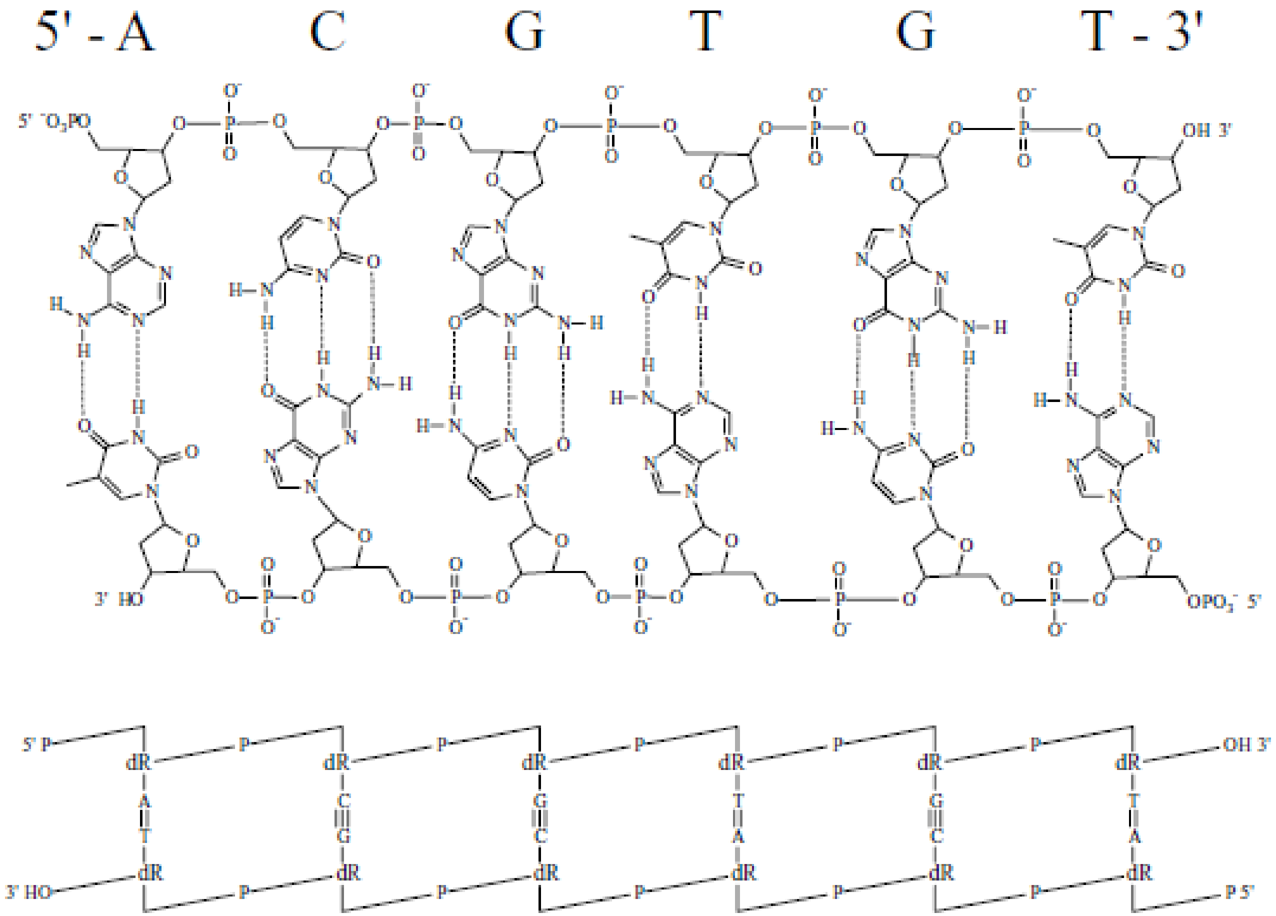
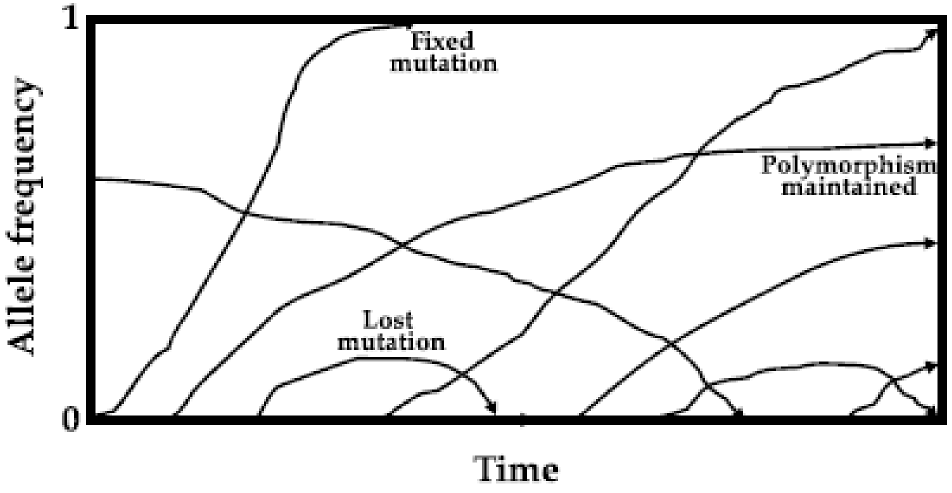
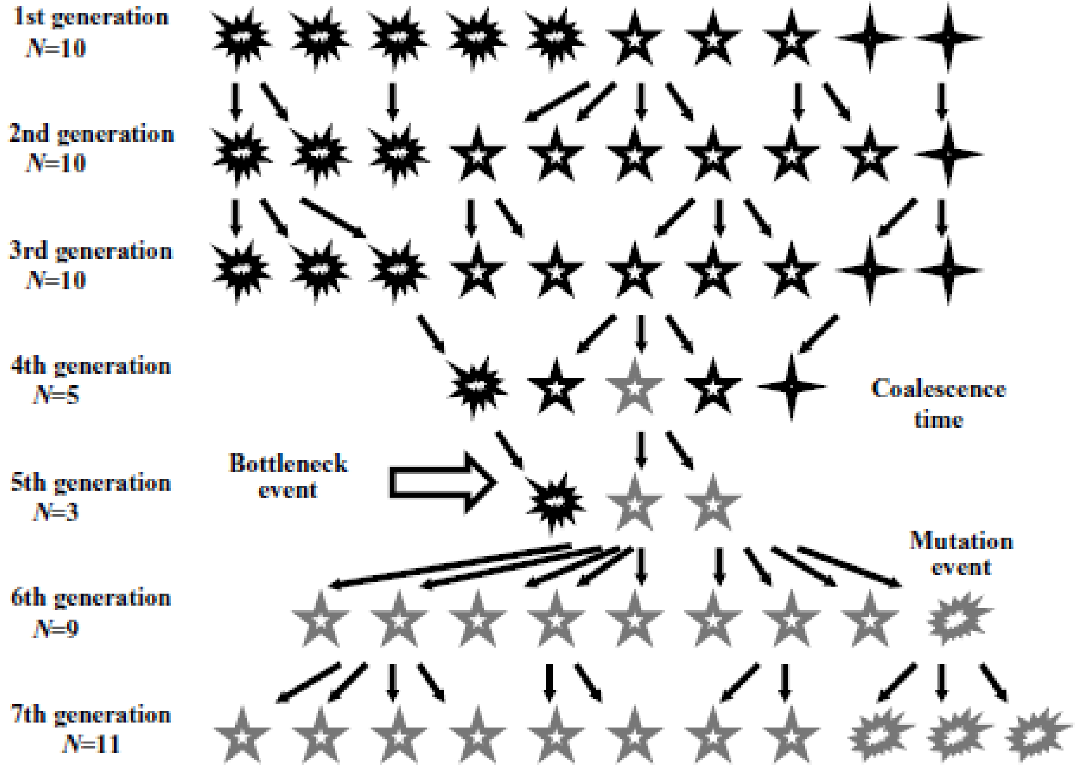
1. Moleküler evrimin temel kavramları



