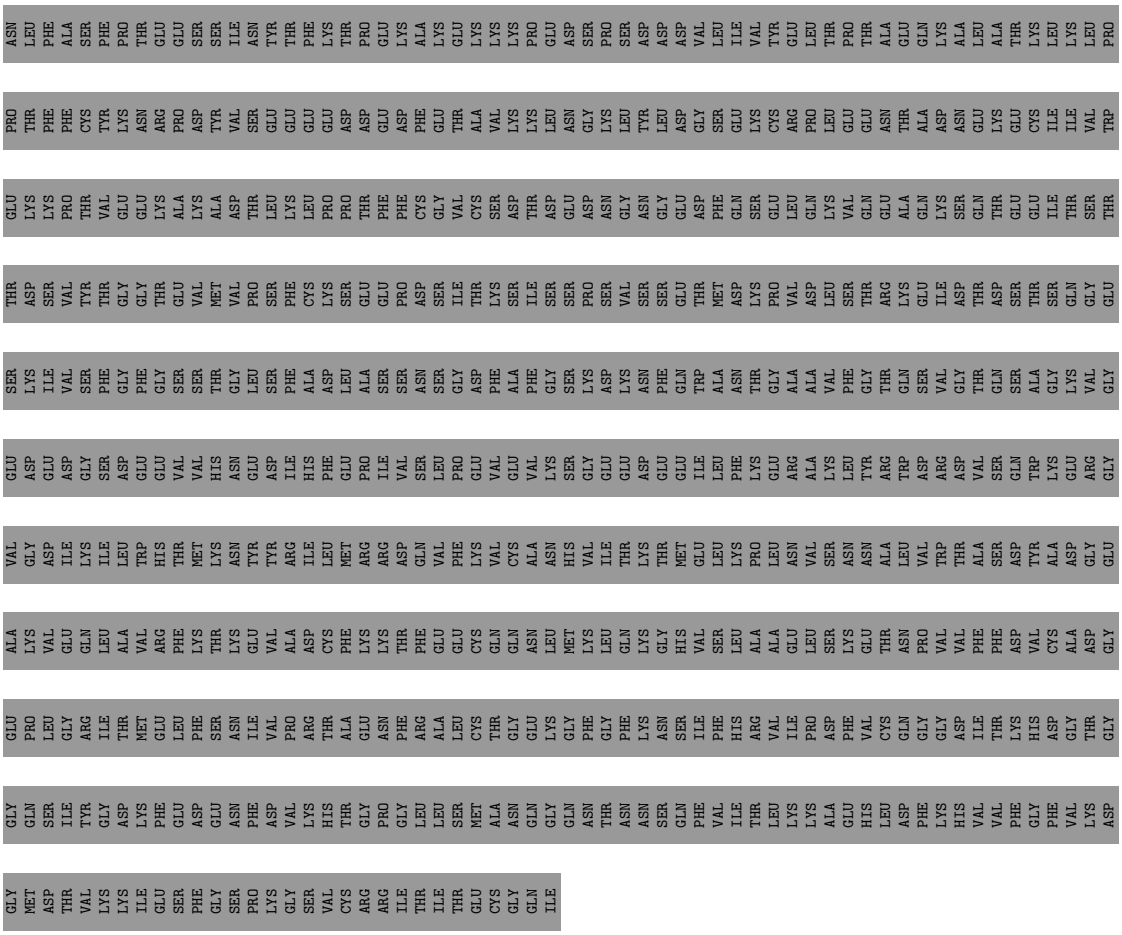
GLU GLU SER ASP VAL THR GLN GLU GLU GLU ARG ASP GLY GLN TYR PHE GLU PRO VAL VAL PRO LEU PRO ASP LEU VAL GLU VAL SER SER GLY GLU GLU ASN GLU GLN VAL VAL PHE SER HIS ARG ALA LYS LEU TYR ARG TYR ASP LYS ASP VAL GLY GLN TRP LYS GLU ARG GLY ILE

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

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

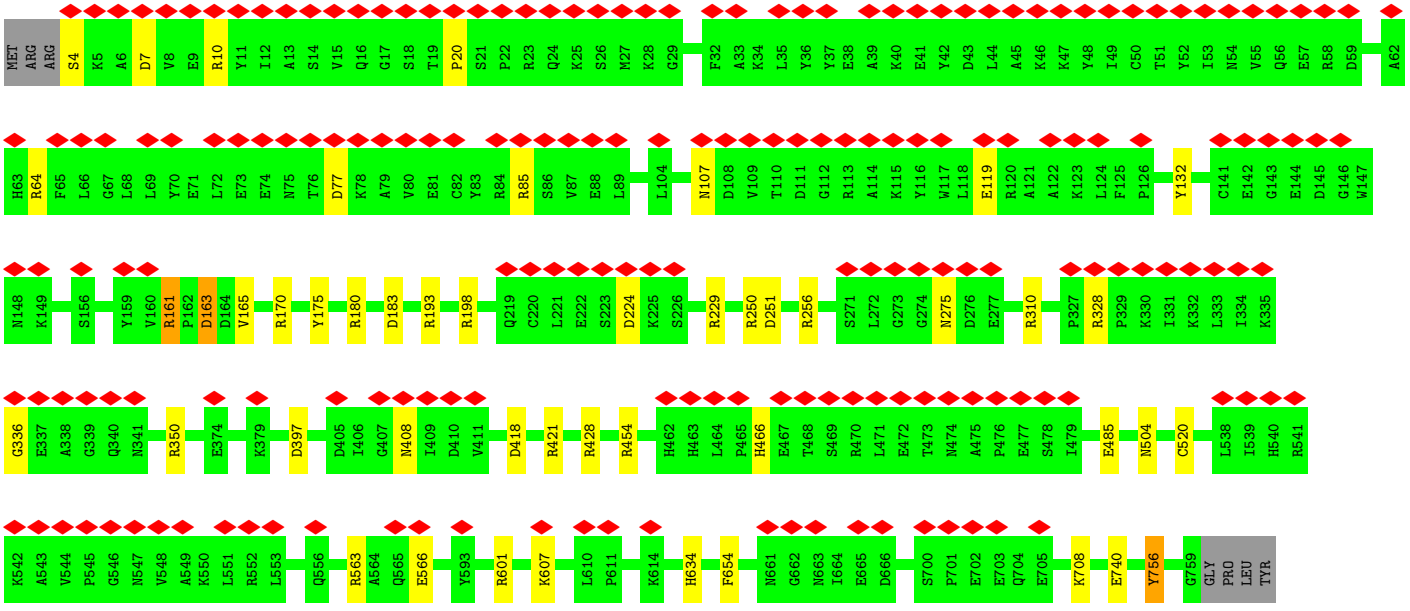
THR THR ARG GLU ARG THR ASP VAL ILE GLN GLY ASP ASP VAL ALA ASP ALA THR SER GLU VAL GLU VAL SER SER THR SER GLU THR THR PRO LYS ALA VAL VAL SER PRO PRO LYS PHE VAL PHE GLY SER GLU SER VAL LYS SER ILE PHE SER SER GLU LYS SER LYS PRO PHE ALA

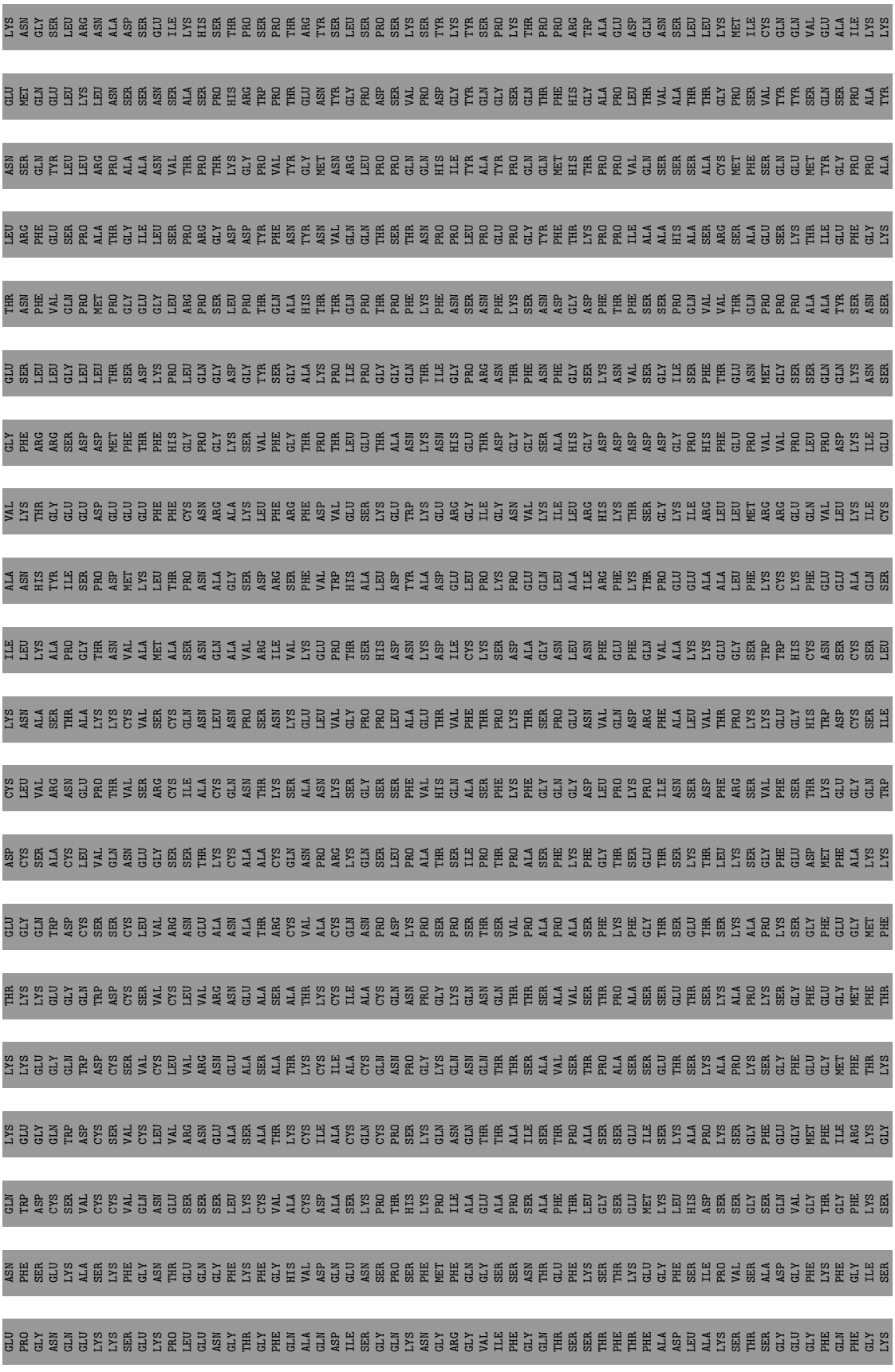
PHE GLY ASN SER SER ALA THR GLY SER LEU PHE GLY PHE SER PHE ASN ALA PRO LEU LYS SER ASN ASN SER GLU THR SER SER VAL ALA GLN SER GLY SER GLU SER LYS VAL GLU PRO LYS LYS CYS GLU LEU SER LYS ASN SER ASP ILE GLU GLN SER SER ASP SER LYS VAL LYS



• Molecule 1: E3 SUMO-protein ligase RanBP2

Chain 03:





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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

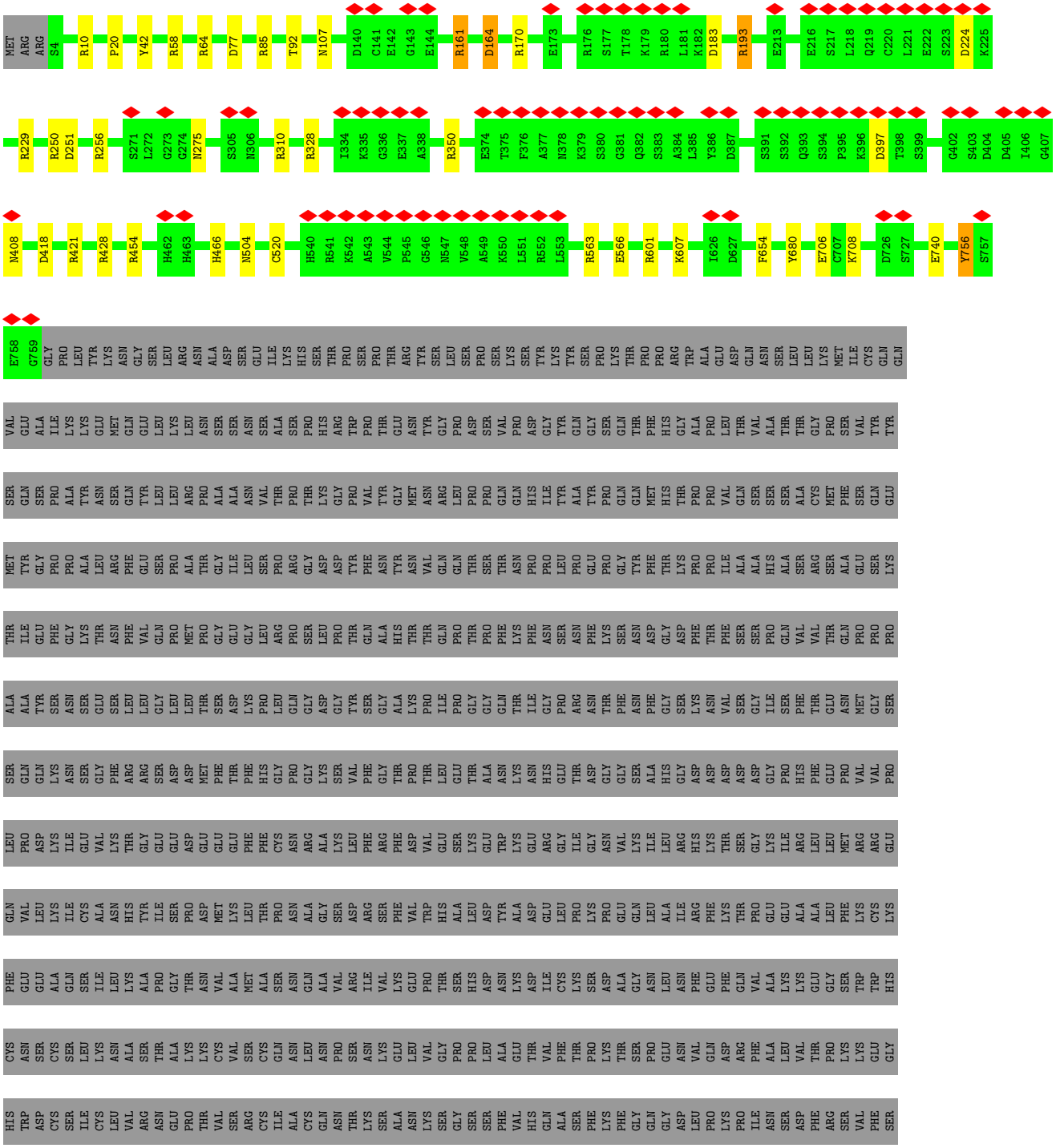
ASN HIS VAL ILE THR LYS THR MET GLU LEU LYS PRO LEU ASN VAL SER ASN ASN ALA LEU VAL TRP THR ALA SER ASP TYR ALA ASP GLY GLU ALA LYS VAL GLU GLN LEU ALA VAL ARG PHE LYS THR LYS GLU VAL ALA ASP CYS PHE LYS LYS THR PHE GLU GLU CYS GLN GLN ASN

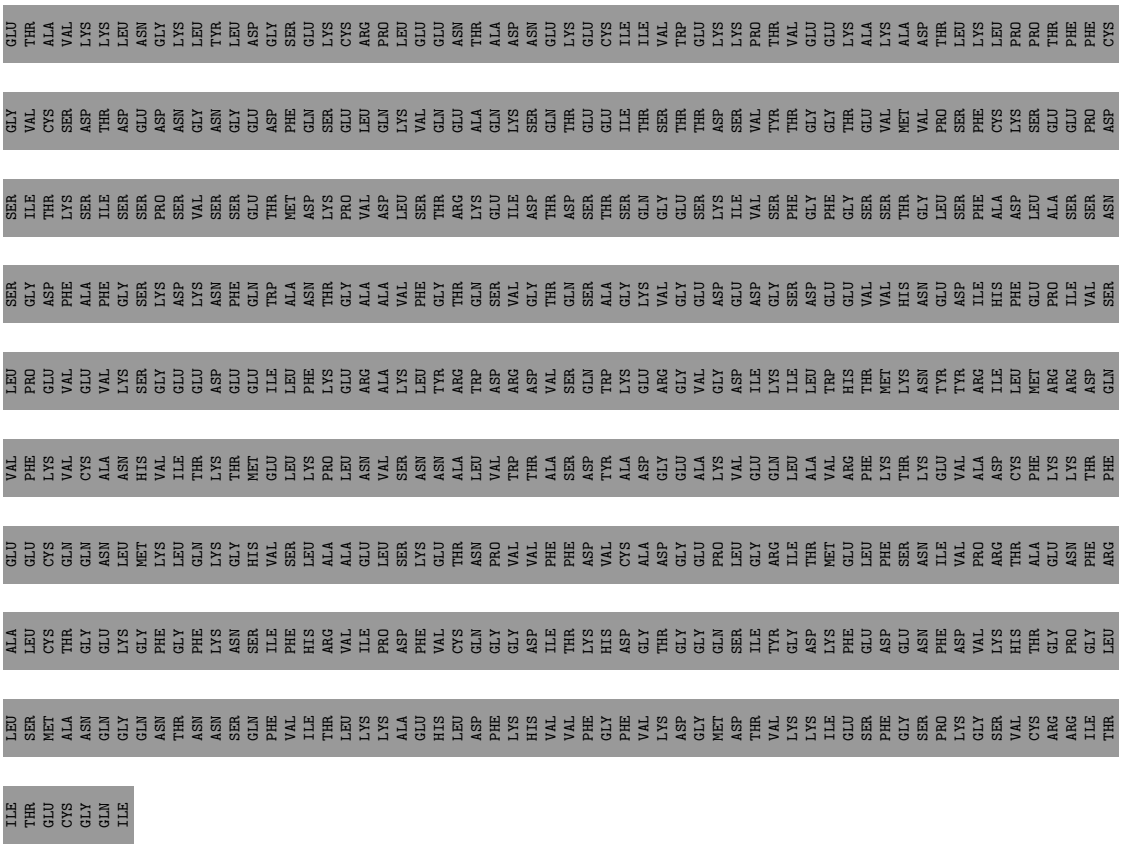
LEU MET LYS LEU GLN LYS GLY HIS VAL SER LEU ALA ALA GLU LEU SER LYS GLU THR ASN PRO VAL VAL PHE PHE ASP VAL CYS ALA ASP GLY GLU PRO LEU GLY ARG ILE THR MET GLU LEU PHE SER ASN ILE VAL PRO ARG THR ALA GLU ASN PHE ARG ALA LEU CYS THR GLY GLU

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

• Molecule 1: E3 SUMO-protein ligase RanBP2

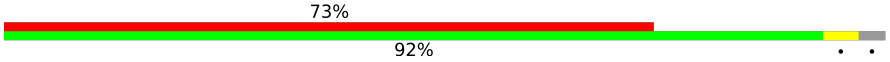
Chain 04:

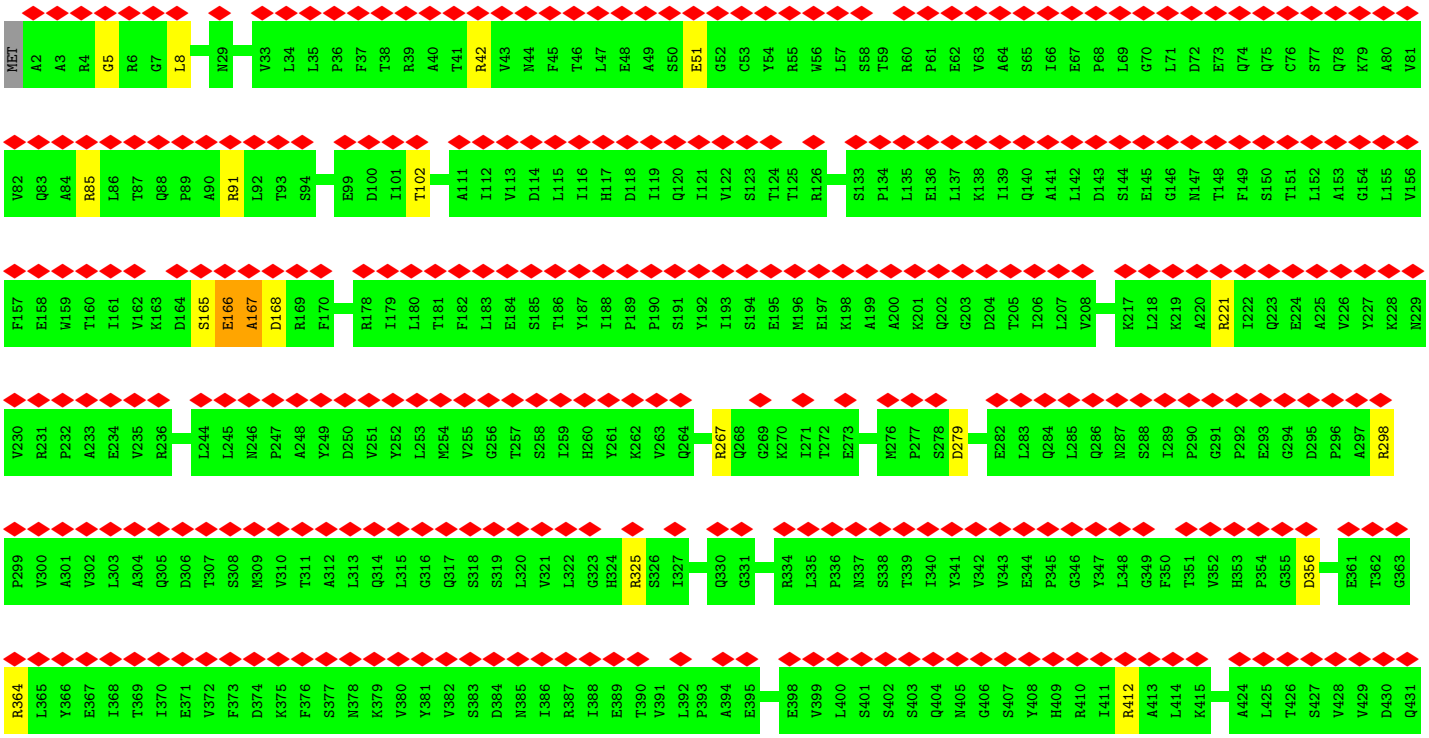


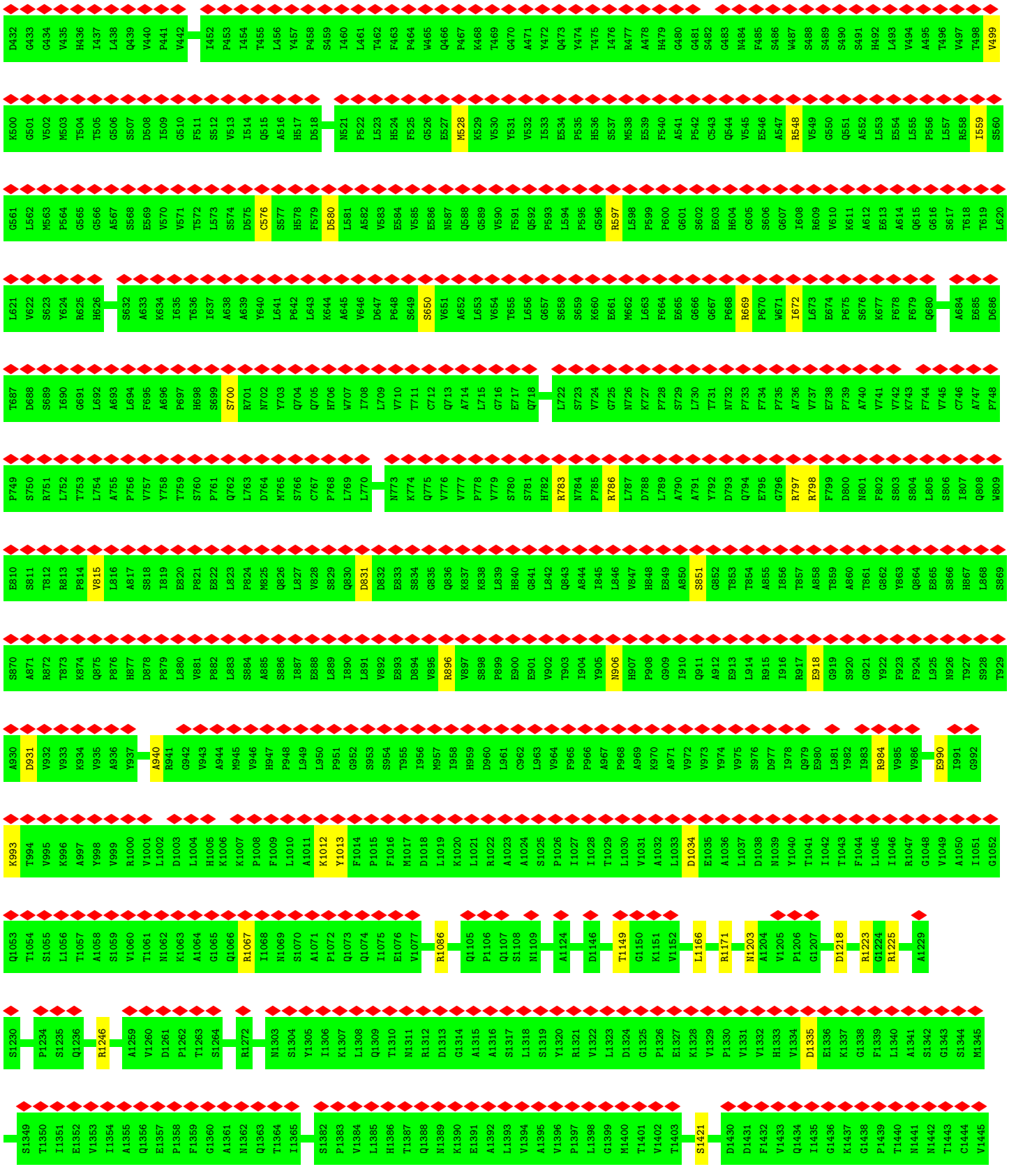


• Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 10:



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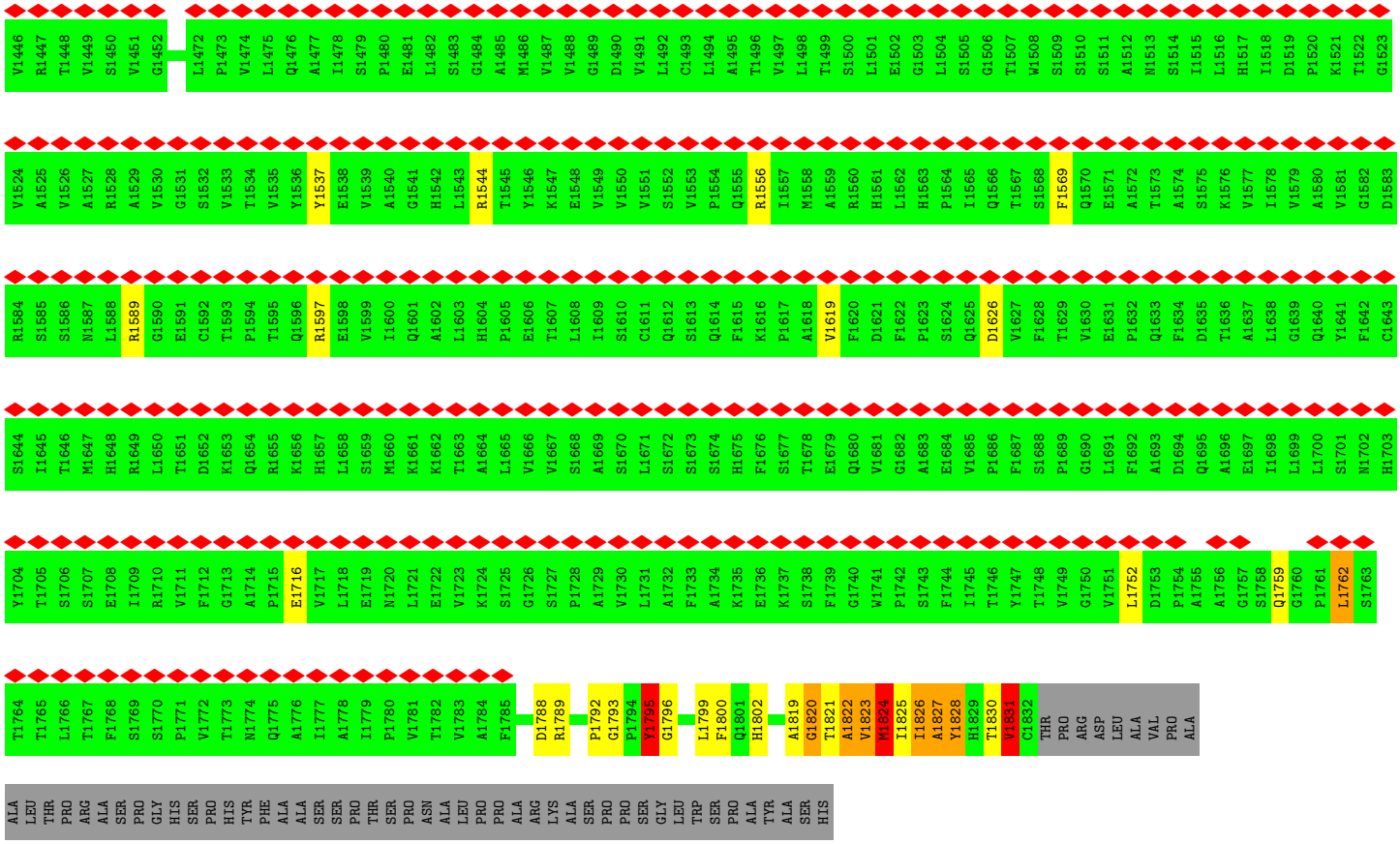
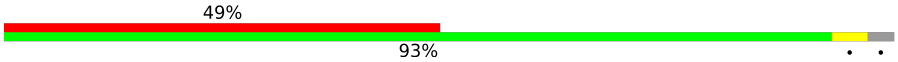
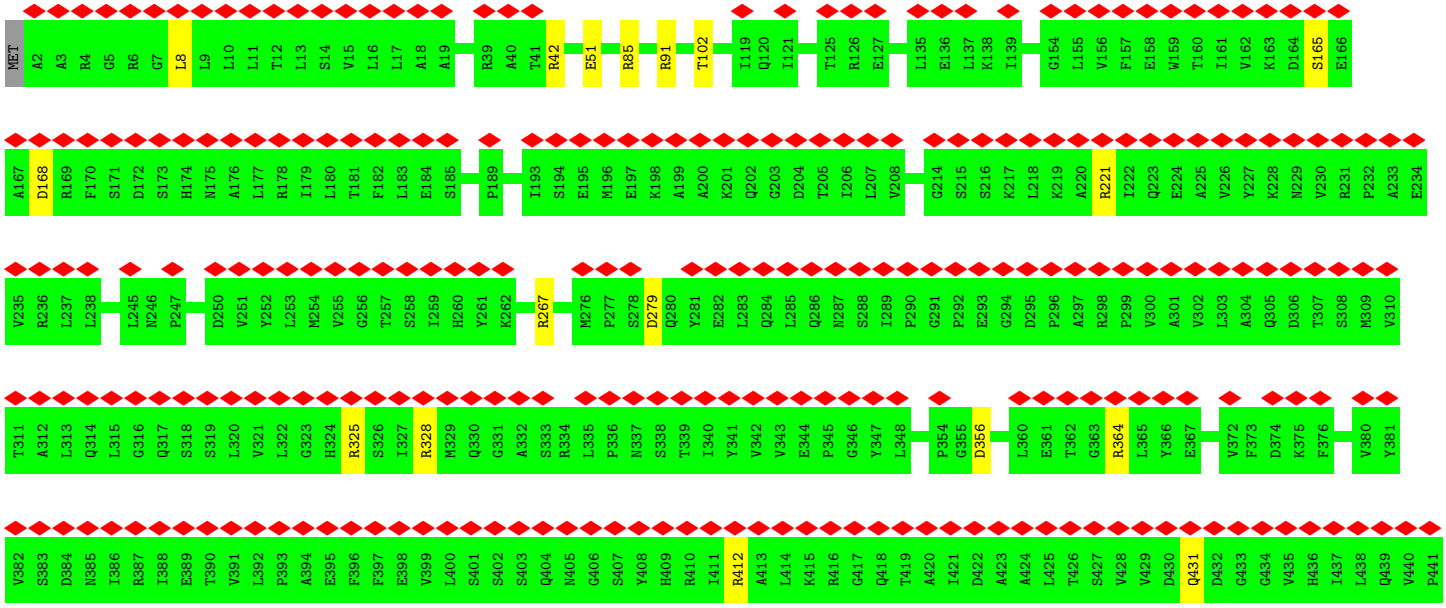
K500 G501 V502 M503 T504 T505 G506 S507 D508 I509 G510 F511 S512 V513 I514 Q515 A516 H517 D518 N521 P522 L523 H524 F525 G526 E527 M528 K529 V530 V531 V532 I533 E534 P535 H536 S537 M538 E539 F540 A541 P542 C543 Q544 V545 E546 A547 R548 V549 G550 Q551 A552 L553 E554 L555 P556 L557 R558 I559 S560
G561 L562 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 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 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 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 W765 S766 C767 P768 L769 L770 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 Q835 Q836 K837 K838 L839 H840 G841 L842 Q843 A844 I845 L846 V847 H848 E849 A850 S851 Q852 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 Q919 S920 G921 Y922 P923 F924 L925 N926 T927 S928 T929
A930 D931 V932 V933 K934 V935 A936 Y937 A940 R941 G942 V943 A944 M945 V946 H947 P948 L949 L950 P951 G952 S953 S954 T955 I956 M957 I958 H959 D960 L961 C962 L963 V964 F965 P966 A967 P968 A969 K970 A971 V972 V973 Y974 V975 S976 D977 I978 Q979 E980 L981 Y982 I983 R984 V985 V986 E990 I991 G992
K993 T994 V995 K996 A997 Y998 V999 R1000 V1001 L1002 D1003 L1004 H1005 K1006 K1007 P1008 F1009 L1010 A1011 K1012 Y1013 F1014 P1015 F1016 M1017 D1018 L1019 K1020 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 R1086 Q1105 P1106 Q1107 S1108 N1109 A1124 D1146 T1149 G1150 K1151 V1152 L1166 R1171 N1203 A1204 V1205 P1206 G1207 D1218 R1223 G1224 R1225 A1229
S1230 P1234 S1235 Q1236 R1246 A1259 V1260 D1261 P1262 T1263 S1264 R1272 N1303 S1304 Y1305 I1306 K1307 L1308 Q1309 T1310 N1311 R1312 D1313 G1314 A1315 A1316 S1317 L1318 S1319 Y1320 R1321 V1322 L1323 D1324 G1325 P1326 E1327 K1328 V1329 P1330 V1331 V1332 H1333 V1334 D1335 E1336 K1337 G1338 F1339 L1340 A1341 S1342 G1343 S1344 M1345
S1349 T1350 I1351 E1352 V1353 I1354 A1355 Q1356 E1357 P1358 F1359 G1360 A1361 N1362 Q1363 T1364 I1365 S1382 P1383 V1384 L1385 H1386 T1387 Q1388 N1389 K1390 E1391 A1392 L1393 V1394 A1395 V1396 P1397 L1398 G1399 M1400 T1401 V1402 T1403 S1421 D1430 D1431 F1432 V1433 Q1434 I1435 G1436 K1437 G1438 P1439 T1440 N1441 N1442 T1443 C1444 V1445

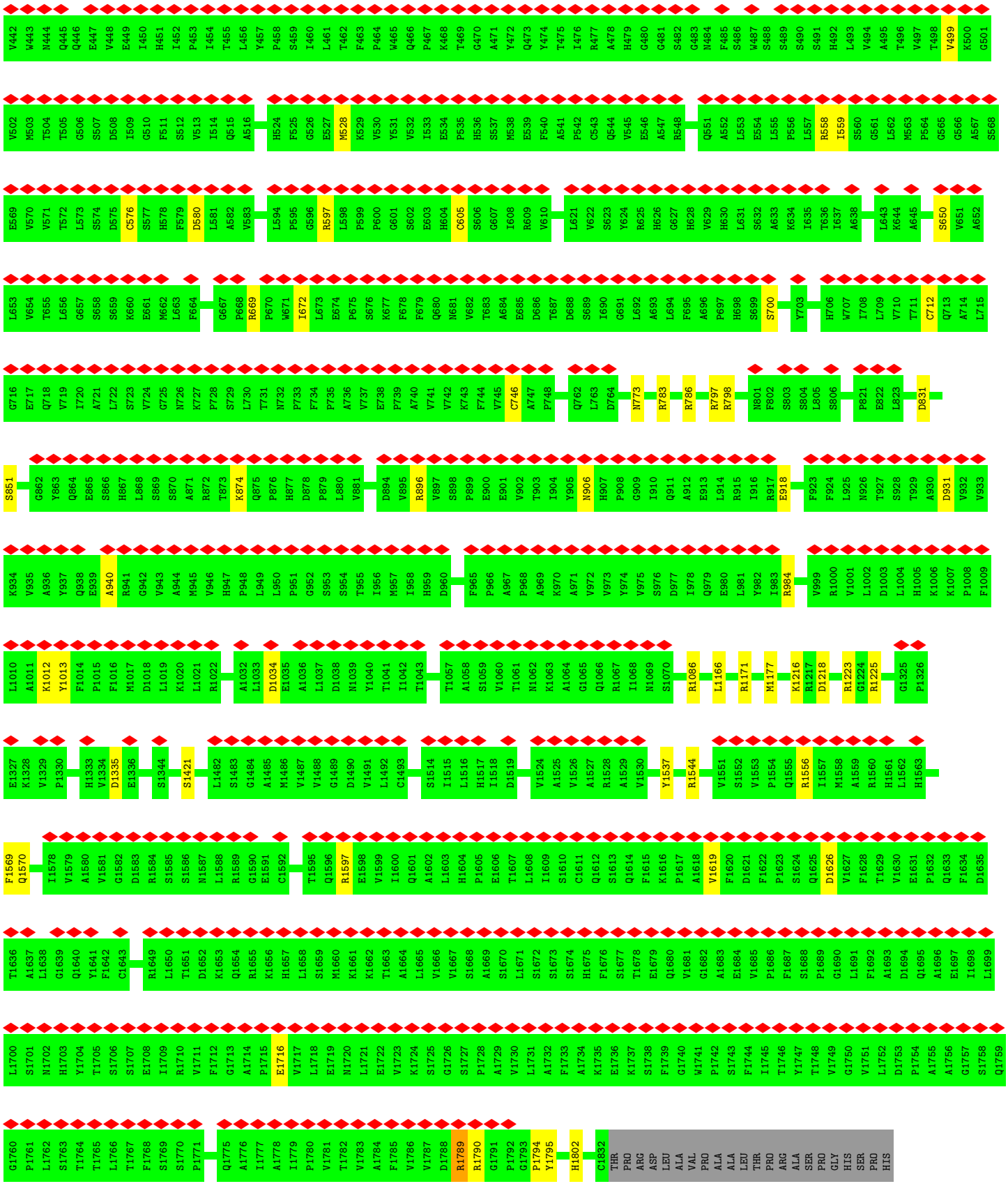


• Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 11:



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V502 M503 T504 T505 G506 S507 D508 I509 G510 F511 S512 V513 I514 Q515 A516 H524 F525 G526 E527 M528 K529 V530 V531 V532 I533 E534 P535 H536 S537 M538 E539 F540 A541 P542 C543 Q544 V545 E546 A547 R548 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 L594 P595 G596 R597 L598 P599 P600 G601 S602 E603 H604 C605 S606 G607 I608 R609 V610 L621 V622 S623 Y624 R625 H626 G627 H628 V629 H630 L631 S632 A633 K634 I635 T636 I637 A638 L643 K644 A645 S650 V651 A652
L653 V654 T655 L656 G657 S658 S659 K660 E661 M662 L663 F664 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 Y703 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 Q762 L763 D764 N773 R783 R786 R797 R798 N801 F802 S803 S804 L805 S806 P821 E822 L823 D831
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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: 31% 93%

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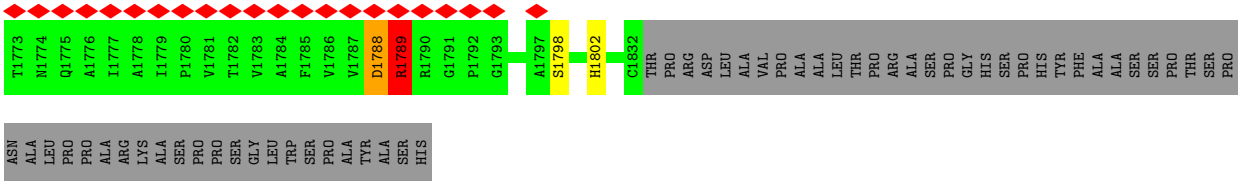
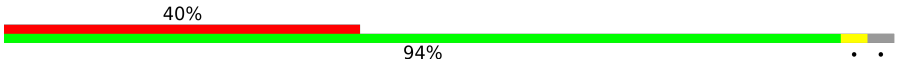
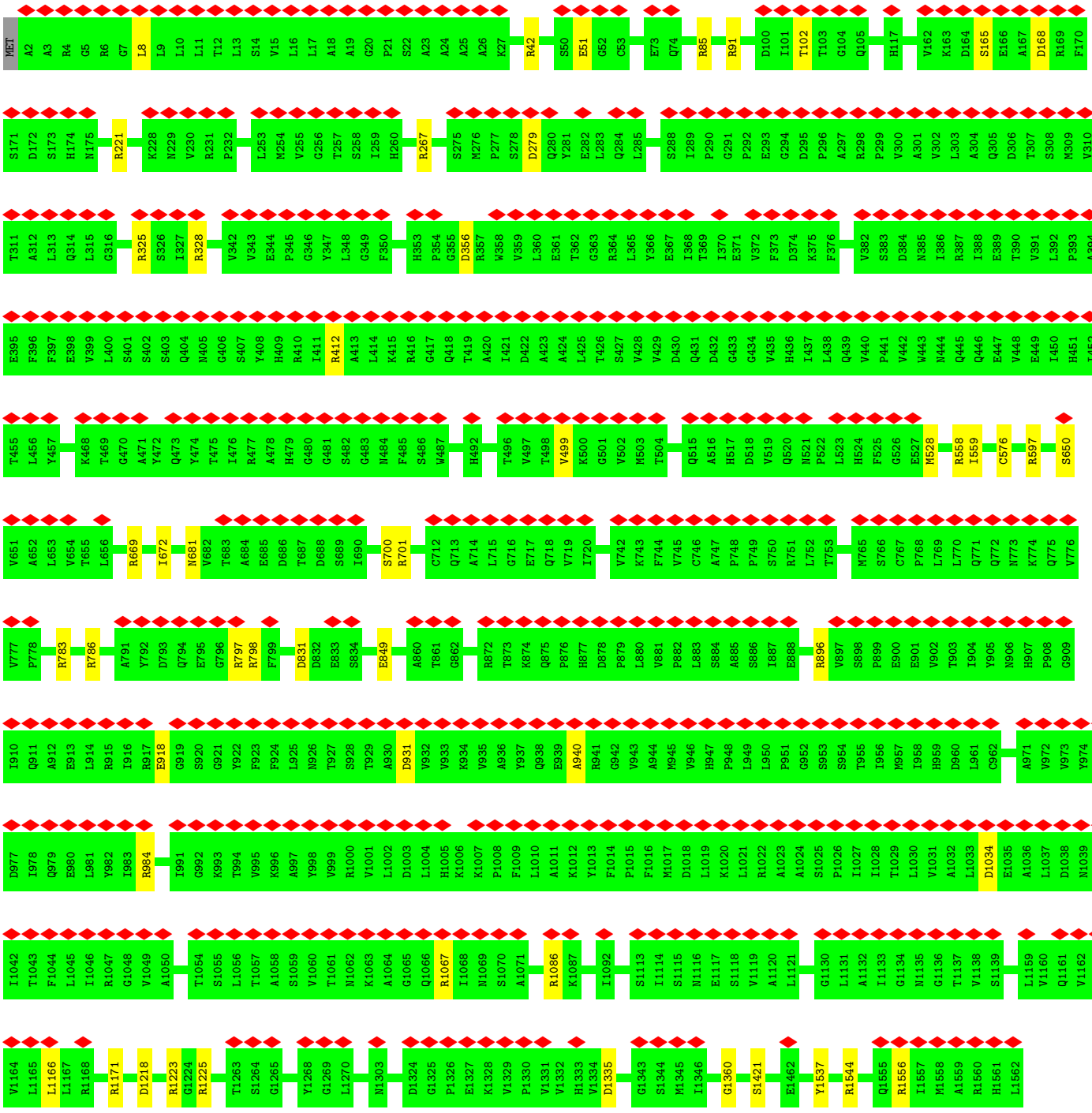
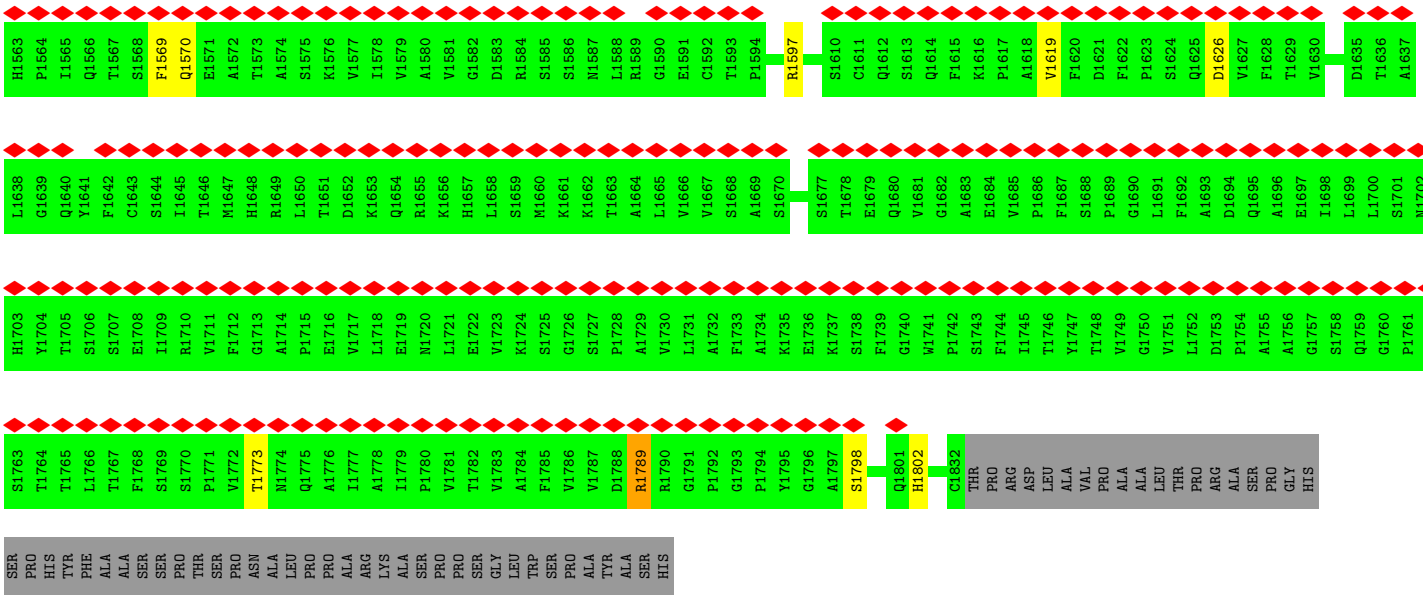


• Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 13:







• Molecule 2: Nuclear pore membrane glycoprotein 210

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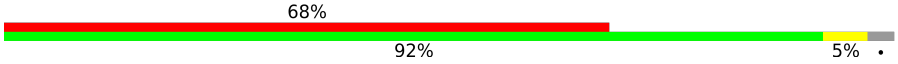

