

Resource Summary Report

Generated by SPARC SAWG on Aug 2, 2026

CEQer

RRID:SCR_010813

Type: Tool

Proper Citation

CEQer (RRID:SCR_010813)

Resource Information

URL: <http://www.ngsbicocca.org/html/ceqer.html>

Proper Citation: CEQer (RRID:SCR_010813)

Description: A graphical, event-driven tool for CNA/AI-coupled analysis of exome sequencing reads.

Abbreviations: CEQer

Synonyms: Comparative Exome Quantification analyzer

Resource Type: software resource

Defining Citation: [PMID:24124457](#)

Keywords: bio.tools

Availability: Commercial license, Free

Resource Name: CEQer

Resource ID: SCR_010813

Alternate IDs: biotools:ceqer, OMICS_00329

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

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190416+0000

Ratings and Alerts

No rating or validation information has been found for CEQer.

No alerts have been found for CEQer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Fontana D, et al. (2024) Late relapse of chronic myeloid leukemia after allogeneic bone marrow transplantation points to KANSARL (KANS1::ARL17A) alteration: a case report with insights on the molecular landscape. *Annals of hematology*, 103(5), 1561.

Franceschi S, et al. (2018) Cancer astrocytes have a more conserved molecular status in long recurrence free survival (RFS) IDH1 wild-type glioblastoma patients: new emerging cancer players. *Oncotarget*, 9(35), 24014.

Piazza R, et al. (2017) OncoScore: a novel, Internet-based tool to assess the oncogenic potential of genes. *Scientific reports*, 7, 46290.

Miyazaki J, et al. (2015) Intragenic duplication in the PKHD1 gene in autosomal recessive polycystic kidney disease. *BMC medical genetics*, 16, 98.

Yin S, et al. (2014) Exome sequencing identifies frequent mutation of MLL2 in non-small cell lung carcinoma from Chinese patients. *Scientific reports*, 4, 6036.

Reimann E, et al. (2014) Whole exome sequencing of a single osteosarcoma case--integrative analysis with whole transcriptome RNA-seq data. *Human genomics*, 8(1), 20.

Piazza R, et al. (2013) CEQer: a graphical tool for copy number and allelic imbalance detection from whole-exome sequencing data. *PLoS one*, 8(10), e74825.