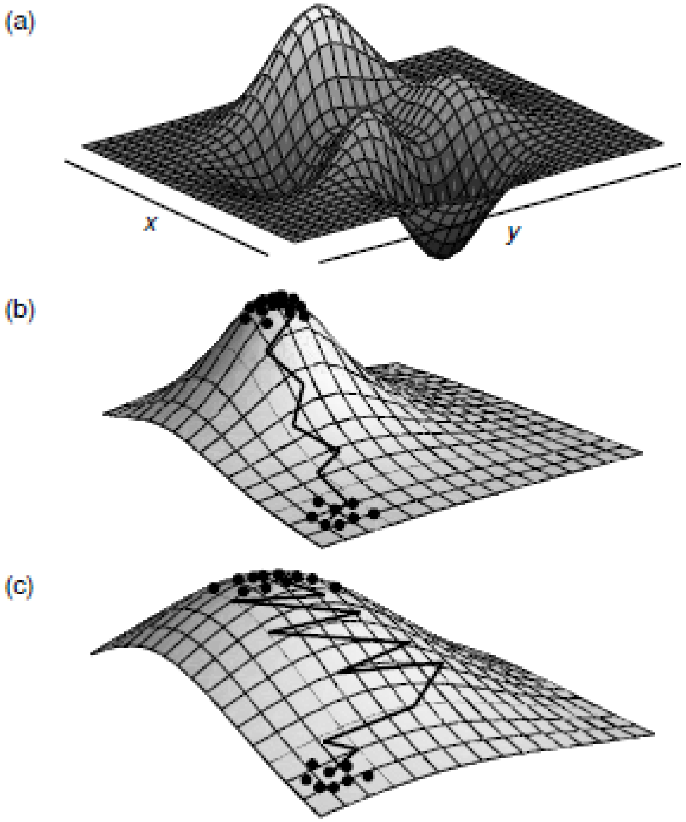
	U		C		A		G		
	Codon	Amino acid	Codon	Amino acid	Codon	Amino acid	Codon	Amino acid	
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	**U**
	UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys	**C**
	UUA	Leu	UCA	Ser	UAA	STOP	UGA	STOP	**A**
	UUG	Leu	UCG	Ser	UAG	STOP	UGG	Trp	**G**
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	**U**
	CUC	Leu	CCC	Pro	CAC	His	CGC	Arg	**C**
	CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg	**A**
	CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg	**G**
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	**U**
	AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser	**C**
	AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg	**A**
	AUG	Met	ACG	Thr	AAG	Lys	AGG	Arg	**G**
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	**U**
	GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly	**C**
	GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly	**A**
	GUG	Val	GCG	Ala	GAG	Glu	GGG	Gly	**G**

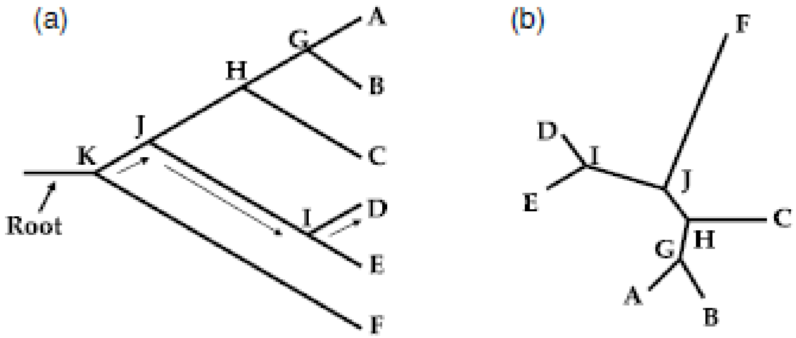
Figures and tables are taken from: Lemey, P., Salemi, M., & Vandamme, A. M. (Eds.). (2009). *The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press. For educational use only.

