Query ID: test183

Query Text: which gene segments code for the variable region of the heavy chain

Retrieved Documents:

1	doc6672	V(D)J recombination. In the developing B cell, the first recombination event to occur is between one D and one J gene segment of the heavy chain locus. Any DNA between these two gene segments is delet
1	doc6669	V(D)J recombination. Each heavy chain and light chain gene contains multiple copies of three different types of gene segments for the variable regions of the antibody proteins. For example, the human
0	doc753720	Genetics. This messenger RNA molecule is then used to produce a corresponding amino acid sequence through a process called translation. Each group of three nucleotides in the sequence, called a codon,
0	doc2473570	Shine-Dalgarno sequence. The Shine-Dalgarno (SD) sequence is a ribosomal binding site in bacterial and archaeal messenger RNA, generally located around 8 bases upstream of the start codon AUG.[1] The
0	doc1030195	DNA ligase. The E. coli DNA ligase is encoded by the lig gene. DNA ligase in E. coli, as well as most prokaryotes, uses energy gained by cleaving nicotinamide adenine dinucleotide (NAD) to create the
0	doc1561520	Pattern recognition receptor. This is another large superfamily of CLRs that includes
0	doc2275296	Yeast artificial chromosome. 2. Chromosome Walking[13]
0	doc1339270	Kill chain. One military kill chain model is the "F2T2EA", which includes the following phases:
0	doc1109708	Sequence alignment. Alignments are commonly represented both graphically and in text format. In almost all sequence alignment representations, sequences are written in rows arranged so that aligned re
0	doc1926701	Chromosome 11. More than 40% of the 856 olfactory receptor genes in the human genome are located in 28 single-gene and multi-gene clusters along the chromosome.
0	doc1720913	Nuclear chain reaction. The region of supercriticality between k = 1 and k = 1/(1-) is known as delayed supercriticality (or delayed criticality). It is in this region that all nuclear power reactors
0	doc2116929	CD4. The short cytoplasmic/intracellular tail (C) of CD4 contains a special sequence of amino acids that allow it to recruit and interact with the tyrosine kinase Lck.
0	doc664723	Genetic linkage. Recombination frequency is a measure of genetic linkage and is used in the creation of a genetic linkage map. Recombination frequency (I) is the frequency with which a single chromos
0	doc2420401	SR protein. SR proteins were discovered independently through the use of two different monoclonal antibodies. The first antibody, mAb104 found SR proteins in the nucleus of amphibian oocytes. The mAb1
0	doc1860147	Gene therapy. In somatic cell gene therapy (SCGT), the therapeutic genes are transferred into any cell other than a gamete, germ cell, gametocyte, or undifferentiated stem cell. Any such modifications
0	doc1286849	Antimicrobial resistance. Recent findings show no necessity of large populations of bacteria for the appearance of antibiotic resistance. Small populations of E.coli in an antibiotic gradient can beco
0	doc162577	DNA profiling. The separated fragments are then transferred to a nitrocellulose or nylon filter; this procedure is called a Southern blot. The DNA fragments within the blot are permanently fixed to th
0	doc1385566	Evolutionary developmental biology. New morphological features and ultimately new species are produced by variations in the toolkit, either when genes are expressed in a new pattern, or when toolkit g
0	doc996840	Monosaccharide. In the Fischer projection, the D- and L- prefixes specifies the configuration at the carbon atom that is second from bottom: D- if the hydroxyl is on the right side, and L- if it is on
0	doc771578	Virus. An enormous variety of genomic structures can be seen among viral species; as a group, they

