

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Amplify

RRID:SCR_002956

Type: Tool

Proper Citation

Amplify (RRID:SCR_002956)

Resource Information

URL: <http://engels.genetics.wisc.edu/amplify/>

Proper Citation: Amplify (RRID:SCR_002956)

Description: A freeware Macintosh program for simulating and testing polymerase chain reactions (PCRs) that can also be used as a tool for designing primers by evaluating candidates. It's a program to simulate the polymerase chain reaction. You specify a target sequence and primers, and it predicts the result. It's useful for planning experiments, testing primers and teaching about PCR. Amplify draws a diagram of the predicted results showing all expected primer matches and amplified fragments. Clicking on any of these objects gives additional information about them.

Abbreviations: Amplify

Synonyms: Amplify 3

Resource Type: simulation software, software application, software resource

Keywords: amplify, simulation, polymerase chain reaction, macos x, primer design, target sequence, primer

Availability: Free, Available for download, Freely available

Resource Name: Amplify

Resource ID: SCR_002956

Alternate IDs: nif-0000-30103

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260903T234554+0000

Ratings and Alerts

No rating or validation information has been found for Amplify.

No alerts have been found for Amplify.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 553 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Tóth AG, et al. (2026) Protocol for the assessment of the impact of mycotoxins and glyphosate residues on the gut microbiome and resistome of European fallow deer. STAR protocols, 7(2), 104498.

Fang X, et al. (2026) Protocol for identifying cell-type-specific genes associated with disease risk using single-cell eQTL data. STAR protocols, 7(2), 104545.

Zhang D, et al. (2026) Protocol for KAT8 conditional knockout mice generation and its application in 4NQO-induced esophageal tumor model. STAR protocols, 7(1), 104384.

Wu S, et al. (2026) Machine learning-driven identification of shared and disease-specific mitochondria-related genes in COPD, NSCLC, and NSCLC with COPD. iScience, 29(3), 114857.

Lukes ME, et al. (2026) Protocol for validating computationally predicted splice-altering variants using full-length gene reporter assays. STAR protocols, 7(1), 104433.

Wu J, et al. (2026) Overexpression of soybean flavonoid 3'-hydroxylase enhances plant salt tolerance by promoting ascorbic acid biosynthesis. Journal of advanced research, 80, 111.

Demirsoy E, et al. (2026) Efficacy and safety evaluation of artificial intelligence-identified antimicrobial peptides targeting avian pathogenic Escherichia coli in broiler chickens. Journal of animal science and biotechnology, 17(1).

Bourner LA, et al. (2026) Protocol to study the role of endogenously produced itaconate using CRISPR-Cas9 technology in THP-1 cells. STAR protocols, 7(1), 104304.

Wang M, et al. (2026) MIR31HG Promotes the Onset and Progression of Peri-Implantitis by Regulating the miR-641 Levels. International dental journal, 76(2), 109375.

Cui B, et al. (2026) Protocol to identify the signaling network of nucleotide second messengers in Shigella sonnei. STAR protocols, 7(1), 104353.

Louis EM, et al. (2026) Protocol for streamlining genotyping of germline-transmissible mutants from genome editing by using a parallel qPCR-based index and R analysis. STAR

protocols, 7(2), 104454.

Xia X, et al. (2026) The Influence of Transgenic Maize on the Endophytic Microorganisms of *Eisenia fetida*. *Microorganisms*, 14(2).

Uddin F, et al. (2026) Protocol to maximize single-nuclei multiome library complexity for limited primary tissues via optimized sample preparation and library synthesis. *STAR protocols*, 7(3), 104640.

Choppavarapu L, et al. (2026) High-resolution Hi-C profiling of human breast tissues using an optimized protocol for clinical samples. *STAR protocols*, 7(1), 104327.

Yan X, et al. (2026) LncRNA SNHG1 Knockdown Ameliorates HIV-1 gp120V3 Loop-Induced Microglial Neuroinflammation by Regulating the Autophagy Process. *Inflammation*, 49(1), 26.

Schroer L, et al. (2025) Orthologues of the human protein histidine methyltransferase METTL9 display distinct substrate specificities. *The Journal of biological chemistry*, 301(7), 110318.

Xiong EH, et al. (2025) Protocol to identify genes important for *Candida albicans* fitness in diverse environmental conditions using pooled bar-seq screening approach. *STAR protocols*, 6(1), 103645.

Fang W, et al. (2025) Genetic analysis of a pedigree with hereditary coagulation factor XII deficiency. *Annals of hematology*, 104(2), 1281.

Fanari O, et al. (2025) Protocol for differential analysis of pseudouridine modifications using nanopore DRS and unmodified transcriptome control. *STAR protocols*, 6(3), 103948.

Schönherr R, et al. (2025) Intracellular protein crystallization in living insect cells. *FEBS open bio*, 15(4), 551.