

# Resource Summary Report

Generated by [NIF](#) on Aug 19, 2026

## NESmapper

RRID:SCR\_012138

Type: Tool

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### Proper Citation

NESmapper (RRID:SCR\_012138)

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### 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:** 20260815T182444+0000

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### Ratings and Alerts

No rating or validation information has been found for NESmapper.

No alerts have been found for NESmapper.

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### Data and Source Information

Source: [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.