Resource Summary Report

Generated by NIF on May 25, 2025

Imprinted Gene Catalogue

RRID:SCR_007737
Type: Tool

Proper Citation

Imprinted Gene Catalogue (RRID:SCR_007737)

Resource Information

URL: http://www.otago.ac.nz/IGC

Proper Citation: Imprinted Gene Catalogue (RRID:SCR_007737)

Description: The Imprinted Gene Catalogue is a database of imprinted genes and related effects in humans and animals. Users can search the Imprinted genes and related effects database by taxon, chromosome, gene name, or a text word from the description. Users can also search the Catalogue of Parental Origin of de novo Mutations by type of mutation, disorder, chromosomal location, inheritance pattern, gene name, or author of publication. There are also many detailed entries which provide a cross-species summary of imprinted genes.

Synonyms: Imprinted Gene Catalogue

Resource Type: data or information resource, database

Funding:

Resource Name: Imprinted Gene Catalogue

Resource ID: SCR_007737

Alternate IDs: nif-0000-03019

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250525T032310+0000

Ratings and Alerts

No rating or validation information has been found for Imprinted Gene Catalogue.

No alerts have been found for Imprinted Gene Catalogue.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Xue H, et al. (2024) Genetic testing for fetal loss of heterozygosity using single nucleotide polymorphism array and whole-exome sequencing. Scientific reports, 14(1), 2190.

Genova F, et al. (2018) First genome-wide CNV mapping in FELIS CATUS using next generation sequencing data. BMC genomics, 19(1), 895.

Hamed M, et al. (2017) Linking Hematopoietic Differentiation to Co-Expressed Sets of Pluripotency-Associated and Imprinted Genes and to Regulatory microRNA-Transcription Factor Motifs. PloS one, 12(1), e0166852.

Andergassen D, et al. (2017) Mapping the mouse Allelome reveals tissue-specific regulation of allelic expression. eLife, 6.

McKean DM, et al. (2016) Loss of RNA expression and allele-specific expression associated with congenital heart disease. Nature communications, 7, 12824.

Andergassen D, et al. (2015) Allelome.PRO, a pipeline to define allele-specific genomic features from high-throughput sequencing data. Nucleic acids research, 43(21), e146.

Tasiou V, et al. (2015) A Mouse Model for Imprinting of the Human Retinoblastoma Gene. PloS one, 10(8), e0134672.

Finn EH, et al. (2014) Maternal bias and escape from X chromosome imprinting in the midgestation mouse placenta. Developmental biology, 390(1), 80.

Hannula-Jouppi K, et al. (2014) Differentially methylated regions in maternal and paternal uniparental disomy for chromosome 7. Epigenetics, 9(3), 351.

Anwar SL, et al. (2012) Loss of imprinting and allelic switching at the DLK1-MEG3 locus in human hepatocellular carcinoma. PloS one, 7(11), e49462.

Berg JS, et al. (2011) Imprinted genes that regulate early mammalian growth are coexpressed in somatic stem cells. PloS one, 6(10), e26410.

Bell CG, et al. (2010) Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. PloS one, 5(11), e14040.

Guo L, et al. (2008) Altered gene expression and methylation of the human chromosome 11 imprinted region in small for gestational age (SGA) placentae. Developmental biology, 320(1), 79.

Eichenlaub-Ritter U, et al. (2007) Gender differences in germ-cell mutagenesis and genetic risk. Environmental research, 104(1), 22.

Reamon-Buettner SM, et al. (2007) A new paradigm in toxicology and teratology: altering gene activity in the absence of DNA sequence variation. Reproductive toxicology (Elmsford, N.Y.), 24(1), 20.

Khatib H, et al. (2007) Comparative analysis of sequence characteristics of imprinted genes in human, mouse, and cattle. Mammalian genome : official journal of the International Mammalian Genome Society, 18(6-7), 538.

Hipp J, et al. (2006) GeneChips in stem cell research. Methods in enzymology, 420, 162.

Glaser RL, et al. (2006) The imprinted gene and parent-of-origin effect database now includes parental origin of de novo mutations. Nucleic acids research, 34(Database issue), D29.

Park CW, et al. (2006) Sleeping Beauty transposition in the mouse genome is associated with changes in DNA methylation at the site of insertion. Genomics, 88(2), 204.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.