



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:27 AM UTC

PDB ID : 5IJN / pdb_00005ijn
EMDB ID : EMD-8085
Title : Composite structure of the inner ring of the human nuclear pore complex (32 copies of Nup205)
Authors : Kosinski, J.; Mosalaganti, S.; von Appen, A.; Beck, M.
Deposited on : 2016-03-02
Resolution : 21.40 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:

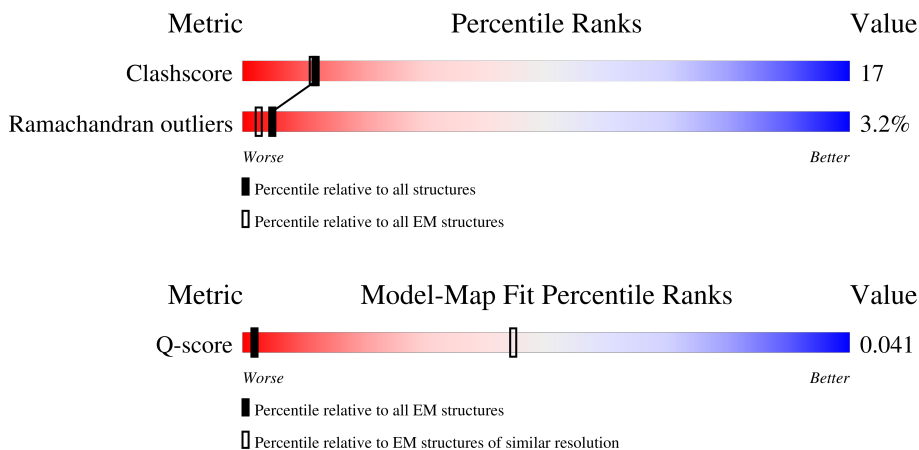
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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





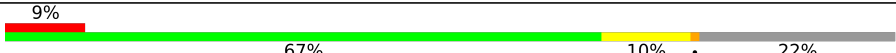
The reported resolution of this entry is 21.40 Å.

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.



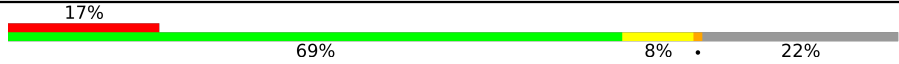


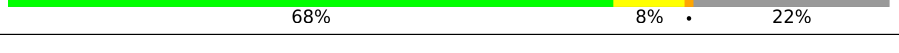
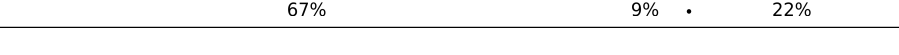
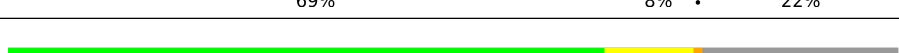
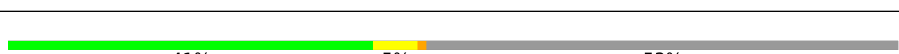






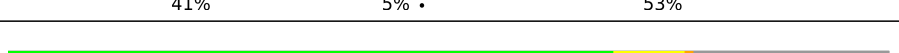
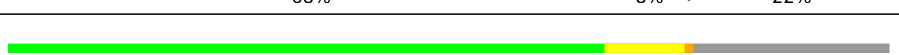
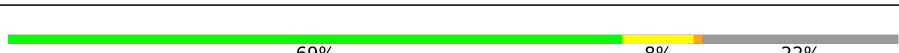






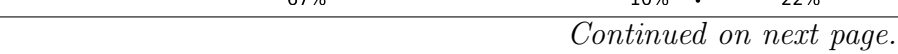


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	9 (21.00 - 21.60)

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	1-A	1391	 41% 5% • 53%
1	1-B	1391	 5% 40% 6% • 53%
1	1-E	1391	 10% 68% 9% • 22%
1	1-K	1391	 35% 69% 8% • 22%
1	1-Q	1391	 9% 67% 10% • 22%

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Mol	Chain	Length	Quality of chain
1	1-W	1391	 17% 69% 8% 22%
1	2-A	1391	 41% 5% 53%
1	2-B	1391	 41% 5% 53%
1	2-E	1391	 68% 8% 22%
1	2-K	1391	 67% 9% 22%
1	2-Q	1391	 69% 8% 22%
1	2-W	1391	 67% 10% 22%
1	3-A	1391	 41% 5% 53%
1	3-B	1391	 41% 5% 53%
1	3-E	1391	 68% 8% 22%
1	3-K	1391	 67% 9% 22%
1	3-Q	1391	 69% 8% 22%
1	3-W	1391	 67% 10% 22%
1	4-A	1391	 41% 5% 53%
1	4-B	1391	 41% 5% 53%
1	4-E	1391	 68% 8% 22%
1	4-K	1391	 67% 9% 22%
1	4-Q	1391	 69% 8% 22%
1	4-W	1391	 67% 10% 22%
1	5-A	1391	 41% 5% 53%
1	5-B	1391	 41% 5% 53%
1	5-E	1391	 68% 8% 22%
1	5-K	1391	 67% 9% 22%
1	5-Q	1391	 69% 8% 22%
1	5-W	1391	 67% 10% 22%

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Mol	Chain	Length	Quality of chain			
1	6-A	1391				
1	6-B	1391				
1	6-E	1391				
1	6-K	1391				
1	6-Q	1391				
1	6-W	1391				
1	7-A	1391				
1	7-B	1391				
1	7-E	1391				
1	7-K	1391				
1	7-Q	1391				
1	7-W	1391				
1	8-A	1391				
1	8-B	1391				
1	8-E	1391				
1	8-K	1391				
1	8-Q	1391				
1	8-W	1391				
2	1-C	819				
2	1-I	819				
2	1-O	819				
2	1-U	819				
2	2-C	819				
2	2-I	819				
2	2-O	819				

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Mol	Chain	Length	Quality of chain			
2	2-U	819	58%	15%	•	22%
2	3-C	819	57%	15%	5%	22%
2	3-I	819	58%	15%	•	22%
2	3-O	819	57%	15%	5%	22%
2	3-U	819	58%	15%	•	22%
2	4-C	819	57%	15%	5%	22%
2	4-I	819	58%	15%	•	22%
2	4-O	819	57%	15%	5%	22%
2	4-U	819	58%	15%	•	22%
2	5-C	819	57%	15%	5%	22%
2	5-I	819	58%	15%	•	22%
2	5-O	819	57%	15%	5%	22%
2	5-U	819	58%	15%	•	22%
2	6-C	819	62%	14%	•	22%
2	6-I	819	62%	14%	•	22%
2	6-O	819	62%	14%	•	22%
2	6-U	819	62%	14%	•	22%
2	7-C	819	57%	16%	5%	22%
2	7-I	819	58%	15%	•	22%
2	7-O	819	57%	15%	5%	22%
2	7-U	819	58%	15%	•	22%
2	8-C	819	57%	15%	5%	22%
2	8-I	819	58%	15%	•	22%
2	8-O	819	57%	15%	5%	22%
2	8-U	819	58%	15%	•	22%

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Mol	Chain	Length	Quality of chain
3	1-D	2012	5% 43% 5% .. 49%
3	1-J	2012	6% 43% 6% .. 49%
3	1-P	2012	5% 43% 5% .. 49%
3	1-V	2012	5% 42% 6% .. 49%
3	2-D	2012	43% 5% .. 49%
3	2-J	2012	43% 5% .. 49%
3	2-P	2012	43% 5% .. 49%
3	2-V	2012	43% 5% .. 49%
3	3-D	2012	43% 5% .. 49%
3	3-J	2012	43% 5% .. 49%
3	3-P	2012	43% 5% .. 49%
3	3-V	2012	43% 5% .. 49%
3	4-D	2012	43% 5% .. 49%
3	4-J	2012	43% 5% .. 49%
3	4-P	2012	43% 5% .. 49%
3	4-V	2012	43% 5% .. 49%
3	5-D	2012	43% 5% .. 49%
3	5-J	2012	43% 5% .. 49%
3	5-P	2012	43% 5% .. 49%
3	5-V	2012	43% 5% .. 49%
3	6-D	2012	45% 5% . 49%
3	6-J	2012	45% 5% . 49%
3	6-P	2012	45% 5% . 49%
3	6-V	2012	45% 5% . 49%
3	7-D	2012	43% 5% .. 49%

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Mol	Chain	Length	Quality of chain
3	7-J	2012	43% 5% .. 49%
3	7-P	2012	43% 5% .. 49%
3	7-V	2012	43% 5% .. 49%
3	8-D	2012	43% 5% .. 49%
3	8-J	2012	43% 5% .. 49%
3	8-P	2012	43% 5% .. 49%
3	8-V	2012	43% 5% .. 49%
4	1-F	507	13% 30% 23% 8% 5% 34%
4	1-L	507	13% 31% 23% 7% 5% 34%
4	1-R	507	15% 30% 23% 8% 5% 34%
4	1-X	507	10% 31% 22% 8% 5% 34%
4	2-F	507	35% 19% 7% 5% 34%
4	2-L	507	35% 19% 7% 5% 34%
4	2-R	507	35% 19% 7% 5% 34%
4	2-X	507	35% 19% 7% 5% 34%
4	3-F	507	35% 19% 7% 5% 34%
4	3-L	507	35% 19% 7% 5% 34%
4	3-R	507	35% 19% 7% 5% 34%
4	3-X	507	35% 19% 7% 5% 34%
4	4-F	507	35% 19% 7% 5% 34%
4	4-L	507	35% 19% 7% 5% 34%
4	4-R	507	35% 19% 7% 5% 34%
4	4-X	507	35% 19% 7% 5% 34%
4	5-F	507	35% 19% 7% 5% 34%
4	5-L	507	35% 19% 7% 5% 34%

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Mol	Chain	Length	Quality of chain
4	5-R	507	35% 19% 7% 5% 34%
4	5-X	507	35% 19% 7% 5% 34%
4	6-F	507	36% 23% 6% 6% 34%
4	6-L	507	36% 23% 6% 6% 34%
4	6-R	507	36% 23% 6% 6% 34%
4	6-X	507	36% 23% 6% 6% 34%
4	7-F	507	35% 19% 7% 5% 34%
4	7-L	507	35% 19% 7% 5% 34%
4	7-R	507	35% 19% 7% 5% 34%
4	7-X	507	35% 19% 7% 5% 34%
4	8-F	507	35% 19% 7% 5% 34%
4	8-L	507	35% 19% 7% 5% 34%
4	8-R	507	35% 19% 7% 5% 34%
4	8-X	507	35% 19% 7% 5% 34%
5	1-G	599	10% 14% 6% 6% 71%
5	1-M	599	10% 14% 6% 6% 71%
5	1-S	599	10% 14% 6% 6% 71%
5	1-Y	599	10% 14% 6% 6% 71%
5	2-G	599	10% 14% 6% 6% 71%
5	2-M	599	10% 14% 6% 6% 71%
5	2-S	599	10% 14% 6% 6% 71%
5	2-Y	599	10% 14% 6% 6% 71%
5	3-G	599	10% 14% 6% 6% 71%
5	3-M	599	10% 14% 6% 6% 71%
5	3-S	599	10% 14% 6% 6% 71%








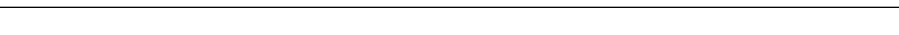
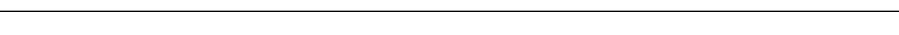
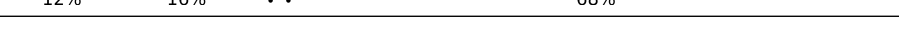
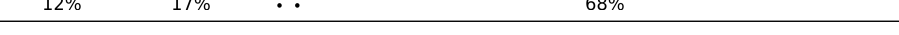
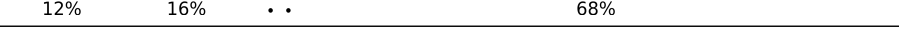













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Mol	Chain	Length	Quality of chain
5	3-Y	599	10% 15% . . 71%
5	4-G	599	10% 14% . . 71%
5	4-M	599	10% 14% . . 71%
5	4-S	599	10% 14% . . 71%
5	4-Y	599	10% 14% . . 71%
5	5-G	599	10% 14% . . 71%
5	5-M	599	10% 14% . . 71%
5	5-S	599	10% 14% . . 71%
5	5-Y	599	10% 14% . . 71%
5	6-G	599	10% 16% . 71%
5	6-M	599	10% 16% . 71%
5	6-S	599	11% 16% . 71%
5	6-Y	599	10% 16% . 71%
5	7-G	599	10% 14% . . 71%
5	7-M	599	10% 14% . . 71%
5	7-S	599	10% 14% . . 71%
5	7-Y	599	10% 14% . . 71%
5	8-G	599	10% 14% . . 71%
5	8-M	599	10% 14% . . 71%
5	8-S	599	10% 14% . . 71%
5	8-Y	599	10% 15% . . 71%
6	1-H	522	6% 12% 16% . . 68%
6	1-N	522	11% 16% . . 68%
6	1-T	522	8% 12% 16% . . 68%
6	1-Z	522	5% 12% 16% . . 68%




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Mol	Chain	Length	Quality of chain
6	2-H	522	 12% 16% .. 68%
6	2-N	522	 12% 17% .. 68%
6	2-T	522	 12% 16% .. 68%
6	2-Z	522	 12% 16% .. 68%
6	3-H	522	 12% 16% .. 68%
6	3-N	522	 11% 17% .. 68%
6	3-T	522	 12% 16% .. 68%
6	3-Z	522	 12% 16% .. 68%
6	4-H	522	 12% 16% .. 68%
6	4-N	522	 12% 17% .. 68%
6	4-T	522	 12% 16% .. 68%
6	4-Z	522	 12% 16% .. 68%
6	5-H	522	 12% 16% .. 68%
6	5-N	522	 12% 17% .. 68%
6	5-T	522	 12% 16% .. 68%
6	5-Z	522	 12% 16% .. 68%
6	6-H	522	 12% 19% . 68%
6	6-N	522	 12% 19% . 68%
6	6-T	522	 12% 18% . 68%
6	6-Z	522	 12% 18% . 68%
6	7-H	522	 12% 16% .. 68%
6	7-N	522	 12% 17% .. 68%
6	7-T	522	 12% 16% .. 68%
6	7-Z	522	 12% 16% .. 68%
6	8-H	522	 12% 16% .. 68%

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Mol	Chain	Length	Quality of chain
6	8-N	522	 11% 17% . . 68%
6	8-T	522	 12% 16% . . 68%
6	8-Z	522	 12% 16% . . 68%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 594304 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 NUCLEAR PORE COMPLEX PROTEIN NUP155.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	1-A	650	3214	1914	650	650	0	0
1	2-A	650	3214	1914	650	650	0	0
1	3-A	650	3214	1914	650	650	0	0
1	4-A	650	3214	1914	650	650	0	0
1	5-A	650	3214	1914	650	650	0	0
1	6-A	650	3214	1914	650	650	0	0
1	7-A	650	3214	1914	650	650	0	0
1	8-A	650	3214	1914	650	650	0	0
1	1-B	650	3214	1914	650	650	0	0
1	2-B	650	3214	1914	650	650	0	0
1	3-B	650	3214	1914	650	650	0	0
1	4-B	650	3214	1914	650	650	0	0
1	5-B	650	3214	1914	650	650	0	0
1	6-B	650	3214	1914	650	650	0	0
1	7-B	650	3214	1914	650	650	0	0
1	8-B	650	3214	1914	650	650	0	0
1	1-E	1083	5366	3200	1083	1083	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	2-E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	3-E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	4-E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	5-E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	6-E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	7-E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	8-E	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	1-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	2-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	3-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	4-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	5-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	6-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	7-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	8-K	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	1-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	2-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	3-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	4-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	5-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	6-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	7-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	8-Q	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	1-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	2-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	3-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	4-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	5-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	6-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	7-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0
1	8-W	1083	Total 5366	C 3200	N 1083	O 1083	0	0

- Molecule 2 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP93.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	2-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	3-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	4-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	5-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	6-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	7-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	8-C	636	Total 3152	C 1880	N 636	O 636	0	0
2	1-I	636	Total 3152	C 1880	N 636	O 636	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	2-I	636	Total 3152	C 1880	N 636	O 636	0	0
2	3-I	636	Total 3152	C 1880	N 636	O 636	0	0
2	4-I	636	Total 3152	C 1880	N 636	O 636	0	0
2	5-I	636	Total 3152	C 1880	N 636	O 636	0	0
2	6-I	636	Total 3152	C 1880	N 636	O 636	0	0
2	7-I	636	Total 3152	C 1880	N 636	O 636	0	0
2	8-I	636	Total 3152	C 1880	N 636	O 636	0	0
2	1-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	2-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	3-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	4-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	5-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	6-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	7-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	8-O	636	Total 3152	C 1880	N 636	O 636	0	0
2	1-U	636	Total 3152	C 1880	N 636	O 636	0	0
2	2-U	636	Total 3152	C 1880	N 636	O 636	0	0
2	3-U	636	Total 3152	C 1880	N 636	O 636	0	0
2	4-U	636	Total 3152	C 1880	N 636	O 636	0	0
2	5-U	636	Total 3152	C 1880	N 636	O 636	0	0
2	6-U	636	Total 3152	C 1880	N 636	O 636	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	7-U	636	Total	C	N	O	0	0
			3152	1880	636	636		
2	8-U	636	Total	C	N	O	0	0
			3152	1880	636	636		

- Molecule 3 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP205.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	1-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	2-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	3-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	4-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	5-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	6-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	7-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	8-D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	1-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	2-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	3-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	4-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	5-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	6-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	7-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	8-J	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	1-P	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	2-P	1028	5094	3038	1028	1028	0	0
3	3-P	1028	5094	3038	1028	1028	0	0
3	4-P	1028	5094	3038	1028	1028	0	0
3	5-P	1028	5094	3038	1028	1028	0	0
3	6-P	1028	5094	3038	1028	1028	0	0
3	7-P	1028	5094	3038	1028	1028	0	0
3	8-P	1028	5094	3038	1028	1028	0	0
3	1-V	1028	5094	3038	1028	1028	0	0
3	2-V	1028	5094	3038	1028	1028	0	0
3	3-V	1028	5094	3038	1028	1028	0	0
3	4-V	1028	5094	3038	1028	1028	0	0
3	5-V	1028	5094	3038	1028	1028	0	0
3	6-V	1028	5094	3038	1028	1028	0	0
3	7-V	1028	5094	3038	1028	1028	0	0
3	8-V	1028	5094	3038	1028	1028	0	0

- Molecule 4 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP54.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	1-F	335	1658	988	335	335	0	0
4	2-F	335	1658	988	335	335	0	0
4	3-F	335	1658	988	335	335	0	0
4	4-F	335	1658	988	335	335	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	5-F	335	1658	988	335	335	0	0
4	6-F	335	1658	988	335	335	0	0
4	7-F	335	1658	988	335	335	0	0
4	8-F	335	1658	988	335	335	0	0
4	1-L	335	1658	988	335	335	0	0
4	2-L	335	1658	988	335	335	0	0
4	3-L	335	1658	988	335	335	0	0
4	4-L	335	1658	988	335	335	0	0
4	5-L	335	1658	988	335	335	0	0
4	6-L	335	1658	988	335	335	0	0
4	7-L	335	1658	988	335	335	0	0
4	8-L	335	1658	988	335	335	0	0
4	1-R	335	1658	988	335	335	0	0
4	2-R	335	1658	988	335	335	0	0
4	3-R	335	1658	988	335	335	0	0
4	4-R	335	1658	988	335	335	0	0
4	5-R	335	1658	988	335	335	0	0
4	6-R	335	1658	988	335	335	0	0
4	7-R	335	1658	988	335	335	0	0
4	8-R	335	1658	988	335	335	0	0
4	1-X	335	1658	988	335	335	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	2-X	335	Total	C	N	O	0	0
			1658	988	335	335		
4	3-X	335	Total	C	N	O	0	0
			1658	988	335	335		
4	4-X	335	Total	C	N	O	0	0
			1658	988	335	335		
4	5-X	335	Total	C	N	O	0	0
			1658	988	335	335		
4	6-X	335	Total	C	N	O	0	0
			1658	988	335	335		
4	7-X	335	Total	C	N	O	0	0
			1658	988	335	335		
4	8-X	335	Total	C	N	O	0	0
			1658	988	335	335		

- Molecule 5 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP58.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	1-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	2-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	3-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	4-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	5-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	6-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	7-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	8-G	171	Total	C	N	O	0	0
			853	511	171	171		
5	1-M	171	Total	C	N	O	0	0
			853	511	171	171		
5	2-M	171	Total	C	N	O	0	0
			853	511	171	171		
5	3-M	171	Total	C	N	O	0	0
			853	511	171	171		
5	4-M	171	Total	C	N	O	0	0
			853	511	171	171		

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Mol	Chain	Residues	Atoms				AltConf	Trace
5	5-M	171	Total 853	C 511	N 171	O 171	0	0
5	6-M	171	Total 853	C 511	N 171	O 171	0	0
5	7-M	171	Total 853	C 511	N 171	O 171	0	0
5	8-M	171	Total 853	C 511	N 171	O 171	0	0
5	1-S	171	Total 853	C 511	N 171	O 171	0	0
5	2-S	171	Total 853	C 511	N 171	O 171	0	0
5	3-S	171	Total 853	C 511	N 171	O 171	0	0
5	4-S	171	Total 853	C 511	N 171	O 171	0	0
5	5-S	171	Total 853	C 511	N 171	O 171	0	0
5	6-S	171	Total 853	C 511	N 171	O 171	0	0
5	7-S	171	Total 853	C 511	N 171	O 171	0	0
5	8-S	171	Total 853	C 511	N 171	O 171	0	0
5	1-Y	171	Total 853	C 511	N 171	O 171	0	0
5	2-Y	171	Total 853	C 511	N 171	O 171	0	0
5	3-Y	171	Total 853	C 511	N 171	O 171	0	0
5	4-Y	171	Total 853	C 511	N 171	O 171	0	0
5	5-Y	171	Total 853	C 511	N 171	O 171	0	0
5	6-Y	171	Total 853	C 511	N 171	O 171	0	0
5	7-Y	171	Total 853	C 511	N 171	O 171	0	0
5	8-Y	171	Total 853	C 511	N 171	O 171	0	0

- Molecule 6 is a protein called Nuclear pore glycoprotein p62.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	1-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	2-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	3-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	4-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	5-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	6-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	7-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	8-H	169	Total	C	N	O	0	0
			842	504	169	169		
6	1-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	2-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	3-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	4-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	5-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	6-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	7-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	8-N	169	Total	C	N	O	0	0
			842	504	169	169		
6	1-T	169	Total	C	N	O	0	0
			842	504	169	169		
6	2-T	169	Total	C	N	O	0	0
			842	504	169	169		
6	3-T	169	Total	C	N	O	0	0
			842	504	169	169		
6	4-T	169	Total	C	N	O	0	0
			842	504	169	169		
6	5-T	169	Total	C	N	O	0	0
			842	504	169	169		
6	6-T	169	Total	C	N	O	0	0
			842	504	169	169		

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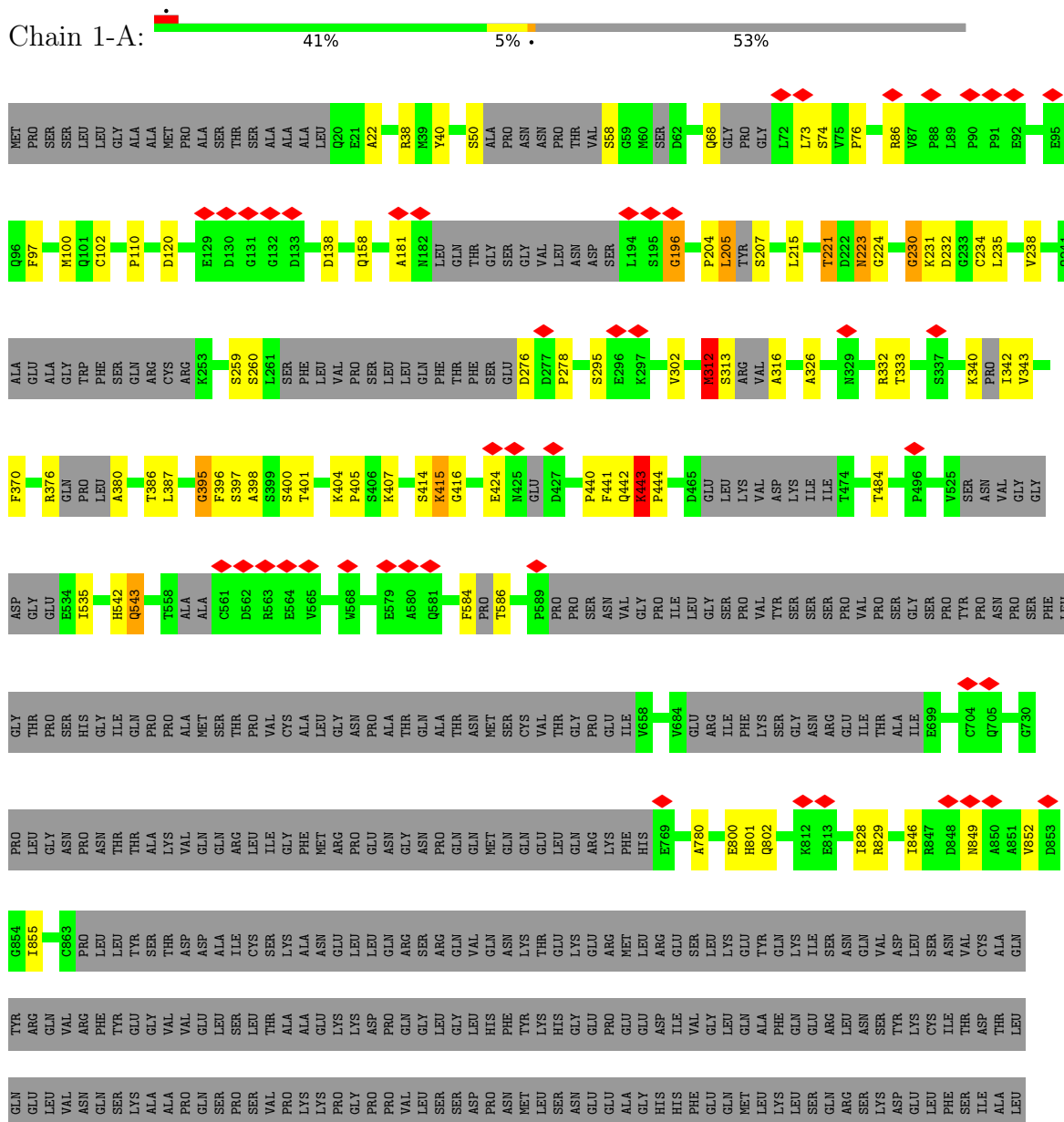
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Mol	Chain	Residues	Atoms				AltConf	Trace
6	7-T	169	Total 842	C 504	N 169	O 169	0	0
6	8-T	169	Total 842	C 504	N 169	O 169	0	0
6	1-Z	169	Total 842	C 504	N 169	O 169	0	0
6	2-Z	169	Total 842	C 504	N 169	O 169	0	0
6	3-Z	169	Total 842	C 504	N 169	O 169	0	0
6	4-Z	169	Total 842	C 504	N 169	O 169	0	0
6	5-Z	169	Total 842	C 504	N 169	O 169	0	0
6	6-Z	169	Total 842	C 504	N 169	O 169	0	0
6	7-Z	169	Total 842	C 504	N 169	O 169	0	0
6	8-Z	169	Total 842	C 504	N 169	O 169	0	0

3 Residue-property plots

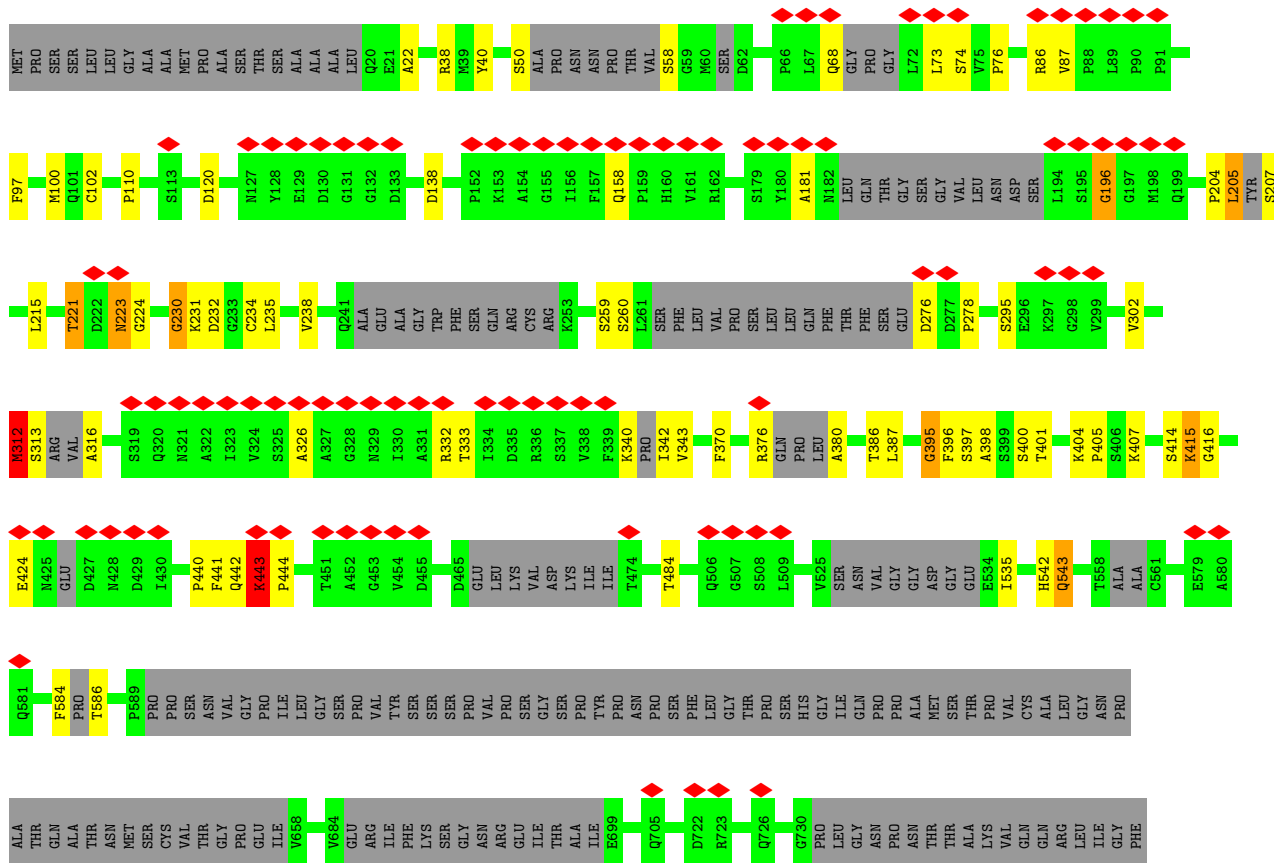
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

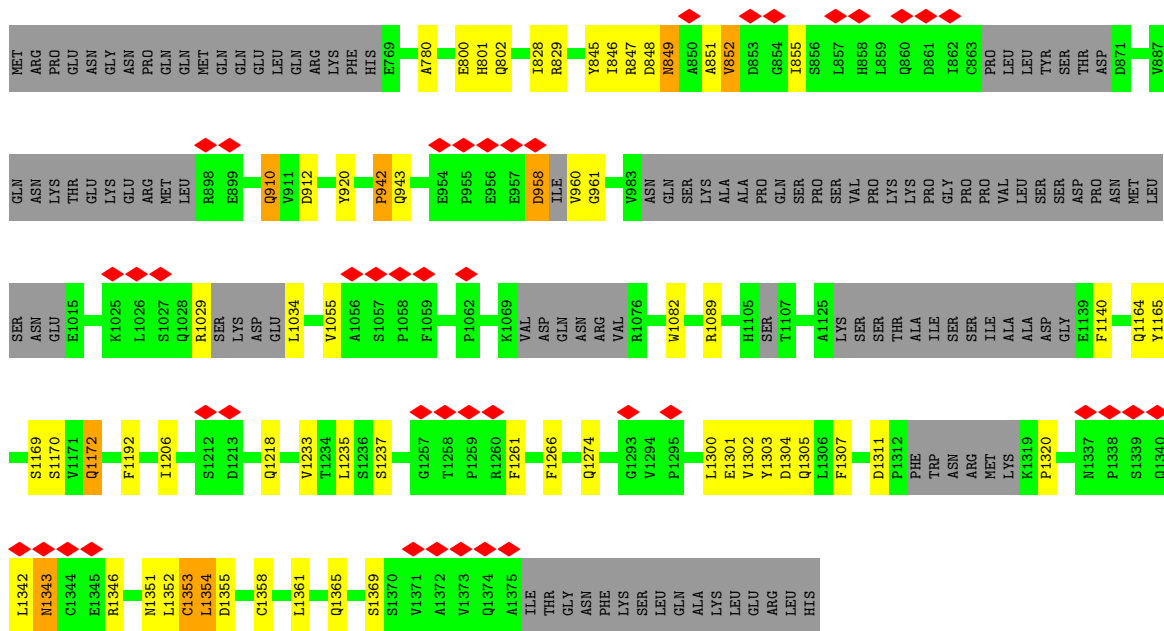
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155



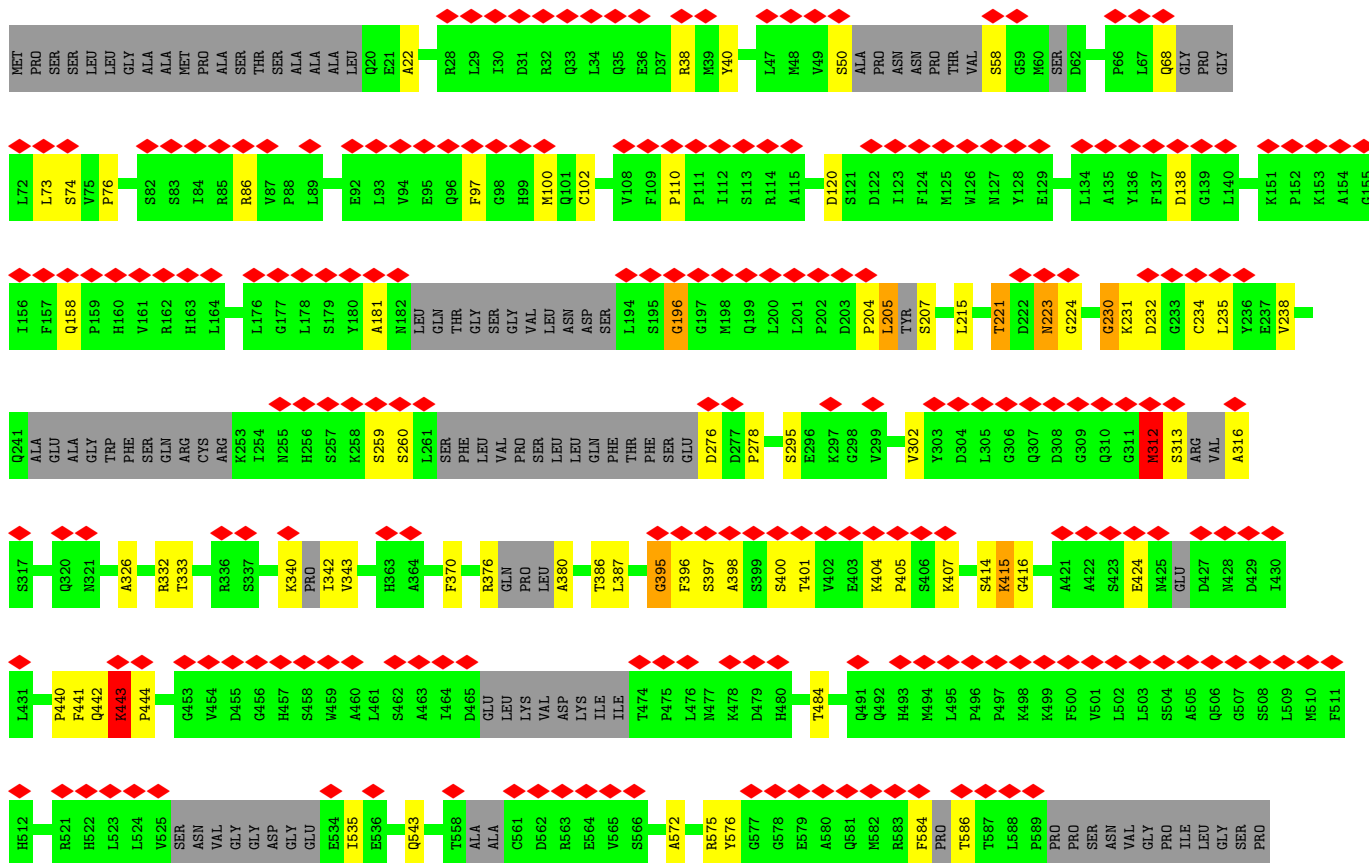
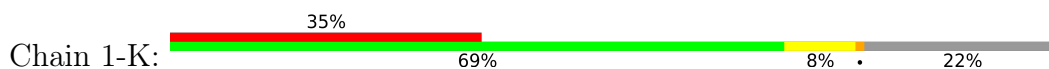
Grid of 25 amino acid sequence diagrams, each showing a short segment of a protein chain with residues highlighted in various colors (green, yellow, orange, red, grey).

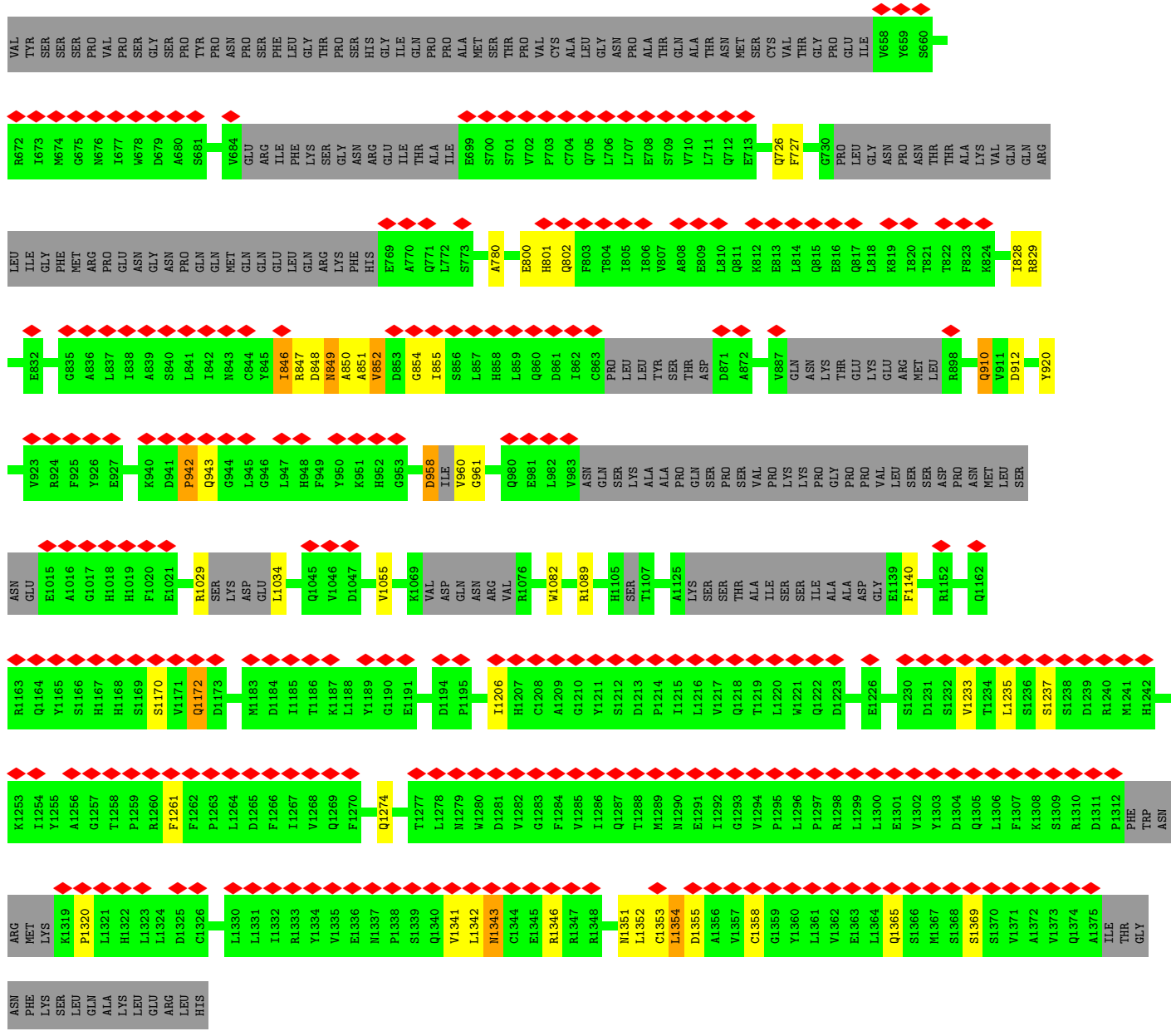
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155



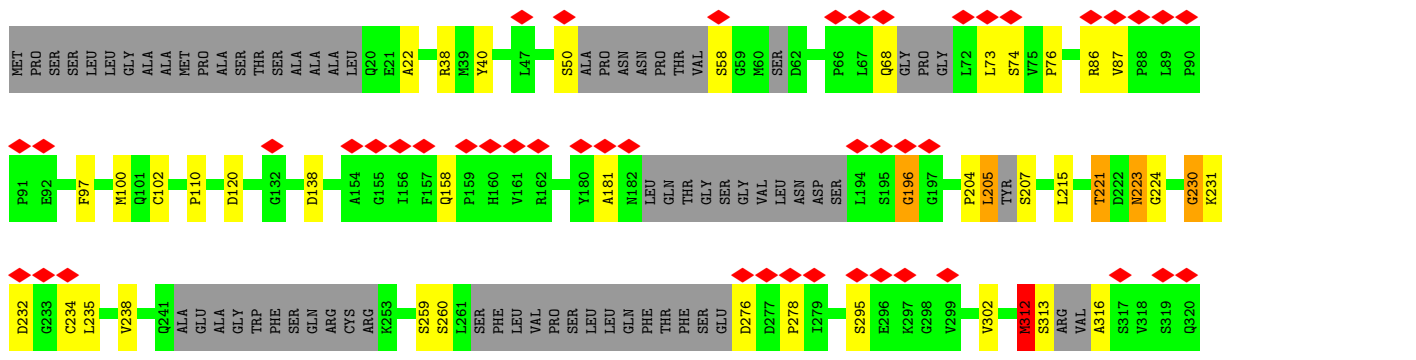


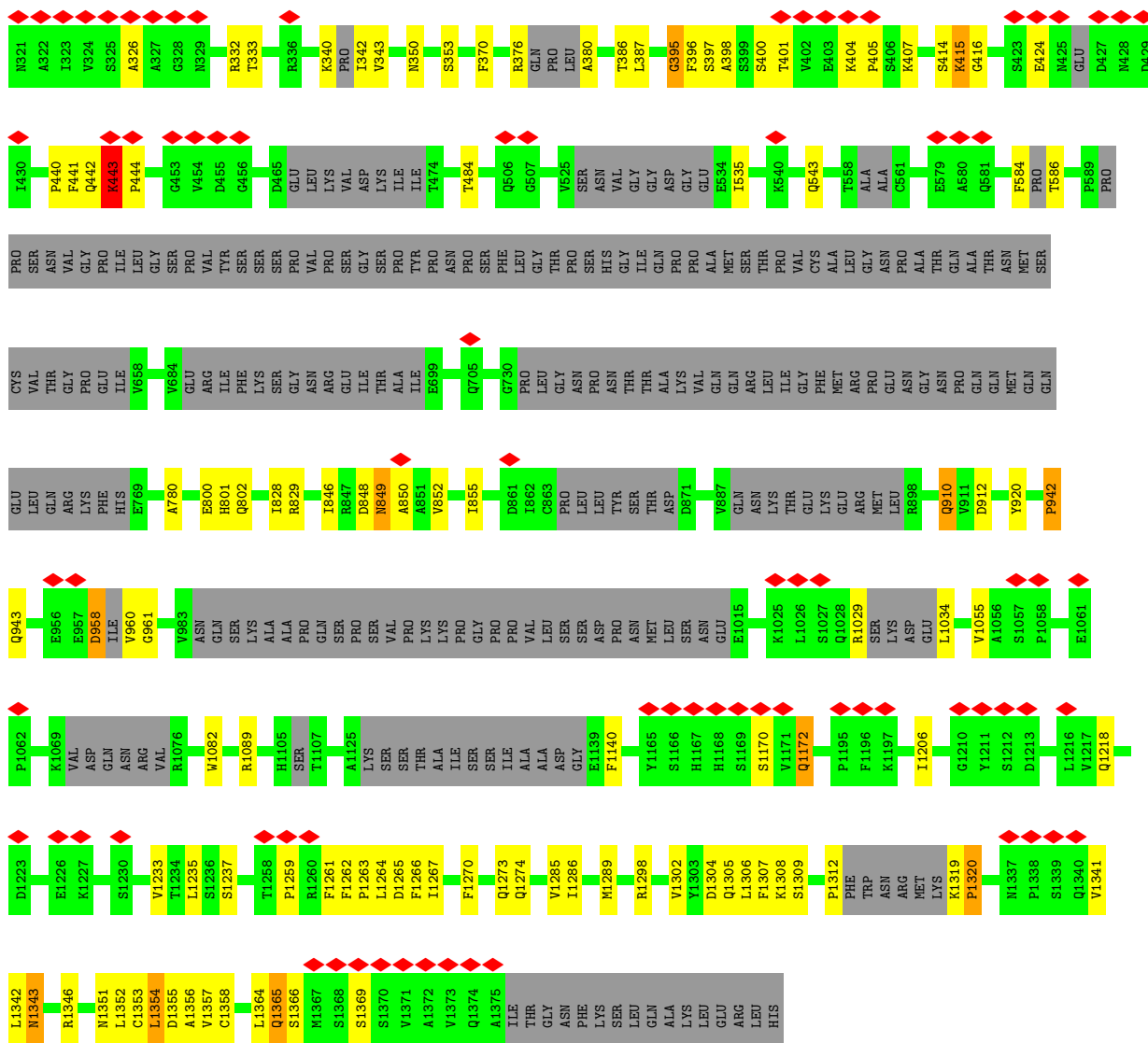
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155



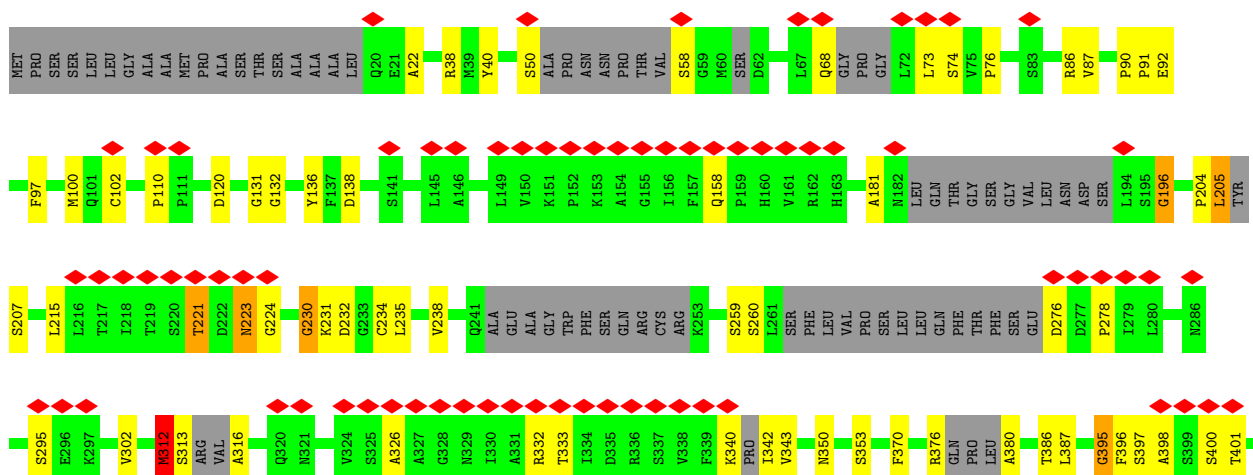
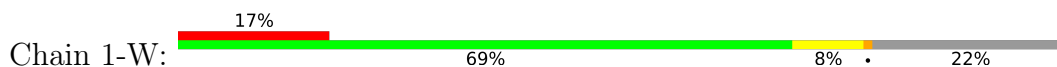


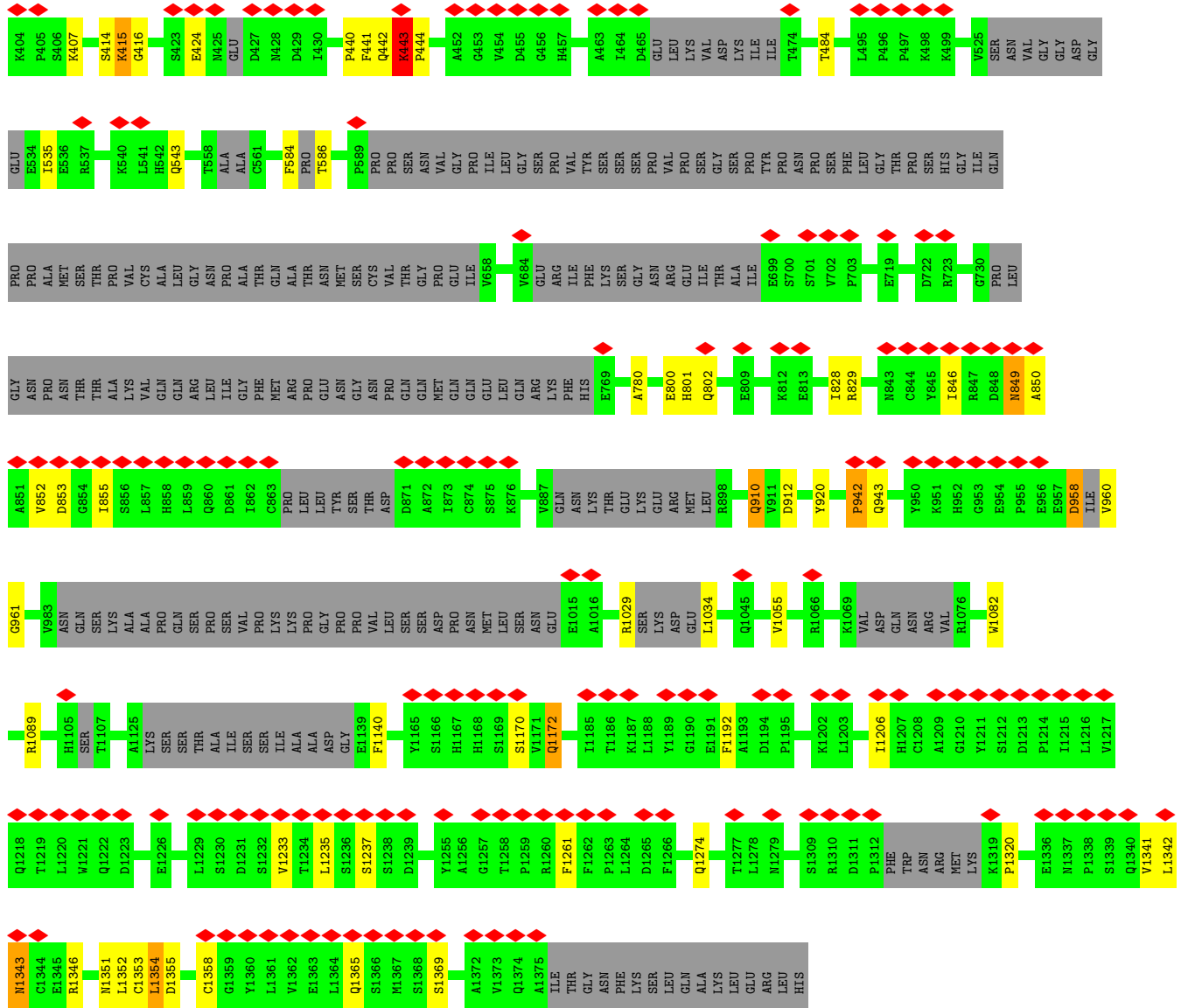
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155





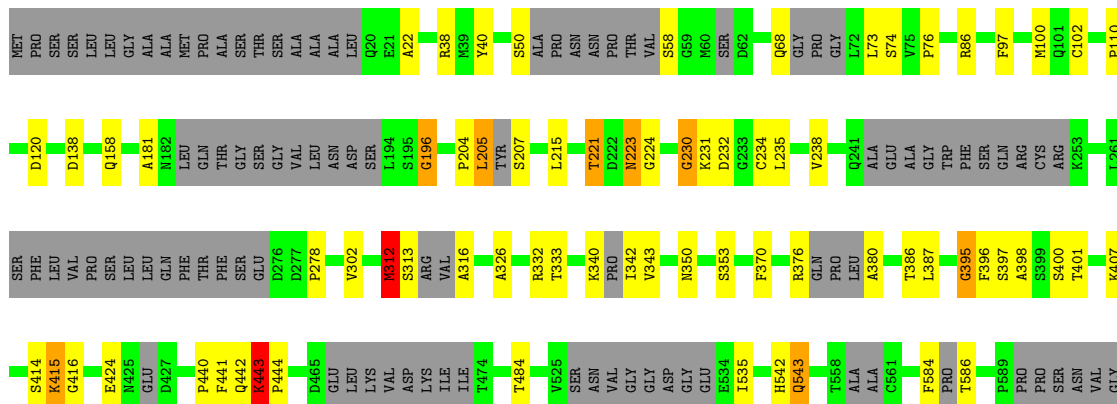
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155





● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

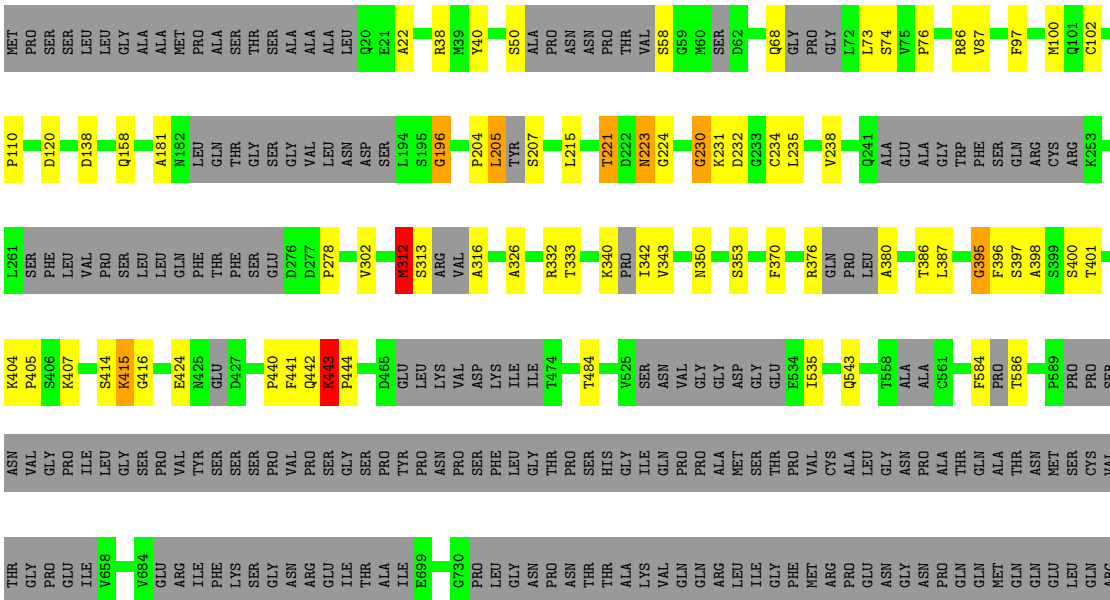
Chain 2-A: 41% 53%

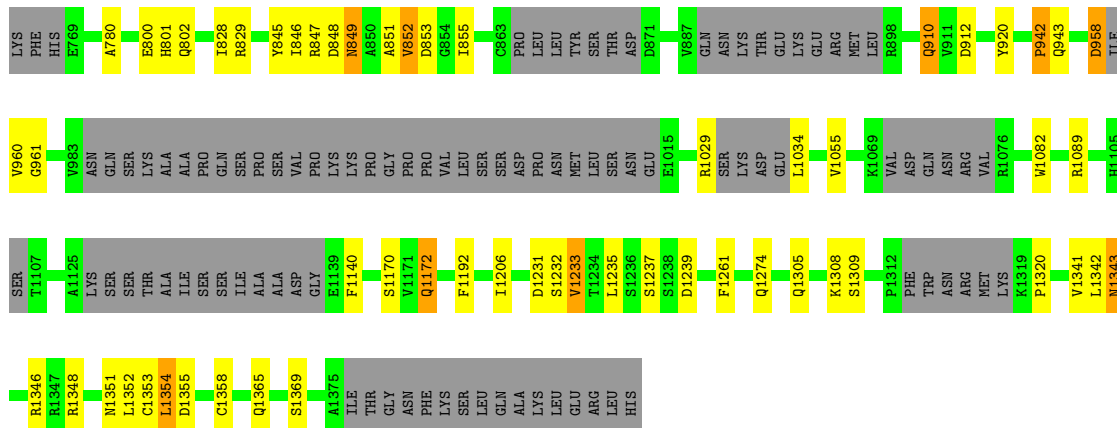




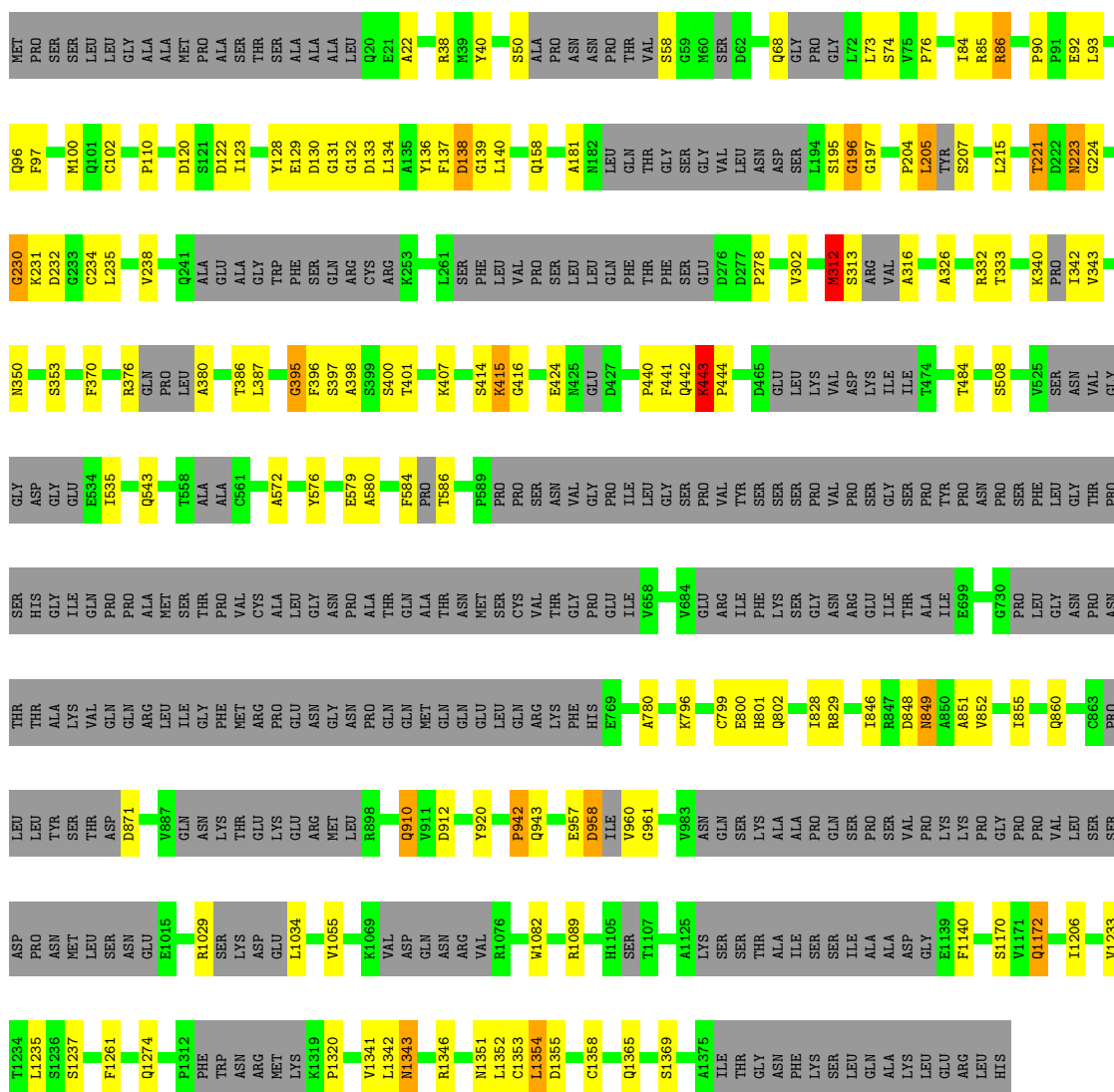
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 2-E: 68% 8% 22%

