

Gene Section

Review

LHCGR (luteinizing hormone / choriogonadotropin receptor)

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Identity

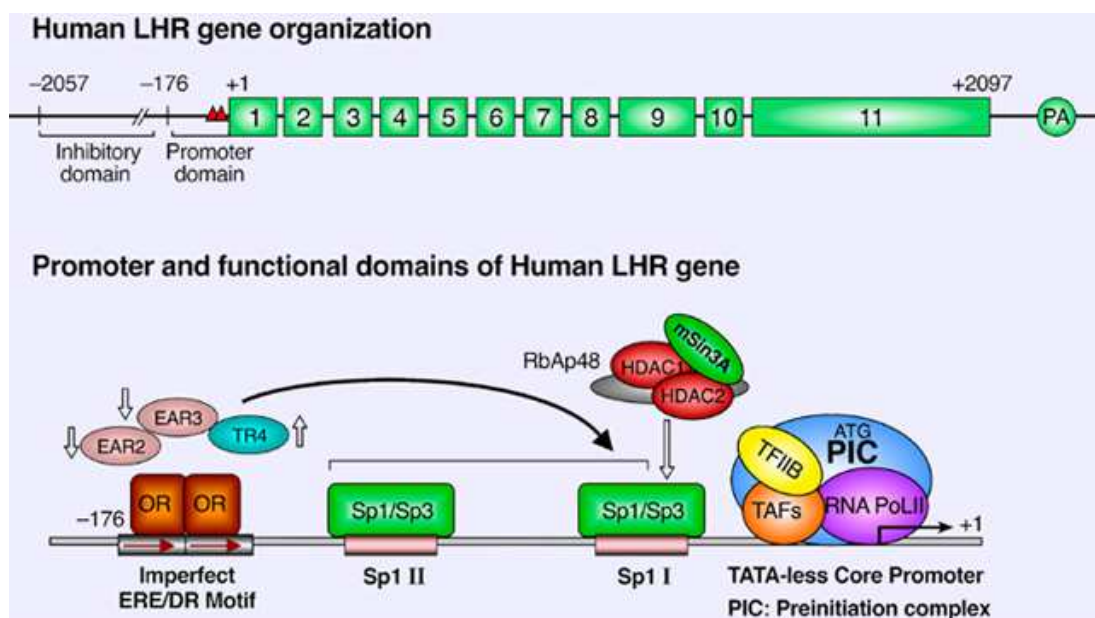
Other names: LHR (Luteinizing hormone receptor); LCGR; LGR2; LHCGR (luteinizing hormone/choriogonadotropin receptor); LH/CG-R, LSH-R (lutropin-choriogonadotropic hormone receptor)

HGNC (Hugo): LHCGR

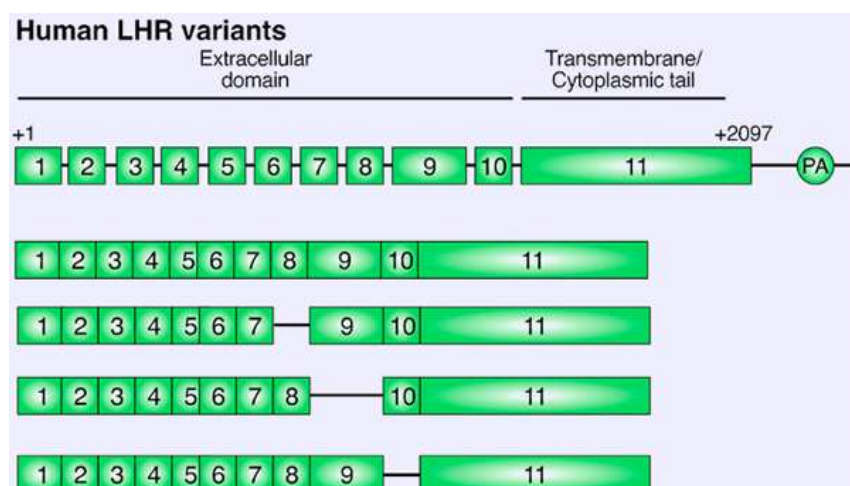
Location: 2p21

Note

The LHR belongs to the glycoprotein hormone receptor subfamily, with leucine rich repeat motifs, of the G protein-coupled receptor family (GPCR).



