

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>

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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 resource, software application

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: 20260801T191122+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 67 mentions in open access literature.

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

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.

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.

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.

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.

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 α signaling regulates cell proliferation and apoptosis of fibroblast-like synoviocytes from patients with rheumatoid arthritis. *Arthritis research & therapy*, 21(1), 78.

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

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).

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.

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.

Ramvalho 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.

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

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.

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.

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

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

Mahesh YU, et al. (2017) Effect of different cryo-devices on in vitro maturation and development of vitrified-warmed immature buffalo oocytes. *Cryobiology*, 75, 106.

Brym P, et al. (2017) Microarray analysis of differential gene expression profiles in blood cells of naturally BLV-infected and uninfected Holstein-Friesian cows. *Molecular biology reports*, 44(1), 109.