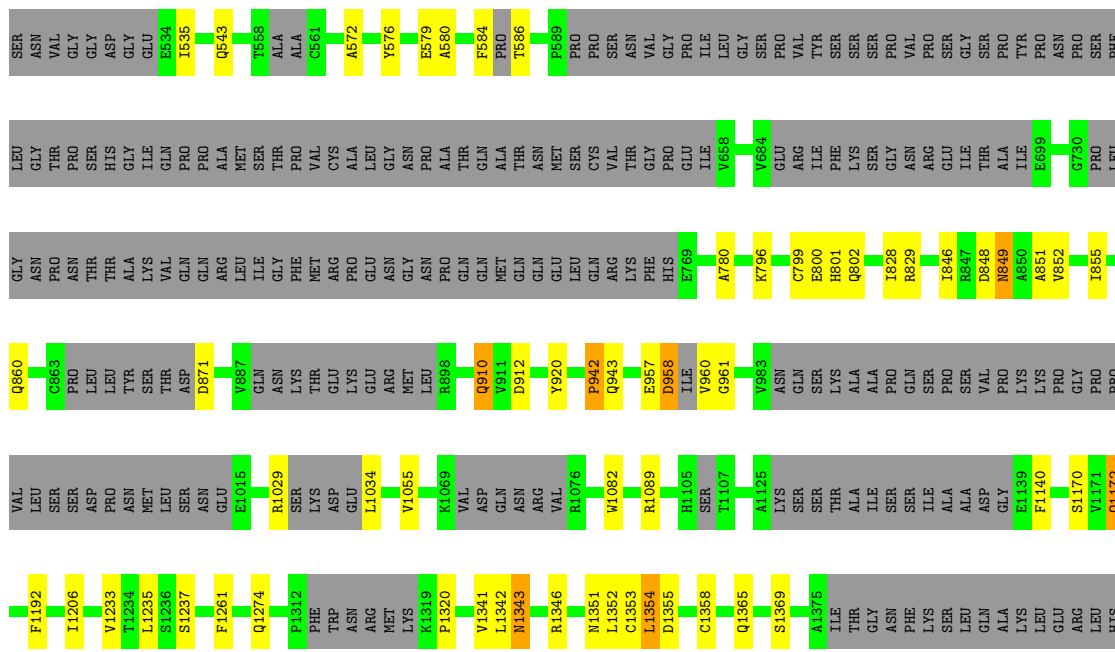




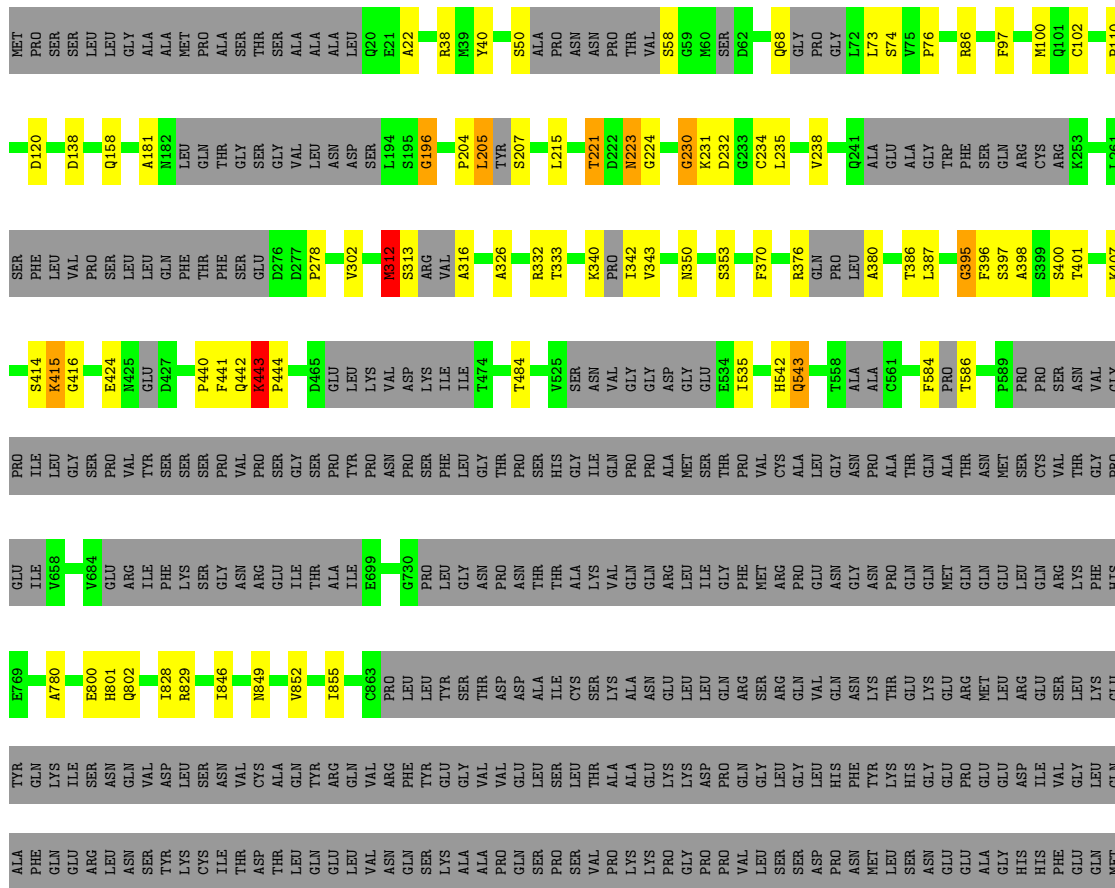
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155



● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

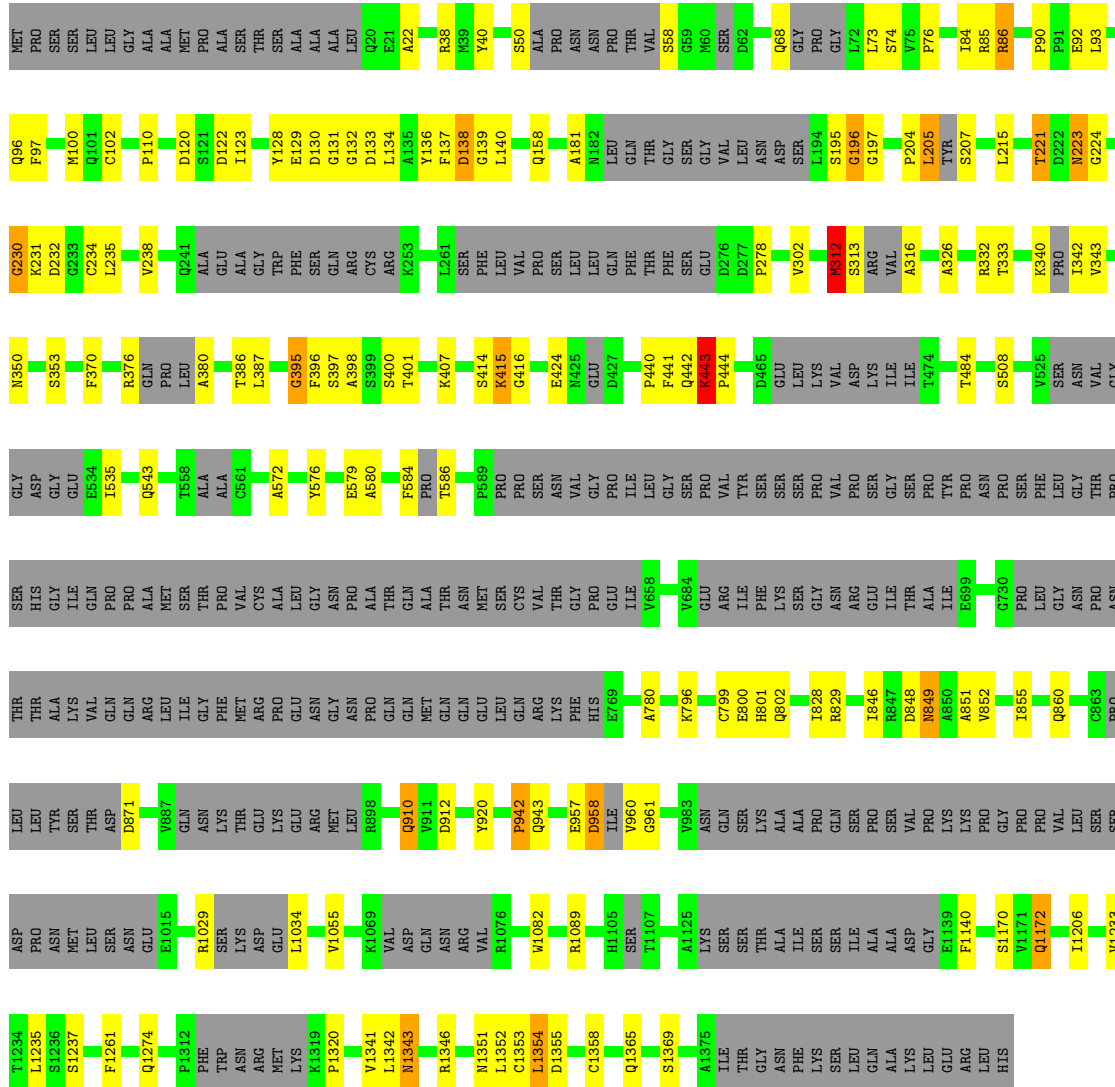


● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155



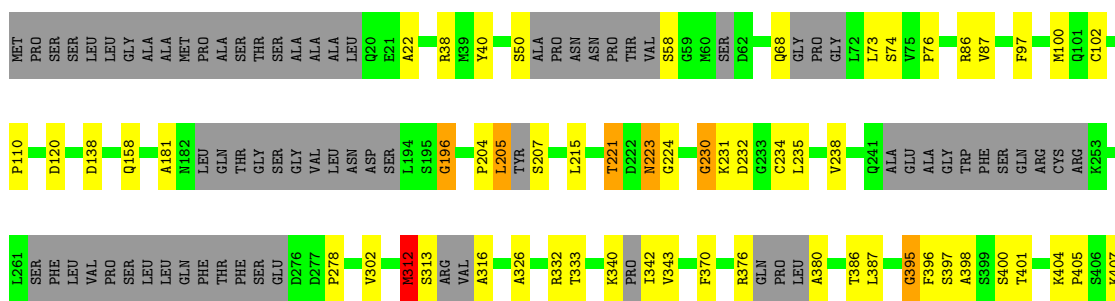
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

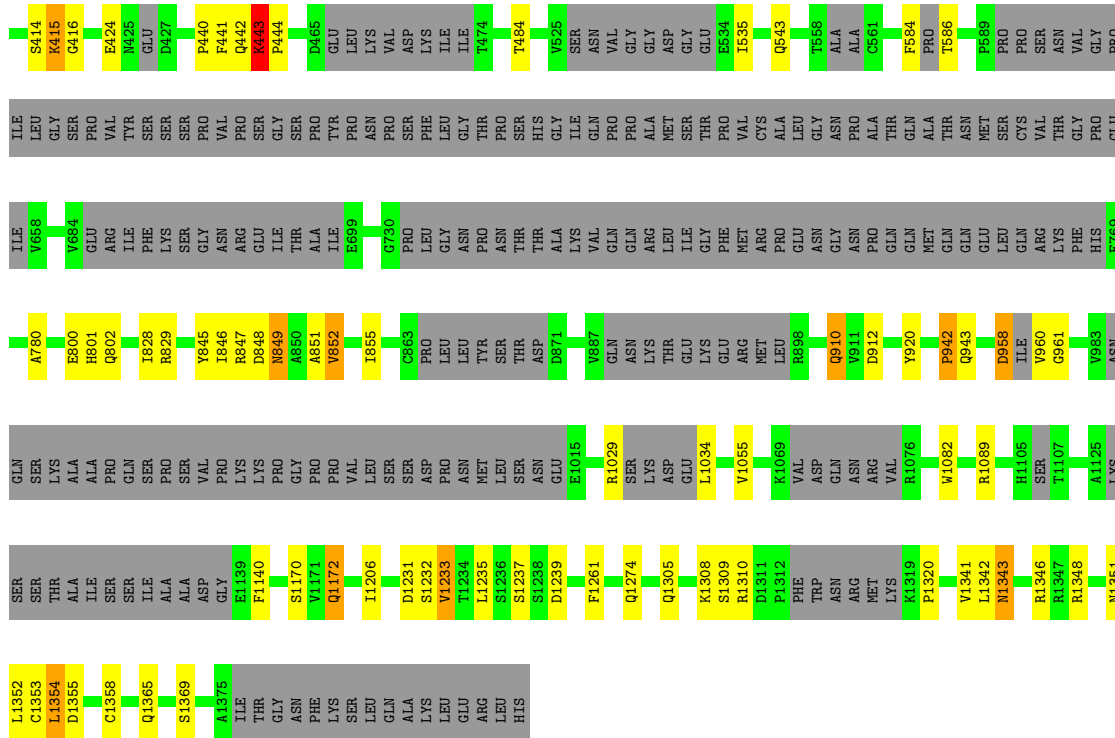
Chain 3-K: 



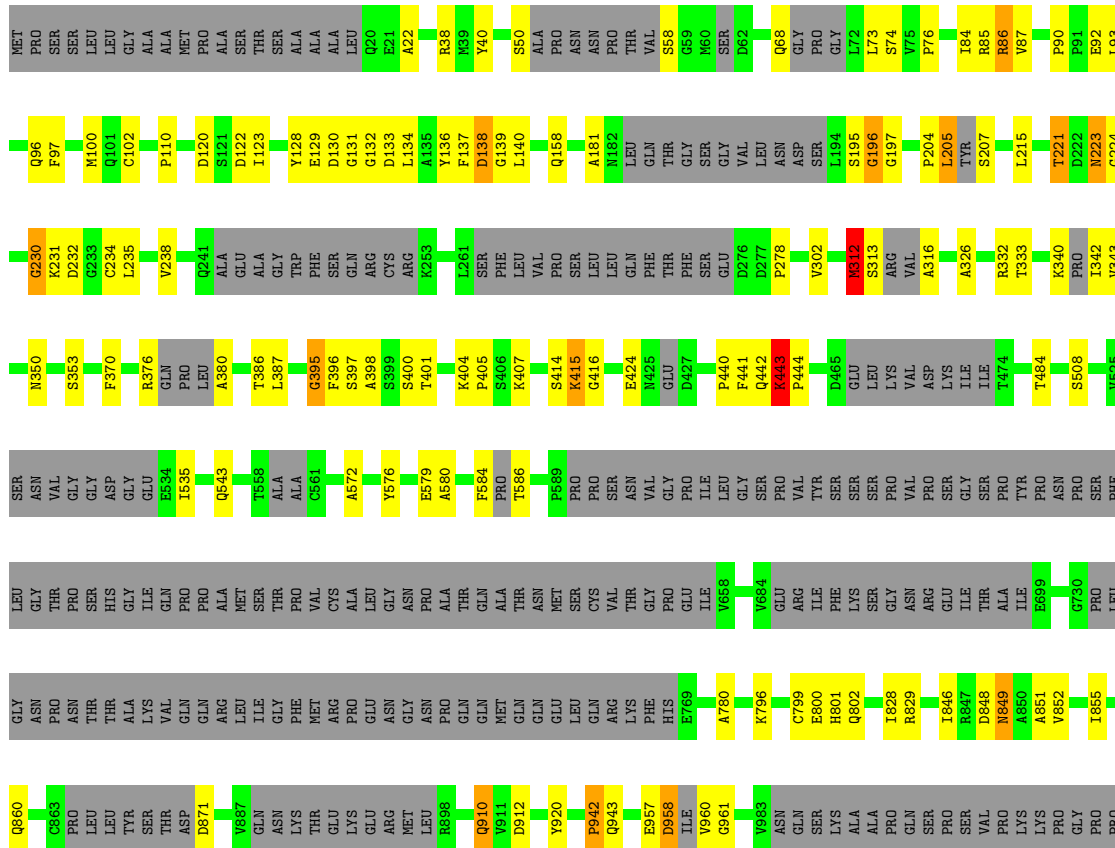
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

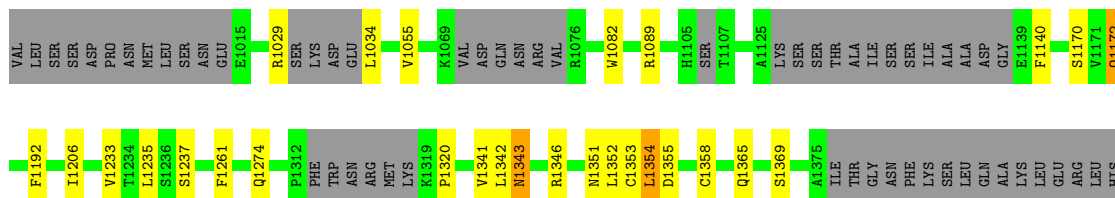
Chain 3-Q: 





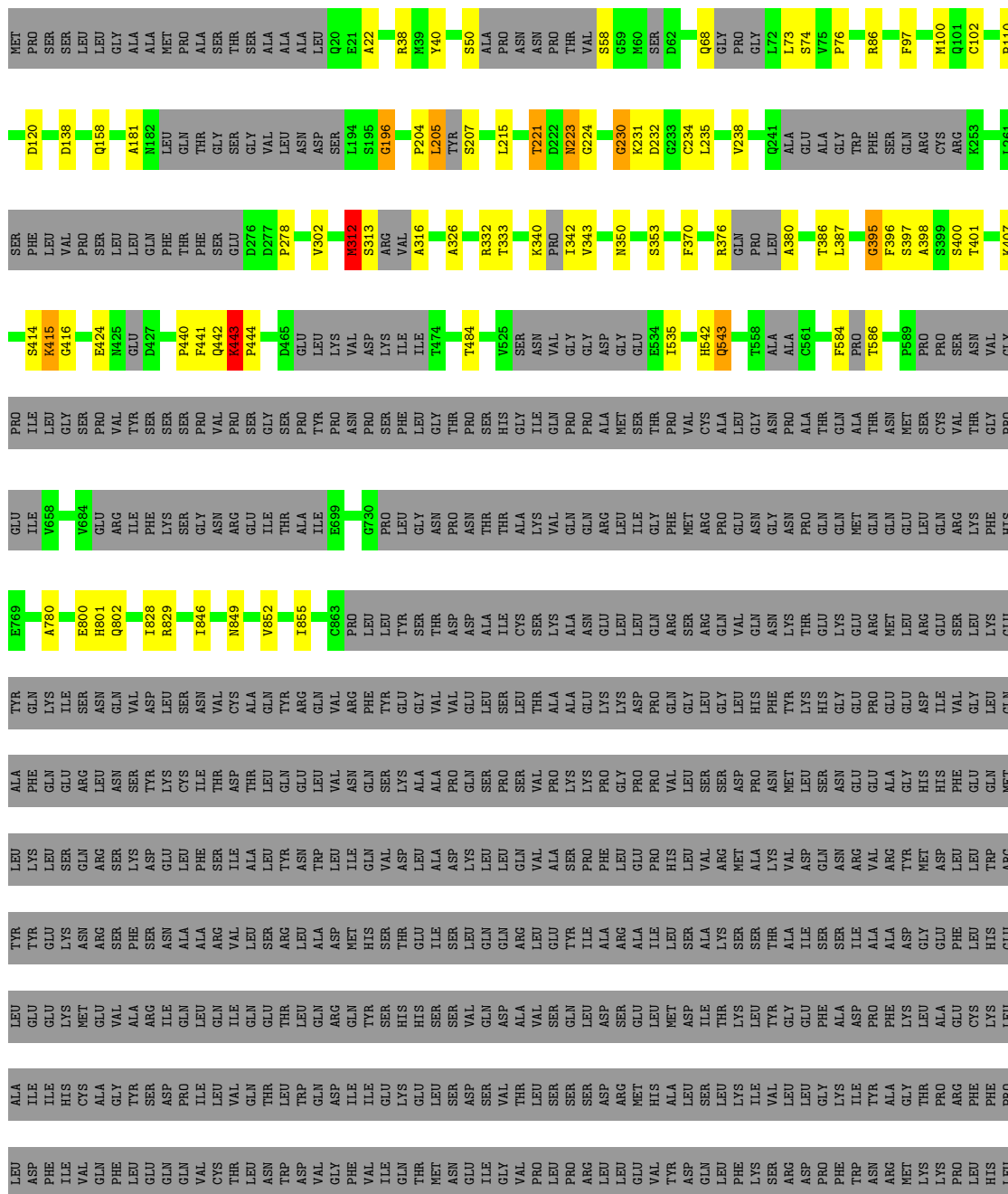
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155





● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

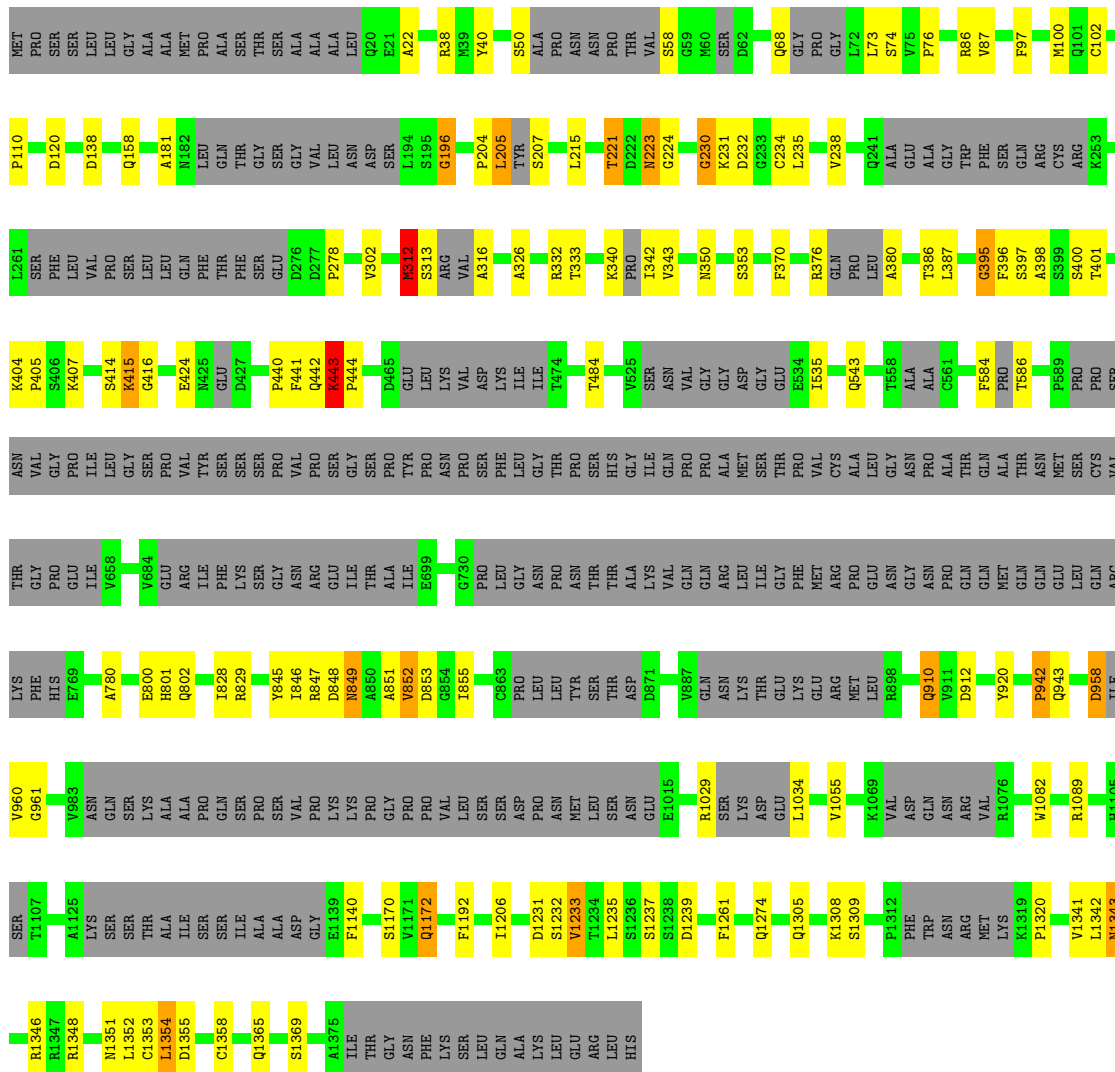
Chain 4-A: 41% 5% 53%



PHE
LYS
SER
LEU
GLN
ALA
LYS
LEU
GLU
ARG
LEU
HIS

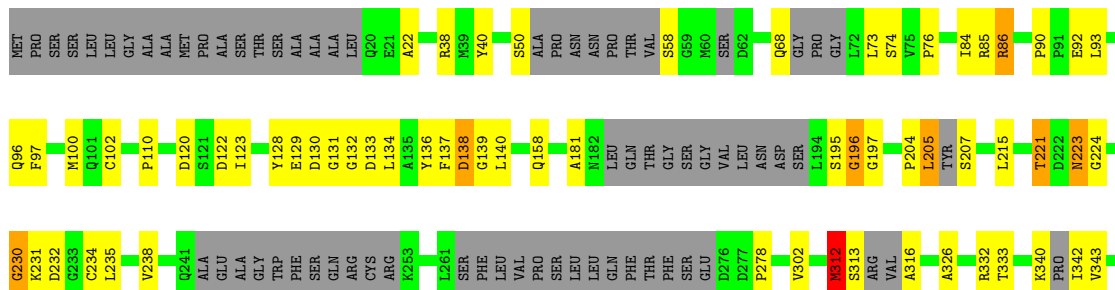
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

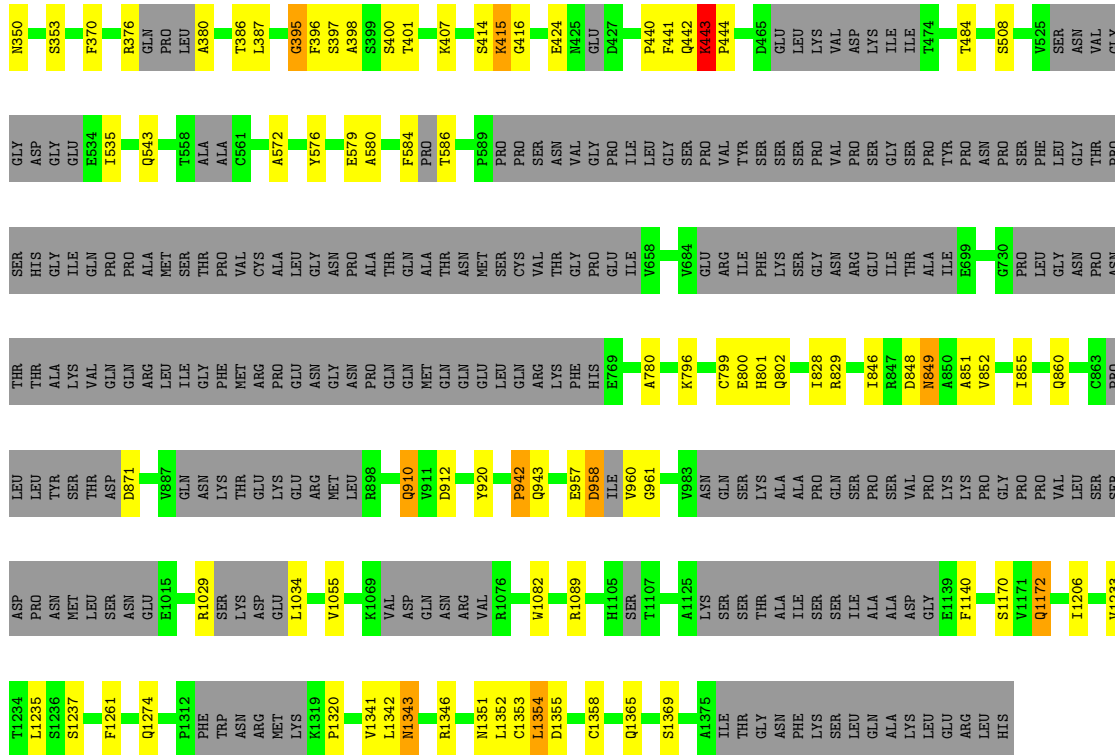
Chain 4-E: 68% 8% 22%



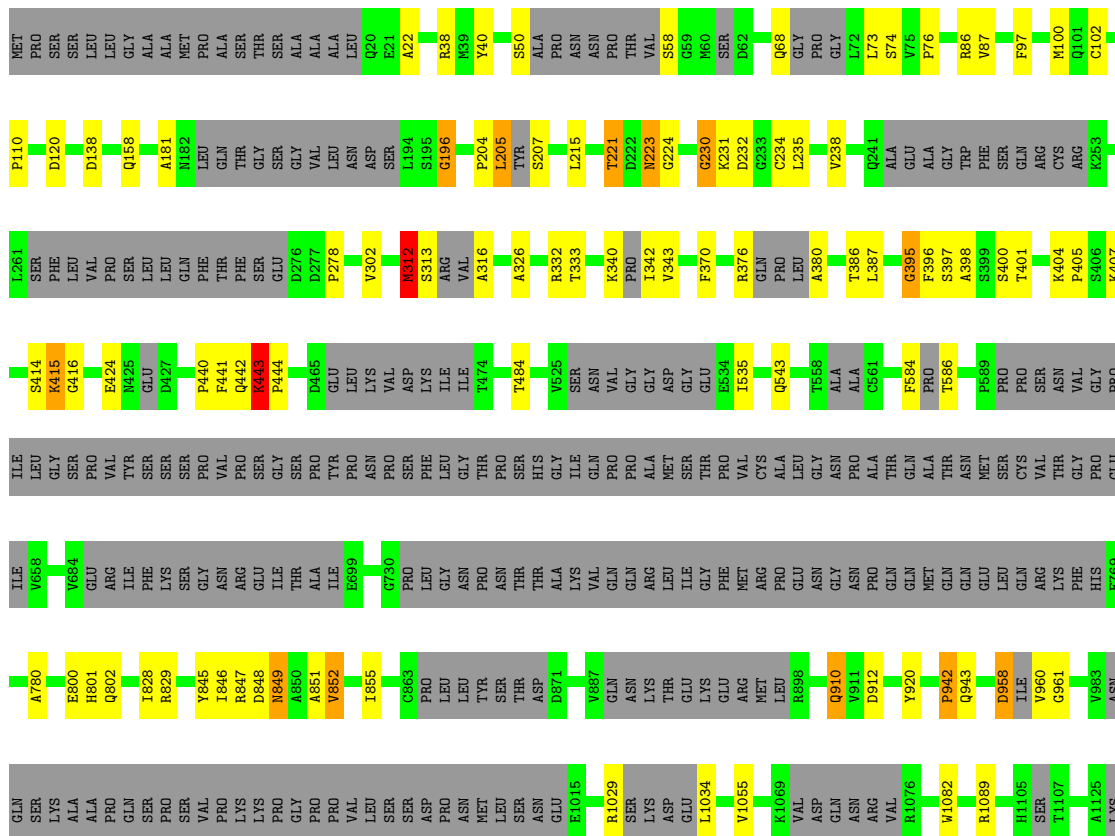
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

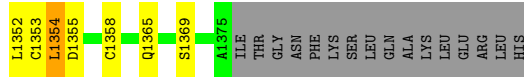
Chain 4-K: 67% 9% 22%



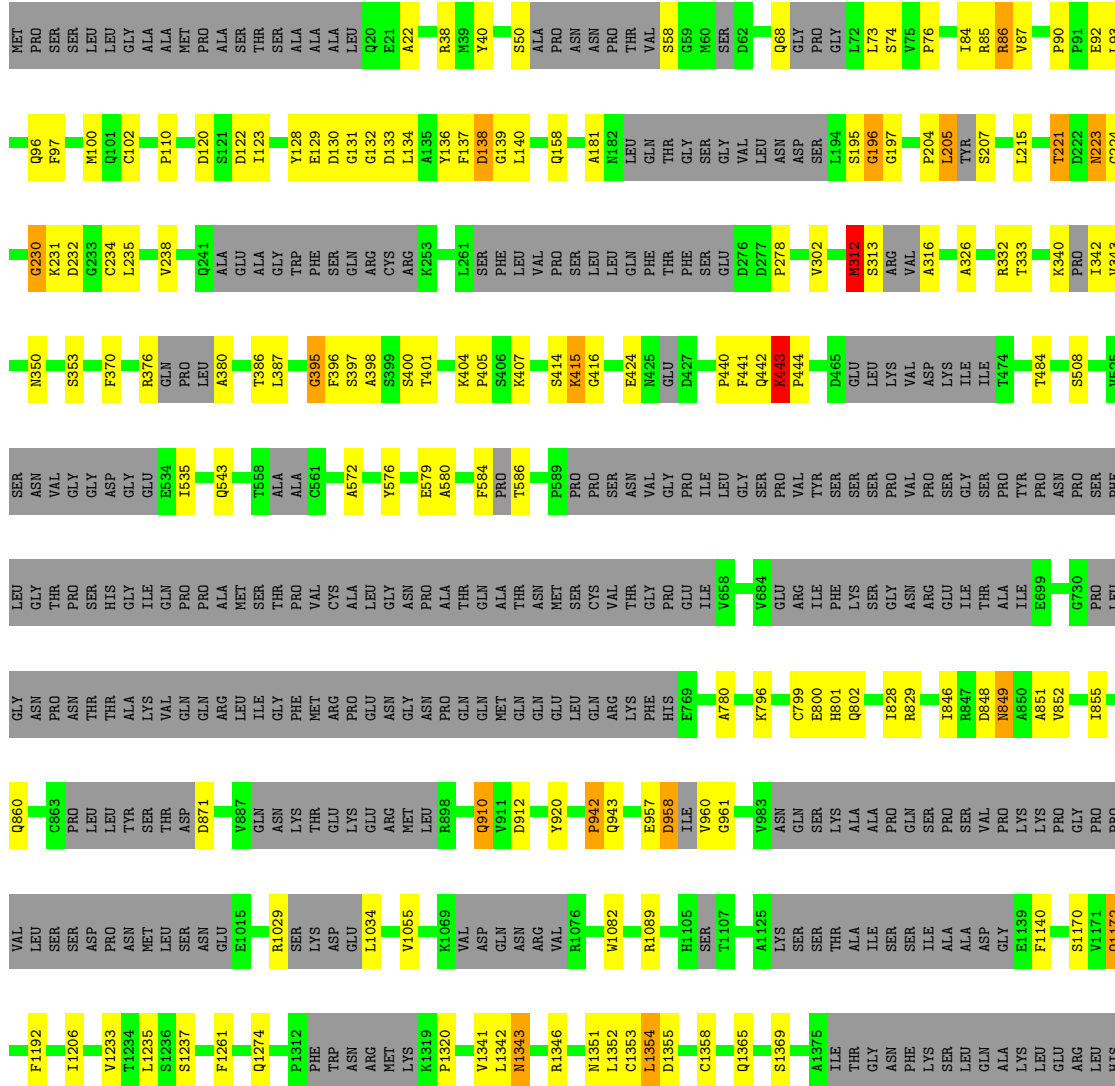


● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

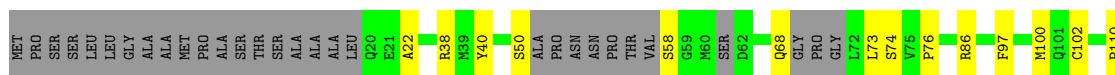


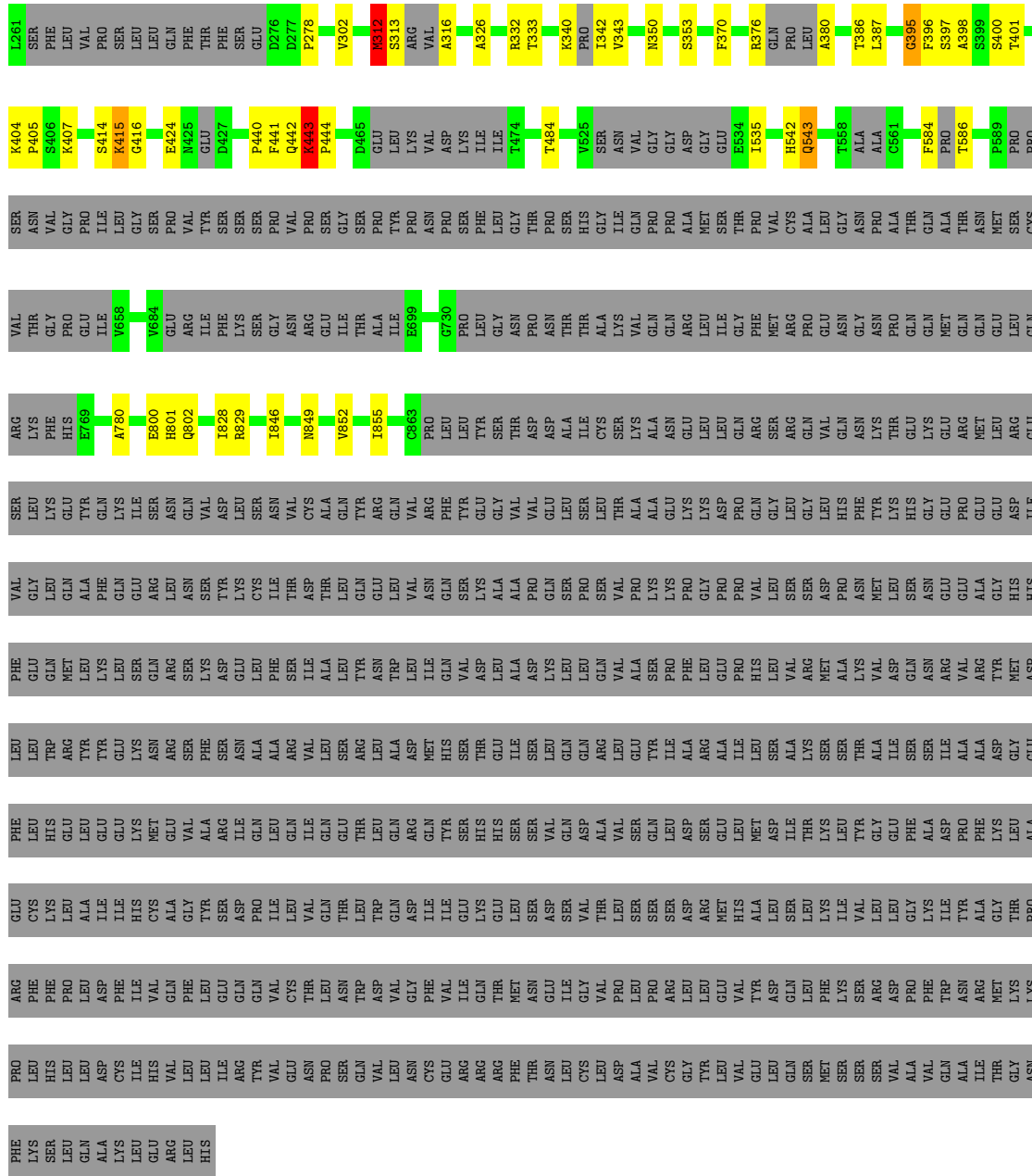


● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

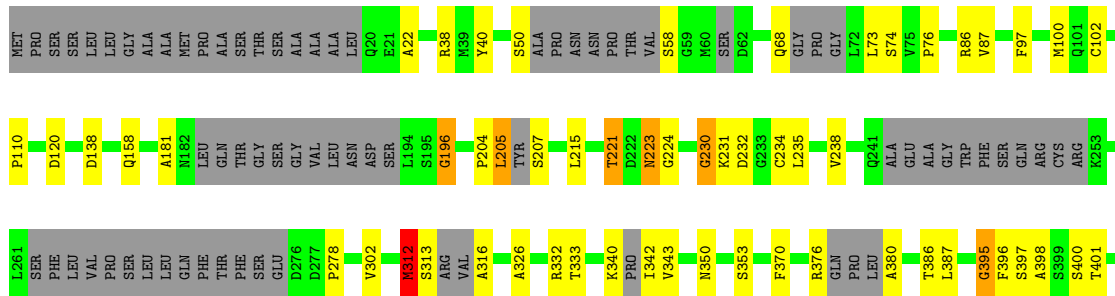


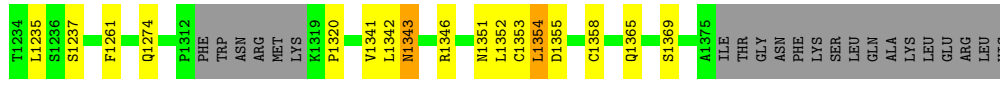
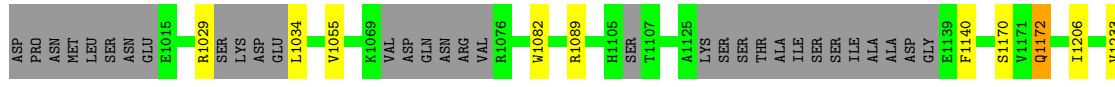
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155





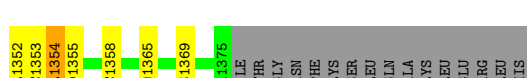
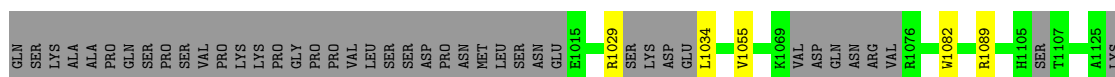
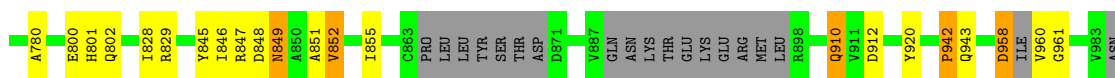
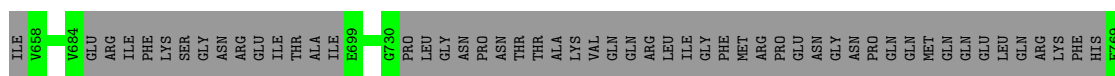
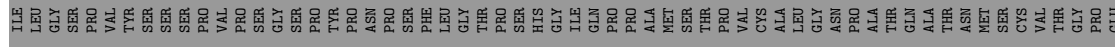
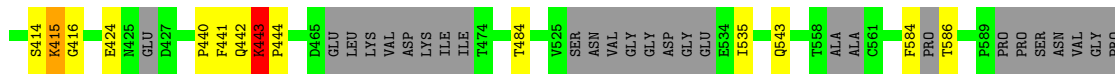
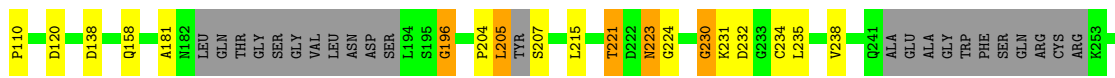
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155





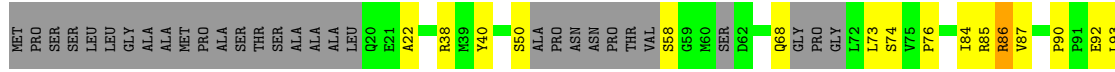
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

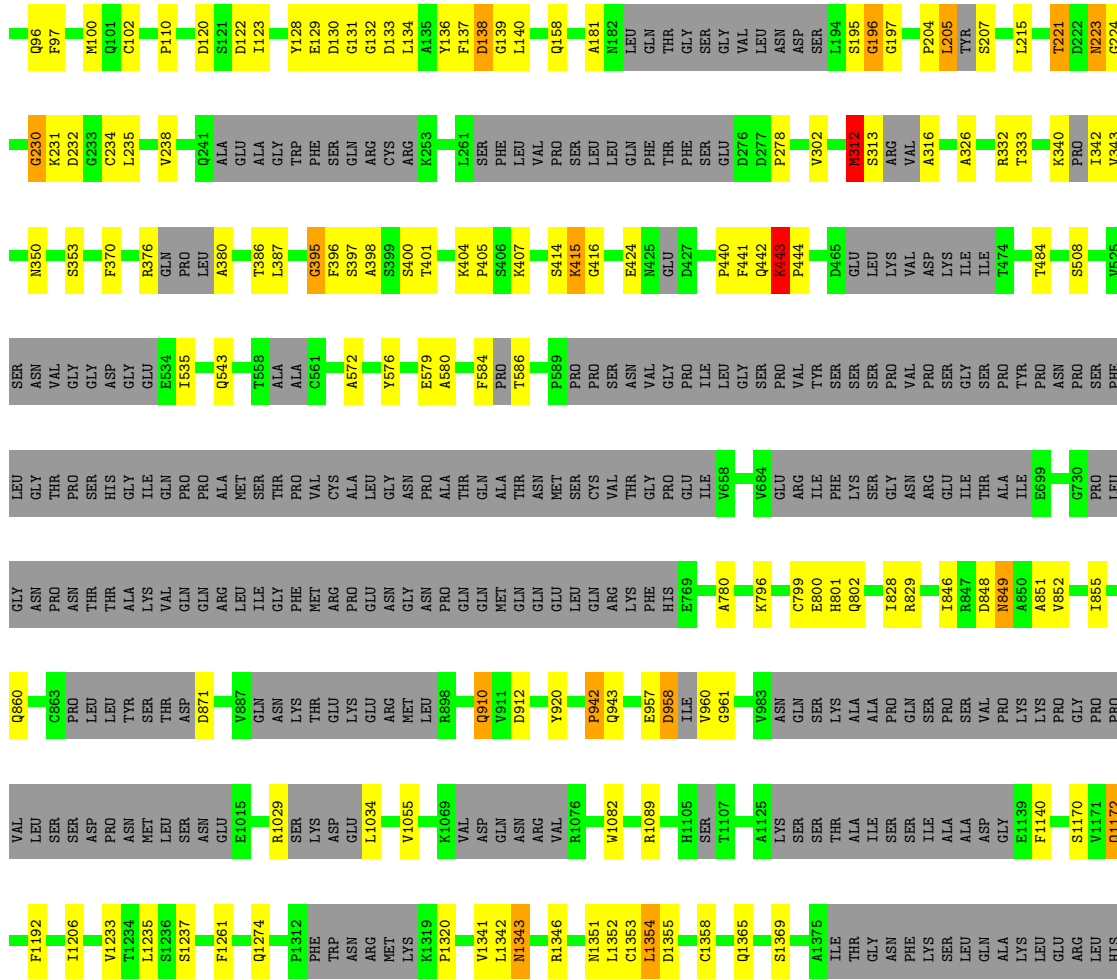
Chain 5-Q: 69% 8% 22%



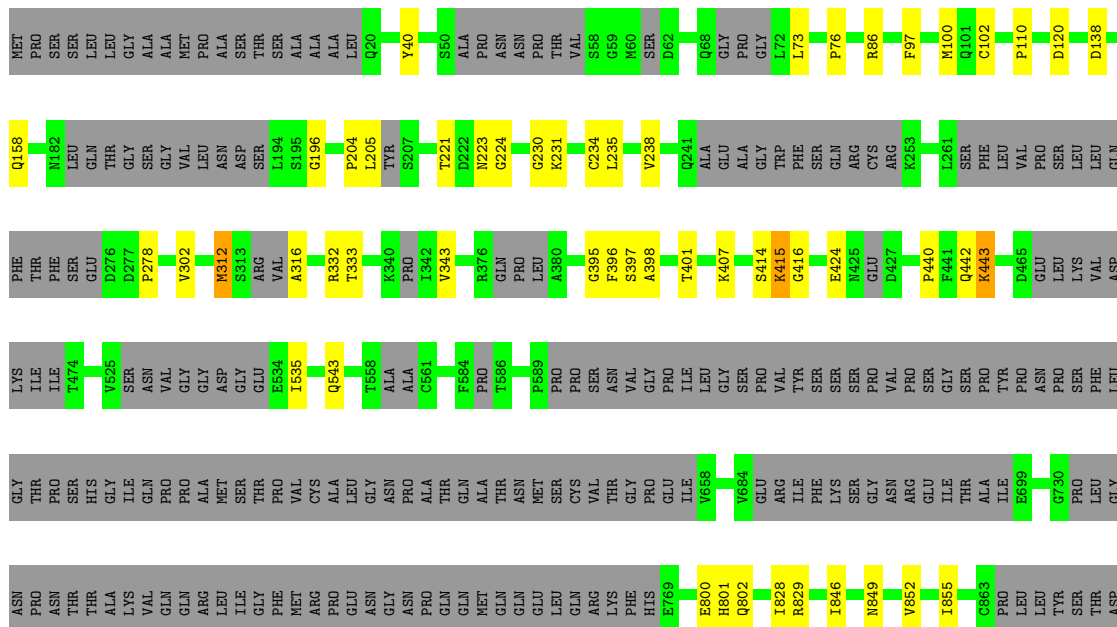
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

