

Resource Summary Report

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NormFinder

RRID:SCR_003387

Type: Tool

Proper Citation

NormFinder (RRID:SCR_003387)

Resource Information

URL: <http://moma.dk/normfinder-software>

Proper Citation: NormFinder (RRID:SCR_003387)

Description: Software for identifying the optimal normalization gene among a set of candidates. It ranks the set of candidate normalization genes according to their expression stability in a given sample set and given experimental design. It can analyze expression data obtained through any quantitative method e.g. real time RT-PCR and microarray based expression analysis. NormFinder.xla adds the NormFinder functionality directly to Excel. A version for R is also available.

Abbreviations: NormFinder

Synonyms: NormFinder software - Determine the optimal normalization gene

Resource Type: software resource

Defining Citation: [PMID:15289330](#)

Keywords: normalization, gene

Availability: Free, Available for download, Freely available

Resource Name: NormFinder

Resource ID: SCR_003387

Alternate IDs: OMICS_02317

Alternate URLs: <https://www.moma.dk/software/normfinder>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260919T195020+0000

Ratings and Alerts

No rating or validation information has been found for NormFinder.

No alerts have been found for NormFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2536 mentions in open access literature.

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

Nong VD, et al. (2026) Identification of stable internal reference genes for expression analysis in the liver and pancreas of diabetic mouse (*Mus musculus* L.) models under physiological, pathological and treatment conditions. *PloS one*, 21(1), e0338403.

Franck E, et al. (2026) Characterization of IFN- γ -mediated cellular responses in the HMC3 cell line. *Biochemistry and cell biology = Biochimie et biologie cellulaire*, 104, 1.

Buson L, et al. (2026) MicroRNAs expression changes associated with trauma-focused psychotherapy efficacy in treatment-resistant depression: An exploratory study. *Neuroscience applied*, 5, 107020.

Peng Y, et al. (2026) Time-resolved transcriptomic profiling of mammary gland tissue during ductal morphogenesis, lactation activation, and involution in sows. *Animal bioscience*, 39(5), 250560.

Cao H, et al. (2026) Quantitative proteomic analysis of longissimus dorsi muscle in Chinese and Western pigs using DIA mass spectrometry with PRM validation. *PloS one*, 21(4), e0346519.

Lee HM, et al. (2026) Synergy between HA cleavage site sequence and NA-mediated plasminogen recruitment as a virulence mechanism for low-pathogenic avian influenza. *mBio*, 17(4), e0246625.

Goryszewska-Szczurek E, et al. (2026) Estradiol-17 β , a key embryonic signal, regulates gene expression and cellular functions in the porcine trophoblast. *Biology of reproduction*, 114(6), 1813.

Ramsaran LN, et al. (2026) Investigation of gene stability in equine luteal tissue during mid-diestrus phase and early pregnancy - Research Article. *BMC veterinary research*.

Maravi J, et al. (2026) Validation of reference genes for RT-qPCR relative expression analysis during cyst-to-early adult development of *Taenia solium*. *PLoS neglected tropical diseases*, 20(1), e0013893.

Ciesielski M, et al. (2026) Association of Selected miRNAs (hsa-miR-27b, hsa-miR-128-3p, hsa-miR-145-5p, hsa-miR-552-3p) with HER2 Status and Chromosome 17 Centromere Copy Number Increase in Gastric Cancer. *International journal of molecular sciences*, 27(12).

Todorova B, et al. (2026) Matrix- and Differentiation Stage-Dependent Variability of Reference Genes: Rethinking Validation Strategies in 3T3-L1 Adipogenic Models. *International journal of molecular sciences*, 27(12).

Li X, et al. (2026) Reference Genes for Expression Analyses by RT-qPCR in *Hyblaea puera* (Lepidoptera: Hyblaeidae). *Insects*, 17(6).

Chen B, et al. (2026) Comparative Analysis of Full-Length Reference Gene Stability in *Phoebe zhennan* Under Primary Abiotic and Biotic Stresses. *Plants (Basel, Switzerland)*, 15(11).

Gu X, et al. (2026) Selection and Validation of Stable Reference Genes for RT-qPCR in *Diaphorencyrtus aligarhensis*-A Predominant Parasitoid of *Diaphorina citri*. *International journal of molecular sciences*, 27(11).

Osorio Zambrano MA, et al. (2026) All roads lead to Rome: integrated physiological and transcriptomic analysis of cacao drought response reveals different ways to achieve tolerance in two hybrid clones. *Frontiers in plant science*, 17, 1764400.

Luo Q, et al. (2026) Transcriptome-Based Selection and Validation of Reference Genes for Gene Expression Analysis in *Roegneria ciliaris* 'Liao Sheng' Across Various Tissues and Under Drought Stress. *Genes*, 17(2).

Vadrot N, et al. (2026) LAP2 Isoform Profile in Heart Ageing and in Cardiac Cell Proliferation and Differentiation: Input From CRISPR-Cas9-mediated LAP2a Knockdown in H9C2. *International journal of medical sciences*, 23(3), 741.

Rädecke K, et al. (2026) CAV1-A Susceptibility Gene for Atrial Fibrillation: The Impact of Coding and Noncoding Variants. *Journal of the American Heart Association*, 15(3), e041586.

Mali? M, et al. (2026) Collagen-hyaluronic acid hydrogel with embedded chondrocytes as a platform for modeling early stages of endochondral ossification in vitro. *Cell transplantation*, 35, 9636897251409464.

Marikova K, et al. (2026) Immediate and Sustained Effects of Intensive Equine-Assisted Physiotherapy Based on Neuroproprioceptive "Facilitation and Inhibition" on Psychomotor Development, Clinical Functions, Quality of Life, and Molecular Biological Indicators in Children With Spinal Muscular Atrophy: Protocol for a Crossover Randomized Controlled Trial. *JMIR research protocols*, 15, e83266.