

Resource Summary Report

Generated by [NIF](#) on Sep 15, 2026

[NSW BioNet](#)

RRID:SCR_019162

Type: Tool

Proper Citation

NSW BioNet (RRID:SCR_019162)

Resource Information

URL: <http://www.bionet.nsw.gov.au/>

Proper Citation: NSW BioNet (RRID:SCR_019162)

Description: Repository for biodiversity data products managed by Department of Planning, Industry and Environment, New South Wales, Australia. It stores species sightings, systematic surveys, threatened biodiversity records and species names.

Synonyms: New South Wales BioNet

Resource Type: data or information resource, data repository, portal, service resource, storage service resource

Keywords: Species sightings, systematic surveys, threatened biodiversity records, species names, data

Availability: Restricted

Resource Name: NSW BioNet

Resource ID: SCR_019162

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260912T195910+0000

Ratings and Alerts

No rating or validation information has been found for NSW BioNet.

No alerts have been found for NSW BioNet.

Data and Source Information

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Odongo R, et al. (2024) A network-based drug prioritization and combination analysis for the MEK5/ERK5 pathway in breast cancer. *BioData mining*, 17(1), 5.

Hughes MDG, et al. (2023) Building block aspect ratio controls assembly, architecture, and mechanics of synthetic and natural protein networks. *Nature communications*, 14(1), 5593.

Bridel C, et al. (2023) Clusters of co-abundant proteins in the brain cortex associated with fronto-temporal lobar degeneration. *Alzheimer's research & therapy*, 15(1), 59.

Li Mow Chee F, et al. (2023) Mena regulates nesprin-2 to control actin-nuclear lamina associations, trans-nuclear membrane signalling and gene expression. *Nature communications*, 14(1), 1602.

Klaile E, et al. (2022) Antibody ligation of CEACAM1, CEACAM3, and CEACAM6, differentially enhance the cytokine release of human neutrophils in responses to *Candida albicans*. *Cellular immunology*, 371, 104459.

Yang X, et al. (2022) BioNet: a large-scale and heterogeneous biological network model for interaction prediction with graph convolution. *Briefings in bioinformatics*, 23(1).

Ruberto AA, et al. (2021) KLF10 integrates circadian timing and sugar signaling to coordinate hepatic metabolism. *eLife*, 10.

Climente-González H, et al. (2021) Boosting GWAS using biological networks: A study on susceptibility to familial breast cancer. *PLoS computational biology*, 17(3), e1008819.

McNellie MJ, et al. (2020) Reference state and benchmark concepts for better biodiversity conservation in contemporary ecosystems. *Global change biology*, 26(12), 6702.

Dorrough J, et al. (2019) Expert predictions of changes in vegetation condition reveal perceived risks in biodiversity offsetting. *PloS one*, 14(5), e0216703.

Wagner KD, et al. (2019) Vascular PPAR γ Promotes Tumor Angiogenesis and Progression. *Cells*, 8(12).

Shi Z, et al. (2018) Exploring the molecular pathogenesis associated with T-cell prolymphocytic leukemia based on a comprehensive bioinformatics analysis. *Oncology letters*, 16(1), 301.

Cheng L, et al. (2018) A random forest classifier predicts recurrence risk in patients with ovarian cancer. *Molecular medicine reports*, 18(3), 3289.

Zhang Y, et al. (2017) Bioinformatics analysis of transcription profiling of solid pseudopapillary neoplasm of the pancreas. *Molecular medicine reports*, 16(2), 1635.

Wanichthanarak K, et al. (2017) Metabox: A Toolbox for Metabolomic Data Analysis, Interpretation and Integrative Exploration. *PloS one*, 12(1), e0171046.

Jones AV, et al. (2017) GWAS of self-reported mosquito bite size, itch intensity and attractiveness to mosquitoes implicates immune-related predisposition loci. *Human molecular genetics*, 26(7), 1391.

Li J, et al. (2016) Identification of rifampin-regulated functional modules and related microRNAs in human hepatocytes based on the protein interaction network. *BMC genomics*, 17 Suppl 7(Suppl 7), 517.

Long J, et al. (2016) Identification of genes and pathways associated with pancreatic ductal adenocarcinoma by bioinformatics analyses. *Oncology letters*, 11(2), 1391.

Shen LI, et al. (2016) Identification of genes and signaling pathways associated with squamous cell carcinoma by bioinformatics analysis. *Oncology letters*, 11(2), 1382.

Choi J, et al. (2016) Network Analysis of Genome-Wide Selective Constraint Reveals a Gene Network Active in Early Fetal Brain Intolerant of Mutation. *PLoS genetics*, 12(6), e1006121.