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File Edit View Tools Sequence Annotate & Predict Help

Back Forward BLAST Workflows Align/Assemble Tree Primers Cloning Back Up Support Help

1 of 9 selected

Name	Description	HQ%	Sequence Le...	# Sequences	%GC	Alignment o...	MFF
COXII CDS aligned	Multiple alignment of 50 Cytochrome C O...	-	705	50	-	Alignment h...	68
HIV env	20 HIV envelope genes	-	-	20	40.2%	-	2,
Ig variable region	5 immunoglobulin heavy chain variable r...	-	-	5	-	-	2f
Ig variable region alignment	Alignment of 5 sequences: JX560779, JX...	-	332	5	54.9%	-	2f
LysR family	7 LysR protein sequences	-	-	7	-	-	3f
Pairwise protein	Pairwise alignment of peptidase from kiw...	-	221	2	-	Global align...	21
People	Multiple alignment of 5 sequences from f...	-	426	5	45.0%	-maxmb 500	3f
Three Kingdoms	Multiple alignment of Alanyl-tRNA synthe...	-	1,156	35	-	-	7?
Transcript variants	Multiple alignment of 4 variants of MAPK...	-	3,106	4	44.4%	Columns wit...	2,

Sequence View Annotations Virtual Gel Lengths Graph Text View Lineage Info

Extract R.C. Translate Add/Edit Annotation Allow Editing Annotate & Predict Save

1. HQ625578 Translation  
 CAGÜGGUAUCAACÜCAACUACUAAÜAAÜGGUAGUCUAGCAA  
 P V V S T Q L L L N G S L A F  
 env CDS  
 subtype: C source Human immunodeficiency virus 1

2. HQ625579 Translation  
 UUAAGCCAGÜGGUAUCAACUCAACUACUGUUGAAÜGGAAAGCCU  
 I K P V V S T Q L L L N G S  
 env CDS  
 subtype: C source Human immunodeficiency virus 1

Live Annotate & Predict

Annotate from...  
 Similarity: 100 %  
 Source: PlasMapper Features  
 Apply Advanced...

Find ORFs (362 new)  
 Minimum size: 100  
 Genetic code: Standard  
 Start codons: CTC TTC ATC

Using 218 / 5996 MB memory

Cursor before base 796.

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