Full wwPDB EM Validation Report ⓘ

Jun 3, 2024 – 11:32 PM JST

PDB ID	:	7FIK
EMDB ID	:	EMD-31600
Title	:	The cryo-EM structure of the CR subunit from X. laevis NPC
Authors	:	Shi, Y.; Huang, G.; Zhan, X.
Deposited on	:	2021-07-31
Resolution	:	3.70 Å(reported)

This is a Full wwPDB EM Validation 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:

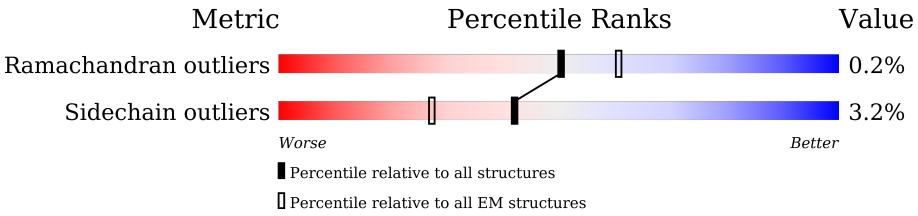
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.70 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)
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	2011	89% 11%
1	a	2011	85% 14%
2	B	653	89% 8%
2	b	653	90% 9%
3	C	375	85% 14%
3	c	375	80% 18%
4	D	360	87% 12%
4	d	360	86% 13%
5	E	1435	24% 90% 9%

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Mol	Chain	Length	Quality of chain
5	e	1435	85% 13%
6	F	326	8% 100%
6	f	326	97%
7	G	1742	31% 67%
7	g	1742	33% 65%
8	H	320	88% 10%
8	h	320	88% 10%
9	I	916	9% 79% 20%
9	i	916	46% 73% 27%
10	J	1140	78% 89% 11%
11	K	2905	5% 24% 76%
11	L	2905	10% 23% 77%
11	M	2905	22% 77%
11	N	2905	6% 24% 76%
11	O	2905	23% 76%
12	P	820	72% 28%
12	S	820	6% 94%
12	p	820	52% 55% 44%
12	s	820	6% 94%
13	W	1388	23% 77%
14	X	161	83% 100%
15	Y	728	38% 46% 53%
16	j	1140	90% 90% 10%

2 Entry composition (i)

There are 16 unique types of molecules in this entry. The entry contains 116163 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 MGC83295 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1795	Total 9238	C 5541	N 1851	O 1841	S 5	0	0
1	a	1725	Total 8811	C 5278	N 1770	O 1757	S 6	0	0

- Molecule 2 is a protein called Nuclear pore complex protein Nup85.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	598	Total 4799	C 3051	N 833	O 878	S 37	0	0
2	b	595	Total 4549	C 2894	N 793	O 829	S 33	0	0

- Molecule 3 is a protein called MGC154553 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	324	Total 2557	C 1590	N 461	O 488	S 18	0	0
3	c	309	Total 2445	C 1518	N 443	O 468	S 16	0	0

- Molecule 4 is a protein called Nucleoporin SEH1-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	316	Total 2473	C 1550	N 443	O 463	S 17	0	0
4	d	312	Total 2435	C 1531	N 435	O 451	S 18	0	0

- Molecule 5 is a protein called outer Nup160.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	1310	Total	C	N	O	S	0	0
			7891	4857	1495	1522	17		
5	e	1247	Total	C	N	O	S	0	0
			8134	5074	1497	1533	30		

- Molecule 6 is a protein called MGC83926 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	326	Total	C	N	O		0	0
			1607	954	326	327			
6	f	322	Total	C	N	O	S	0	0
			2524	1612	436	461	15		

- Molecule 7 is a protein called Nuclear pore complex protein Nup98-Nup96.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	567	Total	C	N	O	S	0	0
			4209	2659	769	764	17		
7	g	603	Total	C	N	O	S	0	0
			4770	3022	868	856	24		

- Molecule 8 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	288	Total	C	N	O	S	0	0
			2235	1417	383	423	12		
8	h	288	Total	C	N	O	S	0	0
			2259	1429	385	433	12		

- Molecule 9 is a protein called Nuclear pore complex protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	729	Total	C	N	O	0	0
			3626	2168	729	729		
9	i	673	Total	C	N	O	0	0
			3347	2001	673	673		

- Molecule 10 is a protein called nuclear pore complex protein Nup133.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	J	1015	Total	C	N	O	0	0
			5029	2999	1015	1015		

- Molecule 11 is a protein called Nup358 complex, clamps.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	697	Total 3460	C 2066	N 697	O 697	0	0
11	L	679	Total 3372	C 2014	N 679	O 679	0	0
11	M	654	Total 3246	C 1938	N 654	O 654	0	0
11	N	701	Total 3480	C 2078	N 701	O 701	0	0
11	O	683	Total 3391	C 2025	N 683	O 683	0	0

- Molecule 12 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	593	Total 2945	C 1759	N 593	O 593		0	0
12	S	52	Total 432	C 272	N 77	O 81	S 2	0	0
12	s	52	Total 432	C 272	N 77	O 81	S 2	0	0
12	p	456	Total 2267	C 1355	N 456	O 456		0	0

- Molecule 13 is a protein called Nup155-prov protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	324	Total 2636	C 1688	N 447	O 485	S 16	0	0

- Molecule 14 is a protein called Nup98.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	X	161	Total 794	C 472	N 161	O 161	0	0

- Molecule 15 is a protein called Nucleoporin Nup88A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	Y	339	Total 1676	C 998	N 339	O 339	0	0

- Molecule 16 is a protein called outer Nup133.

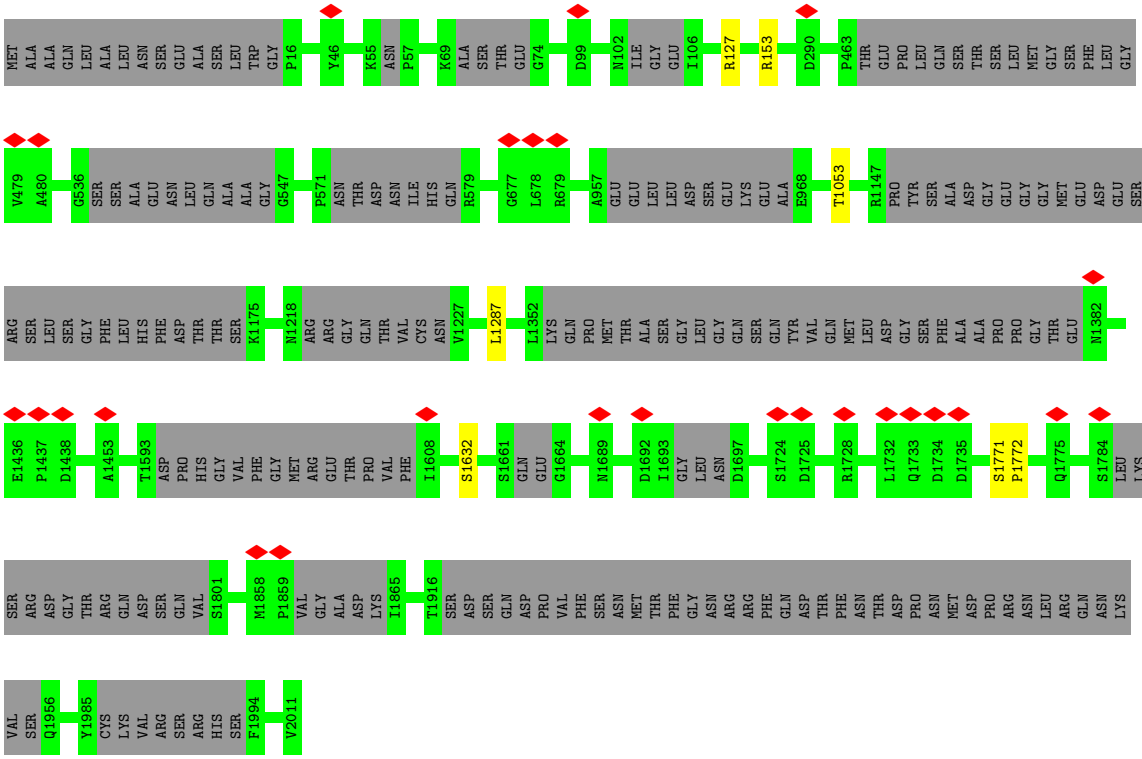
Mol	Chain	Residues	Atoms				AltConf	Trace
16	j	1028	Total 5094	C 3038	N 1028	O 1028	0	0

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.

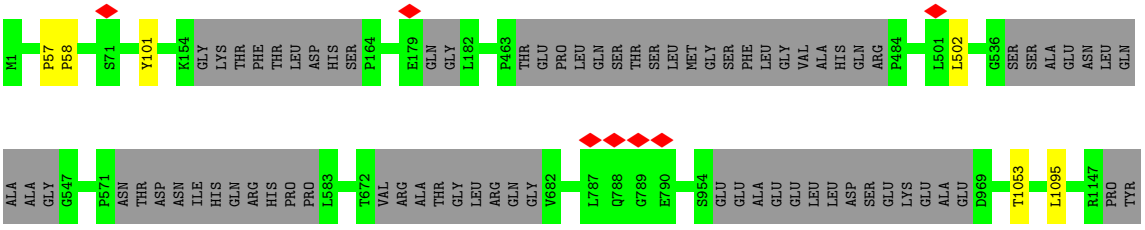
• Molecule 1: MGC83295 protein

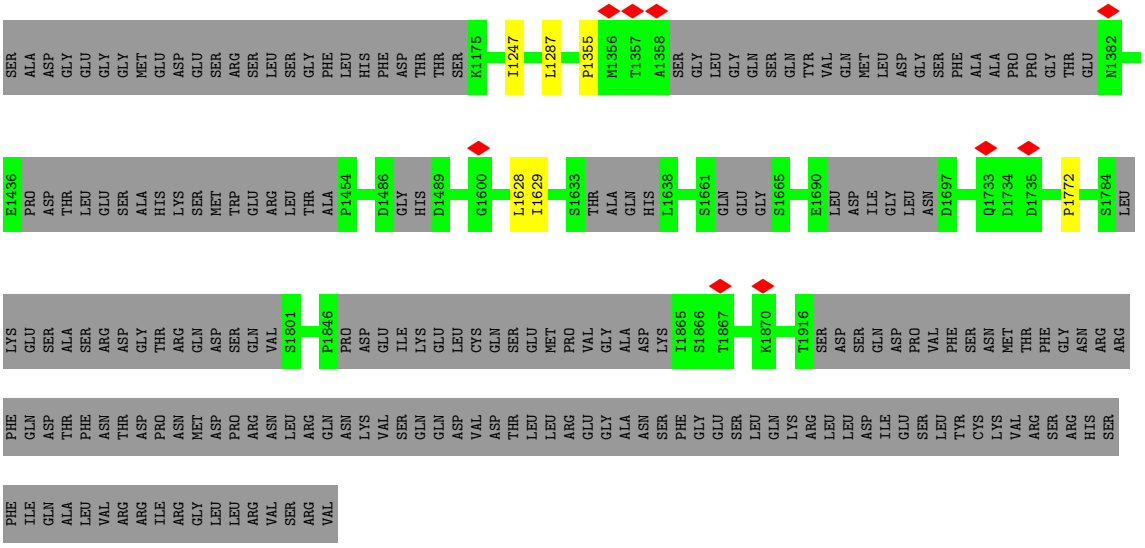
Chain A:



• Molecule 1: MGC83295 protein

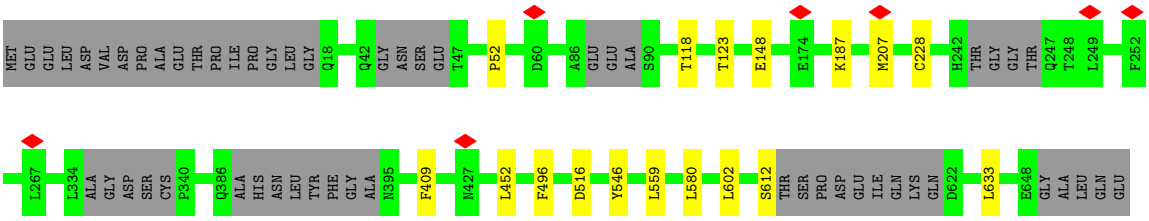
Chain a:





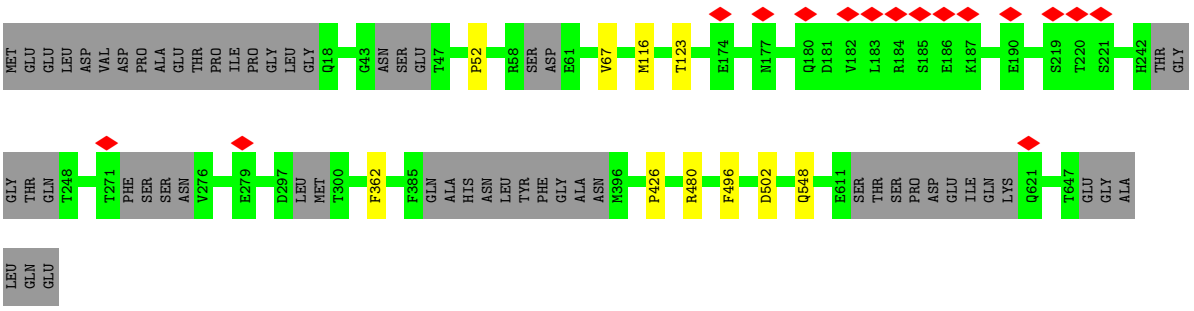
• Molecule 2: Nuclear pore complex protein Nup85

Chain B:



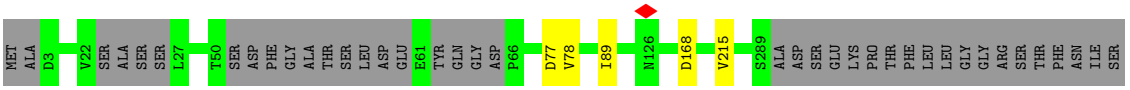
• Molecule 2: Nuclear pore complex protein Nup85

Chain b:



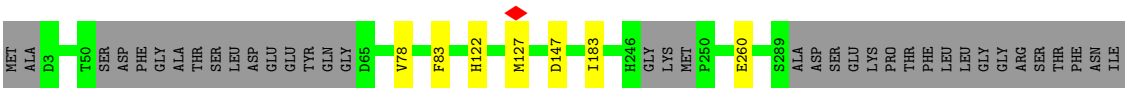
• Molecule 3: MGC154553 protein

Chain C:



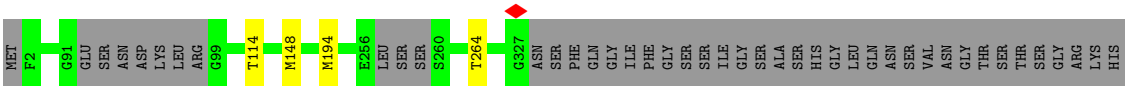
• Molecule 3: MGC154553 protein

Chain c:



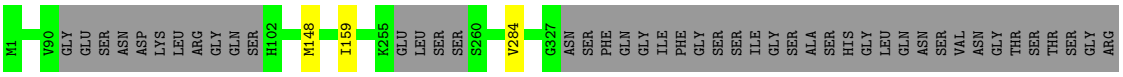
• Molecule 4: Nucleoporin SEH1-B

Chain D:



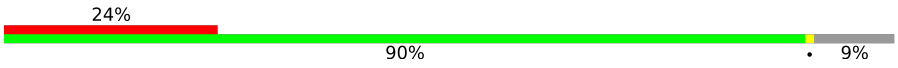
• Molecule 4: Nucleoporin SEH1-B

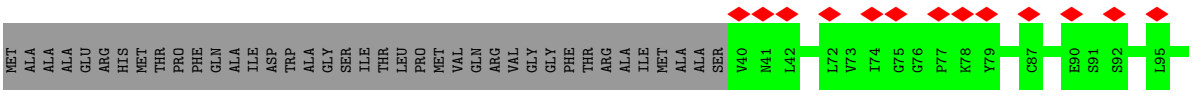
Chain d:

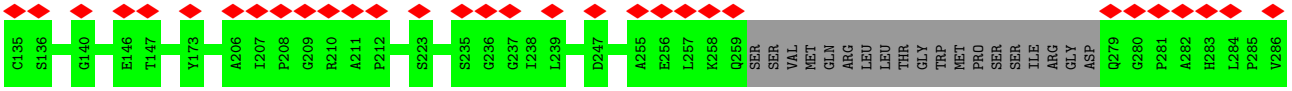


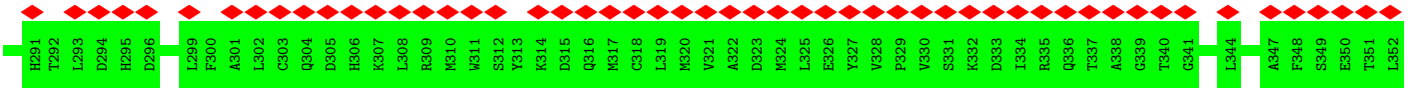
• Molecule 5: outer Nup160

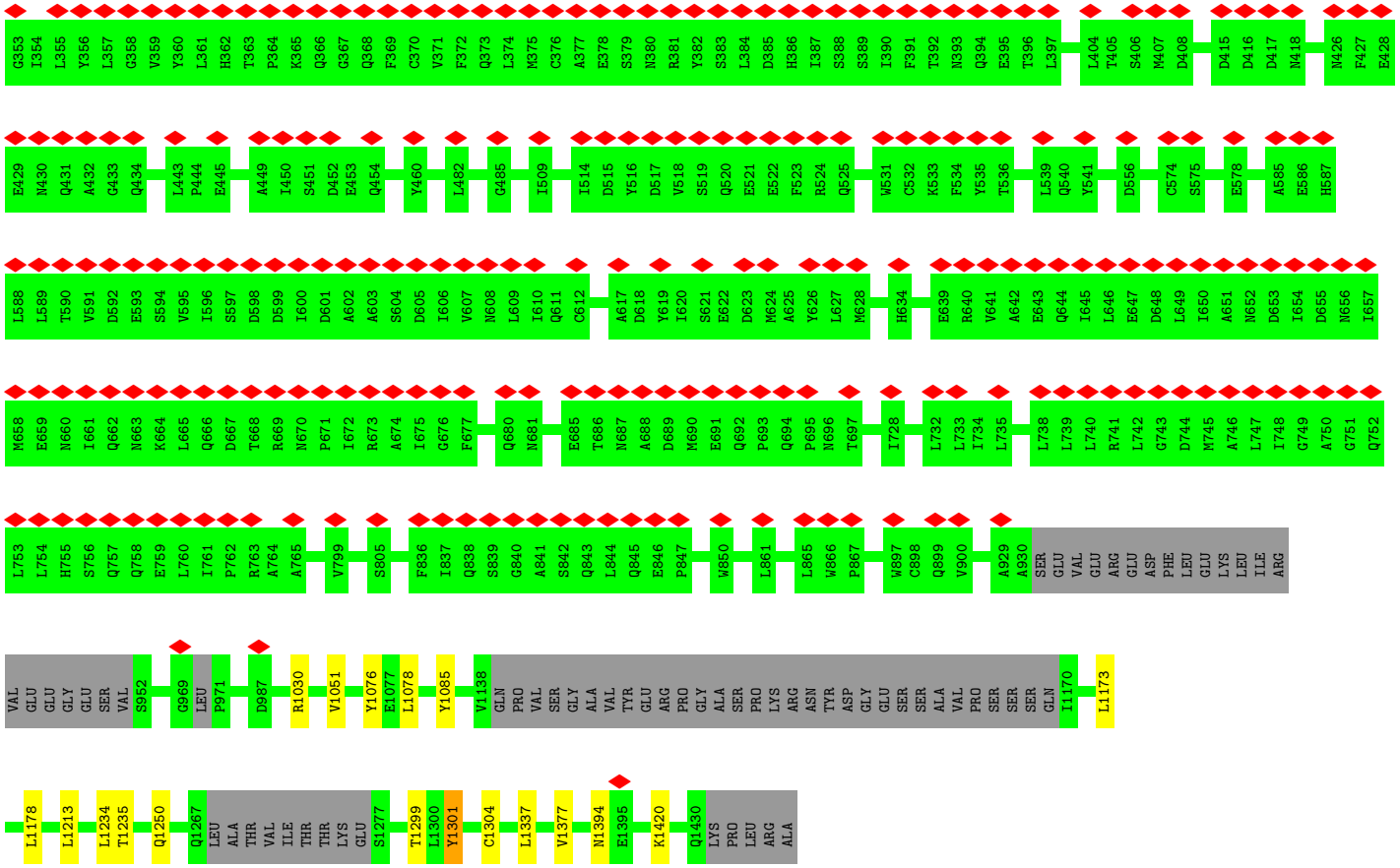
Chain E:





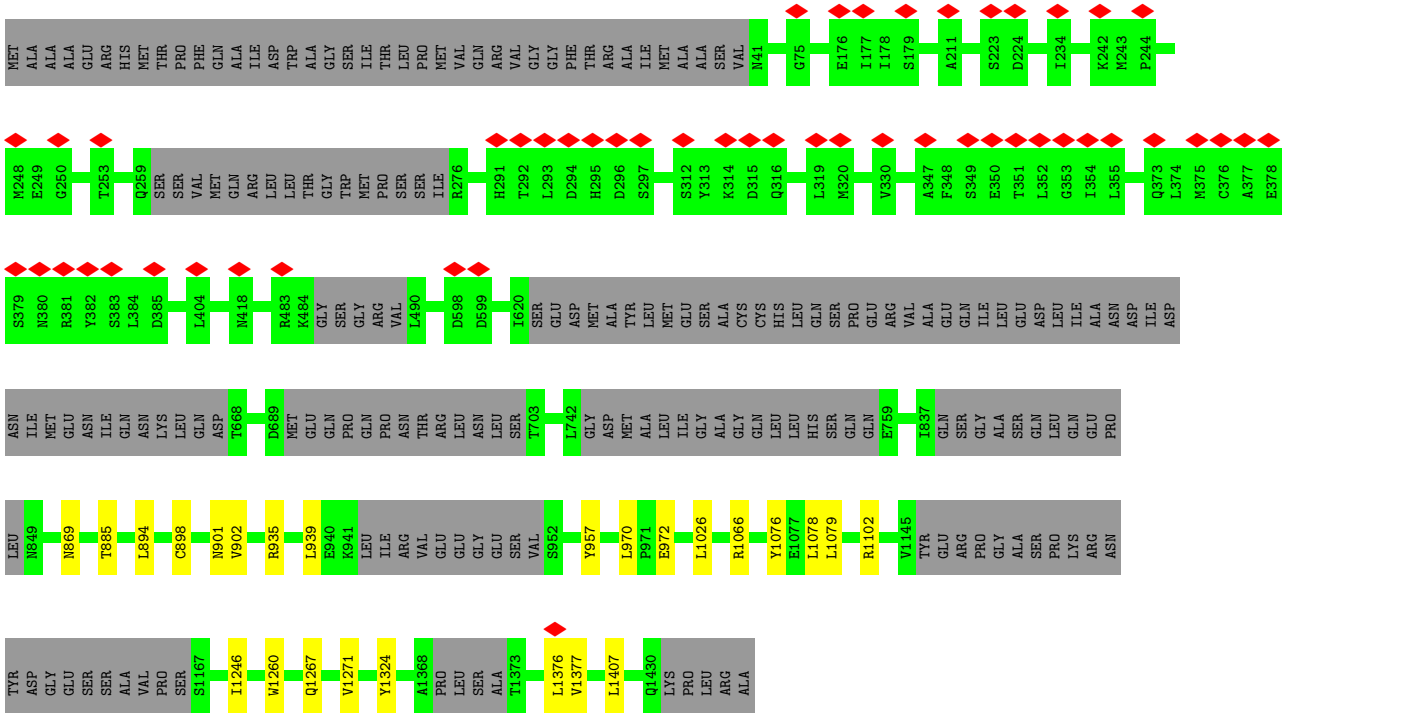






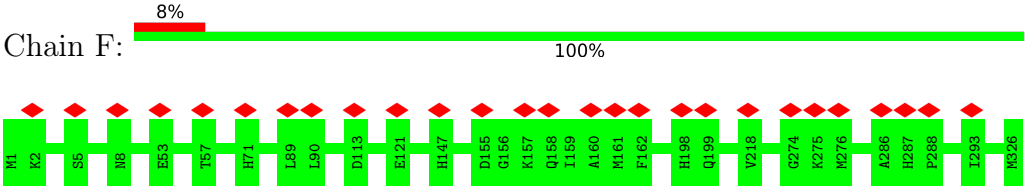
- Molecule 5: outer Nup160

Chain e:



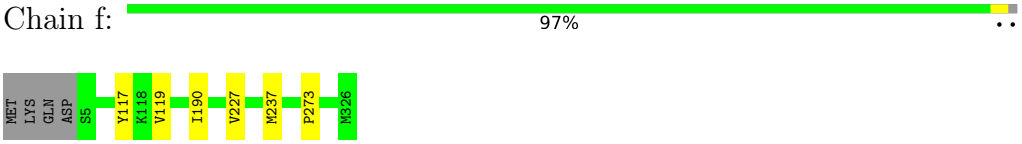
• Molecule 6: MGC83926 protein

Chain F:



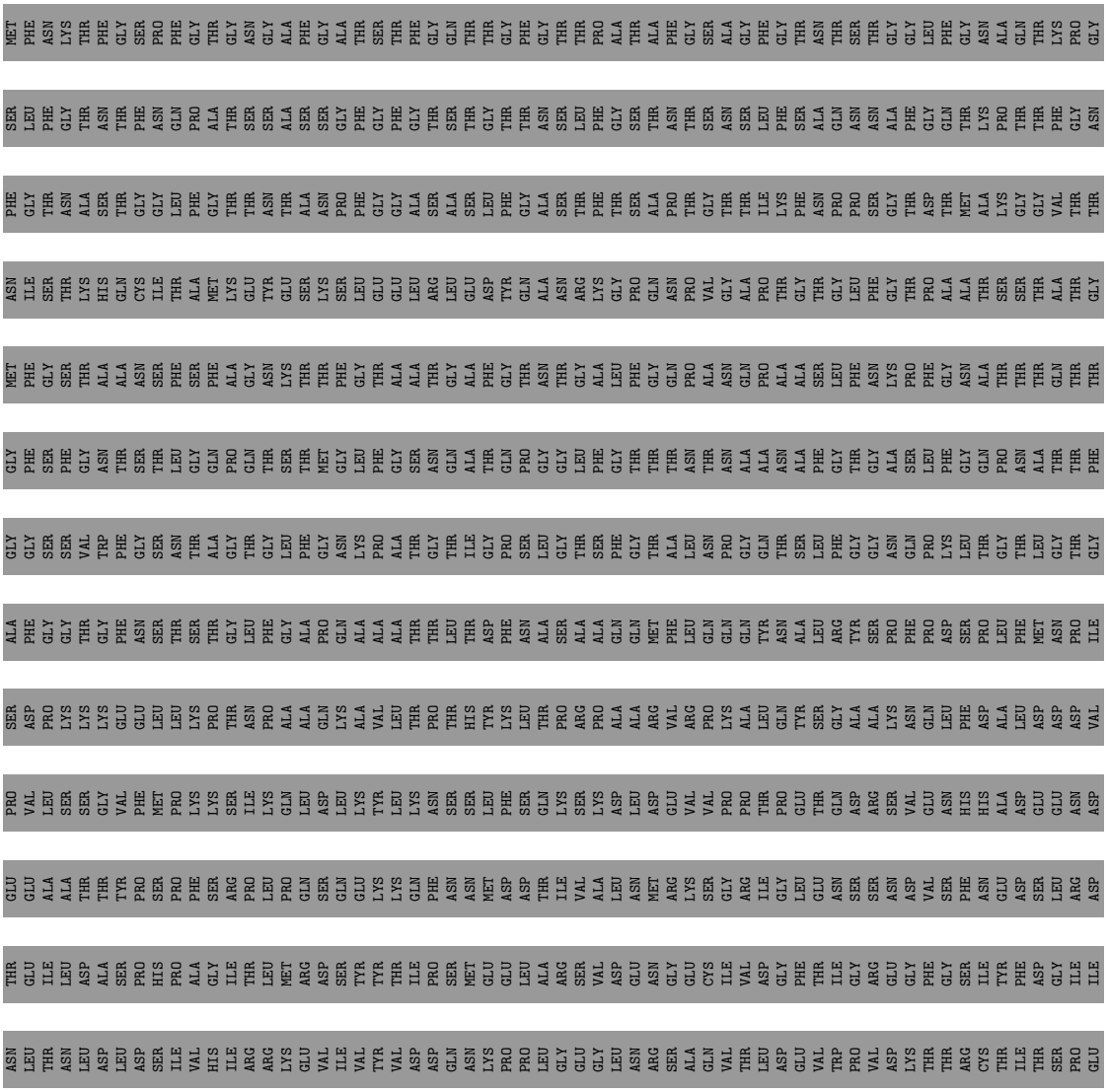
• Molecule 6: MGC83926 protein

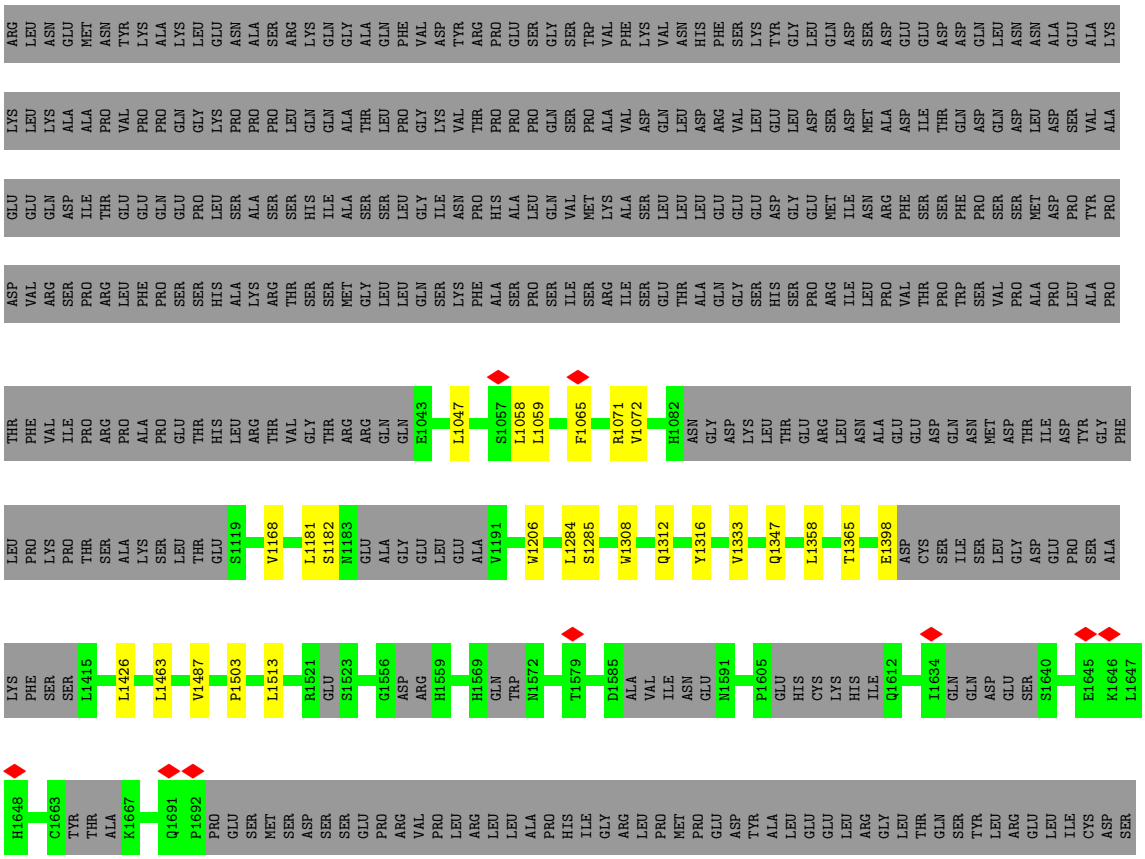
Chain f:



• Molecule 7: Nuclear pore complex protein Nup98-Nup96

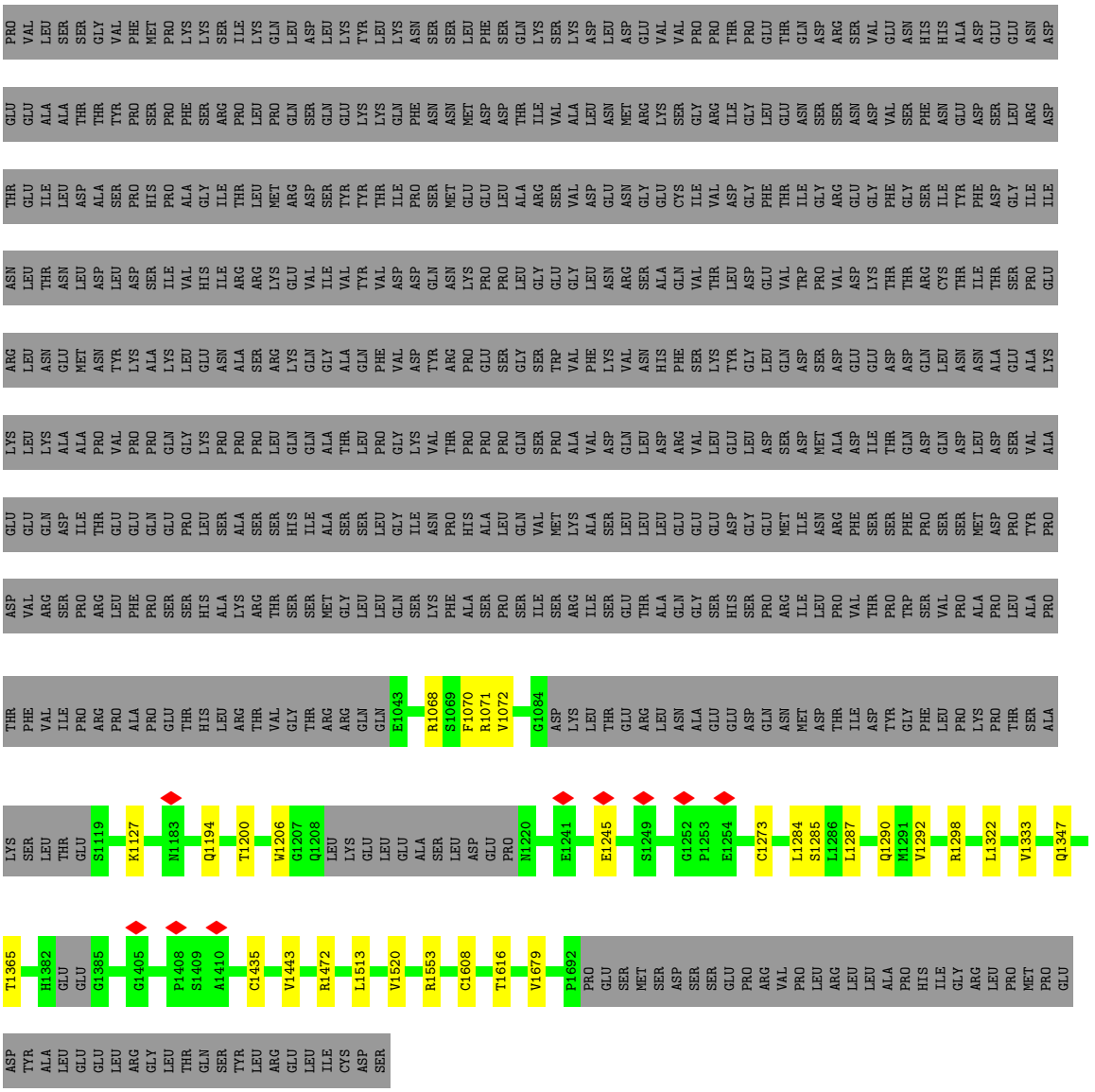
Chain G:





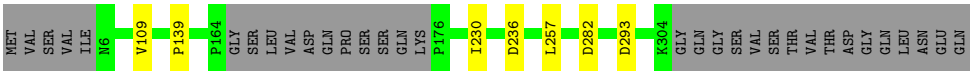
• Molecule 7: Nuclear pore complex protein Nup98-Nup96

Chain g:



• Molecule 8: Protein SEC13 homolog

Chain H:

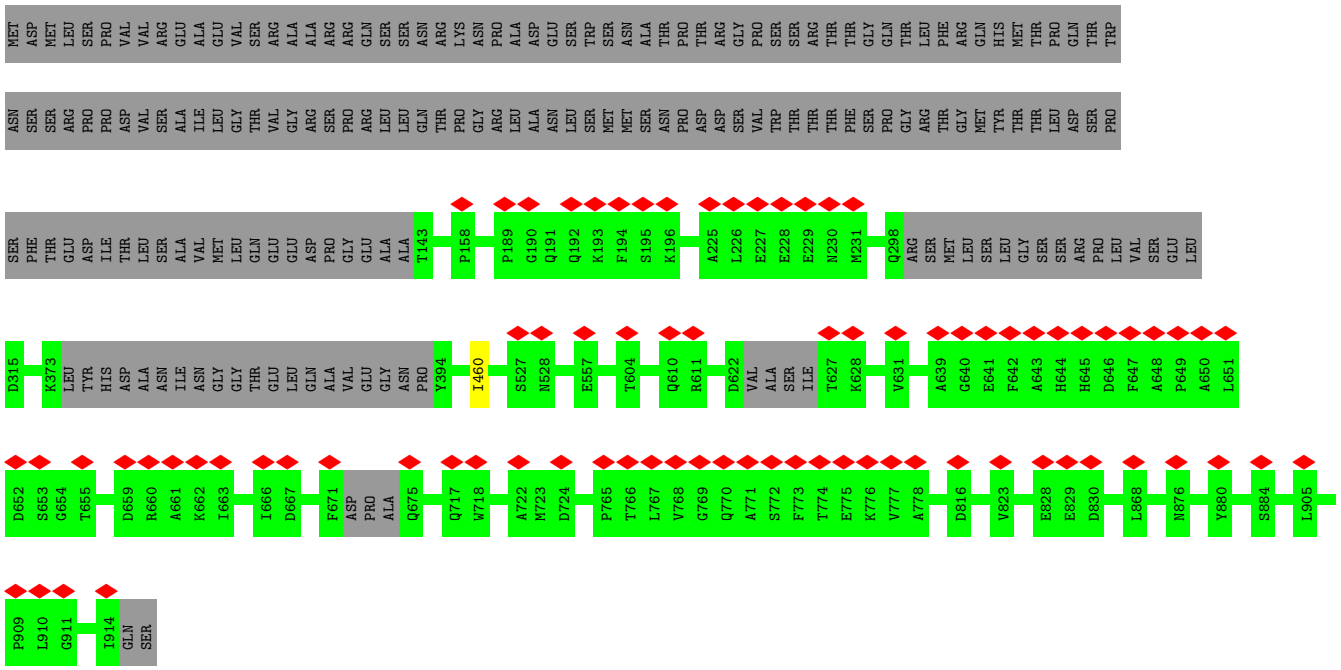


• Molecule 8: Protein SEC13 homolog

Chain h:

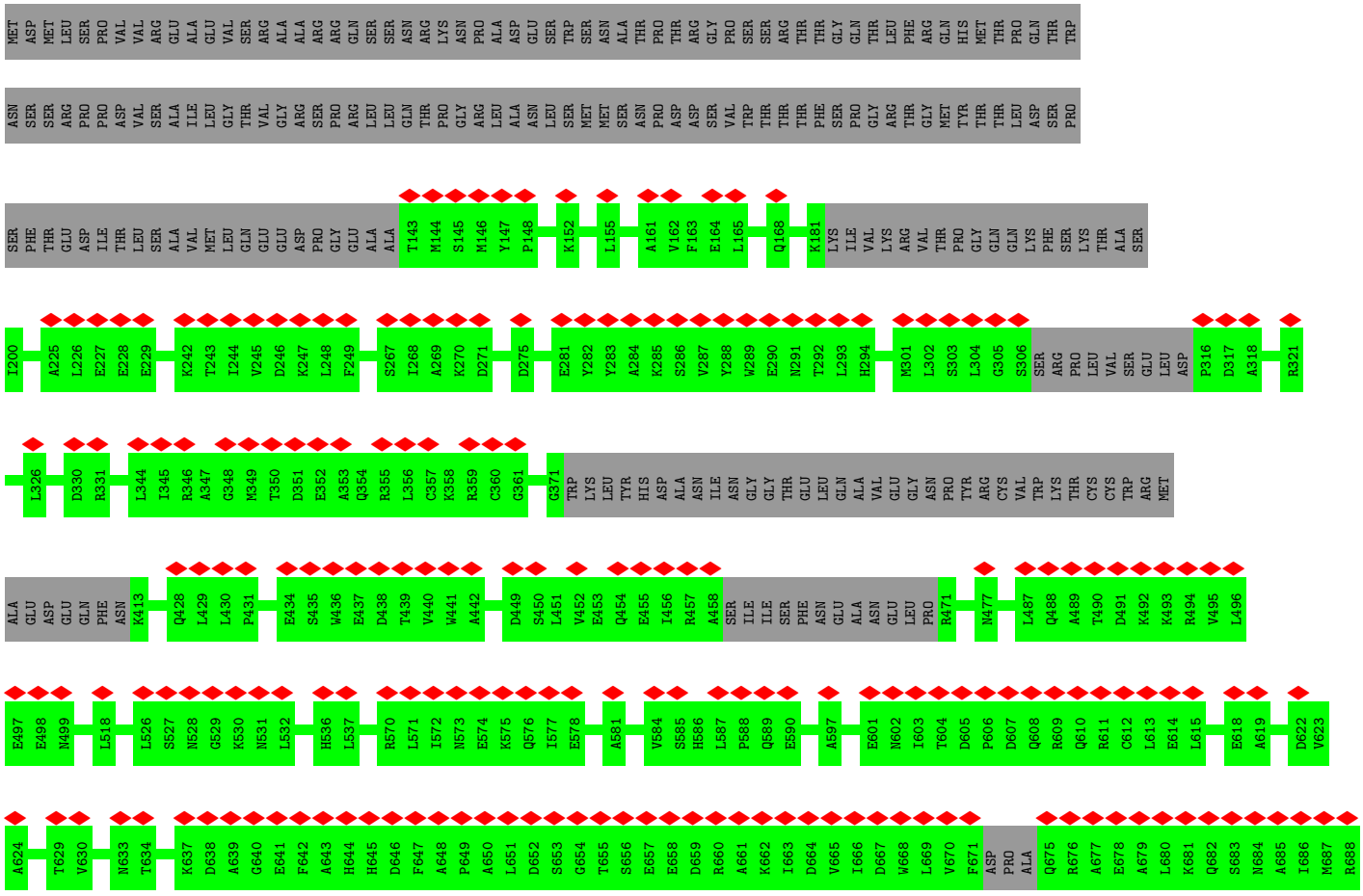
• Molecule 9: Nuclear pore complex protein

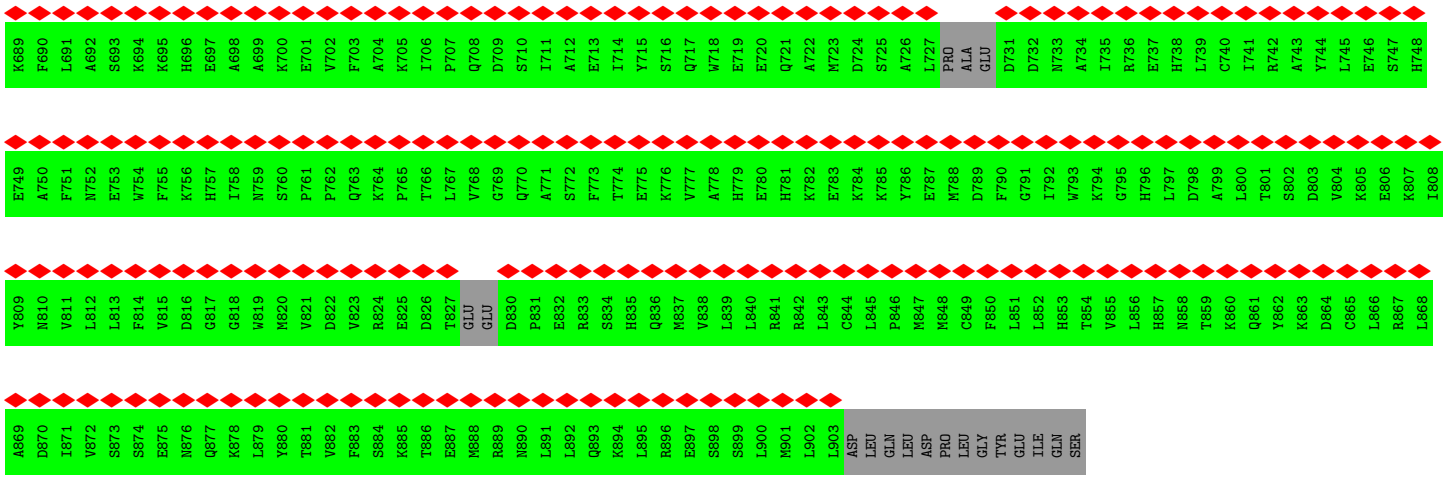
Chain I:



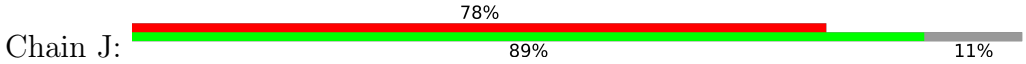
• Molecule 9: Nuclear pore complex protein

