

## SUPPLEMENTAL DATA

### Single molecule real time (SMRT) full length RNA-sequencing reveals novel and distinct mRNA isoforms in human bone marrow cell subpopulations

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## Supplemental Experimental and Computational Procedures

SQANTI2 is a private github repository of Elizabeth Tseng (co-author of this manuscript) and is a modification of the original SQANTI by the Ana Conesa Lab (1).

CAGE Peak data is from Fantom5 (2).

Intropolis is a list of exon-exon junctions across 21,5004 human RNA-seq from the Sequence Read Archive from spliced read alignment to hg19 with Rail-RNA (3).

### Scripts:

#### Transcriptome Alignment and Assembly from Illumina Data.

The specific qsub command for the total bone marrow (T) alignment was:

```
#!/bin/bash
#$ -cwd
#$ -pe orte 32
#$ -N "th.fr.unstr.tot"
#$ -V
export PATH="/mnt/myenv2/bin:/mydata/cufflinks-2.2.1.Linux_x86_64:/mydata/bowtie2-2.2.5:/mydata/samtools-1.2:$PATH"
/mydata/tophat-2.0.14.Linux_x86_64/tophat2 -p 32 -G /results/Homo_sapiens/UCSC/hg19/Annotation/Genes/genes.gtf \
-r200 \
--library-type fr-unstranded \
-o /trimmed_fastq/transcriptome/ill.bm.total/tophat.2.0.14.fr-unstranded.gtf \
/results/Homo_sapiens/UCSC/hg19/Sequence/Bowtie2Index/genome \
/trimmed_fastq/trimmed.fasta.total.bm.non.ss/bm.trimmed.reads.1.fa \
/trimmed_fastq/trimmed.fasta.total.bm.non.ss/bm.trimmed.reads.2.fa
```

The specific command for cufflinks 2 assembly for total bone marrow (T) was:

```
#!/bin/bash
#$ -cwd
#$ -pe orte 32
#$ -N "cf2.tot.fr.un.gtf"
#$ -V
export PATH="/mnt/myenv2/bin:/mydata/cufflinks-2.2.1.Linux_x86_64:/mydata/bowtie2-2.2.1:/mydata/samtools-0.1.19:$PATH"
/mydata/cufflinks-2.2.1.Linux_x86_64/cufflinks -b /results/Homo_sapiens/UCSC/hg19/Sequence/WholeGenomeFasta/genome.fa \
-p 32 \
-g /results/Homo_sapiens/UCSC/hg19/Annotation/Genes/genes.gtf \
-L tot.fr.unstranded.gtf \
-o /trimmed_fastq/transcriptome/ill.bm.total/cufflinks2.2.1.tophat.2.0.14.fr.unstranded.gtf.5.19 \
/trimmed_fastq/transcriptome/ill.bm.total/tophat.2.0.14.fr-unstranded.gtf/accepted_hits.bam
```

The specific qsub command for the lineage-negative (N) alignment was:

```
#!/bin/bash
```

```

##$ -cwd
##$ -pe orte 32
##$ -N "th.neg.gtf"
##$ -V
export PATH="/mnt/myenv2/bin:/mydata/cufflinks-2.2.1.Linux_x86_64:/mydata/bowtie2-2.2.5:/mydata/samtools-1.2:$PATH"
/usr/local/bin/tophat -p 32 -G /results/Homo_sapiens/UCSC/hg19/Annotation/Genes/genes.gtf \
--library-type fr-firststrand \
-r200 \
-o /trimmed_fastq/transcriptome/ill.lin.neg/tophat.2.0.14.fr.firststrand.no.mm.gtf \
/results/Homo_sapiens/UCSC/hg19/Sequence/Bowtie2Index/genome \
/trimmed_fastq/trimmed.fasta.lin.neg.ss/lin.neg.trimmed.reads.1.fa \
/trimmed_fastq/trimmed.fasta.lin.neg.ss/lin.neg.trimmed.reads.2.fa

```

The specific command for cufflinks 2 assembly for lineage-negative (N) was:

```

#!/bin/bash
##$ -cwd
##$ -pe orte 32
##$ -N "cf2.ill.lin.neg.gtf"
##$ -V
export PATH="/mnt/myenv2/bin:/mydata/cufflinks-2.2.1.Linux_x86_64:/mydata/bowtie2-2.2.1:/mydata/samtools-0.1.19:$PATH"
/mydata/cufflinks-2.2.1.Linux_x86_64/cufflinks -b /results/Homo_sapiens/UCSC/hg19/Sequence/WholeGenomeFasta/genome.fa \
-p 32 \
-g /results/Homo_sapiens/UCSC/hg19/Annotation/Genes/genes.gtf \
-L ill.lin.neg.nm.th \
-o /trimmed_fastq/transcriptome/ill.lin.neg/cufflinks2.2.1.no.mm.no.u.gtf \
/trimmed_fastq/transcriptome/ill.lin.neg/tophat.2.0.14.fr.firststrand.no.mm/accepted_hits.bam

```

### Analysis of full length transcript by ToFU:

All processing was done on an amazon cloud instant on which the SMRTAnalysis software was first installed followed by installing the then referred to cDNA\_primer prebam version of ToFU.

Before running the `tofu_wrap.py` software, these files needed to be prepared.

1. CircularConsensus.sh to obtain circular consensus reads (ccs) from movie files
2. Classify to obtain Full length non-chimeric reads (FL) and non-full length (nFL) ccs reads

The ccs reads now classified into FL and nFL are then converted from fastq to fasta files.

So that prior to running `tofu_wrap.py`, one has:

1. Isoseq\_nfl.fasta (nFL) ccs reads
2. Isoseq\_flnc.fasta (FL)
3. Input.fofn (quality information from the movie files)
4. Reads\_of\_insert.fofn (the ccs reads listed as file names)
5. Reference database (hg19)

Then, the ToFU step of final assembly is accomplished with:

```
tofu_wrap.py --nfl_fa isoseq_nfl.fasta \  
--ccs_fofn reads_of_insert.fofn --bas_fofn input.fofn \  
-d clusterOut --quiver --use_sge --max_sge_jobs 120 \  
--gmap_db /home/UNIXHOME/etseng/share/gmap_db_new/ \  
--gmap_name hg19 \  
--output_seqid_prefix tissue1  
isoseq_flnc.fasta final.consensus.fa
```

### Confirmation of novel transcript isoforms with blast

To confirm novel transcripts isoforms, two blastable databases were prepared separately for the total bone marrow (total.bm.non.ss) and lineage-negative short read RNA sequences (lin.neg.ss) using the example script below. The full length RNA-seq reads for each gene was split into single sequence files then batch blasted in a script such as this used for *ANXA1*:

```
#!/bin/bash  
  
endings="aa ab ac ad ae af ag ah ai aj ak al am an ao ap aq ar as at au av aw ax ay az  
      ba bb bc bd be bf bg bh bi bj bk bl bm bn bo bp bq br bs bt bu bv bw bx by bz  
      ca cb cc cd ce cf cg ch ci cj ck cl cm cn co"  
  
#rm ANXA1.lin.neg.coverage.txt  
#rm ANXA1.total.coverage.txt  
  
for end in $endings;  
do  
    echo ANXA1.split."$end"  
    blastn -db ../lin.neg.ss/lin.neg.ss -perc_identity 99 -ungapped -num_threads 32 -max_target_seqs 10000 -query  
ANXA1.split."$end" -outfmt "6 qseqid qstart qend \  
qseq sseq sseqid sstart send" -out ANXA1.split."$end".lin.neg.out  
    blastn -db ../total.bm.non.ss/total.bm.non.ss -perc_identity 99 -ungapped -num_threads 32 -max_target_seqs 10000 -  
query ANXA1.split."$end" -outfmt "6 qseqid \  
qstart qend qseq sseq sseqid sstart send" -out ANXA1.split."$end".total.out  
done
```

Using this output file, a *summarize* script provides the coverage.

```
#!/bin/bash  
  
endings="aa ab ac ad ae af ag ah ai aj ak al am an ao ap aq ar as at au av  
ba bb bc bd be bf bg bh bi bj bk bl bm bn bo bp bq br bs bt bu bv  
ca cb cc cd ce cf cg ch ci cj ck cl cm cn co"  
  
for end in endings  
do  
    echo ANXA1.split."$end"  
    var=$(grep ">" ANXA1.split."$end"  
    var2=${var:1}  
    echo "$var2"  
    grep "$var2" ANXA1.split."$end".lin.neg.out | cut -c -20 > ANXA1.split."$end".lin.neg.num.txt  
    sort -n -k 2,3 ANXA1.split."$end".lin.neg.num.txt > ANXA1."$end" > . "$var2".lin.neg.txt
```

```

sort -n -k 2,3 ANXA1.split."$end".lin.neg.out > ANXA1."$end". "$var2".lin.neg.fa.txt
cat ANXA1."$end" . "$var2".lin.neg.txt >> ANXA1.lin.neg.coverage.txt
grep "$var2" ANXA1.split."$end".total.out | cut -c -20 >ANXA1.split."$end".total.num.txt
sort -n -k 2,3 ANXA1.split."$end".total.num.txt >ANXA1."$end". "$var2".total.txts
sort -n -k 2,3 ANXA1.split."$end".total.out > ANXA1."$end"."$var2".total.fa.txt
cat ANXA1."$end"."$var2".total.txt >> ANXA1.total.coverage.txt
done

```

*Summarize* finds the matches and prepares the coverage file. Next, a series of *awk* scripts find the gaps in coverage as a result of the blast and limits the hits to 100 bp.

The output of the short reads that match each of the novel isoforms were then searched for the full length reads. All genes followed the same stepwise procedure.

step 1 - Simplify the blast output capturing the ends of the hit, and the length of the overlap.

```

cat ANXA1.total.coverage.txt | awk '{print $1 "\t" $2 "\t" $3 "\t" $3-$2+1}' >ANXA1.total.coverage.maths.txt

```

Ensure the hits are at least 100 bp

```

grep "100" ANXA1.total.coverage.maths.txt > ANXA1.total.100.coverage.maths.txt

```

step 2 - preserving the end of the previous line, this awk script identifies gaps.

```

cat ANXA1.total.100.coverage.maths.txt | awk '{print var "\t" $1 "\t" $2 "\t" $3 "\t" $4 "\t" var-$2;var=$3}' >
ANXA1.total.100.coverage.all.txt

```

step 3 - use the end of the match from the previous line to determine if there is a gap

```

grep "\-" ANXA1.total.coverage.all.txt

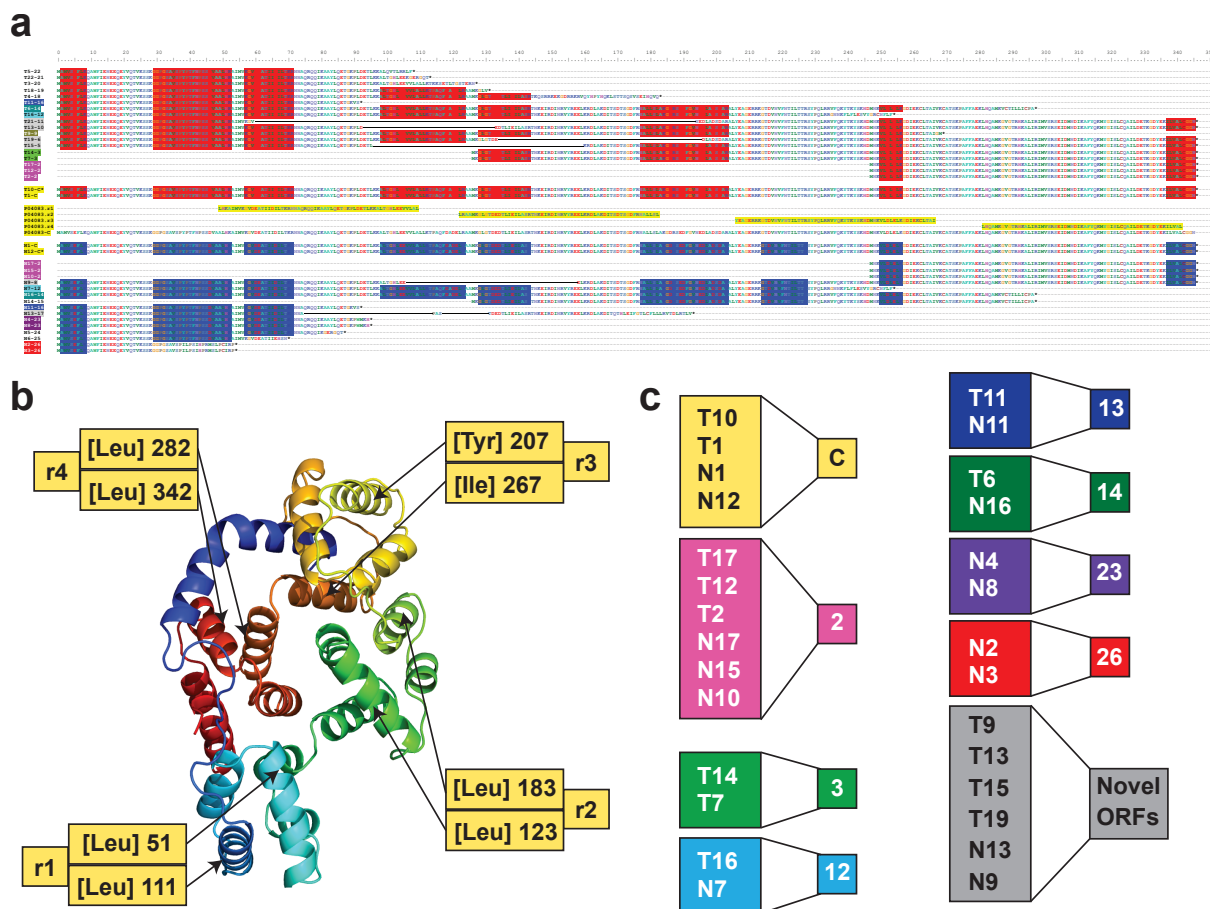
```

The specific command for the Sqanti2 package was:

```
python ~/GitHub/SQANTI2/sqanti_qc2.py -t 30 53A_negative.good.5merge.collapsed.longest_rep.fa
gencode.v29.annotation.gtf /pbi/dept/bifx/etseng/genomes/hg38/hg38_noalt.fa --cage_peak
~/share/FANTOM/hg38.cage_peak_phase1and2combined_coord.bed -c
"Public_Intronpolis/*count_10.*modified" --polyA_motif_list polyA.list
...
"polyA.list"
...
aataaa
attaaa
agtaaa
tataaa
cataaa
gataaa
aatata
aataca
aataga
aaaaag
actaaa
aagaaa
aatgaa
tttaaa
aaaaca
ggggct
...
```

## Supplemental References

1. Tardaguila, M., de la Fuente, L., Marti C., Pereira, C., Pardo-Palacios, F.J., Del Risco, H., Ferrell, M., Mellado, M., Macchietto, M., Verheggen, K., Edelmann, M., Ezkurdia, I., Vazquez, J., Tress, M., Mortazavi, A., Martens, L., Rodriguez-Navarro, S., Moreno-Manzano, V., Conesa, A. (2018) SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification. *Genome Res.* **28**, 396-411
2. Lizio, M, et al. (2015) Gateways to the FANTOM5 promoter level mammalian expression atlas. *Genome Biology* **16**, 22
3. Nellore, A., et al. (2016) Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. *Genome Biology* **17**, 266
4. Shilov, I. V., Seymour, S. L., Patel, A. A., Loboda, A., Tang, W. H., Keating, S. P., Hunter, C. L., Nuwaysir, L. M., and Schaeffer, D. A. (2007) The Paragon Algorithm, a Next Generation Search Engine That Uses Sequence Temperature Values and Feature Probabilities to Identify Peptides from Tandem Mass Spectra. *Molecular & Cellular Proteomics*. **6**, 1638–1655
5. Tang, W. H., Shilov, I. V., and Seymour, S. L. (2008) Nonlinear fitting method for determining local false discovery rates from decoy database searches. *J Proteome Res.* **7**, 3661–3667



**Figure S1.** Amino acid sequence alignment and proteins predicted from the transcript isoforms identified for *ANXA1* (see **Fig. 4c,d**). **(a)** Amino acid sequence alignments including the isoform identifiers. The canonical protein and conserved repeat domains r1 - r4 are highlighted in yellow. ORFs coding for the same protein are shown in matching colors. Note: Solid lines connecting protein fragments indicate contiguous amino acid sequences predicted from the respective transcript isoform. **(b)** Predicted protein structure of the canonical *ANXA1* protein P04083 with repeat domains r1 to r4 indicated. **(c)** Common predicted proteins for groups of transcript isoforms, ORFs 2, 3, 12, 13, 14, 23, 26 and the canonical ORF (C) are listed and shown with the respective color from panel (a). Novel ORFs are indicated.

(A magnified portion of Figure S1a is on the next page.)

	0	10	20	30	40	50	60	70	80	
T5-22	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T22-21	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T3-20	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T18-19	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T4-18	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T11-16	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T6-14	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T16-12	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T21-11	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG			
T13-10	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T9-9	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T19-6	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T15-5	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T14-3										
T7-3										
T17-2										
T12-2										
T2-2										
T10-C*	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
T1-C	MAMVS	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	ATII	ILTKRNNAQRQ	IKAAYLQETG
P04083.r1										
P04083.r2										
P04083.r3										
P04083.r4										
P04083-C	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMVKG	DEATI	IDILTKRNNAQRQ	IKAAYLQETG
N1-C	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N12-C*	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N17-2										
N15-2										
N10-2										
N9-8	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N7-12	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N16-14	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N14-15										
N11-16	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N13-17	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N4-23	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTKRNNAQRQ	IKAAYLQETG
N8-23	MAMVSE	FLRQAWFIENEEQ	EYVQTVKSSK	GGPGSAVS	SPYPTFNPSS	VAALHKA	IMV	GDEATI	IDILTK	

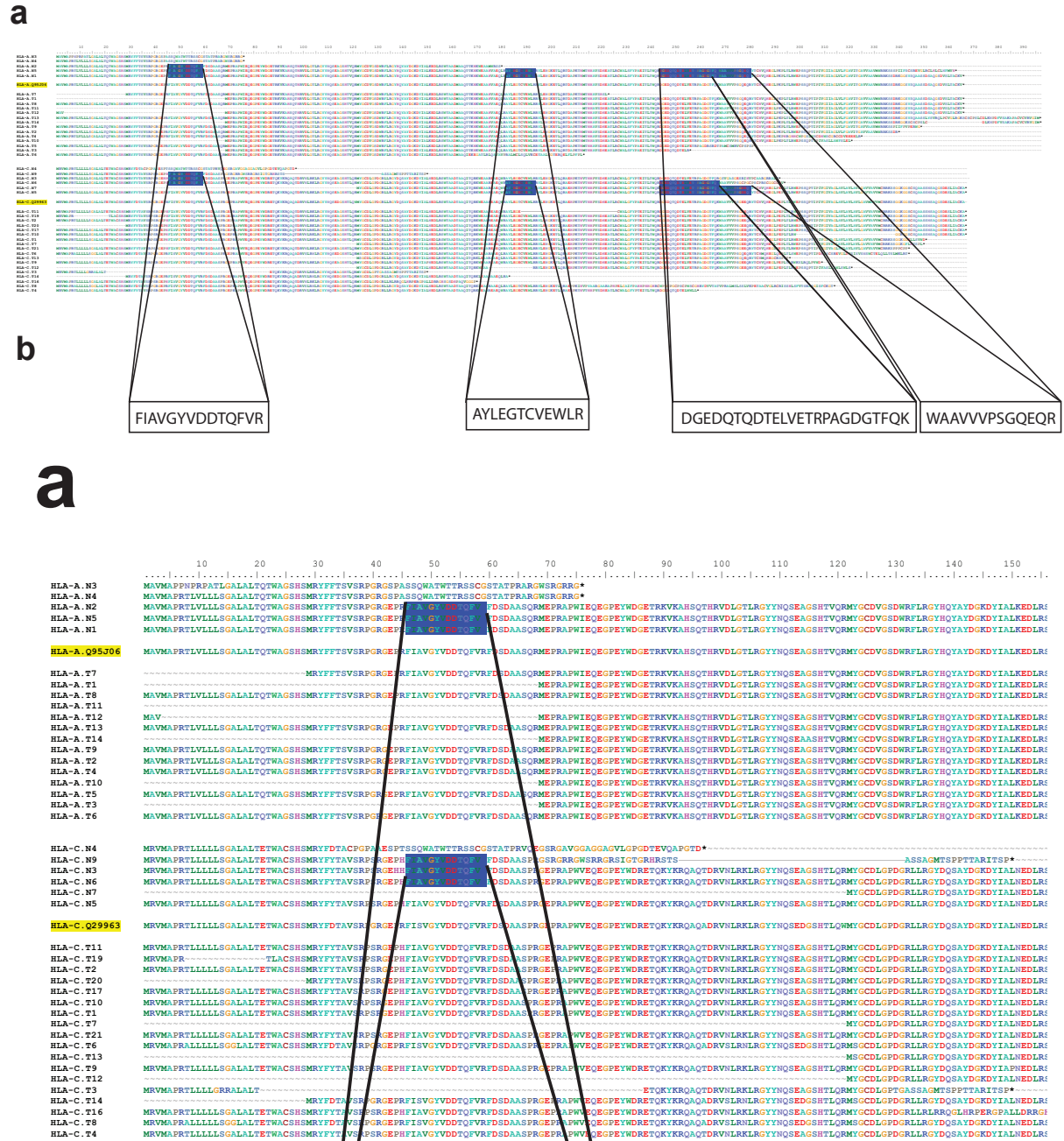
S8





**Figure S2.** Multiple amino acid sequence alignment predicted from transcript isoforms for *ELANE* and *CFD*. The alignment is shown in the top panel. The identifiers of the transcript isoforms are included.

For better readability a magnified portion of the figure is shown as the bottom panel.



**Figure S3.** Multiple amino acid sequence alignment (**a**) and mass spectrometry detected peptides (**b**) for *HLA-A*, *-B* and *-C* transcripts. (**a**) Sequences predicted from transcript isoforms of *HLA-A*, *HLA-B* and *HLA-C*. The identifiers of the transcript isoforms are included. Canonical amino acid sequences are highlighted in yellow. (**b**) Peptide fragments identified by mass spectrometry analysis of tryptic fragments of proteins extracted from lin-neg bone marrow cells. The spectra are shown in Fig. 5d-f.

For better readability a magnified portion of Fig S3a is shown in the bottom panel

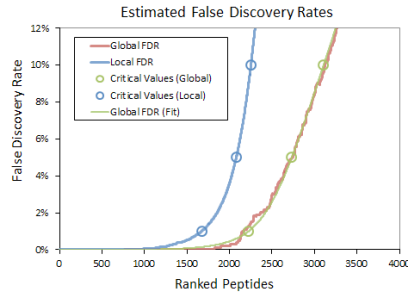
## a lineage-negative bone marrow cells

### Distinct Peptide Level FDR Analysis

Peptides Identified at Critical False Discovery Rates

Number of Peptides Identified			
Critical FDR	Local FDR	Global FDR	Global FDR from Fit
<b>1.0%</b>	<i>1672</i>	<i>2152</i>	<b>2223</b>
<b>5.0%</b>	<b>2080</b>	<i>2740</i>	<i>2792</i>
<b>10.0%</b>	<b>2252</b>	<i>3341</i>	<i>3106</i>

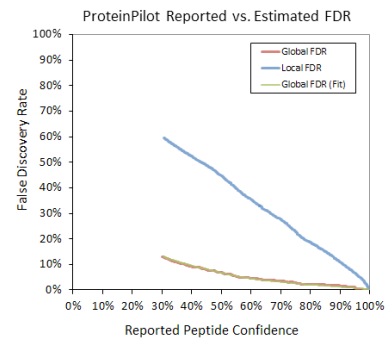
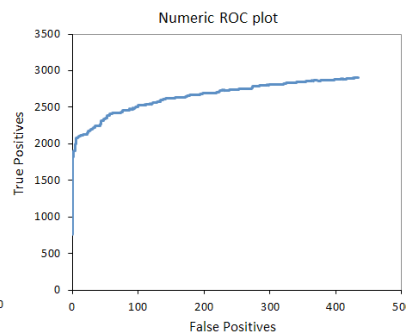
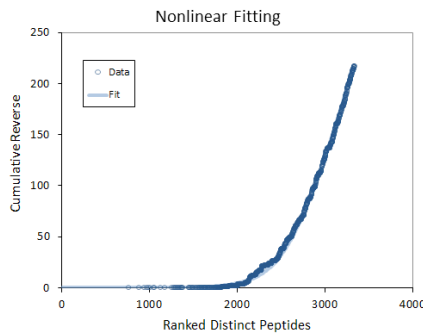
\* It is recommended you use numbers in bold and avoid using numbers in italics.



Correspondence between FDR Levels and ProteinPilot Reported Confidences

Corresponding ProteinPilot Confidence			
Critical FDR	Local FDR	Global FDR	Global FDR from Fit
<b>1.0%</b>	<i>95.5%</i>	<i>95.0%</i>	<b>92.4%</b>
<b>5.0%</b>	<b>96.7%</b>	<i>56.6%</i>	<i>57.1%</i>
<b>10.0%</b>	<b>91.2%</b>	<i>37.8%</i>	<i>38.5%</i>

\* It is recommended you use numbers in bold and avoid using numbers in italics.



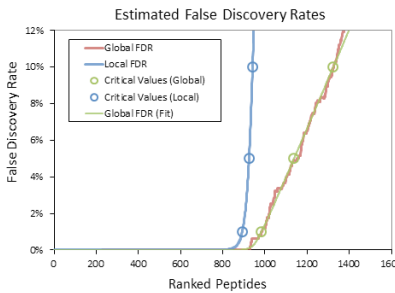
## b lineage-positive bone marrow cells

### Distinct Peptide Level FDR Analysis

Peptides Identified at Critical False Discovery Rates

Number of Peptides Identified			
Critical FDR	Local FDR	Global FDR	Global FDR from Fit
<b>1.0%</b>	<i>891</i>	<i>983</i>	<b>983</b>
<b>5.0%</b>	<b>924</b>	<i>1160</i>	<i>1138</i>
<b>10.0%</b>	<b>940</b>	<i>1434</i>	<i>1223</i>

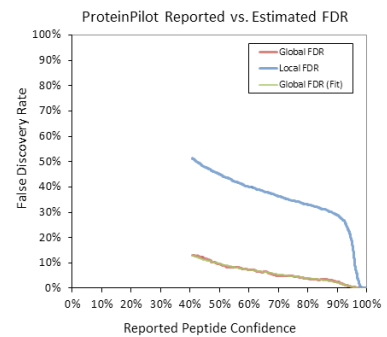
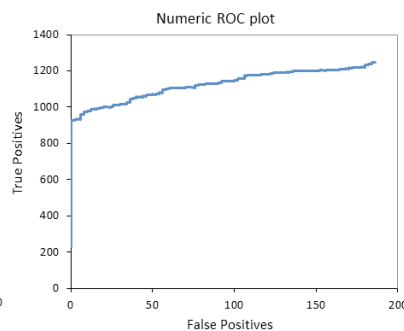
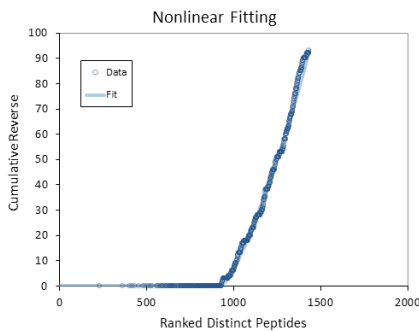
\* It is recommended you use numbers in bold and avoid using numbers in italics.



Correspondence between FDR Levels and ProteinPilot Reported Confidences

Corresponding ProteinPilot Confidence			
Critical FDR	Local FDR	Global FDR	Global FDR from Fit
<b>1.0%</b>	<i>92.7%</i>	<i>93.6%</i>	<b>93.6%</b>
<b>5.0%</b>	<b>96.9%</b>	<i>69.2%</i>	<i>72.7%</i>
<b>10.0%</b>	<b>96.0%</b>	<i>48.7%</i>	<i>49.0%</i>

\* It is recommended you use numbers in bold and avoid using numbers in italics.



**Figure S4.** Summary of the false discovery rate (FDRs) of the shotgun mass spectrometry of proteins extracted from bone marrow-derived cells. FDR analysis was performed on the ProteinPilot platform (4, 5). The cutoff for positive peptide identification was set at an FDR < 1%. The graphs and tables represent the overview of the proteomics analysis of lineage-negative (**a**) and lineage-positive (**b**) bone marrow cells.

**Figure S5.** Blast alignment of EEF1A1 novel transcripts with NCBI EST repository

copied below

**Figure S6.** Blast alignment of ANXA1 novel transcripts with NCBI EST repository

copied further below

RID: 8PV46HTU015

Sequences producing significant alignments:					Score (Bits)	E	Max ident
BX421307.2	BX421307	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1622	0.0	100%		
BX443032.2	BX443032	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1618	0.0	100%		
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	1616	0.0	100%		
BX417098.2	BX417098	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1615	0.0	100%		
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	1611	0.0	100%		
BX441194.2	BX441194	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1611	0.0	100%		
AF541984.3	AF541984	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1609	0.0	100%		
U0409312.1	AGENSCOUT_6795094	NIH MGC_85 Homo sapiens cDNA clone	1607	0.0	100%		
BX417528.2	BX417528	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1604	0.0	100%		
BM477666.1	AGENSCOUT_6482916	NIH MGC_85 Homo sapiens cDNA clone	1602	0.0	100%		

Query	3	TTTTTCGCACGGGTTTGCCGCAACACAGGTGTCGTGAAATACCCCTAAAGCCAAATGGGAAGGAAAGACTCATATCAACATTGTCGTCAATTGGACACGTAGATTCTGGGCAAGTCCACCCTACTGGCCATCTGATCTATA	152
BY794942.2	25	.....	155
DC527884.1	9	.....	158
Query	153	AATGGCGTGGCATCGACAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAGGGCTCCTTCAAGTATGCCTGGGCTTTGGATAAAGCTGAAAGCTGAGCGTGAACGTGGTATCACCATTTGATATCTCCTTTGTGGAAT	302
BY794942.2	156	.....	305
DC527884.1	159	.....T.....	308
Query	303	TTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACAGACAGACTTTATCAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAGA	455
BY794942.2	306	.....	455
DC527884.1	309	.....C.....	458
Query	453	ATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTCGGTGTAAACAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGATATGAGGAATTTGTAAGGAAGTCAGCACTTACATTAAAG	602
BY794942.2	456	.....	605
DC527884.1	459	.....	608
Query	603	AAATTGGCTACAACCCGACACAGTAGCATTTTGTGCCAATTCTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGAACCAACGCTGCTTG	752
BY794942.2	606	.....	755
DC527884.1	609	.....	758
AL541984.3	1	.....	24
Query	757	AGGCTCTGGACTGGTGTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGCTCAAGCTTACACGGAAGTAAATCTGTGAAATGCACCATGAAGCTTTGAGTGAAGCTCTCTCTGGGACAAATGTTGGGCTTCAATGTCAGAATGTTG	902
BX421307.2	23	.....	168
BX443032.2	53	.....	194
BY794942.2	756	.....M.....	768
BY794942.2	871	.....	1012
BX417098.2	16	.....	157
DC527884.1	874	.....	1015
DC527884.1	759	.....	771
BX441194.2	65	.....W.....	206
AL541984.3	140	.....	281
AL541984.3	25	.....	37
BQ049312.1	25	.....	166
BX417528.2	32	.....	173
BM477966.1	9	.....	150
Query	903	CTGTCTAAGGATGTGCTCGTGGCAAGCTTCTGGTGACAGCAAAATGACCCCAATGGAAGCAGCTGCTTCACTGCTCAGGTGATTATCTCTGAACCATCCAGGCCAAATAGCGCCGGCTATGCCCTGTATTGGATTGCCACAG	1052
BX421307.2	169	.....	318
BX443032.2	195	.....	344
BY794942.2	1013	.....	1163
		..... G	
BX417098.2	158	.....	307
DC527884.1	1016	.....	1165
BX441194.2	207	.....	356
AL541984.3	282	.....	431
BQ049312.1	167	.....	316
BX417528.2	174	.....	323
BM477966.1	151	.....	303

Query	1053	GCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAAATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTTCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTC	1202
BX421307.2	319	.....	468
BX443032.2	345	.....	494
BY794942.2	1164	.....	1313
BX417098.2	308	.....	457
DC527884.1	1166	.....	1315
BX441194.2	357	.....	506
AL541984.3	432	.....	581
BQ049312.1	317	.....	466
BX417528.2	324	.....	473
BM477966.1	301	.....	450
Query	1203	TCAGACTATCCACCTTTGGGTCGCTTTGCTGTTGCTGATATGAGACAGACAGTTGCGGTGGGTGTCTCAAAAGCAGTGGACAAGAAGCTGCTGGAGCTGGCAAGTCAACCAAGTCTGCCAGAAAGCTCAGAAGCTAAATGAATATTA	1352
BX421307.2	469	.....	618
BX443032.2	495	.....	644
BY794942.2	1314	.....	1463
BX417098.2	458	.....	607
DC527884.1	1316	.....A.....	1465
BX441194.2	507	.....	656
AL541984.3	582	.....	731
BQ049312.1	467	.....	616
BX417528.2	474	.....	623
BM477966.1	451	.....	600
Query	1353	TCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGGAAGACGGTCTCAGAACTGTTTGTTCATTTGGCCATTTAAAGTTTAGTAGTAAAAGACTGGTAAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAAATggtttt	1502
BX421307.2	619	.....	768
BX443032.2	645	.....	794
BY794942.2	1464	.....	1613
BX417098.2	608	.....	757
DC527884.1	1466	.....C.....	1615
BX441194.2	657	.....	806
AL541984.3	732	.....	881
BQ049312.1	617	.....	766
BX417528.2	624	.....T.....	773
BM477966.1	601	.....	750
Query	1503	gtggaccactttggttttcttttgcgtgtggcagttttaagtattagtttttaaaatcagtagtcttttaATGGAAACAACCTTGACCAAAAATTTGTACAGAAATTTTGGAGCCCATTAAGAAAGTTAAATGAG	1638
BX421307.2	769	.....	904
BX443032.2	795	.....	930
BY794942.2	1614	.....	1749
BX417098.2	758	.....	892
DC527884.1	1616	.....	1751
BX441194.2	807	.....	941
AL541984.3	882	.....K.S.....	1018
BQ049312.1	767	.....M.....T.....	901
BX417528.2	774	.....A.....	907
BM477966.1	751	.....N...A.....	883

Query= T2-C\* [organism=Homo sapiens] eef1a1

Length=1742

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
DC527884.1	DC527884 chimpanzee skin cDNA library PstA Pan trog...	3193	0.0	100%
BY794942.2	BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	3175	0.0	100%
CF111220.1	Shultzomica04471 Rat lung airway and parenchyma cDN...	2361	0.0	91%
BX426149.2	BX426149 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2146	0.0	99%
CO001006.1	OC028 pre-oestrus adult sheep ovary library Ovis ar...	2050	0.0	93%
BX418564.2	BX418564 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2047	0.0	97%
BX426150.2	BX426150 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2037	0.0	99%
AL567209.3	AL567209 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2001	0.0	98%
BX440470.1	BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1999	0.0	98%
BU902062.1	AGENCOURT_10127553 NIH_MGC_71 Homo sapiens cDNA clo...	1999	0.0	98%

# ALIGNMENTS

Query	2	TTTTTCGCAACGGGTTTGCCGCCAGACACAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAGGAAAAGACTCATATCAACATTGTCGTGATTGGACACGTAGATTGGGCAAGTCCACCACTACTGCCATCTGATCTATA	151
DC527884.1	9	.....	158
BY794942.2	25	.....	155
CF111220.1	7	.....T.....G.....T.....G.C...G.....A.....C.....C.....A.....C.....C.....C.....	151
		.....T.....G.....T.....G.C...G.....A.....C.....C.....A.....C.....C.....C.....	

			A	ATTC		
BX426150.2	1		..T.....	.....	126	
BU902062.1	1		.....	.....	137	
Query	152	AATGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGCTCCTCAAGTATGCCTGGGCTTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTTGGGAAAT			301	
DC527884.1	159	.....	.....	.....T.....	308	
BY794942.2	156	.....	.....	.....	305	
CF111220.1	152	.....T.....A.....	.....G.....	.....G.....A.....C.....C.....G.....T.....C.....C.....G.....	301	
BX426150.2	127	.....	.....	.....	276	
BU902062.1	138	.....	.....	.....	287	
Query	302	TTGAGACCAGCAAGTACTATGTGACTATCATTTGATGCCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAGA			451	
DC527884.1	309	.....	.....C.....	.....	458	
BY794942.2	306	.....	.....	.....	455	
CF111220.1	302	.....	.....C.....G.....	.....G.....C.....	451	
CO001006.1	1464	.....	.....T.....C.....	.....C.....C.....C.....	1317	
BX426150.2	277	.....	.....	.....	426	
BU902062.1	288	.....	.....	.....	437	
Query	452	ATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAACAACATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCTTACAGCCAGAAGAGATATGAGGAAATTTGTTAAGGAAGTCAGCACTTACATTAAAG			601	
DC527884.1	459	.....	.....	.....	608	
BY794942.2	456	.....	.....	.....	605	
CF111220.1	452	.....C.....T.....T.....	.....TT.....	.....G.....T.....C.....A.....T.....C.....C.....C.....	601	
BX426149.2	1196	.....	.....	.....-A.....-A.....	1121	
CO001006.1	1316	.....C.....T.....	.....C.....	.....T.....C.....	1167	
BX418564.2	1196	.....	.....	.....YH.VS.-R.....-W.....G.....W.....-R.....M.....K.....-R.....	1125	
BX426150.2	427	.....	.....	.....	576	
AL567209.3	1145	.....	.....	.....S.....-W.....-K.W.....R.....A.M.C.....	1091	
				\		
				M		
BX440470.1	1128	.....	.....	.....	1125	
BU902062.1	438	.....	.....	.....	587	
Query	602	AAATTGGCTACAACCCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCCTTGGTTCAAGGGATGGAAGTCAACCGTAAGGATGGCAATGCCAGTGGAAACACGCTGCTTG			751	
DC527884.1	609	.....	.....	.....	758	
BY794942.2	606	.....	.....	.....	755	
CF111220.1	602	.....T.....	.....	.....T.....G.....C.....A.....G.....C.....G.....	751	
BX426149.2	1120	.....	.....	.....	971	
CO001006.1	1166	.....	.....C.....	.....T.....A.....	1017	
BX418564.2	1124	.....S.....-R.....-R.....	.....	.....C.....	981	
BX426150.2	577	.....	.....	.....	726	
AL567209.3	1090	.....C.....	.....	.....	941	
BX440470.1	1124	.....-W.....	.....-S.M.....Y.....K.....	.....K.....	983	
			\			
			C			
BU902062.1	588	.....	.....	.....	737	
Query	752	AGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACCTGACAAGCCCTTGGCGCTGCCTCTCCAGGATGTCTACAAAATTTGGTGGTATTGGTACTGTTCCTGTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCAACT			901	
DC527884.1	759	.....	.....	.....	908	
BY794942.2	756	.....	.....	.....	905	
CF111220.1	752	.....A.....T.....T.....G.....G.....	.....TC.....A.....C.....	.....T.....C.....C.....C.....G.....A.....T.....T.....	901	
BX426149.2	970	.....	.....	.....	821	
CO001006.1	1016	.....A.....T.....G.....	.....C.....A.....TT.....	.....T.....A.....G.....T.....T.....C.....	867	
BX418564.2	980	.....	.....C.....	.....	831	
BX426150.2	727	.....	.....	.....	876	
AL567209.3	940	.....K.....	.....	.....	791	
BX440470.1	982	.....R.....	.....	.....	833	
BU902062.1	738	.....	.....	.....C.....G.....	887	
Query	902	TTGCTCCAGTCAACGTTACAACGGAAATGTAATCTGTGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGCTGGGCAACGTTGCTGGTGACAGCA			1051	
DC527884.1	909	.....	.....	.....	1058	
BY794942.2	906	.....	.....	.....	1055	
CF111220.1	902	.....T.....A.....T.....C.....G.....G.....	.....G.....A.....C.....A.....C.....A.....A.....T.....G.....	.....	1051	
BX426149.2	820	.....	.....	.....	671	
CO001006.1	866	.....C.....T.....A.....T.....G.....G.....G.....C.....A.....	.....C.....	.....A.....C.....T.....G.....	717	
BX418564.2	830	.....	.....	.....	681	
BX426150.2	877	.....	.....	.....	1025	
			\			
			G			
AL567209.3	790	.....	.....	.....	641	
BX440470.1	832	.....	.....	.....	683	
BU902062.1	888	.....	.....AC.....	.....C.....C.....C.....C.....	1037	
				\		
				G		
Query	1052	AAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGTCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAAGATTG			1201	
DC527884.1	1059	.....	.....	.....	1208	
BY794942.2	1056	.....	.....	.....	1206	

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      |
      G
CF111220.1 1052 .....G..C..T..T.....TC...C.....C...A.....C...T..A..G...C. 1201
BX426149.2 670 .....T...C.....T...C...A.....T.....C..T.GT..A...A...GC.....T...A.....T.....G..... 521
CO001006.1 716 .....T...C.....T...C...A.....T.....C..T.GT..A...A...GC.....T...A.....T.....G..... 567
BX418564.2 680 .....T...C.....T...C...A.....T.....C..T.GT..A...A...GC.....T...A.....T.....G..... 531
BX426150.2 1026 .....T...C.....T...C...A.....T.....C..T.GT..A...A...GC.....T...A.....T.....G..... 1140
AL567209.3 640 .....T...C.....T...C...A.....T.....C..T.GT..A...A...GC.....T...A.....T.....G..... 492
BX440470.1 682 .....T...C.....T...C...A.....T.....C..T.GT..A...A...GC.....T...A.....T.....G..... 532

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      |
      C
BU902062.1 1038 .....C.G.....-.....T.....G.....-.....A.....C..G..T..... 1163

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      |
      C
Query 1202 ATCGCCGTTCTGGTAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGATATGA 1351
DC527884.1 1209 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1358
BY794942.2 1207 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1356
CF111220.1 1202 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1351
BX426149.2 520 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 371
CO001006.1 566 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 417
BX418564.2 530 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 381
AL567209.3 491 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 342
BX440470.1 531 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 382

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      |
      C
Query 1352 GACAGACAGTTGCGGTGGGTGTCAATCAAGCAGTGGACAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAA 1501
DC527884.1 1359 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1508
BY794942.2 1357 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1506
CF111220.1 1352 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1501
BX426149.2 370 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 221
CO001006.1 416 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 267
BX418564.2 380 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 231
AL567209.3 341 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 191

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      |
      A
BX440470.1 381 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 232

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      |
      A
Query 1502 CGGTCTCAGAAGCTGTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACCTTCAGAAGGAAAGGAGAATgttttggaccactttgggttttttttttggtgtggcagttttaag 1651
DC527884.1 1509 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1658
BY794942.2 1507 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1656
CF111220.1 1502 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1640
BX426149.2 220 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 71
CO001006.1 266 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 126

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      |
      T
BX418564.2 230 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 81
AL567209.3 190 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 40

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      |
      G
BX440470.1 231 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 82

      \
      |
      C
Query 1652 ttattagtttttaaaatcagtagtactttttaATGGAACAACCTTGACCAAAAAATTTGTACAGAAATTTTGGAGCCCATTAAGGTTAAATG 1742
DC527884.1 1659 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1749
BY794942.2 1657 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1747
CF111220.1 1641 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1731

