

# 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](http://www.ch.embnet.org/software/COILS_form.html)

**Proper Citation:** COILS: Prediction of Coiled Coil Regions in Proteins (RRID:SCR\_008440)

**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:** software resource, software application, data processing software

**Defining Citation:** [DOI:10.1126/science.252.5009.1162](https://doi.org/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:** 20250411T055214+0000

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## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 164 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

Englich 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.

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

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

Chen W, et al. (2020) E<sub>J</sub>FRI, 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 Phylogenetic 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.

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

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

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.

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.