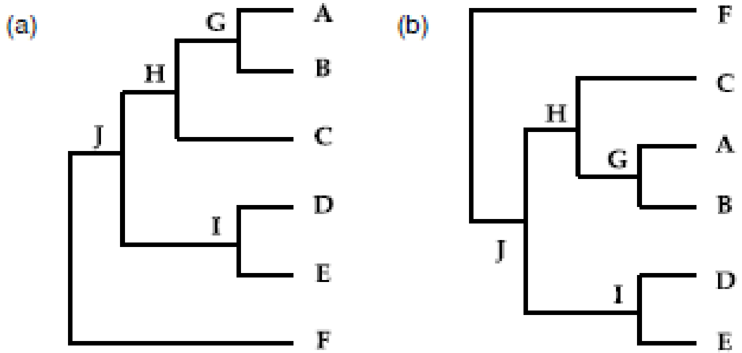




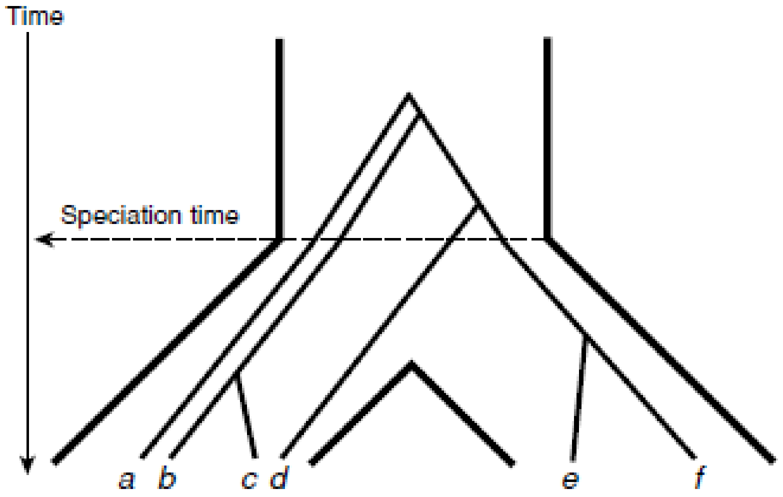
Figures and tables are taken from: Lemey, P., Salemi, M., & Vandamme, A. M. (Eds.). (2009). *The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press. For educational use only.

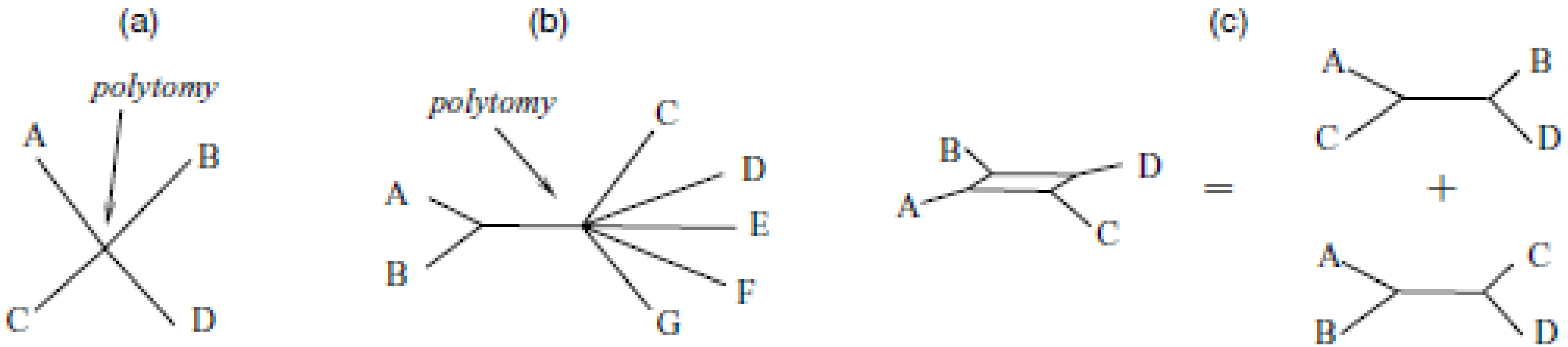






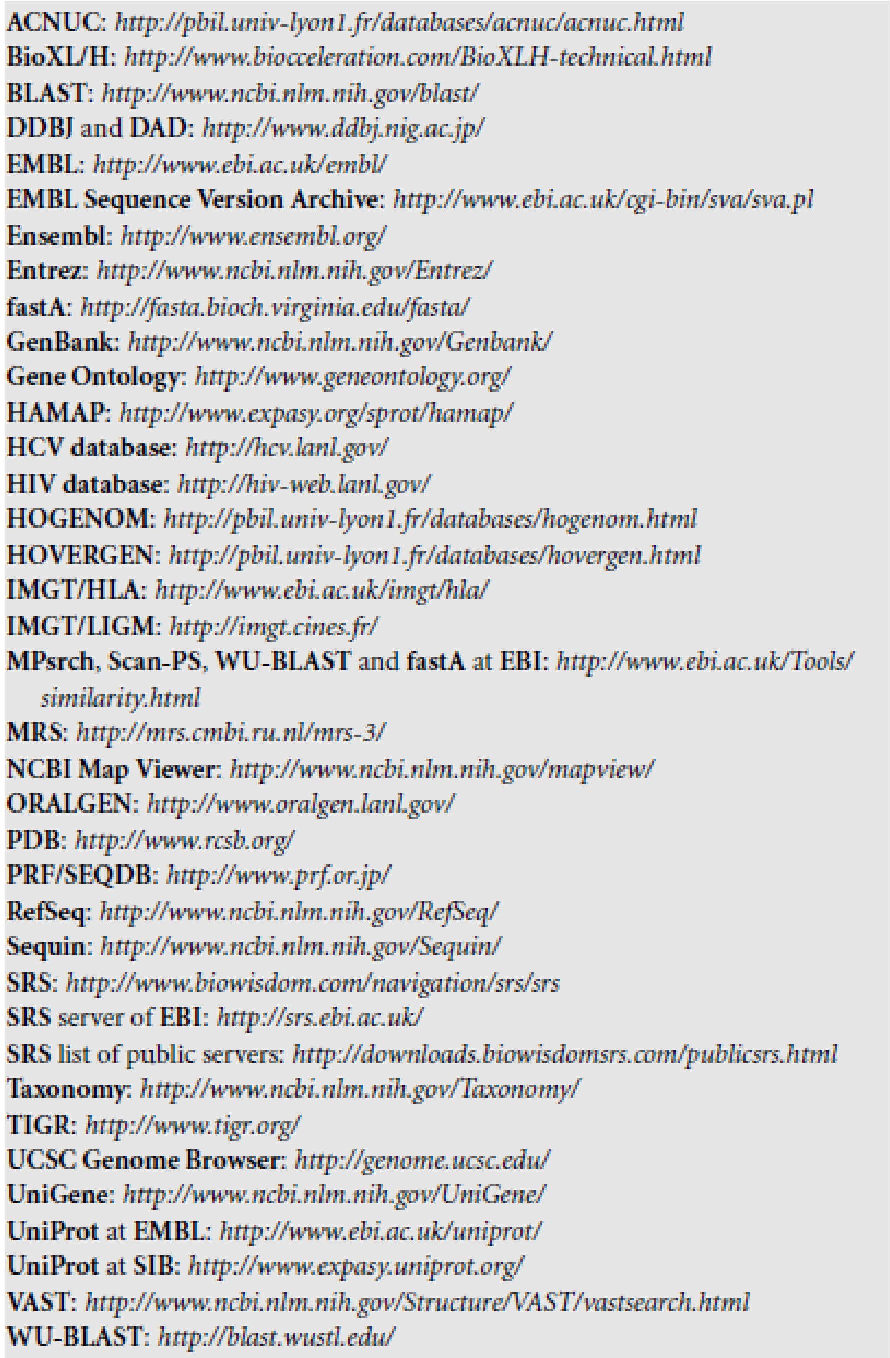
Figures and tables are taken from: Lemey, P., Salemi, M., & Vandamme, A. M. (Eds.). (2009). *The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press. For educational use only.



