

Resource Summary Report

Generated by SPARC SAWG on Jul 29, 2026

PredictNLS

RRID:SCR_003133

Type: Tool

Proper Citation

PredictNLS (RRID:SCR_003133)

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.

Abbreviations: PredictNLS

Synonyms: Prediction and Analysis of Nuclear Localization Signals

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

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

Keywords: bio.tools, nuclear localization signal, protein, protein sequence

Availability: Free, Available for download, Freely available

Resource Name: PredictNLS

Resource ID: SCR_003133

Alternate IDs: nif-0000-31416, OMICS_01633, SCR_008553, biotools:predictnls

Alternate URLs: <https://www.rdocumentation.org/packages/propagate/versions/1.0-4/topics/predictNLS>

Record Creation Time: 20220129T080217+0000

Ratings and Alerts

No rating or validation information has been found for PredictNLS.

No alerts have been found for PredictNLS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Okano K, et al. (2023) Molecular functions of the double-sided and inverted ubiquitin-interacting motif found in *Xenopus tropicalis* cryptochrome 6. *Development, growth & differentiation*, 65(4), 203.

Rafiqi M, et al. (2022) Profile of the in silico secretome of the palm dieback pathogen, *Fusarium oxysporum* f. sp. *albedinis*, a fungus that puts natural oases at risk. *PloS one*, 17(5), e0260830.

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.

Raeispour Shirazi M, et al. (2021) Identification and in-silico characterization of taxadien-5?-ol-O-acetyltransferase (TDAT) gene in *Corylus avellana* L. *PloS one*, 16(8), e0256704.

Poursalavati A, et al. (2021) Toward understanding of the methoxylated flavonoid biosynthesis pathway in *Dracocephalum kotschy* Boiss. *Scientific reports*, 11(1), 19549.

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.

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.

Tao SQ, et al. (2019) Comparative transcriptomics of *Gymnosporangium* spp. teliospores reveals a conserved genetic program at this specific stage of the rust fungal life cycle. *BMC genomics*, 20(1), 723.

Chen G, et al. (2019) Comprehensive Identification and Characterization of Human Secretome Based on Integrative Proteomic and Transcriptomic Data. *Frontiers in cell and developmental biology*, 7, 299.

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.

Marton K, et al. (2018) Comprehensive analysis of *Verticillium nonalfalfae* in silico secretome uncovers putative effector proteins expressed during hop invasion. *PloS one*, 13(6), e0198971.

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.

Evangelisti E, et al. (2017) Time-resolved dual transcriptomics reveal early induced *Nicotiana benthamiana* root genes and conserved infection-promoting *Phytophthora palmivora* effectors. *BMC biology*, 15(1), 39.

Wen F, et al. (2017) Genome-wide survey of heat shock factors and heat shock protein 70s and their regulatory network under abiotic stresses in *Brachypodium distachyon*. *PloS one*, 12(7), e0180352.

Pérez-Miguelsanz J, et al. (2017) Betaine homocysteine S-methyltransferase emerges as a new player of the nuclear methionine cycle. *Biochimica et biophysica acta. Molecular cell research*, 1864(7), 1165.

Liang C, et al. (2016) GhABF2, a bZIP transcription factor, confers drought and salinity tolerance in cotton (*Gossypium hirsutum* L.). *Scientific reports*, 6, 35040.

Dahalan FA, et al. (2016) Phosphorylated and Nonphosphorylated PfMAP2 Are Localized in the Nucleus, Dependent on the Stage of *Plasmodium falciparum* Asexual Maturation. *BioMed research international*, 2016, 1645097.

Levering J, et al. (2016) Genome-Scale Model Reveals Metabolic Basis of Biomass Partitioning in a Model Diatom. *PloS one*, 11(5), e0155038.