

Gene Section

Review

PTPN11 (Protein tyrosine phosphatase, non-receptor type, 11)

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Identity

Other names: SHP-2; SH-PTP2 (Src homology 2 domain-containing protein tyrosine phosphatase 2); PTP2C (Protein tyrosine phosphatase 2C); BPTP3

HGNC (Hugo): PTPN11

Location: 12q24.1

Local order: centromere - FLJ34154 - RPL6 - PTPN11 - RPH3A - OAS1 – telomere.

DNA/RNA

Description

The PTPN11 gene is divided in 16 exons. Exon 1 contains the 5' untranslated region and the translation initiation ATG, and a few additional codons. Exon 15 contains the stop codon and exon 16 contains a major portion of the 3' untranslated region. Other features of the PTPN11 gene, such as the promoter region and enhancer elements have not been delineated.

Transcription

A 7.0-kb transcript is detected in several tissues (heart, brain, lung, liver, skeletal muscle, kidney, and pancreas) with highest steady-state levels in heart and skeletal muscle. The predominant human PTPN11 mRNA contains an open reading frame of 1,779 bases, resulting in a predicted protein of 593 amino acid residues. A second mRNA containing 12 additional base pairs (exon 11) has been identified. Little additional information is available about this alternative transcript.

Pseudogene

A number of PTPN11-related processed pseudogenes, i.e. with no apparent exon structure, have been documented in the human genome. All the pseudogenes share >92% nucleotide identity with the PTPN11 cDNA (including the 5'-UTR and 3'-UTR), but harbour frameshift mutations and multiple stop codons. Three of the five pseudogenes appear to be expressed with distinct tissue distributions and expression levels.

Protein

Description

SHP-2 is a member of a small subfamily of cytoplasmic Src homology 2 (SH2) domain-containing protein tyrosine phosphatases. Both the N-SH2 and C-SH2 domains selectively bind to short amino acid motifs containing a phosphotyrosyl residue and promote SHP-2 association with activated receptors and other signaling partners. Crystallographic data indicate that the N-SH2 domain also interacts with the PTP domain using a separate site. As these subdomains show negative cooperativity, the N-SH2 domain functions as an intramolecular switch controlling SHP-2 catalytic activation. Specifically, the N-SH2 domain interacts with the PTP domain basally, blocking the catalytic site. Binding of the N-SH2 phosphopeptide-binding site to the phosphotyrosyl ligand promotes a conformational change of the domain that weakens the auto-inhibiting intramolecular interaction, making the catalytic site available to substrate, thereby activating the phosphatase.

Expression

Widely expressed in both embryonic and adult tissues.