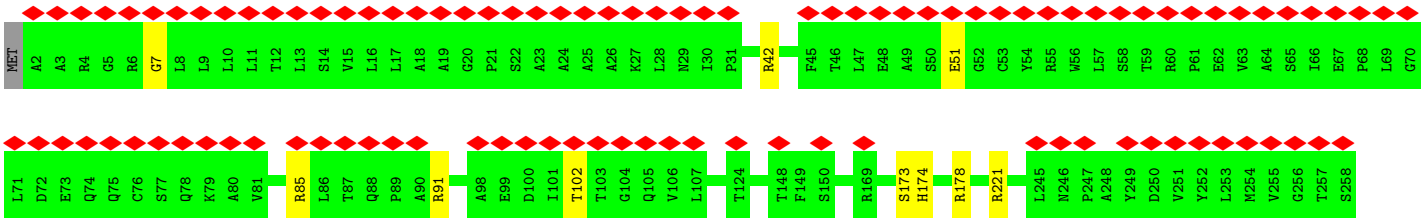

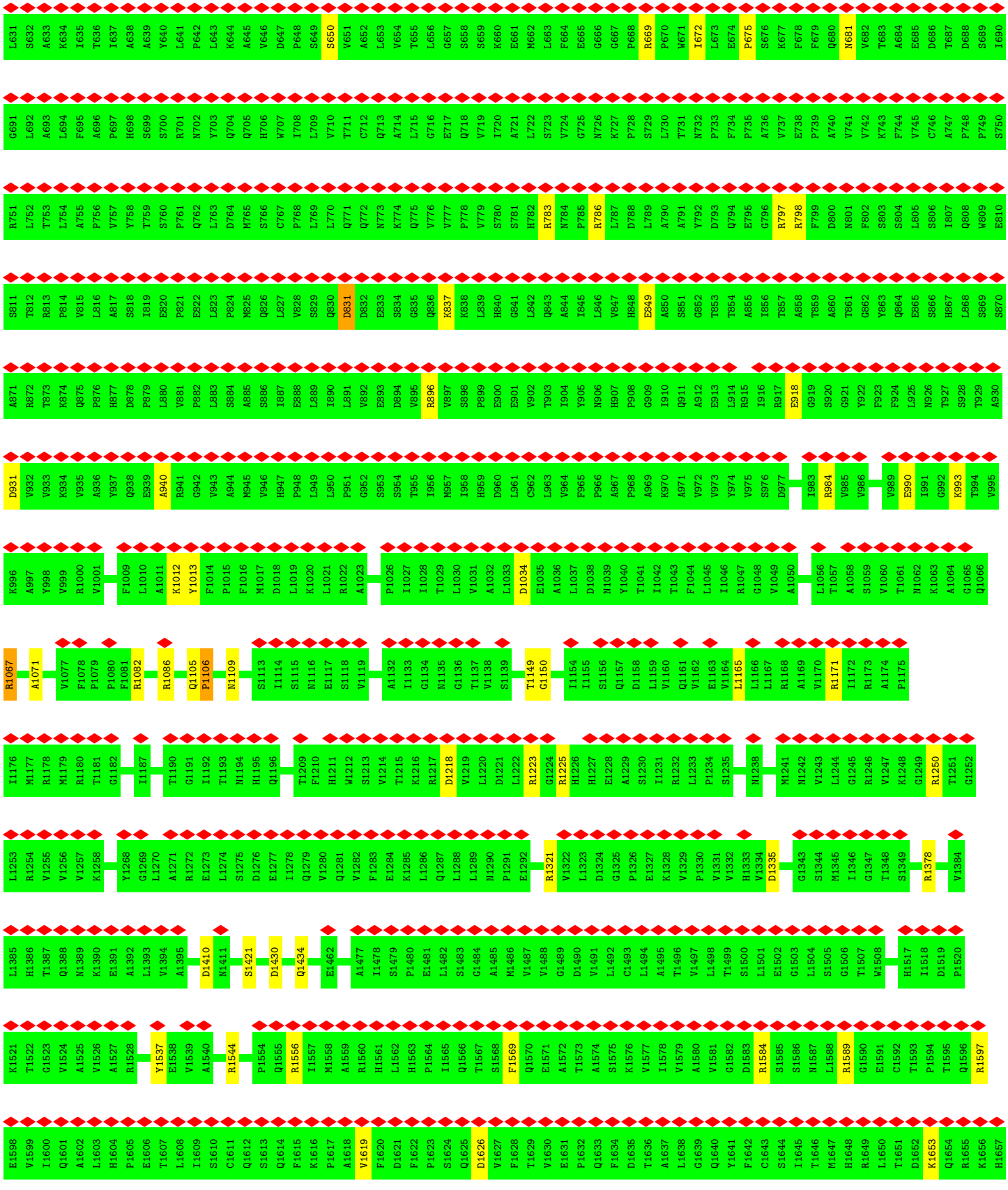
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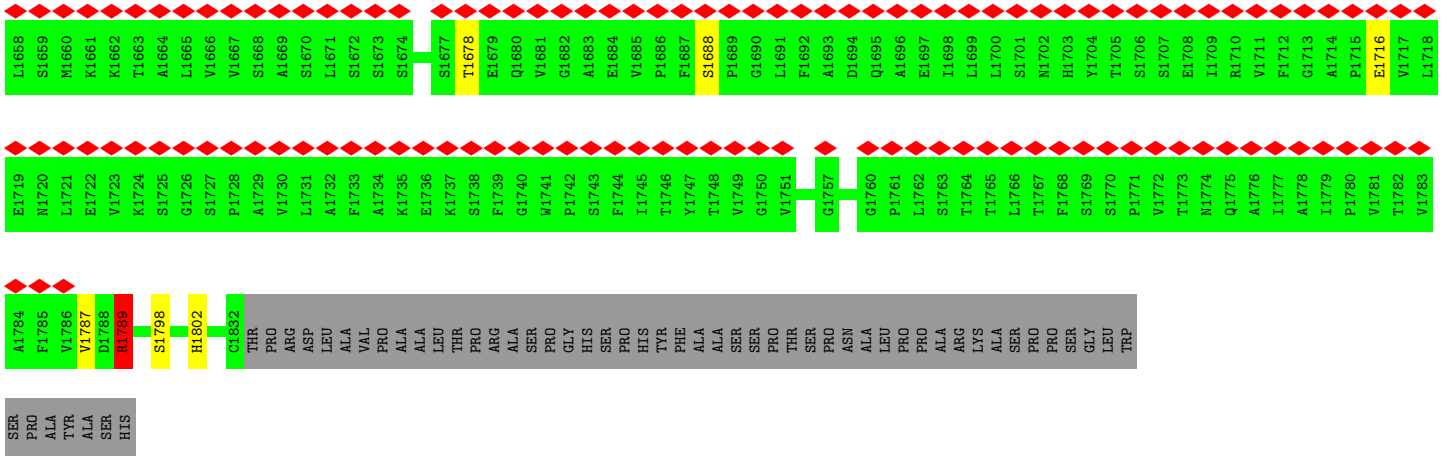
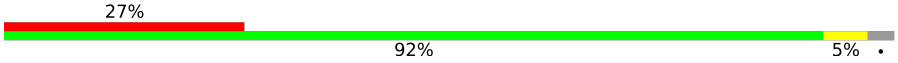
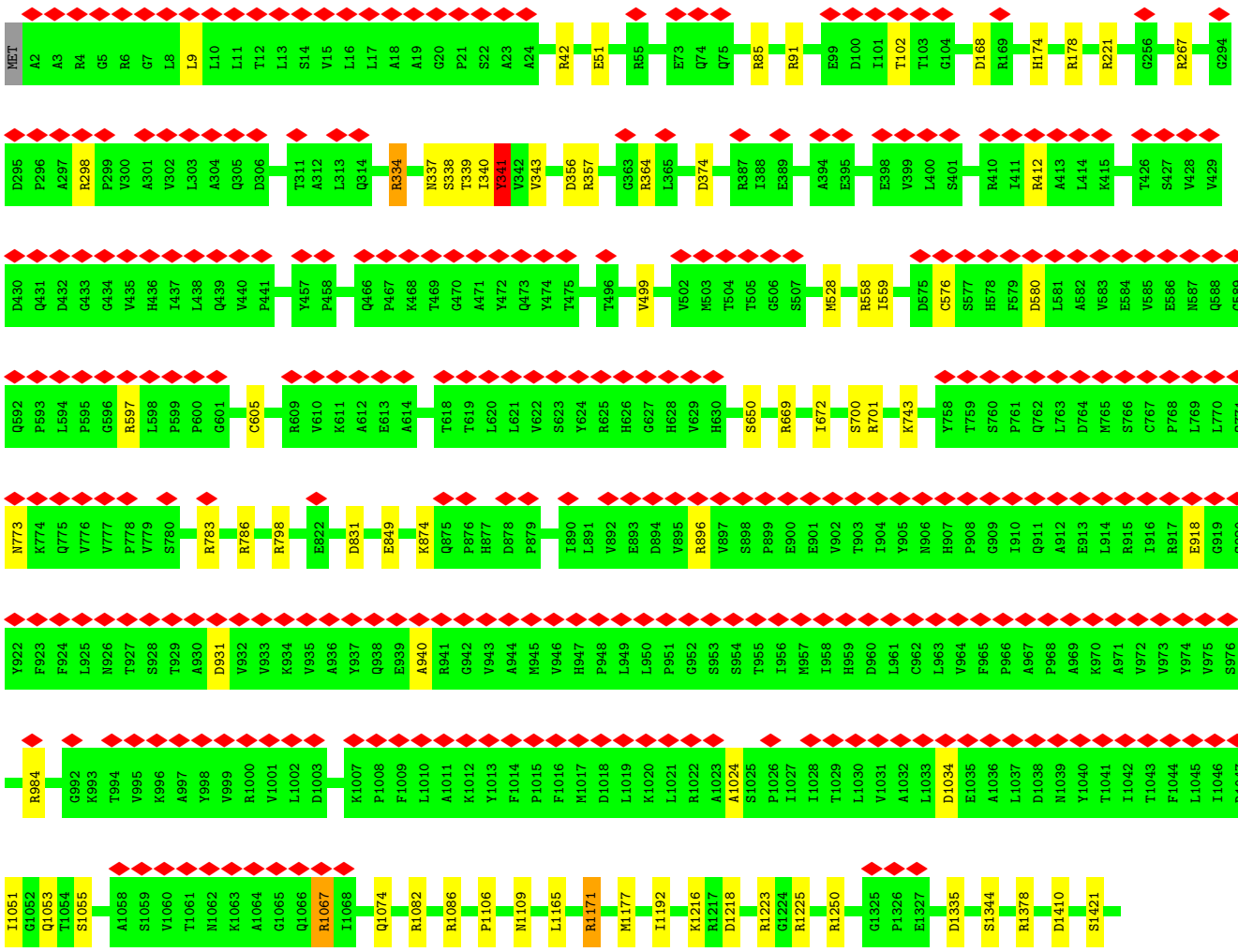
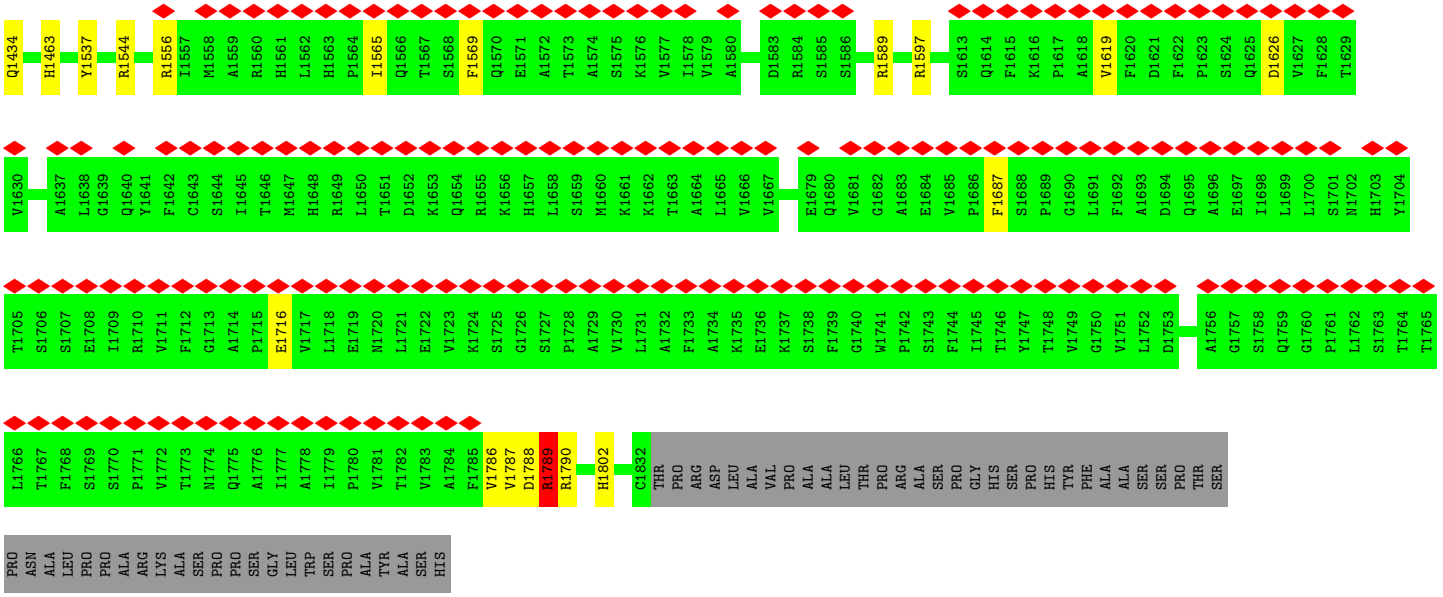


• Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 15:

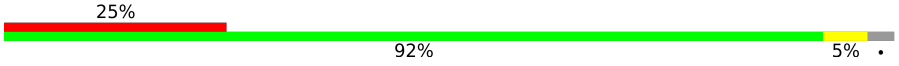


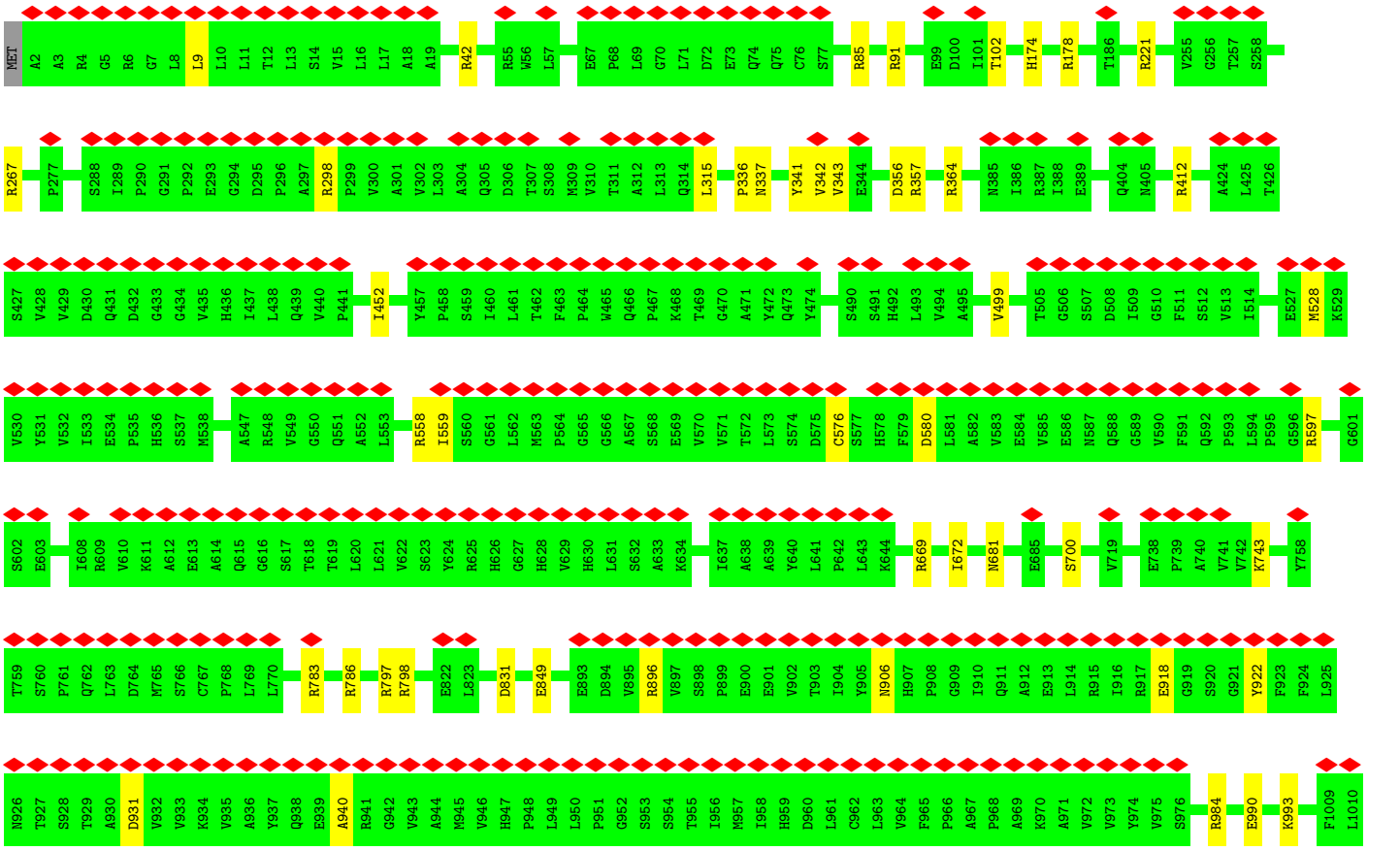


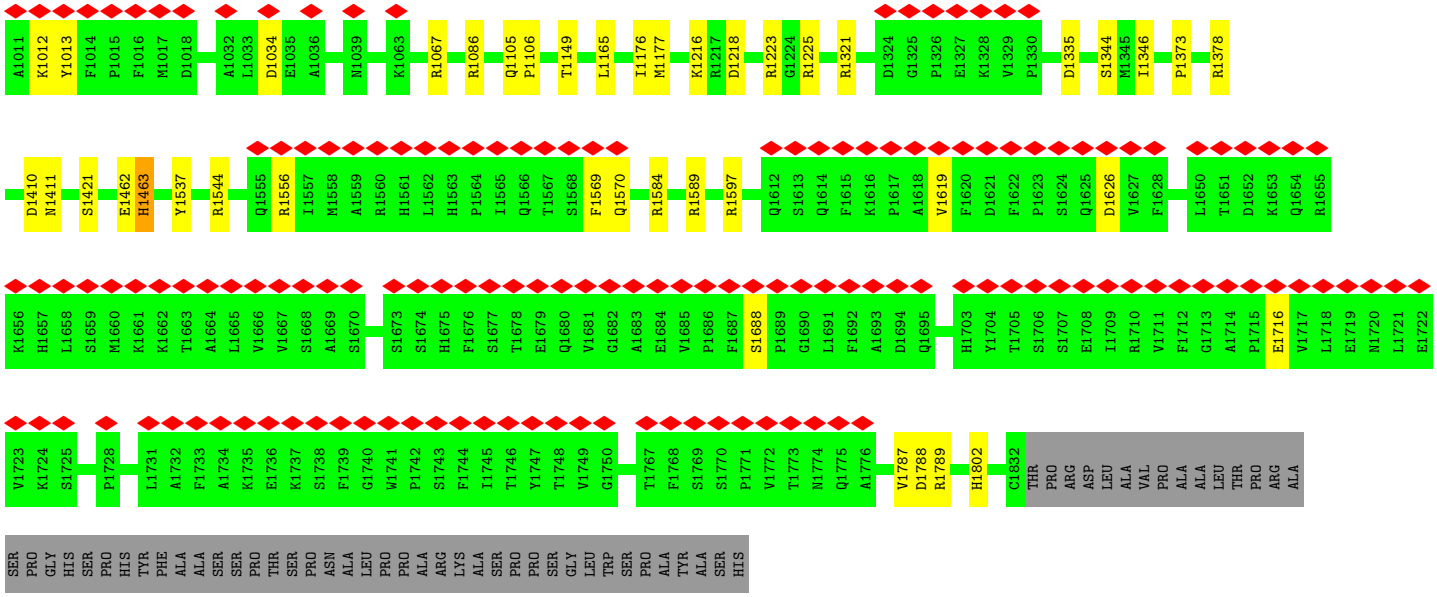


• Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 16:

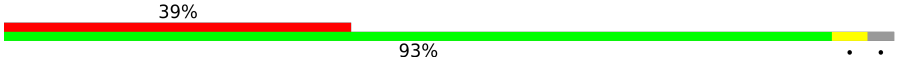


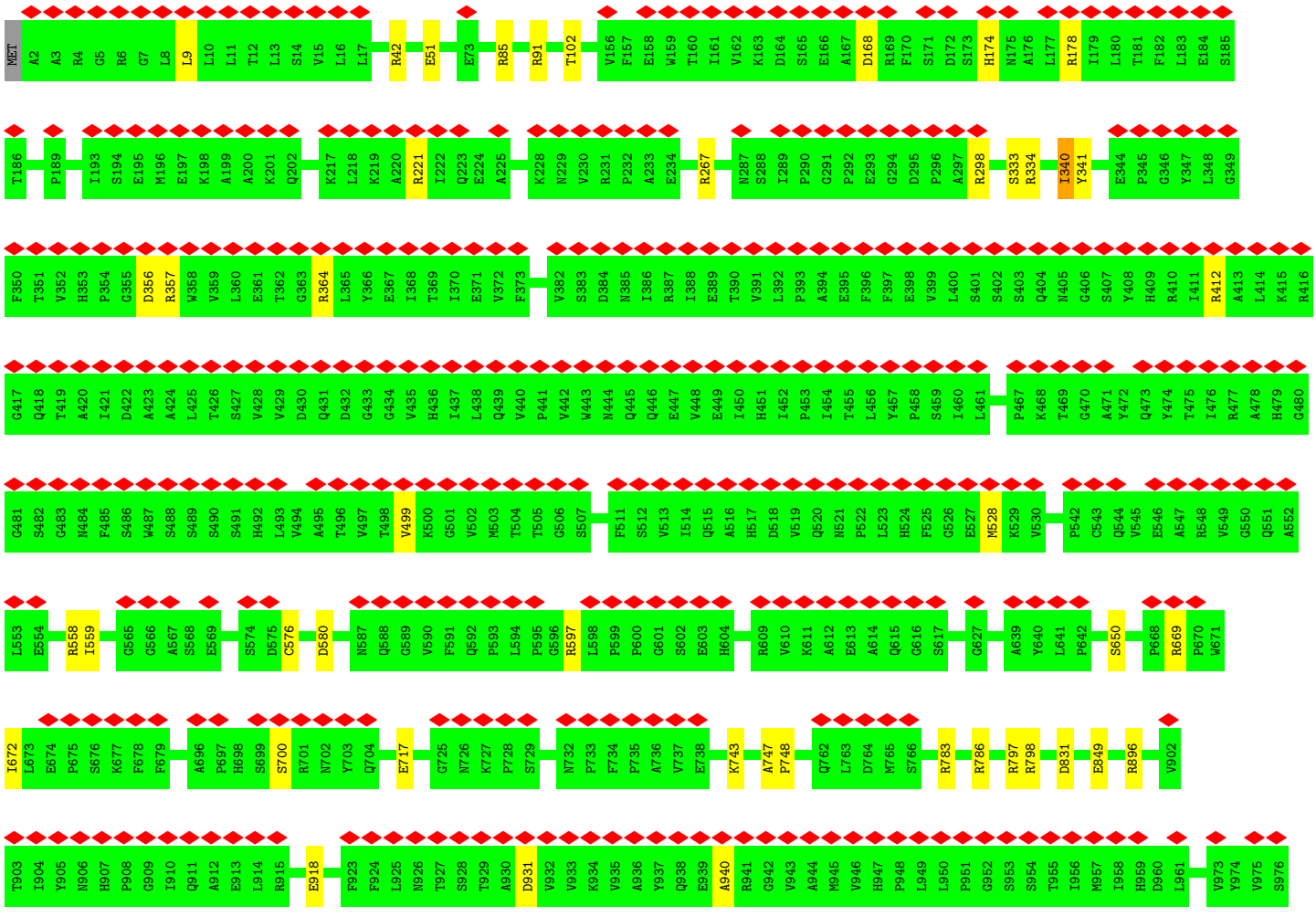


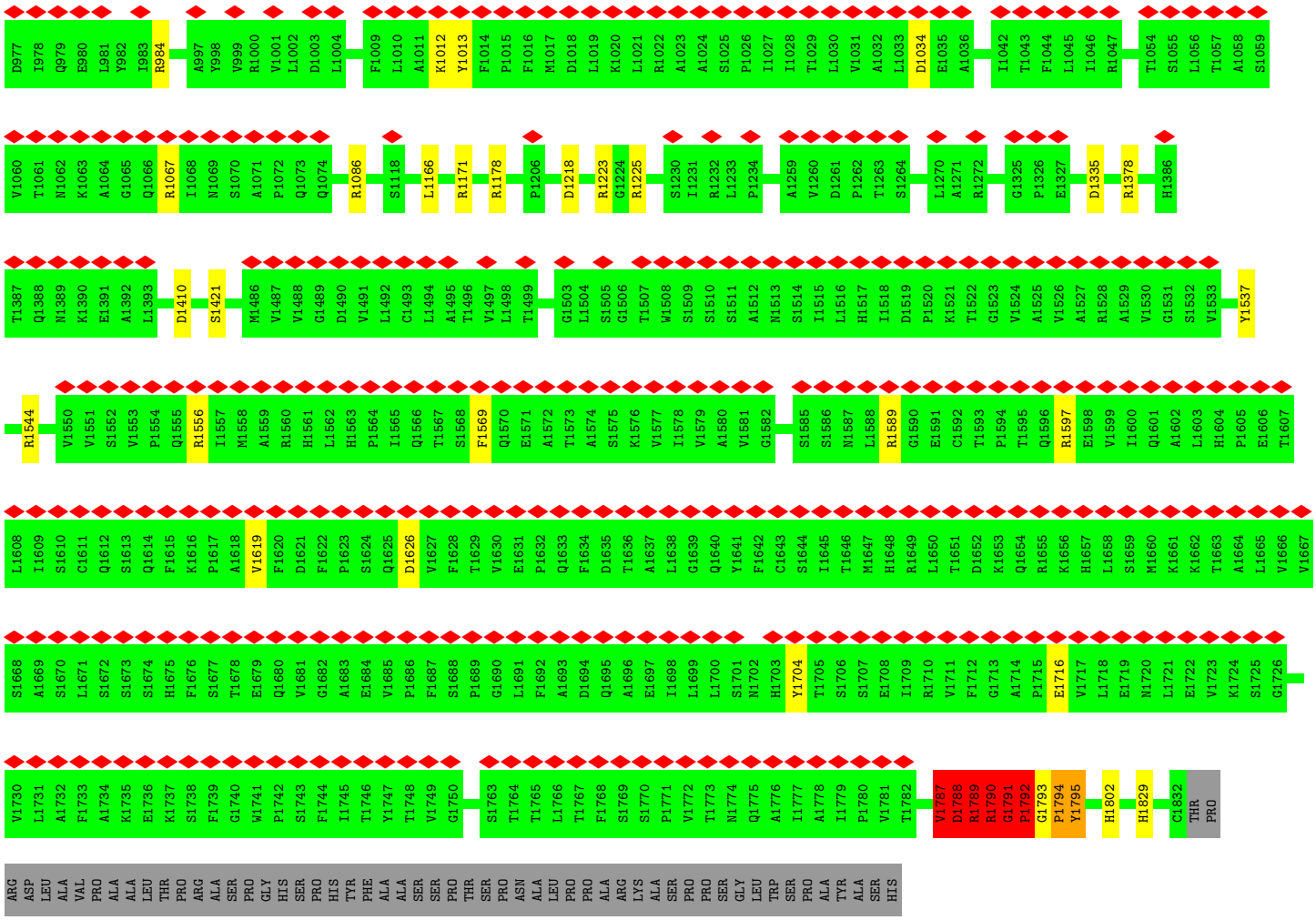


• Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 17:

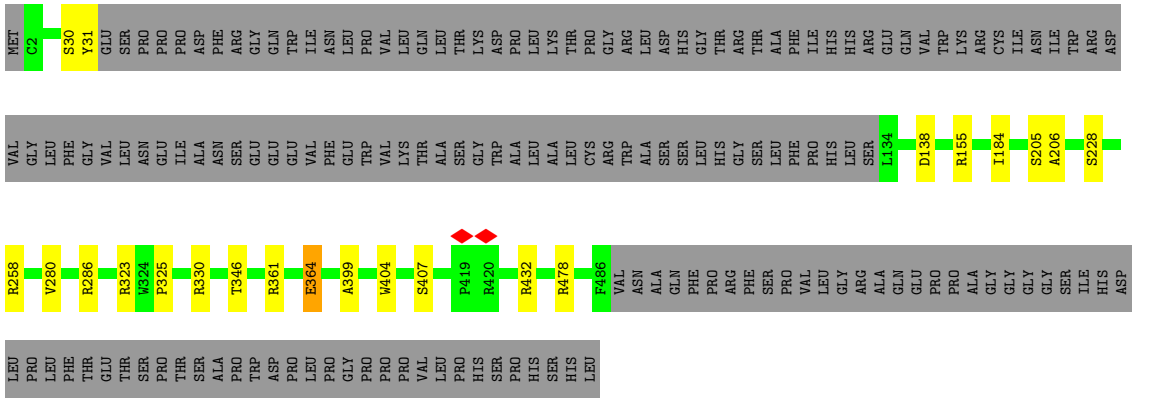






• Molecule 3: Aladin

Chain 40:



• Molecule 3: Aladin

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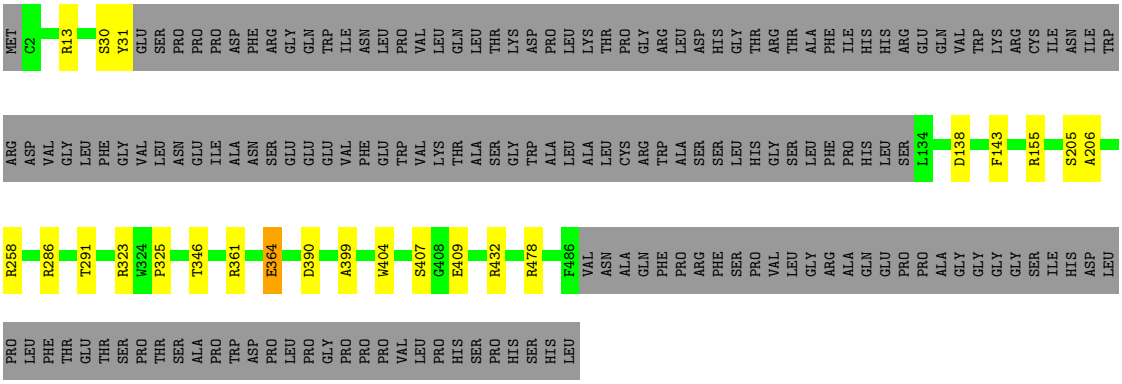
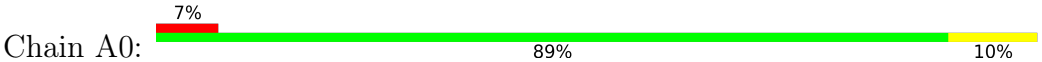
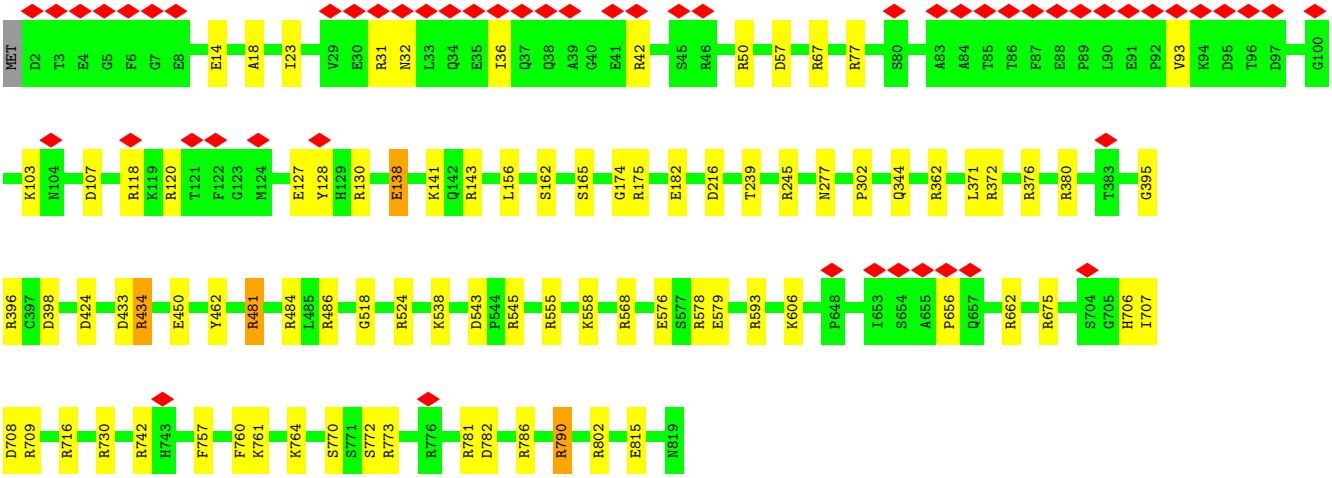
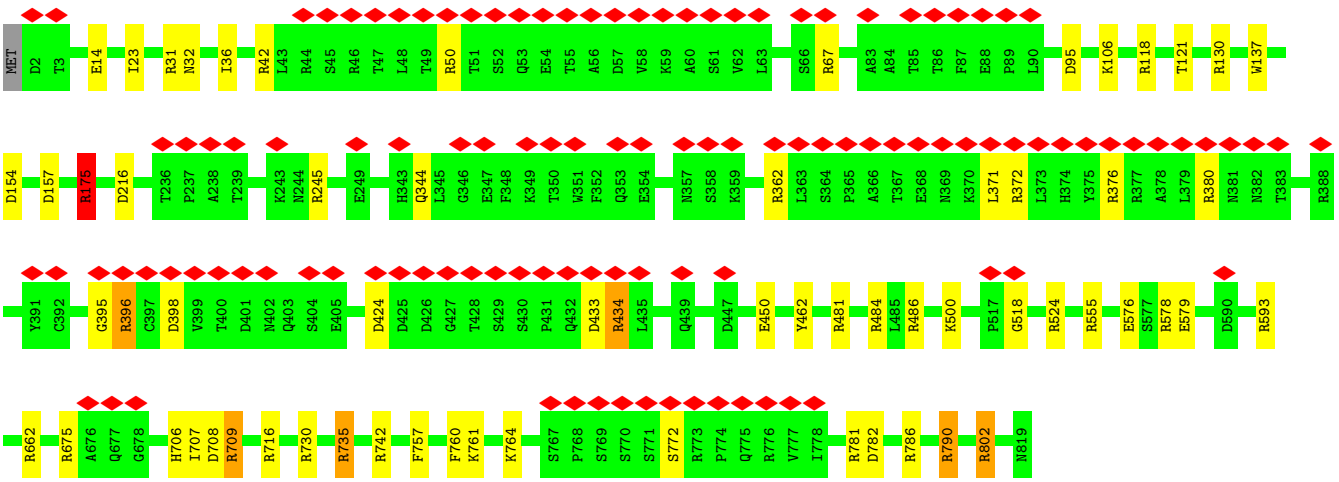


• Molecule 4: Nuclear pore complex protein Nup93



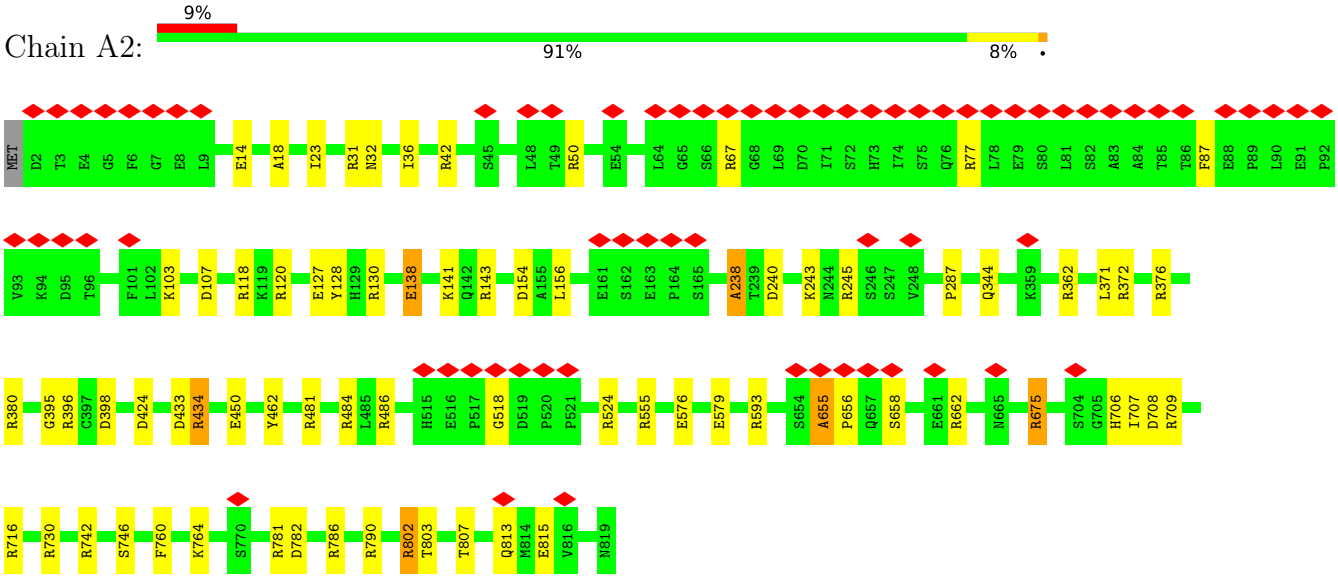


• Molecule 4: Nuclear pore complex protein Nup93



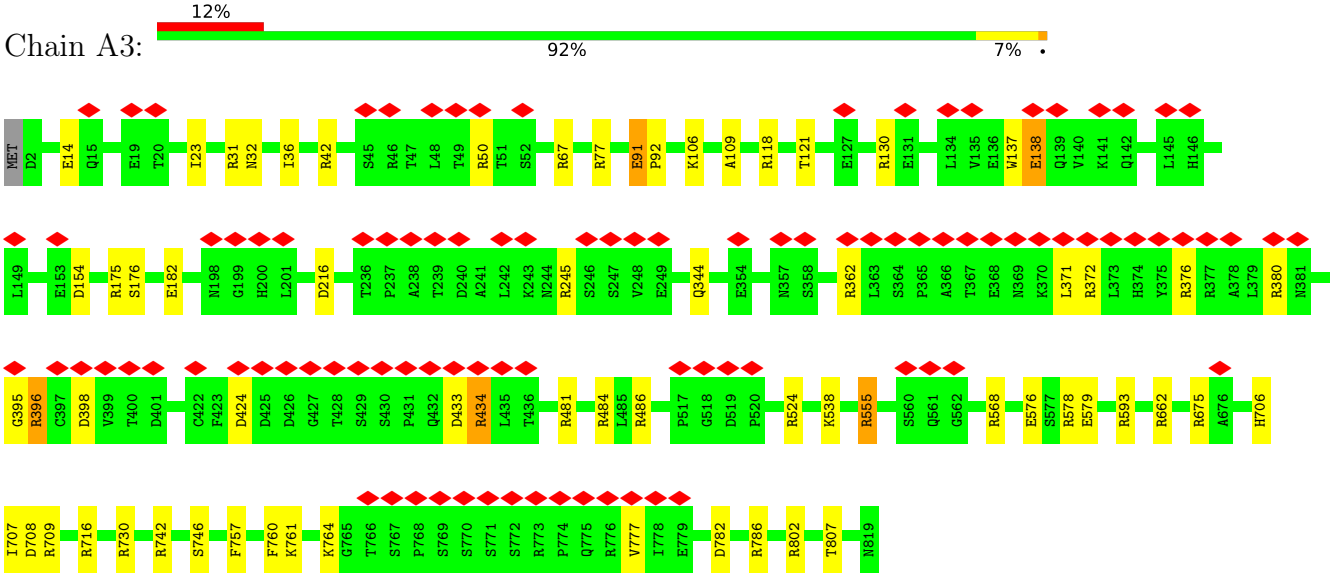
• Molecule 4: Nuclear pore complex protein Nup93

Chain A2:



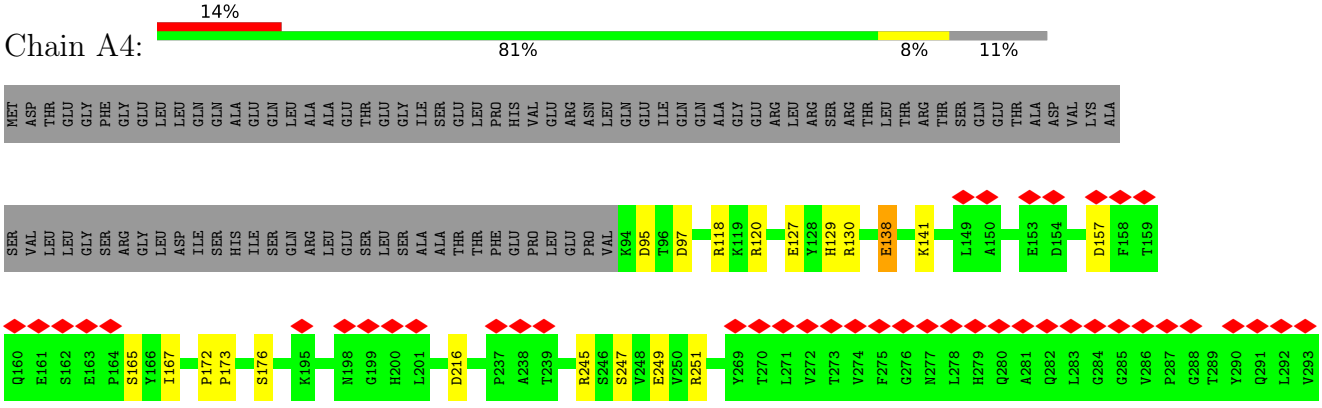
• Molecule 4: Nuclear pore complex protein Nup93

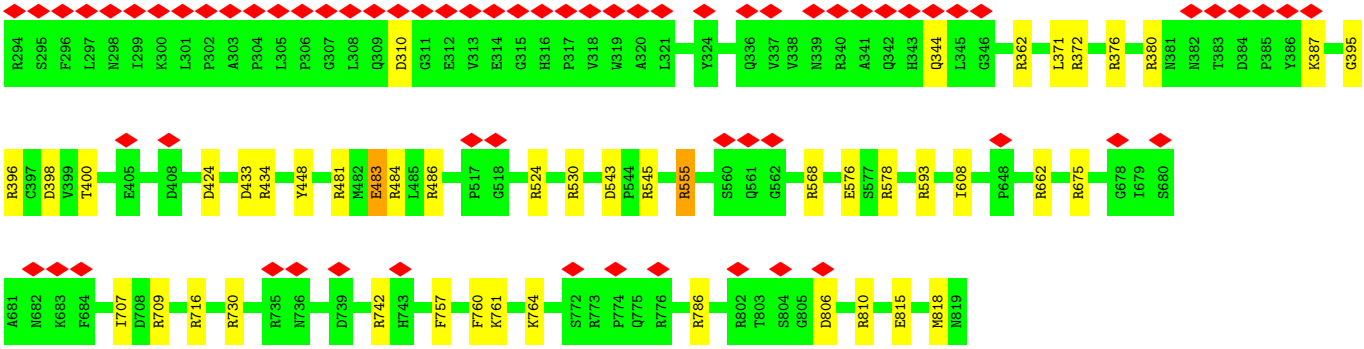
Chain A3:



• Molecule 4: Nuclear pore complex protein Nup93

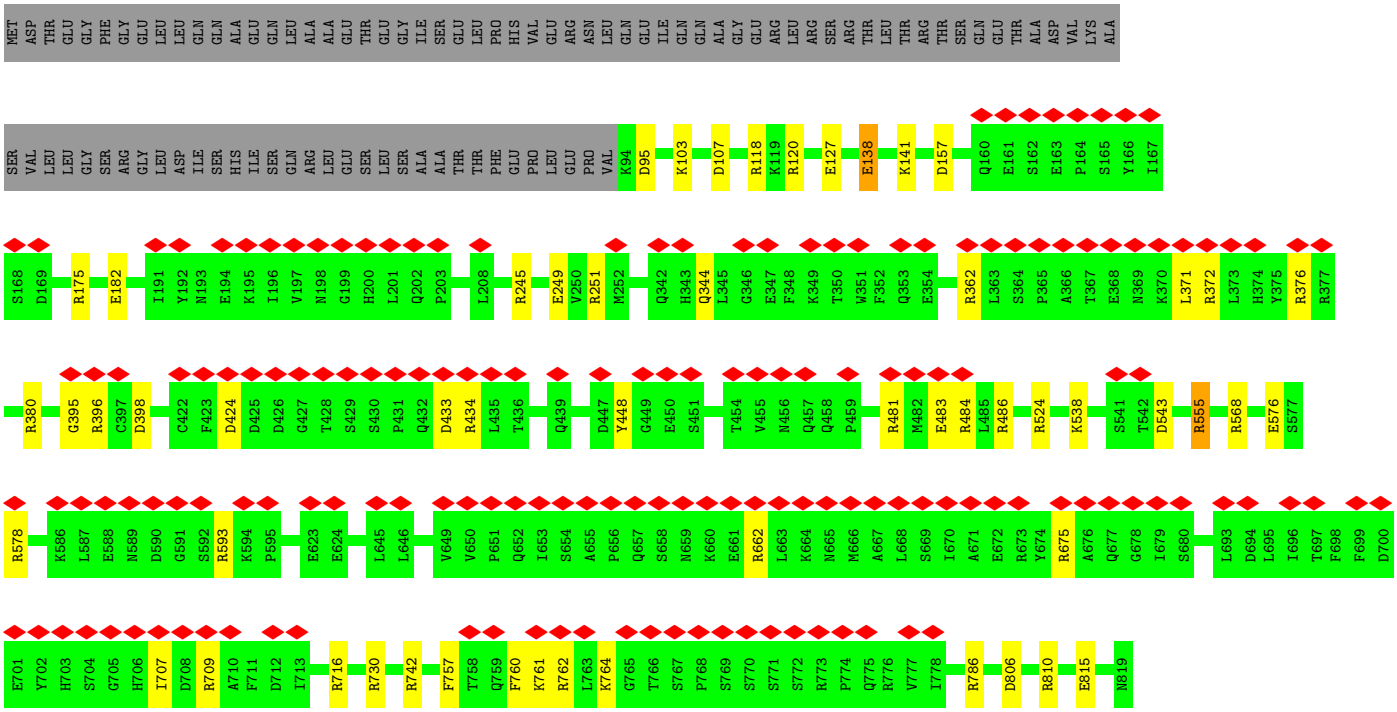
Chain A4:





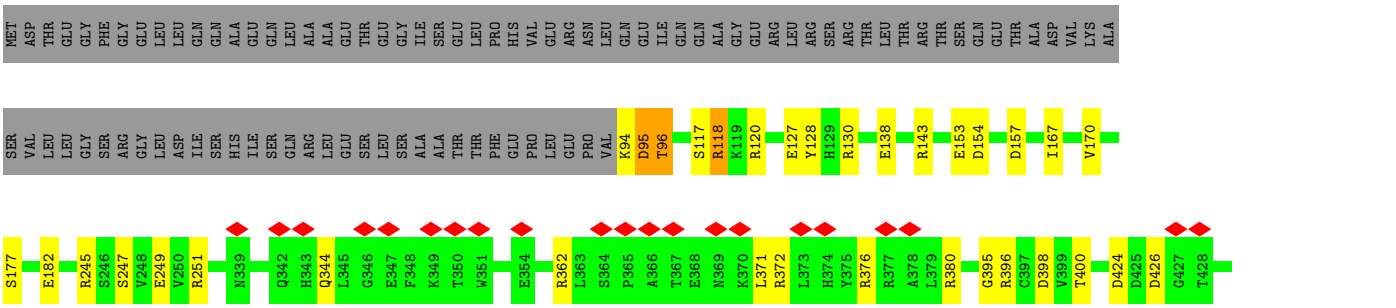
• Molecule 4: Nuclear pore complex protein Nup93

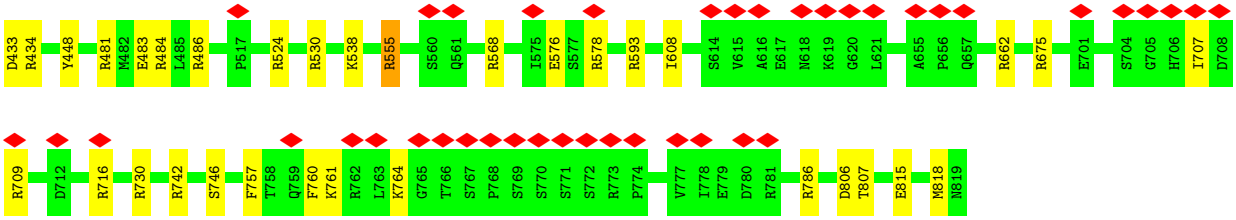
Chain A5:



• Molecule 4: Nuclear pore complex protein Nup93

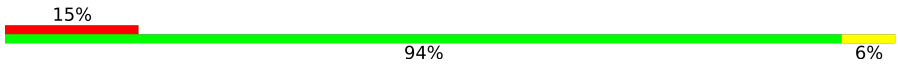
Chain A6:

