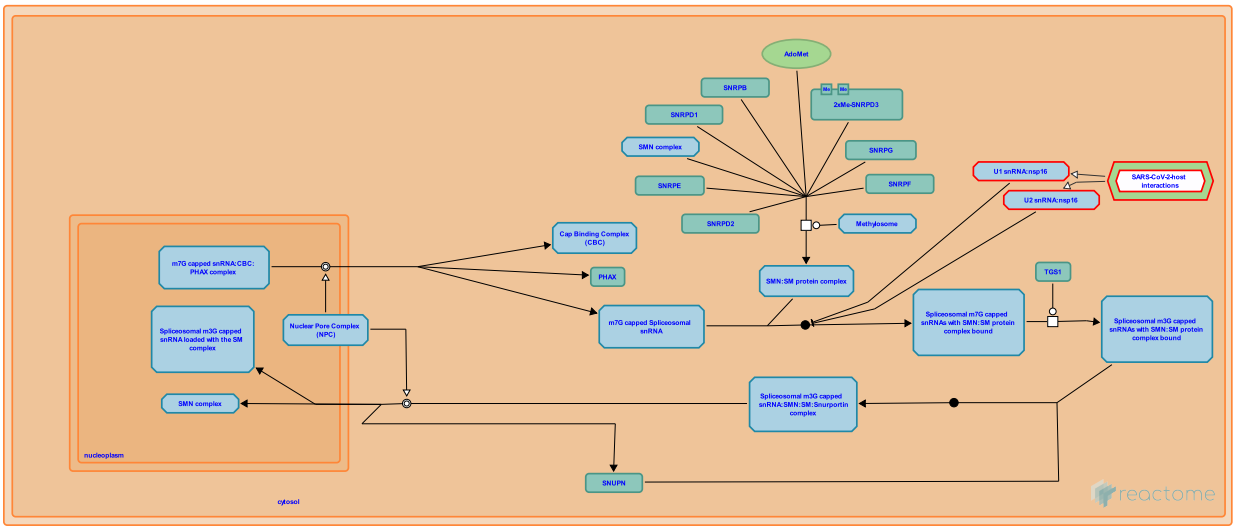
Metabolism of non-coding RNA



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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.
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. ↗

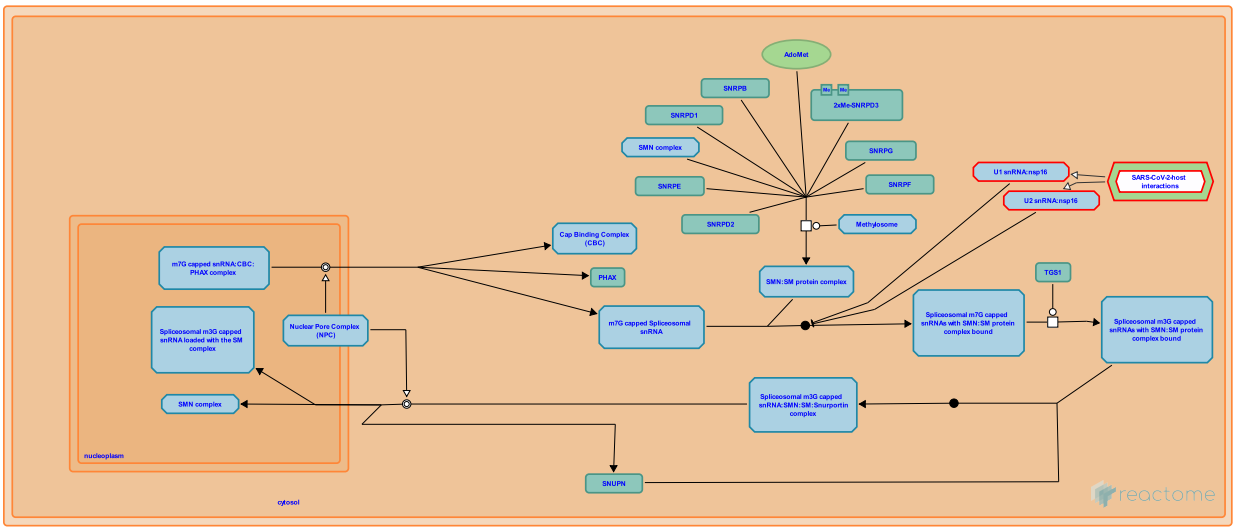
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Reactome database release: 88

