

Resource Summary Report

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FadE

RRID:SCR_003448

Type: Tool

Proper Citation

FadE (RRID:SCR_003448)

Resource Information

URL: <https://code.google.com/p/fade/>

Proper Citation: FadE (RRID:SCR_003448)

Description: A software package designed to determine the methylation parameter at each cytosine or cytosine-guanine position in the human genome. FadE uses color reads produced by the SOLiD sequencer or nucleotide reads produced by the Illumina or 454 sequencing platforms.

Abbreviations: FadE

Synonyms: fade - Estimation of position specific methylation parameters in color or nucleotide space with NR optimization

Resource Type: software resource

Defining Citation: [PMID:22965123](#)

Availability: Free, Available for download, Freely available

Resource Name: FadE

Resource ID: SCR_003448

Alternate IDs: OMICS_00599

Alternate URLs: <https://minituba.hegroup.org/>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260815T182234+0000

Ratings and Alerts

No rating or validation information has been found for FadE.

No alerts have been found for FadE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Dong C, et al. (2026) LDIE-FDNet: Lightweight dynamic image enhancement-enabled real-time fatigue driving detection network. PloS one, 21(4), e0346055.

Franzo G, et al. (2025) Host-driven evolution of PCV2: insights into genetic diversity and adaptation. Frontiers in immunology, 16, 1577436.

Du B, et al. (2025) Multi-Space Feature Fusion and Entropy-Based Metrics for Underwater Image Quality Assessment. Entropy (Basel, Switzerland), 27(2).

Zhang F, et al. (2025) M cells targeted H. pylori antigen SAM-FAdE displayed on bacterium-like particles induce protective immunity. Journal of nanobiotechnology, 23(1), 23.

Fang W, et al. (2025) TBF-YOLOv8n: A Lightweight Tea Bud Detection Model Based on YOLOv8n Improvements. Sensors (Basel, Switzerland), 25(2).

Yoshizato T, et al. (2025) Stable clonal contribution of lineage-restricted stem cells to human hematopoiesis. Nature genetics, 57(12), 3088.

Soch J, et al. (2024) Single-value brain activity scores reflect both severity and risk across the Alzheimer's continuum. Brain : a journal of neurology, 147(11), 3789.

Morel M, et al. (2024) Accurate Detection of Convergent Mutations in Large Protein Alignments With ConDor. Genome biology and evolution, 16(4).

Pei D, et al. (2024) Fuzzy Entropy-Assisted Deconvolution Method and Its Application for Bearing Fault Diagnosis. Entropy (Basel, Switzerland), 26(4).

Benítez-Prián M, et al. (2024) Diversity and Molecular Evolution of Antimicrobial Peptides in Caecilian Amphibians. Toxins, 16(3).

Liu B, et al. (2024) ZYNQ-Based Visible Light Defogging System Design Realization. Sensors (Basel, Switzerland), 24(7).

Zhang F, et al. (2024) An M cell-targeting recombinant L. lactis vaccine against four H. pylori adhesins. Applied microbiology and biotechnology, 108(1), 231.

Giannakopoulou E, et al. (2023) A T cell receptor targeting a recurrent driver mutation in FLT3 mediates elimination of primary human acute myeloid leukemia in vivo. *Nature cancer*, 4(10), 1474.

Richter A, et al. (2023) Single-value scores of memory-related brain activity reflect dissociable neuropsychological and anatomical signatures of neurocognitive aging. *Human brain mapping*, 44(8), 3283.

Soch J, et al. (2022) Structural and Functional MRI Data Differentially Predict Chronological Age and Behavioral Memory Performance. *eNeuro*, 9(6).

Zedan A, et al. (2022) Modelling speech reception thresholds and their improvements due to spatial noise reduction algorithms in bimodal cochlear implant users. *Hearing research*, 420, 108507.

Li Y, et al. (2022) Local hyperthermia therapy induces browning of white fat and treats obesity. *Cell*, 185(6), 949.

Wei Y, et al. (2022) The MYC oncoprotein directly interacts with its chromatin cofactor PNUTS to recruit PP1 phosphatase. *Nucleic acids research*, 50(6), 3505.

Tong C, et al. (2022) Genomic signatures of recent convergent transitions to social life in spiders. *Nature communications*, 13(1), 6967.

Pezzoni G, et al. (2021) Retrospective Characterization of the 2006-2007 Swine Vesicular Disease Epidemic in Northern Italy by Whole Genome Sequence Analysis. *Viruses*, 13(7).