

Resource Summary Report

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Interaction Proteome Project

RRID:SCR_008043

Type: Tool

Proper Citation

Interaction Proteome Project (RRID:SCR_008043)

Resource Information

URL: <http://www.interaction-proteome.org/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on January 28, 2013. (URL is no longer valid) A platform for high-throughput proteomic analysis. Major objectives of IPP include the establishment of a broadly applicable platform of routine methods for the analysis of protein interaction networks in bio-medical research. A multidisciplinary approach will address; * their validation by cell biological, biochemical and biophysical methods. * their collection in a new type of public database. * their exploitation and use for in silico simulations of protein-interaction networks. The innovations generated in IPP will provide the basis for an efficient analysis and systems modeling of fundamental biological processes in health and disease. It will develop novel technology, including a high-end mass spectrometer with extremely large dynamic range, high-density peptide arrays, and improved visualization technology for light and electron microscopy. Additionally, the novel technologies will be validated with selected model systems of high relevance to medicine and biotechnology. Extensive bioinformatics support is a key element in the project to cope with the massive increase in experimental data on protein interactions obtained using the novel technologies. In particular, the efficient integration of disparate data sets represents a key challenge in proteomics and functional genomics. Therefore, the consortium includes the creator of the only European protein-interactions database, MINT. The multi-disciplinary efforts required in the scientific program of IPP are organized into four sub-projects (SP): * SP1: Tools for interaction analysis - SP1 is dedicated to the development of innovative proteomics technology to map protein-interaction networks and their cellular topology for the interaction analyses in SP2 and SP3. * SP2: Identification of interaction partners for protein domains - SP2 will generate (high throughput) data for important protein-protein interactions defined by bioinformatics and biomedical interest and by SP3, utilizing technology developed in SP1. * SP3: Functional analysis of interactions - SP3 focuses on the validation of technologies and tools developed in SP1. It will perform functional analyses of protein-interactions in medically and biochemically relevant prokaryotic and eukaryotic (mammalian) model systems. * SP4: Interactome database and modelling - SP4 provides the required

bioinformatics infrastructure for the project, comprising the improvement of the public MINT database for the collection and dissemination of the interactome data; modelling and simulation of protein-interaction networks characterised in SP2 and SP3; and the dissemination of the technology developments to the scientific community.

Abbreviations: IPP

Synonyms: Interaction Proteome

Resource Type: data or information resource, portal, simulation software, software application, software resource, topical portal

Keywords: electron, eukaryotic, biochemical, bioinformatics, biological, biomedical, biophysical, biotechnology, cell, development, disease, domain, genomics, health, interaction, light, mammalian, map, mass spectrometer, medicine, microscopy, model, modeling, network, peptide array, prokaryotic, protein interaction, proteome, proteomics, silico, simulation, system, technology, tool, protein interaction

Funding: European Union

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Interaction Proteome Project

Resource ID: SCR_008043

Alternate IDs: nif-0000-10259

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260905T132617+0000

Ratings and Alerts

No rating or validation information has been found for Interaction Proteome Project.

No alerts have been found for Interaction Proteome Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Galindo-Romero C, et al. (2016) Neuroprotection by α_2 -Adrenergic Receptor Stimulation after Excitotoxic Retinal Injury: A Study of the Total Population of Retinal Ganglion Cells and Their Distribution in the Chicken Retina. PloS one, 11(9), e0161862.