Resource Summary Report

Generated by RRID on Aug 4, 2026

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 sequencingas.

Resource Type: algorithm resource, software resource, web application

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: 20260804T043821+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 15 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

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

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

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.

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

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.

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.

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.

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.

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).

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.

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.

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.

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.