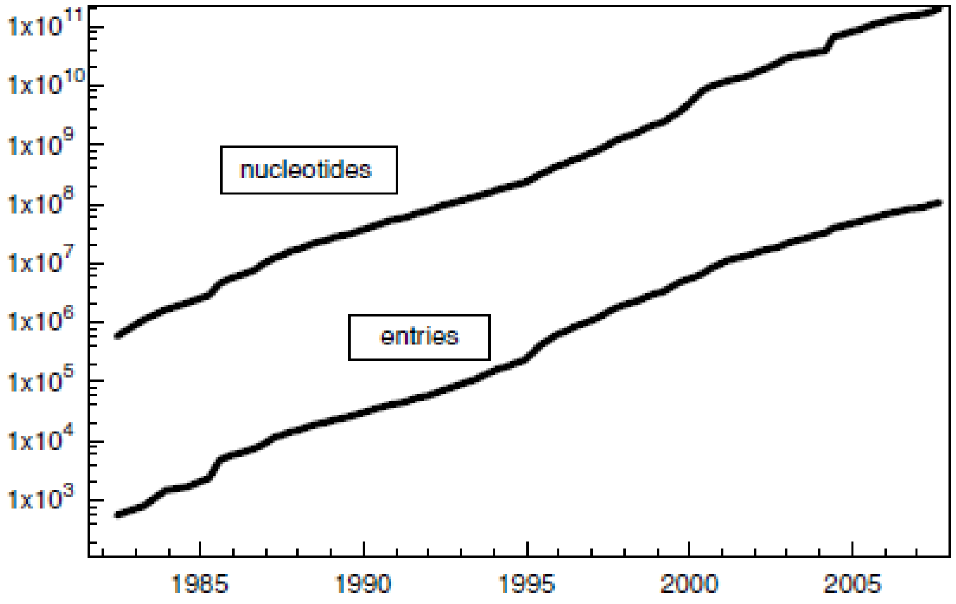


Figures and tables are taken from: Lemey, P., Salemi, M., & Vandamme, A. M. (Eds.). (2009). *The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press. For educational use only.

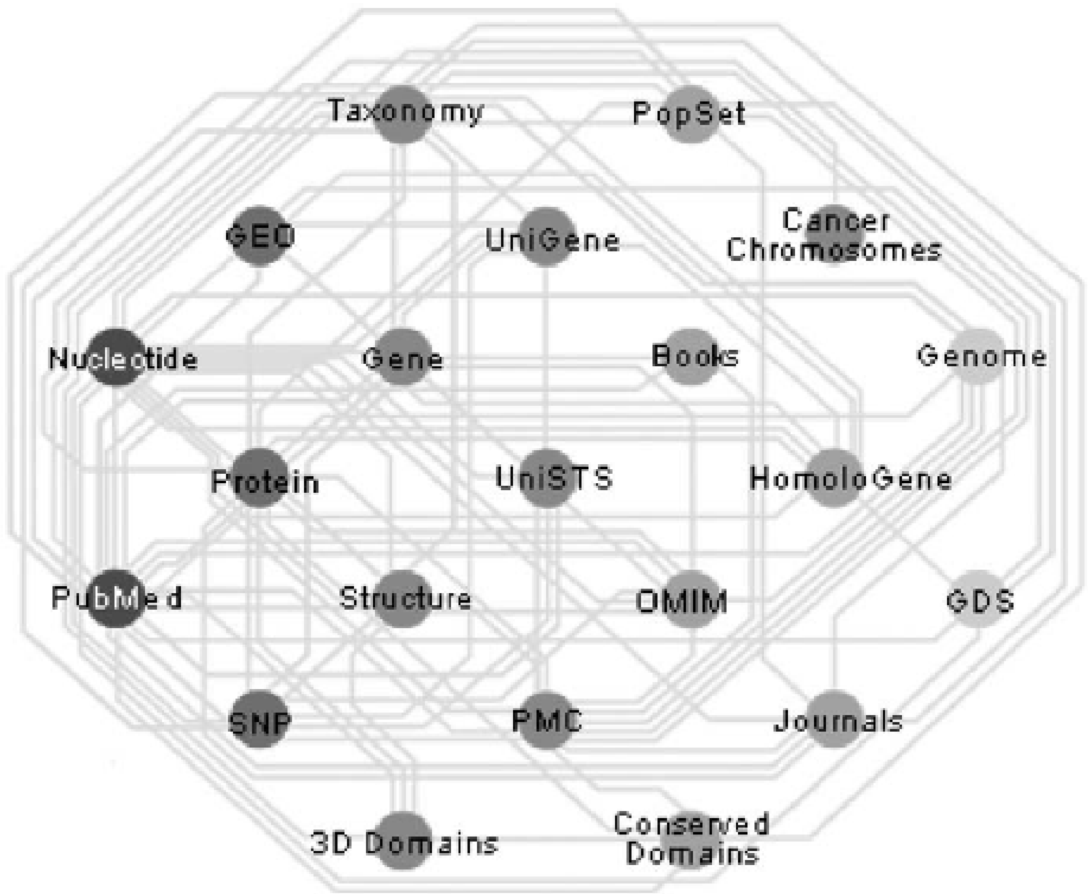
2. DNA dizi veri tabanı ve veri tabanında arama

