# wwPDB EM Validation Summary Report (i)

Mar 4, 2026 – 08:23 PM UTC

| | | |
|---|---|---|
| PDB ID | : | 6LK8 / pdb_00006lk8 |
| EMDB ID | : | EMD-0909 |
| Title | : | Structure of Xenopus laevis Cytoplasmic Ring subunit. |
| Authors | : | Shi, Y.; Huang, G.; Yan, C.; Zhang, Y. |
| Deposited on | : | 2019-12-18 |
| Resolution | : | 5.50 Å(reported) |

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

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

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

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

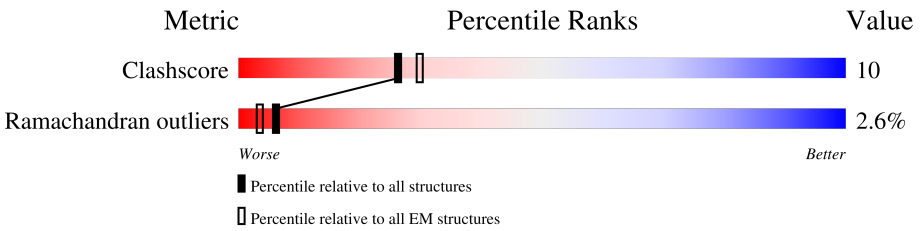
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev132 |
| MolProbity | : | 4-5-2 with Phenix2.0 |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| EM percentile statistics | : | 202505.v01 (Using data in the EMDB archive up until May 2025)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

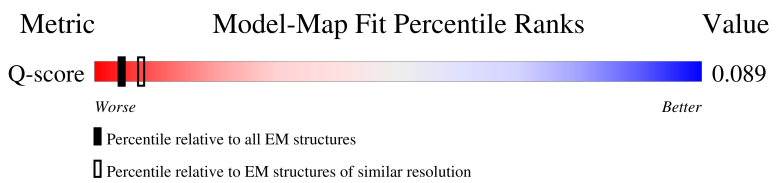
# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 5.50 Å.

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




| Metric | Whole archive (#Entries) | EM structures (#Entries) | Similar EM resolution (#Entries, resolution range(Å)) |
|---|---|---|---|
| Clashscore | 229148 | 23984 | - |
| Ramachandran outliers | 224038 | 23583 | - |
| Q-score | - | 25397 | 520 ( 5.00 - 6.00 ) |

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 | 27% 62% 8% • 30% |
| 1 | a | 2011 | 30% 56% 7% • 37% |
| 2 | B | 653 | 23% 68% 12% • 19% |
| 2 | b | 653 | 22% 64% 14% • 21% |
| 3 | C | 375 | • 66% 10% • 23% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 3 | c | 375 | 5% 70% 8% 22% |
| 4 | D | 322 | 20% 85% 10% 5% |
| 4 | d | 322 | 20% 85% 6% 9% |
| 5 | E | 1435 | 66% 67% 28% |
| 5 | e | 1435 | 64% 72% 5% 23% |
| 6 | F | 326 | 89% 83% 5% 11% |
| 6 | f | 326 | 63% 86% 11% |
| 7 | G | 923 | 23% 50% 13% 33% |
| 7 | g | 923 | 26% 48% 15% 34% |
| 8 | H | 320 | 15% 83% 7% 9% |
| 8 | h | 320 | 21% 81% 9% 10% |
| 9 | I | 916 | 66% 75% 5% 19% |
| 9 | i | 916 | 79% 74% 5% 21% |
| 10 | J | 1140 | 90% 85% 5% 10% |
| 10 | j | 1140 | 90% 84% 5% 10% |
| 11 | S | 2905 | 5% 5% 94% |
| 11 | T | 2905 | 6% 5% 94% |
| 11 | U | 2905 | 6% 5% 94% |
| 11 | V | 2905 | 6% 5% 94% |
| 12 | K | 69 | 100% 97% |
| 13 | L | 80 | 100% 100% |
| 14 | M | 73 | 100% 97% |
| 15 | N | 31 | 48% 100% |
| 16 | O | 35 | 100% 100% |
| 17 | P | 26 | 96% 100% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 18 | Q | 391 | 58% 91% 8% |
| 18 | R | 391 | 87% 72% 18% 10% |

# 2 Entry composition (i)

There are 18 unique types of molecules in this entry. The entry contains 72207 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 |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 1 | A | 1409 | 6934 | 4116 | 1409 | 1409 | 0 | 0 |
| 1 | a | 1272 | 6306 | 3762 | 1272 | 1272 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 2 | B | 532 | 2639 | 1575 | 532 | 532 | 0 | 0 |
| 2 | b | 519 | 2574 | 1536 | 519 | 519 | 0 | 0 |

- Molecule 3 is a protein called MGC154553 protein.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 3 | C | 289 | 1156 | 578 | 289 | 289 | 0 | 0 |
| 3 | c | 292 | 1168 | 584 | 292 | 292 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 4 | D | 307 | 1519 | 905 | 307 | 307 | 0 | 0 |
| 4 | d | 293 | 1450 | 864 | 293 | 293 | 0 | 0 |

- Molecule 5 is a protein called outer Nup160.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 5 | E | 1030 | 5107 | 3047 | 1030 | 1030 | 0 | 0 |
| 5 | e | 1109 | 5497 | 3279 | 1109 | 1109 | 0 | 0 |

- Molecule 6 is a protein called MGC83926 protein.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 6 | F | 289 | 1423 | 845 | 289 | 289 | 0 | 0 |
| 6 | f | 291 | 1433 | 851 | 291 | 291 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 7 | G | 618 | 3064 | 1828 | 618 | 618 | 0 | 0 |
| 7 | g | 607 | 3010 | 1796 | 607 | 607 | 0 | 0 |

- Molecule 8 is a protein called GATOR complex protein SEC13.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 8 | H | 291 | 1419 | 837 | 291 | 291 | 0 | 0 |
| 8 | h | 287 | 1413 | 839 | 287 | 287 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 9 | I | 738 | 3668 | 2192 | 738 | 738 | 0 | 0 |
| 9 | i | 727 | 3613 | 2159 | 727 | 727 | 0 | 0 |

- Molecule 10 is a protein called outer Nup133.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 10 | J | 1026 | 5085 | 3033 | 1026 | 1026 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 10 | j | 1027 | 5090 | 3036 | 1027 | 1027 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 11 | S | 169 | 840 | 502 | 169 | 169 | 0 | 0 |
| 11 | T | 169 | 840 | 502 | 169 | 169 | 0 | 0 |
| 11 | U | 173 | 859 | 513 | 173 | 173 | 0 | 0 |
| 11 | V | 169 | 840 | 502 | 169 | 169 | 0 | 0 |

- Molecule 12 is a protein called Nup214 complex Coiled-coil region 1, helix 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 12 | K | 69 | 345 | 207 | 69 | 69 | 0 | 0 |

- Molecule 13 is a protein called Nup214 complex coiled coil region 1, helix 2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 13 | L | 80 | 400 | 240 | 80 | 80 | 0 | 0 |

- Molecule 14 is a protein called Nup214 complex coiled coil region 1, helix 3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 14 | M | 73 | 365 | 219 | 73 | 73 | 0 | 0 |

- Molecule 15 is a protein called Nup214 complex Coiled coil region 2, helix 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 15 | N | 31 | 155 | 93 | 31 | 31 | 0 | 0 |

- Molecule 16 is a protein called Nup214 complex Coiled coil region 2, helix 2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 16 | O | 35 | 175 | 105 | 35 | 35 | 0 | 0 |

- Molecule 17 is a protein called Nup214 complex Coiled coil region 2, helix 3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 17 | P | 26 | 130 | 78 | 26 | 26 | 0 | 0 |

- Molecule 18 is a protein called bridge domain.

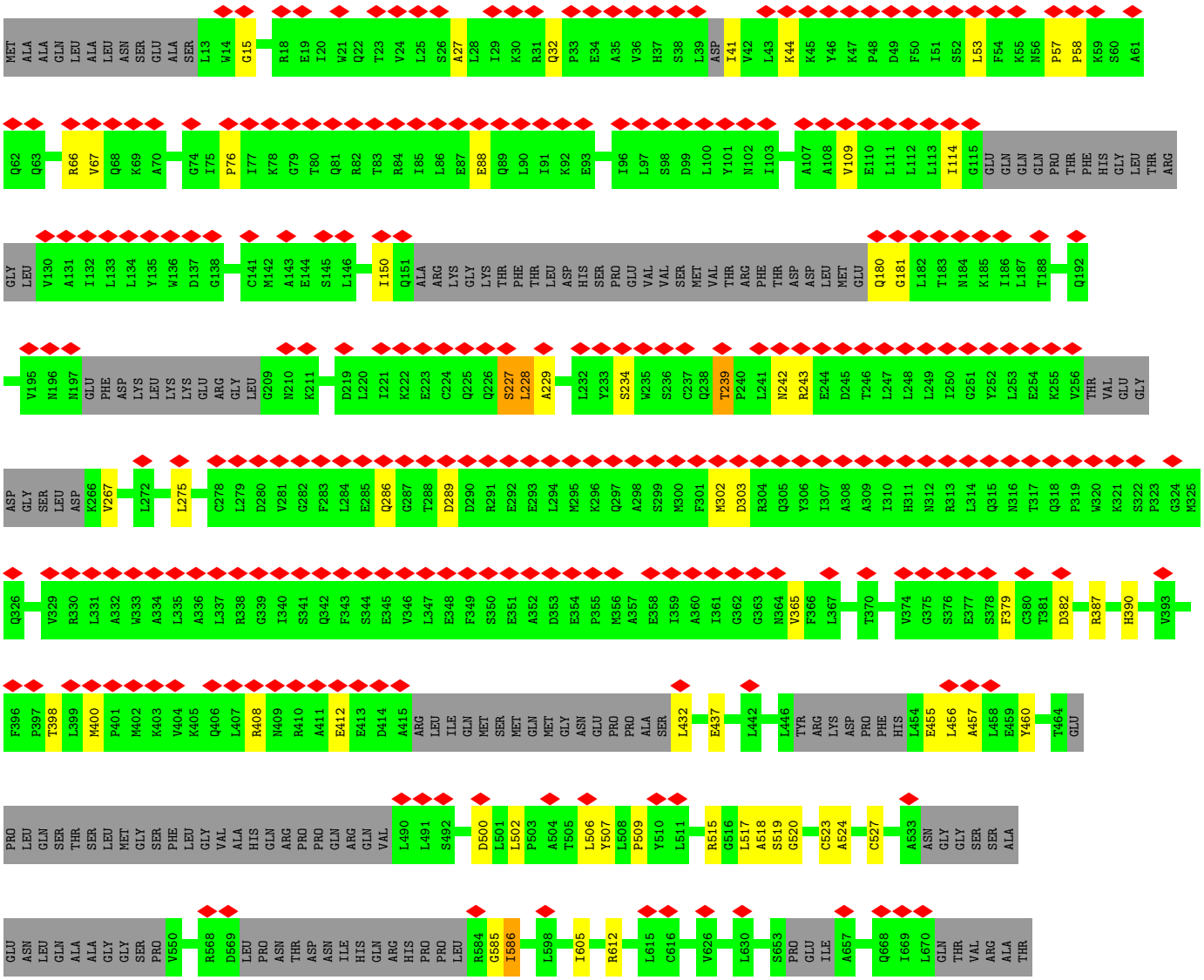
| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 18 | Q | 387 | 1935 | 1161 | 387 | 387 | 0 | 0 |
| 18 | R | 351 | 1755 | 1053 | 351 | 351 | 0 | 0 |

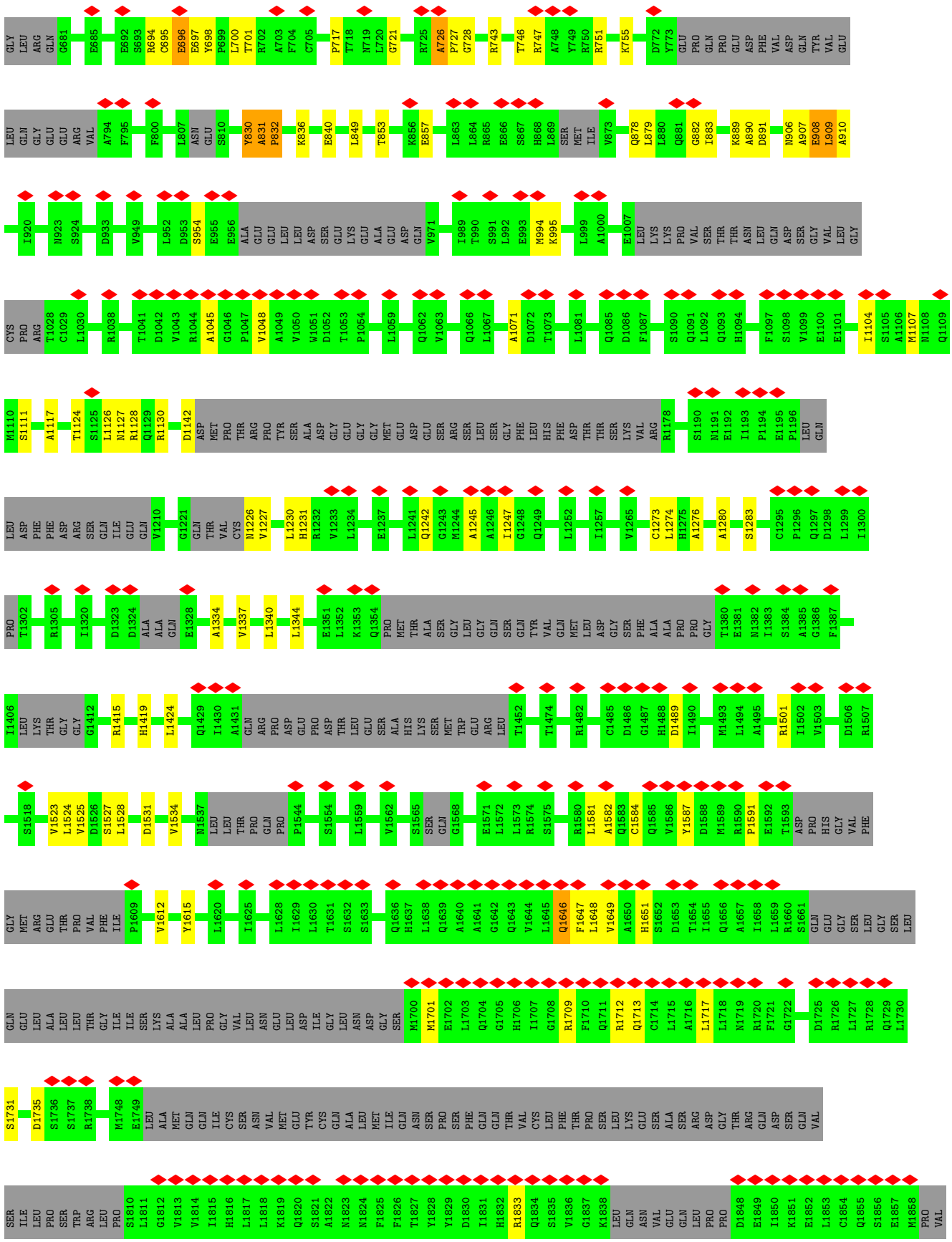
# 3 Residue-property plots (i)

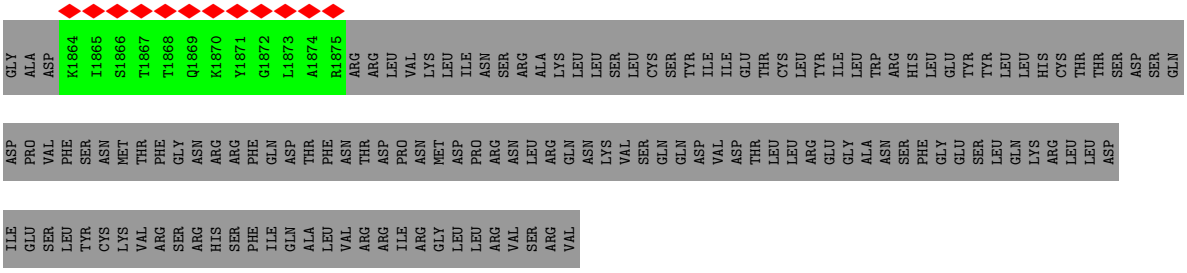
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 27% 62% 8% • 30%

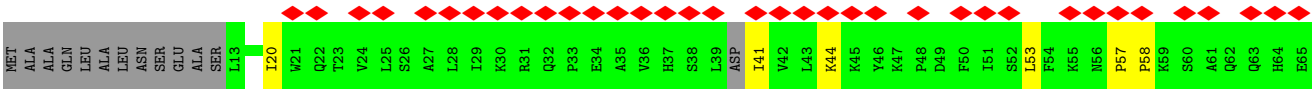


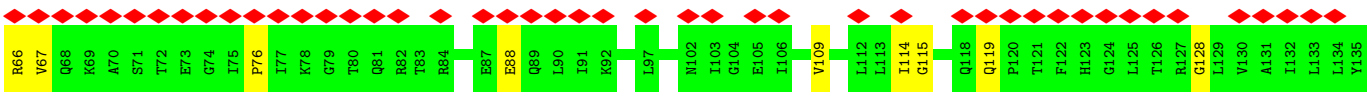

GLY LEU ARG GLN G681 E685 E692 S693 R694 C695 E696 E697 Y698 P699 L700 T701 R702 A703 F704 C705 P717 T718 N719 L720 G721 R725 A726 P727 G728 R743 T746 R747 A748 Y749 R750 R751 K755 D772 Y773 GLU PRO GLN PRO GLU ASP PHE VAL ASP GLN TYR VAL GLU
LEU GLN GLY GLU GLU ARG VAL A794 F795 F800 L807 ASN GLU S810 Y830 A831 P832 K836 E840 L849 T853 K856 E857 L863 L864 R865 E866 S867 H868 L869 SER MET ILE V873 Q878 L879 L880 Q881 G882 I883 K889 A890 D891 N906 A907 E908 L909 A910
I920 N923 S924 D933 V949 L952 D953 S954 E955 E956 ALA GLU GLU LEU LEU ASP SER GLU LYS GLU ALA GLU ASP GLN V971 I989 T990 S991 L992 E993 M994 K995 L999 A1000 E1007 LEU LYS LYS PRO VAL SER THR THR ASN LEU GLN ASP SER GLY VAL LEU GLY
CYS PRO ARG T1028 C1029 L1030 R1038 T1041 D1042 V1043 R1044 A1045 G1046 P1047 V1048 A1049 V1050 W1051 D1052 T1053 P1054 L1059 Q1062 V1063 Q1066 L1067 A1071 D1072 T1073 L1081 Q1085 D1086 F1087 S1090 Q1091 L1092 Q1093 H1094 F1097 S1098 V1099 E1100 E1101 I1104 S1105 A1106 M1107 N1108 Q1109
M1110 S1111 A1117 T1124 S1125 L1126 N1127 R1128 Q1129 R1130 D1142 ASP MET PRO THR ARG PRO TYR SER ALA ASP GLY GLU GLY GLY MET GLU ASP GLU SER ARG SER LEU SER GLY PHE LEU HIS PHE ASP THR THR SER LYS VAL ARG R1178 S1190 N1191 E1192 I1193 P1194 E1195 P1196 LEU GLN
LEU ASP PHE PHE ASP ARG SER GLN ILE GLU GLN V1210 G1221 GLN THR VAL CYS N1226 V1227 L1230 H1231 R1232 V1233 L1234 E1237 L1241 Q1242 G1243 M1244 A1245 A1246 I1247 G1248 Q1249 L1252 I1257 V1265 C1273 L1274 H1275 A1276 A1280 S1283 C1295 P1296 Q1297 D1298 L1299 I1300
PRO T1302 R1305 I1320 D1323 D1324 ALA ALA GLN E1328 A1334 V1337 L1340 L1344 E1351 L1352 K1353 Q1354 PRO MET THR ALA SER GLY LEU GLY GLN SER GLN TYR VAL GLN MET LEU ASP GLY SER PHE ALA ALA PRO PRO GLY T1380 E1381 N1382 I1383 S1384 A1385 G1386 F1387
I1406 LEU LYS THR GLY GLY G1412 R1415 H1419 L1424 Q1429 I1430 A1431 GLN ARG PRO ASP GLU PRO ASP THR LEU GLU SER ALA HIS LYS SER MET TRP GLU ARG LEU T1452 T1474 R1482 C1485 D1486 G1487 H1488 D1489 I1490 M1493 L1494 A1495 R1501 I1502 V1503 D1506 R1507
S1518 V1523 L1524 V1525 D1526 S1527 L1528 D1531 V1534 N1537 LEU LEU THR PRO GLN PRO P1544 S1554 L1559 V1562 S1565 SER GLN G1568 E1571 L1572 L1573 R1574 S1575 R1580 L1581 A1582 Q1583 C1584 Q1585 V1586 Y1587 D1588 M1589 R1590 P1591 E1592 T1593 ASP PRO HIS GLY VAL PHE
GLY MET ARG GLU THR PRO VAL PHE ILE P1609 V1612 Y1615 L1620 I1625 L1628 I1629 L1630 T1631 S1632 S1633 Q1636 H1637 L1638 Q1639 A1640 A1641 G1642 Q1643 V1644 L1645 Q1646 F1647 L1648 V1649 A1650 H1651 S1652 D1653 T1654 I1655 Q1656 A1657 I1658 L1659 R1660 S1661 GLN GLU GLY SER LEU GLY SER LEU
GLN GLU LEU ALA LEU LEU THR GLY ILE ILE SER LYS ALA ALA LEU PRO GLY VAL LEU ASN GLU LEU ASP ILE GLY LEU ASN ASP GLY SER M1700 M1701 E1702 L1703 Q1704 G1705 H1706 I1707 G1708 R1709 F1710 Q1711 R1712 Q1713 C1714 L1715 A1716 L1717 L1718 N1719 R1720 F1721 G1722 D1725 R1726 L1727 R1728 Q1729 L1730
S1731 D1735 S1736 S1737 R1738 M1748 E1749 LEU ALA MET GLN GLN ILE CYS SER ASN VAL MET GLU TYR CYS GLN ALA LEU MET ILE GLN ASN SER PRO SER PHE GLN GLN GLN THR VAL CYS LEU PHE THR PRO SER LEU LYS GLU SER ALA SER ARG ASP GLY THR ARG GLN ASP SER GLN VAL
SER ILE LEU PRO SER TRP ARG LEU PRO S1810 L1811 G1812 V1813 V1814 I1815 H1816 L1817 L1818 K1819 Q1820 S1821 A1822 N1823 N1824 F1825 F1826 T1827 Y1828 Y1829 D1830 I1831 H1832 R1833 Q1834 S1835 V1836 G1837 K1838 LEU GLN ASN VAL GLU GLN LEU PRO PRO D1848 E1849 I1850 K1851 E1852 L1853 C1854 Q1855 S1856 E1857 M1858 PRO VAL

