Resource Summary Report

Generated by RRID on Aug 15, 2026

IntOGen

RRID:SCR_027727
Type: Tool

Proper Citation

IntOGen (RRID:SCR_027727)

Resource Information

URL: https://github.com/bbglab/intogen-plus

Proper Citation: IntOGen (RRID:SCR_027727)

Description: Software tool for automatic and comprehensive knowledge extraction based on mutational data from sequenced tumor samples from patients. Summarizes somatic mutations, genes and pathways involved in tumorigenesis.

Synonyms: , Intogen Plus, IntOGen-mutations platform

Resource Type: source code, software application, software resource

Defining Citation: PMID:24037244

Keywords: Cancer Genes, SNV, indel, knowledge extraction based on mutational data, sequenced tumor samples from patients data,

Availability: Free, Available for download, Freely available

Resource Name: IntOGen

Resource ID: SCR_027727

Alternate URLs: https://bitbucket.org/intogen/intogen-plus/src/master

License URLs: https://github.com/bbglab/intogen-plus?tab=License-1-ov-file#readme

Record Creation Time: 20251209T055452+0000

Record Last Update: 20260815T183307+0000

Ratings and Alerts

No rating or validation information has been found for IntOGen.

No alerts have been found for IntOGen.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Culliford R, et al. (2026) Contrasting Features of Papillary and Chromophobe Renal Cell Carcinoma Revealed by Whole-Genome Sequencing. Molecular cancer research : MCR, 24(5), 327.

Lindner ES, et al. (2026) Genetic landscape of stage II melanoma identifies CBL as a new driver gene and prognostic biomarker. British journal of cancer, 134(12), 1801.

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. Cancer discovery, 16(3), 497.

Qiu C, et al. (2026) A panel of four autoantibodies to tumour-associated antigens in patients with prostate cancer and its potential for multi-cancer detection. British journal of cancer, 134(3), 493.

Kim R, et al. (2026) Whole-genome landscapes of 1,364 breast cancers. Nature, 649(8099), 1282.

Zhang T, et al. (2025) Deciphering lung adenocarcinoma evolution and the role of LINE-1 retrotransposition. bioRxiv : the preprint server for biology.

Yu J, et al. (2025) HCNetlas: A reference database of human cell type-specific gene networks to aid disease genetic analyses. PLoS biology, 23(2), e3002702.

Wang X, et al. (2025) Clonal Hematopoietic Mutations in Plasma Cell Disorders: Clinical Subgroups and Shared Pathogenesis. Genomics, proteomics & bioinformatics, 23(2).

Kinnersley B, et al. (2025) Genomic landscape of diffuse glioma revealed by whole genome sequencing. Nature communications, 16(1), 4233.

McElderry JP, et al. (2025) Microbiome analysis of 940 lung cancers in never-smokers reveals lack of clinically relevant associations. Nature communications, 17(1), 192.

Ren W, et al. (2025) Whole-genome sequencing reveals three follicular lymphoma subtypes with distinct cell of origin and patient outcomes. Cell reports. Medicine, 6(8), 102278.

Parida P, et al. (2025) Precise identification of viral-host integration events in HPV-positive cervical cancers by targeted long-read sequencing. Tumour virus research, 20, 200325.

Zhang T, et al. (2025) APOBEC affects tumor evolution and age at onset of lung cancer in smokers. Nature communications, 16(1), 4711.

Barroux M, et al. (2025) Evolutionary and immune microenvironment dynamics during neoadjuvant treatment of esophageal adenocarcinoma. Nature cancer, 6(5), 820.

Ward JC, et al. (2025) Analysis of IDH1 and IDH2 mutations as causes of the hypermethylator phenotype in colorectal cancer. The Journal of pathology, 267(1), 40.

Khandekar A, et al. (2025) Examining the Role of Extrachromosomal DNA in 1,216 Lung Cancers. bioRxiv : the preprint server for biology.

Espinoza-Ferrao S, et al. (2025) Global analysis of actionable genomic alterations in thyroid cancer and precision-based pharmacogenomic strategies. Frontiers in pharmacology, 16, 1524623.

Pellegrini S, et al. (2025) Oncodrive3D: fast and accurate detection of structural clusters of somatic mutations under positive selection. Nucleic acids research, 53(15).

Calvet F, et al. (2025) Sex and smoking bias in the selection of somatic mutations in human bladder. Nature, 647(8089), 436.

Zhang N, et al. (2024) A novel hypergraph model for identifying and prioritizing personalized drivers in cancer. PLoS computational biology, 20(4), e1012068.