Resource Summary Report

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Integr8 : Access to complete genomes and proteomes

RRID:SCR_007740
Type: Tool

Proper Citation

Integr8 : Access to complete genomes and proteomes (RRID:SCR_007740)

Resource Information

URL: http://www.ebi.ac.uk/integr8/

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Description: The Integr8 web portal provides easy access to integrated information about deciphered genomes and their corresponding proteomes. Available data includes DNA sequences (from databases including the EMBL Nucleotide Sequence Database, Genome Reviews, and Ensembl); protein sequences (from databases including the UniProt Knowledgebase and IPI); statistical genome and proteome analysis (performed using InterPro, CluSTr, and GOA); and information about orthology, paralogy, and synteny.

Synonyms: Integr8

Resource Type: database, data or information resource

Keywords: bio.tools

Funding:

Resource Name: Integr8 : Access to complete genomes and proteomes

Resource ID: SCR_007740

Alternate IDs: nif-0000-03027, biotools:intergr8

Alternate URLs: https://bio.tools/intergr8

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250420T015558+0000

Ratings and Alerts

No rating or validation information has been found for Integr8 : Access to complete genomes and proteomes.

No alerts have been found for Integr8 : Access to complete genomes and proteomes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 52 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Cho DH, et al. (2019) RNA-seq data for olive flounder (Paralichthys olivaceus) according to water temperature. Data in brief, 25, 104384.

Watson DC, et al. (2018) Scalable, cGMP-compatible purification of extracellular vesicles carrying bioactive human heterodimeric IL-15/lactadherin complexes. Journal of extracellular vesicles, 7(1), 1442088.

Mahajan G, et al. (2017) Using structural knowledge in the protein data bank to inform the search for potential host-microbe protein interactions in sequence space: application to Mycobacterium tuberculosis. BMC bioinformatics, 18(1), 201.

Gau D, et al. (2016) Threonine 89 Is an Important Residue of Profilin-1 That Is Phosphorylatable by Protein Kinase A. PloS one, 11(5), e0156313.

Liu S, et al. (2016) Comparative Proteomics Reveals Important Viral-Host Interactions in HCV-Infected Human Liver Cells. PloS one, 11(1), e0147991.

Honvo-Houéto E, et al. (2016) The endoplasmic reticulum and casein-containing vesicles contribute to milk fat globule membrane. Molecular biology of the cell, 27(19), 2946.

Watson DC, et al. (2016) Efficient production and enhanced tumor delivery of engineered extracellular vesicles. Biomaterials, 105, 195.

Miedel MT, et al. (2014) Isolation of serpin-interacting proteins in C. elegans using protein affinity purification. Methods (San Diego, Calif.), 68(3), 536.

Nuss JE, et al. (2014) Multi-faceted proteomic characterization of host protein complement of

Rift Valley fever virus virions and identification of specific heat shock proteins, including HSP90, as important viral host factors. PloS one, 9(5), e93483.

Librado P, et al. (2014) Mycobacterial phylogenomics: an enhanced method for gene turnover analysis reveals uneven levels of gene gain and loss among species and gene families. Genome biology and evolution, 6(6), 1454.

Luo J, et al. (2014) Genetically encoded optochemical probes for simultaneous fluorescence reporting and light activation of protein function with two-photon excitation. Journal of the American Chemical Society, 136(44), 15551.

Dias PJ, et al. (2013) The drug:H? antiporters of family 2 (DHA2), siderophore transporters (ARN) and glutathione:H? antiporters (GEX) have a common evolutionary origin in hemiascomycete yeasts. BMC genomics, 14, 901.

Weng RR, et al. (2013) Large precursor tolerance database search - a simple approach for estimation of the amount of spectra with precursor mass shifts in proteomic data. Journal of proteomics, 91, 375.

Lee NN, et al. (2013) Mtr4-like protein coordinates nuclear RNA processing for heterochromatin assembly and for telomere maintenance. Cell, 155(5), 1061.

Mabey Gilsenan J, et al. (2012) CADRE: the Central Aspergillus Data REpository 2012. Nucleic acids research, 40(Database issue), D660.

Yang C, et al. (2012) Exosomes released from Mycoplasma infected tumor cells activate inhibitory B cells. PloS one, 7(4), e36138.

Collins M, et al. (2012) The RNA-binding motif 45 (RBM45) protein accumulates in inclusion bodies in amyotrophic lateral sclerosis (ALS) and frontotemporal lobar degeneration with TDP-43 inclusions (FTLD-TDP) patients. Acta neuropathologica, 124(5), 717.

Trost B, et al. (2012) Comparing the similarity of different groups of bacteria to the human proteome. PloS one, 7(4), e34007.

Cruz J, et al. (2012) BacMap: an up-to-date electronic atlas of annotated bacterial genomes. Nucleic acids research, 40(Database issue), D599.

Allard JE, et al. (2012) Analysis of PSPHL as a Candidate Gene Influencing the Racial Disparity in Endometrial Cancer. Frontiers in oncology, 2, 65.