

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: 20260801T190146+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 [RRID](#) .

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.