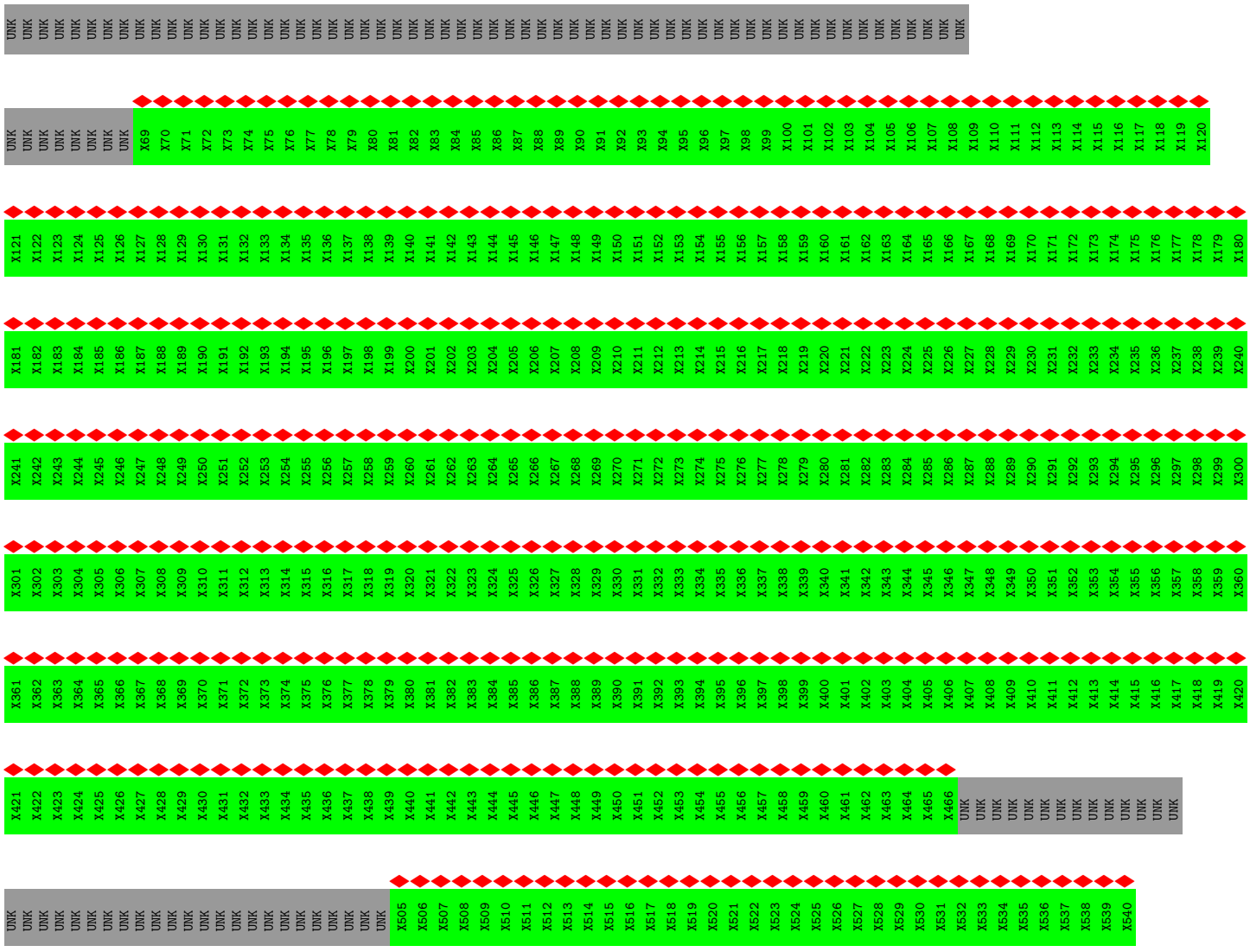
Chain i:

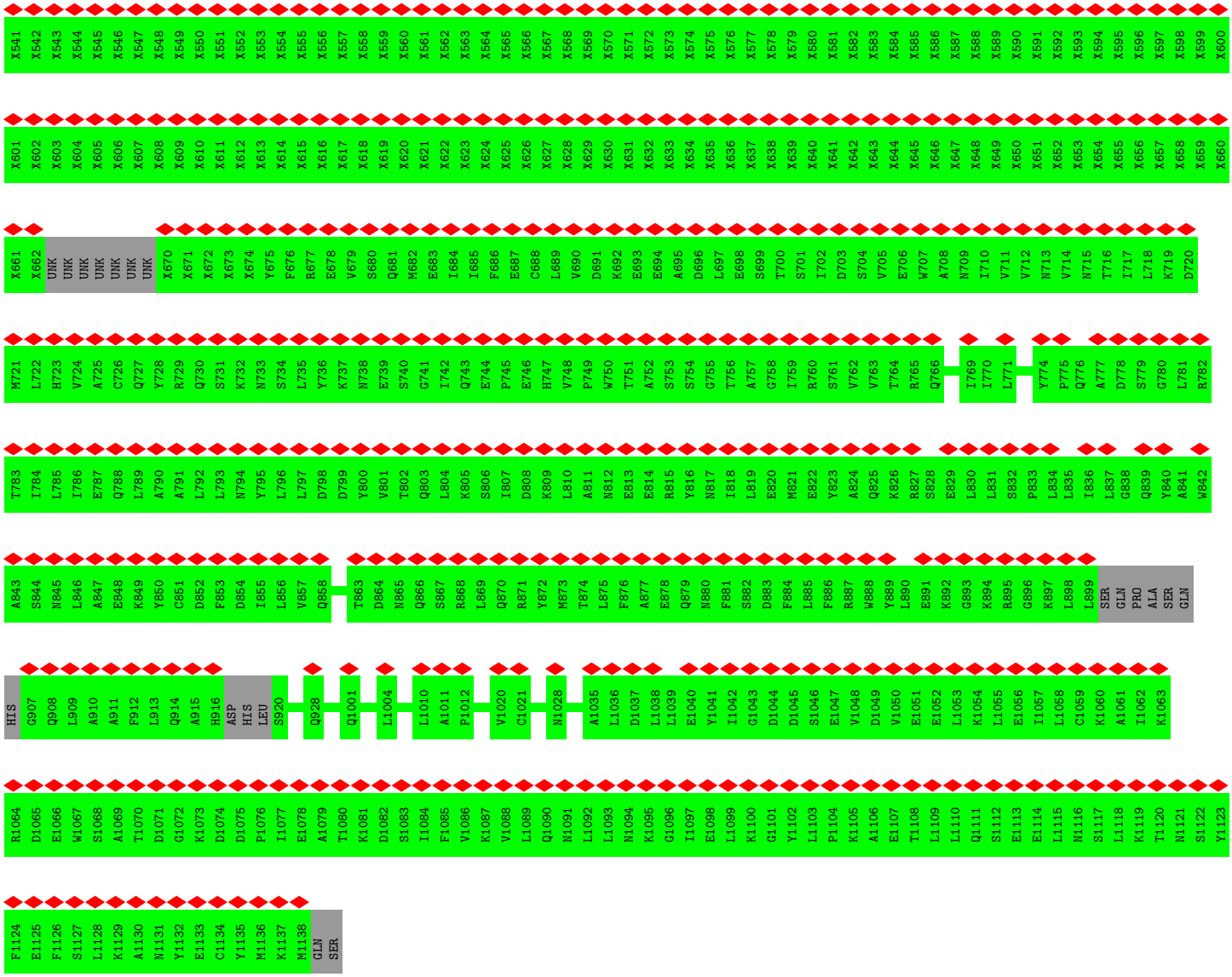




• Molecule 10: nuclear pore complex protein Nup133

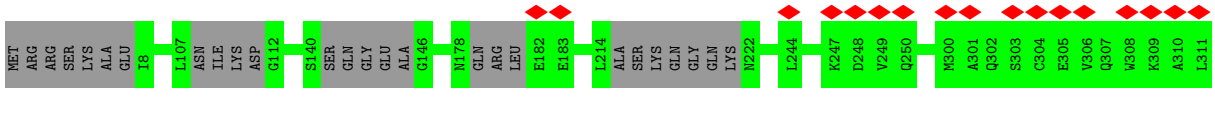


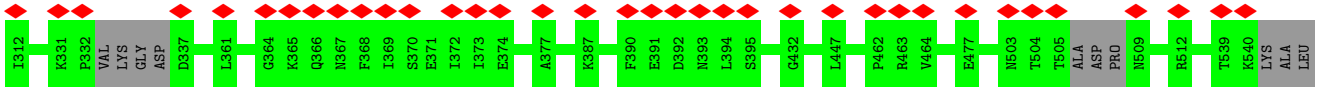

UNK UNK UNK

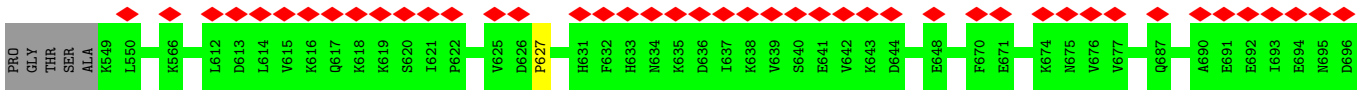


• Molecule 11: Nup358 complex, clamps

Chain K:







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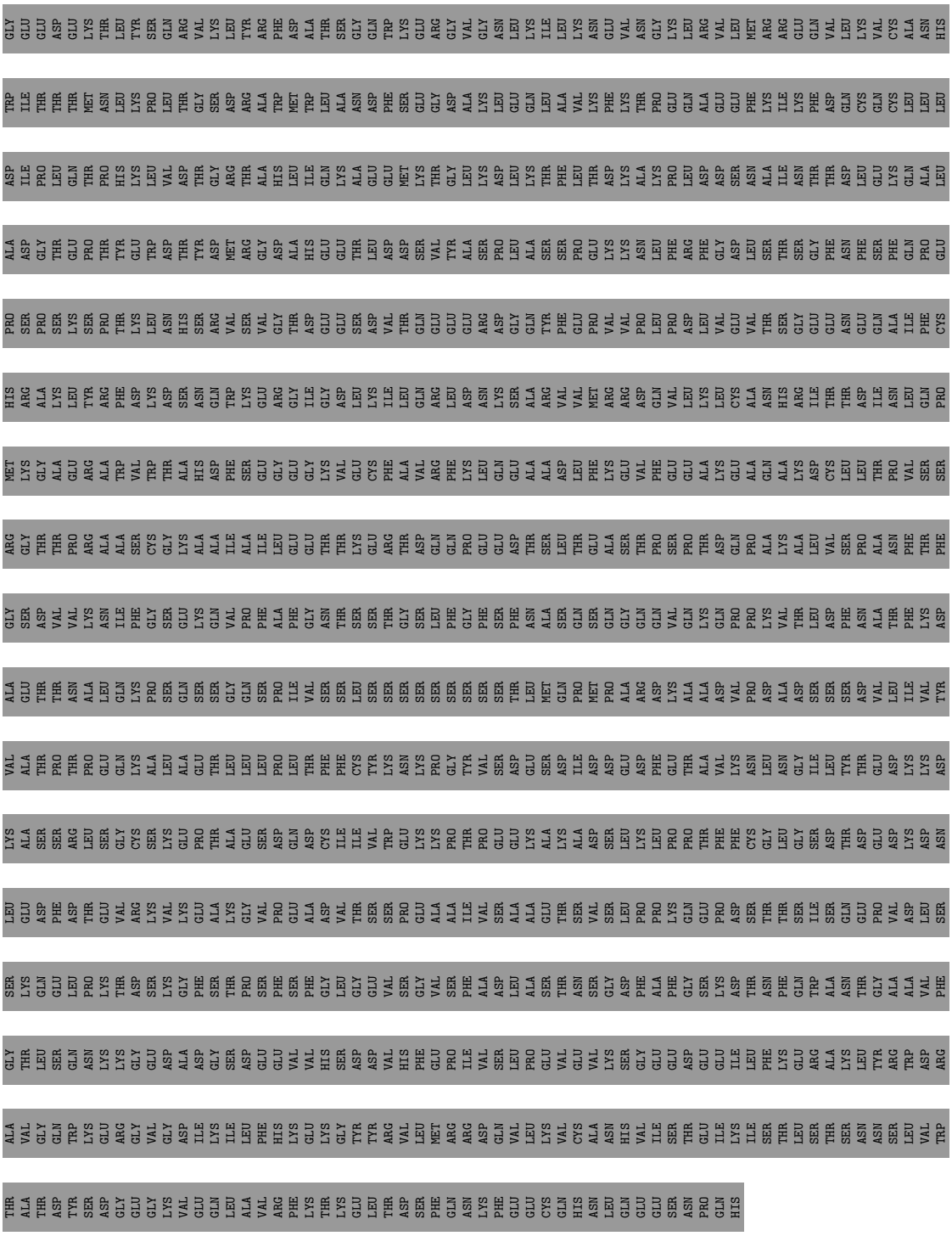
GLU THR VAL PHE GLU MET LEU ASP SER VAL LYS GLN SER LEU GLY GLU ALA MET ASP ASP
HIS SER PRO ALA PHE MET GLU ASN HIS SER VAL LEU THR THR SER ALA ILE LYS HIS SER THR PRO SER PRO THR LYS LEU THR ILE SER PRO SER LYS SER ALA ARG PHE SER PRO LYS THR PRO ARG TRP ALA GLU ASP GLN LYS SER LEU LEU GLU VAL LEU CYS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



• Molecule 11: Nup358 complex, clamps

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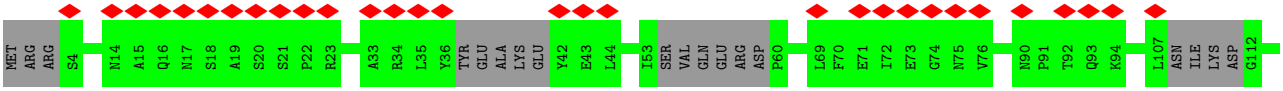
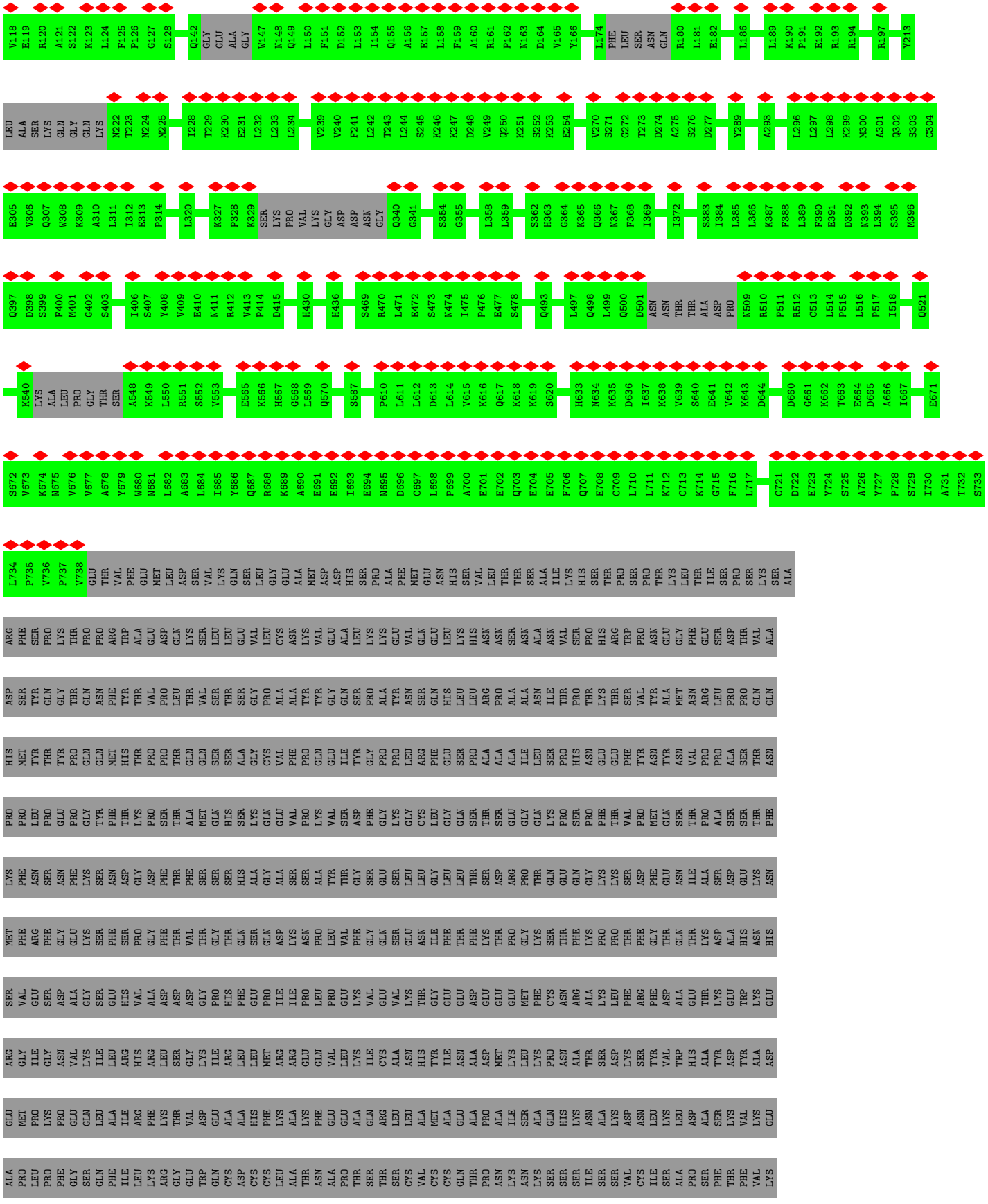
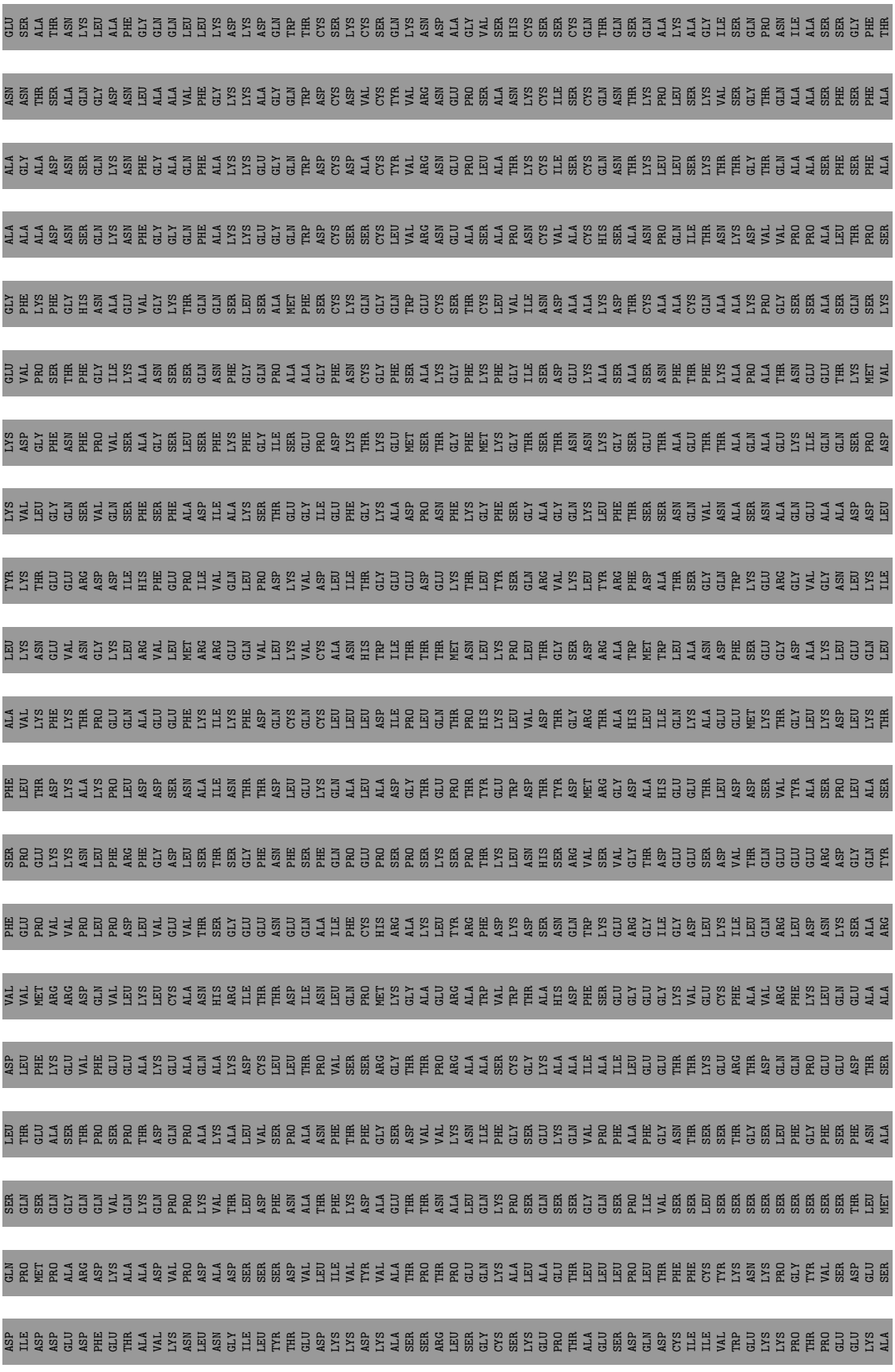



