

Resource Summary Report

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PRED-SIGNAL

RRID:SCR_006181

Type: Tool

Proper Citation

PRED-SIGNAL (RRID:SCR_006181)

Resource Information

URL: <http://bioinformatics.biol.uoa.gr/PRED-SIGNAL/>

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Description: A web tool for prediction of signal peptides in archaea. Computational prediction of signal peptides (SPs) and their cleavage sites is of great importance in computational biology; however, currently there is no available method capable of predicting reliably the SPs of archaea, due to the limited amount of experimentally verified proteins with SPs. We performed an extensive literature search in order to identify archaeal proteins having experimentally verified SP and managed to find 69 such proteins, the largest number ever reported. A detailed analysis of these sequences revealed some unique features of the SPs of archaea, such as the unique amino acid composition of the hydrophobic region with a higher than expected occurrence of isoleucine, and a cleavage site resembling more the sequences of gram-positives with almost equal amounts of alanine and valine at the position-3 before the cleavage site and a dominant alanine at position-1, followed in abundance by serine and glycine. Using these proteins as a training set, we trained a hidden Markov model method that predicts the presence of the SPs and their cleavage sites and also discriminates such proteins from cytoplasmic and transmembrane ones.

Abbreviations: PRED-SIGNAL

Synonyms: PRED-SIGNAL - Prediction of Signal Peptides in Archaea with Hidden Markov Models

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:18988691](#)

Keywords: signal peptide, prediction, protein, bio.tools

Funding: State Scholarships Foundation of Greece

Availability: Free for academic use

Resource Name: PRED-SIGNAL

Resource ID: SCR_006181

Alternate IDs: biotools:pred-signal, nlx_151728

Alternate URLs: <https://bio.tools/pred-signal>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260912T200141+0000

Ratings and Alerts

No rating or validation information has been found for PRED-SIGNAL.

No alerts have been found for PRED-SIGNAL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Stathatos I, et al. (2023) Comparative Analysis of Prokaryotic Extracellular Vesicle Proteins and Their Targeting Signals. Microorganisms, 11(8).

Singhal N, et al. (2021) Efficacy of signal peptide predictors in identifying signal peptides in the experimental secretome of Picrophilous torridus, a thermoacidophilic archaeon. PloS one, 16(8), e0255826.

Sánchez-Ovejero C, et al. (2020) Evaluation of the sensitivity and specificity of GST-tagged recombinant antigens 2B2t, Ag5t and DIPOL in ELISA for the diagnosis and follow up of patients with cystic echinococcosis. PLoS neglected tropical diseases, 14(11), e0008892.

Zhou Z, et al. (2020) Genome- and Community-Level Interaction Insights into Carbon Utilization and Element Cycling Functions of Hydrothermarchaeota in Hydrothermal Sediment. mSystems, 5(1).

Manoharan L, et al. (2019) Metagenomes from Coastal Marine Sediments Give Insights into the Ecological Role and Cellular Features of Loki- and Thorarchaeota. mBio, 10(5).

Zhou Z, et al. (2019) Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermopfundales (MBG-D archaea). The ISME journal, 13(4), 885.

Chen LX, et al. (2018) Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. The ISME journal, 12(3), 756.

Li M, et al. (2016) Genomic and Transcriptomic Resolution of Organic Matter Utilization Among Deep-Sea Bacteria in Guaymas Basin Hydrothermal Plumes. Frontiers in microbiology, 7, 1125.

Li M, et al. (2015) Genomic and transcriptomic evidence for scavenging of diverse organic compounds by widespread deep-sea archaea. Nature communications, 6, 8933.

Arshad A, et al. (2015) A Metagenomics-Based Metabolic Model of Nitrate-Dependent Anaerobic Oxidation of Methane by Methanoperedens-Like Archaea. Frontiers in microbiology, 6, 1423.

Schmid G, et al. (2013) Experimental and computational analysis of the secretome of the hyperthermophilic archaeon Pyrococcus furiosus. Extremophiles : life under extreme conditions, 17(6), 921.

Paramasivam N, et al. (2011) ClubSub-P: Cluster-Based Subcellular Localization Prediction for Gram-Negative Bacteria and Archaea. Frontiers in microbiology, 2, 218.

Ellen AF, et al. (2010) Comparative study of the extracellular proteome of Sulfolobus species reveals limited secretion. Extremophiles : life under extreme conditions, 14(1), 87.