Query ID: test183

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

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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	doc2489121	Polygene. Traditionally, mapping polygenes requires statistical tools available to help measure the effects of polygenes as well as narrow in on single genes. One of these tools is QTL-mapping. QTL-ma
0	doc1316700	Directionality (molecular biology). The 5-untranslated region (5-UTR) is a region of a gene which is transcribed into mRNA, and is located at the 5-end of the mRNA. This region of an mRNA may or ma
0	doc1181933	RNA integrity number. The fast region is the area between the 18S and 5S rRNA peaks on an electropherogram. Initially, as the fast area ratio value increases, it indicates degradation of the 18S and 2
0	doc1885625	Non-coding DNA. Cis-regulatory elements are sequences that control the transcription of a nearby gene. Many such elements are involved in the evolution and control of development.[21] Cis-elements may
0	doc479484	Regulator gene. Other regulatory genes code for activator proteins. An activator binds to a site on the DNA molecule and causes an increase in transcription of a nearby gene. In prokaryotes, a well-kn
0	doc2489120	Polygene. The frequency of the phenotypes of these traits generally follows a normal continuous variation distribution pattern. This results from the many possible allelic combinations. When the value
0	doc6679	V(D)J recombination. V(D)J recombination begins when V(D)J recombinase (through the activity of RAG1) binds an RSS flanking a coding gene segment (V, D, or J) and creates a single-strand nick in the D
0	doc2242522	BLAST. Input sequences (in FASTA or Genbank format) and weight matrix.
0	doc631525	Chromosome conformation capture. The 3-D organization of the genome can also be analyzed via eigendecomposition of the contact matrix. Each eigenvector corresponds to a set of loci, which are not nece
0	doc1411037	Chain letter. There are two main types of chain letters:
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	doc2041702	Chain. The metal link chain has been in use since at least 225A BC.[1]
0	doc2181501	Epistasis. Quantitative genetics focuses on genetic variance due to genetic interactions. Any two locus interactions at a particular gene frequency can be decomposed into eight independent genetic eff
0	doc1885626	Non-coding DNA. Promoters facilitate the transcription of a particular gene and are typically upstream of the coding region. Enhancer sequences may also exert very distant effects on the transcription
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	doc1568424	Protein. Short amino acid sequences within proteins often act as recognition sites for other proteins.[26] For instance, SH3 domains typically bind to short PxxP motifs (i.e. 2 prolines [P], separated
0	doc1293803	Alternative splicing. Pre-mRNAs of the Transformer (Tra) gene of Drosophila melanogaster undergo alternative splicing via the alternative acceptor site mode. The gene Tra encodes a protein that is exp

0	doc1841147	trp operon. At the beginning of the transcribed genes of the trp operon is a sequence of at least 130 nucleotides termed the leader transcript (trpL).[4] Lee and Yanofsky (1977) found that the attenua
0	doc104206	Gene. Transcription produces a single-stranded RNA molecule known as messenger RNA, whose nucleotide sequence is complementary to the DNA from which it was transcribed.[2]:6.1 The mRNA acts as an inte
0	doc56534	DNA. As these DNA targets can occur throughout an organism's genome, changes in the activity of one type of transcription factor can affect thousands of genes.[135] Consequently, these proteins are of
0	doc898696	X chromosome. The following is a partial list of genes on human chromosome X. For complete list, see the link in the infobox on the right.
0	doc1940873	Clostridium tetani. Clostridium tetani has a genome that contains 2.80 Mbp with 2,373 protein coding genes.[9]
0	doc298634	Evolution. Heritable traits are passed from one generation to the next via DNA, a molecule that encodes genetic information.[80] DNA is a long biopolymer composed of four types of bases. The sequence
0	doc1338322	Open reading frame. One common use of closed reading frames (CRF) is as one piece of evidence to assist in gene prediction. Long ORFs are often used, along with other evidence, to initially identify c
0	doc56522	DNA. Genomic DNA is tightly and orderly packed in the process called DNA condensation, to fit the small available volumes of the cell. In eukaryotes, DNA is located in the cell nucleus, with small amo
0	doc1540262	Gene expression. Another modification is 3' cleavage and polyadenylation. They occur if polyadenylation signal sequence (5'- AAUAAA-3') is present in pre-mRNA, which is usually between protein-coding
0	doc56985	Protein biosynthesis. Phenomena of RNA synthesis from DNA template In transcription an mRNA chain is generated, with one strand of the DNA double helix in the genome as a template. This strand is call
0	doc1825924	TATA box. The TATA box is usually located 25-35 base pairs upstream of the transcription start site. Genes containing the TATA box usually require additional promoter elements, including an initiator
0	doc101146	Cell cycle. Current evidence suggests that a semi-autonomous transcriptional network acts in concert with the CDK-cyclin machinery to regulate the cell cycle. Several gene expression studies in Saccha
0	doc2029265	Orthohantavirus. No nonstructural proteins are known unlike the other genera in this family. At the 5' and 3' of each segment are short noncoding sequences: the noncoding segment in all sequences at t
0	doc466017	Eukaryotic transcription. The eukaryotic genome is organized into a compact chromatin structure that allows only regulated access to DNA. The chromatin structure can be globally "open" and more transc
0	doc753723	Genetics. Some DNA sequences are transcribed into RNA but are not translated into protein productsasuch RNA molecules are called non-coding RNA. In some cases, these products fold into structures wh
0	doc2015802	DNA-binding domain. HMG-box domains are found in high mobility group proteins which are involved in a variety of DNA-dependent processes like replication and transcription. They also alter the flexibi
0	doc1558078	DNA microarray. Applications include:
0	doc1985861	RNA polymerase. Rho-independent transcription termination is the termination of transcription without the aid of the rho protein. Transcription of a palindromic region of DNA causes the formation of a
0	doc1845830	Eukaryotic DNA replication. PCNA loading is accomplished by the replication factor C (RFC) complex. The RFC complex is composed of five ATPases: Rfc1, Rfc2, Rfc3, Rfc4 and Rfc5.[86] RFC recognizes pri
0	doc1366281	Restriction enzyme. Recognition sequences in DNA differ for each restriction enzyme, producing differences in the length, sequence and strand orientation (5' end or 3' end) of a sticky-end "overhang"
0	doc2275294	Yeast artificial chromosome. Yeast expression vectors, such as YACs, YIps (yeast integrating plasmids), and YEps (yeast episomal plasmids), have an advantage over bacterial artificial chromosomes (BAC
0	doc1920782	Transformation (genetics). DNA entry into E. coli cells is through channels known as zones of adhesion

