Peptide Design with NCAAs

- Incorporate NCAAs into Rosetta design applications
  - Useful for protein-protein interfaces

- Determine sequence based on predicted binding energy
  - Predict which AA/NCAAs from a given library are likely to help or disfavor binding at protein/protein interface.

Native: (5LY2): Thr-Lys-Ser-Gly

Design: Cycloleucine-dSer-dMet-dAla
