Resource Summary Report

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COILS: Prediction of Coiled Coil Regions in Proteins

RRID:SCR_008440
Type: Tool

Proper Citation

COILS: Prediction of Coiled Coil Regions in Proteins (RRID:SCR_008440)

Resource Information

URL: http://www.ch.embnet.org/software/COILS_form.html

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Description: COILS is a program that compares a sequence to a database of known parallel two-stranded coiled-coils and derives a similarity score. By comparing this score to the distribution of scores in globular and coiled-coil proteins, the program then calculates the probability that the sequence will adopt a coiled-coil conformation.

Synonyms: COILS Server

Resource Type: data processing software, software resource, software application

Defining Citation: DOI:10.1126/science.252.5009.1162

Keywords: software, prediction, database, sequence, coil, globular, protein, probability, bio.tools, FASEB list

Funding:

Resource Name: COILS: Prediction of Coiled Coil Regions in Proteins

Resource ID: SCR_008440

Alternate IDs: biotools:ncoils, OMICS_07850, nif-0000-30263

Alternate URLs: https://bio.tools/ncoils, https://sources.debian.org/src/ncoils/

Old URLs: https://sources.debian.org/src/ncoils/

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250429T055248+0000

Ratings and Alerts

No rating or validation information has been found for COILS: Prediction of Coiled Coil Regions in Proteins.

No alerts have been found for COILS: Prediction of Coiled Coil Regions in Proteins.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 164 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Englisch AS, et al. (2024) Ankrd26 is a retinoic acid-responsive plasma membrane-binding and -shaping protein critical for proper cell differentiation. Cell reports, 43(3), 113939.

Dong C, et al. (2023) Karyotype evolution of the Asterids insights from the first genome sequences of the family Cornaceae. DNA research : an international journal for rapid publication of reports on genes and genomes, 30(1).

Li X, et al. (2023) RPG interacts with E3-ligase CERBERUS to mediate rhizobial infection in Lotus japonicus. PLoS genetics, 19(2), e1010621.

Miller J, et al. (2022) Chromosome-level genome and the identification of sex chromosomes in Uloborus diversus. GigaScience, 12.

Ding H, et al. (2021) Bioinformatics analysis of Myelin Transcription Factor 1. Technology and health care : official journal of the European Society for Engineering and Medicine, 29(S1), 441.

Zheng Y, et al. (2021) Divergence of the genetic contribution of FRIGIDA homologues in regulating the flowering time in Brassica rapa ssp. rapa. Gene, 796-797, 145790.

Wang G, et al. (2021) Genetic structure and evolutionary diversity of mating-type (MAT) loci in Hypsizygus marmoreus. IMA fungus, 12(1), 35.

Stein V, et al. (2021) Targeted Quantification of Phosphorylation Sites Identifies STRIPAK-Dependent Phosphorylation of the Hippo Pathway-Related Kinase SmKIN3. mBio, 12(3).

Chen W, et al. (2020) EjFRI, FRIGIDA (FRI) Ortholog from Eriobotrya japonica, Delays Flowering in Arabidopsis. International journal of molecular sciences, 21(3).

Wei H, et al. (2020) Genomic Organization and Comparative Phylogenic Analysis of NBS-LRR Resistance Gene Family in Solanum pimpinellifolium and Arabidopsis thaliana. Evolutionary bioinformatics online, 16, 1176934320911055.

Wang C, et al. (2020) Donkey genomes provide new insights into domestication and selection for coat color. Nature communications, 11(1), 6014.

Cao Y, et al. (2020) Microtubule Minus-End Binding Protein CAMSAP2 and Kinesin-14 Motor KIFC3 Control Dendritic Microtubule Organization. Current biology : CB, 30(5), 899.

Chen X, et al. (2020) Identification of RNPC3 as a novel JAK2 fusion partner gene in B-acute lymphoblastic leukemia refractory to combination therapy including ruxolitinib. Molecular genetics & genomic medicine, 8(3), e1110.

Tarazona NA, et al. (2019) Role of leucine zipper-like motifs in the oligomerization of Pseudomonas putida phasins. Biochimica et biophysica acta. General subjects, 1863(2), 362.

Jokura K, et al. (2019) CTENO64 Is Required for Coordinated Paddling of Ciliary Comb Plate in Ctenophores. Current biology : CB, 29(20), 3510.

Van de Weyer AL, et al. (2019) A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. Cell, 178(5), 1260.

Yu J, et al. (2019) Molecular cloning and metabolomic characterization of the 5-enolpyruvylshikimate-3-phosphate synthase gene from Baphicacanthus cusia. BMC plant biology, 19(1), 485.

Wang Y, et al. (2019) Three Toxoplasma gondii Dense Granule Proteins Are Required for Induction of Lewis Rat Macrophage Pyroptosis. mBio, 10(1).

Xu X, et al. (2018) A rice class-XIV kinesin enters the nucleus in response to cold. Scientific reports, 8(1), 3588.

He M, et al. (2018) Identification of novel immunoreactive proteins and delineation of a specific epitope of Anaplasma phagocytophilum. Microbial pathogenesis, 125, 183.