

Resource Summary Report

Generated by [dkNET](#) on Aug 24, 2026

geNORM

RRID:SCR_006763

Type: Tool

Proper Citation

geNORM (RRID:SCR_006763)

Resource Information

URL: <https://genorm.cmgg.be/>

Proper Citation: geNORM (RRID:SCR_006763)

Description: Software to determine most stable reference (housekeeping) genes from set of tested candidate reference genes in given sample panel. From this, gene expression normalization factor can be calculated for each sample based geometric mean of user-defined number of reference genes.

Abbreviations: GENORM

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:19131113](#), [PMID:12519963](#)

Keywords: reference gene, quantitative real time pcr

Resource Name: geNORM

Resource ID: SCR_006763

Alternate IDs: nlx_156922, OMICS_02316

Old URLs: <http://medgen.ugent.be/~jvdesomp/genorm/>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260821T193802+0000

Ratings and Alerts

No rating or validation information has been found for geNORM.

No alerts have been found for geNORM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5414 mentions in open access literature.

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

Zhou H, et al. (2026) COP9 Signalosome is Required for Adipose Tissue Maintenance and Metabolic Health. *Journal of lipid research*, 100977.

Liang Y, et al. (2026) A Multigene Signature for Prognostic Stratification of Nasopharyngeal Carcinoma. *Cancers*, 18(8).

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.

Wehling-Henricks M, et al. (2026) CTLA4-Ig reduces proliferation and inflammatory gene expression in muscle fibroblasts, corresponding to less fibrosis and inflammation in mdx muscular dystrophy. *American journal of physiology. Cell physiology*, 330(5), C1172.

Abdo H, et al. (2026) De Novo Gene Transcription of Connexin Mediates Cytoplasmic Fluid Exchange and Flocking Transitions in Physiological and Cancerous Epithelial Systems. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(6), e08648.

Jo M, et al. (2026) Two-Step Algorithmic Selection of Interspecies Sequence-Mismatch-Based Housekeeping Genes for Precise Gene-Expression Assessment in PBMC-Humanized NSG Mice. *ACS omega*, 11(6), 9187.

Kim S, et al. (2026) Improvement of growth, lipid metabolism and innate immune response in Pacific white shrimp (*Penaeus vannamei*) post-larvae through enrichment of live feeds with *Schizochytrium* sp., taurine and inosine monophosphate. *PloS one*, 21(3), e0341999.

Qian K, et al. (2026) Salicylic Acid Enhances Cadmium Tolerance in *Cornus alba* L. Seedlings Through Leaf Transcriptional Regulation and Enhanced Root Heavy Metal Sequestration. *Plants (Basel, Switzerland)*, 15(7).

Gao X, et al. (2026) miRNA Profiling Reveals the Role of Gibberellin Signaling Pathway in Low-Nitrogen Stress Adaptation of Xinjiang Spring Wheat. *Plants (Basel, Switzerland)*, 15(7).

Maurício T, et al. (2026) Integrated Proteomics and Metabolomics Analyses Reveal That Phosphatidylethanolamine Reprograms Macrophage Immunometabolism and Attenuates LPS-Driven Inflammation. *Journal of proteome research*, 25(5), 2437.

Pearson GL, et al. (2026) Time of day alters olfactory bulb immune state with ramifications for intranasal inflammatory challenge. *Cell reports*, 45(4), 117133.

Hibbert TM, et al. (2026) The longitudinal expression of *P. aeruginosa* reference genes in infection-mimicking media. *Microbiology (Reading, England)*, 172(1).

Vardas ?P, et al. (2026) Circulating miR-10b-5p as a candidate biomarker of atrial fibrillation recurrence after catheter ablation: a two-phase translational study. *Europace : European pacing, arrhythmias, and cardiac electrophysiology : journal of the working groups on cardiac pacing, arrhythmias, and cardiac cellular electrophysiology of the European Society of Cardiology*, 28(5).

Wang X, et al. (2026) Transcriptomic Analysis of Bovine Oocytes at GV and MII Stages and Dynamic Changes in Key Gene Expression Patterns. *Biology*, 15(8).

Huang S, et al. (2026) Identification of a novel real-time PCR reference gene panel for EA.hy926 endothelial cells in different growth States and with DHA treatment. *Scientific reports*, 16(1), 2654.

Quarta R, et al. (2026) Best reference genes for unbiased normalized transcript expression in normal and dystrophic human cell models of myogenesis. *PloS one*, 21(3), e0344973.

Bendezu J, et al. (2026) Phenotypic and genotypic characterization of *Plasmodium falciparum* field isolates lacking pfhrp2 gene. *Malaria journal*, 25(1).

Fan Z, et al. (2026) Genome-wide identification, evolution, and expression pattern analysis of the LEA gene family in Tartary Buckwheat (*Fagopyrum tataricum*). *BMC genomics*, 27(1).

Li X, et al. (2026) Suppressive Effects of an Inhibitor Composition on Skin Ulceration and Transcriptomic Analysis in the Sea Cucumber *Apostichopus japonicus* Exposed to No. 0 Diesel Oil. *Biology*, 15(6).

El-Bouhy Z, et al. (2026) Dietary cauliflower (*Brassica oleracea* var. *botrytis*) mitigates benzo[a]pyrene-induced oxidative stress, immune dysfunction, and tissue damage in Nile tilapia. *Scientific reports*, 16(1).