

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, web service, software resource, data access protocol, production service resource, service resource

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: NSF DBI 0543506;
Boston College

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: 20260805T044421+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 47 mentions in open access literature.

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

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.

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.

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.

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.

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.

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.

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.

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.

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

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.

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.

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.

Kim J, et al. (2021) Molecular Characterization of *Paralichthys olivaceus* MAF1 and Its Potential Role as an Anti-Viral Hemorrhagic Septicaemia Virus Factor in Hiram Natural Embryo Cells. *International journal of molecular sciences*, 22(3).

Zhang L, et al. (2021) FoEG1, a secreted glycoside hydrolase family 12 protein from *Fusarium oxysporum*, triggers cell death and modulates plant immunity. *Molecular plant pathology*, 22(5), 522.

Cestero JJ, et al. (2021) A Novel *Salmonella* Periplasmic Protein Controlling Cell Wall Homeostasis and Virulence. *Frontiers in microbiology*, 12, 633701.

Belkahia H, et al. (2021) Screening and Analysis of *Anaplasma marginale* Tunisian Isolates Reveal the Diversity of lipA Phylogeographic Marker and the Conservation of OmpA Protein Vaccine Candidate. *Frontiers in veterinary science*, 8, 731200.

Pan J, et al. (2021) Bacteriophage origin of some minimal ATP-dependent DNA ligases: a new structure from *Burkholderia pseudomallei* with striking similarity to *Chlorella* virus ligase. *Scientific reports*, 11(1), 18693.