Ensembl

seqname : STRING: Name of the chromosome or scaffold

source : STRING : name of the program that generated this feature

feature: STRING : Feature type name {Gene/Strart_Stop_Codon/Transcript/exon/CDS/}

start: INT : Start position of the fature

end : INT : End position of the feature

score : FLOAT :Floating point value indicating the score of a feature

strand : STRING : Defined as a + or -

frame : INT : Frame indicates the number of base pairs before you encounter a full codon

attribute : INT: Additional feature about each feature

Attribute

gene_id : STRING: the stable identifier for the gene

gene_source: STRING: Annotation source for this gene

gene_biotype: STRING : The biotype of the gene

transcript_id : STRING : The stable identifier for this transcript

transcript_source : STRING : The annotation source for this transcript

exon_id : STRING: The stable annotation for this exon

exon_number :STRING: Position of this exon in the transcript

ccds_id: INT: CCDS identifier

protein_id: INT : Stable identifier for this trascript's protein

tag: STRING: A collection of additional key values

Tag

CCDS: STRING : Flag thus transcript as one linked to one CCDS records

seleno: STRING: Flag this transcript as a Selenocysteine edit

cds_end_NF: STRING : The coding region end could not be determined

cds_start_NF: STRING : The coding region start could not be determined

mRNA_end_NF: STRING: mRNA end could not be confirmed

mRNA_start_NF: STRING: mRNA start could not be confirmed