

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 3, 2026

NESmapper

RRID:SCR_012138

Type: Tool

Proper Citation

NESmapper (RRID:SCR_012138)

Resource Information

URL: <http://sourceforge.net/projects/nestmapper/>

Proper Citation: NESmapper (RRID:SCR_012138)

Description: A computational software tool to predict leucine-rich nuclear export signals (NESs) by using profiles that had been further optimized by training and combining the amino acid properties of the NES-flanking regions. It is a multiplatform command-line Perl application with activity-based NES profiles.

Resource Type: software resource

Defining Citation: [PMID:25233087](#)

Keywords: standalone software, perl

Availability: GNU General Public License

Resource Name: NESmapper

Resource ID: SCR_012138

Alternate IDs: OMICS_05911

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260801T190436+0000

Ratings and Alerts

No rating or validation information has been found for NESmapper.

No alerts have been found for NESmapper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Chen W, et al. (2024) Phylogenomics analysis of velvet regulators in the fungal kingdom. Microbiology spectrum, 12(2), e0371723.

Sendino M, et al. (2020) Using a Simple Cellular Assay to Map NES Motifs in Cancer-Related Proteins, Gain Insight into CRM1-Mediated NES Export, and Search for NES-Harboring Micropeptides. International journal of molecular sciences, 21(17).

Tessier TM, et al. (2020) Piggybacking on Classical Import and Other Non-Classical Mechanisms of Nuclear Import Appear Highly Prevalent within the Human Proteome. Biology, 9(8).

??kland AL, et al. (2019) Genomic characterization, phylogenetic position and in situ localization of a novel putative mononegavirus in Lepeophtheirus salmonis. Archives of virology, 164(3), 675.

Liku ME, et al. (2018) NoLogo: a new statistical model highlights the diversity and suggests new classes of Crm1-dependent nuclear export signals. BMC bioinformatics, 19(1), 65.

Cautain B, et al. (2015) Components and regulation of nuclear transport processes. The FEBS journal, 282(3), 445.