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      |
      C
BX426149.2 70 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1
CO001006.1 125 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 35

      \
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BX418564.2 80 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1
AL567209.3 39 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1
BX440470.1 81 .....T.....G.....C.....C.....C.....A.....T...C..T..AC.T...T.....C..... 1

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Query= T3-23 [organism=Homo sapiens] eef1a1

Length=1643

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	2468	0.0	100%



DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog... 2462 0.0 100%  
BX426149.2 BX426149 Homo sapiens NEUROBLASTOMA Homo sapiens cd... 2146 0.0 99%  
BX418564.2 BX418564 Homo sapiens FETAL BRAIN Homo sapiens cDNA... 2047 0.0 97%  
AL567209.3 AL567209 Homo sapiens FETAL BRAIN Homo sapiens cDNA... 2001 0.0 98%  
BX440470.1 BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA... 1999 0.0 98%  
BX420340.1 BX420340 Homo sapiens FETAL BRAIN Homo sapiens cDNA... 1997 0.0 99%  
AL518238.2 AL518238 Homo sapiens NEUROBLASTOMA Homo sapiens cd... 1993 0.0 98%  
BX459625.2 BX459625 Homo sapiens FETAL BRAIN Homo sapiens cDNA... 1993 0.0 99%  
BX418589.2 BX418589 Homo sapiens FETAL BRAIN Homo sapiens cDNA... 1980 0.0 98%

ALIGNMENTS

Query 2 TTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCTGTGAAACTACCCCTAAAAGCCAAATGGGAAAGGAAAGACTCATATCAACATTGTCGTCAATTGGACACGTAGATTTCGGGCAAGTCCACCCTACTGGCCATCTGATCTATA 151  
BY794942.2 25 ..... 155  
DC527884.1 9 ..... 158

Query 152 AATGCGGTGGCATCGACAAAAGTAGCCTGGCTTGGATAAACTGAAAGCGACGCTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTGAGACCAGCAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTATCAA 301  
BY794942.2 156 ..... 177  
BY794942.2 230 ..... 366

.....  
| | | | |  
T G T T A T

DC527884.1 159 ..... 180  
DC527884.1 233 ..... 369

.....  
| | | | |  
T G T T A C

Query 302 ACATGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAGAATGGGACGCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACTAATTGTGCGGTGTTACAAAATGGATTCCACTGAGCCACCCCTACA 451  
BY794942.2 408 ..... 554  
BY794942.2 367 ..... 376

.....  
|  
AA

DC527884.1 411 ..... 557  
DC527884.1 370 ..... 379

.....  
|  
AA

BX426149.2 1196 ..... 1172  
BX418564.2 1196 ..... 1170  
AL567209.3 1145 ..... 1139

Query 452 GCCAGAAGAGATATGAGGAAATTTGTTAAGGAAGTCAGCACTTACATTAAGAAAAATTGGCTACAACCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCCTTGGTTCAAGG 601  
BY794942.2 555 ..... 704  
DC527884.1 558 ..... 707  
BX426149.2 1171 ..... 1022  
BX418564.2 1169 S...-R...-W...-G...W...-R...-M...-K...-R...-S...-R...-C... 1031  
AL567209.3 1138 S...-R...-W...-K...-R...-A...M...C...-C... 992

.....  
|  
M

BX440470.1 1128 ..... 1034

.....  
|  
C

BX420340.1 1117 ..... 1027  
AL518238.2 1148 ..... 1028  
BX459625.2 1118 ..... 1021

.....  
|  
T

BX418589.2 1130 ..... 1033

Query 602 GATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGAACCAACGCTGCTTGAGGCTCTGGAGTCGATCTACCACCACTCGTCCAACCTGACAAGCCCTTGGCCCTGCCTCTCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTC 751  
BY794942.2 705 ..... 854  
DC527884.1 708 ..... 857  
BX426149.2 1021 ..... 872  
BX418564.2 1030 ..... 882  
AL567209.3 991 ..... 842  
BX440470.1 1033 ..... 884  
BX420340.1 1026 ..... 877  
AL518238.2 1027 ..... 877

.....  
|  
A

BX459625.2 1020 ..... 871  
BX418589.2 1032 ..... 883

Query 752 CTGTGGCCGAGTGAGAGATGGTGTCTCAAAACCCGGTATGGTGGTCACTTTTGCTCCAGTCAACGTTACAACGGGAAGTAAATCTGTGCAATGCAACCATGAAGCTTTGAGTGAAGCTCTTCTGGGACAATGTGGGCTTCAATGTCA 901  
BY794942.2 855 ..... 1004  
DC527884.1 858 ..... 1007

Accession	Length	Sequence	Accession	Length	Sequence
BX426149.2	871	.....	722		
BX418564.2	881	.....	732		
AL567209.3	841	.....	692		
BX440470.1	883	.....	734		
BX420340.1	876	.....	727		
AL518238.2	876	.....W.....B.....W.....	727		
BX459625.2	870	.....	721		
BX418589.2	882	.....	733		
Query	902	AGAAATGTCCTGTCAGGATGTCGTCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGTGATTATCTCTGAACCATCCAGGCCAAATAGCGCCGGCTATGCCCTGTATTGGATT	1051		
BY794942.2	1005	.....	1155		
		.....\			
		.....G			
DC527884.1	1008	.....	1117		
BX426149.2	721	.....	572		
BX418564.2	731	.....C.....	582		
AL567209.3	691	.....-.....	543		
BX440470.1	733	.....	584		
BX420340.1	726	.....	577		
AL518238.2	726	.....A.....G.....	577		
BX459625.2	720	.....	571		
BX418589.2	732	.....	583		
Query	1052	GCCACACGGCTCACATTGCATGCAAGTTTGGCTGAGCTGAAGGAAAAGATTGATCGCCGCTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCCTGAAGCTCTGGTGATGCTGCCATTGTTGATATGGTTCTGGCAAGCCCATGTGTGTG	1201		
BY794942.2	1156	.....	1305		
DC527884.1	1158	.....	1307		
BX426149.2	573	.....	422		
BX418564.2	581	.....M.....	432		
AL567209.3	542	.....	393		
BX440470.1	583	.....K.....	433		
		.....\			
		.....I			
		.....C			
BX420340.1	576	.....	427		
AL518238.2	576	.....Y.....	427		
BX459625.2	570	.....	421		
BX418589.2	582	.....Y.S.....	433		
Query	1202	AGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGGCTGTCGTCGATATGAGACAGACAGTTCGCGTGGGTGTCATCAAAAGCAGTGGACAAGAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAGCTCAGAAGGCTAAAT	1351		
BY794942.2	1306	.....	1455		
DC527884.1	1308	.....A.....	1457		
BX426149.2	421	.....	272		
BX418564.2	431	.....	282		
AL567209.3	392	.....M.....Y.....	243		
BX440470.1	432	.....	283		
BX420340.1	426	.....	277		
AL518238.2	426	.....G.....	277		
BX459625.2	420	.....	271		
BX418589.2	432	.....	283		
Query	1352	GATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAAGACGGCTCAGAACTGTTTGTTCATTTGCCATTTAAGTTTAGTATAAAGACTGGTTAATGATTAACATGCATCGTAAACCTTCAGAAGGAAAGGAG	1501		
BY794942.2	1456	.....	1605		
DC527884.1	1458	.....C.....	1607		
BX426149.2	271	.....	122		
BX418564.2	281	.....	132		
AL567209.3	242	.....	92		
		.....\			
		.....A			
BX440470.1	282	.....	133		
BX420340.1	276	.....	127		
AL518238.2	276	.....G.....	127		
BX459625.2	270	.....	121		
BX418589.2	282	.....	133		
Query	1502	AAATGTTTTGTGGACCACTTGGTTTTTTTTTGGTGTGGCAGTTTTAAAGTATTAGTTTTTAAATCAGTACTTTTTAATGGAACAACCTTGACCAAAAATTTGTCACAGAATTTGAGACCCATTAAAAAGTTAAATG	1643		
BY794942.2	1606	.....	1747		
DC527884.1	1608	.....	1749		
BX426149.2	121	.....-.....-.....G.....G.....T.....	1		
BX418564.2	131	.....M.....	1		
AL567209.3	91	.....-.....-.....	1		
		.....\			
		.....G			
BX440470.1	132	.....	1		
BX420340.1	126	.....R.....	1		
AL518238.2	126	.....N.....N.....	1		
		.....\			
		.....N			
BX459625.2	120	.....	1		

BX418589.2 132 .....D.....

1

Query= T4-32 [organism=Homo sapiens] eef1a1

Length=1203

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	1757	0.0	100%
DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog...	1749	0.0	100%
AL541984.3 AL541984 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1749	0.0	100%
BX440470.1 BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1738	0.0	100%
BX420402.2 BX420402 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1736	0.0	100%
BX440308.2 BX440308 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1735	0.0	100%
BX440436.2 BX440436 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1735	0.0	100%
BX325185.1 BX325185 Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1733	0.0	100%
BX440303.2 BX440303 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1731	0.0	100%
BX418589.2 BX418589 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1731	0.0	100%

#### ALIGNMENTS

Query	2	TTTTTCGCAACGGGTTTCCGCCAGAACACAGGTGTCGTGAAAACTACCCCTAAAAAGCCAAAATGGGAAGGAAAAGACTCATATCAACATTGTCGTATTGGACACGTAGATTGGGCAAGTCCACCACTACTGGCCATCTGATCTATA	151
BY794942.2	25	.....	155
DC527884.1	9	.....	158
Query	152	AATGCGGTGGCATCGACAAAAGAACATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGACAAGCCCTTGGCGCTGCCTCTCCAGGATGCTACAAAATTGGTGGTAT	301
BY794942.2	790	.....	843
BY794942.2	156	.....	261
DC527884.1	793	.....	846
DC527884.1	159	.....	264
AL541984.3	59	.....	112
BX440470.1	948	.....	895
BX420402.2	944	.....	891
BX440308.2	947	.....	894
BX440436.2	950	.....R.....	897
BX325185.1	946	.....R.....	893
BX440303.2	946	.....	893
BX418589.2	947	.....	894
Query	302	TGGTACTGTTCTCTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTTGCTCCAGTCAACGTTACAACGGAAGTAAAACTGTGCGAAATGCACCATTGAAGCTTTGAGTGAAGCTCTTCTTGGGGACAATGTGGG	451
BY794942.2	844	.....	993
DC527884.1	847	.....	996
AL541984.3	113	.....	262
BX440470.1	894	.....	745
BX420402.2	890	.....	741
BX440308.2	893	.....	744
BX440436.2	896	.....	747
BX325185.1	892	.....	743
BX440303.2	892	.....	743
BX418589.2	893	.....	744
Query	452	CTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCTCTGAACCATCCAGGCCAAAATAAGCGCCGGCTATGCCCC	601
BY794942.2	994	.....	1144
		\	
		I	
		G	
DC527884.1	997	.....	1146
AL541984.3	263	.....	412
BX440470.1	744	.....	595
BX420402.2	740	.....	591
BX440308.2	743	.....M.....	594
BX440436.2	746	.....	597
BX325185.1	742	.....	593
BX440303.2	742	.....C.....	593
BX418589.2	743	.....	594
Query	602	TGATTATTGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTCTGGCAAGCC	751
BY794942.2	1145	.....	1294
DC527884.1	1147	.....	1296
AL541984.3	413	.....	562
BX440470.1	594	.....	444
		\	
		I	
		C	
BX420402.2	590	.....	441
BX440308.2	593	.....	444
BX440436.2	596	.....	447
BX325185.1	592	.....Y.....	443
BX440303.2	592	.....	443
BX418589.2	593	.....Y.S.....	444

Query 752 CATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAGCAGTGGCAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCA 901  
BY794942.2 1295 ..... 1444  
DC527884.1 1297 ..... A ..... 1446  
AL541984.3 563 ..... 712  
BX440470.1 443 ..... 294  
BX420402.2 440 ..... 291  
BX440308.2 443 ..... 294  
BX440436.2 446 ..... 297  
BX325185.1 442 ..... 293  
BX440303.2 442 ..... 293  
BX418589.2 443 ..... 294

Query 902 GAAGGCTAAATGAATATTTATCCCTAATACTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTTGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAAACTTCAG 1051  
BY794942.2 1445 ..... 1594  
DC527884.1 1447 ..... C ..... 1596  
AL541984.3 713 ..... 862  
BX440470.1 293 ..... 144  
BX420402.2 290 ..... 141  
BX440308.2 293 ..... 144  
BX440436.2 296 ..... 147  
BX325185.1 292 ..... 143  
BX440303.2 292 ..... 143  
BX418589.2 293 ..... 144

Query 1052 AAGGAAAGGAGAATGTTTGTGGACCACtttggtttttcttttgcgtgtggcagttttaagttattagtttttaaaatcagtactttttaATGGAAACAACCTTGACCAAAAATTTGTCACAGAAATTTTGAGACCCATTAAAAAAGTTAAA 1201  
BY794942.2 1595 ..... 1745

DC527884.1 1597 ..... 1747  
AL541984.3 863 ..... K.S ..... 1014  
BX440470.1 143 ..... 1  
BX420402.2 140 ..... 1  
BX440308.2 143 ..... 1  
BX440436.2 146 ..... N ..... 1  
BX325185.1 142 ..... N ..... 1  
BX440303.2 142 ..... 1  
BX418589.2 143 ..... D ..... 1

Query 1202 TG 1203  
BY794942.2 1746 .. 1747  
DC527884.1 1748 .. 1749  
AL541984.3 1015 .. 1016

Query= T5-24 [organism=Homo sapiens] eef1a1

Length=822

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
CR979370.1	CR979370 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	905	0.0	100%
CD522692.1	AGENCOURT_14354560 NIH_MGC_191 Homo sapiens cDNA cl...	905	0.0	100%

BU581210.1 in37g01.x1 Human Fetal Pancreas 1B Homo sapiens cDN... 905 0.0 100%  
BU532443.1 AGENCOURT\_10200888 NIH\_MGC\_126 Homo sapiens cDNA cl... 905 0.0 100%  
BU158477.1 AGENCOURT\_7937274 NIH\_MGC\_92 Homo sapiens cDNA clon... 905 0.0 100%  
BM993568.1 UI-H-DT0-avj-h-01-0-UI.s1 NCI\_CGAP\_DT0 Homo sapiens... 905 0.0 100%  
AU147847.1 AU147847 MAMMA1 Homo sapiens cDNA clone MAMMA100186... 905 0.0 100%  
BE677612.1 7d88f01.x1 Lupski\_dorsal\_root\_ganglion Homo sapiens... 905 0.0 100%  
CN389382.1 17000600087635 GRN\_PRENEU Homo sapiens cDNA 5', mRN... 904 0.0 100%  
CX868104.1 HESC4\_26\_d10.b1\_A037 NIH\_MGC\_262 Homo sapiens cDNA ... 902 0.0 100%

ALIGNMENTS

Query 333 TGATGCTGCCATTGTGTATATGGTTCTCGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCGTTTGTCTGTTGATATGAGACAGACAGTTGCGGTGGGTGTCAATCAAGCAGTGGACAAGAAGGCTGCTGG 482  
CR979370.1 235 ..... 384  
CD522692.1 74 ..... 223  
BU581210.1 492 ..... 343  
BU532443.1 85 ..... 234  
BU158477.1 256 ..... 405  
BM993568.1 508 ..... 359  
AU147847.1 492 ..... 343  
BE677612.1 501 ..... 352  
CN389382.1 145 ..... 294  
CX868104.1 515 ..... 366

Query 483 AGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTGTTGTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGA 632  
CR979370.1 385 ..... 534  
CD522692.1 224 ..... 373  
BU581210.1 342 ..... 193  
BU532443.1 235 ..... 384  
BU158477.1 406 ..... 555  
BM993568.1 358 ..... 209  
AU147847.1 342 ..... 193  
BE677612.1 351 ..... 202  
CN389382.1 295 ..... 444  
CX868104.1 365 ..... 216

Query 633 CTGGTTAATGATAACAATGCATCTGTAACCTTCAGAAGGAAAGGAGAATgtttttgtggaccactttgggtttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagttactttttaATGGAAACAACCTTGACCAAAAAT 782  
CR979370.1 535 ..... 684  
CD522692.1 374 ..... 523  
BU581210.1 192 ..... 43  
BU532443.1 385 ..... 534  
BU158477.1 556 ..... 705  
BM993568.1 208 ..... 59  
AU147847.1 192 ..... 43  
BE677612.1 201 ..... 52  
CN389382.1 445 ..... 594  
CX868104.1 215 ..... 66

Query 783 TTGTACAGAAATTTGAGACCCATTaaaaaaaGTTAAATG 822  
CR979370.1 685 ..... 724  
CD522692.1 524 ..... 563  
BU581210.1 42 ..... 3  
BU532443.1 535 ..... 574  
BU158477.1 706 ..... 745  
BM993568.1 58 ..... 19  
AU147847.1 42 ..... 3  
BE677612.1 51 ..... 12  
CN389382.1 595 ..... 633  
CX868104.1 65 .....N.. 26

Query= T6-31 [organism=Homo sapiens] eef1a1

Length=1168

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	1855	0.0	99%
DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog...	1847	0.0	99%
BX440470.1 BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1832	0.0	99%
AL541984.3 AL541984 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1831	0.0	99%
BX418589.2 BX418589 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1829	0.0	99%
BX442182.2 BX442182 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1823	0.0	99%
BX459625.2 BX459625 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1818	0.0	100%
BX420340.1 BX420340 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1816	0.0	99%
BX418564.2 BX418564 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1814	0.0	99%
BX325185.1 BX325185 Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1810	0.0	99%

ALIGNMENTS

Query 1 TGGTGTGTTGTAATTTGAAGCTGGTATCTCCAAGAAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTAAACAAATGGATTCCACTGAGCCACCTACAGCCAGAGAGATATGA 150  
BY794942.2 723 ..... 723

BY794942.2	421	.....	570
DC527884.1	726	.....	726
DC527884.1	424	.....	573
BX440470.1	1015	.....	1015
BX418589.2	1014	.....	1014
BX442182.2	1007	.....	1007
BX459625.2	1002	.....	1002
BX420340.1	1008	.....	1008
BX418564.2	1013	.....	1013
BX325185.1	1013	.....	1013
Query	151	GGATGGCAATGCCAGTGGGAACACGCTGCTTGAGGCTCTGGACTGCATCCTACACCAACTCGTCCAACCTGACAAGCCCTTGCGCCTGCCTCTCCAGGATGCTACAAAAATTGGTGATTGGTACTGTTCTGTTGGCCGAGTGGAGACT	300
BY794942.2	724	.....	874
		C	
BY794942.2	571	...	573
DC527884.1	727	.....	877
		C	
DC527884.1	574	...	576
BX440470.1	1014	.....R.....	864
		C	
AL541984.3	1	.....	143
		C	
BX418589.2	1013	.....	863
		C	
BX442182.2	1006	.....R...	856
		C	
BX459625.2	1001	.....	851
		C	
BX420340.1	1007	.....A.....R.....	857
		C	
BX418564.2	1012	.....C.....	862
		C	
BX325185.1	1012	.....K.R.M.....K.....A.....R.....	862
		C	
Query	301	GGTGTCTCTCAAACCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGAAGTAAATCTGTGCAAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTCAATGTCAAGATGTGTCTGTCAAGGATGT	450
BY794942.2	875	.....	1026
		C	
DC527884.1	878	.....	1029
		G	
BX440470.1	863	.....	712
		G	
AL541984.3	144	.....	295
		G	
BX418589.2	862	.....	711
		G	
BX442182.2	855	.....	704
		G	
BX459625.2	850	.....	699
		G	

BX420340.1	856	.....	I C	.....	I G	.....	705
BX418564.2	861	.....	I C	.....	I G	.....C.....	710
BX325185.1	861	.....	I C	.....	I G	.....	710
Query	451	TCGTCGTGGCAACGTTGCTGGTGACAGCAAAAAATGACCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCA				600	
BY794942.2	1027	.....	I C	.....	I G	.....	1179
DC527884.1	1030	.....	I C	.....	I G	.....	1181
BX440470.1	711	.....	I C	.....	I C	.....	560
AL541984.3	296	.....	I C	.....	I C	.....	447
BX418589.2	710	.....	I C	.....	I C	.....	559
BX442182.2	703	.....	I C	.....	I C	.....	552
BX459625.2	698	.....	I C	.....	I C	.....	547
BX420340.1	704	.....	I C	.....	I C	.....	553
BX418564.2	709	.....	I C	.....	I C	.....	558
BX325185.1	709	.....	I C	.....	I C	.....Y.....	558
Query	601	AGTTTGCTGAGCTGAAGGAAAAAGATTGATCGCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTT				750	
BY794942.2	1180	.....	I C	.....	I C	.....	1329
DC527884.1	1182	.....	I C	.....	I C	.....	1331
BX440470.1	559	.....	I C	.....	I C	.....	409
AL541984.3	448	.....	I C	.....	I C	.....	597
BX418589.2	558	.....Y.S.....	I C	.....	I C	.....	409
BX442182.2	551	.....	I C	.....	I C	.....	402
BX459625.2	546	.....	I C	.....	I C	.....	397
BX420340.1	552	.....	I C	.....	I C	.....	403
BX418564.2	557	.....M.....	I C	.....	I C	.....	408
BX325185.1	557	.....	I C	.....	I C	.....	408
Query	751	TGGGTCGCTTTGCTGTTCTGATATGAGACAGACAGTTTGGGTGGGTGTCATCAAAGCAGTGGAAGAAGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCA				900	
BY794942.2	1330	.....	I C	.....	I C	.....	1479
DC527884.1	1332	.....A.....	I C	.....	I C	.....	1481
BX440470.1	408	.....	I C	.....	I C	.....	259
AL541984.3	598	.....	I C	.....	I C	.....	747
BX418589.2	408	.....	I C	.....	I C	.....	259
BX442182.2	401	.....	I C	.....	I C	.....	252
BX459625.2	396	.....	I C	.....	I C	.....	247
BX420340.1	402	.....	I C	.....	I C	.....	253
BX418564.2	407	.....	I C	.....	I C	.....	258

BX325185.1 407 ..... 258

Query 901 CCCCACTCTTAATCAGTGGTGAAGAAGCGTCTCAGAACTGTTTGTTCATTTGGCCATTTAAGTTTAGTAGTAAAAAGACTGGTAAATGATAACAATGCATCGTAAACCTTCAGAAGGAAGGAGAAATgttttggaccactttggtt 1050

BY794942.2 1480 ..... 1629

DC527884.1 1482 .....C..... 1631

BX440470.1 258 ..... 109

AL541984.3 748 ..... 897

BX418589.2 258 ..... 109

BX442182.2 251 ..... 102

BX459625.2 246 ..... 97

BX420340.1 252 ..... 103

BX418564.2 257 ..... 108

BX325185.1 257 ..... 108

Query 1051 ttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagtagctttttaatGGAACAACACTTGACCAAAAATTTGTCAAGAAATTTTGAGACCCATTAAAAAGTTAAATG 1168

BY794942.2 1630 ..... 1747

DC527884.1 1632 ..... 1749

BX440470.1 108 ..... 1

AL541984.3 898 .....K.S..... 1016

.....M.....D..... 1

..... 1

.....R..... 1

.....M..... 1

BX325185.1 107 ..... 1

Query= T7-25 [organism=Homo sapiens] eef1a1

Length=1553

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	2710	0.0	100%
DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog...	2693	0.0	100%
BX426149.2 BX426149 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2146	0.0	99%
CO001006.1 OC028 pre-oestrus adult sheep ovary library Ovis ar...	2050	0.0	93%
BX418564.2 BX418564 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2047	0.0	97%
CF111220.1 Shultzomica04471 Rat lung airway and parenchyma cDN...	2034	0.0	92%
AL567209.3 AL567209 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2001	0.0	98%
BX440470.1 BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1999	0.0	98%
BX420340.1 BX420340 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1997	0.0	99%
AL518238.2 AL518238 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1993	0.0	98%

# ALIGNMENTS

Query 2 TTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCTGTGAAAACATACCCCTAAAGCCAAATGGGAAGGAAAAGACTCATATCACCATTGATATCTCCTTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCC 151

BY794942.2 277 ..... 344

BY794942.2 25 .....A..... 98

DC527884.1 280 .....T..... 347

DC527884.1 9 .....A..... 101

CO001006.1 1464 .....T.C..... 1428

CF111220.1 273 .....T....C....C.....G..... 340

Query 152 CAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGCGTGACTGTGCTGCTCTGTTGTTGCTGCTGTTGGTGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACAC 301

BY794942.2 345 ..... 494

DC527884.1 348 .....C..... 497

CO001006.1 1427 .....C....C....C.....C.....T..... 1278

CF111220.1 341 .....C....G....G..C.....C.....G.....C.....T.....T.....TT 490

Query 302 TGGGTGTGAAACAACATAATTGTCGGTGTTAACAAATGGATTCCACTGAGCCACCCCTACAGCCAGAGAGATATGAGGAAATTTGTTAAGGAAGTCAGCACTTACATTAGAAAATTTGGCTACACCCCGACACAGTAGCATTGTGCGCAA 451

BY794942.2 495 ..... 644

DC527884.1 498 ..... 647

BX426149.2 1196 .....A.....A.....G..... 1082

CO001006.1 1277 .....T.....C.....T.....C.....C..... 1128

BX418564.2 1196 .....YH.VS...-R.....W.-G..W...-R.....M.....K.....R.....S.....-R..... 1089

CF111220.1 491 .....G.....T.....C.....C.....A.....T.....C.....C.....T..... 640

AL567209.3 1145 .....S.....W.....-K.W.....R.....A.M.C.....C..... 1052

.....M.....

.....W.....S.M. 1091

.....C.....

.....M.....K.-.M. 1086

.....R.....M.....W..M..V.M..... 1087



Query	452	TTTCTGGTTGGAATGGTGACAACTGCTGGAGCCAAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCACGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACGT	601
BY794942.2	645	.....	784
DC527884.1	648	.....	797
BX426149.2	1081	.....	932
CO001006.1	1127	.....C.....T.....A.....C.....A.....T.....G.....C.....	978
BX418564.2	1088	.....C.....T.....A.....C.....A.....T.....G.....C.....	942
CF111220.1	641	.....T.....G.....C.....A.....G.....C.....G.....A.....T.....T.....G.....G.....	790
AL567209.3	1051	.....K.....	902
BX440470.1	1090	.....Y.....K.....	944
BX420340.1	1085	W.....Y.....T.....D.....K.....T.....Y.....	937
AL518238.2	1086	.....K.....A.....A.....W.....R.....A.....	937
		.....\..... ..... ..... .....A.....	
Query	602	ACAAGCCCTTGGCGCTGCCTCTCCAGGATGCTACAAAAATTGGTGGTATTGGTACTGTTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAAACCCGGTATGGTGGTCACTTTTGCTCCAGTCAACGTTACACGGGAAGTAAAACTCTGTGC	751
BY794942.2	795	.....	944
DC527884.1	798	.....	947
BX426149.2	931	.....	782
CO001006.1	977	.....A.....TT.....T.....A.....G.....T.....T.....T.....C.....C.....T.....A.....T.....G.....G.....C.....A.....	828
BX418564.2	941	.....C.....	792
CF111220.1	791	.....TC.....A.....C.....T.....C.....C.....C.....C.....G.....A.....T.....T.....T.....A.....T.....C.....G.....G.....	940
AL567209.3	901	.....	752
BX440470.1	943	.....	794
BX420340.1	936	.....W.....B.....W.....	787
AL518238.2	936	.....	787
Query	752	AAATGCACCATGAAGCTTTGAGTGAAGCTTCTCCTGGGGACAATGGGGCTTCAATGTCAAGAAATGTGCTGTCAAGGATGTTCTGCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGC	901
BY794942.2	945	.....	1094
DC527884.1	948	.....	1097
BX426149.2	781	.....	632
CO001006.1	827	.....C.....C.....A.....C.....T.....G.....T.....C.....T.....C.....A.....	678
BX418564.2	791	.....	642
CF111220.1	941	.....G.....A.....C.....A.....C.....A.....C.....A.....A.....T.....G.....	1090
AL567209.3	751	.....	603
BX440470.1	793	.....	644
BX420340.1	786	.....	637
AL518238.2	786	.....A.....G.....	637
Query	902	AGGTGATTATCTCGAACCATCCAGGCCAAATAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATGCGATGCAAGTTTGTCTGAGCTGAAGGAAAGATTGATCGCCGTTCTGGTAAAAGCTGGAAGATGGCCCTAAAT	1051
BY794942.2	1095	.....	1245
		.....\..... ..... ..... .....G.....	
DC527884.1	1098	.....	1247
BX426149.2	631	.....T.....C.....T.....GT.....A.....A.....GC.....T.....A.....T.....G.....T.....G.....	482
CO001006.1	677	.....	528
BX418564.2	641	.....	492
CF111220.1	1091	.....G.....C.....T.....T.....TC.....C.....C.....A.....C.....T.....A.....G.....C.....T.....G.....C.....	1240
AL567209.3	602	.....	453
BX440470.1	643	.....	493
		.....\..... ..... ..... .....C.....	
BX420340.1	636	.....Y.....	487
AL518238.2	636	.....	487
Query	1052	TCTTGAAGCTCTGGTGATGCTGCCATTGTGATATGGTTCTGGCAAGCCCATGTGTGTGAGAGCTTCTCAGACTATCCACCTTTGGTGCCTTTGTCTGTTCTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAGCAGTGGACA	1201
BY794942.2	1246	.....	1395
DC527884.1	1248	.....	1397
BX426149.2	481	.....	332
CO001006.1	527	.....A.....C.....C.....T.....C.....T.....T.....T.....T.....C.....C.....T.....G.....C.....C.....T.....	378
BX418564.2	491	.....	342
CF111220.1	1241	.....C.....C.....A.....T.....C.....T.....AC.....T.....T.....C.....G.....T.....C.....	1390
AL567209.3	452	.....K.....	303
BX440470.1	492	.....	343
BX420340.1	486	.....	337
AL518238.2	486	.....	337
Query	1202	AGAAGGCTGCTGGAGCTGGCAAGGTCCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAAGCGGTCTCAGAACTGTTGTTTCAATTGGCCATTTAAGTT	1351
BY794942.2	1396	.....	1545
DC527884.1	1398	.....	1547
BX426149.2	331	.....	182
CO001006.1	377	.....A.....	228
BX418564.2	341	.....	192
CF111220.1	1391	.....A.....A.....C.....G.....	1540
AL567209.3	302	.....M.....Y.....	152
		.....\..... ..... ..... .....A.....	
BX440470.1	342	.....	193
BX420340.1	336	.....	181

AL518238.2	336	.....G.....	187
Query	1352	TAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAGGAAAGGAGAAATgttttgtggaccactttggttttttttgcgtgtggcagttttaagttattagtttttaaaatcagttacttttaATGGAAACAA	1501
BY794942.2	1546	.....	1695
DC527884.1	1548	.....	1697
BX426149.2	181	.....A.....	33
CO001006.1	227	.....A.....	87
		\   T	
BX418564.2	191	.....	42
CF111220.1	1541	.....A.....	1679
AL567209.3	151	.....	4
		\   G	
BX440470.1	192	.....	43
BX420340.1	186	.....	37
AL518238.2	186	.....	37
		\   A	
Query	1502	CTTGACCAAAAATTGTGCACAGAATTTTGAGACCCATTAAGTAAATG	1553
BY794942.2	1696	.....	1747
DC527884.1	1698	.....	1749
BX426149.2	32	.....G.....G.....T..	1
CO001006.1	86	.....C.....T..	35
		\   A	
BX418564.2	41	.....M.....	1
CF111220.1	1680	.....C.....T..	1731
		\   C	
AL567209.3	3	....	1
BX440470.1	42	.....	1
BX420340.1	36	.....R.....	1
AL518238.2	36	.....N.....	1
		\   N	

Query= T8-26 [organism=Homo sapiens] eef1a1  
Length=1631

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	1724	0.0	100%
AL541952.3	AL541952	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1716	0.0	100%
AL559705.3	AL559705	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1711	0.0	100%
AL557904.3	AL557904	Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1711	0.0	100%
AL536241.3	AL536241	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1711	0.0	100%
BX459223.2	BX459223	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1711	0.0	100%
BX459080.2	BX459080	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1711	0.0	100%
BX417904.2	BX417904	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1711	0.0	100%
BX417296.2	BX417296	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1711	0.0	100%
BX440304.2	BX440304	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1707	0.0	100%

ALIGNMENTS				
Query	2	TTTTTCGCAACGGGTTTGCCGCCAGACACAGGTGTCGTGAAAACTACCCCTAAAAAGCCAAAATGGGAAGGAAAAAGACTCATATCAACATTGTCGTGATTGGACACGTAGATTGGGCAAGTCCACCCTACTGCCCTCTGATCTAT	151	
DC527884.1	9	.....	157	
AL541952.3	1	.....A.....	139	
AL559705.3	1	.....A.....	139	
AL557904.3	1	.....A.....	139	
AL536241.3	1	.....A.....	139	
BX459223.2	1	.....A.....	139	
BX459080.2	1	.....A.....	139	
BX417904.2	1	.....A.....	139	
BX417296.2	1	.....A.....	139	
BX440304.2	1	.....A.....	139	
Query	152	AAATGCGGTGGCATCGACAAAAGAACCATTTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGCTCCTTCAAGTATGCTGGGTCTTGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCTTGTGGAAA	301	
DC527884.1	158	.....T.....	307	
AL541952.3	140	.....	289	
AL559705.3	140	.....	289	
AL557904.3	140	.....	289	
AL536241.3	140	.....	289	
BX459223.2	140	.....	289	
BX459080.2	140	.....	289	

BX417904.2	140	.....	289
BX417296.2	140	.....	289
BX440304.2	140	.....	289
Query	302	TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTTATCAAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTGATTGTTGCTGCTGGTGGTGAATTTGAAGCTGGTATCTCCAAG	451
DC527884.1	308	.....C.....	457
AL541952.3	290	.....	439
AL559705.3	290	.....	439
AL557904.3	290	.....	439
AL536241.3	290	.....	439
BX459223.2	290	.....	439
BX459080.2	290	.....	439
BX417904.2	290	.....	439
BX417296.2	290	.....	439
BX440304.2	290	.....	439
Query	452	AATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCCCTACAGCCAGAAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAAG	601
DC527884.1	458	.....	607
AL541952.3	440	.....	589
AL559705.3	440	.....	589
AL557904.3	440	.....	589
AL536241.3	440	.....	589
BX459223.2	440	.....	589
BX459080.2	440	.....	589
BX417904.2	440	.....	589
BX417296.2	440	.....	589
BX440304.2	440	.....	589
Query	602	AAAATTGGCTACAAACCCGACACAGTAGCATTGTGCCAATTTCTGGTTGGAATGGTGACACATGCTGGAGCCAGTGTAAACATGCCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCGCTGCTT	751
DC527884.1	608	.....	757
AL541952.3	590	.....	739
AL559705.3	590	.....	739
AL557904.3	590	.....	739
AL536241.3	590	.....	739
BX459223.2	590	.....	739
BX459080.2	590	.....	739
BX417904.2	590	.....	739
BX417296.2	590	.....	739
BX440304.2	590	.....	740
\			
T			
Query	752	GAGGCTCTGGACTGCATCTTACCACCAACTCGTCCAACCTGACAAGCCCTTGGCGCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGTGTTCCTCAAAACCCGGTATGGTGGTCACC	901
DC527884.1	758	.....	907
AL541952.3	740	.....	889
AL559705.3	740	.....	889
AL557904.3	740	.....	889
AL536241.3	740	.....	889
BX459223.2	740	.....	889
BX459080.2	740	.....	889
BX417904.2	740	.....	889
BX417296.2	740	.....	889
BX440304.2	741	.....	890
Query	902	TTTGCTCCAGTCAACGTTTACAACGGAAGTAAATCTGTGAAAATGACCCCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCT	1051
DC527884.1	908	.....	950
DC527884.1	1059	.....	1168
AL541952.3	890	.....	935
AL559705.3	890	.....	932
AL557904.3	890	.....	932
AL536241.3	890	.....	932
BX459223.2	890	.....	932
BX459080.2	890	.....	932
BX417904.2	890	.....	932
BX417296.2	890	.....	932
BX440304.2	891	.....	933
Query	1052	CACATTGCATGCAAGTTTGTGAGCTGAAGGAAAAGATTGATCGCCGTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTTCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTTGGCAAGCCCATGTGTGTGAGAGCTTTCTCA	1201
DC527884.1	1169	.....	1318
Query	1202	GACTATCCACCTTTGGGTGCTTTTGTGTTCTGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCAGTGGCAAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCC	1351
DC527884.1	1319	.....A.....	1468
Query	1352	CTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAAGCTTTGTTTCAATTGGCCATTAAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAATgtttttgtg	1501
DC527884.1	1469	.....C.....	1618
Query	1502	gaccactttgggttttcttttttgcgtgtggcagttttaagtattagttttttaaatcagtactttttaATGGAAACAACCTTGACCAAAAATTTGTACAGAATTTTGAGACCCATTAAAAAGTTAAAT	1631
DC527884.1	1619	.....	1748

Query= T9-28 [organism=Homo sapiens] eef1a1

Length=1433

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	1969	0.0	100%
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	1945	0.0	100%
DC629953.1	DC629953	macaque bone marrow cDNA library QbmA Maca...	1941	0.0	96%
BX426072.2	BX426072	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1910	0.0	100%
FS580102.1	FS580102	macaque heart cDNA library QhtB Macaca fas...	1906	0.0	99%
BX440468.2	BX440468	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1905	0.0	99%
BX440573.2	BX440573	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1903	0.0	100%
BX426150.2	BX426150	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1899	0.0	99%
BX402793.2	BX402793	Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1899	0.0	99%
AL528506.3	AL528506	Homo sapiens NEUROBLASTOMA COT 25-NORMALIZ...	1897	0.0	99%

ALIGNMENTS

Query	1	CTTTTTCGCAACGGGTTTGC	CGCCAGAACACAGGTGTCGTGAA	AACTACCCCTAAAAAGCCAAAATGGGAAAGGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATT	CGGGCAAGTCCACCACTACTGGCCATCTGATCTA	150
DC527884.1	9	.....	.....	.....	.....	156
BY794942.2	25	.....	.....	.....	.....	153
DC629953.1	1	.....	.....	.....	.....	149
BX426072.2	1	.....	.....	.....	.....	119
FS580102.1	1	.....	.....	.....	.....	149
BX440468.2	1	.....	.....	.....	.....	128
BX440573.2	1	.....	.....	.....	.....	119
BX426150.2	1	.....T.....	.....	.....	.....	124
BX402793.2	6	.....	.....	.....	.....	137
AL528506.3	1	.....	.....	.....	.....	119
Query	151	TAAATGCGGTGGCATCGACAAA	AGAACCATTTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTC	TTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAA	300	
DC527884.1	157	.....	.....	.....T.....	.....	306
BY794942.2	154	.....	.....	.....	.....	303
DC629953.1	150	C.....	.....	.....G.....	.....	299
BX426072.2	120	.....	.....	.....	.....	269
FS580102.1	150	C.....	.....	.....G.....	.....	299
BX440468.2	129	.....	.....	.....	.....	278
BX440573.2	120	.....	.....	.....	.....	269
BX426150.2	125	.....	.....	.....	.....	274
BX402793.2	138	.....	.....	.....	.....	287
AL528506.3	120	.....	.....	.....	.....	269
Query	301	ATTTGAGACCAGCAAGTACTATGT	GACTATCATTGATGCCCCAGGACACAGAGACTTTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGCTCCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAA	450		
DC527884.1	307	.....	.....C.....	.....	.....	456
BY794942.2	304	.....	.....	.....	.....	453
DC629953.1	300	.....T.....	.....C.....	.....	.....	449
BX426072.2	270	.....	.....	.....	.....	419
FS580102.1	300	.....T.....	.....C.....	.....	.....	449
BX440468.2	279	.....	.....	.....	.....	428
BX440573.2	270	.....	.....	.....	.....	419
BX426150.2	275	.....	.....	.....	.....	424
BX402793.2	288	.....	.....	.....	.....	437
AL528506.3	270	.....	.....	.....	.....	419
Query	451	GAATGGGCAGACCCGAGAGCATGCC	CTTCTGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAGAGATATGAGGAAATTTGTTAAGGAAGTCAGCACTTACATTAA	600		
DC527884.1	457	.....	.....	.....	.....	606
BY794942.2	454	.....	.....	.....	.....	603
DC629953.1	450	.....T.....	.....	.....T.....	.....C.....C.....	599
BX426072.2	420	.....	.....	.....	.....	569
FS580102.1	450	.....T.....	.....	.....T.....	.....C.....	599
BX440468.2	429	.....	.....	.....	.....C.....	578
BX440573.2	420	.....	.....	.....	.....	569
BX426150.2	425	.....	.....	.....	.....	574
BX402793.2	438	.....	.....	.....	.....	587
AL528506.3	420	.....	.....	.....	.....	569
Query	601	GAAATTTGGCTACAACCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAAGTGCTAACATGCCCTTG	TTTCAAGGGATGGAAGTCAACCGTAAGGATGGCAATGCCAGTGGAAACCAAGCTGCT	750		
DC527884.1	607	.....	.....	.....	.....	756
BY794942.2	604	.....	.....	.....	.....	753
DC629953.1	600	.....	.....	.....	.....G.....	749
BX426072.2	570	.....	.....	.....	.....	719
FS580102.1	600	.....	.....	.....	.....G.....	749
BX440468.2	579	.....	.....	.....	.....	727
BX440573.2	570	.....	.....	.....	.....	719
BX426150.2	575	.....	.....	.....	.....	724
BX402793.2	588	.....	.....	.....	.....	737
AL528506.3	570	.....	.....	.....	.....	719
Query	751	TGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAATGACAAGCCCTTGC	GCTGCCCTCCAGGATGTTCTACAAAATTTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCAC	900		
DC527884.1	757	.....	.....	.....	.....	906
BY794942.2	754	.....	.....	.....	.....	903



BX442182.2	BX442182	Homo sapiens	FETAL BRAIN	Homo sapiens cDNA...	1871	0.0	100%
BX459625.2	BX459625	Homo sapiens	FETAL BRAIN	Homo sapiens cDNA...	1866	0.0	100%
BX420340.1	BX420340	Homo sapiens	FETAL BRAIN	Homo sapiens cDNA...	1864	0.0	100%
BX418564.2	BX418564	Homo sapiens	FETAL BRAIN	Homo sapiens cDNA...	1862	0.0	99%
BX440436.2	BX440436	Homo sapiens	FETAL BRAIN	Homo sapiens cDNA...	1857	0.0	99%
AL541984.3	AL541984	Homo sapiens	PLACENTA	Homo sapiens cDNA cl...	1855	0.0	100%