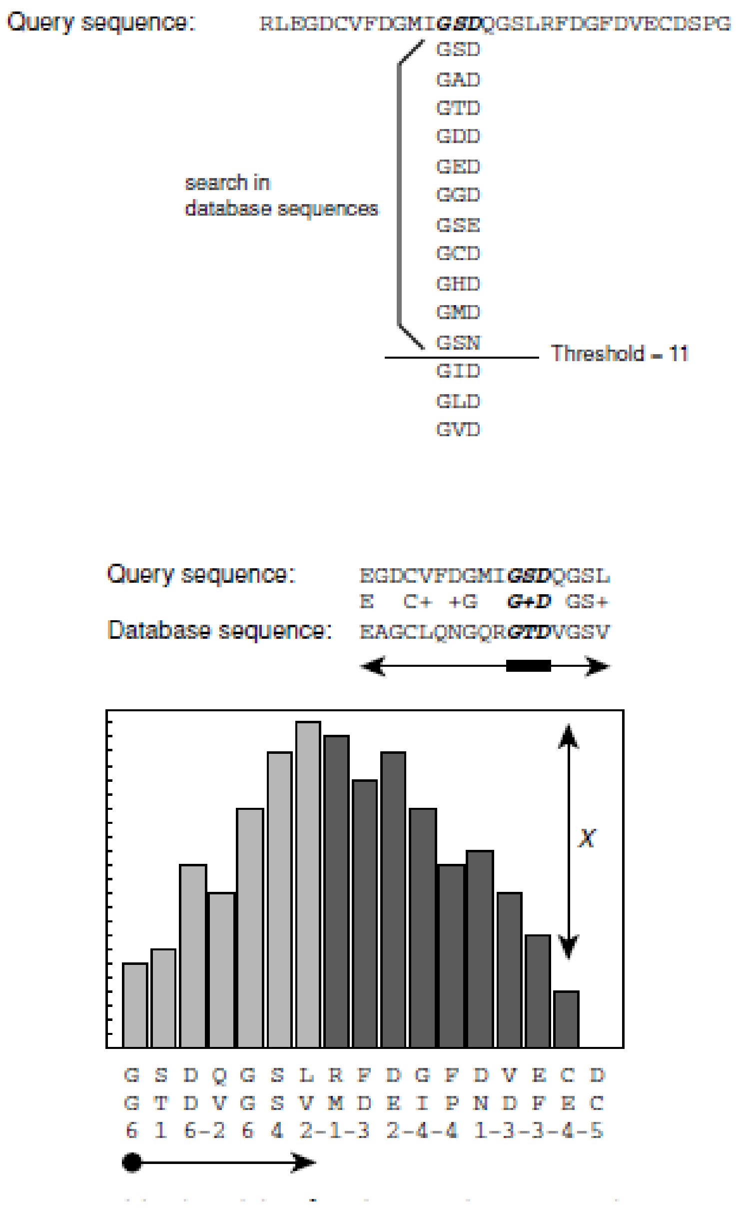


ACNUC: *http://pbil.univ-lyon1.fr/databases/acnuc/acnuc.html*
BioXL/H: *http://www.biocceleration.com/BioXLH-technical.html*
BLAST: *http://www.ncbi.nlm.nih.gov/blast/*
DDBJ and **DAD:** *http://www.ddbj.nig.ac.jp/*
EMBL: *http://www.ebi.ac.uk/embl/*
EMBL Sequence Version Archive: *http://www.ebi.ac.uk/cgi-bin/sva/sva.pl*
Ensembl: *http://www.ensembl.org/*
Entrez: *http://www.ncbi.nlm.nih.gov/Entrez/*
fastA: *http://fasta.bioch.virginia.edu/fasta/*
GenBank: *http://www.ncbi.nlm.nih.gov/Genbank/*
Gene Ontology: *http://www.geneontology.org/*
HAMAP: *http://www.expasy.org/sprot/hamap/*
HCV database: *http://hcv.lanl.gov/*
HIV database: *http://hiv-web.lanl.gov/*
HOGENOM: *http://pbil.univ-lyon1.fr/databases/hogenom.html*
HOVERGEN: *http://pbil.univ-lyon1.fr/databases/hovergen.html*
IMGT/HLA: *http://www.ebi.ac.uk/imgt/hla/*
IMGT/LIGM: *http://imgt.cines.fr/*
MPsrch, **Scan-PS**, **WU-BLAST** and **fastA** at **EBI:** *http://www.ebi.ac.uk/Tools/similarity.html*
MRS: *http://mrs.cmbi.ru.nl/mrs-3/*
NCBI Map Viewer: *http://www.ncbi.nlm.nih.gov/mapview/*
ORALGEN: *http://www.oralgen.lanl.gov/*
PDB: *http://www.rcsb.org/*
PRF/SEQDB: *http://www.prf.or.jp/*
RefSeq: *http://www.ncbi.nlm.nih.gov/RefSeq/*
Sequin: *http://www.ncbi.nlm.nih.gov/Sequin/*
SRS: *http://www.biowisdom.com/navigation/srs/srs*
SRS server of **EBI:** *http://srs.ebi.ac.uk/*
SRS list of public servers: *http://downloads.biowisdomsrs.com/publicsrs.html*
Taxonomy: *http://www.ncbi.nlm.nih.gov/Taxonomy/*
TIGR: *http://www.tigr.org/*
UCSC Genome Browser: *http://genome.ucsc.edu/*
UniGene: *http://www.ncbi.nlm.nih.gov/UniGene/*
UniProt at **EMBL:** *http://www.ebi.ac.uk/uniprot/*
UniProt at **SIB:** *http://www.expasy.uniprot.org/*
VAST: *http://www.ncbi.nlm.nih.gov/Structure/VAST/vastsearch.html*
WU-BLAST: *http://blast.wustl.edu/*



Figures and tables are taken from: Lemey, P., Salemi, M., & Vandamme, A. M. (Eds.). (2009). *The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press. For educational use only.