Human LHR gene organization (Upper panel), 5' flanking regulatory domains and 176 bp promoter with its functional domains, associated transcription factors and silencing regulatory complex (HDAC/mSin3A) (lower panel). Triangle: multiple transcriptional start sites. PA: poly adenylation sites. Open arrow, up: activation, down: inhibition. ERE: estrogen responsive element. DR: direct repeat. OR: orphan receptor. Sp1 I, Sp1 II: Sp1 sites. PIC: preinitiation complex.



Schematic representation of human LHR variants, as deduced from the alternative splicing of the transcripts.

DNA/RNA

Description

The genomic size of human LHR gene is about 80 Kb and consists of 11 coding exons separated by 10 introns. At least three alternatively spliced variants of the hLHR (deletion of exon 8 or 9 or 10) were reported.

Transcription

Multiple LHR mRNA transcriptional start sites are located within the -176 bp TATA-less 5' flanking promoter domain. Additional upstream transcriptional start sites (> -176 bp) were identified in human testicular mRNA and human choriocarcinoma JAR cell. EREhs (-161 to -171 bp) and upstream sequences (-177 to -2056 bp) are inhibitory. Activation of the human LHR promoter through Sp1/3 factors at Sp1 sites is negatively regulated by cross talk among the transcription factors EAR3/COUP-TFI, Sp1, TFIIB, and independently by histone deacetylase-mSin3A complex at the Sp1 I site.

Pseudogene

No known pseudogenes.

Protein

Description

The cDNA for the human LHR encodes 699 amino acids. The receptor is composed of two functional units: the extracellular hormone-binding domain and the seven-membrane transmembrane/cytoplasmic

module, which is the anchoring unit that transduces the signal initiated in the extracellular domain and couples to G proteins. The large extracellular domain binds LH and hCG with high affinity.

Expression

LHR is predominantly expressed in gonads. The LHR has also been identified in several non-gonadal tissues, including human nonpregnant uterus, placenta, fallopian tubes, uterine vessels, umbilical cord, brain, and lymphocyte.

Localisation

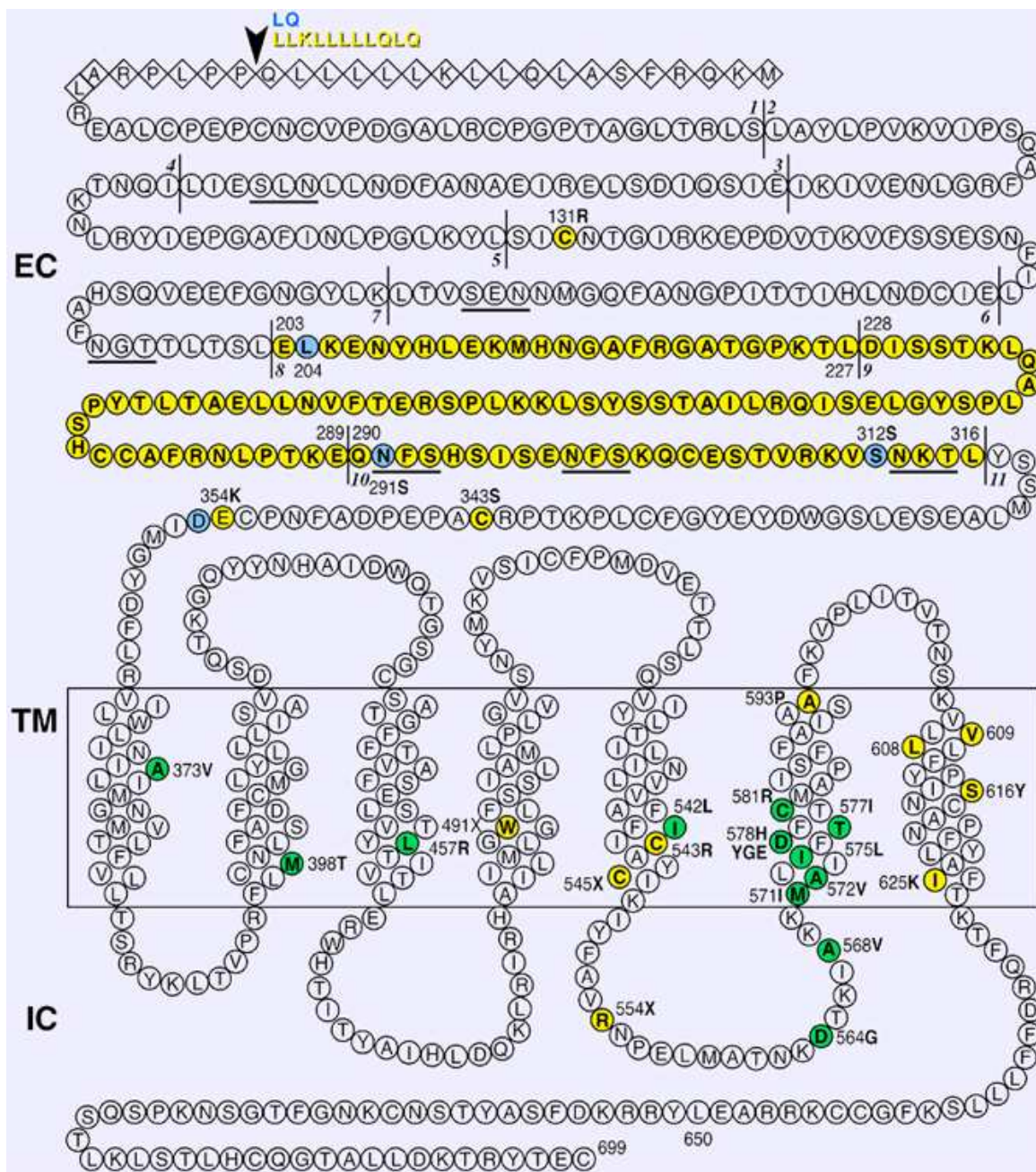
Predominantly localized in the cell membrane.

Function

The LHR mediates gonadotropin signaling and triggers intracellular responses that participate in gonadal maturation and function, as well as in the regulation of steroidogenesis and gametogenesis. Luteinizing hormone through its surface receptors on the Leydig cell maintains general metabolic processes and steroidogenic enzymes to regulate the production of androgens. In the ovary, LH promotes follicular development, at stages beyond early antral follicles including the formation of preovulatory follicles and corpora lutea.

Homology

The percent identity below represents identity using Global pairwise alignment function (GAP): M. musculus: 83.2; R. Norvegicus: 85.2; D. Melanogaster: 40.1; A. gambiae: 39.7; C. elegans: 30.7.



Legend diagram: EC: Extracellular domain. TM: Transmembrane domain. IC: Intracellular domain. Triangle box: the putative signal peptide. Vertical lines indicate exons. Normal amino acid residue (white circle). X: Stop. Activating mutations noted as green in familial male precocious puberty (FMPP)-autosomal dominant and/or sporadic male-limited precocious puberty (SMPP) or other; inactivating mutations in Leydig cells hypoplasia (LCH) noted in yellow. Polymorphism noted in blue. Underlined: N-glycosylation sites.

Mutations

Note

Polymorphism detected in exon 1, 8, 10 and 11. Nucleotides insertion/deletion, single nucleotide mutation detected in exon 1, 5, 7, 8, 10 and 11. Deletions of exon 8 or 9 or 10 (splice variants). Polymorphism: N291S, N312S. Deletion - L204, D355.

Insertion at aa 18 – IQ.

Activating mutation: A373V, M398T, L457R, I542L, D564G, A568V, M571I, A572V, I575L, T577I, D578G/Y/H/E, C581R

Inhibiting mutation: C131R, F194V, C343S, E354K, W491X, C543R, C545X, R554X, A593P, S616Y and I625K. Deletion - L608, V609, aa 203-227 (exon 8), aa 228-289 (exon 9), and aa 290-316 (exon 10). Insertion: aa18 - LLKLLLLLQLQ.

Implicated in

Note

Activating mutations: Human familial male precocious puberty (FMPP) and sporadic male-limited precocious puberty (SMPP) - gonadotropin independent precocious puberty with Leydig cell hyperplasia.

Inactivating mutations: Male: Leydig cell hypoplasia (LCH) with various degree of hypogonadism severity, pseudohermaphroditism. Female: Infertility hypergonadotropic hypogonadism and primary amenorrhea.

Association of FMPP and testicular seminoma (D578G) - 1 patient or nodular Leydig cell hyperplasia (D578G) - 1 patient.

Somatic mutation of the LHR (D578H) with Leydig cell adenoma and no history of FMPP (3 patients).

Mutations may be linked to breast cancer prognosis (18LQ insert).

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