

# Resource Summary Report

Generated by SPARC SAWG on Sep 15, 2026

## CEM

RRID:SCR\_013241

Type: Tool

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### Proper Citation

CEM (RRID:SCR\_013241)

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### Resource Information

**URL:** <http://alumni.cs.ucr.edu/~liw/cem.html>

**Proper Citation:** CEM (RRID:SCR\_013241)

**Description:** An algorithm to assemble transcripts and estimate their expression levels from RNA-Seq reads.

**Abbreviations:** CEM

**Synonyms:** CEM: Transcriptome Assembly and Isoform Expression Level Estimation from Biased RNA-Seq Reads

**Resource Type:** software resource

**Keywords:** bio.tools

**Resource Name:** CEM

**Resource ID:** SCR\_013241

**Alternate IDs:** OMICS\_01271, biotools:cem

**Alternate URLs:** <https://bio.tools/cem>

**Record Creation Time:** 20220129T080315+0000

**Record Last Update:** 20260912T195800+0000

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### Ratings and Alerts

No rating or validation information has been found for CEM.

No alerts have been found for CEM.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Angelini C, et al. (2014) Computational approaches for isoform detection and estimation: good and bad news. BMC bioinformatics, 15, 135.