

Resource Summary Report

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Clemson Computational Biophysics and Bioinformatics

RRID:SCR_005696

Type: Tool

Proper Citation

Clemson Computational Biophysics and Bioinformatics (RRID:SCR_005696)

Resource Information

URL: <http://compbio.clemson.edu/index.html>

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Description: The research in the lab focuses on computational modeling of biological macromolecules and their assemblages and predicting biophysical quantities associated with them. The main focus of the lab is the development and maintenance of the popular software package DelPhi, which calculates electrostatic potential and energies of systems comprised of biological macromolecules. In addition, we are interested in modeling disease-causing missense mutations, pKa's of amino acids and nucleic groups and pH-dependence of stability and binding. In parallel with in silico modeling, the lab actively collaborates with experimentalists to better understand molecular mechanisms of biological reactions and interactions. The combination of the methods of Computational Biophysics and Bioinformatics with experimental results is an essential approach utilized in our research.

Abbreviations: Clemson Computational Biophysics & Bioinformatics

Synonyms: Clemson Computational Biophysics Bioinformatics

Resource Type: data or information resource, laboratory portal, organization portal, portal, software resource

Resource Name: Clemson Computational Biophysics and Bioinformatics

Resource ID: SCR_005696

Alternate IDs: nlx_149145

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260912T195630+0000

Ratings and Alerts

No rating or validation information has been found for Clemson Computational Biophysics and Bioinformatics.

No alerts have been found for Clemson Computational Biophysics and Bioinformatics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Nawab F, et al. (2025) Mutational insights and in silico characterization of NEK family kinases in OSCC patients from the Pakistani population. Frontiers in bioinformatics, 5, 1750649.

Ganakammal SR, et al. (2019) Evaluation of performance of leading algorithms for variant pathogenicity predictions and designing a combinatory predictor method: application to Rett syndrome variants. PeerJ, 7, e8106.