

Resource Summary Report

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RTPrimerDB- The Real-Time PCR and Probe Database

RRID:SCR_007106

Type: Tool

Proper Citation

RTPrimerDB- The Real-Time PCR and Probe Database (RRID:SCR_007106)

Resource Information

URL: <http://medgen.ugent.be/rtpriimerdb/>

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Description: Database for primer and probe sequences used in real-time PCR assays employing popular chemistries (SYBR Green I, Taqman, Hybridization Probes, Molecular Beacon) to prevent time-consuming primer design and experimental optimization, and to introduce a certain level of uniformity and standardization among different laboratories. Researchers are encouraged to submit their validated primer and probe sequence, so that other users can benefit from their expertise. The database can be queried using the official gene name or symbol, Entrez or Ensembl Gene identifier, SNP identifier, or oligonucleotide sequence. Different options make it possible to restrict a query to a particular application (Gene Expression Quantification/Detection, DNA Copy Number Quantification/Detection, SNP Detection, Mutation Analysis, Fusion Gene Quantification/Detection, Chromatin immunoprecipitation (ChIP)), organism (Human, Mouse, Rat, and others) or detection chemistry.

Abbreviations: RTPrimerDB

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:18948285](#), [PMID:16381959](#), [PMID:12519963](#)

Keywords: primer, probe, sequence, real-time pcr, gene, assay, real-time pcr assay, FASEB list

Availability: Public, The community can contribute to this resource

Resource Name: RTPrimerDB- The Real-Time PCR and Probe Database

Resource ID: SCR_007106

Alternate IDs: nif-0000-03431, OMICS_02322

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260919T195124+0000

Ratings and Alerts

No rating or validation information has been found for RTPrimerDB- The Real-Time PCR and Probe Database.

No alerts have been found for RTPrimerDB- The Real-Time PCR and Probe Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Wang T, et al. (2025) DNMBP-AS1/hsa-miR-30a-5p/PGC1? axis suppresses tumor progression of colorectal cancer by inhibiting PKM2-mediated Warburg effect and enhance anti-PD-1 therapy efficacy. Cell death discovery, 11(1), 299.

Daliri K, et al. (2025) Protocol for permanent gene repression by CRISPR-adenine base editing of promoter CCAAT motifs. STAR protocols, 6(3), 104075.

Chen Y, et al. (2024) Long non-coding RNA SRA1 suppresses radiotherapy resistance in esophageal squamous cell carcinoma by modulating glycolytic reprogramming. Open medicine (Warsaw, Poland), 19(1), 20240946.

Wang T, et al. (2023) ESRRG-PKM2 axis reprograms metabolism to suppress esophageal squamous carcinoma progression and enhance anti-PD-1 therapy efficacy. Journal of translational medicine, 21(1), 605.

Kim J, et al. (2021) Single-cell RNA sequencing for the identification of early-stage lung cancer biomarkers from circulating blood. NPJ genomic medicine, 6(1), 87.

Van Hecke C, et al. (2019) Early treated HIV-1 positive individuals demonstrate similar restriction factor expression profile as long-term non-progressors. EBioMedicine, 41, 443.

Liu M, et al. (2017) RHOA GTPase Controls YAP-Mediated EREG Signaling in Small Intestinal Stem Cell Maintenance. Stem cell reports, 9(6), 1961.

Liu S, et al. (2017) An fMRI study of the effects on normal language areas when acupuncture the Tongli (HT5) and Xuanzhong (GB39) acupoints. The Journal of international medical research, 45(6), 1961.

Chen YC, et al. (2015) Expression change in Angiopoietin-1 underlies change in relative brain size in fish. Proceedings. Biological sciences, 282(1810).

Inturi R, et al. (2015) Complementation of the human adenovirus type 5 VA RNAI defect by the Vaccinia virus E3L protein and serotype-specific VA RNAs. Virology, 485, 25.

Scarlet D, et al. (2015) The Orthology Clause in the Next Generation Sequencing Era: Novel Reference Genes Identified by RNA-seq in Humans Improve Normalization of Neonatal Equine Ovary RT-qPCR Data. PloS one, 10(11), e0142122.

Mishto M, et al. (2015) The immunoproteasome $\beta 5i$ subunit is a key contributor to ictogenesis in a rat model of chronic epilepsy. Brain, behavior, and immunity, 49, 188.

Lebreton A, et al. (2014) Structural basis for the inhibition of the chromatin repressor BAHD1 by the bacterial nucleomodulin LntA. mBio, 5(1), e00775.

Guilmot A, et al. (2014) Differential IFN- γ production by adult and neonatal blood CD56+ natural killer (NK) and NK-like-T cells in response to Trypanosoma cruzi and IL-15. Parasite immunology, 36(1), 43.

Stanojevic B, et al. (2014) Low VHL mRNA expression is associated with more aggressive tumor features of papillary thyroid carcinoma. PloS one, 9(12), e114511.

Vanbekbergen N, et al. (2014) Growth differentiation factor 11 is an encephalic regionalizing factor in neural differentiated mouse embryonic stem cells. BMC research notes, 7, 766.

Kohli A, et al. (2014) Oral and vaginal epithelial cell lines bind and transfer cell-free infectious HIV-1 to permissive cells but are not productively infected. PloS one, 9(5), e98077.

Dupasquier S, et al. (2014) Validation of housekeeping gene and impact on normalized gene expression in clear cell renal cell carcinoma: critical reassessment of YBX3/ZONAB/CSDA expression. BMC molecular biology, 15, 9.

Salvestrini C, et al. (2014) Matrix expansion and syncytial aggregation of syndecan-1+ cells underpin villous atrophy in coeliac disease. PloS one, 9(9), e106005.

O'Neill V, et al. (2013) Vitamin D Receptor Gene Expression and Function in a South African Population: Ethnicity, Vitamin D and FokI. PloS one, 8(6), e67663.