

## Gene Section

### Review

# STAT5B (signal transducer and activator of transcription 5B)

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## Identity

**Other names:** STAT5

**HGNC (Hugo):** STAT5B

**Location:** 17q21.2

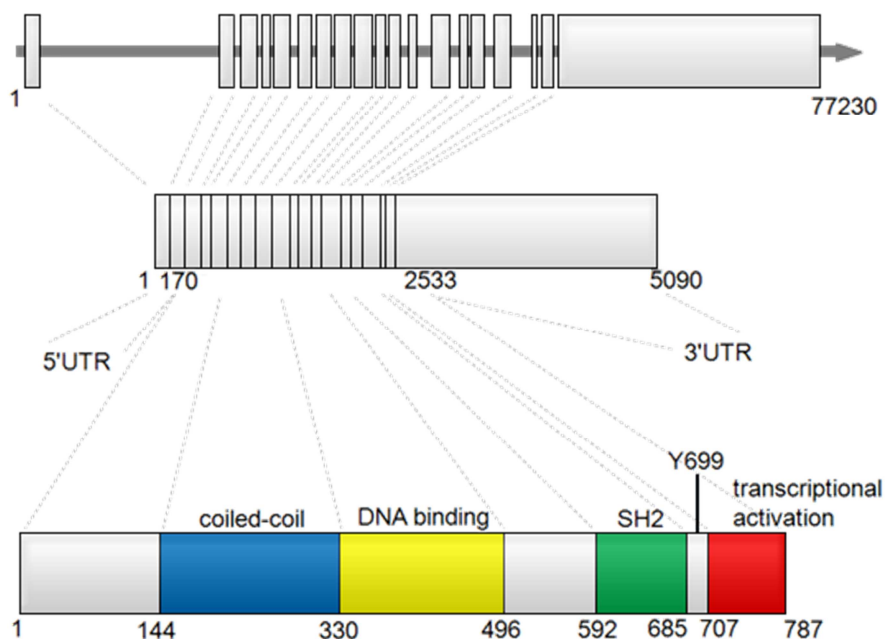
## DNA/RNA

### Description

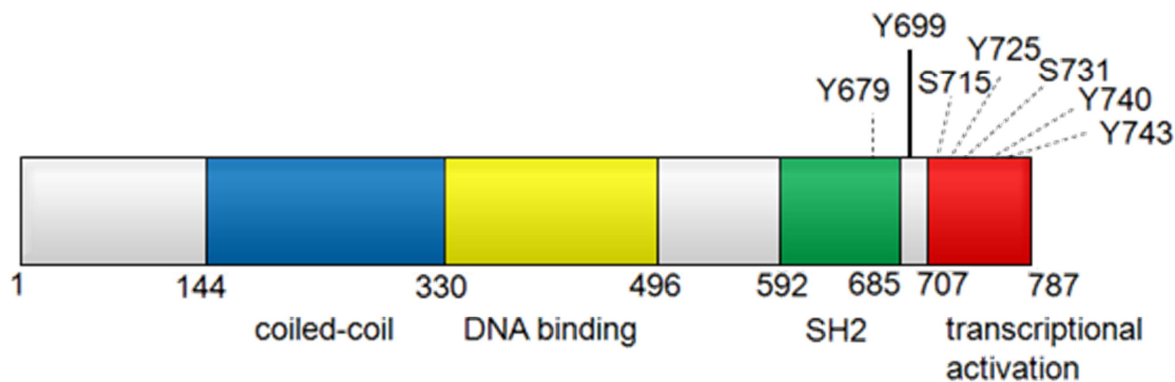
The STAT5b gene is composed of 77229 base pairs and contains 19 exons. As exon 1 contains only the 5' UTR, there are 18 coding exons. The mRNA is composed of 5090 base pairs.

### Transcription

There is one major transcript.



**The STAT5b gene.** The STAT5b gene is composed of 19 exons that are transcribed as a 5090 nucleotide RNA transcript. The RNA is translated into the STAT5b protein containing 787 amino acids.



**Schematic of the STAT5b protein.** The STAT5b protein contains several conserved domains: the coiled-coil domain, the DNA binding domain, the SH2 domain, and the carboxy-terminal transactivation domain. While phosphorylation of Y699 is required for transcriptional activity, there are multiple tyrosine and serine phosphorylation sites that have been identified under specific conditions and in certain cell types.

## Protein

### Note

STAT5b is composed of 787 amino acids (92 kD).

### Description

STAT5b is a member of the signal transducer and activator of transcription (STAT) family. The STAT proteins contain several conserved domains: the coiled-coil domain, the DNA binding domain, the SH2 domain, and the carboxy-terminal transactivation domain. STATs remain latent in the cytoplasm until the binding of a cytokine or growth factor to its receptor, resulting in recruitment of the STAT to the ligand receptor complex (Levy and Darnell, 2002; Herrington et al., 1999; Heim et al., 1995). The STAT protein is then phosphorylated by receptor tyrosine kinases or non-receptor tyrosine kinases, such as Janus kinases (JAKs) and Src family members. This phosphorylation results in SH2 domain mediated dimerization of STATs and their translocation to the nucleus. In the nucleus, STAT dimers bind to consensus DNA sequences and recruit additional transcription machinery to initiate specific gene regulation. To date, seven members of the STAT family have been identified (STAT1, STAT2, STAT3, STAT4, STAT5a, STAT5b, and STAT6) (Silva, 2004; Calò et al., 2003; Moriggl et al., 1996; Liu et al., 1996; Liu et al., 1997).

