

Resource Summary Report

Generated by [dkNET](#) on Sep 2, 2026

GenomonPipeline

RRID:SCR_022989

Type: Tool

Proper Citation

GenomonPipeline (RRID:SCR_022989)

Resource Information

URL: <https://github.com/Genomon-Project>

Proper Citation: GenomonPipeline (RRID:SCR_022989)

Description: Software DNA and RNA sequence analysis pipeline.

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

Keywords: DNA sequence analysis, RNA sequence analysis

Availability: Free, Available for download, Freely available

Resource Name: GenomonPipeline

Resource ID: SCR_022989

Alternate URLs: <https://github.com/Genomon-Project/GenomonPipeline>

License URLs: <https://github.com/Genomon-Project/GenomonPipeline/blob/devel/LICENSE>

Record Creation Time: 20221123T050214+0000

Record Last Update: 20260829T182822+0000

Ratings and Alerts

No rating or validation information has been found for GenomonPipeline.

No alerts have been found for GenomonPipeline.

Data and Source Information

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Kamitori T, et al. (2026) Multi-omics analysis of pediatric minimally differentiated acute myeloid leukemia reveals RUNX1-driven stemness and chemoresistance. *Leukemia*, 40(7), 1427.

Ho K, et al. (2026) Plasma Fibrinogen Predicts Response to Immune Checkpoint Inhibitor by Inflammatory Tumor Microenvironment in Esophageal Cancer. *Cancer medicine*, 15(1), e71548.

Mikami T, et al. (2026) CAR-T cells with the CD38-CD73-Tim-3-HLA-DR+ phenotype predict the efficacy of tisagenlecleucel as a treatment for B cell precursor ALL. *Cell reports. Medicine*, 7(2), 102576.

Ikegami M, et al. (2026) Germline Pathogenic Variant Prediction Model for Tumor-Only Sequencing Based on Japanese Clinicogenomic Database. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(4), 770.

Mikami T, et al. (2025) Multi-omics analysis identifies an M-MDSC-like immunosuppressive phenotype in lineage-switched AML with KMT2A rearrangement. *Nature communications*, 16(1), 7955.

Tiwari A, et al. (2025) Synergistic RAS-MAPK and AKT Activation in MYC-Driven Tumors via Adjacent PVT1 Rearrangements. *bioRxiv : the preprint server for biology*.

Matsumura F, et al. (2025) Multiple Myeloma in a Patient with Birt-Hogg-Dub?? Syndrome. *Internal medicine (Tokyo, Japan)*, 64(18), 2764.

Zeng L, et al. (2025) Hyperactive PLCG1 induces cell-autonomous and bystander T cell activation and drug resistance. *EMBO reports*, 26(18), 4563.

Nishimura T, et al. (2024) Genomic and transcriptomic profiling of pre- and postneoadjuvant chemotherapy triple negative breast cancer tumors. *Cancer science*, 115(12), 3928.

Horaguchi S, et al. (2024) Prognostic Significance of Plasma Neutrophil Extracellular Trap Levels in Patients with Non-Small Cell Lung Cancer Treated with Immune Checkpoint Inhibitors. *Biomedicines*, 12(8).

Xiang H, et al. (2024) Multi-omics analysis-based clinical and functional significance of a novel prognostic and immunotherapeutic gene signature derived from amino acid metabolism pathways in lung adenocarcinoma. *Frontiers in immunology*, 15, 1361992.

Koya J, et al. (2024) Modeling NK-cell lymphoma in mice reveals its cell-of-origin and microenvironmental changes and identifies therapeutic targets. *Nature communications*,

15(1), 9106.

Suma S, et al. (2024) Tumor heterogeneity and immune-evasive T follicular cell lymphoma phenotypes at single-cell resolution. *Leukemia*, 38(2), 340.

Nishimura A, et al. (2023) Myeloid/natural killer (NK) cell precursor acute leukemia as a distinct leukemia type. *Science advances*, 9(50), eadj4407.

Washimi K, et al. (2023) Histological markers, sickle-shaped blood vessels, myxoid area, and infiltrating growth pattern help stratify the prognosis of patients with myxofibrosarcoma/undifferentiated sarcoma. *Scientific reports*, 13(1), 6744.

Suzuki M, et al. (2023) KMT2C expression and DNA homologous recombination repair factors in lung cancers with a high-grade fetal adenocarcinoma component. *Translational lung cancer research*, 12(8), 1738.

Komura K, et al. (2023) Tertiary lymphoid structure and neutrophil-lymphocyte ratio coordinately predict outcome of pembrolizumab. *Cancer science*, 114(12), 4622.

Kawachi K, et al. (2023) Genetic analysis of low-grade adenosquamous carcinoma of the breast progressing to high-grade metaplastic carcinoma. *Breast cancer research and treatment*, 202(3), 563.

Komura K, et al. (2023) The Impact of FGFR3 Alterations on the Tumor Microenvironment and the Efficacy of Immune Checkpoint Inhibitors in Bladder Cancer. *Molecular cancer*, 22(1), 185.

Tsuboi Y, et al. (2023) Triple-negative Thrombocythemia and Subsequent Acute Lymphoblastic Leukemia with Additional Somatic Mutations. *Internal medicine (Tokyo, Japan)*, 62(10), 1527.