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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

Cell lines: Prostate-LnCAP, LAPC4, PC3, DU145, breast-MCF7, melanoma-624mel, 697mel, 888mel, MM331, gastrointestinal tract-MKN45, WiDR, lung-1355.

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

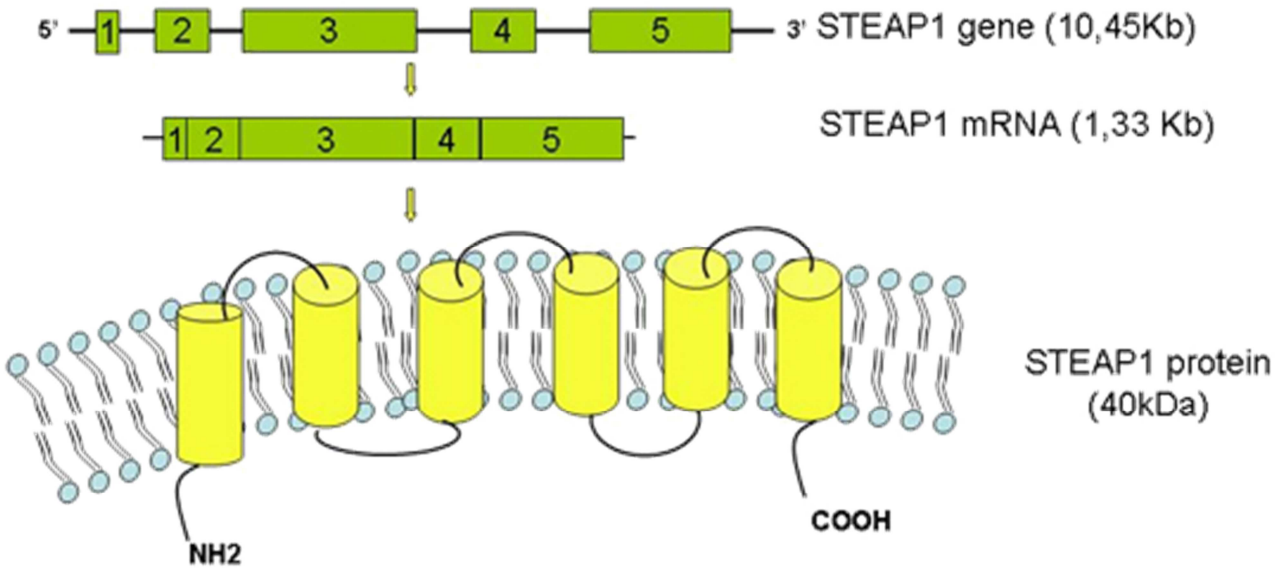
Localisation

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.

Surrounding genes from Entrez (updated 12-Feb-2009).



STEAP gene organization, mRNA transcripts and predicted protein structure. Green boxes correspond to exons.

No.	N terminal	transmembrane region	C terminal	type	length
1	70	QWHLPIKIAAIIASLTFLYTLLR	92	SECONDARY	23
2	114	INKVLPMVSITLLALVYLPGVIA	136	PRIMARY	23
3	163	QFGLLSFFFAVLHAIYSLSYPM	184	SECONDARY	22
4	219	YVSLGIVGLAILALLAVTSIPSV	241	PRIMARY	23
5	254	QSKLGIVSLLLGTIHALIFAWNK	276	SECONDARY	23
6	292	MIAVFLPIVVLIFKSILFLPCL	313	PRIMARY	22

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.

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