ALIGNMENTS

Query	2	TTTTTCGCAACGGGTTTGCCGCCAGACACAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAGGAAAGACTCATATCAACATTGTCGTCTTGGACACGTAGATTGGGCAAGTCCACCACTACTGGCCATCTGATCTATA	151
BY794942.2	25	.....	155
DC527884.1	9	.....	158
Query	152	AATGCGGTGGCATCGACAAAAGAACATTGAAAAATTTGAGAAGGAGCGTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGTCTTGATAAACTGAAAGCTGAGCGTGAACTGGTATCACCATTGATATCTCCTTGTGGAATTT	301
BY794942.2	156	.....	306
DC527884.1	159	.....G.....T.....	309
Query	302	TGAGACAGCAAGTACTATGTGACTATCATTGATGCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTGATTGTGTCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAGAAATG	451
BY794942.2	307	.....	458
DC527884.1	310	.....C.....	461
Query	452	GGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTAAACAAATGGATTCCACTGAGCCACCTTACAGCCAGAAGATATGAGGAAATTGTTAAGGAAGTCAaaaaaaaaaaaaaaaa	601
BY794942.2	459	.....	590
DC527884.1	462	.....	593
Query	602	aaaaaaaaaaaaaaaaTTGTTAAAGGAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACACCGTGCTTGAGGCTCTGGACTGCATCCTACCACTCGTCCAAGTCAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATT	751
BY794942.2	711	.....	835
DC527884.1	714	.....	838
BX440470.1	1027	.....R.....	903
BX418589.2	1026	.....	902
BX442182.2	1019	.....	895
BX459625.2	1014	.....	890
BX420340.1	1020	.....A.....R.....C.....	896
BX418564.2	1025	.....	901
BX440436.2	1026	.....-YK.....R.....	905
AL541984.3	1	.....	104
Query	752	GGTGGTATTGGTACTGTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAAACCCGATGTTGGTGGTCACCTTTTGCTCCAGTCAACGTTACAACGGAAGTAAATCTGTGAAATGCACATGAAGCTTTGAGTGAAGCTCTTCTTGGGGAC	901
BY794942.2	836	.....	985
DC527884.1	839	.....	988
BX440470.1	902	.....	753
BX418589.2	901	.....	752
BX442182.2	894	.....R.....	745
BX459625.2	889	.....	740
BX420340.1	895	.....	746
BX418564.2	900	.....	751
BX440436.2	904	.....	755
AL541984.3	105	.....	254
Query	902	AATGTGGGCTTCAATGTCAGAATGTGTCTGTCAAGGATGTTCTGCTGGCAACGTTGCTGGTGACAGCAAAATGACCCCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCTGAACCATCCAGGCCAAATAAGCGCCGCGC	1051
BY794942.2	986	.....	1136
DC527884.1	989	.....G.....	1138
BX440470.1	752	.....	603
BX418589.2	751	.....	602
BX442182.2	744	.....	595
BX459625.2	739	.....	590
BX420340.1	745	.....	596
BX418564.2	750	.....C.....	601
BX440436.2	754	.....	605
AL541984.3	255	.....	404
Query	1052	TATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAGATTGATCGCCGTTCTGGTAAAAGCTGGAAGATGGCCCTAAATTCCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTCT	1201
BY794942.2	1137	.....	1286
DC527884.1	1139	.....	1288
BX440470.1	602	.....	452

BX418589.2	601	.....C.....Y.S.....	452
BX442182.2	594	.....	445
BX459625.2	589	.....	440
BX420340.1	595	.....	446
BX418564.2	600	.....M.....	451
BX440436.2	604	.....	455
AL541984.3	405	.....	554
Query	1202	GGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGGCTTTGCTGTTGCGTATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAG	1351
BY794942.2	1287	.....	1436
DC527884.1	1289	.....A.....	1438
BX440470.1	451	.....	302
BX418589.2	451	.....	302
BX442182.2	444	.....	295
BX459625.2	439	.....	290
BX420340.1	445	.....	296
BX418564.2	450	.....	301
BX440436.2	454	.....	305
AL541984.3	555	.....	704
Query	1352	AAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAA	1501
BY794942.2	1437	.....	1586
DC527884.1	1439	.....C.....	1588
BX440470.1	301	.....	152
BX418589.2	301	.....	152
BX442182.2	294	.....	145
BX459625.2	289	.....	140
BX420340.1	295	.....	146
BX418564.2	300	.....	151
BX440436.2	304	.....	155
AL541984.3	705	.....	854
Query	1502	ACCTTCAGAAGGAAAGGAGAATgttttggaccactttgggttttttttttgcgtgtggcagttttaagttattagtttttaaaatcagtaactttttaATGGAACAACCTTGACCAAAAATTTGTACAGAATTTTGAGACCCATTAAAA	1651
BY794942.2	1587	.....	1737
		\	
		C	
DC527884.1	1589	.....	1739
		\	
		C	
BX440470.1	151	.....	1
		\	
		C	
BX418589.2	151	.....D.....	1
		\	
		C	
BX442182.2	144	.....	1
		\	
		C	
BX459625.2	139	.....	1
		\	
		C	
BX420340.1	145	.....R.....	1
		\	
		C	
BX418564.2	150	.....M.....	1
		\	
		C	
BX440436.2	154	.....	3
		\ \	
		N N	
AL541984.3	855	.....K.S.....	1006
		\ \	
		C M	
Query	1652	AAGTTAAAT	1660
BY794942.2	1738	.....	1746
DC527884.1	1740	.....	1748
BX440436.2	2	..	1
AL541984.3	1007	.....	1015

Query= T11-30 [organism=Homo sapiens] eef1a1

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
AU120002.1	AU120002 HEMBA1 Homo sapiens cDNA clone HEMBA100713...	1356	0.0	99%
CJ434202.1	CJ434202 macaque brain cDNA library QccE Macaca fas...	1216	0.0	96%
CR976939.1	CR976939 RZPD no.9016 Homo sapiens cDNA clone RZPdp...	1149	0.0	99%
CB138394.1	K-EST0191255 L15CKK1 Homo sapiens cDNA clone L15CKK...	1064	0.0	97%
GR891610.1	CANFLECK JINDO BR_55_A03.abl Jindo brain cDNA libra...	1035	0.0	92%
DC519934.1	DC519934 chimpanzee brain cDNA library PccB Pan tro...	996	0.0	97%
AU296783.1	AU296783 female adult cerebellum, full-length enric...	996	0.0	97%
CD466199.1	LeukoN2_2_E07.g1_A024 Unstimulated peripheral blood...	955	0.0	91%
AU144980.1	AU144980 HEMBA1 Homo sapiens cDNA clone HEMBA100353...	935	0.0	95%
DA429743.1	DA429743 COLON2 Homo sapiens cDNA clone COLON200583...	926	0.0	97%

ALIGNMENTS

Query	3	TTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAACACTACCCTAAAAGCCAAATGGGAAGGAAAGAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAGTCCACCACACTACTGCCCATCTGATCTATA	152
AU120002.1	2	.....	151
CJ434202.1	30	.....	177
CR976939.1	1	.....	33
CB138394.1	1	.....	4
GR891610.1	1	.....C...G....A.....G.....C.....C.....T.....T.....C.	144
		\ \	
		CCC	
		T	
DC519934.1	2	.....N.....	151
AU296783.1	2	.....N.....	151
CD466199.1	2	.....C.....AA.....G.....C.....G.....C.....G.....C.....C.	155
		\ \	
		AA \	
		TCT	
DA429743.1	2	.....	151
Query	153	AATGCGGTGGCCTCGACAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTAGCCTGGGTCCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAAT	302
AU120002.1	152	.....G.....	301
CJ434202.1	178	.....T.....G.....	327
CR976939.1	34	.....	183
CB138394.1	5	.....	154
GR891610.1	145	...T...G...T.C...A.....	294
DC519934.1	152	.....A.....C.....	301
AU296783.1	152	.....T.....	301
CD466199.1	156	.G.....G.....C.G.....C.....A.....G.....C.....	305
DA429743.1	152	.....	302
		\	
		N	
Query	303	TTGAGACCAGCAAGTACTATTGTGACTATTATTGATGCCCCAGGCACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGGTGACTGTGCTGTCTGATTGTGTGCTGCTGGTGTGGTGTCTCTCAAACCCGGTATTGGTGGTCA	452
AU120002.1	302	.....-----	445
CJ434202.1	328	.....C.....	471
CR976939.1	184	.....-----	327
CB138394.1	155	.....	319
GR891610.1	295	.C.....T..C...C.....C.....TGTTGAATTGAAGC.....C...C.-....G..T.....	438
DC519934.1	302	.....C.....	464
AU296783.1	302	.....C.....TGTTGTTGGAGAC.....	464
CD466199.1	306	.C.....T.....C.....C.....C.G.....C.....T.....T.....T.....T.....	449
DA429743.1	303	.....	467
		\ \ \	
		TT GGAGAC	
		C GCCG	
Query	453	CCTTTGCTCCAGTCAACGTTACAACGGAAGTAAATCTGTGAAATGCACCATGAAGCTTTAGTGAAGCTCTTCCTGGGACAAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCGTGGCAACGTTGCTGGTGACA	602
AU120002.1	446	.....	595
CJ434202.1	472	.....T.....	621
CR976939.1	328	.....	472



CB138394.1 320 ..... 469
GR891610.1 439 .....T.....T.....G.....T.....G.....C...A.....A.....T...G..... 588
DC519934.1 465 ..... 594
AU296783.1 465 ..... 594
CD466199.1 450 .....T.....T.....G.....T.....T.....C.....C.....C.....A.....C.....T...G..... 599
AU144980.1 594 ..... 576
DA429743.1 468 ..... 558
Query 603 GCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTGAGCTGAAGGAAAAA 752
AU120002.1 596 ..... 745
CJ434202.1 622 .....C.....G.....A...T.....T.....T...T.....GG.....AAT.....TG.....A..... 772
CR976939.1 478 ..... 627
CB138394.1 470 ..... 619
GR891610.1 589 .....A.....C...T...T...A.....A.....GC.....A...T...A.....CC.....A..... 736
CD466199.1 600 .....T.....A.....C...T...T...G.....A.....GC.....T...A.....T... 724
AU144980.1 575 .....N...N...A...N...N...T.....G.....G.....C.....N...T.....G...T.....T..... 419
Query 753 TTGATCGCTGTTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTATCAAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCA 902
AU120002.1 746 ..... 753
CJ434202.1 773 ..... 779
CR976939.1 628 .....C.... 640
CB138394.1 620 .....C.... 632
AU144980.1 418 ..... 264
Query 903 CTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTTAGTCTAGTAAAGACTGGTAAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAATgttttggaccactttgtttttctt 1052
AU144980.1 263 ..N.....C..... 114
Query 1053 ttttgcgtgtggcagttttaagtattagtttttaaaatcagtactttttaaTGGAACAACCTTGACCAAAAATTTGTACAGAAATTTTGAGACCCATTAAAAAGTTAAAT 1164
AU144980.1 113 ..... 2
Query= T12-29 [organism=Homo sapiens] eef1a1
Length=1240

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	2141	0.0	100%
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	2135	0.0	100%
BX426149.2	BX426149	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2091	0.0	99%
BX418564.2	BX418564	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2025	0.0	98%
BX459625.2	BX459625	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1988	0.0	98%
BX420340.1	BX420340	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1984	0.0	99%
BX440470.1	BX440470	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1980	0.0	98%
AL518238.2	AL518238	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1978	0.0	97%
AL567209.3	AL567209	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1975	0.0	98%
BX418589.2	BX418589	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1962	0.0	98%
ALIGNMENTS					
Query	2	TTTTTCGCAACGGGTTTTCGCCGCCAGACACAGGTGTCTGTGAAAACCTACCCCTAAAAGCCAAATGGGAAGGAAATTTGTTAAGGAAGTCAGCACTTACATTAGAAAAATTTGGCTACAACCCGACACAGTAGCATTTGTGCCAATTTCTG	151		
BY794942.2	570	.....	650		
BY794942.2	25	.....	80		
DC527884.1	573	.....	653		
DC527884.1	9	.....	83		
BX426149.2	1156	.....	1076		
BX418564.2	1153	..W...-R.....M.....K...-R...-S...-R...-K...	1083		
BX459625.2	1118	.....C.MCM...C.....K...W...-KS...-K	1076		
BX420340.1	1117	.....M..M.....K...M.W...YT	1080		
BX440470.1	1128	.....-W...-S.M...Y...-C.....V.M.....	1086		
AL518238.2	1148	.....R...-M...-W...M...V.M.....	1081		
AL567209.3	1125	.....-K.W.....R...-A.M.C.....C.....	1046		
BX418589.2	1130	.....-K...-W...-M...C...M.K...-S...-M	1084		

Query	152	GT TGAATGGTGACAACATGCTGGAGCCAAGTCTAACATGCCTTGGTCAAGGGATGAAAGTCACCCGTAAGGATGGCAATGCCAGTGAACCAACGCTGCTTGAGGCTCTGGA	301
BY794942.2	651	.....	800
DC527884.1	654	.....	803
BX426149.2	1075	.....	926
BX418564.2	1082	.....C.....	936
BX459625.2	1075	.....W.....K.A.....	925
		 T	
BX420340.1	1079	...D...K...T...Y.....A.....R.....	931
BX440470.1	1085	..K.....K.....R.....	938
AL518238.2	1080	-K.....A.....A.....W.....R.....	931
		 A	
AL567209.3	1045	.....K.....	896
BX418589.2	1083	.....-KK.....K.C.....	937
Query	302	CCTTGCCTGCCTCTCCAGGATGCTACAAAAATTGGTGGTATTGGTACTGTTCTGTGGCCGAGTGGAGACTGGTGTCTCAAAACCCGGTATGGTGGTCACTTTGCTCCAGTCAACGTTACACCGGAAGTAAAACTCTGTGAAATGC	451
BY794942.2	801	.....	950
DC527884.1	804	.....	953
BX426149.2	925	.....	776
BX418564.2	935	..C.....	786
BX459625.2	924	.....	775
BX420340.1	930	.....	781
BX440470.1	937	.....	788
AL518238.2	930	.....W.....B.....W.....	781
AL567209.3	895	.....	746
BX418589.2	936	.....	787
Query	452	ACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTCAATGTCAAGAAATGTGTCTGTCAAGGATGTTCTGTCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGA	601
BY794942.2	951	.....	1100
DC527884.1	954	.....	1103
BX426149.2	775	.....	626
BX418564.2	785	.....C.....	636
BX459625.2	774	.....	625
BX420340.1	780	.....	631
BX440470.1	787	.....	638
AL518238.2	780	.....A.....G.....	631
AL567209.3	745	.....	597
BX418589.2	786	.....	637
Query	602	TTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAGATTGATCGCCGTTCTGGTAAAAGCTGGAAGATGGCCCTAAATTCCTTGA	751
BY794942.2	1101	.....	1251
		 G	
DC527884.1	1104	.....	1253
BX426149.2	625	.....	476
BX418564.2	635	.....M.....	486
BX459625.2	624	.....	475
BX420340.1	630	.....	481
BX440470.1	637	.....	487
		 C	
AL518238.2	630	.....Y.....	481
AL567209.3	596	.....	447
BX418589.2	636	.....Y.S.....	487
Query	752	AGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGGTGGTTGTCAATCAAGCAGTGGACAAGAAGG	901
BY794942.2	1252	.....G.....	1401
DC527884.1	1254	.....G.A.....	1403
BX426149.2	475	.....G.....	326
BX418564.2	485	.....G.....	336
BX459625.2	474	.....G.....	325
BX420340.1	480	.....G.....	331
BX440470.1	486	.....G.....	337
AL518238.2	480	.....G.....	331
AL567209.3	446	.....K.....	297
BX418589.2	486	.....G.....	337
Query	902	CTGCTGGAGCTGGCAAGTCAACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTTGGCCATTTAAGTTTAGTAG	1051
BY794942.2	1402	.....	1551
DC527884.1	1404	.....C.....	1553
BX426149.2	325	.....	176
BX418564.2	335	.....	186
BX459625.2	324	.....	175
BX420340.1	330	.....	181
BX440470.1	336	.....	187
AL518238.2	330	.....G.....	181

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AL567209.3 296 .....M.....Y.....\
                                     |
                                     A
BX418589.2 336 .....187
Query      1052 TAAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGAGAAATgttttggaccactttggtttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagttacttttaATGGAACAACCTTGAC 1201
BY794942.2 1552 .....1701
DC527884.1 1554 .....1703
BX426149.2 175 .....28
BX418564.2 185 .....36
BX459625.2 174 .....25
BX420340.1 180 .....31
BX440470.1 186 .....37
AL518238.2 180 .....N.....31
AL567209.3 145 .....1
                                     \
                                     |
                                     G
BX418589.2 186 .....37
Query      1202 CAAAAATTTGTCACAGAAATTTTGACCCATTAAAAAAGTT 1240
BY794942.2 1702 .....1742
                                     \
                                     |
                                     GA
DC527884.1 1704 .....1744
                                     \
                                     |
                                     GA
BX426149.2 27  .G.....G-..G.....5
BX418564.2 35  .....M.....1
                                     \
                                     |
                                     A
BX459625.2 24  .....1
BX420340.1 30  .....7
BX440470.1 36  .....1
                                     \
                                     |
                                     GA
AL518238.2 30  .....N.....6
                                     \
                                     |
                                     N
BX418589.2 36  .....D.....1
                                     \
                                     |
                                     GA

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Query= T13-27 [organism=Homo sapiens] eef1a1

Length=1489

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	2163	0.0	100%
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	2134	0.0	100%
BX426150.2	BX426150	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2037	0.0	99%
BU902062.1	AGENCOURT_10127553	NIH MGC 71 Homo sapiens cDNA clo...	1997	0.0	98%
BX402801.2	BX402801	Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1988	0.0	98%
BX402793.2	BX402793	Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1973	0.0	98%
BX440468.2	BX440468	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1971	0.0	98%
AL513590.3	AL513590	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1967	0.0	97%
AL513664.3	AL513664	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1962	0.0	98%
AL560156.3	AL560156	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1960	0.0	98%

#### ALIGNMENTS

Query	2	TTTTTCGCAACGGGTTTGCCGCCAGACAGGTTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAGGAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAGTCCACCACTACTGGCCATCTGATCTATA	151
DC527884.1	9	.....	158
BY794942.2	25	.....	155
BX426150.2	1	.....T.....	126
BU902062.1	1	.....	137
BX402801.2	1	.....A.....	140
BX402793.2	6	.....	139
BX440468.2	1	.....	130
AL513590.3	2	.....\	123

		C		
AL513664.3	1			130
AL560156.3	1			112
Query	152	AATGCGGTGGCATCGACAAAGAACCATTGAAAAATTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCTTGTGGAAT		301
DC527884.1	159		T	308
BY794942.2	156			305
BX426150.2	127			276
BU902062.1	138			287
BX402801.2	141			290
BX402793.2	140			289
BX440468.2	131			283
AL513590.3	124			273
AL513664.3	131		B	280
AL560156.3	113		Y	267
Query	302	TTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCGCAGGACACAGAGACTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGCTCTGCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAGA		451
DC527884.1	309		C	458
BY794942.2	306			455
BX426150.2	277			426
BU902062.1	288			437
BX402801.2	291			440
BX402793.2	290			439
BX440468.2	281			430
AL513590.3	274			423
AL513664.3	281		K . B . B . K	430
AL560156.3	263		B . Y	412
Query	452	ATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAACAACATTAATGTTCGGTGTAAACAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTTGTTAAGGAAGTCAGCACTTACATTAGA		601
DC527884.1	459			608
BY794942.2	456			605
BX426150.2	427			576
BU902062.1	438			587
BX402801.2	441			590
BX402793.2	440			589
BX440468.2	431			580
AL513590.3	424			573
AL513664.3	421			580
AL560156.3	413			562
Query	602	AAATTGGCTACAACCCCGACACAGTAGCAATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAGGGATGGAAGTCACCCGTAAGGATGGCAATGCCATGGAAACACGCTGCTTG		757
DC527884.1	609			758
BY794942.2	606			755
BX426150.2	577			726
BU902062.1	588			737
BX402801.2	591			740
BX402793.2	590			739
BX440468.2	581			729
AL513590.3	574		Y . . . Y . . . - . . . T . . .	722
AL513664.3	581			730
AL560156.3	563			712
Query	752	AGGCTCTGGACTGCATCTACCACCAACTCGTCCAACATGACAAGCCCTTGGCGCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACTT		901
DC527884.1	759			908
BY794942.2	756			905
BX426150.2	727			878
BU902062.1	738			887
BX402801.2	741			890
BX402793.2	740			889
BX440468.2	730			879
AL513590.3	723			872
AL513664.3	731		Y . . . . .	880
AL560156.3	713			862
Query	902	TTGCTCCAGTCAACGTTACAACGGAAGTAAAACTGTGGAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGACAATGTGGGCTTCAATGTCAAGAATGTGCTGCTCAAGGATGTTCTGCTGGCAACGTTGCTGGTGACAGCA		1051
DC527884.1	909			1058
BY794942.2	906			1055
BX426150.2	877			1025
BU902062.1	888		AC . . . . C . . . C . . .	1037
BX402801.2	891		W . . . . Y . . . . Y . . . T . . . K . T . A . . . M . K . . . S . .	1042
BX402793.2	890		S . . . . - . . . . G . . . TM . A . . . . K . . .	1038
BX440468.2	880		T . . . . T . . . Y . . . R . . . M . . . T . . . M - . . . S - . .	1027
AL513590.3	873		T . . . . T . . . Y . . . R . . . M . . . T . . . M . . . - . . . C . .	1027

AL513664.3 881 .....T.....W.....K.....A.....K.T.....G.....GC.....S.- 1030

AL560156.3 863 .....S. 1013

Query 1052 AAAANTGACCCCAATGGAAGCAGCTGGCTTCAGTGCCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTCTGCCAGAAAGCTCAGAAGGCTA 1201

DC527884.1 1059 .....T... 1188

DC527884.1 1426 ..... 1454

BY794942.2 1056 .....T... 1186

BY794942.2 1424 ..... 1452

BX426150.2 1026 ..... 1140

BU902062.1 1038 .....C..G..T... 1162

BX402801.2 1043 ...W...A.....K.Y.....T..W.....W...S.S-...K.W..... 1144

BX402793.2 1039 ...WKR...M-.....M...Y.....M.M-...M...M-...S... 1121

BX440468.2 1028 .....M.....M.....M(C..R-...A.M-...S...Y-... 1120

AL513590.3 1022 .....Y.....K.C.....W.....M.M-...T...T...M.Y..S.Y.A.....T... 1151

AL513664.3 1031 .....G.....Y.....W.M.....WR.....S.SY-...T..... 1127

AL560156.3 1014 .....K.R.....Y.....W...K..M.M.....W-...Y-... 1103

Query 1202 AATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAG 1351

DC527884.1 1455 .....C..... 1604

BY794942.2 1453 ..... 1602

Query 1352 GAGAATgtttgtggaccactttgttttttttgcgtgtggcagttttaagttattagtttttaaaatcagtaacttttaATGGAACAACCTTGACCAAAAATTTGTACAGAATTTTGAGACCCATTAAAAAG 1489

DC527884.1 1605 ..... 1742

BY794942.2 1603 ..... 1740

Query= T14-34 [organism=Homo sapiens] eef1al

Length=1467

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BX440539.2	BX440539 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1465	0.0	100%
DR763375.1	HESC4_151_G10.g1_A037 NIH_MGC_262 Homo sapiens cDNA...	1463	0.0	100%
DR763172.1	HESC4_149_E01.g1_A037 NIH_MGC_262 Homo sapiens cDNA...	1463	0.0	100%
DR762061.1	HESC4_136_A03.g1_A037 NIH_MGC_262 Homo sapiens cDNA...	1463	0.0	100%
DR158661.1	HESC2_92_H12.g1_A035 NIH_MGC_258 Homo sapiens cDNA ...	1463	0.0	100%
CX870789.1	HESC4_49_D11.g1_A037 NIH_MGC_262 Homo sapiens cDNA ...	1463	0.0	100%
BU846433.1	AGENCOURT_10413493 NIH_MGC_109 Homo sapiens cDNA cl...	1463	0.0	100%
AU119155.1	AU119155 HEMBA1 Homo sapiens cDNA clone HEMBA100515...	1463	0.0	100%
DA738169.1	DA738169 NT2RP4 Homo sapiens cDNA clone NT2RP400261...	1461	0.0	100%
DA418936.1	DA418936 CD34C1 Homo sapiens cDNA clone CD34C100001...	1461	0.0	100%
ALIGNMENTS				
Query	1	CTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCTGGAAGCACTACCCCTAAAAGCCAAATAGGGAAGGAAAGACTCATATCAACATTGTCTGTCATTGGACACGTAGATTGGGCAAGTCCACCACTACTGGCCATCTGATCTAT	150	
BX440539.2	40	.....	189	
DR763375.1	6	.....	154	
DR763172.1	3	.....	151	
DR762061.1	19	.....	167	
DR158661.1	11	.....	159	
CX870789.1	7	.....	155	
BU846433.1	20	.....	168	
AU119155.1	7	.....	155	
DA738169.1	4	.....	153	
DA418936.1	1	.....	150	
Query	151	AAATGCGGTGGCATCGACAAAAGAACCTTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAGGGCTCCTTCAAGTATGCCTGGGCTTTGGATAAACTGAAAGCTGAGCGTGACGTGGTATCACCATTGATATCTCCTTGTGGAAA	300	
BX440539.2	190	.....	339	
DR763375.1	155	.....	304	
DR763172.1	152	.....	301	
DR762061.1	168	.....	317	
DR158661.1	160	.....	309	

CX870789.1	156	.....	305
BU846433.1	169	.....	318
AU119155.1	156	.....	305
DA738169.1	154	.....	303
DA418936.1	151	.....	300
Query 301 TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTCTGATTGTTGCTGCTGGTGGTGAATTTGAAGCTGGTATCTCCAAG 450			
BX440539.2	340	.....	489
DR763375.1	305	.....	454
DR763172.1	302	.....	451
DR762061.1	318	.....	467
DR158661.1	310	.....	459
CX870789.1	306	.....	455
BU846433.1	319	.....	468
AU119155.1	306	.....	455
DA738169.1	304	.....	453
DA418936.1	301	.....	450
Query 451 AATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAACAACATAATTGTCGGTGTAAACAAATGGATTCCACTGAGCCACCTACAGCCAGAAGAGATATGAGGAAATTTGTAAGGAAGTCAGCACTTACATTAAAG 600			
BX440539.2	490	.....	639
DR763375.1	455	.....	604
DR763172.1	452	.....	601
DR762061.1	468	.....	617
DR158661.1	460	.....	609
CX870789.1	456	.....	605
BU846433.1	469	.....	618
AU119155.1	456	.....	605
DA738169.1	454	.....	603
DA418936.1	451	.....	600
Query 601 AAAATTGGCTACAACCCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAAACATGCTGGAGCCCAAGTGCTAACATGCCCTTGGTTCAAGGGATGGAAGTACCCGTAAAGATGGCAATGCCAGTGGAAACCACGCTGCT 750			
BX440539.2	640	.....	788
DR763375.1	605	.....	753
DR763172.1	602	.....	750
DR762061.1	618	.....	766
DR158661.1	610	.....	758
CX870789.1	606	.....	754
BU846433.1	619	.....	767
AU119155.1	606	.....	754
DA738169.1	604	.....	753
<div style="text-align: center;">\</div> <div style="text-align: center;"> </div> <div style="text-align: center;">C</div>			
DA418936.1	601	.....	749
Query 751 TGAGGCTCTGGACTGCACTCTACCACCAACTCGTCCAACCTGACAAGC 797			
BX440539.2	789	.....	835
DR763375.1	754	.....	800
DR763172.1	751	.....	797
DR762061.1	767	.....	813
DR158661.1	759	.....	805
CX870789.1	755	.....	801
BU846433.1	768	.....	814
AU119155.1	755	.....	801
DA738169.1	754	.....	800
DA418936.1	750	.....N.....	796

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions  
 Posted date: Feb 24, 2019 1:46 AM  
 Number of letters in database: 43,200,890,307  
 Number of sequences in database: 77,566,966

Lambda K H  
 1.33 0.621 1.12  
 Gapped  
 Lambda K H  
 1.28 0.460 0.850  
 Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 0, Extension: 0  
 Number of Sequences: 77566966  
 Number of Hits to DB: 11823009  
 Number of extensions: 1013502  
 Number of successful extensions: 1013502  
 Number of sequences better than 10: 34556  
 Number of HSP's better than 10 without gapping: 0  
 Number of HSP's gapped: 528608  
 Number of HSP's successfully gapped: 518797  
 Length of database: 43200890307  
 A: 0  
 X1: 13 (25.0 bits)  
 X2: 32 (59.1 bits)  
 X3: 54 (99.7 bits)

S1: 13 (25.1 bits)

BLASTN 2.9.0+  
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and  
Webb Miller (2000), "A greedy algorithm for aligning DNA  
sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: 8FVG24DZ015

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions  
77,566,966 sequences; 43,200,890,307 total letters  
Query= N1-4 [organism=Homo sapiens] eef1a1

Length=1109

Sequences producing significant alignments:				Score (Bits)	E Value	Max ident
CR982215.1	CR982215	RZPD no.9016	Homo sapiens cDNA clone RZPDp...	1456	0.0	100%
BX443032.2	BX443032	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...		1456	0.0	100%
BX421307.2	BX421307	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...		1456	0.0	100%
BX353545.2	BX353545	Homo sapiens NEUROBLASTOMA COT 25-NORMALIZ...		1456	0.0	100%
CX167214.1	HES2	49 G11.g1_A035 NIH_MGC_258 Homo sapiens cDNA ...		1456	0.0	100%
CA771972.1	io93j08.x1	HR85 islet Homo sapiens cDNA clone IMAGE...		1456	0.0	100%
BU844361.1	AGENCOURT_10414634	NIH_MGC_109 Homo sapiens cDNA cl...		1456	0.0	100%
BX453401.2	BX453401	Homo sapiens T CELLS (JURKAT CELL LINE) Ho...		1454	0.0	100%
CR996534.1	CR996534	RZPD no.9017 Homo sapiens cDNA clone RZPDp...		1452	0.0	100%
BU845975.1	AGENCOURT_10413042	NIH_MGC_109 Homo sapiens cDNA cl...		1452	0.0	100%

ALIGNMENTS

Query	322	TTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCGTCTGAAGGATGTTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGGCTTCACTGCTCAGGTGATTATCCTGAA	471
CR982215.1	6	.....	155
BX443032.2	143	.....	292
BX421307.2	117	.....	266
BX353545.2	22	.....	171
CX167214.1	788	.....	639
CA771972.1	788	.....	639
BU844361.1	795	.....	646
BX453401.2	17	.....	166
CR996534.1	63	.....	212
BU845975.1	786	.....	637
Query	472	CCATCCAGGCCAATAAGCGCCGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAGTTTTCGTGAGCTGAAGGAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTTCTTGAAGTCTGGTGA	621
CR982215.1	156	.....	305
BX443032.2	293	.....	442
BX421307.2	267	.....	416
BX353545.2	172	.....	321
CX167214.1	638	.....	489
CA771972.1	638	.....	489
BU844361.1	645	.....	496
BX453401.2	167	.....	316
CR996534.1	213	.....	362
BU845975.1	636	.....	487
Query	622	TGCTGCCATTGTTGATATGGTTCTTGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTTGGGTGCTTTTGCTGTTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAGCAGTGGACAGAAGGCTGCTGGAGC	771
CR982215.1	306	.....	455
BX443032.2	443	.....	592
BX421307.2	417	.....	566
BX353545.2	322	.....	471
CX167214.1	488	.....	339
CA771972.1	488	.....	339
BU844361.1	495	.....	346
BX453401.2	317	.....	466
CR996534.1	363	.....	512
BU845975.1	486	.....	337
Query	772	TGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTGGCCATTTAAGTTTAGTAGTAAAGACTG	921
CR982215.1	456	.....	605
BX443032.2	593	.....	742
BX421307.2	567	.....	716
BX353545.2	472	.....	621
CX167214.1	338	.....	189
CA771972.1	338	.....	189
BU844361.1	345	.....	196
BX453401.2	467	.....	616
CR996534.1	513	.....	662
BU845975.1	336	.....	187

Query	922	GTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAAATgttttggaccactttggttttcttttttgcgtgtggcagttttaagttattagttttttaaatacagta	1071
CR982215.1	606	.....	755
BX443032.2	743	.....	892
BX421307.2	717	.....	866
BX353545.2	622	.....	771
CX167214.1	188	.....	39
CA771972.1	188	.....	39
BU844361.1	195	.....	46
BX453401.2	617	.....	766
CR996534.1	663	.....	812
BU845975.1	186	.....	37

Query	1072	TCACAGAAATTTTGAGACCCATTAAAAAGTTAAATGAG	1109
CR982215.1	756	.....	793
BX443032.2	893	.....	930
BX421307.2	867	.....	904
BX353545.2	772	.....	809
CX167214.1	38	.....	1
CA771972.1	38	.....	1
BU844361.1	45	.....	8
BX453401.2	767	.....	803
CR996534.1	813	.....	848
BU845975.1	36	.....	1

Query= N2-14 [organism=Homo sapiens] eef1a1

Length=987

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
CN389362.1	17000599951108 GRN PRENEU Homo sapiens cDNA 5', mRN...	952	0.0	100%
CK843266.1	UI-R-AA1-aad-f-05-0-UI.s10 UI-R-AA1 Rattus norvegic...	948	0.0	100%
CK843262.1	UI-R-AA1-aad-c-09-0-UI.s10 UI-R-AA1 Rattus norvegic...	948	0.0	100%
CK843256.1	UI-R-AA1-aac-g-06-0-UI.s10 UI-R-AA1 Rattus norvegic...	948	0.0	100%
CB373762.1	TgESTzyg83g02.x1 TgME49 3 day invitro bradyzoite To...	948	0.0	100%
BQ883373.1	AGENCOURT_7982297 Lupski dorsal_root ganglion Homo ...	948	0.0	100%
BQ788143.1	il48f10.x1 HR85 islet Homo sapiens cDNA clone IMAGE...	948	0.0	100%
BQ787972.1	il45h02.x1 HR85 islet Homo sapiens cDNA clone IMAGE...	948	0.0	100%
BQ787616.1	im13c06.x1 Human insulinoma Homo sapiens cDNA clone...	948	0.0	100%
BQ787579.1	im12e10.x1 Human insulinoma Homo sapiens cDNA clone...	948	0.0	100%

#### ALIGNMENTS

Query	467	GAGAGCATGCCCTAAATTCCTGAAGCTGCTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGATATGAGACAGACAGTTGCGGTGGGTGT	616
CN389362.1	26	.....   G	175
CK843266.1	529	.....	388
CK843262.1	529	.....	388
CK843256.1	529	.....	388
CB373762.1	525	.....	384
BQ883373.1	60	.....	201
BQ788143.1	514	.....	373
BQ787972.1	517	.....	376
BQ787616.1	532	.....	391
BQ787579.1	528	.....	387
Query	617	CATCAAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAAGCTGTTGTTTC	766
CN389362.1	176	.....	325
CK843266.1	387	.....	238
CK843262.1	387	.....	238
CK843256.1	387	.....	238
CB373762.1	383	.....	234
BQ883373.1	202	.....	351
BQ788143.1	372	.....	223
BQ787972.1	375	.....	226
BQ787616.1	390	.....	241
BQ787579.1	386	.....	237
Query	767	AATTGCCCATTTAAGTTTAGTAGTAAAGACTGGTAAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAAATgttttggaccactttggttttcttttttgcgtgtggcagttttaagttattagttttttaaatacagta	916
CN389362.1	326	.....	475
CK843266.1	237	.....	88
CK843262.1	237	.....	88
CK843256.1	237	.....	88
CB373762.1	233	.....	84
BQ883373.1	352	.....	501
BQ788143.1	222	.....	73
BQ787972.1	225	.....	76
BQ787616.1	240	.....	91



B0787579.1 236 ..... 87

Query= N3-8 [organism=Homo sapiens] eef1a1

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
DC635691.1	DC635691 macaque bone marrow cDNA library Qbma Maca...	1504	0.00	96%
U1679280.1	tt2f06.xl NC1_CGAP_Gas4 Homo sapiens cDNA clone IM...	1077	0.00	99%
CA431918.1	UI-H-F070-bhl-c-18-0-UI.xl NC1_CGAP_F70 Homo sapiens...	1075	0.00	99%
BU070293.1	iml1n9.xl Human insulinoma Homo sapiens cDNA clone...	1075	0.00	99%
AI588866.1	tq2e03.xl NC1_CGAP_UT1 Homo sapiens cDNA clone IMA...	1075	0.00	99%
AI554314.1	tq05f11.xl NC1_CGAP_UT1 Homo sapiens cDNA clone IMA...	1075	0.00	99%
AI36170.1	AI36170.1 ScAes fetal lung NHRI9W Homo sapiens cDNA...	1075	0.00	99%
CT005089.1	CT005089 ZRPD. 9017 Homo sapiens cDNA clone ZRPDp...	1074	0.00	100%
CR999820.1	CR999820 ZRPD. no.9017 Homo sapiens cDNA clone ZRPDp...	1074	0.00	100%
CR999128.1	CR999128 ZRPD. no.9017 Homo sapiens cDNA clone ZRPDp...	1074	0.00	100%

Query	1		CTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAACTACCCCATAAAGCCAAATGGGAAGGAAAAGACTCATATCAACATTGTCTGCATTGGACACCTAGATTTCGGGCAAGTCCACCACCTACTGGCCACCTGATCTAT	150
DC635691.1	1		-.....-.....T.....C	149
Query	151		AAATGCGGTGGCATCGACAAGAAGACCATTGAAAAATTTGGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATTCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA	300
DC635691.1	150		.....G.....G.....	299
Query	301		TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAAATTC TTGAAGTCTGGTGATGCTGCCATT	450
DC635691.1	300		.....T.....A.....	467
			\\ \\         TG T G T T G G               T T         C C A C A C A   C	
AI679280.1	604		.....T.....	481
			\             \ G          A C C	
CA431918.1	617		.....A...T.....	495
			\             \ G          C C	
BU070293.1	616		.....A...T.....	494
			\             \ T          C C	
AI588866.1	599		.....T.....	480
			\             \ A C C	
AI554314.1	599		.....A...T.....	477
			\             \ G          C C	
AI336170.1	604		.....A...T.....	482
			\             \ G          C C	
CT005089.1	94		.....	198
CR999820.1	52		.....	156
CR999128.1	166		.....	270
Query	451	GTTGATATGGTTCCTGGCAAGCCCATGTGTTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCGCTTTGCTGTTTCGTGATATGAGACAGACAGITTCGGTGGGTGTCATCAAAGCAGTGGACAAGAGAGGCTGCTGGAGCTGGCAAGGTC	600	
DC635691.1	468	.....T.....G.....	617	

Query	751	CAAAATGCATCGTAAAAACCTTCAGAGAGAAAGGAGATgttttggcgacacttggtttttcttttttgcgtgtgcgagttttaagtattatgatttttaaaatcagtaacttttaATGGAAACACACGACACAAAAATTTGTACACAGATT	900
DC35691.1	768	.....	911
AI679280.1	180	.....	31
CA431918.1	194	.....	45
BU070293.1	193	.....	44
AI588866.1	179	.....	30
AI554314.1	176	.....	27
AI365190.1	181	.....	32
CT005089.1	499	.....	648
CR999820.1	457	.....	606
CR999128.1	571	.....	720

Query= N4-1 [organism=Homo sapiens] eef1a1

Sequences producing significant alignments:				Score (Bits)	E Value	Max ident
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	3184	0.0	100%	
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	3166	0.0	100%	
CF111220.1	Shultzomica04471	Rat lung airway and parenchyma cDN...	2357	0.0	91%	
BX426149.2	BX426149	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2146	0.0	99%	
CO001006.1	OC028	pre-estrum adult sheep ovary library Ovis ar...	2047	0.0	93%	
BX418564.2	BX418564	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2037	0.0	97%	
BX426150	BX426150	Homo sapiens FETAL BRAIN Homo sapiens cD...	2037	0.0	99%	
AL567209.3	AL567209	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2037	0.0	98%	
BX440407.1	BX440407	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1999	0.0	98%	
BU902062.1	AGENCOCURT	10127553 NIH MGC 71 Homo sapiens cDNA clo...	1999	0.0	98%	

[illegible]

[illegible]

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BX440470.1 685 .....535
                                     \
                                     |
                                     C
BU902062.1 1035 .....1163
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               |
               C
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               G
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               |
               T
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               |
               A
               \
               |
               A
Query      1380 TTGATCGCGGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTGATA 1529
DC527884.1 1206 .....1355
BY794942.2 1204 .....1353
CF111220.1 1199 .C...T.....G.....C.....C.....C.....A.....T.....C..T..AC.T...T.....C. 1348
BX426149.2 523 .....374
CO001006.1 569 .....T.....G.....A.....C.....C.....T.....C.....T..T..T...T..C.....C..T.....G.....C. 420
BX418564.2 533 .....384
AL567209.3 494 .....345
BX440470.1 534 .....385
Query      1530 TGAGACGACAGTTGCGGTGGGTGTCATCAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAA 1679
DC527884.1 1356 .....1505
BY794942.2 1354 .....1503
CF111220.1 1349 ...G.....T.....C.....A.....A.....C.....G.....G..... 1498
BX426149.2 373 .....224
CO001006.1 419 .....C..T.....A.....C.....G..... 270
BX418564.2 383 .....234
AL567209.3 344 .....M.....Y.....194
                                     \
                                     |
                                     A
BX440470.1 384 .....235
Query      1680 GAACGGTCTCAGAACTGTTTGTTCAAATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGATgttttgggaccactttggttttcttttttgcgtgtggcagtttt 1829
DC527884.1 1506 .....1655
BY794942.2 1504 .....1653
CF111220.1 1499 .....C.....A.....---.....G..... 1637
BX426149.2 223 .....74
CO001006.1 269 .....C.....A.....-A...-G----- 129
                                     \
                                     |
                                     T
BX418564.2 233 .....84
AL567209.3 193 .....43
                                     \
                                     |
                                     G
BX440470.1 234 .....85
Query      1830 aagttattagtttttaaaatcagttactttttaATGGAAACAACCTTGACCAAAAATTTGTACAGAAATTTTGAGACCCATTAAAAAAGTT 1918
DC527884.1 1656 .....1744
BY794942.2 1654 .....1742
CF111220.1 1638 .....C.....-.....C.....-.....1726
                                     \
                                     |
                                     C
BX426149.2 73 .....1
CO001006.1 128 .....A.....C.....-.....40
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BX418564.2 83 .....M.....1
AL567209.3 42 .....1
BX440470.1 84 .....1

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Query= N5-2 [organism=Homo sapiens] eef1al  
Length=1718

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	3011	0.0	98%
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	2992	0.0	98%
CF111220.1	Shultzomica04471	Rat lung airway and parenchyma cDN...	2206	0.0	90%
BX426149.2	BX426149	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2146	0.0	99%
BX418564.2	BX418564	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2047	0.0	97%
AL567209.3	AL567209	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2001	0.0	98%
BX440470.1	BX440470	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1999	0.0	98%
BX420340.1	BX420340	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1997	0.0	99%
AL518238.2	AL518238	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1993	0.0	98%
BX459625.2	BX459625	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1993	0.0	99%

[illegible]

BX459625.2	1094	....W....-KS.....-K.....W.....K.A.....	946
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Query	752	CAACTCGTCCAACCTGACAAGCCCTTGGCGCTGCCTCTCCAGGATGTCTACAAAAATGGTGGTATTGGTACTGTTCTCTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGG	901
DC527884.1	783	.....	932
BY794942.2	780	.....	929
CF111220.1	776	.....TC..A...C.....T...C..C...C...C...G.....A.....T.....T.....T..A...T..	925
BX426149.2	946	.....	797
BX418564.2	956	.....C.....	807
AL567209.3	916	.....	767
BX440470.1	958	.....	809
BX420340.1	951	.....R.....	802
AL518238.2	951	.....W.....B.....	802
BX459625.2	945	.....	796
Query	902	AAGTAAATCTGTCGAAATGACCATTGAAGCTTTGAGTGAAGCTCTCCTGGGACAAATGTTGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGTCGTGGCAACGTTGCTGGTGACAGCAAAATGACCCACCAATGGAAGCAG	1051
DC527884.1	933	.....	1082
BY794942.2	930	.....	1079
CF111220.1	926	.....C..G...G.....G.....A.....C..A...C.....A..C...A.A.....T.....G.....	1075
BX426149.2	796	.....	647
BX418564.2	806	.....C.....	657
AL567209.3	766	.....	618
BX440470.1	808	.....	659
BX420340.1	801	.....	652
AL518238.2	801	.....W.....A.....	652
BX459625.2	795	.....	646
Query	1052	CTGGCTTCACGTCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGS	1201
DC527884.1	1083	.....	1232
BY794942.2	1080	.....	1230
		<div> <div> <div></div> <div></div> <div>G</div> </div> </div>	
CF111220.1	1076	.....G..C...T..T.....TC...C.....C...A.....C...T..A..G...C...T.....G.....	1225
BX426149.2	646	.....	497
BX418564.2	656	.....	507
AL567209.3	617	.....	468
BX440470.1	658	.....	508
		<div> <div> <div></div> <div></div> <div>C</div> </div> </div>	
BX420340.1	651	.....	502
AL518238.2	651	.....Y.....	502
BX459625.2	645	.....	496
Query	1202	AAGATGGCCCTAAATCTTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCTTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGGTGGGTGTCA	1351
DC527884.1	1233	.....	1382
BY794942.2	1231	.....	1380
CF111220.1	1226	.....C.....C.....C.....A.....T...C...T..AC.T...T.....C...G.....T.....	1375
BX426149.2	496	.....	347
BX418564.2	506	.....	357
AL567209.3	467	.....K.....	318
BX440470.1	507	.....	358
BX420340.1	501	.....	352
AL518238.2	501	.....	352
BX459625.2	495	.....	346
Query	1352	TCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCAACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGGAAGACGGTCTCAGAACTGTTTGTTCAA	1501
DC527884.1	1383	.....	1532
BY794942.2	1381	.....C.....	1530
CF111220.1	1376	.....C.....A.....A.....C.....G.....C.....	1525
BX426149.2	346	.....	197
BX418564.2	356	.....	207
AL567209.3	317	.....M...Y.....	167
		<div> <div> <div></div> <div></div> <div>A</div> </div> </div>	
BX440470.1	357	.....	208
BX420340.1	351	.....	202
AL518238.2	351	.....G.....	202
BX459625.2	345	.....	196
Query	1502	TTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAGGAGAATgttttgtggaccactttgggtttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagtact	1651
DC527884.1	1533	.....	1682
BY794942.2	1531	.....	1680
CF111220.1	1526	.....A.....G.....C.....	1664
BX426149.2	196	.....	47
BX418564.2	206	.....	57
AL567209.3	166	.....	16

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                                     |
                                     G
BX440470.1 207 .....
BX420340.1 201 .....
AL518238.2 201 .....
BX459625.2 195 .....

