Resource Summary Report

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Bioinformatic Harvester IV (beta) at Karlsruhe Institute of Technology

RRID:SCR 008017

Type: Tool

Proper Citation

Bioinformatic Harvester IV (beta) at Karlsruhe Institute of Technology (RRID:SCR_008017)

Resource Information

URL: http://harvester.fzk.de/harvester/

Proper Citation: Bioinformatic Harvester IV (beta) at Karlsruhe Institute of Technology (RRID:SCR_008017)

Description: Harvester is a Web-based tool that bulk-collects bioinformatic data on human proteins from various databases and prediction servers. It is a meta search engine for gene and protein information. It searches 16 major databases and prediction servers and combines the results on pregenerated HTML pages. In this way Harvester can provide comprehensive gene-protein information from different servers in a convenient and fast manner. As full text meta search engine, similar to Google trade mark, Harvester allows screening of the whole genome proteome for current protein functions and predictions in a few seconds. With Harvester it is now possible to compare and check the quality of different database entries and prediction algorithms on a single page. Sponsors: This work has been supported by the BMBF with grants 01GR0101 and 01KW0013.

Synonyms: Harvester IV

Resource Type: data or information resource, database, software resource, data acquisition software, software application, data processing software

Keywords: function, gene, bioinformatics, data, database, human, meta search engine, prediction, protein, bio.tools, FASEB list

Funding:

Resource Name: Bioinformatic Harvester IV (beta) at Karlsruhe Institute of Technology

Resource ID: SCR_008017

Alternate IDs: biotools:harvester, nif-0000-10169

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

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250521T061217+0000

Ratings and Alerts

No rating or validation information has been found for Bioinformatic Harvester IV (beta) at Karlsruhe Institute of Technology.

No alerts have been found for Bioinformatic Harvester IV (beta) at Karlsruhe Institute of Technology.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1480 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

He Y, et al. (2024) Molecular mechanism of resveratrol promoting differentiation of preosteoblastic MC3T3-E1 cells based on network pharmacology and experimental validation. BMC complementary medicine and therapies, 24(1), 108.

Mas-Carrió E, et al. (2024) Niche overlap across landscape variability in summer between two large herbivores using eDNA metabarcoding. PloS one, 19(2), e0279672.

Katru SC, et al. (2024) Identification and characterization of a novel nematode pan allergen (NPA) from Wuchereria bancrofti and their potential role in human filarial tropical pulmonary eosinophilia (TPE). PLoS neglected tropical diseases, 18(2), e0011972.

Peralta-Marzal LN, et al. (2024) A robust microbiome signature for autism spectrum disorder across different studies using machine learning. Scientific reports, 14(1), 814.

Yan HJ, et al. (2024) Proteomic analysis reveals LRPAP1 as a key player in the micropapillary pattern metastasis of lung adenocarcinoma. Heliyon, 10(1), e23913.

Han Y, et al. (2024) Effects of microgravity on neural crest stem cells. Frontiers in

neuroscience, 18, 1379076.

Andreas MP, et al. (2024) Cyclodipeptide oxidase is an enzyme filament. Nature communications, 15(1), 3574.

Gu G, et al. (2024) Endocrine islet ?-cell subtypes with differential function are derived from biochemically distinct embryonic endocrine islet progenitors that are regulated by maternal nutrients. Research square.

Wu J, et al. (2024) Transcriptomic profile of premature ovarian insufficiency with RNA-sequencing. Frontiers in cell and developmental biology, 12, 1370772.

Gu Y, et al. (2024) CYLD regulates cell ferroptosis through Hippo/YAP signaling in prostate cancer progression. Cell death & disease, 15(1), 79.

Hunt AL, et al. (2024) Mapping three-dimensional intratumor proteomic heterogeneity in uterine serous carcinoma by multiregion microsampling. Clinical proteomics, 21(1), 4.

Rahman Z, et al. (2024) Genomic characterization of extended-spectrum beta-lactamase-producing and carbapenem-resistant Escherichia coli from urban wastewater in Australia. MicrobiologyOpen, 13(2), e1403.

Mphephu MM, et al. (2024) Metabolomics approach for predicting stomach and colon contents in dead Arctocephalus pusillus pusillus, Arctocephalus tropicalis, Lobodon carcinophaga and Ommatophoca rossii from sub-Antarctic region. PloS one, 19(4), e0300319.

Ostrov I, et al. (2024) Elemental iron protects gut microbiota against oxygen-induced dysbiosis. PloS one, 19(2), e0298592.

Li J, et al. (2024) UCHL1 contributes to insensitivity to endocrine therapy in triple-negative breast cancer by deubiquitinating and stabilizing KLF5. Breast cancer research: BCR, 26(1), 44.

Nunes SP, et al. (2024) Modulation of tumor microenvironment by targeting histone acetylation in bladder cancer. Cell death discovery, 10(1), 1.

Haugg E, et al. (2024) Comparative transcriptomics of the garden dormouse hypothalamus during hibernation. FEBS open bio, 14(2), 241.

Hooper R, et al. (2024) Ultimate drivers of forced extra-pair copulations in birds lacking a penis: jackdaws as a case-study. Royal Society open science, 11(3), 231226.

Tunsakul N, et al. (2024) Non-significant influence between aerobic and anaerobic sample transport materials on gut (fecal) microbiota in healthy and fat-metabolic disorder Thai adults. PeerJ, 12, e17270.

Conway AM, et al. (2024) A cfDNA methylation-based tissue-of-origin classifier for cancers of unknown primary. Nature communications, 15(1), 3292.