This document contains 2 pathways (see Table of Contents)

Metabolism of non-coding RNA ↗

Stable identifier: R-HSA-194441

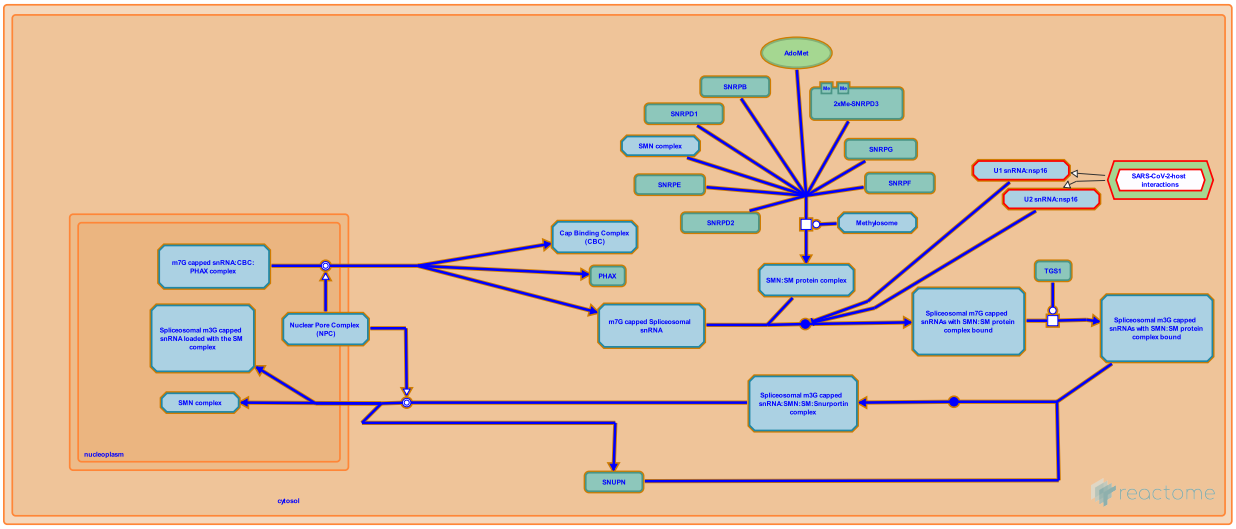


The term non-coding is commonly employed for RNA that does not encode a protein, but this does not mean that such RNAs do not contain information nor have function. There is considerable evidence that the majority of mammalian and other complex organism's genomes is transcribed into non-coding RNAs, many of which are alternatively spliced and/or processed into smaller products. Around 98% of all transcriptional output in humans is non-coding RNA. RNA-mediated gene regulation is widespread in higher eukaryotes and complex genetic phenomena like RNA interference are mediated by such RNAs. These non-coding RNAs are a growing list and include rRNAs, tRNAs, snRNAs, snoRNAs siRNAs, 7SL RNA, 7SK RNA, the RNA component of RNase P RNA, the RNA component of RNase MRP, and the RNA component of telomerase.

snRNP Assembly ↗

Location: Metabolism of non-coding RNA

Stable identifier: R-HSA-191859



Small nuclear ribonucleoproteins (snRNPs) are crucial for pre-mRNA processing to mRNAs. Each snRNP contains a small nuclear RNA (snRNA) and an extremely stable core of seven Sm proteins. The U6 snRNA differs from the other snRNAs; it binds seven Sm-like proteins and its assembly does not involve a cytoplasmic phase. The snRNP biogenesis pathway for all of the other snRNAs is complex, involving nuclear export of snRNA, Sm-core assembly in the cytoplasm and re-import of the mature snRNP. The assembly of the snRNA:Sm-core is carried out by the survival of motor neurons (SMN) complex. The SMN complex stringently scrutinizes RNAs for specific features that define them as snRNAs and binds the RNA-binding Sm proteins.

Literature references

Wan, L., Dreyfuss, G., Yong, J. (2004). Why do cells need an assembly machine for RNA-protein complexes?. *Trends Cell Biol, 14*, 226-32. ↗

Editions

2007-01-30	Authored	Gillespie, ME.
2007-04-30	Reviewed	Luhrmann, R.

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