



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:13 AM UTC

PDB ID : 7R5K / pdb_00007r5k
EMDB ID : EMD-14322
Title : Human nuclear pore complex (constricted)
Authors : Mosalaganti, S.; Obarska-Kosinska, A.; Siggel, M.; Taniguchi, R.; Turonova, B.; Zimmerli, C.E.; Buczak, K.; Schmidt, F.H.; Margiotta, E.; Mackmull, M.T.; Hagen, W.J.H.; Hummer, G.; Kosinski, J.; Beck, M.
Deposited on : 2022-02-10
Resolution : 12.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

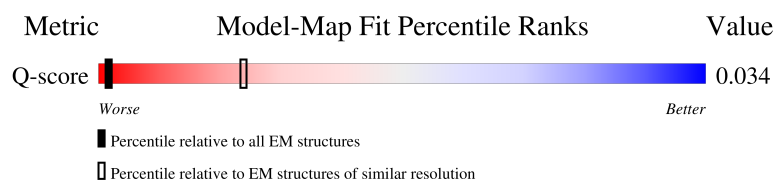
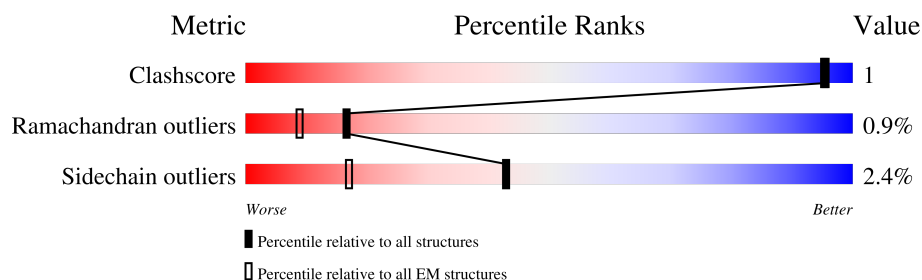
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 12.00 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	00	3224	
1	01	3224	
1	02	3224	
1	03	3224	

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Mol	Chain	Length	Quality of chain
1	04	3224	
2	10	1887	
2	11	1887	
2	12	1887	
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	

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Mol	Chain	Length	Quality of chain
7	D0	1391	
7	D1	1391	
7	D2	1391	
7	D3	1391	
7	D4	1391	
7	D5	1391	
8	E0	674	
8	E1	674	
9	F0	326	
9	F1	326	
9	F2	326	
9	F3	326	
10	H0	507	
10	H1	507	
10	H2	507	
10	H3	507	
11	I0	599	
11	I1	599	
11	I2	599	
11	I3	599	
12	J0	522	
12	J1	522	
12	J2	522	
12	J3	522	
12	J4	522	

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Mol	Chain	Length	Quality of chain
13	K0	1156	
13	K1	1156	
13	K2	1156	
13	K3	1156	
14	L0	925	
14	L1	925	
14	L2	925	
14	L3	925	
15	M0	937	
15	M1	937	
15	M2	937	
15	M3	937	
16	N0	322	
16	N1	322	
16	N2	322	
16	N3	322	
17	O0	360	
17	O1	360	
17	O2	360	
17	O3	360	
18	P0	656	
18	P1	656	
18	P2	656	
18	P3	656	
19	Q0	380	

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Mol	Chain	Length	Quality of chain
19	Q1	380	
19	Q2	380	
19	Q3	380	
20	R0	1436	
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

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	C	N	O	S	0	0
			16013	10208	2753	2965	87		

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

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

- Molecule 8 is a protein called Nucleoporin NDC1.

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

- Molecule 9 is a protein called Nucleoporin NUP35.

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

- 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	C	N	O	S	0	0
			11132	7093	1878	2088	73		

- Molecule 21 is a protein called Nucleoporin Nup37.

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

- Molecule 22 is a protein called Protein ELYS.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
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.

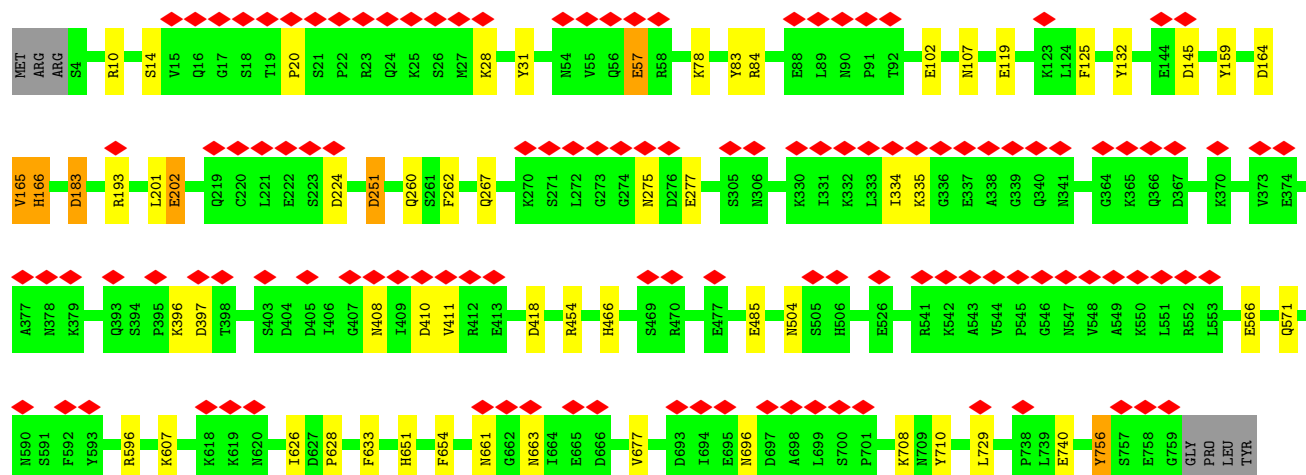
Mol	Chain	Residues	Atoms					AltConf	Trace
25	W0	735	Total	C	N	O	S	0	0
			5836	3714	988	1103	31		

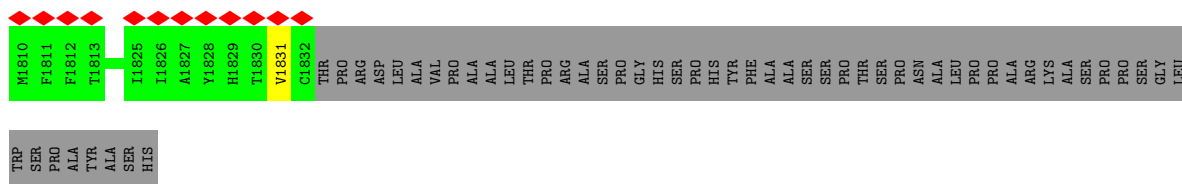


[illegible]

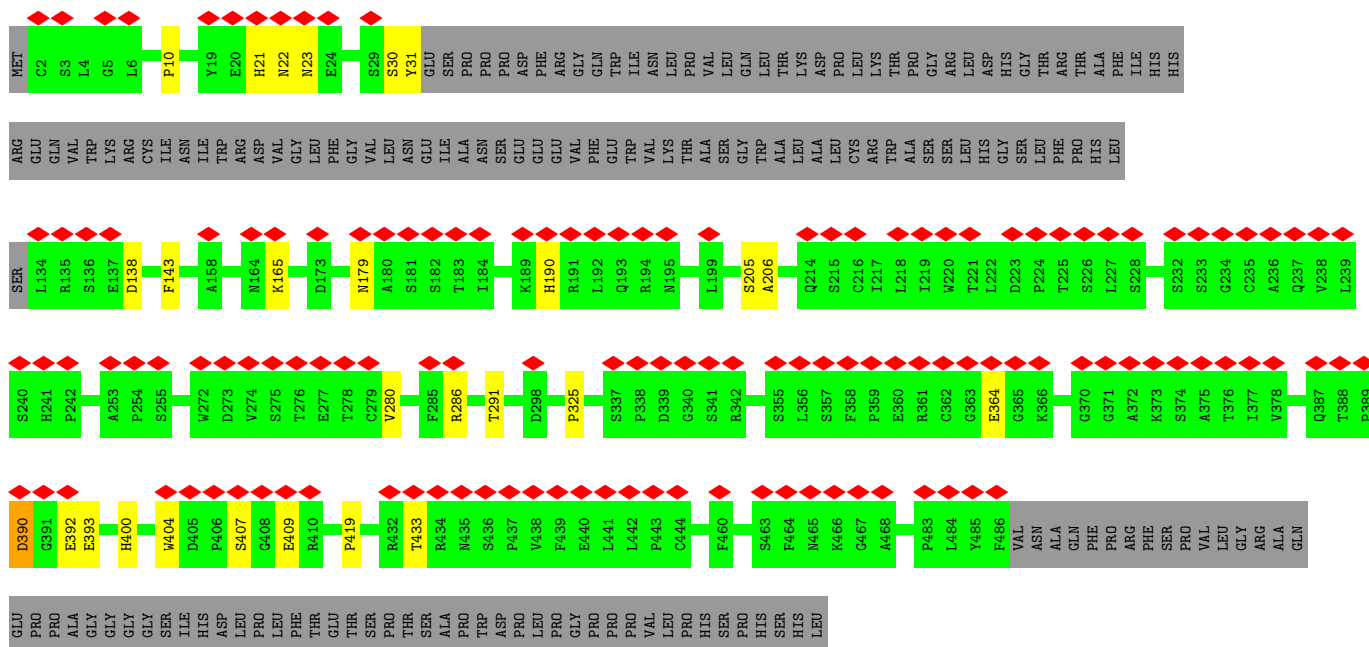
- Molecule 1: E3 SUMO-protein ligase RanBP2

Chain 03: 22% 77%

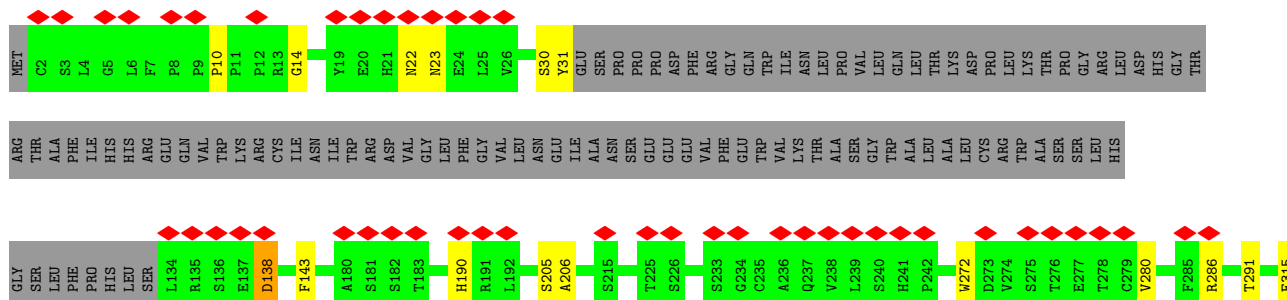


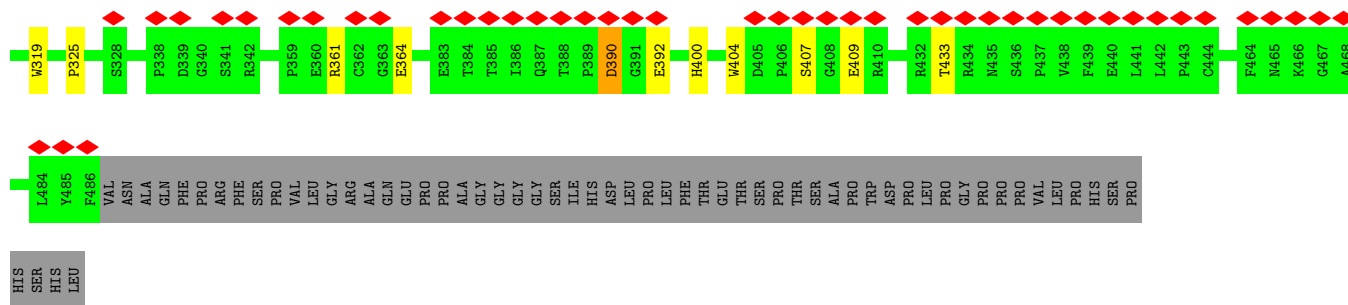


Chain 40: 25% 65% 5% 5%



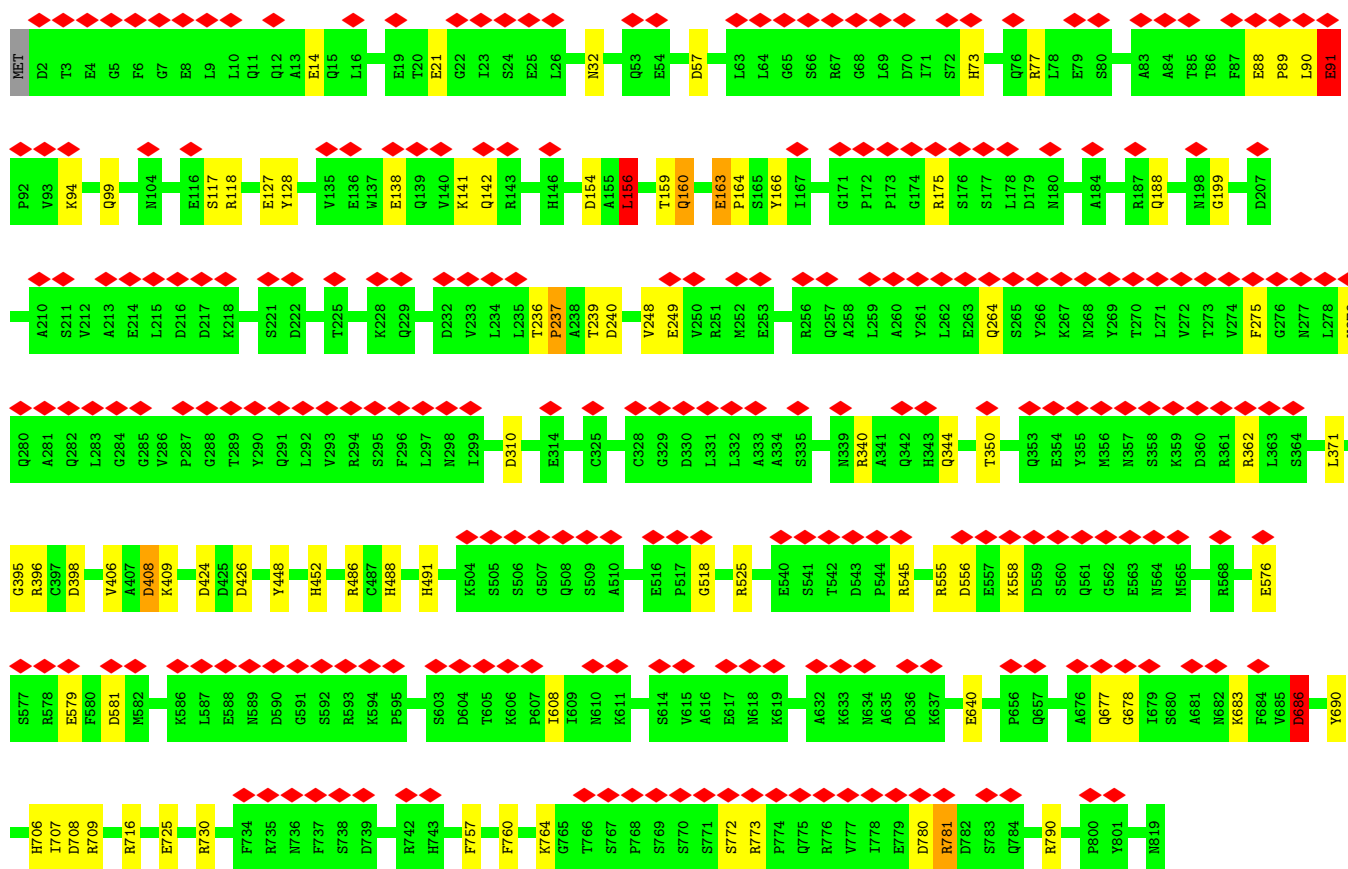
Chain 41:





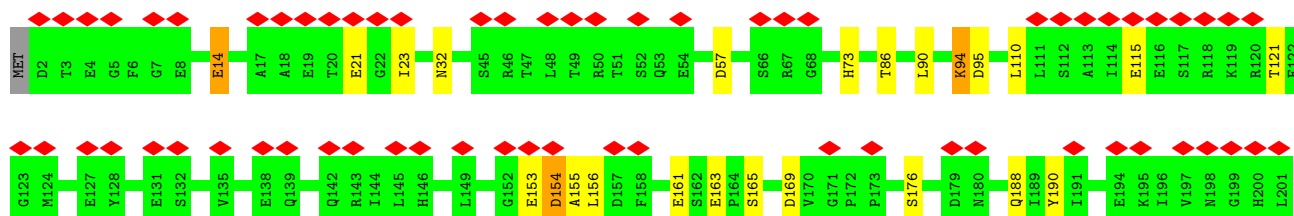
• Molecule 4: Nuclear pore complex protein Nup93

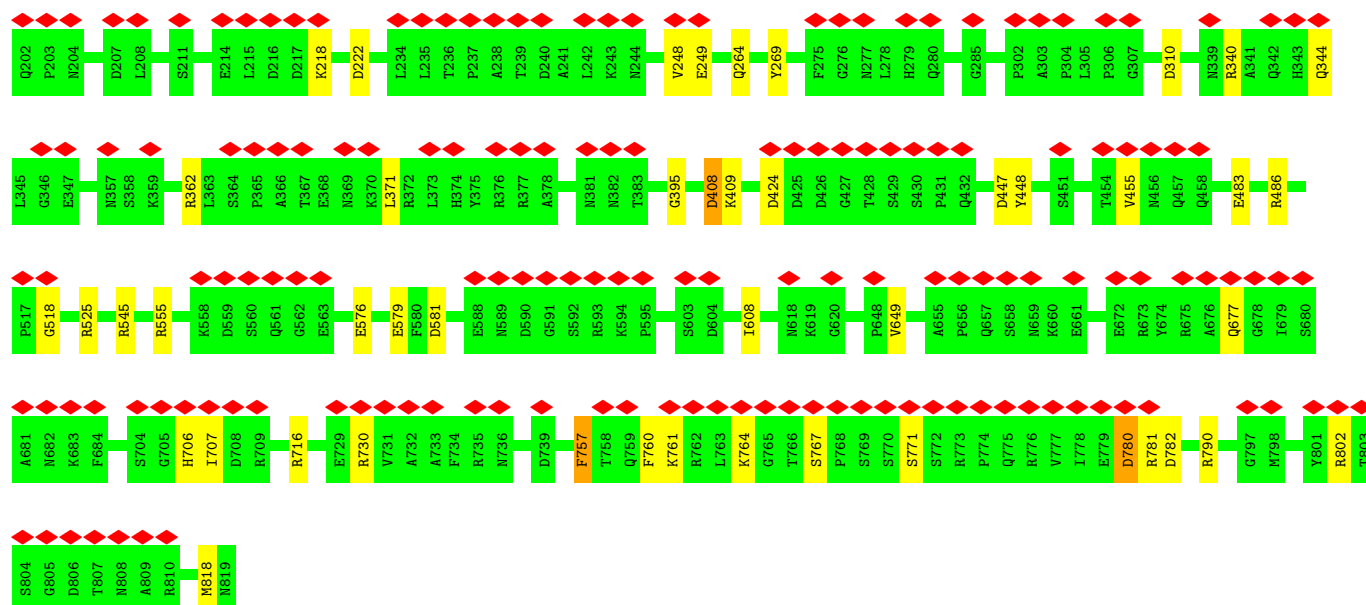
Chain A0: 31% 89% 10%



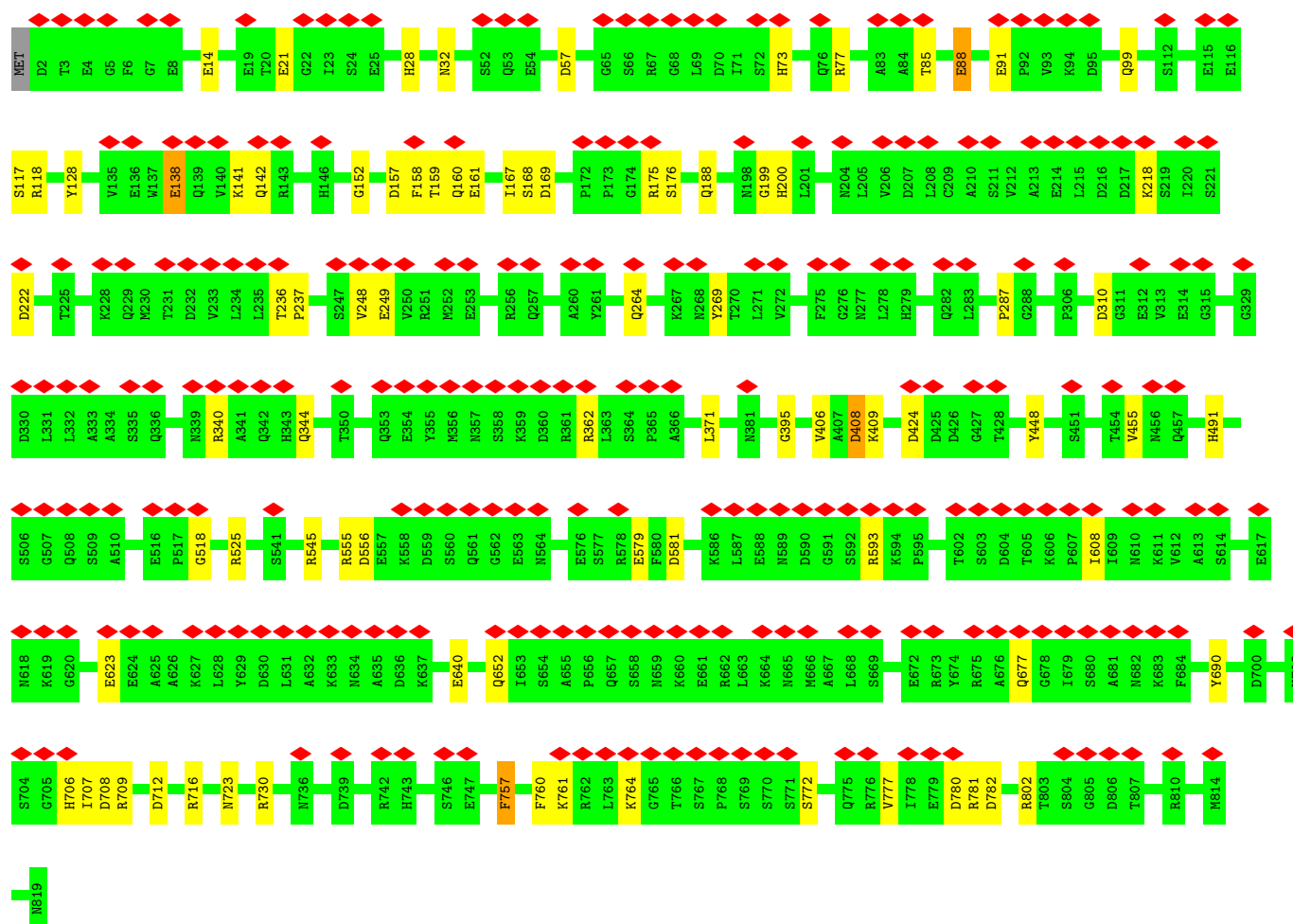
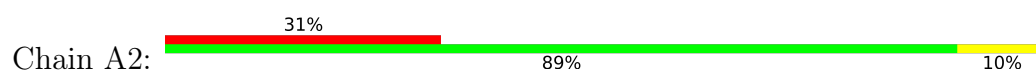
• Molecule 4: Nuclear pore complex protein Nup93

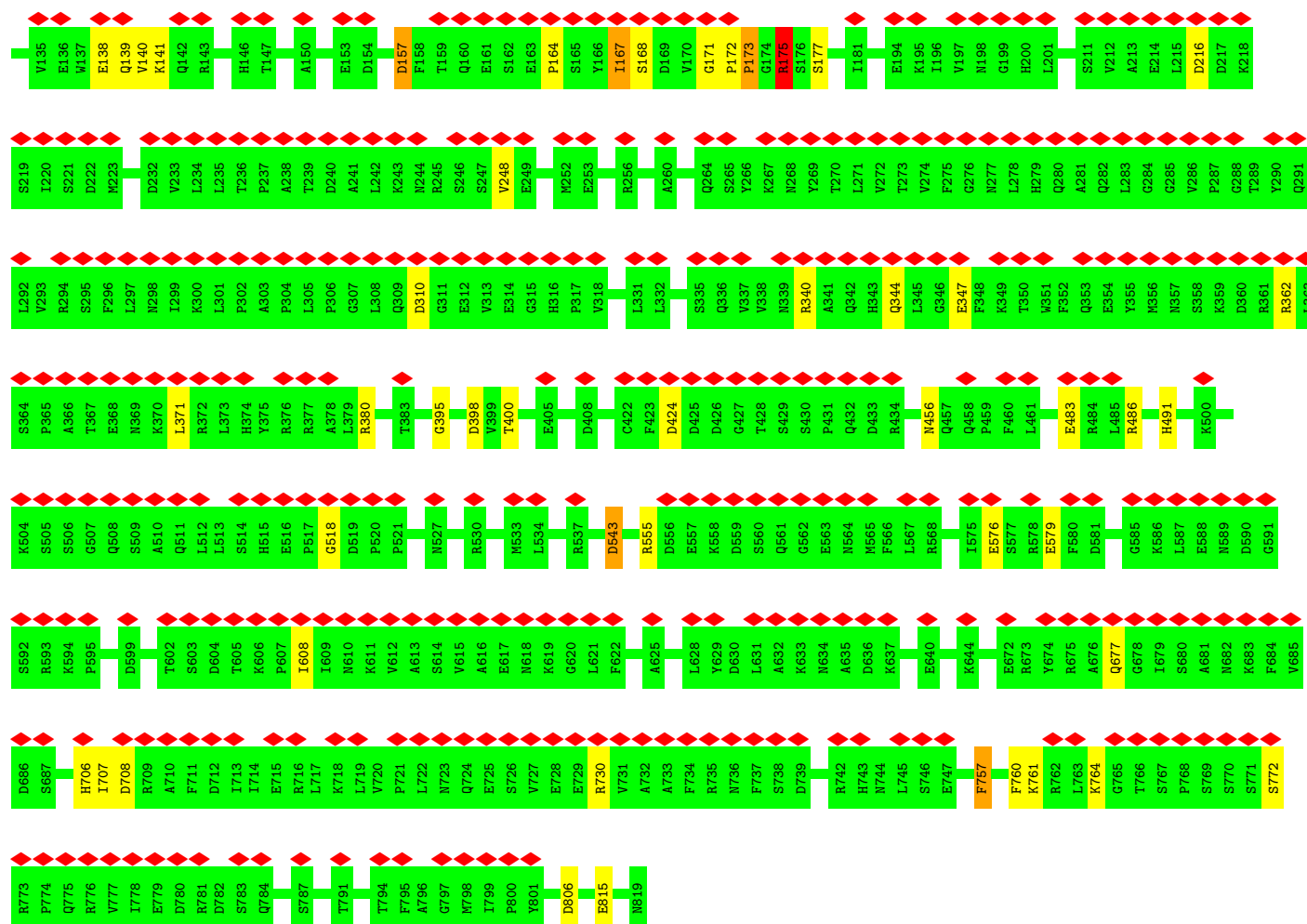
Chain A1: 27% 91% 8%



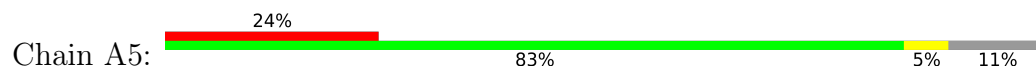


• Molecule 4: Nuclear pore complex protein Nup93

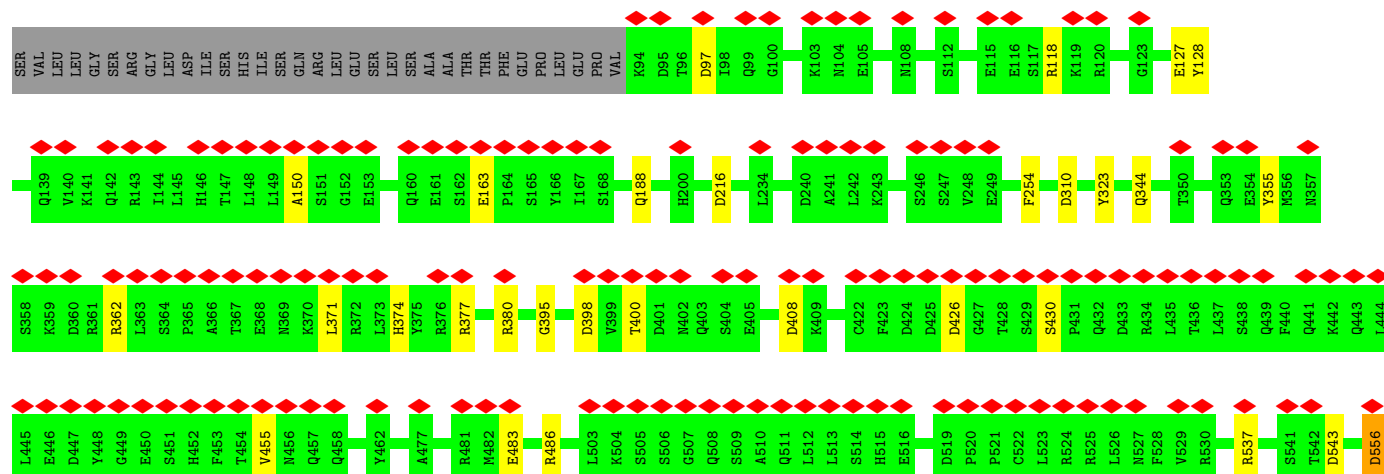


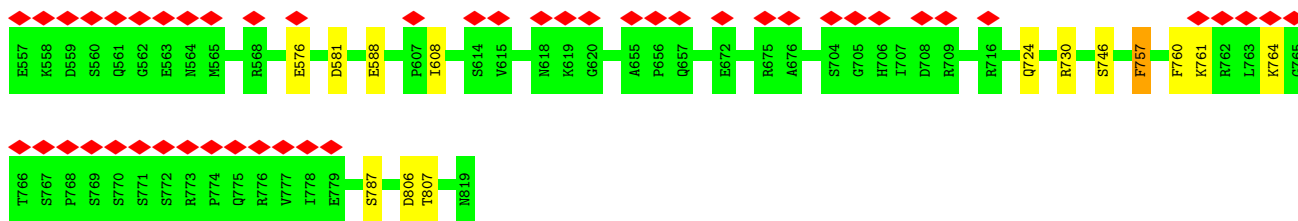


• Molecule 4: Nuclear pore complex protein Nup93

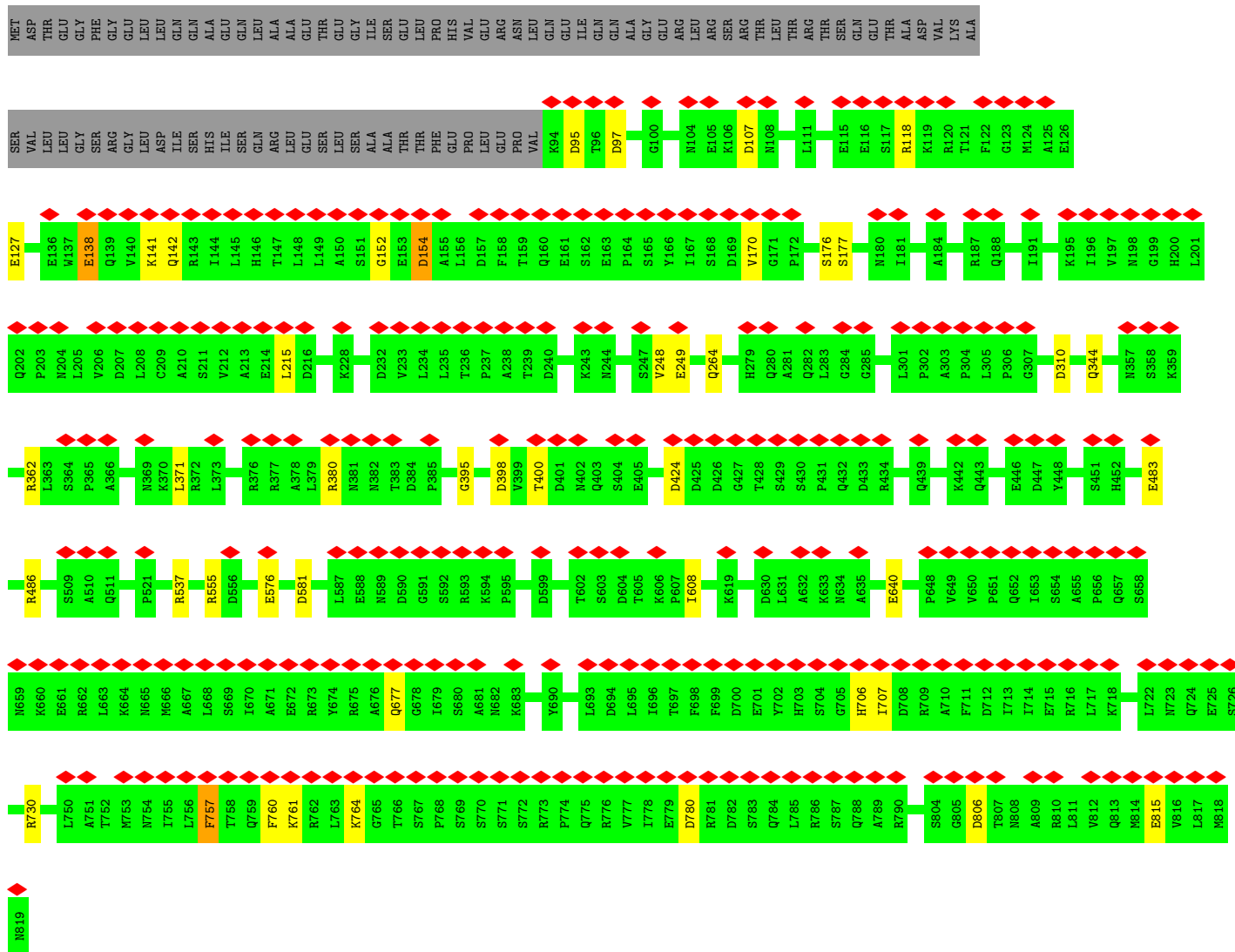
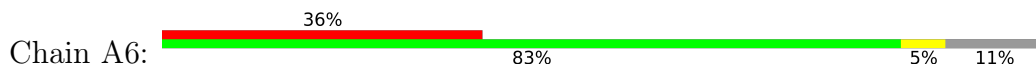


MET	ASP	THR	GLU	GLY	PHE	GLY	GLU	LEU	LEU	LEU	GLN	GLN	ALA	GLU	GLN	LEU	LEU	ALA	ALA	GLU	THR	GLU	GLY	ILE	ILE	SER	GLU	LEU	PRO	HIS	VAL	GLU	LEU	GLU	ARG	ASN	LEU	GLN	ILE	GLN	GLN	ALA	GLY	GLU	ARG	LEU	ARG	SER	THR	LEU	THR	ARG	SER	GLN	GLU	THR	ASP	VAL	LYS	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----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

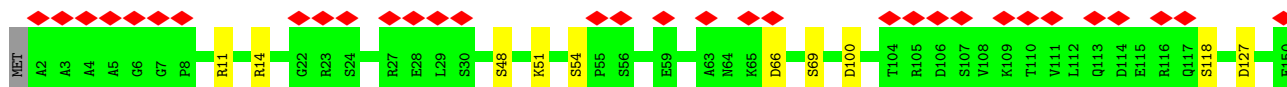


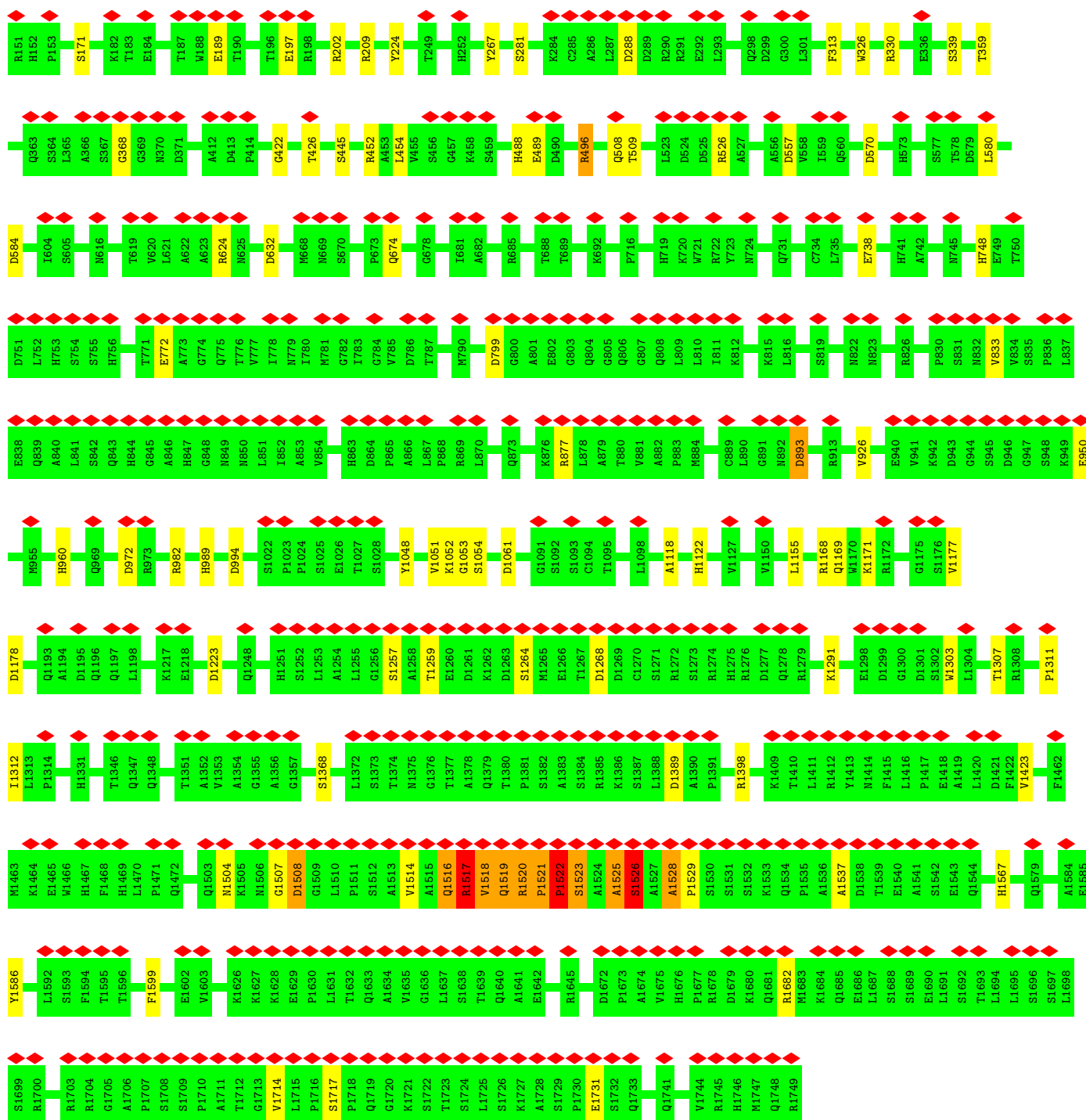


• Molecule 4: Nuclear pore complex protein Nup93



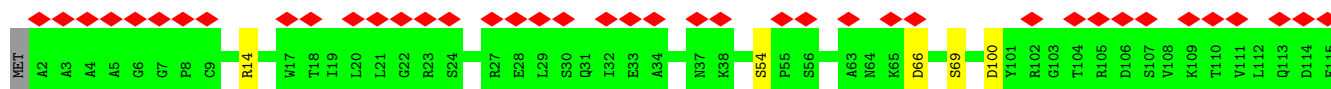
• Molecule 5: Nucleoporin NUP188 homolog

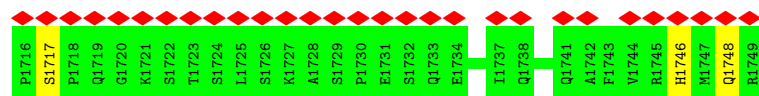
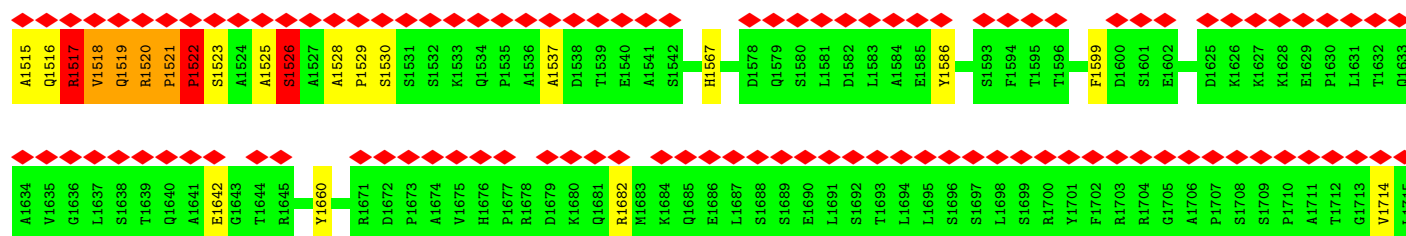




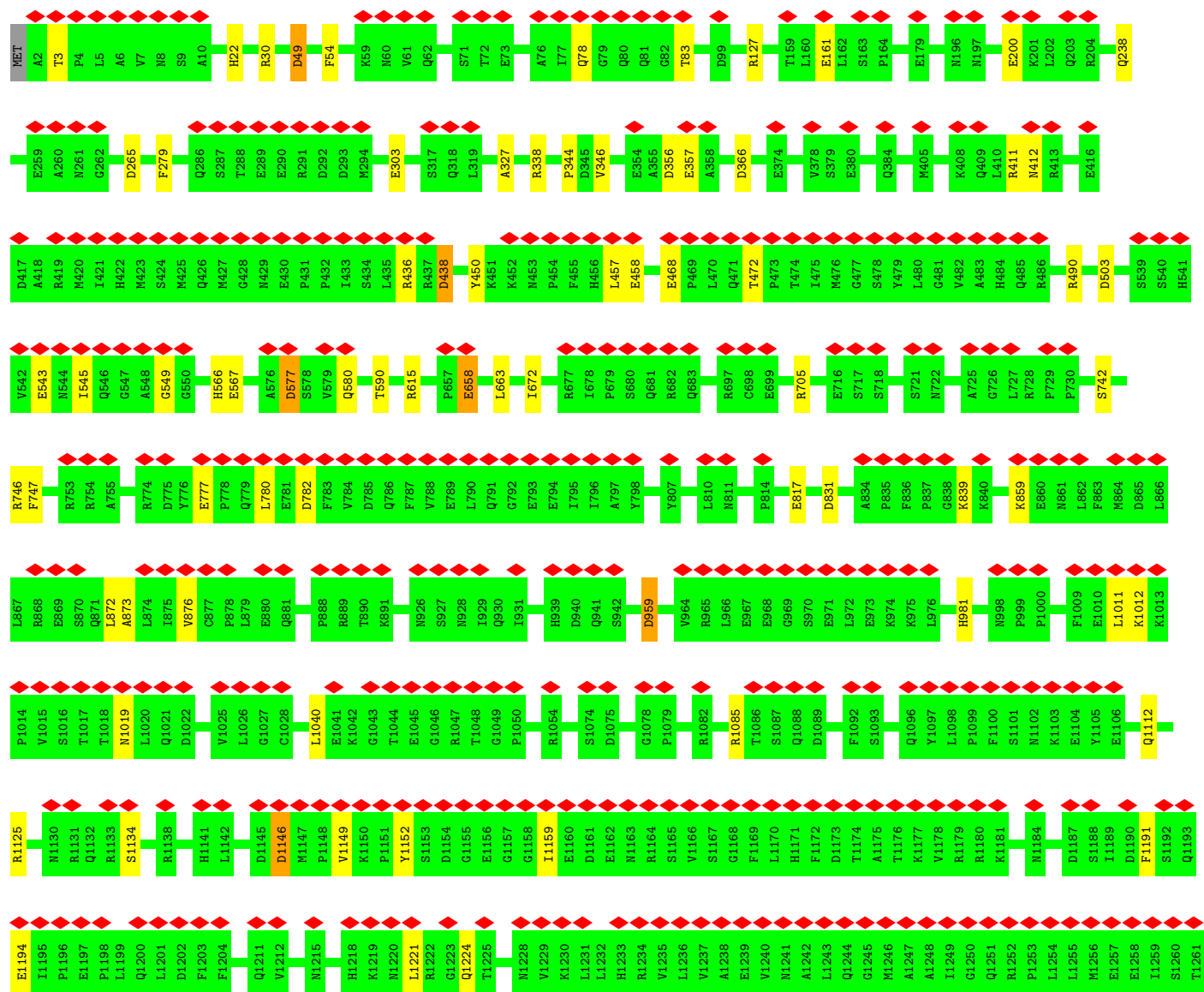
• Molecule 5: Nucleoporin NUP188 homolog

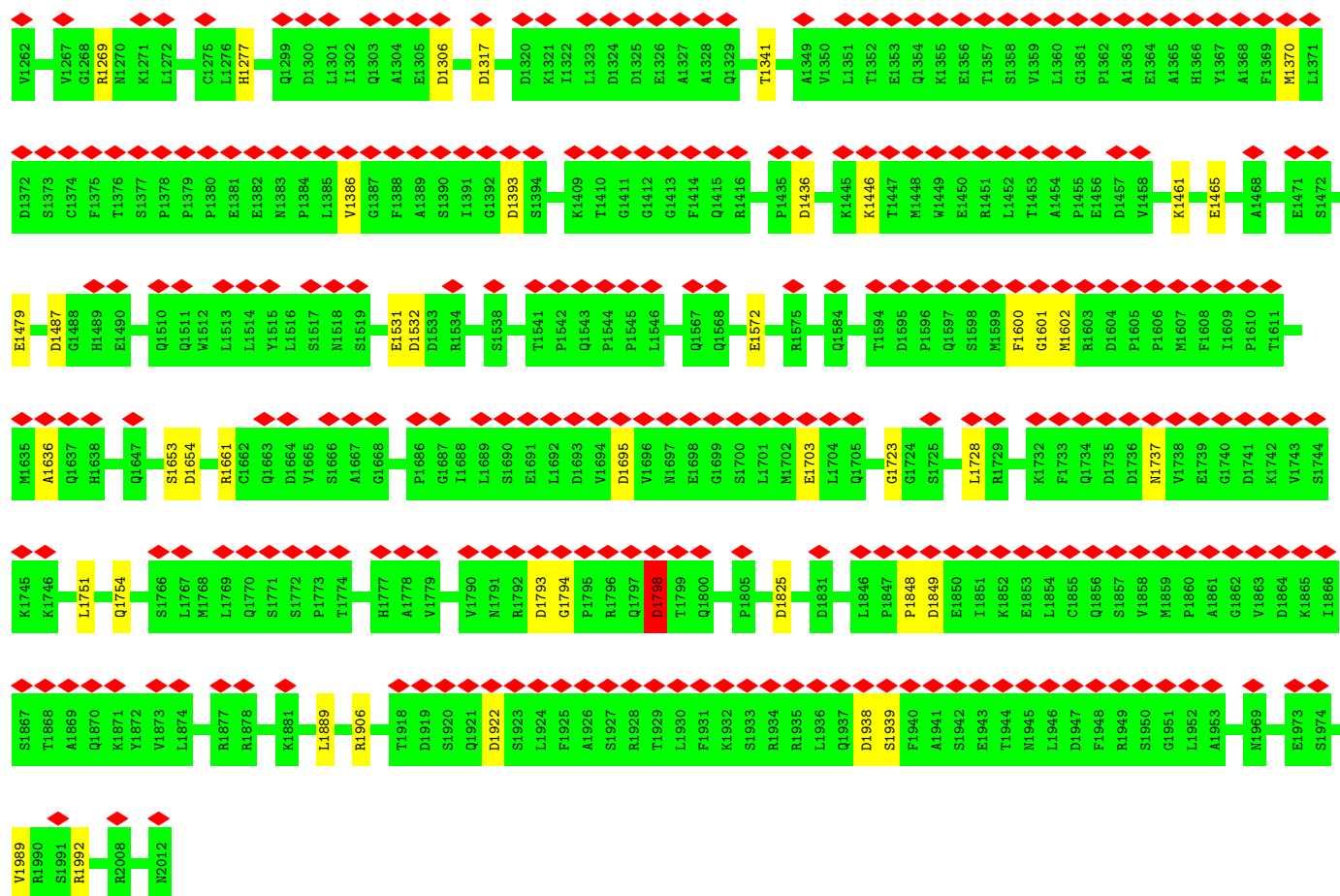
Chain B1: 44% 94% 5%



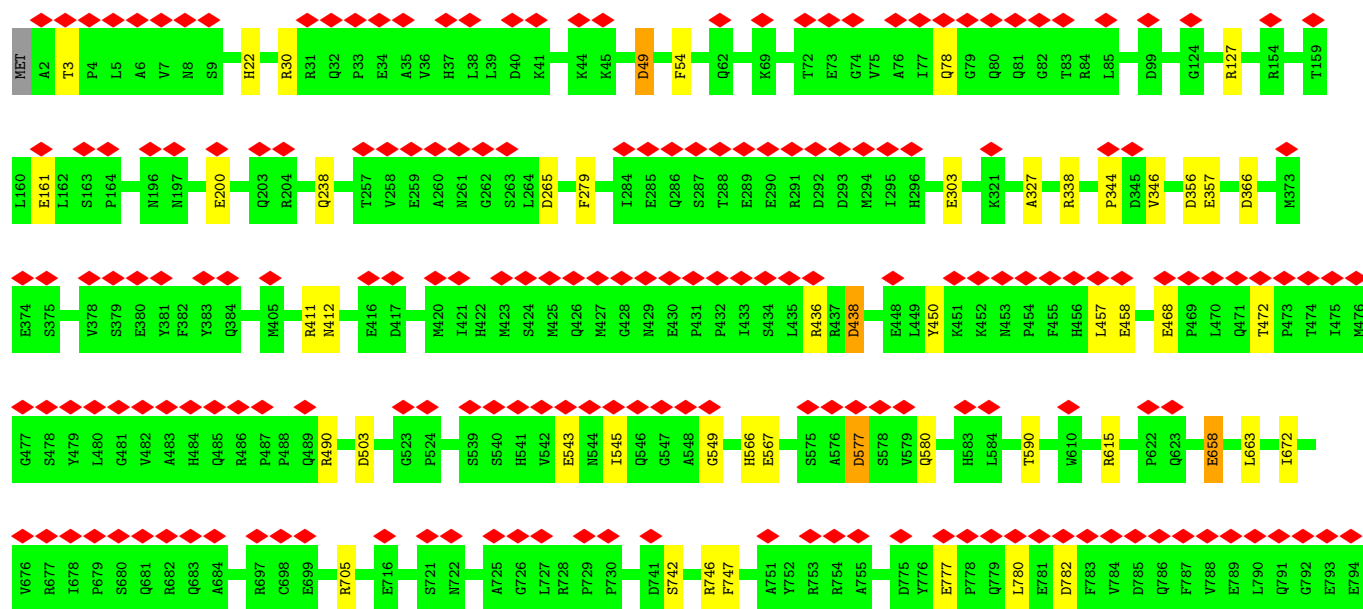


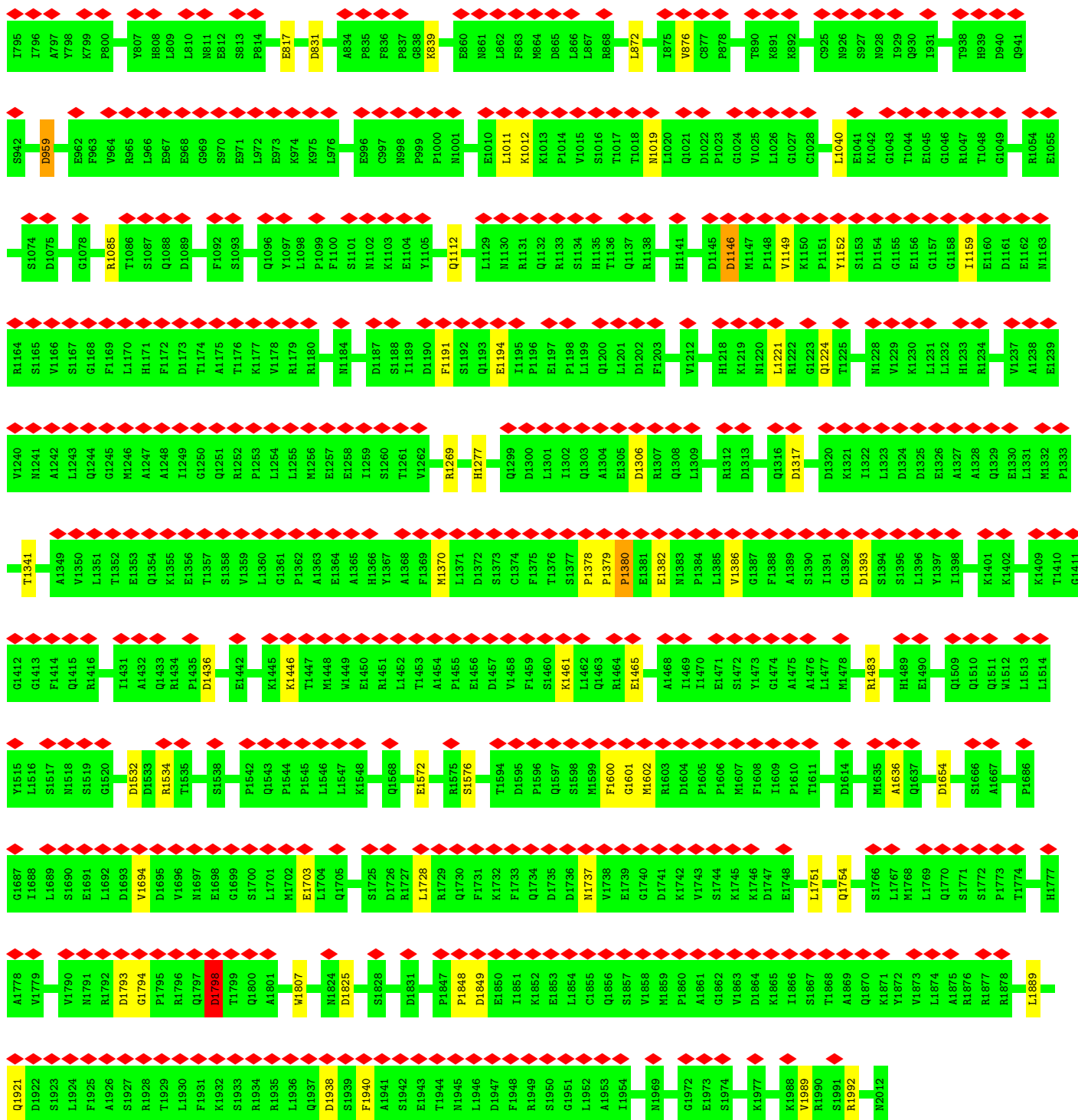
• Molecule 6: Nuclear pore complex protein Nup205



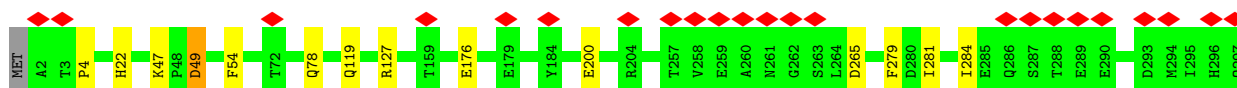


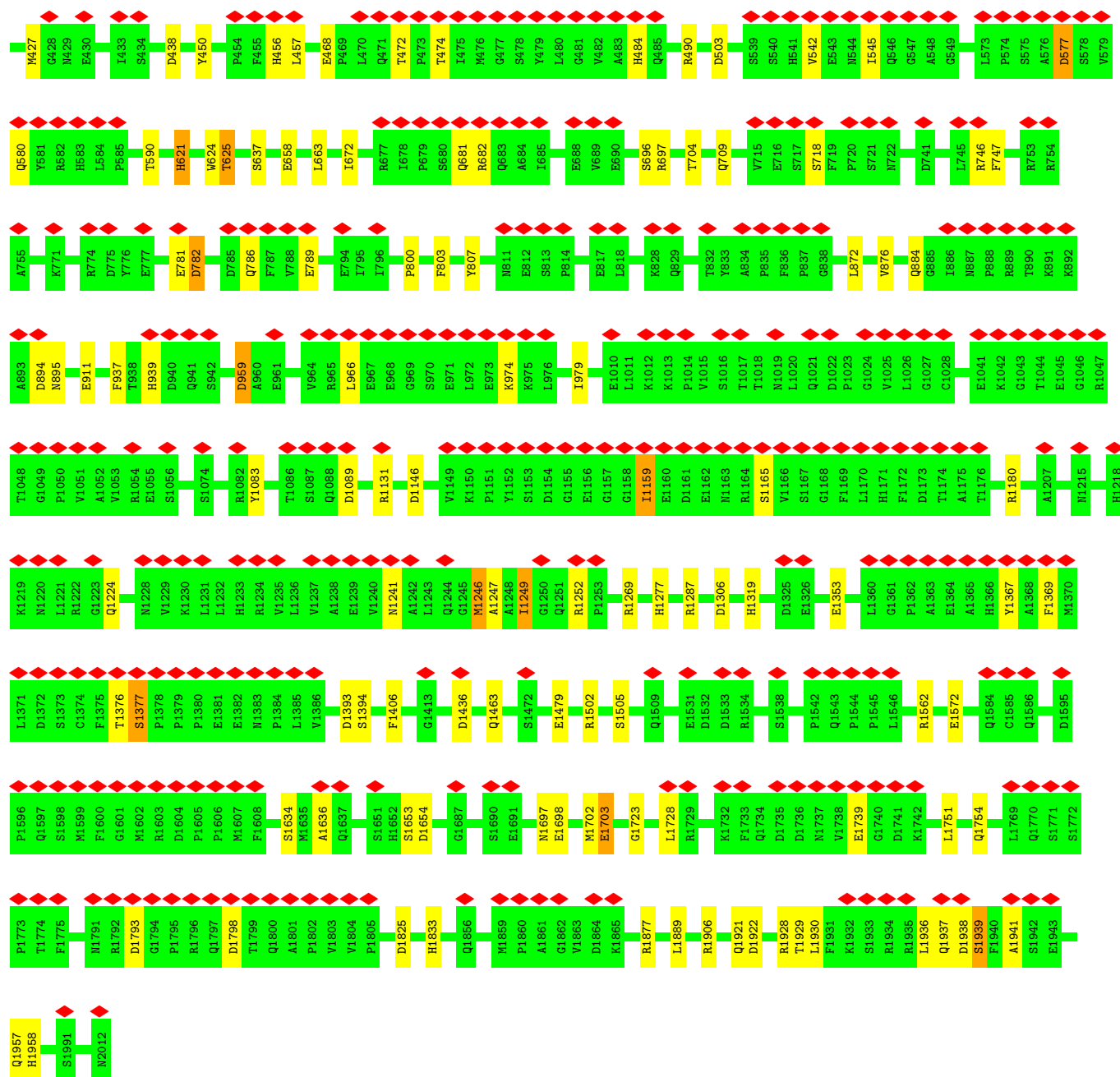
• Molecule 6: Nuclear pore complex protein Nup205



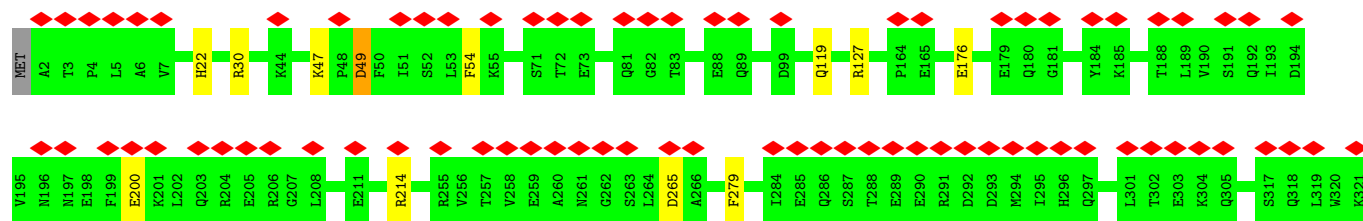
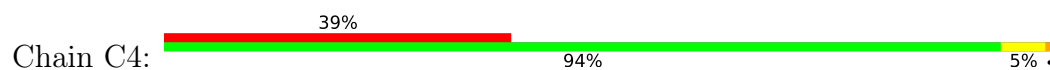


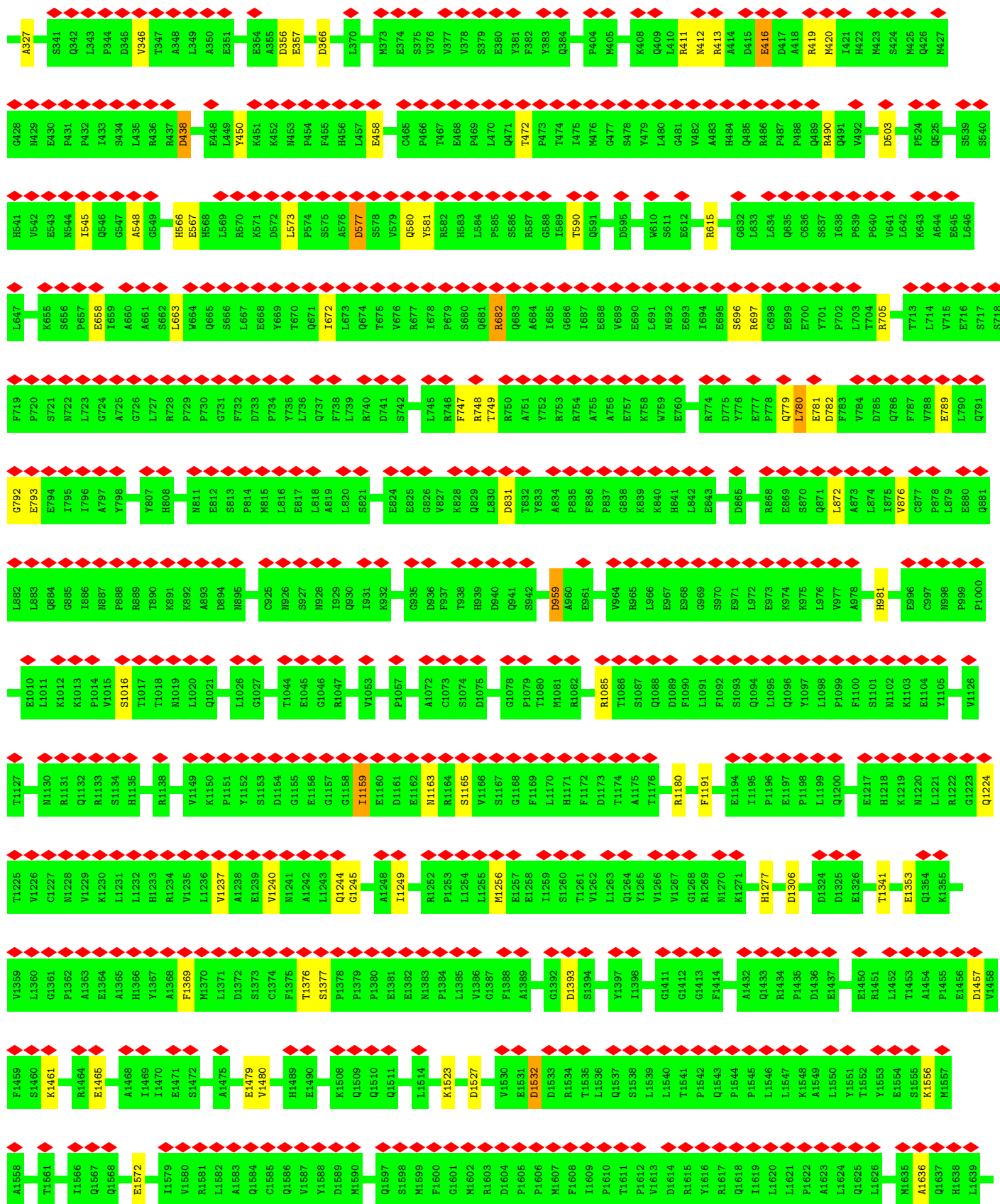
• Molecule 6: Nuclear pore complex protein Nup205

