

Resource Summary Report

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IBIS: Inferred Biomolecular Interactions Server

RRID:SCR_004886

Type: Tool

Proper Citation

IBIS: Inferred Biomolecular Interactions Server (RRID:SCR_004886)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/Structure/ibis/ibis.cgi>

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Description: A web server and database that organizes, analyzes and predicts interactions between proteins and other biomolecules. For a given protein sequence or structure query, it reports protein-protein, protein-small molecule, protein nucleic acids and protein-ion interactions observed in experimentally-determined structural biological assemblies. It also infers/predicts interacting partners and binding sites by homology, by inspecting the protein complexes formed by close homologs of a given query. To ensure biological relevance of inferred binding sites, the IBIS algorithm clusters binding sites formed by homologs based on binding site sequence and structure conservation.

Abbreviations: IBIS

Synonyms: Inferred Biomolecular Interactions Server, NCBI Inferred Biomolecular Interactions Server

Resource Type: data or information resource, database

Defining Citation: [PMID:22102591](#), [PMID:19843613](#)

Keywords: protein interaction, protein protein, protein small molecule, protein nucleic acid, protein ion interaction, interacting partner, binding site, homology, protein complex, structure conservation, nucleic acid, protein dna, protein rna, protein chemical, bio.tools

Resource Name: IBIS: Inferred Biomolecular Interactions Server

Resource ID: SCR_004886

Alternate IDs: OMICS_01917, biotools:ibis_ncbi, nlx_85682

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

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260729T044106+0000

Ratings and Alerts

No rating or validation information has been found for IBIS: Inferred Biomolecular Interactions Server.

No alerts have been found for IBIS: Inferred Biomolecular Interactions Server.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Hashemi ZS, et al. (2021) In silico Approaches for the Design and Optimization of Interfering Peptides Against Protein-Protein Interactions. Frontiers in molecular biosciences, 8, 669431.

Goncearenco A, et al. (2015) Structural Perspectives on the Evolutionary Expansion of Unique Protein-Protein Binding Sites. Biophysical journal, 109(6), 1295.

Nishi H, et al. (2013) Cancer missense mutations alter binding properties of proteins and their interaction networks. PloS one, 8(6), e66273.

Thangudu RR, et al. (2010) Knowledge-based annotation of small molecule binding sites in proteins. BMC bioinformatics, 11, 365.

Hashimoto K, et al. (2010) Functional states of homooligomers: insights from the evolution of glycosyltransferases. Journal of molecular biology, 399(1), 196.