Resource Summary Report

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PeptideMapper

RRID:SCR_005763
Type: Tool

Proper Citation

PeptideMapper (RRID:SCR_005763)

Resource Information

URL: http://edwardslab.bmcb.georgetown.edu/ws/peptideMapper/

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Description: The PeptideMapper Web-Service provides alignments of peptide sequence alignments to proteins, mRNA, EST, and HTC sequences from Genbank, RefSeq, UniProt, IPI, VEGA, EMBL, and HInvDb. This mapping infrastructure is supported, in part, by the compressed peptide sequence database infrastructure (Edwards, 2007) which enables a fast, suffix-tree based mapping of peptide sequences to gene identifiers and a gene-focused detailed mapping of peptide sequences to source sequence evidence. The PeptideMapper Web-Service can be used interactively or as a web-service using either HTTP or SOAP requests. Results of HTTP requests can be returned in a variety of formats, including XML, JSON, CSV, TSV, or XLS, and in some cases, GFF or BED; results of SOAP requests are returned as SOAP responses. The PeptideMapper Web-Service maps at most 20 peptides with length between 5 and 30 amino-acids in each request. The number of alignments returned, per peptide, gene, and sequence type, is set to 10 by default. The default can be changed on the interactive alignments search form or by using the max web-service parameter.

Abbreviations: PeptideMapper

Synonyms: PeptideMapper Web-Service, Peptide Mapper

Resource Type: data access protocol, software resource, web service

Defining Citation: PMID:17437027

Keywords: peptide, sequence, protein, alignment, expressed sequence tag, mrna, est, htc, genbank, refseq, uniprot, ipi, vega, embl, hinvdb

Funding: NCI CA126189

Resource Name: PeptideMapper

Resource ID: SCR_005763

Alternate IDs: nlx_149229

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250524T060050+0000

Ratings and Alerts

No rating or validation information has been found for PeptideMapper.

No alerts have been found for PeptideMapper.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Do K, et al. (2024) A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. mSphere, 9(6), e0079323.

Gómez-Baena G, et al. (2023) Unraveling female communication through scent marks in the Norway rat. Proceedings of the National Academy of Sciences of the United States of America, 120(25), e2300794120.

Fan S-M, et al. (2023) Multi-integrated approach for unraveling small open reading frames potentially associated with secondary metabolism in Streptomyces. mSystems, 8(5), e0024523.

Sánchez LFH, et al. (2019) PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. GigaScience, 8(8).