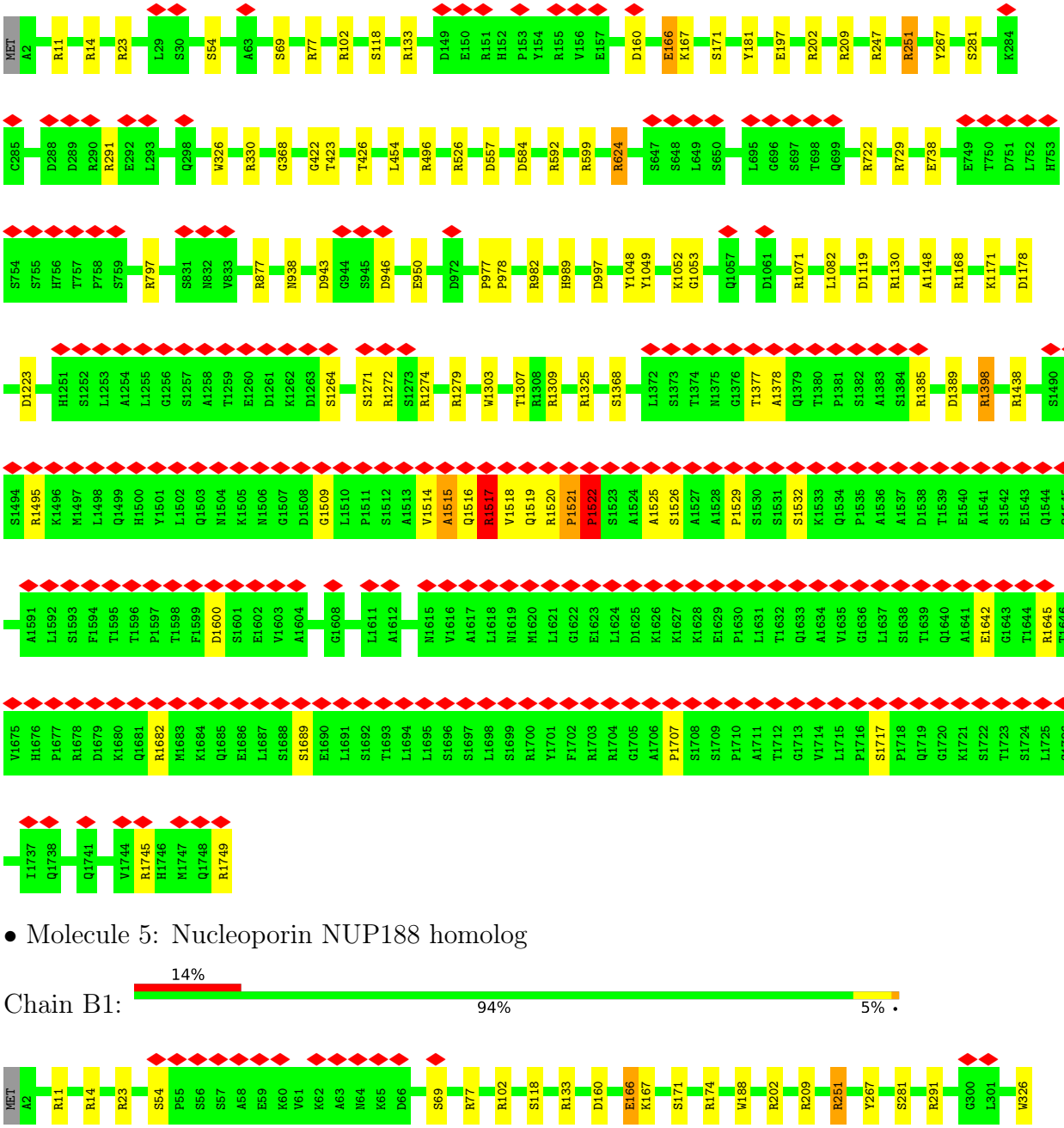




• Molecule 5: Nucleoporin NUP188 homolog

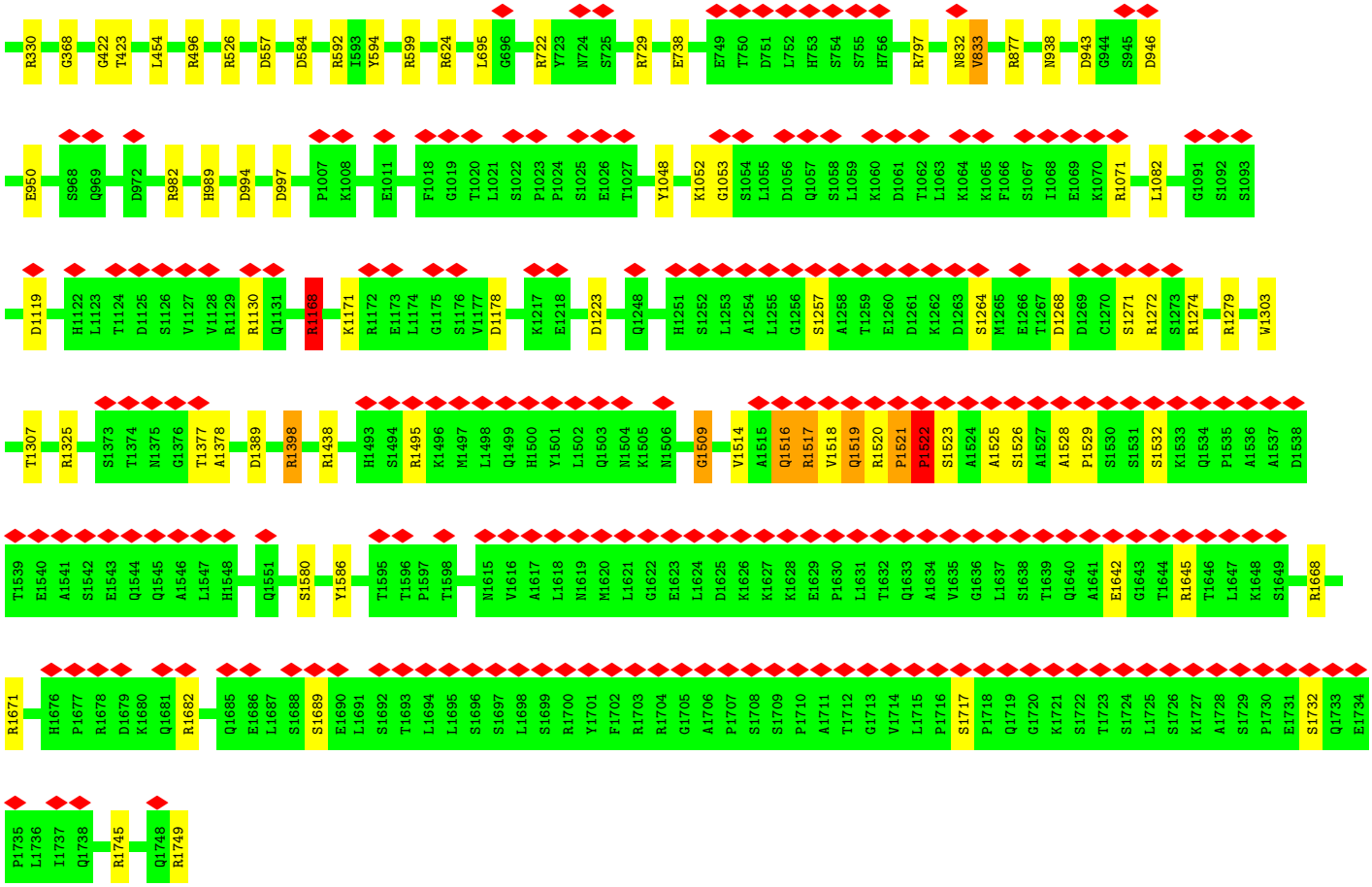
Chain B0:





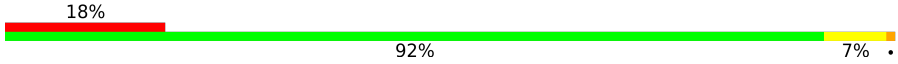
• Molecule 5: Nucleoporin NUP188 homolog

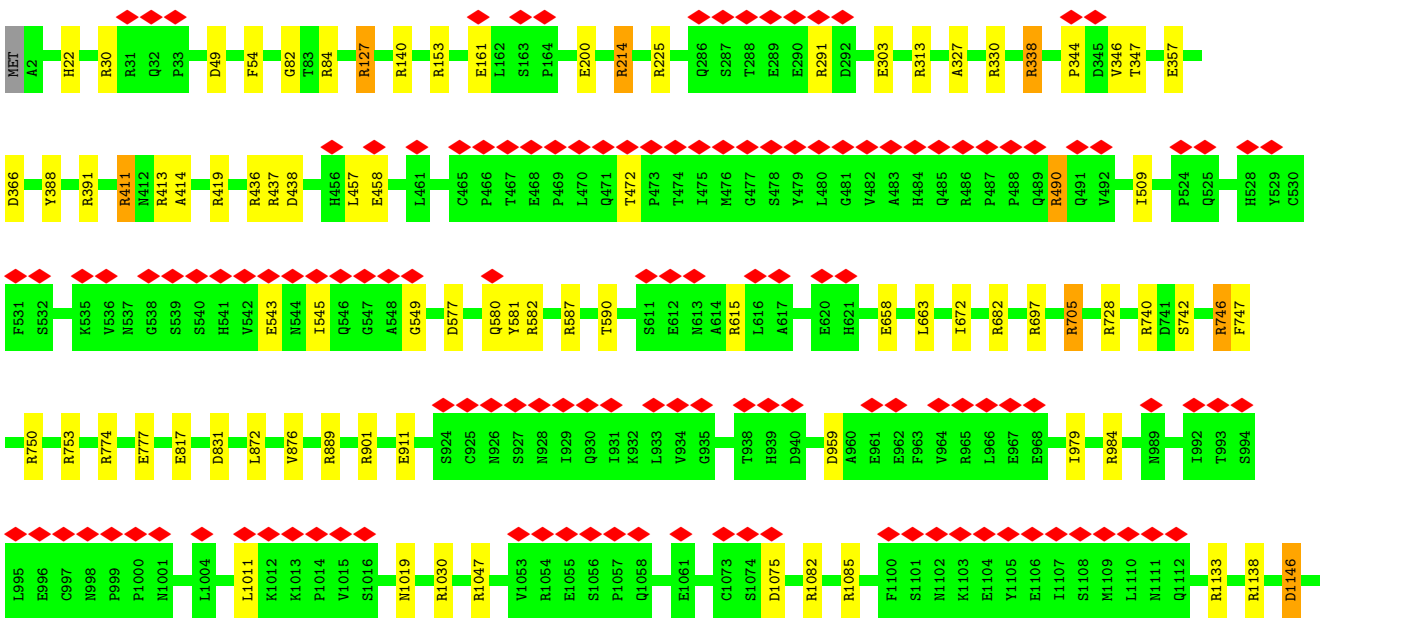
Chain B1:

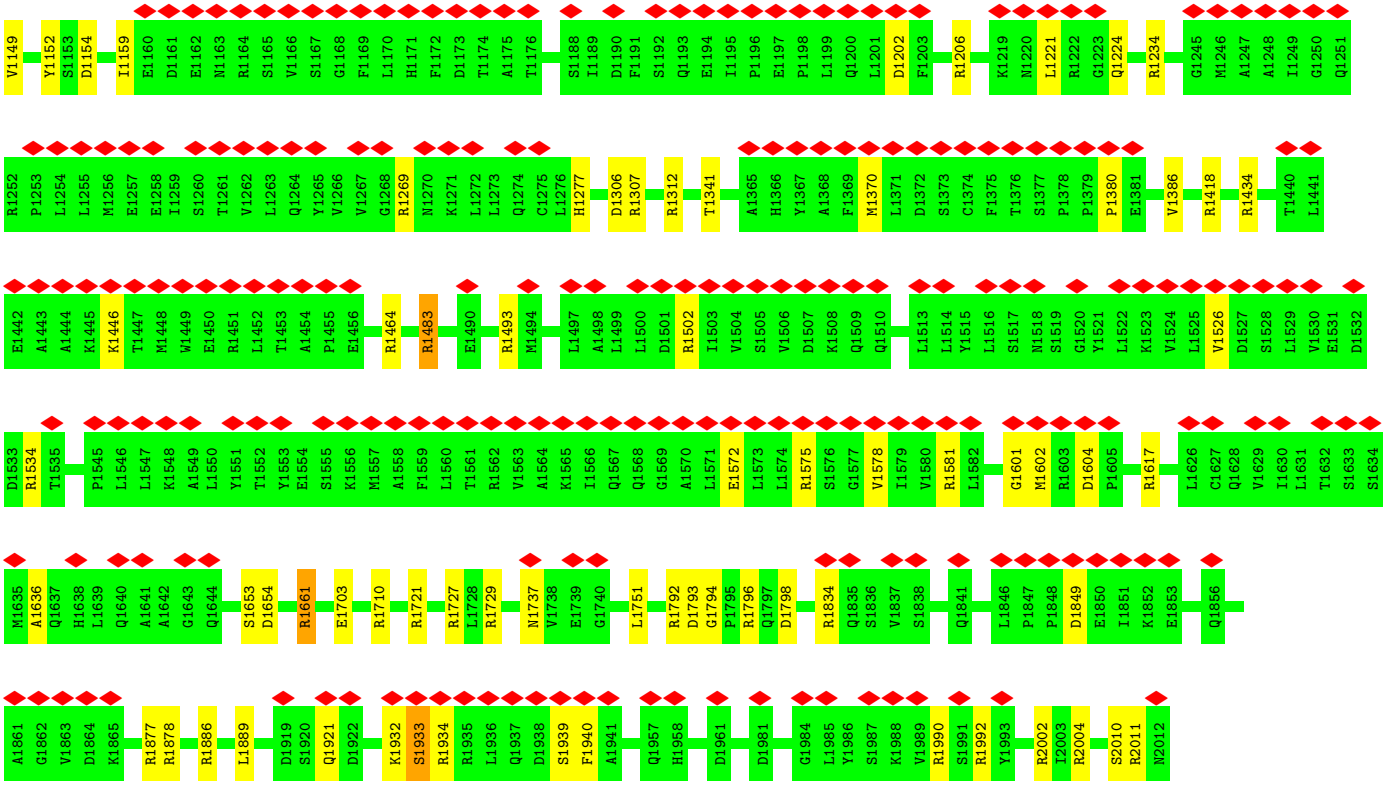


• Molecule 6: Nuclear pore complex protein Nup205

Chain C0:

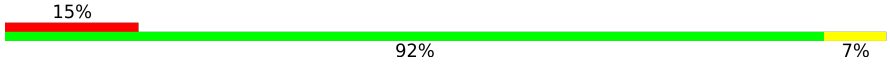


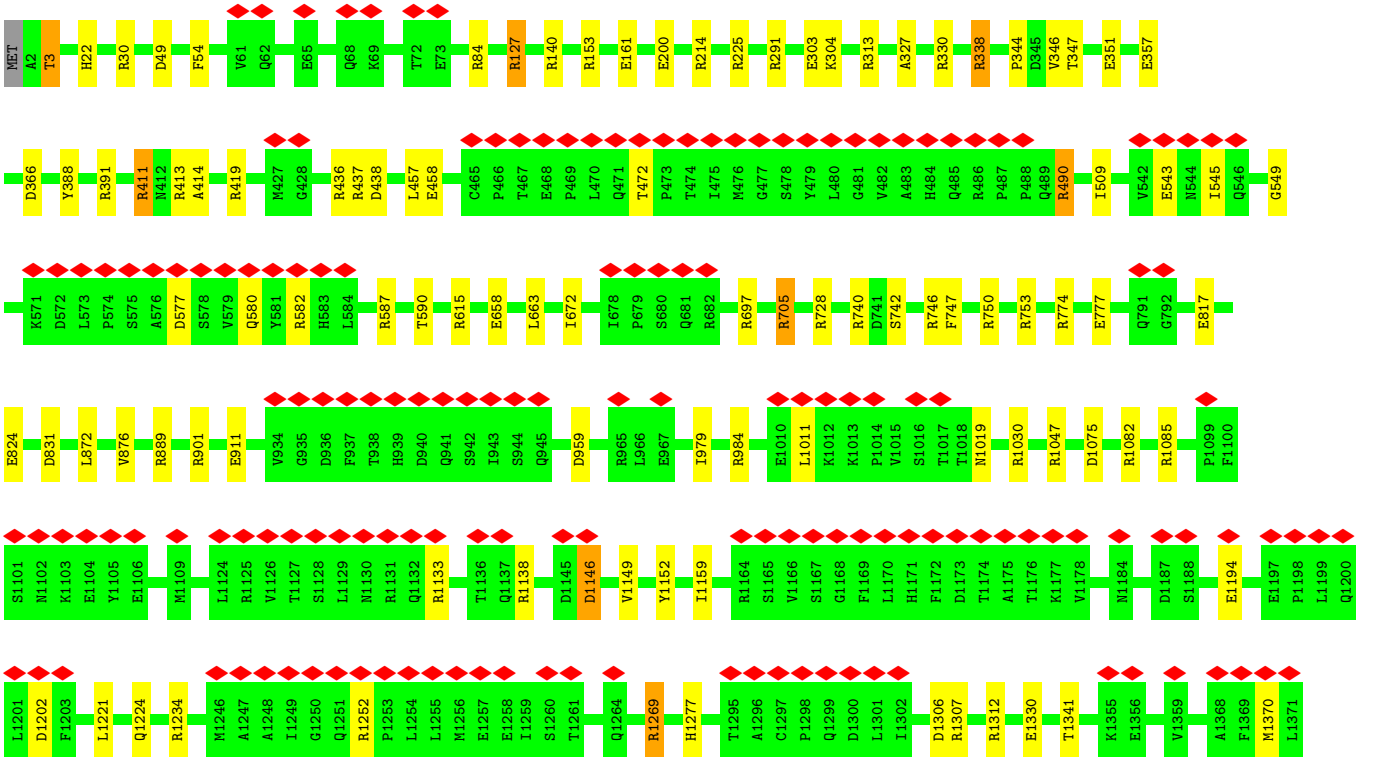


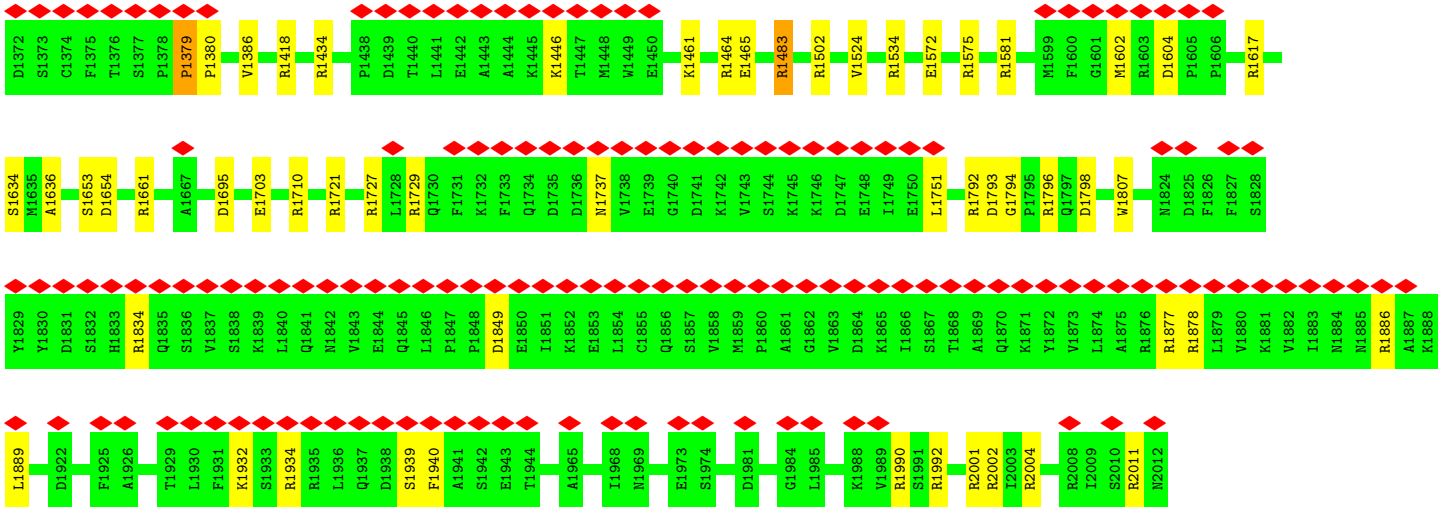


• Molecule 6: Nuclear pore complex protein Nup205

Chain C1:

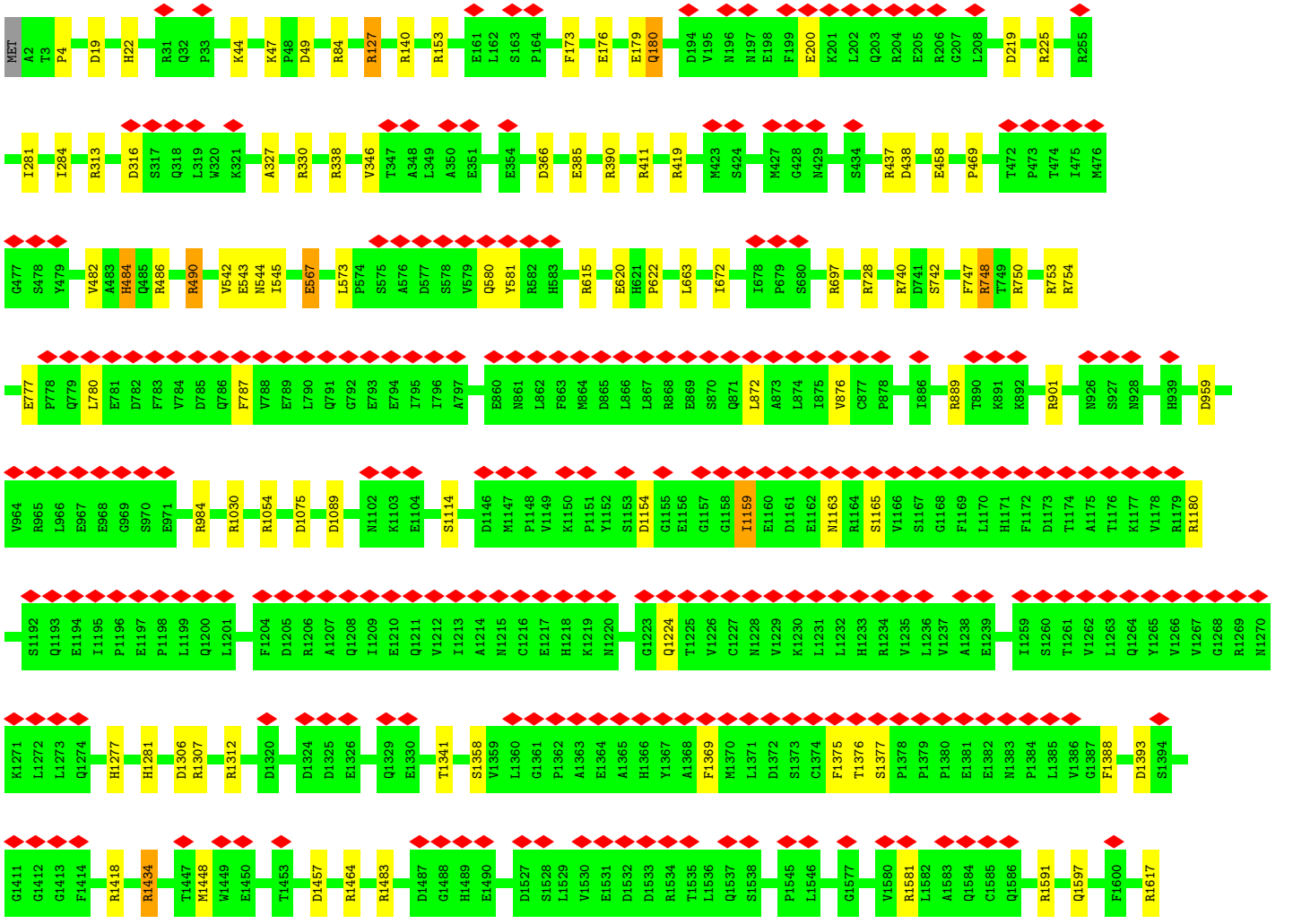


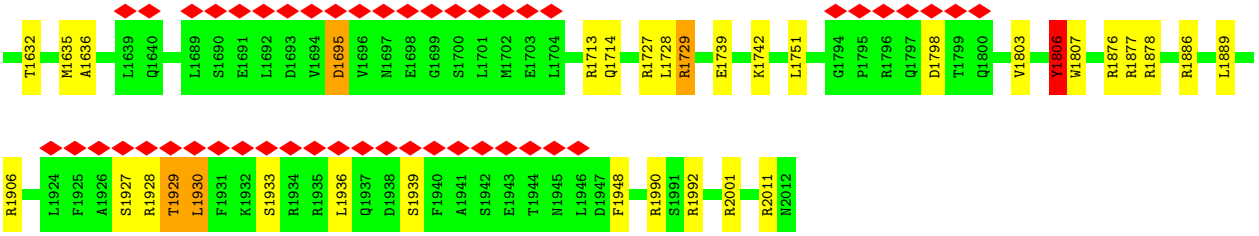




• Molecule 6: Nuclear pore complex protein Nup205

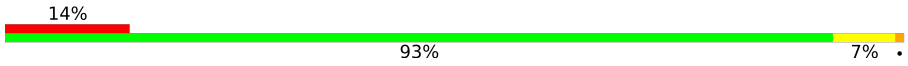
Chain C2:

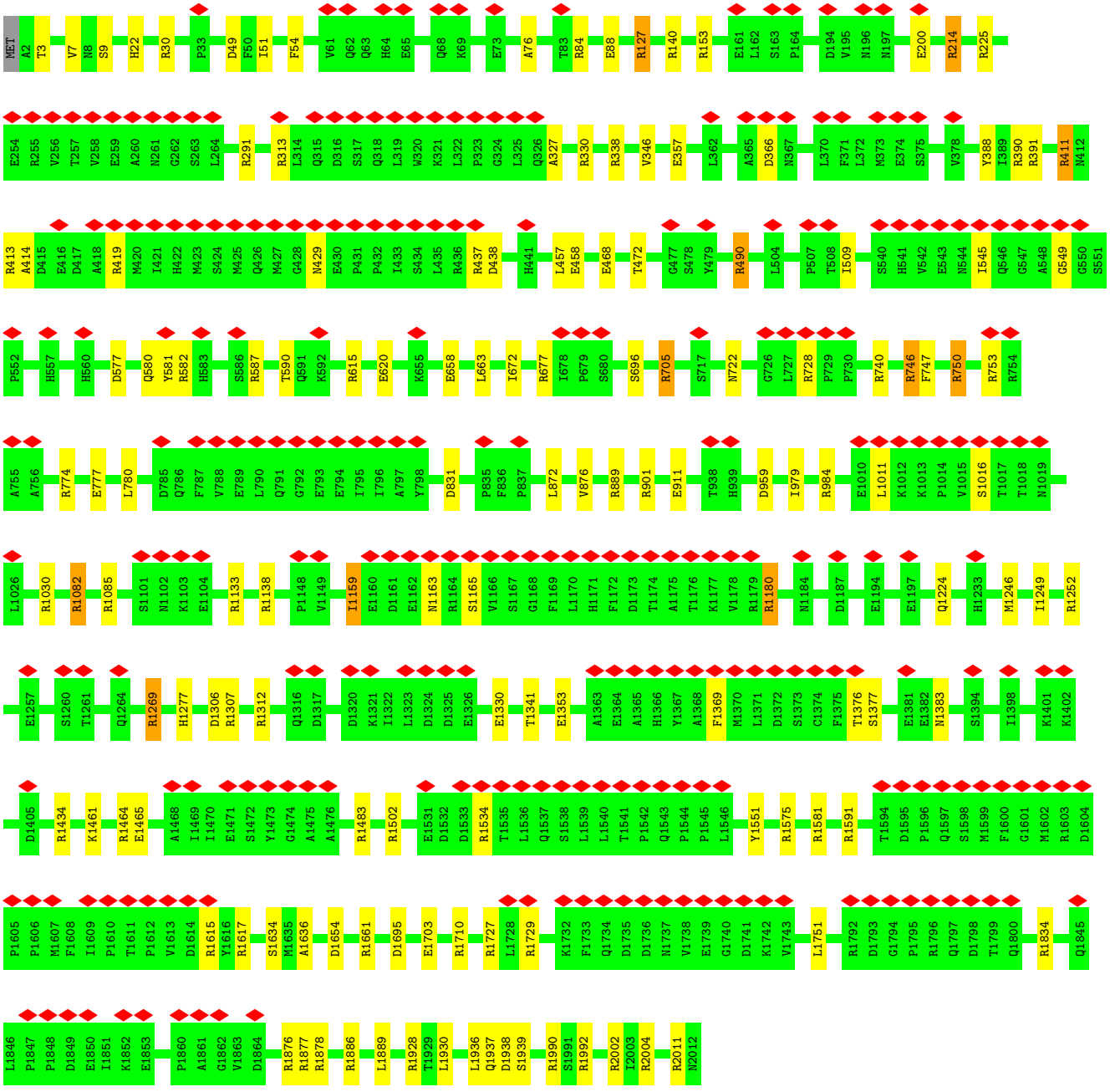




• Molecule 6: Nuclear pore complex protein Nup205

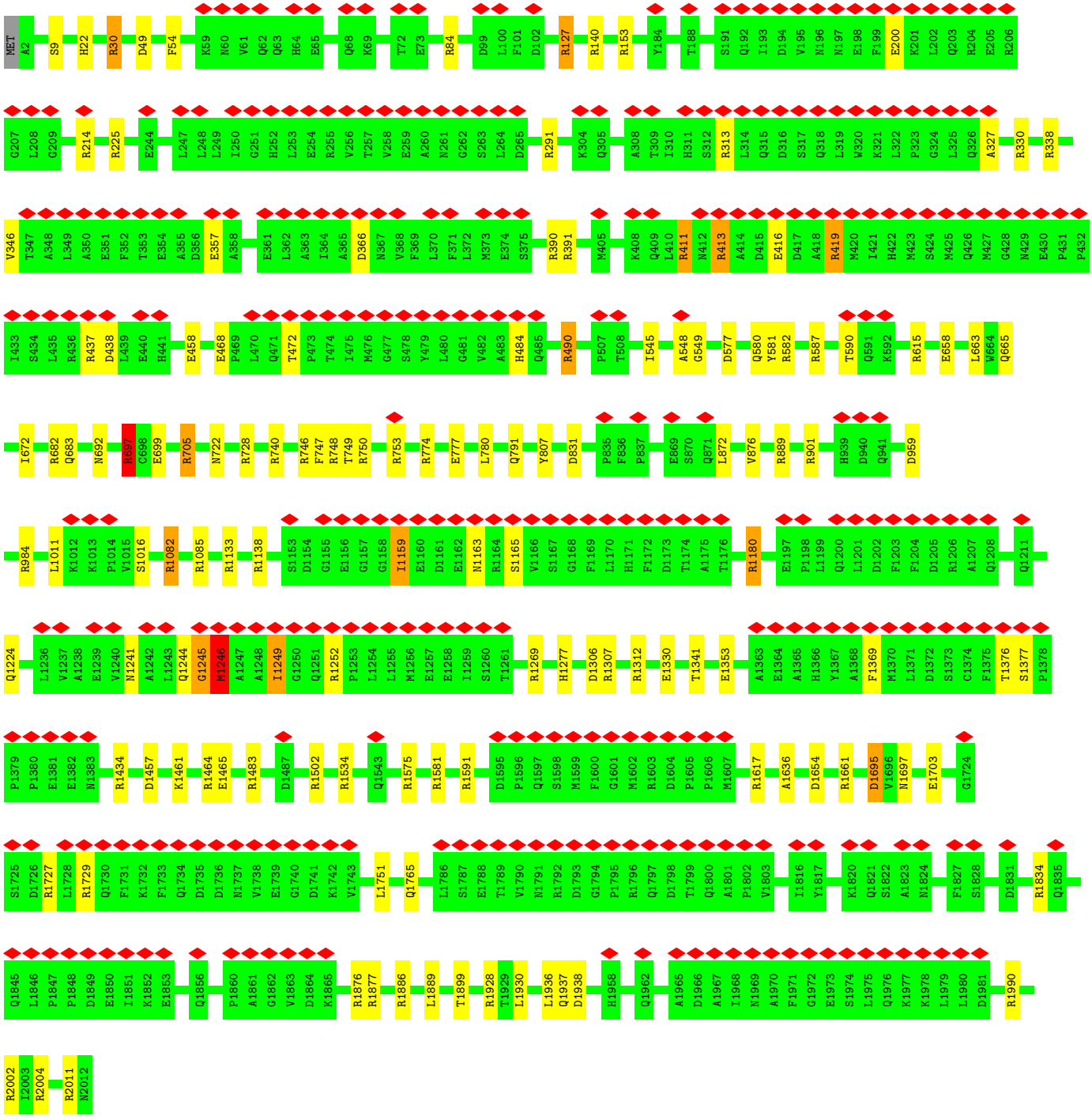
Chain C3:





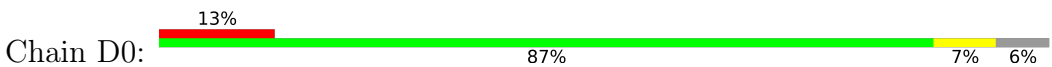
• Molecule 6: Nuclear pore complex protein Nup205

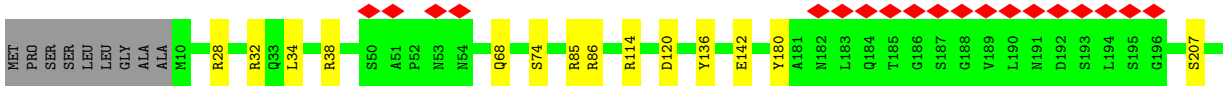
Chain C4:

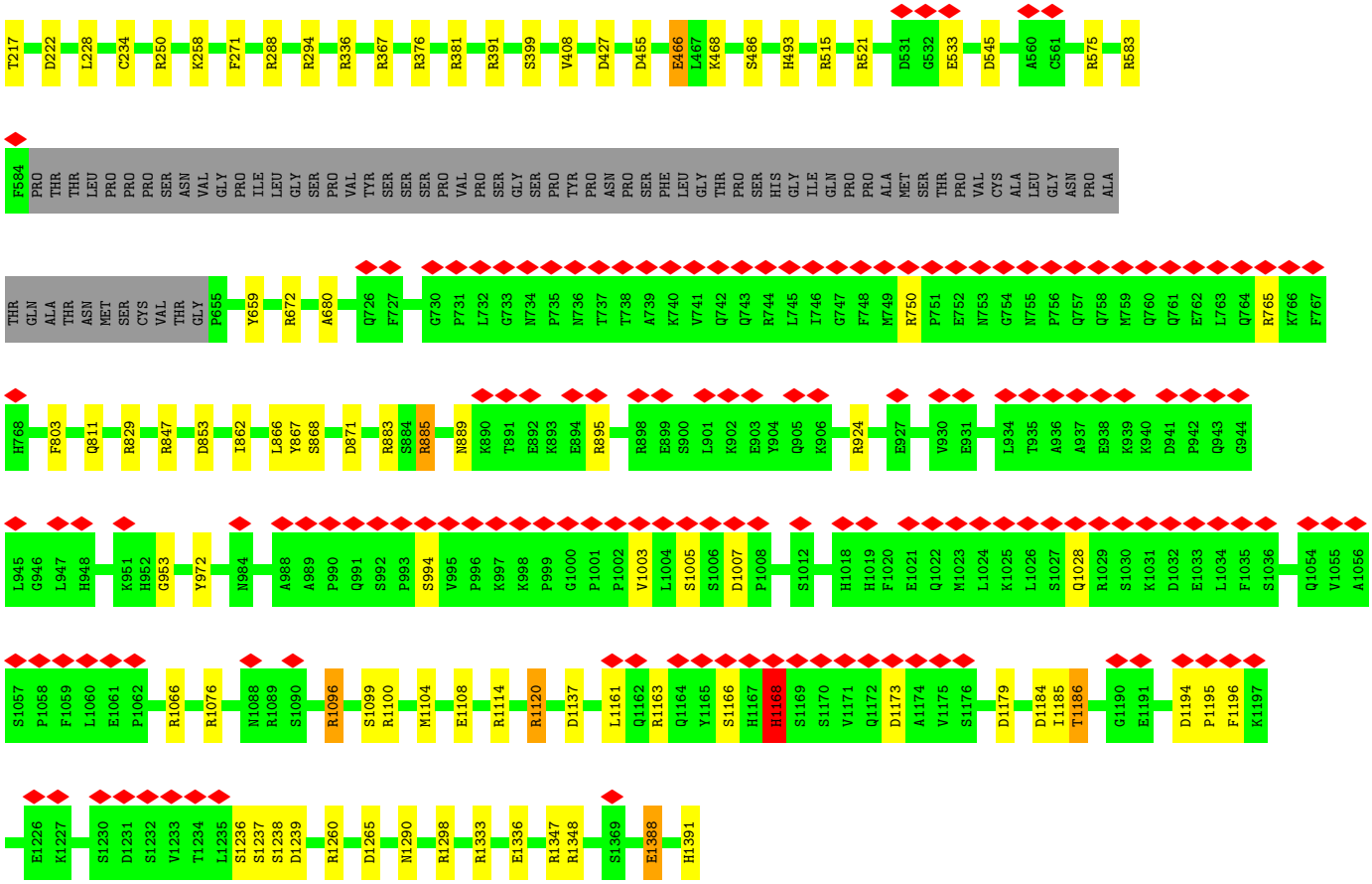


• Molecule 7: Nuclear pore complex protein Nup155

Chain D0:

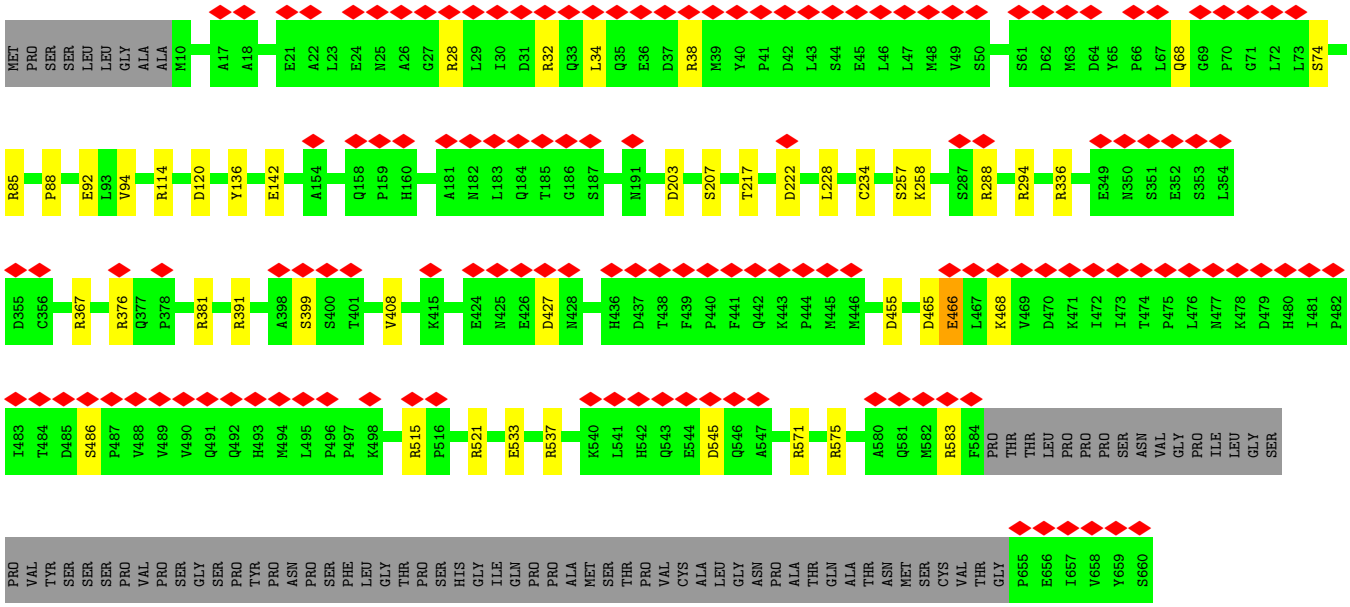


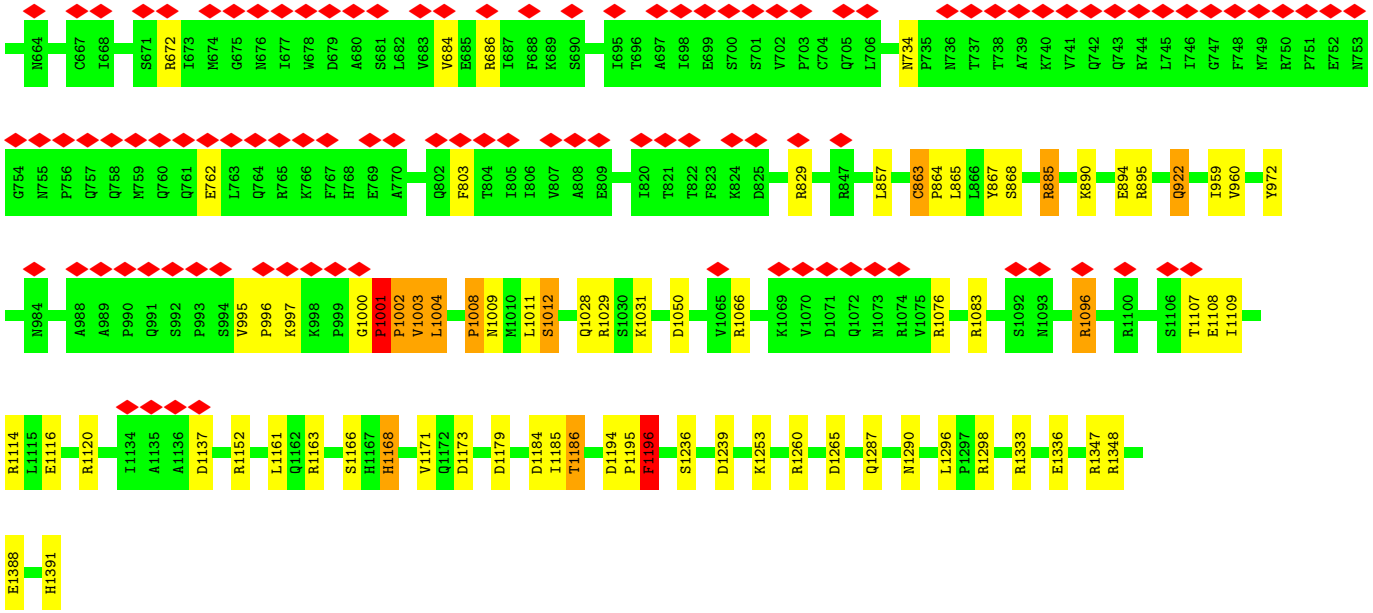




• Molecule 7: Nuclear pore complex protein Nup155

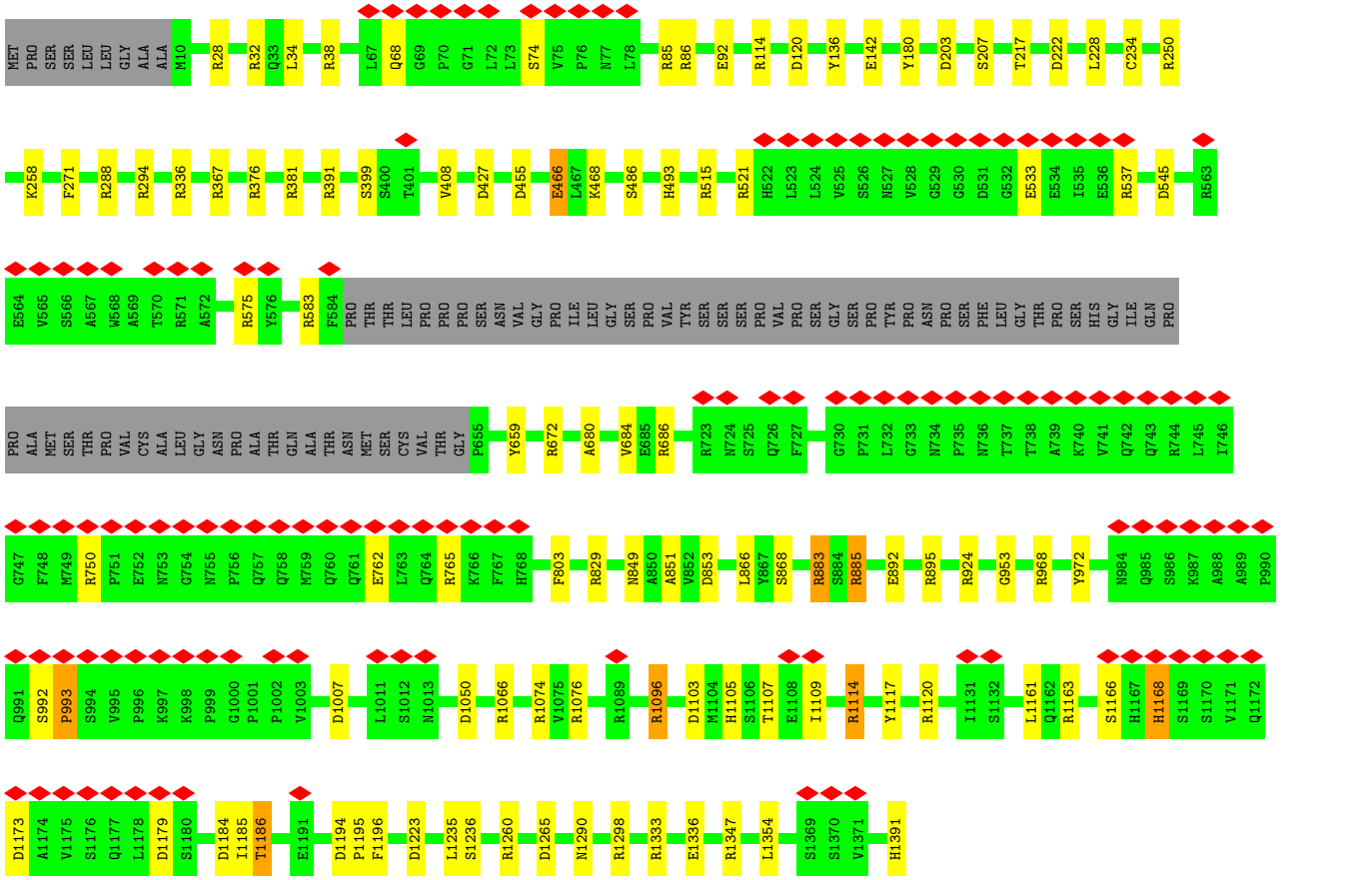
Chain D1:





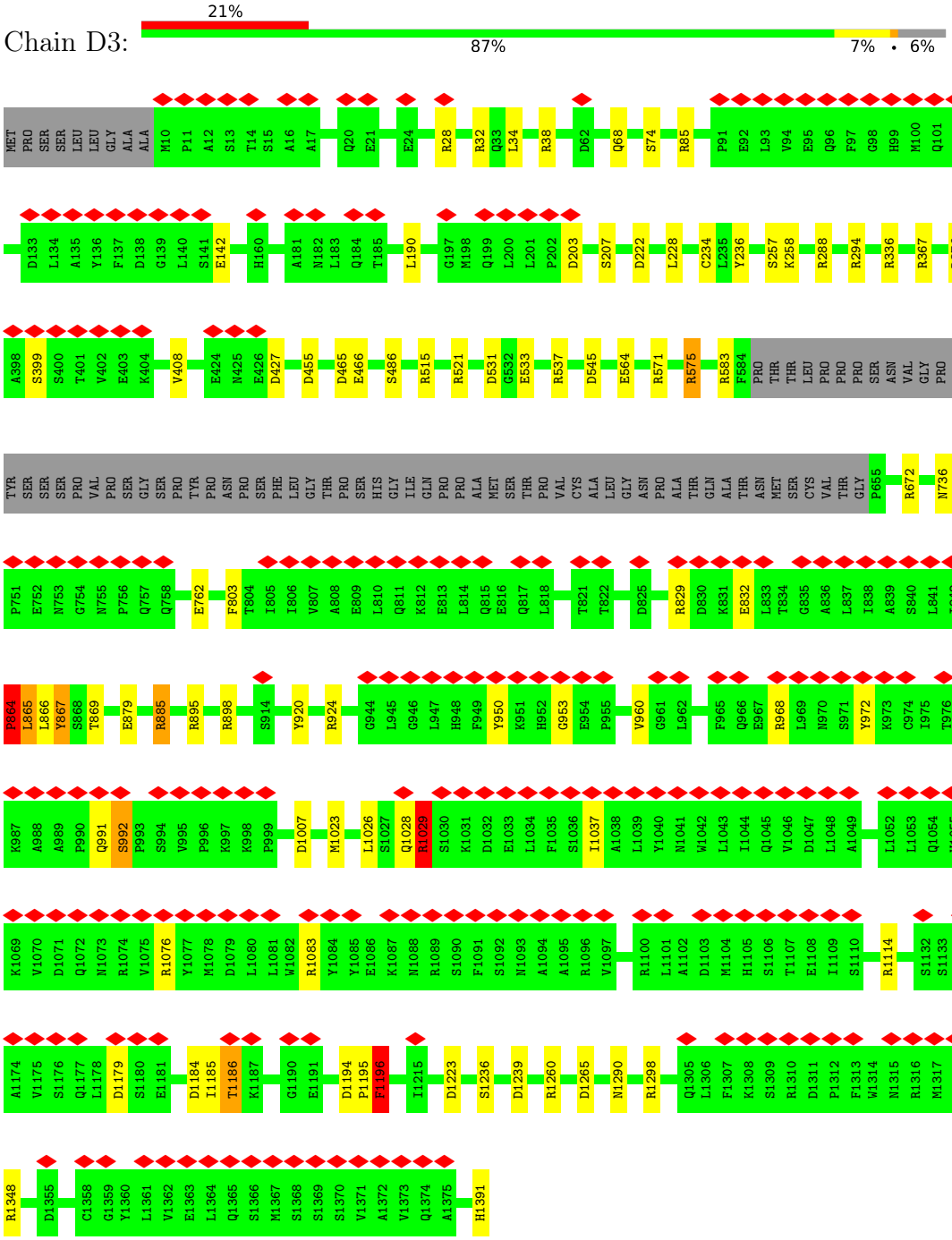
• Molecule 7: Nuclear pore complex protein Nup155

Chain D2:



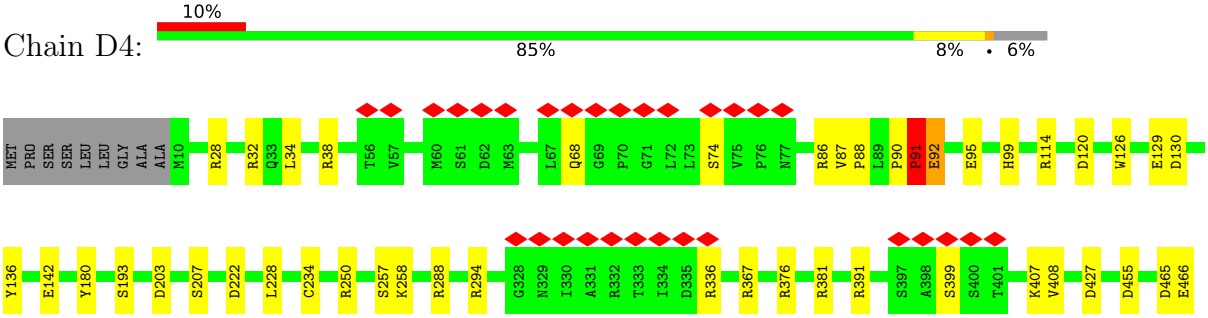
• Molecule 7: Nuclear pore complex protein Nup155

