

# Binding of NEP/NS2 to vRNP:M1

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## Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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## Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

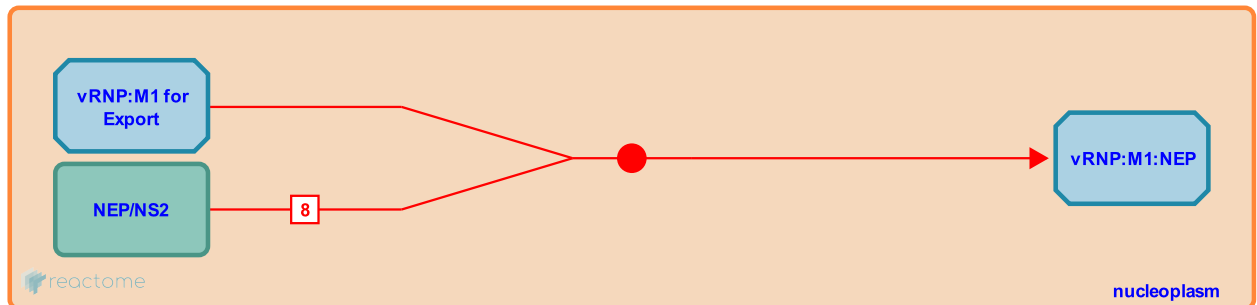
## Binding of NEP/NS2 to vRNP:M1 [↗](#)

**Stable identifier:** R-HSA-168893

**Type:** binding

**Compartments:** nucleoplasm

**Diseases:** influenza



Structural characterization of NEP/NS2 suggests that acidic residues in the C-terminus of NEP/NS2 bind to M1, with Trp78 critical for interaction (Ward, 1995; Yasuda, 1993; Akarsu, 2003).

### Literature references

Macreadie, IG., Castelli, LA., Azad, AA., White, JF., Ward, AC., Lucantoni, AC. (1995). Expression and analysis of the NS2 protein of influenza A virus. *Arch Virol*, 140, 2067-73. [↗](#)

Nakada, S., Yasuda, J., Kato, A., Ishihama, A., Toyoda, T. (1993). Molecular assembly of influenza virus: association of the NS2 protein with virion matrix. *Virology*, 196, 249-55. [↗](#)

### Editions

|            |          |                              |
|------------|----------|------------------------------|
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