## **Resource Summary Report**

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# **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:** software application, data analysis software, sequence analysis software, data processing software, software resource

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

**Funding:** 

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: 20250401T061129+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 772 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

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

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).

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.

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.

He T, et al. (2024) Development of an orally bioavailable mSWI/SNF ATPase degrader and acquired mechanisms of resistance in prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 121(15), e2322563121.

Bhattacharyya N, et al. (2024) Deciphering novel TCF4-driven mechanisms underlying a common triplet repeat expansion-mediated disease. PLoS genetics, 20(5), e1011230.

Zhang M, et al. (2024) A gut microbiota rheostat forecasts responsiveness to PD-L1 and VEGF blockade in mesothelioma. Nature communications, 15(1), 7187.

Nishijima A, et al. (2024) Integrated genomic/epigenomic analysis stratifies subtypes of clear cell ovarian carcinoma, highlighting their cellular origin. Scientific reports, 14(1), 18797.

Peterson KM, et al. (2024) Serum-deprivation response of ARPE-19 cells; expression patterns relevant to age-related macular degeneration. PloS one, 19(9), e0293383.

Bhérer C, et al. (2024) A cost-effective sequencing method for genetic studies combining high-depth whole exome and low-depth whole genome. NPJ genomic medicine, 9(1), 8.

Dimitrova-Paternoga L, et al. (2024) Structural basis of ribosomal 30S subunit degradation by RNase R. Nature, 626(8001), 1133.

Murray JC, et al. (2024) Elucidating the Heterogeneity of Immunotherapy Response and Immune-Related Toxicities by Longitudinal ctDNA and Immune Cell Compartment Tracking in Lung Cancer. Clinical cancer research: an official journal of the American Association for Cancer Research, 30(2), 389.

Nokin MJ, et al. (2024) RAS-ON inhibition overcomes clinical resistance to KRAS G12C-OFF covalent blockade. Nature communications, 15(1), 7554.

Nederlof I, et al. (2024) Neoadjuvant nivolumab or nivolumab plus ipilimumab in early-stage triple-negative breast cancer: a phase 2 adaptive trial. Nature medicine, 30(11), 3223.

Zhao X, et al. (2024) Phosphorylation of AGO2 by TBK1 Promotes the Formation of Oncogenic miRISC in NSCLC. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(15), e2305541.

Selvaraju D, et al. (2024) Experimentally evolving Drosophila erecta populations may fail to establish an effective piRNA-based host defense against invading P-elements. Genome research, 34(3), 410.

Peirone S, et al. (2024) Impaired neutrophil-mediated cell death drives Ewing's Sarcoma in the background of Down syndrome. Frontiers in oncology, 14, 1429833.

Shea A, et al. (2024) Modeling Drug Responses and Evolutionary Dynamics using Patient-Derived Xenografts Reveals Precision Medicine Strategies for Triple Negative Breast Cancer. Cancer research.

Lacin H, et al. (2024) A genetic screen in Drosophila uncovers a role for senseless-2 in

surface glia in the peripheral nervous system to regulate CNS morphology. G3 (Bethesda, Md.), 14(9).