RNP association

Marsh, G., Rush, MG., Squires, B.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

22/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗

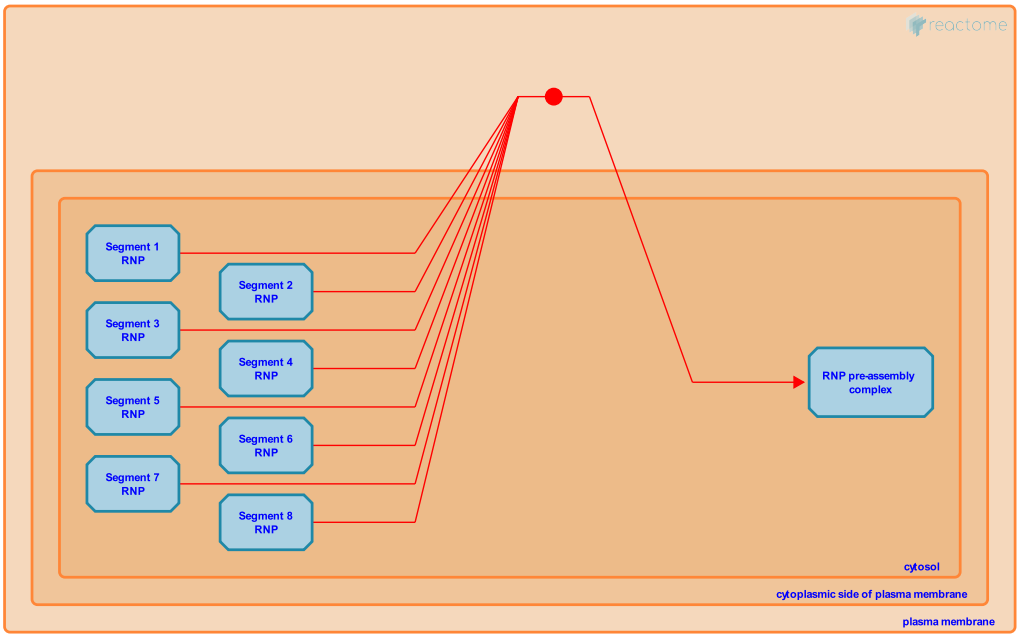
RNP association ↗

Stable identifier: R-HSA-168895

Type: binding

Compartments: plasma membrane

Diseases: influenza



The random incorporation model as its name suggests proposes that there is no selection at all on which vRNPs are packaged. It is assumed that each vRNP has equal probability of being packaged, and that if enough vRNPS are packaged a particular percentage of budding virions will receive at least one copy of each genome segment. This model is supported by evidence that infectious virions may possess more than eight vRNPs assuring the presence of a full complement of eight vRNPs in a significant percentage of virus particles. Mathematical analysis of packaging suggested that twelve RNA segments would need to be packaged in order to obtain approximately 10% of virus particles that are fully infectious (Enami, 1991), a number that is compatible with experimental data (Donald, 1954). Due to the low amount of RNA per virion (estimated at 1-2% w/w), enumeration of the precise number of RNAs packaged in a virion is difficult.

Literature references

ISAACS, A., DONALD, HB. (1954). Counts of influenza virus particles. *J Gen Microbiol, 10*, 457-64. ↗

Benham, C., Sharma, G., Palese, P., Enami, M. (1991). An influenza virus containing nine different RNA segments. *Virology, 185*, 291-8. ↗

Editions

2007-05-01	Authored	Marsh, G.
2007-05-01	Reviewed	Rush, MG., Squires, B.