

Resource Summary Report

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abSENSE

RRID:SCR_023223

Type: Tool

Proper Citation

abSENSE (RRID:SCR_023223)

Resource Information

URL: <https://github.com/caraweisman/abSENSE>

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Description: Software to interpret undetected homolog.Method that calculates probability that homolog of given gene would fail to be detected by homology search in given species, even if homolog were present and evolving normally.

Resource Type: source code, software resource

Defining Citation: [PMID:33137085](#)

Keywords: undetected homolog, gene homolog detection failure, homology search, lineage-specific genes, homology detection failure

Funding: Howard Hughes Medical Institute ;
NHGRI R01-HG009116;
NIGMS RO1-GM43987;
NSF 1764269;
Simons Center for the Mathematical and Statistical Analysis of Biology 594596;
Harvard University

Availability: Free, Available for download, Freely available

Resource Name: abSENSE

Resource ID: SCR_023223

Alternate URLs: <http://www.eddylab.org/abSENSE/>

Record Creation Time: 20230202T050240+0000

Record Last Update: 20260729T044553+0000

Ratings and Alerts

No rating or validation information has been found for abSENSE.

No alerts have been found for abSENSE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Chang CH, et al. (2023) Expansion and loss of sperm nuclear basic protein genes in *Drosophila* correspond with genetic conflicts between sex chromosomes. *eLife*, 12.