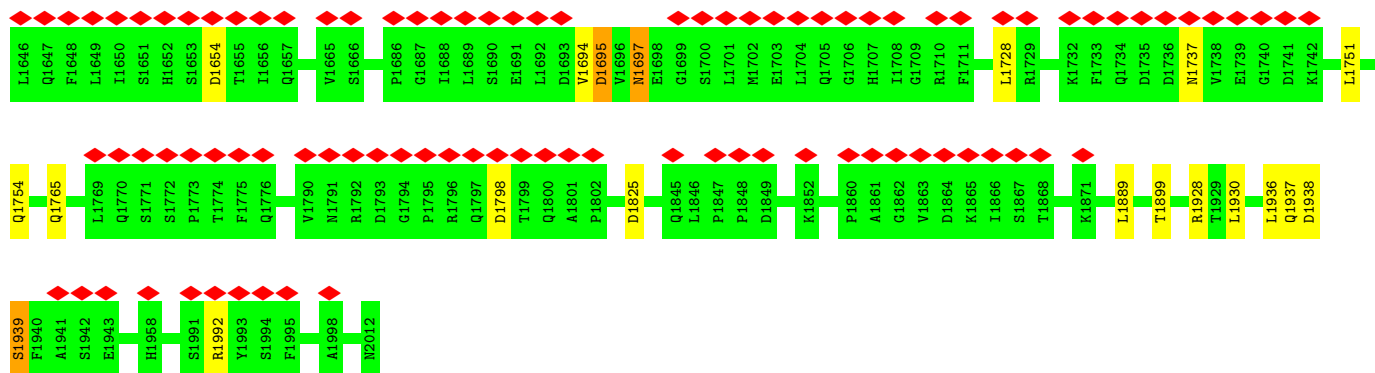




• Molecule 6: Nuclear pore complex protein Nup205

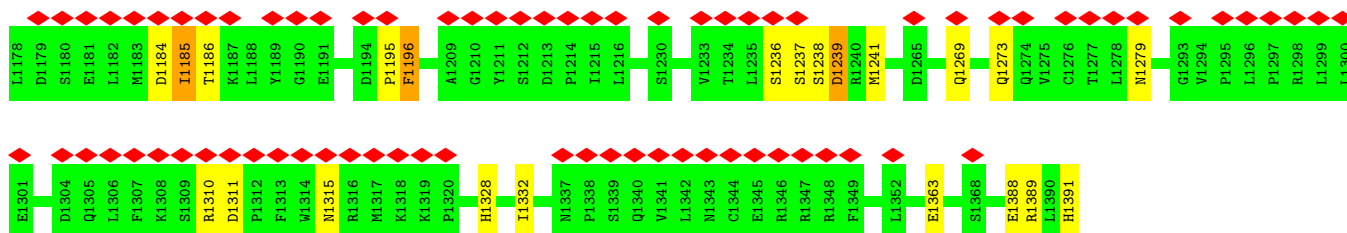
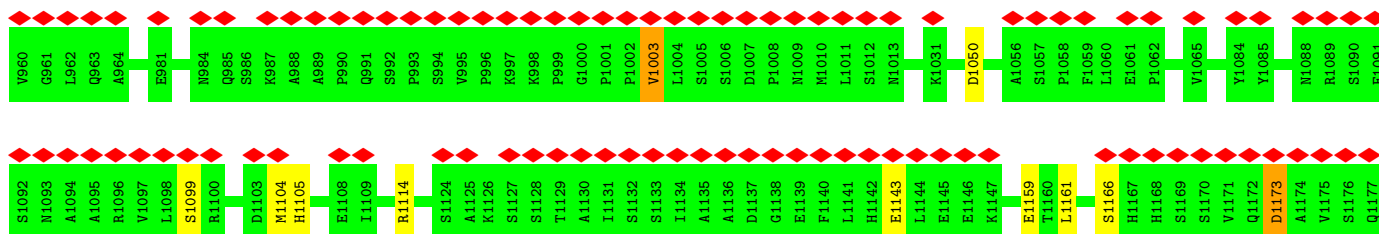




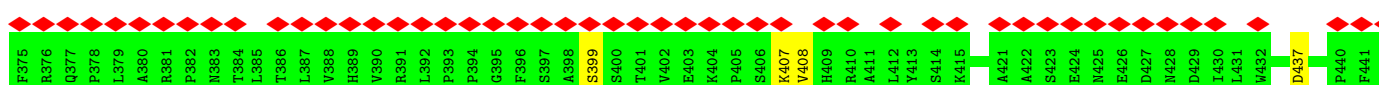
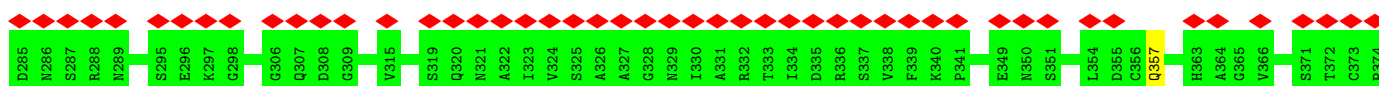
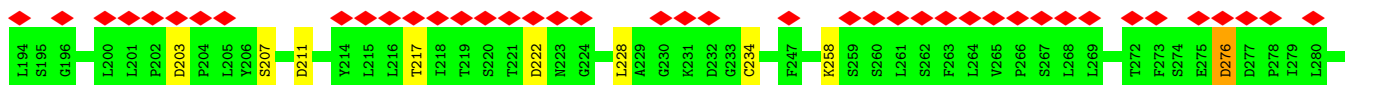
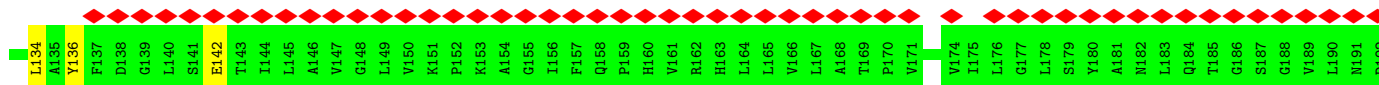
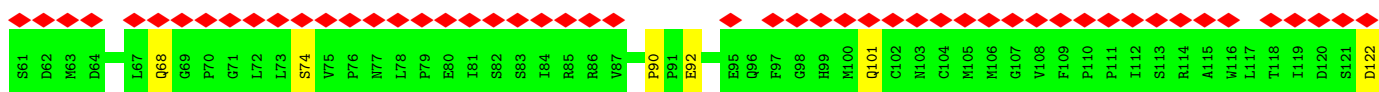
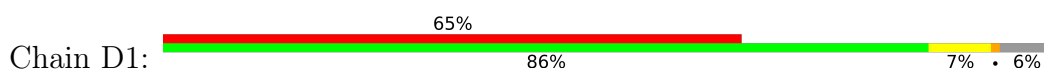


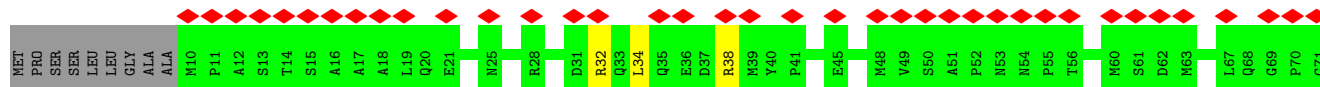
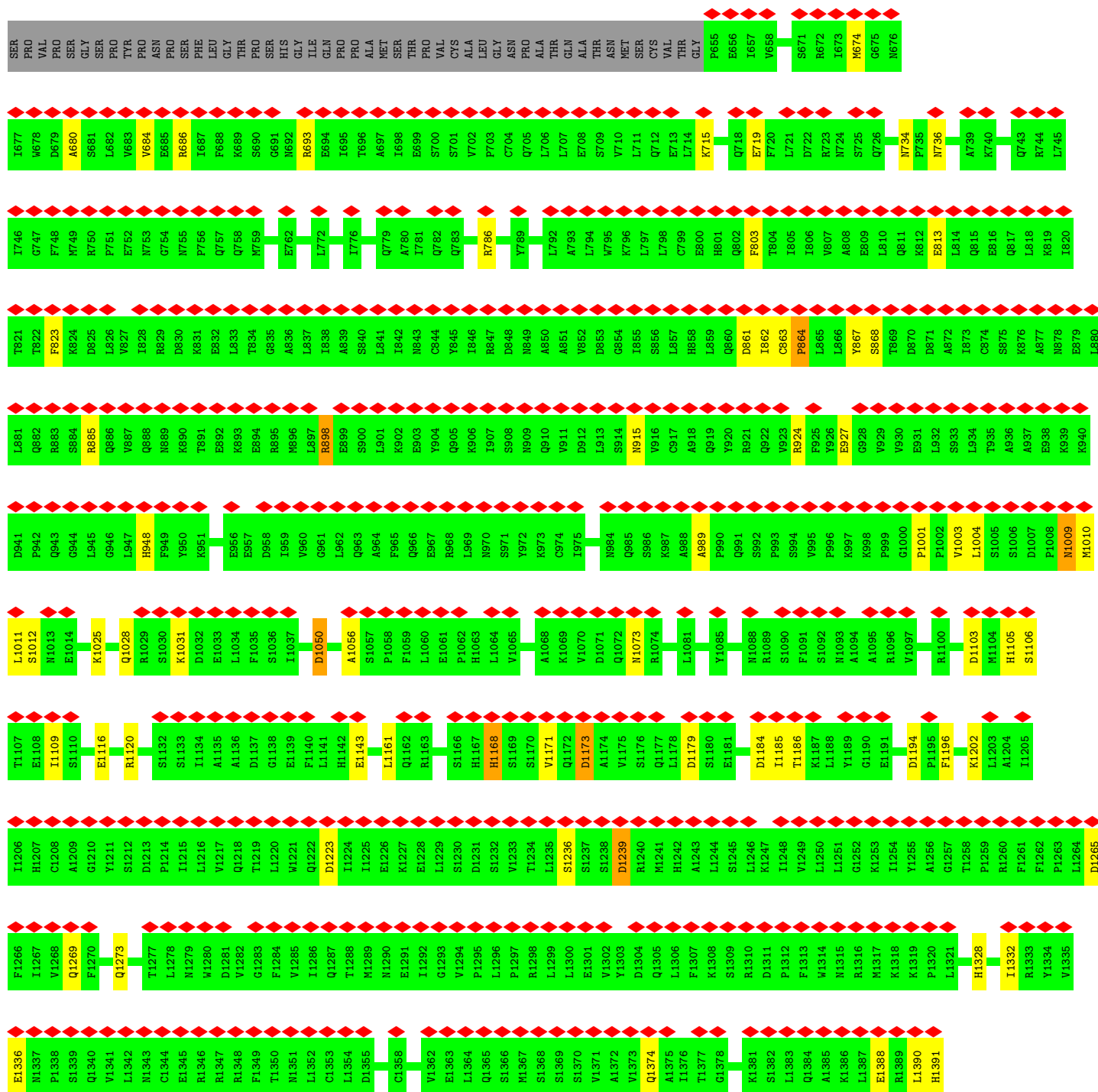
• Molecule 7: Nuclear pore complex protein Nup155

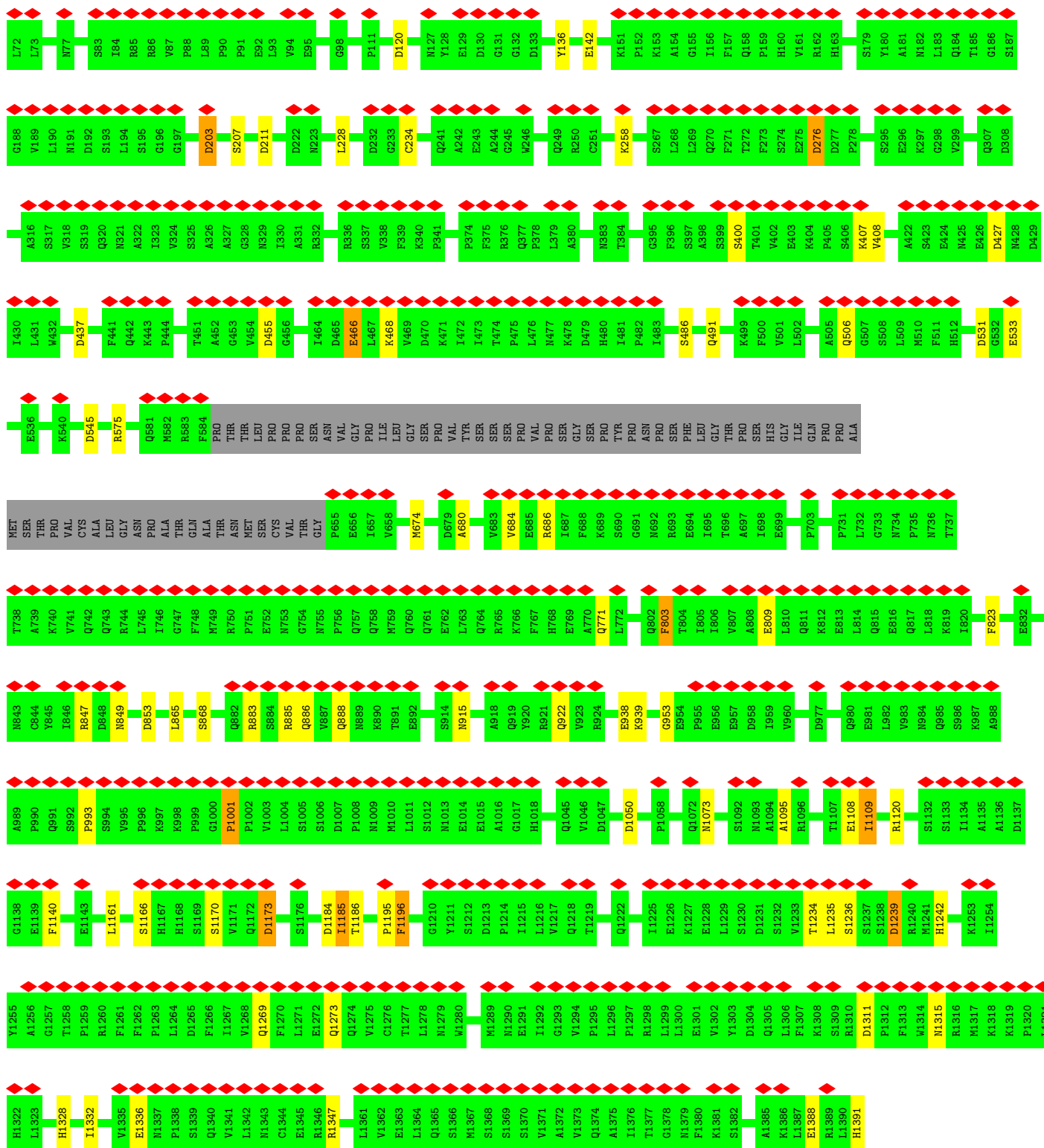




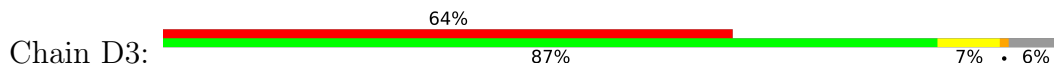
• Molecule 7: Nuclear pore complex protein Nup155

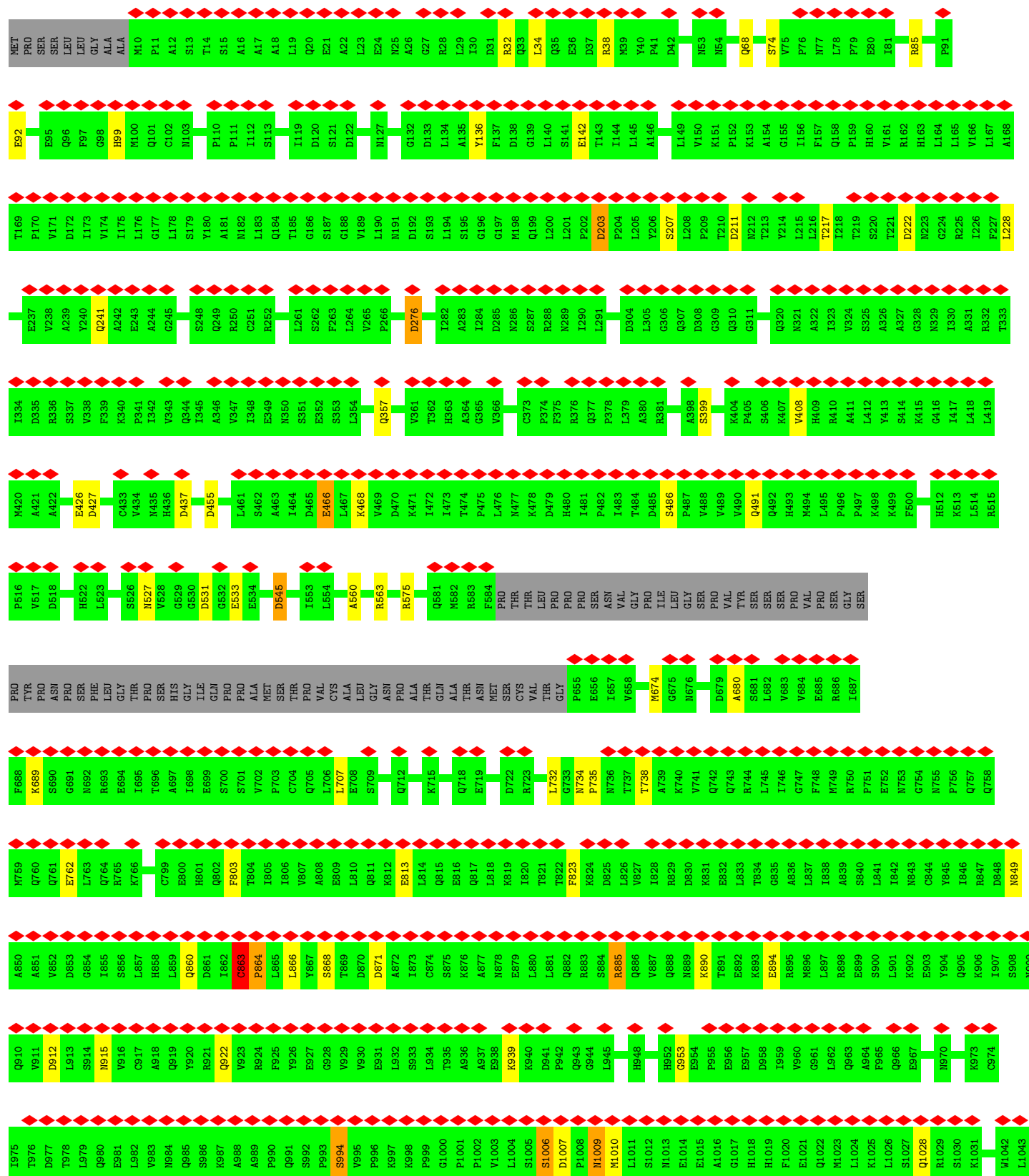


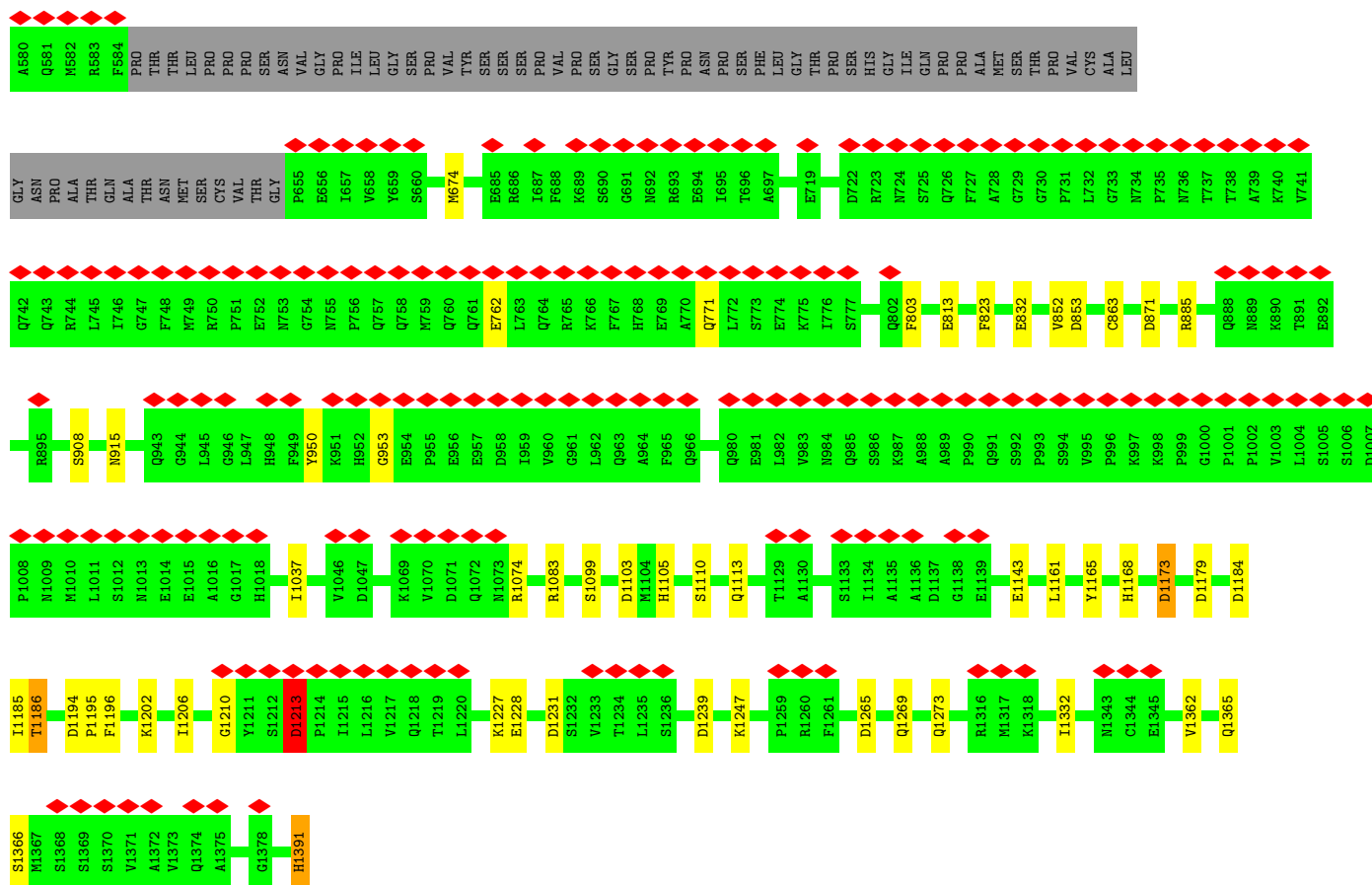




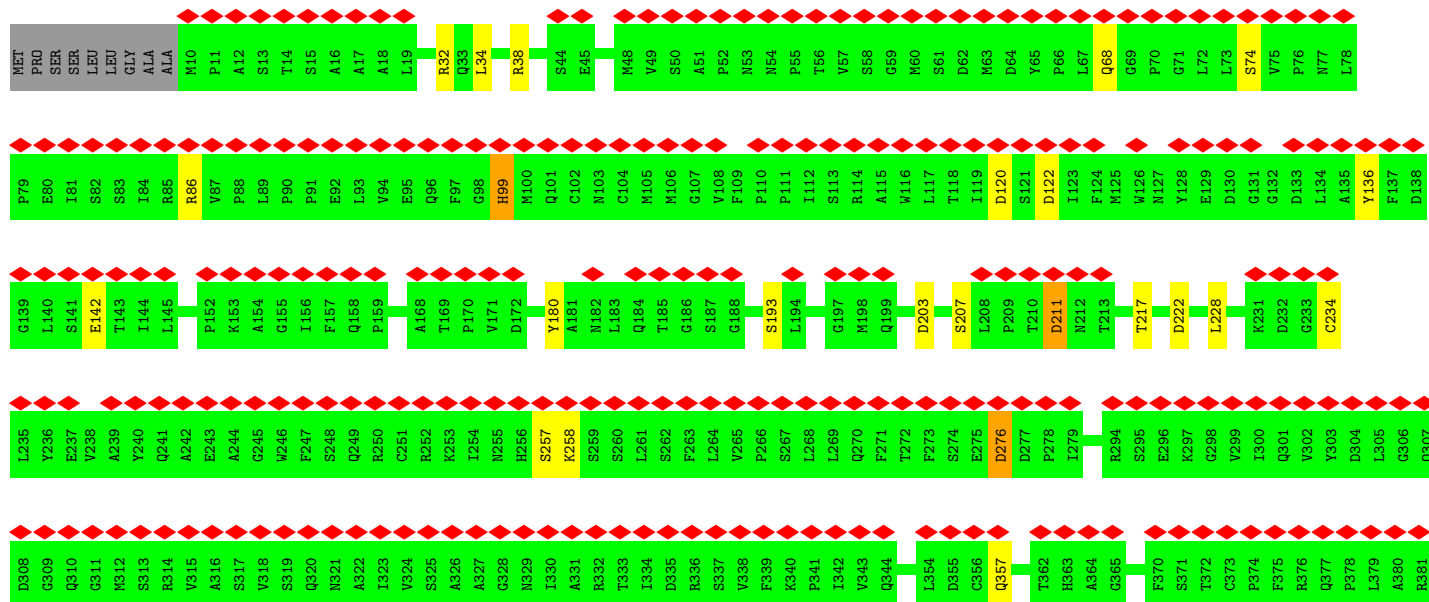
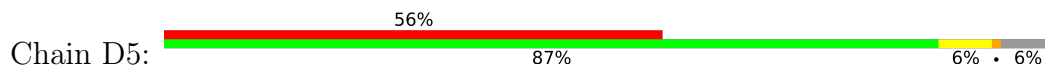
• Molecule 7: Nuclear pore complex protein Nup155

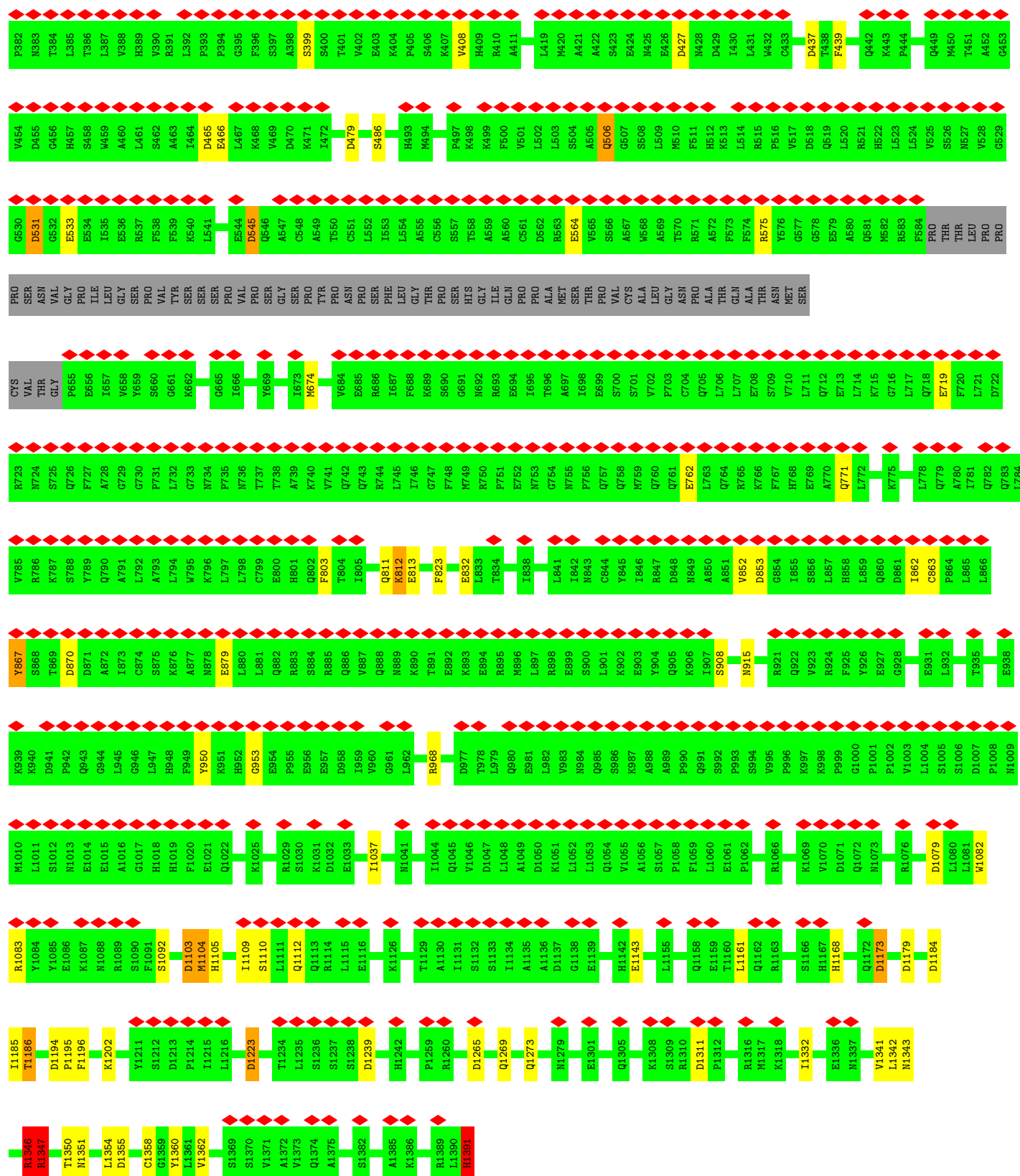


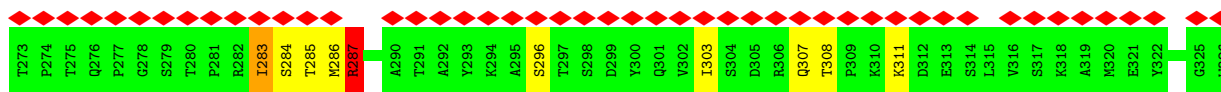




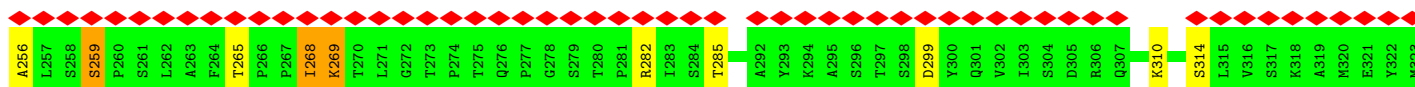
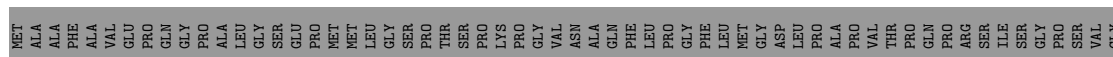
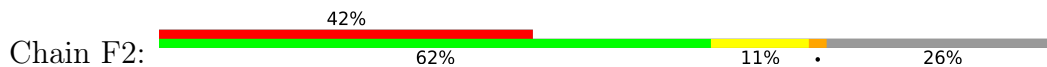
• Molecule 7: Nuclear pore complex protein Nup155



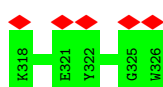
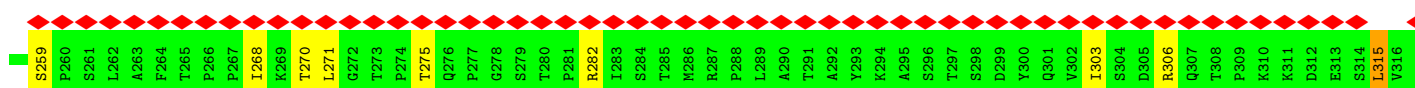
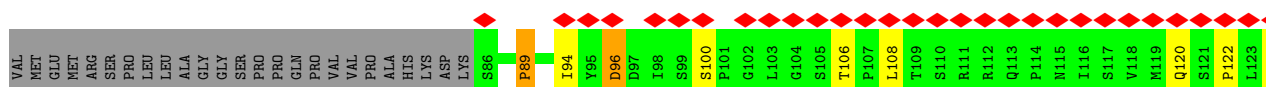
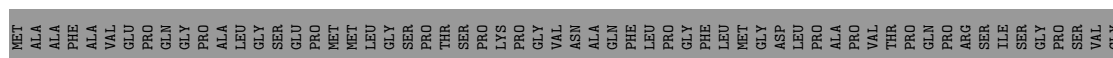
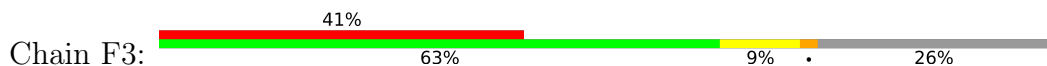




