

Resource Summary Report

Generated by [RRID](#) on Aug 9, 2026

nTrackAnnotator

RRID:SCR_028789

Type: Tool

Proper Citation

nTrackAnnotator (RRID:SCR_028789)

Resource Information

URL:

<https://www.sciencedirect.com/science/article/abs/pii/S2452014417300055?via%3Dihub>

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Description: Standalone, Windows-based software program designed to identify and annotate low-complexity purine and pyrimidine regions as well as user-defined nucleotide sequences within prokaryotic and eukaryotic genomes. It features a graphical user interface and performs rapid "one-go" genome analyses without requiring high-performance computing clusters. Software for detection and annotation of sequence tracks of chosen nucleic acid bases with defined length in genome. Used to identify low-complexity regions containing DNA sequences of selected nucleotide(s) and to annotate the data with the support of NCBI/Genome database.

Resource Type: standalone software, software resource, software application

Defining Citation: [DOI:10.1016/j.genrep.2017.01.004](https://doi.org/10.1016/j.genrep.2017.01.004)

Keywords: identify low-complexity regions containing DNA sequences, detection and annotation of sequence tracks, chosen nucleic acid bases, defined length in genome,

Funding: ICMR ;
New Delhi ;
India

Availability: Restricted

Resource Name: nTrackAnnotator

Resource ID: SCR_028789

Old URLs: <http://www.aiims.edu/images/depart/biochem/nTrackAnnotator.rar>

Record Creation Time: 20260805T044609+0000

Record Last Update: 20260808T190834+0000

Ratings and Alerts

No rating or validation information has been found for nTrackAnnotator.

No alerts have been found for nTrackAnnotator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.