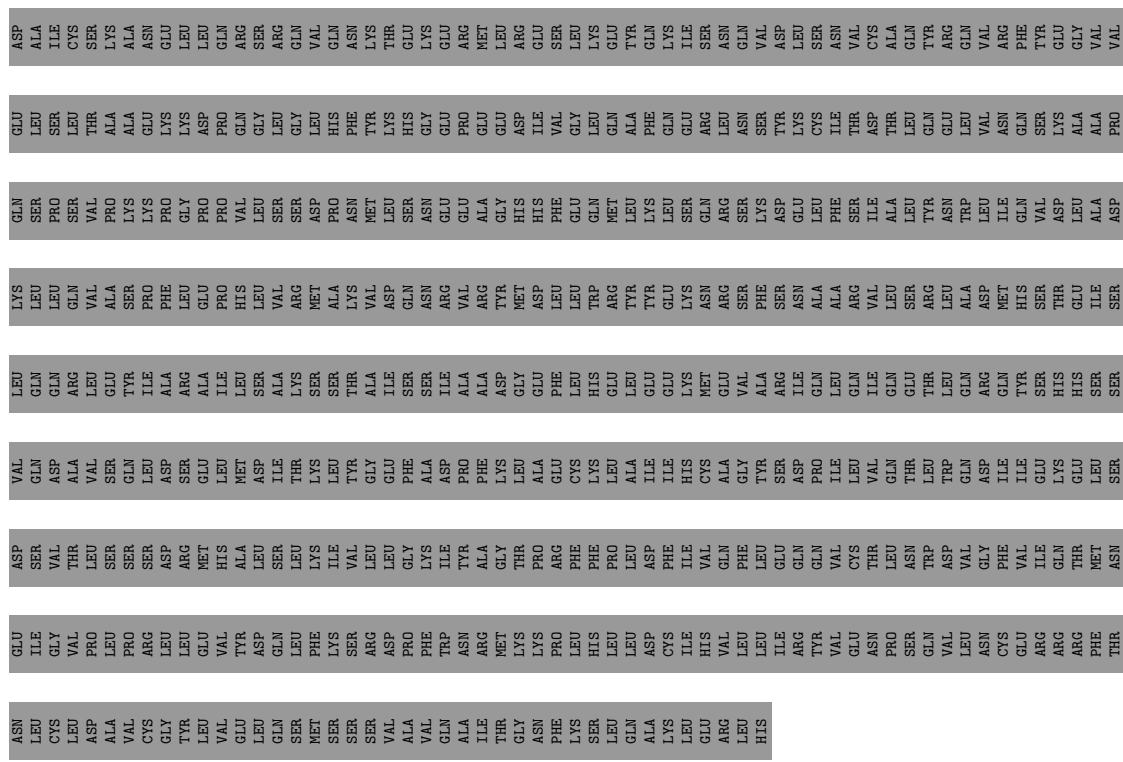
Chain 5-W: 67% 10% 22%



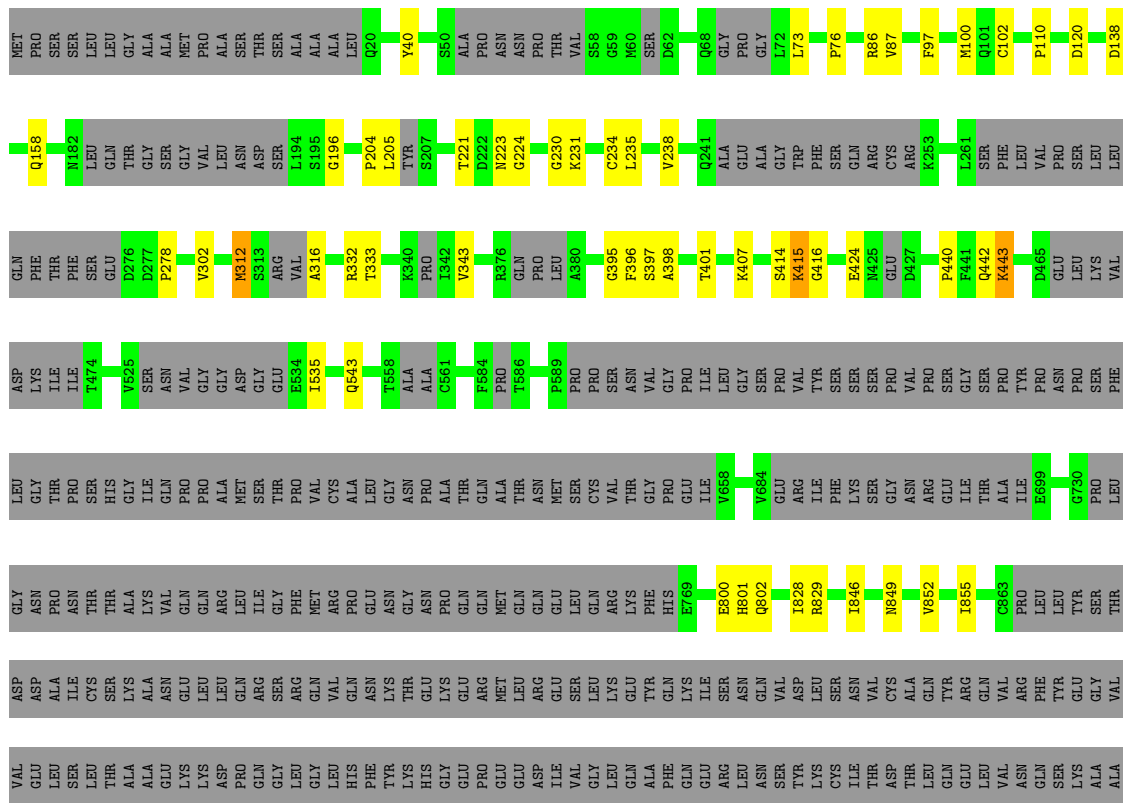


● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

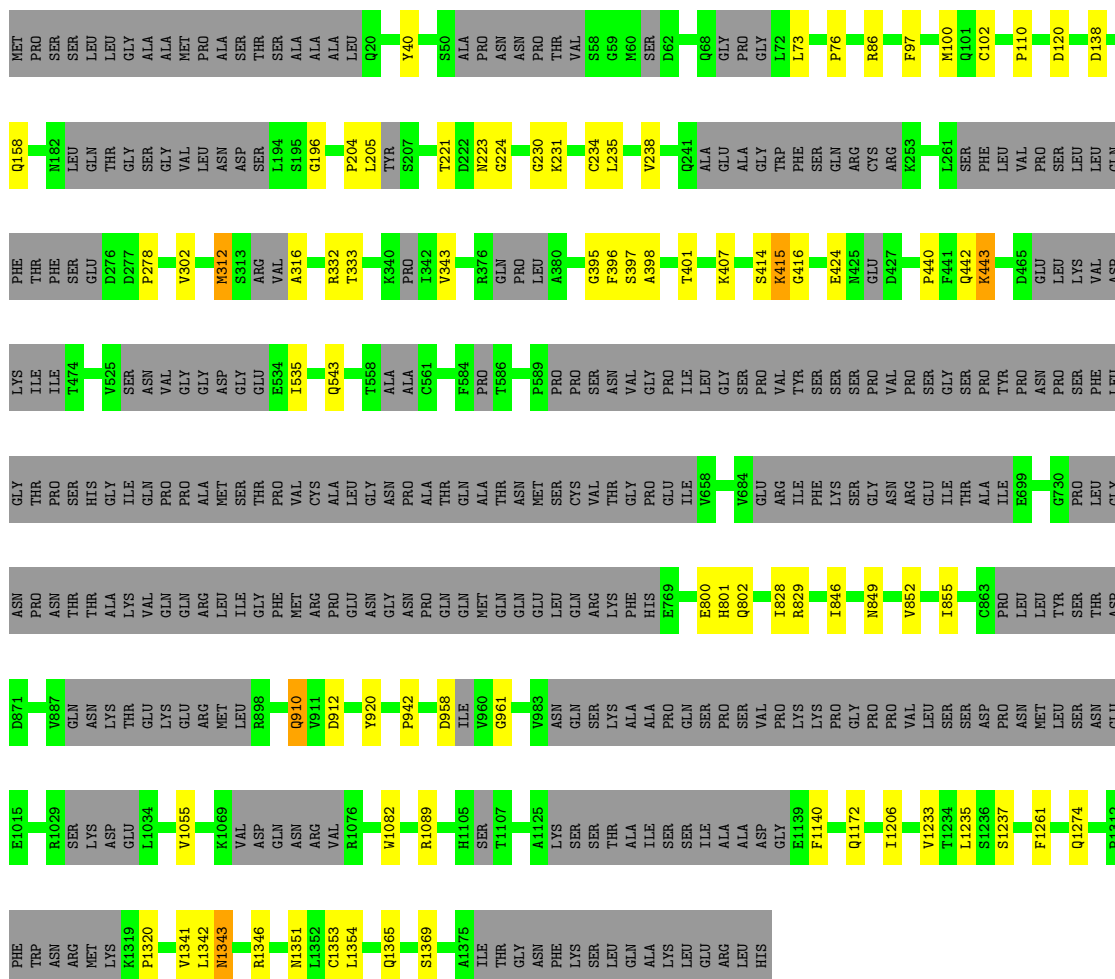




● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

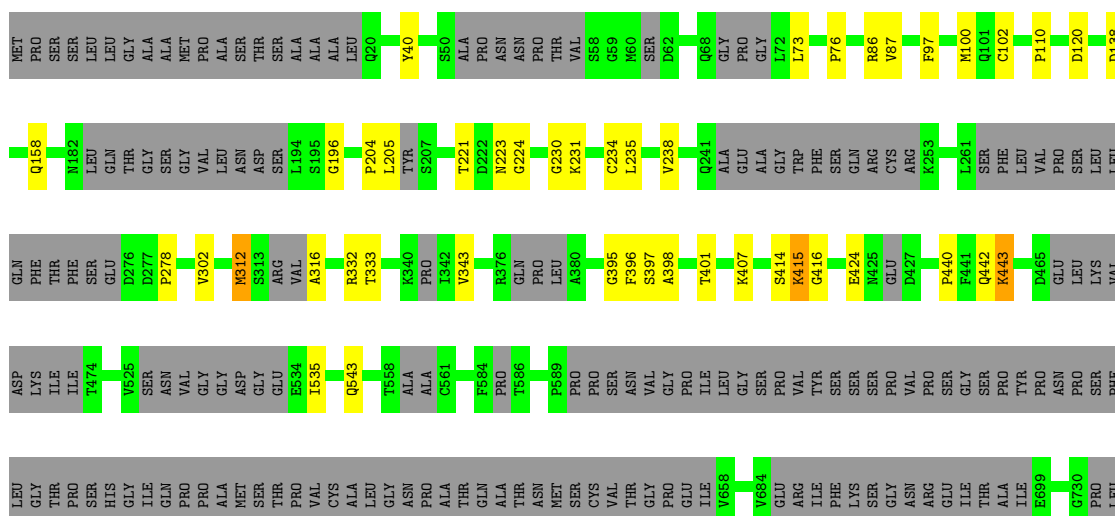


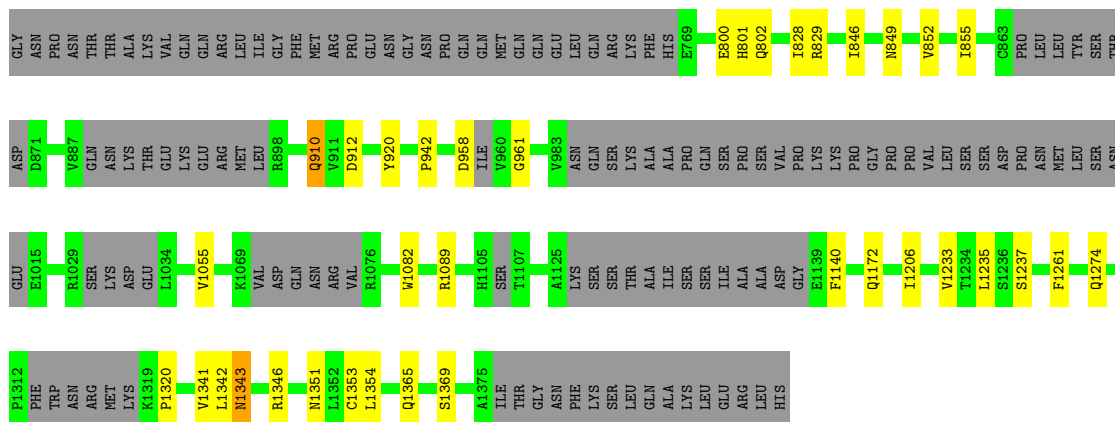
Chain 6-K: 72% 5% 22%



● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

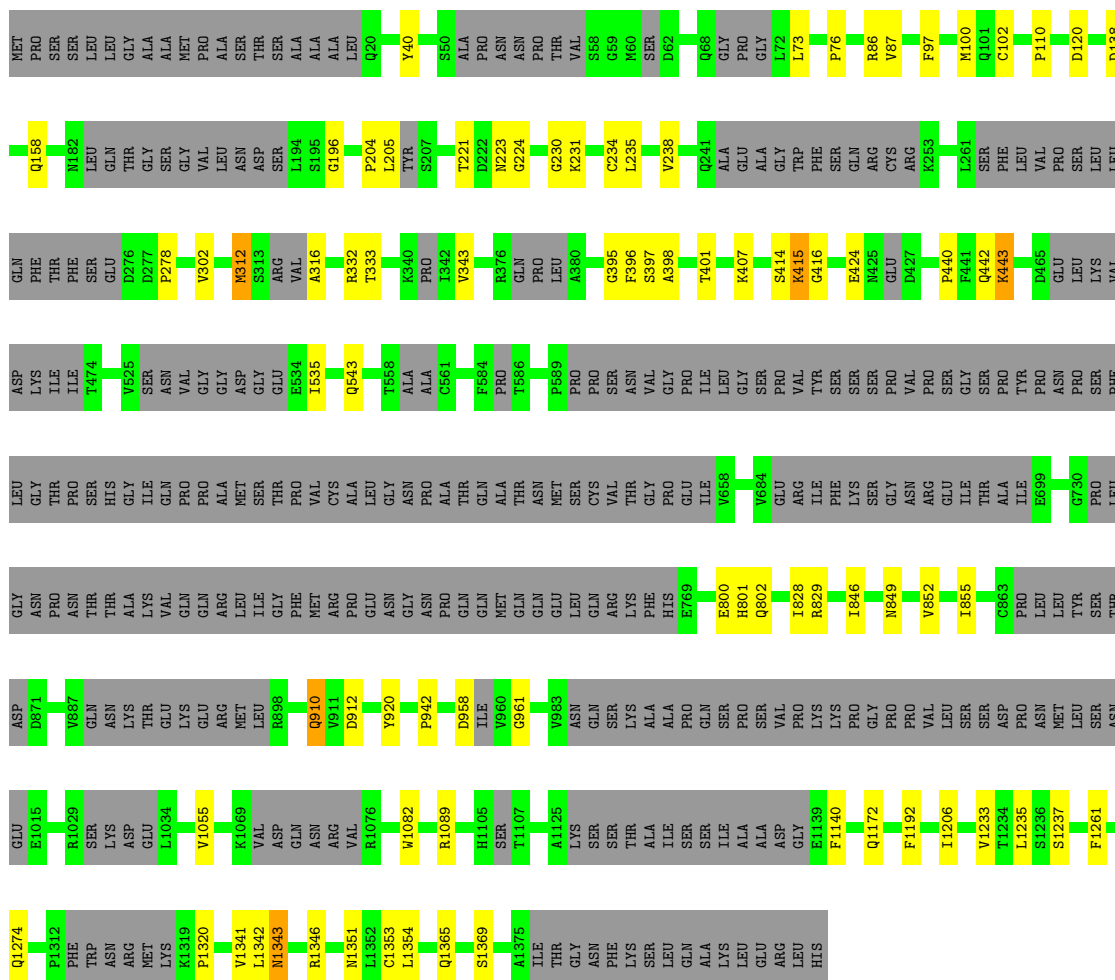
Chain 6-Q: 72% 5% 22%





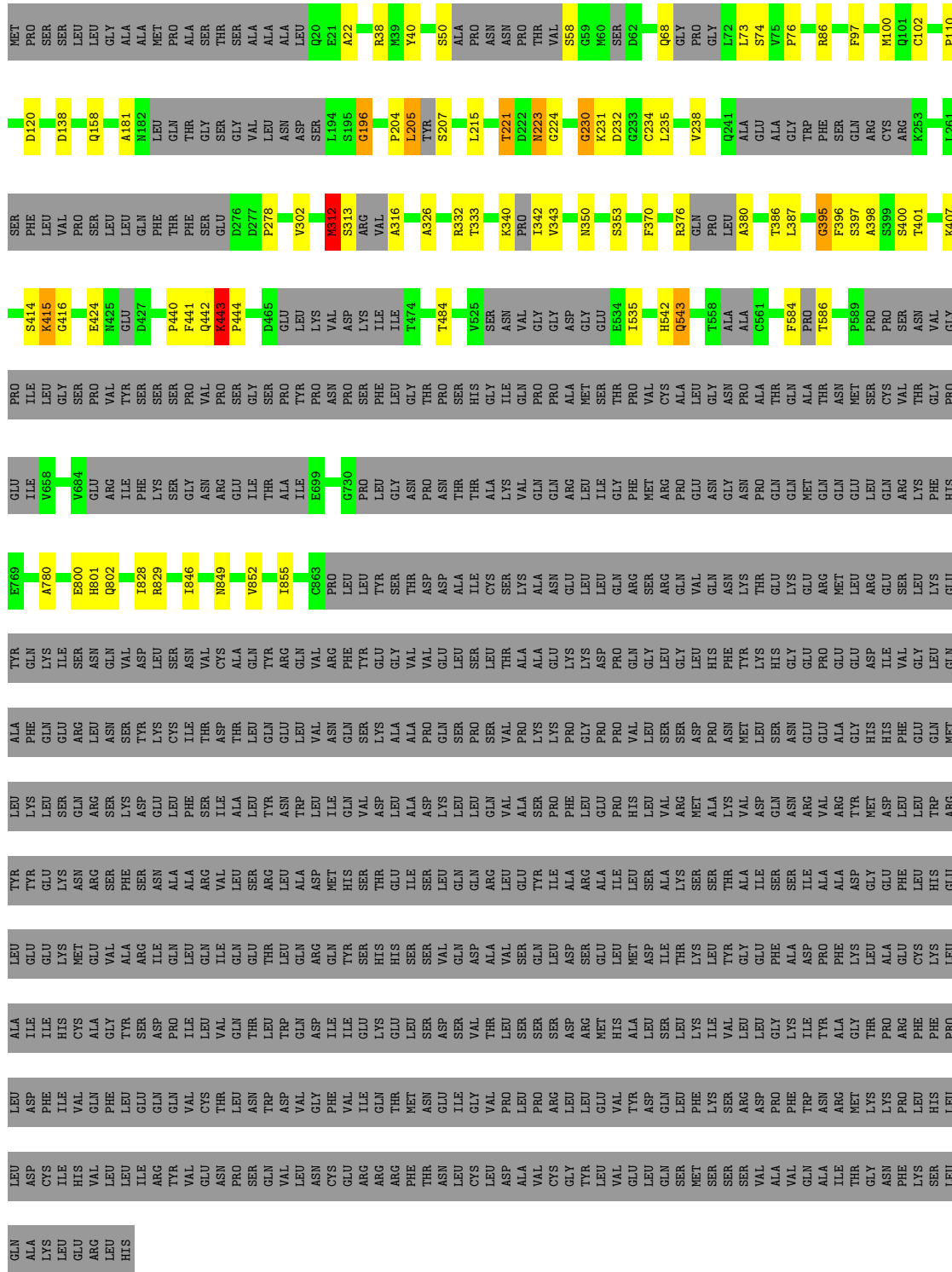
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 6-W: 72% 6% 22%

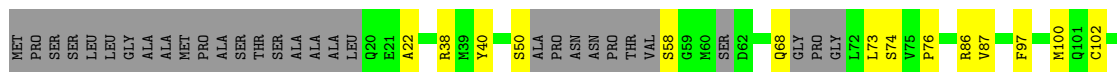


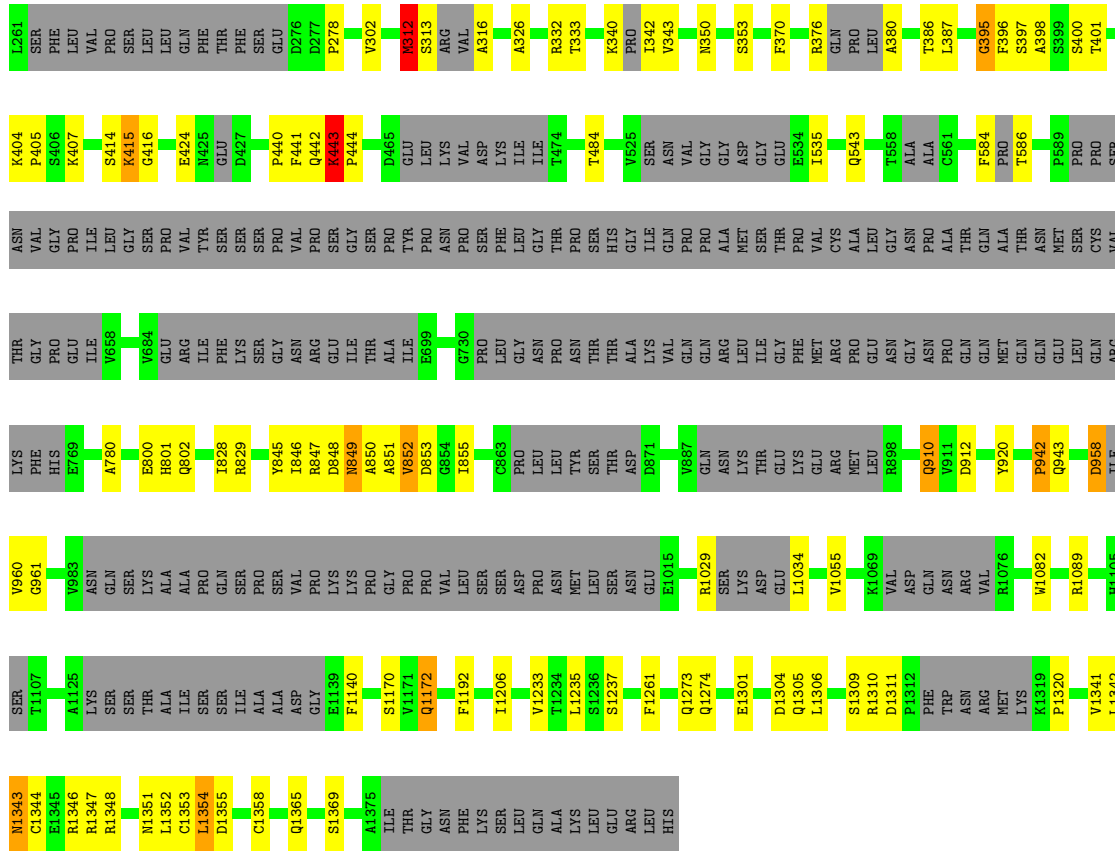
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 7-A: 41% 5% 53%

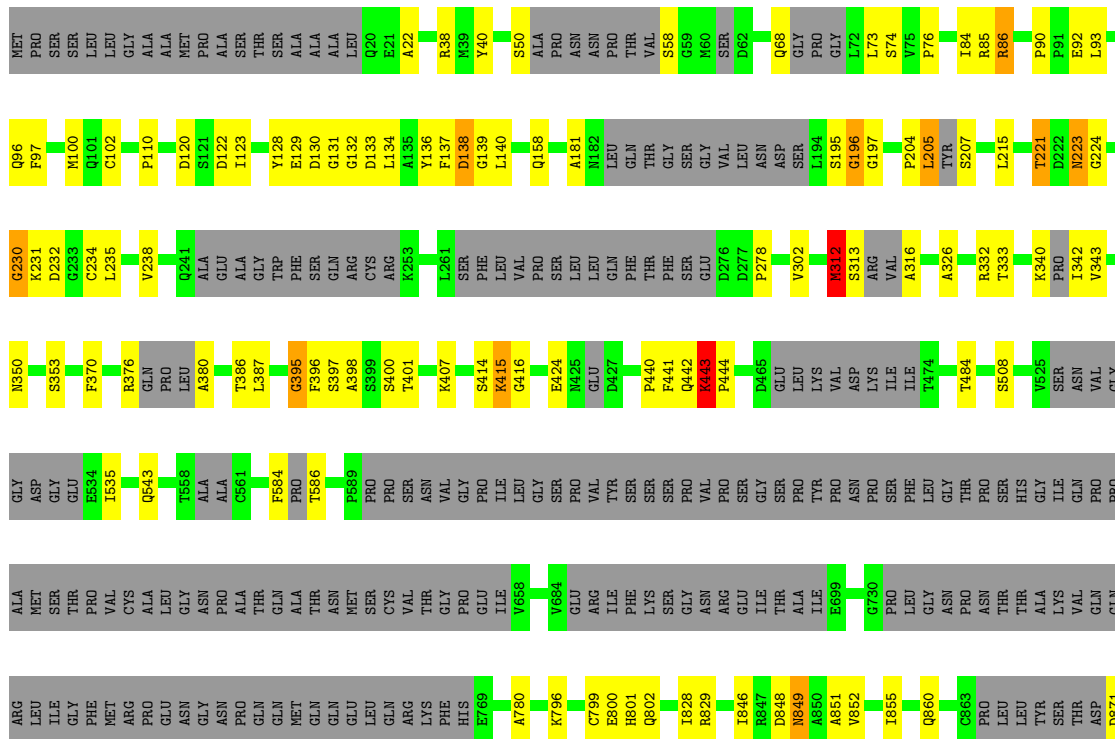


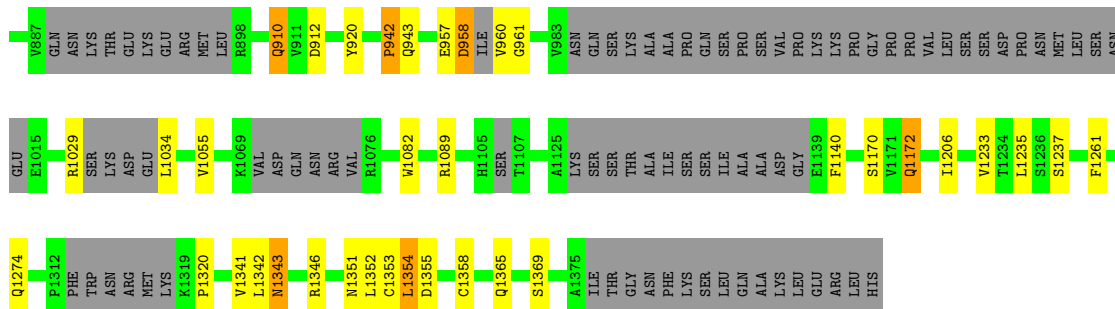
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155



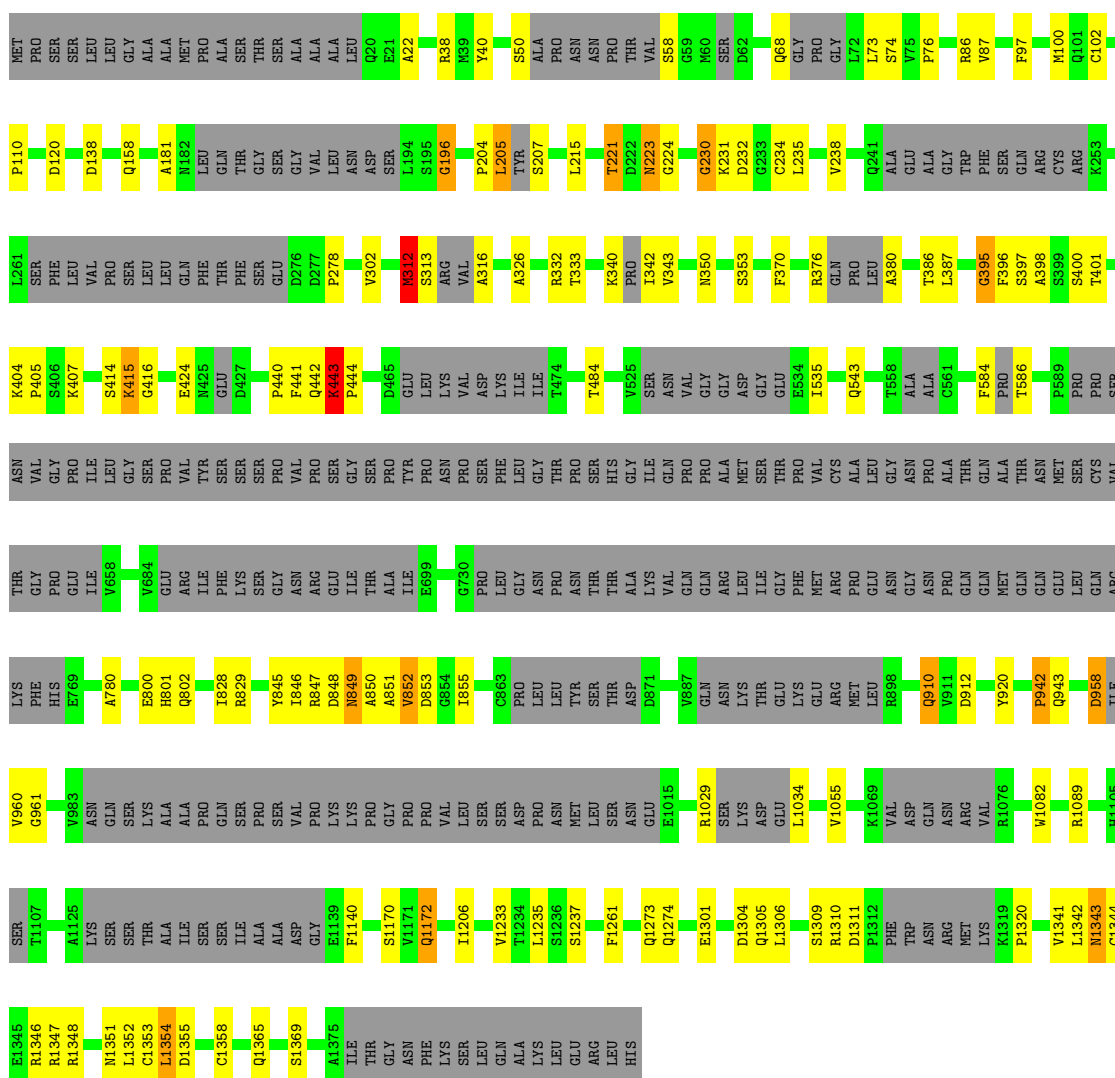


• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155



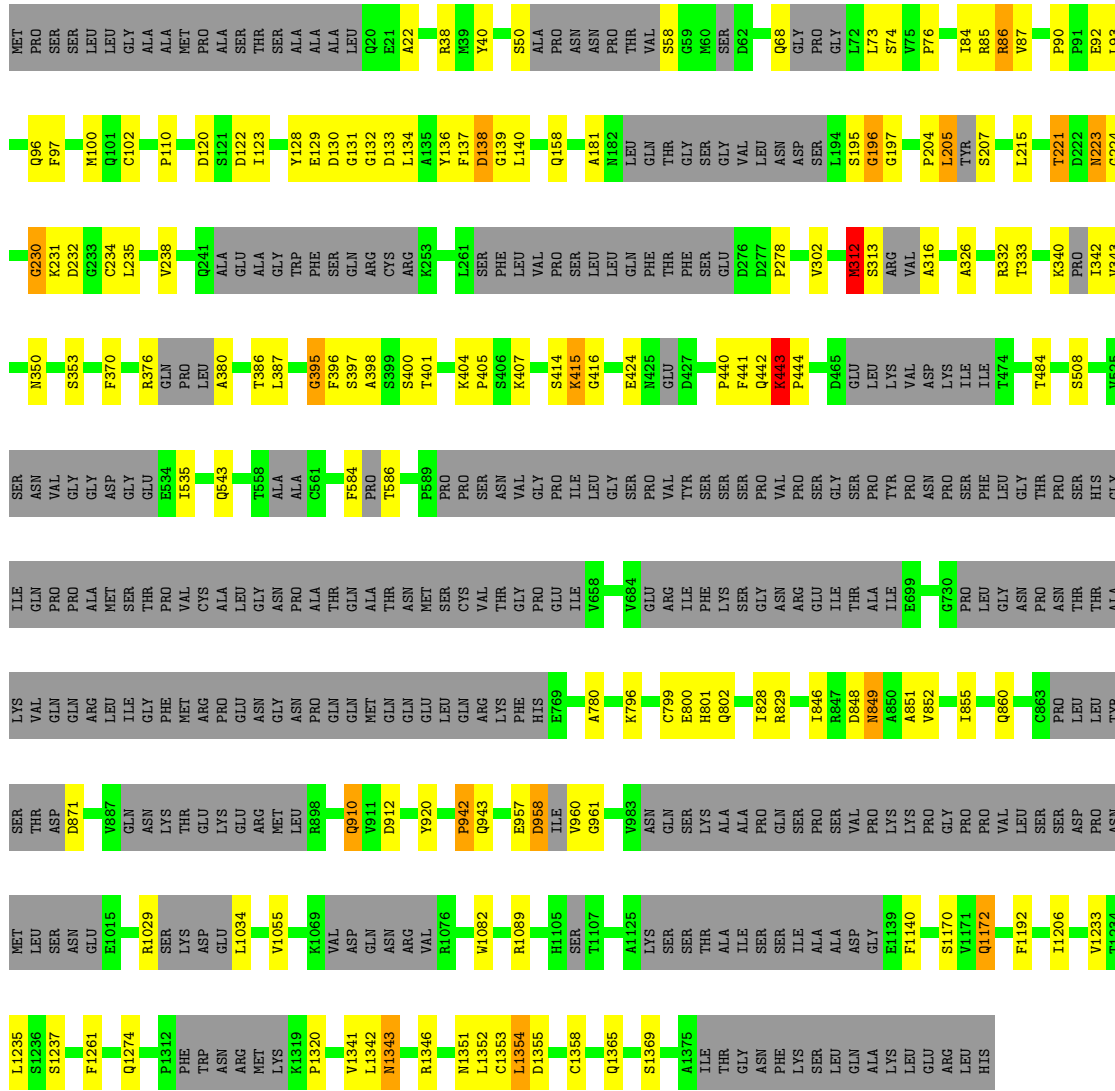


● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

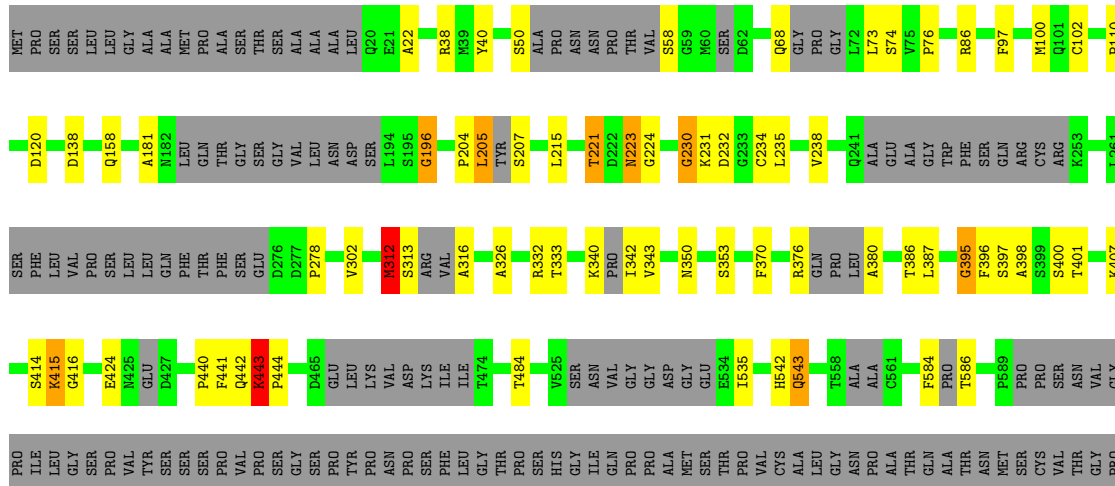


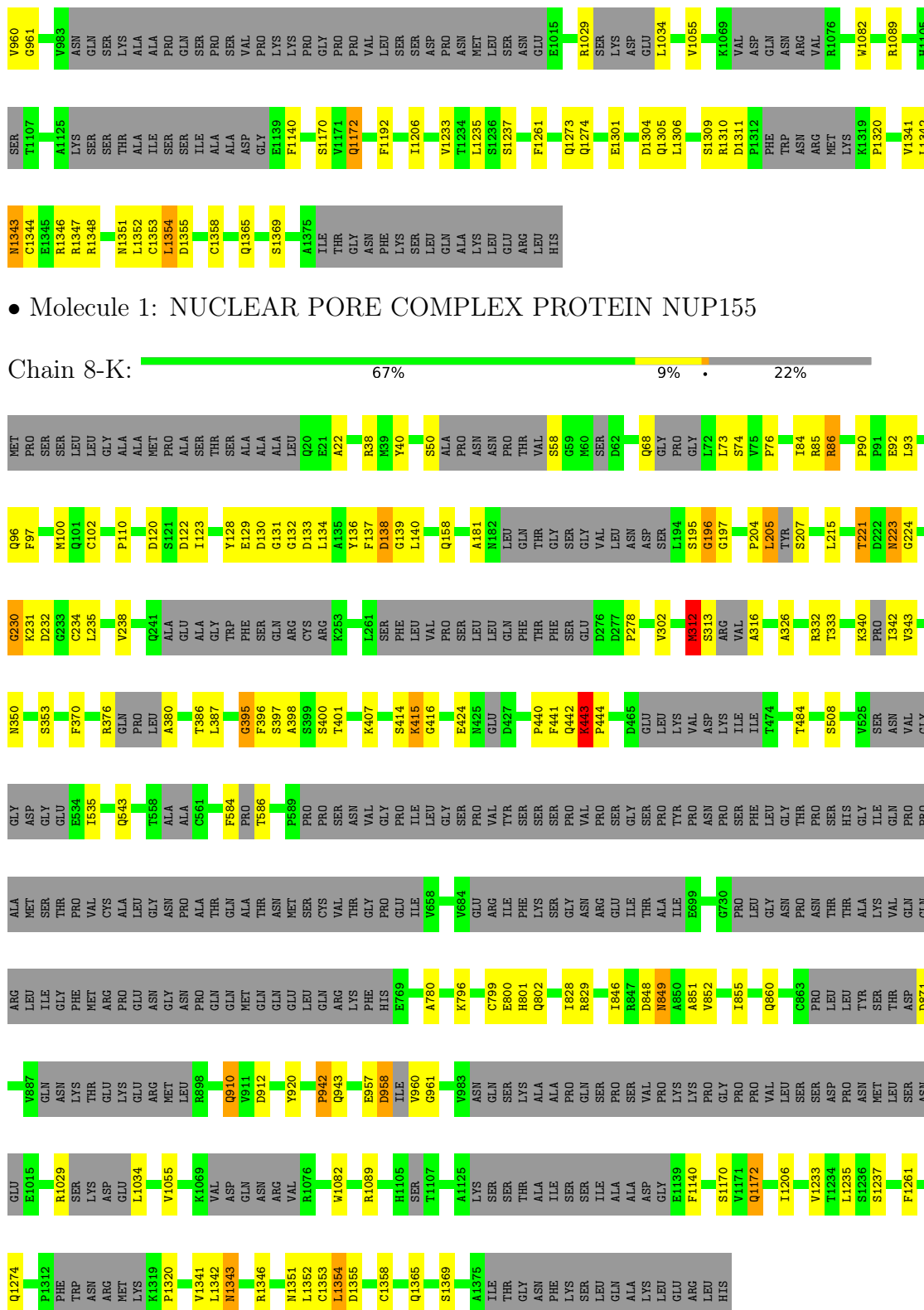
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155





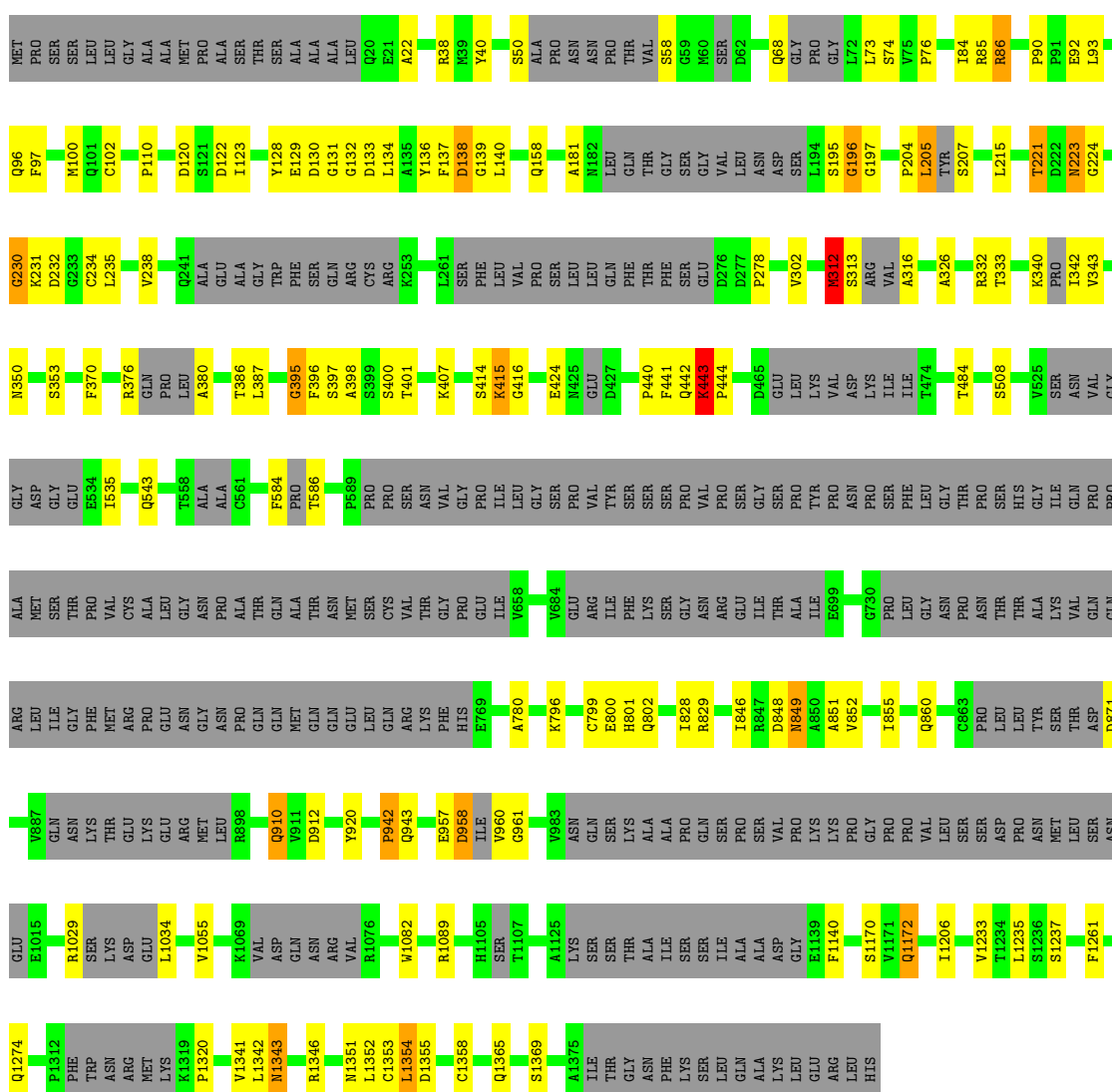
● Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155





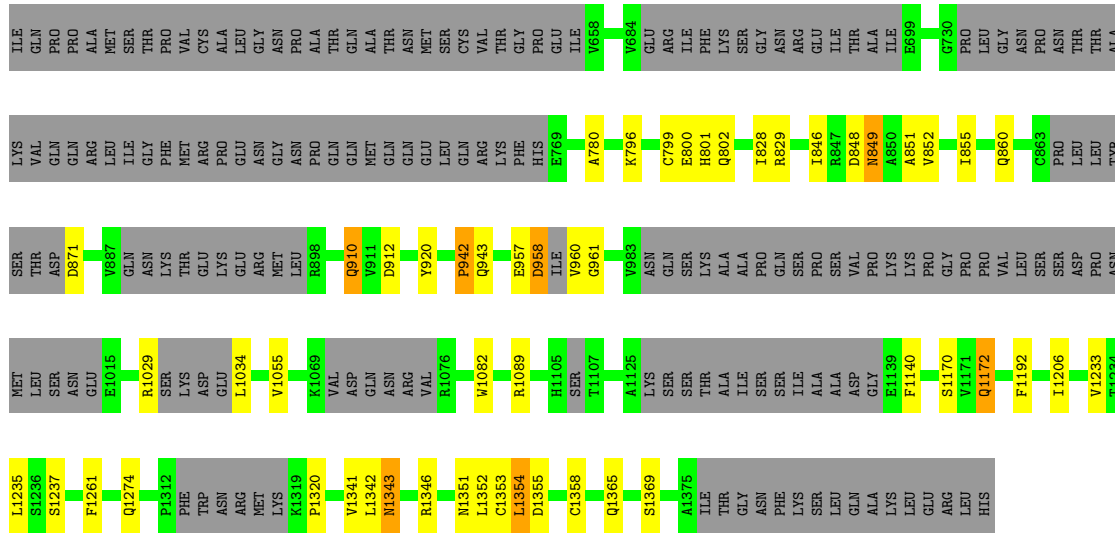
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 8-K: 67% 9% 22%

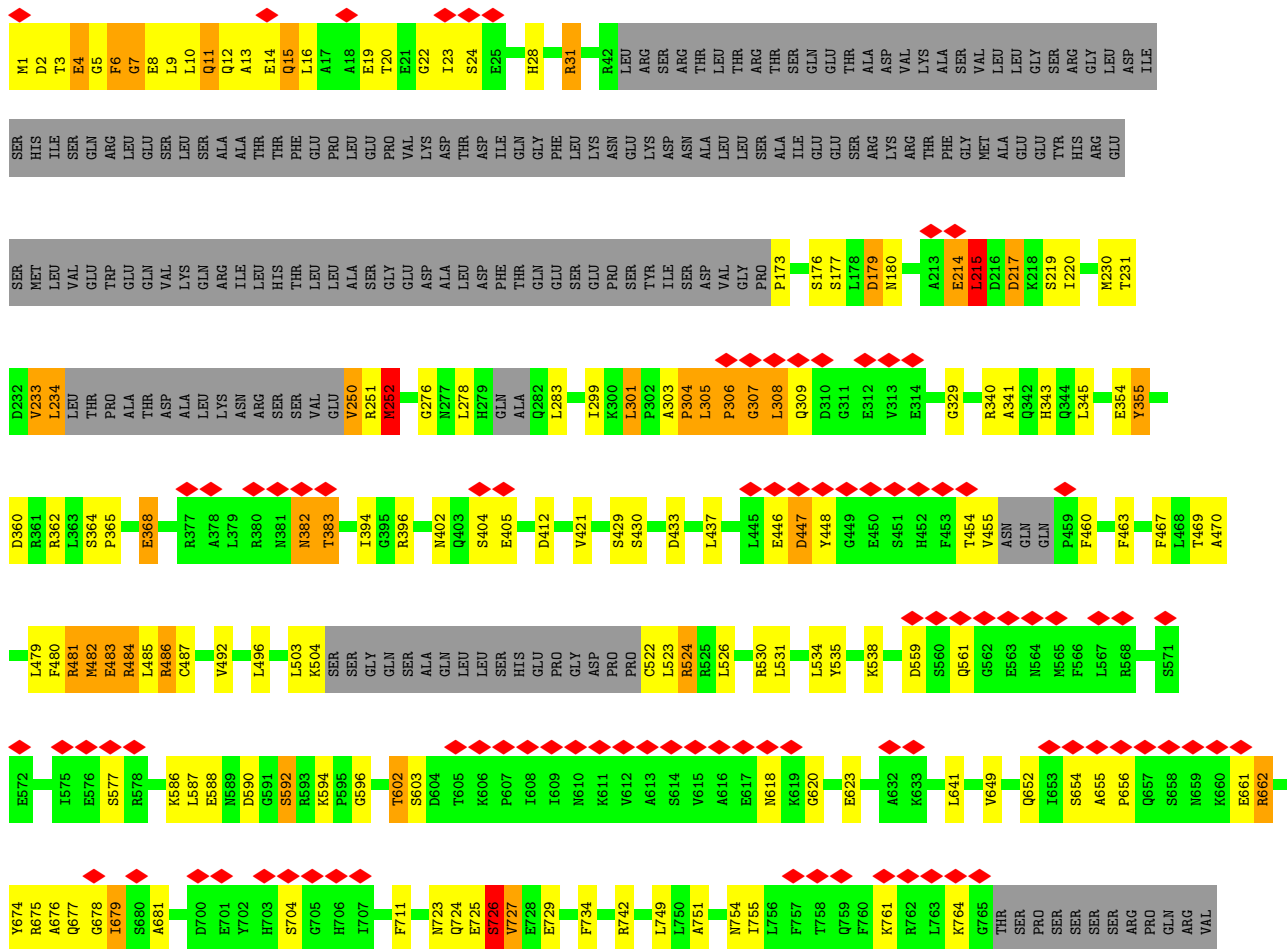


• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 8-Q: 68% 9% 22%

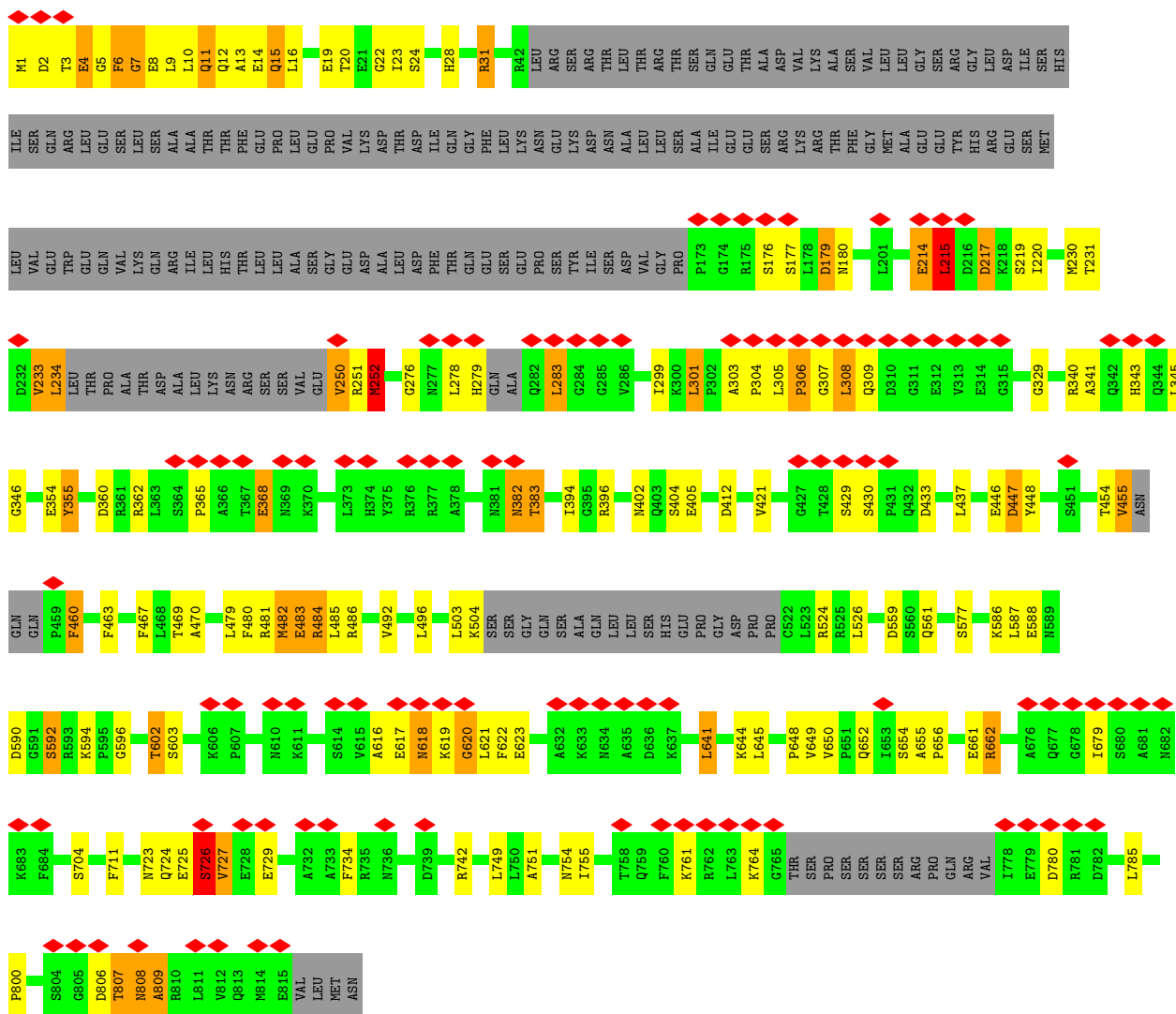


● Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

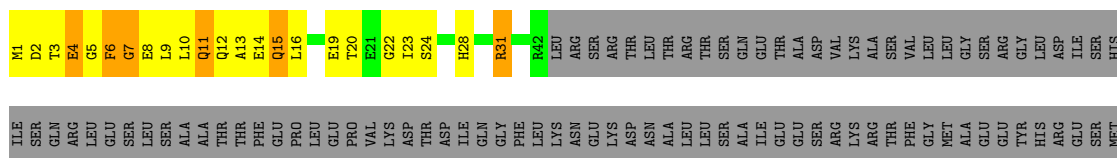


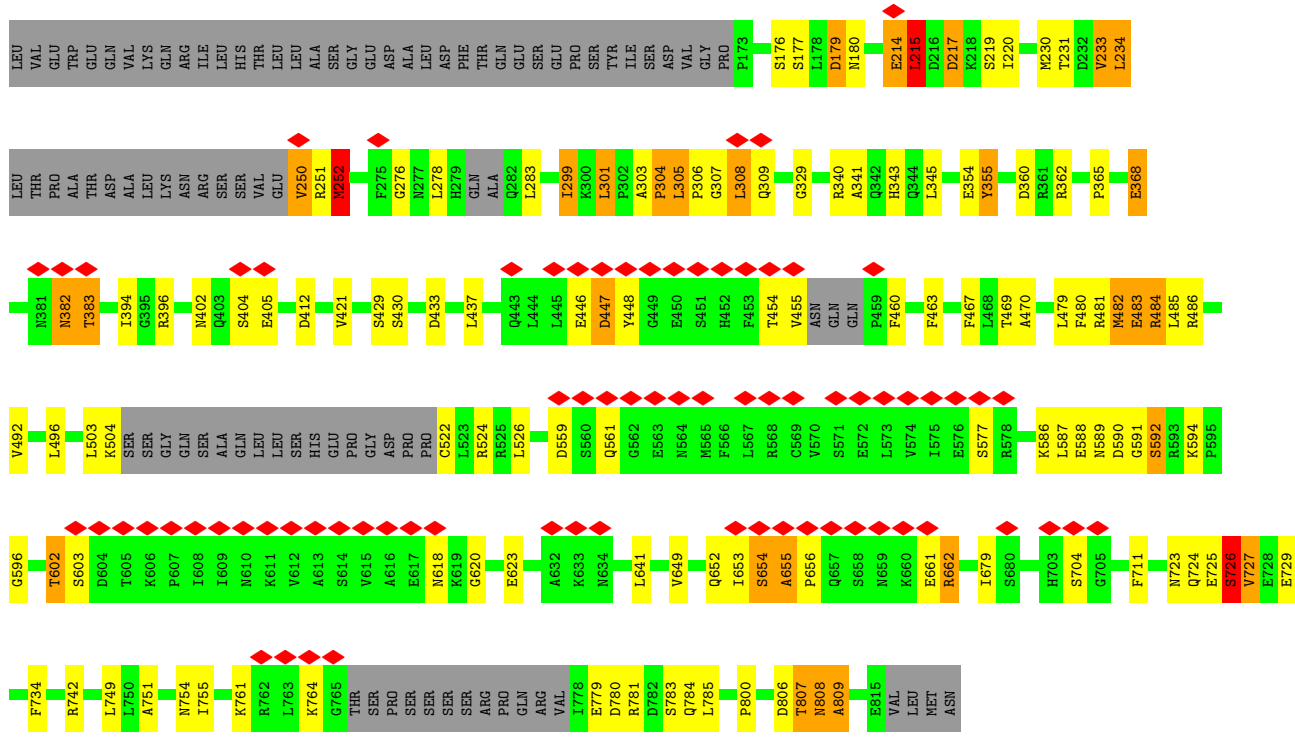


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

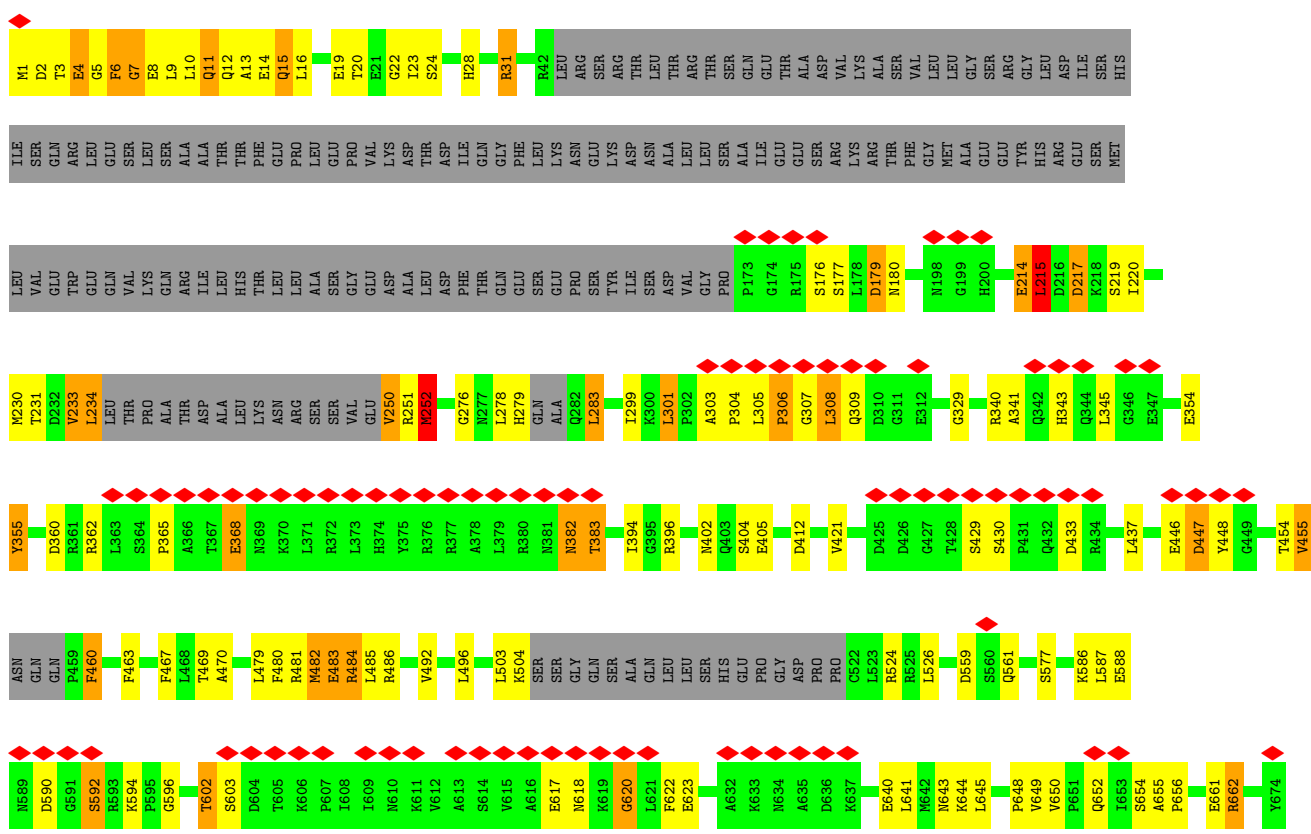


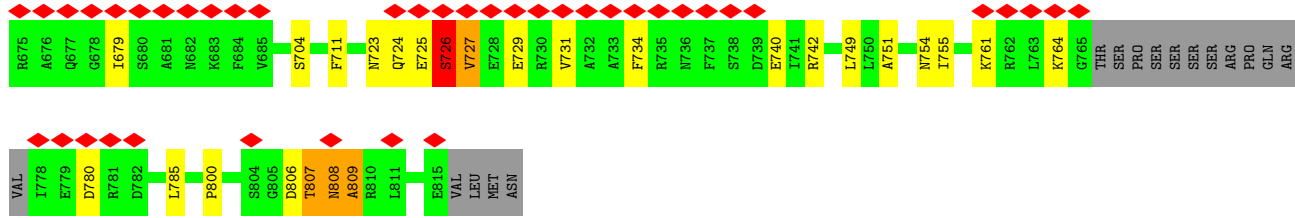
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93



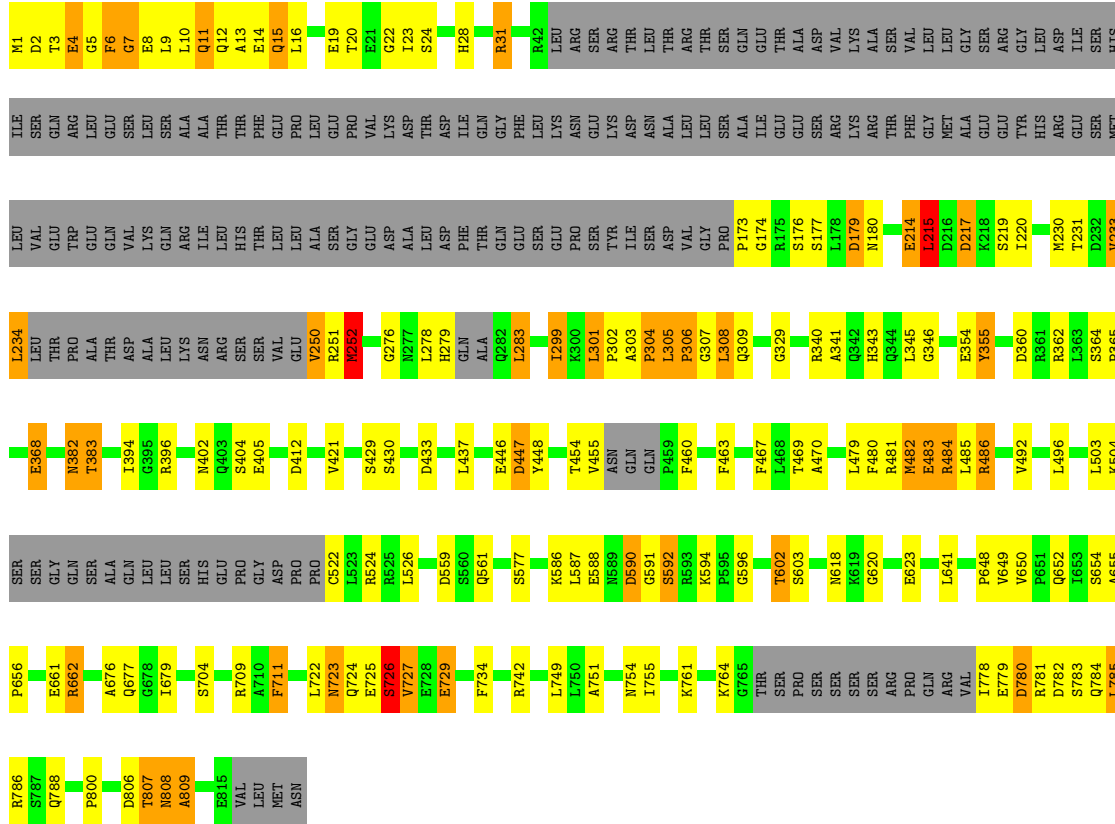


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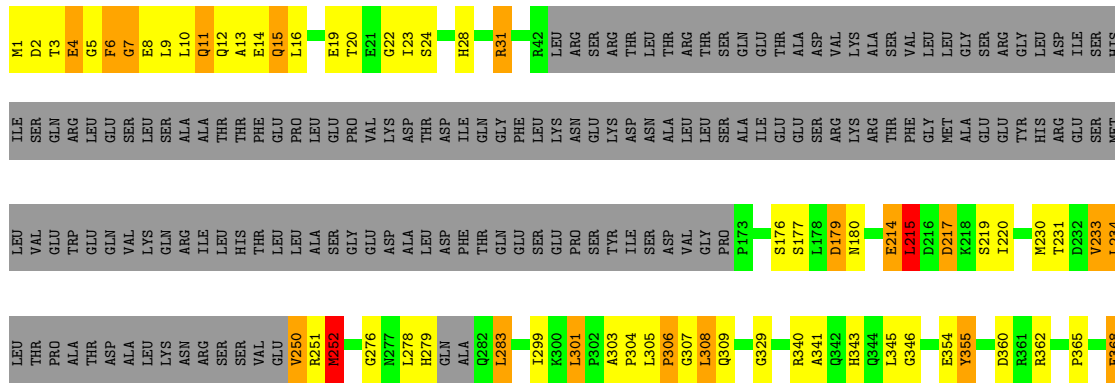


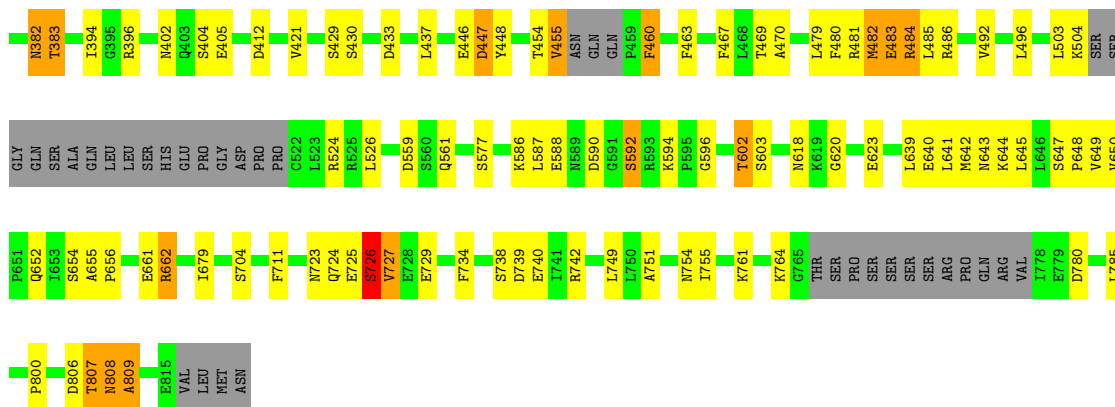


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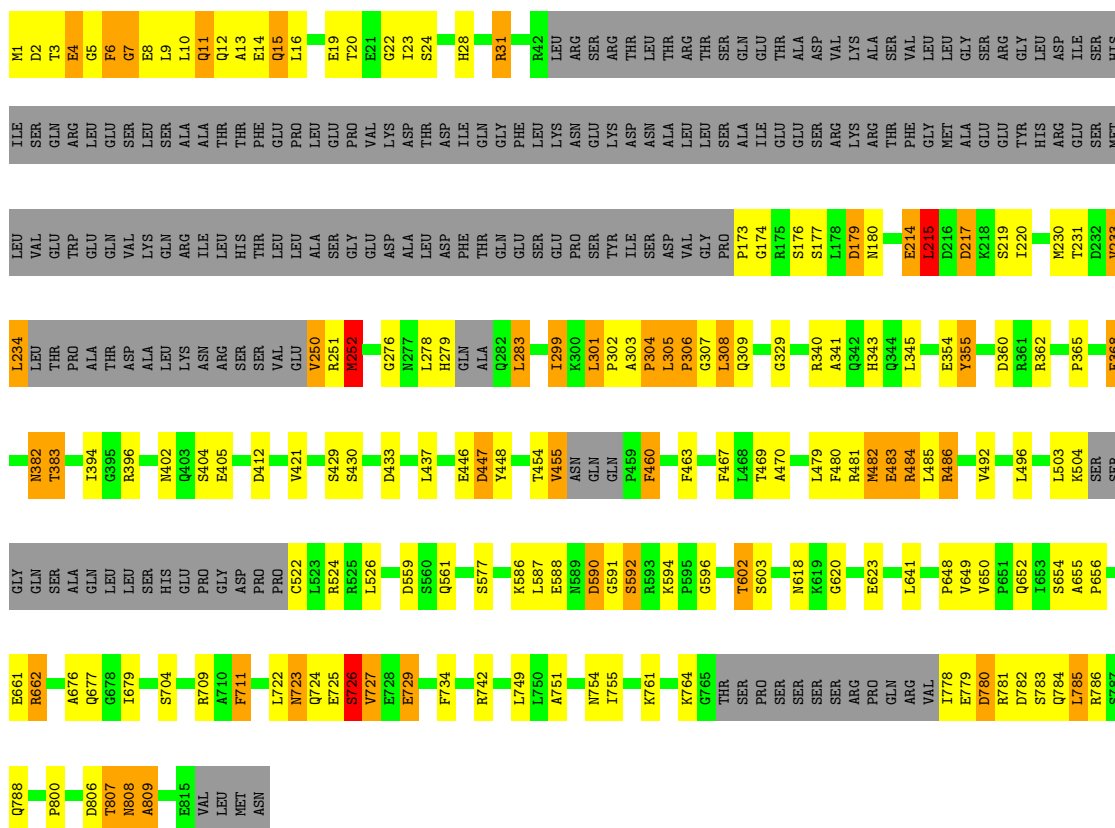


