Resource Summary Report

Generated by NIF on Apr 8, 2025

InterEvol database

RRID:SCR_006054
Type: Tool

Proper Citation

InterEvol database (RRID:SCR_006054)

Resource Information

URL: http://biodev.cea.fr/interevol/

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Description: InterEvol database is designed for the analysis of co-evolution events at the interface of known structures of hetero- and homo-oligomers. The database can be search and analyzed through 3 interconnected levels of analysis: * From a Keyword or the PDB entry of a complex, you can browse: ** structural homologs for every chain in other complexes ** structural interologs for every interface ** retrieve pre-computed sequence alignments in diverse species * From 1 or 2 sequences of interacting partners: ** build 2 multiple sequence alignments with the same species ordered in each ** query the InterEvol database with alignments using profile-profile comparison method * Visualize structure vs sequence alignment at the complex interface ** A dedicated Pymol plugin is provided ** Alignment views in Pymol are interactively restricted to the residues selected at the interface

Abbreviations: InterEvol

Resource Type: analysis service resource, data analysis service, production service resource, service resource, database, data or information resource, software resource

Defining Citation: PMID:22053089

Keywords: structure, evolution, protein complex, interface, protein complex, sequence alignment, plug in, protein structure, visualization, pymol plugin, structural homolog, structural interolog, bio.tools

Funding: Commissariat a lEnergie Atomique ;
ANR HPGenVar

Availability: Free and open to all users - no login requirement

Resource Name: InterEvol database

Resource ID: SCR_006054

Alternate IDs: nlx_151453, biotools:interevol

Alternate URLs: https://bio.tools/interevol

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250407T215600+0000

Ratings and Alerts

No rating or validation information has been found for InterEvol database.

No alerts have been found for InterEvol database.

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 NIF.

Marelli S, et al. (2020) Antagonism of PP2A is an independent and conserved function of HIV-1 Vif and causes cell cycle arrest. eLife, 9.

Bakail M, et al. (2019) Design on a Rational Basis of High-Affinity Peptides Inhibiting the Histone Chaperone ASF1. Cell chemical biology, 26(11), 1573.

Chen YQ, et al. (2018) Influenza Infection in Humans Induces Broadly Cross-Reactive and Protective Neuraminidase-Reactive Antibodies. Cell, 173(2), 417.

Caillet-Saguy C, et al. (2017) Regulation of the Human Phosphatase PTPN4 by the inter-domain linker connecting the PDZ and the phosphatase domains. Scientific reports, 7(1), 7875.

Launay G, et al. (2017) Non-interacting proteins may resemble interacting proteins: prevalence and implications. Scientific reports, 7, 40419.

Martin OM, et al. (2016) Implication of Terminal Residues at Protein-Protein and Protein-DNA Interfaces. PloS one, 11(9), e0162143.

Alsop JD, et al. (2015) Interolog interfaces in protein-protein docking. Proteins, 83(11), 1940.

Vasudevan HN, et al. (2014) SRF regulates craniofacial development through selective recruitment of MRTF cofactors by PDGF signaling. Developmental cell, 31(3), 332.

Hopf TA, et al. (2014) Sequence co-evolution gives 3D contacts and structures of protein complexes. eLife, 3.

Galperin MY, et al. (2012) The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. Nucleic acids research, 40(Database issue), D1.