V118 E119 R120 A121 S122 K123 L124 F125 P126 G127 S128 Q142 GLY GLU ALA GLY W147 N148 Q149 L150 F151 D152 L153 I154 Q155 A156 E157 L158 F159 A160 R161 P162 N163 D164 V165 Y166 L174 PHE LEU SER ASN GLN R180 L181 E182 L186 L189 K190 P191 E192 R193 R194 R197 Y213
LEU ALA SER LYS GLN GLY GLN LYS N222 T223 N224 M225 T228 T229 K230 E231 L232 L233 L234 V239 V240 F241 L242 T243 L244 S245 K246 K247 D248 V249 Q250 K251 S252 K253 E254 V270 S271 G272 T273 D274 A275 S276 D277 Y289 A293 L296 L297 L298 K299 M300 A301 Q302 S303 C304
E305 V306 Q307 W308 K309 A310 L311 I312 E313 P314 L320 K327 P328 K329 SER LYS PRO VAL LYS GLY ASP ASP ASN GLY Q340 G341 S354 G355 L358 L359 S362 H363 G364 K365 Q366 N367 F368 I369 I372 S383 I384 L385 L386 K387 F388 L389 F390 E391 D392 N393 L394 S395 M396
Q397 D398 S399 F400 M401 G402 S403 I406 S407 Y408 V409 E410 N411 R412 V413 P414 D415 H430 H436 S469 R470 L471 E472 S473 N474 I475 P476 E477 S478 Q493 L497 Q498 L499 Q500 D501 ASN ASN THR THR ALA ASP PRO N509 R510 P511 R512 C513 L514 P515 L516 P517 I518 Q521
K540 LYS ALA LEU PRO GLY THR SER A548 K549 L550 R551 S552 V553 E565 K566 H567 G568 L569 Q570 S587 P610 L611 L612 D613 L614 V615 K616 Q617 K618 K619 S620 H633 N634 K635 D636 I637 K638 V639 S640 E641 V642 K643 D644 D660 G661 K662 T663 E664 D665 A666 I667 E671
S672 V673 K674 N675 V676 V677 A678 Y679 W680 N681 L682 A683 L684 I685 Y686 Q687 R688 K689 A690 E691 E692 I693 E694 N695 D696 C697 L698 P699 A700 E701 E702 Q703 E704 E705 F706 Q707 E708 C709 L710 L711 K712 C713 K714 G715 F716 L717 C721 D722 E723 Y724 S725 A726 Y727 P728 S729 I730 A731 T732 S733
L734 P735 V736 P737 V738 GLU THR VAL PHE GLU MET LEU ASP SER VAL LYS GLN SER LEU GLY GLU ALA MET ASP ASP HIS SER PRO ALA PHE MET GLU ASN 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 LYS THR PRO PRO ARG TRP ALA GLU ASP GLN LYS SER LEU LEU GLU VAL LEU LEU CYS ASN LYS VAL GLU ALA LEU LYS LYS GLU VAL GLN GLU GLU LEU LYS HIS ASN 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 ALA TYR TYR GLY GLN SER PRO ALA TYR ASN SER GLN HIS LEU LEU ARG PRO 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 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 HIS 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 SER SER SER HIS ALA ALA GLY ALA SER SER ALA TYR THR GLY SER GLU SER LEU LEU LEU GLY LEU 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 SER ASP LYS ASN PRO LEU VAL PHE GLY GLY GLN SER GLU SER LEU PHE PHE THR PHE LYS SER THR PHE LYS PRO 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 ASP GLU GLU GLU MET PHE CYS ASN ARG ALA LYS LEU PHE ARG PHE ASP ALA GLU THR LYS GLU TRP 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 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 GLN ALA ALA HIS PHE LYS ALA ALA LYS PHE GLU GLU ALA ILE ARG CYS CYS LEU ALA ALA THR ASN ALA PRO THR SER THR SER THR SER CYS VAL CYS CYS GLN THR PRO ASN LYS ASN LYS SER SER SER ILE SER SER VAL CYS ILE SER ALA PRO SER PHE THR PHE VAL LYS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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 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 SER ALA THR 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 ASP ASN SER GLN LYS ASN PHE GLY GLY LYS GLN PHE ALA LYS LYS GLU GLY GLN TRP ASP CYS SER SER CYS LEU VAL ARG ASN GLU ALA SER ALA THR 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 GLY LYS THR GLN GLN SER LEU SER ALA MET PHE SER CYS LYS GLN GLY GLN LYS ASP THR CYS SER GLY GLN LYS ASP THR CYS ALA LEU SER GLN SER LYS
GLU VAL PRO SER THR PHE GLY ILE LYS ALA ASN SER SER GLN ASN PHE GLY GLN PRO ALA ALA GLY PHE ASN CYS GLY PHE SER ASP GLU LYS ALA ALA SER ALA SER ASN PHE THR PHE LYS ALA PRO ALA THR ASN GLY PHE THR LYS VAL
LYS ASP GLY PHE ASN PHE PRO VAL SER ALA 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 GLN SER PHE SER PHE SER ALA ASP ILE ALA LYS SER THR GLU GLY ILE GLU PHE GLY LYS ALA ASP PRO ASN PHE PHE SER GLY ALA GLY GLN LYS LEU PHE THR SER SER ASN GLN VAL ASN ALA ALA SER ASN GLN ALA GLN ALA ASP ASP
TYR LYS THR GLU GLU ARG 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 GLY GLN TRP LYS THR GLU GLY GLY ARG GLY VAL GLY ASN LEU LYS ILE
LEU LYS ASN GLU VAL ASN GLY LYS LEU ARG VAL LEU MET ARG ARG GLU GLN VAL LEU LYS VAL CYS ALA ASN HIS TRP ILE THR THR MET ASN LEU LYS PRO LEU THR GLY SER ASP ARG ALA TRP MET TRP LEU ALA ASN ASP PHE SER GLU GLY GLN ALA LYS LEU VAL GLN LEU
ALA VAL LYS PHE LYS THR PRO GLU GLN ALA GLU GLU PHE LYS ILE LYS PHE ASP GLN CYS GLN CYS LEU LEU LEU ASP ILE PRO LEU GLN THR PRO THR THR GLU ASP ARG ALA HIS LEU ILE GLN LYS ALA GLU GLU THR LEU ALA GLN LYS VAL ASP THR GLY ARG THR ALA LEU ILE LEU LEU LYS LYS THR
PHE LEU THR ASP LYS PRO LEU ASP SER ASN ALA ILE ASN THR THR GLU PRO THR TYR GLU TRP ASP THR TYR ASP MET ARG GLY ASP ALA HIS GLU GLU THR LEU ASP ASP SER VAL TYR ALA SER PRO LEU ALA SER
SER PRO GLU LYS LYS ASN PHE ARG PHE GLY ASP LEU SER THR SER GLY GLY PHE ASN PHE SER PHE GLN PRO GLU PRO SER PRO SER LYS SER PRO PRO THR LYS LEU ASN HIS SER ARG VAL SER VAL GLY THR ASP GLU GLU SER ASP VAL THR GLN GLU GLU GLU ARG ASP GLY GLN TYR
PHE GLU PRO VAL VAL PRO LEU LEU VAL GLU PRO ASP LEU ALA ILE PHE CYS HIS ARG ALA LYS LEU TYR ARG PHE ASP LYS ASP SER ASN GLN TRP LYS GLU ARG GLY ILE GLY ASP LEU LYS ILE LEU GLN ARG LEU ASP ASN LYS SER ALA ARG
VAL VAL MET ARG ARG ASP HIS ARG ILE THR ASP ILE ASN LEU GLN PRO MET LYS GLY ALA GLU ARG ALA TRP VAL TRP THR ASP ALA HIS ASP PHE SER GLU GLY GLY THR ALA ASP PHE LYS LEU GLN GLN ALA ALA
ASP LEU PHE LYS GLU ALA ALA GLN LYS ALA ALA SER CYS GLY LYS ALA ALA ILE ALA ILE LEU GLU GLN GLN PRO GLU ARG THR ASP GLN GLN ARG
LEU THR GLU ALA SER PRO THR ASP GLN GLY PHE THR SER GLY SER GLU LYS ASN ILE PHE GLY VAL PRO PHE ALA PHE GLY ASN THR SER SER THR GLY PHE GLY PHE SER PHE ASN ALA
SER GLN SER GLN GLN PRO LYS VAL THR LEU ASP PHE ASN ALA THR PHE LYS ASP ALA GLU THR THR ASN ALA LEU GLN LYS PRO SER GLN SER PRO ILE VAL SER SER LEU SER SER SER LEU SER SER SER SER SER SER SER SER THR LEU MET
GLN PRO MET PRO ALA ARG ASP LYS ALA ALA VAL PRO ASP ALA ALA ASP VAL LEU ILE VAL TYR VAL ALA THR PRO PRO GLU GLN LEU ALA LEU LEU LEU PRO LEU THR PHE CYS TYR LYS ASN LYS LYS PRO GLY TYR VAL SER GLU THR VAL
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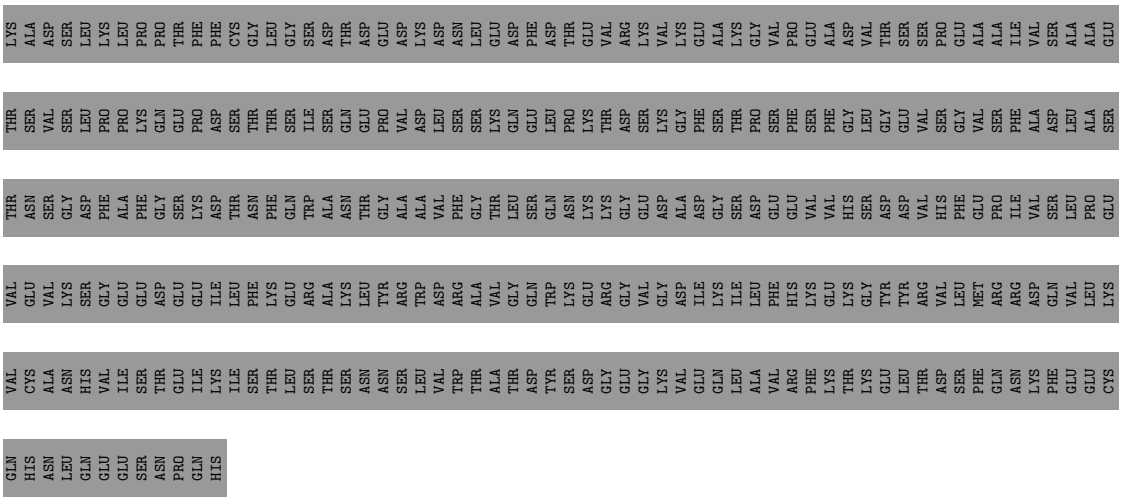
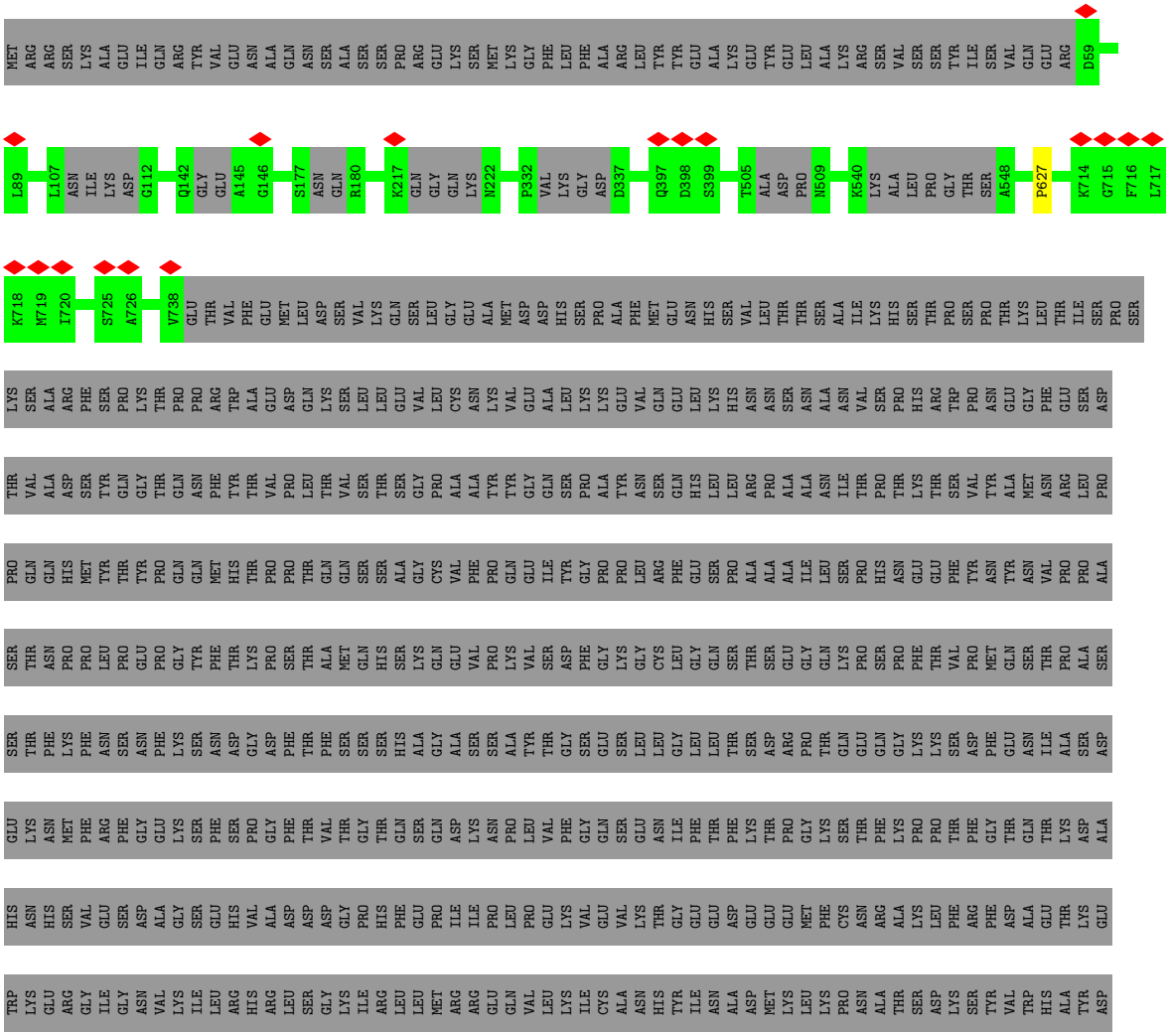
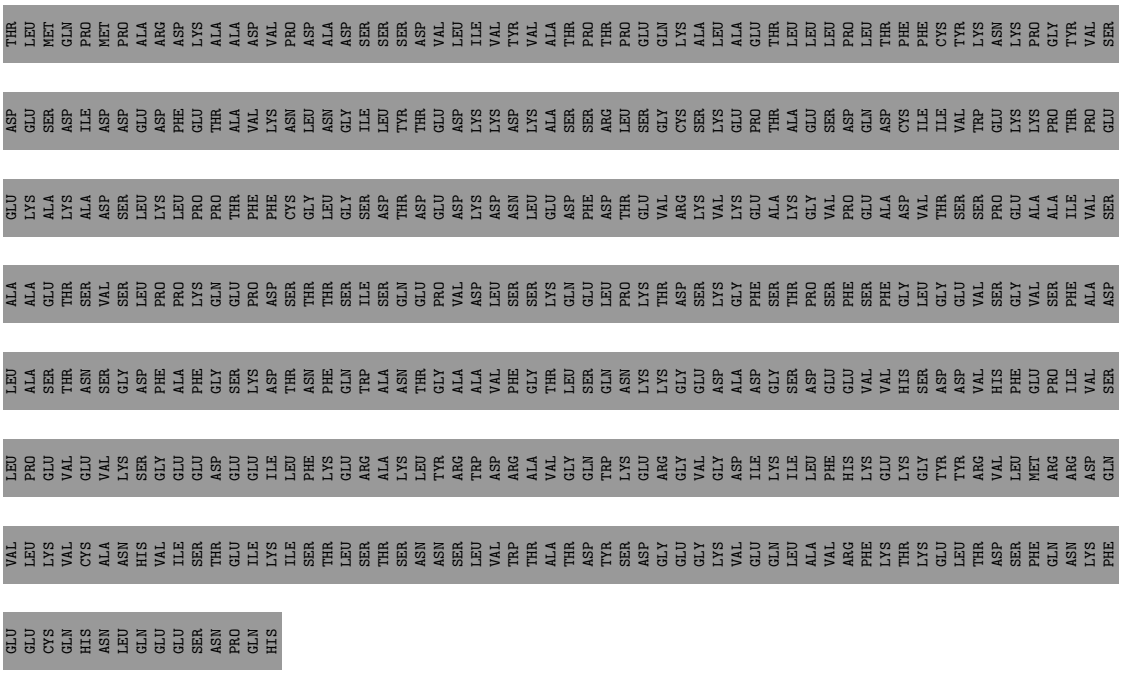


• Molecule 11: Nup358 complex, clamps

Chain M:





• Molecule 11: Nup358 complex, clamps

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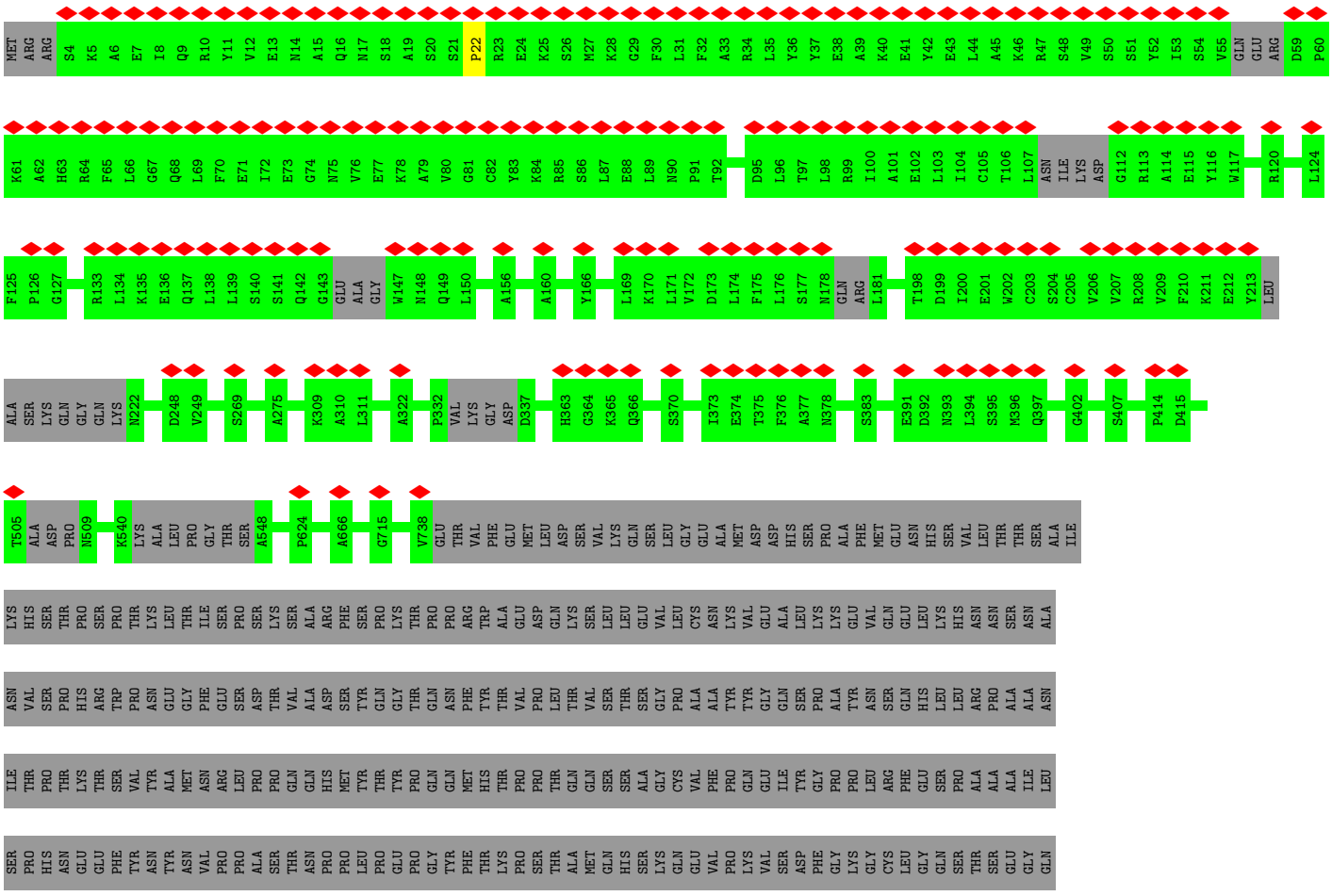

