wwPDB EM Validation Summary Report (i)

Nov 19, 2022 – 02:38 pm GMT

PDB ID	:	5IJN
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 (i) symbol.

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

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

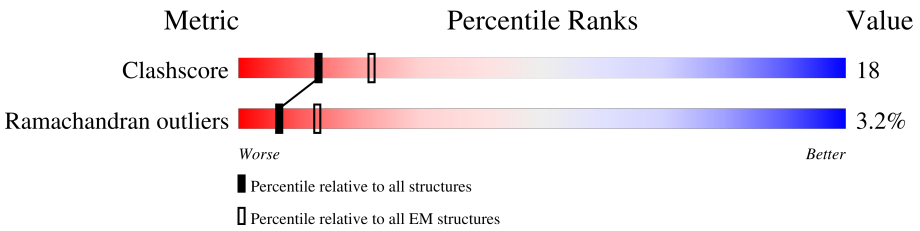
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023

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

Mol	Chain	Length	Quality of chain
1	1-A	1391	• 43% • 53%
1	1-B	1391	5% 43% • 53%
1	1-E	1391	10% 72% 5% • 22%
1	1-K	1391	35% 73% 5% • 22%
1	1-Q	1391	9% 71% 6% • 22%
1	1-W	1391	17% 73% 5% 22%
1	2-A	1391	44% • 53%
1	2-B	1391	44% • 53%
1	2-E	1391	73% 5% 22%

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Mol	Chain	Length	Quality of chain
1	2-K	1391	71% 6% 22%
1	2-Q	1391	73% 5% 22%
1	2-W	1391	71% 6% 22%
1	3-A	1391	44% • 53%
1	3-B	1391	44% • 53%
1	3-E	1391	73% 5% 22%
1	3-K	1391	71% 6% 22%
1	3-Q	1391	73% 5% 22%
1	3-W	1391	71% 6% 22%
1	4-A	1391	44% • 53%
1	4-B	1391	44% • 53%
1	4-E	1391	73% 5% 22%
1	4-K	1391	71% 6% 22%
1	4-Q	1391	73% 5% 22%
1	4-W	1391	71% 6% 22%
1	5-A	1391	44% • 53%
1	5-B	1391	44% • 53%
1	5-E	1391	73% 5% 22%
1	5-K	1391	71% 6% 22%
1	5-Q	1391	73% 5% 22%
1	5-W	1391	71% 6% 22%
1	6-A	1391	44% • 53%
1	6-B	1391	44% • 53%
1	6-E	1391	72% 5% 22%
1	6-K	1391	71% 6% 22%

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Mol	Chain	Length	Quality of chain
1	6-Q	1391	72% 5% 22%
1	6-W	1391	71% 6% 22%
1	7-A	1391	44% • 53%
1	7-B	1391	44% • 53%
1	7-E	1391	72% 5% 22%
1	7-K	1391	71% 6% 22%
1	7-Q	1391	72% 5% 22%
1	7-W	1391	71% 6% 22%
1	8-A	1391	44% • 53%
1	8-B	1391	44% • 53%
1	8-E	1391	72% 5% 22%
1	8-K	1391	71% 6% 22%
1	8-Q	1391	72% 5% 22%
1	8-W	1391	71% 6% 22%
2	1-C	819	12% 64% 11% • 22%
2	1-I	819	14% 65% 11% • 22%
2	1-O	819	9% 65% 10% • 22%
2	1-U	819	16% 65% 11% • 22%
2	2-C	819	63% 13% • 22%
2	2-I	819	65% 11% • 22%
2	2-O	819	63% 12% • 22%
2	2-U	819	65% 11% • 22%
2	3-C	819	63% 13% • 22%
2	3-I	819	65% 11% • 22%
2	3-O	819	63% 12% • 22%

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Mol	Chain	Length	Quality of chain
2	3-U	819	65% 11% • 22%
2	4-C	819	63% 13% • 22%
2	4-I	819	65% 11% • 22%
2	4-O	819	63% 12% • 22%
2	4-U	819	65% 11% • 22%
2	5-C	819	63% 13% • 22%
2	5-I	819	65% 11% • 22%
2	5-O	819	63% 12% • 22%
2	5-U	819	65% 11% • 22%
2	6-C	819	63% 13% • 22%
2	6-I	819	65% 11% • 22%
2	6-O	819	63% 12% • 22%
2	6-U	819	65% 11% • 22%
2	7-C	819	63% 13% • 22%
2	7-I	819	65% 11% • 22%
2	7-O	819	63% 12% • 22%
2	7-U	819	65% 11% • 22%
2	8-C	819	63% 13% • 22%
2	8-I	819	65% 11% • 22%
2	8-O	819	63% 12% • 22%
2	8-U	819	65% 11% • 22%
3	1-D	2012	5% 45% • •• 49%
3	1-J	2012	6% 45% • •• 49%
3	1-P	2012	5% 46% • •• 49%
3	1-V	2012	5% 44% • •• 49%

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Mol	Chain	Length	Quality of chain
3	2-D	2012	45% 49%
3	2-J	2012	46% 49%
3	2-P	2012	45% 49%
3	2-V	2012	46% 49%
3	3-D	2012	45% 49%
3	3-J	2012	46% 49%
3	3-P	2012	45% 49%
3	3-V	2012	46% 49%
3	4-D	2012	46% 49%
3	4-J	2012	46% 49%
3	4-P	2012	46% 49%
3	4-V	2012	46% 49%
3	5-D	2012	46% 49%
3	5-J	2012	46% 49%
3	5-P	2012	46% 49%
3	5-V	2012	46% 49%
3	6-D	2012	46% 49%
3	6-J	2012	46% 49%
3	6-P	2012	46% 49%
3	6-V	2012	46% 49%
3	7-D	2012	46% 49%
3	7-J	2012	46% 49%
3	7-P	2012	46% 49%
3	7-V	2012	46% 49%
3	8-D	2012	46% 49%

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Mol	Chain	Length	Quality of chain
3	8-J	2012	46% · · · 49%
3	8-P	2012	46% · · · 49%
3	8-V	2012	46% · · · 49%
4	1-F	507	13% 35% 16% 9% 5% 34%
4	1-L	507	13% 35% 16% 9% 5% 34%
4	1-R	507	15% 35% 16% 9% 5% 34%
4	1-X	507	10% 36% 16% 9% 5% 34%
4	2-F	507	43% 12% 7% 5% 34%
4	2-L	507	43% 12% 6% 5% 34%
4	2-R	507	43% 11% 7% 5% 34%
4	2-X	507	43% 12% 6% 5% 34%
4	3-F	507	43% 12% 7% 5% 34%
4	3-L	507	43% 11% 7% 5% 34%
4	3-R	507	43% 11% 7% 5% 34%
4	3-X	507	43% 12% 7% 5% 34%
4	4-F	507	43% 12% 7% 5% 34%
4	4-L	507	43% 12% 6% 5% 34%
4	4-R	507	43% 12% 7% 5% 34%
4	4-X	507	43% 12% 6% 5% 34%
4	5-F	507	43% 12% 7% 5% 34%
4	5-L	507	43% 12% 6% 5% 34%
4	5-R	507	43% 12% 7% 5% 34%
4	5-X	507	43% 12% 6% 5% 34%
4	6-F	507	43% 12% 7% 5% 34%
4	6-L	507	43% 12% 6% 5% 34%

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Mol	Chain	Length	Quality of chain
4	6-R	507	43% 12% 7% 5% 34%
4	6-X	507	43% 12% 6% 5% 34%
4	7-F	507	43% 12% 7% 5% 34%
4	7-L	507	43% 12% 6% 5% 34%
4	7-R	507	43% 12% 7% 5% 34%
4	7-X	507	43% 12% 6% 5% 34%
4	8-F	507	43% 12% 7% 5% 34%
4	8-L	507	43% 11% 7% 5% 34%
4	8-R	507	43% 12% 7% 5% 34%
4	8-X	507	43% 12% 7% 5% 34%
5	1-G	599	17% 7% • • 71%
5	1-M	599	17% 7% • • 71%
5	1-S	599	17% 7% • • 71%
5	1-Y	599	17% 7% • • 71%
5	2-G	599	17% 7% • • 71%
5	2-M	599	17% 7% • • 71%
5	2-S	599	17% 7% • • 71%
5	2-Y	599	17% 7% • • 71%
5	3-G	599	17% 7% • • 71%
5	3-M	599	17% 7% • • 71%
5	3-S	599	17% 7% • • 71%
5	3-Y	599	17% 7% • • 71%
5	4-G	599	17% 7% • • 71%
5	4-M	599	17% 7% • • 71%
5	4-S	599	17% 7% • • 71%

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Mol	Chain	Length	Quality of chain
5	4-Y	599	17% 7% 71%
5	5-G	599	17% 7% 71%
5	5-M	599	17% 7% 71%
5	5-S	599	17% 7% 71%
5	5-Y	599	17% 7% 71%
5	6-G	599	17% 7% 71%
5	6-M	599	17% 7% 71%
5	6-S	599	17% 7% 71%
5	6-Y	599	17% 7% 71%
5	7-G	599	17% 7% 71%
5	7-M	599	17% 7% 71%
5	7-S	599	17% 7% 71%
5	7-Y	599	17% 7% 71%
5	8-G	599	17% 7% 71%
5	8-M	599	17% 7% 71%
5	8-S	599	17% 7% 71%
5	8-Y	599	17% 7% 71%
6	1-H	522	6% 18% 11% 68%
6	1-N	522	18% 11% 68%
6	1-T	522	8% 18% 11% 68%
6	1-Z	522	5% 18% 11% 68%
6	2-H	522	18% 11% 68%
6	2-N	522	18% 11% 68%
6	2-T	522	18% 10% 68%
6	2-Z	522	18% 11% 68%

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Mol	Chain	Length	Quality of chain
6	3-H	522	18% 11% • • 68%
6	3-N	522	18% 11% • • 68%
6	3-T	522	18% 10% • • 68%
6	3-Z	522	18% 11% • • 68%
6	4-H	522	18% 11% • • 68%
6	4-N	522	18% 11% • • 68%
6	4-T	522	18% 11% • • 68%
6	4-Z	522	18% 11% • • 68%
6	5-H	522	18% 11% • • 68%
6	5-N	522	18% 11% • • 68%
6	5-T	522	18% 11% • • 68%
6	5-Z	522	18% 11% • • 68%
6	6-H	522	18% 11% • • 68%
6	6-N	522	18% 11% • • 68%
6	6-T	522	18% 11% • • 68%
6	6-Z	522	18% 11% • • 68%
6	7-H	522	18% 11% • • 68%
6	7-N	522	18% 11% • • 68%
6	7-T	522	18% 11% • • 68%
6	7-Z	522	18% 11% • • 68%
6	8-H	522	18% 11% • • 68%
6	8-N	522	18% 11% • • 68%
6	8-T	522	18% 11% • • 68%
6	8-Z	522	18% 11% • • 68%

2 Entry composition (i)

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
			Total	C	N	O		
1	2-E	1083	5366	3200	1083	1083	0	0
1	3-E	1083	5366	3200	1083	1083	0	0
1	4-E	1083	5366	3200	1083	1083	0	0
1	5-E	1083	5366	3200	1083	1083	0	0
1	6-E	1083	5366	3200	1083	1083	0	0
1	7-E	1083	5366	3200	1083	1083	0	0
1	8-E	1083	5366	3200	1083	1083	0	0
1	1-K	1083	5366	3200	1083	1083	0	0
1	2-K	1083	5366	3200	1083	1083	0	0
1	3-K	1083	5366	3200	1083	1083	0	0
1	4-K	1083	5366	3200	1083	1083	0	0
1	5-K	1083	5366	3200	1083	1083	0	0
1	6-K	1083	5366	3200	1083	1083	0	0
1	7-K	1083	5366	3200	1083	1083	0	0
1	8-K	1083	5366	3200	1083	1083	0	0
1	1-Q	1083	5366	3200	1083	1083	0	0
1	2-Q	1083	5366	3200	1083	1083	0	0
1	3-Q	1083	5366	3200	1083	1083	0	0
1	4-Q	1083	5366	3200	1083	1083	0	0
1	5-Q	1083	5366	3200	1083	1083	0	0
1	6-Q	1083	5366	3200	1083	1083	0	0

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

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

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

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

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

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

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

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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
			Total	C	N	O		
4	2-X	335	1658	988	335	335	0	0
4	3-X	335	1658	988	335	335	0	0
4	4-X	335	1658	988	335	335	0	0
4	5-X	335	1658	988	335	335	0	0
4	6-X	335	1658	988	335	335	0	0
4	7-X	335	1658	988	335	335	0	0
4	8-X	335	1658	988	335	335	0	0

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

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

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

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

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

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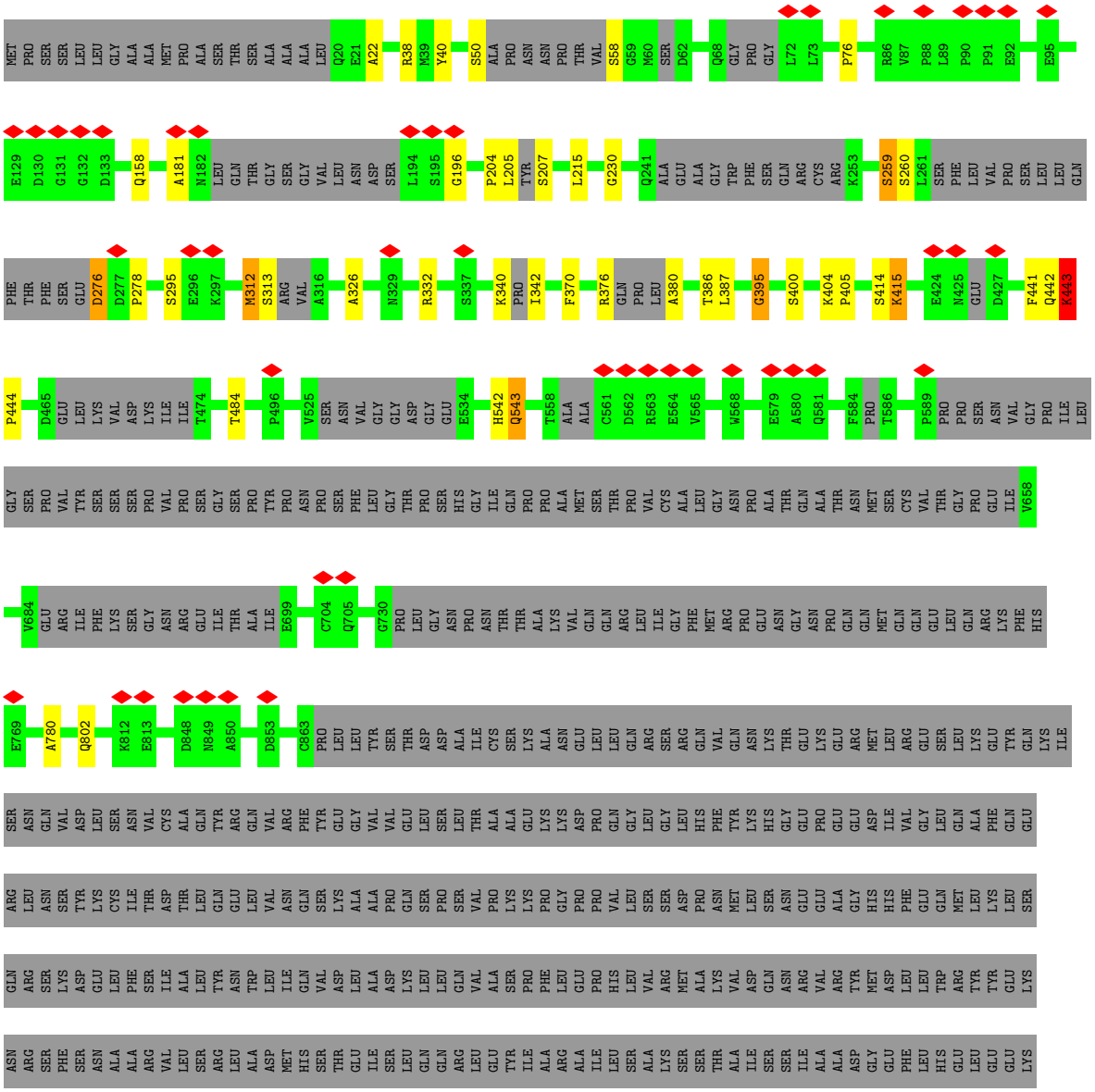
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	7-T	169	842	504	169	169	0	0
6	8-T	169	842	504	169	169	0	0
6	1-Z	169	842	504	169	169	0	0
6	2-Z	169	842	504	169	169	0	0
6	3-Z	169	842	504	169	169	0	0
6	4-Z	169	842	504	169	169	0	0
6	5-Z	169	842	504	169	169	0	0
6	6-Z	169	842	504	169	169	0	0
6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

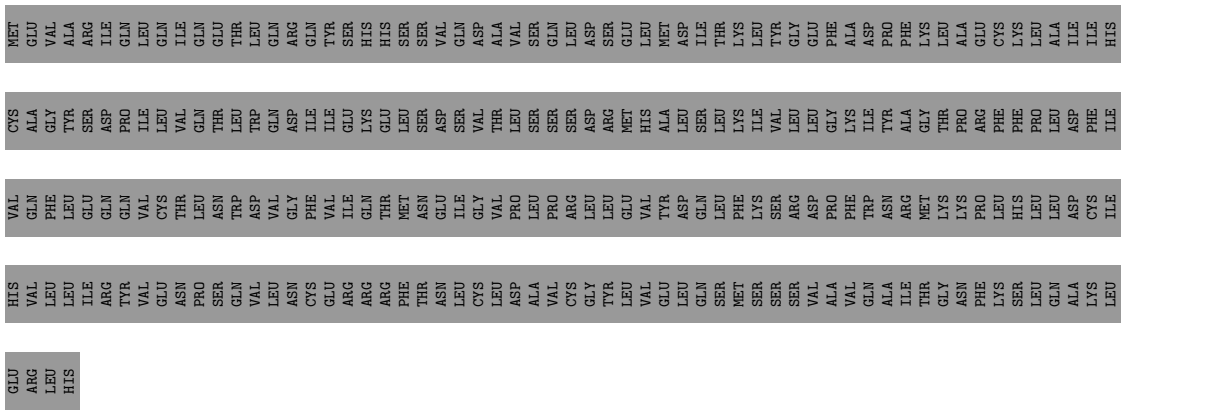
3 Residue-property plots (i)

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

- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

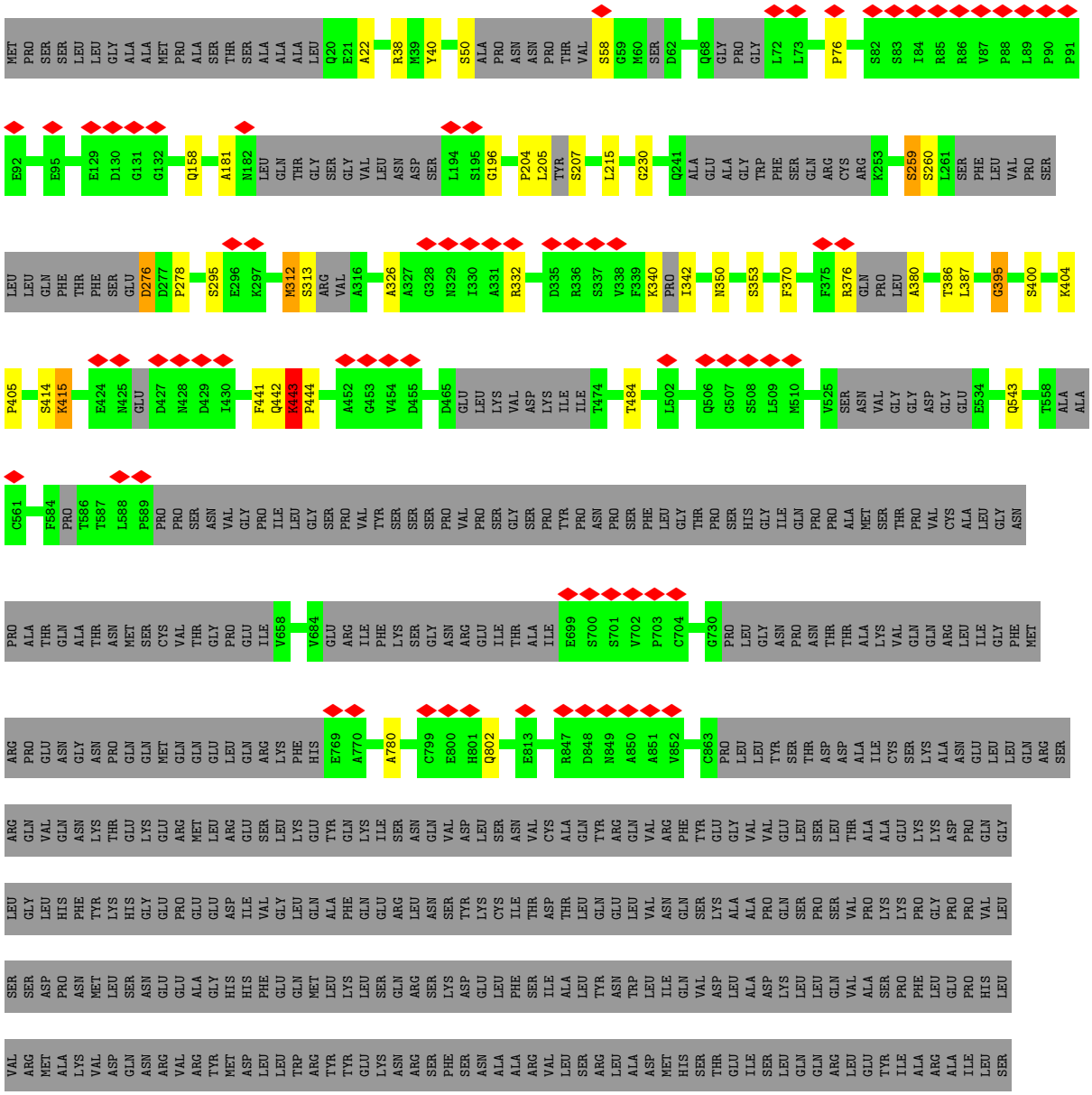
Chain 1-A:

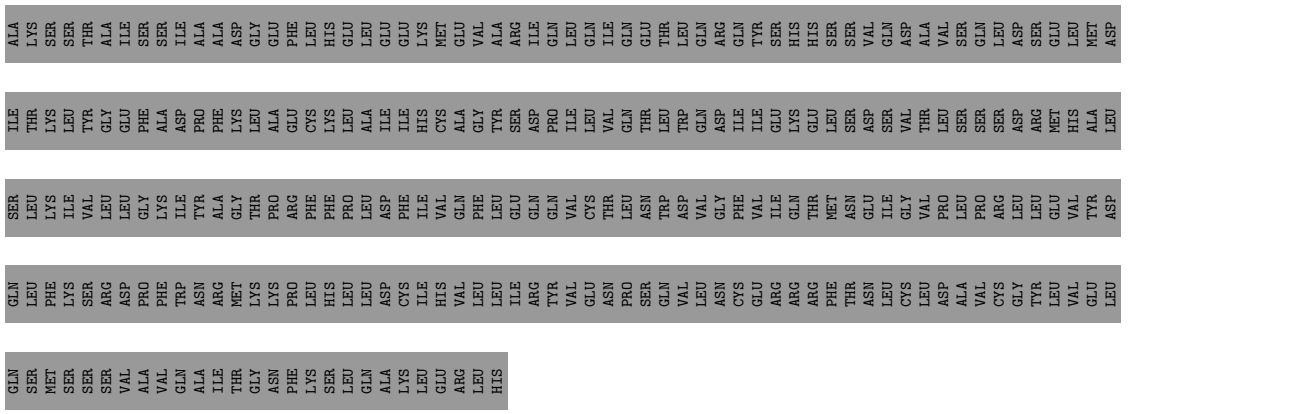




• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

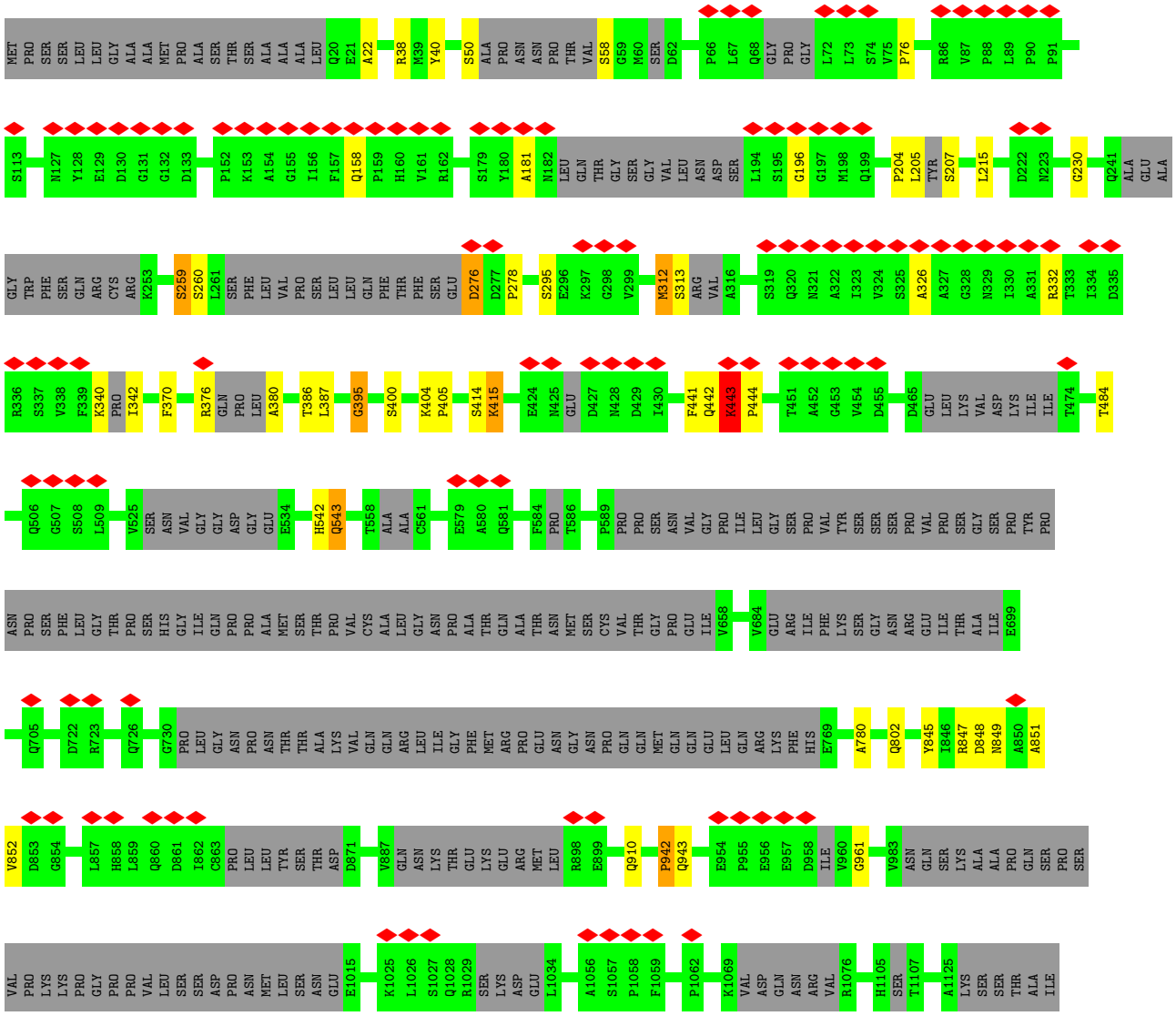
Chain 1-B: 5% 43% • 53%

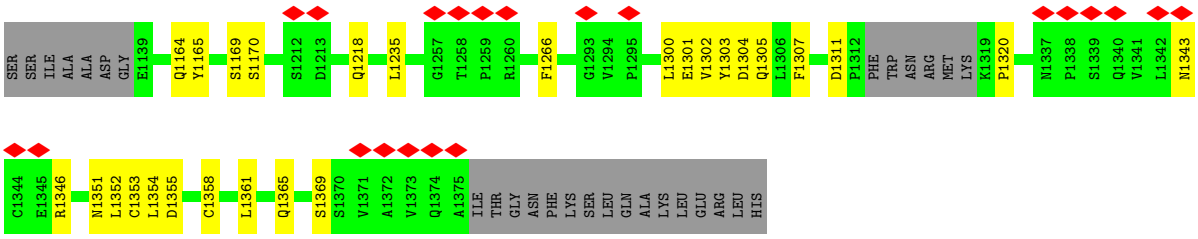




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

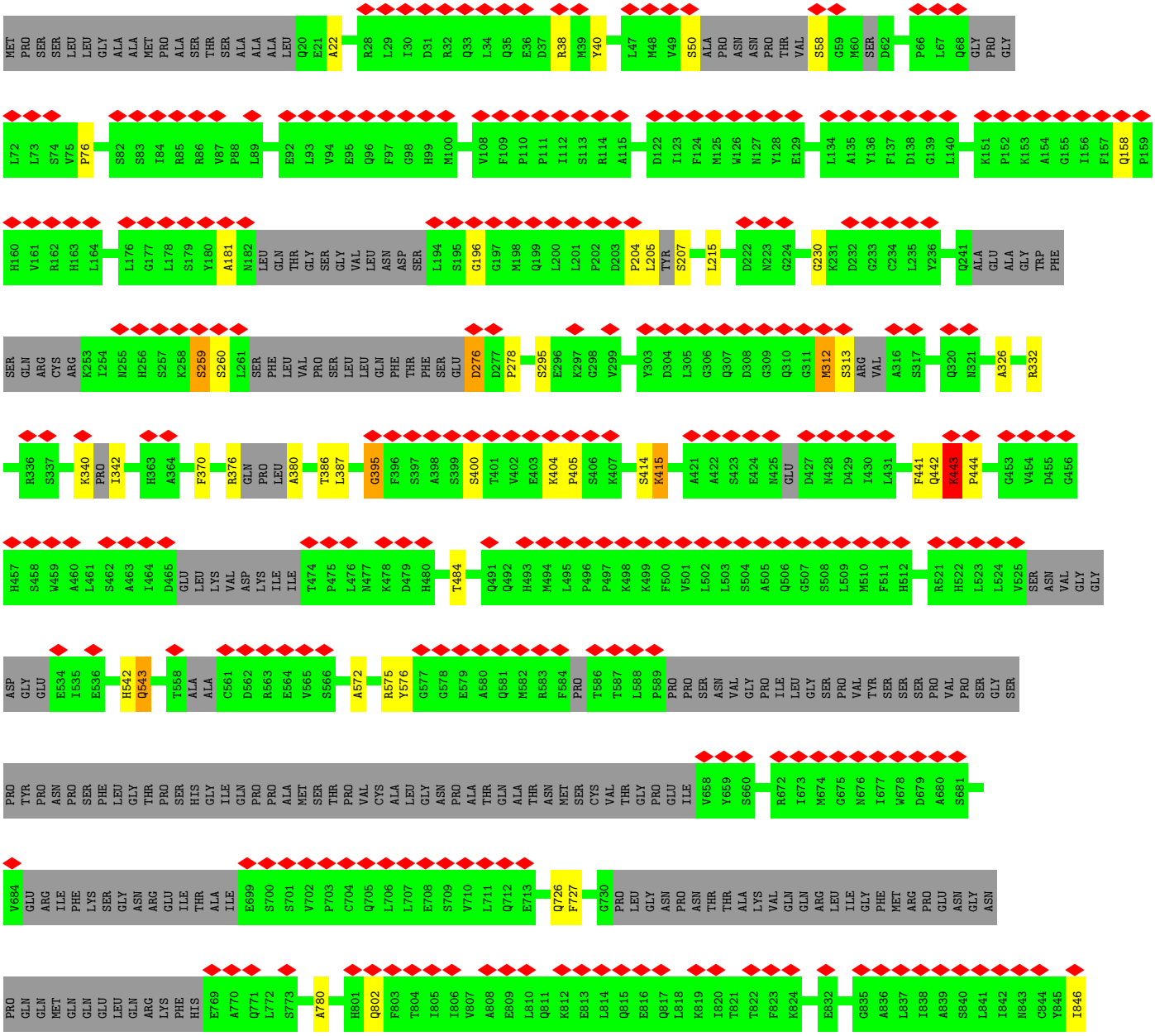
Chain 1-E:

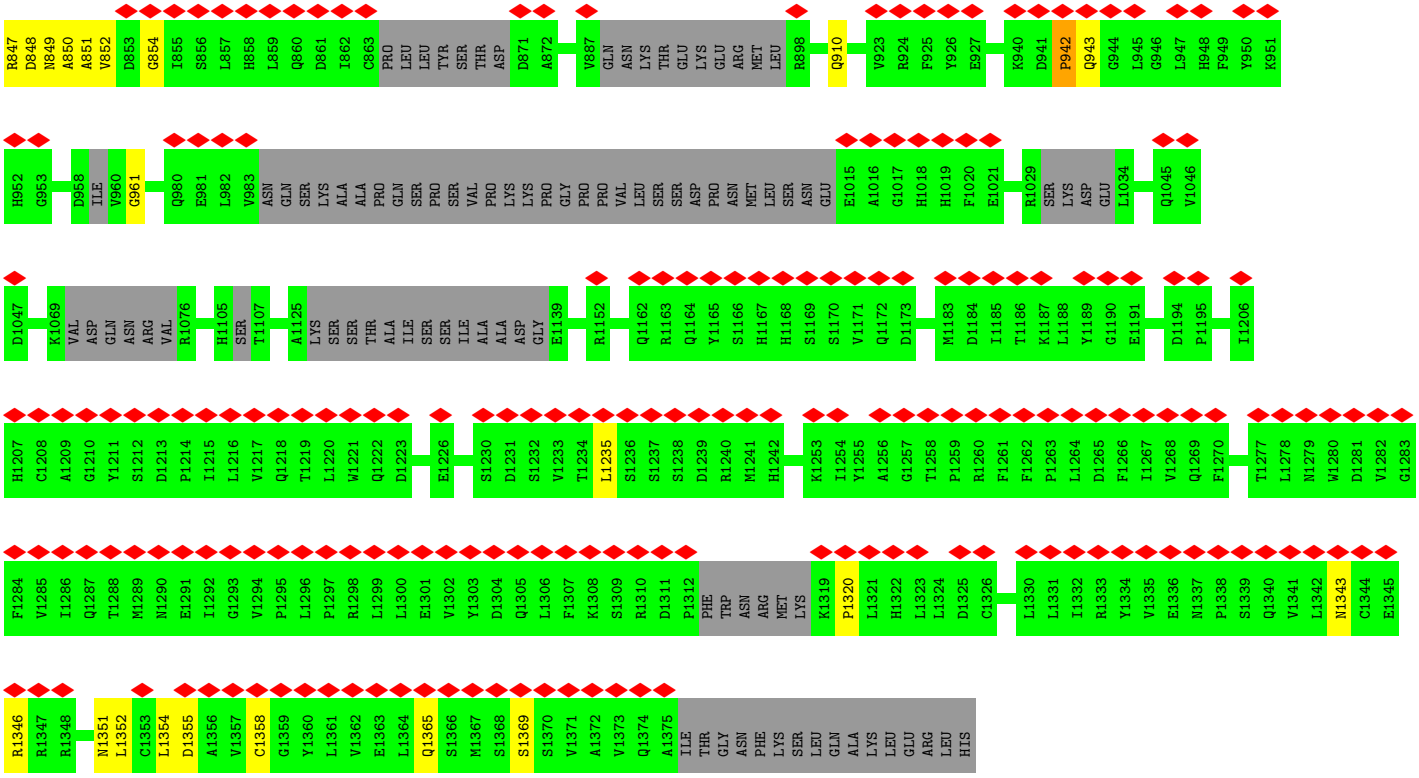




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

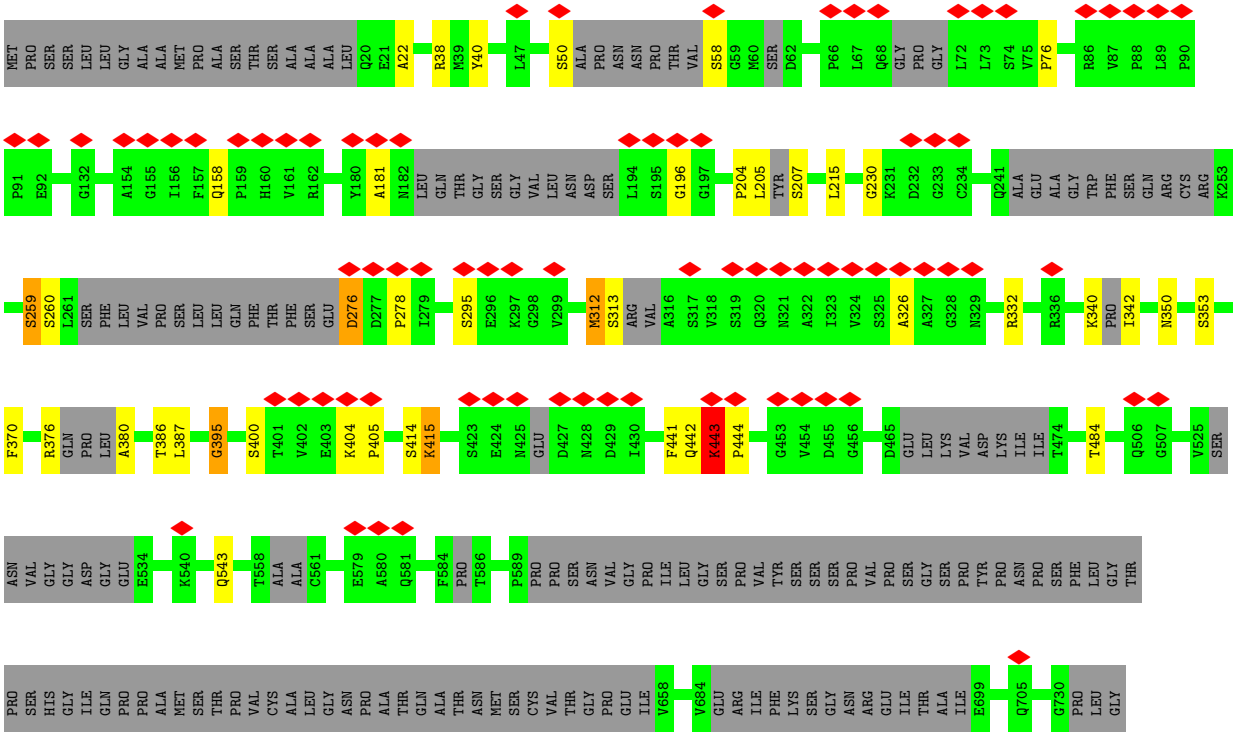
Chain 1-K:

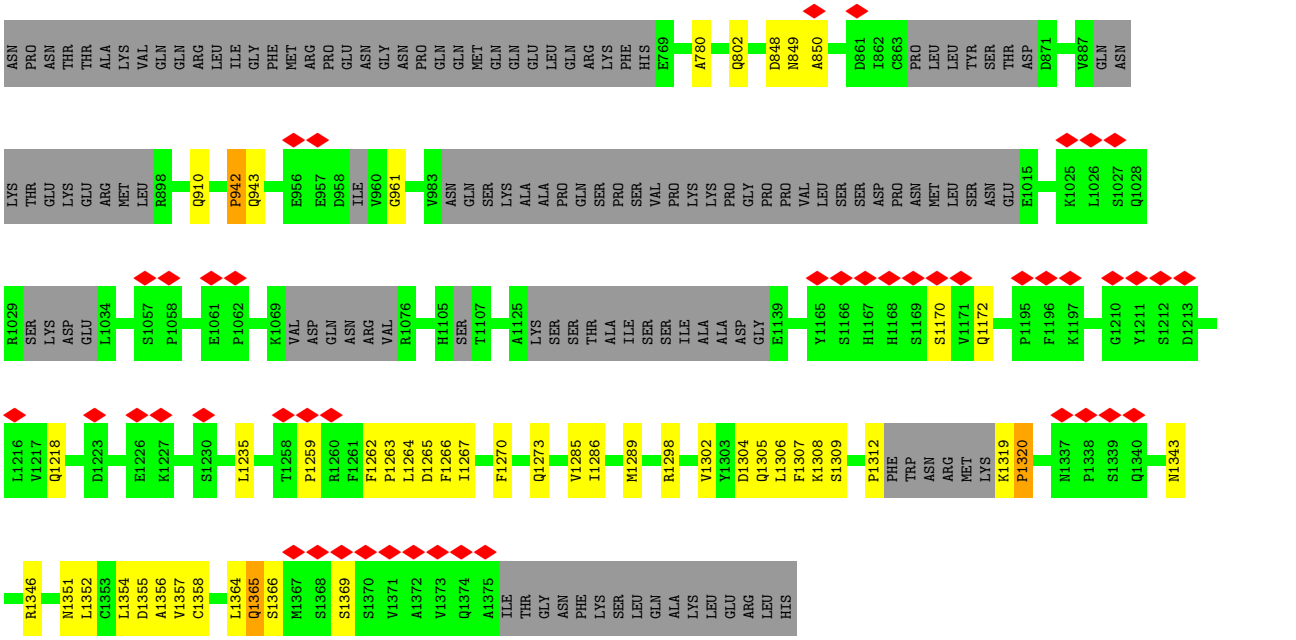




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

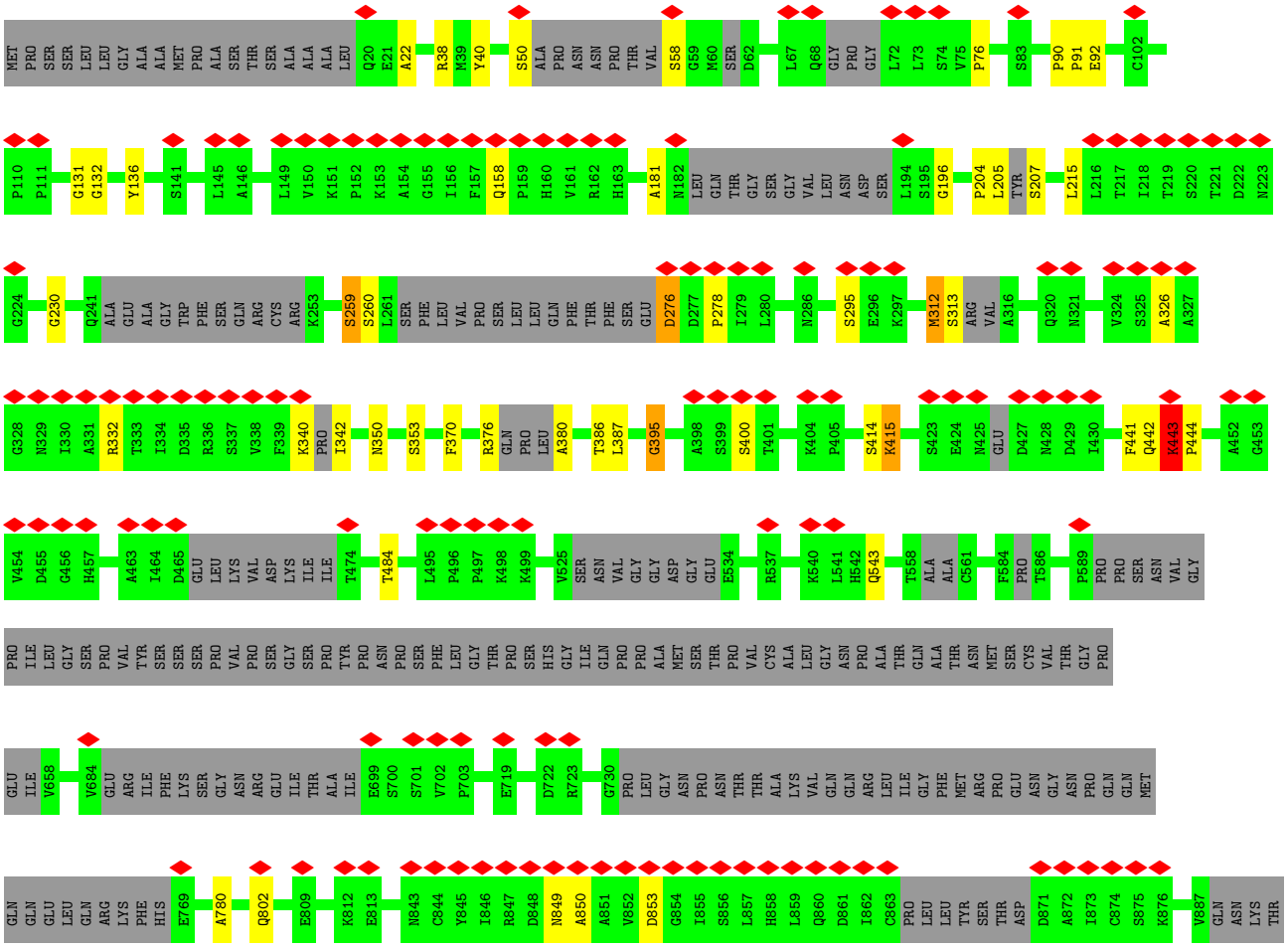
Chain 1-Q:

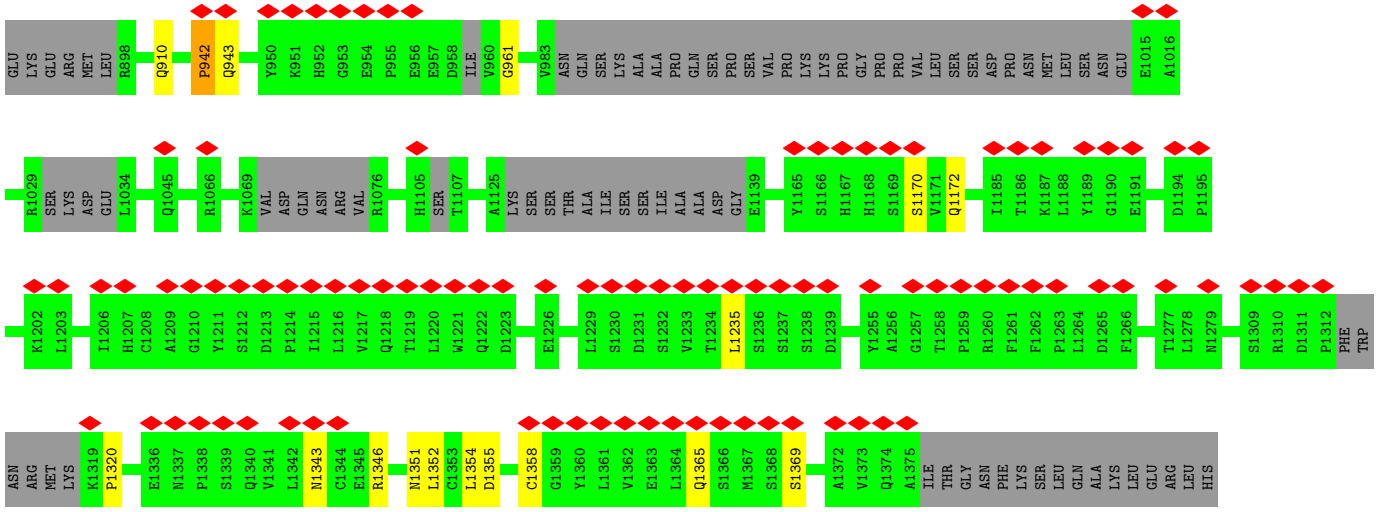




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

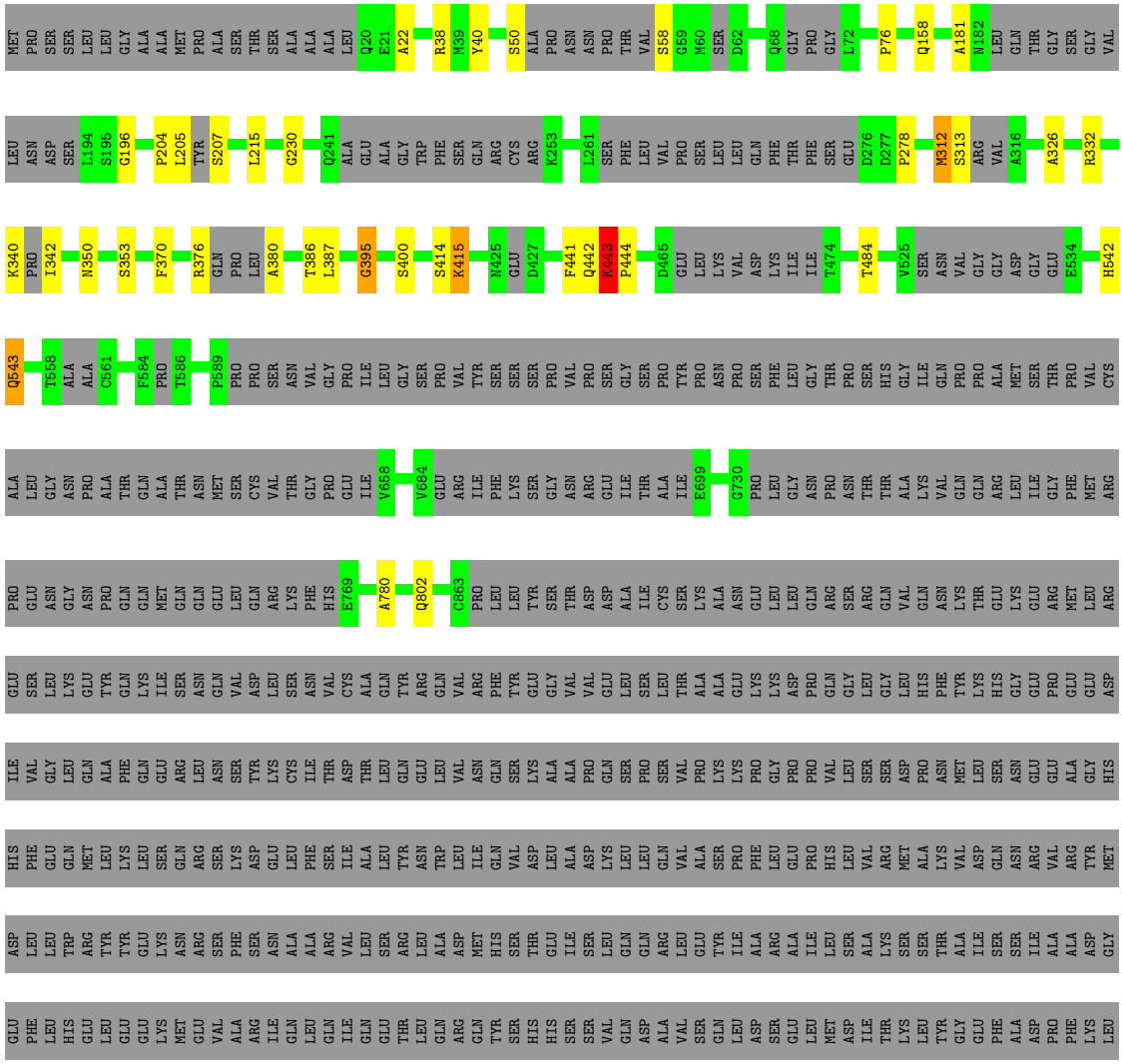
Chain 1-W:

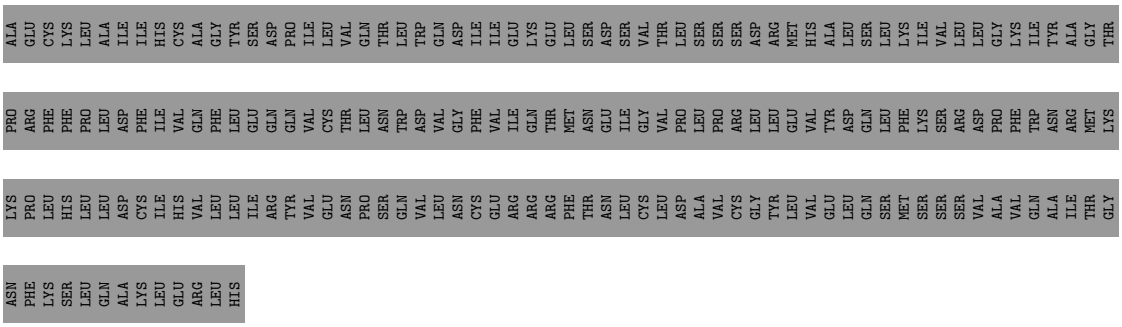




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

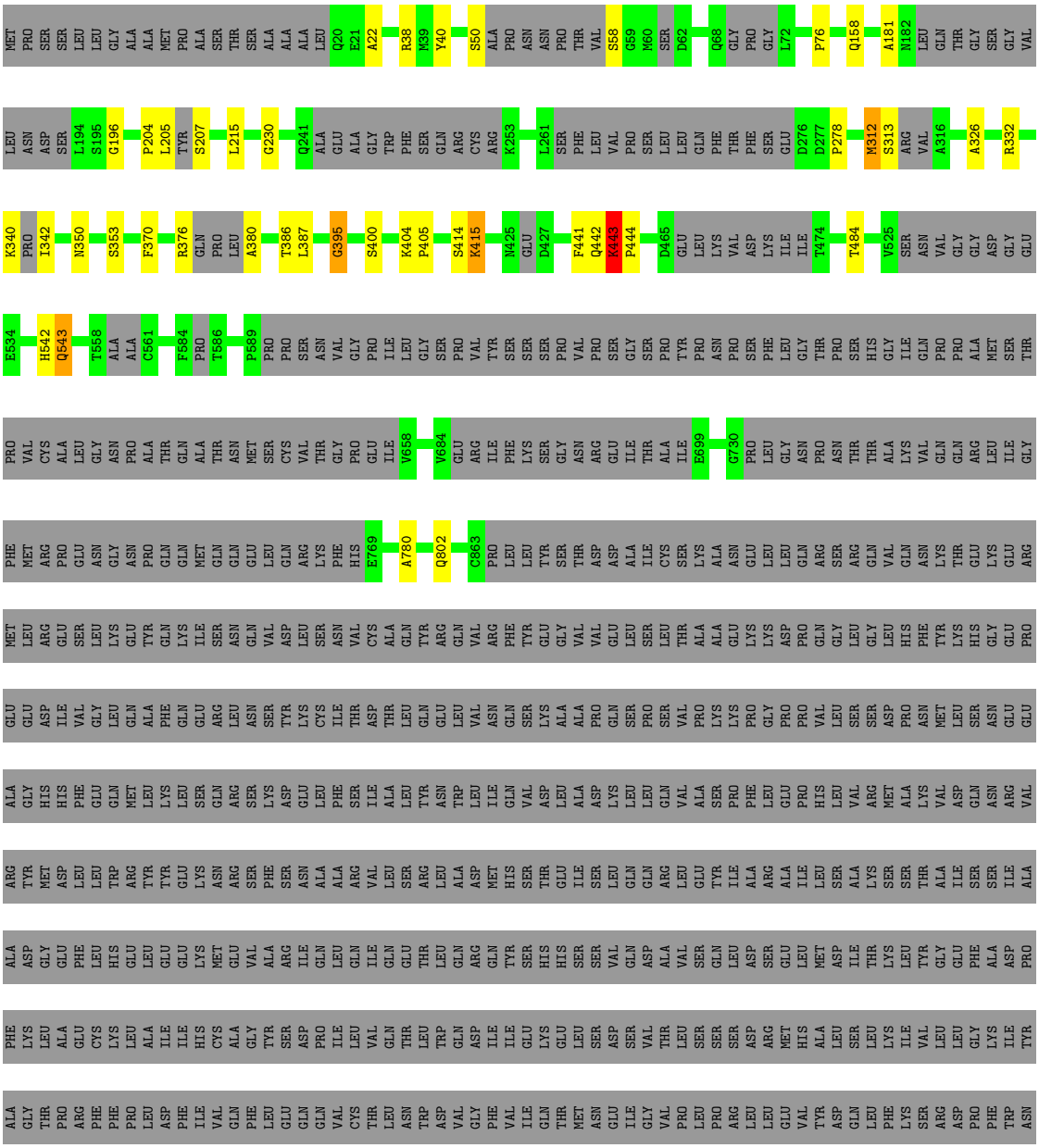
Chain 2-A: 44% • 53%





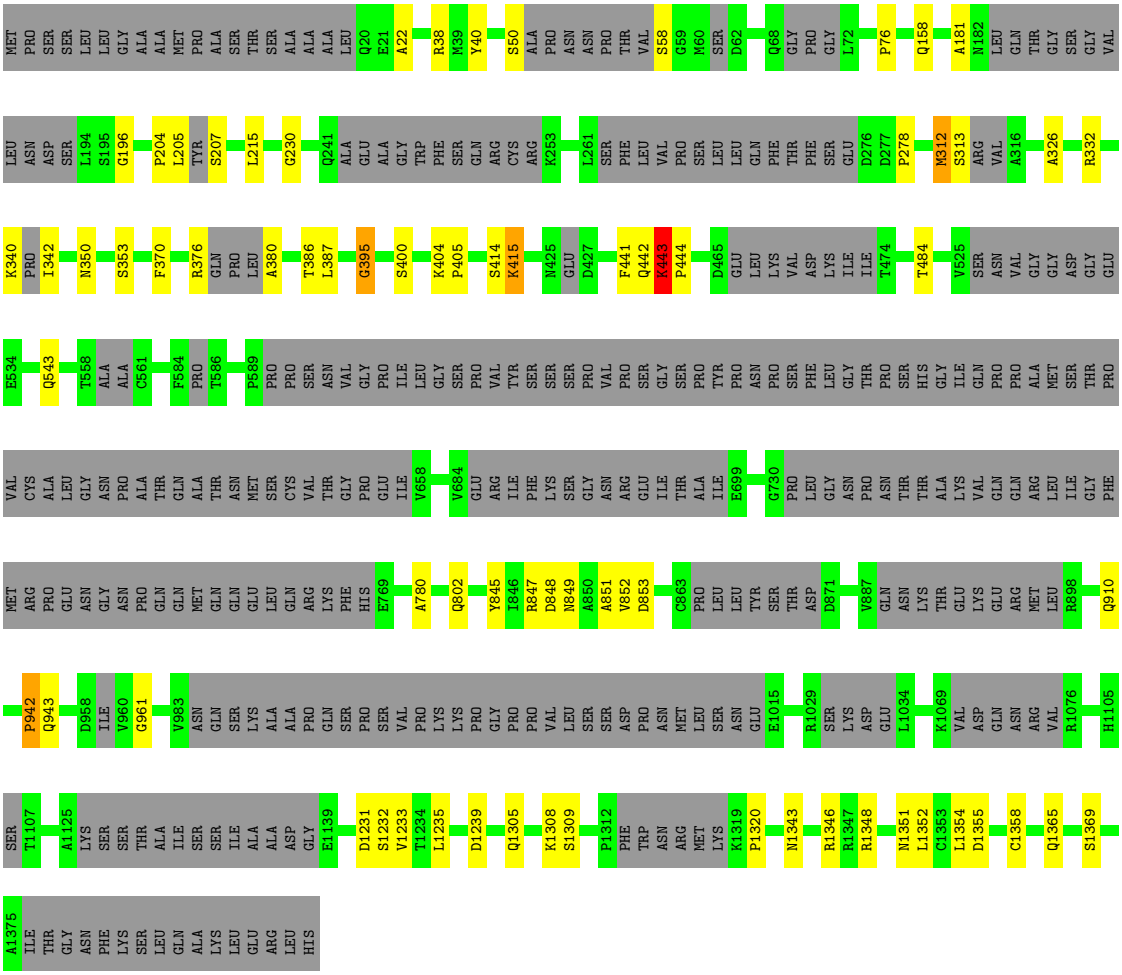
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 2-B: 44% • 53%



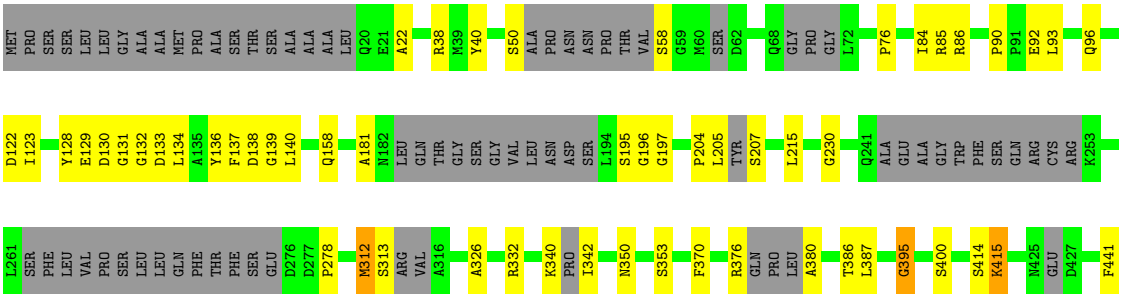
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

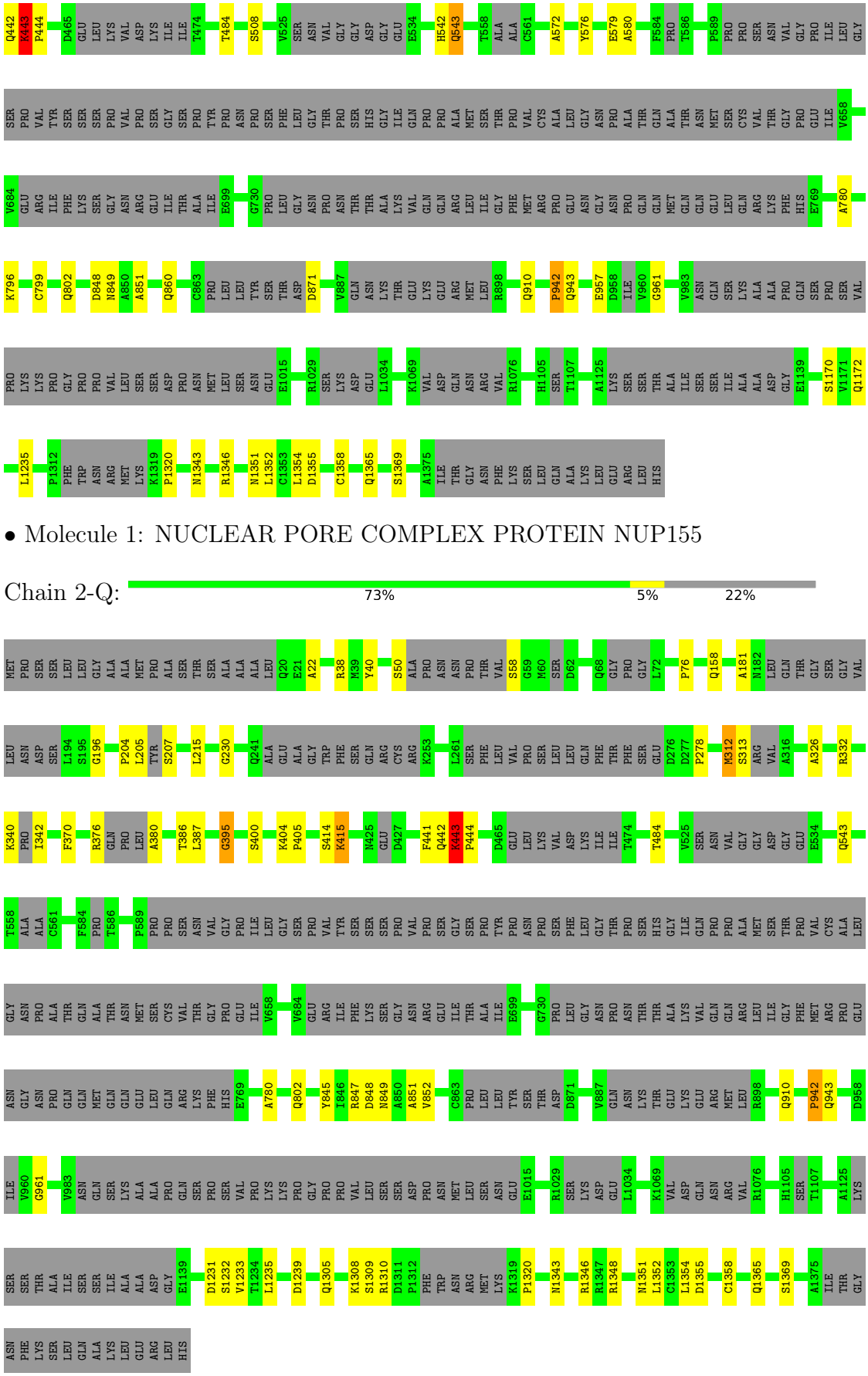
Chain 2-E:



• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 2-K:



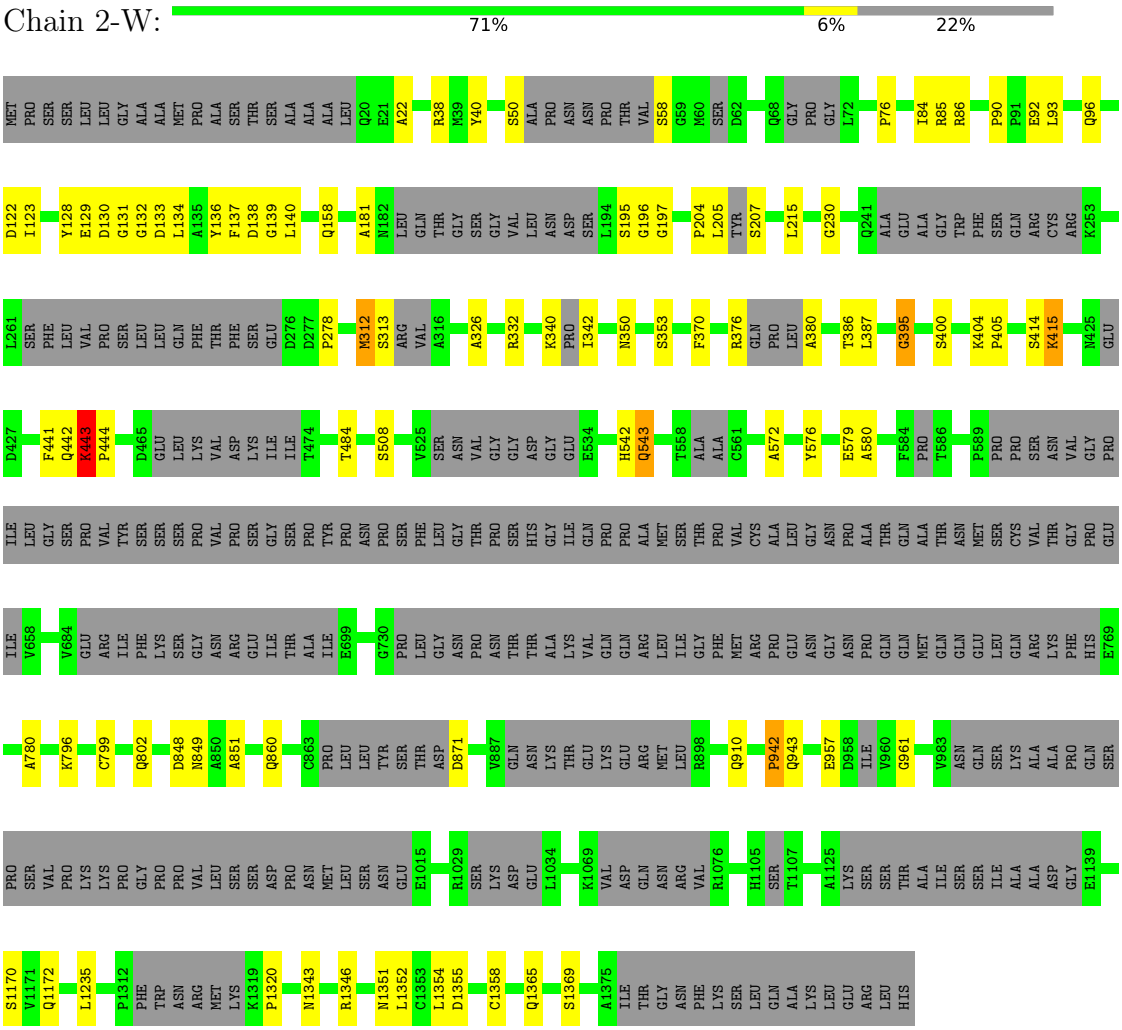


• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 2-Q: 73% 5% 22%

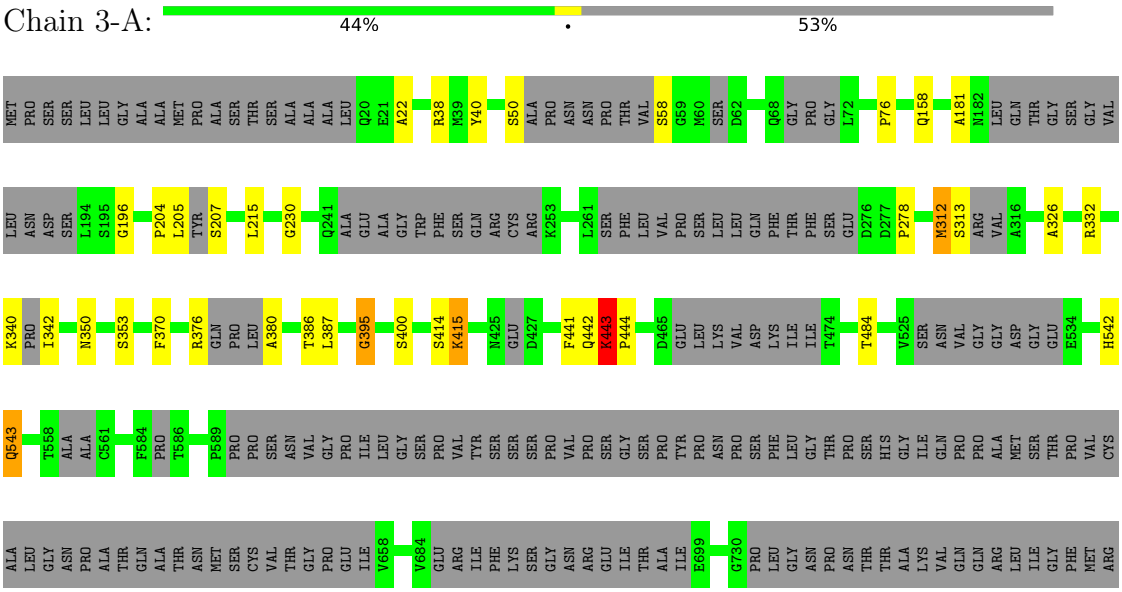
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 2-W:



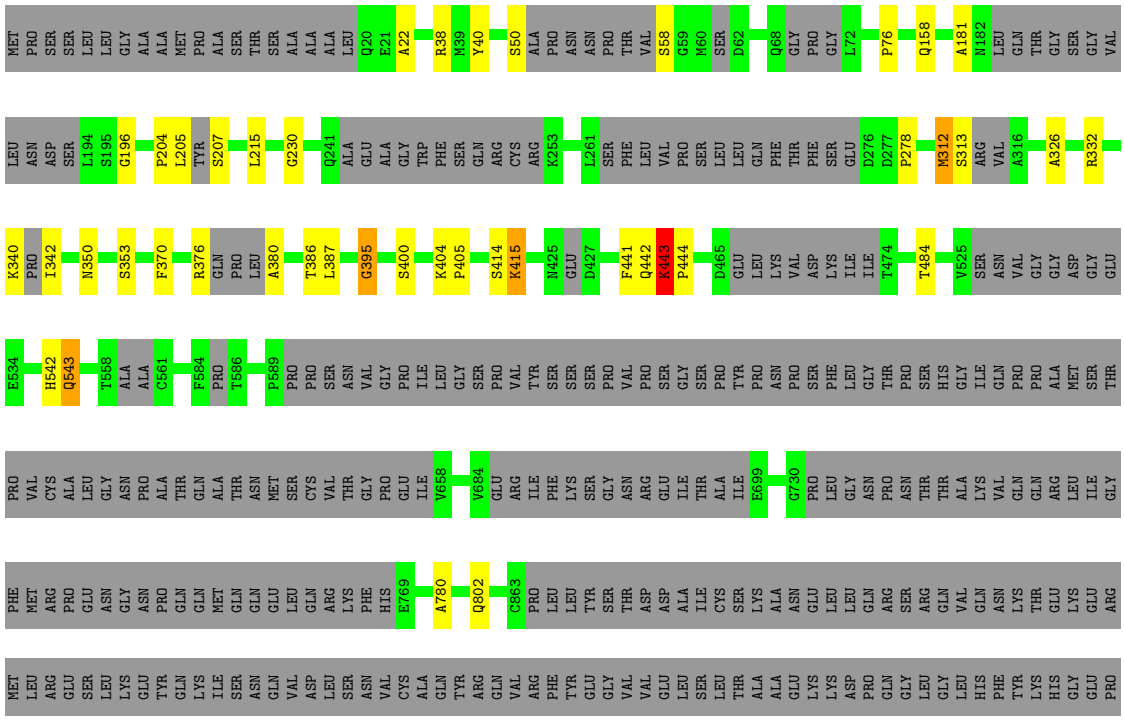
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

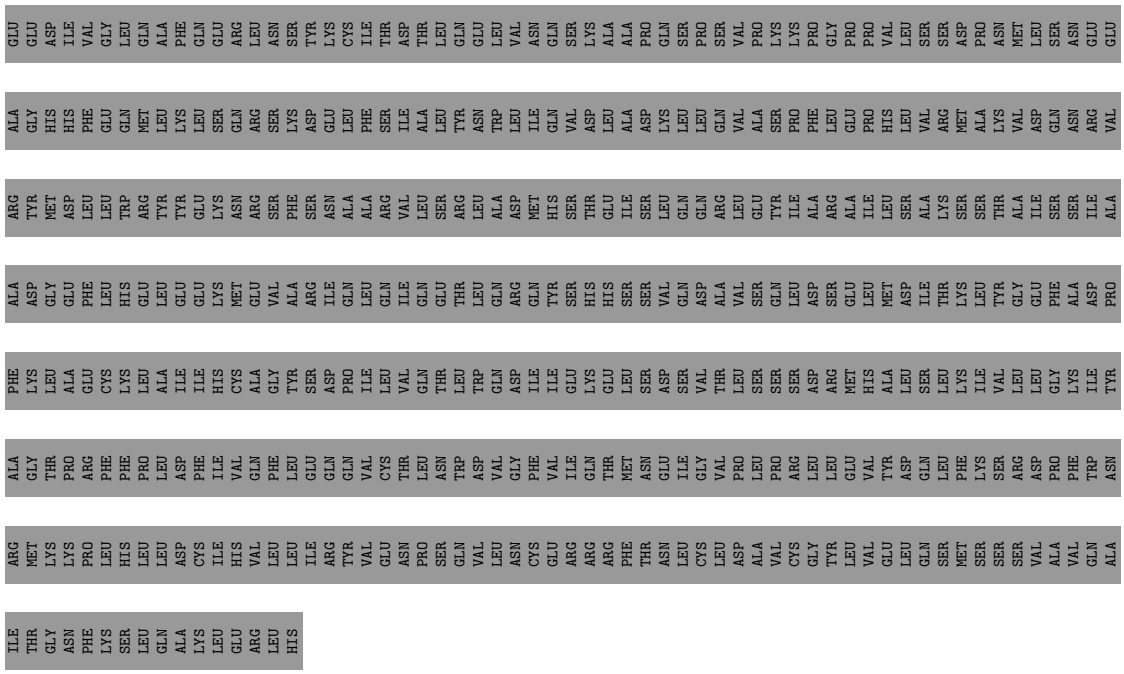
Chain 3-A:



• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

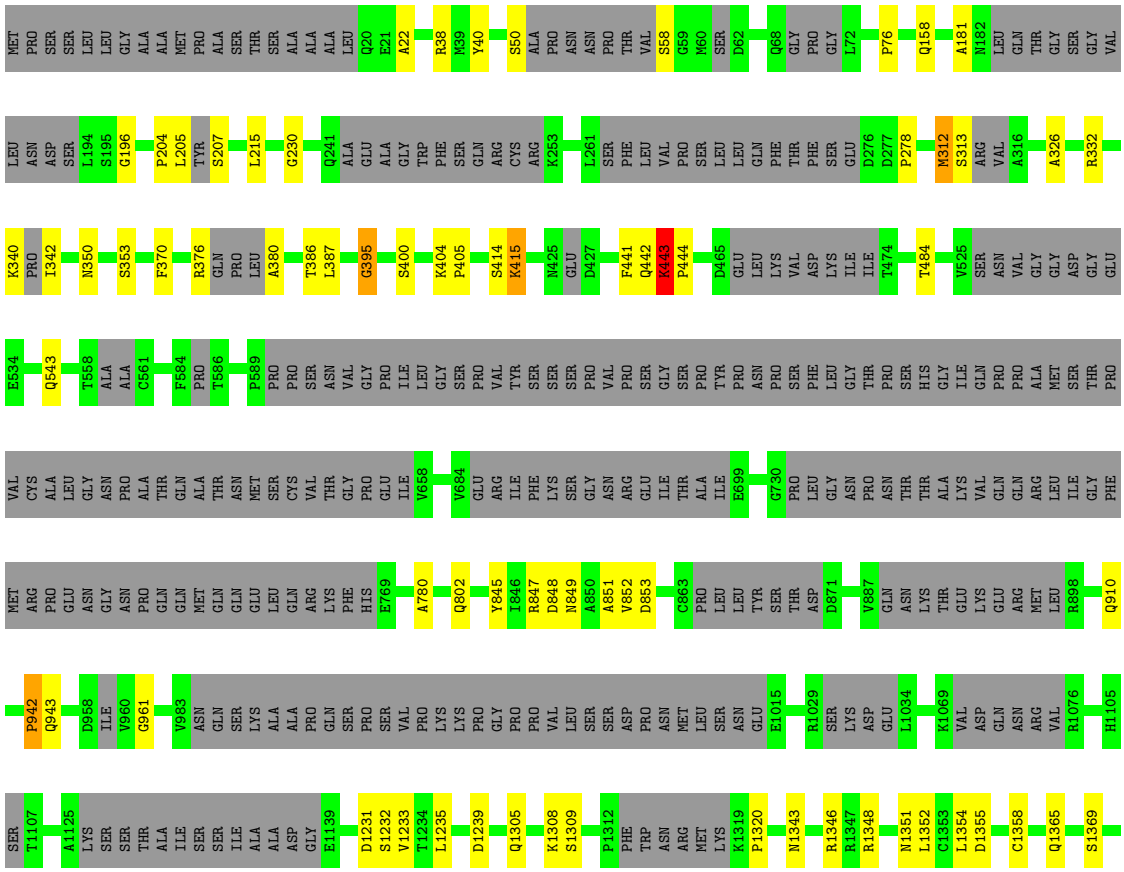
Chain 3-B: 44% • 53%

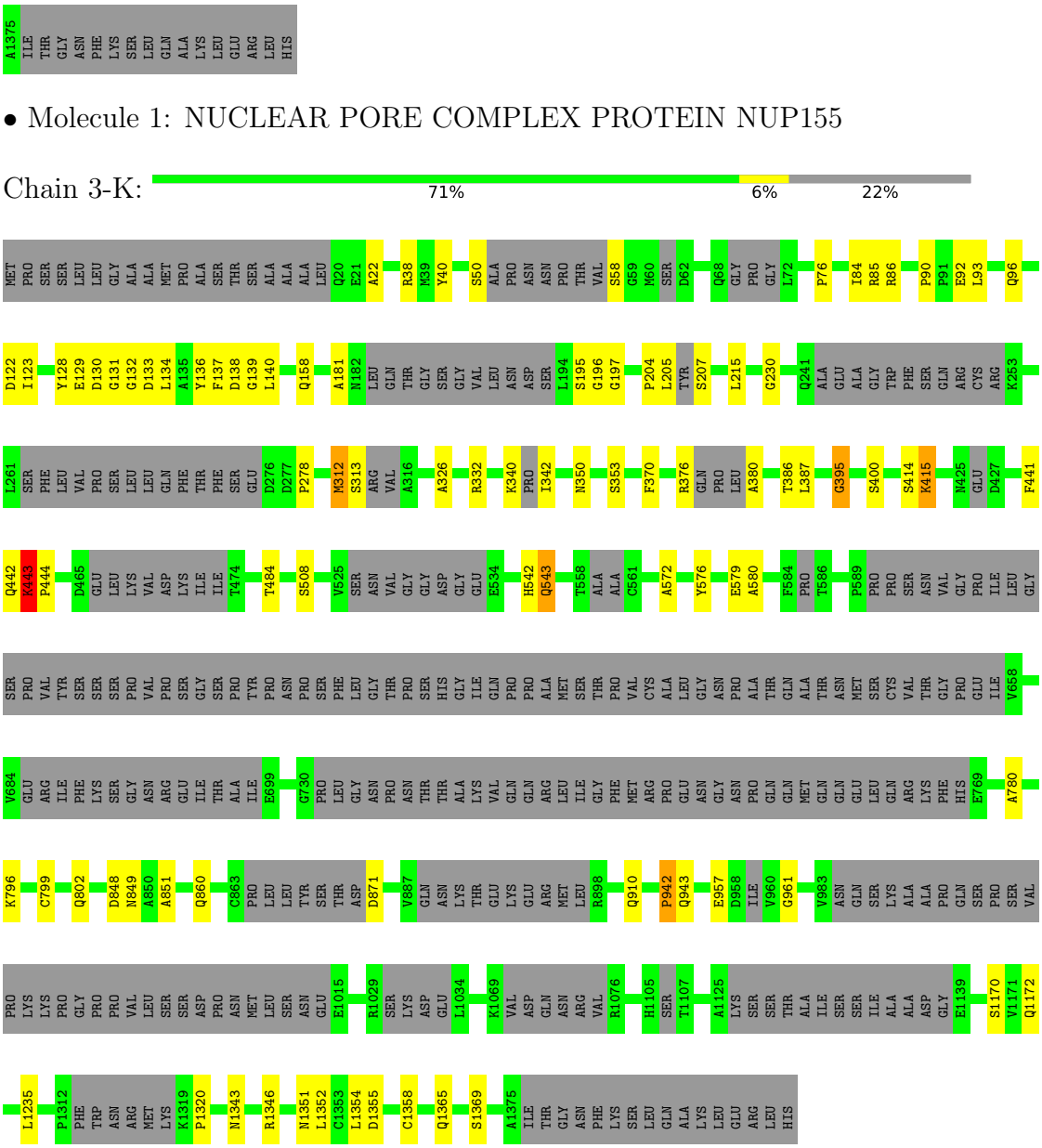




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 3-E: 73% 5% 22%



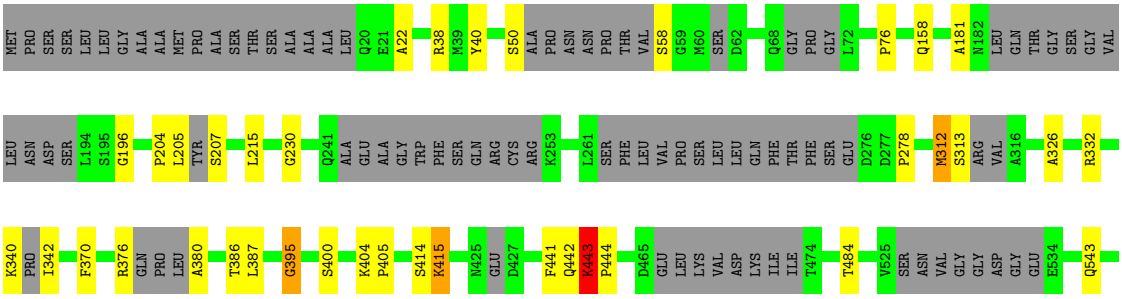


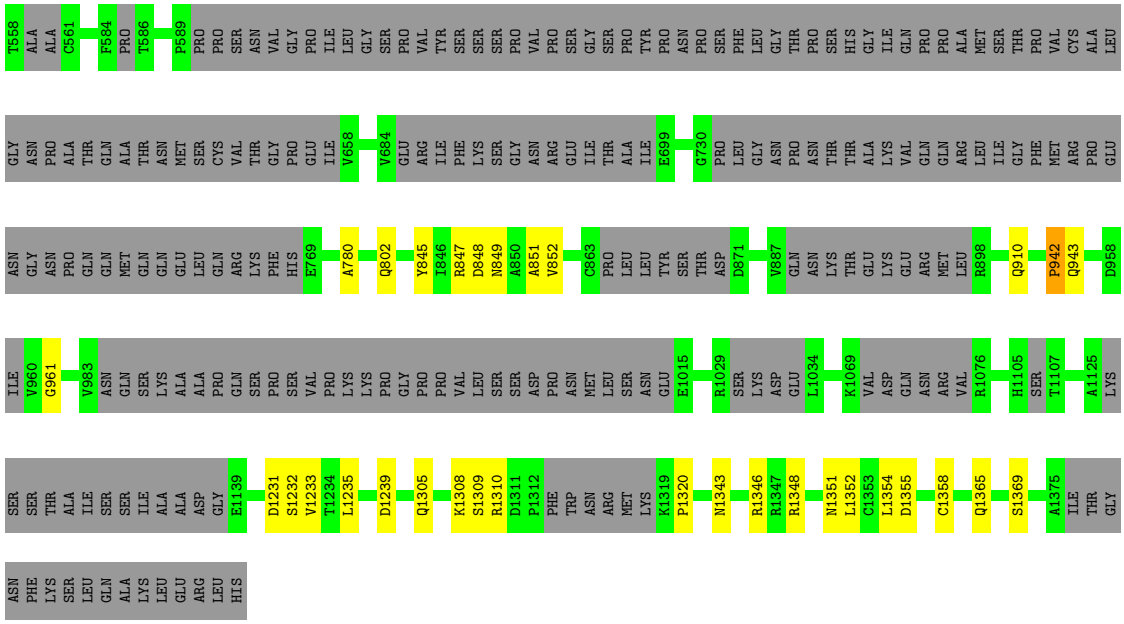
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 3-K: 71% 6% 22%

• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

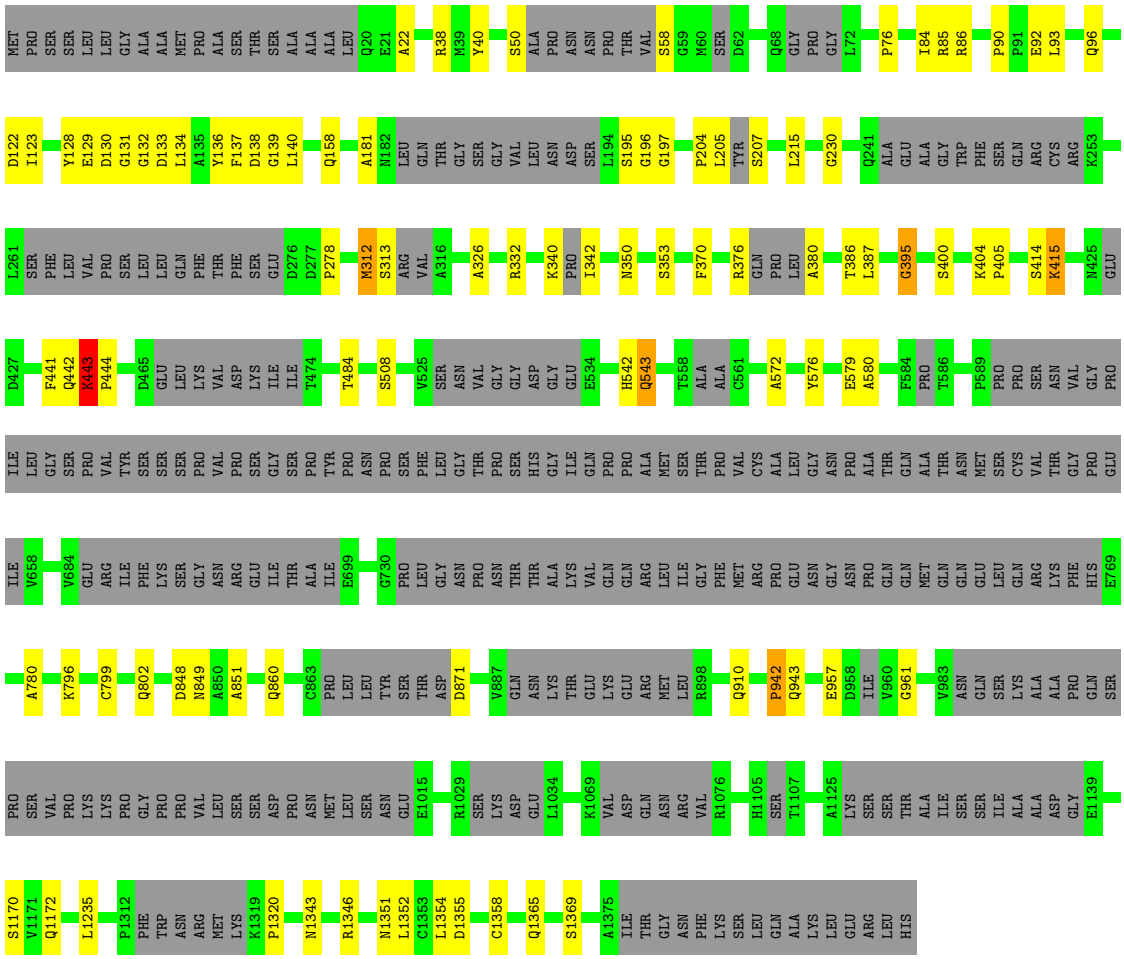
Chain 3-Q: 73% 5% 22%





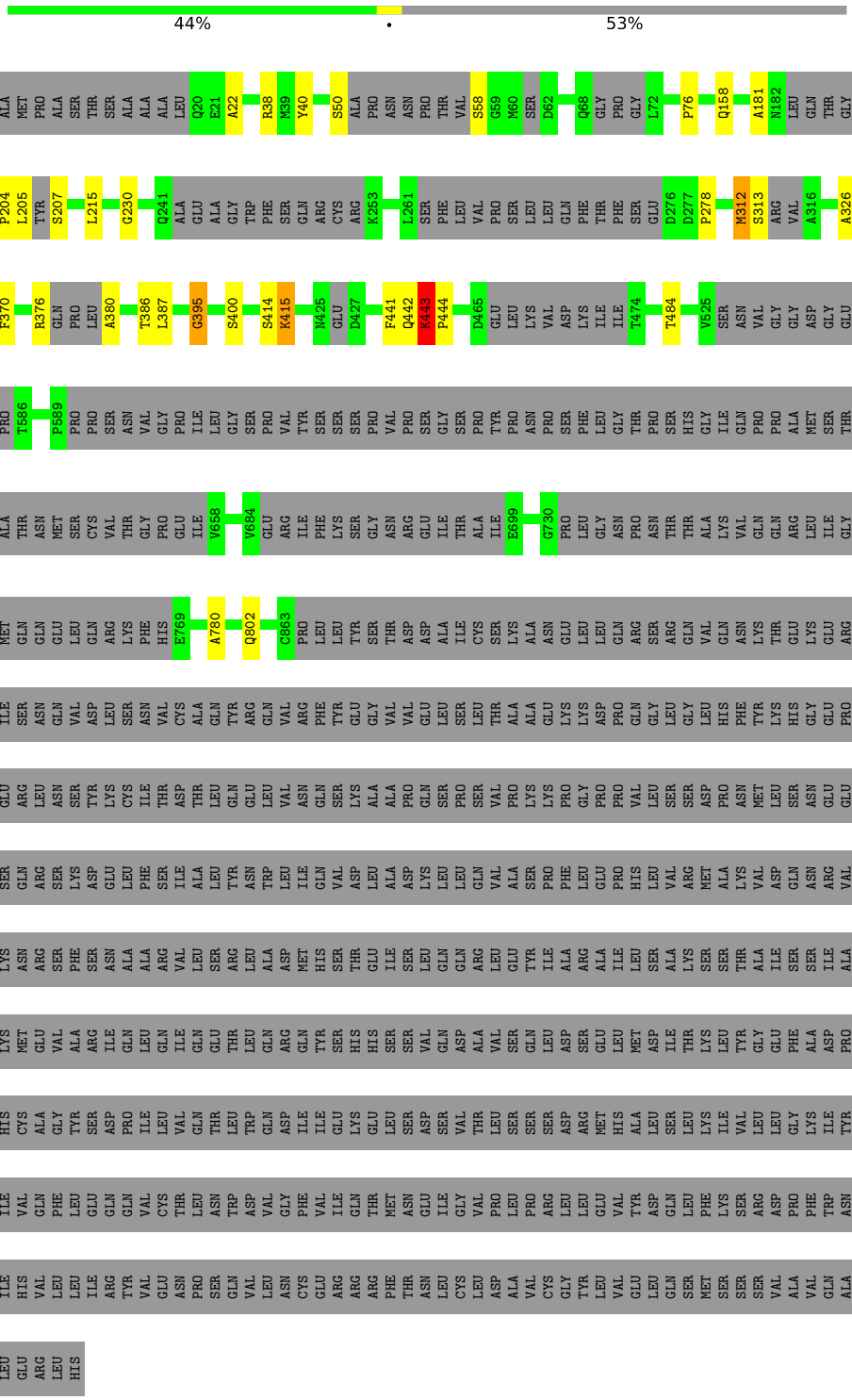
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 3-W: 71% 6% 22%



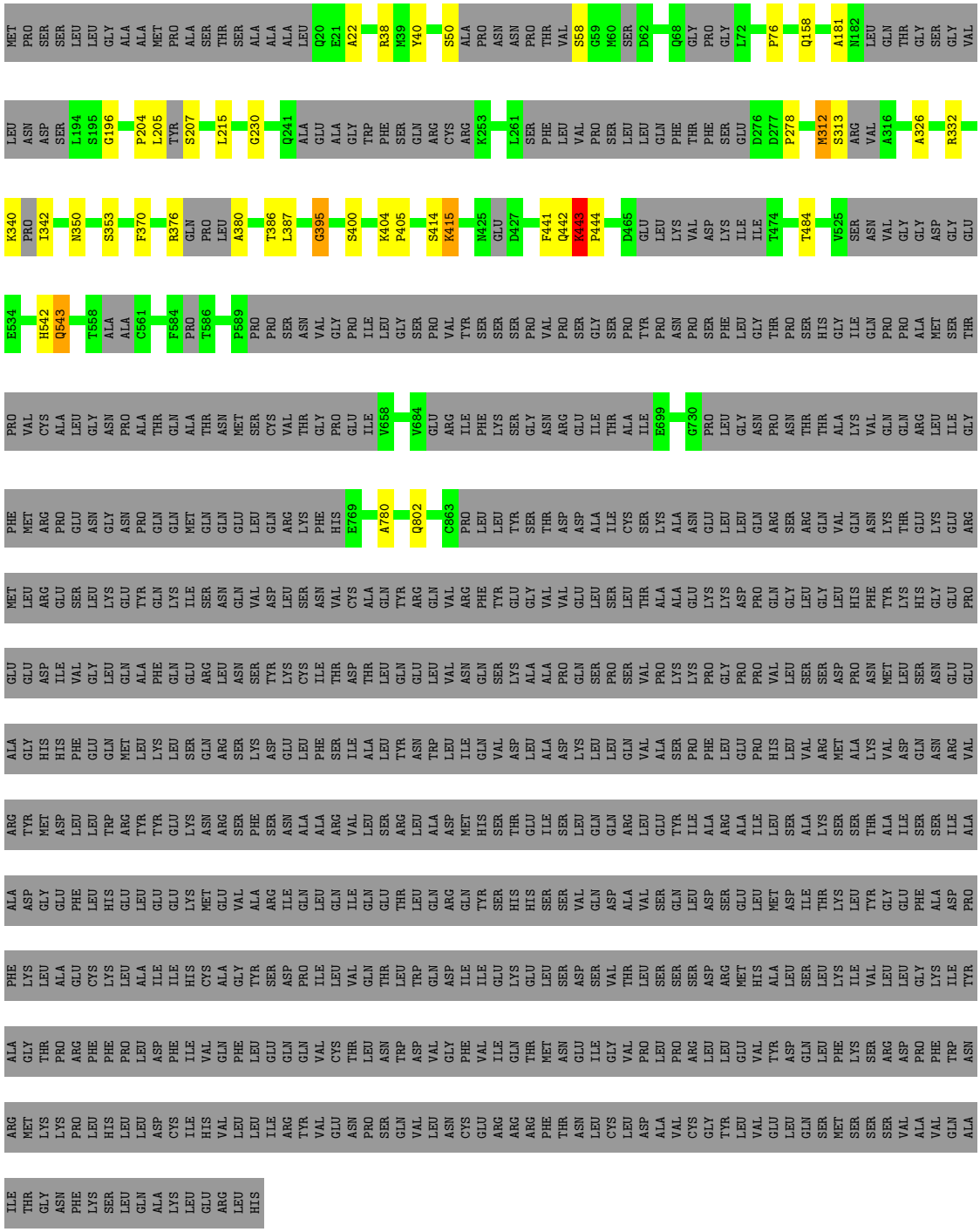
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 4-A:



