

# Resource Summary Report

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## nTrackAnnotator

RRID:SCR\_028789

Type: Tool

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### Proper Citation

nTrackAnnotator (RRID:SCR\_028789)

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### 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:** software application, software resource, standalone software

**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:** 20260829T183549+0000

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## Ratings and Alerts

No rating or validation information has been found for nTrackAnnotator.

No alerts have been found for nTrackAnnotator.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.