• Molecule 9: Nucleoporin NUP35

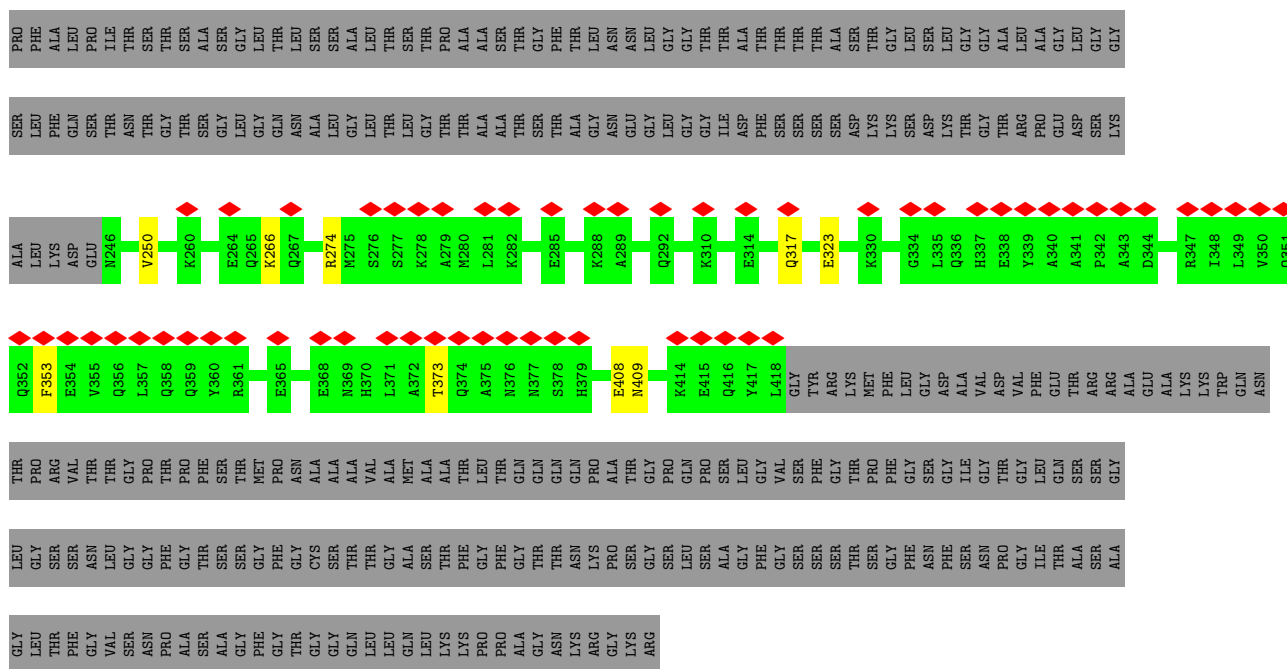


• Molecule 9: Nucleoporin NUP35

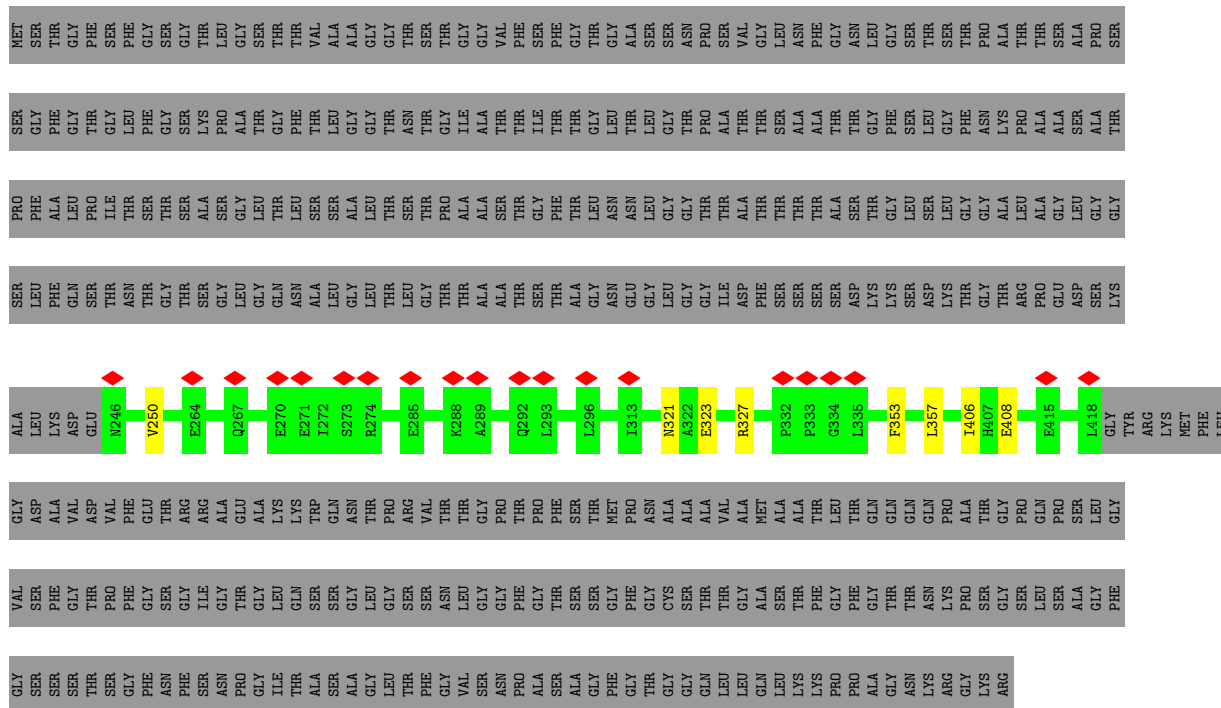


• Molecule 10: Nucleoporin p54

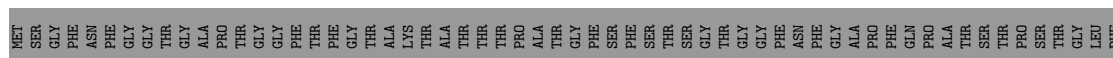


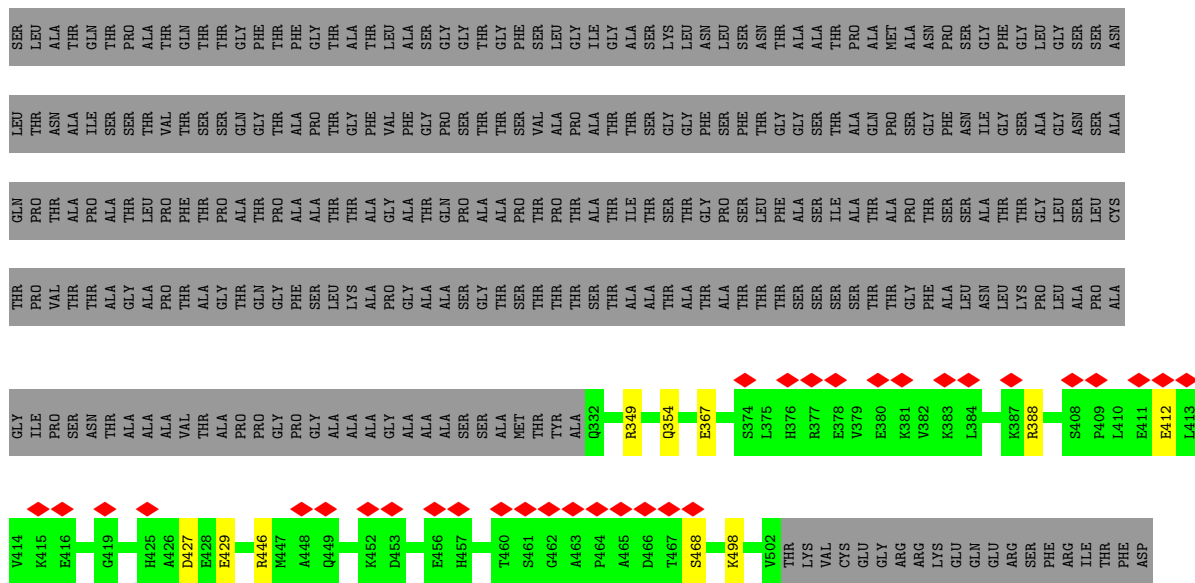


- Molecule 11: Nucleoporin p58/p45

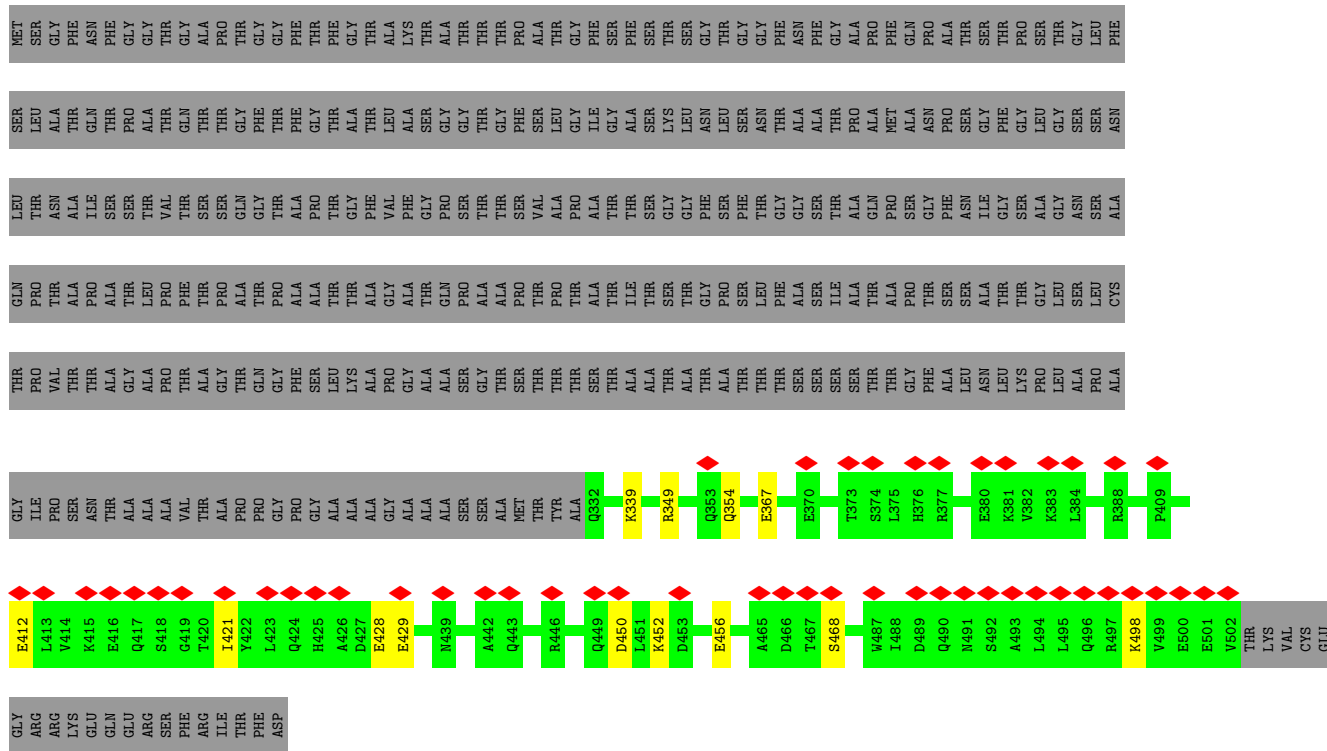


- Molecule 12: Nuclear pore glycoprotein p62

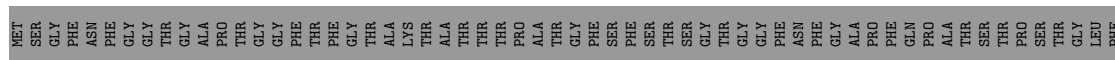




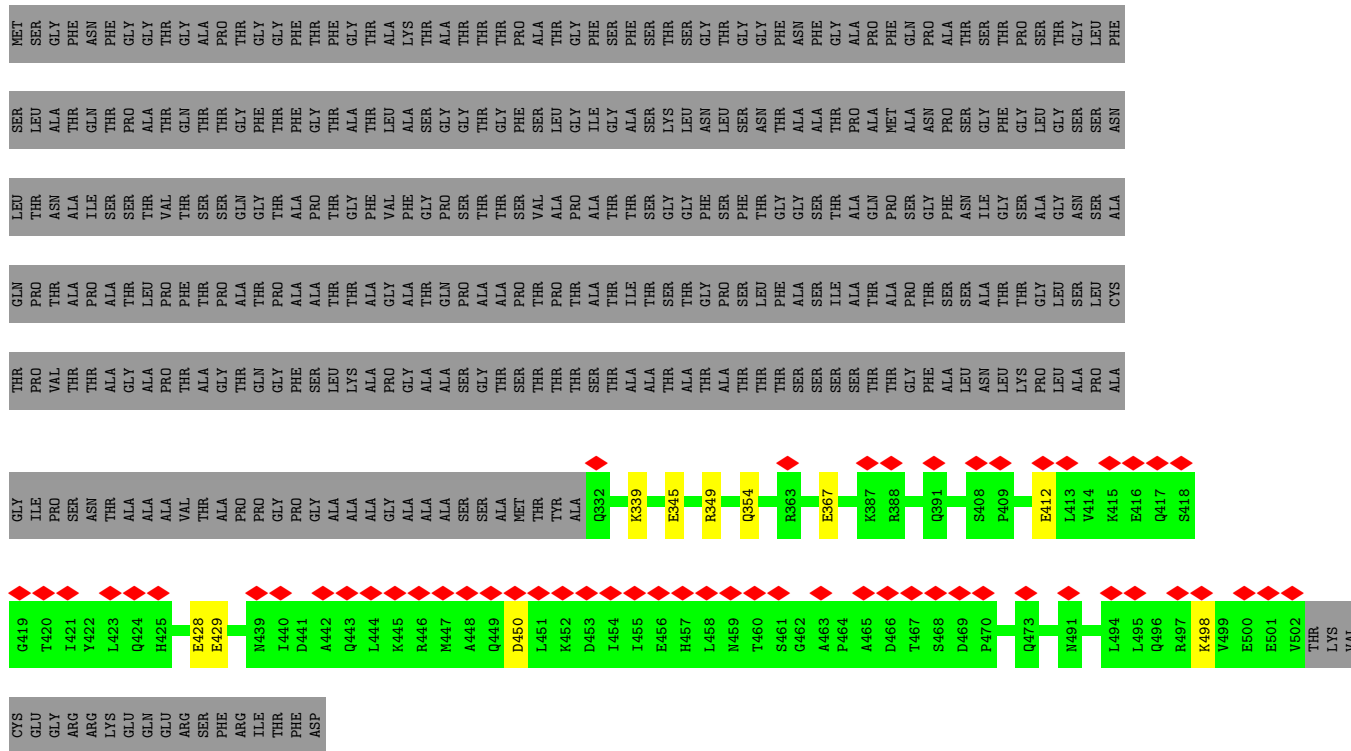
- Molecule 12: Nuclear pore glycoprotein p62



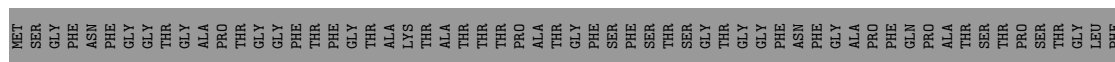
- Molecule 12: Nuclear pore glycoprotein p62

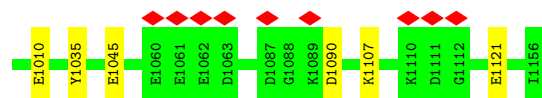


- Molecule 12: Nuclear pore glycoprotein p62



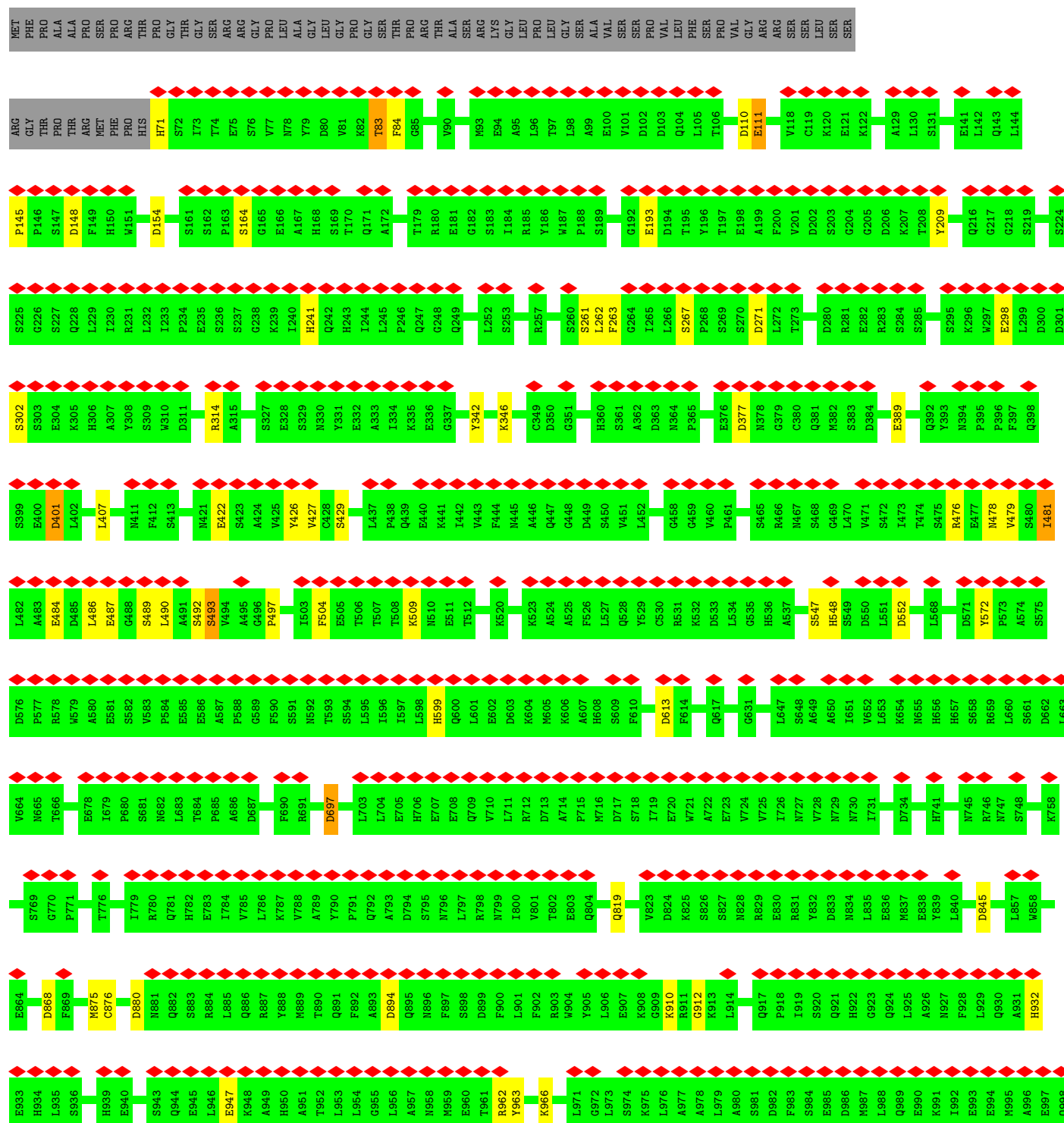
- Molecule 12: Nuclear pore glycoprotein p62

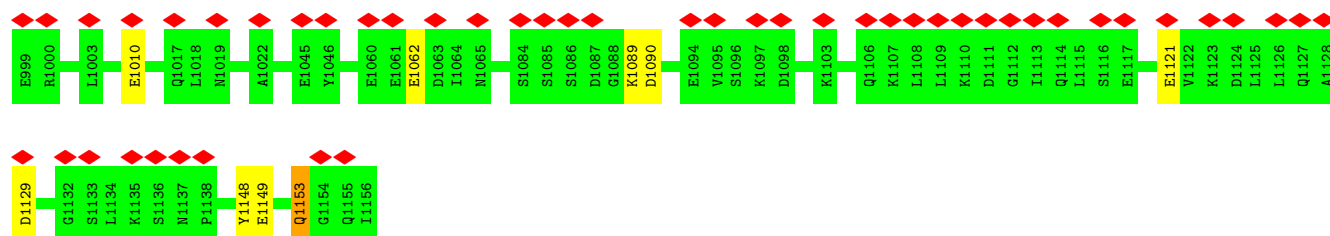




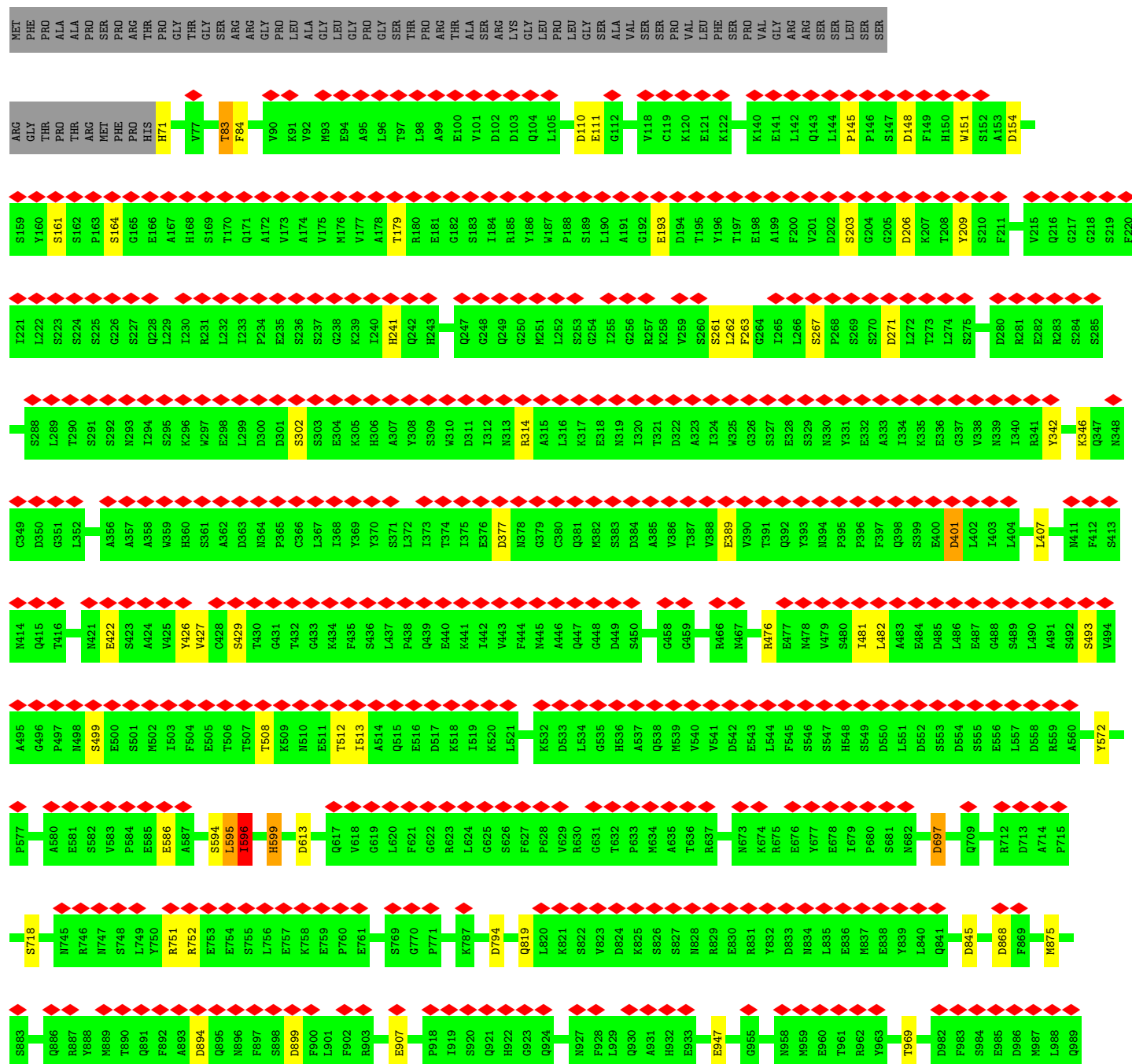
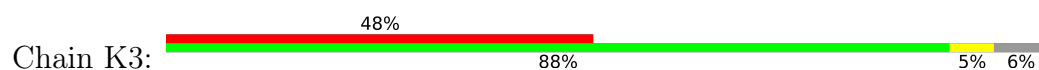
• Molecule 13: Nuclear pore complex protein Nup133

Chain K2: 51% 88% 6% • 6%

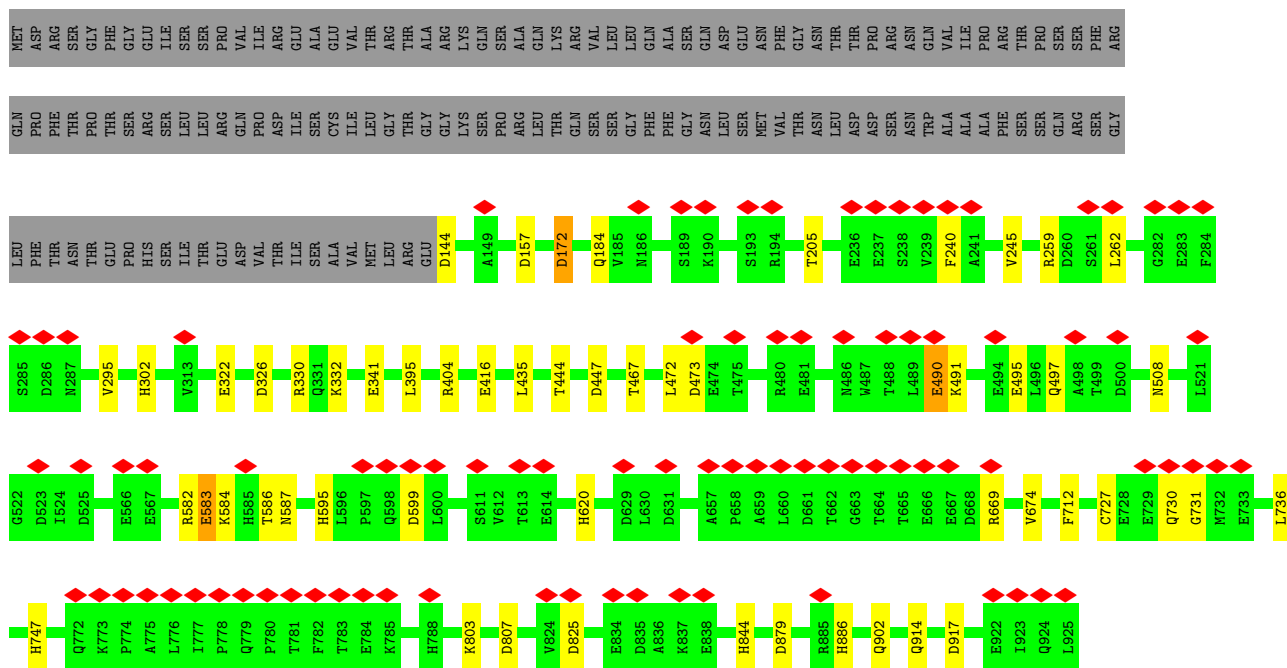
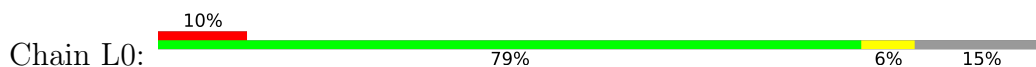




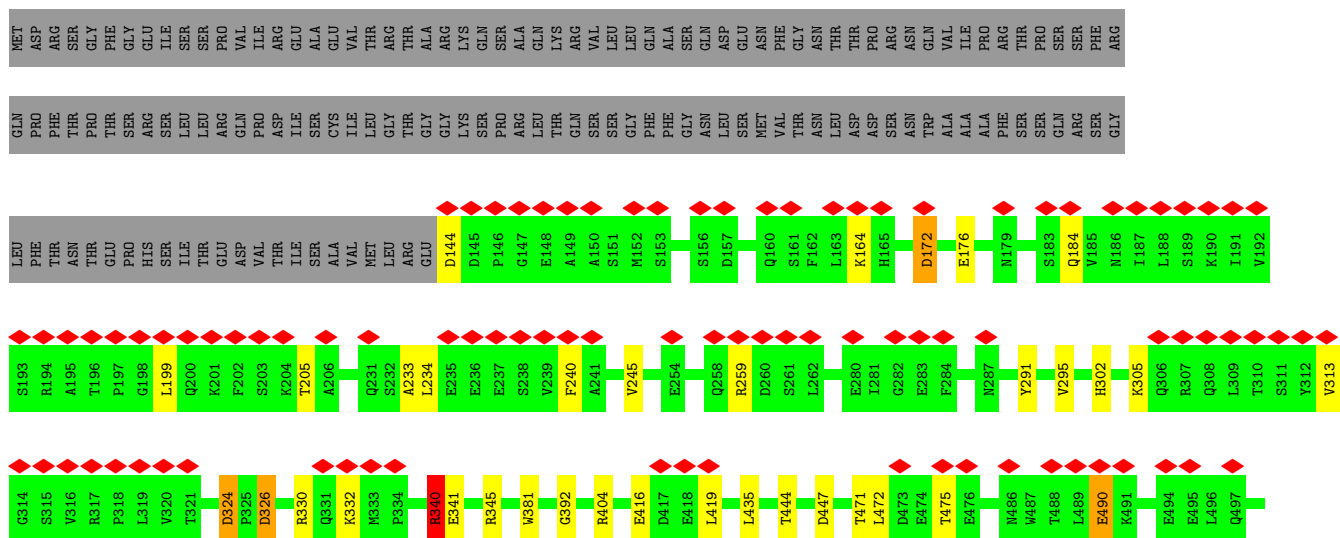
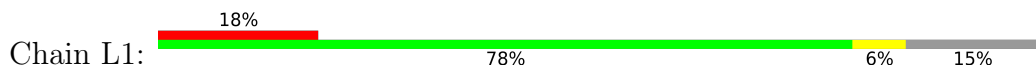
• Molecule 13: Nuclear pore complex protein Nup133

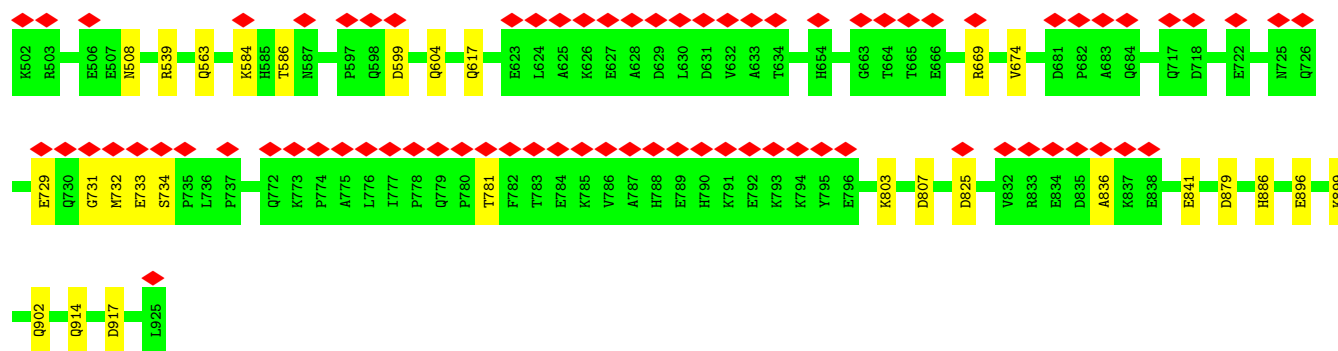


- Molecule 14: Nuclear pore complex protein Nup107

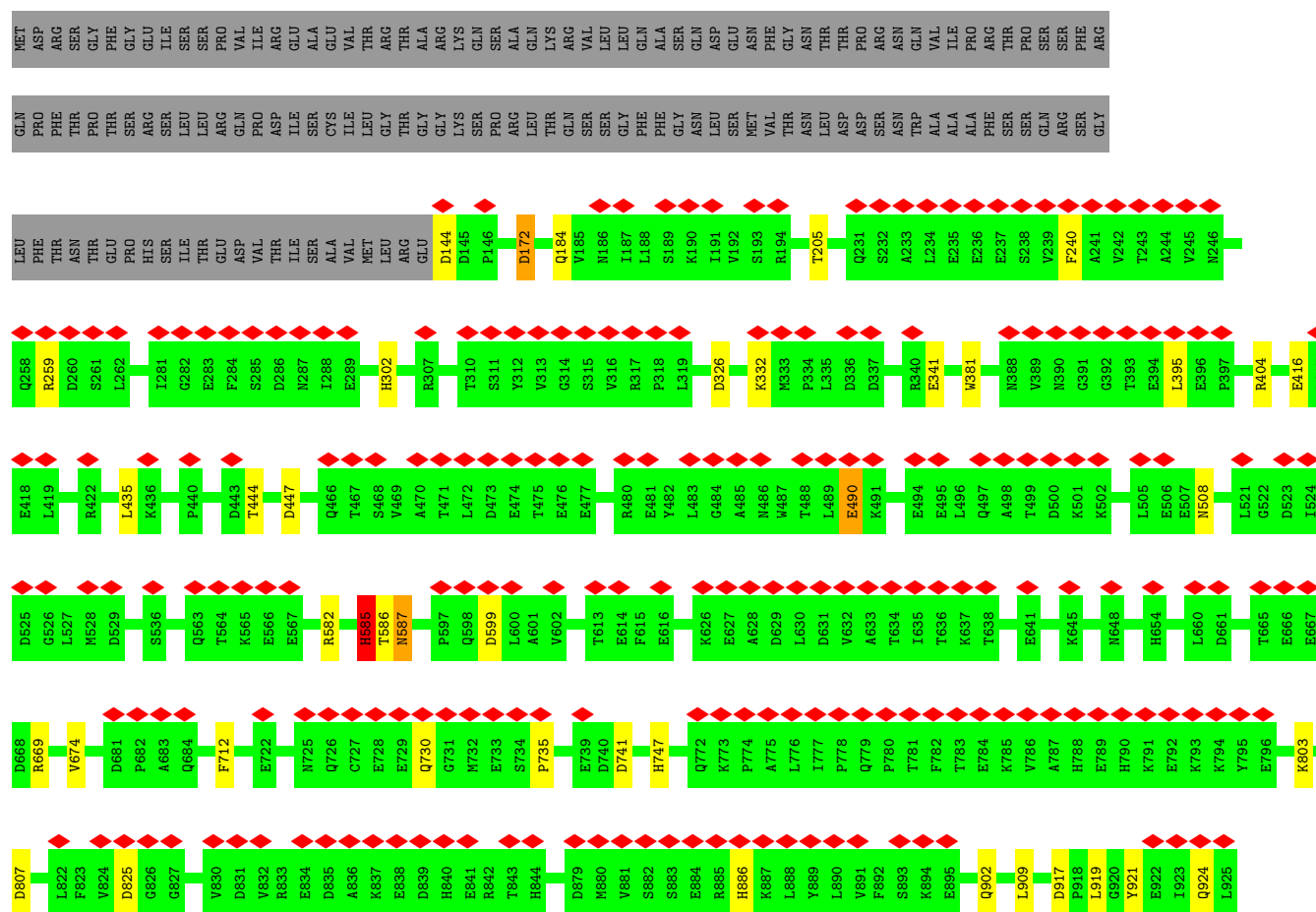
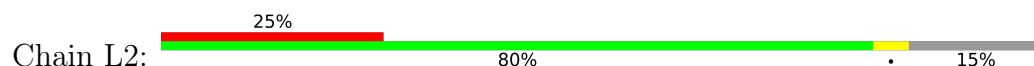


