

# Resource Summary Report

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## UT Genome Browser (Medaka)

RRID:SCR\_005857

Type: Tool

### Proper Citation

UT Genome Browser (Medaka) (RRID:SCR\_005857)

### Resource Information

**URL:** <http://medaka.utgenome.org/>

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**Description:** A website containing the complete sequenced genome of the medaka fish. It presents a high-quality draft genome sequence of a small egg-laying freshwater teleost, medaka (*Oryzias latipes*). Medaka is native to East Asia and an excellent model system for a wide range of biology, including ecotoxicology, carcinogenesis, sex determination<sup>4</sup>, 5, 6 and developmental genetics<sup>7</sup>. In the assembled medaka genome (700 megabases), which is less than half of the zebrafish genome, we predicted 20,141 genes, including approx 2,900 new genes, using 5'??-end serial analysis of gene expression tag information. We found single nucleotide polymorphisms (SNPs) at an average rate of 3.42% between the two inbred strains derived from two regional populations; this is the highest SNP rate seen in any vertebrate species. Analyses based on the dense SNP information show a strict genetic separation of 4 million years (Myr) between the two populations, and suggest that differential selective pressures acted on specific gene categories. Four-way comparisons with the human, pufferfish (*Tetraodon*), zebrafish and medaka genomes revealed that eight major interchromosomal rearrangements took place in a remarkably short period of approx 50 Myr after the whole-genome duplication event in the teleost ancestor and afterwards, intriguingly, the medaka genome preserved its ancestral karyotype for more than 300 Myr.

**Synonyms:** UTGB medaka

**Resource Type:** database, data or information resource

**Resource Name:** UT Genome Browser (Medaka)

**Resource ID:** SCR\_005857

**Alternate IDs:** nif-0000-03618

**Record Creation Time:** 20220129T080232+0000

## Ratings and Alerts

No rating or validation information has been found for UT Genome Browser (Medaka).

No alerts have been found for UT Genome Browser (Medaka).

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Salindeho RA, et al. (2024) Re-sequencing of the complete chloroplast genome of *Cinnamomum burmanni* (Nees & T.Nees) Blume (Lauraceae) from Indonesia using MinION Oxford Nanopore Technologies. *F1000Research*, 13, 127.

Ishikawa T, et al. (2010) High-resolution melting curve analysis for rapid detection of mutations in a Medaka TILLING library. *BMC molecular biology*, 11, 70.

Sasado T, et al. (2008) Distinct contributions of CXCR4b and CXCR7/RDC1 receptor systems in regulation of PGC migration revealed by medaka mutants *kazura* and *yanagi*. *Developmental biology*, 320(2), 328.

Sugawara H, et al. (2007) DDBJ working on evaluation and classification of bacterial genes in INSDC. *Nucleic acids research*, 35(Database issue), D13.

Del Bene F, et al. (2007) In vivo validation of a computationally predicted conserved *Ath5* target gene set. *PLoS genetics*, 3(9), 1661.

Soroldoni D, et al. (2007) Dynamic expression pattern of Nodal-related genes during left-right development in medaka. *Gene expression patterns : GEP*, 7(1-2), 93.

Hochmann S, et al. (2007) Expression of marker genes during early ear development in medaka. *Gene expression patterns : GEP*, 7(3), 355.

Saito D, et al. (2007) Proliferation of germ cells during gonadal sex differentiation in medaka: Insights from germ cell-depleted mutant *zenzai*. *Developmental biology*, 310(2), 280.

Su F, et al. (2007) Radiation hybrid maps of Medaka chromosomes LG 12, 17, and 22. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 14(3), 135.

Yoshihama M, et al. (2006) Analysis of ribosomal protein gene structures: implications for intron evolution. *PLoS genetics*, 2(3), e25.