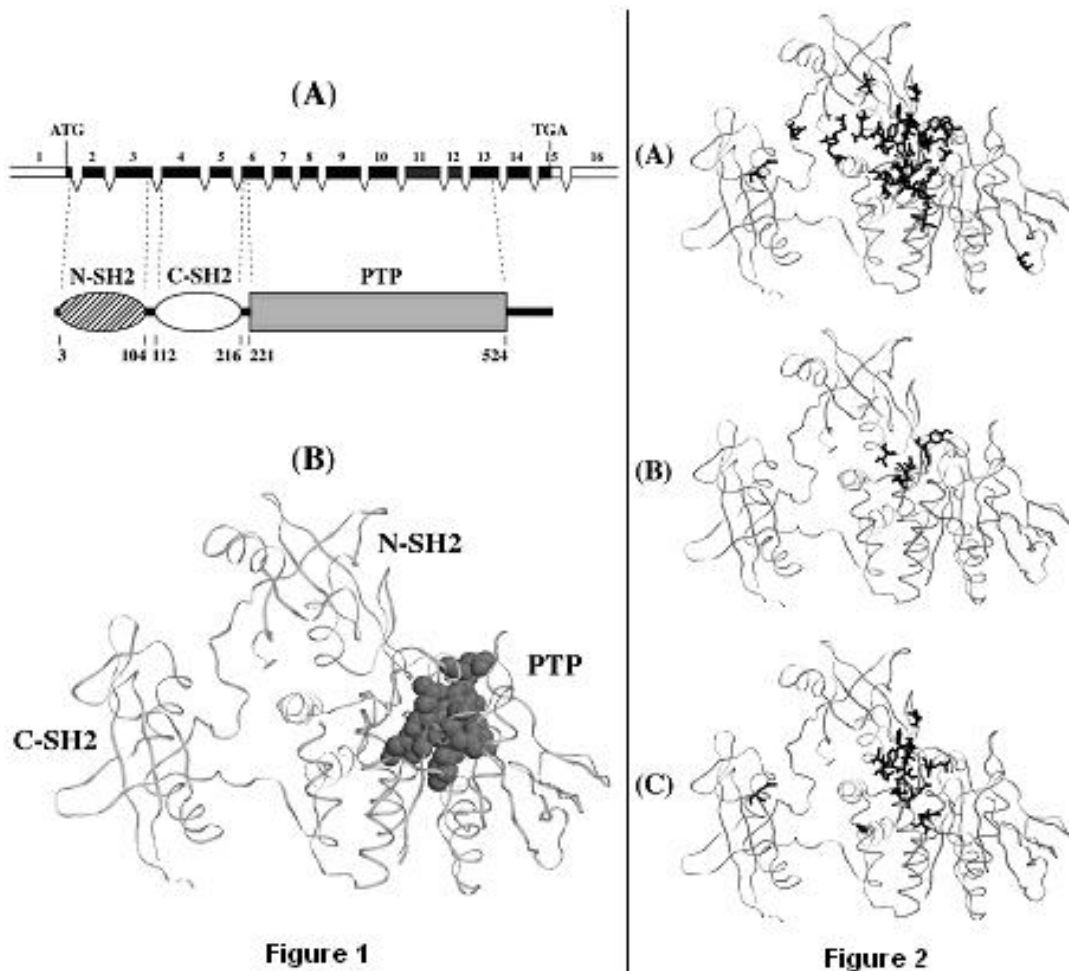
Localisation

Cytoplasmic. It binds to activated cell surface receptors, cell adhesion molecules and scaffolding adapters.

Function

SHP-2 functions as an intracellular signal transducer. It positively modulates signal flow in most circumstances, but can also function as negative regulator depending upon its binding partner and interactions with downstream signaling networks. SHP-2 positively controls the activation of the RAS/MAPK cascade induced by several growth factors, and

negatively regulates JAK/STAT signaling. In most cases, SHP-2's function in intracellular signaling appears to be immediately proximal to activated receptors and upstream to RAS. The mechanisms of SHP-2's action and its physiological substrates are still poorly defined. However, both membrane translocation and PTPase activity are required for SHP-2 function. SHP-2 is required during development. Embryos nullizygous for Shp-2 have defects in gastrulation and mesodermal patterning resulting in severe abnormalities in axial and paraxial mesodermal structures. Shp-2 function is also required for development of terminal and skeletal structures, semilunar valvulogenesis in the heart, and hematopoiesis.



PTPN11 genomic organization and SHP-2 domain structure:

Figure 1 : (A) The PTPN11 gene and SHP-2 domain characterization. The coding exons are shown as numbered filled boxes. The functional domains of the protein, comprising two tandemly arranged SH2 domains at the N terminus (N-SH2 and C-SH2) followed by a protein tyrosine phosphatase (PTP) domain, are shown below. Numbers below the domain structure indicate the amino-acid boundaries of those domains. (B) Three-dimensional structure of SHP-2 in its catalytically inactive conformation, as determined by Hof et al. (1998). Residues involved in catalysis are shown (space fill).

Figure 2 : Location of SHP-2 mutated residues in human disease. (A) Noonan syndrome and LEOPARD syndrome (germ-line origin; N=224); (B) Noonan syndrome with juvenile myelomonocytic leukemia (germ-line origin; N=11); (C) hematologic malignancies, including juvenile myelomonocytic leukemia, acute myeloid leukemia, acute lymphoblastic leukemia, myelodysplastic syndromes and chronic myelomonocytic leukemia (somatic origin; N=97). The pictures show the C trace of SHP-2 in its catalytically inactive conformation. Affected residues are indicated with their side chains as black sticks.

