

Resource Summary Report

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GOLD.db - Genomics Of Lipid-associated Disorders

RRID:SCR_000736

Type: Tool

Proper Citation

GOLD.db - Genomics Of Lipid-associated Disorders (RRID:SCR_000736)

Resource Information

URL: <http://genome.tugraz.at/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented July 22, 2016. A database that integrates information on the function and properties of genes and their protein products relevant to lipid-associated disorders. GOLD.db provides information such as the biology, diagnosis management, treatment and prevention of such disorders like non-insulin dependent diabetes, various hyperlipidemias, high blood pressure and atherosclerosis. Resources include the biological pathways, data sets, microarray protocols and other experimental standards, analytical tools, and reagents.

Synonyms: Genomics Of Lipid-associated Disorders database, GOLD.db Genomics Of Lipid-associated Disorders, GOLD.db

Resource Type: data or information resource, database

Defining Citation: [PMID:15588328](#)

Keywords: lipid, disorder, diabetes, insulin, hyperlipidemia, blood pressure, atherosclerosis, microarray, reagent, biology

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GOLD.db - Genomics Of Lipid-associated Disorders

Resource ID: SCR_000736

Alternate IDs: nif-0000-02919

Alternate URLs: <http://gold.tugraz.at>

Record Creation Time: 20220129T080203+0000

Ratings and Alerts

No rating or validation information has been found for GOLD.db - Genomics Of Lipid-associated Disorders.

No alerts have been found for GOLD.db - Genomics Of Lipid-associated Disorders.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Huang WQ, et al. (2018) DNA Methylation Profiling Reveals the Change of Inflammation-Associated ZC3H12D in Leukoaraiosis. *Frontiers in aging neuroscience*, 10, 143.

Wang X, et al. (2018) An Integrated Approach of Proteomics and Computational Genetic Modification Effectiveness Analysis to Uncover the Mechanisms of Flood Tolerance in Soybeans. *International journal of molecular sciences*, 19(5).

Lian C, et al. (2018) Exploration of ABA Responsive miRNAs Reveals a New Hormone Signaling Crosstalk Pathway Regulating Root Growth of *Populus euphratica*. *International journal of molecular sciences*, 19(5).

Sang H, et al. (2018) A Xenobiotic Detoxification Pathway through Transcriptional Regulation in Filamentous Fungi. *mBio*, 9(4).

Surles-Zeigler MC, et al. (2018) Transcriptomic analysis of neuregulin-1 regulated genes following ischemic stroke by computational identification of promoter binding sites: A role for the ETS-1 transcription factor. *PloS one*, 13(6), e0197092.

Ma Y, et al. (2017) Overexpression of OsRRK1 Changes Leaf Morphology and Defense to Insect in Rice. *Frontiers in plant science*, 8, 1783.

Glaser LV, et al. (2017) EBF1 binds to EBNA2 and promotes the assembly of EBNA2 chromatin complexes in B cells. *PLoS pathogens*, 13(10), e1006664.

Kim S, et al. (2016) Impact of suppression of tumorigenicity 14 (ST14)/serine protease 14 (Prss14) expression analysis on the prognosis and management of estrogen receptor negative breast cancer. *Oncotarget*, 7(23), 34643.

Martin K, et al. (2016) Dynamic transcriptome profiling of Bean Common Mosaic Virus (BCMV) infection in Common Bean (*Phaseolus vulgaris* L.). *BMC genomics*, 17(1), 613.

- Wang Y, et al. (2016) Identification and Profiling of microRNAs Expressed in Elongating Cotton Fibers Using Small RNA Deep Sequencing. *Frontiers in plant science*, 7, 1722.
- Olivier JD, et al. (2014) The effects of antenatal depression and antidepressant treatment on placental gene expression. *Frontiers in cellular neuroscience*, 8, 465.
- Routaboul JM, et al. (2012) Metabolite profiling and quantitative genetics of natural variation for flavonoids in *Arabidopsis*. *Journal of experimental botany*, 63(10), 3749.
- O'Keefe DD, et al. (2012) Combinatorial control of temporal gene expression in the *Drosophila* wing by enhancers and core promoters. *BMC genomics*, 13, 498.
- Petitdemange C, et al. (2011) Unconventional repertoire profile is imprinted during acute chikungunya infection for natural killer cells polarization toward cytotoxicity. *PLoS pathogens*, 7(9), e1002268.
- Borjabad A, et al. (2011) Significant effects of antiretroviral therapy on global gene expression in brain tissues of patients with HIV-1-associated neurocognitive disorders. *PLoS pathogens*, 7(9), e1002213.
- Le Nou??n C, et al. (2011) Low CCR7-mediated migration of human monocyte derived dendritic cells in response to human respiratory syncytial virus and human metapneumovirus. *PLoS pathogens*, 7(6), e1002105.
- Xu L, et al. (2011) Lignin metabolism has a central role in the resistance of cotton to the wilt fungus *Verticillium dahliae* as revealed by RNA-Seq-dependent transcriptional analysis and histochemistry. *Journal of experimental botany*, 62(15), 5607.
- Votavova H, et al. (2011) Differential expression of microRNAs in CD34+ cells of 5q-syndrome. *Journal of hematology & oncology*, 4, 1.
- Palyada K, et al. (2009) Characterization of the oxidative stress stimulon and PerR regulon of *Campylobacter jejuni*. *BMC genomics*, 10, 481.
- Guo P, et al. (2009) Differentially expressed genes between drought-tolerant and drought-sensitive barley genotypes in response to drought stress during the reproductive stage. *Journal of experimental botany*, 60(12), 3531.