

Egr2 (Krox20) activates Hoxb2 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

- 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

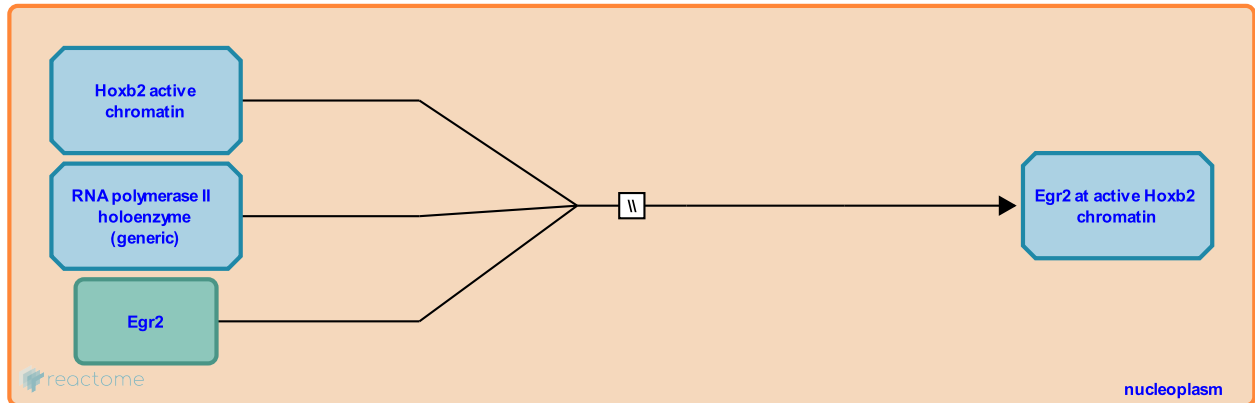
This document contains 1 reaction ([see Table of Contents](#))

Egr2 (Krox20) activates Hoxb2 expression ↗

Stable identifier: R-MMU-5619430

Type: omitted

Compartments: nucleoplasm



Egr2 (Krox20) binds three sites in the 5' region of the Hoxb2 gene and activates expression in rhombomere 3 (r3) and r5 (Sham et al. 1993, Maconochie et al. 2001, Ferrai et al. 2009). Hoxb1 activates Hoxb2 in r4 and expression is also observed in r6 and r7.

Literature references

Krumlauf, R., Nonchev, S., Marshall, H., Frain, M., Sham, MH., Vesque, C. et al. (1993). The zinc finger gene Krox20 regulates HoxB2 (Hox2.8) during hindbrain segmentation. *Cell*, 72, 183-96. ↗

Krumlauf, R., Nonchev, S., Manzanares, M., Marshall, H., Maconochie, MK. (2001). Differences in Krox20-dependent regulation of Hoxa2 and Hoxb2 during hindbrain development. *Dev. Biol.*, 233, 468-81. ↗

Editions

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