

Resource Summary Report

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Picard

RRID:SCR_006525

Type: Tool

Proper Citation

Picard (RRID:SCR_006525)

Resource Information

URL: <http://broadinstitute.github.io/picard/>

Proper Citation: Picard (RRID:SCR_006525)

Description: Java toolset for working with next generation sequencing data in the BAM format.

Resource Type: software resource, software toolkit, source code

Keywords: next generation sequencing, java, bam

Availability: Available for download, Free

Resource Name: Picard

Resource ID: SCR_006525

Alternate IDs: OMICS_01066

Alternate URLs: <http://sourceforge.net/projects/picard/>,
<https://github.com/broadinstitute/picard>, <https://sources.debian.org/src/picard-tools/>

License: Apache License, v2, MIT License

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260829T183153+0000

Ratings and Alerts

- Used for sequencing service by the Human Islet Research Network community.
Contact(s): [Golnaz Vahedi](#), [Klaus Kaestner](#) - Human Islets Research Network

No alerts have been found for Picard.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15653 mentions in open access literature.

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

Wang X, et al. (2026) Clinicogenomic Characterization of Primary Sclerosing Cholangitis-Associated Biliary Tract Cancers. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(2), 363.

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. *Cancer discovery*, 16(2), 296.

Yun KH, et al. (2026) Phase IB/II Trial with Correlative Analyses of Doxorubicin plus Durvalumab Combination in Patients with Advanced Soft Tissue Sarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1686.

Yang Q, et al. (2026) Molecular mechanism of resistance to Ionafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a Ionafarnib-derived antiviral PROTAC. *Journal of virology*, 100(1), e0148725.

Stanojcic S, et al. (2026) Stranded short nascent strand sequencing reveals the topology of DNA replication origins in *Trypanosoma brucei*. *eLife*, 14.

Kim H, et al. (2026) Thyroid cancer-associated EZH1 Q571R mutation drives chromatin compaction and H3K27me3 invasion into active chromatin. *Molecular cell*, 86(14), 2739.

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(12), 2413.

Adams NM, et al. (2026) Chromatin-mediated anticipatory control of type I interferon production in plasmacytoid dendritic cells. *Immunity*, 59(2), 270.

Patel UA, et al. (2026) CRISPR Screen Identifies HDAC3 as a Novel Radiosensitizing Target in Small Cell Lung Cancer. *Molecular cancer therapeutics*, 25(1), 183.

Brodsky AL, et al. (2026) Combination Therapy with Copanlisib and Niraparib in Patients with Recurrent Endometrial and Ovarian Cancer (COPANIRA): Efficacy, Toxicity, and Translational Insights. *Clinical cancer research : an official journal of the American*

Association for Cancer Research, 32(7), 1234.

Friske JD, et al. (2026) A Conserved Enhancer Locus in Extrachromosomal DNA and Homogeneously Staining Regions Activates MYC Transcription in Group 3 Medulloblastoma. *Cancer research*, 86(13), 3160.

Sun W, et al. (2026) Reconstruction of T cell infiltration in an osteosarcoma PDX-organoid interactive biobank for personalized immunotherapy. *Cell reports. Medicine*, 7(3), 102644.

Zhang Y, et al. (2026) Co-occurrence of transcriptionally distinct persister cell states underpins neoadjuvant therapy resistance in triple-negative breast cancer. *Genome medicine*, 18(1).

Vasseur D, et al. (2026) Transcription Factor Subtype Governs Response and Resistance to DLL3-Directed T-Cell Engagement in Small Cell Lung Cancer. *bioRxiv : the preprint server for biology*.

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Chmelova L, et al. (2026) High-depth whole genome sequencing of premalignant breast lesions reveals rearrangement hotspots and personalized management opportunities. *Nature communications*, 17(1).

Xie S, et al. (2026) Fallen Leaves to Their Roots: genome-wide evidence for two independent colonizations of the Taiwan island by *Mogera* moles. *Molecular phylogenetics and evolution*, 222, 108640.

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

Kryeziu K, et al. (2026) Patient-derived organoids from metastatic colorectal cancer mirror tumor heterogeneity and predict patient survival and drug sensitivity. *Cell reports. Medicine*, 7(6), 102840.

Bakhmet EI, et al. (2026) PCBP1 orchestrates amino acid metabolism burst during the naïve-to-primed pluripotency transition. *Stem cell reports*, 21(7), 102950.