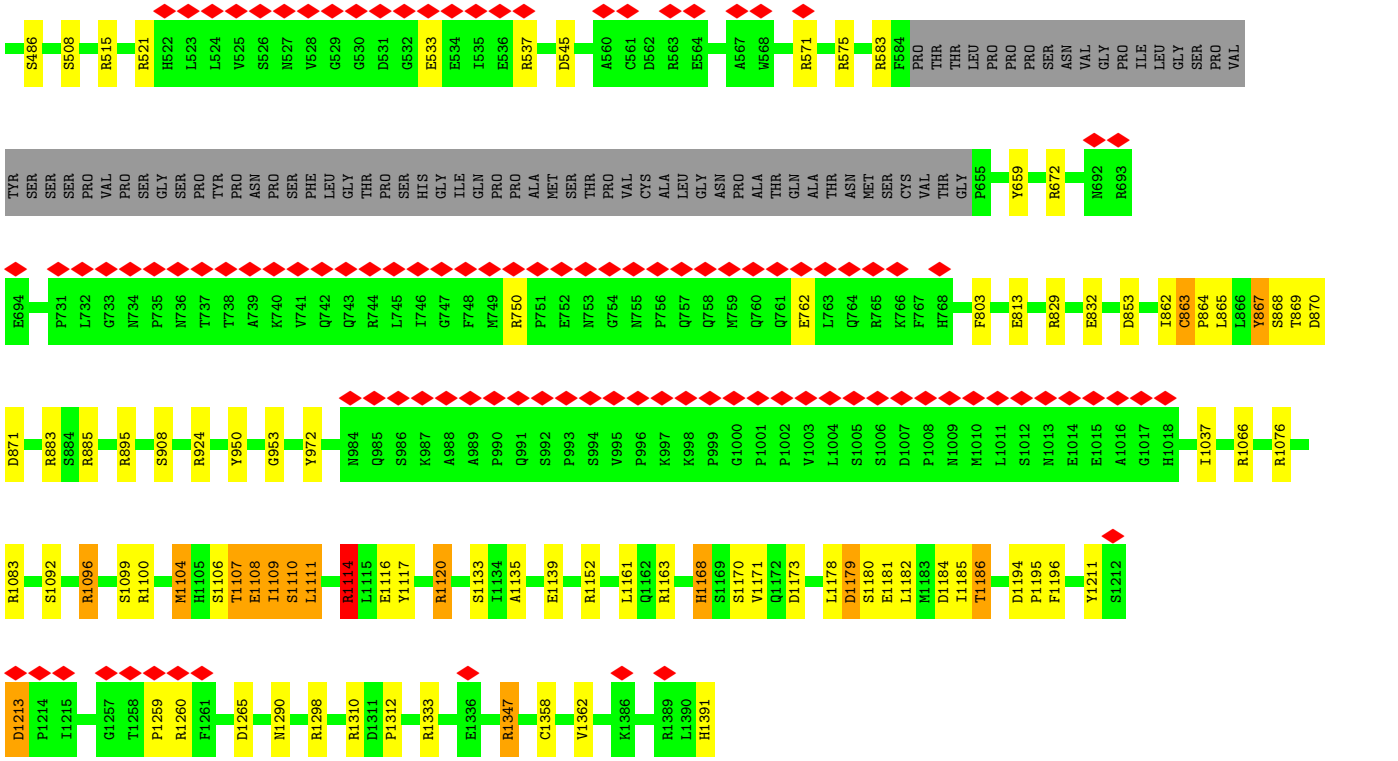
Chain D3:



• Molecule 7: Nuclear pore complex protein Nup155

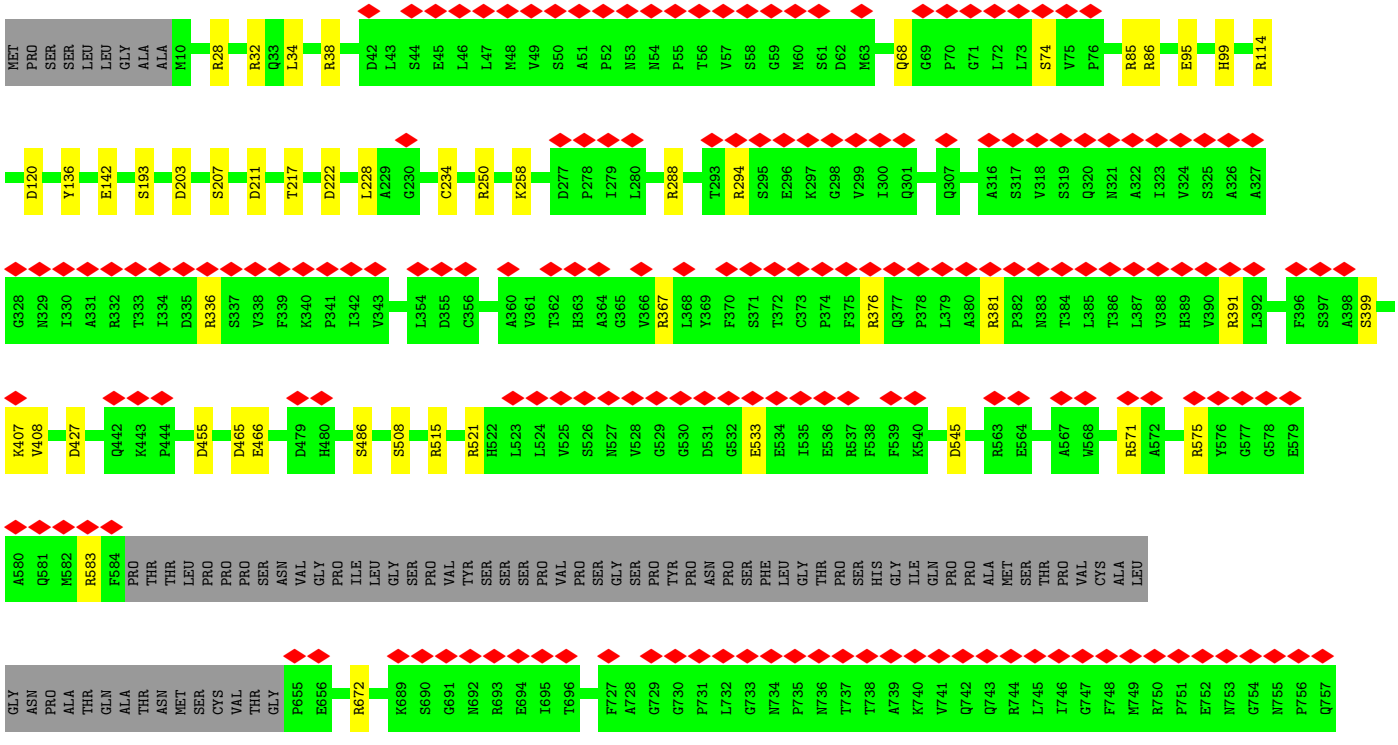
Chain D4:





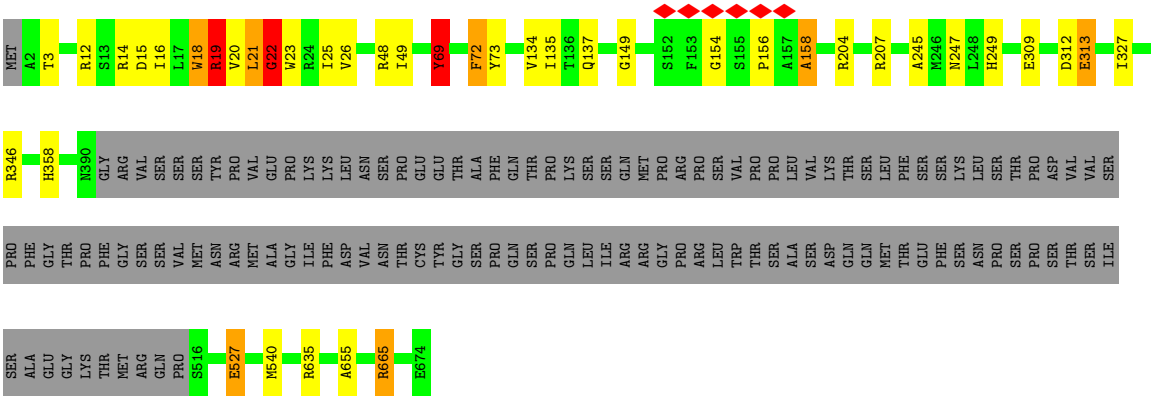
• Molecule 7: Nuclear pore complex protein Nup155

Chain D5:



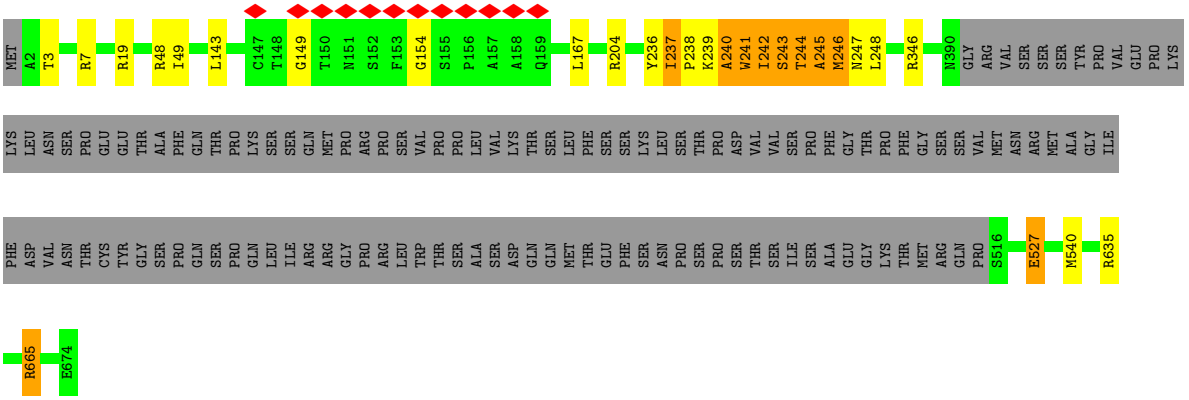
• Molecule 8: Nucleoporin NDC1

Chain E0:



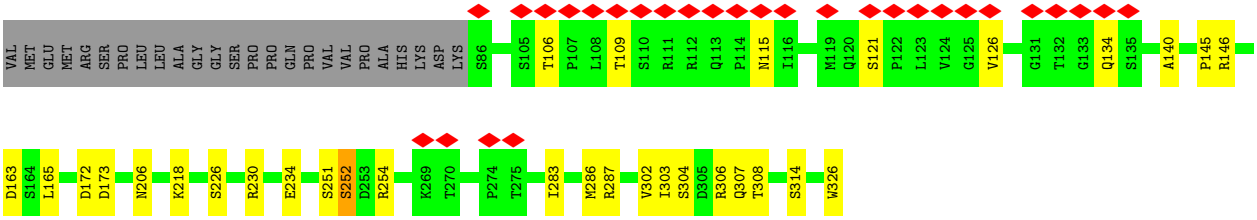
• Molecule 8: Nucleoporin NDC1

Chain E1:



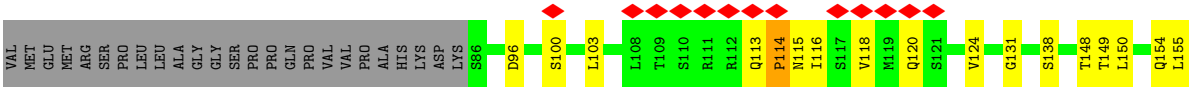
• Molecule 9: Nucleoporin NUP35

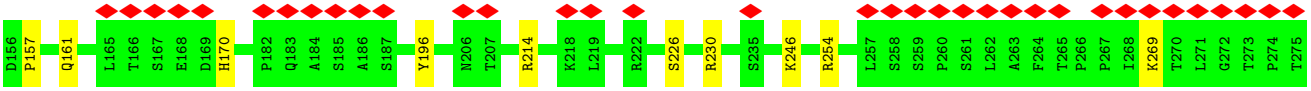
Chain F0:

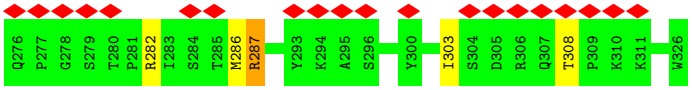


• Molecule 9: Nucleoporin NUP35

Chain F1:

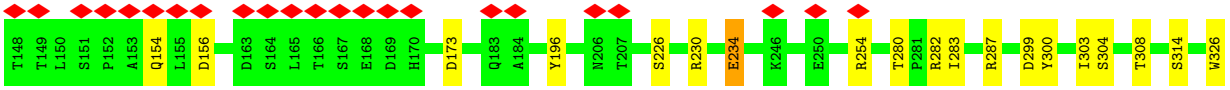






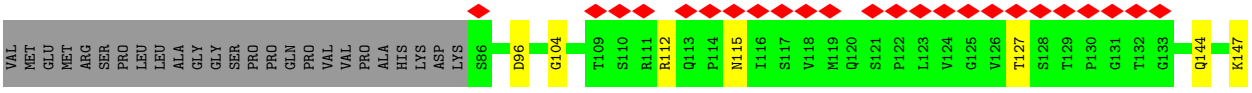
• Molecule 9: Nucleoporin NUP35

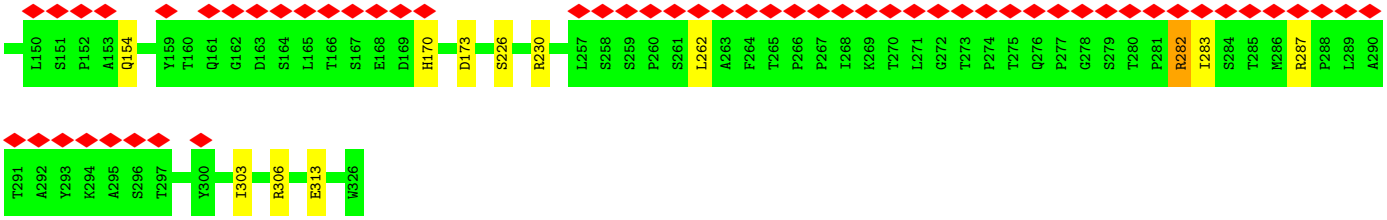
Chain F2:



• Molecule 9: Nucleoporin NUP35

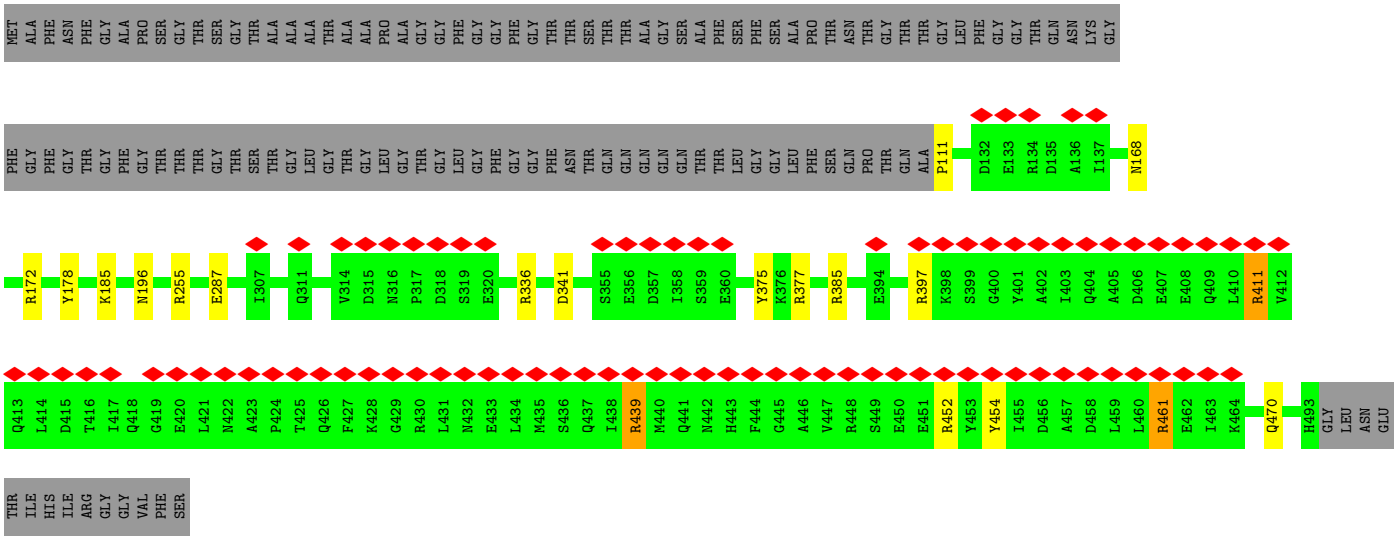
Chain F3:





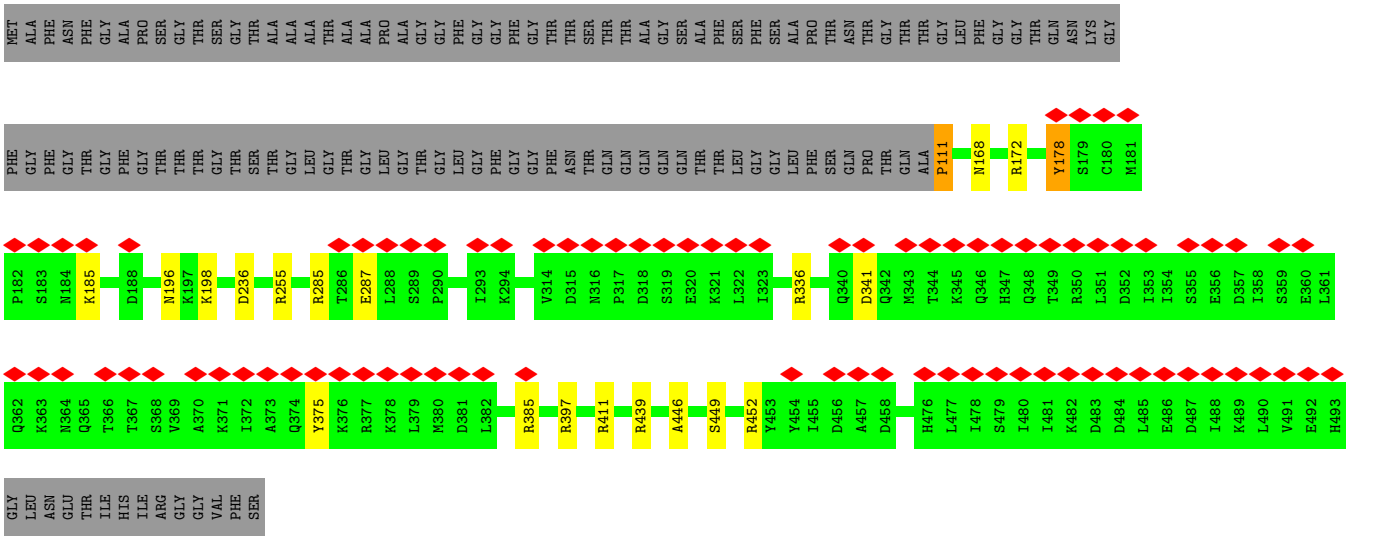
• Molecule 10: Nucleoporin p54

Chain H0:



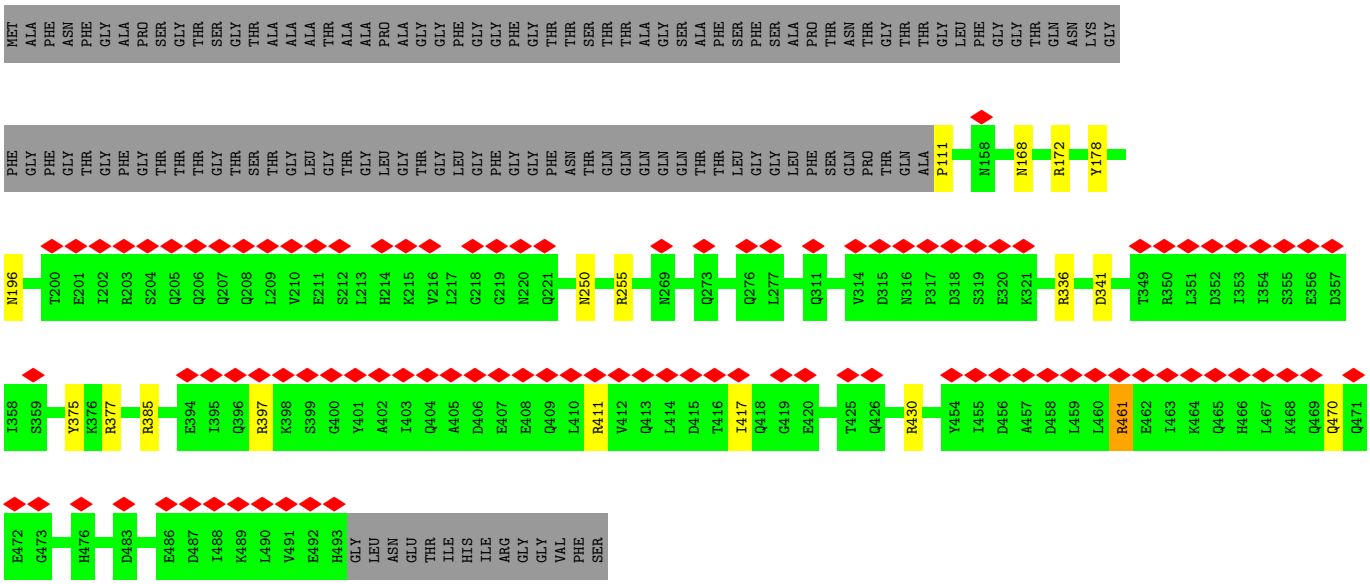
• Molecule 10: Nucleoporin p54

Chain H1:



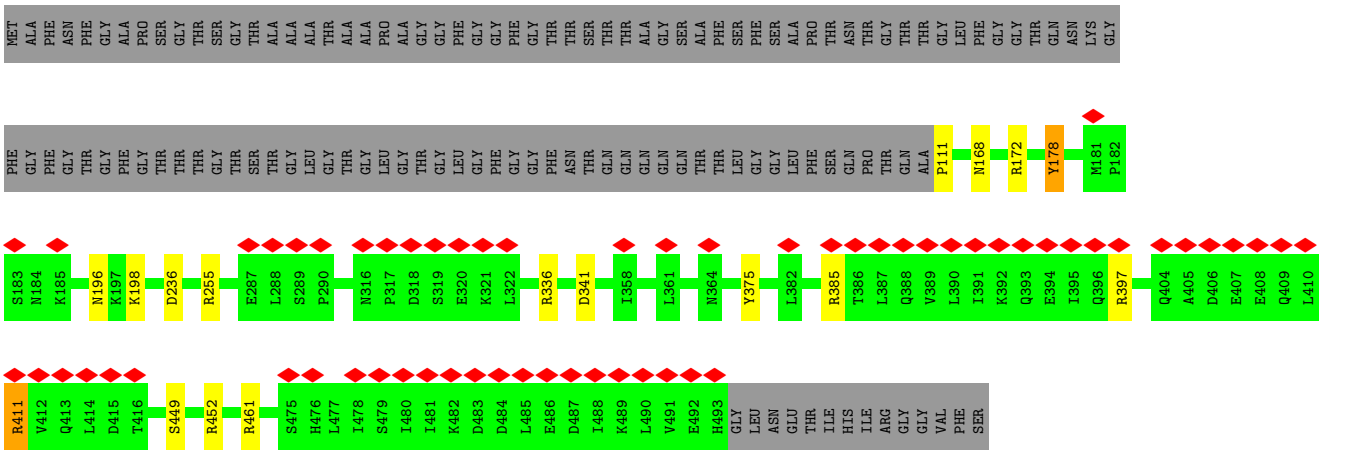
• Molecule 10: Nucleoporin p54

Chain H2:



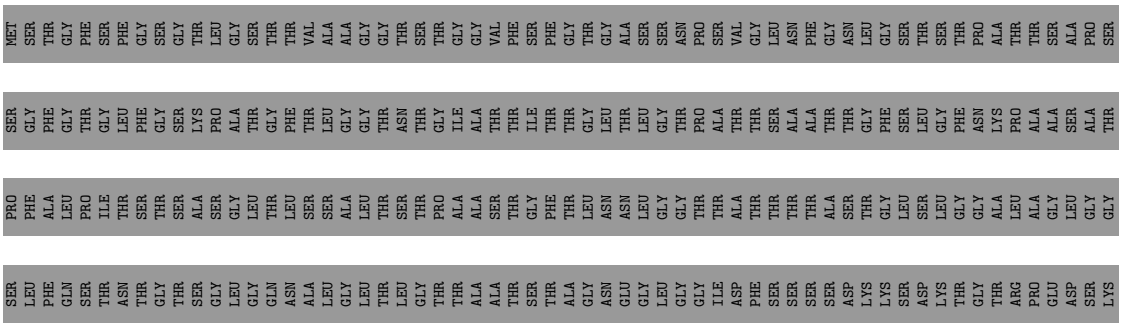
• Molecule 10: Nucleoporin p54

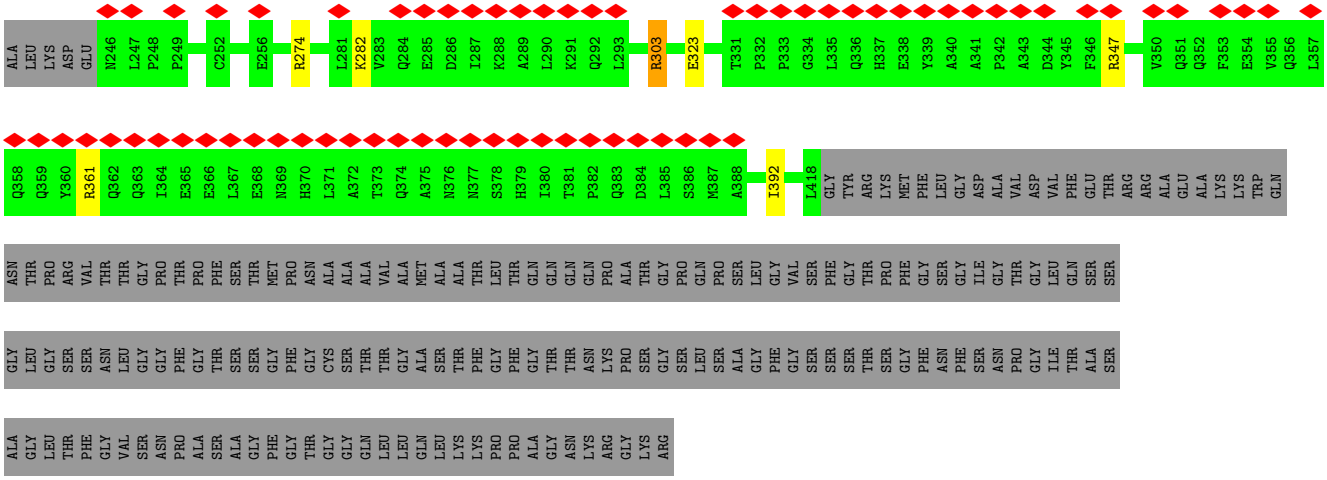
Chain H3:



• Molecule 11: Nucleoporin p58/p45

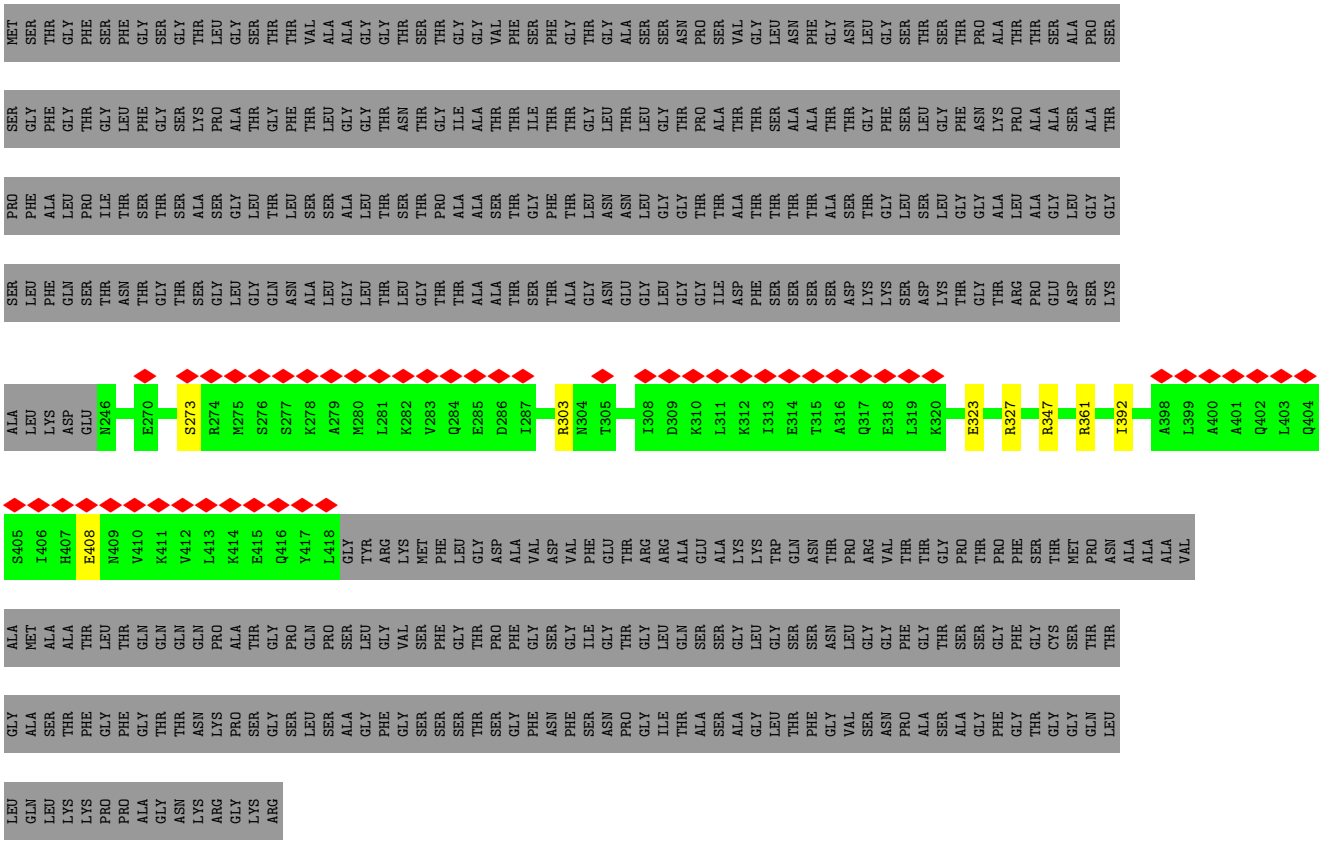
Chain I0:





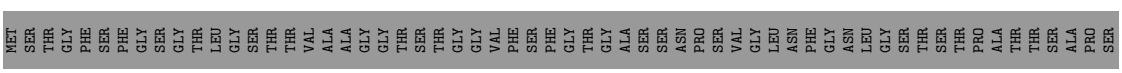
- Molecule 11: Nucleoporin p58/p45

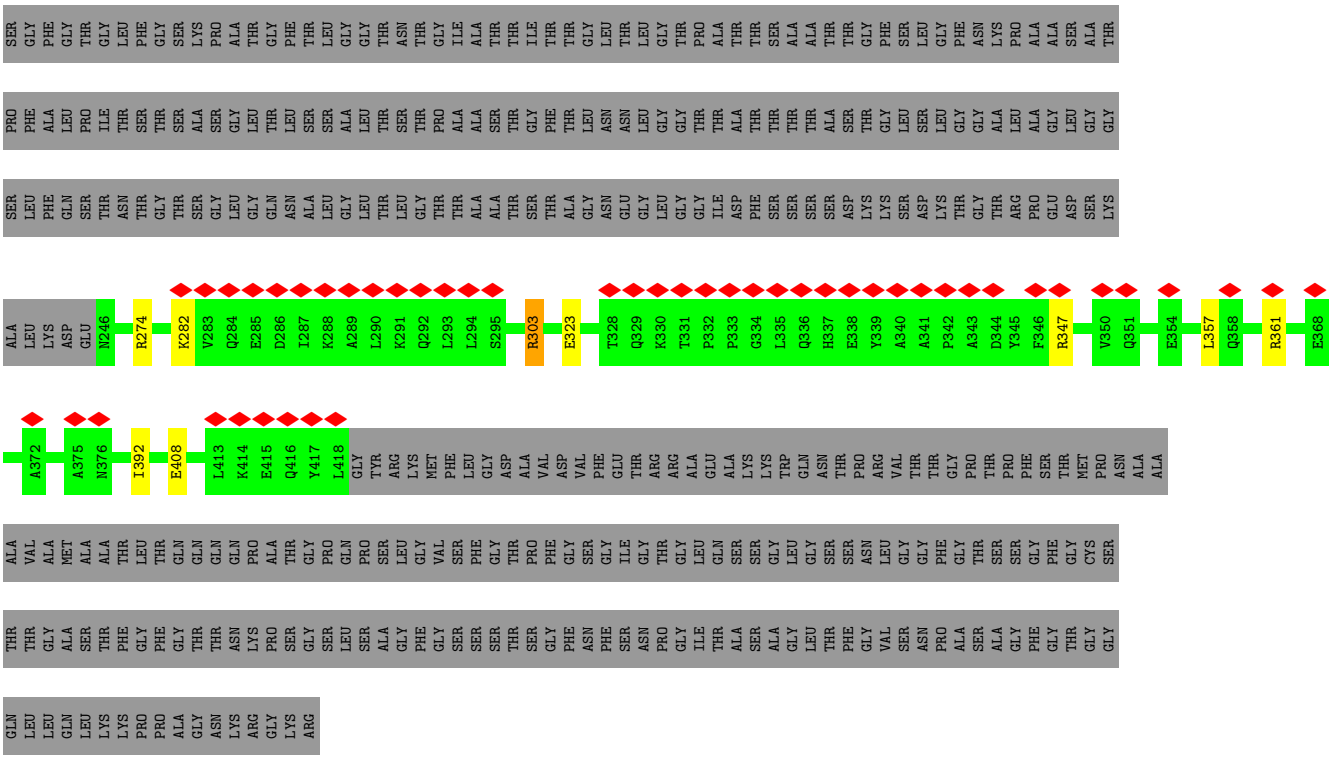
Chain I1:



- Molecule 11: Nucleoporin p58/p45

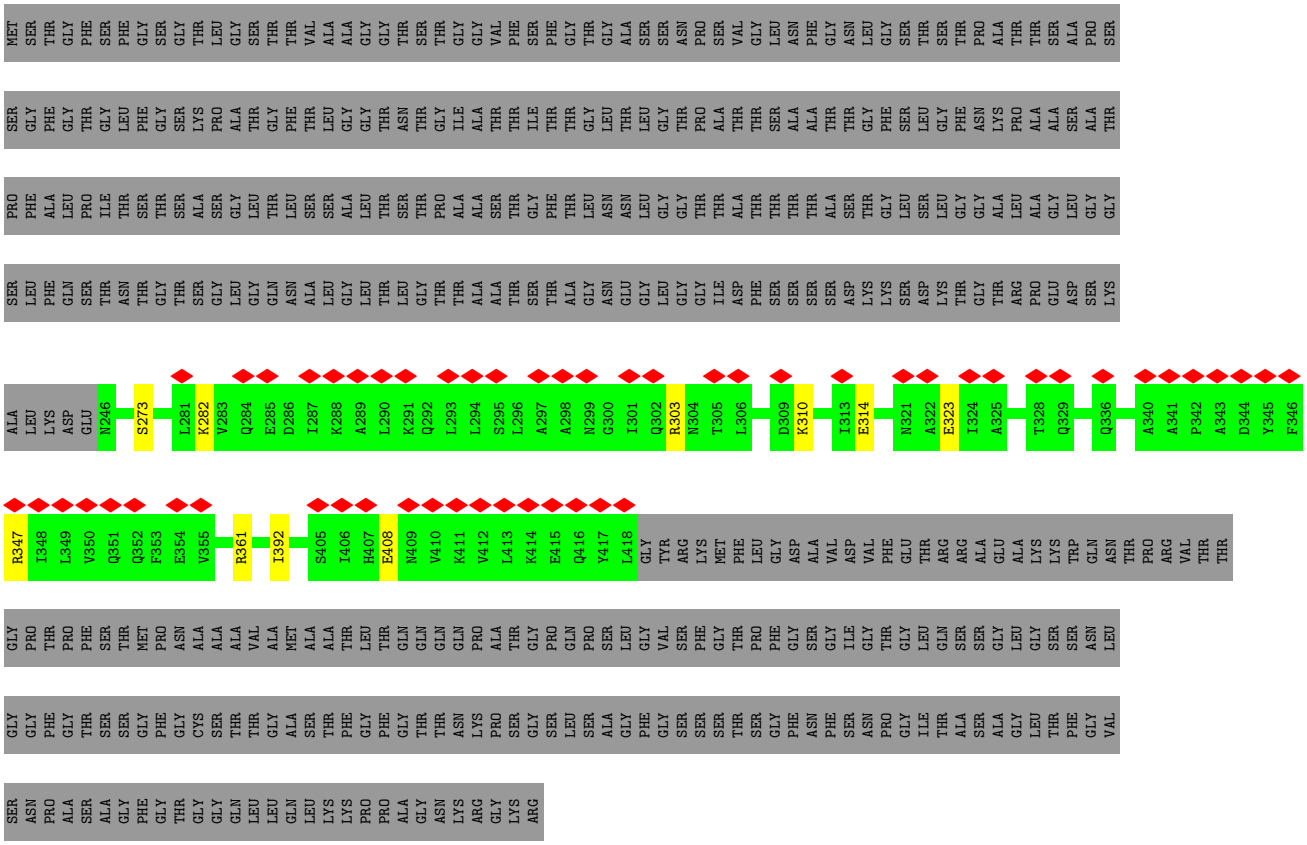
Chain I2:





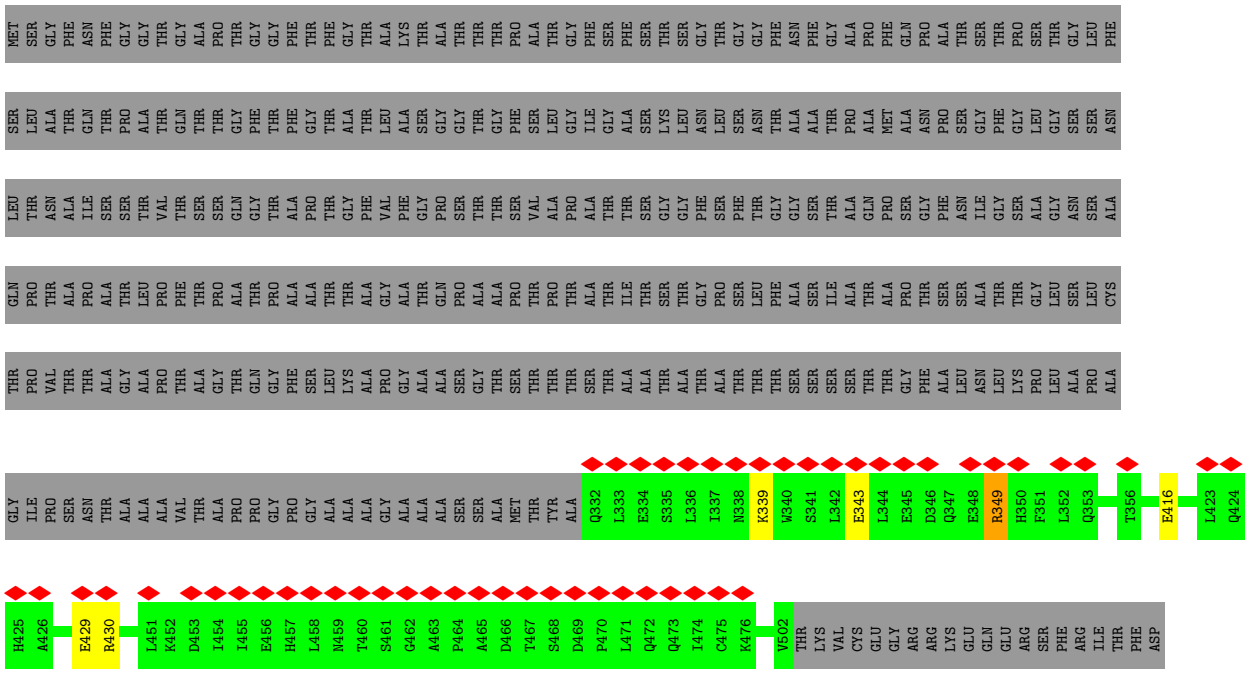
• Molecule 11: Nucleoporin p58/p45

Chain I3:



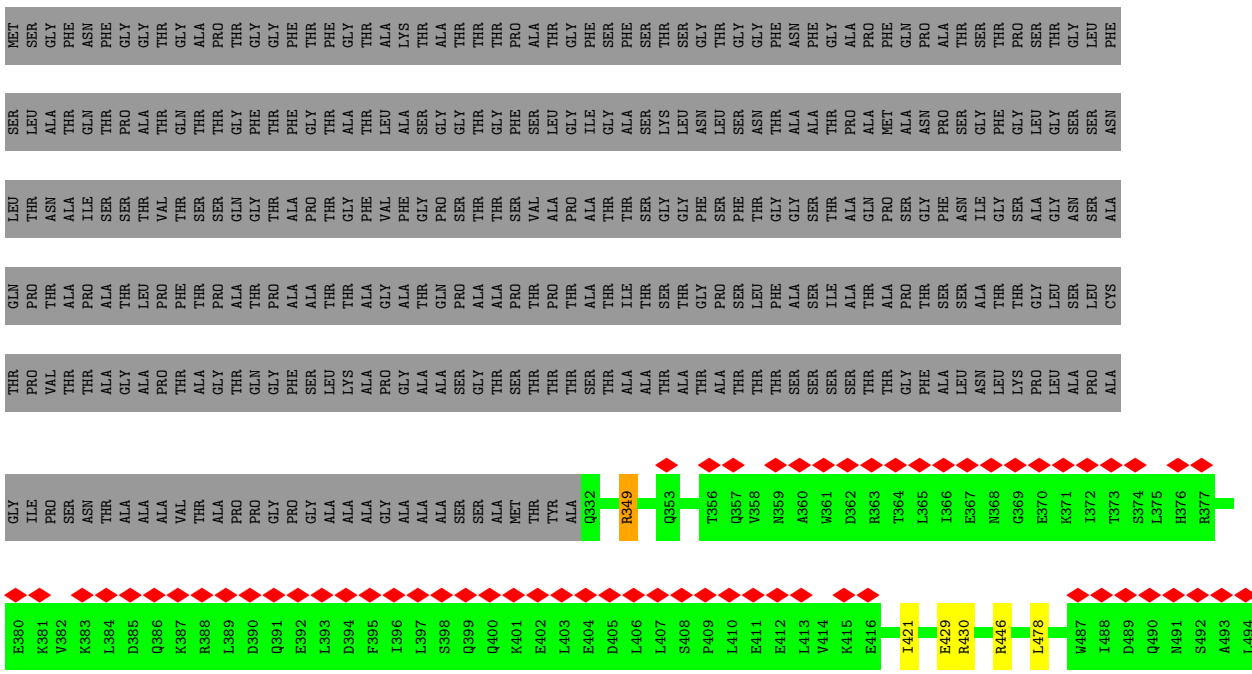
• Molecule 12: Nuclear pore glycoprotein p62

Chain J0:



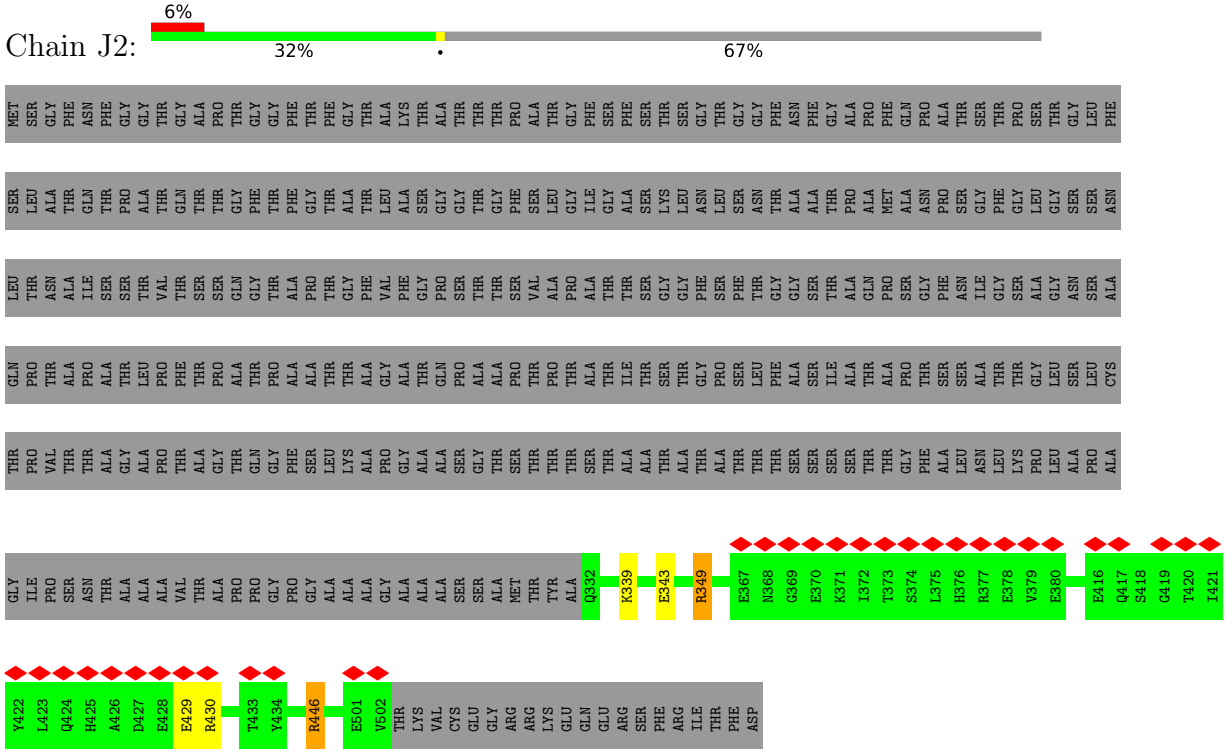
• Molecule 12: Nuclear pore glycoprotein p62

Chain J1:



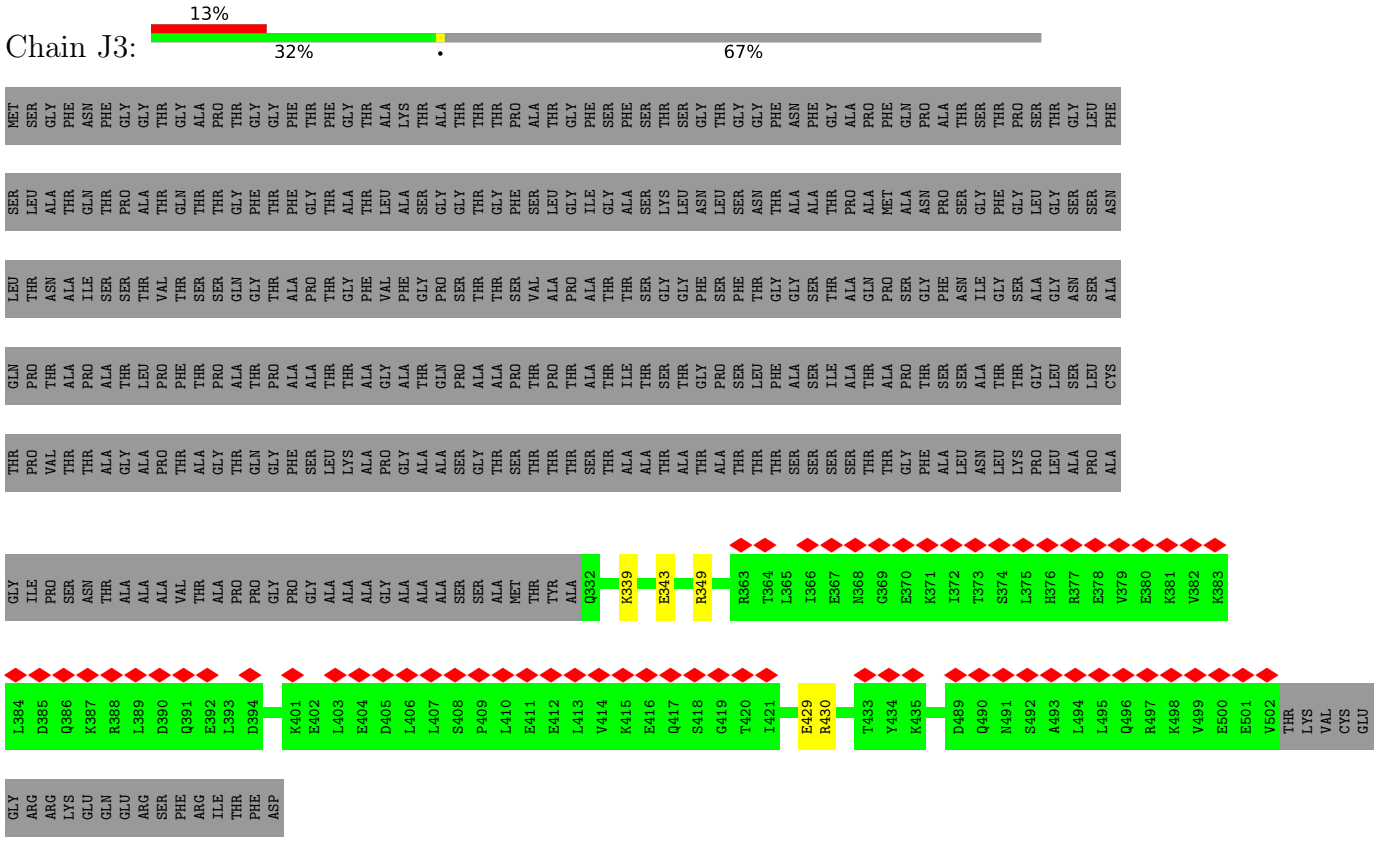
• Molecule 12: Nuclear pore glycoprotein p62

Chain J2:



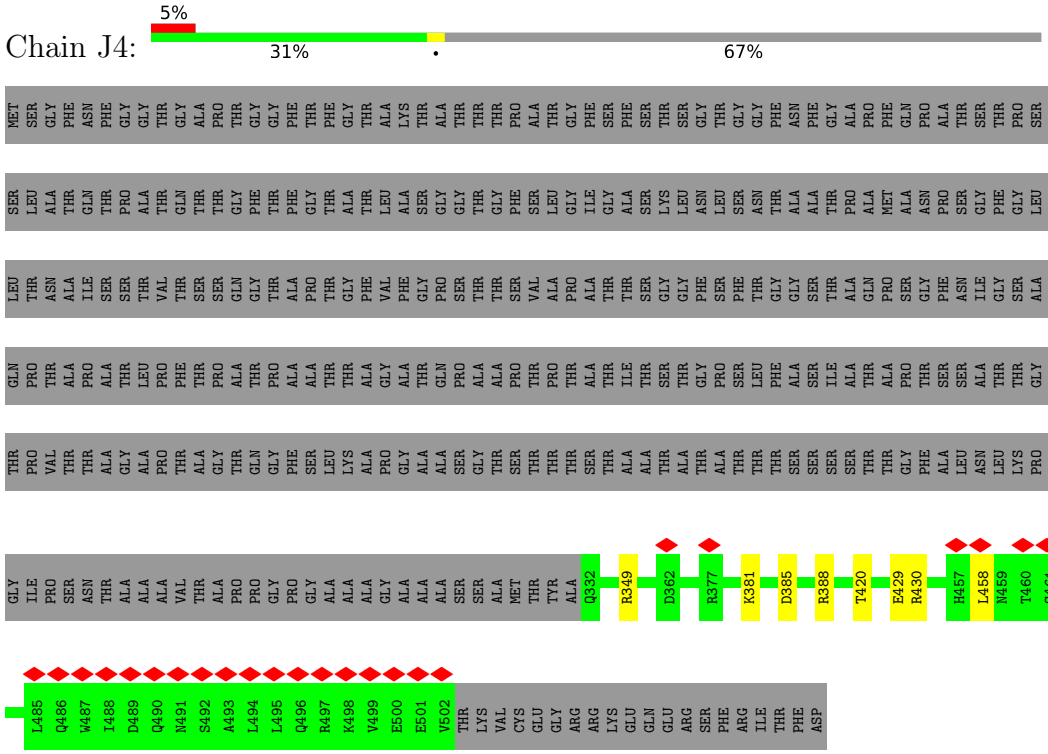
• Molecule 12: Nuclear pore glycoprotein p62

