

```
858     FALSE     FALSE     THR
859     FALSE     FALSE     LYS
860     FALSE     FALSE     VAL
861     FALSE     FALSE     ASP
862     FALSE     FALSE     LYS
863     FALSE     FALSE     ARG
864     FALSE     FALSE     VAL
865     FALSE     FALSE     GLU
866     FALSE     FALSE     PRO
867     FALSE     FALSE     LYS
868     FALSE     FALSE     SER:CtermProteinFull
```

```
core.pack.interaction_graph.interaction_graph_factory: Instantiating DensePDInteractionGraph
core.pack.pack_rotamers: built 8 rotamers at 1 positions.
core.pack.pack_rotamers: IG: 820 bytes
core.conformation.Conformation: [ WARNING ] missing heavyatom: CG on residue ARG 18
core.conformation.Conformation: [ WARNING ] missing heavyatom: CD on residue ARG 18
core.conformation.Conformation: [ WARNING ] missing heavyatom: NE on residue ARG 18
core.conformation.Conformation: [ WARNING ] missing heavyatom: CZ on residue ARG 18
core.conformation.Conformation: [ WARNING ] missing heavyatom: NH1 on residue ARG 18
core.conformation.Conformation: [ WARNING ] missing heavyatom: NH2 on residue ARG 18
core.conformation.Conformation: [ WARNING ] missing heavyatom: CG on residue GLN:NtermProteinFull 214
core.conformation.Conformation: [ WARNING ] missing heavyatom: CD on residue GLN:NtermProteinFull 214
core.conformation.Conformation: [ WARNING ] missing heavyatom: OE1 on residue GLN:NtermProteinFull 214
core.conformation.Conformation: [ WARNING ] missing heavyatom: NE2 on residue GLN:NtermProteinFull 214
core.conformation.Conformation: [ WARNING ] missing heavyatom: CG on residue ARG 452
core.conformation.Conformation: [ WARNING ] missing heavyatom: CD on residue ARG 452
core.conformation.Conformation: [ WARNING ] missing heavyatom: NE on residue ARG 452
core.conformation.Conformation: [ WARNING ] missing heavyatom: CZ on residue ARG 452
core.conformation.Conformation: [ WARNING ] missing heavyatom: NH1 on residue ARG 452
core.conformation.Conformation: [ WARNING ] missing heavyatom: NH2 on residue ARG 452
core.conformation.Conformation: [ WARNING ] missing heavyatom: CG on residue GLN:NtermProteinFull 648
core.conformation.Conformation: [ WARNING ] missing heavyatom: CD on residue GLN:NtermProteinFull 648
core.conformation.Conformation: [ WARNING ] missing heavyatom: OE1 on residue GLN:NtermProteinFull 648
core.conformation.Conformation: [ WARNING ] missing heavyatom: NE2 on residue GLN:NtermProteinFull 648
core.conformation.Conformation: Found disulfide between residues 23 88
core.conformation.Conformation: current variant for 23 CYS
core.conformation.Conformation: current variant for 88 CYS
core.conformation.Conformation: current variant for 23 CYD
core.conformation.Conformation: current variant for 88 CYD
core.conformation.Conformation: Found disulfide between residues 134 194
core.conformation.Conformation: current variant for 134 CYS
core.conformation.Conformation: current variant for 194 CYS
core.conformation.Conformation: current variant for 134 CYD
core.conformation.Conformation: current variant for 194 CYD
core.conformation.Conformation: Found disulfide between residues 235 308
core.conformation.Conformation: current variant for 235 CYS
core.conformation.Conformation: current variant for 308 CYS
core.conformation.Conformation: current variant for 235 CYD
core.conformation.Conformation: current variant for 308 CYD
core.conformation.Conformation: Found disulfide between residues 359 415
core.conformation.Conformation: current variant for 359 CYS
core.conformation.Conformation: current variant for 415 CYS
core.conformation.Conformation: current variant for 359 CYD
core.conformation.Conformation: current variant for 415 CYD
core.conformation.Conformation: Found disulfide between residues 457 522
core.conformation.Conformation: current variant for 457 CYS
core.conformation.Conformation: current variant for 522 CYS
core.conformation.Conformation: current variant for 457 CYD
core.conformation.Conformation: current variant for 522 CYD
core.conformation.Conformation: Found disulfide between residues 568 628
core.conformation.Conformation: current variant for 568 CYS
core.conformation.Conformation: current variant for 628 CYS
core.conformation.Conformation: current variant for 568 CYD
core.conformation.Conformation: current variant for 628 CYD
core.conformation.Conformation: Found disulfide between residues 669 742
core.conformation.Conformation: current variant for 669 CYS
core.conformation.Conformation: current variant for 742 CYS
core.conformation.Conformation: current variant for 669 CYD
core.conformation.Conformation: current variant for 742 CYD
core.conformation.Conformation: Found disulfide between residues 793 849
core.conformation.Conformation: current variant for 793 CYS
core.conformation.Conformation: current variant for 849 CYS
core.conformation.Conformation: current variant for 793 CYD
core.conformation.Conformation: current variant for 849 CYD
core.pack.task: Packer task: initialize from command line<
core.pack.pack_missing_sidechains: packing residue number 18 because of missing atom number 6 atom name CG
core.pack.pack_missing_sidechains: packing residue number 214 because of missing atom number 6 atom name CG
core.pack.pack_missing_sidechains: packing residue number 452 because of missing atom number 6 atom name CG
core.pack.pack_missing_sidechains: packing residue number 648 because of missing atom number 6 atom name CG
core.scoring.ScoreFunctionFactory: SCOREFUNCTION: talaris2013
core.pack.interaction_graph.interaction_graph_factory: Instantiating DensePDInteractionGraph
core.pack.pack_rotamers: built 91 rotamers at 4 positions.
core.pack.pack_rotamers: IG: 2076 bytes
core.scoring.ScoreFunctionFactory: SCOREFUNCTION: talaris2013
core.pack.task: Packer task: initialize from command line<
core.pack.interaction_graph.interaction_graph_factory: Instantiating PDInteractionGraph
core.pack.pack_rotamers: built 16 rotamers at 1 positions.
core.pack.pack_rotamers: IG: 2392 bytes
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D:\PyRosetta>
```