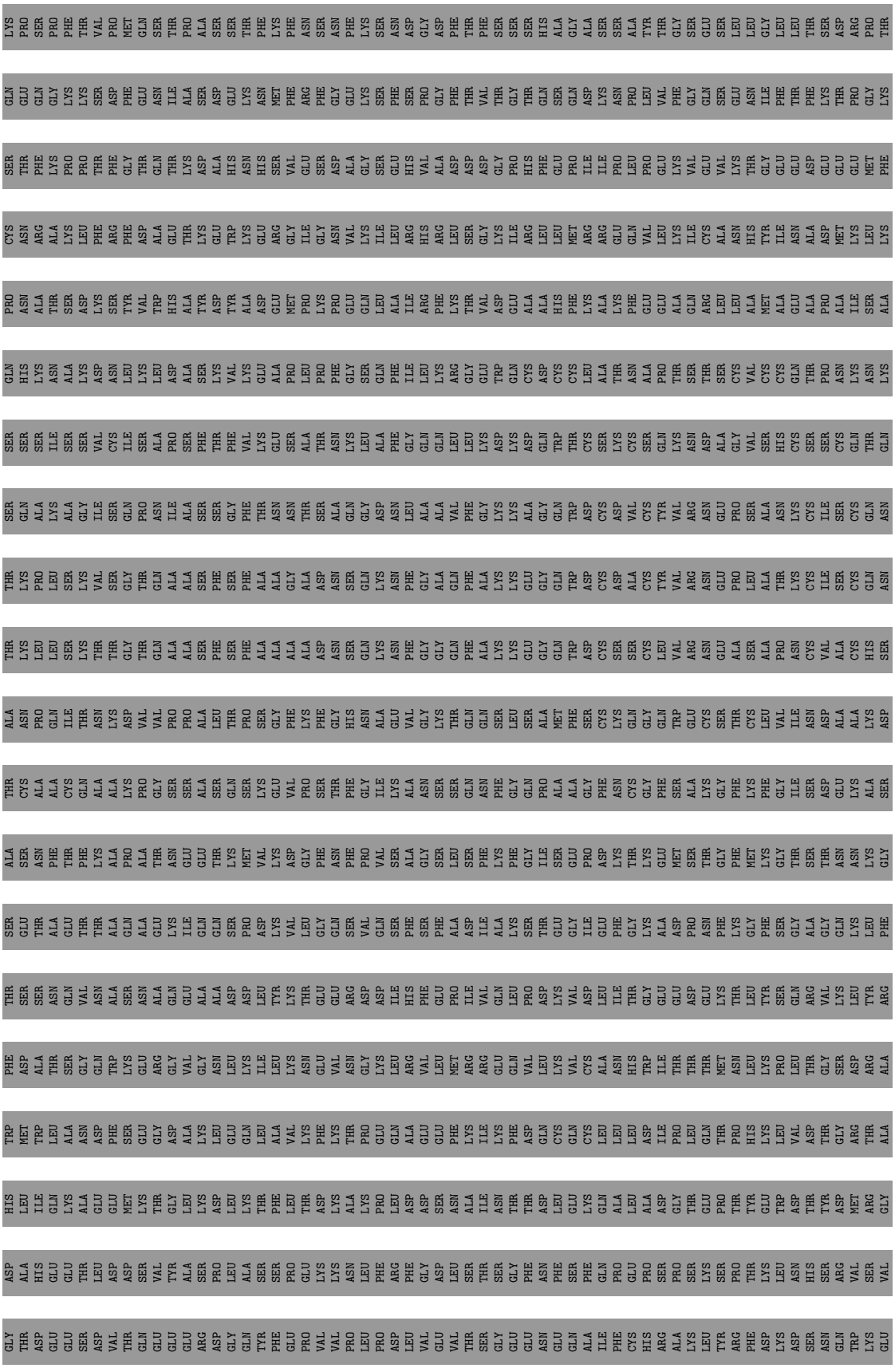
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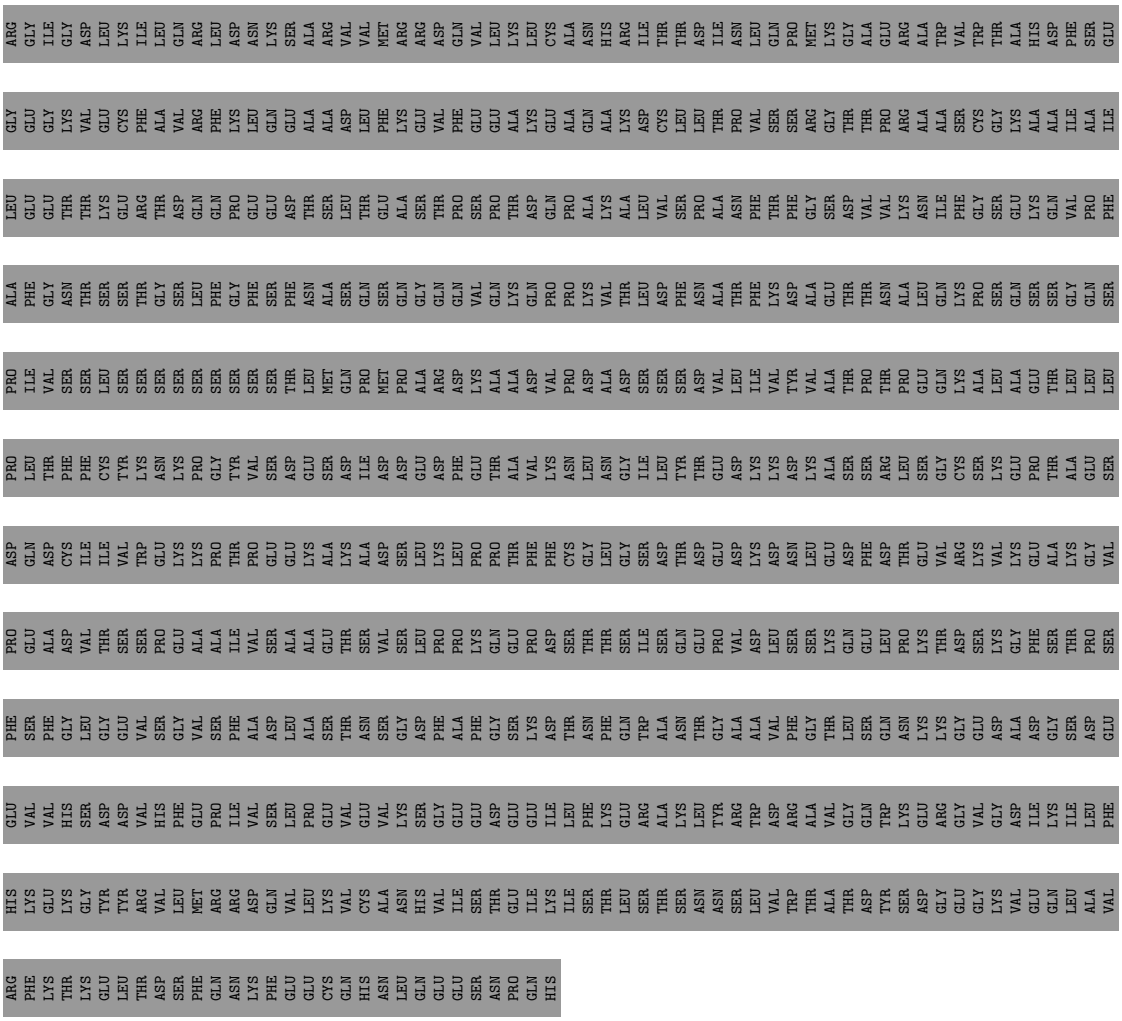
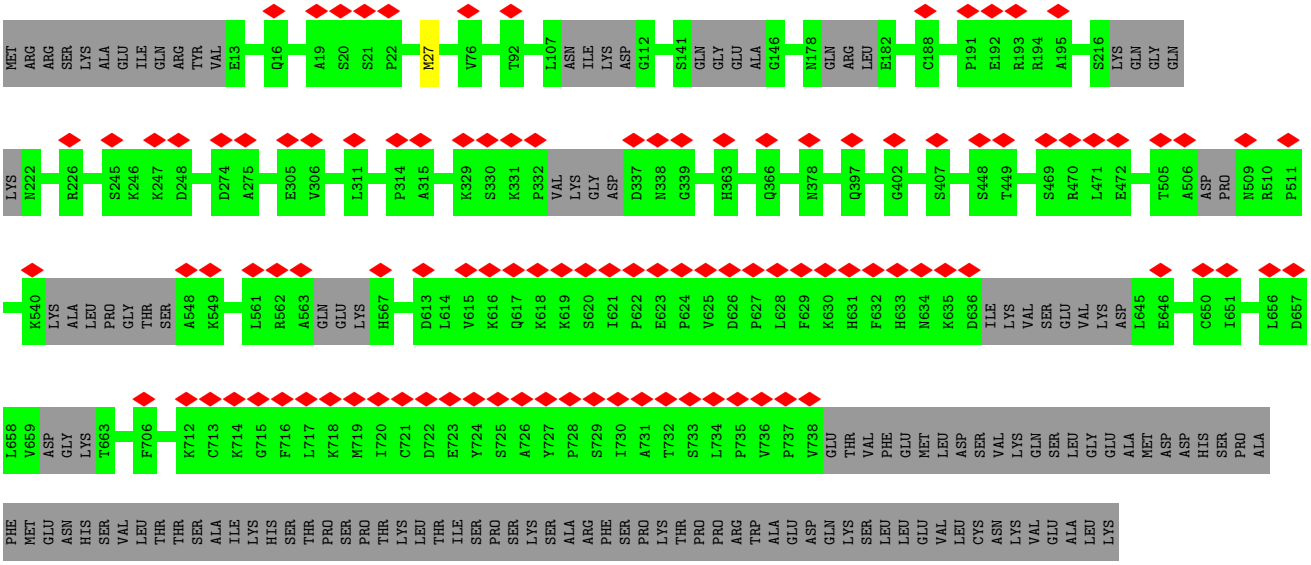
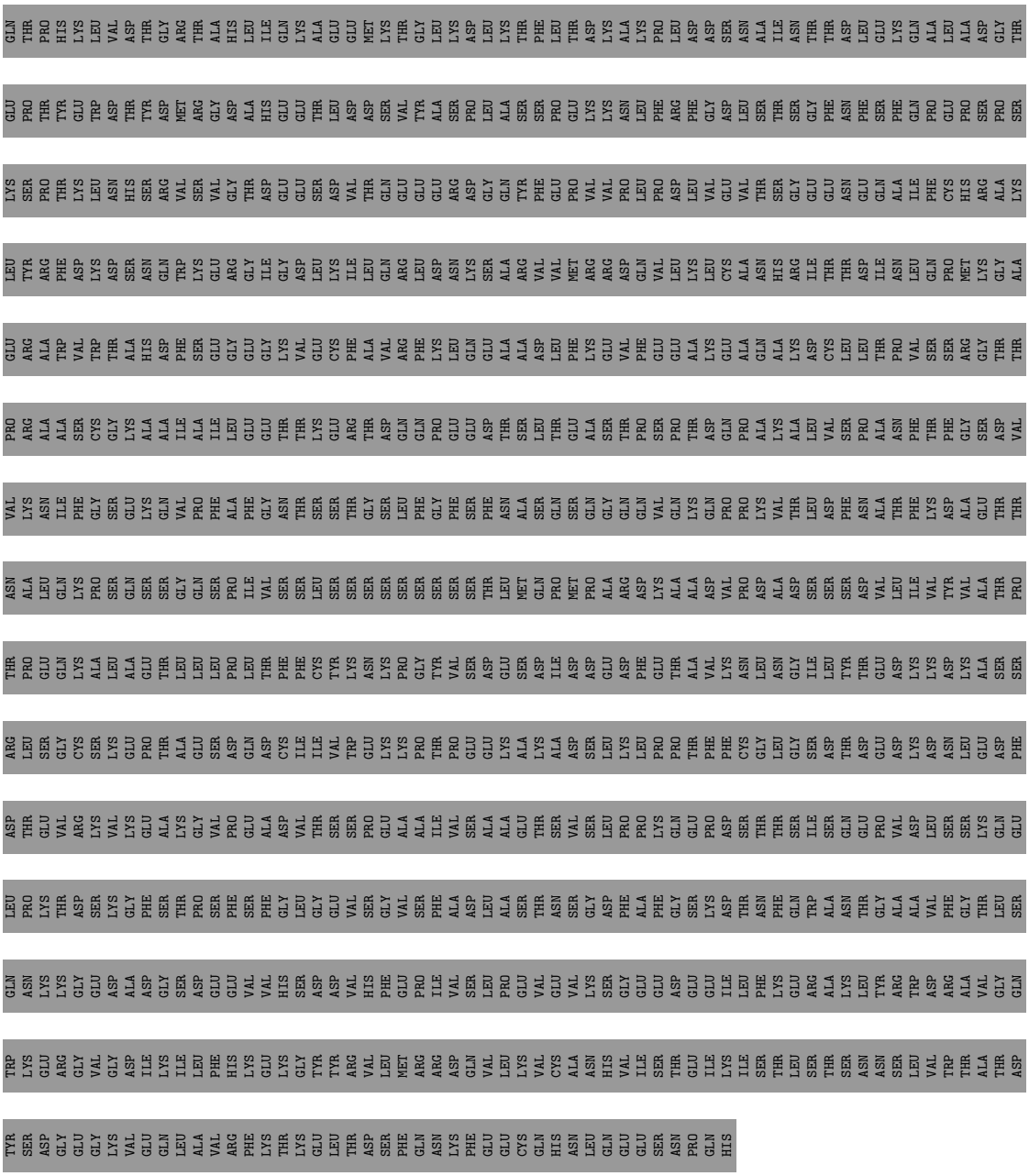
GLN GLU GLN GLY LYS LYS SER ASP PHE GLU ASN ILE ALA SER ASP GLU LYS ASN MET PHE ARG PHE GLY GLU LYS SER PHE SER PRO GLY PHE THR VAL THR GLY THR GLN SER GLU ASN ILE ILE PHE THR PHE GLY LYS PRO GLY
SER THR PHE LYS PRO PRO THR PHE GLY THR GLN THR LYS ASP ALA HIS ASN HIS SER VAL GLU SER ASP ALA GLY SER GLU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



• Molecule 11: Nup358 complex, clamps

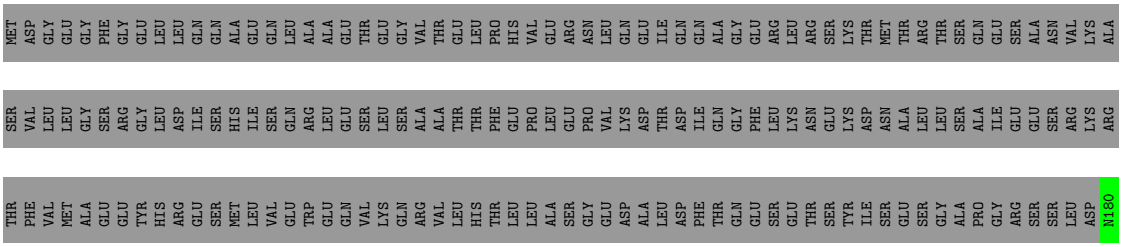
Chain O:

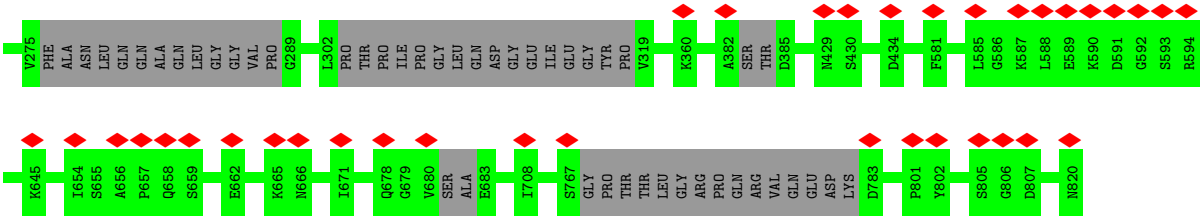




• Molecule 12: Nuclear pore complex protein Nup93

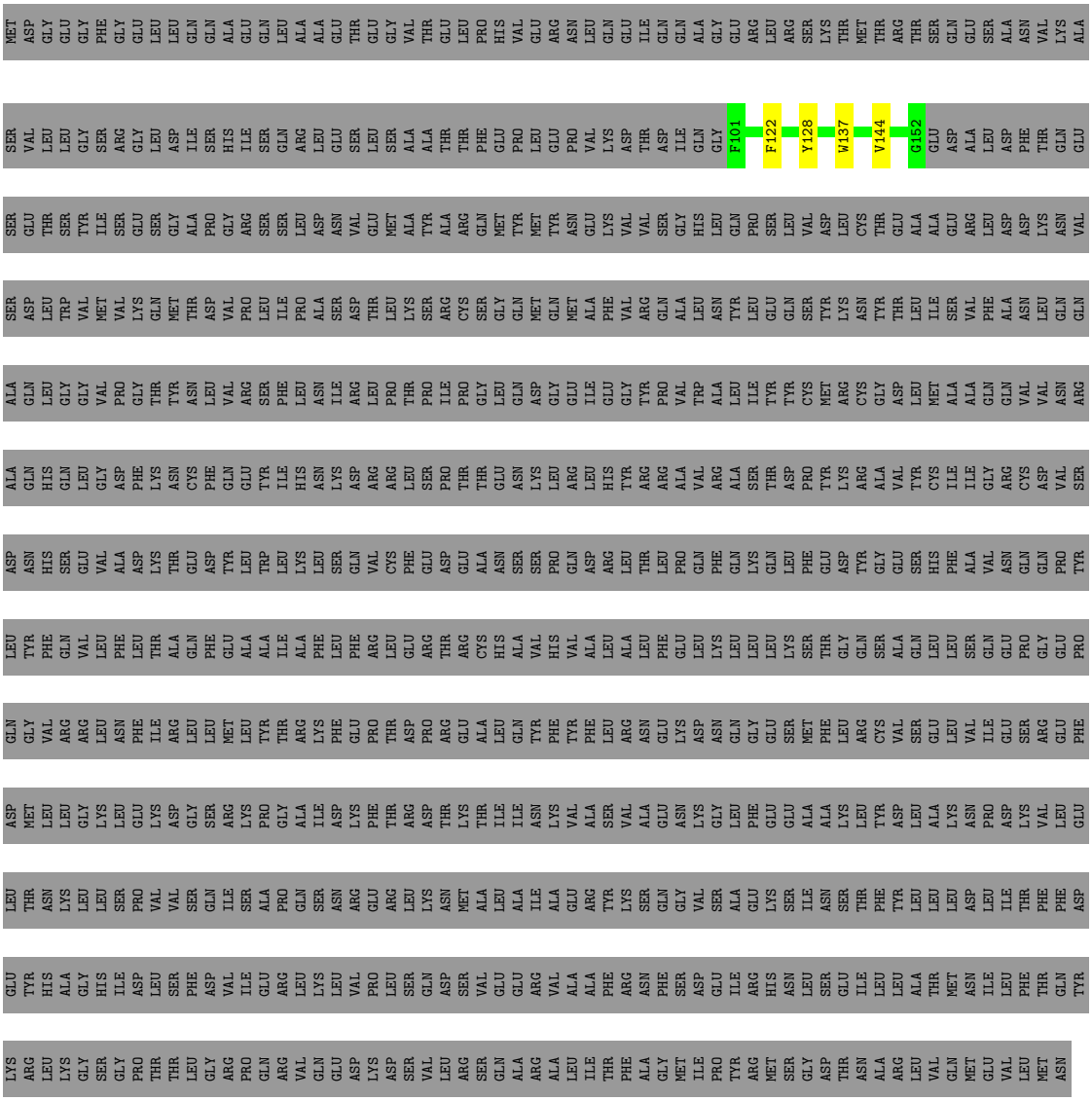
Chain P:





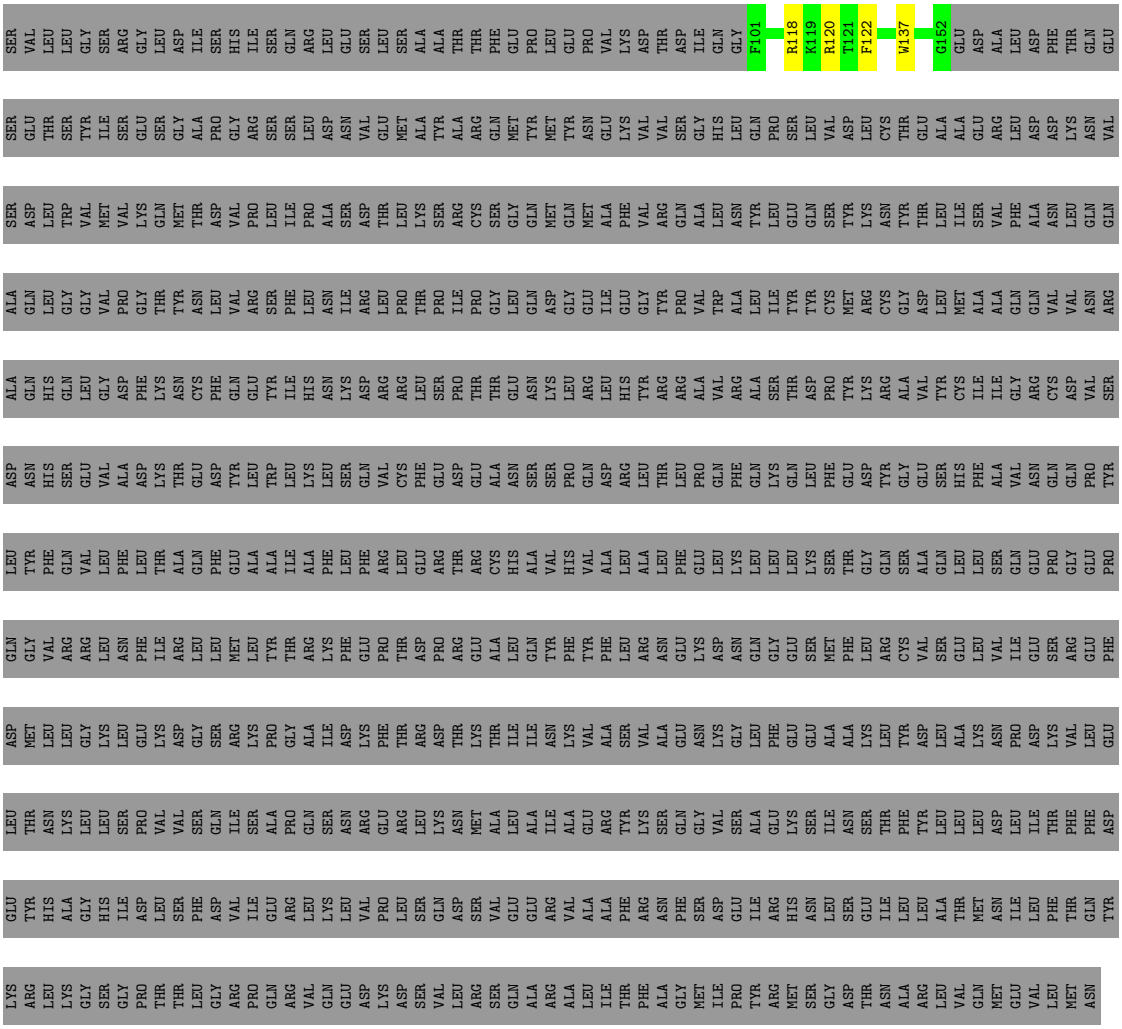
• Molecule 12: Nuclear pore complex protein Nup93

Chain S: 6% 94%



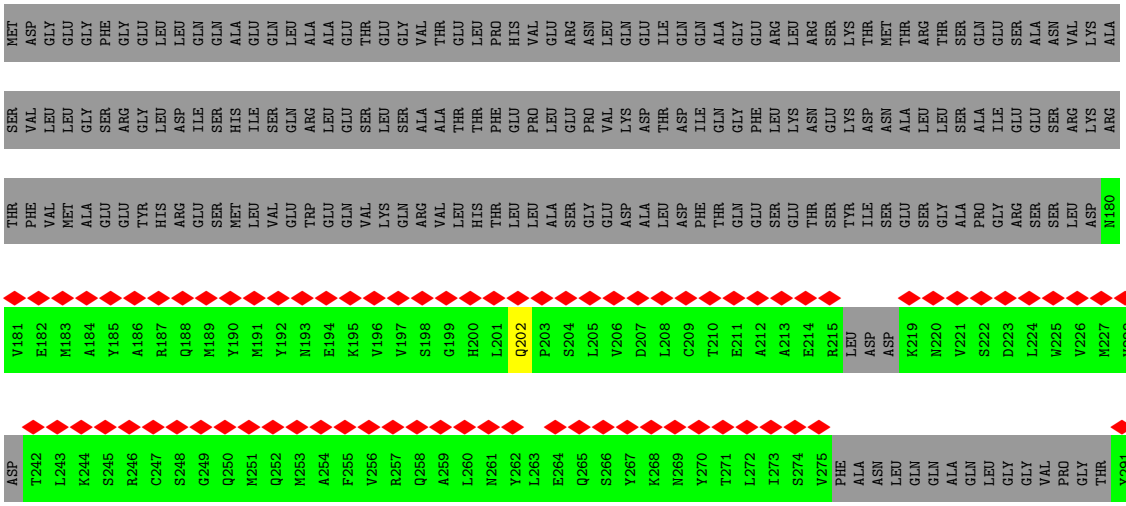
• Molecule 12: Nuclear pore complex protein Nup93