- Molecule 14: Nuclear pore complex protein Nup107

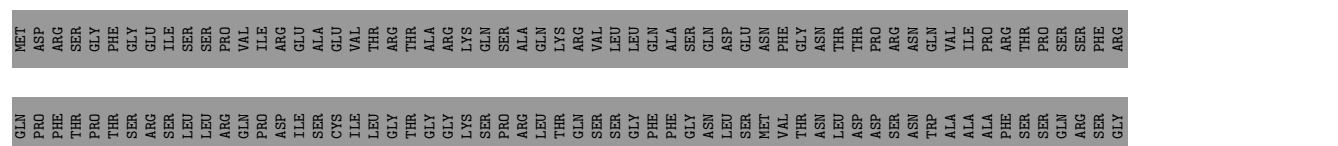
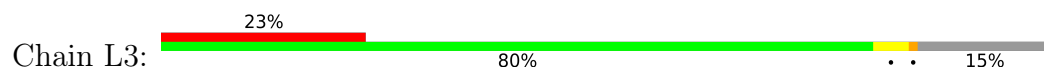




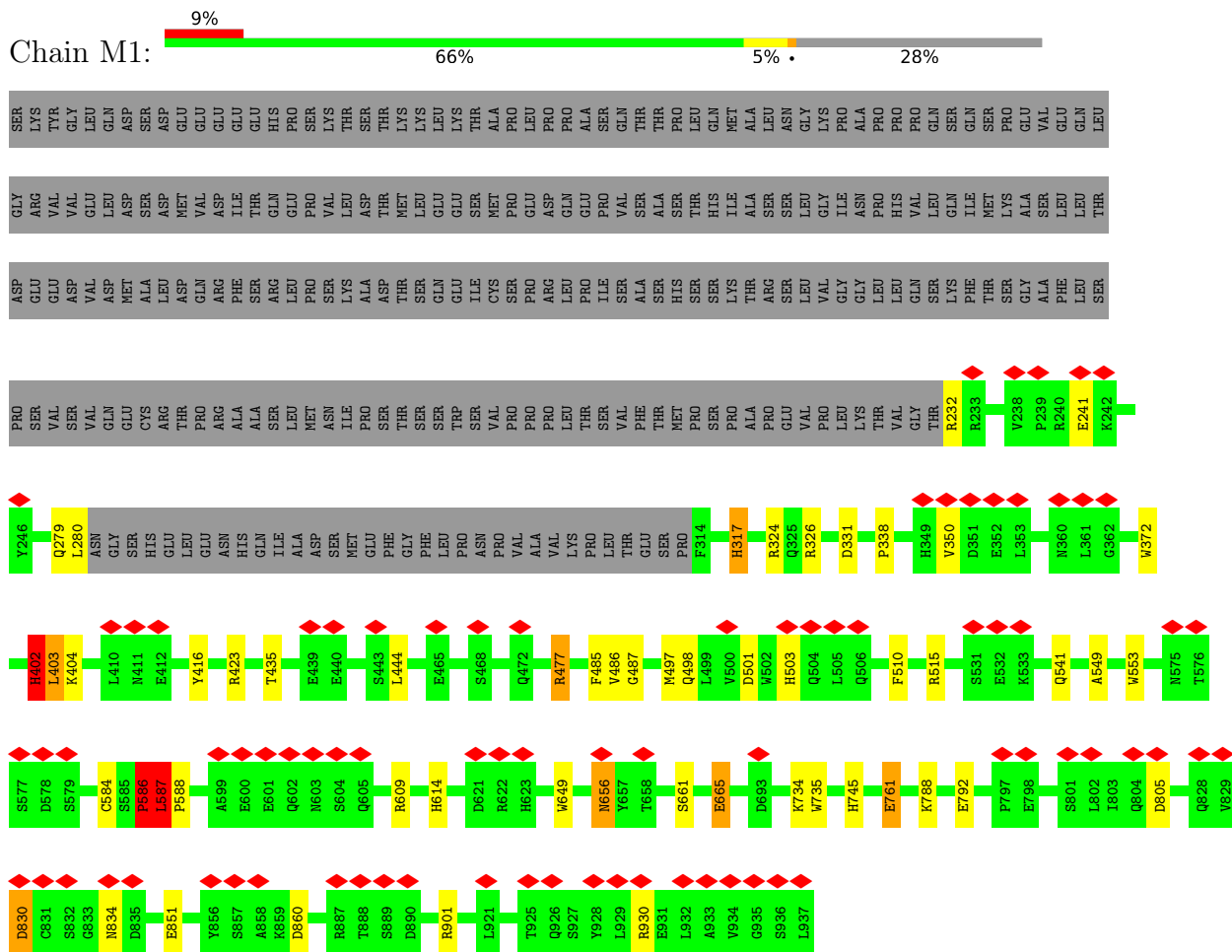
• Molecule 14: Nuclear pore complex protein Nup107



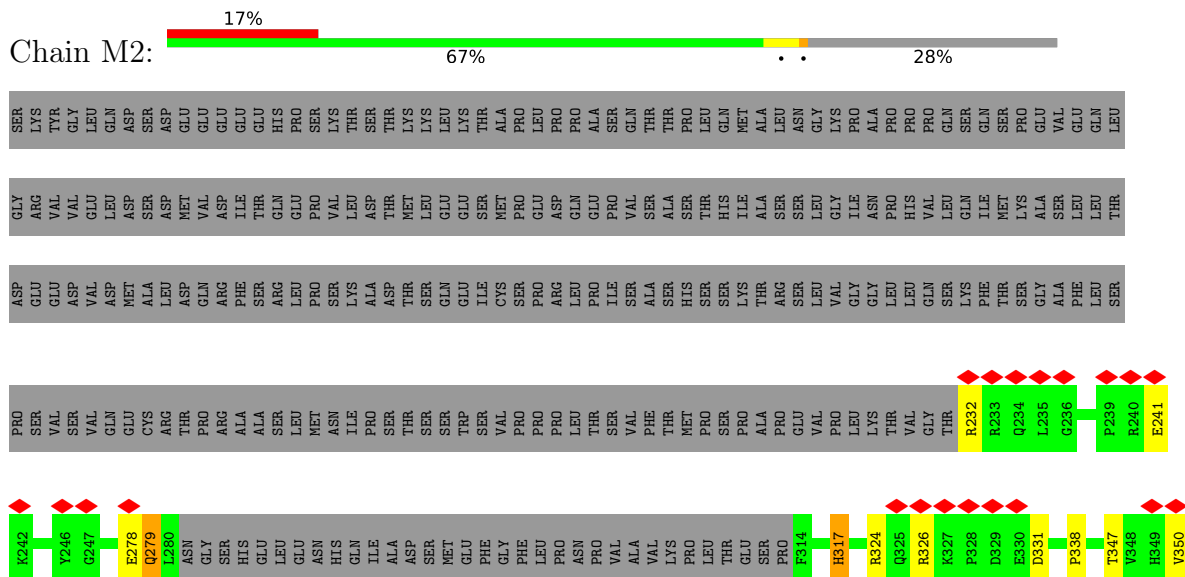
• Molecule 14: Nuclear pore complex protein Nup107

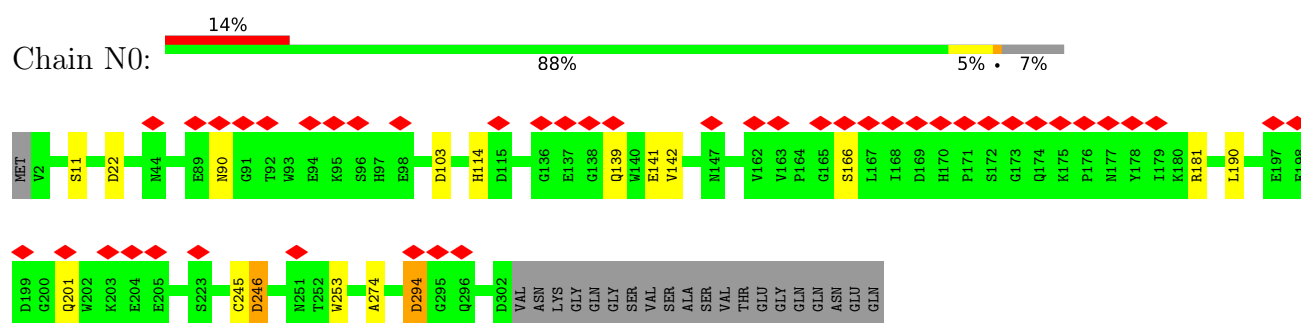


Chain M1:

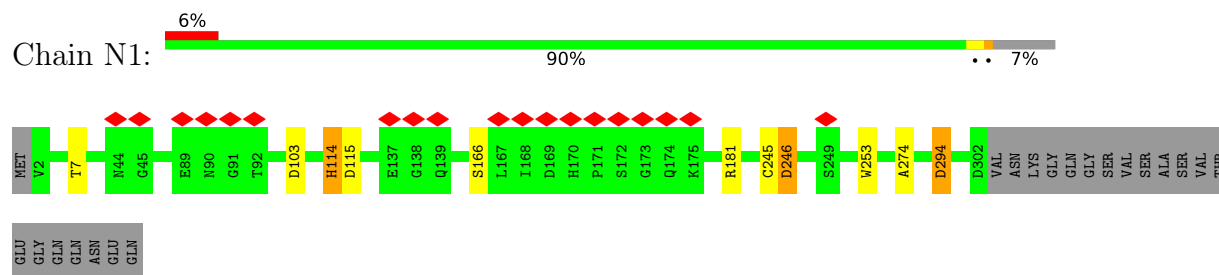


Chain M2:

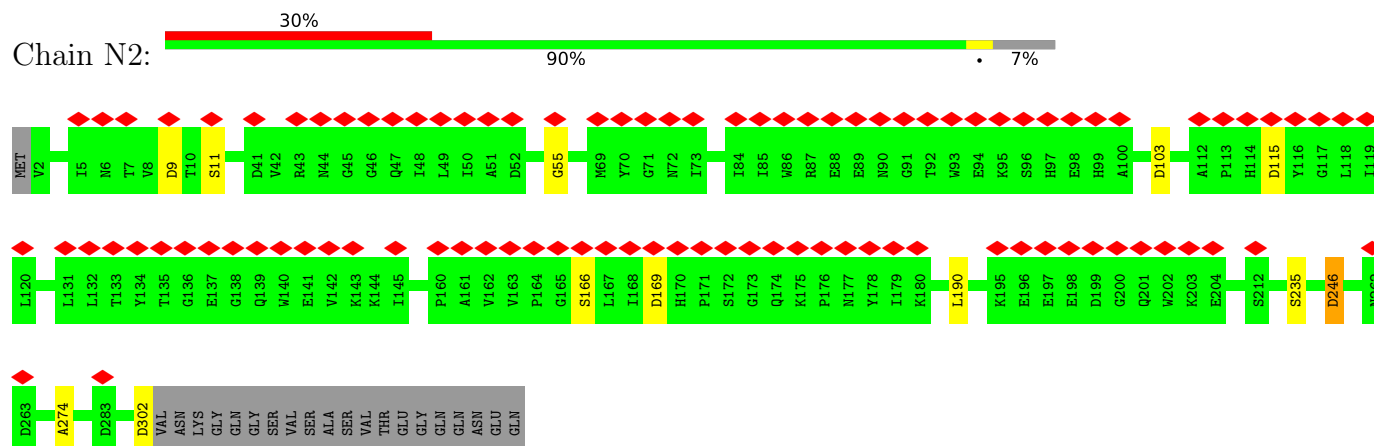




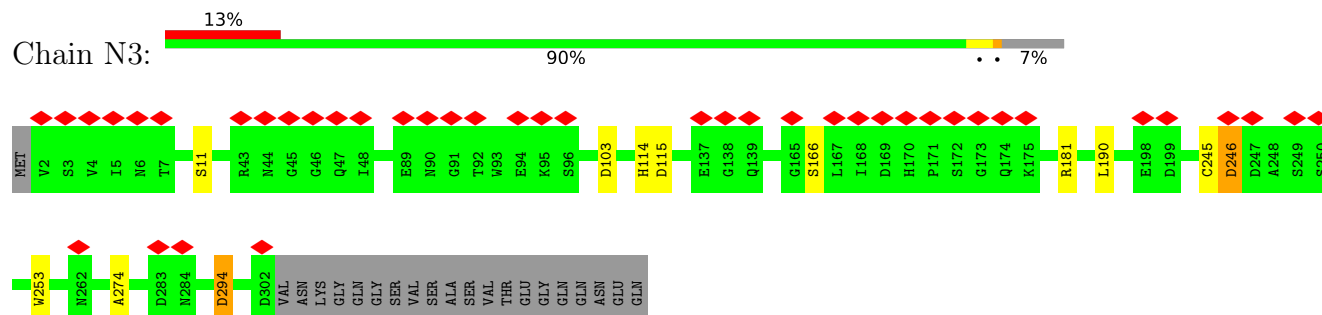
- Molecule 16: Protein SEC13 homolog



- Molecule 16: Protein SEC13 homolog



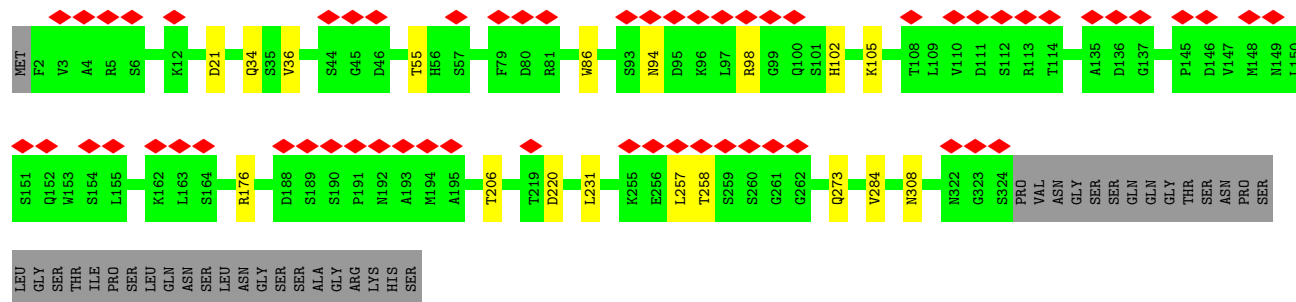
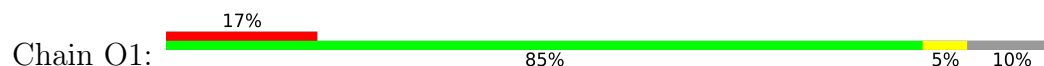
- Molecule 16: Protein SEC13 homolog



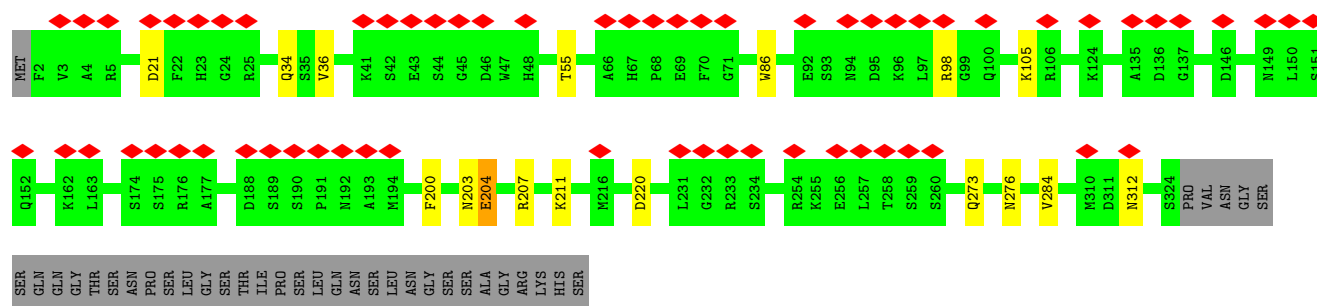
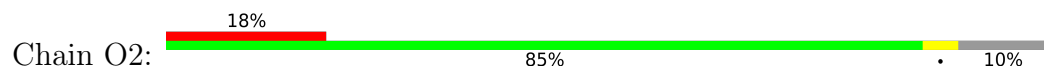
- Molecule 17: Nucleoporin SEH1



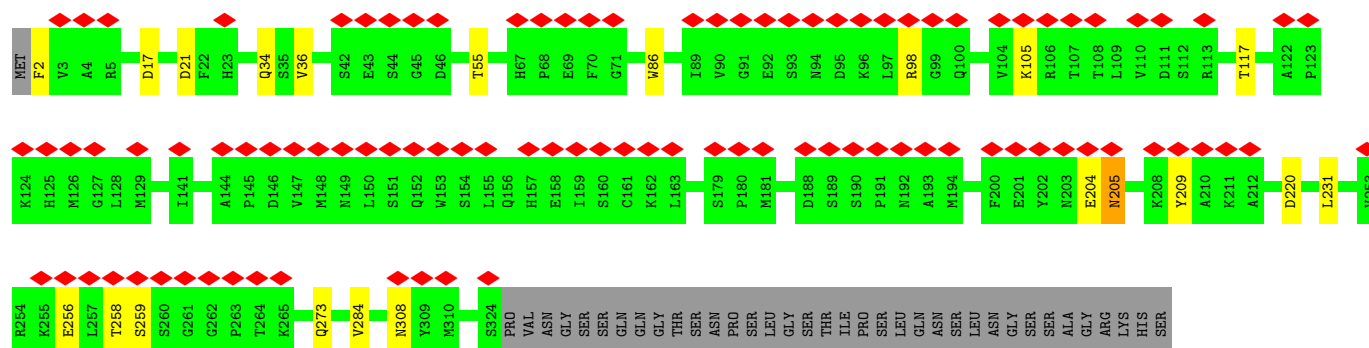
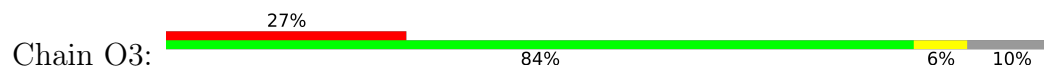
- Molecule 17: Nucleoporin SEH1



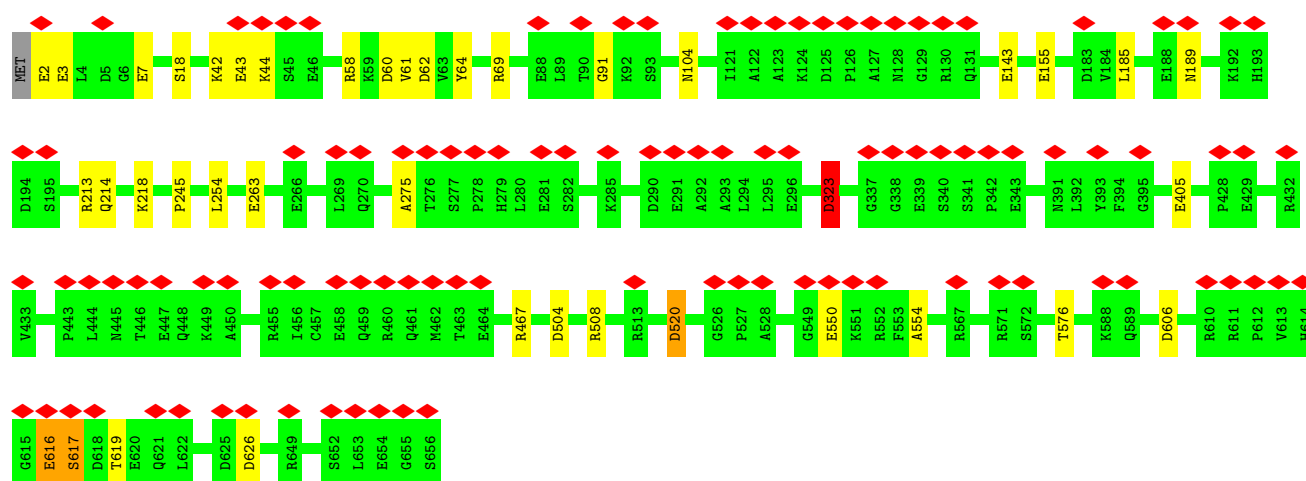
- Molecule 17: Nucleoporin SEH1



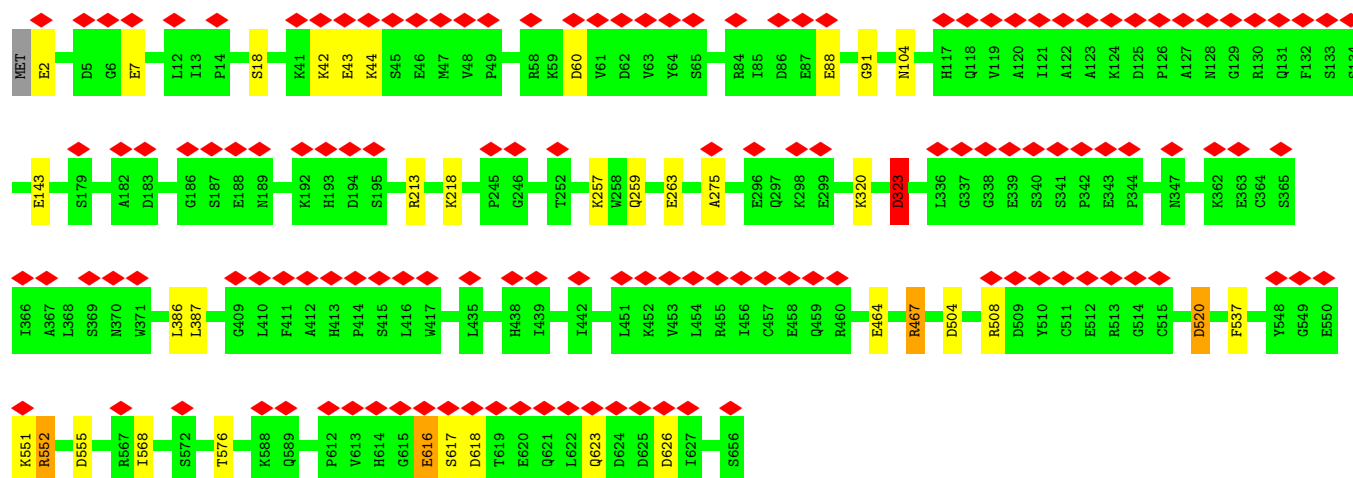
- Molecule 17: Nucleoporin SEH1



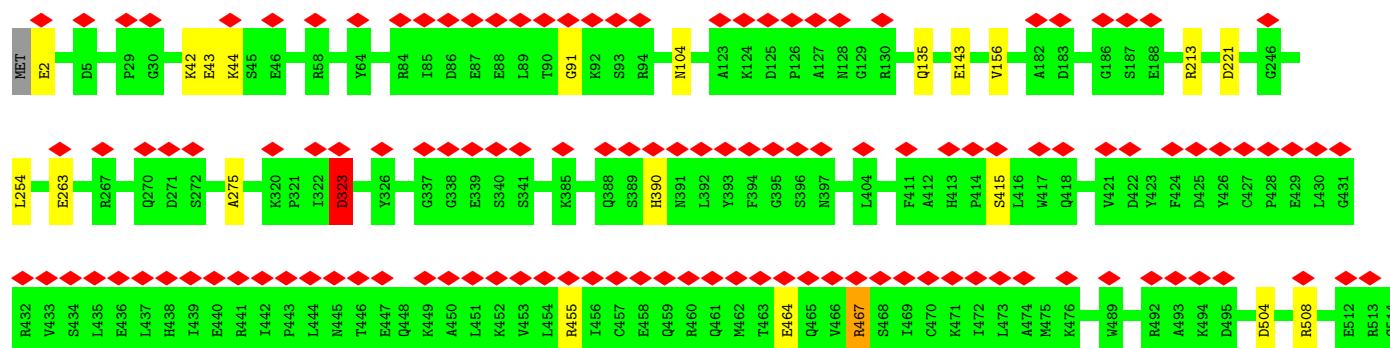
- Molecule 18: Nuclear pore complex protein Nup85

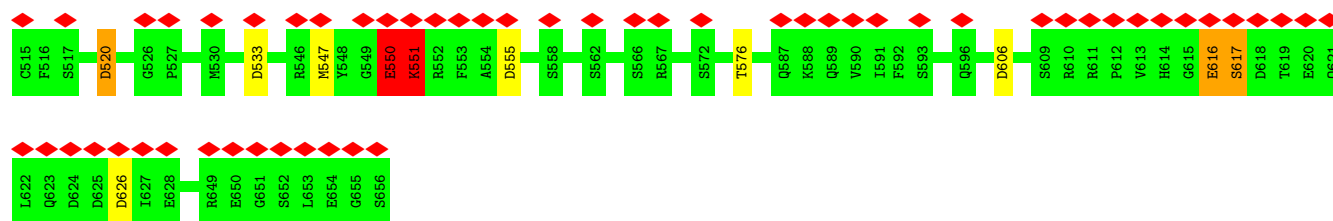


• Molecule 18: Nuclear pore complex protein Nup85

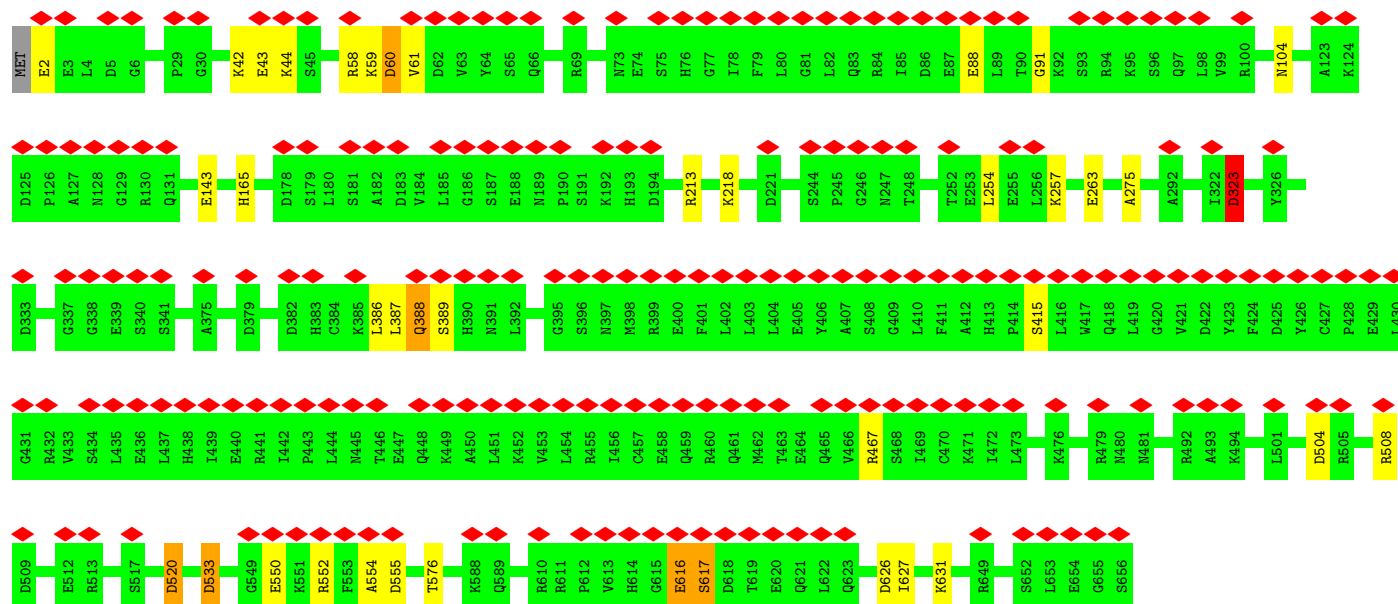


• Molecule 18: Nuclear pore complex protein Nup85

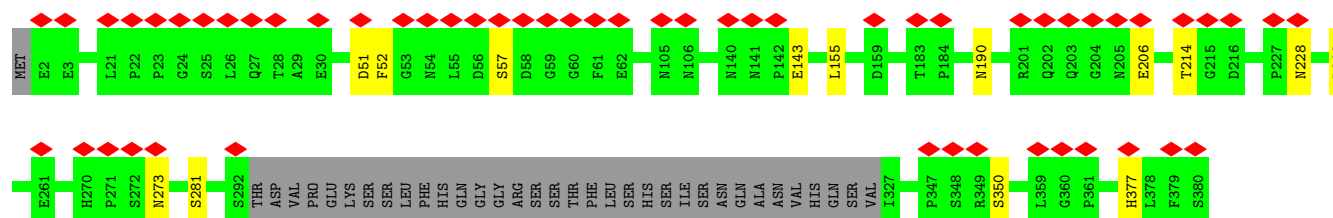
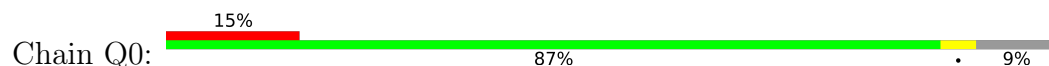




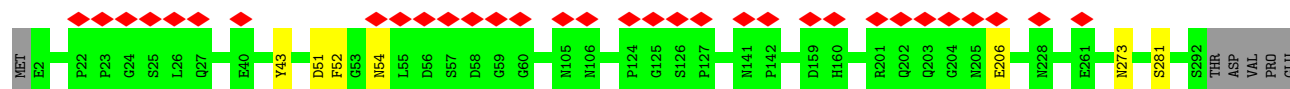
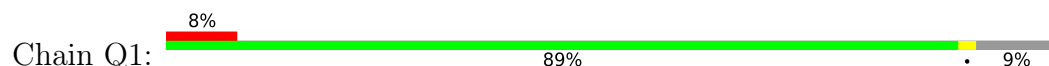
• Molecule 18: Nuclear pore complex protein Nup85

