

Resource Summary Report

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Bionemo

RRID:SCR_007565

Type: Tool

Proper Citation

Bionemo (RRID:SCR_007565)

Resource Information

URL: <http://bionemo.bioinfo.cnio.es>

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Description: Bionemo stores manually curated information about proteins and genes directly implicated in biodegradation metabolism. The database includes information on sequence, domains and structures for proteins; and sequence, regulatory elements and transcription units for genes. Bionemo complements other biodegradation databases such as the University of Minnesota Biocatalysis/Biodegradation Database, or Metarouter, which focus on the biochemical aspects of biodegradation. Bionemo has been built by manually associating sequences databases entries to biodegradation reactions, using the information extracted from published articles. Information on transcription units and their regulation was also extracted from the literature for biodegradation genes, and linked to the underlying biochemical network.

Synonyms: Bionemo

Resource Type: data or information resource, database

Keywords: gene sequence, biodegradation, metabolism, protein domain, protein sequence, protein structure, regulatory elements, transcription unit

Resource Name: Bionemo

Resource ID: SCR_007565

Alternate IDs: nif-0000-02610

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260729T044148+0000

Ratings and Alerts

No rating or validation information has been found for Bionemo.

No alerts have been found for Bionemo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Haddad R, et al. (2025) Targeted molecular generation with latent reinforcement learning. Scientific reports, 15(1), 15202.

Sotelo J, et al. (2025) Neurobiological and Chemical Characterization of the Cyanobacterial Metabolite Veraguamide E. bioRxiv : the preprint server for biology.

Kamuntavičius G, et al. (2025) Benchmarking ML in ADMET predictions: the practical impact of feature representations in ligand-based models. Journal of cheminformatics, 17(1), 108.

Sevgen E, et al. (2025) ProT-VAE: Protein Transformer Variational AutoEncoder for functional protein design. Proceedings of the National Academy of Sciences of the United States of America, 122(41), e2408737122.

Hetmann M, et al. (2024) Folding the human proteome using BioNeMo: A fused dataset of structural models for machine learning purposes. Scientific data, 11(1), 591.

Tellechea-Luzardo J, et al. (2023) Sensbio: an online server for biosensor design. BMC bioinformatics, 24(1), 71.

Parigger L, et al. (2023) AI-assisted structural consensus-proteome prediction of human monkeypox viruses isolated within a year after the 2022 multi-country outbreak. Microbiology spectrum, 11(6), e0231523.

Mishra S, et al. (2021) Recent Advanced Technologies for the Characterization of Xenobiotic-Degrading Microorganisms and Microbial Communities. Frontiers in bioengineering and biotechnology, 9, 632059.

Jaiswal S, et al. (2019) Gene Editing and Systems Biology Tools for Pesticide Bioremediation: A Review. Frontiers in microbiology, 10, 87.

Koch M, et al. (2018) A dataset of small molecules triggering transcriptional and translational cellular responses. Data in brief, 17, 1374.

Delépine B, et al. (2016) SensiPath: computer-aided design of sensing-enabling metabolic pathways. Nucleic acids research, 44(W1), W226.

Arora PK, et al. (2014) Integration of bioinformatics to biodegradation. Biological procedures online, 16, 8.