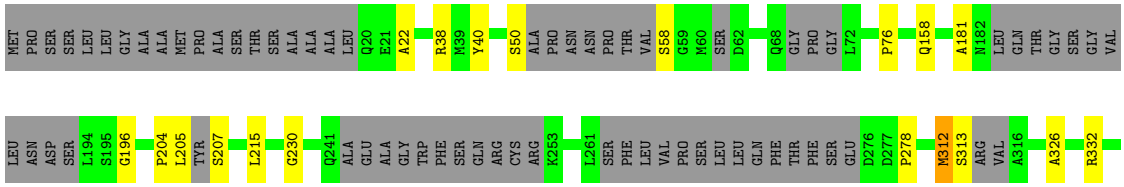
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

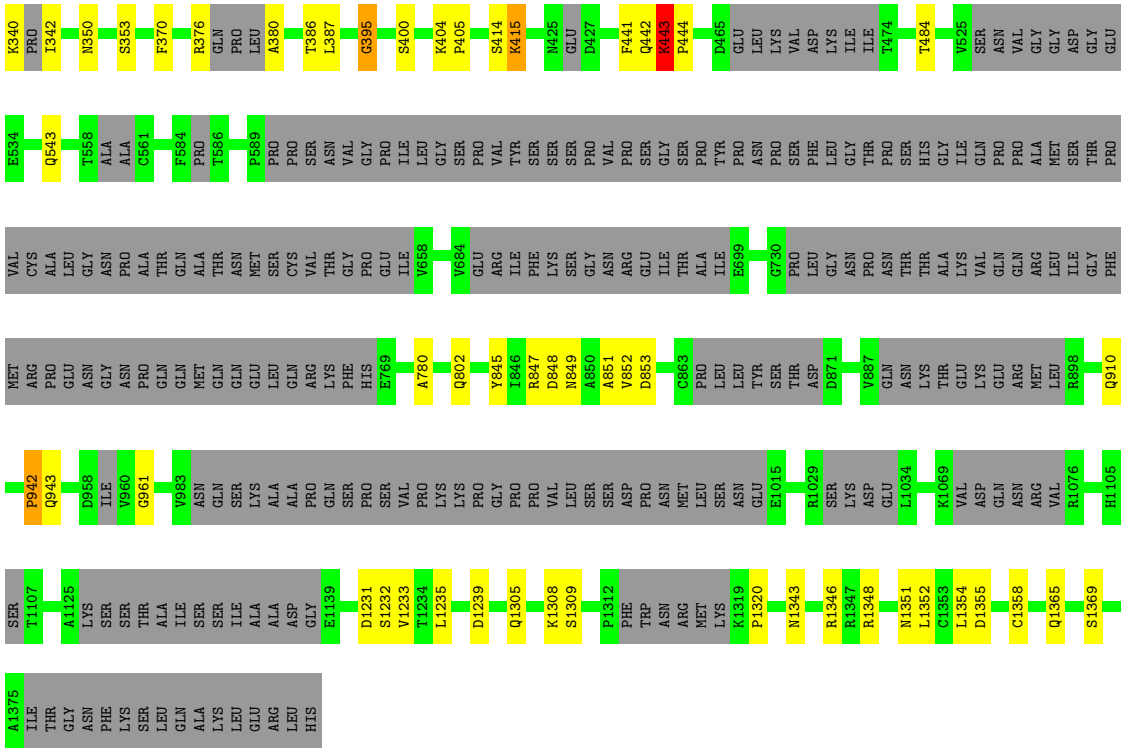
Chain 4-B:



- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

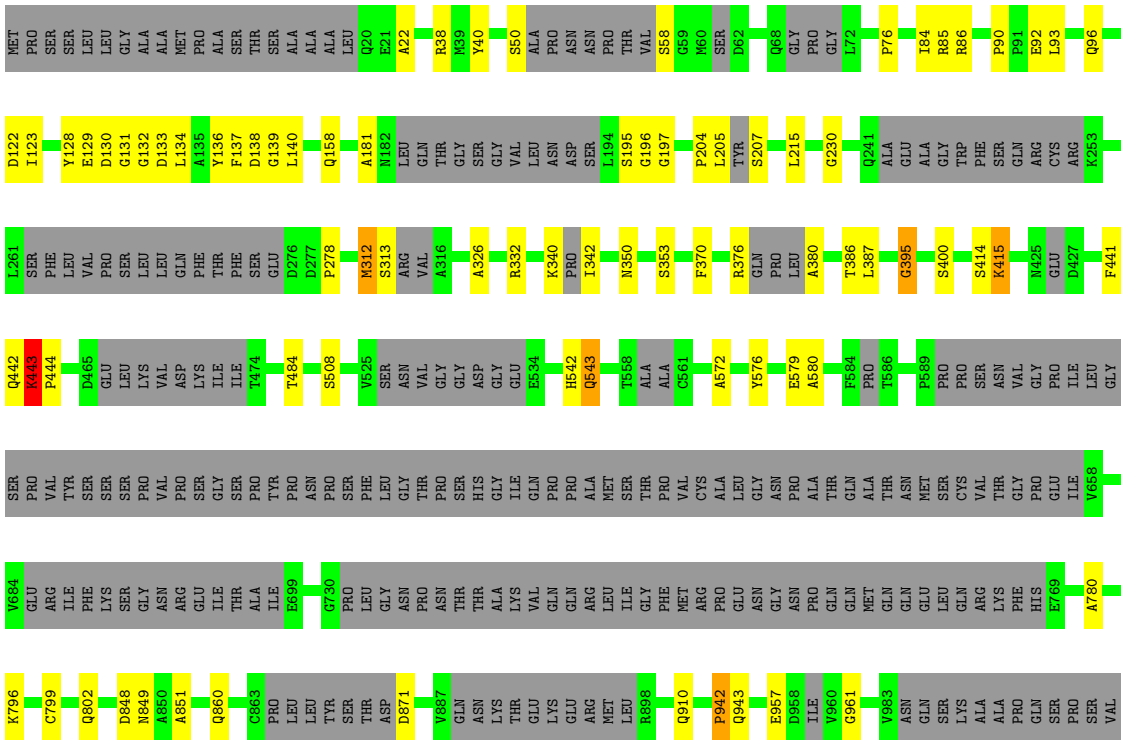
Chain 4-E:

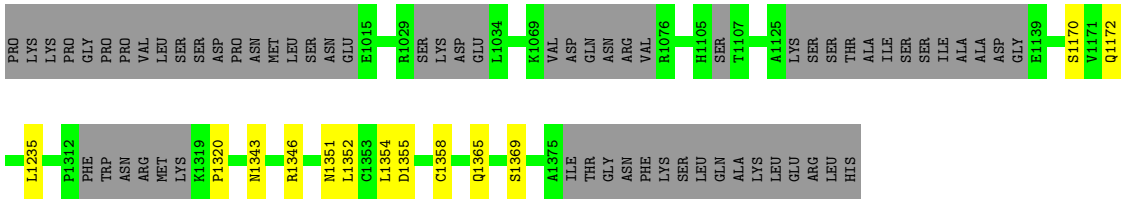




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

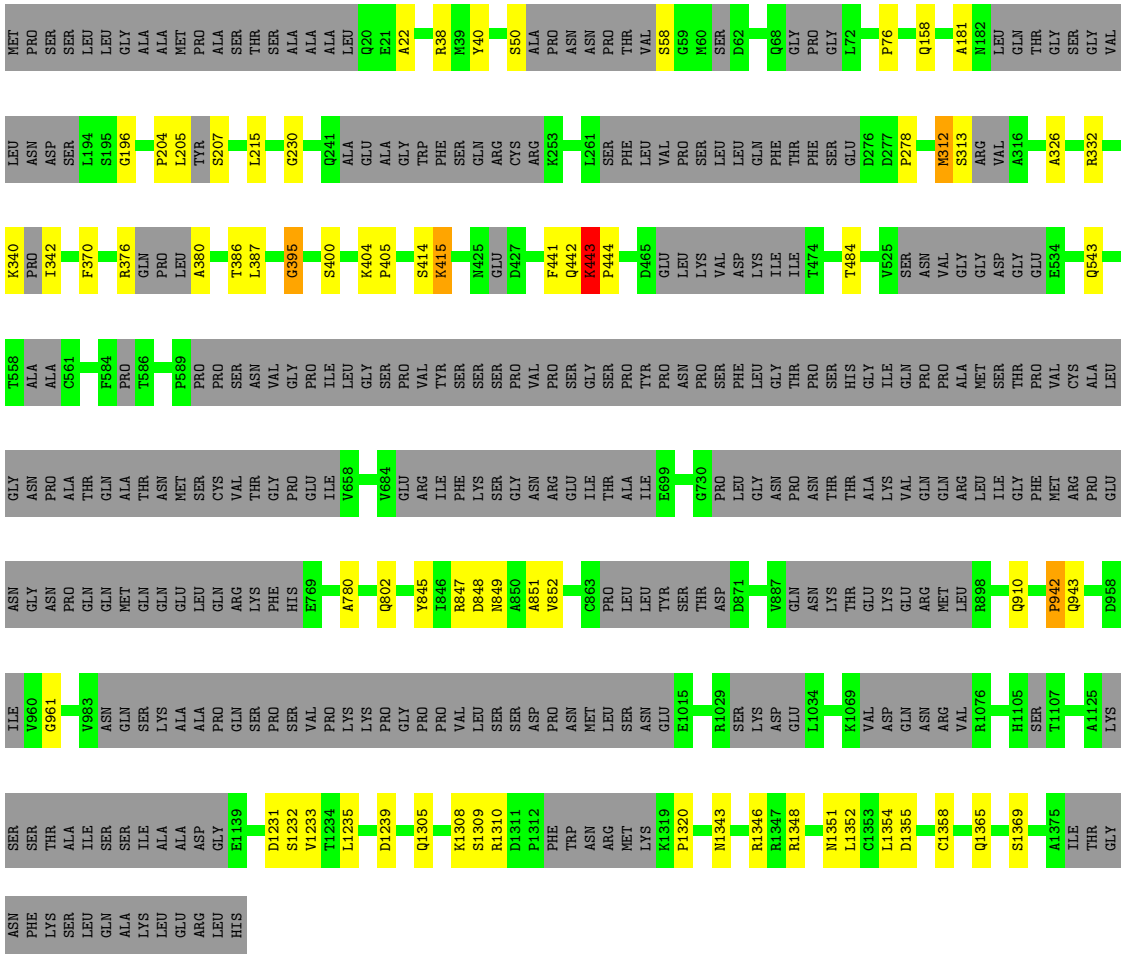
Chain 4-K:





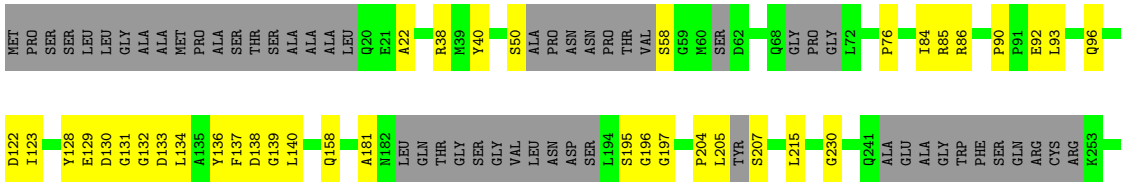
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

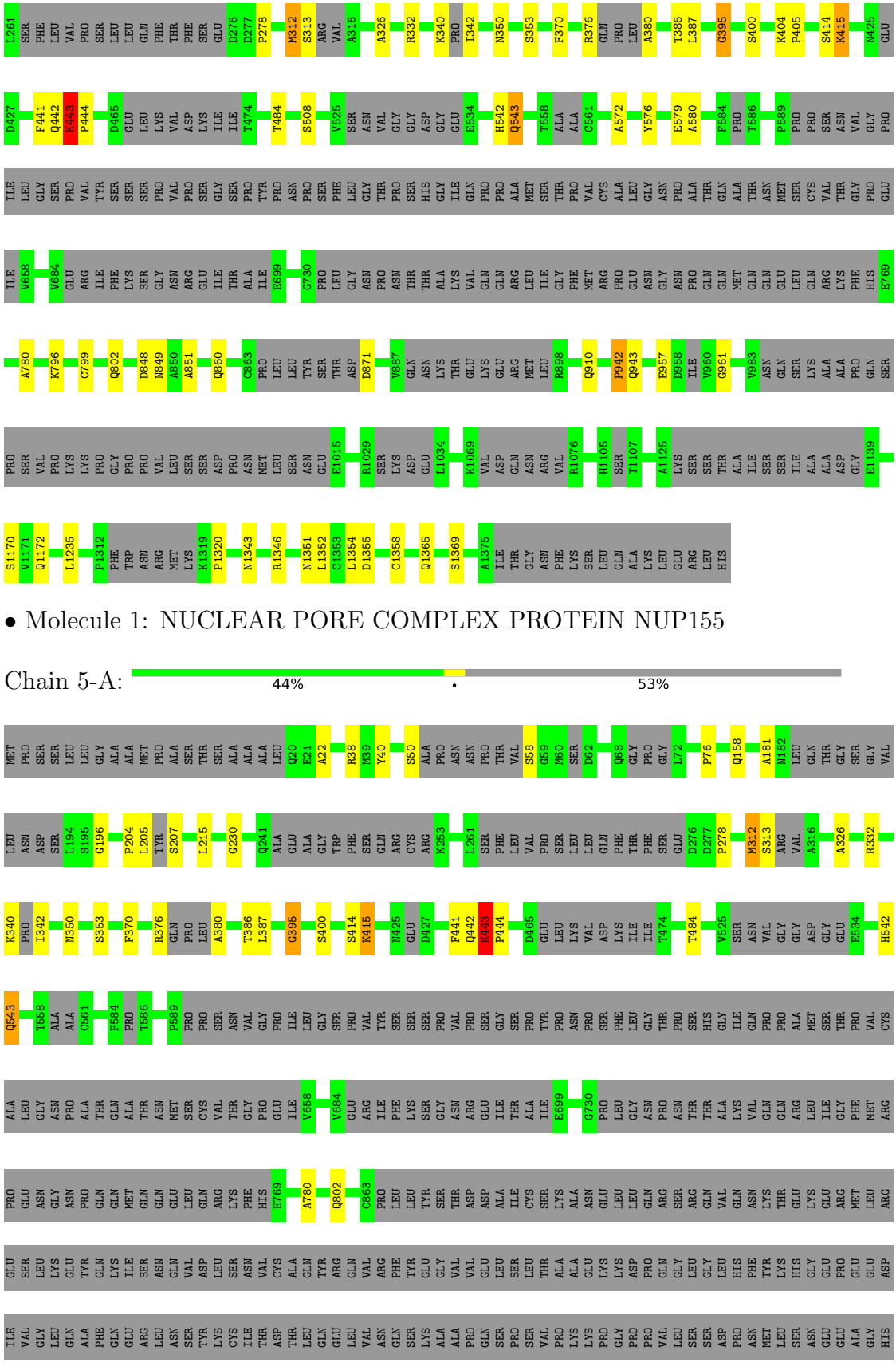
Chain 4-Q:



- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 4-W:



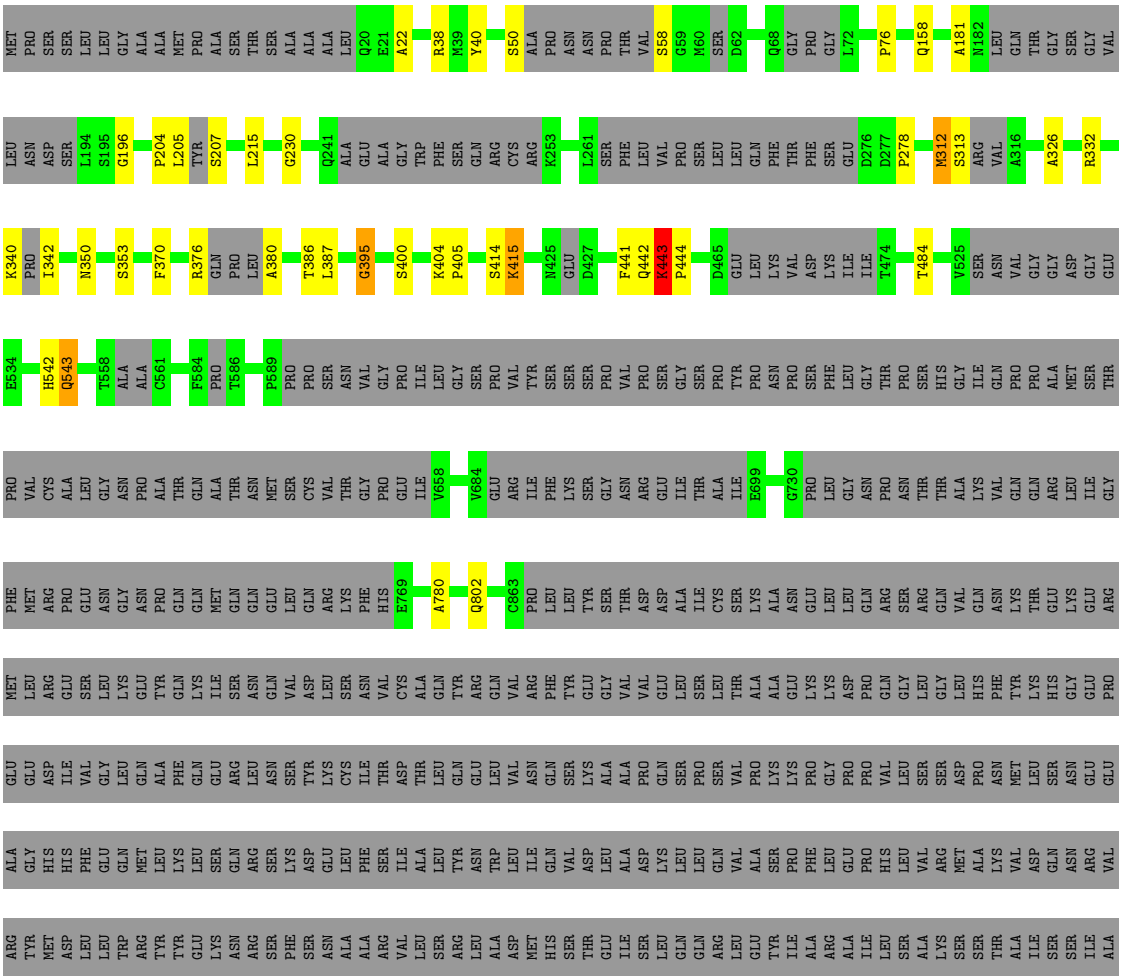


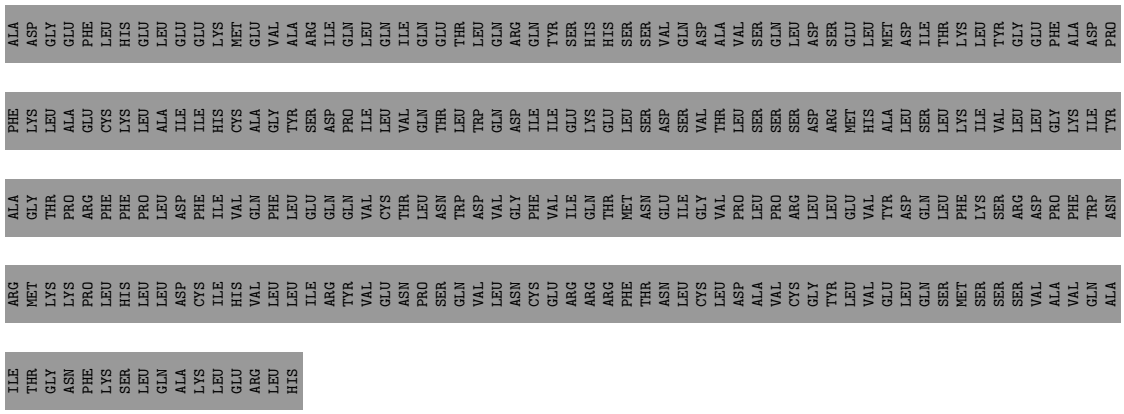
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 5-A: 44% • 53%

- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

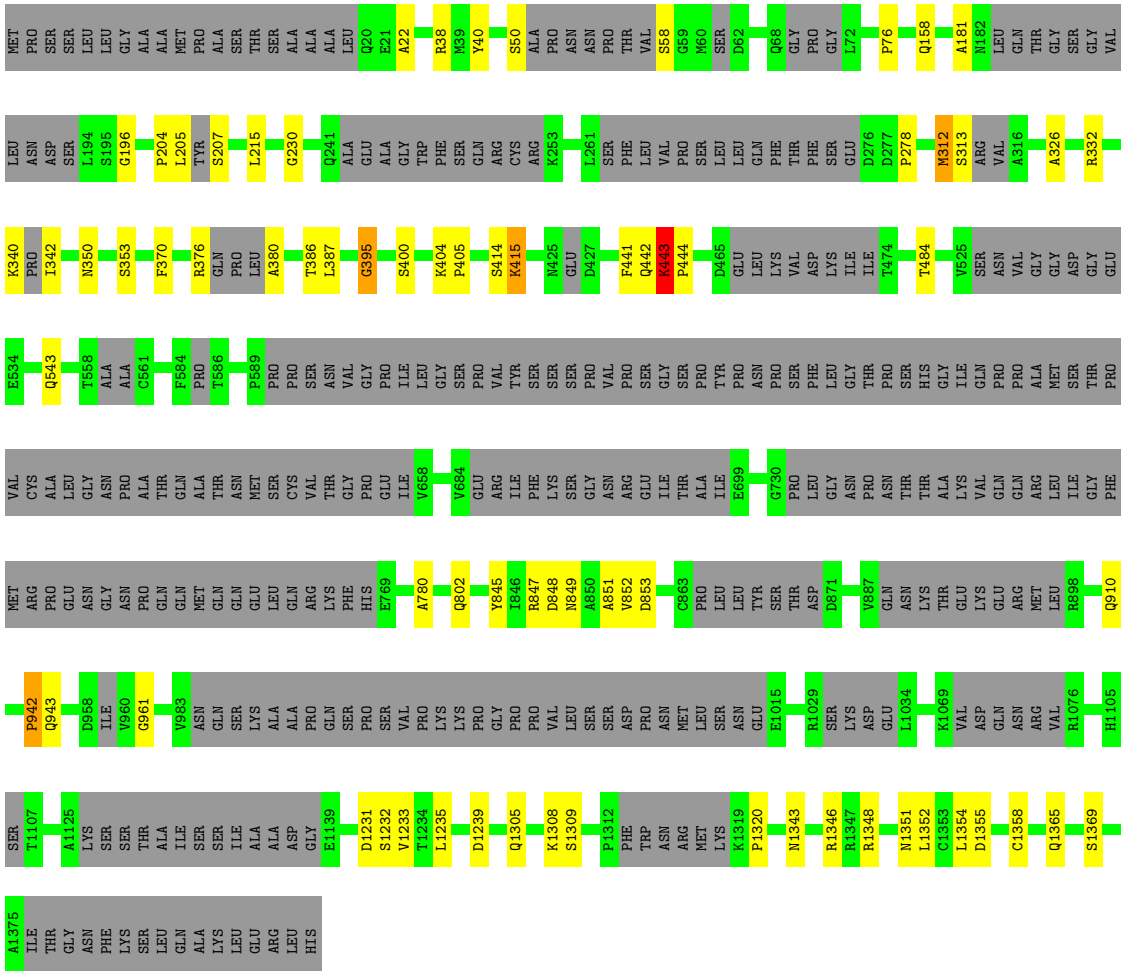
Chain 5-B:





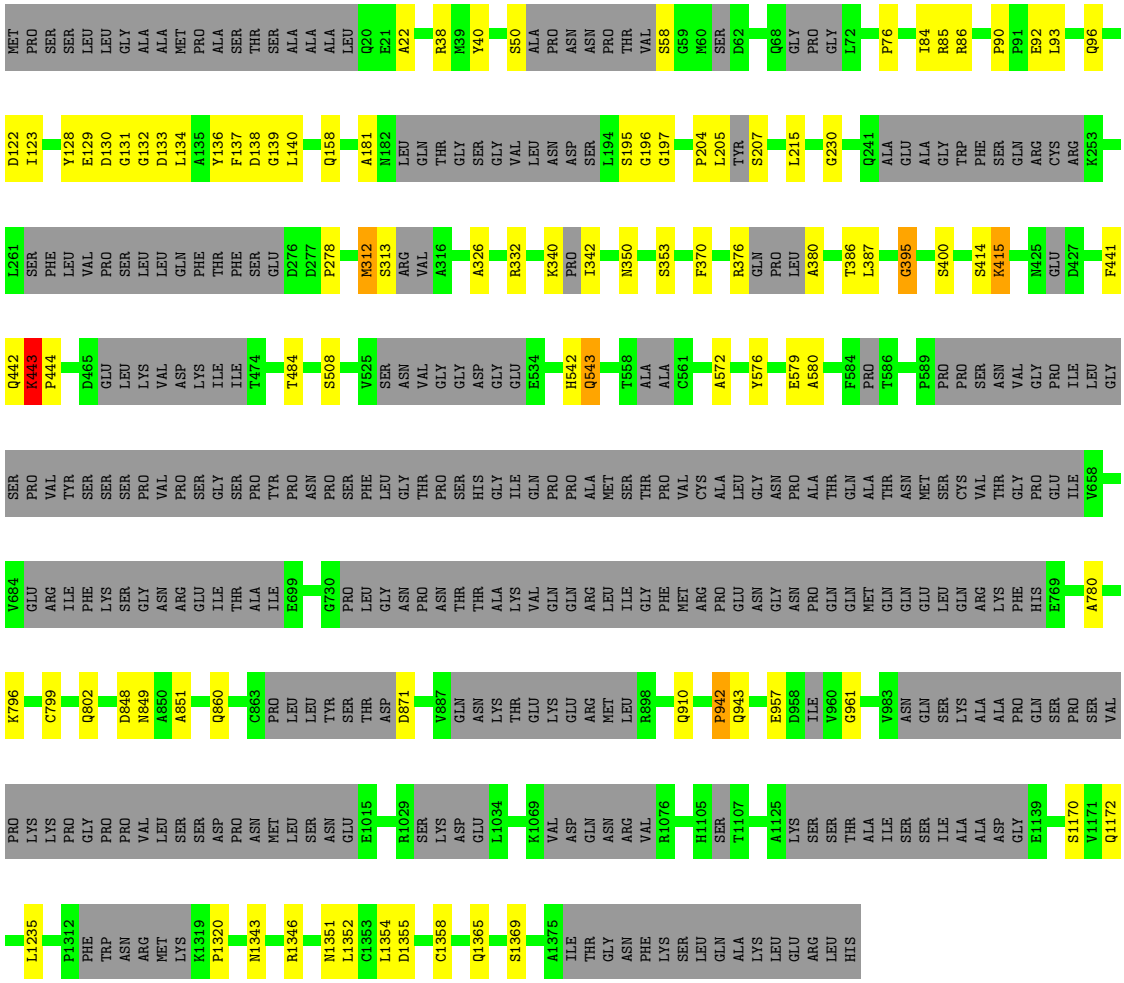
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 5-E:



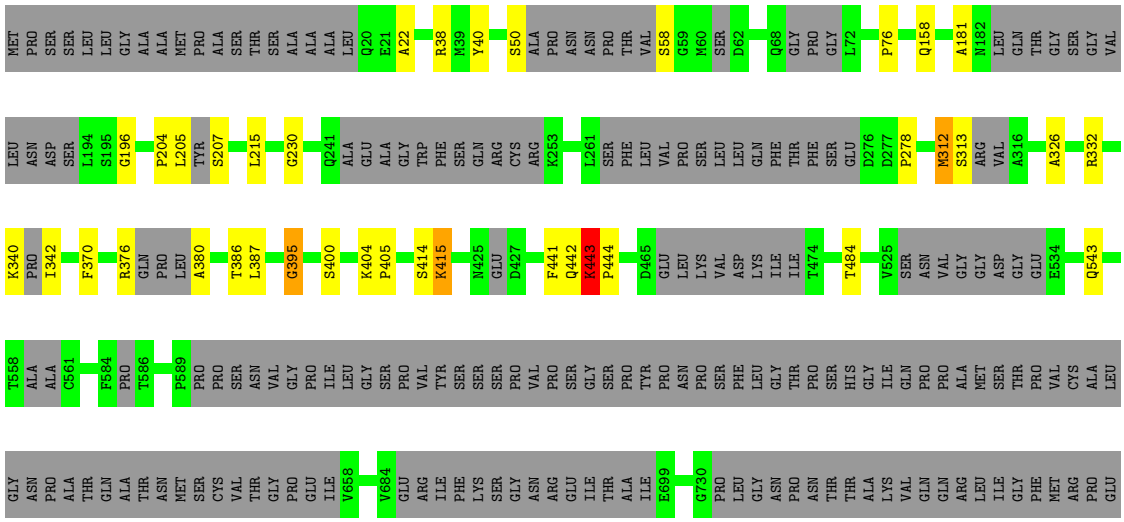
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

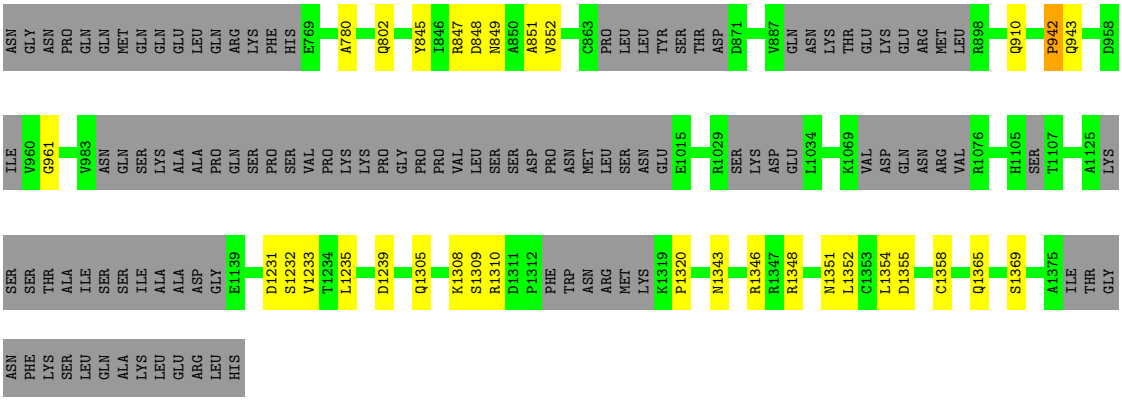
Chain 5-K:



- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

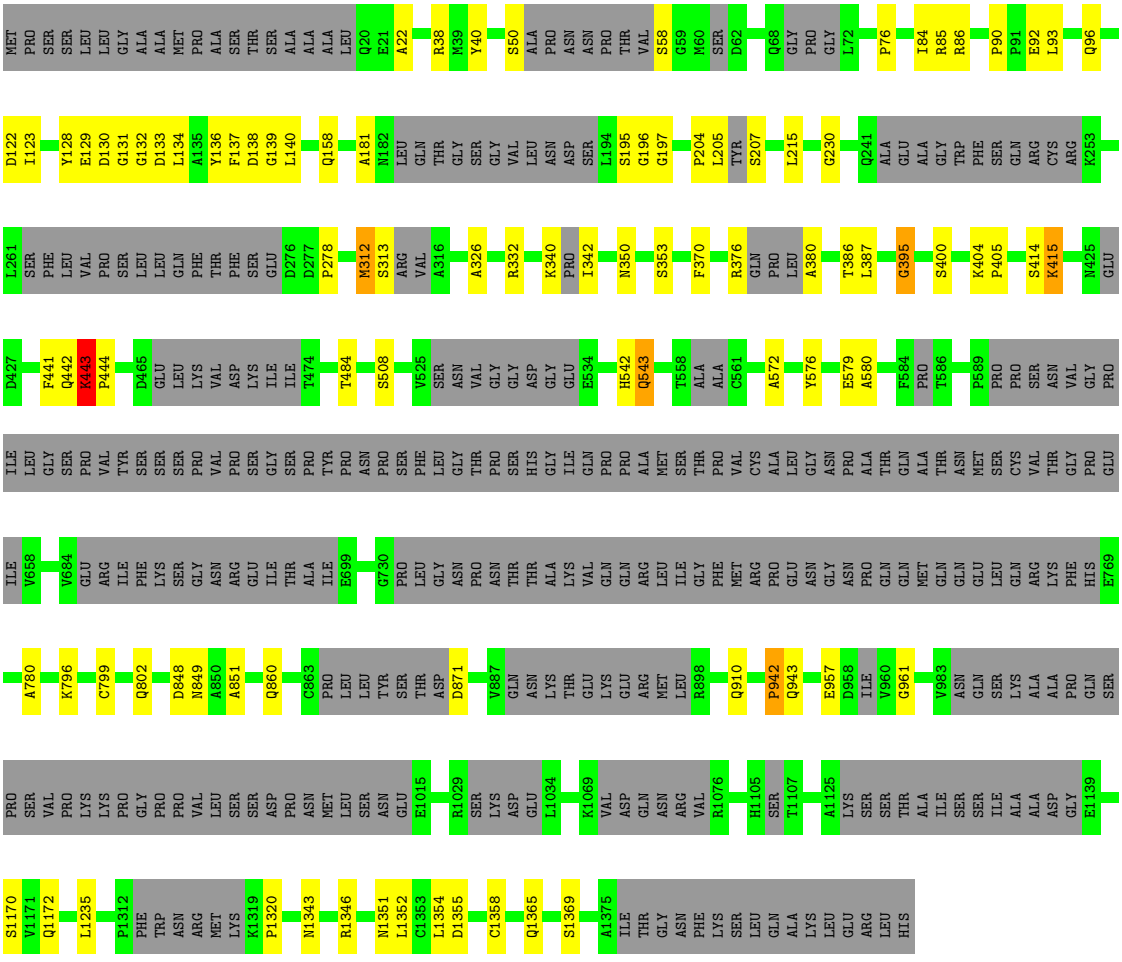
Chain 5-Q:





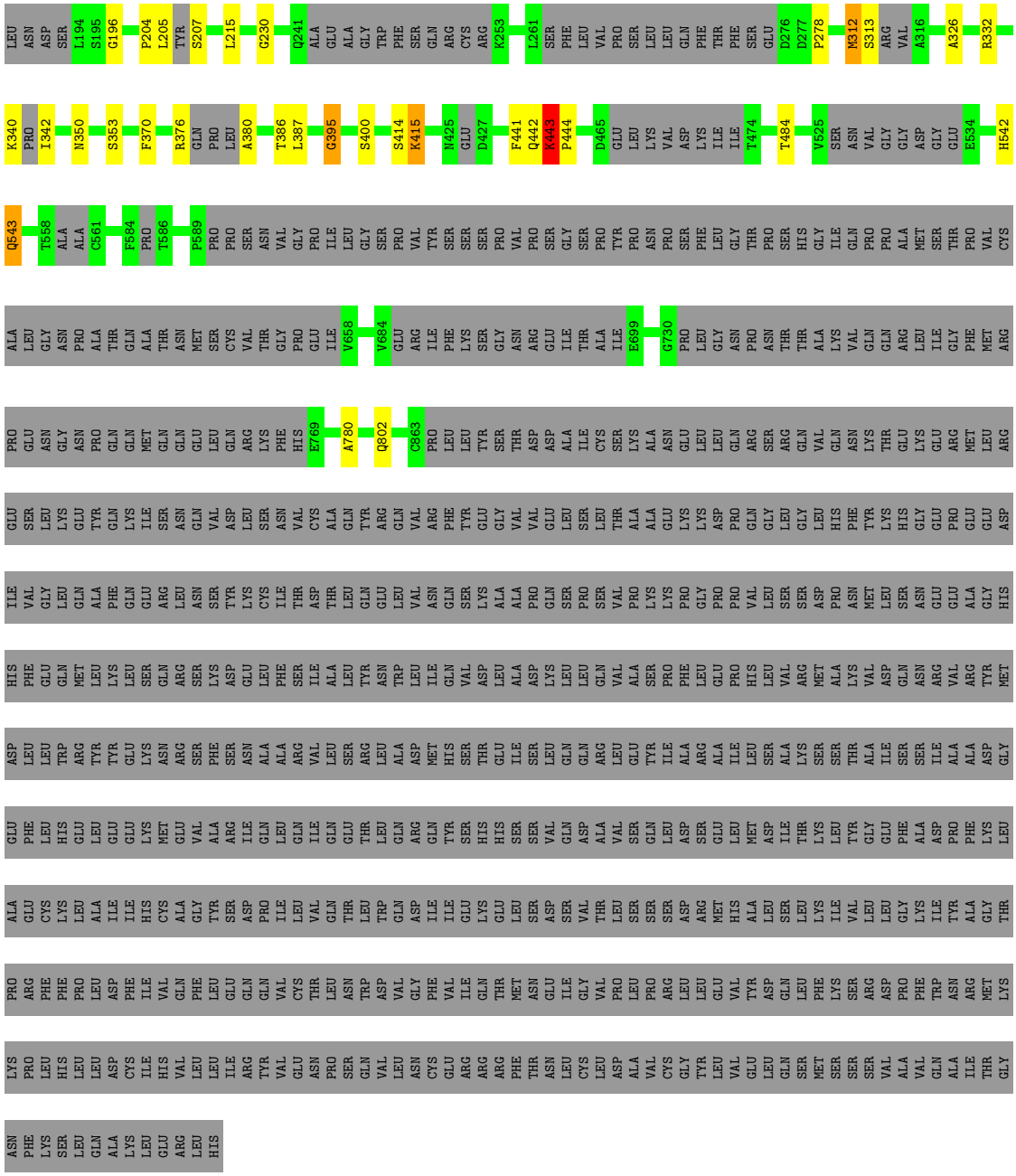
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 5-W:



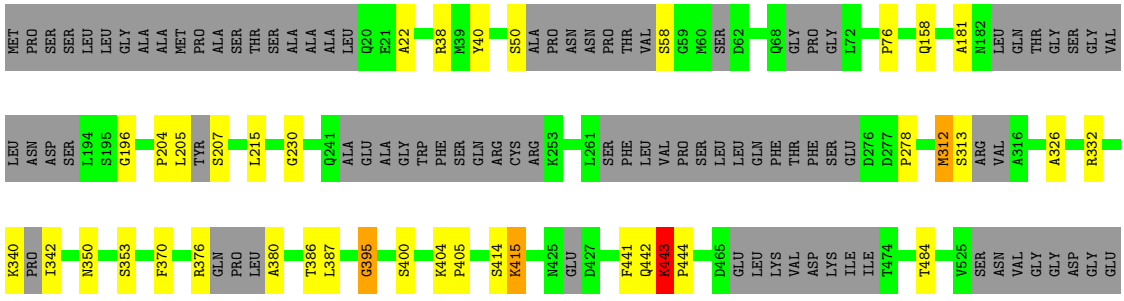
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

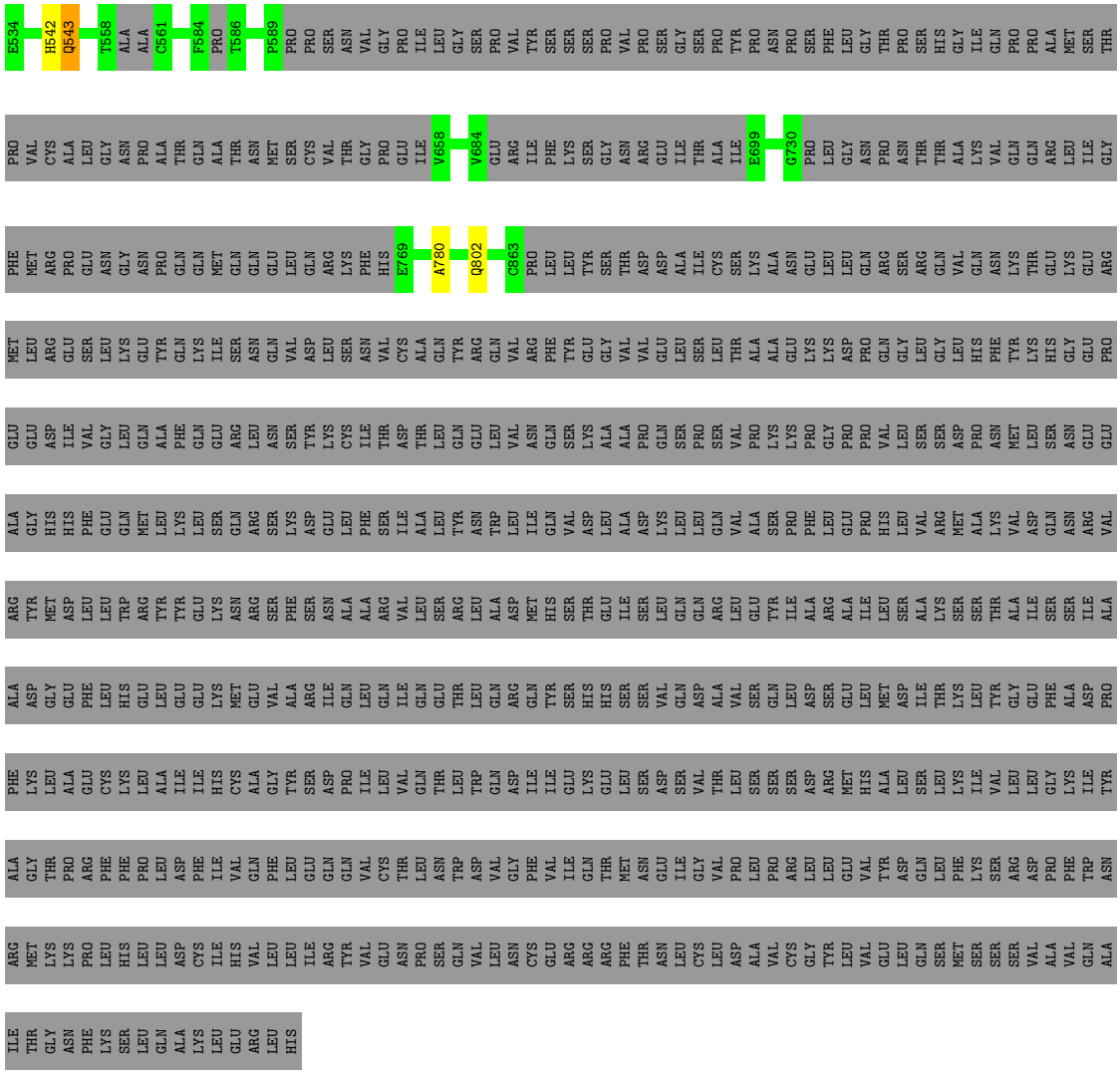
Chain 6-A:



- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

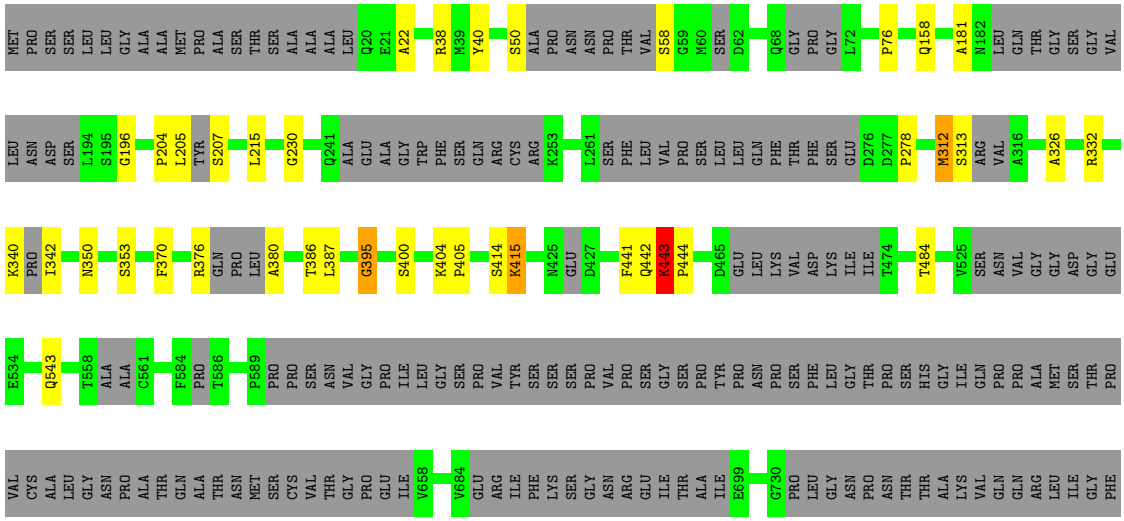
Chain 6-B:

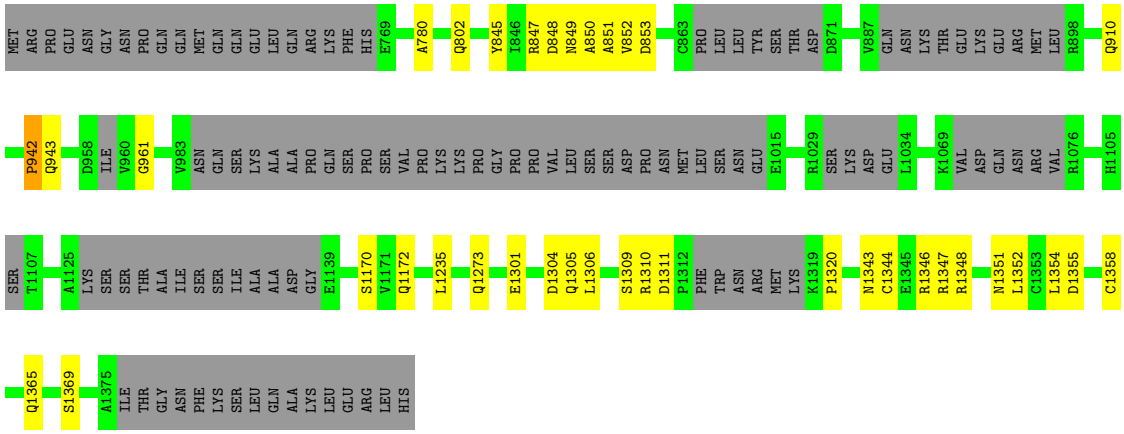




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

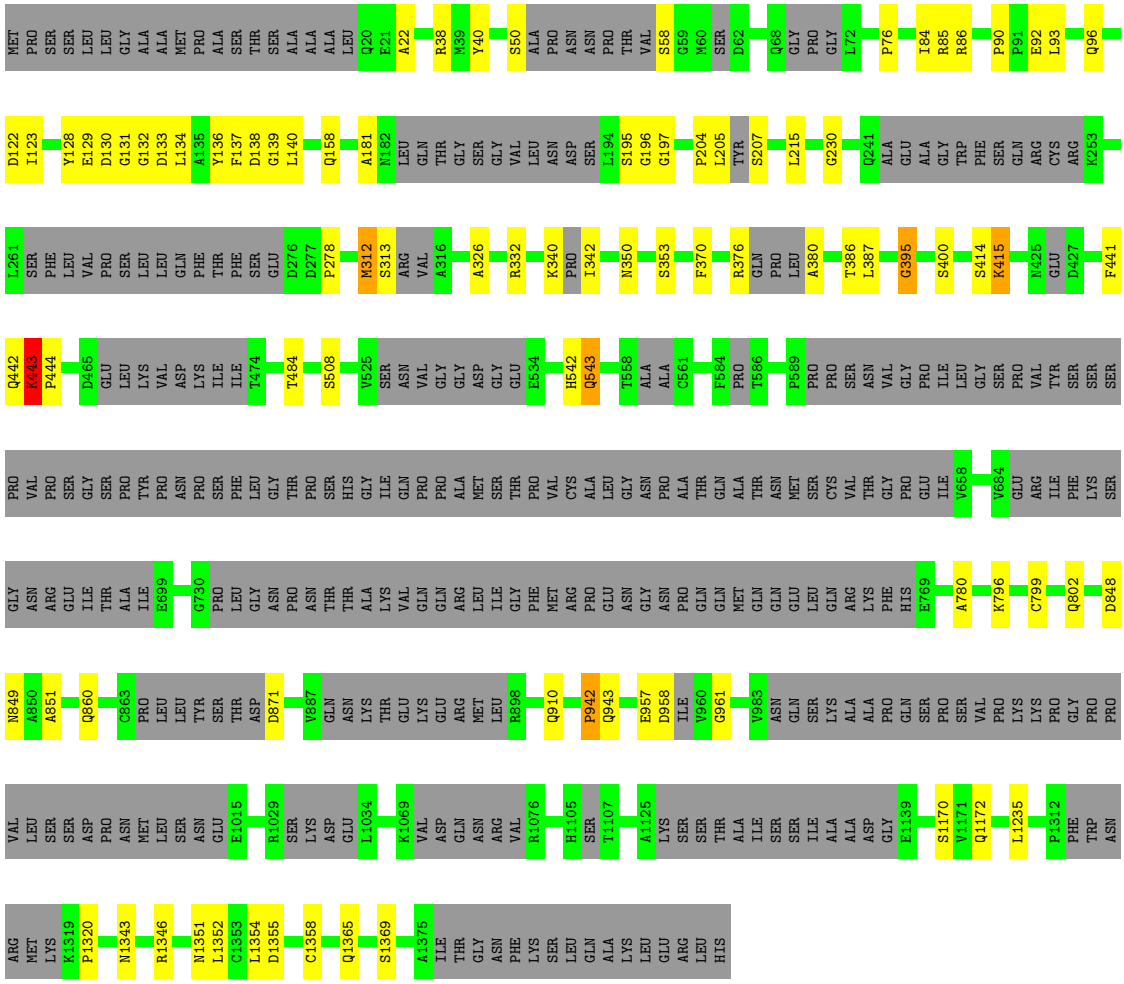
Chain 6-E: 72% 5% 22%





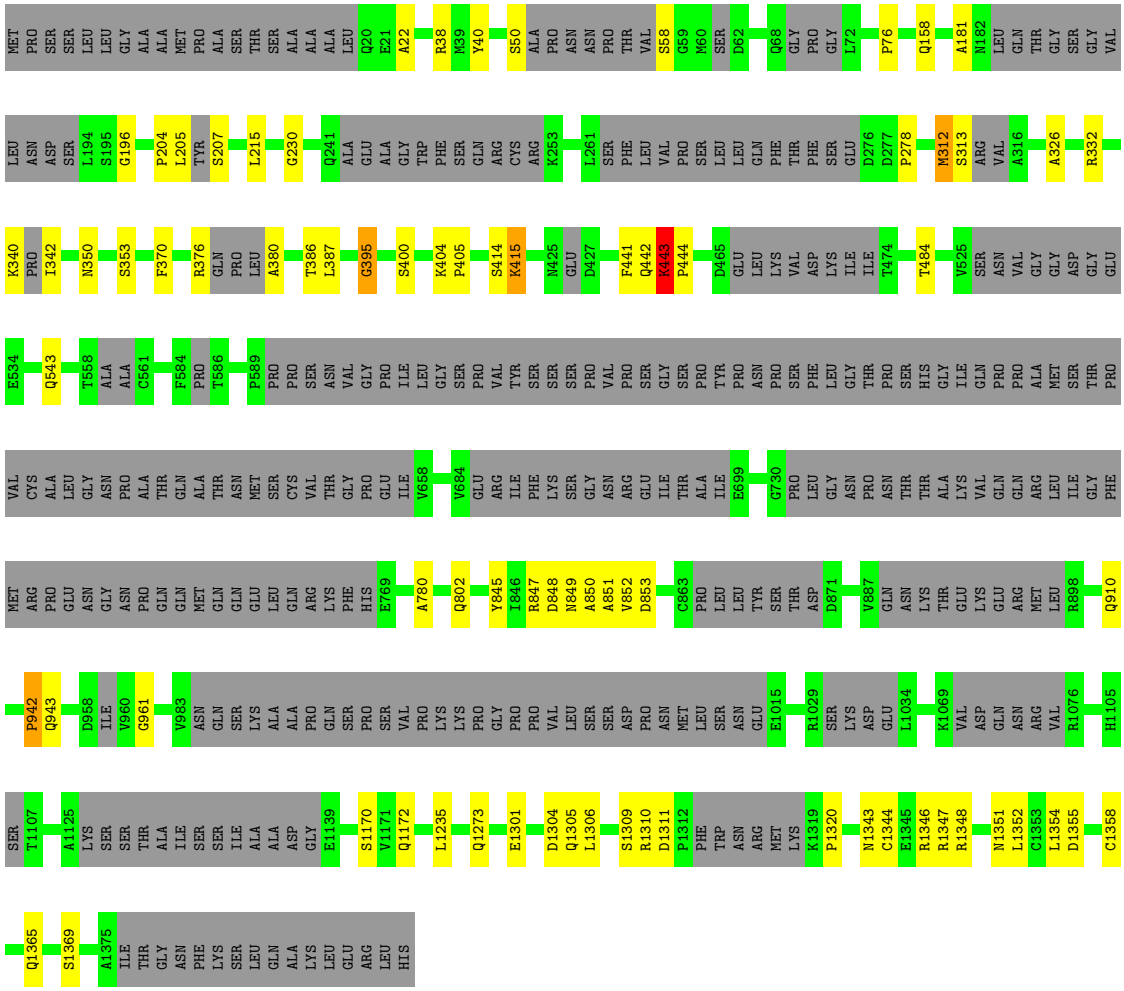
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 6-K:



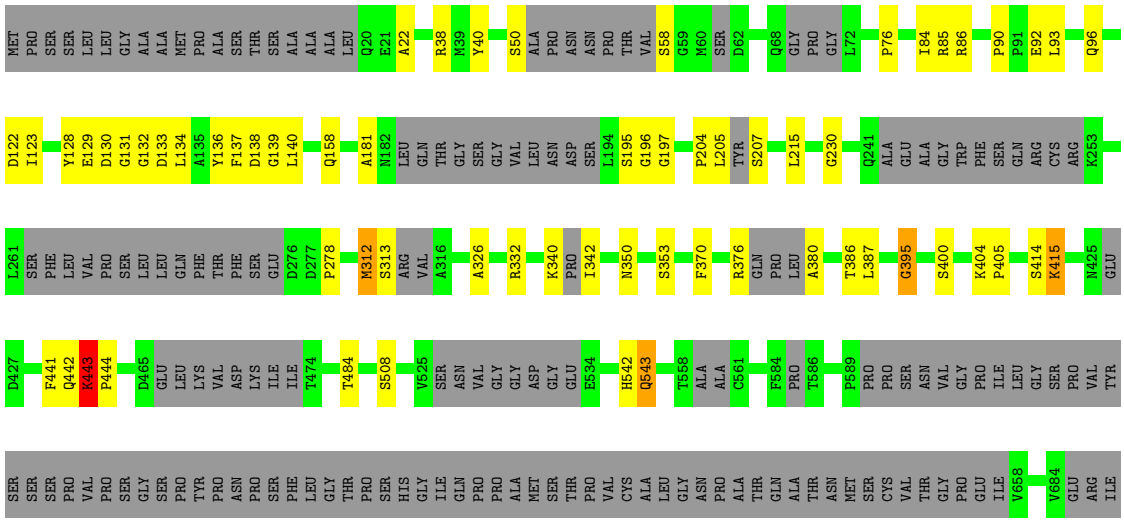
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 6-Q:



- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 6-W: 71% 6% 22%



PHE LYS SER GLY ASN ARG GLU ILE THR ALA ILE E699 G730 PRO LEU GLY ASN PRO ASN THR THR ALA LYS VAL GLN GLN ARG LEU ILE GLY PHE MET ARG PRO GLU ASN GLY ASN PRO GLN GLN MET GLN GLN GLU LEU GLN ARG LYS PHE HIS E769 A780 K796 C799

Q802 D848 N849 A850 A851 Q860 C863 PRO LEU LEU TYR SER THR ASP D871 V887 GLN ASN LYS THR GLU LYS GLU ARG MET LEU R898 Q910 P942 Q943 E957 D958 ILE V960 G961 V983 ASN GLN SER LYS ALA ALA PRO GLN SER PRO PRO SER VAL PRO LYS LYS PRO

GLY PRO PRO VAL LEU SER SER ASP PRO ASN MET LEU SER ASN GLU E1015 R1029 SER LYS ASP GLU L1034 K1069 VAL ASP GLN ASN ARG VAL R1076 H1105 SER T1107 A1125 LYS SER SER THR ALA ILE SER SER ILE ALA ALA ASP GLY E1139 S1170 V1171 Q1172 L1235 P1312

PHE TRP ASN ARG MET LYS K1319 P1320 N1343 R1346 N1351 L1352 C1353 L1354 D1355 C1358 Q1365 S1369 A1375 ILE THR GLY ASN PHE LYS SER LEU GLN ALA LYS LEU GLU ARG LEU HIS

- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 7-A: 44% 53%

MET PRO SER SER LEU LEU GLY ALA ALA MET PRO ALA SER THR SER ALA ALA ALA LEU Q20 E21 A22 R38 M39 Y40 S50 ALA PRO ASN ASN PRO THR VAL S58 G59 M60 SER D62 Q68 GLY PRO GLY L72 P76 Q158 A181 N182 LEU GLN THR GLY SER GLY VAL

LEU ASN ASP SER L194 S195 G196 P204 L205 TYR S207 L215 G230 Q241 ALA GLU ALA GLY TRP PHE SER GLN ARG CYS ARG K253 L261 SER PHE LEU VAL PRO SER LEU LEU GLN PHE THR PHE SER GLU D276 D277 P278 N312 S313 ARG VAL A316 A326 R332

K340 PRO I342 N350 S353 F370 R376 GLN PRO LEU A380 T386 L387 G395 S400 S414 K415 N425 GLU D427 F441 Q442 K443 P444 D465 GLU LEU LYS VAL ASP LYS ILE ILE T474 T484 V525 SER ASN VAL GLY GLY ASP GLY GLU E534 H542

Q543 T558 ALA ALA C561 F584 PRO T586 F589 PRO PRO SER ASN VAL GLY PRO ILE LEU GLY SER PRO VAL TYR SER SER SER PRO VAL PRO SER GLY SER PRO TYR PRO PRO PRO SER PHE LEU GLY THR PRO SER HIS GLY ILE GLN PRO PRO ALA MET SER THR PRO VAL CYS

ALA LEU GLY ASN PRO ALA THR GLN ALA THR ASN MET SER CYS VAL THR GLY PRO GLU ILE V658 V684 GLU ARG ILE PHE LYS SER GLY ASN ARG GLU ILE THR ALA ILE E699 G730 PRO LEU GLY ASN PRO ASN THR THR ALA LYS VAL GLN ARG LEU ILE GLY PHE MET ARG

PRO GLU ASN GLY ASN PRO GLN GLN MET GLN GLN GLU LEU LEU GLN ARG LYS PHE HIS E769 A780 Q802 C863 PRO LEU LEU TYR SER THR ASP ASP ALA ILE CYS SER LYS ALA ASN GLU LEU LEU GLN ARG SER ARG GLN VAL GLN ASN LYS THR GLU LYS GLU ARG MET LEU ARG

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

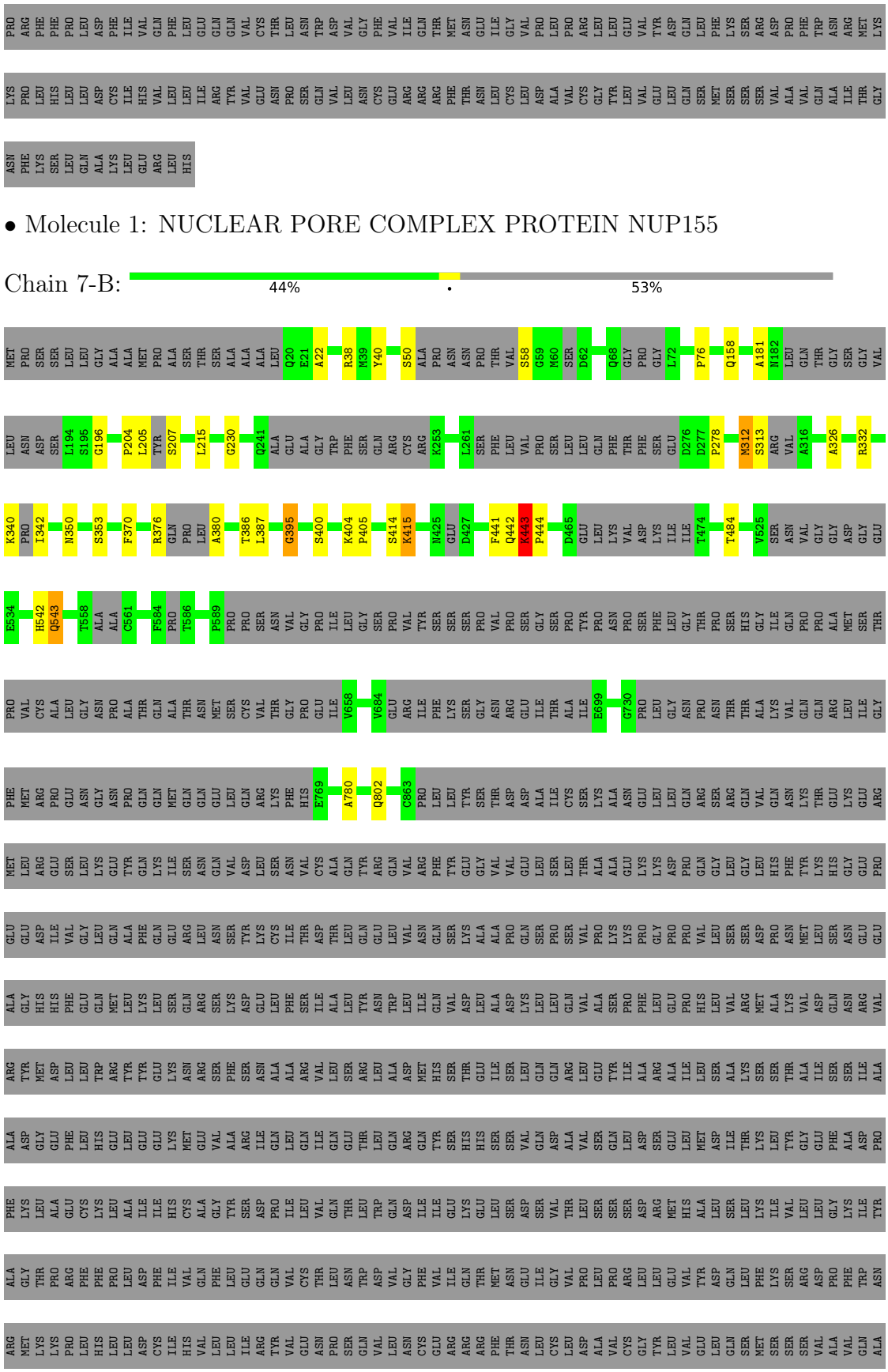
ILE VAL GLY LEU GLN ALA PHE GLN GLU ARG LEU ASN SER TYR LYS CYS ILE THR ASP THR LEU GLN LEU VAL ASN GLN SER LYS ALA ALA PRO GLN SER PRO SER VAL PRO LYS LYS PRO GLY PRO PRO VAL LEU SER SER ASP PRO ASN GLU GLU GLU GLU ALA GLY HIS

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

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

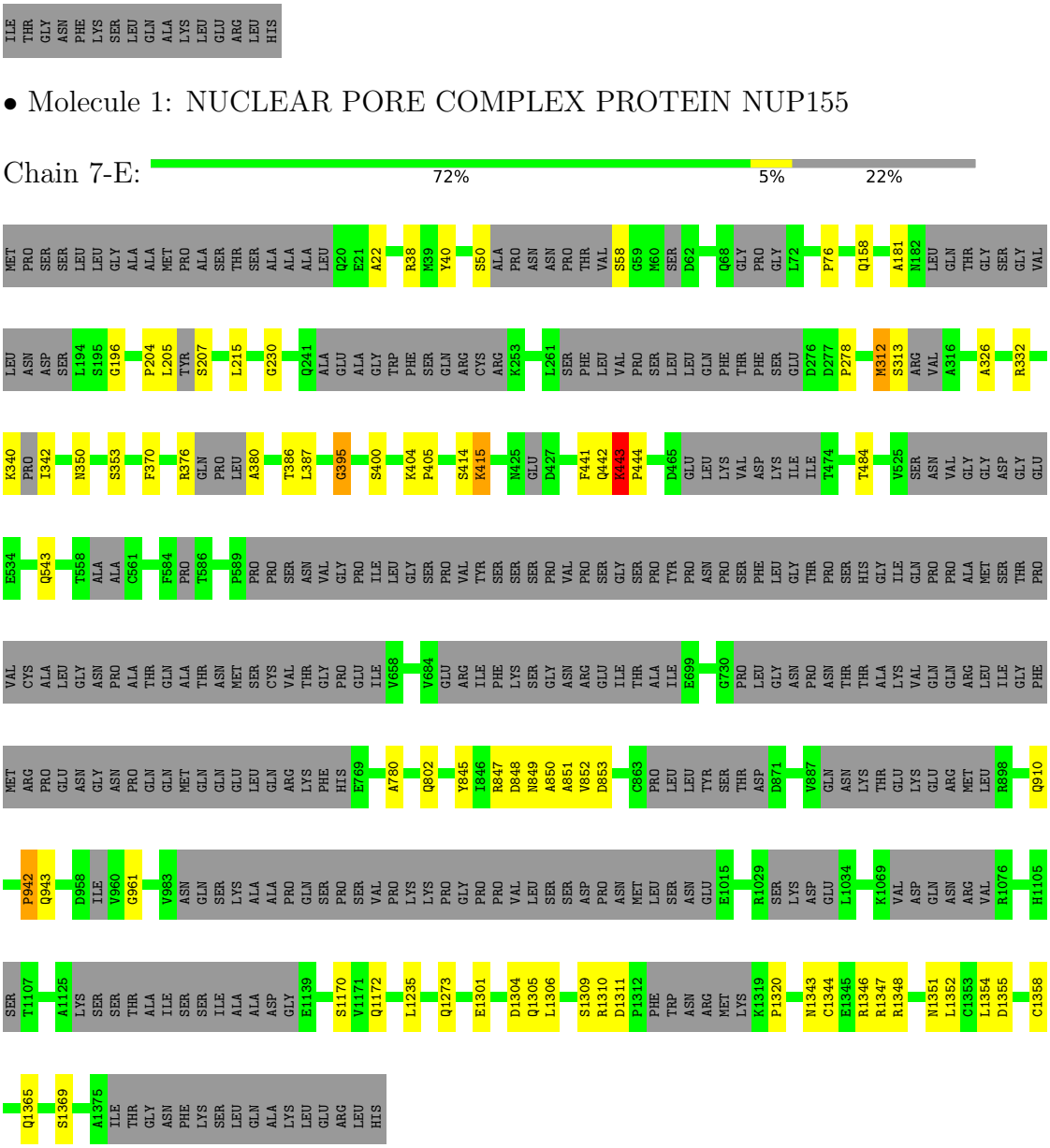
GLU PHE LEU HIS GLU LEU GLU GLU LYS MET GLU VAL ALA ARG ILE GLN LEU GLN ILE GLN GLU THR LEU GLN ARG ARG TYR SER HIS HIS SER SER VAL GLN ASP ARG LEU LEU GLN ILE ALA VAL SER GLN LEU LEU ASP ILE THR LYS LEU TYR LYS GLU GLU PHE ALA ALA LEU LYS LEU

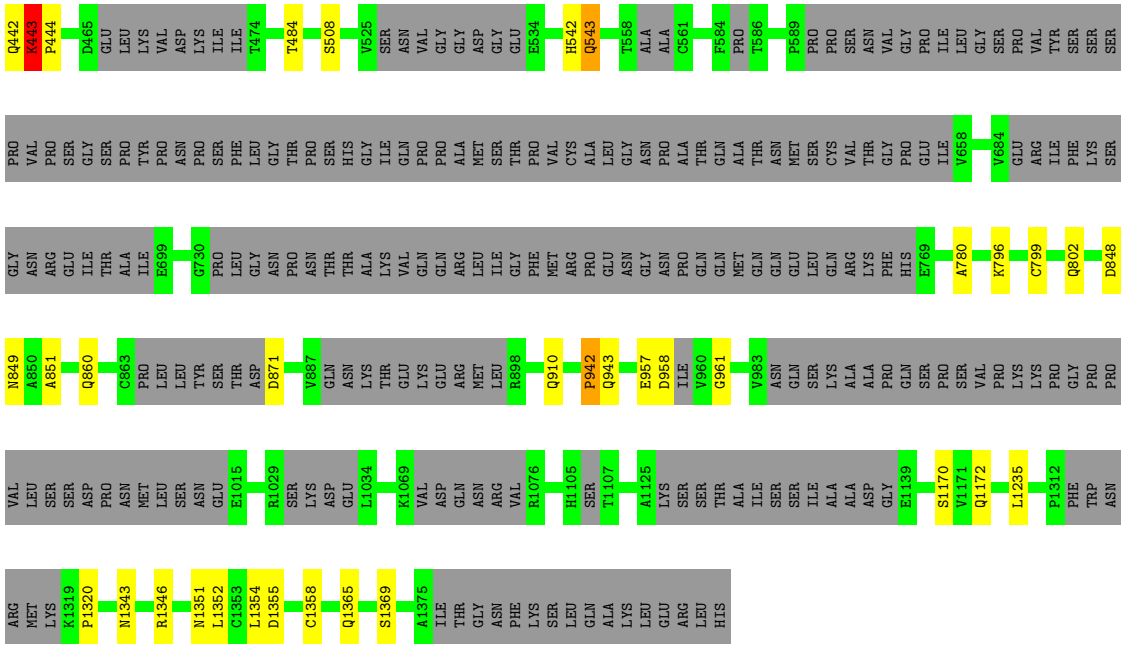
ALA GLU CYS LYS LEU ALA ILE ILE HIS CYS ALA GLY TYR SER ASP PRO ILE LEU VAL GLN THR LEU TRP GLN ASP ILE ILE GLU LYS GLU LEU SER ASP SER VAL THR LEU SER SER SER ASP ARG MET HIS ALA LEU SER LEU LYS ILE VAL LEU LEU GLY LYS ILE LYS ILE TYR ALA GLY HIS



• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

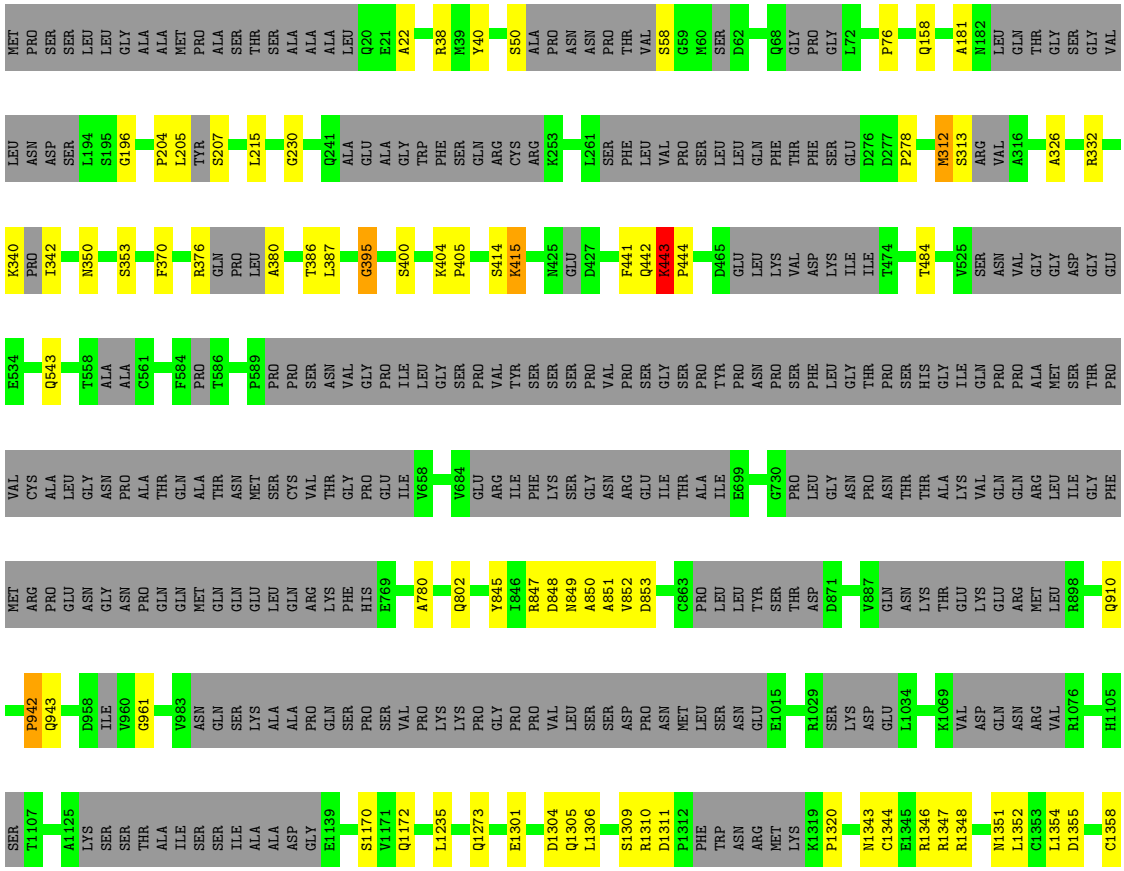
Chain 7-B: 44% • 53%


ILE THR GLY ASN PHE LYS SER LEU GLN ALA LYS LEU GLU ARG LEU HIS
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155
Chain 7-E:
72%
5%
22%
MET PRO SER SER LEU LEU GLY ALA ALA MET PRO ALA SER THR SER ALA ALA ALA LEU Q20 E21 A22 R38 M39 Y40 S50 ALA PRO ASN ASN PRO THR VAL S58 G59 M60 SER D62 Q68 GLY PRO GLY L72 P76 Q158 A181 N182 LEU GLN THR GLY SER GLY VAL
LEU ASN ASP SER L194 S195 G196 P204 L205 TYR S207 L215 G230 Q241 ALA GLU ALA GLY TRP PHE SER GLN ARG CYS ARG K253 L261 SER PHE LEU VAL PRO SER LEU LEU GLN PHE THR PHE SER GLU D276 D277 P278 M312 S313 ARG VAL A316 A326 R332
K340 PRO I342 N350 S353 F370 R376 GLN PRO LEU A380 T386 L387 G395 S400 K404 P405 S414 K415 N425 GLU D427 F441 Q442 K443 P444 D465 GLU LEU LYS VAL ASP LYS ILE ILE T474 T484 V525 SER ASN VAL GLY GLY ASP GLY GLU
E534 Q543 T558 ALA ALA C561 F584 PRO T586 P589 PRO PRO SER ASN VAL GLY PRO ILE LEU GLY SER PRO VAL TYR SER SER SER PRO VAL PRO SER GLY SER PRO TYR PRO ASN PRO SER PHE LEU GLY THR PRO SER HIS GLY ILE GLN PRO PRO ALA MET SER THR PRO
VAL CYS ALA LEU GLY ASN PRO ALA THR GLN ALA THR ASN MET SER CYS VAL THR GLY PRO GLU ILE V658 V684 GLU ARG ILE PHE LYS SER GLY ASN ARG GLU ILE THR ALA ILE E699 G730 PRO LEU GLY ASN PRO ASN THR THR ALA LYS VAL GLN GLN ARG LEU ILE GLY PHE
MET ARG PRO GLU ASN GLY ASN PRO GLN GLN MET GLN GLN GLU LEU GLN ARG LYS PHE HIS E769 A780 Q802 Y845 I846 R847 D848 N849 A850 A851 V852 D853 C863 PRO LEU LEU TYR SER THR ASP D871 V887 GLN ASN LYS THR GLU LYS GLU ARG MET LEU R898 Q910
P942 Q943 D968 ILE V960 G961 V983 ASN GLN SER LYS ALA ALA PRO GLN SER PRO SER VAL PRO LYS LYS PRO GLY PRO PRO VAL LEU SER SER ASP PRO ASN MET LEU SER ASN GLU E1015 R1029 SER LYS ASP GLU L1034 K1069 VAL ASP GLN ASN ARG VAL R1076 H1105
SER T1107 A1125 LYS SER SER THR ALA ILE SER SER ILE ILE ALA ALA ASP GLY E1139 S1170 V1171 Q1172 L1235 Q1273 E1301 D1304 Q1305 L1306 S1309 R1310 D1311 P1312 PHE TRP ASN ARG MET LYS K1319 P1320 N1343 C1344 E1345 R1346 R1347 R1348 N1351 L1352 C1353 L1354 D1355 C1358
Q1365 S1369 A1375 ILE THR GLY ASN PHE LYS SER LEU GLN ALA LYS LEU GLU ARG LEU HIS
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155
Chain 7-K:
71%
6%
22%
MET PRO SER SER LEU LEU GLY ALA ALA MET PRO ALA SER THR SER ALA ALA ALA LEU Q20 E21 A22 R38 M39 Y40 S50 ALA PRO ASN ASN PRO THR VAL S58 G59 M60 SER D62 Q68 GLY PRO GLY L72 P76 I84 R85 R86 P90 P91 E92 L93 Q96
D122 I123 Y128 E129 D130 G131 G132 D133 L134 A135 Y136 F137 D138 G139 L140 Q158 A181 N182 LEU GLN THR GLY SER GLY VAL LEU ASN ASP SER L194 S195 G196 G197 P204 L205 TYR S207 L215 G230 Q241 ALA GLU ALA GLY TRP PHE SER GLN ARG CYS ARG K253
L261 SER PHE LEU VAL PRO SER LEU LEU GLN PHE THR PHE SER GLU D276 D277 P278 M312 S313 ARG VAL A316 A326 R332 K340 PRO I342 N350 S353 F370 R376 GLN PRO LEU A380 T386 L387 G395 S400 S414 K415 N425 GLU D427 F441



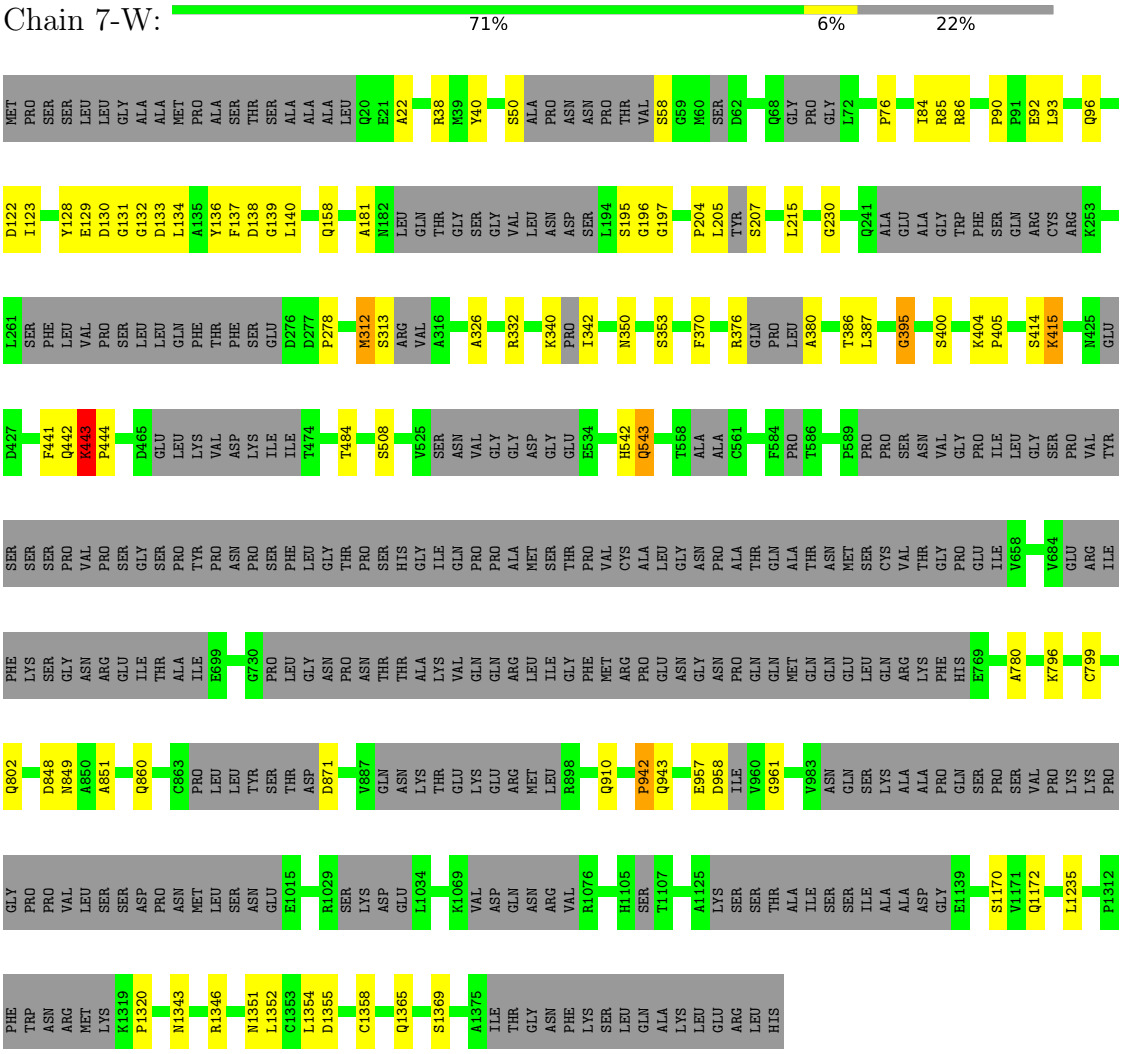
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

Chain 7-Q:



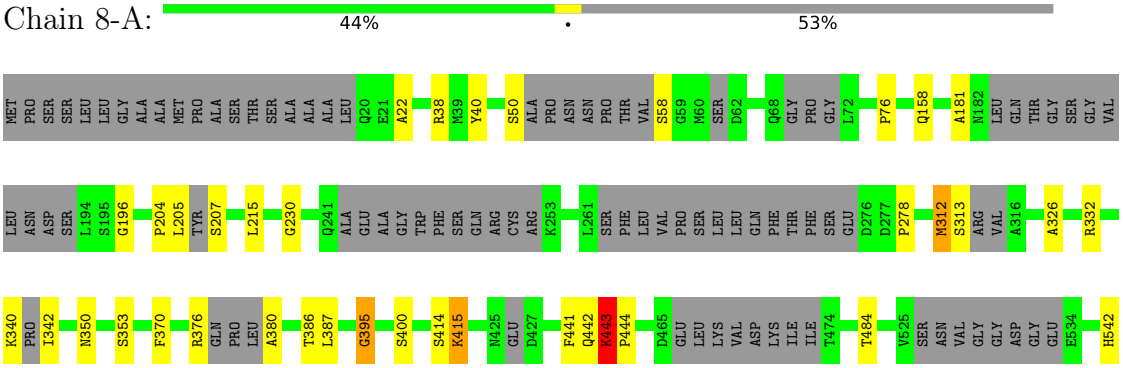
• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

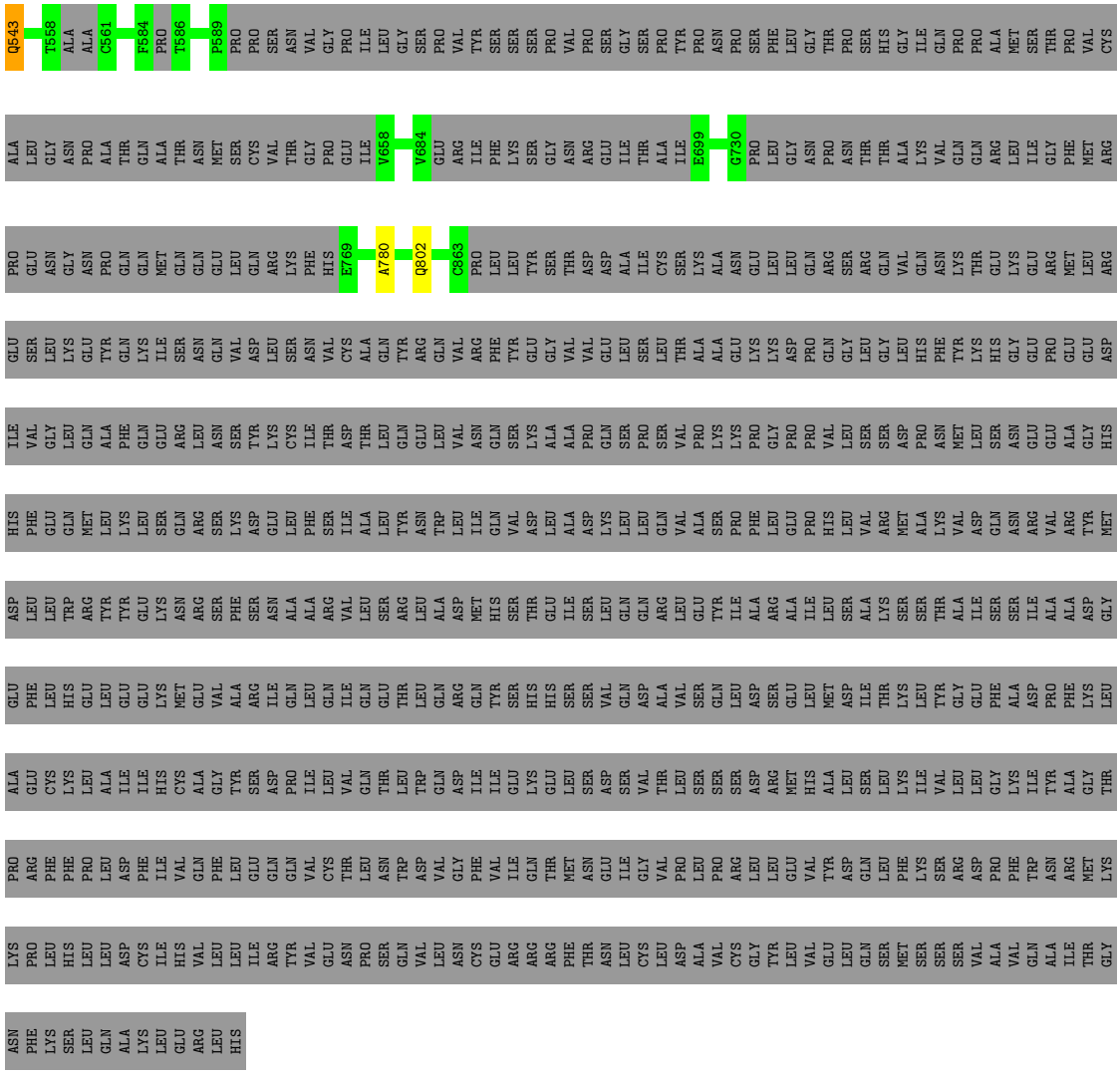
Chain 7-W:



• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

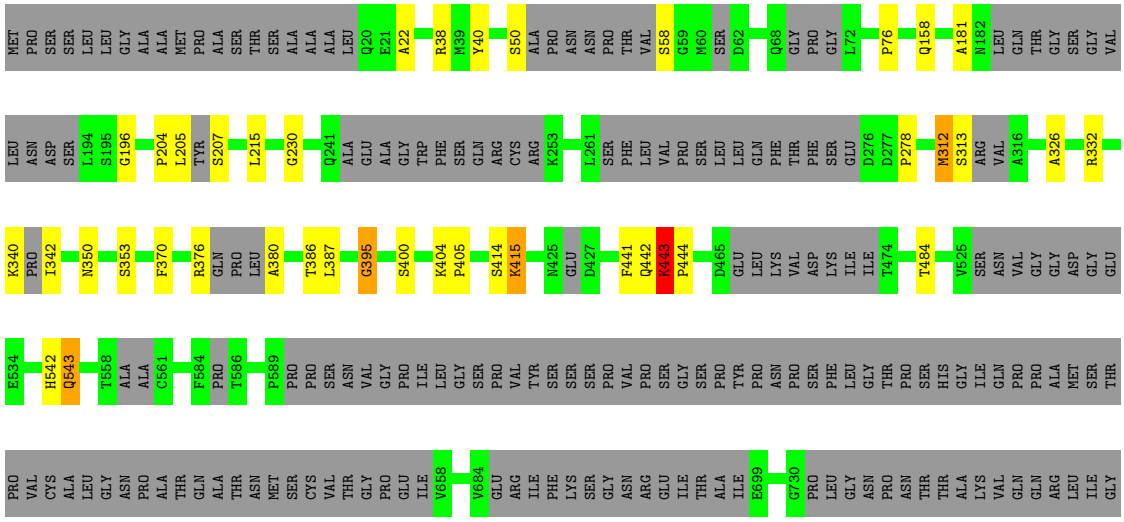
Chain 8-A:

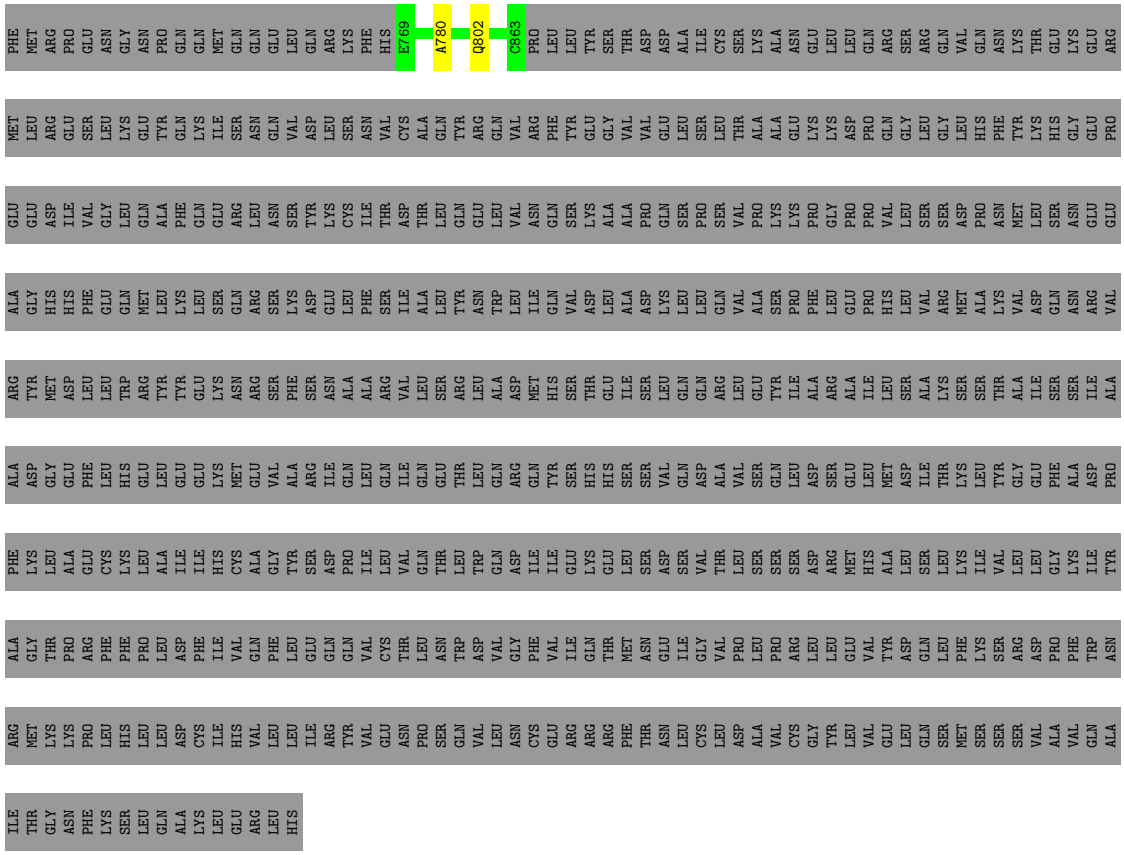




• Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

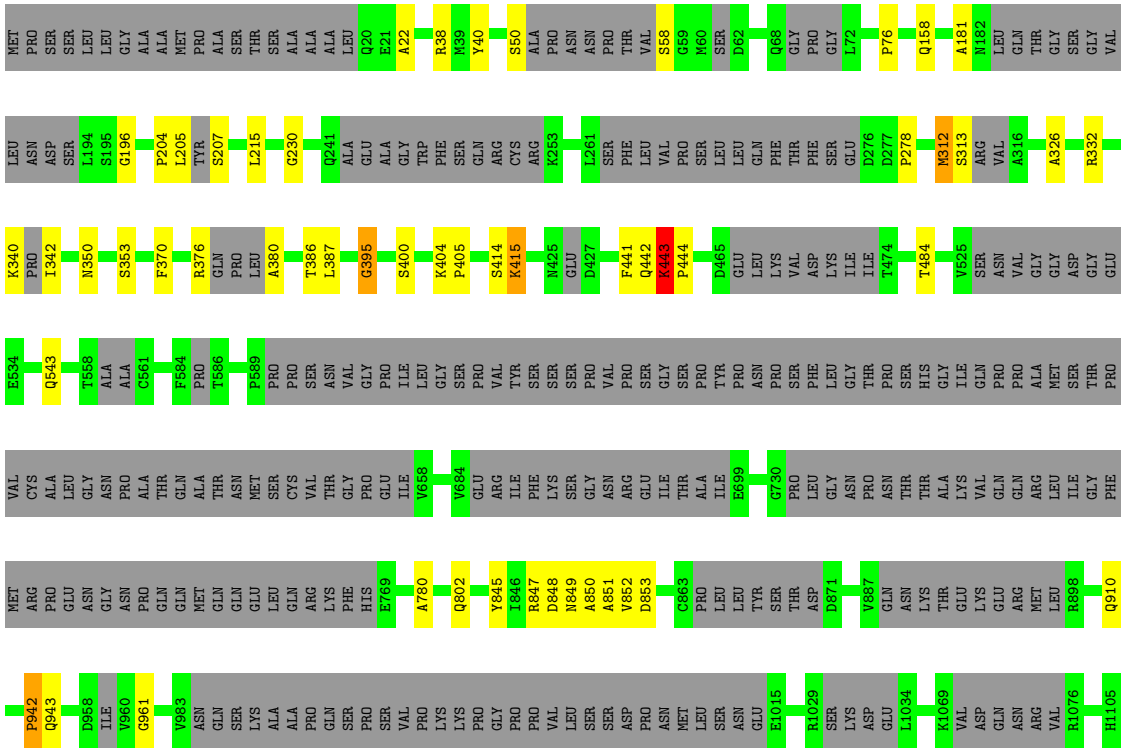
Chain 8-B: 44% • 53%

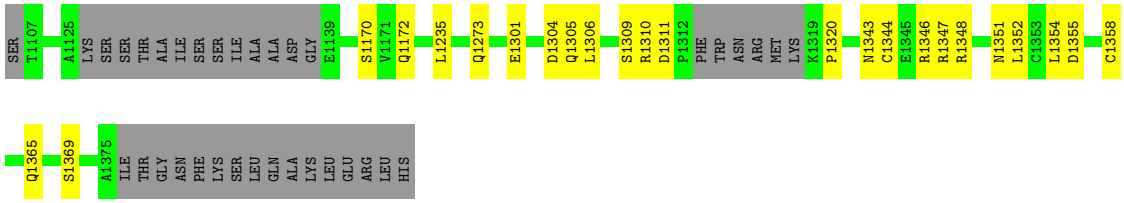




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

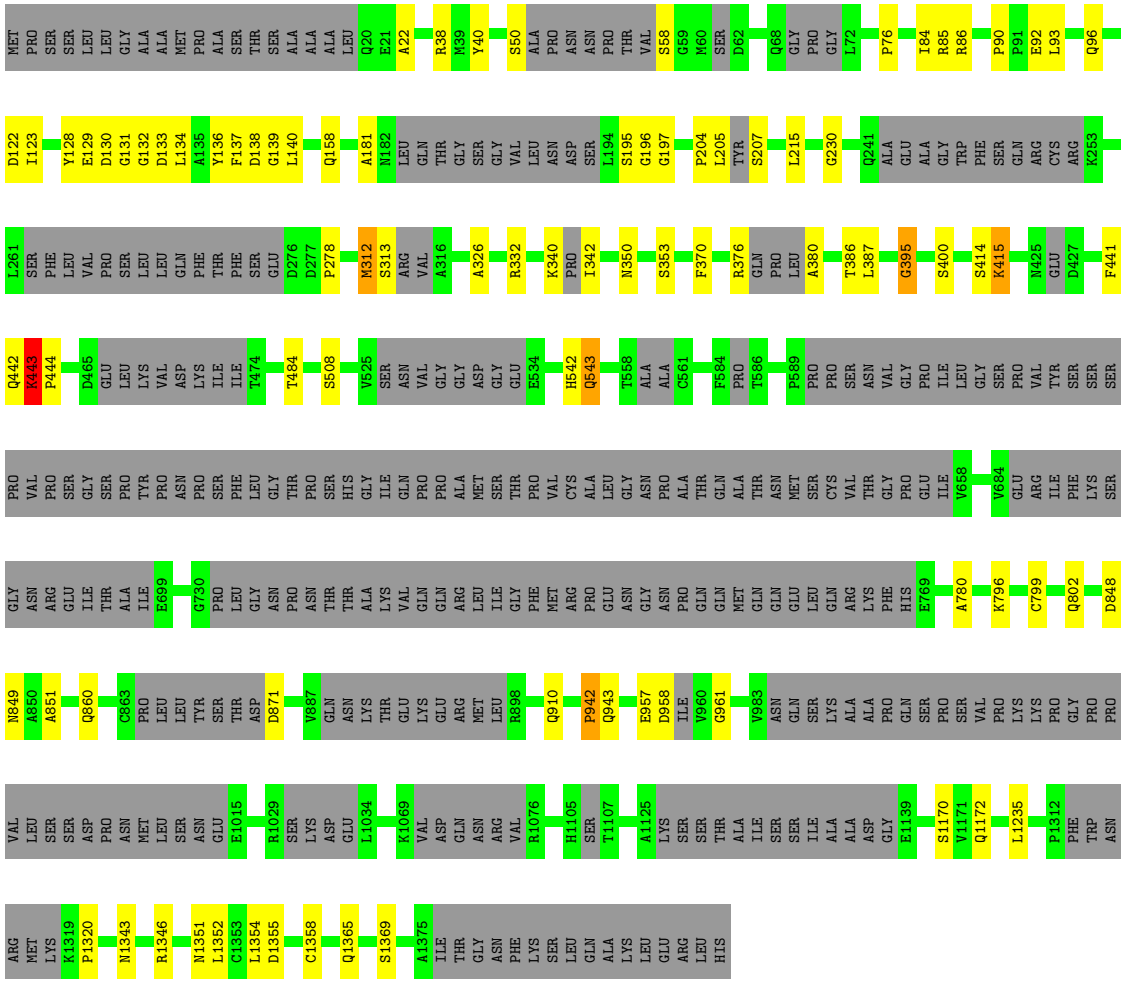
Chain 8-E:





