Resource Summary Report

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Online Encyclopedia for Genetic Epidemiology studies

RRID:SCR_001825
Type: Tool

Proper Citation

Online Encyclopedia for Genetic Epidemiology studies (RRID:SCR_001825)

Resource Information

URL: http://www.oege.org/

Proper Citation: Online Encyclopedia for Genetic Epidemiology studies (RRID:SCR_001825)

Description: Portal for researchers to locate information relevant to interpretation and follow-up of human genetic epidemiological discoveries, including: a range of population and case and family genetic epidemiological studies, relevant gene and sequence databases, genetic variation databases, trait measurement, resource labs, journals, software, general information, disease genes and genetic diversity.

Abbreviations: OEGE

Synonyms: OEGE - Online Encyclopedia for Genetic Epidemiology studies

Resource Type: data or information resource, topical portal, portal

Keywords: encyclopedia, epidemiology, gene, genealogist, genetic, genetic variation, diversity, health, journal, molecular genealogy, population genetics, sequence, software, trait, genome wide association study, genotyping, phenotyping, next generation sequencing, gene association study

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Online Encyclopedia for Genetic Epidemiology studies

Resource ID: SCR_001825

Alternate IDs: nif-0000-10388

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260729T044016+0000

Ratings and Alerts

No rating or validation information has been found for Online Encyclopedia for Genetic Epidemiology studies.

No alerts have been found for Online Encyclopedia for Genetic Epidemiology studies.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Fawzy MS, et al. (2022) MicroRNA-499a (rs3746444A/G) gene variant and susceptibility to type 2 diabetes-associated end-stage renal disease. Experimental and therapeutic medicine, 23(1), 63.

Opdal SH, et al. (2021) Aquaporin-1 and aquaporin-9 gene variations in sudden infant death syndrome. International journal of legal medicine, 135(3), 719.

Huang Y, et al. (2019) Biochemical metabolic levels and vitamin D receptor Fok??? gene polymorphisms in Uyghur children with urolithiasis. PloS one, 14(2), e0212183.

Arama C, et al. (2018) Malaria severity: Possible influence of the E670G PCSK9 polymorphism: A preliminary case-control study in Malian children. PloS one, 13(2), e0192850.

Shumay E, et al. (2017) New Repeat Polymorphism in the AKT1 Gene Predicts Striatal Dopamine D2/D3 Receptor Availability and Stimulant-Induced Dopamine Release in the Healthy Human Brain. The Journal of neuroscience : the official journal of the Society for Neuroscience, 37(19), 4982.

Neamati N, et al. (2017) The ENPP1 K121Q polymorphism modulates developing of bone disorders in type 2 diabetes: A cross sectional study. Gene, 637, 100.

Aslam R, et al. (2016) SOCS3 mRNA expression and polymorphisms as pretreatment predictor of response to HCV genotype 3a IFN-based treatment. SpringerPlus, 5(1), 1826.

Smolarz B, et al. (2015) Gly322Asp and Asn127Ser single nucleotide polymorphisms (SNPs) of hMSH2 mismatch repair gene and the risk of triple-negative breast cancer in Polish women. Familial cancer, 14(1), 81.

Lou DI, et al. (2014) Rapid evolution of BRCA1 and BRCA2 in humans and other primates. BMC evolutionary biology, 14, 155.

Schmid F, et al. (2012) SNPs in the coding region of the metastasis-inducing gene MACC1 and clinical outcome in colorectal cancer. Molecular cancer, 11, 49.

Nava-Salazar S, et al. (2011) Polymorphisms in the hypoxia-inducible factor 1 alpha gene in Mexican patients with preeclampsia: A case-control study. BMC research notes, 4, 68.

Heino S, et al. (2008) Non-synonymous sequence variants within the oxygen-dependent degradation domain of the HIF1A gene are not associated with pre-eclampsia in the Finnish population. BMC medical genetics, 9, 96.