Resource Summary Report

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pipasic

RRID:SCR_024165
Type: Tool

Proper Citation

pipasic (RRID:SCR_024165)

Resource Information

URL: https://sourceforge.net/projects/pipasic/

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Description: Software tool for similarity and expression correction for strain level identification and quantification in metaproteomics. Peptide intensity weighted proteome abundance similarity correction tool to correct identification and spectral counting based quantification results. Pipasic has distinct advantages over approaches only regarding unique peptides or aggregating results to the lowest common ancestor.

Resource Type: software resource, software application, data analysis software, data processing software

Defining Citation: PMID:24931978

Keywords: similarity and expression correction, strain level identification and quantification, metaproteomics, peptide intensity weighted proteome abundance similarity, correct identification and spectral counting, quantification results, peptide similarity estimation and expression level weighting within non-negative lasso framework,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: pipasic

Resource ID: SCR_024165

Old URLs: https://sources.debian.org/src/pipasic/

License: BSD License

Record Creation Time: 20230824T050212+0000

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Ratings and Alerts

No rating or validation information has been found for pipasic.

No alerts have been found for pipasic.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.