Homology

PTPN6 (protein tyrosine phosphatase, non-receptor type, 6) previously known as SHP1 or SHP-1 (Src homology 2 domain-containing protein tyrosine phosphatase, 1).

Mutations

Note

At least two distinct classes of PTPN11 mutations have been identified in humans.

The first group, which has germ-line origin, causes Noonan syndrome and closely related developmental disorders.

The second group, acquired as a somatic event, has been documented in a heterogeneous group of hematologic malignancies and pre-leukemic disorders, and rarely in certain solid tumors.

The vast majority of mutations affect residues residing at or close to the interface between the N-SH2 and PTP domains. Increasing evidence supports that both germ-line and somatic mutations promote SHP-2 gain-of-function by destabilizing the catalytically inactive conformation of the protein, and prolong signal flux through the RAS/MAPK pathway in a ligand-dependent manner.

A mouse model bearing the NS-causative D61G mutation in the Ptpn11 gene has been recently generated and characterized. The Ptpn11^{D61G/D61G} genotype is embryonic lethal. At day E13.5, these embryos are grossly edematous and hemorrhagic, have diffuse liver necrosis and severe cardiac defects. Heterozygous embryos exhibit cardiac defects, proportionate growth failure and perturbed craniofacial development. Hematologic anomalies include a mild myeloproliferative disease. Ptpn11^{D61G/+} embryonic fibroblasts exhibit a three-fold increased Shp-2 activity and increased association of Shp-2 with Gab1 after stimulation with EGF. Cell culture and whole embryo studies reveal that increased RAS/MAPK signaling is variably present, appearing to be cell-context specific.

Germinal

Selection: 124A>G (T42A), 179-181delGTG (delGly60), 181-183delGAT (delAsp61), 182A>G (D61G), 184T>G (Y62D), 188A>G (Y63C), 214G>T (A72S), 215C>G (A72G), 218C>T (T73I), 228G>T,C (E76D), 236A>G (N79R), 317A>C (D106A), 836A>G (Y279C), 922A>G (N308D), 1403C>T (T468M), 1510A>G (M504V).

Somatic

Selection: 181G>T (D61Y), 182A>T (D61V), 205G>A (E69K), 211-213TTT>AAA (F71K), 214G>A (A72T), 215C>T (A72V), 226G>A (E76K), 226G>C (E76Q), 227A>T (E76V), 227A>G (E76G), 227A>C (E76A),

1471C>T (P491S), 1472C>T (P491L), 1504T>C (S502P), 1504T>G (S502A), 1520C>A (T507K), 1528C>A (Q510K).

Implicated in

Noonan syndrome, Noonan-like/multiple giant cell lesion syndrome and LEOPARD syndrome

Note

Germ-line origin. Gain-of-function mutations. Increased basal protein tyrosine phosphatase activity. Prolonged ligand-dependent activation of the RAS/MAPK cascade.

Disease

Noonan syndrome is a genetically heterogeneous and clinically variable developmental disorder defined by short stature, facial dysmorphism and a wide spectrum of congenital heart defects. The distinctive facial features consist of a broad forehead, hypertelorism, down-slanting palpebral fissures, ptosis, high-arched palate and low-set, posteriorly rotated ears. Cardiovascular abnormalities, primarily pulmonic stenosis and hypertrophic cardiomyopathy, are present in up to 85% of affected individuals. Additional relatively frequent features are multiple skeletal defects, webbed neck, mental retardation, cryptorchidism and bleeding diathesis. Children with Noonan syndrome are predisposed to a spectrum of hematologic abnormalities, including transient monocytosis, thrombocytopenia and rarely juvenile myelomonocytic leukemia and acute leukemia.

Juvenile myelomonocytic leukemia, acute myeloid leukemia, acute lymphoblastic leukemia, myelodysplastic syndromes, chronic myelomonocytic leukemia, melanoma, neuroblastoma, lung adenocarcinoma, colon cancer

Note

Somatic origin.

Prognosis

No data are currently available.

Oncogenesis

Gain-of-function mutations. Increased basal protein tyrosine phosphatase activity. Prolonged ligand-dependent activation of the RAS/MAPK cascade.

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