Gene Section
Mini Review

STEAP1 (Six Transmembrane Epithelial Antigene of the Prostate 1)
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Identity
Other names: STEAP; PRSS24; MGC19484
HGNC (Hugo): STEAP1
Location: 7q21.13
Local order: Other genes in the vicinity of STEAP1 include ZNF804B (zinc finger protein 804B), dpy-19-like 2 pseudogene 4 (from C. elegans) and STEAP2.

DNA/RNA
Description
10.4 kb consisting of 5 exons.

Transcription
1,330 kb transcript; 1195 bp ORF.

Protein
Description
339 amino acids (NCBI: AF186249); MW 40 kDa, contains 6 transmembrane helical domains (table 1) and a theoretical pI of 9.28.

Expression
Normal murine tissues: bone marrow, brain, colon, duodenum, liver, heart, ileum, kidney, lung, pancreas, placenta, prostate, skeletal muscle, thymus, testis.

Localisation
Cell membrane.

Function
STEAP1 was first identified as a prostate-specific cell-surface antigen, over-expressed in human prostate cancer, and in the spontaneous transgenic mouse model of prostate cancer, by suppressive subtractive hybridization. It is also expressed in several human cancer cell lines obtained from prostate, breast, pancreas, bladder, gastrointestinal tract, testis, ovary, cervix, Ewing sarcoma, and melanomas, and in malignant tumours from several different tissues (eg. prostate, breast, bladder, lung), with little or no expression in vital organs. Recent data showed that STEAP1 is involved in intercellular communication between adjacent cells in culture, and that it seems to favour tumour development.
STEAP gene organization, mRNA transcripts and predicted protein structure. Green boxes correspond to exons.

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Table 1—Sequence of the 6 transmembrane helices.

Its structure prediction, and location at cell-cell junctions, suggest that STEAP1 must be a channel, or a transport protein. Its cell surface location in all tumour types analyzed so far, and its absence in most vital organs in humans, turned STEAP1 into a potential target for anti-tumour immunotherapy, which has already been used in animal models of cancer with promising results. In addition, high levels of STEAP mRNA have been detected in the circulation of cancer patients increasing the potential of STEAP as a diagnosing marker for human cancer.

**Homology**

Highest levels of homology with the other members of the family in the following order: STEAP2, STEAP3 and STEAP4.

**Mutations**

**Note**
No mutations have been identified so far.

**Implicated in**

**Various cancers**

**Note**
Prostate cancer, breast cancer, bladder cancer, lung cancer. STEAP1 is overexpressed in all these types of tumours compared to normal tissue.

**References**


This article should be referenced as such: