Disintegration of matrix layer

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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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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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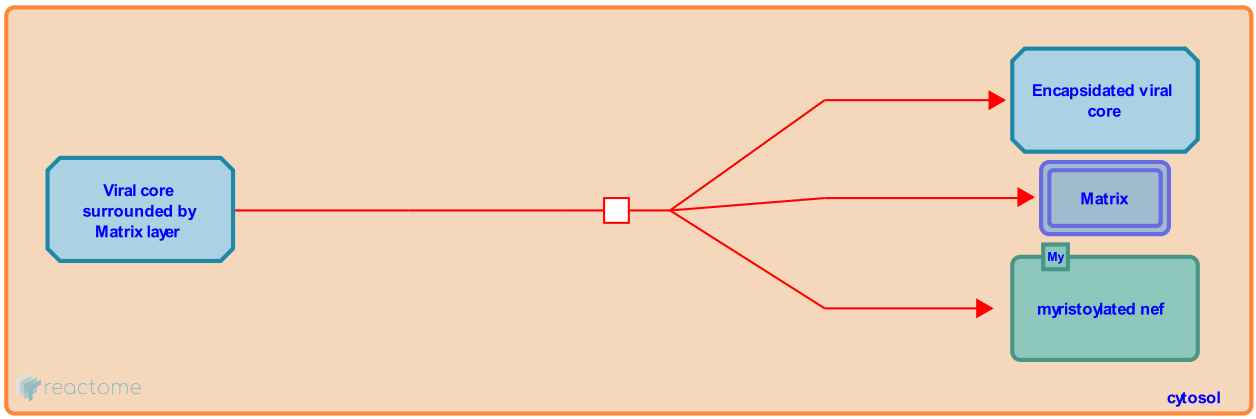
Stable identifier: R-HSA-173642

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



After fusion of the viral membrane with the target cell membrane, the viral core, which is surrounded by a layer of Matrix (p17) proteins, is exposed to the cytoplasm. Disintegration of the Matrix layer allows for the conical-shaped viral core to be fully released, and allow for viral capsid dissociation and eventually reverse transcription. Dissociation of the Matrix layer is not well characterized, but is believed to occur due to disruption of protein-protein interactions as a result of the conditions of the cytoplasm (including pH), which differ from that of the internal viral structure.

Literature references

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Editions

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