

# Resource Summary Report

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## TAPyR

RRID:SCR\_000588

Type: Tool

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### Proper Citation

TAPyR (RRID:SCR\_000588)

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### Resource Information

**URL:** <http://www.tapyr.net/>

**Proper Citation:** TAPyR (RRID:SCR\_000588)

**Description:** An efficient software tool for the local alignment of pyrosequencing reads produced by the GS FLX (454) Genome Analyzer technology against a reference genome sequence. The approach explores the characteristics of the data in re-sequencing applications and uses state of the art BWT-based indexing techniques combined with a flexible seed-based approach, leading to a fast and accurate algorithm which needs very little user parameterization. Although initially developed having this specific technology in mind, this software performs equally well on any other platform that can return its sequencing reads in the FASTA, FASTQ or SFF formats, including Illumina, Ion Torrent and Pacific Biosciences technologies.

**Synonyms:** Tool for Alignment of Pyrosequencing Reads

**Resource Type:** software resource

**Defining Citation:** [PMID:21672185](#)

**Keywords:** gs flx, genome analyzer, bwt, fasta, fastq, sff formats, pyrosequencing reads, bio.tools

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

**Resource Name:** TAPyR

**Resource ID:** SCR\_000588

**Alternate IDs:** biotools:tapyr, OMICS\_00693

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

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

**Record Last Update:** 20260919T194926+0000

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## Ratings and Alerts

No rating or validation information has been found for TAPyR.

No alerts have been found for TAPyR.

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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 [nidm-terms](#) .

Fernandes F, et al. (2011) Efficient alignment of pyrosequencing reads for re-sequencing applications. BMC bioinformatics, 12, 163.