Resource Summary Report

Generated by NIF on Apr 19, 2025

Pegasus-fus

RRID:SCR_012118
Type: Tool

Proper Citation

Pegasus-fus (RRID:SCR_012118)

Resource Information

URL: http://sourceforge.net/projects/pegasus-fus/

Proper Citation: Pegasus-fus (RRID:SCR_012118)

Description: Software that annotates biologically functional gene fusion candidates.

Resource Type: software resource

Defining Citation: PMID:25183062

Keywords: standalone software, unix/linux, java, perl, python

Funding:

Resource Name: Pegasus-fus

Resource ID: SCR_012118

Alternate IDs: OMICS_05584

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014607+0000

Ratings and Alerts

No rating or validation information has been found for Pegasus-fus.

No alerts have been found for Pegasus-fus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Saxe HJ, et al. (2021) Two UGT84A Family Glycosyltransferases Regulate Phenol, Flavonoid, and Tannin Metabolism in Juglans regia (English Walnut). Frontiers in plant science, 12, 626483.

Le Moal M, et al. (2021) Is the Cyanobacterial Bloom Composition Shifting Due to Climate Forcing or Nutrient Changes? Example of a Shallow Eutrophic Reservoir. Toxins, 13(5).

Zhang Y, et al. (2020) A moonlighting role for enzymes of glycolysis in the co-localization of mitochondria and chloroplasts. Nature communications, 11(1), 4509.

Wu L, et al. (2020) An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature communications, 11(1), 3905.

Cheng W, et al. (2020) Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits. PLoS genetics, 16(6), e1008855.

McGuirl MR, et al. (2020) Detecting Shared Genetic Architecture Among Multiple Phenotypes by Hierarchical Clustering of Gene-Level Association Statistics. Genetics, 215(2), 511.

Li B, et al. (2020) Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. Nature methods, 17(8), 793.

Müller C, et al. (2019) The Global Gridded Crop Model Intercomparison phase 1 simulation dataset. Scientific data, 6(1), 50.

Harcourt D, et al. (2017) A study protocol of the effectiveness of PEGASUS: a multi-centred study comparing an intervention to promote shared decision making about breast reconstruction with treatment as usual. BMC medical informatics and decision making, 17(1), 143.

Schauberger B, et al. (2017) Consistent negative response of US crops to high temperatures in observations and crop models. Nature communications, 8, 13931.

Nakka P, et al. (2016) Gene and Network Analysis of Common Variants Reveals Novel Associations in Multiple Complex Diseases. Genetics, 204(2), 783.

Zhao C, et al. (2016) Field warming experiments shed light on the wheat yield response to

temperature in China. Nature communications, 7, 13530.

Harcourt D, et al. (2016) The acceptability of PEGASUS: an intervention to facilitate shared decision-making with women contemplating breast reconstruction. Psychology, health & medicine, 21(2), 248.

Fentzke RC, et al. (1999) Impaired cardiomyocyte relaxation and diastolic function in transgenic mice expressing slow skeletal troponin I in the heart. The Journal of physiology, 517 (Pt 1)(Pt 1), 143.