Resource Summary Report

Generated by dkNET on Apr 29, 2025

SBEAMS

RRID:SCR_011830
Type: Tool

Proper Citation

SBEAMS (RRID:SCR_011830)

Resource Information

URL: http://www.sbeams.org/

Proper Citation: SBEAMS (RRID:SCR_011830)

Description: Software providing a framework for collecting, storing, and accessing data produced by a wide variety of experiments.

Abbreviations: SBEAMS

Synonyms: Systems Biology Experiment Analysis Management System

Resource Type: software resource

Defining Citation: PMID:16756676

Keywords: proteomics, microarray

Funding:

Resource Name: SBEAMS

Resource ID: SCR_011830

Alternate IDs: OMICS_01011

Record Creation Time: 20220129T080306+0000

Record Last Update: 20250420T014600+0000

Ratings and Alerts

No rating or validation information has been found for SBEAMS.

No alerts have been found for SBEAMS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Panchaud A, et al. (2008) Experimental and computational approaches to quantitative proteomics: status quo and outlook. Journal of proteomics, 71(1), 19.

Zhang Q, et al. (2008) A mouse plasma peptide atlas as a resource for disease proteomics. Genome biology, 9(6), R93.

Deutsch EW, et al. (2008) PeptideAtlas: a resource for target selection for emerging targeted proteomics workflows. EMBO reports, 9(5), 429.

Ingalls BP, et al. (2007) Systems level modeling of the cell cycle using budding yeast. Cancer informatics, 3, 357.

Bodenmiller B, et al. (2007) PhosphoPep--a phosphoproteome resource for systems biology research in Drosophila Kc167 cells. Molecular systems biology, 3, 139.

Bonneau R, et al. (2007) A predictive model for transcriptional control of physiology in a free living cell. Cell, 131(7), 1354.

Zhang H, et al. (2006) UniPep--a database for human N-linked glycosites: a resource for biomarker discovery. Genome biology, 7(8), R73.

King NL, et al. (2006) Analysis of the Saccharomyces cerevisiae proteome with PeptideAtlas. Genome biology, 7(11), R106.

Marzolf B, et al. (2006) SBEAMS-Microarray: database software supporting genomic expression analyses for systems biology. BMC bioinformatics, 7, 286.