Chain J3:



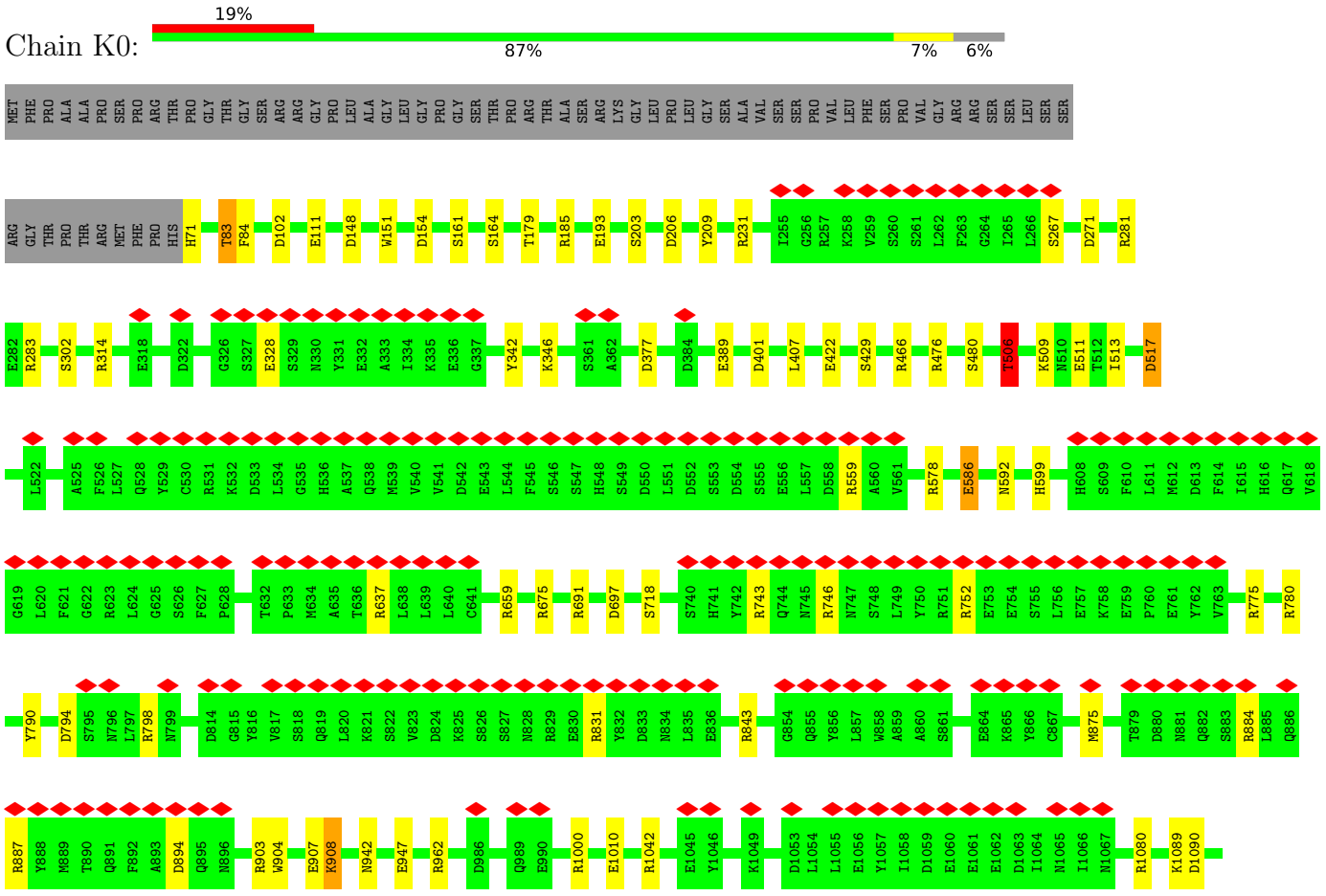
• Molecule 12: Nuclear pore glycoprotein p62

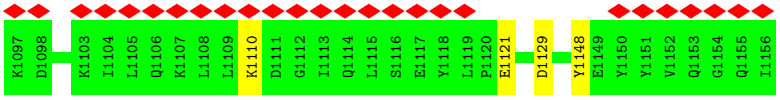
Chain J4:



- Molecule 13: Nuclear pore complex protein Nup133

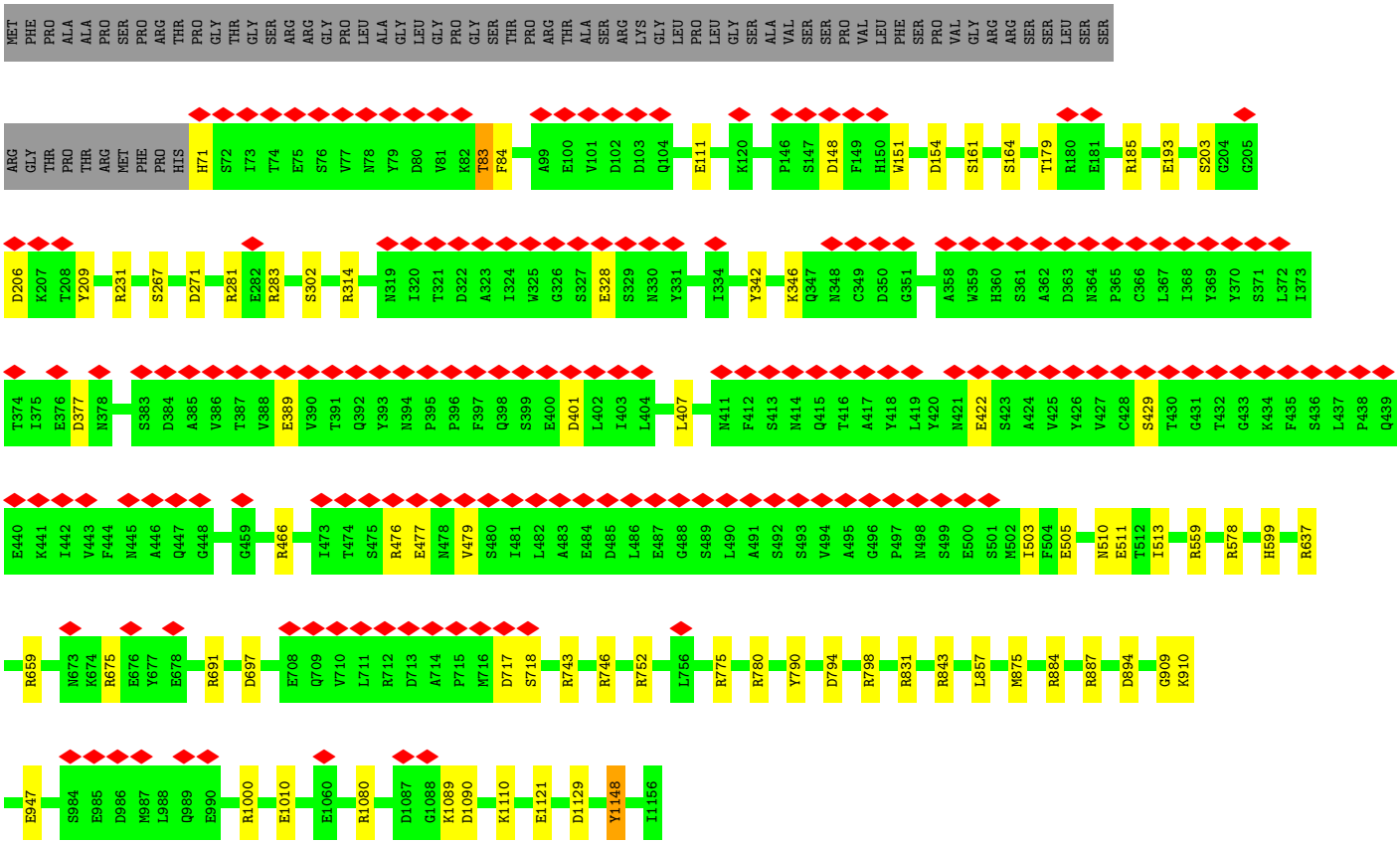
Chain K0:





• Molecule 13: Nuclear pore complex protein Nup133

Chain K1:



• Molecule 13: Nuclear pore complex protein Nup133

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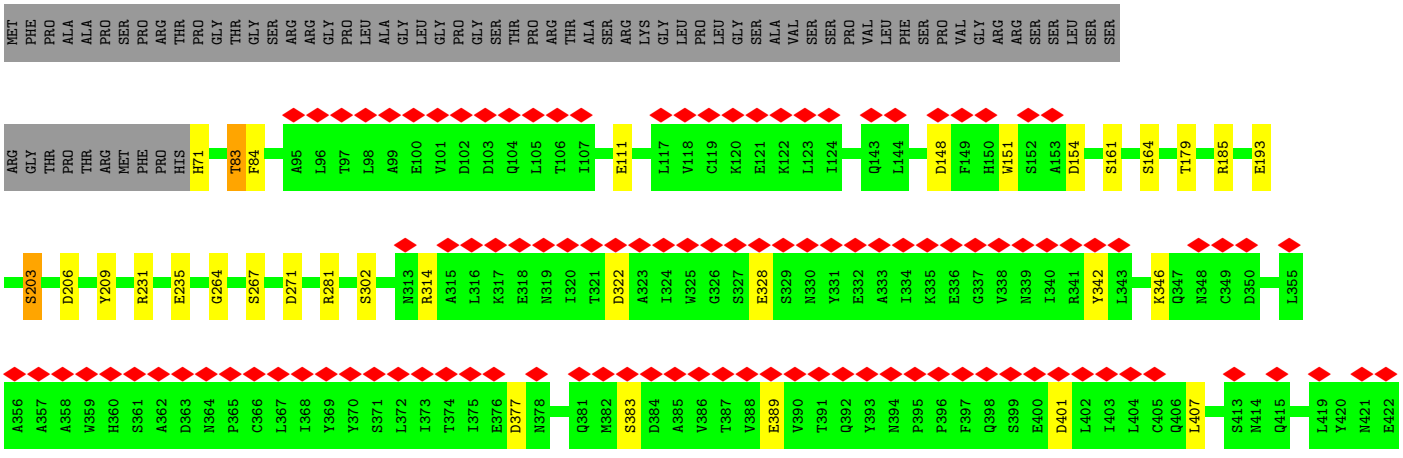
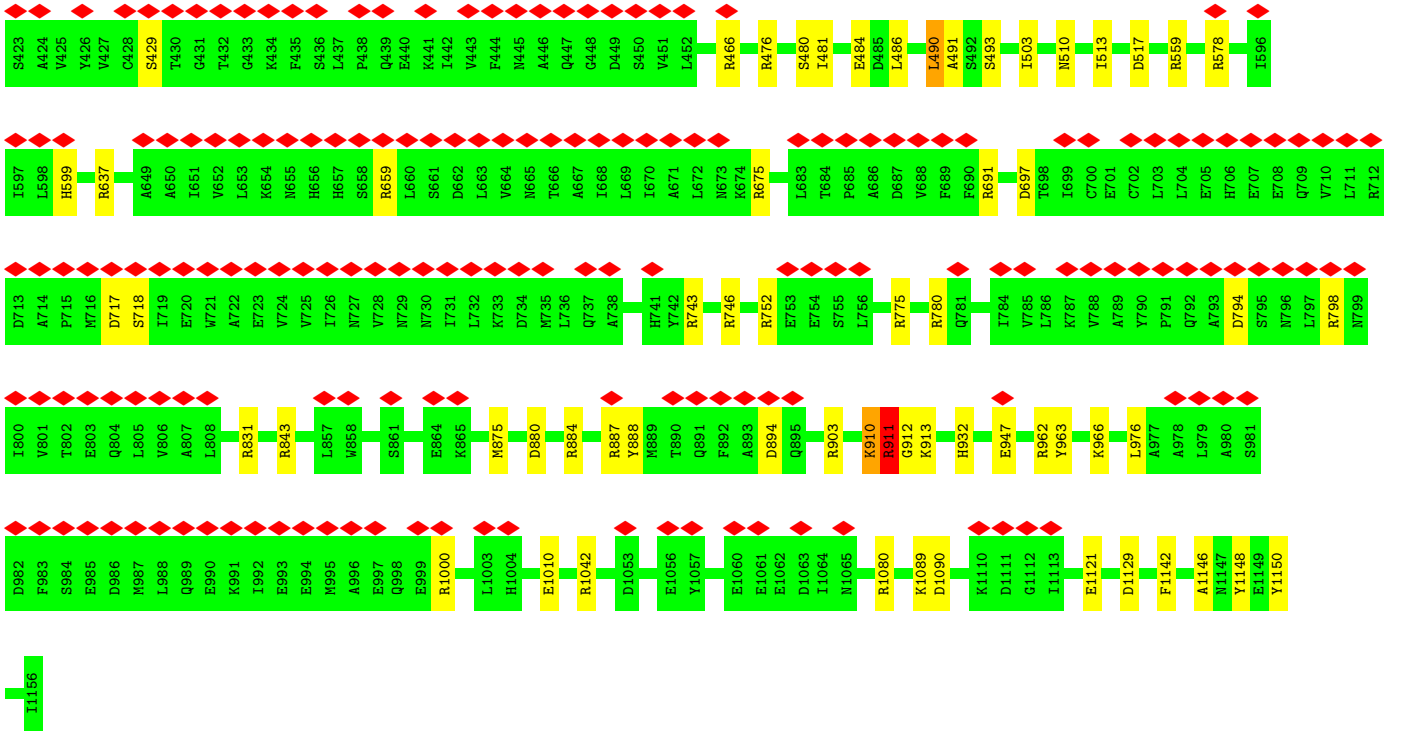
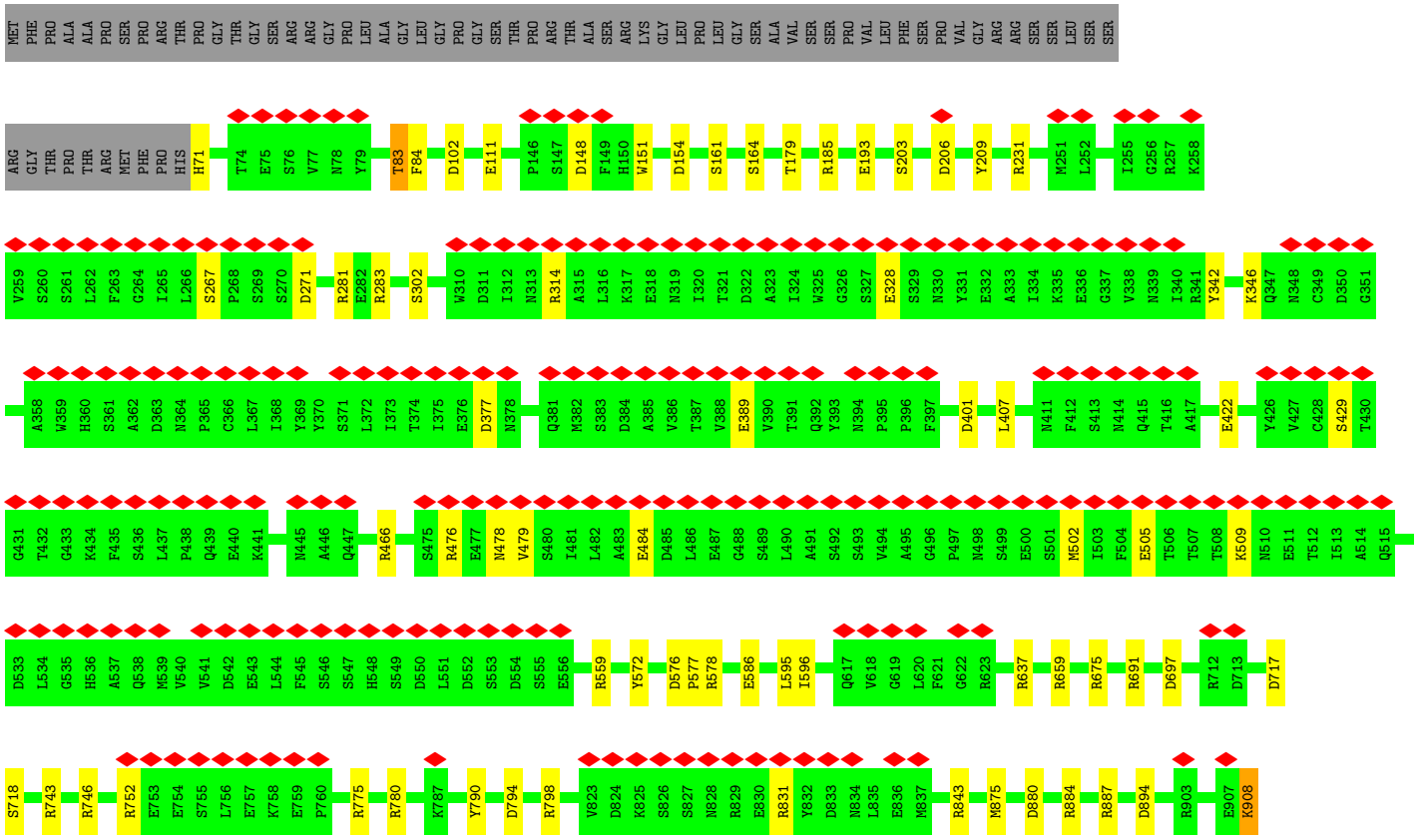
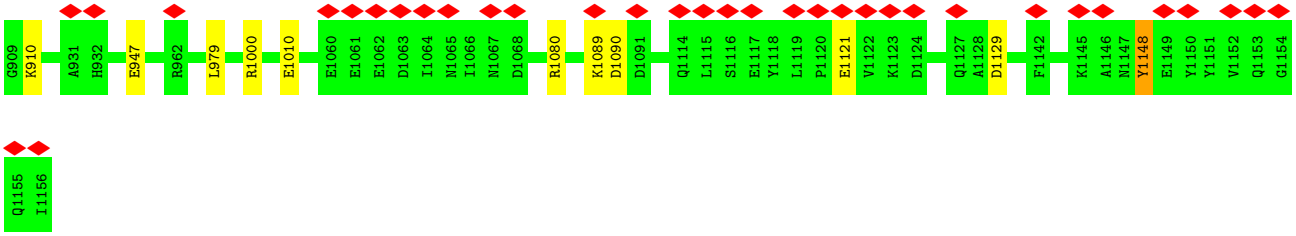




- Molecule 13: Nuclear pore complex protein Nup133

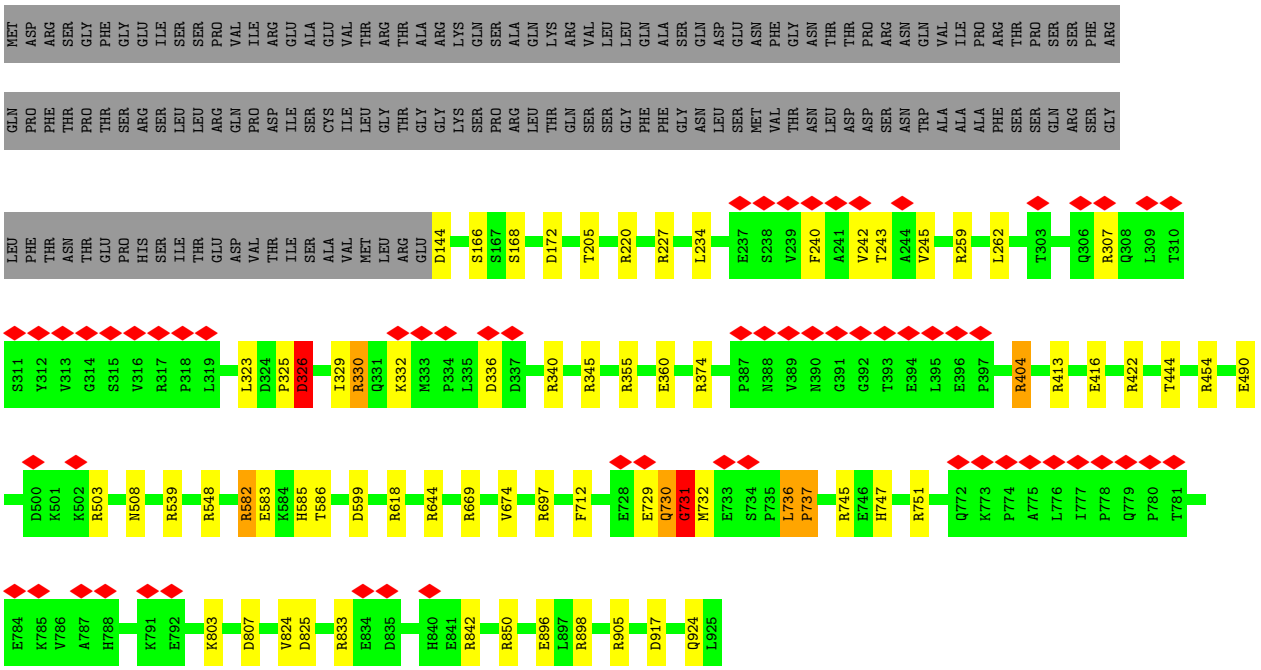
Chain K3:





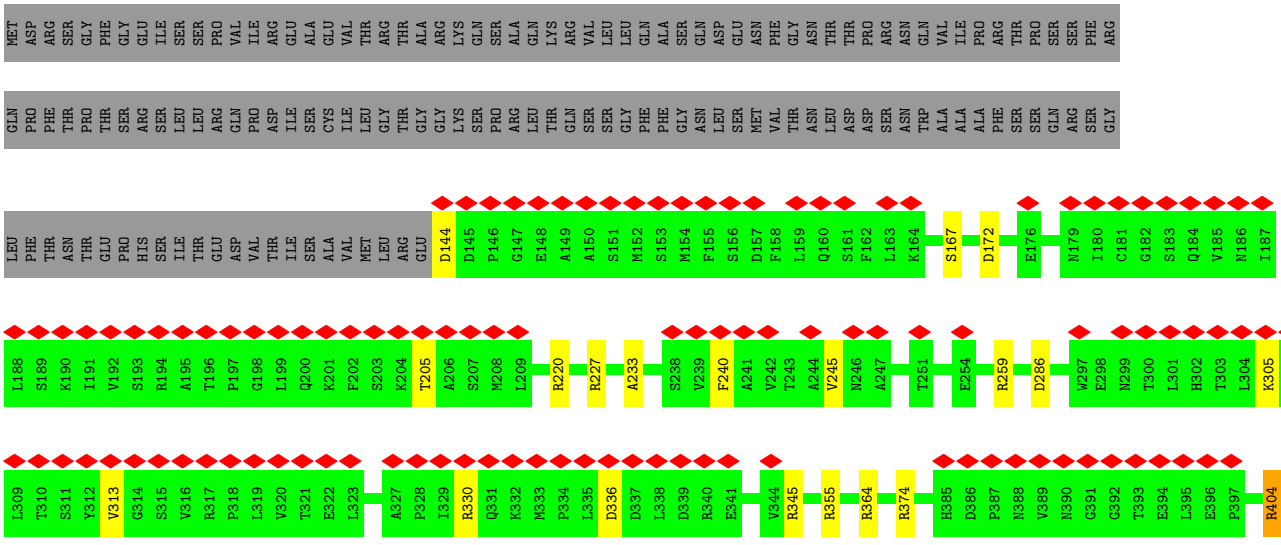
• Molecule 14: Nuclear pore complex protein Nup107

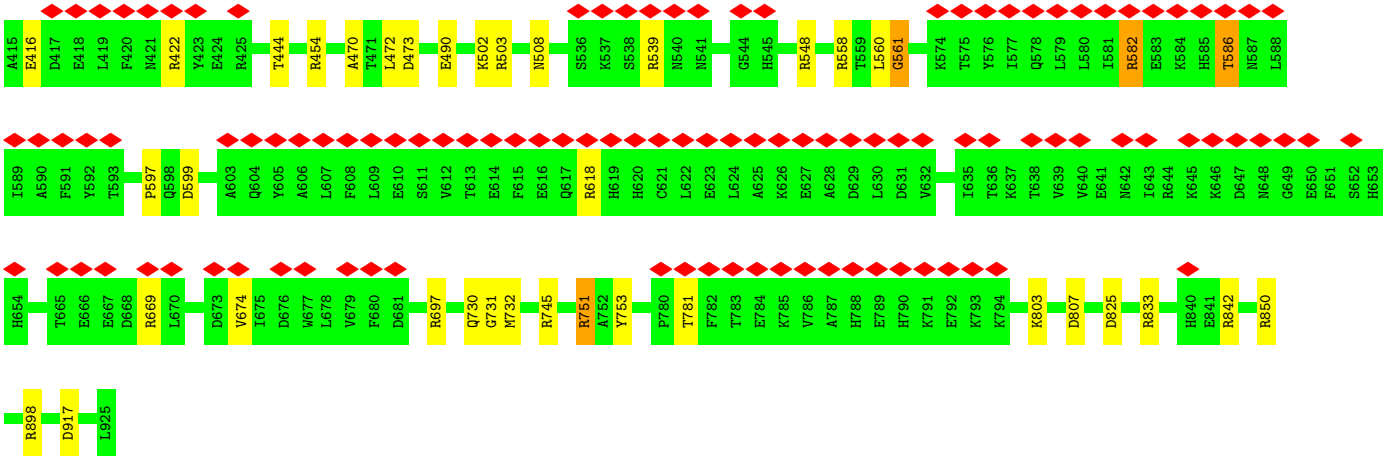
Chain L0:



• Molecule 14: Nuclear pore complex protein Nup107

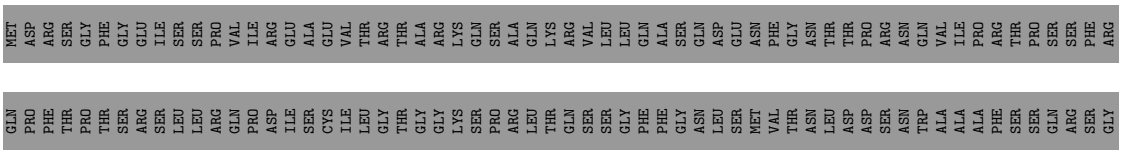
Chain L1:

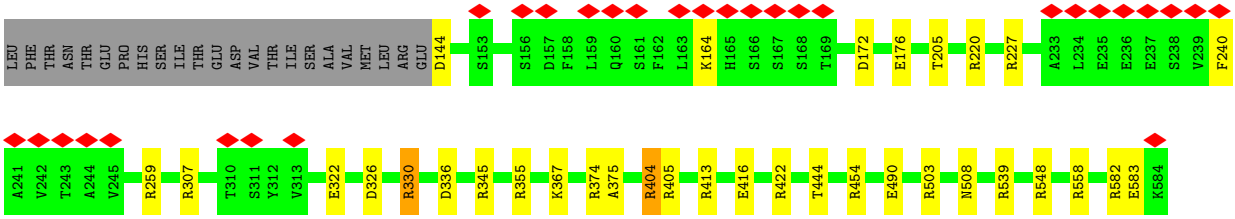




• Molecule 14: Nuclear pore complex protein Nup107

Chain L2:





• Molecule 14: Nuclear pore complex protein Nup107

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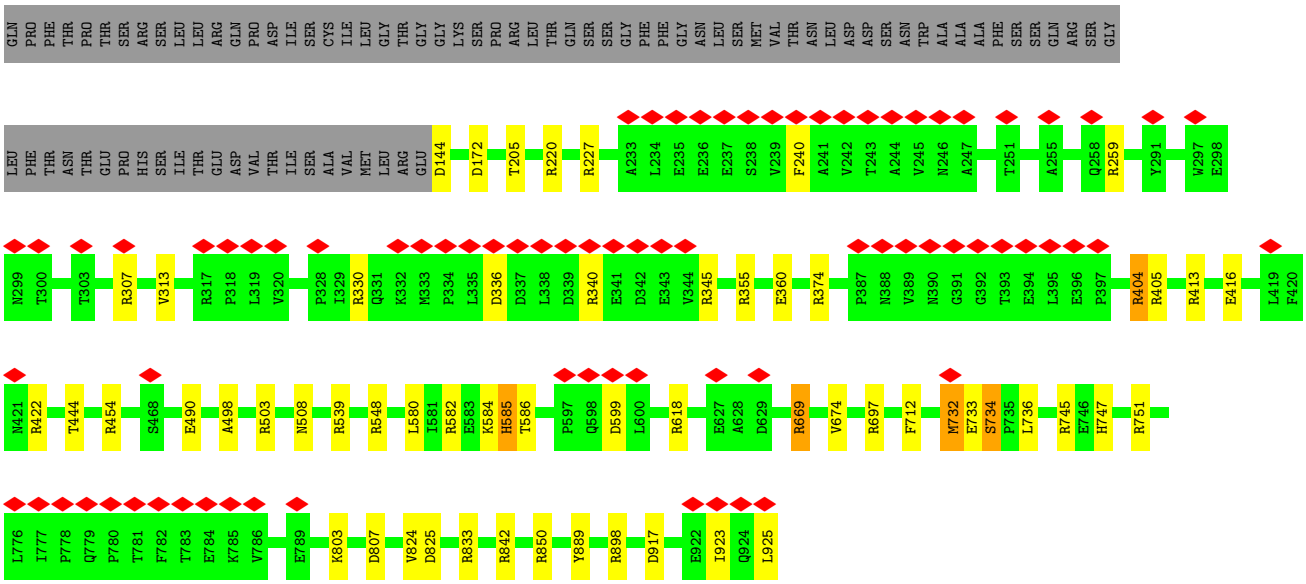
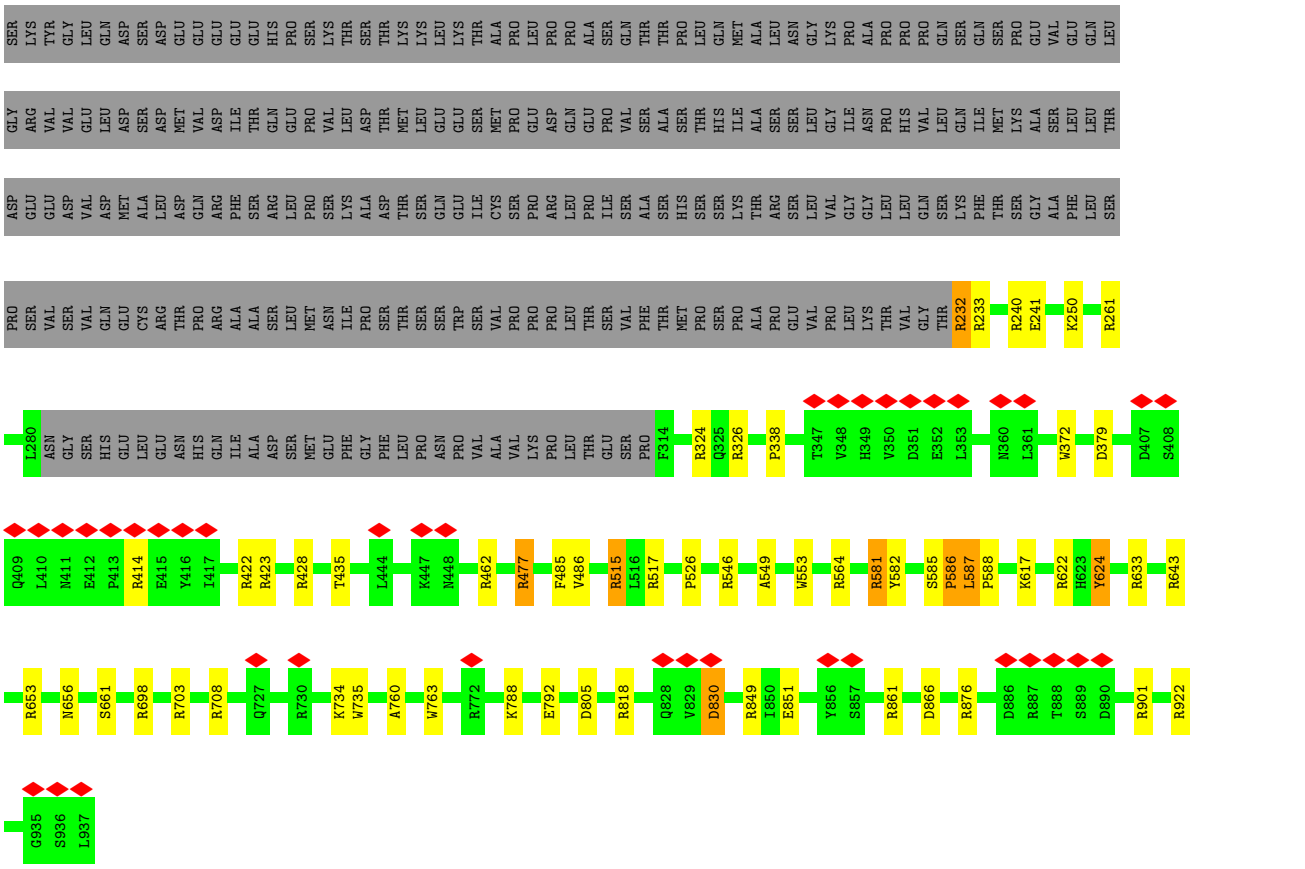


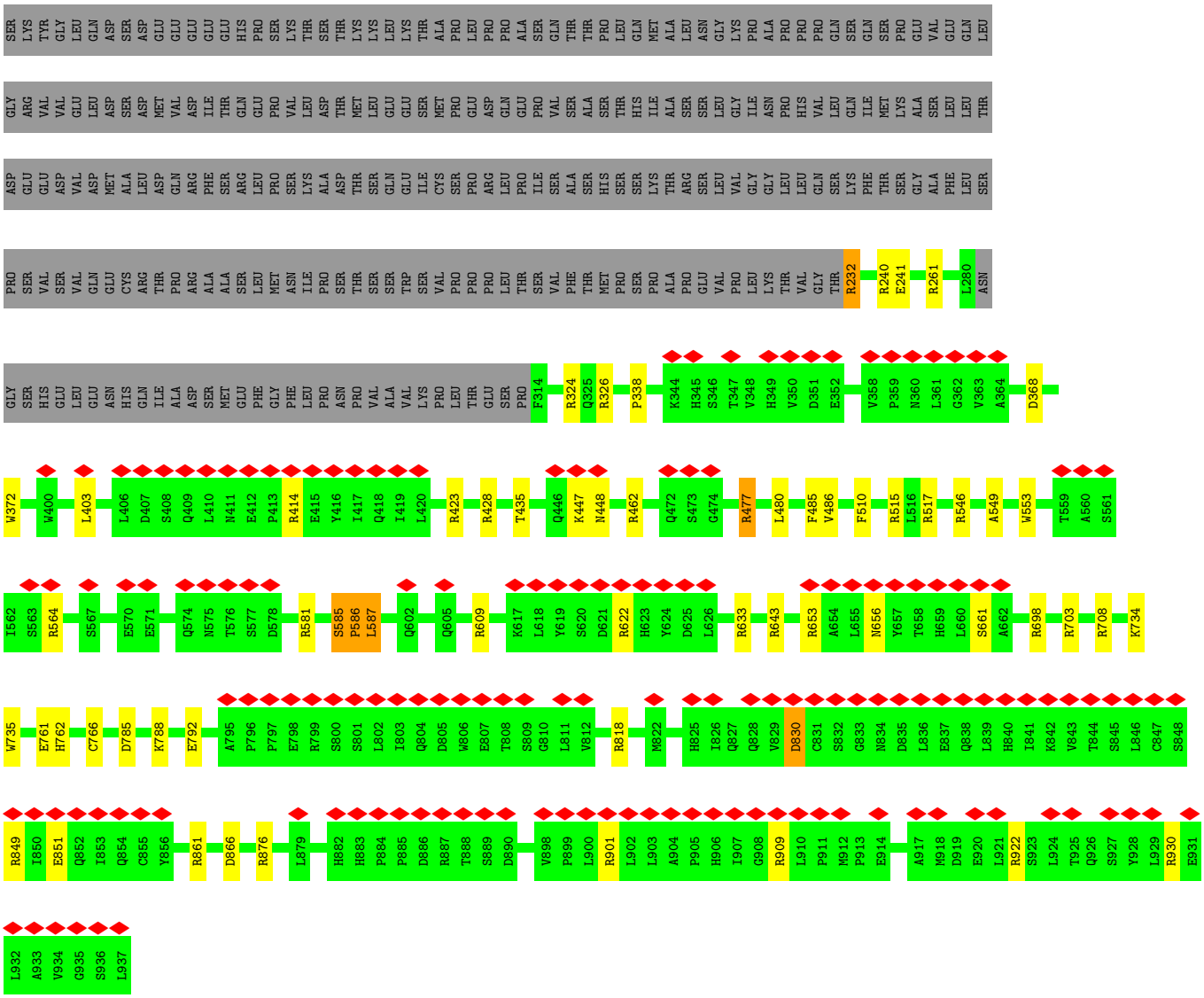
• Molecule 15: Nuclear pore complex protein Nup96

Chain M0:



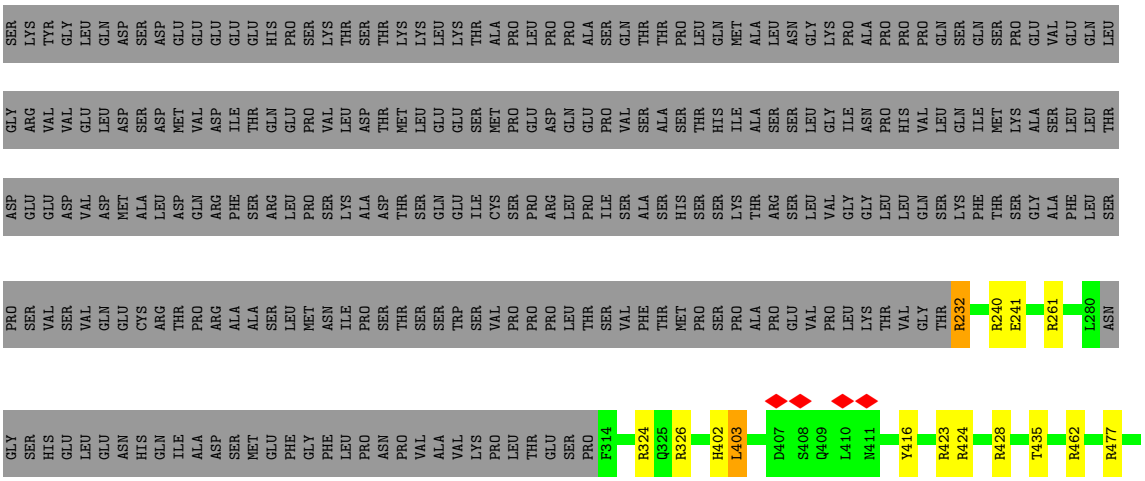
• Molecule 15: Nuclear pore complex protein Nup96

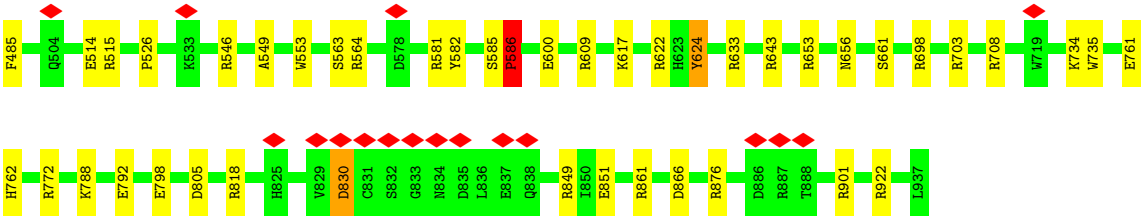
Chain M1:



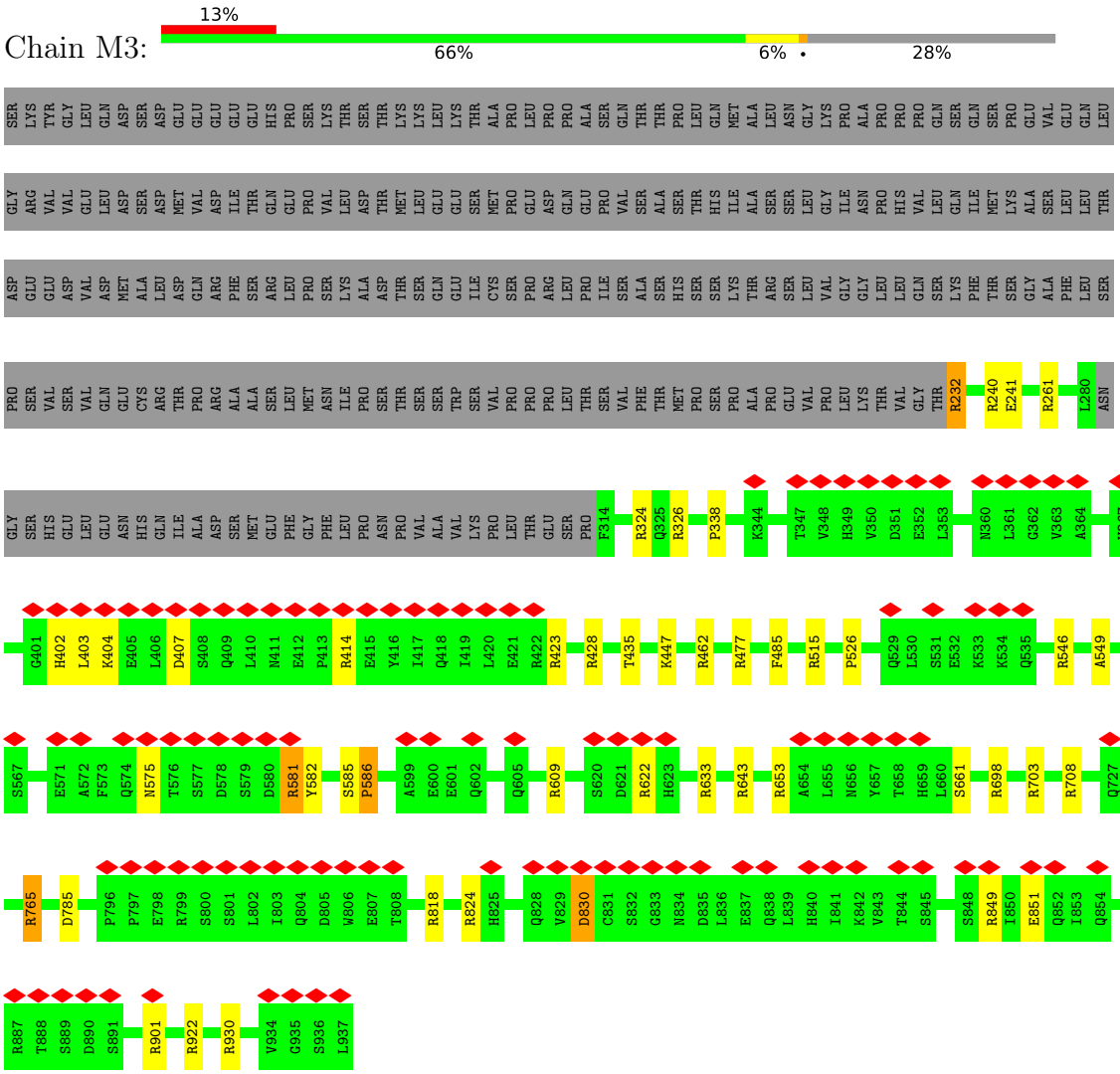
• Molecule 15: Nuclear pore complex protein Nup96

Chain M2:

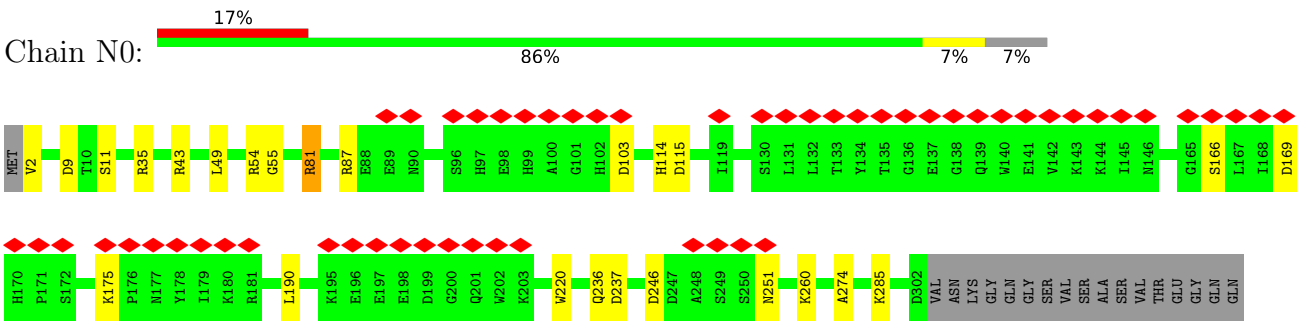




• Molecule 15: Nuclear pore complex protein Nup96

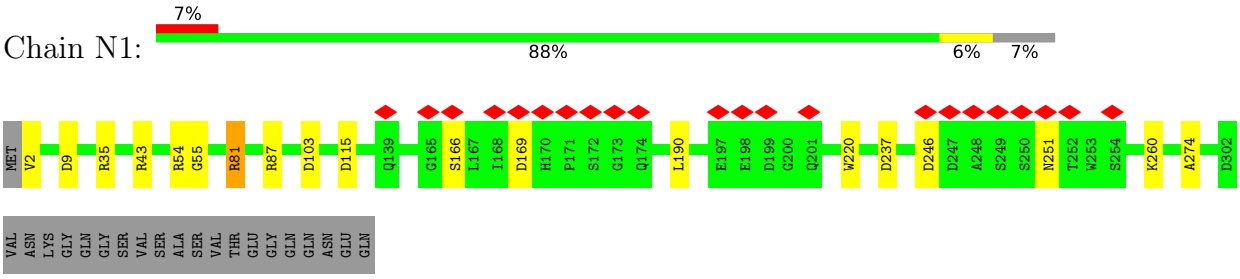


• Molecule 16: Protein SEC13 homolog



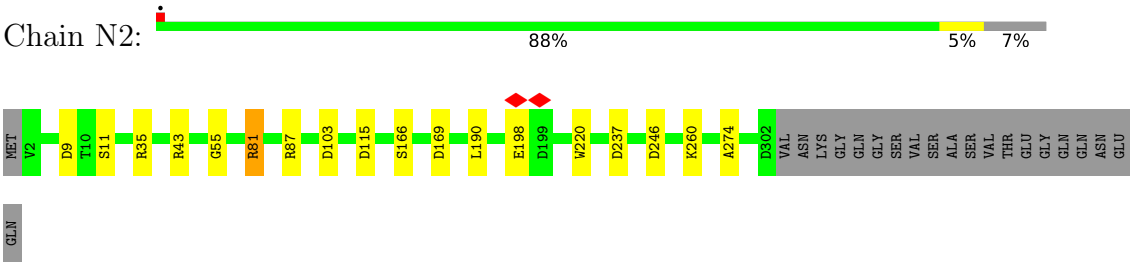
• Molecule 16: Protein SEC13 homolog

Chain N1:



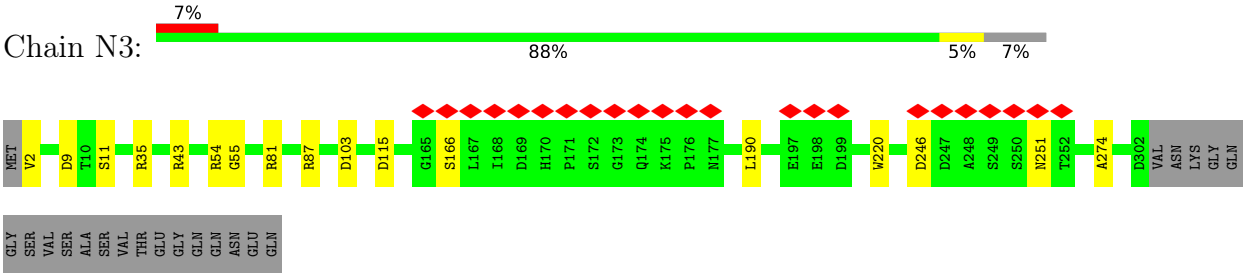
• Molecule 16: Protein SEC13 homolog

Chain N2:



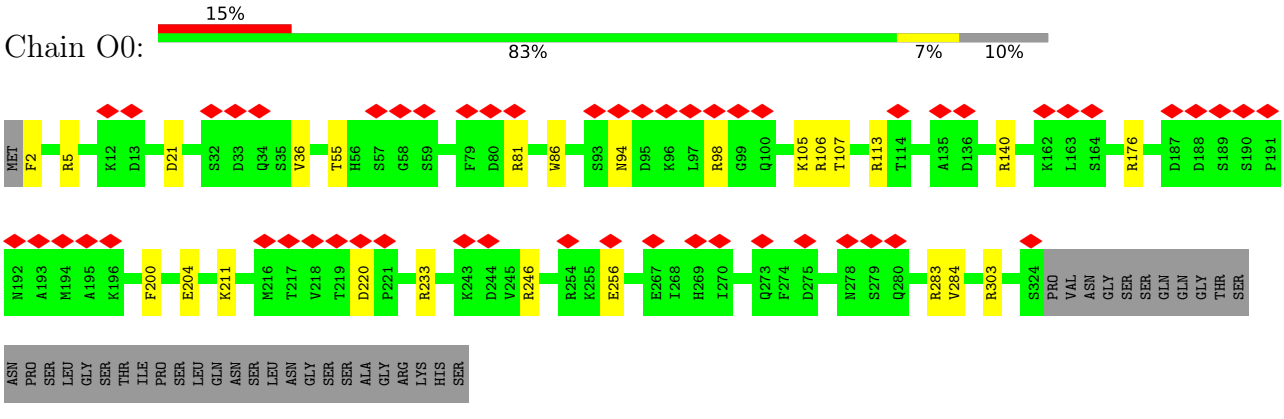
• Molecule 16: Protein SEC13 homolog

Chain N3:



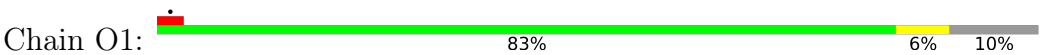
• Molecule 17: Nucleoporin SEH1

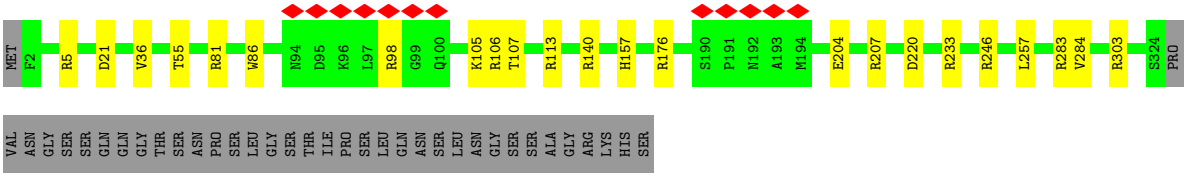
Chain O0:



• Molecule 17: Nucleoporin SEH1

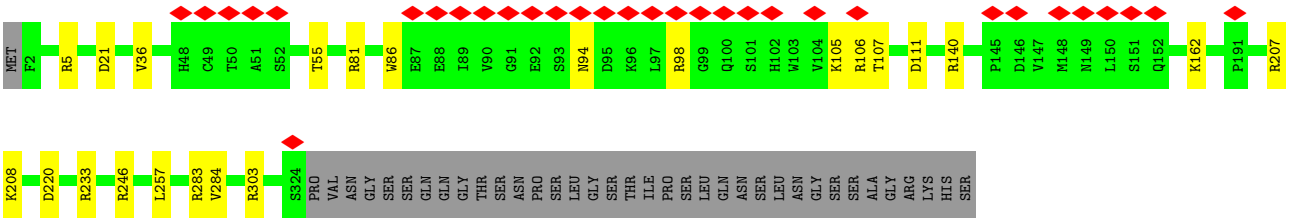
Chain O1:





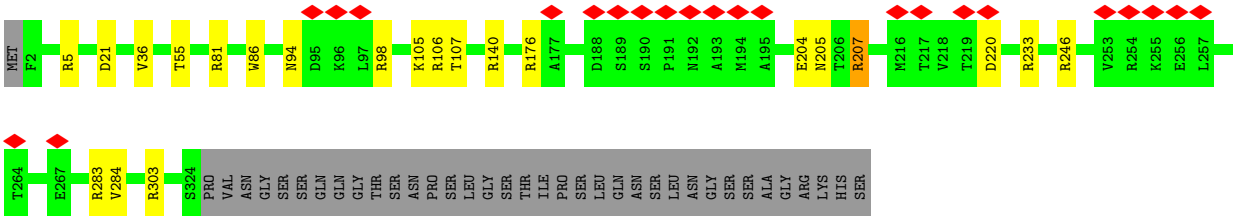
• Molecule 17: Nucleoporin SEH1

Chain O2:



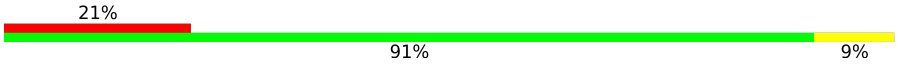
• Molecule 17: Nucleoporin SEH1

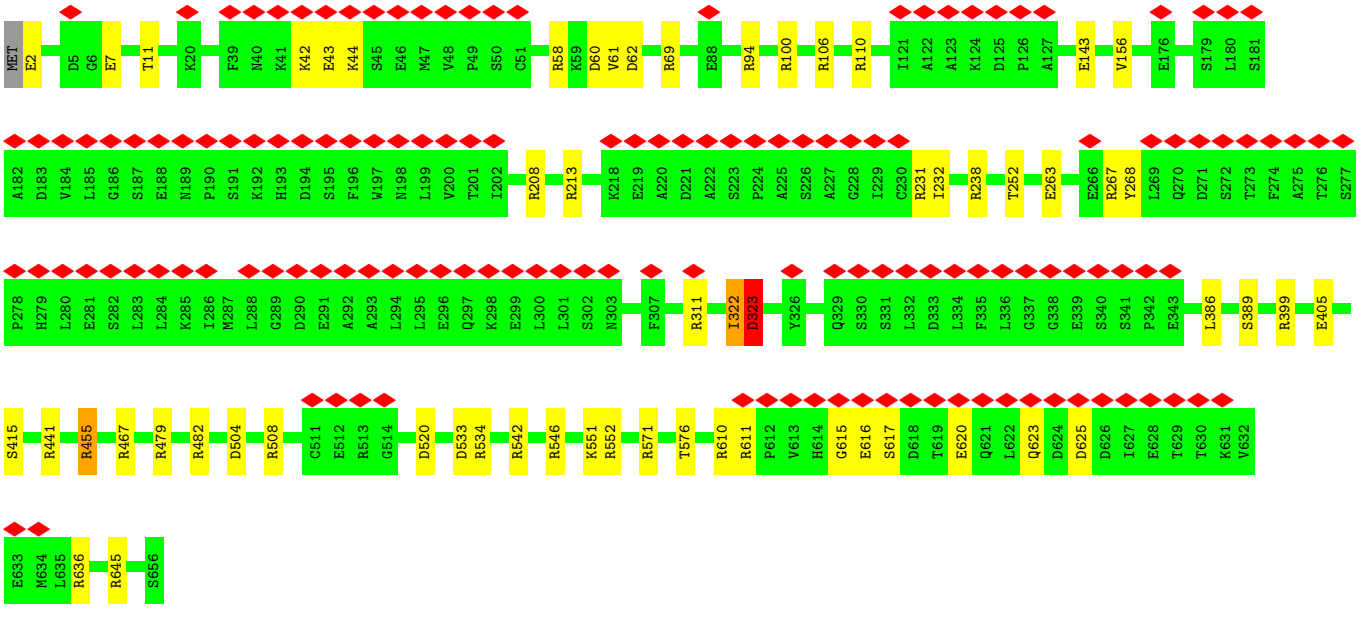
Chain O3:



• Molecule 18: Nuclear pore complex protein Nup85

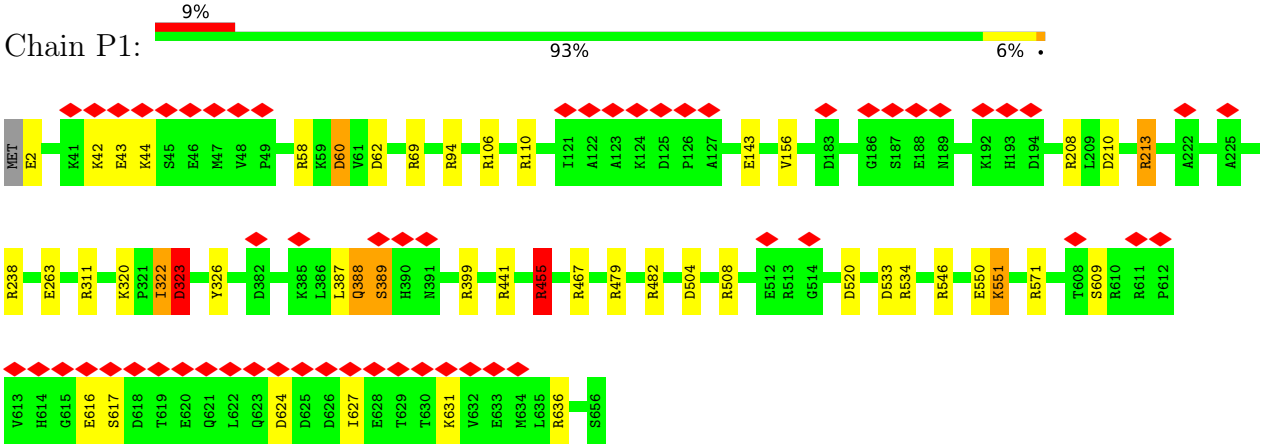
Chain P0:





• Molecule 18: Nuclear pore complex protein Nup85

Chain P1:



• Molecule 18: Nuclear pore complex protein Nup85

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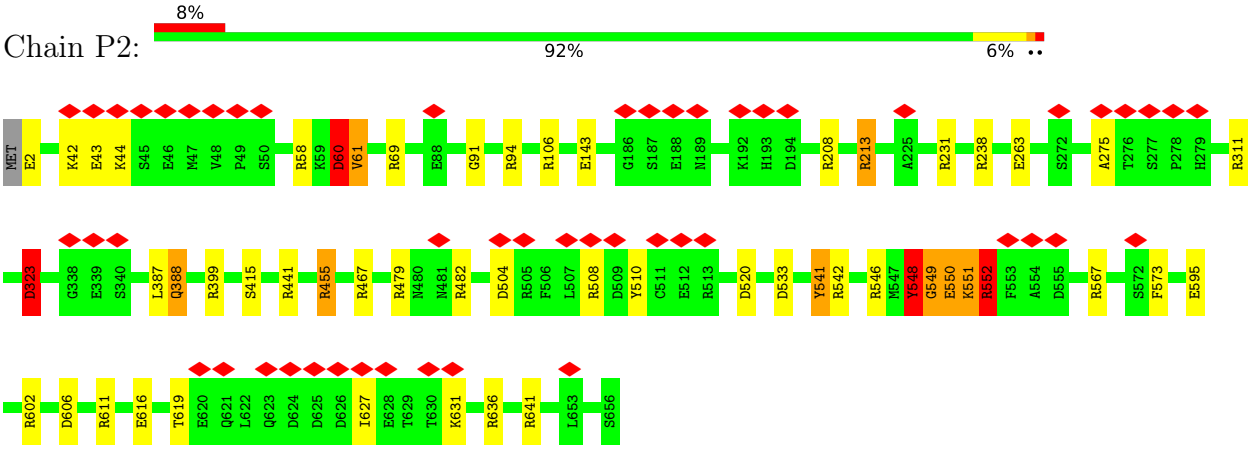
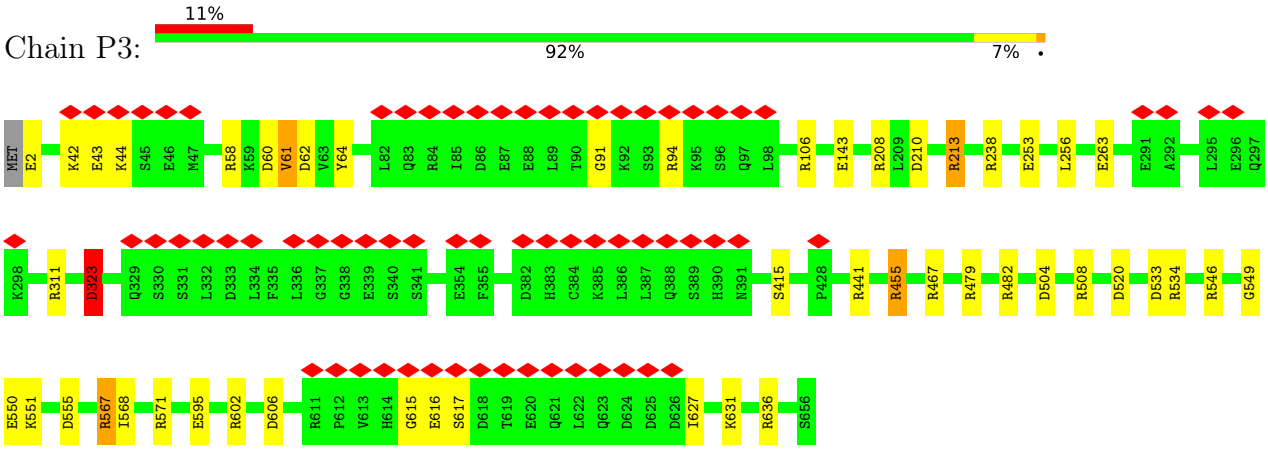


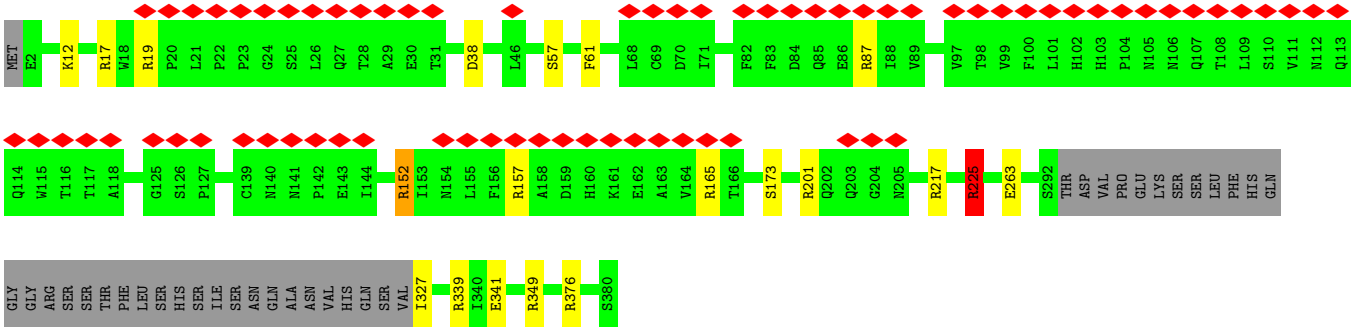
• Molecule 18: Nuclear pore complex protein Nup85

Chain P3:

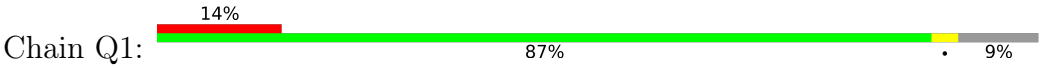


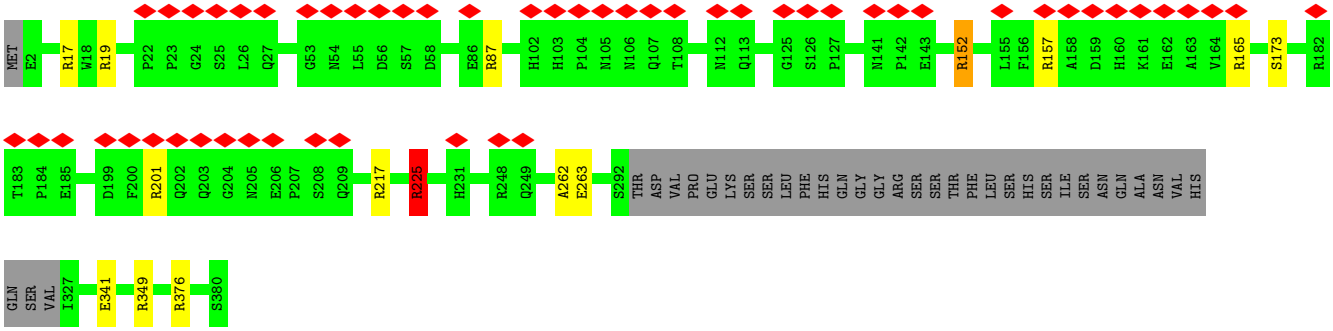
• Molecule 19: Nucleoporin Nup43

Chain Q0:

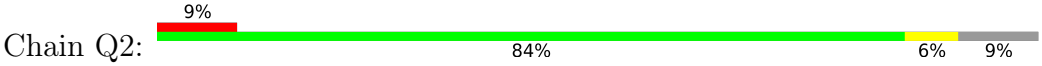


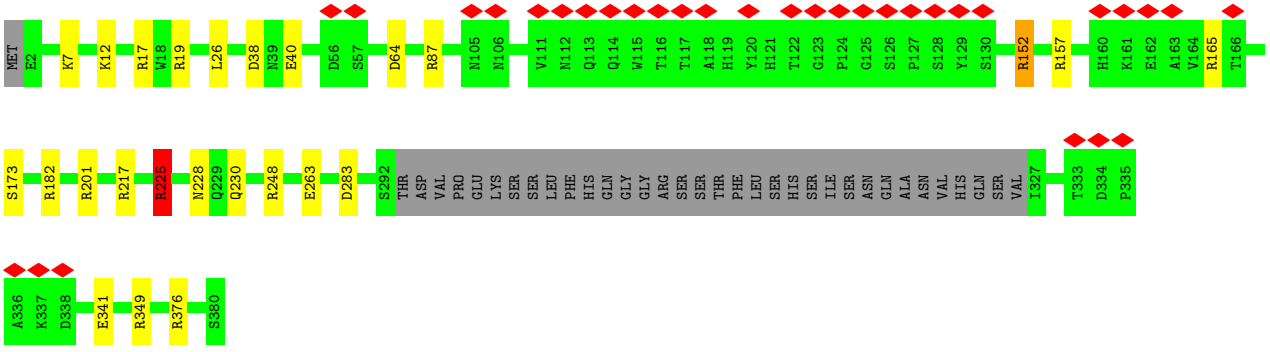
• Molecule 19: Nucleoporin Nup43



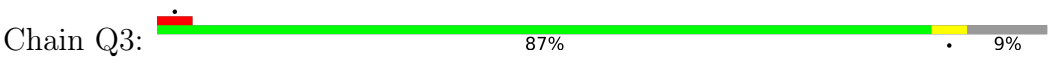


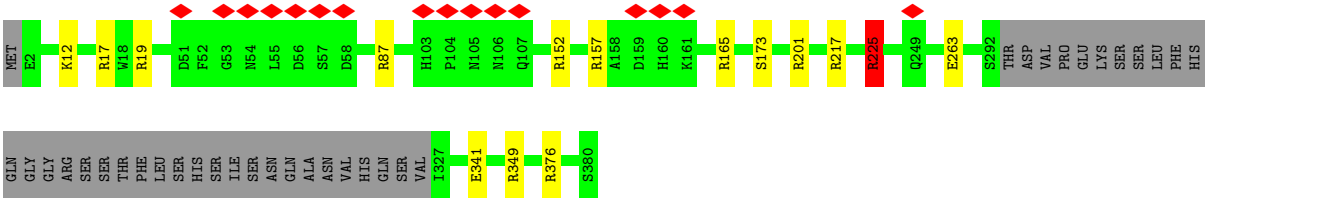
• Molecule 19: Nucleoporin Nup43





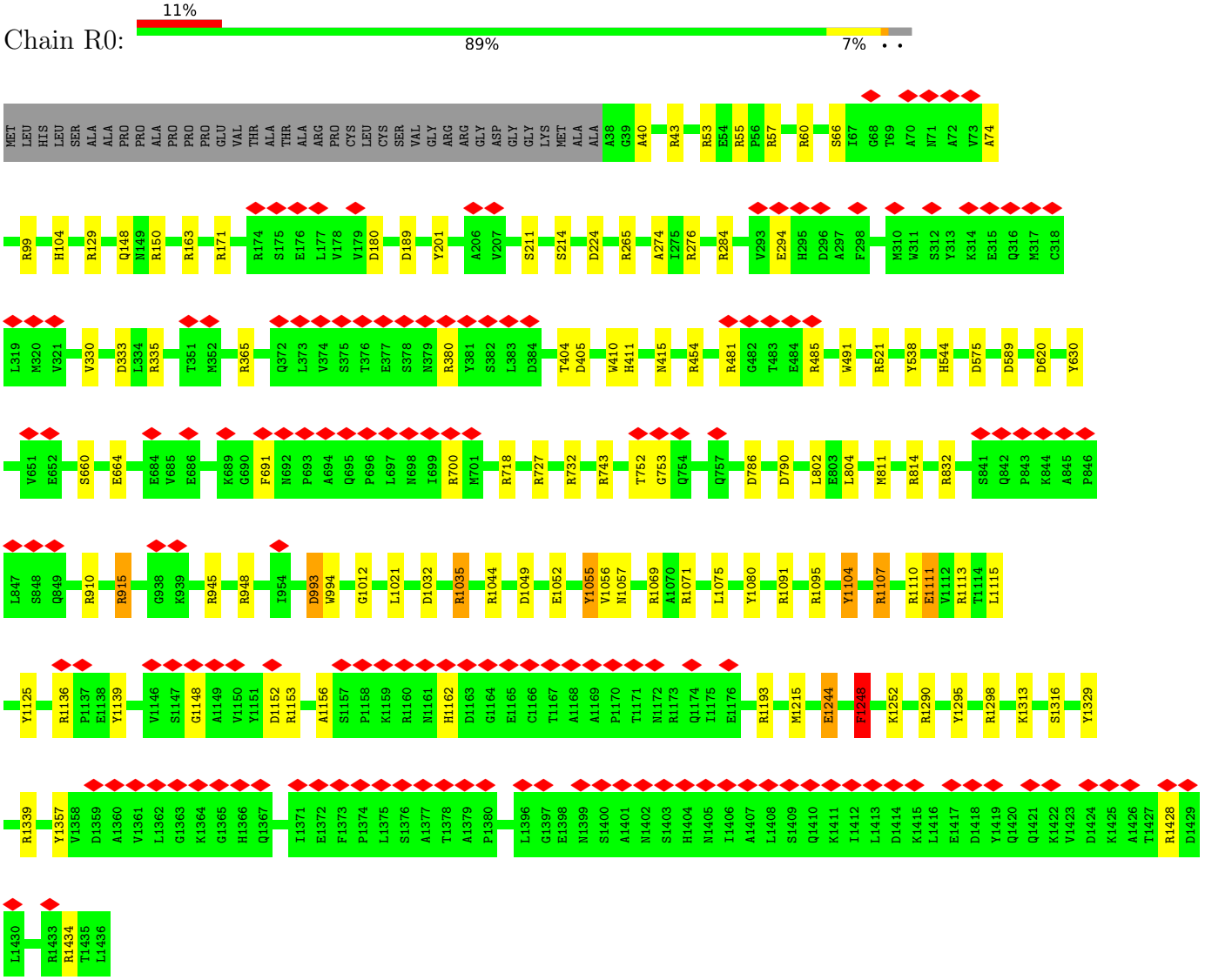
• Molecule 19: Nucleoporin Nup43





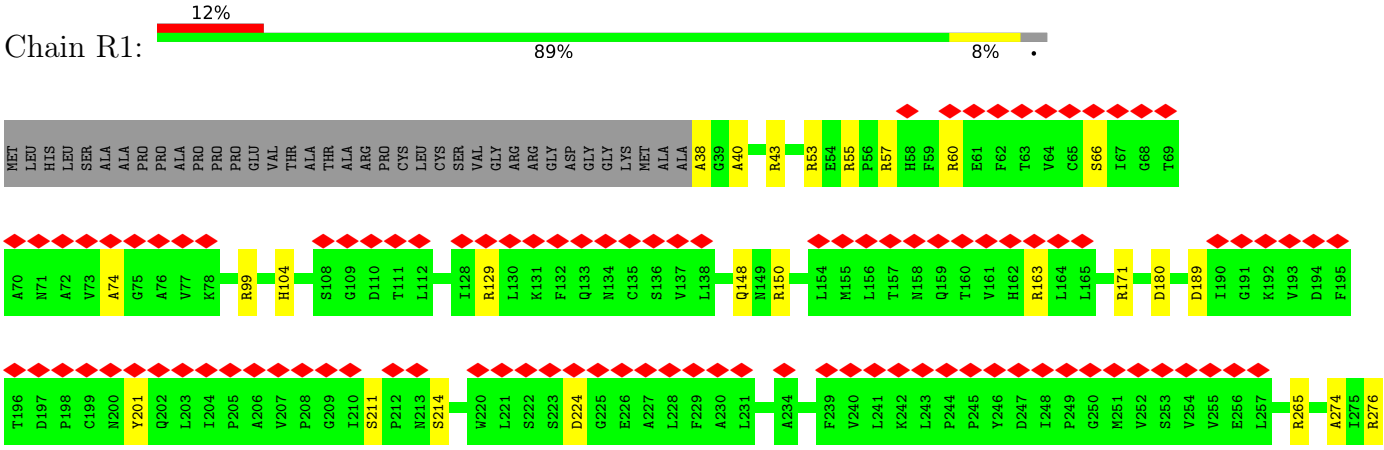
• Molecule 20: Nuclear pore complex protein Nup160

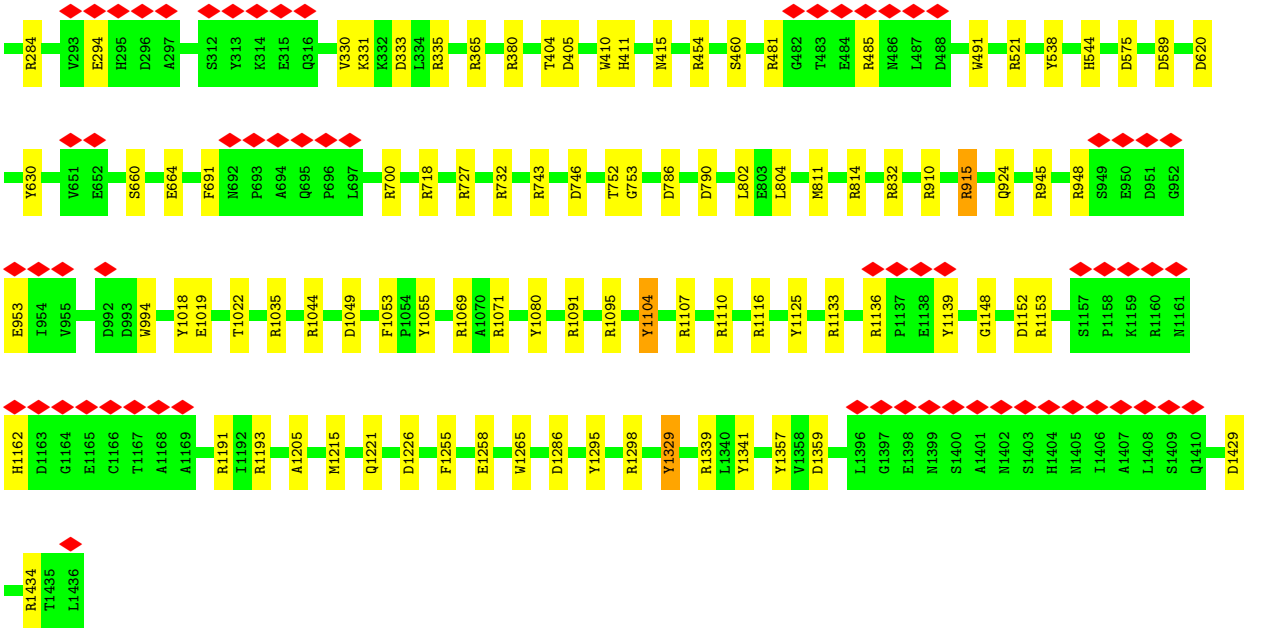
Chain R0:



• Molecule 20: Nuclear pore complex protein Nup160

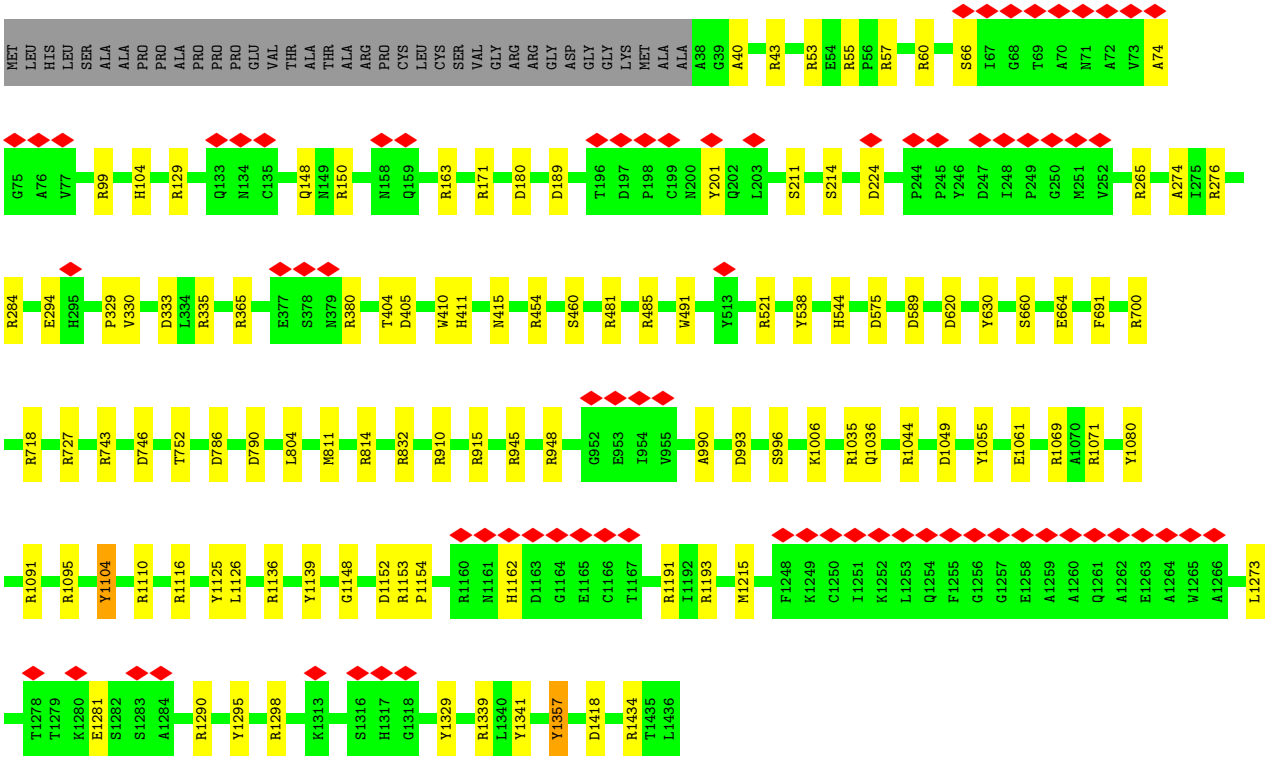
Chain R1:





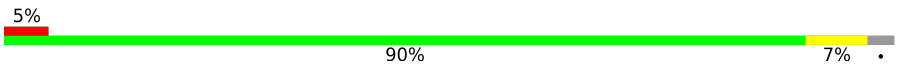
• Molecule 20: Nuclear pore complex protein Nup160

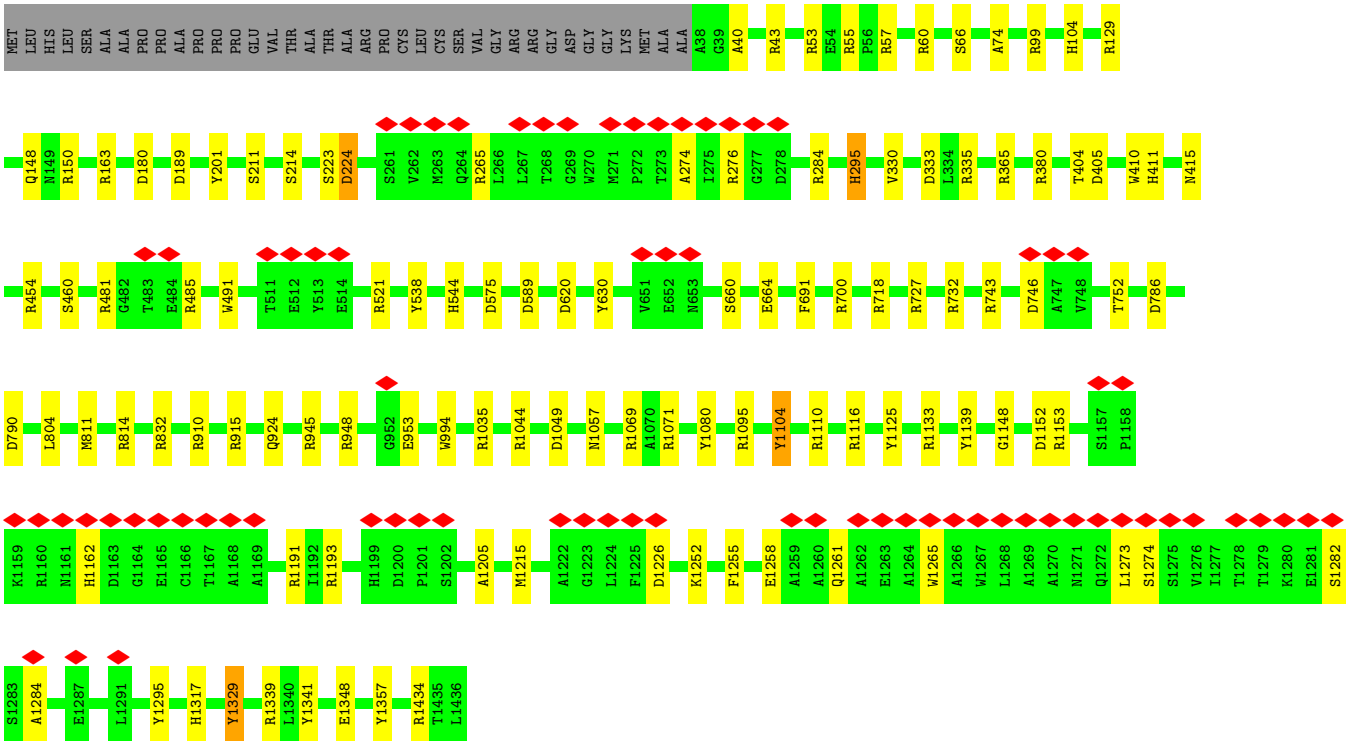
Chain R2:



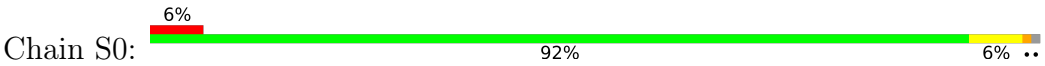
• Molecule 20: Nuclear pore complex protein Nup160

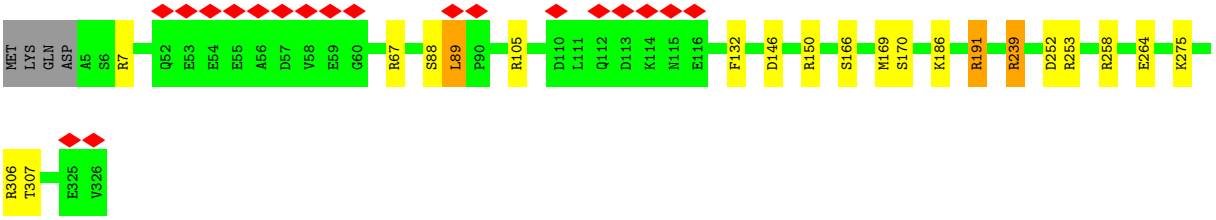
Chain R3:



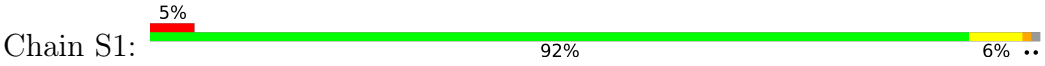


• Molecule 21: Nucleoporin Nup37

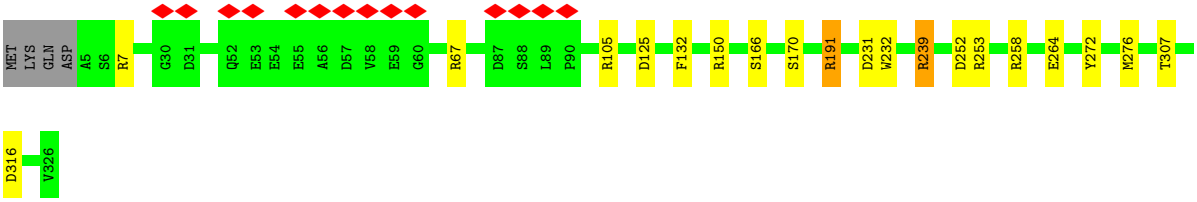




• Molecule 21: Nucleoporin Nup37

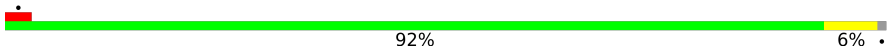


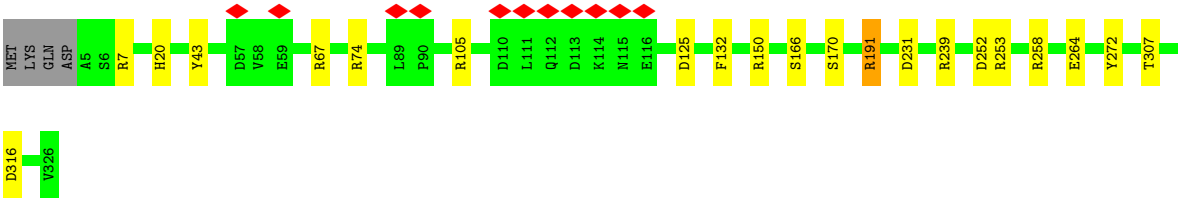
• Molecule 21: Nucleoporin Nup37



• Molecule 21: Nucleoporin Nup37

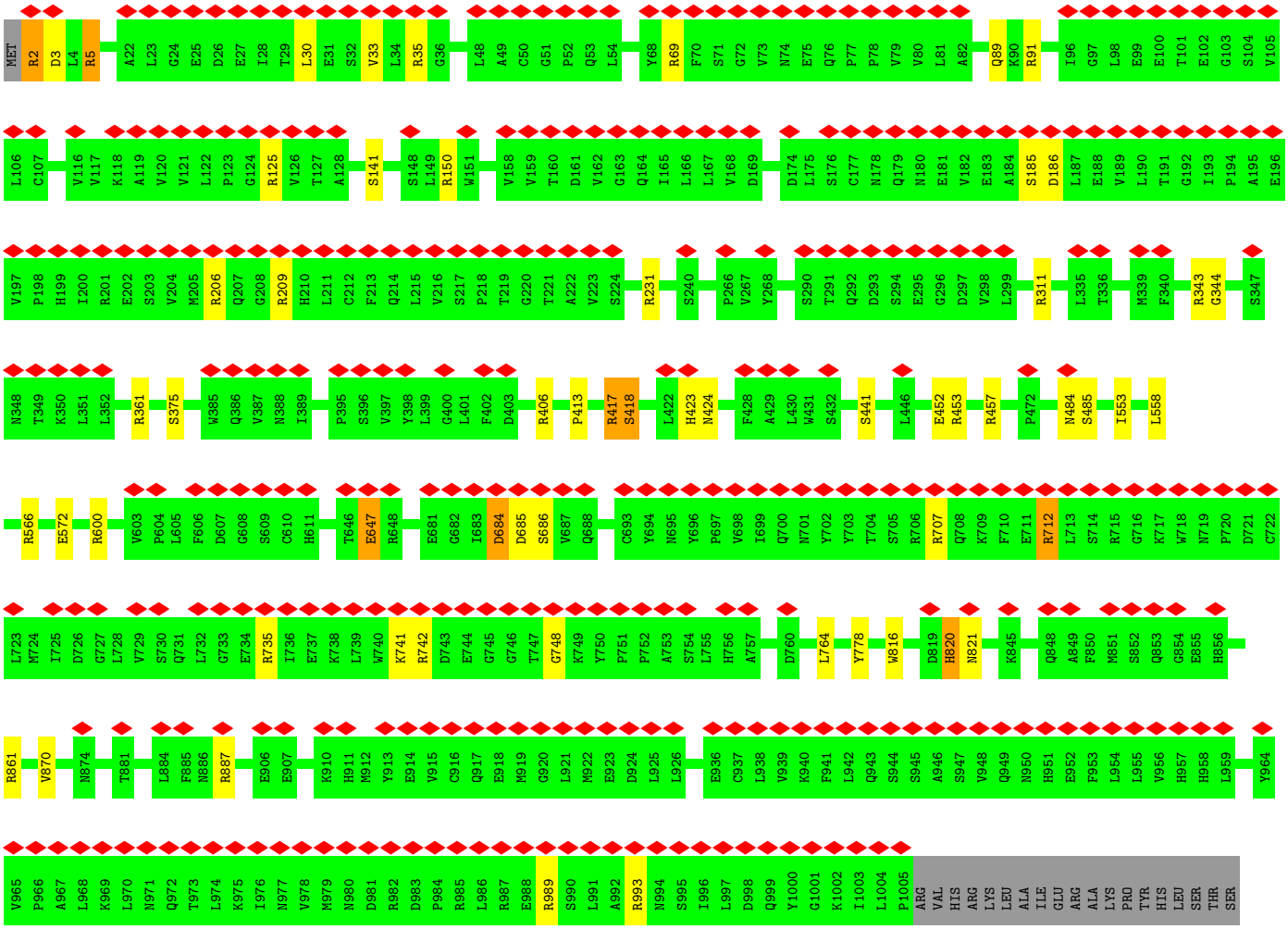
Chain S3:





• Molecule 22: Protein ELYS

Chain T0:



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

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

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

LYS LYS LYS LEU THR LYS LYS THR GLU SER GLN SER GLN LYS ARG SER LEU HIS SER VAL SER GLU 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 SER SER ARG THR ARG SER SER LYS ALA

ILE LEU LEU PRO ASP LEU SER GLU PRO ASN ASN GLU PRO LEU VAL PHE SER PRO ALA SER GLU VAL PRO ARG LYS 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 LEU GLU ASP GLU LEU LYS 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 22: Protein ELYS

Chain T1: 36% 42% 56%

MET R2 D3 L4 R5 A6 Q7 T19 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 E55 V56 V57 R64 L65 S66 A67 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 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 L226 S227 Y228 I229 S230 R231 T232 N233 Q234 L235 A236 V237 G238 F239 S240 D241 G242 Y243 L244 A245 L246 W247 N248 M249 K250 S251 M252 K253 R254 E255 Y256

Y257 I258 Q259 L260 E261 S262 G263 Q264 V265 P266 V267 Y268 A269 V270 T271 P272 Q273 E274 P275 E276 N277 D278 P279 R280 N281 C282 C283 Y284 L285 W286 A287 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 L351 L352 G353 C354 Q355 S356 I357 E358 K359 F360 R361 S362 H363 G364 D365 R366 E367 E368 G369 V370 N371 E372 A373 L374 S375 P376

D377 T378 S379 V380 S381 V382 F383 T384 W385 Q386 V387 N388 I389 Y390 P395 S396 V397 Y398 L399 G400 L401 F402 D403 I404 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 S432 L433 E434 S435 S441 G444

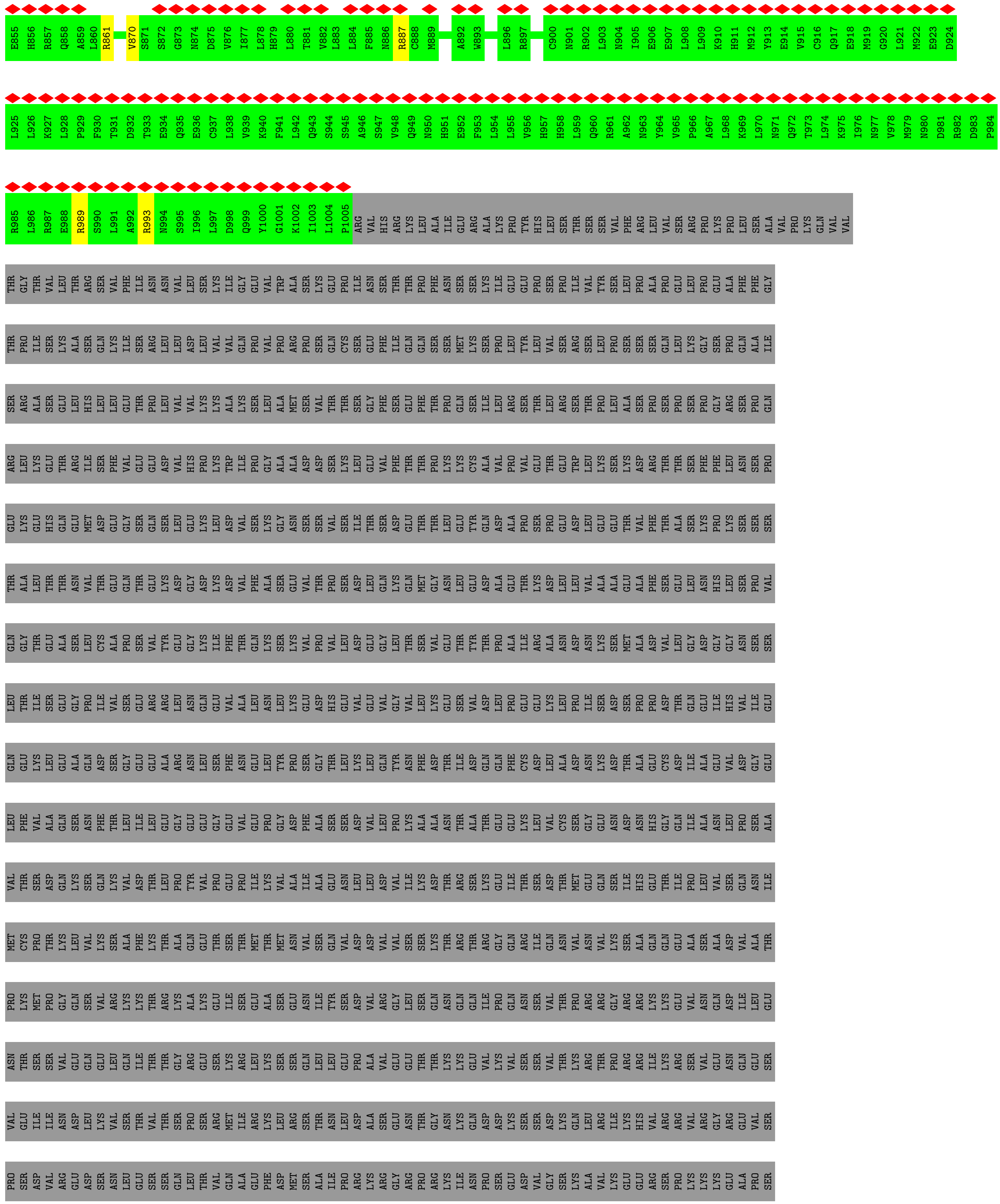
I445 L446 D447 I448 L449 V450 H451 E452 R453 S454 L455 N456 R457 G458 V459 P460 P461 S462 Y463 P464 P465 P466 E467 Q468 F469 F470 N471 P472 S473 T474 Y475 N476 F477 L482 L483 N484 S485 T491 C492 T493 G494 F495 Q496 K497 E498 T499 L500 T501 F502 L503 K504 K505 S506 G507 P508 S509 L510 N511

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 E571 E572 Q573 P574 N575 S576 A577 T578 N579 L580 R581 F582

V583 L584 E585 R600 V603 P604 L605 F606 D607 G608 S609 C610 H611 F612 E644 I645 T646 E647 R648 G649 L650 I651 D652 N655 L678 L679 P680 E681 G682 I683 D684 D685 S686 V687 Q688 L689 S690 R691 L692 C693 Y694 N695 Y696 P697 V698 I699 Q700 N701 Y702 Y703 T704 S705 R706 R707 Q708

K709 F710 E711 R712 L713 S714 R715 G716 K717 W718 N719 P720 D721 C722 L723 M724 I725 D726 G727 L728 V729 S730 Q731 L732 G733 E734 R735 I736 E737 K738 L739 W740 K741 R742 D743 E744 G745 G746 T747 G748 K749 Y750 P751 P752 A753 S754 L755 H756 A757 V758 L759 D760 M761 Y762 L763 L764 D765 G766 V767

