wwPDB EM Validation Summary Report

Jun 11, 2024 – 08:02 PM JST

PDB ID	:	7VOP
EMDB ID	:	EMD-32056
Title	:	Cryo-EM structure of Xenopus laevis nuclear pore complex cytoplasmic ring subunit
Authors	:	Tai, L.; Zhu, Y.; Sun, F.
Deposited on	:	2021-10-14
Resolution	:	8.70 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

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

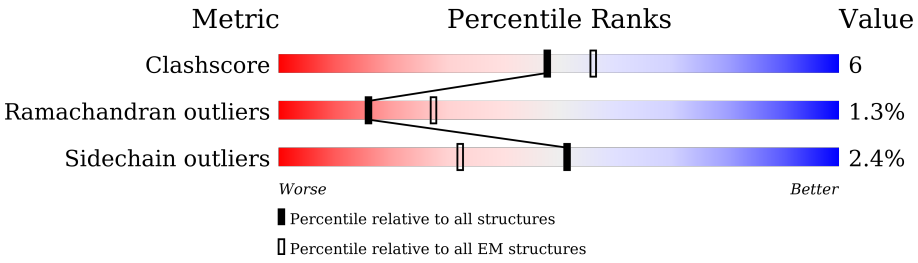
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 8.70 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	653	10% 83% 17% ·
1	J	653	19% 79% 19% ·
2	B	375	21% 72% 27% ·
2	K	375	29% 73% 25% ·
3	C	360	6% 74% 18% · 8%
3	L	360	11% 75% 14% · 10%
4	D	1414	28% 80% 18% ··
4	M	1414	53% 79% 19% ··

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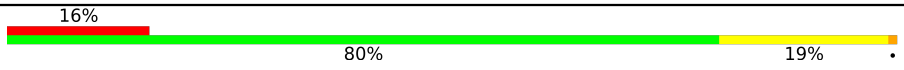
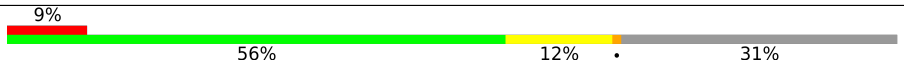
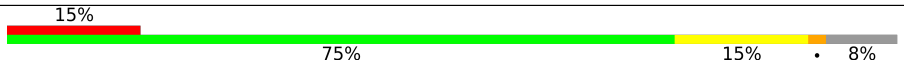
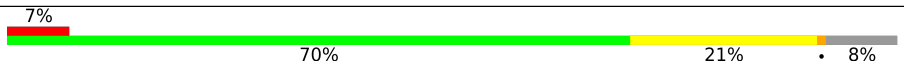
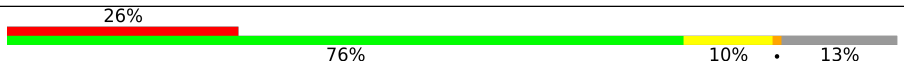
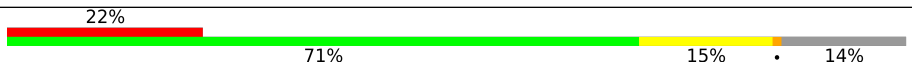
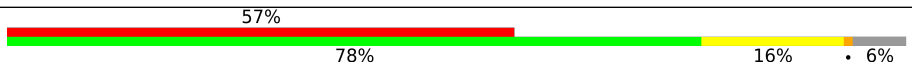
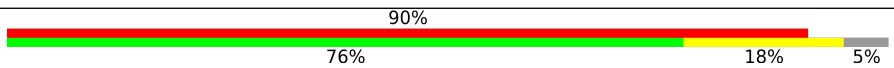
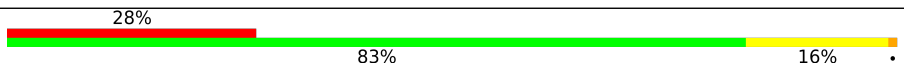
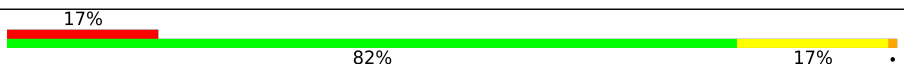
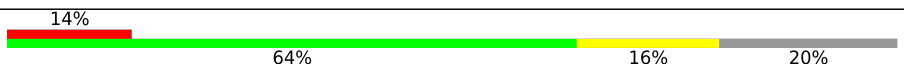
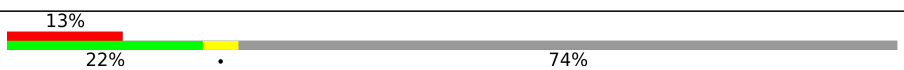
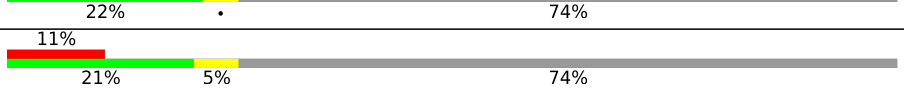
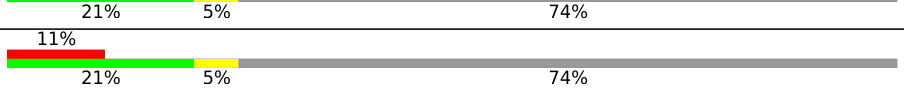
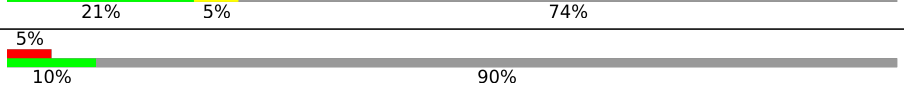
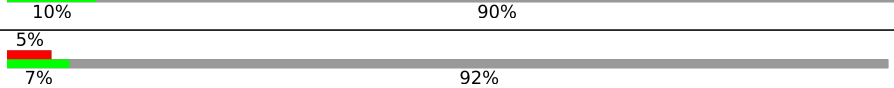
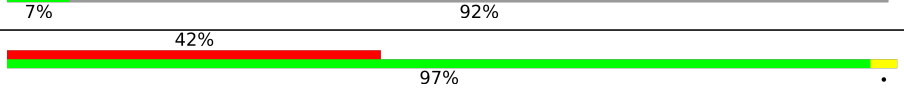
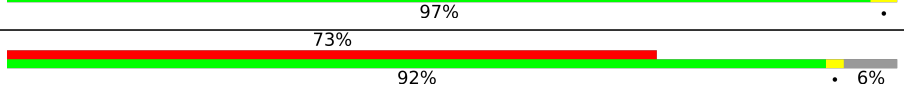
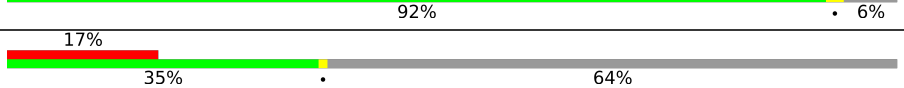
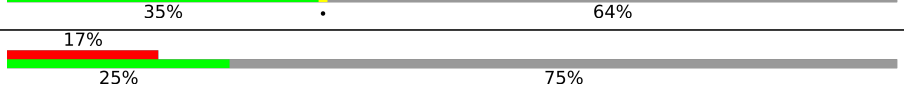
Mol	Chain	Length	Quality of chain
5	E	326	
5	N	326	
6	F	924	
6	O	924	
7	G	320	
7	P	320	
8	H	916	
8	Q	916	
9	I	1140	
9	R	1140	
10	S	2011	
10	T	2011	
11	U	820	
12	V	2931	
12	W	2931	
12	X	2931	
12	Y	2931	
12	Z	2931	
13	a	2037	
13	e	2037	
14	b	728	
14	d	728	
15	c	547	
15	f	547	

2 Entry composition (i)

There are 15 unique types of molecules in this entry. The entry contains 178773 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 Nup85.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	653	Total	C	N	O	S	0	0
			5268	3341	904	984	39		
1	J	653	Total	C	N	O	S	0	0
			5268	3341	904	984	39		

- Molecule 2 is a protein called MGC154553 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	375	Total	C	N	O	S	0	0
			2927	1813	524	571	19		
2	K	375	Total	C	N	O	S	0	0
			2927	1813	524	571	19		

- Molecule 3 is a protein called Nucleoporin SEH1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	333	Total	C	N	O	S	0	0
			2607	1632	466	491	18		
3	L	325	Total	C	N	O	S	0	0
			2546	1592	455	482	17		

- Molecule 4 is a protein called Nucleoporin 160kDa.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1394	Total	C	N	O	S	0	0
			11118	7052	1912	2086	68		
4	M	1394	Total	C	N	O	S	0	0
			11118	7052	1912	2086	68		

- Molecule 5 is a protein called MGC83926 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	326	Total	C	N	O	S	0	0
			2573	1640	443	473	17		
5	N	326	Total	C	N	O	S	0	0
			2573	1640	443	473	17		

- Molecule 6 is a protein called Nuclear pore complex protein Nup96.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	638	Total	C	N	O	S	0	0
			5177	3287	912	949	29		
6	O	637	Total	C	N	O	S	0	0
			5168	3282	911	946	29		

- Molecule 7 is a protein called GATOR complex protein SEC13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	294	Total	C	N	O	S	0	0
			2300	1454	394	440	12		
7	P	294	Total	C	N	O	S	0	0
			2300	1454	394	440	12		

- Molecule 8 is a protein called Nuclear pore complex protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	798	Total	C	N	O	S	0	0
			6494	4126	1096	1240	32		
8	Q	790	Total	C	N	O	S	0	0
			6430	4085	1087	1226	32		

- Molecule 9 is a protein called outer Nup133.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	1076	Total	C	N	O	S	0	0
			8482	5362	1409	1661	50		
9	R	1082	Total	C	N	O	S	0	0
			8536	5397	1420	1669	50		

- Molecule 10 is a protein called MGC83295 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	S	2011	Total	C	N	O	S	0	0
			15974	10112	2785	2978	99		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	T	2011	Total	C	N	O	S	0	0
			15974	10112	2785	2978	99		

- Molecule 11 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	U	654	Total	C	N	O	S	0	0
			5260	3328	918	986	28		

- Molecule 12 is a protein called Nup358.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	V	772	Total	C	N	O	S	0	0
			6225	3966	1061	1166	32		
12	W	756	Total	C	N	O	S	0	0
			6100	3890	1040	1139	31		
12	X	767	Total	C	N	O	S	0	0
			6190	3944	1056	1158	32		
12	Y	761	Total	C	N	O	S	0	0
			6139	3912	1047	1149	31		
12	Z	758	Total	C	N	O	S	0	0
			6116	3898	1042	1145	31		

There are 130 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	2480	GLY	-	insertion	UNP A0A1L8HGL2
V	2481	PHE	-	insertion	UNP A0A1L8HGL2
V	2482	ASN	-	insertion	UNP A0A1L8HGL2
V	2483	PHE	-	insertion	UNP A0A1L8HGL2
V	2484	SER	-	insertion	UNP A0A1L8HGL2
V	2485	LEU	-	insertion	UNP A0A1L8HGL2
V	2486	PHE	-	insertion	UNP A0A1L8HGL2
V	2487	LYS	-	insertion	UNP A0A1L8HGL2
V	2488	SER	-	insertion	UNP A0A1L8HGL2
V	2489	ASN	-	insertion	UNP A0A1L8HGL2
V	2490	PRO	-	insertion	UNP A0A1L8HGL2
V	2491	ARG	-	insertion	UNP A0A1L8HGL2
V	2492	ALA	-	insertion	UNP A0A1L8HGL2
V	2493	PHE	-	insertion	UNP A0A1L8HGL2
V	2494	TRP	-	insertion	UNP A0A1L8HGL2
V	2495	THR	-	insertion	UNP A0A1L8HGL2

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Chain	Residue	Modelled	Actual	Comment	Reference
V	2496	CYS	-	insertion	UNP A0A1L8HGL2
V	2497	THR	-	insertion	UNP A0A1L8HGL2
V	2498	SER	-	insertion	UNP A0A1L8HGL2
V	2499	SER	-	insertion	UNP A0A1L8HGL2
V	2500	SER	-	insertion	UNP A0A1L8HGL2
V	2501	LYS	-	insertion	UNP A0A1L8HGL2
V	2502	PRO	-	insertion	UNP A0A1L8HGL2
V	2503	GLU	-	insertion	UNP A0A1L8HGL2
V	2504	VAL	-	insertion	UNP A0A1L8HGL2
V	2505	GLU	-	insertion	UNP A0A1L8HGL2
W	2480	GLY	-	insertion	UNP A0A1L8HGL2
W	2481	PHE	-	insertion	UNP A0A1L8HGL2
W	2482	ASN	-	insertion	UNP A0A1L8HGL2
W	2483	PHE	-	insertion	UNP A0A1L8HGL2
W	2484	SER	-	insertion	UNP A0A1L8HGL2
W	2485	LEU	-	insertion	UNP A0A1L8HGL2
W	2486	PHE	-	insertion	UNP A0A1L8HGL2
W	2487	LYS	-	insertion	UNP A0A1L8HGL2
W	2488	SER	-	insertion	UNP A0A1L8HGL2
W	2489	ASN	-	insertion	UNP A0A1L8HGL2
W	2490	PRO	-	insertion	UNP A0A1L8HGL2
W	2491	ARG	-	insertion	UNP A0A1L8HGL2
W	2492	ALA	-	insertion	UNP A0A1L8HGL2
W	2493	PHE	-	insertion	UNP A0A1L8HGL2
W	2494	TRP	-	insertion	UNP A0A1L8HGL2
W	2495	THR	-	insertion	UNP A0A1L8HGL2
W	2496	CYS	-	insertion	UNP A0A1L8HGL2
W	2497	THR	-	insertion	UNP A0A1L8HGL2
W	2498	SER	-	insertion	UNP A0A1L8HGL2
W	2499	SER	-	insertion	UNP A0A1L8HGL2
W	2500	SER	-	insertion	UNP A0A1L8HGL2
W	2501	LYS	-	insertion	UNP A0A1L8HGL2
W	2502	PRO	-	insertion	UNP A0A1L8HGL2
W	2503	GLU	-	insertion	UNP A0A1L8HGL2
W	2504	VAL	-	insertion	UNP A0A1L8HGL2
W	2505	GLU	-	insertion	UNP A0A1L8HGL2
X	2480	GLY	-	insertion	UNP A0A1L8HGL2
X	2481	PHE	-	insertion	UNP A0A1L8HGL2
X	2482	ASN	-	insertion	UNP A0A1L8HGL2
X	2483	PHE	-	insertion	UNP A0A1L8HGL2
X	2484	SER	-	insertion	UNP A0A1L8HGL2
X	2485	LEU	-	insertion	UNP A0A1L8HGL2

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Chain	Residue	Modelled	Actual	Comment	Reference
X	2486	PHE	-	insertion	UNP A0A1L8HGL2
X	2487	LYS	-	insertion	UNP A0A1L8HGL2
X	2488	SER	-	insertion	UNP A0A1L8HGL2
X	2489	ASN	-	insertion	UNP A0A1L8HGL2
X	2490	PRO	-	insertion	UNP A0A1L8HGL2
X	2491	ARG	-	insertion	UNP A0A1L8HGL2
X	2492	ALA	-	insertion	UNP A0A1L8HGL2
X	2493	PHE	-	insertion	UNP A0A1L8HGL2
X	2494	TRP	-	insertion	UNP A0A1L8HGL2
X	2495	THR	-	insertion	UNP A0A1L8HGL2
X	2496	CYS	-	insertion	UNP A0A1L8HGL2
X	2497	THR	-	insertion	UNP A0A1L8HGL2
X	2498	SER	-	insertion	UNP A0A1L8HGL2
X	2499	SER	-	insertion	UNP A0A1L8HGL2
X	2500	SER	-	insertion	UNP A0A1L8HGL2
X	2501	LYS	-	insertion	UNP A0A1L8HGL2
X	2502	PRO	-	insertion	UNP A0A1L8HGL2
X	2503	GLU	-	insertion	UNP A0A1L8HGL2
X	2504	VAL	-	insertion	UNP A0A1L8HGL2
X	2505	GLU	-	insertion	UNP A0A1L8HGL2
Y	2480	GLY	-	insertion	UNP A0A1L8HGL2
Y	2481	PHE	-	insertion	UNP A0A1L8HGL2
Y	2482	ASN	-	insertion	UNP A0A1L8HGL2
Y	2483	PHE	-	insertion	UNP A0A1L8HGL2
Y	2484	SER	-	insertion	UNP A0A1L8HGL2
Y	2485	LEU	-	insertion	UNP A0A1L8HGL2
Y	2486	PHE	-	insertion	UNP A0A1L8HGL2
Y	2487	LYS	-	insertion	UNP A0A1L8HGL2
Y	2488	SER	-	insertion	UNP A0A1L8HGL2
Y	2489	ASN	-	insertion	UNP A0A1L8HGL2
Y	2490	PRO	-	insertion	UNP A0A1L8HGL2
Y	2491	ARG	-	insertion	UNP A0A1L8HGL2
Y	2492	ALA	-	insertion	UNP A0A1L8HGL2
Y	2493	PHE	-	insertion	UNP A0A1L8HGL2
Y	2494	TRP	-	insertion	UNP A0A1L8HGL2
Y	2495	THR	-	insertion	UNP A0A1L8HGL2
Y	2496	CYS	-	insertion	UNP A0A1L8HGL2
Y	2497	THR	-	insertion	UNP A0A1L8HGL2
Y	2498	SER	-	insertion	UNP A0A1L8HGL2
Y	2499	SER	-	insertion	UNP A0A1L8HGL2
Y	2500	SER	-	insertion	UNP A0A1L8HGL2
Y	2501	LYS	-	insertion	UNP A0A1L8HGL2

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	2502	PRO	-	insertion	UNP A0A1L8HGL2
Y	2503	GLU	-	insertion	UNP A0A1L8HGL2
Y	2504	VAL	-	insertion	UNP A0A1L8HGL2
Y	2505	GLU	-	insertion	UNP A0A1L8HGL2
Z	2480	GLY	-	insertion	UNP A0A1L8HGL2
Z	2481	PHE	-	insertion	UNP A0A1L8HGL2
Z	2482	ASN	-	insertion	UNP A0A1L8HGL2
Z	2483	PHE	-	insertion	UNP A0A1L8HGL2
Z	2484	SER	-	insertion	UNP A0A1L8HGL2
Z	2485	LEU	-	insertion	UNP A0A1L8HGL2
Z	2486	PHE	-	insertion	UNP A0A1L8HGL2
Z	2487	LYS	-	insertion	UNP A0A1L8HGL2
Z	2488	SER	-	insertion	UNP A0A1L8HGL2
Z	2489	ASN	-	insertion	UNP A0A1L8HGL2
Z	2490	PRO	-	insertion	UNP A0A1L8HGL2
Z	2491	ARG	-	insertion	UNP A0A1L8HGL2
Z	2492	ALA	-	insertion	UNP A0A1L8HGL2
Z	2493	PHE	-	insertion	UNP A0A1L8HGL2
Z	2494	TRP	-	insertion	UNP A0A1L8HGL2
Z	2495	THR	-	insertion	UNP A0A1L8HGL2
Z	2496	CYS	-	insertion	UNP A0A1L8HGL2
Z	2497	THR	-	insertion	UNP A0A1L8HGL2
Z	2498	SER	-	insertion	UNP A0A1L8HGL2
Z	2499	SER	-	insertion	UNP A0A1L8HGL2
Z	2500	SER	-	insertion	UNP A0A1L8HGL2
Z	2501	LYS	-	insertion	UNP A0A1L8HGL2
Z	2502	PRO	-	insertion	UNP A0A1L8HGL2
Z	2503	GLU	-	insertion	UNP A0A1L8HGL2
Z	2504	VAL	-	insertion	UNP A0A1L8HGL2
Z	2505	GLU	-	insertion	UNP A0A1L8HGL2

- Molecule 13 is a protein called Nucleoporin CAN.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	a	209	Total	C	N	O	S	0	0
			1738	1086	308	341	3		
13	e	155	Total	C	N	O	S	0	0
			1282	797	224	258	3		

- Molecule 14 is a protein called Nup88A protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	b	728	Total	C	N	O	S	0	0
			5787	3645	991	1119	32		
14	d	683	Total	C	N	O	S	0	0
			5414	3413	919	1051	31		

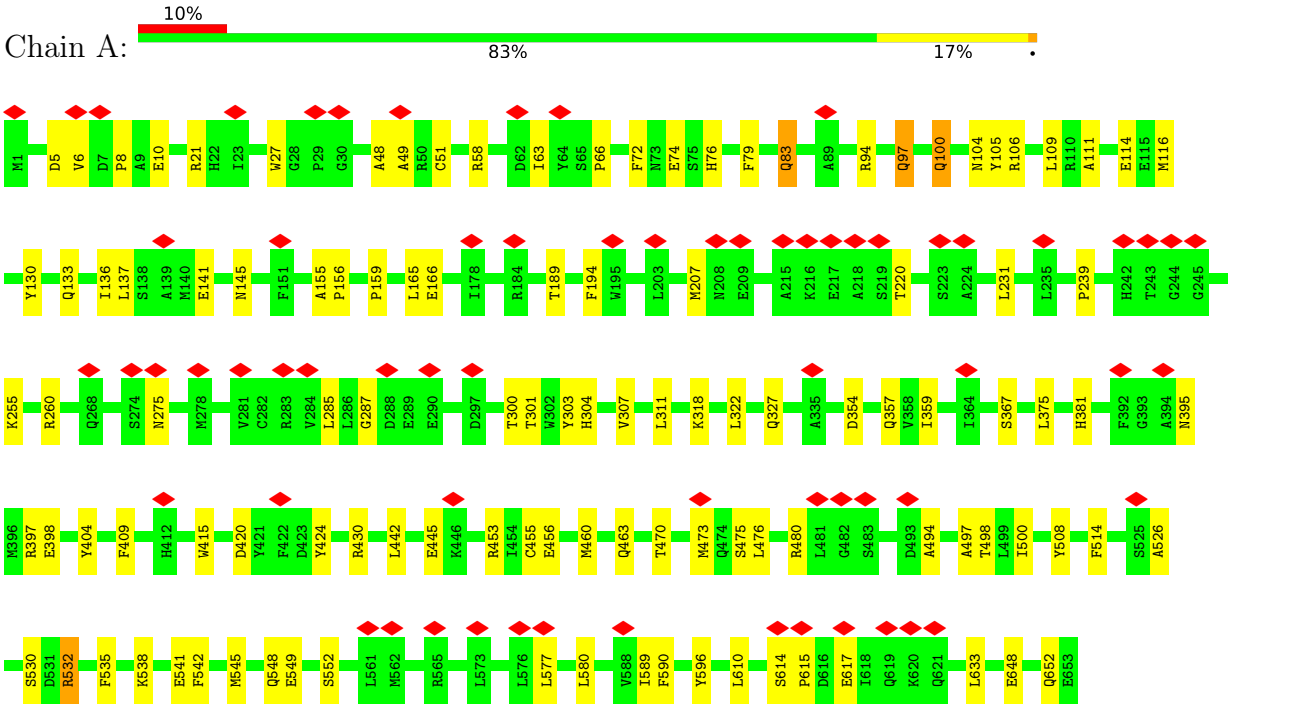
- Molecule 15 is a protein called IL4I1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	c	198	Total	C	N	O	S	0	0
			1621	1001	286	327	7		
15	f	138	Total	C	N	O	S	0	0
			1141	708	197	232	4		

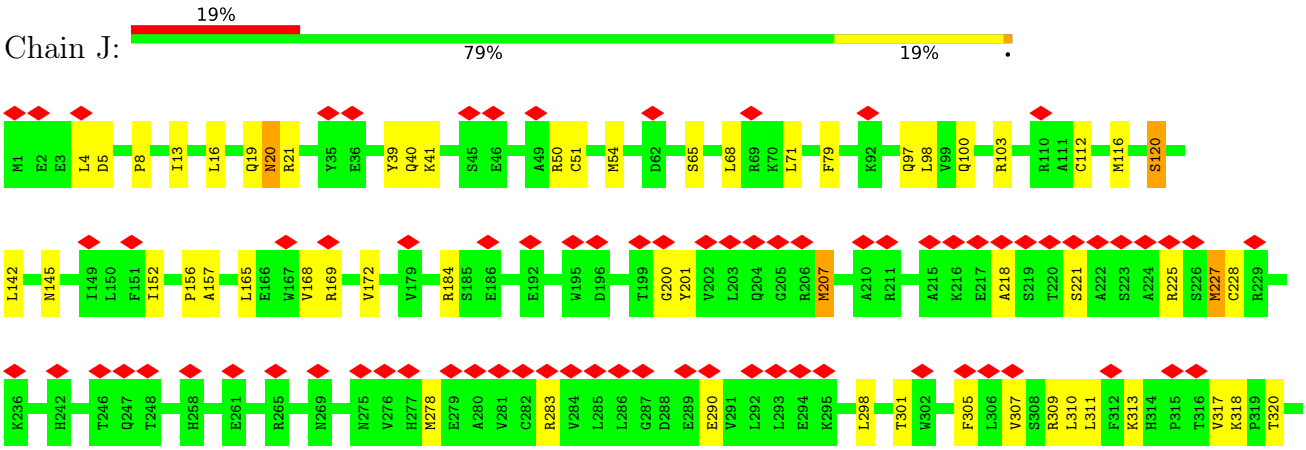
3 Residue-property plots (i)

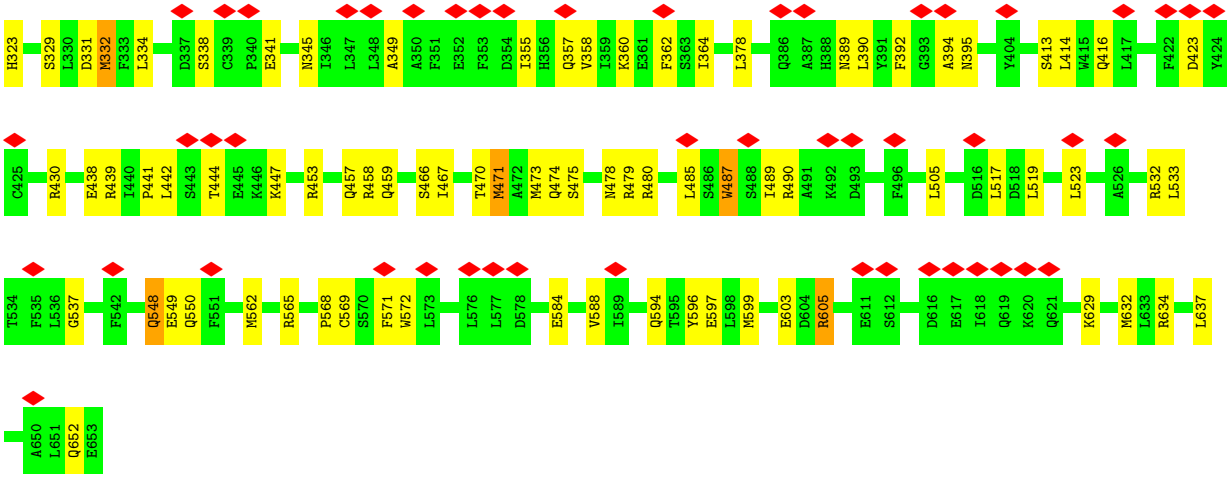
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 Nup85



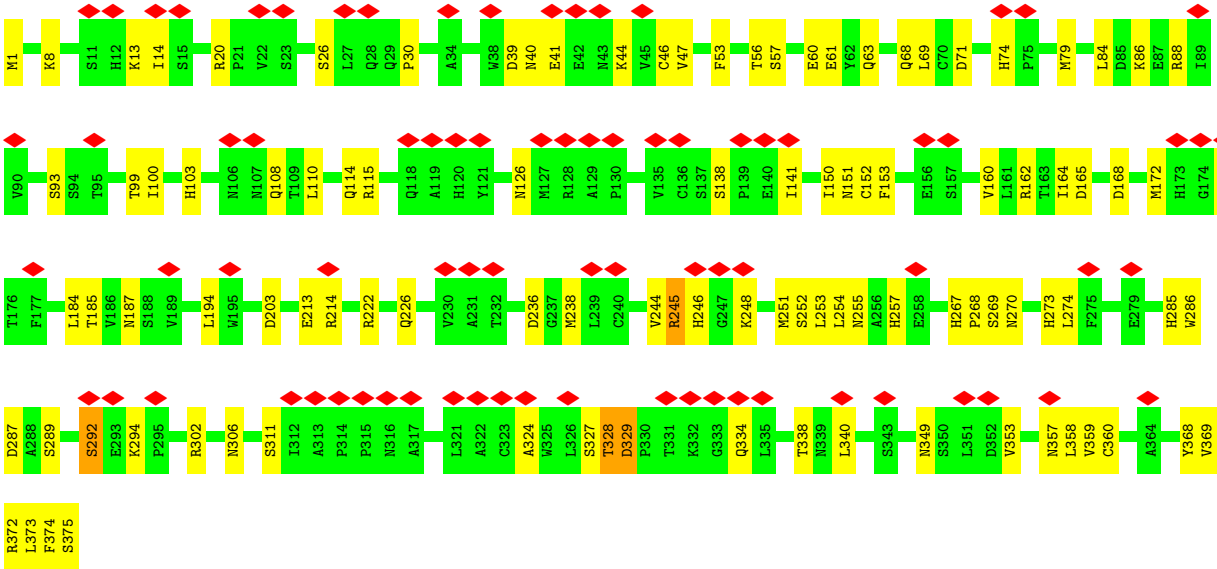
• Molecule 1: Nuclear pore complex protein Nup85





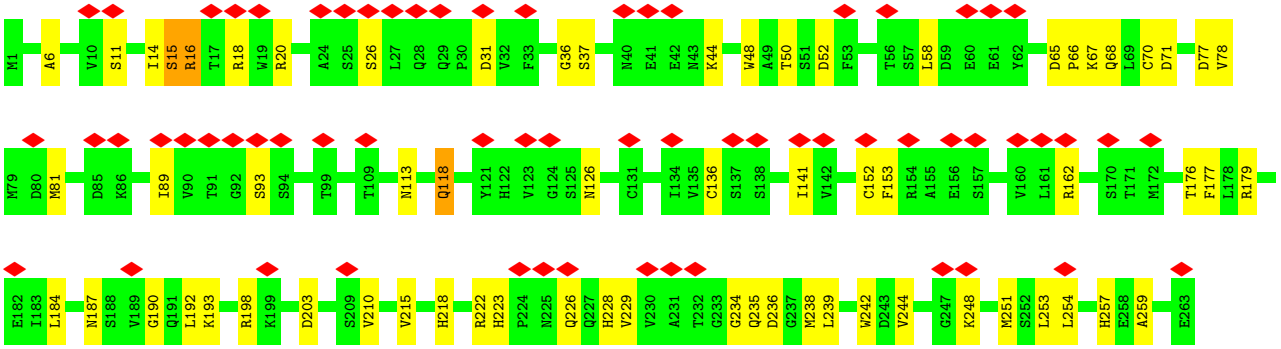
• Molecule 2: MGC154553 protein

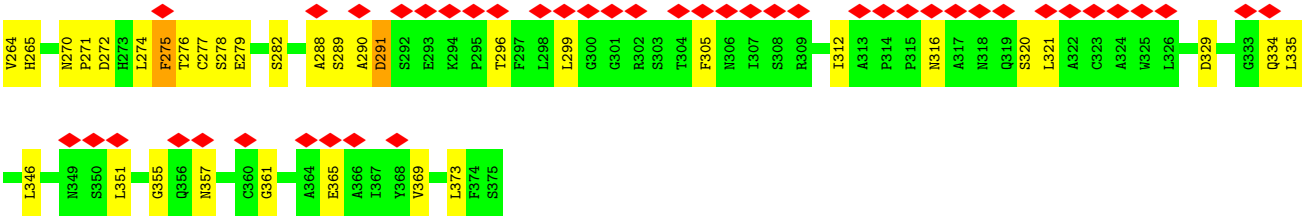
Chain B:



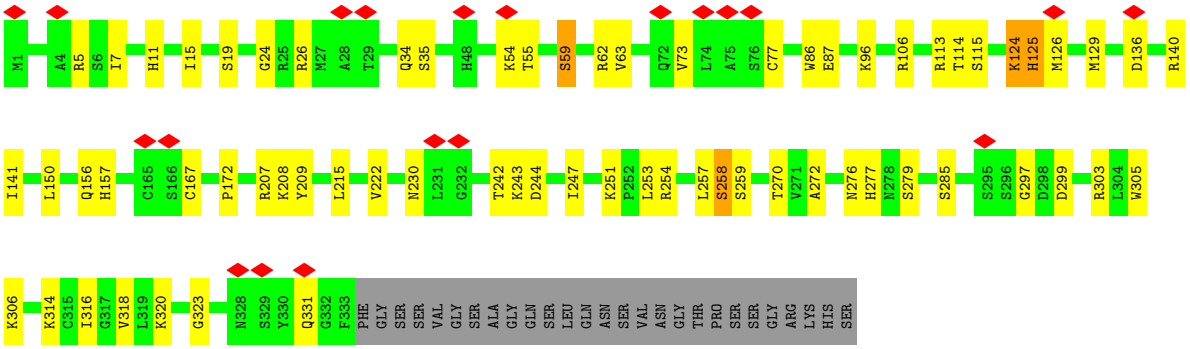
• Molecule 2: MGC154553 protein

Chain K:

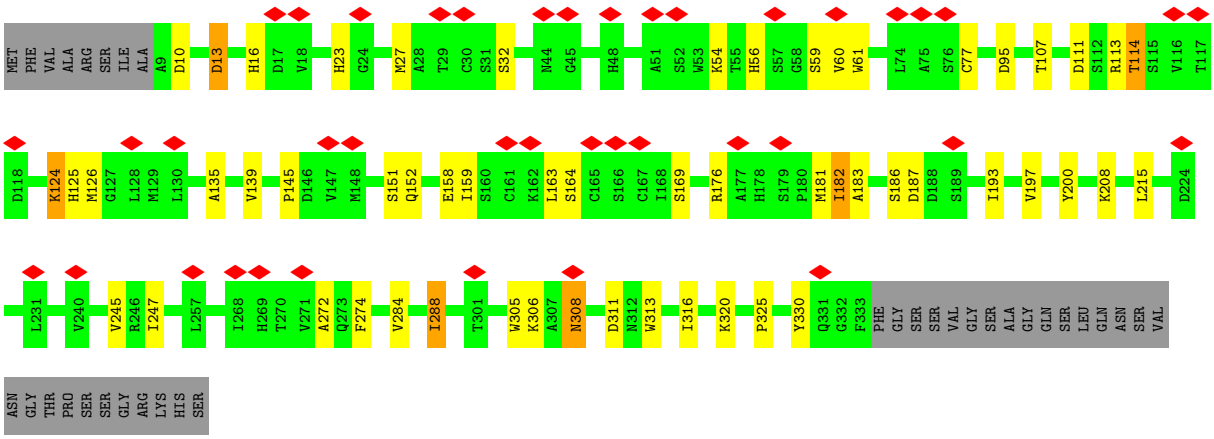




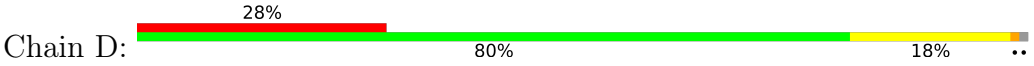
• Molecule 3: Nucleoporin SEH1-A

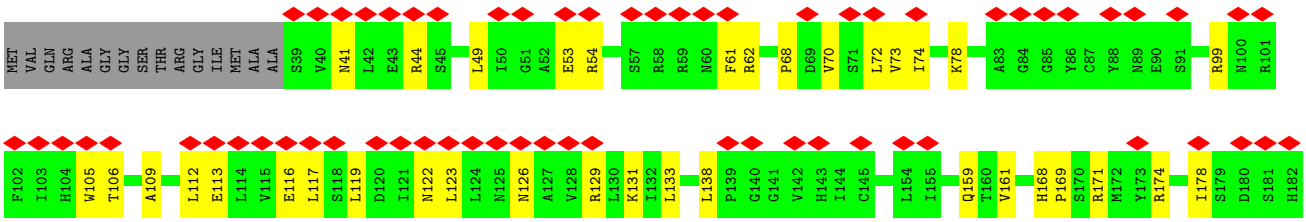


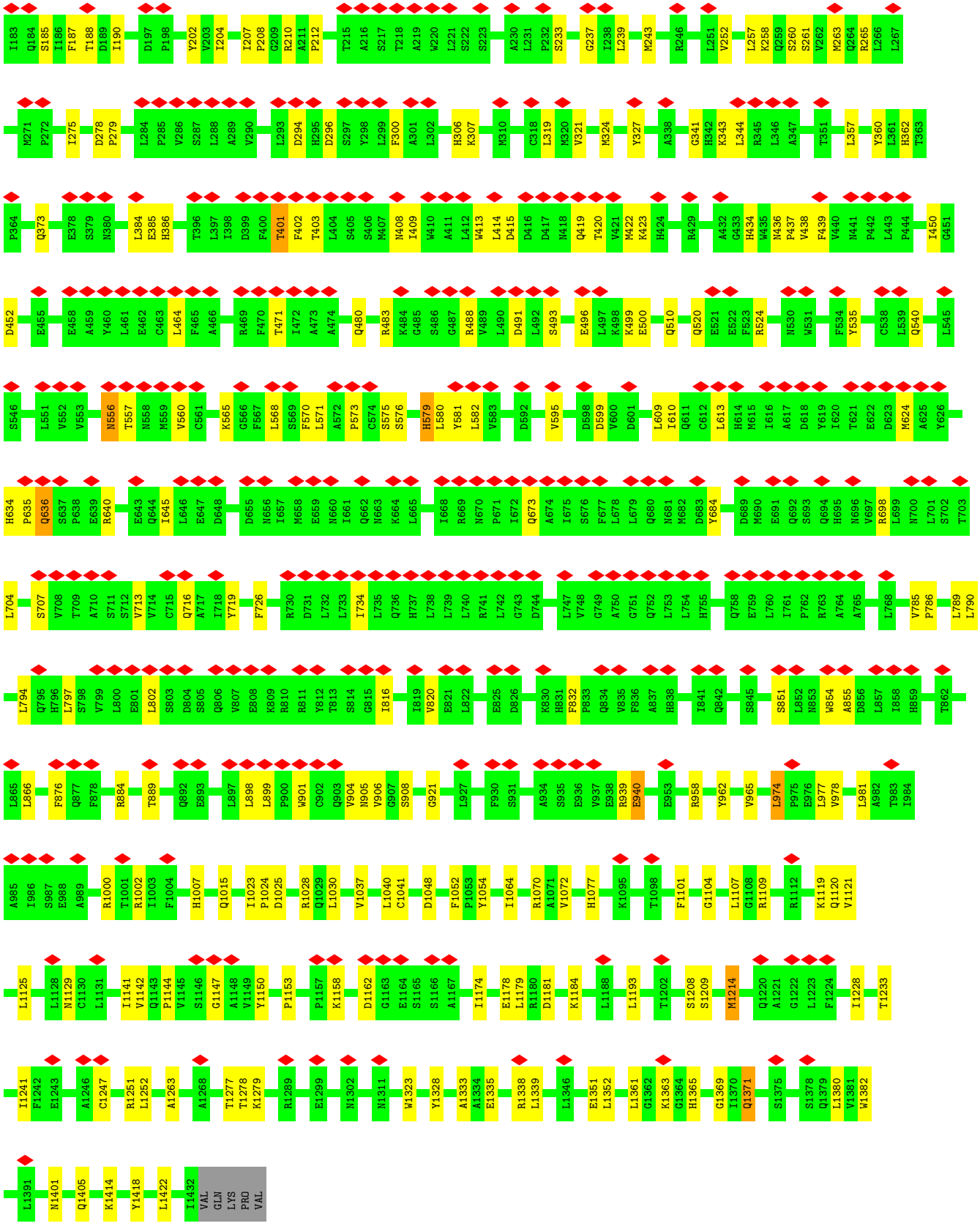
• Molecule 3: Nucleoporin SEH1-A



• Molecule 4: Nucleoporin 160kDa

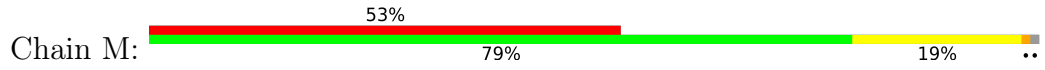


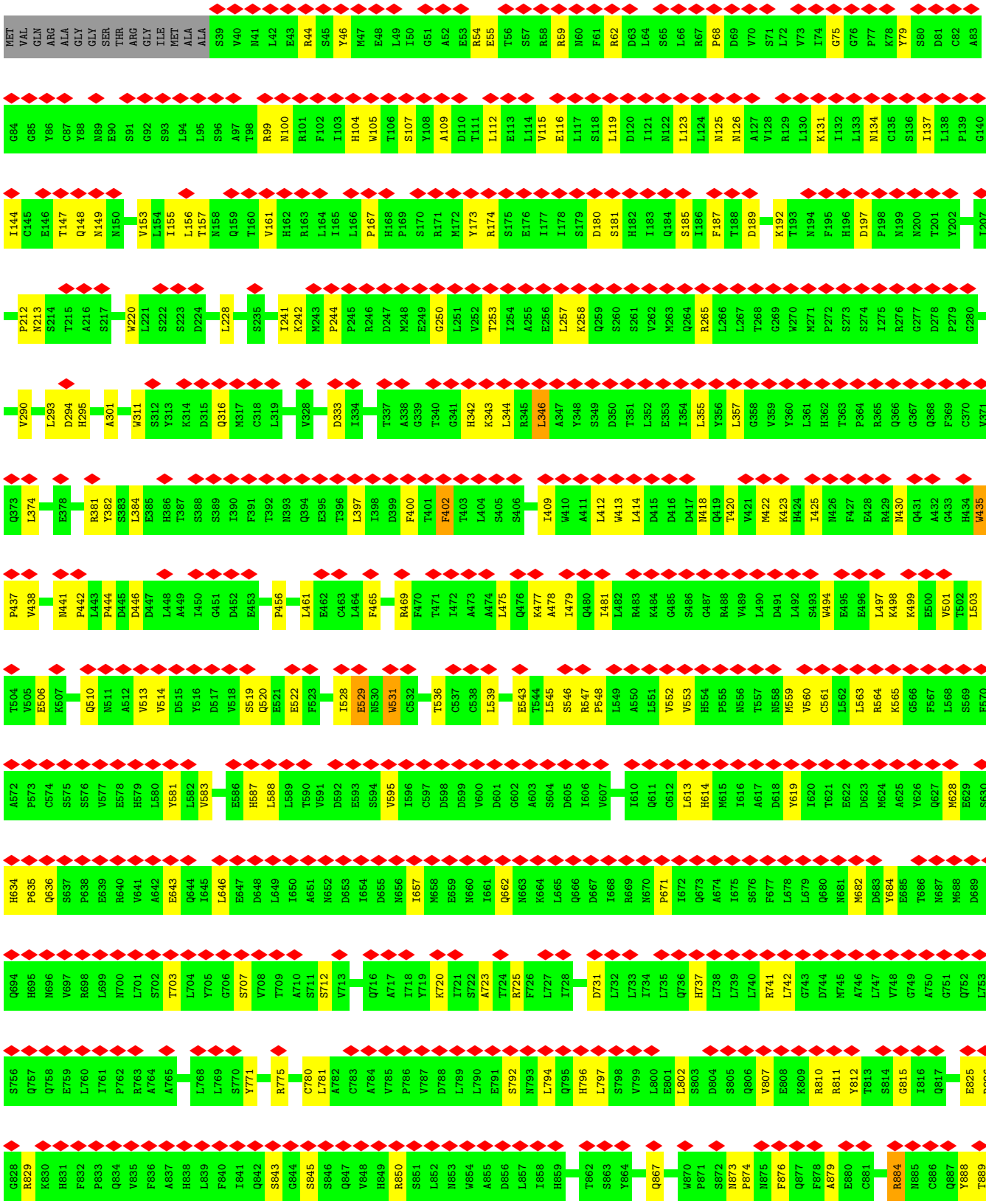




• Molecule 4: Nucleoporin 160kDa

Chain M:


53%
79%
19%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G84 G85 Y86 C87 Y88 N89 E90 S91 G92 S93 L94 L95 S96 A97 T98 R99 N100 R101 F102 I103 H104 W105 T106 S107 Y108 A109 D110 T111 L112 E113 L114 V115 E116 L117 S118 L119 D120 I121 N122 L123 L124 N125 N126 A127 V128 R129 L130 K131 I132 L133 N134 C135 S136 I137 L138 P139 G140 G141 V142 H143
I144 C145 E146 T147 Q148 N149 N150 V153 L154 I155 L156 T157 N158 Q159 T160 V161 H162 R163 L164 I165 L166 P167 H168 P169 S170 R171 N172 Y173 R174 S175 E176 I177 I178 S179 D180 S181 H182 I183 Q184 S185 I186 F187 T188 D189 K192 T193 N194 F195 H196 D197 P198 N199 N200 T201 Y202 I207 P208
P212 N213 S214 T215 A216 S217 W220 L221 S222 S223 D224 L228 S235 I241 K242 M243 P244 P245 R246 D247 M248 E249 G250 L251 V252 T253 I254 A255 E256 L257 K258 Q259 S260 S261 V262 M263 Q264 R265 L266 L267 T268 G269 W270 M271 P272 S273 S274 I275 R276 G277 D278 P279 G280 P285
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T504 Y505 E506 K507 Q510 N511 A512 V513 V514 D515 Y516 D517 V518 S519 Q520 E521 E522 F523 I528 E529 N530 W531 C532 T536 C537 C538 L539 E543 T544 L545 S546 R547 P548 L549 A550 L551 V552 V553 H554 P555 N556 T557 N558 M559 V560 C561 L562 L563 R564 K565 G566 F567 L568 S569 F570 L571
A572 P573 C574 S575 S576 V577 E578 H579 L580 Y581 L582 V583 E586 H587 L588 L589 T590 V591 D592 E593 S594 V595 I596 C597 D598 D599 V600 D601 G602 A603 S604 D605 I606 V607 I610 Q611 C612 L613 H614 M615 I616 A617 D618 Y619 I620 T621 E622 D623 M624 A625 Y626 Q627 M628 E629 S630 A631 C632 C633
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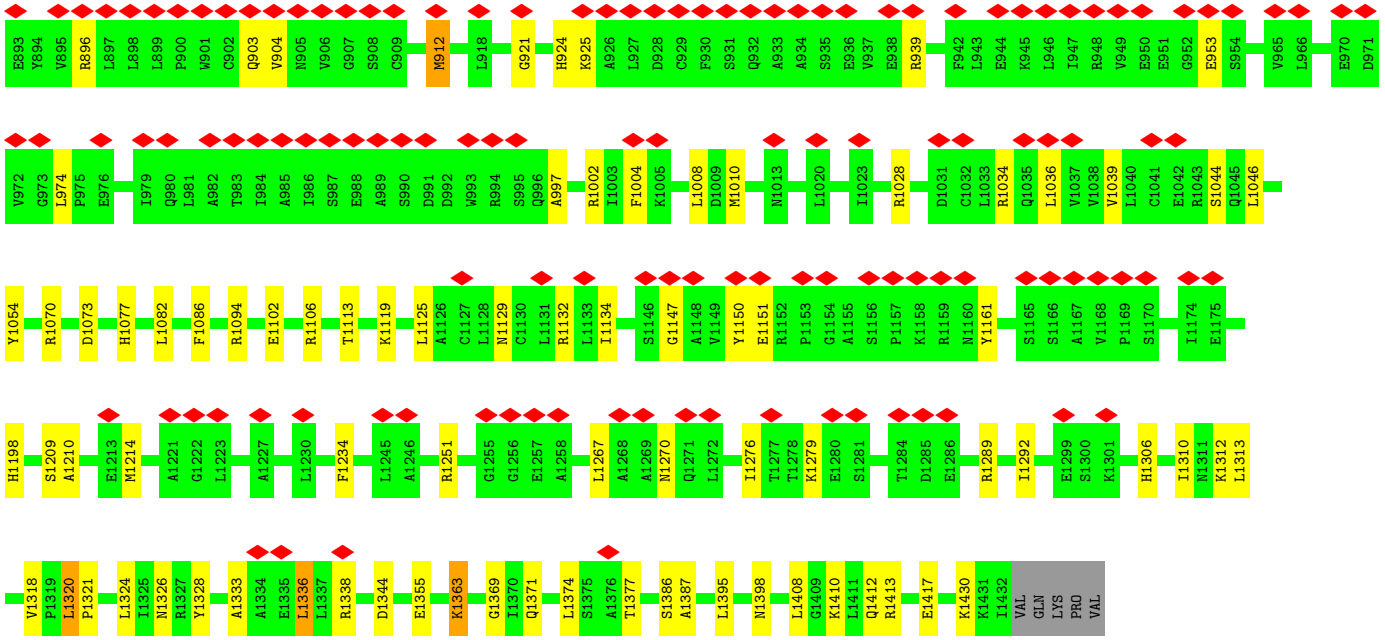
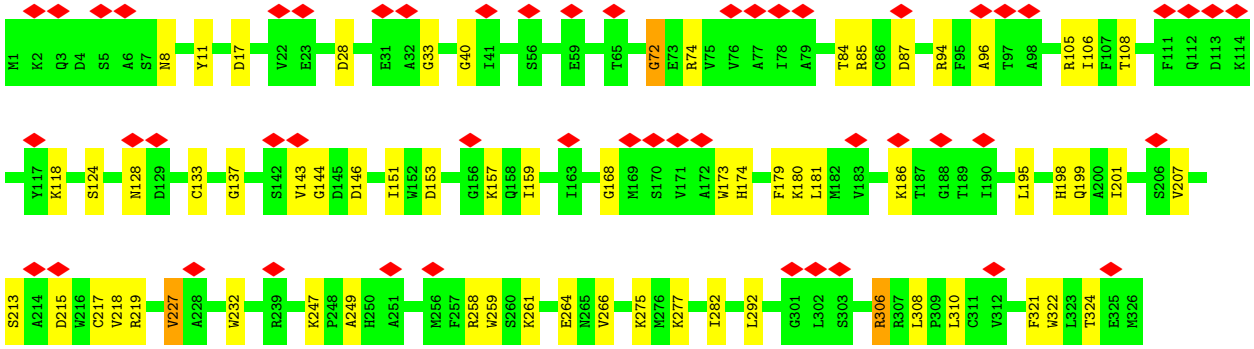
S756 Q757 Q758 E759 L760 I761 P762 R763 A764 A765 L768 L769 S770 Y771 R775 C780 L781 A782 C783 A784 V785 P786 V787 D788 L789 L790 E791 S792 N793 L794 Q795 H796 L797 S798 V799 L800 E801 L802 S803 D804 S805 Q806 V807 E808 K809 R810 R811 Y812 T813 S814 G815 I816 Q817 E825 D826 V827
G828 R829 K830 H831 F832 P833 Q834 V835 F836 A837 H838 L839 F840 I841 Q842 S843 G844 S845 S846 Q847 V848 H849 R850 S851 L852 N853 W854 A855 D856 L857 I858 H859 T862 S863 Y864 Q867 W870 P871 S872 N873 P874 N875 F876 Q877 F878 A879 E880 C881 R884 N885 C886 Q887 Y888 T889 Q892



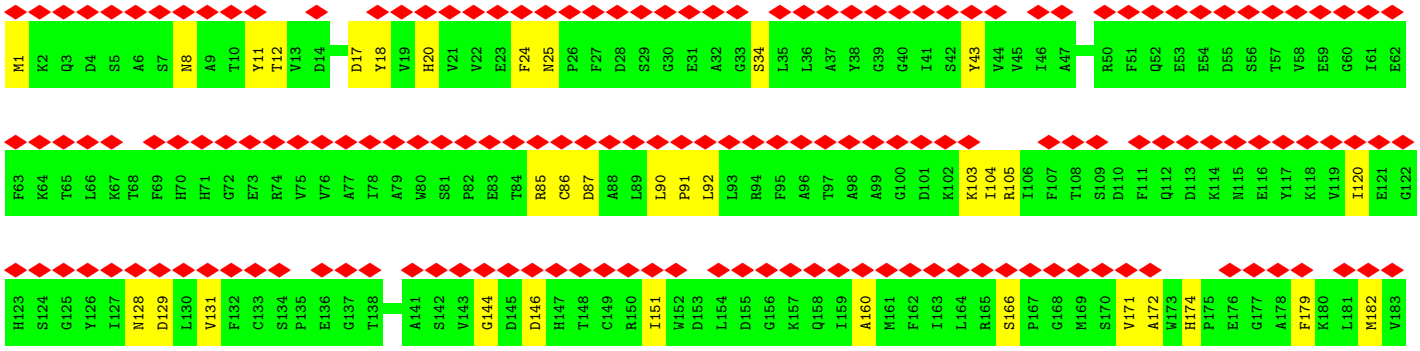
• Molecule 5: MGC83926 protein

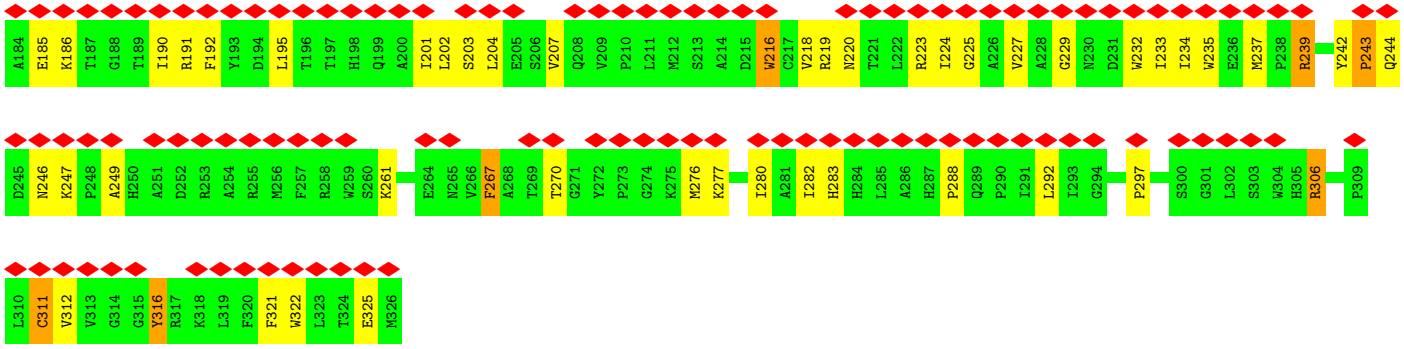
Chain E:



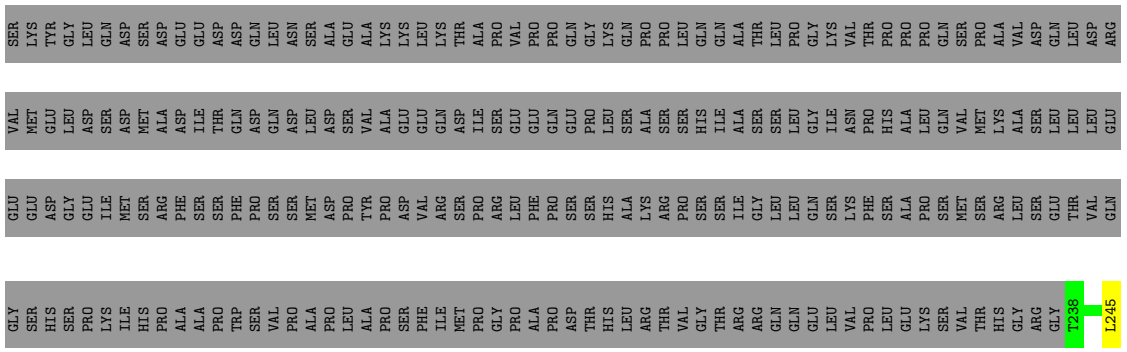
• Molecule 5: MGC83926 protein

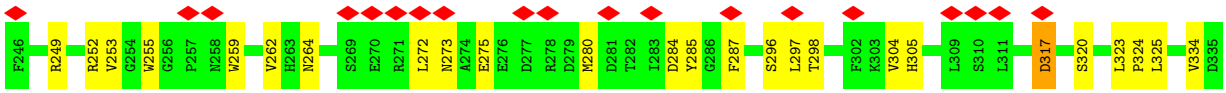
Chain N:

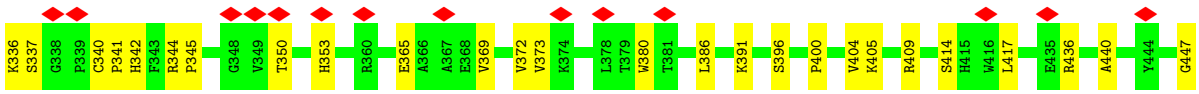


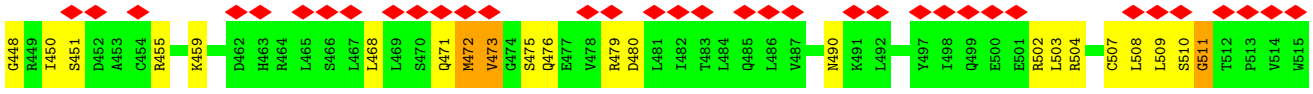


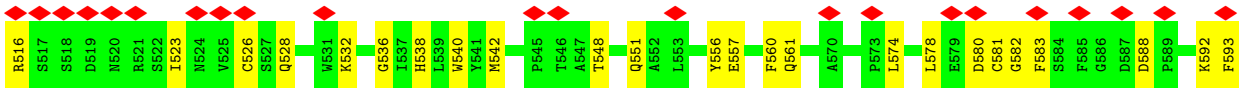
• Molecule 6: Nuclear pore complex protein Nup96

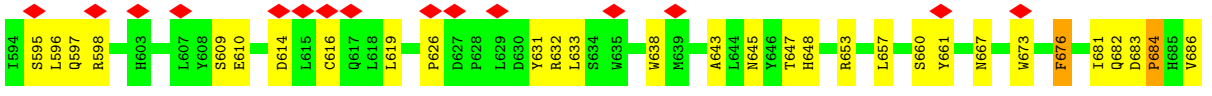






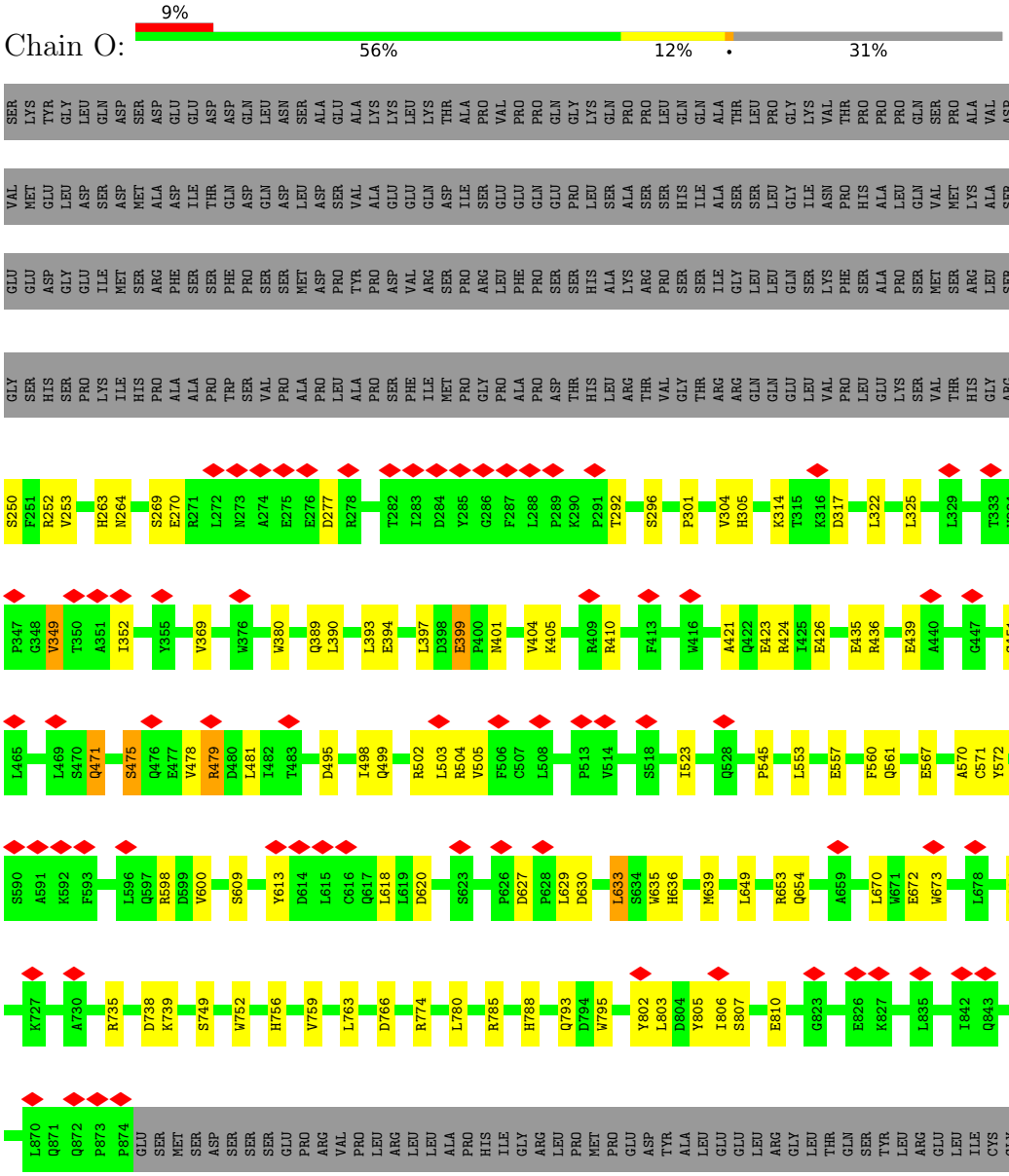






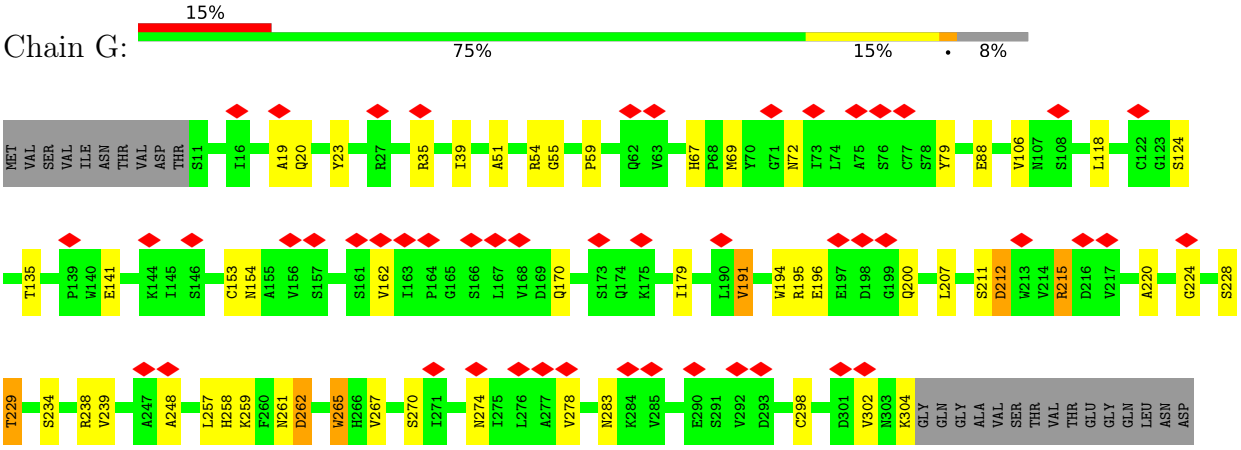
• Molecule 6: Nuclear pore complex protein Nup96

Chain O:

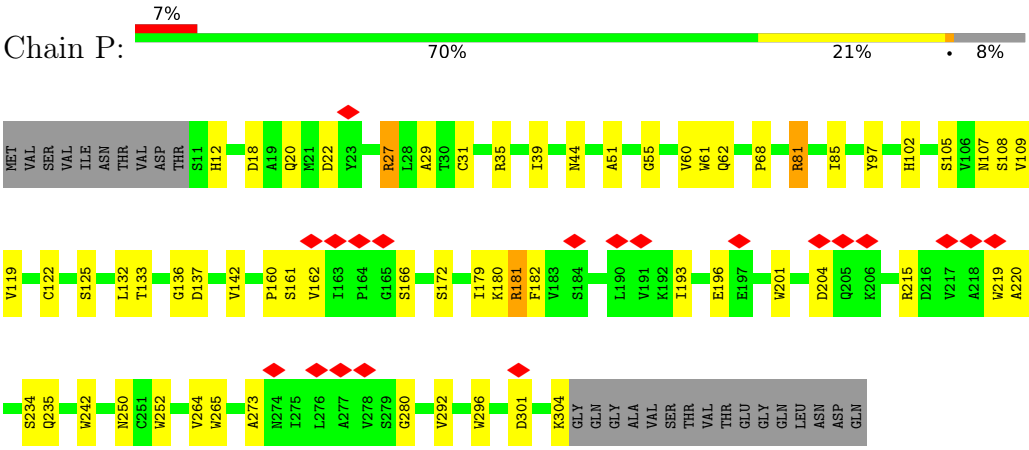


• Molecule 7: GATOR complex protein SEC13

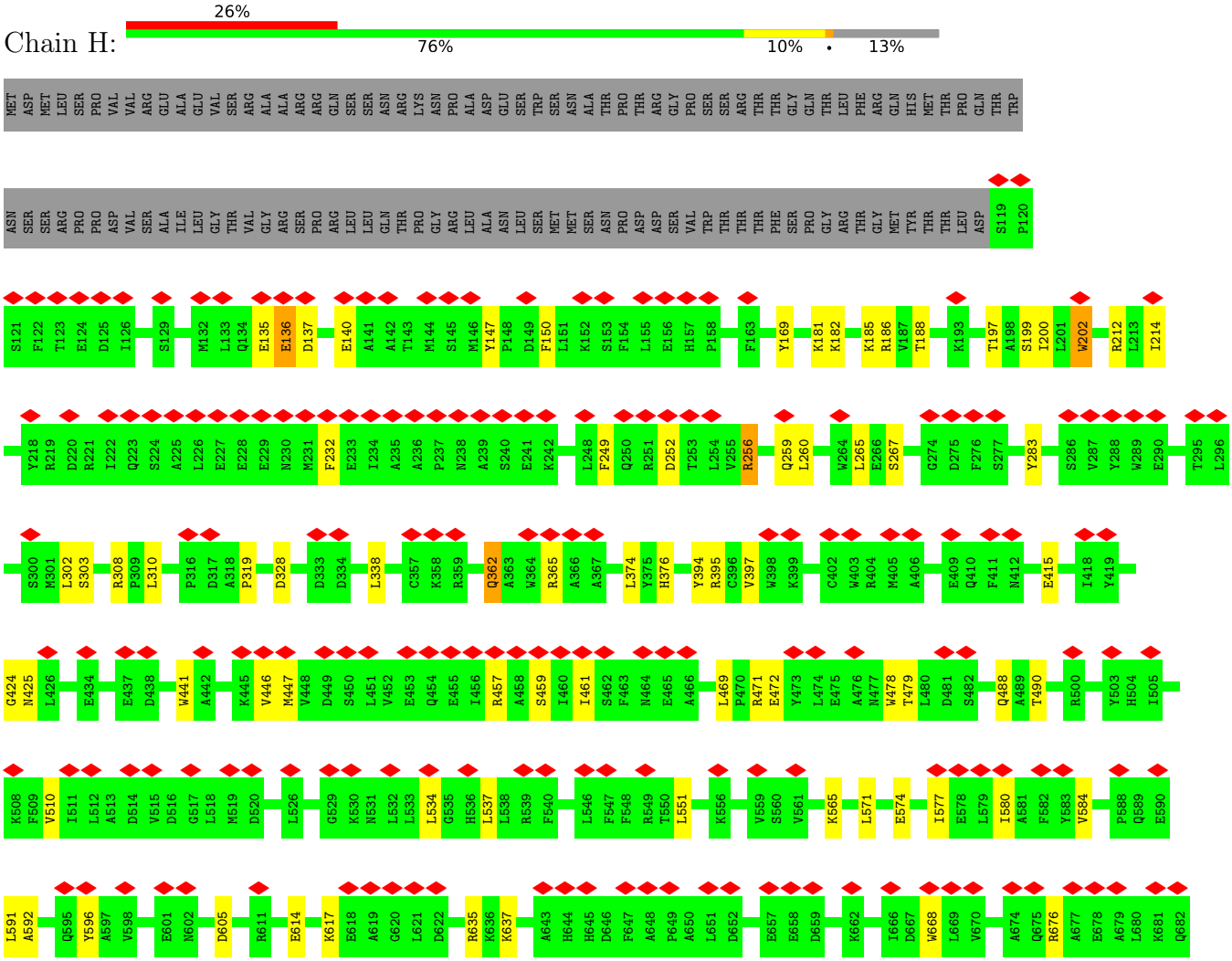
Chain G:

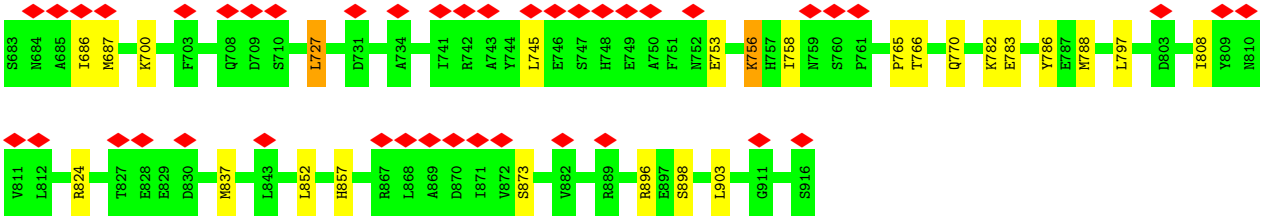


• Molecule 7: GATOR complex protein SEC13



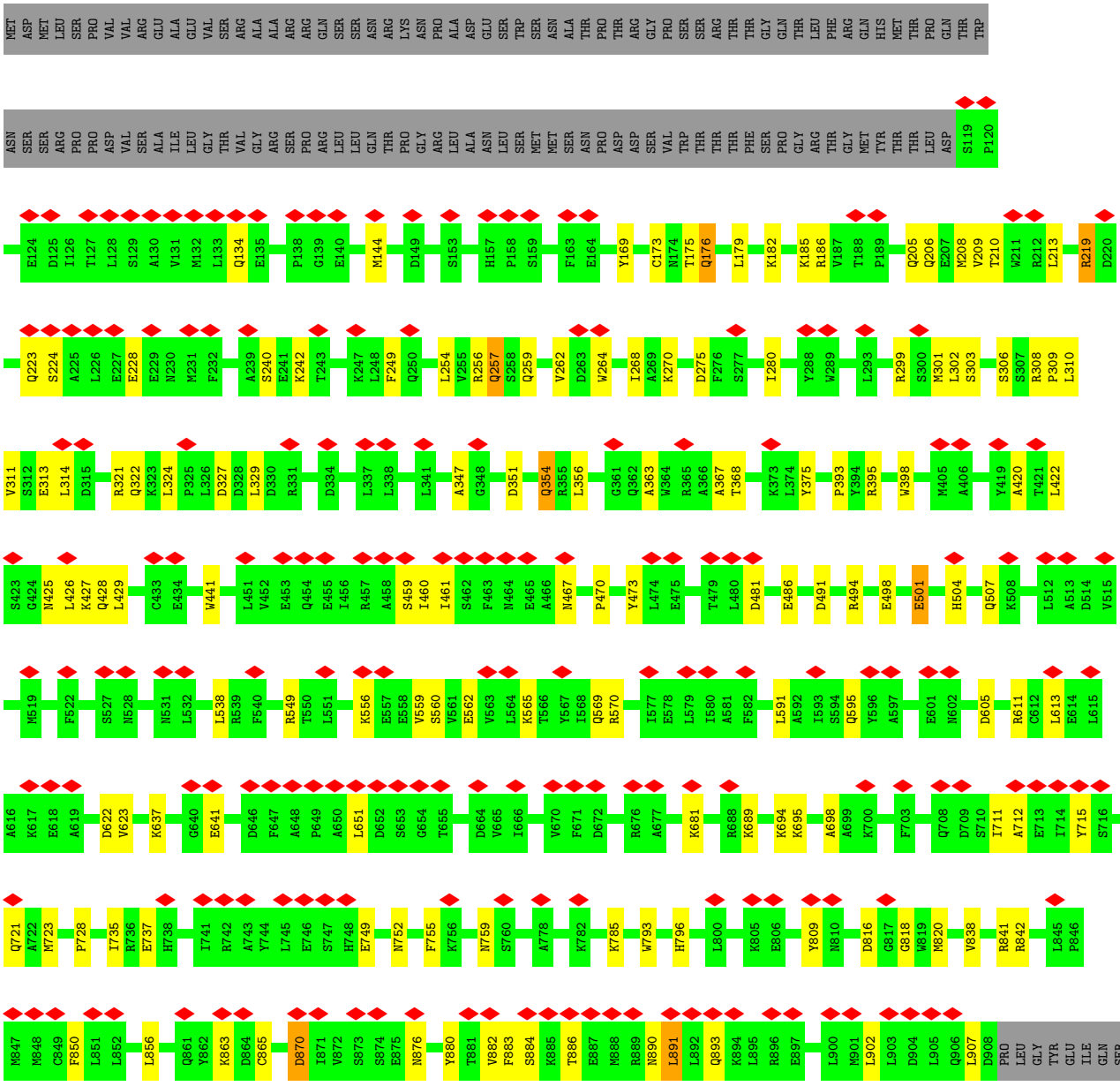
• Molecule 8: Nuclear pore complex protein





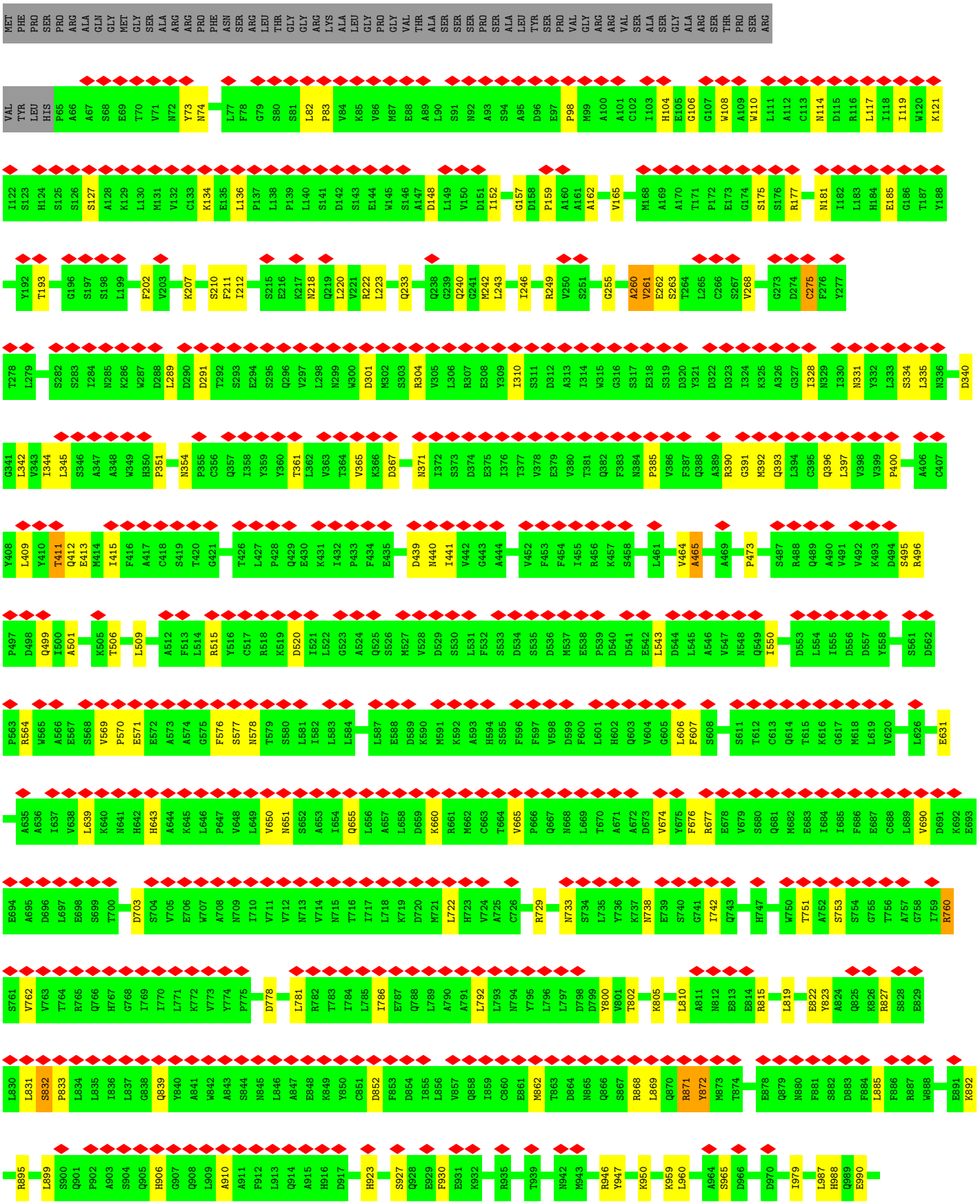
• Molecule 8: Nuclear pore complex protein

Chain Q:



• Molecule 9: outer Nup133

Chain I: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VAL TYR LEU HIS P65 A66 A67 S68 E69 T70 V71 N72 Y73 N74 L77 F78 G79 S80 S81 L82 P83 V84 K85 V86 H87 E88 A89 L90 S91 N92 A93 S94 A95 D96 E97 P98 M99 A100 A101 C102 I103 H104 E105 G106 G107 W108 A109 W110 L111 A112 C113 N114 D115 R116 L117 I118 I119 W120 K121
I122 S123 H124 S125 S126 S127 A128 K129 L130 M131 V132 C133 K134 E135 L136 P137 L138 P139 L140 S141 D142 S143 E144 W145 S146 A147 D148 L149 V150 D151 I152 G157 D158 P159 A160 A161 A162 V165 M168 A169 A170 T171 P172 E173 G174 S175 S176 R177 N181 I182 L183 H184 E185 G186 T187 Y188
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T278 L279 S282 S283 I284 N285 K286 W287 D288 L289 D290 D291 T292 S293 E294 S295 Q296 V297 L298 N299 W300 D301 M302 S303 R304 V305 L306 R307 E308 Y309 I310 S311 D312 A313 I314 W315 G316 S317 E318 S319 D320 Y321 D322 D323 I324 K325 A326 G327 I328 N329 I330 N331 Y332 L333 S334 L335 N336 D340
G341 L342 Y343 I344 L345 S346 A347 A348 W349 H350 P351 N354 P355 C356 Q357 I358 Y359 Y360 T361 L362 V363 T364 Y365 K366 D367 N371 I372 S373 D374 E375 I376 T377 V378 E379 V380 T381 Q382 F383 N384 P385 V386 F387 Q388 A389 R390 G391 M392 Q393 L394 C395 Q396 L397 V398 V399 P400 A406 C407
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P497 D498 Q499 I500 A501 K505 T506 L509 A512 F513 L514 R515 Y516 C517 R518 K519 D520 I521 L522 G523 A524 Q525 S526 M527 V528 D529 S530 L531 F532 S533 D534 S535 D536 M537 E538 P539 D540 D541 E542 L543 D544 L545 A546 V547 N548 Q549 I550 D553 L554 I555 D556 D557 Y558 S561 D562
P563 R564 W565 A566 E567 S568 V569 P570 E571 E572 A573 A574 G575 F576 S577 N578 T579 S580 L581 I582 L583 L584 L587 E588 D589 K590 M591 K592 A593 H594 S595 F596 F597 V598 D599 F600 L601 H602 Q603 V604 G605 L606 F607 S608 S611 T612 C613 Q614 T615 K616 G617 M618 L619 V620 L626 E631
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E694 A695 D696 L697 E698 S699 T700 D703 S704 V705 E706 W707 A708 N709 I710 V711 V712 N713 V714 N715 T716 I717 L718 K719 D720 M721 L722 H723 V724 A725 C726 R729 N733 S734 L735 V736 K737 N738 E739 S740 G741 I742 Q743 H747 W750 T751 A752 S753 S754 G755 T756 A757 G758 I759 R760
S761 V762 V763 T764 R765 Q766 H767 G768 I769 I770 L771 K772 V773 Y774 P775 D778 L781 R782 T783 I784 L785 T786 E787 Q788 L789 A790 A791 L792 L793 N794 Y795 L796 L797 D798 D799 Y800 V801 T802 K805 L810 A811 N812 E813 E814 R815 L819 E822 Y823 A824 Q825 K826 R827 S828 E829
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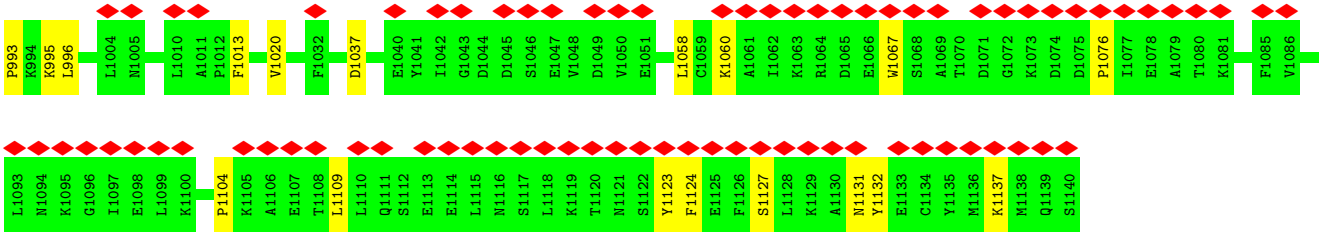
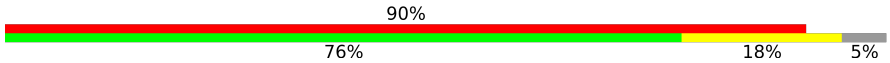
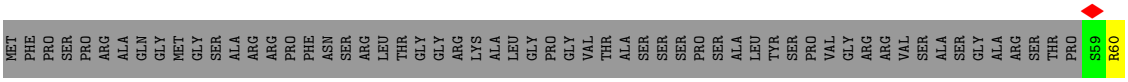
R895 L899 S900 Q901 P902 A903 S904 Q905 H906 G907 Q908 L909 A910 A911 F912 L913 Q914 A915 H916 D917 H923 S927 Q928 E929 F930 E931 K932 R935 T939 N942 M943 R946 Y947 K960 K959 L960 A964 S965 D966 D970 I979 L987 H988 Q989 E990

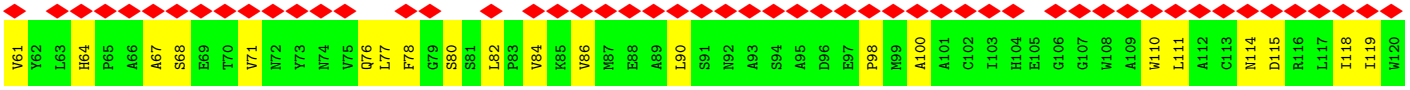


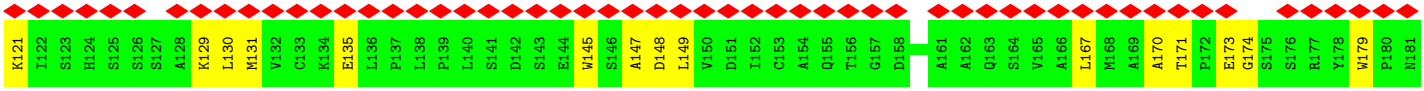
• Molecule 9: outer Nup133

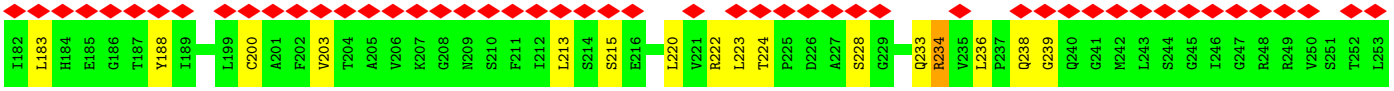
Chain R:

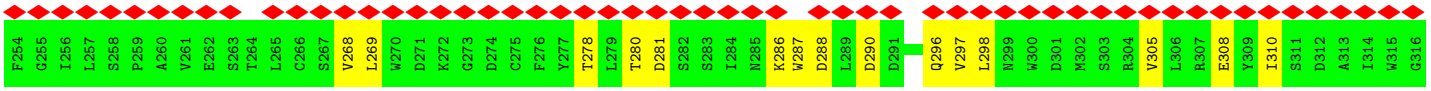


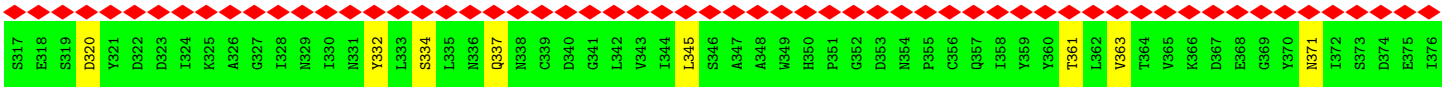


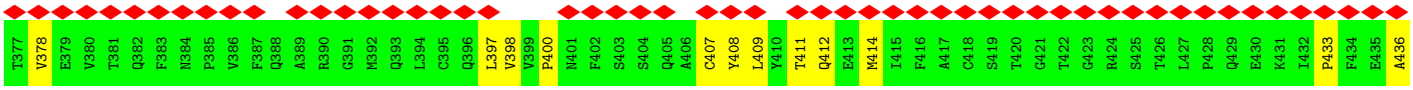


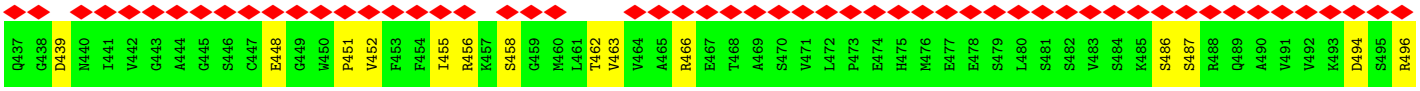


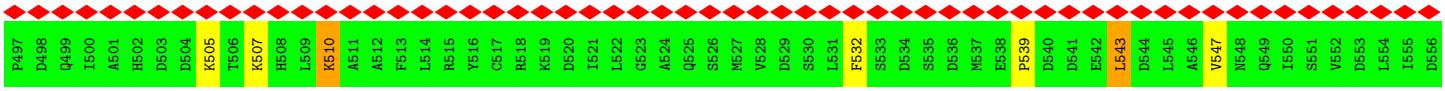


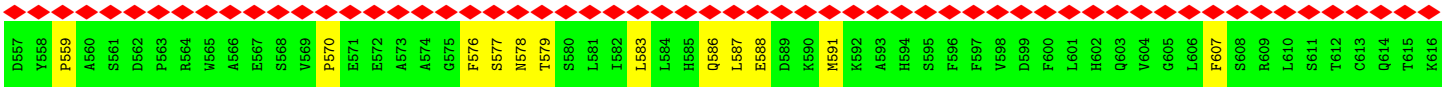


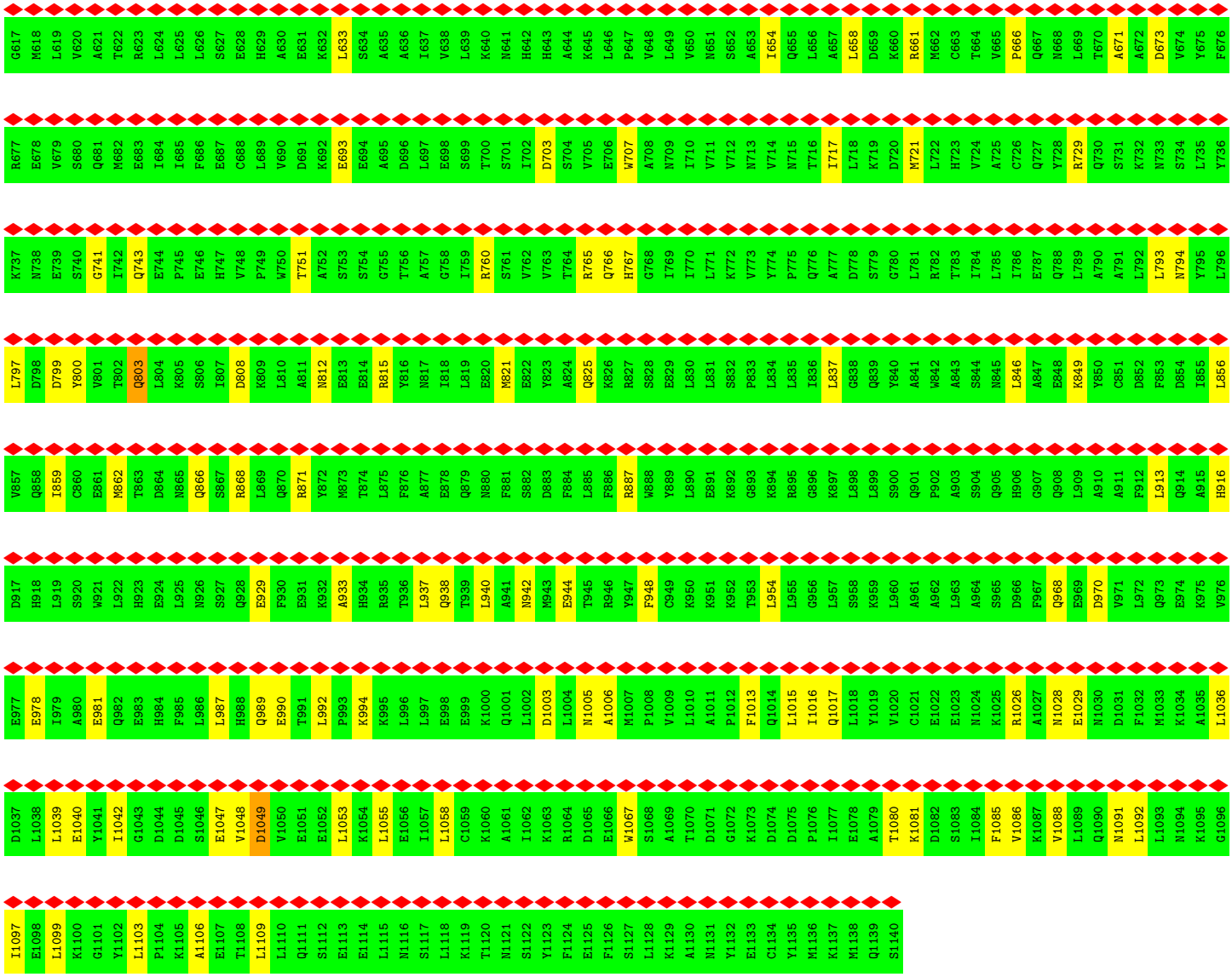






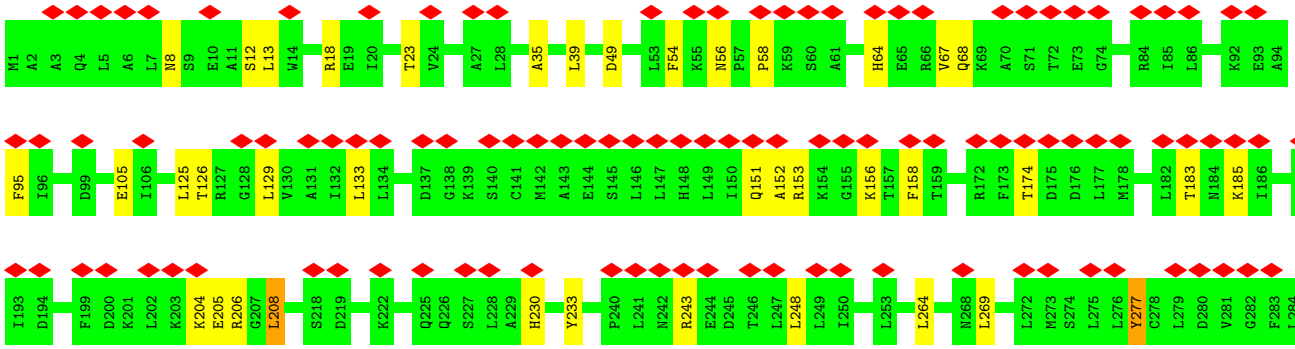


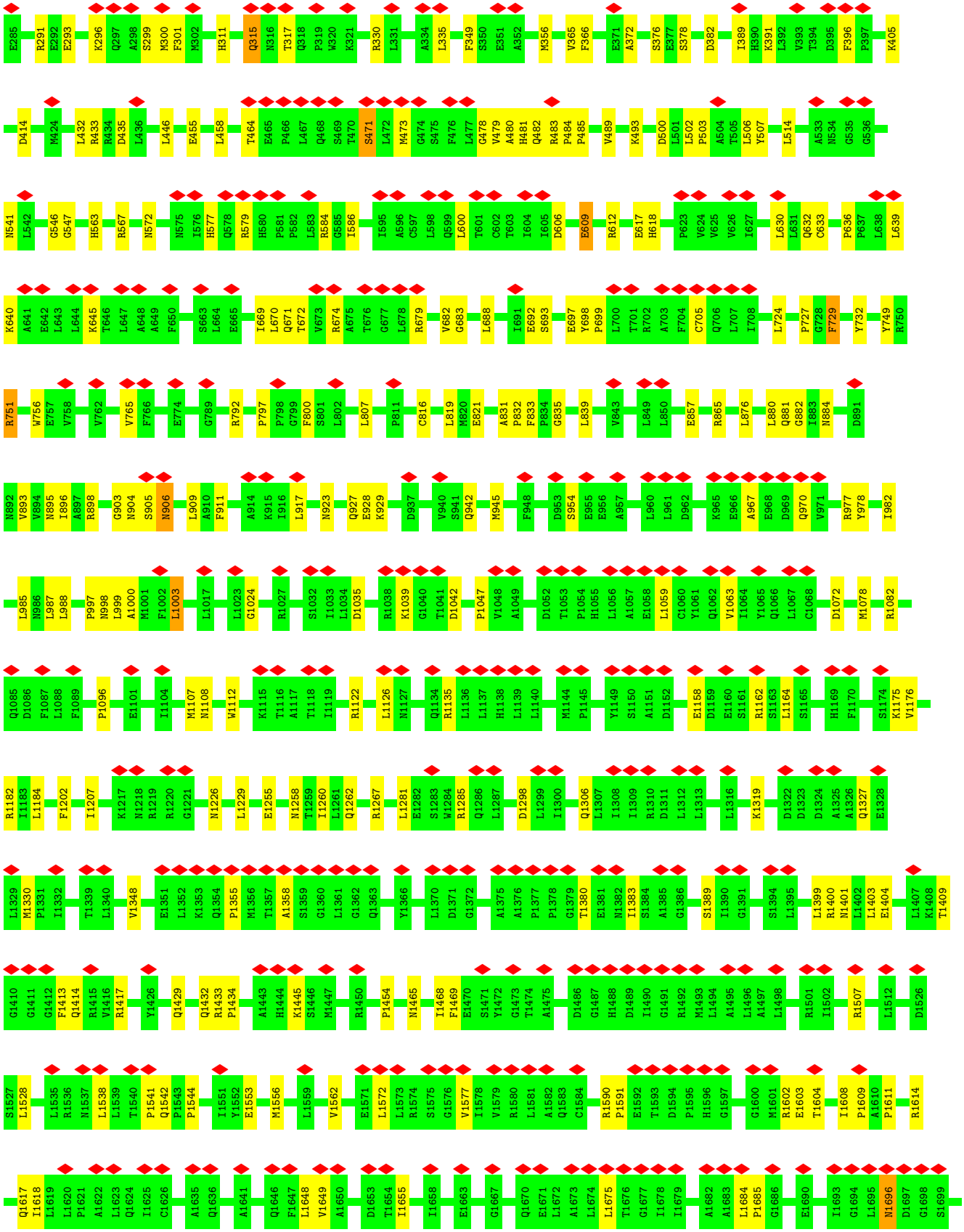




• Molecule 10: MGC83295 protein

Chain S:

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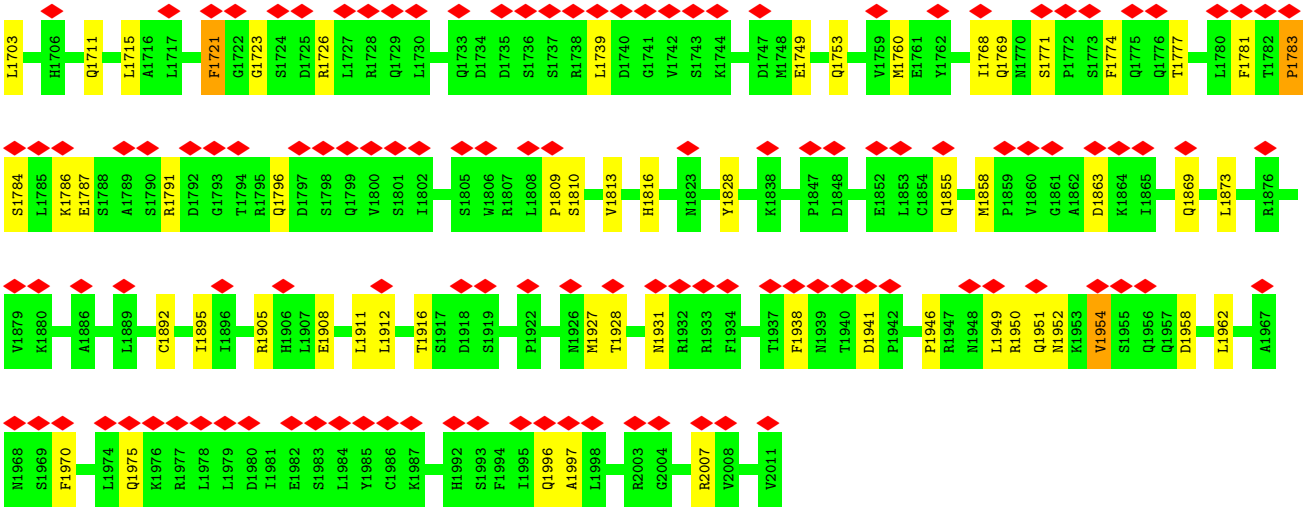
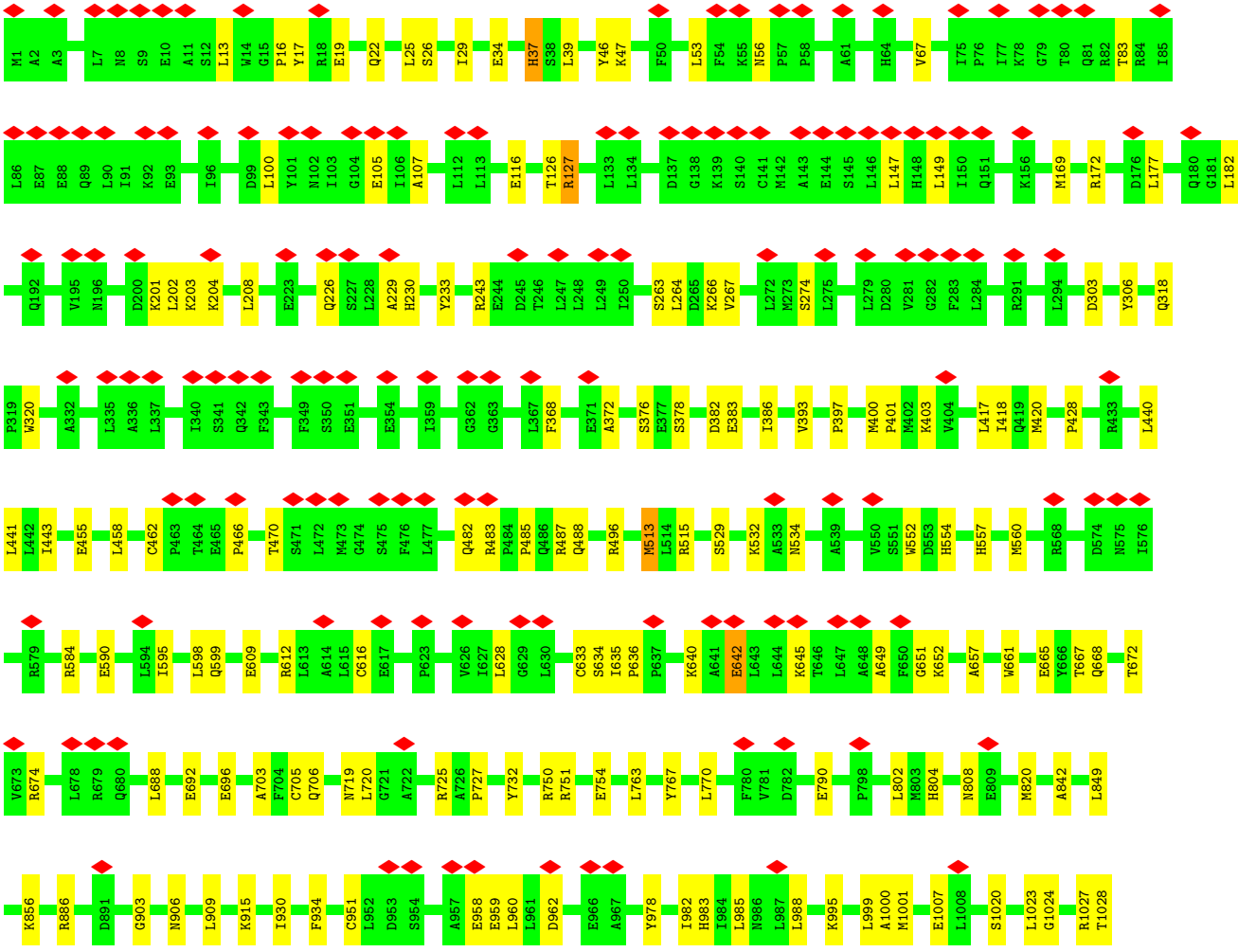


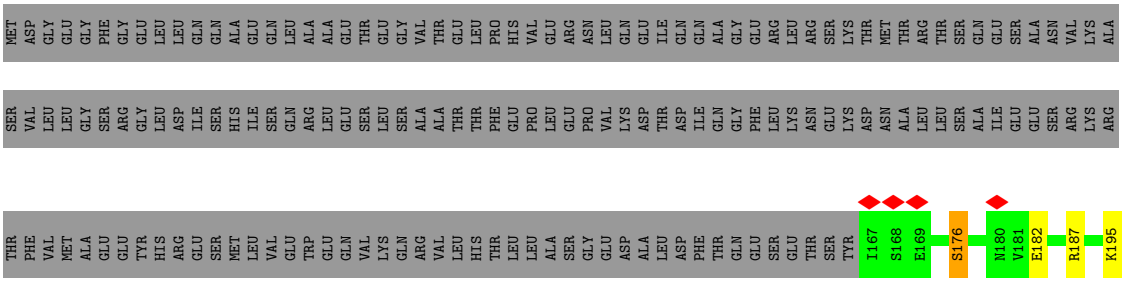
- Molecule 10: MGC83295 protein

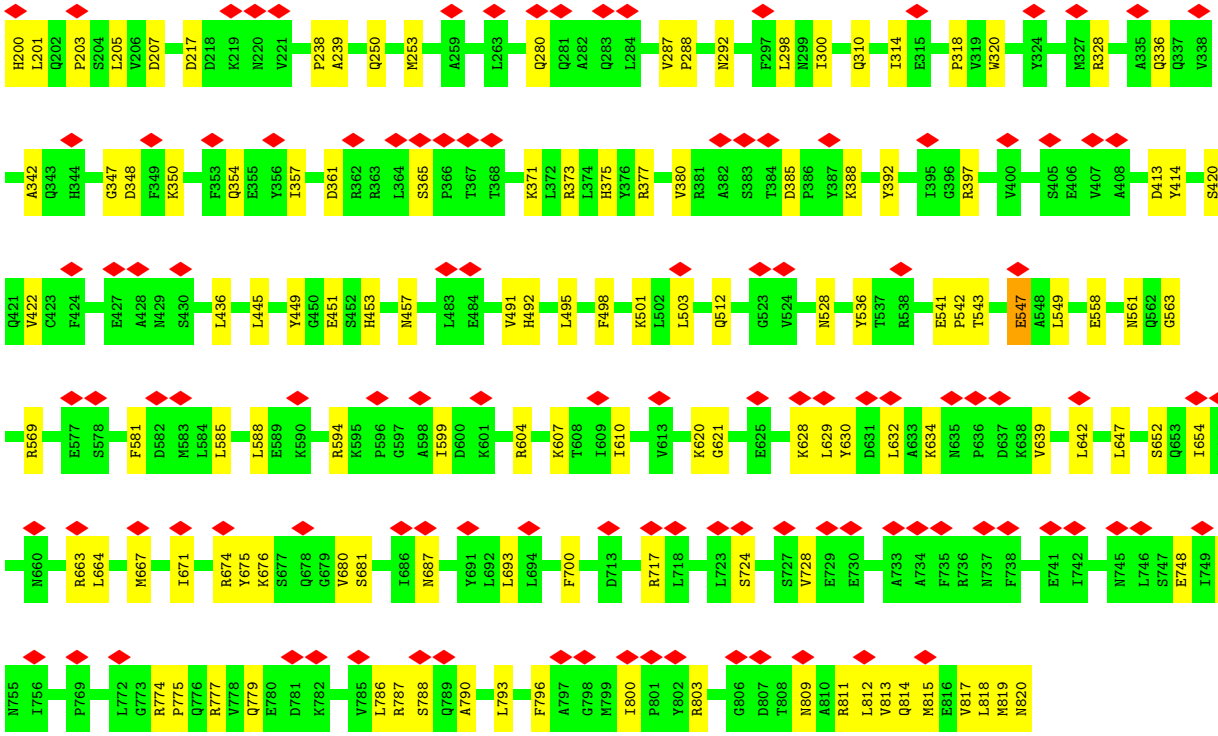
Chain T:



• Molecule 11: Nuclear pore complex protein Nup93

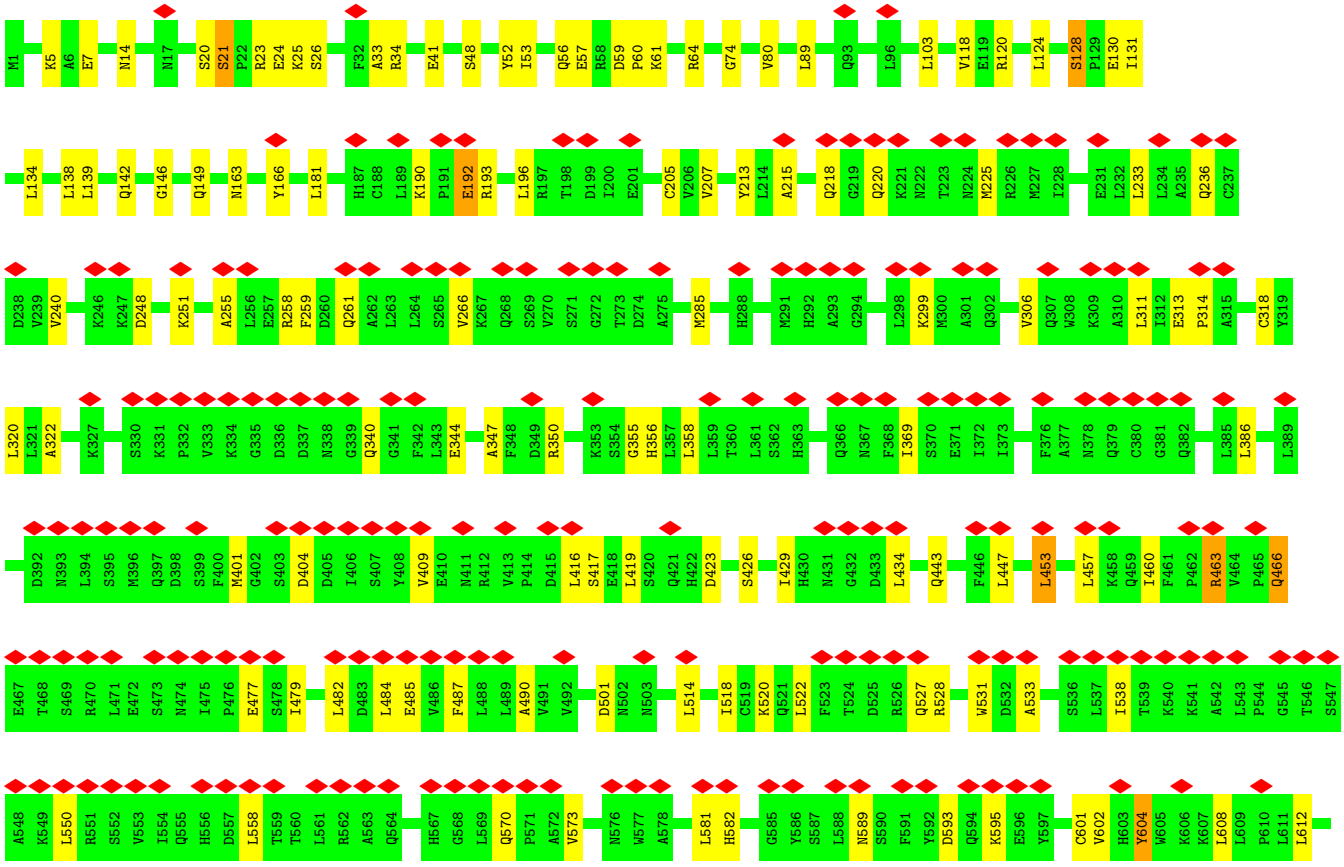
Chain U:

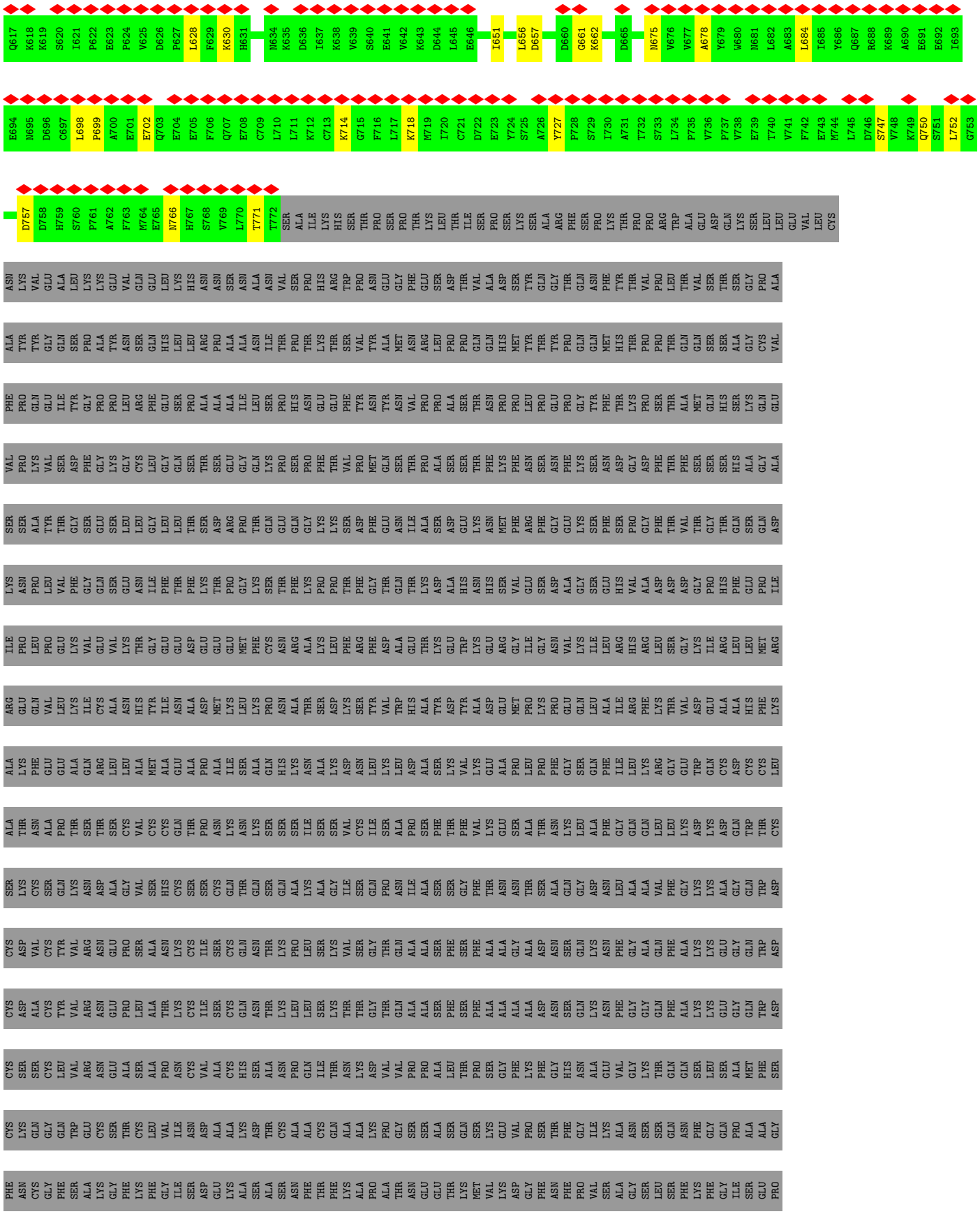




• Molecule 12: Nup358

Chain V:

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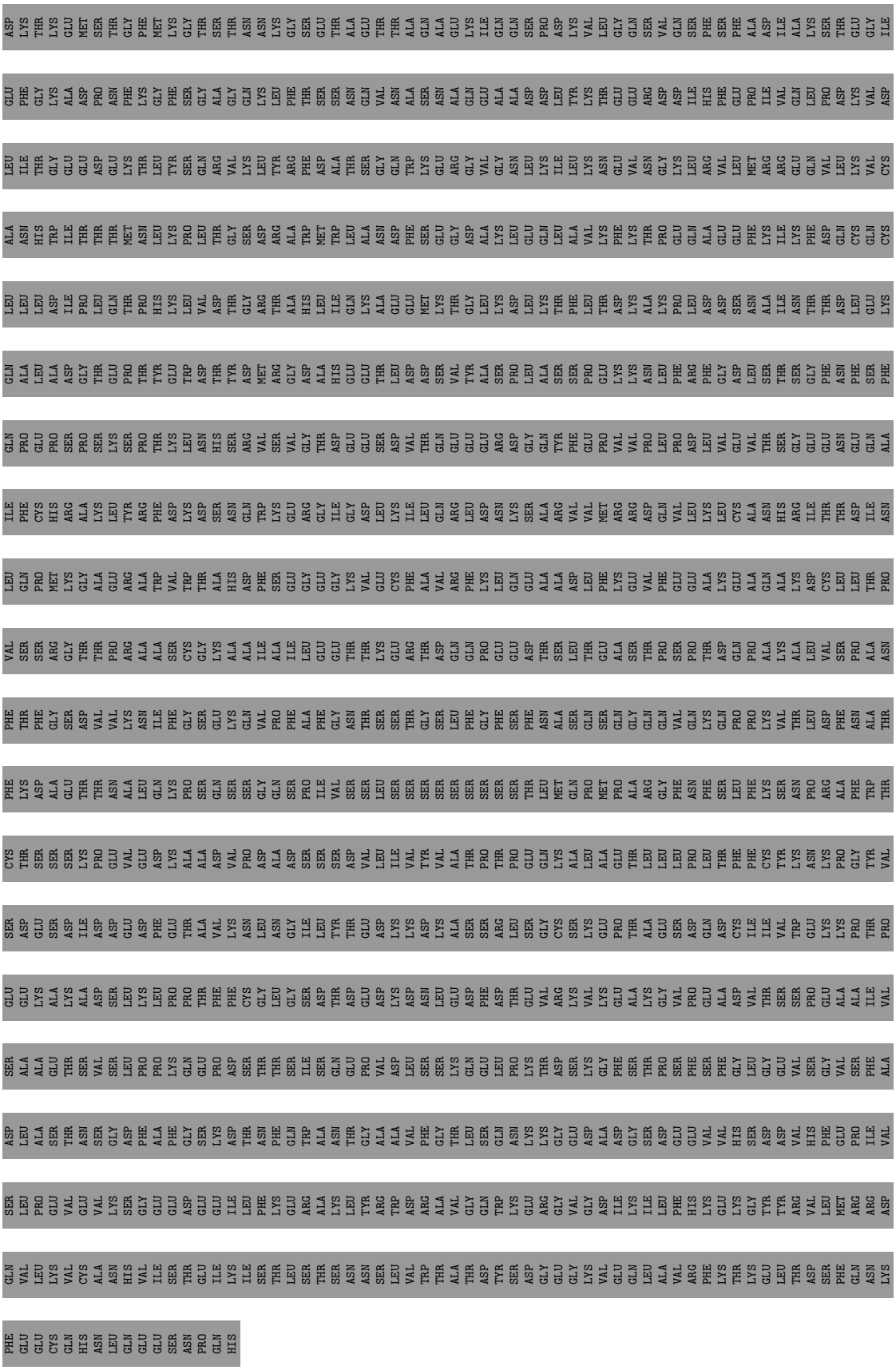
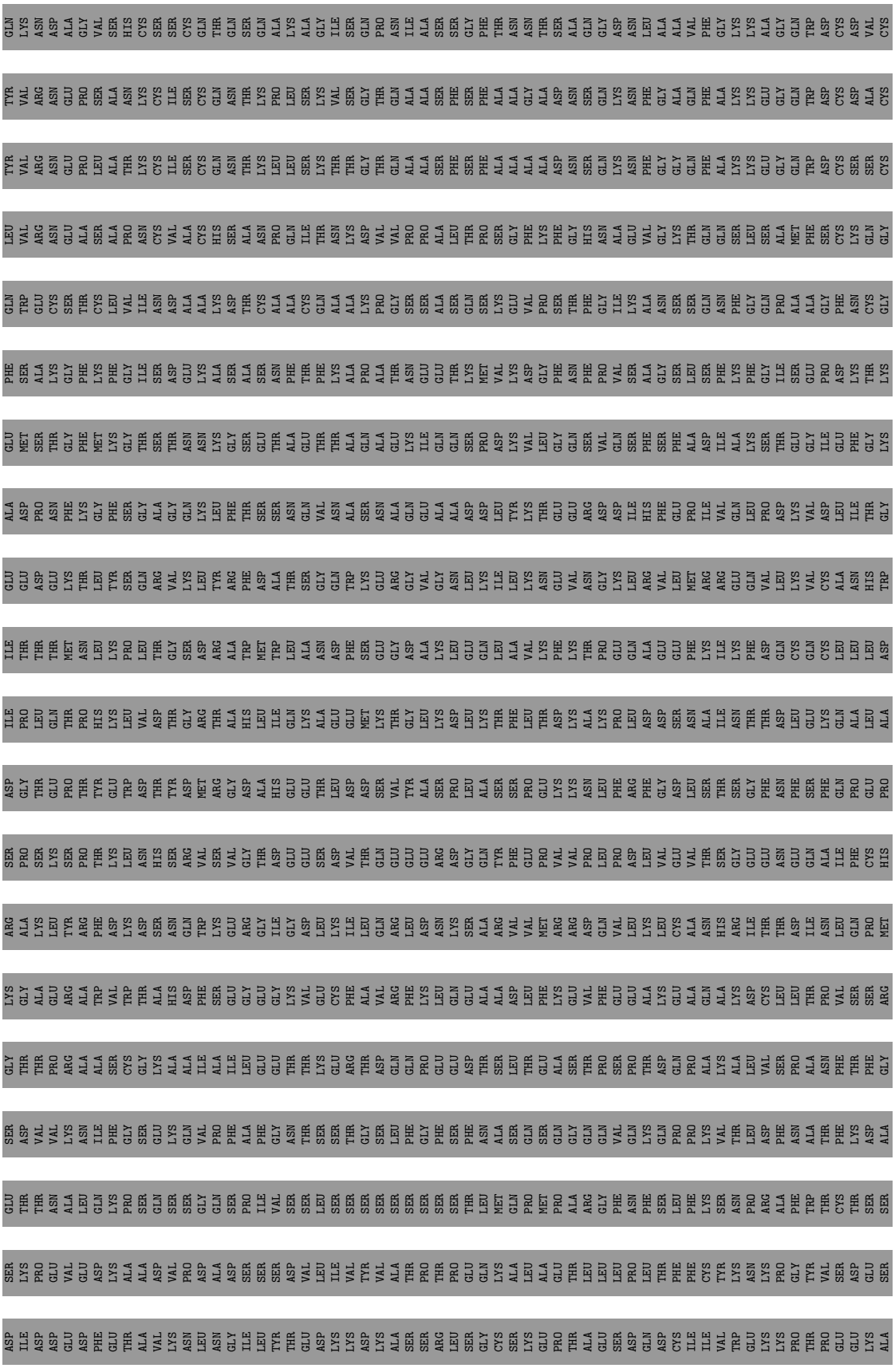
E694 N695 D696 C697 L698 P699 A700 E701 E702 Q703 E704 E705 F706 Q707 E708 C709 L710 L711 K712 C713 K714 G715 F716 L717 K718 M719 I720 C721 D722 E723 Y724 S725 A726 Y727 F728 S729 I730 A731 T732 S733 L734 P735 V736 P737 V738 E739 T740 V741 F742 E743 M744 L745 D746 S747 V748 K749 Q750 S751 L752 G753
D757 D758 H759 S760 P761 A762 F763 M764 E765 N766 H767 S768 V769 L770 T771 T772 SER ALA ILE LYS HIS SER THR PRO SER PRO THR LYS LEU THR ILE SER PRO SER LYS SER ALA ARG PHE SER PRO LYS THR PRO PRO ARG TRP ALA GLU ASP GLN LYS SER LEU LEU GLU VAL LEU CYS
ASN LYS VAL GLU ALA LEU LYS LYS GLU VAL GLN GLU LEU LYS HIS ASN ASN SER ASN ALA ASN VAL SER PRO HIS ARG TRP PRO ASN GLU GLY PHE GLU SER ASP THR VAL ALA ASP SER TYR GLN GLY THR GLN ASN PHE TYR THR VAL PRO LEU THR VAL SER THR SER GLY PRO ALA
ALA TYR TYR GLY GLN SER PRO ALA TYR ASN SER GLN HIS LEU LEU LEU ARG PRO ALA ASN ILE THR PRO THR LYS THR SER VAL TYR ALA MET ASN ARG LEU PRO PRO GLN HIS MET TYR THR TYR PRO GLN GLN MET HIS THR PRO PRO THR GLN GLN SER SER ALA GLY CYS VAL
PHE PRO GLN GLU ILE TYR GLY PRO PRO LEU ARG PHE GLU SER PRO ALA ALA ALA ILE LEU SER PRO HIS ASN GLU GLU PHE TYR ASN TYR ASN VAL PRO PRO ALA SER THR ASN PRO PRO LEU PRO GLU PRO PRO GLY TYR PHE PHE THR LYS PRO SER THR ALA MET GLN HIS SER LYS GLN GLU
VAL PRO LYS VAL SER ASP PHE GLY LYS GLY CYS LEU GLY GLN SER THR SER GLU GLY LEU LYS PRO SER PRO HIS ASN GLU GLU PHE THR VAL PRO MET GLN SER THR PRO ALA SER SER SER THR PHE LYS PHE ASN SER ASN PHE LYS PRO SER SER ASN ASP GLY ASP PHE THR PHE SER SER SER HIS ALA GLY ALA
SER SER ALA TYR THR GLY SER GLU SER LEU LEU GLY LEU LEU THR SER ASP ARG PRO THR GLN GLU GLN GLY LYS LYS SER ASP PHE GLU ASN ILE ALA SER ASP GLU LYS ASN MET PHE ARG PHE GLY GLU LYS SER PHE SER PRO GLY PHE THR VAL THR GLY THR GLN ASP PHE THR GLN
LYS ASN PRO LEU VAL PHE GLY GLN SER GLU ASN ILE PHE THR PHE LYS THR PRO GLY LYS SER THR PHE PHE PRO LYS PRO PRO THR PHE GLY THR GLN THR LYS ASP ALA HIS ASN HIS SER VAL GLU SER ASP ALA GLY SER GLU HIS VAL ALA ASP ASP ASP GLY PRO HIS PHE GLU PRO ILE
ILE PRO LEU PRO GLU LYS VAL GLU VAL LYS THR GLY GLU GLU GLU MET PHE CYS ASN ARG ALA LYS LEU PHE ARG PHE ASP ALA GLU GLU GLU GLU ASP GLU LYS GLU ARG GLY ILE GLY ASN VAL LYS ILE LEU ARG HIS ARG LEU SER GLY LYS ILE ARG LEU LEU MET ARG
ARG GLU GLN VAL LEU LYS ILE CYS ALA ASN HIS TYR ILE ASN ALA ASP MET LYS LEU LYS PRO ASN ALA ALA THR SER ASP LYS SER TYR VAL TRP HIS ALA TYR ASP TYR ALA ASP GLU MET PRO LYS PRO GLU GLN LEU ALA ALA ILE ARG PHE LYS THR VAL ASP GLU ALA ALA HIS PHE LYS
ALA LYS PHE GLU GLU ALA GLN ARG LEU LEU ALA MET ALA GLU GLU ALA PRO ALA ILE SER ALA GLN HIS LYS ASN ALA LYS ASP ASN LEU LYS LEU ASP ALA SER LYS VAL LYS GLU ALA PRO LEU PRO PHE GLY SER GLN PHE ILE LEU LYS ARG GLY GLU TRP GLN CYS ASP CYS CYS LEU
ALA THR ASN ALA PRO THR SER THR SER CYS VAL CYS CYS GLN THR PRO ASN LYS ASN SER THR SER SER VAL CYS ILE SER ALA PRO SER PHE THR PHE VAL LYS GLU SER ALA THR ASN ASN LYS LEU ALA PHE GLY GLN GLN LEU LEU LEU LYS ASP LYS ASP GLN TRP THR CYS
SER LYS CYS SER GLN LYS ASN ASP ALA GLY VAL CYS SER GLN ALA LYS ALA GLY ILE SER GLN PRO ASN ILE ALA ALA SER SER GLY PHE THR ASN ASN THR SER ALA GLN GLY ASP ASN LEU ALA ALA VAL PHE GLY LYS LYS ALA GLY GLN TRP ASP
CYS ASP VAL CYS TYR VAL ARG ASN GLU PRO LEU LEU ALA THR LYS CYS ILE SER CYS GLN ASN THR LYS PRO LEU SER LYS VAL SER GLY THR GLN ALA ALA SER PHE SER PHE ALA ALA GLY ALA ASP ASN SER GLN LYS ASN PHE GLY ALA GLN PHE ALA LYS LYS GLU GLY GLN TRP ASP
CYS ASP ALA CYS TYR VAL ARG ASN GLU PRO LEU LEU ALA THR LYS CYS ILE SER CYS GLN ASN THR LYS PRO LEU LEU SER LYS THR THR GLY GLY THR GLN ALA ALA SER PHE SER PHE ALA ALA ASP ASN SER GLN LYS ASN PHE GLY ALA GLN PHE ALA LYS LYS GLU GLY GLN TRP ASP
CYS SER SER CYS LEU VAL ARG ASN GLU ALA SER ALA PRO ASN CYS VAL ALA CYS HIS SER ALA ASN PRO GLN ILE THR ASN LYS ASP VAL VAL PRO PRO ALA LEU THR PRO SER GLY PHE LYS PHE GLY HIS ASN ALA GLU VAL GLY LYS THR GLN GLN SER LEU SER ALA MET PHE SER
CYS LYS GLN GLY GLN TRP GLU CYS SER THR CYS LEU VAL ILE ASN ASP ALA ALA CYS GLN ALA ALA LYS PRO GLY CYS SER SER GLU VAL PRO SER THR PHE GLY ILE LYS ALA ASN SER GLN ASN PHE GLY GLN PRO ALA ILE GLY
PHE ASN CYS GLY PHE SER ALA LYS GLY PHE ALA ASP SER ALA ALA PRO THR PHE LYS ALA THR ASN GLU GLU THR LYS MET VAL LYS ASP GLY PHE ASN PHE PRO VAL SER ALA GLY SER LEU SER PHE LYS PHE GLY ILE SER GLU PRO



- Molecule 12: Nup358

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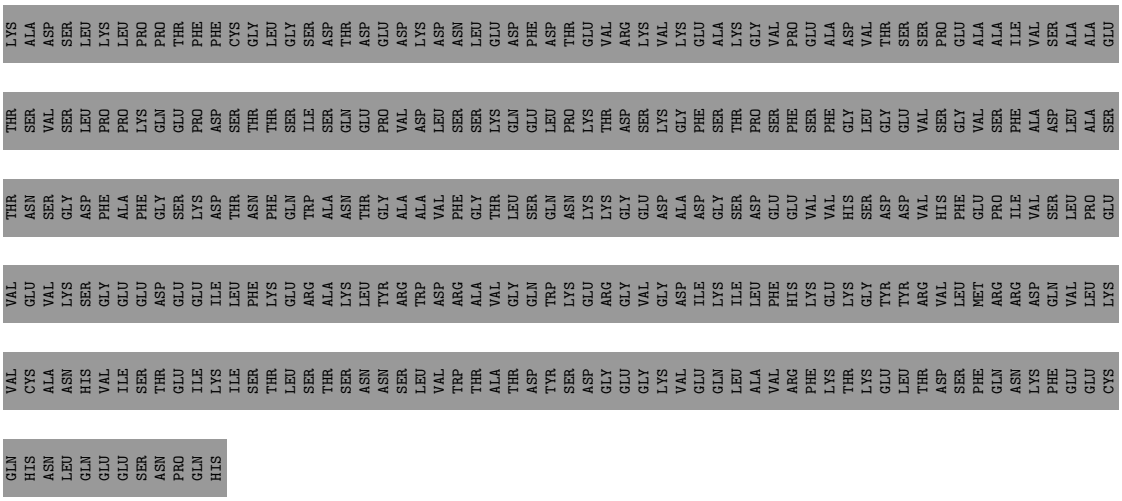
TYR VAL ARG ASN GLU PRO SER ALA ASN LYS CYS ILE SER CYS GLN ASN THR LYS PRO LEU SER LYS VAL SER GLY THR GLN ALA ALA SER PHE SER PHE ALA ALA GLY ALA ASP ASN SER GLN LYS ASN PHE GLY ALA GLN PHE ALA LYS LYS GLU GLY GLN TRP ASP CYS ASP ALA CYS
TYR VAL ARG ASN GLU PRO LEU ALA THR LYS CYS ILE SER CYS GLN ASN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



