NGF-stimulated transcription

Aletta, J M., Castagnoli, L., Jassal, B., Le Novere, N., Rothfels, K.

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

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20/02/2022
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


Reactome database release: 79

This document contains 1 pathway and 37 reactions (see Table of Contents)
NGF-stimulated transcription

Stable identifier: R-HSA-9031628

NGF stimulation induces expression of a wide array of transcriptional targets. In rat PC12 cells, a common model for NGF signaling, stimulation with NGF causes cells to exit the cell cycle and undergo a differentiation program leading to neurite outgrowth. This program is driven by the expression of immediate early genes (IEGs), which frequently encode transcription factors regulating the activity of NGF-specific delayed response genes (reviewed in Sheng and Greenberg, 1990; Flavell and Grennberg, 2008; Santiago and Bashaw, 2014).

Literature references


Editions

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<td>Authored</td>
<td>Rothfels, K.</td>
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<tr>
<td>2020-01-17</td>
<td>Reviewed</td>
<td>Aletta, J M.</td>
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<tr>
<td>2020-02-24</td>
<td>Edited</td>
<td>Rothfels, K.</td>
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p-S133 CREB1, MEF2D and SRF bind the ARC gene

Location: NGF-stimulated transcription

Stable identifier: R-HSA-9031610