Resource Summary Report

Generated by dkNET on Apr 19, 2025

Decoys-R-Us

RRID:SCR_007622
Type: Tool

Proper Citation

Decoys-R-Us (RRID:SCR_007622)

Resource Information

URL: http://dd.compbio.washington.edu/

Proper Citation: Decoys-R-Us (RRID:SCR_007622)

Description: Decoys-R-Us is a database of decoys, computer-generated conformations of protein sequences that possess some characteristics of native proteins, but are not biologically real. The primary use of decoys is to test scoring, or energy, functions. All the decoys in the Decoys "R" Us database can be downloaded.

Synonyms: Decoys-R-Us

Resource Type: database, data or information resource

Keywords: decoy, protein sequence conformation

Funding:

Resource Name: Decoys-R-Us

Resource ID: SCR_007622

Alternate IDs: nif-0000-02743

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250412T055204+0000

Ratings and Alerts

No rating or validation information has been found for Decoys-R-Us.

No alerts have been found for Decoys-R-Us.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Park J, et al. (2014) ROTAS: a rotamer-dependent, atomic statistical potential for assessment and prediction of protein structures. BMC bioinformatics, 15(1), 307.

Carlsen M, et al. (2014) On the importance of the distance measures used to train and test knowledge-based potentials for proteins. PloS one, 9(11), e109335.

Chakraborty S, et al. (2013) Protein structure quality assessment based on the distance profiles of consecutive backbone C? atoms. F1000Research, 2, 211.

Chakraborty S, et al. (2013) The electrostatic profile of consecutive C? atoms applied to protein structure quality assessment. F1000Research, 2, 243.

Zhao F, et al. (2012) A position-specific distance-dependent statistical potential for protein structure and functional study. Structure (London, England : 1993), 20(6), 1118.

Liu Y, et al. (2012) Using the unfolded state as the reference state improves the performance of statistical potentials. Biophysical journal, 103(9), 1950.

Zhou H, et al. (2011) GOAP: a generalized orientation-dependent, all-atom statistical potential for protein structure prediction. Biophysical journal, 101(8), 2043.

Moughon SE, et al. (2011) LoCo: a novel main chain scoring function for protein structure prediction based on local coordinates. BMC bioinformatics, 12, 368.

Zhang J, et al. (2010) A novel side-chain orientation dependent potential derived from random-walk reference state for protein fold selection and structure prediction. PloS one, 5(10), e15386.

Arab S, et al. (2010) A pairwise residue contact area-based mean force potential for discrimination of native protein structure. BMC bioinformatics, 11, 16.