

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

Funding:

Resource Name: CAGE

Resource ID: SCR_007574

Alternate IDs: nif-0000-02631

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250410T065558+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 242 mentions in open access literature.

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

Wang Y, et al. (2025) Integrating single-cell RNA and T?cell/B?cell receptor sequencing with mass cytometry reveals dynamic trajectories of human peripheral immune cells from birth to old age. *Nature immunology*, 26(2), 308.

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

Wiechens E, et al. (2025) Gene regulation by convergent promoters. *Nature genetics*, 57(1), 206.

Abiy E, et al. (2024) Insecticide susceptibility status of *Anopheles stephensi* against novel insecticides in Eastern Ethiopia. *Research square*.

Wei S, et al. (2024) Reaction Mechanism and Performance of Innovative 2D Germanane-Silicane Alloys: SixGe1- xH Electrodes in Lithium-Ion Batteries. *Advanced science* (Weinheim, Baden-Wurtemberg, Germany), 11(24), e2308955.

Li R, et al. (2024) Enhancing the Photosensitivity of Hypocrellin A by Perylene Diimide Metallacage-Based Host-Guest Complexation for Photodynamic Therapy. *Nano-micro letters*, 16(1), 226.

Abugessaisa I, et al. (2024) OVCH1 Antisense RNA 1 is differentially expressed between non-frail and frail old adults. *GeroScience*, 46(2), 2063.

Said AA, et al. (2024) Sublimed C60 for efficient and repeatable perovskite-based solar cells. *Nature communications*, 15(1), 708.

Nakamura T, et al. (2024) Human RFX6 regulates endoderm patterning at the primitive gut

tube stage. PNAS nexus, 3(1), pgae001.

Simachew A, et al. (2024) Neurocognitive impairment and its associated factors among patients with diabetes mellitus who have follow up at referral hospital in Northwest, Ethiopia. *Frontiers in endocrinology*, 15, 1459585.

Poonia P, et al. (2024) Yeast poly(A)-binding protein (Pab1) controls translation initiation in vivo primarily by blocking mRNA decapping and decay. *bioRxiv : the preprint server for biology*.

Salvotti HV, et al. (2024) Three distinct patterns of mental health response following accidents in mountain sports: a follow-up study of individuals treated at a tertiary trauma center. *European archives of psychiatry and clinical neuroscience*, 274(6), 1289.

Jerez PÁ, et al. (2024) African ancestry neurodegeneration risk variant disrupts an intronic branchpoint in GBA1. *medRxiv : the preprint server for health sciences*.

Yoshida M, et al. (2024) Transcriptome analysis of long non-coding RNAs in *Mycobacterium avium* complex-infected macrophages. *Frontiers in immunology*, 15, 1374437.

Hofwimmer K, et al. (2024) IL-1 β promotes adipogenesis by directly targeting adipocyte precursors. *Nature communications*, 15(1), 7957.

Garma LD, et al. (2024) Applicability of epigenetic age models to next-generation methylation arrays. *Genome medicine*, 16(1), 116.

Yamagami K, et al. (2024) Progranulin enhances the engraftment of transplanted human iPS cell-derived cerebral neurons. *Stem cells translational medicine*, 13(11), 1113.

Gosai SJ, et al. (2024) Machine-guided design of cell-type-targeting cis-regulatory elements. *Nature*, 634(8036), 1211.

Álvarez Jerez P, et al. (2024) African ancestry neurodegeneration risk variant disrupts an intronic branchpoint in GBA1. *Nature structural & molecular biology*, 31(12), 1955.

Hu Y, et al. (2024) T4SEpp: A pipeline integrating protein language models to predict bacterial type IV secreted effectors. *Computational and structural biotechnology journal*, 23, 801.