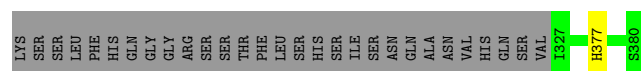


• Molecule 19: Nucleoporin Nup43

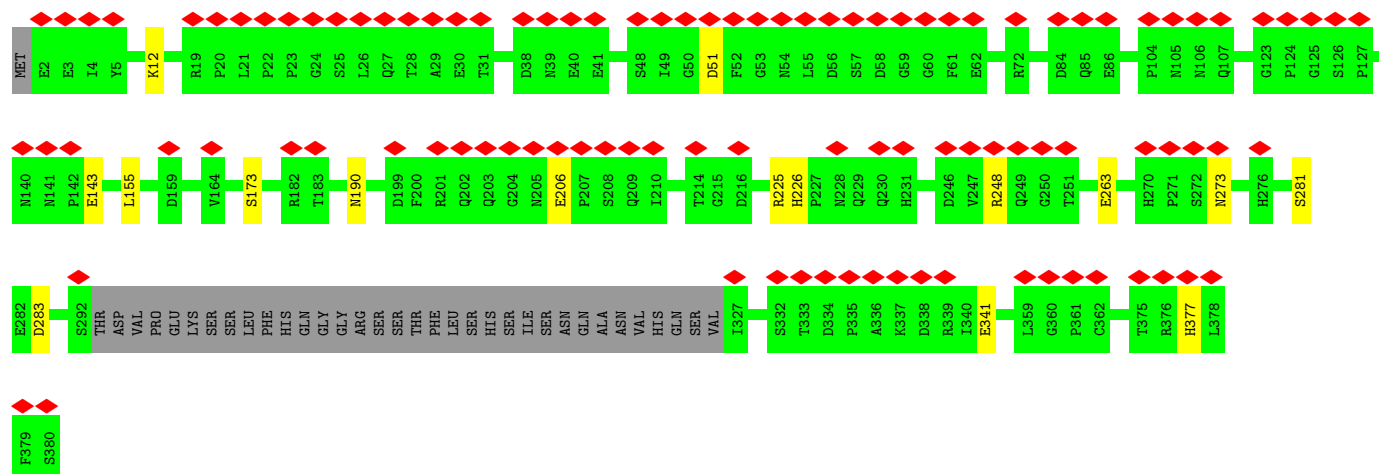
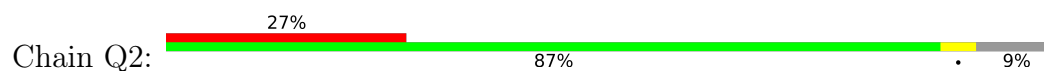


• Molecule 19: Nucleoporin Nup43

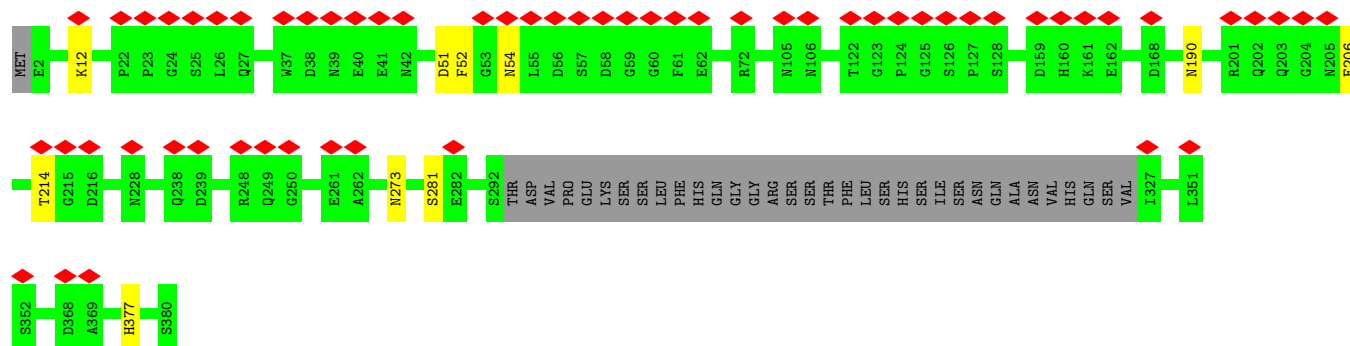
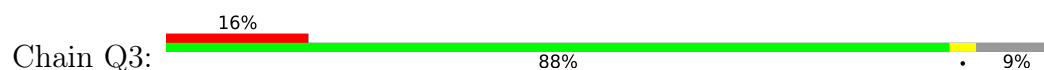




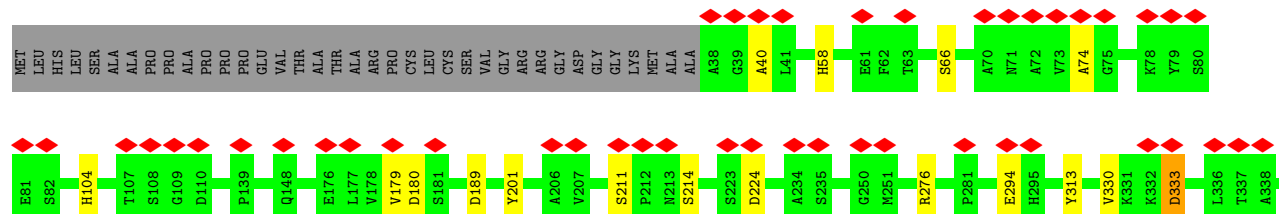
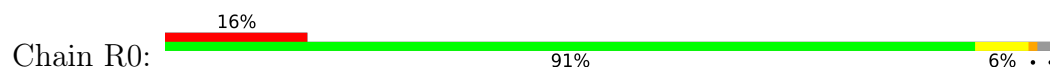
• Molecule 19: Nucleoporin Nup43

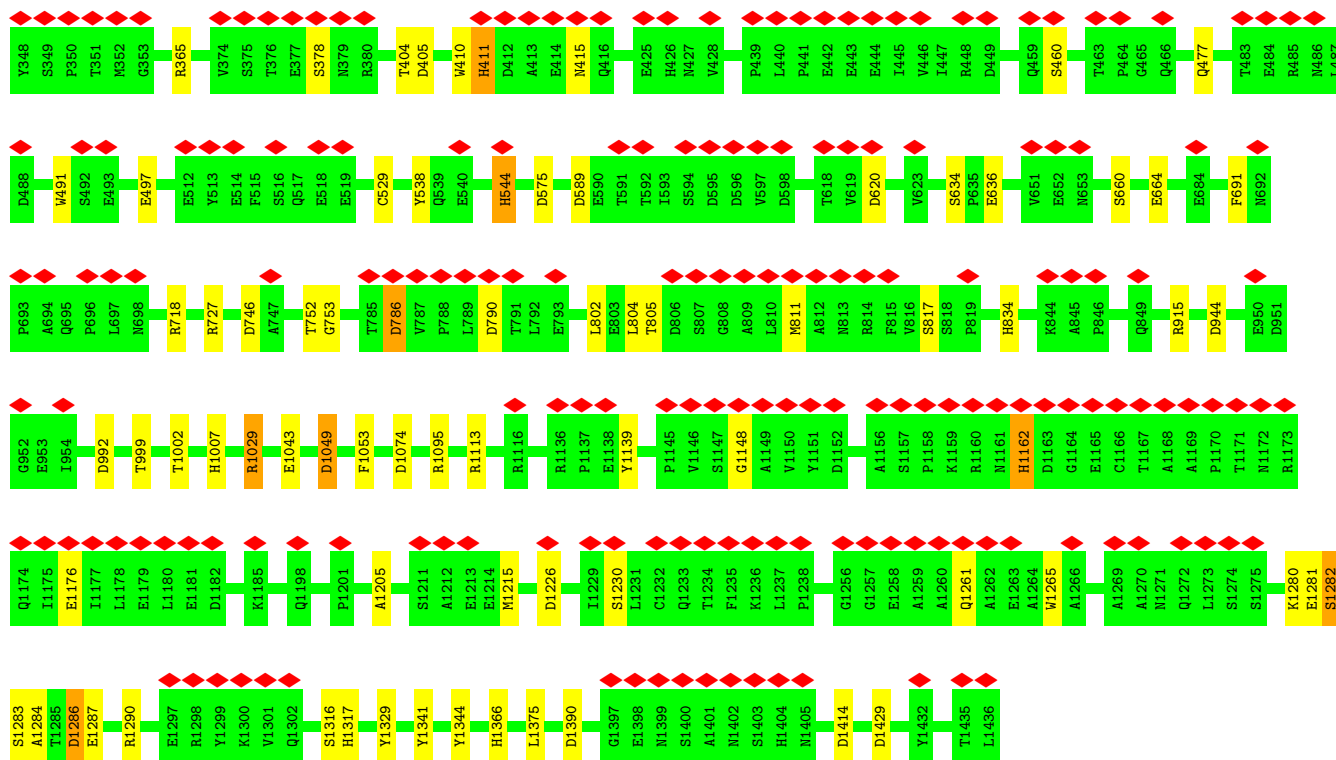


• Molecule 19: Nucleoporin Nup43

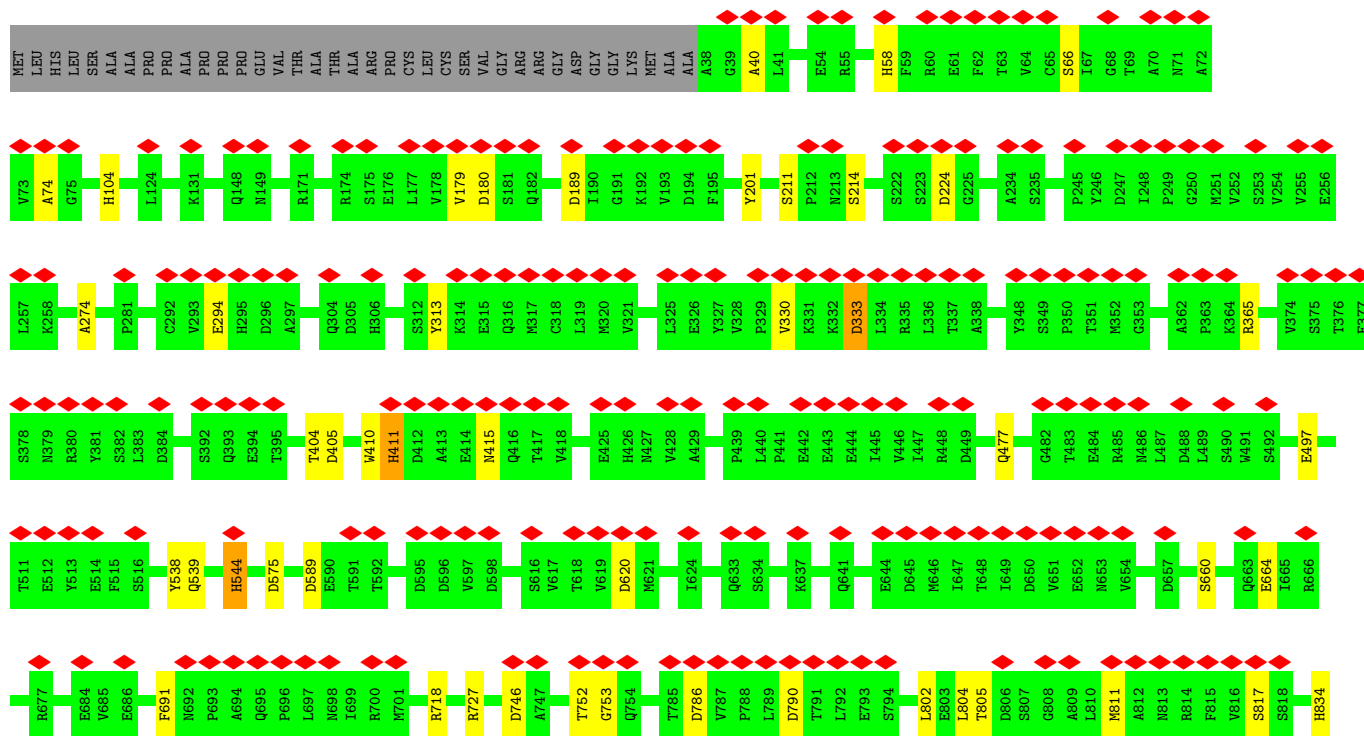


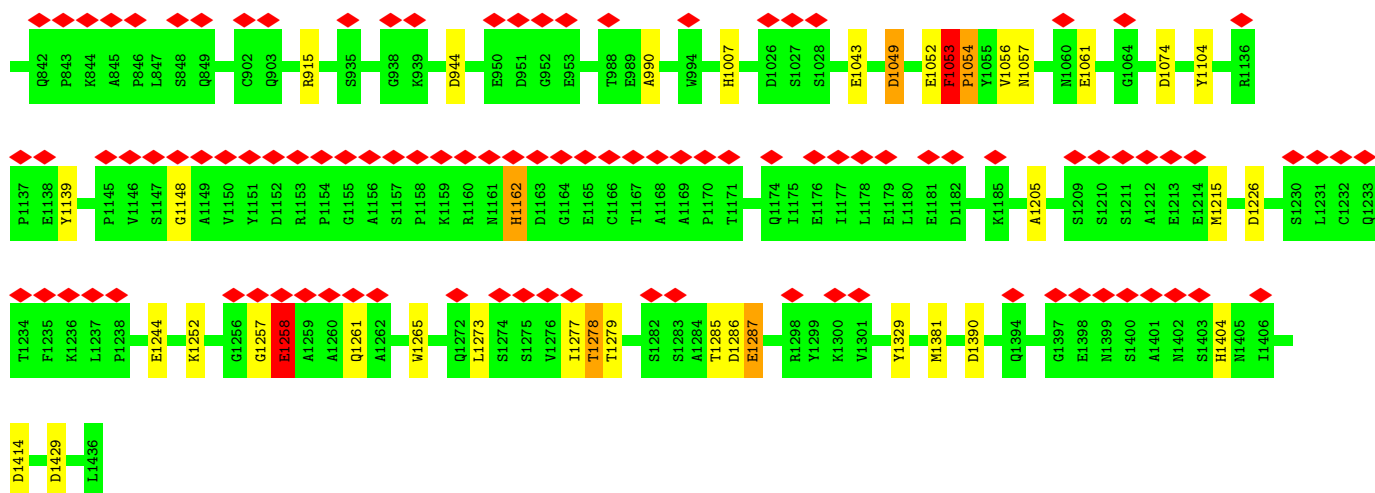
• Molecule 20: Nuclear pore complex protein Nup160



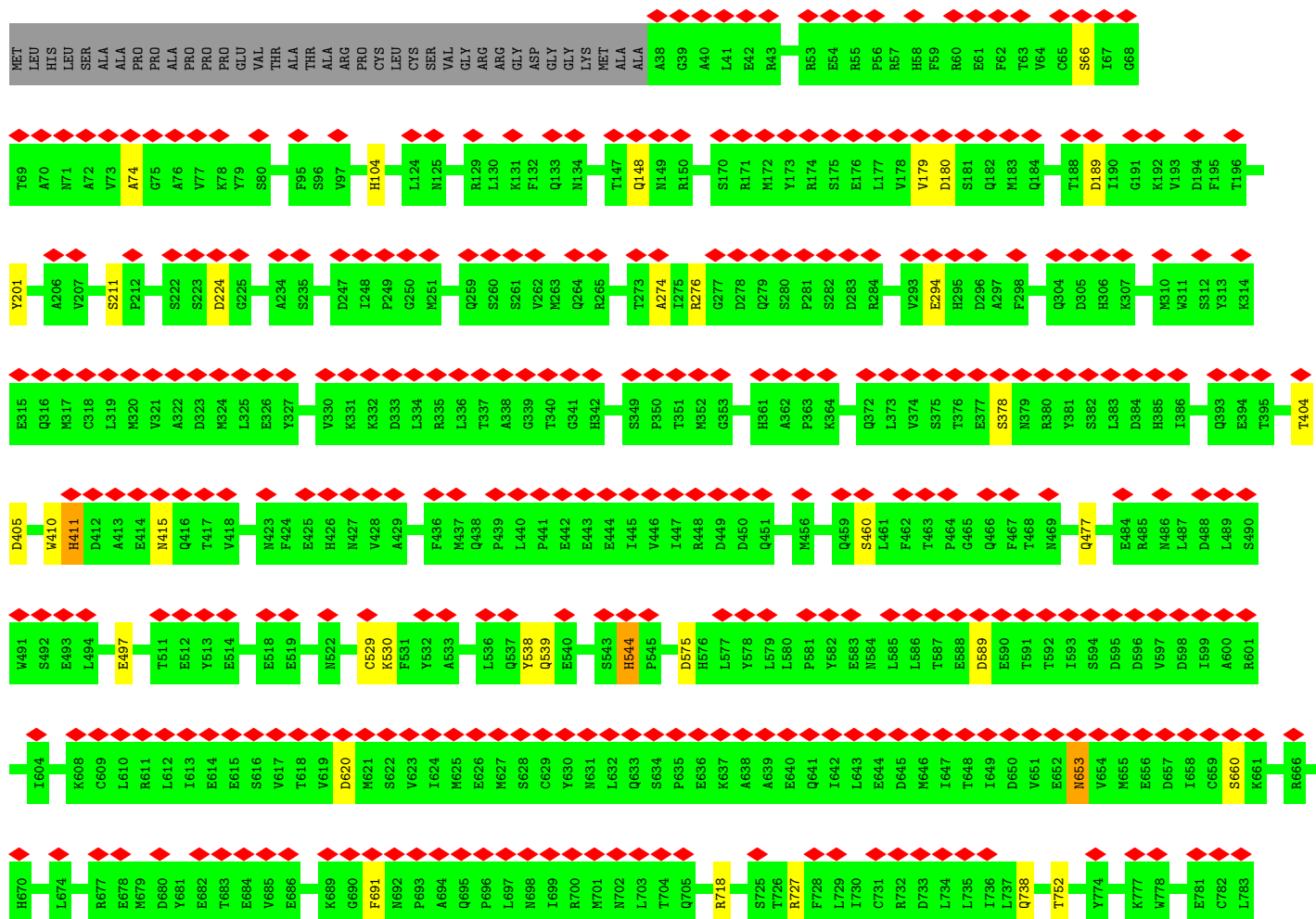
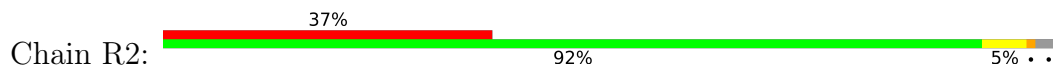


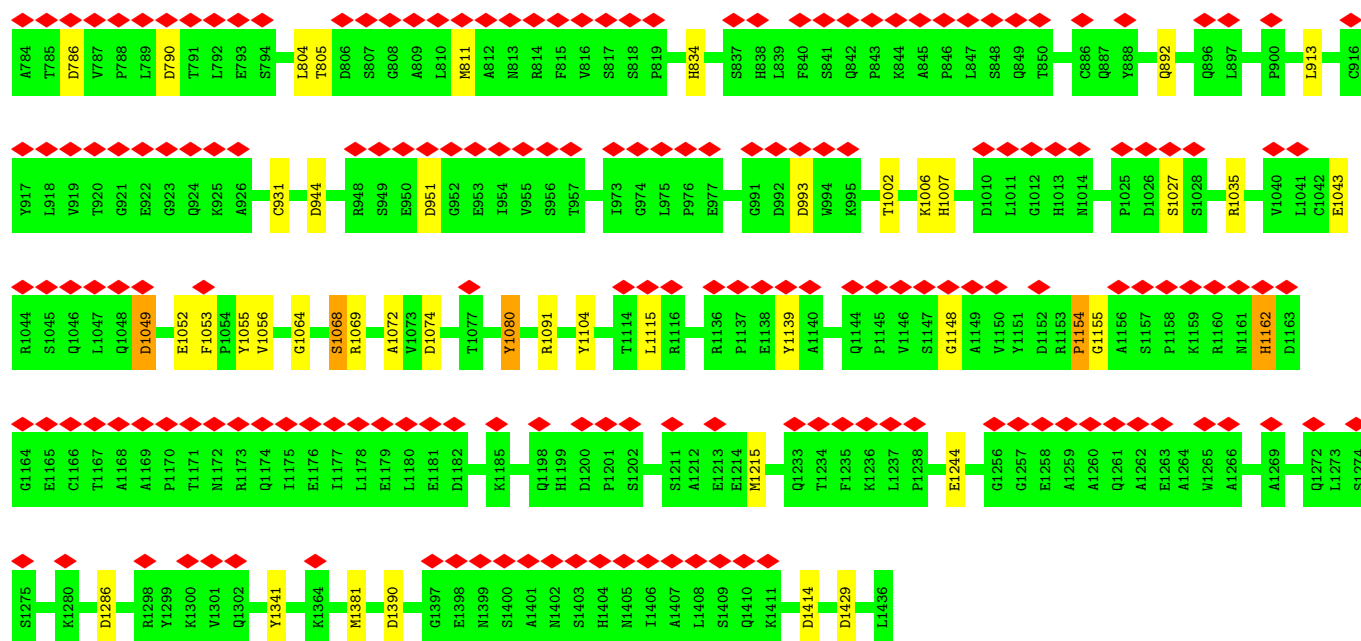
• Molecule 20: Nuclear pore complex protein Nup160



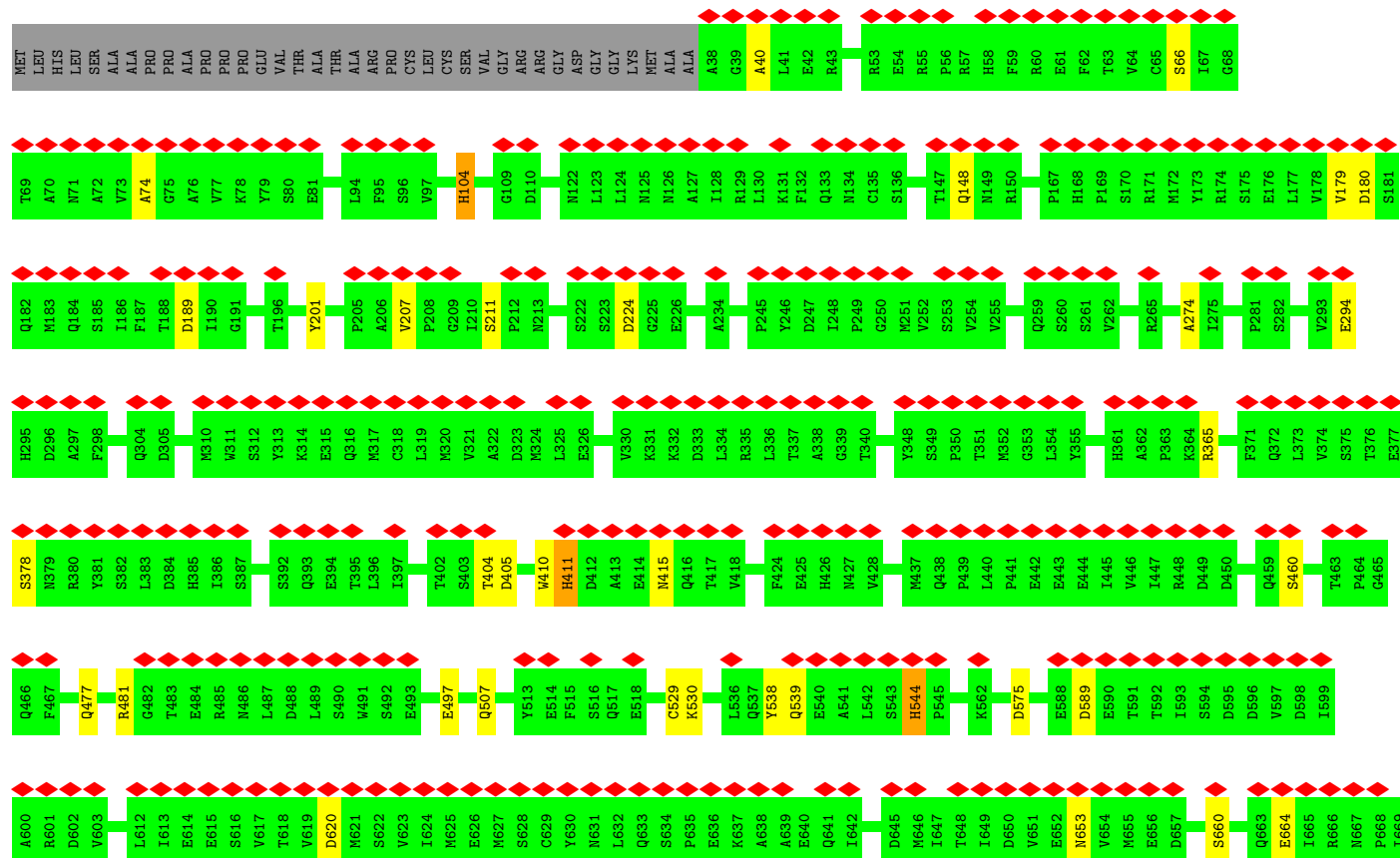
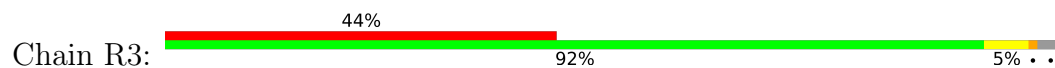


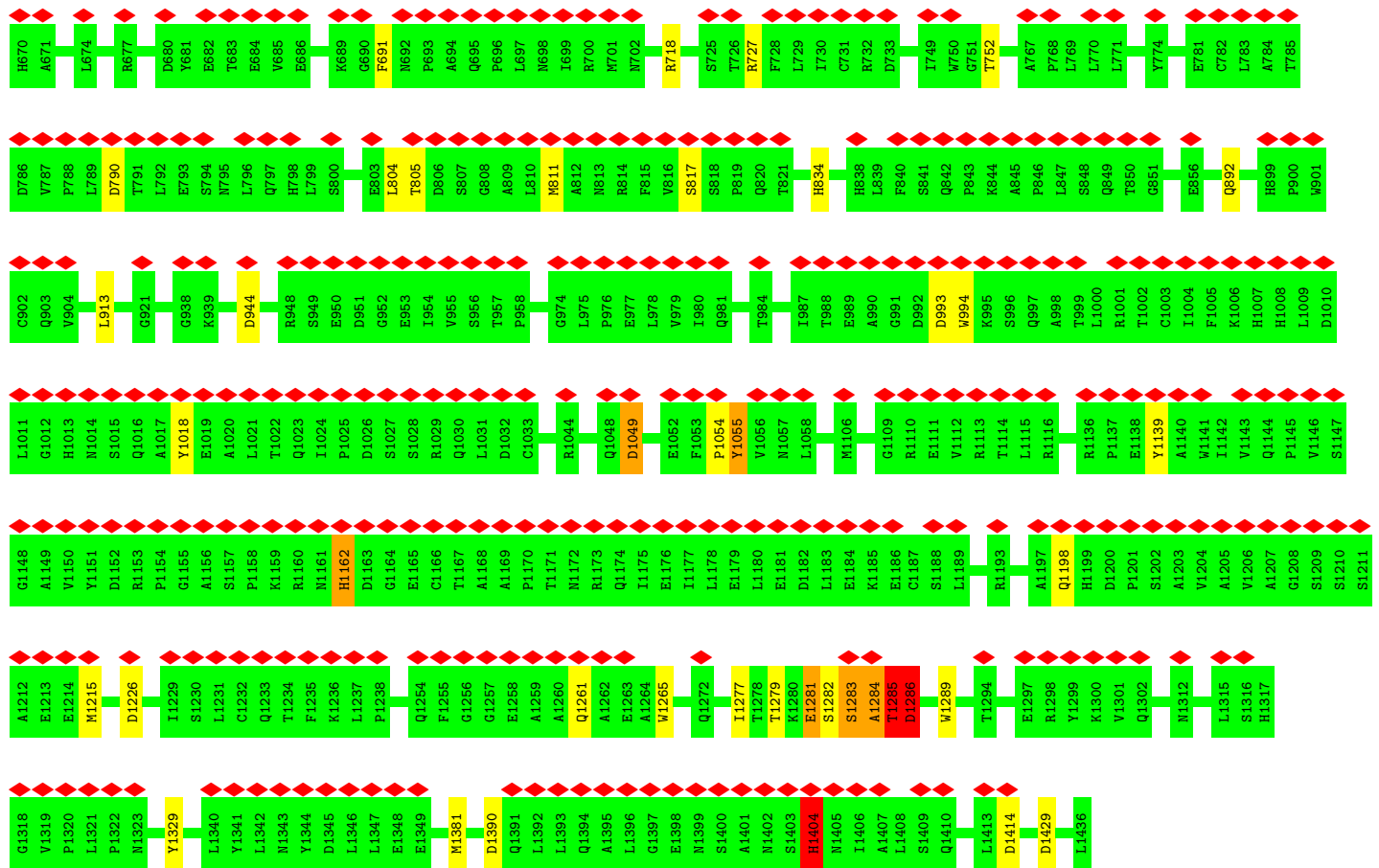
• Molecule 20: Nuclear pore complex protein Nup160



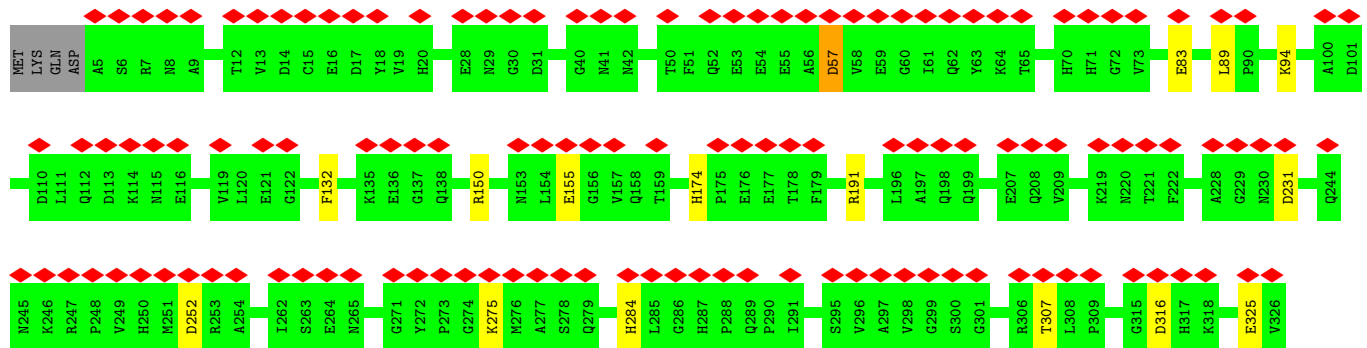
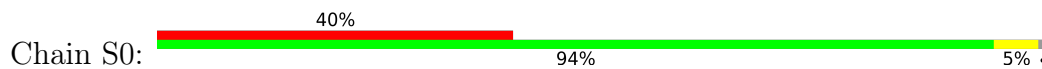


• Molecule 20: Nuclear pore complex protein Nup160

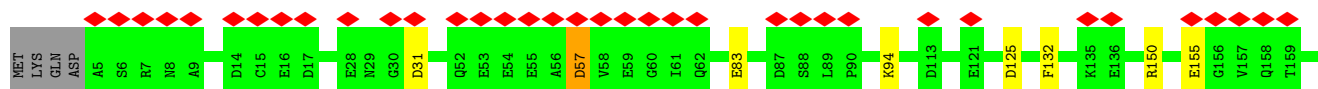
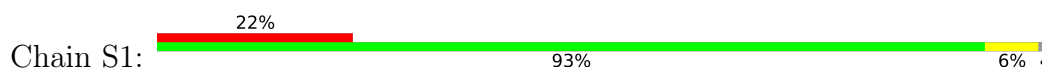


