

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

CorQ

RRID:SCR_000660

Type: Tool

Proper Citation

CorQ (RRID:SCR_000660)

Resource Information

URL: 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 [PRECISE-TBI](#) .

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