

## Gene Section

### Review

# GPC1 (glypican 1)

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## Abstract

Review on GPC1, with data on DNA/RNA, on the protein encoded and where the gene is implicated.

## Identity

**Other names:** glypican

**HGNC (Hugo):** GPC1

**Location:** 2q37.3

## DNA/RNA

### Description

The gene spans 32381 pb of DNA, comprising 9 exons.

### Transcription

1676 bp open reading frame.

## Protein

### Description

The glypican-1 gene codes for a protein of 558 amino acids with a predicted molecular weight of 62 kDa. It is a cell surface, lipid-raft-associated heparan sulfate proteoglycan (HSPG), composed of a glycosylphosphatidylinositol (GPI)-anchored core protein substituted with a three chains of heparan sulfate near its C-terminus. It shares, along with all other glypicans, an N-terminal secretory signal, heparan sulfate attachment sites, 14 evolutionary conserved cysteine residues and hydrophobic domain near the C-terminus for the addition of the glycosylphosphatidylinositol (GPI) anchor. Also, the glypican-1 core protein contains two N-glycosylation sites at Asn79 & Asn116, which are found to be invariably occupied. The N-linked

glycans at these sites affect Gpc-1 protein expression and heparan sulfate substitution. Nevertheless the protein is folded correctly even in the absence of N-linked glycans (Svensson et al., 2011). Recently, the structure of C-terminally truncated human N-glycosylated Gpc-1 core protein was determined at 2.55 Å resolution (Svensson et al., 2012; Awad et al., 2013), which revealed a highly extended, cylindrical (dimensions 120 x 30 x 30 Å), stable all- $\alpha$ -helical fold. Its structural similarity to the Dally-like protein from *Drosophila* (Kim et al., 2011) confirmed a conserved overall fold for the glypican family. The Gpc-1 structure consists of 14  $\alpha$ -helices ( $\alpha$ 1-  $\alpha$ 14) and three major loops (L1-L3). The extended helix  $\alpha$ 2 (83Å) traverses the whole protein, carrying two N-linked glycans close to its ends. The Gpc-1 structure revealed the complete arrangement of the 14 Cys residues conserved across the glypican family, in 7 disulfide bonds, 6 of them located near the molecule N terminus at a region termed "Cys-rich lobe". This lobe is followed by a region forms the heart of the structure called the "central lobe". This lobe is stabilized by evolutionary conserved hydrophobic centers. The last region of the Gpc-1 molecule is termed the "protease site lobe" because of the presence of a protease site in this part. No additional electron density was observed in the electron density maps from crystals of non-truncated glypican-1 containing the HS attachment region near the C-terminus, which suggests that this part is highly disordered. This extended long C terminus (50 residues) might thus give the core protein a freedom in its orientation when Gpc-1 is anchored to the cell membrane (Svensson et al., 2012).



et al., 2005; O'Callaghan et al., 2008; Timmer et al., 2009; Cheng et al., 2011), prion disease (Cheng et al., 2006; Löfgren et al., 2008; Taylor et al., 2009; Hooper, 2011), and Niemann-Pick type C1 disease (Mani et al., 2006). GPC1 has been localized to the amyloid plaques of Alzheimer's disease. Both nitric oxide- and heparanase-induced degraded GPC1 HS have found to be associated with amyloid deposits, including the toxic amyloid  $\beta$  peptide aggregates in brain of human Alzheimer's patients and transgenic Alzheimer's mice (Sandwall et al., 2010; Cheng et al., 2011). Further, it has been shown that the HS oligosaccharides released from GPC1 by Cu/NO-vitamin C form conjugates with amyloid  $\beta$  peptides, thereby modulating and suppressing oligomerization of amyloid  $\beta$  and dissolving toxic amyloid  $\beta$  oligomers in hippocampal slices from Alzheimer's mice (Cheng et al., 2011). Other studies have shown that amyloid  $\beta$  toxicity is attenuated in cells overexpressing heparanase, suggesting that HS oligosaccharides generated by cleavage with heparanase could also have a protective effect (Sandwall et al., 2010; Zhang et al., 2012).

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