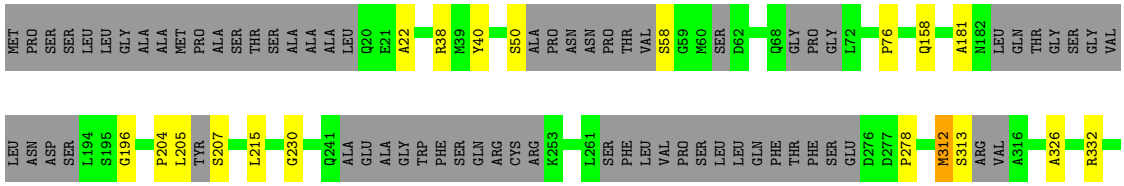
- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

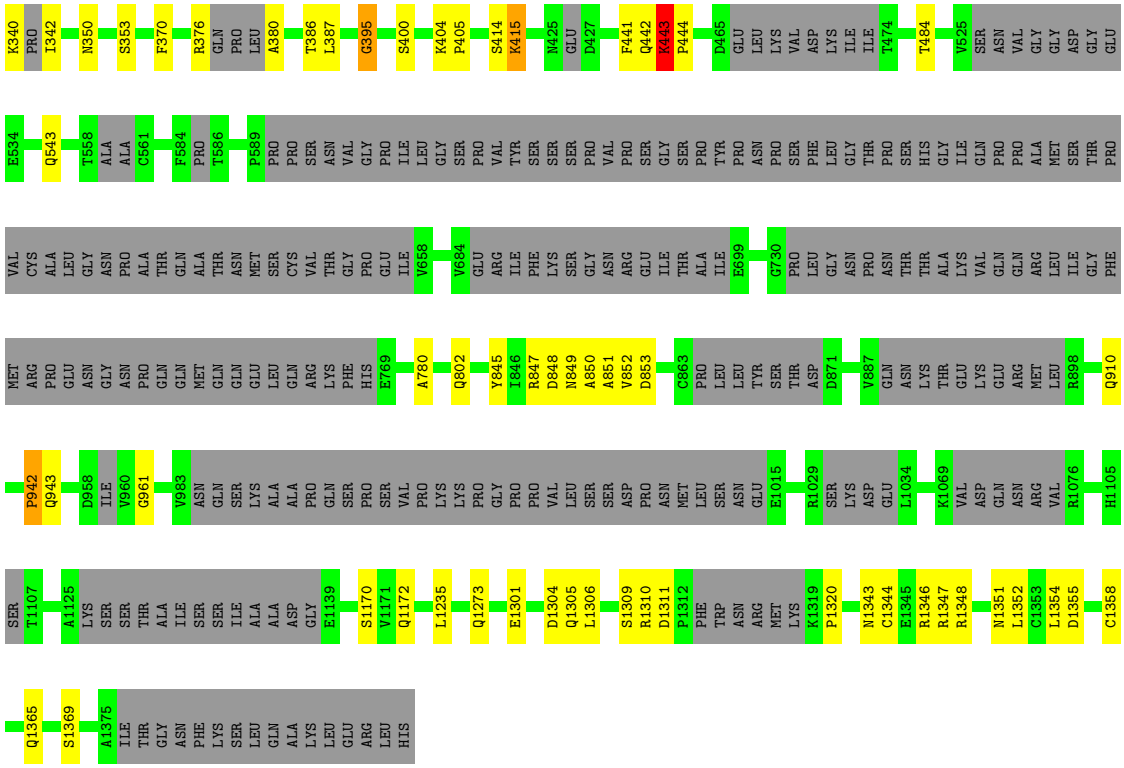
Chain 8-K:



- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

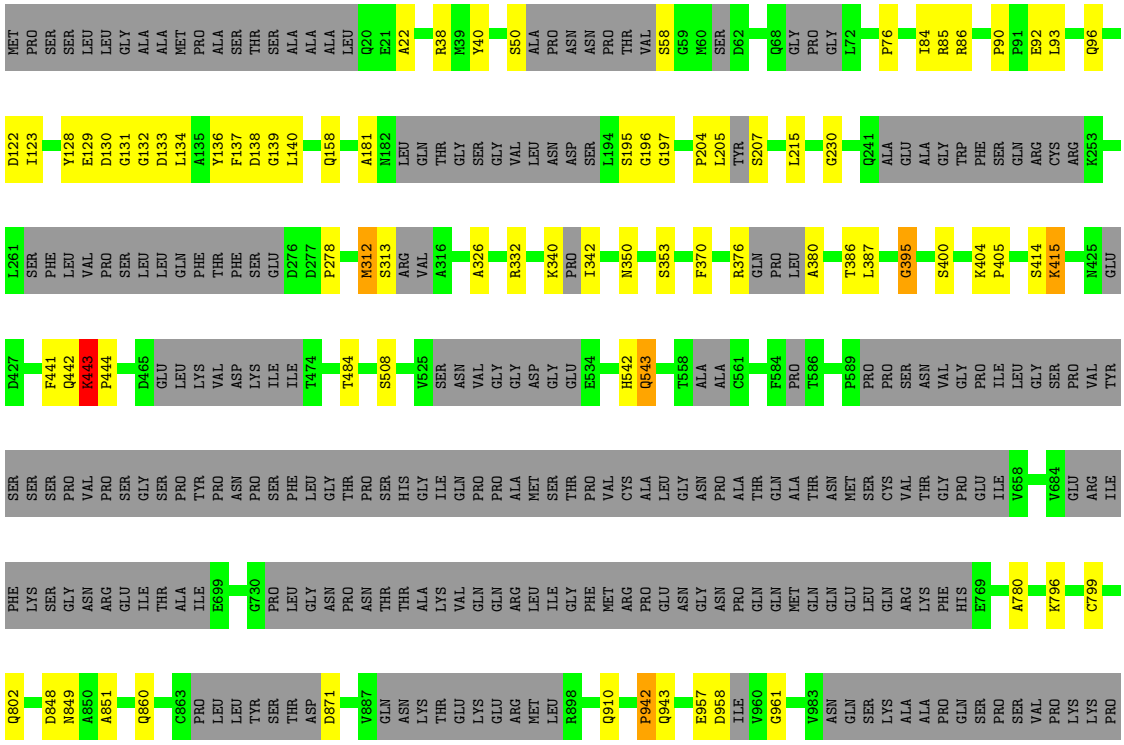
Chain 8-Q:

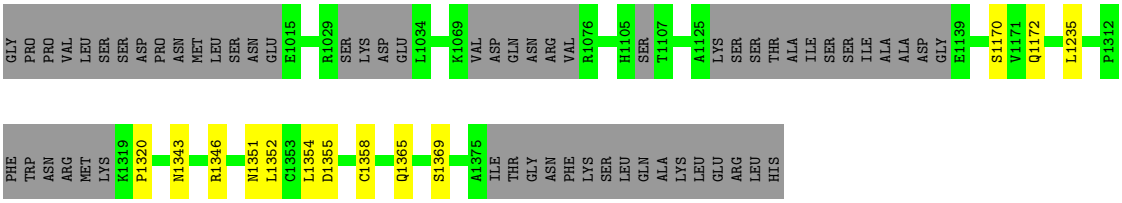




- Molecule 1: NUCLEAR PORE COMPLEX PROTEIN NUP155

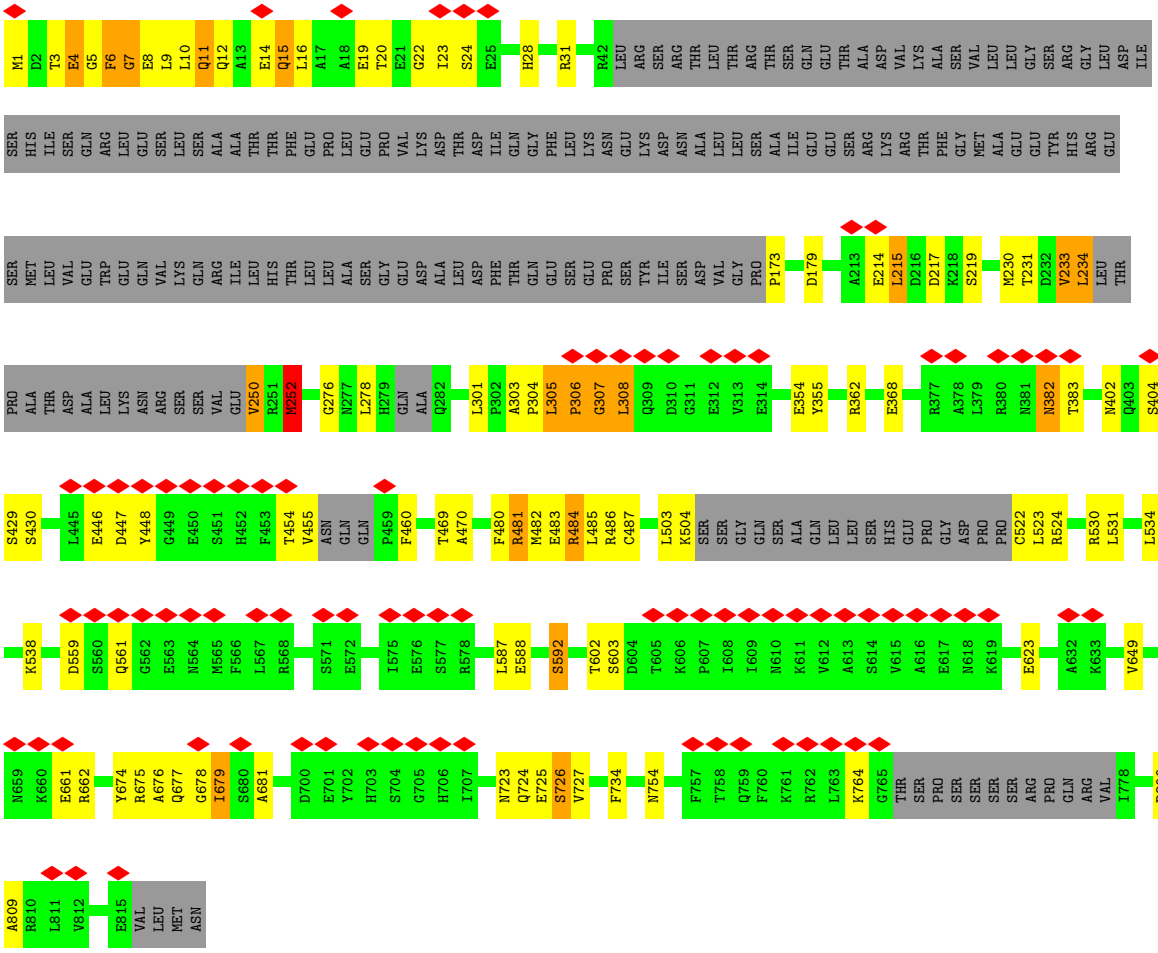
Chain 8-W: 71% 6% 22%





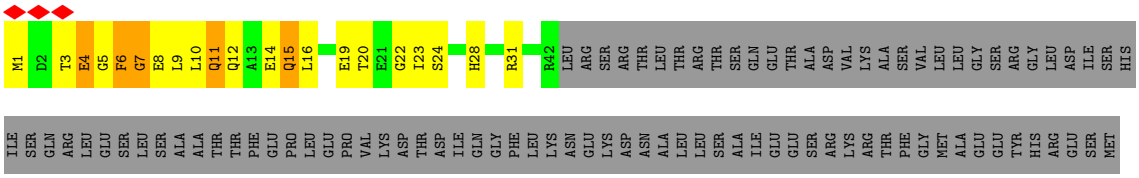
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

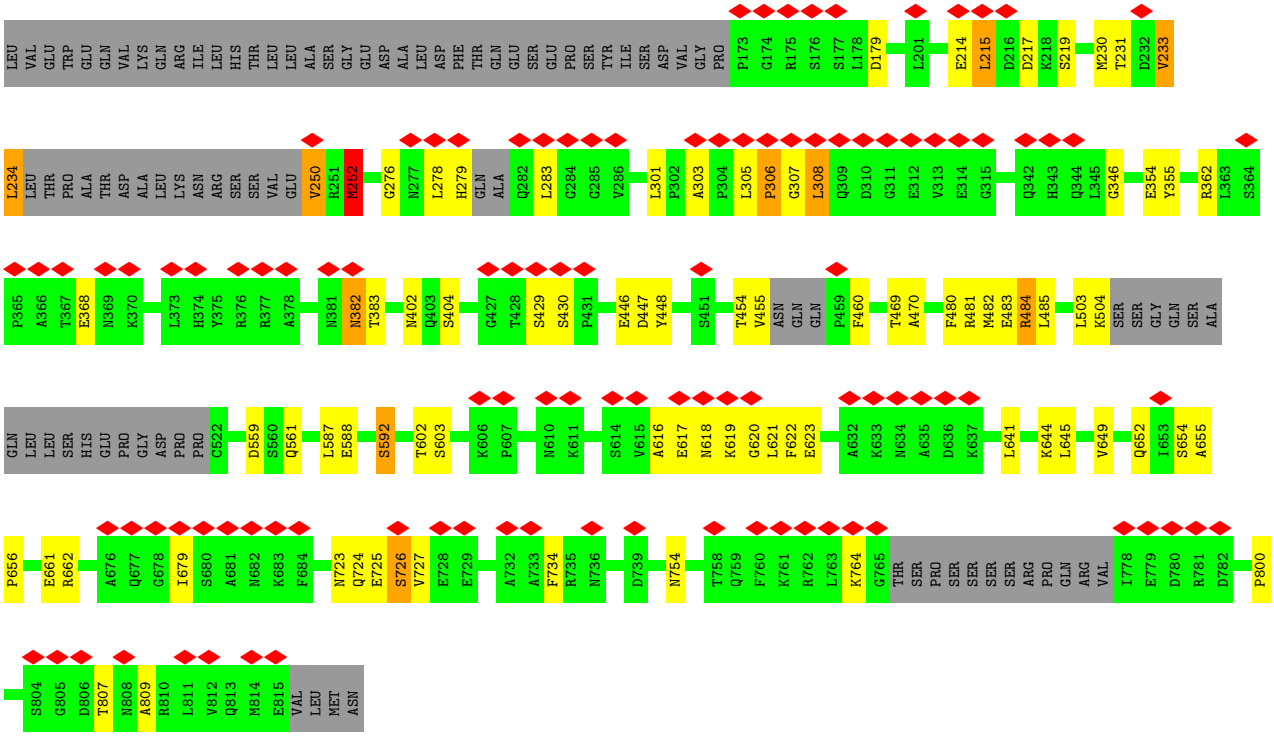
Chain 1-C:



• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

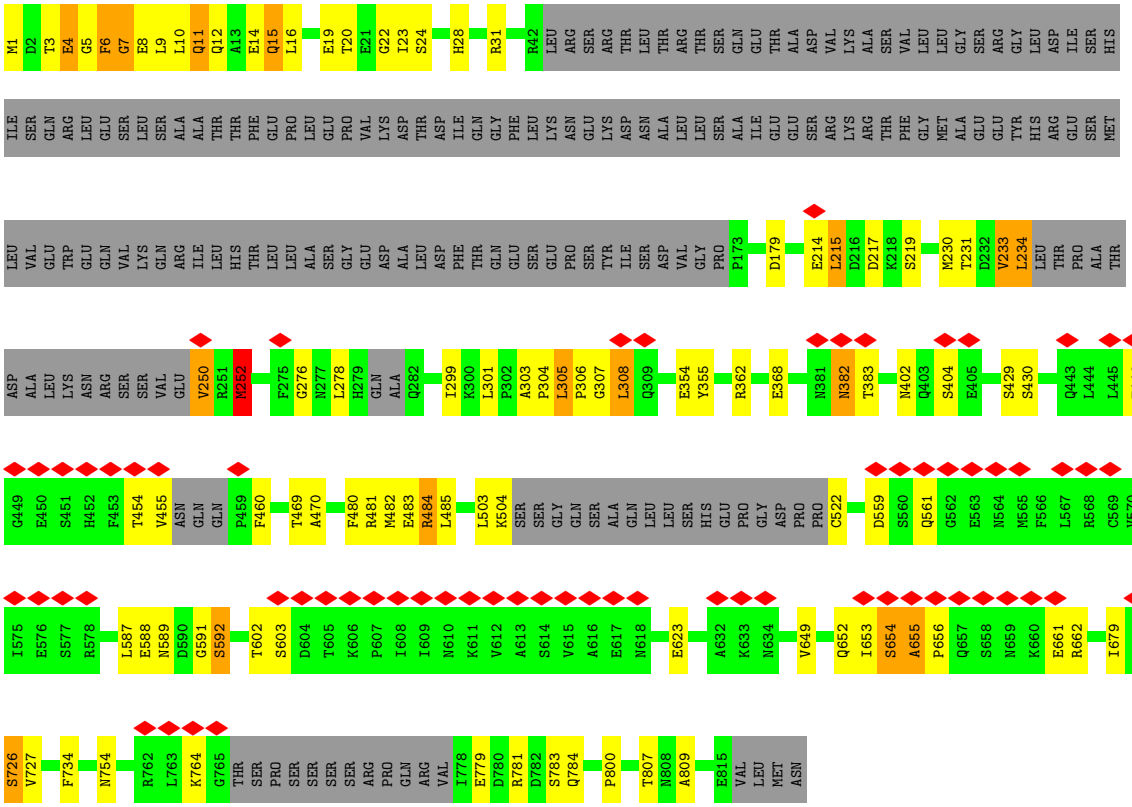
Chain 1-I:





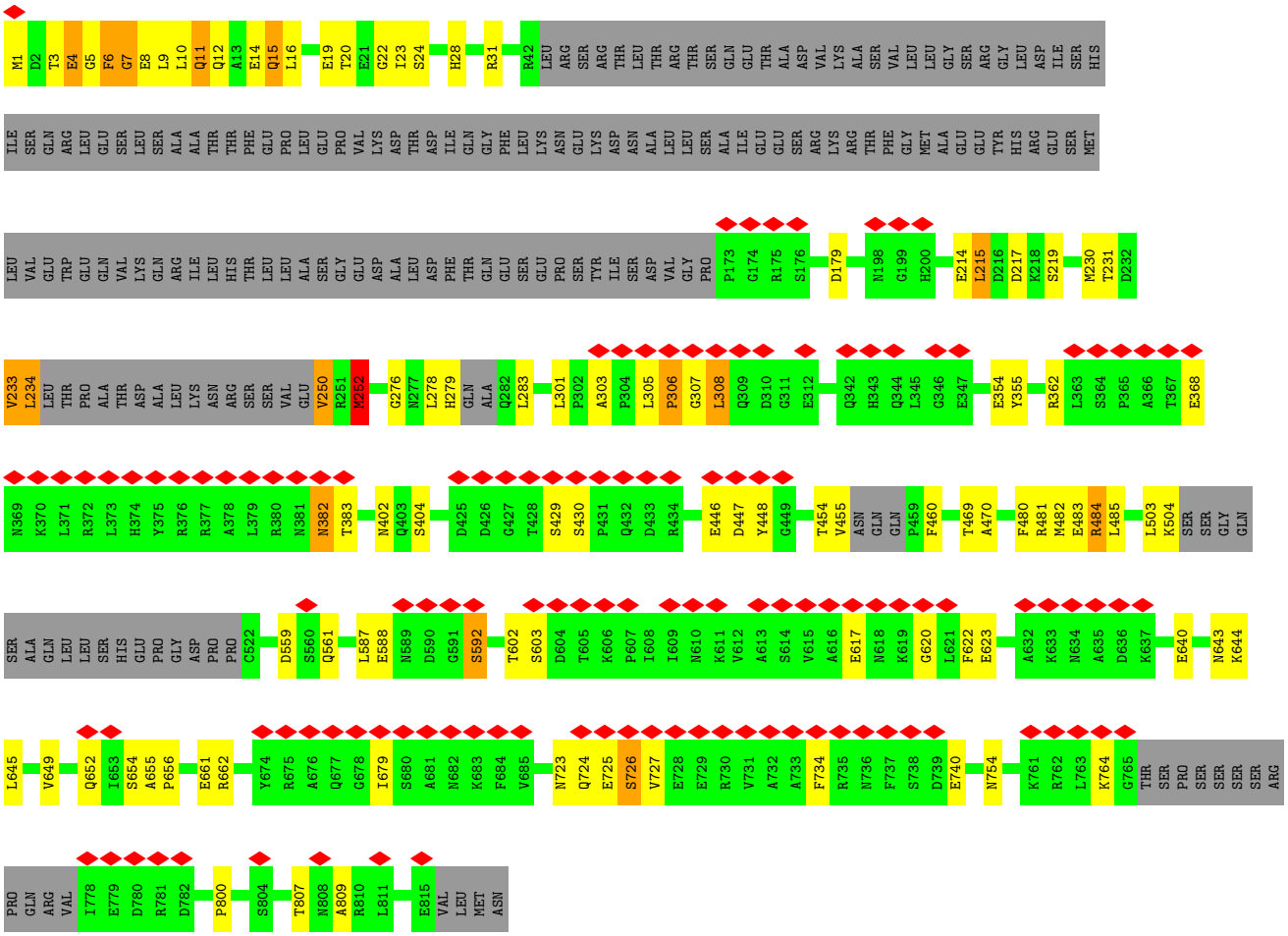
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 1-O:



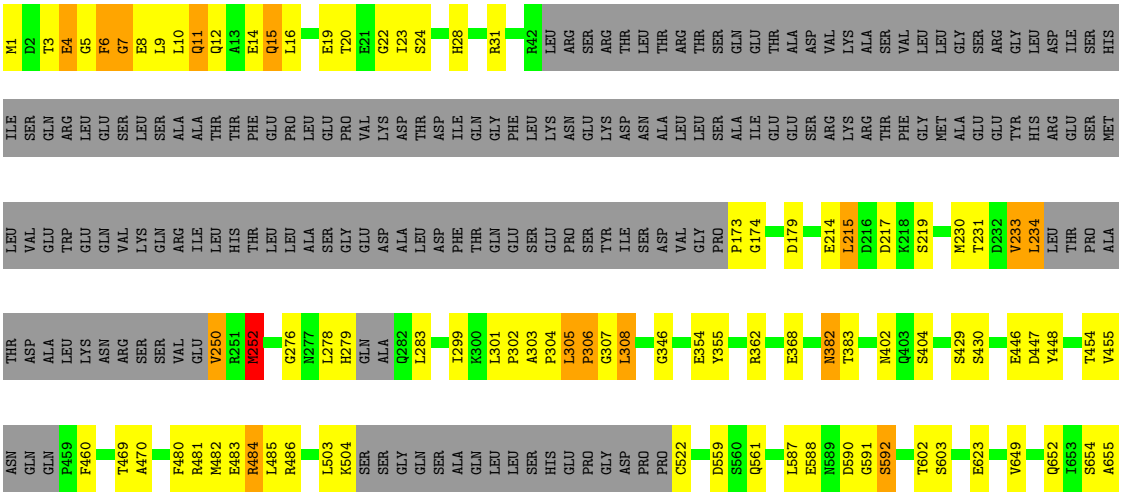
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

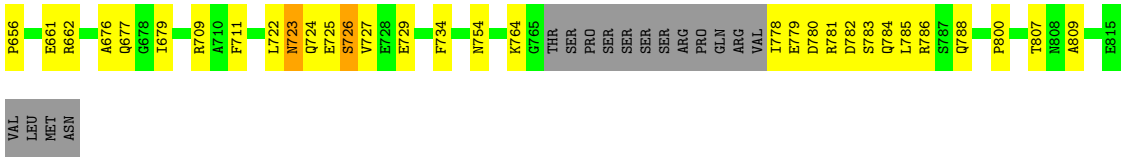
Chain 1-U:



- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

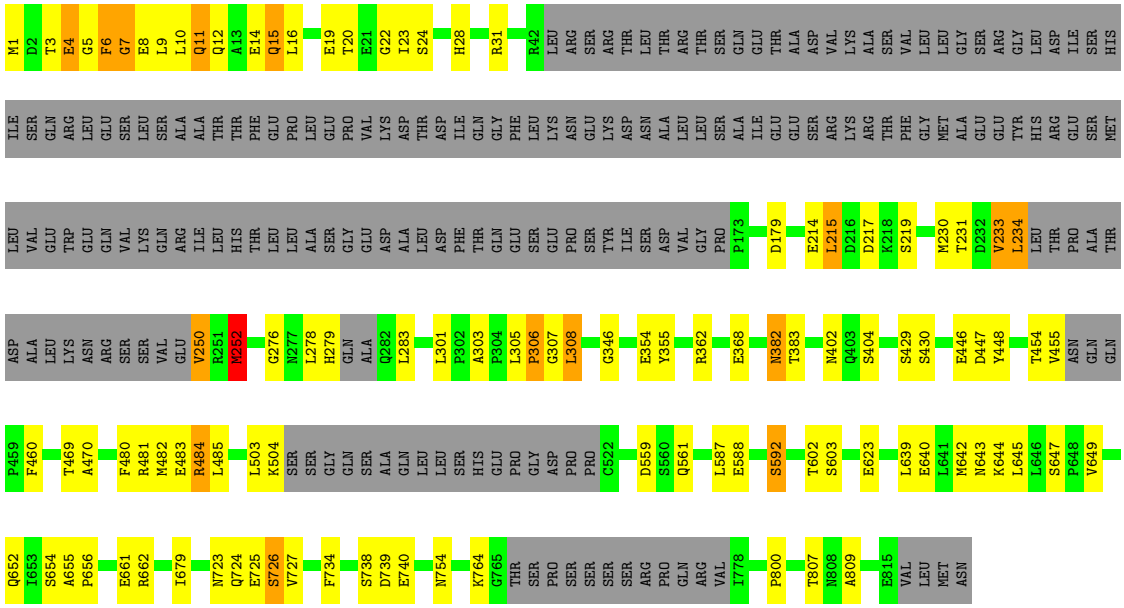
Chain 2-C:





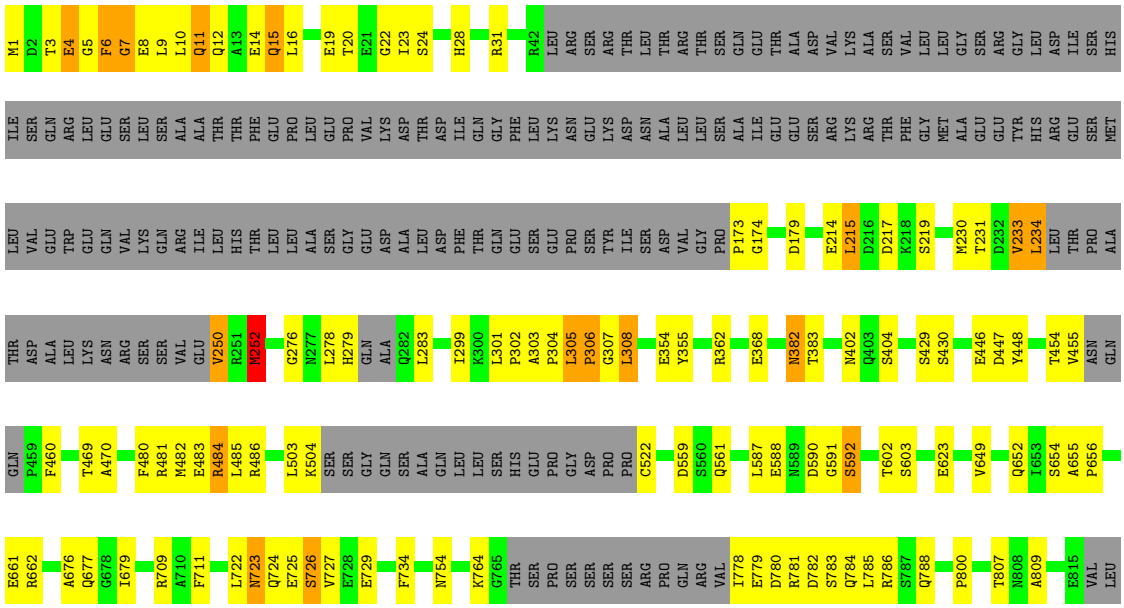
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 2-I: 65% 11% • 22%



• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 2-O: 63% 12% • 22%



MET
ASN

• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 2-U: 65% 11% • 22%

M1 D2 T3 E4 G5 F6 G7 E8 L9 L10 Q11 Q12 A13 E14 Q15 L16 E19 T20 E21 G22 I23 S24 H28 R31 R42 LEU ARG SER ARG THR LEU THR ARG THR SER GLN GLU THR ALA ASP VAL LYS ALA SER VAL LEU LEU GLY SER ARG GLY LEU ASP ILE SER HIS

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

LEU VAL GLU TRP GLU GLN VAL LYS GLN ARG ILE LEU HIS THR LEU LEU ALA SER GLY GLU ASP ALA LEU ASP PHE THR GLN GLU SER GLU PRO SER TYR ILE SER ASP VAL GLY PRO P173 D179 E214 L215 D216 D217 K218 S219 M230 T231 D232 V233 L234 LEU THR PRO ALA THR

ASP ALA LEU LYS ASN ARG SER SER VAL GLU V250 R251 M252 G276 N277 L278 H279 GLN ALA Q282 L283 L301 P302 A303 P304 L305 P306 G307 L308 G346 E354 Y355 R362 E368 N382 T383 N402 Q403 S404 S429 S430 E446 D447 Y448 T454 V455 ASN GLN GLN

P459 F460 T469 A470 F480 R481 M482 E483 R484 L485 L503 K504 SER SER GLY GLN SER ALA GLN LEU LEU SER HIS GLU PRO GLY ASP PRO PRO C522 D559 S560 Q561 L587 E588 S592 T602 S603 E623 L639 E640 L641 M642 N643 K644 L645 L646 S647 F648 V649

Q652 I653 S654 A655 P656 E661 R662 I679 N723 Q724 E725 S726 V727 F734 S738 D739 E740 N754 K764 G765 THR SER PRO SER SER SER SER ARG PRO GLN ARG VAL I778 P800 T807 N808 A809 E815 VAL LEU MET ASN

• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 3-C: 63% 13% • 22%

M1 D2 T3 E4 G5 F6 G7 E8 L9 L10 Q11 Q12 A13 E14 Q15 L16 E19 T20 E21 G22 I23 S24 H28 R31 R42 LEU ARG SER ARG THR LEU THR ARG THR SER GLN GLU THR ALA ASP VAL LYS ALA SER VAL LEU LEU GLY SER ARG GLY LEU ASP ILE SER HIS

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

LEU VAL GLU TRP GLU GLN VAL LYS GLN ARG ILE LEU HIS THR LEU LEU ALA SER GLY GLU ASP ALA LEU ASP PHE THR GLN GLU SER GLU PRO SER TYR ILE SER ASP VAL GLY PRO P173 G174 D179 E214 L215 D216 D217 K218 S219 M230 T231 D232 V233 L234 LEU THR PRO ALA

THR ASP ALA LEU LYS ASN ARG SER SER VAL GLU V250 R251 M252 G276 N277 L278 H279 GLN ALA Q282 L283 I299 K300 L301 P302 A303 P304 L305 P306 G307 L308 G346 E354 Y355 R362 E368 N382 T383 N402 Q403 S404 S429 S430 E446 D447 Y448 T454 V455

ASN GLN GLN P459 F460 T469 A470 F480 R481 M482 E483 R484 L485 R486 L503 K504 SER SER GLY GLN SER ALA GLN LEU LEU SER HIS GLU PRO GLY ASP PRO PRO C522 D559 S560 Q561 L587 E588 N589 D590 G591 S592 T602 S603 E623 V649 Q652 I653 S654 A655

P656 E661 R662 A676 Q677 G678 I679 R709 A710 F711 L722 N723 Q724 E725 S726 V727 E728 E729 F734 N754 K764 G765 THR SER PRO SER SER SER SER ARG PRO GLN ARG VAL I778 E779 D780 R781 D782 S783 Q784 L785 R786 S787 Q788 P800 T807 N808 A809 E815

VAL
LEU
MET
ASN

• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 3-I: 65% 11% • 22%

M1 D2 T3 E4 G5 F6 G7 E8 L9 L10 Q11 Q12 A13 E14 Q15 L16 E19 T20 E21 G22 I23 S24 H28 R31 R42 LEU ARG SER ARG THR LEU THR ARG THR SER GLN GLU THR ALA ASP VAL LYS ALA SER VAL LEU LEU GLY SER ARG GLY LEU ASP ILE SER HIS

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

LEU VAL GLU TRP GLU GLN VAL LYS GLN ARG ILE LEU HIS THR LEU LEU ALA SER GLY GLU ASP ALA LEU ASP PHE THR GLN GLU SER GLU PRO SER TYR ILE SER ASP VAL GLY PRO P173 D179 E214 L215 D216 D217 K218 S219 M230 T231 D232 V233 L234 LEU THR PRO ALA THR

ASP ALA LEU LYS ASN ARG SER SER VAL GLU V250 R251 M252 G276 N277 L278 H279 GLN ALA Q282 L283 L301 P302 A303 P304 L305 P306 G307 L308 G346 E354 Y355 R362 E368 N382 T383 N402 Q403 S404 S429 S430 E446 D447 Y448 T454 V455 ASN GLN GLN

P459 F460 T469 A470 F480 R481 M482 E483 R484 L485 L503 K504 SER SER GLY GLN SER ALA GLN LEU LEU SER HIS GLU PRO GLY ASP PRO PRO C522 D559 S560 Q561 L587 E588 S592 T602 S603 E623 L639 E640 L641 M642 N643 K644 L645 L646 S647 P648 V649

Q652 I653 S654 A655 P656 E661 R662 I679 N723 Q724 E725 S726 V727 F734 S738 D739 E740 N754 K764 G765 THR SER PRO SER SER SER SER ARG PRO GLN ARG VAL I778 P800 T807 N808 A809 E815 VAL LEU MET ASN

• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 3-O: 63% 12% • 22%

M1 D2 T3 E4 G5 F6 G7 E8 L9 L10 Q11 Q12 A13 E14 Q15 L16 E19 T20 E21 G22 I23 S24 H28 R31 R42 LEU ARG SER ARG THR LEU THR ARG THR SER GLN GLU THR ALA ASP VAL LYS ALA SER VAL LEU LEU GLY SER ARG GLY LEU ASP ILE SER HIS

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

LEU VAL GLU TRP GLU GLN VAL LYS GLN ARG ILE LEU HIS THR LEU LEU ALA SER GLY GLU ASP ALA LEU ASP PHE THR GLN GLU SER GLU PRO SER TYR ILE SER ASP VAL GLY PRO P173 G174 D179 E214 L215 D216 D217 K218 S219 M230 T231 D232 V233 L234 LEU THR PRO ALA

THR ASP ALA LEU LYS ASN ARG SER SER VAL GLU V250 R251 M252 G276 N277 L278 H279 GLN ALA Q282 L283 I299 K300 L301 P302 A303 P304 L305 P306 G307 L308 E354 Y355 R362 E368 N382 T383 N402 Q403 S404 S429 S430 E446 D447 Y448 T454 V455 ASN GLN

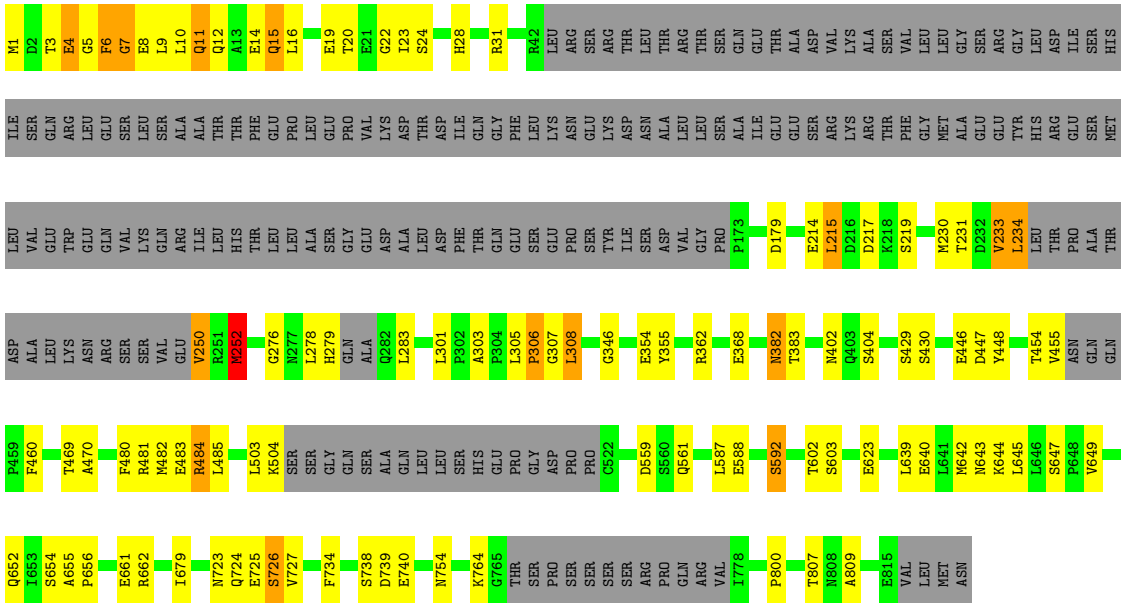
GLN P459 F460 T469 A470 F480 R481 M482 E483 R484 L485 R486 L503 K504 SER SER GLY GLN SER ALA GLN LEU LEU SER HIS GLU PRO GLY ASP PRO PRO C522 D559 S560 Q561 L587 E588 N589 D590 G591 S592 T602 S603 E623 V649 Q652 I653 S654 A655 P656

E661 R662 A676 Q677 G678 I679 R709 A710 F711 L722 N723 Q724 E725 S726 V727 E728 E729 F734 N754 K764 G765 THR SER PRO SER SER SER SER ARG PRO GLN ARG VAL I778 E779 D780 R781 D782 S783 Q784 L785 R786 S787 Q788 P800 T807 N808 A809 E815 VAL LEU

MET ASN

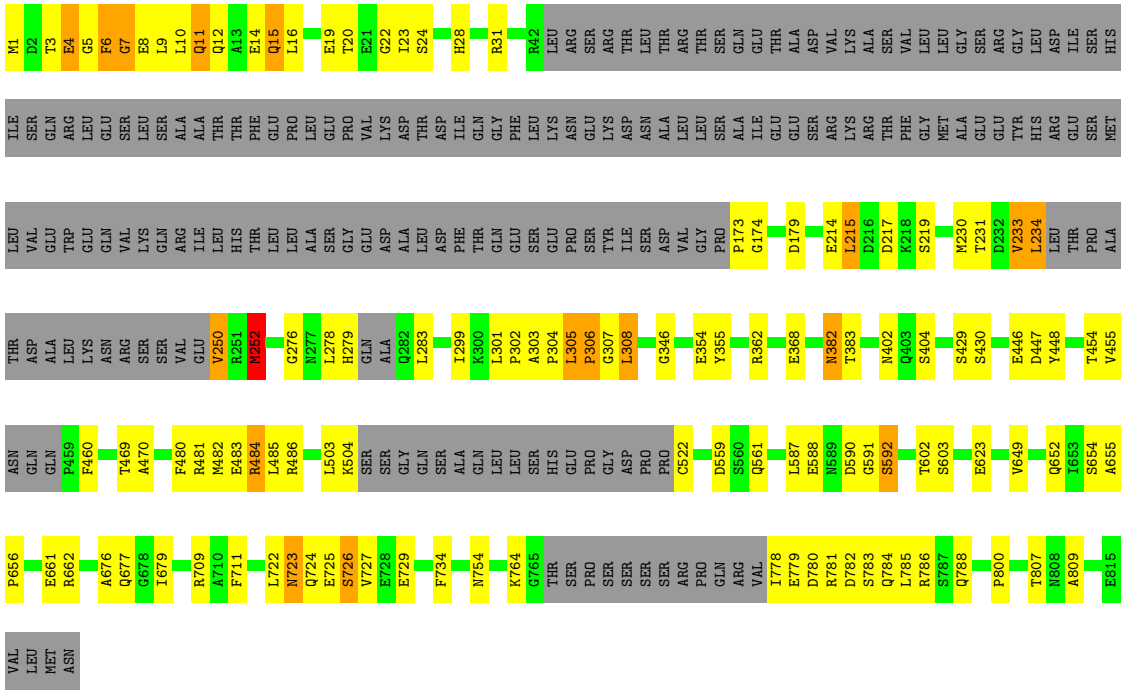
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 3-U: 65% 11% • 22%



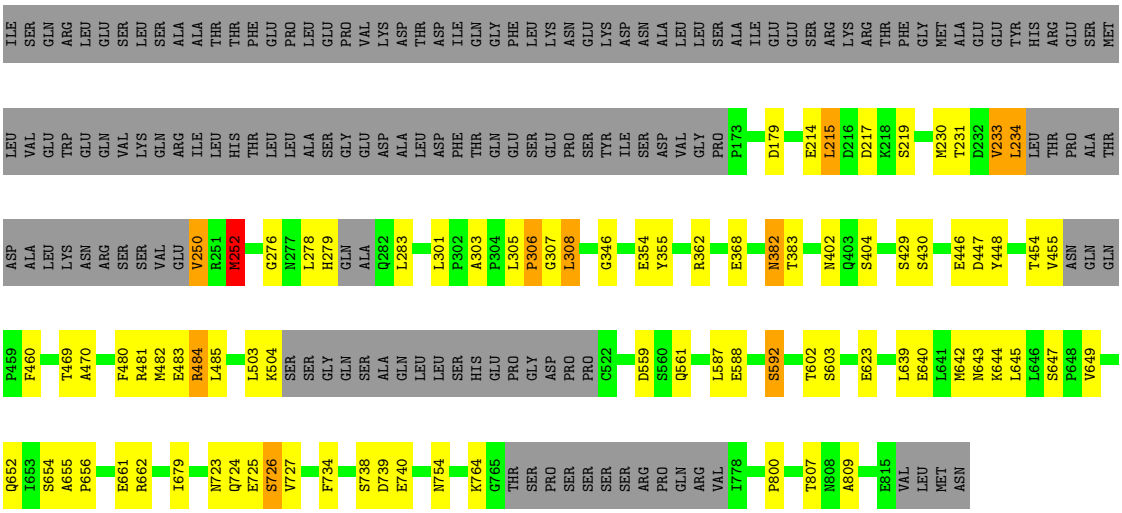
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 4-C:



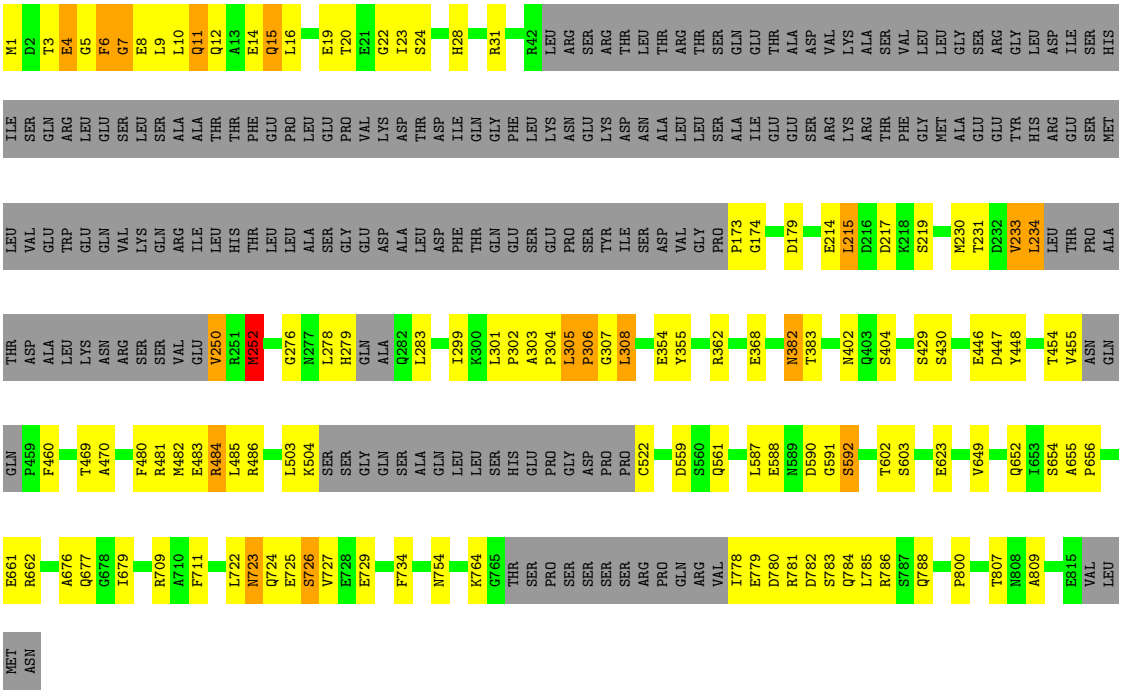
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 4-I:



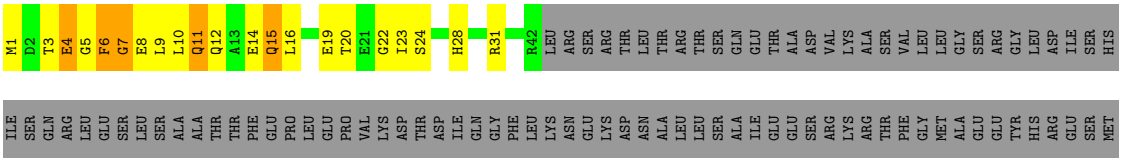
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

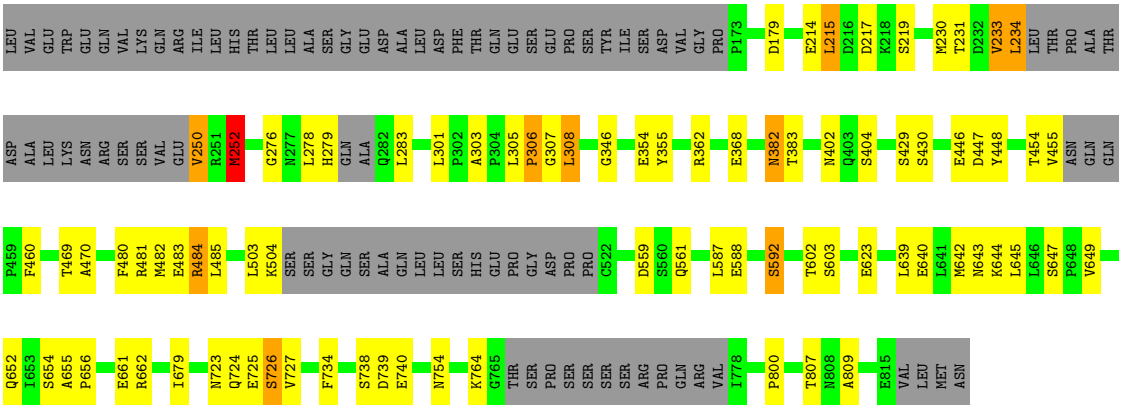
Chain 4-O:



- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

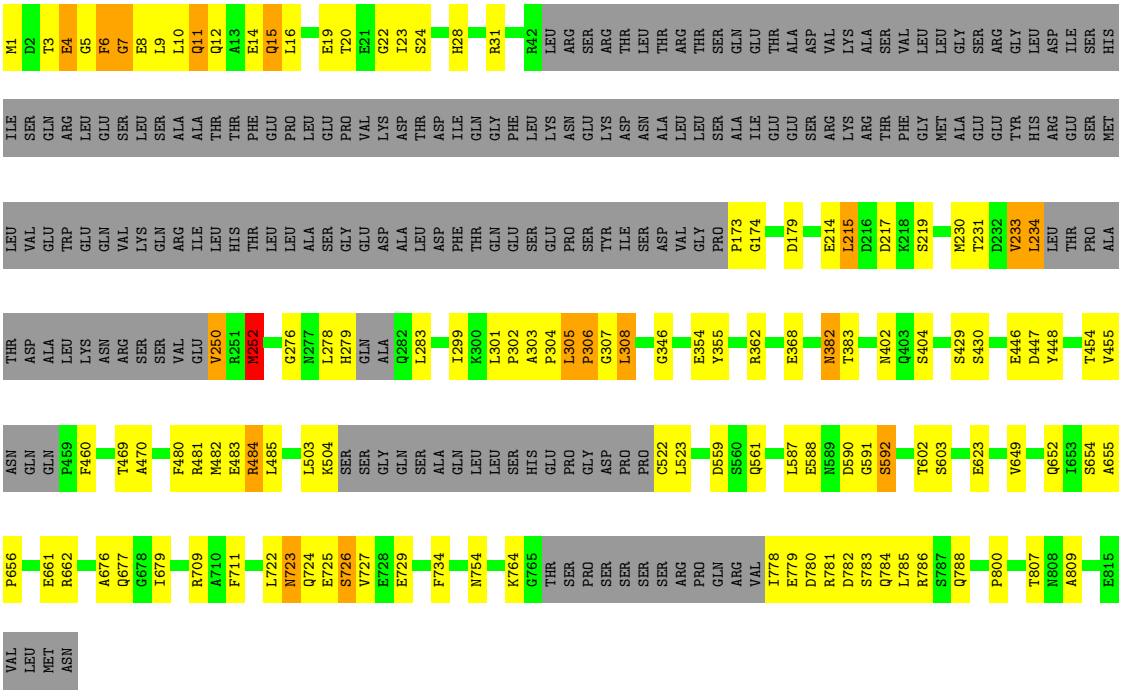
Chain 4-U:





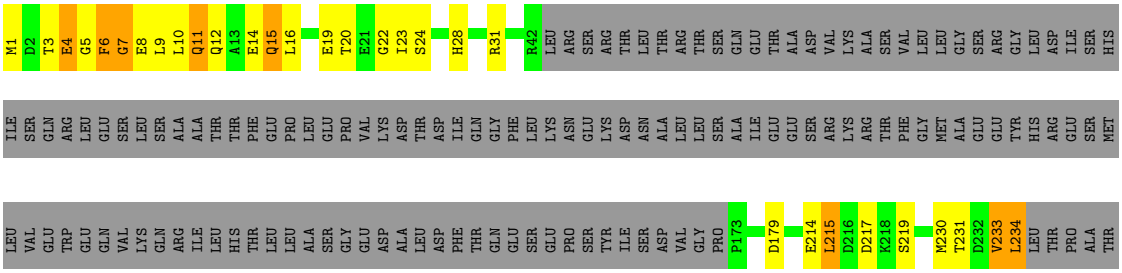
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

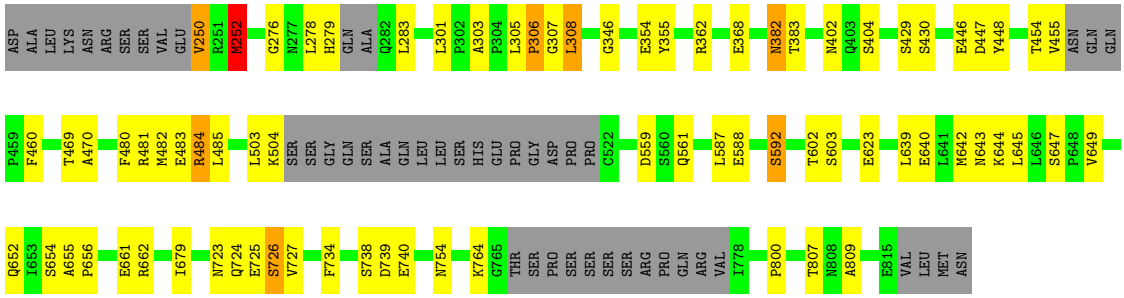
Chain 5-C:



• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

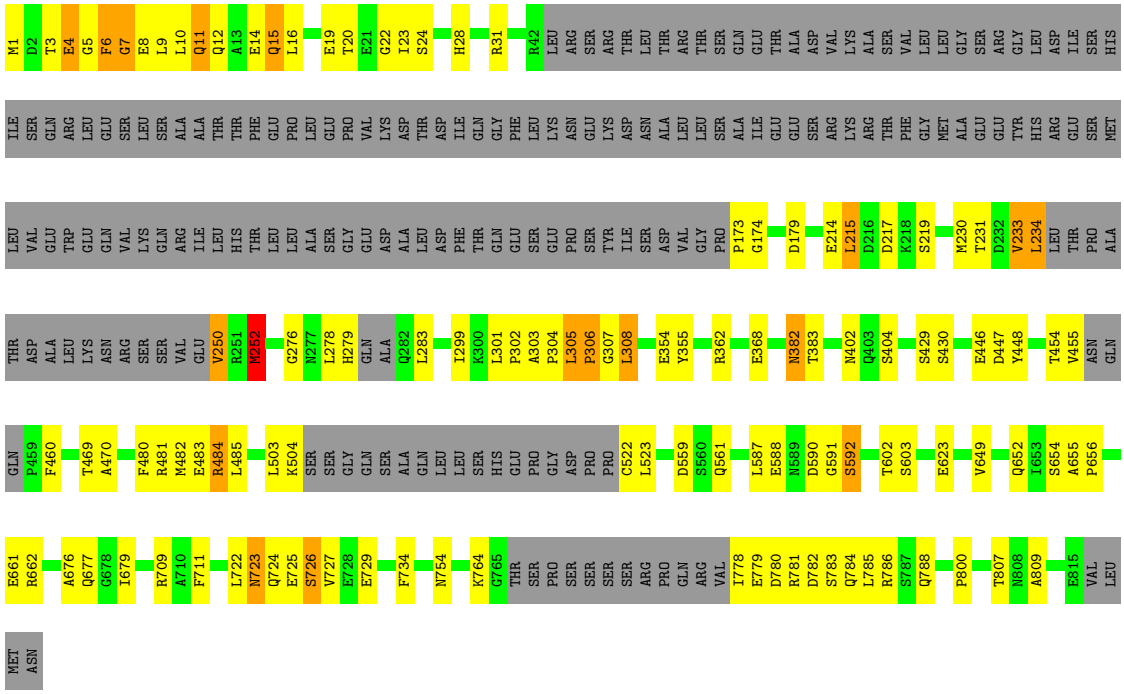
Chain 5-I:





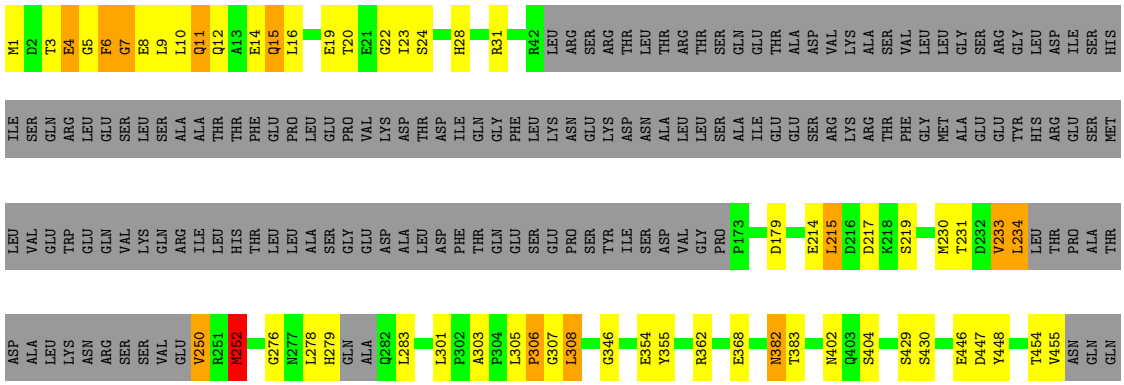
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

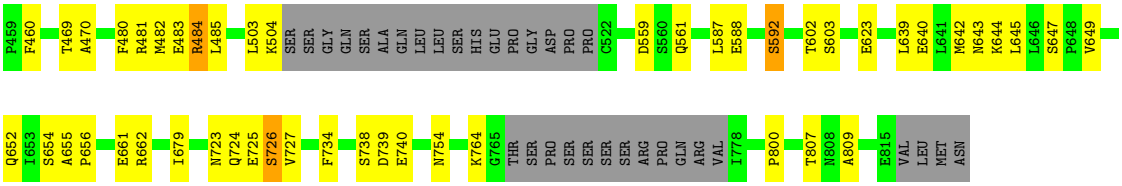
Chain 5-O:



- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

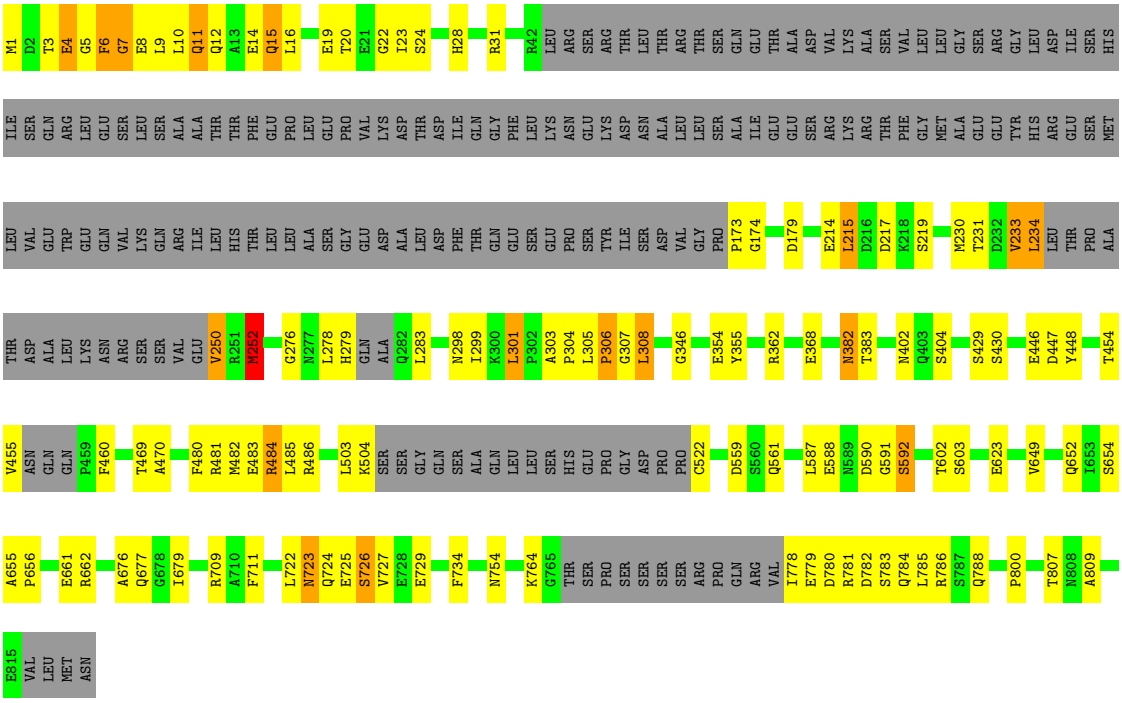
Chain 5-U:





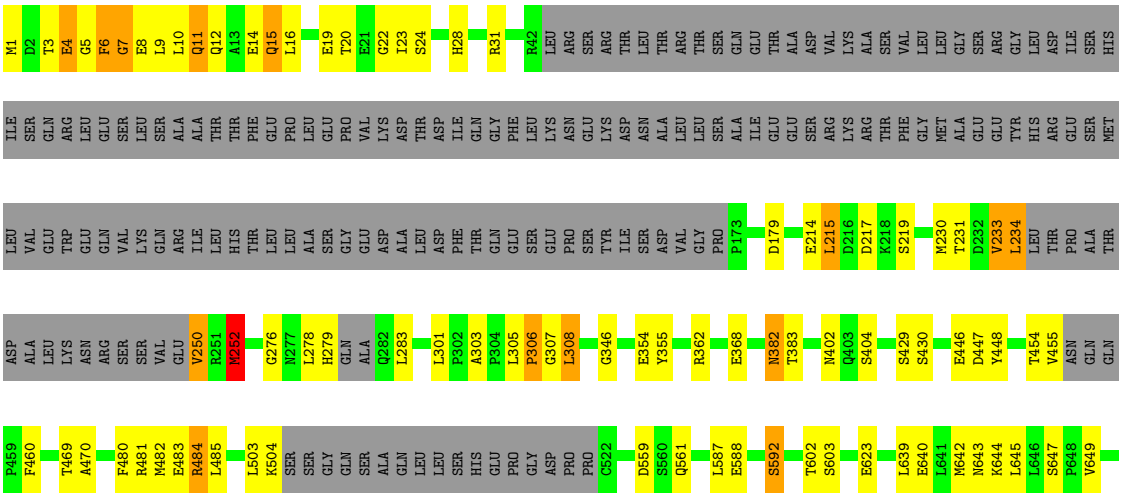
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

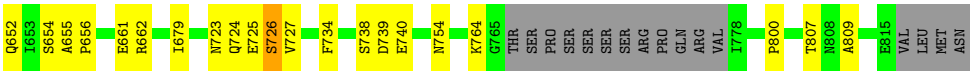
Chain 6-C: 63% 13% • 22%



• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

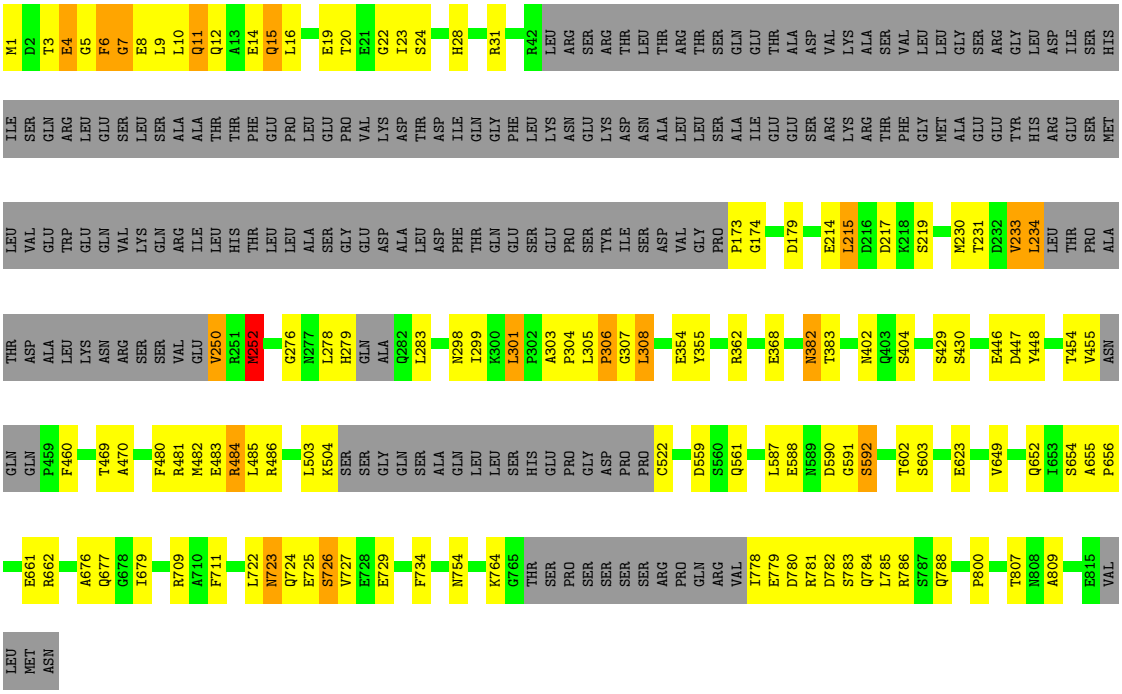
Chain 6-I: 65% 11% • 22%





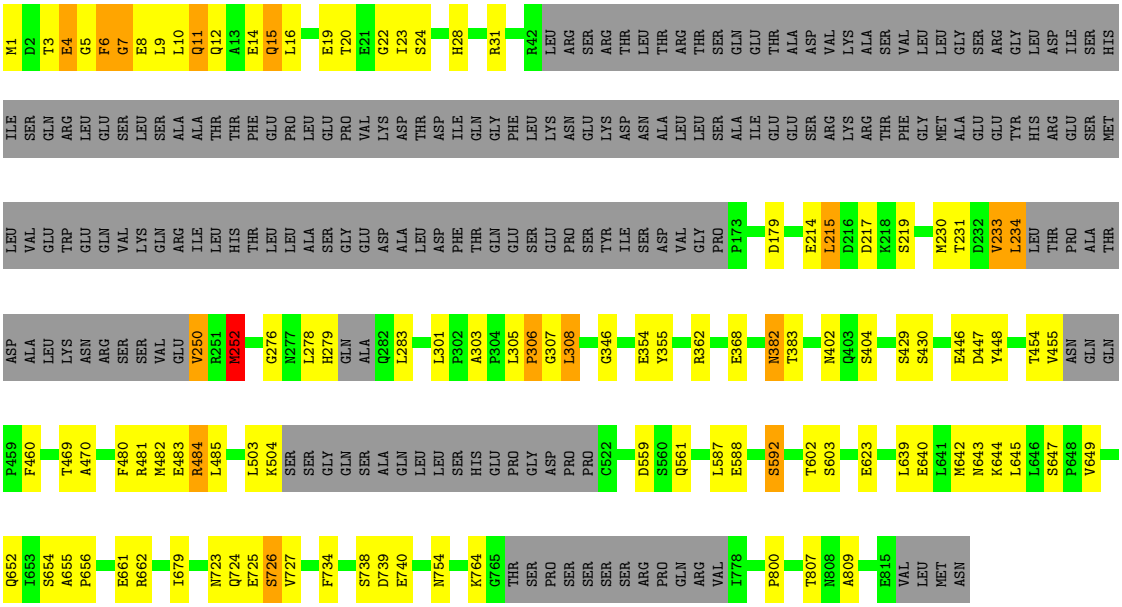
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 6-O:



• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 6-U:



• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 7-C: 63% 13% • 22%

M1 D2 T3 E4 G5 F6 G7 E8 L9 L10 Q11 Q12 A13 E14 Q15 L16 E19 T20 E21 G22 I23 S24 H28 R31 R42 LEU ARG SER ARG THR LEU THR ARG THR SER GLN GLU THR ALA ASP VAL LYS ALA SER VAL LEU LEU GLY SER ARG GLY LEU ASP ILE SER HIS

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

LEU VAL GLU TRP GLU GLN VAL LYS GLN ARG ILE LEU HIS THR LEU LEU ALA SER GLY GLU ASP ALA LEU ASP PHE THR GLN GLU SER GLU PRO SER TYR ILE SER ASP VAL GLY PRO P173 G174 D179 E214 L215 D216 D217 K218 S219 M230 T231 D232 V233 L234 LEU THR PRO ALA

THR ASP ALA LEU LYS ASN ARG SER SER VAL GLU V250 R251 M252 G276 N277 L278 H279 GLN ALA Q282 L283 N298 I299 K300 L301 P302 A303 P304 L305 P306 G307 L308 G346 E354 Y355 R362 E368 N382 T383 N402 Q403 S404 S429 S430 E446 D447 Y448 T454

V455 ASN GLN GLN P459 F460 T469 A470 F480 R481 M482 E483 R484 L485 L503 K504 SER SER GLY GLN SER ALA GLN LEU LEU SER HIS GLU PRO GLY ASP PRO PRO C522 L523 D559 S560 Q561 L587 E588 N589 D590 G591 S592 T602 S603 E623 V649 Q652 I653 S654

A655 P656 E661 R662 A676 Q677 G678 I679 R709 A710 F711 L722 N723 Q724 E725 S726 V727 E728 E729 F734 N754 K764 G765 THR SER PRO SER SER SER SER ARG PRO GLN ARG VAL I778 E779 D780 R781 D782 S783 Q784 L785 R786 S787 Q788 P800 T807 N808 A809

E815 VAL LEU MET ASN

• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 7-I: 65% 11% • 22%

M1 D2 T3 E4 G5 F6 G7 E8 L9 L10 Q11 Q12 A13 E14 Q15 L16 E19 T20 E21 G22 I23 S24 H28 R31 R42 LEU ARG SER ARG THR LEU THR ARG THR SER GLN GLU THR ALA ASP VAL LYS ALA SER VAL LEU LEU GLY SER ARG GLY LEU ASP ILE SER HIS

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

LEU VAL GLU TRP GLU GLN VAL LYS GLN ARG ILE LEU HIS THR LEU LEU ALA SER GLY GLU ASP ALA LEU ASP PHE THR GLN GLU SER GLU PRO SER TYR ILE SER ASP VAL GLY PRO P173 D179 E214 L215 D216 D217 K218 S219 M230 T231 D232 V233 L234 LEU THR PRO ALA THR

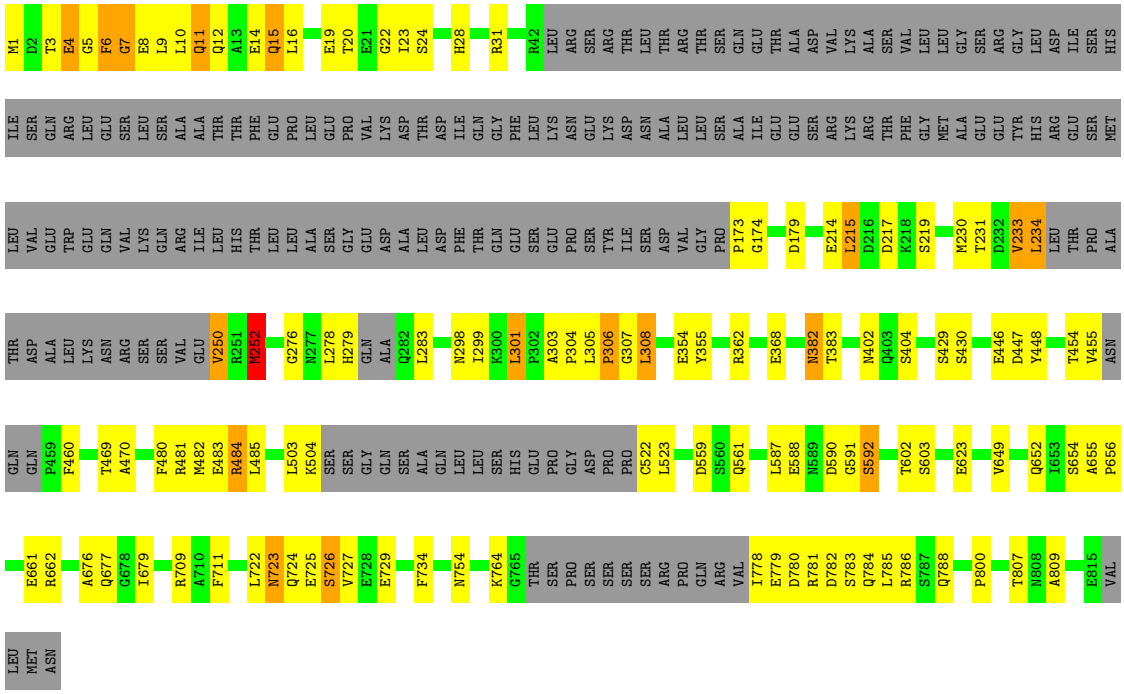
ASP ALA LEU LYS ASN ARG SER SER VAL GLU V250 R251 M252 G276 N277 L278 H279 GLN ALA Q282 L283 L301 P302 A303 P304 L305 P306 G307 L308 G346 E354 Y355 R362 E368 N382 T383 N402 Q403 S404 S429 S430 E446 D447 Y448 T454 V455 ASN GLN GLN

P459 F460 T469 A470 F480 R481 M482 E483 R484 L485 L503 K504 SER SER GLY GLN SER ALA GLN LEU LEU SER HIS GLU PRO PRO GLY ASP PRO PRO C522 D559 S560 Q561 L587 E588 S592 T602 S603 E623 L639 E640 L641 M642 N643 K644 L645 L646 S647 F648 V649

Q652 I653 S654 A655 P656 E661 R662 I679 N723 Q724 E725 S726 V727 F734 S738 D739 E740 N754 K764 G765 THR SER PRO SER SER SER SER ARG PRO GLN ARG VAL I778 P800 T807 N808 A809 E815 VAL LEU MET ASN

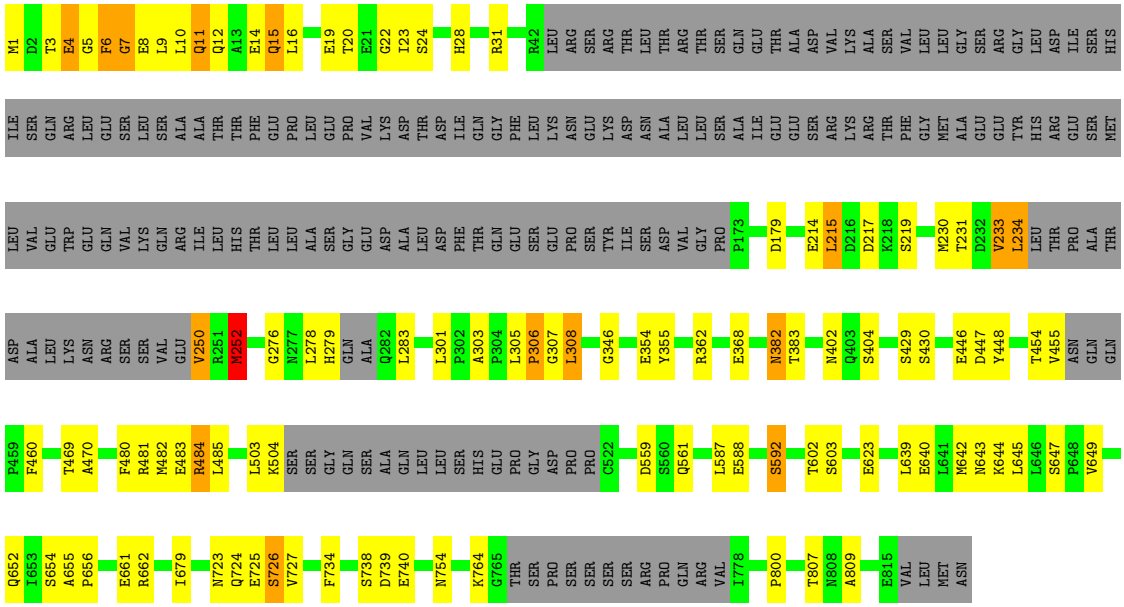
• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 7-O: 63% 12% • 22%



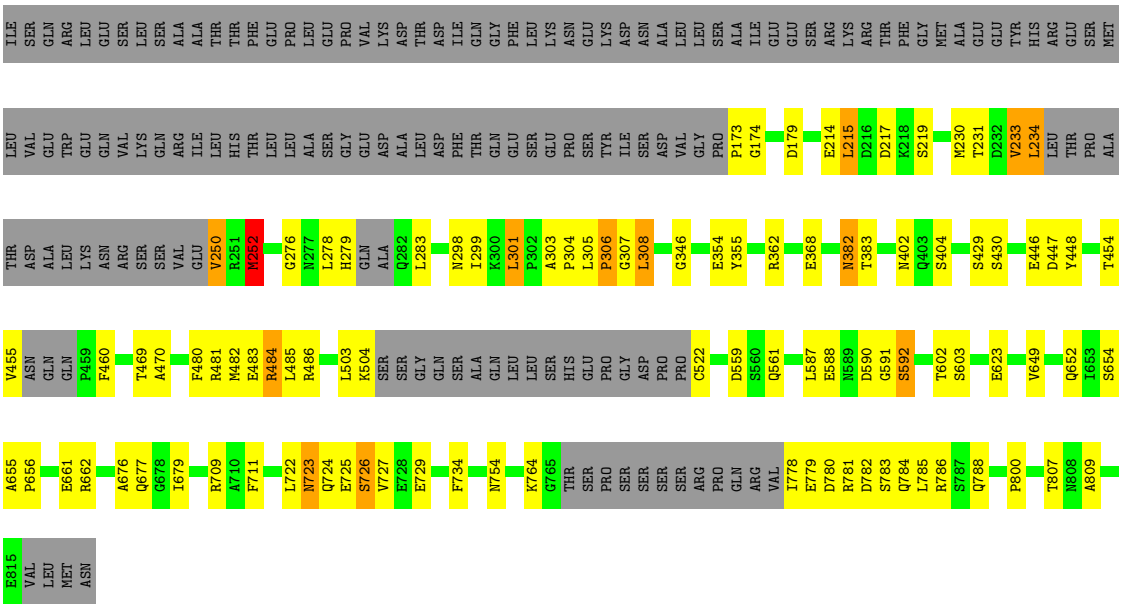
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 7-U:



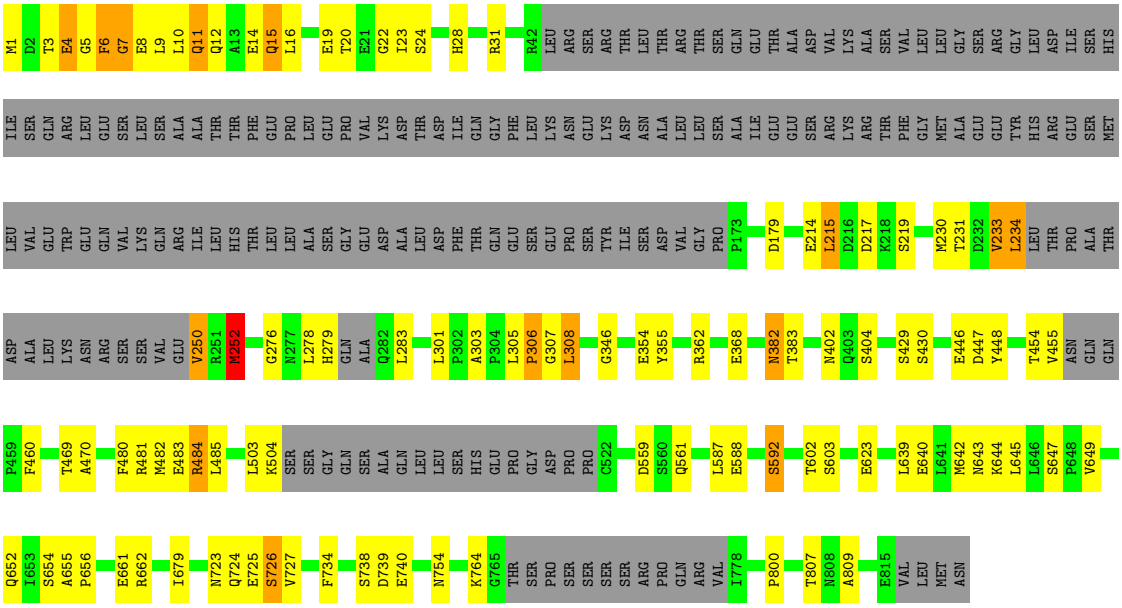
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

Chain 8-C:



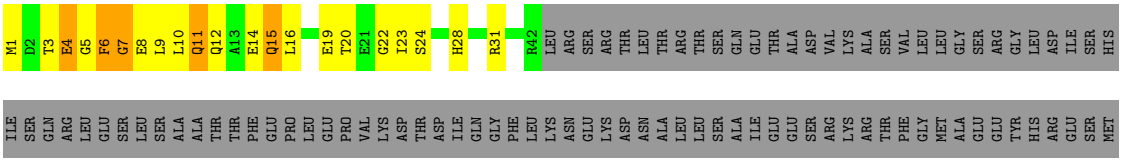
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

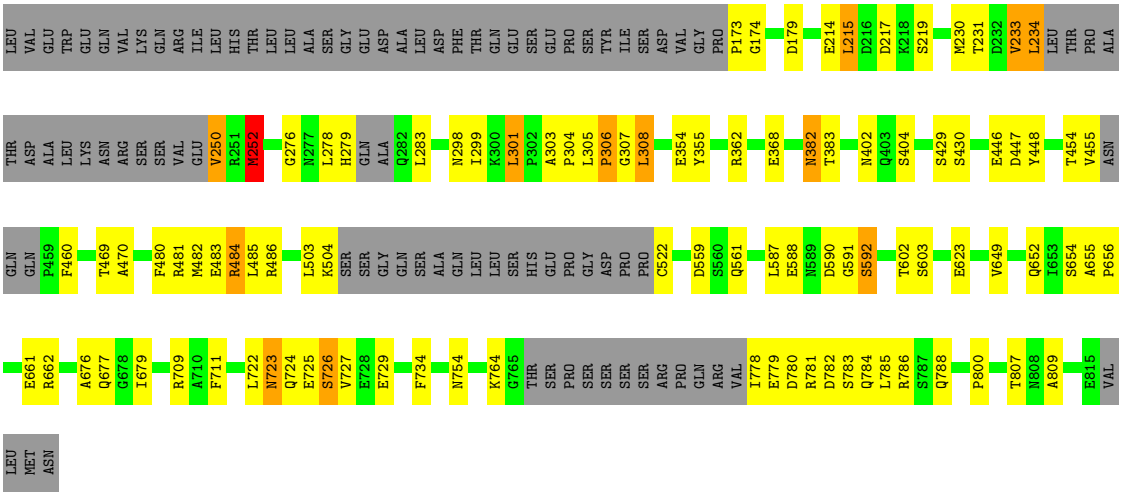
Chain 8-I:



- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

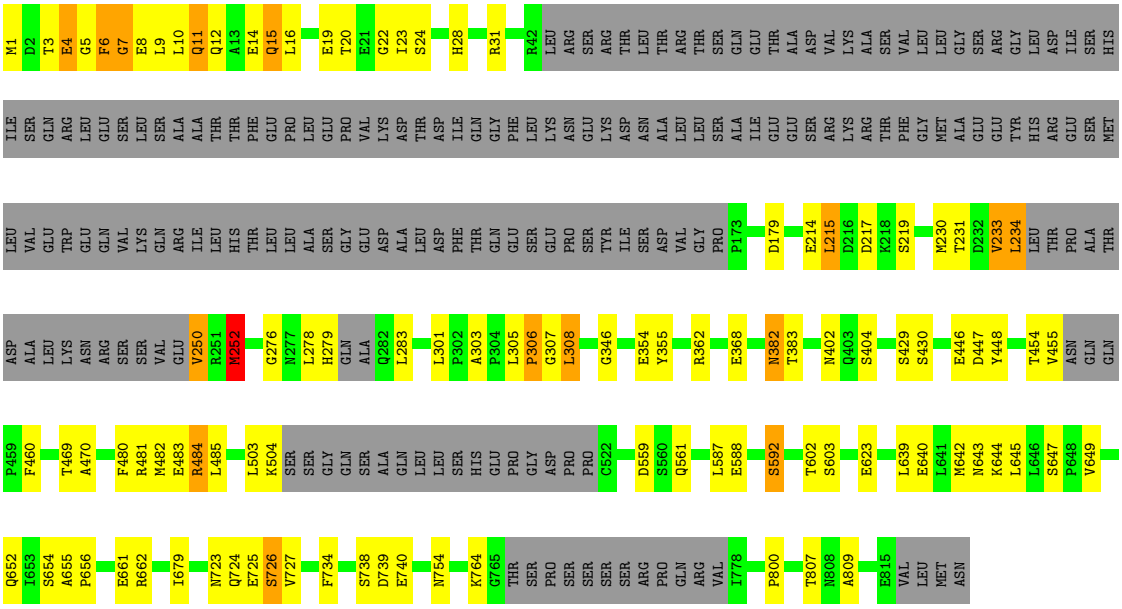
Chain 8-O:





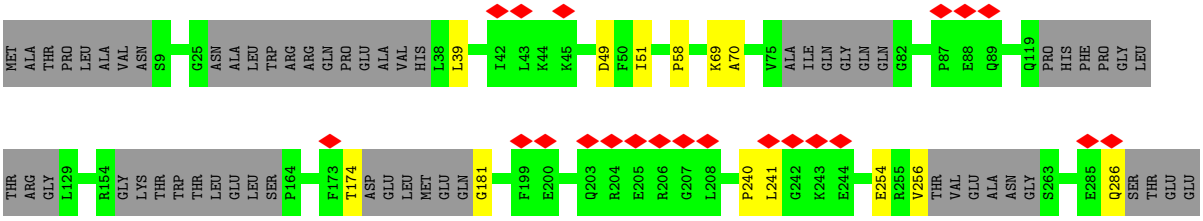
- Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP93

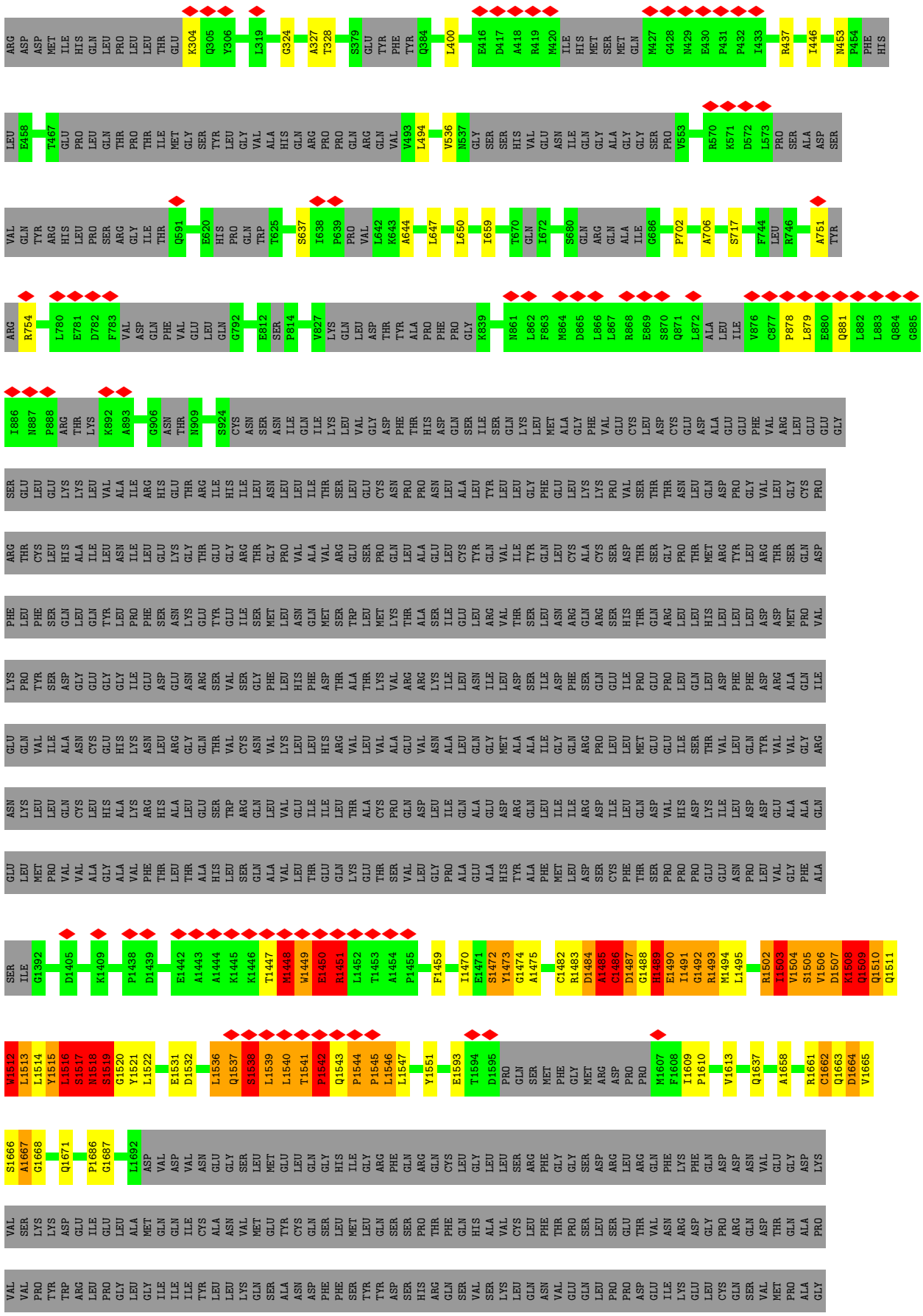
Chain 8-U:

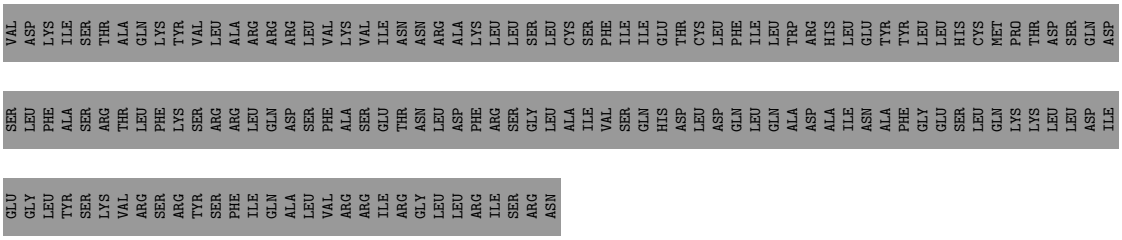


- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 1-D:

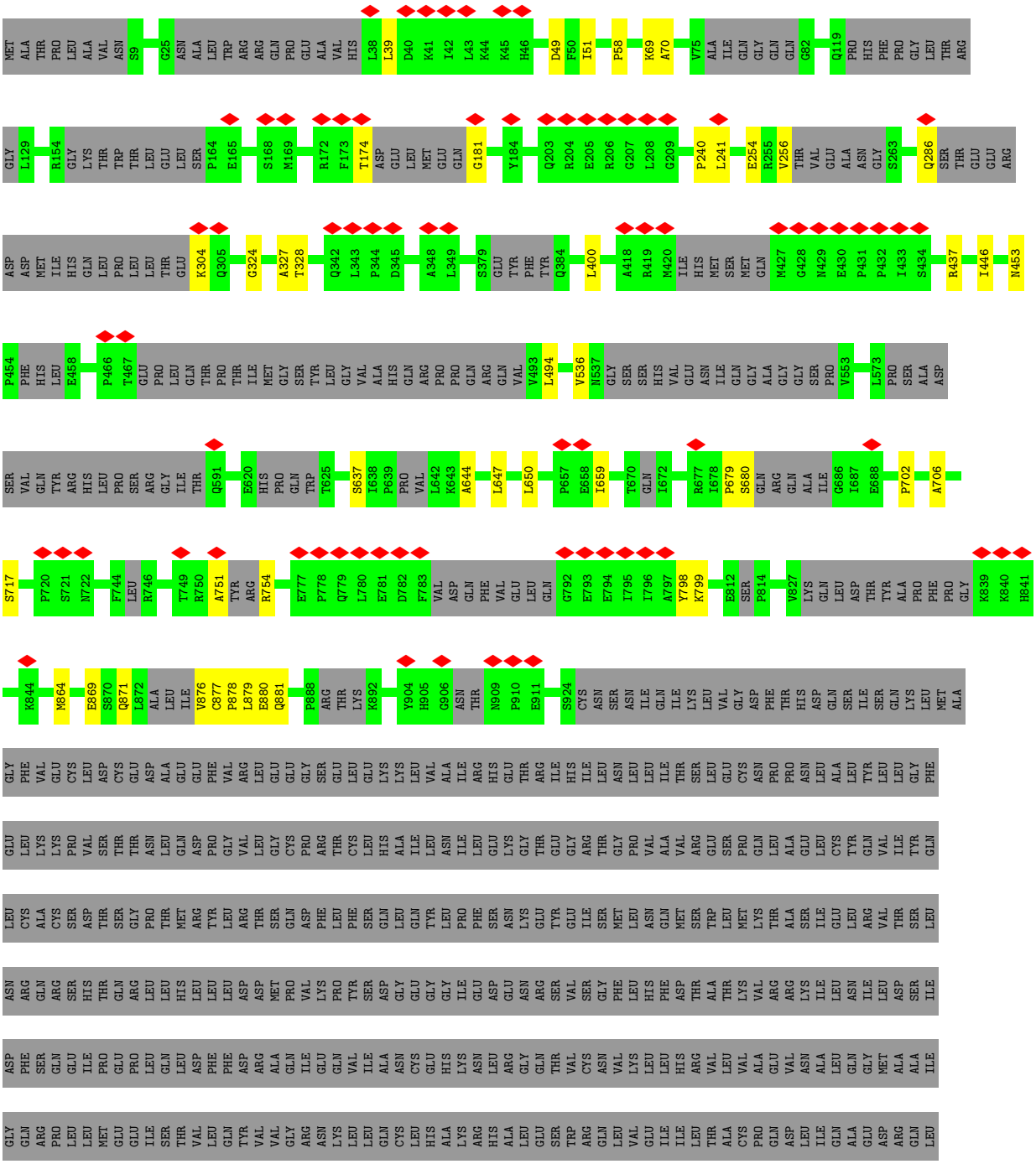


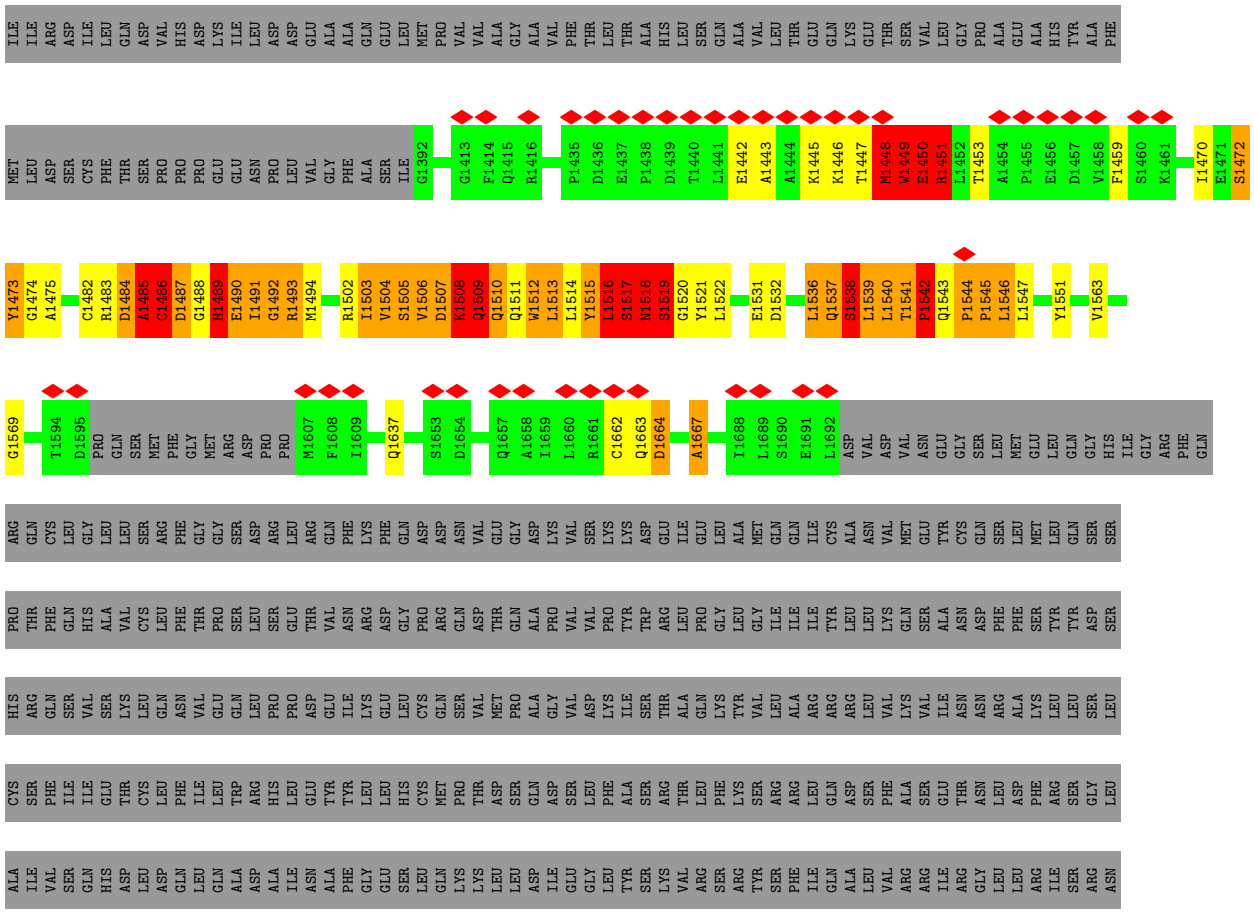

ARG ASP ASP MET ILE HIS GLN LEU PRO LEU LEU THR GLU K304 Q305 Y306 L319 G324 A327 T328 S379 GLU TYR PHE TYR Q384 L400 E416 D417 A418 R419 M420 ILE HIS MET SER MET GLN M427 G428 N429 E430 P431 P432 I433 R437 I446 N453 P454 PHE HIS
LEU E458 T467 GLU PRO LEU GLN THR PRO THR ILE MET GLY SER TYR LEU GLY VAL ALA HIS GLN ARG PRO PRO GLN ARG GLN VAL V493 L494 V536 N537 GLY SER SER HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 R570 K571 D572 L573 PRO SER ALA ASP SER
VAL GLN TYR ARG HIS LEU PRO SER ARG GLY ILE THR Q591 E620 HIS PRO GLN TRP T625 S637 I638 P639 PRO VAL L642 K643 A644 L647 L650 I659 T670 GLN I672 S680 GLN ARG GLN ALA ILE G686 P702 A706 S717 F744 LEU R746 A751 TYR
ARG R754 L780 E781 D782 F783 VAL ASP GLN PHE VAL GLU LEU GLN G792 E812 SER P814 V827 LYS GLN LEU ASP THR TYR ALA PRO PHE PRO GLY K839 N861 L862 F863 M864 D865 L866 L867 R868 E869 S870 Q871 L872 ALA LEU ILE V876 C877 P878 L879 E880 Q881 L882 L883 Q884 G885
I886 N887 P888 ARG THR LYS K892 A893 G906 ASN THR N909 S924 CYS ASN SER ASN ILE GLN ILE LYS LEU VAL GLY ASP PHE THR HIS ASP GLN SER ILE SER GLN LYS LEU MET ALA GLY PHE VAL GLU CYS LEU ASP CYS GLU ASP ALA GLU GLU PHE VAL ARG LEU GLU GLU GLY
SER GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE LEU ASN LEU LEU ILE ILE THR SER LEU GLU CYS ASN PRO PRO ASN LEU ALA LEU TYR LEU LEU GLY PHE GLU LEU LYS LYS PRO VAL SER THR THR ASN LEU GLN ASP PRO GLY VAL LEU GLY CYS PRO
ARG THR CYS LEU HIS ALA ILE LEU ASN ILE LEU GLU LYS GLY THR GLU GLY ARG THR GLY PRO VAL ALA VAL ARG GLU SER PRO GLN LEU ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU CYS ALA CYS SER ASP THR SER GLY PRO THR MET ARG TYR LEU ARG THR SER GLN ASP
PHE LEU PHE SER GLN LEU GLN TYR LEU PRO PHE SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR ALA SER ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG SER HIS THR GLN ARG LEU LEU HIS LEU LEU LEU LEU ASP ASP MET PRO VAL
LYS PRO TYR SER ASP GLY GLU GLY GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS VAL ARG ARG LYS ILE LEU ASN ILE LEU ASP SER ILE ASP PHE SER GLN GLU ILE PRO GLU PRO LEU GLN GLU ASP ARG ALA GLN ILE
GLU GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU LEU LEU HIS ARG VAL LEU VAL VAL ALA GLU VAL ASN ASN ALA LEU GLN GLY MET ALA ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU ILE SER THR VAL LEU GLN TYR VAL VAL GLY ARG
ASN LYS LEU LEU GLN CYS LEU HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ARG GLN LEU VAL GLU ILE ILE LEU THR ALA CYS PRO GLN ASP LEU ILE ALA GLU ALA GLN LEU ILE ILE ARG ASP ILE LEU GLN ASP VAL HIS ASP LYS ILE GLN ALA ALA GLN
GLU LEU MET PRO VAL VAL ALA GLY ALA VAL PHE THR LEU THR ALA HIS LEU SER GLN ALA VAL LEU THR GLU GLN LYS GLU THR SER VAL LEU GLY VAL ALA GLU ALA ALA HIS TYR ALA PHE MET LEU ASP SER CYS PHE THR SER PRO PRO LEU PRO GLU GLU GLU ASN PRO LEU VAL PHE ALA
SER ILE G1392 D1405 K1409 P1438 D1439 E1442 A1443 A1444 K1445 K1446 T1447 M1448 W1449 E1450 R1451 L1452 T1453 A1454 P1455 F1459 I1470 E1471 S1472 Y1473 G1474 A1475 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511
W1512 L1513 L1514 Y1515 L1516 S1517 N1518 S1519 G1520 Y1521 L1522 E1531 D1532 L1536 Q1537 S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 Y1551 E1593 T1594 D1595 PRO GLN SER MET PHE GLY MET ARG ASP PRO PRO M1607 F1608 I1609 P1610 V1613 Q1637 A1658 R1661 C1662 Q1663 D1664 V1665
S1666 A1667 G1668 Q1671 P1686 G1687 L1692 ASP VAL ASP VAL ASN GLU GLY SER LEU MET GLU LEU GLN GLY HIS ILE GLY ARG PHE GLN ARG GLN CYS LEU GLY LEU LEU SER ARG PHE GLY GLY SER ASP ARG LEU ARG GLN PHE LYS PHE GLY ASP ASN VAL GLU GLY ASP LYS
VAL SER LYS LYS ASP GLU ILE GLU LEU ALA MET GLN GLN ILE CYS ALA ASN VAL MET GLU TYR CYS GLN SER LEU MET LEU GLN SER SER PRO THR PHE GLN HIS ALA VAL CYS LEU PHE THR GLY PRO SER LEU LEU SER GLU THR VAL ARG GLN ASP THR GLN ALA PRO
VAL VAL PRO TYR TRP ARG LEU PRO GLY LEU GLY ILE ILE ILE TYR LEU LEU LYS GLN SER ALA ASN ASP PHE PHE SER TYR TYR ASP SER HIS ARG GLN SER VAL SER LYS LEU GLN ASN VAL GLU GLN LEU PRO PRO ASP GLU ILE LYS GLU LEU CYS GLN SER VAL MET PRO ALA GLY



• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

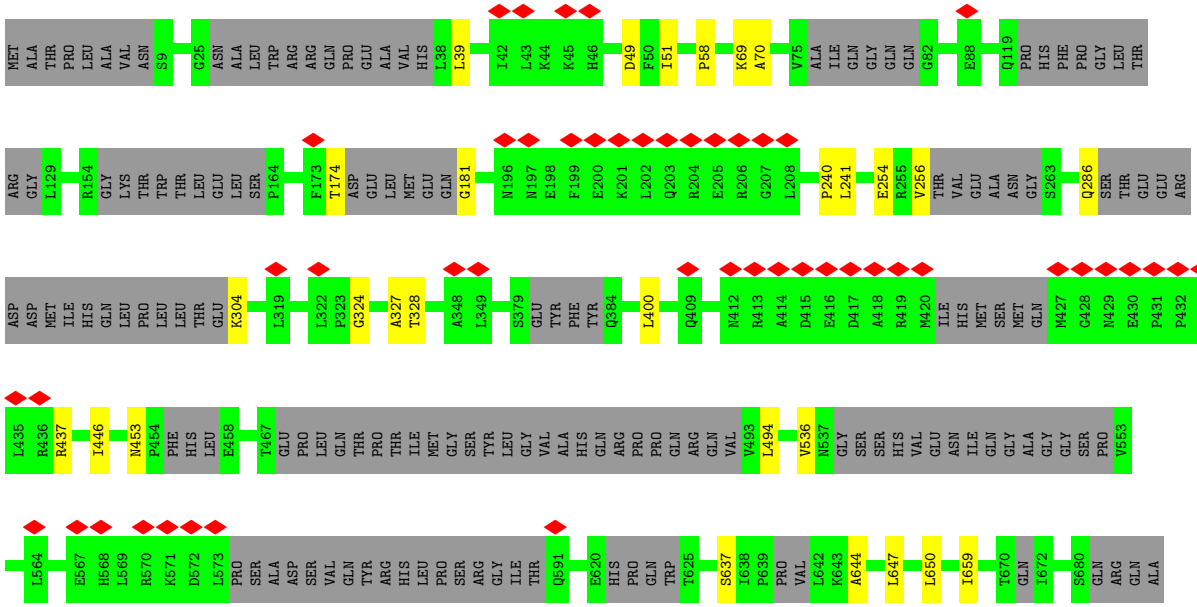
Chain 1-J:

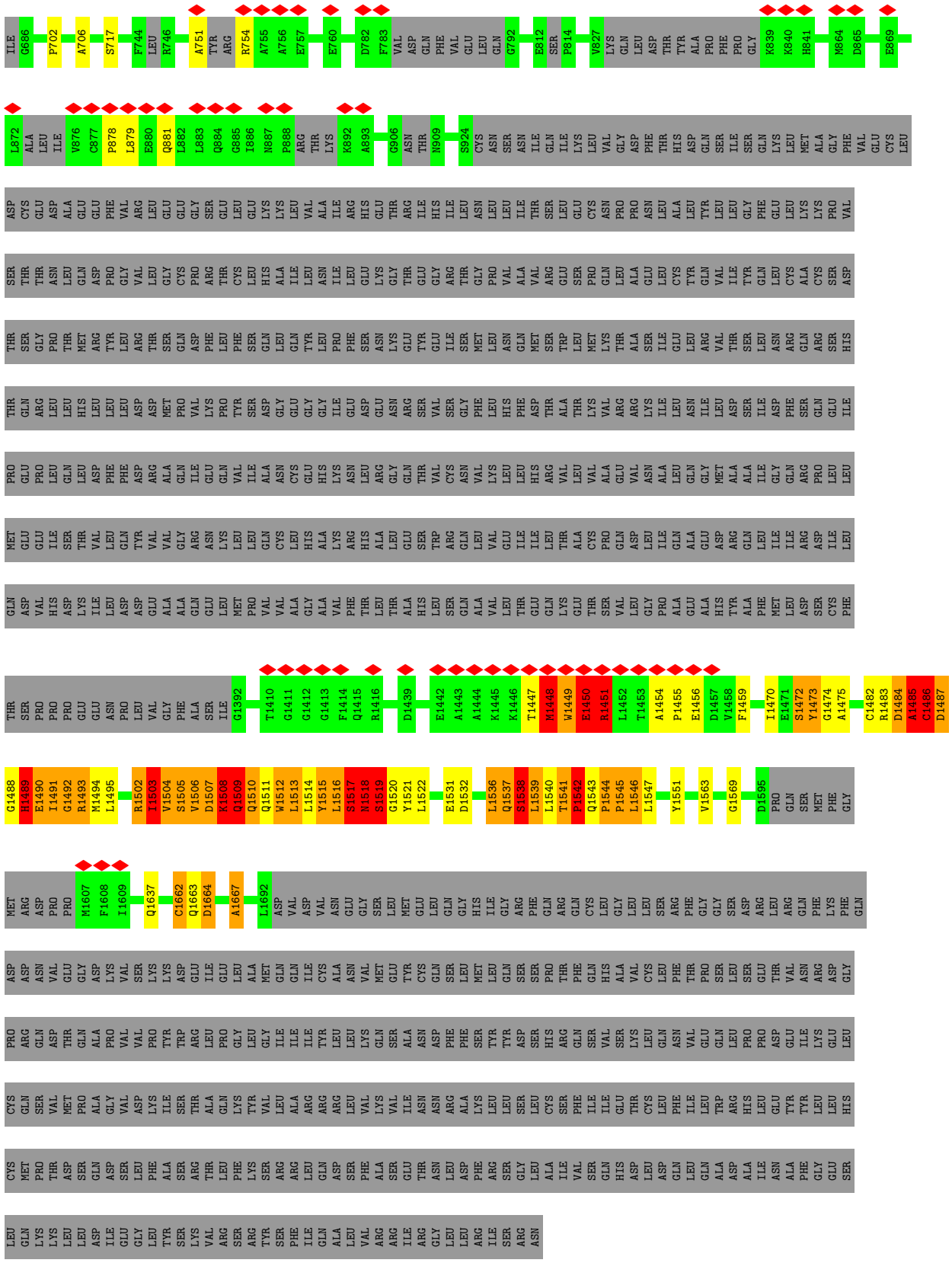




• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 1-P:

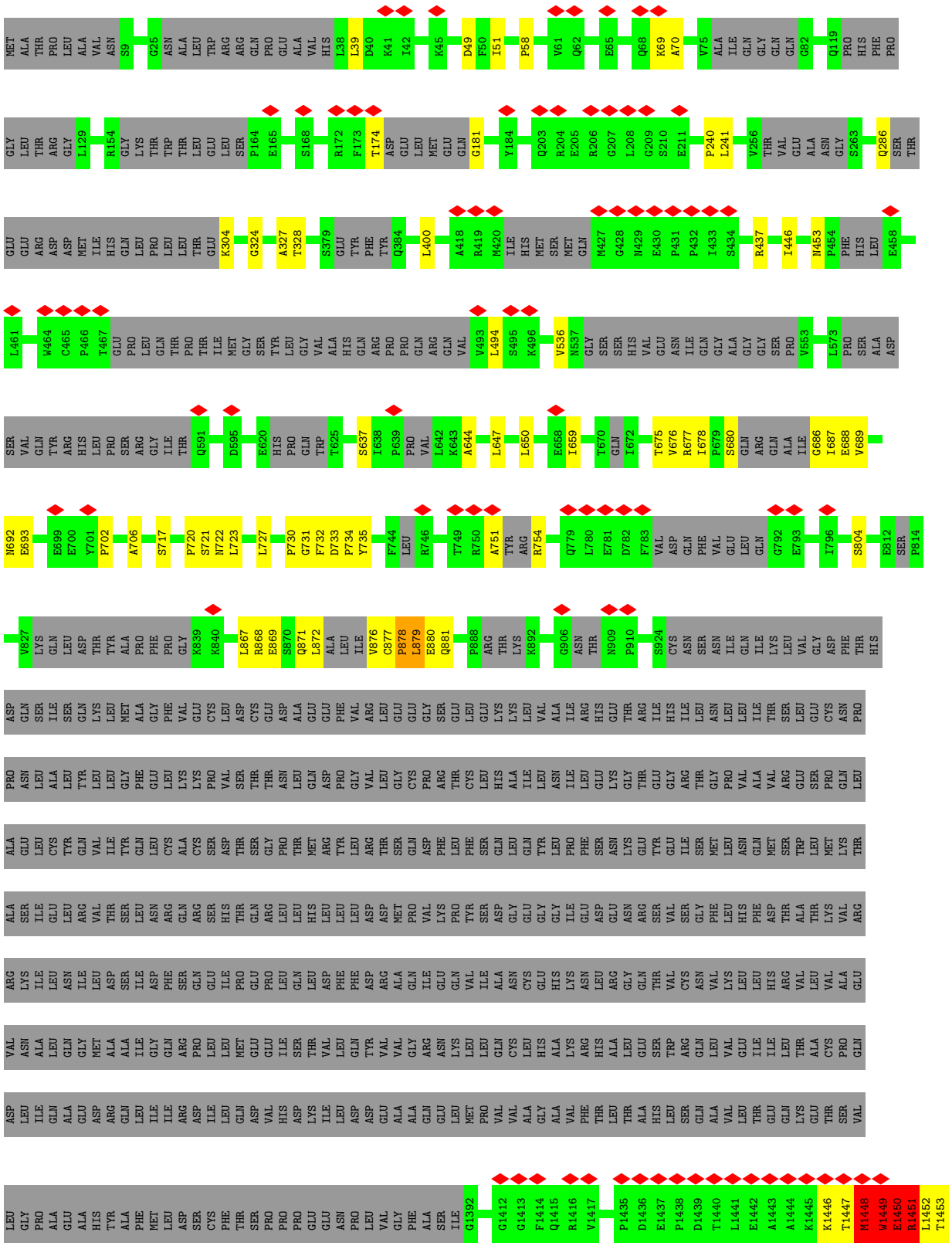


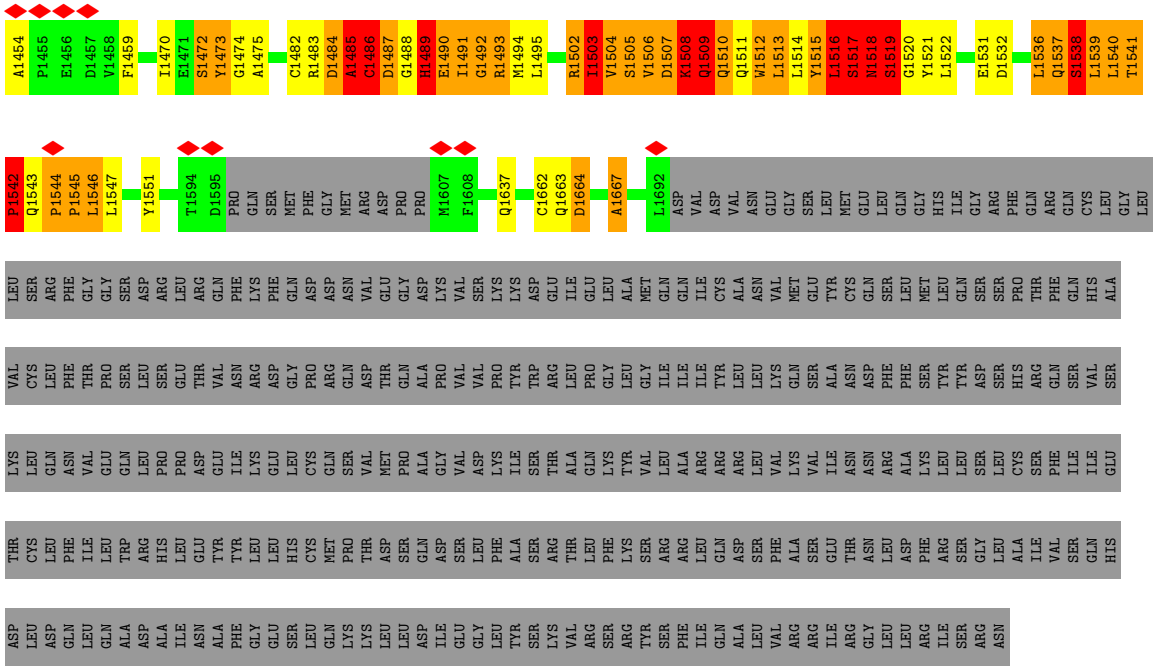


- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 1-V:

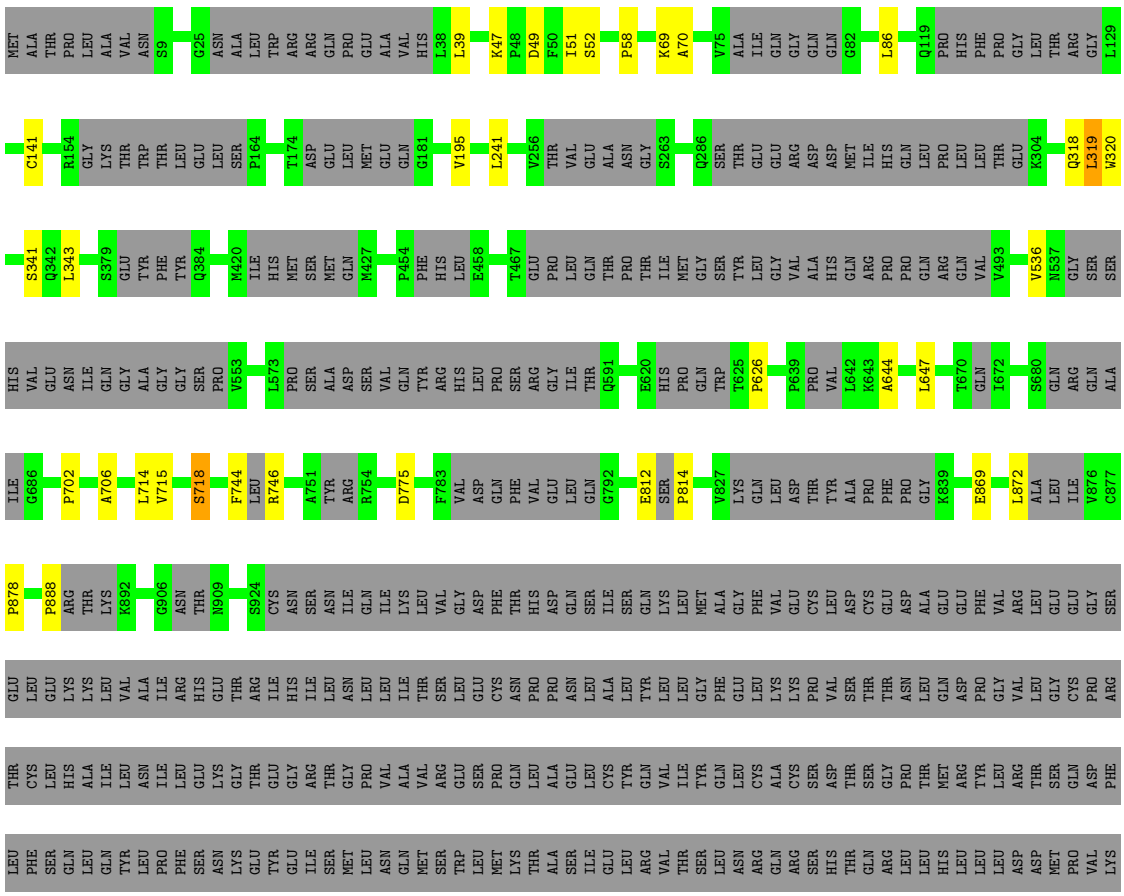
5%
44%
49%

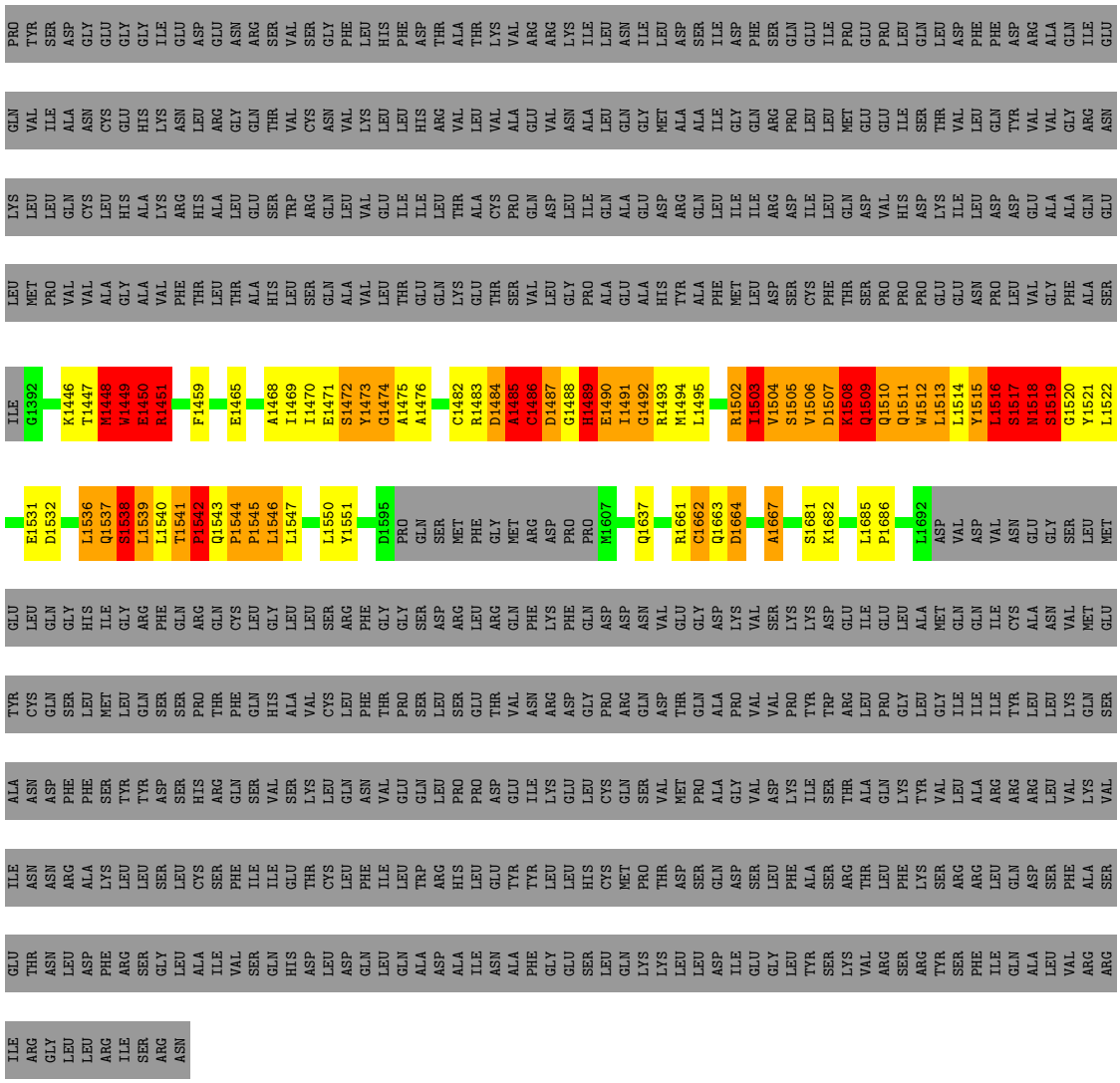

MET ALA THR PRO LEU ALA VAL ASN S9 G25 ASN ALA LEU TRP ARG ARG GLN PRO GLU ALA VAL HIS L38 L39 D40 K41 I42 K45 D49 F50 I51 P58 V61 Q62 E65 Q68 K69 A70 V75 ALA ILE GLN GLY GLN GLN G82 Q119 PRO HIS PHE PRO
GLY LEU THR ARG GLY L129 R154 GLY LYS THR TRP THR LEU GLU LEU SER P164 E165 S168 R172 F173 T174 ASP GLU LEU MET GLU GLN G181 Y184 Q203 R204 E205 R206 G207 L208 G209 S210 E211 P240 L241 V256 THR VAL GLU ALA ASN GLY S263 Q286 SER THR
GLU GLU ARG ASP ASP MET ILE HIS GLN LEU PRO LEU LEU THR GLU K304 G324 A327 T328 S379 GLU TYR PHE TYR Q384 L400 A418 R419 M420 ILE HIS MET SER MET GLN M427 G428 N429 E430 P431 P432 I433 S434 R437 I446 N453 P454 PHE HIS LEU E458
L461 W464 C465 P466 T467 GLU PRO LEU GLN THR PRO THR ILE MET GLY SER TYR LEU GLY VAL ALA HIS GLN ARG PRO PRO GLN ARG GLN VAL V493 L494 S495 K496 V536 N537 GLY SER SER HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 L573 PRO SER ALA ASP
SER VAL GLN TYR ARG HIS LEU PRO SER ARG GLY ILE THR Q591 D595 E620 HIS PRO GLN TRP T625 S637 I638 P639 PRO VAL L642 K643 A644 L647 L650 E658 I659 T670 GLN I672 T675 V676 R677 I678 P679 S680 GLN ARG GLN ALA ILE G686 I687 E688 V689
N692 E693 E699 E700 Y701 P702 A706 S717 P720 S721 N722 L723 L727 P730 G731 F732 D733 P734 Y735 F744 LEU R746 T749 R750 A751 TYR ARG R754 Q779 L780 E781 D782 F783 VAL ASP GLN PHE VAL GLU LEU GLN G792 E793 I796 S804 E812 SER P814
V827 LYS GLN LEU ASP THR TYR ALA PRO PHE PRO GLY K839 K840 L867 R868 E869 S870 Q871 L872 ALA LEU ILE V876 C877 P878 L879 E880 Q881 P888 ARG THR LYS K892 G906 ASN THR N909 P910 S924 CYS ASN SER ASN ILE GLN ILE LYS LEU VAL GLY ASP PHE THR HIS
ASP GLN SER ILE SER GLN LYS LYS LEU MET ALA GLY PHE VAL GLU CYS LEU ASP CYS GLU ASP ALA GLU GLU PHE VAL ARG LEU GLU GLU GLY SER GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE LEU ASN LEU LEU ILE THR SER LEU GLU GLU CYS ASN PRO
PRO ASN LEU ALA LEU TYR LEU LEU LEU GLY PHE GLU GLU LEU LYS LYS PRO VAL SER SER THR THR ASN LEU GLN ASP PRO GLY VAL LEU GLY CYS PRO ARG THR CYS LEU HIS ALA ILE LEU ASN ILE LEU GLU LYS GLY THR GLU GLU GLY ARG THR GLY PRO VAL ALA VAL ARG GLU SER PRO GLN LEU
ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU CYS ALA CYS SER ASP THR SER GLY PRO THR MET ARG TYR LEU ARG THR SER GLN ASP PHE LEU PHE SER GLN LEU GLN TYR LEU PRO PHE SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR
ALA SER ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG SER HIS THR GLN ARG LEU LEU HIS LEU LEU LEU LEU ASP ASP MET PRO VAL LYS PRO TYR SER SER ASP GLY GLU GLY GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS LYS VAL ARG
ARG LYS ILE LEU ASN ILE LEU ASP SER ILE ASP PHE SER GLN GLU ILE PRO GLU PRO LEU GLN LEU ASP PHE PHE ASP ARG ALA GLN ILE GLU GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU GLU ILE HIS ARG VAL LEU THR ALA LYS VAL ALA GLU
VAL ASN ALA LEU GLN GLY MET ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU ILE SER THR VAL LEU GLN TYR VAL VAL GLY ARG ASN LYS LEU LEU GLN CYS LEU HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ARG GLN LEU VAL LEU GLU ILE ILE LEU THR ALA CYS PRO GLN
ASP LEU ILE GLN ALA GLU ASP ARG GLN ILE ILE ILE ARG ASP ILE LEU GLN ASP VAL HIS ASP LYS ILE LEU ASP ASP ARG GLU GLU LEU MET PRO VAL VAL ALA GLY ALA VAL PHE THR LEU THR ALA HIS LEU SER GLN GLU ALA VAL LEU LEU THR GLU GLN GLN VAL THR SER
LEU GLY PRO ALA GLU ALA HIS TYR ALA PHE MET LEU ASP SER CYS PHE THR SER PRO PRO PRO GLU GLU ASN PRO LEU VAL GLY PHE ALA SER ILE G1392 G1412 G1413 F1414 Q1415 R1416 V1417 P1435 D1436 E1437 P1438 D1439 T1440 L1441 E1442 A1443 A1444 K1445 K1446 T1447 M1448 W1449 E1450 R1451 L1452 T1453



• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

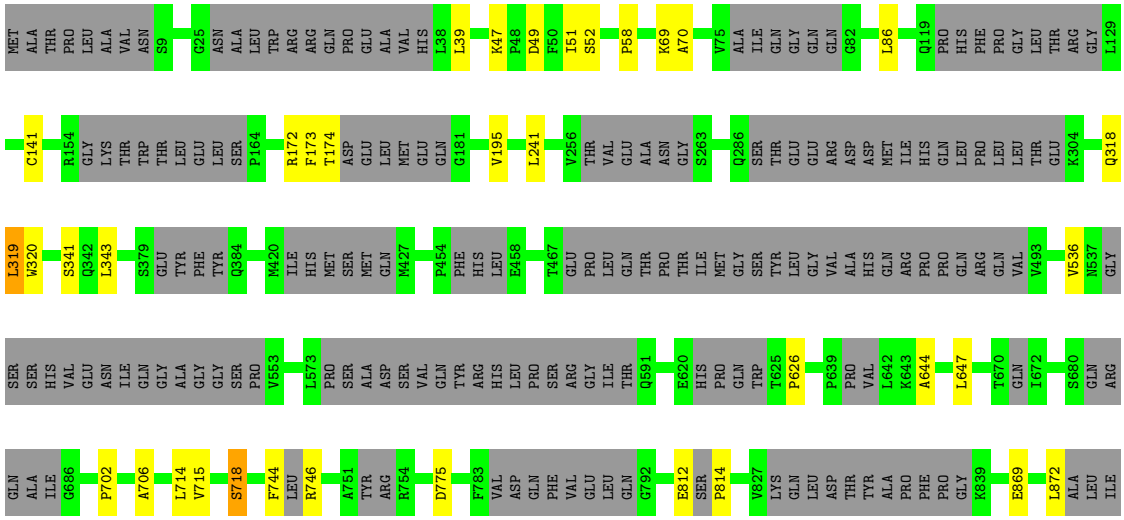
Chain 2-D: 45% 49%

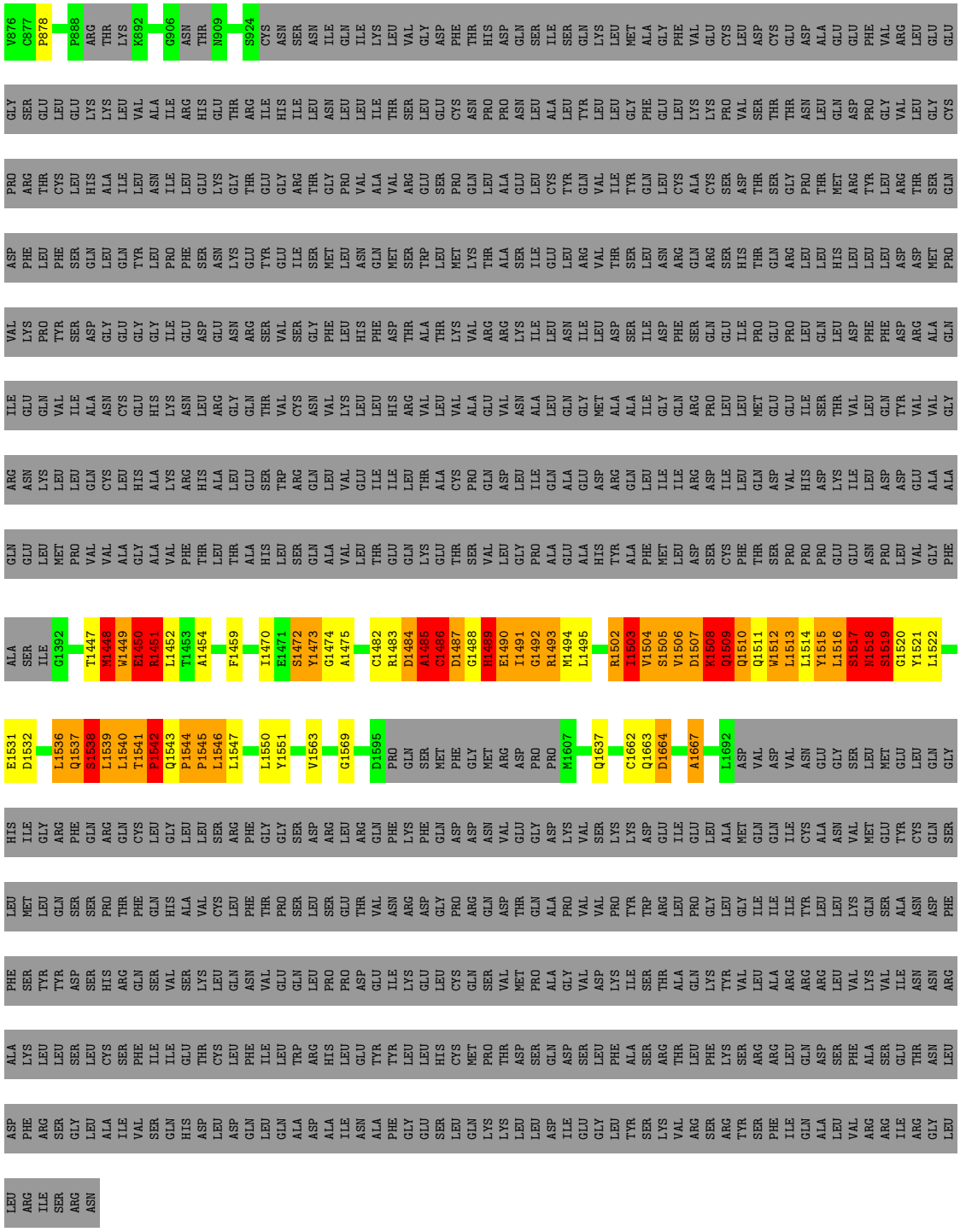




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 2-J:

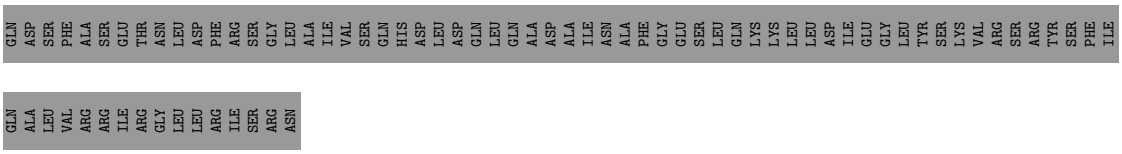




• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

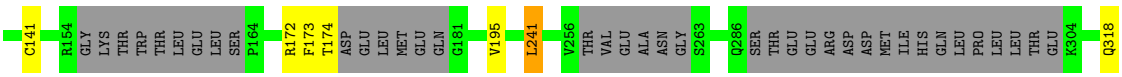
Chain 2-P:

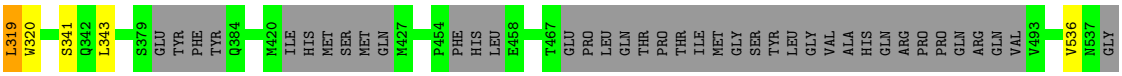
C141 R154 P164 T174 G181 V195 L241 V256 S263 Q286 K304 Q318 L319 W320
S341 Q342 L343 S379 Q384 M420 M427 P454 E458 T467 V493 V536 N537
HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 L573 PRO SER ALA ASP SER VAL GLN TYR ARG HIS LEU PRO SER ARG GLY ILE THR Q591 E620 HIS PRO GLN TRP T625 P626 P639 PRO VAL L642 K643 A644 L647 T670 GLN I672 S680 GLN ARG GLN ALA
ILE G686 P702 A706 L714 V715 S718 F744 LEU R746 A751 TYR ARG R754 D775 F783 VAL ASP GLN PHE VAL GLU LEU GLN G792 E812 SER P814 V827 LYS GLN LEU ASP THR TYR ALA PRO PHE PRO GLY K839 E869 L872 ALA LEU ILE V876 C877
P878 L879 E880 L883 Q884 N887 P888 ARG THR LYS K892 G906 ASN THR N909 S924 CYS ASN SER ASN ILE GLN ILE LYS LEU VAL GLY ASP PHE THR HIS ASP GLN SER ILE SER GLN LYS LEU MET ALA GLY PHE VAL GLU CYS LEU ASP CYS GLU ASP ALA GLU GLU PHE PHE VAL
ARG LEU GLU GLU GLY SER GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE ILE LEU ASN LEU LEU ILE THR SER LEU GLU GLU CYS ASN PRO ASN LEU ALA LEU TYR LEU LEU GLY PHE GLU LEU LYS LYS PRO VAL SER THR THR ASN LEU GLN LYS PRO GLY
VAL LEU GLY CYS PRO ARG THR CYS LEU HIS ALA ILE LEU ASN ILE LEU LEU CYS THR GLY THR GLY PRO VAL ALA VAL ARG GLU GLU SER PRO GLN LEU ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU LEU ASP THR SER GLY PRO GLN CYS SER ASP THR SER GLY PRO GLN LYS THR GLN LEU LEU
ARG THR SER GLN ASP PHE LEU PHE SER GLN LEU GLN TYR LEU PRO PHE SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR ALA SER ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG SER HIS THR GLN ARG LEU LEU HIS LEU LEU LEU
ASP ASP MET PRO VAL LYS PRO TYR SER ASP GLY GLU GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS VAL ARG ARG LYS ILE LEU ASN ILE LEU ASP PHE ILE PHE GLU GLN ILE GLY PHE PRO GLN PRO GLU LEU ASP PHE PRO GLN LEU LEU ASP PHE PHE
ASP ARG ALA GLN ILE GLU GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU LEU HIS ARG VAL LEU VAL ALA ALA ASN ALA LEU GLN GLU GLY MET ALA ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU GLU ILE SER THR VAL LEU GLN
TYR VAL VAL GLY ARG ASN LYS LEU LEU GLU CYS LEU HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ARG GLN LEU VAL GLU ILE LEU THR ALA CYS PRO GLN ASP LEU ILE GLN ALA GLU ASP ARG GLN LEU ILE ILE ARG ASP ILE LEU LEU GLN GLN ILE LEU HIS LYS ILE LEU ASP
ASP GLU ALA ALA GLN GLU LEU MET PRO VAL VAL ALA GLY HIS VAL LEU THR LYS GLU GLN LYS GLU THR SER GLN ALA VAL LEU GLY PRO ALA GLU ALA HIS TYR ALA PHE MET LEU ASP PRO SER VAL ALA ALA ILE GLY GLN GLU LEU ILE ARG PRO LEU LEU ASP SER CYS PHE THR GLN MET GLU GLU VAL PRO HIS ASP LYS ILE LEU ASN PRO
LEU VAL GLY PHE ALA SER ILE G1392 K1446 T1447 M1448 W1449 E1450 R1451 F1459 E1465 A1468 I1469 I1470 E1471 S1472 Y1473 G1474 A1475 A1476 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511 W1512 L1513 L1514 Y1515 L1516
S1517 N1518 S1519 G1520 Y1521 L1522 E1531 D1532 L1536 Q1537 S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 L1550 Y1551 D1595 PRO GLN SER MET PHE GLY MET ARG ASP PRO PRO M1607 Q1637 R1661 C1662 Q1663 D1664 A1667 S1681 K1682 L1685 P1686 L1692 ASP VAL ASP VAL
ASN GLU GLY SER LEU MET GLU LEU GLN GLY HIS ILE GLY ARG PHE GLY GLY GLY ASP ARG LEU ARG GLN PHE LYS PHE GLU ASP ASP ASN VAL GLU GLY ASP LYS VAL SER LYS LYS ASP ILE ARG ILE LEU ALA MET GLN GLN ILE
CYS ALA ASN VAL MET GLU TYR CYS GLN SER LEU MET LEU GLN SER SER PRO THR PHE GLN HIS ALA VAL CYS LEU PHE THR PRO SER LEU SER GLU THR VAL ASN ARG ASP GLY PRO ARG GLN ASP THR GLN ALA PRO VAL VAL PRO TYR TRP ARG LEU ILE ILE
TYR LEU LEU LYS GLN SER ALA ASN ASP PHE PHE SER TYR TYR PHE SER HIS ARG GLN GLN ASP VAL GLU GLN LEU PRO PRO ASP GLU ILE LYS GLU LEU CYS GLN SER VAL GLU LYS LYS LYS ILE LYS TYR VAL LEU ILE
ARG ARG LEU VAL LYS LYS ILE LEU LEU SER LEU CYS SER PHE ILE ILE GLU LEU LEU HIS CYS MET PRO THR ASP SER GLN ASP SER LEU PHE ALA SER ARG THR ARG LEU LEU ARG HIS LEU GLU TYR LEU LEU CYS LEU PHE ILE LEU TRP ARG ALA LYS LEU LEU SER LEU LEU LEU LEU

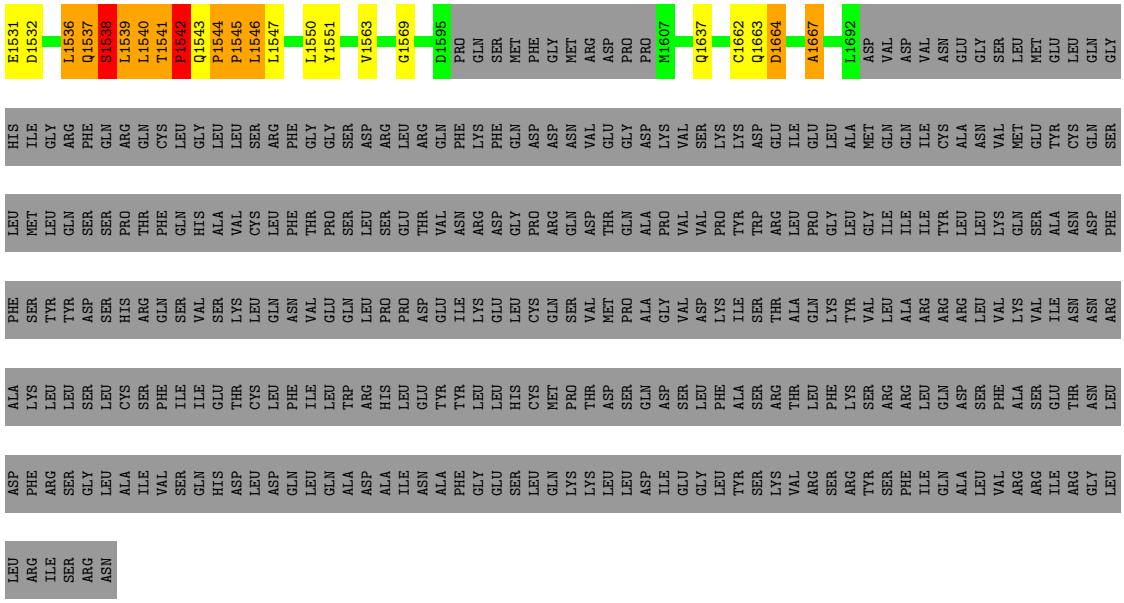


• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 2-V:

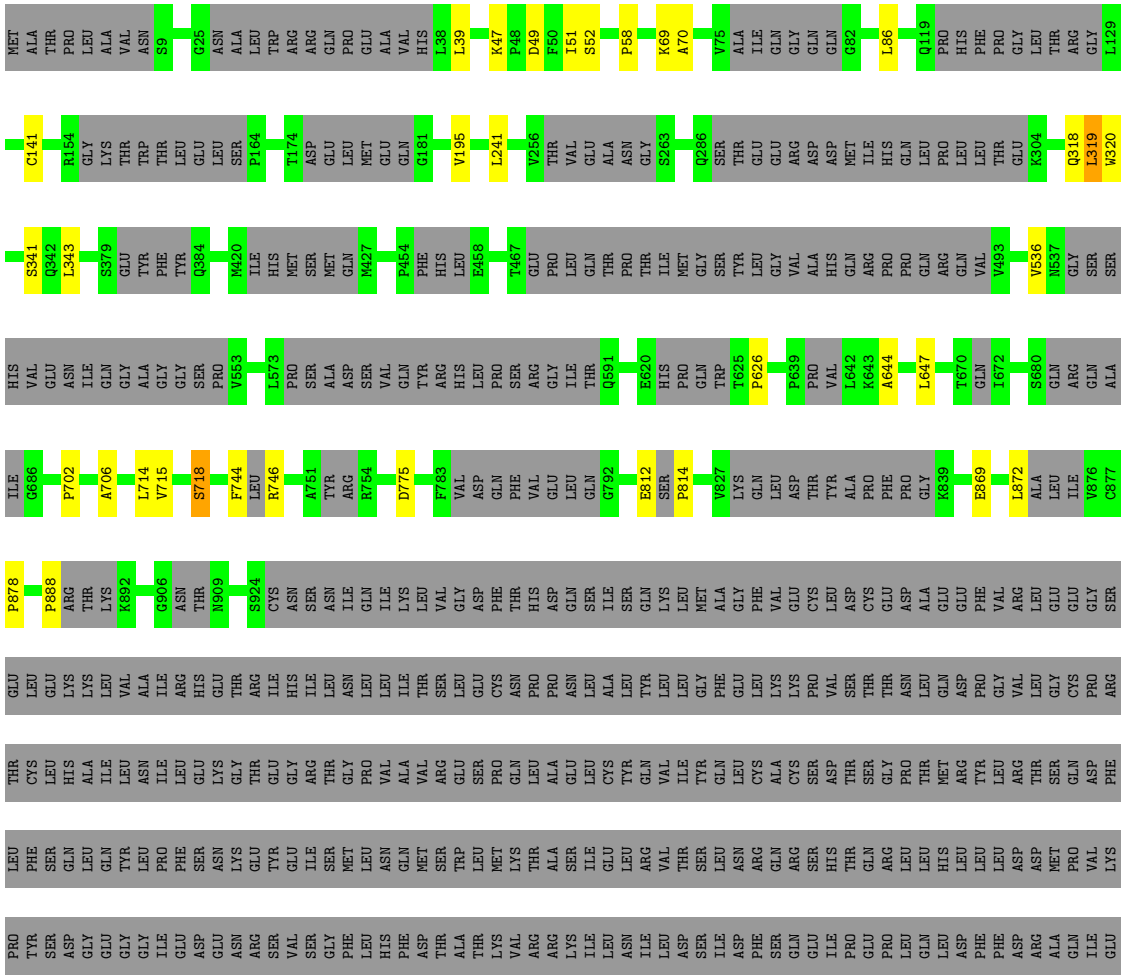


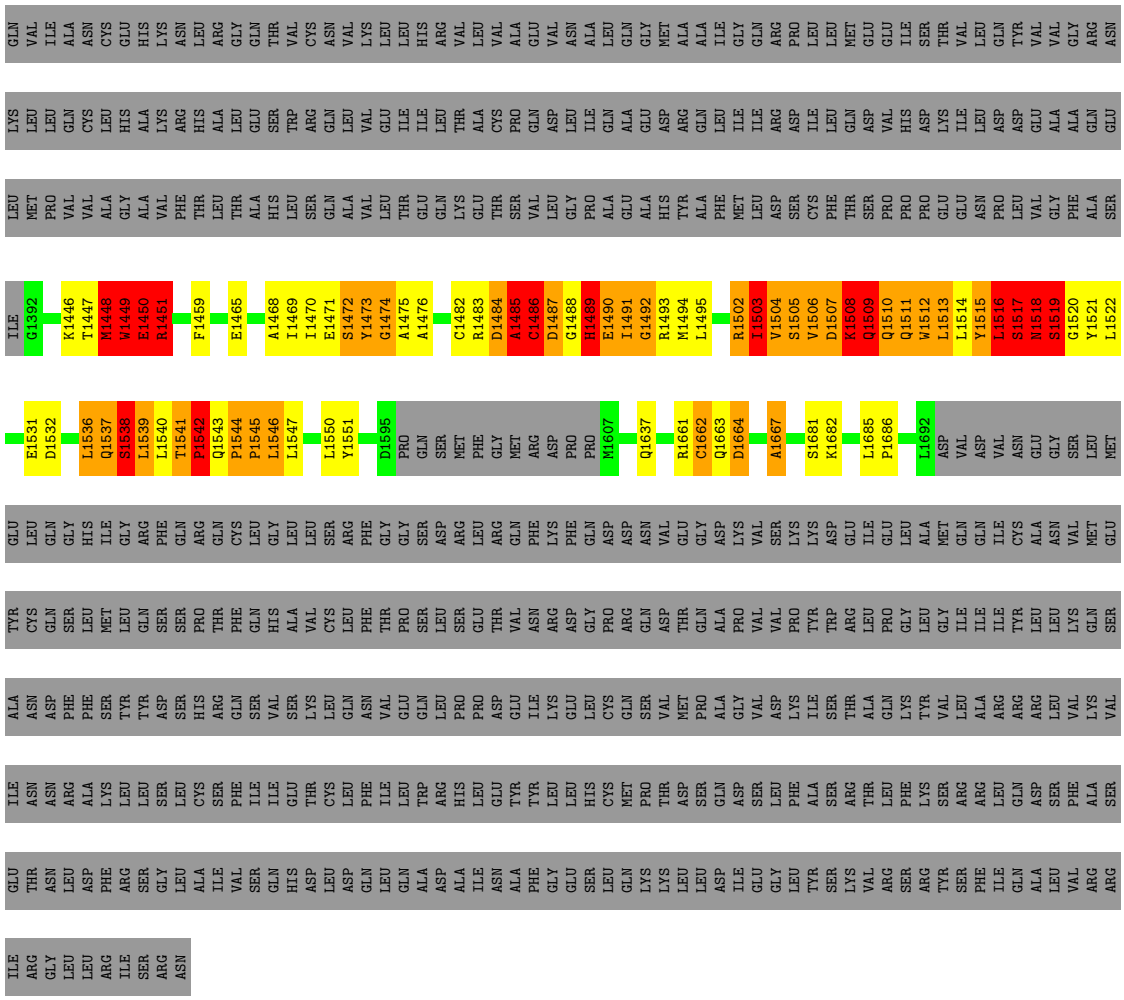




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

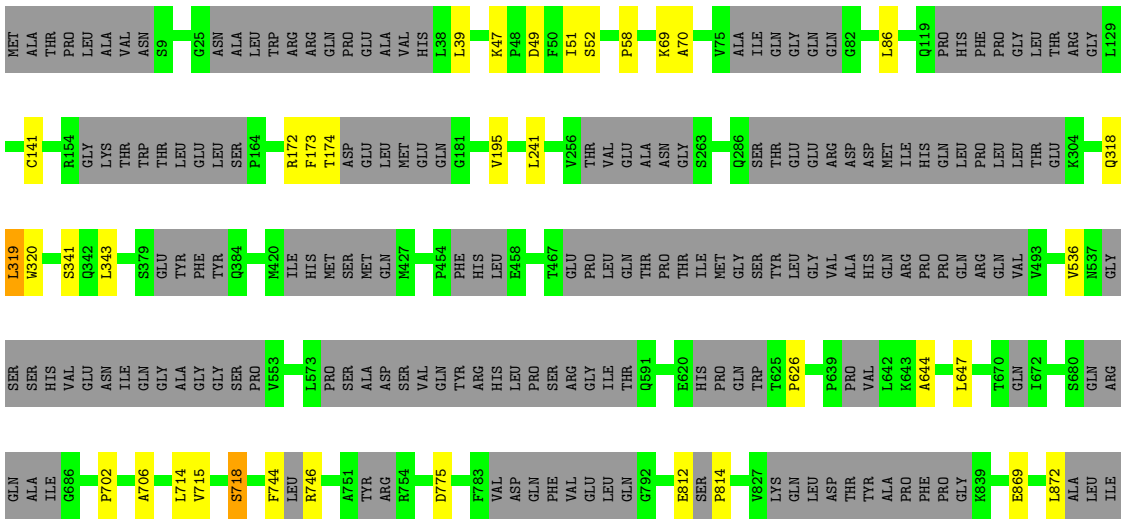
Chain 3-D:

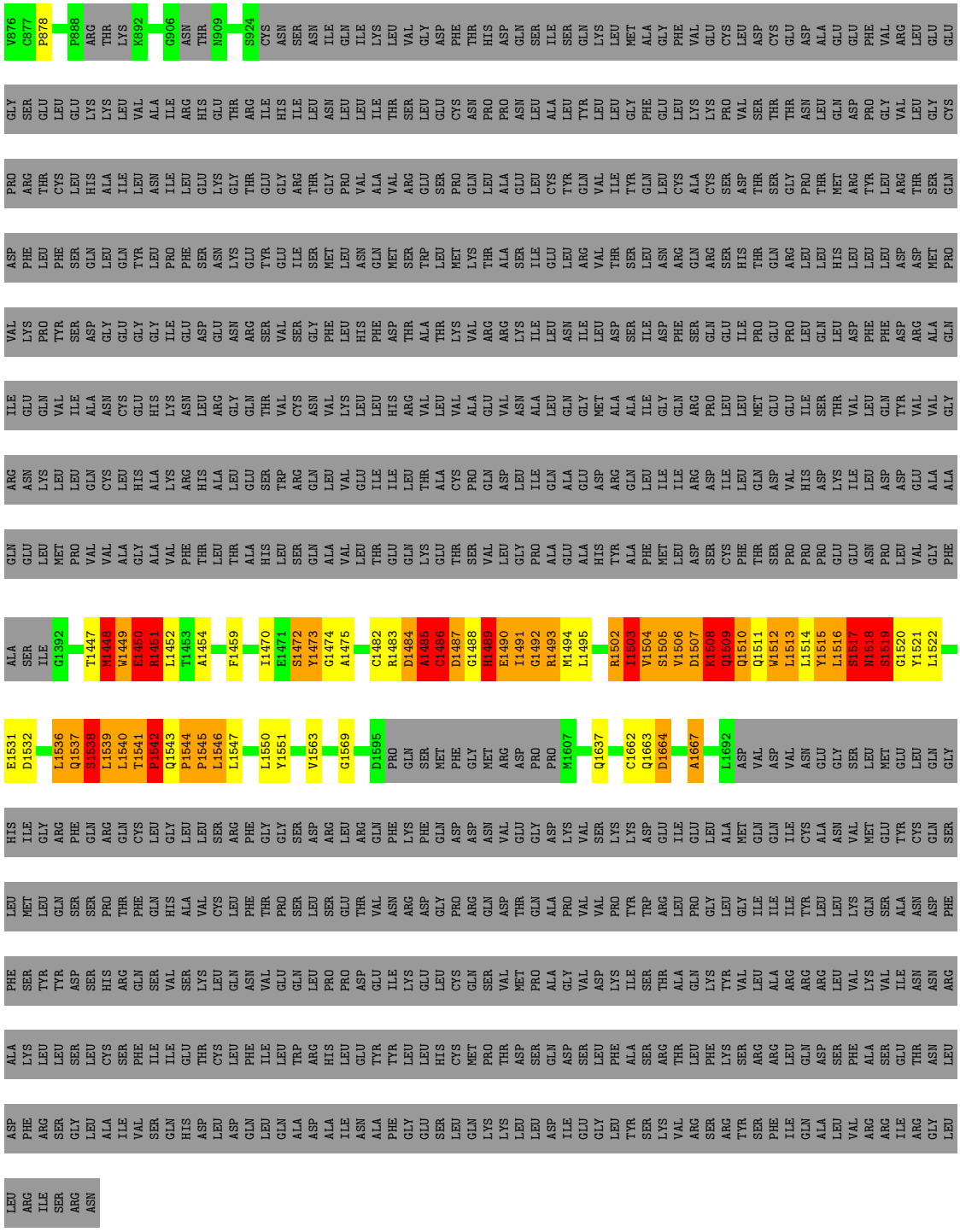




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 3-J:





• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 3-P: 45% 49%

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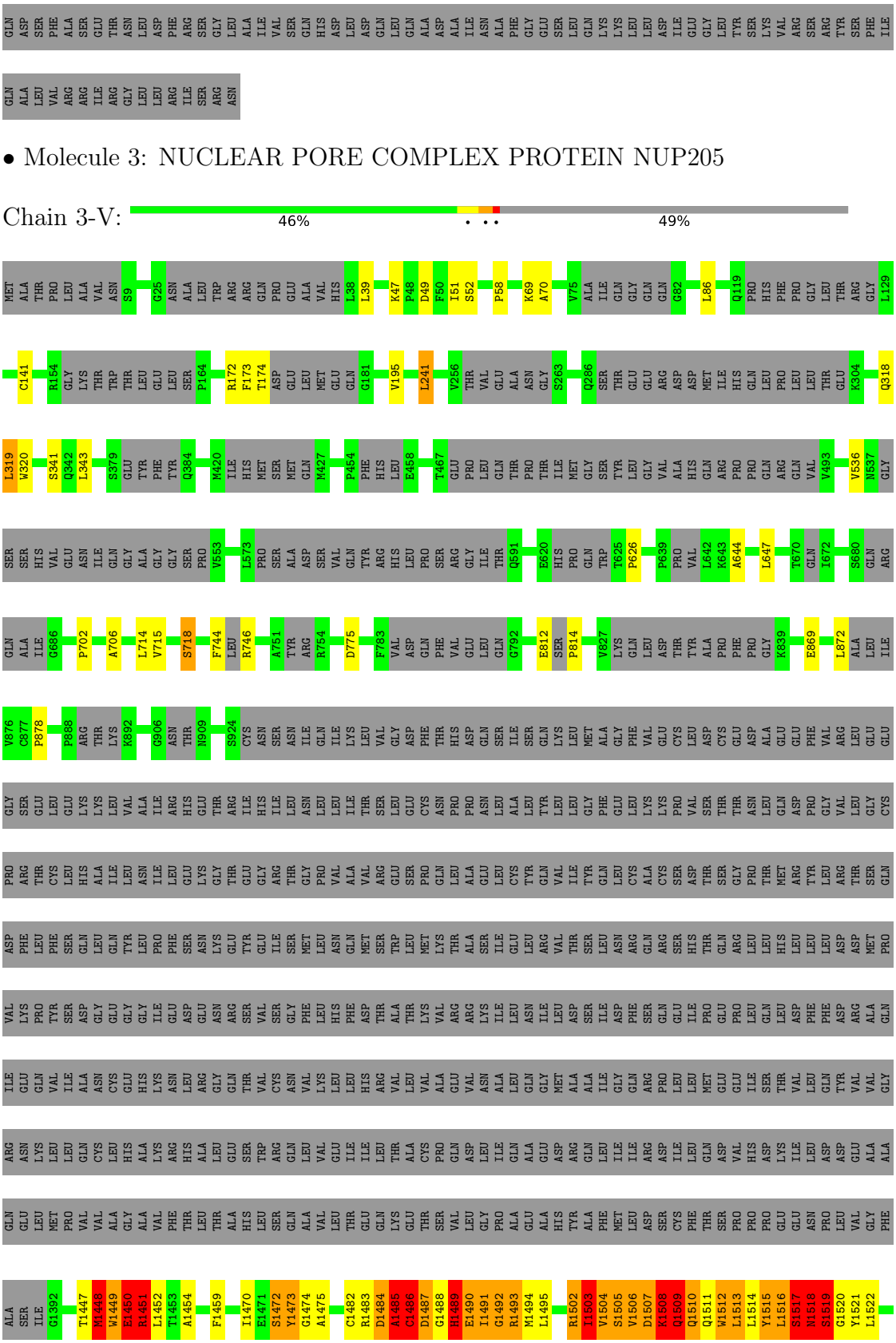
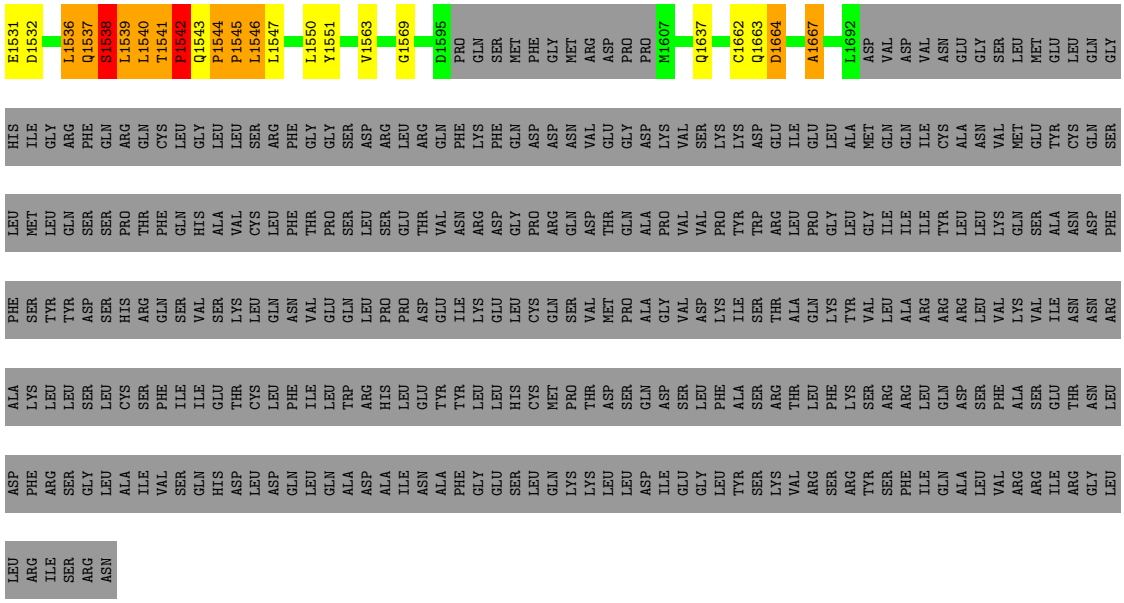
S341 Q342 L343 S379 Q384 M420 M427 P454 E458 T467 V493 V536 N537
V553 L573 Q591 E620 T625 P626 P639 L642 K643 A644 L647 T670 I672 S680
G686 P702 A706 L714 V715 S718 F744 R746 A751 R754 D775 F783 Q792 E812 P814 V827 K839 E869 L872 V876 C877
P878 L879 E880 L883 Q884 N887 P888 K892 G906 N909 S924
S1517 N1518 S1519 G1520 Y1521 L1522 E1531 D1532 L1536 Q1537 S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 L1550 Y1551 D1595 M1607 Q1637 R1661 C1662 Q1663 D1664 A1667 S1681 K1682 L1685 P1686 L1692
G1392 K1446 T1447 M1448 W1449 E1450 R1451 F1459 E1465 A1468 I1469 I1470 E1471 S1472 Y1473 G1474 A1475 A1476 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511 W1512 L1513 L1514 Y1515 L1516



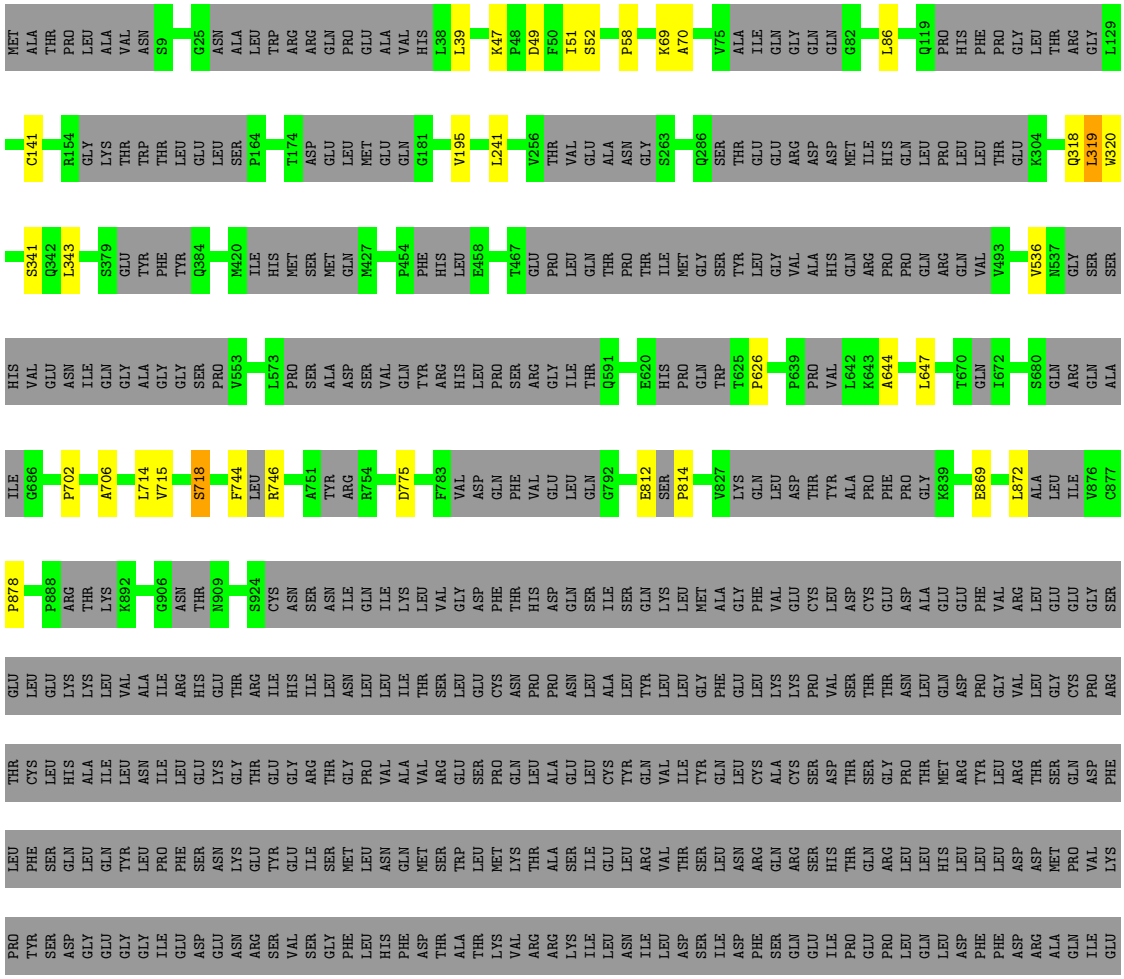
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

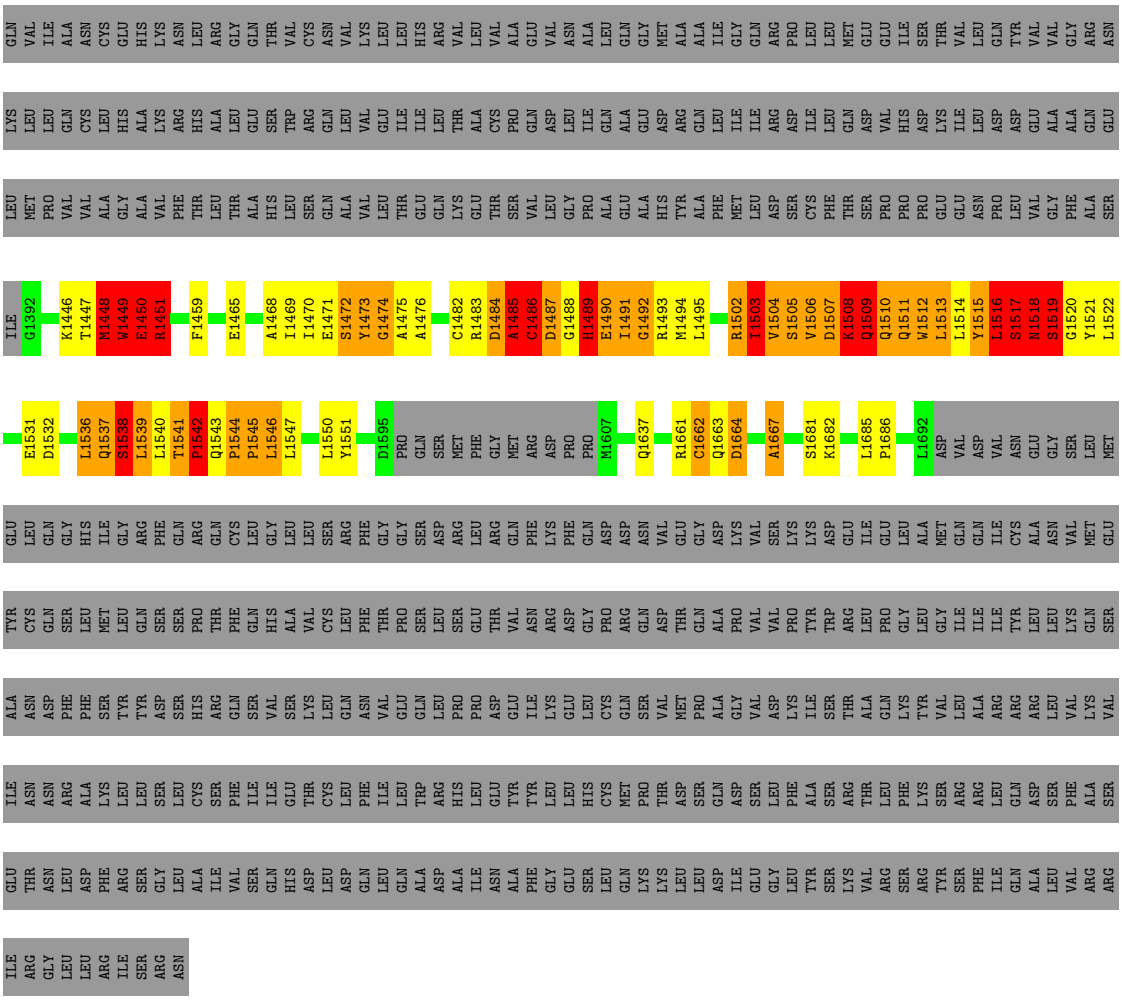
Chain 3-V: 46% • • • 49%



- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

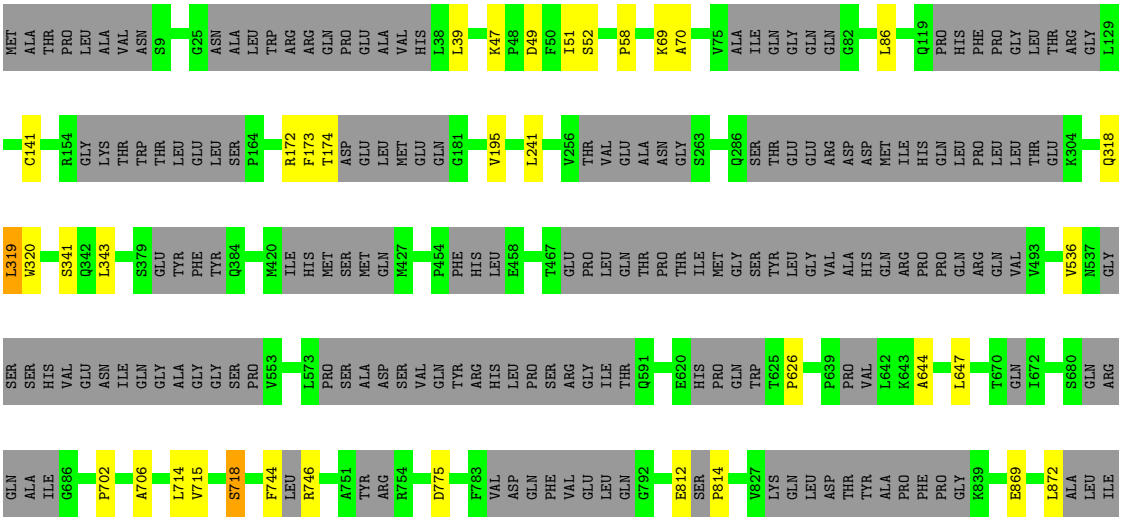
Chain 4-D:

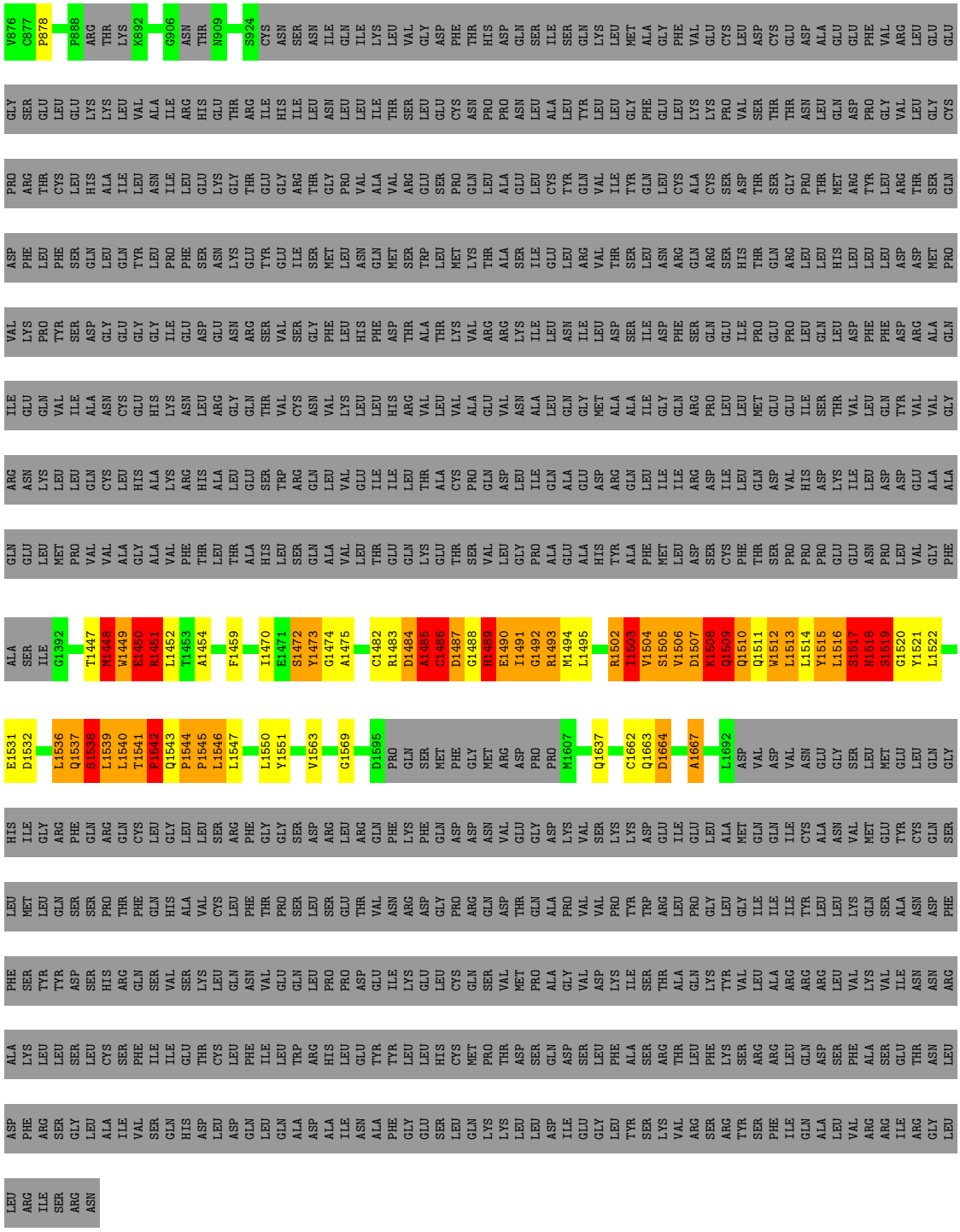




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 4-J:

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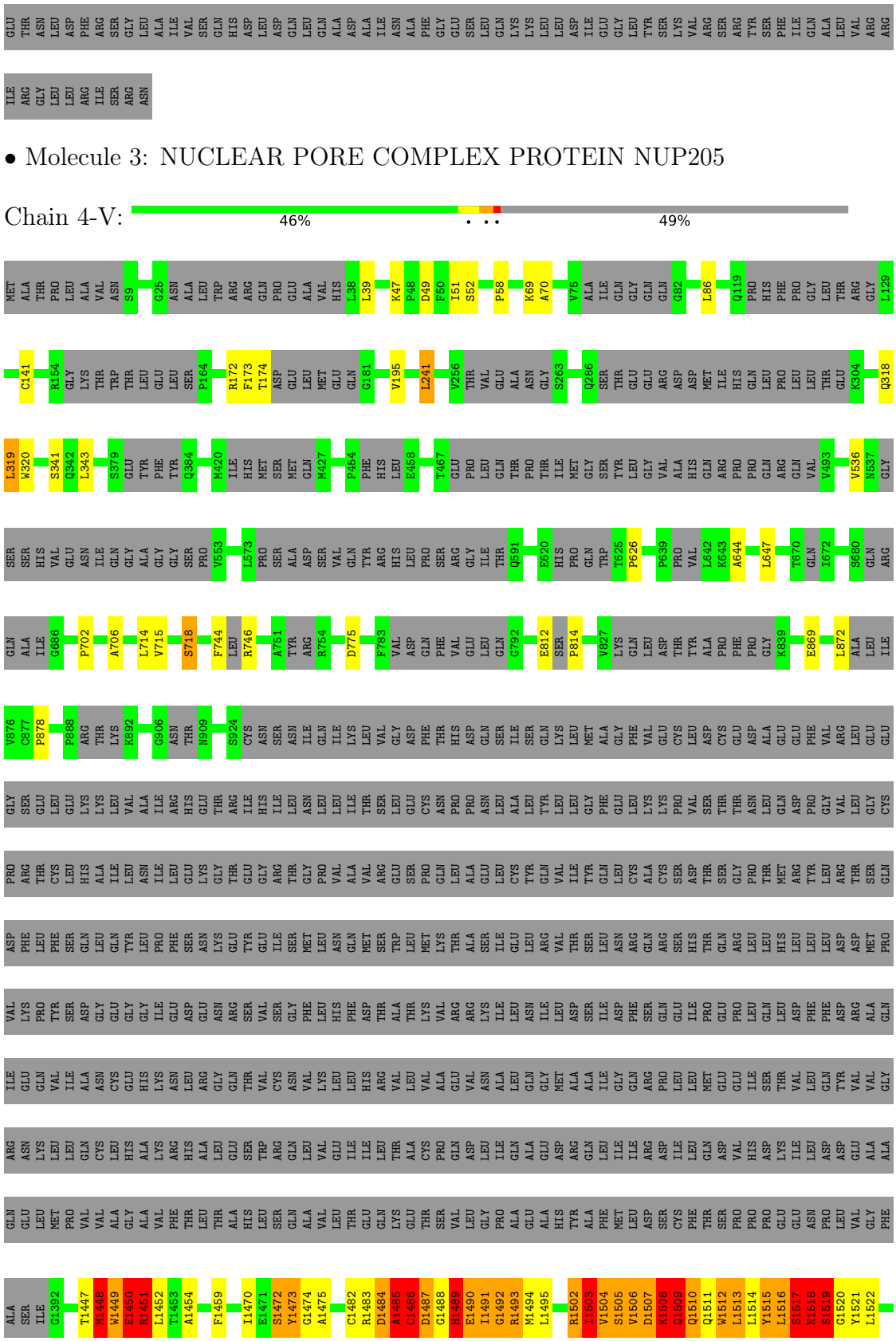
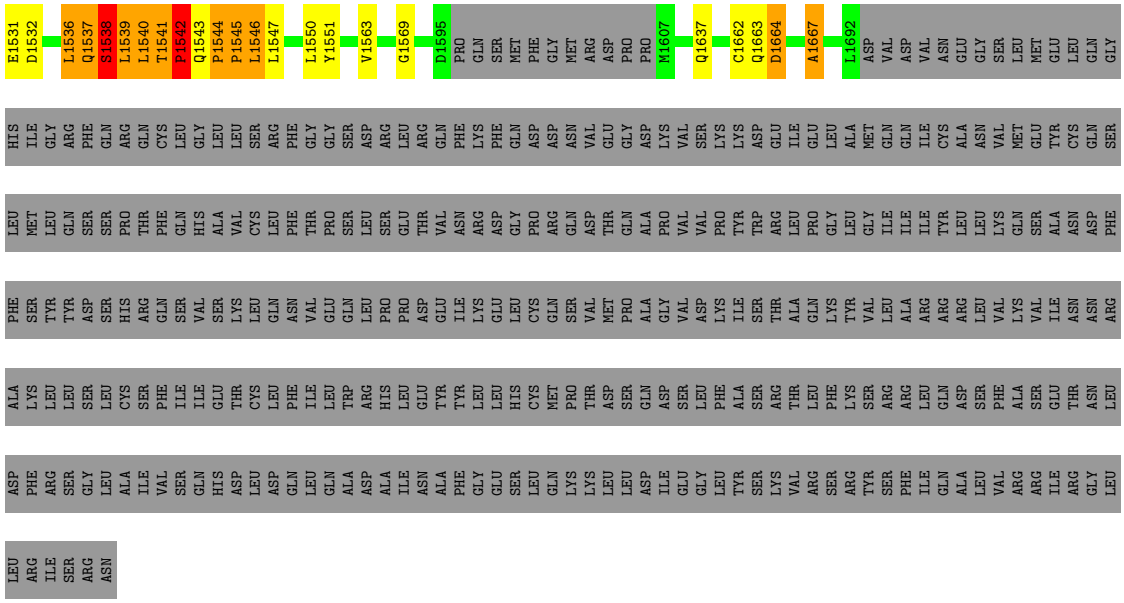
C141 R154 P164 T174 G181 V195 L241 V256 S263 Q286 K304 Q318 L319 W320
S341 Q342 L343 S379 Q384 M420 M427 P454 E458 T467 V493 V536 N537
HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 L573 Q591 E620 T625 P626 P639 L642 K643 A644 L647 T670 I672 S680
ILE G686 P702 A706 L714 V715 S718 F744 R746 A751 R754 D775 F783 Q792 E812 P814 V827 K839 E869 L872 V876 C877
P878 P888 K892 G906 N909 S924
GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE ASN LEU ILE THR SER LEU GLU CYS ASN PRO PRO ASN LEU ALA LEU LEU TYR GLN VAL LEU LEU GLY PHE GLU LEU LYS LYS PRO VAL SER THR THR ASN LEU GLN ASP PRO GLY VAL LEU LEU GLY CYS PRO ARG
THR CYS LEU HIS ALA ILE LEU ASN ILE LEU GLU LYS GLY THR GLU GLY ARG THR GLY PRO VAL ALA VAL ARG GLU SER PRO GLN LEU ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU CYS ALA CYS SER ASP THR SER GLY PRO THR MET ARG TYR LEU ARG THR SER GLN ASP PHE
LEU PHE SER GLN LEU GLN LYS TYR LEU LEU PRO PHE SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR ALA SER ILE ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG HIS THR GLN LEU LEU LEU LEU ASP ASP MET PRO VAL LYS
PRO TYR SER ASP GLY GLU GLY GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS VAL ARG ARG LYS ILE LEU ASP SER ILE ASP PHE SER GLN GLU ILE PRO GLU PRO LEU LEU GLN LEU ASP PHE PHE ASP ARG ALA GLN GLU
GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU LEU HIS ARG VAL LEU VAL ALA GLU VAL ASN ALA LEU GLN GLY MET ALA ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU LEU LEU ILE SER THR SER ARG LEU LEU ILE GLN TYR VAL VAL VAL GLY ARG ASN
LYS LEU LEU GLN CYS LEU HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ARG GLN LEU VAL GLU ILE ILE LEU THR ALA CYS PRO GLN ASP LEU ILE GLN ALA GLU ARG ASP ILE LEU LEU ASP VAL HIS LYS ILE LEU ASP ASP GLU ALA ALA GLN GLU
LEU MET PRO VAL VAL ALA ALA GLY ALA ALA VAL PHE THR LEU SER LEU GLN GLN LYS GLU THR SER VAL LEU GLY PRO ALA GLU ALA HIS TYR ALA PHE MET LEU ASP SER CYS PHE THR SER PRO PRO GLU LEU GLU GLU ASP ILE GLY ARG ALA SER
ILE G1392 K1446 T1447 M1448 W1449 E1450 R1451 F1459 E1465 A1468 I1469 I1470 E1471 S1472 Y1473 G1474 A1475 A1476 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511 W1512 L1513 L1514 Y1515 L1516 S1517 N1518 S1519 G1520 Y1521 L1522
E1531 D1532 L1536 Q1537 S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 L1550 Y1551 D1595 M1607 Q1637 R1661 C1662 Q1663 D1664 A1667 S1681 K1682 L1685 P1686 L1692
GLU LEU GLN GLY HIS ILE GLY ARG PHE GLN ARG GLN CYS LEU GLY LEU LEU SER ARG PHE GLY GLY SER ASP ARG LEU ARG GLN PHE LYS PHE GLN ASP ASP ARG ASN VAL GLU GLY ASP LYS VAL SER LYS LYS ASP GLU ILE PRO VAL ASP ASP ILE GLU LEU ASN ILE ILE CYS GLN SER VAL THR ARG THR LEU PHE LYS LYS GLN GLN ALA GLN GLU GLU LEU GLY LEU ALA MET GLN GLN ILE ILE ILE CYS ASN GLU GLY ARG ARG LEU ASN VAL VAL MET GLU
TYR CYS GLN SER LEU MET LEU GLN SER SER PRO THR PHE GLN HIS ALA VAL CYS LEU PHE THR PRO SER LEU SER GLU THR VAL ASN ARG ASP PRO THR TYR TRP ARG LEU PRO GLY LEU LEU ILE ILE ILE PRO VAL GLN ASP ARG GLN ASP VAL ASP VAL PRO VAL LYS LYS ASP GLU ILE ILE ILE CYS VAL ASP ASP ARG LYS LYS LYS LYS VAL SER
ALA ASN ASP PHE PHE SER TYR TYR ASP SER HIS ARG GLN SER VAL ALA LYS LEU GLN ASN VAL GLU GLU ASP GLU LEU PRO ASP GLU ILE LYS GLU LEU CYS GLN SER VAL MET PRO ALA GLY VAL ASP LYS SER THR ALA ARG LEU ARG ARG ARG LEU LEU VAL LEU LEU ALA ILE ILE ILE TYR LEU LEU VAL
ILE ASN ASN ARG ALA LYS LEU LEU SER LEU CYS SER PHE ILE LEU THR CYS PHE LEU LEU HIS CYS MET PRO THR ASP SER GLN ASP SER LEU PHE ALA SER ARG THR ARG LEU PHE LYS LYS LEU GLN ARG ARG LEU ARG ARG LEU GLN ASP SER PHE ALA SER
WORLDWIDE PDB PROTEIN DATA BANK



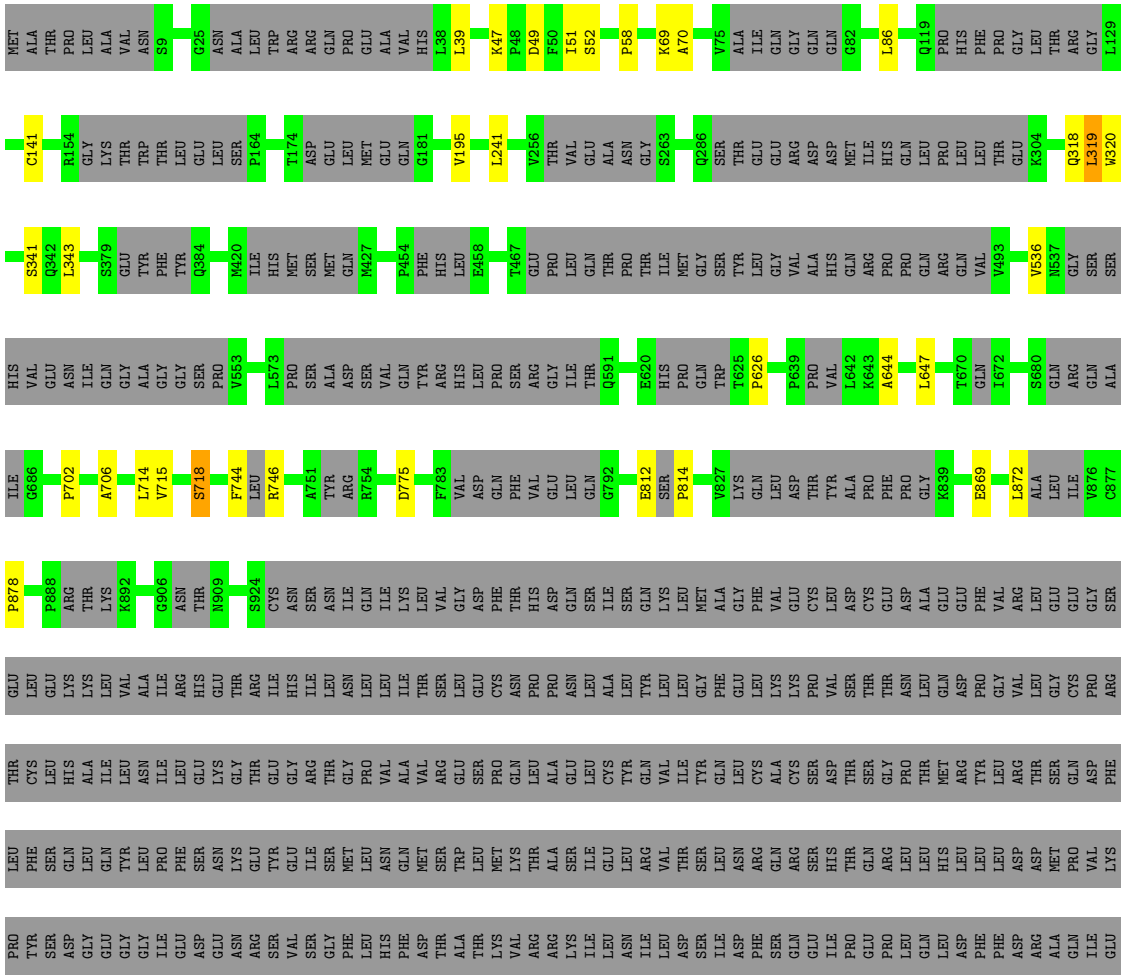
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

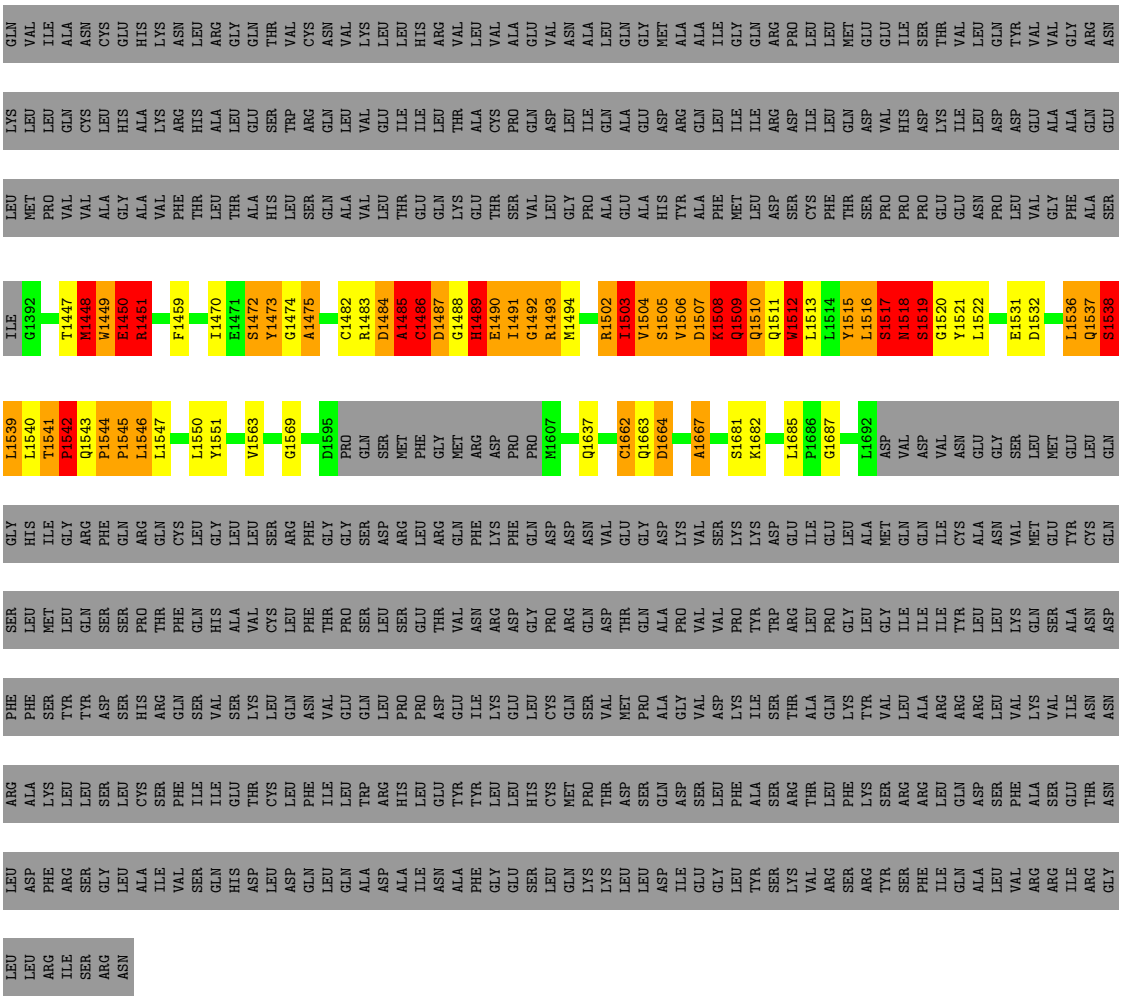
Chain 4-V: 46% 49%



• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

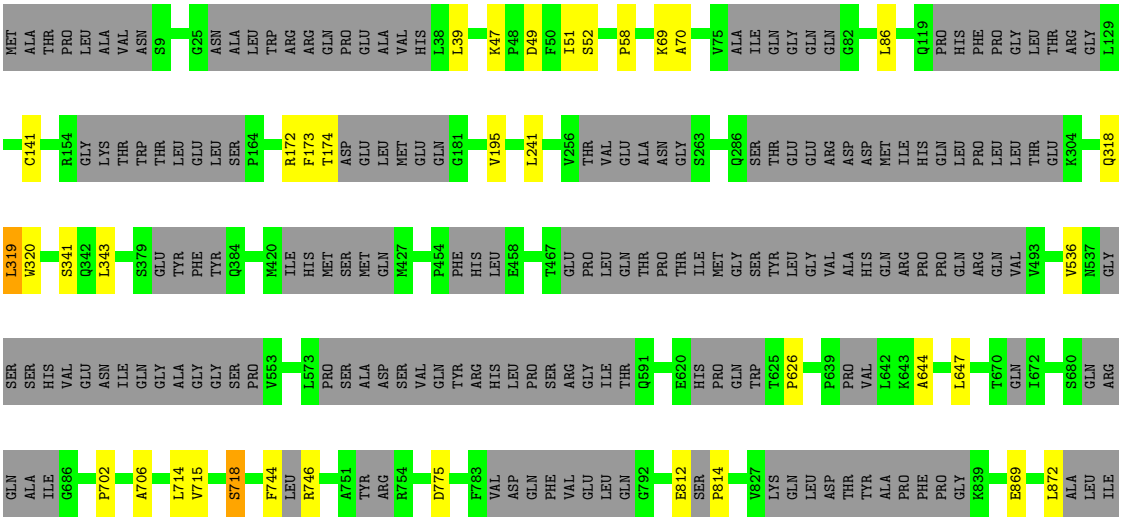
Chain 5-D:

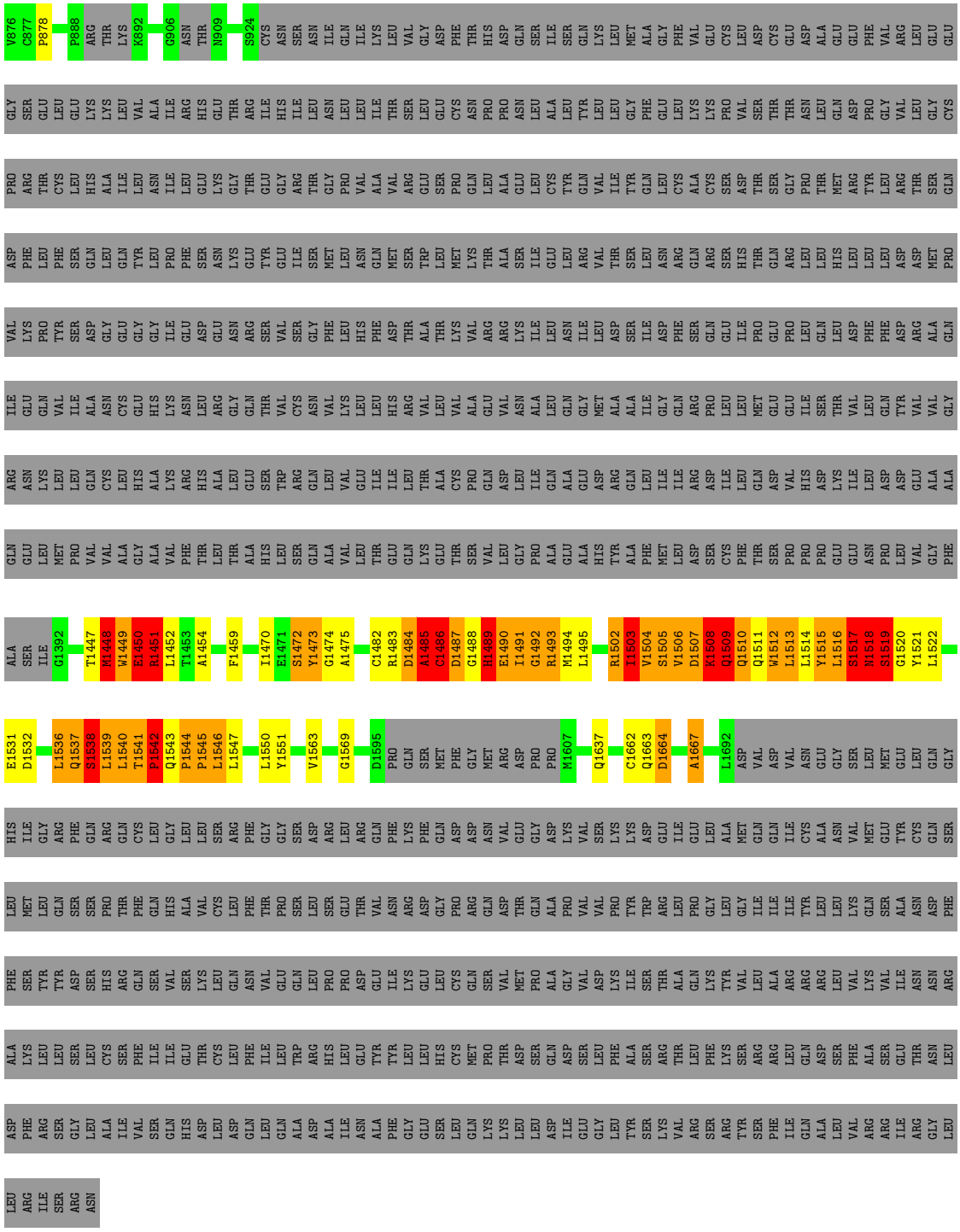




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 5-J:

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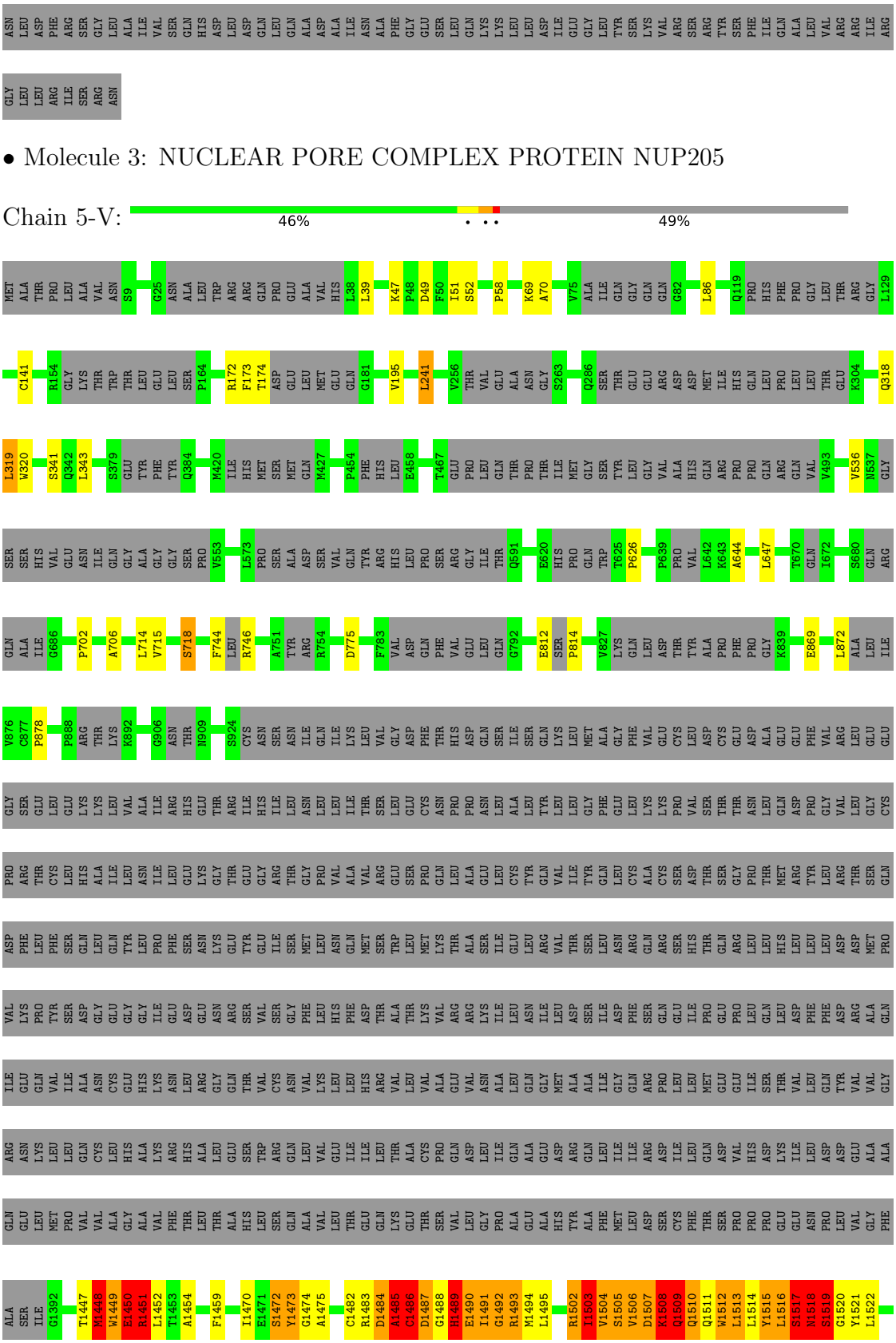
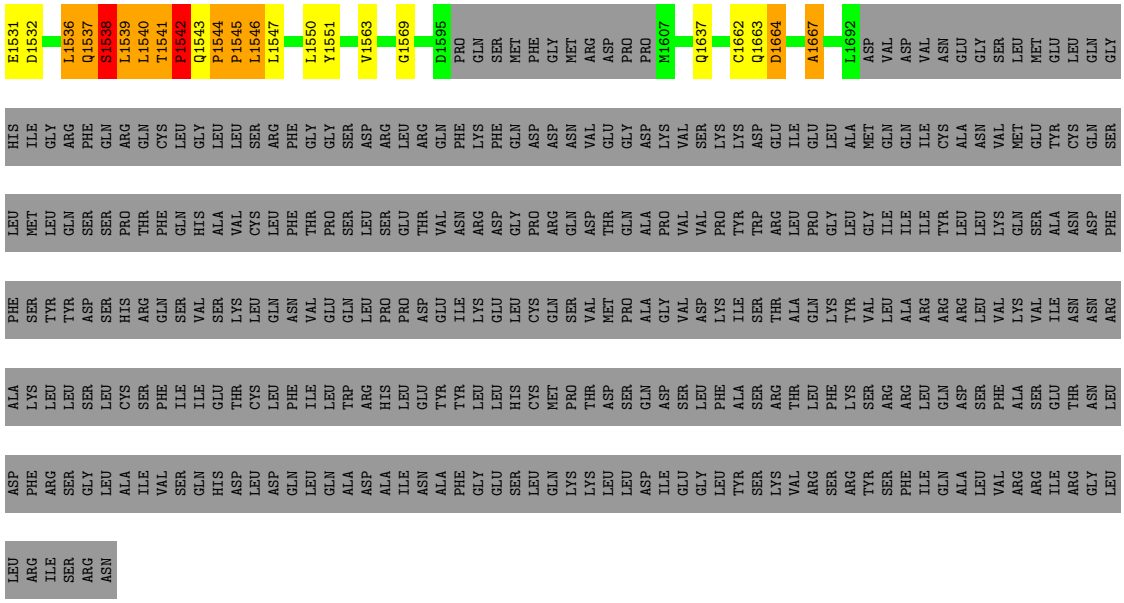
C141 R154 P164 T174 G181 V195 L241 V256 S263 Q286 K304 Q318 L319 W320
S341 Q342 L343 S379 Q384 M420 M427 P454 E458 T467 V493 V536 N537
HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 L573 Q591 E620 T625 P626 P639 L642 K643 A644 L647 T670 I672 S680
ILE G686 P702 A706 L714 V715 S718 F744 R746 A751 R754 D775 F783 Q792 E812 P814 V827 K839 E869 L872 V876 C877
P878 P888 K892 G906 N909 S924
GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE LEU ASN LEU LEU ILE THR SER LEU GLU CYS ASN PRO PRO ASN LEU ALA LEU TYR LEU LEU LEU GLY PHE GLU LEU LYS LYS PRO VAL SER THR THR ASN LEU LEU GLN ASP PRO GLY VAL LEU GLY VAL PRO ARG
THR CYS LEU HIS ALA ILE LEU ASN ILE LEU CYS GLY THR GLU GLY GLY ARG THR GLY PRO VAL ALA VAL ARG GLU GLU SER PRO GLN GLN LEU ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU CYS ALA CYS SER ASP THR SER GLY PRO THR MET ARG TYR LEU ARG THR SER GLN ASP PHE
LEU PHE SER GLN LEU GLN TYR GLU SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR ALA SER ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG SER HIS THR GLN ARG LEU LEU LEU LEU LEU ASP ASP MET PRO VAL LYS
PRO TYR SER ASP GLY GLU GLY GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS VAL ARG ARG LYS ILE LEU ASP SER ILE ASP PHE SER GLN GLU ILE PRO GLU PRO LEU GLN LEU ASP ARG ALA GLN GLU GLU
GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU LEU HIS ARG VAL LEU VAL ALA GLU VAL ASN ALA LEU GLN GLY MET ALA ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU GLU ILE ARG LEU LEU VAL VAL GLY ARG ASN
LYS LEU LEU GLN CYS LEU HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ARG GLN LEU VAL GLU VAL THR ALA CYS PRO GLN ASP LEU ILE GLN ALA GLU ASP ARG GLN LEU ILE ILE ARG GLN GLN ASP VAL HIS LEU LEU ASP ASP GLU ALA ALA GLN GLU
LEU MET PRO VAL VAL ALA ALA GLY ALA VAL PHE THR LEU THR ALA HIS LEU SER GLN ALA VAL LEU THR GLU LEU GLY LYS GLU THR SER SER VAL LEU GLY PRO ALA GLU ALA HIS TYR ALA PHE MET LEU ASP SER CYS PHE THR SER PRO PRO GLU GLU ASN PRO LEU VAL GLY PHE ALA SER
ILE G1392 T1447 M1448 W1449 E1450 R1451 F1459 I1470 E1471 S1472 Y1473 G1474 A1475 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511 W1512 L1513 L1514 Y1515 L1516 S1517 N1518 S1519 G1520 Y1521 L1522 E1531 D1532 L1536 Q1537
S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 L1550 Y1551 V1563 G1569 D1595 PRO GLN SER MET PHE GLY MET ARG ASP PRO PRO M1607 Q1637 C1662 Q1663 D1664 A1667 S1681 K1682 L1685 P1686 G1687 L1692 ASP VAL ASP GLU GLY SER LEU MET GLU GLU LEU
GLN GLY HIS ILE GLY ARG PHE GLN ARG GLN CYS LEU GLY LEU SER ARG PHE GLY GLY SER ASP ARG LEU ARG GLN PHE LYS PHE GLN ASP ASP ASN VAL SER LYS ASP GLU ILE LYS ALA MET GLN LYS ILE ILE ILE ALA ALA ASN VAL MET GLU TYR CYS
GLN SER LEU MET LEU GLN SER SER PRO THR PHE GLN HIS ALA VAL CYS LEU PHE THR PRO ARG GLN SER LEU SER GLU THR VAL ASN ARG ASP GLY PRO ARG GLN ASP THR GLN ALA TRP VAL VAL PRO TYR TRP ARG LEU PRO GLY LEU GLY ILE ILE TYR TYR LEU LEU LYS SER ALA ASN
ASP PHE PHE SER TYR TYR ASP SER HIS ARG GLN SER VAL SER LYS LEU GLN ASN VAL GLU GLN GLN LEU PRO PRO ASP GLU ILE LYS ARG LEU CYS GLN SER VAL MET PRO ALA PRO VAL ASP PRO LEU VAL ARG ARG LEU ALA ARG ARG LEU LYS VAL ILE ASN
ASN ARG ALA LYS LEU LEU SER PHE ILE ILE LEU TRP ARG HIS LEU GLU TYR TYR LEU LEU HIS CYS MET PRO THR ASP SER GLN ASP SER LEU PHE ALA SER ARG THR LEU PHE LYS SER ARG ARG LEU GLN ASP PHE LEU LEU PHE ILE ILE ILE LEU GLU GLN ARG ARG LEU ALA ASN VAL MET GLU ILE ALA SER GLU THR



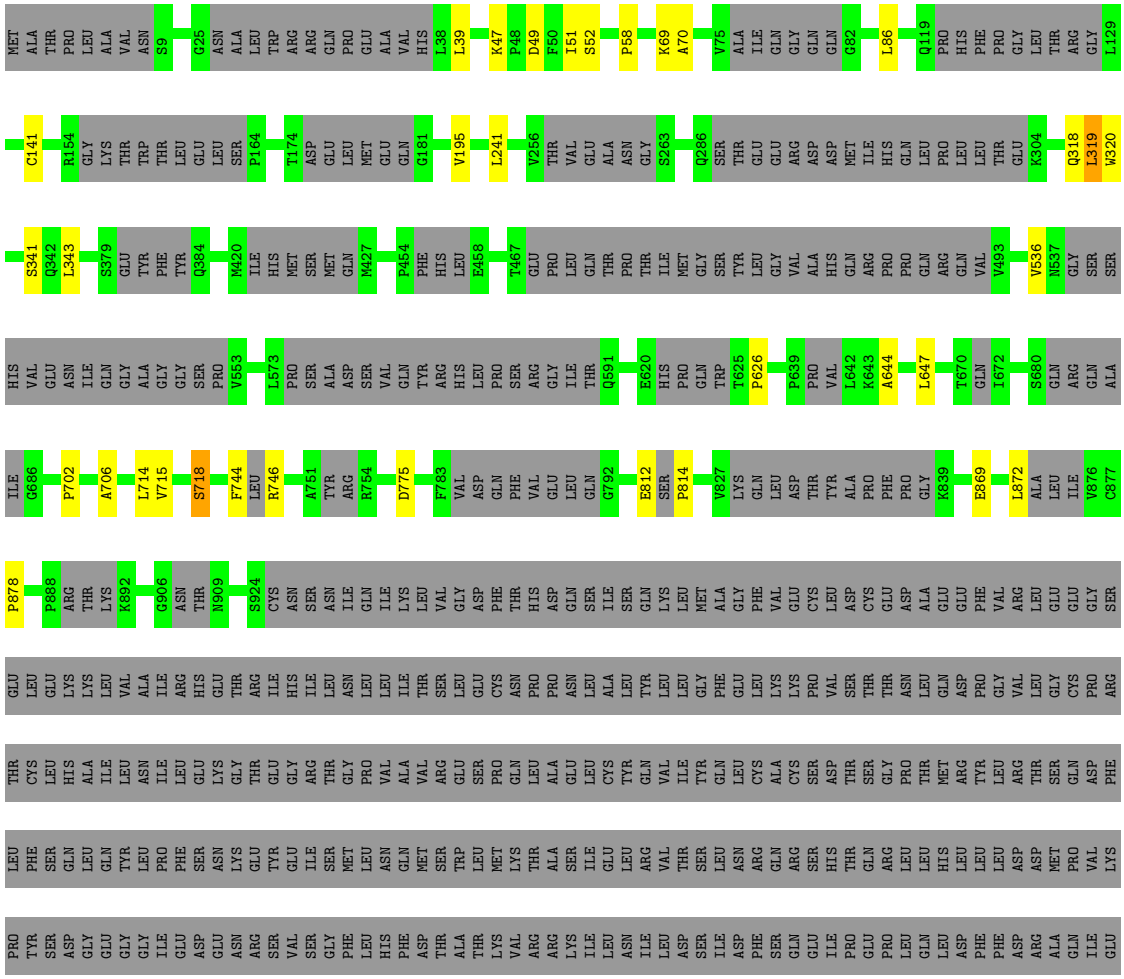
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

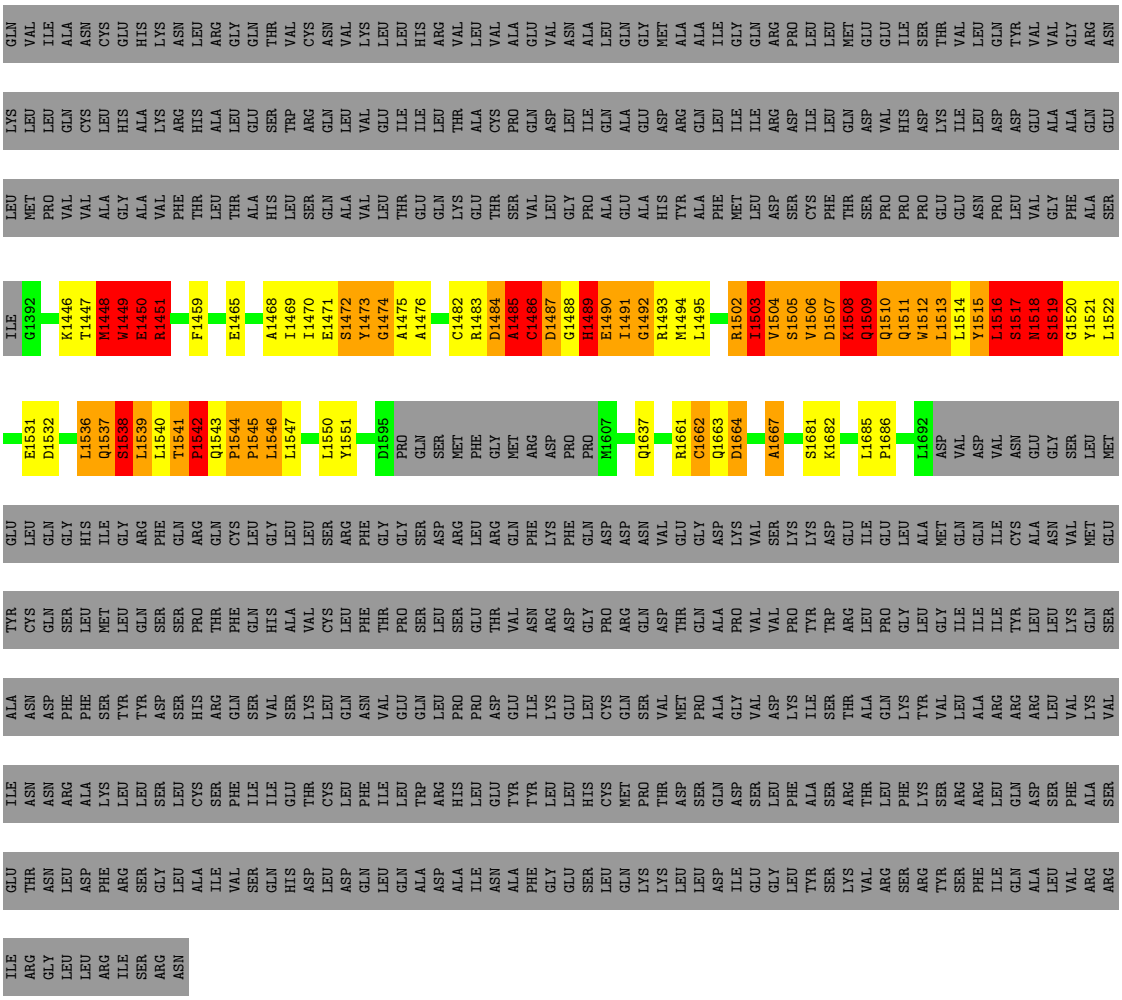
Chain 5-V: 46% • • • 49%



- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

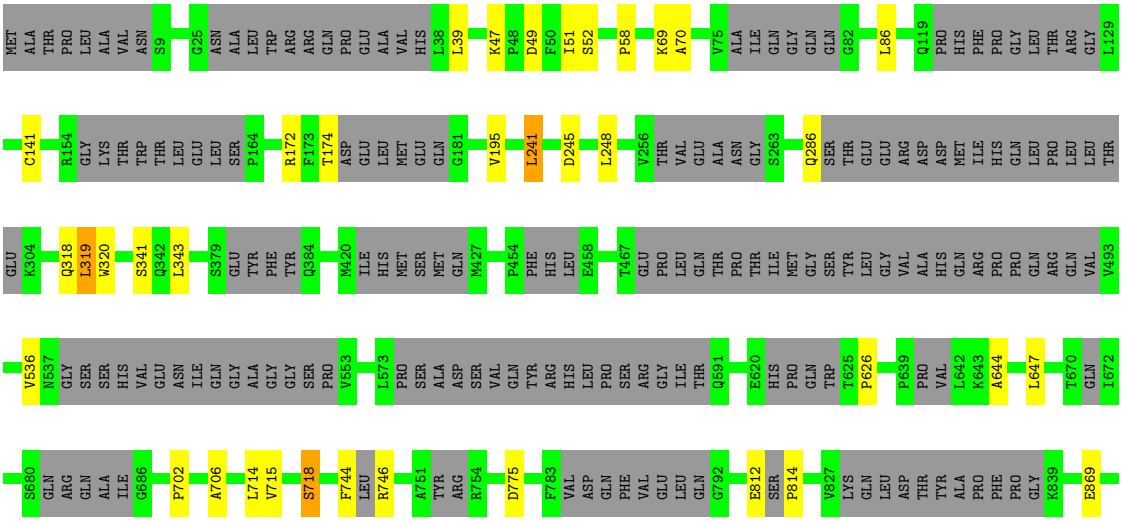
Chain 6-D:

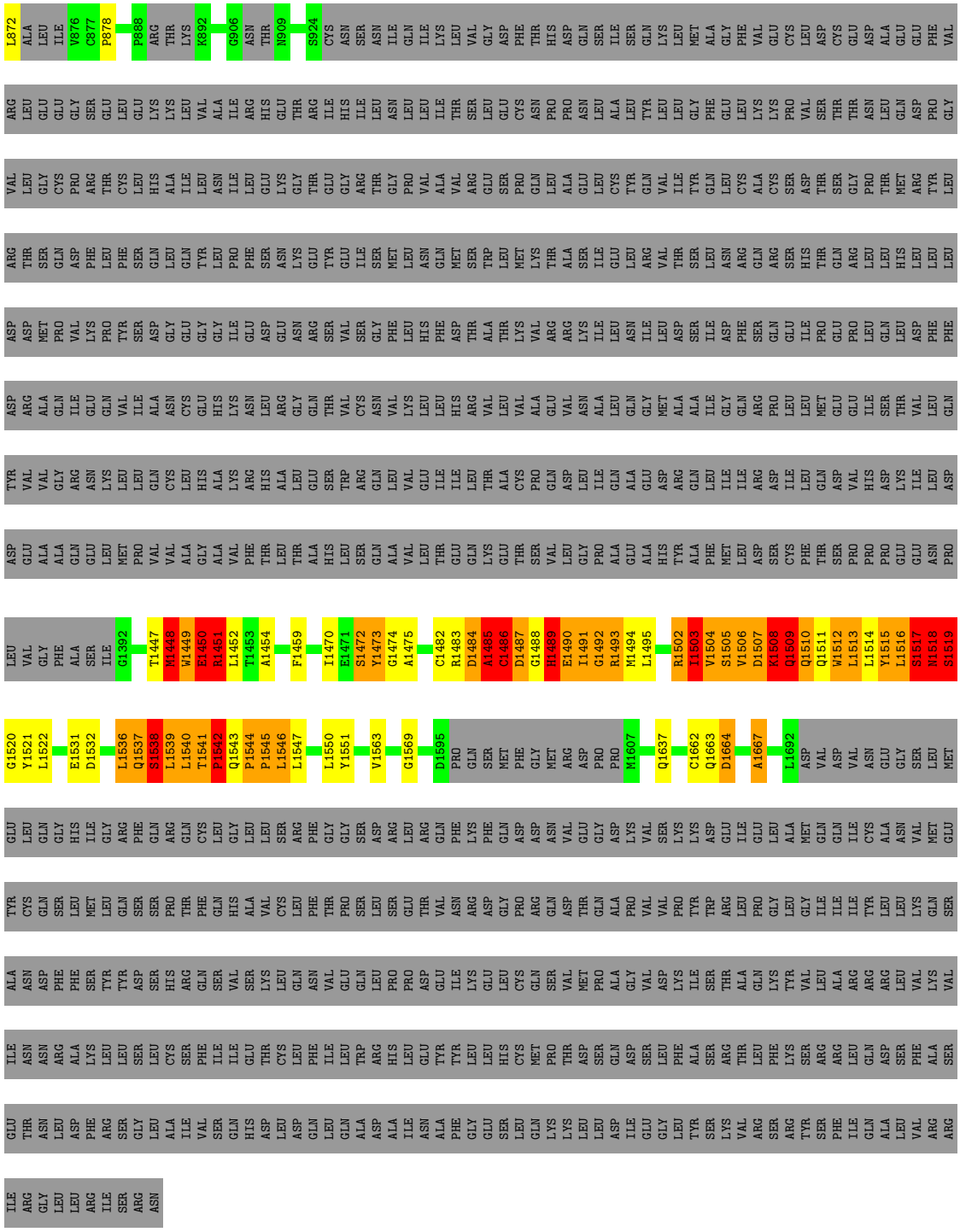




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 6-J:

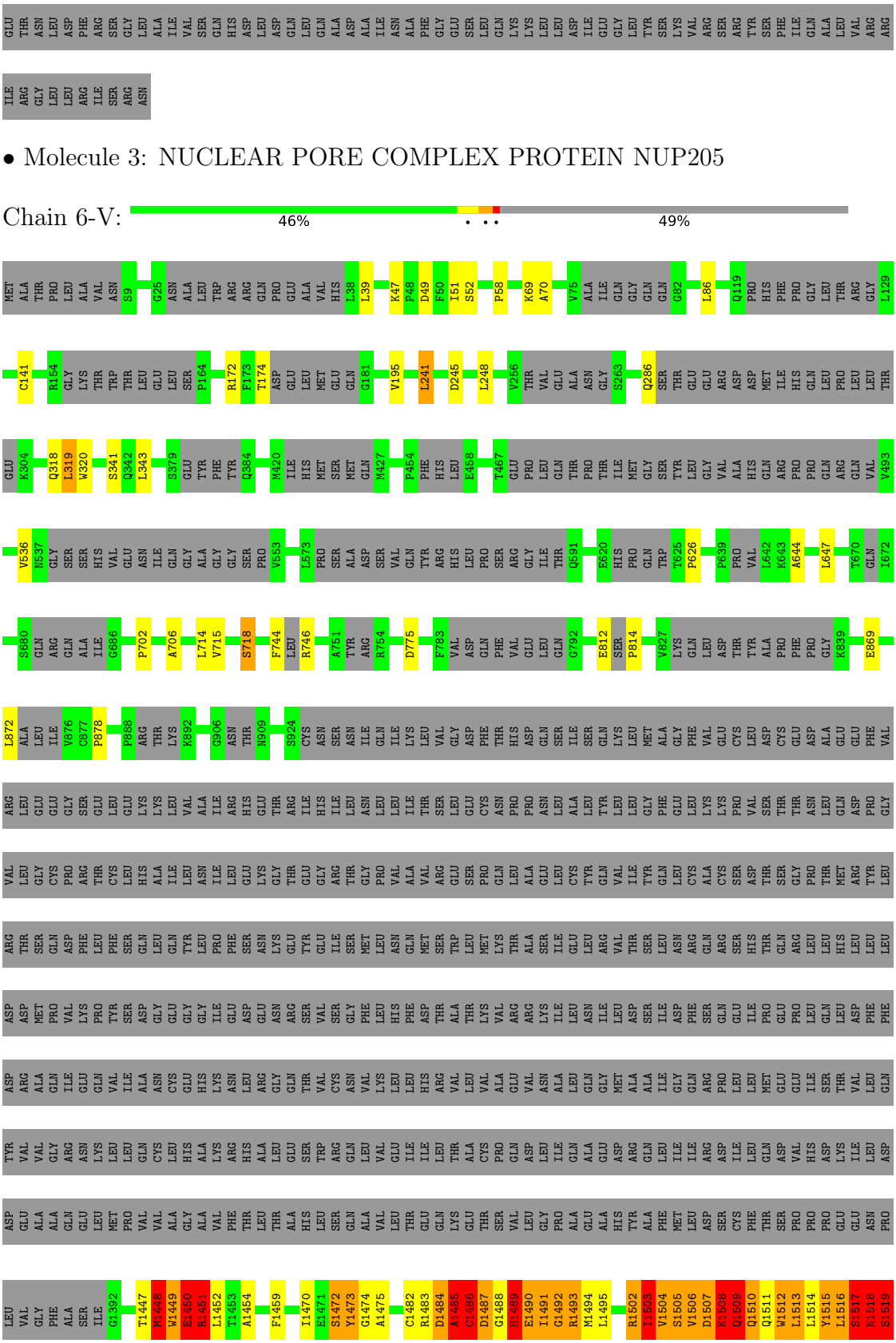




• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

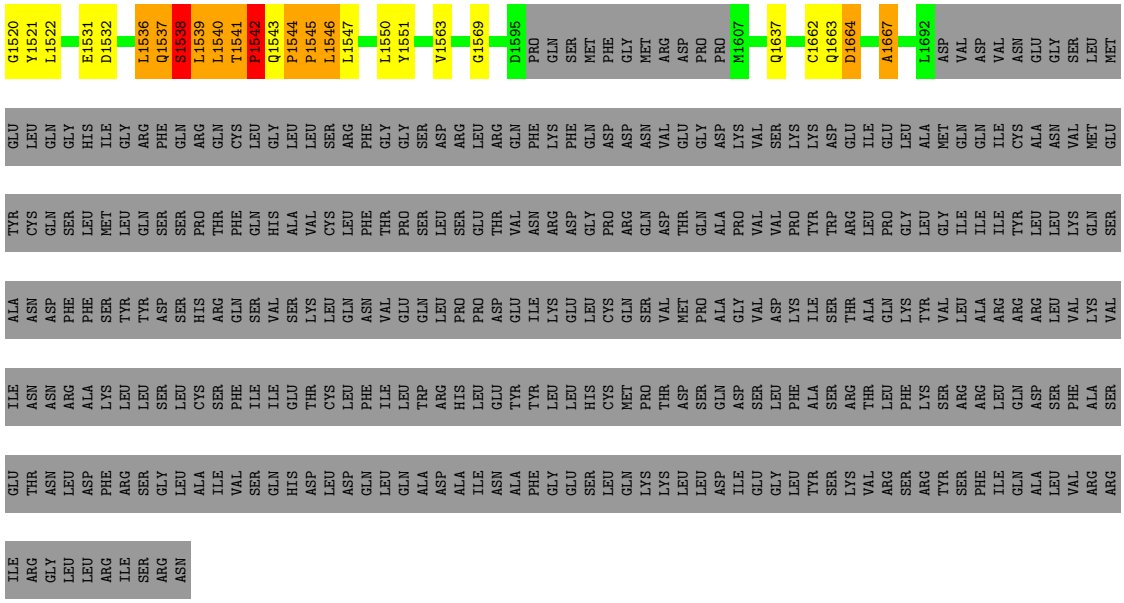
Chain 6-P: 46% 49%

C141 R154 P164 T174 G181 V195 L241 V256 S263 Q286 K304 Q318 L319 W320
S341 Q342 L343 S379 Q384 M420 M427 P454 E458 T467 V493 V536 N537
HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 L573 Q591 E620 T625 P626 P639 L642 K643 A644 L647 T670 I672 S680
ILE G686 P702 A706 L714 V715 S718 F744 R746 A751 R754 D775 F783 Q792 E812 P814 V827 K839 E869 L872 V876 C877
P878 P888 K892 G906 N909 S924
GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE LEU ASN LEU LEU ILE THR SER LEU GLU CYS ASN PRO PRO ASN LEU LEU ALA LEU LEU TYR TYR LEU LEU LYS LYS PRO VAL SER THR THR ASN LEU LEU GLN ASP PRO GLY VAL LEU LEU GLY CYS PRO ARG
THR CYS LEU HIS ALA ILE LEU ASN ILE LEU GLU LYS GLY THR GLU GLY ARG THR GLY PRO VAL ALA VAL ARG GLU SER PRO GLN LEU ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU CYS ALA CYS SER ASP THR SER GLY PRO THR MET ARG TYR LEU ARG THR SER GLN ASP PHE
LEU PHE SER GLN LEU GLN TYR LEU LEU PRO PHE SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR ALA SER ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG SER HIS THR GLN ARG LEU LEU LEU LEU LEU ASP ASP MET PRO VAL LYS
PRO TYR SER ASP GLY GLU GLY GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS VAL ARG ARG LYS ILE LEU ASP SER ILE ASP PHE SER GLN GLU ILE PRO GLU PRO LEU LEU GLN LEU ASP PHE PHE ASP ARG ALA GLN GLU
GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU LEU HIS ARG VAL LEU VAL ALA GLU VAL ASN ALA LEU GLN LYS MET ALA ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU ILE SER THR ILE LEU ARG GLN TYR VAL VAL GLY ARG ASN
LYS LEU LEU GLN CYS LEU HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ARG GLN LEU VAL GLU LEU ILE ILE LEU THR ALA CYS PRO GLN ASP LEU ILE GLN ALA GLU ASP ARG GLN LEU ILE ARG ASP ILE LEU GLN VAL ASP ASP LYS ILE LEU GLU ALA GLU GLU ALA ALA GLN GLU
LEU MET PRO VAL VAL ALA ALA GLY ALA ALA VAL PHE THR LEU THR LEU GLN GLU LYS GLU THR SER VAL LEU GLY PRO ALA GLU ALA HIS TYR ALA PHE MET LEU ASP SER CYS PHE THR SER PRO PRO PRO GLU GLU ASN PRO LEU VAL GLY PHE ALA GLN ASN
ILE G1392 K1446 T1447 M1448 W1449 E1450 R1451 F1459 E1465 A1468 I1469 I1470 E1471 S1472 Y1473 G1474 A1475 A1476 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511 W1512 L1513 L1514 Y1515 L1516 S1517 N1518 S1519 G1520 Y1521 L1522
E1531 D1532 L1536 Q1537 S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 L1550 Y1551 D1595 PRO GLN SER MET PHE GLY MET ARG ASP PRO PRO M1607 Q1637 R1661 C1662 Q1663 D1664 A1667 S1681 K1682 L1685 P1686 L1692 ASP VAL ASP VAL ASN GLU GLY SER VAL MET MET GLU
GLU LEU GLN GLY HIS ILE GLY ARG PHE GLN GLN CYS LEU GLY LEU SER ARG PHE GLY GLY GLN ASP ASN ARG ASP GLN PHE LYS PHE GLN ASP ASP ARG ASN VAL GLU GLY ASP LYS VAL SER LYS LYS ASP GLU ILE GLU GLN ARG ILE ILE CYS ASN GLN ILE ILE ALA ILE ILE ALA GLN ILE
TYR CYS GLN SER LEU MET LEU GLN SER SER PRO THR PHE GLN HIS ALA VAL CYS LEU PHE THR PRO SER LEU SER GLU THR VAL ASN ARG ASP PRO GLY PRO ARG GLN ASP THR ARG VAL VAL PRO TYR TYR ARG LEU PRO GLY LEU ALA MET GLN GLN ILE ILE CYS ASN SER
ALA ASN ASP PHE PHE SER TYR TYR ASP SER HIS ARG GLN SER LYS VAL LYS LEU GLN ASP PRO ASP GLU ILE LYS GLU LEU CYS GLN SER VAL MET PRO ALA GLY VAL ASP LYS SER THR ALA LYS TYR VAL ASN ARG ARG ARG LEU LEU VAL LYS GLN GLN LYS
ILE ASN ASN ARG ALA LYS LEU LEU SER LEU CYS SER PHE ILE ILE LEU HIS CYS MET PRO THR ASP SER GLN ASP SER LEU PHE ALA SER ARG THR ARG LEU ARG ARG LEU GLN ASP PHE ILE LEU LEU GLU TYR TYR LEU LEU LEU CYS ASP ARG ARG ARG LEU PHE LYS SER ARG ARG LEU ALA ILE ILE ILE PHE ALA
GLU ASN ARG GLN GLN LEU GLU GLU LEU SER LEU GLU GLN GLN LEU LYS LYS LEU LYS LYS LYS



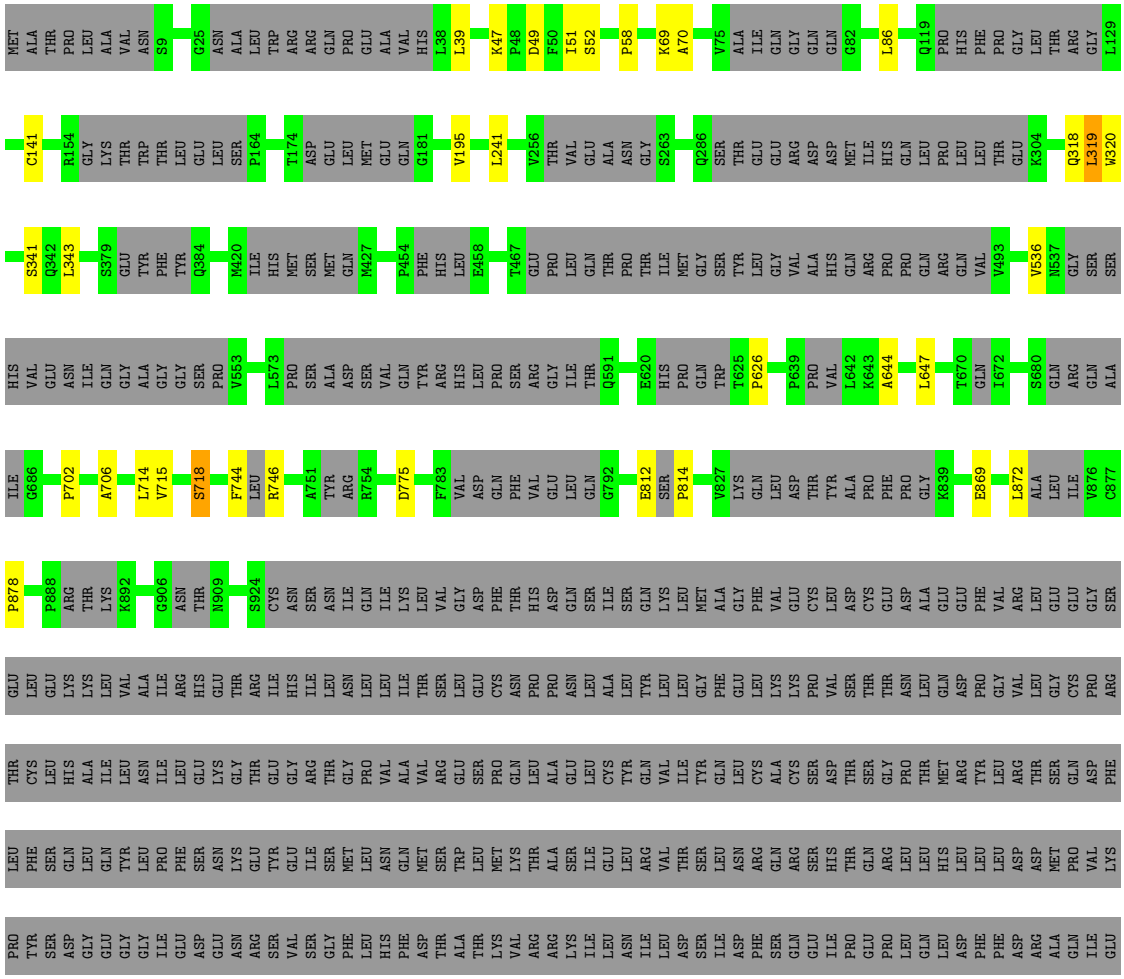
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

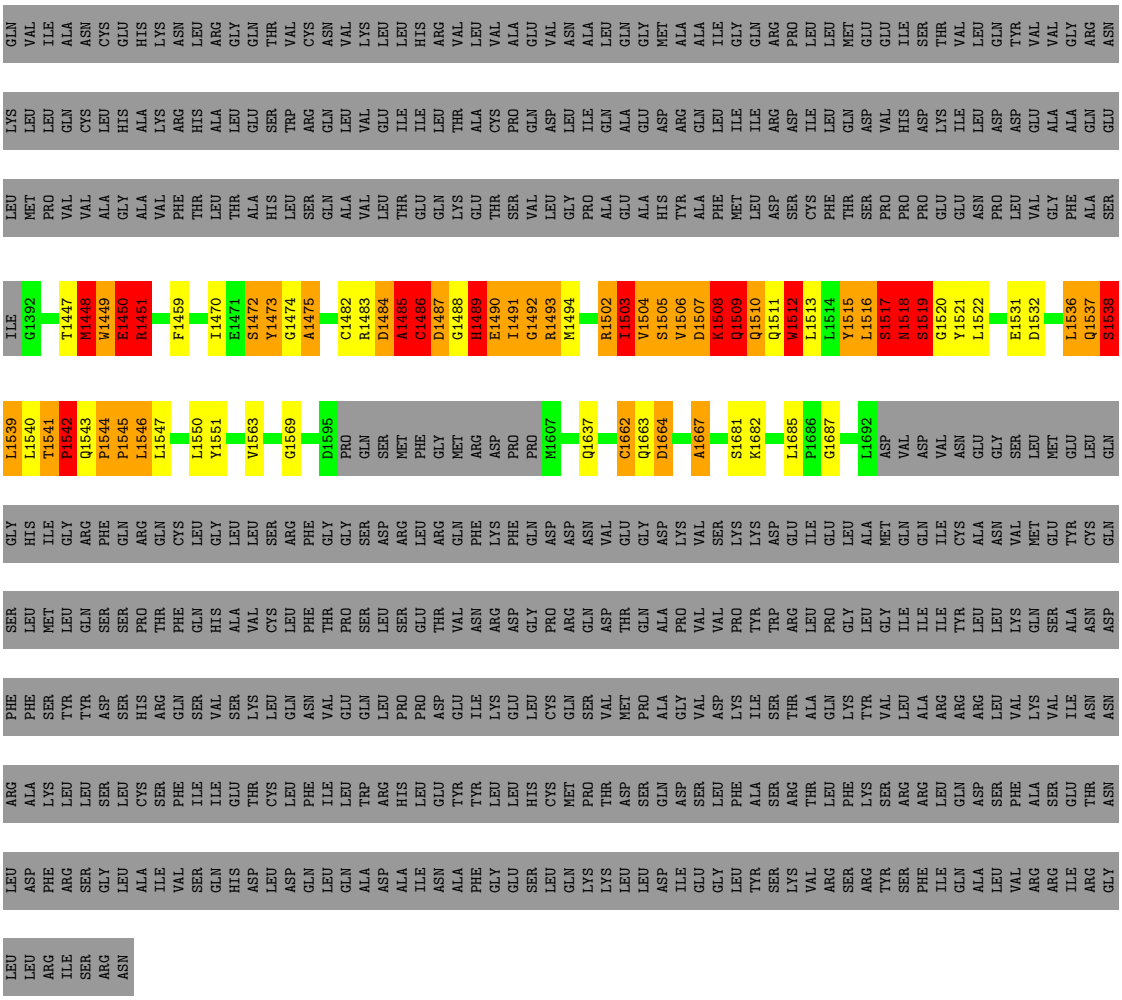
Chain 6-V: 46% 49%



• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

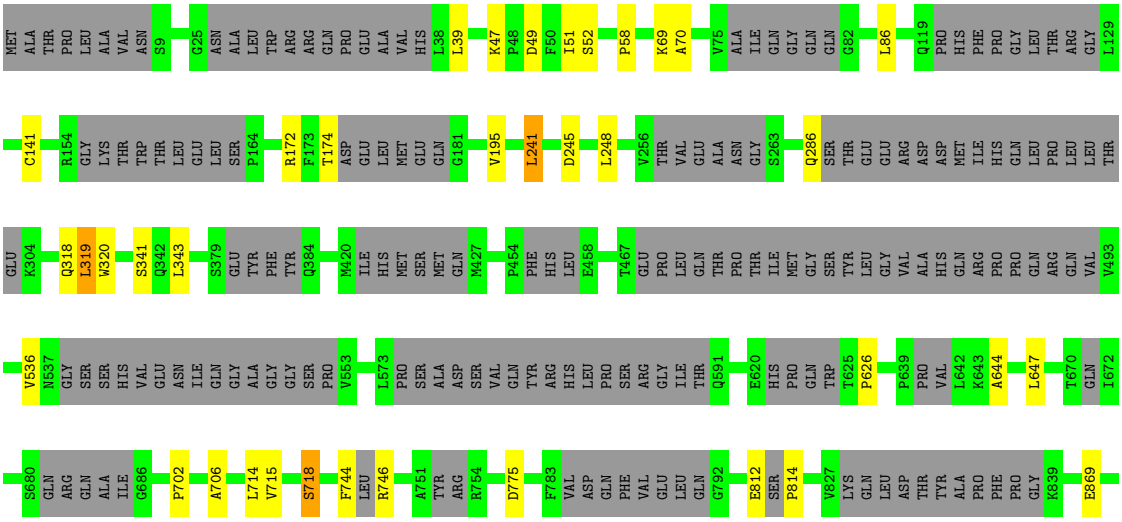
Chain 7-D: 46% 49%

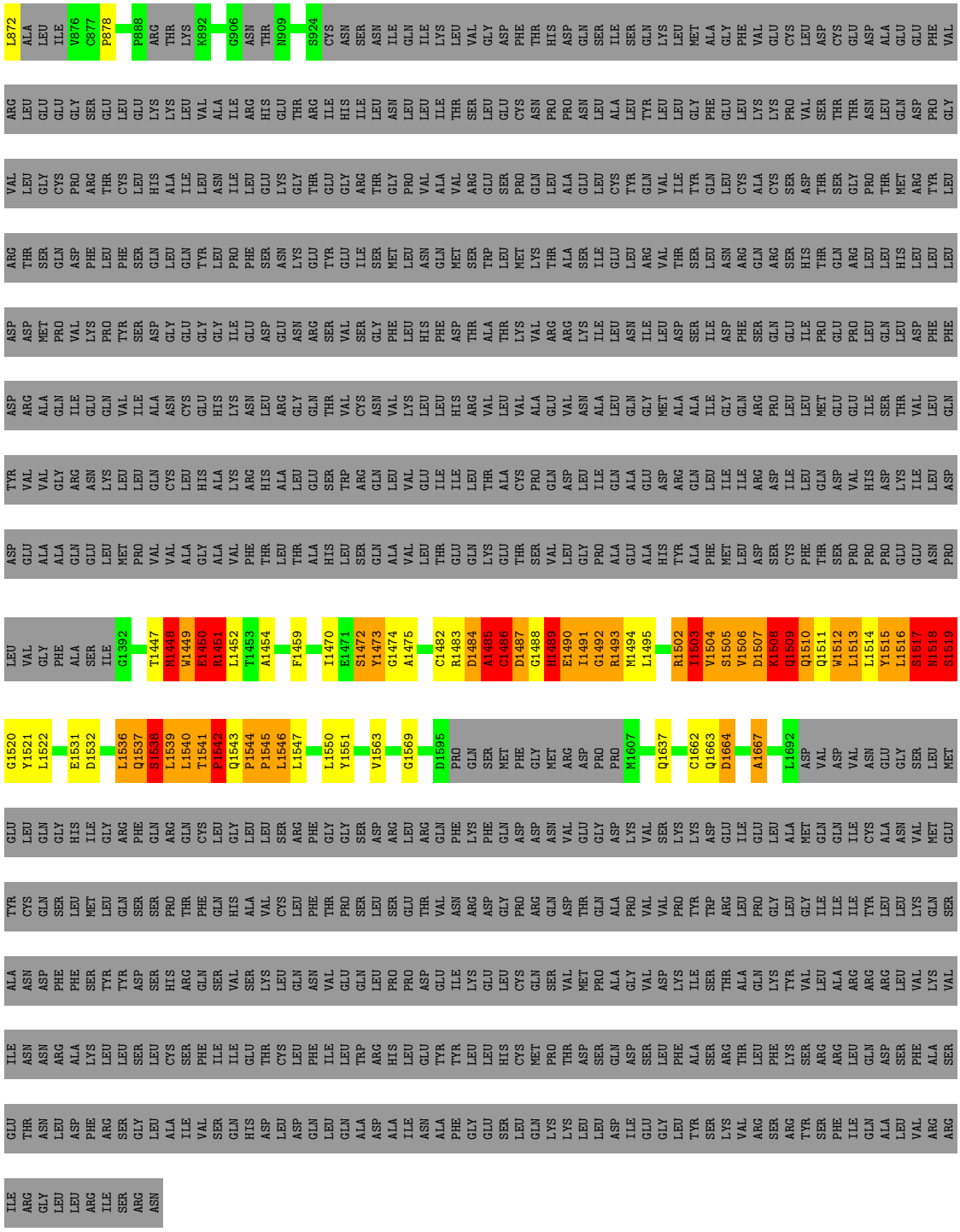




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 7-J:

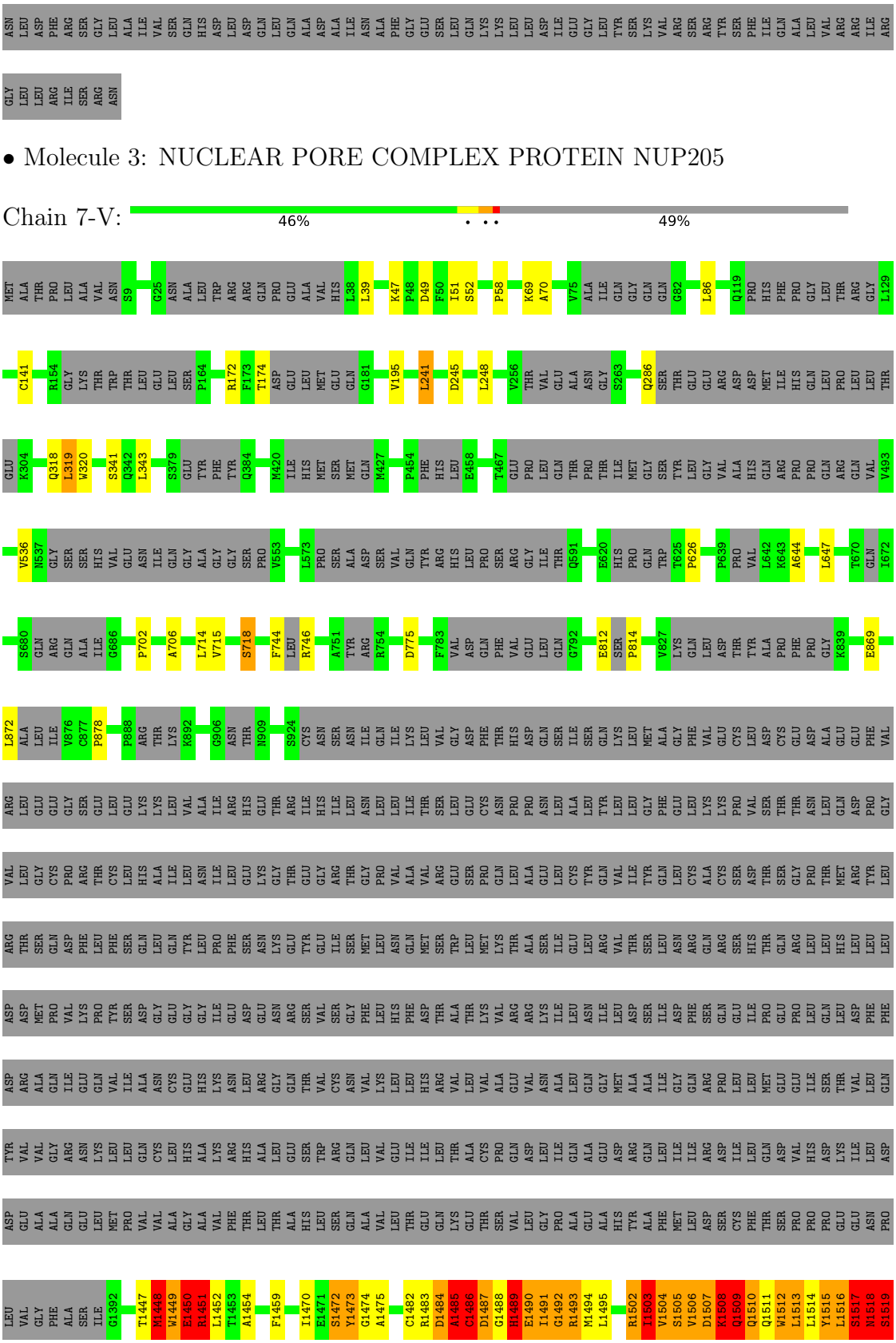




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

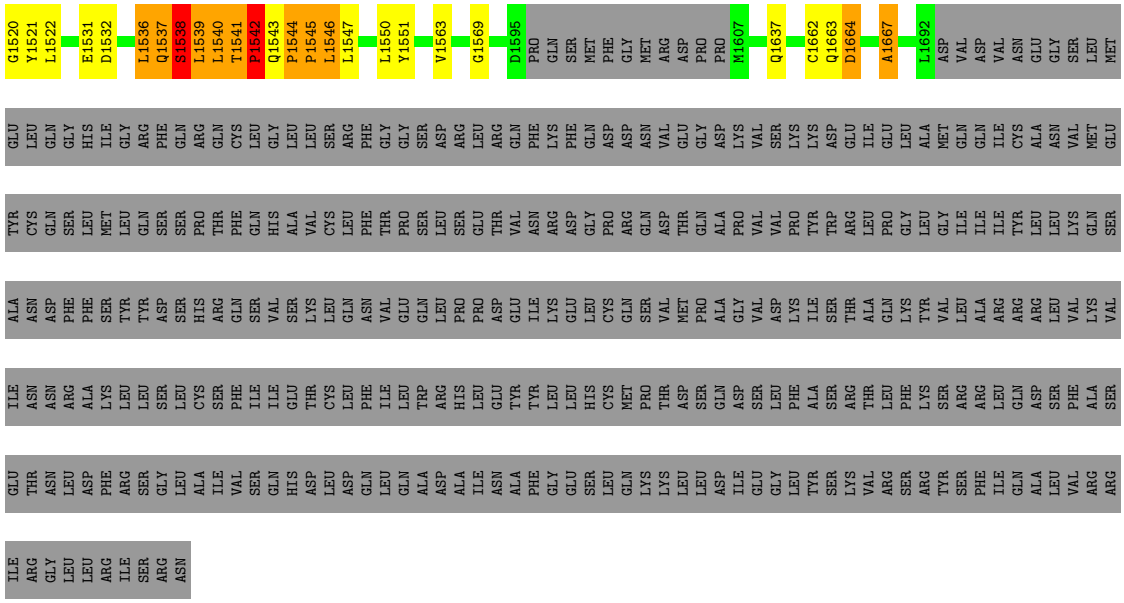
Chain 7-P:

C141 R154 P164 T174 G181 V195 L241 V256 S263 Q286 K304 Q318 L319 W320
S341 Q342 L343 S379 Q384 M420 M427 P454 E458 T467 V493 V536 N537
HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 L573 Q591 E620 T625 P626 P639 L642 K643 A644 L647 T670 I672 S680
ILE G686 P702 A706 L714 V715 S718 F744 R746 A751 R754 D775 F783 Q792 E812 P814 V827 K839 E869 L872 V876 C877
P878 P888 K892 G906 N909 S924
GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE ASN LEU LEU ILE THR SER LEU GLU CYS ASN PRO PRO ASN LEU ALA LEU LEU LEU LYS LYS PRO VAL SER THR THR ASN LEU GLN ASP PRO GLY VAL LEU GLY CYS PRO ARG
THR CYS LEU HIS ALA ILE LEU ASN ILE LEU GLU LYS GLY THR GLU GLY ARG THR GLY PRO VAL ALA VAL ARG GLU GLU SER PRO GLN LEU ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU CYS ALA CYS SER ASP THR SER GLY PRO THR MET ARG TYR LEU ARG THR SER GLN ASP PHE
LEU PHE SER GLN LEU GLN TYR LEU PRO PHE SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR ALA SER ILE ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG SER HIS THR GLN ARG LEU LEU LEU LEU LEU ASP ASP MET PRO VAL LYS
PRO TYR SER ASP GLY GLU GLY GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS VAL ARG ARG LYS ILE LEU ASP SER ILE ASP PHE SER GLN GLU ILE PRO GLU PRO LEU GLN LEU ILE LEU ASP PHE ASP ARG ALA GLN GLU
GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU LEU HIS ARG VAL LEU VAL ALA GLU VAL ASN ALA LEU GLN GLY MET ALA ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU LEU THR SER GLN TYR VAL VAL GLY ARG ASN
LYS LEU LEU GLN CYS LEU HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ALA GLN LEU VAL GLU VAL THR ALA CYS PRO GLN ASP LEU ILE GLN ALA GLU ASP ARG GLN LEU ILE ILE ARG GLN GLU ASP VAL HIS ASP ASP ILE LEU GLN ASP ILE LEU GLN LEU ILE LEU ASP ASP GLU ALA ALA GLN GLU
LEU MET PRO VAL VAL ALA GLY ALA VAL PHE THR LEU THR ALA HIS LEU SER GLN ALA VAL LEU THR GLU ILE ILE LEU LYS GLU THR SER VAL VAL ALA GLU GLU GLN LEU GLY PRO ALA GLU ALA HIS TYR ALA PHE MET LEU ASP SER CYS PHE THR SER PRO PRO GLU GLU ASN PRO LEU VAL HIS ASP LYS ILE LEU ASP PHE ASP ARG ALA GLY VAL GLY PHE ALA SER
ILE G1392 T1447 M1448 W1449 E1450 R1451 F1459 I1470 E1471 S1472 Y1473 G1474 A1475 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511 W1512 L1513 L1514 Y1515 L1516 S1517 N1518 S1519 G1520 Y1521 L1522 E1531 D1532 L1536 Q1537
S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 L1550 Y1551 V1563 G1569 D1595 PRO GLN SER MET PHE GLY MET ARG ASP PRO PRO M1607 Q1637 C1662 Q1663 D1664 A1667 S1681 K1682 L1685 P1686 G1687 L1692 ASP VAL ASP GLU GLY SER LEU MET GLU GLU LEU
GLN GLY HIS ILE GLY ARG PHE GLN ARG GLN CYS LEU GLY LEU SER VAL ARG PHE GLY GLY SER ASP MET LEU ARG GLN PHE LYS PHE GLN ASP ASP ASN VAL SER LYS ASP VAL LYS ILE SER THR GLU VAL MET PRO ALA GLY VAL ASP LYS TYR VAL LEU ALA MET GLN ILE ILE CYS ALA ASN VAL MET GLU TYR CYS
GLN SER LEU MET LEU GLN SER SER PRO THR PHE GLN HIS ALA VAL CYS LEU PHE THR PRO SER LEU SER GLU THR VAL ASN ARG ASP GLY PRO ARG GLN ASP THR GLN ALA THR VAL PRO TYR TRP ARG LEU PRO GLY LEU LEU LEU ILE ILE ILE ILE CYS ALA LEU LEU ILE ILE ALA ALA GLN SER ALA ASN
ASP PHE PHE SER TYR TYR ASP SER HIS ARG GLN SER VAL SER LYS LEU GLN ASN VAL LEU GLN LEU PRO PRO ASP GLU ILE LYS ARG LEU CYS GLN SER VAL MET PRO ALA GLY VAL ASP LYS TYR VAL LEU ARG ARG ARG LEU LYS GLN SER VAL ILE ASN
ASN ARG ALA LYS LEU LEU SER LEU CYS SER PHE ILE ILE LEU TRP ARG HIS LEU GLU TYR TYR LEU LEU LEU HIS CYS MET PRO THR ASP SER GLN ASP SER LEU PHE ALA SER ARG THR ALA PHE LYS ARG ARG LEU ASP PHE ALA SER GLU GLU ILE ILE ILE ARG ARG LEU ASN GLN ASP SER PHE ALA SER GLU GLU THR



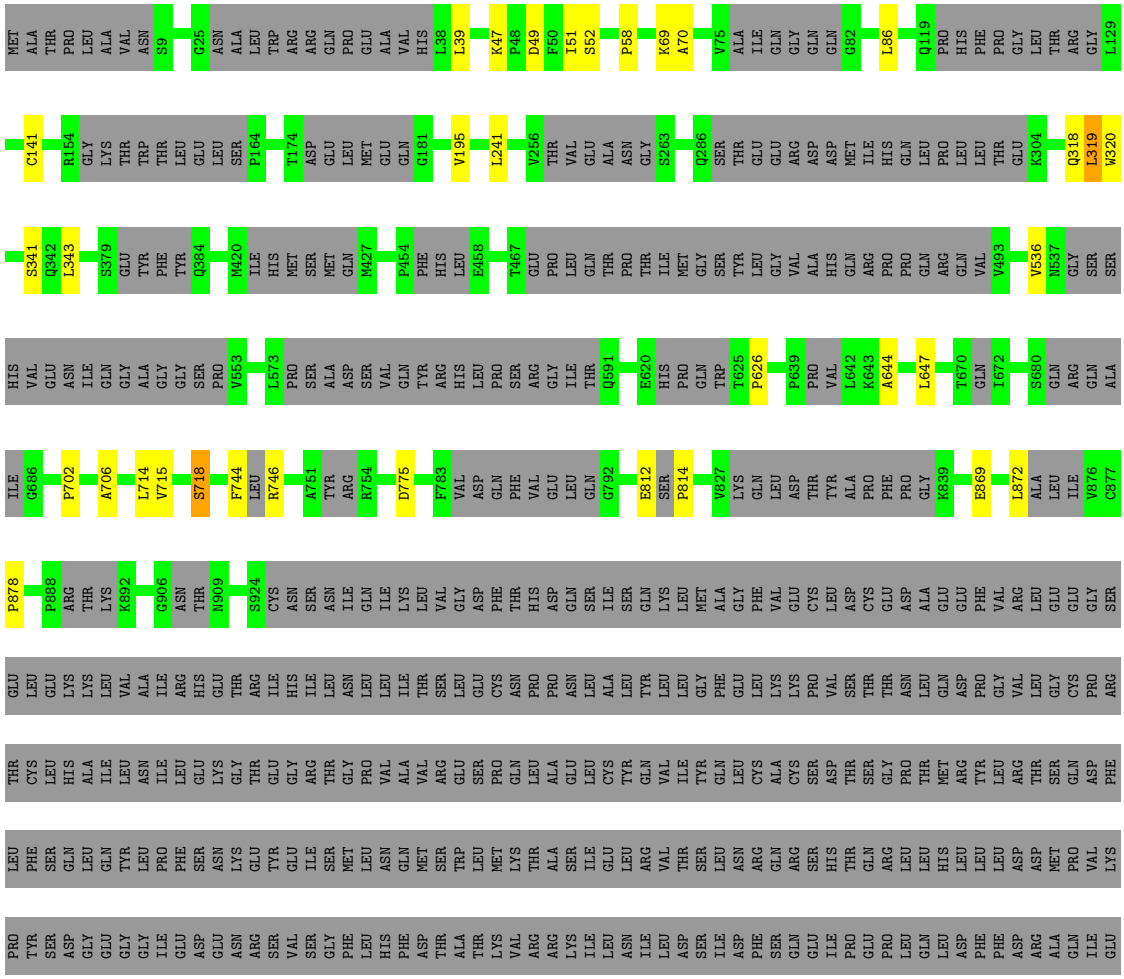
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

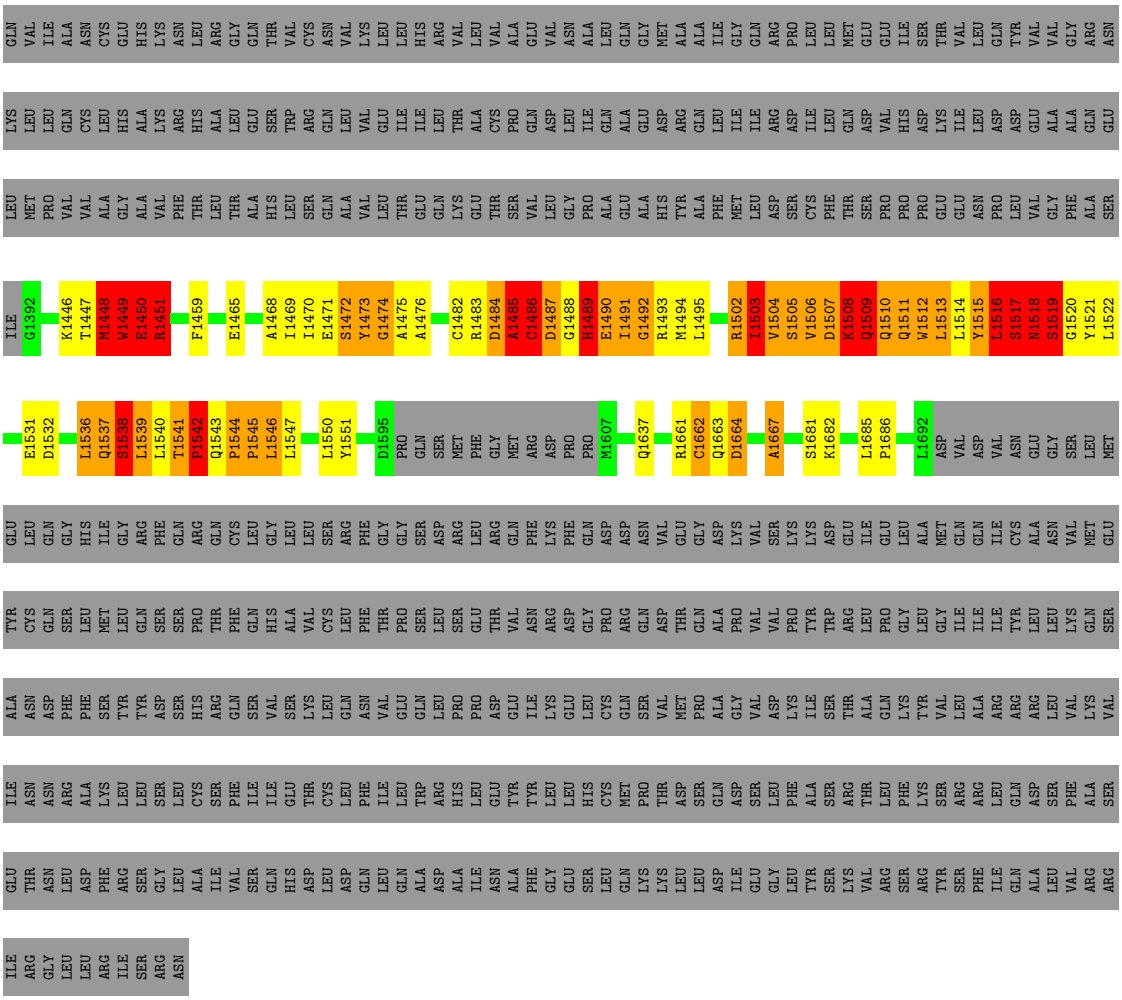
Chain 7-V: 46% 49%



- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

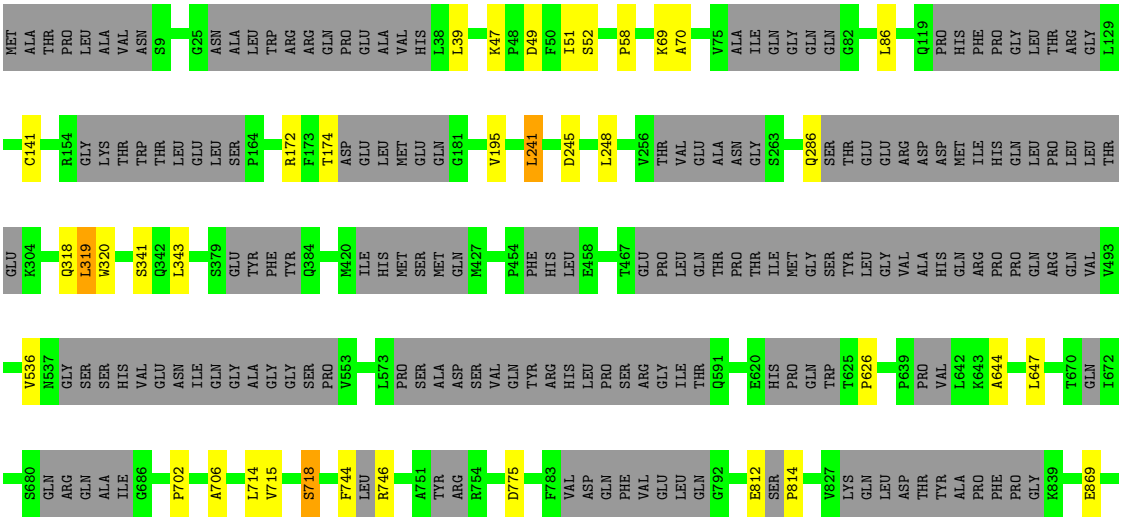
Chain 8-D:

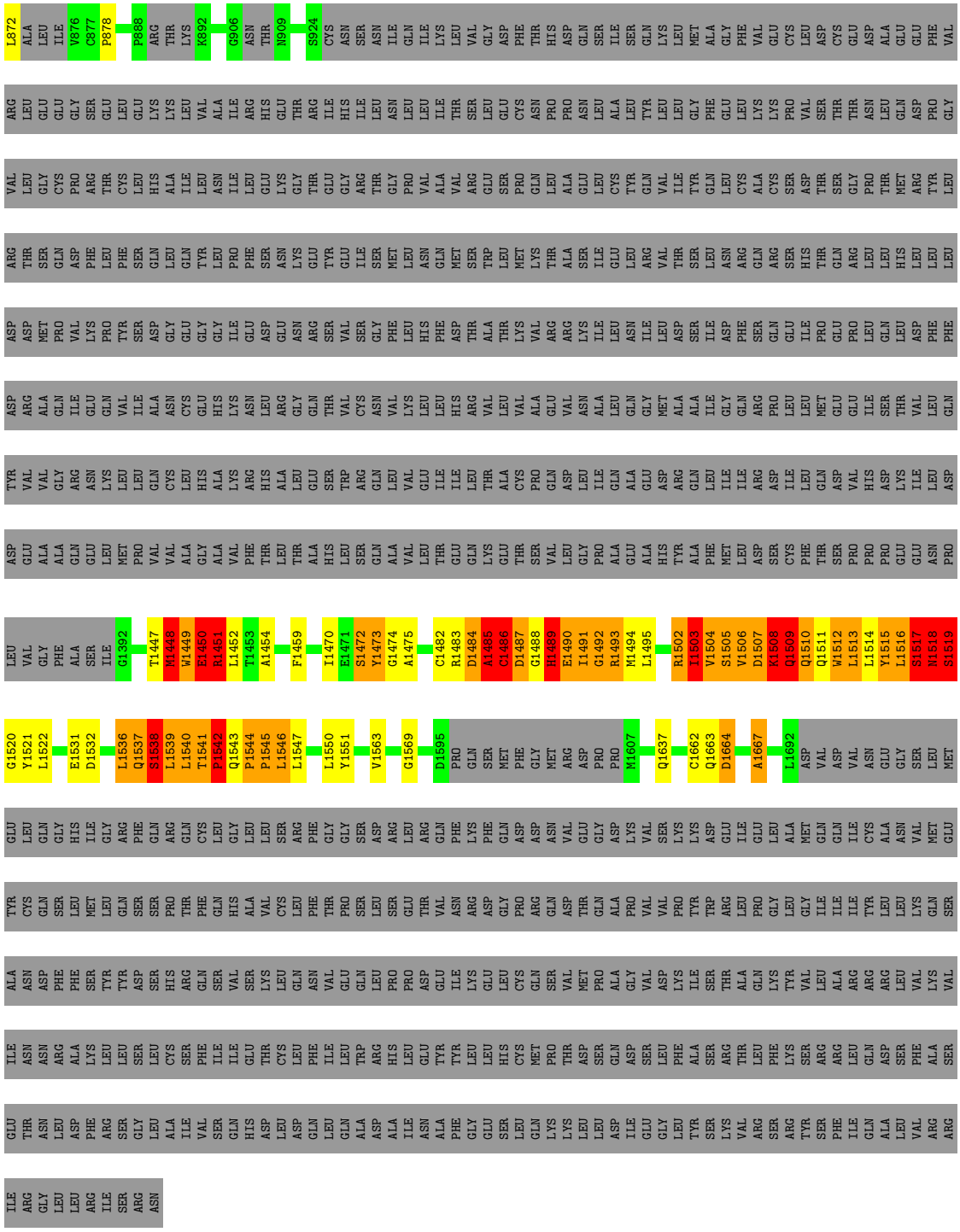




- Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 8-J:

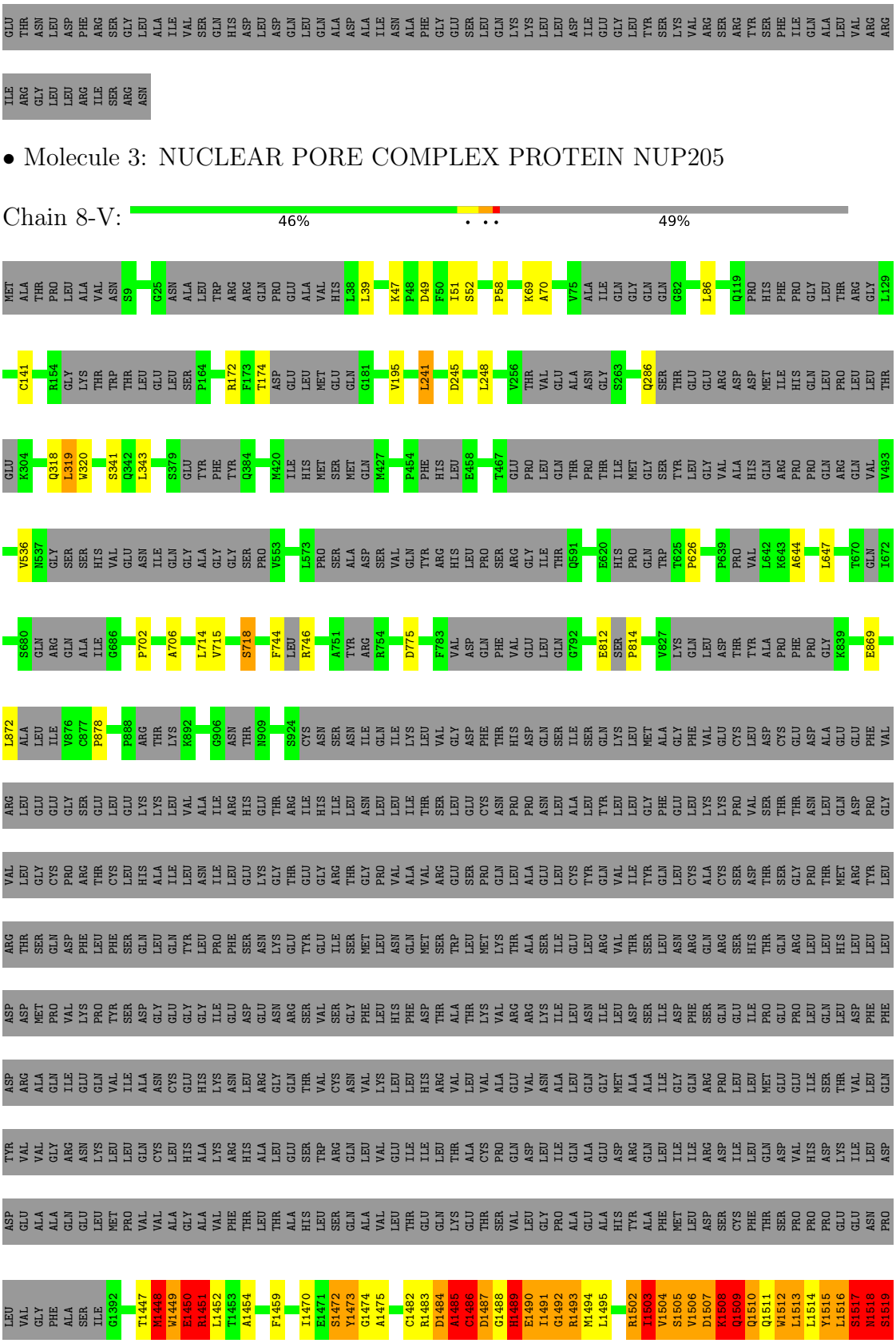




• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

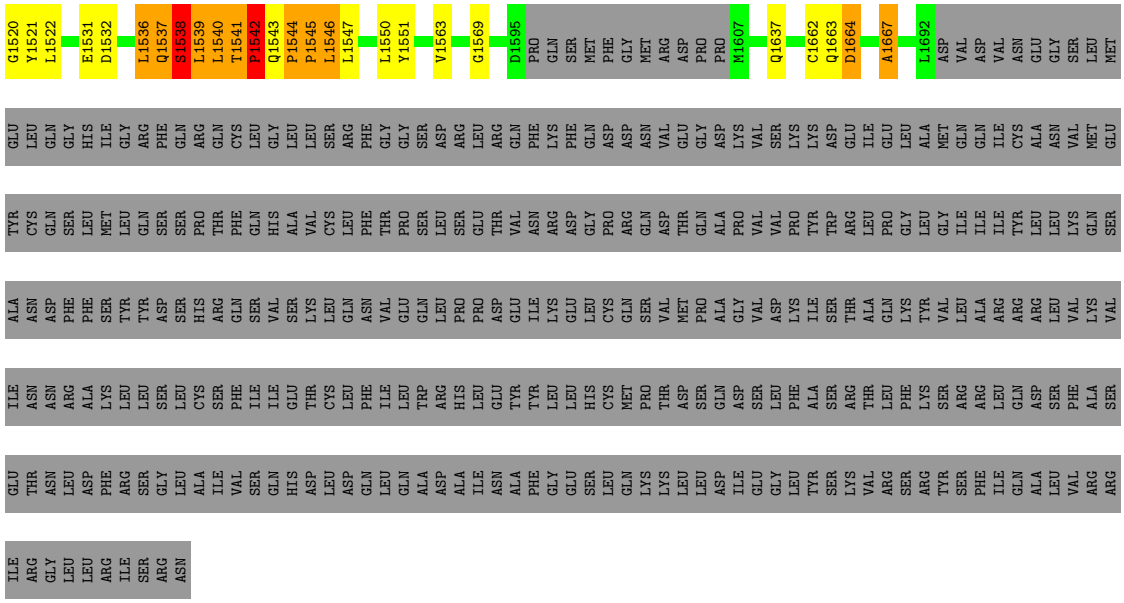
Chain 8-P:

C141 R154 P164 T174 G181 V195 L241 V256 S263 Q286 K304 Q318 L319 W320
S341 Q342 L343 S379 Q384 M420 M427 P454 E458 T467 V493 V536 N537
HIS VAL GLU ASN ILE GLN GLY ALA GLY GLY SER PRO V553 L573 PRO SER ALA ASP SER VAL GLN TYR ARG HIS LEU PRO SER ARG GLY ILE THR Q591 E620 HIS PRO GLN TRP T625 P626 P639 PRO VAL L642 K643 A644 L647 T670 GLN I672 S680 GLN ARG GLN ALA
ILE G686 P702 A706 L714 V715 S718 F744 LEU R746 A751 TYR ARG R754 D775 F783 VAL ASP GLN PHE VAL GLU LEU GLN G792 E812 SER P814 V827 LYS GLN LEU ASP THR TYR ALA PRO PHE PRO GLY K839 E869 L872 ALA LEU ILE V876 C877
P878 P888 ARG THR LYS K892 G906 ASN THR N909 S924 CYS ASN SER ASN ILE GLN ILE LYS LEU VAL GLY ASP PHE THR HIS ASP GLN SER ILE SER GLN LYS LEU MET ALA GLY PHE VAL GLU CYS LEU ASP CYS GLU ASP ALA GLU GLU PHE VAL ARG LEU GLU SER
GLU LEU GLU LYS LYS LEU VAL ALA ILE ARG HIS GLU THR ARG ILE HIS ILE LEU ASN LEU LEU ILE THR SER LEU GLU CYS ASN PRO PRO ASN LEU ALA LEU CYS TYR LEU TYR THR GLN VAL LEU LYS LYS PRO VAL SER THR THR ASN LEU GLN ASP PRO PRO GLY VAL LEU LEU GLY CYS PRO ARG
THR CYS LEU HIS ALA ILE LEU ASN ILE LEU LYS GLY THR GLU GLY ARG THR GLY PRO VAL ALA VAL ARG GLU GLU SER PRO GLN LEU ALA GLU LEU CYS TYR GLN VAL ILE TYR GLN LEU CYS ALA CYS SER ASP THR SER GLY PRO THR MET ARG TYR LEU ARG THR SER GLN ASP PHE
LEU PHE SER GLN LEU GLN TYR LEU LEU PRO PHE SER ASN LYS GLU TYR GLU ILE SER MET LEU ASN GLN MET SER TRP LEU MET LYS THR ALA SER ILE GLU LEU ARG VAL THR SER LEU ASN ARG GLN ARG SER HIS THR GLN ARG LEU LEU LEU LEU LEU ASP PHE VAL LYS
PRO TYR SER ASP GLY GLU GLY GLY ILE GLU ASP GLU ASN ARG SER VAL SER GLY PHE LEU HIS PHE ASP THR ALA THR LYS VAL ARG ARG LYS ILE LEU ASP SER GLN GLU ILE ASP PHE SER GLN GLU ILE LEU ASP PRO GLU PRO LEU GLN LEU ASP PHE ASP ARG ALA GLN GLU
GLN VAL ILE ALA ASN CYS GLU HIS LYS ASN LEU ARG GLY GLN THR VAL CYS ASN VAL LYS LEU LEU HIS ARG VAL LEU VAL ALA GLU VAL ASN ALA LEU GLN GLY MET ALA ALA ILE GLY GLN ARG PRO LEU LEU MET GLU GLU LEU TYR ARG GLN VAL VAL GLY ARG ASN
LYS LEU LEU GLN CYS LEU HIS HIS ALA LYS ARG HIS ALA LEU GLU SER TRP ARG GLN LEU VAL GLU LEU THR ALA CYS PRO GLN ASP LEU ILE GLN ALA GLU ASP GLU ILE ILE LEU LEU ILE GLN GLU ILE ILE GLN GLU LYS ILE LEU GLN ILE LEU GLU ALA ALA GLU
LEU MET PRO VAL VAL PHE THR LEU THR ALA ALA HIS LEU SER GLN ALA VAL LEU THR GLU GLN LYS GLY THR SER VAL LEU GLY PRO ALA GLU ALA HIS TYR ALA PHE MET LEU ASP SER CYS PHE THR SER PRO PRO PRO GLU LEU VAL LEU ASP PHE ASP ALA GLY PHE ALA SER
ILE G1392 K1446 T1447 M1448 W1449 E1450 R1451 F1459 E1465 A1468 I1469 I1470 E1471 S1472 Y1473 G1474 A1475 A1476 C1482 R1483 D1484 A1485 C1486 D1487 G1488 H1489 E1490 I1491 G1492 R1493 M1494 L1495 R1502 I1503 V1504 S1505 V1506 D1507 K1508 Q1509 Q1510 Q1511 W1512 L1513 L1514 Y1515 L1516 S1517 N1518 S1519 G1520 Y1521 L1522
E1531 D1532 L1536 Q1537 S1538 L1539 L1540 T1541 P1542 Q1543 P1544 P1545 L1546 L1547 L1550 Y1551 D1595 PRO GLN SER MET PHE GLY MET ARG ASP PRO PRO M1607 Q1637 R1661 C1662 Q1663 D1664 A1667 S1681 K1682 L1685 P1686 L1692 ASP VAL ASP VAL ASN GLU GLY SER VAL MET
GLU LEU GLN GLY HIS ILE GLY ARG PHE GLN CYS LEU GLY LEU LEU SER ARG PHE GLY GLY SER ASP ARG LEU ARG GLN PHE LYS PHE GLN ASP ASP ASN VAL GLU GLY ASP LYS VAL SER LYS LYS ASP GLU ILE GLU LEU ALA MET GLN GLN ILE ILE CYS TYR GLU
TYR CYS GLN SER LEU MET LEU GLN SER SER PRO THR PHE GLN HIS ALA VAL CYS LEU PHE THR PRO SER LEU SER ASP ARG GLN ASP PRO GLN ARG ASP PRO GLY PRO ARG GLN ASP THR ARG VAL VAL PRO TYR TRP ARG LEU PRO GLY LEU ILE ILE TYR LEU
ALA ASN ASP PHE PHE SER TYR TYR ASP SER HIS ARG GLN SER LYS LEU GLN ASN VAL GLU GLU ASP GLU LEU CYS GLN SER VAL MET PRO ALA GLY VAL ASP LYS ILE SER THR ALA LEU ALA ARG ARG ARG LEU ALA VAL
ILE ASN ASN ARG ALA LYS LEU LEU SER LEU CYS SER PHE ILE ILE LEU GLU THR CYS PHE ILE ILE LEU LEU ARG HIS LEU LEU GLU HIS CYS MET PRO THR ASP SER GLN ASP SER LEU PHE ALA SER ARG THR ALA LEU ARG ARG LEU ASP PHE ALA SER



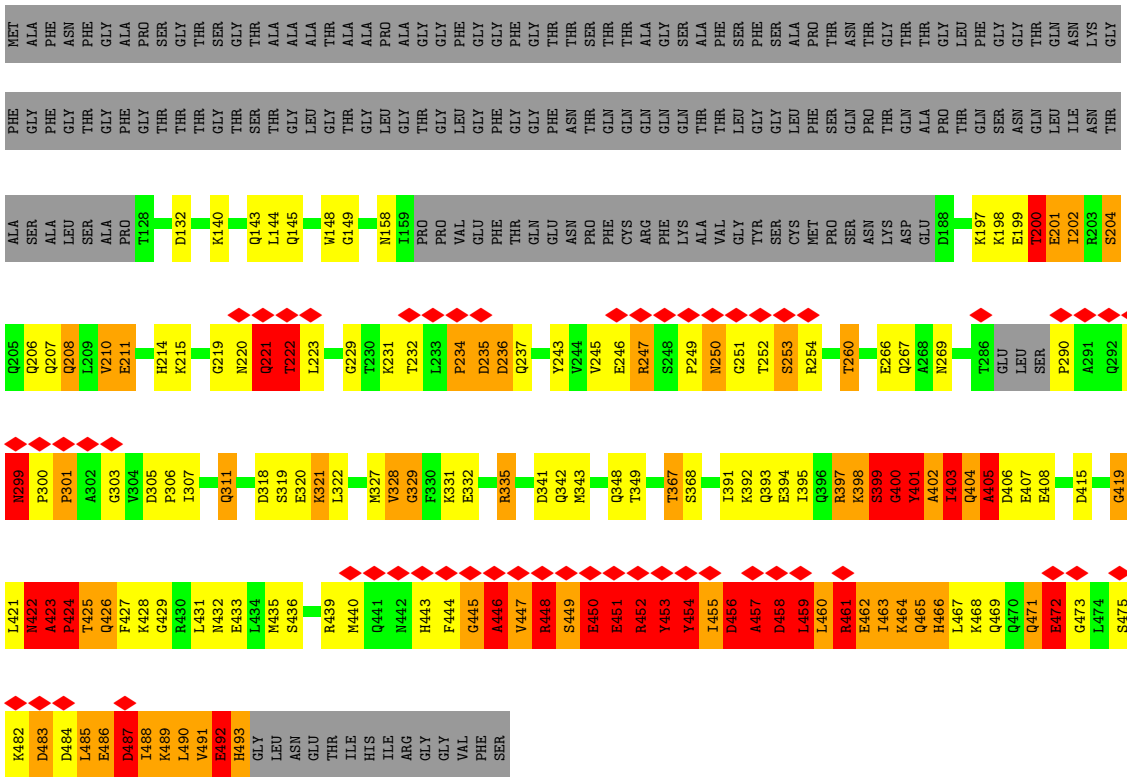
• Molecule 3: NUCLEAR PORE COMPLEX PROTEIN NUP205

Chain 8-V: 46% 49%



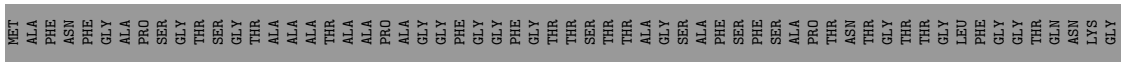
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