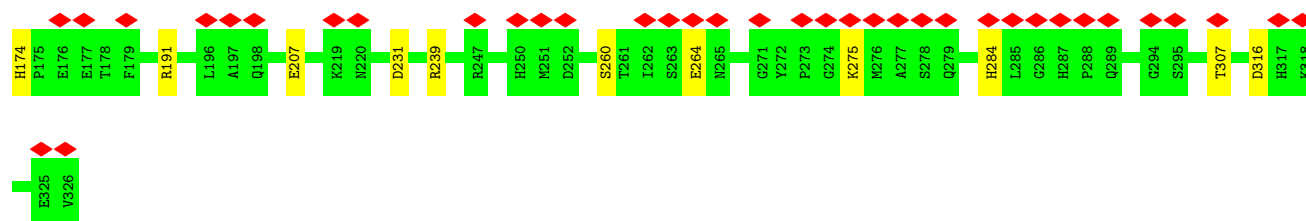


• Molecule 21: Nucleoporin Nup37



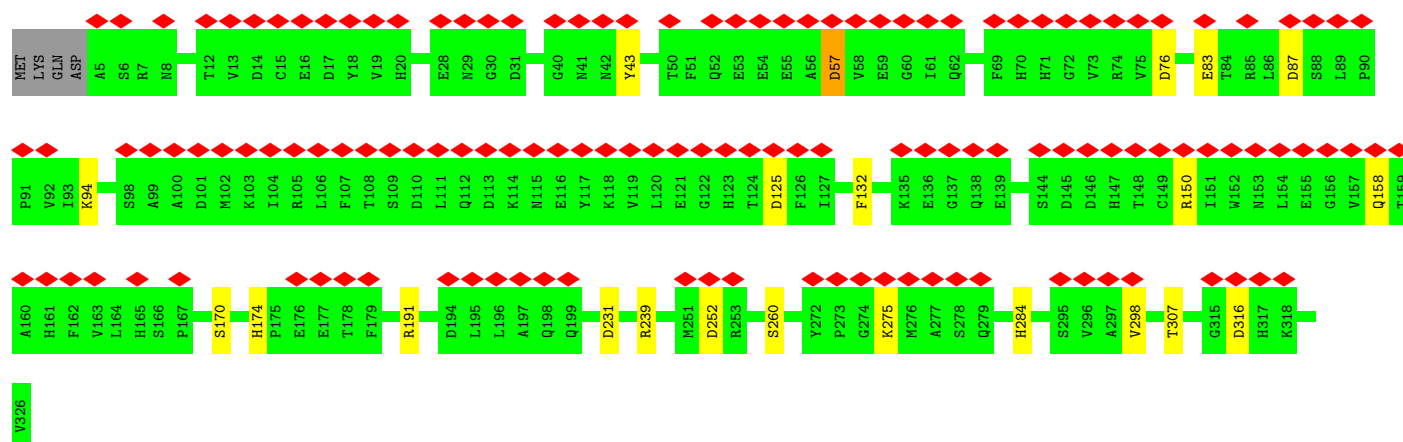
• Molecule 21: Nucleoporin Nup37





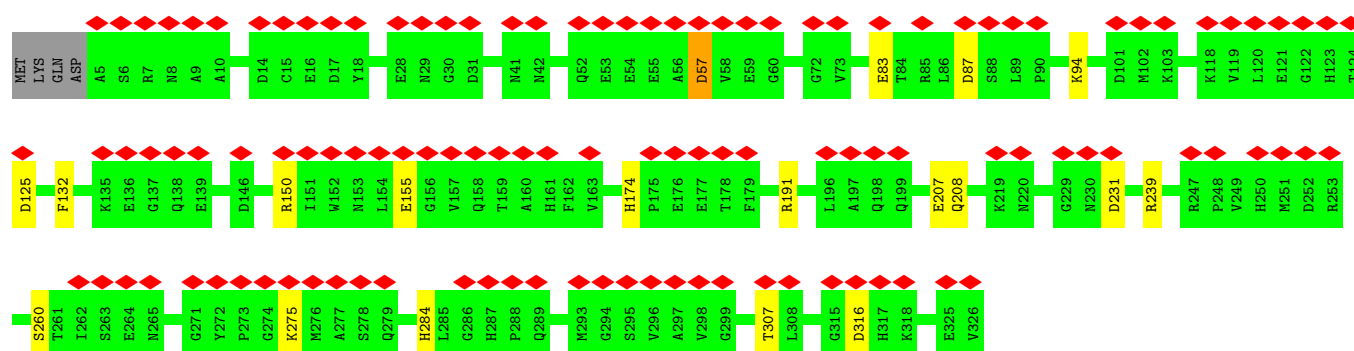
• Molecule 21: Nucleoporin Nup37

Chain S2: 41% 92% 6%



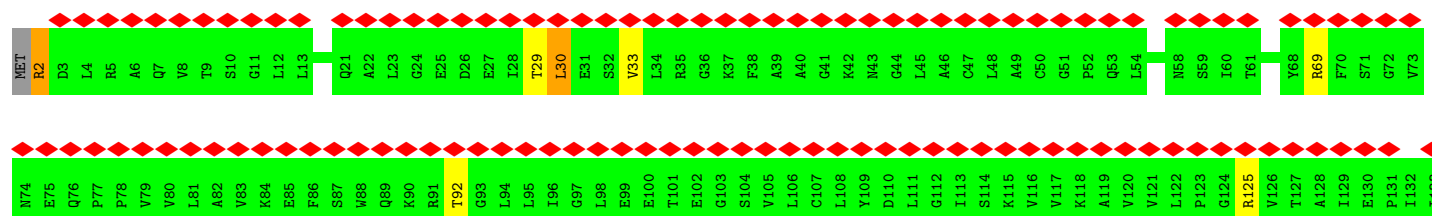
• Molecule 21: Nucleoporin Nup37

Chain S3: 36% 93% 6%



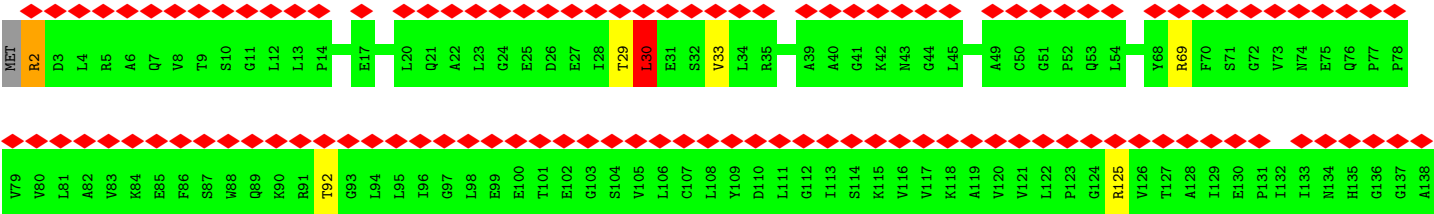
• Molecule 22: Protein ELYS

Chain T0: 25% 42% 56%



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

● Molecule 22: Protein ELYS





- Molecule 23: Nuclear pore complex protein Nup98



- [illegible]



[illegible]

- Molecule 23: Nuclear pore complex protein Nup98

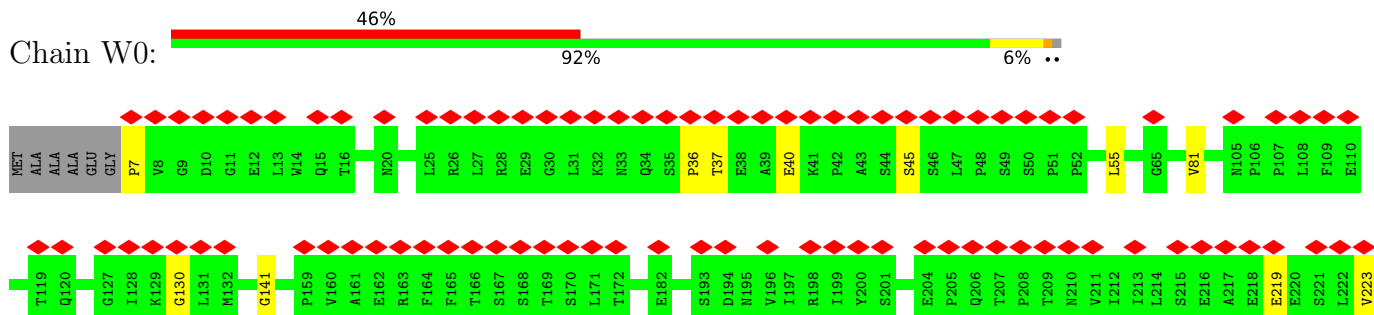
Chain U5:  98%

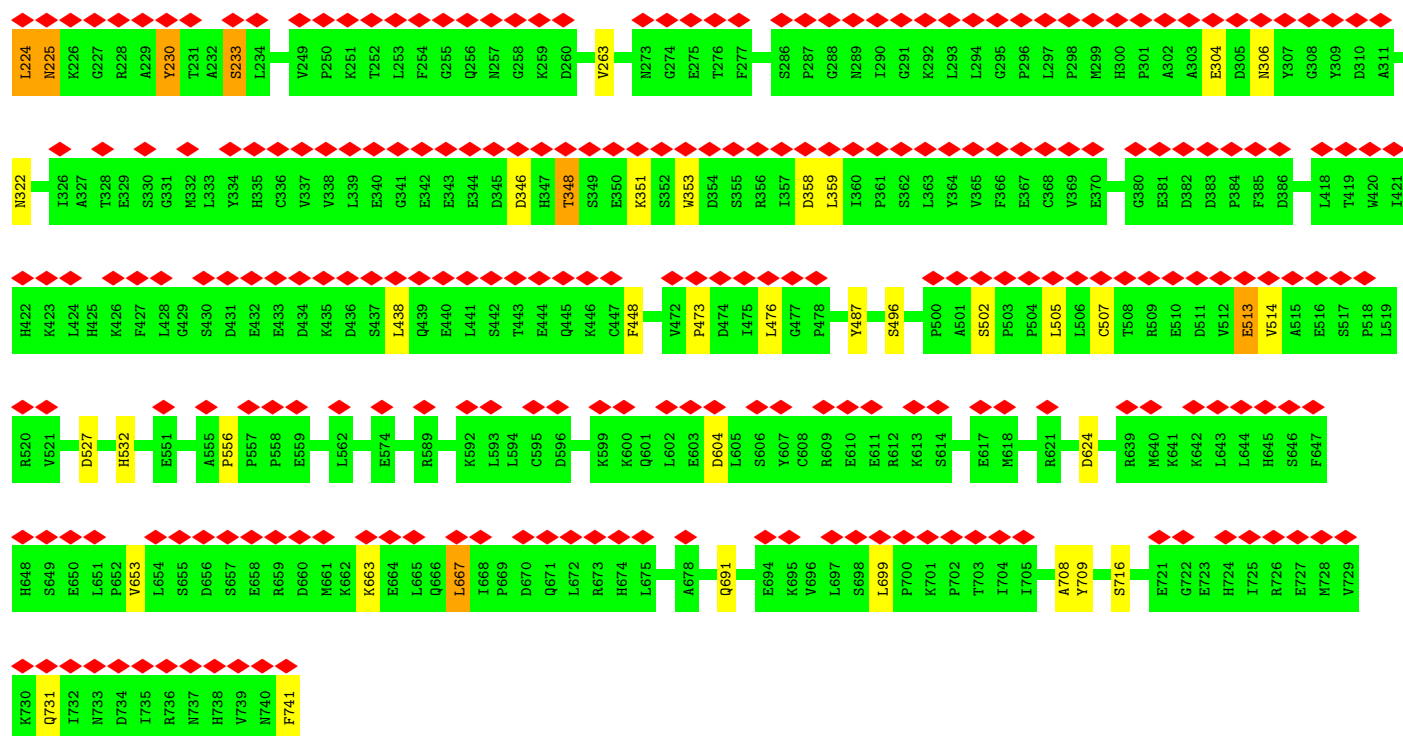
[illegible]



[illegible]

- Molecule 25: Nuclear pore complex protein Nup88





4 Experimental information

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	00	0.84	0/6212	1.44	24/8405 (0.3%)
1	01	0.83	0/6212	1.41	20/8405 (0.2%)
1	02	0.83	0/6212	1.41	17/8405 (0.2%)
1	03	0.84	0/6212	1.41	21/8405 (0.2%)
1	04	0.83	0/6212	1.41	18/8405 (0.2%)
2	10	0.81	0/14350	1.36	30/19560 (0.2%)
2	11	0.81	0/14350	1.37	25/19560 (0.1%)
2	12	0.81	0/14350	1.36	27/19560 (0.1%)
2	13	0.81	0/14350	1.36	26/19560 (0.1%)
2	14	0.81	0/14350	1.36	30/19560 (0.2%)
2	15	0.81	0/14350	1.36	30/19560 (0.2%)
2	16	0.81	0/14350	1.36	27/19560 (0.1%)
2	17	0.81	0/14350	1.36	22/19560 (0.1%)
3	40	0.86	1/3007 (0.0%)	1.33	7/4114 (0.2%)
3	41	0.86	1/3007 (0.0%)	1.33	6/4114 (0.1%)
4	A0	0.85	0/6687	1.42	21/9036 (0.2%)
4	A1	0.84	0/6687	1.41	25/9036 (0.3%)
4	A2	0.85	0/6687	1.41	22/9036 (0.2%)
4	A3	0.83	0/6687	1.39	25/9036 (0.3%)
4	A4	0.83	0/5972	1.39	17/8068 (0.2%)
4	A5	0.82	0/5972	1.41	12/8068 (0.1%)
4	A6	0.83	1/5972 (0.0%)	1.37	13/8068 (0.2%)
5	B0	0.85	1/14018 (0.0%)	1.40	46/19022 (0.2%)
5	B1	0.85	1/14018 (0.0%)	1.40	44/19022 (0.2%)
6	C0	0.85	0/16330	1.40	44/22131 (0.2%)
6	C1	0.85	1/16330 (0.0%)	1.40	38/22131 (0.2%)
6	C2	0.84	0/16330	1.38	41/22131 (0.2%)
6	C3	0.84	1/16330 (0.0%)	1.42	57/22131 (0.3%)
6	C4	0.84	0/16330	1.38	30/22131 (0.1%)
7	D0	0.82	0/10568	1.40	23/14320 (0.2%)
7	D1	0.83	2/10568 (0.0%)	1.40	28/14320 (0.2%)
7	D2	0.82	0/10568	1.39	25/14320 (0.2%)
7	D3	0.83	0/10568	1.42	33/14320 (0.2%)
7	D4	0.81	0/10568	1.38	23/14320 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	D5	0.82	0/10568	1.41	39/14320 (0.3%)
8	E0	0.84	0/4563	1.34	6/6214 (0.1%)
8	E1	0.84	0/4563	1.33	4/6214 (0.1%)
9	F0	0.91	0/1882	1.49	9/2556 (0.4%)
9	F1	0.88	0/1882	1.44	6/2556 (0.2%)
9	F2	0.91	0/1882	1.50	7/2556 (0.3%)
9	F3	0.89	1/1882 (0.1%)	1.45	8/2556 (0.3%)
10	H0	0.82	1/3114 (0.0%)	1.40	12/4211 (0.3%)
10	H1	0.81	0/3114	1.40	13/4211 (0.3%)
10	H2	0.81	0/3114	1.40	13/4211 (0.3%)
10	H3	0.81	0/3114	1.41	15/4211 (0.4%)
11	I0	0.81	0/1416	1.42	3/1911 (0.2%)
11	I1	0.81	0/1416	1.42	6/1911 (0.3%)
11	I2	0.81	0/1416	1.42	3/1911 (0.2%)
11	I3	0.81	0/1416	1.41	4/1911 (0.2%)
12	J0	0.80	0/1420	1.40	4/1915 (0.2%)
12	J1	0.80	0/1420	1.39	5/1915 (0.3%)
12	J2	0.80	0/1420	1.37	2/1915 (0.1%)
12	J3	0.80	0/1420	1.39	3/1915 (0.2%)
12	J4	0.80	0/1420	1.44	2/1915 (0.1%)
13	K0	0.84	0/8740	1.40	32/11848 (0.3%)
13	K1	0.83	1/8740 (0.0%)	1.43	23/11848 (0.2%)
13	K2	0.83	0/8740	1.37	19/11848 (0.2%)
13	K3	0.83	1/8740 (0.0%)	1.37	16/11848 (0.1%)
14	L0	0.85	0/6518	1.39	16/8819 (0.2%)
14	L1	0.85	0/6518	1.41	21/8819 (0.2%)
14	L2	0.84	0/6518	1.39	15/8819 (0.2%)
14	L3	0.88	3/6518 (0.0%)	1.44	33/8819 (0.4%)
15	M0	0.87	0/5588	1.43	18/7581 (0.2%)
15	M1	0.87	0/5588	1.42	12/7581 (0.2%)
15	M2	0.87	0/5588	1.41	9/7581 (0.1%)
15	M3	0.86	0/5588	1.41	21/7581 (0.3%)
16	N0	0.84	0/2419	1.35	3/3301 (0.1%)
16	N1	0.84	0/2419	1.33	3/3301 (0.1%)
16	N2	0.85	0/2419	1.35	5/3301 (0.2%)
16	N3	0.83	0/2419	1.33	3/3301 (0.1%)
17	O0	0.83	0/2593	1.32	4/3520 (0.1%)
17	O1	0.83	0/2593	1.32	6/3520 (0.2%)
17	O2	0.84	0/2593	1.34	5/3520 (0.1%)
17	O3	0.83	0/2593	1.33	3/3520 (0.1%)
18	P0	0.85	0/5365	1.39	17/7257 (0.2%)
18	P1	0.85	0/5365	1.39	10/7257 (0.1%)
18	P2	0.85	0/5365	1.39	12/7257 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	P3	0.85	0/5365	1.39	15/7257 (0.2%)
19	Q0	0.86	0/2775	1.36	4/3786 (0.1%)
19	Q1	0.85	0/2775	1.35	3/3786 (0.1%)
19	Q2	0.86	0/2775	1.39	6/3786 (0.2%)
19	Q3	0.85	0/2775	1.36	4/3786 (0.1%)
20	R0	0.85	0/11371	1.38	29/15446 (0.2%)
20	R1	0.85	1/11371 (0.0%)	1.39	36/15446 (0.2%)
20	R2	0.85	0/11371	1.38	28/15446 (0.2%)
20	R3	0.84	0/11371	1.38	34/15446 (0.2%)
21	S0	0.83	0/2623	1.32	3/3568 (0.1%)
21	S1	0.82	0/2623	1.31	5/3568 (0.1%)
21	S2	0.83	0/2623	1.33	7/3568 (0.2%)
21	S3	0.83	0/2623	1.32	7/3568 (0.2%)
22	T0	0.84	0/8141	1.38	20/11065 (0.2%)
22	T1	0.83	0/8141	1.36	19/11065 (0.2%)
23	U0	0.85	0/1217	1.34	2/1644 (0.1%)
23	U1	0.87	0/152	1.91	6/204 (2.9%)
23	U2	1.05	0/152	2.09	7/204 (3.4%)
23	U3	1.20	1/152 (0.7%)	2.02	6/204 (2.9%)
23	U4	1.21	2/152 (1.3%)	2.09	10/204 (4.9%)
23	U5	1.07	1/152 (0.7%)	1.82	4/204 (2.0%)
23	U6	0.86	0/152	1.84	4/204 (2.0%)
24	V0	0.86	0/2240	1.47	7/3019 (0.2%)
25	W0	0.84	1/5972 (0.0%)	1.38	18/8105 (0.2%)
All	All	0.84	22/630097 (0.0%)	1.39	1651/855041 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	00	0	6
1	01	0	3
1	02	0	4
1	03	0	5
1	04	0	4
2	10	0	11
2	11	0	13
2	12	0	10
2	13	0	13
2	14	0	11

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

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

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	L3	727	CYS	CA-C	9.14	1.64	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	U3	610	LEU	N-CA	-8.09	1.36	1.46
14	L3	731	GLY	CA-C	7.49	1.62	1.51
14	L3	731	GLY	N-CA	7.03	1.55	1.45
6	C1	1379	PRO	CA-C	6.18	1.55	1.51

The worst 5 of 1651 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	15	5	GLY	O-C-N	-38.98	78.22	123.44
2	10	5	GLY	O-C-N	-38.55	78.72	123.44
2	13	5	GLY	O-C-N	-38.52	78.75	123.44
2	14	5	GLY	O-C-N	-38.46	78.83	123.44
2	17	5	GLY	O-C-N	-38.45	78.84	123.44

5 of 11 chirality outliers are listed below:

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

5 of 728 planarity outliers are listed below:

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

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	00	6085	0	6080	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	01	6085	0	6080	27	0
1	02	6085	0	6080	10	0
1	03	6085	0	6080	40	0
1	04	6085	0	6080	12	0
2	10	14046	0	14194	21	0
2	11	14046	0	14194	27	0
2	12	14046	0	14194	33	0
2	13	14046	0	14194	22	0
2	14	14046	0	14194	26	0
2	15	14046	0	14194	16	0
2	16	14046	0	14194	12	0
2	17	14046	0	14194	11	0
3	40	2922	0	2899	4	0
3	41	2922	0	2899	3	0
4	A0	6568	0	6527	70	0
4	A1	6568	0	6527	11	0
4	A2	6568	0	6527	24	0
4	A3	6568	0	6527	10	0
4	A4	5860	0	5828	25	0
4	A5	5860	0	5828	5	0
4	A6	5860	0	5828	7	0
5	B0	13746	0	13949	7	0
5	B1	13746	0	13949	10	0
6	C0	16013	0	16224	13	0
6	C1	16013	0	16224	14	0
6	C2	16013	0	16224	94	0
6	C3	16013	0	16224	72	0
6	C4	16013	0	16224	62	0
7	D0	10363	0	10400	50	0
7	D1	10363	0	10400	118	0
7	D2	10363	0	10400	58	0
7	D3	10363	0	10400	70	0
7	D4	10363	0	10400	59	0
7	D5	10363	0	10400	59	0
8	E0	4432	0	4472	14	0
8	E1	4432	0	4472	1	0
9	F0	1837	0	1825	13	0
9	F1	1837	0	1825	5	0
9	F2	1837	0	1825	3	0
9	F3	1837	0	1825	11	0
10	H0	3066	0	3103	26	0
10	H1	3066	0	3103	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	H2	3066	0	3103	2	0
10	H3	3066	0	3103	4	0
11	I0	1398	0	1431	26	0
11	I1	1398	0	1431	3	0
11	I2	1398	0	1431	2	0
11	I3	1398	0	1431	2	0
12	J0	1403	0	1391	2	0
12	J1	1403	0	1391	3	0
12	J2	1403	0	1391	1	0
12	J3	1403	0	1391	0	0
12	J4	1403	0	1391	0	0
13	K0	8574	0	8438	17	0
13	K1	8574	0	8438	17	0
13	K2	8574	0	8438	22	0
13	K3	8574	0	8438	21	0
14	L0	6383	0	6313	24	0
14	L1	6383	0	6313	36	0
14	L2	6383	0	6313	13	0
14	L3	6383	0	6313	12	0
15	M0	5461	0	5443	11	0
15	M1	5461	0	5443	14	0
15	M2	5461	0	5443	6	0
15	M3	5461	0	5443	8	0
16	N0	2352	0	2220	17	0
16	N1	2352	0	2220	2	0
16	N2	2352	0	2220	0	0
16	N3	2352	0	2220	1	0
17	O0	2528	0	2444	45	0
17	O1	2528	0	2444	6	0
17	O2	2528	0	2444	6	0
17	O3	2528	0	2444	18	0
18	P0	5257	0	5249	9	0
18	P1	5257	0	5249	8	0
18	P2	5257	0	5249	4	0
18	P3	5257	0	5249	11	0
19	Q0	2703	0	2555	16	0
19	Q1	2703	0	2555	0	0
19	Q2	2703	0	2555	5	0
19	Q3	2703	0	2555	1	0
20	R0	11132	0	11066	74	0
20	R1	11132	0	11066	19	0
20	R2	11132	0	11066	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R3	11132	0	11066	27	0
21	S0	2552	0	2452	5	0
21	S1	2552	0	2452	1	0
21	S2	2552	0	2452	2	0
21	S3	2552	0	2452	1	0
22	T0	7960	0	7896	6	0
22	T1	7960	0	7896	4	0
23	U0	1193	0	1188	7	0
23	U1	151	0	167	25	0
23	U2	151	0	167	25	0
23	U3	151	0	167	20	0
23	U4	151	0	167	26	0
23	U5	151	0	167	25	0
23	U6	151	0	167	26	0
24	V0	2203	0	2226	21	0
25	W0	5836	0	5850	14	0
All	All	617133	0	616873	1222	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 1222 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C2:1249:ILE:HG21	20:R0:1284:ALA:CB	1.29	1.54
6:C2:622:PRO:HB3	20:R0:1316:SER:CB	1.44	1.47
6:C2:788:VAL:CG2	17:O0:258:THR:HG21	1.53	1.39
6:C2:1249:ILE:CG2	20:R0:1284:ALA:HB2	1.58	1.33
6:C2:622:PRO:CB	20:R0:1316:SER:HB3	1.56	1.33

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	00	754/3224 (23%)	703 (93%)	43 (6%)	8 (1%)	11	46
1	01	754/3224 (23%)	706 (94%)	42 (6%)	6 (1%)	16	54
1	02	754/3224 (23%)	707 (94%)	44 (6%)	3 (0%)	30	67
1	03	754/3224 (23%)	700 (93%)	45 (6%)	9 (1%)	10	44
1	04	754/3224 (23%)	702 (93%)	49 (6%)	3 (0%)	30	67
2	10	1829/1887 (97%)	1726 (94%)	94 (5%)	9 (0%)	24	63
2	11	1829/1887 (97%)	1725 (94%)	93 (5%)	11 (1%)	21	59
2	12	1829/1887 (97%)	1724 (94%)	95 (5%)	10 (0%)	24	63
2	13	1829/1887 (97%)	1711 (94%)	107 (6%)	11 (1%)	21	59
2	14	1829/1887 (97%)	1731 (95%)	90 (5%)	8 (0%)	30	67
2	15	1829/1887 (97%)	1733 (95%)	87 (5%)	9 (0%)	24	63
2	16	1829/1887 (97%)	1734 (95%)	86 (5%)	9 (0%)	24	63
2	17	1829/1887 (97%)	1724 (94%)	95 (5%)	10 (0%)	24	63
3	40	379/546 (69%)	350 (92%)	28 (7%)	1 (0%)	36	72
3	41	379/546 (69%)	348 (92%)	29 (8%)	2 (0%)	24	63
4	A0	816/819 (100%)	741 (91%)	65 (8%)	10 (1%)	10	44
4	A1	816/819 (100%)	753 (92%)	54 (7%)	9 (1%)	11	46
4	A2	816/819 (100%)	756 (93%)	50 (6%)	10 (1%)	10	44
4	A3	816/819 (100%)	755 (92%)	55 (7%)	6 (1%)	18	56
4	A4	724/819 (88%)	680 (94%)	40 (6%)	4 (1%)	21	59
4	A5	724/819 (88%)	688 (95%)	31 (4%)	5 (1%)	18	56
4	A6	724/819 (88%)	674 (93%)	47 (6%)	3 (0%)	30	67
5	B0	1746/1749 (100%)	1634 (94%)	93 (5%)	19 (1%)	11	46
5	B1	1746/1749 (100%)	1626 (93%)	103 (6%)	17 (1%)	12	49
6	C0	2009/2012 (100%)	1878 (94%)	111 (6%)	20 (1%)	12	49
6	C1	2009/2012 (100%)	1879 (94%)	109 (5%)	21 (1%)	12	49
6	C2	2009/2012 (100%)	1886 (94%)	106 (5%)	17 (1%)	16	54
6	C3	2009/2012 (100%)	1876 (93%)	118 (6%)	15 (1%)	18	56
6	C4	2009/2012 (100%)	1873 (93%)	123 (6%)	13 (1%)	21	59
7	D0	1308/1391 (94%)	1207 (92%)	89 (7%)	12 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	D1	1308/1391 (94%)	1209 (92%)	88 (7%)	11 (1%)	16	54
7	D2	1308/1391 (94%)	1218 (93%)	81 (6%)	9 (1%)	18	56
7	D3	1308/1391 (94%)	1210 (92%)	85 (6%)	13 (1%)	12	49
7	D4	1308/1391 (94%)	1221 (93%)	77 (6%)	10 (1%)	16	54
7	D5	1308/1391 (94%)	1233 (94%)	65 (5%)	10 (1%)	16	54
8	E0	544/674 (81%)	516 (95%)	26 (5%)	2 (0%)	30	67
8	E1	544/674 (81%)	514 (94%)	29 (5%)	1 (0%)	43	78
9	F0	239/326 (73%)	189 (79%)	33 (14%)	17 (7%)	1	11
9	F1	239/326 (73%)	192 (80%)	33 (14%)	14 (6%)	1	13
9	F2	239/326 (73%)	177 (74%)	45 (19%)	17 (7%)	1	11
9	F3	239/326 (73%)	188 (79%)	39 (16%)	12 (5%)	1	16
10	H0	381/507 (75%)	365 (96%)	16 (4%)	0	100	100
10	H1	381/507 (75%)	364 (96%)	16 (4%)	1 (0%)	36	72
10	H2	381/507 (75%)	366 (96%)	15 (4%)	0	100	100
10	H3	381/507 (75%)	363 (95%)	16 (4%)	2 (0%)	24	63
11	I0	171/599 (28%)	168 (98%)	3 (2%)	0	100	100
11	I1	171/599 (28%)	167 (98%)	3 (2%)	1 (1%)	21	59
11	I2	171/599 (28%)	167 (98%)	4 (2%)	0	100	100
11	I3	171/599 (28%)	167 (98%)	4 (2%)	0	100	100
12	J0	169/522 (32%)	166 (98%)	3 (2%)	0	100	100
12	J1	169/522 (32%)	168 (99%)	1 (1%)	0	100	100
12	J2	169/522 (32%)	167 (99%)	2 (1%)	0	100	100
12	J3	169/522 (32%)	166 (98%)	2 (1%)	1 (1%)	21	59
12	J4	169/522 (32%)	168 (99%)	1 (1%)	0	100	100
13	K0	1084/1156 (94%)	985 (91%)	85 (8%)	14 (1%)	9	42
13	K1	1084/1156 (94%)	990 (91%)	78 (7%)	16 (2%)	8	40
13	K2	1084/1156 (94%)	992 (92%)	82 (8%)	10 (1%)	14	51
13	K3	1084/1156 (94%)	1001 (92%)	70 (6%)	13 (1%)	10	44
14	L0	780/925 (84%)	734 (94%)	42 (5%)	4 (0%)	24	63
14	L1	780/925 (84%)	734 (94%)	38 (5%)	8 (1%)	12	49
14	L2	780/925 (84%)	732 (94%)	45 (6%)	3 (0%)	30	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	L3	780/925 (84%)	731 (94%)	43 (6%)	6 (1%)	16	54
15	M0	669/937 (71%)	609 (91%)	50 (8%)	10 (2%)	8	40
15	M1	669/937 (71%)	613 (92%)	48 (7%)	8 (1%)	10	44
15	M2	669/937 (71%)	618 (92%)	45 (7%)	6 (1%)	14	51
15	M3	669/937 (71%)	612 (92%)	50 (8%)	7 (1%)	12	49
16	N0	299/322 (93%)	277 (93%)	19 (6%)	3 (1%)	12	49
16	N1	299/322 (93%)	277 (93%)	20 (7%)	2 (1%)	18	56
16	N2	299/322 (93%)	277 (93%)	19 (6%)	3 (1%)	12	49
16	N3	299/322 (93%)	278 (93%)	18 (6%)	3 (1%)	12	49
17	O0	321/360 (89%)	304 (95%)	14 (4%)	3 (1%)	14	51
17	O1	321/360 (89%)	302 (94%)	15 (5%)	4 (1%)	10	44
17	O2	321/360 (89%)	302 (94%)	18 (6%)	1 (0%)	36	72
17	O3	321/360 (89%)	299 (93%)	19 (6%)	3 (1%)	14	51
18	P0	653/656 (100%)	607 (93%)	40 (6%)	6 (1%)	14	51
18	P1	653/656 (100%)	612 (94%)	35 (5%)	6 (1%)	14	51
18	P2	653/656 (100%)	610 (93%)	36 (6%)	7 (1%)	11	46
18	P3	653/656 (100%)	611 (94%)	35 (5%)	7 (1%)	11	46
19	Q0	341/380 (90%)	320 (94%)	20 (6%)	1 (0%)	36	72
19	Q1	341/380 (90%)	322 (94%)	18 (5%)	1 (0%)	36	72
19	Q2	341/380 (90%)	320 (94%)	20 (6%)	1 (0%)	36	72
19	Q3	341/380 (90%)	323 (95%)	17 (5%)	1 (0%)	36	72
20	R0	1397/1436 (97%)	1288 (92%)	93 (7%)	16 (1%)	11	46
20	R1	1397/1436 (97%)	1285 (92%)	94 (7%)	18 (1%)	9	42
20	R2	1397/1436 (97%)	1298 (93%)	87 (6%)	12 (1%)	14	51
20	R3	1397/1436 (97%)	1294 (93%)	93 (7%)	10 (1%)	18	56
21	S0	320/326 (98%)	292 (91%)	26 (8%)	2 (1%)	21	59
21	S1	320/326 (98%)	293 (92%)	24 (8%)	3 (1%)	14	51
21	S2	320/326 (98%)	290 (91%)	28 (9%)	2 (1%)	21	59
21	S3	320/326 (98%)	292 (91%)	25 (8%)	3 (1%)	14	51
22	T0	1002/2266 (44%)	927 (92%)	62 (6%)	13 (1%)	9	42
22	T1	1002/2266 (44%)	931 (93%)	58 (6%)	13 (1%)	9	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	U0	148/880 (17%)	140 (95%)	8 (5%)	0	100	100
23	U1	17/880 (2%)	16 (94%)	1 (6%)	0	100	100
23	U2	17/880 (2%)	15 (88%)	2 (12%)	0	100	100
23	U3	17/880 (2%)	15 (88%)	1 (6%)	1 (6%)	1	13
23	U4	17/880 (2%)	15 (88%)	2 (12%)	0	100	100
23	U5	17/880 (2%)	14 (82%)	2 (12%)	1 (6%)	1	13
23	U6	17/880 (2%)	16 (94%)	1 (6%)	0	100	100
24	V0	271/2090 (13%)	255 (94%)	12 (4%)	4 (2%)	8	40
25	W0	733/741 (99%)	688 (94%)	40 (6%)	5 (1%)	18	56
All	All	77792/109146 (71%)	72515 (93%)	4606 (6%)	671 (1%)	16	51

