MECOM (EVI1) recruits polycomb repressor complexes (PRCs) to the PTEN gene promoter

Carracedo, A., Orlic-Milacic, M., Salmena, L.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

03/05/2024

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

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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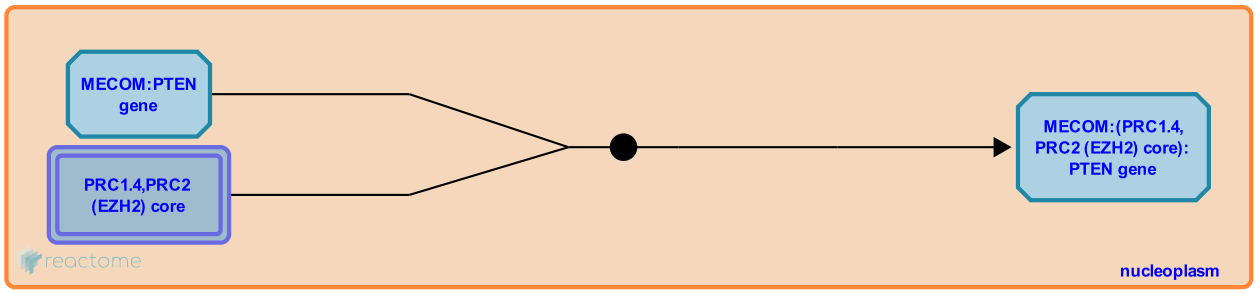
Stable identifier: R-HSA-8943817

Type: binding

Compartments: nucleoplasm



The transcription factor MECOM (EVI1) can associate with the polycomb repressor complexes (PRCs) and recruit them to the promoter of the PTEN gene (Song et al. 2009). Both the BMI1-containing PRC, supposedly PRC1.4, and the EZH2-containing PRC2 complex are recruited to the PTEN promoter, resulting in transcriptional silencing of the PTEN gene (Song et al. 2009, Yoshimi et al. 2011). Since the exact composition of the EZH2-containing PRC2 at the PTEN promoter is not known, the core EZH2-PRC2 complex is shown.

Literature references

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Editions

2016-08-11	Authored	Carracedo, A., Salmena, L.
2016-10-30	Authored	Orlic-Milacic, M.
2017-05-09	Edited	Orlic-Milacic, M.