

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: 20260725T190539+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 34 mentions in open access literature.

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

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.

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.

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.

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.

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

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.

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).

Schädler MR, et al. (2021) Thoughts on the potential to compensate a hearing loss in noise. *F1000Research*, 10, 311.