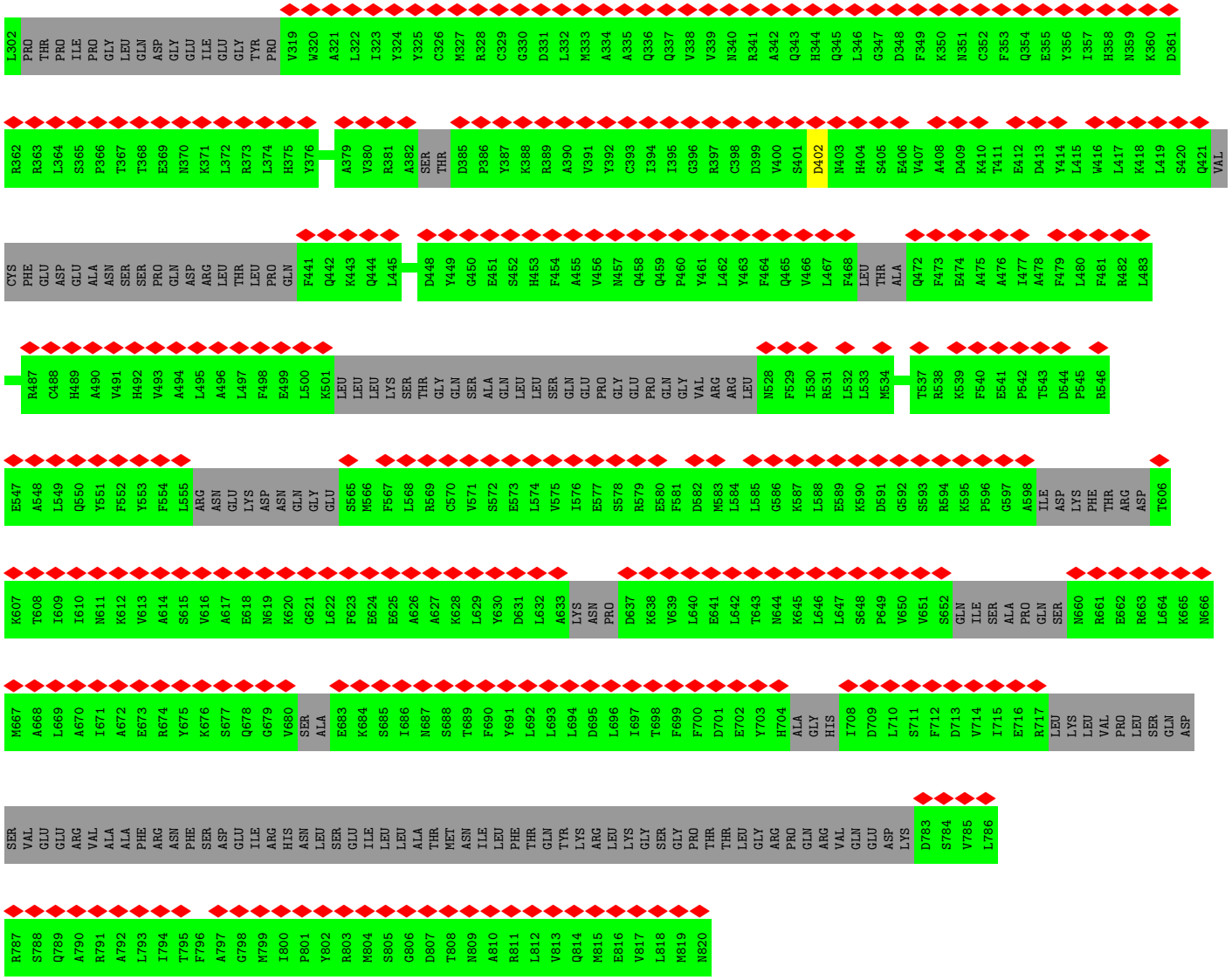
Chain s: 6% 94%



• Molecule 12: Nuclear pore complex protein Nup93

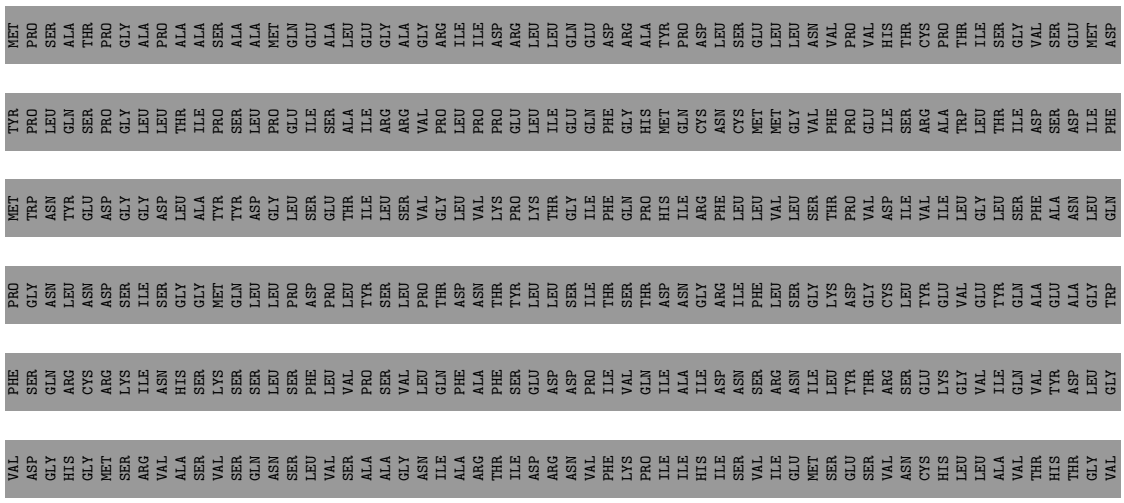
Chain p:

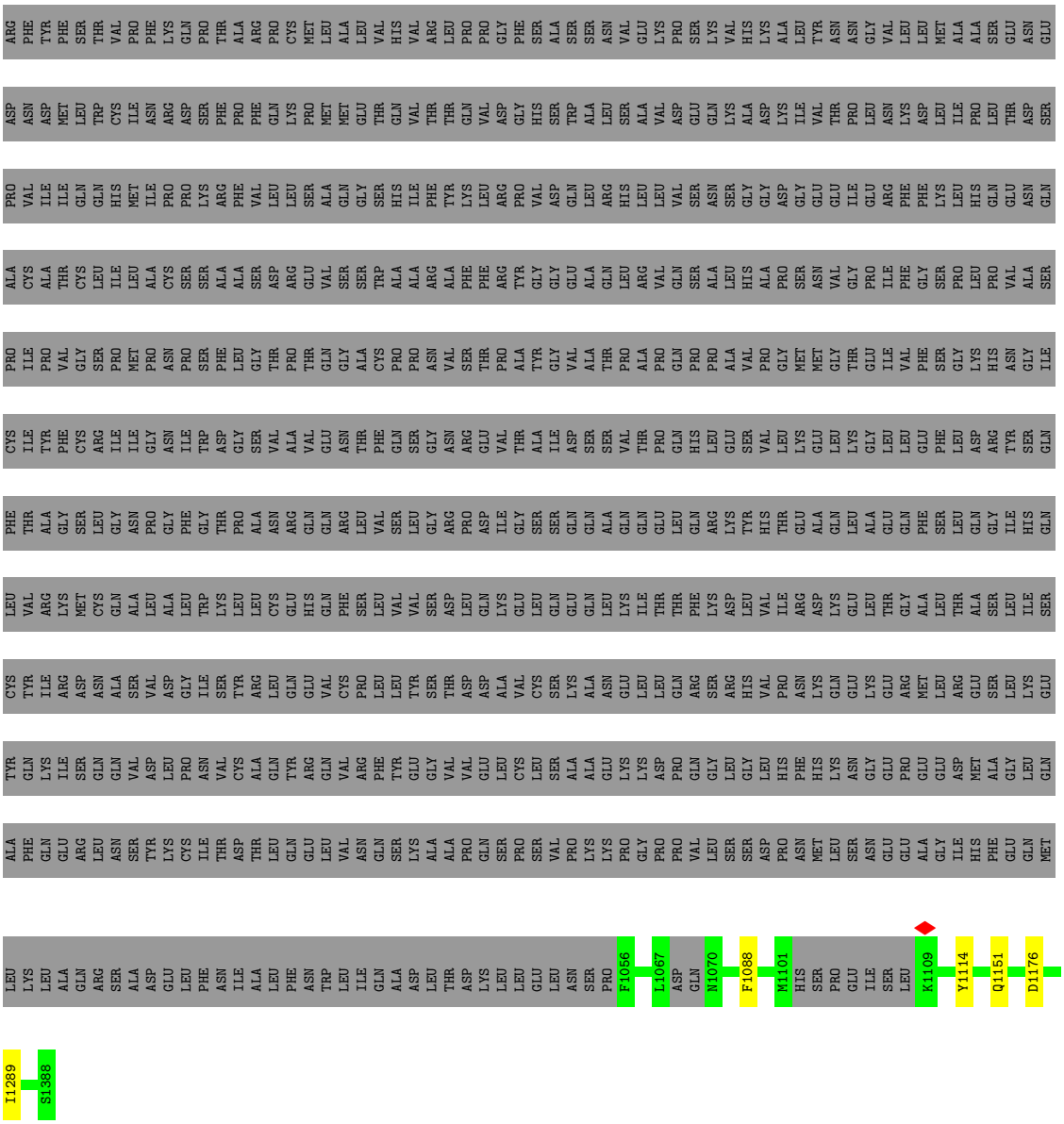




• Molecule 13: Nup155-prov protein

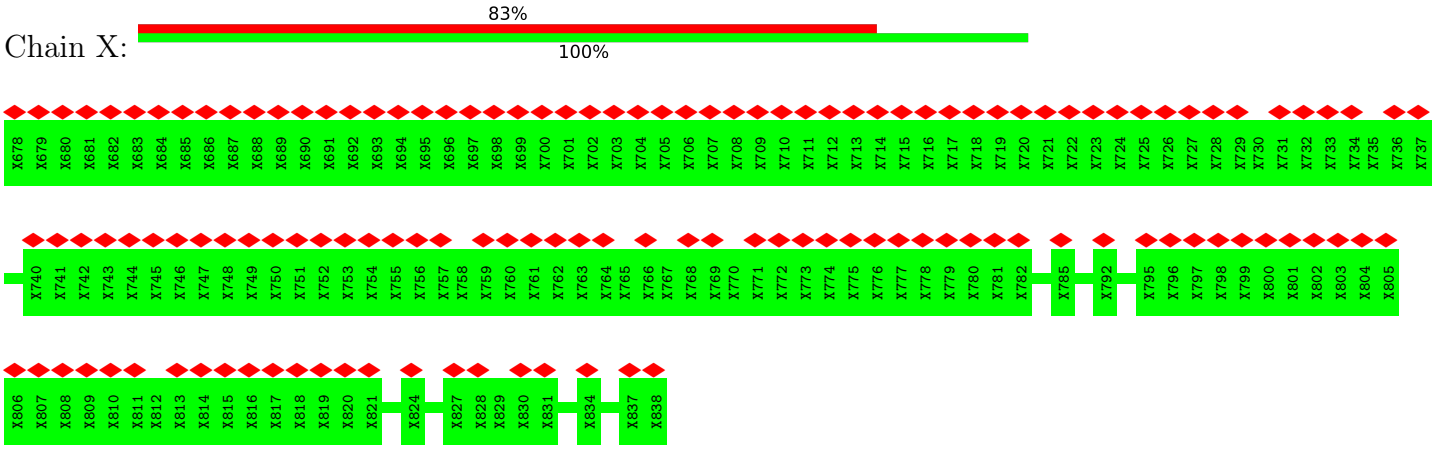
Chain W:





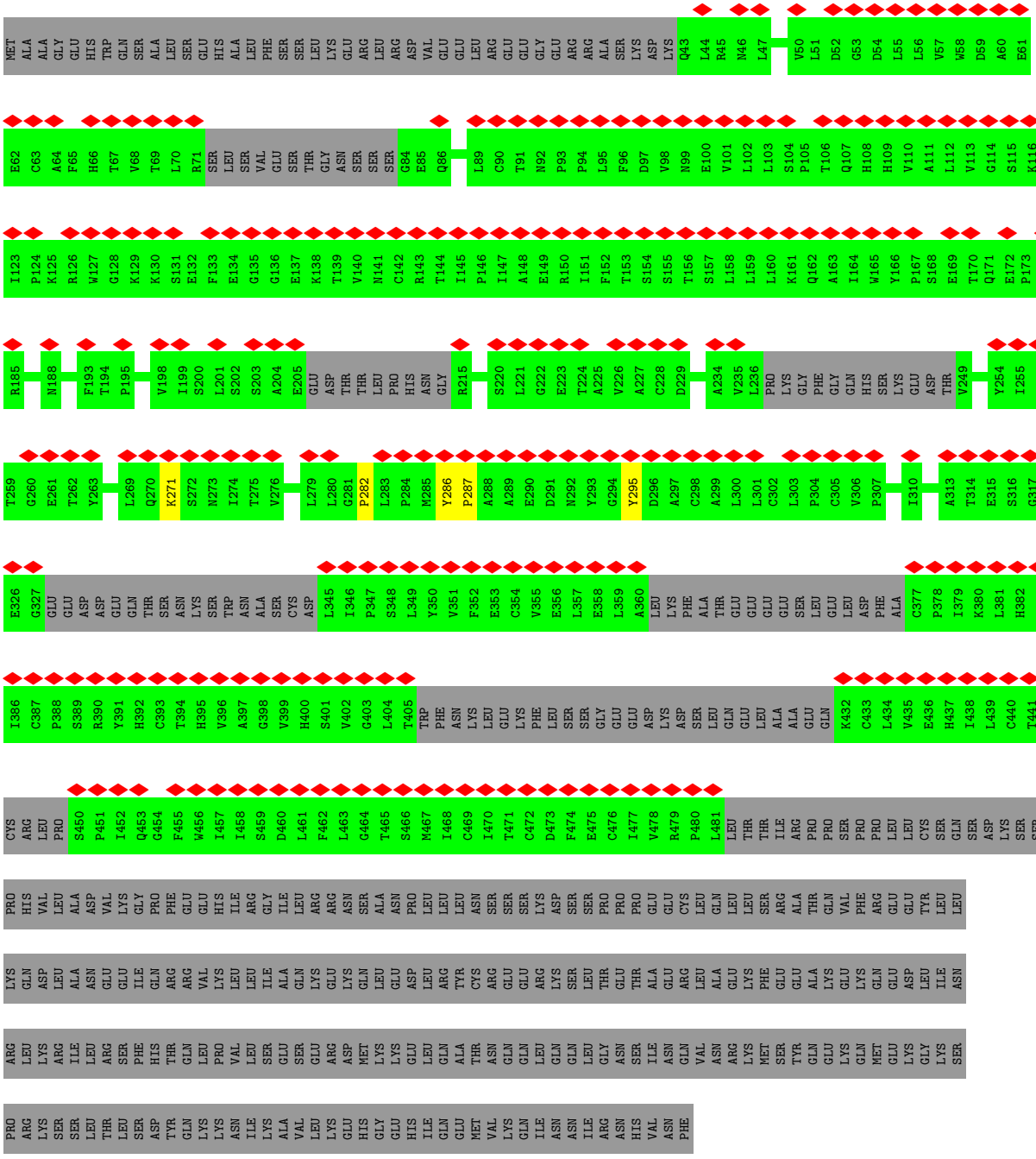
• Molecule 14: Nup98

Chain X:



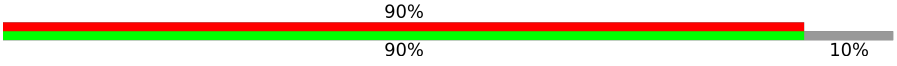
• Molecule 15: Nucleoporin Nup88A

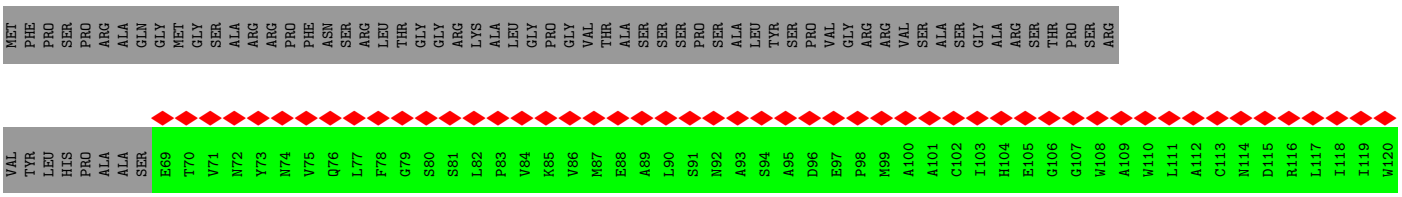
Chain Y:

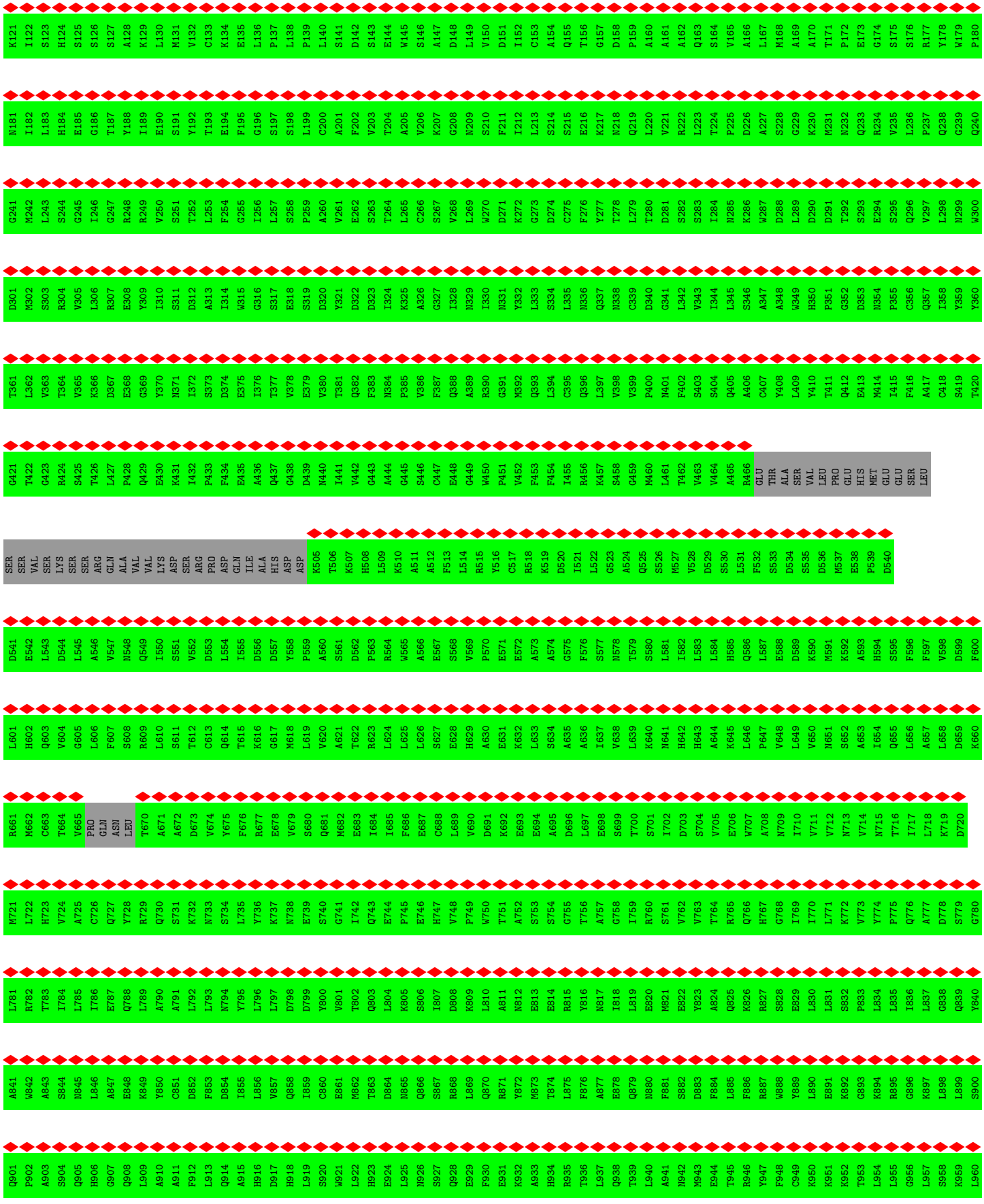


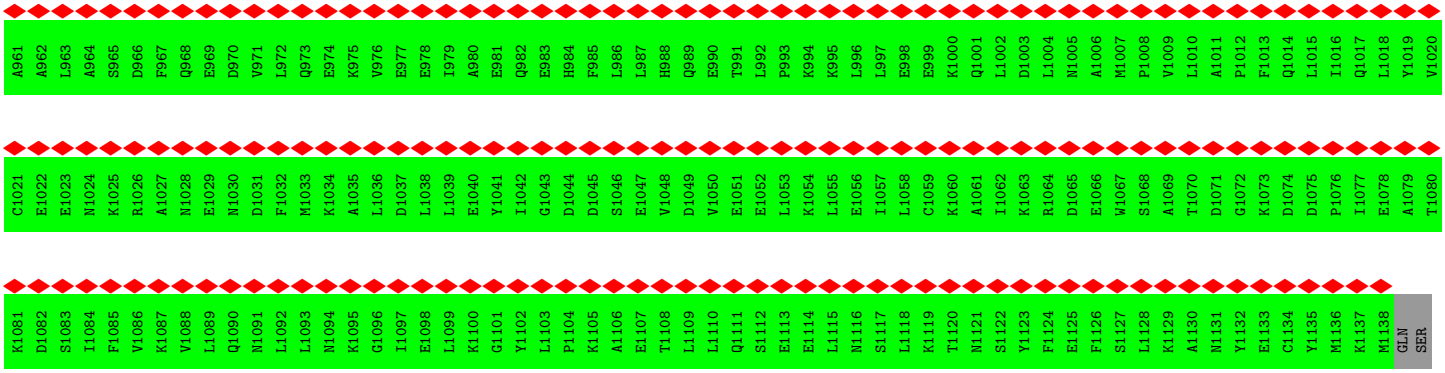
• Molecule 16: outer Nup133

Chain j:






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 C153 A154 Q155 T156 G157 D158 P159 A160 A161 A162 Q163 S164 V165 A166 L167 M168 A169 A170 T171 P172 E173 G174 S175 S176 R177 Y178 W179 P180
N181 I182 L183 H184 E185 G186 T187 Y188 I189 E190 S191 Y192 T193 E194 F195 G196 S197 S198 L199 C200 A201 F202 V203 T204 A205 V206 K207 G208 N209 S210 F211 I212 L213 S214 S215 E216 K217 N218 Q219 L220 V221 R222 L223 T224 P225 D226 A227 S228 G229 K230 M231 N232 Q233 R234 V235 L236 P237 Q238 G239 Q240
G241 M242 L243 S244 G245 I246 G247 R248 R249 V250 S251 T252 L253 F254 G255 I256 L257 S258 P259 A260 V261 E262 S263 T264 L265 C266 S267 V268 L269 W270 D271 K272 G273 D274 C275 F276 Y277 T278 L279 T280 D281 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 Q337 N338 C339 D340 G341 L342 V343 I344 L345 S346 A347 A348 W349 H350 P351 G352 D353 N354 P355 C356 Q357 I358 Y359 Y360
T361 L362 V363 T364 V365 K366 D367 E368 G369 Y370 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 N401 F402 S403 S404 Q405 A406 C407 Y408 L409 Y410 T411 Q412 E413 M414 I415 F416 A417 C418 S419 T420
G421 T422 G423 R424 S425 T426 L427 P428 Q429 E430 K431 I432 P433 F434 E435 A436 Q437 G438 D439 N440 I441 V442 G443 A444 G445 S446 C447 E448 G449 W450 P451 V452 F453 F454 I455 R456 K457 S458 G459 M460 L461 T462 V463 V464 A465 R466 GLU THR ALA SER VAL LEU PRO GLU HIS MET GLU GLU SER LEU
SER SER VAL SER LYS SER SER ARG GLN ALA VAL VAL LYS ASP SER ARG PRO ASP GLN ILE ALA HIS ASP ASP K505 T506 K507 H508 L509 K510 A511 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 S551 V552 D553 L554 I555 D556 D557 Y558 P559 A560 S561 D562 P563 R564 W565 A566 E567 S568 V569 P570 E571 E572 A573 A574 G575 F576 S577 N578 T579 S580 L581 I582 L583 L584 H585 Q586 L587 E588 D589 K590 M591 K592 A593 H594 S595 F596 F597 V598 D599 F600
L601 H602 Q603 V604 G605 L606 F607 S608 R609 L610 S611 T612 C613 Q614 T615 K616 G617 M618 L619 V620 A621 T622 R623 L624 L625 L626 S627 E628 H629 A630 E631 K632 L633 S634 A635 A636 I637 V638 L639 K640 N641 H642 H643 A644 K645 L646 P647 V648 L649 V650 N651 S652 A653 I654 Q655 L656 A657 L658 D659 K660
R661 M662 C663 T664 V665 PRO GLN ASN LEU T670 A671 A672 D673 V674 Y675 F676 R677 E678 V679 S680 Q681 M682 E683 I684 I685 F686 E687 C688 L689 V690 D691 K692 E693 E694 A695 D696 L697 E698 S699 T700 S701 I702 D703 S704 V705 E706 W707 A708 N709 I710 V711 V712 N713 V714 N715 T716 I717 L718 K719 D720
M721 L722 H723 V724 A725 C726 Q727 Y728 R729 Q730 S731 K732 N733 S734 L735 Y736 K737 N738 E739 S740 G741 I742 Q743 E744 P745 E746 H747 V748 P749 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 Q776 A777 D778 S779 G780
L781 R782 T783 I784 L785 I786 E787 Q788 L789 A790 A791 L792 L793 N794 Y795 L796 L797 D798 D799 Y800 V801 T802 Q803 L804 K805 S806 I807 D808 K809 L810 A811 N812 E813 E814 R815 Y816 N817 I818 L819 E820 M821 E822 Y823 A824 Q825 K826 R827 S828 E829 L830 L831 S832 P833 L834 L835 I836 L837 Q838 Q839 Y840
A841 W842 A843 S844 N845 L846 A847 E848 K849 Y850 C851 D852 F853 D854 I855 L856 V857 Q858 I859 C860 E861 M862 T863 D864 N865 Q866 S867 R868 L869 Q870 R871 Y872 M873 T874 L875 F876 A877 E878 Q879 N880 F881 S882 D883 F884 L885 F886 R887 W888 Y889 L890 E891 K892 G893 K894 R895 G896 K897 L898 L899 S900
Q901 P902 A903 S904 Q905 H906 G907 Q908 L909 A910 A911 F912 L913 Q914 A915 H916 D917 H918 L919 S920 W921 L922 H923 E924 L925 N926 S927 Q928 E929 F930 E931 K932 A933 H934 R935 T936 L937 Q938 T939 L940 A941 N942 M943 E944 T945 R946 Y947 F948 C949 K950 K951 K952 T953 L954 L955 G956 L957 S958 K959 L960


