

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## CorQ

RRID:SCR\_000660

Type: Tool

---

### Proper Citation

CorQ (RRID:SCR\_000660)

---

### Resource Information

**URL:** [http://mullinslab.microbiol.washington.edu/publications/iyer\\_2012/](http://mullinslab.microbiol.washington.edu/publications/iyer_2012/)

**Proper Citation:** CorQ (RRID:SCR\_000660)

**Description:** A set of perl programs that correct errors in 454 pyrosequences by identifying and flagging poor quality insertions, deletions and substitutions within an alignment. The algorithm utilizes the inherent base quality in sequence-specific context to correct for homopolymer and non-homopolymer insertion and deletion errors. CorQ also takes uneven read mapping into account for correcting pyrosequencing miscall errors and it identifies and corrects carry forward errors.

**Resource Type:** software resource

**Defining Citation:** [PMID:24039850](#)

**Keywords:** homopolymer, indel, corq, uneven read mapping, pyrosequence error, forward errors

**Resource Name:** CorQ

**Resource ID:** SCR\_000660

**Alternate IDs:** OMICS\_01039

**Record Creation Time:** 20220129T080202+0000

**Record Last Update:** 20260725T190450+0000

---

### Ratings and Alerts

No rating or validation information has been found for CorQ.

No alerts have been found for CorQ.

## 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 [nidm-terms](#) .

Iyer S, et al. (2013) Quality score based identification and correction of pyrosequencing errors. PloS one, 8(9), e73015.