

Resource Summary Report

Generated by [nidm-terms](#) on Aug 9, 2026

RefFinder

RRID:SCR_000472

Type: Tool

Proper Citation

RefFinder (RRID:SCR_000472)

Resource Information

URL: <http://fulxie.0fees.us/?type=reference&ckattempt=1>

Proper Citation: RefFinder (RRID:SCR_000472)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 1,2023. Web-based tool for evaluating and screening reference genes from extensive experimental datasets. It integrates major computational programs (geNorm, Normfinder, BestKeeper, and the comparative delta-Ct method) to compare and rank the tested candidate reference genes. Based on the rankings from each program, it assigns an appropriate weight to an individual gene and calculated the geometric mean of their weights for the overall final ranking., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: RefFinder

Resource Type: web service, production service resource, software resource, data access protocol, analysis service resource, service resource

Keywords: gene, gene expression, reference gene, web based tool

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RefFinder

Resource ID: SCR_000472

Alternate IDs: OMICS_02321

Old URLs: <http://www.leonxie.com/referencegene.php>

Record Creation Time: 20220129T080201+0000

Record Last Update: 20260808T185716+0000

Ratings and Alerts

No rating or validation information has been found for RefFinder.

No alerts have been found for RefFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

de Miranda FS, et al. (2024) MicroRNA as a promising molecular biomarker in the diagnosis of breast cancer. *Frontiers in molecular biosciences*, 11, 1337706.

Gorji-Bahri G, et al. (2021) RAB5A is associated with genes involved in exosome secretion: Integration of bioinformatics analysis and experimental validation. *Journal of cellular biochemistry*, 122(3-4), 425.

Bilandžija H, et al. (2020) Phenotypic plasticity as a mechanism of cave colonization and adaptation. *eLife*, 9.

Gilbert SJ, et al. (2018) Inflammatory and degenerative phases resulting from anterior cruciate rupture in a non-invasive murine model of post-traumatic osteoarthritis. *Journal of orthopaedic research : official publication of the Orthopaedic Research Society*, 36(8), 2118.

Songsasen N, et al. (2017) Short-term hypertonic exposure enhances in vitro follicle growth and meiotic competence of enclosed oocytes while modestly affecting mRNA expression of aquaporin and steroidogenic genes in the domestic cat model. *Theriogenology*, 90, 228.

Sadangi C, et al. (2017) Validation of reference genes for quantitative gene expression analysis in experimental epilepsy. *Journal of neuroscience research*, 95(12), 2357.

Bause M, et al. (2016) Glypican1/2/4/6 and sulfated glycosaminoglycans regulate the patterning of the primary body axis in the cnidarian *Nematostella vectensis*. *Developmental biology*, 414(1), 108.

Pan H, et al. (2015) Selection of Reference Genes for RT-qPCR Analysis in the Monarch Butterfly, *Danaus plexippus* (L.), a Migrating Bio-Indicator. *PloS one*, 10(6), e0129482.

Yang C, et al. (2015) Stably expressed housekeeping genes across developmental stages in the two-spotted spider mite, *Tetranychus urticae*. *PloS one*, 10(3), e0120833.

Niu L, et al. (2015) Selection of Reliable Reference Genes for Gene Expression Studies of a Promising Oilseed Crop, *Plukenetia volubilis*, by Real-Time Quantitative PCR. *International journal of molecular sciences*, 16(6), 12513.

Neubauer K, et al. (2015) Nampt/PBEF/visfatin upregulation in colorectal tumors, mirrored in normal tissue and whole blood of colorectal cancer patients, is associated with metastasis, hypoxia, IL1?, and anemia. *BioMed research international*, 2015, 523930.

Chen IH, et al. (2015) Selection of suitable reference genes for normalization of quantitative RT-PCR in peripheral blood samples of bottlenose dolphins (*Tursiops truncatus*). *Scientific reports*, 5, 15425.

Resnyk CW, et al. (2015) RNA-Seq Analysis of Abdominal Fat in Genetically Fat and Lean Chickens Highlights a Divergence in Expression of Genes Controlling Adiposity, Hemostasis, and Lipid Metabolism. *PloS one*, 10(10), e0139549.

Margue C, et al. (2015) Comparison of a healthy miRNome with melanoma patient miRNomes: are microRNAs suitable serum biomarkers for cancer? *Oncotarget*, 6(14), 12110.

Tarzemany R, et al. (2015) Expression and function of connexin 43 in human gingival wound healing and fibroblasts. *PloS one*, 10(1), e0115524.

Bansal R, et al. (2015) Recommended Reference Genes for Quantitative PCR Analysis in Soybean Have Variable Stabilities during Diverse Biotic Stresses. *PloS one*, 10(8), e0134890.

Yang C, et al. (2015) Temperature and Development Impacts on Housekeeping Gene Expression in Cowpea Aphid, *Aphis craccivora* (Hemiptera: Aphididae). *PloS one*, 10(6), e0130593.

Yang C, et al. (2015) Stable Reference Gene Selection for RT-qPCR Analysis in Nonviruliferous and Viruliferous *Frankliniella occidentalis*. *PloS one*, 10(8), e0135207.

Zhu X, et al. (2015) Selection of reference genes for microRNA quantitative expression analysis in Chinese perch, *Siniperca chuatsi*. *International journal of molecular sciences*, 16(4), 8310.

Leal MF, et al. (2015) Identification of Suitable Reference Genes for Investigating Gene Expression in Anterior Cruciate Ligament Injury by Using Reverse Transcription-Quantitative PCR. *PloS one*, 10(7), e0133323.