

Resource Summary Report

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Fugu Genome Project

RRID:SCR_013014

Type: Tool

Proper Citation

Fugu Genome Project (RRID:SCR_013014)

Resource Information

URL: <http://www.fugu-sg.org/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE,documented on August 16, 2019. Fugu genome is among the smallest vertebrate genomes and has proved to be a valuable reference genome for identifying genes and other functional elements such as regulatory elements in the human and other vertebrate genomes, and for understanding the structure and evolution of vertebrate genomes. This site presents version 4 of the Fugu genome, released in October 2004 by the International Fugu Genome Consortium. Fugu rubripes has a very compact genome, with less than 15 consisting of dispersed repetitive sequence, which makes it ideal for gene discovery. A draft sequence of the fugu genome was determined by the International Fugu Genome Consortium in 2002 using the "whole-genome shotgun" sequencing strategy. Fugu is the second vertebrate genome to be sequenced, the first being the human genome. This webpage presents the annotation made on the fourth assembly by the IMCB team using the Ensembl annotation pipeline. We are continuing with the gap filling work and linking of the scaffolds to obtain super-contigs.

Synonyms: FGP

Resource Type: data or information resource, database

Keywords: element, evolution, fish, fugu, functional, gene, genome, human, pufferfish, regulatory, rubripes, structure, vertebrate, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Fugu Genome Project

Resource ID: SCR_013014

Alternate IDs: biotools:fugu-sg, nif-0000-20988

Alternate URLs: <https://bio.tools/fugu-sg>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260905T133203+0000

Ratings and Alerts

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

No alerts have been found for Fugu Genome Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Amini-Farsani Z, et al. (2020) The impact of miR-183/182/96 gene regulation on the maturation, survival, and function of photoreceptor cells in the retina. The Journal of comparative neurology, 528(9), 1616.

Shakur Ahammad AK, et al. (2019) Multiple transcription factors mediating the expressional regulation of myosin heavy chain gene involved in the indeterminate muscle growth of fish. Gene, 687, 308.

Fu X, et al. (2017) Immunoglobulin light chain (IGL) genes in torafugu: Genomic organization and identification of a third teleost IGL isotype. Scientific reports, 7, 40416.

Shahjahan M, et al. (2015) Differential expression patterns of PQRamide peptide and its two receptor genes in the brain and pituitary of grass puffer during the reproductive cycle. General and comparative endocrinology, 210, 152.

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

Luo J, et al. (2014) Teaching the ABCs of bioinformatics: a brief introduction to the Applied Bioinformatics Course. Briefings in bioinformatics, 15(6), 1004.

Hiller M, et al. (2013) Computational methods to detect conserved non-genic elements in phylogenetically isolated genomes: application to zebrafish. Nucleic acids research, 41(15), e151.

Rakshambikai R, et al. (2012) Repertoire of Protein Kinases Encoded in the Genome of Takifugu rubripes. Comparative and functional genomics, 2012, 258284.

Kai W, et al. (2011) Integration of the genetic map and genome assembly of fugu facilitates insights into distinct features of genome evolution in teleosts and mammals. *Genome biology and evolution*, 3, 424.

Oba Y, et al. (2011) Purification and characterization of tributyltin-binding protein of tiger puffer, *Takifugu rubripes*. *Comparative biochemistry and physiology. Toxicology & pharmacology : CBP*, 153(1), 17.

Tognoli C, et al. (2010) Acute stress alters transcript expression pattern and reduces processing of proBDNF to mature BDNF in *Dicentrarchus labrax*. *BMC neuroscience*, 11, 4.

Zenke K, et al. (2008) Novel fugu U6 promoter driven shRNA expression vector for efficient vector based RNAi in fish cell lines. *Biochemical and biophysical research communications*, 371(3), 480.

Wang Y, et al. (2008) Comparative genomic study reveals a transition from TA richness in invertebrates to GC richness in vertebrates at CpG flanking sites: an indication for context-dependent mutagenicity of methylated CpG sites. *Genomics, proteomics & bioinformatics*, 6(3-4), 144.

Aihara Y, et al. (2007) Transgenic labeling of taste receptor cells in model fish under the control of the 5'-upstream region of medaka phospholipase C-beta 2 gene. *Gene expression patterns : GEP*, 7(1-2), 149.

Venkatesh B, et al. (2006) Fugu genome does not contain mitochondrial pseudogenes. *Genomics*, 87(2), 307.

Cockram GP, et al. (2006) Identification and characterization of the DNA-binding properties of a Zhangfei homologue in Japanese pufferfish, *Takifugu rubripes*. *Biochemical and biophysical research communications*, 339(4), 1238.

Eckert D, et al. (2005) The AP-2 family of transcription factors. *Genome biology*, 6(13), 246.

Fuchs C, et al. (2005) Duplicated cytoglobin genes in teleost fishes. *Biochemical and biophysical research communications*, 337(1), 216.

Bekpen C, et al. (2005) The interferon-inducible p47 (IRG) GTPases in vertebrates: loss of the cell autonomous resistance mechanism in the human lineage. *Genome biology*, 6(11), R92.

Lethimonier C, et al. (2004) Evolutionary aspects of GnRHs, GnRH neuronal systems and GnRH receptors in teleost fish. *General and comparative endocrinology*, 135(1), 1.