

Resource Summary Report

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TIGER Data Portal

RRID:SCR_023626

Type: Tool

Proper Citation

TIGER Data Portal (RRID:SCR_023626)

Resource Information

URL: <http://tiger.bsc.es>

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Description: Resource enables integrative exploration of genetic and epigenetic basis of development of Type 2 Diabetes, together with other associated functional, molecular and clinical data, centered in biology and role of pancreatic beta cells. The gene expression regulatory variation landscape of human pancreatic islets.

Synonyms: Translational Human Pancreatic Islet Genotype Tissue-Expression Resource

Resource Type: disease-related portal, data or information resource, topical portal, portal

Defining Citation: [PMID:34644572](#)

Keywords: Type 2 Diabetes, genetic and epigenetic, functional data, molecular data, clinical data, pancreatic beta cells.

Related Condition: Type 2 Diabetes

Funding: European Union Horizon 2020 ;
Spanish government ;
Swiss State Secretariat for Education??? Research and Innovation ;
American Diabetes Association Innovative and Clinical Translational Award ;
Research England ;
Wellcome Trust ;
NIDDK U01 DK105535;
NIDDK U01 DK085545

Resource Name: TIGER Data Portal

Resource ID: SCR_023626

Record Creation Time: 20230527T050216+0000

Ratings and Alerts

No rating or validation information has been found for TIGER Data Portal.

No alerts have been found for TIGER Data Portal.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Zhang J, et al. (2025) The landscape of immunogenic cell death-related genes predicts the overall survival and immune infiltration status of non-small-cell lung carcinoma. *Heliyon*, 11(1), e40869.

Bocher O, et al. (2025) Unravelling the molecular mechanisms causal to type 2 diabetes across global populations and disease-relevant tissues. *medRxiv : the preprint server for health sciences*.

Kuo P, et al. (2025) Histone variant H2A.W7 represses meiotic crossover formation in *Arabidopsis* heterochromatin. *Proceedings of the National Academy of Sciences of the United States of America*, 122(22), e2414166122.

Yu SL, et al. (2024) Speeding genomic island discovery through systematic design of reference database composition. *PloS one*, 19(3), e0298641.

Zhu L, et al. (2024) The kinase ATR controls meiotic crossover distribution at the genome scale in *Arabidopsis*. *The Plant cell*, 37(1).

Nelson HM, et al. (2024) Transfer of miR-100 and miR-125b increases 3D growth and invasiveness in recipient cancer cells. *Extracellular vesicles and circulating nucleic acids*, 5(3), 397.

Huerta-Chagoya A, et al. (2024) Rare variant analyses in 51,256 type 2 diabetes cases and 370,487 controls reveal the pathogenicity spectrum of monogenic diabetes genes. *Nature genetics*, 56(11), 2370.

Meulebrouck S, et al. (2024) Functional genetics reveals the contribution of delta opioid receptor to type 2 diabetes and beta-cell function. *Nature communications*, 15(1), 6627.

Maina JG, et al. (2023) Bidirectional Mendelian Randomization and Multiphenotype GWAS Show Causality and Shared Pathophysiology Between Depression and Type 2 Diabetes. *Diabetes care*, 46(9), 1707.

Erlenbach T, et al. (2023) Investigating the phylogenetic history of toxin tolerance in mushroom-feeding *Drosophila*. *Ecology and evolution*, 13(12), e10736.

Schroeder P, et al. (2023) Rare variant association analysis in 51,256 type 2 diabetes cases and 370,487 controls informs the spectrum of pathogenicity of monogenic diabetes genes. *medRxiv : the preprint server for health sciences*.

Lagou V, et al. (2023) GWAS of random glucose in 476,326 individuals provide insights into diabetes pathophysiology, complications and treatment stratification. *Nature genetics*, 55(9), 1448.

Karvinen S, et al. (2023) Extracellular vesicles and high-density lipoproteins: Exercise and oestrogen-responsive small RNA carriers. *Journal of extracellular vesicles*, 12(2), e12308.

Lambing C, et al. (2020) ASY1 acts as a dosage-dependent antagonist of telomere-led recombination and mediates crossover interference in *Arabidopsis*. *Proceedings of the National Academy of Sciences of the United States of America*, 117(24), 13647.

Turmel M, et al. (2017) Divergent copies of the large inverted repeat in the chloroplast genomes of ulvophyceean green algae. *Scientific reports*, 7(1), 994.

Lu TM, et al. (2017) The phylogenetic position of dicyemid mesozoans offers insights into spiralian evolution. *Zoological letters*, 3, 6.

Sahoo RK, et al. (2017) Hostplant change and paleoclimatic events explain diversification shifts in skipper butterflies (Family: Hesperiidae). *BMC evolutionary biology*, 17(1), 174.

Yelina NE, et al. (2015) DNA methylation epigenetically silences crossover hot spots and controls chromosomal domains of meiotic recombination in *Arabidopsis*. *Genes & development*, 29(20), 2183.