MYC trancscription is negatively regulated by SMAD2/3:SMAD4:RBL1:E2F4/5:DP1/2 complex

Contreras, O., Huang, T., Jassal, B., Orlic-Milacic, M.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of Creative Commons Attribution 4.0 International (CC BY 4.0) License. For more information see our license.

01/05/2024

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

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. ↗

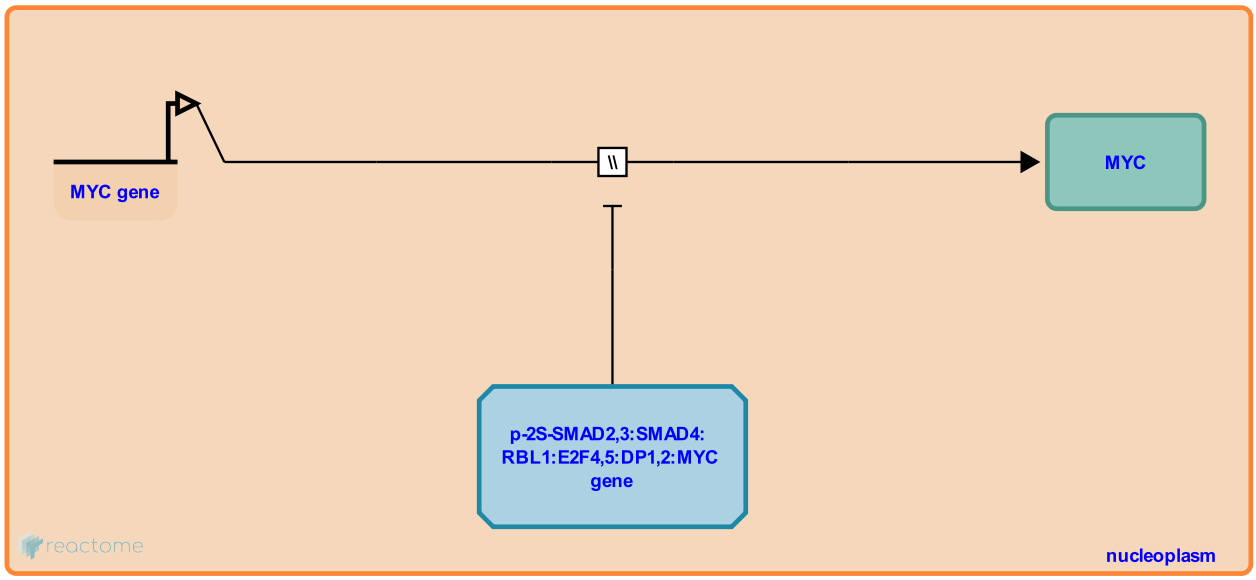
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

MYC trancscription is negatively regulated by SMAD2/3:SMAD4:RBL1:E2F4/5:DP1/2 complex ↗

Stable identifier: R-HSA-1484099

Type: omitted

Compartments: nucleoplasm



Complex formed by RBL1 (p107), E2F4/5, DP1/2 and a trimer of phosphorylated R-SMADs (SMAD2/3) and SMAD4 (Co-SMAD) cooperatively binds to TIE (TGF-beta inhibitory element) and E2F sites in the MYC promoter and promotes cell-cycle independent inhibition of MYC transcription in response to TGF-beta stimulation (Chen et al. 2002).

Literature references

Massague, J., Siegel, PM., Chen, CR., Kang, Y. (2002). E2F4/5 and p107 as Smad cofactors linking the TGFbeta receptor to c-myc repression. *Cell, 110*, 19-32. ↗

Editions

2012-04-05	Authored	Orlic-Milacic, M.
2012-04-10	Edited	Jassal, B.
2012-05-14	Reviewed	Huang, T.
2022-05-02	Reviewed	Contreras, O.
2022-05-09	Edited	Orlic-Milacic, M.