		or Bayer's junction, with a typical cell carrying as many as 400 such zones. Their role was estab
0	doc1497434	Sanger sequencing. Technical variations of chain-termination sequencing include tagging with nucleotides containing radioactive phosphorus for radiolabelling, or using a primer labeled at the 5' end w
0	doc1779227	Reporter gene. Many methods of transfection and transformation two ways of expressing a foreign or modified gene in an organism are effective in only a small percentage of a population subjected t
0	doc2181476	Epistasis. Terminology about epistasis can vary between scientific fields. Geneticists often refer to wild type and mutant alleles where the mutation is implicitly deleterious and may talk in terms of
0	doc2289734	Genomic library. N = l n (1 P) l n (1 i g) {\displaystyle N={\frac {ln(1-P)}{ln(1-{\frac {i}{g}})}}}
0	doc1636652	Genetic code. Despite these differences, all known naturally occurring codes are very similar. The coding mechanism is the same for all organisms: three-base codons, tRNA, ribosomes, single direction
0	doc2674775	Herpes simplex virus. Animal herpes viruses all share some common properties. The structure of herpes viruses consists of a relatively large double-stranded, linear DNA genome encased within an icosah
0	doc2674057	Polymorphism (biology). Whereas a gene family (several tightly linked genes performing similar or identical functions) arises by duplication of a single original gene, this is usually not the case wit

0	doc490541	RuBisCO. The chloroplast gene rbcL, which codes for the large subunit of RuBisCO has been widely used as an appropriate locus for analysis of phylogenetics in plant taxonomy.[32]
0	doc2309639	Polyadenylation. The process of polyadenylation begins as the transcription of a gene terminates. The 3'-most segment of the newly made pre-mRNA is first cleaved off by a set of proteins; these protei
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	doc2345423	Protein structure prediction. motif (structural context)A
0	doc665443	Origin of replication. Many bacteria, including E. coli, contain plasmids that each contain an origin of replication. These are separate from the origins of replication that are used by the bacteria t
0	doc2617864	Terminator (genetics). In eukaryotic transcription of mRNAs, terminator signals are recognized by protein factors that are associated with the RNA polymerase II and which trigger the termination proce
0	doc2345446	Protein structure prediction. The modern versions of these libraries as used in most software are presented as multidimensional distributions of probability or frequency, where the peaks correspond to
0	doc593979	Macromolecule. In most cases, the monomers within the chain have a strong propensity to interact with other amino acids or nucleotides. In DNA and RNA, this can take the form of Watson-Crick base pair
0	doc631515	Chromosome conformation capture. These methods have revealed large-scale organization of the genome into topologically associating domains (TADs), which correlate with epigenetic markers. Some TADs ar
0	doc1181932	RNA integrity number. For the height of 28S peak, a large value is desired. 28S, the most prominent rRNA species, is used in RIN calculation as it is typically degraded more quickly than 18S rRNA, and
0	doc1561520	Pattern recognition receptor. This is another large superfamily of CLRs that includes
0	doc1540284	Gene expression. The activity of transcription factors is further modulated by intracellular signals causing protein post-translational modification including phosphorylated, acetylated, or glycosylat

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