

Resource Summary Report

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DiANNA

RRID:SCR_018529

Type: Tool

Proper Citation

DiANNA (RRID:SCR_018529)

Resource Information

URL: <http://clavius.bc.edu/~clotelab/DiANNA/>

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Description: Neural network and web server, which determines cysteine oxidation state and disulfide connectivity of protein, given only its amino acid sequence. Used to predict disulfide connectivity topology. Predicts which half-cystines are covalently bound to which other half-cystines. DiANNA 1.1 is extension of DiANNA web server for ternary cysteine classification.

Synonyms: DiANNA 1.1

Resource Type: analysis service resource, data access protocol, production service resource, service resource, software resource, web service

Defining Citation: [PMID:16844987](#), [PMID:15980459](#)

Keywords: Ternary cysteine classification, cysteine oxidation, disulfide protein connectivity, amino acid sequence, predict disulfide connectivity, connectivity topology, cysteine covalent bound,

Funding: Boston College ;
NSF DBI 0543506

Availability: Free, Freely available

Resource Name: DiANNA

Resource ID: SCR_018529

Alternate URLs: <http://bioinformatics.bc.edu/clotelab/DiANNA/>

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260912T195902+0000

Ratings and Alerts

No rating or validation information has been found for DiANNA.

No alerts have been found for DiANNA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Chen Y, et al. (2026) PDIA6 promotes the cell proliferation of ESCC by enhancing the disulfide bond formation in TRAF4. Cellular & molecular biology letters, 31(1).

Mashhadi Abolghasem Shirazi M, et al. (2025) Novel bioinformatics approaches to design epitope-based vaccine against HIV latency by inquiring CTL epitopes and built-in adjuvants. Scientific reports, 15(1), 32809.

Huang X, et al. (2025) Decoding sugarcane smut: the role of effector SsEF83 in fungal virulence and plant interaction. Frontiers in microbiology, 16, 1586720.

De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. Frontiers in plant science, 16, 1588802.

Abid A, et al. (2024) Reverse Vaccinology Approach to Identify Novel and Immunogenic Targets against Streptococcus gordonii. Biology, 13(7).

Pei T, et al. (2024) Molecular characterization and induced changes of histone acetyltransferases in the tick Haemaphysalis longicornis in response to cold stress. Parasites & vectors, 17(1), 218.

Pei T, et al. (2023) Molecular characterization and modulated expression of histone acetyltransferases during cold response of the tick Dermacentor silvarum (Acari: Ixodidae). Parasites & vectors, 16(1), 358.

Liu Z, et al. (2023) Identification of gene modules and hub genes associated with Colletotrichum siamense infection in mango using weighted gene co-expression network analysis. BMC genomics, 24(1), 710.

Yang Y, et al. (2023) Convergent evolution of plant pattern recognition receptors sensing cysteine-rich patterns from three microbial kingdoms. Nature communications, 14(1), 3621.

Tan Q, et al. (2023) Functional Characterization of *Verticillium dahliae* Race 3-Specific Gene VdR3e in Virulence and Elicitation of Plant Immune Responses. *Microbiology spectrum*, 11(4), e0108323.

Khosravi F, et al. (2023) Identification and characterization of inulinases by bioinformatics analysis of bacterial glycoside hydrolases family 32 (GH32). *Engineering in life sciences*, 23(8), e2300003.

Lu X, et al. (2023) Molecular Analysis and Sex-specific Response of the Hepcidin Gene in Yellow Perch (*Perca Flavescens*) Following Lipopolysaccharide Challenge. *Probiotics and antimicrobial proteins*, 15(2), 215.

Remans K, et al. (2022) Protein purification strategies must consider downstream applications and individual biological characteristics. *Microbial cell factories*, 21(1), 52.

Akter S, et al. (2022) Immunoinformatics approach to epitope-based vaccine design against the SARS-CoV-2 in Bangladeshi patients. *Journal, genetic engineering & biotechnology*, 20(1), 136.

Chen HD, et al. (2022) UMOD Mutations in Chronic Kidney Disease in Taiwan. *Biomedicines*, 10(9).

Porf??rio CTMN, et al. (2022) Serine carboxypeptidases from the carnivorous plant *Nepenthes mirabilis*: Partial characterization and heterologous expression. *International journal of biological macromolecules*, 198, 77.

Ghaffari AD, et al. (2021) Immunoinformatic analysis of immunogenic B- and T-cell epitopes of MIC4 protein to designing a vaccine candidate against *Toxoplasma gondii* through an in-silico approach. *Clinical and experimental vaccine research*, 10(1), 59.

Xin A, et al. (2021) Cutin:cutin-acid endo-transacylase (CCT), a cuticle-remodelling enzyme activity in the plant epidermis. *The Biochemical journal*, 478(4), 777.

Ebrahim-Saraie HS, et al. (2021) Functional and Structural Characterization of SARS-Cov-2 Spike Protein: An In Silico Study. *Ethiopian journal of health sciences*, 31(2), 213.

Mondal R, et al. (2021) In silico analysis and expression profiling of S-domain receptor-like kinases (SD-RLKs) under different abiotic stresses in *Arabidopsis thaliana*. *BMC genomics*, 22(1), 817.