Resource Summary Report

Generated by RRID on Aug 4, 2026

NovoAlign

RRID:SCR_014818
Type: Tool

Proper Citation

NovoAlign (RRID:SCR_014818)

Resource Information

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

Proper Citation: NovoAlign (RRID:SCR_014818)

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: sequence analysis software, software application, data processing software, data analysis software, 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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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 787 mentions in open access literature.

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

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

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).

Laiho JE, et al. (2025) Detection of enterovirus RNA in pancreas and lymphoid tissues of organ donors with type 1 diabetes. Diabetologia, 68(6), 1211.

Srivastav MK, et al. (2025) PhpCNF-Y transcription factor infiltrates heterochromatin to generate cryptic intron-containing transcripts crucial for small RNA production. Nature communications, 16(1), 268.

Tong X, et al. (2025) Genome-Wide Characterization of Extrachromosomal Circular DNA in the Midgut of BmCPV-Infected Silkworms and Its Potential Role in Antiviral Responses. International journal of molecular sciences, 26(2).

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.

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.

Miao J, et al. (2025) GASZ directly recruits MILI to the intermitochondrial cement for piRNA biogenesis and male germ cell development. Nucleic acids research, 53(18).

K??odawska M, et al. (2025) Seeing in the Deep: Evolution of the Opsin Gene Expression in Bermin Crater Lake Cichlids. Molecular biology and evolution, 42(11).

Niu L, et al. (2025) Machine learning model for early diagnosis of breast cancer based on PiRNA expression with CA153. Scientific reports, 15(1), 30586.

Banning A, et al. (2025) Structural and Functional Characterization of N-Glycanase-1 Pathogenic Variants. Cells, 14(13).

Dunn-Davies H, et al. (2025) Systematic mapping of small nucleolar RNA interactions in human cells. RNA biology, 22(1), 1.

Yi C, et al. (2025) ZBTB16/PLZF regulates juvenile spermatogonial stem cell development through an extensive transcription factor poising network. Nature structural & molecular biology, 32(7), 1213.

Deng R, et al. (2025) The mutation landscape of Daphnia obtusa reveals evolutionary forces shaping genome stability. bioRxiv : the preprint server for biology.

Gambardella A, et al. (2025) PAK3 pathogenic variant associated with sleep-related hypermotor epilepsy in a family with parental mosaicism. Epilepsia open, 10(2), 593.

Ali A, et al. (2025) Chromosome level genome assembly and annotation of the Swanson rainbow trout homozygous line. Scientific data, 12(1), 345.

Yao S, et al. (2024) Xist RNA binds select autosomal genes and depends on Repeat B to regulate their expression. bioRxiv : the preprint server for biology.

Laverty DJ, et al. (2024) ATM inhibition exploits checkpoint defects and ATM-dependent double strand break repair in TP53-mutant glioblastoma. Nature communications, 15(1), 5294.