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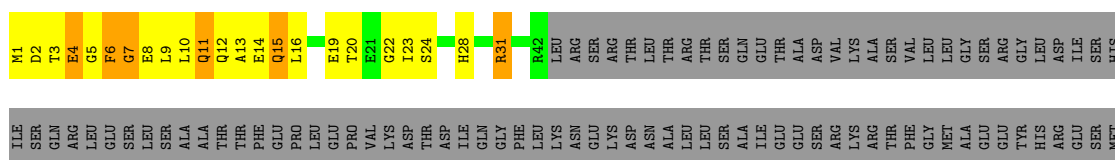


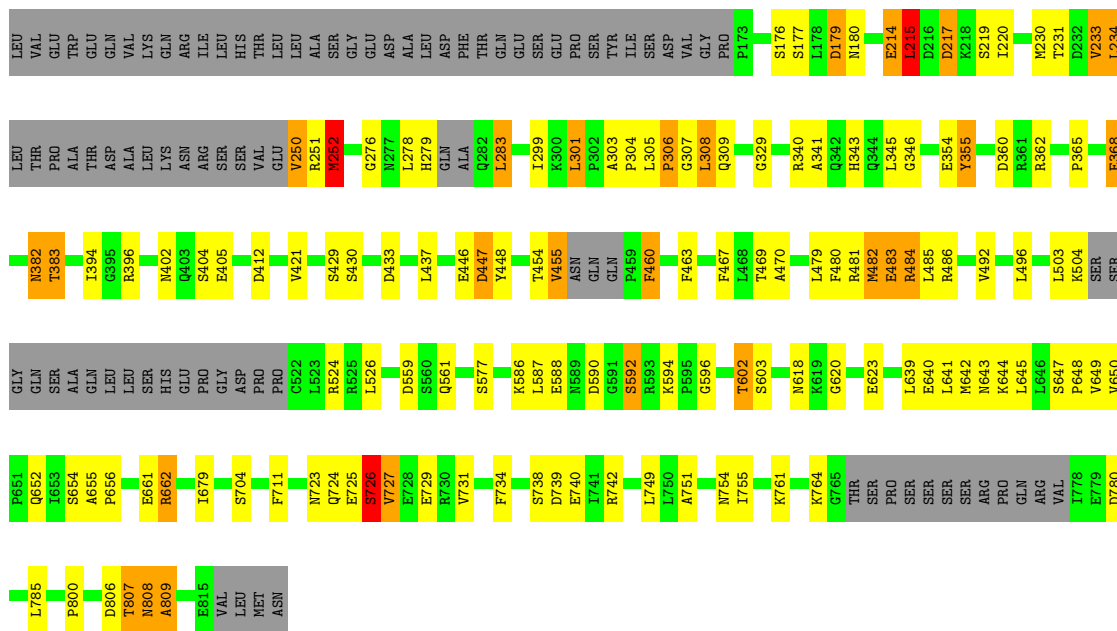


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

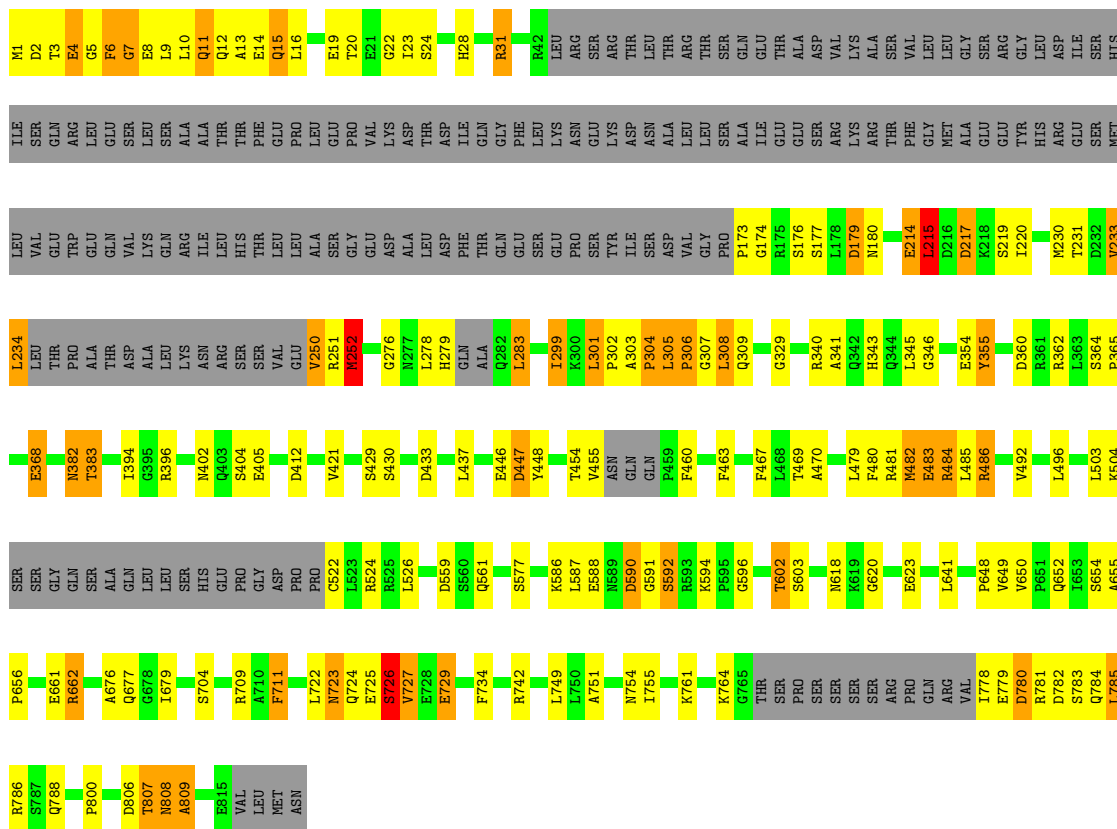


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93



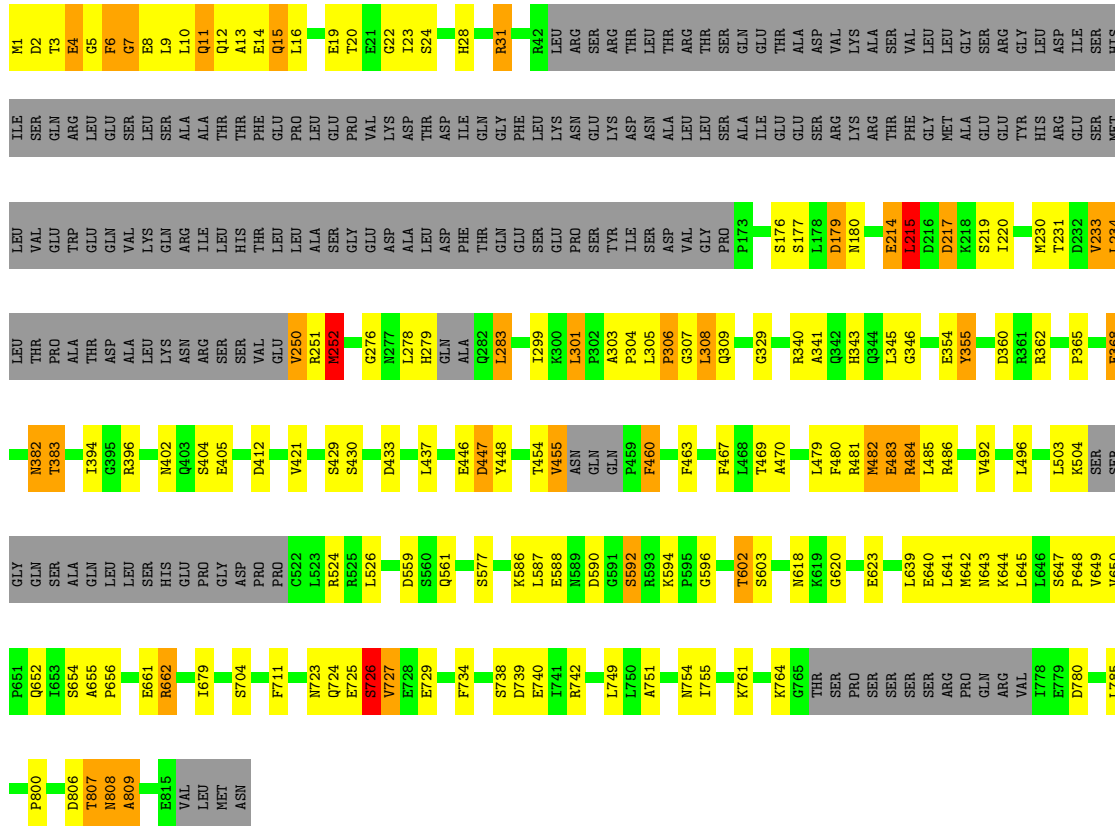


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

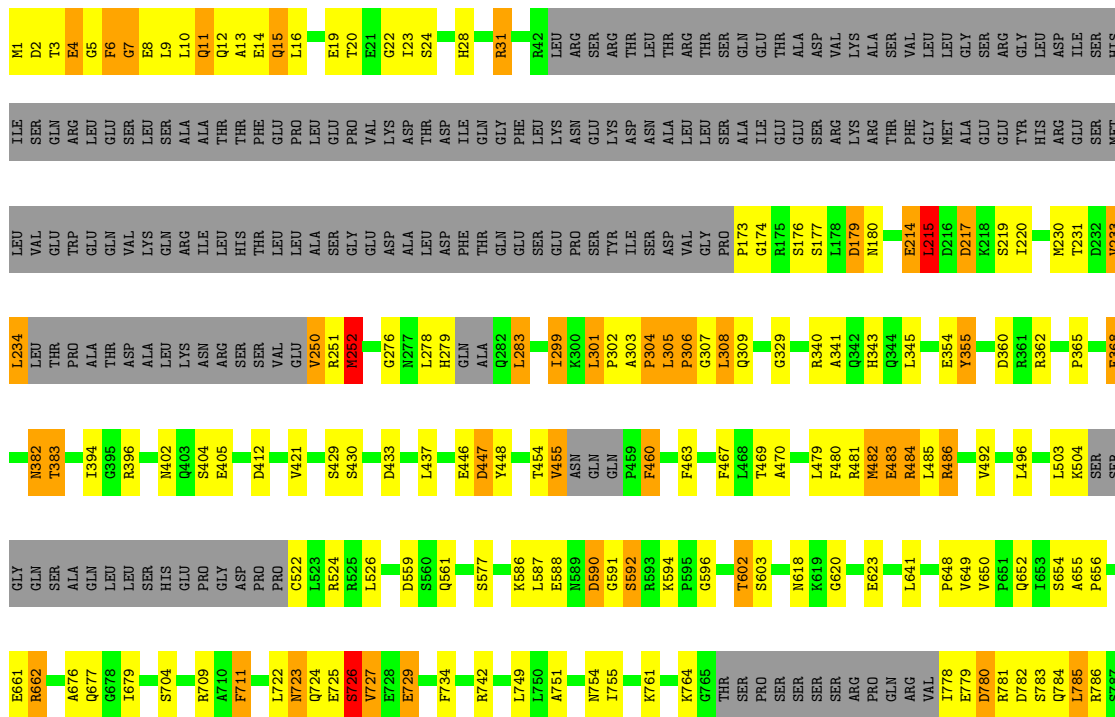


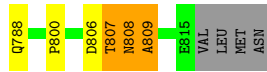
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93



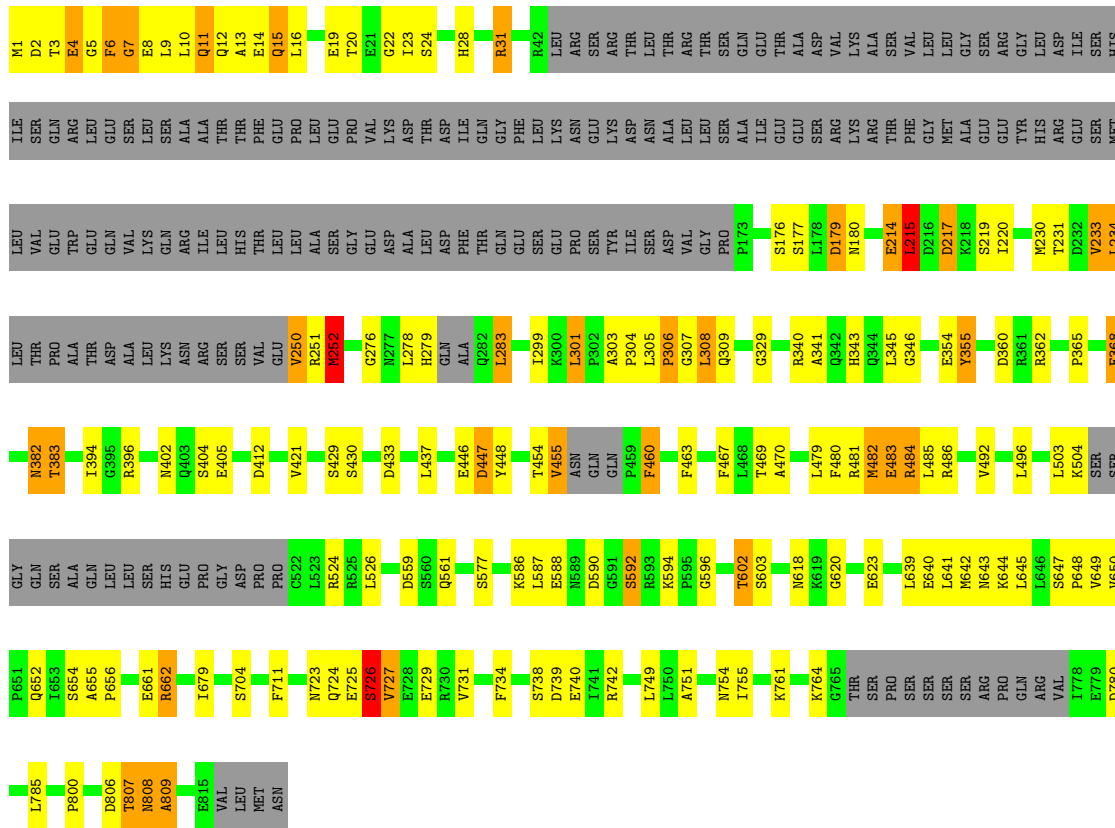


● Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

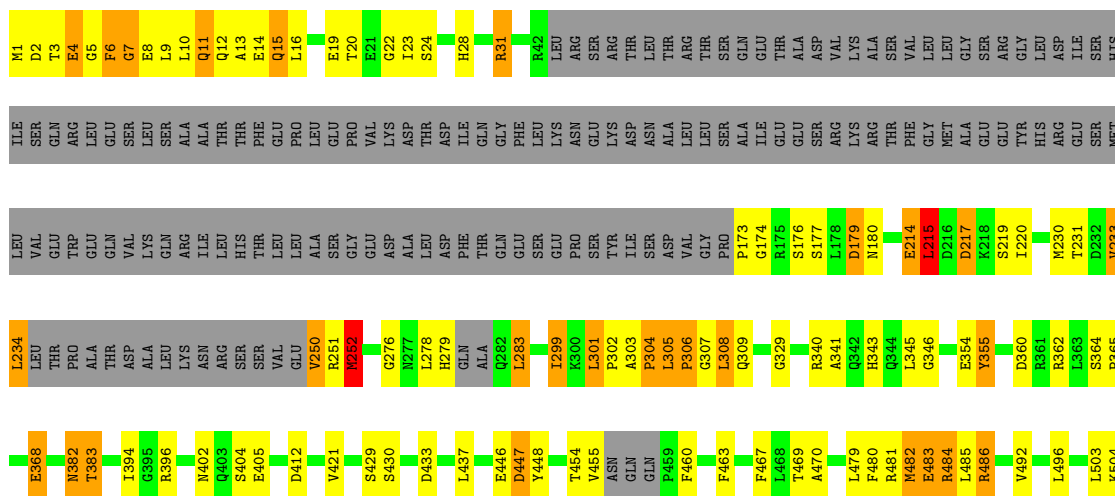


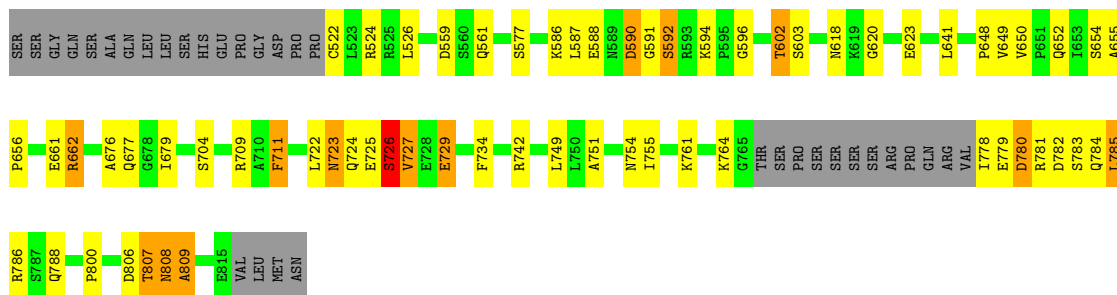


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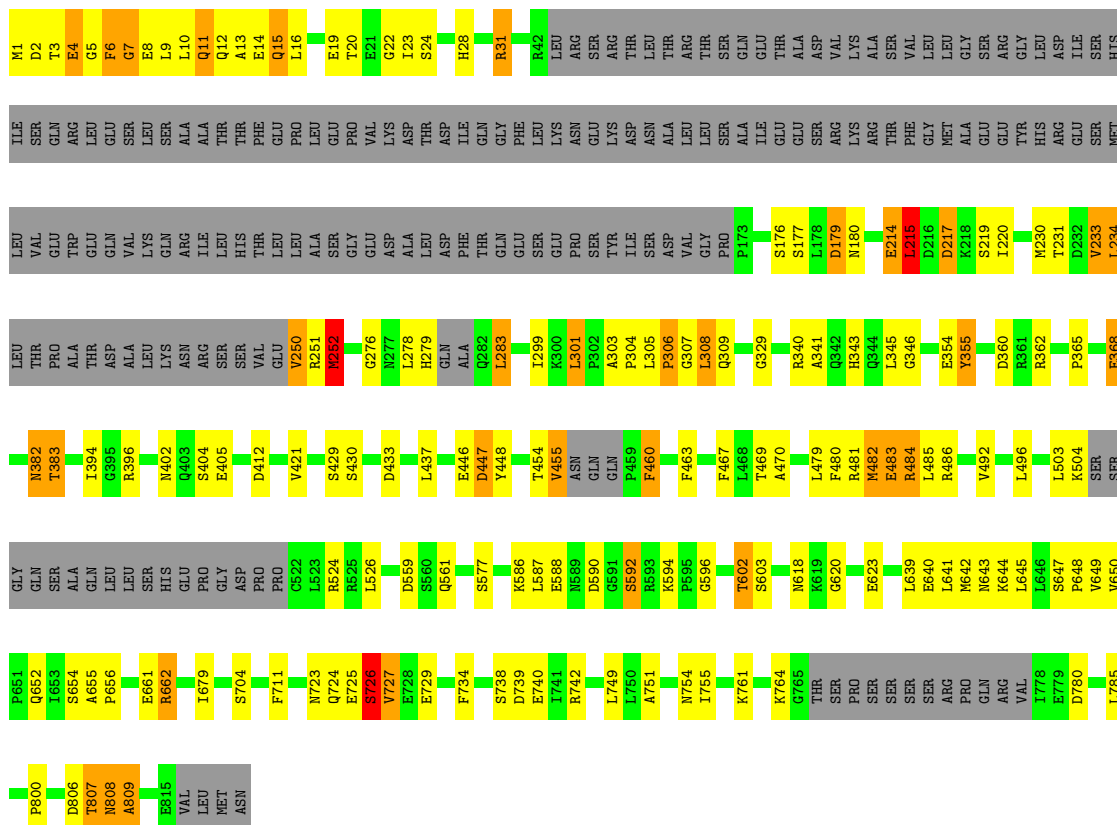


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

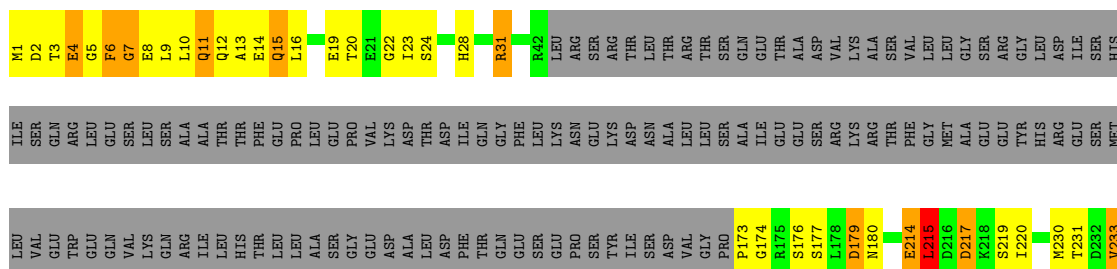




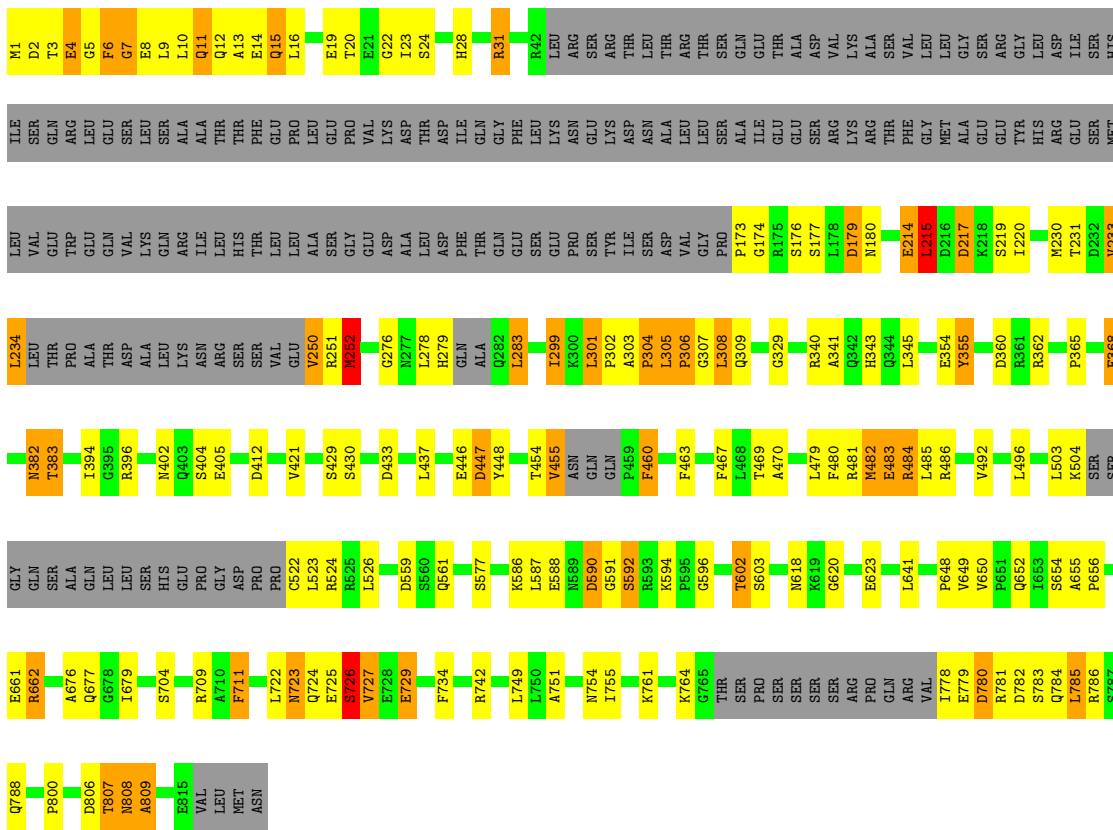
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93



• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

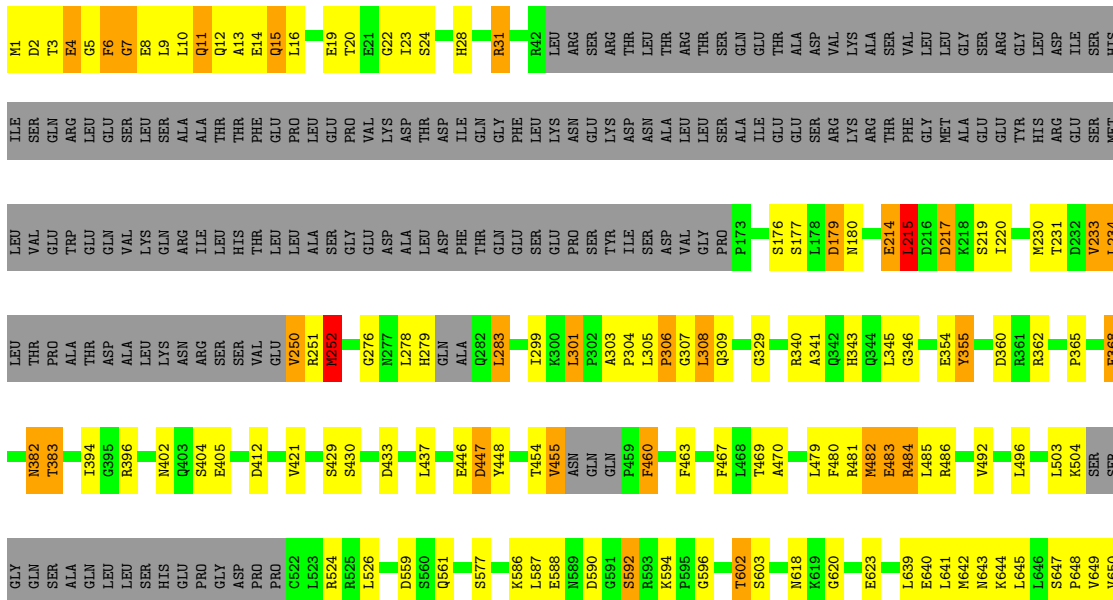


Chain 5-O: 57% 15% 5% 22%



● Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

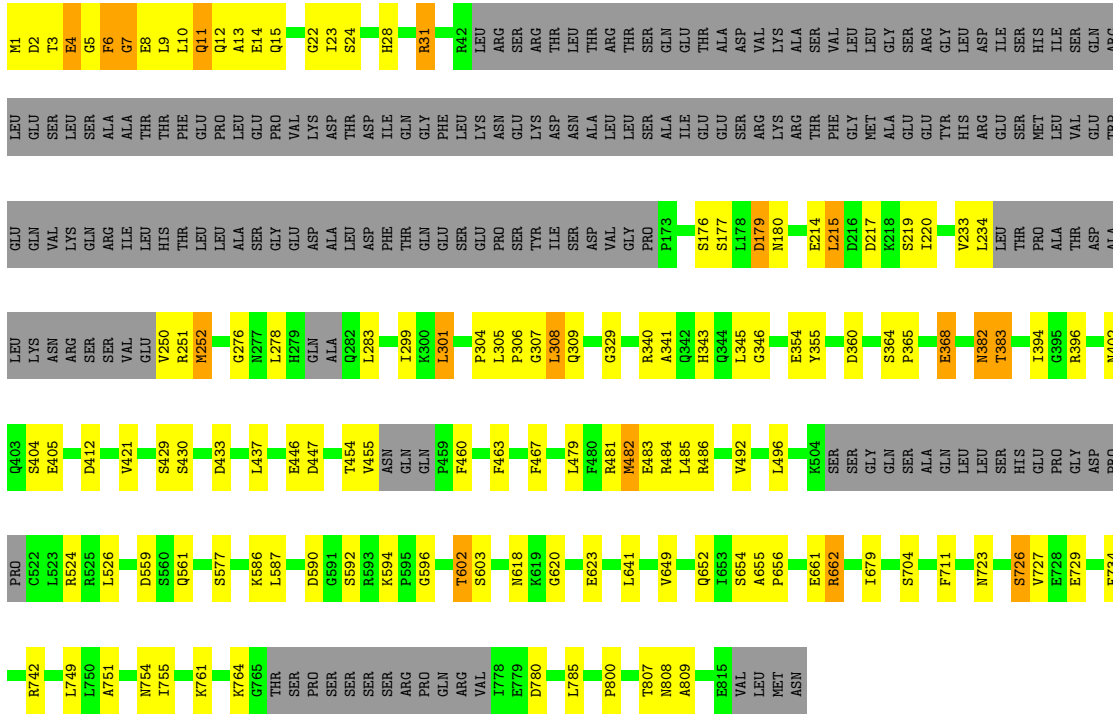
Chain 5-U: 58% 15% 22%





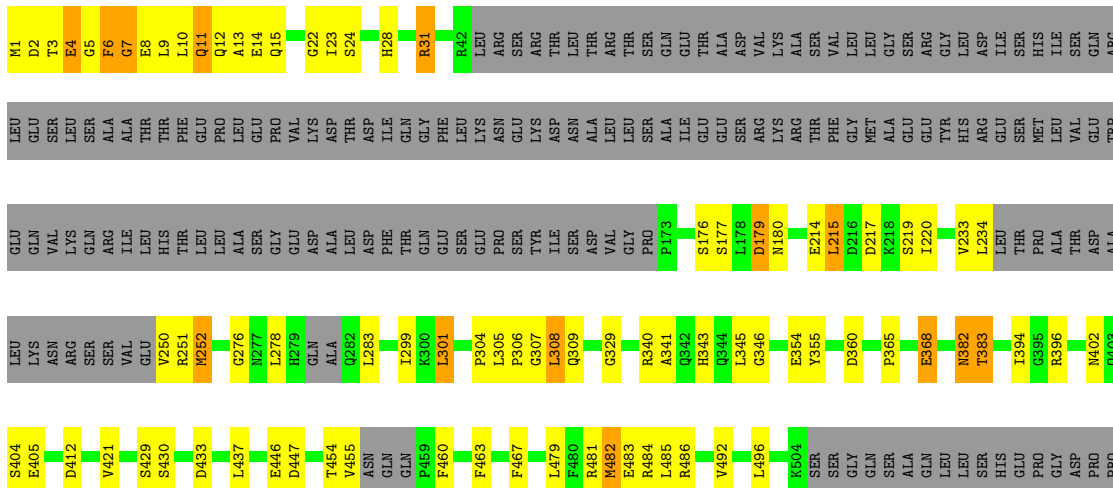
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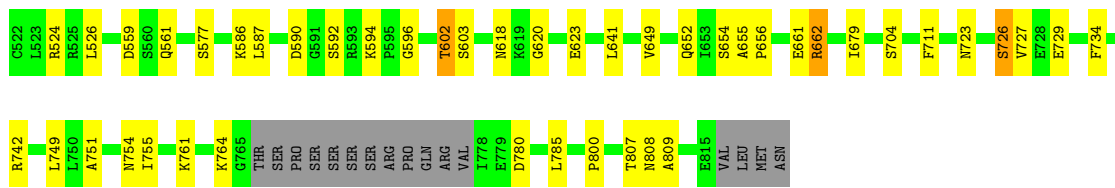
Chain 6-C: 62% 14% 22%



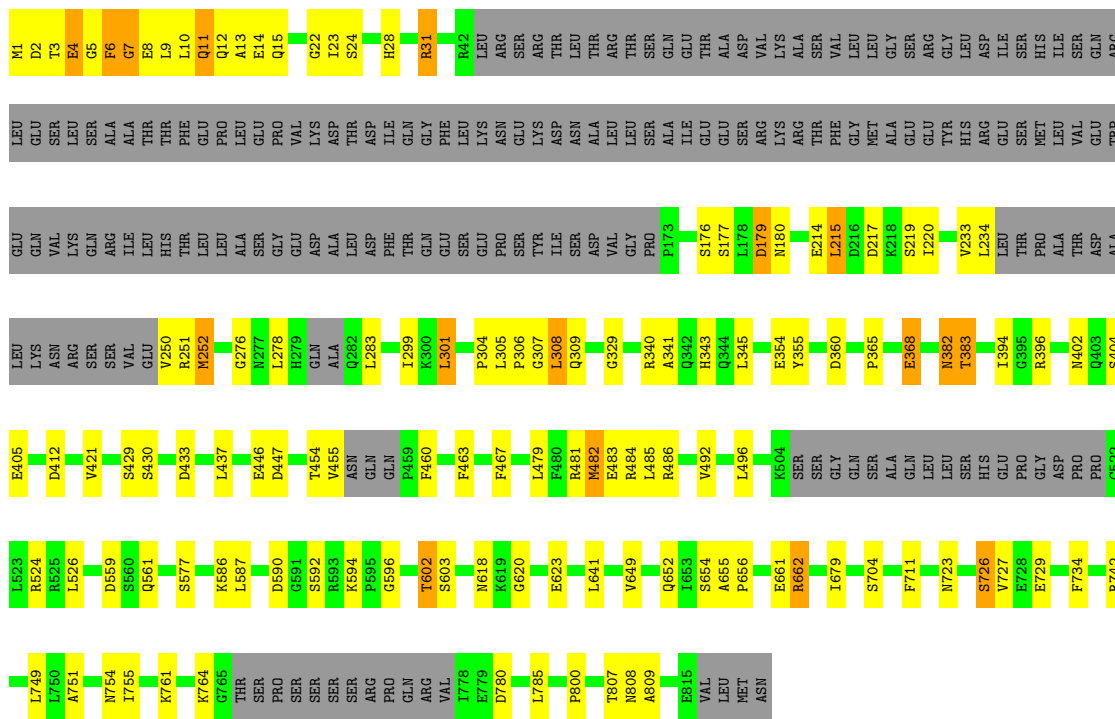
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 6-I: 62% 14% 22%

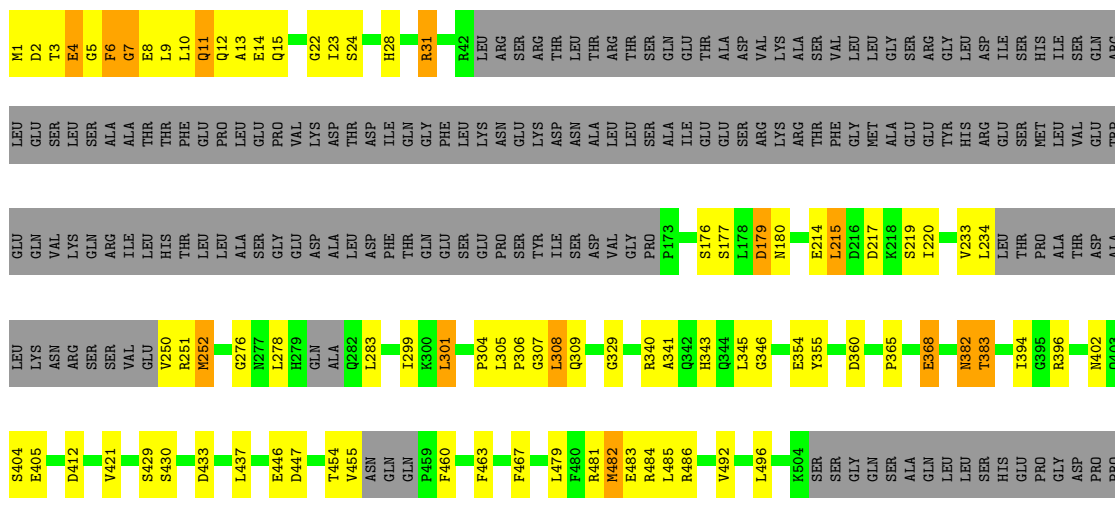


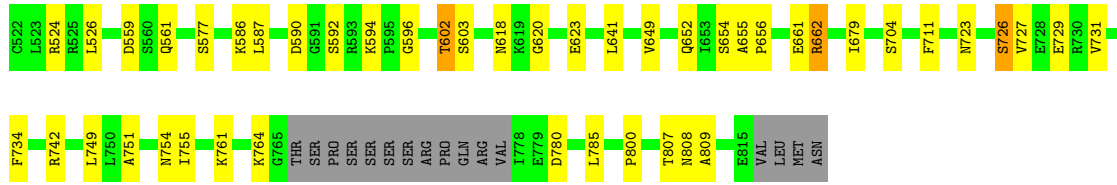


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

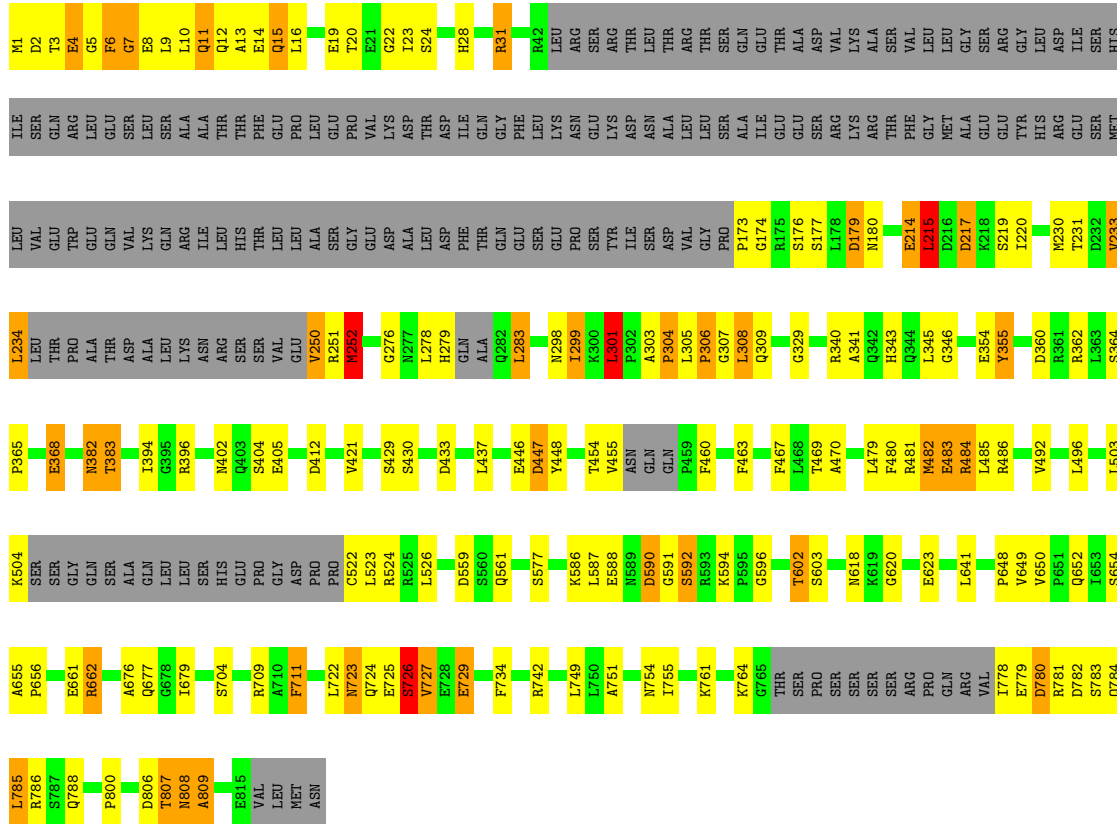


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

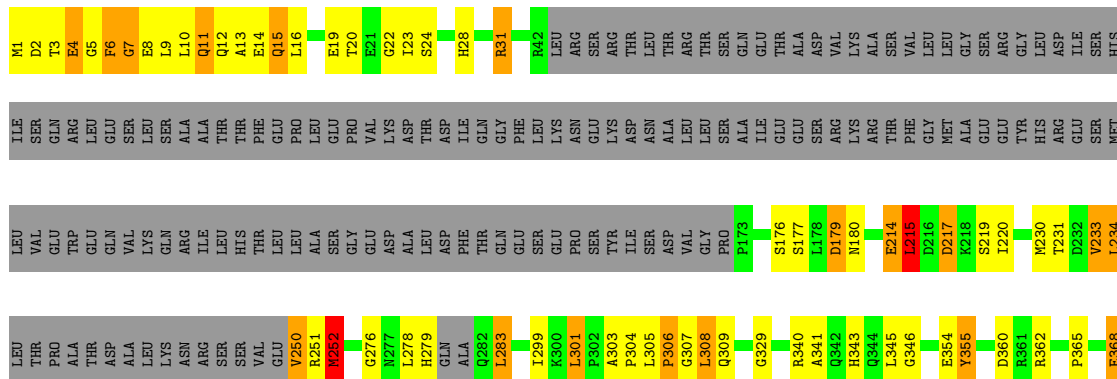


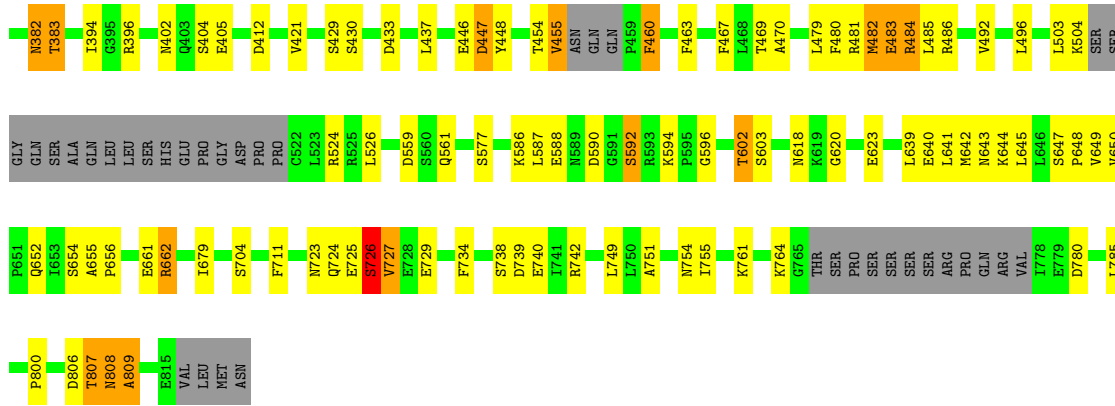


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

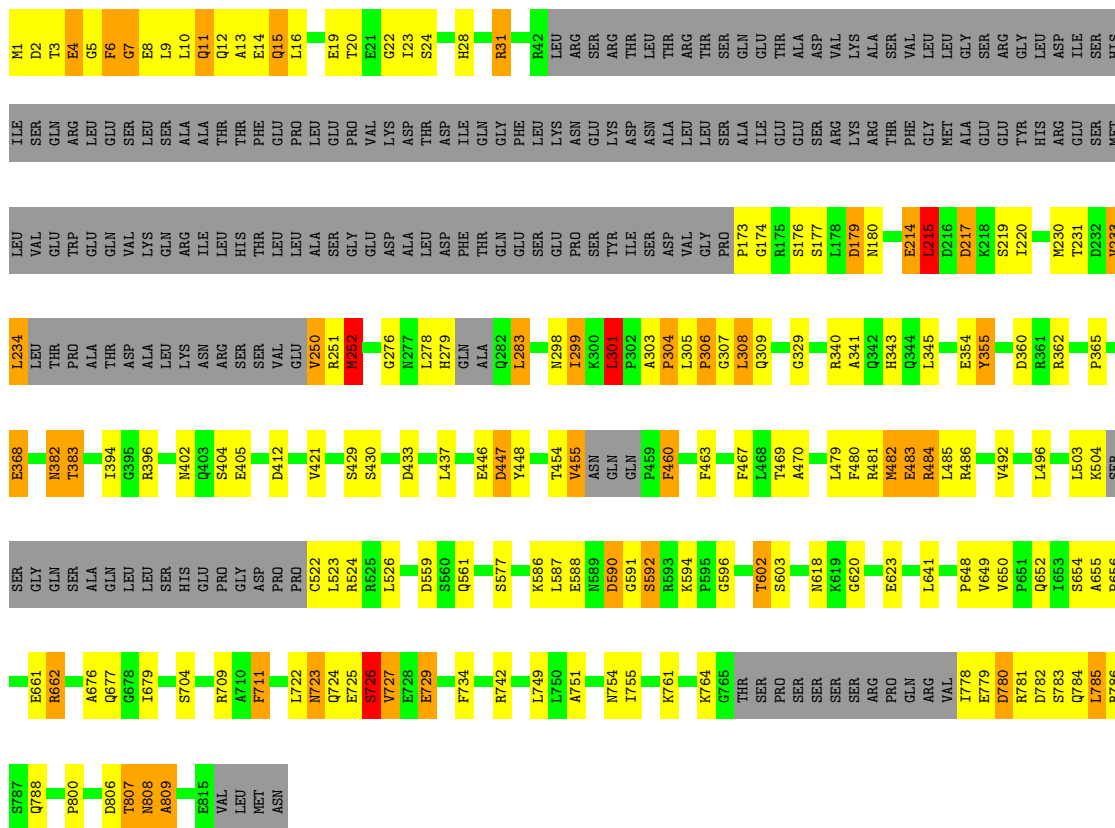


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

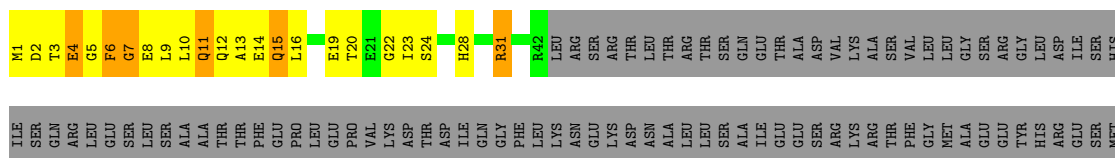


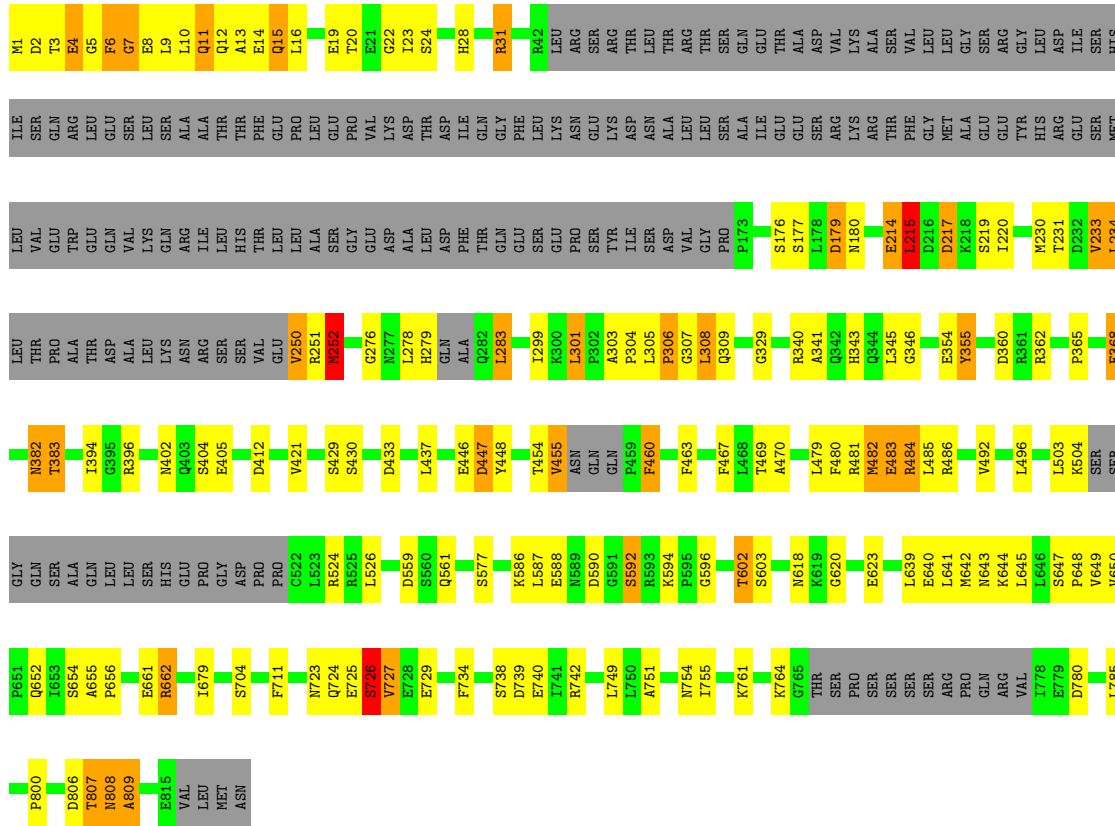


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

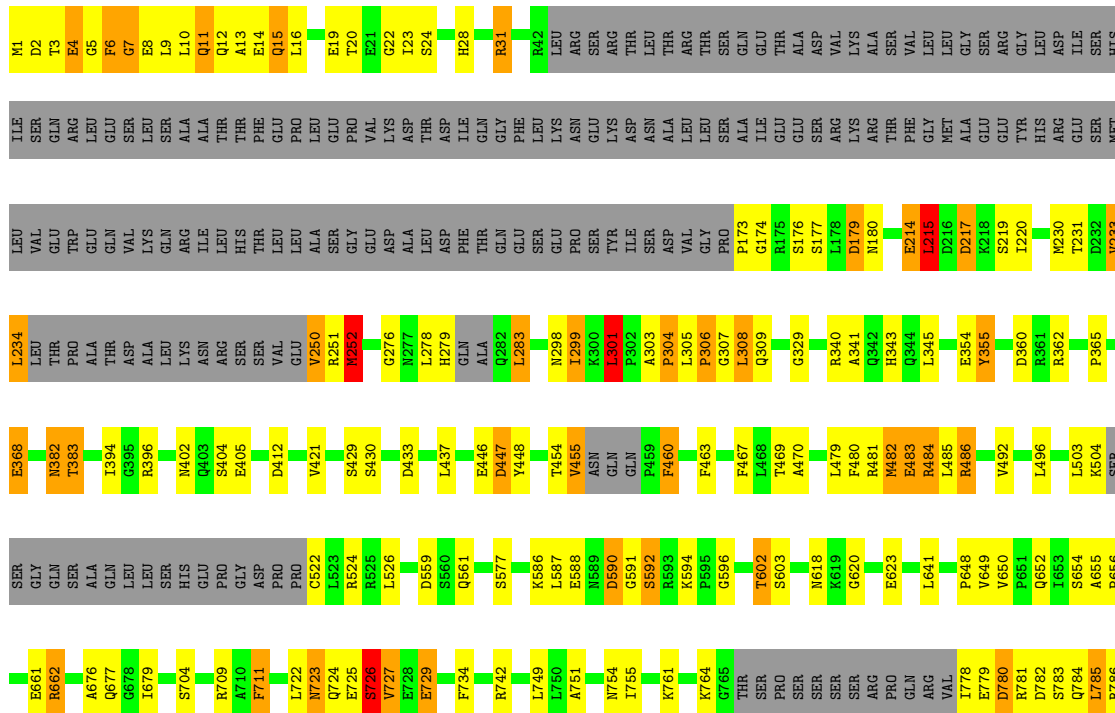


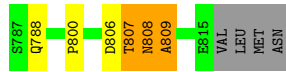
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93



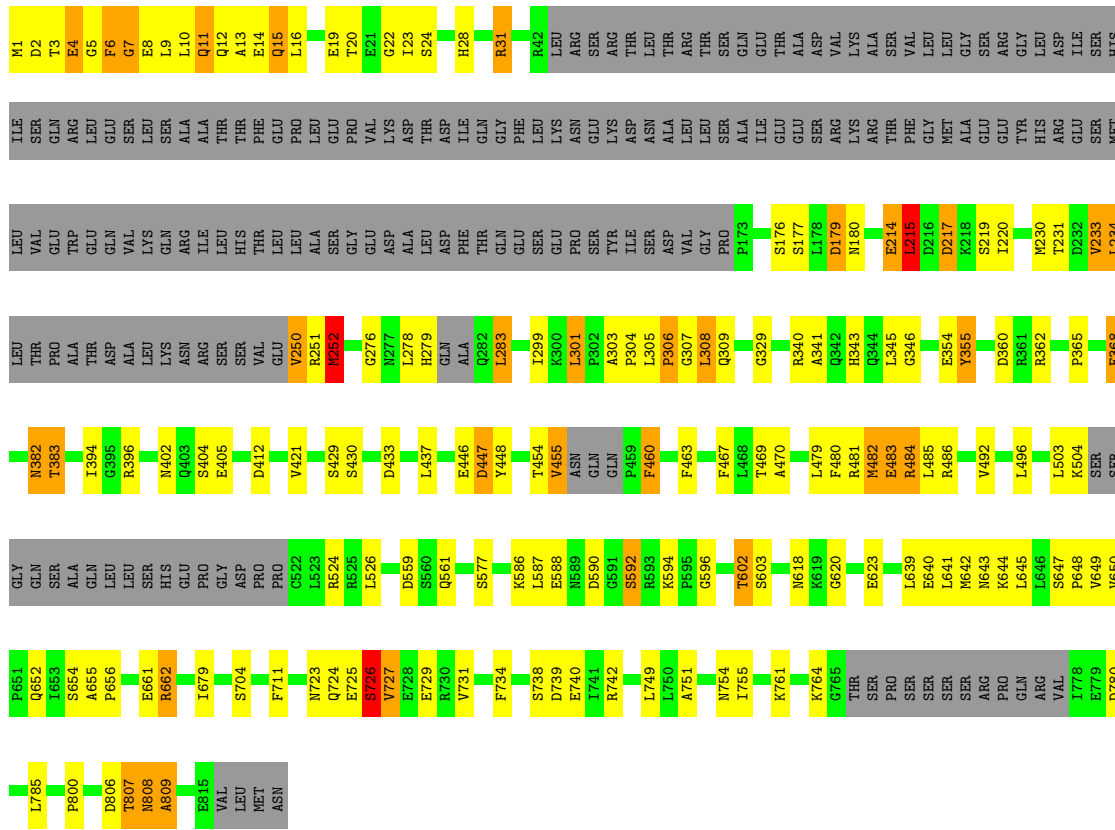


● Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

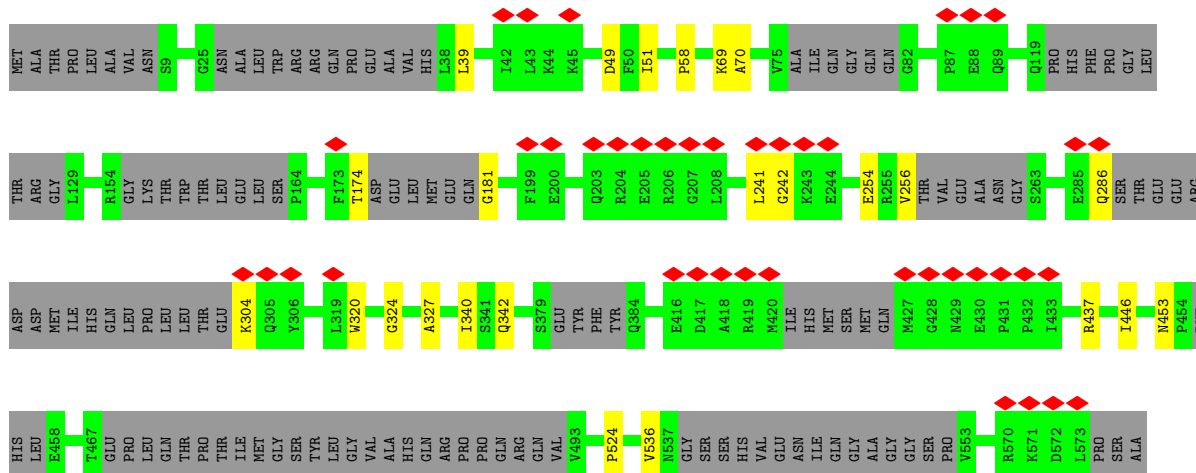
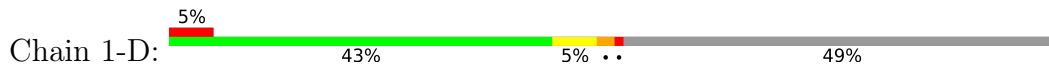


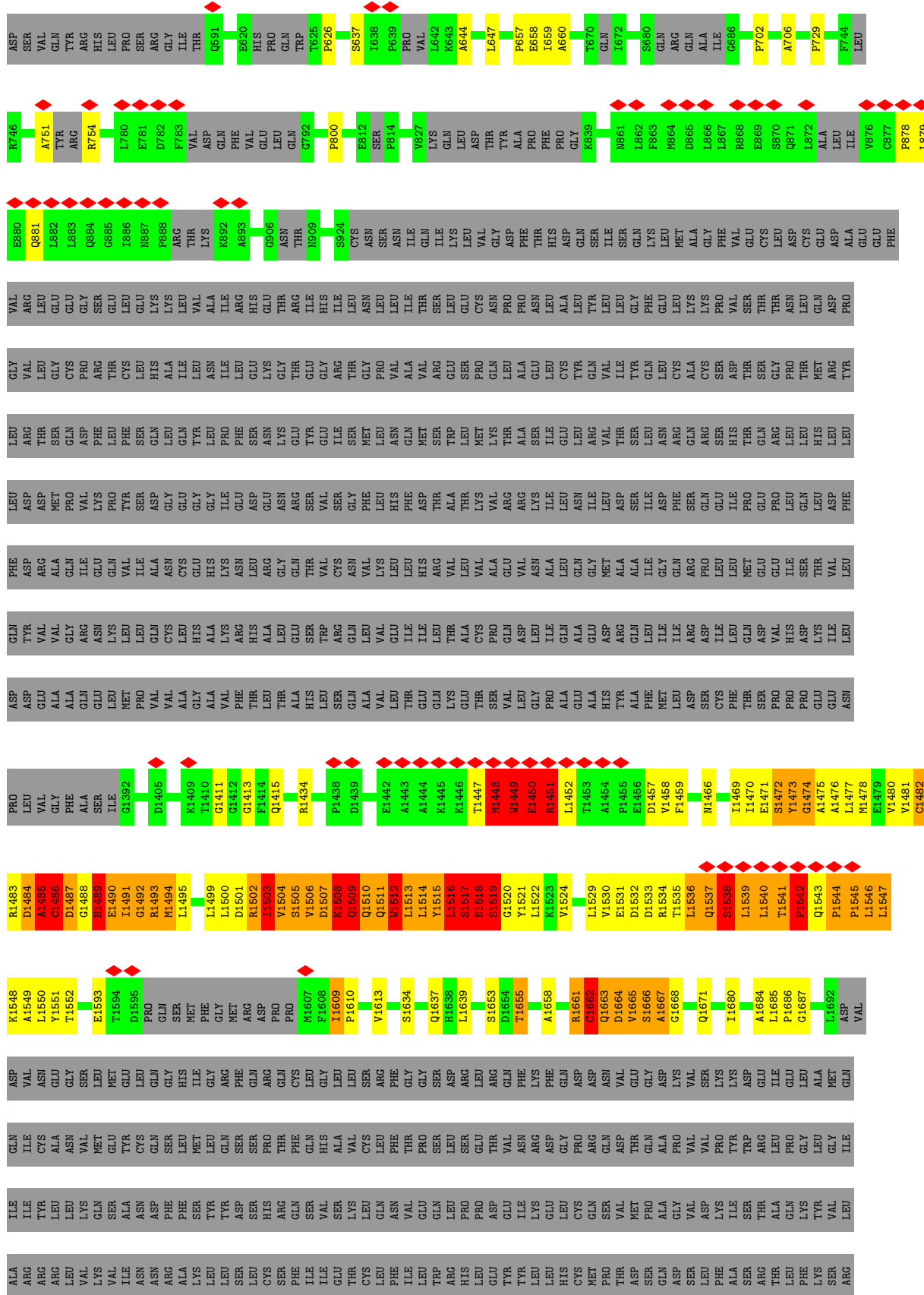


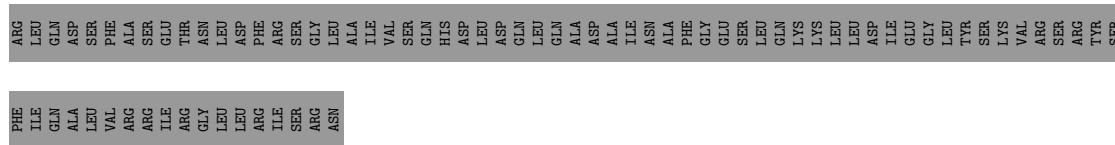
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93



