SKI complexes with the Smad complex, suppressing BMP2 signalling

Heldin, CH., Huminiecki, L., Mi, H., Moustakas, A.

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

17/05/2024

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. ↗

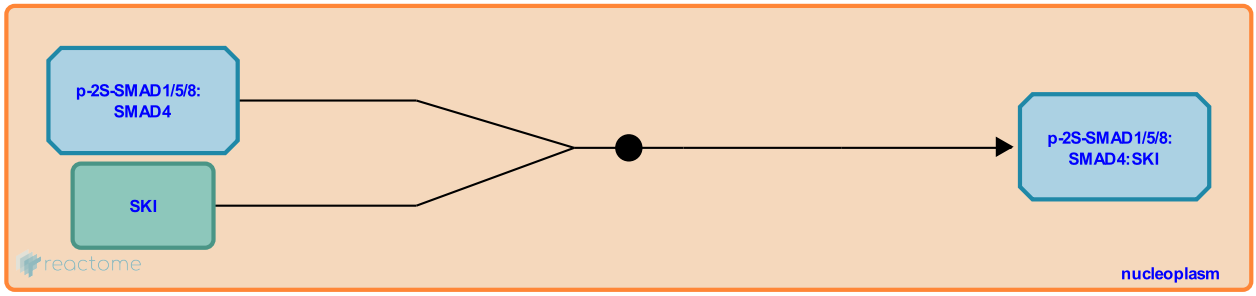
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

SKI complexes with the Smad complex, suppressing BMP2 signalling ↗

Stable identifier: R-HSA-201423

Type: binding

Compartments: nucleoplasm



SKI and SKIL (SNO) are able to recruit NCOR and possibly other transcriptional repressors to SMAD2/3:SMAD4 complex, inhibiting SMAD2/3:SMAD4-mediated transcription (Sun et al. 1999, Luo et al. 1999, Strochein et al. 1999). Experimental findings suggest that SMAD2 and SMAD3 may target SKI and SKIL for degradation (Strochein et al. 1999, Sun et al. 1999 PNAS, Bonni et al. 2001), and that the ratio of SMAD2/3 and SKI/SKIL determines the outcome (inhibition of SMAD2/3:SMAD4-mediated transcription or degradation of SKI/SKIL). SKI and SKIL are overexpressed in various cancer types and their oncogenic effect is connected with their ability to inhibit signaling by TGF-beta receptor complex.

Literature references

Wang, W., Luo, K., Harland, RM., Mariani, FV. (2000). Ski represses bone morphogenic protein signaling in Xenopus and mammalian cells. *Proc Natl Acad Sci U S A, 97*, 14394-9. ↗

Editions

2007-11-07	Authored	Moustakas, A., Huminiecki, L.
2007-11-12	Reviewed	Heldin, CH.
2019-02-08	Revised	Mi, H.