Resource Summary Report

Generated by RRID on Sep 19, 2026

AACR GENIE cBioPortal

RRID:SCR_026217
Type: Tool

Proper Citation

AACR GENIE cBioPortal (RRID:SCR_026217)

Resource Information

URL: https://genie.cbioportal.org/

Proper Citation: AACR GENIE cBioPortal (RRID:SCR_026217)

Description: International data-sharing consortium focused on generating an evidence base for precision cancer medicine by integrating clinical-grade cancer genomic data with clinical outcome data of cancer patients treated at multiple institutions worldwide.

Resource Type: consortium, data or information resource, organization portal, portal

Defining Citation: PMID:28572459

Keywords: International data-sharing consortium, generating an evidence base, precision cancer medicine, integrating clinical-grade cancer genomic data, clinical outcome data, cancer patients,

Funding: Howard Hughes Medical Institute ;
NCI 2P30CA006516;
NCI 5P30CA068485;
NCI 5P50CA083639;
NCI 5P50CA098258;
NCI 5U01CA168394;
NCI CA006973;
NCI CA008748;
NCI CA121113;
NCI CA180950;
NCI U24CA209851;
NCI U24CA210950;
NHGRI U54HG008100

Availability: Restricted

Resource Name: AACR GENIE cBioPortal

Resource ID: SCR_026217

Record Creation Time: 20250103T053333+0000

Record Last Update: 20260919T200044+0000

Ratings and Alerts

No rating or validation information has been found for AACR GENIE cBioPortal.

No alerts have been found for AACR GENIE cBioPortal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Dundr P, et al. (2026) CTNNB1 mutation represents a recurrent driver molecular alteration in a subset of endometrial stromal tumors. Virchows Archiv : an international journal of pathology, 488(3), 661.

Ojala VK, et al. (2026) Recurrent cancer-associated ERBB4 mutations are transforming and confer resistance to targeted therapies. Molecular oncology, 20(5), 1323.

Chakroborty D, et al. (2026) Database of recurrent mutations, an unbiased web resource to browse recurrent mutations in cancers. iScience, 29(2), 114561.

Russolillo JK, et al. (2026) Comprehensive Genomic Profiling of Acral Melanoma: Insights From the AACR Project GENIE Database. The American Journal of dermatopathology, 48(5), 354.

Junttila MR, et al. (2026) Enozertinib Is a Selective, Brain-Penetrant EGFR Inhibitor for Treating Non-Small Cell Lung Cancers with EGFR Exon 20 and Atypical Mutations. Cancer research, 86(3), 759.

Lock IC, et al. (2025) Mis-splicing drives loss of function of p53E224D point mutation. PloS one, 20(3), e0318856.

Outani H, et al. (2025) Age-related genomic alterations and chemotherapy sensitivity in osteosarcoma: insights from cancer genome profiling analyses. International journal of clinical oncology, 30(2), 397.

Khalil A, et al. (2025) DiffInvex identifies evolutionary shifts in driver gene repertoires during tumorigenesis and chemotherapy. Nature communications, 16(1), 4209.

Tsilimigras DI, et al. (2025) Genomic Profiling of Biliary Tract Cancers: Comprehensive Assessment of Anatomic and Geographic Heterogeneity, Co-Alterations and Outcomes. Journal of surgical oncology, 131(7), 1352.

Boni J, et al. (2025) Concurrence of FGFR1 mutations modulates oncogenesis in glioneuronal tumors. The EMBO journal, 44(24), 7513.

Arter ZL, et al. (2025) Comprehensive Survey of AACR GENIE Database of Tumor Mutation Burden (TMB) Among All Three Classes (I, II, III) of BRAF Mutated (BRAF+) NSCLC. Lung Cancer (Auckland, N.Z.), 16, 1.

Broseghini E, et al. (2025) Exploring the Common Mutational Landscape in Cutaneous Melanoma and Pancreatic Cancer. Pigment cell & melanoma research, 38(1), e13210.

Rominger MC, et al. (2025) Mutant RIT1 cooperates with YAP to drive an EMT-like lung cancer state. Cell reports, 44(10), 116185.

Cox AD, et al. (2025) "Undruggable KRAS": druggable after all. Genes & development, 39(1-2), 132.

Lee CK, et al. (2025) Olaparib, durvalumab, and cyclophosphamide, and a prognostic blood signature in platinum-sensitive ovarian cancer: the randomized phase 2 SOLACE2 trial. Nature communications, 16(1), 9756.

Rodriquenz MG, et al. (2025) Comprehensive Molecular Screening by Next Generation Sequencing of Gastrointestinal Stromal Tumors (GISTs): In Silico Analysis and Classification of Rare KIT Exon 11 Mutations. Cancer medicine, 14(23), e71430.

Brlek P, et al. (2025) In Silico Validation of OncoOrigin: An Integrative AI Tool for Primary Cancer Site Prediction with Graphical User Interface to Facilitate Clinical Application. International journal of molecular sciences, 26(6).

Monge C, et al. (2025) Detecting PI3K and TP53 Pathway Disruptions in Early-Onset Colorectal Cancer Among Hispanic/Latino Patients. Cancer medicine, 14(7), e70791.

Dhotare PS, et al. (2025) Landscape of cancer associated EpCAM mutations: molecular modeling, predictive insights and impact on patient survival. BMC cancer, 25(1), 1066.

Zhu M, et al. (2025) Large language model trained on clinical oncology data predicts cancer progression. NPJ digital medicine, 8(1), 397.