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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

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: 88

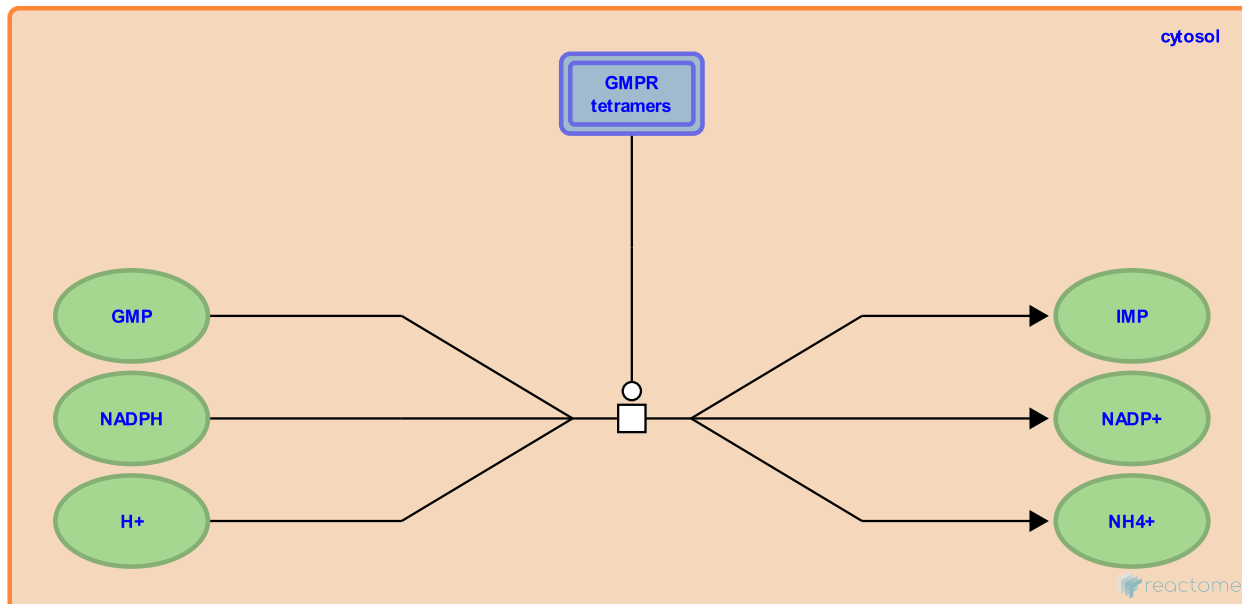
This document contains 1 reaction ([see Table of Contents](#))

**GMP + NADPH + H+ => IMP + NADP+ + NH4+ (GMPR,GMPR2)** ↗

**Stable identifier:** R-HSA-514604

**Type:** transition

**Compartments:** cytosol



Cytosolic GMP reductase (GMPR) catalyzes the reaction of GMP and NADPH + H<sup>+</sup> to yield IMP and NADP<sup>+</sup> + NH<sub>4</sub><sup>+</sup> (Spector et al. 1979; Deng et al. 2002). Two GMPR proteins have been identified, GMPR and GMPR2. Both proteins form homotetramers (GMPR - unpublished crystallographic data PDB 2BLE; GMPR2 - Li et al. 2006).

## Literature references

- Deng, Y., Qiu, R., Gu, X., Chen, F., Li, J., Xie, Y. et al. (2006). Crystal structure of human guanosine monophosphate reductase 2 (GMPR2) in complex with GMP. *J Mol Biol*, 355, 980-8. ↗
- Gu, S., Deng, Y., Wang, Y., Huang, Y., Ying, K., Gu, X. et al. (2002). NADPH-dependent GMP reductase isoenzyme of human (GMPR2). Expression, purification, and kinetic properties. *Int J Biochem Cell Biol*, 34, 1035-50. ↗
- Miller, RL., Jones, TE., Spector, T. (1979). Reaction mechanism and specificity of human GMP reductase. Substrates, inhibitors, activators, and inactivators. *J Biol Chem*, 254, 2308-15. ↗

## Editions

2010-02-18	Authored, Edited	D'Eustachio, P.
2024-03-06	Reviewed	Rush, MG., Graves, L.