

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 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: 20260725T190732+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

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.