

Resource Summary Report

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Prediction and Analysis of Nuclear Localization Signals

RRID:SCR_008553

Type: Tool

Proper Citation

Prediction and Analysis of Nuclear Localization Signals (RRID:SCR_008553)

Resource Information

URL: <https://roslab.org/owiki/index.php/PredictNLS>

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Description: Software automated tool for analysis and determination of Nuclear Localization Signals (NLS). Predicts that your protein is nuclear or finds out whether your potential NLS is found in our database. The program also compiles statistics on the number of nuclear/non-nuclear proteins in which your potential NLS is found. Finally, proteins with similar NLS motifs are reported, and the experimental paper describing the particular NLS are given.

Synonyms: PredictNLS

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

Defining Citation: [DOI:10.1093/embo-reports/kvd092](https://doi.org/10.1093/embo-reports/kvd092), [DOI:10.1093/embo-reports/kvd092](https://doi.org/10.1093/embo-reports/kvd092)

Keywords: bio.tools

Resource Name: Prediction and Analysis of Nuclear Localization Signals

Resource ID: SCR_008553

Alternate IDs: nif-0000-31416, OMICS_01633, biotools:predictnls

Alternate URLs: <http://www.roslab.org/services/predictNLS/>, <https://bio.tools/predictnls>, <https://sources.debian.org/src/predictnls/>

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260903T235005+0000

Ratings and Alerts

No rating or validation information has been found for Prediction and Analysis of Nuclear Localization Signals.

No alerts have been found for Prediction and Analysis of Nuclear Localization Signals.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Reis LM, et al. (2021) Comprehensive phenotypic and functional analysis of dominant and recessive FOXE3 alleles in ocular developmental disorders. Human molecular genetics, 30(17), 1591.

Yang Y, et al. (2020) Identification of the Repressive Domain of the Negative Circadian Clock Component CHRONO. International journal of molecular sciences, 21(7).

Wang H, et al. (2020) Transcription factor LkWOX4 is involved in adventitious root development in Larix kaempferi. Gene, 758, 144942.

Feng JM, et al. (2020) Identification and evolutionary analysis of the nucleolar proteome of Giardia lamblia. BMC genomics, 21(1), 269.

Chen K, et al. (2020) Overexpression of GmUBC9 Gene Enhances Plant Drought Resistance and Affects Flowering Time via Histone H2B Monoubiquitination. Frontiers in plant science, 11, 555794.

Li X, et al. (2018) Nuclear Klf4 accumulation is associated with cetuximab drug-resistance and predicts poor prognosis of nasopharyngeal carcinoma. Journal of translational medicine, 16(1), 183.

Wang J, et al. (2018) Genome-wide analysis of the plant-specific PLATZ proteins in maize and identification of their general role in interaction with RNA polymerase III complex. BMC plant biology, 18(1), 221.

Pan X, et al. (2014) Structural and temporal requirements of Wnt/PCP protein Vangl2 function for convergence and extension movements and facial branchiomotor neuron migration in zebrafish. Mechanisms of development, 131, 1.

Narsai R, et al. (2013) Rice DB: an Oryza Information Portal linking annotation, subcellular location, function, expression, regulation, and evolutionary information for rice and Arabidopsis. The Plant journal : for cell and molecular biology, 76(6), 1057.

Nag A, et al. (2012) Enhancing a Pathway-Genome Database (PGDB) to capture subcellular localization of metabolites and enzymes: the nucleotide-sugar biosynthetic pathways of *Populus trichocarpa*. Database : the journal of biological databases and curation, 2012, bas013.