

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Pre Ensembl

RRID:SCR_006766

Type: Tool

Proper Citation

Pre Ensembl (RRID:SCR_006766)

Resource Information

URL: <http://pre.ensembl.org/index.html>

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Description: Database of genomes that are in the process of being annotated are provided as an early access site for users. Genomes are here when the initial BLAST analysis on a new assembly has been done but the gene build has not been completed. Owing to the preliminary nature of the data, Pre-Ensembl provides views of the assembly, BLAST against the assembly and download of portions of the assembly - and little else. A number of ready-made tools for processing your data are also available. In general a full Ensembl release takes months depending on how complex the data are and the time constraints of people in the team. Occasionally a more complete gene build will be released on this site, but without any comparative genomics, variation or other additional data. Many other species with fully annotated genomic data, more website features and documentation are available at www.ensembl.org

Abbreviations: Pre Ensembl, Pre-Ensembl, Pre!Ensembl, Pre! Ensembl

Synonyms: Ensemble Pre-release Genome Browser, Ensembl pre-build, PreEnsembl

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Keywords: genome, annotation, blast, blat, assembly

Resource Name: Pre Ensembl

Resource ID: SCR_006766

Alternate IDs: nlx_152112

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260905T132600+0000

Ratings and Alerts

No rating or validation information has been found for Pre Ensembl.

No alerts have been found for Pre Ensembl.

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](#) .

Chen S, et al. (2026) Diversity-triggered 2-naphthoic acid exudation recruits keystone microbial taxa to promote soybean drought tolerance. *Cell host & microbe*, 34(5), 844.

Diao C, et al. (2018) Identification and analysis of key genes in osteosarcoma using bioinformatics. *Oncology letters*, 15(3), 2789.

Hultqvist G, et al. (2017) Emergence and evolution of an interaction between intrinsically disordered proteins. *eLife*, 6.

Åberg E, et al. (2017) Evolution of the p53-MDM2 pathway. *BMC evolutionary biology*, 17(1), 177.

Yates A, et al. (2016) Ensembl 2016. *Nucleic acids research*, 44(D1), D710.

Grone BP, et al. (2015) A second corticotropin-releasing hormone gene (CRH2) is conserved across vertebrate classes and expressed in the hindbrain of a basal neopterygian fish, the spotted gar (*Lepisosteus oculatus*). *The Journal of comparative neurology*, 523(7), 1125.

Cunningham F, et al. (2015) Ensembl 2015. *Nucleic acids research*, 43(Database issue), D662.

Onimaru K, et al. (2015) A shift in anterior-posterior positional information underlies the fin-to-limb evolution. *eLife*, 4.

Schwarze K, et al. (2015) The Full Globin Repertoire of Turtles Provides Insights into Vertebrate Globin Evolution and Functions. *Genome biology and evolution*, 7(7), 1896.

Irwin DM, et al. (2014) Evolution of receptors for peptides similar to glucagon. *General and comparative endocrinology*, 209, 50.

Mulley JF, et al. (2014) Genomic organisation of the seven ParaHox genes of coelacanth. *Journal of experimental zoology. Part B, Molecular and developmental evolution*, 322(6), 352.

Yao Q, et al. (2014) Molecular cloning, expression and characterization of Pekin duck interferon- γ . *Gene*, 548(1), 29.

Bhat R, et al. (2014) Structural divergence in vertebrate phylogeny of a duplicated prototype galectin. *Genome biology and evolution*, 6(10), 2721.

Pasquier J, et al. (2014) Looking for the bird Kiss: evolutionary scenario in sauropsids. *BMC evolutionary biology*, 14(1), 30.

Henriksen C, et al. (2013) Molecular cloning and characterization of porcine Na⁺/K⁺-ATPase isoforms α 1, α 2, α 3 and the ATP1A3 promoter. *PloS one*, 8(11), e79127.

Crespo B, et al. (2013) foxl2 and foxl3 are two ancient paralogs that remain fully functional in teleosts. *General and comparative endocrinology*, 194, 81.

Paixão-Côrtes VR, et al. (2013) Evolutionary history of chordate PAX genes: dynamics of change in a complex gene family. *PloS one*, 8(9), e73560.

Bhuiyan SS, et al. (2013) Evolution of the myosin heavy chain gene MYH14 and its intronic microRNA miR-499: muscle-specific miR-499 expression persists in the absence of the ancestral host gene. *BMC evolutionary biology*, 13, 142.

Jiang Z, et al. (2011) Evolution of trefoil factor(s): genetic and spatio-temporal expression of trefoil factor 2 in the chicken (*Gallus gallus domesticus*). *PloS one*, 6(7), e22691.

Nascimento FF, et al. (2011) Evolution of endogenous retroviruses in the Suidae: evidence for different viral subpopulations in African and Eurasian host species. *BMC evolutionary biology*, 11, 139.