

# Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

## Catalyst Framework

RRID:SCR\_000703

Type: Tool

### Proper Citation

Catalyst Framework (RRID:SCR\_000703)

### Resource Information

**URL:** <http://www.catalystframework.org>

**Proper Citation:** Catalyst Framework (RRID:SCR\_000703)

**Description:** A web application framework that helps build applications or run protocols for the web. It allows the user to manage various tasks being run on the web both manually and through existing Perl modules.

**Synonyms:** Catalyst

**Resource Type:** web application, software resource

**Keywords:** web, application, framework, development, developer, perl, programmer

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Catalyst Framework

**Resource ID:** SCR\_000703

**Alternate IDs:** nif-0000-30301

**License:** GNU General Public License, Artistic License

**Record Creation Time:** 20220129T080203+0000

**Record Last Update:** 20260808T190250+0000

### Ratings and Alerts

No rating or validation information has been found for Catalyst Framework.

No alerts have been found for Catalyst Framework.

## 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 [SPARC SAWG](#) .

Diehl AG, et al. (2018) Conserved and species-specific transcription factor co-binding patterns drive divergent gene regulation in human and mouse. *Nucleic acids research*, 46(4), 1878.

Boeuf D, et al. (2015) MicRhoDE: a curated database for the analysis of microbial rhodopsin diversity and evolution. *Database : the journal of biological databases and curation*, 2015.

Harris TW, et al. (2014) WormBase 2014: new views of curated biology. *Nucleic acids research*, 42(Database issue), D789.

Akiyama K, et al. (2014) RARGE II: an integrated phenotype database of Arabidopsis mutant traits using a controlled vocabulary. *Plant & cell physiology*, 55(1), e4.

Brodin J, et al. (2013) A multiple-alignment based primer design algorithm for genetically highly variable DNA targets. *BMC bioinformatics*, 14, 255.

Zucker FH, et al. (2012) PROSPERO: online prediction of crystallographic success from experimental results and sequence. *Journal of applied crystallography*, 45(Pt 3), 598.

Yao H, et al. (2010) Use of ITS2 region as the universal DNA barcode for plants and animals. *PloS one*, 5(10).

O'Connor BD, et al. (2008) GMODWeb: a web framework for the Generic Model Organism Database. *Genome biology*, 9(6), R102.