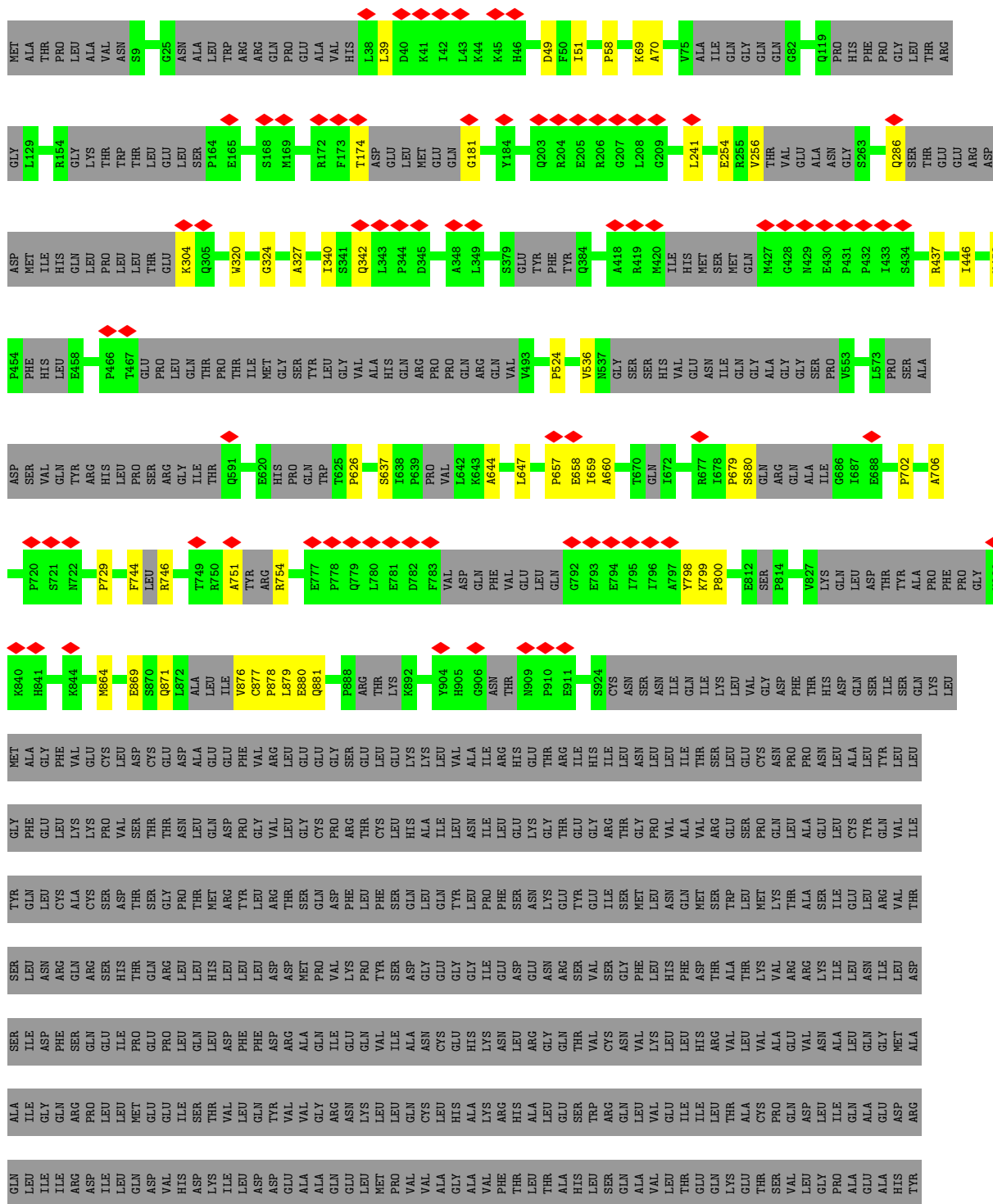
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

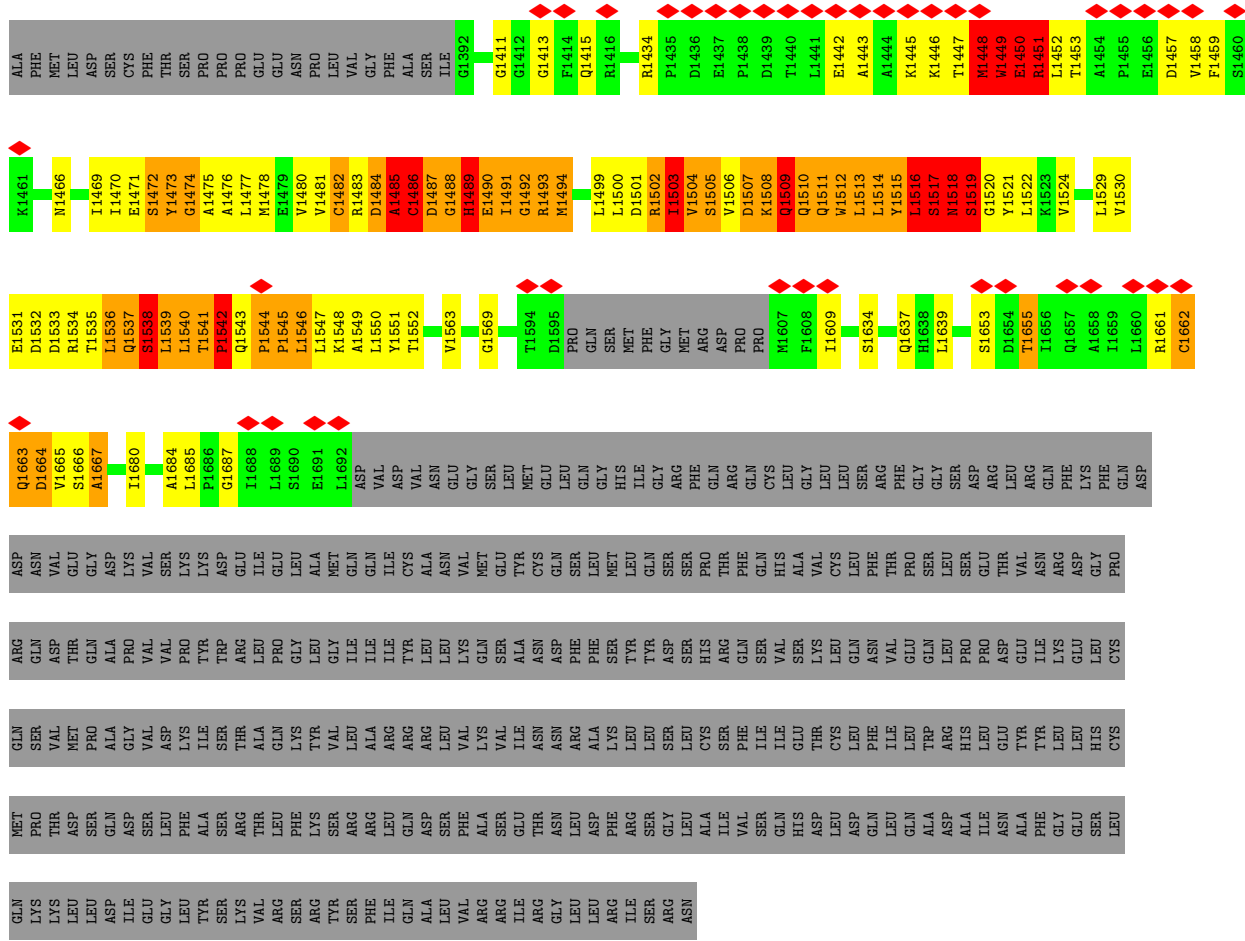




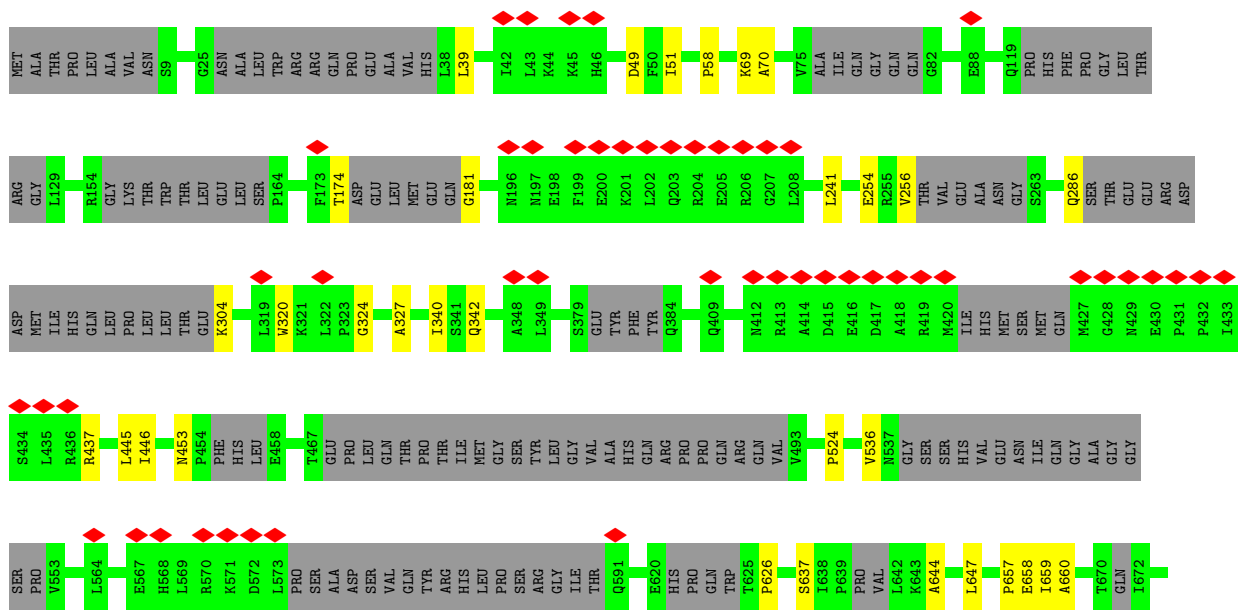


● Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

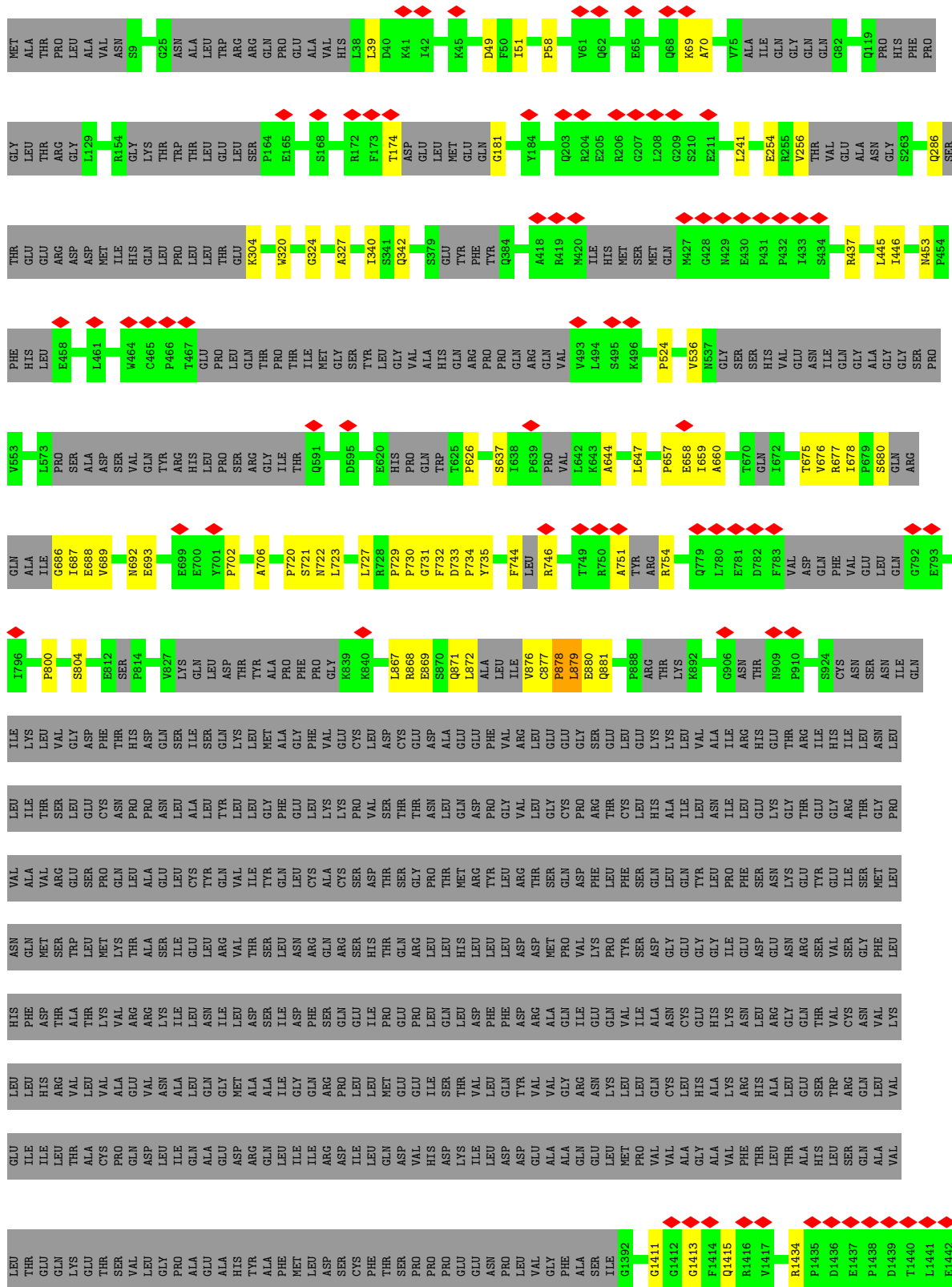
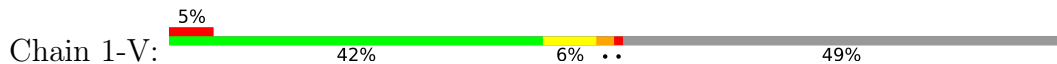




● Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205



● Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205



GLY	SER	GLN	ARG	GLU	ILE	GLY	ASN	LEU	ILE	PRO	P553	PRO	SER	ALA	ASP	SER	THR	GLN	TYR	ARG	ARG	HIS	LEU	ILE	THR	GLY	ASP	GLN	PRO	HIS	GLN	PRO	T626	P626	P639	PRO	VAL	I642	K643	A644	L647	P657	T670	GLN	I672										
S660	GLN	ARG	GLU	ALA	ILE	G666	P702	A706	L714	V715	S718	P729	F744	R746	A751	ARG	R764	R774	D775	Y776	F783	VAL	ASP	GLN	PHE	VAL	GLU	LEU	GLN	TRP	T625	P800	E812	P814	V827	LYS	GLN	LEU	ASP	THR	TYR	ALA	PRO	PHE	PRO										
K839	GLY	E869	L872	ALA	LEU	ILE	V876	C877	P878	L879	P888	ARG	THR	LYS	P892	G906	ASN	THR	N909	S924	CYS	ASN	LEU	ILE	GLY	ASP	PHE	GLY	ASP	ILE	ALA	SER	GLN	P814	P814	L642	K643	A644	L647	P657	T670	GLN	I672												
ASP	ALA	GLU	PHE	VAL	ARG	LEU	GLY	CYS	PRO	THR	LEU	GLY	ALA	ILE	ILE	ASP	HIS	GLU	ASN	THR	ARG	ILE	GLY	LEU	GLY	GLY	CYS	PHE	ALA	LEU	ALA	LEU	TYR	LEU	GLY	PHE	GLY	LEU	ASP	THR	VAL	THR	THR	THR											
ASN	LEU	GLN	ASP	PRO	GLY	VAL	LEU	CYS	ARG	THR	LEU	GLY	ALA	ILE	ILE	ASP	HIS	GLU	ASN	THR	ARG	ILE	GLY	LEU	GLY	GLY	CYS	PHE	ALA	LEU	ALA	LEU	TYR	LEU	GLY	PHE	GLY	LEU	ASP	THR	VAL	THR	THR	THR											
PRO	THR	MET	ARG	TYR	LEU	ARG	THR	ASP	THR	ARG	THR	SER	GLN	ILE	PRO	PHE	SER	THR	ASN	GLU	GLY	THR	LEU	ASN	LEU	ASN	LEU	GLY	ASP	VAL	GLN	TYR	LEU	LEU	MET	LYS	VAL	VAL	GLN	GLY	GLN	GLN	GLN	ARG											
LEU	HIS	LEU	LEU	LEU	ASP	ASP	MET	PRO	VAL	TYR	SER	ASP	GLY	GLY	ILE	GLU	GLU	ASP	GLU	ASN	GLY	THR	LEU	ASN	LEU	HIS	PHE	ALA	LEU	ALA	LEU	LEU	LEU	LEU	ILE	ILE	SER	ILE	ILE	PHE	ASP	GLN	PRO	PRO	PRO										
LEU	GLN	LEU	ASP	PHE	ARG	VAL	VAL	ALA	GLY	ILE	ALA	ASN	CYS	HIS	GLY	HIS	ASN	ARG	GLY	ALA	LEU	GLY	GLN	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLN	GLY	ILE	ILE	GLY	GLY	GLY	GLY	VAL											
ILE	SER	THR	VAL	GLN	TYR	ASP	VAL	ALA	GLY	ILE	ALA	ASN	CYS	HIS	GLY	HIS	ASN	ARG	GLY	ALA	LEU	GLY	GLN	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLN	GLY	ILE	ILE	GLY	GLY	VAL											
HIS	ASP	ILE	LEU	LEU	ASP	ASP	GLU	ALA	GLN	GLY	MET	PRO	VAL	VAL	ALA	VAL	PHE	THR	THR	LEU	LEU	ALA	ALA	HIS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL										
PRO	PRO	GLU	ASN	PRO	LEU	VAL	VAL	GLY	ILE	G1392	G1411	G1411	G1412	G1413	F1414	Q1415	R1434	T1447	M1448	V1449	E1450	R1451	L1452	T1453	A1454	D1457	V1458	F1459	M1466	I1469	I1470	A1471	S1472	Y1473	G1474	A1475	A1476	L1477	M1478	E1479	V1480	V1481	C1482	R1483	D1484	A1485	C1486	D1487	H1488	E1490					
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G1569	DI595	GLN	GLN	SER	MET	PHE	GLY	GLY	MET	ARG	PRO	M1607	F1608	I1609	S1634	Q1637	H1638	L1639	S1653	D1654	T1655	R1661	Q1662	Q1663	D1664	V1665	S1666	A1667	I1680	A1684	L1685	P1686	G1687	L1692	ASP	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
GLY	ARG	PHE	GLN	ARG	GLN	CYS	LEU	LEU	PHE	GLY	GLY	GLY	SER	SER	ARG	LEU	ARG	LEU	LEU	GLN	ASP	ASP	ASP	GLY	ASP	ASP	GLY	LYS	ASP	GLU	GLY	LEU	MET	GLN	GLN	GLN	ILE	ILE	ILE	ILE	CYS	ALA	ASN	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
LEU	GLN	SER	SER	THR	PHE	GLN	HIS	GLY	HIS	VAL	VAL	THR	PRO	TRP	GLN	ASP	THR	ASN	THR	ASP	GLY	PRO	CYS	GLY	PRO	ARG	GLN	PRO	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
TYR	TYR	ASP	SER	HIS	ARG	ARG	SER	GLN	THR	VAL	SER	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
LEU	LEU	SER	CYS	ALA	VAL	THR	ASP	CYS	LEU	PHE	LEU	ILE	LEU	TRP	ALA	HIS	GLY	THR	LEU	HIS	LEU	MET	GLY	THR	ASP	GLN	ASP	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		
ARG	SER	GLY	LEU	ALA	VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU

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● Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 2-P:  43% 5% .. 49%

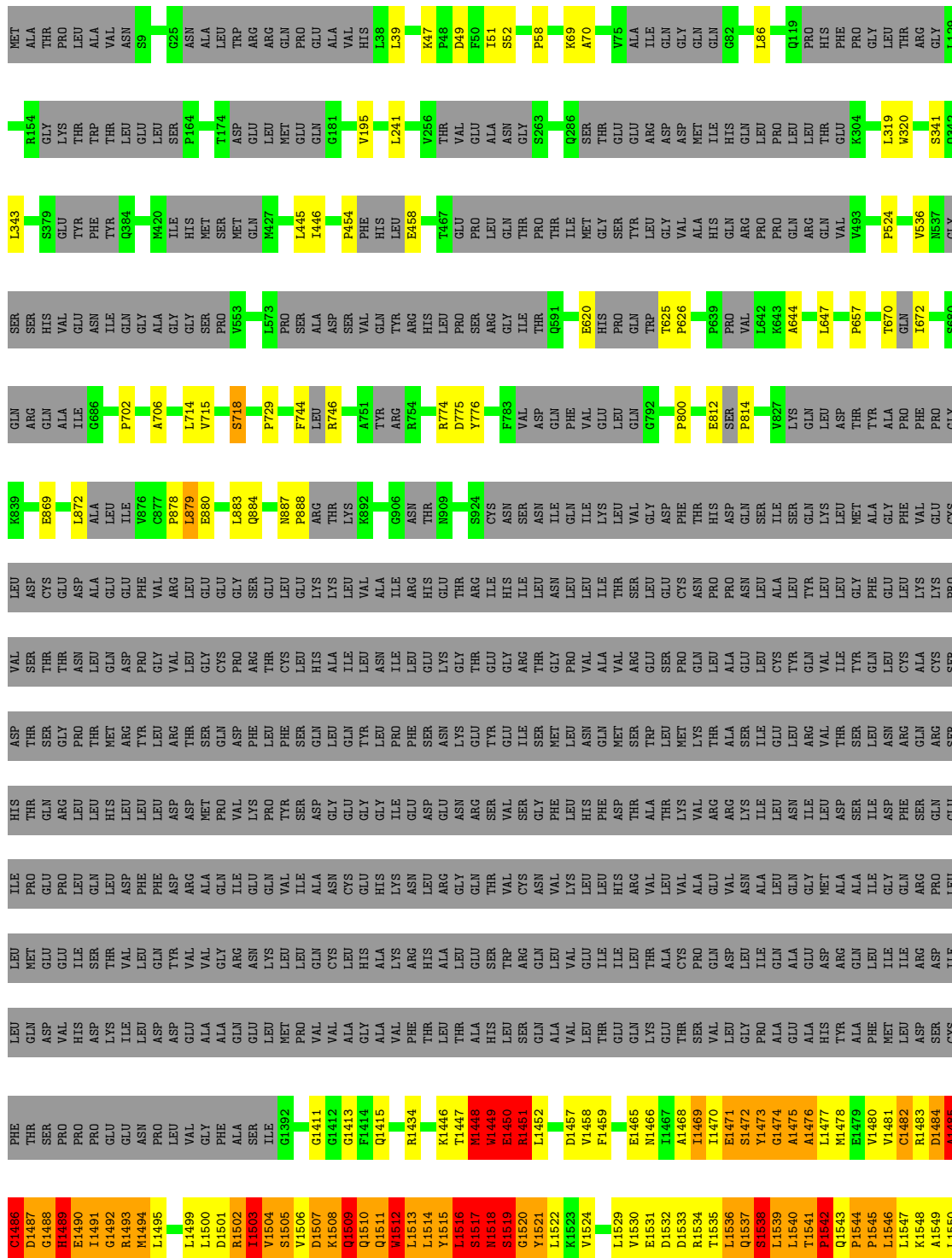
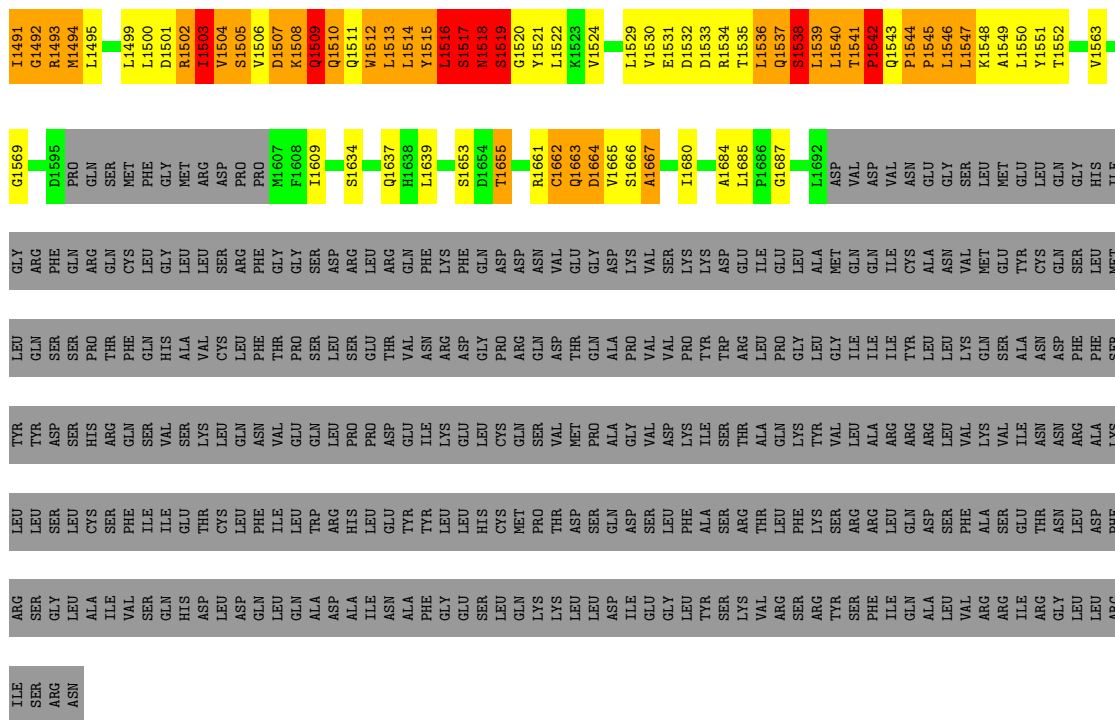
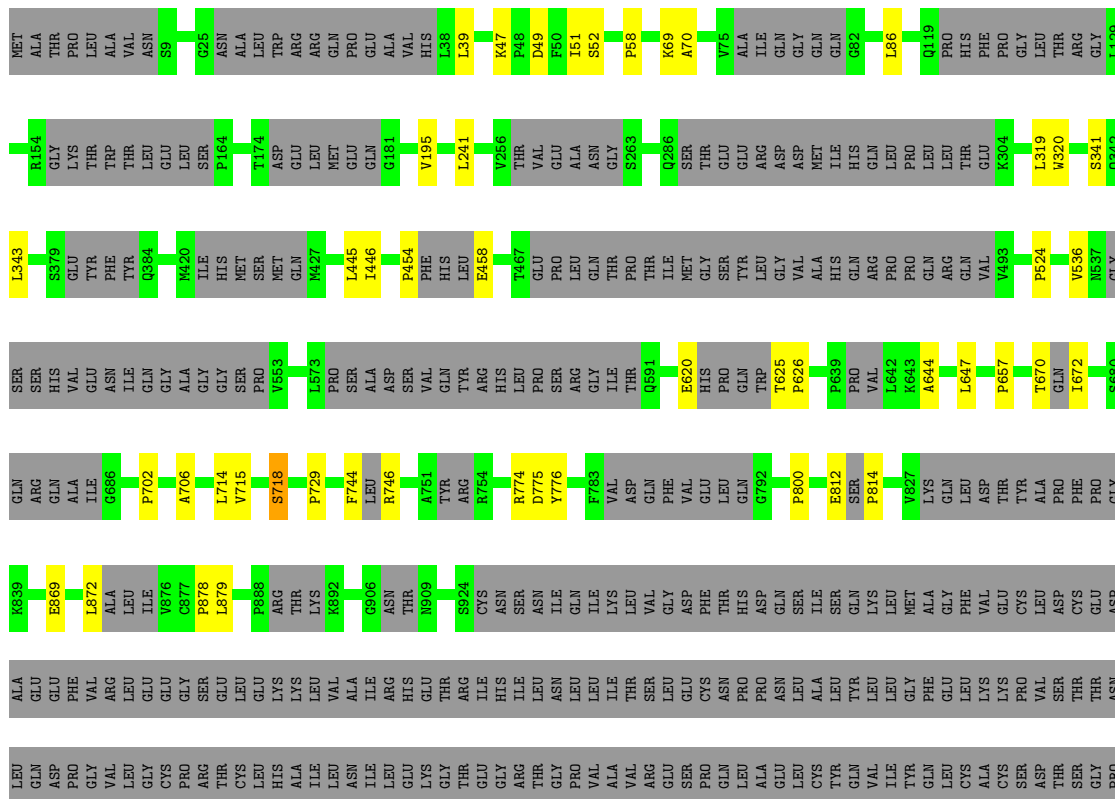




Table of amino acid residues for Chain 3-J, showing residue type, ID, and validation status (color-coded by quality).



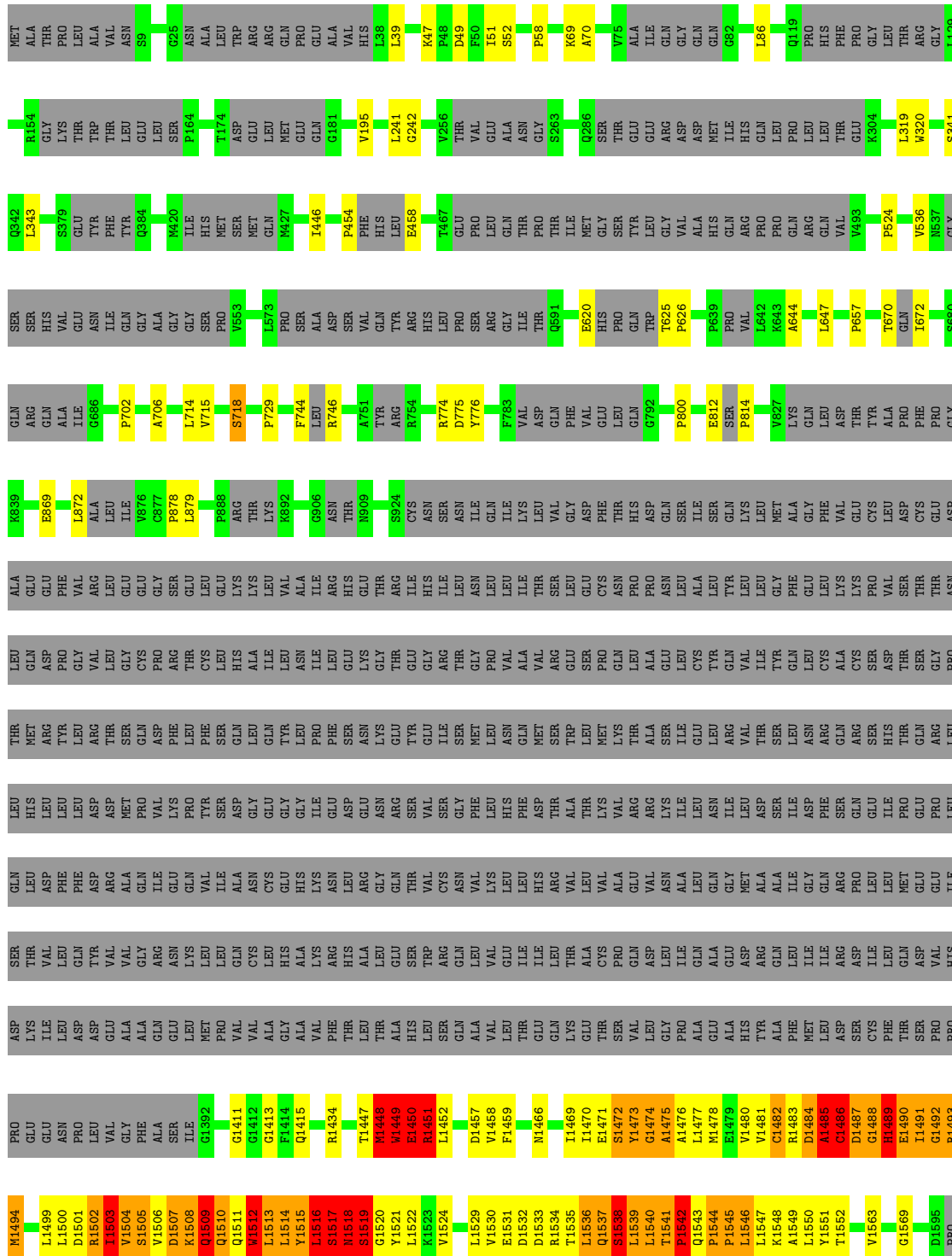
● Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

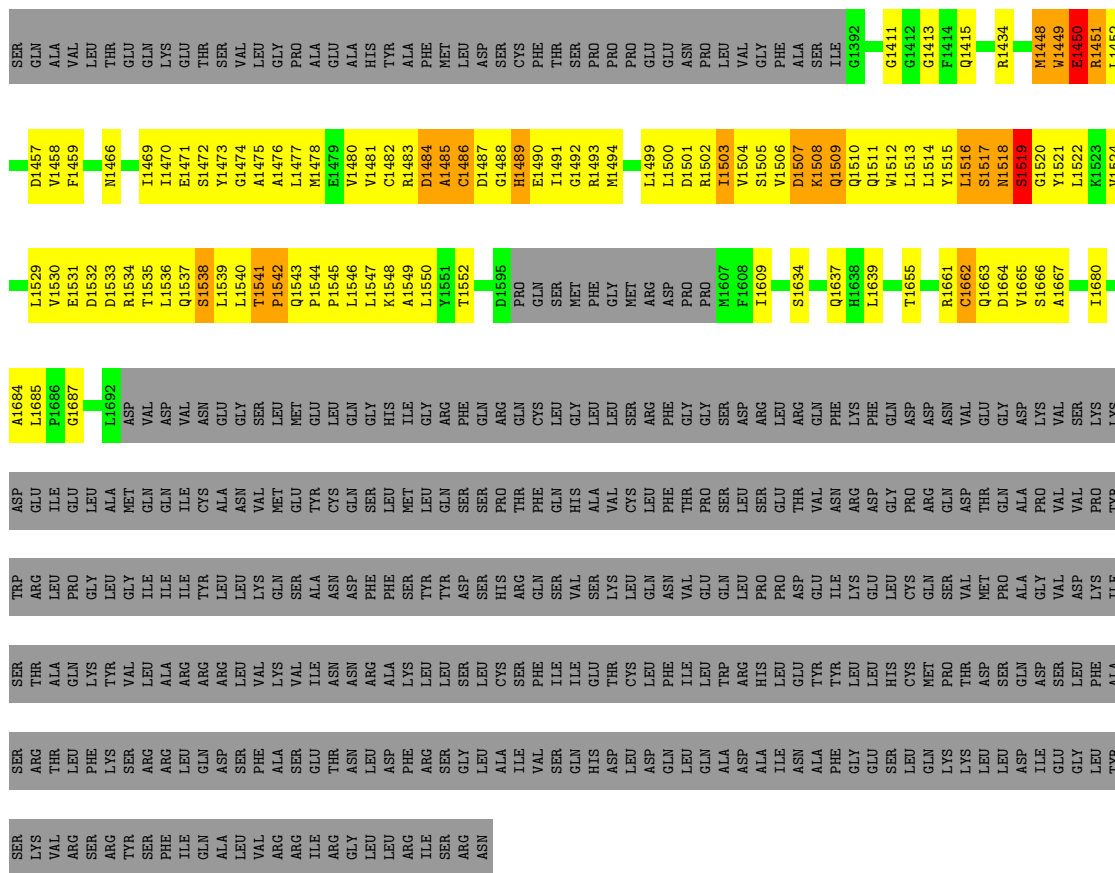


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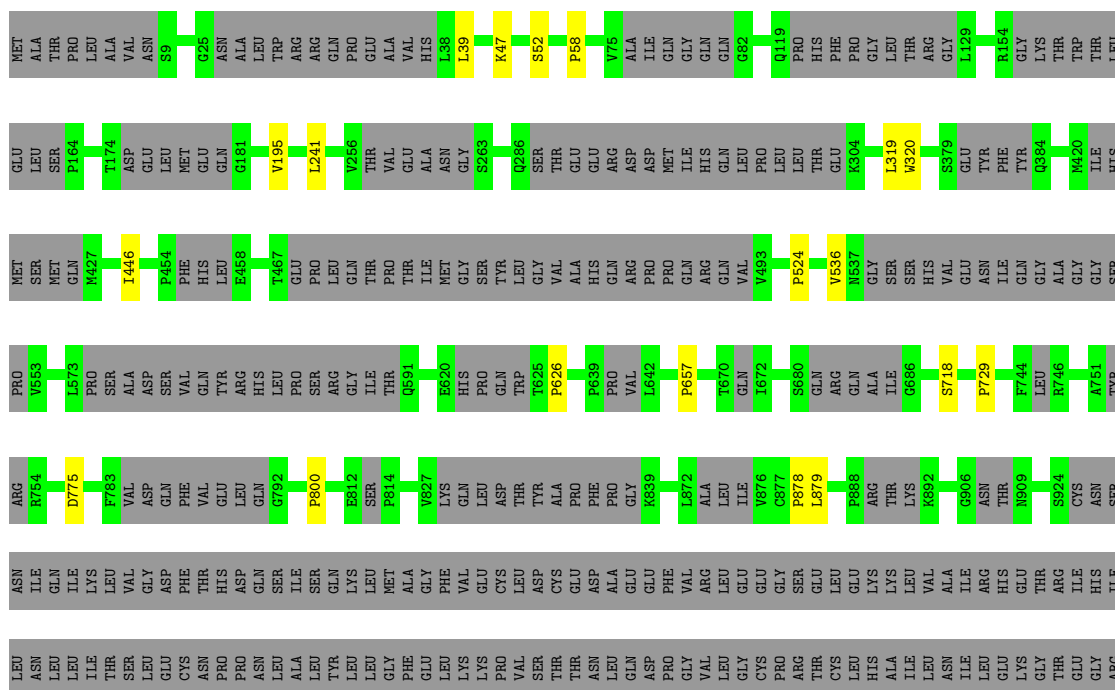
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

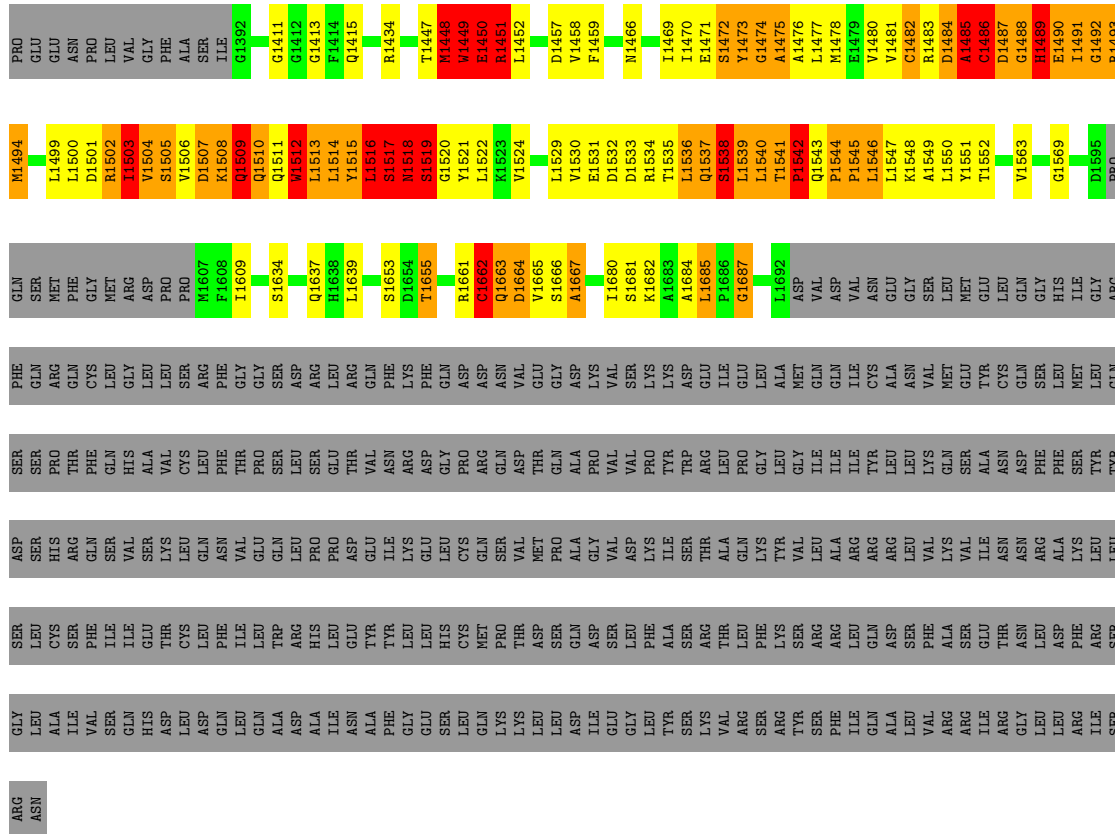
Chain 5-D: 43% 5% 49%



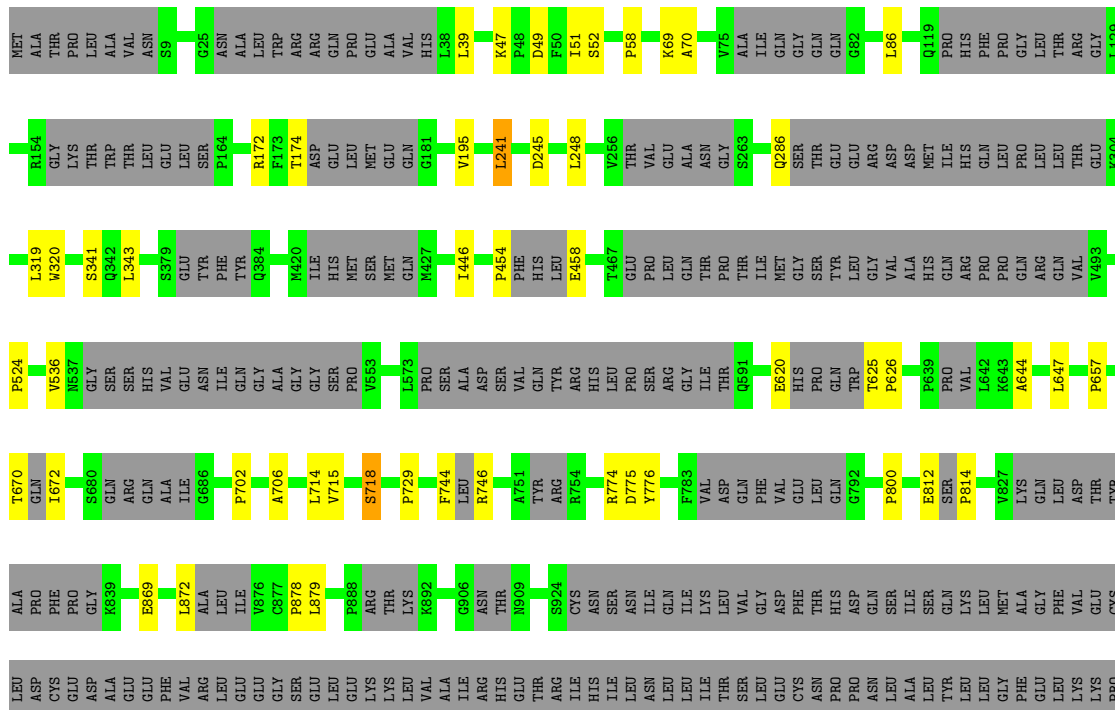


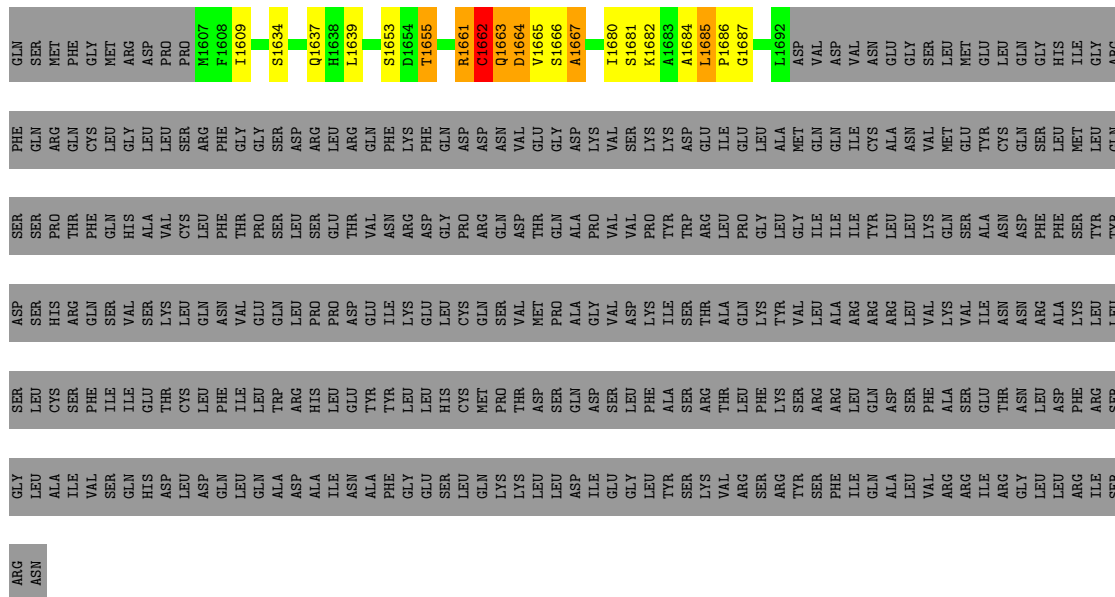
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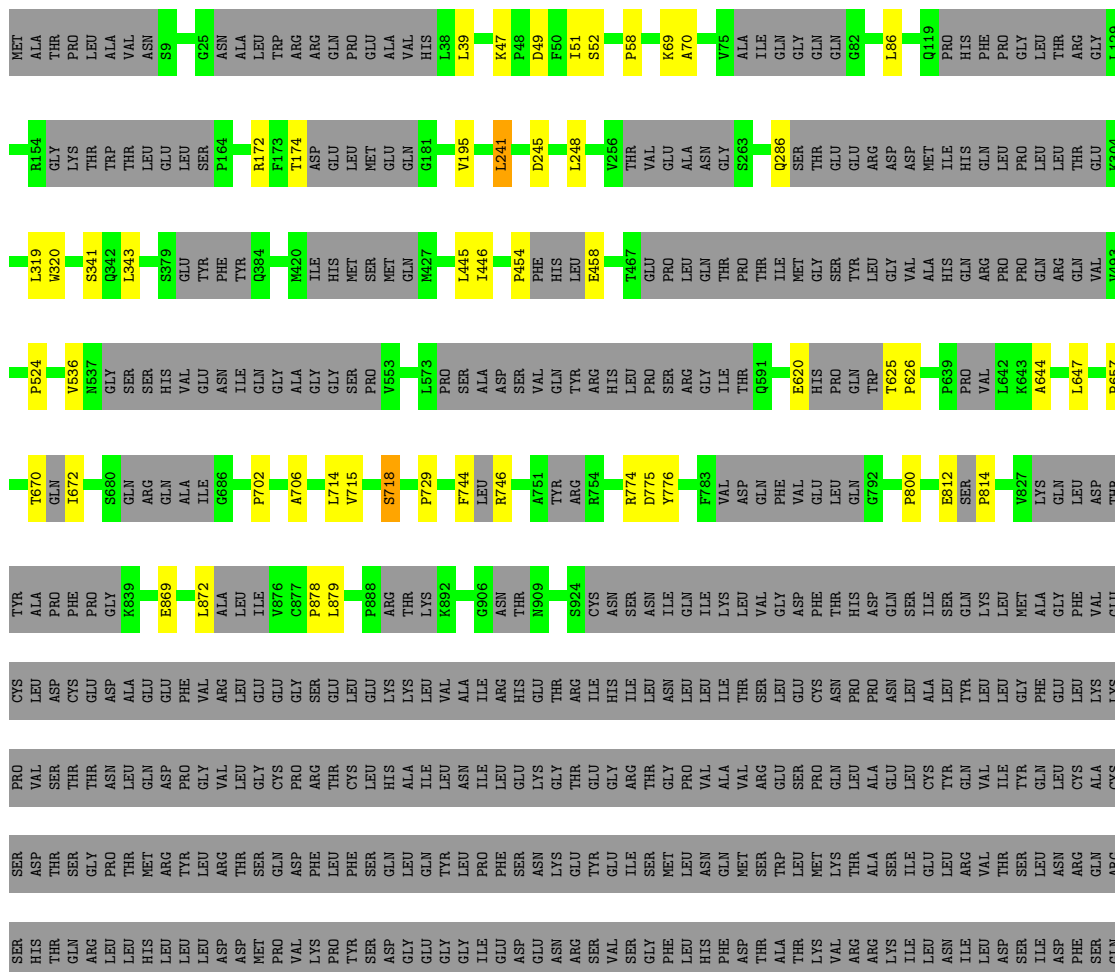


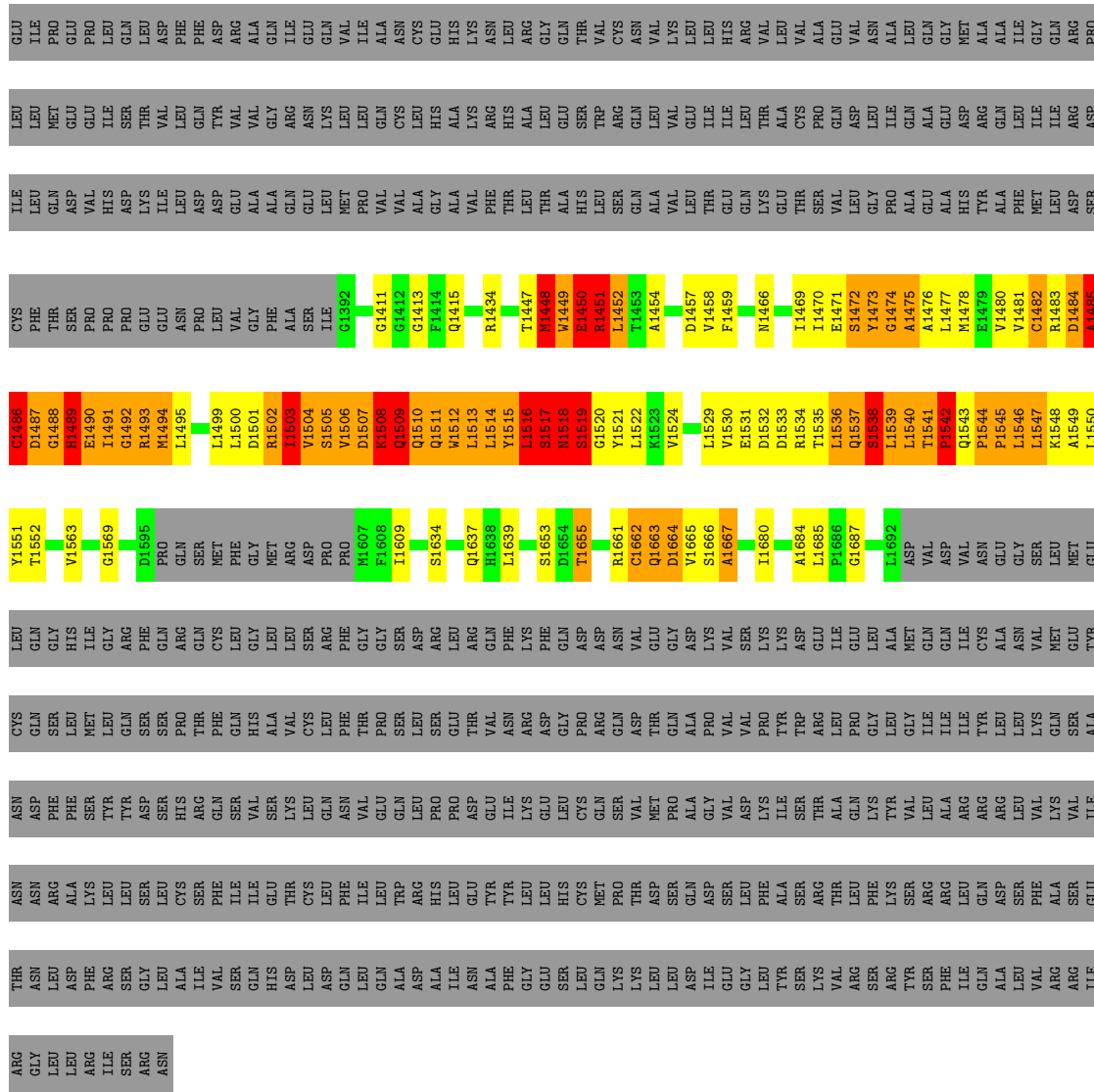
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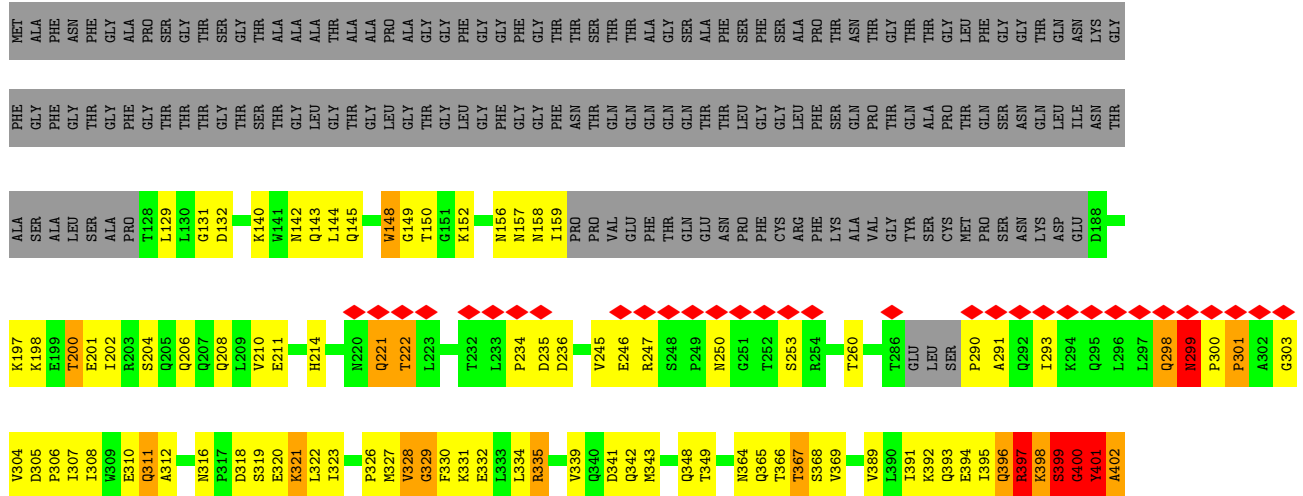
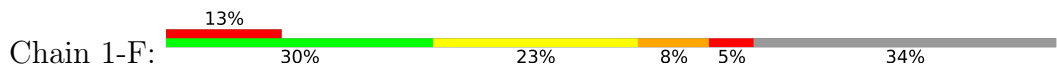


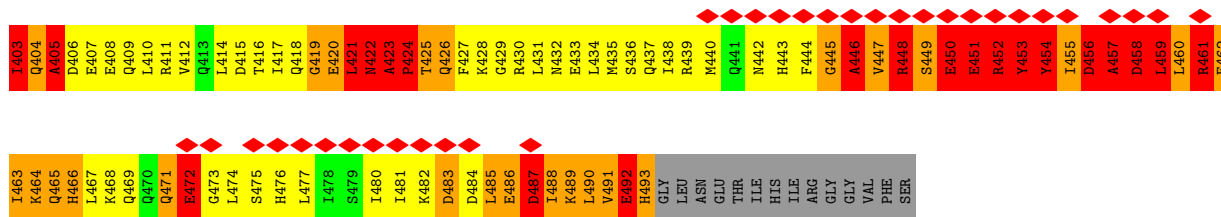
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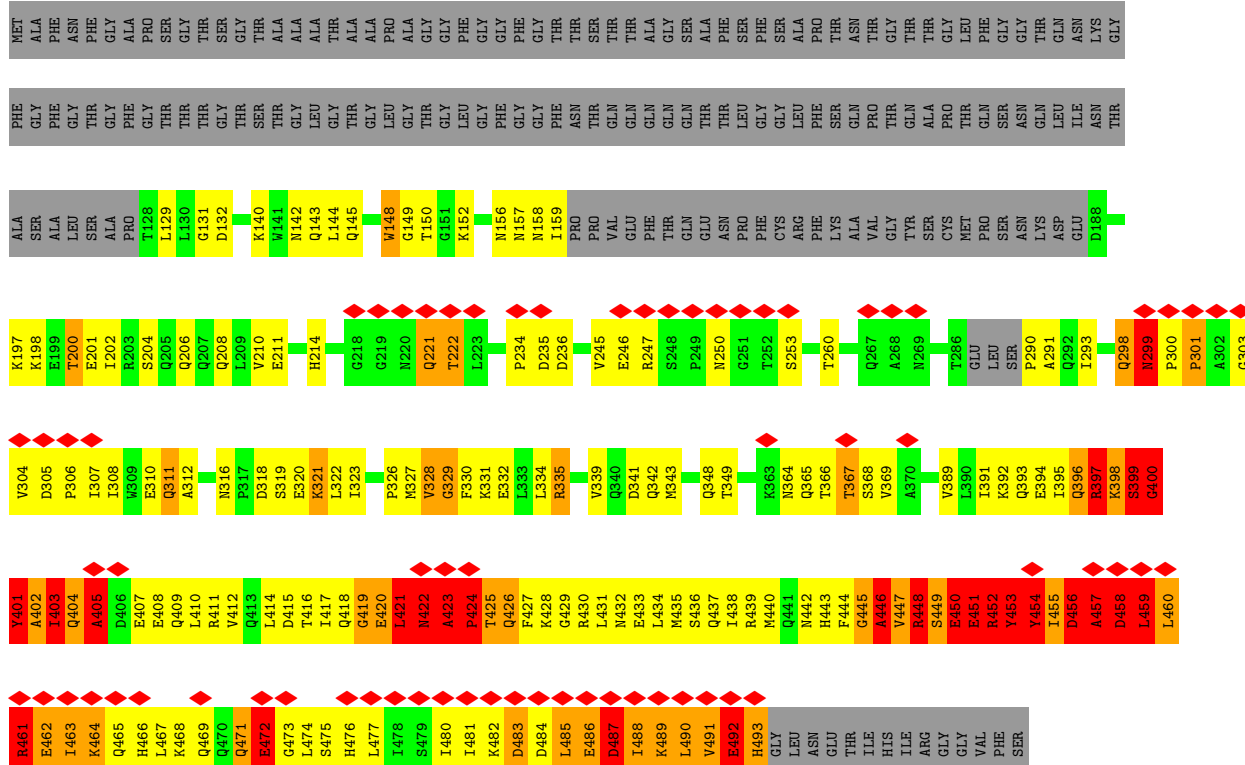
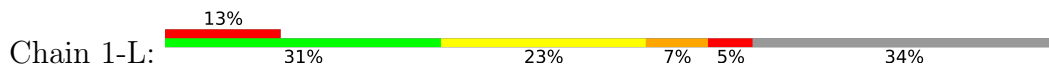


• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

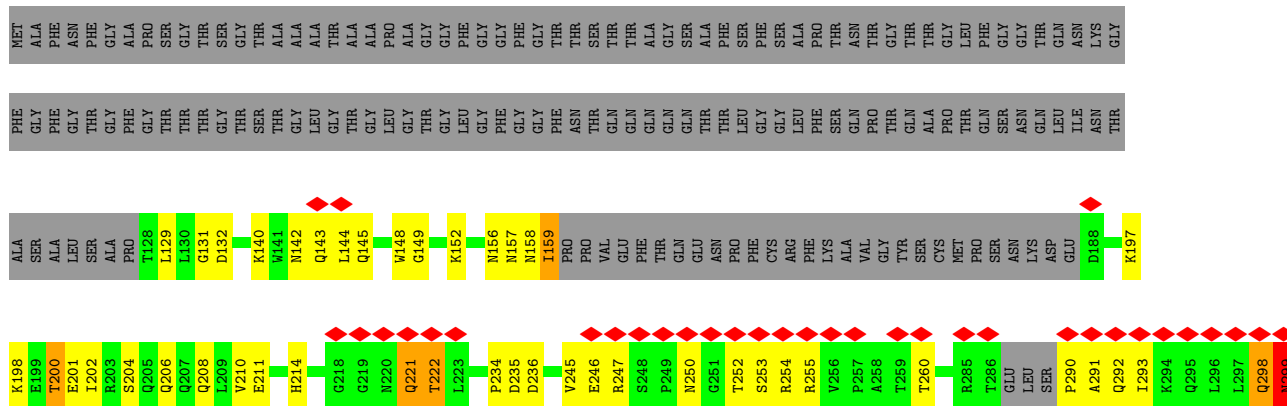
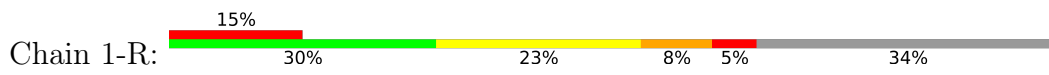


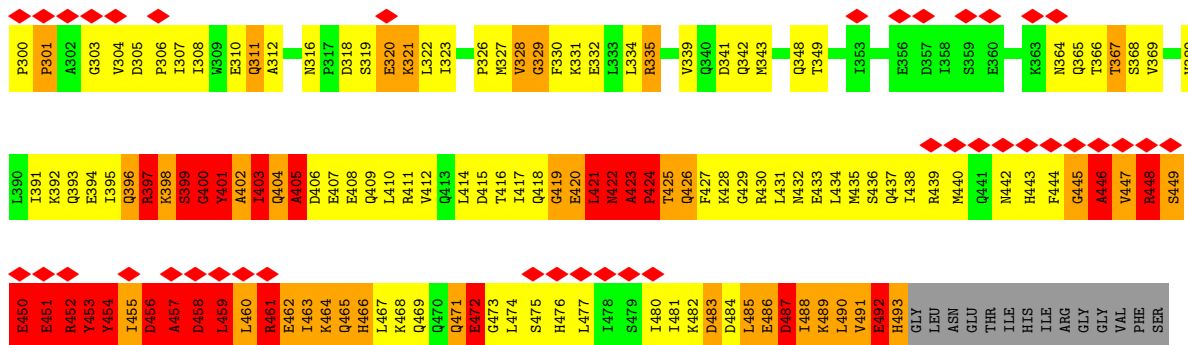


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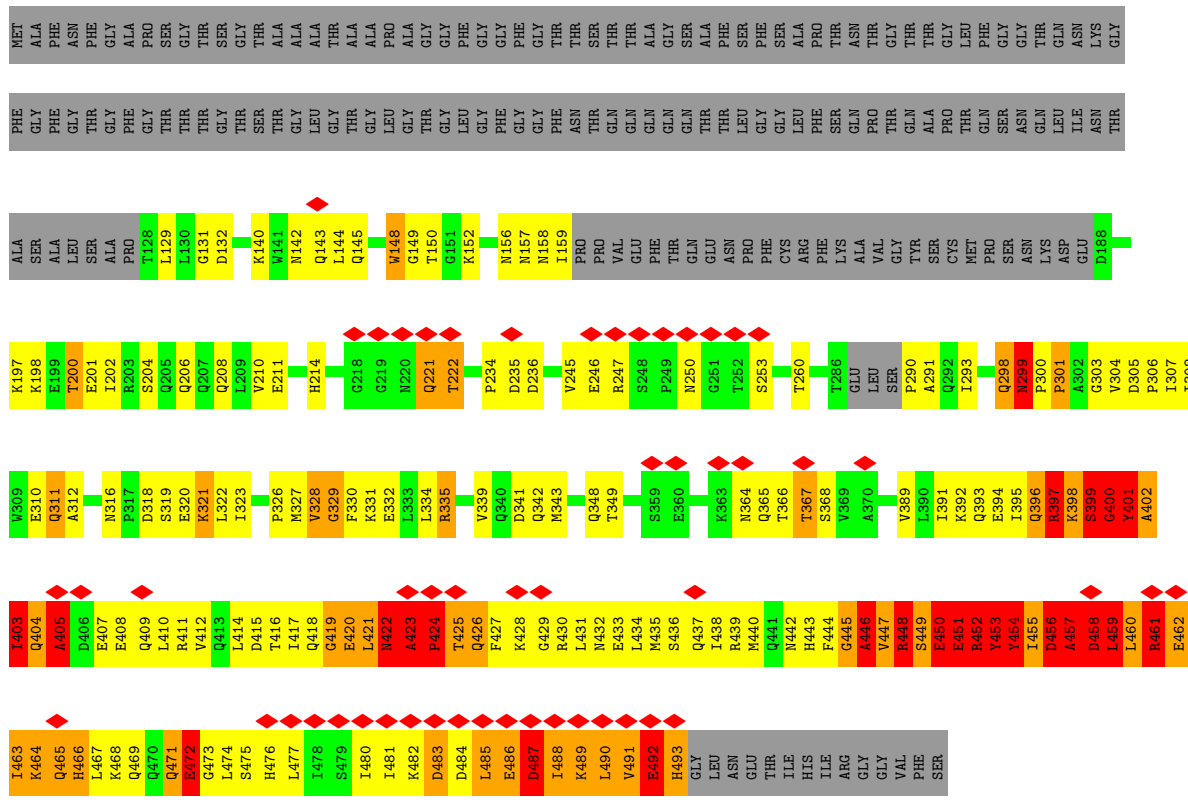
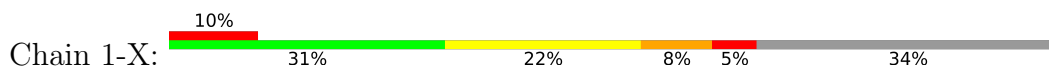


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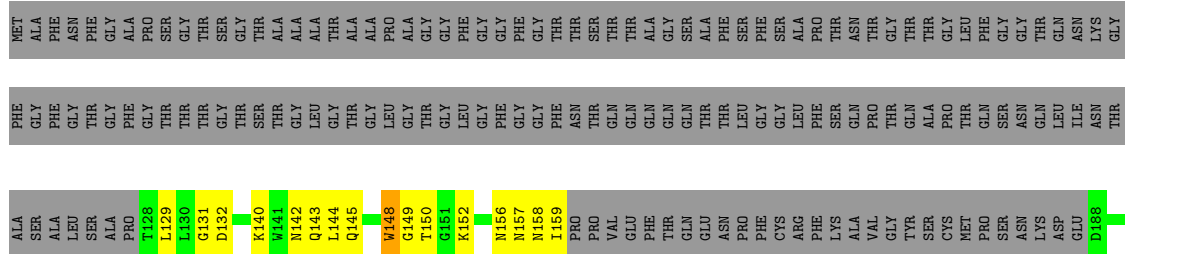
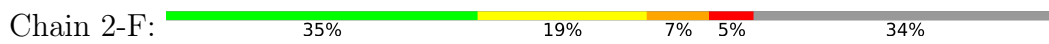


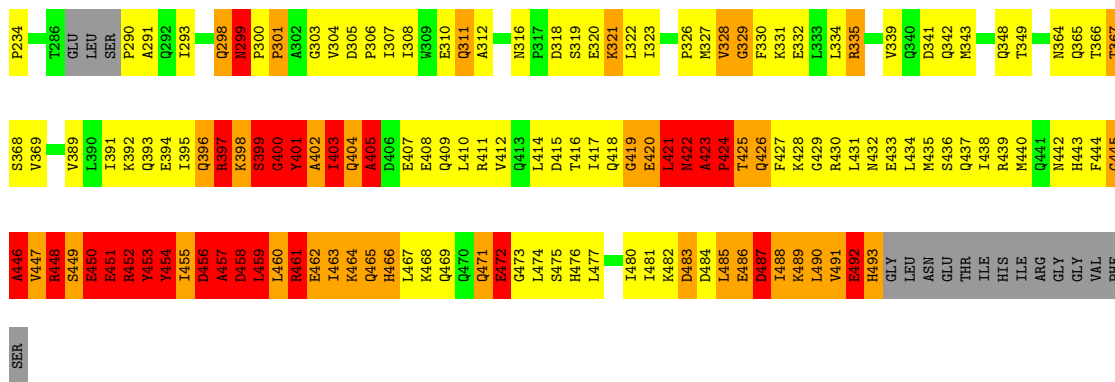


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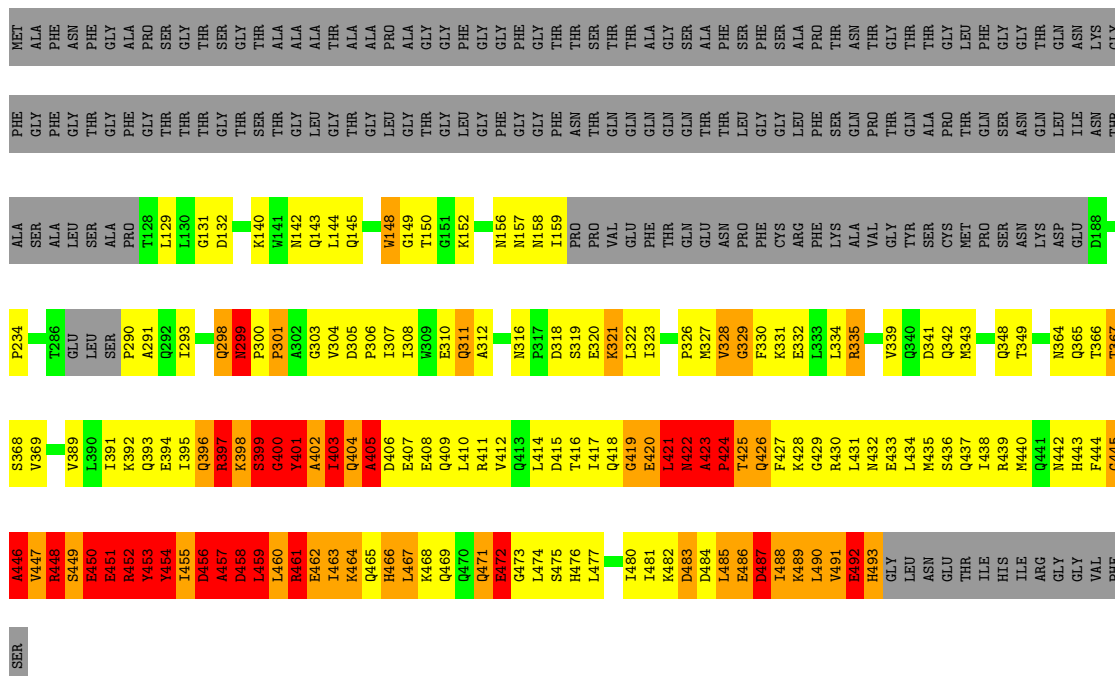


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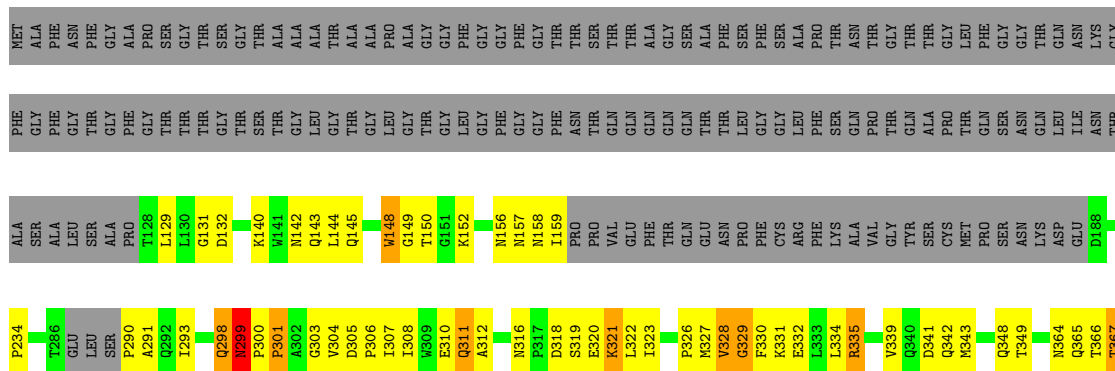
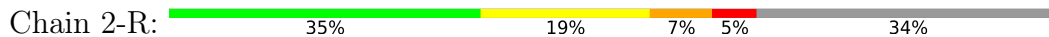


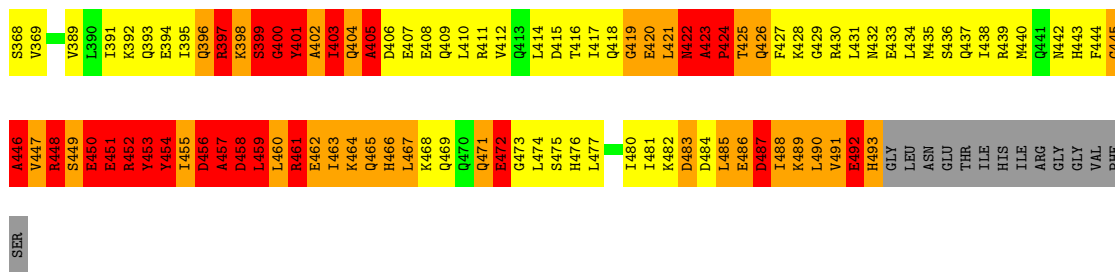


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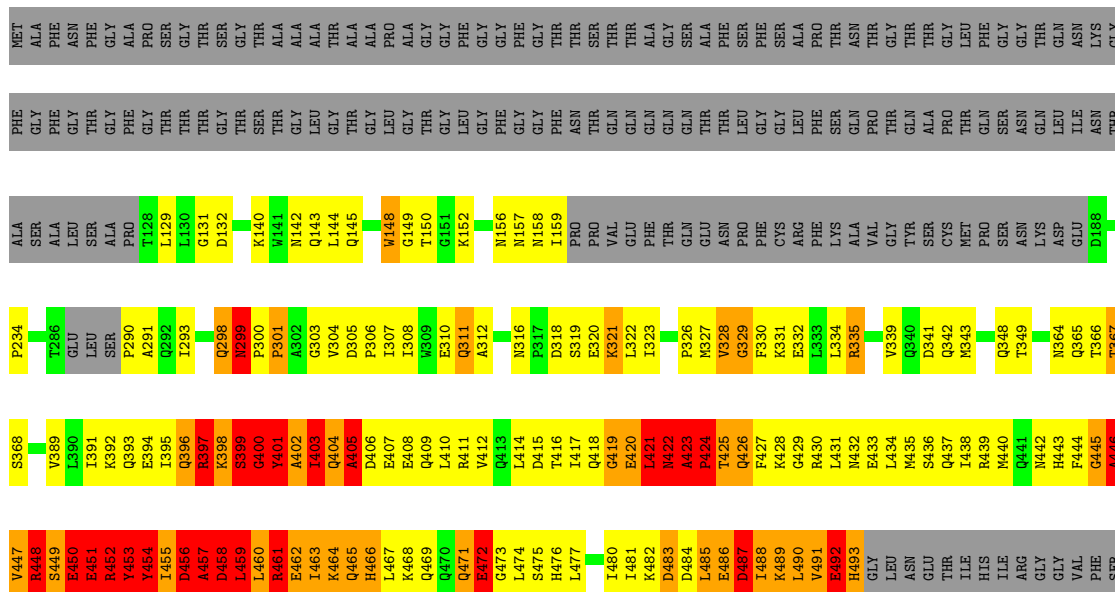


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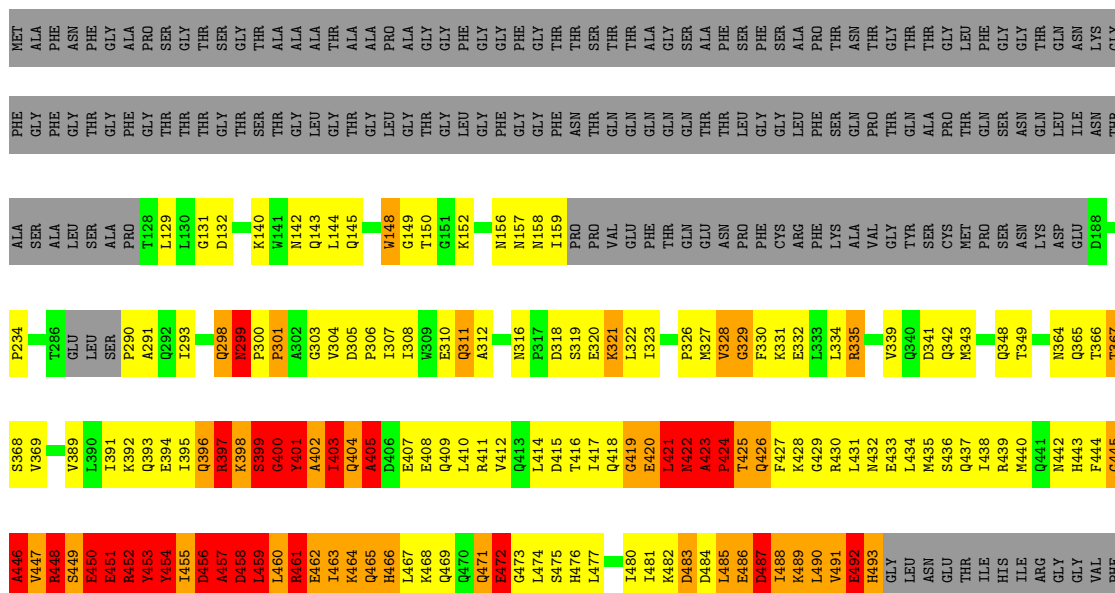
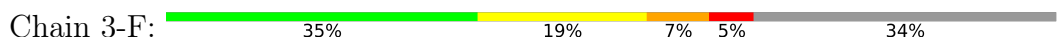




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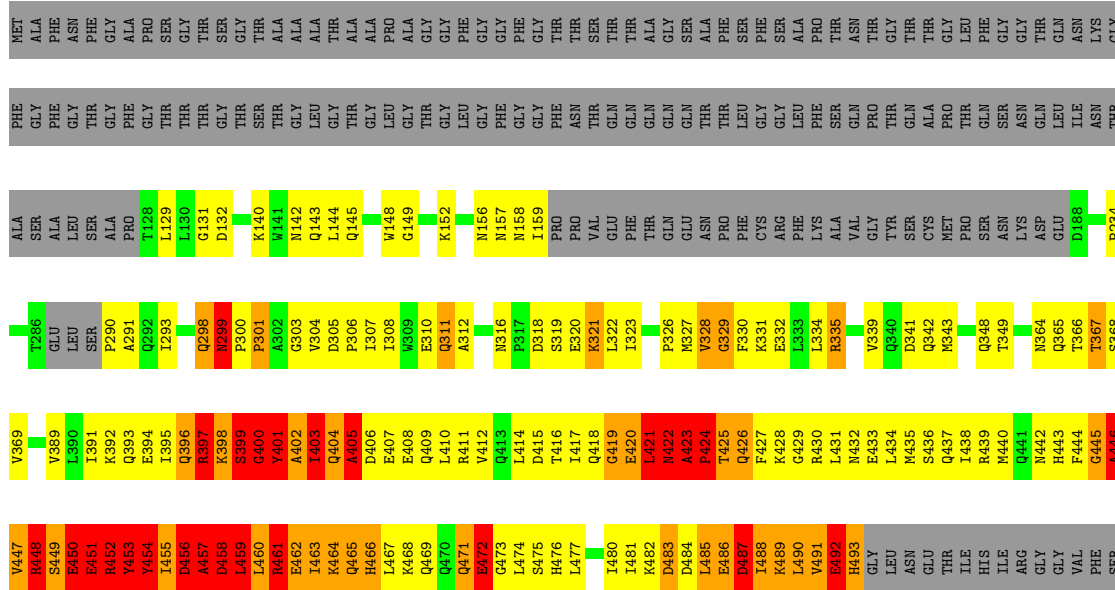
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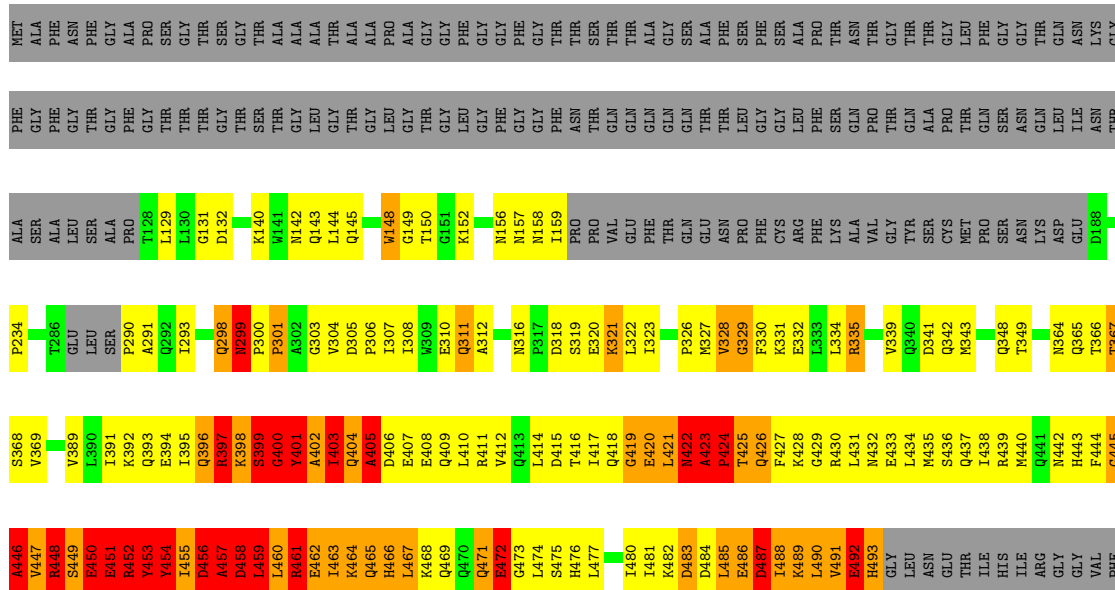
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 3-L: 35% 19% 7% 5% 34%



• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

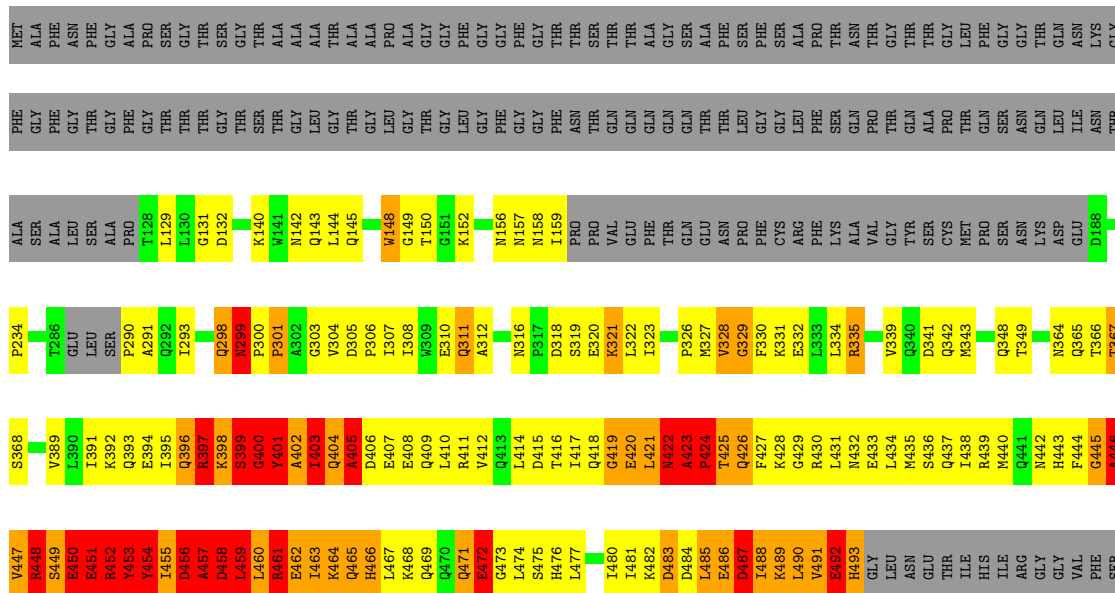
Chain 3-R: 35% 19% 7% 5% 34%



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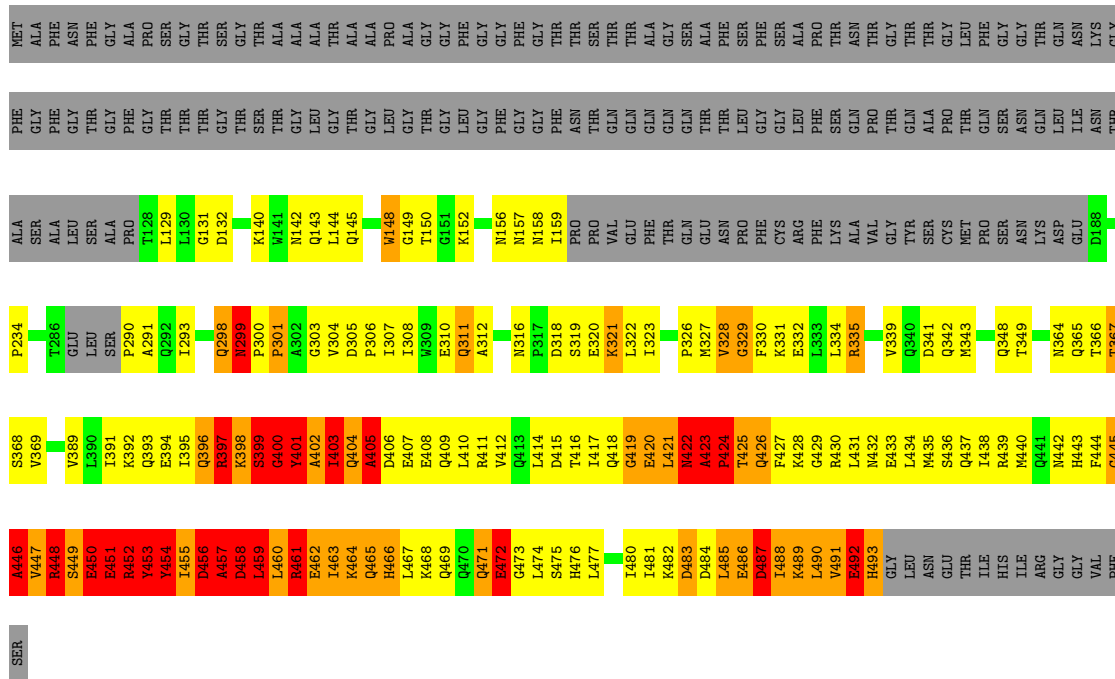
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 3-X: 35% 19% 7% 5% 34%



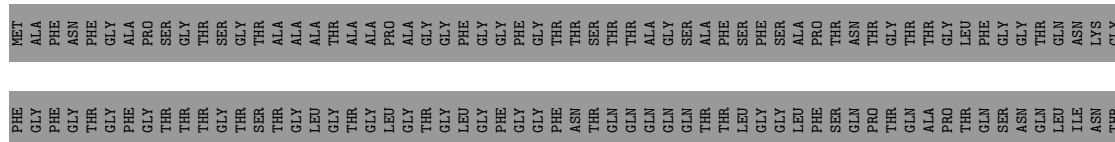
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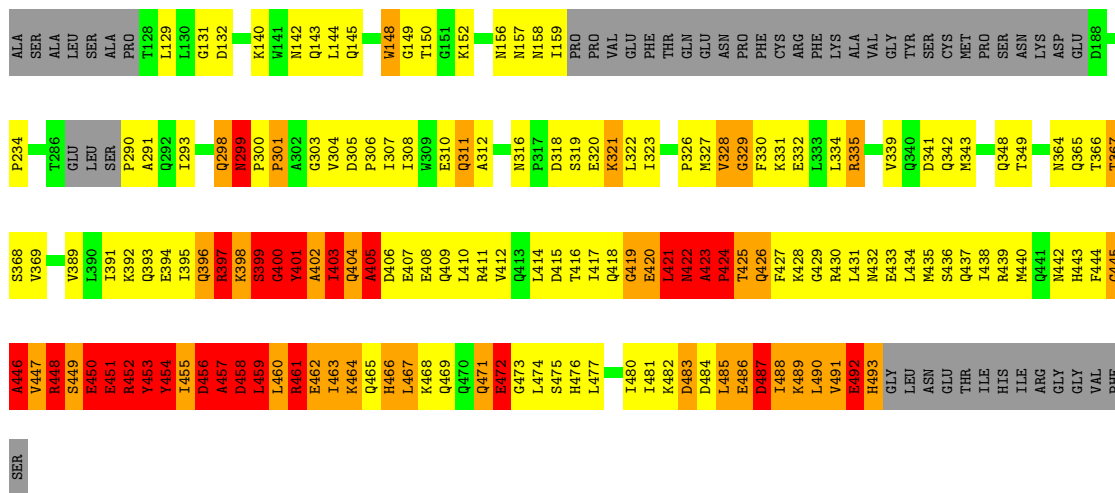
Chain 4-F: 35% 19% 7% 5% 34%



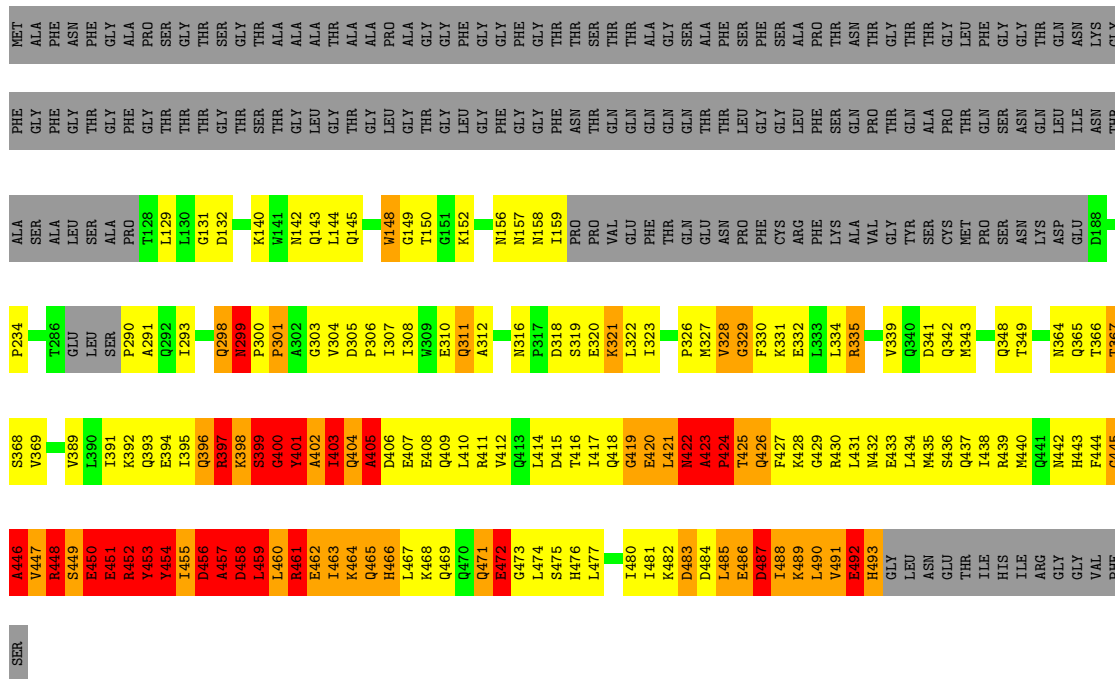
● Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 4-L: 35% 19% 7% 5% 34%

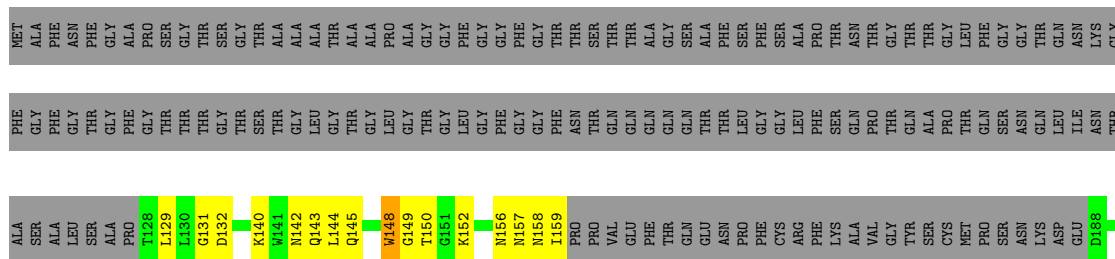
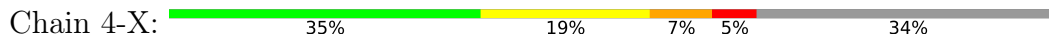


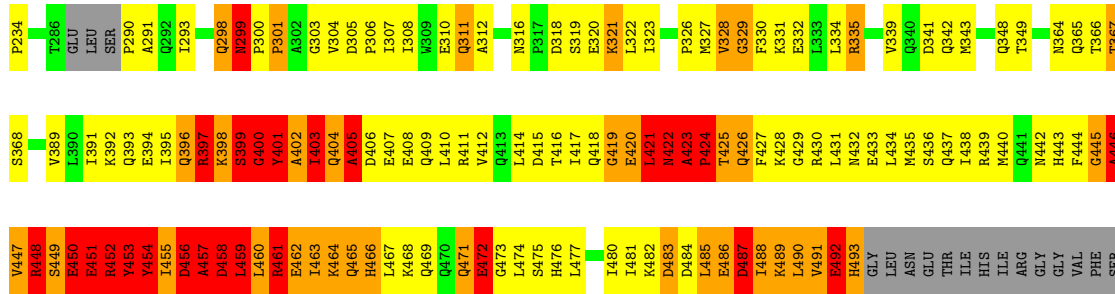


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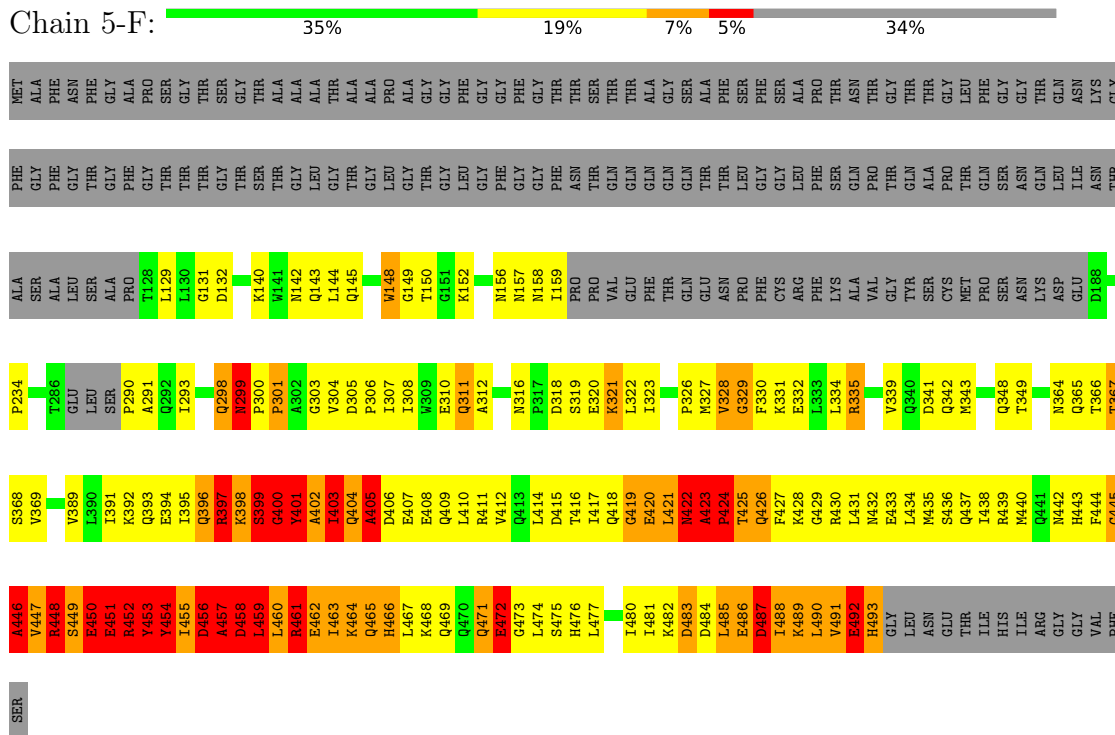


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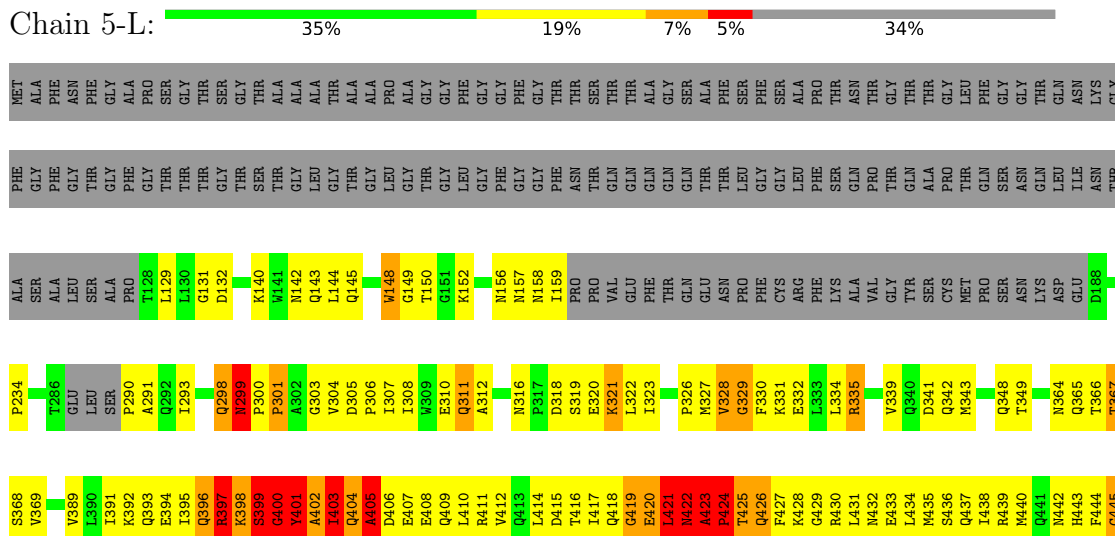


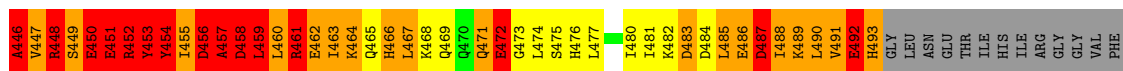


• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54



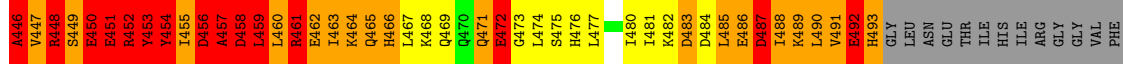
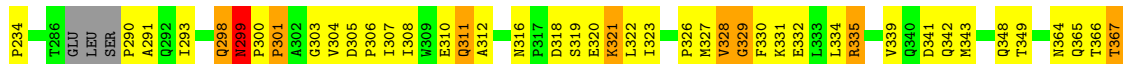
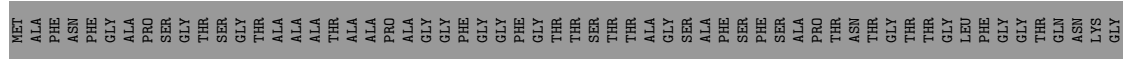
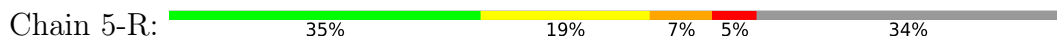
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54





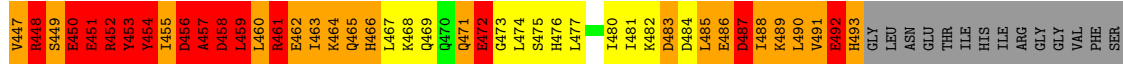
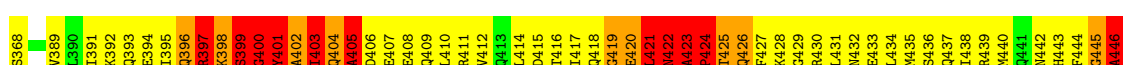
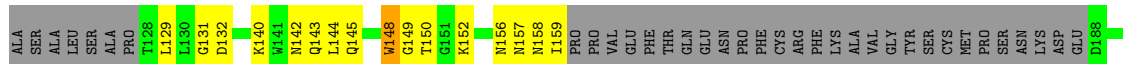
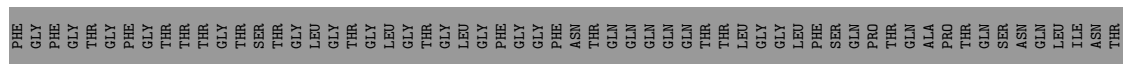
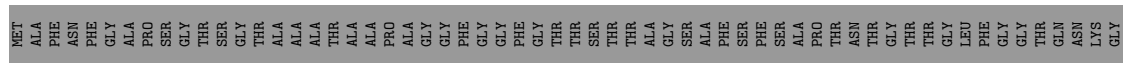
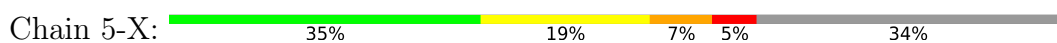
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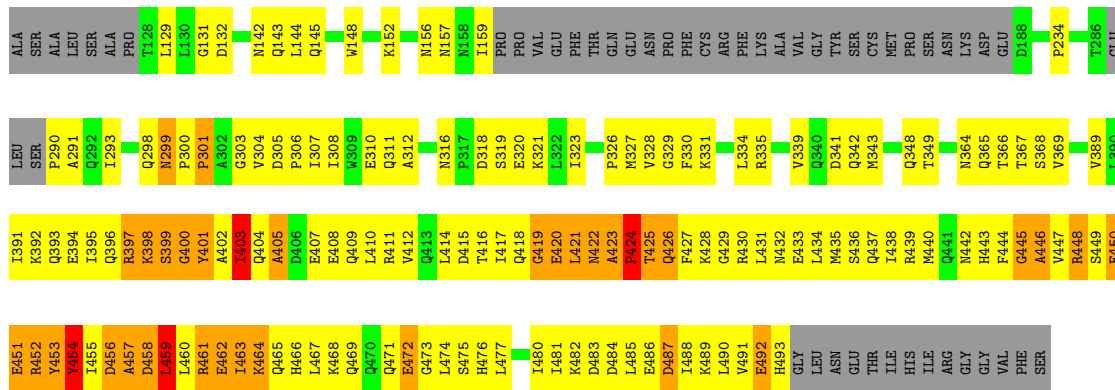
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54



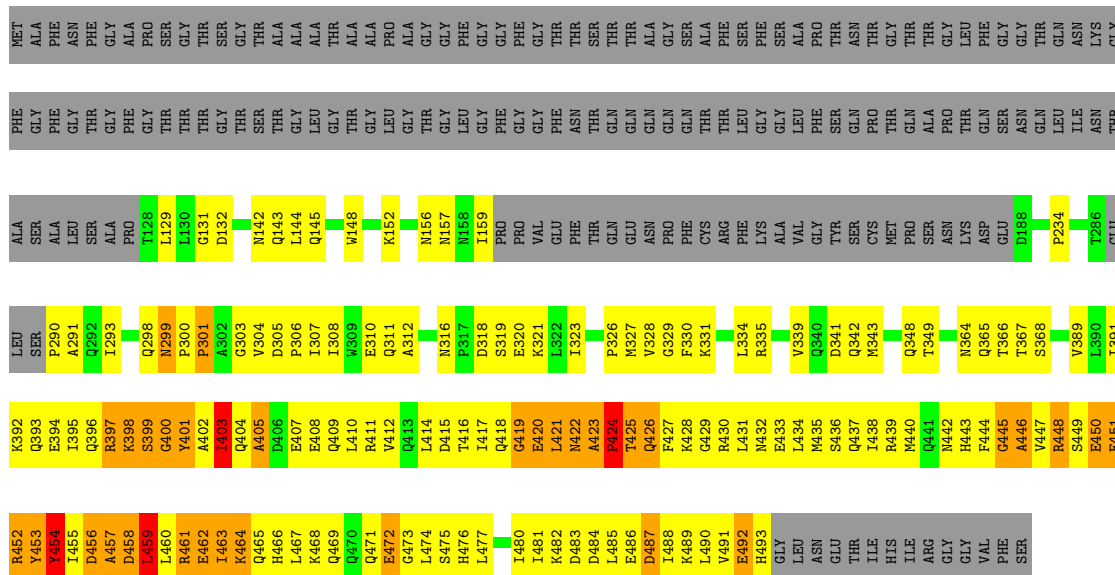
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• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

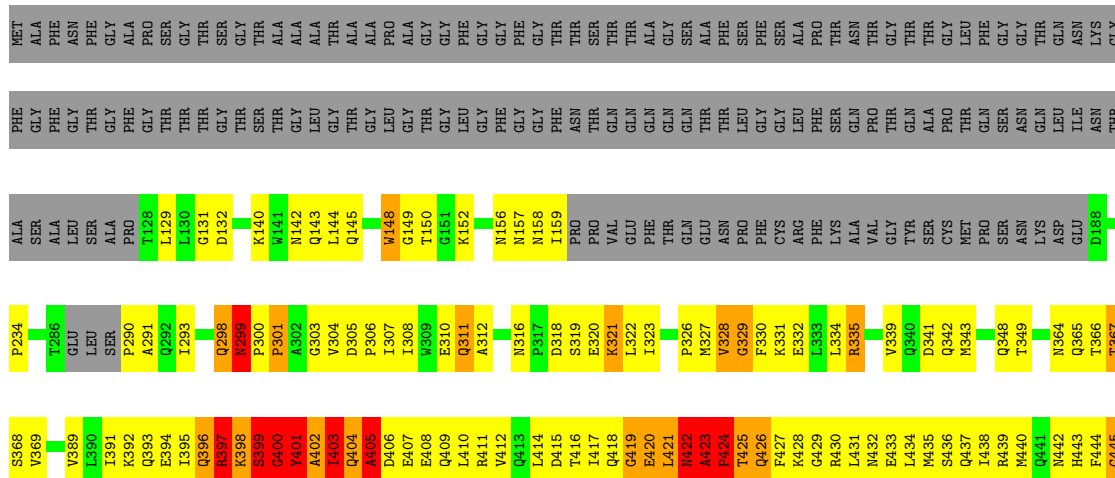


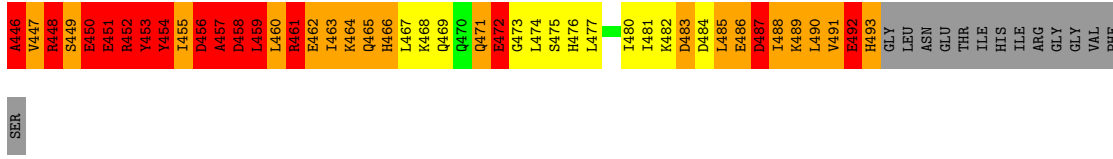


● Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

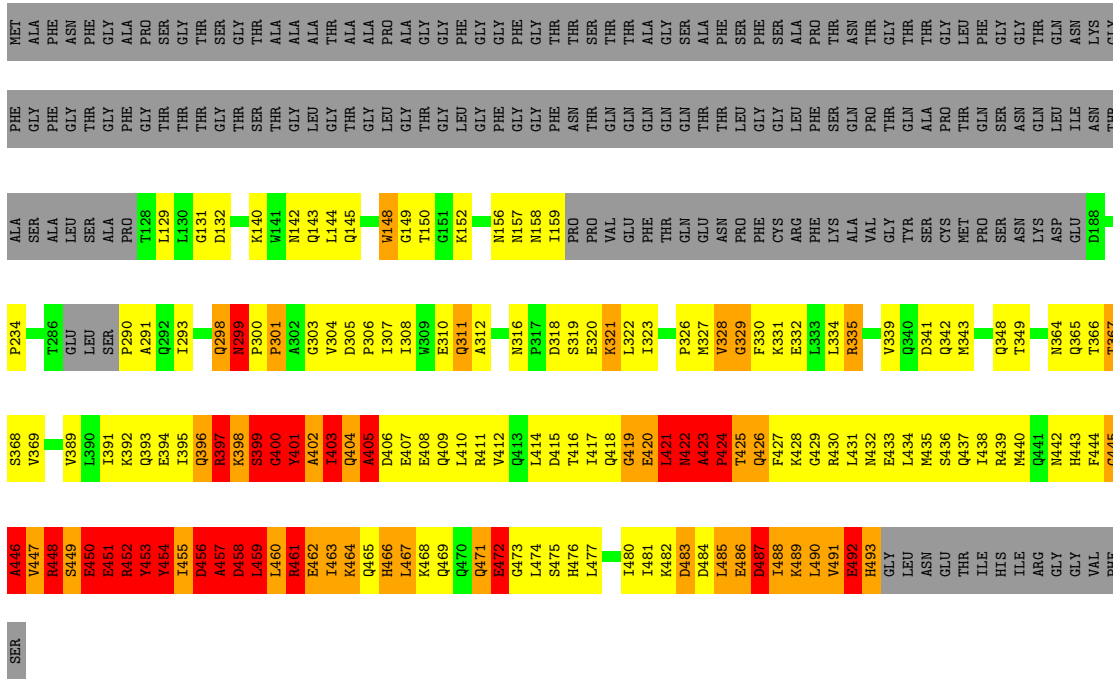
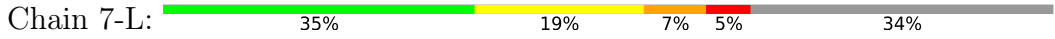


● Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

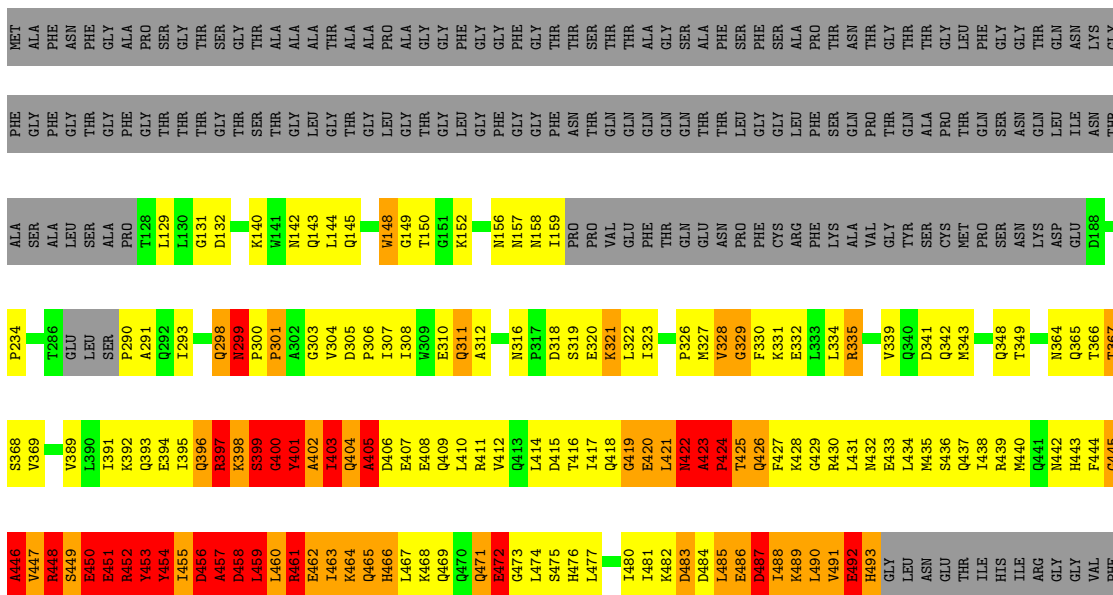
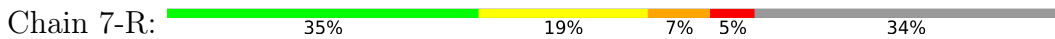


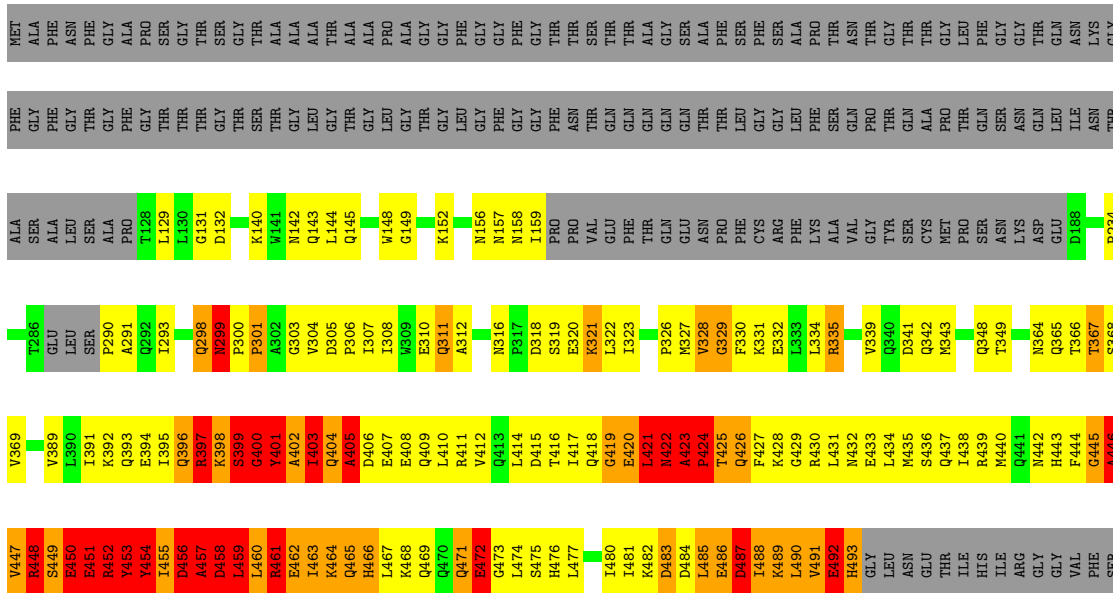


• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

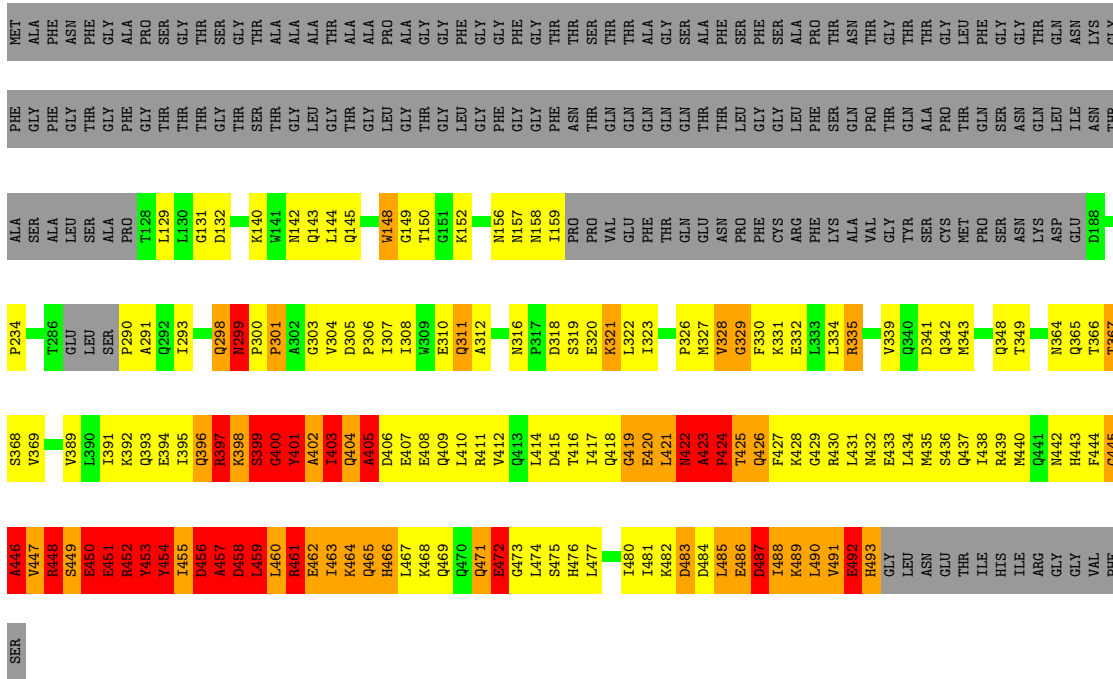
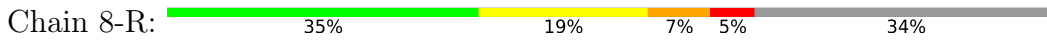


• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

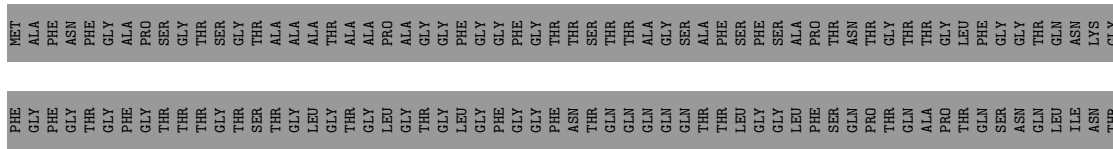
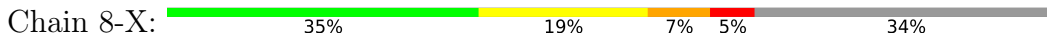


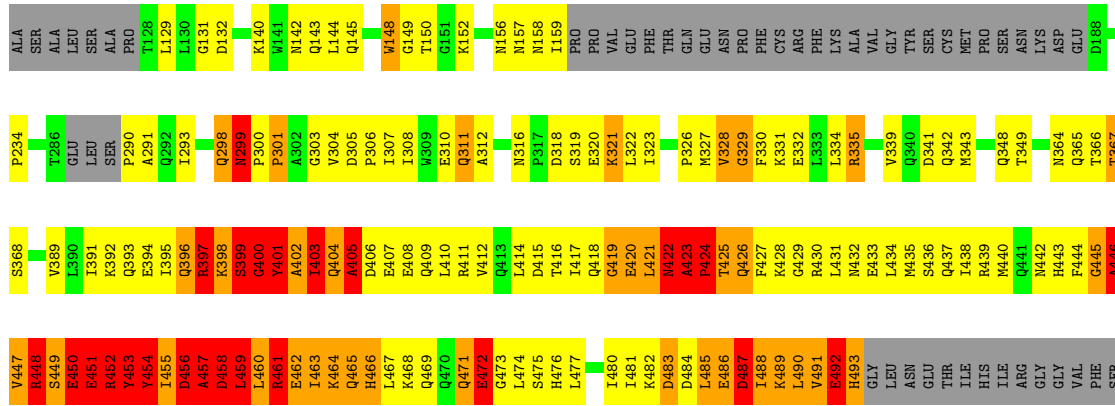


• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

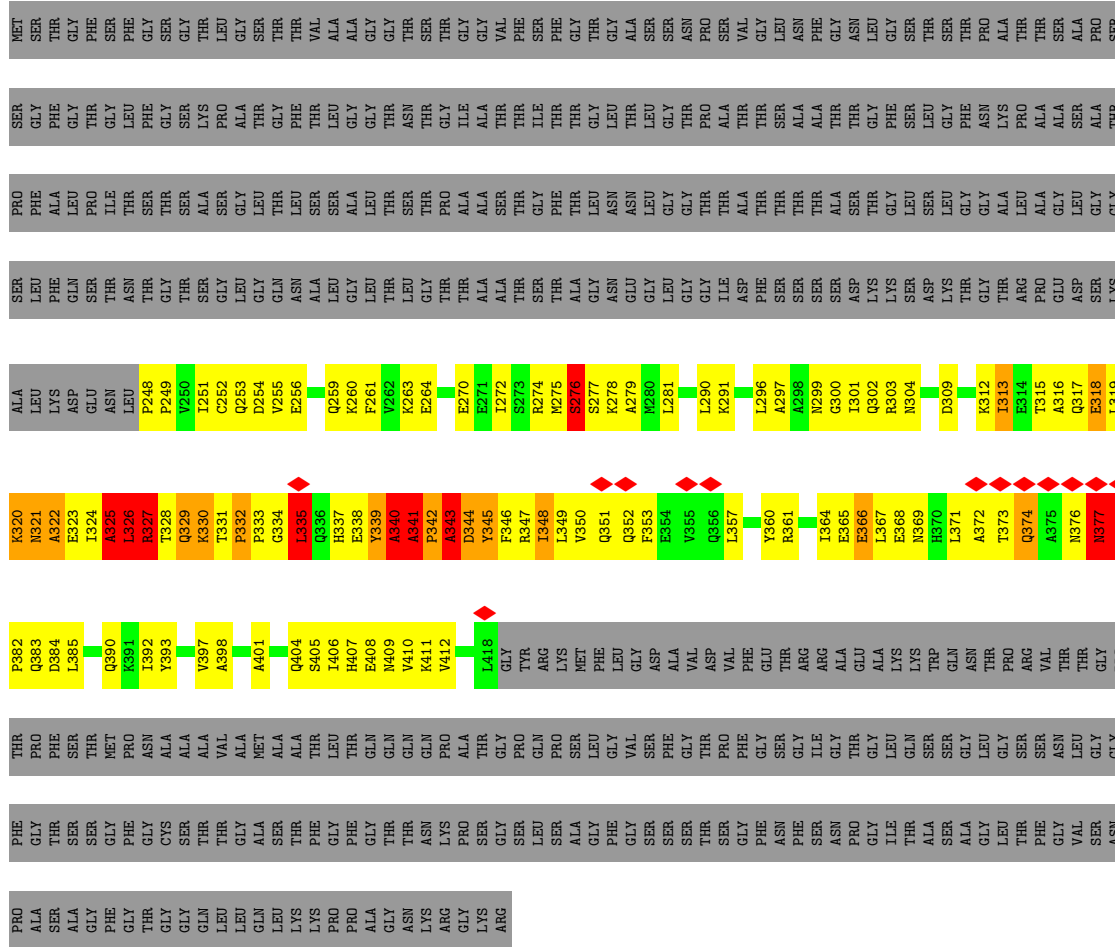


• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54





● Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58



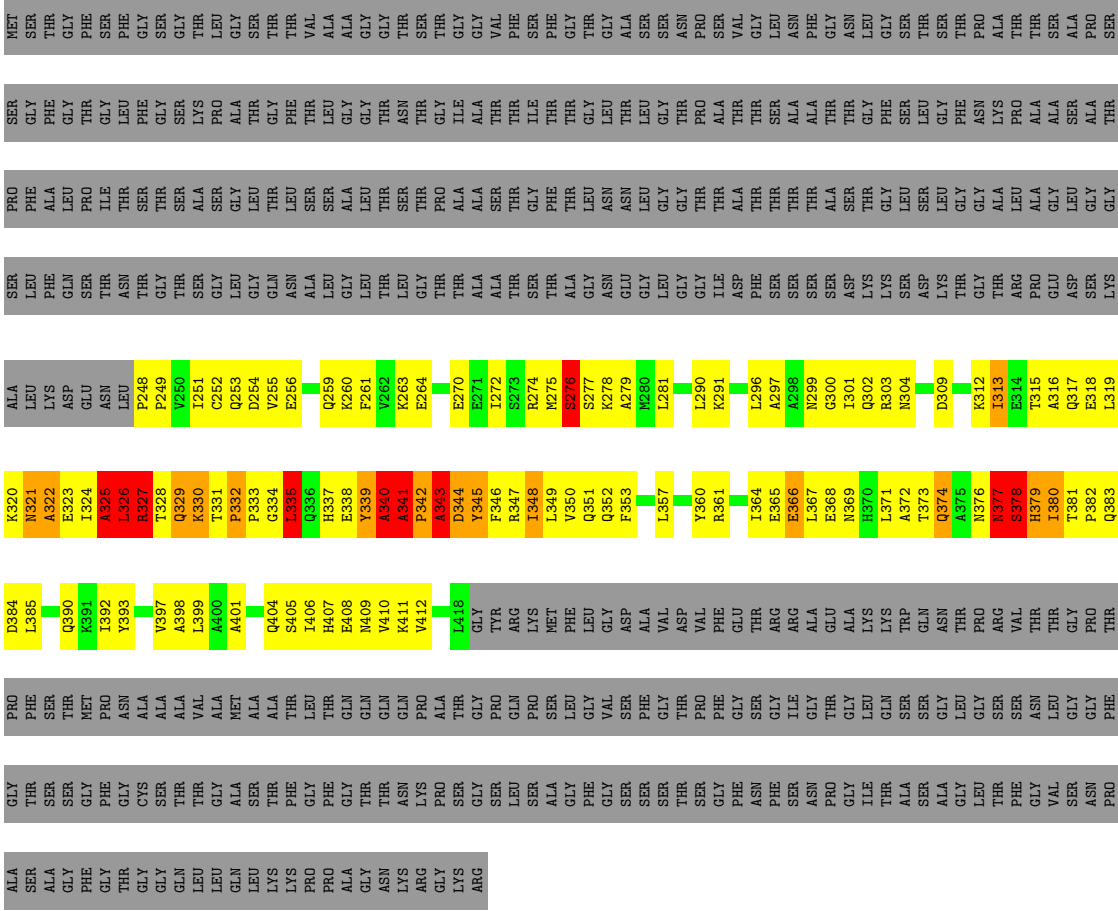
● Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58



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

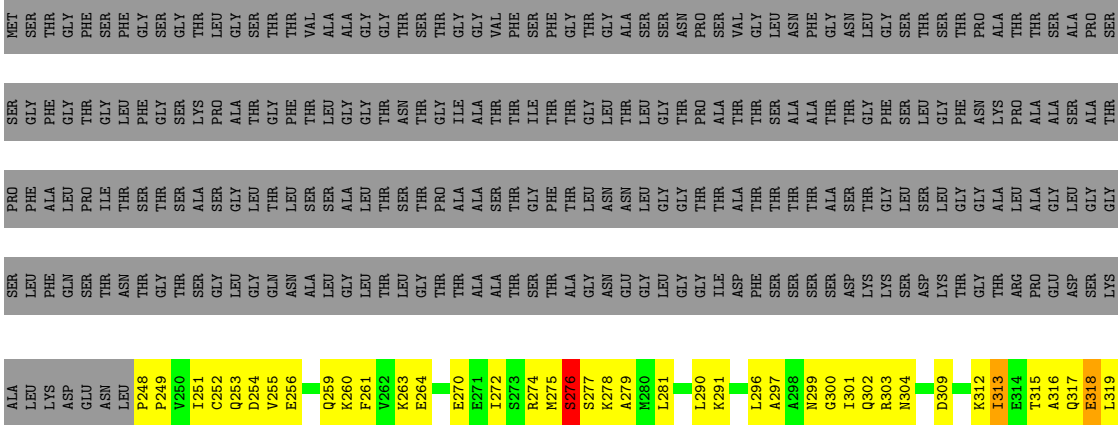
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

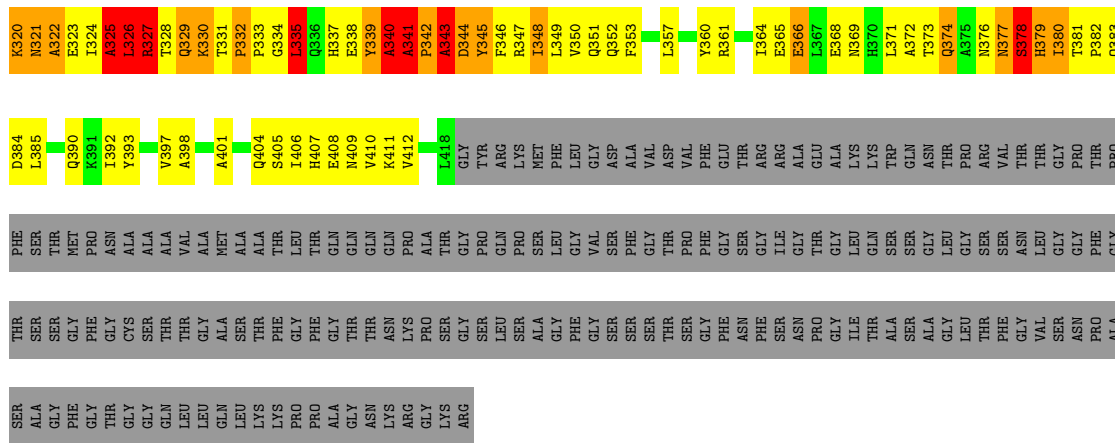
Chain 3-Y: 10% 15% . . . 71%



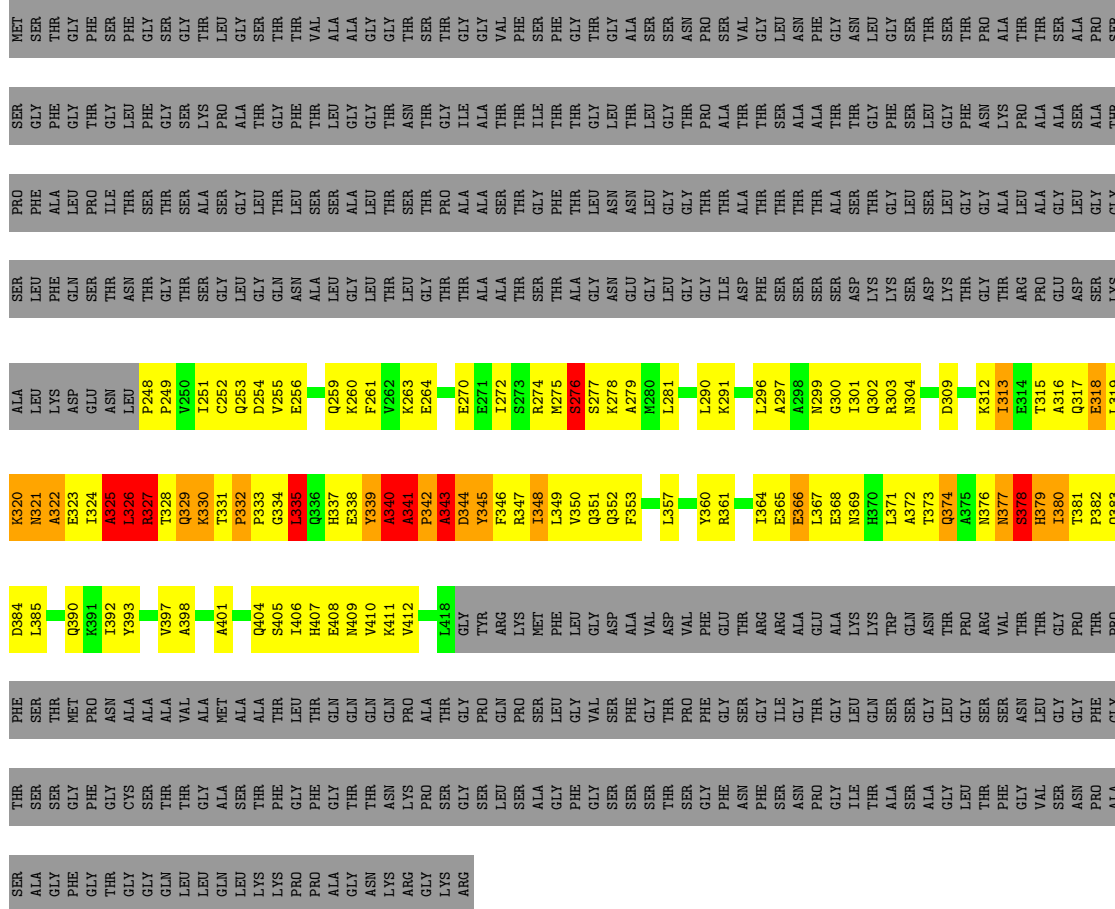
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 4-G: 10% 14% . . . 71%





● Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58



● Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58



ALA	K320	D384	PHE	THR	SER	SER	ALA
LEU	N321	L385	SER	SER	GLY	ALA	GLY
LYS	A322	Q390	THR	GLY	PHE	GLY	THR
ASP	E323	K391	MET	GLY	THR	THR	THR
GLU	I324	I392	PHE	THR	GLY	GLY	GLY
ASN	A325	Y393	GLY	GLY	ASN	GLY	GLY
LEU	L326	R327	ALA	PHE	GLY	GLY	GLY
P248	R328	V397	ALA	GLY	THR	GLN	GLN
P249	T328	A398	ALA	SER	THR	LEU	LEU
V250	Q329	K330	VAL	THR	THR	LEU	LEU
I251	K330	K330	VAL	THR	THR	LEU	LEU
C252	T331	T331	ALA	GLY	THR	LEU	LEU
Q253	P332	A401	MET	ALA	ALA	GLN	GLN
D254	P333	Q404	ALA	SER	ALA	LEU	LEU
V255	G334	S405	ALA	THR	THR	LEU	LEU
E256	L335	I406	PHE	THR	THR	LEU	LEU
Q259	Q336	H407	THR	THR	THR	LEU	LEU
K260	H337	E408	ALA	ALA	ALA	GLY	GLY
F261	E338	N409	ALA	GLY	GLY	GLY	GLY
V262	Y339	V410	THR	THR	THR	GLY	GLY
K262	A340	K411	GLN	ASN	ASN	GLN	GLN
E264	P342	V412	ALA	PRO	PRO	ALA	ALA
E270	A343	L418	THR	THR	THR	GLY	GLY
E271	D344	L418	GLY	GLY	GLY	THR	THR
I272	Y345	TYR	PRO	PRO	PRO	GLY	GLY
S273	F346	ARG	LEU	LEU	LEU	SER	SER
R274	R347	ARG	LEU	LEU	LEU	THR	THR
M275	I348	LYS	SER	SER	SER	THR	THR
S276	L349	ALA	GLY	GLY	GLY	THR	THR
S277	V350	PHE	THR	THR	THR	THR	THR
K278	Q351	GLY	THR	THR	THR	THR	THR
A279	Q352	VAL	THR	THR	THR	THR	THR
M280	F353	VAL	THR	THR	THR	THR	THR
L281	L357	ASP	THR	THR	THR	THR	THR
L290	Y360	VAL	PRO	PRO	PRO	PRO	PRO
K291	R361	PHE	GLY	GLY	GLY	GLY	GLY
L296	I364	THR	ASN	ASN	ASN	ASN	ASN
A297	E365	GLY	PHE	PHE	PHE	PHE	PHE
A298	E366	ARG	THR	THR	THR	THR	THR
N299	L367	ALA	ASN	ASN	ASN	ASN	ASN
G300	E368	GLU	GLY	GLY	GLY	GLY	GLY
I301	N369	ALA	ILE	ILE	ILE	ILE	ILE
Q302	H370	LYS	THR	THR	THR	THR	THR
R303	L371	TRP	GLN	GLN	GLN	GLN	GLN
N304	A372	GLN	ALA	ALA	ALA	ALA	ALA
D309	T373	ASN	GLY	GLY	GLY	GLY	GLY
K312	Q374	THR	LEU	LEU	LEU	LEU	LEU
I313	A375	PRO	GLY	GLY	GLY	GLY	GLY
E314	N376	ARG	THR	THR	THR	THR	THR
T315	S377	VAL	PHE	PHE	PHE	PHE	PHE
A316	S378	THR	GLY	GLY	GLY	GLY	GLY
A318	H379	VAL	ASN	ASN	ASN	ASN	ASN
E318	I380	THR	LEU	LEU	LEU	LEU	LEU
L319	T381	GLY	SER	SER	SER	SER	SER
L319	P382	THR	PRO	PRO	PRO	PRO	PRO
L319	Q383	PRO	ALA	ALA	ALA	ALA	ALA

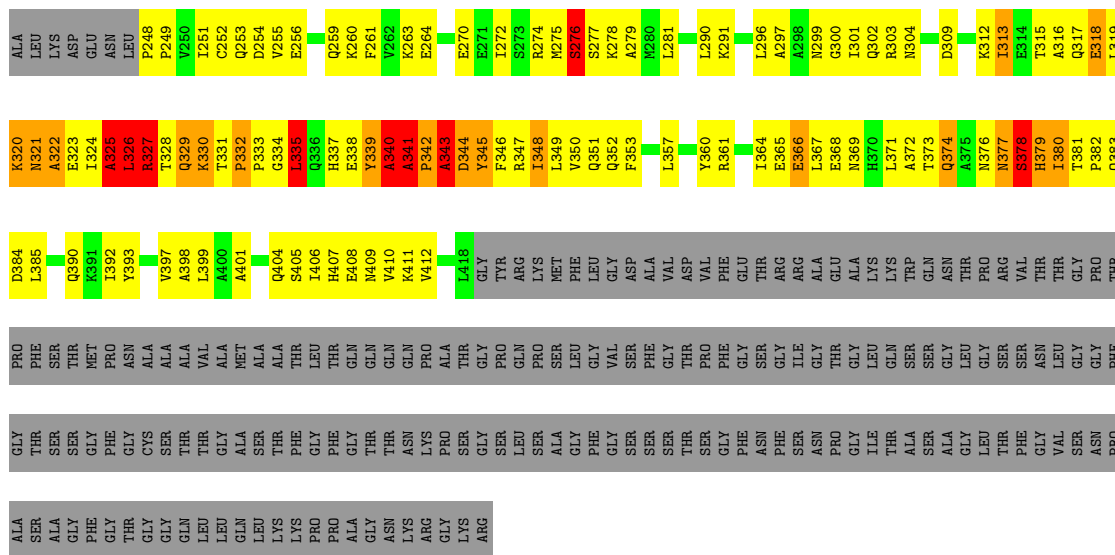
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58



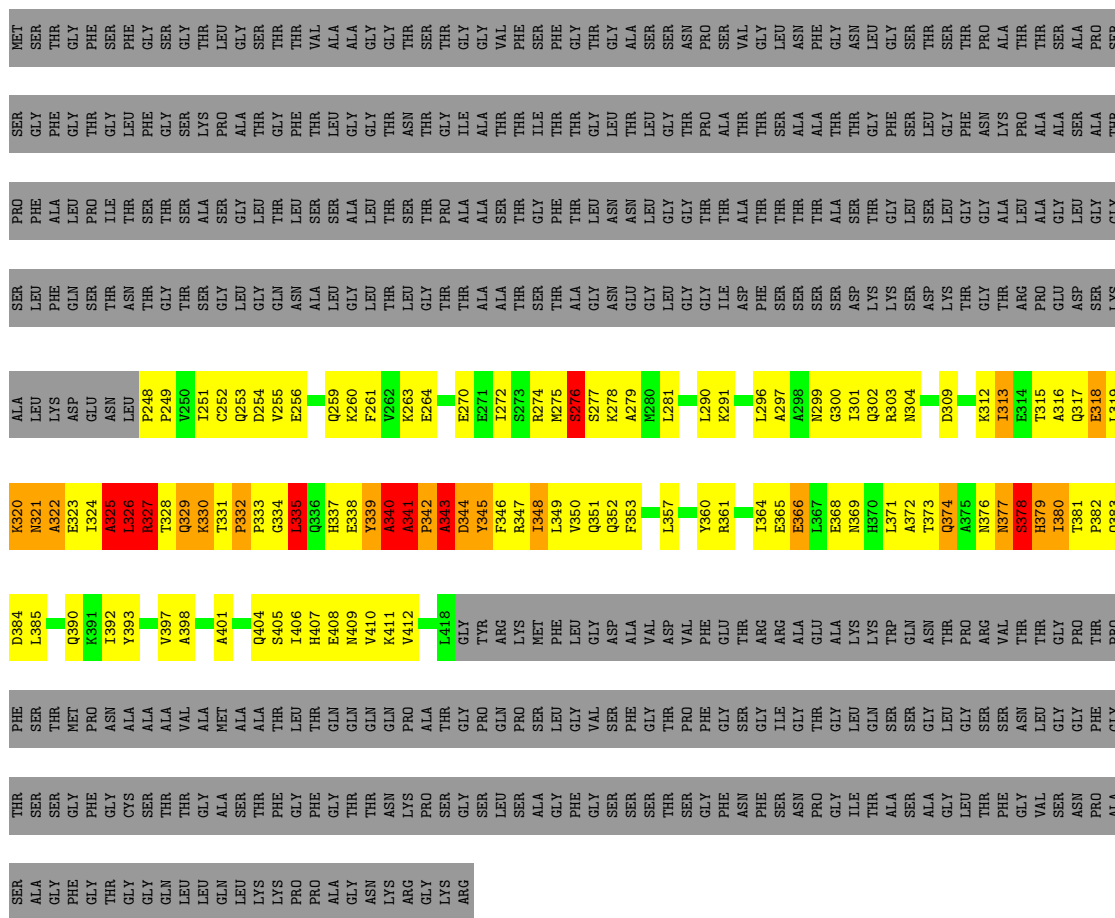
MET	K320	D384	SER	THR	SER	SER	ALA
SER	N321	L385	GLY	PHE	GLY	ALA	GLY
THR	A322	Q390	PHE	GLY	THR	THR	THR
GLY	E323	K391	GLY	THR	GLY	GLY	GLY
PHE	I324	I392	THR	GLY	ASN	GLY	GLY
ASN	A325	Y393	GLY	THR	THR	GLY	GLY
LEU	L326	R327	LEU	PHE	GLY	GLY	GLY
P248	R328	V397	PHE	GLY	THR	GLN	GLN
P249	T328	A398	ALA	SER	THR	LEU	LEU
V250	Q329	K330	VAL	THR	THR	LEU	LEU
I251	K330	K330	VAL	THR	THR	LEU	LEU
C252	T331	T331	ALA	GLY	THR	LEU	LEU
Q253	P332	A401	MET	ALA	ALA	GLN	GLN
D254	P333	Q404	ALA	SER	ALA	LEU	LEU
V255	G334	S405	ALA	THR	THR	LEU	LEU
E256	L335	I406	PHE	THR	THR	LEU	LEU
Q259	Q336	H407	THR	THR	THR	LEU	LEU
K260	H337	E408	ALA	ALA	ALA	GLY	GLY
F261	E338	N409	ALA	GLY	GLY	GLY	GLY
V262	Y339	V410	THR	THR	THR	GLY	GLY
K262	A340	K411	GLN	ASN	ASN	GLN	GLN
E264	P342	V412	ALA	PRO	PRO	ALA	ALA
E270	A343	L418	THR	THR	THR	GLY	GLY
E271	D344	L418	GLY	GLY	GLY	THR	THR
I272	Y345	TYR	PRO	PRO	PRO	GLY	GLY
S273	F346	ARG	LEU	LEU	LEU	SER	SER
R274	R347	ARG	LEU	LEU	LEU	THR	THR
M275	I348	LYS	SER	SER	SER	THR	THR
S276	L349	PHE	THR	THR	THR	THR	THR
S277	V350	PHE	THR	THR	THR	THR	THR
K278	Q351	GLY	THR	THR	THR	THR	THR
A279	Q352	VAL	THR	THR	THR	THR	THR
M280	F353	VAL	THR	THR	THR	THR	THR
L281	L357	ASP	THR	THR	THR	THR	THR
L290	Y360	VAL	PRO	PRO	PRO	PRO	PRO
K291	R361	PHE	GLY	GLY	GLY	GLY	GLY
L296	I364	THR	ASN	ASN	ASN	ASN	ASN
A297	E365	GLY	PHE	PHE	PHE	PHE	PHE
A298	E366	ARG	THR	THR	THR	THR	THR
N299	L367	ALA	ASN	ASN	ASN	ASN	ASN
G300	E368	GLU	GLY	GLY	GLY	GLY	GLY
I301	N369	ALA	ILE	ILE	ILE	ILE	ILE
Q302	H370	LYS	THR	THR	THR	THR	THR
R303	L371	TRP	GLN	GLN	GLN	GLN	GLN
N304	A372	GLN	ALA	ALA	ALA	ALA	ALA
D309	T373	ASN	GLY	GLY	GLY	GLY	GLY
K312	Q374	THR	LEU	LEU	LEU	LEU	LEU
I313	A375	PRO	GLY	GLY	GLY	GLY	GLY
E314	N376	ARG	THR	THR	THR	THR	THR
T315	S377	VAL	PHE	PHE	PHE	PHE	PHE
A316	S378	THR	GLY	GLY	GLY	GLY	GLY
A318	H379	VAL	ASN	ASN	ASN	ASN	ASN
E318	I380	THR	LEU	LEU	LEU	LEU	LEU
L319	T381	GLY	SER	SER	SER	SER	SER
L319	P382	THR	PRO	PRO	PRO	PRO	PRO
L319	Q383	PRO	ALA	ALA	ALA	ALA	ALA

• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58



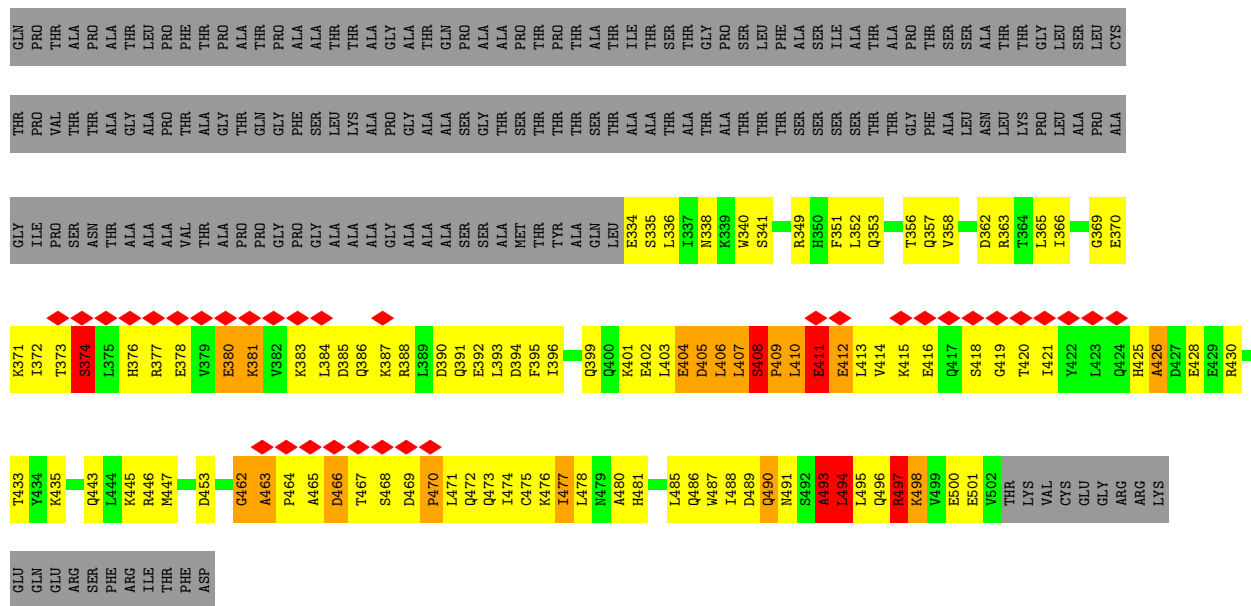


● Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58



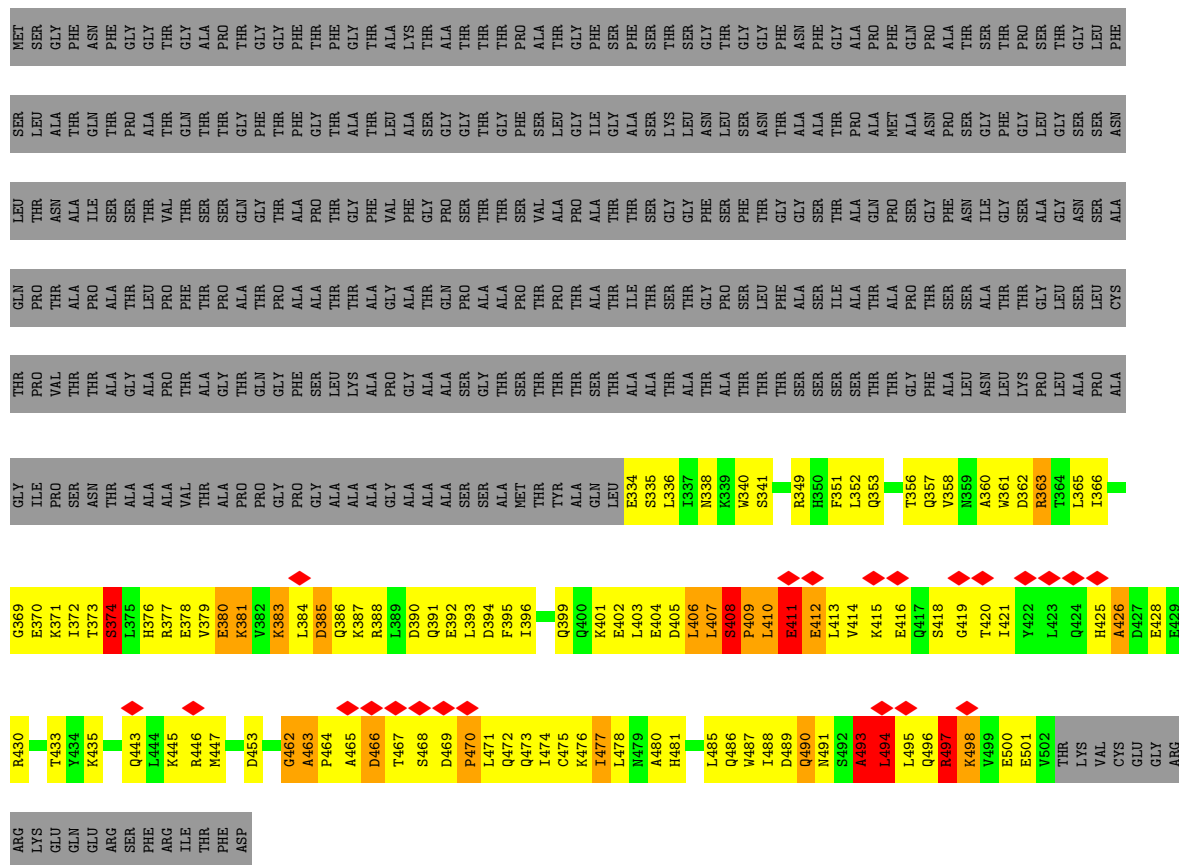
● Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58





- Molecule 6: Nuclear pore glycoprotein p62

Chain 1-N:

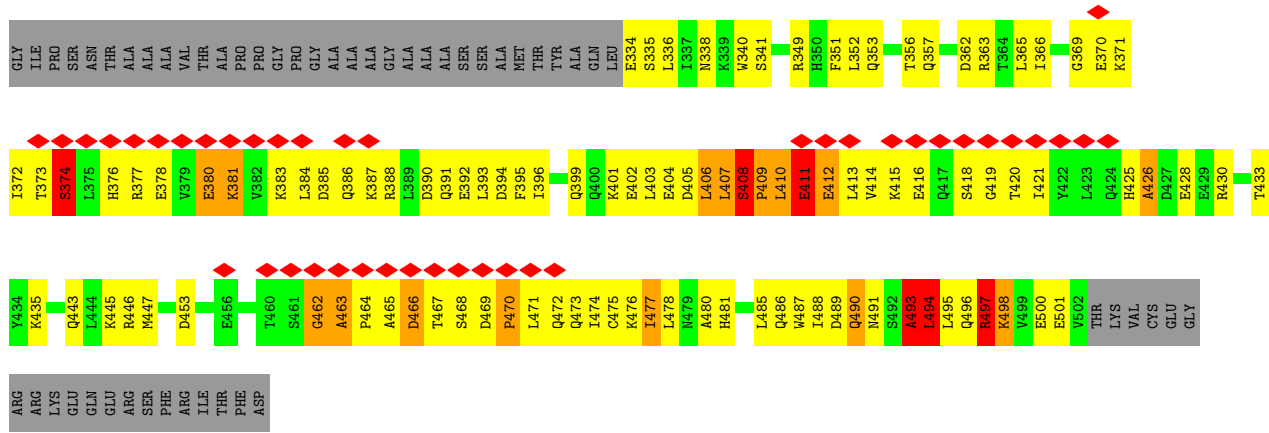


- Molecule 6: Nuclear pore glycoprotein p62

Chain 1-T:



Table of amino acid residues for the protein chain, including MET, SER, LEU, THR, ALA, ASN, PHE, GLY, and others.

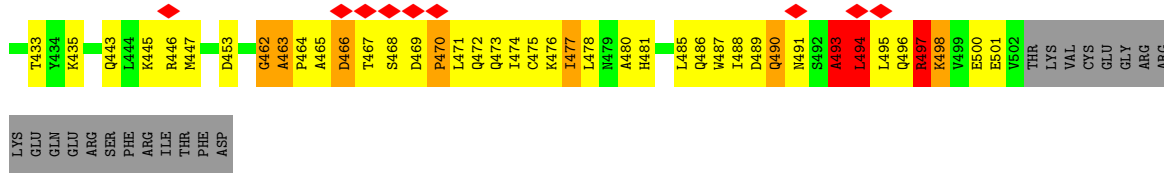


• Molecule 6: Nuclear pore glycoprotein p62



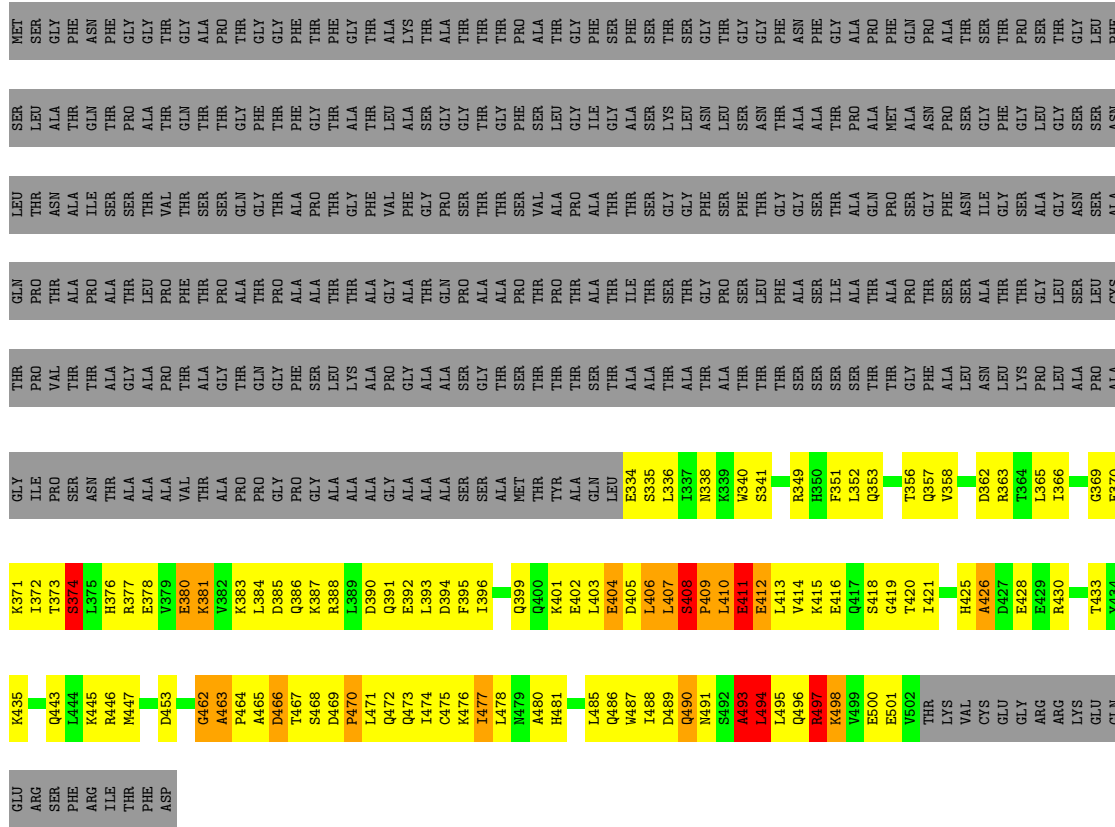
Table of amino acid residues for Chain 1-Z, including MET, SER, LEU, THR, ALA, ASN, PHE, GLY, and others.

Summary table of residue numbers and their corresponding amino acid types for Chain 1-Z.



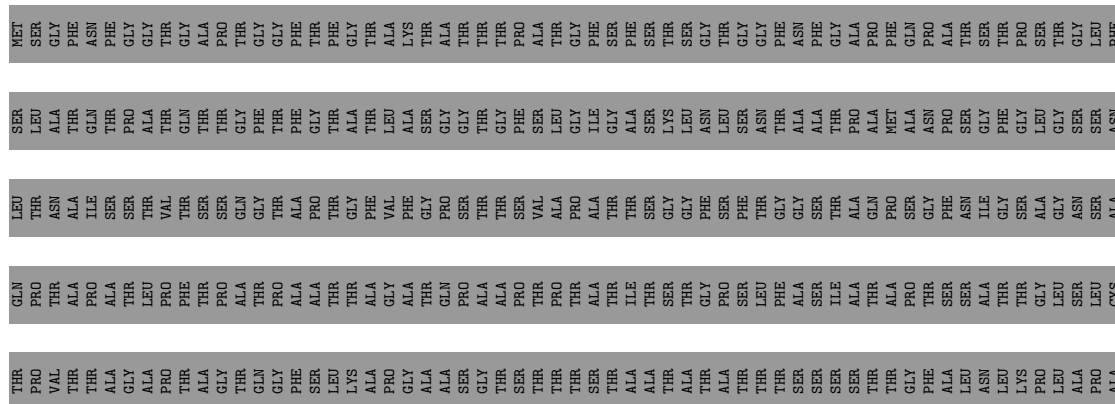
• Molecule 6: Nuclear pore glycoprotein p62

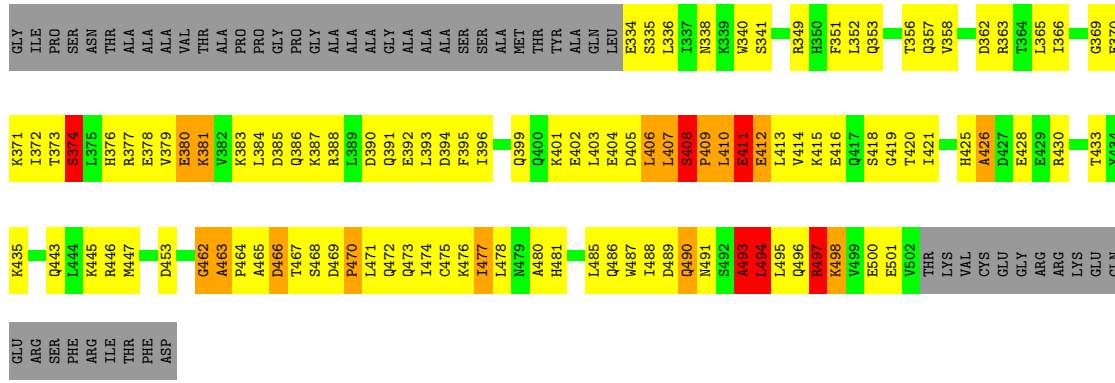
Chain 2-H: 12% 16% .. 68%



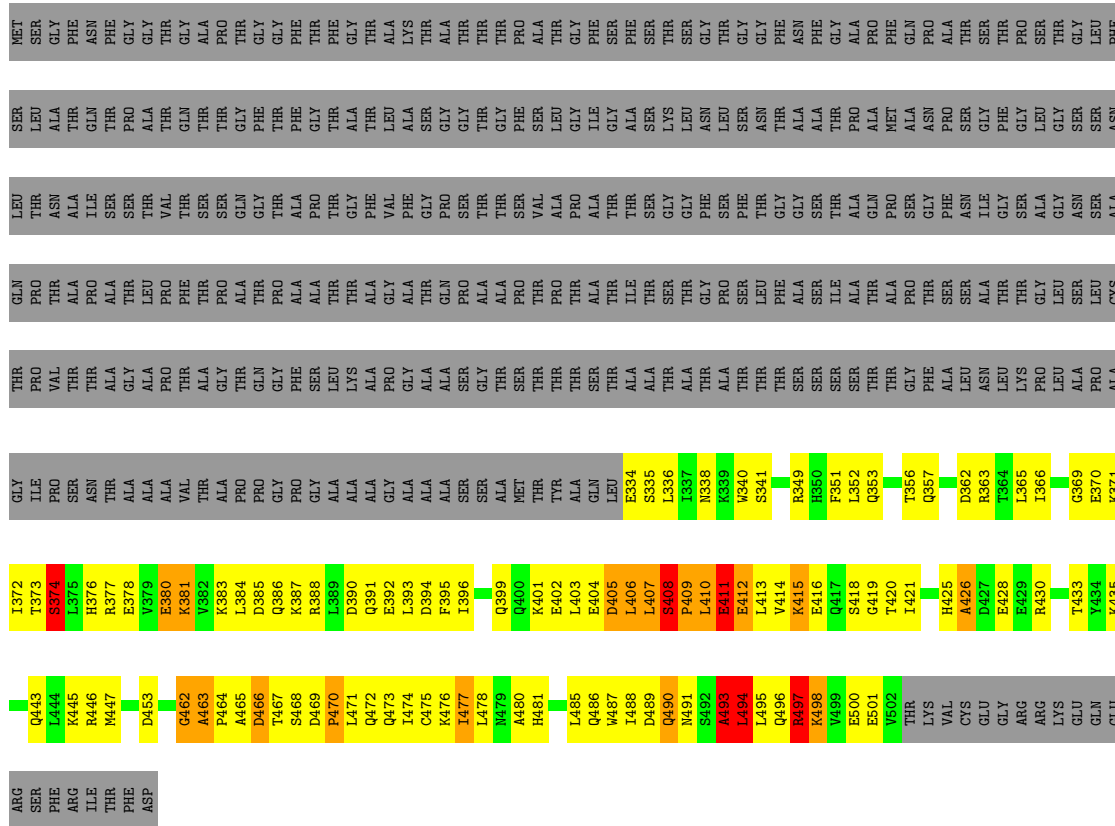
• Molecule 6: Nuclear pore glycoprotein p62

Chain 2-N: 12% 17% .. 68%

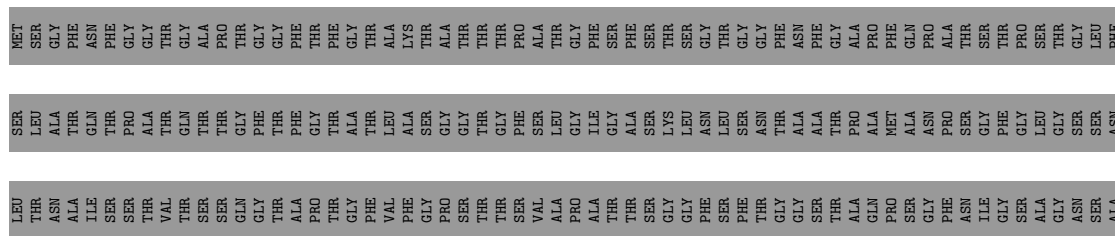


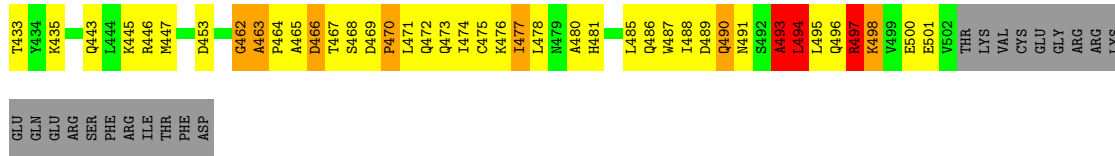


• Molecule 6: Nuclear pore glycoprotein p62

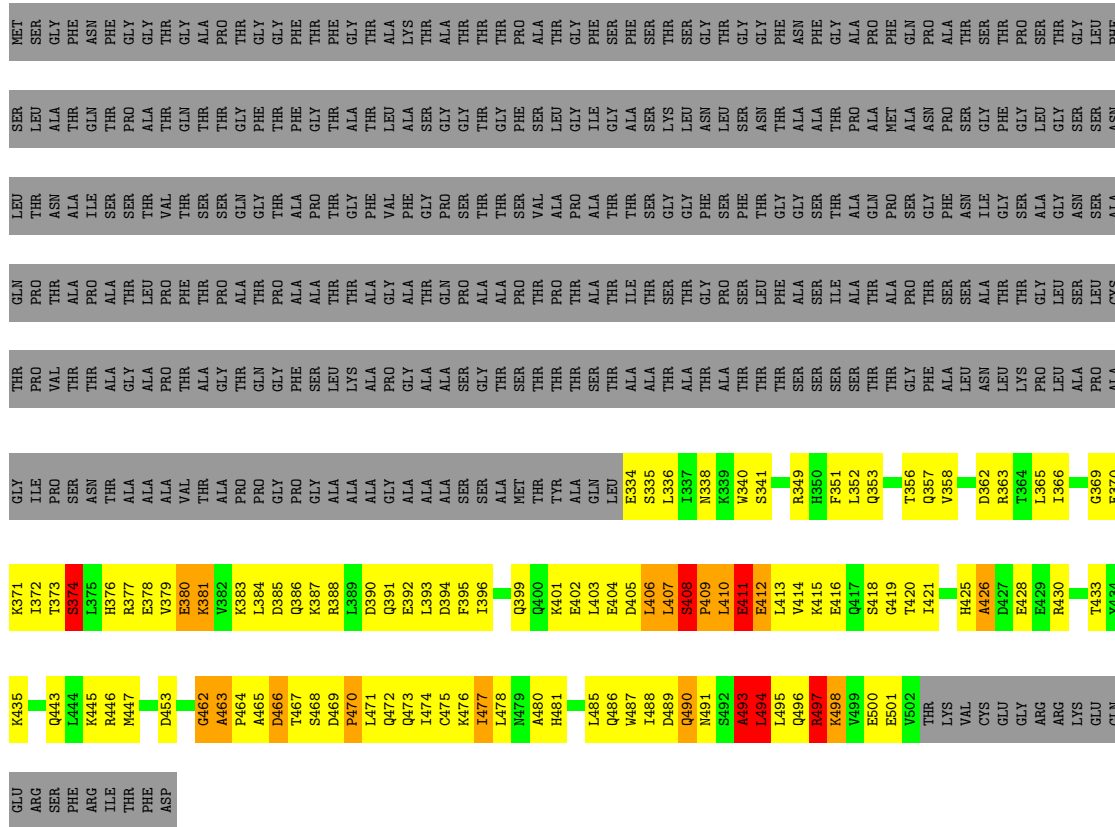


• Molecule 6: Nuclear pore glycoprotein p62



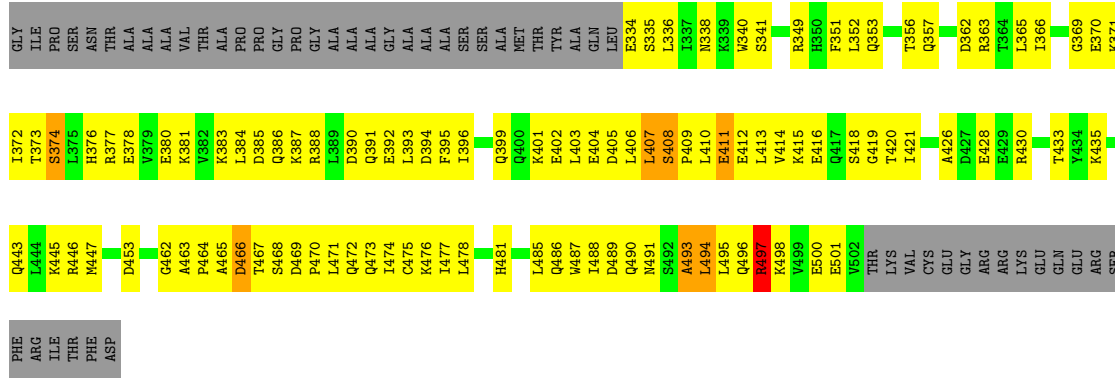


• Molecule 6: Nuclear pore glycoprotein p62

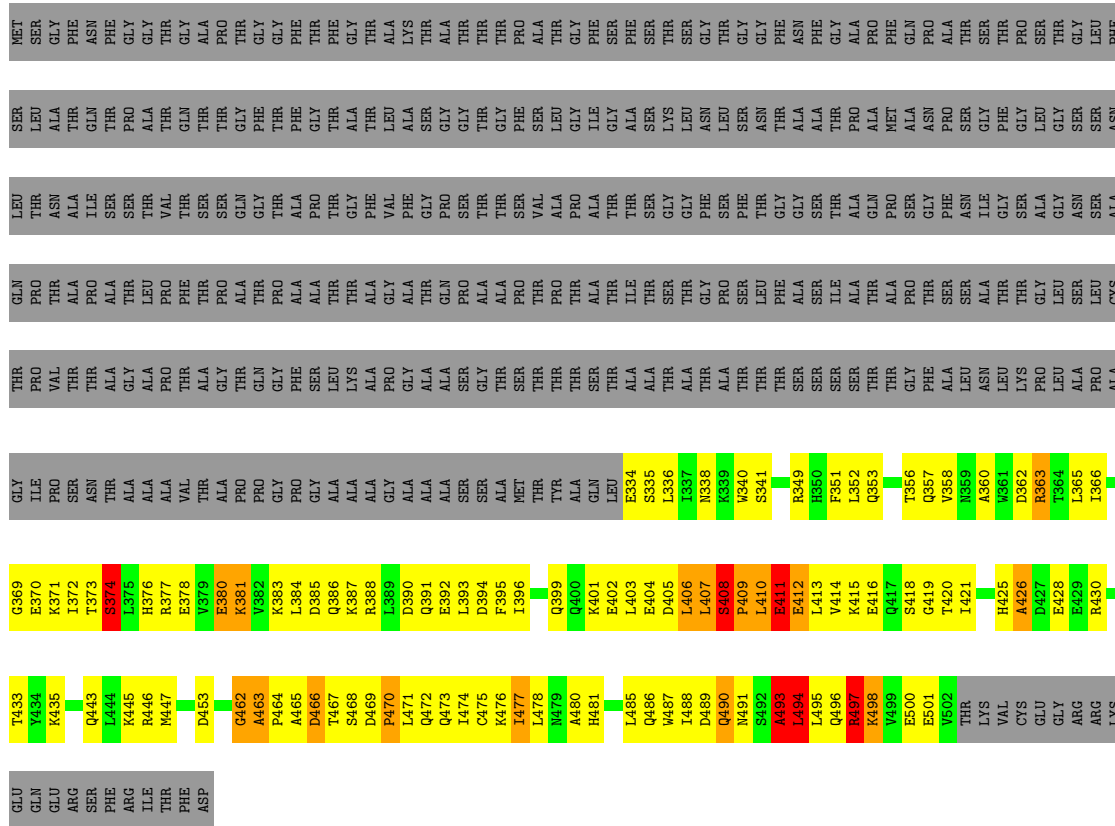


• Molecule 6: Nuclear pore glycoprotein p62

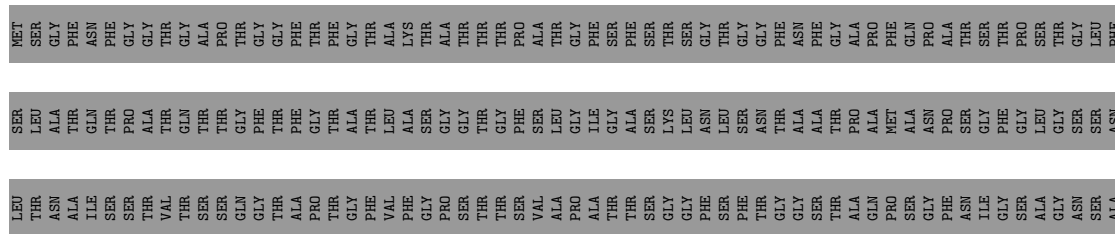




• Molecule 6: Nuclear pore glycoprotein p62



• Molecule 6: Nuclear pore glycoprotein p62



GLN	THR	GLY	K371	K435	GLU
PRO	PRO	ILE	I372	K435	ARG
THR	VAL	PRO	I373	Q443	ARG
ALA	THR	SER	S374	L444	PHE
ALA	THR	ASN	L375	K445	ASN
ALA	ALA	THR	H376	R446	ARG
LEU	GLY	ALA	R377	M447	ILE
LEU	PRO	ALA	E378	D453	THR
PHE	THR	VAL	E380	G462	PHE
ALA	ALA	THR	K381	A463	ASP
PRO	GLY	ALA	V382	P464	
ALA	THR	PRO	K383	A465	
ALA	GLN	PRO	L384	D466	
THR	GLY	GLY	D385	T467	
THR	PHE	PRO	Q386	S468	
THR	ALA	GLY	K387	D469	
ALA	ALA	ALA	R388	P470	
THR	LYS	ALA	L389	L471	
ALA	ALA	ALA	D390	L472	
ALA	PRO	GLY	Q391	Q473	
ALA	GLY	ALA	E392	Q473	
ALA	ALA	ALA	L393	I474	
ALA	ALA	ALA	D394	C475	
PRO	ALA	ALA	F395	K476	
GLN	SER	SER	I396	L477	
ALA	GLY	ALA	Q399	L478	
ALA	THR	ALA	M479	M479	
ALA	THR	THR	A480	A480	
ALA	THR	THR	K401	H481	
ALA	THR	THR	E402	L485	
ALA	SER	ALA	L403	Q486	
ALA	THR	LEU	E404	W487	
ILE	ALA	ALA	D405	I488	
ALA	ALA	ALA	S335	I488	
ALA	ALA	THR	L336	I489	
THR	THR	THR	L407	D489	
SER	SER	ALA	S408	Q490	
THR	GLY	THR	I337	M491	
GLY	THR	ALA	M338	A492	
PRO	ALA	ALA	R389	S492	
PRO	THR	THR	W340	A493	
THR	THR	THR	S341	L494	
LEU	THR	PHE	E412	L495	
ALA	THR	THR	E413	Q496	
ALA	SER	ALA	R349	V414	
ALA	THR	ALA	H350	K415	
ALA	SER	THR	F351	E416	
ILE	SER	THR	L352	V499	
ALA	SER	ALA	Q353	E500	
ALA	THR	THR	T356	E501	
ALA	THR	ALA	Q357	V502	
PRO	GLY	ALA	T420	THR	
THR	PHE	ALA	I421	LYS	
SER	ALA	LEU	H425	VAL	
SER	ASN	ALA	A426	CYS	
ALA	LEU	ALA	D362	GLU	
ALA	THR	THR	R363	GLY	
THR	LYS	THR	T364	ARG	
THR	PRO	THR	E428	ARG	
GLY	LEU	THR	E429	LYS	
LEU	LEU	SER	R430	GLN	
SER	ALA	THR	T433		
SER	PRO	PRO	E370		
CYS	ALA	ALA			