Figures and tables are taken from: Lemey, P., Salemi, M., & Vandamme, A. M. (Eds.). (2009). *The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press. For educational use only.

Search across databases: "human papillomavirus type 13"

- Result counts displayed in gray indicate one or more terms not found

8	**PubMed:** biomedical literature citations and abstracts	69	**Books:** online books
8	**PubMed Central:** free, full text journal articles	7	**OMIM:** online Mendelian Inheritance in Man
1	**Site Search:** NCBI web and FTP sites	none	**OMIA:** online Mendelian Inheritance in Animals

5	**CoreNucleotide:** Core subset of nucleotide sequence records	none	**dbGaP:** genotype and phenotype
none	**EST:** Expressed Sequence Tag records	none	**UniGene:** gene-oriented clusters of transcript sequences
none	**GSS:** Genome Survey Sequence records	none	**CDD:** conserved protein domain database
50	**Protein:** sequence database	none	**3D Domains:** domains from Entrez Structure
none	**Genome:** whole genome sequences	none	**UniSTS:** markers and mapping data
none	**Structure:** three-dimensional macromolecular structures	none	**PopSet:** population study data sets
1	**Taxonomy:** organisms in GenBank	none	**GEO Profiles:** expression and molecular abundance profiles
none	**SNP:** single nucleotide polymorphism	none	**GEO DataSets:** experimental sets of GEO data
1	**Gene:** gene-centered information	none	**Cancer Chromosomes:** cytogenetic databases
none	**HomoloGene:** eukaryotic homology groups	none	**PubChem BioAssay:** bioactivity screens of chemical substances
none	**PubChem Compound:** unique small molecule chemical structures	none	**GENSAT:** gene expression atlas of mouse central nervous system
none	**PubChem Substance:** deposited chemical substance records	none	**Probe:** sequence-specific reagents
none	**Genome Project:** genome project information	none	**Protein Clusters:** a collection of related protein sequences

NCBI/ BLAST/ blastn suite: BLASTN programs search nucleotide databases using a nucleotide query.

Enter Query Sequence

Enter accession number, gi, or FASTA sequence

```
ACTCCTGACAGAACCCCTGAGTCTGCCCTGCGGCCCACAGCTTCTCCCAAGCGTGCATCA
CTGCAAACCACAAGGAGTCCATGCTATACAAAGAAGAAGAGAGAAGCTGCCCTGTGTGC
CGGATCAGTTACCAGCCTGAGAATATACAGCCTAATCGGCATGTAGCCAACATAGTGCA
GAACCTCAGAGAGGTCAAGTTGAGCCCAGAAGAGCGGCAGAAGC
TTGATCACTGTGCACGCCATGGAGAGAAACTCCTACTCTTCTGTCAGGAGGACAGCAAG
```

Query subrange
From
To

Or, upload file: no file selected

Job Title: AY843504

Enter a descriptive title for your BLAST search

Choose Search Set

Database: ○ Human genomic + transcript ○ Mouse genomic + transcript ● Others (nr etc.):

Nucleotide collection (nr/nt)

Organism Optional: Enter organism name or id—completions will be suggested

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query Optional:

Enter an Entrez query to limit search

Program Selection

Optimize for
○ Highly similar sequences (megablast)
○ More dissimilar sequences (discontiguous megablast)
● Somewhat similar sequences (blastn)

Choose a BLAST algorithm

Search database nr using Blastn (Optimize for somewhat similar sequences)

