

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

TRiCoLOR

RRID:SCR_018801

Type: Tool

Proper Citation

TRiCoLOR (RRID:SCR_018801)

Resource Information

URL: <https://github.com/davidebolo1993/TRiCoLOR>

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Description: Command line application for tandem repeats profiling from error prone long read sequencing data. Works on data from Oxford Nanopore Technologies and Pacific Biosciences sequencers. Used on whole genome alignments.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Keywords: Tandem repeat, long read sequencing data, whole genome alignment, data analysis, sequence analysis, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: TRiCoLOR

Resource ID: SCR_018801

Alternate IDs: biotools:tricolor

Alternate URLs: <https://bio.tools/tricolor>

License: GNU Lesser General Public License v3.0

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260912T195906+0000

Ratings and Alerts

No rating or validation information has been found for TRiCoLOR.

No alerts have been found for TRiCoLOR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Walker K, et al. (2022) The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. F1000Research, 11, 530.

Bolognini D, et al. (2020) TRiCoLOR: tandem repeat profiling using whole-genome long-read sequencing data. GigaScience, 9(10).