Resource Summary Report

Generated by T1D on Aug 4, 2026

Scalpel

RRID:SCR_012107
Type: Tool

Proper Citation

Scalpel (RRID:SCR_012107)

Resource Information

URL: http://scalpel.sourceforge.net/

Proper Citation: Scalpel (RRID:SCR_012107)

Description: A software package for detecting INDELs (INsertions and DELetions) mutations in a reference genome which has been sequenced with next-generation sequencing technology (e.g., Illumina).

Resource Type: software resource

Defining Citation: PMID:25128977

Keywords: software package, c++, perl, bio.tools

Resource Name: Scalpel

Resource ID: SCR_012107

Alternate IDs: biotools:scalpel, OMICS_05395

Alternate URLs: https://bio.tools/scalpel

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260801T190435+0000

Ratings and Alerts

No rating or validation information has been found for Scalpel.

No alerts have been found for Scalpel.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 57 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Ake F, et al. (2025) Quantification of transcript isoforms at the single-cell level using SCALPEL. Nature communications, 16(1), 6402.

Fu Y, et al. (2025) Integrated circulating tumor DNA-based prognostic algorithm for limited stage small-cell lung cancer under definitive chemoradiotherapy and utility in consolidation immunotherapy benefit prediction. Cell communication and signaling : CCS, 23(1), 480.

Zhang Y, et al. (2024) Toripalimab plus anlotinib in patients with recurrent or metastatic nasopharyngeal carcinoma: A multicenter, single-arm phase 2 trial (TORAL). Cell reports. Medicine, 5(12), 101833.

Hobor S, et al. (2024) Mixed responses to targeted therapy driven by chromosomal instability through p53 dysfunction and genome doubling. Nature communications, 15(1), 4871.

Guille A, et al. (2024) A benchmarking study of individual somatic variant callers and voting-based ensembles for whole-exome sequencing. Briefings in bioinformatics, 26(1).

Hariprakash JM, et al. (2024) Leveraging Tissue-Specific Enhancer-Target Gene Regulatory Networks Identifies Enhancer Somatic Mutations That Functionally Impact Lung Cancer. Cancer research, 84(1), 133.

Malamon JS, et al. (2024) A comparative study of structural variant calling in WGS from Alzheimer's disease families. Life science alliance, 7(5).

Caswell DR, et al. (2024) The role of APOBEC3B in lung tumor evolution and targeted cancer therapy resistance. Nature genetics, 56(1), 60.

Elhassan YS, et al. (2024) Primary unilateral macronodular adrenal hyperplasia with concomitant glucocorticoid and androgen excess and KDM1A inactivation. European journal of endocrinology, 191(3), 334.

Feng J, et al. (2023) Primary papillary epithelial tumor of the sella and posterior pituitary tumor show similar (epi)genetic features and constitute a single neuro-oncological entity. Neuro-oncology, 25(8), 1487.

Spain L, et al. (2023) Late-Stage Metastatic Melanoma Emerges through a Diversity of Evolutionary Pathways. Cancer discovery, 13(6), 1364.

Wei Y, et al. (2023) Human 8-cell embryos enable efficient induction of disease-preventive mutations without off-target effect by cytosine base editor. Protein & cell, 14(6), 416.

Valero C, et al. (2023) Clinical-genomic determinants of immune checkpoint blockade response in head and neck squamous cell carcinoma. The Journal of clinical investigation, 133(19).

Wobser M, et al. (2022) Panel Sequencing of Primary Cutaneous B-Cell Lymphoma. Cancers, 14(21).

Freed-Pastor WA, et al. (2021) The CD155/TIGIT axis promotes and maintains immune evasion in neoantigen-expressing pancreatic cancer. Cancer cell, 39(10), 1342.

Au L, et al. (2021) Determinants of anti-PD-1 response and resistance in clear cell renal cell carcinoma. Cancer cell, 39(11), 1497.

Leoni G, et al. (2021) VENUS, a Novel Selection Approach to Improve the Accuracy of Neoantigens' Prediction. Vaccines, 9(8).

Zhang Z, et al. (2021) Protocol for detecting plastic changes in defined neuronal populations in neuropathic mice. STAR protocols, 2(3), 100698.

Jones W, et al. (2021) A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome biology, 22(1), 111.

Ma Y, et al. (2021) Copy number loss in granzyme genes confers resistance to immune checkpoint inhibitor in nasopharyngeal carcinoma. Journal for immunotherapy of cancer, 9(3).