☐ Show results in a new window

Note: Parameter values that differ from the default are highlighted in yellow

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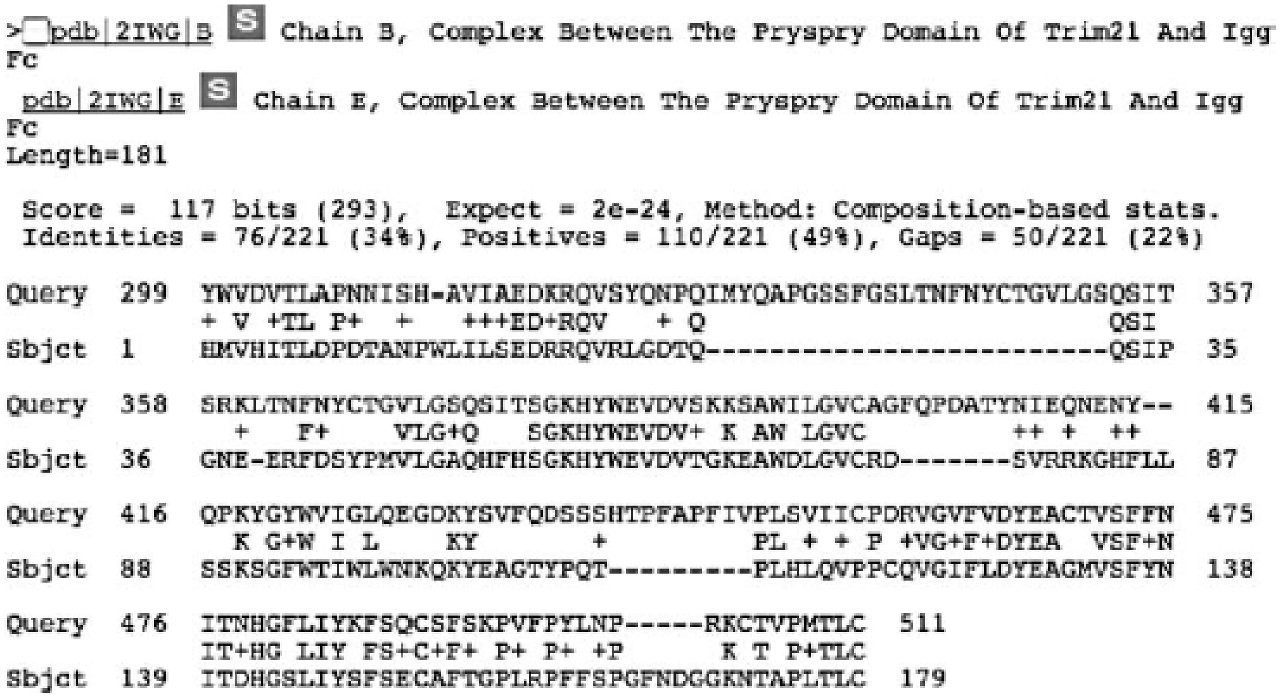
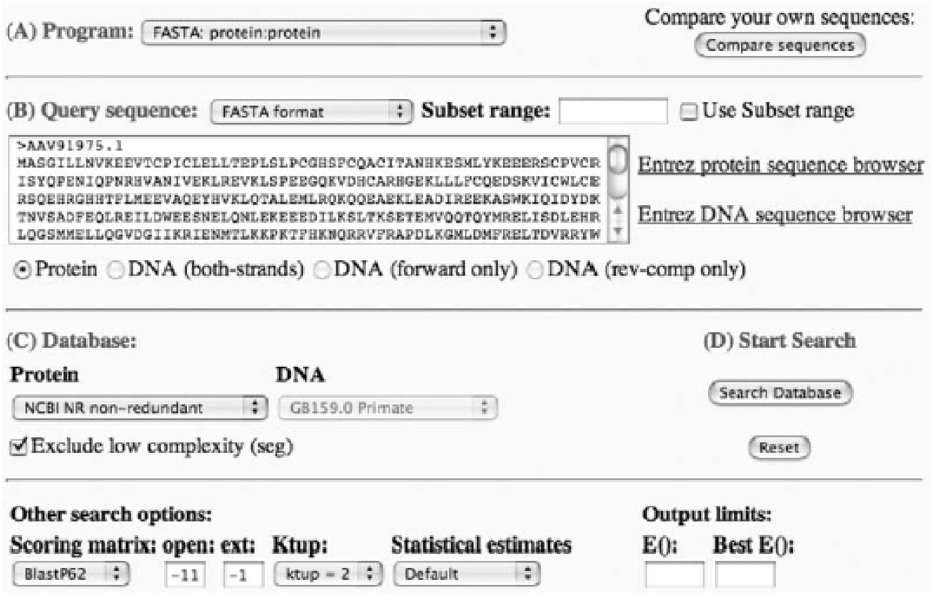


```
>pdb|2IWG|B  S  Chain B, Complex Between The Pryspry Domain Of Trim21 And Igg
Fc
 pdb|2IWG|E  S  Chain E, Complex Between The Pryspry Domain Of Trim21 And Igg
Fc
Length=181

 Score =  117 bits (293),  Expect = 2e-24, Method: Composition-based stats.
 Identities = 76/221 (34%), Positives = 110/221 (49%), Gaps = 50/221 (22%)

Query  299  YWVDVTLAPNNISH-AVIAEDKRQVSYQNPQIMYQAPGSSFGSLTNFNYCTGVLGSQSIT  357
            + V +TL P+  +   +++ED+RQV   + Q                        QSI
Sbjct  1    HMVHITLDPDTANPWLILSEDRRQVRLGDTQ-------------------------QSIP  35

Query  358  SRKLTNFNYCTGVLGSQSITSGKHYWEVDVSKKSAWILGVCAGFQPDATYNIEQNENY--  415
              +   F+    VLG+Q   SGKHYWEVDV+ K AW LGVC         ++ +  ++
Sbjct  36   GNE-ERFDSYPMVLGAQHFHSGKHYWEVDVTGKEAWDLGVCRD-------SVRRKGHFLL  87

Query  416  QPKYGYWVIGLQEGDKYSVFQDSSSHTPFAPFIVPLSVIICPDRVGVFVDYEACTVSFFN  475
              K G+W I L    KY      +          PL + + P +VG+F+DYEA  VSF+N
Sbjct  88   SSKSGFWTIWLWNKQKYEAGTYPQT---------PLHLQVPPCQVGIFLDYEAGMVSFYN  138

Query  476  ITNHGFLIYKFSQCSFSKPVFPYLNP-----RKCTVPMTLC  511
            IT+HG LIY FS+C+F+ P+ P+ +P      K T P+TLC
Sbjct  139  ITDHGSLIYSFSECAFTGPLRPFFSPGFNDGGKNTAPLTLC  179
```



(A) Program: FASTA: protein:protein

Compare your own sequences:

(B) Query sequence: FASTA format **Subset range:** ☐ Use Subset range

```
>AAV91975.1
MASGILLNVKEEVTCPICLELLTEPLSLPCGHSFCQACITANHKESMLYKEEERSCPVCR
ISYQPENIQPNRHVANIVEKLREVKLSPEEGQKVDHCARHGEKLLLFCQEDSKVICWLCE
RSQEHRGHHTFLMEEVAQEYHVKLQTALEMLRQKQQEAEKLEADIREEKASWKIQIDYDK
TNVSADFEQLREILDWEESNELQNLEKEEEDILKSLTKSETEMVQQTQYMRELISDLEHR
LQGSMMELLQGVDGIIKRIENMTLKKPKTFHKNQRRVFRAPDLKGMLDMFRELTDVRRYW
```

● Protein ○ DNA (both-strands) ○ DNA (forward only) ○ DNA (rev-comp only)

(C) Database:

Protein: NCBI NR non-redundant

DNA: GB159.0 Primate

☑ Exclude low complexity (seg)

(D) Start Search

Other search options:

Scoring matrix: BlastP62 **open:** -11 **ext:** -1 **Ktup:** ktup = 2 **Statistical estimates:** Default

