

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## Pegasus-fus

RRID:SCR\_012118

Type: Tool

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### Proper Citation

Pegasus-fus (RRID:SCR\_012118)

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### 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

**Resource Name:** Pegasus-fus

**Resource ID:** SCR\_012118

**Alternate IDs:** OMICS\_05584

**Record Creation Time:** 20220129T080308+0000

**Record Last Update:** 20260725T190729+0000

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### Ratings and Alerts

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

No alerts have been found for Pegasus-fus.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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### Usage and Citation Metrics

We found 14 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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).

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.

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

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.

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.

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.

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.

Zhao C, et al. (2016) Field warming experiments shed light on the wheat yield response to temperature in China. *Nature communications*, 7, 13530.

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.