

# Expression of STAT3-upregulated nuclear proteins

Jupe, S., Leibovich, SJ.

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

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

- 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. [↗](#)

Reactome database release: 88

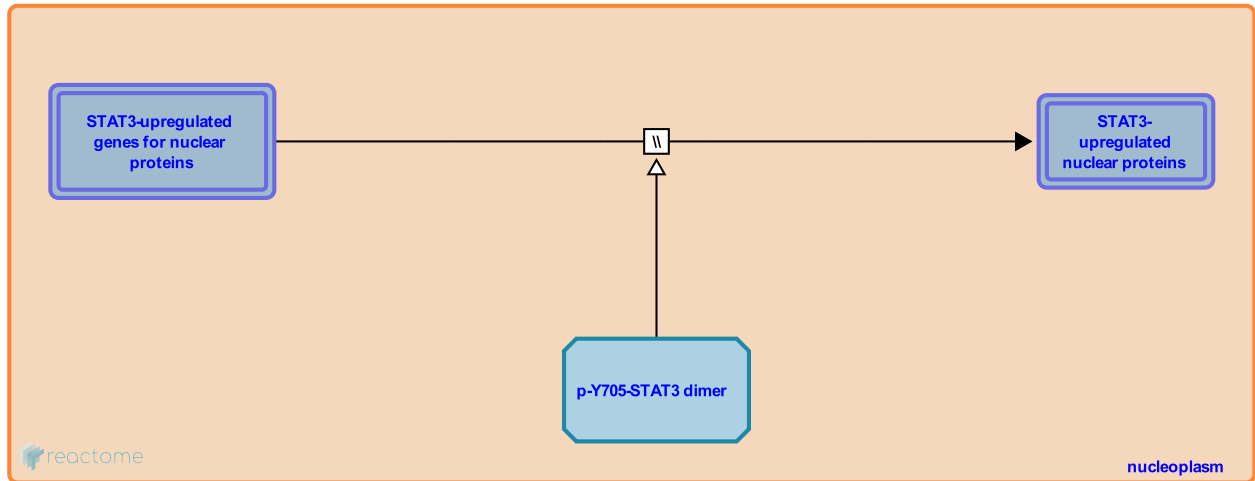
This document contains 1 reaction ([see Table of Contents](#))

## Expression of STAT3-upregulated nuclear proteins ↗

**Stable identifier:** R-HSA-6790036

**Type:** omitted

**Compartments:** nucleoplasm



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 nuclear proteins upregulated by STAT3 include CCAAT/enhancer-binding protein delta (CEBPD) (Hutt et al. 2000), B-cell lymphoma 6 protein (BCL6) (Reljic et al. 2000), Myc proto-oncogene protein (MYC) (Kiuchi et al. 1999, Bowman et al. 2001), Proto-oncogene c-Fos (FOS) (Yang et al. 2003), Hypoxia-inducible factor 1-alpha (HIF1A) (Niu et al. 2008), Transcription factor SOX-2 (SOX2) (Foshay & Gallicano 2008), the homeobox protein NANOG (Okumura et al. 2011), Twist-related protein 1 (TWIST1) (Lo et al. 2007, Cheng et al. 2008), Zinc finger E-box-binding homeobox 1 (ZEB1) (Xiong et al. 2012), POU domain, class 2, transcription factor 1 (POU2F1) (OCT1) (Wang et al. 2013), Baculoviral IAP repeat-containing protein 5 (BIRC5, Survivin) (Gritsko et al. 2006), G1/S-specific cyclin-D1 (CCND1) (Leslie et al. 2006), Serine/threonine-protein kinase PIM1 (Przanowski et al. 2014), Forkhead box protein O1 (FOXO1), FOXO3 (Oh et al. 2011), Nuclear receptor ROR-alpha (RORA), RORC, Basic leucine zipper transcriptional factor ATF-like (BATF) (Durant et al. 2010) and Transcription factor JUNB (Coffer et al. 1995).

### Literature references

- Pestell, R., Albanese, C., Darnell, JE., Leslie, K., Azare, J., Bromberg, J. et al. (2006). Cyclin D1 is transcriptionally regulated by and required for transformation by activated signal transducer and activator of transcription 3. *Cancer Res.*, 66, 2544-52. ↗
- Hu, F., Dabrowski, M., Ellert-Miklaszewska, A., Kaminska, B., Ronowicz, A., Kettenmann, H. et al. (2014). The signal transducers Stat1 and Stat3 and their novel target Jmjd3 drive the expression of inflammatory genes in microglia. *J. Mol. Med.*, 92, 239-54. ↗
- Kaneko, S., Diaz, N., Gritsko, T., Bowman, T., Lee, JH., Eschrich, S. et al. (2006). Persistent activation of stat3 signaling induces survivin gene expression and confers resistance to apoptosis in human breast cancer cells. *Clin. Cancer Res.*, 12, 11-9. ↗
- Gunduz, M., Lo, HW., Xia, W., Bartholomeusz, G., Ali-Seyed, M., Hung, MC. et al. (2005). Nuclear interaction of EGFR and STAT3 in the activation of the iNOS/NO pathway. *Cancer Cell*, 7, 575-89. ↗
- Yang, E., Darnell, JE., Besser, D., Lerner, L. (2003). Independent and cooperative activation of chromosomal c-fos promoter by STAT3. *J. Biol. Chem.*, 278, 15794-9. ↗

**Editions**

2015-07-01	Authored	Jupe, S.
2016-09-02	Edited	Jupe, S.
2016-09-02	Reviewed	Leibovich, SJ.