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Query      1652 ttttaATGGAACAACCTTGACCAAAAATTTGTACAGAATTTTGAGAGCCCATTAAGTAAATG 1718
DC527884.1 1683 .....
BY794942.2 1681 .....
CF111220.1 1665 .....C.....T..... 1731

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                                     |
                                     C
BX426149.2 46 .....-.....G.....G.-..G.....T.. 1
BX418564.2 56 .....M..... 1
AL567209.3 15 ..... 1
BX440470.1 57 ..... 1
BX420340.1 51 .....R..... 1
AL518238.2 51 .....N.....N..... 1

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BX459625.2 45 ..... 1

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Query= N6-15 [organism=Homo sapiens] eef1a1

Length=1144

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
CR996534.1	CR996534	RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1437	0.0	100%
CR982215.1	CR982215	RZPD no.9016 Homo sapiens cDNA clone RZPDp...	1437	0.0	100%
BX453401.2	BX453401	Homo sapiens T CELLS (JURKAT CELL LINE) Ho...	1437	0.0	100%
BX443032.2	BX443032	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1437	0.0	100%
BX421307.2	BX421307	Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1437	0.0	100%
BX353545.2	BX353545	Homo sapiens NEUROBLASTOMA COT 25-NORMALIZ...	1437	0.0	100%
CX167214.1	HESC2_49	G11.g1 A035 NIH MGC 258 Homo sapiens cDNA ...	1437	0.0	100%
CA771972.1	ic93g08.x1	HR85 islet Homo sapiens cDNA clone IMAGE...	1437	0.0	100%
BU845975.1	AGENCOURT_10413042	NIH_MGC_109 Homo sapiens cDNA cl...	1437	0.0	100%
BU844361.1	AGENCOURT_10414634	NIH_MGC_109 Homo sapiens cDNA cl...	1437	0.0	100%

#### ALIGNMENTS

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Query      357 CTTTAGAGTGAAGCTCTTCTGGGGACAAATGTGGGCTTCAATGTCAAGAATGTTGTCGTCAAGGATGTTGTCGTGGCAACGTTGCTGGTGACAGCAAAATGACCCACCAATGGAAAGCTGGGCTTCACTGCTCAGGTGATTATCCTG 506
CR996534.1 62 .....
CR982215.1 5 .....
BX453401.2 16 .....
BX443032.2 142 .....
BX421307.2 116 .....
BX353545.2 21 .....
CX167214.1 789 .....
CA771972.1 789 .....
BU845975.1 787 .....
BU844361.1 796 .....

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Query      507 AACCATCCAGGCCAAATAAGCCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAGATTGATCGCCGTTCTGGTAAAGCTGGAAGATGGCCCTAAATTCCTGAAGTCTGGTG 656
CR996534.1 211 .....

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                                     |
                                     C
CR982215.1 154 .....

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                                     |
                                     C
BX453401.2 165 .....

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                                     |
                                     C
BX443032.2 291 .....

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                                     \
                                     |
                                     C
BX421307.2 265 .....

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                                     \
                                     |
                                     C
BX353545.2 170 .....

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CX167214.1	640	.....	c	.....	490
			\		
CA771972.1	640	.....	c	.....	490
			\		
BU845975.1	638	.....	c	.....	488
			\		
BU844361.1	647	.....	c	.....	497
			\		
			c		

Query	657	ATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTTGCTGTTCTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAG	806
CR996534.1	362	.....	511
CR982215.1	305	.....	454
BX453401.2	316	.....	465
BX443032.2	442	.....	591
BX421307.2	416	.....	565
BX353545.2	321	.....	470
CX167214.1	489	.....	340
CA771972.1	489	.....	340
BU845975.1	487	.....	338
BU844361.1	496	.....	347

Query	807	CTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTGGCCATTTAAGTTTAGTAGTAAAGACT	956
CR996534.1	512	.....	661
CR982215.1	455	.....	604
BX453401.2	466	.....	615
BX443032.2	592	.....	741
BX421307.2	566	.....	715
BX353545.2	471	.....	620
CX167214.1	339	.....	190
CA771972.1	339	.....	190
BU845975.1	337	.....	188
BU844361.1	346	.....	197

Query	957	GGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAATgttttgtggaccactttgttttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagtagctttttaATGGAAACAACCTTGACCAAAAATTT	1106
CR996534.1	662	.....	811
CR982215.1	605	.....	754
BX453401.2	616	.....	765
BX443032.2	742	.....	891
BX421307.2	716	.....	865
BX353545.2	621	.....	770
CX167214.1	189	.....	40
CA771972.1	189	.....	40
BU845975.1	187	.....	38
BU844361.1	196	.....	47

Query	1107	GTCACCAGAAATTTTGAGACCCATTAAAAAAGTTAAATG	1144
CR996534.1	812	.....	848
CR982215.1	755	.....	791
BX453401.2	766	.....	802
BX443032.2	892	.....	928
BX421307.2	866	.....	902
BX353545.2	771	.....	807
CX167214.1	39	.....	3
CA771972.1	39	.....	3
BU845975.1	37	.....	1
BU844361.1	46	.....	10

Query= N7-11 [organism=Homo sapiens] eef1a1

Length=972

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
CT005089.1	CT005089 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR999128.1	CR999128 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR996969.1	CR996969 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR996534.1	CR996534 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR982215.1	CR982215 RZPD no.9016 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR977084.1	CR977084 RZPD no.9016 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR975903.1	CR975903 RZPD no.9016 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
BQ776023.1	UI-H-FH0-bck-l-16-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1201	0.0	100%



BQ775888.1 UI-H-FH0-bcg-o-05-0-UI.s1 NCI\_CGAP\_FH0 Homo sapiens... 1201 0.0 100%  
BQ775886.1 UI-H-FH0-bcg-o-01-0-UI.s1 NCI\_CGAP\_FH0 Homo sapiens... 1201 0.0 100%

ALIGNMENTS

Query	323	GTGATTATTCCTGAACCATCCAGGCCAAATAAGCGCCGCTATGCCCTGTATTGGATTGCCACCGGTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTC	472
CT005089.1	25	.....	174
CR999128.1	97	.....	246
CR996969.1	130	.....	279
CR996534.1	199	.....	348
CR982215.1	142	.....	291
CR977084.1	88	.....	237
CR975903.1	19	.....	168
BQ776023.1	668	.....	519
BQ775888.1	668	.....	519
BQ775886.1	668	.....	519
Query	473	TTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTGTGCTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCAGTGGACAAG	622
CT005089.1	175	.....	324
CR999128.1	247	.....	396
CR996969.1	280	.....	429
CR996534.1	349	.....	498
CR982215.1	292	.....	441
CR977084.1	238	.....	387
CR975903.1	169	.....	318
BQ776023.1	518	.....	369
BQ775888.1	518	.....	369
BQ775886.1	518	.....	369
Query	623	AAGGCTGCTGGAGCTGGCAAGGTCAACAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGGAAGACGGTCTCAGAACTGTTGTTTCAATTGGCCATTTAAGTTTA	772
CT005089.1	325	.....	474
CR999128.1	397	.....	546
CR996969.1	430	.....	579
CR996534.1	499	.....	648
CR982215.1	442	.....	591
CR977084.1	388	.....	537
CR975903.1	319	.....	468
BQ776023.1	368	.....	219
BQ775888.1	368	.....	219
BQ775886.1	368	.....	219
Query	773	GTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAGAAGGAAGGAGATgttttgtggaccacttttggttttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagtaactttttaATGGAACAACAT	922
CT005089.1	475	.....	624
CR999128.1	547	.....	696
CR996969.1	580	.....	729
CR996534.1	649	.....	798
CR982215.1	592	.....	741
CR977084.1	538	.....	687
CR975903.1	469	.....	618
BQ776023.1	218	.....	69
BQ775888.1	218	.....	69
BQ775886.1	218	.....	69
Query	923	TGACCAAAAAATTTGTACAGAATTTTGAGACCCATTAAAAAAGTTAAATG	972
CT005089.1	625	.....	674
CR999128.1	697	.....	746
CR996969.1	730	.....	779
CR996534.1	799	.....	848
CR982215.1	742	.....	791
CR977084.1	688	.....	737
CR975903.1	619	.....	668
BQ776023.1	68	.....	19
BQ775888.1	68	.....	19
BQ775886.1	68	.....	19

Query= N8-C\* [organism=Homo sapiens] eef1a1

Length=1830

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	3155	0.0	100%
DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog...	3138	0.0	100%
CF111220.1 Shultzomica04471 Rat lung airway and parenchyma cDN...	2344	0.0	91%
BX426149.2 BX426149 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2146	0.0	99%
CO001006.1 OC028 pre-oestrus adult sheep ovary library Ovis ar...	2050	0.0	93%
BX418564.2 BX418564 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2047	0.0	97%
BX426150.2 BX426150 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2032	0.0	99%
AL567209.3 AL567209 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2001	0.0	98%
BX440470.1 BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1999	0.0	98%

## ALIGNMENTS

ATTC

Query	417	TCATTCGATGCCCCAGGACACAGAGAC	TCATCAAAAACATGATTACAGGACATCTCAGGCTGACTGTGCTGCTCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAGAAATGGGCAGACCCGAGAGCATGCCCTC	566
RY794942.2	333	.....	.....	482
DC527884.1	336	.....C.....	.....	485
CF111220.1	329	.....C.....G.....	.....G.....C.....T.....T.....	478
CO001006.1	1439	.....C.....C.....C.....	.....C.....C.....T.....	1290
BX426150.2	304	.....	.....	453

Query	567	TGCGCTTACACACTGGGTTGTAACAAC	.....TTGTCGGTGTAAACAAATGGGATTCACACTGAGCACCCCTACAGCCAGGAAGAGATATGAGGAAATTTGTAAAGGAAGTCAGCACTTACATTAAAGAAAAATGGGCTACACACCCCGACACACAGTAG	716
BY94942.2	483	.....	.....	632
DC527884.1	486	.....	.....	635
CF111220.1	479	.....TT.....G.....T.....C.....	.....A.....C.....A.....T.....C.....C.....C.....T.....	628
BX426149.2	1196	.....	.....A.....C.....A.....T.....G.....C.....C.....	1094
CO001006.1	1289	.....C.....T.....C.....	.....T.....C.....C.....M.....C.....	1140
BX418564.2	1196	.....	.....VHVS.....R.....N.....G.....W.....R.....M.....K.....R.....S.....	1100
BX426150.2	454	.....	.....	603
AL567209.3	1145	.....	.....S.....W.....T.....R.....K.....W.....R.....A.....M.....C.....C.....	1064

M

1

Query	717	CATTGTGCCAATTCTGGTGGAGTGCACCAATGCTGGAGGACAGCTGAACATGCCTGGTTCAGGGATGGAAGTCAACCGTAGGATGGCAATGCCAGTGGGAACACGCTGCTTGAGGCTCTGGAGCTGCATCTACACCA	866
BY794942.2	633	.....	782
DC527884.1	636	.....	785
CF111220.1	629	.....T.....G.....C.A.....G.....C.....G.A.....T.....T.G.G.....	778
BX426149.2	1093	.....	944
CO001006.1	1139	.....C.....T.....A.....C.....C.....A.....T.....G.....	990
BX418564.2	1099	.....-.....-.....-.....	954
BX426150.2	604	.....C.....T.....A.....C.....C.....A.....T.....G.....	753
AL567209.3	1063	.....-.....S.M.....Y.....K.....	914
BX440470.1	1100	.....K.....M.M.....Y.T.....D.....K.....T.....T.....Y.....K.....A.....R.....	956
BX420340.1	1096	.....K.....M.M.....Y.T.....D.....K.....T.....T.....Y.....K.....A.....R.....	949

Query	867	CTCGTCAACTGACAAAGCCCTTGGCACTCTCCAGGATGTCTACAAAATGGTGGTATTGGTACTGTTCCTGTTGGCCGAGTGAGACTGGTGTCTCAAAACCGGTATGGTGGTCACTTTGCTCCAGTCAACGGTTACAAAGGAAG	1016
BY794942.2	783	.....	932
DC527884.1	786	.....	935
CF111220.1	779	.....TC...A...C.....T...C.C...C...C...G...A...T...T...T.A...T...	928
BX426149.2	943	.....	794
CO001006.1	989	...C...A...TT...T...A...G.T.T...T.C...C...T.A...T.G...	840
EX418564.2	953	.....C.....	804
BX426150.2	754	.....	903
AL567209.3	913	.....	764
BX440470.1	955	.....	806
BX420340.1	948	.....R.....	799

$$\frac{1}{2}$$

AL567209.3	763	.....-	615
BX440470.1	805	.....	656

BX420340.1	798	.....	649
Query	1167	GCTTCACTGCTCAGGTGATTATCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAG	1316
BY794942.2	1083	.....	1233
		<div> <div>\</div> <div> </div> <div>G</div> </div>	
DC527884.1	1086	.....	1235
CF111220.1	1079	.....G..C..T..T.....TC...C...C...A...C...T..A...G...C...T.....G.....	1228
BX426149.2	643	.....	494
CO001006.1	689	.....C...A.....T.....C..T..GT..A...A...GC...T...A...T.....G...M.....T.....G.....	540
BX418564.2	653	.....	504
BX426150.2	1051	.....	1140
AL567209.3	614	.....	465
BX440470.1	655	.....	505
		<div> <div>\</div> <div> </div> <div>C</div> </div>	
BX420340.1	648	.....	499
Query	1317	ATGGCCCTAAATCTTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTGTGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTGATATGAGACAGACAGTTGCGGTGGGTGTCATCA	1466
BY794942.2	1234	.....	1383
DC527884.1	1236	.....	1385
CF111220.1	1229	.....C.....C...C.....A...T...C...T..AC..T...T.....C...G...T.....	1378
BX426149.2	493	.....	344
CO001006.1	539	.....A.....C.....C.....T.....C.....T..T...T...T...C...C...T...G...C.....C..T.....	390
BX418564.2	503	.....	354
AL567209.3	464	.....K.....	315
BX440470.1	504	.....	355
BX420340.1	498	.....	349
Query	1467	AAGCAGTGGACAAGAAGCTGCTGGAGCTGGCAAGSTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAAGCGTCTCAGAACTGTTTGTTCAAATTG	1616
BY794942.2	1384	.....	1533
DC527884.1	1386	.....	1535
CF111220.1	1379	.....C.....A.....A.....C.....G.....C.....	1528
BX426149.2	343	.....	194
CO001006.1	389	.....A.....C.....G.....C.....	240
BX418564.2	353	.....	204
AL567209.3	314	.....M...Y.....	164
		<div> <div>\</div> <div> </div> <div>A</div> </div>	
BX440470.1	354	.....	205
BX420340.1	348	.....	199
Query	1617	GCCATTAAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAGGAGAAATgttttgtggaccactttgttttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagtaactttt	1766
BY794942.2	1534	.....	1683
DC527884.1	1536	.....	1685
CF111220.1	1529	.....A.....G.....C.....	1667
BX426149.2	193	.....	44
CO001006.1	239	.....A.....A.....G.....G.....	99
		<div> <div>\</div> <div> </div> <div>T</div> </div>	
BX418564.2	203	.....	54
AL567209.3	163	.....	13
		<div> <div>\</div> <div> </div> <div>G</div> </div>	
BX440470.1	204	.....	55
BX420340.1	198	.....	49
Query	1767	taATGGAAACAACCTTGACCAAAAATTTGTCACAGAATTTTGAGACCCATTAAAAAAGTTAAATG	1830
BY794942.2	1684	.....	1747
DC527884.1	1686	.....	1749
CF111220.1	1668	.....C.....T.....	1731
		<div> <div>\</div> <div> </div> <div>C</div> </div>	
BX426149.2	43	.....G.....G.....G.....T..	1
CO001006.1	98	.....A.....C.....T.....	35
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BX418564.2	53	.....M-.....	1
AL567209.3	12	.....	1
BX440470.1	54	.....	1
BX420340.1	48	.....R.....	1

Query= N9-C\* [organism=Homo sapiens] eef1a1

Length=2090

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	3155	0.0	100%
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	3138	0.0	100%
CF111220.1	Shultzomlca0471	Rat lung airway and parenchyma cDN...	2344	0.0	91%
BX426149.2	BX426149	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2146	0.0	99%
CO001006.1	OC028	pre-oestrus adult sheep ovary library Ovis ar...	2050	0.0	93%
BX418564.2	BX418564	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2047	0.0	97%
BX426150.2	BX426150	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2034	0.0	99%
AL567209.3	AL567209	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2001	0.0	98%
BX440470.1	BX440470	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1999	0.0	98%
BX420340.1	BX420340	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1997	0.0	99%
ALIGNMENTS					
Query	376	TCAAAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAGGAAAAGACTCATATCAACATTGTCGTCA			525
BY794942.2	33	..C.....			181
DC527884.1	36	..C.....			184
CF111220.1	28	.....T.....G.C...G.....A.....C.....C.....A.....C.....A..C.....C.....C.....T.....A.....			177
		\			
		ATTC			
BX426150.2	3	...C.....			152
Query	526	ATTGAAAAATTTGAGAAGGAGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCTGGGTCTTGGATAA			675
BY794942.2	182	.....			331
DC527884.1	185	.....			334
CF111220.1	178	.....G.....G.....A.....C.....C.....G.....T.....C.....C.....G.....			327
CO001006.1	1464	.....			1441
BX426150.2	153	.....			302
Query	676	ATCATTGATGCCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGACATCTCAGGCTGACTGTGCTGTCTG			825
BY794942.2	332	.....			481
DC527884.1	335	.....C.....			484
CF111220.1	328	.....C.....G.....G.....C.....C.....G.....C.....T.....T.....			477
CO001006.1	1440	.....C.....C.....C.....C.....C.....C.....T.....			1291
BX426150.2	303	.....			452
Query	826	CTGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCC			975
BY794942.2	482	.....			631
DC527884.1	485	.....			634
CF111220.1	478	.....TT.....G.....T.....C.....A.....A.....T.....G.....C.....C.....T.....			627
BX426149.2	1196	.....			1095
CO001006.1	1290	.....C.....T.....C.....T.....C.....C.....C.....C.....C.....C.....			1141
BX418564.2	1196	.....YH.VS.-.R.-.W.-.G.W.-.R.-.M.-.K.-.R.-.S.-.R.-.			1101
BX426150.2	453	.....			602
AL567209.3	1145	.....S.....W.....K.W.....R.....A.M.C.....C.....			1065
		\			
		M			
BX440470.1	1128	.....-W.-.....			1102
		\			
		C			
BX420340.1	1117	.....M..M.....			1098
Query	976	GCATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAAGTGCTAACATGCCTTGGTTC			1125
BY794942.2	632	.....			781
DC527884.1	635	.....			784
CF111220.1	628	.....T.....G.....C.....A.....G.....C.....G.....A.....T.....T.....G.....G.....			777
BX426149.2	1094	.....			945
CO001006.1	1140	.....C.....T.....A.....C.....C.....C.....C.....A.....T.....G.....			991
BX418564.2	1100	.....			955
BX426150.2	603	.....			752
AL567209.3	1064	.....K.....			915
BX440470.1	1101	.....S.M...Y.-.K.....K.....R.....			957
BX420340.1	1097	.....K.-..M.W...YT...D...K.....T.....Y.....A.....			950
Query	1126	ACTCGTCCAACCTGACAAGCCCTTGGCCTGCCTCTCCAGGATGCTACAAAATTTGGTGGTATTGGTACTGTTC			1275
BY794942.2	782	.....			931
DC527884.1	785	.....			934
CF111220.1	778	.....TC..A.....C.....T.....C.....C.....C.....G.....A.....T.....T.....T.....A.....T.....			927
BX426149.2	944	.....			795
CO001006.1	990	.....C.....A.....TT.....T.....A.....G..T..T.....T.....C.....C.....T.....A.....T.....G.....			841
BX418564.2	954	.....C.....			805
BX426150.2	753	.....			902
AL567209.3	914	.....			765
BX440470.1	956	.....			807
BX420340.1	949	.....R.....			800

Query	1276	GTAAATCTGTCGAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGACAAATGTGGGCTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGCTGGCAACGTTGCTGGTGACAGCAAAAATGAACCAACCAATGGAGCAGCT	1425
BY794942.2	932	.....	1081
DC527884.1	935	.....	1084
CF111220.1	928	.C..G...G.....G.....A.....C..A..C.....A..C..A.A.....T.....G.....	1077
BX426149.2	794	.....	645
CO001006.1	840	.G..G..C..A.....C.....C.....A..C.....T..G.....T..C.....T.....	691
BX418564.2	804	.....	655
BX426150.2	903	.....	1049
		<div> <div> </div> <div> </div> <div> </div> </div>	
AL567209.3	764	.....	616
BX440470.1	806	.....	657
BX420340.1	799	.....	650
Query	1426	GGCTTCAGTGTCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAA	1575
BY794942.2	1082	.....	1232
		<div> <div> </div> <div> </div> <div> </div> </div>	
DC527884.1	1085	.....	1234
CF111220.1	1078	.....G..C..T..T.....TC...C.....C.....A.....C.....T..A..G.....C.....T.....G.....	1227
BX426149.2	644	.....	495
CO001006.1	690	...C..A.....T.....C..T.GT..A..A..GC.....T..A.....T.....G.....T.....G.....	541
BX418564.2	654	.....	505
BX426150.2	1050	.....	1140
AL567209.3	615	.....	466
BX440470.1	656	.....	506
		<div> <div> </div> <div> </div> <div> </div> </div>	
BX420340.1	649	.....	500
Query	1576	GATGGCCCTAAATCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGGTGGGTGTCACT	1725
BY794942.2	1233	.....	1382
DC527884.1	1235	.....	1384
CF111220.1	1228	.....C.....C.....C.....A.....T.....C..T..AC.T.....T.....C.....G.....T.....	1377
BX426149.2	494	.....	345
CO001006.1	540	.....A.....C.....C.....T.....C.....T..T..T.....T..C.....C..T.....G.....C.....C..T.....	391
BX418564.2	504	.....	355
AL567209.3	465	.....K.....	316
BX440470.1	505	.....	356
BX420340.1	499	.....	350
Query	1726	AAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAANTGAATATTTATCCCTAATACCTGGCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTT	1875
BY794942.2	1383	.....	1532
DC527884.1	1385	.....	1534
CF111220.1	1378	....C.....A.....A.....C.....G.....C.....C.....	1527
BX426149.2	344	.....	195
CO001006.1	390	.....A.....C.....C.....G.....C.....C.....	241
BX418564.2	354	.....	205
AL567209.3	315	.....M.....Y.....	165
		<div> <div> </div> <div> </div> <div> </div> </div>	
BX440470.1	355	.....	206
BX420340.1	349	.....	200
Query	1876	GGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAGGAGAATgttttgtggaccactttgttttttttttgcgtgtggcagttttaagttattagtttttaaaatcagttacttt	2025
BY794942.2	1533	.....	1682
DC527884.1	1535	.....	1684
CF111220.1	1528	.....A.....G.....C.....	1666
BX426149.2	194	.....	45
CO001006.1	240	.....A.....A.....G.....	100
		<div> <div> </div> <div> </div> <div> </div> </div>	
BX418564.2	204	.....	55
AL567209.3	164	.....	14
		<div> <div> </div> <div> </div> <div> </div> </div>	
BX440470.1	205	.....	56
BX420340.1	199	.....	50
Query	2026	ttaATGGAAACAACCTTGACCAAAAAATTTGTACAGAAATTTTGAGACCCATTAAAAAAGTTAAATG	2090
BY794942.2	1683	.....	1747
DC527884.1	1685	.....	1749
CF111220.1	1667	.....C.....T.....	1731
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Query	751	.....TGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGGCGCTGGCTCTCCAGGATGCTACAAAAATTGGTGGTATTGGTACTGTTCCCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCAC	900
DC527884.1	757	.....	906
BY794942.2	754	.....	903
CF111220.1	750	G..A..T.....T..G..G.....TC..A...C.....T.....C..C..C..C..G.....A.....T.....T.....	899
BX426149.2	972	.....	823
CO001006.1	1018	..A.....T.....G.....C.....A.....TT.....T.....A..G..T..T.....T..C.....	869
BX418564.2	982	.....	833
BX426150.2	725	.....C.....	874
AL567209.3	942	.....K.....	793
BX440470.1	984	.....R.....	835
BX420340.1	977	.....A.....R.....	828
Query	901	CTTTGCTCCAGTCAACGTTACAACGGAAGTAAAACTGTGCGAAATGCACCACTGAAGCTTTGAGTGAAGCTCTTCTCTGGGACAATGTGGGCTTCAATGTCAAGAATGTCTGTCTGCAAGGATGTTCTGCTGGCAACGTTGCTGTTGACAG	1050
DC527884.1	907	.....	1056
BY794942.2	904	.....	1053
CF111220.1	900	.....T..A.....T.....C..G...G.....G.....A.....C...A...C.....A..C...A.A.....T.....G.....	1049
BX426149.2	822	.....	673
CO001006.1	868	.....C.....T..A.....T..G..G..G..C..A.....C.....C.....A...C.....T..G.....	719
BX418564.2	832	.....	683
BX426150.2	875	.....	1023
		.....G.....	
AL567209.3	792	.....	643
BX440470.1	834	.....	685
BX420340.1	827	.....	678
Query	1051	CAAAAATGACCCACCAATGGAAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAAGAT	1200
DC527884.1	1057	.....	1206
BY794942.2	1054	.....	1204
		.....G.....	
CF111220.1	1050	.....G..C..T..T.....TC...C.....C.....A.....C.....T..A..G.....	1199
BX426149.2	672	.....	523
CO001006.1	718	.....T.....C.....T.....C...A.....T.....C..T.GT..A...A...GC.....T...A.....T.....G.....	569
BX418564.2	682	.....	533
BX426150.2	1024	.....-.....-.....-.....-.....-.....-.....T..-.....	1140
AL567209.3	642	.....-.....-.....-.....-.....-.....-.....	494
BX440470.1	684	.....	534
		.....C.....	
BX420340.1	677	.....	528
Query	1201	TGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTTCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTCTGGCAAGCCCATGTGTGTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCTTTTGCTGTCTGTGATAT	1350
DC527884.1	1207	.....	1356
BY794942.2	1205	.....	1354
CF111220.1	1200	C.....T.....G.....C.....C.....C.....A.....T.....C..T..AC.T.....T.....C.....	1349
BX426149.2	522	.....	373
CO001006.1	568	.....T.....G.....A.....C.....C.....T.....C.....T..T..T.....T..C.....C..T.....G..C.....	419
BX418564.2	532	.....	383
AL567209.3	493	.....K.....	344
BX440470.1	533	.....	384
BX420340.1	527	.....	378
Query	1351	GAGACAGACAGTTGGCGTGGGTGTCTATCAAGCAGTGGACAGAAGGCTGTCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATATATCCCTAATACCTGCCACCCCACTCTTAATCAGTCGTTGGAAG	1500
DC527884.1	1397	.....A.....	1506
BY794942.2	1355	.....	1504
CF111220.1	1350	..G.....T.....C.....A.....A.....A.....C.....G.....	1499
BX426149.2	372	.....	223
CO001006.1	418	.....C..T.....A.....C.....C.....C.....G.....	269
BX418564.2	382	.....	233
AL567209.3	343	.....M.....Y.....	193
		.....A.....	
BX440470.1	383	.....	234
BX420340.1	377	.....	228
Query	1501	AACGGTCTCAGAACTGTTTGTTCATTTGGCCATTTAAGTTTAGTAGTAAAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAGGAGAAATgtttttgtggaccacttttggtttcttttttgcgtgtggcagtttta	1650
DC527884.1	1507	.....	1656
BY794942.2	1505	.....	1654
CF111220.1	1500	.....C.....A.....	1638
BX426149.2	222	.....	73
CO001006.1	268	.....C.....A.....	128
		.....T.....	
BX418564.2	232	.....	83
AL567209.3	192	.....	42





BY794942.2	606	.....	755
CF111220.1	602	.....T.....G.....C.A.....G.....C.....G.....	751
BX426149.2	1120	.....	971
CO001006.1	1166	.....C.....T.....A.....C.....C.....	1017
BX418564.2	1124	.....S.....-.....R.....-.....-.....C.....-.....	981
BX426150.2	577	.....	726
AL567209.3	1090	.....C.....	941
BX440470.1	1124	.....-W.....-.....-S.M.Y.-K.....-.....K.....	983
BX420340.1	1117	.....M.M.....C.....K.-..M.W...YT...D...K.-.....T.....Y.....	976
Query	752	AGGCTCTGACTGCATCCTACACCAACTCGTCAACTGACAACTTTGCGCCTGCCTCTCCAGGATGTTCTACAAAATGTGTATTGGTACTGTTCTGTGTGGCCGAGTGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAG	901
DC527884.1	759	.....	917
BY794942.2	756	.....	914
CF111220.1	752	.A..T.....T..C.G.....A.....C.....T.....G.C.....C.....G.....A.....T.....T.....	910
BX426149.2	970	.....	812
CO001006.1	1016	.A.....T.....C.....C.....TT.....T.....A.....G..T..T.....T..C.....C.....	858
BX418564.2	980	.....	822
BX426150.2	727	.....	885
AL567209.3	940	.....	782
BX440470.1	982	.....	824
BX420340.1	975	.....	817
Query	902	TCAACGTTTACAACGGAAGTAAAAATCTGTGCAAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTCTGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAATGACC	1051
DC527884.1	918	.....	1067
BY794942.2	915	.....	1064
CF111220.1	911	.....T..A.....T.....C..G.....G.....G.....A.....C..A.....C.....A..C.....A.A.....T.....G.....	1060
BX426149.2	811	.....	662
CO001006.1	857	.....T..A.....T..G..G..G..C..A.....C.....C.....A.....C.....T..G.....T.....	708
BX418564.2	821	.....	672
BX426150.2	886	.....	1034
AL567209.3	781	.....	633
BX440470.1	823	.....	674
BX420340.1	816	.....	667
Query	1052	CACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCTGTAACCATCCAGGCCAAATAAGCGCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCGTT	1201
DC527884.1	1068	.....	1217
BY794942.2	1065	.....	1215



BX442182.2	BX442182	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1873	0.0	99%
BX418589.2	BX418589	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1873	0.0	99%
BX418564.2	BX418564	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1868	0.0	99%
BX420340.1	BX420340	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1866	0.0	99%
BX459625.2	BX459625	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1860	0.0	99%
AL517685.3	AL517685	Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1845	0.0	98%
BX440303.2	BX440303	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1845	0.0	98%

ALIGNMENTS

Query	2	TTTTTCGCAACGGGTTTGCCCGCAGAACACAGGTGTCGTGAAAACCTACCCCTAAAGCCAAATGGGAAGGAAAGACTCATATCAACATTGTCTGTCATTGGACACGTAGATTTCGGCAAGTCCACCACTACTGGCCATCTGATCTATA	151
BY794942.2	25	.....	155
DC527884.1	9	.....	158
Query	152	AATGCGGTGSCATCGACAAAAGAACCATTTGAAAAATTTGAGAAGGAGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCTTTGGTTCAAGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCAAGCTGCTTGAGGCTC	301
BY794942.2	689	.....	761
BY794942.2	156	.....G...	243
		G	
DC527884.1	692	.....	764
DC527884.1	159	.....G...	246
		G	
BX440470.1	1049	.....K.....	977
BX442182.2	1041	.....	969
BX418589.2	1048	.....K.C.....	976
BX418564.2	1046	.....	975
BX420340.1	1042	.....	970
BX459625.2	1036	.....K.A.....	964
AL517685.3	2	.....	74
BX440303.2	1044	.....K.....R.....M.....N.....R.....	974
Query	302	TGGACTGCATCCTACCACCAACTCGTCCAAGTACCAAGCCCTTGGCGCTGCTCTCCAGGATGTCTACAAAATTTGGTGGTATTGGTACTGTTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAAACCGGTATGGTGGTCAACCTTTGCTC	451
BY794942.2	762	.....	911
DC527884.1	765	.....	914
BX440470.1	976	..R.....	827
BX442182.2	968	.....R.....	819
BX418589.2	975	.....	826
BX418564.2	974	.....C.....	825
BX420340.1	969	..A.....R.....	820
BX459625.2	963	.....	814
AL517685.3	75	.....	224
BX440303.2	973	.....	825
Query	452	CAGTCAACGTACAAACGGAAGTAAATCTGTGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCCTGGGGACAATGTGGCTTCATGTCAAGAAATGTGTCTGTCAAGGATGTTCTGCTGGTGCACGTTGCTGGTGAAGCAAAATG	601
BY794942.2	912	.....	1061
DC527884.1	915	.....	1064
BX440470.1	826	.....	677
BX442182.2	818	.....	669
BX418589.2	825	.....	676
BX418564.2	824	.....C.....	675
BX420340.1	819	.....	670
BX459625.2	813	.....	664
AL517685.3	225	.....	374
BX440303.2	824	.....C.....	675
Query	602	ACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCTTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGGCTGAGCTGAAGGAAAAGATTGATCGCCG	751
BY794942.2	1062	.....	1213
		G	
DC527884.1	1065	.....	1215
		C	
BX440470.1	676	.....	525
		C	
BX442182.2	668	.....	518
		C	
BX418589.2	675	.....Y.S.....	525
		C	
BX418564.2	674	.....M.....	524

BX420340.1	669	.....	c	.....	519
			c		
BX459625.2	663	.....			513
			c		
AL517685.3	375	.....			525
			c		
BX440303.2	674	.....			524
			c		
Query	752	TTCTGGTAAAAAGCTGGAAGATGGCCCTAAATCTTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCATGTGTGTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTTGCTGTTCTGATATGAGACAGACA			901
BY794942.2	1214	.....			1364
			c		
DC527884.1	1216	.....			1366
			c		
BX440470.1	524	.....			374
			c		
BX442182.2	517	.....			367
			c		
BX418589.2	524	.....			374
			c		
BX418564.2	523	.....			373
			c		
BX420340.1	518	.....			368
			c		
BX459625.2	512	.....			362
			c		
AL517685.3	526	.....M.....			676
			c		
BX440303.2	523	.....			373
			c		
Query	902	GTTCGGTGGGTGTTCATCAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGA			1051
BY794942.2	1365	.....			1516
			c		
DC527884.1	1367	.....A.....			1518
			c		
BX440470.1	373	.....			222
			c		
BX442182.2	366	.....			215
			c		
BX418589.2	373	.....			222
			c		
BX418564.2	372	.....			221
			c		



Query= N13-10 [organism=Homo sapiens] eef1a1  
Length=1650

## ALIGNMENTS

			I C		
Query	752	TCCAAC	TGACAAGCCCTTGC	GCCTGCCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAATGTGGGCTTC	901
DC855699.1	753	.....	.....	.....	876
DC527884.1	987	.....	.....	.....	1000
DC527884.1	790	.....	.....	.....	929
BY794942.2	984	.....	.....	.....	997
BY794942.2	787	.....	.....	.....	926
CR996969.1	17	.....	.....	.....	30
CR996534.1	86	.....	.....	.....	99
CR996534.1	1	.....	.....	.....	28
CR982215.1	29	.....	.....	.....	42
BX453401.2	40	.....	.....	.....	53
BX443032.2	166	.....	.....	.....	179
BX443032.2	1	.....	.....	.....	108
BX421307.2	140	.....	.....	.....	153
BX421307.2	23	.....	.....	.....	82
			\ I T		
BX353545.2	45	.....	.....	.....	58
Query	902	AATGTC	AAGAATGTGTCTGTCAAGGATGTTCTGTCGTGGCAACGTTGCTGGTGACAGCAAAAAATGACCCCAATGGAAGCAGCTGGCTTC	ACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAAATAAGCGCCGGTATGCCCTGTGA	1051
DC527884.1	1001	.....	.....	.....	1150
BY794942.2	998	.....	.....	.....	1148
			\ I G		
CR996969.1	31	.....	.....	.....	180
CR996534.1	100	.....	.....	.....	249
CR982215.1	43	.....	.....	.....	192
BX453401.2	54	.....	.....	.....	203
BX443032.2	180	.....	.....	.....	329
BX421307.2	154	.....	.....	.....	303
BX353545.2	59	.....	.....	.....	208
Query	1052	TTGGATTGCC	CACCGCTCACATTCGATGCAAGTTTGGTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGTGGCCCTAAATTTCTTGAAGTCTGGT	GATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATG	1201
DC527884.1	1151	.....	.....	.....	1300
BY794942.2	1149	.....	.....	.....	1298
CR996969.1	181	.....	.....	.....	330
CR996534.1	250	.....	.....	.....	399
CR982215.1	193	.....	.....	.....	342
BX453401.2	204	.....	.....	.....	353
BX443032.2	330	.....	.....	.....	479
BX421307.2	304	.....	.....	.....	453
BX353545.2	209	.....	.....	.....	358
Query	1202	TGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTTGCTGTTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGTCTGCCAGAAAAGCTCAGAAG			1351
DC527884.1	1301	.....	.....	.....	1450
BY794942.2	1299	.....	.....	.....	1448
CR996969.1	331	.....	.....	.....	480
CR996534.1	400	.....	.....	.....	549
CR982215.1	343	.....	.....	.....	492
BX453401.2	354	.....	.....	.....	503
BX443032.2	480	.....	.....	.....	629
BX421307.2	454	.....	.....	.....	603
BX353545.2	359	.....	.....	.....	508
Query	1352	GCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAAGCGTCTCAGAACTGTTTGTGTTCAATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGG			1501
DC527884.1	1451	.....	.....	.....	1600
BY794942.2	1449	.....	.....	.....	1598
CR996969.1	481	.....	.....	.....	630
CR996534.1	550	.....	.....	.....	699
CR982215.1	493	.....	.....	.....	642
BX453401.2	504	.....	.....	.....	653
BX443032.2	630	.....	.....	.....	779
BX421307.2	604	.....	.....	.....	753
BX353545.2	509	.....	.....	.....	658
Query	1502	AAAGGAGAAATgtttt	gtggaccactttgggtttttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagtagctttttaATGGAACAACCTTGACCAAAAATTTGTCACAGAATTTTGAGACCCATTAAAAAGTTAAATG		1650
DC527884.1	1601	.....	.....	.....	1749
BY794942.2	1599	.....	.....	.....	1747
CR996969.1	631	.....	.....	.....	779
CR996534.1	700	.....	.....	.....	848
CR982215.1	643	.....	.....	.....	791
BX453401.2	654	.....	.....	.....	802
BX443032.2	780	.....	.....	.....	928
BX421307.2	754	.....	.....	.....	902
BX353545.2	659	.....	.....	.....	807

Query= N14-17 [organism=Homo sapiens] eef1a1

Length=1118

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
BU845975.1 AGENCOURT_10413042 NIH_MGC_109 Homo sapiens cDNA cl...	1592	0.0	100%
BX421307.2 BX421307 Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1591	0.0	100%
BX443032.2 BX443032 Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1587	0.0	100%
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	1585	0.0	100%
BU192437.1 AGENCOURT_7938567 NIH_MGC_92 Homo sapiens cDNA clon...	1585	0.0	100%
BX417098.2 BX417098 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1583	0.0	100%
DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog...	1580	0.0	100%
BX441194.2 BX441194 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1580	0.0	100%
BQ049312.1 AGENCOURT_6795094 NIH_MGC_85 Homo sapiens cDNA clon...	1580	0.0	100%
BM477966.1 AGENCOURT_6482916 NIH_MGC_85 Homo sapiens cDNA clon...	1580	0.0	100%

ALIGNMENTS

Query	2	TTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAACCTACCCCTAAAAAGCAAAATGGGAAAGGAAAAGACTCATATCAACATTGTCGTATTGGACACGTAGATTTCGGGCAAGTCCACCCTACTGGCCATCTGATCTAT	151
BU794942.2	25	.....	154
DC527884.1	9	.....	157
Query	152	AAATGCGGTGGCATCGACAAAAAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCTGGGTCTTGGATAAACTCAAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAAACGGA	301
BU845975.1	867	.....N.....	817
BX421307.2	37	.....	86
BX443032.2	63	.....	112
BY794942.2	881	.....	930
BY794942.2	155	...G...	259
BU192437.1	8	.....	57
BX417098.2	26	.....	75
DC527884.1	884	.....	933
DC527884.1	158	...G...	262
BX441194.2	75	.....W.....	124
BQ049312.1	35	.....	84
BM477966.1	19	.....	68
Query	302	AGTAAATCTGTGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTCAATGTCAAGATGTGTCTGTCAGGATGTTCTGCTGGCAACGTTGCTGGTGACAGCAAAAAATGACCCACCAATGGAAGCAGC	451
BU845975.1	816	.....	667
BX421307.2	87	.....	236
BX443032.2	113	..M.....	262
BY794942.2	931	.....	1080
BU192437.1	58	.....	207
BX417098.2	76	.....	225
DC527884.1	934	.....	1083
BX441194.2	125	.....	274
BQ049312.1	85	.....	234
BM477966.1	69	.....	218
Query	452	TGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGA	601
BU845975.1	666	.....	517
BX421307.2	237	.....	386
BX443032.2	263	.....	412
BY794942.2	1081	.....	1231
		\   G	
BU192437.1	208	.....	357
BX417098.2	226	.....	375
DC527884.1	1084	.....	1233
BX441194.2	275	.....	424
BQ049312.1	235	.....	384
BM477966.1	219	.....	368
Query	602	AGATGGCCCTAAATTCCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTTGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCTTTGCTGTTTCGTGATATGAGACAGACAGTTGCGGTGGGTGCAT	751
BU845975.1	516	.....	367
BX421307.2	387	.....	536
BX443032.2	413	.....	562
BY794942.2	1232	.....	1381
BU192437.1	358	.....	507
BX417098.2	376	.....	525
DC527884.1	1234	.....A.....	1383
BX441194.2	425	.....	574
BQ049312.1	385	.....	534
BM477966.1	369	.....	518
Query	752	CAAAGCAGTGGAACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCAT	901
BU845975.1	366	.....	217
BX421307.2	537	.....	686
BX443032.2	563	.....	712
BY794942.2	1382	.....	1531