5 of 671 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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%)	655 (97%)	20 (3%)	36	57
1	01	675/2818 (24%)	656 (97%)	19 (3%)	38	60
1	02	675/2818 (24%)	654 (97%)	21 (3%)	35	56
1	03	675/2818 (24%)	655 (97%)	20 (3%)	36	57
1	04	675/2818 (24%)	654 (97%)	21 (3%)	35	56
2	10	1565/1608 (97%)	1543 (99%)	22 (1%)	59	72
2	11	1565/1608 (97%)	1535 (98%)	30 (2%)	50	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	12	1565/1608 (97%)	1541 (98%)	24 (2%)	57	72
2	13	1565/1608 (97%)	1535 (98%)	30 (2%)	50	67
2	14	1565/1608 (97%)	1543 (99%)	22 (1%)	59	72
2	15	1565/1608 (97%)	1539 (98%)	26 (2%)	53	69
2	16	1565/1608 (97%)	1539 (98%)	26 (2%)	53	69
2	17	1565/1608 (97%)	1542 (98%)	23 (2%)	57	72
3	40	323/463 (70%)	312 (97%)	11 (3%)	32	54
3	41	323/463 (70%)	313 (97%)	10 (3%)	35	56
4	A0	725/726 (100%)	700 (97%)	25 (3%)	32	54
4	A1	725/726 (100%)	705 (97%)	20 (3%)	38	60
4	A2	725/726 (100%)	700 (97%)	25 (3%)	32	54
4	A3	725/726 (100%)	704 (97%)	21 (3%)	37	58
4	A4	647/726 (89%)	629 (97%)	18 (3%)	38	60
4	A5	647/726 (89%)	633 (98%)	14 (2%)	45	64
4	A6	647/726 (89%)	629 (97%)	18 (3%)	38	60
5	B0	1540/1541 (100%)	1504 (98%)	36 (2%)	44	64
5	B1	1540/1541 (100%)	1502 (98%)	38 (2%)	42	63
6	C0	1776/1777 (100%)	1732 (98%)	44 (2%)	42	63
6	C1	1776/1777 (100%)	1737 (98%)	39 (2%)	45	64
6	C2	1776/1777 (100%)	1742 (98%)	34 (2%)	50	67
6	C3	1776/1777 (100%)	1736 (98%)	40 (2%)	44	64
6	C4	1776/1777 (100%)	1740 (98%)	36 (2%)	48	66
7	D0	1157/1222 (95%)	1128 (98%)	29 (2%)	42	63
7	D1	1157/1222 (95%)	1126 (97%)	31 (3%)	39	61
7	D2	1157/1222 (95%)	1135 (98%)	22 (2%)	50	67
7	D3	1157/1222 (95%)	1117 (96%)	40 (4%)	32	53
7	D4	1157/1222 (95%)	1125 (97%)	32 (3%)	38	60
7	D5	1157/1222 (95%)	1117 (96%)	40 (4%)	32	53
8	E0	489/604 (81%)	484 (99%)	5 (1%)	68	78
8	E1	489/604 (81%)	484 (99%)	5 (1%)	68	78
9	F0	210/277 (76%)	195 (93%)	15 (7%)	13	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	F1	210/277 (76%)	199 (95%)	11 (5%)	21	42
9	F2	210/277 (76%)	192 (91%)	18 (9%)	10	29
9	F3	210/277 (76%)	196 (93%)	14 (7%)	15	36
10	H0	345/425 (81%)	340 (99%)	5 (1%)	59	72
10	H1	345/425 (81%)	339 (98%)	6 (2%)	53	69
10	H2	345/425 (81%)	339 (98%)	6 (2%)	53	69
10	H3	345/425 (81%)	338 (98%)	7 (2%)	48	66
11	I0	155/459 (34%)	151 (97%)	4 (3%)	40	62
11	I1	155/459 (34%)	152 (98%)	3 (2%)	50	67
11	I2	155/459 (34%)	150 (97%)	5 (3%)	34	56
11	I3	155/459 (34%)	152 (98%)	3 (2%)	50	67
12	J0	158/401 (39%)	154 (98%)	4 (2%)	42	63
12	J1	158/401 (39%)	153 (97%)	5 (3%)	34	56
12	J2	158/401 (39%)	154 (98%)	4 (2%)	42	63
12	J3	158/401 (39%)	153 (97%)	5 (3%)	34	56
12	J4	158/401 (39%)	155 (98%)	3 (2%)	50	67
13	K0	958/1013 (95%)	924 (96%)	34 (4%)	32	53
13	K1	958/1013 (95%)	934 (98%)	24 (2%)	42	63
13	K2	958/1013 (95%)	929 (97%)	29 (3%)	36	57
13	K3	958/1013 (95%)	932 (97%)	26 (3%)	39	61
14	L0	701/827 (85%)	682 (97%)	19 (3%)	39	61
14	L1	701/827 (85%)	680 (97%)	21 (3%)	36	57
14	L2	701/827 (85%)	688 (98%)	13 (2%)	50	67
14	L3	701/827 (85%)	686 (98%)	15 (2%)	47	65
15	M0	602/840 (72%)	586 (97%)	16 (3%)	39	61
15	M1	602/840 (72%)	583 (97%)	19 (3%)	34	56
15	M2	602/840 (72%)	585 (97%)	17 (3%)	38	60
15	M3	602/840 (72%)	588 (98%)	14 (2%)	44	64
16	N0	255/272 (94%)	250 (98%)	5 (2%)	48	66
16	N1	255/272 (94%)	251 (98%)	4 (2%)	55	70
16	N2	255/272 (94%)	251 (98%)	4 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	N3	255/272 (94%)	251 (98%)	4 (2%)	55	70
17	O0	279/310 (90%)	275 (99%)	4 (1%)	59	72
17	O1	279/310 (90%)	275 (99%)	4 (1%)	59	72
17	O2	279/310 (90%)	274 (98%)	5 (2%)	51	68
17	O3	279/310 (90%)	274 (98%)	5 (2%)	51	68
18	P0	584/585 (100%)	570 (98%)	14 (2%)	43	64
18	P1	584/585 (100%)	571 (98%)	13 (2%)	45	64
18	P2	584/585 (100%)	571 (98%)	13 (2%)	45	64
18	P3	584/585 (100%)	568 (97%)	16 (3%)	39	61
19	Q0	303/335 (90%)	300 (99%)	3 (1%)	68	78
19	Q1	303/335 (90%)	301 (99%)	2 (1%)	76	81
19	Q2	303/335 (90%)	301 (99%)	2 (1%)	76	81
19	Q3	303/335 (90%)	300 (99%)	3 (1%)	68	78
20	R0	1233/1259 (98%)	1200 (97%)	33 (3%)	39	61
20	R1	1233/1259 (98%)	1204 (98%)	29 (2%)	43	64
20	R2	1233/1259 (98%)	1206 (98%)	27 (2%)	45	64
20	R3	1233/1259 (98%)	1205 (98%)	28 (2%)	44	64
21	S0	278/282 (99%)	273 (98%)	5 (2%)	51	68
21	S1	278/282 (99%)	272 (98%)	6 (2%)	45	64
21	S2	278/282 (99%)	272 (98%)	6 (2%)	45	64
21	S3	278/282 (99%)	274 (99%)	4 (1%)	59	72
22	T0	891/2037 (44%)	878 (98%)	13 (2%)	57	72
22	T1	891/2037 (44%)	874 (98%)	17 (2%)	50	67
23	U0	131/703 (19%)	127 (97%)	4 (3%)	35	56
23	U1	19/703 (3%)	16 (84%)	3 (16%)	2	11
23	U2	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U3	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U4	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U5	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U6	19/703 (3%)	17 (90%)	2 (10%)	6	21
24	V0	249/1685 (15%)	237 (95%)	12 (5%)	23	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
25	W0	661/663 (100%)	643 (97%)	18 (3%)	39 61
All	All	68601/94353 (73%)	66987 (98%)	1614 (2%)	43 64

5 of 1614 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	D5	1391	HIS
13	K3	271	ASP
25	W0	81	VAL
9	F1	108	LEU
7	D5	1347	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 920 such sidechains are listed below:

Mol	Chain	Res	Type
6	C4	928	ASN
21	S0	244	GLN
7	D5	782	GLN
20	R3	924	GLN
18	P1	388	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

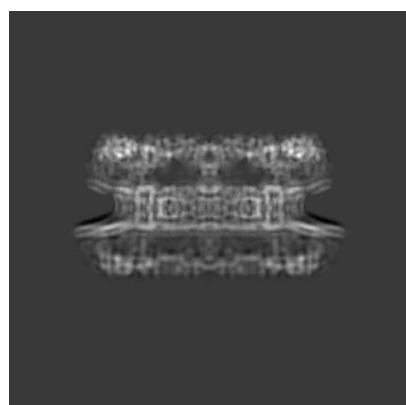
6 Map visualisation [i](#)

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

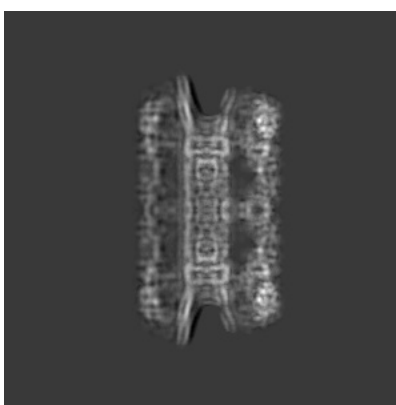
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

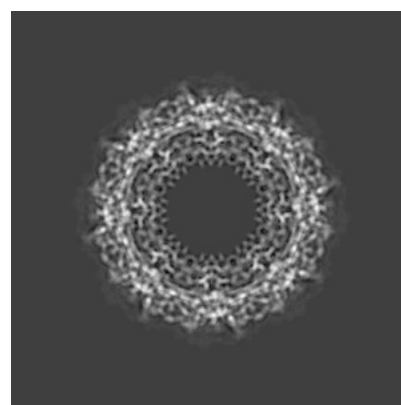
6.1.1 Primary map



X



Y

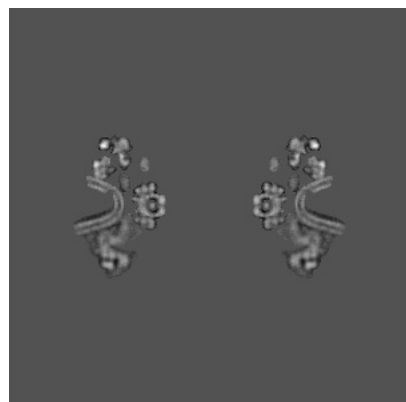


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 288



Y Index: 288



Z Index: 288

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

6.3 Largest variance slices [i](#)

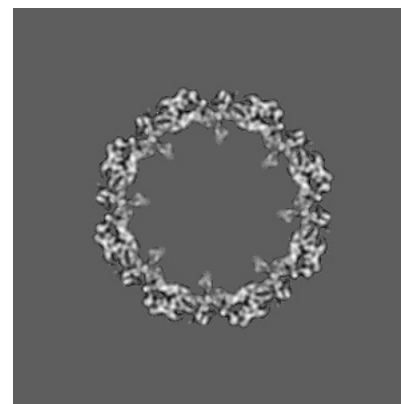
6.3.1 Primary map



X Index: 404



Y Index: 172

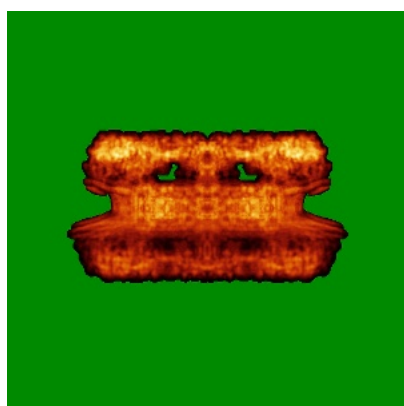


Z Index: 370

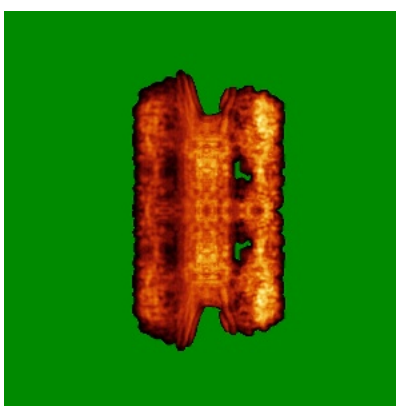
The images above show the largest variance slices of the map in three orthogonal directions.

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

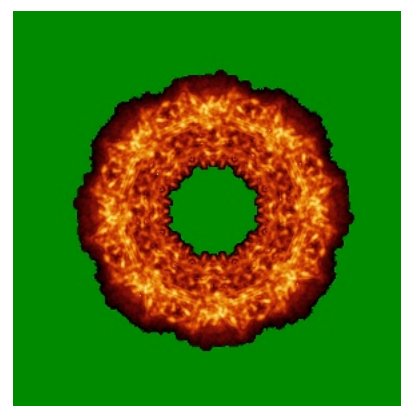
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

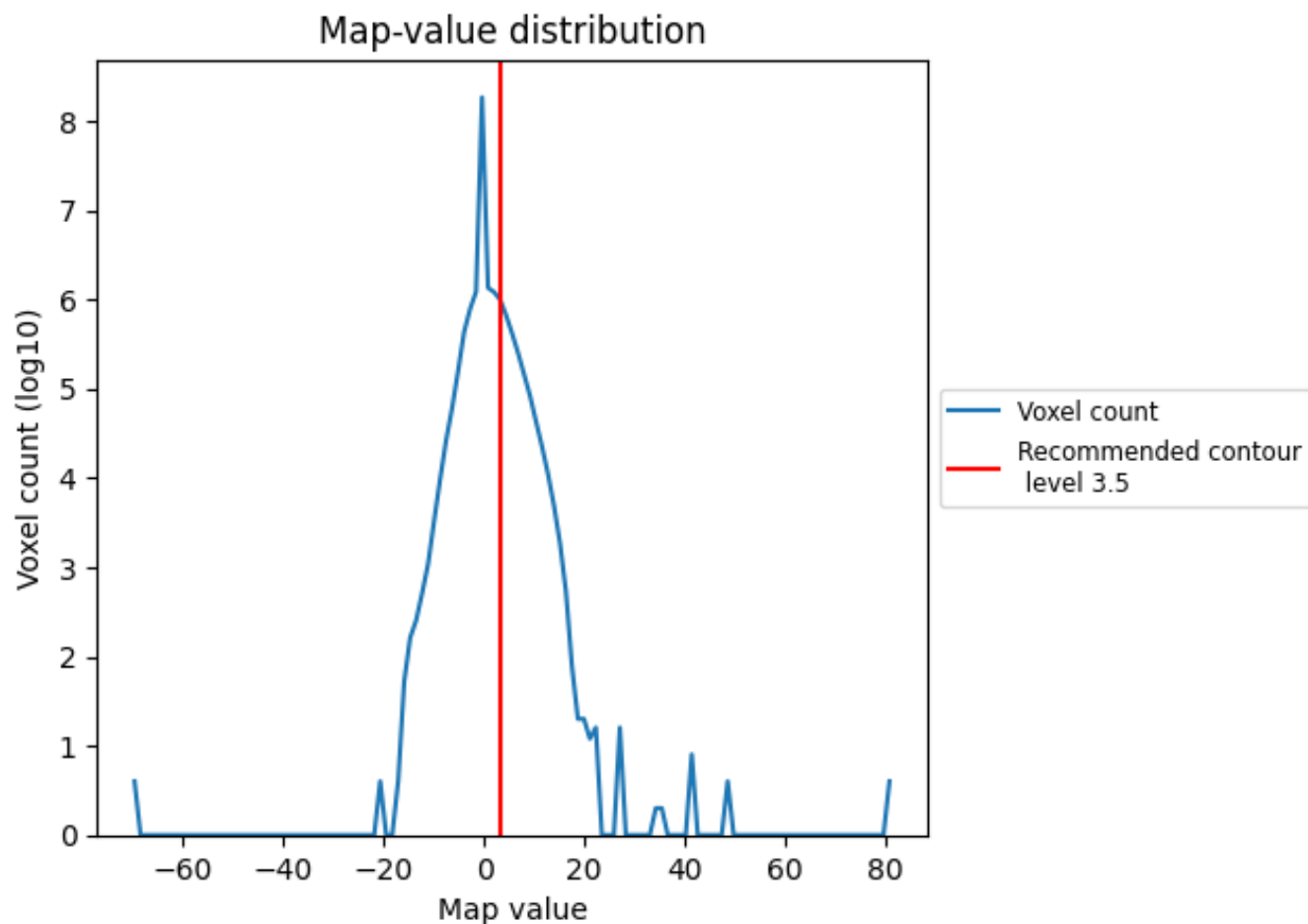
6.6 Mask visualisation

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

7 Map analysis [i](#)

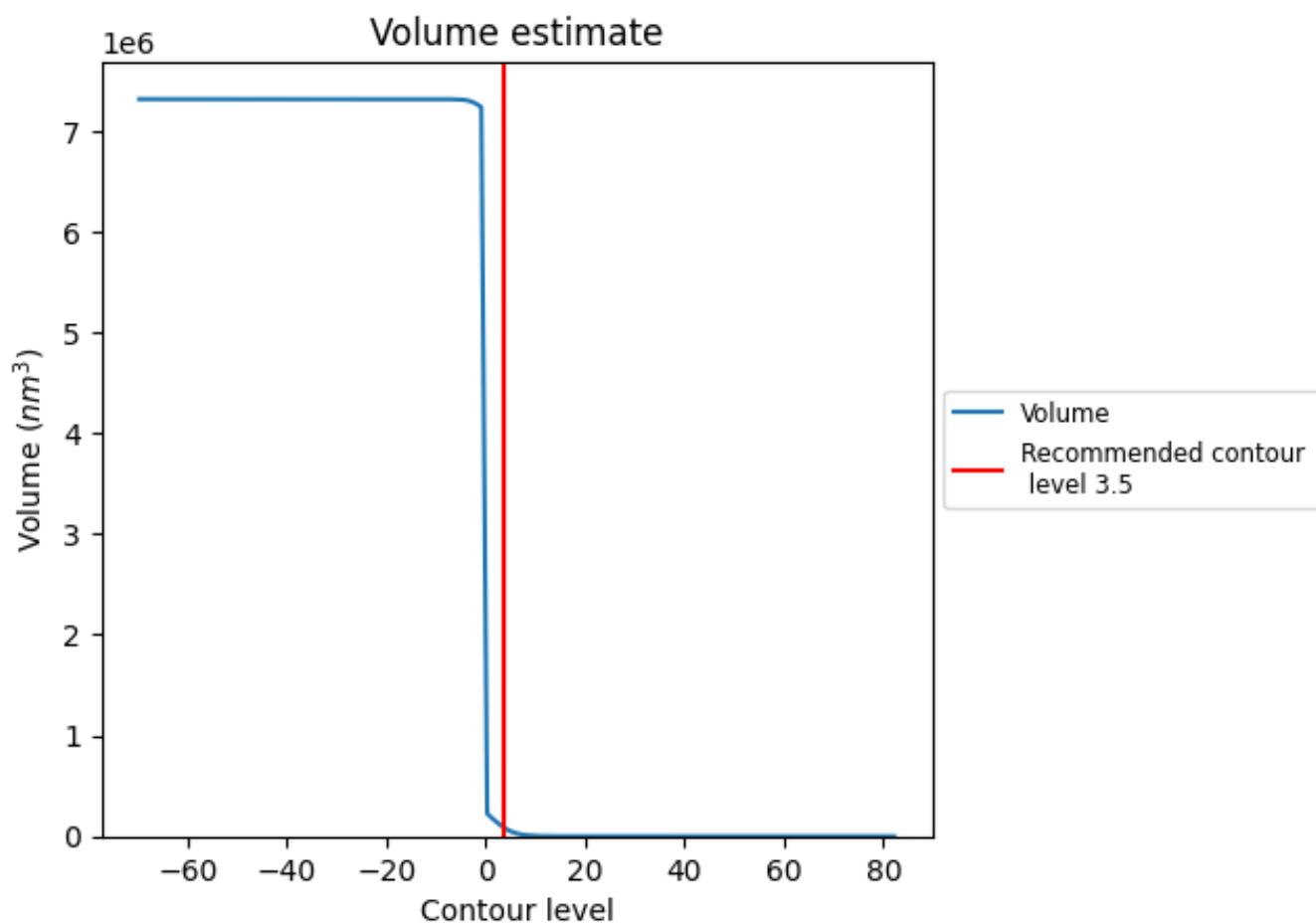
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

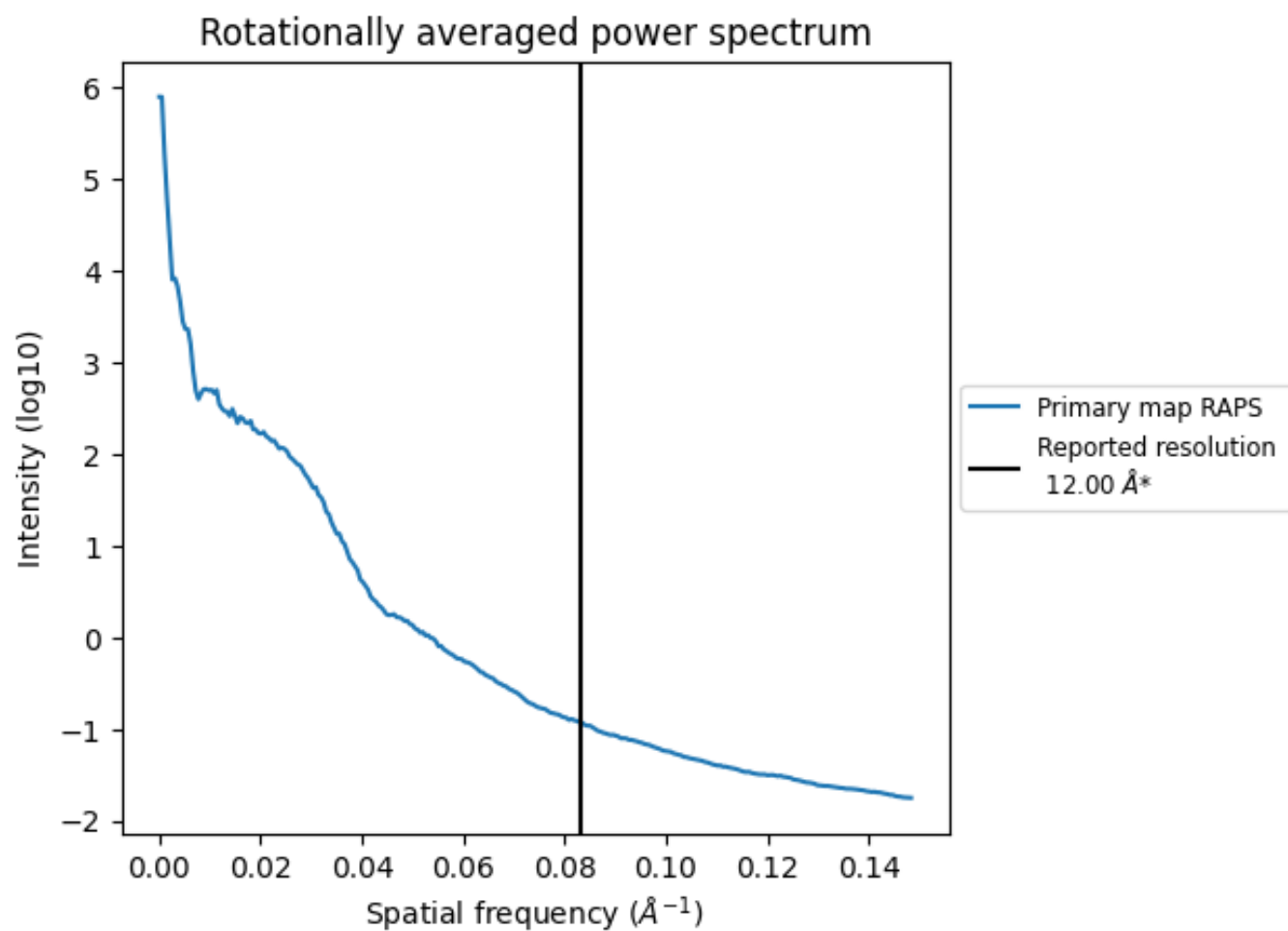
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 93549 nm³; this corresponds to an approximate mass of 84505 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.083 Å⁻¹

8 Fourier-Shell correlation

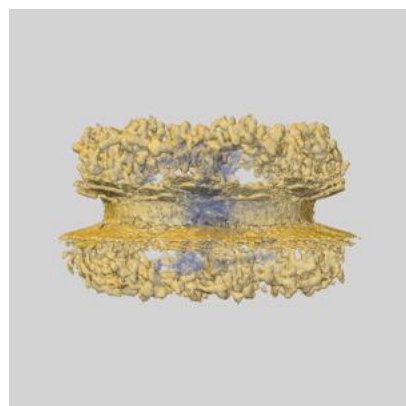
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit ⓘ

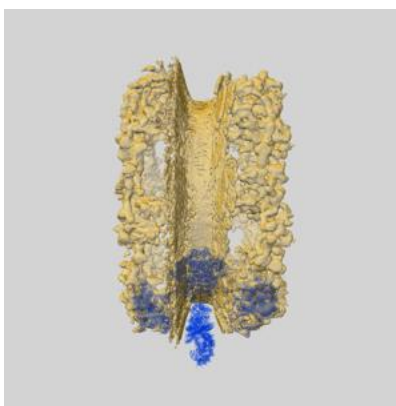
This section contains information regarding the fit between EMDB map EMD-14322 and PDB model 7R5K. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlays

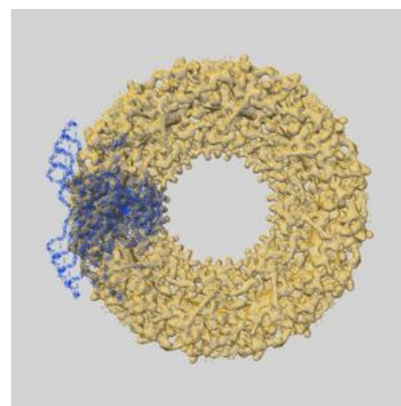
9.1.1 Map-model overlay ⓘ



X



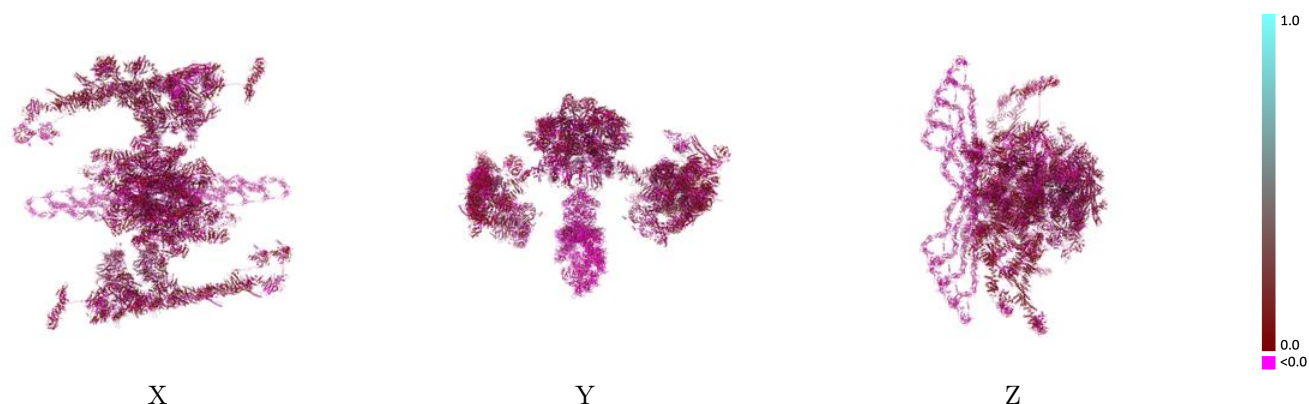
Y



Z

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

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

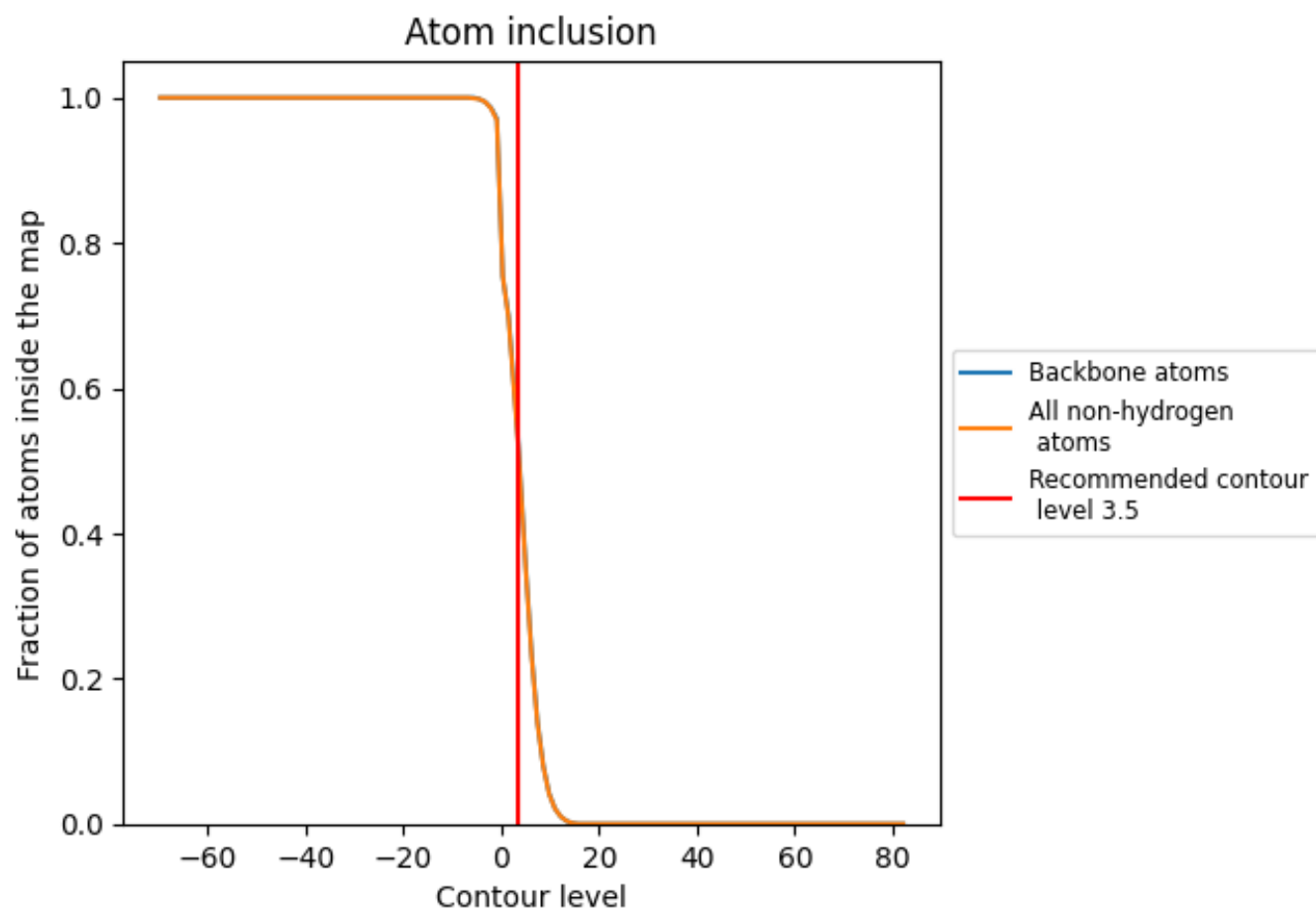


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



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

9.5 Map-model fit summary ⓘ

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

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



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

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Chain	Atom inclusion	Q-score
P2	 0.7050	 0.0450
P3	 0.6510	 0.0390
Q0	 0.8020	 0.0550
Q1	 0.8860	 0.0590
Q2	 0.6720	 0.0420
Q3	 0.7960	 0.0480
R0	 0.8160	 0.0500
R1	 0.7570	 0.0390
R2	 0.6000	 0.0360
R3	 0.5240	 0.0350
S0	 0.5650	 0.0350
S1	 0.7370	 0.0430
S2	 0.5650	 0.0290
S3	 0.6200	 0.0350
T0	 0.4250	 0.0380
T1	 0.1950	 0.0270
U0	 0.1440	 -0.0010
U1	 1.0000	 0.0840
U2	 0.0000	 -0.0540
U3	 0.0000	 -0.0440
U4	 0.0070	 -0.0040
U5	 0.0000	 -0.0250
U6	 0.2720	 0.0500
V0	 0.3540	 0.0120
W0	 0.5130	 0.0120