

## STAT3 (Signal Transducer and Activator of Transcription 3)

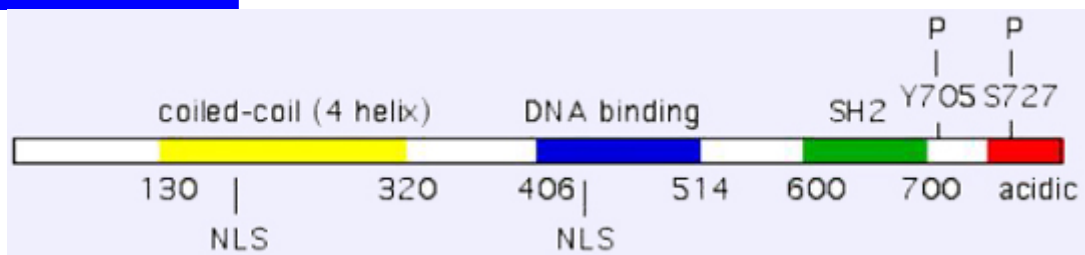
### Identity

Other names **Acute Phase Response Factor, APRF**  
 Hugo **STAT3**  
 Location 17q21.2  
 STAT3 is flanked by STAT5a and PTRF

### DNA/RNA

Note 24 exons spanning 74444 bp.  
 Transcription There are two major transcripts, STAT3a and STAT3b. STAT3a mRNA is 4973 bp. The STAT3b arises due to an alternate splice acceptor site in exon 23 which gives rise to a protein that is essentially truncated after amino acid 715. Another variant differs by 1 amino acid.

### Protein



Description There are two major isoforms of STAT3. The long form is known as STAT3 (or STAT3a) and is a 770 amino acid protein (93 kDa on gels). Notable features are STAT family DNA binding domain, an SH2 domain, a major tyrosine phosphorylation site at Y705 and a major serine phosphorylation site at S727. Phosphorylation leads to dimerization of STAT3 via intermolecular pTyr-SH2 interactions. STAT3 can also heterodimerize with STAT1. (Recent data suggests that STAT3 can possibly form a dimer without tyrosine phosphorylation and that phosphorylation leads to changes dimer conformation). Tyrosine of the protein activates its high affinity DNA binding activity (TTCNNGGAA) and can stimulate nuclear translocation of the protein. Stimulation of STAT3 tyrosine phosphorylation occurs in response to a variety of cytokines and growth factors including LIF, OSM, IL-6, leptin, EGF, PDGF, and HGF. The C terminal domain is a transcriptional activation domain whose activity is enhanced by phosphorylation of serine 727. The STAT3 beta isoform (84 kDa) is missing this domain (1-715 + 7 unique amino acids resulting from frameshift) and is sometimes used as a dominant negative though there is also evidence that it regulates distinct genes as well.

Expression near ubiquitous

Localisation Cytoplasmic, but translocates to the nucleus upon tyrosine phosphorylation.

Function Transcription regulation.

Homology Shares homology with the other 6 mammalian STAT genes: STAT1,

STAT2, STAT4, STAT5A, STAT5B, STAT6.

## Implicated in

Disease Upregulated in many cancers including [glioblastoma](#), [head and neck cancer](#), prostate cancer, and [breast cancer](#). A constitutively active form of STAT3 is oncogenic, though these mutations have not been identified in human cancer as yet. STAT 3 activation is associated with Crohn's disease, and other inflammatory diseases such as pulmonary fibrosis and acute lung injury. STAT3 is critical for leptin signaling and its mutation leads to obesity in mice.

## External links

Nomenclature	
<a href="#">Hugo</a>	<a href="#">STAT3</a>
<a href="#">GDB</a>	<a href="#">STAT3</a>
<a href="#">Entrez Gene</a>	<a href="#">STAT3 6774</a> signal transducer and activator of transcription 3 (acute-phase response factor)
Cards	
<a href="#">Atlas</a>	<a href="#">STAT3ID444</a>
<a href="#">GeneCards</a>	<a href="#">STAT3</a>
<a href="#">Ensembl</a>	<a href="#">STAT3</a>
<a href="#">CancerGene</a>	<a href="#">STAT3</a>
<a href="#">Genatlas</a>	<a href="#">STAT3</a>
<a href="#">GeneLynx</a>	<a href="#">STAT3</a>
<a href="#">eGenome</a>	<a href="#">STAT3</a>
<a href="#">euGene</a>	<a href="#">6774</a>
Genomic and cartography	
<a href="#">GoldenPath</a>	<a href="#">STAT3 - 17q21.2 chr17:37718869-37794039 - 17q21.2</a> (hg17-May_2004)
<a href="#">Ensembl</a>	<a href="#">STAT3 - 17q21.2 [CytoView]</a>
<a href="#">NCBI</a>	<a href="#">Genes Cyto</a> <a href="#">Gene Seq</a> [Map View - NCBI]
<a href="#">OMIM</a>	<a href="#">Disease map [OMIM]</a>
<a href="#">HomoloGene</a>	<a href="#">STAT3</a>
Gene and transcription	
<a href="#">Genbank</a>	<a href="#">AF332508</a> [SRS] <a href="#">AF332508</a> [ENTREZ]
<a href="#">Genbank</a>	<a href="#">AY572796</a> [SRS] <a href="#">AY572796</a> [ENTREZ]
<a href="#">Genbank</a>	<a href="#">AF029311</a> [SRS] <a href="#">AF029311</a> [ENTREZ]
<a href="#">Genbank</a>	<a href="#">AI631896</a> [SRS] <a href="#">AI631896</a> [ENTREZ]
<a href="#">Genbank</a>	<a href="#">AJ012463</a> [SRS] <a href="#">AJ012463</a> [ENTREZ]
<a href="#">RefSeq</a>	<a href="#">NM_003150</a> [SRS] <a href="#">NM_003150</a> [ENTREZ]
<a href="#">RefSeq</a>	<a href="#">NM_139276</a> [SRS] <a href="#">NM_139276</a> [ENTREZ]
<a href="#">RefSeq</a>	<a href="#">NM_213662</a> [SRS] <a href="#">NM_213662</a> [ENTREZ]
<a href="#">RefSeq</a>	<a href="#">NT_086877</a> [SRS] <a href="#">NT_086877</a> [ENTREZ]
<a href="#">AceView</a>	<a href="#">STAT3</a> AceView - NCBI
<a href="#">TRASER</a>	<a href="#">STAT3</a> Traser - Stanford
<a href="#">Unigene</a>	<a href="#">Hs.463059</a> [SRS] <a href="#">Hs.463059</a> [NCBI] <a href="#">HS463059</a> [spliceNest]
Protein : pattern, domain, 3D structure	
<a href="#">SwissProt</a>	<a href="#">P40763</a> [SRS] <a href="#">P40763</a> [EXPASY] <a href="#">P40763</a> [INTERPRO]
<a href="#">Prosite</a>	<a href="#">PS50001 SH2</a> [SRS] <a href="#">PS50001 SH2</a> [Expasy]
<a href="#">Interpro</a>	<a href="#">IPR008967 P53 like DNA_bnd</a> [SRS] <a href="#">IPR008967 P53 like DNA_bnd</a> [EBI]

[Interpro](#) [IPR000980 SH2](#) [ SRS ] [IPR000980 SH2](#) [ EBI ]  
[Interpro](#) [IPR001217 STAT](#) [ SRS ] [IPR001217 STAT](#) [ EBI ]  
[CluSTr](#) [P40763](#)  
[Pfam](#) [PF00017 SH2](#) [ SRS ] [PF00017 SH2](#) [ Sanger ] [pfam00017](#) [ NCBI-CDD ]  
[Pfam](#) [PF01017 STAT\\_alpha](#) [ SRS ] [PF01017 STAT\\_alpha](#) [ Sanger ]  
[Pfam](#) [PF02864 STAT\\_bind](#) [ SRS ] [PF02864 STAT\\_bind](#) [ Sanger ]  
[Pfam](#) [PF02865 STAT\\_int](#) [ SRS ] [PF02865 STAT\\_int](#) [ Sanger ] [pfam02865](#) [ NCBI-CDD ]  
[Blocks](#) [P40763](#)

### Polymorphism : SNP, mutations, diseases

[OMIM](#) [102582](#) [ map ]  
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[SNP](#) [STAT3](#) [dbSNP-NCBI]  
[SNP](#) [NM\\_003150](#) [SNP-NCI]  
[SNP](#) [NM\\_139276](#) [SNP-NCI]  
[SNP](#) [NM\\_213662](#) [SNP-NCI]  
[SNP](#) [STAT3](#) [GeneSNPs - Utah] [STAT3](#) [SNP - CSHL] [STAT3](#) [HGBASE - SRS]

### General knowledge

[Family Browser](#) [STAT3](#) [UCSC Family Browser]  
[SOURCE](#) [NM\\_003150](#)  
[SOURCE](#) [NM\\_139276](#)  
[SOURCE](#) [NM\\_213662](#)  
[SMD](#) [Hs.463059](#)  
[SAGE](#) [Hs.463059](#)  
[Amigo](#) [process|JAK-STAT cascade](#)  
[Amigo](#) [process|acute-phase response](#)  
[Amigo](#) [function|calcium ion binding](#)  
[Amigo](#) [process|cell motility](#)  
[Amigo](#) [component|cytoplasm](#)  
[Amigo](#) [function|hematopoietin/interferon-class \(D200-domain\) cytokine receptor signal transducer activity](#)  
[Amigo](#) [process|intracellular signaling cascade](#)  
[Amigo](#) [process|negative regulation of transcription from Pol II promoter](#)  
[Amigo](#) [process|neurogenesis](#)  
[Amigo](#) [component|nucleus](#)  
[Amigo](#) [component|nucleus](#)  
[Amigo](#) [process|regulation of transcription, DNA-dependent](#)  
[Amigo](#) [function|signal transducer activity](#)  
[Amigo](#) [function|transcription factor activity](#)  
[Amigo](#) [function|transcription factor activity](#)  
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[BIOCARTA](#) [Erk1/Erk2 Mapk Signaling pathway](#)  
[BIOCARTA](#) [Role of ERBB2 in Signal Transduction and Oncology](#)  
[BIOCARTA](#) [IL22 Soluble Receptor Signaling](#)  
[BIOCARTA](#) [IL 6 signaling pathway](#)  
[BIOCARTA](#) [Signaling of Hepatocyte Growth Factor Receptor](#)  
[BIOCARTA](#) [PDGF Signaling Pathway](#)  
[BIOCARTA](#) [Stat3 Signaling Pathway](#)

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[STAT3](#)

**Other databases**

**Probes**

[Probe](#)

[STAT3 Related clones \(RZPD - Berlin\)](#)

**PubMed**

[PubMed](#)

[127 Pubmed reference\(s\) in LocusLink](#)

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Medline [14729509](#)

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**Contributor(s)**

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