Expression of DPPA4

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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. ↗

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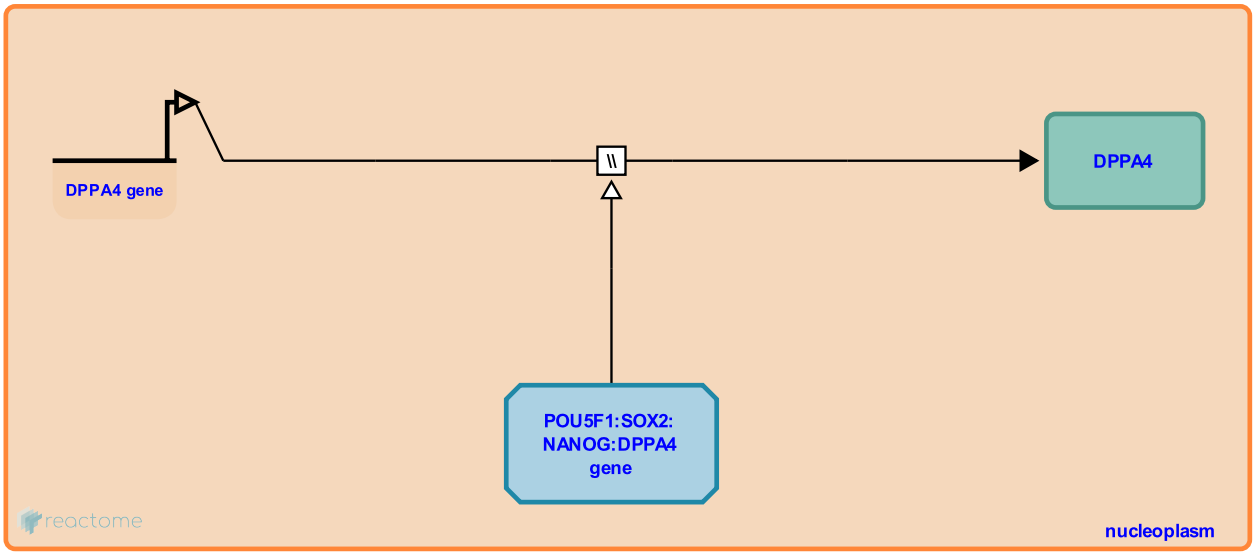
Stable identifier: R-HSA-452701

Type: omitted

Compartments: nucleoplasm



DPPA4 is expressed in pluripotent stem cells. The promoter of the DPPA4 gene binds OCT4 (POU5F1), SOX2, and NANOG (Player et al. 2006, Boyer et al. 2007, inferred from mouse homologs in Chakravarthy et al. 2008). OCT4 Knockdown experiments show OCT4 enhances expression of DPPA4 (Babaie et al. 2007).

Literature references

Desler, M., McKeithan, TW., Mallanna, SK., Boer, B., Rizzino, A., Chakravarthy, H. (2008). Identification of DPPA4 and other genes as putative Sox2:Oct-3/4 target genes using a combination of in silico analysis and transcription-based assays. *J Cell Physiol, 216*, 651-62.

Gifford, DK., Jaenisch, R., Lee, TI., Young, RA., Kumar, RM., Guenther, MG. et al. (2005). Core transcriptional regulatory circuitry in human embryonic stem cells. *Cell, 122*, 947-56.

Player, A., Rao, M., Puri, RK., Wang, Y., Kawasaki, ES., Bhattacharya, B. (2006). Comparisons between transcriptional regulation and RNA expression in human embryonic stem cell lines. *Stem Cells Dev, 15*, 315-23.

Babaie, Y., Groth, D., Wruck, W., Greber, B., Lehrach, H., Brink, TC. et al. (2007). Analysis of Oct4-dependent transcriptional networks regulating self-renewal and pluripotency in human embryonic stem cells. *Stem Cells, 25*, 500-10.

Editions

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