

EGR2 and SOX10 bind the MBP gene

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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](#))

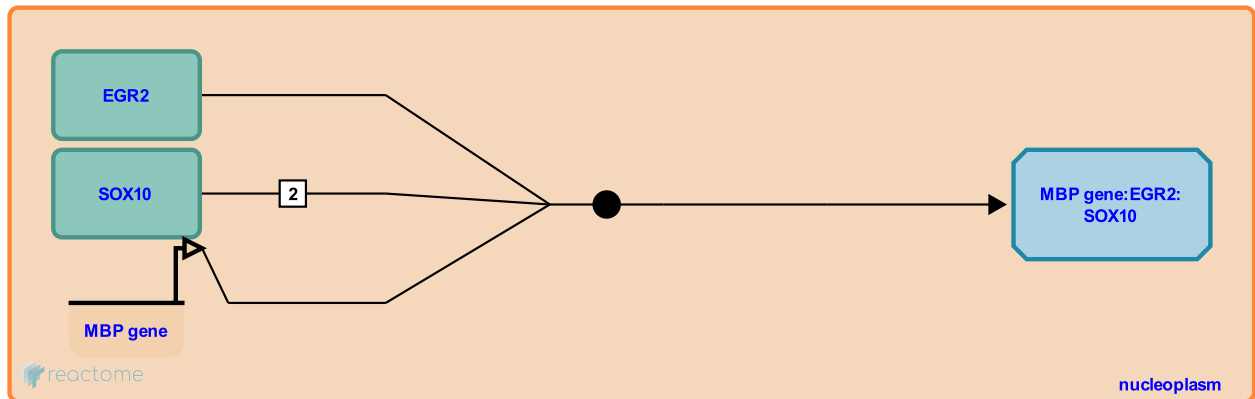
EGR2 and SOX10 bind the MBP gene [↗](#)

Stable identifier: R-HSA-9615638

Type: binding

Compartments: nucleoplasm

Inferred from: [Egr2 and Sox10 bind Mbp1 gene \(Rattus norvegicus\)](#)



Myelin basic protein (MBP) is a key component in the myelin sheath that coats axons of the peripheral nervous system. MBP expression is regulated by EGR2 binding to sites in an enhancer that lies ~9kb upstream of the transcriptional start site, as well as to a binding site in the first intron (Forgahni et al, 2001; Denarier et al, 2005; Jang et al, 2006; Jones et al, 2007). Based on conservation of binding sites, SOX10 is predicted to also contribute to MBP expression during myelination (Jones et al, 2007), and this is substantiated by ChIP seq analysis and Sox10 knockdown studies in mouse (Arido-Lopez et al, 2015).

Literature references

- Koenning, M., Keles, S., Emery, B., Lopez-Anido, C., Sun, G., Hung, HA. et al. (2015). Differential Sox10 genomic occupancy in myelinating glia. *Glia*, 63, 1897-1914. [↗](#)
- Nagarajan, R., Jones, EA., Mager, GM., Ward, RM., Chang, LW., Svaren, J. et al. (2007). Interactions of Sox10 and Egr2 in myelin gene regulation. *Neuron Glia Biol.*, 3, 377-87. [↗](#)
- Wrabetz, L., Svaren, J., Leblanc, SE., Jang, SW., Roopra, A. (2006). In vivo detection of Egr2 binding to target genes during peripheral nerve myelination. *J. Neurochem.*, 98, 1678-87. [↗](#)
- Friedman, HC., Forghani, R., Hudson, TJ., Dib, S., Peterson, A., Drouin, R. et al. (2005). Functional organization of a Schwann cell enhancer. *J. Neurosci.*, 25, 11210-7. [↗](#)
- Forghani, R., Hudson, TJ., Tretjakoff, I., Peterson, A., Lepage, P., Garofalo, L. et al. (2001). A distal upstream enhancer from the myelin basic protein gene regulates expression in myelin-forming schwann cells. *J. Neurosci.*, 21, 3780-7. [↗](#)

Editions

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