		contain more structural genomic diversity than plants, animals, archaea, or bacteria. There are milli
0	doc1335622	Negative binomial distribution. The negative binomial distribution is also commonly used to model gene expression in the form of discrete read count data from high-throughput RNA sequencing experiment
0	doc690286	Hubble sequence. On the right of the Hubble sequence diagram are two parallel branches encompassing the spiral galaxies. A spiral galaxy consists of a flattened disk, with stars forming a (usually two
0	doc1049452	Cellular differentiation. The problem, of course, is that the candidacy of these signaling pathways was inferred primarily on the basis of their role in development and cellular differentiation. While
0	doc1722551	Primitive streak. The formation of the primitive streak relies on a complex network of signaling pathways that work together to ensure that this process is highly regulated. Activation of various secr
0	doc2674031	Polymorphism (biology). Three mechanisms may cause polymorphism:[3]
0	doc2620790	Histone acetylation and deacetylation. Based on different cardiac hypertrophy models, it has been demonstrated that cardiac stress can result in gene expression changes and alter cardiac function.[33]
0	doc1568440	Protein. The study of proteins in vivo is often concerned with the synthesis and localization of the protein within the cell. Although many intracellular proteins are synthesized in the cytoplasm and
0	doc694379	Metaphase. The analysis of metaphase chromosomes is one of the main tools of classical cytogenetics and cancer studies. Chromosomes are condensed (thickened) and highly coiled in metaphase, which make
0	doc1128847	Membrane transport. There are several databases which attempt to construct phylogenetic trees detailing the creation of transporter proteins. One such resource is the Transporter Classification databa
0	doc104614	Glycogenin. The main enzyme involved in glycogen polymerisation, glycogen synthase, can only add to an existing chain of at least 4 glucose residues. Glycogenin acts as the primer, to which further gl
0	doc698521	Secretion. Secretion is not unique to eukaryotes alone, it is present in bacteria and archaea as well. ATP binding cassette (ABC) type transporters are common to all the three domains of life. The Sec
0	doc1995536	Steroid hormone receptor. Type II receptors are located in the nucleus. Thus, their ligands pass through the cell membrane and cytoplasm and enter the nucleus where they activate the receptor without
0	doc4941	Cell nucleus. Specialized export proteins exist for translocation of mature mRNA and tRNA to the cytoplasm after post-transcriptional modification is complete. This quality-control mechanism is import
0	doc2657032	List of North American Volkswagen engines. ID code- UM
0	doc2024349	Nissan Sentra. All engines in the B14 line up came with timing chains, designed to last the vehicle's lifetime.
0	doc2598417	Most recent common ancestor. In biology and genealogy, the most recent common ancestor (MRCA, also last common ancestor LCA, or concestor[1]) of any set of organisms is the most recent individual from
0	doc1204595	Operon. Operons are related to regulons, stimulons and modulons; whereas operons contain a set of genes regulated by the same operator, regulons contain a set of genes under regulation by a single reg
0	doc2088294	Drug design. Binding site identification is the first step in structure based design.[14][38] If the structure of the target or a sufficiently similar homolog is determined in the presence of a bound
0	doc1301603	Thalamus. The exposure to SHH leads to differentiation of thalamic neurons. SHH signaling from the MDO induces a posterior-to-anterior wave of expression the proneural gene Neurogenin1 in the major (c
0	doc720786	Safety stock. and the expected number of units out of stock during and order cycle is given by IL(z).[16]
0	doc2100496	Chromatin remodeling. Chromatin remodeling plays a central role in the regulation of gene expression by providing the transcription machinery with dynamic access to an otherwise tightly packaged genom
0	doc1106427	Japanese people. A 2011 SNP consortium study done by the Chinese Academy of Sciences and Max Planck Society consisting of 1719 DNA samples determined that Koreans and Japanese clustered near to each o

0	doc1379147	Evidence of common descent. The proteomic evidence also supports the universal ancestry of life. Vital proteins, such as the ribosome, DNA polymerase, and RNA polymerase, are found in everything from
0	doc2132002	Weaving. The raising and lowering sequence of warp threads in various sequences gives rise to many possible weave structures:
0	doc623459	Telomerase. TERT is a reverse transcriptase, which is a class of enzyme that creates single-stranded DNA using single-stranded RNA as a template.
0	doc1766957	Corn smut. When grown in the lab on very simple media, it behaves like baker's yeast, forming single cells called sporidia. These cells multiply by budding off daughter cells. When two compatible spor
0	doc1056209	Har Gobind Khorana. Har Gobind Khorana (9 January 1922 9 November 2011)[1][2][3] was an Indian American biochemist.[4] While on the faculty of the University of Wisconsin, he shared the 1968 Nobel P
0	doc1278705	Code-division multiple access. If sender0 has code (1, a1) and data (1, 0, 1, 1), and sender1 has code (1, 1) and data (0, 0, 1, 1), and both senders transmit simultaneously, then this table describ
0	doc1781847	H II region. Chemically, H II regions consist of about 90% hydrogen. The strongest hydrogen emission line at 656.3 nm gives H II regions their characteristic red colour. Most of the rest of an H II re
0	doc1766435	Genetic variation. Polyploidy is an example of chromosomal mutation. Polyploidy is a condition wherein organisms have three or more sets of genetic variation (3n or more).
0	doc1198567	Human genome. Most studies of human genetic variation have focused on single-nucleotide polymorphisms (SNPs), which are substitutions in individual bases along a chromosome. Most analyses estimate tha
0	doc2210197	RNA splicing. Because spliceosomal introns are not conserved in all species, there is debate concerning when spliceosomal splicing evolved. Two models have been proposed: the intron late and intron e
0	doc63817	StarLink corn recall. StarLink is a genetically modified maize, containing two modifications: a gene for resistance to glufosinate, and a variant of the bacillus thuringiensis (Bt) protein called Cry9
0	doc682237	Protease. Proteases can be classified into seven broad groups:[1]
0	doc1781844	H II region. There are also "ultra-dense HA II" regions (UDHII).[22]
0	doc2025250	microRNA. For partially complementary microRNAs to recognise their targets, nucleotides 27 of the miRNA (its 'seed region'[10][20]) must be perfectly complementary.[93] Animal miRNAs inhibit protein
0	doc1095667	Nuclear binding energy. E = m c2,
0	doc1158999	South Western Railway zone. The South Western Railway (abbreviated SWR and) is one of the 16 railway zones in India.
0	doc2599342	Leptin. The discovery of leptin also is documented in a series of books including Fat: Fighting the Obesity Epidemic by Robert Pool,[34] The Hungry Gene by Ellen Ruppel Shell, and Rethinking Thin: The
0	doc800696	Taxonomic rank. Classifications of five species follow: the fruit fly so familiar in genetics laboratories (Drosophila melanogaster), humans (Homo sapiens), the peas used by Gregor Mendel in his disco

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