BU192437.1	508	.....	657
BX417098.2	526	.....	675
DC527884.1	1384	.....C.....	1533
BX441194.2	575	.....	724
BQ049312.1	535	.....	684
BM477966.1	519	.....	668

Query	902	TGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAGGAGAAATgtttgtggaccacttgggttttttttgcgtgtggcagtttaagttattagtttttaaaatcagttactt	1051
BU845975.1	216	.....	67
BX421307.2	687	.....	836
BX443032.2	713	.....	862
BY794942.2	1532	.....	1681
BU192437.1	658	.....A.....	807
BX417098.2	676	.....	825
DC527884.1	1534	.....	1683
BX441194.2	725	.....	874
BQ049312.1	685	.....	834
BM477966.1	669	.....-	817

Query	1052	tttaATGGAACAACCTTGACCAAAAATTTGTCACAGAATTTTGAGACCCATTaaaaaaGTTAAATG	1118
BU845975.1	66	.....-	1
BX421307.2	837	.....-	902
BX443032.2	863	.....-	928
BY794942.2	1682	.....-	1747
BU192437.1	808	.....C.....	874
BX417098.2	826	.....-	890
DC527884.1	1684	.....	1749
BX441194.2	875	.....	939
BQ049312.1	835	.....T.....	901

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BM477966.1	818	.....N.....-	883
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Query= N15-19 [organism=Homo sapiens] eef1a1

Length=933

		Score	E	Max
Sequences producing significant alignments:		(Bits)	Value	ident
DC635691.1	DC635691 macaque bone marrow cDNA library QbmA Maca...	1150	0.0	97%
BQ005659.1	UI-H-ED0-ayr-1-05-0-UI.s1 NCI CGAP ED0 Homo sapiens...	1153	0.0	100%
BM997474.1	UI-H-DH0-aug-1-16-0-UI.s1 NCI CGAP DH0 Homo sapiens...	1153	0.0	100%
CT005089.1	CT005089 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1151	0.0	100%
CR999820.1	CR999820 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1151	0.0	100%
CR999128.1	CR999128 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1151	0.0	100%
CR996969.1	CR996969 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1151	0.0	100%
CR996534.1	CR996534 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1151	0.0	100%
CR989971.1	CR989971 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1151	0.0	100%
CR987376.1	CR987376 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1151	0.0	100%

# ALIGNMENTS

Query	1	CTTTTCGCAACGGGTTTGCCGCCAGACACAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAGGAAAAGACTCATATCAACATTGTCGTGATTGGACACGTAGATTGGGCAAGTCCACCACTACTGCCATCTGATCTAT	150
DC635691.1	1	.....-.....	149

Query	151	AAATCGCGTGGCATCGACAAAAGAACCATTGAAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA	300
DC635691.1	150	.....G.....	299

Query	301	TTTGAGACCAAATAAGCGCCTGCTATGCCCTGTATTGGATTGCCACACGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATCTTGAAGTCTGGTGATG	450
DC635691.1	300	.....T.A..T.....G.....A.....A.....	459

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| | | | | | | |  
GC G TT A AT  
|  
T G

BQ005659.1	648	..N.....G.....	503
BM997474.1	648	..N.....G.....	503
CT005089.1	45	..G.....G.....	190
CR999820.1	3	..G.....G.....	148
CR999128.1	117	..G.....G.....	262
CR996969.1	150	..G.....G.....	295
CR996534.1	219	..G.....G.....	364
CR989971.1	75	..G.....G.....	220
CR987376.1	12	..G.....G.....	157

Query	451	CTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCTTGTGCTGTCGTGATATGAGACAGAGTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTG	600
DC635691.1	460	.....T.....G.....	609
BQ005659.1	502	.....	353
BM997474.1	502	.....	353

CT005089.1	191	.....	340
CR999820.1	149	.....	298
CR999128.1	263	.....	412
CR996969.1	296	.....	445
CR996534.1	365	.....	514
CR989971.1	221	.....	370
CR987376.1	158	.....	307

Query	601	GCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTTGCCATTTAAGTTTAGTAGTAAAGACTGGT	750
DC635691.1	610	.....	759
BQ005659.1	352	.....	203
BM997474.1	352	.....	203
CT005089.1	341	.....	490
CR999820.1	299	.....	448
CR999128.1	413	.....	562
CR996969.1	446	.....	595
CR996534.1	515	.....	664
CR989971.1	371	.....	520
CR987376.1	308	.....	457

Query	751	TAATGATAACAATGCATCGTAAACCTTCAGAAGGAAGGAGAATgttttgggaccactttgggtttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagtagtttttaATGGAACAACCTTGACCAAAAATTTGTC	900
DC635691.1	760	.....	904
BQ005659.1	202	.....	53
BM997474.1	202	.....	53
CT005089.1	491	.....	640
CR999820.1	449	.....	598
CR999128.1	563	.....	712
CR996969.1	596	.....	745
CR996534.1	665	.....	814
CR989971.1	521	.....	670
CR987376.1	458	.....	607

Query	901	ACAGAATTTTGAGACCCATTAAAAAGTTAAAT	933
DC635691.1	905	.....	929
BQ005659.1	52	.....	20
BM997474.1	52	.....	20
CT005089.1	641	.....	673
CR999820.1	599	.....	631
CR999128.1	713	.....	745
CR996969.1	746	.....	778
CR996534.1	815	.....	847
CR989971.1	671	.....	703
CR987376.1	608	.....	640

Query= N16-18 [organism=Homo sapiens] eef1a1

Length=970

Sequences producing significant alignments:				Score (Bits)	E Value	Max ident
CR999128.1	CR999128	RZPD	no.9017 Homo sapiens cDNA clone RZPD...	1247	0.0	100%
CR996969.1	CR996969	RZPD	no.9017 Homo sapiens cDNA clone RZPD...	1247	0.0	100%
CR996534.1	CR996534	RZPD	no.9017 Homo sapiens cDNA clone RZPD...	1247	0.0	100%
CR989971.1	CR989971	RZPD	no.9017 Homo sapiens cDNA clone RZPD...	1247	0.0	100%
CR982215.1	CR982215	RZPD	no.9016 Homo sapiens cDNA clone RZPD...	1247	0.0	100%
CR977084.1	CR977084	RZPD	no.9016 Homo sapiens cDNA clone RZPD...	1247	0.0	100%
BX453401.2	BX453401	Homo sapiens	T CELLS (JURKAT CELL LINE) Ho...	1247	0.0	100%
BX453399.2	BX453399	Homo sapiens	T CELLS (JURKAT CELL LINE) Ho...	1247	0.0	100%
BX443032.2	BX443032	Homo sapiens	B CELLS (RAMOS CELL LINE) Hom...	1247	0.0	100%
BX426531.2	BX426531	Homo sapiens	T CELLS (JURKAT CELL LINE) Ho...	1247	0.0	100%

# ALIGNMENTS

Query	296	TGGAAGCAGCTGGCTTCACTGCTCAGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTA	445
CR999128.1	71	.....	220
CR996969.1	104	.....	253
CR996534.1	173	.....	322
CR989971.1	29	.....	178
CR982215.1	116	.....	265
CR977084.1	62	.....	211
BX453401.2	127	.....	276
BX453399.2	681	.....	532
BX443032.2	253	.....	402
BX426531.2	72	.....	221

Query	446	AAAAGCTGGAAGATGGCCCTAAATTTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGG	595
CR999128.1	221	.....	370
CR996969.1	254	.....	403
CR996534.1	323	.....	472
CR989971.1	179	.....	328

CR982215.1	266	.....	415
CR977084.1	212	.....	361
BX453401.2	277	.....	426
BX453399.2	531	.....	382
BX443032.2	403	.....	552
BX426531.2	222	.....	371

Query	596	TGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGT	745
CR999128.1	371	.....	520
CR996969.1	404	.....	553
CR996534.1	473	.....	622
CR989971.1	329	.....	478
CR982215.1	416	.....	565
CR977084.1	362	.....	511
BX453401.2	427	.....	576
BX453399.2	381	.....	232
BX443032.2	553	.....	702
BX426531.2	372	.....	521

Query	746	TGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGAGAAATgttttgggaccactttgggtttcttttttgcgtgtggcagttttaagttattagtttttaaa	895
CR999128.1	521	.....	670
CR996969.1	554	.....	703
CR996534.1	623	.....	772
CR989971.1	479	.....	628
CR982215.1	566	.....	715
CR977084.1	512	.....	661
BX453401.2	577	.....	726
BX453399.2	231	.....	82
BX443032.2	703	.....	852
BX426531.2	522	.....	671

Query	896	atcagtagcttttttaATGGAAACAACCTTGACCAAAAATTTGTACAGAAATTTTGAGACCCATTAAAAAGTTAAAT	970
CR999128.1	671	.....	745
CR996969.1	704	.....	778
CR996534.1	773	.....	847
CR989971.1	629	.....	703
CR982215.1	716	.....	790
CR977084.1	662	.....	736
BX453401.2	727	.....	801
BX453399.2	81	.....	7
BX443032.2	853	.....	927
BX426531.2	672	.....	746

Query= N17-21 [organism=Homo sapiens] eeflal

Length=1093

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
CA442866.1 UI-H-DP0-avr-n-20-0-UI.s1 NCI_CGAP_Fs1 Homo sapiens...	1247	0.0	100%
CA417999.1 UI-H-FH0-bcc-k-24-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1247	0.0	100%
CA414363.1 UI-H-EZ0-bas-d-03-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens...	1247	0.0	100%
CX758265.1 AGENCOURT_41351531 NIH_MGC_278 Homo sapiens cDNA cl...	1245	0.0	100%
CT005089.1 CT005089 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1243	0.0	100%
CR999128.1 CR999128 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1243	0.0	100%
CR996969.1 CR996969 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1243	0.0	100%
CR996534.1 CR996534 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1243	0.0	100%
CR989971.1 CR989971 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1243	0.0	100%
CR982215.1 CR982215 RZPD no.9016 Homo sapiens cDNA clone RZPDp...	1243	0.0	100%

# ALIGNMENTS

Query	416	AATTTGAAGCAGCTGGCTTCACGTGCTCAGGTGATTTATCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTG	565
CA442866.1	697	...G.....	548
CA417999.1	697	...G.....	548
CA414363.1	699	...G.....	550
CX758265.1	704	.....	559
CT005089.1	1	.....	145
CR999128.1	73	.....	217
CR996969.1	106	.....	250
CR996534.1	175	.....	319
CR989971.1	31	.....	175
CR982215.1	118	.....	262
Query	566	GTA AAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTATGAGACAGACAGTTG	715
CA442866.1	547	.....	398
CA417999.1	547	.....	398
CA414363.1	549	.....	400
CX758265.1	558	.....	409
CT005089.1	146	.....	295

Query	866	TGTTTGTTTCAATTGGCCATTAAAGTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAGGAAGGAGAAATgttttgtggaccactttggttttcttttttgcgtgtggcagttttaagtattatagttttt	1015
CA442866.1	247	.....	98
CA417999.1	247	.....	98
CA414363.1	249	.....	100
CX758265.1	258	.....	109
CT005089.1	446	.....	595
CR999128.1	518	.....	667
CR996969.1	551	.....	700
CR996534.1	620	.....	769
CR989971.1	476	.....	625
CR982215.1	563	.....	712

Query= N18-C\* [organism=Homo sapiens] eef1a1

Length=1742

## ALIGNMENTS

[illegible]

Query	303	TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACCTTTATCAAAAAATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAG	452
DC527884.1	308	.....C.....	457
BY794942.2	305	.....	454
CF111220.1	301	.....C...G...G...C.....C.....G.....	450
CO001006.1	1464	.....T..C.....C.....C.....C.....	1318
BX426150.2	276	.....C.....	425
BU902062.1	287	.....	436
Query	453	AATGGGCAGACCCGAGAGCATGCCCTCTCGGCTTACACACTGGGTGTGAACAACTAATTGTGGTGTAAACAAATGGATTCCACTGAGCCACCCCTACAGCCAGAGATATGAGGAATTTGTAAGGAAGTCAGCACTTACATTAAG	602
DC527884.1	458	.....	607
BY794942.2	455	.....	604
CF111220.1	451	..C.....T.....T.....TT.....G.....T.....C.....A.....T.....C.....C.....C.....	600
BX426149.2	1196	.....-A.....-A.....G.....	1122
CO001006.1	1317	..C.....T.....C.....T..C.....T.....T.....C.....C.....C.....	1168
BX418564.2	1196	.....-.....-.....-.....YH.VS...-R.....-W...-G...W...-R.....M.....K...-R.....	1125
BX426150.2	426	.....	575
AL567209.3	1145	.....S.....-W...-K.W.....R.....-A.M.....	1092
BU902062.1	437	.....M.....	586
BX440470.1	1128	.....	1125
Query	603	AAAAATTGGCTACAACCCCGACACAGTAGCAATTTGTGCCAATTTCTGGTTGGAATGGTGACAAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCCAGCTGCTT	752
DC527884.1	608	.....	757
BY794942.2	605	.....	754
CF111220.1	601	.....T.....G.....C..A.....G.....C.....G.....	750
BX426149.2	1121	.....	972
CO001006.1	1167	.....C.....T.....A.....C.....C.....C.....	1018
BX418564.2	1124	.....S.....-R.....-.....C.....-.....	982
BX426150.2	576	.....	725
AL567209.3	1091	C.....C.....	942
BU902062.1	587	.....	736
BX440470.1	1124	.....-W...-S.M...Y...-K.....-.....K.....	984
Query	753	GAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACCTGACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTCTGTTGGCCGAGTGGAGACTGGTGTTCACAAACCCGGTATGGTGGTCACC	902
DC527884.1	758	.....	907
BY794942.2	755	.....	904
CF111220.1	751	..A..T.....T..G..G.....TC..A..C.....T.....C..C.....C.....G.....A.....T.....T.....	900
BX426149.2	971	.....	822
CO001006.1	1017	..A.....T.....G.....C.....A.....TT.....T.....A.....G..T..T.....T..C.....	868
BX418564.2	981	.....C.....	832
BX426150.2	726	.....	875
AL567209.3	941	.....K.....	792
BU902062.1	737	.....	886
BX440470.1	983	.....R.....	834
Query	903	TTTGCTCCAGTCAACGTTTACAACGGAAGTAAAACTGTGCAAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTCAATGTCAAGAATGTGTCTGTCAGGATGTTCTGTCGTGGCAACGTTGCTGGTGACAGC	1052
DC527884.1	908	.....	1057
BY794942.2	905	.....	1054
CF111220.1	901	.....T..A.....T.....C..G...G.....G.....A.....C..A.....C.....A..C...A.A.....T.....G.....	1050
BX426149.2	821	.....	672
CO001006.1	867	.....C.....T..A.....T..G..G..C..A.....C.....C.....A.....C.....T..G.....	718
BX418564.2	831	.....	682
BX426150.2	876	.....	1024
AL567209.3	791	.....G.....	642
BU902062.1	887	.....AC.....C..C.....C..C.....	1036
BX440470.1	833	.....G.....	684
Query	1053	AAAAATGACCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCTGTAACCATCCAGGCCAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATT	1202
DC527884.1	1058	.....	1207
BY794942.2	1055	.....	1205
CF111220.1	1051	.....G..C..T..T.....TC...C.....C.....A.....C.....T..A..G...C.....	1200
BX426149.2	671	.....T.....C.....T.....C..A.....T.....C..T..G..A...A...GC.....T...A.....T.....G.....	522
CO001006.1	717	.....	568
BX418564.2	681	.....	532
BX426150.2	1025	.....	1140
AL567209.3	641	.....	493
BU902062.1	1037	.....C.G...-.....T.....G.....-A.....C..G..T...-.....	1163



## ALIGNMENTS

[illegible]

BX443032.2	507	.....	656
BX412224.1	424	.....	275
BY794942.2	1326	.....	1475
BX441194.2	519	.....	668
BX417098.2	470	.....	619
BU844361.1	431	.....	282
Query	1221	GCCACCCACTCTTAATCAGTGGTGGGAAGACGGTCTCAGAACTGTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAA	1370
CR996534.1	577	.....	726
BX421307.2	631	.....	780
CX167214.1	274	.....	125
BU845975.1	272	.....	123
BX443032.2	657	.....	806
BX412224.1	274	.....	125
BY794942.2	1476	.....	1625
BX441194.2	669	.....	818
BX417098.2	620	.....	769
BU844361.1	281	.....	132
Query	1371	ggttttcttttttgcggtgtggcagttttaagttattagtttttaaaatcagttcttttaATGGAAACAACCTTGACCAAAAAATTTGTCACAGAATTTTGAGACCCATTAAAAAGTTAAAT	1492
CR996534.1	727	.....	847
BX421307.2	781	.....	901
CX167214.1	124	.....	4
BU845975.1	122	.....	2
BX443032.2	807	.....	927
BX412224.1	124	.....	3
BY794942.2	1626	.....	1746
BX441194.2	819	.....	938
BX417098.2	770	.....	889
BU844361.1	131	.....	11

Query= N20-6 [organism=Homo sapiens] eef1a1

Length=1602

	Score (Bits)	E Value	Max ident
Sequences producing significant alignments:			
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	1873	0.0	100%
DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog...	1866	0.0	100%
BX418589.2 BX418589 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1853	0.0	100%
BX440470.1 BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1853	0.0	100%
BX442182.2 BX442182 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1849	0.0	100%
AL541984.3 AL541984 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1845	0.0	99%
BX418564.2 BX418564 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1845	0.0	99%
BX459625.2 BX459625 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1844	0.0	100%
BX420340.1 BX420340 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1840	0.0	100%
BX440308.2 BX440308 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1836	0.0	99%

# ALIGNMENTS

Query	2	TTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAGGAAAGACTCATATCAACATTGTCGTATTGGACACGTAGATTTCGGGCAAGTCCACCCTACTGCCCATCTGATCTAT	151
BY794942.2	25	.....	154
DC527884.1	8	.....	157
Query	152	AAATGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA	301
BY794942.2	155	.....	304
DC527884.1	158	.....T.....	307
Query	302	TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGCTCCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAG	451
BY794942.2	305	.....	454
DC527884.1	308	.....C.....	457
Query	452	AATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTTAACAAAATGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGATGGCAATGCCAGTGGAAACC	601
BY794942.2	721	.....	745
BY794942.2	455	.....	585
DC527884.1	724	.....	748
DC527884.1	458	.....	588
BX418589.2	1016	.....	992
BX440470.1	1017	.....	993
BX442182.2	1009	.....	985
AL541984.3	1	.....	14
BX418564.2	1015	.....	991
BX459625.2	1004	.....	980
BX420340.1	1010	.....	986
BX440308.2	1014	.....-K.....	992
Query	602	ACGTCGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAATGACAAGCCCTTGGCCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATG	751



BY794942.2	746	.....	895
DC527884.1	749	.....	898
BX418589.2	991	.....	842
BX440470.1	992	.....R.....	843
BX442182.2	984	.....R.....	835
AL541984.3	15	.....C.....	164
BX418564.2	990	.....	841
BX459625.2	979	.....A.....R.....	830
BX420340.1	985	.....	836
BX440308.2	991	M.....R.....M.....	842
Query	752	GTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAAATGTGCTGTCAAGGATGTTCTGCTGTGGCAACGTTGCT	901
BY794942.2	896	.....	1045
DC527884.1	899	.....	1048
BX418589.2	841	.....	692
BX440470.1	842	.....	693
BX442182.2	834	.....	685
AL541984.3	165	.....	314
BX418564.2	840	.....C.....	691
BX459625.2	829	.....	680
BX420340.1	835	.....	686
BX440308.2	841	.....	692
Query	902	GGTGACAGCAAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACCTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAG	1051
BY794942.2	1046	.....	1196
		\   G	
DC527884.1	1049	.....	1198
BX418589.2	691	.....	542
BX440470.1	692	.....	543
BX442182.2	684	.....	535
AL541984.3	315	.....	464
BX418564.2	690	.....	541
BX459625.2	679	.....	530
BX420340.1	685	.....	536
BX440308.2	691	.....M.....	542
Query	1052	GAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTTCTGAAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTT	1201
BY794942.2	1197	.....	1346
DC527884.1	1199	.....	1348
BX418589.2	541	.....Y.S.....	392
BX440470.1	542	.....	392
		\   C	
BX442182.2	534	.....	385
AL541984.3	465	.....	614
BX418564.2	540	.....M.....	391
BX459625.2	529	.....	380
BX420340.1	535	.....	386
BX440308.2	541	.....	392
Query	1202	CGTGATATGAGACAGACAGTTGCGGTGGGTGTCTCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAANTGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGT	1351
BY794942.2	1347	.....	1496
DC527884.1	1349	.....A.....	1498
BX418589.2	391	.....C.....	242
BX440470.1	391	.....	242
BX442182.2	384	.....	235
AL541984.3	615	.....	764
BX418564.2	390	.....	241
BX459625.2	379	.....	230
BX420340.1	385	.....	236
BX440308.2	391	.....	242
Query	1352	GGTGAAGAACGGTCTCAGAACTGTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAAATgttttgggacactttggtttttcttttttgcgtgtgg	1501
BY794942.2	1497	.....	1646
DC527884.1	1499	.....	1648
BX418589.2	241	.....	92
BX440470.1	241	.....	92
BX442182.2	234	.....	85
AL541984.3	765	.....K.....	914
BX418564.2	240	.....	91
BX459625.2	229	.....	80
BX420340.1	235	.....	86
BX440308.2	241	.....	92
Query	1502	cagttttaagttattagttttttaaatcagtagctttttaATGGAACAACCTTGACCAAAAAATTTGTACAGAAATTTGAGACCCCACTTAAAAAAGTTAAAT	1602
BY794942.2	1647	.....	1746
		\   T	

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DC527884.1 1649 .....-..... 1748
                                     \
                                     |
                                     T
BX418589.2 91 .....-..... 1
                                     \
                                     |
                                     D
BX440470.1 91 .....-..... 1
                                     \
                                     |
                                     T
BX442182.2 84 .....-..... 1
                                     \
                                     |
                                     T
AL541984.3 915 S.....-..... 1015
                                     \
                                     |
                                     M
BX418564.2 90 .....-..... 1
BX459625.2 79 .....-..... 4
BX420340.1 85 .....-..... 2
                                     \
                                     |
                                     T
BX440308.2 91 .....-..... 1

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Query= N21-3 [organism=Homo sapiens] eef1a1

Length=656

		Score	E	Max
Sequences producing significant alignments:		(Bits)	Value	ident
BX441194.2	BX441194 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1205	0.0	100%
BX417098.2	BX417098 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1205	0.0	100%
CA422292.1	UI-H-FG0-bdg-d-06-0-UI.s1 NCI_CGAP_EN1_2 Homo sapie...	1203	0.0	100%
BU628737.1	UI-H-FG0-bdg-k-06-0-UI.s1 NCI_CGAP_EN1_2 Homo sapie...	1203	0.0	100%
BU628664.1	UI-H-FG0-bdf-1-02-0-UI.s1 NCI_CGAP_EN1_2 Homo sapie...	1203	0.0	100%
CT005089.1	CT005089 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR999128.1	CR999128 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR996969.1	CR996969 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR996534.1	CR996534 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%
CR989971.1	CR989971 RZPD no.9017 Homo sapiens cDNA clone RZPDp...	1201	0.0	100%

#### ALIGNMENTS

Query	1	TGCTCAGGTGATTATCTGGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCC	150
BX441194.2	284	.....	433
BX417098.2	235	.....	384
CA422292.1	678	.....	529
BU628737.1	678	.....	529
BU628664.1	678	.....	529
CT005089.1	18	.....	167
CR999128.1	90	.....	239
CR996969.1	123	.....	272
CR996534.1	192	.....	341
CR989971.1	48	.....	197
Query	151	TAAATTCCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTTGGCAAGCCCATGTGTTGTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGATATGAGACAGACAGTTGCGGTGGGTGTCAATCAAGCAGT	300
BX441194.2	434	.....	583
BX417098.2	385	.....	534
CA422292.1	528	.....	379
BU628737.1	528	.....	379
BU628664.1	528	.....	379
CT005089.1	168	.....	317
CR999128.1	240	.....	389
CR996969.1	273	.....	422
CR996534.1	342	.....	491
CR989971.1	198	.....	347
Query	301	GGACAAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAAGCTGTTTGTCAATTGGCCATTT	450
BX441194.2	584	.....	733
BX417098.2	535	.....	684
CA422292.1	378	.....	229
BU628737.1	378	.....	229
BU628664.1	378	.....	229
CT005089.1	318	.....	467
CR999128.1	390	.....	539
CR996969.1	423	.....	572

CR996534.1	492	.....	641
CR989971.1	348	.....	497
Query	451	AAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCGACGGAAGGAGAGAAATgttttggaccactttggtttctcttttttgcgtgtggcagttttaagtattagtttttaaatacagtaacttttaATGGA	600
EX441194.2	734	.....	883
EX417098.2	685	.....	834
CA422292.1	228	.....	79
BU628737.1	228	.....	79
BU628664.1	228	.....	79
CT005089.1	468	.....	617
CR999128.1	540	.....	689
CR996969.1	573	.....	722
CR996534.1	642	.....	791
CR989971.1	498	.....	647

CR	BU	CT	CR	CR	CR	CR	CR
222222.1	78	.....	.....	.....	.....	.....	.....
BU628737.1	78	.....N.....	.....	.....	.....	.....	.....
BU628664.1	78	.....N.....	.....	.....	.....	.....	.....
CT005089.1	618	.....-.....	.....	.....	.....	.....	.....
CR999128.1	690	.....-.....	.....	.....	.....	.....	.....
CR996969.1	723	.....-.....	.....	.....	.....	.....	.....
CR996534.1	792	.....-.....	.....	.....	.....	.....	.....
CR989971.1	648	.....-.....	.....	.....	.....	.....	.....

Sequences producing significant alignments:					Score (Bits)	E	Max ident
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan trog...	3053	0.0	99%		
BY794942.2	BY794942	Homo sapiens eye Homo sapiens cDNA clone H...	3037	0.0	99%		
BX461649.2	BX426149	Homo sapiens NEUROBLASTOMA Homo sapiens c...	2012	0.0	97%		
BX418564.2	BX418564	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1932	0.0	96%		
BX440470.1	BX440470	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1929	0.0	100%		
BX418589.2	BX418589	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1921	0.0	100%		
BX442182.2	BX442182	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1910	0.0	100%		
BX420340.1	BX420340	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1917	0.0	100%		
BX459625.2	BX459625	Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1910	0.0	100%		
BX325185.1	BX325185	Homo sapiens T CELLS (JURKAT CELL LINE) Co...	1892	0.0	99%		

Query	2	TTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAATACCCCTAAAAGCCAAATGGGAAAGGAAAAGACTCATATCAACATTTGCTGTCATTGGACACGTAGATTTCGGGCAAGTCACCACACTACTGCCCATCTGATCTATA	151
DC527884.1	9		158
BY794942.2	25		155
Query	152	AATGCGGTGGCATCGACAAAGAACCATTGAAAAATTTGAGAGGAGGCTGCTGAGATGSGAAAGGGCTCCTTCAAGTATGCCTGGGTCCTGGATAAATGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAAT	301
DC527884.1	159		308
BY794942.2	156		305
Query	302	TTGAGACGACGAACTACTATGTGACTATCATTTGATGCCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCCTGATTGTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAGA	451
DC527884.1	309		458

BY794942.2	306	.....	455
Query	452	ATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCTTACAGCCAGAGAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAAG	601
DC527884.1	459	.....	608
BY794942.2	456	.....	605
BX426149.2	1196	.....A.....A.....G.....	1121
BX418564.2	1196	.....YH.VS.....R.....W.....G.W.....R.....M.....K.....R.....	1125
Query	602	AAATTGGCTACAACCCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCCCTTGGTTCAAGGGATGGAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCACGCTGCTTGAGGCTCTGGACTGCATCCTAC	751
DC527884.1	609	.....	779
BY794942.2	606	.....AACATGCTGGAGCCAAGTGCT.....	776
BX426149.2	1120	.....AACATGCTGGAGCCAAGTGCT.....	950
BX418564.2	1124	.....S.....-R.....-.....TGGAGCCAAGTGCTAACATGC.....	960
BX440470.1	1052	.....C.....K.....	962
BX418589.2	1051	.....K.C.....	961
BX442182.2	1041	.....	954
BX420340.1	1045	.....A.....	955
BX459625.2	1039	.....K.A.....	949
BX325185.1	1050	.....C.Y.....K.M.....W.....K.R.M.....K.....A.....	960
Query	752	CACCAACTCGTCCAACGTGACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCACAAAAATGGTGGTATTGGTACTGTTCCTGTTGGCCGAGTGGAGACTGGTGTTCACAAACCCGGTATGGTGGTCACTTTGCTCCAGTCAACGTTACAA	901
DC527884.1	780	.....	929
BY794942.2	777	.....	926
BX426149.2	949	.....	800
BX418564.2	959	.....C.....	810
BX440470.1	961	.....	812
BX418589.2	960	.....R.....	811
BX442182.2	953	.....	804
BX420340.1	954	.....R.....	805
BX459625.2	948	.....	799
BX325185.1	959	.....R.....	810
Query	902	CGGAAGTAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTCAATGTCAAGAAATGTGTCTGTCAAGGATGTTGCTGCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCCAATGGAAG	1051
DC527884.1	930	.....	1079
BY794942.2	927	.....	1076
BX426149.2	799	.....	650
BX418564.2	809	.....C.....	660
BX440470.1	811	.....	662
BX418589.2	810	.....	661
BX442182.2	803	.....	654
BX420340.1	804	.....	655
BX459625.2	798	.....	649
BX325185.1	809	.....	660
Query	1052	CAGCTGGCTTCACTGCTCAGGTGATTATCTGAAACCATCCAGGCCAAAATAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTGAGCTGAAGGAAAAGATTGATGCGCGTCTTGGTAAAAAGC	1201
DC527884.1	1080	.....	1229
BY794942.2	1077	.....G.....	1227
BX426149.2	649	.....M.....	500
BX418564.2	659	.....	510
BX440470.1	661	.....C.....Y.S.....	511
BX418589.2	660	.....	511
BX442182.2	653	.....	504
BX420340.1	654	.....	505
BX459625.2	648	.....Y.....	499
BX325185.1	659	.....	510
Query	1202	TGGAAGATGGCCCTAAATTCCTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTGATATGAGACAGACAGTTGCGGTGGGTC	1351
DC527884.1	1230	.....A.....	1379
BY794942.2	1228	.....	1377
BX426149.2	499	.....	350

BX418564.2	509	.....	360
BX440470.1	510	.....	361
BX418589.2	510	.....	361
BX442182.2	503	.....	354
BX420340.1	504	.....	355
BX459625.2	498	.....	349
BX325185.1	509	.....	360

Query	1352	TCATCAAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGANGAACGGTCTCAGAACGTGTTGTTT	1501
DC527884.1	1380	.....C.....	1529
BY794942.2	1378	.....	1527
BX426149.2	349	.....	200
BX418564.2	359	.....	210
BX440470.1	360	.....	211
BX418589.2	360	.....	211
BX442182.2	353	.....	204
BX420340.1	354	.....	205
BX459625.2	348	.....	199
BX325185.1	359	.....	210

Query	1502	CAATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCTAAACCTTCAGAAGGAAAGGAGAATgttttgtggaccactttggttttcttttttgcgtgtggcagttttaagttattagtttttaaaatcagt	1651
DC527884.1	1530	.....	1679
BY794942.2	1528	.....	1677
BX426149.2	199	.....	50
BX418564.2	209	.....	60
BX440470.1	210	.....	61
BX418589.2	210	.....	61
BX442182.2	203	.....	54
BX420340.1	204	.....	55
BX459625.2	198	.....	49
BX325185.1	209	.....	60

Query	1652	acttttttaATGGAAACACTTGACCACAAAATTGTGCACAGATTTTGTAGACCCATTAAAAAGTTAAA	1719
DC527884.1	1680	.....	1747
BY794942.2	1678	.....	1745
BX426149.2	49	.....-.....-.....G.....G.....G.....T..	1
BX418564.2	59	.....M.....	1
BX440470.1	60	.....	1
BX418589.2	60	.....D.....	1
BX442182.2	53	.....	1
BX420340.1	54	.....R.....	1
BX459625.2	48	.....	1
BX325185.1	59	.....	1

Query= N23-12 [organism=Homo sapiens] eef1a1

Length=1128

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
CD684311.1 EST831 human nasopharynx Homo sapiens cDNA, mRNA se...	1136	0.0	98%
CR768893.1 DKFPz468L0412_r1 468 (synonym: phrt1) Pongo abelii ...	1072	0.0	100%
DA037335.1 DA037335 BGGI11 Homo sapiens cDNA clone BGGI1100023...	1072	0.0	100%
DA085397.1 DA085397 BRACE2 Homo sapiens cDNA clone BRACE203976...	1072	0.0	100%
DB247234.1 DB247234 UTERU1 Homo sapiens cDNA clone UTERU100011...	1072	0.0	100%
DB246583.1 DB246583 UMVEN1 Homo sapiens cDNA clone UMVEN100002...	1072	0.0	100%
DB100941.1 DB100941 THYMU1 Homo sapiens cDNA clone THYMU100016...	1072	0.0	100%
DB100909.1 DB100909 THYMU1 Homo sapiens cDNA clone THYMU100013...	1072	0.0	100%
DB194465.1 DB194465 TRACH1 Homo sapiens cDNA clone TRACH100013...	1072	0.0	100%
DB194442.1 DB194442 TRACH1 Homo sapiens cDNA clone TRACH100011...	1072	0.0	100%

ALIGNMENTS

Query	1	CTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAACTACCCCTAAAAAGCCAAAAATGGGAAAGGAAAGAACTCATATCAACATTGTGTCATTGGACACGTAGATTTCGGGCAAGTCCACCACTACTGGCCATCTGATCT	150
CD684311.1	24	.....-.....	169
CR768893.1	2	.....	150
DA037335.1	1	.....	149
DA085397.1	1	.....	149
DB247234.1	1	.....	149
DB246583.1	1	.....	149
DB100941.1	1	.....	149
DB100909.1	1	.....	149
DB194465.1	4	.....	152
DB194442.1	1	.....	149
Query	151	ATAAATGCGGTGGCATCGACAAAAGAACATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCTCTGTGGA	300
CD684311.1	170	.....	319
CR768893.1	151	.....	300
DA037335.1	150	.....	299
DA085397.1	150	.....	299

DB247234.1	150	299
DB246583.1	150	299
DB100941.1	150	299
DB100909.1	150	299
DB194465.1	153	302
DB194442.1	150	299

Query	451	AGAATGGGCGAGACCCGAGAGCATGCCCTTGGCTTACACATGGGTGTGAAACCACTAATTTGTGGTGTAAACAAAATGGATTCCACTGAGCCACCCCTACAGCCAGAAAGAGATATGAGGAAATTTGTAAGGAAAAGATTGATCGCGT	607
CD684311.1	470	.....	607
CR768893.1	451	.....	584
DA037335.1	450	.....	583
DA085397.1	450	.....	583
DB247234.1	450	.....	583
DB246583.1	450	.....	583
DB100941.1	450	.....	583
DB100909.1	450	.....	583
DB194465.1	453	.....	586
DB194442.1	450	.....	583

Query= N24-22 [organism=Homo sapiens] eef1a1

Sequences producing significant alignments:						Score (Bits)	E	Max ident
BX421307.2	BX421307	Homo sapiens	B CELLS (RAMOS CELL LINE) Hom...	1596	0.0	100%		
BX440302.2	BX440302	Homo sapiens	B CELLS (RAMOS CELL LINE) Hom...	1592	0.0	100%		
BY794942.2	BY794942	Homo sapiens	eye Homo sapiens cDNA clone H...	1592	0.0	100%		
BQ049312.1	AGENCOCURT	6795094 NIH_MGC_85	Homo sapiens cDNA clon...	1592	0.0	100%		
BX417098.2	BX417098	Homo sapiens	PLACENTA Homo sapiens cDNA c...	1591	0.0	100%		
BX441194.2	BX441194	Homo sapiens	FETAL BRAIN Homo sapiens cDNA...	1587	0.0	100%		
DC27884.1	DC27884	Japanese skin	cDNA library TetA Pan trop...	1587	0.0	100%		
AL541918.3	AL541918	Homo sapiens	PLACENTA Homo sapiens cDNA c...	1585	0.0	100%		
CR984260.1	CR984260	RZPD no.9017	Homo sapiens cDNA clone RZPD...	1583	0.0	100%		
BX440436.2	BX440436	Homo sapiens	FETAL BRAIN Homo sapiens cDNA...	1583	0.0	100%		

Query	1	GAAGTCAGCACTTACATTAAGAAAATGGGTACAACCCCGACACAGTAGCATTTGTGCCAATTTCCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAGTCACCGTAAGGATGGCAATG	150
BY794942.2	584	.....	734
		\	
		I	
		C	
DC527884.1	587	.....	737
		\	
		I	
		C	
AL541984.3	1		3
BX440436.2	1087	.....-K.....Y.....S.....-K.....-	1004
		\	
		I	
		C	
Query	151	CCAGTGAACCA CGCTGCTTGAGGCTCTGGACTGCATCTACCAACCACTCGTCCA ACTGACAAGCCTTGCGCTGCTCTCCAGGATGTCTACAAAACTGGTGTTCTCAAACC CGGTATGGTGGTCACCTTTGCTCCAGTCAACGTATA	300
BX421307.2	30	.....	79
BX443032.2	56	.....	105
EY794942.2	874	.....	923
BY794942.2	735	.....	839
		\	
		I	
		C	
BQ049312.1	28		77
BX417098.2	19		68
BX441194.2	68		117
DC527884.1	877		92

DC527884.1	738	.....		842
			\	
			C	
AL541984.3	143	.....		192
AL541984.3	4	.....		108
			\	
			C	
CR984260.1	46	.....		95
BX440436.2	866	.....		817
BX440436.2	1003	.....-YK.....		901
			\	
			C	
Query	301	CAACGGAAGTAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTGTCGTCACGTTGCTGGTGACAGCAAAATGACCCACCAATGG	450	
BX421307.2	80	.....		229
BX443032.2	106	.....M.....		255
BY794942.2	924	.....		1073
BQ049312.1	78	.....		227
BX417098.2	69	.....		218
BX441194.2	118	.....		267
DC527884.1	927	.....		1076
AL541984.3	193	.....		342
CR984260.1	96	.....		245
BX440436.2	816	.....		667
Query	451	AAGCAGCTGGCTTCACCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAGTTTGTCTGAGCTGAAGGAAAAGATTGATGCCGTTCTTGSTAAAAA	600	
BX421307.2	230	.....		380
			\	
			C	
BX443032.2	256	.....		406
			\	
			C	
BY794942.2	1074	.....		1225
		\		
		G		
BQ049312.1	228	.....		378
			\	
			C	
BX417098.2	219	.....		369
			\	
			C	
BX441194.2	268	.....		418
			\	
			C	
DC527884.1	1077	.....		1227
			\	
			C	
AL541984.3	343	.....		493
			\	
			C	
CR984260.1	246	.....		396
			\	
			C	
BX440436.2	666	.....		516
			\	
			C	
Query	601	GCTGGAAGATGGCCCTAAATCTTGAAGTCTGGTGATGCTGCCATTGTGATATGGTTCTTGCCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCTTTGCTGTTGATATGAGACAGACAGTTGCCGTGGG	750	
BX421307.2	381	.....		530
BX443032.2	407	.....		556
BY794942.2	1226	.....		1375
BQ049312.1	379	.....		528
BX417098.2	370	.....		519
BX441194.2	419	.....		568
DC527884.1	1228	.....		1377
AL541984.3	494	.....		643
CR984260.1	397	.....		546
BX440436.2	515	.....		366

Query	751	TGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGGAAGACGGTCTCAGAACTGTTTGT	900
BX421307.2	531	.....	680
BX443032.2	557	.....	706
BY794942.2	1376	.....	1525
BQ049312.1	529	.....	678
BX417098.2	520	.....	669
BX441194.2	569	.....	718
DC527884.1	1378	A.....C.....	1527
AL541984.3	644	.....	793
CR984260.1	547	.....	696
BX440436.2	365	.....	216
Query	901	TTCAATTGGCCATTTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGATGttttgtggaccactttgttttctttttgcgtgtggcagttttaagttattagtttttaaaatca	1050
BX421307.2	681	.....	830
BX443032.2	707	.....	856
BY794942.2	1526	.....	1675
BQ049312.1	679	.....	828
BX417098.2	670	.....	819
BX441194.2	719	.....	868
DC527884.1	1528	.....	1677
AL541984.3	794	.....K.S.....	943
CR984260.1	697	.....N.....	846
BX440436.2	215	.....	66

Query	1051	gtacttttttaATGGAAACAACCTTGACCAAAAAATTTGTACAGAAATTTTGGAGCCCAATTAATAAAGT	1117
BX421307.2	831	.....	897
BX443032.2	857	.....	923
BY794942.2	1676	.....	1742
BQ049312.1	829	.....	896
		\	
		A	
BX417098.2	820	.....-	885
BX441194.2	869	.....-	934
DC527884.1	1678	.....	1744
AL541984.3	944	.....	1011
		\	
		M	
CR984260.1	847	.....N.....	912
BX440436.2	65	.....N.....	1
		\	
		N	

Query= N25-C\* [organism=Homo sapiens] eef1a1

Length=1832

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
BY794942.2	BY794942	Homo sapiens eye cDNA clone H...	3147	0.0	100%
DC527884.1	DC527884	chimpanzee skin cDNA library PstA Pan troglodytes	3131	0.0	100%
CF111220.1	Shultzomica04471	Rat lung airway and parenchyma cDNA	2346	0.0	92%
BX426149.2	BX426149	Homo sapiens NEUROBLASTOMA Homo sapiens cDNA	2146	0.0	99%
CO001006.1	OC028	pre-oestrus adult sheep ovary library Ovis aries	2047	0.0	93%
BX418564.2	BX418564	Homo sapiens FETAL BRAIN Homo sapiens cDNA	2047	0.0	97%
BX426150.2	BX426150	Homo sapiens NEUROBLASTOMA Homo sapiens cDNA	2034	0.0	99%
AL567209.3	AL567209	Homo sapiens FETAL BRAIN Homo sapiens cDNA	2001	0.0	98%
BX440470.1	BX440470	Homo sapiens FETAL BRAIN Homo sapiens cDNA	1999	0.0	98%
BX420340.1	BX420340	Homo sapiens FETAL BRAIN Homo sapiens cDNA	1997	0.0	99%

