Resource Summary Report

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Genotype-to-Phenotype Databases: A Holistic Solution

RRID:SCR_013704
Type: Tool

Proper Citation

Genotype-to-Phenotype Databases: A Holistic Solution (RRID:SCR_013704)

Resource Information

URL: http://www.gen2phen.org/

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Description: The Genotype-to-Phenotype Databases (GEN2PHEN) consortium aims to create a web-based platform to capture and unify genetic information associated with health and disease progression. The focus of the consortium is to create an integrated genetic variation catalogue for the research community, with a focus on disorders such as diabetes, obesity, heart disease and cancer.

Abbreviations: GEN2PHEN

Resource Type: organization portal, data or information resource, consortium, portal

Keywords: data-sharing enabler, genetic information, diabetes, obesity, heart disease, cancer,

Funding: European Union FP7 Health Thematic Area of the Cooperation Programme

Resource Name: Genotype-to-Phenotype Databases: A Holistic Solution

Resource ID: SCR_013704

Record Creation Time: 20220129T080317+0000

Record Last Update: 20260903T235218+0000

Ratings and Alerts

No rating or validation information has been found for Genotype-to-Phenotype Databases: A Holistic Solution.

No alerts have been found for Genotype-to-Phenotype Databases: A Holistic Solution.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

C??rdova LDS, et al. (2021) Clinical characteristics of older patients with COVID-19: a systematic review of case reports. Dementia & neuropsychologia, 15(1), 1.

Viennas E, et al. (2017) Expanded national database collection and data coverage in the FINDbase worldwide database for clinically relevant genomic variation allele frequencies. Nucleic acids research, 45(D1), D846.

Adamusiak T, et al. (2014) Next generation phenotyping using the unified medical language system. JMIR medical informatics, 2(1), e5.

Cutting GR, et al. (2014) Annotating DNA variants is the next major goal for human genetics. American journal of human genetics, 94(1), 5.

Byrne M, et al. (2012) VarioML framework for comprehensive variation data representation and exchange. BMC bioinformatics, 13, 254.

Joly Y, et al. (2012) Data sharing in the post-genomic world: the experience of the International Cancer Genome Consortium (ICGC) Data Access Compliance Office (DACO). PLoS computational biology, 8(7), e1002549.

Georgitsi M, et al. (2011) FINDbase: a worldwide database for genetic variation allele frequencies updated. Nucleic acids research, 39(Database issue), D926.

Saccone SF, et al. (2010) SPOT: a web-based tool for using biological databases to prioritize SNPs after a genome-wide association study. Nucleic acids research, 38(Web Server issue), W201.

Mottaz A, et al. (2010) Easy retrieval of single amino-acid polymorphisms and phenotype information using SwissVar. Bioinformatics (Oxford, England), 26(6), 851.

Desmet FO, et al. (2009) Human Splicing Finder: an online bioinformatics tool to predict splicing signals. Nucleic acids research, 37(9), e67.

Thorisson GA, et al. (2009) HGVbaseG2P: a central genetic association database. Nucleic acids research, 37(Database issue), D797.