

Resource Summary Report

Generated by NIF on Sep 1, 2026

GenExpress: an intellectual system for analysis of genomic regulatory sequences of humans and higher eukaryotes

RRID:SCR_010647

Type: Tool

Proper Citation

GenExpress: an intellectual system for analysis of genomic regulatory sequences of humans and higher eukaryotes (RRID:SCR_010647)

Resource Information

URL: <http://wwwmgs.bionet.nsc.ru/mgs/papers/kol/geneexp/>

Proper Citation: GenExpress: an intellectual system for analysis of genomic regulatory sequences of humans and higher eukaryotes (RRID:SCR_010647)

Description: The intellectual system GenExpress designed for analysis of genomic regulatory sequences of higher eukaryotes comprises the following major units: (1) the database of transcription regulatory regions of eukaryotic genes TRRD that contains the description of regulatory regions of 427 eukaryotic genes, including 2133 transcription factor binding sites, 78 composite regulatory elements, 593 enhancers, and other types of transcription-regulating elements; (2) the database Activity that comprises the available data on the activity of the sites involved in the regulation of gene expression as well as the physico-chemical, conformational, and statistical DNA/RNA properties significant for the activity of these sites; (3) the database for gene networks GeneNet that contains the information on groups of the genes functioning coordinately to provide expression of genetic information; (4) a set of programs for detecting functional sites and predicting their activity; (5) programs for visualization of the information contained in the listed databases and the results of analysis; (6) semantic means to provide user's navigation in the system. SRS (Sequence Retrieval System) query language was chosen for the system GenExpress, as it is widespread and Internet-compatible. GenExpress is available at /mgs/systems/geneexpress/. Applications of the system to analysis of the structure-function organization of human genomic nucleotide sequences are considered.

Synonyms: GenExpress

Resource Type: data or information resource, database, portal, service resource, topical portal

Resource Name: GenExpress: an intellectual system for analysis of genomic regulatory sequences of humans and higher eukaryotes

Resource ID: SCR_010647

Alternate IDs: nlx_66659

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260829T182334+0000

Ratings and Alerts

No rating or validation information has been found for GenExpress: an intellectual system for analysis of genomic regulatory sequences of humans and higher eukaryotes.

No alerts have been found for GenExpress: an intellectual system for analysis of genomic regulatory sequences of humans and higher eukaryotes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Surtees R, et al. (2025) Machine learning-supported framework for the classification of mpox infection and MVA immunization from multiplexed serology data. Nature communications, 16(1), 10943.

Sáez-López E, et al. (2024) Amoxicillin/clavulanate in combination with rifampicin/clarithromycin is bactericidal against Mycobacterium ulcerans. PLoS neglected tropical diseases, 18(4), e0011867.

Arranz-Solís D, et al. (2023) Late Embryogenesis Abundant Proteins Contribute to the Resistance of Toxoplasma gondii Oocysts against Environmental Stresses. mBio, 14(2), e0286822.

Rohde C, et al. (2022) Ebola Virus Activates IRE1 α -Dependent XBP1u Splicing. Viruses, 15(1).

Saar M, et al. (2021) RLEP LAMP for the laboratory confirmation of leprosy: towards a point-of-care test. BMC infectious diseases, 21(1), 1186.

El Wahed AA, et al. (2021) Suitcase Lab for Rapid Detection of SARS-CoV-2 Based on Recombinase Polymerase Amplification Assay. Analytical chemistry, 93(4), 2627.

Pietsch H, et al. (2020) Detection of parvovirus mRNAs as markers for viral activity in endomyocardial biopsy-based diagnosis of patients with unexplained heart failure. *Scientific reports*, 10(1), 22354.

Surtees R, et al. (2020) Development of a multiplex microsphere immunoassay for the detection of antibodies against highly pathogenic viruses in human and animal serum samples. *PLoS neglected tropical diseases*, 14(10), e0008699.

Andersson MI, et al. (2020) SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. *Wellcome open research*, 5, 181.

Mayer FJ, et al. (2020) Development of a fully automated high throughput PCR for the detection of SARS-CoV-2: The need for speed. *Virulence*, 11(1), 964.

Beissner M, et al. (2019) Development of a combined RLEP/16S rRNA (RT) qPCR assay for the detection of viable *M. leprae* from nasal swab samples. *BMC infectious diseases*, 19(1), 753.

Torelli F, et al. (2018) Recombinant IFN- γ from the bank vole *Myodes glareolus*: a novel tool for research on rodent reservoirs of zoonotic pathogens. *Scientific reports*, 8(1), 2797.

Van Linthout S, et al. (2018) Telbivudine in chronic lymphocytic myocarditis and human parvovirus B19 transcriptional activity. *ESC heart failure*, 5(5), 818.

Abd El Wahed A, et al. (2017) Rapid Molecular Detection of Zika Virus in Acute-Phase Urine Samples Using the Recombinase Polymerase Amplification Assay. *PLoS currents*, 9.

Köller T, et al. (2016) Implementation and Evaluation of a Fully Automated Multiplex Real-Time PCR Assay on the BD Max Platform to Detect and Differentiate Herpesviridae from Cerebrospinal Fluids. *PloS one*, 11(4), e0153991.

Schunk M, et al. (2015) Use of Occult Blood Detection Cards for Real-Time PCR-Based Diagnosis of *Schistosoma Mansoni* Infection. *PloS one*, 10(9), e0137730.

Abd-Alla AM, et al. (2009) Quantitative PCR analysis of the salivary gland hypertrophy virus (GpSGHV) in a laboratory colony of *Glossina pallidipes*. *Virus research*, 139(1), 48.

Hemdan NY, et al. (2006) The in vitro immune modulation by cadmium depends on the way of cell activation. *Toxicology*, 222(1-2), 37.