#### ALIGNMENTS

Query	124	CGCAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAGGAAAGACTCATATCAACATTGTCTGTCATTGGACACGTAGATTTCGGGCAAGTCCACCACTACTGGCCATCTGATCTATAAATGCGGTGGCATCGACAAAAGAACCA	273
BY794942.2	35	.....	182
DC527884.1	38	.....	185
CF111220.1	25	.....T.....G.C...G.....A.....C.....C.....A.....C.....A.....C.....C.....T.....A.....	178
		\	
		ATTC	
BX426150.2	6	.....	153
Query	274	TTGAAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGCTTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTA	423
BY794942.2	183	.....	332
DC527884.1	186	.....T.....	335
CF111220.1	179	.....G.....G.....A.....C.....C.....G.....T.....C.....C.....G.....	328
CO001006.1	1464	.....	1440
BX426150.2	154	.....	303



Query	424	TCATTGATGCCCCAGGCACACAGAGACTTTAATCAAAAACATGATTACAGGGACATCTCAGCGTGACTGTGCTGTCCCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTC	573
BY794942.2	333	.....	482
DC527884.1	336	.....C.....	485
CF111220.1	329	...C...G....G..C.....C.....T.....T.....	478
CO001006.1	1439	.....C.....C.....C.....C.....T.....	1290
BX426150.2	304	.....C.....C.....C.....C.....T.....	453
Query	574	TGGCTTACACACTGGGTGTGAAACAACATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAAGAAAATTGGCTACAACCCCGACACAGTAG	723
BY794942.2	483	.....	632
DC527884.1	486	.....	635
CF111220.1	479	.....TT.....G.....T.....C.....C.....A.....T.....C.....C.....C.....T.....	628
BX426149.2	1196	.....-A.....-A.....-A.....G.....	1094
CO001006.1	1289	.....C.....T.....C.....T.....C.....C.....C.....C.....	1140
BX418564.2	1196	.....YH.VS...R...W...G.W...R...M.K...R...S...-R...	1100
BX426150.2	454	.....S.....W...K.W...R...A.M.C.....C.....	603
AL567209.3	1145	.....S.....W...K.W...R...A.M.C.....C.....	1064
		M	
BX440470.1	1128	.....-W.....	1101
		C	
BX420340.1	1117	...M..M.....	1097
Query	724	CATTTGTGCCAATTTCTGGTGGGAATGGTGACAACTGCTGGAGCCAAAGTGCTAACATGCCCTGGTTCAAGGGATGGAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCACGCTGCTTGAGGCTCTGGACTGCATCTACCAACCAA	873
BY794942.2	633	.....	782
DC527884.1	636	.....	785
CF111220.1	629	.....T.G.....C.A...G.....C.....G.A.T.....T.G.G.....	778
BX426149.2	1093	.....C.....T.A.....C.....C.....C.....A.....T.....G.....	944
CO001006.1	1139	.....C.....T.A.....C.....C.....C.....A.....T.....G.....	929
BX418564.2	1099	.....C.....T.A.....C.....C.....C.....A.....T.....G.....	954
BX426150.2	604	.....C.....T.A.....C.....C.....C.....A.....T.....G.....	753
AL567209.3	1063	.....C.....T.A.....C.....C.....C.....A.....T.....G.....	914
BX440470.1	1100	...-S.M...Y.-K.....K.....K.....R.....	956
BX420340.1	1096	...K.-..S.M.W...YT..D..K.-..T.....Y.....A.....	949
Query	874	CTCGTCCAACGTACAAGCCCTTGGCGCTGCCTCTCCAGGATGTCTACAAAAATGGTGGTATTGGTACTGTTCTCTGTTGGCCGAGTGAGAGCTGGTGTCTCAAAACCCGGTATGGTGTGCACCTTTGCTCCAGTCAACGTTACACGGGAAG	1023
BY794942.2	783	.....	932
DC527884.1	786	.....	935
CF111220.1	779	.....TC..A...C.....T.....C..C.....C.....G.....A.....T.....T.....T.....A..A..T.....	928
BX426149.2	943	.....A.....C.....T.....C.....C.....C.....G.....A.....T.....T.....T.....A..A..T.....	794
CO001006.1	989	.....C.....A...C...TT.....T.....A.....G..T..T.....T.....C.....T.....T.....A..A..T.....G.....	840
BX418564.2	953	.....C.....A...C...TT.....T.....A.....G..T..T.....T.....C.....T.....T.....A..A..T.....G.....	804
BX426150.2	754	.....C.....A...C...TT.....T.....A.....G..T..T.....T.....C.....T.....T.....A..A..T.....G.....	903
AL567209.3	913	.....C.....A...C...TT.....T.....A.....G..T..T.....T.....C.....T.....T.....A..A..T.....G.....	764
BX440470.1	955	.....C.....A...C...TT.....T.....A.....G..T..T.....T.....C.....T.....T.....A..A..T.....G.....	806
BX420340.1	948	.....R.....	799
Query	1024	TAAAACTCTGTCGAAATGCACCATGAAGCTTTTGAGTGAAGCTCTTCTCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGCTGGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTG	1173
BY794942.2	933	.....	1082
DC527884.1	936	.....	1085
CF111220.1	929	.C..G...G.....G.....A.....C.A...C.....A..C..A.A.....T.....G.....	1078
BX426149.2	793	.G..G..C..A.....C.....C.....A.....C.....T.....G.....	644
CO001006.1	839	.G..G..C..A.....C.....C.....A.....C.....T.....G.....	690
BX418564.2	803	.G..G..C..A.....C.....C.....A.....C.....T.....G.....	654
BX426150.2	904	.G..G..C..A.....C.....C.....A.....C.....T.....G.....	1050
		G	
AL567209.3	763	.....	615
BX440470.1	805	.....	656
BX420340.1	798	.....	649
Query	1174	GCTTCACCTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTCTTGGTAAAAAGCTGGAAG	1323
BY794942.2	1083	.....	1233
		G	
DC527884.1	1086	.....	1235
CF111220.1	1079	.....G..C..T..T.....TC..C.....C.....A.....C.....T..A..G...C...T.....G.....	1228
BX426149.2	643	.....C..A.....T.....C..T.GT..A...A...GC.....T..A.....T.....G.....	494
CO001006.1	689	.....C..A.....T.....C..T.GT..A...A...GC.....T..A.....T.....G.....	540
BX418564.2	653	.....C..A.....T.....C..T.GT..A...A...GC.....T..A.....T.....G.....	504
BX426150.2	1051	.....C..A.....T.....C..T.GT..A...A...GC.....T..A.....T.....G.....	1140
AL567209.3	614	.....C..A.....T.....C..T.GT..A...A...GC.....T..A.....T.....G.....	465
BX440470.1	655	.....C..A.....T.....C..T.GT..A...A...GC.....T..A.....T.....G.....	505
		C	
BX420340.1	648	.....	499

Query 1324 ATGGCCCTAAATCTTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTGCTTTGCTGTTGATATGAGACAGACAGTTGCGGTGGGTGTCATCA 1473  
BY794942.2 1234 ..... 1383  
DC527884.1 1236 .....A..... 1385  
CF111220.1 1229 .....C.....C.....A.....T.....C..T..AC.T.....T.....C.....G.....T..... 1378  
BX426149.2 493 ..... 344  
CO001006.1 539 .....A.....C.....C.....T.....C.....T..T..T..T..C.....C..T.....G.....C.....C..T..... 390  
BX418564.2 503 ..... 354  
AL567209.3 464 .....K..... 315  
BX440470.1 504 ..... 355  
BX420340.1 498 ..... 349

Query 1474 AAGCAGTGGACAAGAAGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAAGCGGTCTCAGAACTGTTGTTCAATTG 1623  
BY794942.2 1384 ..... 1533  
DC527884.1 1386 .....C..... 1535  
CF111220.1 1379 .....C.....A.....A.....C.....G.....C..... 1528  
BX426149.2 343 ..... 194  
CO001006.1 389 .....A.....C.....G.....C..... 240  
BX418564.2 353 ..... 204  
AL567209.3 314 .....M.....Y..... 164

BX440470.1 354 .....A..... 205  
BX420340.1 348 ..... 199

Query 1624 GCCATTTAAGTTTAGTAGTAAAGACTGGTAAATGATAACAAATGCATCGTAAACCTTCAGAAGGAAAGGAGAAATgtttttgtggaccacttttggttttttttttgcgtgtggcagttttaagttattagtttttaaaatcagttactttt 1773  
BY794942.2 1534 ..... 1683  
DC527884.1 1536 .....G.....C..... 1685  
CF111220.1 1529 .....A..... 1667  
BX426149.2 193 .....-.....G.....-..... 44  
CO001006.1 239 .....A.....-.....A.....G.....-.....-..... 99

BX418564.2 203 .....T..... 54  
AL567209.3 163 ..... 13

BX440470.1 204 .....G..... 55  
BX420340.1 198 ..... 49

Query 1774 taATGGAACAACCTTGACCAAAAAATTTGTCACAGAAATTTTGAGACCCATTAAAAAAGTT 1832  
BY794942.2 1684 ..... 1742  
DC527884.1 1686 ..... 1744  
CF111220.1 1668 .....C..... 1726

BX426149.2 43 .....G.....G.....G.....T..... 1  
CO001006.1 98 .....A.....C.....-..... 40

BX418564.2 53 .....M..... 1  
AL567209.3 12 ..... 1  
BX440470.1 54 ..... 1  
BX420340.1 48 .....R..... 1

Query= N26-20 [organism=Homo sapiens] eef1a1

Length=1067

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
BX421307.2 BX421307 Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1592	0.0	100%
BX443032.2 BX443032 Homo sapiens B CELLS (RAMOS CELL LINE) Hom...	1589	0.0	100%
BY794942.2 BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	1589	0.0	100%
BQ049312.1 AGENCOURT 6795094 NIH_MGC 85 Homo sapiens cDNA clon...	1589	0.0	100%
BX417098.2 BX417098 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1587	0.0	100%
BX441194.2 BX441194 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1583	0.0	100%
BX440436.2 BX440436 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1583	0.0	100%
BX440470.1 BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1583	0.0	100%
DC527884.1 DC527884 chimpanzee skin cDNA library PstA Pan trog...	1581	0.0	100%
AL541984.3 AL541984 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1581	0.0	100%

ALIGNMENTS

Query 1 GAAAGAAAAAGACTCATATCAACATTGTCGTCAATTGGACACGTAGATTCGGGCAAGTCCACCACTACTGGCCATCTGATCTATAAATGCGGTGGCATTGACAAAAGAACATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGG 150  
BY794942.2 72 ..... 221

[illegible]

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      c
BX440436.2 318 ..... 168
      |
      c
BX440470.1 315 ..... 165
      |
      c
DC527884.1 1425 .....C..... 1575
      |
      c
AL541984.3 691 ..... 841
      |
      c

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Query      901  AATGCATCGTAAACCTTCAGAAGGAAAGGAGAAATgttttggaccactttggttttctttttgcgtgtggcagttttaagttattagtttttaaaatcagttacttttaATGGAAACAACTTGACCAAAAATTTGCACAGATTTT 1050
BX421307.2 729 ..... 878
BX443032.2 755 ..... 904
BY794942.2 1574 ..... 1723
BQ049312.1 727 ..... 876
BX417098.2 718 ..... 867
BX441194.2 767 ..... 916
BX440436.2 167 .....N..... 17

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      |
      N
BX440470.1 164 ..... 15
      |
      N
DC527884.1 1576 ..... 1725
AL541984.3 842 .....K.S..... 992
      |
      M

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Query      1051  GAGACCCATTAAAAAAG 1067
BX421307.2 879 ..... 895
BX443032.2 905 ..... 921
BY794942.2 1724 ..... 1740
BQ049312.1 877 ..... 894
      |
      A
BX417098.2 868 ..... 883
BX441194.2 917 ..... 932
BX440436.2 16 ..... 1
BX440470.1 14 ..... 1
DC527884.1 1726 ..... 1742
AL541984.3 993 ..... 1009

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Query= N27-C\* [organism=Homo sapiens] eef1a1  
Length=1807

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BY794942.2	BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	3134	0.0	100%
DC527884.1	DC527884 chimpanzee skin cDNA library PstA Pan trog...	3116	0.0	100%
CF111220.1	Shultzomica04471 Rat lung airway and parenchyma cDN...	2331	0.0	92%
BX426149.2	BX426149 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2143	0.0	99%
CO001006.1	OC028 pre-oestrus adult sheep ovary library Ovis ar...	2041	0.0	93%
BX418564.2	BX418564 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2041	0.0	97%
BX426150.2	BX426150 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2028	0.0	99%
AL567209.3	AL567209 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	2001	0.0	98%
BX440470.1	BX440470 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1993	0.0	98%
BX420340.1	BX420340 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1991	0.0	98%

