

Resource Summary Report

Generated by [dkNET](#) on Sep 1, 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: 20260829T182436+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 [dkNET](#) .

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.