

Resource Summary Report

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

TAPyR

RRID:SCR_000588

Type: Tool

Proper Citation

TAPyR (RRID:SCR_000588)

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: 20260905T132423+0000

Ratings and Alerts

No rating or validation information has been found for TAPyR.

No alerts have been found for TAPyR.

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 [Kravitz](#) .

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