

# GNPDA1,2 hexamers deaminate GlcN6P to Fru(6)P

D'Eustachio, P., Jassal, B.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

## 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: 70

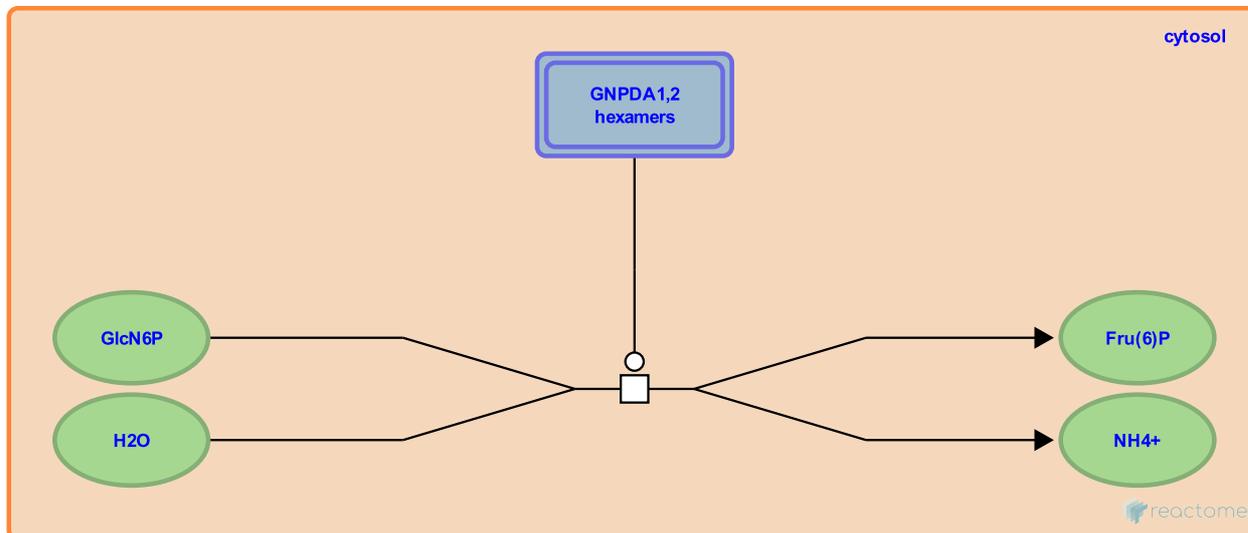
This document contains 1 reaction ([see Table of Contents](#))

## GNPDA1,2 hexamers deaminate GlcN6P to Fru(6)P ↗

**Stable identifier:** R-HSA-6799604

**Type:** transition

**Compartments:** cytosol



Glucosamine-6-phosphate isomerases 1 and 2 (GNPDA1, 2) catalyse the reversible deamination and with an aldo/keto isomerisation of D-glucosamine 6-phosphate (GlcN6P) to D-fructose 6-phosphate (Fru(6)P) and ammonia (NH<sub>3</sub>). GNDPA1 and 2 function as homohexamers in the cytosol. This reaction could provide a source of energy from catabolic pathways of hexosamines found in glycoproteins and glycolipids (Wolosker et al. 1998, Zhang et al. 2003, Arreola et al. 2003).

### Literature references

Wolosker, H., Kline, D., Bian, Y., Blackshaw, S., Cameron, AM., Fralich, TJ. et al. (1998). Molecularly cloned mammalian glucosamine-6-phosphate deaminase localizes to transporting epithelium and lacks oscillin activity. *FASEB J.*, 12, 91-9. ↗

Arreola, R., Valderrama, B., Morante, ML., Horjales, E. (2003). Two mammalian glucosamine-6-phosphate deaminases: a structural and genetic study. *FEBS Lett.*, 551, 63-70. ↗

Zhang, J., Zhang, W., Zou, D., Chen, G., Wan, T., Li, N. et al. (2003). Cloning and functional characterization of GNPI2, a novel human homolog of glucosamine-6-phosphate isomerase/oscillin. *J. Cell. Biochem.*, 88, 932-40. ↗

### Editions

2015-09-25	Authored, Edited	Jassal, B.
2016-01-11	Reviewed	D'Eustachio, P.