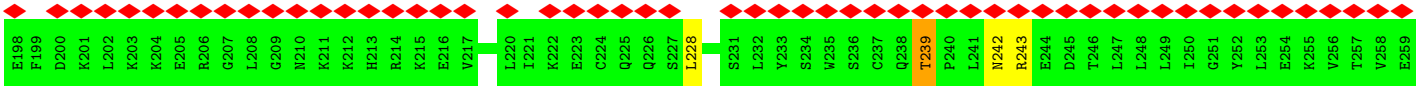


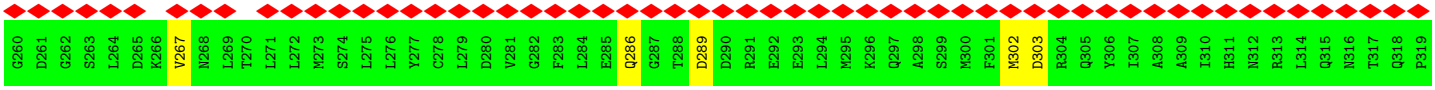

- Molecule 1: MGC83295 protein

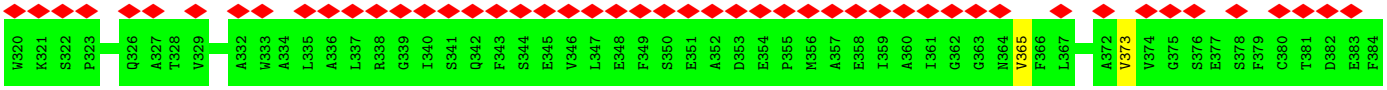
Chain a:

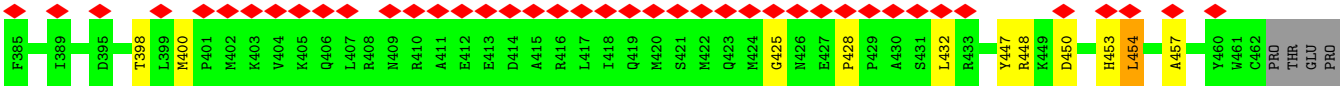


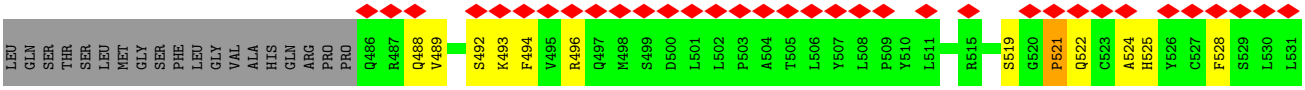



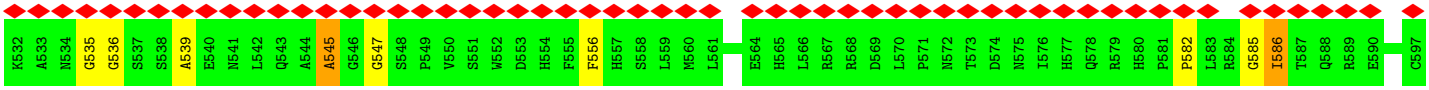


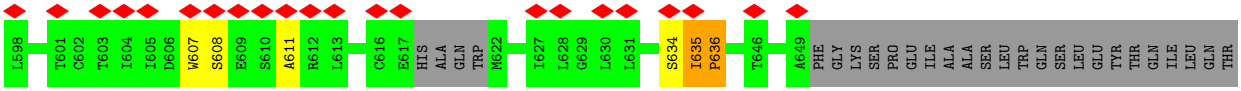



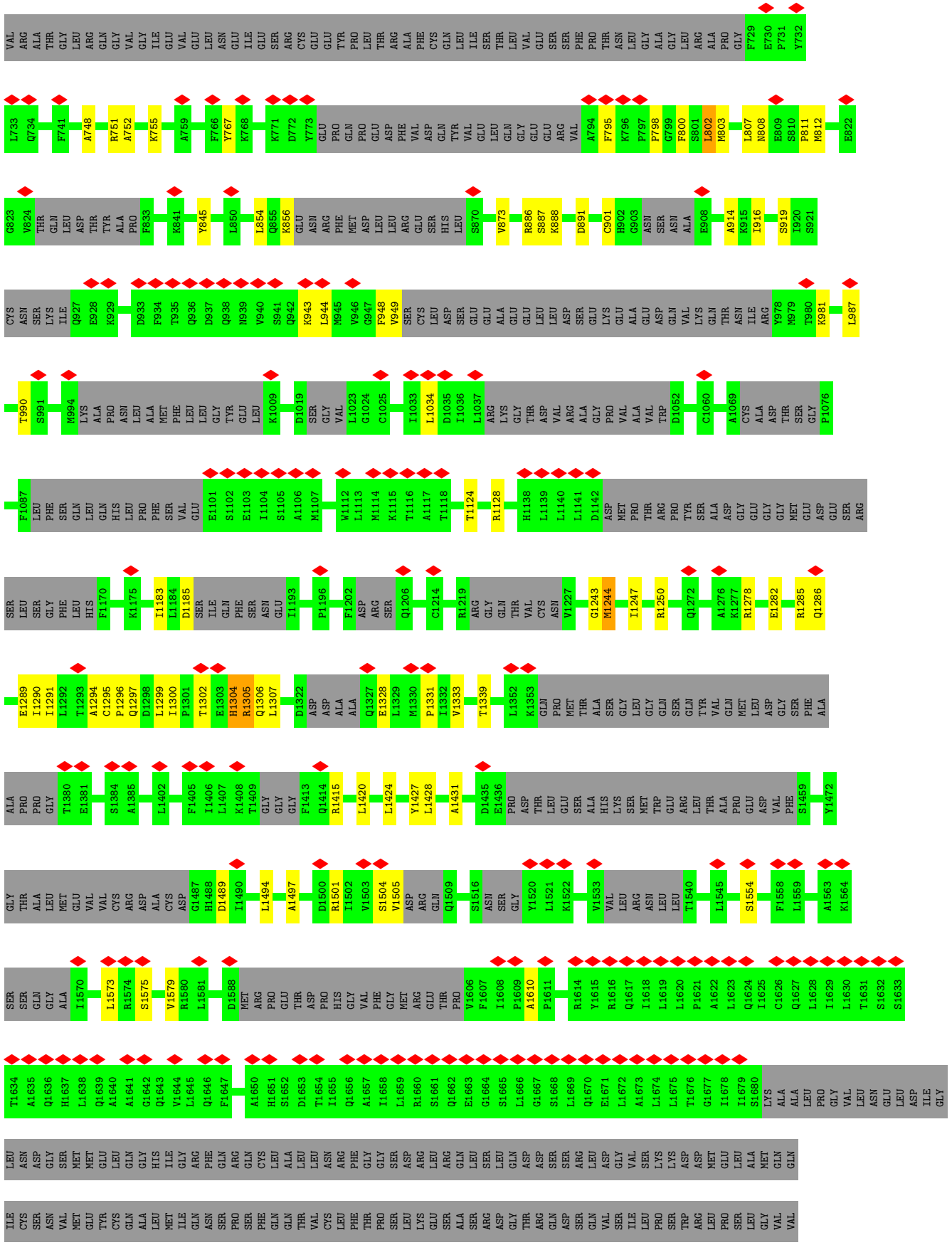




VAL ARG ALA THR GLY LEU ARG GLN GLY VAL GLY ILE GLU VAL GLU LEU ASN GLU ILE GLU SER ARG CYS GLU GLU TYR PRO LEU THR ARG ALA PHE CYS GLN LEU ILE SER THR LEU VAL GLU SER SER PHE PRO THR ASN LEU GLY ALA GLY LEU ARG ALA PRO GLY F729 E730 P731 Y732
L733 Q734 F741 A748 R751 A752 K755 A759 F766 Y767 K768 K771 D772 Y773 GLU PRO GLN PRO GLU ASP PHE VAL ASP GLN TYR VAL GLU LEU GLN GLY GLU GLU ARG VAL A794 F795 K796 P797 P798 G799 F800 S801 L802 M803 L807 N808 E809 S810 P811 M812 E822
G823 V824 THR GLN LEU ASP THR TYR ALA PRO F833 K841 Y845 L850 L854 Q855 K856 GLU ASN ARG PHE MET ASP LEU LEU ARG GLU SER HIS LEU S870 V873 R886 S887 K888 D891 C901 H902 C903 ASN SER ASN ALA E908 A914 K915 I916 S919 I920 S921
CYS ASN SER LYS ILE Q927 E928 K929 D933 F934 T935 Q936 D937 Q938 N939 V940 S941 Q942 K943 L944 M945 V946 G947 F948 V949 SER CYS LEU ASP SER GLU GLU ALA GLU GLU GLU LEU LEU ASP SER GLU LYS GLU ALA GLU ASP GLN VAL LYS GLN THR ASN ILE ARG Y978 M979 T980 K981 L987
T990 S991 M994 LYS ALA PRO ASN LEU ALA MET PHE LEU LEU GLY TYR GLU LEU K1009 D1019 SER GLY VAL L1023 G1024 C1025 I1033 L1034 D1035 I1036 L1037 ARG LYS GLY THR ASP VAL ARG ALA GLY PRO VAL ALA VAL TRP D1052 C1060 A1069 CYS ALA ASP THR SER GLY P1076
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SER SER GLN GLY ALA I1570 L1573 R1574 S1575 V1579 R1580 L1581 D1588 MET ARG PRO GLU THR ASP PRO HIS GLY VAL PHE GLY MET MET ARG GLU THR PRO V1606 F1607 I1608 P1609 A1610 P1611 R1614 Y1615 R1616 Q1617 I1618 I1619 L1620 P1621 A1622 L1623 Q1624 I1625 C1626 Q1627 L1628 I1629 L1630 T1631 S1632 S1633
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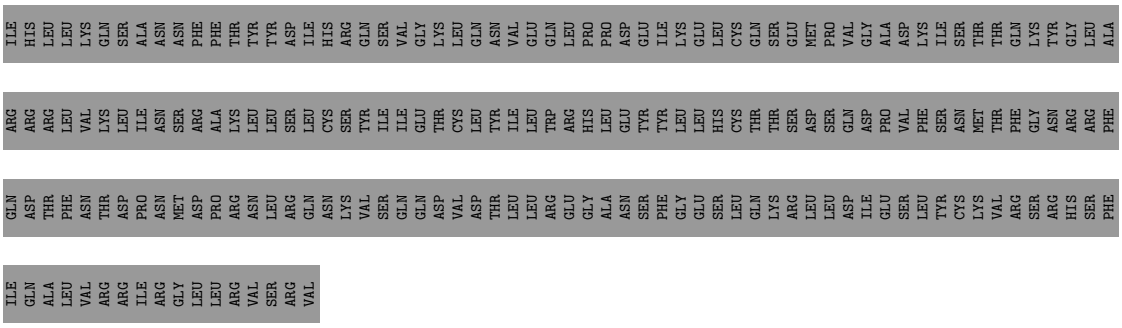


- Molecule 2: Nuclear pore complex protein Nup85

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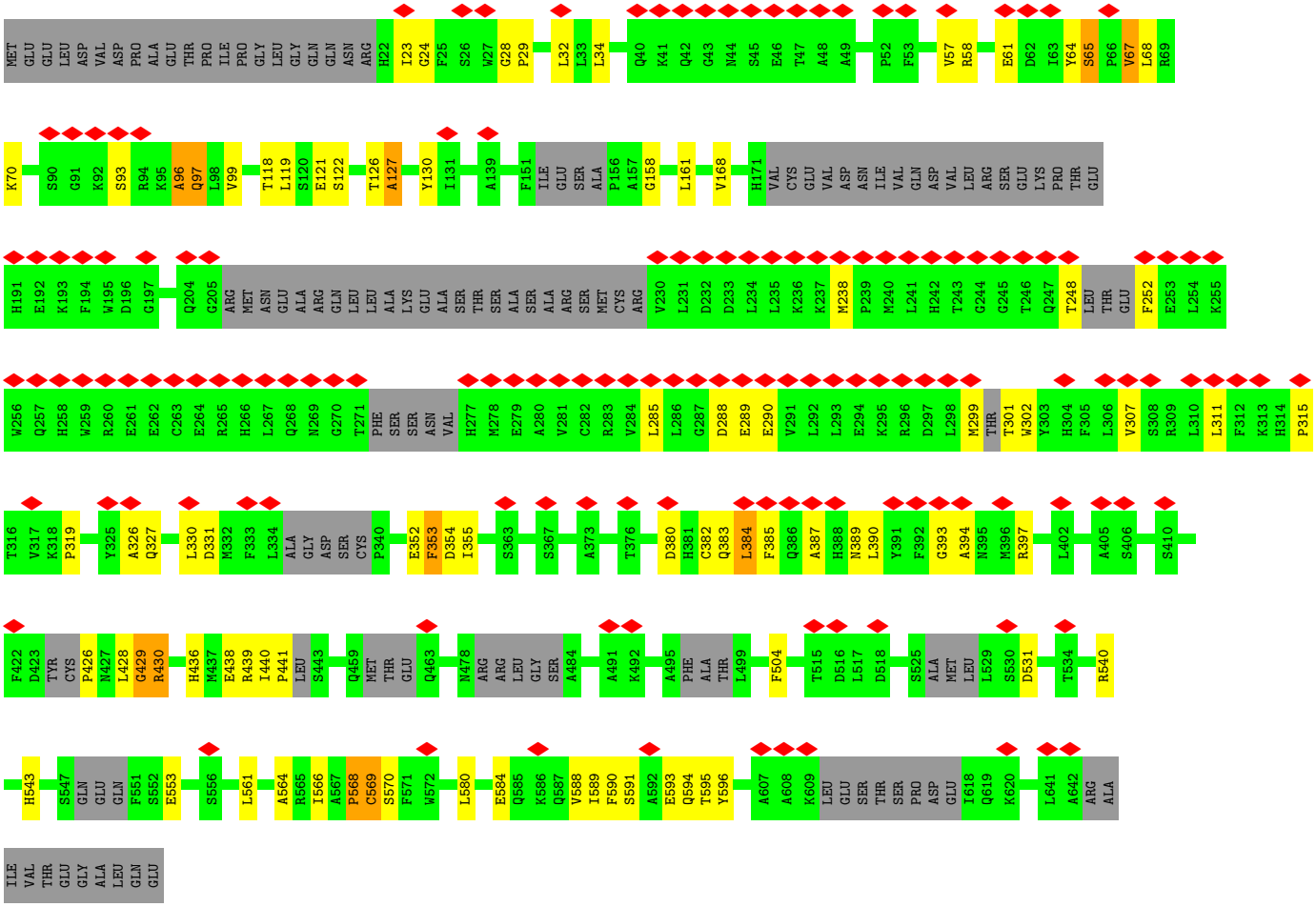
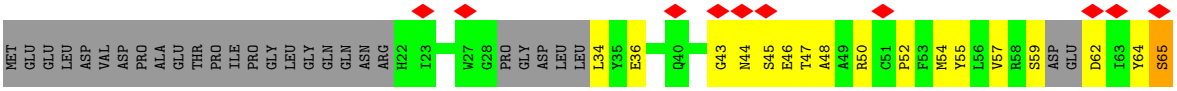
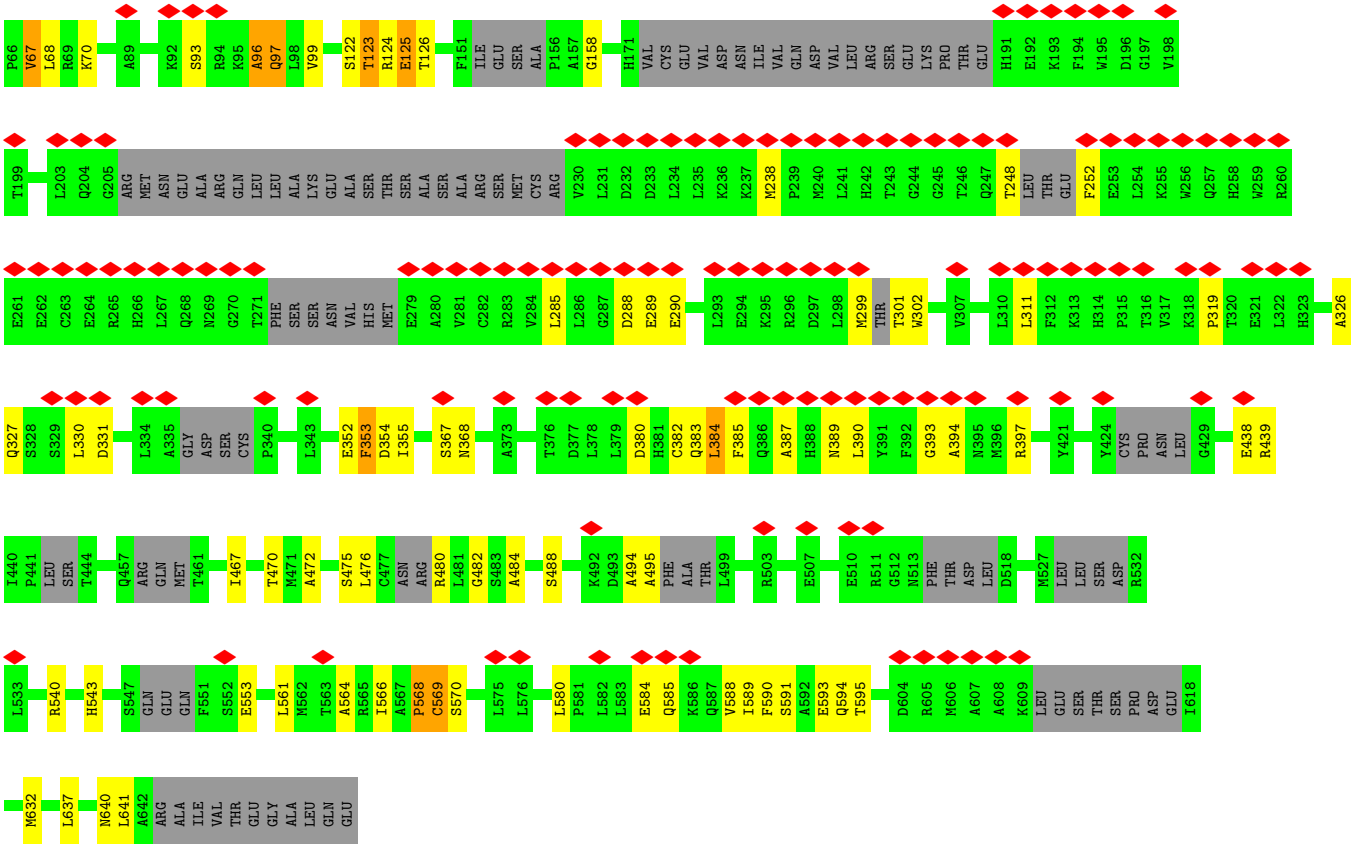



- Molecule 2: Nuclear pore complex protein Nup85

Chain b:






- Molecule 3: MGC154553 protein

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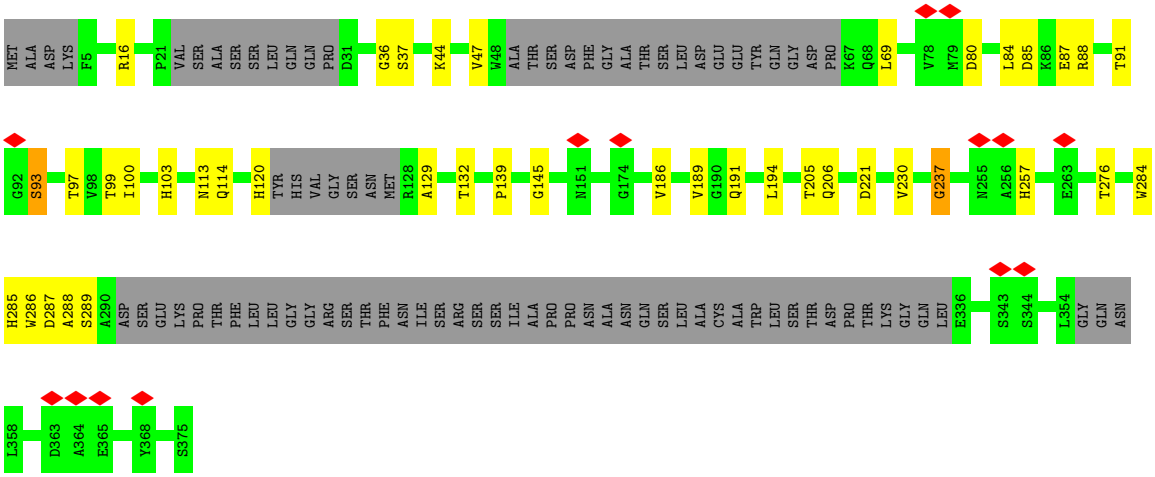


- Molecule 3: MGC154553 protein

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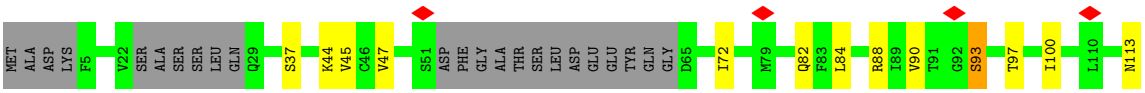

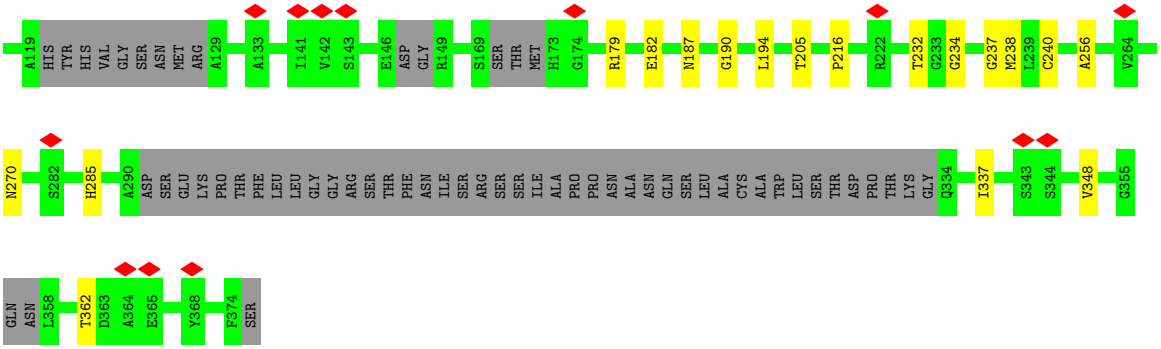


- Molecule 4: Nucleoporin SEH1-A

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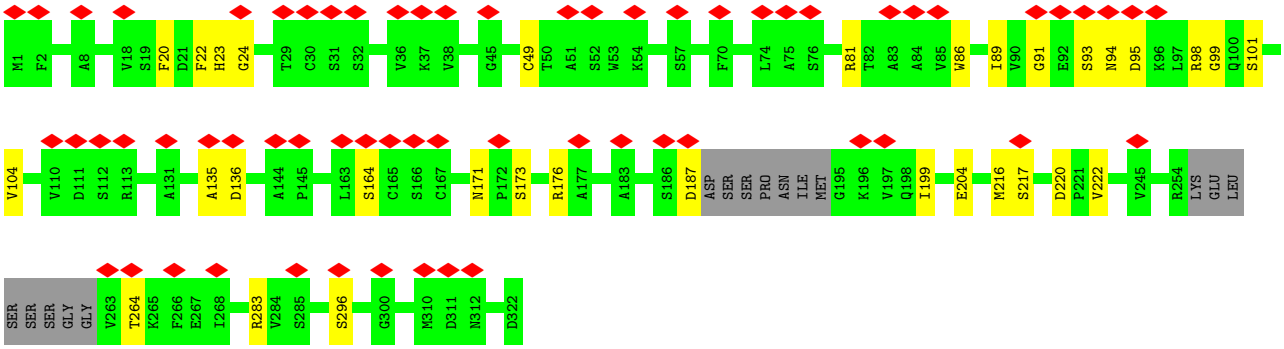


- Molecule 4: Nucleoporin SEH1-A

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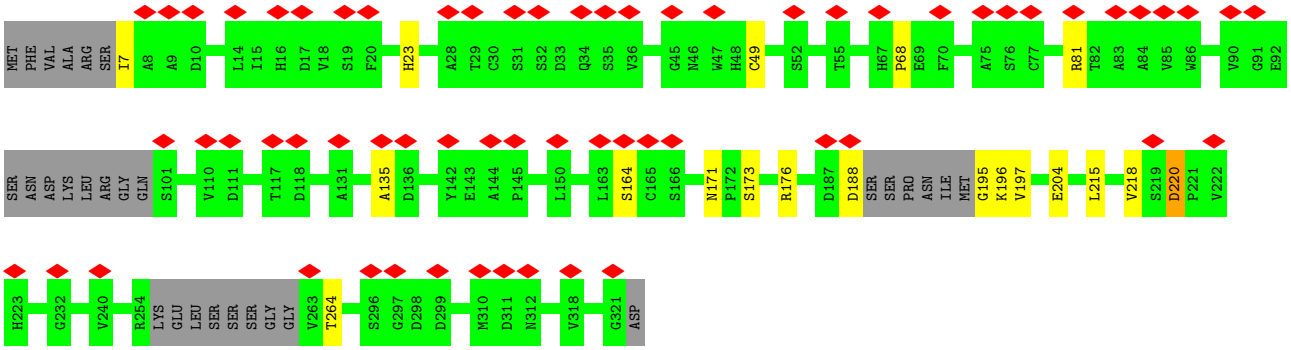


- Molecule 5: outer Nup160

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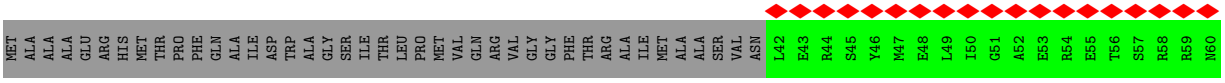

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GLY GLY GLU ALA ALA GLN ALA GLU ALA TRP GLU TRP LEU ALA ALA ASN GLN LEU ALA THR VAL ILE THR THR LYS GLU SER SER ALA THR ASP GLU ALA TRP ARG LEU MET ILE SER TYR LEU ASP LYS TYR GLU ALA LYS ASN THR LEU TYR HIS HIS CYS ILE ILE ASN LYS LEU LEU

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

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

LYS PRO LEU ARG ALA

- Molecule 5: outer Nup160

Chain e:

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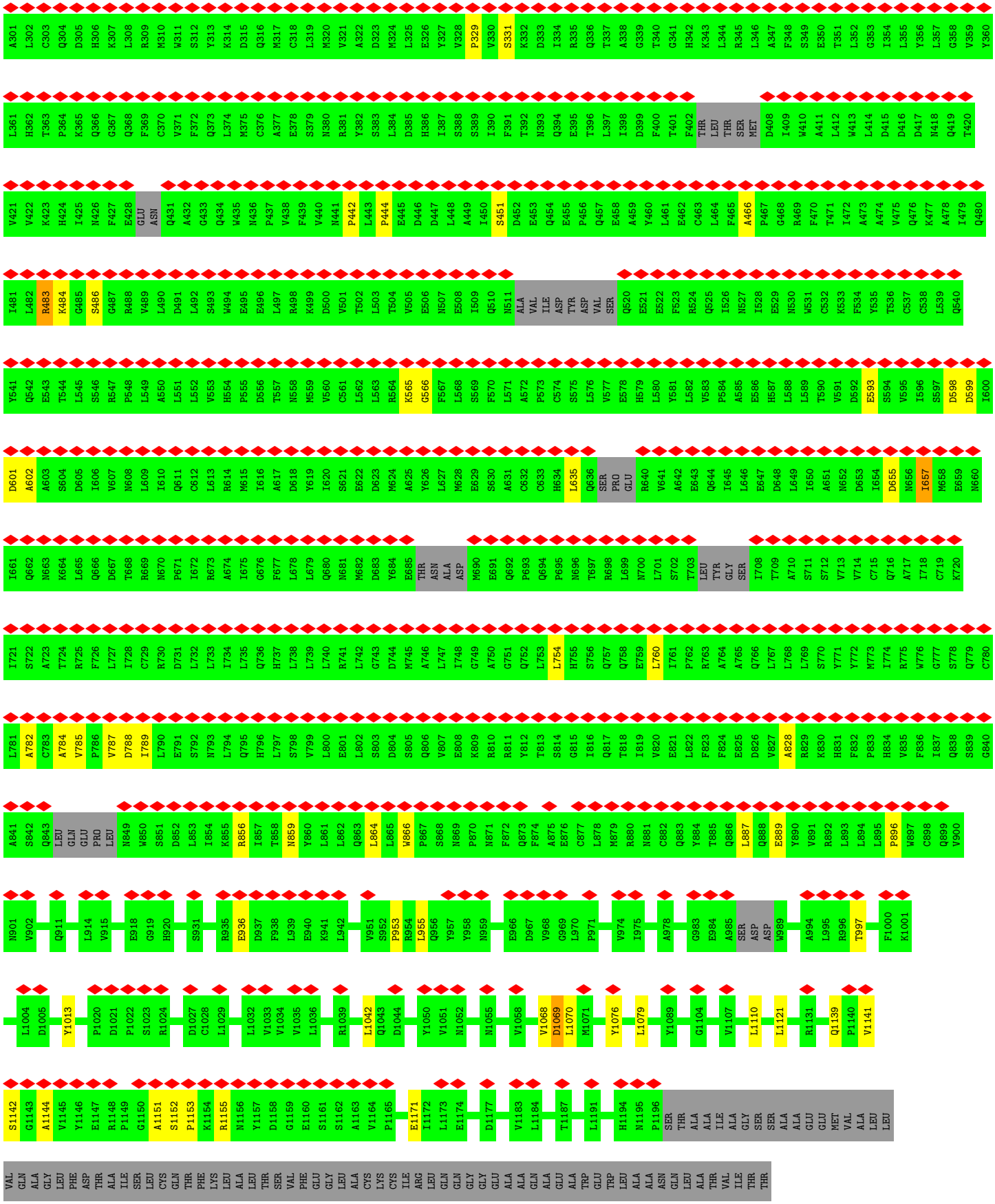
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S1142 G1143 A1144 V1145 Y1146 E1147 R1148 P1149 G1150 A1151 S1152 P1153 K1154 R1155 N1156 Y1157 D1158 G1159 E1160 S1161 S1162 A1163 V1164 P1165 E1171 I1172 L1173 E1174 D1177 V1183 L1184 T1187 L1191 H1194 N1195 P1196 SER THR ALA ALA ILE ALA GLY SER SER ALA ALA GLU GLU GLU MET VAL ALA LEU LEU
VAL GLN ALA GLY LEU PHE ASP THR ALA ILE SER LEU CYS GLN THR PHE LYS LEU ALA LEU THR SER VAL PHE GLU GLY LEU ALA CYS LYS CYS ILE ARG LEU GLN GLN GLY GLY GLU ALA ALA GLN ALA GLU ALA TRP GLU TRP LEU ALA ALA ASN GLN LEU ALA THR VAL ILE THR THR

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

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

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

- Molecule 6: MGC83926 protein

Chain F: 89% 83% 5% • 11%

MET LYS GLN ASP SER ALA SER ASN A9 T10 Y11 T12 V13 D14 C15 E16 D17 Y18 V19 H20 V21 V22 E23 F24 N25 P26 PHE ASP SER GLY GLU ALA G33 S34 L35 L36 A37 Y38 G39 G40 I41 S42 Y43 V44 V45 I46 A47 S48 C49 R50 F51 Q52 E53 E54 D55 S56 T57 V58 E59 G60

I61 E62 F63 K64 T65 L66 K67 T68 F69 H70 H71 G72 E73 R74 V75 V76 A77 I78 A79 W80 S81 P82 E83 T84 R85 C86 D87 A88 L89 L90 P91 L92 L93 R94 F95 A96 T97 A98 A99 G100 D101 K102 K103 I104 R105 I106 F107 T108 SER ASP F111 Q112 D113 K114 N115 E116 Y117 K118 V119 T120

E121 G122 H123 S124 G125 Y126 T127 N128 D129 L130 V131 F132 C133 S134 P135 E136 G137 T138 D139 A79 I140 A141 S142 V143 G144 D145 D146 H147 T148 C149 R150 T151 W152 D153 L154 ASP G156 K157 Q158 I159 A160 M161 F162 I163 L164 R165 S166 P167 G168 M169 S170 V171 A172 W173 H174 P175 E176 G177 A178 F179 K180

L181 M182 V183 A184 E185 K186 T187 G188 T189 I190 R191 F192 Y193 D194 L195 T196 T197 H198 Q199 A200 I201 L202 S203 L204 E205 SER VAL GLN VAL PRO LEU M212 S213 A214 D215 W216 C217 V218 R219 N220 T221 L222 R223 I224 G225 A226 V227 A228 G229 N230 D231 W232 I233 I234 W235 E236 M237 PRO ARG SER

SER TYR PRO Q244 D245 N246 K247 P248 A249 H250 A251 D252 R253 ALA R255 M256 F257 R258 W259 S260 K261 C262 N263 E264 N265 V266 F267 A268 T269 T270 G271 Y272 P273 GLY LYS MET K277 S278 Q279 I280 A281 I282 H283 H284 LEU ALA HIS P288 Q289 P290 I291 L292 I293 G294 T295 ALA P297 V298 G299 S300

G301 L302 S303 W304 H305 R306 R307 L308 P309 L310 C311 V312 V313 G314 G315 Y316 R317 K318 L319 F320 F321 W322 L323 T324 E325 M326

- Molecule 6: MGC83926 protein

Chain f: 63% 86% • 11%

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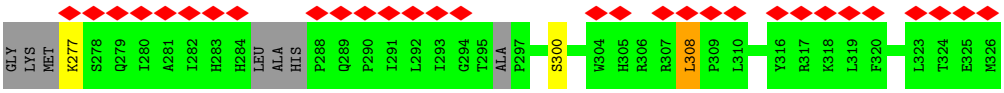
T65 L66 K67 T68 F69 H70 H71 G72 S81 P82 E83 T84 R85 C86 D87 A88 L89 L90 P91 L92 L93 A96 D101 K102 K103 I104 R105 I106 F107 T108 SER ASP F111 Q112 D113 K114 N115 E116 Y117 K118 V119 I120 E121 G122 H123 S124 N128 D129 L130 V131 F132 C133 S134 P135 E136 G137

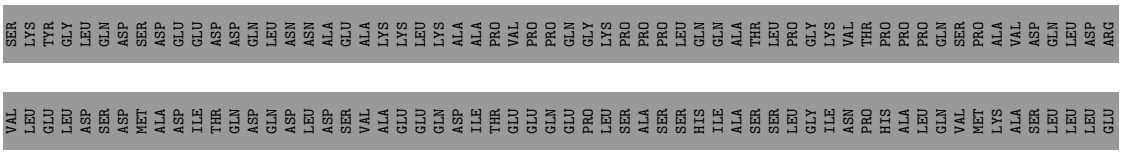
T138 D139 T148 C149 R150 I151 W152 D153 L154 ASP G156 K157 Q158 I159 A160 M161 F162 I163 S166 P167 G168 M169 S170 V171 A172 W173 H174 P175 E176 G177 A178 F179 K180 L181 M182 V183 A184 T187 G188 T189 I190 R191 F192 Y193 D194 L195 T196 T197 H198 Q199 A200 I201 L202 S203 L204 E205 SER

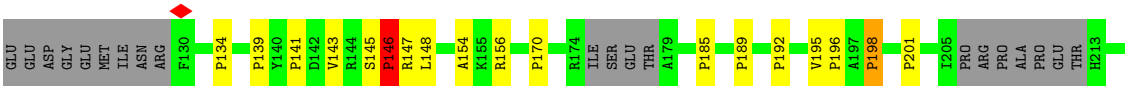
VAL GLN VAL PRO LEU M212 S213 A214 D215 W216 C217 V218 R219 N220 T221 L222 R223 I224 G225 A226 V227 A228 G229 N230 D231 W232 I233 I234 W235 E236 M237 PRO ARG SER SER TYR PRO Q244 D245 N246 K247 P248 A249 H250 A251 D252 R253 ALA R255 R258 E264 N265 V266 F267 A268 T269 P273

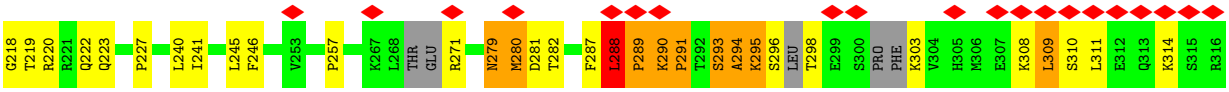


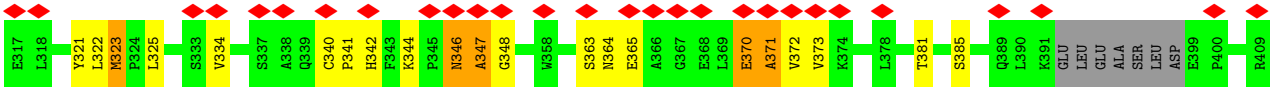

- Molecule 7: Nuclear pore complex protein Nup96

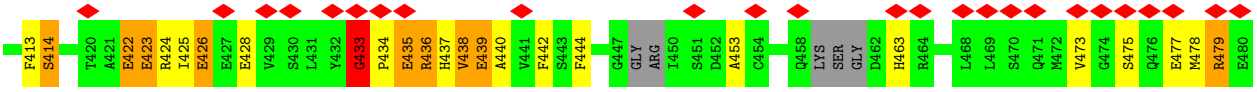
Chain G:

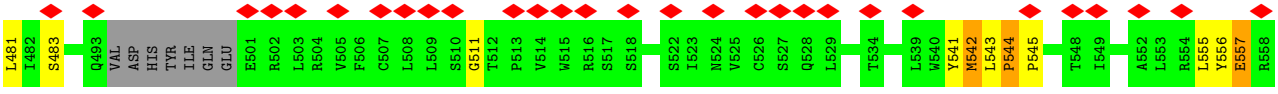


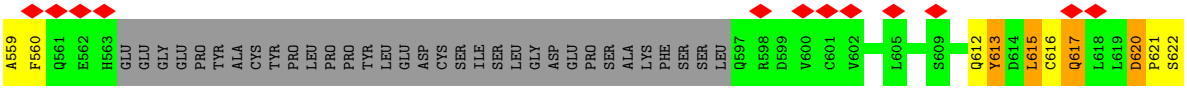



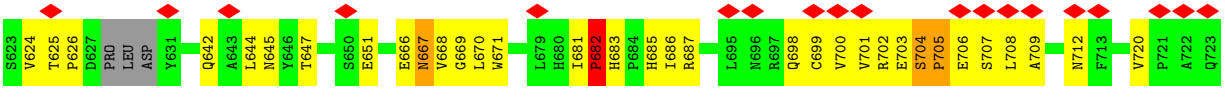



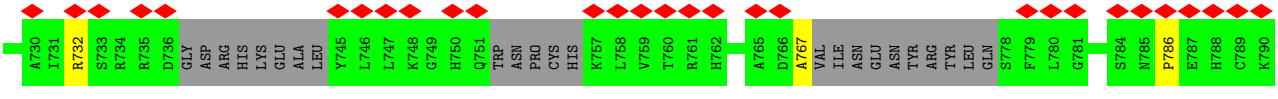



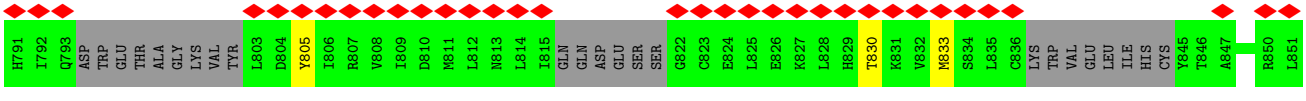



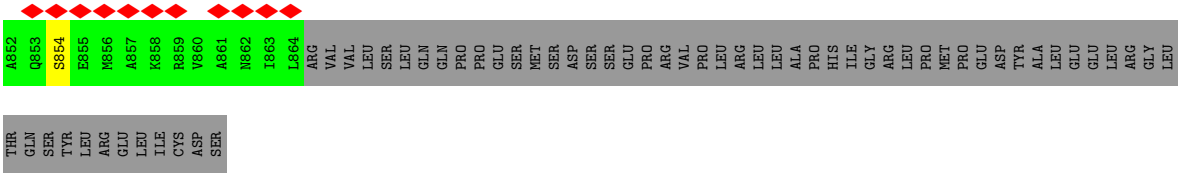



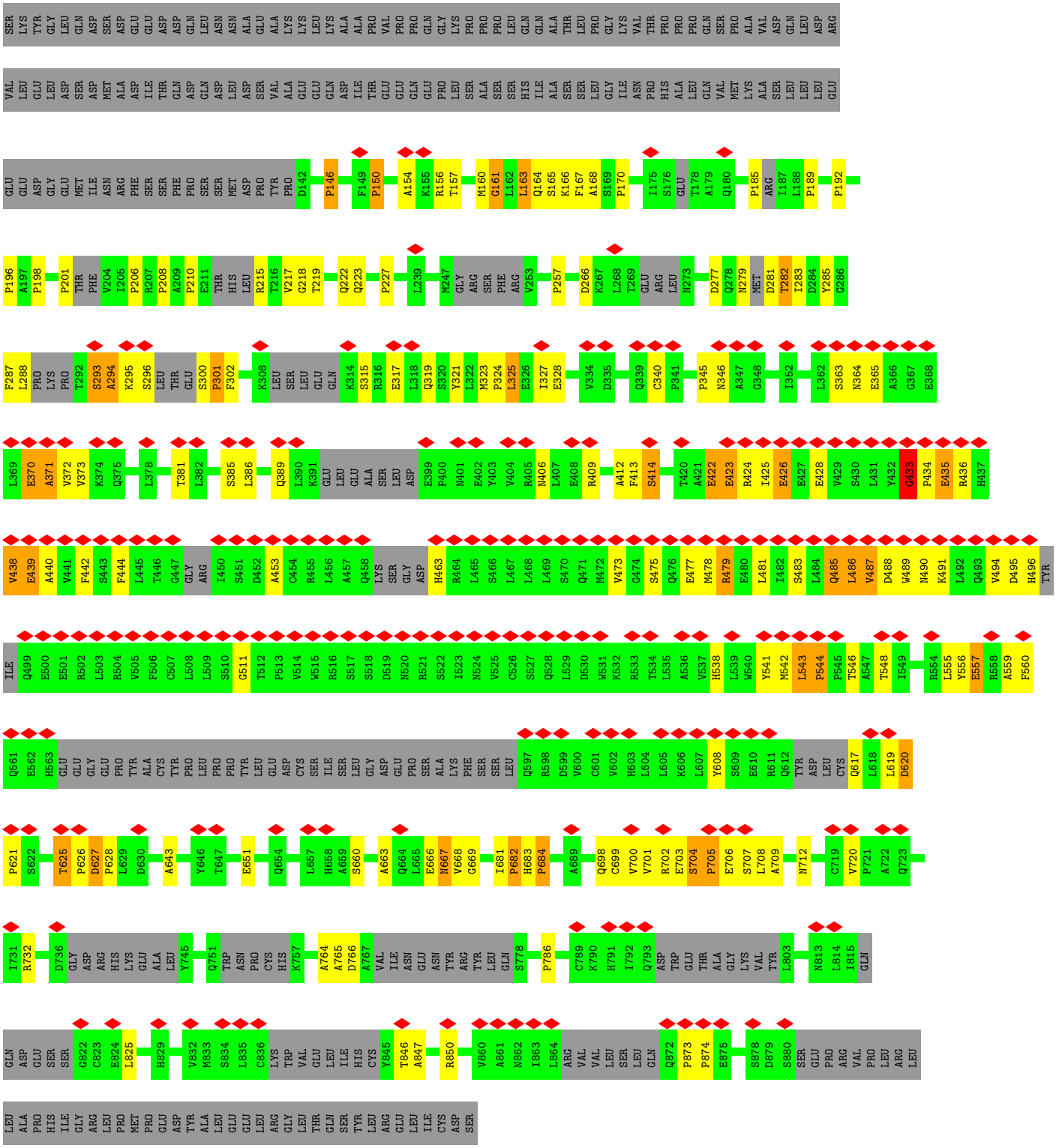



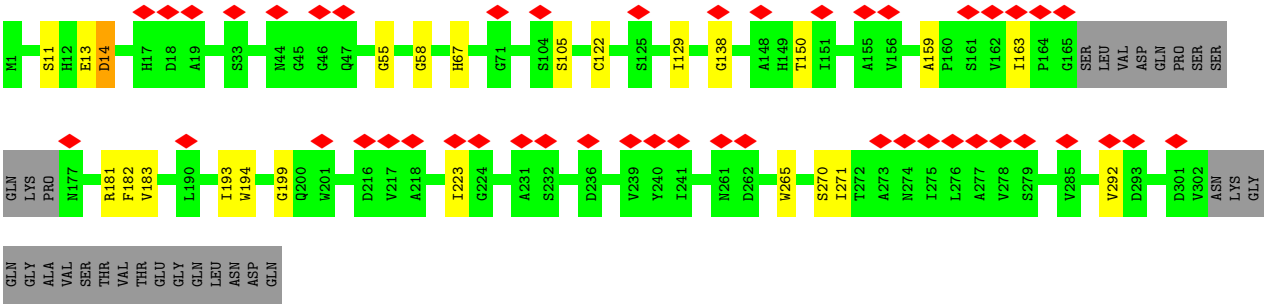
- Molecule 7: Nuclear pore complex protein Nup96

Chain g:



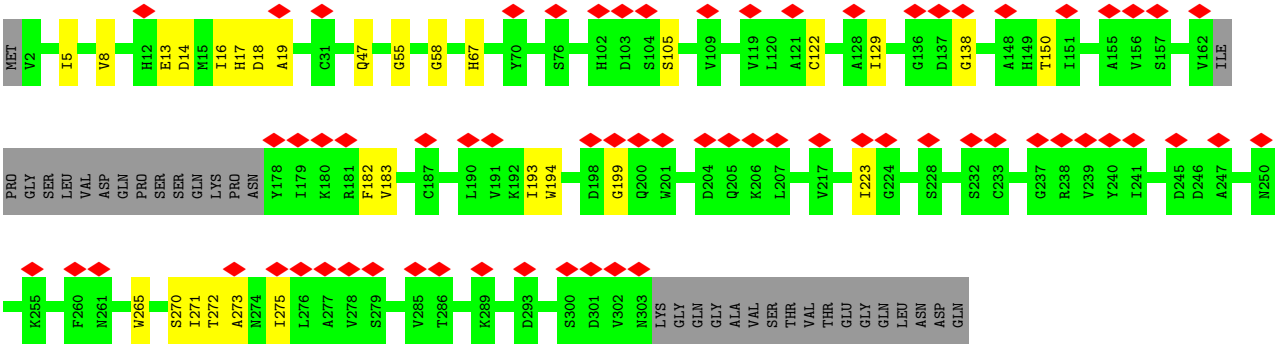
- Molecule 8: GATOR complex protein SEC13

Chain H:



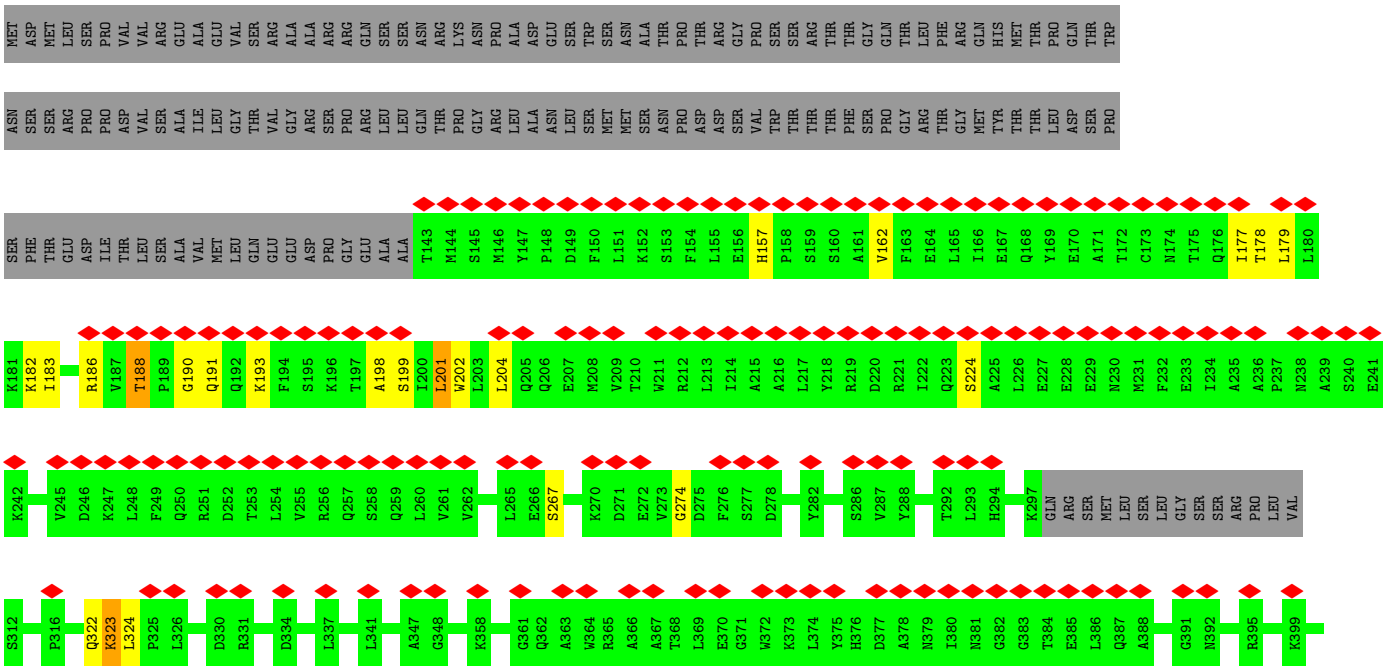

- Molecule 8: GATOR complex protein SEC13

Chain h:




- Molecule 9: Nuclear pore complex protein

Chain I:



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R471 E472 Y473 I474 E475 A476 N477 W478 T479 L480 D481 S482 V483 F484 E485 A486 L487 Q488 A489 K493 R494 V495 L496 E497 E498 N499 Q507 K508 F509 V510 I511 L512 A513 D514 V515 D516 G517 L518 M519 D520 E521 F522 S523 E524 W525 L526 S527 N528 G529 K530 N531 L532 L533 L534 G535 H536 L537 L538

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F599 L600 E601 N602 I603 T604 ASP PRO ASP GLN R609 Q610 R611 C612 L613 E614 L615 A616 K617 E618 A619 G620 L621 D622 V623 ALA SER ILE T627 K628 T629 V630 V631 E632 N633 T634 R635 K636 K637 D638 A639 G640 GLU PHE ALA HIS HIS ASP PHE ALA PRO ALA L651 D652 S653 G654 T655 S656 E657 E658

D659 R660 A661 K662 I663 D664 V665 I666 D667 W668 L669 V670 F671 ASP PRO ALA Q675 R676 A677 E678 A679 L680 K681 Q682 S683 N684 A685 I686 M687 R688 K689 F690 L691 A692 S693 K694 K695 H696 E697 A698 A699 K700 E701 V702 F703 A704 K705 I706 P707 Q708 D709 S710 I711 A712 E713 I714 Y715 S716 Q717 W718

E719 E720 Q721 A722 M723 D724 S725 A726 L727 P728 A729 E730 D731 D732 N733 A734 I735 R736 E737 H738 L739 C740 I741 R742 A743 Y744 L745 E746 S747 H748 E749 A750 F751 N752 E753 W754 F755 K756 H757 I758 N759 S760 P761 P762 Q763 K764 P765 T766 L767 V768 G769 Q770 A771 S772 F773 T774 E775 K776 V777 A778

H779 E780 H781 K782 E783 K784 K785 Y786 E787 M788 D789 F790 G791 I792 W793 K794 G795 H796 L797 D798 A799 L800 T801 S802 D803 V804 K805 E806 K807 I808 Y809 N810 V811 L812 L813 F814 V815 D816 G817 G818 W819 M820 V821 D822 V823 R824 E825 D826 T827 E828 E829 D830 P831 E832 R833 S834 H835 Q836 M837 V838

L839 L840 R841 R842 L843 C844 L845 P846 M847 M848 C849 F850 L851 L852 H853 T854 V855 L856 H857 N858 T859 K860 Q861 Y862 K863 D864 C865 L866 R867 L868 A869 D870 I871 V872 S873 S874 E875 N876 Q877 K878 L879 Y880 T881 V882 F883 S884 K885 T886 E887 M888 R889 N890 L891 L892 Q893 K894 L895 R896 E897 S898

S899 L900 M901 L902 L903 D904 L905 Q906 L907 D908 P909 L910 G911 Y912 E913 I914 GLN SER

- Molecule 9: Nuclear pore complex protein

Chain i:

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

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

SER PHE THR GLU ASP ILE THR LEU SER ALA VAL MET LEU GLN GLU GLU ASP PRO GLY GLU ALA ALA T143 M144 S145 M146 Y147 P148 D149 F150 L151 K152 S153 F154 L155 E156 H157 P158 S159 S160 A161 V162 F163 E164 L165 I166 E167 Q168 Y169 E170 A171 T172 C173 N174 T175 Q176 I177 T178 L179 L180

K181 K182 I183 V184 K185 R186 V187 T188 P189 G190 Q191 Q192 K193 F194 S195 K196 T197 A198 S199 I200 L201 W202 L203 L204 Q205 Q206 E207 M208 V209 T210 W211 R212 L213 I214 A215 A216 L217 Y218 R219 D220 R221 I222 Q223 S224 A225 LEU GLU GLU GLU ASN MET PHE GLU ILE ALA ALA PRO ASN A239 S240

E241 K242 T243 I244 V245 D246 K247 L248 F249 Q250 R251 D252 T253 L254 V255 R256 Q257 S258 Q259 L260 V261 V262 D263 W264 L265 E266 S267 I268 A269 K270 D271 E272 V273 G274 D275 F276 S277 D278 N279 I280 E281 Y282 Y283 A284 K285 S286 V287 Y288 W289 E290 N291 T292 L293 H294 T295 L296 K297 GLN ARG SER

MET LEU SER LEU GLY SER SER ARG PRO LEU VAL SER GLU LEU ASP PRO D317 A318 P319 I320 R321 Q322 K323 L324 P325 L326 D327 D328 L329 D330 R331 E332 D333 D334 I335 R336 L337 I338 K339 Y340 L341 F342 T343 L344 I345 R346 A347 G348 M349 T350 D351 E352 A353 Q354 R355 L356 C357 K358 R359 C360

G361 Q362 A363 W364 R365 A366 A367 T368 L369 E370 G371 W372 K373 L374 Y375 H376 D377 A378 N379 I380 N381 G382 G383 T384 E385 L386 Q387 A388 V389 E390 G391 N392 P393 Y394 R395 C396 V397 W398 K399 T400 C401 C402 W403 R404 M405 A406 E407 D408 E409 Q410 F411 N412 K413 Y414 E415 R416 A417 I418 Y419 A420

T421 L422 S423 G424 N425 L426 K427 Q428 L429 L430 P431 V432 C433 E434 S435 W436 E437 D438 T439 V440 W441 A442 H443 F444 K445 V446 M447 V448 D449 S450 L451 V452 E453 Q454 E455 I456 R457 A458 S459 I460 I461 S462 F463 M464 E465 A466 N467 E468 L469 P470 R471 E472 Y473 L474 E475 A476 M477 W478 T479 L480

D481 S482 V483 F484 E485 E486 L487 Q488 A489 T490 D491 K492 K493 R494 V495 L496 E497 E498 M499 R500 E501 H502 Y503 H504 I505 I506 Q507 K508 F509 V510 I511 L512 A513 D514 V515 D516 G517 L518 M519 D520 E521 F522 S523 E524 W525 L526 S527 N528 G529 K530 N531 L532 L533 L534 G535 H536 L537 L538 R539 F540

M541 T542 H543 L544 L545 L546 F547 F548 R549 T550 L551 G552 L553 Q554 A555 K556 E557 E558 V559 S560 V561 E562 V563 L564 K565 T566 Y567 I568 Q569 R570 L571 I572 N573 E574 K575 Q576 I577 E578 L579 I580 A581 F582 Y583 V584 S585 H586 L587 P588 Q589 E590 L591 A592 I593 S594 Q595 Y596 A597 V598 F599 L600

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H781 K782 E783 K784 K785 Y786 E787 M788 D789 F790 G791 I792 W793 K794 G795 H796 L797 D798 A799 L800 T801 S802 D803 V804 K805 E806 K807 I808 Y809 N810 V811 L812 L813 F814 V815 D816 G817 G818 W819 M820 V821 D822 V823 R824 E825 D826 T827 E828 E829 D830 P831 E832 R833 S834 H835 Q836 M837 V838 L839 L840

R841 R842 L843 C844 L845 P846 M847 M848 C849 F850 L851 L852 H853 T854 V855 L856 H857 N858 T859 K860 Q861 Y862 K863 D864 C865 L866 R867 L868 A869 D870 I871 V872 S873 S874 E875 N876 Q877 K878 L879 Y880 T881 V882 F883 S884 K885 T886 E887 M888 R889 N890 L891 L892 Q893 K894 L895 R896 E897 S898 S899 L900

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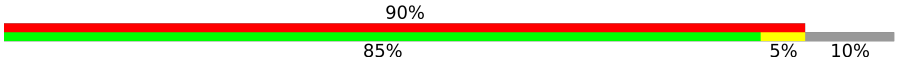
- Molecule 10: outer Nup133

Chain J:




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

VAL TYR LEU HIS PRO ALA ALA SER E69 T70 V71 N72 Y73 N74 V75 Q76 L77 F78 G79 S80 S81 L82 P83 V84 K85 V86 M87 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

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N181 I182 L183 H184 E185 G186 T187 Y188 I189 E190 S191 Y192 T193 E194 F195 G196 S197 SER 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 LYS GLY 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 E467 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

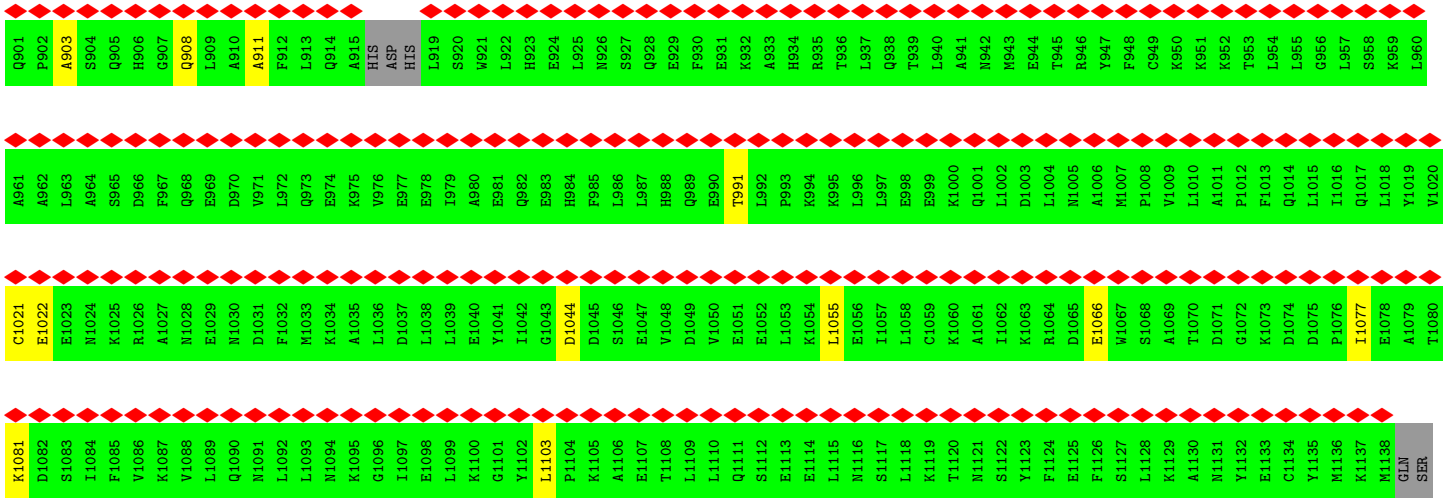
L601 H602 Q603 V604 G605 L606 F607 S608 R609 L610 SER T612 C613 Q614 T615 K616 G617 M618 L619 V620 A621 T622 R623 L624 L625 L626 S627 E628 H629 A630 E631 K632 L633 S634 A635 A636 I637 V638 L639 K640 N641 H642 H643 A644 K645 L646 P647 V648 L649 V650 N651 S652 A653 I654 Q655 L656 A657 L658 D659 K660

R661 M662 C663 T664 V665 P666 Q667 N668 L669 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

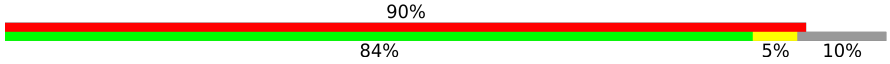
L781 R782 T783 I784 L785 I786 E787 Q788 L789 A790 A791 L792 L793 N794 Y795 L796 L797 D798 D799 Y800 V801 T802 Q803 L804 K805 S806 I807 D808 K809 L810 A811 N812 E813 E814 R815 Y816 N817 I818 L819 E820 M821 E822 Y823 A824 Q825 K826 R827 S828 E829 L830 L831 S832 P833 L834 L835 I836 L837 G838 Q839 Y840

