

# EGR2, SOX10 and SMARCA4 bind the MPZ gene

Aletta, J M., Rothfels, K.

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

07/05/2024

## 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: 88

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

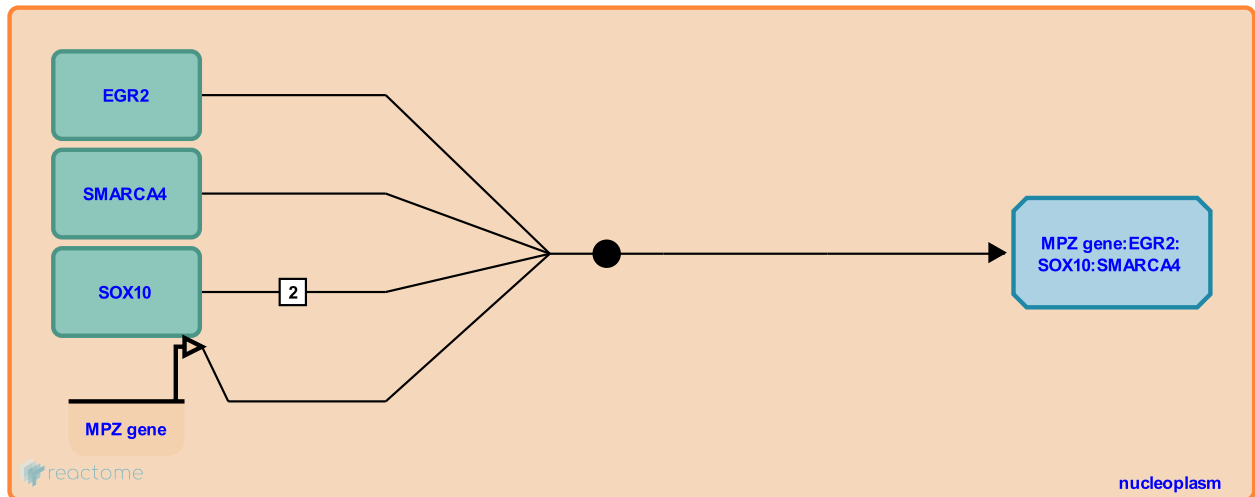
## EGR2, SOX10 and SMARCA4 bind the MPZ gene [↗](#)

**Stable identifier:** R-HSA-9614790

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [Egr2, Sox10 and Smarca4 bind the Mpz gene \(Rattus norvegicus\)](#)



MPZ is a key component of the myelin sheath that surrounds axons of the peripheral nervous system. Expression of MPZ is dependent on binding of transcriptional regulators EGR2 and SOX10 to response elements in intron 1, where they recruit SMARCA4 to the gene (Le Blanc et al, 2006; Le Blanc et al, 2007; Marathe et al, 2013). SOX10 additionally binds to elements in the promoter of MPZ (Peirano et al, 2000).

### Literature references

- Goerich, DE., Wegner, M., Riethmacher, D., Peirano, RI. (2000). Protein zero gene expression is regulated by the glial transcription factor Sox10. *Mol. Cell. Biol.*, 20, 3198-209. [↗](#)
- Yeung, KC., Datar, I., Zhang, X., Mehta, G., Marathe, HG., Mehrotra, A. et al. (2013). SWI/SNF enzymes promote SOX10-mediated activation of myelin gene expression. *PLoS ONE*, 8, e69037. [↗](#)
- Ward, RM., Svaren, J., Leblanc, SE. (2007). Neuropathy-associated Egr2 mutants disrupt cooperative activation of myelin protein zero by Egr2 and Sox10. *Mol. Cell. Biol.*, 27, 3521-9. [↗](#)
- Wrabetz, L., Ward, RM., Svaren, J., Jang, SW., Leblanc, SE. (2006). Direct regulation of myelin protein zero expression by the Egr2 transactivator. *J. Biol. Chem.*, 281, 5453-60. [↗](#)

### Editions

2019-08-16	Authored	Rothfels, K.
2020-01-17	Reviewed	Aletta, J M.
2020-02-24	Edited	Rothfels, K.