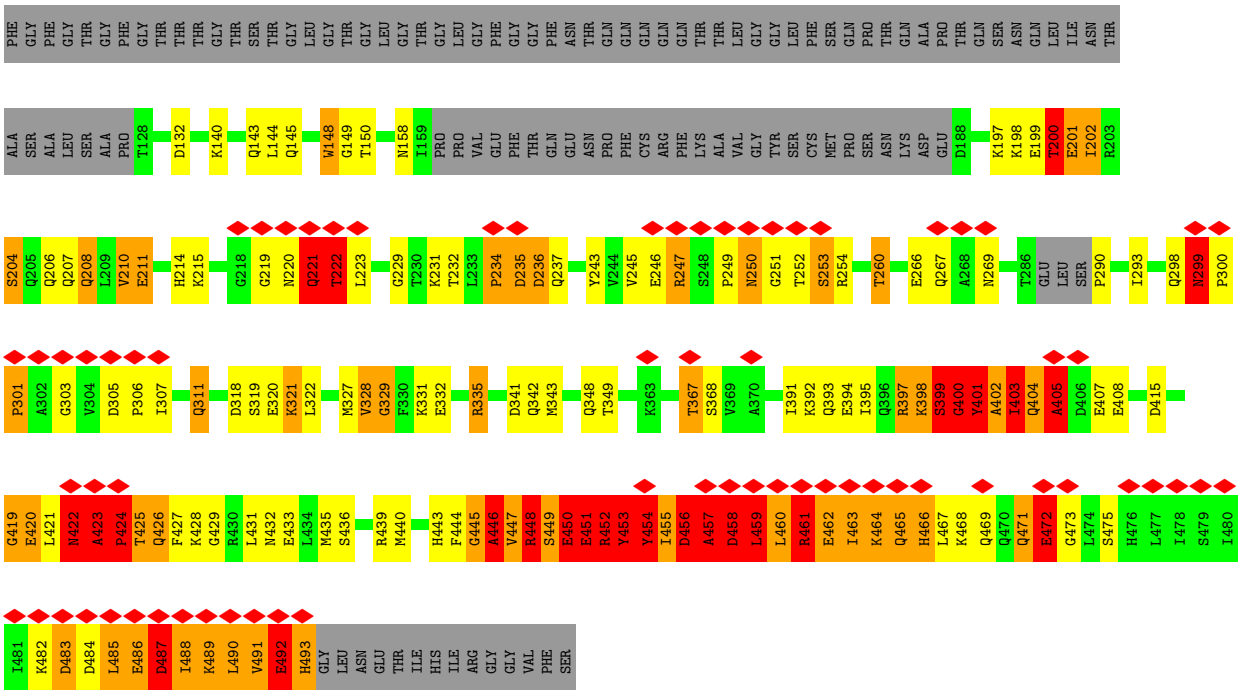
Chain 1-F:



• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

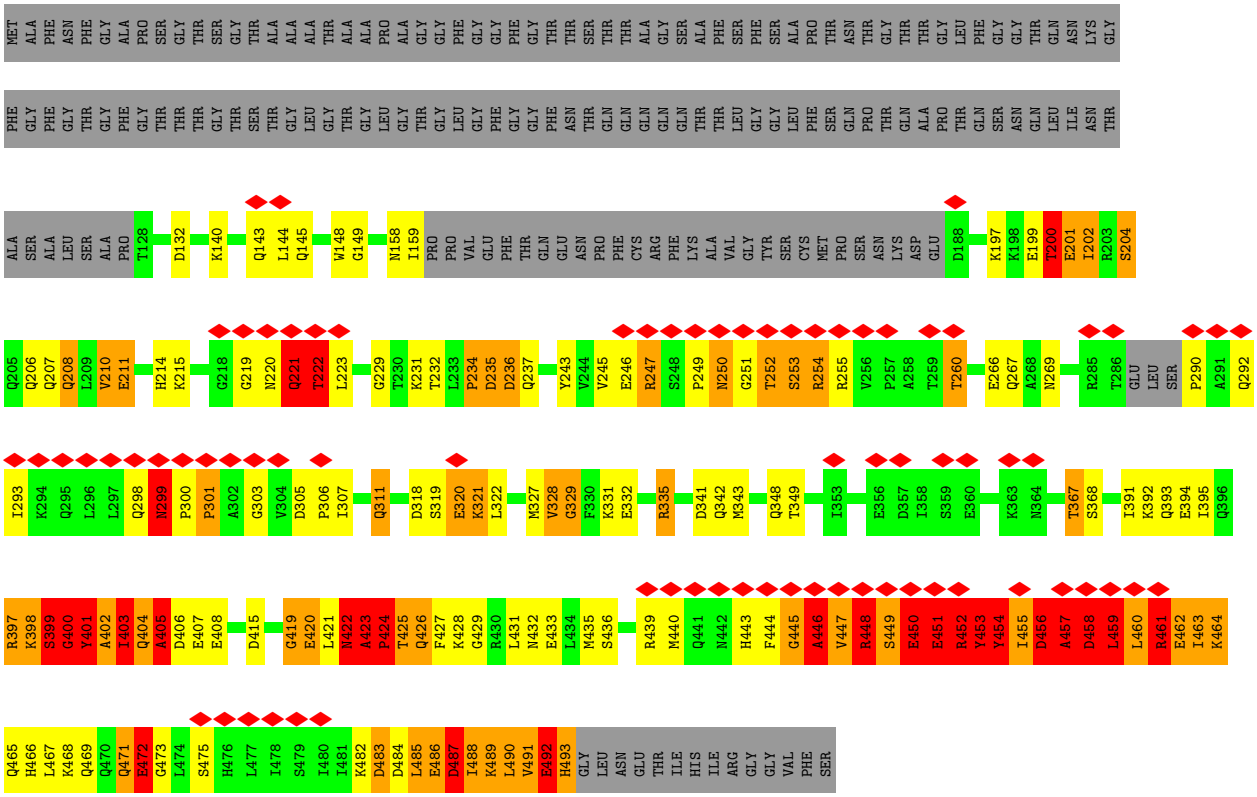
Chain 1-L:





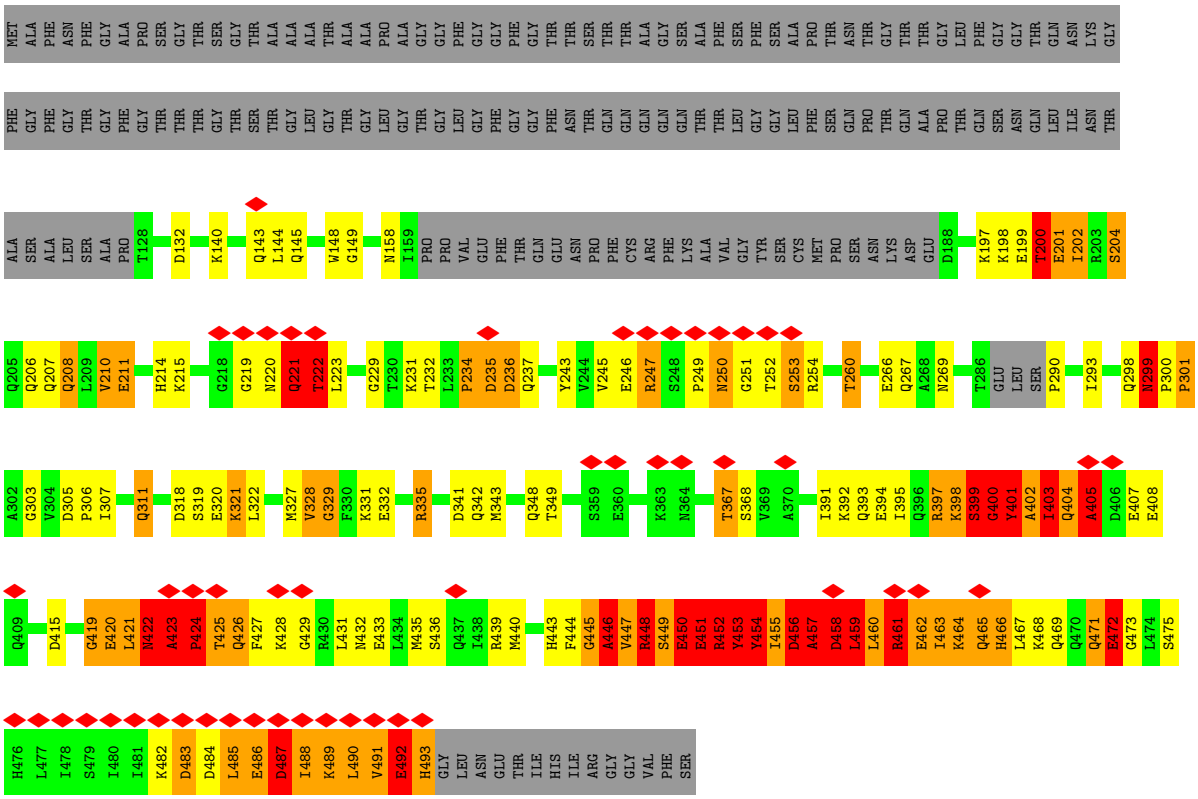
- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 1-R:



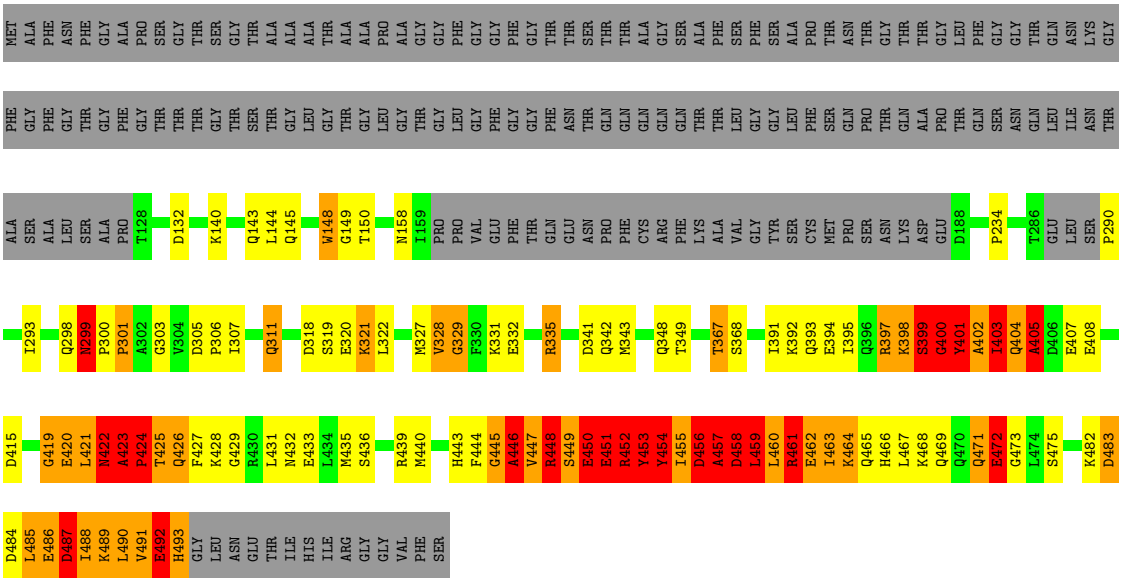
- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 1-X:



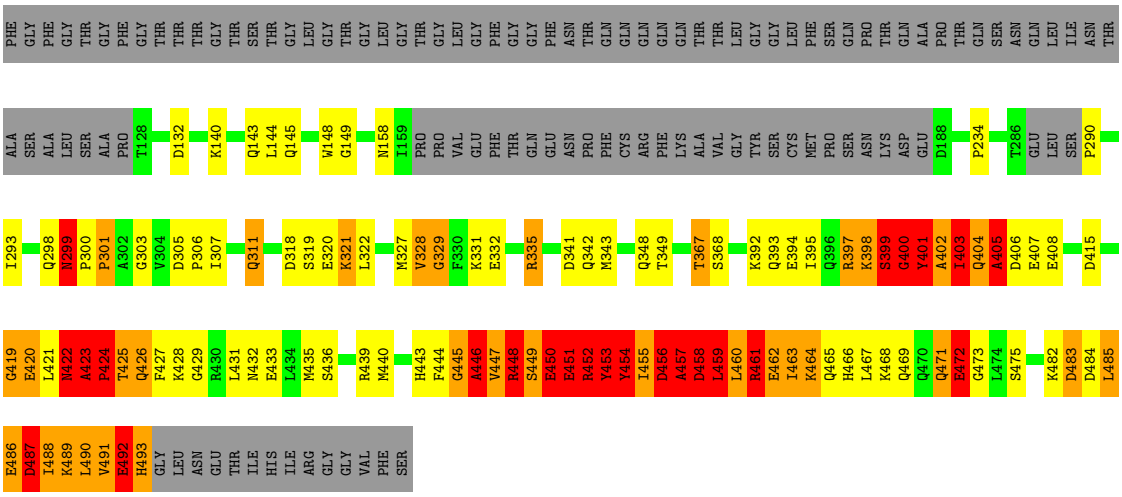
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 2-F: 43% 12% 7% 5% 34%



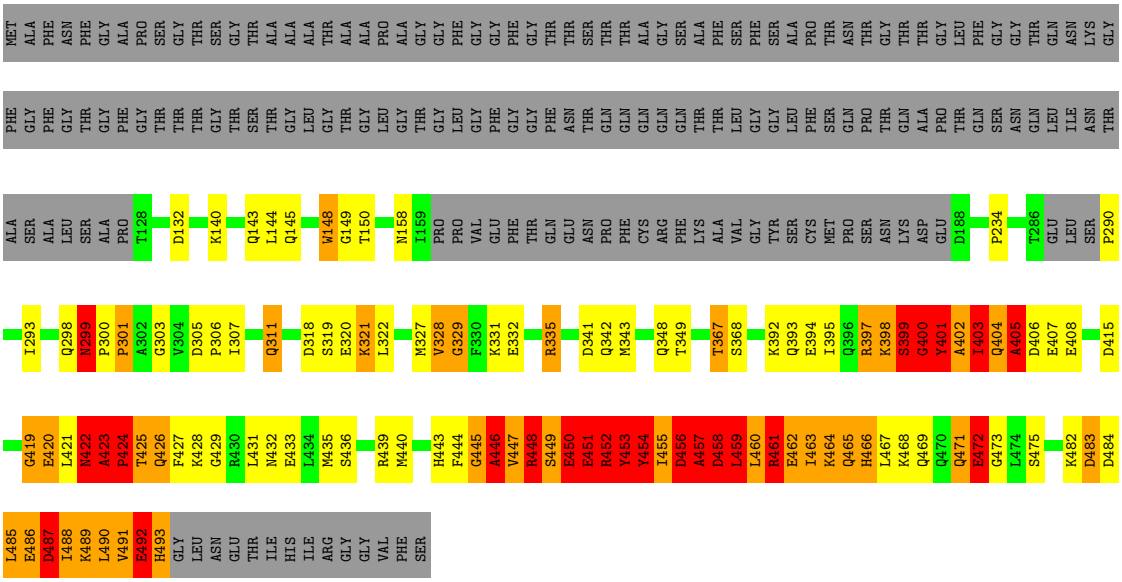
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 2-L: 43% 12% 6% 5% 34%



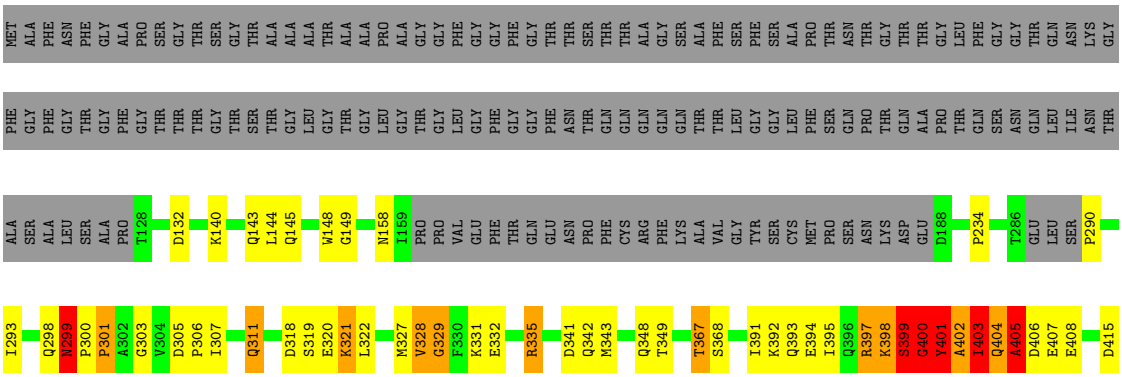
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 2-R: 43% 11% 7% 5% 34%



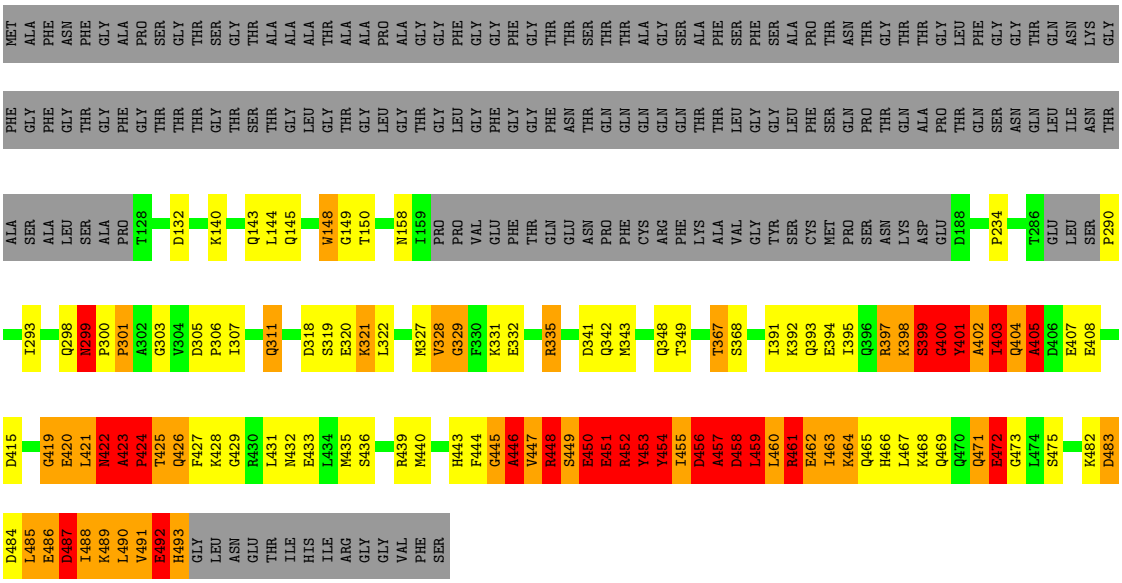
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 2-X: 43% 12% 6% 5% 34%



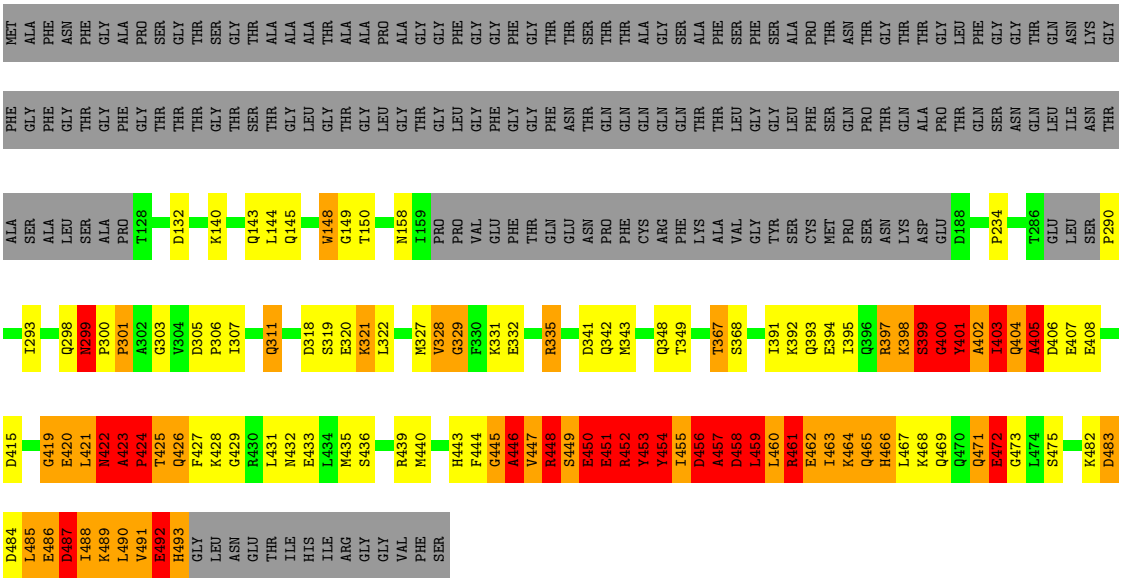
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 3-F: 43% 12% 7% 5% 34%



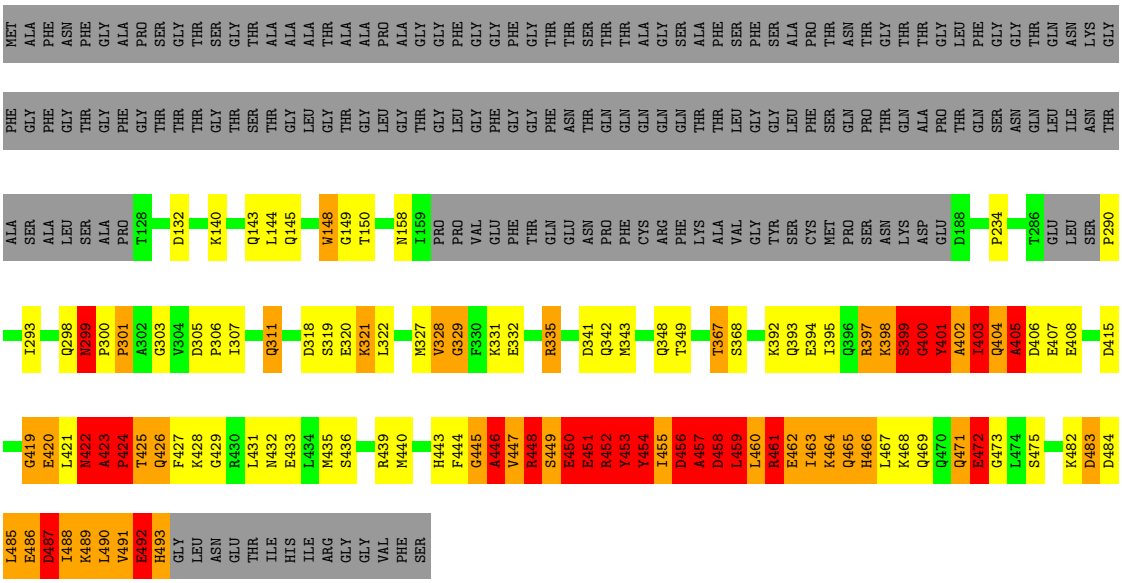
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 3-L: 43% 11% 7% 5% 34%



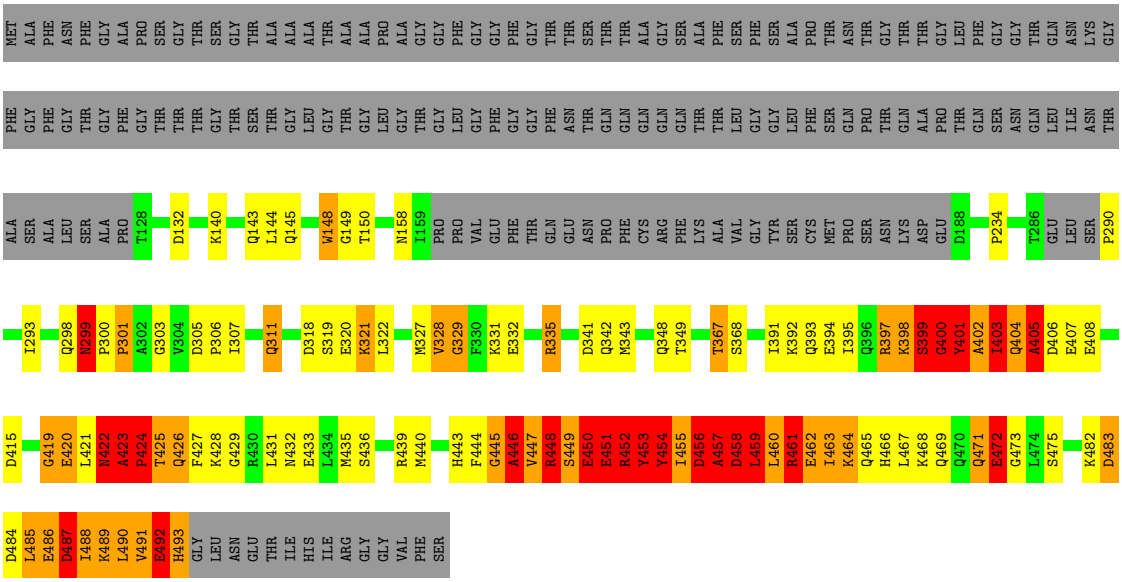
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 3-R: 43% 11% 7% 5% 34%



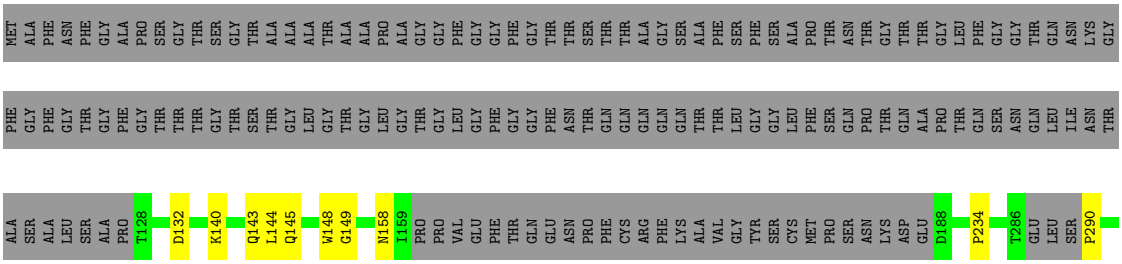
- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

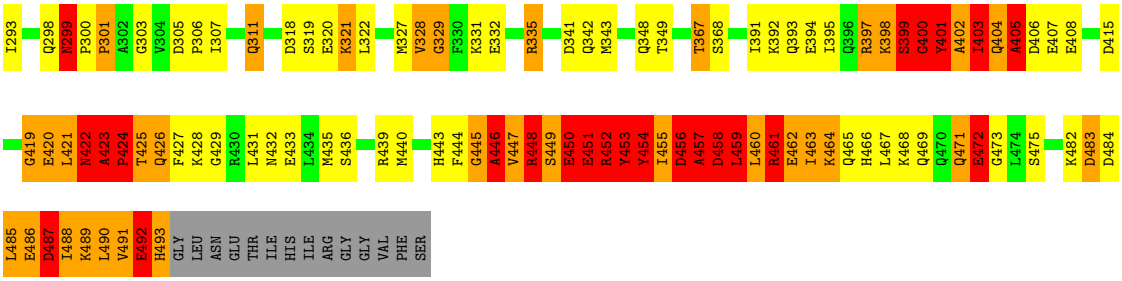
Chain 3-X: 43% 12% 7% 5% 34%



- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

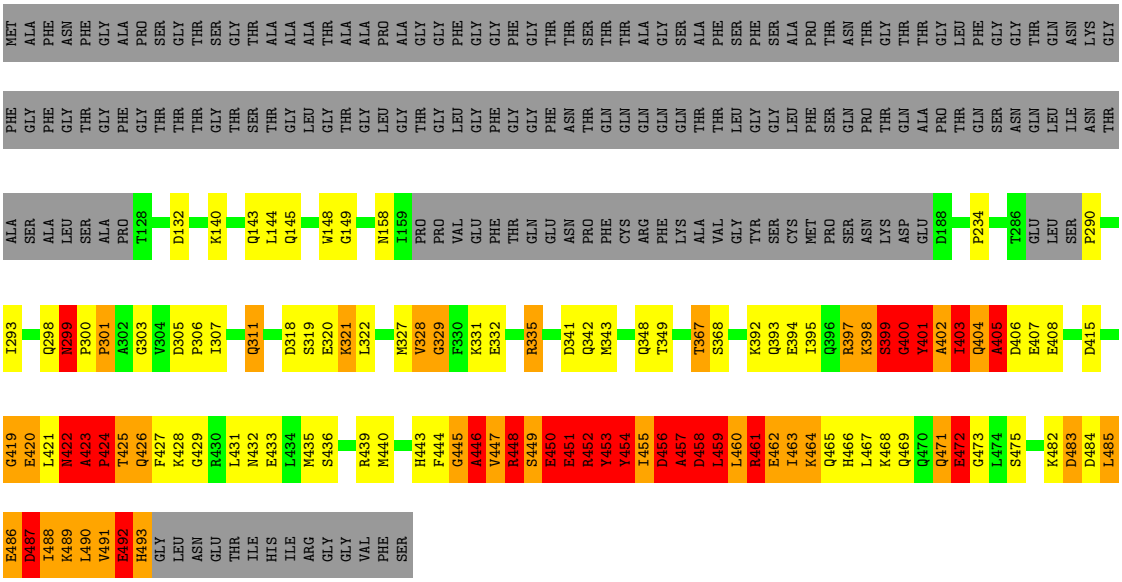
Chain 4-F: 43% 12% 7% 5% 34%





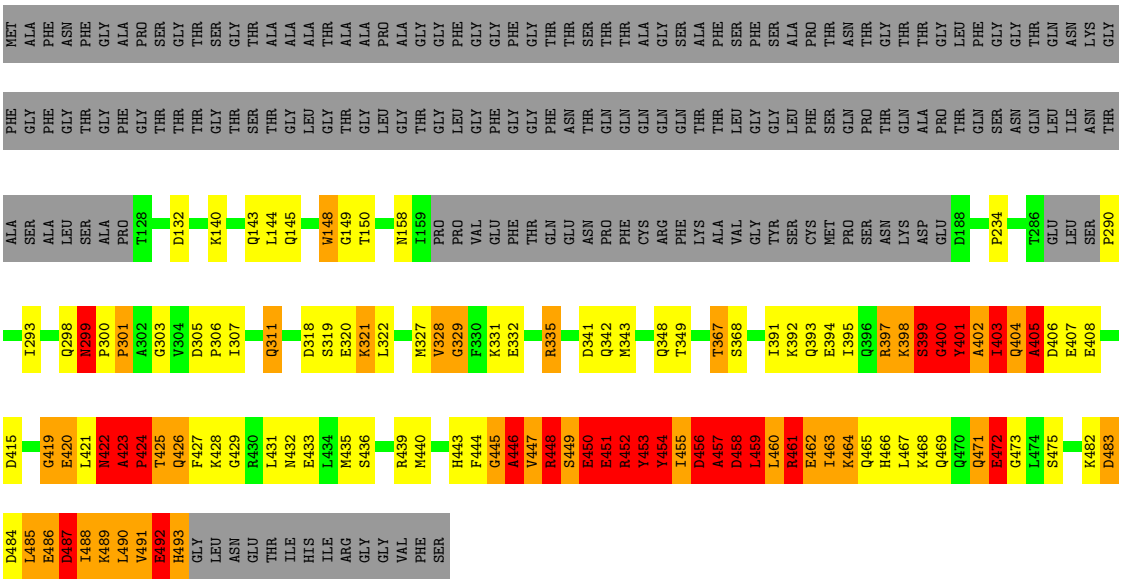
- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 4-L: 43% 12% 6% 5% 34%



- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 4-R: 43% 12% 7% 5% 34%



- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 4-X: 43% 12% 6% 5% 34%

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

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

ALA SER ALA LEU SER ALA PRO T128 D132 K140 Q143 L144 Q145 W148 G149 N158 I159 PRO PRO VAL GLU PHE THR GLN GLU ASN PRO PHE CYS ARG PHE LYS ALA VAL GLY TYR SER CYS MET PRO SER ASN LYS ASP GLU D188 P234 T286 GLU LEU SER P290

I293 Q298 N299 P300 P301 A302 G303 V304 D305 P306 I307 Q311 D318 S319 E320 K321 L322 M327 V328 G329 F330 K331 E332 R335 D341 Q342 M343 Q348 T349 T367 S368 I391 K392 Q393 E394 I395 Q396 R397 K398 S399 G400 Y401 A402 I403 Q404 A405 D406 E407 E408 D415

G419 E420 L421 N422 A423 P424 T425 Q426 F427 K428 G429 R430 L431 N432 E433 L434 M435 S436 R439 M440 H443 F444 G445 A446 V447 R448 S449 E450 E451 R452 Y453 Y454 I455 D456 A457 D458 L459 L460 R461 E462 I463 K464 Q465 H466 L467 K468 Q469 Q470 Q471 E472 G473 L474 S475 K482 D483 D484

L485 E486 D487 I488 K489 L490 V491 E492 H493 GLY LEU ASN GLU THR ILE HIS ILE ARG GLY GLY VAL PHE SER

- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 5-F: 43% 12% 7% 5% 34%

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

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

ALA SER ALA LEU SER ALA PRO T128 D132 K140 Q143 L144 Q145 W148 G149 N158 I159 PRO PRO VAL GLU PHE THR GLN GLU ASN PRO PHE CYS ARG PHE LYS ALA VAL GLY TYR SER CYS MET PRO SER ASN LYS ASP GLU D188 P234 T286 GLU LEU SER P290

I293 Q298 N299 P300 P301 A302 G303 V304 D305 P306 I307 Q311 D318 S319 E320 K321 L322 M327 V328 G329 F330 K331 E332 R335 D341 Q342 M343 Q348 T349 T367 S368 I391 K392 Q393 E394 I395 Q396 R397 K398 S399 G400 Y401 A402 I403 Q404 A405 D406 E407 E408 D415

G419 E420 L421 N422 A423 P424 T425 Q426 F427 K428 G429 R430 L431 N432 E433 L434 M435 S436 R439 M440 H443 F444 G445 A446 V447 R448 S449 E450 E451 R452 Y453 Y454 I455 D456 A457 D458 L459 L460 R461 E462 I463 K464 Q465 H466 L467 K468 Q469 Q470 Q471 E472 G473 L474 S475 K482 D483 D484

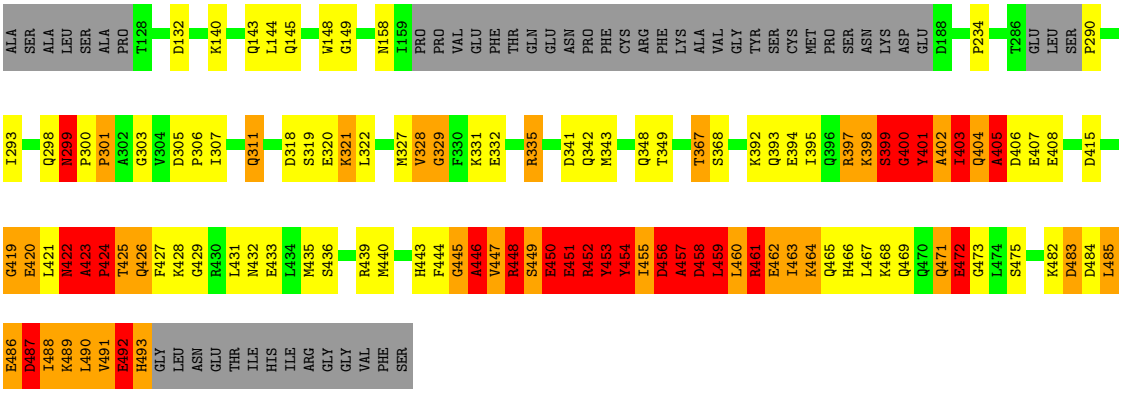
L485 E486 D487 I488 K489 L490 V491 E492 H493 GLY LEU ASN GLU THR ILE HIS ILE ARG GLY GLY VAL PHE SER

- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 5-L: 43% 12% 6% 5% 34%

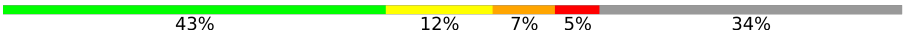
MET ALA PHE ASN PHE GLY ALA PRO SER GLY THR SER GLY THR ALA ALA ALA THR ALA ALA PRO ALA GLY GLY PHE GLY GLY PHE GLY THR THR SER THR THR ALA GLY SER ALA PHE SER PHE SER ALA PRO THR ASN THR GLY THR THR GLY LEU PHE GLY GLY THR GLN LYS GLY

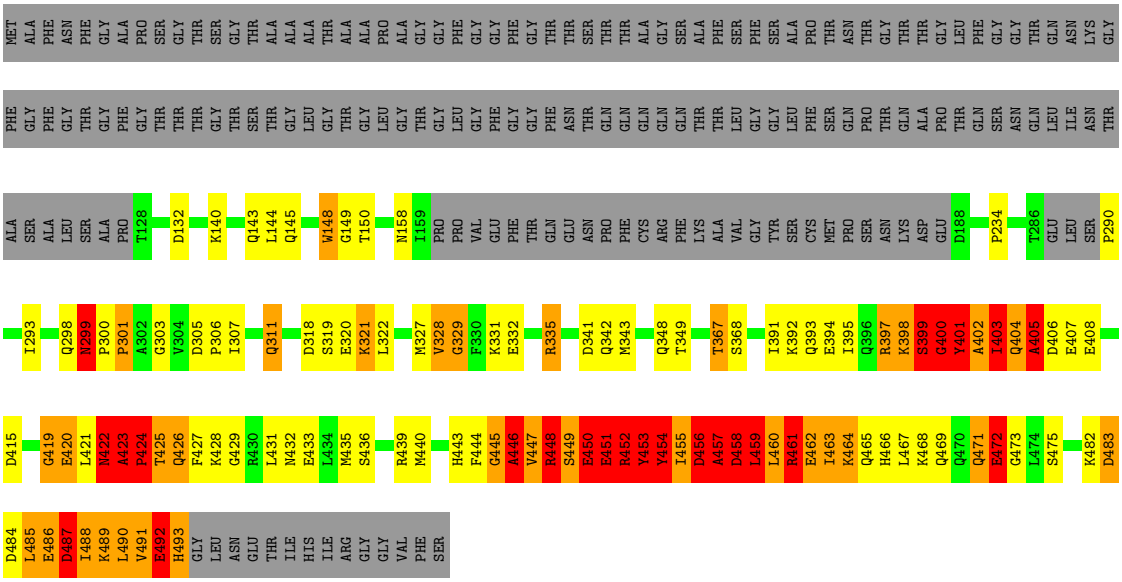
PHE GLY PHE GLY THR GLY PHE GLY THR THR GLY THR SER THR GLY LEU GLY THR GLY LEU GLY PHE GLY GLY PHE ASN THR GLN GLN GLN GLN GLN THR THR LEU GLY GLY LEU PHE SER GLN PRO THR GLN ALA PRO THR GLN SER ASN GLN LEU ILE ASN THR



- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

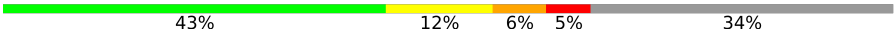
Chain 5-R:

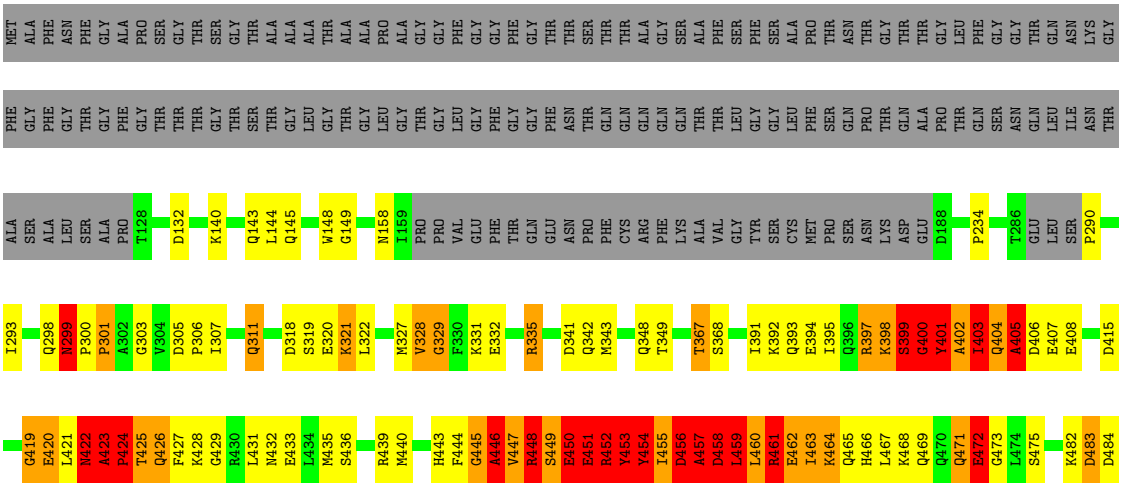


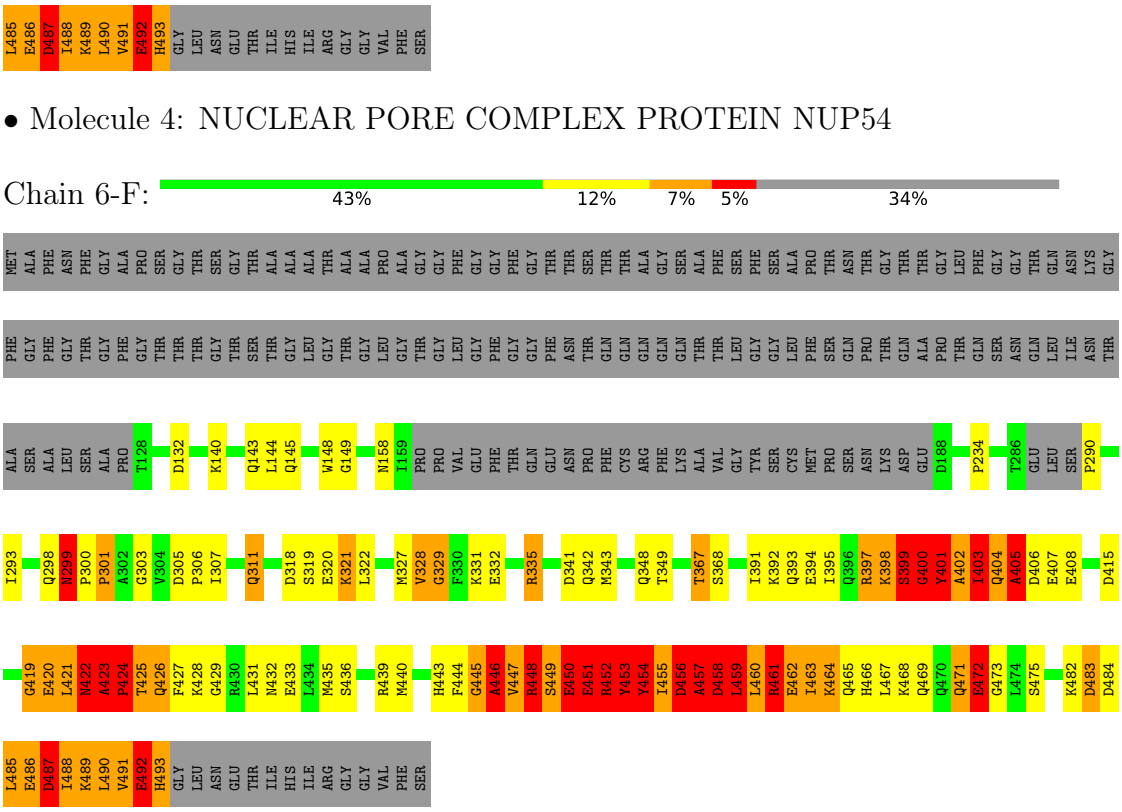


- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 5-X:





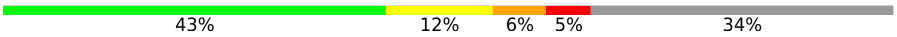


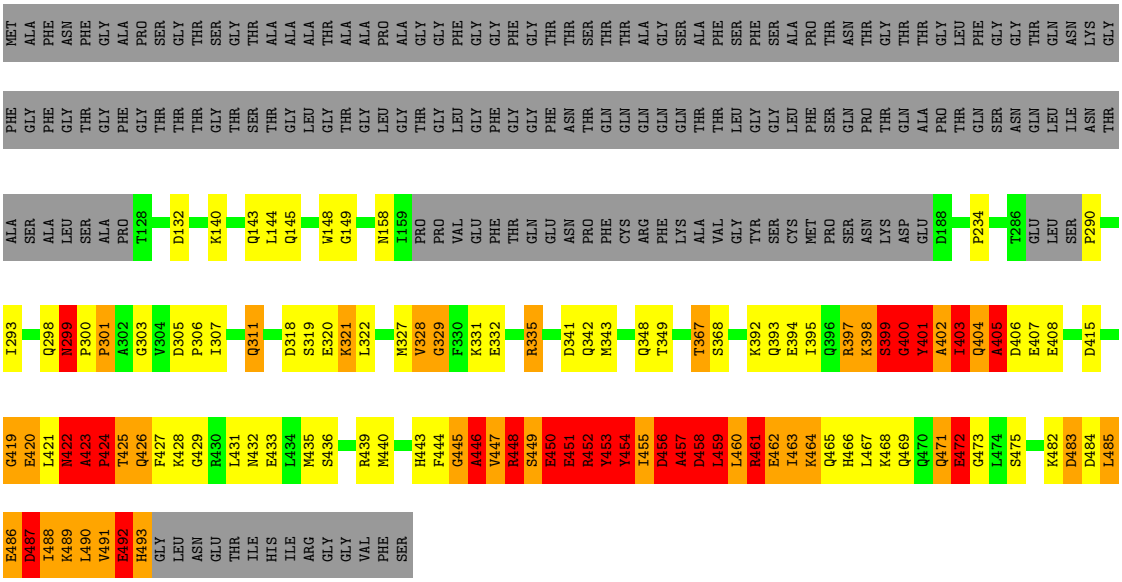
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 6-F:

• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

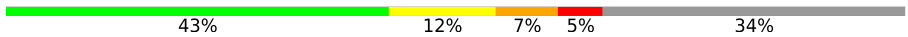
Chain 6-L:

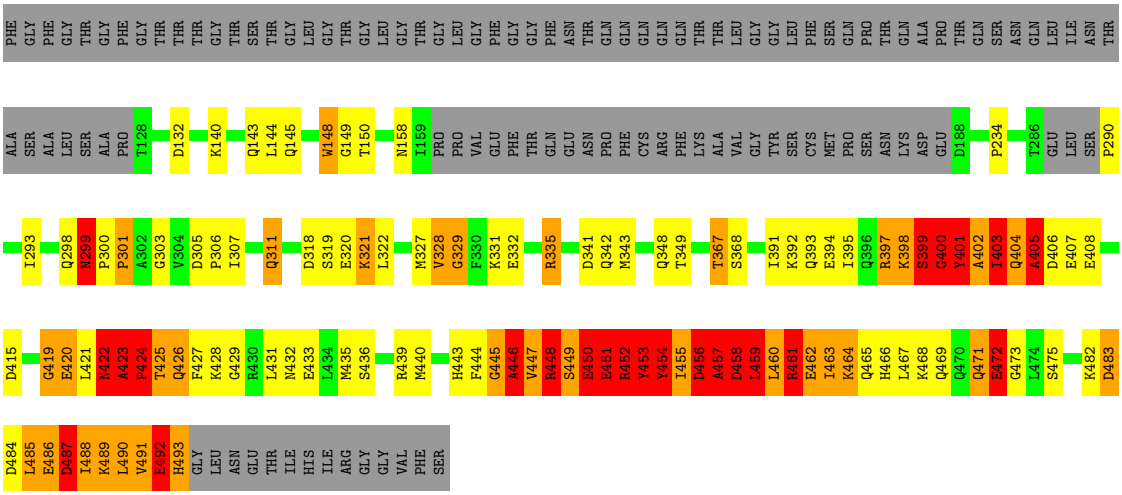




• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

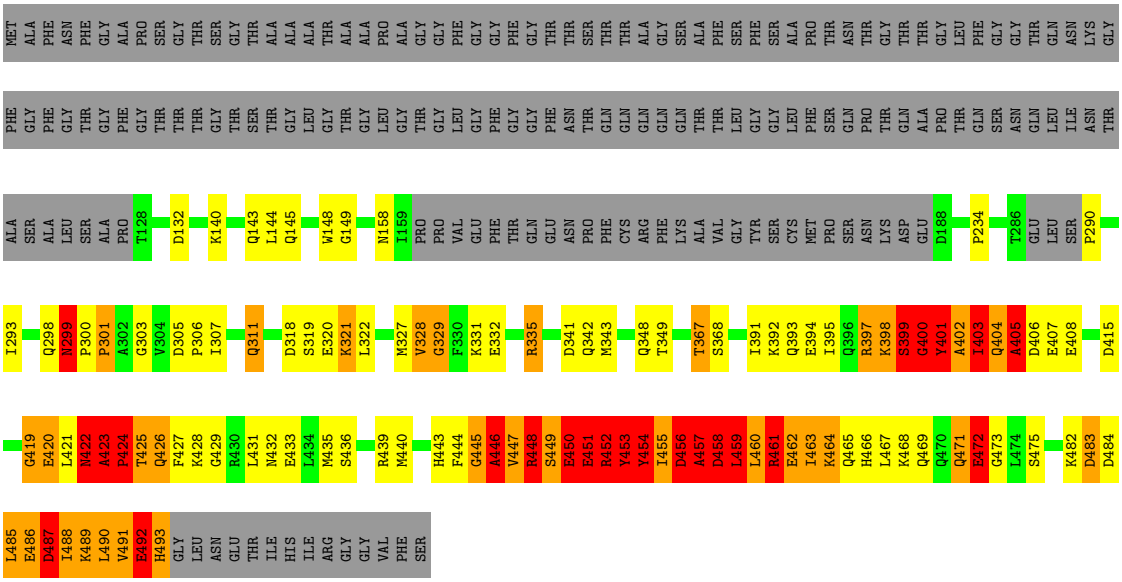
Chain 6-R:





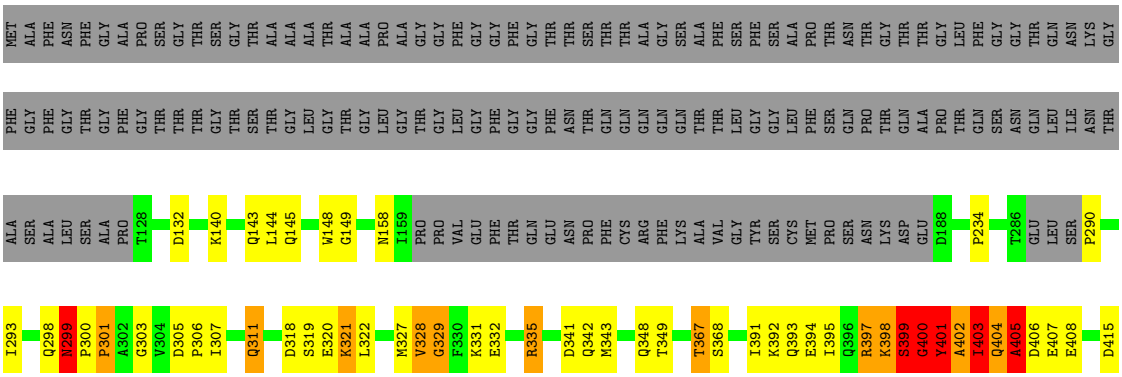
- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 6-X: 43% 12% 6% 5% 34%



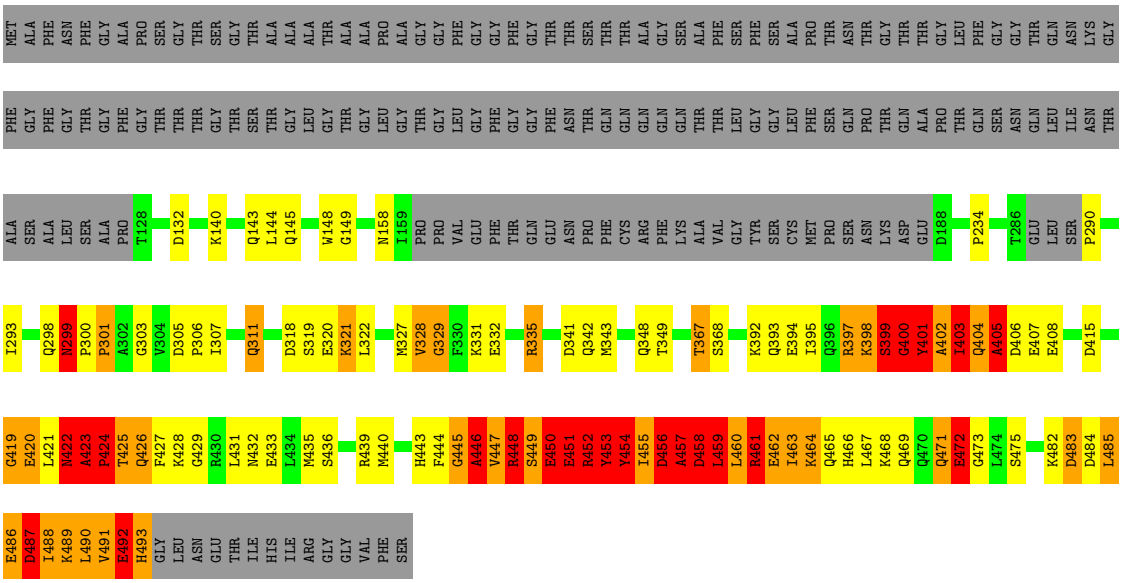
- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 7-F: 43% 12% 7% 5% 34%



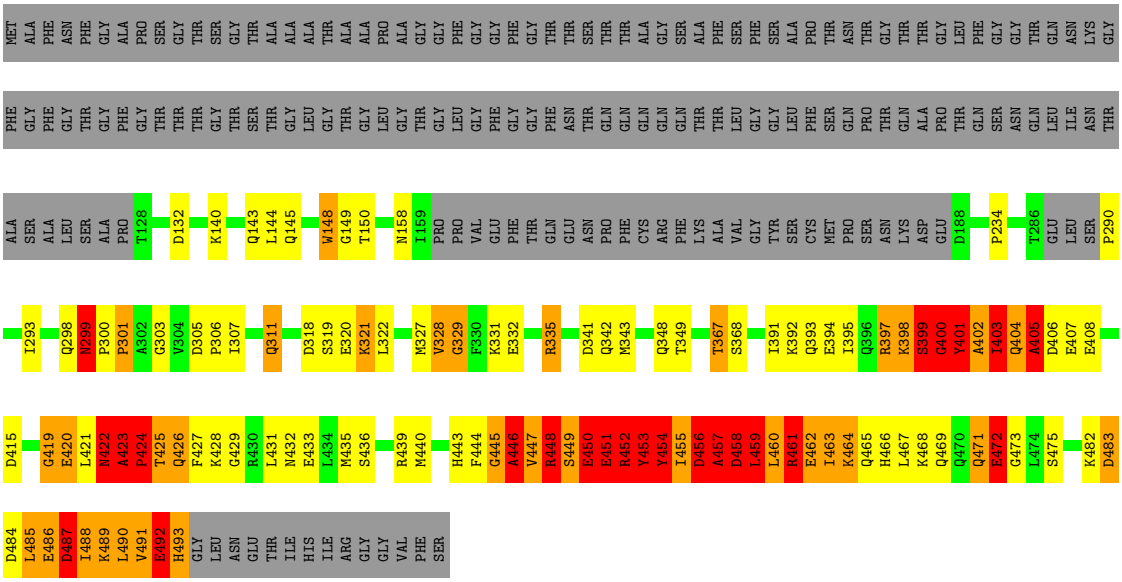
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 7-L: 43% 12% 6% 5% 34%



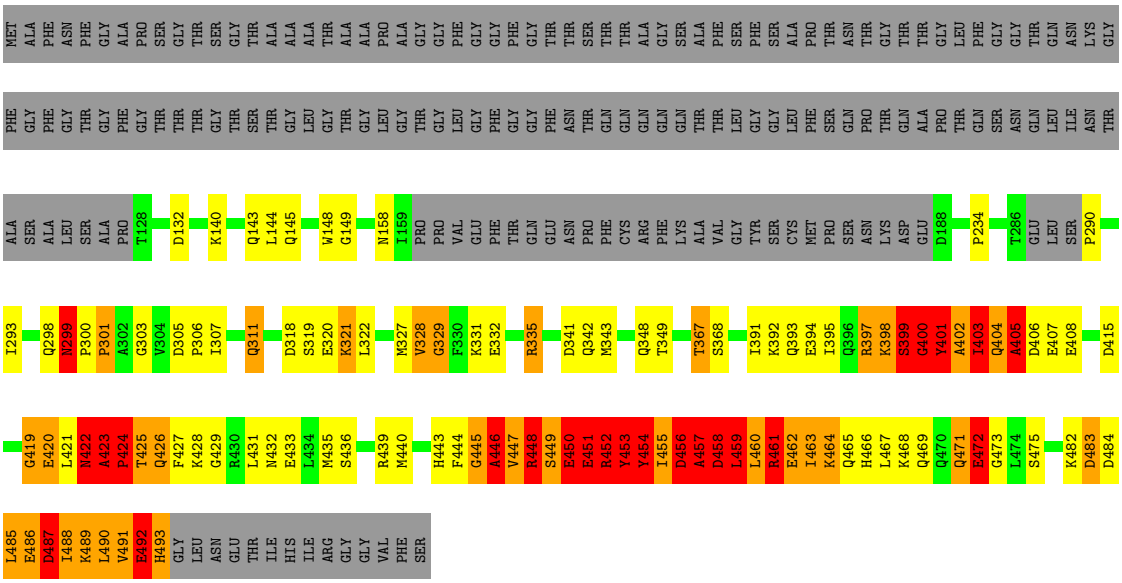
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 7-R: 43% 12% 7% 5% 34%



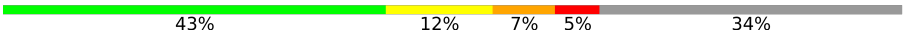
• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

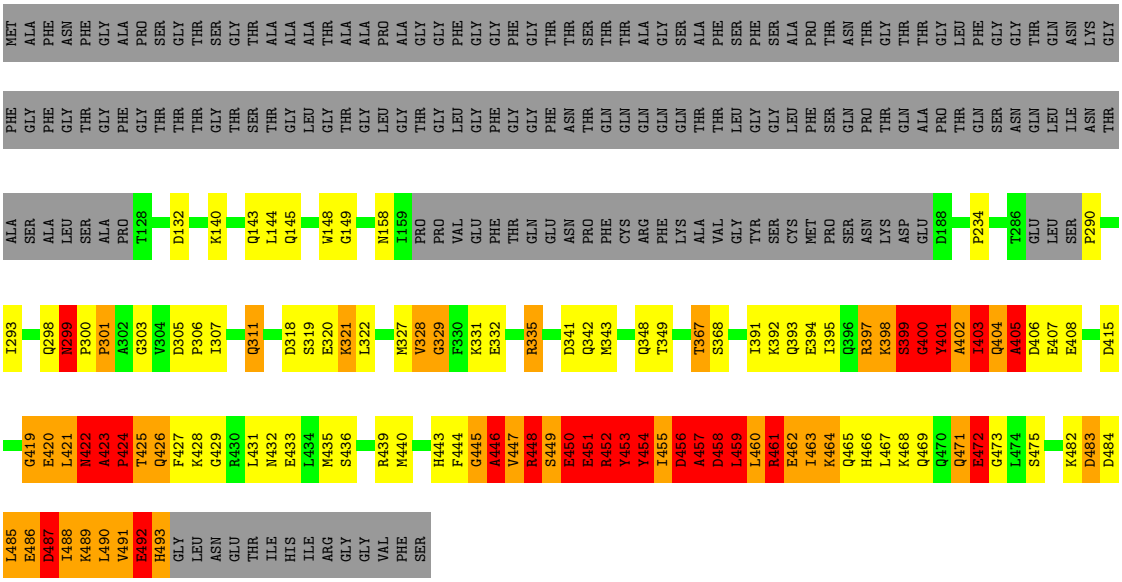
Chain 7-X: 43% 12% 6% 5% 34%



- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

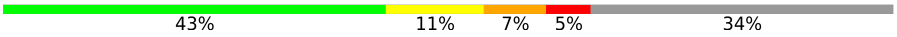
Chain 8-F:

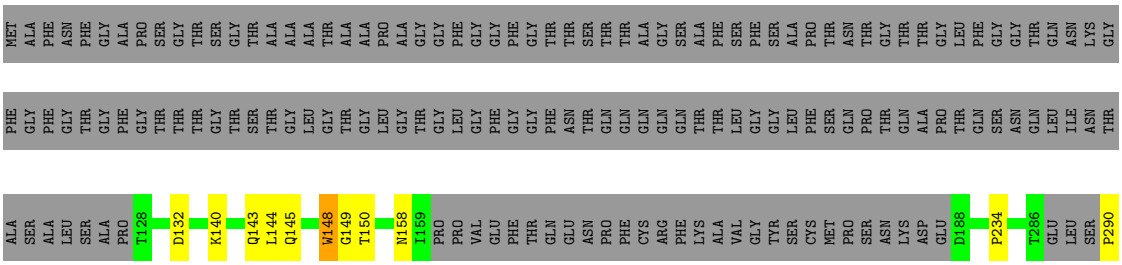


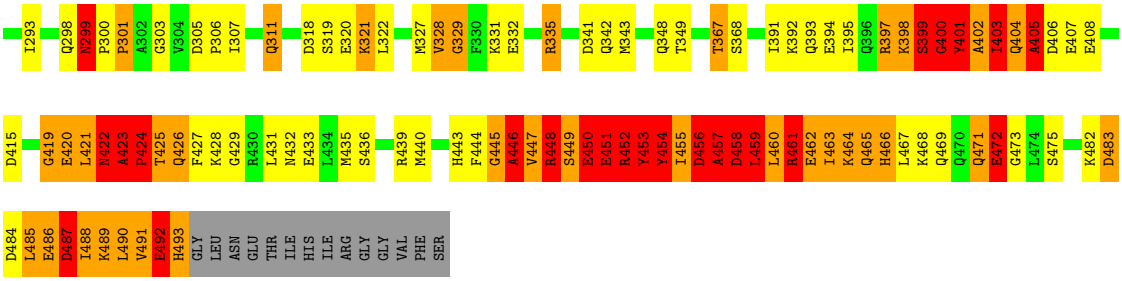


- Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

Chain 8-L:

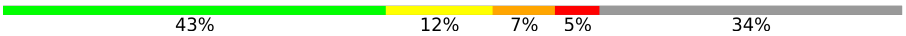


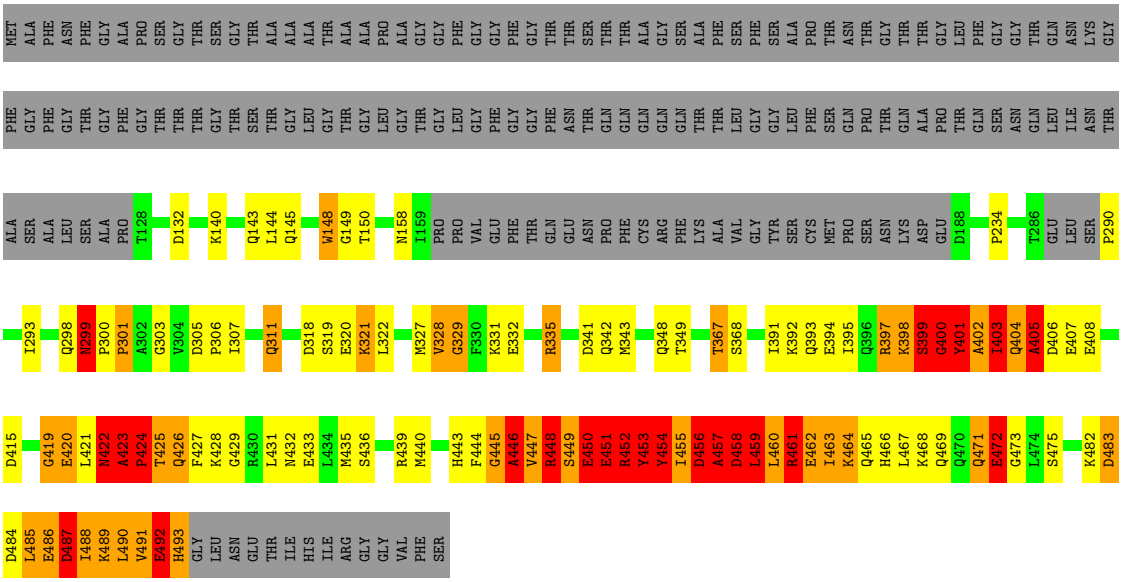




• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

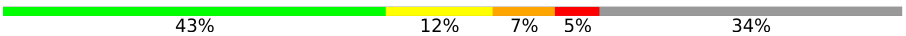
Chain 8-R:

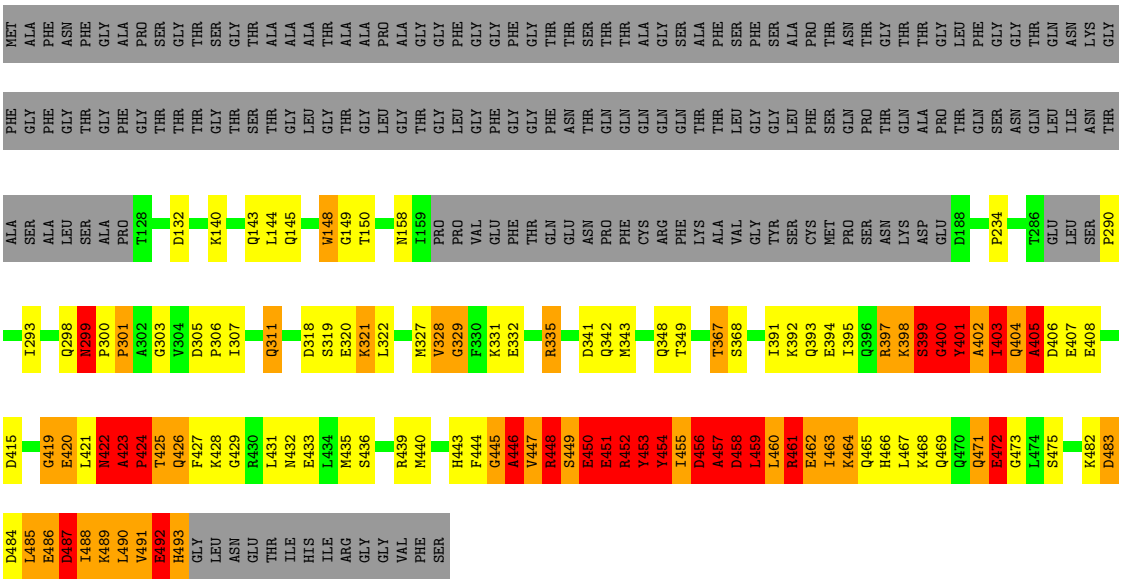




• Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP54

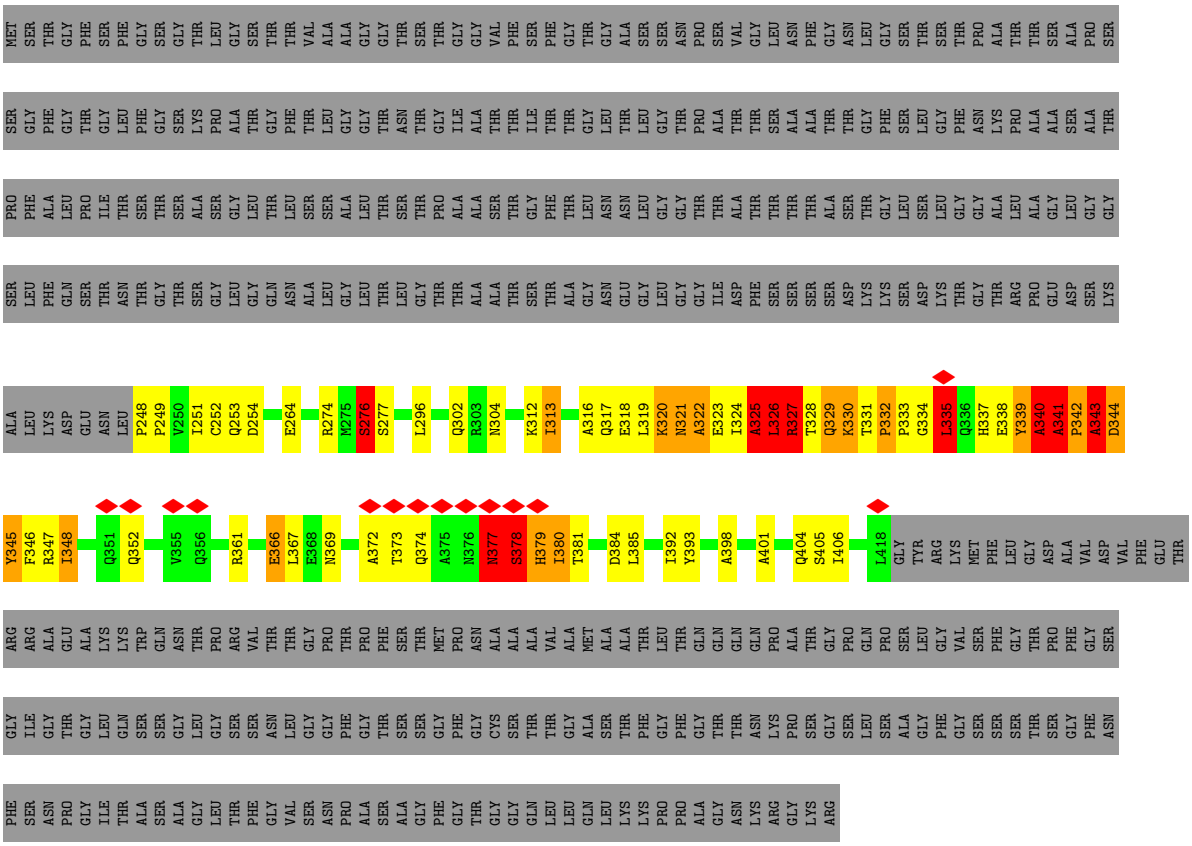
Chain 8-X:





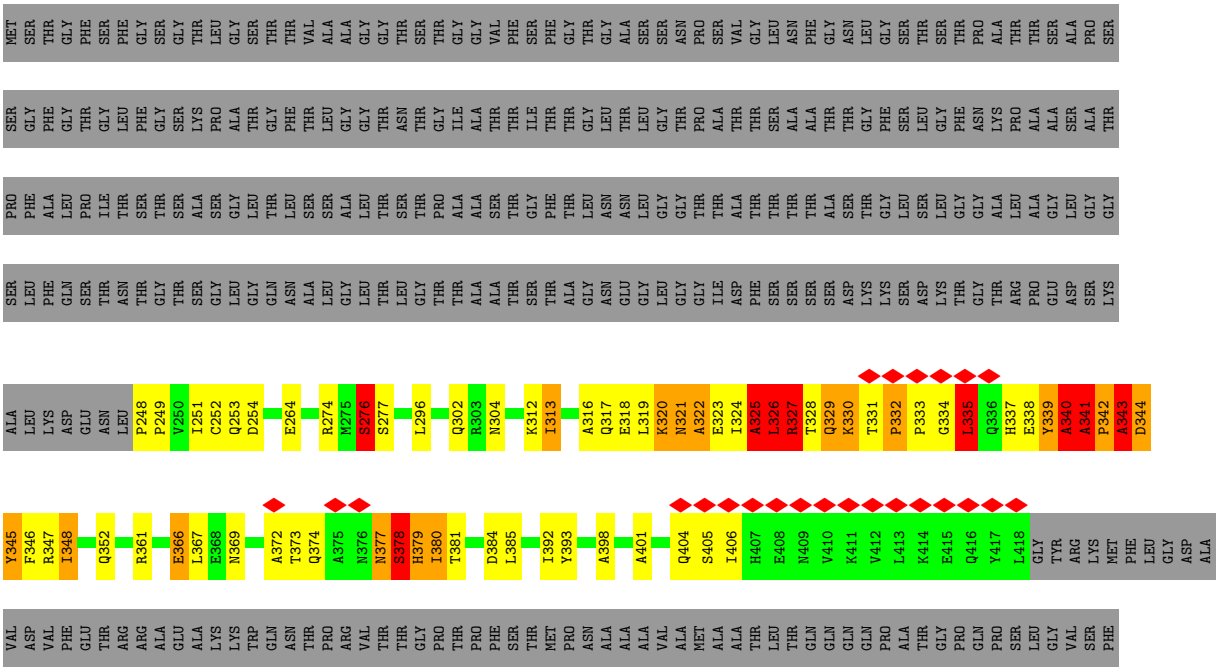
- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

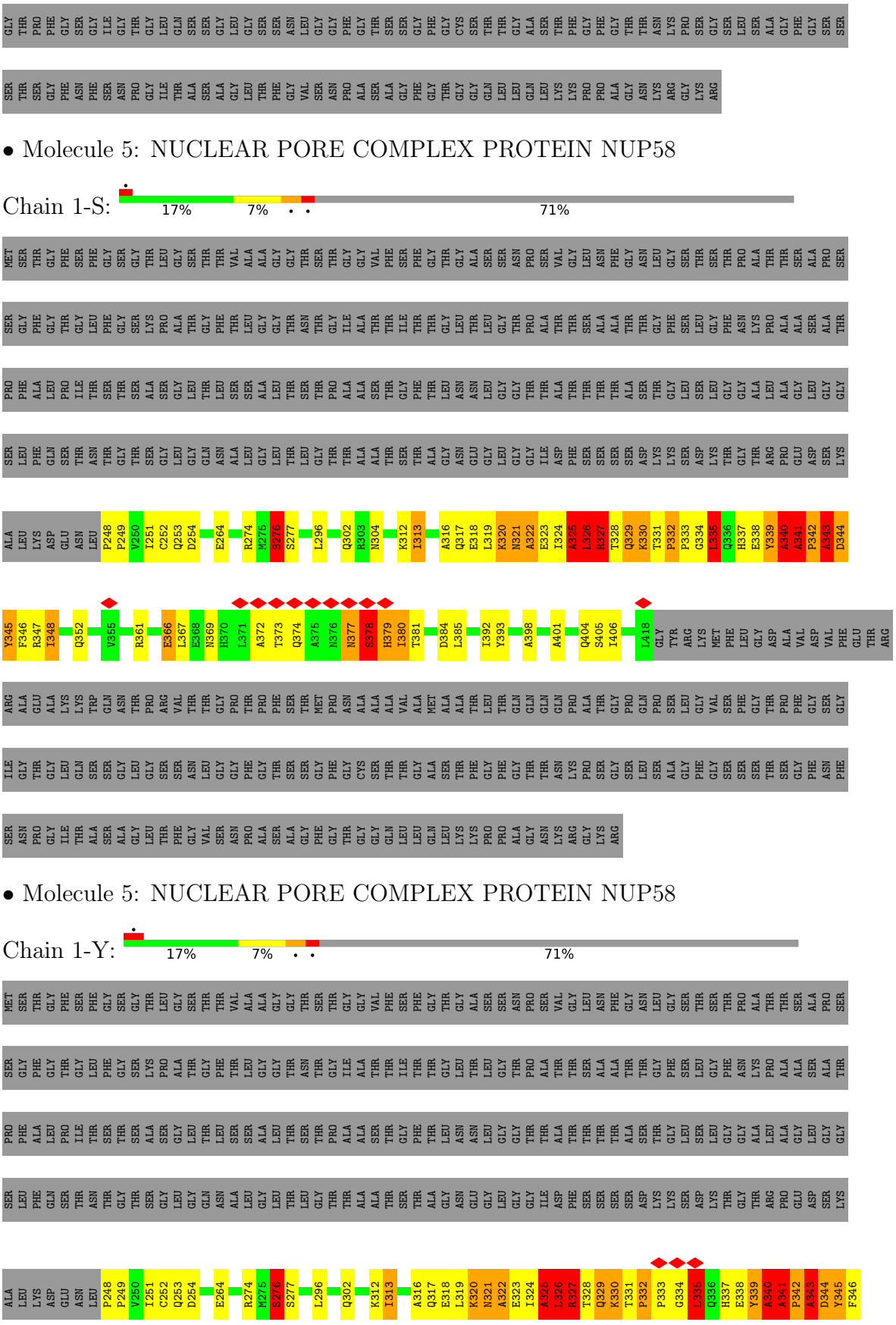
Chain 1-G:

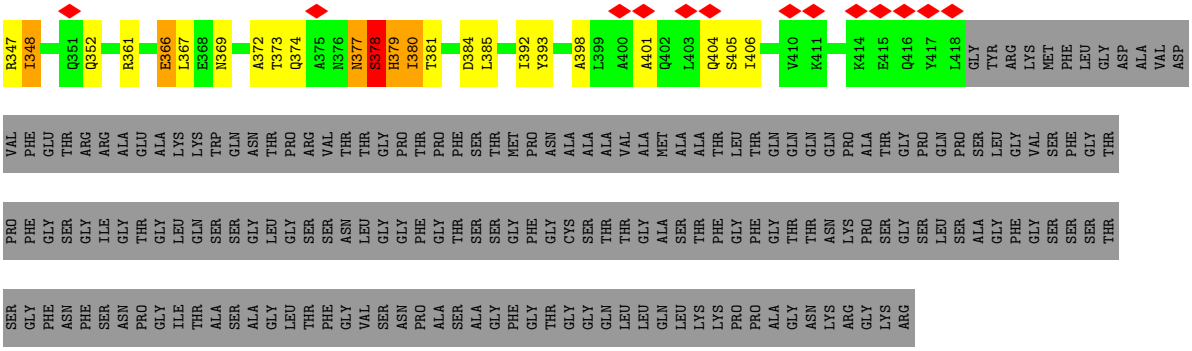


- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 1-M:

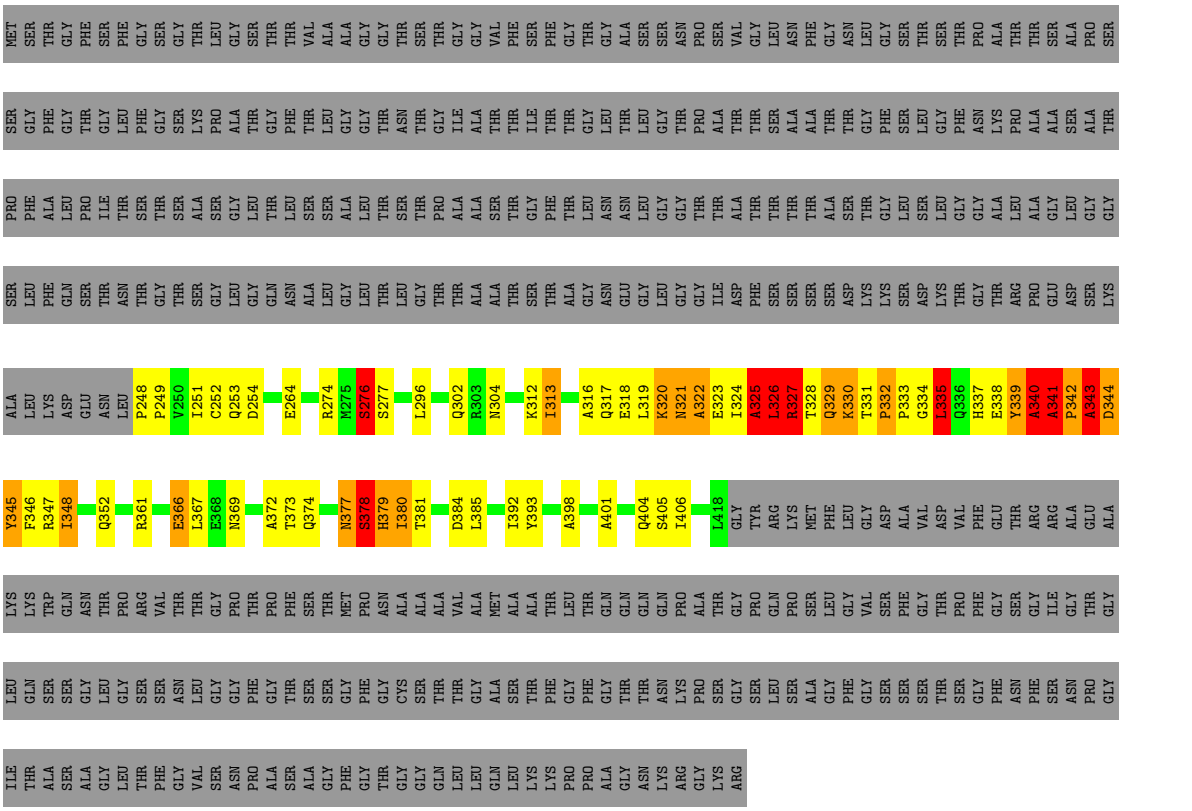



GLY THR PRO PHE GLY SER GLY ILE GLY THR GLY LEU GLN SER SER GLY LEU GLY SER SER ASN LEU GLY GLY PHE GLY GLY THR SER SER GLY PHE GLY CYS SER THR THR GLY ALA SER THR PHE GLY PHE GLY THR THR ASN LYS PRO SER GLY SER LEU SER ALA GLY PHE GLY SER SER
SER THR SER GLY PHE ASN PHE SER ASN PRO GLY ILE THR ALA SER ALA GLY LEU THR PHE GLY VAL SER ASN PRO ALA SER ALA GLY PHE GLY THR GLY GLY GLN LEU LEU GLN LEU LYS LYS PRO PRO ALA GLY ASN LYS ARG GLY LYS ARG
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58
Chain 1-S:
17%
7%
71%
MET SER THR GLY PHE SER PHE GLY SER GLY THR LEU GLY SER THR THR VAL ALA ALA GLY GLY THR SER THR GLY GLY VAL PHE SER PHE GLY THR GLY ALA SER SER ASN PRO SER VAL GLY LEU ASN PHE GLY ASN LEU GLY SER THR SER THR PRO ALA THR THR SER ALA PRO SER
SER GLY PHE GLY THR GLY LEU PHE GLY SER LYS PRO ALA THR GLY PHE THR LEU GLY GLY THR ASN THR GLY ILE ALA THR THR ILE THR THR GLY LEU THR LEU GLY THR PRO ALA THR THR SER ALA ALA THR THR GLY PHE SER LEU GLY PHE ASN LYS PRO ALA ALA SER ALA THR
PRO PHE ALA LEU PRO ILE THR SER THR SER ALA SER GLY LEU THR LEU SER SER SER ALA LEU THR SER THR PRO ALA ALA SER THR GLY PHE THR LEU ASN ASN LEU GLY GLY THR THR ALA ALA THR THR THR THR ALA SER THR GLY LEU SER LEU GLY GLY ALA LEU ALA GLY LEU GLY GLY
SER LEU PHE GLN SER THR ASN THR GLY THR SER GLY LEU GLY GLN ASN ALA LEU GLY LEU THR LEU GLY GLY THR THR ALA ALA THR SER THR ALA ALA GLY GLY LEU GLY GLY ILE ASP PHE SER SER SER SER ASP LYS LYS SER ASP LYS THR GLY THR ARG PRO GLU ASP SER LYS
ALA LEU LYS ASP GLU ASN LEU P248 P249 V250 I251 C252 Q253 D254 E264 R274 M275 S276 S277 L296 Q302 R303 N304 K312 I313 A316 Q317 E318 L319 K320 N321 A322 E323 I324 A325 L326 R327 T328 Q329 K330 T331 P332 P333 G334 L335 Q336 H337 E338 Y339 A340 A341 P342 A343 D344
Y345 F346 R347 I348 Q352 V355 R361 E366 L367 E368 N369 H370 L371 A372 T373 Q374 A375 N376 N377 S378 H379 I380 T381 D384 L385 I392 Y393 A398 A401 Q404 S405 I406 L418 GLY TYR ARG LYS MET PHE LEU GLY ASP ALA VAL ASP VAL PHE GLU THR ARG
ARG ALA GLU ALA LYS LYS TRP GLN ASN THR PRO ARG VAL THR THR GLY PRO THR PRO PHE SER THR MET PRO ASN ALA ALA ALA VAL ALA MET ALA ALA THR LEU THR GLN GLN GLN GLN PRO ALA THR GLY PRO GLN PRO SER LEU GLY VAL SER PHE GLY THR PRO PHE GLY SER GLY
ILE GLY THR GLY LEU GLN SER SER GLY LEU GLY SER SER ASN LEU GLY GLY PHE GLY THR SER SER GLY PHE GLY CYS SER THR THR GLY ALA SER THR PHE GLY PHE GLY THR THR ASN LYS PRO SER GLY SER LEU SER ALA GLY PHE GLY SER SER SER THR SER GLY PHE ASN PHE
SER ASN PRO GLY ILE THR ALA SER ALA GLY LEU THR PHE GLY VAL SER ASN PRO ALA SER ALA GLY PHE GLY THR GLY GLY GLN LEU LEU LYS LYS PRO PRO ALA GLY ASN LYS ARG GLY LYS ARG
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58
Chain 1-Y:
17%
7%
71%
MET SER THR GLY PHE SER PHE GLY SER GLY THR LEU GLY SER THR THR VAL ALA ALA GLY GLY THR SER THR GLY GLY VAL PHE SER PHE GLY THR GLY ALA SER SER ASN PRO SER VAL GLY LEU ASN PHE GLY ASN LEU GLY SER THR SER THR PRO ALA THR THR SER ALA PRO SER
SER GLY PHE GLY THR GLY LEU PHE GLY SER LYS PRO ALA THR GLY PHE THR LEU GLY GLY THR ASN THR GLY ILE ALA THR THR ILE THR THR GLY LEU THR LEU GLY THR PRO ALA THR THR SER ALA ALA THR THR GLY PHE SER LEU GLY PHE ASN LYS PRO ALA ALA SER ALA THR
PRO PHE ALA LEU PRO ILE THR SER THR SER ALA SER GLY LEU THR LEU SER SER SER ALA LEU THR SER THR PRO ALA ALA SER THR GLY PHE THR LEU ASN ASN LEU GLY GLY THR THR ALA ALA THR THR THR THR ALA SER THR GLY LEU SER LEU GLY GLY ALA LEU ALA GLY LEU GLY GLY
SER LEU PHE GLN SER THR ASN THR GLY THR SER GLY LEU GLY GLN ASN ALA LEU GLY LEU THR LEU GLY GLY THR THR ALA ALA THR SER THR ALA ALA GLY GLY LEU GLY GLY ILE ASP PHE SER SER SER SER ASP LYS LYS SER ASP LYS THR GLY THR ARG PRO GLU ASP SER LYS
ALA LEU LYS ASP GLU ASN LEU P248 P249 V250 I251 C252 Q253 D254 E264 R274 M275 S276 S277 L296 Q302 K312 I313 A316 Q317 E318 L319 K320 N321 A322 E323 I324 A325 L326 R327 T328 Q329 K330 T331 P332 P333 G334 L335 Q336 H337 E338 Y339 A340 A341 P342 A343 D344 Y345 F346



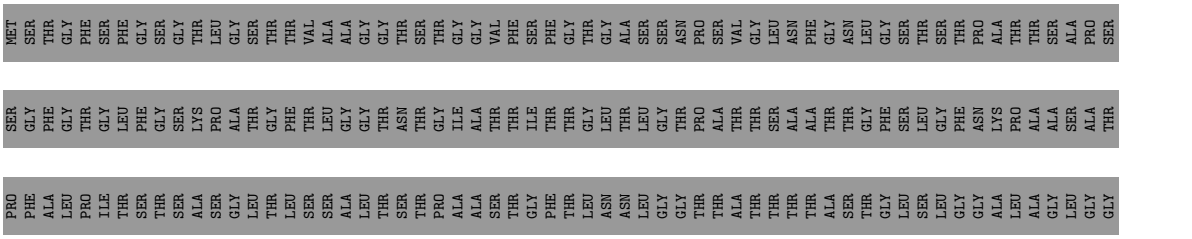
- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

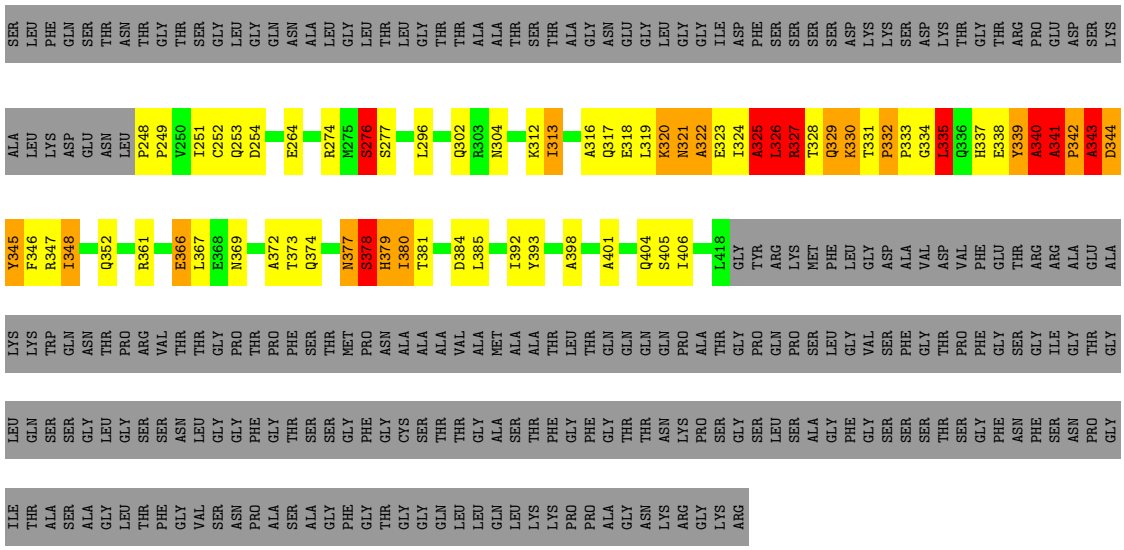
Chain 2-G: 17% 7% • • 71%



- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

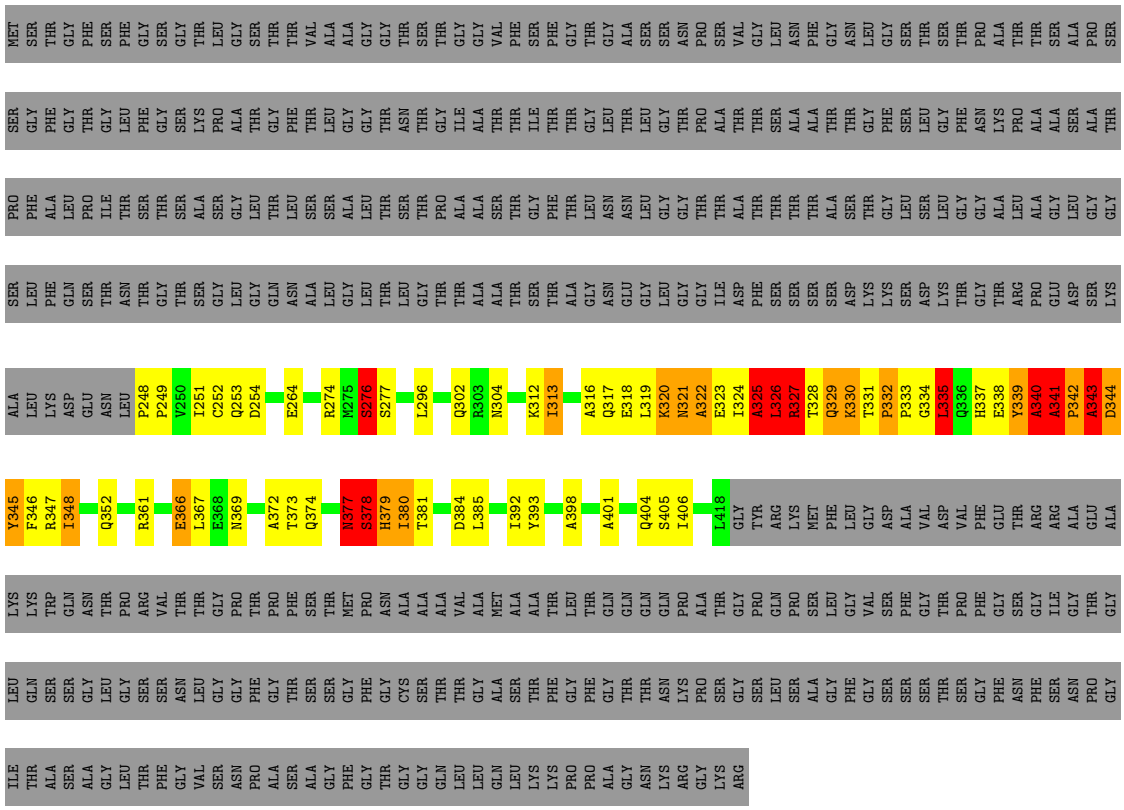
Chain 2-M: 17% 7% • • 71%





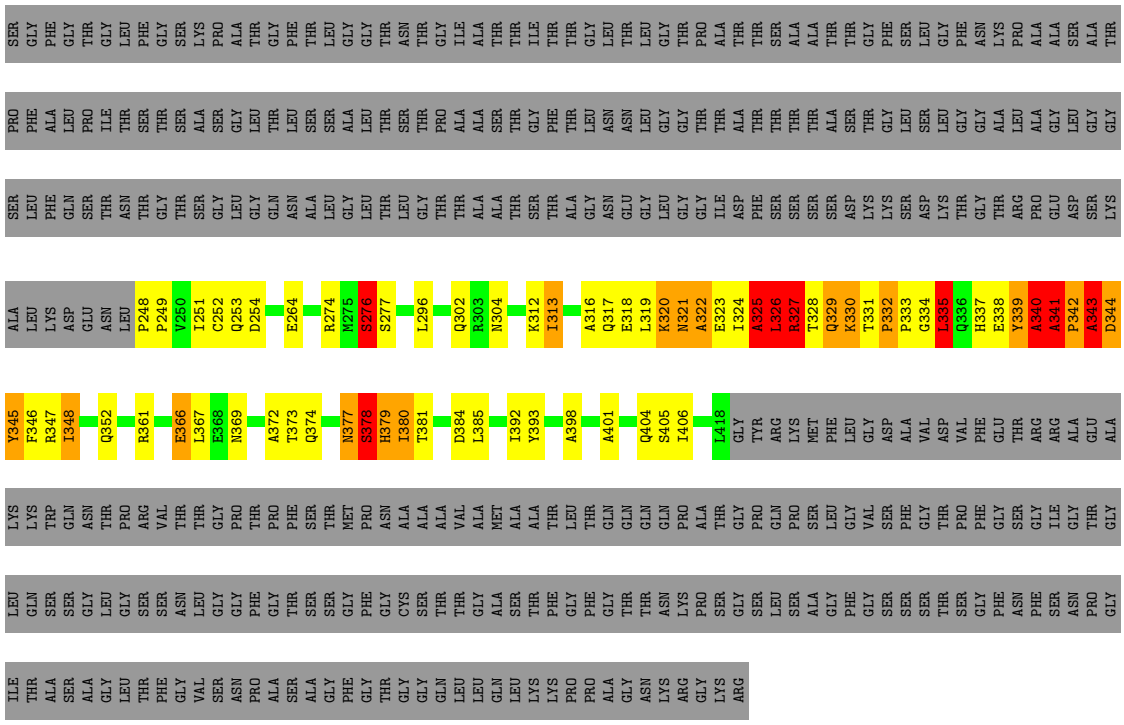
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 2-S: 17% 7% • • 71%



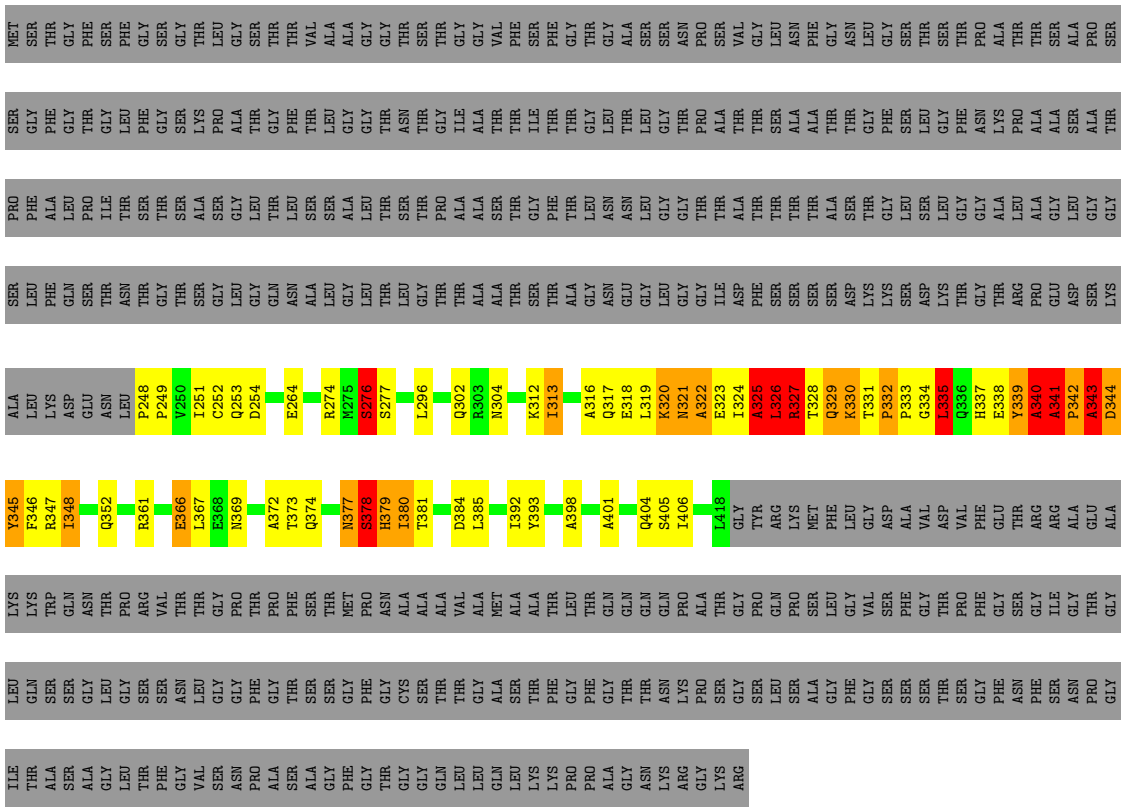
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 2-Y: 17% 7% • • 71%



• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 3-G: 17% 7% • • 71%



• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 3-M: 17% 7% • • 71%

MET SER THR GLY PHE SER PHE GLY SER GLY THR LEU GLY SER THR THR VAL ALA ALA GLY GLY THR SER THR GLY GLY VAL PHE SER PHE GLY THR GLY ALA SER SER ASN PRO SER VAL GLY LEU ASN PHE GLY ASN LEU GLY SER THR SER THR PRO ALA THR THR SER ALA PRO SER

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

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

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

ALA LEU LYS ASP GLU ASN LEU P248 P249 V250 I251 C252 Q253 D254 E264 R274 M275 S276 S277 L296 Q302 R303 N304 K312 I313 A316 Q317 E318 L319 K320 N321 A322 E323 I324 A325 L326 R327 T328 Q329 K330 T331 P332 P333 G334 L335 Q336 H337 E338 Y339 A340 A341 P342 A343 D344

Y345 F346 R347 I348 Q352 R361 E366 L367 E368 N369 A372 T373 Q374 N377 S378 H379 I380 T381 D384 L385 I392 Y393 A398 A401 Q404 S405 I406 L418 GLY TYR ARG LYS MET PHE LEU GLY ASP ALA VAL ASP VAL PHE GLU THR ARG ARG ALA GLU ALA

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

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

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

• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 3-S: 17% 7% • • 71%

MET SER THR GLY PHE SER PHE GLY SER GLY THR LEU GLY SER THR THR VAL ALA ALA GLY GLY THR SER THR GLY GLY VAL PHE SER PHE GLY THR GLY ALA SER SER ASN PRO SER VAL GLY LEU ASN PHE GLY ASN LEU GLY SER THR SER THR PRO ALA THR THR SER ALA PRO SER

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

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

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

ALA LEU LYS ASP GLU ASN LEU P248 P249 V250 I251 C252 Q253 D254 E264 R274 M275 S276 S277 L296 Q302 R303 N304 K312 I313 A316 Q317 E318 L319 K320 N321 A322 E323 I324 A325 L326 R327 T328 Q329 K330 T331 P332 P333 G334 L335 Q336 H337 E338 Y339 A340 A341 P342 A343 D344

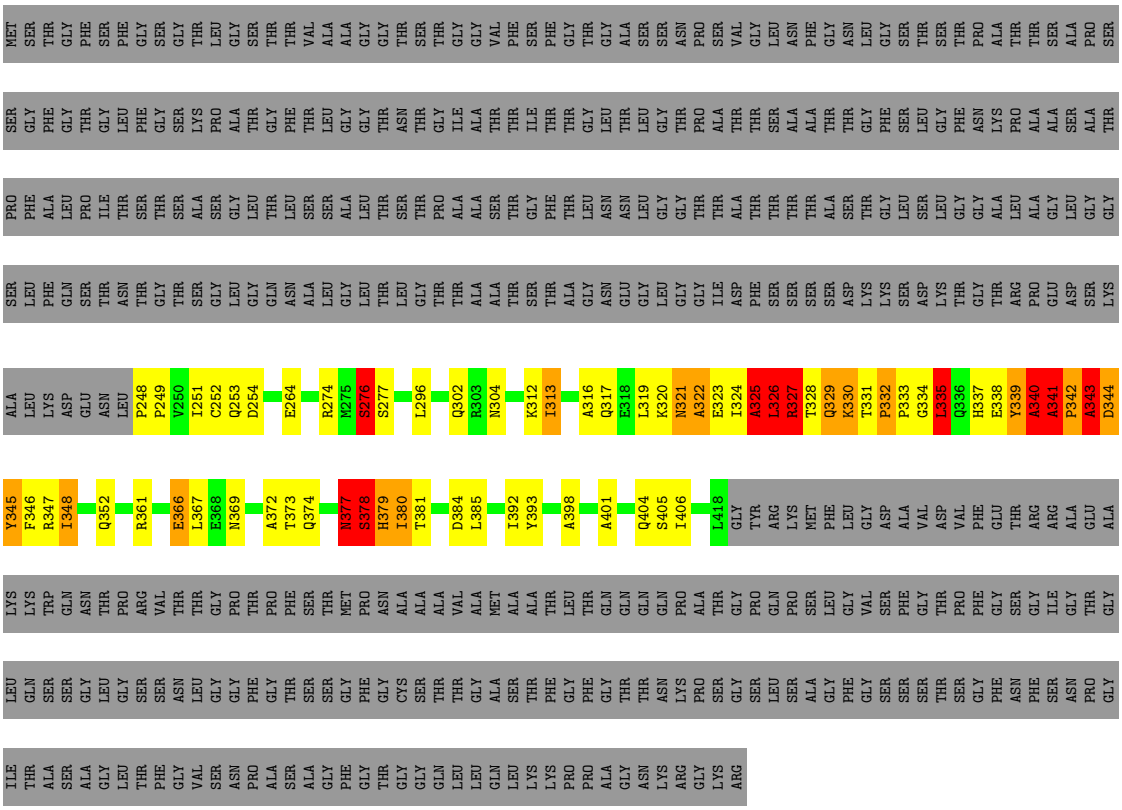
Y345 F346 R347 I348 Q352 R361 E366 L367 E368 N369 A372 T373 Q374 N377 S378 H379 I380 T381 D384 L385 I392 Y393 A398 A401 Q404 S405 I406 L418 GLY TYR ARG LYS MET PHE LEU GLY ASP ALA VAL ASP VAL PHE GLU THR ARG ARG ALA GLU ALA

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

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

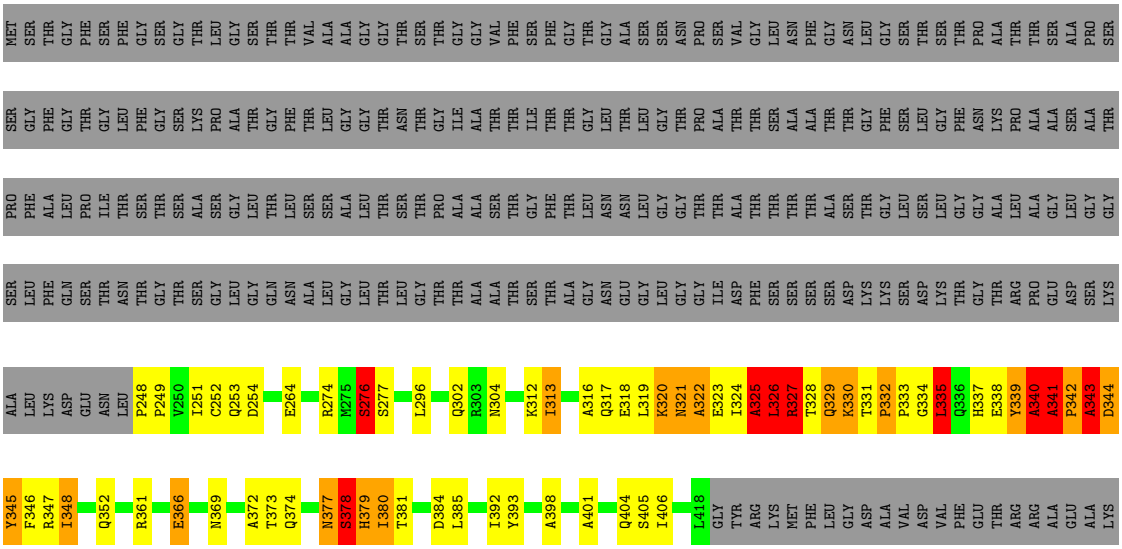
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

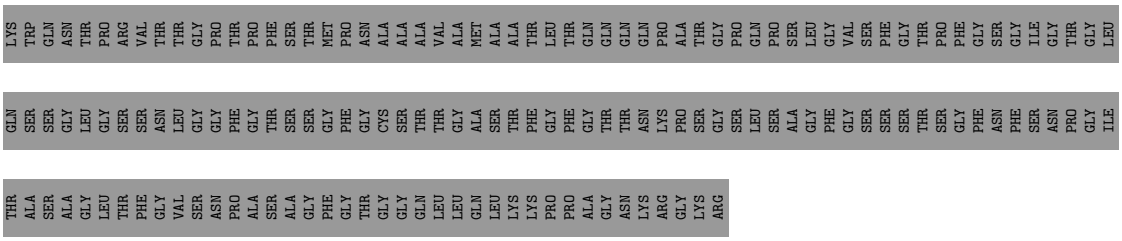
Chain 3-Y:



• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

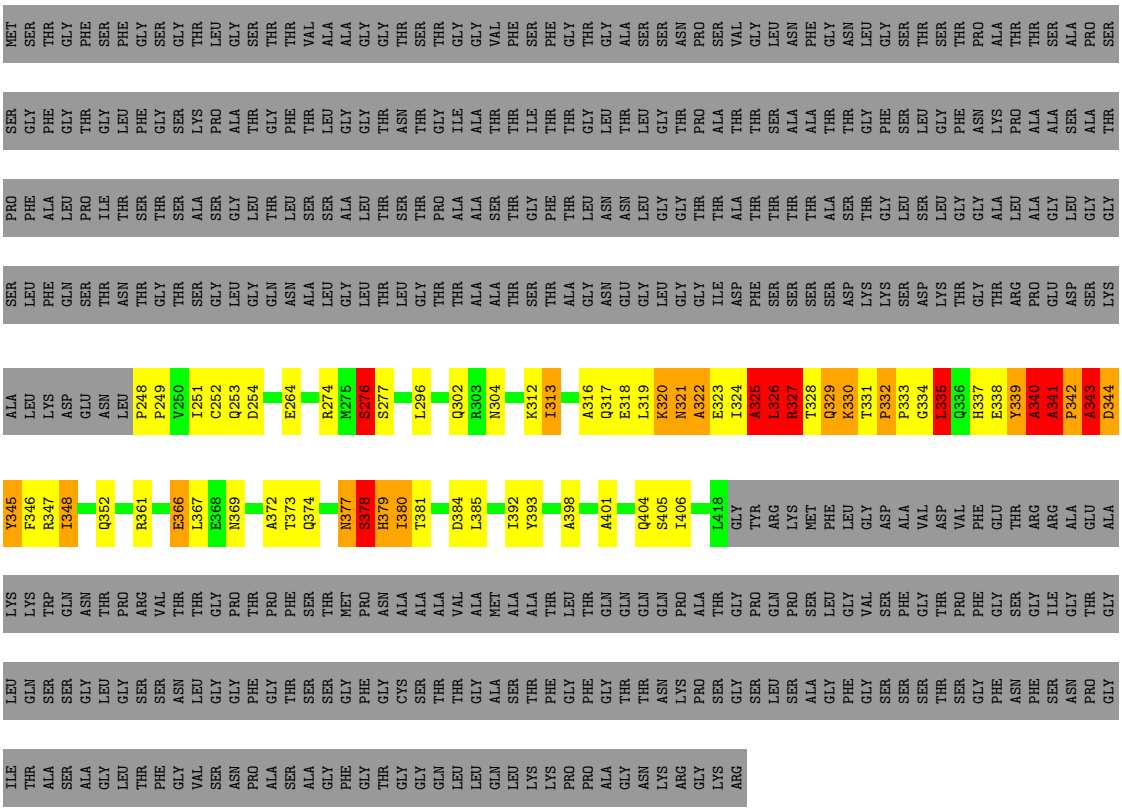
Chain 4-G:





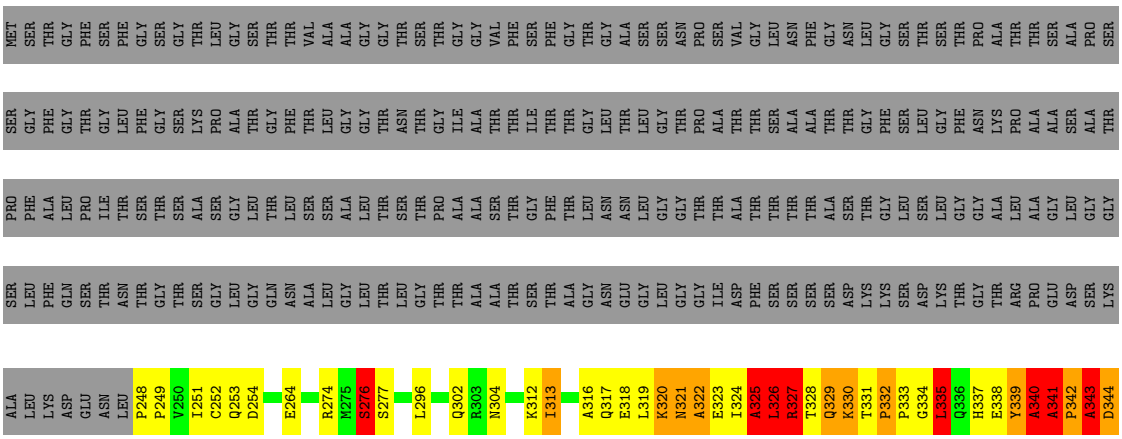
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

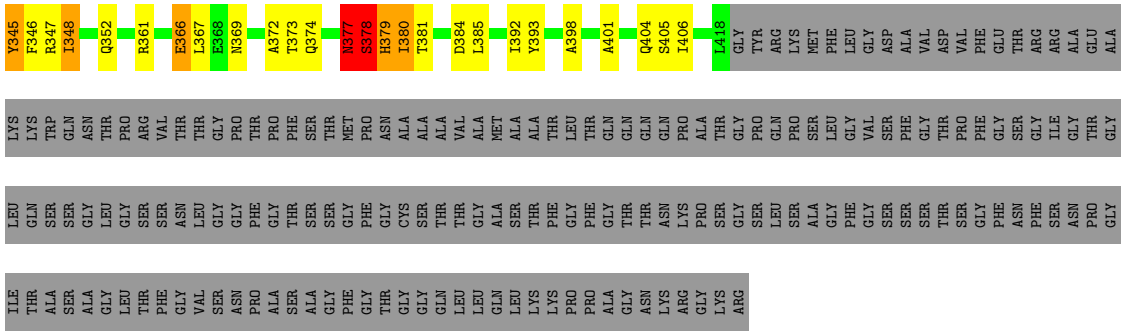
Chain 4-M: 17% 7% • • 71%



• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

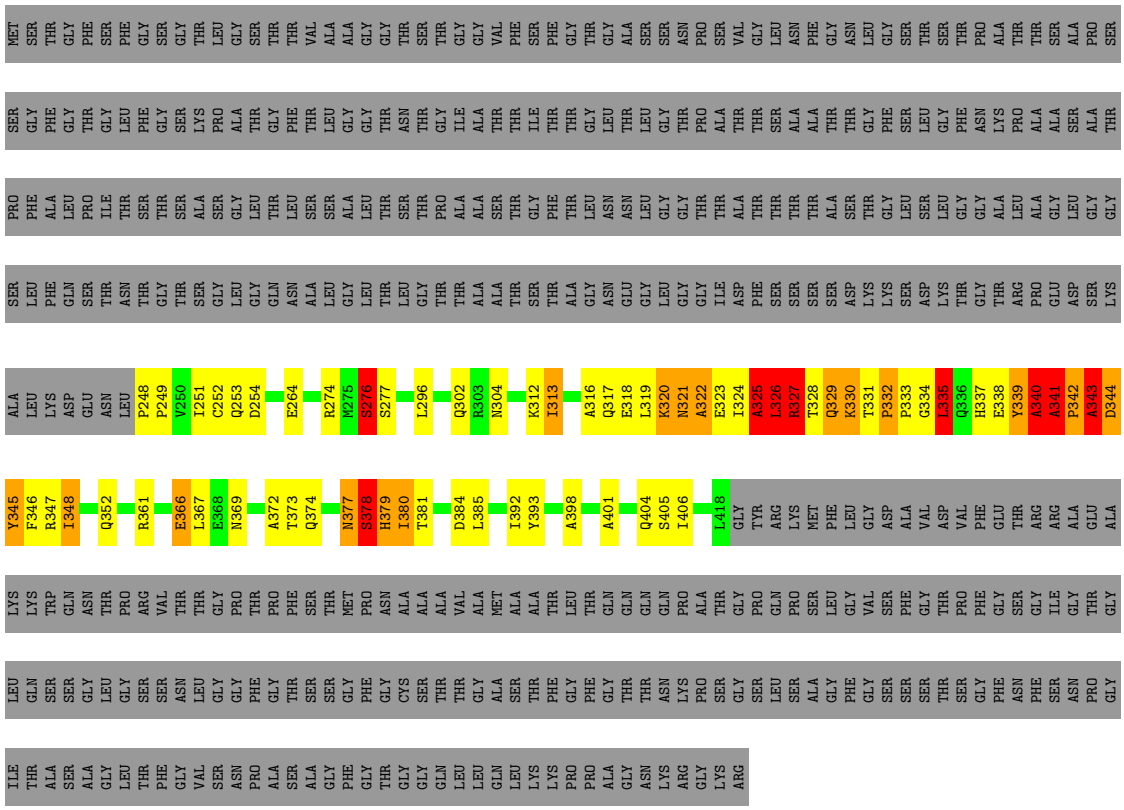
Chain 4-S: 17% 7% • • 71%





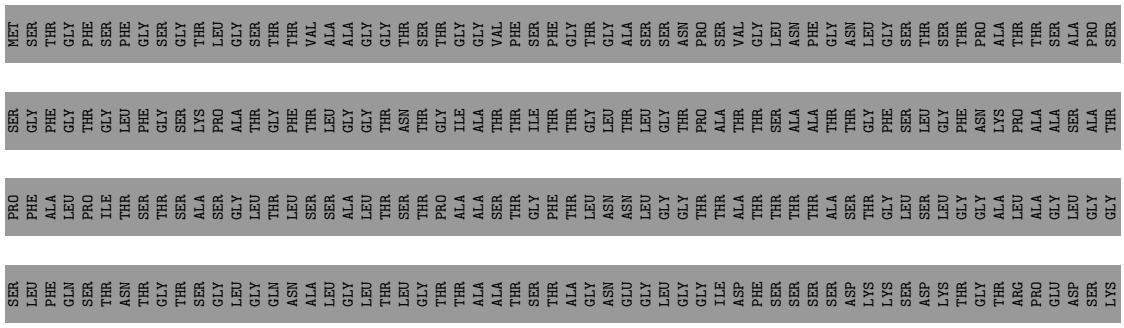
- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

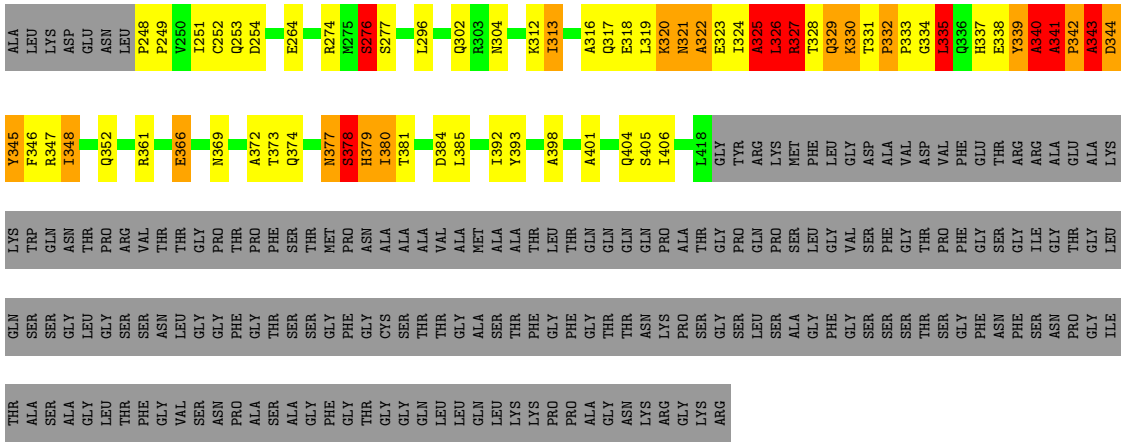
Chain 4-Y: 17% 7% • • 71%



- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

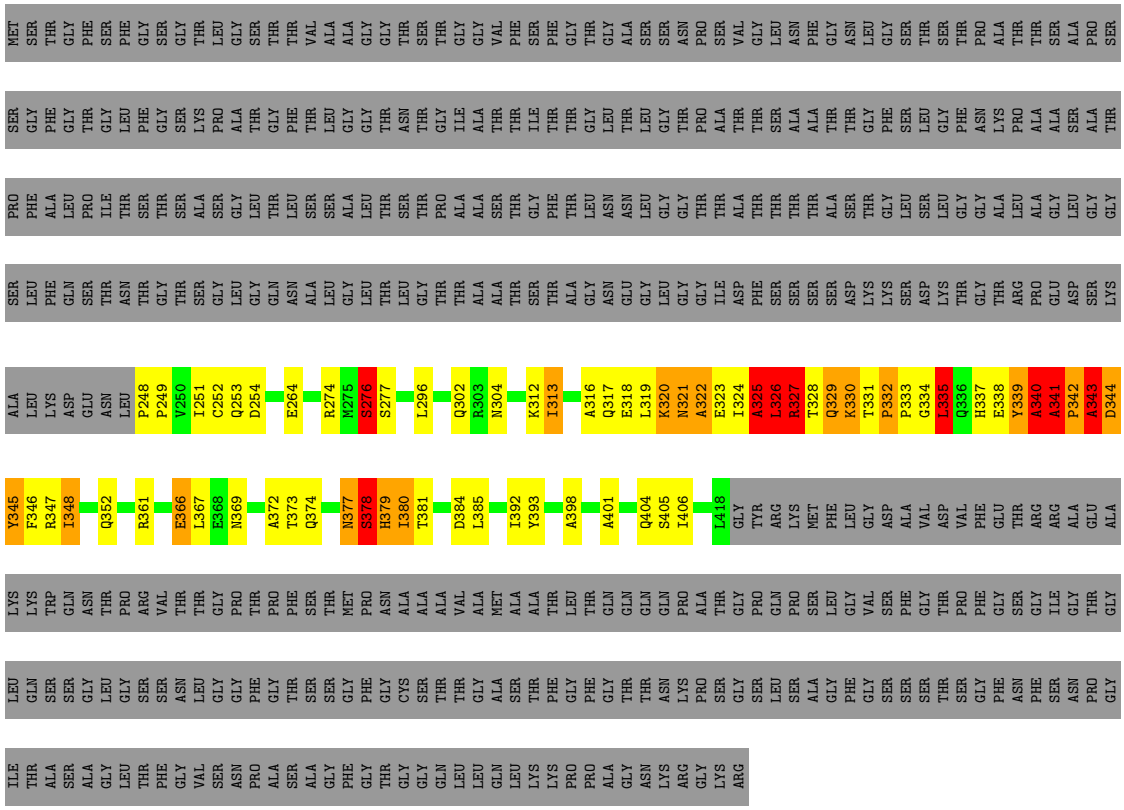
Chain 5-G: 17% 7% • • 71%





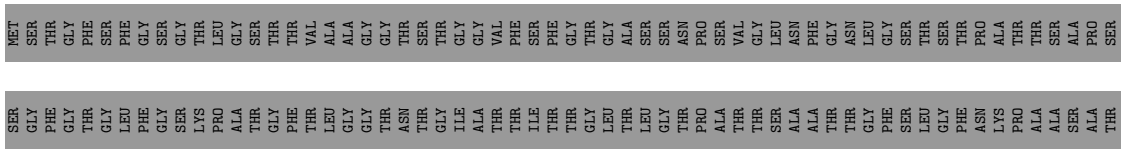
- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

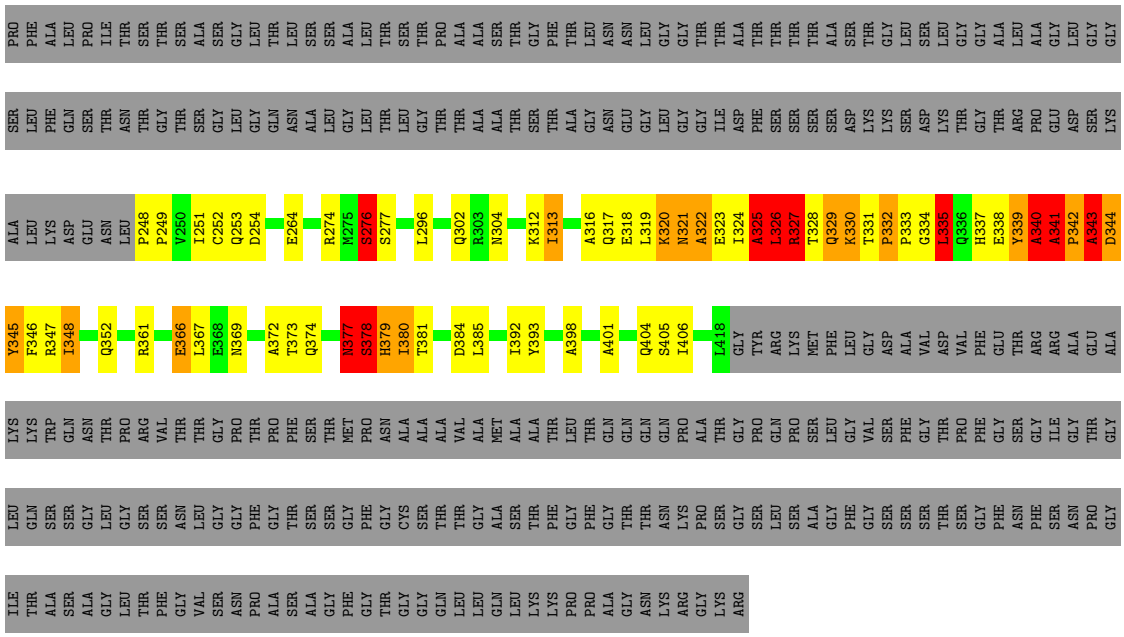
Chain 5-M: 17% 7% • • 71%



- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

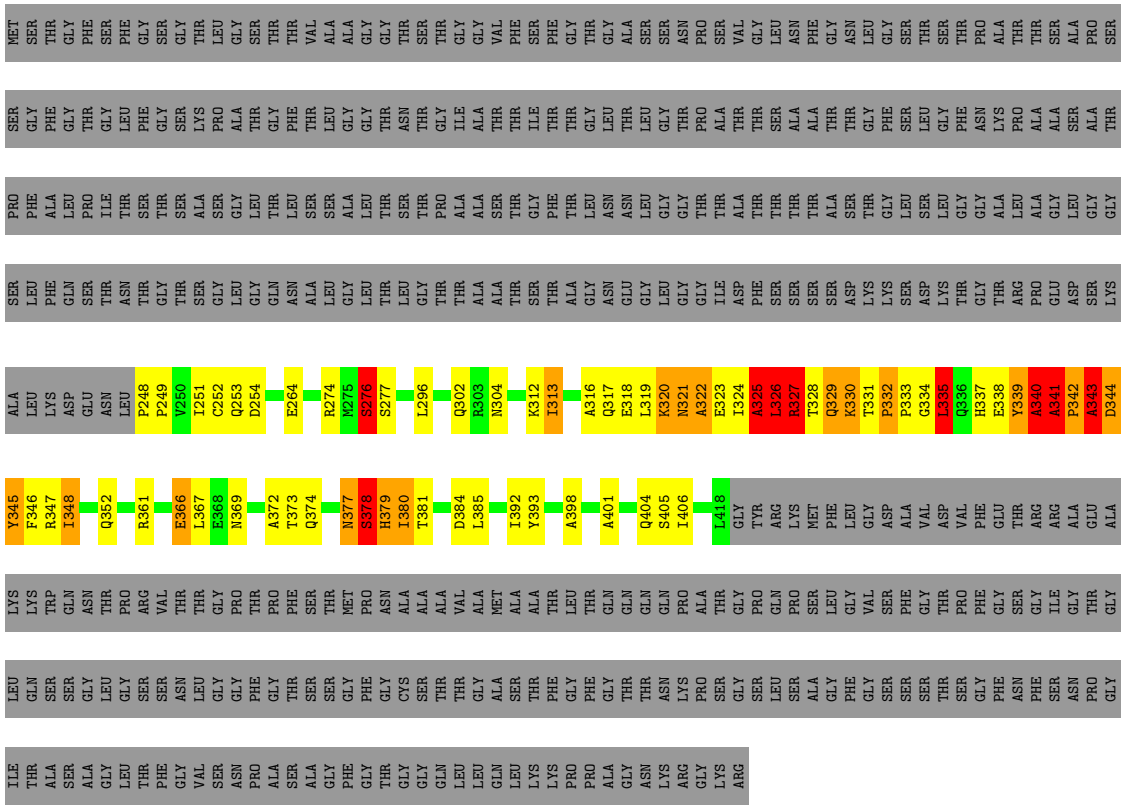
Chain 5-S: 17% 7% • • 71%





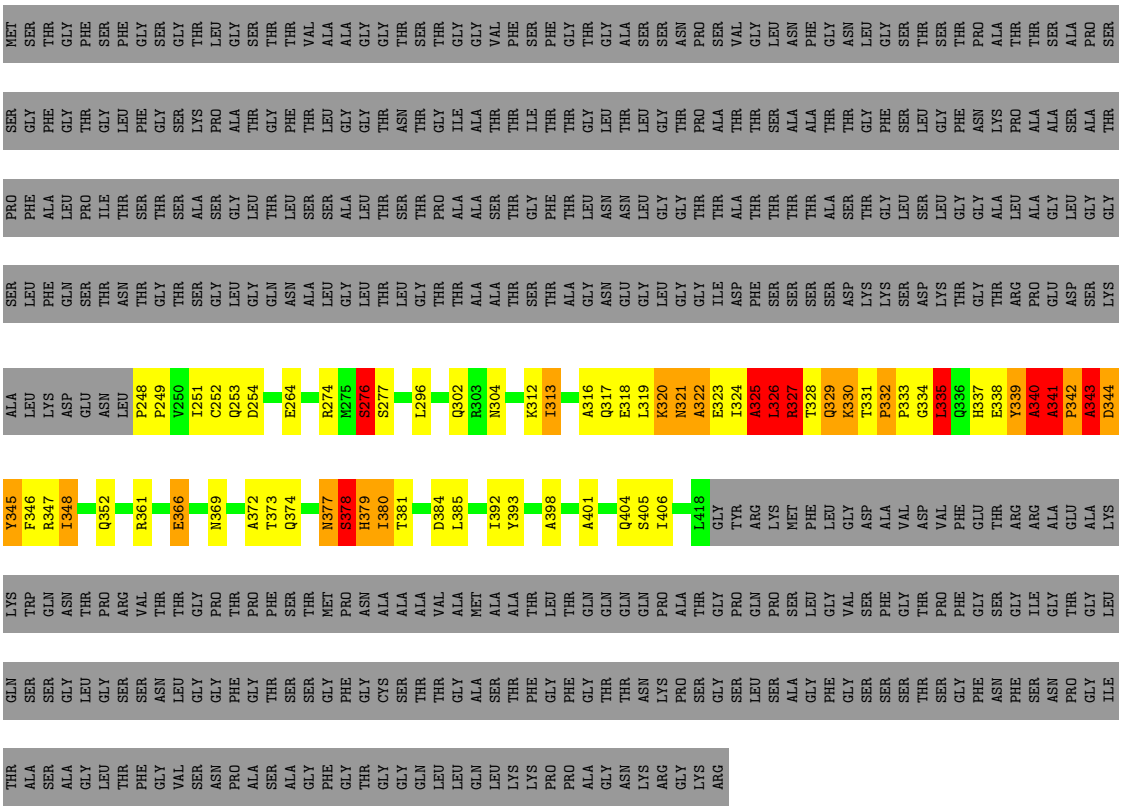
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 5-Y: 17% 7% • • 71%



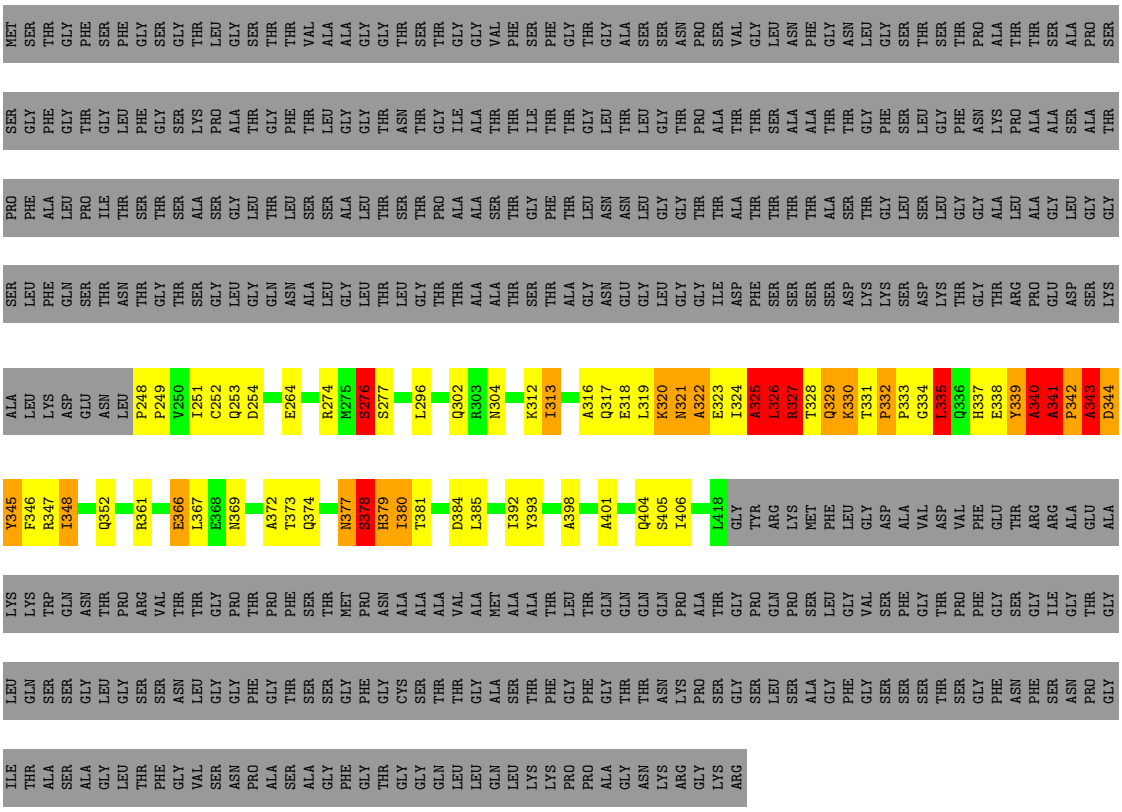
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 6-G: 17% 7% • • 71%



- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 6-M: 17% 7% • • 71%



- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 6-S: 17% 7% • • 71%

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

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

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

ALA LEU LYS ASP GLU ASN LEU P248 P249 V250 I251 C252 Q253 D254 E264 R274 M275 S276 S277 L296 Q302 R303 N304 K312 I313 A316 Q317 E318 L319 K320 N321 A322 E323 I324 A325 L326 R327 T328 Q329 K330 T331 P332 P333 G334 L335 Q336 H337 E338 Y339 A340 A341 P342 A343 D344

Y345 F346 R347 I348 Q352 R361 E366 L367 E368 N369 A372 T373 Q374 N377 S378 H379 I380 T381 D384 L385 I392 Y393 A398 A401 Q404 S405 I406 L418 GLY TYR ARG LYS MET PHE LEU GLY ASP ALA VAL ASP VAL PHE GLU THR ARG ARG ALA GLU ALA

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

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

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

- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 6-Y: 17% 7% • • 71%

MET SER THR GLY PHE SER PHE GLY SER GLY THR LEU GLY SER THR THR VAL ALA ALA GLY GLY THR SER THR GLY GLY VAL PHE SER PHE GLY THR GLY ALA SER SER ASN PRO SER VAL GLY LEU ASN PHE GLY ASN LEU GLY SER THR SER THR PRO ALA THR THR SER ALA PRO SER

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

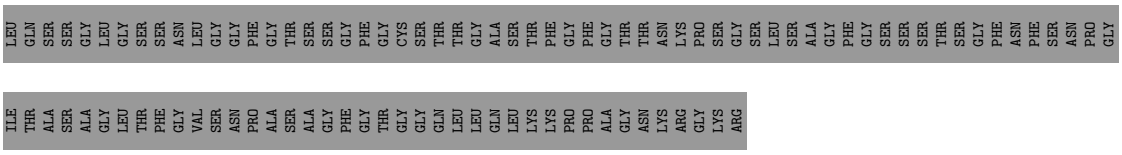
PRO PHE ALA LEU PRO ILE THR SER THR SER ALA SER GLY LEU THR LEU SER SER ALA LEU THR SER THR PRO ALA ALA SER THR GLY PHE THR LEU ASN ASN LEU GLY GLY THR THR ALA THR THR THR ALA SER THR GLY LEU SER LEU GLY GLY ALA LEU ALA GLY LEU GLY GLY

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

ALA LEU LYS ASP GLU ASN LEU P248 P249 V250 I251 C252 Q253 D254 E264 R274 M275 S276 S277 L296 Q302 R303 N304 K312 I313 A316 Q317 E318 L319 K320 N321 A322 E323 I324 A325 L326 R327 T328 Q329 K330 T331 P332 P333 G334 L335 Q336 H337 E338 Y339 A340 A341 P342 A343 D344

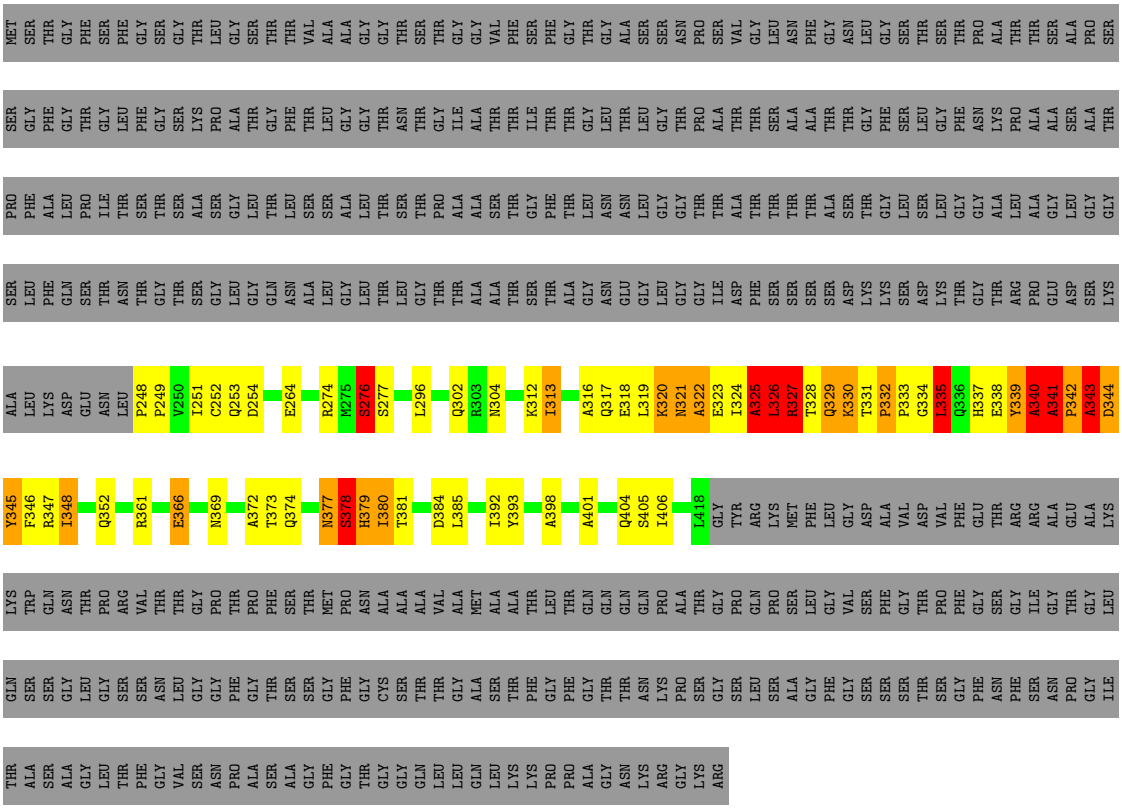
Y345 F346 R347 I348 Q352 R361 E366 L367 E368 N369 A372 T373 Q374 N377 S378 H379 I380 T381 D384 L385 I392 Y393 A398 A401 Q404 S405 I406 L418 GLY TYR ARG LYS MET PHE LEU GLY ASP ALA VAL ASP VAL PHE GLU THR ARG ARG ALA GLU ALA

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



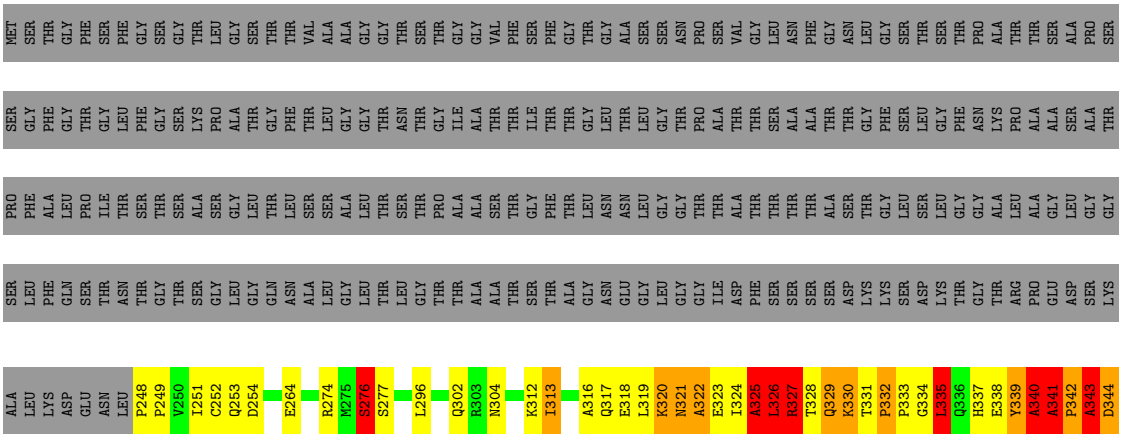
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

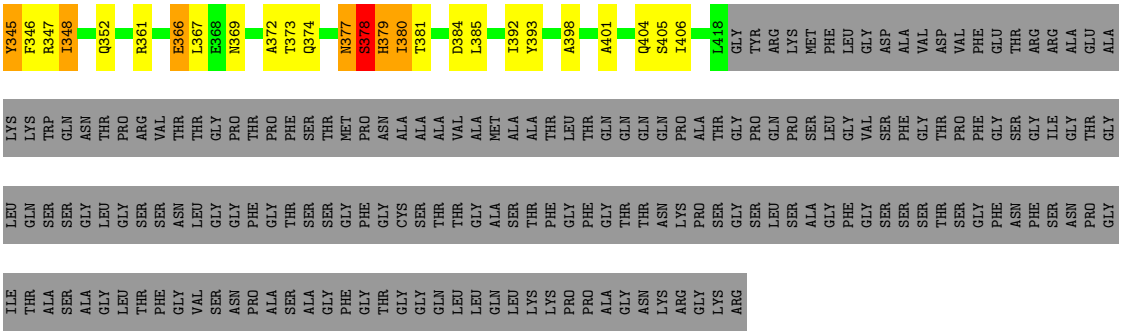
Chain 7-G: 17% 7% • • 71%



• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

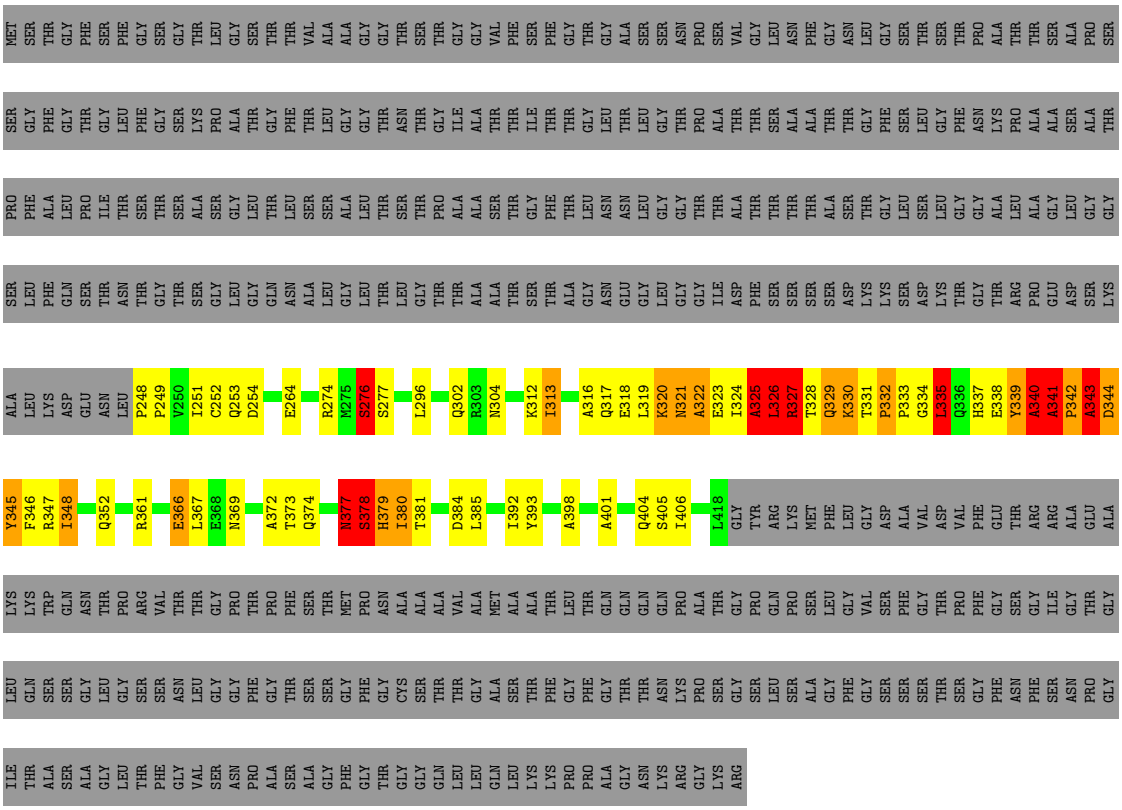
Chain 7-M: 17% 7% • • 71%





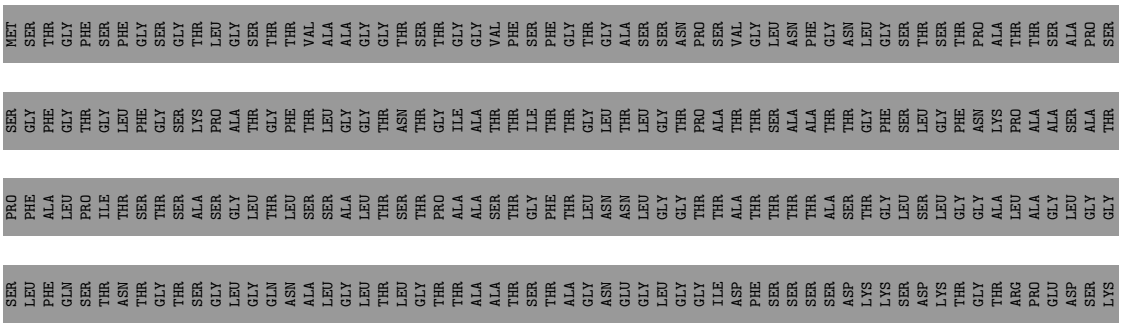
- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

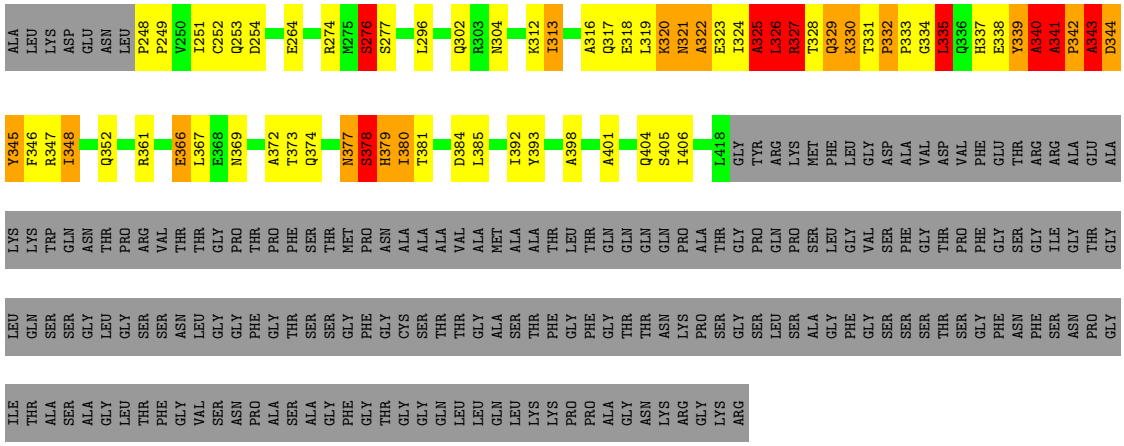
Chain 7-S: 17% 7% • • 71%



- Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

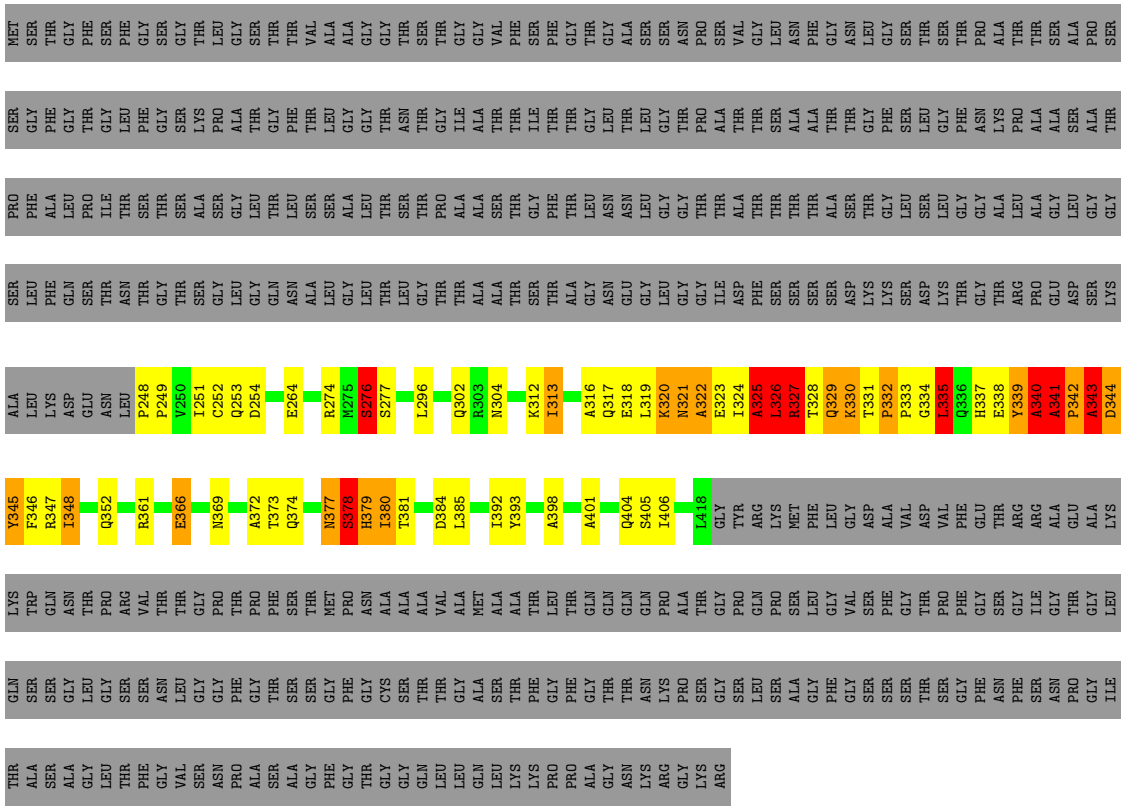
Chain 7-Y: 17% 7% • • 71%





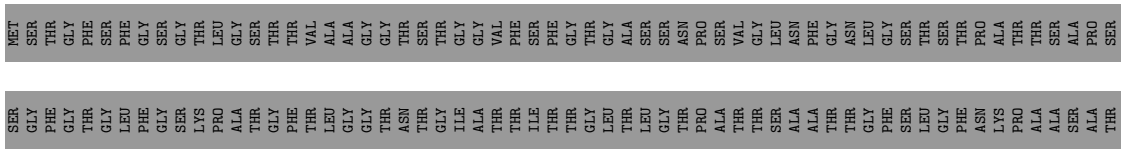
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

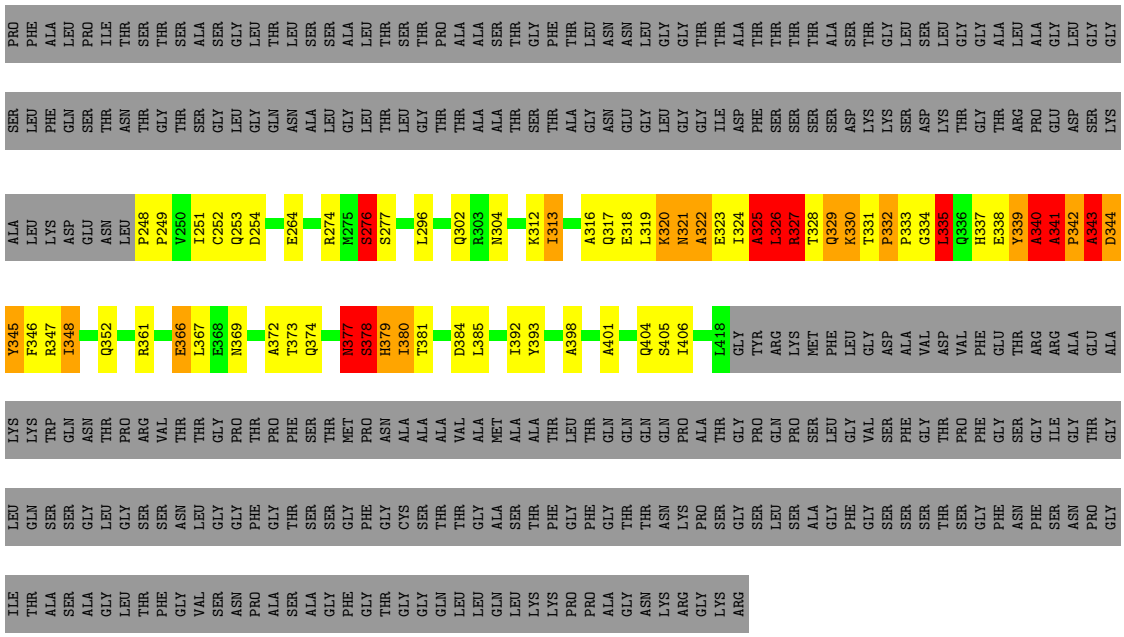
Chain 8-G: 17% 7% • • 71%



• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

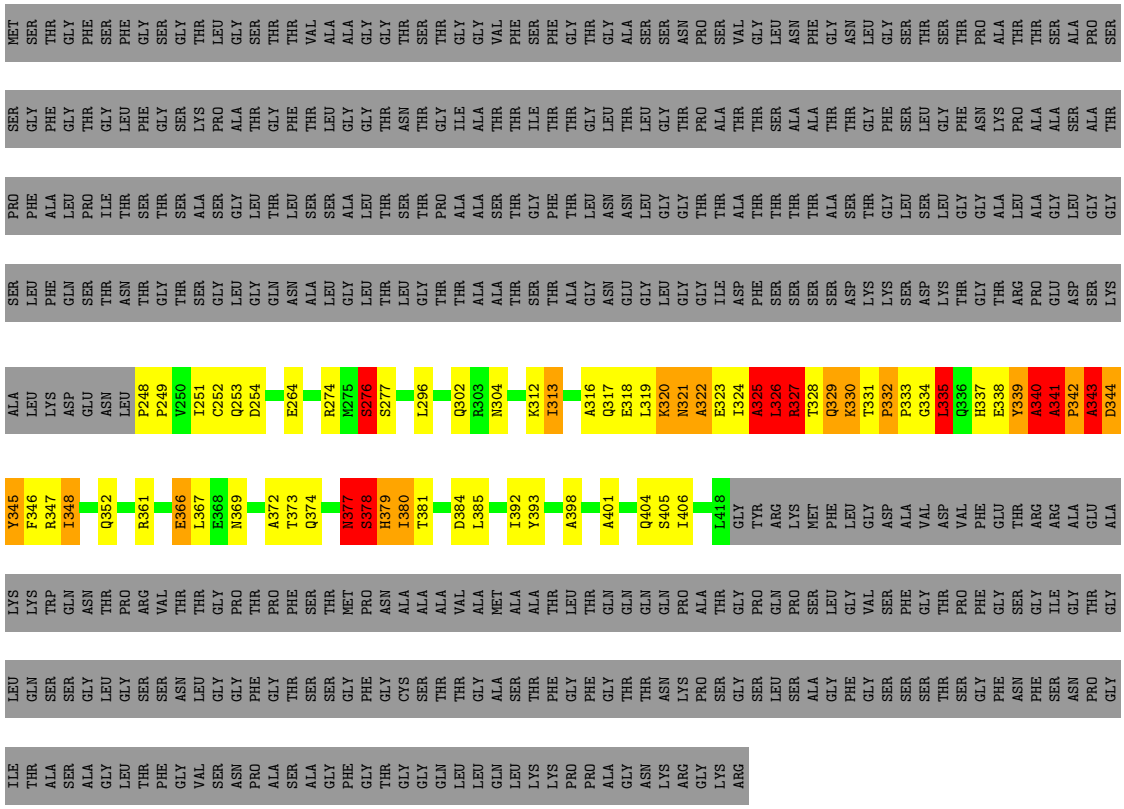
Chain 8-M: 17% 7% • • 71%





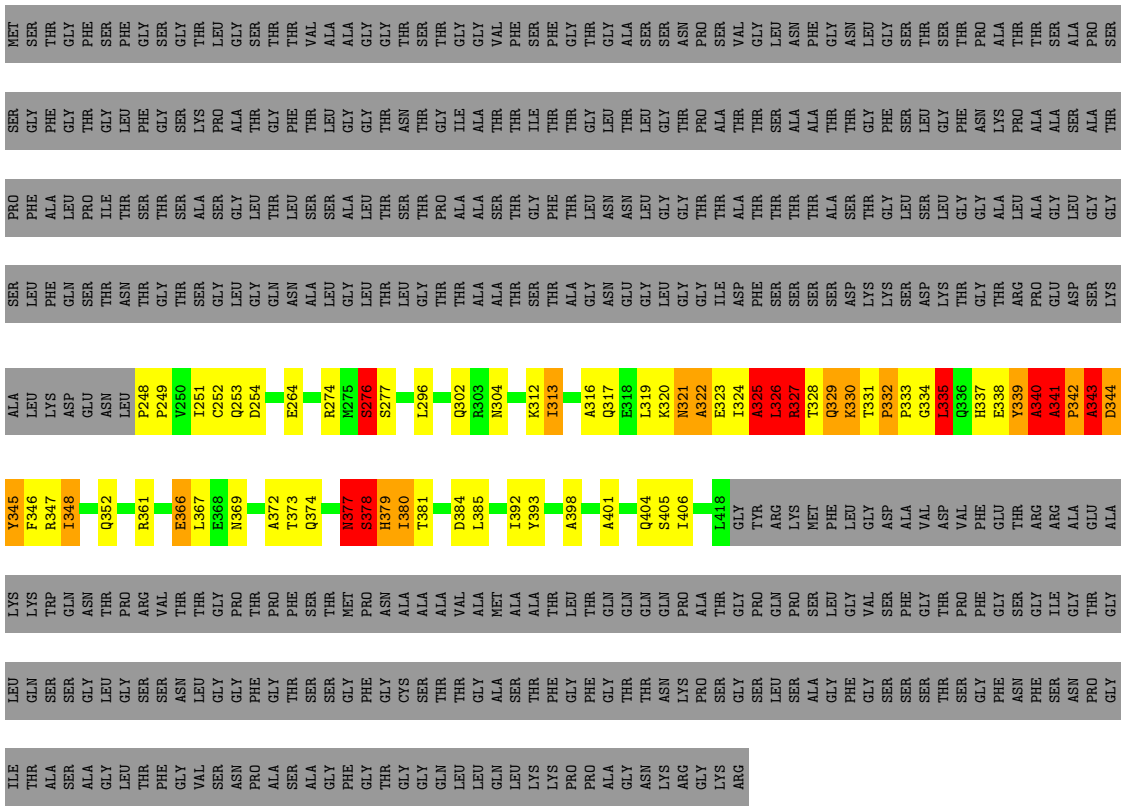
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 8-S: 17% 7% • • 71%



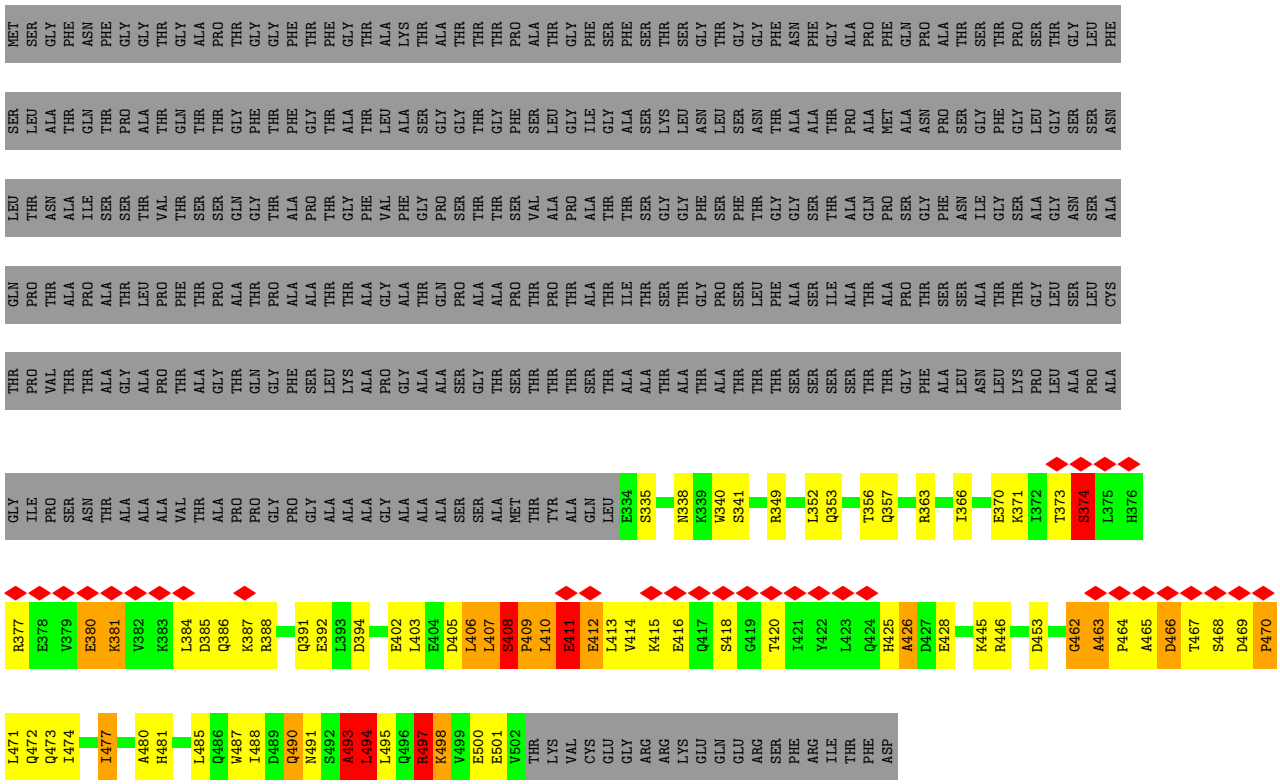
• Molecule 5: NUCLEAR PORE COMPLEX PROTEIN NUP58

Chain 8-Y: 17% 7% • • 71%



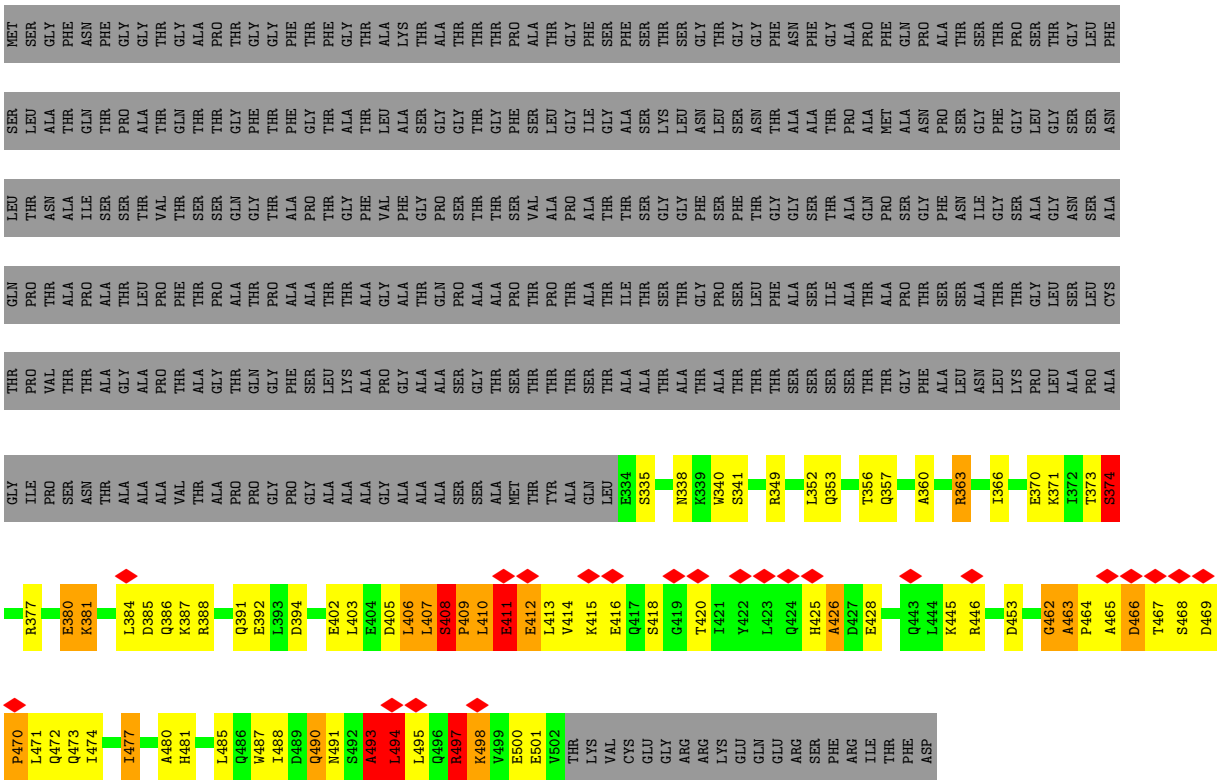
- Molecule 6: Nuclear pore glycoprotein p62

Chain 1-H:



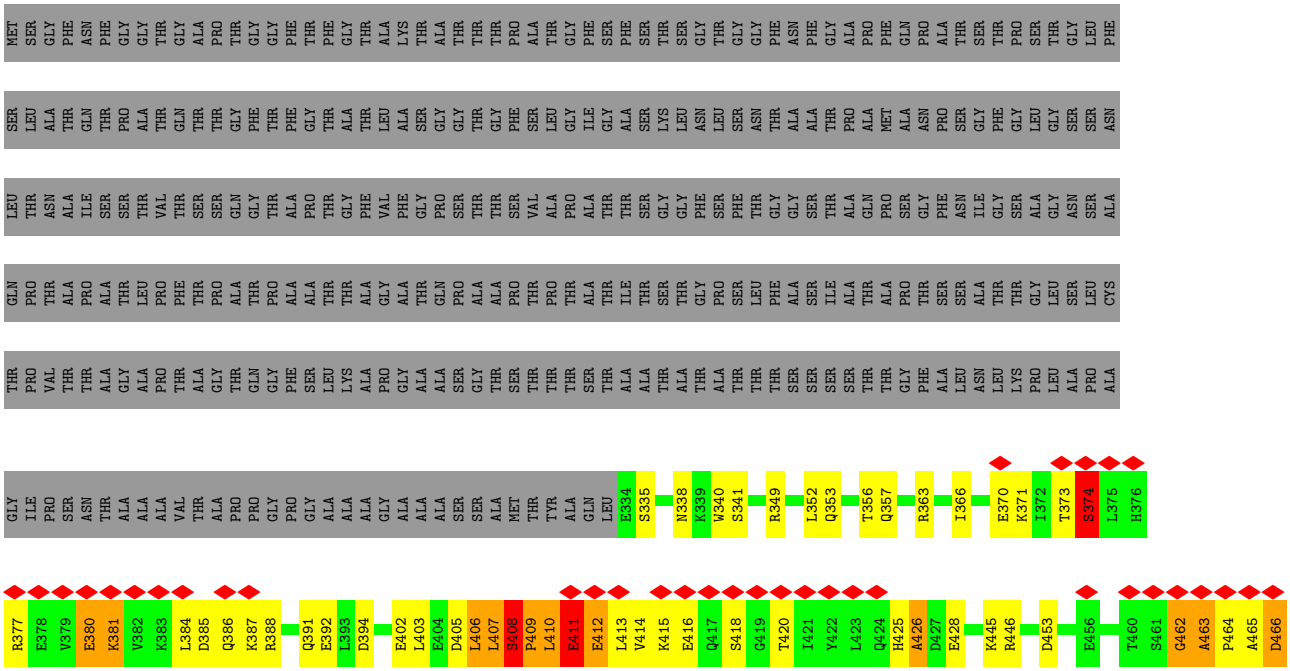
- Molecule 6: Nuclear pore glycoprotein p62

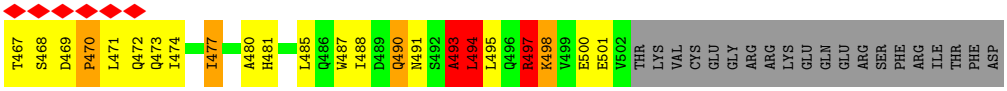
Chain 1-N:



- Molecule 6: Nuclear pore glycoprotein p62

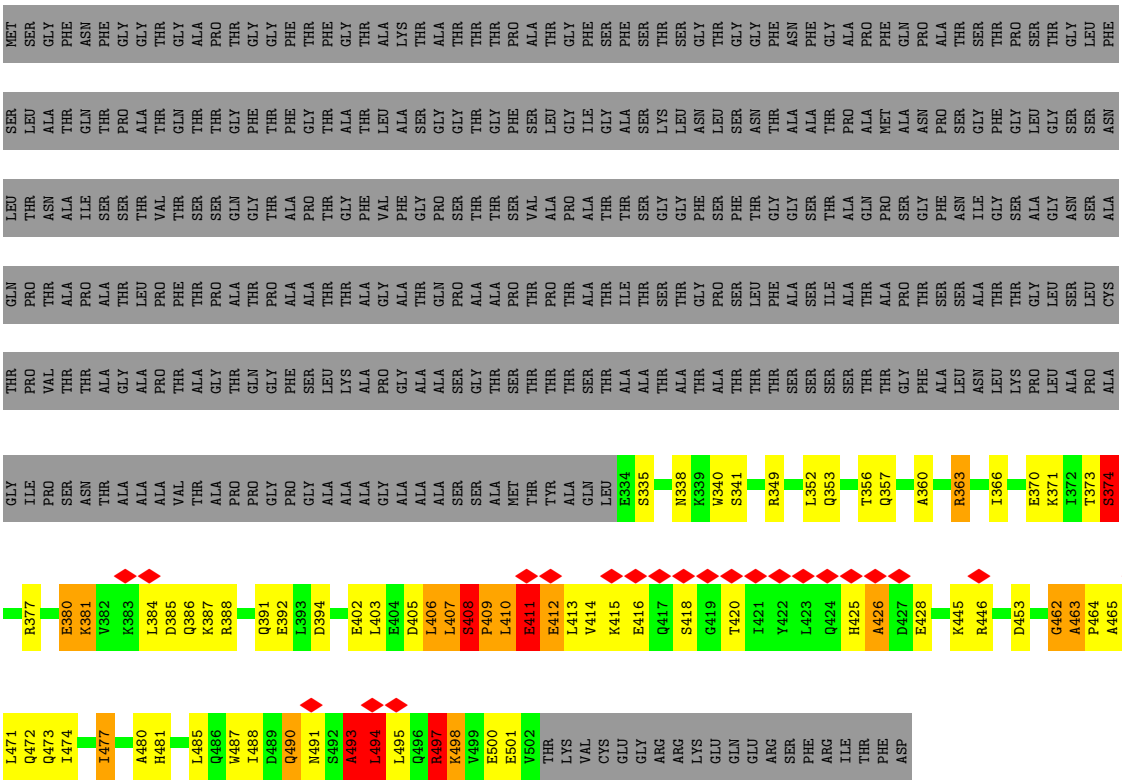
Chain 1-T:





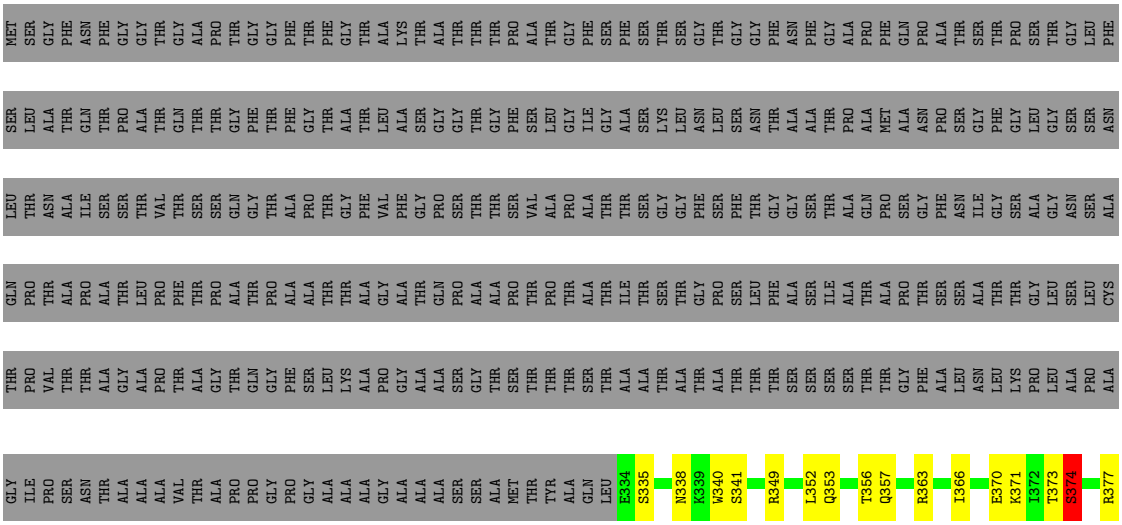
- Molecule 6: Nuclear pore glycoprotein p62

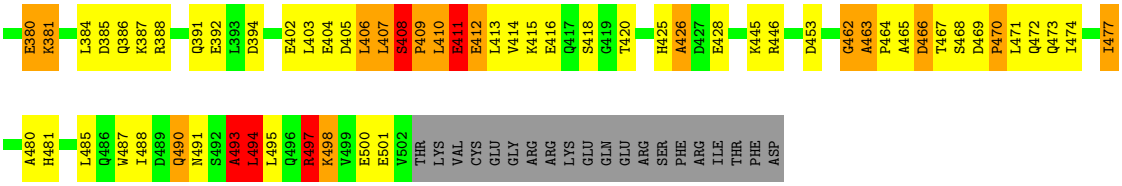
Chain 1-Z:



- Molecule 6: Nuclear pore glycoprotein p62

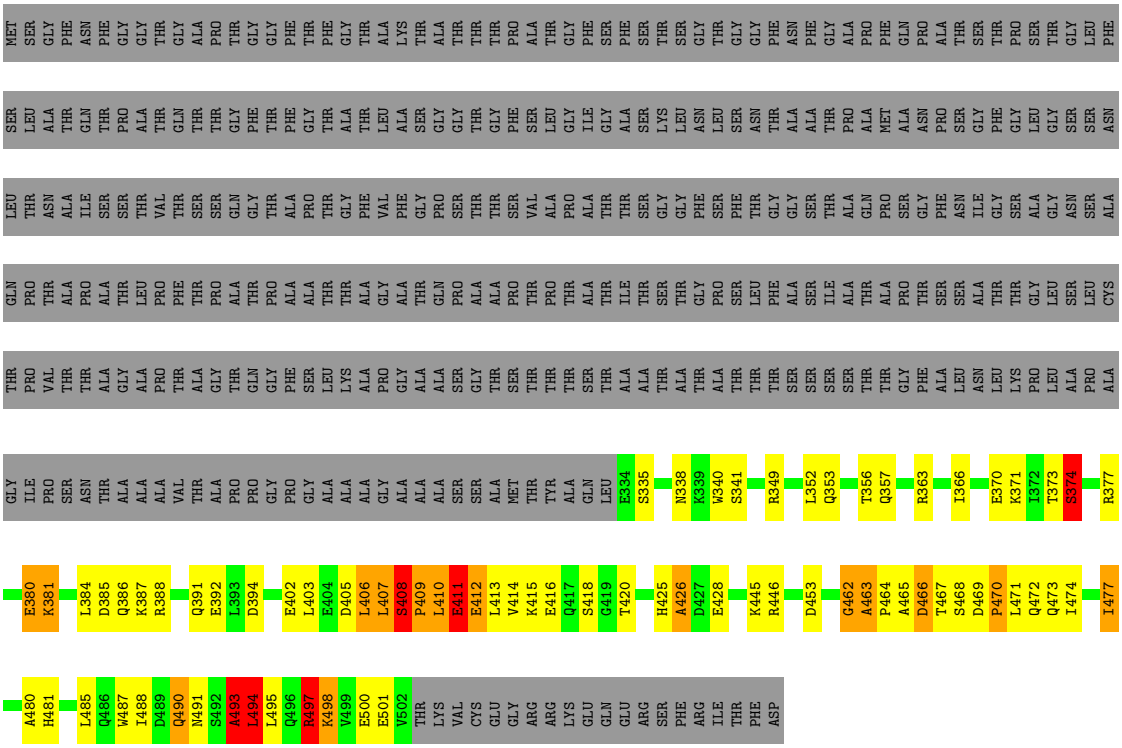
Chain 2-H:





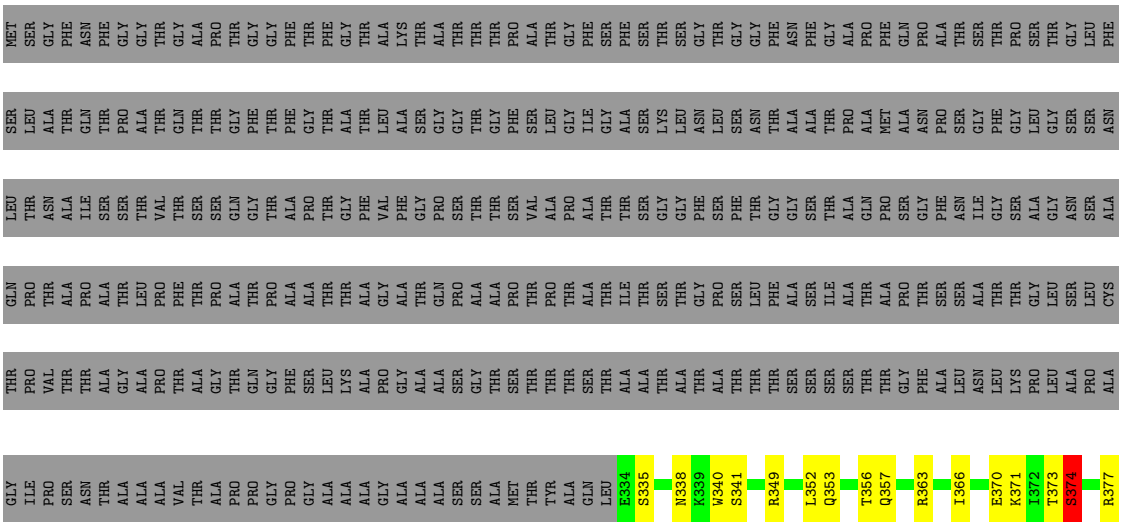
- Molecule 6: Nuclear pore glycoprotein p62

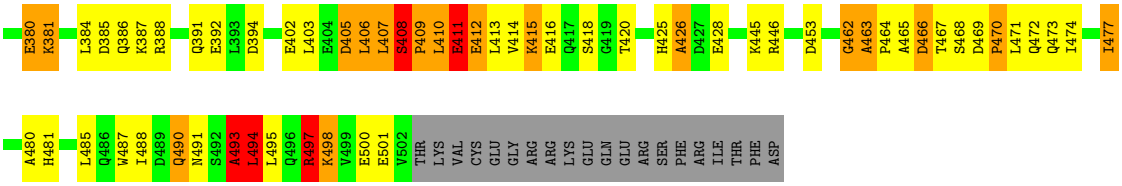
Chain 2-N: 18% 11% • • 68%



- Molecule 6: Nuclear pore glycoprotein p62

Chain 2-T: 18% 10% • • 68%



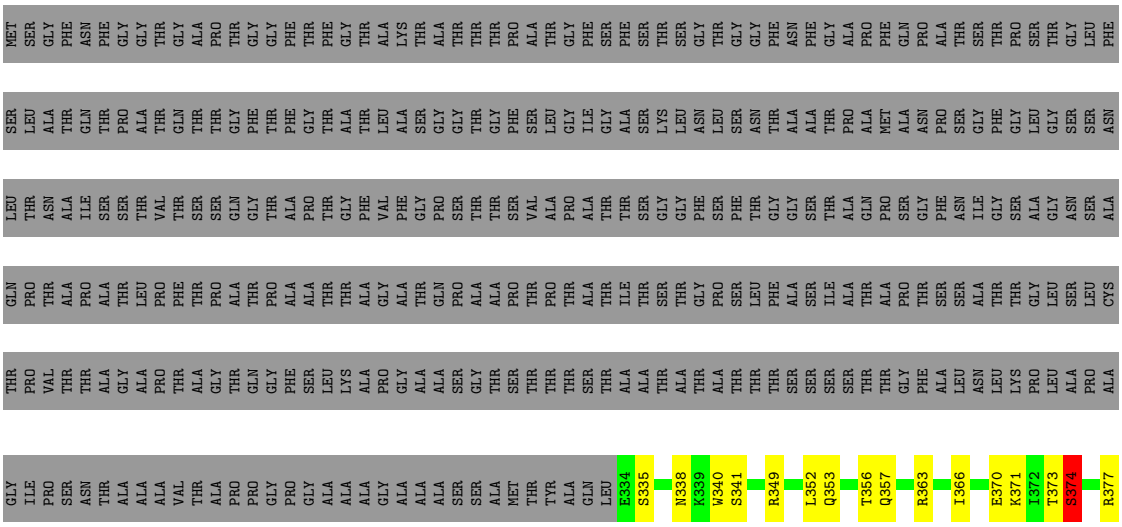


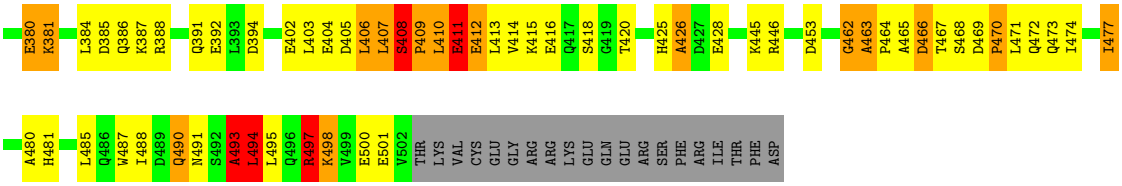
- Molecule 6: Nuclear pore glycoprotein p62

Chain 2-Z:

- Molecule 6: Nuclear pore glycoprotein p62

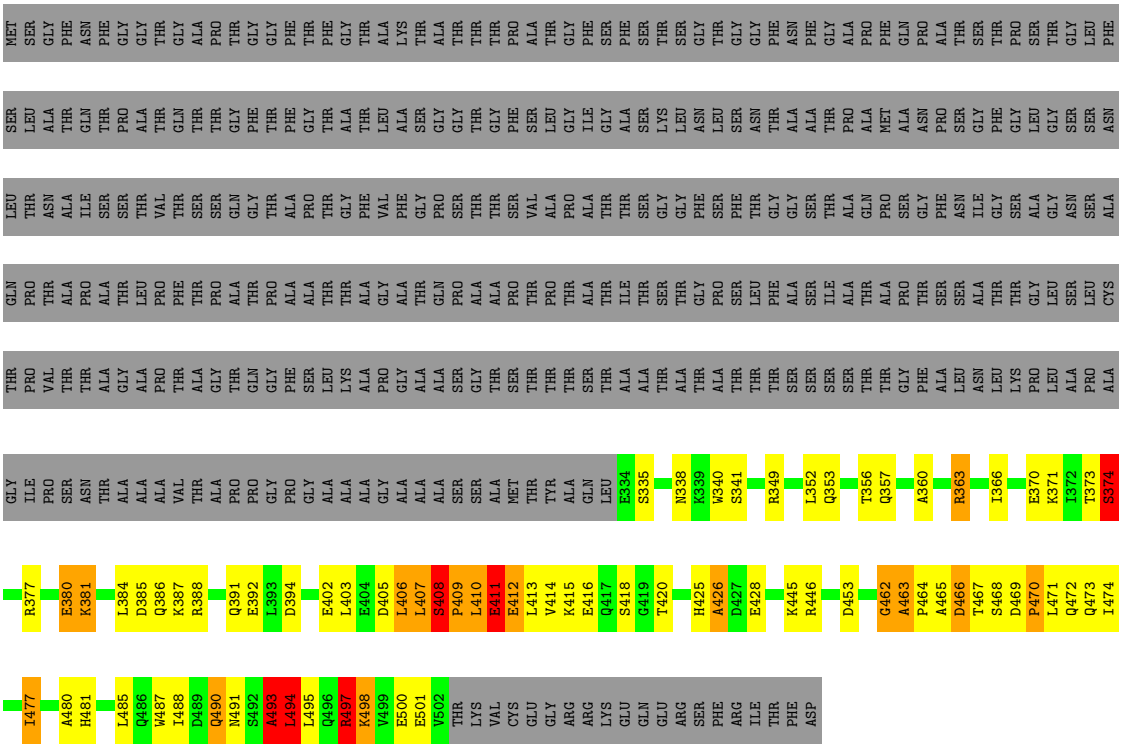
Chain 3-H:





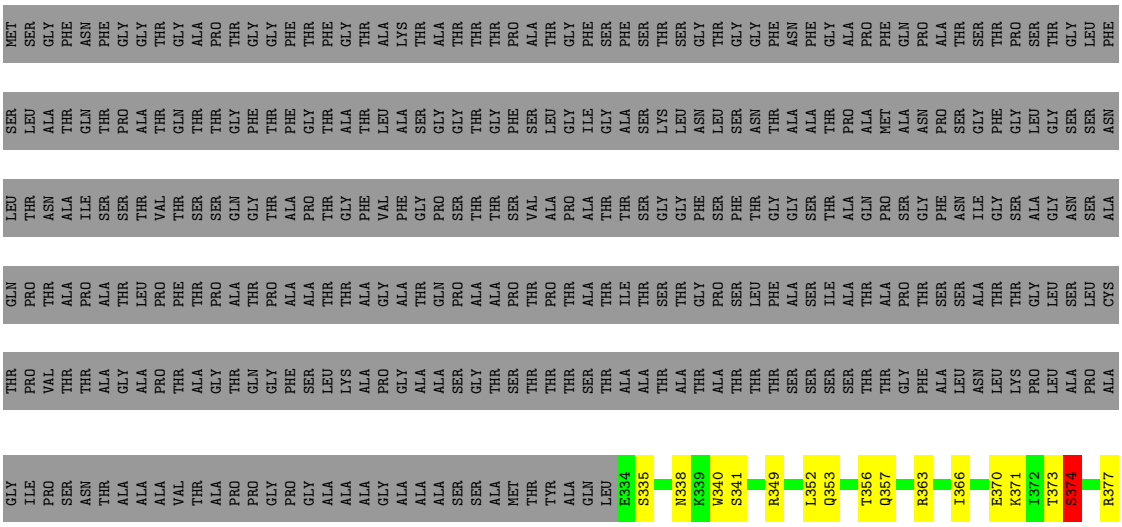
- Molecule 6: Nuclear pore glycoprotein p62

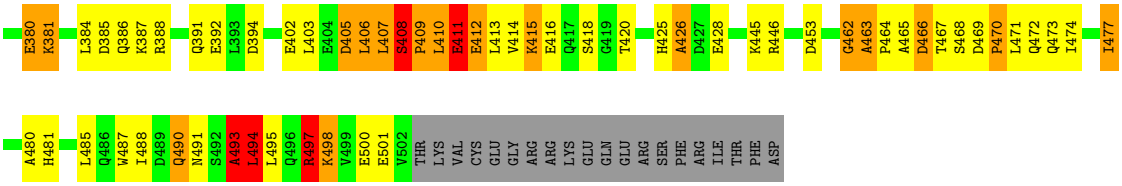
Chain 3-N: 18% 11% • • 68%



- Molecule 6: Nuclear pore glycoprotein p62

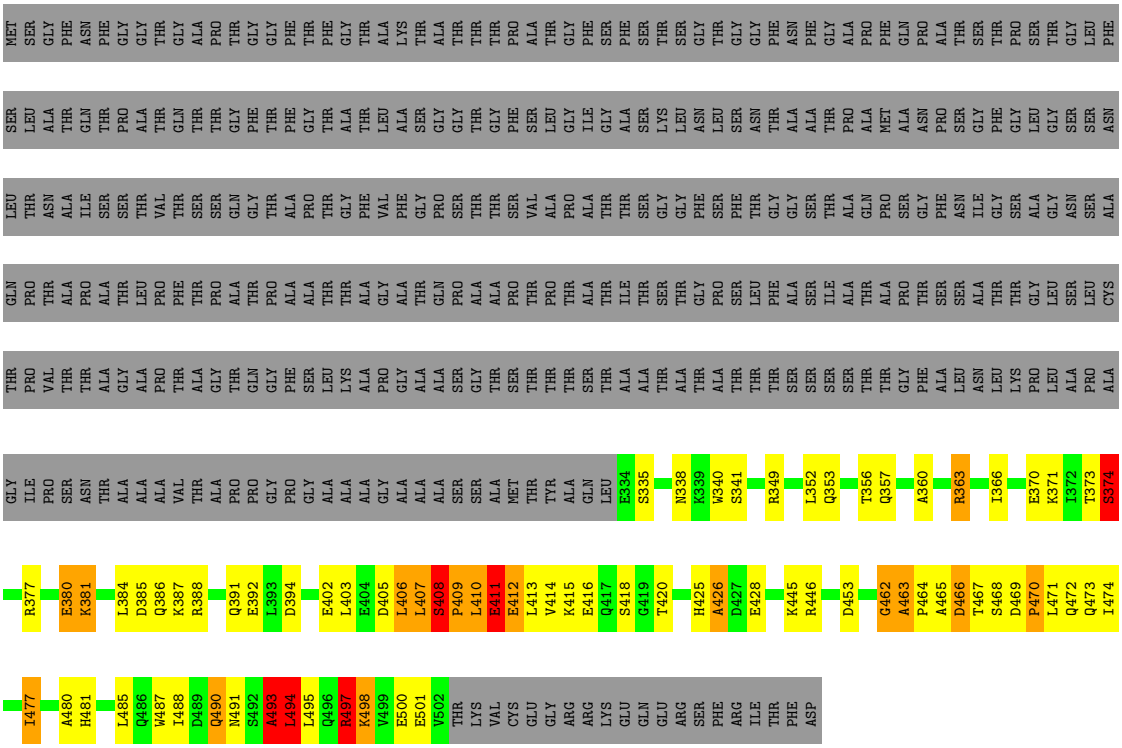
Chain 3-T: 18% 10% • • 68%





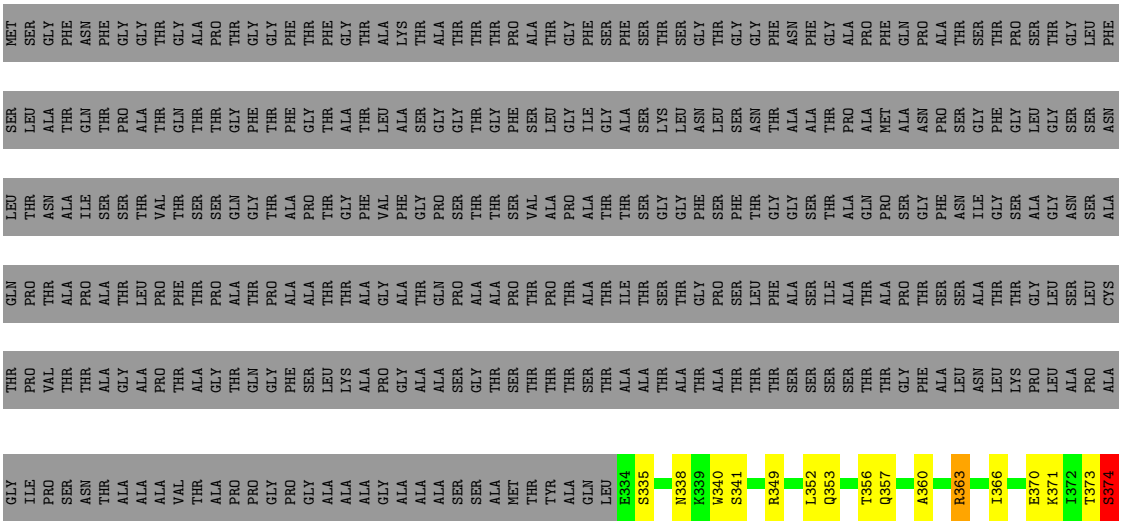
- Molecule 6: Nuclear pore glycoprotein p62

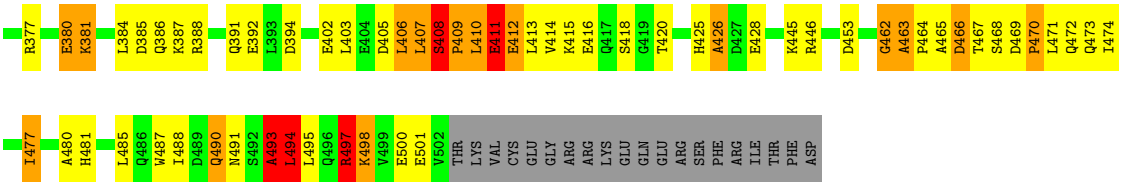
Chain 3-Z:



- Molecule 6: Nuclear pore glycoprotein p62

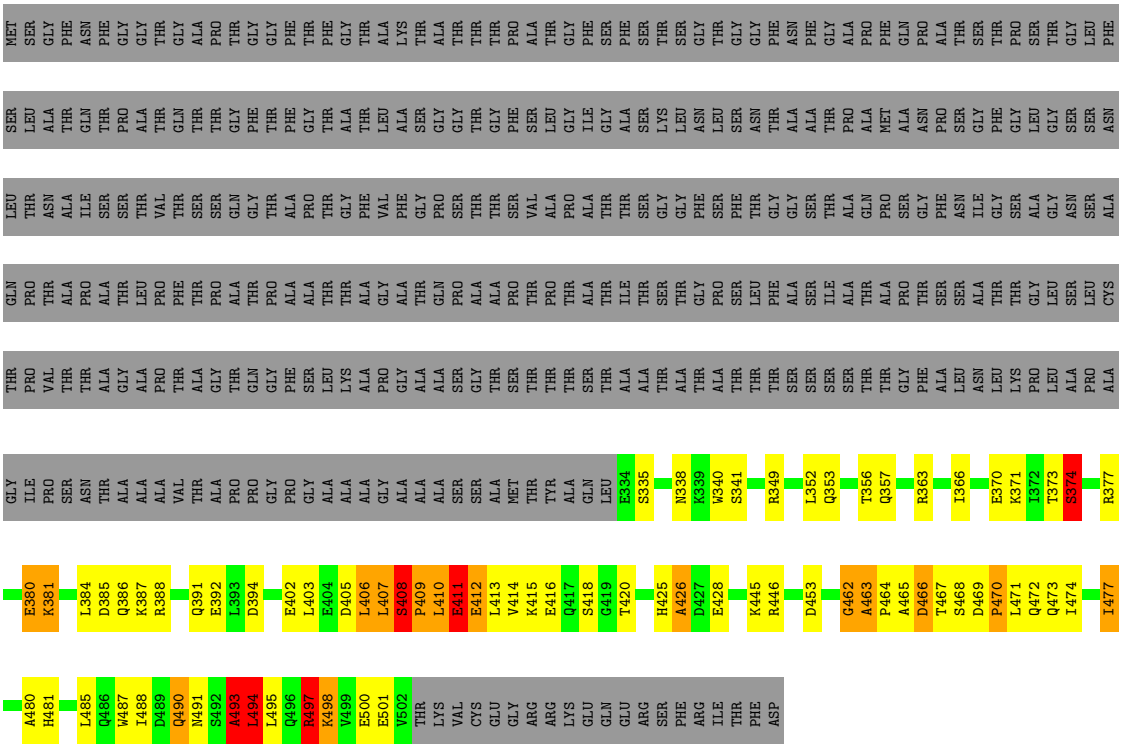
Chain 4-H:





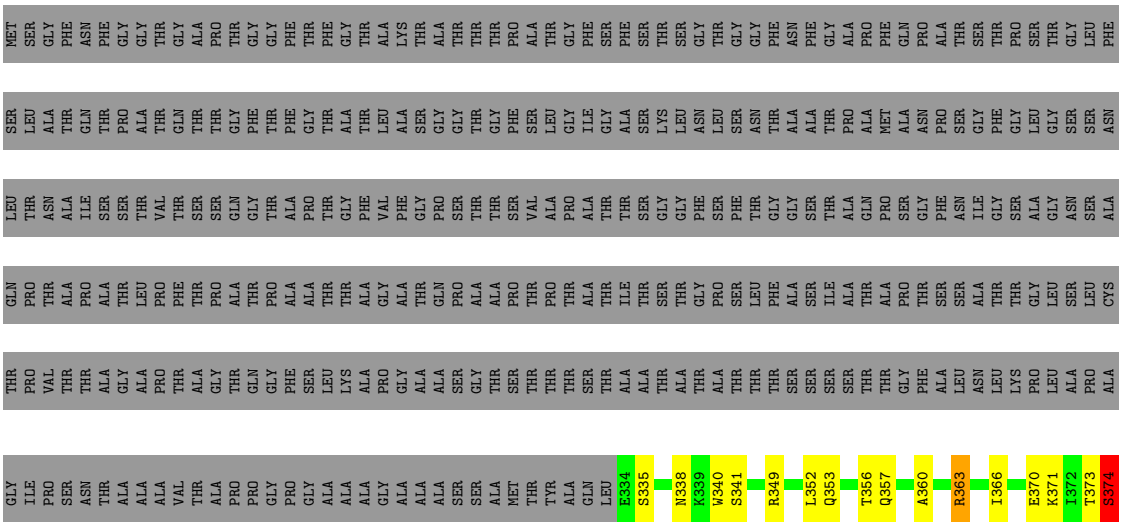
- Molecule 6: Nuclear pore glycoprotein p62

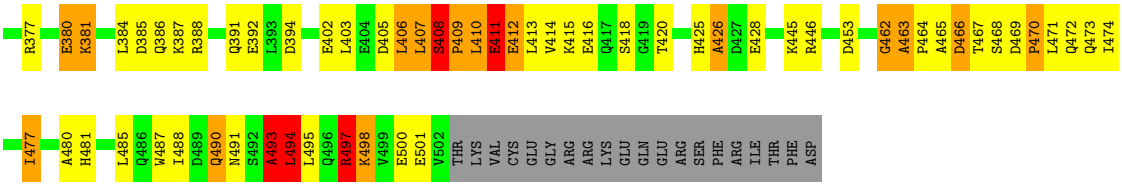
Chain 4-N:



- Molecule 6: Nuclear pore glycoprotein p62

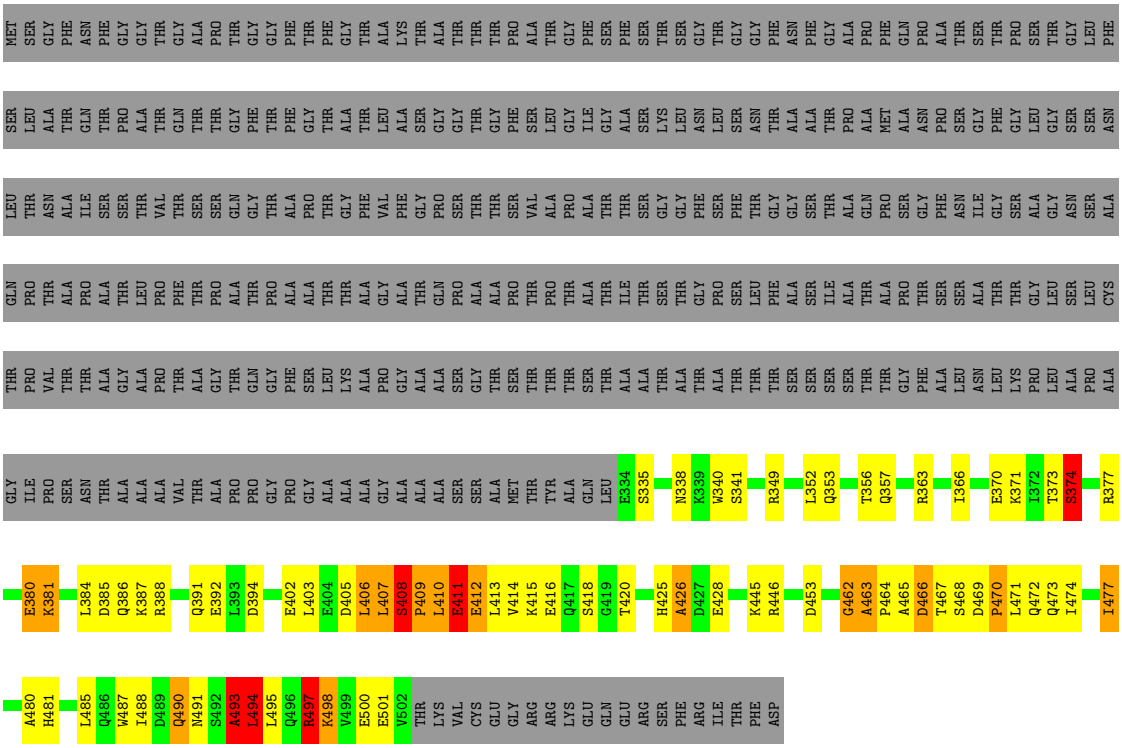
Chain 4-T:





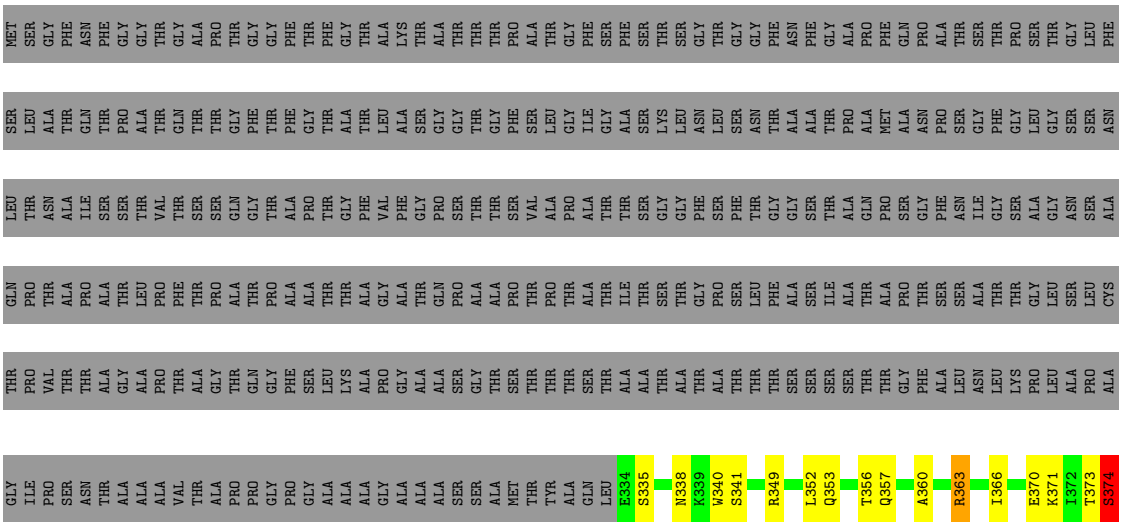
- Molecule 6: Nuclear pore glycoprotein p62

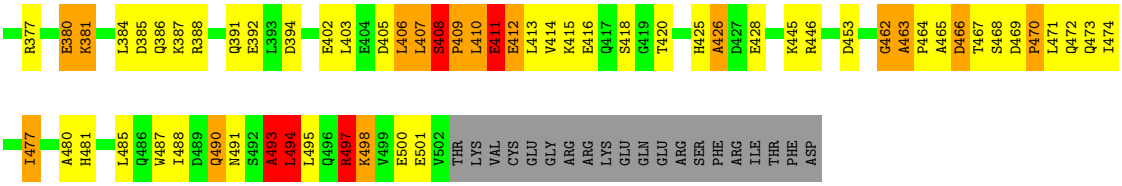
Chain 4-Z:



- Molecule 6: Nuclear pore glycoprotein p62

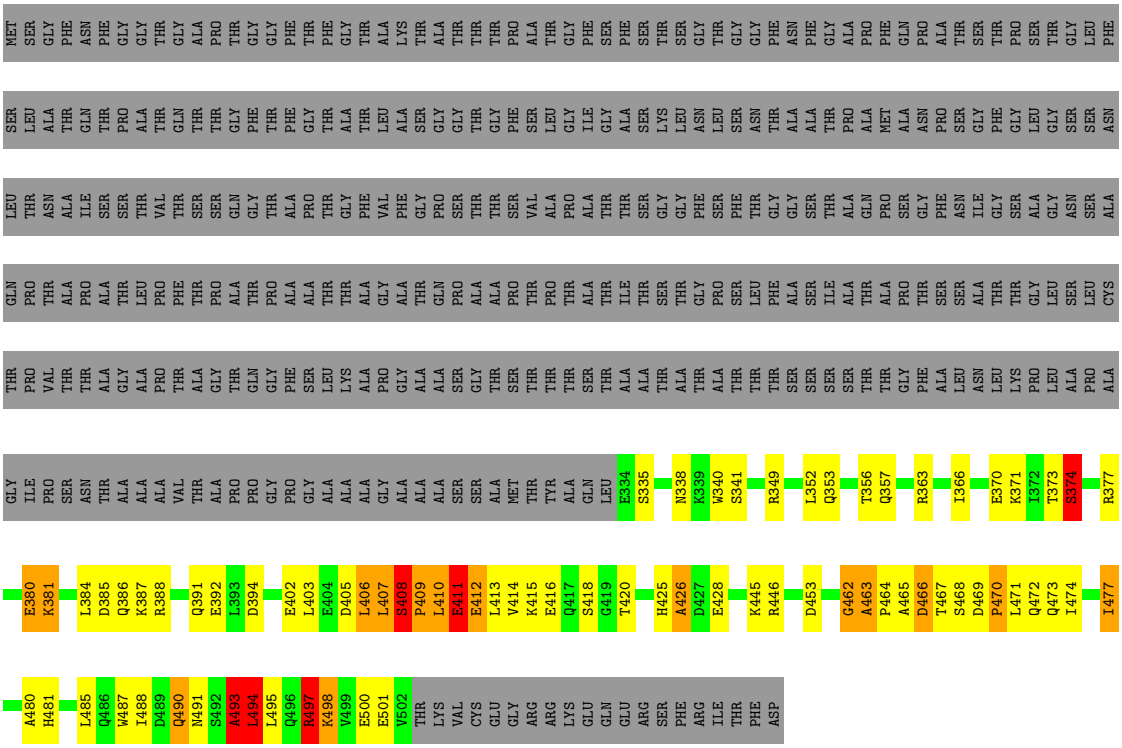
Chain 5-H:





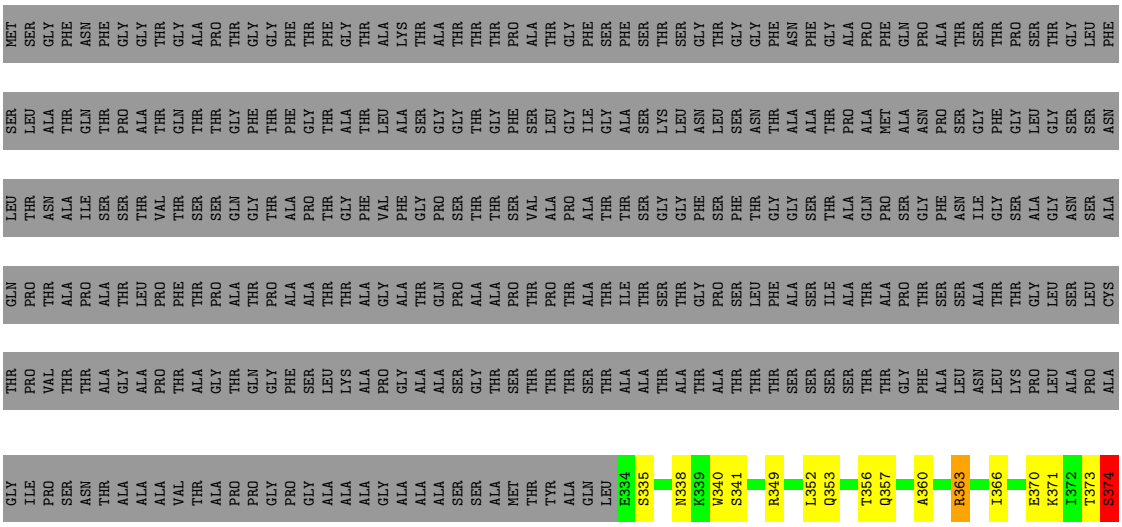
- Molecule 6: Nuclear pore glycoprotein p62

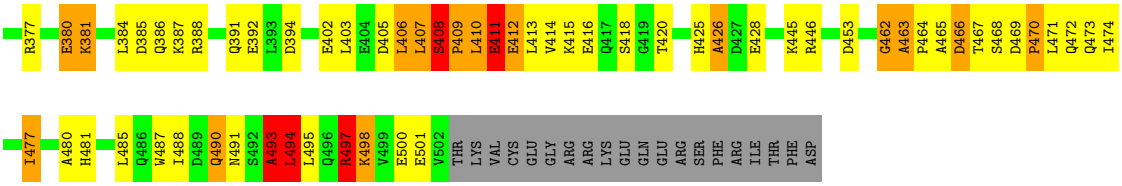
Chain 5-N:



- Molecule 6: Nuclear pore glycoprotein p62

Chain 5-T:





- Molecule 6: Nuclear pore glycoprotein p62

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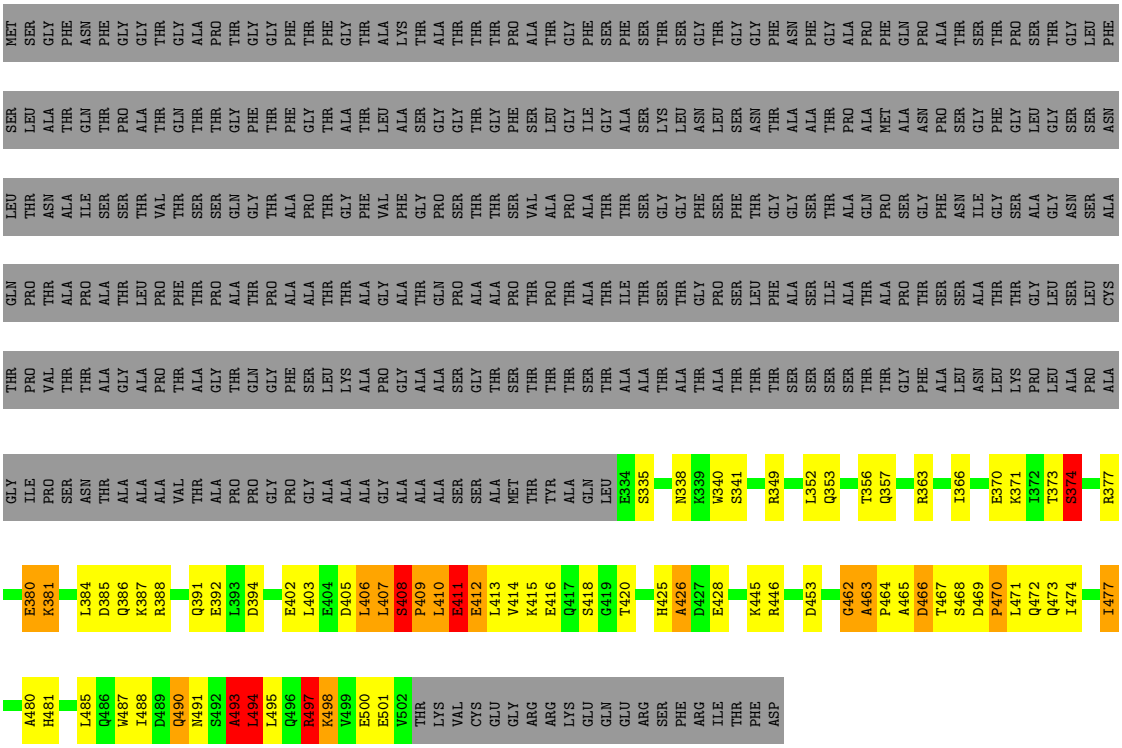

- Molecule 6: Nuclear pore glycoprotein p62

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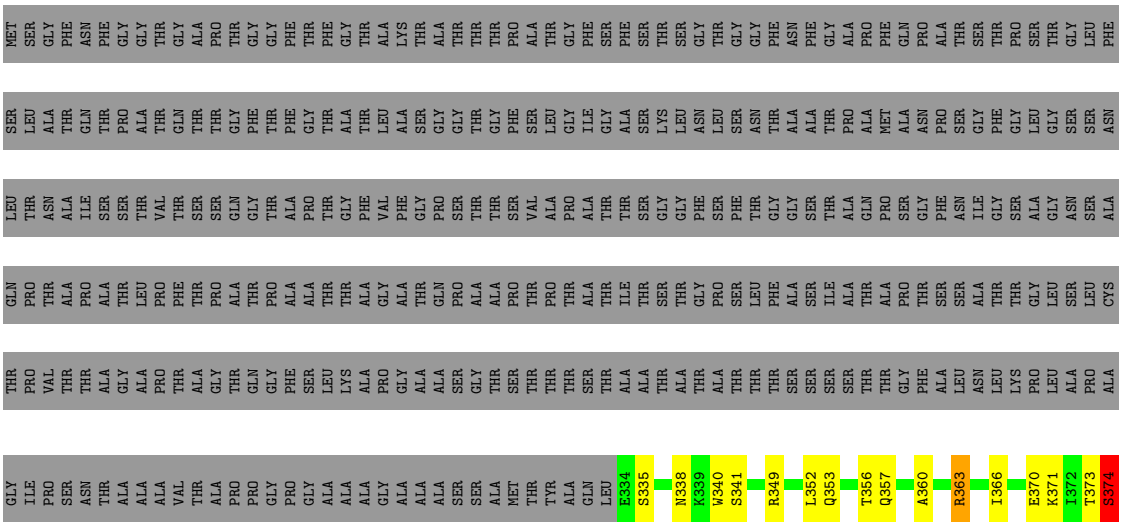
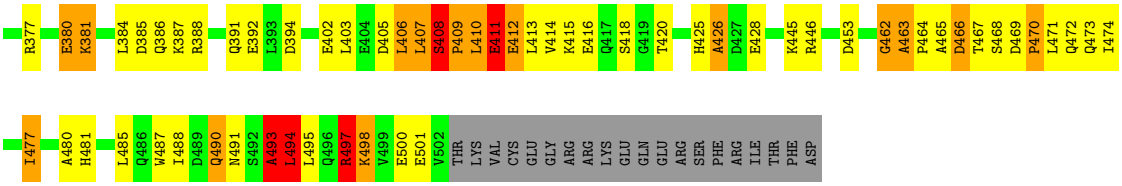
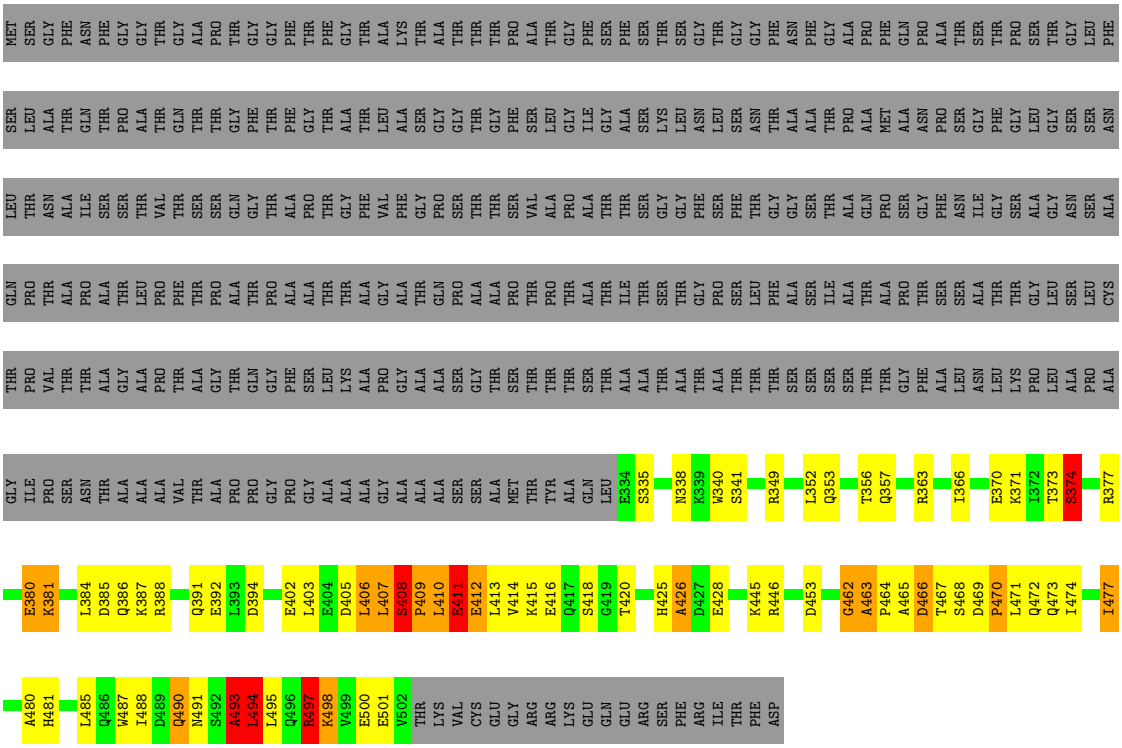




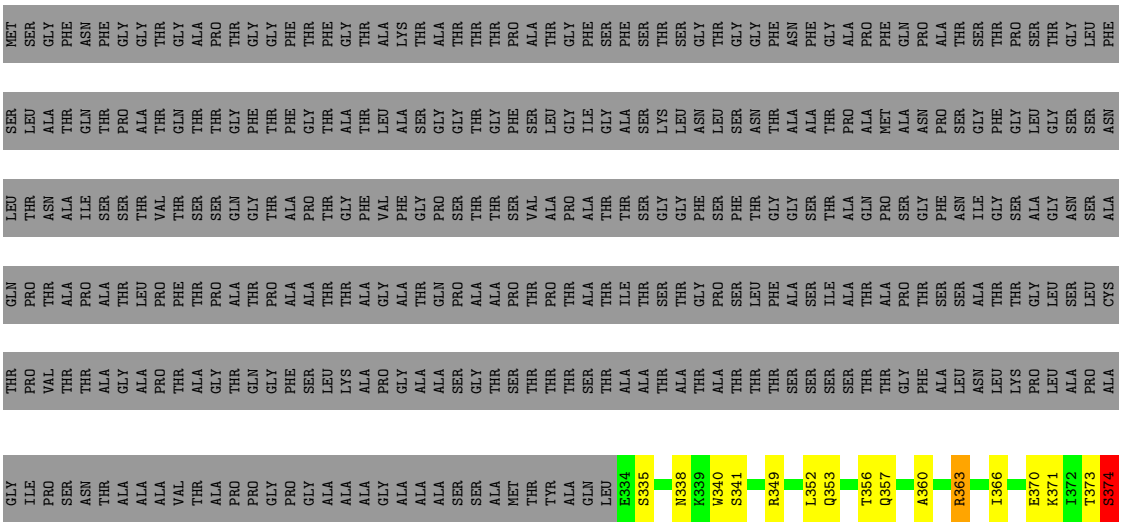
- Molecule 6: Nuclear pore glycoprotein p62

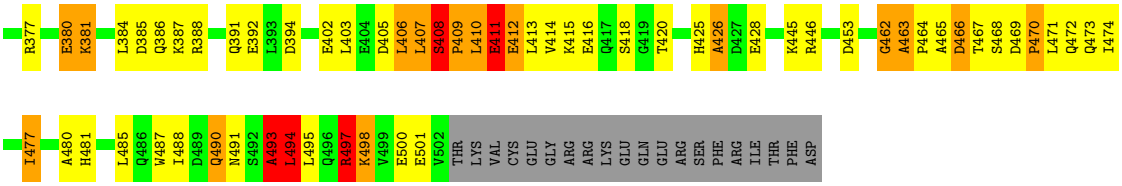
Chain 6-N: 18% 11% • • 68%



- Molecule 6: Nuclear pore glycoprotein p62

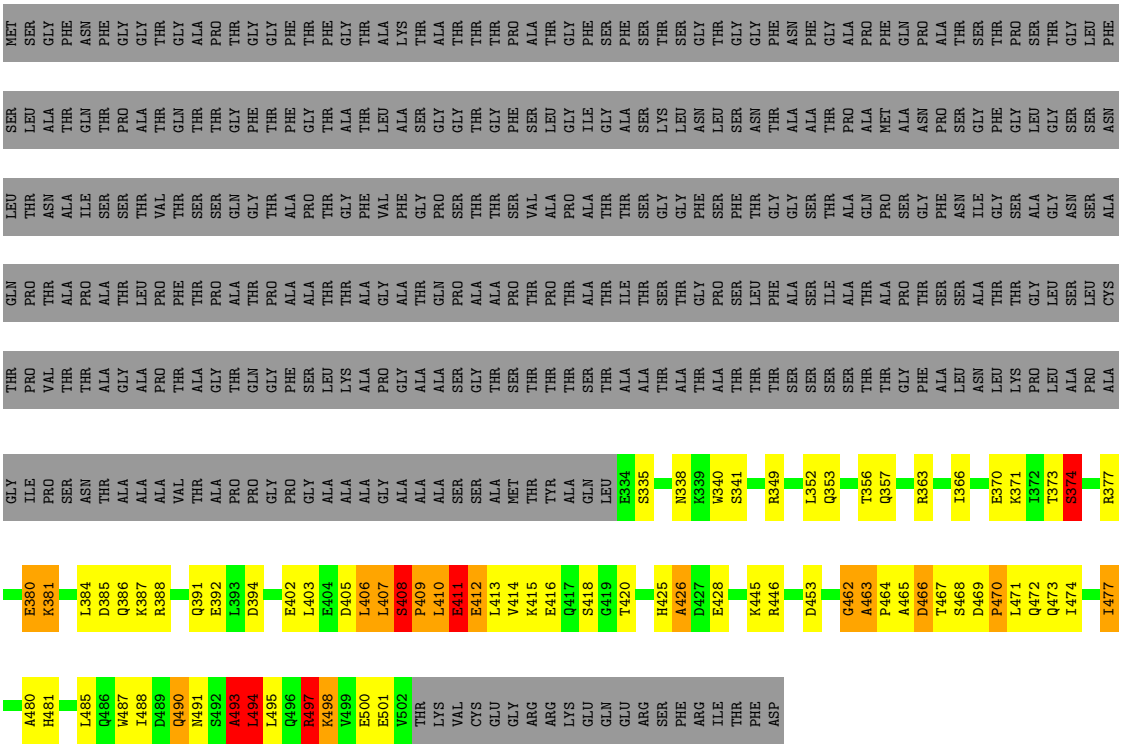
Chain 6-T: 18% 11% • • 68%





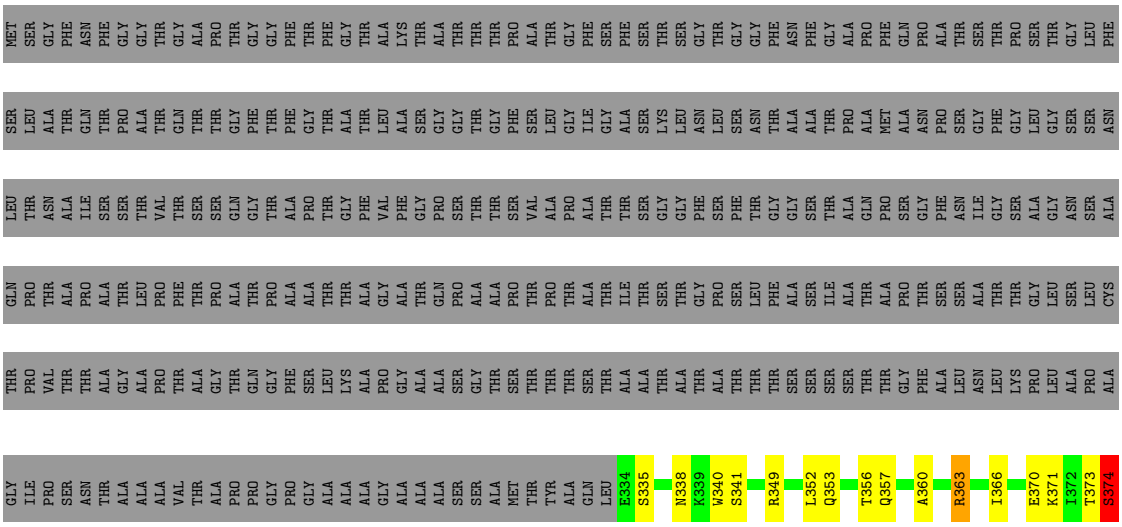
- Molecule 6: Nuclear pore glycoprotein p62

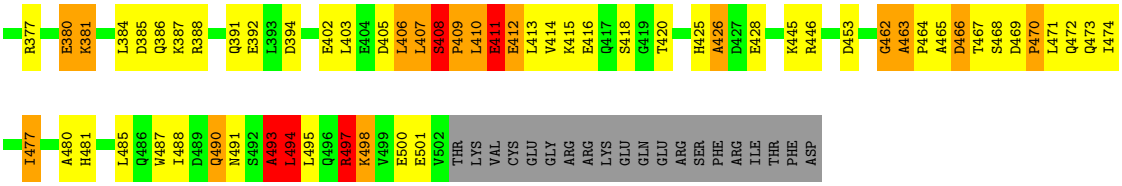
Chain 6-Z:



- Molecule 6: Nuclear pore glycoprotein p62

Chain 7-H:





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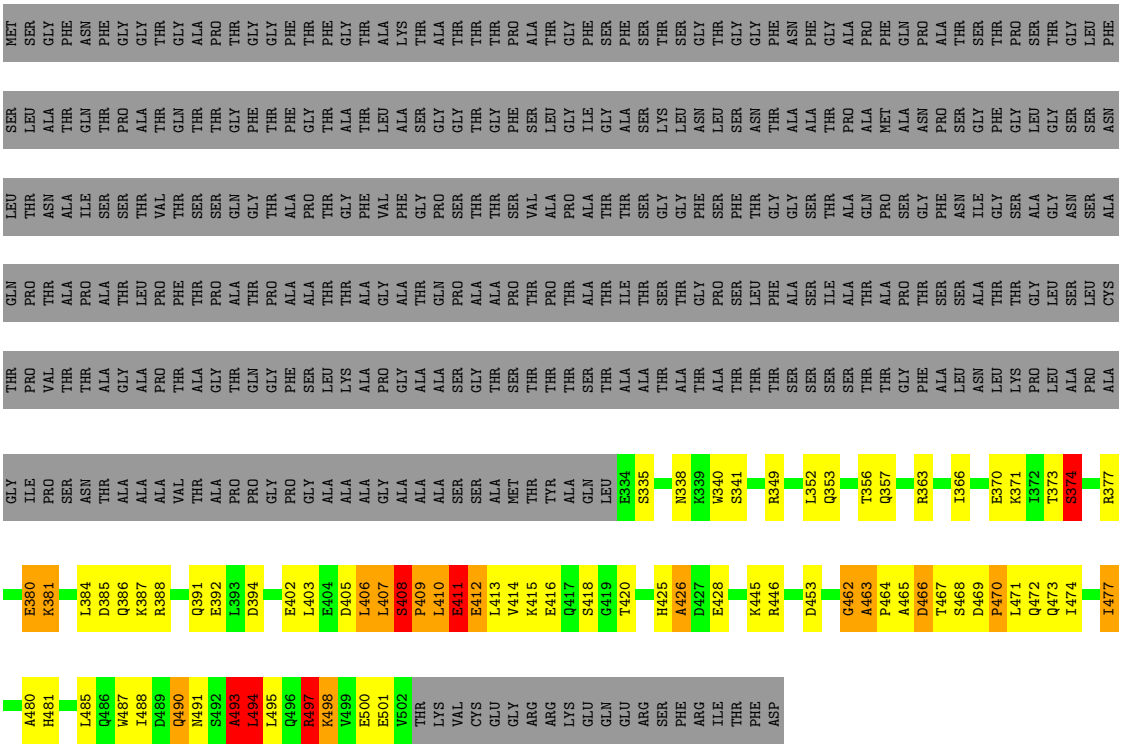
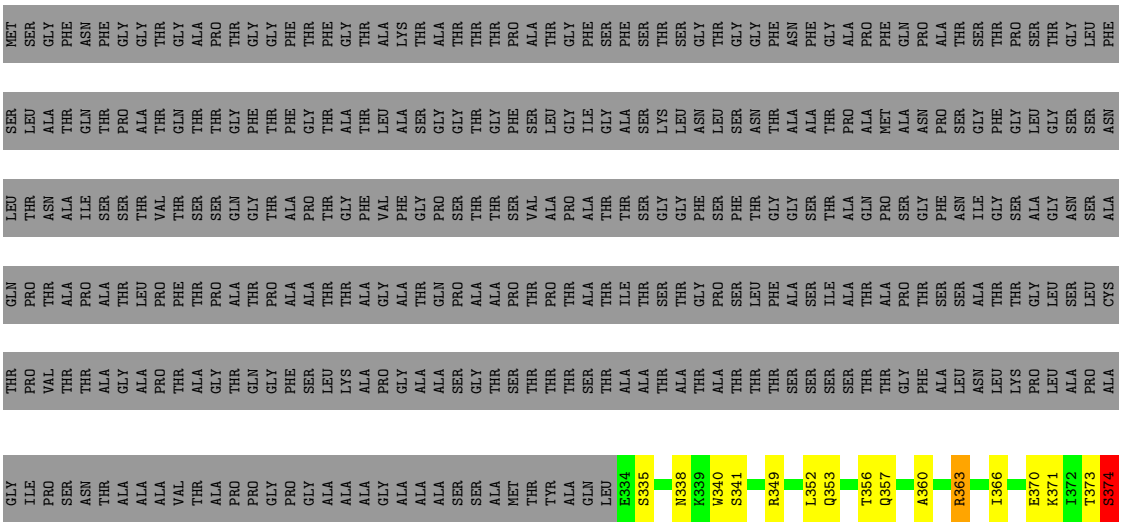
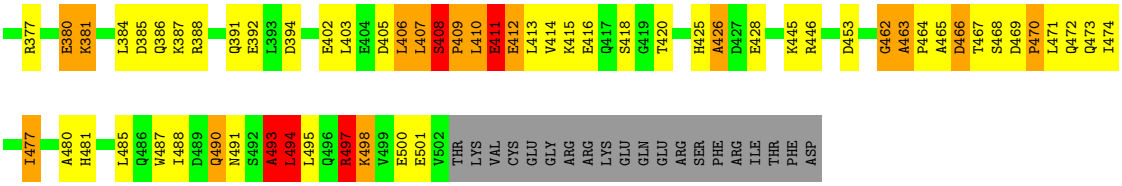


- Molecule 6: Nuclear pore glycoprotein p62

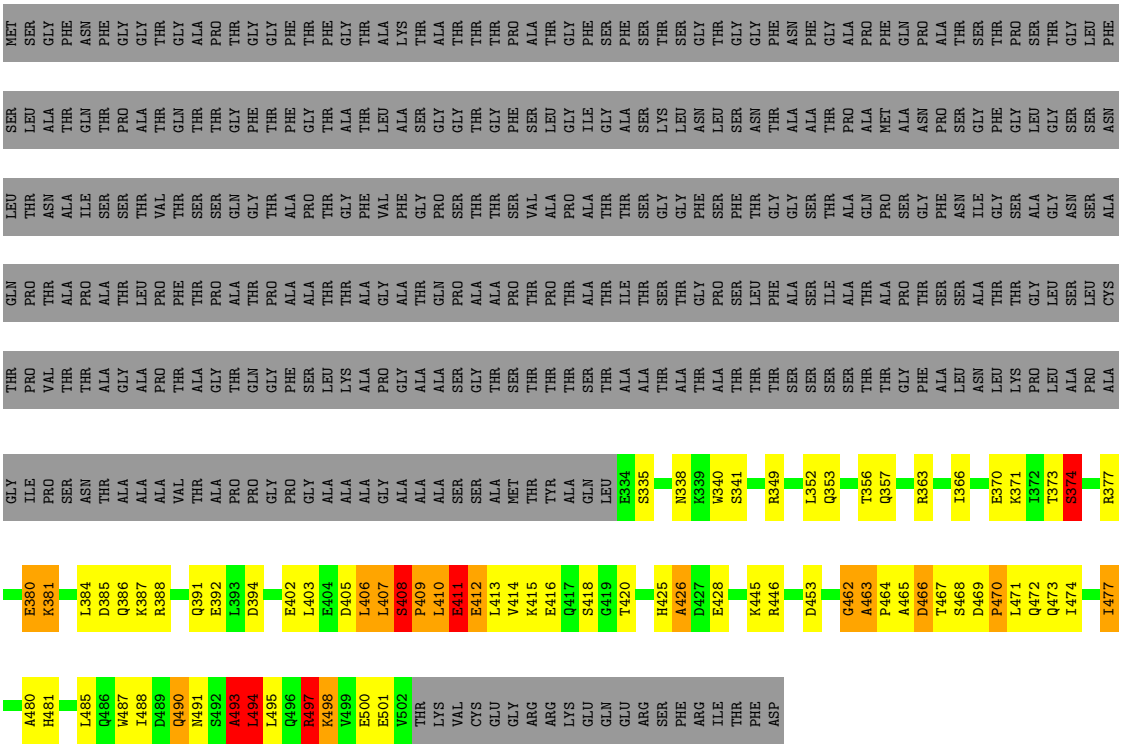
Chain 7-T:





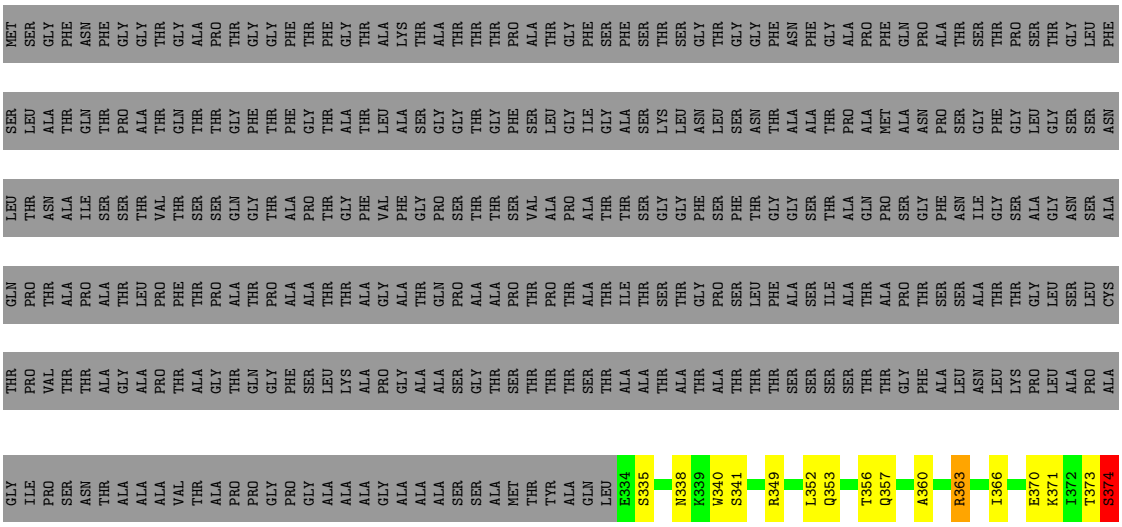
- Molecule 6: Nuclear pore glycoprotein p62

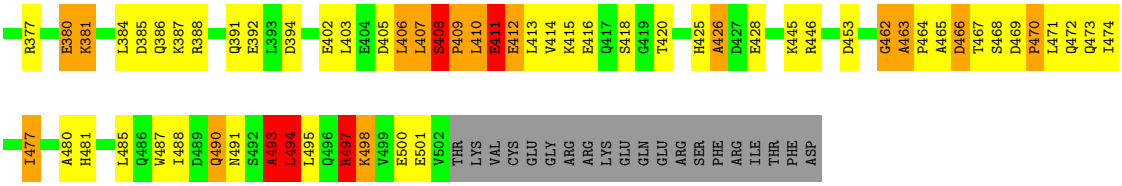
Chain 7-Z:



- Molecule 6: Nuclear pore glycoprotein p62

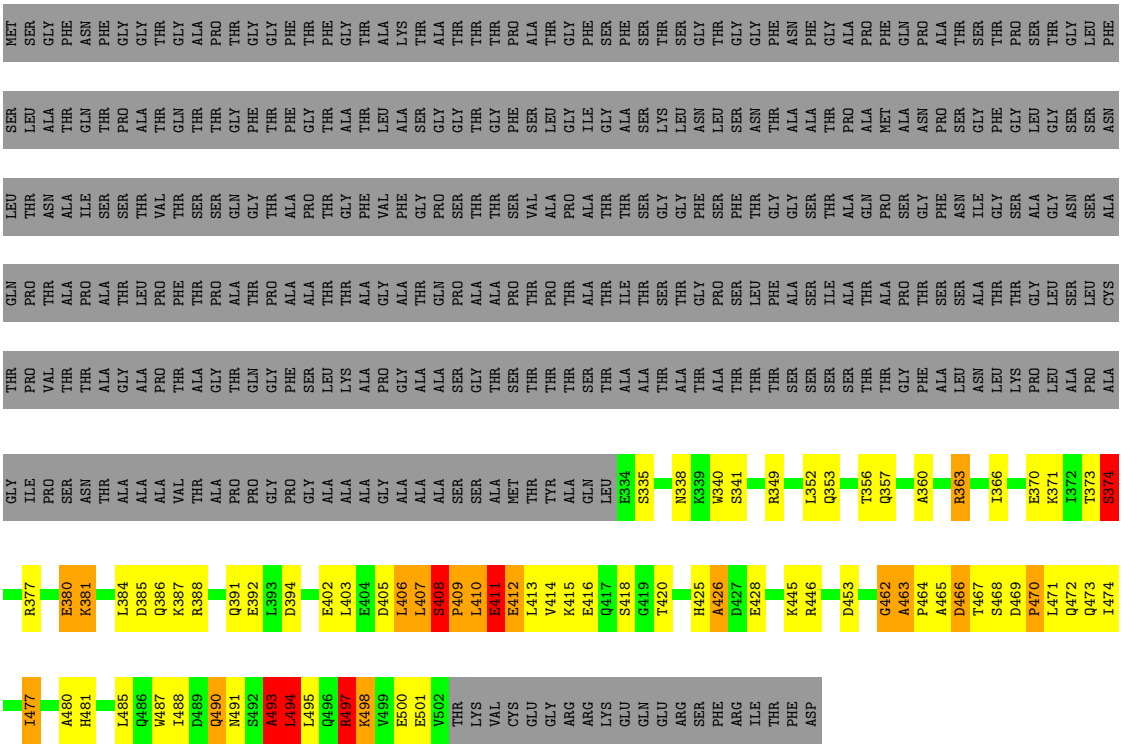
Chain 8-H:





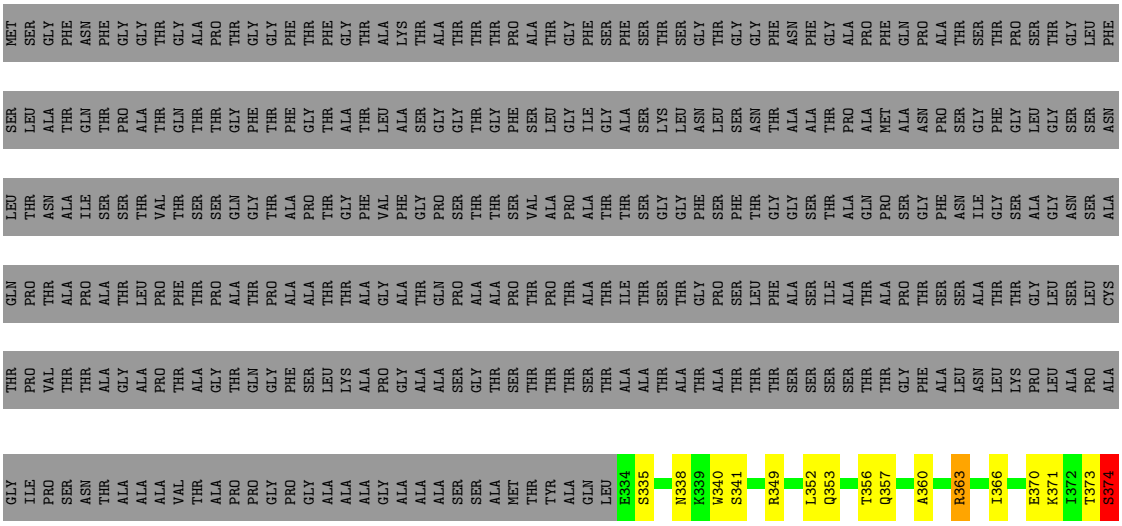
- Molecule 6: Nuclear pore glycoprotein p62

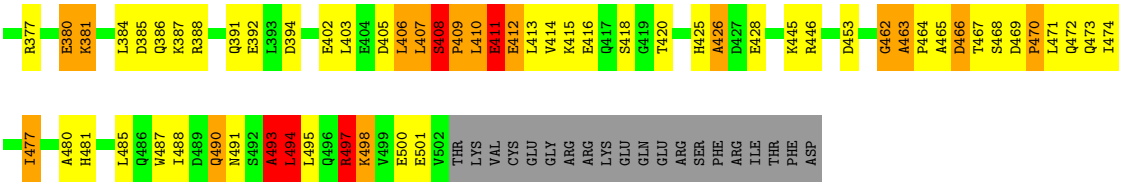
Chain 8-N:



- Molecule 6: Nuclear pore glycoprotein p62

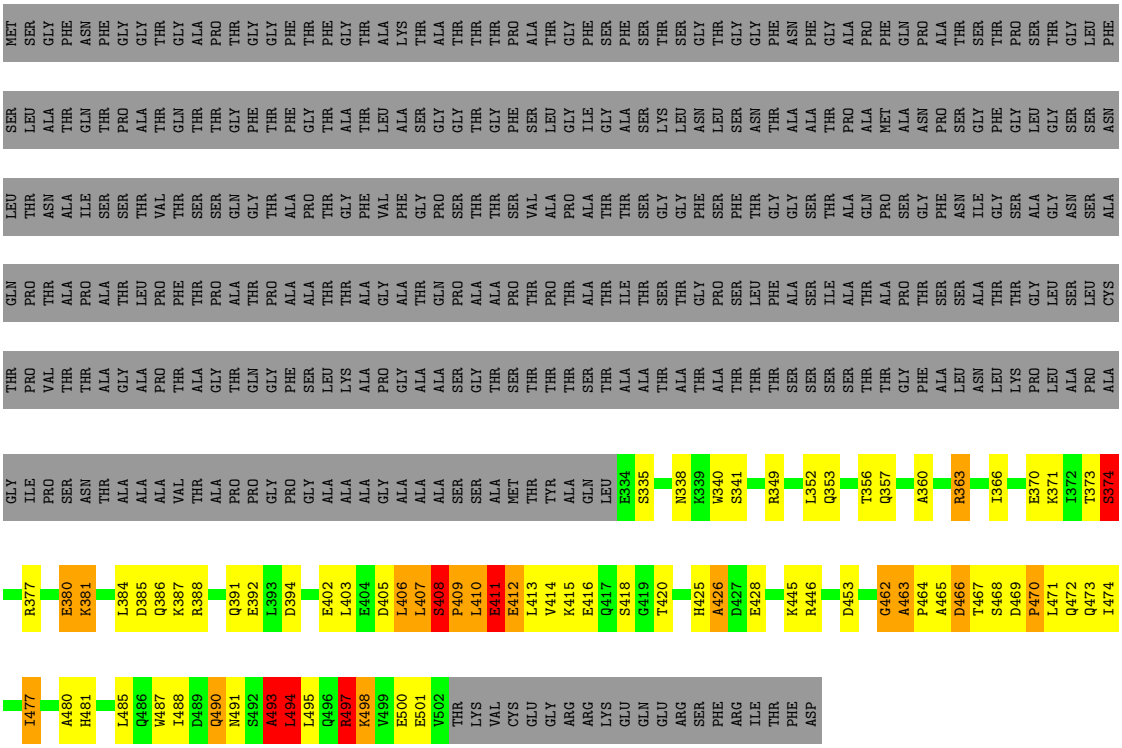
Chain 8-T:





• Molecule 6: Nuclear pore glycoprotein p62

Chain 8-Z: 18% 11% • • 68%



4 Experimental information (i)

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 ($e^-/Å^2$)	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 (Å)	964.8, 964.8, 964.8	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.94	0/3195	1.25	10/4421 (0.2%)
1	1-B	0.94	0/3195	1.25	10/4421 (0.2%)
1	1-E	0.93	0/5338	1.17	10/7399 (0.1%)
1	1-K	0.93	0/5338	1.18	10/7399 (0.1%)
1	1-Q	0.93	0/5338	1.17	10/7399 (0.1%)
1	1-W	0.93	0/5338	1.17	10/7399 (0.1%)
1	2-A	0.94	0/3195	1.16	6/4421 (0.1%)
1	2-B	0.94	0/3195	1.16	6/4421 (0.1%)
1	2-E	0.92	0/5338	1.12	6/7399 (0.1%)
1	2-K	0.93	0/5338	1.12	6/7399 (0.1%)
1	2-Q	0.93	0/5338	1.12	6/7399 (0.1%)
1	2-W	0.93	0/5338	1.12	6/7399 (0.1%)
1	3-A	0.94	0/3195	1.16	6/4421 (0.1%)
1	3-B	0.94	0/3195	1.16	6/4421 (0.1%)
1	3-E	0.92	0/5338	1.12	6/7399 (0.1%)
1	3-K	0.93	0/5338	1.12	6/7399 (0.1%)
1	3-Q	0.93	0/5338	1.12	6/7399 (0.1%)
1	3-W	0.93	0/5338	1.12	6/7399 (0.1%)
1	4-A	0.94	0/3195	1.16	6/4421 (0.1%)
1	4-B	0.94	0/3195	1.16	6/4421 (0.1%)
1	4-E	0.92	0/5338	1.12	6/7399 (0.1%)
1	4-K	0.93	0/5338	1.12	6/7399 (0.1%)
1	4-Q	0.93	0/5338	1.12	6/7399 (0.1%)
1	4-W	0.93	0/5338	1.12	6/7399 (0.1%)
1	5-A	0.94	0/3195	1.16	6/4421 (0.1%)
1	5-B	0.94	0/3195	1.16	6/4421 (0.1%)
1	5-E	0.92	0/5338	1.12	6/7399 (0.1%)
1	5-K	0.93	0/5338	1.12	6/7399 (0.1%)
1	5-Q	0.93	0/5338	1.12	6/7399 (0.1%)
1	5-W	0.93	0/5338	1.12	6/7399 (0.1%)
1	6-A	0.94	0/3195	1.16	6/4421 (0.1%)
1	6-B	0.94	0/3195	1.16	6/4421 (0.1%)
1	6-E	0.93	0/5338	1.12	6/7399 (0.1%)
1	6-K	0.93	0/5338	1.12	6/7399 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	6-Q	0.93	0/5338	1.12	6/7399 (0.1%)
1	6-W	0.93	0/5338	1.12	6/7399 (0.1%)
1	7-A	0.94	0/3195	1.16	6/4421 (0.1%)
1	7-B	0.94	0/3195	1.16	6/4421 (0.1%)
1	7-E	0.93	0/5338	1.12	6/7399 (0.1%)
1	7-K	0.93	0/5338	1.12	6/7399 (0.1%)
1	7-Q	0.93	0/5338	1.12	6/7399 (0.1%)
1	7-W	0.93	0/5338	1.12	6/7399 (0.1%)
1	8-A	0.94	0/3195	1.16	6/4421 (0.1%)
1	8-B	0.94	0/3195	1.16	6/4421 (0.1%)
1	8-E	0.93	0/5338	1.12	6/7399 (0.1%)
1	8-K	0.93	0/5338	1.12	6/7399 (0.1%)
1	8-Q	0.93	0/5338	1.12	6/7399 (0.1%)
1	8-W	0.93	0/5338	1.12	6/7399 (0.1%)
2	1-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	1-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	1-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	1-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	2-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	2-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	2-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	2-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	3-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	3-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	3-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	3-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	4-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	4-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	4-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	4-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	5-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	5-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	5-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	5-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	6-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	6-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	6-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	6-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	7-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	7-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	7-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	7-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	8-C	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	8-I	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	8-O	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
2	8-U	1.13	13/3143 (0.4%)	1.44	45/4369 (1.0%)
3	1-D	1.22	38/5066 (0.8%)	1.74	122/7020 (1.7%)
3	1-J	1.22	37/5066 (0.7%)	1.74	121/7020 (1.7%)
3	1-P	1.22	38/5066 (0.8%)	1.74	121/7020 (1.7%)
3	1-V	1.22	37/5066 (0.7%)	1.74	121/7020 (1.7%)
3	2-D	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	2-J	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	2-P	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	2-V	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	3-D	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	3-J	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	3-P	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	3-V	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	4-D	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	4-J	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	4-P	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	4-V	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	5-D	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	5-J	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	5-P	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	5-V	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	6-D	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	6-J	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	6-P	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	6-V	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	7-D	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	7-J	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	7-P	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	7-V	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	8-D	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	8-J	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	8-P	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
3	8-V	1.22	39/5066 (0.8%)	1.69	117/7020 (1.7%)
4	1-F	4.14	197/1655 (11.9%)	4.03	272/2302 (11.8%)
4	1-L	4.14	197/1655 (11.9%)	4.03	272/2302 (11.8%)
4	1-R	4.14	197/1655 (11.9%)	4.03	272/2302 (11.8%)
4	1-X	4.14	199/1655 (12.0%)	4.03	273/2302 (11.9%)
4	2-F	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	2-L	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	2-R	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	2-X	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
4	3-F	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	3-L	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	3-R	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	3-X	3.74	153/1655 (9.2%)	3.77	224/2302 (9.7%)
4	4-F	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	4-L	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	4-R	3.74	153/1655 (9.2%)	3.77	223/2302 (9.7%)
4	4-X	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	5-F	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	5-L	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	5-R	3.74	153/1655 (9.2%)	3.77	223/2302 (9.7%)
4	5-X	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	6-F	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	6-L	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	6-R	3.74	153/1655 (9.2%)	3.77	223/2302 (9.7%)
4	6-X	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	7-F	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	7-L	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	7-R	3.74	153/1655 (9.2%)	3.77	223/2302 (9.7%)
4	7-X	3.74	153/1655 (9.2%)	3.77	222/2302 (9.6%)
4	8-F	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	8-L	3.74	154/1655 (9.3%)	3.77	223/2302 (9.7%)
4	8-R	3.74	153/1655 (9.2%)	3.77	223/2302 (9.7%)
4	8-X	3.74	153/1655 (9.2%)	3.77	224/2302 (9.7%)
5	1-G	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	1-M	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	1-S	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	1-Y	3.95	85/852 (10.0%)	3.81	120/1190 (10.1%)
5	2-G	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	2-M	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	2-S	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	2-Y	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	3-G	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	3-M	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	3-S	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	3-Y	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	4-G	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	4-M	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	4-S	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	4-Y	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	5-G	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	5-M	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	5-S	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	5-Y	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	6-G	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	6-M	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	6-S	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	6-Y	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	7-G	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	7-M	3.95	84/852 (9.9%)	3.81	121/1190 (10.2%)
5	7-S	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	7-Y	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	8-G	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	8-M	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
5	8-S	3.95	85/852 (10.0%)	3.81	121/1190 (10.2%)
5	8-Y	3.95	83/852 (9.7%)	3.81	121/1190 (10.2%)
6	1-H	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	1-N	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	1-T	3.44	83/841 (9.9%)	3.09	109/1174 (9.3%)
6	1-Z	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	2-H	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	2-N	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	2-T	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	2-Z	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	3-H	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	3-N	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	3-T	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	3-Z	3.43	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	4-H	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	4-N	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	4-T	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	4-Z	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	5-H	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	5-N	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	5-T	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	5-Z	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	6-H	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	6-N	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	6-T	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	6-Z	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	7-H	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	7-N	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	7-T	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	7-Z	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	8-H	3.44	83/841 (9.9%)	3.10	110/1174 (9.4%)
6	8-N	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
6	8-T	3.44	83/841 (9.9%)	3.10	109/1174 (9.3%)
6	8-Z	3.43	83/841 (9.9%)	3.10	109/1174 (9.3%)
All	All	1.87	12085/591760 (2.0%)	2.01	20213/821264 (2.5%)

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 12085 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1-S	380	ILE	N-CA	38.58	2.23	1.46
5	1-M	380	ILE	N-CA	38.56	2.23	1.46
5	1-G	380	ILE	N-CA	38.55	2.23	1.46
5	2-M	380	ILE	N-CA	38.55	2.23	1.46
5	4-M	380	ILE	N-CA	38.55	2.23	1.46

The worst 5 of 20213 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	2-R	452	ARG	CA-C-N	-39.55	30.18	117.20
4	3-R	452	ARG	CA-C-N	-39.55	30.18	117.20
4	1-X	452	ARG	CA-C-N	-39.55	30.19	117.20
4	1-F	452	ARG	CA-C-N	-39.54	30.20	117.20
4	1-R	452	ARG	CA-C-N	-39.54	30.20	117.20

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	23	0
1	1-B	3214	0	1424	23	0
1	1-E	5366	0	2362	86	0
1	1-K	5366	0	2360	73	0
1	1-Q	5366	0	2357	167	0
1	1-W	5366	0	2364	56	0
1	2-A	3214	0	1424	21	0
1	2-B	3214	0	1424	22	0
1	2-E	5366	0	2363	75	0
1	2-K	5366	0	2359	148	0
1	2-Q	5366	0	2363	80	0
1	2-W	5366	0	2361	153	0
1	3-A	3214	0	1424	21	0
1	3-B	3214	0	1424	22	0
1	3-E	5366	0	2363	75	0
1	3-K	5366	0	2359	148	0
1	3-Q	5366	0	2363	80	0
1	3-W	5366	0	2361	153	0
1	4-A	3214	0	1424	21	0
1	4-B	3214	0	1424	22	0
1	4-E	5366	0	2363	75	0
1	4-K	5366	0	2359	148	0
1	4-Q	5366	0	2363	80	0
1	4-W	5366	0	2361	153	0
1	5-A	3214	0	1424	21	0
1	5-B	3214	0	1424	22	0
1	5-E	5366	0	2363	75	0
1	5-K	5366	0	2359	148	0
1	5-Q	5366	0	2363	80	0
1	5-W	5366	0	2361	153	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	6-A	3214	0	1424	21	0
1	6-B	3214	0	1424	22	0
1	6-E	5366	0	2363	85	0
1	6-K	5366	0	2359	130	0
1	6-Q	5366	0	2363	85	0
1	6-W	5366	0	2361	132	0
1	7-A	3214	0	1424	21	0
1	7-B	3214	0	1424	22	0
1	7-E	5366	0	2363	85	0
1	7-K	5366	0	2359	130	0
1	7-Q	5366	0	2363	85	0
1	7-W	5366	0	2361	132	0
1	8-A	3214	0	1424	21	0
1	8-B	3214	0	1424	22	0
1	8-E	5366	0	2363	85	0
1	8-K	5366	0	2359	130	0
1	8-Q	5366	0	2363	85	0
1	8-W	5366	0	2361	132	0
2	1-C	3152	0	1401	155	0
2	1-I	3152	0	1406	72	0
2	1-O	3152	0	1403	88	0
2	1-U	3152	0	1404	61	0
2	2-C	3152	0	1401	172	0
2	2-I	3152	0	1403	60	0
2	2-O	3152	0	1401	171	0
2	2-U	3152	0	1403	60	0
2	3-C	3152	0	1401	172	0
2	3-I	3152	0	1403	60	0
2	3-O	3152	0	1401	171	0
2	3-U	3152	0	1403	59	0
2	4-C	3152	0	1401	172	0
2	4-I	3152	0	1403	60	0
2	4-O	3152	0	1401	172	0
2	4-U	3152	0	1403	60	0
2	5-C	3152	0	1401	174	0
2	5-I	3152	0	1403	60	0
2	5-O	3152	0	1401	173	0
2	5-U	3152	0	1403	60	0
2	6-C	3152	0	1399	184	0
2	6-I	3152	0	1403	60	0
2	6-O	3152	0	1399	185	0
2	6-U	3152	0	1403	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	7-C	3152	0	1399	186	0
2	7-I	3152	0	1403	60	0
2	7-O	3152	0	1399	186	0
2	7-U	3152	0	1403	60	0
2	8-C	3152	0	1399	184	0
2	8-I	3152	0	1403	60	0
2	8-O	3152	0	1399	185	0
2	8-U	3152	0	1403	59	0
3	1-D	5094	0	2272	121	0
3	1-J	5094	0	2271	129	0
3	1-P	5094	0	2273	77	0
3	1-V	5094	0	2267	197	0
3	2-D	5094	0	2270	147	0
3	2-J	5094	0	2272	97	0
3	2-P	5094	0	2270	179	0
3	2-V	5094	0	2272	97	0
3	3-D	5094	0	2270	147	0
3	3-J	5094	0	2272	97	0
3	3-P	5094	0	2270	179	0
3	3-V	5094	0	2272	97	0
3	4-D	5094	0	2270	146	0
3	4-J	5094	0	2272	97	0
3	4-P	5094	0	2270	149	0
3	4-V	5094	0	2272	97	0
3	5-D	5094	0	2273	88	0
3	5-J	5094	0	2272	97	0
3	5-P	5094	0	2273	89	0
3	5-V	5094	0	2272	97	0
3	6-D	5094	0	2270	146	0
3	6-J	5094	0	2271	110	0
3	6-P	5094	0	2270	149	0
3	6-V	5094	0	2271	109	0
3	7-D	5094	0	2273	88	0
3	7-J	5094	0	2271	110	0
3	7-P	5094	0	2273	89	0
3	7-V	5094	0	2271	109	0
3	8-D	5094	0	2270	146	0
3	8-J	5094	0	2271	110	0
3	8-P	5094	0	2270	149	0
3	8-V	5094	0	2271	109	0
4	1-F	1658	0	715	168	0
4	1-L	1658	0	715	169	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	1-R	1658	0	714	169	0
4	1-X	1658	0	715	168	0
4	2-F	1658	0	715	154	0
4	2-L	1658	0	715	153	0
4	2-R	1658	0	715	152	0
4	2-X	1658	0	715	151	0
4	3-F	1658	0	715	154	0
4	3-L	1658	0	715	156	0
4	3-R	1658	0	715	152	0
4	3-X	1658	0	715	154	0
4	4-F	1658	0	715	150	0
4	4-L	1658	0	715	153	0
4	4-R	1658	0	715	152	0
4	4-X	1658	0	715	151	0
4	5-F	1658	0	715	150	0
4	5-L	1658	0	715	153	0
4	5-R	1658	0	715	152	0
4	5-X	1658	0	715	151	0
4	6-F	1658	0	715	150	0
4	6-L	1658	0	715	153	0
4	6-R	1658	0	715	152	0
4	6-X	1658	0	715	151	0
4	7-F	1658	0	715	150	0
4	7-L	1658	0	715	153	0
4	7-R	1658	0	715	152	0
4	7-X	1658	0	715	151	0
4	8-F	1658	0	715	150	0
4	8-L	1658	0	715	156	0
4	8-R	1658	0	715	152	0
4	8-X	1658	0	715	154	0
5	1-G	853	0	384	57	0
5	1-M	853	0	384	55	0
5	1-S	853	0	384	55	0
5	1-Y	853	0	384	57	0
5	2-G	853	0	384	56	0
5	2-M	853	0	384	55	0
5	2-S	853	0	384	56	0
5	2-Y	853	0	384	55	0
5	3-G	853	0	384	56	0
5	3-M	853	0	384	56	0
5	3-S	853	0	384	56	0
5	3-Y	853	0	384	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	4-G	853	0	384	54	0
5	4-M	853	0	384	55	0
5	4-S	853	0	384	57	0
5	4-Y	853	0	384	55	0
5	5-G	853	0	384	54	0
5	5-M	853	0	384	55	0
5	5-S	853	0	384	57	0
5	5-Y	853	0	384	55	0
5	6-G	853	0	384	54	0
5	6-M	853	0	384	55	0
5	6-S	853	0	384	57	0
5	6-Y	853	0	384	55	0
5	7-G	853	0	384	54	0
5	7-M	853	0	384	55	0
5	7-S	853	0	384	57	0
5	7-Y	853	0	384	55	0
5	8-G	853	0	384	54	0
5	8-M	853	0	384	56	0
5	8-S	853	0	384	57	0
5	8-Y	853	0	384	54	0
6	1-H	842	0	365	36	0
6	1-N	842	0	365	39	0
6	1-T	842	0	365	38	0
6	1-Z	842	0	365	38	0
6	2-H	842	0	365	39	0
6	2-N	842	0	365	35	0
6	2-T	842	0	365	68	0
6	2-Z	842	0	365	35	0
6	3-H	842	0	365	39	0
6	3-N	842	0	365	38	0
6	3-T	842	0	365	68	0
6	3-Z	842	0	365	39	0
6	4-H	842	0	365	39	0
6	4-N	842	0	365	35	0
6	4-T	842	0	365	40	0
6	4-Z	842	0	365	35	0
6	5-H	842	0	365	39	0
6	5-N	842	0	365	35	0
6	5-T	842	0	365	40	0
6	5-Z	842	0	365	35	0
6	6-H	842	0	365	39	0
6	6-N	842	0	365	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	6-T	842	0	365	40	0
6	6-Z	842	0	365	35	0
6	7-H	842	0	365	39	0
6	7-N	842	0	365	35	0
6	7-T	842	0	365	40	0
6	7-Z	842	0	365	35	0
6	8-H	842	0	365	39	0
6	8-N	842	0	365	38	0
6	8-T	842	0	365	40	0
6	8-Z	842	0	365	39	0
All	All	594304	0	262731	15656	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 18.

The worst 5 of 15656 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
6:H:490:GLN:CA	6:H:490:GLN:CB	1.75	1.65

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%)	7 38
1	1-B	612/1391 (44%)	562 (92%)	38 (6%)	12 (2%)	7 38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-E	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	7	36
1	1-K	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	7	36
1	1-Q	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	7	36
1	1-W	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	7	36
1	2-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	2-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	2-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	2-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	2-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	7	38
1	2-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	3-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	3-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	3-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	3-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	3-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	7	38
1	3-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	4-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	4-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	4-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	4-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	4-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	7	38
1	4-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	5-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	5-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	5-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	5-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	5-Q	1027/1391 (74%)	950 (92%)	56 (6%)	21 (2%)	7	38
1	5-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	6-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	6-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	6-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	6-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	6-Q	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	6-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	7-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	7-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	7-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	7-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	7-Q	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	7-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	8-A	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	8-B	612/1391 (44%)	564 (92%)	37 (6%)	11 (2%)	8	40
1	8-E	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	8-K	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	8-Q	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
1	8-W	1027/1391 (74%)	949 (92%)	57 (6%)	21 (2%)	7	38
2	1-C	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	14
2	1-I	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	14
2	1-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	14
2	1-U	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	14
2	2-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	14
2	2-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	14
2	2-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	14
2	2-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	14
2	3-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	14
2	3-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	14
2	3-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	14
2	3-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	14
2	4-C	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	14
2	4-I	618/819 (76%)	515 (83%)	59 (10%)	44 (7%)	1	14
2	4-O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	14
2	4-U	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	14

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	4-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	5-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	5-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	5-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	5-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	6-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	6-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	6-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	6-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	7-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	7-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	7-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	7-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	8-D	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	8-J	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	8-P	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
3	8-V	972/2012 (48%)	911 (94%)	46 (5%)	15 (2%)	10	46
4	1-F	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	15
4	1-L	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	15
4	1-R	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	15
4	1-X	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	15
4	2-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	2-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	2-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	2-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	3-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	3-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	3-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	3-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	4-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	4-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	4-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	5-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	5-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	5-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	5-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	6-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	6-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	6-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	6-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	7-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	7-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	7-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	7-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	8-F	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	8-L	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	8-R	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
4	8-X	329/507 (65%)	295 (90%)	16 (5%)	18 (6%)	2	19
5	1-G	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	1-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	1-S	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	1-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	2-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	2-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	2-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	2-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	3-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	3-M	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	3-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	3-Y	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	4-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	4-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	4-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	4-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	5-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	5-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	5-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	5-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	6-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	6-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	6-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	6-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	7-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	7-M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	7-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	7-Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	8-G	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	4	28
5	8-M	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	8-S	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
5	8-Y	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	3	25
6	1-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	1-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	1-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	1-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	2-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	2-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	2-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	2-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	3-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	3-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	3-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	3-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	4-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	4-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	4-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	4-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	5-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	5-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	5-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	5-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	6-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	6-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	6-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	6-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	7-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	7-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	7-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	7-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	8-H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	8-N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	8-T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
6	8-Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	3	22
All	All	114816/209456 (55%)	104157 (91%)	6943 (6%)	3716 (3%)	7	26

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

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

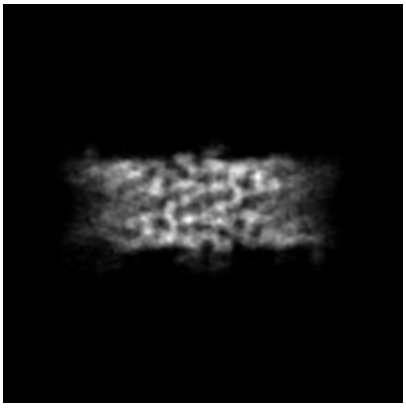
6 Map visualisation (i)

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.

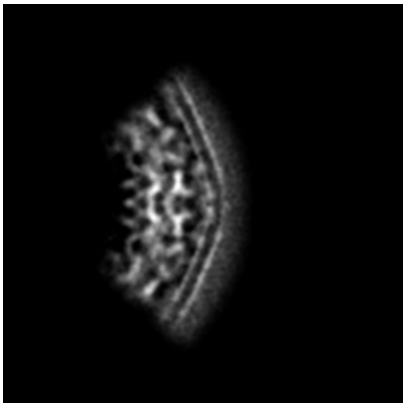
6.1 Orthogonal projections (i)

6.1.1 Primary map



X

Y



Z

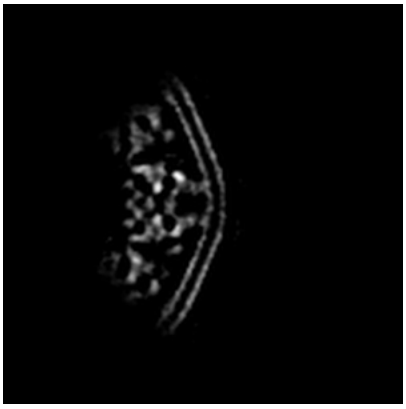
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map

X Index: 72

Y Index: 72

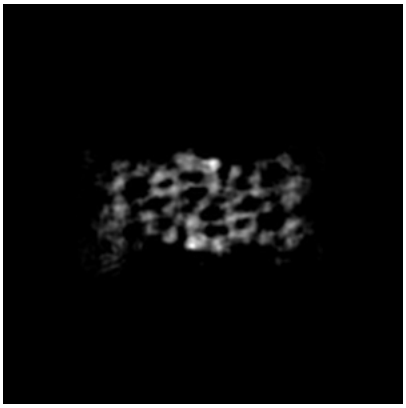


Z Index: 72

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

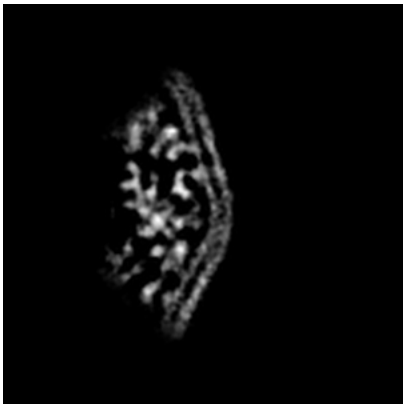
6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 53

Y Index: 76



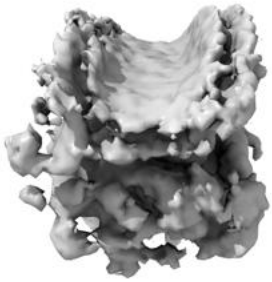
Z Index: 78

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X



Y

Z

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.

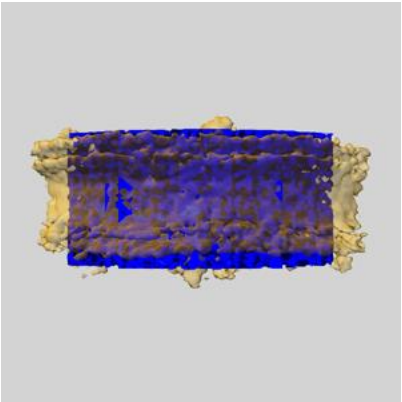
6.5 Mask visualisation (i)

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

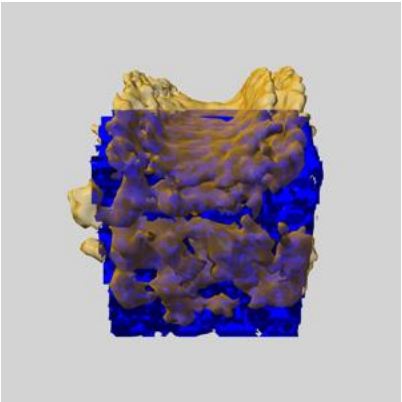
A mask typically either:

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

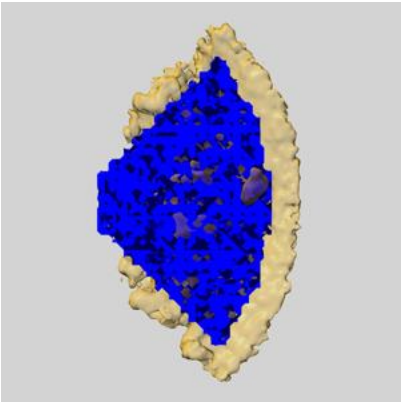
6.5.1 emd_8085_msk_1.map (i)



X



Y

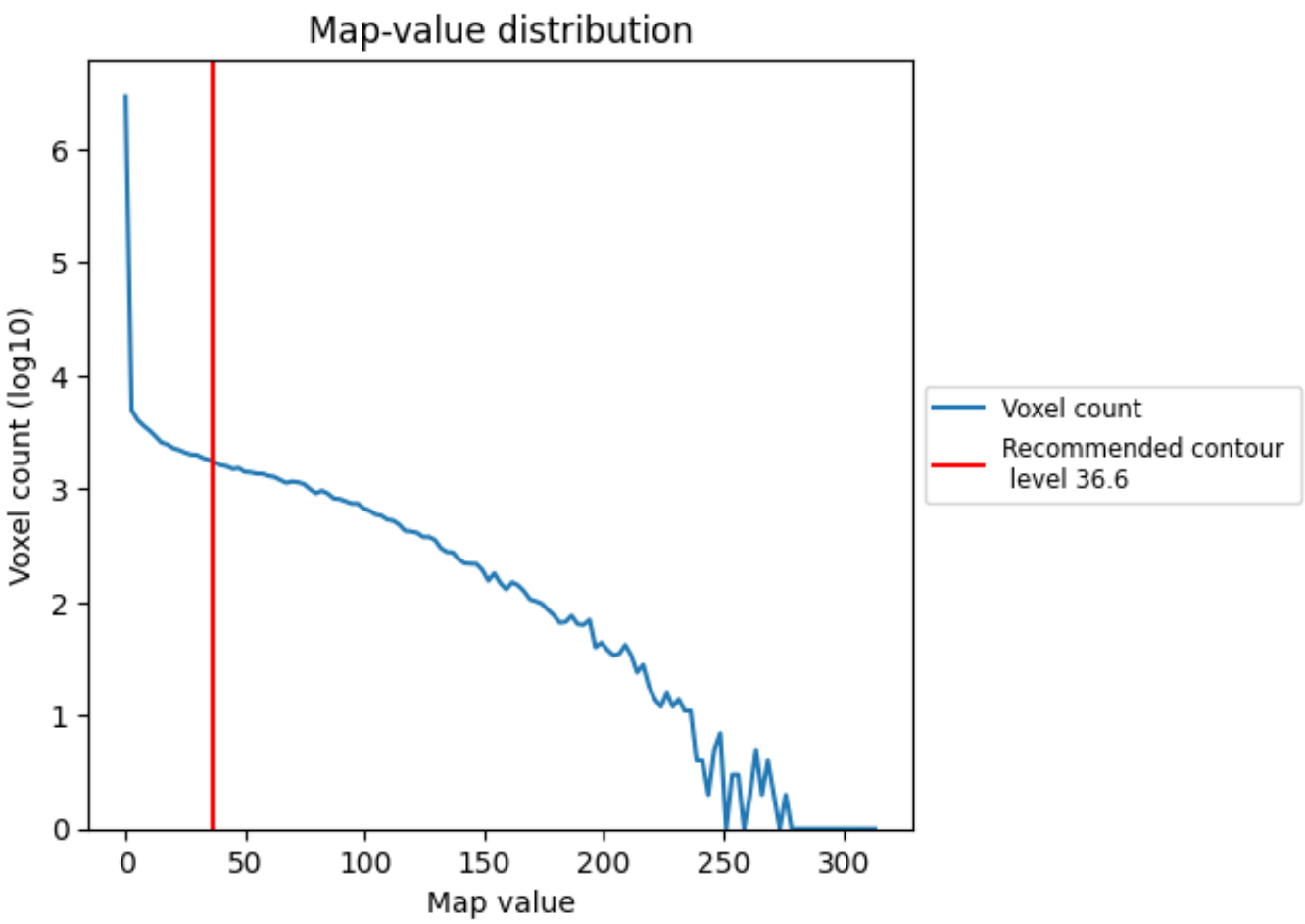


Z

7 Map analysis (i)

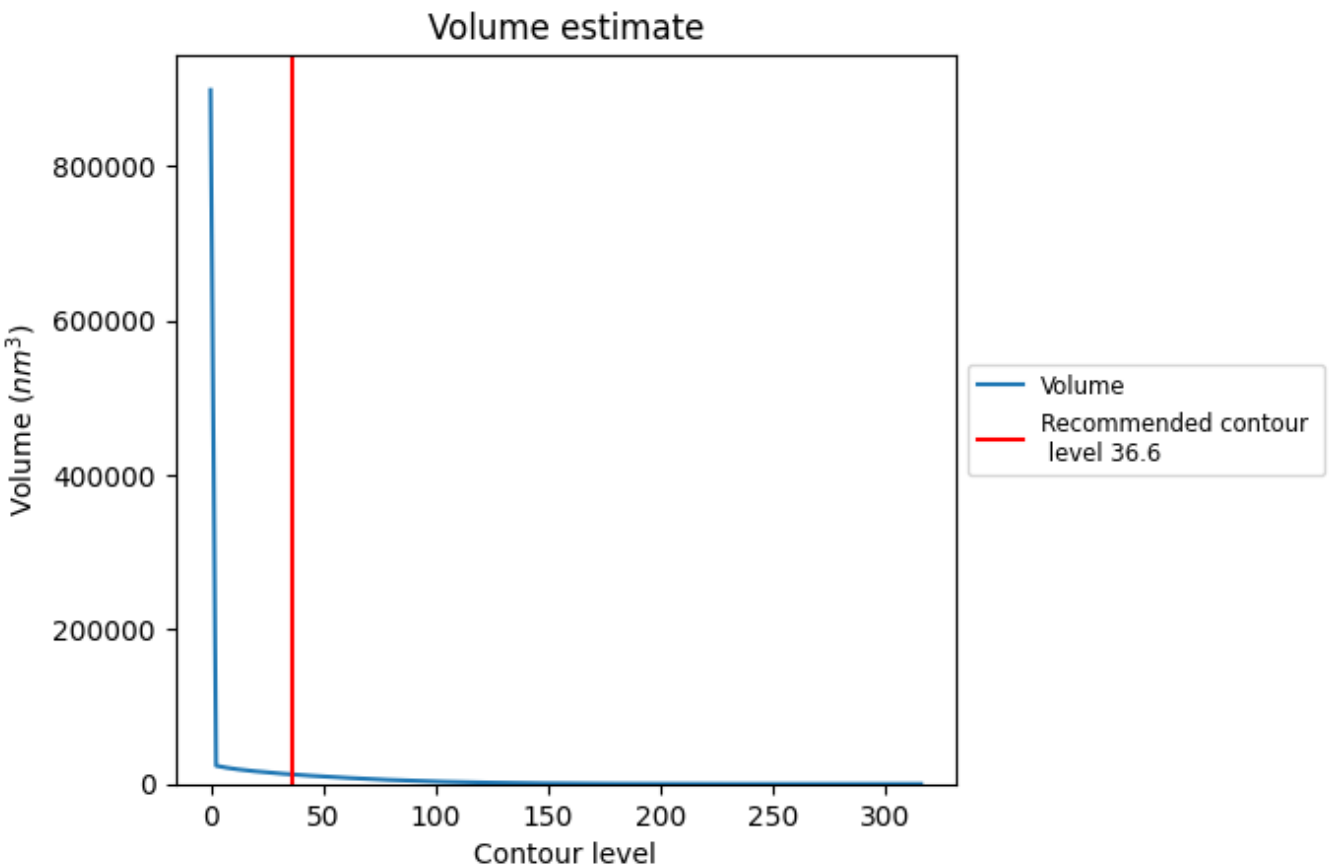
This section contains the results of statistical analysis of the map.

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.

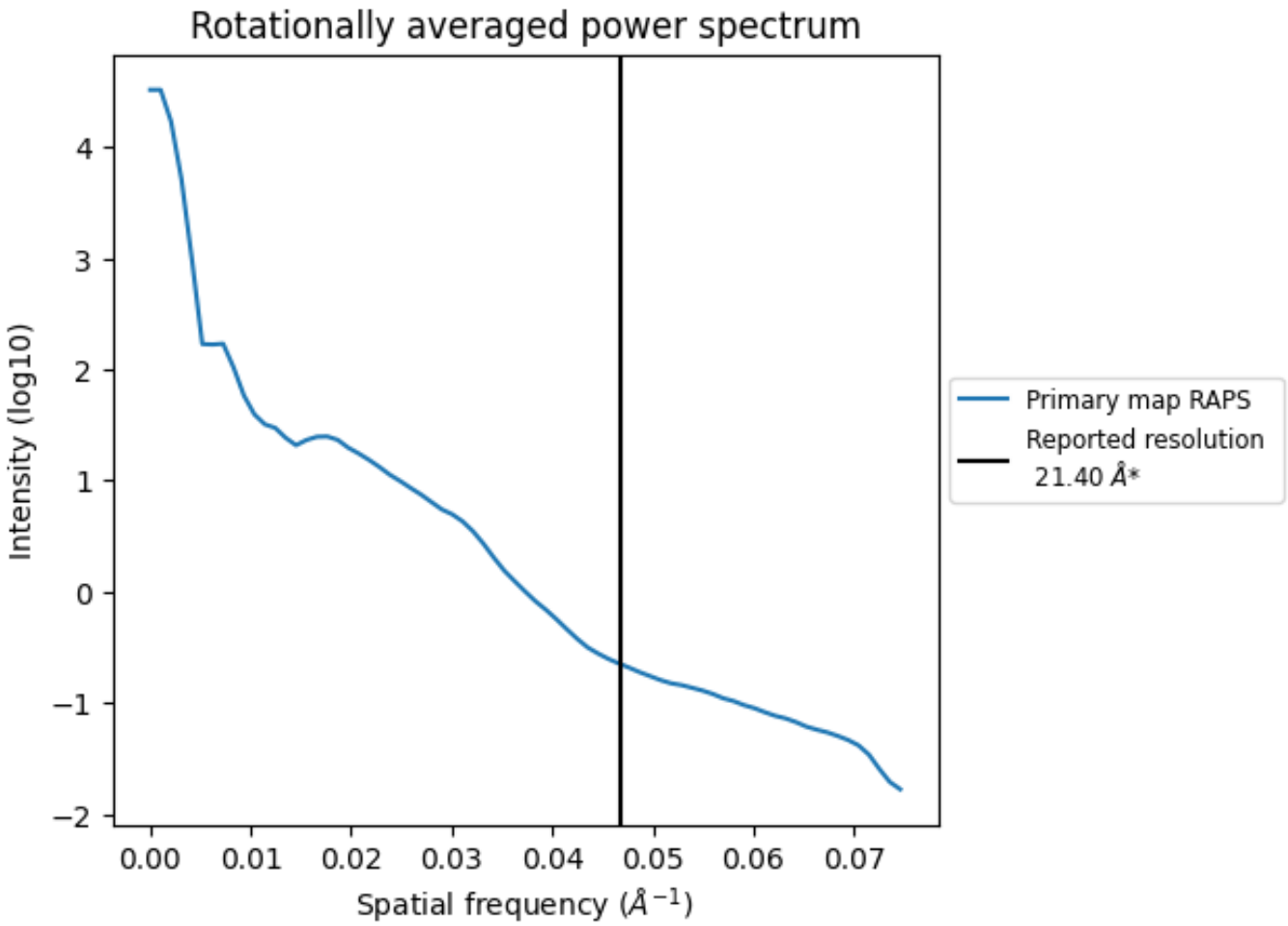
7.2 Volume estimate (i)



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}

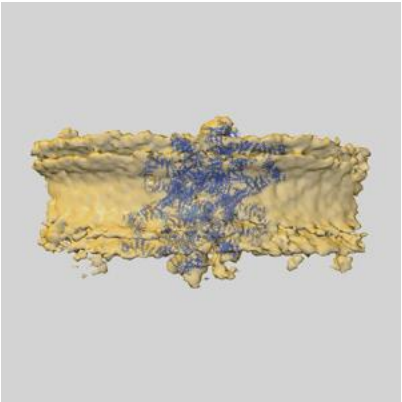
8 Fourier-Shell correlation (i)

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

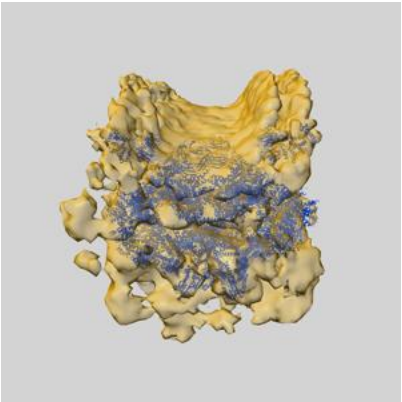
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8085 and PDB model 5IJN. Per-residue inclusion information can be found in section 3 on page 22.

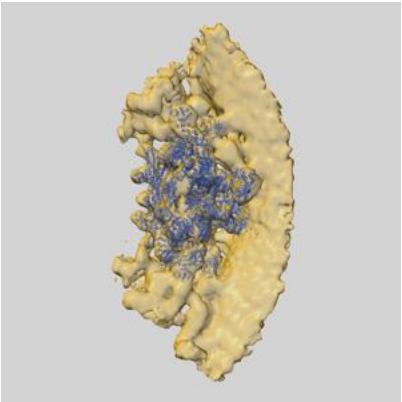
9.1 Map-model overlay (i)



X



Y



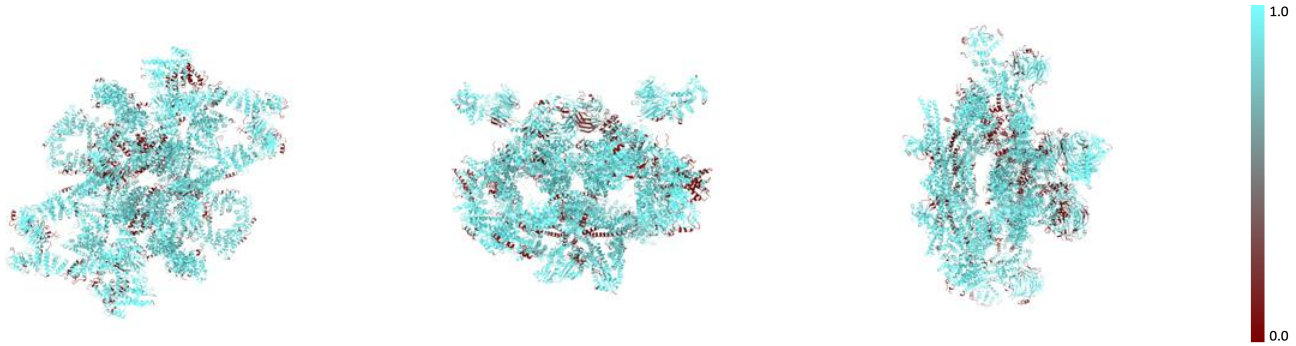
Z

The images above show the 3D surface view of the map at the recommended contour level 36.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)

This section was not generated.

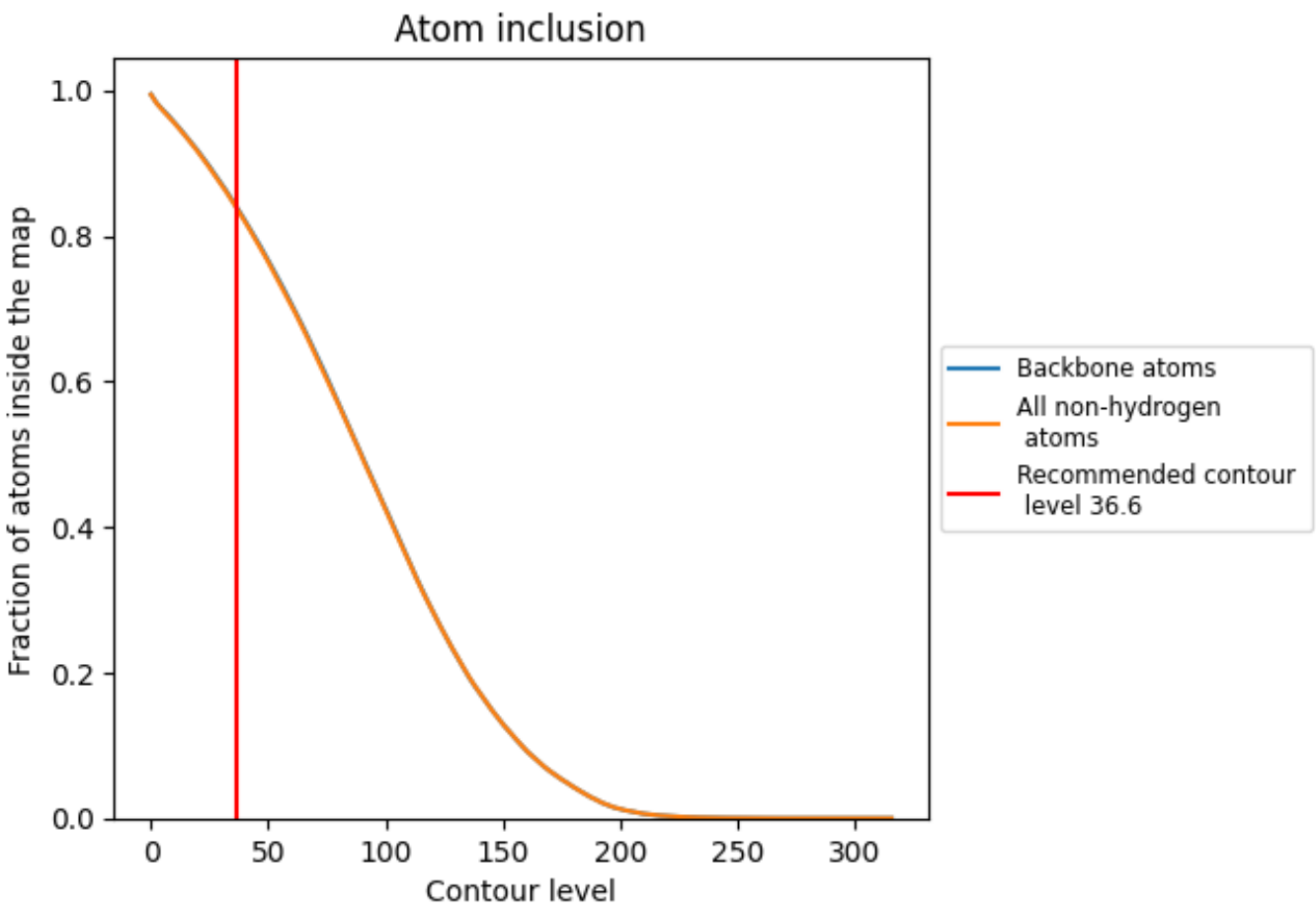
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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

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
All	0.8379
A	0.9291
B	0.8787
C	0.8493
D	0.8983
E	0.8658
F	0.8100
G	0.9039
H	0.7993
I	0.8271
J	0.8801
K	0.5460
L	0.7986
M	0.8453
N	0.8729
O	0.8782
P	0.8971
Q	0.8813
R	0.7762
S	0.9332
T	0.7482
U	0.8004
V	0.9066
W	0.7753
X	0.8372
Y	0.9004
Z	0.8492