# NP binds vRNA

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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

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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. ↗

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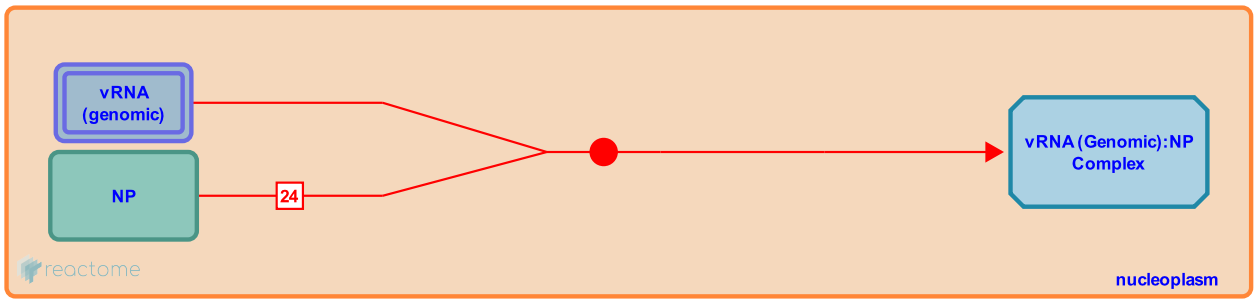
## NP binds vRNA ↗

**Stable identifier:** R-HSA-192912

**Type:** binding

**Compartments:** nucleoplasm

**Diseases:** influenza




Viral genomic RNA (vRNA) and complementary RNA (cRNA) are likely bound by the influenza nucleoprotein (NP) immediately upon synthesis. Although two nuclear localization signals have been mapped in the NP, an unconventional N-terminal NLS and a bipartite NLS within amino acids 198-216 (Wang, 1997; Neumann, 1997; Ozawa, 2007), the crystal structure of the NP suggests that only the unconventional NLS is exposed and can be used as a functional NLS (Ye, 2006). This unconvenetional NLS interacts with importins alpha-1 and -2 (Cros et al., 2005; Wang et al., 1997; Buolo et al., 2006). The three-dimensional structure of NP has revealed that NP molecules associate as a trimer, interacting through beta-sheets b5, b6, and b7 in the C-terminal domain of the protein; the viral RNA likely wraps around the outside of the complex (Ye, 2006).

## Literature references

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## Editions

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