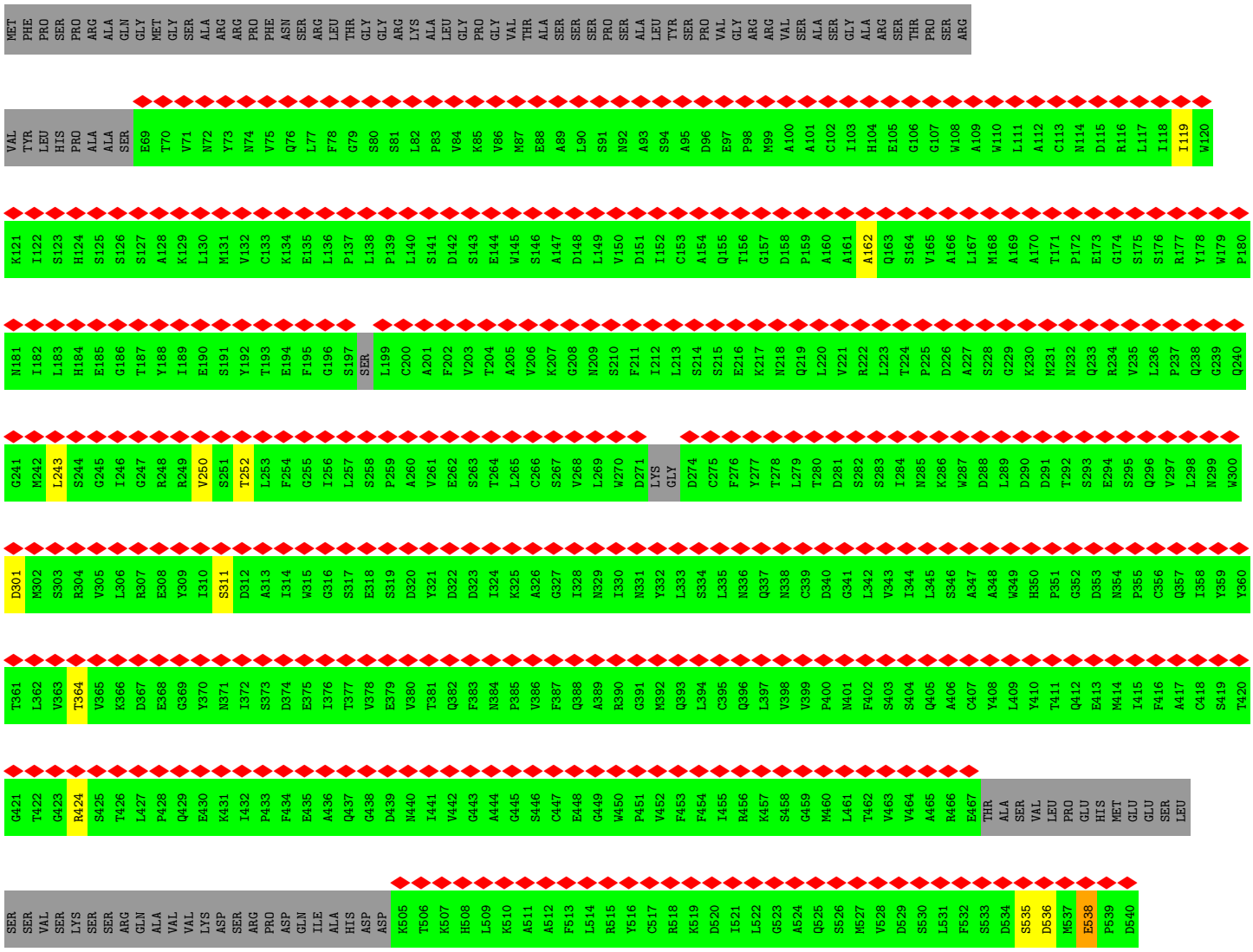
A841 W842 A843 S844 N845 L846 A847 E848 K849 Y850 C851 D852 P853 D854 I855 L856 V857 Q858 I859 C860 E861 M862 T863 D864 N865 Q866 S867 R868 L869 Q870 R871 Y872 M873 T874 L875 F876 A877 E878 Q879 N880 F881 S882 D883 F884 L885 F886 R887 W888 Y889 L890 E891 K892 G893 K894 R895 G896 K897 L898 L899 S900




- Molecule 10: outer Nup133

Chain j:



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L601 H602 Q603 V604 G605 L606 F607 S608 R609 L610 SER 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 P666 Q667 N668 L669 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 G838 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 ALA SER GLN 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 N943 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

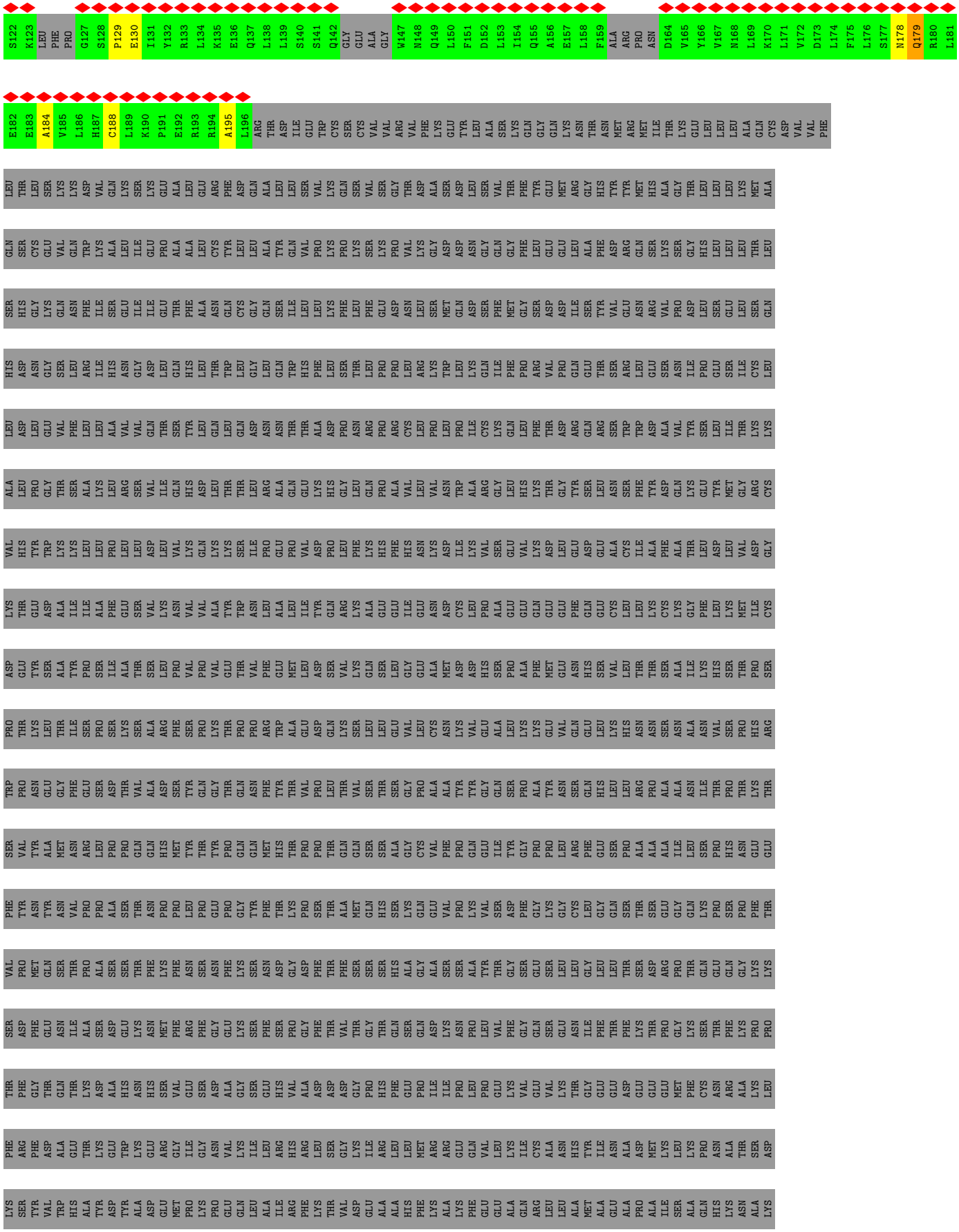
K1081 D1082 S1083 I1084 F1085 V1086 K1087 V1088 L1089 Q1090 N1091 L1092 L1093 N1094 K1095 G1096 I1097 E1098 L1099 K1100 G1101 Y1102 L1103 P1104 K1105 A1106 E1107 T1108 L1109 L1110 Q1111 S1112 E1113 E1114 L1115 N1116 S1117 L1118 K1119 T1120 N1121 S1122 Y1123 F1124 E1125 F1126 S1127 L1128 K1129 A1130 N1131 Y1132 E1133 C1134 Y1135 M1136 K1137 M1138 Q1139 SER

- Molecule 11: Nup358 complex, clamps

Chain S: 5% 5% • 94%

MET ARG ARG SER LYS ALA GLU I8 Q9 R10 Y11 N14 A15 Q16 N17 S18 A19 S20 S21 P22 ARG GLU K25 S26 M27 K28 G29 F30 L31 F32 A33 R34 L35 Y36 Y37 E38 ALA LYS E41 Y42 E43 L44 A45 K46 R47 S48 V49 S50 S51 Y52 I53 S54 V55 Q56 E57 R58 D59 P60 K61

A62 H63 R64 F65 L66 G67 Q68 L69 F70 E71 I72 E73 G74 N75 V76 E77 K78 A79 V80 G81 C82 Y83 K84 R85 S86 L87 E88 L89 N90 P91 Y92 Q93 K94 ASP L96 T97 L98 R99 I100 A101 E102 L103 I104 C105 T106 L107 N108 ILE LYS ASP GLY R113 A114 E115 Y116 W117 V118 E119 R120 A121


S122 K123 LEU PHE PRO G127 S128 P129 E130 I131 Y132 R133 L134 K135 E136 Q137 L138 L139 S140 S141 Q142 GLY GLU ALA GLY W147 N148 Q149 L150 F151 D152 L153 I154 Q155 A156 E157 L158 F159 ALA ARG PRO ASN D164 V165 Y166 V167 N168 L169 K170 L171 V172 D173 L174 F175 L176 S177 N178 Q179 R180 L181
E182 E183 A184 V185 L186 H187 C188 L189 K190 P191 E192 R193 R194 A195 L196 ARG THR ASP ILE GLU TRP CYS SER CYS VAL VAL ARG VAL PHE LYS GLU TYR LEU ALA SER LYS GLN GLY GLN LYS ASN THR ASN MET ARG MET ILE THR LYS GLU LEU LEU LEU LEU ALA GLN CYS ASP VAL VAL PHE
LEU THR LEU SER LYS LYS ASP VAL GLN LYS LYS LYS GLU GLU ARG PHE ASP GLN ALA LEU LEU SER VAL LYS GLN SER SER VAL SER GLY THR ASP ALA SER ASP LEU SER VAL THR PHE TYR GLU MET ARG GLY HIS TYR TYR MET HIS ALA GLY THR LEU LEU LEU LYS MET ALA
GLN SER CYS GLU VAL GLN TRP LYS ALA LEU ILE GLU PRO ALA ALA LEU CYS TYR LEU LEU ALA TYR GLN VAL PRO LYS PRO LYS SER LYS PRO VAL LYS GLY ASP ASN GLY GLN GLY PHE LEU GLU GLU LEU ALA PHE ASP ARG GLN SER LYS SER GLY HIS LEU LEU LEU LEU THR LEU
SER HIS GLY LYS GLN ASN PHE ILE SER GLU ILE ILE ILE GLU THR PHE ALA ASN GLN CYS GLY GLN SER ILE LEU LEU LYS PHE LEU PHE GLU ASP ASN LEU SER MET GLN ASP SER PHE MET GLY SER ASP ILE SER TYR VAL GLU ASN ARG VAL PRO ASP LEU SER GLU LEU SER GLN
HIS ASP ASN GLY SER LEU ARG ILE HIS ASN GLY ASP LEU GLN HIS LEU THR TRP LEU GLY GLY LEU GLN TRP HIS PHE LEU SER THR LEU PRO PRO LEU ARG LYS GLN ILE PHE PRO ARG VAL PRO GLN GLU THR SER ARG LEU GLU SER ASN ILE PRO GLU SER ILE CYS LEU
LEU ASP LEU GLU VAL PHE LEU LEU ALA VAL VAL GLN THR SER TYR LEU GLN LEU GLN ASN ASN THR THR ALA ASP PRO ASN ARG PRO ARG CYS LEU PRO LEU LEU PRO ILE CYS LYS GLN LEU PHE THR ASP ARG GLN ARG SER TRP TRP ASP ALA VAL TYR SER LEU ILE THR LYS LYS
ALA LEU PRO GLY THR SER ALA LYS LEU ARG SER VAL ILE GLN HIS ASP LEU THR THR LEU ARG ALA GLN GLU LYS HIS GLY LEU GLN PRO ALA VAL LEU VAL ASN TRP ALA ARG GLY LEU HIS LYS THR GLY TYR SER LEU ASN SER PHE TYR ASP GLN LYS GLU TYR MET GLY ARG CYS
VAL HIS TYR TRP LYS LYS LEU LEU PRO LEU LEU ASP LEU VAL LYS GLN LYS LYS SER ILE PRO GLU PRO VAL ASP PRO LEU PHE LYS HIS PHE HIS ASN LYS ASP ILE LYS VAL SER GLU VAL LYS ASP LEU GLU ALA CYS ILE ALA PHE ALA THR LEU ASP GLY
LYS THR GLU ASP ALA ILE ILE ALA PHE GLU SER VAL LYS ASN VAL VAL ALA TYR TRP ASN LEU ALA LEU ILE TYR GLN ARG LYS ALA GLU GLU ILE GLU ASN ASP CYS LEU PRO ALA GLU GLU GLN GLU GLU PHE GLN GLU CYS LEU LEU LYS CYS LYS LYS GLY PHE LEU LYS MET ILE CYS
ASP GLU TYR SER ALA TYR PRO SER ILE ALA THR SER LEU PRO VAL PRO VAL 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 CYS ASN LYS VAL GLU ALA LEU LYS LYS GLU VAL LEU GLU 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 ASN THR SER GLY 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 GLN GLN SER SER ALA GLY CYS VAL PHE PRO GLU ILE ILE ILE TYR GLY PRO GLN PHE GLU LEU LYS HIS ASN ASN SER ASN ALA ILE LEU LEU SER PRO HIS ASN GLU GLU
PHE TYR ASN TYR ASN VAL PRO PRO ALA SER THR ASN 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 PRO LYS PRO PRO SER PRO PHE THR
VAL PRO MET GLN SER THR PRO ALA SER SER THR PHE LYS PHE THR PHE SER SER HIS ALA ALA GLY ASP PHE THR PHE SER SER SER HIS ALA GLY PRO PRO ALA ALA SER GLU SER LEU LEU GLY LEU LEU THR SER ASP ARG PRO THR GLN GLU GLN GLN LYS THR
SER ASP PHE GLU ASN ILE ALA SER GLU LYS ASN MET PHE ARG PHE GLY GLU LYS SER PHE SER PRO GLY PHE THR VAL THR GLY THR GLN SER GLN HIS ASN ILE ALA ASP LYS ASN PRO LEU VAL PHE GLY GLN SER GLU ASN ILE PHE THR PHE LYS GLN GLU GLU GLN LYS PRO SER
THR PHE GLY THR GLN THR HIS ASN HIS SER VAL GLU SER ASP ALA GLY SER GLU ASP ALA ALA ASP GLY PRO HIS PHE GLU PRO ILE ILE PRO LEU PRO LYS VAL GLU VAL LYS THR GLY PRO HIS PHE CYS ASN ARG ALA LYS LEU
PHE ARG PHE ASP ALA GLU THR LYS ASP ILE ARG GLY ILE GLY ASN VAL LYS ILE LEU ARG HIS ARG LEU SER GLY LYS ILE ARG LEU LEU MET 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 MET PRO GLU GLN ILE ILE ALA ILE ARG PHE LYS THR VAL ASP GLU ALA HIS PHE LYS ALA LYS PHE GLU GLU ALA GLN ARG LEU LEU ALA MET ALA 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 LYS SER SER ILE SER SER

VAL CYS 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 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 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 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 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 LYS ASP THR CYS ALA ALA CYS GLN

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

ASN ALA SER ASN ALA GLN GLU 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 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 GLU 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 THR MET ASN LEU LYS PRO LEU THR GLY SER ASP ARG ALA TRP MET TRP LEU ALA ASN

ASP PHE SER GLU GLY ASP ALA LYS LEU GLU 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 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 HIS GLU GLU THR

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

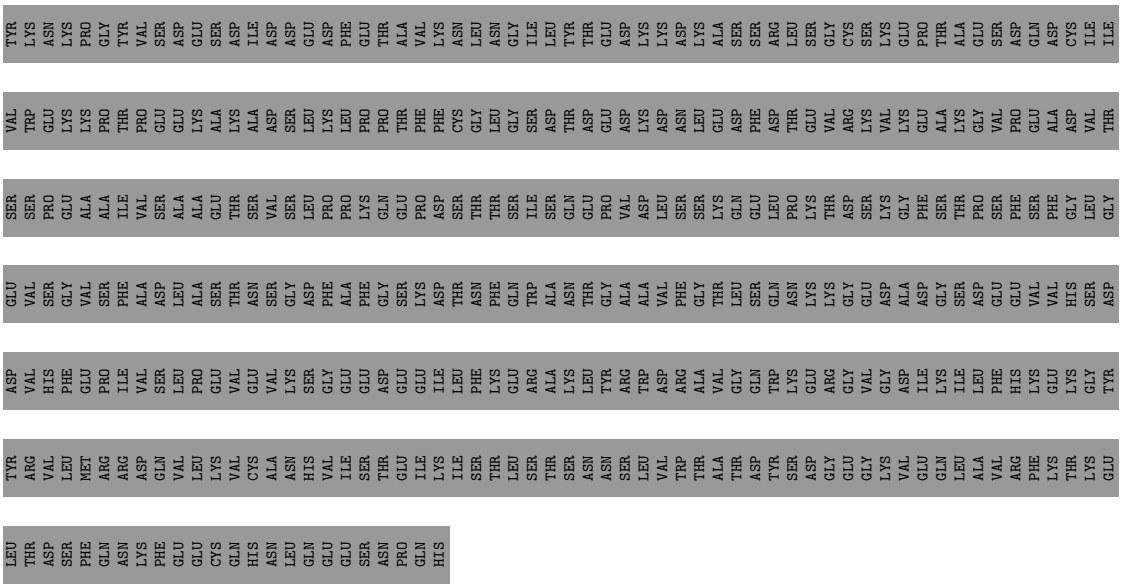
LYS ILE LEU GLN ARG LEU ASP ASN LYS SER ALA ARG VAL VAL MET ARG ARG ASP GLN VAL LEU LYS LEU CYS ALA ASN HIS ARG ILE THR THR ASP ILE ASN LEU GLN PRO MET LYS GLY ALA GLU ARG ALA TRP VAL TRP THR ALA HIS ASP PHE SER GLU GLY GLU GLY LYS VAL GLU

CYS PHE ALA VAL ARG PHE LYS LEU GLN GLU ALA 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 ALA ILE ALA ILE LEU GLU GLU THR THR LYS

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

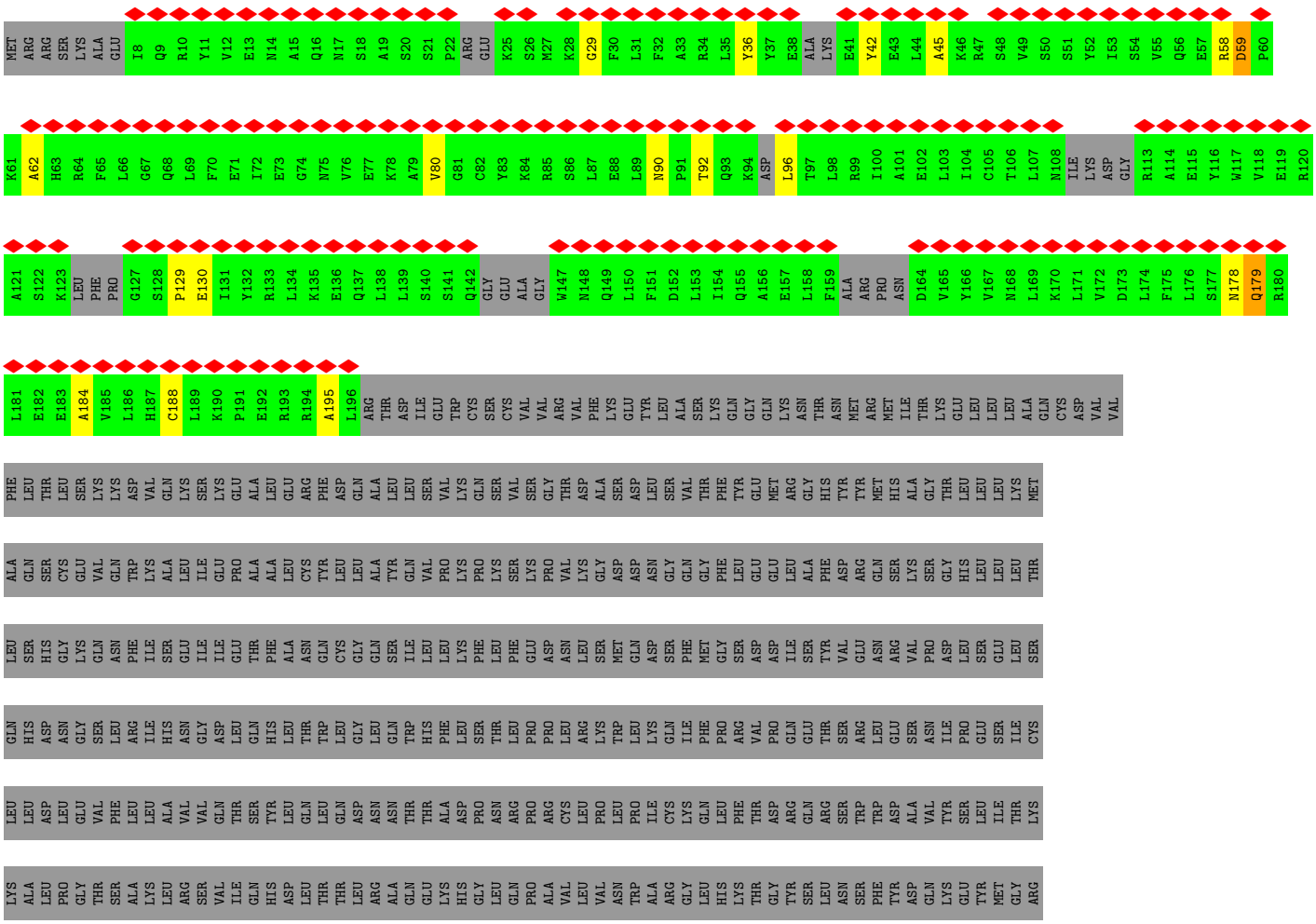
SER THR GLY SER LEU PHE GLY PHE SER PHE ASN ALA SER GLN SER GLN GLY GLN GLN VAL GLN LYS GLN PRO PRO LYS VAL THR LEU ASP PHE ASN ALA THR PHE LYS ASP ALA GLU THR THR ASN ALA LEU GLN LYS PRO SER GLN GLN SER SER GLY GLN SER PRO ILE VAL SER SER LEU