A771 K772 H773 S774 I775 T776 I777 Y778 L779 L780 L781 D782 I783 M784 Y785 S786 F787 P788 W789 K790 T791 D792 V809 K810 L811 I812 Q813 G814 F815 W816 L817 I818 D819 N820 N821 D822 Y823 E824 S825 G826 L827 D828 L829 L830 W841 Q842 H843 S844 K845 I846 I847 Q848 A849 F850 M851 S852 Q853 G854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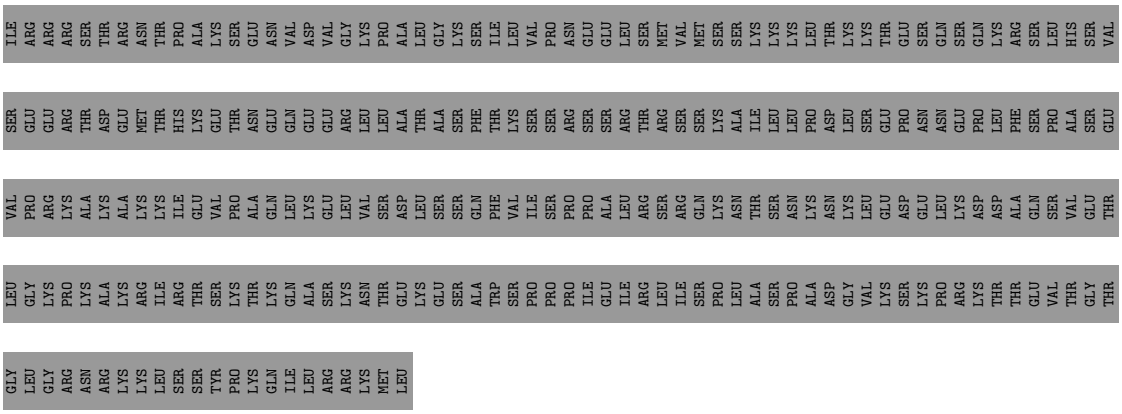
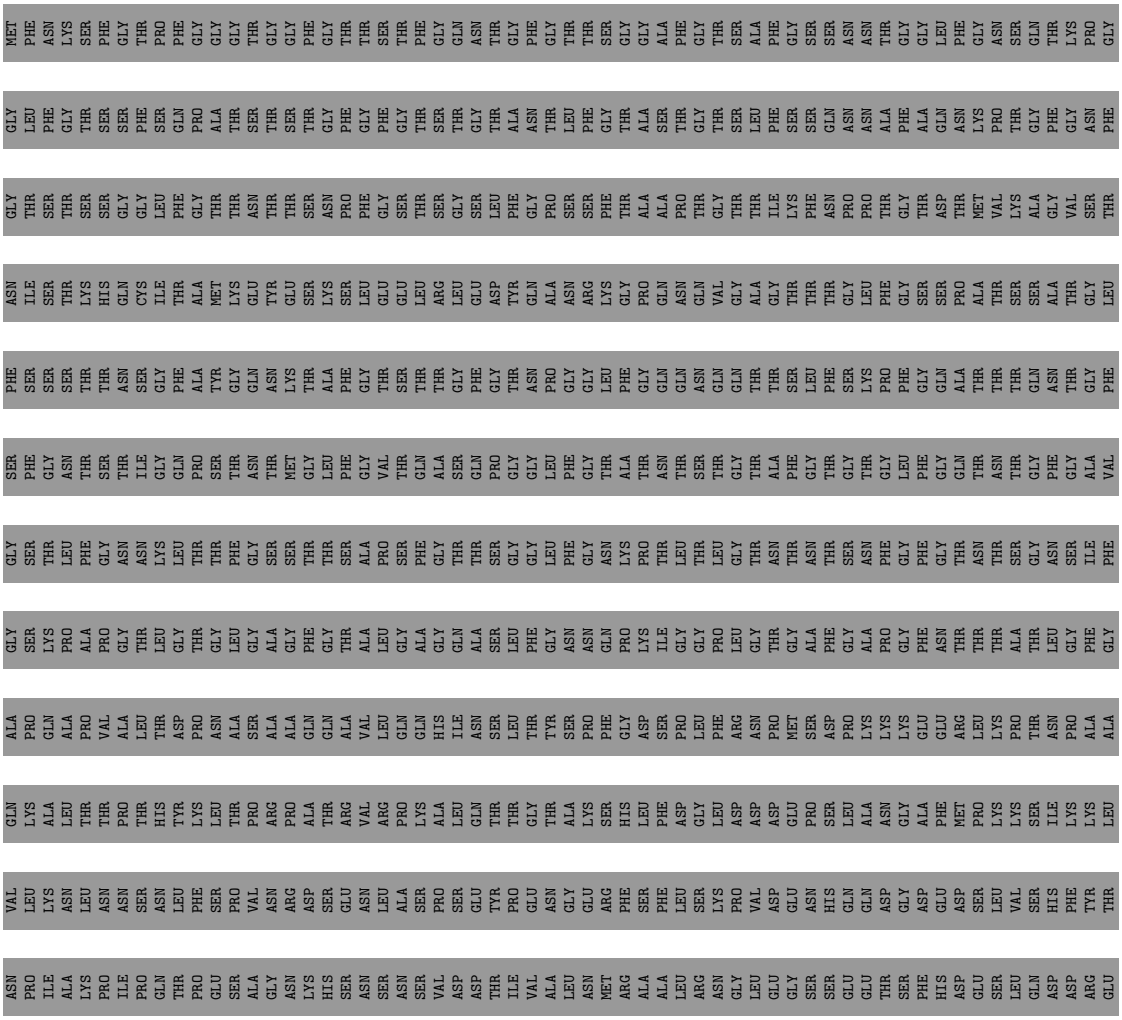
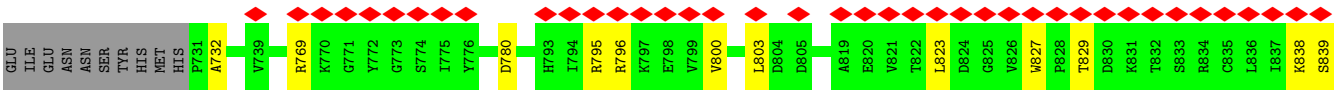
L925 L926 K927 L928 P929 F930 T931 D932 T933 E934 Q935 E936 C937 L938 V939 K940 F941 L942 Q943 S944 S945 A946 S947 V948 Q949 N950 H951 E952 F953 L954 L955 V956 H957 H958 L959 Q960 R961 A962 N963 Y964 V965 P966 A967 L968 K969 L970 N971 Q972 T973 L974 K975 I976 N977 V978 M979 N980 D981 R982 D983 P984
R985 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 GLN GLU MET ASP GLU GLY SER GLN SER LEU GLU LYS LEU ASP 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 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 ASP VAL PHE ALA SER GLU VAL THR PRO SER 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 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 SER GLU ARG ARG LEU ASN GLN GLU VAL ALA LEU ASN LEU LYS GLU ASP HIS GLU VAL GLU VAL GLY VAL LEU LYS GLU SER VAL ASP LEU PRO GLU GLU LYS LEU PRO ILE SER ASP SER PRO PRO ASP THR GLN 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 LEU TYR PRO SER GLY THR LEU LYS LEU GLN TYR ASN PHE ASP THR ILE ASP GLN GLN PHE CYS ASP LEU ALA ASP ASN LYS ASP THR ALA GLU CYS ASP 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 ASN HIS GLY 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 ASN LEU LEU 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 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 THR ARG GLY GLN ARG ILE GLN ASN VAL ASN VAL LYS SER ALA GLN GLU GLU ALA SER ALA ASP VAL ALA THR
PRO LYS MET PRO GLY GLN SER VAL ARG LYS LYS THR ARG LYS ALA LYS GLU ILE SER GLU ALA SER GLU ASN ILE TYR SER ASP VAL ARG GLY LEU SER GLN ASN 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 VAL GLU GLN GLU LEU GLN ILE THR THR GLY ARG GLU SER LYS ARG LEU LYS SER SER GLN LEU LEU GLU PRO ALA VAL GLU GLU THR THR 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 SER LYS ALA VAL LYS GLU GLU ARG SER PRO LYS LYS LYS GLU ALA PRO SER

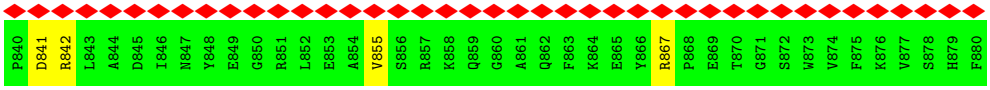


• Molecule 23: Nuclear pore complex protein Nup98

Chain U0: 9% 15% 83%

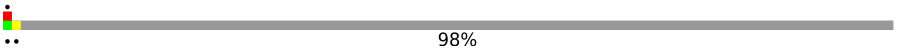


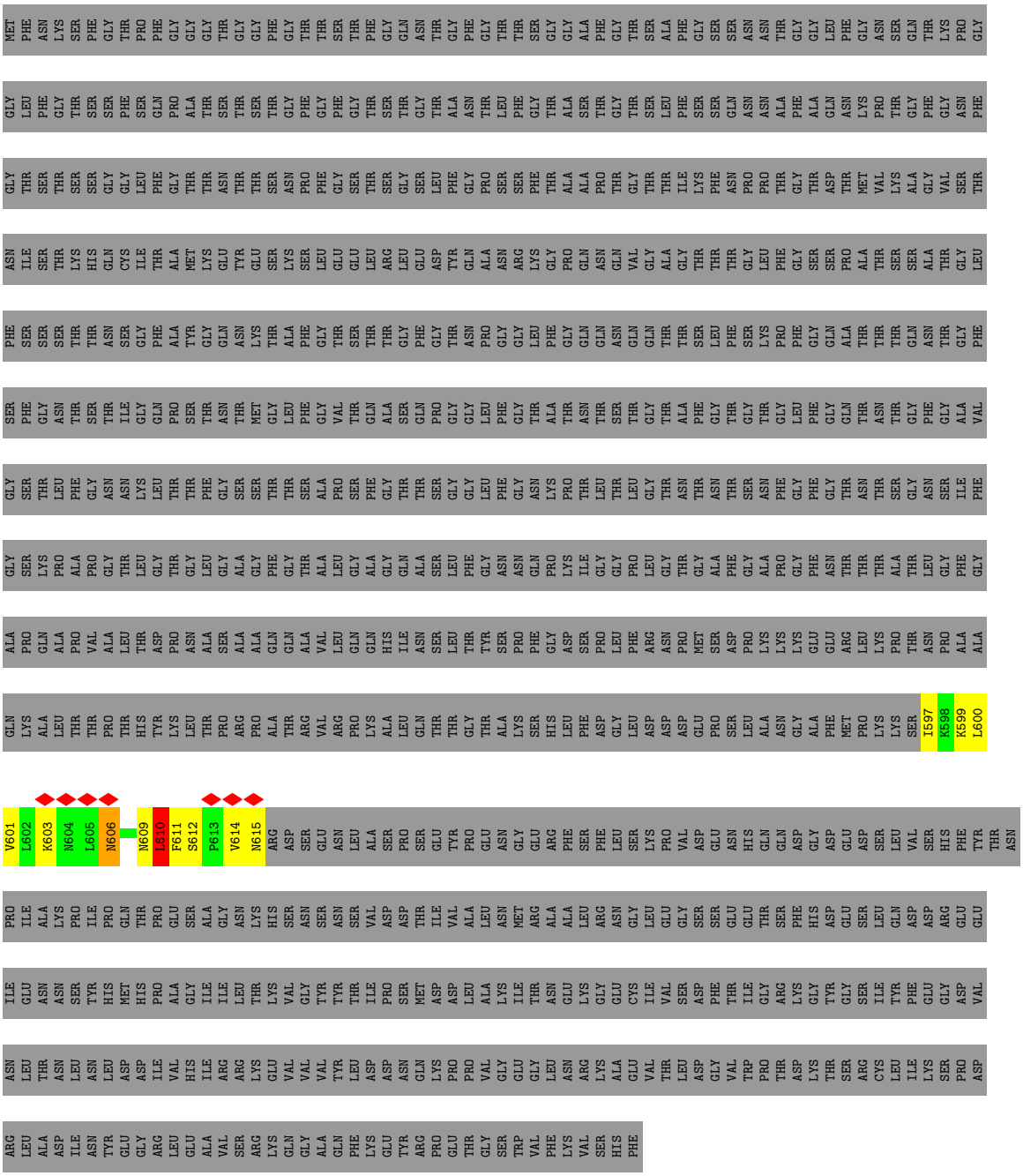




• Molecule 23: Nuclear pore complex protein Nup98

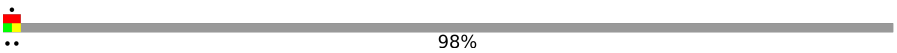
Chain U1:

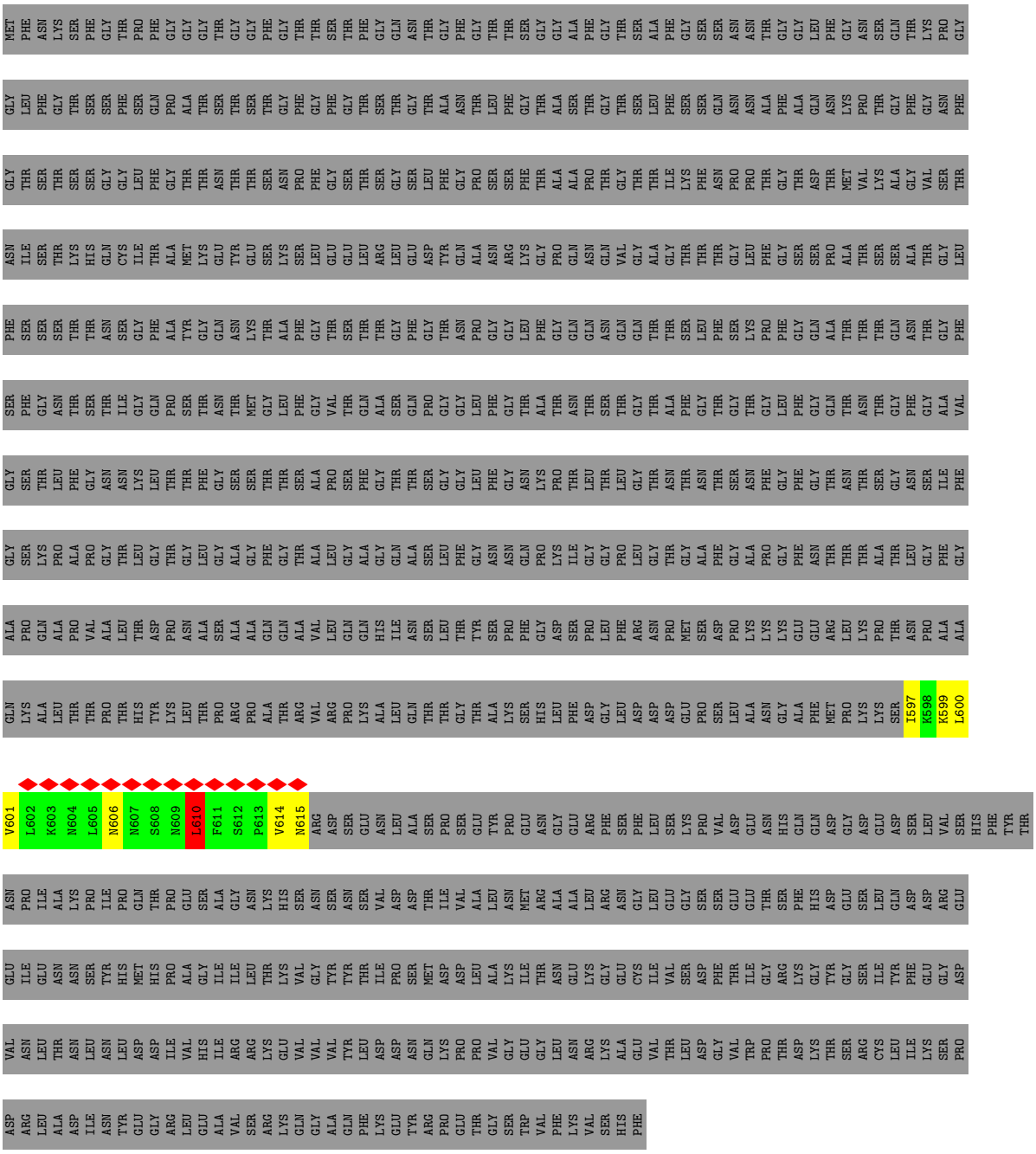




• Molecule 23: Nuclear pore complex protein Nup98

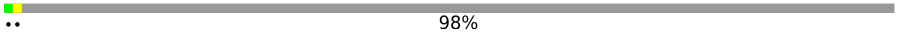
Chain U2:

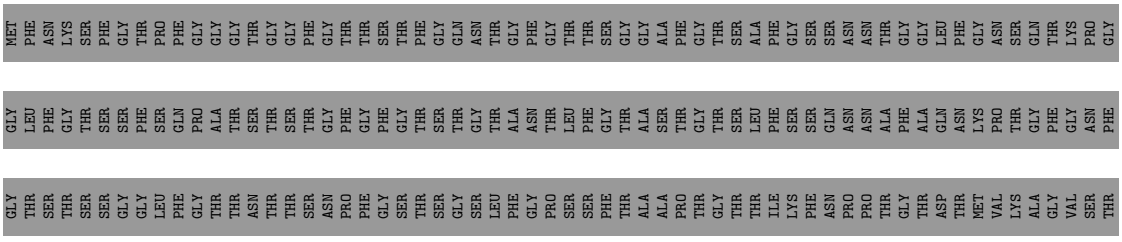


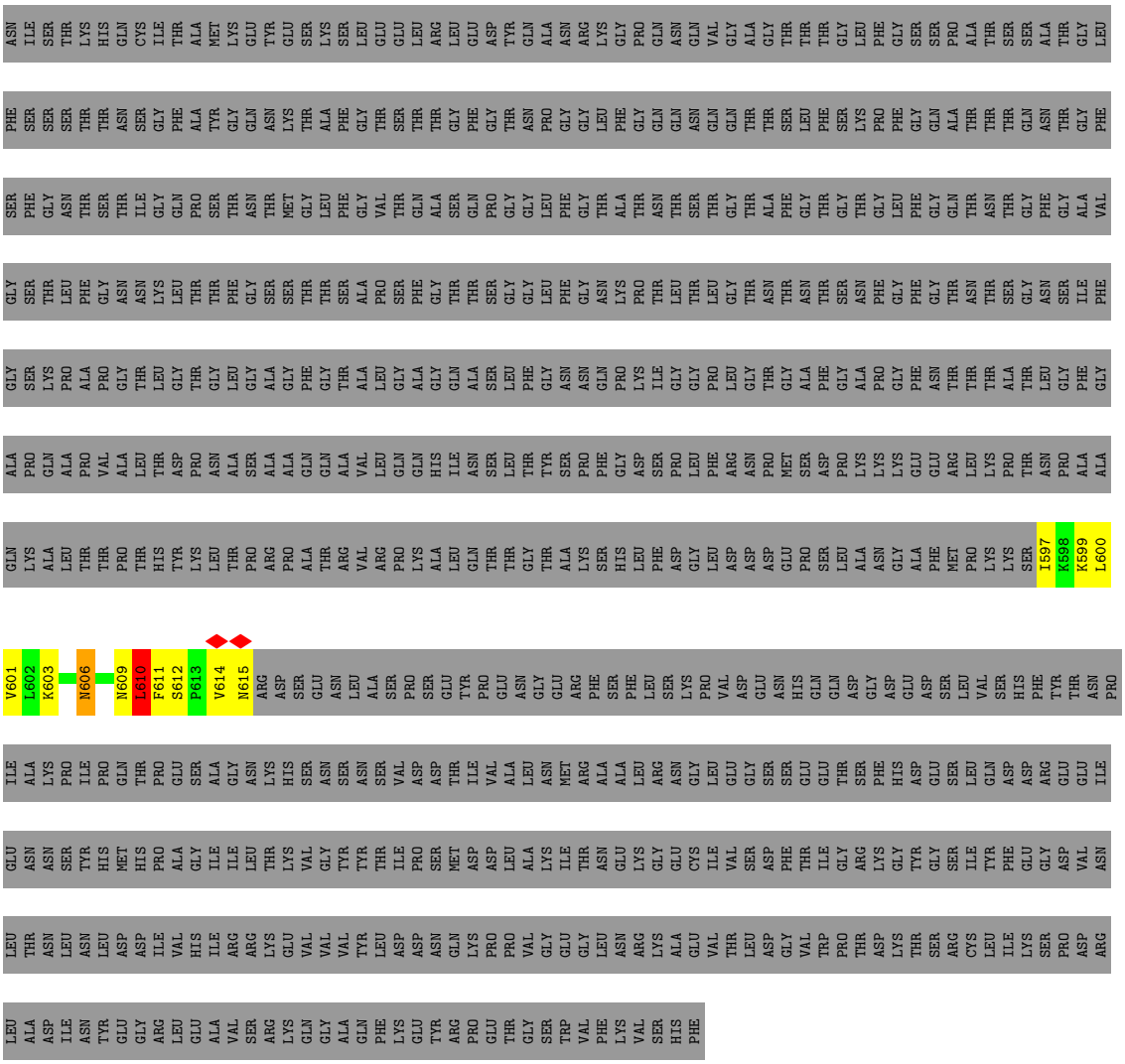


• Molecule 23: Nuclear pore complex protein Nup98

Chain U3:

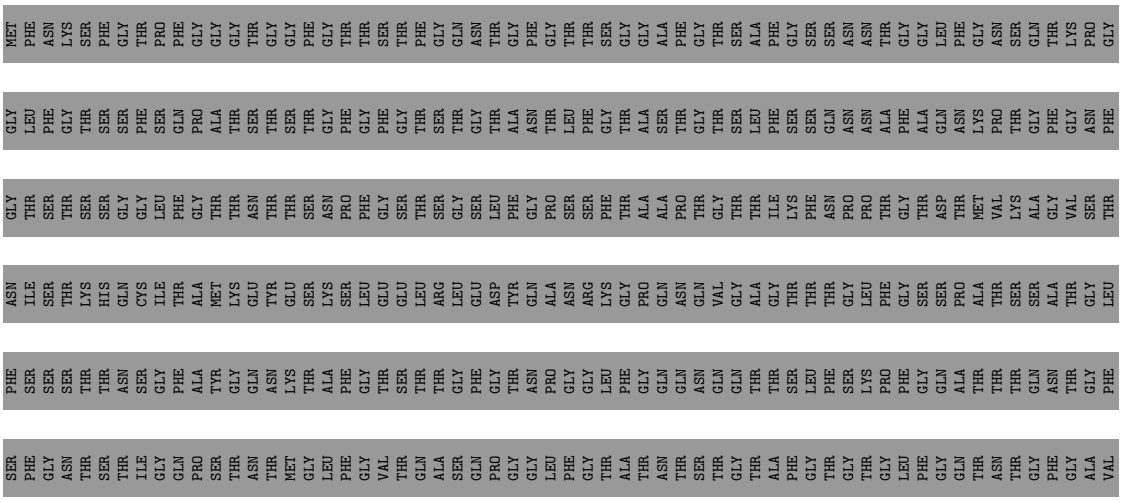


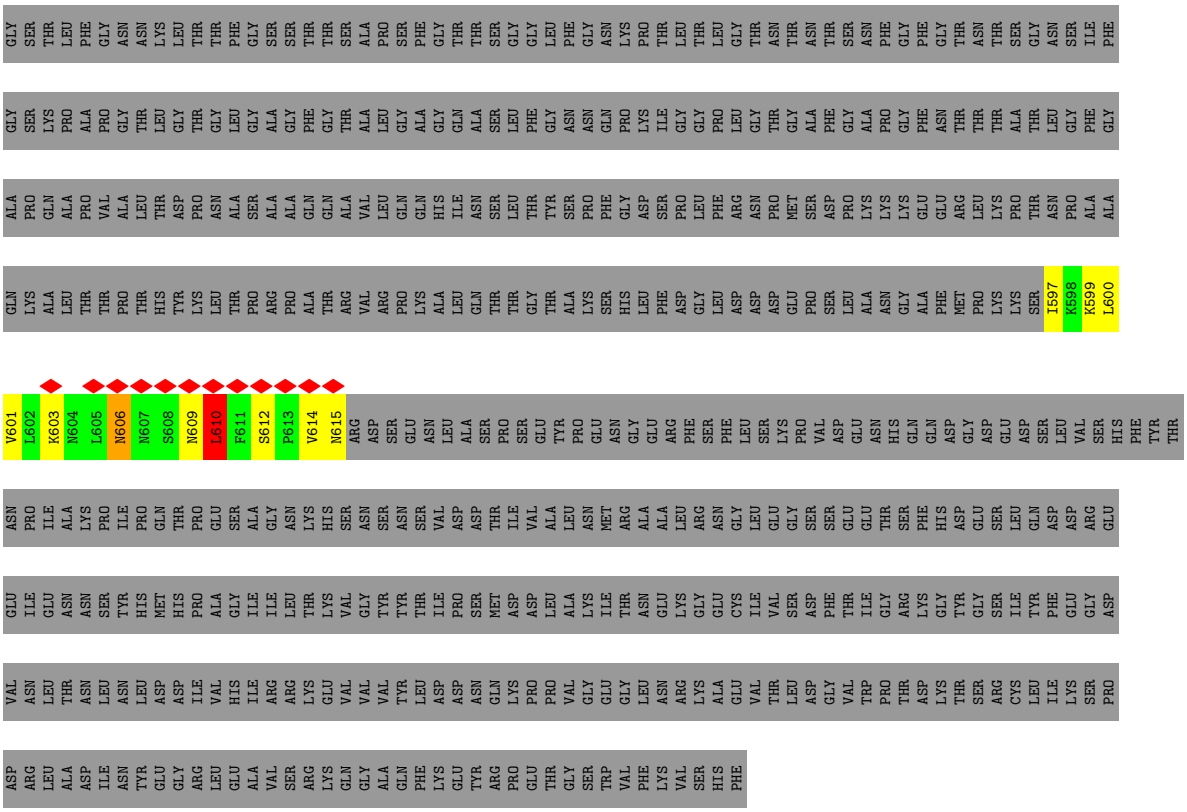




• Molecule 23: Nuclear pore complex protein Nup98

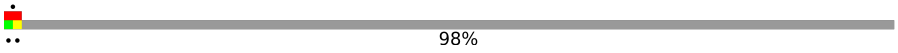
Chain U4:

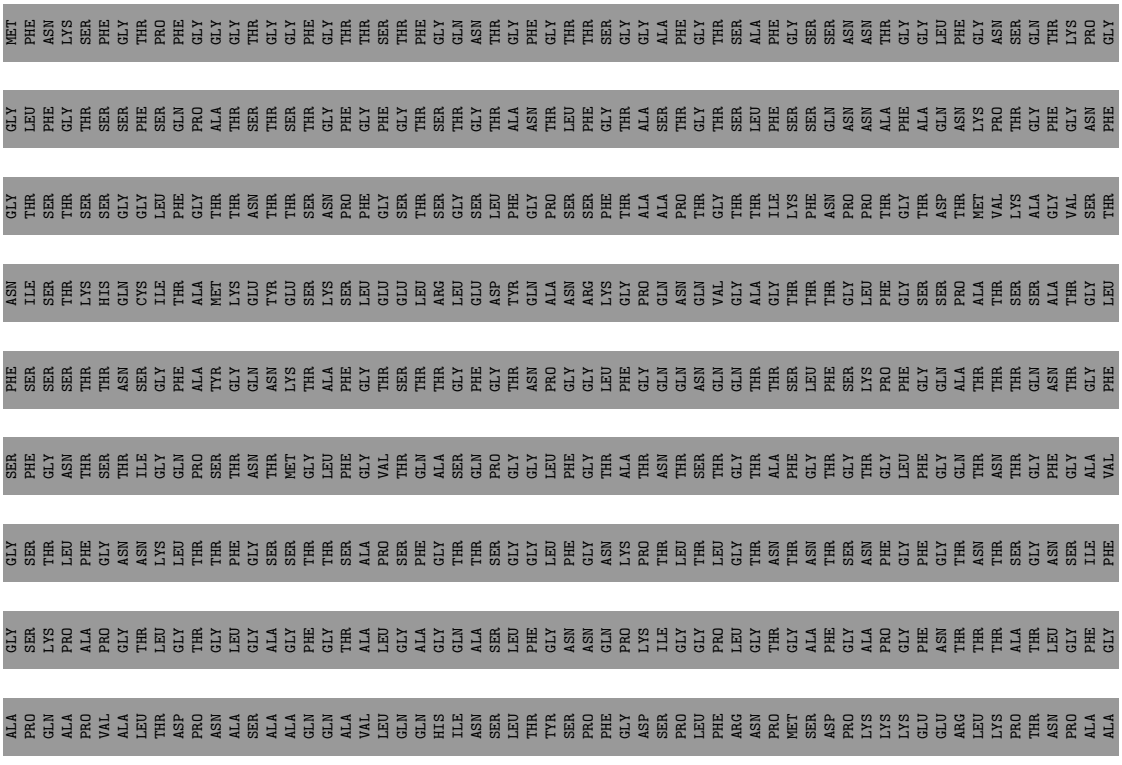


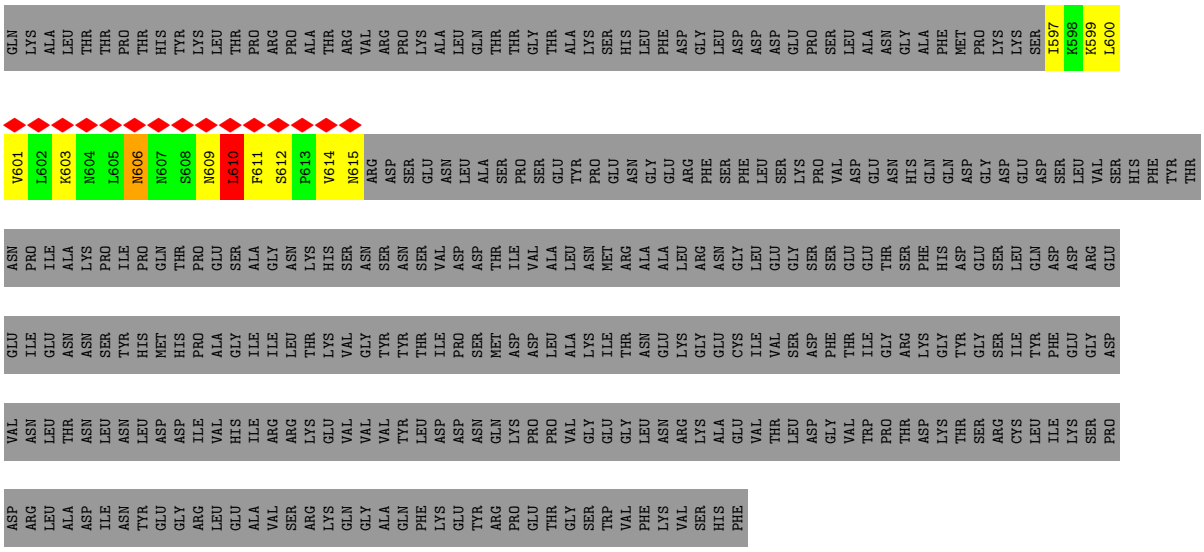


• Molecule 23: Nuclear pore complex protein Nup98

Chain U5:

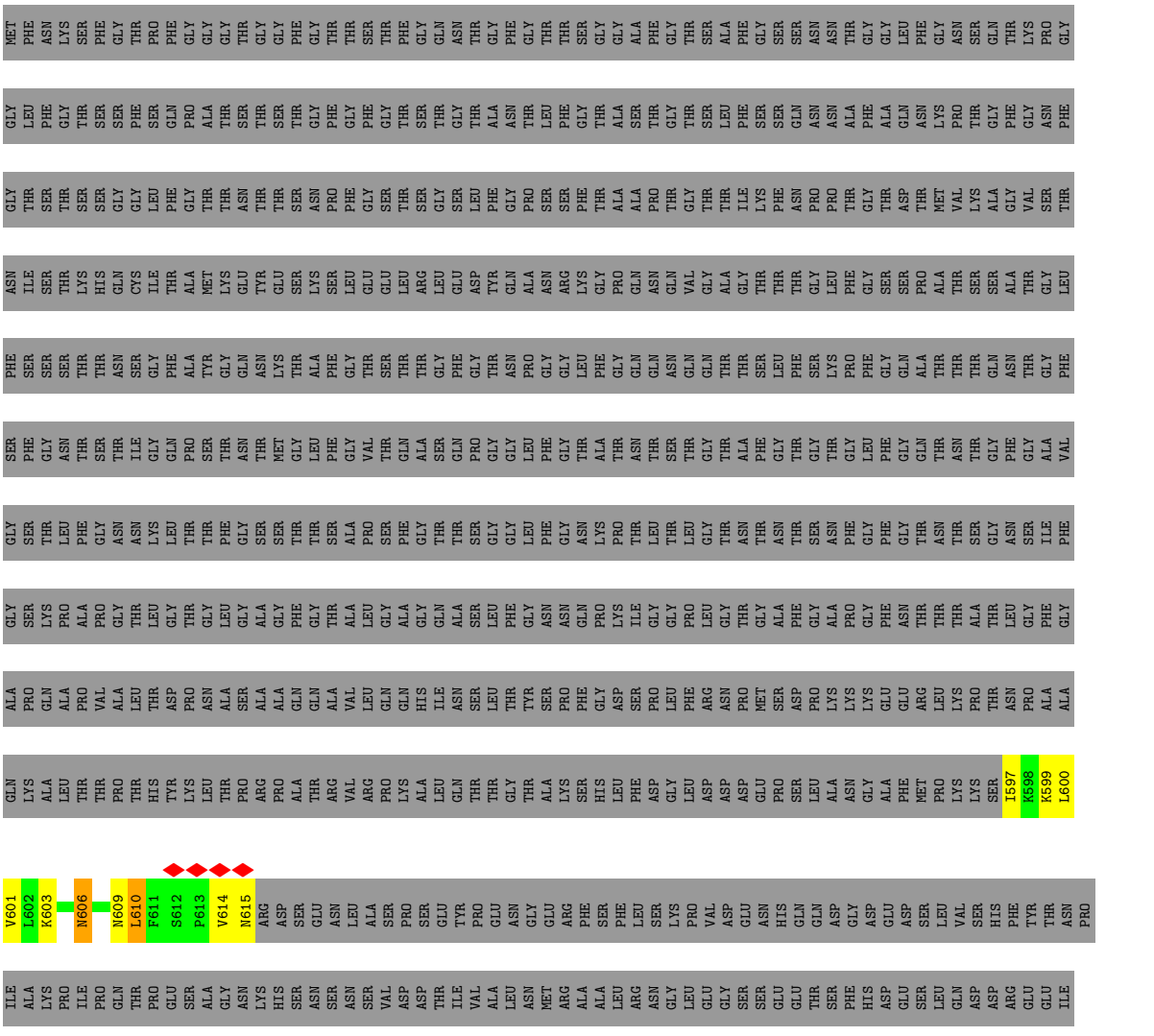


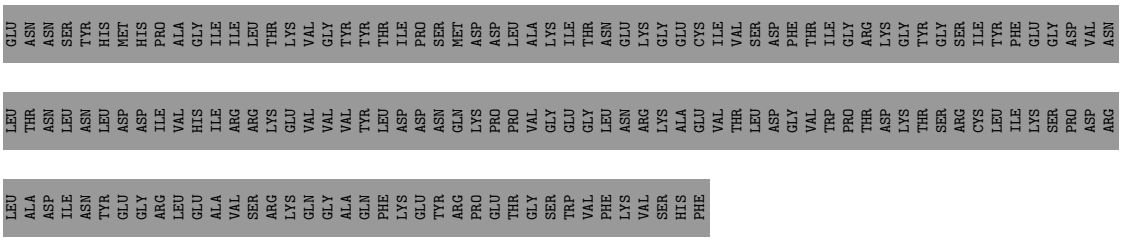




• Molecule 23: Nuclear pore complex protein Nup98

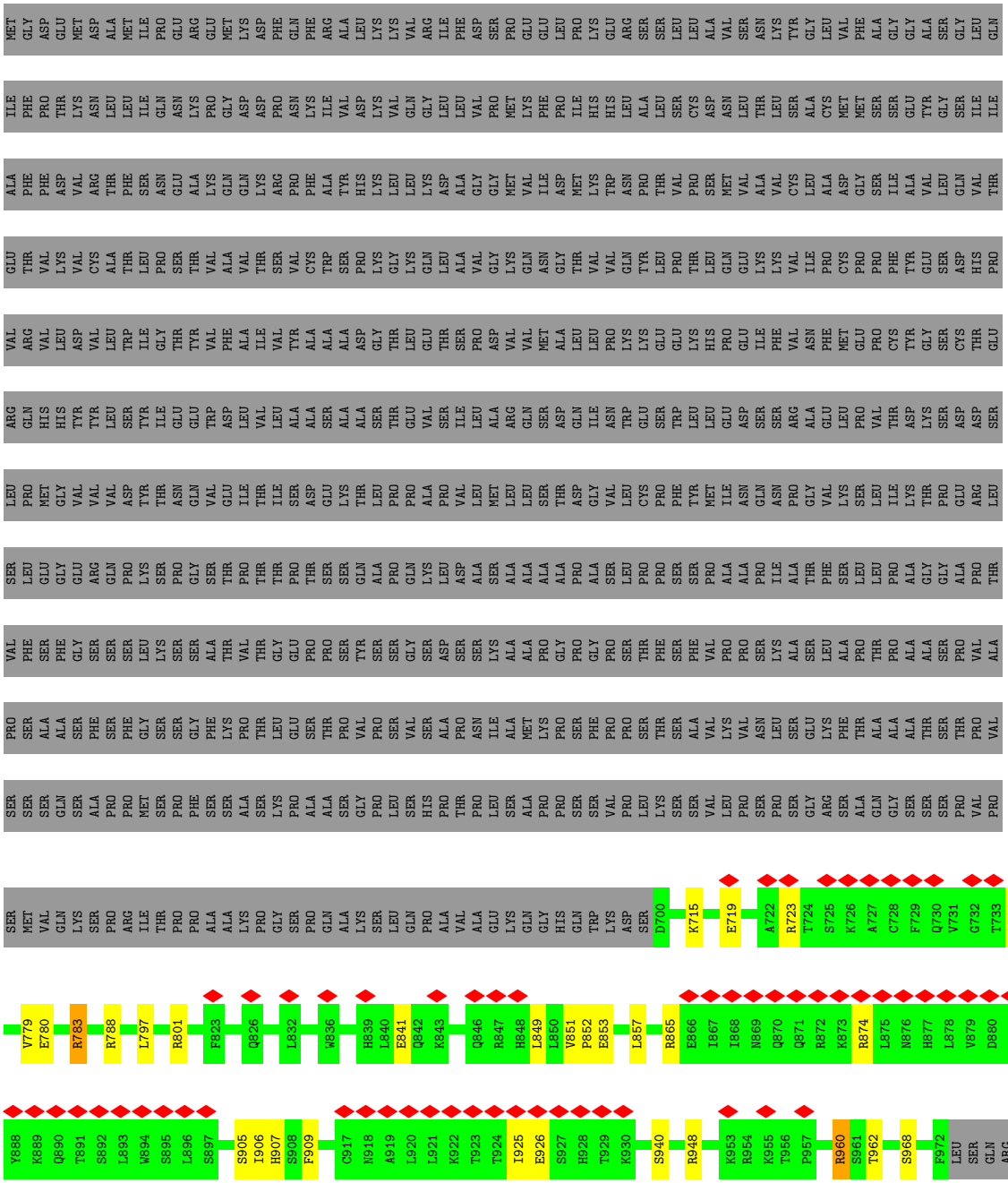
Chain U6: 98%





• Molecule 24: Nuclear pore complex protein Nup214

Chain V0:



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

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THR 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

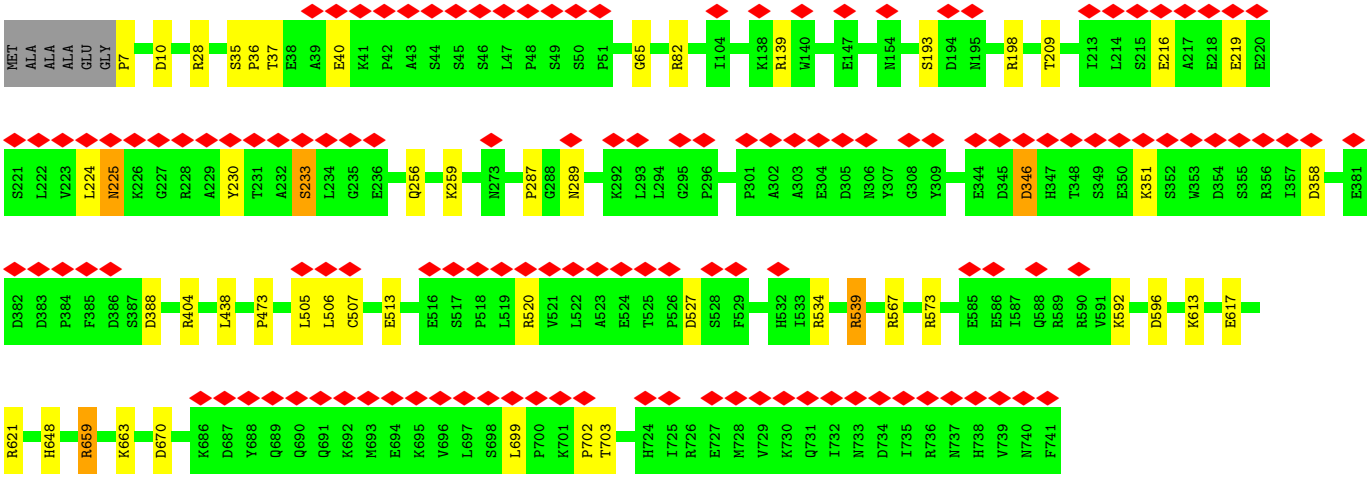
LEU GLY SER THR GLY GLY LYS VAL PHE GLY GLU GLY THR ALA ALA ALA SER ALA GLY GLY PHE GLY PHE GLY SER SER ASN THR THR SER PHE GLY THR LEU ALA SER GLN ASN ALA PRO THR PHE GLY SER LEU SER GLN GLN THR SER GLY PHE GLY THR GLN SER SER GLY PHE

SER GLY PHE GLY SER 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

18%

Chain W0: 92% 6% ••


MET ALA ALA ALA GLU GLY P7 D10 R28 S35 P36 T37 E38 A39 E40 K41 P42 A43 S44 S45 S46 L47 P48 S49 S50 P51 G65 R82 I104 K138 R139 W140 E147 N154 S193 D194 N195 R198 T209 I213 L214 S215 E216 A217 E218 E219 E220
S221 L222 V223 L224 N225 K226 G227 R228 A229 Y230 T231 A232 S233 L234 G235 E236 Q256 K259 N273 P287 G288 N289 K292 L293 L294 G295 P296 P301 A302 A303 E304 D305 N306 Y307 G308 Y309 E344 D345 D346 H347 T348 S349 E350 K351 S352 W353 D354 S355 R356 I357 D358 E381
D382 D383 P384 F385 D386 S387 D388 R404 L438 P473 L505 L506 C507 E513 E516 S517 P518 L519 R520 V521 L522 A523 E524 T525 P526 D527 S528 F529 H532 I533 R534 R539 R567 R573 E585 E586 I587 Q588 R589 R590 V591 K592 D596 K613 E617
R621 H648 R659 K663 D670 K686 D687 Y688 Q689 Q690 Q691 K692 M693 E694 K695 V696 L697 S698 L699 P700 K701 P702 T703 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, Not provided	
Number of subtomograms used	150	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	130	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.878	Depositor
Minimum map value	-0.768	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.0891	Depositor
Map size (Å)	1987.2001, 1987.2001, 1987.2001	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	13.8, 13.8, 13.8	Depositor

5 Model quality (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	1.04	21/8405 (0.2%)
1	01	0.69	0/6212	1.04	20/8405 (0.2%)
1	02	0.69	0/6212	1.04	18/8405 (0.2%)
1	03	0.69	0/6212	1.04	19/8405 (0.2%)
1	04	0.69	0/6212	1.04	21/8405 (0.2%)
2	10	1.01	5/14350 (0.0%)	1.01	49/19560 (0.3%)
2	11	0.65	0/14350	0.97	32/19560 (0.2%)
2	12	0.65	0/14350	0.97	37/19560 (0.2%)
2	13	0.65	0/14350	0.97	35/19560 (0.2%)
2	14	0.66	0/14350	0.98	42/19560 (0.2%)
2	15	0.65	0/14350	0.98	38/19560 (0.2%)
2	16	0.65	0/14350	0.98	38/19560 (0.2%)
2	17	0.68	7/14350 (0.0%)	1.01	51/19560 (0.3%)
3	40	0.68	0/3007	1.04	7/4114 (0.2%)
3	41	0.68	0/3007	1.04	7/4114 (0.2%)
4	A0	0.71	0/6687	1.07	31/9036 (0.3%)
4	A1	0.70	0/6687	1.06	31/9036 (0.3%)
4	A2	0.71	0/6687	1.08	29/9036 (0.3%)
4	A3	0.70	0/6687	1.05	29/9036 (0.3%)
4	A4	0.71	0/5972	1.05	27/8068 (0.3%)
4	A5	0.71	0/5972	1.03	25/8068 (0.3%)
4	A6	0.71	0/5972	1.04	27/8068 (0.3%)
5	B0	0.68	0/14018	1.02	44/19022 (0.2%)
5	B1	0.68	0/14018	1.01	36/19022 (0.2%)
6	C0	0.69	0/16330	1.04	76/22131 (0.3%)
6	C1	0.69	0/16330	1.04	73/22131 (0.3%)
6	C2	0.92	5/16330 (0.0%)	1.00	52/22131 (0.2%)
6	C3	0.69	0/16330	1.03	69/22131 (0.3%)
6	C4	0.69	0/16330	1.03	67/22131 (0.3%)
7	D0	0.67	0/10568	1.03	42/14320 (0.3%)
7	D1	0.98	3/10568 (0.0%)	1.05	48/14320 (0.3%)
7	D2	0.67	0/10568	1.02	39/14320 (0.3%)
7	D3	0.68	0/10568	1.02	36/14320 (0.3%)
7	D4	0.85	5/10568 (0.0%)	1.05	46/14320 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
7	D5	0.67	0/10568	1.01	36/14320 (0.3%)
8	E0	1.17	11/4563 (0.2%)	1.11	28/6214 (0.5%)
8	E1	0.79	2/4563 (0.0%)	1.06	23/6214 (0.4%)
9	F0	0.70	0/1882	1.08	3/2556 (0.1%)
9	F1	0.70	0/1882	1.05	4/2556 (0.2%)
9	F2	0.71	0/1882	1.11	5/2556 (0.2%)
9	F3	0.72	0/1882	1.05	3/2556 (0.1%)
10	H0	0.64	0/3114	1.02	13/4211 (0.3%)
10	H1	0.64	0/3114	1.01	12/4211 (0.3%)
10	H2	0.64	0/3114	1.00	11/4211 (0.3%)
10	H3	0.64	0/3114	1.01	12/4211 (0.3%)
11	I0	0.65	0/1416	0.97	4/1911 (0.2%)
11	I1	0.65	0/1416	0.98	4/1911 (0.2%)
11	I2	0.65	0/1416	0.97	4/1911 (0.2%)
11	I3	0.65	0/1416	0.97	3/1911 (0.2%)
12	J0	0.63	0/1420	0.95	2/1915 (0.1%)
12	J1	0.63	0/1420	0.97	2/1915 (0.1%)
12	J2	0.64	0/1420	0.98	3/1915 (0.2%)
12	J3	0.63	0/1420	0.97	1/1915 (0.1%)
12	J4	0.63	0/1420	0.98	3/1915 (0.2%)
13	K0	0.68	0/8740	1.01	27/11848 (0.2%)
13	K1	0.68	0/8740	1.01	25/11848 (0.2%)
13	K2	0.68	0/8740	1.01	27/11848 (0.2%)
13	K3	0.68	0/8740	1.01	24/11848 (0.2%)
14	L0	0.71	0/6518	1.09	35/8819 (0.4%)
14	L1	0.70	0/6518	1.06	34/8819 (0.4%)
14	L2	0.70	0/6518	1.07	29/8819 (0.3%)
14	L3	0.71	0/6518	1.06	29/8819 (0.3%)
15	M0	0.70	0/5588	1.11	31/7581 (0.4%)
15	M1	0.70	0/5588	1.11	37/7581 (0.5%)
15	M2	0.70	0/5588	1.10	31/7581 (0.4%)
15	M3	0.70	0/5588	1.10	33/7581 (0.4%)
16	N0	0.67	0/2419	1.07	7/3301 (0.2%)
16	N1	0.67	0/2419	1.08	7/3301 (0.2%)
16	N2	0.67	0/2419	1.05	4/3301 (0.1%)
16	N3	0.67	0/2419	1.07	7/3301 (0.2%)
17	O0	0.68	0/2593	1.07	12/3520 (0.3%)
17	O1	0.68	0/2593	1.08	12/3520 (0.3%)
17	O2	0.67	0/2593	1.06	10/3520 (0.3%)
17	O3	0.67	0/2593	1.08	10/3520 (0.3%)
18	P0	0.70	0/5365	1.07	31/7257 (0.4%)
18	P1	0.70	0/5365	1.04	26/7257 (0.4%)
18	P2	0.71	0/5365	1.07	34/7257 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	P3	0.70	0/5365	1.03	20/7257 (0.3%)
19	Q0	0.67	0/2775	1.06	13/3786 (0.3%)
19	Q1	0.67	0/2775	1.05	12/3786 (0.3%)
19	Q2	0.67	0/2775	1.07	15/3786 (0.4%)
19	Q3	0.67	0/2775	1.05	12/3786 (0.3%)
20	R0	1.12	2/11371 (0.0%)	1.07	61/15446 (0.4%)
20	R1	0.70	0/11371	1.05	54/15446 (0.3%)
20	R2	0.70	0/11371	1.05	53/15446 (0.3%)
20	R3	0.70	0/11371	1.04	48/15446 (0.3%)
21	S0	0.70	0/2623	1.05	10/3568 (0.3%)
21	S1	0.70	0/2623	1.04	10/3568 (0.3%)
21	S2	0.70	0/2623	1.03	8/3568 (0.2%)
21	S3	0.70	0/2623	1.03	8/3568 (0.2%)
22	T0	0.70	0/8141	1.03	26/11065 (0.2%)
22	T1	0.70	0/8141	1.02	25/11065 (0.2%)
23	U0	0.72	0/1217	1.06	4/1644 (0.2%)
23	U1	0.94	0/152	1.56	5/204 (2.5%)
23	U2	0.95	0/152	1.45	3/204 (1.5%)
23	U3	0.93	0/152	1.51	4/204 (2.0%)
23	U4	1.03	0/152	1.48	3/204 (1.5%)
23	U5	0.95	0/152	1.54	5/204 (2.5%)
23	U6	0.92	0/152	1.40	3/204 (1.5%)
24	V0	0.67	0/2240	1.06	10/3019 (0.3%)
25	W0	0.69	0/5972	1.02	12/8105 (0.1%)
All	All	0.72	40/630097 (0.0%)	1.03	2384/855041 (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	4
1	01	0	4
1	02	0	3
1	03	0	3
1	04	0	1
2	10	1	9
2	11	0	3
2	12	1	7
2	13	1	3
2	14	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	15	0	7
2	16	0	7
2	17	0	8
3	40	0	5
3	41	0	4
4	A0	0	11
4	A1	0	12
4	A2	0	12
4	A3	0	9
4	A4	0	7
4	A5	0	6
4	A6	1	9
5	B0	0	22
5	B1	0	26
6	C0	1	17
6	C1	1	13
6	C2	1	17
6	C3	1	15
6	C4	1	15
7	D0	0	16
7	D1	0	13
7	D2	0	18
7	D3	0	14
7	D4	1	19
7	D5	0	15
8	E0	0	5
8	E1	0	2
9	F0	0	3
9	F1	0	2
9	F2	0	3
9	F3	0	1
10	H0	0	5
10	H1	0	1
10	H2	0	2
10	H3	0	2
12	J0	0	1
12	J1	0	1
12	J2	0	1
12	J3	0	1
13	K0	0	10
13	K1	0	9
13	K2	0	12

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	K3	0	8
14	L0	0	8
14	L1	0	5
14	L2	0	6
14	L3	0	6
15	M0	0	7
15	M1	0	5
15	M2	0	9
15	M3	1	6
16	N0	0	4
16	N1	0	2
16	N2	0	2
16	N3	0	2
17	O0	0	1
17	O1	0	2
17	O2	0	2
17	O3	0	2
18	P0	0	9
18	P1	0	10
18	P2	1	17
18	P3	0	10
19	Q0	0	3
19	Q1	0	3
19	Q2	0	3
19	Q3	0	2
20	R0	0	15
20	R1	0	16
20	R2	0	15
20	R3	0	15
21	S0	0	4
21	S1	0	5
21	S2	0	5
21	S3	0	5
22	T0	2	13
22	T1	2	14
24	V0	0	5
25	W0	0	7
All	All	16	676

The worst 5 of 40 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	R0	1111	GLU	CD-OE1	92.11	2.27	1.25
2	10	1824	MET	N-CA	90.35	3.27	1.46
7	D1	1002	PRO	CA-C	73.09	2.99	1.52
6	C2	484	HIS	CD2-NE2	41.61	2.29	1.38
6	C2	484	HIS	CG-CD2	39.34	2.02	1.35

