

Resource Summary Report

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ISB Cancer Genomics Cloud

RRID:SCR_017681

Type: Tool

Proper Citation

ISB Cancer Genomics Cloud (RRID:SCR_017681)

Resource Information

URL: <https://isb-cgc.appspot.com/>

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Description: Web tool as flexible cloud-based platform for cancer genomics research. Platform that serves as large-scale repository and provides computational infrastructure necessary to carry out cancer genomics research at unprecedented scales. ISB-CGC is providing access to TCGA data and computation on Google Cloud Platform.

Abbreviations: ISB-CGC

Synonyms: ISB Cancer Genomics Cloud, Institute for Systems Biology Cancer Genomics Cloud

Resource Type: web application, software resource, service resource, storage service resource, data repository

Defining Citation: [PMID:29092928](#)

Keywords: Cancer, genomics, repository, data

Funding: National Cancer Institute ;
National Institutes of Health

Availability: Restricted

Resource Name: ISB Cancer Genomics Cloud

Resource ID: SCR_017681

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260808T190111+0000

Ratings and Alerts

No rating or validation information has been found for ISB Cancer Genomics Cloud.

No alerts have been found for ISB Cancer Genomics Cloud.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Modi SR, et al. (2026) BHLHE40 Is a Transcriptional Regulatory Target of NFE2L3 in Triple-Negative Breast Cancer. *Oncology research*, 34(2), 14.

Kim H, et al. (2024) Mapping extrachromosomal DNA amplifications during cancer progression. *Nature genetics*, 56(11), 2447.

Kim E, et al. (2024) NCI Cancer Research Data Commons: Lessons Learned and Future State. *Cancer research*, 84(9), 1404.

Luebeck J, et al. (2023) Extrachromosomal DNA in the cancerous transformation of Barrett's oesophagus. *Nature*, 616(7958), 798.

Tercan B, et al. (2022) SL-Cloud: A Cloud-based resource to support synthetic lethal interaction discovery. *F1000Research*, 11, 493.

Elmarakeby HA, et al. (2021) Biologically informed deep neural network for prostate cancer discovery. *Nature*, 598(7880), 348.

He MX, et al. (2021) Transcriptional mediators of treatment resistance in lethal prostate cancer. *Nature medicine*, 27(3), 426.

Leclair NK, et al. (2020) Poison Exon Splicing Regulates a Coordinated Network of SR Protein Expression during Differentiation and Tumorigenesis. *Molecular cell*, 80(4), 648.

Kim H, et al. (2020) Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. *Nature genetics*, 52(9), 891.

Cao S, et al. (2020) Discovery of driver non-coding splice-site-creating mutations in cancer. *Nature communications*, 11(1), 5573.

Park S, et al. (2019) Differential Functions of Splicing Factors in Mammary Transformation and Breast Cancer Metastasis. *Cell reports*, 29(9), 2672.