

Resource Summary Report

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Zebrafish Genome Project

RRID:SCR_013157

Type: Tool

Proper Citation

Zebrafish Genome Project (RRID:SCR_013157)

Resource Information

URL: http://www.sanger.ac.uk/Projects/D_rerio/

Proper Citation: Zebrafish Genome Project (RRID:SCR_013157)

Description: Database of zebrafish genome.

Synonyms: Danio rerio Sequencing Project

Resource Type: data or information resource, database

Keywords: Zebrafish, genome

Availability: Free, Freely available

Resource Name: Zebrafish Genome Project

Resource ID: SCR_013157

Alternate IDs: SCR_017503, nif-0000-31931

Alternate URLs: <https://www.sanger.ac.uk/science/data/zebrafish-genome-project>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260804T043509+0000

Ratings and Alerts

No rating or validation information has been found for Zebrafish Genome Project.

No alerts have been found for Zebrafish Genome Project.

Data and Source Information

Usage and Citation Metrics

We found 67 mentions in open access literature.

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

Kuo MW, et al. (2021) Yulink, predicted from evolutionary analysis, is involved in cardiac function. *Journal of biomedical science*, 28(1), 7.

Garland MA, et al. (2019) Glucocorticoid receptor-dependent induction of cripto-1 (one-eyed pinhead) inhibits zebrafish caudal fin regeneration. *Toxicology reports*, 6, 529.

Celauro E, et al. (2017) Functional analysis of the cfdp1 gene in zebrafish provides evidence for its crucial role in craniofacial development and osteogenesis. *Experimental cell research*, 361(2), 236.

Orosz F, et al. (2015) On the tubulin polymerization promoting proteins of zebrafish. *Biochemical and biophysical research communications*, 457(3), 267.

Caballero J, et al. (2014) Realistic artificial DNA sequences as negative controls for computational genomics. *Nucleic acids research*, 42(12), e99.

Zhou Y, et al. (2014) A vertebrate model for the study of lipid binding/transfer protein function: conservation of OSBP-related proteins between zebrafish and human. *Biochemical and biophysical research communications*, 446(3), 675.

Nemudryi AA, et al. (2014) TALEN and CRISPR/Cas Genome Editing Systems: Tools of Discovery. *Acta naturae*, 6(3), 19.

Schneider VA, et al. (2013) Clone DB: an integrated NCBI resource for clone-associated data. *Nucleic acids research*, 41(Database issue), D1070.

Thomas-Jinu S, et al. (2013) Dynamic expression of neurexophilin1 during zebrafish embryonic development. *Gene expression patterns : GEP*, 13(8), 395.

Fritz JV, et al. (2013) From meta-omics to causality: experimental models for human microbiome research. *Microbiome*, 1(1), 14.

Sun C, et al. (2012) LTR retrotransposons contribute to genomic gigantism in plethodontid salamanders. *Genome biology and evolution*, 4(2), 168.

Fang L, et al. (2012) Emerging applications for zebrafish as a model organism to study oxidative mechanisms and their roles in inflammation and vascular accumulation of oxidized lipids. *Free radical biology & medicine*, 53(7), 1411.

Goldsmith JR, et al. (2012) Think small: zebrafish as a model system of human pathology. *Journal of biomedicine & biotechnology*, 2012, 817341.

Voz ML, et al. (2012) Fast homozygosity mapping and identification of a zebrafish ENU-induced mutation by whole-genome sequencing. *PloS one*, 7(4), e34671.

Graham LA, et al. (2012) Smelt was the likely beneficiary of an antifreeze gene laterally transferred between fishes. *BMC evolutionary biology*, 12, 190.

Yuelling LW, et al. (2012) Autotaxin/ENPP2 regulates oligodendrocyte differentiation in vivo in the developing zebrafish hindbrain. *Glia*, 60(10), 1605.

Costa AC, et al. (2012) Multidimensional scaling applied to histogram-based DNA analysis. *Comparative and functional genomics*, 2012, 289694.

Marianes AE, et al. (2011) Targets of somatic hypermutation within immunoglobulin light chain genes in zebrafish. *Immunology*, 132(2), 240.

Baldo L, et al. (2011) Comparative transcriptomics of Eastern African cichlid fishes shows signs of positive selection and a large contribution of untranslated regions to genetic diversity. *Genome biology and evolution*, 3, 443.

Jain RA, et al. (2011) Molecular-genetic mapping of zebrafish mutants with variable phenotypic penetrance. *PloS one*, 6(10), e26510.