

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

INCLUSive

RRID:SCR_013488

Type: Tool

Proper Citation

INCLUSive (RRID:SCR_013488)

Resource Information

URL: <http://tomcatbackup.esat.kuleuven.be/inclusive/>

Proper Citation: INCLUSive (RRID:SCR_013488)

Description: A suit of algorithms and tools for the analysis of gene expression data and the discovery of cis-regulatory sequence elements.

Abbreviations: INCLUSive

Resource Type: software resource

Defining Citation: [PMID:12824346](#)

Keywords: bio.tools

Availability: Acknowledgement requested

Resource Name: INCLUSive

Resource ID: SCR_013488

Alternate IDs: OMICS_00766, biotools:inclusive

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

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260801T190448+0000

Ratings and Alerts

No rating or validation information has been found for INCLUSive.

No alerts have been found for INCLUSive.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Taskiran II, et al. (2024) Cell-type-directed design of synthetic enhancers. *Nature*, 626(7997), 212.

Melendez-Torres GJ, et al. (2022) Effects of a Whole-School Health Intervention on Clustered Adolescent Health Risks: Latent Transition Analysis of Data from the INCLUSIVE Trial. *Prevention science : the official journal of the Society for Prevention Research*, 23(1), 1.

Melendez-Torres GJ, et al. (2022) Locating and testing the healthy context paradox: examples from the INCLUSIVE trial. *BMC medical research methodology*, 22(1), 57.

M??ller JV, et al. (2019) A university's response to people with disabilities in Worcester, Western Cape. *African journal of disability*, 8, 439.

Pilalis E, et al. (2011) Escherichia coli genome-wide promoter analysis: identification of additional AtoC binding target elements. *BMC genomics*, 12(1), 238.

Monsieurs P, et al. (2006) More robust detection of motifs in coexpressed genes by using phylogenetic information. *BMC bioinformatics*, 7, 160.

Vandepoele K, et al. (2006) Identification of novel regulatory modules in dicotyledonous plants using expression data and comparative genomics. *Genome biology*, 7(11), R103.