**Introduction to CABS-based tools for protein modeling: CABS-flex, CABS-fold and py-CABS**  
  
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**Abstract:**

CABS is a coarse-grained protein model that has been well tested in a wide variety of protein simulation tasks. Based on the CABS model, we recently developed automated protocols for modeling and analysis of protein dynamics and structure: CABS-flex, CABS-fold and py-CABS.

CABS-flex [1, 2] is a web server for fast simulations of short-term dynamics of globular proteins and characterization of their fluctuations (available at <http://biocomp.chem.uw.edu.pl/CABSflex/‎>). CABS-fold [3] is a web server  for de novo and consensus-based prediction of protein structure (available at <http://biocomp.chem.uw.edu.pl/CABSfold/>‎). py-CABS [4] is a software package of python modules for the simulations of long-term dynamics of globular proteins (available at <http://biocomp.chem.uw.edu.pl/pycabs/>).

During my presentation I will shortly introduce these tools and give examples of their capabilities, usage and limitations.

**References:**

[1] Jamroz M, Kolinski A, Kmiecik S. *CABS-flex: server for fast simulation of protein structure fluctuations*. Nucleic Acids Research, 41:W427-W431, 2013.  
  
[2] Jamroz M, Kolinski A, Kmiecik S. *CABS-flex predictions of protein flexibility compared with NMR ensembles*. Bioinformatics, doi: 10.1093/bioinformatics/btu184, 2014.  
  
[3] Blaszczyk M, Jamroz M, Kmiecik S, Kolinski A. *CABS-fold: server for the de novo and consensus-based prediction of protein structure*. Nucleic Acids Research, 41:W406-W411, 2013.

[4] Jamroz M, Kolinski A, Kmiecik S. *Protocols for efficient simulations of long time protein dynamics using coarse-grained CABS model*. Methods in Molecular Biology, 1137:235-250, 2014.