• Molecule 12: Nup358

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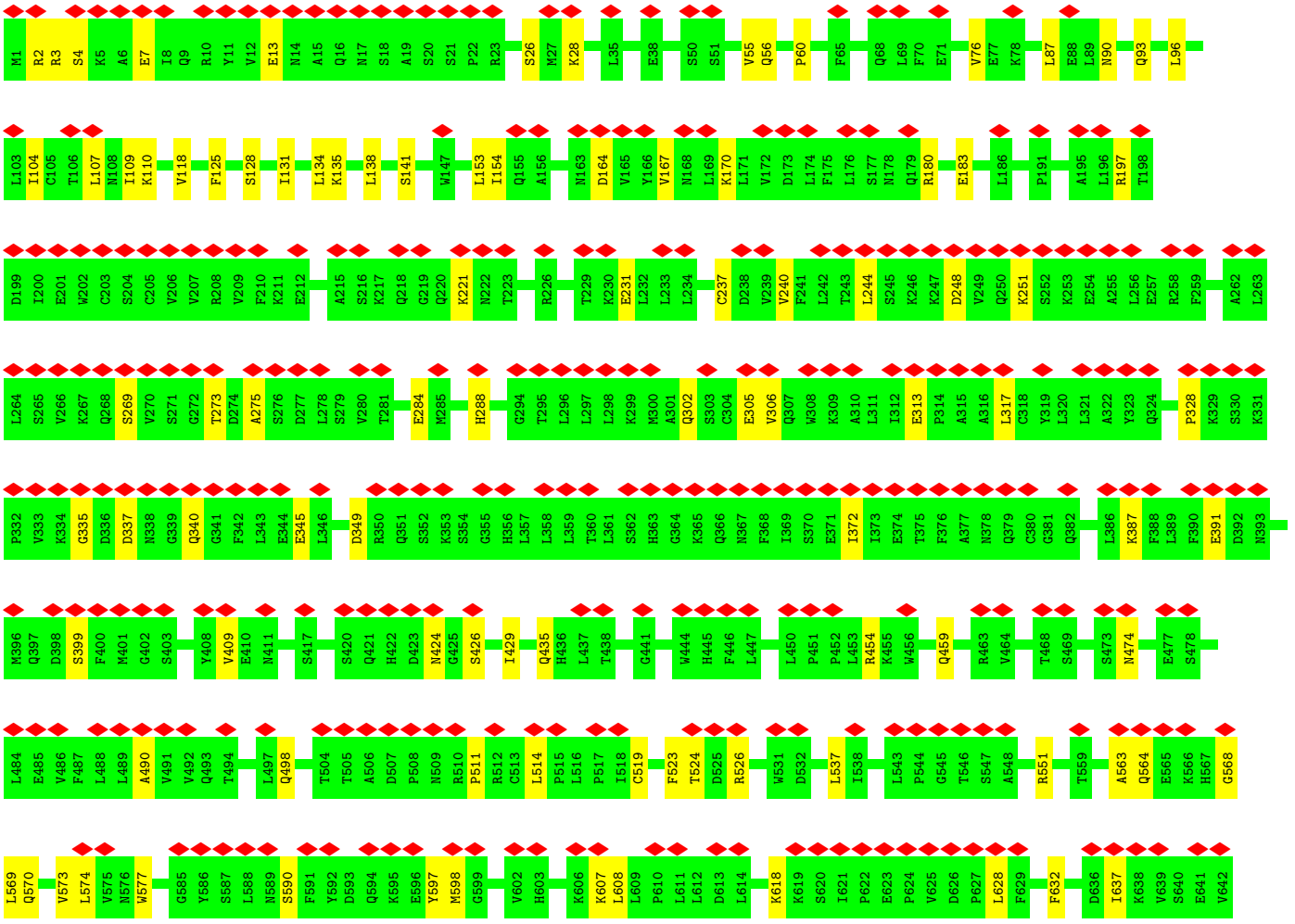

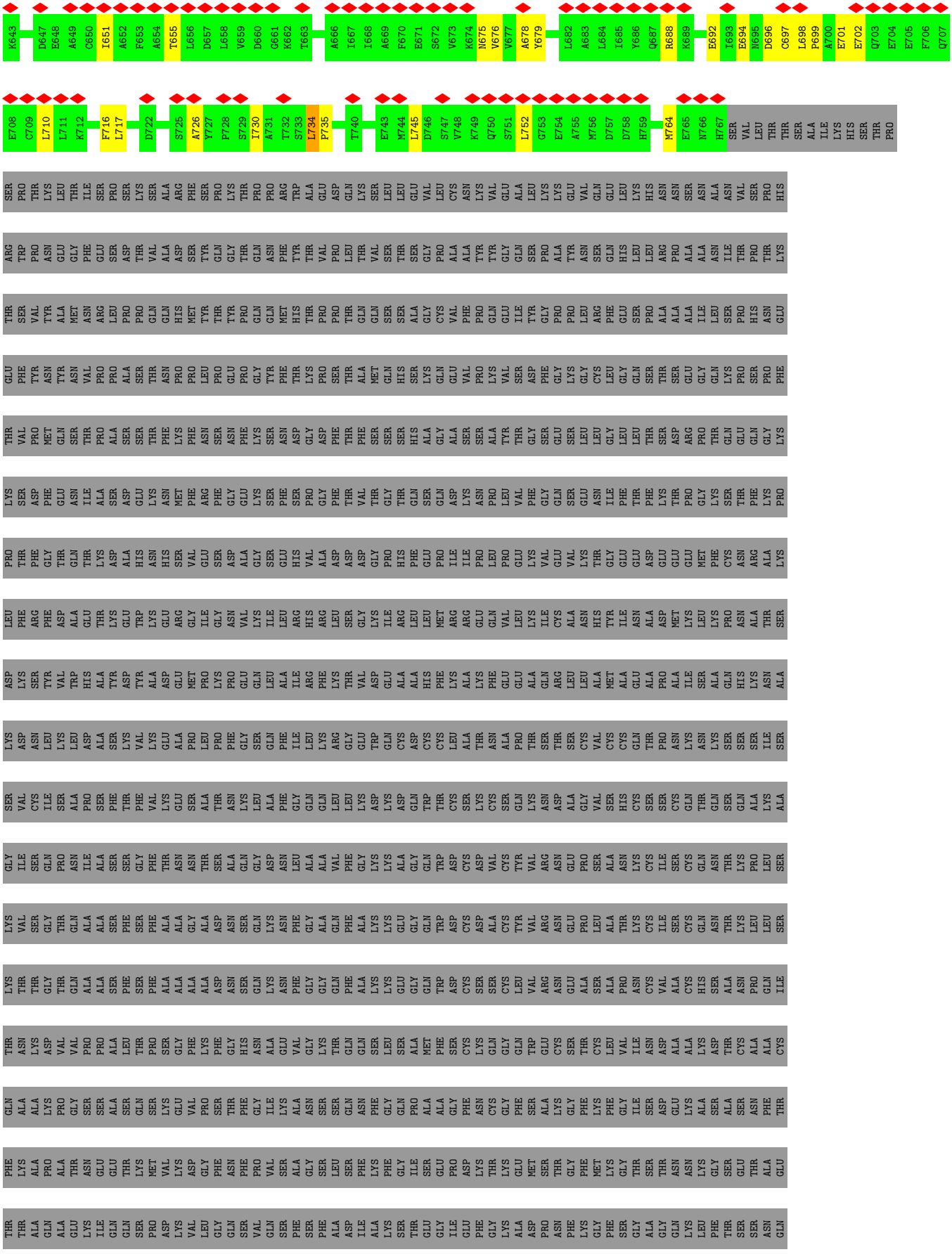
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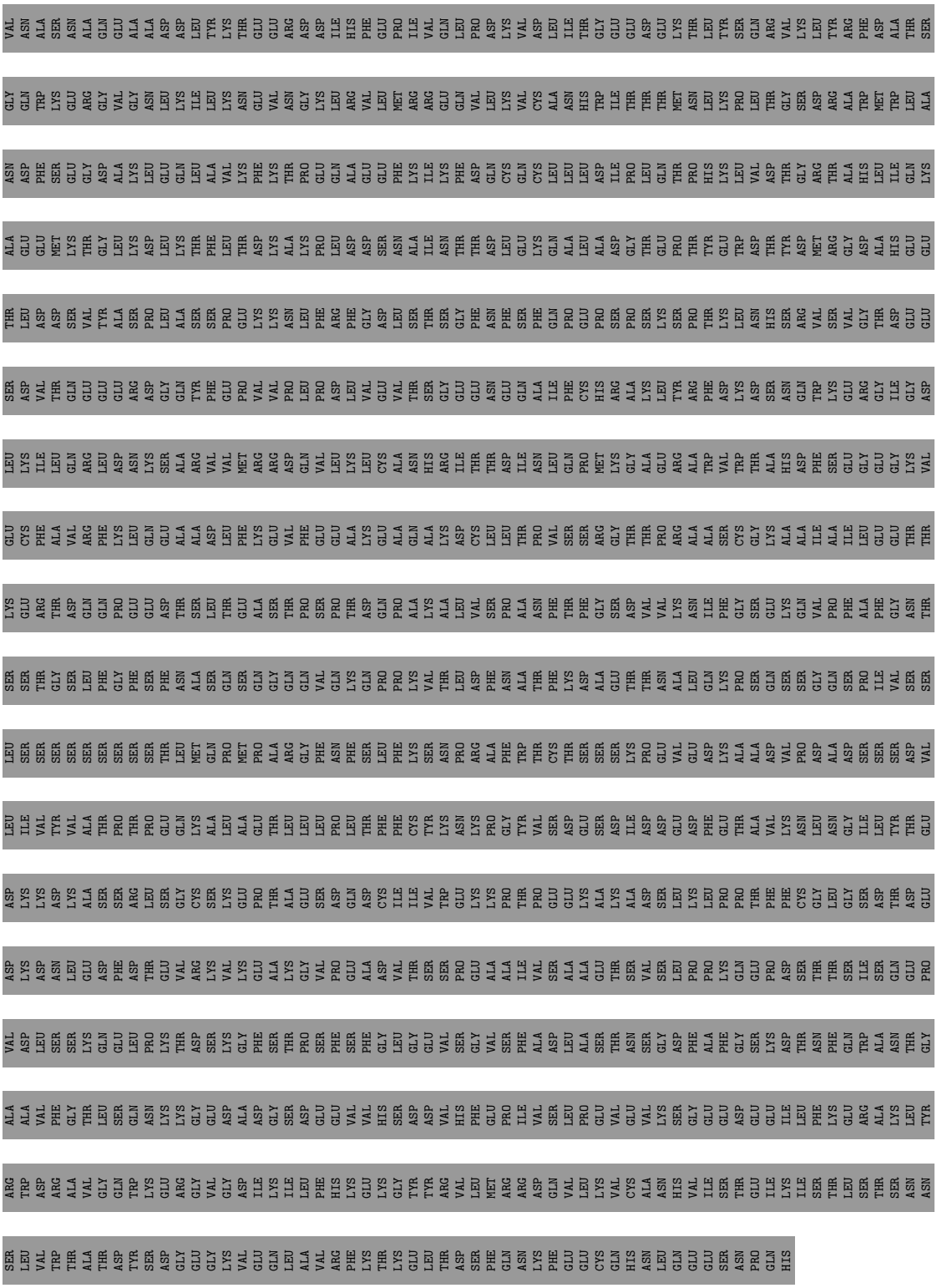
E708 C709 L710 L711 K712 F716 L717 D722 S725 A726 Y727 P728 S729 I730 A731 T732 S733 L734 P735 T740 E743 M744 L745 D746 S747 V748 K749 Q750 S751 L752 G753 E754 A755 M756 D757 D758 H759 M764 E765 N766 H767 SER VAL LEU THR THR SER ALA ILE LYS HIS SER THR PRO



• Molecule 12: Nup358

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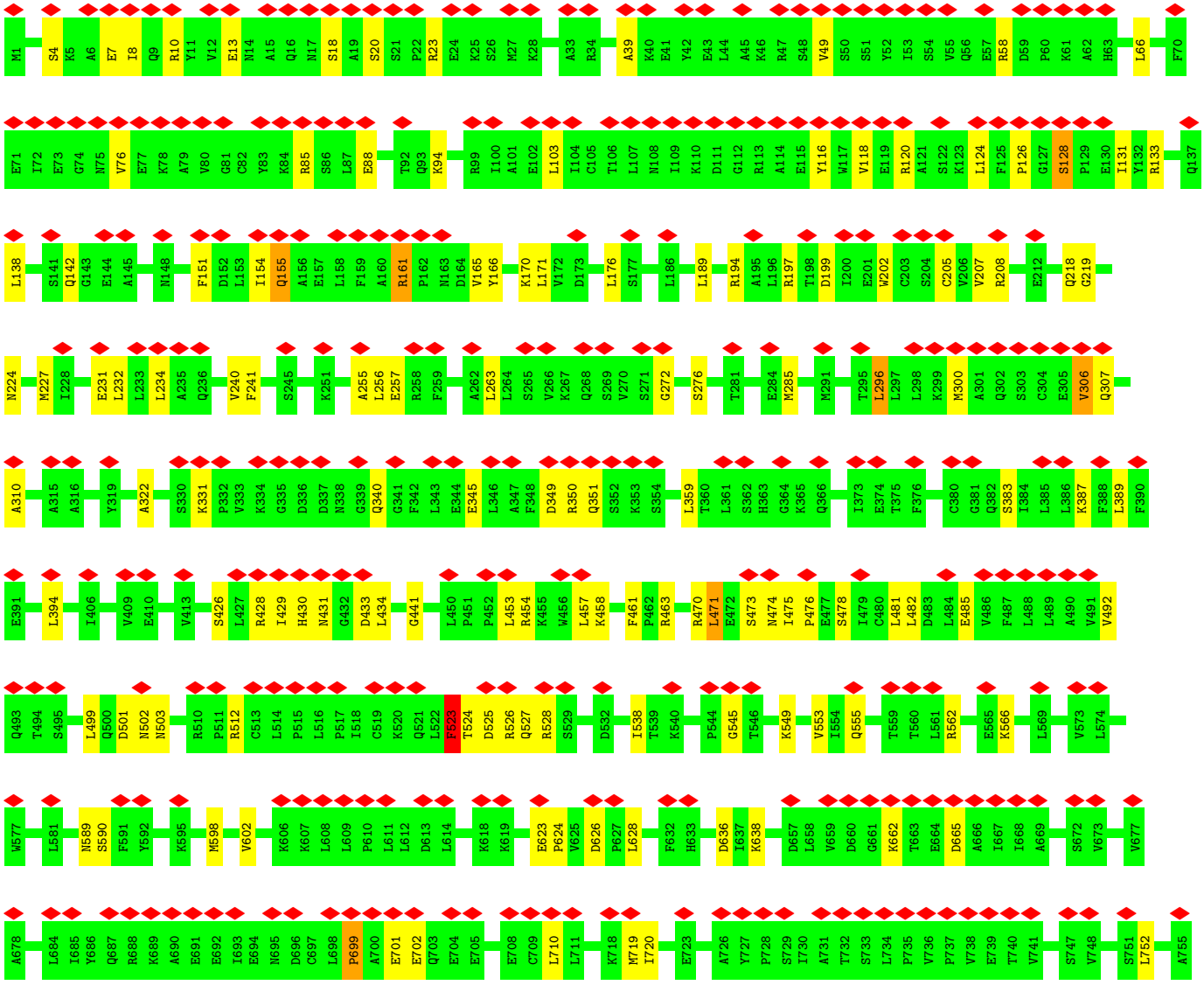
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E71 I72 E73 G74 N75 V76 E77 K78 A79 V80 G81 C82 Y83 K84 R85 S86 L87 E88 T92 Q93 K94 R99 I100 A101 E102 L103 I104 C105 T106 L107 N108 I109 K110 D111 G112 R113 A114 E115 Y116 W117 V118 E119 R120 A121 S122 K123 L124 F125 P126 G127 S128 P129 E130 T131 Y132 R133 Q137
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E391 L394 I406 V409 E410 V413 S426 L427 R428 I429 H430 N431 G432 D433 L434 G441 L450 P451 P452 L453 R454 K455 W456 L457 K458 F461 P462 R463 R470 L471 E472 S473 N474 I475 P476 E477 S478 I479 C480 L481 L482 D483 L484 E485 V486 F487 L488 L489 A490 V491 V492
Q493 T494 S495 L499 Q500 D501 N502 N503 R510 P511 R512 C513 L514 P515 L516 P517 I518 C519 K520 Q521 L522 P523 T524 D525 R526 Q527 R528 S529 D532 I538 T539 K540 P544 G545 T546 K549 V553 I554 Q555 T559 T560 L561 R562 E565 K566 L569 V573 L574
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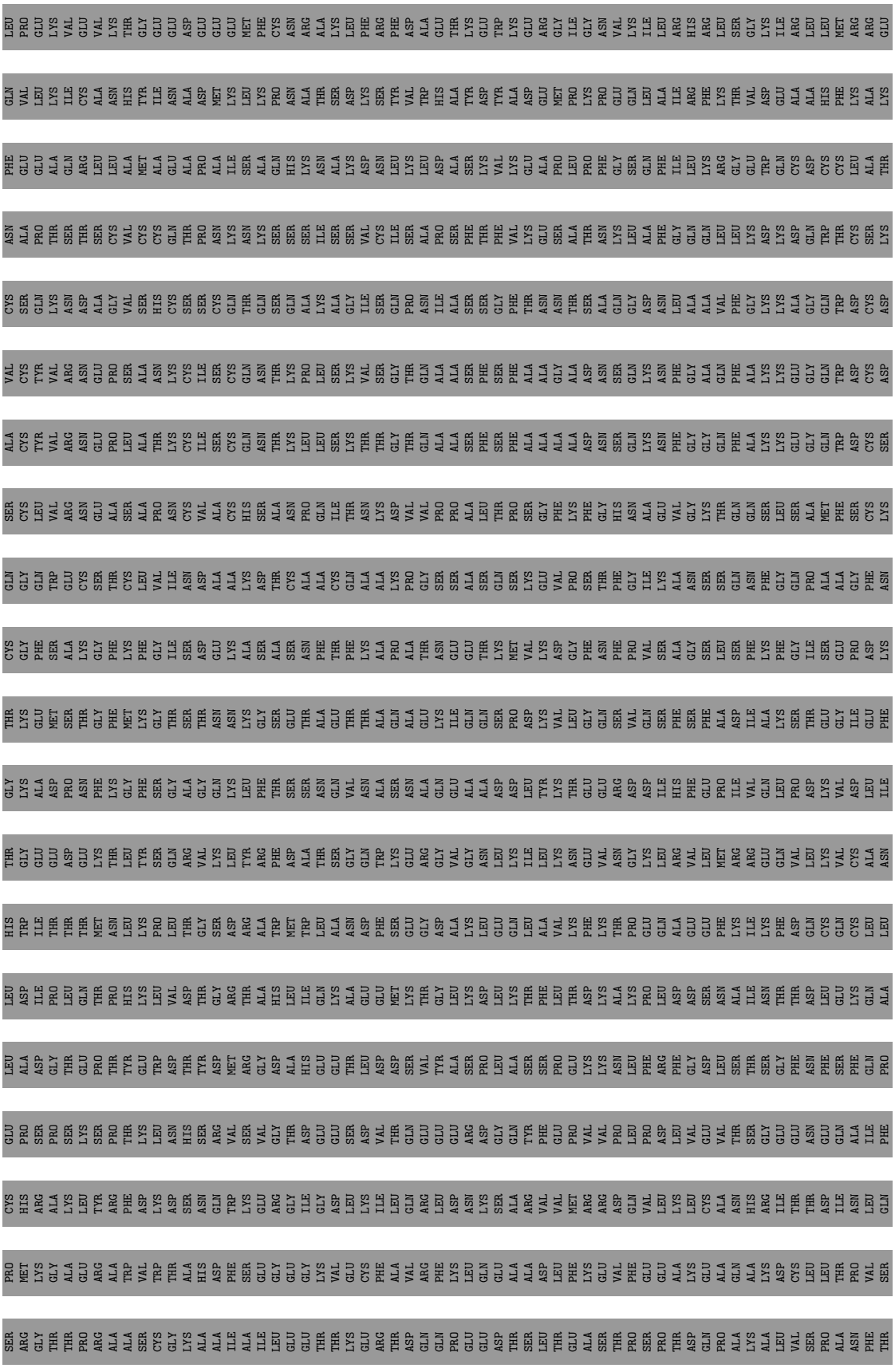
M756 D757 P761 ALA PHE MET GLU ASN HIS SER VAL LEU THR THR SER ALA ILE LYS HIS SER THR PRO HIS PRO SER PRO THR LYS LEU THR ILE SER PRO SER LYS SER ALA ARG PHE SER PRO LYS THR PRO PRO ARG TRP ALA GLU ASP GLN LYS SER LEU LEU GLU VAL LEU CYS ASN LYS
VAL GLU ALA LEU LYS LYS GLU VAL GLN GLU LEU LYS HIS ASN ASN SER ALA ASN ALA ASN VAL SER PRO HIS ARG TRP PRO ASN GLU GLY PHE GLU SER ASP THR VAL ALA ASP SER TYR GLN GLY THR GLN ASN PHE TYR THR VAL PRO LEU THR VAL SER THR SER GLY PRO LEU ALA ALA PHE
TYR GLY GLN SER PRO ALA TYR ASN SER GLN HIS LEU LEU ARG PRO ALA ALA ALA ASN ILE THR PRO THR LYS THR SER VAL TYR ALA MET ASN ARG LEU PRO PRO GLN GLN HIS MET TYR THR TYR PRO GLN GLN MET HIS THR PRO PRO THR GLN GLN SER SER ALA GLY CYS VAL PHE PRO
GLN GLU ILE TYR GLY PRO PRO LEU ARG PHE GLU GLU SER PRO ALA ALA ALA ILE LEU LEU SER PRO HIS ASN GLU GLU PHE TYR ASN TYR ASN VAL PRO PRO ALA SER THR ASN PRO PRO GLU PRO GLY TYR PHE THR LYS PRO SER THR ALA MET GLN HIS SER LYS GLN LEU PRO GLU VAL PRO
LYS VAL SER ASP PHE GLY LYS GLY CYS LEU GLY GLN SER THR SER GLU GLY GLN LYS PRO SER PRO PHE THR VAL PRO MET GLN SER THR PRO ALA SER SER THR PHE LYS PHE ASN SER ASN PHE LYS SER ASN ASP GLY ASP PHE THR PHE THR PHE SER SER SER HIS ALA GLY ALA SER
ALA TYR THR GLY SER GLU SER LEU LEU LEU THR SER ASP ARG PRO THR LYS SER LEU LEU ALA SER ASP GLU LYS ASN MET PHE ARG PHE GLY GLU LYS SER PHE SER PRO GLY GLY PHE THR GLY GLN SER SER ILE LYS GLN GLU GLN GLY LYS LYS SER ASP PHE GLU ASN ILE ALA SER ASP GLU LYS ASN MET PHE ARG PHE GLY GLU LYS SER PHE SER PRO GLY GLY PHE THR VAL THR GLY GLY THR SER GLN ASP GLU VAL
PRO LEU VAL PHE GLY GLN SER GLU ASN ILE PHE THR PHE LYS THR PRO GLY LYS SER THR PHE LYS PRO PRO THR PHE GLY THR GLN THR LYS ASP ALA HIS ASN HIS SER VAL GLU SER ASP ALA GLY SER GLU HIS VAL ALA ASP ASP GLY PRO HIS PHE GLU PRO ILE ILE PRO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GLN VAL LEU LYS ILE CYS ALA ASN HIS TYR ILE ASN ALA ASP MET LYS LEU LYS PRO ASN ALA THR SER ASP LYS SER TYR VAL TRP HIS ALA TYR ASP TYR ALA ASP GLU MET PRO LYS PRO GLU GLN LEU ALA ILE ARG PHE LYS THR VAL ASP GLU ALA ALA HIS PHE LYS ALA
PHE GLU GLU ALA GLN ARG LEU ALA MET ALA GLU ALA PRO ALA ILE SER ALA GLN HIS LYS ASN SER ALA LYS ASP ASN LEU LYS LEU ASP ALA SER GLU LYS VAL LYS GLU ALA PRO LEU PRO PHE GLY SER GLN PHE ILE LEU LYS ARG GLY GLU TRP GLN CYS ASP CYS CYS LEU LEU ALA THR
ASN ALA PRO THR SER THR SER CYS VAL CYS CYS GLN THR PRO ASN LYS ASN LYS SER SER SER ILE SER ALA PRO ALA SER VAL CYS ILE SER ALA PRO ASN ILE ALA PHE THR PHE VAL LYS GLU SER ALA THR ASN LYS LEU ALA PHE GLY GLN GLN LEU LEU LYS ASP LYS ASP GLN TRP THR CYS SER LYS
CYS SER GLN LYS ASN ASP ALA GLY VAL PRO ASP SER CYS GLN THR GLN SER GLN PRO ASN ILE ALA SER SER GLY ASN ALA ALA VAL PHE GLY GLY ASP ASP CYS CYS ASP
VAL CYS TYR VAL ARG ASN GLU PRO SER ALA ASN LYS CYS ILE SER CYS GLN ASN THR LYS PRO LEU SER CYS GLN THR GLN ALA ALA SER SER GLY THR GLN ALA ALA SER PHE SER GLY PHE THR ASN ASN SER GLN LYS ASN PHE GLY ALA GLN PHE ALA LYS LYS GLU GLY GLN TRP ASP CYS ASP
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SER CYS LEU VAL ARG ASN GLU ALA SER ALA PRO ASN CYS VAL ALA CYS HIS SER ALA ASN PRO GLN ILE THR ASN LYS ASP VAL VAL PRO PRO ALA LEU THR PRO SER GLY PHE LYS PHE GLY HIS ASN ALA GLU VAL GLY LYS THR GLN GLN GLN SER LEU SER ALA MET PHE SER CYS LYS
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CYS GLY GLY PHE SER ALA LYS GLY PHE GLY ILE SER ASP GLU LYS ALA SER ALA SER ASN PHE THR PHE LYS ALA PRO ALA THR ASN GLU GLU THR LYS MET VAL LYS ASP GLY PHE ASN PHE PRO VAL SER ALA GLY GLY SER LEU SER PHE LYS PHE GLY ILE SER GLU PRO ASP LYS
THR LYS GLU MET SER THR GLY PHE MET LYS GLY THR SER THR ASN ASN LYS GLY SER GLU THR ALA GLU THR THR ALA GLN ALA GLU ALA GLU LYS ILE GLN GLN SER PRO ASP LYS VAL LEU GLY GLN SER VAL GLN SER PHE SER PHE SER ALA ASP GLU ILE GLU PHE
GLY LYS ALA ASP PRO ASN PHE LYS GLY PHE SER GLY ALA GLY GLN LYS LEU PHE THR SER SER ASN GLN VAL ASN ALA SER ASN ALA GLN GLU GLU ALA ASP PHE TYR ARG ASP ASP ILE HIS PHE GLU PRO ILE VAL GLN LEU PRO ASP LYS LEU ILE
THR GLY GLU GLU ASP GLU THR LEU TYR SER GLN ARG VAL LYS LEU TYR ARG PHE ASP ALA THR SER GLY GLN TRP LYS GLU GLY GLY VAL GLY ASN LEU LYS GLU ARG GLY VAL ASN GLY LYS LEU ARG VAL GLU PHE ASP ALA ASN
HIS TRP ILE THR THR MET ASN LEU LYS PRO LEU THR GLY ASP ALA ASN ASP PHE SER GLU GLY ASP ALA LYS LEU GLU GLN LEU ALA ASP ALA VAL LYS PHE LYS THR PRO GLU GLN GLN ALA ASP GLU GLU PHE LYS ILE ARG VAL GLU PHE ASP GLN CYS GLN CYS ALA LEU LEU
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LEU ALA ASP GLY THR PRO THR TYR ASP SER VAL TYR ALA SER PRO LEU ALA SER SER PRO GLU PRO LEU ASP LYS ALA ASN LEU PHE ARG PHE GLY ASP SER THR SER GLY PHE ASN PHE GLU PRO
GLU PRO SER PRO SER LYS LEU ASN HIS SER ARG VAL SER VAL GLY THR ASP GLU GLU SER ASP VAL THR GLN GLU GLU GLU GLU ARG ASP GLY GLN TYR PHE GLU PRO VAL VAL PRO LEU PRO ASP LEU VAL GLU VAL GLU PRO ALA ILE PHE
CYS HIS ARG ALA LYS LEU TYR ARG PHE ASP LYS ILE LEU GLN ARG LEU ASP ASN LYS SER ALA ARG VAL VAL MET ARG ARG ASP GLN VAL LEU CYS ALA ASN HIS ARG ILE THR THR ASP ILE ASN LEU GLN
PRO MET LYS GLY ALA GLU VAL ARG PHE LYS LEU GLN GLU GLU ALA ALA ASP LEU PHE LYS GLU VAL PHE GLU GLU ALA GLN ALA LYS ASP CYS LEU LEU LEU THR ALA SER
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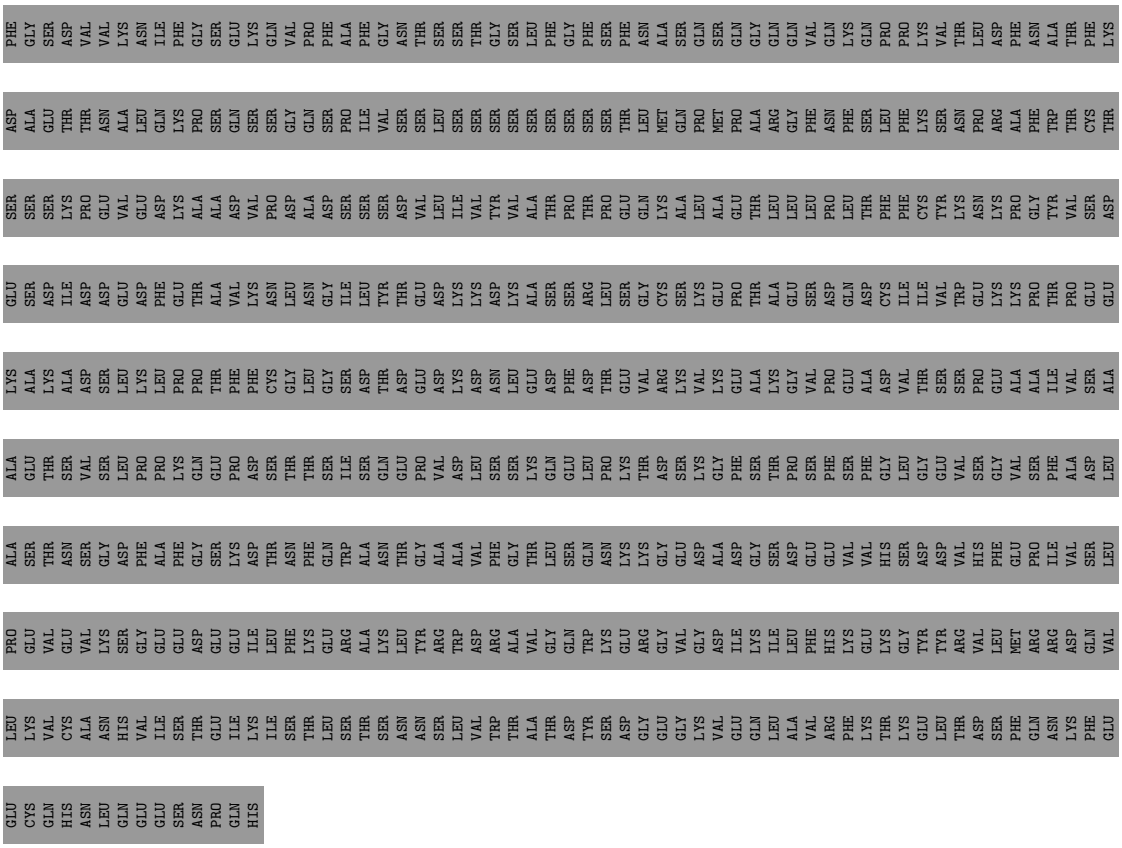

• Molecule 12: Nup358

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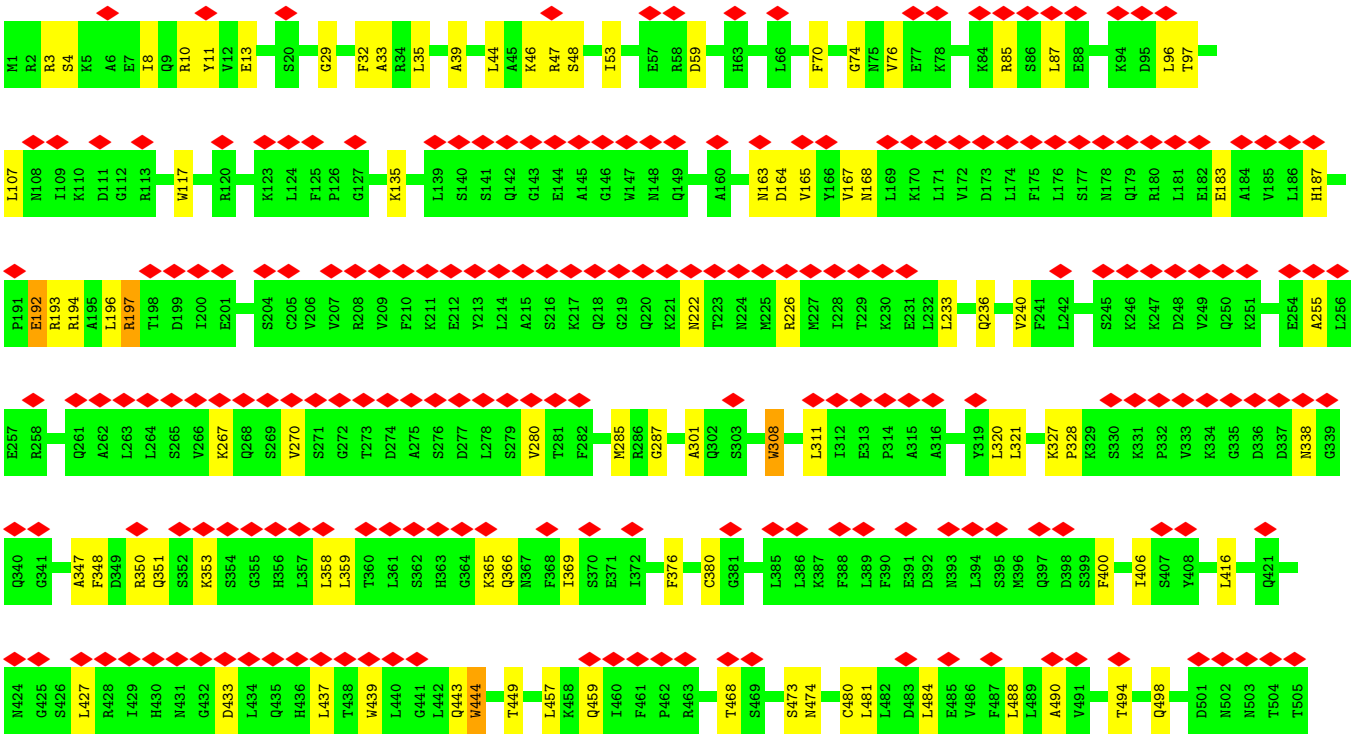

