Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

CleanEx

RRID:SCR_012911
Type: Tool

Proper Citation

CleanEx (RRID:SCR_012911)

Resource Information

URL: http://www.cleanex.isb-sib.ch/

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Description: CleanEx is a database which provides access to public gene expression data via unique approved gene symbols and which represents heterogeneous expression data produced by different technologies in a way that facilitates joint analysis and cross-dataset comparisons. To achieve this goal, each single gene expression experiment is regularly mapped on a permanent target identifier consisting of a physical description of the targeted RNA. There is one entry per gene. To have a complete view of the transcript and its product, we also link each entry to the corresponding protein. We further provide the genomic position of the transcription start site from EPD, when available. Otherwise we give the annotated start site position in Ensembl.

Synonyms: CleanEx

Resource Type: data or information resource, database

Keywords: gene expression, data comparison, heterogeneous expression, bio.tools

Resource Name: CleanEx

Resource ID: SCR_012911

Alternate IDs: nif-0000-02667, biotools:cleanex

Alternate URLs: https://bio.tools/cleanex

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260905T133203+0000

Ratings and Alerts

No rating or validation information has been found for CleanEx.

No alerts have been found for CleanEx.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Palte RL, et al. (2026) WRN structural flexibility showcased through fragment-based lead discovery of inhibitors. Nature communications, 17(1), 79.

Neißner K, et al. (2025) NMR Solution Structure of the N-Terminal GSPII Domain from the Thermus Thermophilus Traffic ATPase PilF and Reconstruction of its c-di-GMP Binding Capability. Chembiochem : a European journal of chemical biology, 26(7), e202400959.

Vasconcelos AA, et al. (2025) Surface hydrophobic clusters modulate the folding stability and molecular recognition of the disintegrin jarastatin. The Journal of biological chemistry, 301(3), 108294.

Müller-Hermes C, et al. (2025) Unique conformational dynamics and protein recognition of A-to-I hyper-edited dsRNA. Nucleic acids research, 53(12).

Koduru T, et al. (2024) A molten globule ensemble primes Arf1-GDP for the nucleotide switch. Proceedings of the National Academy of Sciences of the United States of America, 121(39), e2413100121.

Wang Y, et al. (2023) Structural insights into the activity regulation of full-length non-structural protein 1 from SARS-CoV-2. Structure (London, England : 1993), 31(2), 128.

Bershatsky YV, et al. (2023) Diversity of Structural, Dynamic, and Environmental Effects Explain a Distinctive Functional Role of Transmembrane Domains in the Insulin Receptor Subfamily. International journal of molecular sciences, 24(4).

Forsythe HM, et al. (2021) Multivalent binding of the partially disordered SARS-CoV-2 nucleocapsid phosphoprotein dimer to RNA. Biophysical journal, 120(14), 2890.

Okuda M, et al. (2021) Structural and dynamical insights into the PH domain of p62 in human TFIIH. Nucleic acids research, 49(5), 2916.

Schedlbauer A, et al. (2021) A conserved rRNA switch is central to decoding site maturation on the small ribosomal subunit. Science advances, 7(23).

Ogden TEH, et al. (2021) Dynamics of the HD regulatory subdomain of PARP-1; substrate access and allostery in PARP activation and inhibition. Nucleic acids research, 49(4),

2266.

Alburquerque-González B, et al. (2021) The FDA-Approved Antiviral Raltegravir Inhibits Fascin1-Dependent Invasion of Colorectal Tumor Cells In Vitro and In Vivo. Cancers, 13(4).

Bertuzzi S, et al. (2020) Unravelling the Time Scale of Conformational Plasticity and Allostery in Glycan Recognition by Human Galectin-1. Chemistry (Weinheim an der Bergstrasse, Germany), 26(67), 15643.

Schiavina M, et al. (2020) Ensemble description of the intrinsically disordered N-terminal domain of the Nipah virus P/V protein from combined NMR and SAXS. Scientific reports, 10(1), 19574.

Mateos B, et al. (2020) The Ambivalent Role of Proline Residues in an Intrinsically Disordered Protein: From Disorder Promoters to Compaction Facilitators. Journal of molecular biology, 432(9), 3093.

Jespersen NE, et al. (2019) The LC8-RavP ensemble Structure Evinces A Role for LC8 in Regulating Lyssavirus Polymerase Functionality. Journal of molecular biology, 431(24), 4959.

Mineev KS, et al. (2017) Spatial structure of TLR4 transmembrane domain in bicelles provides the insight into the receptor activation mechanism. Scientific reports, 7(1), 6864.

Gladkova C, et al. (2017) An invisible ubiquitin conformation is required for efficient phosphorylation by PINK1. The EMBO journal, 36(24), 3555.

Rennella E, et al. (2017) RNA binding and chaperone activity of the E. coli cold-shock protein CspA. Nucleic acids research, 45(7), 4255.

Perez-Borrajero C, et al. (2016) Structural and Dynamics Studies of Pax5 Reveal Asymmetry in Stability and DNA Binding by the Paired Domain. Journal of molecular biology, 428(11), 2372.