• Molecule 6: Nuclear pore glycoprotein p62

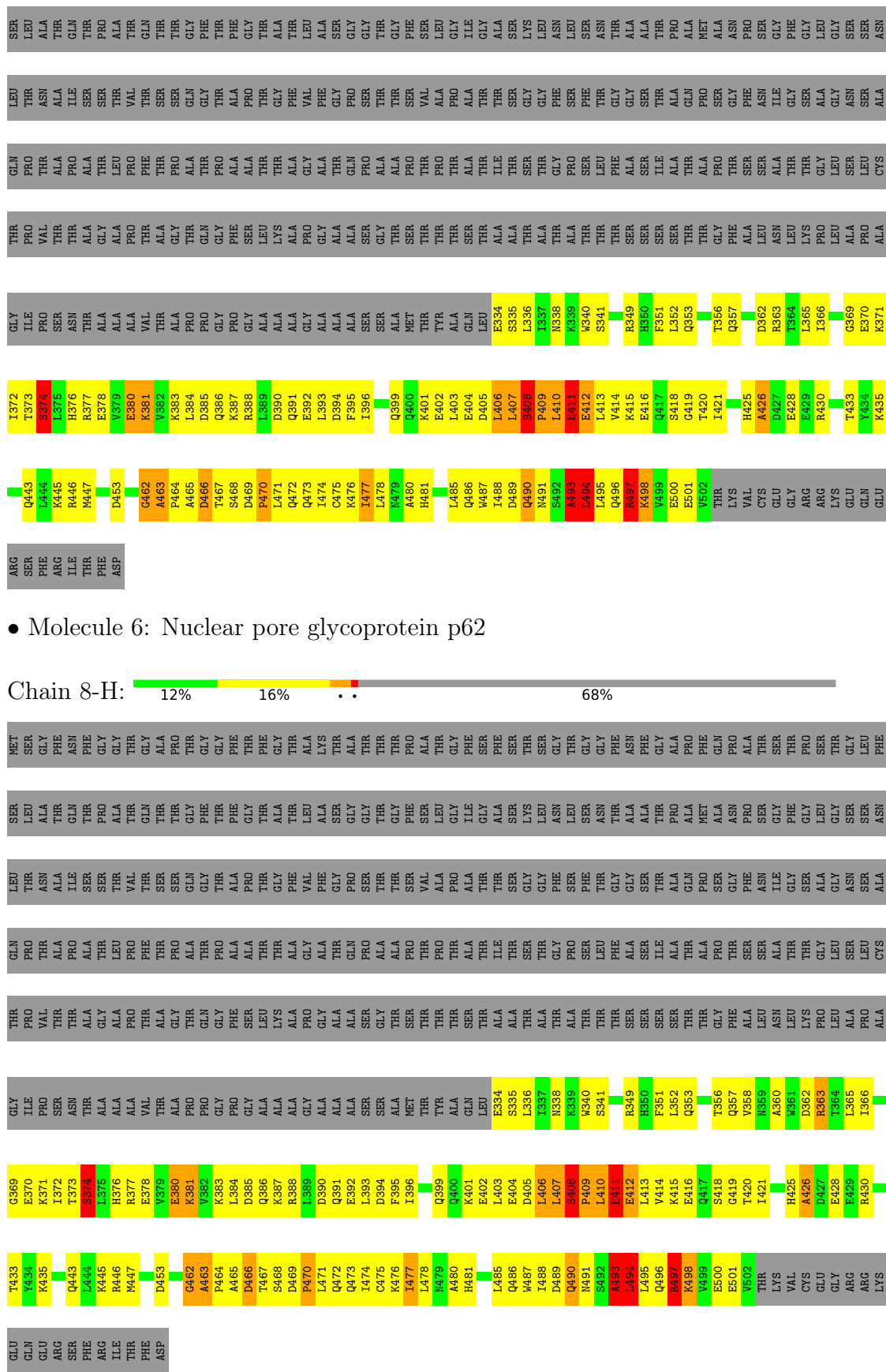


MET	SER	GLY	E370	Y484	GLN
SER	GLY	ILE	K371	K435	PRO
PHE	PHE	PRO	I372	Q443	THR
ASN	ASN	SER	S374	L444	VAL
THR	THR	ASN	L375	K445	THR
ALA	THR	THR	H376	R446	ALA
ALA	GLY	ALA	R377	M447	ALA
ALA	GLY	ALA	E378	D453	ALA
VAL	THR	VAL	V379	G462	VAL
GLN	GLY	GLN	E380	A463	THR
THR	PRO	THR	K381	P464	ALA
ALA	THR	ALA	V382	A465	GLY
ALA	THR	ALA	K383	D466	THR
ALA	GLY	GLY	L384	T467	GLY
ALA	GLY	GLY	D385	S468	GLY
ALA	PHE	ALA	Q386	D469	ALA
ALA	THR	ALA	K387	P470	ALA
ALA	THR	THR	R388	L471	ALA
ALA	ALA	ALA	L389	L472	ALA
ALA	ALA	ALA	D390	Q473	ALA
GLY	GLY	GLY	Q391	Q473	LYS
GLY	GLY	ALA	E392	I474	THR
ALA	ALA	ALA	L393	I474	ALA
ALA	ALA	ALA	D394	C475	ALA
ALA	ALA	ALA	F395	K476	ALA
SER	SER	SER	I396	L477	THR
SER	THR	THR	Q399	L478	THR
THR	THR	THR	M479	M479	THR
ALA	ALA	ALA	A480	A480	ALA
GLY	GLY	GLY	K401	H481	GLY
PHE	PHE	ALA	E402	L485	PHE
SER	SER	ALA	L403	Q486	SER
THR	THR	LEU	E404	W487	THR
THR	THR	ALA	D405	I488	THR
ALA	ALA	ALA	S335	I488	ALA
ALA	ALA	THR	L336	I489	ALA
ALA	ALA	ALA	L407	D489	ALA
THR	THR	THR	S408	Q490	THR
ALA	THR	ALA	I337	M491	ALA
ALA	ALA	ALA	M338	A492	ALA
ALA	THR	THR	R389	S492	THR
THR	THR	THR	W340	A493	THR
THR	THR	THR	S341	L494	THR
THR	THR	THR	E412	L495	THR
ASN	ASN	ALA	R349	Q496	ASN
ALA	ALA	ALA	H350	K415	ALA
ALA	ALA	ALA	F351	E416	ALA
ALA	ALA	THR	L352	V499	ALA
ALA	ALA	THR	Q353	E500	ALA
ALA	THR	THR	T356	E501	ALA
GLN	GLY	ALA	Q357	V502	GLN
ALA	THR	ALA	T420	THR	ALA
ALA	ALA	ALA	I421	LYS	ALA
LEU	LEU	THR	H425	VAL	LEU
ALA	ASN	THR	A426	CYS	ALA
ALA	LEU	THR	D362	GLU	ALA
LYS	PRO	THR	R363	GLY	LYS
THR	THR	THR	T364	ARG	THR
LEU	LEU	THR	L365	ARG	LEU
ALA	ALA	THR	I366	LYS	ALA
PRO	PRO	THR	T433	GLU	PRO
ALA	ALA	PHE			ALA

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MET	SER	GLY	E370	Y484	GLN
SER	GLY	ILE	K371	K435	PRO
PHE	PHE	PRO	I372	Q443	THR
ASN	ASN	SER	S374	L444	VAL
THR	THR	ASN	L375	K445	THR
ALA	THR	THR	H376	R446	ALA
ALA	GLY	ALA	R377	M447	ALA
ALA	GLY	ALA	E378	D453	ALA
VAL	THR	VAL	V379	G462	VAL
GLN	GLY	GLN	E380	A463	THR
THR	PRO	THR	K381	P464	ALA
ALA	THR	ALA	V382	A465	GLY
ALA	THR	ALA	K383	D466	THR
ALA	GLY	GLY	L384	T467	GLY
ALA	GLY	GLY	D385	S468	GLY
ALA	PHE	ALA	Q386	D469	ALA
ALA	THR	ALA	K387	P470	ALA
ALA	THR	THR	R388	L471	ALA
ALA	ALA	ALA	L389	L472	ALA
ALA	ALA	ALA	D390	Q473	ALA
GLY	GLY	GLY	Q391	Q473	LYS
GLY	GLY	ALA	E392	I474	THR
ALA	ALA	ALA	L393	I474	ALA
ALA	ALA	ALA	D394	C475	ALA
THR	THR	THR	F395	K476	ALA
THR	THR	THR	I396	L477	THR
THR	THR	THR	Q399	L478	THR
PRO	PRO	THR	M479	M479	THR
ALA	ALA	ALA	A480	A480	ALA
GLY	GLY	GLY	K401	H481	GLY
PHE	PHE	ALA	E402	L485	PHE
SER	SER	ALA	L403	Q486	SER
THR	THR	LEU	E404	W487	THR
THR	THR	ALA	D405	I488	THR
ALA	ALA	ALA	S335	I488	ALA
ALA	ALA	THR	L336	I489	ALA
ALA	ALA	ALA	L407	D489	ALA
THR	THR	THR	S408	Q490	THR
ALA	THR	ALA	I337	M491	ALA
ALA	ALA	ALA	M338	A492	ALA
ALA	THR	THR	R389	S492	THR
THR	THR	THR	W340	A493	THR
THR	THR	THR	S341	L494	THR
THR	THR	THR	E412	L495	THR
ASN	ASN	ALA	R349	Q496	ASN
ALA	ALA	ALA	H350	K415	ALA
ALA	ALA	THR	F351	E416	ALA
ALA	ALA	THR	L352	V499	ALA
ALA	THR	THR	Q353	E500	ALA
ALA	THR	ALA	T356	E501	ALA
GLN	GLY	ALA	Q357	V502	GLN
ALA	THR	ALA	T420	THR	ALA
ALA	ALA	ALA	I421	LYS	ALA
LEU	LEU	THR	H425	VAL	LEU
THR	ASN	THR	A426	CYS	THR
SER	LEU	THR	D362	GLU	SER
THR	LYS	THR	R363	GLY	THR
THR	PRO	THR	T364	ARG	THR
THR	THR	THR	E428	ARG	THR
GLY	LEU	THR	E429	LYS	GLY
LEU	LEU	SER	R430	GLN	LEU
SER	ALA	THR	T433		SER
PRO	PRO	PRO			PRO
PHE	ALA	ALA			PHE



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4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	8400	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	315.784	Depositor
Minimum map value	0.000	Depositor
Average map value	1.328	Depositor
Map value standard deviation	10.659	Depositor
Recommended contour level	36.6	Depositor
Map size (\AA)	964.8, 964.8, 964.8	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	6.7, 6.7, 6.7	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	1-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	1-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	1-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	1-K	1.54	0/5338	1.77	85/7399 (1.1%)
1	1-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	1-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	2-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	2-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	2-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	2-K	1.54	0/5338	1.77	85/7399 (1.1%)
1	2-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	2-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	3-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	3-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	3-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	3-K	1.54	0/5338	1.77	85/7399 (1.1%)
1	3-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	3-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	4-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	4-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	4-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	4-K	1.54	0/5338	1.77	85/7399 (1.1%)
1	4-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	4-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	5-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	5-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	5-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	5-K	1.54	0/5338	1.77	85/7399 (1.1%)
1	5-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	5-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	6-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	6-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	6-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	6-K	1.54	0/5338	1.77	85/7399 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	6-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	6-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	7-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	7-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	7-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	7-K	1.54	0/5338	1.77	85/7399 (1.1%)
1	7-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	7-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	8-A	1.55	0/3195	1.79	59/4421 (1.3%)
1	8-B	1.55	1/3195 (0.0%)	1.79	59/4421 (1.3%)
1	8-E	1.53	1/5338 (0.0%)	1.77	86/7399 (1.2%)
1	8-K	1.54	0/5338	1.77	85/7399 (1.1%)
1	8-Q	1.53	1/5338 (0.0%)	1.77	85/7399 (1.1%)
1	8-W	1.54	1/5338 (0.0%)	1.77	86/7399 (1.2%)
2	1-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	1-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	1-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	1-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	2-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	2-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	2-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	2-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	3-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	3-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	3-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	3-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	4-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	4-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	4-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	4-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	5-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	5-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	5-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	5-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	6-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	6-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	6-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	6-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	7-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	7-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	7-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	7-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
2	8-C	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	8-I	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	8-O	1.85	32/3143 (1.0%)	2.22	154/4369 (3.5%)
2	8-U	1.85	31/3143 (1.0%)	2.22	155/4369 (3.5%)
3	1-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	1-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	1-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	1-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	2-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	2-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	2-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	2-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	3-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	3-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	3-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	3-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	4-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	4-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	4-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	4-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	5-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	5-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	5-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	5-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	6-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	6-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	6-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	6-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	7-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	7-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	7-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	7-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	8-D	1.94	100/5066 (2.0%)	2.79	254/7020 (3.6%)
3	8-J	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
3	8-P	1.94	100/5066 (2.0%)	2.79	253/7020 (3.6%)
3	8-V	1.95	100/5066 (2.0%)	2.79	252/7020 (3.6%)
4	1-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	1-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	1-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	1-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)
4	2-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	2-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	2-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	2-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	3-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	3-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	3-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	3-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)
4	4-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	4-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	4-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	4-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)
4	5-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	5-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	5-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	5-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)
4	6-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	6-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	6-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	6-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)
4	7-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	7-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	7-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	7-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)
4	8-F	5.96	263/1655 (15.9%)	5.12	360/2302 (15.6%)
4	8-L	5.96	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	8-R	5.97	263/1655 (15.9%)	5.12	362/2302 (15.7%)
4	8-X	5.97	262/1655 (15.8%)	5.12	362/2302 (15.7%)
5	1-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	1-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	1-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)
5	1-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
5	2-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	2-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	2-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)
5	2-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
5	3-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	3-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	3-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)
5	3-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
5	4-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	4-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	4-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)
5	4-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
5	5-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	5-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	5-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	5-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
5	6-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	6-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	6-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)
5	6-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
5	7-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	7-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	7-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)
5	7-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
5	8-G	6.67	152/852 (17.8%)	5.77	239/1190 (20.1%)
5	8-M	6.67	151/852 (17.7%)	5.77	240/1190 (20.2%)
5	8-S	6.67	150/852 (17.6%)	5.77	239/1190 (20.1%)
5	8-Y	6.67	153/852 (18.0%)	5.77	242/1190 (20.3%)
6	1-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	1-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)
6	1-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	1-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
6	2-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	2-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)
6	2-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	2-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
6	3-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	3-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)
6	3-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	3-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
6	4-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	4-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)
6	4-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	4-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
6	5-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	5-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)
6	5-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	5-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
6	6-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	6-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)
6	6-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	6-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
6	7-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	7-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)
6	7-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	7-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
6	8-H	5.51	133/841 (15.8%)	4.99	244/1174 (20.8%)
6	8-N	5.51	134/841 (15.9%)	4.99	246/1174 (21.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	8-T	5.51	132/841 (15.7%)	4.99	246/1174 (21.0%)
6	8-Z	5.51	132/841 (15.7%)	4.99	248/1174 (21.1%)
All	All	3.02	21744/591760 (3.7%)	3.03	43832/821264 (5.3%)

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	1-A	0	1
1	1-B	0	1
1	1-E	0	1
1	1-K	0	1
1	1-Q	0	1
1	1-W	0	1
2	1-C	1	4
2	1-I	1	4
2	1-O	1	4
2	1-U	1	4
2	2-C	1	4
2	2-I	1	4
2	2-O	1	4
2	2-U	1	4
2	3-C	1	4
2	3-I	1	4
2	3-O	1	4
2	3-U	1	4
2	4-C	1	4
2	4-I	1	4
2	4-O	1	4
2	4-U	1	4
2	5-C	1	4
2	5-I	1	4
2	5-O	1	4
2	5-U	1	4
2	6-C	1	4
2	6-I	1	4
2	6-O	1	4
2	6-U	1	4
2	7-C	1	4
2	7-I	1	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	7-O	1	4
2	7-U	1	4
2	8-C	1	4
2	8-I	1	4
2	8-O	1	4
2	8-U	1	4
3	1-D	0	21
3	1-J	0	20
3	1-P	0	20
3	1-V	0	20
3	2-D	0	20
3	2-J	0	20
3	2-P	0	21
3	2-V	0	20
3	3-D	0	20
3	3-J	0	20
3	3-P	0	21
3	3-V	0	20
3	4-D	0	20
3	4-J	0	20
3	4-P	0	21
3	4-V	0	20
3	5-D	0	21
3	5-J	0	20
3	5-P	0	21
3	5-V	0	20
3	6-D	0	20
3	6-J	0	20
3	6-P	0	21
3	6-V	0	20
3	7-D	0	21
3	7-J	0	20
3	7-P	0	21
3	7-V	0	20
3	8-D	0	20
3	8-J	0	20
3	8-P	0	21
3	8-V	0	20
4	1-F	10	40
4	1-L	10	40
4	1-R	10	40
4	1-X	10	40

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	2-F	7	31
4	2-L	7	31
4	2-R	7	31
4	2-X	7	31
4	3-F	7	31
4	3-L	7	31
4	3-R	7	31
4	3-X	7	31
4	4-F	7	31
4	4-L	7	31
4	4-R	7	31
4	4-X	7	31
4	5-F	7	31
4	5-L	7	31
4	5-R	7	31
4	5-X	7	31
4	6-F	7	31
4	6-L	7	31
4	6-R	7	31
4	6-X	7	31
4	7-F	7	31
4	7-L	7	31
4	7-R	7	31
4	7-X	7	31
4	8-F	7	31
4	8-L	7	31
4	8-R	7	31
4	8-X	7	31
5	1-G	9	10
5	1-M	9	10
5	1-S	9	10
5	1-Y	9	10
5	2-G	9	10
5	2-M	9	10
5	2-S	9	10
5	2-Y	9	10
5	3-G	9	10
5	3-M	9	10
5	3-S	9	10
5	3-Y	9	10
5	4-G	9	10
5	4-M	9	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	4-S	9	10
5	4-Y	9	10
5	5-G	9	10
5	5-M	9	10
5	5-S	9	10
5	5-Y	9	10
5	6-G	9	10
5	6-M	9	10
5	6-S	9	10
5	6-Y	9	10
5	7-G	9	10
5	7-M	9	10
5	7-S	9	10
5	7-Y	9	10
5	8-G	9	10
5	8-M	9	10
5	8-S	9	10
5	8-Y	9	10
6	1-H	5	5
6	1-N	5	5
6	1-T	5	4
6	1-Z	5	5
6	2-H	5	5
6	2-N	5	5
6	2-T	5	4
6	2-Z	5	5
6	3-H	5	5
6	3-N	5	5
6	3-T	5	4
6	3-Z	5	5
6	4-H	5	5
6	4-N	5	5
6	4-T	5	5
6	4-Z	5	5
6	5-H	5	5
6	5-N	5	5
6	5-T	5	5
6	5-Z	5	5
6	6-H	5	5
6	6-N	5	5
6	6-T	5	5
6	6-Z	5	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	7-H	5	5
6	7-N	5	5
6	7-T	5	5
6	7-Z	5	5
6	8-H	5	5
6	8-N	5	5
6	8-T	5	5
6	8-Z	5	5
All	All	716	2289

The worst 5 of 21744 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1-M	379	HIS	CA-C	72.08	2.49	1.52
5	2-M	379	HIS	CA-C	72.08	2.49	1.52
5	3-M	379	HIS	CA-C	72.08	2.49	1.52
5	4-M	379	HIS	CA-C	72.08	2.49	1.52
5	5-M	379	HIS	CA-C	72.08	2.49	1.52

The worst 5 of 43832 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	1-S	341	ALA	CA-C-N	-52.55	63.48	119.19
5	1-S	341	ALA	C-N-CA	-52.55	63.48	119.19
5	2-S	341	ALA	CA-C-N	-52.55	63.48	119.19
5	2-S	341	ALA	C-N-CA	-52.55	63.48	119.19
5	3-S	341	ALA	CA-C-N	-52.55	63.48	119.19

5 of 716 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	1-C	11	GLN	CA
4	1-F	200	THR	CA
4	1-F	210	VAL	CA
4	1-F	211	GLU	CA
4	1-F	305	ASP	CA

5 of 2289 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	259	SER	Mainchain
1	1-B	259	SER	Mainchain

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Mol	Chain	Res	Type	Group
2	1-C	4	GLU	Mainchain
2	1-C	6	PHE	Mainchain
2	1-C	7	GLY	Mainchain

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	1-A	3214	0	1424	27	0
1	1-B	3214	0	1424	28	0
1	1-E	5366	0	2362	98	0
1	1-K	5366	0	2360	82	0
1	1-Q	5366	0	2357	178	0
1	1-W	5366	0	2364	65	0
1	2-A	3214	0	1424	26	0
1	2-B	3214	0	1424	28	0
1	2-E	5366	0	2363	85	0
1	2-K	5366	0	2359	158	0
1	2-Q	5366	0	2363	89	0
1	2-W	5366	0	2361	163	0
1	3-A	3214	0	1424	26	0
1	3-B	3214	0	1424	28	0
1	3-E	5366	0	2363	85	0
1	3-K	5366	0	2359	158	0
1	3-Q	5366	0	2363	89	0
1	3-W	5366	0	2361	163	0
1	4-A	3214	0	1424	26	0
1	4-B	3214	0	1424	28	0
1	4-E	5366	0	2363	85	0
1	4-K	5366	0	2359	158	0
1	4-Q	5366	0	2363	89	0
1	4-W	5366	0	2361	163	0
1	5-A	3214	0	1424	26	0
1	5-B	3214	0	1424	28	0
1	5-E	5366	0	2363	85	0
1	5-K	5366	0	2359	158	0
1	5-Q	5366	0	2363	89	0
1	5-W	5366	0	2361	163	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	6-A	3214	0	0	0	0
1	6-B	3214	0	0	0	0
1	6-E	5366	0	0	0	0
1	6-K	5366	0	0	0	0
1	6-Q	5366	0	0	0	0
1	6-W	5366	0	0	0	0
1	7-A	3214	0	1424	26	0
1	7-B	3214	0	1424	28	0
1	7-E	5366	0	2363	95	0
1	7-K	5366	0	2359	139	0
1	7-Q	5366	0	2363	95	0
1	7-W	5366	0	2361	141	0
1	8-A	3214	0	1424	26	0
1	8-B	3214	0	1424	28	0
1	8-E	5366	0	2363	95	0
1	8-K	5366	0	2359	139	0
1	8-Q	5366	0	2363	95	0
1	8-W	5366	0	2361	141	0
2	1-C	3152	0	1403	163	0
2	1-I	3152	0	1408	80	0
2	1-O	3152	0	1405	94	0
2	1-U	3152	0	1406	69	0
2	2-C	3152	0	1403	178	0
2	2-I	3152	0	1405	67	0
2	2-O	3152	0	1403	178	0
2	2-U	3152	0	1405	68	0
2	3-C	3152	0	1403	178	0
2	3-I	3152	0	1405	67	0
2	3-O	3152	0	1403	178	0
2	3-U	3152	0	1405	67	0
2	4-C	3152	0	1403	178	0
2	4-I	3152	0	1405	67	0
2	4-O	3152	0	1403	178	0
2	4-U	3152	0	1405	68	0
2	5-C	3152	0	1403	180	0
2	5-I	3152	0	1405	67	0
2	5-O	3152	0	1403	180	0
2	5-U	3152	0	1405	68	0
2	6-C	3152	0	0	0	0
2	6-I	3152	0	0	0	0
2	6-O	3152	0	0	0	0
2	6-U	3152	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	7-C	3152	0	1401	193	0
2	7-I	3152	0	1405	67	0
2	7-O	3152	0	1401	194	0
2	7-U	3152	0	1405	68	0
2	8-C	3152	0	1401	191	0
2	8-I	3152	0	1405	67	0
2	8-O	3152	0	1401	192	0
2	8-U	3152	0	1405	67	0
3	1-D	5094	0	2272	130	0
3	1-J	5094	0	2271	142	0
3	1-P	5094	0	2273	87	0
3	1-V	5094	0	2267	210	0
3	2-D	5094	0	2270	163	0
3	2-J	5094	0	2272	108	0
3	2-P	5094	0	2270	193	0
3	2-V	5094	0	2272	112	0
3	3-D	5094	0	2270	163	0
3	3-J	5094	0	2272	108	0
3	3-P	5094	0	2270	193	0
3	3-V	5094	0	2272	112	0
3	4-D	5094	0	2270	162	0
3	4-J	5094	0	2272	108	0
3	4-P	5094	0	2270	162	0
3	4-V	5094	0	2272	112	0
3	5-D	5094	0	2273	102	0
3	5-J	5094	0	2272	108	0
3	5-P	5094	0	2273	104	0
3	5-V	5094	0	2272	112	0
3	6-D	5094	0	0	0	0
3	6-J	5094	0	0	0	0
3	6-P	5094	0	0	0	0
3	6-V	5094	0	0	0	0
3	7-D	5094	0	2273	102	0
3	7-J	5094	0	2271	122	0
3	7-P	5094	0	2273	104	0
3	7-V	5094	0	2271	125	0
3	8-D	5094	0	2270	162	0
3	8-J	5094	0	2271	122	0
3	8-P	5094	0	2270	162	0
3	8-V	5094	0	2271	125	0
4	1-F	1658	0	715	180	0
4	1-L	1658	0	715	178	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	1-R	1658	0	714	181	0
4	1-X	1658	0	715	179	0
4	2-F	1658	0	715	163	0
4	2-L	1658	0	715	165	0
4	2-R	1658	0	715	164	0
4	2-X	1658	0	715	163	0
4	3-F	1658	0	715	163	0
4	3-L	1658	0	715	165	0
4	3-R	1658	0	715	164	0
4	3-X	1658	0	715	165	0
4	4-F	1658	0	715	161	0
4	4-L	1658	0	715	165	0
4	4-R	1658	0	715	162	0
4	4-X	1658	0	715	163	0
4	5-F	1658	0	715	161	0
4	5-L	1658	0	715	165	0
4	5-R	1658	0	715	162	0
4	5-X	1658	0	715	163	0
4	6-F	1658	0	0	0	0
4	6-L	1658	0	0	0	0
4	6-R	1658	0	0	0	0
4	6-X	1658	0	0	0	0
4	7-F	1658	0	715	161	0
4	7-L	1658	0	715	165	0
4	7-R	1658	0	715	162	0
4	7-X	1658	0	715	163	0
4	8-F	1658	0	715	161	0
4	8-L	1658	0	715	165	0
4	8-R	1658	0	715	162	0
4	8-X	1658	0	715	165	0
5	1-G	853	0	384	58	0
5	1-M	853	0	384	58	0
5	1-S	853	0	384	60	0
5	1-Y	853	0	384	58	0
5	2-G	853	0	384	59	0
5	2-M	853	0	384	59	0
5	2-S	853	0	384	59	0
5	2-Y	853	0	384	59	0
5	3-G	853	0	384	59	0
5	3-M	853	0	384	59	0
5	3-S	853	0	384	59	0
5	3-Y	853	0	384	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	4-G	853	0	384	59	0
5	4-M	853	0	384	59	0
5	4-S	853	0	384	59	0
5	4-Y	853	0	384	59	0
5	5-G	853	0	384	59	0
5	5-M	853	0	384	59	0
5	5-S	853	0	384	59	0
5	5-Y	853	0	384	59	0
5	6-G	853	0	0	0	0
5	6-M	853	0	0	0	0
5	6-S	853	0	0	0	0
5	6-Y	853	0	0	0	0
5	7-G	853	0	384	59	0
5	7-M	853	0	384	59	0
5	7-S	853	0	384	59	0
5	7-Y	853	0	384	59	0
5	8-G	853	0	384	59	0
5	8-M	853	0	384	59	0
5	8-S	853	0	384	59	0
5	8-Y	853	0	384	59	0
6	1-H	842	0	365	38	0
6	1-N	842	0	365	41	0
6	1-T	842	0	365	39	0
6	1-Z	842	0	365	39	0
6	2-H	842	0	365	39	0
6	2-N	842	0	365	37	0
6	2-T	842	0	365	69	0
6	2-Z	842	0	365	37	0
6	3-H	842	0	365	39	0
6	3-N	842	0	365	39	0
6	3-T	842	0	365	69	0
6	3-Z	842	0	365	39	0
6	4-H	842	0	365	40	0
6	4-N	842	0	365	37	0
6	4-T	842	0	365	40	0
6	4-Z	842	0	365	37	0
6	5-H	842	0	365	40	0
6	5-N	842	0	365	37	0
6	5-T	842	0	365	40	0
6	5-Z	842	0	365	37	0
6	6-H	842	0	0	0	0
6	6-N	842	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	6-T	842	0	0	0	0
6	6-Z	842	0	0	0	0
6	7-H	842	0	365	40	0
6	7-N	842	0	365	37	0
6	7-T	842	0	365	40	0
6	7-Z	842	0	365	37	0
6	8-H	842	0	365	40	0
6	8-N	842	0	365	39	0
6	8-T	842	0	365	40	0
6	8-Z	842	0	365	39	0
All	All	594304	0	229951	14969	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 17.

The worst 5 of 14969 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:H:490:GLN:CA	6:H:490:GLN:CB	1.75	1.65
6:H:490:GLN:CA	6:H:490:GLN:CB	1.75	1.65
6:H:490:GLN:CA	6:H:490:GLN:CB	1.75	1.65
6:H:490:GLN:CA	6:H:490:GLN:CB	1.75	1.65
5:S:366:GLU:CA	5:S:366:GLU:CB	1.76	1.64

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	1-A	612/1391 (44%)	562 (92%)	38 (6%)	12 (2%)	6	31
1	1-B	612/1391 (44%)	562 (92%)	38 (6%)	12 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-E	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
1	1-K	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
1	1-Q	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
1	1-W	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
1	2-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	2-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	2-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	2-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	2-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	6	31
1	2-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	3-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	3-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	3-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	3-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	3-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	6	31
1	3-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	4-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	4-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	4-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	4-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	4-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	6	31
1	4-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	5-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	5-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	5-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	5-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	5-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	6	31
1	5-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	6-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	6-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	6-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	6-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	6-Q	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	6-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	7-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	7-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	7-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	7-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	7-Q	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	7-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	8-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	8-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	6	34
1	8-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	8-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	8-Q	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
1	8-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	6	31
2	1-C	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	1-I	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	1-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	1-U	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	2-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	2-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	11
2	2-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	2-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	3-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	3-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	11
2	3-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	3-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	4-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	4-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	11
2	4-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	4-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	5-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	5-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	11
2	5-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	5-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	6-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	6-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	11
2	6-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	6-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	7-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	7-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	11
2	7-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	7-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	8-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	8-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	11
2	8-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	8-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
3	1-D	972/2012 (48%)	899 (92%)	59 (6%)	14 (1%)	9	40
3	1-J	972/2012 (48%)	899 (92%)	59 (6%)	14 (1%)	9	40
3	1-P	972/2012 (48%)	899 (92%)	59 (6%)	14 (1%)	9	40
3	1-V	972/2012 (48%)	899 (92%)	59 (6%)	14 (1%)	9	40
3	2-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	2-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	2-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	2-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	3-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	3-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	3-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	3-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	4-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	4-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	4-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	4-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	5-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	5-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	5-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	5-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	6-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	6-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	6-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	6-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	7-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	7-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	7-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	7-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	8-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	8-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	8-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
3	8-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	8	40
4	1-F	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
4	1-L	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
4	1-R	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
4	1-X	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
4	2-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	2-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	2-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	2-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	3-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	3-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	3-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	3-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	4-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	4-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	4-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	5-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	5-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	5-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	5-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	6-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	6-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	6-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	6-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	7-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	7-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	7-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	7-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	8-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	8-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	8-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
4	8-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	1	15
5	1-G	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	1-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	1-S	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	1-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	2-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	2-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	2-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	2-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	3-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	3-M	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	3-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	3-Y	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	4-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	4-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	4-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	4-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	5-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	5-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	5-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	5-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	6-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	6-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	6-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	6-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	7-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	7-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	7-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	7-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	8-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	8-M	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	8-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	8-Y	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
6	1-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	1-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	1-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	1-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	2-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	2-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	2-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	2-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	3-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	3-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	3-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	3-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	4-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	4-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	4-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	4-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	5-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	5-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	5-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	5-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	6-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	6-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	6-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	6-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	7-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	7-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	7-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	7-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	8-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	8-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	8-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	8-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
All	All	114816/209456 (55%)	104157 (91%)	6943 (6%)	3716 (3%)	5	21

5 of 3716 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	332	ARG
1	1-A	443	LYS
1	1-A	543	GLN
1	1-A	802	GLN
1	1-B	332	ARG

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	1-F	6
4	1-L	6
4	1-R	6
4	1-X	6
4	2-F	5
4	2-L	5
4	2-R	5
4	2-X	5
4	3-F	5
4	3-L	5
4	3-R	5
4	3-X	5
4	4-F	5
4	4-L	5
4	4-R	5
4	4-X	5

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Mol	Chain	Number of breaks
4	5-F	5
4	5-L	5
4	5-R	5
4	5-X	5
4	6-F	5
4	6-L	5
4	6-R	5
4	6-X	5
4	7-F	5
4	7-L	5
4	7-R	5
4	7-X	5
4	8-F	5
4	8-L	5
4	8-R	5
4	8-X	5
2	1-C	3
2	1-I	3
2	1-O	3
2	1-U	3
2	2-C	3
2	2-I	3
2	2-O	3
2	2-U	3
2	3-C	3
2	3-I	3
2	3-O	3
2	3-U	3
2	4-C	3
2	4-I	3
2	4-O	3
2	4-U	3
2	5-C	3
2	5-I	3
2	5-O	3
2	5-U	3
2	6-C	3
2	6-I	3
2	6-O	3
2	6-U	3
2	7-C	3
2	7-I	3

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Mol	Chain	Number of breaks
2	7-O	3
2	7-U	3
2	8-C	3
2	8-I	3
2	8-O	3
2	8-U	3
5	1-M	3
5	1-Y	3
5	2-G	3
5	2-S	3
5	2-Y	3
5	3-G	3
5	3-M	3
5	3-S	3
5	3-Y	3
5	4-G	3
5	4-S	3
5	4-Y	3
5	5-G	3
5	5-S	3
5	5-Y	3
5	6-G	3
5	6-S	3
5	6-Y	3
5	7-G	3
5	7-S	3
5	7-Y	3
5	8-G	3
5	8-M	3
5	8-S	3
5	8-Y	3
5	1-G	3
5	1-S	3
5	2-M	3
5	4-M	3
5	5-M	3
5	6-M	3
5	7-M	3
6	1-H	3
6	1-N	3
6	1-T	3
6	1-Z	3

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Mol	Chain	Number of breaks
6	2-H	3
6	2-N	3
6	2-T	3
6	2-Z	3
6	3-H	3
6	3-N	3
6	3-T	3
6	3-Z	3
6	4-H	3
6	4-N	3
6	4-T	3
6	4-Z	3
6	5-H	3
6	5-N	3
6	5-T	3
6	5-Z	3
6	6-H	3
6	6-N	3
6	6-T	3
6	6-Z	3
6	7-H	3
6	7-N	3
6	7-T	3
6	7-Z	3
6	8-H	3
6	8-N	3
6	8-T	3
6	8-Z	3

The worst 5 of 452 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	483:GLU	C	484:ARG	N	4.02
1	I	483:GLU	C	484:ARG	N	4.02
1	O	483:GLU	C	484:ARG	N	4.02
1	U	483:GLU	C	484:ARG	N	4.02
2	C	483:GLU	C	484:ARG	N	4.02

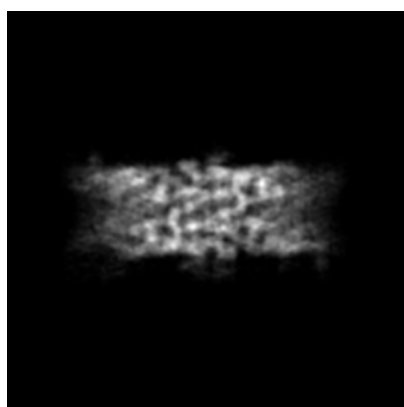
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8085. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

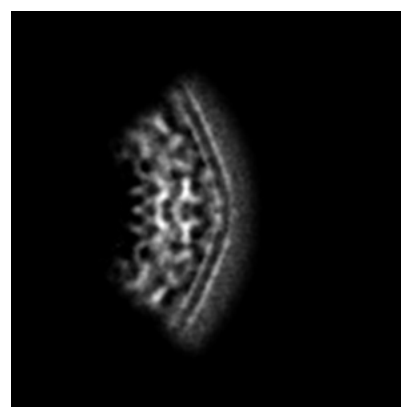
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 72



Y Index: 72

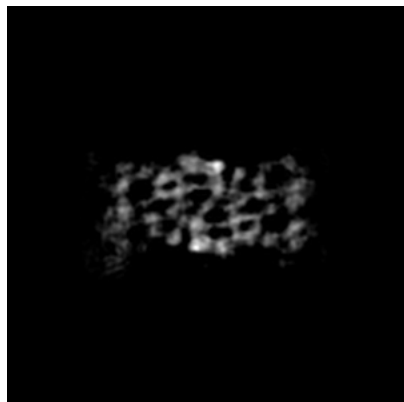


Z Index: 72

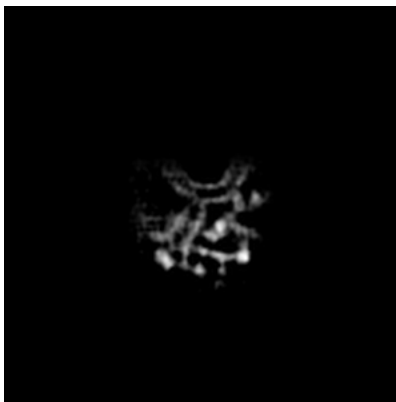
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 53



Y Index: 76

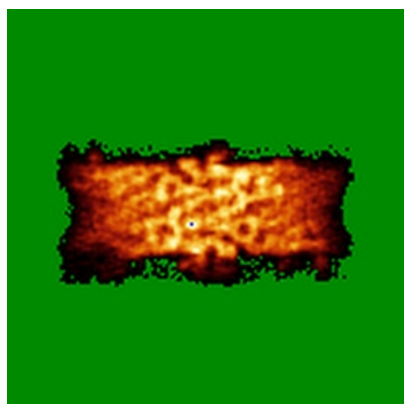


Z Index: 78

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

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

6.4.1 Primary map



X



Y

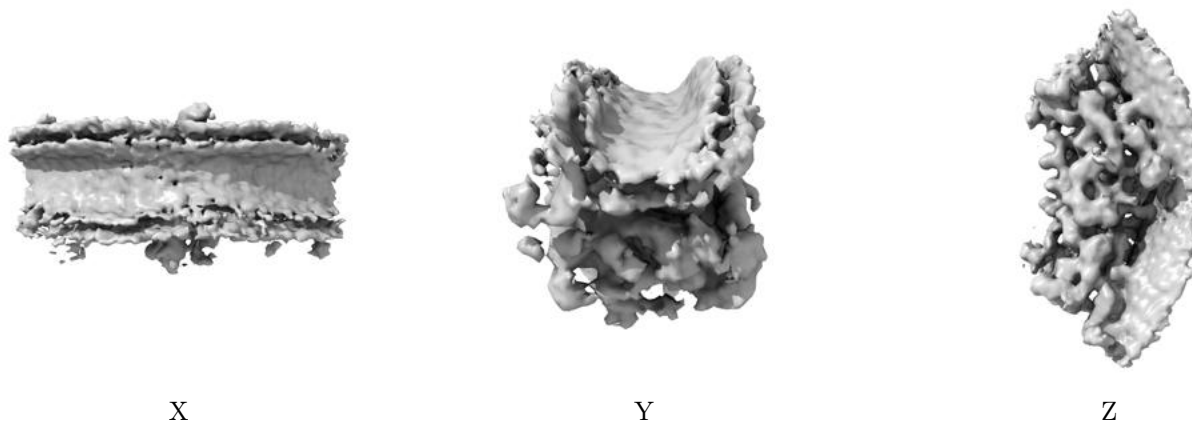


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 36.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

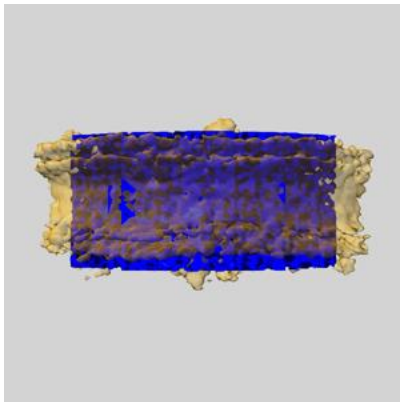
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

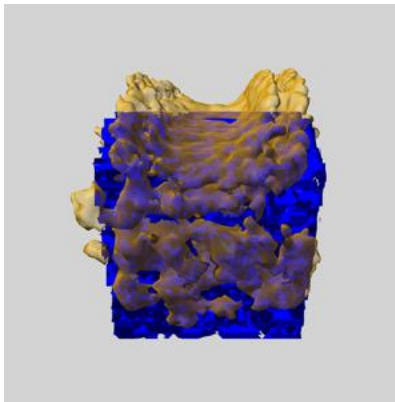
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

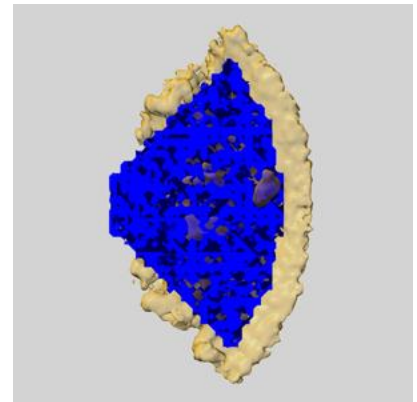
6.6.1 emd_8085_msk_1.map [i](#)



X



Y

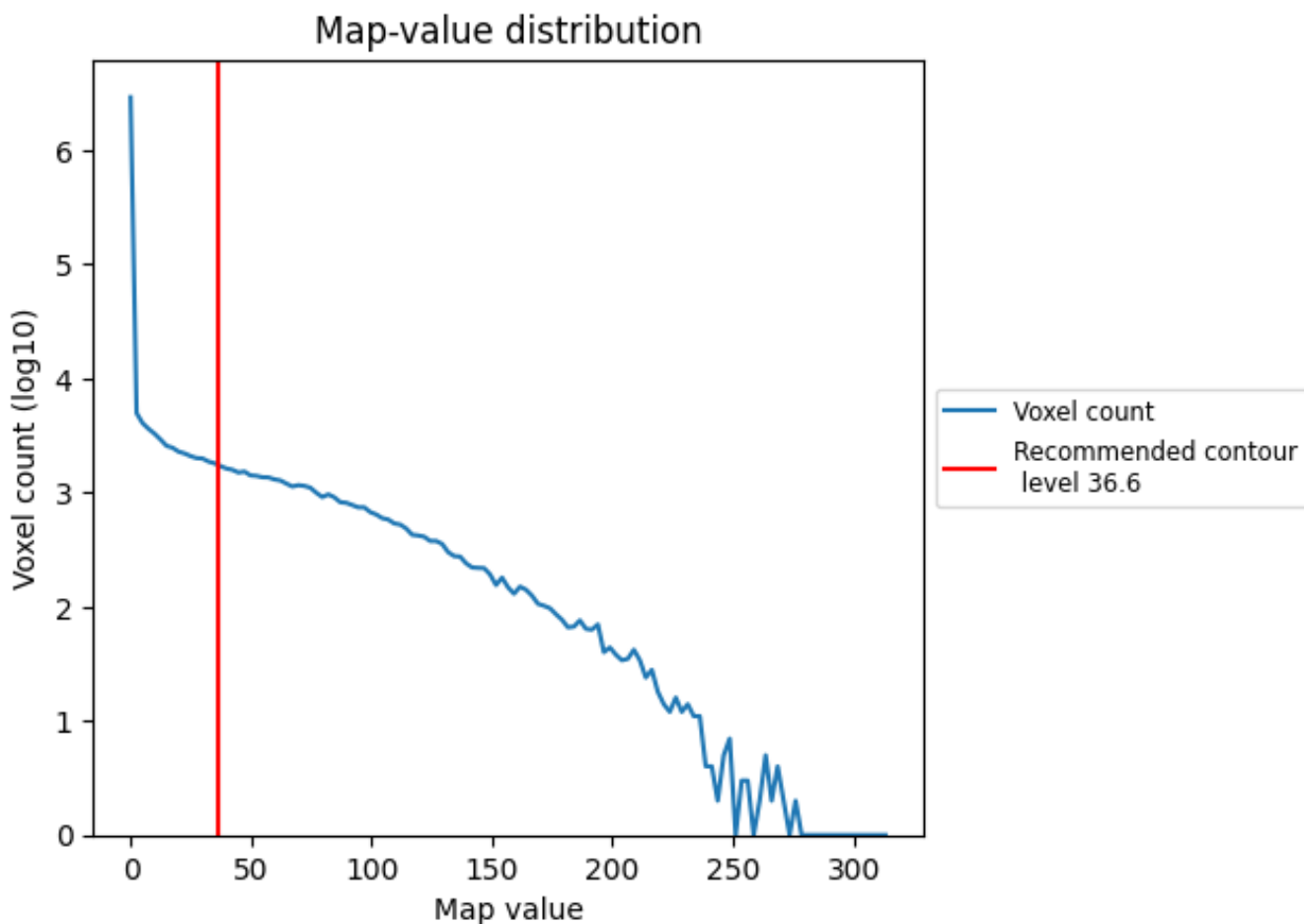


Z

7 Map analysis [i](#)

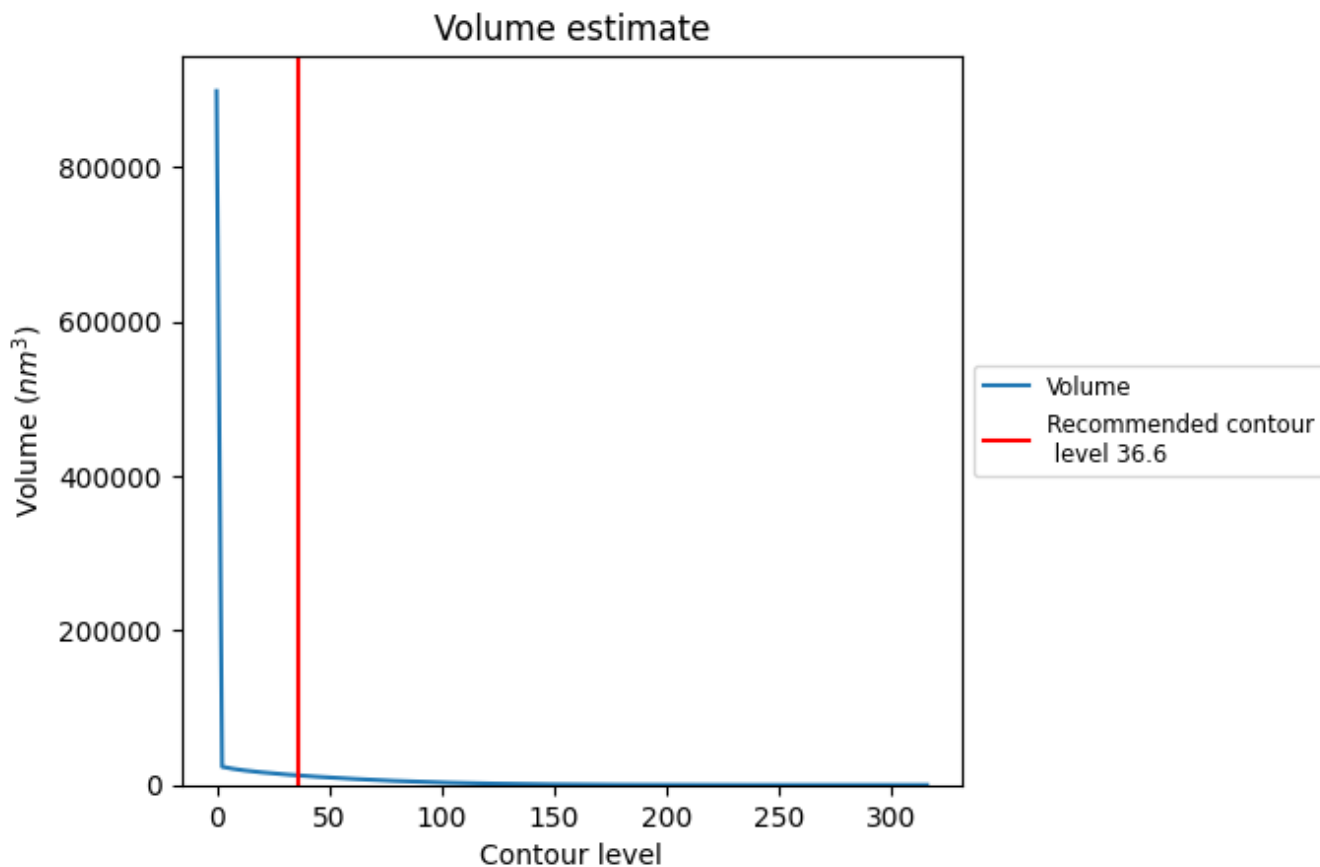
This section contains the results of statistical analysis of the map.

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.

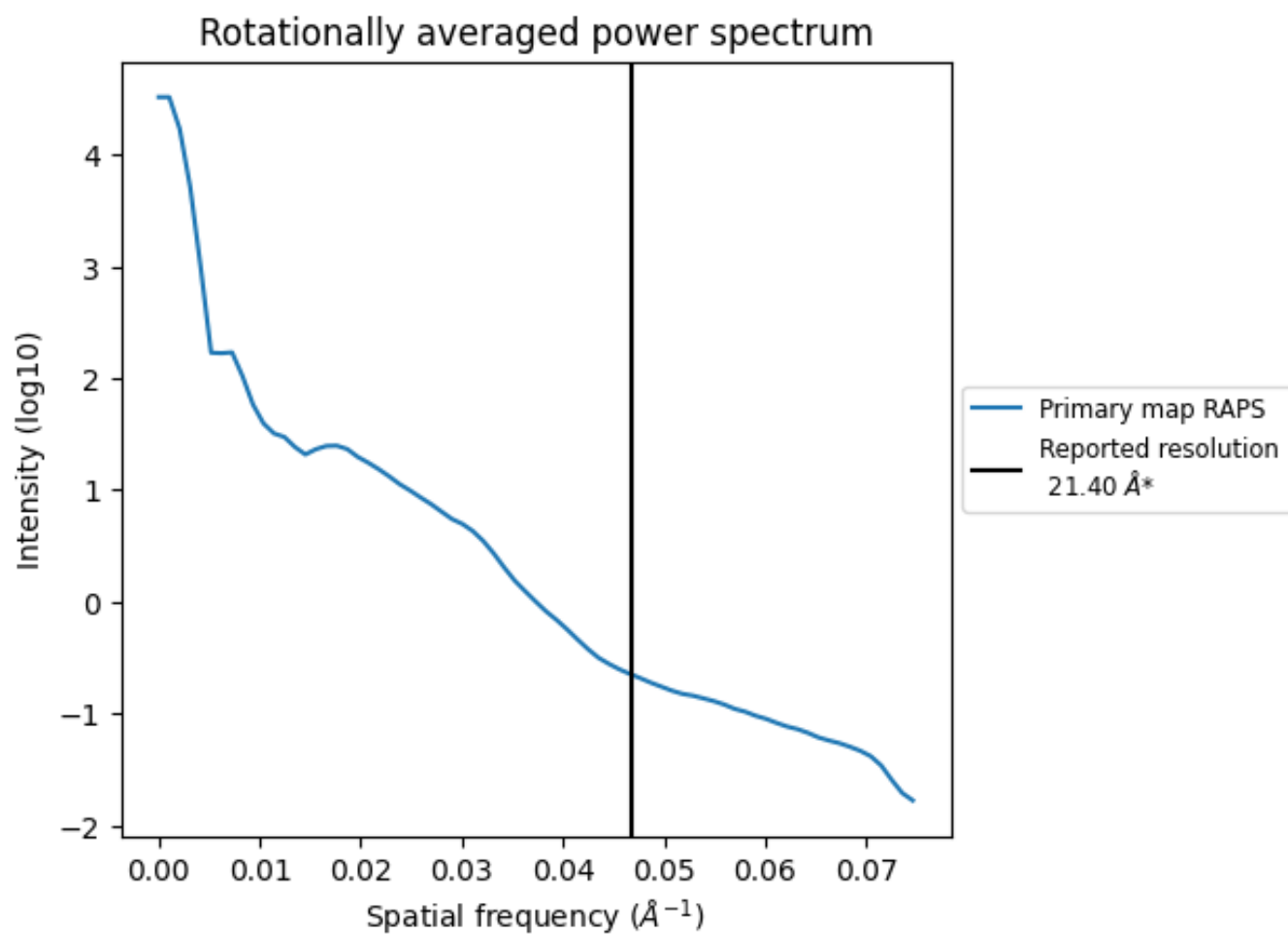
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 12255 nm^3 ; this corresponds to an approximate mass of 11070 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 0.047 Å⁻¹

8 Fourier-Shell correlation

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

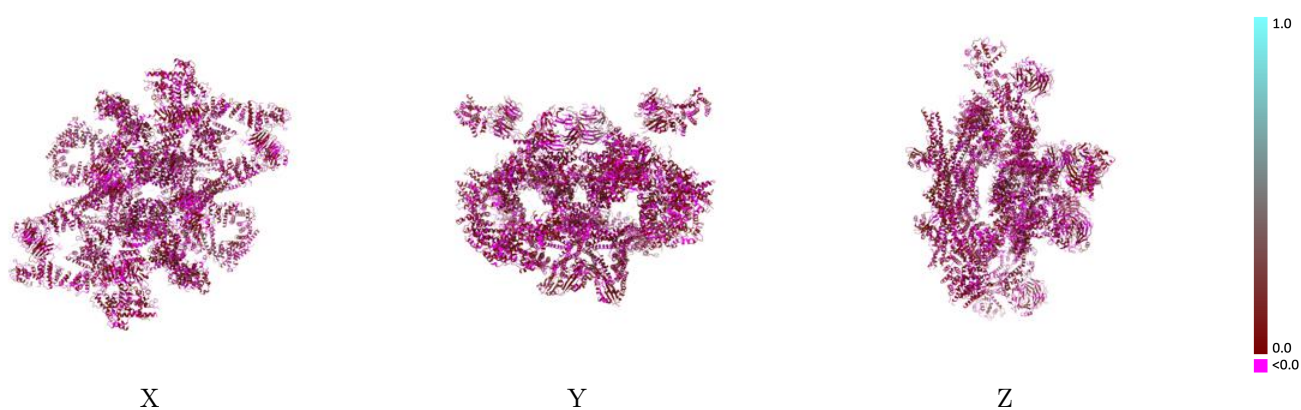
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8085 and PDB model 5IJN. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)

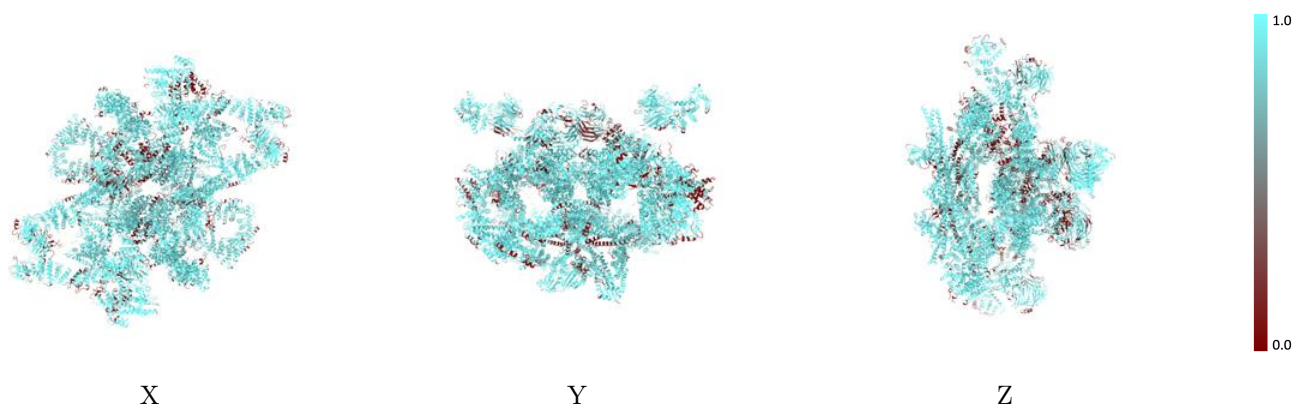
This section was not generated.

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



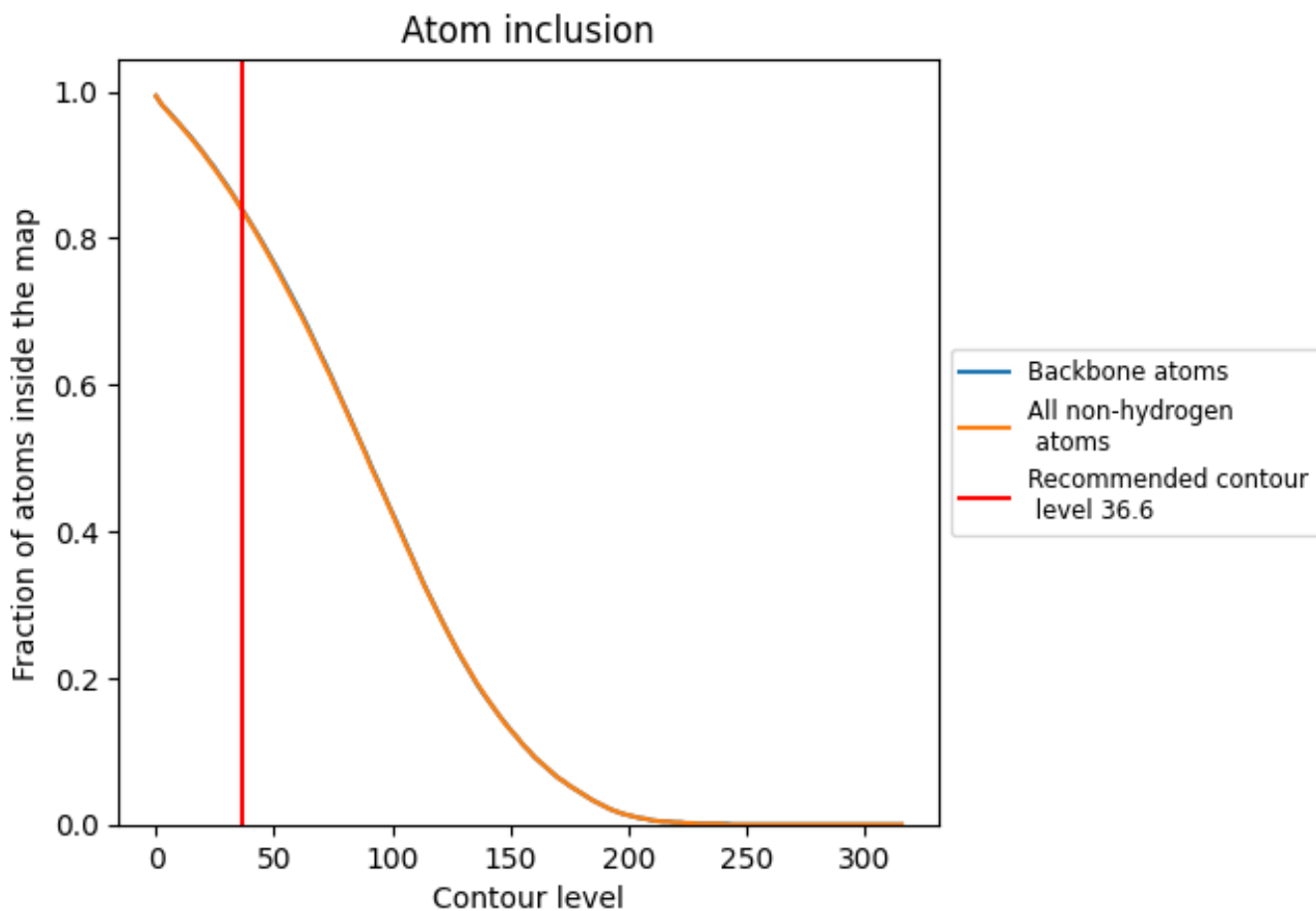
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (36.6).























































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% 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 (36.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.0410
A	 0.9290	 0.0440
B	 0.8790	 0.0450
C	 0.8490	 0.0370
D	 0.8980	 0.0440
E	 0.8660	 0.0390
F	 0.8100	 0.0350
G	 0.9040	 0.0420
H	 0.7990	 0.0240
I	 0.8270	 0.0450
J	 0.8800	 0.0520
K	 0.5460	 0.0180
L	 0.7990	 0.0280
M	 0.8450	 0.0490
N	 0.8730	 0.0700
O	 0.8780	 0.0410
P	 0.8970	 0.0520
Q	 0.8810	 0.0430
R	 0.7760	 0.0280
S	 0.9330	 0.0520
T	 0.7480	 0.0290
U	 0.8000	 0.0380
V	 0.9070	 0.0510
W	 0.7750	 0.0340
X	 0.8370	 0.0380
Y	 0.9000	 0.0550
Z	 0.8490	 0.0460

