

Resource Summary Report

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EXProt- database for EXPerimentally verified Protein functions

RRID:SCR_007652

Type: Tool

Proper Citation

EXProt- database for EXPerimentally verified Protein functions (RRID:SCR_007652)

Resource Information

URL: <http://www.cmbi.kun.nl/EXProt/>

Proper Citation: EXProt- database for EXPerimentally verified Protein functions (RRID:SCR_007652)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 23, 2016. EXProt (database for EXPerimentally verified Protein functions) is a new non-redundant database containing protein sequences for which the function has been experimentally verified. EXProt is a selection of 6491 entries which are described to have an experimentally verified function. The entries in EXProt all have a unique ID number and provide information about organism, protein sequence, functional annotation, link to entry in original database, and if known, gene name and link to references in PubMed. The EXProt database can be searched with BLAST or FASTA with amino acid or nucleotide sequence as query sequence. Note that only the sequence goes into the field. EXProt database is also searchable in SRS6 at CMBI. In a near future entries from the genome project of *Lactobacillus plantarum* by Wageningen Centre for Food Sciences (WCFS) will be added to EXProt.

Synonyms: EXProt

Resource Type: data or information resource, database

Keywords: protein function, protein sequence

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: EXProt- database for EXPerimentally verified Protein functions

Resource ID: SCR_007652

Alternate IDs: nif-0000-02828

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260821T193822+0000

Ratings and Alerts

No rating or validation information has been found for EXProt- database for EXPerimentally verified Protein functions.

No alerts have been found for EXProt- database for EXPerimentally verified Protein functions.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Vazquez-Vilar M, et al. (2017) GB3.0: a platform for plant bio-design that connects functional DNA elements with associated biological data. Nucleic acids research, 45(4), 2196.

Adhikary T, et al. (2017) Interferon signaling in ascites-associated macrophages is linked to a favorable clinical outcome in a subgroup of ovarian carcinoma patients. BMC genomics, 18(1), 243.

Finkernagel F, et al. (2016) The transcriptional signature of human ovarian carcinoma macrophages is associated with extracellular matrix reorganization. Oncotarget, 7(46), 75339.

Nurizzo D, et al. (2016) RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. Acta crystallographica. Section D, Structural biology, 72(Pt 8), 966.

Zhang Y, et al. (2016) Uncovering three-dimensional gradients in fibrillar orientation in an impact-resistant biological armour. Scientific reports, 6, 26249.

Malagarriga D, et al. (2015) Mesoscopic segregation of excitation and inhibition in a brain network model. PLoS computational biology, 11(2), e1004007.

Thibeault CM, et al. (2014) Analyzing large-scale spiking neural data with HRLAnalysis(???). Frontiers in neuroinformatics, 8, 17.

Wang A, et al. (2014) A web-server of cell type discrimination system. TheScientificWorldJournal, 2014, 459064.

Gafni E, et al. (2014) COSMOS: Python library for massively parallel workflows. *Bioinformatics* (Oxford, England), 30(20), 2956.

Clos LJ, et al. (2013) NMRbot: Python scripts enable high-throughput data collection on current Bruker BioSpin NMR spectrometers. *Metabolomics : Official journal of the Metabolomic Society*, 9(3), 558.

Kim S, et al. (2013) Virmid: accurate detection of somatic mutations with sample impurity inference. *Genome biology*, 14(8), R90.

Williams DS, et al. (2010) Nonsense mediated decay resistant mutations are a source of expressed mutant proteins in colon cancer cell lines with microsatellite instability. *PloS one*, 5(12), e16012.

Chandran D, et al. (2009) TinkerCell: modular CAD tool for synthetic biology. *Journal of biological engineering*, 3, 19.

Malik A, et al. (2007) Databases and QSAR for cancer research. *Cancer informatics*, 2, 99.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.