A961 A962 L963 A964 S965 D966 F967 Q968 E969 D970 V971 L972 Q973 E974 K975 V976 E977 E978 I979 A980 E981 Q982 E983 H984 F985 L986 L987 H988 Q989 E990 T991 L992 P993 K994 K995 L996 L997 E998 E999 K1000 Q1001 L1002 D1003 L1004 N1005 A1006 M1007 P1008 V1009 L1010 A1011 P1012 F1013 Q1014 L1015 I1016 Q1017 L1018 Y1019 V1020
C1021 E1022 E1023 N1024 K1025 R1026 A1027 N1028 E1029 N1030 D1031 F1032 M1033 K1034 A1035 L1036 D1037 L1038 L1039 E1040 Y1041 I1042 G1043 D1044 D1045 S1046 E1047 V1048 D1049 V1050 E1051 E1052 L1053 K1054 L1055 E1056 I1057 L1058 C1059 K1060 A1061 I1062 K1063 R1064 D1065 E1066 W1067 S1068 A1069 T1070 D1071 G1072 K1073 D1074 D1075 P1076 I1077 E1078 A1079 T1080
K1081 D1082 S1083 I1084 F1085 V1086 K1087 V1088 L1089 Q1090 N1091 L1092 L1093 N1094 K1095 G1096 I1097 E1098 L1099 K1100 G1101 Y1102 L1103 P1104 K1105 A1106 E1107 T1108 L1109 L1110 Q1111 S1112 E1113 E1114 L1115 N1116 S1117 L1118 K1119 T1120 N1121 S1122 Y1123 F1124 E1125 F1126 S1127 L1128 K1129 A1130 N1131 Y1132 E1133 C1134 Y1135 M1136 K1137 M1138 GLN SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1279270	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 ($e^-/Å^2$)	75	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.334	Depositor
Minimum map value	-0.334	Depositor
Average map value	0.040	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	710.144, 710.144, 710.144	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.387, 1.387, 1.387	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	0.31	0/9232	0.46	0/12806
1	a	0.27	0/8804	0.43	0/12220
2	B	0.34	0/4893	0.47	0/6602
2	b	0.36	0/4636	0.49	0/6272
3	C	0.27	0/2615	0.48	0/3550
3	c	0.28	0/2500	0.49	0/3394
4	D	0.27	0/2536	0.46	0/3442
4	d	0.27	0/2498	0.45	0/3392
5	E	0.33	0/7960	0.51	0/10948
5	e	0.34	0/8229	0.51	0/11264
6	F	0.28	0/1606	0.48	0/2231
6	f	0.27	0/2594	0.46	0/3526
7	G	0.33	0/4299	0.49	0/5856
7	g	0.38	0/4888	0.54	0/6644
8	H	0.28	0/2299	0.46	0/3139
8	h	0.28	0/2322	0.46	0/3169
9	I	0.24	0/3621	0.40	0/5050
9	i	0.23	0/3339	0.37	0/4651
10	J	0.23	0/2253	0.37	0/3141
11	K	0.25	0/3452	0.43	0/4805
11	L	0.24	0/3362	0.42	0/4677
11	M	0.26	0/3238	0.46	0/4506
11	N	0.25	0/3471	0.45	0/4830
11	O	0.24	0/3380	0.43	0/4700
12	P	0.25	0/2939	0.39	0/4093
12	S	0.35	0/438	0.46	0/586
12	p	0.44	0/2251	0.43	0/3118
12	s	0.32	0/438	0.45	0/586
13	W	0.35	0/2692	0.49	0/3638
15	Y	0.32	0/1668	0.71	0/2311
16	j	0.24	0/5091	0.41	0/7095
All	All	0.30	0/113544	0.46	0/156242

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	A	0	2
1	a	0	2
6	f	0	1
15	Y	0	1
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1053	THR	Peptide
1	A	1771	SER	Peptide
15	Y	286	TYR	Peptide
1	a	1053	THR	Peptide
1	a	1355	PRO	Peptide
6	f	237	MET	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1759/2011 (88%)	1626 (92%)	129 (7%)	4 (0%)	47 78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	1691/2011 (84%)	1552 (92%)	131 (8%)	8 (0%)	29	66
2	B	584/653 (89%)	564 (97%)	19 (3%)	1 (0%)	47	78
2	b	579/653 (89%)	562 (97%)	15 (3%)	2 (0%)	41	74
3	C	315/375 (84%)	303 (96%)	12 (4%)	0	100	100
3	c	299/375 (80%)	284 (95%)	14 (5%)	1 (0%)	41	74
4	D	310/360 (86%)	298 (96%)	12 (4%)	0	100	100
4	d	306/360 (85%)	293 (96%)	13 (4%)	0	100	100
5	E	1298/1435 (90%)	1239 (96%)	56 (4%)	3 (0%)	47	78
5	e	1227/1435 (86%)	1167 (95%)	59 (5%)	1 (0%)	51	83
6	F	324/326 (99%)	312 (96%)	12 (4%)	0	100	100
6	f	320/326 (98%)	308 (96%)	11 (3%)	1 (0%)	41	74
7	G	545/1742 (31%)	508 (93%)	35 (6%)	2 (0%)	34	69
7	g	595/1742 (34%)	543 (91%)	50 (8%)	2 (0%)	41	74
8	H	284/320 (89%)	274 (96%)	9 (3%)	1 (0%)	34	69
8	h	284/320 (89%)	274 (96%)	8 (3%)	2 (1%)	22	59
9	I	719/916 (78%)	675 (94%)	43 (6%)	1 (0%)	51	83
9	i	657/916 (72%)	628 (96%)	29 (4%)	0	100	100
10	J	449/1140 (39%)	422 (94%)	27 (6%)	0	100	100
11	K	681/2905 (23%)	623 (92%)	57 (8%)	1 (0%)	51	83
11	L	659/2905 (23%)	614 (93%)	45 (7%)	0	100	100
11	M	638/2905 (22%)	575 (90%)	62 (10%)	1 (0%)	47	78
11	N	683/2905 (24%)	614 (90%)	68 (10%)	1 (0%)	51	83
11	O	661/2905 (23%)	613 (93%)	47 (7%)	1 (0%)	47	78
12	P	581/820 (71%)	539 (93%)	42 (7%)	0	100	100
12	S	50/820 (6%)	49 (98%)	1 (2%)	0	100	100
12	p	424/820 (52%)	401 (95%)	21 (5%)	2 (0%)	29	66
12	s	50/820 (6%)	46 (92%)	4 (8%)	0	100	100
13	W	318/1388 (23%)	305 (96%)	12 (4%)	1 (0%)	41	74
15	Y	323/728 (44%)	308 (95%)	11 (3%)	4 (1%)	13	48
16	j	1022/1140 (90%)	960 (94%)	62 (6%)	0	100	100
All	All	18635/38477 (48%)	17479 (94%)	1116 (6%)	40 (0%)	50	78

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	I	460	ILE
15	Y	271	LYS
1	a	57	PRO
1	a	58	PRO
1	a	1095	LEU
1	a	1628	LEU
1	a	1629	ILE
1	a	1772	PRO
7	g	1616	THR
1	A	153	ARG
1	A	1632	SER
5	E	1301	TYR
7	G	1463	LEU
2	b	426	PRO
3	c	127	MET
12	p	202	GLN
1	a	101	TYR
8	h	139	PRO
12	p	402	ASP
1	A	127	ARG
5	E	1299	THR
11	O	27	MET
15	Y	282	PRO
15	Y	287	PRO
7	g	1068	ARG
1	A	1772	PRO
5	e	1066	ARG
2	B	52	PRO
5	E	1051	VAL
15	Y	295	TYR
1	a	502	LEU
6	f	273	PRO
8	H	139	PRO
11	N	22	PRO
13	W	1289	ILE
2	b	52	PRO
11	M	627	PRO
7	G	1503	PRO
11	K	627	PRO
8	h	5	ILE

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	100/1779 (6%)	99 (99%)	1 (1%)	76	86
1	a	77/1779 (4%)	75 (97%)	2 (3%)	46	69
2	B	517/580 (89%)	501 (97%)	16 (3%)	40	65
2	b	447/580 (77%)	439 (98%)	8 (2%)	59	77
3	C	288/329 (88%)	282 (98%)	6 (2%)	53	74
3	c	276/329 (84%)	268 (97%)	8 (3%)	42	66
4	D	273/310 (88%)	269 (98%)	4 (2%)	65	81
4	d	266/310 (86%)	263 (99%)	3 (1%)	73	85
5	E	382/1256 (30%)	366 (96%)	16 (4%)	30	59
5	e	545/1256 (43%)	521 (96%)	24 (4%)	28	58
6	f	266/275 (97%)	262 (98%)	4 (2%)	65	81
7	G	384/1474 (26%)	361 (94%)	23 (6%)	19	50
7	g	490/1474 (33%)	463 (94%)	27 (6%)	21	53
8	H	236/273 (86%)	230 (98%)	6 (2%)	47	70
8	h	245/273 (90%)	240 (98%)	5 (2%)	55	74
12	S	47/721 (6%)	43 (92%)	4 (8%)	10	40
12	s	47/721 (6%)	43 (92%)	4 (8%)	10	40
13	W	295/1219 (24%)	291 (99%)	4 (1%)	67	82
All	All	5181/14938 (35%)	5016 (97%)	165 (3%)	42	65

All (165) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1287	LEU
2	B	118	THR
2	B	123	THR
2	B	148	GLU
2	B	187	LYS
2	B	207	MET

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Mol	Chain	Res	Type
2	B	228	CYS
2	B	409	PHE
2	B	452	LEU
2	B	496	PHE
2	B	516	ASP
2	B	546	TYR
2	B	559	LEU
2	B	580	LEU
2	B	602	LEU
2	B	612	SER
2	B	633	LEU
3	C	77	ASP
3	C	78	VAL
3	C	89	ILE
3	C	168	ASP
3	C	215	VAL
3	C	351	LEU
4	D	114	THR
4	D	148	MET
4	D	194	MET
4	D	264	THR
5	E	1030	ARG
5	E	1076	TYR
5	E	1078	LEU
5	E	1085	TYR
5	E	1173	LEU
5	E	1178	LEU
5	E	1213	LEU
5	E	1234	LEU
5	E	1235	THR
5	E	1250	GLN
5	E	1301	TYR
5	E	1304	CYS
5	E	1337	LEU
5	E	1377	VAL
5	E	1394	ASN
5	E	1420	LYS
7	G	1047	LEU
7	G	1058	LEU
7	G	1059	LEU
7	G	1065	PHE
7	G	1071	ARG

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Mol	Chain	Res	Type
7	G	1072	VAL
7	G	1168	VAL
7	G	1181	LEU
7	G	1182	SER
7	G	1206	TRP
7	G	1284	LEU
7	G	1285	SER
7	G	1308	TRP
7	G	1312	GLN
7	G	1316	TYR
7	G	1333	VAL
7	G	1347	GLN
7	G	1358	LEU
7	G	1365	THR
7	G	1398	GLU
7	G	1426	LEU
7	G	1487	VAL
7	G	1513	LEU
8	H	109	VAL
8	H	230	ILE
8	H	236	ASP
8	H	257	LEU
8	H	282	ASP
8	H	293	ASP
12	S	122	PHE
12	S	128	TYR
12	S	137	TRP
12	S	144	VAL
13	W	1088	PHE
13	W	1114	TYR
13	W	1151	GLN
13	W	1176	ASP
12	s	118	ARG
12	s	120	ARG
12	s	122	PHE
12	s	137	TRP
1	a	1247	ILE
1	a	1287	LEU
2	b	67	VAL
2	b	116	MET
2	b	123	THR
2	b	362	PHE

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Mol	Chain	Res	Type
2	b	480	ARG
2	b	496	PHE
2	b	502	ASP
2	b	548	GLN
3	c	78	VAL
3	c	83	PHE
3	c	122	HIS
3	c	147	ASP
3	c	183	ILE
3	c	260	GLU
3	c	337	ILE
3	c	371	ARG
4	d	148	MET
4	d	159	ILE
4	d	284	VAL
5	e	869	ASN
5	e	885	THR
5	e	894	LEU
5	e	898	CYS
5	e	901	ASN
5	e	902	VAL
5	e	935	ARG
5	e	939	LEU
5	e	957	TYR
5	e	970	LEU
5	e	972	GLU
5	e	1026	LEU
5	e	1076	TYR
5	e	1078	LEU
5	e	1079	LEU
5	e	1102	ARG
5	e	1246	ILE
5	e	1260	TRP
5	e	1267	GLN
5	e	1271	VAL
5	e	1324	TYR
5	e	1376	LEU
5	e	1377	VAL
5	e	1407	LEU
6	f	117	TYR
6	f	119	VAL
6	f	190	ILE

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Mol	Chain	Res	Type
6	f	227	VAL
7	g	1070	PHE
7	g	1071	ARG
7	g	1072	VAL
7	g	1127	LYS
7	g	1194	GLN
7	g	1200	THR
7	g	1206	TRP
7	g	1245	GLU
7	g	1273	CYS
7	g	1284	LEU
7	g	1285	SER
7	g	1287	LEU
7	g	1290	GLN
7	g	1292	VAL
7	g	1298	ARG
7	g	1322	LEU
7	g	1333	VAL
7	g	1347	GLN
7	g	1365	THR
7	g	1435	CYS
7	g	1443	VAL
7	g	1472	ARG
7	g	1513	LEU
7	g	1520	VAL
7	g	1553	ARG
7	g	1608	CYS
7	g	1679	VAL
8	h	14	ASP
8	h	47	GLN
8	h	74	LEU
8	h	109	VAL
8	h	223	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (68) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1206	GLN
1	A	1268	ASN
2	B	22	HIS
2	B	40	GLN
2	B	42	GLN

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Mol	Chain	Res	Type
2	B	257	GLN
2	B	395	ASN
3	C	113	ASN
3	C	273	HIS
4	D	11	HIS
4	D	56	HIS
4	D	198	GLN
4	D	273	GLN
5	E	1025	GLN
5	E	1083	HIS
5	E	1228	GLN
5	E	1318	ASN
5	E	1416	GLN
7	G	1165	ASN
7	G	1180	ASN
7	G	1220	ASN
7	G	1290	GLN
7	G	1347	GLN
7	G	1370	GLN
7	G	1431	GLN
7	G	1515	ASN
8	H	261	ASN
12	S	142	GLN
13	W	1204	HIS
12	s	142	GLN
1	a	1286	GLN
2	b	22	HIS
2	b	40	GLN
2	b	257	GLN
2	b	314	HIS
3	c	114	GLN
3	c	151	ASN
4	d	152	GLN
4	d	268	ASN
4	d	276	ASN
4	d	278	ASN
4	d	280	GLN
5	e	869	ASN
5	e	920	HIS
5	e	1003	HIS
5	e	1054	HIS
5	e	1083	HIS

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Mol	Chain	Res	Type
5	e	1125	ASN
5	e	1195	ASN
5	e	1228	GLN
5	e	1249	GLN
5	e	1267	GLN
5	e	1298	ASN
5	e	1318	ASN
5	e	1367	GLN
7	g	1083	ASN
7	g	1150	ASN
7	g	1165	ASN
7	g	1180	ASN
7	g	1220	ASN
7	g	1290	GLN
7	g	1309	ASN
7	g	1347	GLN
7	g	1370	GLN
7	g	1467	HIS
7	g	1499	HIS
7	g	1515	ASN
8	h	261	ASN

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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

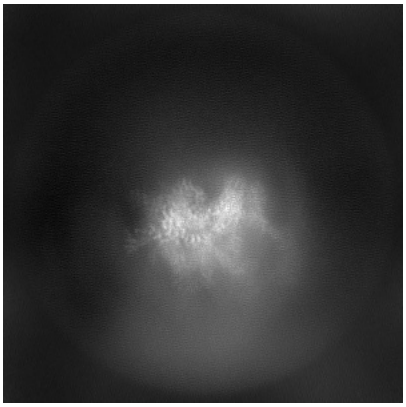
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-31600. These allow visual inspection of the internal detail of the map and identification of artifacts.

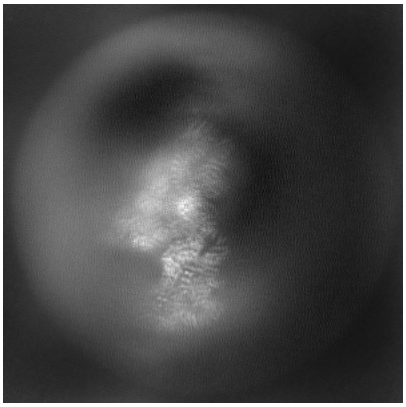
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

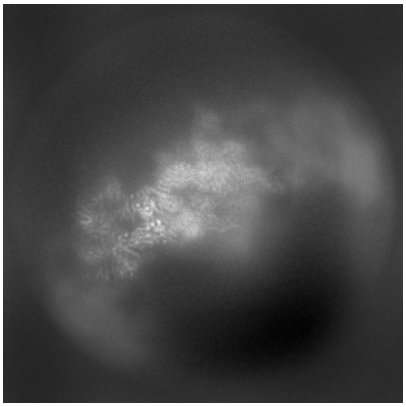
6.1.1 Primary map



X



Y

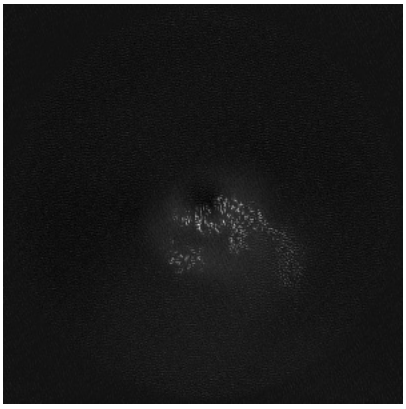


Z

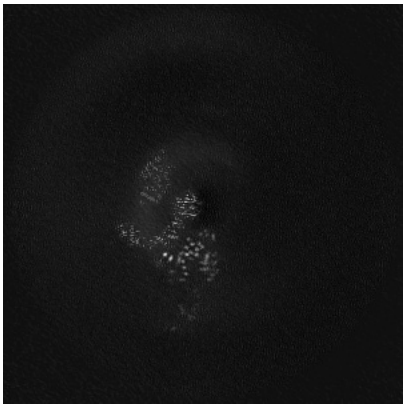
The images above show the map projected in three orthogonal directions.

6.2 Central slices

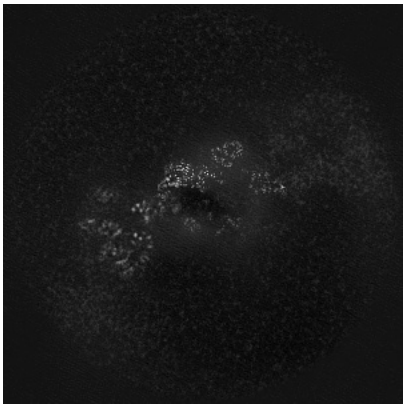
6.2.1 Primary map



X Index: 256



Y Index: 256

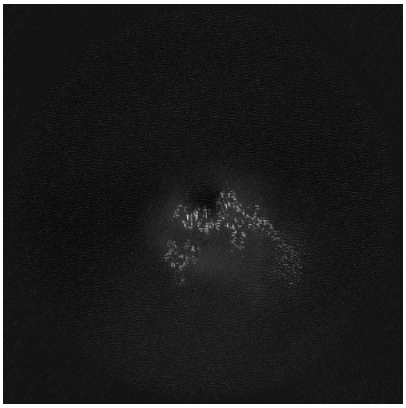


Z Index: 256

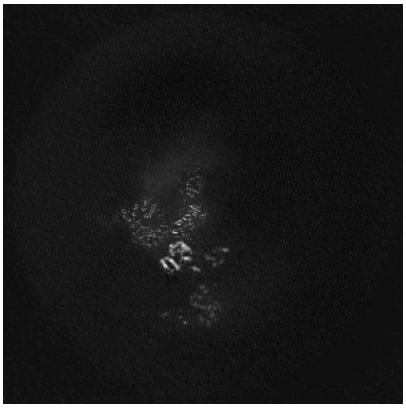
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

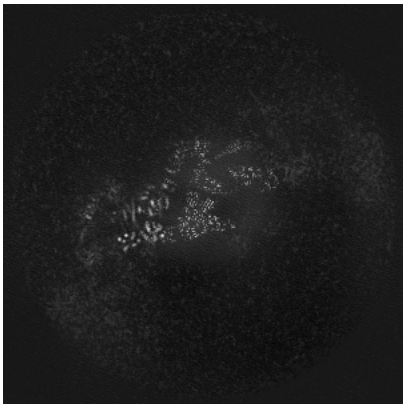
6.3.1 Primary map



X Index: 252



Y Index: 223

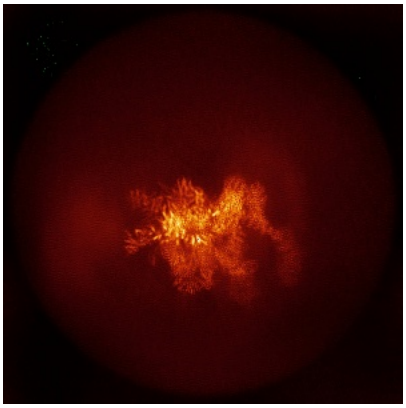


Z Index: 236

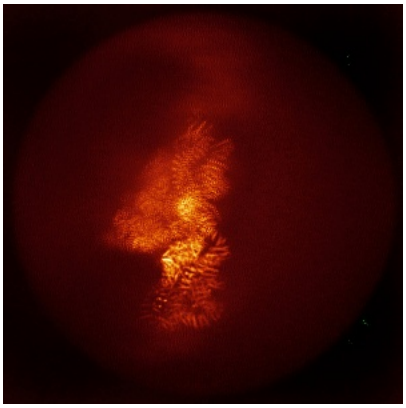
The images above show the largest variance slices of the map in three orthogonal directions.