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



- Molecule 11: Nup358 complex, clamps

Chain T: 6% 5% 94%



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

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

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

SER VAL CYS 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 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 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 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 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 LYS ASP THR CYS ALA ALA CYS

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

VAL ASN ALA SER ASN ALA GLN GLU 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 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 GLU 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 THR MET ASN LEU LYS PRO LEU THR GLY SER ASP ARG ALA TRP MET TRP LEU ALA

ASN ASP PHE SER GLU GLY ASP ALA LYS LEU GLU 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 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 HIS GLU GLU

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

GLU CYS PHE ALA VAL ARG PHE LYS LEU GLN GLU ALA 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 ALA ILE ALA ILE LEU GLU GLU THR THR

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

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

CYS TYR LYS ASN LYS PRO GLY TYR VAL SER ASP GLU SER ASP ILE ASP 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 ALA GLU SER ASP GLN ASP CYS ILE

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

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

GLY GLU VAL SER GLY VAL SER PHE ALA ASP LEU ALA SER THR ASN SER GLY ASP PHE ALA PHE GLY SER LYS ASP THR ASN PHE GLN TRP ALA ASN THR GLY ALA ALA VAL PHE GLY THR LEU SER GLN ASN LYS LYS GLY GLU ASP ALA ASP GLY SER ASP GLU GLU VAL VAL HIS SER

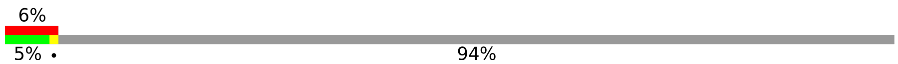
ASP ASP VAL HIS PHE GLU PRO ILE VAL SER LEU PRO GLU VAL GLU VAL LYS SER GLY GLU GLU ASP GLU GLU ILE LEU PHE LYS GLU ARG ALA LYS LEU TYR ARG TRP ASP ARG ALA VAL GLY GLN TRP LYS GLU ARG GLY VAL GLY ASP ILE LYS ILE LEU PHE HIS LYS GLU LYS GLY

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

GLU LEU THR ASP SER PHE GLN ASN LYS PHE GLU GLU CYS GLN HIS ASN LEU GLN GLU GLU SER ASN PRO GLN HIS

- Molecule 11: Nup358 complex, clamps

Chain U:



MET ARG ARG SER LYS ALA GLU I8 Q9 R10 Y11 V12 E13 N14 A15 Q16 N17 S18 A19 S20 S21 P22 R23 E24 K25 S26 M27 K28 G29 F30 L31 F32 A33 R34 L35 Y36 Y37 E38 A39 K40 E41 Y42 E43 L44 A45 K46 R47 S48 V49 S50 S51 Y52 I53 S54 V55 GLN GLU R58 D59 P60
K61 A62 H63 R64 F65 L66 G67 Q68 L69 F70 E71 I72 E73 G74 N75 V76 E77 K78 A79 V80 G81 C82 Y83 K84 R85 S86 L87 E88 L89 N90 P91 T92 Q93 K94 D95 L96 T97 L98 R99 I100 A101 E102 L103 I104 C105 T106 LEU ASN ILE LYS D111 G112 R113 A114 E115 Y116 W117 V118 E119 R120
A121 S122 K123 L124 F125 P126 G127 S128 P129 E130 I131 Y132 R133 L134 K135 E136 Q137 L138 L139 SER SER GLN GLY GLU ALA GLY W147 N148 Q149 L150 F151 D152 L153 I154 Q155 A156 E157 L158 F159 A160 ARG PRO N163 D164 V165 Y166 V167 N168 L169 K170 L171 V172 D173 L174 F175 L176 S177 N178 GLN ARG
L181 E182 E183 A184 V185 L186 H187 C188 L189 K190 P191 E192 R193 R194 A195 L196 R197 THR ASP ILE GLU TRP CYS SER CYS VAL VAL ARG VAL PHE LYS GLU TYR LEU ALA SER LYS GLN GLY GLN LYS ASN THR ASN MET ARG MET ILE THR LYS GLU LEU LEU LEU ALA GLN CYS ASP VAL VAL
PHE LEU THR LEU SER LYS LYS ASP VAL GLN GLN LYS SER LYS GLU ALA LEU GLU ARG PHE ASP GLN ALA LEU LEU SER VAL LYS GLN SER VAL SER GLY THR ASP ALA SER ASP LEU SER VAL THR PHE TYR GLU MET ARG GLY HIS TYR TYR MET HIS ALA GLY THR LEU LEU LEU LEU LYS MET
ALA GLN SER CYS GLU VAL GLN TRP LYS ALA LEU ILE GLU PRO ALA ALA LEU CYS TYR LEU LEU ALA TYR GLN VAL PRO LYS PRO LYS SER LYS PRO VAL LYS GLY ASP ASP ASN GLY GLN GLY PHE LEU GLU GLU LEU ALA PHE ASP ARG GLN SER LYS SER GLY HIS LEU LEU LEU THR
LEU SER HIS GLY LYS GLN ASN PHE ILE SER GLU ILE ILE GLU THR PHE ALA ASN GLN CYS GLY GLN SER ILE LEU LEU LYS PHE LEU PHE GLU ASP ASN LEU SER MET GLN ASP SER PHE MET GLY SER ASP ASP ILE SER TYR VAL GLU ASN ARG VAL PRO ASP LEU SER SER SER
GLN HIS ASP ASN GLY SER LEU ARG ILE HIS ASN GLY ASP LEU GLN HIS LEU THR TRP LEU GLY LEU GLN TRP HIS PHE LEU SER THR LEU PRO PRO LEU ARG LYS TRP LEU LYS GLN ILE PHE PRO ARG VAL PRO GLN GLU THR SER ARG LEU GLU ASN SER ASN ILE PRO GLU SER ILE CYS
LEU LEU ASP LEU GLU VAL PHE LEU LEU LEU ALA VAL VAL GLN THR SER TYR LEU GLN LEU GLN ASP ASN ASN THR THR ALA ASP PRO ASN ARG PRO ARG CYS LEU PRO LEU PRO ILE CYS LYS GLN LEU PHE THR ASP ARG GLN ARG SER TRP TRP ASP ALA VAL TYR SER ILE ILE THR LYS
LYS ALA LEU PRO GLY THR SER ALA LYS LEU ARG SER VAL ILE GLN HIS ASP LEU THR THR LEU ARG ALA GLN GLU LYS HIS GLY LEU GLN PRO ALA VAL LEU VAL ASN TRP ALA ARG GLY LEU HIS LYS THR GLY TYR SER LEU ASN SER PHE TYR ASP GLN LYS GLU TYR MET GLY ARG
CYS VAL HIS TYR TRP LYS LYS LEU LEU PRO LEU LEU SER LYS LYS GLN SER ILE PRO GLU PRO VAL ASP PRO LEU PHE LYS HIS PHE HIS ASN LYS ASP ILE LYS VAL SER GLU VAL LYS ASP GLU GLU ASP LEU GLU ALA ILE ALA ALA PHE ALA THR LEU ASP LEU LEU VAL ASP
GLY LYS THR GLU ASP ALA ILE ILE ALA PHE GLU SER VAL LYS ASN VAL VAL ALA TYR TRP ASN LEU ALA LEU ILE TYR GLN ARG LYS ALA GLU GLU ILE GLU ASN ASP CYS LEU PRO ALA GLU GLU GLN GLU GLU PHE GLN GLU CYS LEU LEU LYS CYS LYS GLY PHE LEU LYS GLY ILE
CYS ASP GLU TYR SER ALA TYR PRO SER ILE ALA THR SER LEU PRO VAL PRO VAL GLU THR VAL PHE GLU MET LEU ASP SER LEU LEU GLY GLU ALA 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 ALA ARG PHE SER PRO LYS THR PRO PRO PRO ARG TYR 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 GLU LEU GLU ASN ALA ALA ILE LYS HIS SER THR PRO
ARG TRP PRO ASN GLU GLY PHE GLU SER ASP THR VAL ALA ASP PRO THR GLN PRO SER THR VAL PRO VAL GLN GLN SER THR SER GLY PRO ALA TYR ASN SER GLN GLU LEU 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 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 LEU ASN ILE THR PRO HIS ASN GLU
GLU PHE TYR ASN TYR ASN VAL PRO PRO ALA PRO SER THR ASN PRO PRO ALA PHE TYR GLU PRO GLY TYR PHE HIS LYS PRO SER THR ALA MET GLN HIS SER HIS LYS GLN GLU VAL PRO LYS GLY LYS GLY CYS LEU GLY GLN SER THR SER GLY GLY GLN LYS
THR VAL PRO MET GLN SER SER THR PHE ASP ALA SER SER PHE THR PHE SER SER GLY ASP PHE SER GLU SER LEU LEU LEU GLY LEU LEU THR SER ARG PRO ALA ALA ALA ILE LEU LEU SER PRO LYS GLU GLY GLN LYS
LYS SER ASP PHE GLU ASN ILE ALA SER ASP PHE ARG PHE GLY GLU LYS SER PHE ASN ASP PRO GLY PHE THR VAL THR GLY THR GLN SER GLU ASN PRO GLY GLN SER GLU ASN ILE PHE THR PHE LYS THR PHE GLY PRO PRO PHE

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

SER VAL CYS 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 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 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 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 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 GLY GLN TRP GLU CYS SER THR CYS LEU VAL ILE ASN ASP ALA ALA LYS ASP THR CYS ALA ALA CYS

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

VAL ASN ALA SER ASN ALA GLN GLU 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 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 GLU 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 THR MET ASN LEU LYS PRO LEU THR GLY SER ASP ARG ALA TRP MET TRP LEU ALA

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

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

GLU CYS PHE ALA VAL ARG PHE LYS LEU GLN GLU ALA 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 ALA ILE ALA ILE LEU GLU GLU THR THR

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

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

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

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

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

GLY GLU VAL SER GLY VAL SER PHE ALA ASP LEU ALA SER THR ASN SER GLY ASP PHE ALA PHE GLY SER LYS ASP THR ASN PHE GLN TRP ALA ASN THR GLY ALA ALA VAL PHE GLY THR LEU SER GLN ASN LYS LYS GLY GLU ASP ALA ASP GLY SER ASP GLU GLU VAL VAL HIS SER

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

GLU LEU THR ASP SER PHE GLN ASN LYS PHE GLU GLU CYS GLN HIS ASN LEU GLN GLU GLU SER ASN PRO GLN HIS

- Molecule 11: Nup358 complex, clamps

Chain V: 6% 5% 94%

MET ARG ARG SER LYS ALA GLU T8 Q9 R10 Y11 V12 E13 N14 A15 Q16 N17 S18 A19 S20 S21 P22 ARG GLU K25 S26 M27 K28 G29 F30 L31 F32 A33 R34 L35 Y36 Y37 E38 ALA LYS E41 Y42 E43 L44 A45 K46 R47 S48 V49 S50 S51 Y52 I53 S54 V55 Q56 E57 R58 D59 P60

K61 A62 H63 R64 F65 L66 G67 Q68 L69 F70 E71 I72 E73 G74 N75 V76 E77 K78 A79 V80 G81 C82 Y83 K84 R85 S86 L87 E88 L89 N90 P91 T92 Q93 K94 ASP L96 T97 L98 R99 I100 A101 E102 L103 I104 C105 T106 L107 N108 ILE LYS ASP GLY R113 A114 E115 Y116 W117 V118 E119 R120

A121 S122 K123 LEU PHE PRO G127 S128 P129 E130 I131 Y132 R133 L134 K135 E136 Q137 L138 L139 S140 S141 Q142 GLY GLU ALA GLY W147 N148 Q149 L150 F151 D152 L153 I154 Q155 A156 E157 L158 F159 ALA ARG PRO ASN D164 V165 Y166 V167 N168 L169 K170 L171 V172 D173 L174 F175 L176 S177 N178 Q179 R180

L181 E182 E183 A184 V185 L186 H187 C188 L189 K190 P191 E192 R193 R194 A195 L196 ARG THR ASP ILE GLU TRP CYS SER CYS VAL VAL ARG VAL PHE LYS GLU TYR LEU ALA SER LYS GLN GLY GLN LYS ASN THR ASN MET ARG MET ILE THR LYS GLU LEU LEU LEU ALA GLN CYS ASP VAL VAL

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

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

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

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

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

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

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

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

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

SER VAL CYS 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 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 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 SER 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 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 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 LYS ASP THR CYS ALA ALA CYS

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

VAL ASN ALA SER ASN ALA GLN GLU 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 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 GLU 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 THR MET ASN LEU LYS PRO LEU THR GLY SER ASP ARG ALA TRP MET TRP LEU ALA

ASN ASP PHE SER GLU GLY ASP ALA LYS LEU GLU 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 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 HIS GLU GLU

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

GLU CYS PHE ALA VAL ARG PHE LYS LEU GLN GLU ALA 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 ALA ILE ALA ILE LEU GLU GLU THR THR

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

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

CYS TYR LYS ASN LYS PRO GLY TYR VAL SER ASP GLU SER ASP ILE ASP 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 ALA GLU SER ASP GLN ASP CYS ILE

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

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

GLY GLU VAL SER GLY VAL SER PHE ALA ASP LEU ALA SER THR ASN SER GLY ASP PHE ALA PHE GLY SER LYS ASP THR ASN PHE GLN TRP ALA ASN THR GLY ALA ALA VAL PHE GLY THR LEU SER GLN ASN LYS LYS GLY GLU ASP ALA ASP GLY SER ASP GLU GLU VAL VAL HIS SER

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

GLU LEU THR ASP SER PHE GLN GLN ASN LYS PHE GLU GLU CYS GLN HIS ASN LEU GLN GLU GLU SER ASN PRO GLN HIS

- Molecule 12: Nup214 complex Coiled-coil region 1, helix 1

Chain K: 100% 97%

X355 X356 X357 X358 X359 X360 X361 X362 X363 X364 X365 X366 X367 X368 X369 X370 X371 X372 X373 X374 X375 X376 X377 X378 X379 X380 X381 X382 X383 X384 X385 X386 X387 X388 X389 X390 X391 X392 X393 X394 X395 X396 X397 X398 X399 X400 X401 X402 X403 X404 X405 X406 X407 X408 X409 X410 X411 X412 X413 X414

X415 X416 X417 X418 X419 X420 X421 X422 X423

- Molecule 13: Nup214 complex coiled coil region 1, helix 2

Chain L: 100% 100%

X286 X287 X288 X289 X290 X291 X292 X293 X294 X295 X296 X297 X298 X299 X300 X301 X302 X303 X304 X305 X306 X307 X312 X313 X314 X315 X316 X317 X318 X319 X320 X321 X322 X323 X324 X325 X326 X327 X328 X329 X330 X331 X332 X333 X334 X335 X336 X337 X338 X339 X340 X341 X342 X343 X344 X345 X346 X347 X348 X349

X350 X351 X352 X353 X354 X355 X356 X357 X358 X359 X360 X361 X362 X363 X364 X365 X366 X367 X368 X369

- Molecule 14: Nup214 complex coiled coil region 1, helix 3

Chain M: 100% 97%

X358 X359 X360 X361 X362 X363 X364 X365 X366 X367 X368 X369 X370 X371 X372 X373 X374 X375 X376 X377 X378 X379 X380 X381 X382 X383 X384 X385 X386 X387 X388 X389 X390 X391 X392 X393 X394 X395 X396 X397 X398 X399 X400 X401 X402 X403 X404 X405 X406 X407 X408 X409 X410 X411 X412 X413 X414 X415 X416 X417

X418 X419 X420 X421 X422 X423 X424 X425 X426 X427 X428 X429 X430

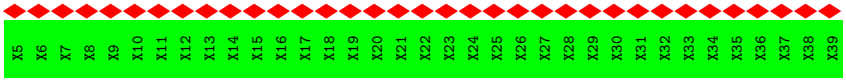
- Molecule 15: Nup214 complex Coiled coil region 2, helix 1

Chain N: 48% 100%

X7 X11 X12 X13 X14 X15 X18 X22 X25 X26 X31 X32 X33 X34 X35 X36 X37

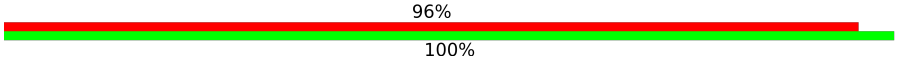
- Molecule 16: Nup214 complex Coiled coil region 2, helix 2

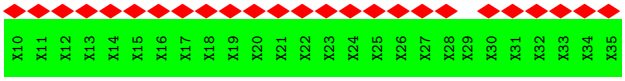
Chain O: 100% 100%




• Molecule 17: Nup214 complex Coiled coil region 2, helix 3

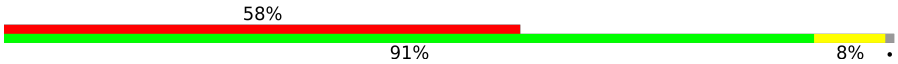
Chain P:

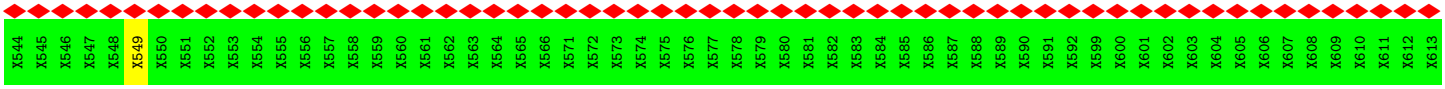


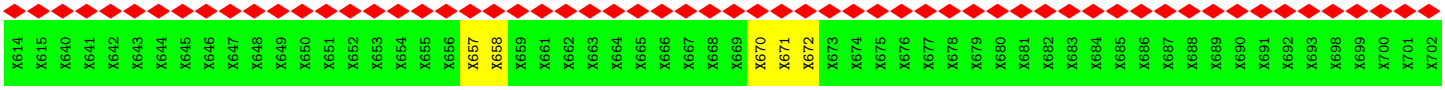



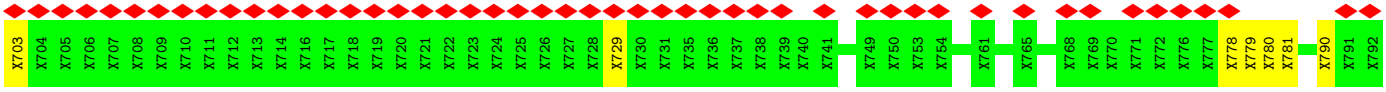

• Molecule 18: bridge domain

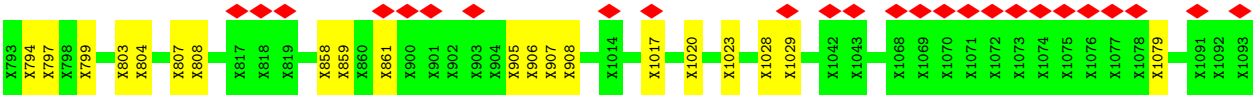
Chain Q:

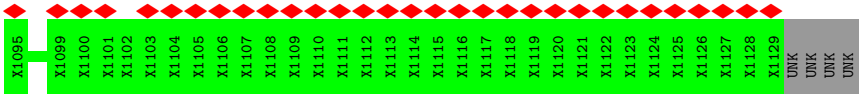


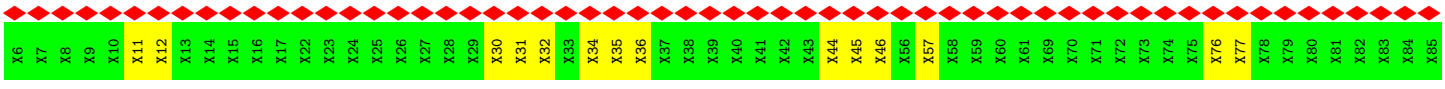



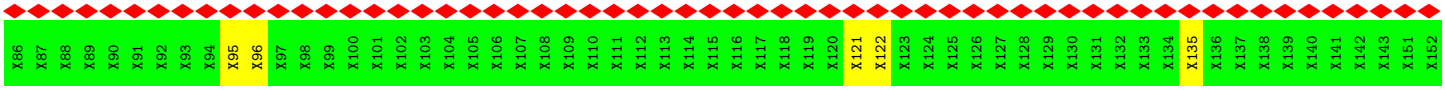



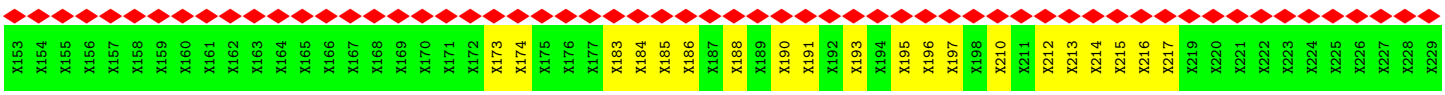




• Molecule 18: bridge domain

Chain R:



X230 X231 X232 X233 X234 X235 X245 X246 X247 X248 X249 X250 X251 X252 X253 X254 X255 X256 X257 X258 X259 X260 X261 X262 X263 X264 X265 X266 X267 X268 X269 X270 X271 X272 X273 X274 X275 X276 X277 X278 X279 X280 X281 X282 X284 X285 X286 X287 X288 X289 X290 X299 X300 X301 X302 X303 X304 X305 X306 X307
X308 X309 X310 X311 X312 X313 X314 X315 X316 X317 X319 X320 X321 X322 X323 X324 X325 X326 X327 X328 X329 X330 X331 X332 X333 X334 X335 X336 X337 X338 X339 X340 X341 X342 X343 X345 X346 X347 X348 X349 X350 X351 X352 X353 X354 X356 X357 X358 X359 X360 X361 X362 X363 X364 X365 X366 X367 X369 X373
X374 X375 X376 X377 X378 X379 X380 X381 X382 X385 X386 X387 X416 X417 X418 X419 X420 X421 X422 X423 X424 X425 X426 X427 X428 X430 X431 X432 X433 X434 X435 X436 X437 X438 X439 X440 X441 X442 X443 X444 X445 X446 X447 X448 X449 X451 X452 UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK
UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 616547 | 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) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 0.151 | Depositor |
| Minimum map value | -0.091 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.006 | Depositor |
| Recommended contour level | 0.03 | Depositor |
| Map size (Å) | 568.832, 568.832, 568.832 | wwPDB |
| Map dimensions | 256, 256, 256 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 2.222, 2.222, 2.222 | Depositor |

# 5 Model quality (i)

## 5.1 Standard geometry (i)

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

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 1 | A | 0.73 | 2/6901 (0.0%) | 1.41 | 44/9542 (0.5%) |
| 1 | a | 0.84 | 1/6275 (0.0%) | 1.63 | 63/8703 (0.7%) |
| 2 | B | 0.52 | 0/2623 | 1.10 | 11/3634 (0.3%) |
| 2 | b | 0.50 | 0/2555 | 1.08 | 9/3534 (0.3%) |
| 3 | C | 0.69 | 1/1150 (0.1%) | 1.13 | 4/1427 (0.3%) |
| 3 | c | 0.61 | 0/1160 | 1.03 | 5/1436 (0.3%) |
| 4 | D | 1.07 | 0/1516 | 1.54 | 10/2108 (0.5%) |
| 4 | d | 1.10 | 0/1446 | 1.58 | 9/2009 (0.4%) |
| 5 | E | 0.95 | 0/5091 | 1.73 | 47/7076 (0.7%) |
| 5 | e | 0.95 | 0/5486 | 1.73 | 48/7634 (0.6%) |
| 6 | F | 1.02 | 0/1413 | 1.50 | 6/1949 (0.3%) |
| 6 | f | 1.02 | 0/1423 | 1.50 | 6/1963 (0.3%) |
| 7 | G | 0.65 | 2/3046 (0.1%) | 1.33 | 39/4220 (0.9%) |
| 7 | g | 0.63 | 6/2986 (0.2%) | 1.32 | 43/4127 (1.0%) |
| 8 | H | 1.06 | 0/1417 | 1.54 | 11/1959 (0.6%) |
| 8 | h | 1.06 | 0/1411 | 1.55 | 12/1959 (0.6%) |
| 9 | I | 0.90 | 0/3662 | 1.70 | 26/5104 (0.5%) |
| 9 | i | 0.91 | 0/3607 | 1.72 | 30/5027 (0.6%) |
| 10 | J | 0.98 | 2/5079 (0.0%) | 1.68 | 41/7074 (0.6%) |
| 10 | j | 0.98 | 2/5084 (0.0%) | 1.70 | 47/7081 (0.7%) |
| 11 | S | 0.67 | 0/832 | 1.51 | 10/1149 (0.9%) |
| 11 | T | 0.67 | 0/832 | 1.51 | 10/1149 (0.9%) |
| 11 | U | 0.68 | 0/853 | 1.52 | 12/1181 (1.0%) |
| 11 | V | 0.67 | 0/832 | 1.50 | 8/1149 (0.7%) |
| All | All | 0.86 | 16/66680 (0.0%) | 1.55 | 551/92194 (0.6%) |

The worst 5 of 16 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 3 | C | 289 | SER | CA-C | -7.89 | 1.42 | 1.52 |
| 7 | g | 625 | THR | C-N | 6.93 | 1.41 | 1.34 |
| 10 | J | 1077 | ILE | CA-CB | -6.77 | 1.46 | 1.54 |
| 10 | j | 1077 | ILE | CA-CB | -6.64 | 1.46 | 1.54 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 7 | g | 543 | LEU | C-N | 6.54 | 1.41 | 1.33 |

The worst 5 of 551 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 10 | j | 1007 | MET | CA-C-N | 14.59 | 134.47 | 120.03 |
| 10 | j | 1007 | MET | C-N-CA | 14.59 | 134.47 | 120.03 |
| 7 | G | 671 | TRP | N-CA-C | 11.78 | 124.12 | 111.28 |
| 1 | a | 1573 | LEU | N-CA-C | 10.32 | 123.49 | 111.11 |
| 1 | A | 1528 | LEU | N-CA-C | -10.28 | 99.28 | 112.23 |

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 | 6934 | 0 | 3045 | 142 | 0 |
| 1 | a | 6306 | 0 | 2772 | 108 | 0 |
| 2 | B | 2639 | 0 | 1163 | 74 | 0 |
| 2 | b | 2574 | 0 | 1141 | 85 | 0 |
| 3 | C | 1156 | 0 | 304 | 21 | 0 |
| 3 | c | 1168 | 0 | 303 | 15 | 0 |
| 4 | D | 1519 | 0 | 694 | 32 | 0 |
| 4 | d | 1450 | 0 | 658 | 17 | 0 |
| 5 | E | 5107 | 0 | 2254 | 18 | 0 |
| 5 | e | 5497 | 0 | 2427 | 51 | 0 |
| 6 | F | 1423 | 0 | 645 | 12 | 0 |
| 6 | f | 1433 | 0 | 653 | 0 | 0 |
| 7 | G | 3064 | 0 | 1339 | 139 | 0 |
| 7 | g | 3010 | 0 | 1311 | 182 | 0 |
| 8 | H | 1419 | 0 | 647 | 15 | 0 |
| 8 | h | 1413 | 0 | 649 | 27 | 0 |
| 9 | I | 3668 | 0 | 1635 | 32 | 0 |
| 9 | i | 3613 | 0 | 1617 | 38 | 0 |
| 10 | J | 5085 | 0 | 2301 | 23 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 10 | j | 5090 | 0 | 2300 | 35 | 0 |
| 11 | S | 840 | 0 | 366 | 9 | 0 |
| 11 | T | 840 | 0 | 366 | 5 | 0 |
| 11 | U | 859 | 0 | 382 | 14 | 0 |
| 11 | V | 840 | 0 | 366 | 7 | 0 |
| 12 | K | 345 | 0 | 72 | 1 | 0 |
| 13 | L | 400 | 0 | 84 | 0 | 0 |
| 14 | M | 365 | 0 | 75 | 1 | 0 |
| 15 | N | 155 | 0 | 34 | 0 | 0 |
| 16 | O | 175 | 0 | 37 | 0 | 0 |
| 17 | P | 130 | 0 | 28 | 0 | 0 |
| 18 | Q | 1935 | 0 | 438 | 27 | 0 |
| 18 | R | 1755 | 0 | 443 | 58 | 0 |
| All | All | 72207 | 0 | 30549 | 1042 | 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 10.

The worst 5 of 1042 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) |
|---|---|---|---|
| 7:g:285:TYR:CB | 7:g:294:ALA:HA | 1.27 | 1.63 |
| 9:i:888:MET:CB | 10:j:964:ALA:CB | 1.76 | 1.57 |
| 2:B:23:ILE:CB | 4:D:296:SER:CB | 1.77 | 1.56 |
| 1:A:517:LEU:CB | 1:A:527:CYS:CB | 1.80 | 1.54 |
| 9:I:186:ARG:CB | 9:I:191:GLN:HA | 1.36 | 1.51 |

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 | 1343/2011 (67%) | 1264 (94%) | 50 (4%) | 29 (2%) | 5 | 28 |
| 1 | a | 1210/2011 (60%) | 1131 (94%) | 53 (4%) | 26 (2%) | 5 | 29 |
| 2 | B | 500/653 (77%) | 471 (94%) | 18 (4%) | 11 (2%) | 5 | 28 |
| 2 | b | 481/653 (74%) | 454 (94%) | 15 (3%) | 12 (2%) | 4 | 25 |
| 3 | C | 277/375 (74%) | 211 (76%) | 65 (24%) | 1 (0%) | 30 | 67 |
| 3 | c | 276/375 (74%) | 212 (77%) | 63 (23%) | 1 (0%) | 30 | 67 |
| 4 | D | 301/322 (94%) | 275 (91%) | 20 (7%) | 6 (2%) | 6 | 30 |
| 4 | d | 285/322 (88%) | 261 (92%) | 20 (7%) | 4 (1%) | 9 | 39 |
| 5 | E | 998/1435 (70%) | 900 (90%) | 71 (7%) | 27 (3%) | 4 | 25 |
| 5 | e | 1087/1435 (76%) | 967 (89%) | 87 (8%) | 33 (3%) | 3 | 22 |
| 6 | F | 269/326 (82%) | 244 (91%) | 17 (6%) | 8 (3%) | 3 | 22 |
| 6 | f | 271/326 (83%) | 245 (90%) | 18 (7%) | 8 (3%) | 3 | 22 |
| 7 | G | 582/923 (63%) | 473 (81%) | 56 (10%) | 53 (9%) | 0 | 8 |
| 7 | g | 559/923 (61%) | 475 (85%) | 39 (7%) | 45 (8%) | 1 | 9 |
| 8 | H | 287/320 (90%) | 257 (90%) | 24 (8%) | 6 (2%) | 5 | 29 |
| 8 | h | 283/320 (88%) | 255 (90%) | 24 (8%) | 4 (1%) | 9 | 39 |
| 9 | I | 726/916 (79%) | 692 (95%) | 28 (4%) | 6 (1%) | 16 | 54 |
| 9 | i | 715/916 (78%) | 681 (95%) | 27 (4%) | 7 (1%) | 12 | 48 |
| 10 | J | 1014/1140 (89%) | 925 (91%) | 69 (7%) | 20 (2%) | 6 | 30 |
| 10 | j | 1015/1140 (89%) | 930 (92%) | 67 (7%) | 18 (2%) | 6 | 33 |
| 11 | S | 153/2905 (5%) | 146 (95%) | 2 (1%) | 5 (3%) | 3 | 20 |
| 11 | T | 153/2905 (5%) | 146 (95%) | 2 (1%) | 5 (3%) | 3 | 20 |
| 11 | U | 161/2905 (6%) | 148 (92%) | 9 (6%) | 4 (2%) | 4 | 25 |
| 11 | V | 153/2905 (5%) | 146 (95%) | 2 (1%) | 5 (3%) | 3 | 20 |
| All | All | 13099/28462 (46%) | 11909 (91%) | 846 (6%) | 344 (3%) | 6 | 25 |

5 of 344 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 227 | SER |
| 1 | A | 228 | LEU |
| 1 | A | 239 | THR |
| 1 | A | 586 | ILE |
| 1 | A | 696 | GLU |

#### 5.3.2 Protein sidechains (i)

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

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry (i)

There are no ligands in this entry.

### 5.7 Other polymers (i)

There are no such residues in this entry.

### 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|---|---|---|
| 18 | Q | 21 |
| 18 | R | 18 |
| 13 | L | 1 |

The worst 5 of 40 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | R | 235:UNK | C | 245:UNK | N | 21.64 |
| 1 | Q | 861:UNK | C | 900:UNK | N | 21.11 |
| 1 | R | 387:UNK | C | 416:UNK | N | 18.78 |
| 1 | Q | 1112:UNK | C | 1113:UNK | N | 18.48 |

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| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | R | 198:UNK | C | 210:UNK | N | 17.94 |

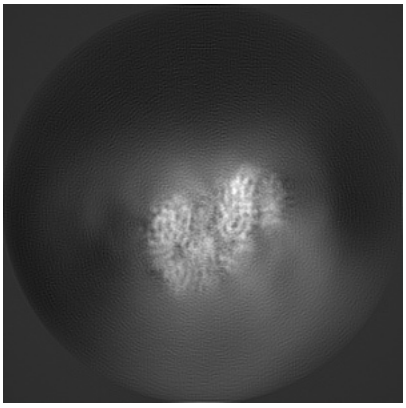
# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0909. These allow visual inspection of the internal detail of the map and identification of artifacts.

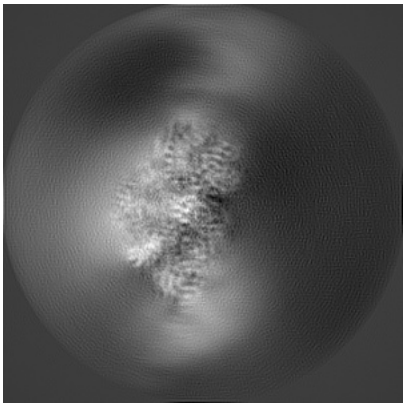
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections (i)

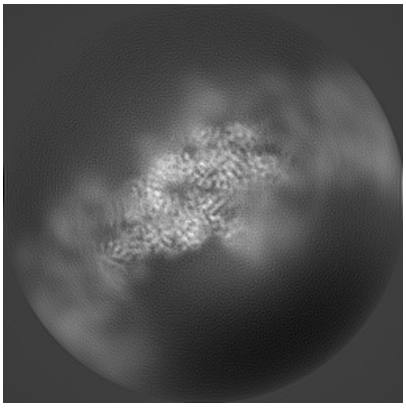
### 6.1.1 Primary map



X



Y

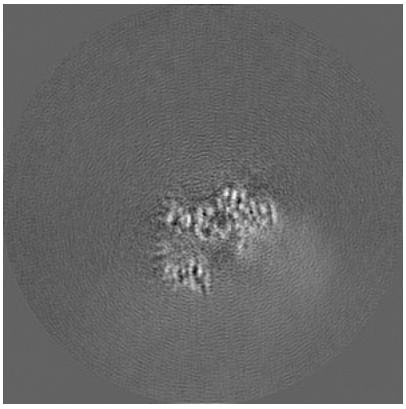


Z

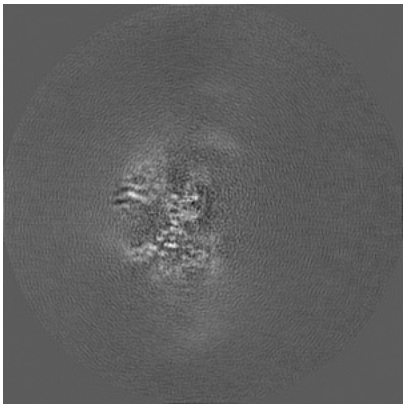
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

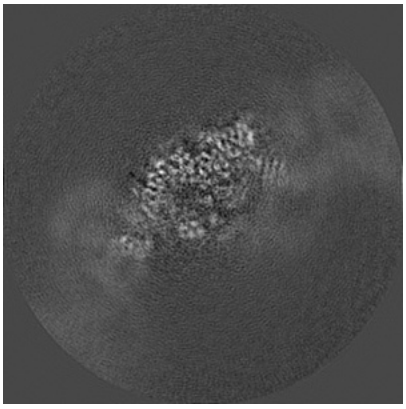
### 6.2.1 Primary map



X Index: 128



Y Index: 128

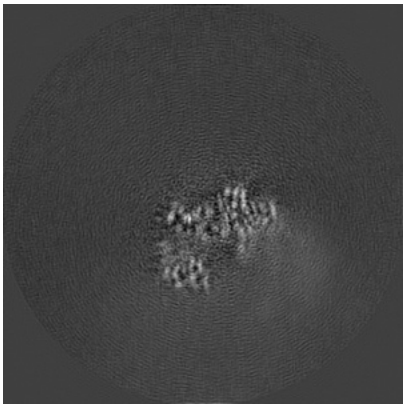


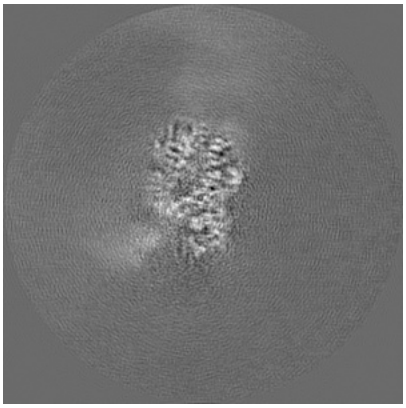
Z Index: 128

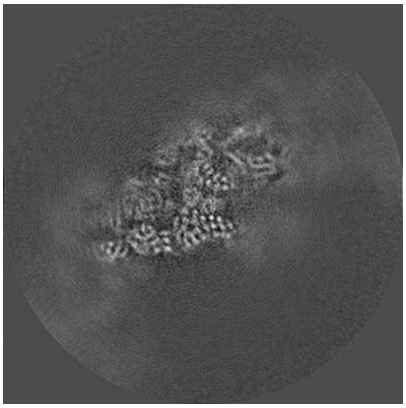
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

### 6.3.1 Primary map


X Index: 127

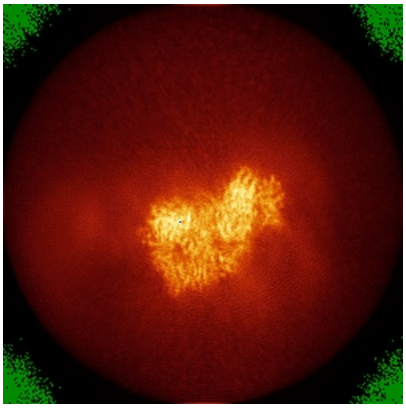

Y Index: 152

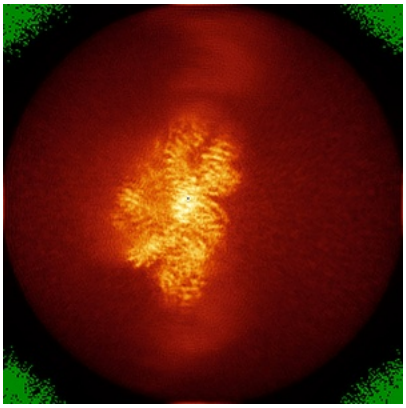

Z Index: 117

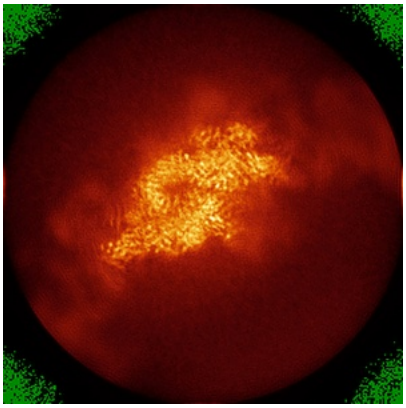
The images above show the largest variance slices of the map in three orthogonal directions.

## 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)

This section was not generated.