The worst 5 of 2384 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	17	1788	ASP	C-N-CA	16.59	163.16	121.70
8	E1	240	ALA	CB-CA-C	14.66	132.09	110.10
20	R0	1111	GLU	CG-CD-OE2	-13.88	90.54	118.30
8	E0	19	ARG	NE-CZ-NH1	13.82	127.21	120.30
8	E1	243	SER	CA-C-O	-12.90	93.01	120.10

5 of 16 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	10	167	ALA	CA
2	12	167	ALA	CA
2	13	1773	THR	CA
4	A6	96	THR	CA
6	C0	174	THR	CB

5 of 676 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	00	132	TYR	Sidechain
1	00	161	ARG	Peptide
1	00	175	TYR	Sidechain
1	00	193	ARG	Sidechain
1	01	11	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	35	0
1	01	6085	0	6080	38	0
1	02	6085	0	6080	7	0
1	03	6085	0	6080	9	0
1	04	6085	0	6080	9	0
2	10	14046	0	14194	127	0
2	11	14046	0	14194	23	0
2	12	14046	0	14194	19	0
2	13	14046	0	14194	8	0
2	14	14046	0	14194	27	0
2	15	14046	0	14194	60	0
2	16	14046	0	14194	49	0
2	17	14046	0	14193	75	0
3	40	2922	0	2899	4	0
3	41	2922	0	2899	2	0
4	A0	6568	0	6527	43	0
4	A1	6568	0	6527	7	0
4	A2	6568	0	6527	32	0
4	A3	6568	0	6527	9	0
4	A4	5860	0	5828	27	0
4	A5	5860	0	5828	8	0
4	A6	5860	0	5828	8	0
5	B0	13746	0	13949	12	0
5	B1	13746	0	13949	14	0
6	C0	16013	0	16224	19	0
6	C1	16013	0	16224	28	0
6	C2	16013	0	16224	67	0
6	C3	16013	0	16224	44	0
6	C4	16013	0	16224	38	0
7	D0	10363	0	10400	63	0
7	D1	10363	0	10400	132	0
7	D2	10363	0	10400	53	0
7	D3	10363	0	10400	81	0
7	D4	10363	0	10400	129	0
7	D5	10363	0	10400	51	0
8	E0	4432	0	4472	133	0
8	E1	4432	0	4472	64	0
9	F0	1837	0	1825	1	0
9	F1	1837	0	1825	14	0
9	F2	1837	0	1825	0	0
9	F3	1837	0	1825	0	0
10	H0	3066	0	3103	3	0
10	H1	3066	0	3103	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	H2	3066	0	3103	4	0
10	H3	3066	0	3103	1	0
11	I0	1398	0	1431	4	0
11	I1	1398	0	1431	2	0
11	I2	1398	0	1431	5	0
11	I3	1398	0	1431	2	0
12	J0	1403	0	1391	1	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	2	0
13	K0	8574	0	8438	9	0
13	K1	8574	0	8438	5	0
13	K2	8574	0	8438	47	0
13	K3	8574	0	8438	30	0
14	L0	6383	0	6313	30	0
14	L1	6383	0	6313	59	0
14	L2	6383	0	6313	25	0
14	L3	6383	0	6313	12	0
15	M0	5461	0	5443	10	0
15	M1	5461	0	5443	12	0
15	M2	5461	0	5443	10	0
15	M3	5461	0	5443	6	0
16	N0	2352	0	2220	19	0
16	N1	2352	0	2220	1	0
16	N2	2352	0	2220	2	0
16	N3	2352	0	2220	0	0
17	O0	2528	0	2444	8	0
17	O1	2528	0	2444	2	0
17	O2	2528	0	2444	2	0
17	O3	2528	0	2444	5	0
18	P0	5257	0	5249	15	0
18	P1	5257	0	5249	9	0
18	P2	5257	0	5249	4	0
18	P3	5257	0	5249	6	0
19	Q0	2703	0	2555	12	0
19	Q1	2703	0	2555	1	0
19	Q2	2703	0	2555	15	0
19	Q3	2703	0	2555	1	0
20	R0	11132	0	11066	39	0
20	R1	11132	0	11066	13	0
20	R2	11132	0	11066	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R3	11132	0	11066	26	0
21	S0	2552	0	2452	4	0
21	S1	2552	0	2452	1	0
21	S2	2552	0	2452	3	0
21	S3	2552	0	2452	1	0
22	T0	7960	0	7896	13	0
22	T1	7960	0	7896	1	0
23	U0	1193	0	1188	4	0
23	U1	151	0	167	60	0
23	U2	151	0	167	36	0
23	U3	151	0	167	47	0
23	U4	151	0	167	36	0
23	U5	151	0	167	47	0
23	U6	151	0	167	36	0
24	V0	2203	0	2226	12	0
25	W0	5836	0	5850	20	0
All	All	617133	0	616872	1415	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 1415 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)
8:E0:18:TRP:CD2	8:E0:18:TRP:CG	1.82	1.64
8:E1:244:THR:N	8:E1:244:THR:CA	1.69	1.52
2:17:1788:ASP:C	2:17:1788:ASP:CA	1.75	1.51
2:10:1824:MET:C	2:10:1824:MET:CA	1.75	1.50
8:E0:18:TRP:NE1	8:E0:18:TRP:CE2	1.80	1.49

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%)	707 (94%)	43 (6%)	4 (0%)	29	69
1	01	754/3224 (23%)	705 (94%)	44 (6%)	5 (1%)	22	63
1	02	754/3224 (23%)	703 (93%)	46 (6%)	5 (1%)	22	63
1	03	754/3224 (23%)	705 (94%)	43 (6%)	6 (1%)	19	60
1	04	754/3224 (23%)	704 (93%)	47 (6%)	3 (0%)	34	72
2	10	1829/1887 (97%)	1727 (94%)	90 (5%)	12 (1%)	22	63
2	11	1829/1887 (97%)	1742 (95%)	80 (4%)	7 (0%)	34	72
2	12	1829/1887 (97%)	1738 (95%)	86 (5%)	5 (0%)	41	77
2	13	1829/1887 (97%)	1735 (95%)	88 (5%)	6 (0%)	41	77
2	14	1829/1887 (97%)	1714 (94%)	103 (6%)	12 (1%)	22	63
2	15	1829/1887 (97%)	1725 (94%)	85 (5%)	19 (1%)	15	55
2	16	1829/1887 (97%)	1731 (95%)	88 (5%)	10 (0%)	29	69
2	17	1829/1887 (97%)	1720 (94%)	95 (5%)	14 (1%)	19	60
3	40	379/546 (69%)	352 (93%)	26 (7%)	1 (0%)	41	77
3	41	379/546 (69%)	349 (92%)	29 (8%)	1 (0%)	41	77
4	A0	816/819 (100%)	761 (93%)	47 (6%)	8 (1%)	15	55
4	A1	816/819 (100%)	760 (93%)	52 (6%)	4 (0%)	29	69
4	A2	816/819 (100%)	765 (94%)	45 (6%)	6 (1%)	22	63
4	A3	816/819 (100%)	762 (93%)	48 (6%)	6 (1%)	22	63
4	A4	724/819 (88%)	683 (94%)	37 (5%)	4 (1%)	25	66
4	A5	724/819 (88%)	685 (95%)	37 (5%)	2 (0%)	41	77
4	A6	724/819 (88%)	683 (94%)	37 (5%)	4 (1%)	25	66
5	B0	1746/1749 (100%)	1629 (93%)	97 (6%)	20 (1%)	14	52
5	B1	1746/1749 (100%)	1633 (94%)	88 (5%)	25 (1%)	11	46
6	C0	2009/2012 (100%)	1875 (93%)	111 (6%)	23 (1%)	14	52
6	C1	2009/2012 (100%)	1874 (93%)	113 (6%)	22 (1%)	14	52
6	C2	2009/2012 (100%)	1886 (94%)	107 (5%)	16 (1%)	19	60
6	C3	2009/2012 (100%)	1873 (93%)	122 (6%)	14 (1%)	22	63
6	C4	2009/2012 (100%)	1866 (93%)	127 (6%)	16 (1%)	19	60
7	D0	1308/1391 (94%)	1215 (93%)	79 (6%)	14 (1%)	14	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	D1	1308/1391 (94%)	1208 (92%)	84 (6%)	16 (1%)	13	50
7	D2	1308/1391 (94%)	1211 (93%)	85 (6%)	12 (1%)	17	57
7	D3	1308/1391 (94%)	1218 (93%)	78 (6%)	12 (1%)	17	57
7	D4	1308/1391 (94%)	1209 (92%)	81 (6%)	18 (1%)	11	46
7	D5	1308/1391 (94%)	1221 (93%)	75 (6%)	12 (1%)	17	57
8	E0	544/674 (81%)	516 (95%)	25 (5%)	3 (1%)	25	66
8	E1	544/674 (81%)	518 (95%)	22 (4%)	4 (1%)	22	63
9	F0	239/326 (73%)	193 (81%)	31 (13%)	15 (6%)	1	17
9	F1	239/326 (73%)	191 (80%)	33 (14%)	15 (6%)	1	17
9	F2	239/326 (73%)	187 (78%)	41 (17%)	11 (5%)	2	21
9	F3	239/326 (73%)	190 (80%)	41 (17%)	8 (3%)	4	26
10	H0	381/507 (75%)	369 (97%)	12 (3%)	0	100	100
10	H1	381/507 (75%)	363 (95%)	17 (4%)	1 (0%)	41	77
10	H2	381/507 (75%)	368 (97%)	13 (3%)	0	100	100
10	H3	381/507 (75%)	366 (96%)	15 (4%)	0	100	100
11	I0	171/599 (28%)	170 (99%)	1 (1%)	0	100	100
11	I1	171/599 (28%)	170 (99%)	0	1 (1%)	25	66
11	I2	171/599 (28%)	170 (99%)	1 (1%)	0	100	100
11	I3	171/599 (28%)	170 (99%)	0	1 (1%)	25	66
12	J0	169/522 (32%)	167 (99%)	2 (1%)	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%)	167 (99%)	2 (1%)	0	100	100
12	J4	169/522 (32%)	167 (99%)	2 (1%)	0	100	100
13	K0	1084/1156 (94%)	997 (92%)	77 (7%)	10 (1%)	17	57
13	K1	1084/1156 (94%)	996 (92%)	77 (7%)	11 (1%)	15	55
13	K2	1084/1156 (94%)	996 (92%)	75 (7%)	13 (1%)	13	50
13	K3	1084/1156 (94%)	990 (91%)	82 (8%)	12 (1%)	14	52
14	L0	780/925 (84%)	731 (94%)	43 (6%)	6 (1%)	19	60
14	L1	780/925 (84%)	733 (94%)	40 (5%)	7 (1%)	17	57
14	L2	780/925 (84%)	736 (94%)	40 (5%)	4 (0%)	29	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	L3	780/925 (84%)	737 (94%)	35 (4%)	8 (1%)	15	55
15	M0	669/937 (71%)	616 (92%)	46 (7%)	7 (1%)	15	55
15	M1	669/937 (71%)	618 (92%)	45 (7%)	6 (1%)	17	57
15	M2	669/937 (71%)	616 (92%)	47 (7%)	6 (1%)	17	57
15	M3	669/937 (71%)	616 (92%)	48 (7%)	5 (1%)	22	63
16	N0	299/322 (93%)	272 (91%)	24 (8%)	3 (1%)	15	55
16	N1	299/322 (93%)	272 (91%)	25 (8%)	2 (1%)	22	63
16	N2	299/322 (93%)	273 (91%)	23 (8%)	3 (1%)	15	55
16	N3	299/322 (93%)	271 (91%)	25 (8%)	3 (1%)	15	55
17	O0	321/360 (89%)	300 (94%)	21 (6%)	0	100	100
17	O1	321/360 (89%)	299 (93%)	20 (6%)	2 (1%)	25	66
17	O2	321/360 (89%)	300 (94%)	19 (6%)	2 (1%)	25	66
17	O3	321/360 (89%)	299 (93%)	21 (6%)	1 (0%)	41	77
18	P0	653/656 (100%)	613 (94%)	35 (5%)	5 (1%)	19	60
18	P1	653/656 (100%)	614 (94%)	33 (5%)	6 (1%)	17	57
18	P2	653/656 (100%)	609 (93%)	34 (5%)	10 (2%)	10	46
18	P3	653/656 (100%)	613 (94%)	34 (5%)	6 (1%)	17	57
19	Q0	341/380 (90%)	321 (94%)	19 (6%)	1 (0%)	41	77
19	Q1	341/380 (90%)	319 (94%)	21 (6%)	1 (0%)	41	77
19	Q2	341/380 (90%)	322 (94%)	18 (5%)	1 (0%)	41	77
19	Q3	341/380 (90%)	318 (93%)	22 (6%)	1 (0%)	41	77
20	R0	1397/1436 (97%)	1291 (92%)	88 (6%)	18 (1%)	12	48
20	R1	1397/1436 (97%)	1299 (93%)	84 (6%)	14 (1%)	15	55
20	R2	1397/1436 (97%)	1297 (93%)	87 (6%)	13 (1%)	17	57
20	R3	1397/1436 (97%)	1295 (93%)	89 (6%)	13 (1%)	17	57
21	S0	320/326 (98%)	287 (90%)	33 (10%)	0	100	100
21	S1	320/326 (98%)	287 (90%)	32 (10%)	1 (0%)	41	77
21	S2	320/326 (98%)	289 (90%)	30 (9%)	1 (0%)	41	77
21	S3	320/326 (98%)	288 (90%)	31 (10%)	1 (0%)	41	77
22	T0	1002/2266 (44%)	920 (92%)	68 (7%)	14 (1%)	11	46
22	T1	1002/2266 (44%)	922 (92%)	65 (6%)	15 (2%)	10	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
23	U0	148/880 (17%)	137 (93%)	10 (7%)	1 (1%)	22 63
23	U1	17/880 (2%)	15 (88%)	2 (12%)	0	100 100
23	U2	17/880 (2%)	14 (82%)	2 (12%)	1 (6%)	1 17
23	U3	17/880 (2%)	15 (88%)	2 (12%)	0	100 100
23	U4	17/880 (2%)	14 (82%)	2 (12%)	1 (6%)	1 17
23	U5	17/880 (2%)	15 (88%)	2 (12%)	0	100 100
23	U6	17/880 (2%)	14 (82%)	3 (18%)	0	100 100
24	V0	271/2090 (13%)	250 (92%)	16 (6%)	5 (2%)	8 40
25	W0	733/741 (99%)	684 (93%)	37 (5%)	12 (2%)	9 44
All	All	77792/109146 (71%)	72581 (93%)	4536 (6%)	675 (1%)	21 57

5 of 675 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	10	167	ALA
2	14	174	HIS
2	14	1688	SER
2	15	174	HIS
2	15	1788	ASP

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%)	656 (97%)	19 (3%)	43 65
1	01	675/2818 (24%)	657 (97%)	18 (3%)	44 65
1	02	675/2818 (24%)	658 (98%)	17 (2%)	47 68
1	03	675/2818 (24%)	660 (98%)	15 (2%)	52 71
1	04	675/2818 (24%)	659 (98%)	16 (2%)	49 69
2	10	1565/1608 (97%)	1539 (98%)	26 (2%)	60 78
2	11	1565/1608 (97%)	1542 (98%)	23 (2%)	65 80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	12	1565/1608 (97%)	1538 (98%)	27 (2%)	60	78
2	13	1565/1608 (97%)	1543 (99%)	22 (1%)	67	80
2	14	1565/1608 (97%)	1541 (98%)	24 (2%)	65	80
2	15	1565/1608 (97%)	1542 (98%)	23 (2%)	65	80
2	16	1565/1608 (97%)	1541 (98%)	24 (2%)	65	80
2	17	1565/1608 (97%)	1539 (98%)	26 (2%)	60	78
3	40	323/463 (70%)	317 (98%)	6 (2%)	57	75
3	41	323/463 (70%)	315 (98%)	8 (2%)	47	68
4	A0	725/726 (100%)	708 (98%)	17 (2%)	50	70
4	A1	725/726 (100%)	709 (98%)	16 (2%)	52	71
4	A2	725/726 (100%)	710 (98%)	15 (2%)	53	72
4	A3	725/726 (100%)	710 (98%)	15 (2%)	53	72
4	A4	647/726 (89%)	631 (98%)	16 (2%)	47	68
4	A5	647/726 (89%)	635 (98%)	12 (2%)	57	75
4	A6	647/726 (89%)	628 (97%)	19 (3%)	42	64
5	B0	1540/1541 (100%)	1512 (98%)	28 (2%)	59	77
5	B1	1540/1541 (100%)	1512 (98%)	28 (2%)	59	77
6	C0	1776/1777 (100%)	1743 (98%)	33 (2%)	57	75
6	C1	1776/1777 (100%)	1738 (98%)	38 (2%)	53	72
6	C2	1776/1777 (100%)	1743 (98%)	33 (2%)	57	75
6	C3	1776/1777 (100%)	1743 (98%)	33 (2%)	57	75
6	C4	1776/1777 (100%)	1741 (98%)	35 (2%)	55	74
7	D0	1157/1222 (95%)	1127 (97%)	30 (3%)	46	66
7	D1	1157/1222 (95%)	1123 (97%)	34 (3%)	42	64
7	D2	1157/1222 (95%)	1126 (97%)	31 (3%)	44	65
7	D3	1157/1222 (95%)	1124 (97%)	33 (3%)	42	64
7	D4	1157/1222 (95%)	1117 (96%)	40 (4%)	36	59
7	D5	1157/1222 (95%)	1128 (98%)	29 (2%)	47	68
8	E0	489/604 (81%)	483 (99%)	6 (1%)	71	83
8	E1	489/604 (81%)	485 (99%)	4 (1%)	81	89
9	F0	210/277 (76%)	200 (95%)	10 (5%)	25	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	F1	210/277 (76%)	201 (96%)	9 (4%)	29	53
9	F2	210/277 (76%)	202 (96%)	8 (4%)	33	57
9	F3	210/277 (76%)	202 (96%)	8 (4%)	33	57
10	H0	345/425 (81%)	342 (99%)	3 (1%)	78	87
10	H1	345/425 (81%)	341 (99%)	4 (1%)	71	83
10	H2	345/425 (81%)	342 (99%)	3 (1%)	78	87
10	H3	345/425 (81%)	341 (99%)	4 (1%)	71	83
11	I0	155/459 (34%)	153 (99%)	2 (1%)	69	81
11	I1	155/459 (34%)	153 (99%)	2 (1%)	69	81
11	I2	155/459 (34%)	152 (98%)	3 (2%)	57	75
11	I3	155/459 (34%)	152 (98%)	3 (2%)	57	75
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%)	157 (99%)	1 (1%)	86	92
12	J4	158/401 (39%)	156 (99%)	2 (1%)	69	81
13	K0	958/1013 (95%)	929 (97%)	29 (3%)	41	63
13	K1	958/1013 (95%)	930 (97%)	28 (3%)	42	64
13	K2	958/1013 (95%)	928 (97%)	30 (3%)	40	62
13	K3	958/1013 (95%)	929 (97%)	29 (3%)	41	63
14	L0	701/827 (85%)	685 (98%)	16 (2%)	50	70
14	L1	701/827 (85%)	690 (98%)	11 (2%)	62	79
14	L2	701/827 (85%)	689 (98%)	12 (2%)	60	78
14	L3	701/827 (85%)	688 (98%)	13 (2%)	57	75
15	M0	602/840 (72%)	591 (98%)	11 (2%)	59	77
15	M1	602/840 (72%)	588 (98%)	14 (2%)	50	70
15	M2	602/840 (72%)	591 (98%)	11 (2%)	59	77
15	M3	602/840 (72%)	589 (98%)	13 (2%)	52	71
16	N0	255/272 (94%)	247 (97%)	8 (3%)	40	62
16	N1	255/272 (94%)	247 (97%)	8 (3%)	40	62
16	N2	255/272 (94%)	248 (97%)	7 (3%)	44	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	N3	255/272 (94%)	249 (98%)	6 (2%)	49	69
17	O0	279/310 (90%)	274 (98%)	5 (2%)	59	77
17	O1	279/310 (90%)	274 (98%)	5 (2%)	59	77
17	O2	279/310 (90%)	273 (98%)	6 (2%)	52	71
17	O3	279/310 (90%)	274 (98%)	5 (2%)	59	77
18	P0	584/585 (100%)	570 (98%)	14 (2%)	49	69
18	P1	584/585 (100%)	572 (98%)	12 (2%)	53	72
18	P2	584/585 (100%)	573 (98%)	11 (2%)	57	75
18	P3	584/585 (100%)	570 (98%)	14 (2%)	49	69
19	Q0	303/335 (90%)	300 (99%)	3 (1%)	76	86
19	Q1	303/335 (90%)	301 (99%)	2 (1%)	84	90
19	Q2	303/335 (90%)	299 (99%)	4 (1%)	69	81
19	Q3	303/335 (90%)	301 (99%)	2 (1%)	84	90
20	R0	1233/1259 (98%)	1207 (98%)	26 (2%)	53	72
20	R1	1233/1259 (98%)	1204 (98%)	29 (2%)	49	69
20	R2	1233/1259 (98%)	1202 (98%)	31 (2%)	47	68
20	R3	1233/1259 (98%)	1206 (98%)	27 (2%)	52	71
21	S0	278/282 (99%)	273 (98%)	5 (2%)	59	77
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%)	271 (98%)	7 (2%)	47	68
22	T0	891/2037 (44%)	881 (99%)	10 (1%)	73	84
22	T1	891/2037 (44%)	879 (99%)	12 (1%)	69	81
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%)	17 (90%)	2 (10%)	7	24
23	U4	19/703 (3%)	18 (95%)	1 (5%)	22	47
23	U5	19/703 (3%)	17 (90%)	2 (10%)	7	24
23	U6	19/703 (3%)	18 (95%)	1 (5%)	22	47
24	V0	249/1685 (15%)	241 (97%)	8 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
25	W0	661/663 (100%)	648 (98%)	13 (2%)	55 74
All	All	68601/94353 (73%)	67169 (98%)	1432 (2%)	56 72

5 of 1432 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	K0	790	TYR
16	N2	246	ASP
13	K1	790	TYR
13	K0	718	SER
14	L1	205	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 135 such sidechains are listed below:

Mol	Chain	Res	Type
23	U1	604	ASN
23	U2	609	ASN
23	U6	604	ASN
6	C2	854	ASN
6	C2	544	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no 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

This section contains visualisations of the EMDB entry EMD-14321. These allow visual inspection of the internal detail of the map and identification of artifacts.

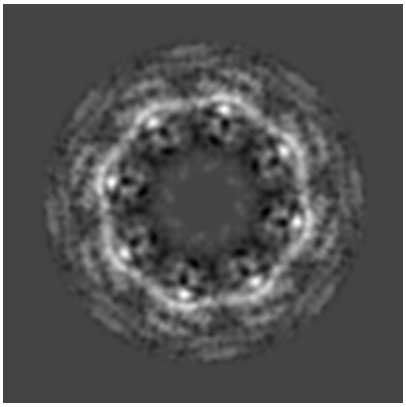
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

6.1.1 Primary map

X

Y



Z

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

6.2 Central slices

6.2.1 Primary map

X Index: 72

Y Index: 72

Z Index: 72

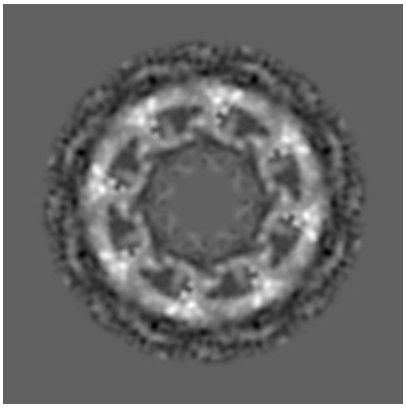
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 36

Y Index: 36

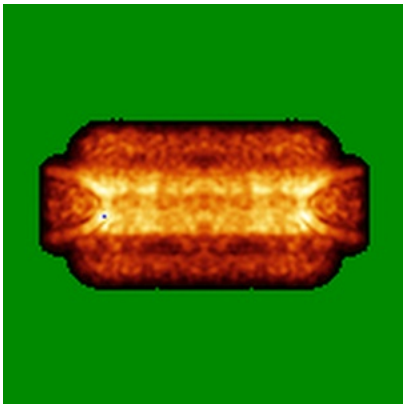


Z Index: 77

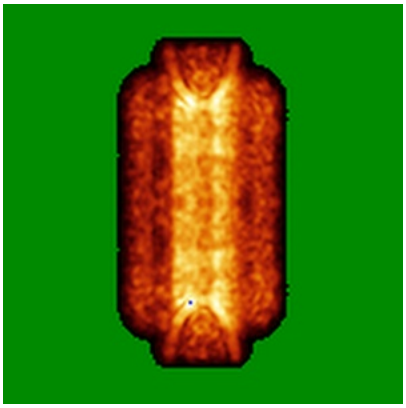
The images above show the largest variance slices of the map in three orthogonal directions.

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

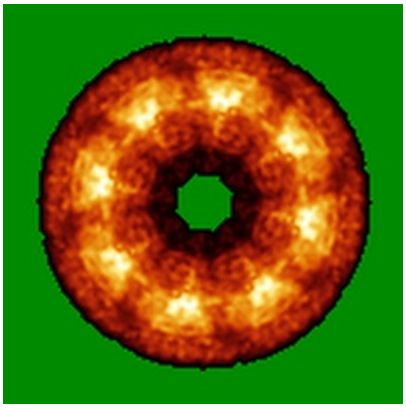
6.4.1 Primary map



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 0.0891. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

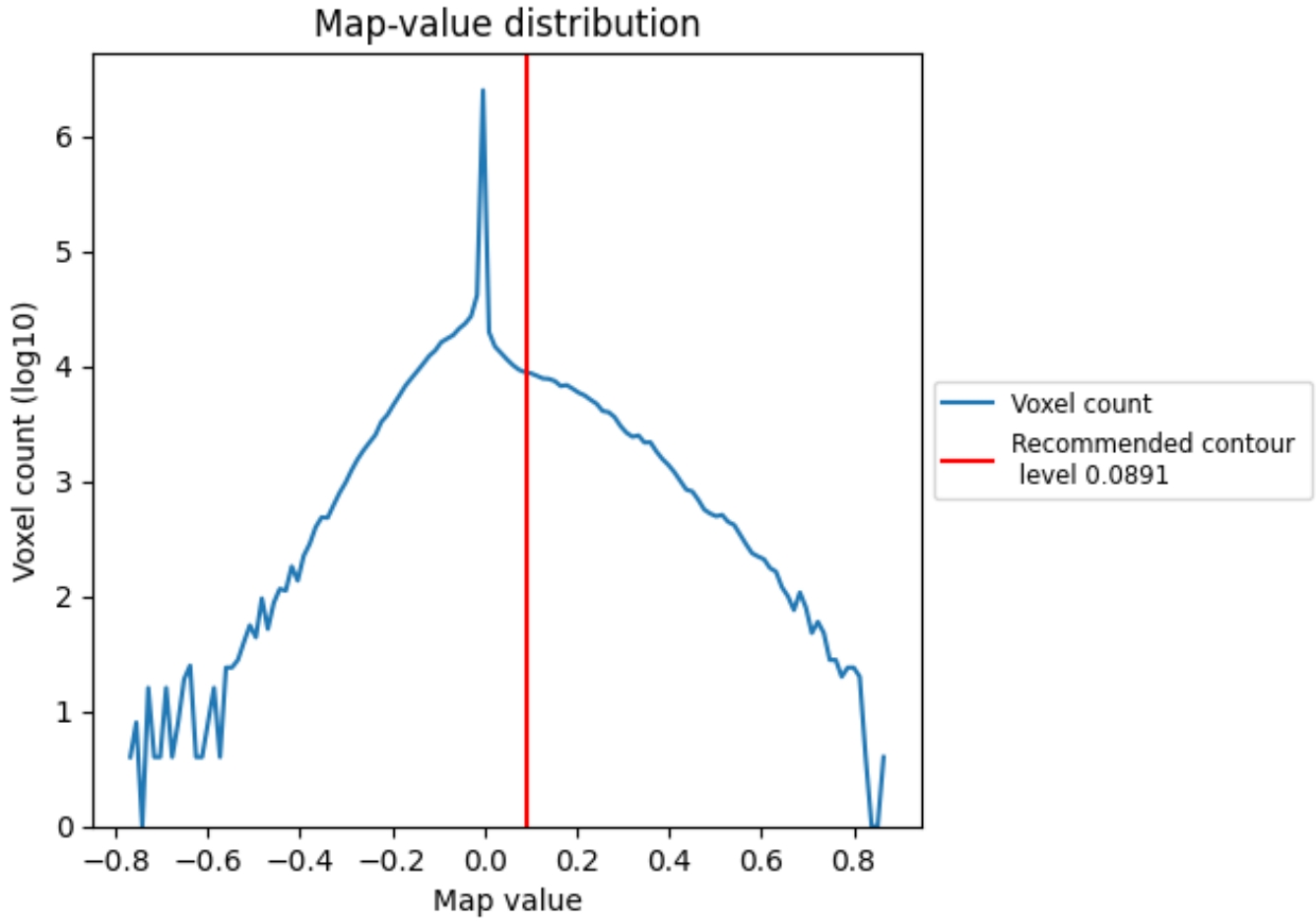
6.6 Mask visualisation (i)

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

7 Map analysis

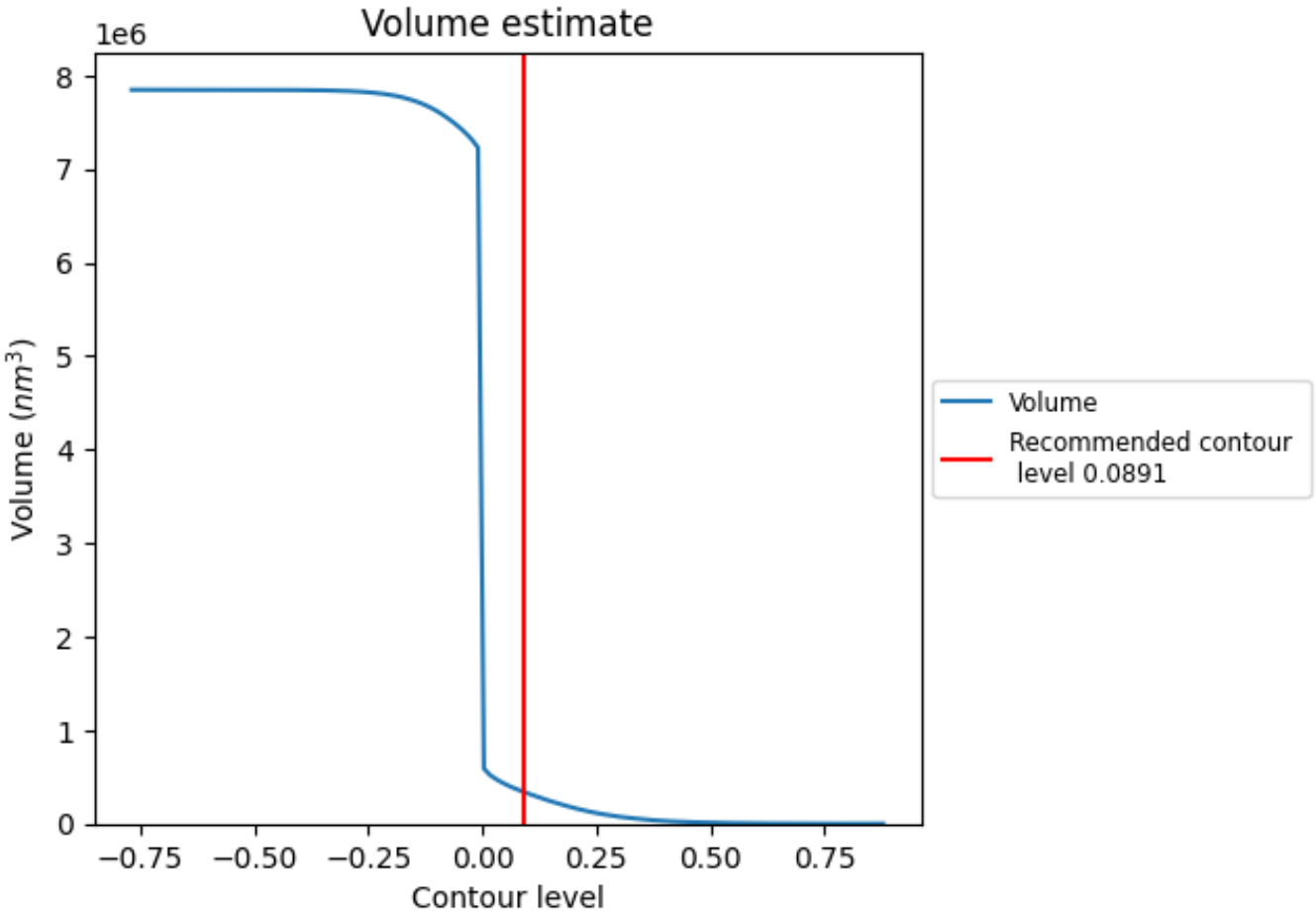
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

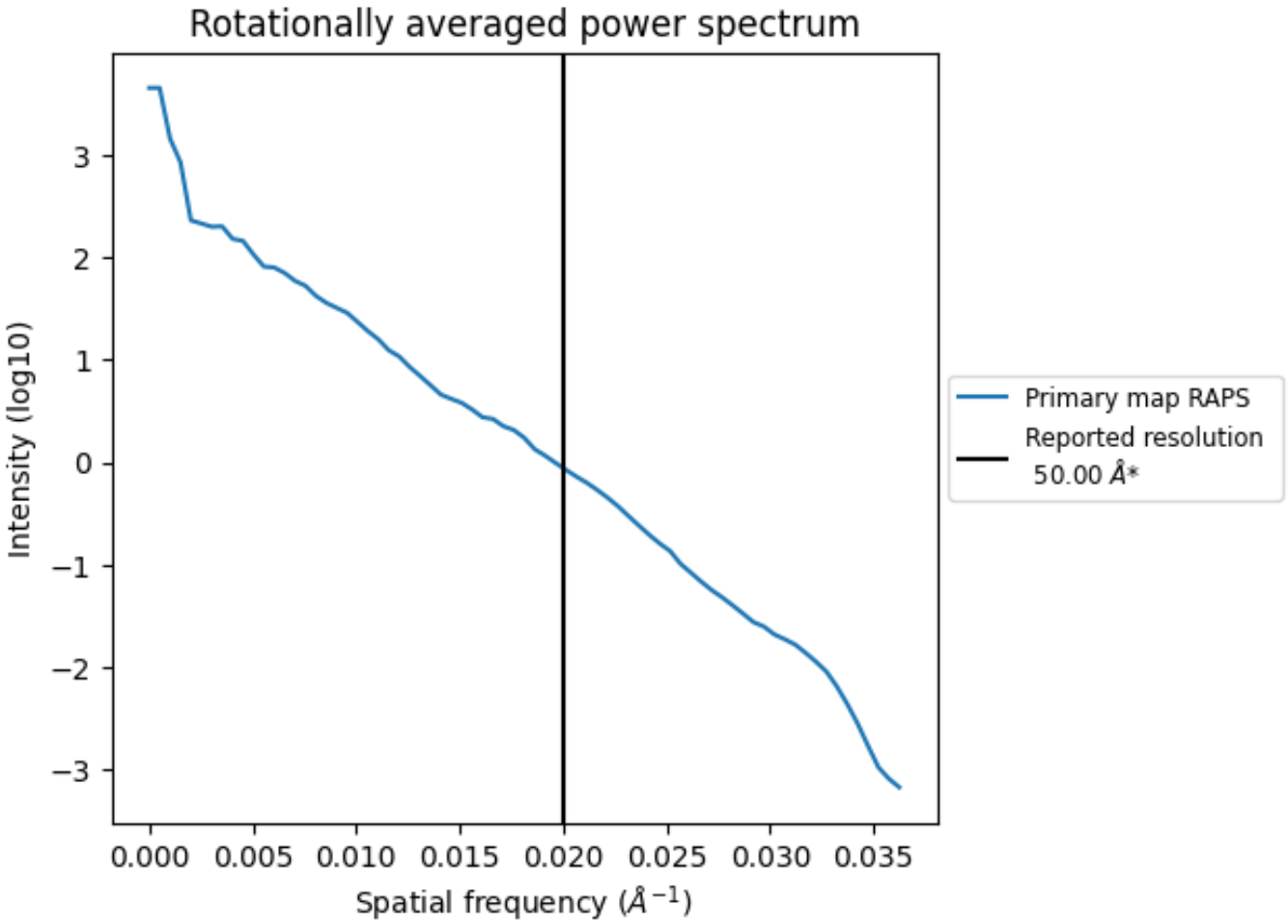
7.2 Volume estimate (i)



The volume at the recommended contour level is 342613 nm^3; this corresponds to an approximate mass of 309491 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 0.020 Å^{-1}

8 Fourier-Shell correlation

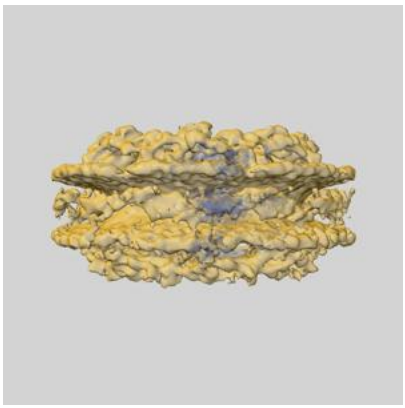
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

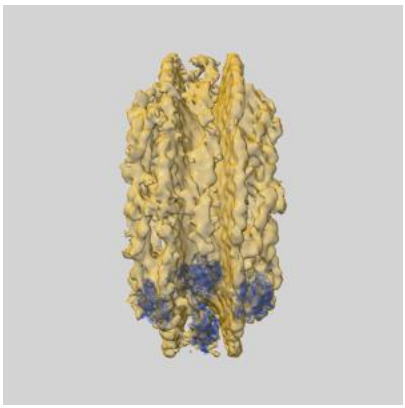
This section contains information regarding the fit between EMDB map EMD-14321 and PDB model 7R5J. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlays

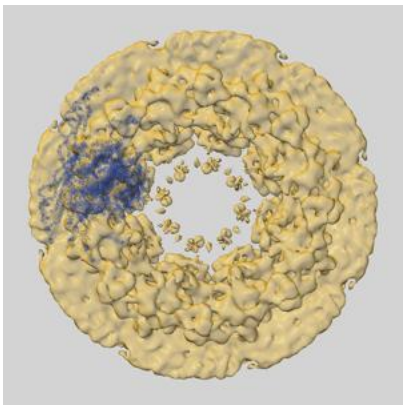
9.1.1 Map-model overlay



X

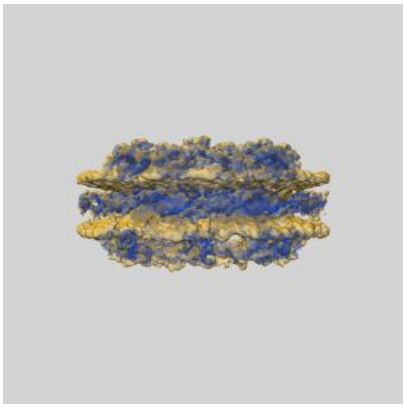


Y

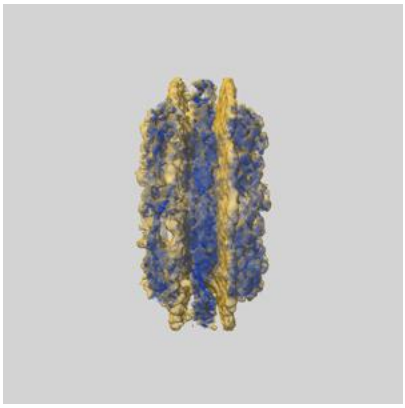


Z

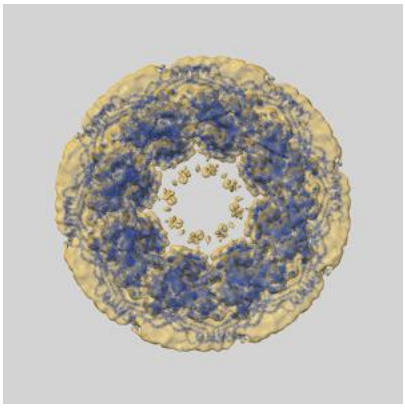
9.1.2 Map-model assembly overlay



X



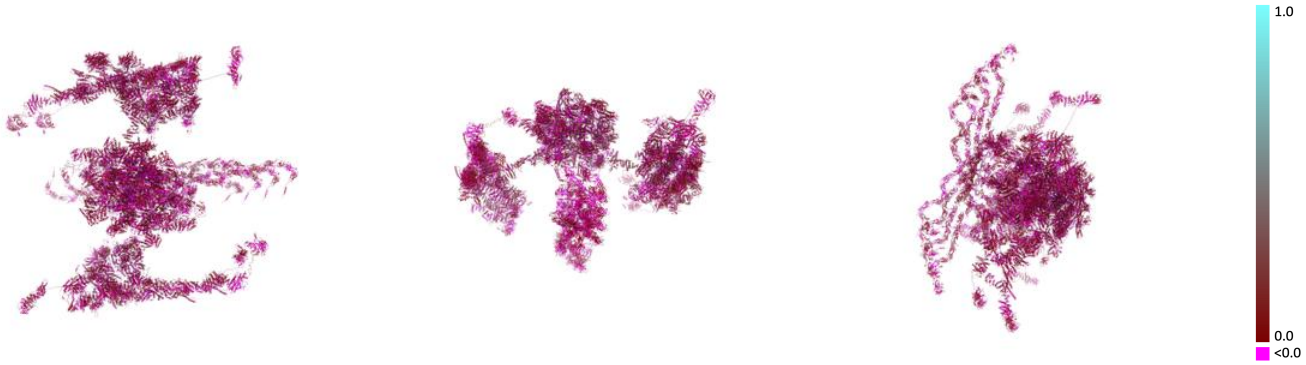
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0891 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

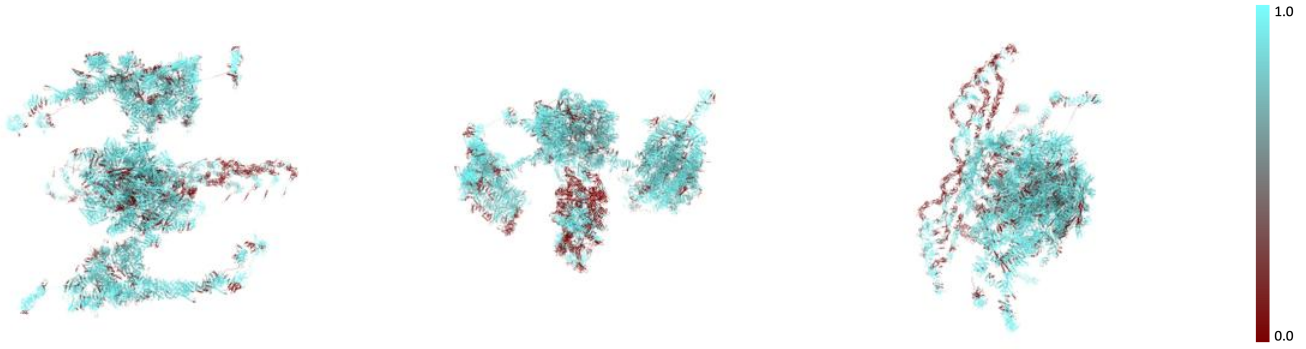
9.2 Q-score mapped to coordinate model



X Y Z

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

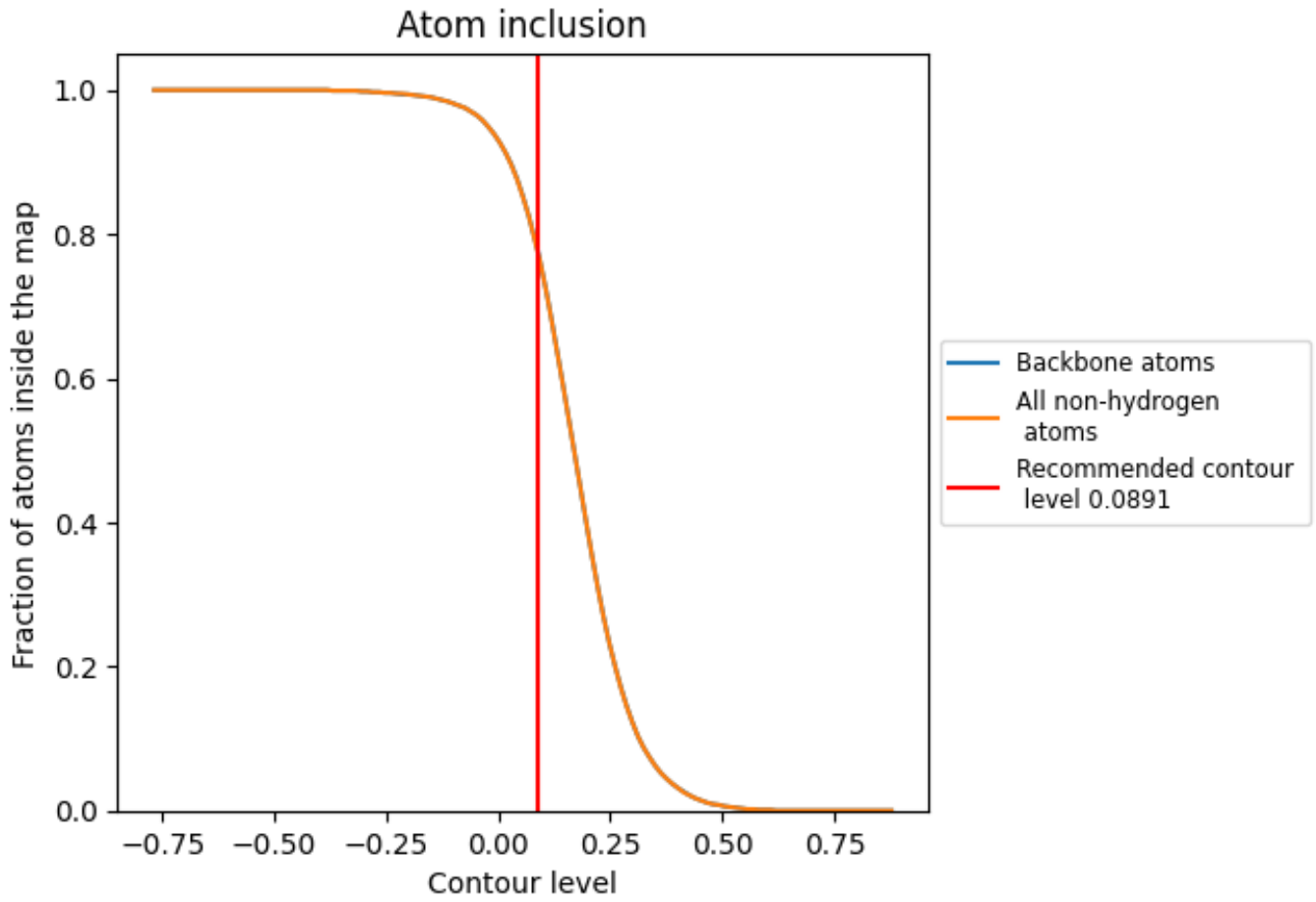
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0891).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0891) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7740	0.0260
00	0.6940	0.0260
01	0.8320	0.0420
02	0.8560	0.0400
03	0.7250	0.0340
04	0.8890	0.0480
10	0.2440	0.0150
11	0.4850	0.0150
12	0.6710	0.0220
13	0.5790	0.0240
14	0.2910	0.0000
15	0.7150	0.0220
16	0.7300	0.0210
17	0.5870	0.0250
40	0.9960	0.0240
41	0.9990	0.0270
A0	0.9250	0.0230
A1	0.8520	0.0330
A2	0.9070	0.0210
A3	0.8760	0.0420
A4	0.8380	0.0400
A5	0.7590	0.0160
A6	0.9110	0.0340
B0	0.8480	0.0340
B1	0.8550	0.0320
C0	0.8060	0.0240
C1	0.8360	0.0180
C2	0.8300	0.0340
C3	0.8520	0.0170
C4	0.8220	0.0280
D0	0.8470	0.0270
D1	0.8020	0.0260
D2	0.8970	0.0310
D3	0.7720	0.0200
D4	0.8920	0.0350

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Chain	Atom inclusion	Q-score
D5	0.8260	0.0310
E0	0.9900	0.0160
E1	0.9800	0.0080
F0	0.8740	0.0280
F1	0.7040	0.0170
F2	0.7790	0.0280
F3	0.6710	0.0170
H0	0.7580	0.0260
H1	0.7630	0.0350
H2	0.7230	0.0180
H3	0.8260	0.0390
I0	0.5810	0.0190
I1	0.6700	0.0260
I2	0.7210	0.0430
I3	0.6500	0.0200
J0	0.6840	0.0250
J1	0.5620	0.0110
J2	0.7980	0.0440
J3	0.5780	0.0030
J4	0.8320	0.0220
K0	0.7780	0.0200
K1	0.8210	0.0400
K2	0.7120	0.0140
K3	0.7450	0.0430
L0	0.9130	0.0390
L1	0.7030	0.0100
L2	0.7540	0.0260
L3	0.8890	0.0310
M0	0.9300	0.0420
M1	0.7500	0.0430
M2	0.9600	0.0380
M3	0.8000	0.0370
N0	0.7930	0.0160
N1	0.9130	0.0400
N2	0.9890	0.0250
N3	0.9200	0.0380
O0	0.8330	0.0330
O1	0.9650	0.0360
O2	0.8840	0.0290
O3	0.9170	0.0240
P0	0.7830	0.0380
P1	0.9050	0.0250

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Chain	Atom inclusion	Q-score
P2	0.9040	0.0330
P3	0.8850	0.0300
Q0	0.7680	0.0330
Q1	0.8240	0.0380
Q2	0.8960	0.0260
Q3	0.9450	0.0330
R0	0.8850	0.0290
R1	0.8770	0.0250
R2	0.9450	0.0280
R3	0.9440	0.0240
S0	0.9310	0.0430
S1	0.9470	0.0370
S2	0.9460	0.0200
S3	0.9570	0.0410
T0	0.6370	-0.0040
T1	0.1820	-0.0130
U0	0.4430	0.0070
U1	0.5560	0.0070
U2	0.2650	0.0290
U3	0.9200	0.0140
U4	0.3840	0.0040
U5	0.1990	0.0090
U6	0.7880	0.0380
V0	0.7210	0.0220
W0	0.8030	0.0250