Loading and methylation of Sm proteins onto SMN Complexes

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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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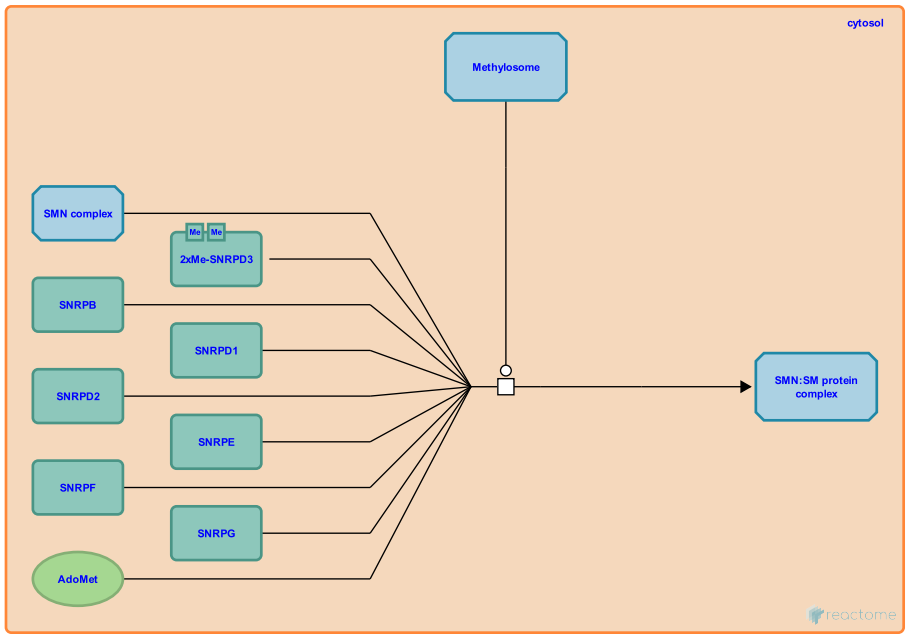
Stable identifier: R-HSA-191790

Type: transition

Compartments: cytosol



The survival of motor neurons (SMN) complex binds to Sm proteins and small nuclear RNAs (snRNAs) in the cytoplasm. Sm is part the SMN multiprotein complex that contains Gemins 2 – 7, including the DEAD-box RNA helicase Gemin3. The binding of the SMN complex to the snRNAs depends on the presence of specific, high-affinity (nanomolar) binding domains in the snRNAs. The SMN complex binds the Sm proteins through the Sm domains interaction with the Gemins, the TUDOR domain, and through unique arginine- and glycine-rich (RG) domains found in three of these, SmB, SmD1 and SmD3. The association with RG domains is strongly enhanced by the post-translational symmetric dimethylation of specific arginines in these domains, a process that is carried out by the methylosome (JBP1 or PRMT5) complex.

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Editions

2007-01-30	Authored	Gillespie, ME.
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