Resource Summary Report

Generated by dkNET on Sep 14, 2026

NovoAlign

RRID:SCR_014818
Type: Tool

Proper Citation

NovoAlign (RRID:SCR_014818)

Resource Information

URL: http://www.novocraft.com/products/novoalign/

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Description: Software tool designed for mapping short reads onto a reference genome generated from Illumina, Ion Torrent, and 454 NGS platforms. Its features include paired end alignment, methylation status analysis, automatic base quality calibration, and in built adapter trimming and base quality trimming.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Keywords: sequence analysis software, short read, map, genome, illumina, ion torrent, 454 ngs

Availability: Commercially available, Trial available by request

Resource Name: NovoAlign

Resource ID: SCR_014818

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Record Creation Time: 20220129T080322+0000

Record Last Update: 20260912T200017+0000

Ratings and Alerts

No rating or validation information has been found for NovoAlign.

No alerts have been found for NovoAlign.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 809 mentions in open access literature.

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

Mayanagi T, et al. (2026) Inter-individual differentially methylated region-targeted EWAS reveals epigenetic signatures of early childhood adversity. Epigenomics, 18(1), 89.

Sethumadhavan A, et al. (2026) Identification of a novel TLR7 gain-of-function variant that underlies systemic lupus erythematosus. Journal of human immunity, 2(3), e20250194.

Tirtei E, et al. (2026) Mapping Genomic Heterogeneity in Pediatric and Adolescent-Young Adult Sarcomas: Insights from the Italian SAR-GEN2016 and SAR-GEN_ITA Prospective Multicenter Trials. Cancer research communications, 6(4), 857.

Azouzi C, et al. (2026) Ribosomal RNA synthesis by RNA polymerase I is subject to premature termination of transcription. eLife, 14.

Hu M, et al. (2026) A Phase II Trial of Perioperative Camrelizumab Plus Neoadjuvant Chemotherapy in Resectable Stage IIB-IIIB Lung Squamous Cell Carcinoma. MedComm, 7(7), e70793.

Hafner J, et al. (2026) Sni445 recruits box C/D snoRNPs snR4 and snR45 to guide ribosomal RNA acetylation by Kre33. Nucleic acids research, 54(3).

Janevska S, et al. (2026) Facultative heterochromatin mediated by core and accessory chromosome-encoded H3K27-specific methyltransferases controls virulence in a fungal phytopathogen. Nucleic acids research, 54(1).

Zhou Z, et al. (2026) Targeting the TRIM25-AGO2-miR-148b-5p-ABCC1 axis overcomes chemoresistance in non-small cell lung cancer. Cell death & disease, 17(1).

Deng R, et al. (2026) The mutation landscape of Daphnia obtusa reveals evolutionary forces shaping genome stability. Molecular biology and evolution, 43(2).

Fu L, et al. (2026) Completely resolved structural variants by optical genome mapping with adaptive sampling from CNV discovery. NPJ genomic medicine, 11(1).

Torner B, et al. (2026) The role of miRNAs in the development of brain metastases originating from lung adenocarcinoma. Frontiers in genetics, 17, 1769972.

Ali A, et al. (2026) De Novo Genome Assemblies of Four Rainbow Trout Genetic Lines Reveal Structural Variants in Pursuit of a Pangenome Reference. Molecular ecology resources, 26(5), e70167.

Chen Y, et al. (2026) Accurate detection of tumor clonality and ongoing expansion mode from genomic data. bioRxiv : the preprint server for biology.

Yao S, et al. (2025) Xist RNA binds select autosomal genes and depends on Repeat B to regulate their expression. eLife, 13.

Tsukamura A, et al. (2025) KNTC1 introduces segmental heterogeneity to mitochondria. Disease models & mechanisms, 18(3).

Hasegawa N, et al. (2025) DNA demethylating agents suppress preclinical models of synovial sarcoma. The Journal of clinical investigation, 135(13).

Kang YS, et al. (2025) Leveraging a new data resource to define the response of Cryptococcus neoformans to environmental signals. Genetics, 229(1), 1.

Zhao X, et al. (2025) Comparative mitochondrial genome and transcriptome analyses reveal strain-specific features of RNA editing in Trypanosoma brucei. Nucleic acids research, 53(13).

Fennell DA, et al. (2025) Constitutive inflammation and epithelial-mesenchymal transition dictate sensitivity to nivolumab in CONFIRM: a placebo-controlled, randomised phase III trial. Nature communications, 16(1), 6688.

Marocco F, et al. (2025) Negative regulation of miRNA sorting into EVs is mediated by the capacity of RBP PCBP2 to impair the SYNCRIP-dependent miRNA loading. eLife, 14.