#### ALIGNMENTS

```

Query      105  GTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAAGGAAAGACTCATATCAACATTGTCTGTCATTGGACACGTAGATTGGGGCAAGTCCACCACTACTGGCCATCTGATCTATAAATGCGGTGGCATCGACAAAAGAACCATTTGAA 254
BY794942.2 38 ..... 187
DC527884.1 41 ..... 190
CF111220.1 55 .....A.....C.....C.....A.....C.....A..C.....C.....C.....T.....A..... 183
BX426150.2 9 ..... 158

Query      255  AAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGCTTGGATAAACTGAAAGCTGAGCGTGAACGGTGATCACCATTGATATCTCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATT 404
BY794942.2 188 ..... 337
DC527884.1 191 ..... 340
CF111220.1 184 ..G.....G.....A.....C.....C.....G.....T.....T.....C.....C.....G..... 333

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[illegible]

BX420340.1 643 ..... C ..... 494

Query 1305 CCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCTGTATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCA 1454

BY794942.2 1239 ..... 1388

DC527884.1 1241 ..... A ..... 1390

CF111220.1 1234 ..C.....C.....C.....A.....T.....C..T..AC.T.....T.....C.....G.....T.....C 1383

BX426149.2 488 ..... 339

CO001006.1 534 ..... A.....C.....C.....T.....C.....T..T..T.....T..C.....C..T.....G.....C.....C..T..... 385

BX418564.2 498 ..... 349

AL567209.3 459 ..... K ..... 310

BX440470.1 499 ..... 350

BX420340.1 493 ..... 344

Query 1455 GTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCAACAACTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTTGGCCAT 1604

BY794942.2 1389 ..... 1538

DC527884.1 1391 ..... C ..... 1540

CF111220.1 1384 ..... A.....A.....C.....G.....C..... 1533

BX426149.2 338 ..... 189

CO001006.1 384 ..... A.....C.....G.....C..... 235

BX418564.2 348 ..... 199

AL567209.3 309 ..... M.....Y..... 159

..... \ .....  
..... | .....  
..... A .....  
BX440470.1 349 ..... 200

BX420340.1 343 ..... 194

Query 1605 TTAAGTTTAGTAGTAAAGACTGGTTAATGATAACAAATGCATCGTAAACCTTCAGAAGGAAGGAGAAATgttttggaccactttgggttttcttttttgcgtgtggcagttttaagtatttagtttttaaaatcagtaactttttaATG 1754

BY794942.2 1539 ..... 1688

DC527884.1 1541 ..... 1690

CF111220.1 1534 ..... A.....-..-..-..G..-..-..C..... 1672

BX426149.2 188 ..... 39

CO001006.1 234 ..... A.....-..A.....G..-..-..-..-..-..-.. 94

..... \ .....  
..... | .....  
..... T .....  
BX418564.2 198 ..... 49

AL567209.3 158 ..... 9

..... \ .....  
..... | .....  
..... G .....  
BX440470.1 199 ..... 50

BX420340.1 193 ..... 44

Query 1755 GAAACAACCTTGACAAAAATTTGTACACAGAATTTTGTGAGACCCATTAAAAAAG 1807

BY794942.2 1689 ..... 1740

DC527884.1 1691 ..... 1742

CF111220.1 1673 ..... C.....-..-..-.. 1724

..... \ .....  
..... | .....  
..... C .....  
BX426149.2 38 -..-..-..G.....G.....-..T.. 1

CO001006.1 93 A.....C.....-..-..-.. 44

BX418564.2 48 ..... M..... 1

AL567209.3 8 -..-..-.. 1

BX440470.1 49 ..... 1

BX420340.1 43 ..... R..... 1

Query= N28-13 [organism=Homo sapiens] eef1a1

Length=1189

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
DC527884.1	DC527884 chimpanzee skin cDNA library PstA Pan trog...	2182	0.0	100%
BY794942.2	BY794942 Homo sapiens eye Homo sapiens cDNA clone H...	2152	0.0	100%
BX426150.2	BX426150 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	2037	0.0	99%
BU902062.1	AGENCOCURT_10127553 NIH MGC 71 Homo sapiens cDNA clo...	1999	0.0	98%
BX402801.2	BX402801 Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1988	0.0	98%
AL513590.3	AL513590 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1977	0.0	97%
BX402793.2	BX402793 Homo sapiens T CELLS (JURKAT CELL LINE) CO...	1973	0.0	98%
BX440468.2	BX440468 Homo sapiens FETAL BRAIN Homo sapiens cDNA...	1971	0.0	98%
AL513664.3	AL513664 Homo sapiens NEUROBLASTOMA Homo sapiens cD...	1962	0.0	98%
DC852462.1	DC852462 macaque spleen cDNA library QspA Macaca fa...	1960	0.0	97%

ALIGNMENTS

Query 2 CTTTTTCGCAACGGGTTTGCCGCCAGAAACACAGGTGTCGTGAAAACTACCCCTAAAGCCAAAATGGGAAGGAAAGAACTCATATCAACATTGTCGTCAATTGGACACGTAGATTGGGGCAAGTCCAACCACTACTGGCCATCTGATCTAT 151

DC527884.1 9 ..... 157

BY794942.2	25	.....	151
BX426150.2	1	.....T.....	125
BU902062.1	1	.....	136
BX402801.2	1	.....A.....	139
AL513590.3	2	.....	122
		.....\..... .....C.....	
BX402793.2	6	.....	138
BX440468.2	1	.....	129
AL513664.3	1	.....	129
DC852462.1	1	.....C.....	150
Query	152	AAATGGCGGTGCGCATCGACAAAGAACCATTTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGCTCCTTCAGTATGCTGGGTCTTTGGATAAACTGAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCTTGTGGAA	301
DC527884.1	158	.....T.....	307
BY794942.2	155	.....	304
BX426150.2	126	.....	275
BU902062.1	137	.....	286
BX402801.2	140	.....	289
AL513590.3	123	.....B.....	272
BX402793.2	139	.....	288
BX440468.2	130	.....	279
AL513664.3	130	.....G.....Y.....	279
DC852462.1	151	.....G.....	300
Query	302	TTTGGAGCCAGCAAGTACTATGTGACTATCATTTGATGCCCCAGGACACAGAGACTTTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGCTCCTGATTGTTGCTGCTGGTGTGGTGAATTTGAAGCTGGTATCTCAG	451
DC527884.1	308	.....C.....	457
BY794942.2	305	.....	454
BX426150.2	276	.....	425
BU902062.1	287	.....	436
BX402801.2	290	.....	439
AL513590.3	273	.....K..B..B.....K..	422
BX402793.2	289	.....	438
BX440468.2	280	.....Y.....	429
AL513664.3	280	.....	429
DC852462.1	301	.....T.....C.....	450
Query	452	AAATGGGCGAGCCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAACAACCTAATTTGTCGGTGTTAACAAAATGGATTCCACTGAGCCACCCCTACAGCCAGAAGAGATATGAGGAAATTTGTTAAGGAAGTCAGCACTTACATTAAG	601
DC527884.1	458	.....	607
BY794942.2	455	.....	604
BX426150.2	426	.....	575
BU902062.1	437	.....	586
BX402801.2	440	.....	589
AL513590.3	423	.....	572
BX402793.2	439	.....	588
BX440468.2	430	.....	579
AL513664.3	430	.....T.....T.....C.....	579
DC852462.1	451	.....T.....C.....	600
Query	602	AAAAATGGCTACAAACCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAAATGGTGACAAATGCTGGAGCCAAATGCTAACATGCCTTGGTTCAAGGGATGGAAGTCACCCGTAAAGGATGGCAATGCCAGTGGAAACCAAGCTGCTT	751
DC527884.1	608	.....	754
BY794942.2	605	.....	751
BX426150.2	576	.....	725
BU902062.1	587	.....	736
BX402801.2	590	.....	739
AL513590.3	573	.....Y.....Y.....-.....T.....	722
BX402793.2	589	.....	738
BX440468.2	580	.....-.....	728
AL513664.3	580	.....K.....	729
DC852462.1	601	.....G.....	750
Query	752	GAGGCTCTGGACTGCATCTTACCACCAACTCGTCCAACCTGACAAGCCCTTGCGCCCTGCCTCCAGGATGCTACAAAAATTTGGTGGTATTTGGTACTGTTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACC	901
DC527884.1	758	.....	907
BY794942.2	755	.....	904
BX426150.2	726	.....	875
BU902062.1	737	.....C..G.....	886
BX402801.2	740	.....	889
AL513590.3	722	.....Y.....	871
BX402793.2	739	.....	888
BX440468.2	729	.....	878
AL513664.3	730	.....	879
DC852462.1	751	.....	900
Query	902	TTTGCTCCAGTCACAGTTACAACGGAATAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTCTGGGGCAATGTGGGCTTCAATGTCAAGAATGTGCTGTCAAGGATGTTCTGCTGGCAACGTGCTGGTGACAGC	1051
DC527884.1	908	.....	1057
BY794942.2	905	.....	1054
BX426150.2	876	.....\..... .....G.....	1024
BU902062.1	887	.....-.....AC.....C...C.....C...C.....\.....	1036

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BX402801.2 890 .....W.....Y.....Y.....T.....K.T.A.....M.K.....S. 1041
                                     \
                                     | G
                                     |
AL513590.3 872 .....T.....T.....Y.....R.....M.....T.....C. 1020
BX402793.2 889 .....S.....TM.A.....R.....S. 1037
EX440468.2 879 .....W.....R.....M.....S- 1026
AL513664.3 880 .....T.....W.....K.....A.....K.T.....G.....GC.....S. 1030
                                     \
                                     | G
                                     |
DC852462.1 901 .....T.....-.....-.....-.....-.....-.....-.....-..... 1045
Query      1052 AAAAATGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTG 1189
DC527884.1 1058 ..... 1195
BY794942.2 1055 ..... 1193
                                     \
                                     | G
                                     |
BX426150.2 1025 .....-.....-.....-.....-.....-.....T..... 1140
BU902062.1 1037 .....C.G.....-.....T.....G.....A.....C.G..T..... 1163
                                     \
                                     | C
                                     |
BX402801.2 1042 ...W..A.....K..Y.....T.W.....W.....S.S-.....K.W..... 1144
                                     \
                                     | G
                                     |
AL513590.3 1021 .....Y.....K.C.....W.....M.M.-.....T.....T...M.Y...S.Y.A..... 1153
                                     \
                                     | C
                                     |
BX402793.2 1038 ...WKR...M.....M...Y.....M.M...M...M.....S... 1121
BX440468.2 1027 .....M.....M.....M.....MWC..R.....A..M...S...Y- 1120
AL513664.3 1031 .....G.....Y.....W.M.....WR...S.SY-.....T..... 1127
DC852462.1 1046 .....C-.....-.....-.....-.....T-..T-.....G-..A..G.....A.....-C-..... 1168
                                     \
                                     | G
                                     |

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Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions

Posted date: Feb 24, 2019 1:46 AM  
Number of letters in database: 43,200,890,307  
Number of sequences in database: 77,566,966

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Lambda      K      H
  1.33    0.621    1.12
Gapped
Lambda      K      H
  1.28    0.460    0.850
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 77566966
Number of Hits to DB: 3956718
Number of extensions: 27026
Number of successful extensions: 27026
Number of sequences better than 10: 972
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 23040
Number of HSP's successfully gapped: 22826
Length of database: 43200890307
A: 0
X1: 13 (25.0 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 13 (25.1 bits)

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BLASTN 2.9.0+  
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and  
Webb Miller (2000), "A greedy algorithm for aligning DNA  
sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: 8R733CVH014

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions  
77,566,966 sequences; 43,200,890,307 total letters  
Query= Tl-C [organism=Homo sapiens] anxl  
Length=1480

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BU508007.1	AGENCOURT_10128424 NIH_MGC_71 Homo sapiens cDNA clo...	1929	0.0	98%
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1910	0.0	98%
AL544231.3	AL544231 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1905	0.0	98%
DC631365.1	DC631365 macaque bone marrow cDNA library Qbma Maca...	1879	0.0	94%
DC636772.1	DC636772 macaque bone marrow cDNA library Qbma Maca...	1853	0.0	94%
AL541874.3	AL541874 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1853	0.0	99%
BU902298.1	AGENCOURT_10127317 NIH_MGC_71 Homo sapiens cDNA clo...	1847	0.0	96%
BX438944.2	BX438944 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1844	0.0	99%
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1831	0.0	98%
AL570884.3	AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1825	0.0	97%
ALIGNMENTS				
Query	87	AGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAGAGGTAGAGATAAAGACACTTTTTCAAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATTGAAAAATGAAGAGCAGGAATATGTTCAAACCTGTGA	236	
BU508007.1	1	.....\	131	
		N		
AL544231.3	19	..T.....	151	
DC631365.1	1	.....C.C.....	149	
DC636772.1	1	.....C.C.....	149	
AL541874.3	1	.....	125	
BU902298.1	24	.....\	164	
		N		
BX438944.2	1	.....	133	
Query	237	AGTCATCCAAAGGTGGTCCCGATCAGCGGTGAGCCCTATCCTACCTTCAATCCATCCTCGGATGTGCTGCTTGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTCTAACTAAGCGAAACAATGCAC	386	
BU508007.1	132	.....	281	
AL570428.3	1088	.....-T.....-..	1068	
AL544231.3	152	.....T.....A.....T.....C.....	301	
DC631365.1	150	.A.....T.....A.....T.....C.....	299	
DC636772.1	150	.A.....T.....A.....C.....	299	
AL541874.3	126	.....C.....	275	
BU902298.1	165	.....	314	
BX438944.2	134	.....	283	
Query	387	AGCGTCAACAGATCAAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCTGGATGAAACACTGAAGAAAGCCCTTACAGGTACCTTGAGGAGGTTGTTTGTAGCTCTGCTAAAAACTCCAGCGCAATTTGATGCTGATGAACCTCGTGCTG	536	
BU508007.1	282	..T.....A.....W.....GC.....-Y.....	431	
AL570428.3	1067	.....	922	
AL544231.3	302	.....TG.....G.....	451	
DC631365.1	300	.....TG.....G.....	449	
DC636772.1	300	.....G.TG.....G.....	449	
AL541874.3	276	.....	425	
BU902298.1	315	.....	464	
BX438944.2	284	.....	433	
AL576223.3	1050	.....-W.....-R.....-Y.....-R.....-D.....-WR.....-A.....-V.....	917	
AL570884.3	1059	.....T.....T.....C.....Y.....W.....RS.....W.....Y.M.....R.....T.....K.....YY..S.W.....C.....K...S	924	
		M		
Query	537	CCATGAAGGGCCTTGAAGACTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTACAGGGTCTACAGAGAGGAAGAGAGATCTGCCAAAGACATAACCTCAGACACATCTGGAGATT	686	
BU508007.1	432	.....M.....	581	
AL570428.3	921	.....W.....	772	
AL544231.3	452	.....	601	
DC631365.1	450	.....C.....G.....G.....	599	
DC636772.1	450	.....C.....G.....	599	
AL541874.3	426	.....	575	
BU902298.1	465	.....	614	
BX438944.2	434	.....	583	
AL576223.3	916	.....W.AAR.....	767	

AL570884.3	923	.....	774
Query	687	TTCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTGAGTCCAGGGCCCTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACGTTCTCAATACCATCCTTA	836
BU508007.1	582	.....	731
AL570428.3	771	.....R.....N.....	622
AL544231.3	602	.....	751
DC631365.1	600	.....G.....T.....	749
DC636772.1	600	.....G.....T.....	749
AL541874.3	576	.....G.....T.....	725
BU902298.1	615	.....	764
BX438944.2	584	.....	733
AL576223.3	766	.....	617
AL570884.3	773	.....	624
Query	837	CCACCAGAAGCTATCCACAACCTTCGCAGAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGGCCACAAGCAAAACAG	986
BU508007.1	732	.....	881
AL570428.3	621	.....A.....	472
AL544231.3	752	.....C.....T.....	900
DC631365.1	750	.....C.....T.....	899
DC636772.1	750	.....C.....T.....	899
AL541874.3	726	.....	875
BU902298.1	765	.....A.....TG.....	914
BX438944.2	734	.....	883
AL576223.3	616	.....	467
AL570884.3	623	.....	474
Query	987	CTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTGTGAACTCGCATTAAGGCATTGATCAGGATTATGGTTTCCCGTCTCGAAATGACATGAATGATATCAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAG	1136
BU508007.1	882	.....C.....G.....G.....C.....	1032
AL570428.3	471	.....G.....A.....T.....C.....	322
AL544231.3	901	.....G.W.....WY.....	1048
DC631365.1	900	.....A.....G.....C.....A.....	1048
DC636772.1	900	.....A.....G.....C.....A.....	1048
AL541874.3	876	.....T.....G.....T.....W.K.....	1019
BU902298.1	915	.....C.....GA.....G.....T.....A.....C.....T.....A.....A.G.....A.....C.....G.....C.....	1067
BX438944.2	884	.....K.....R.....S.....D.....R.....Y.....W.KD.....Y.....	1030
AL576223.3	466	.....A.....	317
AL570884.3	473	.....	324
Query	1137	CCATCCTGGATGAAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTC	1286
BU508007.1	1033	..T...G.....C.....GA...T..TA.....C.....C.....	1123
AL570428.3	321	.....G.....A.....T.....AG.....	172
AL544231.3	1049	..MWY.....R.....Y..K.....K.....R.....	1102
DC631365.1	1049	.....A.....CA...G.....C.....C.....	1173
DC636772.1	1049	.....GG.....GA.....C.....G.....C.....	1174
AL541874.3	1020	..M.....C.....G.....A.....A.....C.....G.....A.....AA.....	1029
BU902298.1	1068	.....T.....G.....A.....A.....C.....G.....A.....AA.....	1152
AL576223.3	316	.....G.....G.....G.....G.....T.....A.....T.....	167
AL570884.3	323	.....C.....	174
Query	1287	AACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCAAAACCATAAAACCCATACAAAGTTGTTCTAGTAACAAT	1436
AL570428.3	171	.....T.....	22
DC631365.1	1174	.....C.....T.....C.....A.....	1216

DC636772.1 1175 .....G...-A...-T-.....T...GG...A...A..... 1231

AL576223.3 166 .....B..... 17

AL570884.3 173 .....RW...V.....N...N...W 23

Query 1437 ACATGAGAAAGATGTCTATGT 1457

AL570428.3 21 ..... 1

AL576223.3 16 ..... 1

AL570884.3 22 .....A..... 1

Query= T2-2 [organism=Homo sapiens] anxa1

Length=1065

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
BQ228162.1	AGENCOURT_7258587 NIH_MGC_71 Homo sapiens cDNA clon...	1707	0.0	99%	
AL574991.3	AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1676	0.0	100%	
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1661	0.0	99%	
AL570884.3	AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1655	0.0	99%	
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1655	0.0	99%	
AL576603.2	AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1652	0.0	99%	
AL575425.3	AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1644	0.0	99%	
AL576340.3	AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1642	0.0	99%	
BM555842.1	AGENCOURT_6544353 NIH_MGC_88 Homo sapiens cDNA clon...	1639	0.0	99%	
AL553095.3	AL553095 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1615	0.0	98%	

ALIGNMENTS

Query	123	AAAGGGCCTTGGAACATGATGAAGATACTCTAATTGAGATTTTGGCATAAAGAACTAACCAAGGATTAACAGGGTCTACAGAGAGGAAGTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCG	272
BQ228162.1	25	.....	173
AL574991.3	911	.....	763
AL576223.3	911	.....W.AAR.....	763
AL570884.3	918	.....	770
AL570428.3	916	.....M.....	768
AL576603.2	912	.....WM.....	770
AL575425.3	930	.....R.....R.....	781
AL576340.3	915	.....RW.....	774
BM555842.1	1	.....	132
AL553095.3	917	.....	769
Query	273	GAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTGAGATGCCAGGGCCCTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACGCTGTTCATACCATCCTTACCAC	422
BQ228162.1	174	.....	323
AL574991.3	762	.....	613
AL576223.3	762	.....	613
AL570884.3	769	.....	620
AL570428.3	767	.....R.....N.....	618
AL576603.2	769	.....	620
AL575425.3	780	.....R.....B.....S.....T.....	631
AL576340.3	773	.....	624
BM555842.1	133	.....	282
AL553095.3	768	.....	619
Query	423	CAGAAGCTATCCACAACCTTCGCAGAGTGTTCAGAAATACACCAAGTACAGTAAAGCATGACATGAACAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGGGCCACAAGCAACAGCTTT	572
BQ228162.1	324	.....	473
AL574991.3	612	.....	463
AL576223.3	612	.....	463
AL570884.3	619	.....	470
AL570428.3	617	.....A.....	468
AL576603.2	619	.....N.....	470
AL575425.3	630	.....N.....N.....	481
AL576340.3	623	.....	474
BM555842.1	283	.....	432
AL553095.3	618	.....	469
Query	573	CTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTGGAACCTGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCAT	722
BQ228162.1	474	.....	623
AL574991.3	462	.....W.....	313
AL576223.3	462	.....	313
AL570884.3	469	.....	320

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AL570428.3 467 .....A.....T.....318
AL576603.2 469 .....320
AL575425.3 480 .....331
AL576340.3 473 .....324
BM555842.1 433 .....582
AL553095.3 468 ..V.....C.....V.....S..S.....RK..R..G..R.....319

Query      723 CCTGGATGAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACCTTAATTATATATTTTCATCCTATAAGCTTAATAGGAAAGTTTCTTCAACA 872
BQ228162.1 624 .....774

                                     \
                                     A

AL574991.3 312 .....Y.....163
AL576223.3 312 .....163
AL570884.3 319 .....170
AL570428.3 317 .....168
AL576603.2 319 .....170
AL575425.3 330 .....181
AL576340.3 323 .....R.....R.....174
BM555842.1 583 .....732
AL553095.3 318 .....K..G.....R.....169

Query      873 GGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATTATACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCAAACCATAAACCCCTATACAAGTTGTTCTAGTAACAATACAT 1022
BQ228162.1 775 .....925

                                     \
                                     G

AL574991.3 162 .....13
AL576223.3 162 .....B.....13
AL570884.3 169 .....RW...V.....N...N...W...18

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                                     N
                                     |
                                     N

AL570428.3 167 .....T.....18
AL576603.2 169 .....A.....19

                                     \
                                     C
                                     |
                                     N

AL575425.3 180 .....N.....31
AL576340.3 173 .....23

                                     \
                                     N
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                                     N

BM555842.1 733 .....888

                                     \
                                     A
                                     |
                                     C
                                     |
                                     C
                                     |
                                     N
                                     |
                                     C
                                     |
                                     N

AL553095.3 168 .....18

                                     \
                                     N

Query      1023 GAGAAAGATGCTCTATGTAGCTGAAAAATAAAATGACGTC 1060
BQ228162.1 926 .....965

      \      \
      G      A

AL574991.3 12 .....1
AL576223.3 12 .....1
AL570884.3 17 .....A.....1
AL570428.3 17 .....1
AL576603.2 18 .....1
AL575425.3 30 .....G.....17
AL576340.3 22 .....5
BM555842.1 889 .....922

      \      \      \
      A      C      G

AL553095.3 17 .....G..1

Query= T3-20 [organism=Homo sapiens] anxl
Length=1346

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Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
BQ228162.1 AGENCOURT 7258587 NIH MGC 71 Homo sapiens cDNA clon...	1607	0.0	99%
AL576603.2 AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1583	0.0	100%
AL576340.3 AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1581	0.0	100%
AL576223.3 AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1580	0.0	100%

AL574991.3	AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1576	0.0	100%
BM555842.1	AGENCOCURT_6544353 NIH_MGC_88 Homo sapiens cDNA clon...	1570	0.0	99%
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1559	0.0	99%
AL570884.3	AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1555	0.0	99%
AL575425.3	AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1543	0.0	99%
BE614257.1	601504294T1 NIH_MGC_71 Homo sapiens cDNA clone IMAG...	1528	0.0	99%

ALIGNMENTS

Query	324	TCTAACTAAGCGAAACAATGCACAGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCTGGATGAACACTGAAGAAAGCCCTTACAGGTACCTTTGAGGAGGTGTTTGTAGCTCTGCTAAAAACAAGAAATCAGA	473
BQ228162.1	79		93
AL576603.2	864		850
AL576340.3	868		854
AL576223.3	857		843
AL574991.3	857		843
BM555842.1	38		52
AL570428.3	862		848
AL570428.3	1088	.....-T.....-.....T.....-A.....-W.....-.....GC.....Y.....	957
AL570884.3	864		850
AL575425.3	875		861
AL575425.3	1037	.....-.....-.....M.....M.....KG.....C.....	970
BE614257.1	871		862

Query	474	GACATTAAACAGGGTCTACAGAGAGGAACCTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGAT	623
BQ228162.1	94		243
AL576603.2	849		700
AL576340.3	853		704
AL576223.3	842		693
AL574991.3	842		693
BM555842.1	53		202
AL570428.3	847	.....W.....	698
AL570884.3	849		700
AL575425.3	860	R.....R.....R.....B.....S.....	711
BE614257.1	861	.....-.....A.T.....A.....C.....-.....	713

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	A	G

Query	624	TCAGATGCCAGGCGCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACCGTGTTCATACCATCTTACCACCAGAAGCTATCCAACTTCGCAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAA	773
BQ228162.1	244		393
AL576603.2	699		550
AL576340.3	703		554
AL576223.3	692		543
AL574991.3	692		543
BM555842.1	203		352
AL570428.3	697	.....N.....	548
AL570884.3	699		550
AL575425.3	710	.....T.....	561
BE614257.1	712		563

Query	774	GTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAAACGAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACTCGCCATAAGGCATTGATCAGGATTATG	923
BQ228162.1	394		543
AL576603.2	549		400
AL576340.3	553		404
AL576223.3	542		393
AL574991.3	542		393
BM555842.1	353		502
AL570428.3	547		398
AL570884.3	549	.....N.....	400
AL575425.3	560		411
BE614257.1	562		413

Query	924	GTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCTGGATGAAACCAAGGAGATTATGAGAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCTCT	1073
BQ228162.1	544		693
AL576603.2	399		250
AL576340.3	403	.....R.....R.....	254
AL576223.3	392		243
AL574991.3	392	.....W.....	243
BM555842.1	503		652
AL570428.3	397	.....A.....T.....	248
AL570884.3	399		250
AL575425.3	410		261
BE614257.1	412		263

Query	1074	TGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATACTCTGTA	1223
BQ228162.1	694		844

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	A

AL576603.2	249		100
AL576340.3	253		104
AL576223.3	242		93

AL574991.3	242	.....Y.....	93
BM555842.1	653	.....	802
AL570428.3	247	.....	98
AL570884.3	249	.....	100
AL575425.3	260	.....N.....	111
BE614257.1	262	.....	113
Query	1224	TAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCAAAACCATAAAACCCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGTCTGAAAAATAAAATGACGTC	1341
BQ228162.1	845	.....G.....	965
		\                  \                  \	
		G                  G                  A	
AL576603.2	99	.....A.....	1
		C	
AL576340.3	103	.....	5
		N	
AL576223.3	92	.....B.....	1
AL574991.3	92	.....	1
BM555842.1	803	.....	922
		\          \          \          \          \          \          \	
		A          C          C          N          C          N          A          C          G	
AL570428.3	97	.T.....	1
AL570884.3	99	.....RW...V.....N...N...W...A.....	1
		N          N          N	
AL575425.3	110	.....N...N...G.....	17
BE614257.1	112	.....T.A.....	6
		T	

Query= T4-18 [organism=Homo sapiens] anxal

Length=1226

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
CB306442.1 UI-CF-EN1-aej-e-15-0-UI.s1 UI-CF-EN1 Homo sapiens c...	1295	0.0	100%
CA447733.1 UI-H-EI0-ayf-a-16-0-UI.s1 NCI_CGAP_EI0 Homo sapiens...	1295	0.0	100%
CA447223.1 UI-H-EI0-ayd-b-19-0-UI.s1 NCI_CGAP_EI0 Homo sapiens...	1295	0.0	100%
CA419844.1 UI-H-FH0-bcm-d-16-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1295	0.0	100%
CA417462.1 UI-H-FE0-bbw-c-13-0-UI.s1 NCI_CGAP_FE0 Homo sapiens...	1295	0.0	100%
CA415613.1 UI-H-EZ0-bay-p-10-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens...	1295	0.0	100%
CA414702.1 UI-H-EZ0-bar-e-18-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens...	1295	0.0	100%
BU633206.1 UI-H-FL1-bgt-f-12-0-UI.s1 NCI_CGAP_FL1 Homo sapiens...	1295	0.0	100%
BQ776306.1 UI-H-FH0-bcn-i-12-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1295	0.0	100%
BQ775850.1 UI-H-FH0-bcg-g-15-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1295	0.0	100%

#### ALIGNMENTS

Query	526	AAGCAGGAGAAAGGAGAAAGGGGACAGCGTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTTCGCAGAGTGTTTCAGAAATACACCAAGTACAGTAAAGTCTGGACCTGGAGTTGAAAG	675
CB306442.1	719	.....	570
CA447733.1	719	.....	570
CA447223.1	719	.....	570
CA419844.1	719	.....	570
CA417462.1	716	.....	567
CA415613.1	721	.....	572
CA414702.1	721	.....	572
BU633206.1	719	.....	570
BQ776306.1	719	.....	570
BQ775850.1	716	.....	567
Query	676	GTGACATTGAGAAATGCCTCACGCTATCGTGAAGTGCGCCACAAGCAAAACAGCTTTCTTTTCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACTCGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACA	825
CB306442.1	569	.....	420
CA447733.1	569	.....	420
CA447223.1	569	.....	420
CA419844.1	569	.....	420
CA417462.1	566	.....	417
CA415613.1	571	.....	422
CA414702.1	571	.....	422
BU633206.1	569	.....	420
BQ776306.1	569	.....	420
BQ775850.1	566	.....	417

Query	826	TGAATGATATCAAAAGCATTCATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAGGAGATTATGAGAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCA	975
CB306442.1	419	.....	270
CA447733.1	419	.....	270
CA447223.1	419	.....	270
CA419844.1	419	.....	270
CA417462.1	416	.....	267
CA415613.1	421	.....	272
CA414702.1	421	.....	272
BU633206.1	419	.....	270
BQ776306.1	419	.....	270
BQ775850.1	416	.....	267

Query	976	GAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATTTATAACTCTGTATAATAGAGATAAGTCCATTTTT	1125
CB306442.1	269	.....	120
CA447733.1	269	.....	120
CA447223.1	269	.....	120
CA419844.1	269	.....	120
CA417462.1	266	.....	117
CA415613.1	271	.....	122
CA414702.1	271	.....	122
BU633206.1	269	.....	120
BQ776306.1	269	.....	120
BQ775850.1	266	.....	117

Query	1126	TAAAAATGTTTTCCCAAAACCAATAAACCCCTATACAAGTTGTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAAATGACGTCACAAG	1226
CB306442.1	119	.....	19
CA447733.1	119	.....	19
CA447223.1	119	.....	19
CA419844.1	119	.....	19
CA417462.1	116	.....	16
CA415613.1	121	.....	21
CA414702.1	121	.....	21
BU633206.1	119	.....	19
BQ776306.1	119	.....	19
BQ775850.1	116	.....	16

Query= T5-22 [organism=Homo sapiens] anxl

Length=1238

Sequences producing significant alignments:				
	Score (Bits)	E Value	Max ident	
CA446942.1 UI-H-ED0-aya-g-19-0-UI.s1 NCI_CGAP_ED0 Homo sapiens...	1260	0.0	100%	
CA442733.1 UI-H-DP0-avr-a-19-0-UI.s1 NCI_CGAP_Fs1 Homo sapiens...	1260	0.0	100%	
CA419750.1 UI-H-FH0-bcm-o-09-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	
CA418232.1 UI-H-FH0-bcf-o-06-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	
CA418210.1 UI-H-FH0-bcf-i-22-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	
BU615320.1 UI-H-FH0-bcf-e-10-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	
BQ774950.1 UI-H-FH0-bcd-n-16-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	
BQ774641.1 UI-H-FH0-bcc-1-13-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	
BQ774017.1 UI-H-FH0-bce-a-18-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	
BQ773942.1 UI-H-FH0-bce-c-05-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1260	0.0	100%	

ALIGNMENTS

Query	557	GAGAAAGGGACAGCTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTCGCAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAA	706
CA446942.1	705	.....	556
CA442733.1	705	.....	556
CA419750.1	705	.....	556
CA418232.1	705	.....	556
CA418210.1	702	.....	553
BU615320.1	705	.....	556
BQ774950.1	705	.....	556
BQ774641.1	705	.....	556
BQ774017.1	702	.....	553
BQ773942.1	705	.....	556

Query	707	TGCTTCACAGCTATCGTGAAGTGCGCCACAAGCAAAACAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTGCCATAAGGCATTGATCAGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAA	856
CA446942.1	555	.....	406
CA442733.1	555	.....	406
CA419750.1	555	.....	406
CA418232.1	555	.....	406
CA418210.1	552	.....	403
BU615320.1	555	.....	406
BQ774950.1	555	.....	406
BQ774641.1	555	.....	406
BQ774017.1	552	.....	403
BQ773942.1	555	.....	406

Query	857	GCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAGGAGATTATGAGAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTA	1006
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CA446942.1	405	.....	256
CA442733.1	405	.....	256
CA419750.1	405	.....	256
CA418232.1	405	.....	256
CA418210.1	402	.....	253
BU615320.1	405	.....	256
BQ774950.1	405	.....	256
BQ774641.1	405	.....	256
BQ774017.1	402	.....	253
BQ773942.1	405	.....	256

Query	1007	TATATTTTCATCCTTATAAGCTTAAATAGGAAAGTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATTATAACTCTGTATAATAGAGATAGTCCATTTTTAAAAATGTTTCC	1156
CA446942.1	255	.....	106
CA442733.1	255	.....	106
CA419750.1	255	.....	106
CA418232.1	255	.....	106
CA418210.1	252	.....	103
BU615320.1	255	.....	106
BQ774950.1	255	.....	106
BQ774641.1	255	.....	106
BQ774017.1	252	.....	103
BQ773942.1	255	.....	106

Query	1157	CCAAACCATAAAACCCCTATACAAGTTGTCTTAGTAAACAATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAAATGACGTC	1238
CA446942.1	105	.....	24
CA442733.1	105	.....	24
CA419750.1	105	.....	24
CA418232.1	105	.....	24
CA418210.1	102	.....	21
BU615320.1	105	.....	24
BQ774950.1	105	.....	24
BQ774641.1	105	.....	24
BQ774017.1	102	.....	21
BQ773942.1	105	.....	24

Query= T6-14 [organism=Homo sapiens] anx1

Length=2854

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
AL544959.3 AL544959 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1701	0.0	100%
BX438944.2 BX438944 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1698	0.0	100%
AL551427.3 AL551427 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1696	0.0	100%
AL540651.3 AL540651 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1692	0.0	100%
AL551980.3 AL551980 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1687	0.0	100%
AL544231.3 AL544231 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1685	0.0	100%
AL541874.3 AL541874 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1683	0.0	100%
BU902298.1 AGENCOURT_10127317 NIH_MGC_71 Homo sapiens cDNA clo...	1683	0.0	99%
BU508007.1 AGENCOURT_10128424 NIH_MGC_71 Homo sapiens cDNA clo...	1681	0.0	100%
AL553114.3 AL553114 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1677	0.0	99%

ALIGNMENTS

Query	1	AGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAGAGGTAGAGATAAAGACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCTCANGCAGGCTGGTTTATTGAAAAATGAAGCAGGAATATGTTCAAACTGTGA	150
AL544959.3	1	.....	142
BX438944.2	1	.....	133
AL551427.3	1	..T.....	135
AL540651.3	19	..T.....	151
AL551980.3	22	..T.....	152
AL544231.3	19	..T.....	151
AL541874.3	1	.....	125
BU902298.1	24	.....	164
		\	
		I	
		N	
BU508007.1	1	.....	131
		\	
		I	
		N	
AL553114.3	107	.....	256
Query	151	AGTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCCATCCTACCTTCAATCCATCCTCGGATGTCGCTGCTTGATAGGCCATAATGGTTAAAGGTGGATGAAGCAACCATCATTGACATTCTAACTAAGCGAAACAATGCAC	300
AL544959.3	143	.....	292
BX438944.2	134	.....	283
AL551427.3	136	.....	285
AL540651.3	152	.....	301
AL551980.3	153	.....	302
AL544231.3	152	.....	301
AL541874.3	126	.....	275



BU902298.1	165	.....	314
BU508007.1	132	.....	281
AL553114.3	257	.....	406
Query	301	AGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAAAGGAAAGCCCTGGATGAAACACTGAAGAAAGCCCTTACAGGTCACCTTGAGGAGGTGTTTTAGCTCTGCTAAAAACTCAGCGCAATTTGATGCTGATGAACCTCGTGCTG	450
AL544959.3	293	.....	442
BX438944.2	284	.....	433
AL551427.3	286	.....	435
AL540651.3	302	.....	451
AL551980.3	303	.....	452
AL544231.3	302	.....	451
AL541874.3	276	.....	425
BU902298.1	315	.....	464
BU508007.1	282	.....	431
AL553114.3	407	.....	556
Query	451	CCATGAAGGGCCTTGGAACTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAATT	600
AL544959.3	443	.....	592
BX438944.2	434	.....	583
AL551427.3	436	.....	585
AL540651.3	452	.....	601
AL551980.3	453	.....	602
AL544231.3	452	.....	601
AL541874.3	426	.....	575
BU902298.1	465	.....	614
BU508007.1	432	.....	581
AL553114.3	557	.....	706
Query	601	TTCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGAACGATCTGAGGACTTTGGTGTAATGAAGACTTGGCTGATTTCAGATGCCAGGGCCCTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTA	750
AL544959.3	593	.....	742
BX438944.2	584	.....	733
AL551427.3	586	.....	735
AL540651.3	602	.....	751
AL551980.3	603	.....	752
AL544231.3	602	.....	751
AL541874.3	576	.....	725
BU902298.1	615	.....	764
BU508007.1	582	.....	731
AL553114.3	707	.....	856
Query	751	CCACCAGAAGCTATCCACAACCTTCGACAGTGTTTCAGAAATACCAAGTACAGTAAGCATGACATGAACAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAAACGAG	900
AL544959.3	743	.....M.....M.....	893
		$\begin{array}{c} \backslash \\   \\ T \end{array}$	
BX438944.2	734	.....	883
AL551427.3	736	.....	885
AL540651.3	752	.....	901
AL551980.3	753	.....M.....	902
AL544231.3	752	.....-.....	900
AL541874.3	726	.....	875
BU902298.1	765	.....A.....TG.....	914
BU508007.1	732	.....	881
AL553114.3	857	.....W.....-.....-.....	1003
Query	901	CTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGTATGTACCATTCTACTTATATGTCCTGCTTAGAGGAAGAATTATTTGTAGAAGAACAGAAAACCTCATGTTGTTGAAAAATCTCACATTTAATATCTTCCCATTAATGAGAAT	1050
AL544959.3	894	.....	929
BX438944.2	884	.....	919
AL551427.3	886	.....	921
AL540651.3	902	.....	937
AL551980.3	903	.....	938
AL544231.3	901	.....	936
AL541874.3	876	.....	911
BU902298.1	915	.....C.....	950
BU508007.1	882	.....-.....	916
AL553114.3	1004	.....-.....-.....M.....	1036
Query	1051	CATTGTCTTATTGTATGAAAAGAGTAATACACTACTTCTCAGAAATAAATCTCTGTAGATTTCGGTGCTtttttttACAGATGAGATTGTAAAGTGAGCTGTAAGTGATTTCACGGTCACCTTGTTGCTTAAAAATGTTGTCACACGGS	1200
Query	1201	AAGGTGATGTACTTCTTTTAACTGTAAATTTAGTGGCTACTTCTCTAAGGTGTGAGTTTATAATCTCCACCTTATGAGTCTGATTTGTGTTTATTATCTGTCTTTTATGCCACAGATTAATAGTTGAAACTTTGAAATG	1350
Query	1351	TCATTCTATGATTAAAGGATGTAGAATGATGATTTGAGATCAACTATGTCACCTTTAACTTTACTGTCTGACATGCATGGTATTATACAAGGTACCTCTTCTATTCTGACATTTTGAGCCCAAAATGAATAGTTATGAAGTTATCTTCCT	1500
Query	1501	TTTTCTTTGCAGCTCCAAAATAAGGAGGTTTTTAgagagagagagagAAGAAAGATCTAACTattttgaataaatatgaaggaatattttgaatatatatgaataatttgaataaatatgaaatgataGACATGCTAGGTACTGCTCTGTAGTG	1650
Query	1651	GTTAGCATAGTTGCTGCCCTTTCTGCCATAGTCTAGTGTGATATTTCTGTTGGTAAATGATGAATACCTGGTGCCATGGAAGAGAAAGTGACATATATCTCCAGACTTTGGAAATCCAGGTAGCATTTGCTGTGAGCTAAATAACACCTG	1800
Query	1801	AAGTTTAAATAGAAATGAGCAGATGAGGCGAAGAGTGGAGAGATGGGATAAAGCAAGGGTGGTCCAAGAGGAAGAAGTAAACCCACACACAGGCTTGAAGGCAAAGGTAACATAACCTTCTCAAGACAGTAAGTATAGAGTATGATGGTGC	1950
Query	1951	ACACTGGAAGAGATGGTAGAATTAGGCAGGATATTGTAAGCCTTGAAAAAGAATTAGGCAGGATATCGGAAGCCCTGATTAGATTCTATCCTAAGAGCAACAGAAGTACCTGACAGTGTTTAAATAGATAGACTAGTTTATTAGATTGG	2100
Query	2101	CAGTTTAGAAGTTCCTtttttttGTAATTATTGGACAGTGTAGAGACCGGATGGTGAGAGATGAGTTAGGAAGTTGTGACAGCTCTCTATACCTACCGCTAATGTAGAGGATTATTATTATTTTCATTTCATTACCATTCGTGTAAGgtgtgt	2250

Query	2401	AACTCGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTCTTGAATTGACATGAATGATATCAAGCATCTTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAGGAGATTATGAGAAAACTCCTGGT	2550
BX438944.2	927	R.....S.....D.....R=...Y.....W.KD=.Y.....Y...	1030

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**AG**

Length=2231

## ALIGNMENTS

Query	613	TGCTGCTGTCAATAAGAATATGGTCTGATTGAAATGTACTAATATTTAACTGAACGTGTTAATGCCTAAATTTTATATATAATCTACTTTAAAAATAAGCCTTATGTCITTTATACCAAATAGAGTAGTTTCTAAAGCAATGAAA	762
BX417009.2	602	.....	751

[illegible]

AL575425.3	1037	.....M.....	1010
AL553095.3	1020	.....-R.....-YK.....	994
AL576340.3	1011	.....G.....	987

Query	1213	CAGGTCACCTTGAGGAGGTTGTTT	TAGTCTCTGCTAAAAA	CTCCAGCGCAATTTGATGCTGATGAAC	TCGTGCTGCCATGAAGGGCCTT	GGAAC	TGATGAAGAT	CTCTAATTGAGATTTT	GGCATCAAGAACTAA	CAAGAATCAGAG	1362
AL570428.3	996	.....	.....	.....	.....	.....	.....	.....	.....	.....	847
AL574991.3	989	.CR.....	.....K.....	.....	.....	.....	.....	.....	.....	.....	842
AL576223.3	987	...D...WR.....	...A...V.....	.....	.....	.....	.....	.....	W...AAR.....	.....	842
AL570884.3	998	...Y.M...R...T...K...YY...S.W...C.....	.....	.....	.....	K...S.....	.....	.....	.....	.....	849
AL575425.3	1009	...M.....	.....KG.....C.....	.....	.....	C.C...S...A.....	.....	.....	.....	.....	860
AL553095.3	993	.....	.....	.....	.....	.....	.....	.....	.....	.....	848
BQ228162.1	12	.....	.....	.....	.....	.....	.....	.....	.....	.....	94
AL576340.3	986	.....Y.....	.....	.....	.....	.....	.....	.....	.....	.....	853
AL576603.2	917	.....	.....	.....	.....	.....	.....	.....	.....	.....	849
Query	1363	ACATTAA	CAGGGCTACAGAGAGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGCTTTCTCTGCTAAGGGTGACCGATCTGAGGACTTTGGTGGAATGAAGACTTGGCTGATT	1512							
AL570428.3	846	.....	W.....	.....	.....	.....	.....	.....	.....	.....	697
AL574991.3	841	.....	.....	.....	.....	.....	.....	.....	.....	.....	692
AL576223.3	841	.....	.....	.....	.....	.....	.....	.....	.....	.....	699
AL570884.3	848	.....	.....	.....	.....	.....	.....	.....	.....	.....	699
AL575425.3	859	.....	.....	.....	.....	.....	.....	.....	.....	.....	710
AL553095.3	847	.....	.....	.....	.....	.....	.....	.....	.....	.....	698
BQ228162.1	95	.....	.....	.....	.....	.....	.....	.....	.....	.....	244
AL576340.3	852	.....	.....	.....	.....	.....	.....	.....	.....	.....	703
AL576603.2	848	.....	.....	.....	.....	.....	.....	.....	.....	.....	699
Query	1513	CAGATGCCAGGGCCTTGATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTTGTCATACCACCTCTTACCACCAAGACTATCCACAACCTTCGACAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAG	1662								
AL570428.3	696	.....	.....	.....	.....	N.....	.....	.....	.....	A.....	547
AL574991.3	691	.....	.....	.....	.....	.....	.....	.....	.....	.....	542
AL576223.3	691	.....	.....	.....	.....	.....	.....	.....	.....	.....	542
AL570884.3	698	.....	.....	.....	.....	.....	.....	.....	.....	.....	549
AL575425.3	709	.....	.....	.....	.....	.....	.....	.....	.....	.....	560
AL553095.3	697	.....	.....	.....	.....	T.....	.....	.....	.....	N.....	548
BQ228162.1	245	.....	.....	.....	.....	.....	.....	.....	.....	.....	394
AL576340.3	702	.....	.....	.....	.....	.....	.....	.....	.....	.....	553
AL576603.2	698	.....	.....	.....	.....	.....	.....	.....	.....	.....	549
Query	1663	TTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCTGTAAGTGCGCCACAAGCAAAACAGCTTTCTTTGACAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAAC	1812								
AL570428.3	546	.....	.....	.....	.....	.....	.....	.....	.....	.....	397
AL574991.3	541	.....	.....	.....	.....	.....	.....	.....	.....	.....	392
AL576223.3	541	.....	.....	.....	.....	.....	.....	.....	.....	.....	392
AL570884.3	548	.....	.....	.....	.....	.....	.....	.....	.....	.....	399
AL575425.3	559	.....	.....	.....	.....	N.....	.....	.....	.....	.....	410
AL553095.3	547	.....	.....	.....	.....	.....	YY...V.....	.....	C.....	.....	398
BQ228162.1	395	.....	.....	.....	.....	.....	.....	.....	.....	V.....	544
AL576340.3	552	.....	.....	.....	.....	.....	.....	.....	.....	.....	403
AL576603.2	548	.....	.....	.....	.....	.....	.....	.....	.....	.....	399
Query	1813	TTTCCCGTTCTGAAATTGACATGAATGATATCAAGACATCTATCAGAAGATGATGGTATCTCCCTTTGCCAAGCCATCTGGATGAACCAAGGAGATTATGAGAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTT	1962								
AL570428.3	396	.....	.....	.....	.....	A.....	.....	.....	.....	.....	247
AL574991.3	391	.....	.....	.....	.....	.....	.....	.....	.....	.....	242
AL576223.3	391	.....	.....	.....	.....	.....	.....	.....	.....	.....	242
AL570884.3	398	.....	.....	.....	.....	.....	.....	.....	.....	.....	249
AL575425.3	409	.....	.....	.....	.....	.....	.....	.....	.....	.....	260
AL553095.3	397	.....	.....	S...S.....	.....	RK...R...G...R.....	.....	K...G.....	.....	R.....	248
BQ228162.1	545	.....	.....	.....	.....	.....	.....	.....	.....	.....	694
AL576340.3	402	.....	.....	.....	.....	.....	.....	R.....	.....	R.....	253
AL576603.2	398	.....	.....	.....	.....	.....	.....	.....	.....	.....	249
Query	1963	GATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATATAACTCTGTAT	2229								
AL570428.3	246	.....	.....	.....	.....	.....	.....	.....	.....	.....	97
AL574991.3	241	.....	Y.....	.....	.....	.....	.....	.....	.....	.....	92
AL576223.3	241	.....	.....	.....	.....	.....	.....	.....	.....	.....	92
AL570884.3	248	.....	.....	.....	.....	.....	.....	.....	.....	.....	99
AL575425.3	259	.....	.....	.....	.....	.....	.....	.....	.....	.....	110
AL553095.3	247	.....	.....	.....	.....	.....	.....	.....	N.....	.....	98
BQ228162.1	695	.....	.....	.....	.....	.....	.....	.....	.....	.....	845
AL576340.3	252	.....	.....	.....	.....	.....	.....	.....	.....	.....	103
AL576603.2	248	.....	.....	.....	.....	.....	.....	.....	.....	.....	99
Query	2113	AATAGAGATAAGTCCATTTTTT	AAAAATGTTTTC	CCCAACCATAAAACCC	TATACAAAGTTGTTCTAGTAACAATACATGAGAAAGATGCTCTATGTAGCTGAAAAATAAAATGACGTC	2229					
AL570428.3	96	T.....	.....	.....	.....	.....	1				
AL574991.3	91	.....	.....	.....	.....	.....	1				
AL576223.3	91	.....	.....	.....	.....	.....	1				
AL570884.3	98	.....	.....	RW...V.....	.....	N...N...W...A.....	1				
AL575425.3	109	.....	.....	.....	.....	.....	.....	.....	.....	.....	17
AL553095.3	97	.....	.....	.....	.....	.....	.....	.....	.....	.....	1

Query= T9-9 [organism=Homo sapiens] anxa1  
Length=2698

AL540651.3 451 ..... 600  
AL553679.3 441 ..... 590  
AL553164.3 452 ..... 601

Query 601 TTTCGGAACGCTTTGCTTTCTCTTGGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTAGATGCCAGGGCCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACCGTGTCAATACCATCCCTT 750  
AL553114.3 706 ..... 855  
AL544959.3 592 ..... 741  
BM458053.1 610 ..... 759  
BX438944.2 583 ..... 732  
AL551427.3 585 ..... 734  
BU902298.1 614 ..... 763  
AL544231.3 601 ..... 750  
AL540651.3 601 ..... 750  
AL553679.3 591 ..... 740  
AL553164.3 602 ..... 751

Query 751 ACCACCAGAAGCTATCCACAACCTTCGACAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTACAGCTATCGGTATGTAGTCCAGCAGTTGAAAG 900  
AL553114.3 856 ..... 981  
AL544959.3 742 ..... 869

BM458053.1 760 ..... 889

AL553164.3 752 ..... 877

Query 901 AGTTTTCTAAGTAAATTTGATTTTCAAAGCTATCCTATACTTaaacaagaacaacagcaacaaaaccaataaaagaaaaacaaaaacaaTCAGAAGTAGTGATCTGTTTCAATTGAAGCAACGTAAAAGATTGGCAAAGTACTATAAC 1050

Query 1051 CTTAATAACAATAGATATTATTCCCTTTTCAAAAATAGAGAGATAGACTATACTTTATTGAGCACCTACTTATATCAAACAATGTACAGGCTGGGCACACCACAGAGGCAATTCAGAATGGTCACTGAGAGCATGGGATCTGGAATA 1200

Query 1201 AATGTAACATCTGGATAAATGTAACCTCAAGTCCTGGTCTACTGCTTGTAAATTGTACAATCTTGGGAGGTCCAGGAGAGTCTGATTAGTGGGTCGAGTTGGCCTCTAAAAATCGGTACTTTTTAAAGATCTCCAGGTTATTCAGA 1350

Query 1351 CAACCATCAGGGTTGGGGAACCTATGTTCTCAAGCAGTGTCTCTCATTCAGTACTATGCACCTGAATCCCTGGAAAGCTTGTAAATGCAGATTCTGATTCCTCCAGGTCTGGGGTGAGCTTAGATTCTGCTTTTCTAACAGCTCCC 1500

Query 1501 CATTGATGCCAATGCTGTTGGTCCATAGATCTCGACAAGATGAAGAACACTATGAACTGGAATGTGCTAGTATTATTTGGGTTCTGTTTTATTTTAAAGCCCATCCTATCCAGAGttttttcttcaatttattcaatttttttaattat 1650

Query 1651 ttgtttgtGCAACTCTTACTTTAGACACAGAGGTACATGTGCACGTTTGTTCATGGGTGTTCTGCACCTCAGGCAGTGAGCATAGTACCCAATAAGTAGTTTTTTGACCAATGCCCTTCTCTCCCTGCCCTCTCTAGTAGTCTGCAGTG 1800

Query 1801 TCTGTTGTTCATAGGGTGTCTTTTTAAATGTTCTTATAGTAACATAAATAAAGATTATTACATAGGCTTGAACACCTAGTGGCTTCTCCACTCCCAAGGAGATATATGTTGGATAGCGCAACTACTGAAGTTGCTCTTGAGATGTATT 1950

Query 1951 TAAGGTAATaaaaaaTTGATCGTCAGGGAAGAATATTCAAACCACCATCTAGAGAGTCACAAACTCTCTCAGAAGTTAACTGCCCTATATTGGGAGATGAGAGGTGAAGATGATGATGAGGGATAGAACACTGTGTGGCAAAAT 2100

Query 2101 TCTATATTTCTGTTCTTTTCATATGGATATTTTCATTTTTTCATGGTAAATACATCAACTAAAATTTTCTCTCTAACAGTGAAGTGGCCACAAGCAAAACAGCTTTCTTTTGACAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAAC 2250  
AL544959.3 869 ..... 939  
BX438944.2 859 ..... 929  
AL551427.3 861 ..... 930  
BU902298.1 894 ..... 960  
AL544231.3 877 ..... 946  
AL540651.3 877 ..... 937  
AL553164.3 877 ..... 936

Query 2251 TCGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAACCAAAAGGAGATTATGAGAAATCCTGGTGGC 2400  
AL544959.3 940 ..... 983  
BX438944.2 930 ..... 1030

AL551427.3 931 ..... 1038  
BU902298.1 961 ..... 1116

AL544231.3 947 ..... 1089

Query 2401 TCTTTGTGGAGGAACTAAACATTCCCTTGA 2431  
BU902298.1 1118 ..... 1152

AL544231.3 1090 ..... 1102

Query= T10-C\* [organism=Homo sapiens] anxa1

Length=1518

Sequences producing significant alignments:

	Score (Bits)	E Value	Max ident
AL542692.3 AL542692 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1914	0.0	98%
AL570428.3 AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1910	0.0	98%
BU508007.1 AGENCOURT 10128424 NIH MGC 71 Homo sapiens cDNA clo...	1858	0.0	98%
AL544231.3 AL544231 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1834	0.0	98%
AL576223.3 AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1831	0.0	98%
AL570884.3 AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1825	0.0	97%
AL574991.3 AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1810	0.0	98%
AL541874.3 AL541874 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1792	0.0	99%
DC631365.1 DC631365 macaque bone marrow cDNA library QbmA Maca...	1788	0.0	94%
AL575425.3 AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1788	0.0	98%

ALIGNMENTS

Query	1	AGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAGAAGGTAGAGATAAAGAGTCTTGTTATGTGCGCCAGGATGGAGTGTAGTGGTACAATCTCGGCTCACTGCAGCCTCCGCCTCTTCTGGGTTCAAGTGATTCTCTCT	150
AL542692.3	19	..T.....	151
BU508007.1	1	.....	41
AL544231.3	19	..T.....	62
AL541874.3	1	.....	36
DC631365.1	1	.....C.C.....	60
Query	151	GCCTCAGCCTCTCTGAGTAGATGGGACTACAGACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCTGGTTTATTGAAAATGAAGAGCAGGAATATGTTCAAACTGTGAAGTCATCCAAAGGTGGTCCCGGATCAGCG	300
AL542692.3	152	.....	301
BU508007.1	36	..A..... \   N	160
AL544231.3	57	..A.....	180
AL541874.3	31	..A.....	154
DC631365.1	55	..A.....A.....T.....A	178
Query	301	GTGAGCCCTTCTCTACCTTCAATCCATCCTCGGATGTCGCTGCCTGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTTCTAACTAAGCGAAACAATGCACAGCGTCAACAGATCAAAAGCAGCATATCTC	450
AL542692.3	302	.....	451
AL570428.3	1088	.....-T.....T.....A.....W.....	1041
BU508007.1	161	.....	310
AL544231.3	181	.....	330
AL576223.3	1050	.....-W.....-R.....Y.....	1030
AL570884.3	1059	.....T..... \   M	1045
AL541874.3	155	.....	304
DC631365.1	179	.....T.....C.....	328
Query	451	CAGGAAACAGGAAAGCCCTGGATGAAACACTGAAGAAAGCCCTTACAGGTACACCTTGAGGAGGTTGTTTGTAGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGATGAACCTTCGTCTGCCATGAAGGGCCTTGGAACTGATGAAGAT	600
AL542692.3	452	.....	601
AL570428.3	1040	...-.....GC.....-Y.....M.....	893
BU508007.1	311	.....	460
AL544231.3	331	.....	480
AL576223.3	1029	..-.....-R.....-D.....WR.....-A.....-V.....	888
AL570884.3	1044	.T.....C...Y...W...RS...W...Y.M...R...T...K...YY...S.W...C.....K...S.....	895
AL574991.3	1017	.....-R.....-K.....RS...-CR...Y.M...R...T...K...YY...S.W...C.....K...S.....	888
AL541874.3	305	.....TG.....G.....C.....	454
DC631365.1	329	.....TG.....G.....C.....	478
AL575425.3	1037	.....-.....M.....M.....KG.....C.....C.C...S...A.....	906
Query	601	ACTCTAATTGAGATTTTGGCATCAGAACTAAACAAGAAATCAGAGACATTAAACAGGGCTCTACAGAGAGAACTGAAGAGAGATCTGGCCAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGCTTTCTCTGCTAAG	750
AL542692.3	602	.....	751
AL570428.3	892	.....W.....	743
BU508007.1	461	.....	610
AL544231.3	481	.....	630
AL576223.3	887	...W...AAR.....	738
AL570884.3	894	.....	745
AL574991.3	887	.....	738
AL541874.3	455	.....	604
DC631365.1	479	...G.....G.....	628
AL575425.3	905	.....R.....R.....	756
Query	751	GGTGACCGATCTGAGACTTTGGTGTGAATGAAGACTTTGGCTGATTTCAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCATACCATCCTTACCACCAAGCTATCCACAACCTTCGCAGA	900
AL542692.3	752	.....R.....	901
AL570428.3	742	.....R.....N.....	593
BU508007.1	611	.....	760
AL544231.3	631	.....	780
AL576223.3	737	.....	588
AL570884.3	744	.....	595



DB013065.1 DB013065 TESOP2 Homo sapiens cDNA clone TESOP200154... 1040 0.0 100%  
DB328492.1 DB328492 PLACE6 Homo sapiens cDNA clone PLACE600972... 948 0.0 100%  
BG231632.1 naf37c05.xl Soares NPRMC Homo sapiens cDNA clone IM... 942 0.0 100%  
BU674442.1 UI-CF-DU0-aab-j-09-0-UI.s1 UI-CF-DU0 Homo sapiens c... 935 0.0 100%

ALIGNMENTS

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Query      1      AGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTCTTTTGCAAGAAGGTAGAGATAAAGACACTTTTTCAAAATGGCAATGGTATCAGAAATTCCTCAAGCAGGCCTGGTTTATTGAAAAATGAAGCAGGAATATGTTCAAACCTGTGA 150
BX417009.2 1      .....
AU134300.1 1      .....
AU138502.1 1      .....C.....
BF107418.1 1      .....
                                           133

Query      151     AGTCATCCAAAGGTGGTCCCGATCAGCGGTGAGCCCTATCCTACCTTCAATCCATCCTCGGATGTGCTGCTTGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTTGACATTTCACTAAGCGAAACAATGCAC 300
BX417009.2 139     .....
AU134300.1 151     .....
AU138502.1 151     .....
BF107418.1 134     .....
                                           283

Query      301     AGCGTCAACAGATCAAAGCAGCATATCTCCAGGAACAGGAAAGGTAAGTAGAGTGGTAAATTTAGATATTTAATTTTACAGCATAGTTATACTTAACCATGGATTCGGAAGCACAGTTACCTAGTTCTTTAAGGTTCTAACCACTGTTTT 450
BX417009.2 289     .....
AU134300.1 301     .....
AU138502.1 301     .....
BF107418.1 284     .....
                                           433

Query      451     CTCATTACATCTATGATTGGGATTGCAGTGTTTATCCACTTTGTGCAATTTAATCAAATTTTATCAAATTTCTATTTTTATACATTAGTCATCTTGGTGTATATTGTTTGCAGATGTGGTGCTCTGGGGACAAATTTTAAATTTGAACG 600
BX417009.2 439     .....
AU134300.1 451     .....N.....
AU138502.1 451     .....
BF107418.1 434     .....G.....
DB013065.1 1      .....
                                           62

Query      601     TAAACATCAGAGATTGCTGCTGTCAATAAAGAATATGGTCTGATTGAAATGTACTAATATTTAAACTGAACTGTTTAAATGCCTAAATTTATATATAATTTCTACTTTAAAAATAGCCTTATGTCTTTTATACCAATATGAGTAGTTTTC 750
BX417009.2 589     .....
AU134300.1 601     .....-.....
AU138502.1 601     .....A.....G.....N.....G.....N.....
                                           760
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           NG

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BF107418.1 580     .T..AT.....TG..G....C.... 610
DB013065.1 63      .....
           \
           |
           T

Query      751     TAAAGCAATGAAATAGAAAACTATATAATTTTCAATATCTGATTATATCTGCTTGTATTTGAGAAGTACAAACCTCAAAGATTGGAACATGAATATATTATTTTAAAGTAATTTTACTTCTGTTTTCTGTTAGCACACAGTCCTCTGT 900
BX417009.2 739     .....
AU134300.1 750     .....N.....-.....
AU138502.1 761     C.....
           \
           |
           G

DB013065.1 214     .....
                                           363

Query      901     GTTTTGATCTTTTGATTCTCCCTCTGTATAAGATTACTAACCCCTATGCTTTAAGAAGTTATTGATGAATTCAGTAAATTTTATTTTAATCCCTCTAGATCTGGAAGGTAAGATAATGTTTCAAAATATTTGGTACACTTTGTATGT 1050
BX417009.2 889     .....-.....-.....-.....-.....W.....-.....
DB013065.1 364     .....
                                           513

Query      1051     GAAGGGAAGAAGCTCTAAAAGATGGTTGGGTTTAGGGATGAGTTGTACGATGACCTAAAGTCAGGTAATATCACATTTTTTAACTAGCATGTTACTTATTTGGAAGTCTGATTCTAATCtttttttttGAGCCCTGGATGAAACACT 1200
DB013065.1 514     .....
                                           567

Query      1201     GAAGAAAGCCCTTACAGGTCACCTTGAGGAGGTTGTTTGTGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGATGAACCTCTGCTGCCCATGAAGGCCTTGGAACCTGATGAAGATACCTCTAATTGAGATTTTGGCATCAAGAATAA 1350
CA421424.1 727     .....-.....-.....
AI764962.1 731     ...-.....C.....A.....-.....C.....-.....CT.....C.....G.C.....-.....T. 586
           \
           |
           G

Query      1351     CAAAGAAATCAGAGACATTAAACAGGCTTACAGAGAGGAACCTGAAGAGAGATCTGGCAGAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGA 1500
CA421424.1 604     .....
AI764962.1 585     .C.G...T.....C.....C.....C.....C.....C.....-.....C.....T..... 437
DB328492.1 528     .....
BG231632.1 525     .....
BU674442.1 536     .....
                                           455

Query      1501     AGACTTGGCTGATTACAGATCCAGGCGCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACGTTGTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTTCGAGAGGTAACAATAAATTTCTTTTTCTGGAATCTGT 1650
CA421424.1 454     .....
AI764962.1 436     .....
DB328492.1 442     .....
BG231632.1 442     .....
                                           293
```



BU674442.1	454	.....C.....	305
Query	1651	TTATGGAAGATGCAATTTTCTTTTTTGTATGACAAATAAGAGAAAGTAAAAACAGAACCTTTTTCAATTACTACTCTGTATCAAAACAGATACAGTGTTCCTGACCCATTGTTATTGTCAATTTTGCCAATTTTGTACAGCCGCTACTTT	1800
CA421424.1	304	.....	155
AI764962.1	286	.....	137
DB328492.1	292	.....	143
BG231632.1	292	.....	143
BU674442.1	304	.....	155

Query	1801	ATCATATTTAATACATTTTGTGACTTGGGCATGTGGAACATAATTTGTTATTTTCACTGCCTTTTACTCCCTAAAGATTGGGAATATGTGTGGGAAAAGACATGCATAACAGAACAAATGAAATT	1927
CA421424.1	154	.....	28
AI764962.1	136	.....	10
DB328492.1	142	.....	16
BG231632.1	142	.....	16
BU674442.1	154	.....	28

Query= T12-2 [organism=Homo sapiens] anxl

Length=1027

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
CB306442.1 UI-CF-EN1-aej-e-15-0-UI.s1 UI-CF-EN1 Homo sapiens c...	1279	0.0	100%
CA447733.1 UI-H-E10-ayf-a-16-0-UI.s1 NCI_CGAP_E10 Homo sapiens...	1279	0.0	100%
CA447223.1 UI-H-E10-ayd-b-19-0-UI.s1 NCI_CGAP_E10 Homo sapiens...	1279	0.0	100%
CA422748.1 UI-H-FL0-bdr-g-09-0-UI.s1 NCI_CGAP_FL0 Homo sapiens...	1279	0.0	100%
CA419844.1 UI-H-FH0-bcm-d-16-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1279	0.0	100%
CA417462.1 UI-H-FE0-bbw-c-13-0-UI.s1 NCI_CGAP_FE0 Homo sapiens...	1279	0.0	100%
CA415613.1 UI-H-EZ0-bay-p-10-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens...	1279	0.0	100%
CA414702.1 UI-H-EZ0-bar-e-18-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens...	1279	0.0	100%
BU633206.1 UI-H-FL1-bgt-f-12-0-UI.s1 NCI_CGAP_FL1 Homo sapiens...	1279	0.0	100%
BQ776306.1 UI-H-FH0-bcn-i-12-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1279	0.0	100%

#### ALIGNMENTS

Query	330	CAGGAACAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTTCGACAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTG	479
CB306442.1	716	.....G.A.....	567
CA447733.1	716	.....G.A.....	567
CA447223.1	716	.....G.A.....	567
CA422748.1	718	.....G.A.....	569
CA419844.1	716	.....G.A.....	567
CA417462.1	713	.....G.A.....	564
CA415613.1	718	.....G.A.....	569
CA414702.1	718	.....G.A.....	569
BU633206.1	716	.....G.A.....	567
BQ776306.1	716	.....G.A.....	567

Query	480	ACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAACACAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTGGAACTCGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGA	629
CB306442.1	566	.....	417
CA447733.1	566	.....	417
CA447223.1	566	.....	417
CA422748.1	568	.....	419
CA419844.1	566	.....	417
CA417462.1	563	.....	414
CA415613.1	568	.....	419
CA414702.1	568	.....	419
BU633206.1	566	.....	417
BQ776306.1	566	.....	417

Query	630	ATGATATCAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAACCAAGGAGATTATGAGAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAA	779
CB306442.1	416	.....	267
CA447733.1	416	.....	267
CA447223.1	416	.....	267
CA422748.1	418	.....	269
CA419844.1	416	.....	267
CA417462.1	413	.....	264
CA415613.1	418	.....	269
CA414702.1	418	.....	269
BU633206.1	416	.....	267
BQ776306.1	416	.....	267

Query	780	GACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTAA	929
CB306442.1	266	.....	117
CA447733.1	266	.....	117
CA447223.1	266	.....	117
CA422748.1	268	.....	119
CA419844.1	266	.....	117
CA417462.1	263	.....	114
CA415613.1	268	.....	119
CA414702.1	268	.....	119

BU633206.1	266	.....	117
BQ776306.1	266	.....	117
Query	930	AAATGTTTTCCTCCCAACCATAAAACCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAATGACGTCACAAG	1027
CB306442.1	116	.....	19
CA447733.1	116	.....	19
CA447223.1	116	.....	19
CA422748.1	118	.....	21
CA419844.1	116	.....	19
CA417462.1	113	.....	16
CA415613.1	118	.....	21
CA414702.1	118	.....	21
BU633206.1	116	.....	19
BQ776306.1	116	.....	19

Query= T13-10 [organism=Homo sapiens] anxa1

Length=1277

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
BQ228162.1	AGENCOURT_7258587 NIH_MGC_71 Homo sapiens cDNA clon...	1679	0.0	99%	
AL574991.3	AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1648	0.0	100%	
BM555842.1	AGENCOURT_6544353 NIH_MGC_88 Homo sapiens cDNA clon...	1639	0.0	99%	
AL576603.2	AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1635	0.0	99%	
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1633	0.0	99%	
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1631	0.0	99%	
AL570884.3	AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1628	0.0	99%	
AL576340.3	AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1624	0.0	99%	
AL575425.3	AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1615	0.0	99%	
AL553095.3	AL553095 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1587	0.0	98%	

#### ALIGNMENTS

Query	351	GATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAACAGGGTCTACAGAGAGGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAAACGCTTTGCTTTCT	500
BQ228162.1	40	.....	189
AL574991.3	896	.....	747
BM555842.1	1	.....	148
AL576603.2	901	.....-NM.....-	754
AL576223.3	896	.....W.AAR.....	747
AL570428.3	901	.....W.....	752
AL570884.3	903	.....	754
AL576340.3	896	.....	758
AL575425.3	914	.....R.....R.....	765
AL553095.3	902	.....	753
Query	501	CTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGCGTGATTTCAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACGCTGTTCAATACCATCCTTACCACCAGAAGCTATCCAAA	650
BQ228162.1	190	.....	339
AL574991.3	746	.....	597
BM555842.1	149	.....	298
AL576603.2	753	.....	604
AL576223.3	746	.....	597
AL570428.3	751	.....R.....N.....	602
AL570884.3	753	.....	604
AL576340.3	757	.....	608
AL575425.3	764	.....R.....B.....S.....T.....	615
AL553095.3	752	.....	603
Query	651	CTTCGCAGAGTGTTCAGAAATACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCAGAGTATCGTGAAGTGCGCCACAAGCAACACAGCTTTCTTTGCAGAGAAGCTT	800
BQ228162.1	340	.....	489
AL574991.3	596	.....	447
BM555842.1	299	.....	448
AL576603.2	603	.....	454
AL576223.3	596	.....	447
AL570428.3	601	.....A.....	452
AL570884.3	603	.....	454
AL576340.3	607	.....	458
AL575425.3	614	.....N.....N.....	465
AL553095.3	602	.....YY...V.....C	453
Query	801	CATCAAGCCATGAAAGGTGTTGGAATCGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAGCATTTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAA	950
BQ228162.1	490	.....	639
AL574991.3	446	.....W.....	297
BM555842.1	449	.....	598
AL576603.2	453	.....	304
AL576223.3	446	.....	297
AL570428.3	451	.....A.....T.....	302
AL570884.3	453	.....	304
AL576340.3	457	.....R.....	308
AL575425.3	464	.....	315

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AL553095.3 452 .....S..S.....RK..R..G..R.....K..G.....303
Query      951 GGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCT 1100
BQ228162.1 640 .....                               790
                                     |
                                     A
AL574991.3 296 .....Y.....147
BM555842.1 599 .....748
AL576603.2 303 .....154
AL576223.3 296 .....147
AL570428.3 301 .....152
AL570884.3 303 .....154
AL576340.3 307 ..R.....158
AL575425.3 314 ..R.....165
AL553095.3 302 ..R.....153
Query      1101 ACCTACATGCTGAAAAATATAGCCTTAAATCATTTTATATATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCCAAACCATAAAACCTATACAAGTTGTTCTAGTAAACAATACATGAGAAAGATGTCCTATG 1250
BQ228162.1 791 .....                               942
                                     |
                                     G
AL574991.3 146 .....1
BM555842.1 749 .....907
                                     |
                                     A
                                     |
                                     C
AL576603.2 153 .....3
                                     |
                                     C
                                     |
                                     N
AL576223.3 146 .....B.....1
AL570428.3 151 .....T.....2
AL570884.3 153 .....RW..V.....2
                                     |
                                     N
                                     |
                                     N
AL576340.3 157 .....7
                                     |
                                     N
AL575425.3 164 ..N.....17
AL553095.3 152 .....G.....2
                                     |
                                     N
Query      1251 TAGCTGAAAAATAAAATGACGTC 1272
BQ228162.1 943 .....965
                                     |
                                     A
BM555842.1 908 .....922
AL576603.2 2 ..1
AL570428.3 1 ..1
AL570884.3 1 ..1
AL576340.3 6 ..5
AL553095.3 1 ..1

Query= T14-11 [organism=Homo sapiens] anxal
Length=1348

Sequences producing significant alignments:

Score      E      Max
(Bits)     Value  ident

AL570428.3 AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1908      0.0   98%
AL576223.3 AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1831      0.0   98%
AL570884.3 AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1825      0.0   97%
AL574991.3 AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1810      0.0   98%
AL575425.3 AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1788      0.0   98%
AL553095.3 AL553095 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1762      0.0   97%
FS581262.1 FS581262 macaque heart cDNA library QhtB Macaca fas... 1742      0.0   96%
BQ228162.1 AGENCOURT 7258587 NIH_MGC_71 Homo sapiens cDNA clon... 1731      0.0   99%
AL576340.3 AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1729      0.0   97%
AL576603.2 AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho... 1655      0.0   99%

ALIGNMENTS

Query      1      AGTGTGAAATCTTCAGAGAAGAATTCTCTTTAGTTCTTTTGCAAGAAGGTAGAGATATAAGACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCCTCAAGCAGGCCTGGTTTATTGAAAATGAAGACAGGAATATGTTCAAACCTGTG 150
FS581262.1 1      .....C.C.....144

