WBSCR22:TRMT112 methylates guanosine-1639 of 18S rRNA yielding 7-methylguanosine-1639

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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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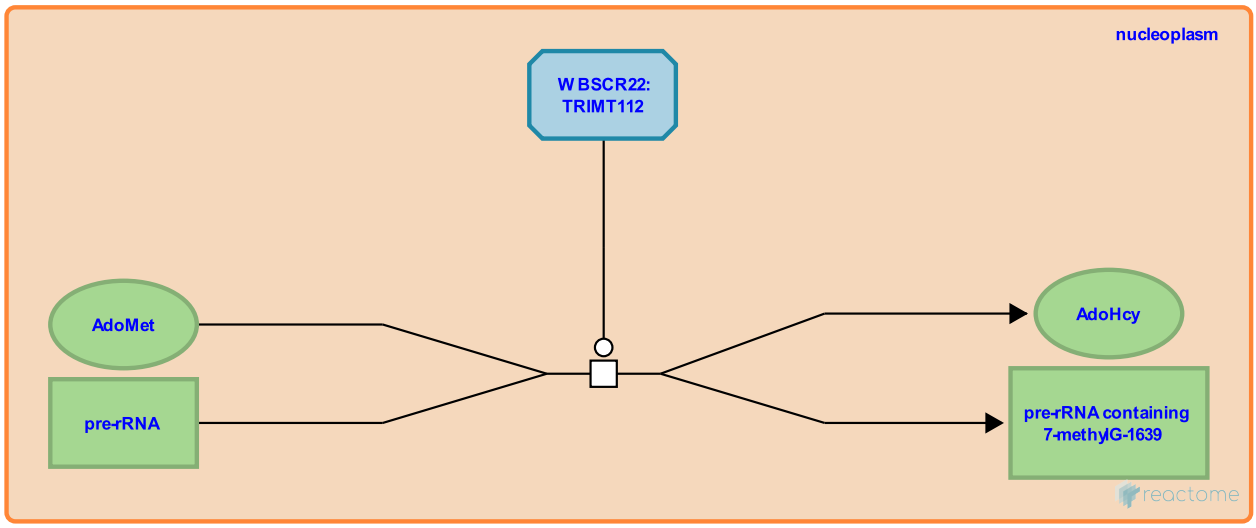
Stable identifier: R-HSA-6790982

Type: transition

Compartments: nucleoplasm



The WBSCR22:TRMT112 complex, homolog of the Bud23:Trm112 complex in yeast (Ounap et al. 2013), methylates guanosine-1639 of 18S rRNA at the N(7) position of the guanine base (Haag et al. 2015, Zorbas et al. 2015). The WBSCR22:TRMT112 complex but not its methylase activity is required for efficient processing of precursor rRNA at site 2 and site 3 (Haag et al. 2015, Zorbas et al. 2015). Hemizygosity at the region containing WBSCR22 causes Williams-Beuren syndrome (Doll and Grzeschik 2001).

Literature references

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Editions

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