

Resource Summary Report

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CAGE

RRID:SCR_007574

Type: Tool

Proper Citation

CAGE (RRID:SCR_007574)

Resource Information

URL: http://www.dnaform.jp/products/cage_e.html

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Description: Expression profiling and promoter identification software tool for transcriptional network analysis and transcriptome characterization. DeepCAGE, the combination of next-generation sequencing with next generation expression profiling provides unsurpassed solutions for expression profiling and genome annotation. CAGE will be the experimental approach at need to link gene expression and control regions in the genome. With the availability of next-generation sequencing methods, DNAFORM now offers DeepCAGE services. DeepCAGE libraries are prepared for direct analysis by an Illumina/Solexa Sequencer. One sequencing run using one channel on an Illumina/Solexa Sequencer can yield in over 4,000,000 reads per sample. CAGE is based on our full-length cDNA library technology, where an adaptor is ligated to the 5'-end of full-length cDNAs, which introduces a recognition site for a Class IIs restriction endonuclease adjacent to the 5'-end of the cDNA. The Class IIs restriction endonuclease, here MmeI, allows for the cloning of short tags as derived from the 5'-end of transcripts into concatemers for high-throughput sequencing. CAGE tags are further characterized by mapping to genomic sequences, which enables the identification of transcriptional start sites. As such CAGE can contribute to projects in Gene Discovery, Gene Expression, and Promoter Identification. After the genome sequencing projects have provided us with the genetic blueprints for many organisms, new questions have to be answered on how to correlate the observed genotypes with related phenotypes, and how to understand the regulation of genetic information in time and space. The dynamics of living systems and the functional behavior of cells in multicellular organisms has thus become the subject of the emerging field of system biology. Integration of experimental approaches and computer aided theories on a system level will be the fundamental principle to drive systems biology in order to understand the principles behind complex regulatory networks, which will be an ambitious goal requiring new approaches in life sciences. For ordering and additional information, please contact us under [contact_at_dnaform.jp](#)

Abbreviations: CAGE

Synonyms: DeepCAGE, Cap-Analysis-Gene-Expression, CAGE Library, Cap analysis of gene expression

Resource Type: software resource

Keywords: gene, gene expression, transcriptome, expression profiling, promoter identification, promoter, gene discovery, cdna, cdna library, genome annotation, genome, annotation, rna library, rna, mrna

Resource Name: CAGE

Resource ID: SCR_007574

Alternate IDs: nif-0000-02631

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260912T195657+0000

Ratings and Alerts

No rating or validation information has been found for CAGE.

No alerts have been found for CAGE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 267 mentions in open access literature.

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

Yoshikawa R, et al. (2026) Novel therapeutic strategy targeting STMN1 using chlorambucil-conjugated pyrrole-imidazole polyamide in small cell lung cancer. International journal of cancer, 158(5), 1336.

Zhang Y, et al. (2026) TEITbase: a database for transposable element (TE)-initiated transcripts in human cancers. Database : the journal of biological databases and curation, 2026.

Bou K, et al. (2026) Introns as Protective Buffers Against Transposable Elements Invasion During Genome Gigantism in a Newt. Genes to cells : devoted to molecular & cellular mechanisms, 31(2), e70102.

Chen J, et al. (2025) Piwi regulates the usage of alternative transcription start sites in the Drosophila ovary. Nucleic acids research, 53(1).

- Kohno S, et al. (2025) RB1 controls differentiation through positive regulation of phosphoglycerate mutases. *Cell death & disease*, 16(1), 559.
- Furukawa TA, et al. (2025) Personalised & optimised therapy (POT) algorithm using five cognitive and behavioural skills for subthreshold depression. *NPJ digital medicine*, 8(1), 531.
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- Ma Y, et al. (2025) Enhancer RNA-mediated transcriptional regulatory programs reveal the malignant progression of glioma. *Science advances*, 11(23), eadu9487.
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- Khmelinskaia A, et al. (2025) Local structural flexibility drives oligomorphism in computationally designed protein assemblies. *Nature structural & molecular biology*, 32(6), 1050.
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- Nakano Y, et al. (2025) Epigenetic Regulation of G6PD Drives Metabolic Reprogramming in Intrahepatic Cholangiocarcinoma. *Cancer science*, 116(12), 3352.
- Wiechens E, et al. (2025) Gene regulation by convergent promoters. *Nature genetics*, 57(1), 206.
- Costa BNL, et al. (2025) Smart Polymeric 3D Microscaffolds Hosting Spheroids for Neuronal Research via Quantum Metrology. *Advanced healthcare materials*, 14(7), e2403875.
- Hübner JM, et al. (2025) The Missing Link in the Monogermanide Series: YbGe. *Chemistry (Weinheim an der Bergstrasse, Germany)*, 31(13), e202404515.
- Wang Y, et al. (2025) Adhesive micro-liquid for efficient removal of bacterial biofilm infection. *Materials today. Bio*, 31, 101525.
- Kurata D, et al. (2025) Unstable anthocyanin pigmentation in *Streptocarpus* sect. *Saintpaulia* (African violet) is due to transcriptional selectivity of a single MYB gene. *The New phytologist*, 247(3), 1426.