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

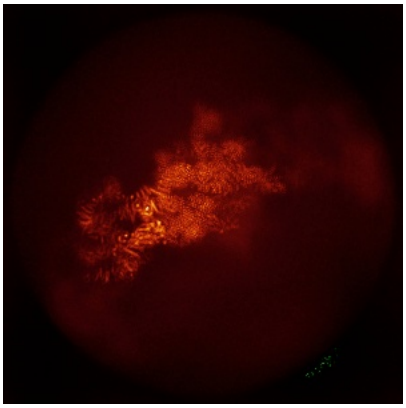
6.4.1 Primary map



X



Y

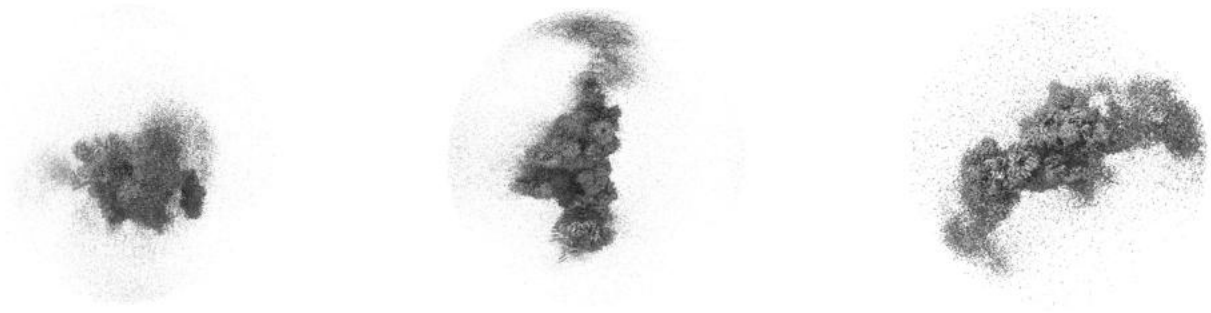


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

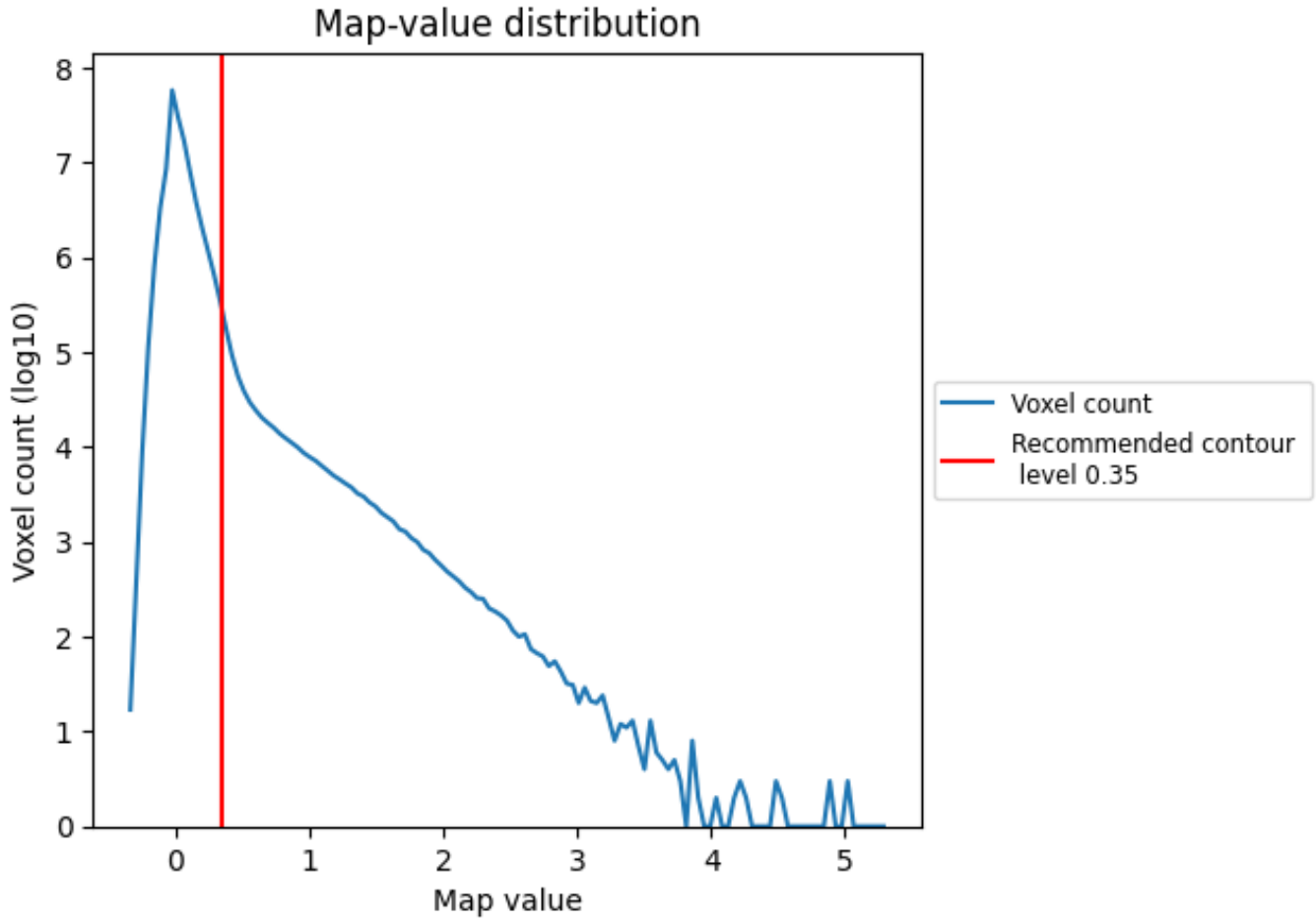
6.6 Mask visualisation (i)

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

7 Map analysis

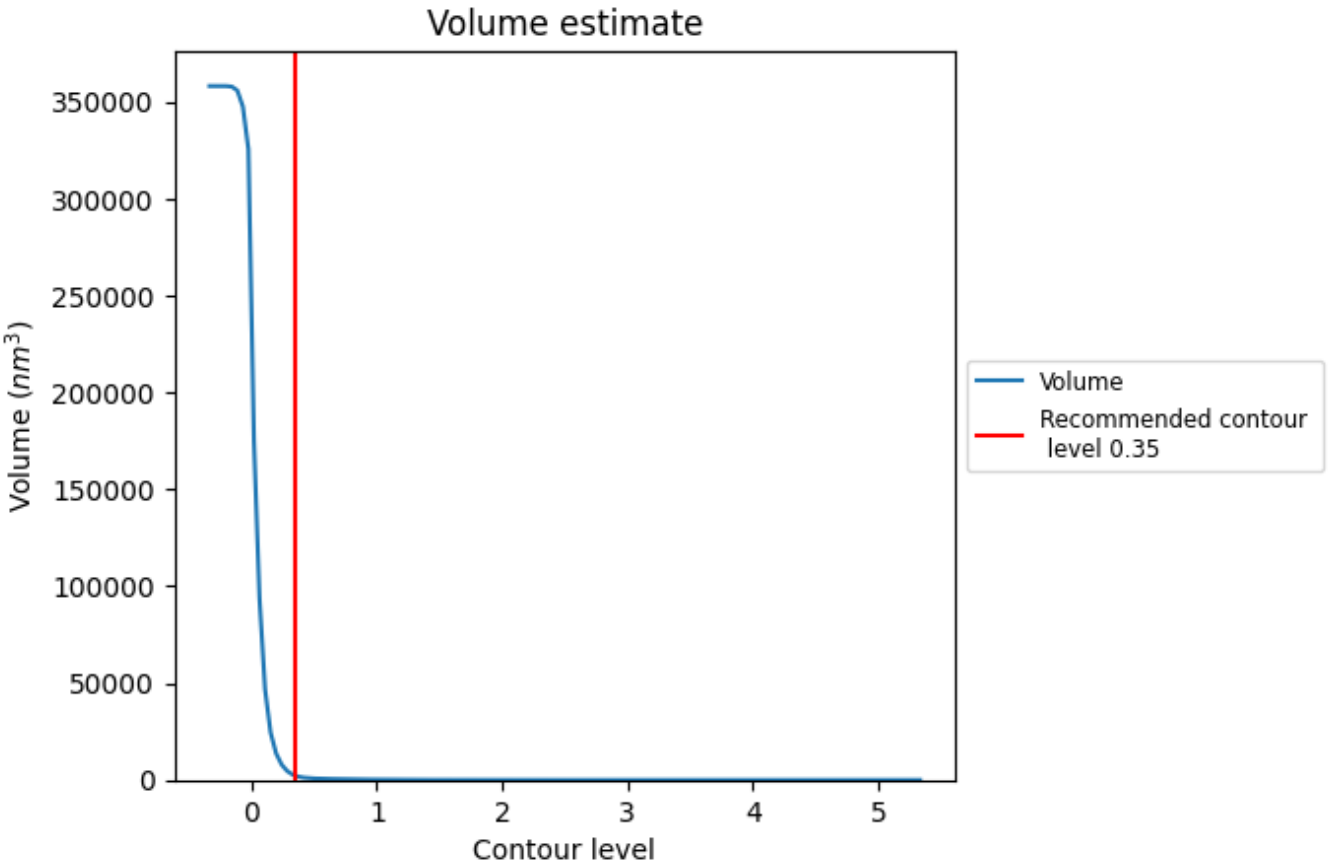
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

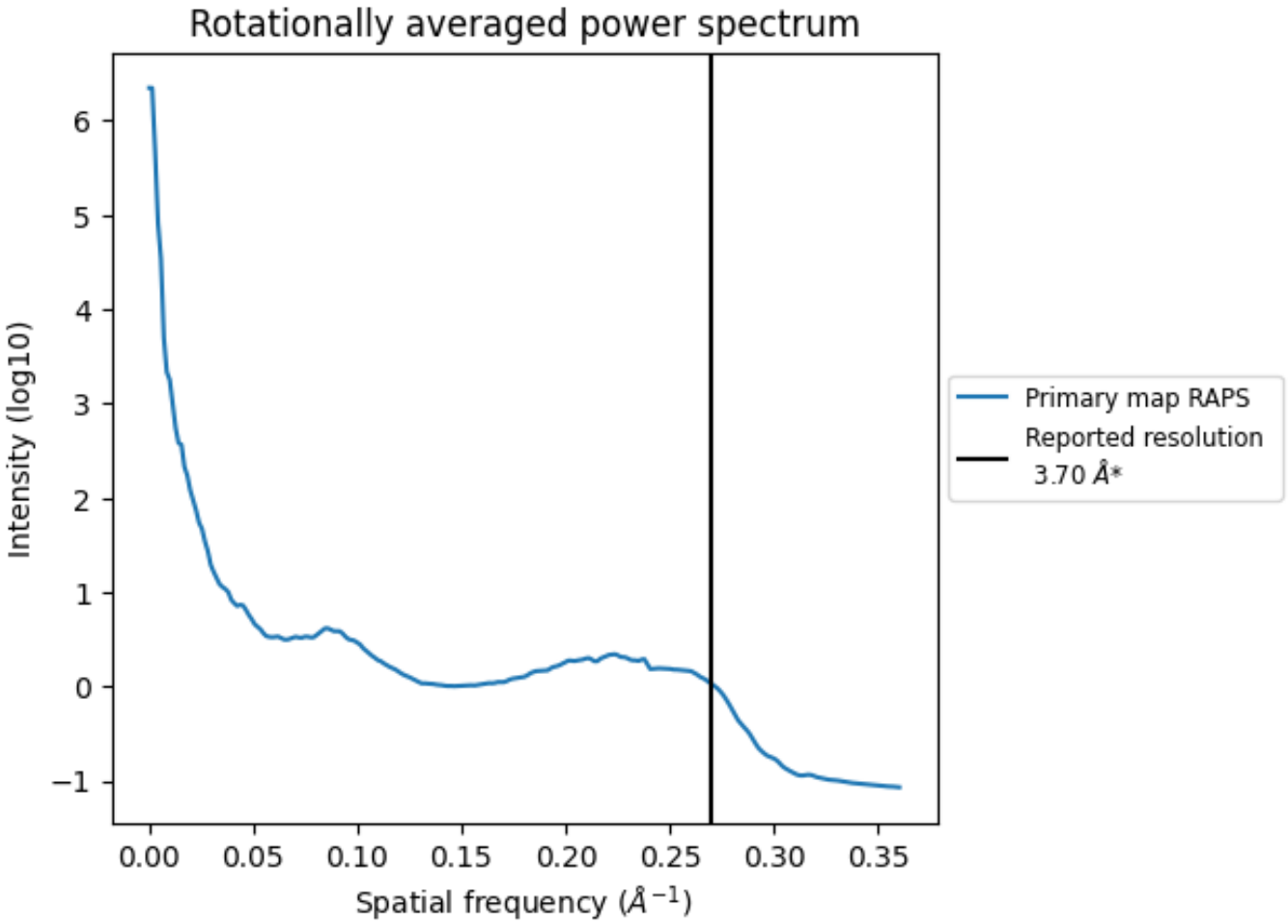
7.2 Volume estimate



The volume at the recommended contour level is 2248 nm^3; this corresponds to an approximate mass of 2031 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 0.270 Å^{-1}

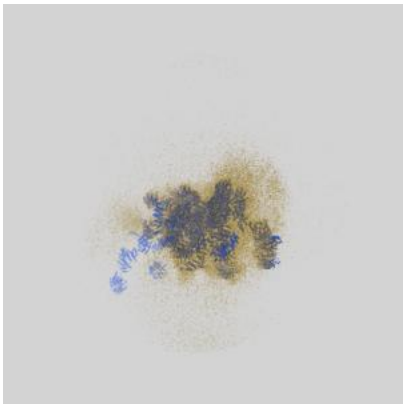
8 Fourier-Shell correlation

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

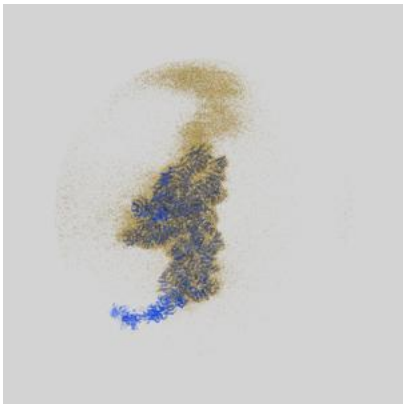
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-31600 and PDB model 7FIK. Per-residue inclusion information can be found in section 3 on page 8.

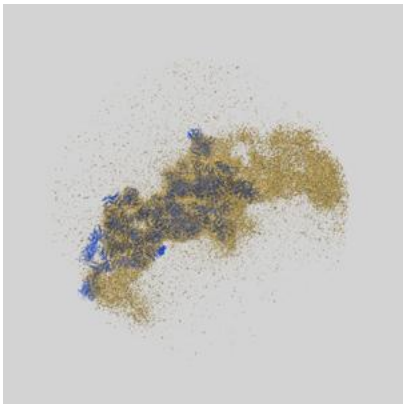
9.1 Map-model overlay



X



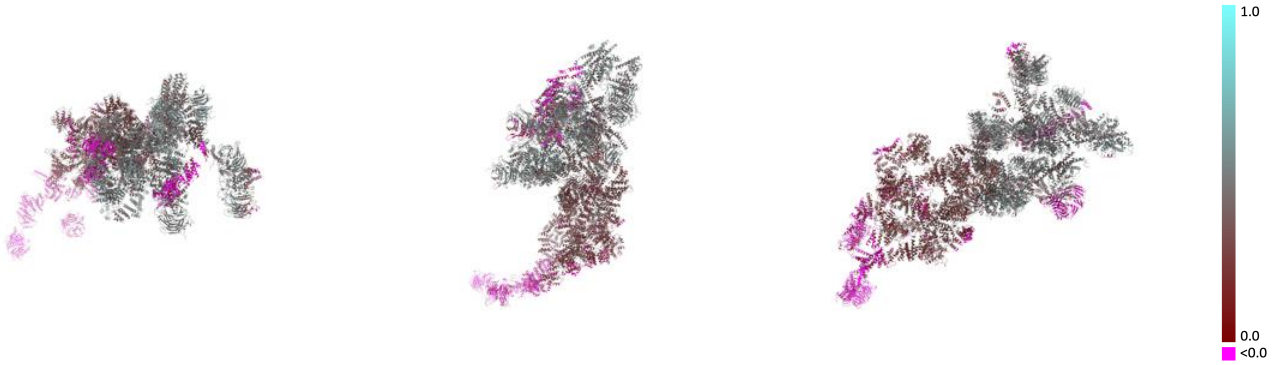
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.35 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.

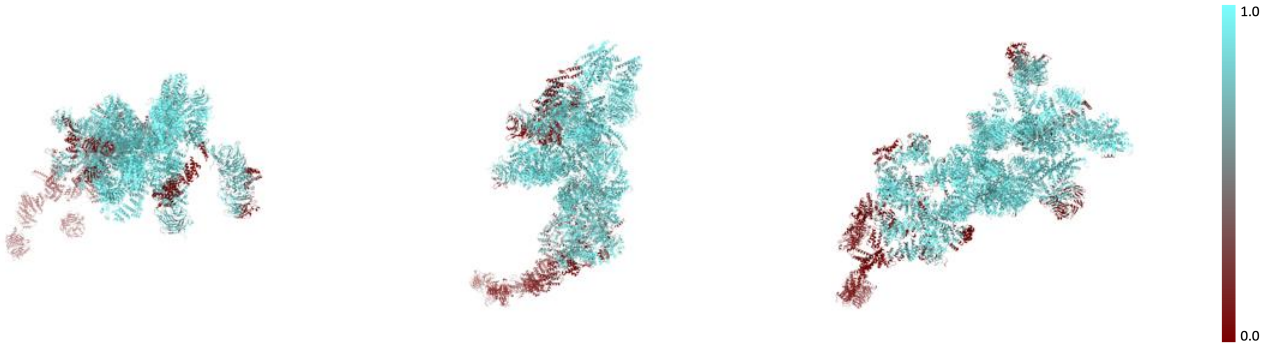
9.2 Q-score mapped to coordinate model (i)



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.

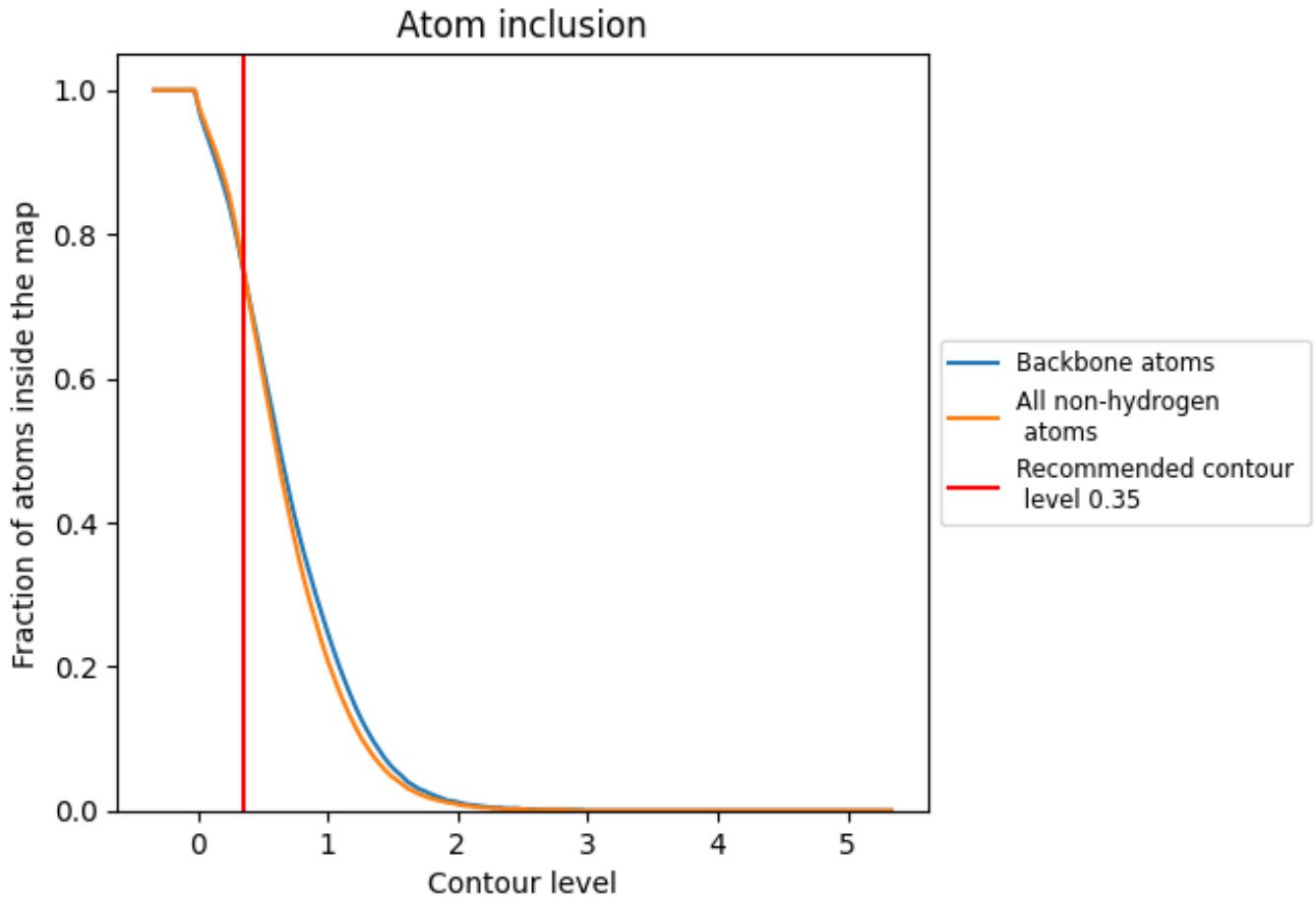
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.35).

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 75% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7540	0.3460
A	0.9580	0.4790
B	0.8710	0.4340
C	0.9490	0.5030
D	0.9220	0.4710
E	0.7110	0.4090
F	0.7750	0.4700
G	0.8890	0.3440
H	0.9590	0.4710
I	0.8330	0.2830
J	0.1110	0.0820
K	0.7490	0.2950
L	0.5250	0.2780
M	0.9400	0.3220
N	0.6850	0.2870
O	0.7840	0.2290
P	0.8780	0.2830
S	0.9190	0.4340
W	0.9640	0.4950
X	0.2370	0.0090
Y	0.2550	-0.0240
a	0.9670	0.4830
b	0.8760	0.4240
c	0.9290	0.4670
d	0.9660	0.4690
e	0.8850	0.4500
f	0.9850	0.5100
g	0.8900	0.3330
h	0.9510	0.3740
i	0.3530	0.1570
j	0.0000	-0.0560
p	0.1080	-0.0130
s	0.9530	0.3980