EGR2 gene expression

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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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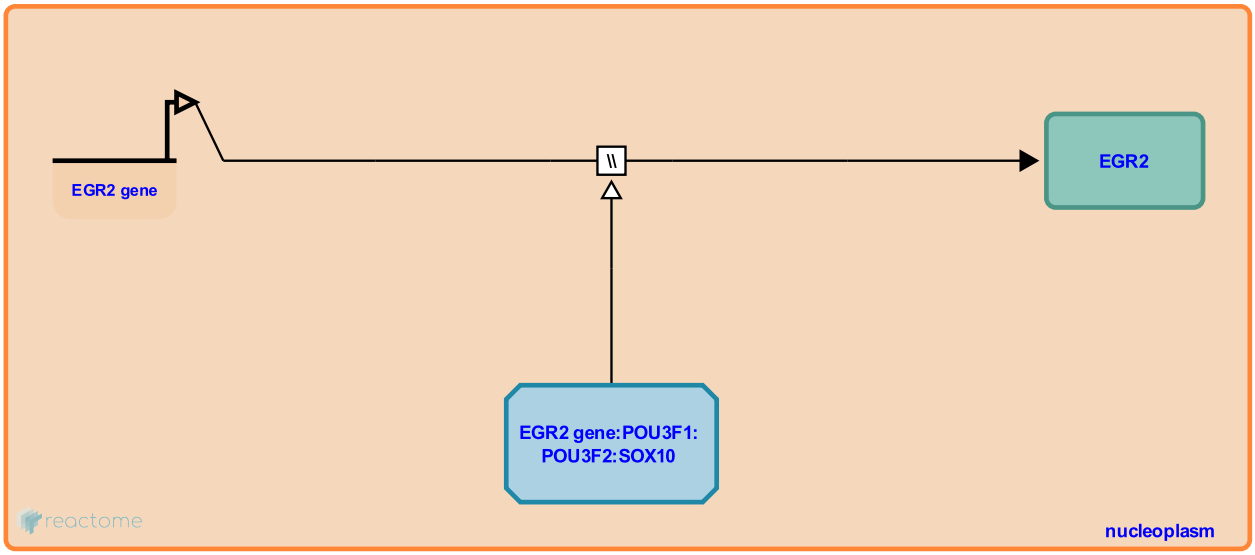
Stable identifier: R-HSA-9613760

Type: omitted

Compartments: nucleoplasm



EGR2 (also known as KROX20) is a member of the Early Growth Response (EGR) gene family encoding sequence-specific Cys2-His2 DNA binding transcription factors. The EGR family are immediate early genes (IEGs) whose expression is rapidly upregulated in response to a number of external stimuli to control activation of genes involved in stress response and differentiation (reviewed in Pagel and Deindl, 2001; Bahrami and Drabløs, 2016). Roles for EGR proteins are well established in the nervous system, with EGR target genes contributing to synaptic plasticity, long-term potentiation, peripheral nerve myelination and NGF-induced neurite outgrowth (reviewed in Perez-Cadahia et al, 2011; Herdegen and Leah, 1998; O'Donovan et al, 1999)
In addition to its other roles, EGR2 is a critical regulator of myelination by Schwann cells in the peripheral nervous system (reviewed in Svaren and Meijer, 2008). Consistent with this, Schwann cells are blocked at the promyelinating stage in EGR2 knockouts in mice (Topilko et al, 1994). Expression of EGR2 during the myelination process is controlled by a myelinating Schwann cell enhancer (MSE) 35 kb downstream of the gene (Ghislain et al, 2002). The MSE is bound by SOX10, POU3F1 and POU3F2 (Ghislain and Charnay, 2006; Reiprich et al, 2010). SOX10 in turn recruits SMARCA4, HDAC1 and HDAC2 to play overlapping but non-redundant roles in activating EGR2 expression (Jacob et al, 2011; Chen et al, 2011; Weider et al, 2012).

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Editions

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