# **Resource Summary Report**

Generated by NIF on May 20, 2025

## **BlindCall**

RRID:SCR\_001280

Type: Tool

### **Proper Citation**

BlindCall (RRID:SCR\_001280)

#### **Resource Information**

URL: http://cbcb.umd.edu/~hcorrada/secgen/

Proper Citation: BlindCall (RRID:SCR\_001280)

Description: Software for ultra-fast base-calling of second-generation sequencing data by

blind deconvolution.

Abbreviations: BlindCall

Resource Type: software resource

**Defining Citation:** PMID:24413520

Keywords: base-calling, second-generation sequencing, blind deconvolution

**Funding:** 

Resource Name: BlindCall

Resource ID: SCR\_001280

Alternate IDs: OMICS\_02216

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20250519T203122+0000

## Ratings and Alerts

No rating or validation information has been found for BlindCall.

No alerts have been found for BlindCall.

## **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 1 mentions in open access literature.

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

Wang B, et al. (2017) An adaptive decorrelation method removes Illumina DNA base-calling errors caused by crosstalk between adjacent clusters. Scientific reports, 7, 41348.