

Resource Summary Report

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CoryneRegNet

RRID:SCR_002255

Type: Tool

Proper Citation

CoryneRegNet (RRID:SCR_002255)

Resource Information

URL: <http://www.coryneregnet.de>

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Description: Reference database and analysis platform for corynebacterial transcription factors and gene regulatory networks. It generates links to genome annotations, to identified transcription factors and to the corresponding cis-regulatory elements. CoryneRegNet is based on a multi-layered, hierarchical and modular concept of transcriptional regulation and was implemented by using the relational database management system MySQL and an ontology-based data structure.

Abbreviations: CoryneRegNet

Resource Type: data or information resource, database

Defining Citation: [PMID:22080556](#), [PMID:19498379](#), [PMID:18426593](#), [PMID:17986320](#), [PMID:17229482](#), [PMID:16478536](#)

Keywords: gene, regulatory network, transcription factor, interaction, cis-regulatory element, bio.tools

Availability: Free, Freely available

Resource Name: CoryneRegNet

Resource ID: SCR_002255

Alternate IDs: biotools:coryneregnet, nif-0000-02689, OMICS_01858

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

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260801T190909+0000

Ratings and Alerts

No rating or validation information has been found for CoryneRegNet.

No alerts have been found for CoryneRegNet.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Yu C, et al. (2025) Elucidating the Mechanism of Temporal Adaptation to Hydrogen Peroxide-Induced Oxidative Stress in *Corynebacterium glutamicum*. *Microbial biotechnology*, 18(6), e70170.

Parise D, et al. (2021) On the Consistency between Gene Expression and the Gene Regulatory Network of *Corynebacterium glutamicum*. *Network and systems medicine*, 4(1), 51.

Graf M, et al. (2019) Continuous Adaptive Evolution of a Fast-Growing *Corynebacterium glutamicum* Strain Independent of Protocatechuate. *Frontiers in microbiology*, 10, 1648.

Haas T, et al. (2019) Identifying the Growth Modulon of *Corynebacterium glutamicum*. *Frontiers in microbiology*, 10, 974.

Ibraim IC, et al. (2019) Transcriptome profile of *Corynebacterium pseudotuberculosis* in response to iron limitation. *BMC genomics*, 20(1), 663.

Ko YJ, et al. (2018) Biosynthesis of organic photosensitizer Zn-porphyrin by diphtheria toxin repressor (DtxR)-mediated global upregulation of engineered heme biosynthesis pathway in *Corynebacterium glutamicum*. *Scientific reports*, 8(1), 14460.

Dostálová H, et al. (2018) Overlap of Promoter Recognition Specificity of Stress Response Sigma Factors SigD and SigH in *Corynebacterium glutamicum* ATCC 13032. *Frontiers in microbiology*, 9, 3287.

Lee HN, et al. (2018) *Corynebacterium* Cell Factory Design and Culture Process Optimization for Muconic Acid Biosynthesis. *Scientific reports*, 8(1), 18041.

Catarina Teodoro Castro B, et al. (2018) UvrB protein of *Corynebacterium pseudotuberculosis* complements the phenotype of knockout *Escherichia coli* and recognizes DNA damage caused by UV radiation but not 8-oxoguanine in vitro. *Gene*, 639, 34.

Zhang H, et al. (2018) Understanding the high L-valine production in *Corynebacterium glutamicum* VWB-1 using transcriptomics and proteomics. *Scientific reports*, 8(1), 3632.

O'Neill PK, et al. (2016) Parametric bootstrapping for biological sequence motifs. *BMC bioinformatics*, 17(1), 406.

Lubitz D, et al. (2016) Ciprofloxacin triggered glutamate production by *Corynebacterium glutamicum*. *BMC microbiology*, 16(1), 235.

Taniguchi H, et al. (2015) Exploring the role of sigma factor gene expression on production by *Corynebacterium glutamicum*: sigma factor H and FMN as example. *Frontiers in microbiology*, 6, 740.

Rees MA, et al. (2015) Changes in protein abundance are observed in bacterial isolates from a natural host. *Frontiers in cellular and infection microbiology*, 5, 71.

Heider SA, et al. (2012) Carotenoid biosynthesis and overproduction in *Corynebacterium glutamicum*. *BMC microbiology*, 12, 198.

Pacheco LG, et al. (2012) A Role for Sigma Factor σ^E in *Corynebacterium pseudotuberculosis* Resistance to Nitric Oxide/Peroxide Stress. *Frontiers in microbiology*, 3, 126.

Baumbach J, et al. (2007) CoryneRegNet 4.0 - A reference database for corynebacterial gene regulatory networks. *BMC bioinformatics*, 8, 429.