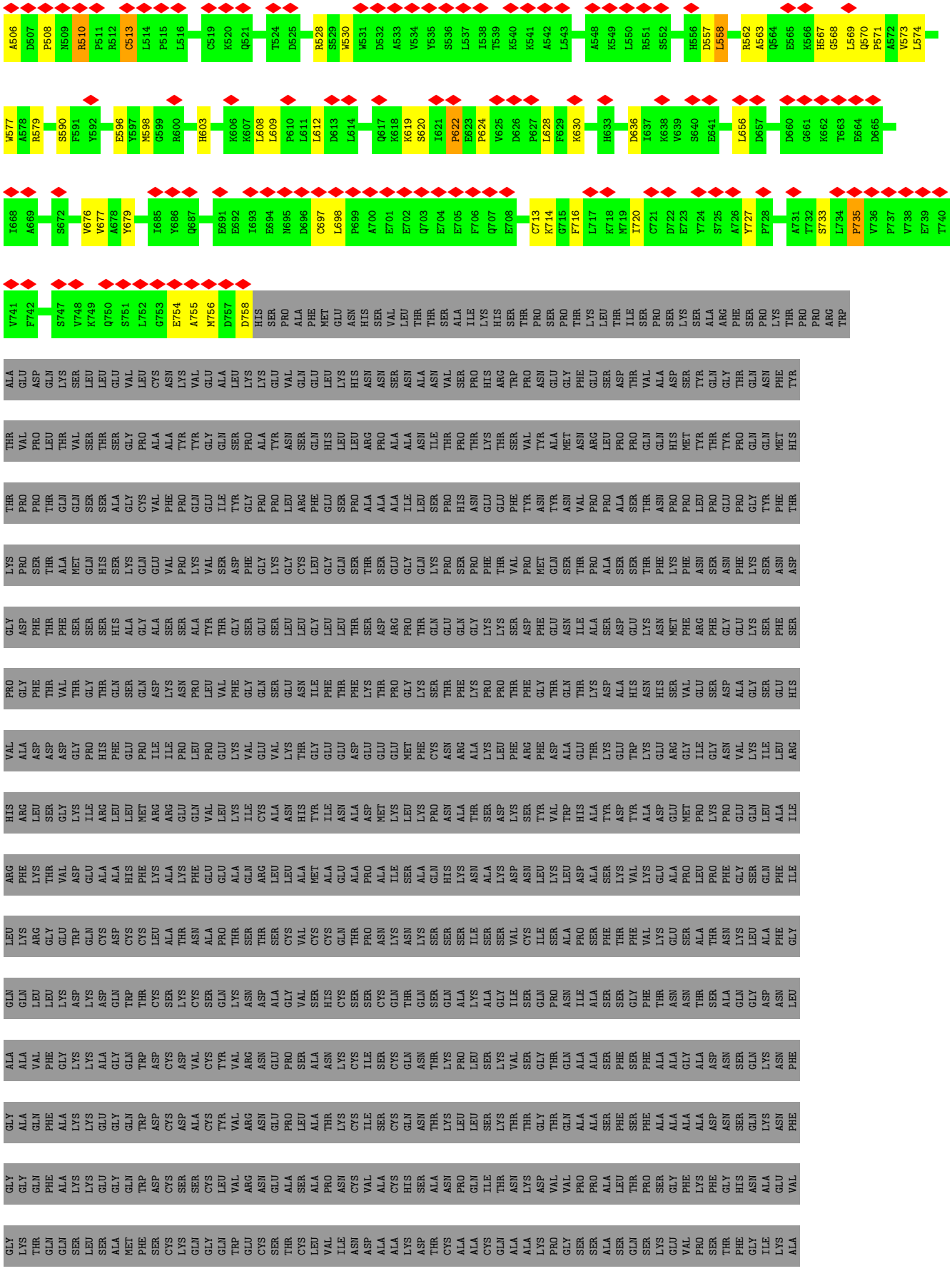
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V741 F742 S747 V748 K749 Q750 S751 L752 G753 E754 A755 M756 D757 D758 HIS SER PRO ALA PHE MET GLU GLN HIS SER VAL LEU THR THR SER ALA ILE LYS HIS SER THR PRO SER PRO THR LYS LEU THR ILE SER PRO SER LYS SER ALA ARG PHE SER PRO PRO THR PRO PRO ARG TRP
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THR PRO PRO THR GLN GLN SER SER ALA GLY CYS VAL PHE PRO GLN GLU ILE TYR GLY PRO PRO LEU ARG PHE GLU SER PRO ALA ALA ALA ILE LEU SER PRO HIS ASN GLU GLU PHE TYR ASN TYR ASN VAL PRO PRO ALA SER THR ASN PRO PRO LEU PRO GLU PRO GLY TYR PHE THR
LYS PRO SER THR ALA MET GLN HIS SER LYS GLN GLU VAL PRO LYS VAL SER ASP PHE GLY LYS GLY CYS LEU GLY GLN SER THR SER GLU GLY GLN LYS PRO SER PRO PHE THR VAL PRO MET GLN SER THR PRO ALA SER SER SER THR PHE LYS PHE ASN SER ASN PHE LYS SER ASN ASP
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PRO GLY PHE THR VAL THR GLY THR GLN SER GLN ASP LYS ASN PRO LEU PRO GLU VAL LEU VAL PHE GLY GLN SER GLU ASN ILE PHE THR PHE LYS SER THR PHE LYS PRO PRO THR PHE GLY THR GLN THR LYS ASP ALA HIS ASN HIS SER VAL GLU SER ASP ALA GLY GLU HIS
VAL ALA ASP ASP ASP GLY PRO HIS PHE GLU PRO ILE ILE PRO LEU PRO GLU GLU LYS VAL GLU VAL LYS THR GLY GLU GLU GLU GLU MET PHE CYS ASN ARG ALA LYS LEU PHE ARG PHE ASP ALA GLU GLU THR LYS GLU TRP LYS GLU ARG GLY ILE GLY ASN VAL LYS LEU ILE LEU ARG
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ARG PHE LYS THR VAL ASP HIS PHE LYS ALA LYS PHE GLU GLU ALA GLN ARG LEU LEU ALA MET ALA GLU GLU ALA PRO ALA ILE SER ALA GLN HIS LYS ASN ALA LYS ASP ASN LEU LYS LEU ASP ALA SER LYS VAL LYS GLU ALA PRO LEU PRO PHE GLY SER GLN LEU ILE PHE
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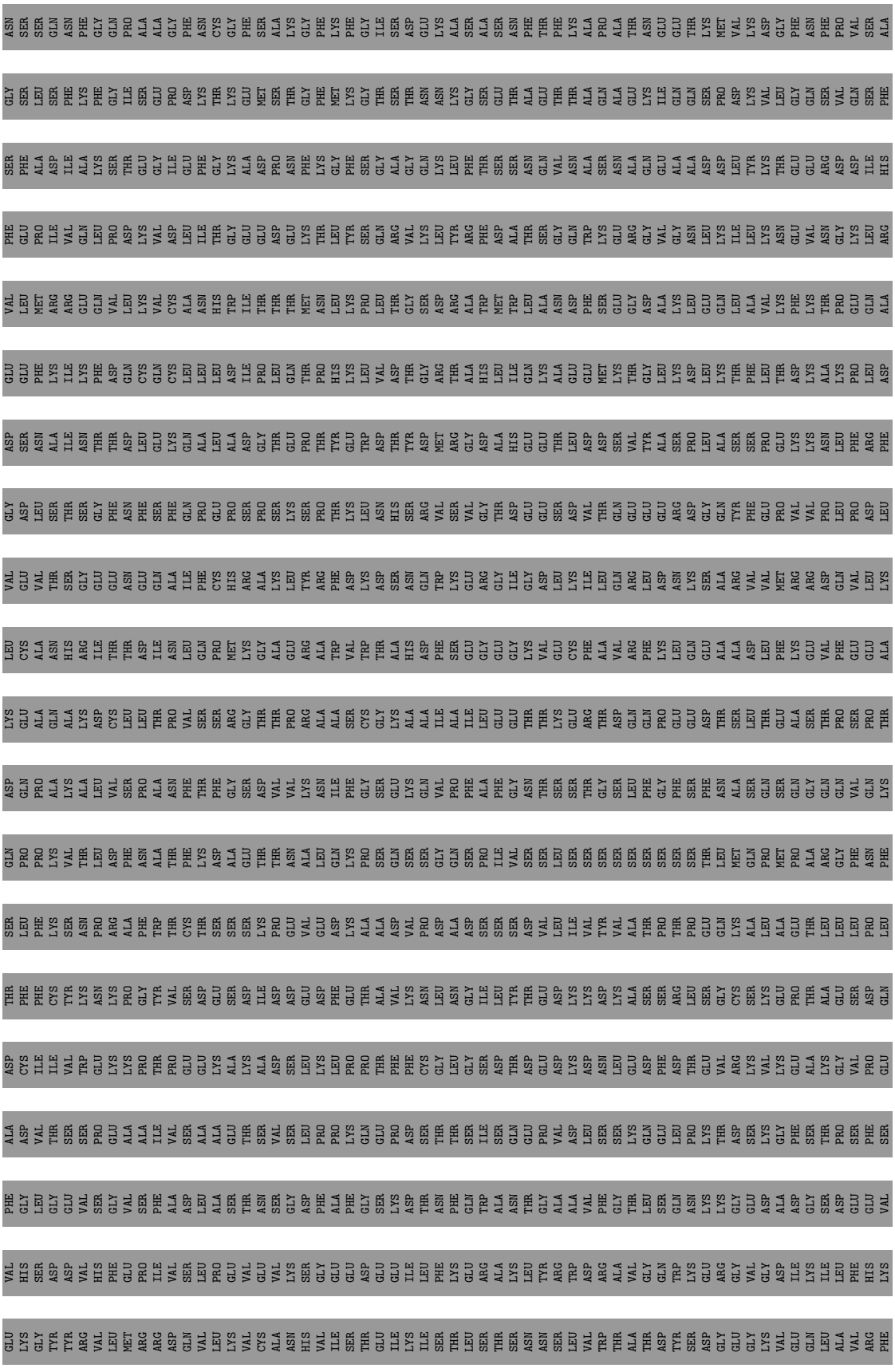
GLY ALA GLN PHE ALA LYS LYS GLU GLY GLN TRP ASP CYS ASP ALA CYS TYR VAL ARG ASN GLU PRO LEU ALA THR LYS CYS ILE SER CYS GLN ASN THR LYS LEU LEU SER LYS THR THR GLY THR GLN ALA ALA ALA SER PHE SER PHE ALA ALA ALA ALA ASP ASN SER GLN LYS ASN PHE
GLY GLY GLN PHE ALA LYS LYS GLU GLY GLN TRP ASP CYS SER ALA CYS TYR LEU VAL ARG ASN GLU ALA SER ALA ALA CYS HIS SER ASN GLU ALA ASN SER ALA LEU THR PRO SER ALA PHE ASN SER GLY LYS PHE LYS PHE GLY HIS ASN ALA GLU VAL
GLY LYS THR GLN SER LEU SER ALA MET PHE SER CYS LYS GLN GLY GLN TRP GLU CYS SER CYS GLN LEU VAL ILE ASN ASP THR CYS ALA ALA ALA LYS ASP THR CYS GLN ALA ALA LYS PRO GLY SER SER ALA SER GLN SER LYS GLU VAL PRO SER THR PHE GLY ILE LYS VAL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GLY SER LEU SER PHE LYS PHE GLY ILE SER GLU PRO ASP LYS THR LYS GLU MET SER THR GLY PHE MET LYS GLY THR SER THR ASN ASN LYS GLY SER GLU THR ALA GLU THR THR ALA GLN ALA GLU LYS ILE GLN GLN SER PRO ASP LYS VAL LEU GLY GLN SER VAL SER PHE
SER PHE ALA ASP ILE ALA LYS SER THR GLU GLY ILE GLU PHE GLY LYS ALA ASP PRO ASN PHE LYS GLY PHE SER GLY ALA GLN LYS LEU PHE THR SER SER ASN GLN VAL ASN ALA SER ASN ALA GLN GLU LYS ILE GLN GLN ALA ALA ASP ASP LEU TYR LYS THR GLU GLU ARG ASP PRO ASP ASP ILE HIS
PHE GLU PRO ILE VAL GLN LEU PRO ASP LYS VAL ASP LEU ILE THR GLY GLU GLU ASP GLU LYS THR LEU TYR SER GLN ARG VAL LYS LEU TYR ARG PHE ASP ALA THR SER GLN TRP LYS GLU ARG GLY VAL GLY ASN LEU LYS ILE LEU LEU LYS ASN GLU VAL ASN GLY LYS LEU ARG
VAL LEU MET ARG ARG GLU GLN VAL LEU LYS VAL CYS GLN LEU LEU ALA ASN HIS TRP ILE THR THR THR MET ASN LEU LYS PRO LEU THR GLY LEU TYR GLU ASP ARG ALA TRP MET TRP LEU ALA ASN ASP PHE SER GLU GLY ASP ALA LYS LEU GLU GLN LEU GLU ASP ALA
GLU GLU PHE LYS ILE LYS PHE ASP GLN CYS GLN CYS LEU LEU LEU ASP ILE PRO LEU GLN THR HIS LYS LEU VAL ASP THR GLY ARG THR ALA HIS LEU ILE GLN LYS ALA GLU GLU MET LYS THR GLY LEU LYS ASP LEU LYS THR PHE LEU THR ASP LYS ALA LYS PRO LEU ASP
ASP SER ASN ALA ILE ASN THR THR ASP LEU GLU LYS GLN ALA LEU ALA ASP GLY THR GLU PRO THR TYR GLU TRP ASP THR TYR ASP MET ARG GLY ASP ALA ALA HIS GLU GLU THR LEU ASP ASP SER VAL TYR ALA SER PRO LEU ALA SER PRO GLU LYS LYS ASN LEU PHE ARG PHE
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LEU CYS ALA ASN HIS ARG ILE THR THR ASP ILE ASN LEU GLN PRO MET LYS GLY ALA GLU ARG ALA TRP VAL TRP THR HIS ASP PHE SER GLU GLN GLU ALA ALA ASP ASP PHE LYS LEU GLN GLU ALA ASP LEU PHE LYS GLU VAL PHE GLU GLU ALA
LYS GLU ALA GLN ALA LYS ASP CYS LEU LEU THR PRO VAL SER SER ARG GLY THR THR PRO ARG ALA ALA SER CYS GLY LYS ALA ILE ALA ILE GLU GLU GLY GLU THR LYS GLU ARG THR ASP GLN GLN PRO GLU GLU ASP THR SER ALA LEU THR GLU ALA SER THR PRO PRO THR
ASP GLN PRO ALA LYS ALA LEU VAL SER PRO ALA ASN PHE THR PHE LYS ASP GLY SER ASP VAL LYS ASN ILE PHE GLY SER GLU LYS GLN VAL PRO PHE ALA PHE GLY GLN GLU ALA ASP SER GLN SER SER SER THR GLY SER LEU PHE GLY PHE SER PHE ASN ALA SER GLN SER GLY GLN GLY LYS VAL LEU PHE
GLN PRO PRO LYS VAL THR LEU ASP PHE ASN ALA THR PHE PHE LYS ASP ALA GLU GLN LYS PRO SER GLN SER SER GLY GLN SER PRO ILE VAL SER SER LEU SER SER SER SER SER SER SER SER SER THR LEU MET GLN PRO MET PRO ALA ARG GLY PHE ASN PHE
SER LEU PHE LYS SER ASN PRO ASP ALA ARG ALA ALA ASP VAL PRO ASP ALA ASP SER VAL LEU ILE VAL TYR VAL ALA THR PRO THR PRO GLU GLN LYS ALA LEU ALA THR GLU THR LEU SER PRO GLU LEU PRO LEU
THR PHE PHE CYS TYR LYS ASN PRO GLY TYR VAL SER ASP GLU ASP PHE GLU THR ALA VAL LYS ASN LEU ASN GLY ILE LEU TYR THR GLU ASP LYS LYS ASP LYS ALA SER SER ARG LEU SER GLY CYS SER LYS GLU PRO THR LEU ALA GLN ASP
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ALA ASP VAL THR SER ALA ALA GLU THR SER VAL SER LEU PRO PRO LYS GLN GLU PRO VAL ASP LEU SER SER LYS GLN GLU LEU PRO GLU SER LYS GLY PHE SER THR PRO SER PHE SER
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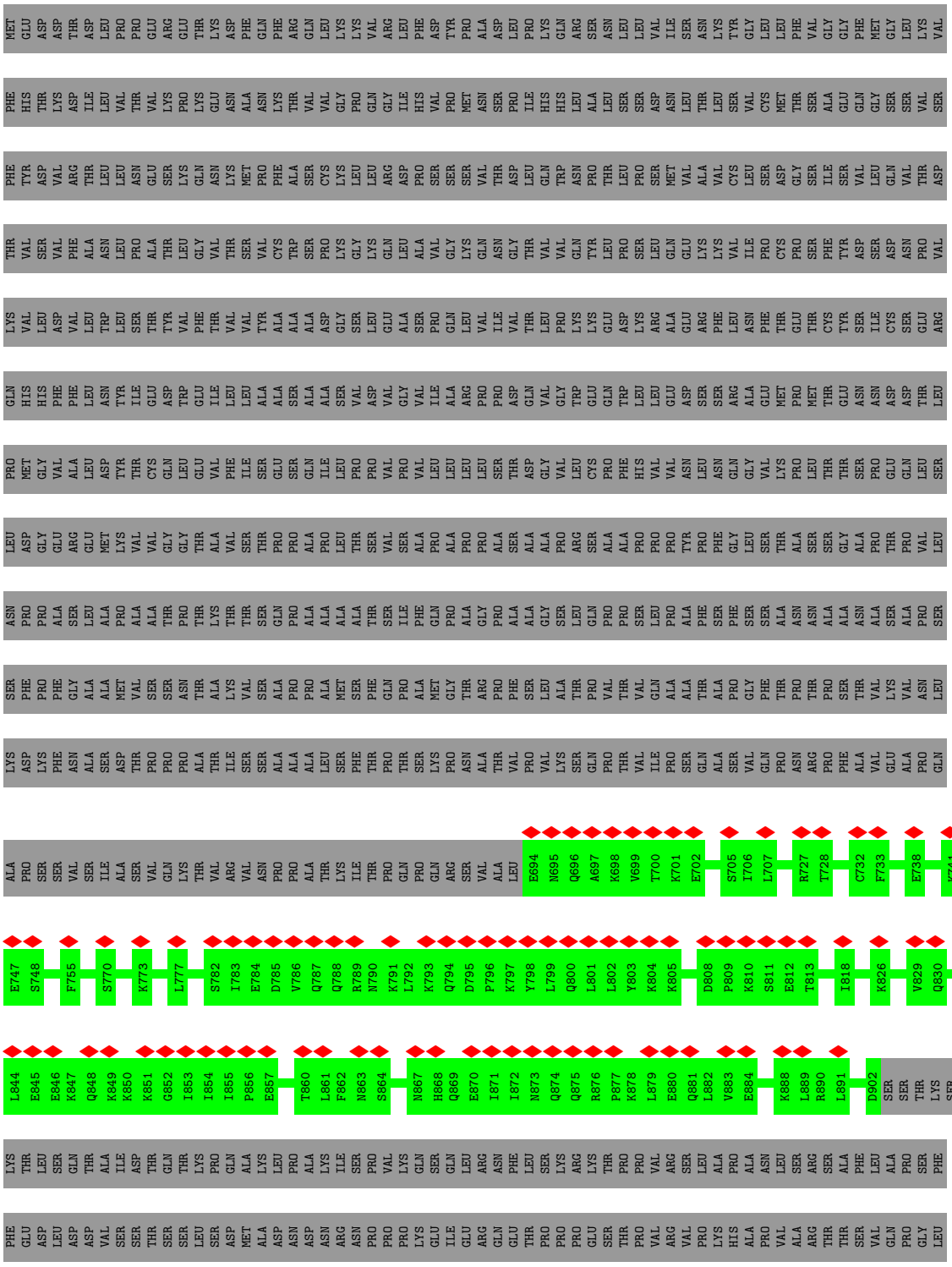
VAL HIS SER ASP VAL PRO ILE VAL GLU VAL LYS SER GLY GLU GLU ASP GLU ARG ALA LYS LEU TYR ARG TRP ASP ARG ALA VAL GLY GLN TRP LYS GLU ARG GLY VAL GLY ASP ILE LYS ILE LEU PHE HIS LYS
GLU LYS GLY TYR TYR ARG VAL LEU MET ARG ASP GLN VAL LEU PRO GLU LYS VAL CYS ALA ASN HIS VAL ILE SER THR GLU ILE LYS ILE SER THR LEU SER ASN ASN SER LEU VAL TRP THR ALA THR ASP TYR SER ASP GLY GLU GLY LYS VAL GLU GLN LEU ALA VAL ARG PHE

• Molecule 13: Nucleoporin CAN



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

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

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

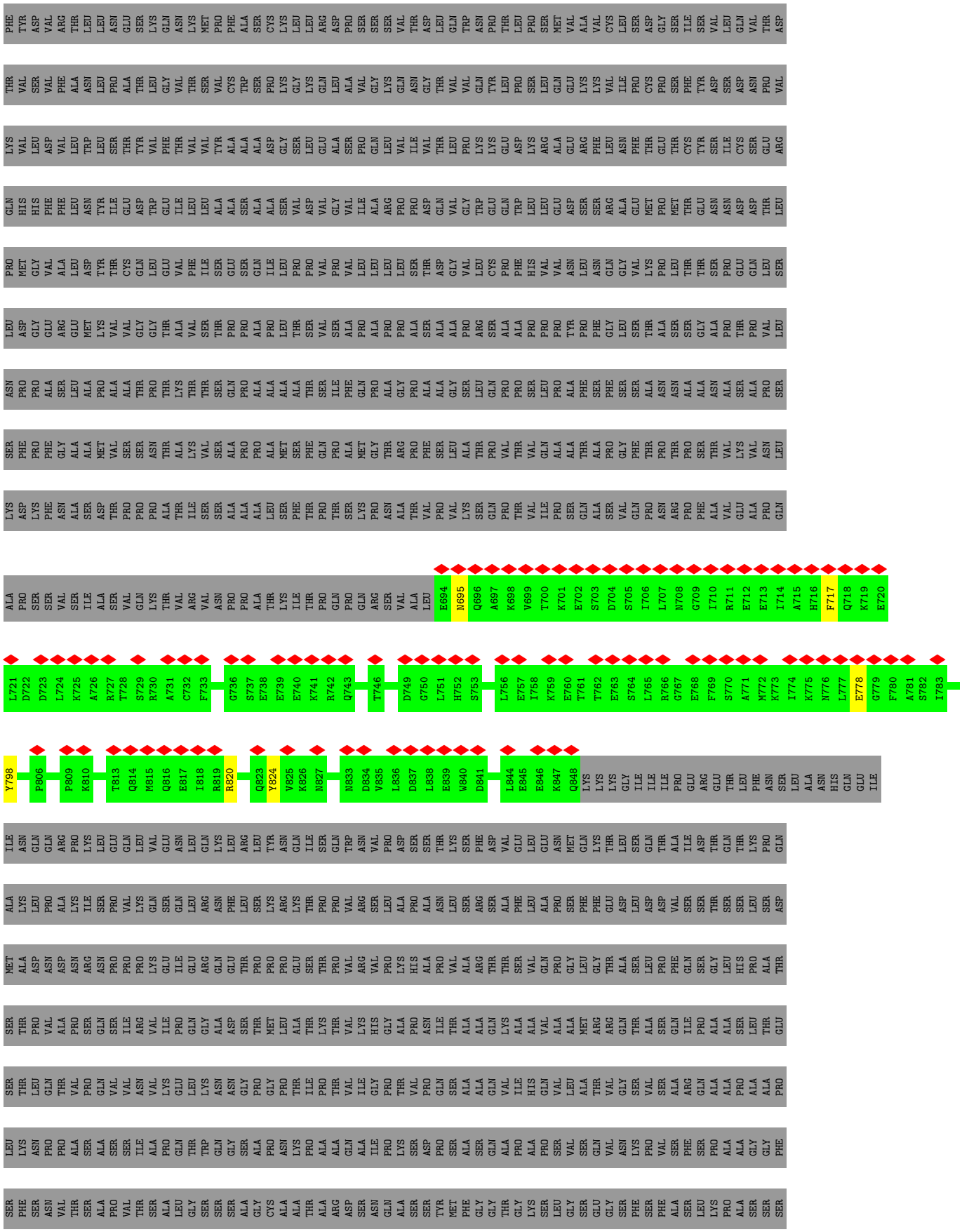
GLY GLY GLN SER SER GLY PHE GLY ALA ALA ALA GLY ASN THR GLY GLY PHE GLY PHE GLY VAL SER ASN PRO THR SER PRO GLY PHE GLY CYS TRP ARG SER

• Molecule 13: Nucleoporin CAN

Chain e: 5% 7% 92%

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

PHE HIS THR LYS ASP ILE LEU VAL THR VAL LYS PRO LYS GLU ASN ALA ASN LYS THR VAL VAL GLY PRO GLN GLY ILE HIS VAL PRO MET ASN SER PRO ILE HIS HIS LEU ALA LEU SER SER ASP ASN LEU THR LEU SER VAL CYS MET THR SER ALA GLU GLN GLY SER SER VAL SER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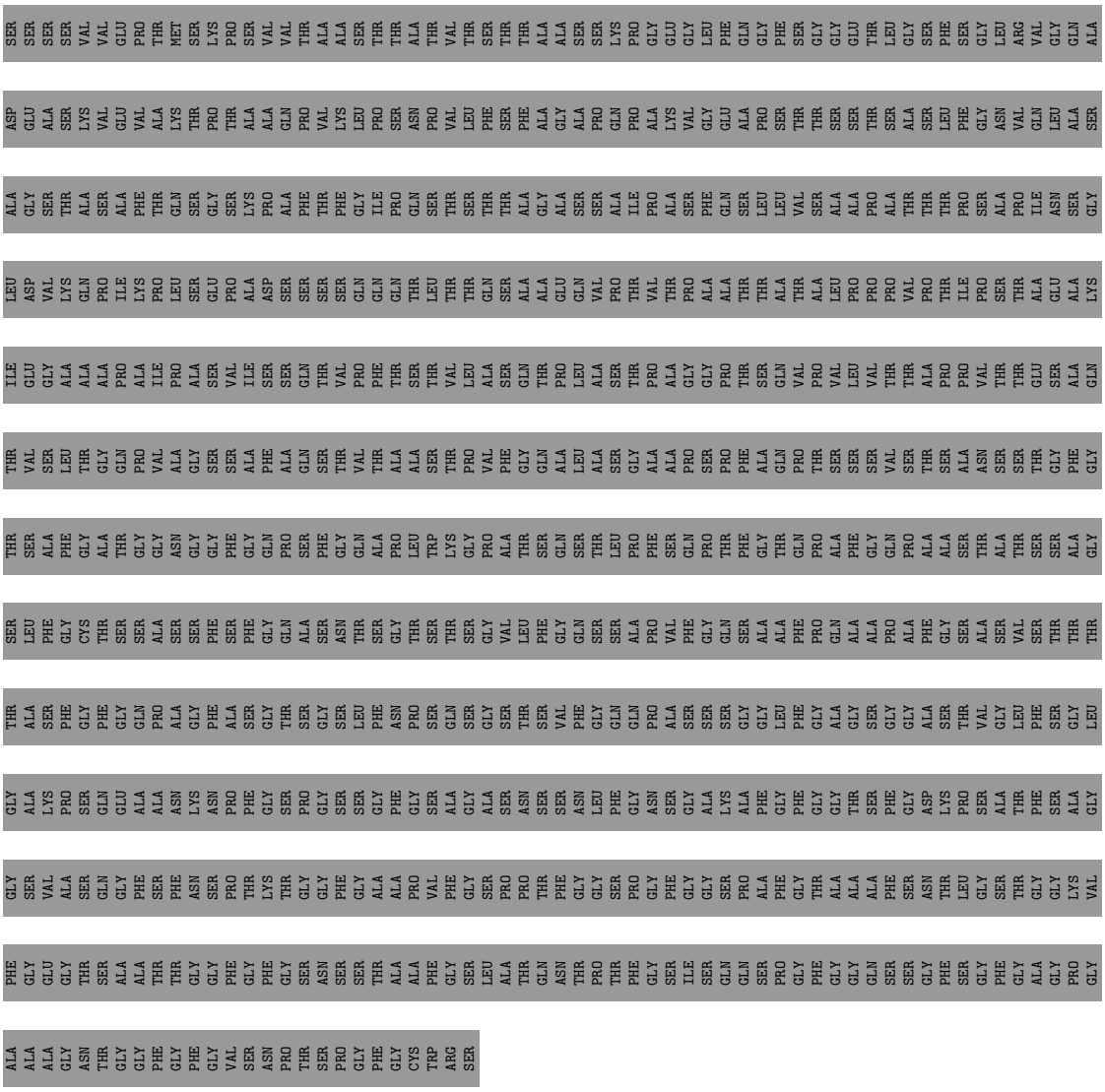
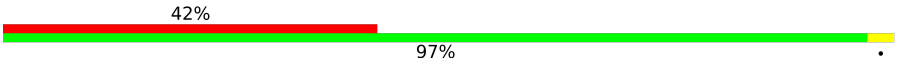
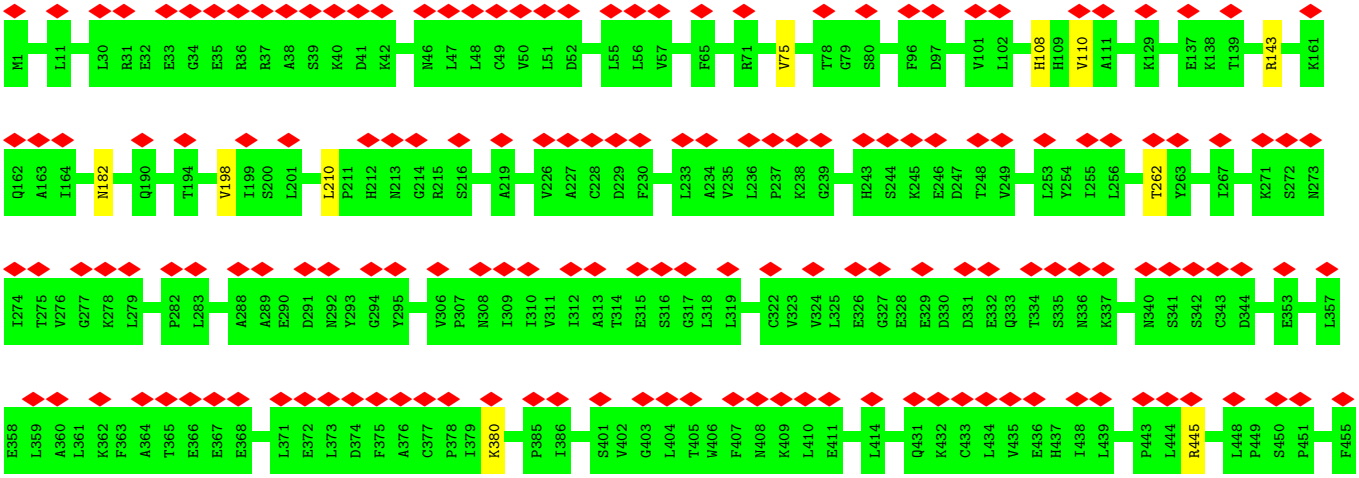
L721 D722 D723 L724 K725 A726 R727 T728 S729 R730 A731 C732 F733 G736 S737 E738 E739 E740 K741 R742 Q743 T746 D749 G750 L751 H752 S753 L756 E757 I758 K759 E760 T761 T762 E763 S764 L765 R766 G767 E768 F769 S770 A771 M772 K773 I774 K775 N776 L777 E778 G779 F780 A781 S782 I783
Y798 P806 P809 K810 T813 Q814 M815 Q816 E817 I818 R819 R820 Q823 Y824 V825 K826 N827 N833 D834 V835 L836 D837 L838 E839 W840 D841 L844 E845 E846 K847 Q848

