

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## QC-Chain

RRID:SCR\_005438

Type: Tool

---

### Proper Citation

QC-Chain (RRID:SCR\_005438)

---

### Resource Information

**URL:** <http://www.computationalbioenergy.org/qc-chain.html>

**Proper Citation:** QC-Chain (RRID:SCR\_005438)

**Description:** A software package of quality control tools for next generation sequencing (NGS) data, consisting of both raw reads quality evaluation and de novo contamination screening, which could identify all possible contamination sequences. This QC pipeline supplies a fast, easy-to-use, and parallel processing approach to accomplish the comprehensive QC steps, which could be applied widely to almost all kinds of NGS reads, including genomic, transcriptomic and metagenomic data.

**Abbreviations:** QC-Chain

**Resource Type:** software resource

**Keywords:** next generation sequencing

**Resource Name:** QC-Chain

**Resource ID:** SCR\_005438

**Alternate IDs:** OMICS\_01070

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20260905T132535+0000

---

### Ratings and Alerts

No rating or validation information has been found for QC-Chain.

No alerts have been found for QC-Chain.

---

### Data and Source Information

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

---

## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Mills RJ, et al. (2019) Drug Screening in Human PSC-Cardiac Organoids Identifies Pro-proliferative Compounds Acting via the Mevalonate Pathway. Cell stem cell, 24(6), 895.

Escobar-Zepeda A, et al. (2015) The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. Frontiers in genetics, 6, 348.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Zhou Q, et al. (2013) QC-Chain: fast and holistic quality control method for next-generation sequencing data. PloS one, 8(4), e60234.