Output limits: **E():** **Best E():**

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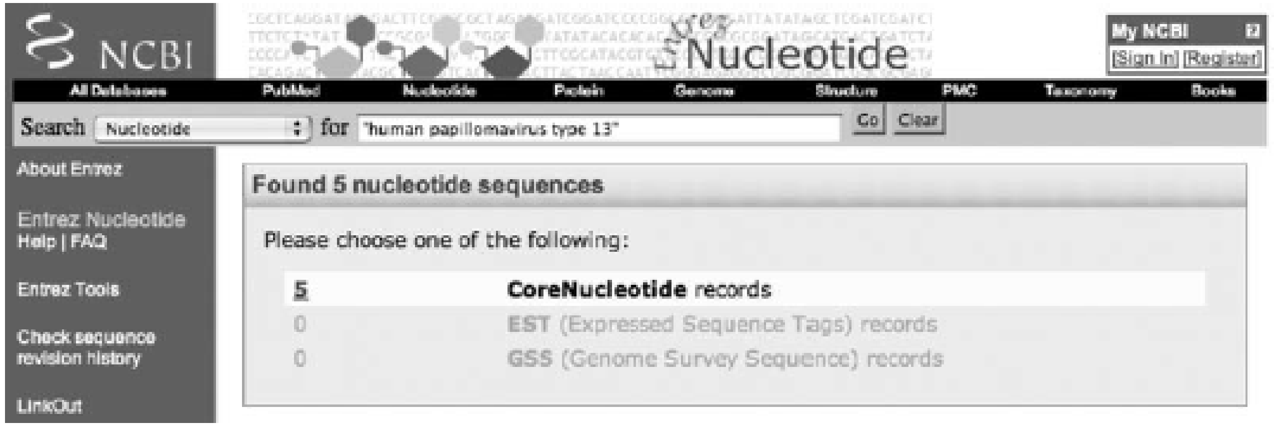
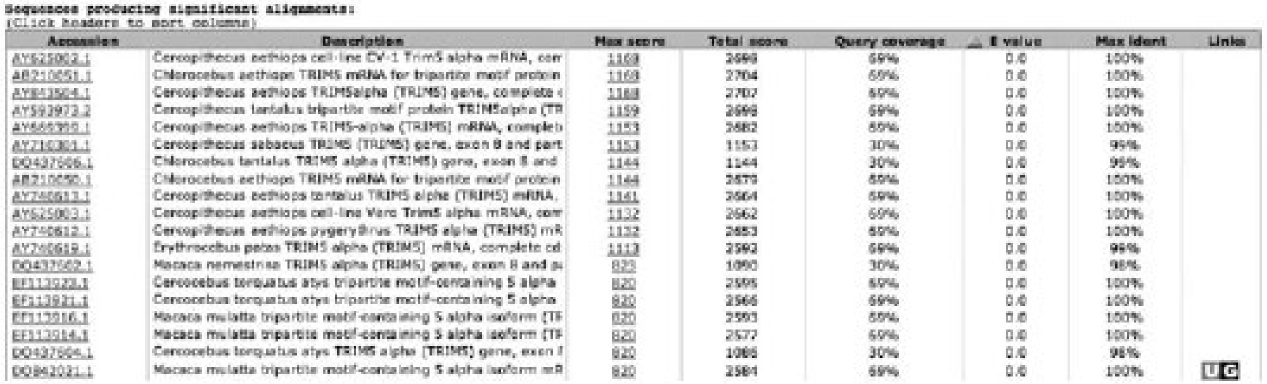


Search Nucleotide for "human papillomavirus type 13"

Found 5 nucleotide sequences

Please choose one of the following:

5	**CoreNucleotide** records
0	**EST** (Expressed Sequence Tags) records
0	**GSS** (Genome Survey Sequence) records



Sequences producing significant alignments:
(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
AY625002.1	Cercopithecus aethiops cell-line CV-1 Trim5 alpha mRNA, com	1169	2699	69%	0.0	100%	
AB210051.1	Chlorocebus aethiops TRIM5 mRNA for tripartite motif protein	1169	2704	69%	0.0	100%	
AY843504.1	Cercopithecus aethiops TRIM5alpha (TRIM5) gene, complete c	1168	2707	69%	0.0	100%	
AY593973.2	Cercopithecus tantalus tripartite motif protein TRIM5alpha (TR	1159	2699	69%	0.0	100%	
AY669399.1	Cercopithecus aethiops TRIM5-alpha (TRIM5) mRNA, complet	1153	2682	69%	0.0	100%	
AY710301.1	Cercopithecus sabaeus TRIM5 (TRIM5) gene, exon 8 and part	1153	1153	30%	0.0	99%	
DQ437606.1	Chlorocebus tantalus TRIM5 alpha (TRIM5) gene, exon 8 and	1144	1144	30%	0.0	99%	
AB210050.1	Chlorocebus aethiops TRIM5 mRNA for tripartite motif protein	1144	2679	69%	0.0	100%	
AY740613.1	Cercopithecus aethiops tantalus TRIM5 alpha (TRIM5) mRNA,	1141	2664	69%	0.0	100%	
AY625003.1	Cercopithecus aethiops cell-line Vero Trim5 alpha mRNA, com	1132	2662	69%	0.0	100%	
AY740612.1	Cercopithecus aethiops pygerythrus TRIM5 alpha (TRIM5) mR	1132	2653	69%	0.0	100%	
AY740619.1	Erythrocebus patas TRIM5 alpha (TRIM5) mRNA, complete cd	1113	2592	69%	0.0	96%	
DQ437592.1	Macaca nemestrina TRIM5 alpha (TRIM5) gene, exon 8 and p	823	1090	30%	0.0	98%	
EF113923.1	Cercocebus torquatus atys tripartite motif-containing 5 alpha	820	2595	69%	0.0	100%	
EF113921.1	Cercocebus torquatus atys tripartite motif-containing 5 alpha	820	2566	69%	0.0	100%	
EF113916.1	Macaca mulatta tripartite motif-containing 5 alpha isoform (TR	820	2593	69%	0.0	100%	
EF113914.1	Macaca mulatta tripartite motif-containing 5 alpha isoform (TR	820	2577	69%	0.0	100%	
DQ437604.1	Cercocebus torquatus atys TRIM5 alpha (TRIM5) gene, exon 8	820	1086	30%	0.0	98%	
DQ842021.1	Macaca mulatta tripartite motif-containing 5 alpha isoform mR	820	2581	69%	0.0	100%	UG

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