

Resource Summary Report

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Relative Expression Software Tool

RRID:SCR_023755

Type: Tool

Proper Citation

Relative Expression Software Tool (RRID:SCR_023755)

Resource Information

URL: <https://www.gene-quantification.de/rest.html>

Proper Citation: Relative Expression Software Tool (RRID:SCR_023755)

Description: Software tool for group wise comparison and statistical analysis of relative expression results in real-time PCR. Used to compute expression ratio, based on real-time PCR efficiency and crossing point deviation of unknown sample versus control. Compares two groups, with up to 16 data points in sample and 16 in control group, for reference and up to four target genes.

Abbreviations: REST

Resource Type: software application, software resource

Defining Citation: [PMID:11972351](#)

Keywords: relative quantification analysis, group wise comparison, relative expression statistical analysis, RT PCR results analysis, target genes, compute expression ratio,

Availability: Free, Freely available

Resource Name: Relative Expression Software Tool

Resource ID: SCR_023755

Record Creation Time: 20230708T050227+0000

Record Last Update: 20260905T133315+0000

Ratings and Alerts

No rating or validation information has been found for Relative Expression Software Tool.

No alerts have been found for Relative Expression Software Tool.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 69 mentions in open access literature.

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

Hajiabadi S, et al. (2023) Immunotherapy with STING and TLR9 agonists promotes synergistic therapeutic efficacy with suppressed cancer-associated fibroblasts in colon carcinoma. *Frontiers in immunology*, 14, 1258691.

Mirabedini Z, et al. (2023) The effects of Leishmania RNA virus 2 (LRV2) on the virulence factors of *L. major* and pro-inflammatory biomarkers: an in vitro study on human monocyte cell line (THP-1). *BMC microbiology*, 23(1), 398.

Ghanbari Moheb Seraj R, et al. (2022) Metabolomics analysis of milk thistle lipids to identify drought-tolerant genes. *Scientific reports*, 12(1), 12827.

Said-Salman IH, et al. (2019) Global gene expression analysis of *Escherichia coli* K-12 DH5 α after exposure to 2.4 GHz wireless fidelity radiation. *Scientific reports*, 9(1), 14425.

Pong LY, et al. (2019) MicroRNA profiling of mouse liver in response to DENV-1 infection by deep sequencing. *PeerJ*, 7, e6697.

Hong M, et al. (2019) Comparative analysis of the liver transcriptome in the red-eared slider *Trachemys scripta elegans* under chronic salinity stress. *PeerJ*, 7, e6538.

Do TD, et al. (2019) Molecular Characterization and Gene Expression of Glutathione Peroxidase 1 in *Tor tambroides* Exposed to Temperature Stress. *Evolutionary bioinformatics online*, 15, 1176934319853580.

Sheikhbahaei S, et al. (2019) Can MiR-503 be used as a marker in diabetic patients with ischemic stroke? *BMC endocrine disorders*, 19(1), 42.

Szmidt M, et al. (2019) Graphene oxide down-regulates genes of the oxidative phosphorylation complexes in a glioblastoma. *BMC molecular biology*, 20(1), 2.

Yu S, et al. (2019) Hypoxia-induced miR-191-C/EBP β signaling regulates cell proliferation and apoptosis of fibroblast-like synoviocytes from patients with rheumatoid arthritis. *Arthritis research & therapy*, 21(1), 78.

Kunde DA, et al. (2018) TRPV1 mediates capsaicin-stimulated metabolic activity but not cell death or inhibition of interleukin-1 β release in human THP-1 monocytes. *Toxicology and applied pharmacology*, 360, 9.

Barnett AM, et al. (2018) Metabolism of Caprine Milk Carbohydrates by Probiotic Bacteria and Caco-2:HT29 α MTX Epithelial Co-Cultures and Their Impact on Intestinal Barrier Integrity. *Nutrients*, 10(7).

Kiani S, et al. (2018) Purified sulforaphane from broccoli (*Brassica oleracea* var. *italica*) leads to alterations of CDX1 and CDX2 expression and changes in miR-9 and miR-326 levels in human gastric cancer cells. *Gene*, 678, 115.

Gaye A, et al. (2018) Whole-genome transcriptomic insights into protective molecular mechanisms in metabolically healthy obese African Americans. *NPJ genomic medicine*, 3, 4.

Ramalho JC, et al. (2018) Stress cross-response of the antioxidative system promoted by superimposed drought and cold conditions in *Coffea* spp. *PloS one*, 13(6), e0198694.

Hajizadeh N, et al. (2018) Effect of MTA and CEM on Mineralization-Associated Gene Expression in Stem Cells Derived from Apical Papilla. *Iranian endodontic journal*, 13(1), 94.

Sheshadri SA, et al. (2018) Effect of Melatonin on the stability and expression of reference genes in *Catharanthus roseus*. *Scientific reports*, 8(1), 2222.

Goyal RK, et al. (2018) Analysis of MAPK and MAPKK gene families in wheat and related *Triticeae* species. *BMC genomics*, 19(1), 178.

Dash SK, et al. (2018) Induction profiles of mRNA of toll like receptors and cytokines in chickens pre-exposed to low pathogenic avian influenza H9N2 virus followed by challenge with highly pathogenic avian influenza H5N1 virus. *Microbial pathogenesis*, 117, 200.

Gupta A, et al. (2017) Transcriptomic difference in bovine blastocysts following vitrification and slow freezing at morula stage. *PloS one*, 12(11), e0187268.