

# Synthesis of GAG polypeptide

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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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- 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 1 reaction ([see Table of Contents](#))

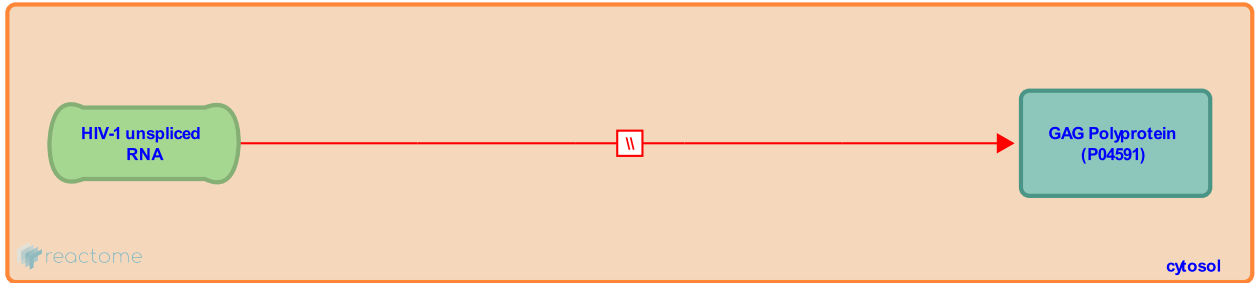
# Synthesis of GAG polyprotein ↗

**Stable identifier:** R-HSA-187213

**Type:** omitted

**Compartments:** cytosol

**Diseases:** Human immunodeficiency virus infectious disease



Gag is translated from the unspliced viral RNA on free ribosomes in the cytoplasm. The products of the pro and pol genes are also synthesized from the unspliced viral RNA, but never as parts of an independent polyprotein. They are initially contained within the Gag-Pro or Gag-Pro-Pol fusion protein, the product of translational readthrough

## Literature references

Varmus, HE., Hughes, SH., Coffin, JM. (1997). Synthesis, Assembly, and Processing of Viral Proteins, Retroviruses.

## Editions

2013-03-07	Authored	Gillespie, ME.
2013-05-21	Reviewed	Dube, M.