

Resource Summary Report

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Alfred

RRID:SCR_023354

Type: Tool

Proper Citation

Alfred (RRID:SCR_023354)

Resource Information

URL: <https://github.com/tobiasrausch/alfred>

Proper Citation: Alfred (RRID:SCR_023354)

Description: Web application as interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing.

Resource Type: algorithm resource, web application, software resource

Defining Citation: [PMID:30520945](#)

Keywords: alignment, BAM, quality control, cell barcode splitting, annotation directed improvement, BAM alignment statistics, feature counting, feature annotation.

Funding: NHGRI U41HG007497

Availability: Free, Available for download, Freely available

Resource Name: Alfred

Resource ID: SCR_023354

Alternate URLs: <https://bio.tools/alfred>

License: BSD-3-Clause

Record Creation Time: 20230311T050215+0000

Record Last Update: 20260815T182737+0000

Ratings and Alerts

No rating or validation information has been found for Alfred.

No alerts have been found for Alfred.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Helsmoortel M, et al. (2026) Oxford Nanopore enhanced accuracy of long-read amplicons applied to microbial whole-genome sequencing. *Microbiology spectrum*, 14(4), e0285625.

Vidak S, et al. (2026) Transcriptional profiling of Hutchinson-Gilford progeria patients identifies primary target pathways of progerin. *Nucleus (Austin, Tex.)*, 17(1), 2611484.

Zapater LJ, et al. (2026) A transposase-derived gene required for human brain development. *Science advances*, 12(3), eadv7530.

Acebrón SP, et al. (2026) Morphogen Gradients as Drivers of Mosaicism During Early Human Development. *BioEssays : news and reviews in molecular, cellular and developmental biology*, 48(3), e70128.

Munsif M, et al. (2025) Return-to-work in lung transplant recipients: an Australian perspective. *Internal medicine journal*, 55(3), 415.

Gavriouchkina D, et al. (2025) A single-cell atlas of the bobtail squid visual and nervous system highlights molecular principles of convergent evolution. *Nature ecology & evolution*, 9(7), 1245.

Cockle E, et al. (2025) Cortical stimulation predicts language decline following SEEG radiofrequency thermocoagulation. *Brain : a journal of neurology*, 148(9), 3314.

Schulte LA, et al. (2025) Unveiling the intriguing relationship: oncogenic KRAS, morphological shifts, and mutational complexity in pancreatic mucinous cystic neoplasms. *The Journal of pathology*, 265(4), 401.

Arvidsson L, et al. (2025) Double trouble! Concomitant distal ulna fractures predict worse 1-year outcome in distal radius fractures: a registry-based cohort study of 5,536 patients. *Acta orthopaedica*, 96, 606.

Vidak S, et al. (2025) Transcriptional profiling of Hutchinson-Gilford Progeria patients identifies primary target pathways of progerin. *bioRxiv : the preprint server for biology*.

Lysenkova Wiklander M, et al. (2024) A multiomic characterization of the leukemia cell line REH using short- and long-read sequencing. *Life science alliance*, 7(8).

Sanchez-Flores M, et al. (2024) Novel genotype-phenotype correlations, differential cerebellar allele-specific methylation, and a common origin of the (ATTTC)_n insertion in

spinocerebellar ataxia type 37. Human genetics, 143(3), 211.

Yang J, et al. (2024) Modeling the United Oscillation and Wave of economic policy and urban planning employing spatial population dynamics. PloS one, 19(7), e0305465.

Beschorner N, et al. (2024) Preclinical toxicity analyses of lentiviral vectors expressing the HIV-1 LTR-specific designer-recombinase Brec1. PloS one, 19(3), e0298542.

Cosentino C, et al. (2024) Ex-SPECTing success: Predictors of successful SPECT radiotracer injection during presurgical video-EEG admissions. Epilepsia open, 9(5), 1685.

Sahuquillo-Arce JM, et al. (2024) Actinotignum schaalii infection: Challenges in diagnosis and treatment. Heliyon, 10(7), e28589.

Ordóñez CD, et al. (2023) A primer-independent DNA polymerase-based method for competent whole-genome amplification of intermediate to high GC sequences. NAR genomics and bioinformatics, 5(3), lqad073.

Singh A, et al. (2023) Exploring late Pleistocene bioturbation on Yermak Plateau to assess sea-ice conditions and primary productivity through the Ethological Ichno Quotient. Scientific reports, 13(1), 17416.