

Resource Summary Report

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EBCall

RRID:SCR_006791

Type: Tool

Proper Citation

EBCall (RRID:SCR_006791)

Resource Information

URL: <https://github.com/friend1ws/EBCall>

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Description: A software package for somatic mutation detection (including InDels). EBCall uses not only paired tumor/normal sequence data of a target sample, but also multiple non-paired normal reference samples for evaluating distribution of sequencing errors, which leads to an accurate mutaiton detection even in case of low sequencing depths and low allele frequencies.

Abbreviations: EBCall

Synonyms: EBCall (Empirical Baysian mutation Calling), Empirical Baysian mutation Calling

Resource Type: software resource

Defining Citation: [PMID:23471004](#)

Keywords: mutation, cancer, genome, sequencing, bio.tools

Availability: Copyright conditions, Acknowledgement required

Resource Name: EBCall

Resource ID: SCR_006791

Alternate IDs: biotools:ebcall, OMICS_00084

Alternate URLs: <https://bio.tools/ebcall>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260801T190317+0000

Ratings and Alerts

No rating or validation information has been found for EBCall.

No alerts have been found for EBCall.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Yoshizato T, et al. (2025) Stable clonal contribution of lineage-restricted stem cells to human hematopoiesis. *Nature genetics*, 57(12), 3088.

Fukumoto T, et al. (2024) Steroids-producing nodules: a two-layered adrenocortical nodular structure as a precursor lesion of cortisol-producing adenoma. *EBioMedicine*, 103, 105087.

Nagayama S, et al. (2023) Mutated genes on ctDNA detecting postoperative recurrence presented reduced neoantigens in primary tumors in colorectal cancer cases. *Scientific reports*, 13(1), 1366.

Shah RK, et al. (2023) Utilizing immunogenomic approaches to prioritize targetable neoantigens for personalized cancer immunotherapy. *Frontiers in immunology*, 14, 1301100.

Tabata M, et al. (2023) Inter- and intra-tumor heterogeneity of genetic and immune profiles in inherited renal cell carcinoma. *Cell reports*, 42(7), 112736.

Takeda J, et al. (2022) Amplified EPOR/JAK2 Genes Define a Unique Subtype of Acute Erythroid Leukemia. *Blood cancer discovery*, 3(5), 410.

Skowron P, et al. (2021) The transcriptional landscape of Shh medulloblastoma. *Nature communications*, 12(1), 1749.

Hurst CD, et al. (2021) Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. *Cell reports. Medicine*, 2(12), 100472.

Fujii Y, et al. (2021) Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. *Cancer cell*, 39(6), 793.

Xu Y, et al. (2021) Technological advances in cancer immunity: from immunogenomics to single-cell analysis and artificial intelligence. *Signal transduction and targeted therapy*, 6(1), 312.

Inagaki-Kawata Y, et al. (2020) Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. *Communications biology*, 3(1), 578.

Chen CCL, et al. (2020) Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. *Cell*, 183(6), 1617.

Kawasaki K, et al. (2020) An Organoid Biobank of Neuroendocrine Neoplasms Enables Genotype-Phenotype Mapping. *Cell*, 183(5), 1420.

Sato K, et al. (2020) Genetic landscape of external auditory canal squamous cell carcinoma. *Cancer science*, 111(8), 3010.

Suzuki H, et al. (2019) Recurrent noncoding U1 snRNA mutations drive cryptic splicing in SHH medulloblastoma. *Nature*, 574(7780), 707.

Xue R, et al. (2019) Genomic and Transcriptomic Profiling of Combined Hepatocellular and Intrahepatic Cholangiocarcinoma Reveals Distinct Molecular Subtypes. *Cancer cell*, 35(6), 932.

Bohannan ZS, et al. (2019) Calling Variants in the Clinic: Informed Variant Calling Decisions Based on Biological, Clinical, and Laboratory Variables. *Computational and structural biotechnology journal*, 17, 561.

Krøigård AB, et al. (2016) Evaluation of Nine Somatic Variant Callers for Detection of Somatic Mutations in Exome and Targeted Deep Sequencing Data. *PloS one*, 11(3), e0151664.

Shiraishi Y, et al. (2014) Integrated analysis of whole genome and transcriptome sequencing reveals diverse transcriptomic aberrations driven by somatic genomic changes in liver cancers. *PloS one*, 9(12), e114263.