

Research Project

CAMEO - Continuous Automated Model EvaluatiOn

Project funded by own resources

Project title CAMEO - Continuous Automated Model EvaluatiOn

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Organisation / Research unit

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Project Website <https://cameo3d.org/>

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Probable end 31.12.2025

Status Active

0.0.1 Computational Modeling of 3D Protein Structures

Proteins are the key tools of the cell and are responsible for the most important functions of living organisms. The specific spatial structures of proteins are determining their function. Computer simulations aim at reliably modeling the properties of three-dimensional protein structures that have not previously been elucidated experimentally. By providing information about their function at an atomic level of detail, modeling is applied in basic research on protein function as well as in drug development.

0.0.2 Assessing the Reliability of Protein Structure Models

As it is crucial to regularly assess the reliability of protein structure predictions, the "Continuous Automated Model EvaluatiOn (CAMEO)" platform conducts fully automated blind prediction assessments based on the weekly pre-release of sequences of those structures, which are going to be published in the next release of the PDB Protein Data Bank. CAMEO publishes weekly benchmarking results based on models collected during a 4-day prediction window, on average assessing ca. 100 targets during a time frame of 5 weeks. CAMEO benchmarking data is generated consistently for all participating methods at the same point in time, enabling developers to benchmark and cross-validate their method's performance, and directly refer to the benchmarking results in publications. In order to facilitate server development and promote shorter release cycles, CAMEO sends weekly email with submission statistics and low performance warnings. CAMEO offers a variety of scores to allow benchmarking diverse aspects of structure prediction methods, including introducing new scoring schemes. In summary, CAMEO facilitates new development in structure prediction in areas of active research, for example, modeling quaternary structure, complexes, or ligand binding sites.

Beside Protein Structure Modeling, CAMEO also features a separate category for "Model Quality Estimation" and the prediction of residue-residue contacts.

Keywords Benchmarking, Continuous Automated Model Evaluation, Protein Structure Modeling, Protein Structure Prediction, Assessment

Financed by

Other funds

Add publication

Published results

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