

Resource Summary Report

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SLqPCR

RRID:SCR_001669

Type: Tool

Proper Citation

SLqPCR (RRID:SCR_001669)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/SLqPCR.html>

Proper Citation: SLqPCR (RRID:SCR_001669)

Description: Software functions for analysis of real-time quantitative PCR data at SIRS-Lab GmbH.

Synonyms: SLqPCR - Functions for analysis of real-time quantitative PCR data at SIRS-Lab GmbH

Resource Type: software resource

Keywords: standalone software, mac os x, unix/linux, windows, r, microtitre plate assay, qpcr

Availability: Free, Available for download, Freely available

Resource Name: SLqPCR

Resource ID: SCR_001669

Alternate IDs: OMICS_04010

License: GNU General Public License, v2 or greater

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260725T190506+0000

Ratings and Alerts

No rating or validation information has been found for SLqPCR.

No alerts have been found for SLqPCR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Sécula A, et al. (2022) Maternal dietary methionine restriction alters hepatic expression of one-carbon metabolism and epigenetic mechanism genes in the ducklings. BMC genomics, 23(1), 823.

Chamas L, et al. (2022) A Fine Regulation of the Hippocampal Thyroid Signalling Protects Hypothyroid Mice against Glial Cell Activation. International journal of molecular sciences, 23(19).

Debackere K, et al. (2021) Fusion transcripts FYN-TRAF3IP2 and KHDRBS1-LCK hijack T cell receptor signaling in peripheral T-cell lymphoma, not otherwise specified. Nature communications, 12(1), 3705.

Lamelas L, et al. (2020) Integrative analysis of the nuclear proteome in Pinus radiata reveals thermoprimering coupled to epigenetic regulation. Journal of experimental botany, 71(6), 2040.

Massimino W, et al. (2020) Ontogeny of hepatic metabolism in mule ducks highlights different gene expression profiles between carbohydrate and lipid metabolic pathways. BMC genomics, 21(1), 742.

Dwivedi N, et al. (2020) Relative quantification of BCL2 mRNA for diagnostic usage needs stable uncontrolled genes as reference. PloS one, 15(8), e0236338.

Kirschman LJ, et al. (2020) Early life disruption of the microbiota affects organ development and cytokine gene expression in threespine stickleback. Integrative and comparative biology, 63(1), 250.

Christenson SA, et al. (2019) An airway epithelial IL-17A response signature identifies a steroid-unresponsive COPD patient subgroup. The Journal of clinical investigation, 129(1), 169.

Terrien J, et al. (2019) Reduced central and peripheral inflammatory responses and increased mitochondrial activity contribute to diet-induced obesity resistance in WSB/EiJ mice. Scientific reports, 9(1), 19696.

Smitha PK, et al. (2019) Genome wide search to identify reference genes candidates for gene expression analysis in Gossypium hirsutum. BMC plant biology, 19(1), 405.

Lorenzetti WR, et al. (2018) Identification of endogenous normalizing genes for expression studies in inguinal ring tissue for scrotal hernias in pigs. PloS one, 13(9), e0204348.

Reichel M, et al. (2018) Chronic Psychosocial Stress in Mice Is Associated With Increased Acid Sphingomyelinase Activity in Liver and Serum and With Hepatic C16:0-Ceramide Accumulation. *Frontiers in psychiatry*, 9, 496.

Köglberger S, et al. (2017) Gender-Specific Expression of Ubiquitin-Specific Peptidase 9 Modulates Tau Expression and Phosphorylation: Possible Implications for Tauopathies. *Molecular neurobiology*, 54(10), 7979.

Cedraz de Oliveira H, et al. (2017) Influence of heat stress, sex and genetic groups on reference genes stability in muscle tissue of chicken. *PloS one*, 12(5), e0176402.

Vantangoli MM, et al. (2016) Morphologic effects of estrogen stimulation on 3D MCF-7 microtissues. *Toxicology letters*, 248, 1.

Vantangoli MM, et al. (2016) Estradiol Exposure Differentially Alters Monolayer versus Microtissue MCF-7 Human Breast Carcinoma Cultures. *PloS one*, 11(7), e0157997.

Marabita F, et al. (2016) Normalization of circulating microRNA expression data obtained by quantitative real-time RT-PCR. *Briefings in bioinformatics*, 17(2), 204.

Pascual J, et al. (2016) The variations in the nuclear proteome reveal new transcription factors and mechanisms involved in UV stress response in *Pinus radiata*. *Journal of proteomics*, 143, 390.

Gunsalus KT, et al. (2016) Manipulation of Host Diet To Reduce Gastrointestinal Colonization by the Opportunistic Pathogen *Candida albicans*. *mSphere*, 1(1).

Gotanda K, et al. (2016) Circulating intestine-derived exosomal miR-328 in plasma, a possible biomarker for estimating BCRP function in the human intestines. *Scientific reports*, 6, 32299.