

Expression of STAT3-upregulated cytosolic

proteins

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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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Signal transducer and activator of transcription 3 (STAT3) is a key regulator of gene expression in response to signaling of many cytokines including interleukin-6 (IL6), Oncostatin M, and leukemia inhibitory factor. Using microarray techniques, hundreds of genes have been reported as potential STAT3 target genes (Dauer et al. 2005, Hsieh et al. 2005). Some of these genes have been proven to be direct STAT3 targets using genome-wide chromatin immunoprecipitation screening (Snyder et al. 2008, Carpenter & Lo 2014). Genes for cytoplasmic proteins upregulated by STAT3 include Suppressor of cytokine signaling 3 (SOCS3) (He et al. 2003), Induced myeloid leukemia cell differentiation protein Mcl-1 (MCL1) (Becker et al. 2014), Heat shock protein HSP 90-alpha (HSP90AA1) (Chen et al. 2007), Fascin (FSCN1) (Snyder et al. 2009), RAC-alpha serine/threonine-protein kinase (AKT1) (Xu et al. 2005), Cyclin-dependent kinase inhibitor 1 (CDKN1A) (Bellido et al. 1998), Phosphatidylinositol 3-kinase regulatory subunit alpha (PIK3R1) (Abell et al. 2005), Signal transducer and activator of transcription 1 (STAT1) (Han et al. 2013), Interferon regulatory factor 4 (IRF4) (Durant et al. 2010) and Nitric oxide synthase, inducible (NOS2) (Lo et al. 2005).

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Editions

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