

Resource Summary Report

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Phenote: A Phenotype Annotation Tool using Ontologies

RRID:SCR_008334

Type: Tool

Proper Citation

Phenote: A Phenotype Annotation Tool using Ontologies (RRID:SCR_008334)

Resource Information

URL: <http://www.phenote.org/>

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Description: Phenote is both a complete piece of software and a software toolkit designed to facilitate the annotation of biological phenotypes using ontologies. It provides an interface and infrastructure to record genotype-phenotype pairs, together with the provenance for the annotation. Typical users of Phenote include literature curators, laboratory researchers, and clinicians looking for a method to record data in a user-friendly and computable way. Features of Phenote include the use of any OBO-format ontology, ontology navigation and term information display, bulk sort, copy, edit, and delete of phenotype-genotype character entries, and a variety of export formats. Phenote is a project of the Berkeley Bioinformatics Open-Source Projects (BBOP).

Synonyms: Phenote

Resource Type: software resource, software toolkit

Keywords: biological, genotype, literature, ontology, phenotype, research, software, toolkit

Resource Name: Phenote: A Phenotype Annotation Tool using Ontologies

Resource ID: SCR_008334

Alternate IDs: nif-0000-24915

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260905T133240+0000

Ratings and Alerts

No rating or validation information has been found for Phenote: A Phenotype Annotation Tool using Ontologies.

No alerts have been found for Phenote: A Phenotype Annotation Tool using Ontologies.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Wang RL, et al. (2019) Ontology-based semantic mapping of chemical toxicities. Toxicology, 412, 89.

Oellrich A, et al. (2016) The digital revolution in phenotyping. Briefings in bioinformatics, 17(5), 819.

Costa M, et al. (2013) The Drosophila anatomy ontology. Journal of biomedical semantics, 4(1), 32.

Van Auken K, et al. (2012) Text mining in the biocuration workflow: applications for literature curation at WormBase, dictyBase and TAIR. Database : the journal of biological databases and curation, 2012, bas040.

Schindelman G, et al. (2011) Worm Phenotype Ontology: integrating phenotype data within and beyond the C. elegans community. BMC bioinformatics, 12, 32.