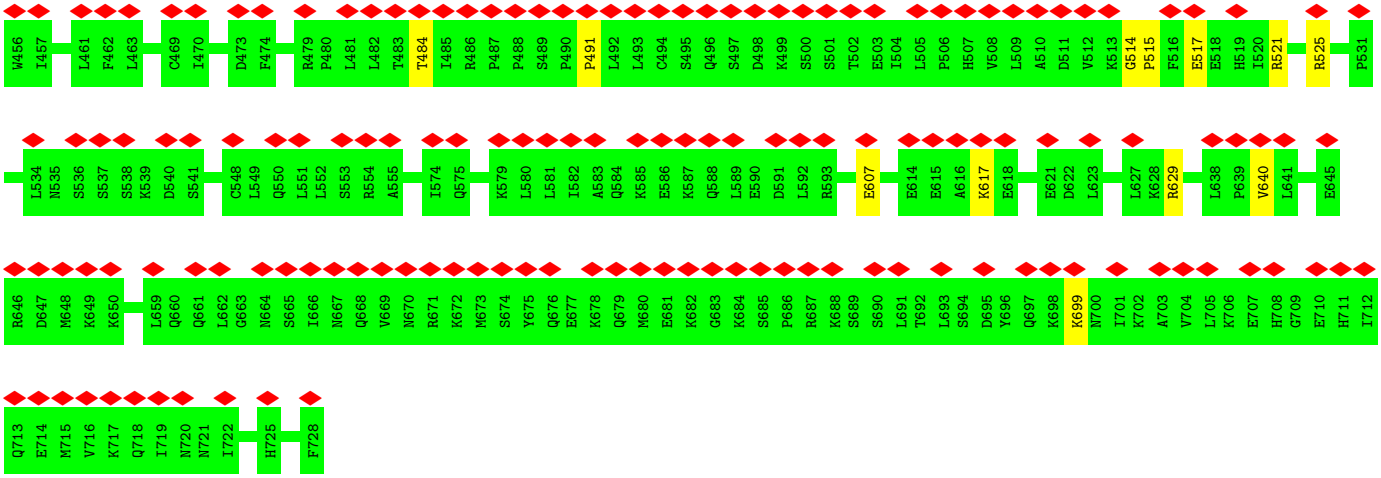


• Molecule 14: Nup88A protein

Chain b:

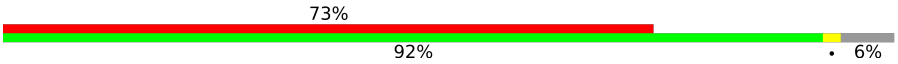


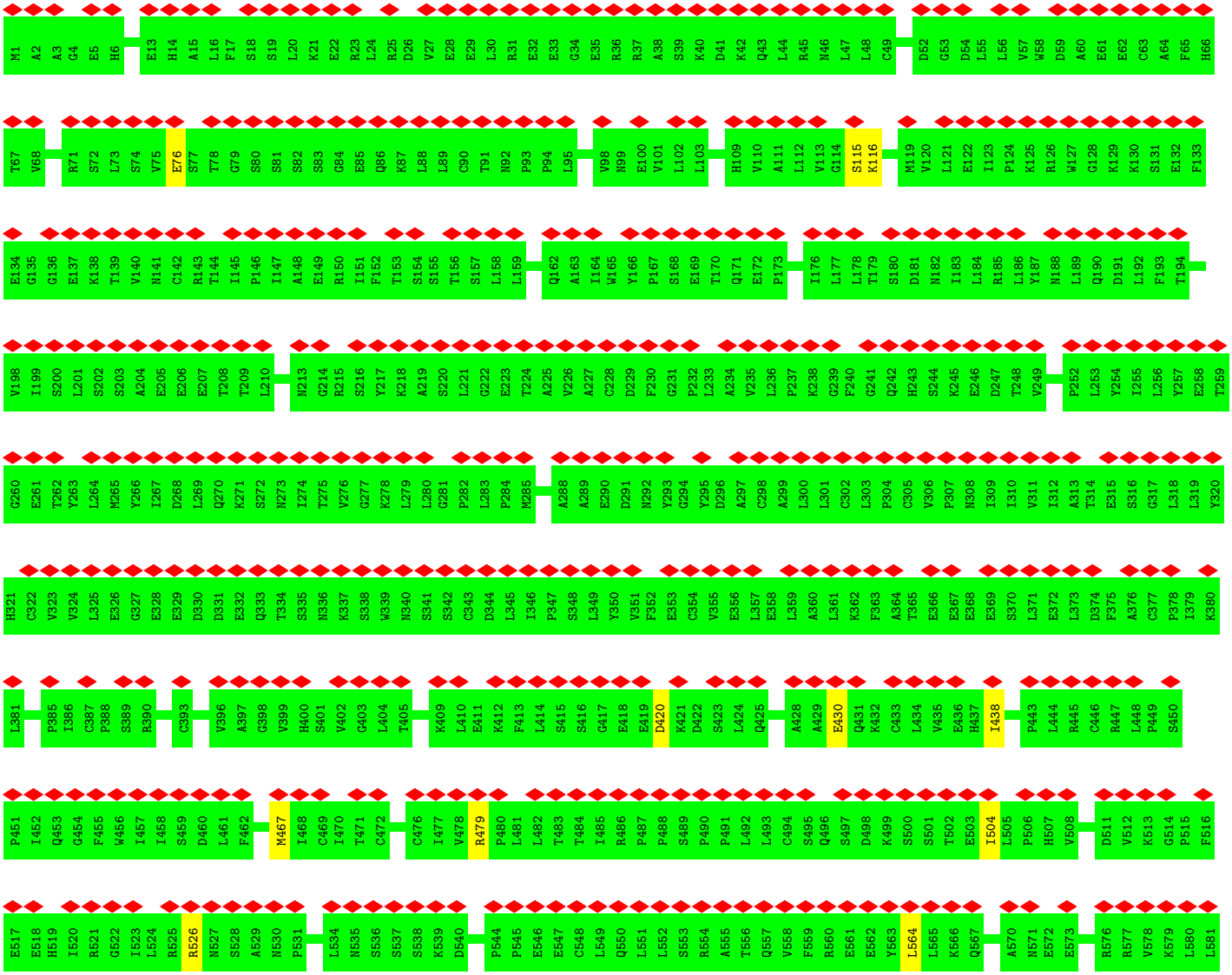


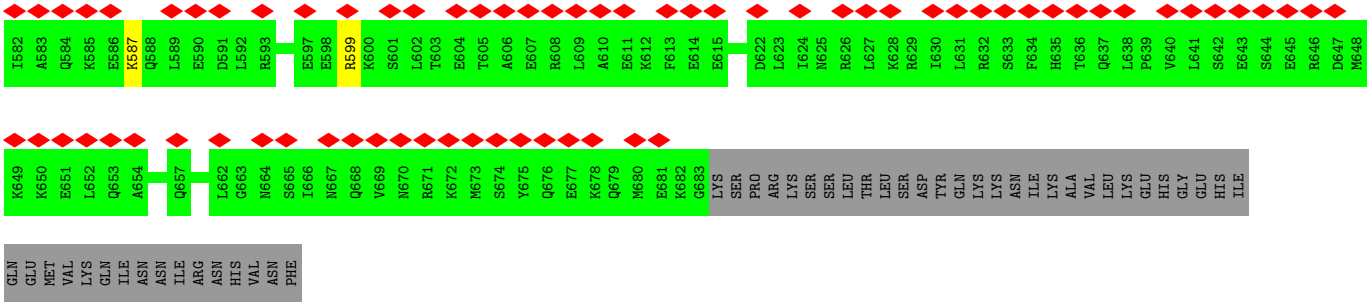


• Molecule 14: Nup88A protein

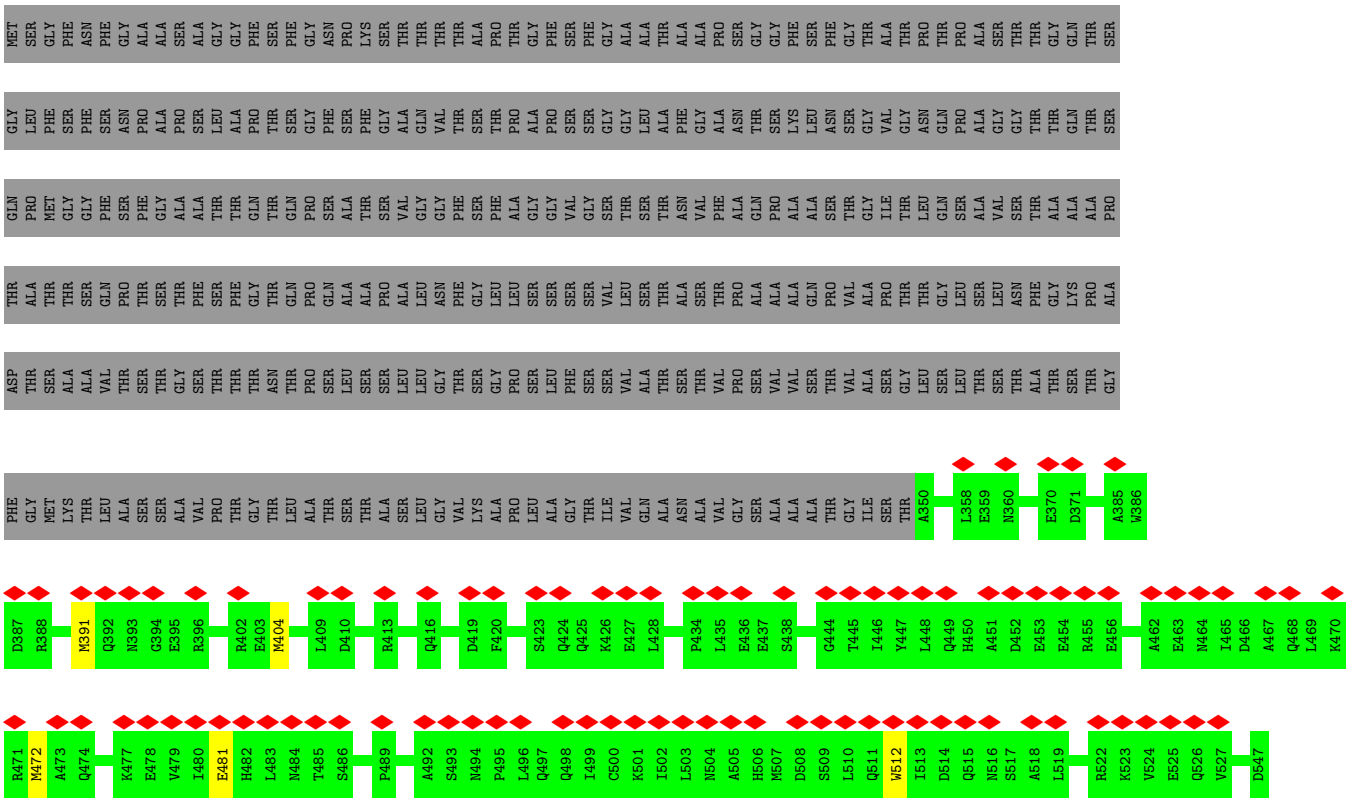
Chain d:



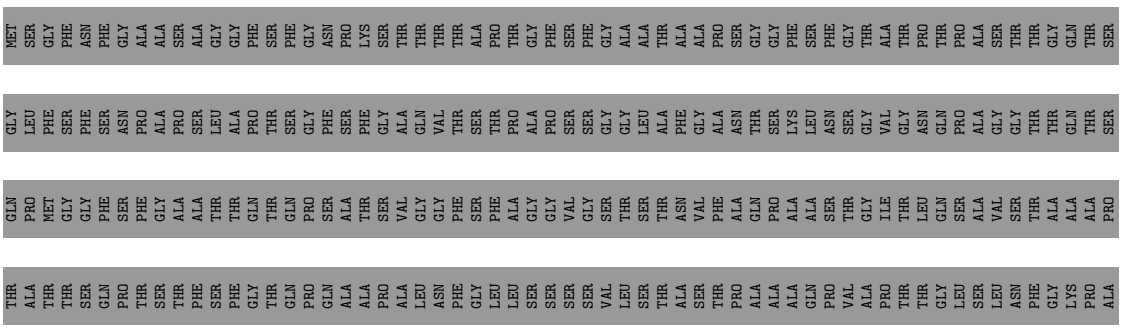


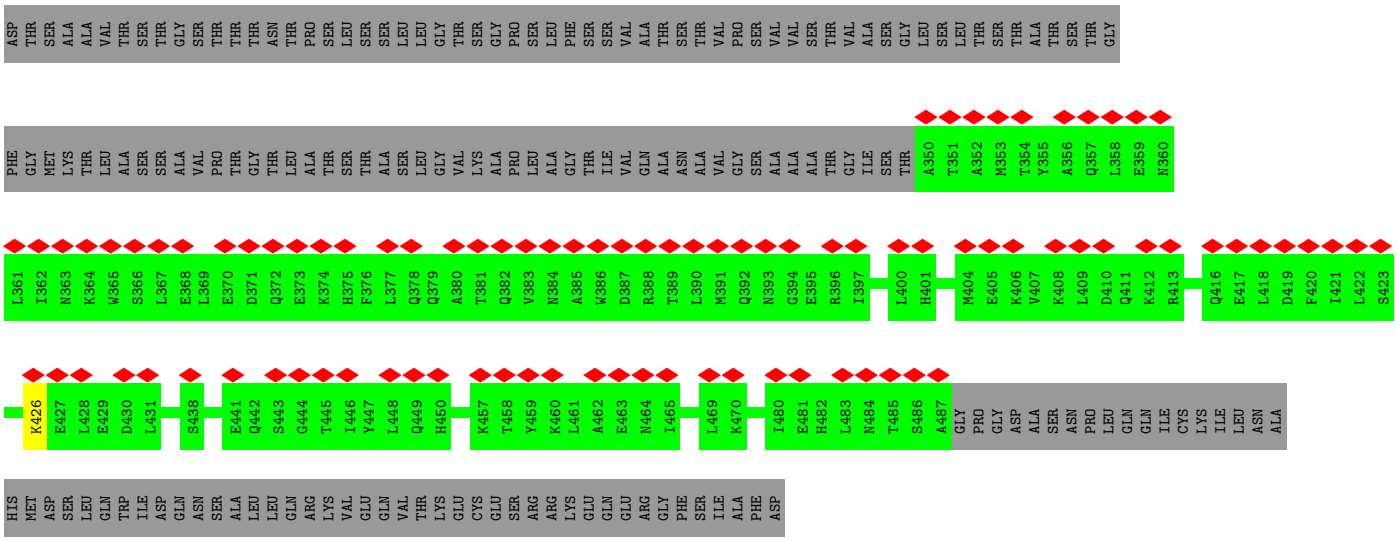


• Molecule 15: IL4I1 protein



• Molecule 15: IL4I1 protein

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PHE GLY MET LYS THR LEU ALA SER SER ALA VAL PRO THR GLY THR LEU ALA THR SER THR ALA SER LEU LEU GLY VAL LYS ALA PRO LEU ALA GLY THR ILE VAL GLN ALA ASN ALA VAL GLY SER ALA ALA ALA THR GLY ILE SER THR A350 T351 A352 M353 T354 Y355 A356 Q357 L358 E359 N360
L361 I362 N363 K364 W365 S366 L367 E368 L369 E370 D371 Q372 E373 K374 H375 F376 L377 Q378 Q379 A380 T381 Q382 V383 N384 A385 W386 D387 R388 T389 L390 M391 Q392 N393 G394 E395 R396 I397 L400 H401 M404 E405 K406 V407 K408 L409 D410 Q411 K412 R413 Q416 E417 L418 D419 F420 I421 L422 S423
K426 E427 L428 E429 D430 L431 S438 E441 Q442 S443 G444 T445 I446 Y447 L448 Q449 H450 K457 T458 Y459 K460 L461 A462 E463 N464 I465 L469 K470 I480 E481 H482 L483 N484 T485 S486 A487 GLY PRO GLY ASP ALA SER ASN PRO LEU GLN GLN ILE CYS LYS ILE LEU ASN ALA
HIS MET ASP SER LEU GLN TRP ILE ASP GLN ASN SER ALA LEU LEU GLN ARG LYS VAL GLU GLN VAL THR LYS GLU CYS GLU SER ARG ARG LYS GLU GLN GLU ARG GLY PHE SER ILE ALA PHE ASP

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	354460	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	3.582	Depositor
Minimum map value	-2.369	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.112	Depositor
Recommended contour level	0.505	Depositor
Map size (Å)	716.8, 716.8, 716.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.24, 2.24, 2.24	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.23	0/5377	0.44	0/7265
1	J	0.89	7/5377 (0.1%)	0.48	2/7265 (0.0%)
2	B	0.23	0/2996	0.47	0/4074
2	K	0.24	0/2996	0.48	0/4074
3	C	0.24	0/2674	0.48	0/3628
3	L	0.23	0/2612	0.46	0/3545
4	D	0.23	0/11349	0.43	0/15414
4	M	0.23	0/11349	0.43	0/15414
5	E	0.24	0/2643	0.46	0/3587
5	N	0.24	0/2643	0.47	0/3587
6	F	0.23	0/5308	0.43	0/7201
6	O	0.23	0/5299	0.44	0/7189
7	G	0.23	0/2367	0.44	0/3231
7	P	0.23	0/2367	0.45	0/3231
8	H	0.23	0/6628	0.41	0/8968
8	Q	0.23	0/6562	0.42	0/8879
9	I	0.23	0/8647	0.41	0/11720
9	R	0.23	0/8703	0.42	0/11797
10	S	0.23	0/16272	0.44	0/22021
10	T	0.23	0/16272	0.43	0/22021
11	U	0.24	0/5360	0.45	0/7239
12	V	0.23	0/6356	0.41	0/8594
12	W	0.23	0/6227	0.41	0/8417
12	X	0.23	0/6321	0.41	0/8545
12	Y	0.23	0/6268	0.40	0/8474
12	Z	1.17	8/6243 (0.1%)	0.52	4/8439 (0.0%)
13	a	0.23	0/1762	0.40	0/2365
13	e	0.23	0/1298	0.39	0/1738
14	b	0.23	0/5896	0.45	0/7976
14	d	0.23	0/5517	0.45	0/7471
15	c	0.23	0/1641	0.39	0/2206
15	f	0.23	0/1154	0.39	0/1553
All	All	0.35	15/182484 (0.0%)	0.44	6/247128 (0.0%)

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	Z	308	TRP	CE3-CZ3	61.34	2.42	1.38
1	J	487	TRP	CE3-CZ3	38.83	2.04	1.38
12	Z	308	TRP	CZ3-CH2	38.33	2.01	1.40
12	Z	308	TRP	CE2-CZ2	32.92	1.95	1.39
12	Z	308	TRP	CD2-CE2	27.05	1.73	1.41

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	Z	510	ARG	CD-NE-CZ	22.20	154.69	123.60
1	J	471	MET	CG-SD-CE	16.96	127.33	100.20
12	Z	510	ARG	NE-CZ-NH1	12.45	126.53	120.30
12	Z	308	TRP	CE3-CZ3-CH2	-8.84	111.47	121.20
12	Z	510	ARG	CG-CD-NE	6.80	126.08	111.80

There are no chirality outliers.

There are no planarity outliers.

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	A	5268	0	5226	61	0
1	J	5268	0	5226	100	0
2	B	2927	0	2800	63	0
2	K	2927	0	2800	48	0
3	C	2607	0	2513	40	0
3	L	2546	0	2444	32	0
4	D	11118	0	11035	144	0
4	M	11118	0	11035	166	0
5	E	2573	0	2503	36	0
5	N	2573	0	2503	50	0
6	F	5177	0	5086	81	0
6	O	5168	0	5080	67	0
7	G	2300	0	2180	30	0
7	P	2300	0	2180	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	6494	0	6413	52	0
8	Q	6430	0	6353	82	0
9	I	8482	0	8354	106	0
9	R	8536	0	8407	113	0
10	S	15974	0	16156	175	0
10	T	15974	0	16156	201	0
11	U	5260	0	5256	78	0
12	V	6225	0	6236	84	0
12	W	6100	0	6128	59	0
12	X	6190	0	6197	67	0
12	Y	6139	0	6155	83	0
12	Z	6116	0	6136	113	0
13	a	1738	0	1741	0	0
13	e	1282	0	1269	0	0
14	b	5787	0	5811	0	0
14	d	5414	0	5424	0	0
15	c	1621	0	1597	0	0
15	f	1141	0	1127	0	0
All	All	178773	0	177527	2026	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 6.

The worst 5 of 2026 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)
1:J:487:TRP:CZ2	1:J:487:TRP:CE2	1.76	1.70
1:J:487:TRP:CH2	1:J:487:TRP:CZ3	1.81	1.63
12:Z:308:TRP:CZ2	12:Z:308:TRP:CE2	1.95	1.51
12:Z:510:ARG:CD	12:Z:510:ARG:NE	1.75	1.49
12:Z:308:TRP:CZ3	12:Z:510:ARG:NE	1.73	1.47

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	A	651/653 (100%)	584 (90%)	60 (9%)	7 (1%)	14	52
1	J	651/653 (100%)	590 (91%)	53 (8%)	8 (1%)	13	50
2	B	373/375 (100%)	300 (80%)	64 (17%)	9 (2%)	6	33
2	K	373/375 (100%)	306 (82%)	53 (14%)	14 (4%)	3	24
3	C	331/360 (92%)	286 (86%)	40 (12%)	5 (2%)	10	46
3	L	323/360 (90%)	268 (83%)	49 (15%)	6 (2%)	8	38
4	D	1392/1414 (98%)	1227 (88%)	144 (10%)	21 (2%)	10	46
4	M	1392/1414 (98%)	1254 (90%)	125 (9%)	13 (1%)	17	57
5	E	324/326 (99%)	275 (85%)	46 (14%)	3 (1%)	17	57
5	N	324/326 (99%)	273 (84%)	45 (14%)	6 (2%)	8	38
6	F	636/924 (69%)	530 (83%)	91 (14%)	15 (2%)	6	33
6	O	635/924 (69%)	560 (88%)	68 (11%)	7 (1%)	14	52
7	G	292/320 (91%)	251 (86%)	35 (12%)	6 (2%)	7	36
7	P	292/320 (91%)	235 (80%)	50 (17%)	7 (2%)	6	33
8	H	796/916 (87%)	736 (92%)	53 (7%)	7 (1%)	17	57
8	Q	788/916 (86%)	704 (89%)	75 (10%)	9 (1%)	14	52
9	I	1074/1140 (94%)	926 (86%)	131 (12%)	17 (2%)	9	44
9	R	1080/1140 (95%)	957 (89%)	113 (10%)	10 (1%)	17	57
10	S	2009/2011 (100%)	1790 (89%)	193 (10%)	26 (1%)	12	48
10	T	2009/2011 (100%)	1815 (90%)	171 (8%)	23 (1%)	14	52
11	U	652/820 (80%)	593 (91%)	51 (8%)	8 (1%)	13	50
12	V	770/2931 (26%)	702 (91%)	59 (8%)	9 (1%)	13	50
12	W	754/2931 (26%)	690 (92%)	57 (8%)	7 (1%)	17	57
12	X	765/2931 (26%)	698 (91%)	62 (8%)	5 (1%)	22	63
12	Y	759/2931 (26%)	699 (92%)	49 (6%)	11 (1%)	11	46
12	Z	756/2931 (26%)	688 (91%)	58 (8%)	10 (1%)	12	48
13	a	207/2037 (10%)	202 (98%)	5 (2%)	0	100	100
13	e	153/2037 (8%)	149 (97%)	3 (2%)	1 (1%)	22	63
14	b	726/728 (100%)	653 (90%)	65 (9%)	8 (1%)	14	52
14	d	681/728 (94%)	609 (89%)	65 (10%)	7 (1%)	15	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	c	196/547 (36%)	192 (98%)	4 (2%)	0	100	100
15	f	136/547 (25%)	136 (100%)	0	0	100	100
All	All	22300/38977 (57%)	19878 (89%)	2137 (10%)	285 (1%)	16	48

5 of 285 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	178	ILE
4	D	565	LYS
9	R	837	LEU
11	U	203	PRO
12	W	271	SER

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	580/580 (100%)	560 (97%)	20 (3%)	37	60
1	J	580/580 (100%)	557 (96%)	23 (4%)	31	55
2	B	329/329 (100%)	321 (98%)	8 (2%)	49	69
2	K	329/329 (100%)	317 (96%)	12 (4%)	35	59
3	C	288/309 (93%)	282 (98%)	6 (2%)	53	72
3	L	282/309 (91%)	275 (98%)	7 (2%)	47	68
4	D	1230/1244 (99%)	1206 (98%)	24 (2%)	55	74
4	M	1230/1244 (99%)	1198 (97%)	32 (3%)	46	66
5	E	275/275 (100%)	271 (98%)	4 (2%)	65	80
5	N	275/275 (100%)	264 (96%)	11 (4%)	31	55
6	F	564/816 (69%)	538 (95%)	26 (5%)	27	52
6	O	563/816 (69%)	542 (96%)	21 (4%)	34	58
7	G	250/272 (92%)	241 (96%)	9 (4%)	35	59
7	P	250/272 (92%)	242 (97%)	8 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	712/816 (87%)	692 (97%)	20 (3%)	43	65
8	Q	705/816 (86%)	682 (97%)	23 (3%)	38	61
9	I	944/993 (95%)	931 (99%)	13 (1%)	67	80
9	R	950/993 (96%)	926 (98%)	24 (2%)	47	68
10	S	1779/1779 (100%)	1741 (98%)	38 (2%)	53	72
10	T	1779/1779 (100%)	1730 (97%)	49 (3%)	43	65
11	U	577/721 (80%)	566 (98%)	11 (2%)	57	75
12	V	692/2545 (27%)	682 (99%)	10 (1%)	67	80
12	W	677/2545 (27%)	669 (99%)	8 (1%)	71	83
12	X	687/2545 (27%)	681 (99%)	6 (1%)	78	87
12	Y	682/2545 (27%)	665 (98%)	17 (2%)	47	68
12	Z	679/2545 (27%)	667 (98%)	12 (2%)	59	77
13	a	195/1634 (12%)	195 (100%)	0	100	100
13	e	143/1634 (9%)	138 (96%)	5 (4%)	36	59
14	b	660/660 (100%)	646 (98%)	14 (2%)	53	72
14	d	617/660 (94%)	611 (99%)	6 (1%)	76	86
15	c	179/429 (42%)	174 (97%)	5 (3%)	43	65
15	f	126/429 (29%)	125 (99%)	1 (1%)	81	89
All	All	19808/33718 (59%)	19335 (98%)	473 (2%)	51	69

5 of 473 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	O	714	LEU
14	b	143	ARG
9	R	868	ARG
12	Z	444	TRP
12	W	23	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 254 such sidechains are listed below:

Mol	Chain	Res	Type
8	Q	507	GLN
12	Y	759	HIS
10	S	884	ASN

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Mol	Chain	Res	Type
12	Y	675	ASN
14	b	109	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

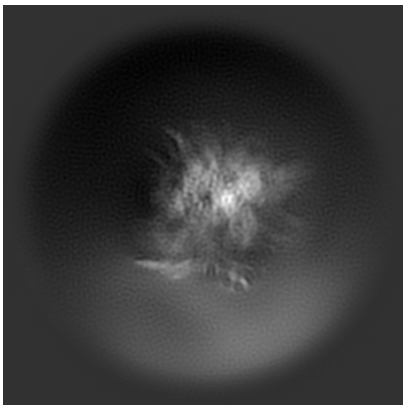
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32056. These allow visual inspection of the internal detail of the map and identification of artifacts.

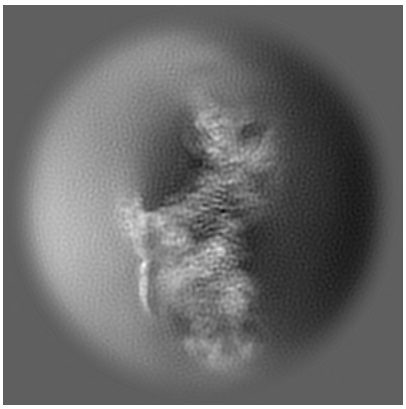
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

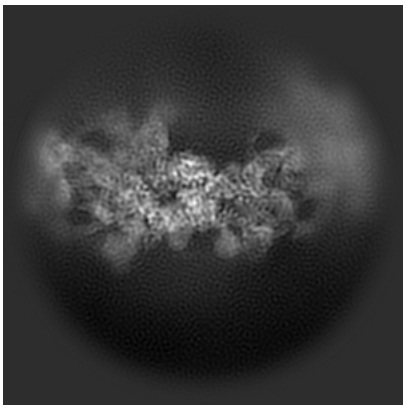
6.1.1 Primary map



X

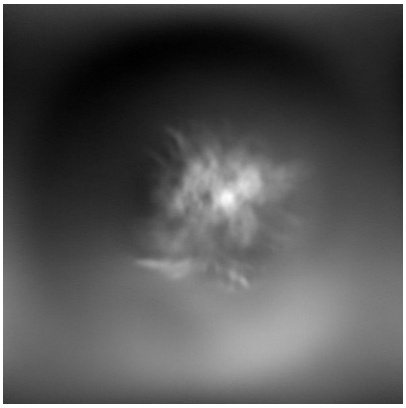


Y

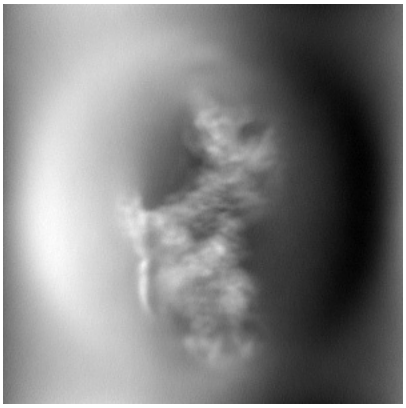


Z

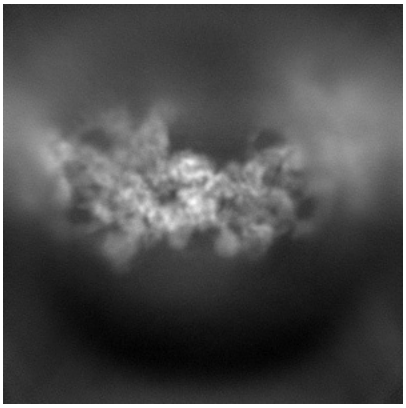
6.1.2 Raw map



X



Y

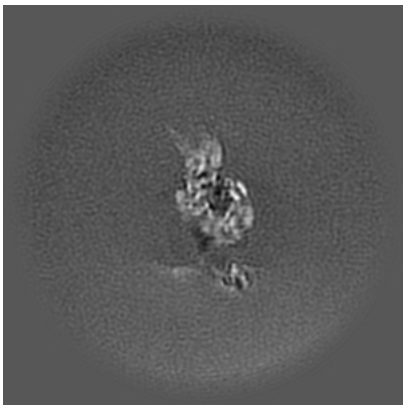


Z

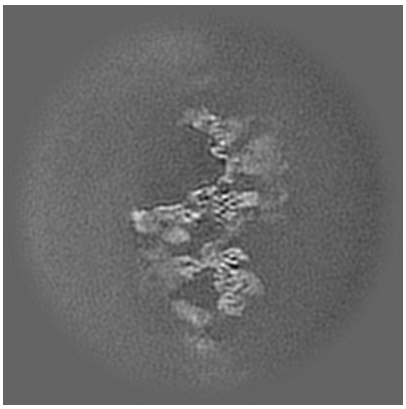
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

