# Resource Summary Report

Generated by RRID on Apr 9, 2025

## EBCall

RRID:SCR_006791
Type: Tool

### Proper Citation

EBCall (RRID:SCR_006791)

### Resource Information

**URL:** https://github.com/friend1ws/EBCall

**Proper Citation:** EBCall (RRID:SCR_006791)

**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

**Funding:**

**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:** 20250214T183058+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 18 mentions in open access literature.

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

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.

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

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.

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.

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.

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

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

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

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.

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.