

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## Pyrocleaner

RRID:SCR\_000584

Type: Tool

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### Proper Citation

Pyrocleaner (RRID:SCR\_000584)

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### Resource Information

**URL:** <https://mulcyber.toulouse.inra.fr/plugins/mediawiki/wiki/ng6/index.php/Pyrocleaner>

**Proper Citation:** Pyrocleaner (RRID:SCR\_000584)

**Description:** A software module for cleaning 454 pyrosequencing reads using filters such as read duplication, length, complexity, base-pair quality and number of undetermined bases. The software also uses flowgram files of paired-end sequences to validate paired-ends files of another file.

**Abbreviations:** Pyrocleaner

**Resource Type:** software resource

**Defining Citation:** [PMID:21615897](#)

**Keywords:** pyrosequence, assembly, rna, dna, duplication, length, complexity, bases, flowgram, paired end

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Pyrocleaner

**Resource ID:** SCR\_000584

**Alternate IDs:** OMICS\_01069

**License:** GNU General Public License

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

**Record Last Update:** 20260801T190125+0000

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### Ratings and Alerts

No rating or validation information has been found for Pyrocleaner.

No alerts have been found for Pyrocleaner.

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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 [RRID](#) .

Jérôme M, et al. (2011) Assessment of replicate bias in 454 pyrosequencing and a multi-purpose read-filtering tool. BMC research notes, 4, 149.