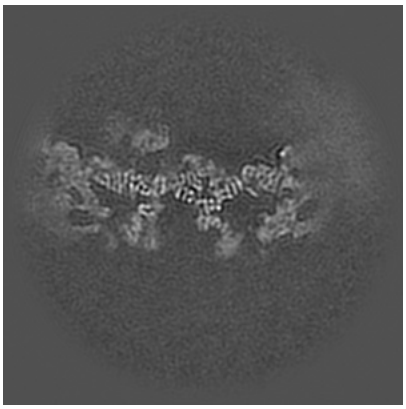
6.2.1 Primary map



X Index: 160

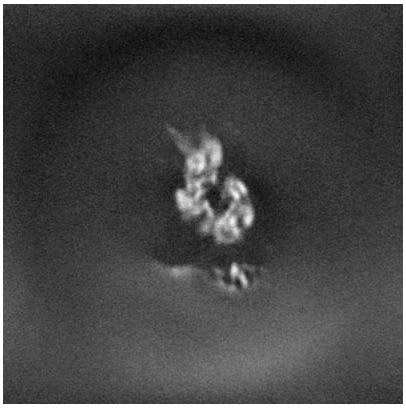


Y Index: 160

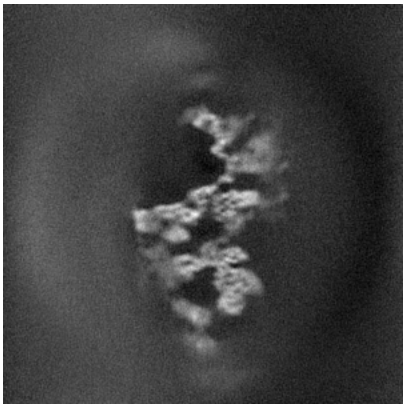


Z Index: 160

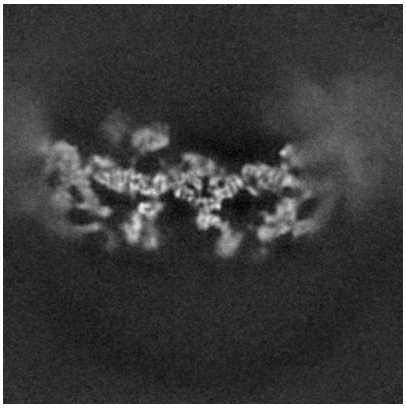
6.2.2 Raw map



X Index: 160



Y Index: 160

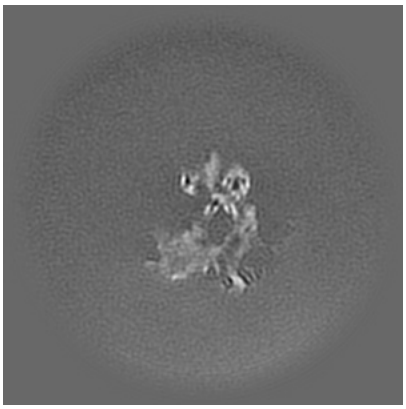


Z Index: 160

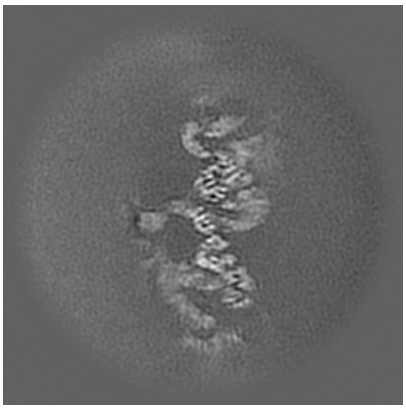
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

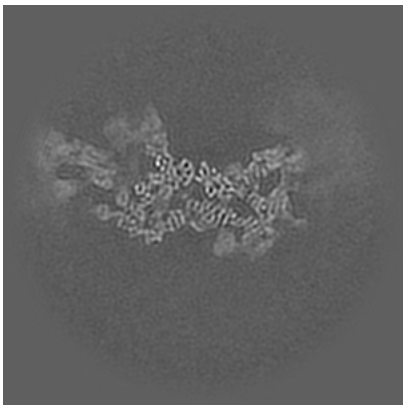
6.3.1 Primary map



X Index: 143

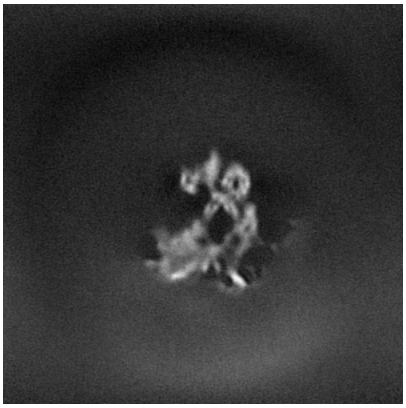


Y Index: 169

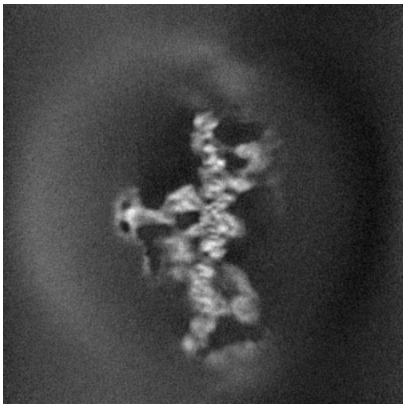


Z Index: 171

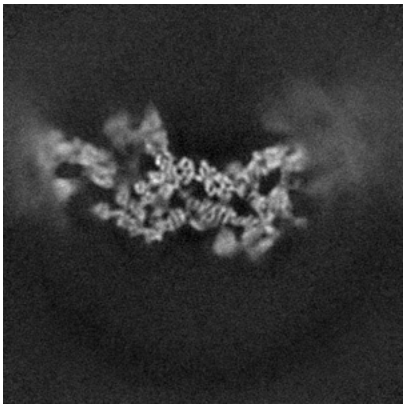
6.3.2 Raw map



X Index: 143



Y Index: 182

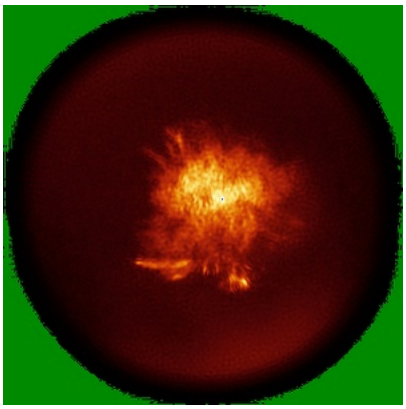


Z Index: 171

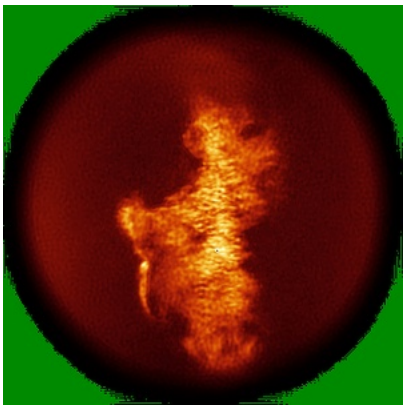
The images above show the largest variance slices of the map in three orthogonal directions.

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

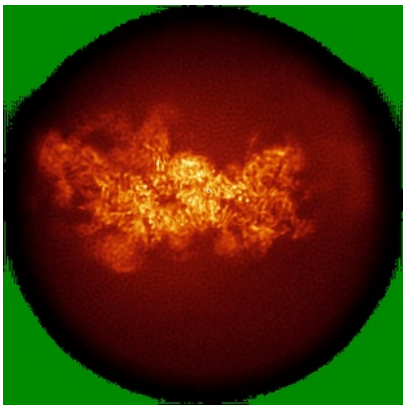
6.4.1 Primary map



X

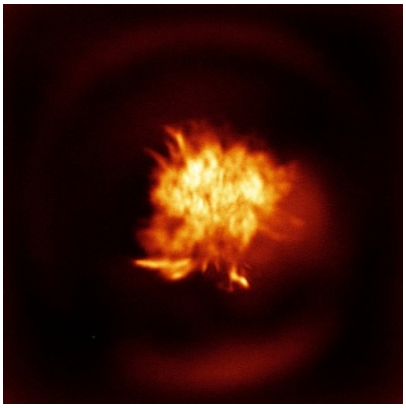


Y

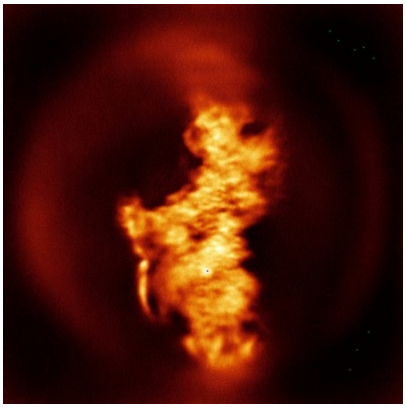


Z

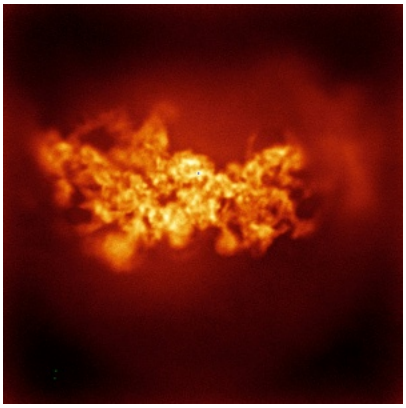
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.505. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

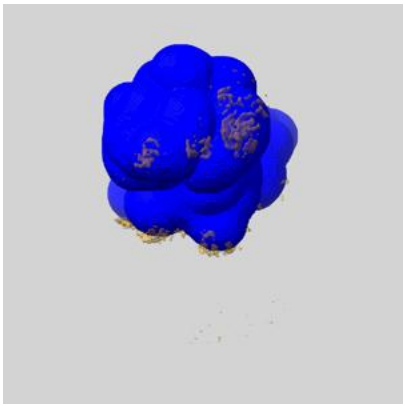
6.6 Mask visualisation (i)

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

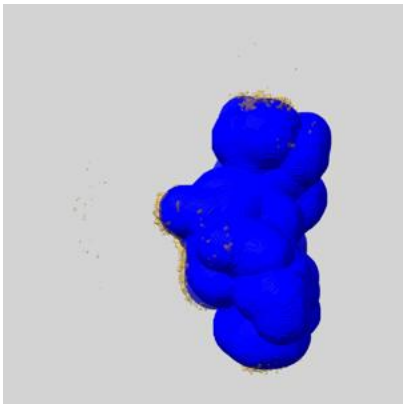
A mask typically either:

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

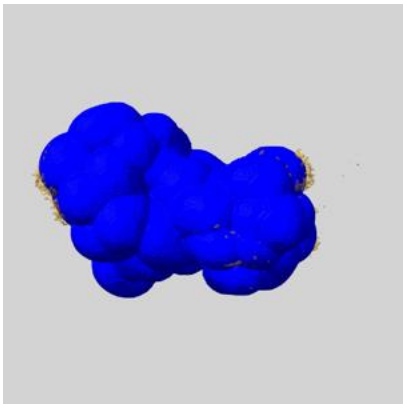
6.6.1 emd_32056_msk_1.map (i)



X



Y

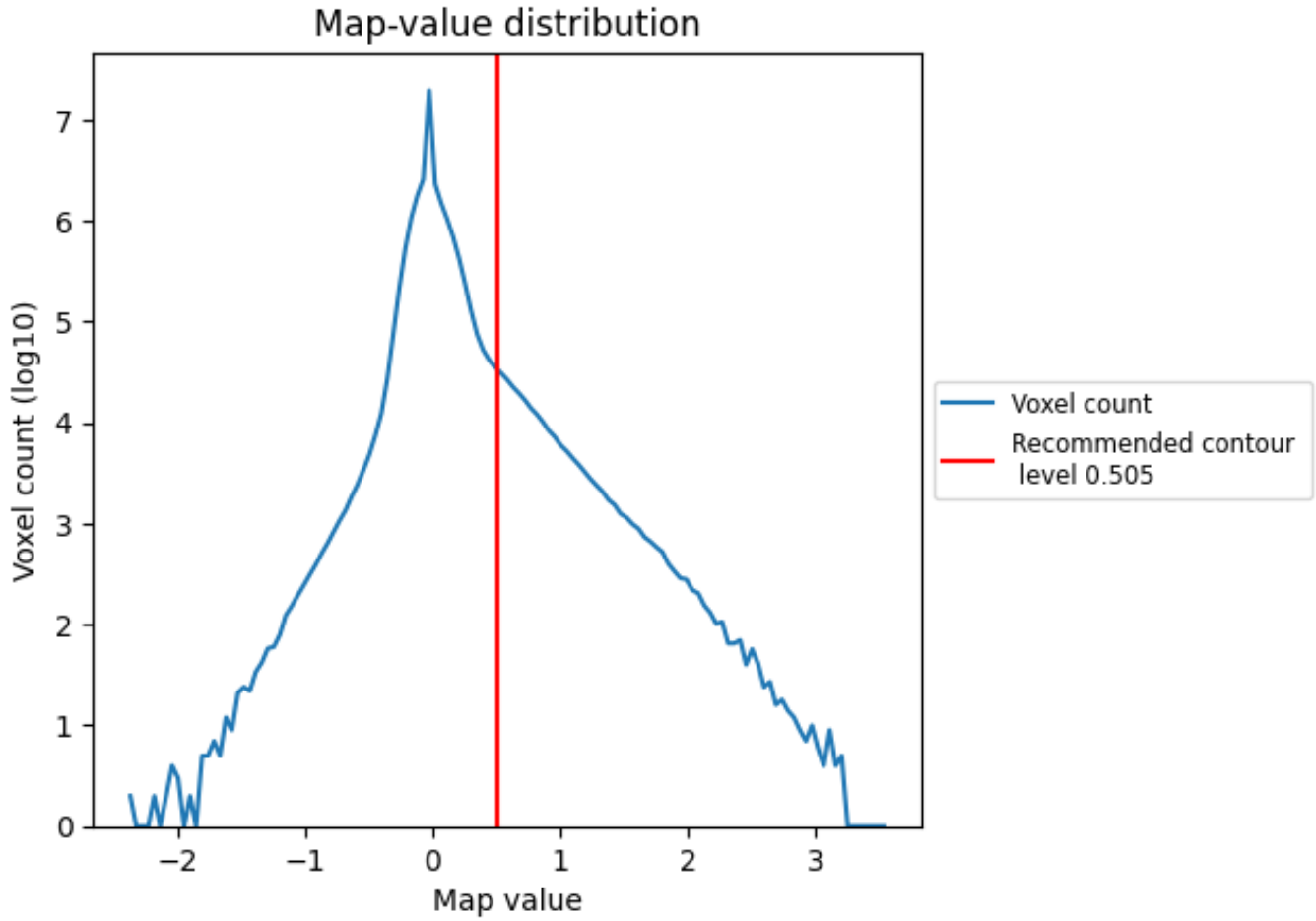


Z

7 Map analysis

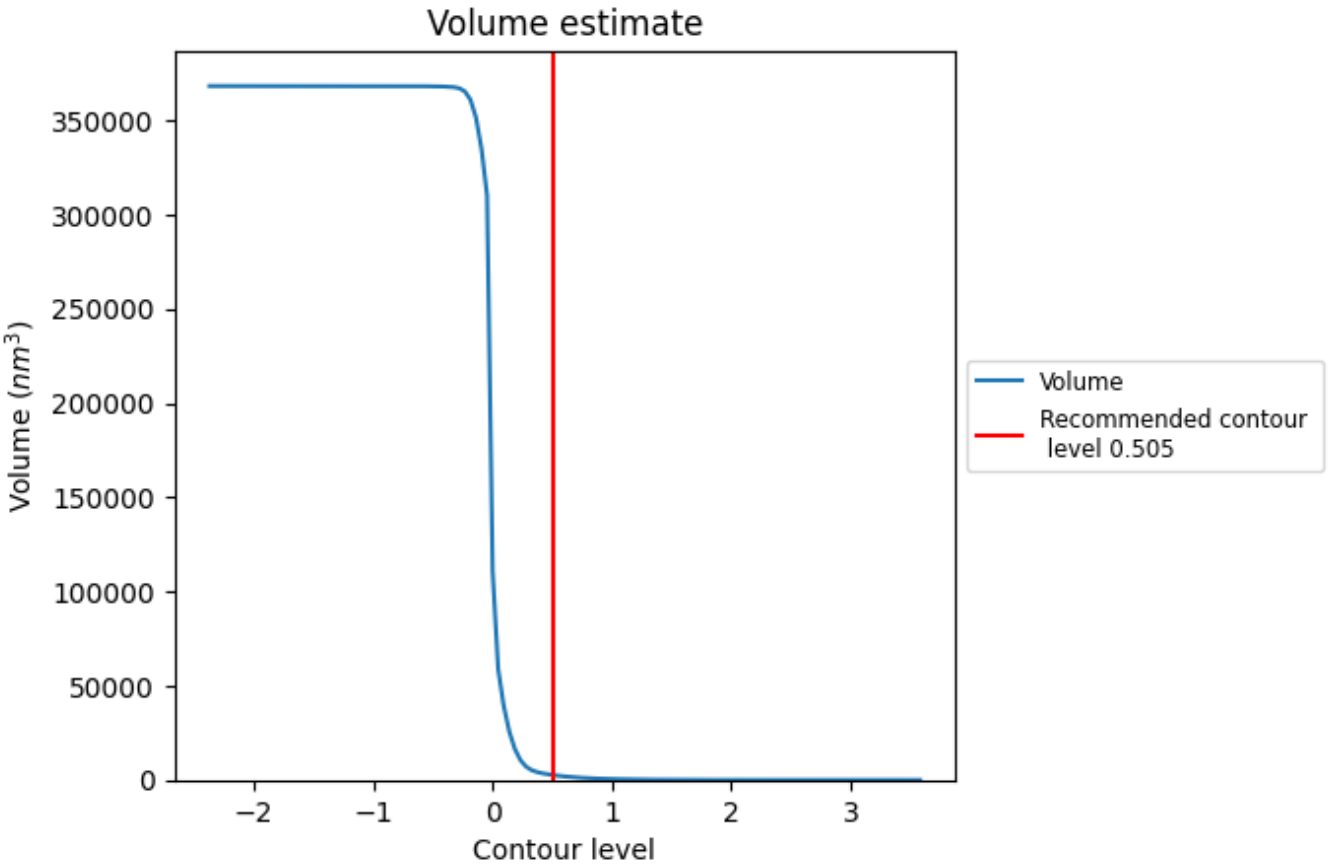
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

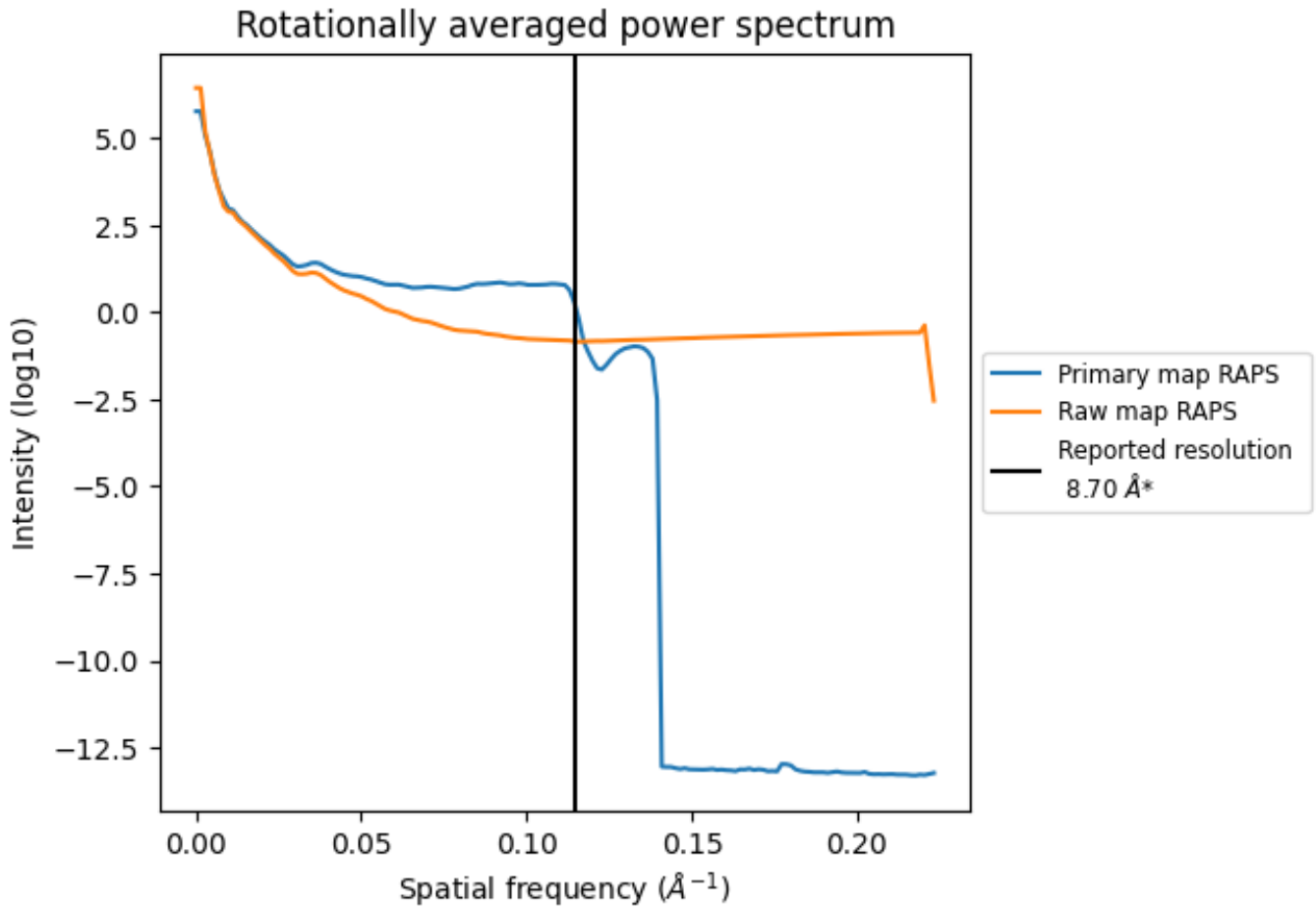
7.2 Volume estimate (i)



The volume at the recommended contour level is 2642 nm^3; this corresponds to an approximate mass of 2387 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)

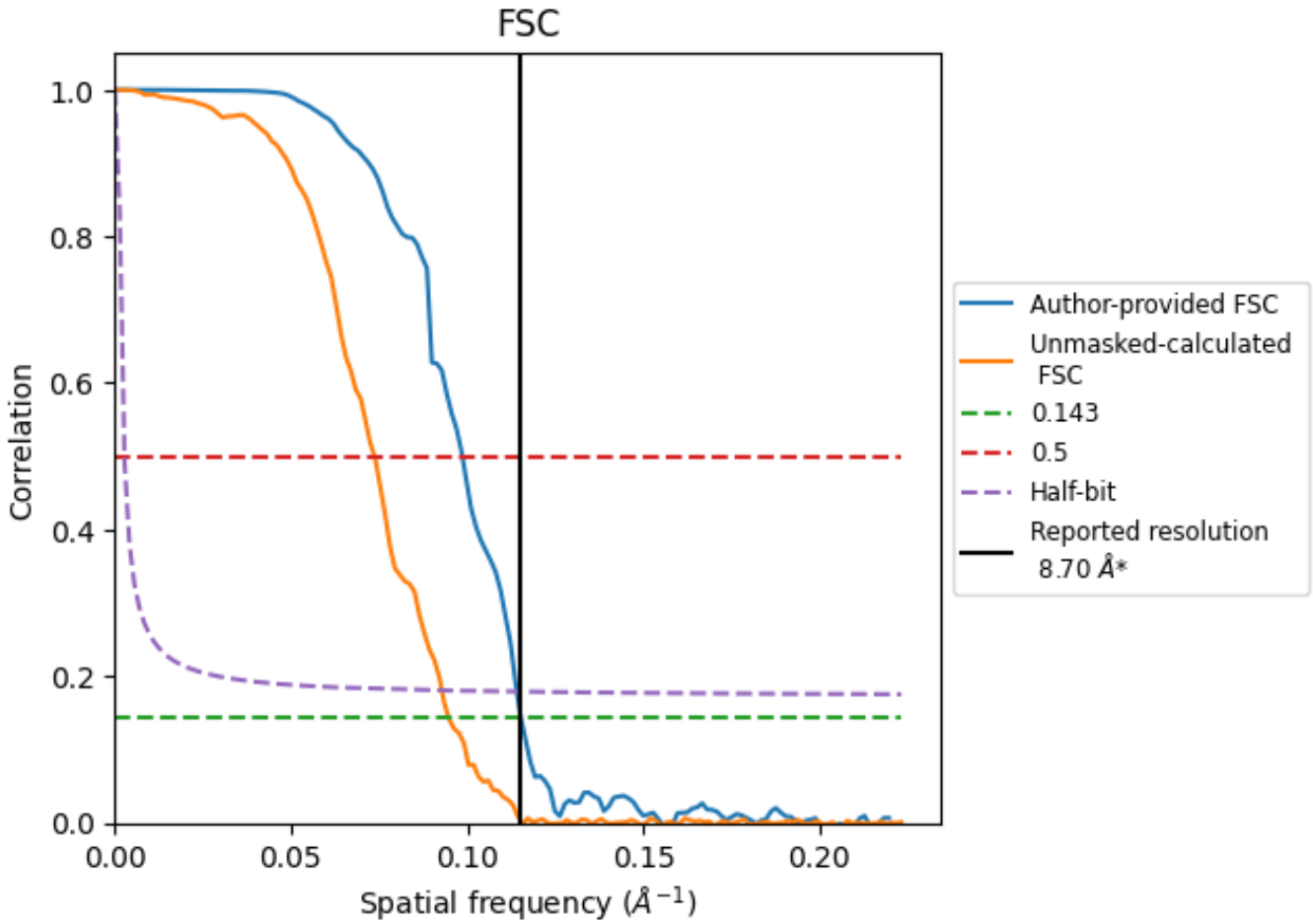


*Reported resolution corresponds to spatial frequency of 0.115 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.115 Å^{-1}

8.2 Resolution estimates (i)

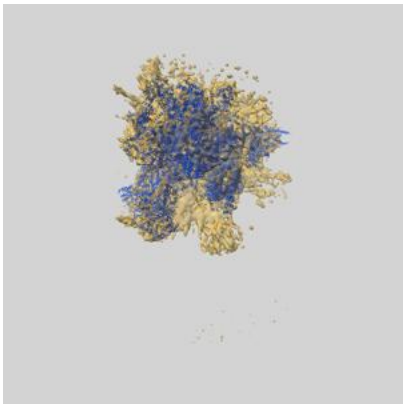
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.70	-	-
Author-provided FSC curve	8.68	10.14	8.76
Unmasked-calculated*	10.56	13.55	10.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.56 differs from the reported value 8.7 by more than 10 %

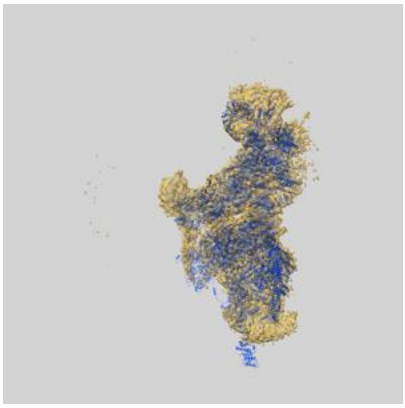
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-32056 and PDB model 7VOP. Per-residue inclusion information can be found in section 3 on page 11.

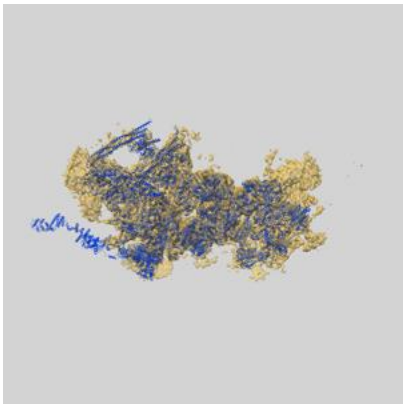
9.1 Map-model overlay



X



Y



Z

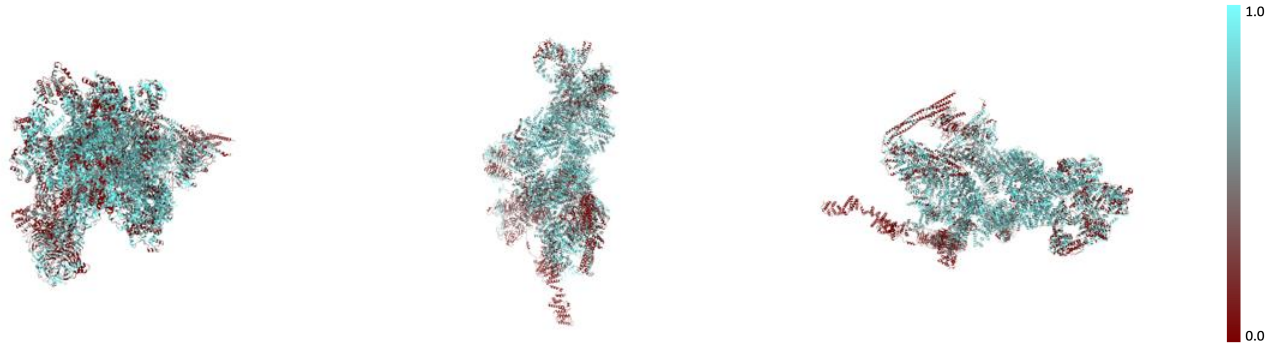
The images above show the 3D surface view of the map at the recommended contour level 0.505 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)

X Y Z

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

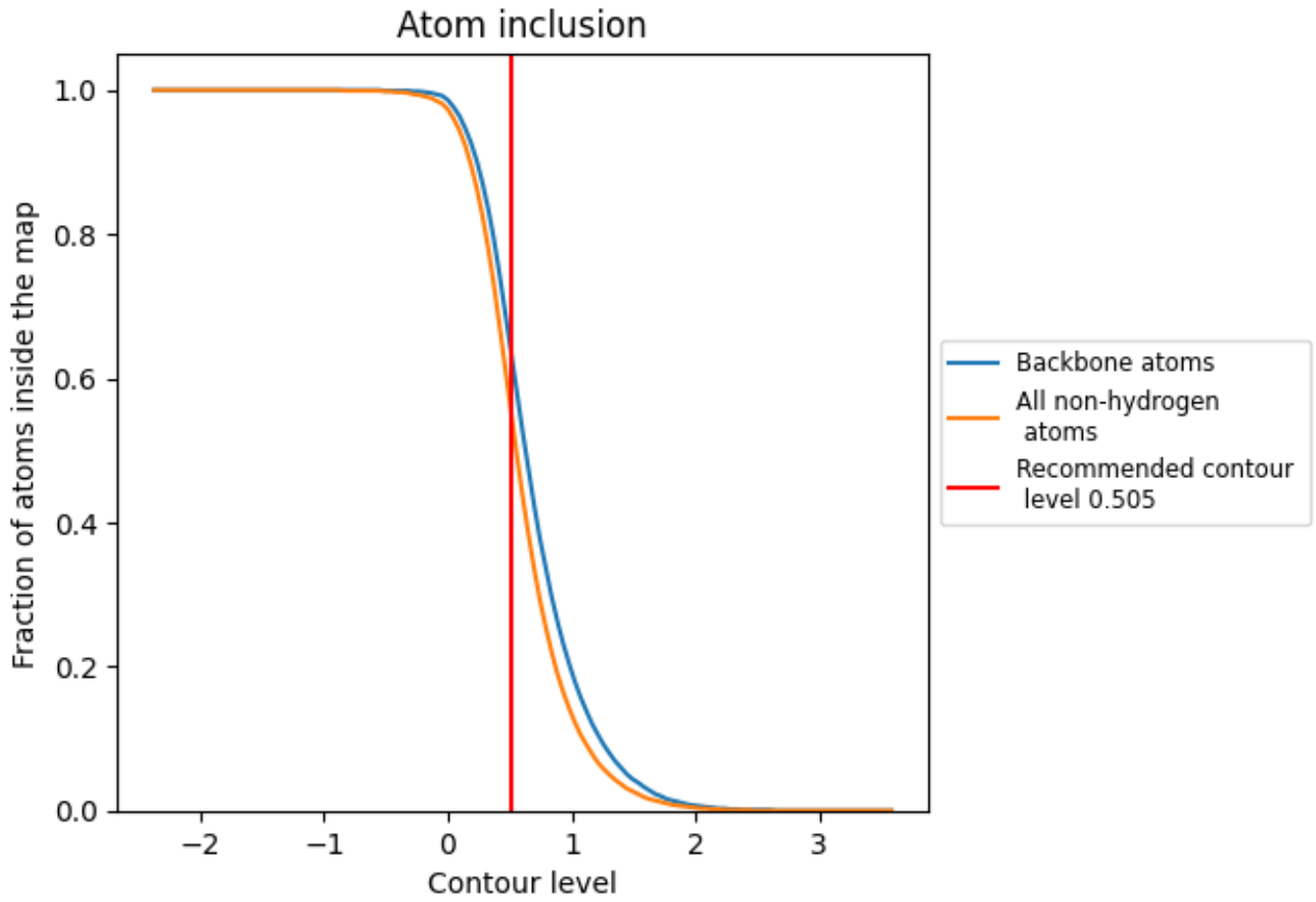
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.505).

9.4 Atom inclusion (i)



At the recommended contour level, 64% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.505) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5610	0.0860
A	0.7260	0.1500
B	0.6850	0.0950
C	0.8050	0.1310
D	0.6360	0.0820
E	0.7930	0.0860
F	0.7050	0.1140
G	0.7030	0.1080
H	0.6260	0.0910
I	0.3520	0.0610
J	0.6650	0.1240
K	0.6430	0.0790
L	0.7590	0.1190
M	0.4190	0.0550
N	0.1560	0.0390
O	0.7360	0.1380
P	0.8080	0.1180
Q	0.6300	0.1170
R	0.0450	0.0030
S	0.6450	0.1010
T	0.7120	0.1190
U	0.7090	0.1000
V	0.5220	0.0830
W	0.7180	0.1070
X	0.4620	0.0360
Y	0.5210	0.0410
Z	0.5150	0.0490
a	0.4520	0.1090
b	0.4980	0.0840
c	0.4480	0.1040
d	0.2060	0.0500
e	0.3420	0.0740
f	0.3160	0.0280