STAT5b is activated by a variety of stimuli, including interleukins, erythropoietin, growth hormone (GH), prolactin (Prl), and epidermal growth factor (EGF). Activation of STAT5b results in phosphorylation of tyrosine 699. Phosphorylation of this tyrosine is required for DNA binding and transcriptional activity. Mutation of Y699 of STAT5b inhibits stimulant-induced tyrosine phosphorylation, DNA binding, and transcriptional activity (Gebert et al., 1997; Gouilleux et al., 1994; Kloth et al., 2003). Additional tyrosine phosphorylation sites (Y679, Y725, Y740, and Y743) and serine phosphorylation sites (S715, S731) have been shown to alter STAT5b transcriptional activity (Kloth et al., 2002; Weaver and Silva, 2006; Yamashita

et al., 2001; Park et al., 2001; Decker and Kovarik, 2000).

While no classic nuclear localization signal (NLS) composed of a cluster of basic amino acids has been reported for the STAT5b, the STAT5b dimer is actively translocated through the nuclear pore complex and accumulates in the nucleus upon phosphorylation (Xu and Massagué, 2004).

STAT5b can be negatively regulated by phosphatase-mediated dephosphorylation, ubiquitination-promoting proteasome degradation, or by negative feedback loops.

### Expression

Ubiquitous.

### Localisation

STAT5b is localized in the cytoplasm and translocates to the nucleus upon phosphorylation of Y699. However, unphosphorylated STAT5b has also been reported to be found in the nucleus (Brown and Zeidler, 2008; Iyer and Reich, 2008; Zeng et al., 2002).

### Function

Transcription factor. STAT5b mediates the transcription of numerous genes in various cell signaling pathways involved in cellular proliferation, differentiation, and cell survival. The STATs bind TTC(N3)GAA gamma-interferon-activating sequence (GAS) sites in the promoters of target genes.

### Homology

Shares homology with the other STAT family members (STAT1, 2, 3, 4, 5a, and 6). Additionally, STAT5a and STAT5b are 94% similar at the amino acid level, differing primarily at the C-terminus (Teglund et al., 1998; Silva et al., 1996; Lin et al., 1996; Liu et al., 1995).

## Mutations

### Note

To date, there are 6 reported cases of humans having a mutant STAT5b, and these cases result from five

different STAT5b mutations. The first STAT5b mutation in a human to be reported was the A630P STAT5b mutant. This single point mutation in the SH2 domain causes misfolding of STAT5b. A nonsense mutation in the coiled-coil domain (R152X) results in the absence of detectable STAT5b protein. Insertion of a nucleotide in the DBD at position 1102 (Q368fsX376) or 1191 (N398E) causes a frameshift mutation resulting in a non-functional truncated STAT5b. Likewise, a single nucleotide deletion in the linker domain at position 1680 (E561R) also results in a truncated STAT5b. In each of the 6 cases, STAT5b protein is not detectable, but STAT5a protein levels are unchanged. These reports are from homozygous patients while the parents are heterozygous for the STAT5b mutation and display a normal phenotype. The phenotype of each STAT5b mutant is similar: pronounced short stature, growth hormone insensitivity despite normal to high levels of GH in the serum, and extremely low IGF-I and IGFBP-3 levels (Chia et al., 2006; Hwa et al., 2007; Nadeau et al., 2011).

## Implicated in

### Solid tumors

#### Note

STAT5b is implicated in prostate cancer (Koptyra et al., 2011; Clevenger, 2004), breast cancer (Bernaciak et al., 2009; Peck et al., 2011; Strauss et al., 2006; Sultan et al., 2005; Yamashita et al., 2003), lung cancer (Sánchez-Ceja et al., 2006), head and neck cancer (Koppikar et al., 2008), ovarian cancer (Chen et al., 2004), hepatocellular carcinoma (Lee et al., 2006), cervical cancer (Lopez et al., 2011), and colorectal cancer (Du et al., 2011).

### Leukemias and lymphomas

#### Note

STAT5b is involved in the proliferation of chronic myeloid leukemia (CML) and acute myeloid leukemia (AML) cells (Bańkiewicz-Masiuk and Machaliński, 2004; Sternberg and Gilliland, 2004; Hoover et al., 2001; de Groot et al., 1999). Additionally, STAT5b has been found to fuse with the retinoic acid receptor-alpha (RARalpha) gene in a subset of acute promyelocytic leukemias (APL) (Arnould et al., 1999). Furthermore, STAT5b plays a role in the development of lymphoblastic lymphoma (Bessette et al., 2008; Nieborowska-Skorska et al., 2001).

### Laron type dwarfism II

#### Note

Laron type dwarfism II (LTD2) is mediated by defects in STAT5b (Nadeau et al., 2011; Freeth et al., 1998; Chia et al., 2006).

### Graft-versus-host disease

#### Note

Constitutively active STAT5b increases expansion of

regulatory T cells (Treg), and these Tregs are more potent suppressors of graft-versus-host disease in vivo, compared to wild-type Tregs (Vogtenhuber et al., 2010).

### Crohn's disease/colitis

#### Note

Growth hormone reduces mucosal inflammation in colitis by activating STAT5b, such that STAT5b deficient mice demonstrated more severe colitis compared to wild-type mice (Han et al., 2006).

### Diabetes and metabolic disorder

#### Note

Upon leptin stimulation, the leptin receptor can mediate STAT5b tyrosine phosphorylation and transcriptional activity in the liver, gastrointestinal tract, and brain (Mütze et al., 2007; Ghilardi et al., 1996; Gong et al., 2007).

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