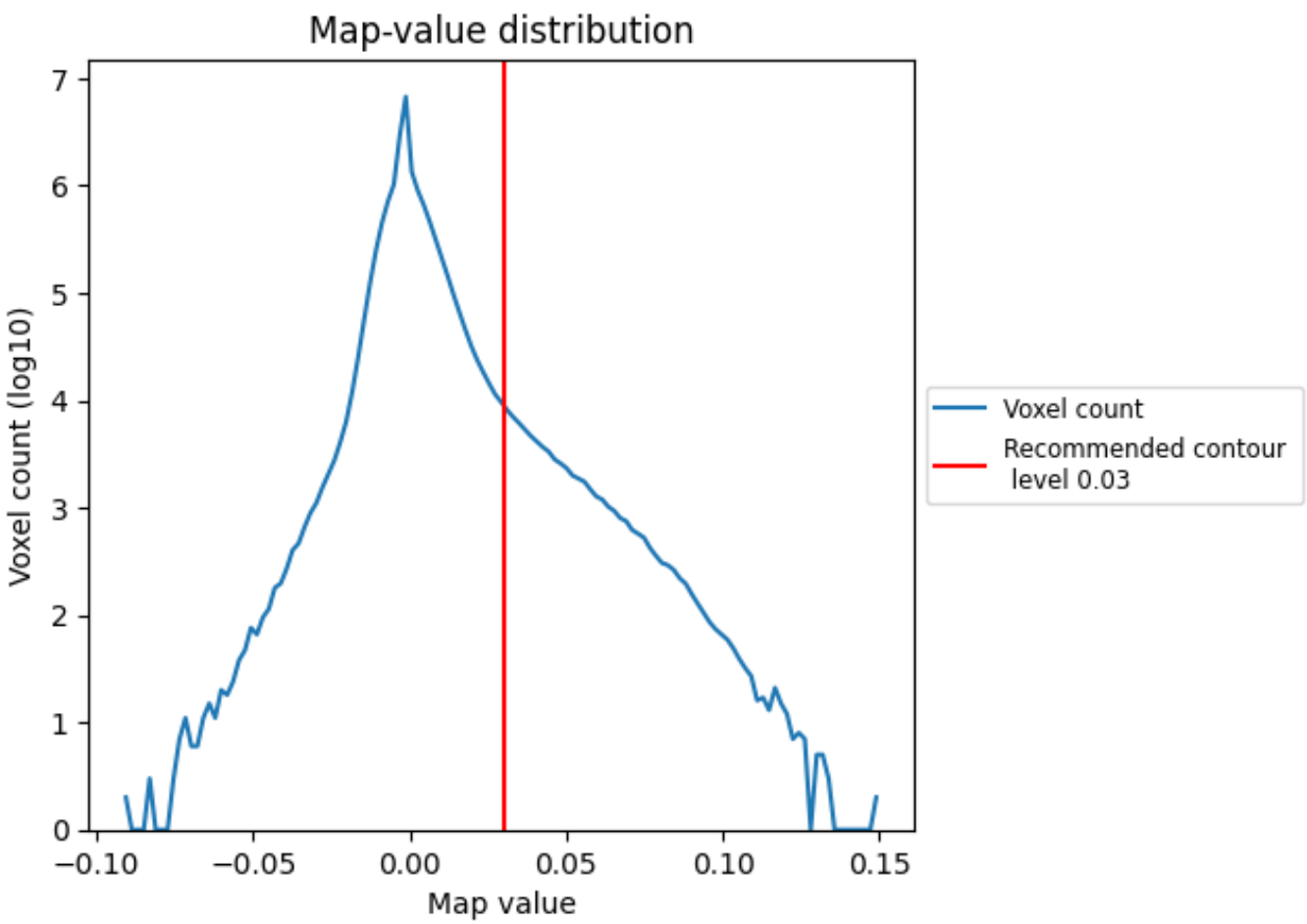
## 6.6 Mask visualisation (i)

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

# 7 Map analysis (i)

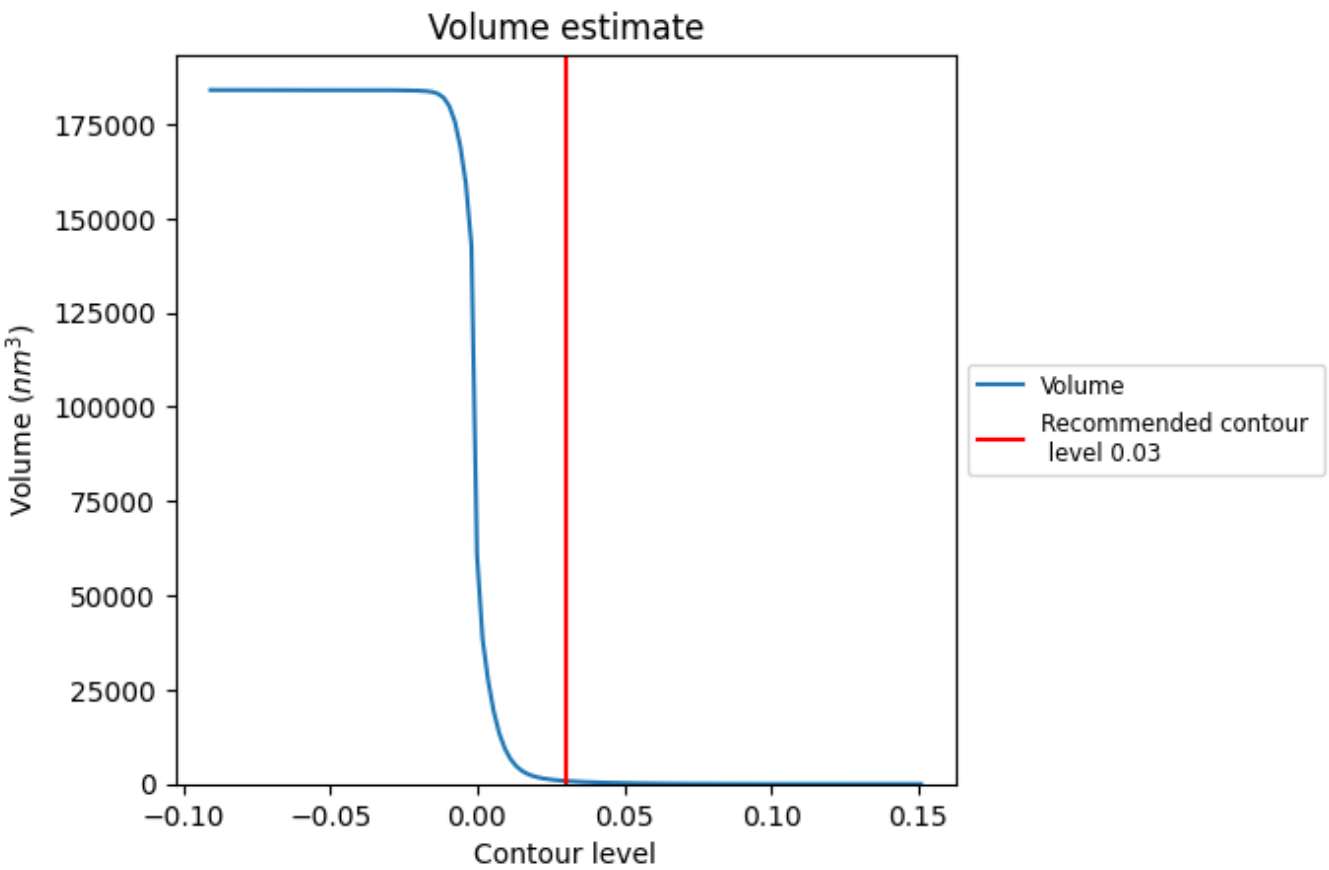
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution (i)




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

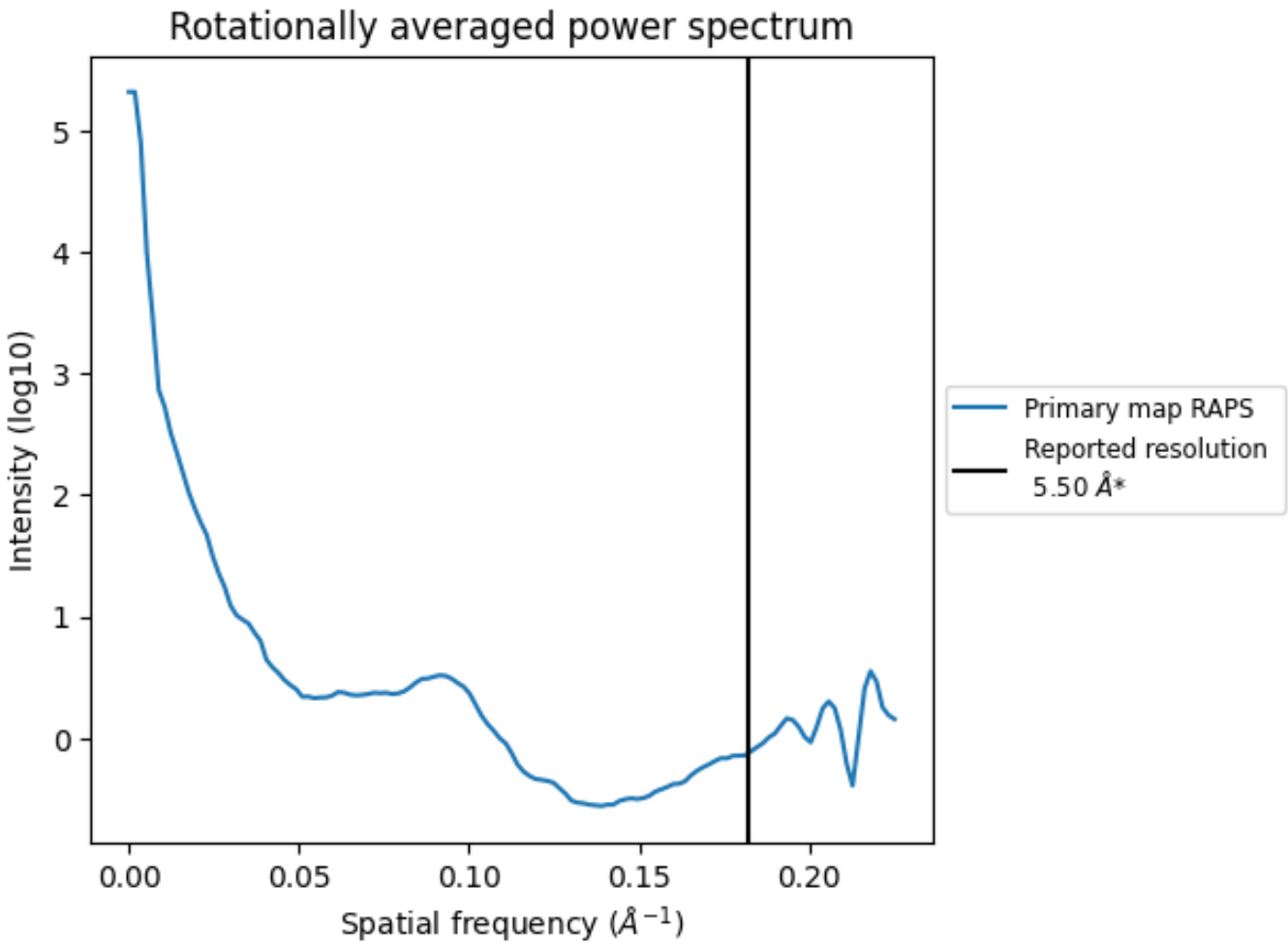
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 803 $nm^3$; this corresponds to an approximate mass of 725 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 0.182 Å$^{-1}$

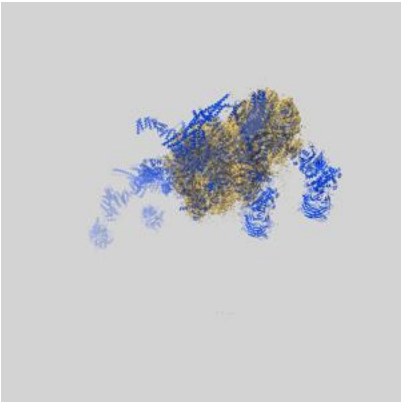
# 8 Fourier-Shell correlation (i)

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

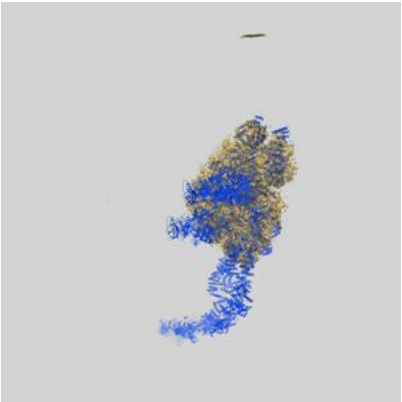
# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-0909 and PDB model 6LK8. Per-residue inclusion information can be found in section 3 on page 9.

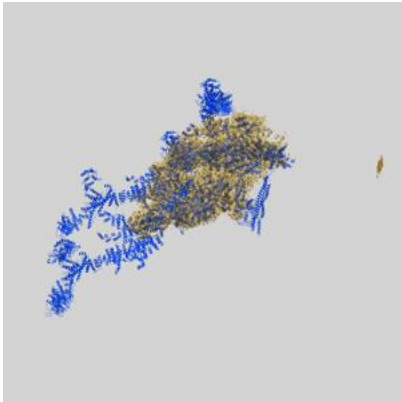
## 9.1 Map-model overlay (i)



X



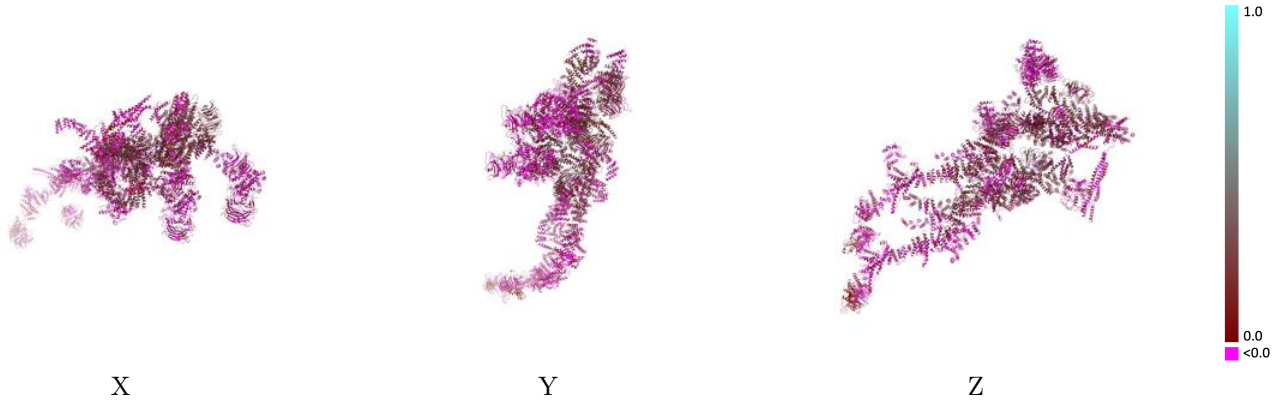
Y



Z

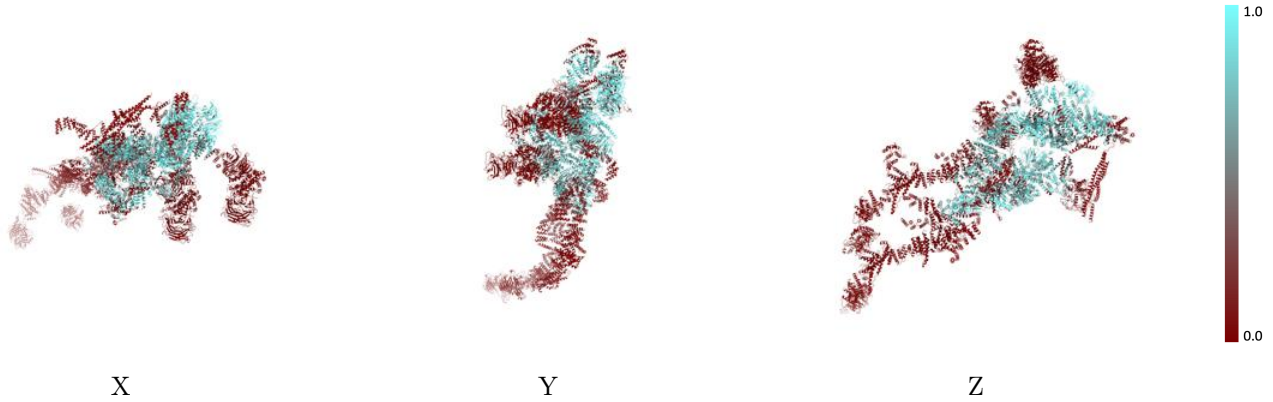
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



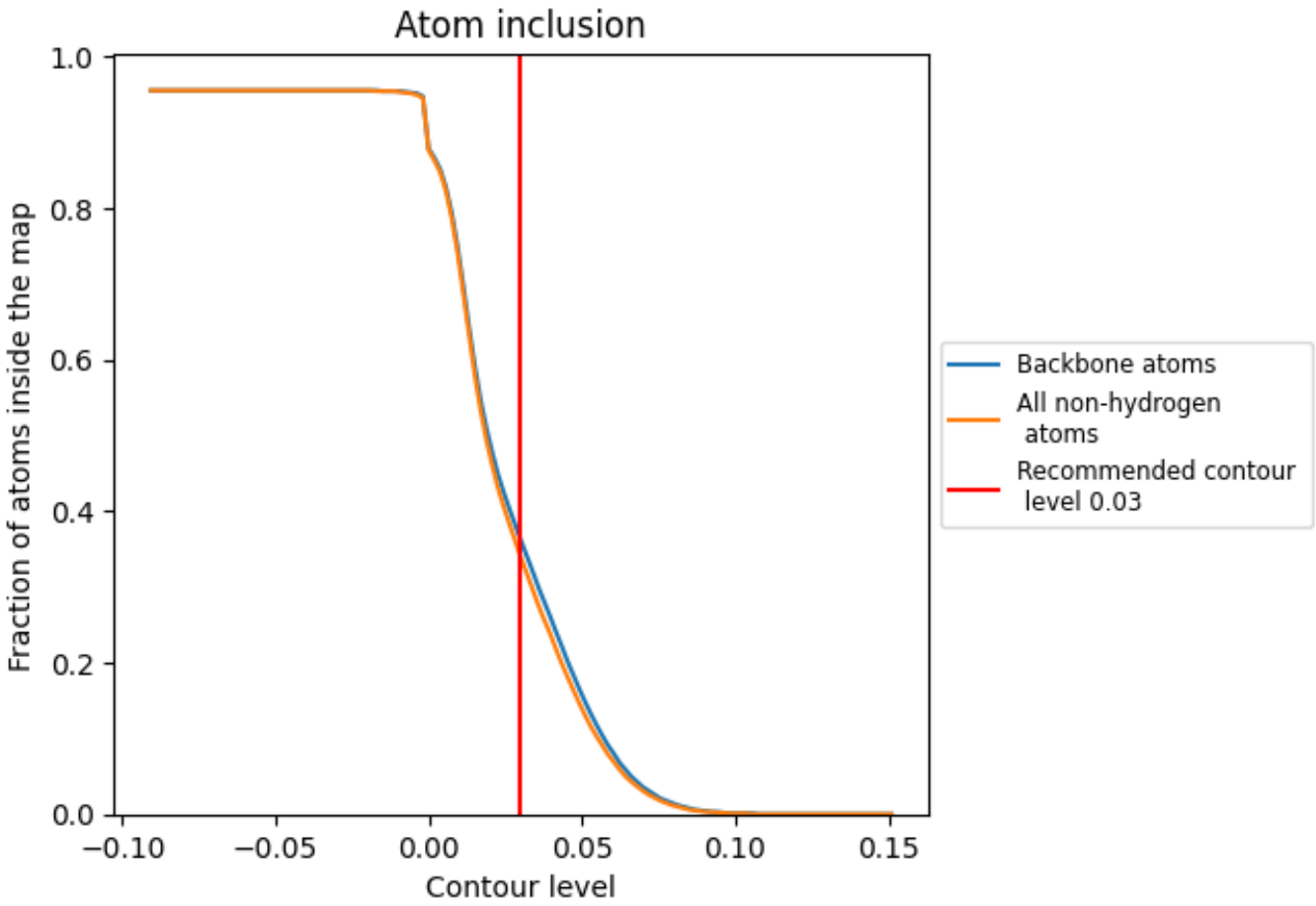

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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




The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

## 9.4 Atom inclusion (i)




At the recommended contour level, 36% of all backbone atoms, 34% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.3390 | 0.0890 |
| A | 0.6000 | 0.1430 |
| B | 0.6840 | 0.1880 |
| C | 0.8950 | 0.2270 |
| D | 0.7460 | 0.1650 |
| E | 0.0750 | 0.0220 |
| F | 0.0000 | 0.0160 |
| G | 0.6470 | 0.1730 |
| H | 0.7810 | 0.1790 |
| I | 0.1830 | 0.0930 |
| J | 0.0000 | 0.0030 |
| K | 0.0000 | 0.0110 |
| L | 0.0000 | 0.0100 |
| M | 0.0000 | 0.0220 |
| N | 0.4520 | 0.1270 |
| O | 0.0800 | 0.0580 |
| P | 0.0850 | 0.0380 |
| Q | 0.4120 | 0.1510 |
| R | 0.0550 | 0.0080 |
| S | 0.0670 | 0.0560 |
| T | 0.0500 | 0.0150 |
| U | 0.0000 | 0.0300 |
| V | 0.0000 | 0.0190 |
| a | 0.5030 | 0.1030 |
| b | 0.6740 | 0.1800 |
| c | 0.8780 | 0.2470 |
| d | 0.7290 | 0.1740 |
| e | 0.1730 | 0.0260 |
| f | 0.2990 | 0.0300 |
| g | 0.5760 | 0.1550 |
| h | 0.7090 | 0.1850 |
| i | 0.0000 | 0.0190 |
| j | 0.0000 | 0.0120 |