

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

Baitfisher

RRID:SCR_015985

Type: Tool

Proper Citation

Baitfisher (RRID:SCR_015985)

Resource Information

URL: <https://github.com/cmayer/BaitFisher-package>

Proper Citation: Baitfisher (RRID:SCR_015985)

Description: Software toolkit for multispecies target DNA enrichment probe design. It consists of two programs: BaitFisher and BaitFilter, which are designed to construct hybrid enrichment baits for multiple sequence alignments or annotated features in multiple sequence alignments.

Resource Type: image analysis software, software toolkit, alignment software, software application, data processing software, software resource

Defining Citation: [PMID:27009209](#), [DOI:10.1093/molbev/msw056](#)

Keywords: software, package, multispecies, comparative, genomics, hybrid, enrichment, DNA, probe, design, sequence, alignments

Funding: German Research Foundation (DFG) OH81/9-1; NI 1387/1-1;
Spanish Ministry of Science and Education (MEC) RYC-2014-15615

Availability: Free, Available for download

Resource Name: Baitfisher

Resource ID: SCR_015985

Alternate IDs: OMICS_11740

Old URLs: <https://sources.debian.org/src/baitview/>

License: GPL-3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260801T190533+0000

Ratings and Alerts

No rating or validation information has been found for Baitfisher.

No alerts have been found for Baitfisher.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Loera-S??nchez M, et al. (2022) A multispecies amplicon sequencing approach for genetic diversity assessments in grassland plant species. *Molecular ecology resources*, 22(5), 1725.

Alanko JN, et al. (2022) Syotti: scalable bait design for DNA enrichment. *Bioinformatics* (Oxford, England), 38(Suppl 1), i177.

Stringer DN, et al. (2021) Development and evaluation of a custom bait design based on 469 single-copy protein-coding genes for exon capture of isopods (Philosciidae: Haloniscus). *PloS one*, 16(9), e0256861.

Quek RZB, et al. (2020) Transcriptome-based target-enrichment baits for stony corals (Cnidaria: Anthozoa: Scleractinia). *Molecular ecology resources*, 20(3), 807.

Sann M, et al. (2018) Phylogenomic analysis of Apoidea sheds new light on the sister group of bees. *BMC evolutionary biology*, 18(1), 71.