

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

Selectome: a Database of Positive Selection

RRID:SCR_004542

Type: Tool

Proper Citation

Selectome: a Database of Positive Selection (RRID:SCR_004542)

Resource Information

URL: <http://selectome.unil.ch/>

Proper Citation: Selectome: a Database of Positive Selection (RRID:SCR_004542)

Description: Database of positive selection based on a rigorous branch-site specific likelihood test. Positive selection is detected using CODEML on all branches of animal gene trees.

Synonyms: Selectome

Resource Type: data or information resource, database

Defining Citation: [PMID:24225318](#)

Keywords: duplication, events, gene, animal, positive selection, speciation, p-value, speciation, duplication, selectome, phylogenetic, bio.tools

Resource Name: Selectome: a Database of Positive Selection

Resource ID: SCR_004542

Alternate IDs: nif-0000-03451, biotools:selectome

Alternate URLs: <https://bio.tools/selectome>

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260729T044104+0000

Ratings and Alerts

No rating or validation information has been found for Selectome: a Database of Positive Selection.

No alerts have been found for Selectome: a Database of Positive Selection.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Bhuiyan SA, et al. (2023) Harmonized cross-species cell atlases of trigeminal and dorsal root ganglia. bioRxiv : the preprint server for biology.

Jaron KS, et al. (2022) Convergent consequences of parthenogenesis on stick insect genomes. Science advances, 8(8), eabg3842.

Ahmad HI, et al. (2020) Adaptive evolution of peptidoglycan recognition protein family regulates the innate signaling against microbial pathogens in vertebrates. Microbial pathogenesis, 147, 104361.

Li Y, et al. (2020) Pacific Biosciences assembly with Hi-C mapping generates an improved, chromosome-level goose genome. GigaScience, 9(10).

Davydov II, et al. (2019) Large-Scale Comparative Analysis of Codon Models Accounting for Protein and Nucleotide Selection. Molecular biology and evolution, 36(6), 1316.

Daub JT, et al. (2017) Detection of Pathways Affected by Positive Selection in Primate Lineages Ancestral to Humans. Molecular biology and evolution, 34(6), 1391.

Bakken TE, et al. (2016) A comprehensive transcriptional map of primate brain development. Nature, 535(7612), 367.

Pybus M, et al. (2014) 1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. Nucleic acids research, 42(Database issue), D903.