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Query	151	AAGTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCTATCTCACTTCAAATCCATCATTTGAACATTGATCTCTAACTAACTAAGCGAAACAATGCACAGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAGCCCT	300
AL570428.3	1087	.....T.....T.....A.....W.....GC.....	1022
AL576223.3	1050	.....W.....R.....Y.....	1012
AL570884.3	1059	.....T.....T.....C.....Y.....	1025
		\	
		M	
AL574991.3	1017	.....	1011
AL575425.3	1037	.....	1034
AL553095.3	1020	.....	1017
FS581262.1	149	..A.....T.....A.....-.....CAACC.T.....-A.-T.....	295
AL576340.3	1011	.....	1008
Query	301	GGATGAAACACTGAAGAAAGCCCTTACAGGTCACCTTGAGGAGTTGTTTGTAGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGTGAACCTTCGTCTGCCATGAAGGCGCTTGGAACCTGATGAAGATACTCTAATTGAGATTTTGGC	450
AL570428.3	1021	.....Y.....D.....WR.....A.....V.....M.....	873
AL576223.3	1011	..R.....D.....A.....V.....W...AAR.....	868
AL570884.3	1024	..W.....RS...W...Y.M...R...T...K...YY...S.W...C.....K...S.....	875
AL574991.3	1010	..R.....K.....RS...CR...K.....	868
AL575425.3	1033	.....M.....M.....KG...C.....C.C...S...A.....	886
AL553095.3	1016	..R.....YK.....-.....-.....C.....G.....	874
FS581262.1	296	.....C.TG.....G.....C.....G.....	445
BQ228162.1	12	.....G.....Y.....-.....K.....-.....RW.....	68
AL576340.3	1007	.....G.....Y.....-.....K.....-.....RW.....	878
AL576603.2	917	.....-.....WM.....	875
Query	451	ATCAAGAACTAACAAGAAATCAGAGACATTAAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGCTTTCTCTTGTCTAAGGGTGACCGATCTGAGGACTT	600
AL570428.3	872	.....W.....	723
AL576223.3	867	.....	718
AL570884.3	874	.....	725
AL574991.3	867	.....	718
AL575425.3	885	.....R.....R.....	736
AL553095.3	873	.....	724
FS581262.1	446	.....	595
BQ228162.1	69	.....	218
AL576340.3	877	.....	729
AL576603.2	874	.....	725
Query	601	TGGTGTGAATGAAGACTTGGCTGATTGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACAGAAGCTATCCACAACCTTCGAGAGTGTTCAGAAATACACAA	750
AL570428.3	722	.....R.....N.....	573
AL576223.3	717	.....	568
AL570884.3	724	.....	575
AL574991.3	717	.....	568
AL575425.3	735	.....B.....S.....T.....	586
AL553095.3	723	.....	574
FS581262.1	596	.....G.....T.....C.....T.....	745
BQ228162.1	219	.....	368
AL576340.3	728	.....	579
AL576603.2	724	.....	575
Query	751	GTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCCTACAGCTATCGTGAAGTGCGCCACAAGCAAACGAGCTTTCTTTGAGAGAGCTTCATCAAGCCATGAAAGGTGTTGGAACTCG	900
AL570428.3	572	.....A.....	423
AL576223.3	567	.....	418
AL570884.3	574	.....	425
AL574991.3	567	.....	418
AL575425.3	585	.....N.....N.....	436
AL553095.3	573	.....YY...V.....A...C.....V.....	424
FS581262.1	746	.....T.....	895
BQ228162.1	369	.....	518
AL576340.3	578	.....	429
AL576603.2	574	.....	425
Query	901	CCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGATTCATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAACCAAAGGAGATTATGAGAAATCCTGGTGGCTCT	1050
AL570428.3	422	.....A.....T.....	273
AL576223.3	417	.....	268
AL570884.3	424	.....	275
AL574991.3	417	.....W.....	268
AL575425.3	435	.....	286
AL553095.3	423	.....S...S.....RK...R...G...R.....K...G...R.....	274
FS581262.1	896	.....A.....-.....-.....-.....-.....	1038
BQ228162.1	519	.....	668
AL576340.3	428	.....R.....R.....	279
AL576603.2	424	.....	275
Query	1051	TTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTATCTCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAA	1200
AL570428.3	272	.....	123
AL576223.3	267	.....	118
AL570884.3	274	.....Y.....	125
AL574991.3	267	.....	118
AL575425.3	285	.....	136
AL553095.3	273	.....N.....	124
FS581262.1	1039	.....	1072



BQ228162.1 420 ..... 569  
 AL576603.2 523 ..... 374  
 AL576340.3 527 ..... 378  
 AL576223.3 516 ..... 367  
 AL574991.3 516 ..... 367  
 BM555842.1 379 ..... 528  
 AL570428.3 521 ..... A. 372  
 BE614257.1 536 ..... 387  
 AL570884.3 523 ..... 374  
 BU857810.1 267 ..... 416  
  
 Query 810 TGATATCAAAGCATTCATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCTGGATGAAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAG 959  
 BQ228162.1 570 ..... 719  
 AL576603.2 373 ..... 224  
 AL576340.3 377 ..... R. R. 228  
 AL576223.3 366 ..... 217  
 AL574991.3 366 ..... W. Y. 217  
 BM555842.1 529 ..... 678  
 AL570428.3 371 ..... T. 222  
 BE614257.1 386 ..... 237  
 AL570884.3 373 ..... 224  
 BU857810.1 417 ..... 566  
  
 Query 960 ACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATTATAAATCTGTATAATAGAGATAAGTCCATTTTAAAA 1109  
 BQ228162.1 720 ..... 870  
  
 AL576603.2 223 ..... 74  
 AL576340.3 227 ..... 78  
 AL576223.3 216 ..... 67  
 AL574991.3 216 ..... 67  
 BM555842.1 679 ..... 828  
 AL570428.3 221 ..... T. 72  
 BE614257.1 236 ..... 87  
 AL570884.3 223 ..... 74  
 BU857810.1 567 ..... N. N. 716  
  
 Query 1110 AATGTTTTCCCAACCATAAAACCCATACAAGTTGTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAATGACGTC 1201  
 BQ228162.1 871 ..... G. 965  
  
 AL576603.2 73 ..... 1  
  
 AL576340.3 77 ..... 5  
  
 AL576223.3 66 ..... B. N. 1  
 AL574991.3 66 ..... 1  
 BM555842.1 829 ..... G. 922  
  
 AL570428.3 71 ..... 1  
 BE614257.1 86 ..... T. A- 6  
  
 AL570884.3 73 ..... RW...V...N...N...W...A... 1  
  
 BU857810.1 717 ..... N. N. 808  
  
 Query= T16-12 [organism=Homo sapiens] anxa1  
 Length=1094

Sequences producing significant alignments:			Score (Bits)	E Value	Max Ident
AL553114.3	AL553114	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1441	0.0	100%
CX870542.1	HESC4_46_F03.g1_A037	NIH MGC 262 Homo sapiens cDNA ...	1441	0.0	100%
BQ953713.1	AGENCOURT_8786826	NIH MGC 43 Homo sapiens cDNA clon...	1432	0.0	100%
BM458053.1	AGENCOURT_6411336	NIH MGC 71 Homo sapiens cDNA clon...	1430	0.0	100%
AL544959.3	AL544959	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1426	0.0	100%
AU117349.1	AU117349	HEMBA1 Homo sapiens cDNA clone HEMBA100120...	1426	0.0	100%

AL553679.3	AL553679	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1419	0.0	100%
BQ962441.1	AGENCOURT_10056322	NIH_MGC_71 Homo sapiens cDNA clo...	1419	0.0	100%
BU902298.1	AGENCOURT_10127317	NIH_MGC_71 Homo sapiens cDNA clo...	1417	0.0	100%
EB387180.1	nbj26d10.y1	Human optic nerve. Unnormalized (nbj) H...	1415	0.0	100%

ALIGNMENTS

Query	1	AGTGTGAAATCTTCAGAGAAGAATTCTCTTTAGTCTTTTGAAGAAGGTAGAGATAAAGACACTTTTTCAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATTGAAAATGAAGAGCAGGAATATGTTCAAACTGTGA	150
AL553114.3	107	.....	256
CX870542.1	29	.....	178
BQ953713.1	1	.....	145
BM458053.1	11	.....	160
AL544959.3	1	.....	142
AU117349.1	1	.....	150
AL553679.3	1	.....	142
BQ962441.1	1	.....	138
BU902298.1	24	.....	164

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|  
N

EB387180.1	1	.....	136
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Query	151	AGTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCTATCCTACCTTCAATCCATCCTCGGATGTCGCTGCCTTGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCTTGACATTCTAACTAAGCGAAACAATGCAC	300
AL553114.3	257	.....	406
CX870542.1	179	.....	328
BQ953713.1	146	.....	295
BM458053.1	161	.....	310
AL544959.3	143	.....	292
AU117349.1	151	.....	300
AL553679.3	143	.....	292
BQ962441.1	139	.....	288
BU902298.1	165	.....	314
EB387180.1	137	.....	286

Query	301	AGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCTGGATGAAACACTGAAGAAAGCCCTTACAGGTACCTTGAGGAGGTGTGTTTAGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGAACTTCGTGCTG	450
AL553114.3	407	.....	556
CX870542.1	329	.....	478
BQ953713.1	296	.....	445
BM458053.1	311	.....	460
AL544959.3	293	.....	442
AU117349.1	301	.....	450
AL553679.3	293	.....C.....	441
BQ962441.1	289	.....	438
BU902298.1	315	.....	464
EB387180.1	287	.....	436

Query	451	CCATGAAGGCCTTGGAACTGATGAAGTACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAAACAGGCTCTACAGAGAGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATT	600
AL553114.3	557	.....	706
CX870542.1	479	.....	628
BQ953713.1	446	.....	595
BM458053.1	461	.....	610
AL544959.3	443	.....	592
AU117349.1	451	.....	600
AL553679.3	442	.....	591
BQ962441.1	439	.....	588
BU902298.1	465	.....	614
EB387180.1	437	.....	586

Query	601	TTCGGAACGCTTTGCTTTCTCTTGTCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTGATGCCAGGCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTTTCAATACCATCCTTA	750
AL553114.3	707	.....	856
CX870542.1	629	.....	778
BQ953713.1	596	.....	745
BM458053.1	611	.....	760
AL544959.3	593	.....T.....	742
AU117349.1	601	.....	750
AL553679.3	592	.....N.....	741
BQ962441.1	589	.....	738
BU902298.1	615	.....	764
EB387180.1	587	.....	736

Query	751	CCACCAGAAGCTATCCACAACCTTCGCAGAG	780
AL553114.3	857	.....	886
CX870542.1	779	.....	808
BQ953713.1	746	.....	775
BM458053.1	761	.....	791

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C

AL544959.3	743	.....	772
AU117349.1	751	.....	777
AL553679.3	742	.....	771
BQ962441.1	739	.....	768

BU902298.1 765 ..... 794  
EB387180.1 737 ..... 766

Query= T17-2 [organism=Homo sapiens] anxl

Length=1103

Sequences producing significant alignments:			Score	E	Max
			(Bits)	Value	ident
BU857810.1	AGENCOURT_10474308 NIH_MGC_107 Homo sapiens cDNA cl...	1386	0.0	99%	
CN386790.1	17000599887650 GRN PRENEU Homo sapiens cDNA 5', mRN...	1378	0.0	100%	
BQ228162.1	AGENCOURT_7258587 NIH_MGC_71 Homo sapiens cDNA clon...	1376	0.0	99%	
CA447733.1	UI-H-EI0-ayf-a-16-0-UI.s1 NCI_CGAP_EI0 Homo sapiens...	1371	0.0	100%	
CA423056.1	UI-H-FL0-bdk-f-10-0-UI.s1 NCI_CGAP_FL0 Homo sapiens...	1365	0.0	100%	
BE614257.1	601504294T1 NIH_MGC_71 Homo sapiens cDNA clone IMAG...	1358	0.0	99%	
BQ776006.1	UI-H-FH0-bck-h-18-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1356	0.0	100%	
AL576603.2	AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1352	0.0	100%	
AL576340.3	AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1351	0.0	100%	
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1349	0.0	100%	

ALIGNMENTS

Query	346	CCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTACAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGCGTAAACGTGTTCAATACCATCCTTACCAACCAGAAGCTATCCACAACCTCGCAGAGTGTT	495
BU857810.1	51	.....	200
CN386790.1	18	.....	167
BQ228162.1	204	.....	353
CA447733.1	765	.....	632
CA423056.1	767	.....	634
BE614257.1	752	.....	603
BQ776006.1	765	.....N	632
		\	
		I	
		T	
AL576603.2	739	.....	590
AL576340.3	743	.....	594
AL576223.3	732	.....	583
Query	496	TCGAAATACACCAAGTACAGTAAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCTTCACAGCTATCGTGAAGTGCGCCACAAGCAAAACAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAA	645
BU857810.1	201	.....	350
CN386790.1	168	.....	317
BQ228162.1	354	.....	503
CA447733.1	631	.....	482
CA423056.1	633	.....	484
BE614257.1	602	.....	453
BQ776006.1	631	.....	482
AL576603.2	589	.....	440
AL576340.3	593	.....	444
AL576223.3	582	.....	433
Query	646	AGGTGTTGGAACCTGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAGGAGATTATGAGAA	795
BU857810.1	351	.....	500
CN386790.1	318	.....	467
BQ228162.1	504	.....	653
CA447733.1	481	.....	332
CA423056.1	483	.....	334
BE614257.1	452	.....	303
BQ776006.1	481	.....	332
AL576603.2	439	.....	290
AL576340.3	443	.....R.....R.....	294
AL576223.3	432	.....	283
Query	796	AATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTGGATGGCTCAAGCTATGATCAGAAGACTTTAAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTTACCTACATGCTGAA	945
BU857810.1	501	.....N.....	650
CN386790.1	468	.....	617
BQ228162.1	654	.....	804
		\	
		I	
		A	
CA447733.1	331	.....	182
CA423056.1	333	.....	184
BE614257.1	302	.....	153
BQ776006.1	331	.....	182
AL576603.2	289	.....	140
AL576340.3	293	.....	144
AL576223.3	282	.....	133
Query	946	AAATATAGCCTTTAAATCATTTTATATATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTTCCCAAAACCATAAACCCCTATACAAGTTGTTCTAGTAAACAATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAA	1095
BU857810.1	651	.....N.....	800
CN386790.1	618	.....N.....G.....	766
BQ228162.1	805	.....G.....	957



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      |      |      |
      G      G      A
CA447733.1 181 ..... 32
CA423056.1 183 ..... 34
BE614257.1 152 ..... 6
      \
      |
      T
BQ776006.1 181 ..... 32
AL576603.2 139 ..... 1
      \
      |
      C
AL576340.3 143 ..... 5
      \
      |
      N
AL576223.3 132 ..... 1
      \
      |
      B
Query      1096  ATGACGTC  1103
BU857810.1 801 ..... 808
BQ228162.1 958 ..... 965
CA447733.1 31 ..... 24
CA423056.1 33 ..... 26
BQ776006.1 31 ..... 24
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Query= T18-19 [organism=Homo sapiens] anxa1  
Length=1170

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
CA447733.1	UI-H-EI0-ayf-a-16-0-UI.s1	NCI_CGAP_EI0 Homo sapiens...	1319	0.0	100%
CB306442.1	UI-CF-EN1-aej-e-15-0-UI.s1	UI-CF-EN1 Homo sapiens c...	1315	0.0	100%
CA418062.1	UI-H-FH0-bcc-j-24-0-UI.s1	NCI_CGAP_FH0 Homo sapiens...	1315	0.0	100%
BQ776006.1	UI-H-FH0-bcc-h-18-0-UI.s1	NCI_CGAP_FH0 Homo sapiens...	1315	0.0	100%
CA423056.1	UI-H-FL0-bdk-f-10-0-UI.s1	NCI_CGAP_FL0 Homo sapiens...	1314	0.0	100%
CA418210.1	UI-H-FH0-bcf-i-22-0-UI.s1	NCI_CGAP_FH0 Homo sapiens...	1312	0.0	100%
CA443862.1	UI-H-DP0-avg-a-20-0-UI.s1	NCI_CGAP_Fs1 Homo sapiens...	1310	0.0	100%
BQ774641.1	UI-H-FH0-bcc-l-13-0-UI.s1	NCI_CGAP_FH0 Homo sapiens...	1308	0.0	100%
CA447223.1	UI-H-EI0-ayd-b-19-0-UI.s1	NCI_CGAP_EI0 Homo sapiens...	1303	0.0	100%
BQ775843.1	UI-H-FH0-bcg-e-23-0-UI.s1	NCI_CGAP_FH0 Homo sapiens...	1301	0.0	100%

#### ALIGNMENTS

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Query      457  AGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTTAAACGTGTTCAATACCATCCTTACCACGAGCTATCCACAACCTTCGCAGAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGAC 606
CA447733.1 732 ..... 583
CB306442.1 732 ...N..... 583
CA418062.1 732 .....N..... 583
BQ776006.1 732 .....N..... 583
CA423056.1 734 ..... 585
CA418210.1 728 ..... 580
CA443862.1 732 .....C.....N..... 583
BQ774641.1 729 ..... 583
CA447223.1 723 ..... 583
BQ775843.1 721 .....N..... 580

Query      607  CTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAAACCAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTGGAACCTGCCATAAGGCATTGATCAGGATTATGGTTTCCCGT 756
CA447733.1 582 ..... 433
CB306442.1 582 ..... 433
CA418062.1 582 ..... 433
BQ776006.1 582 ..... 433
CA423056.1 584 ..... 435
CA418210.1 579 ..... 430
CA443862.1 582 ..... 433
BQ774641.1 582 ..... 433
CA447223.1 582 ..... 433
BQ775843.1 579 ..... 430

Query      757  TCTGAAATTGACATGAATGATATCAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCTCGATGAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCT 906
CA447733.1 432 ..... 283
CB306442.1 432 ..... 283
CA418062.1 432 ..... 283
BQ776006.1 432 ..... 283
CA423056.1 434 ..... 285
CA418210.1 429 ..... 280
CA443862.1 432 ..... 283
BQ774641.1 432 ..... 283
CA447223.1 432 ..... 283
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BQ775843.1	429	.....	280
Query	907	CAAGCTATGATCAGAAGCTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAACTCTGTATAATAGAGA	1056
CA447733.1	282	.....	133
CB306442.1	282	.....	133
CA418062.1	282	.....	133
BQ776006.1	282	.....	133
CA423056.1	284	.....	135
CA418210.1	279	.....	130
CA443862.1	282	.....	133
BQ774641.1	282	.....	133
CA447223.1	282	.....	133
BQ775843.1	279	.....	130

Query	1057	TAAGTCCATTTTTTAAAAATGTTTTTCCCAAACCATAAAAACCTATACAAGTTGTTCTAGTAACANTACATGAGAAAGATGTTCTATGTAGCTGAAAAATAAATGACGTCACAAG	1170
CA447733.1	132	.....	19
CB306442.1	132	.....	19
CA418062.1	132	.....	19
BQ776006.1	132	.....	19
CA423056.1	134	.....G.....	21
CA418210.1	129	.....	16
CA443862.1	132	.....	19
BQ774641.1	132	.....	19
CA447223.1	132	.....	19
BQ775843.1	129	.....	16

Query= T19-6 [organism=Homo sapiens] anxl

Length=1210

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
CA447733.1 UI-H-EI0-ayf-a-16-0-UI.s1 NCI_CGAP_EI0 Homo sapiens...	1360	0.0	100%
CA423056.1 UI-H-FL0-bdk-f-10-0-UI.s1 NCI_CGAP_FL0 Homo sapiens...	1354	0.0	100%
BQ776006.1 UI-H-FH0-bck-h-18-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1345	0.0	99%
BU857810.1 AGENCOURT_10474308 NIH_MGC_107 Homo sapiens cDNA cl...	1336	0.0	99%
CB306442.1 UI-CF-EN1-aej-e-15-0-UI.s1 UI-CF-EN1 Homo sapiens c...	1330	0.0	100%
CA418062.1 UI-H-FH0-bcc-j-24-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1330	0.0	100%
BM981135.1 UI-CF-EN1-adg-a-11-0-UI.s1 UI-CF-EN1 Homo sapiens c...	1330	0.0	99%
CN386790.1 17000599887650 GRN_PRENEU Homo sapiens cDNA 5', mRN...	1328	0.0	100%
CA418210.1 UI-H-FH0-bcf-i-22-0-UI.s1 NCI_CGAP_FH0 Homo sapiens...	1328	0.0	100%
CA443862.1 UI-H-DP0-avg-a-20-0-UI.s1 NCI_CGAP_Fs1 Homo sapiens...	1327	0.0	99%

#### ALIGNMENTS

Query	472	ATGAAGACTTGGCTGATTGATCAGATGCCAGGGCCTTGATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACGTTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTTCGCAGAGTGTTCAGAAATACACCAAGTACAGTA	621
CA447733.1	758	.....	609
CA423056.1	760	.....	611
BQ776006.1	758	.....-.....N.....	609

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BU857810.1	74	.....	223
CB306442.1	744	.....N.....	609
CA418062.1	744	.....N.....	609
BM981135.1	754	.....-.....N.....	609
CN386790.1	41	.....	190
CA418210.1	740	.....-.....	606
CA443862.1	748	.....C.....N.....	609

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Query	622	AGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAACGAGCTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTGCCATAAGS	771
CA447733.1	608	.....	459
CA423056.1	610	.....	461
BQ776006.1	608	.....	459
BU857810.1	224	.....	373
CB306442.1	608	.....	459
CA418062.1	608	.....	459
BM981135.1	608	.....	459
CN386790.1	191	.....	340
CA418210.1	605	.....	456
CA443862.1	608	.....	459

Query	772	CATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCAATTTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAAGGAGATTATGAGAAAAATCCTGGTGGCTCTTTGTGGAG	921
CA447733.1	458	.....	309
CA423056.1	460	.....	311
BQ776006.1	458	.....	309
BU857810.1	374	.....	523

CB306442.1	458	.....	309
CA418062.1	458	.....	309
BM981135.1	458	.....	309
CN386790.1	341	.....	490
CA418210.1	455	.....	306
CA443862.1	458	.....	309
Query	922	GAAACTAAACATTCCCTTGTGCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCTTTAAATCATTTTT	1071
CA447733.1	308	.....	158
CA423056.1	310	.....	160
BQ776006.1	308	.....	158
BU857810.1	524	.....N.....	674
CB306442.1	308	.....	158
CA418062.1	308	.....	158
BM981135.1	308	.....	158
CN386790.1	491	.....	641
CA418210.1	305	.....	155
CA443862.1	308	.....	158
Query	1072	ATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCAAACCATAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTTCTATGTAGCTGAAAAATAAAATGACGTCACAAG	1210
CA447733.1	157	.....	19
CA423056.1	159	.....G.....	21
BQ776006.1	157	.....	19
BU857810.1	675	.....N.....N.....	808
CB306442.1	157	.....	19
CA418062.1	157	.....	19
BM981135.1	157	.....	19
CN386790.1	642	.....G.....	766
CA418210.1	154	.....	16
CA443862.1	157	.....	19

Query= T21-l1 [organism=Homo sapiens] anxa1

Length=989

Sequences producing significant alignments:			
	Score (Bits)	E Value	Max ident
CA447733.1 UI-H-EI0-ayf-a-16-0-UI.s1 NCI_CGAP EI0 Homo sapiens...	1369	0.0	100%
CA423056.1 UI-H-FL0-bdk-f-10-0-UI.s1 NCI_CGAP FL0 Homo sapiens...	1363	0.0	100%
BU857810.1 AGENCOURT_10474308 NIH_MGC_107 Homo sapiens cDNA cl...	1354	0.0	99%
BQ776006.1 UI-H-FH0-bck-h-18-0-UI.s1 NCI_CGAP FH0 Homo sapiens...	1354	0.0	100%
CN386790.1 17000599887650 GRN PRENEU Homo sapiens cDNA 5', mRN...	1349	0.0	100%
BQ228162.1 AGENCOURT_7258587 NIH_MGC_71 Homo sapiens cDNA clon...	1345	0.0	99%
BM981135.1 UI-CF-EN1-adq-a-11-0-UI.s1 UI-CF-EN1 Homo sapiens c...	1338	0.0	99%
BE614257.1 601504294T1 NIH_MGC_71 Homo sapiens cDNA clone IMAG...	1328	0.0	99%
CB306442.1 UI-CF-EN1-aej-e-15-0-UI.s1 UI-CF-EN1 Homo sapiens c...	1327	0.0	100%
CA418062.1 UI-H-FH0-bcc-j-24-0-UI.s1 NCI_CGAP FH0 Homo sapiens...	1327	0.0	100%

ALIGNMENTS

Query	249	GGTGTGAATGAAGACTTGGCTGATTGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTTTCAATACCATCCTTACCACGAGAAGCTATCCACAACCTTCGAGAGTGTTCAGAAATACCCANG	398
CA447733.1	765	.....	616
CA423056.1	767	.....	618
BU857810.1	67	.....	216
BQ776006.1	765	.....N.....	616
		<div> <div> </div> <div> </div> <div> </div> </div>	
CN386790.1	34	.....	183
BQ228162.1	220	.....	369
BM981135.1	760	.....N.....	616
BE614257.1	736	.....	587
CB306442.1	744	.....N.....	616
CA418062.1	744	.....N.....	616
Query	399	TACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAACCCAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTGGAACTCGC	548
CA447733.1	615	.....	466
CA423056.1	617	.....	468
BU857810.1	217	.....	366
BQ776006.1	615	.....	466
CN386790.1	184	.....	333
BQ228162.1	370	.....	519
BM981135.1	615	.....	466
BE614257.1	586	.....	437
CB306442.1	615	.....	466
CA418062.1	615	.....	466
Query	549	CATAAGGCATTGATCAGGATTATGTTTCCCGTCTGAAATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAAGGAGATTATGAGAAAATCCTGGTGGCTCTT	698
CA447733.1	465	.....	316
CA423056.1	467	.....	318
BU857810.1	367	.....	516
BQ776006.1	465	.....	316
CN386790.1	334	.....	483
BQ228162.1	520	.....	669
BM981135.1	465	.....	316
BE614257.1	436	.....	287
CB306442.1	465	.....	316
CA418062.1	465	.....	316
Query	699	TGTGGAGAAACTAAACATTCCCTTGTATGGTCTCAAGCTATGATCAGAAGACTTTAAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAA	848
CA447733.1	315	.....	166
CA423056.1	317	.....	168
BU857810.1	517	.....N.....	666
BQ776006.1	315	.....	166
CN386790.1	484	.....	633
BQ228162.1	670	.....	820
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BM981135.1	315	.....	166
BE614257.1	286	.....	137
CB306442.1	315	.....	166
CA418062.1	315	.....	166
Query	849	TCATTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTAAAAATGTTTCCCCAAACCATAAACCCATATACAGTTGTTCTAGTAACATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAATGACGT	989
CA447733.1	165	.....	25
CA423056.1	167	.....G.....	27
BU857810.1	667	.....N.....N.....	807
BQ776006.1	165	.....	25
CN386790.1	634	.....G.....	766
BQ228162.1	821	.....G.....	964
		<div> <div> </div> <div> </div> <div> </div> </div>	
BM981135.1	165	.....	25
BE614257.1	136	.....T.A-.....	6
		<div> <div> </div> <div> </div> <div> </div> </div>	
CB306442.1	165	.....	25
CA418062.1	165	.....	25

Query= T22-21 [organism=Homo sapiens] anxa1

Length=1084

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
CB306442.1 UI-CF-EN1-aej-e-15-0-UI.s1 UI-CF-EN1 Homo sapiens c...	1288	0.0	100%
CA447733.1 UI-H-EI0-ayf-a-16-0-UI.s1 NCI_CGAP_EI0 Homo sapiens...	1288	0.0	100%

CA447223.1	UI-H-EI0-ayd-b-19-0-UI.s1	NCI_CGAP_EI0	Homo sapiens...	1288	0.0	100%
CA422748.1	UI-H-FL0-bdr-g-09-0-UI.s1	NCI_CGAP_FL0	Homo sapiens...	1288	0.0	100%
CA419844.1	UI-H-FH0-bcm-d-16-0-UI.s1	NCI_CGAP_FH0	Homo sapiens...	1288	0.0	100%
CA417462.1	UI-H-FE0-bbw-c-13-0-UI.s1	NCI_CGAP_FE0	Homo sapiens...	1288	0.0	100%
CA415613.1	UI-H-EZ0-bay-p-10-0-UI.s1	NCI_CGAP_Ch1	Homo sapiens...	1288	0.0	100%
CA414702.1	UI-H-EZ0-bar-e-18-0-UI.s1	NCI_CGAP_Ch1	Homo sapiens...	1288	0.0	100%
BU633206.1	UI-H-FL1-bgt-f-12-0-UI.s1	NCI_CGAP_FL1	Homo sapiens...	1288	0.0	100%
BQ776306.1	UI-H-FH0-bcn-i-12-0-UI.s1	NCI_CGAP_FH0	Homo sapiens...	1288	0.0	100%

ALIGNMENTS

Query	388	AGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTTCGCAGAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGA	537
CB306442.1	715	.....	566
CA447733.1	715	.....	566
CA447223.1	715	.....	566
CA422748.1	717	.....	568
CA419844.1	715	.....	566
CA417462.1	712	.....	563
CA415613.1	717	.....	568
CA414702.1	717	.....	568
BU633206.1	715	.....	566
BQ776306.1	715	.....	566
Query	538	CATTGAGAAATGCCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAAACGAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTCGCCATAAGGCATTGATCAGGATTATGGTTTCCGGTCTGAAATTGACATGAA	687
CB306442.1	565	.....	416
CA447733.1	565	.....	416
CA447223.1	565	.....	416
CA422748.1	567	.....	418
CA419844.1	565	.....	416
CA417462.1	562	.....	413
CA415613.1	567	.....	418
CA414702.1	567	.....	418
BU633206.1	565	.....	416
BQ776306.1	565	.....	416
Query	688	TGATATCAAAGCATTCATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAG	837
CB306442.1	415	.....	266
CA447733.1	415	.....	266
CA447223.1	415	.....	266
CA422748.1	417	.....	268
CA419844.1	415	.....	266
CA417462.1	412	.....	263
CA415613.1	417	.....	268
CA414702.1	417	.....	268
BU633206.1	415	.....	266
BQ776306.1	415	.....	266
Query	838	ACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATTTATACTCTGTATAATAGAGATAAGTCATTTTTTAA	987
CB306442.1	265	.....	116
CA447733.1	265	.....	116
CA447223.1	265	.....	116
CA422748.1	267	.....	118
CA419844.1	265	.....	116
CA417462.1	262	.....	113
CA415613.1	267	.....	118
CA414702.1	267	.....	118
BU633206.1	265	.....	116
BQ776306.1	265	.....	116
Query	988	AATGTTTTCCCCAAACCATAAAACCCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCATATGTAGCTGAAAAATAAAATGACGTCACAAG	1084
CB306442.1	115	.....	19
CA447733.1	115	.....	19
CA447223.1	115	.....	19
CA422748.1	117	.....	21
CA419844.1	115	.....	19
CA417462.1	112	.....	16
CA415613.1	117	.....	21
CA414702.1	117	.....	21
BU633206.1	115	.....	19
BQ776306.1	115	.....	19

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions  
Posted date: Feb 24, 2019 1:46 AM  
Number of letters in database: 43,200,890,307  
Number of sequences in database: 77,566,966

Lambda	K	H
1.33	0.621	1.12
Gapped		
Lambda	K	H
1.28	0.460	0.850

Matrix: blastn matrix:1 ~2

Gap Penalties: Existence: 0, Extension: 0  
Number of Sequences: 77566966  
Number of Hits to DB: 3240899  
Number of extensions: 1347  
Number of successful extensions: 1347  
Number of sequences better than 10: 64  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 1343  
Number of HSP's successfully gapped: 1343  
Length of database: 43200890307  
A: 0  
X1: 13 (25.0 bits)  
X2: 32 (59.1 bits)  
X3: 54 (99.7 bits)  
S1: 13 (25.1 bits)  
BLASTN 2.9.0+  
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and  
Webb Miller (2000), "A greedy algorithm for aligning DNA  
sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: 8RBRB7KC015

Database: Database of GenBank+EMBL+DBJ sequences from EST Divisions  
77,566,966 sequences; 43,200,890,307 total letters  
Query= N1-C [organism=Homo sapiens] anxa1  
Length=1485

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BU508007.1	AGENCOURT_10128424 NIH MGC 71 Homo sapiens cDNA clo...	1929	0.0	98%
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1910	0.0	98%
AL544231.3	AL544231 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1905	0.0	98%
DC631365.1	DC631365 macaque bone marrow cDNA library Qbma Maca...	1879	0.0	94%
DC636772.1	DC636772 macaque bone marrow cDNA library Qbma Maca...	1853	0.0	94%
AL541874.3	AL541874 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1853	0.0	99%
BU902298.1	AGENCOURT_10127317 NIH MGC 71 Homo sapiens cDNA clo...	1847	0.0	96%
BX438944.2	BX438944 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1844	0.0	99%
AL553114.3	AL553114 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1842	0.0	99%
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1831	0.0	98%
ALIGNMENTS				
Query	2	AAACAGAGGCCCAATTACTAATCTCTGGTTGCTAGGTGTGGCTTCCTTTAAAAATCCTATAAAATCAGAGCCCAAGTCTCCACTGCCAGTGTGAAATCTTCAGAGAAGATTCTCTTTAGTTCTTTGCAAGAAGGTAGAGATAAAG	151	
BU508007.1	1	.....	40	
AL544231.3	19	.....T.....	61	
DC631365.1	1	.....-.....C.C.....	59	
DC636772.1	1	.....-.....C.C.....	59	
AL541874.3	1	.....	35	
BU902298.1	24	.....	73	
BX438944.2	1	.....	43	
AL553114.3	17	.....	166	
Query	152	ACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATTGAAAATGAAGAGCAGGAATATGTTCAAAGTGTGAAGTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCTATCCTACCTTCAATCCATCCT	301	
BU508007.1	41	.....	191	
		\   N		
AL544231.3	62	.....	211	
DC631365.1	60	.....A.....T.....A.....	209	
DC636772.1	60	.....A.....T.....A.....	209	
AL541874.3	36	.....	185	
BU902298.1	74	.....	224	
		\   N		
BX438944.2	44	.....	193	
AL553114.3	167	.....	316	
Query	302	CGGATGTCGCTCCTTCGATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATTCATTGACATTCTAACTAAGCGAAACAATGCACAGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCTGGATGAAACAC	451	
BU508007.1	192	.....	341	
AL570428.3	1088	.....-T.....-.....T.....-A...-.....W.....-.....GC.....	1011	
AL544231.3	212	.....	361	
DC631365.1	210	.....T.....C.....	359	
DC636772.1	210	.....C.....	359	
AL541874.3	186	.....	335	
BU902298.1	225	.....	374	
BX438944.2	194	.....	343	

AL553114.3	317	.....	466
AL576223.3	1050	.....-W.....-R.....-Y.....-.....-R.....	1002
Query	452	TGAAGAAAGCCCTTACAGGTCACCTTGAGGAGGTGTTTTAGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGATGAACCTCGTGCTGCCATGAAGGGCCTTGGAACTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTA	601
BU508007.1	342	.....	491
AL570428.3	1010	.....-Y.....	862
AL544231.3	362	.....	511
DC631365.1	360	.....TG.....G.....C.....G.....	509
DC636772.1	360	.....G.TG.....G.....C.....G.....	509
AL541874.3	336	.....	485
BU902298.1	375	.....	524
BX438944.2	344	.....	493
AL553114.3	467	.....	616
AL576223.3	1001	.....-.....-D.....-WR.....-.....A.....-V.....-.....W.....AAR.....	857
Query	602	ACAAAGAAATCAGAGACATTAAACAGGCTCTACAGAGAGGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATG	751
BU508007.1	492	.....	641
AL570428.3	861	.....W.....	712
AL544231.3	512	.....	661
DC631365.1	510	.....G.....	659
DC636772.1	510	.....	659
AL541874.3	486	.....	635
BU902298.1	525	.....	674
BX438944.2	494	.....	643
AL553114.3	617	.....	766
AL576223.3	856	.....	707
Query	752	AAGACTTGGCTGATTCAGATGCCAGGGCCTTGATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACCAAGCTATCCACAACCTTCGAGAGTGTTTCAGAAATACACCAAGTACAGTAAGC	901
BU508007.1	642	.....	791
AL570428.3	711	.....R.....N.....	562
AL544231.3	662	.....	811
DC631365.1	660	.....G.....T.....C.....T.....	809
DC636772.1	660	.....G.....T.....C.....T.....	809
AL541874.3	636	.....	785
BU902298.1	675	.....	824
BX438944.2	644	.....	793
AL553114.3	767	.....	916
AL576223.3	706	.....	557
Query	902	ATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCGCTCACAGCTATCGTGAAGTGCGCCAAGCAACACAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTGCCATAAGGCAT	1051
BU508007.1	792	.....	940
AL570428.3	561	.....A.....	412
AL544231.3	812	.....	960
DC631365.1	810	.....T.....A.....G.....C.....	959
DC636772.1	810	.....T.....A.....G.....C.....	959
AL541874.3	786	.....	935
BU902298.1	825	.....	974
BX438944.2	794	.....A.....TG.....C.....	943
AL553114.3	917	.....W.....-.....-.....-.....-.....-.....M.....	1035
AL576223.3	556	.....	407
Query	1052	TGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTCATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAA	1201
BU508007.1	941	.....G.....G.....C.....T.....G.....C.....GA.....T.....TA.....	1093
AL570428.3	411	.....G.....A.....T.....C.....G.....	262
AL544231.3	961	.....G.W.....WY.....WY.....R.....Y.....K.....K.....R.....	1102
DC631365.1	960	.....A.....	1096
DC636772.1	960	.....G.....A.....GG.....	1099
AL541874.3	936	.....G.....T.....W.....K.....M.....	1029
BU902298.1	975	.....GA.....G.....T.....A.....C.....T.....A.....A.....G.....A.....C.....G.....C.....C.....T.....G.....A.....C.....G.....A.....	1132
BX438944.2	944	.....D.....R.....Y.....W.....KD.....Y.....Y.....	1030
AL576223.3	406	.....A.....	257

Query 1202 ACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATATTTTCATCCTATAAGCTAAATAGGAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTAT 1351  
BU508007.1 1094 .....C.....C..... 1123  
          \          \          \  
          A          T          AG  
AL570428.3 261 ..... 112  
DC631365.1 1097 .....A.....CA..G.....C.....C.....C.....C.....T.....C.....A..... 1216  
                                  \  
                                  A  
DC636772.1 1100 .....GA.....C.....G.....C.....G.....A.....T.....GG.....A.....A..... 1229  
                                  \  
                                  G  
BU902298.1 1133 .AA..... 1152  
          \          \          \  
          T          A          T  
AL576223.3 256 ..... 107  
Query 1352 ATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCAAACCATAAACCCTATACAAGTTGTCTAGTAAACAATACATGAGAAAGATGTCTATGT 1462  
AL570428.3 111 .....T..... 1  
DC636772.1 1230 .. 1231  
AL576223.3 106 .....B..... 1

Query= N2-26 [organism=Homo sapiens] anxal  
Length=988

Sequences producing significant alignments:				Score (Bits)	E Value	Max ident
CA447733.1	UI-H-EI0-ayf-a-16-0-UI.s1	NCI_CGAP_EI0	Homo sapiens...	1349	0.0	99%
CA423056.1	UI-H-FL0-bdk-f-10-0-UI.s1	NCI_CGAP_FL0	Homo sapiens...	1343	0.0	99%
BQ776006.1	UI-H-FH0-bck-h-18-0-UI.s1	NCI_CGAP_FH0	Homo sapiens...	1334	0.0	99%
BU857810.1	AGENCOURT_10474308	NIH_MGC_107	Homo sapiens cDNA cl...	1330	0.0	99%
CN386790.1	17000599887650	GRN_PRENEU	Homo sapiens cDNA 5', mRN...	1323	0.0	99%
BQ228162.1	AGENCOURT_7258587	NIH_MGC_71	Homo sapiens cDNA clon...	1321	0.0	99%
BM981135.1	UI-CF-EN1-adg-a-11-0-UI.s1	UI-CF-EN1	Homo sapiens c...	1317	0.0	99%
CB306442.1	UI-CF-EN1-aej-e-15-0-UI.s1	UI-CF-EN1	Homo sapiens c...	1306	0.0	99%
CA418062.1	UI-H-FH0-bcc-j-24-0-UI.s1	NCI_CGAP_FH0	Homo sapiens...	1306	0.0	99%
CA418210.1	UI-H-FH0-bcf-i-22-0-UI.s1	NCI_CGAP_FH0	Homo sapiens...	1303	0.0	99%

ALIGNMENTS

Query 249 GGTGTGAATGAAGACTTTGGCTGATTCAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCATACCATCCTTACCACGAGAGCTATCCACAACTTCGCAGAGTGTTCAGAAATACACCAAG 398  
CA447733.1 765 ..... 616  
CA423056.1 767 ..... 618  
BQ776006.1 765 .....N..... 616  
                                  \  
                                  T  
BU857810.1 67 ..... 216  
CN386790.1 34 ..... 183  
BQ228162.1 220 ..... 369  
BM981135.1 760 .....N..... 616  
CB306442.1 744 .....N..... 616  
CA418062.1 744 .....N..... 616  
CA418210.1 740 ..... 613  
Query 399 TACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAACCAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTCGC 548  
CA447733.1 615 ..... 466  
CA423056.1 617 ..... 468  
BQ776006.1 615 ..... 466  
BU857810.1 217 ..... 366  
CN386790.1 184 ..... 333  
BQ228162.1 370 ..... 519  
BM981135.1 615 ..... 466  
CB306442.1 615 ..... 466  
CA418062.1 615 ..... 466  
CA418210.1 612 ..... 463  
Query 549 CATAAGGCATTGATCAGGATTATGGTTCCCGTCTGAAATTGACATGAATGATATCAAGACATTCTATCAGAAGATGTATGGTATCTCTTTGCCAAGCCATCCTGGATGAAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTT 698  
CA447733.1 465 ..... 315  
                                  \  
                                  C  
CA423056.1 467 ..... 317  
                                  \  
                                  C



BQ776006.1	465	.....	.....	315
			\	
			C	
BU857810.1	367	.....	.....	517
			\	
			C	
CN386790.1	334	.....	.....	484
			\	
			C	
BQ228162.1	520	.....	.....	670
			\	
			C	
BM981135.1	465	.....	.....	315
			\	
			C	
CB306442.1	465	.....	.....	315
			\	
			C	
CA418062.1	465	.....	.....	315
			\	
			C	
CA418210.1	462	.....	.....	312
			\	
			C	
Query	699	GTGGAGGAAACTAAACATTTCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATC	848	
CA447733.1	314	.....	.....	164
			\	
			C	
CA423056.1	316	.....	.....	166
			\	
			C	
BQ776006.1	314	.....	.....	164
			\	
			C	
BU857810.1	518	.....	.....N.....N...	668
			\	
			C	
CN386790.1	485	.....	.....	635
			\	
			C	
BQ228162.1	671	.....	.....	822
			\	
			C	
BM981135.1	314	.....	.....	164
			\	
			C	
CB306442.1	314	.....	.....	164
			\	
			C	
CA418062.1	314	.....	.....	164
			\	
			C	
CA418210.1	311	.....	.....	161
			\	
			C	
Query	849	ATTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTAAAAATGTTTCCCAACCATAAAACCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGCTCTATGTAGCTGAAAAATAAATGACGTCAC	988	
CA447733.1	163	.....	.....	22
			\	
			C	
			\	
			C	
CA423056.1	165	.....	.....G.....	24
			\	
			\	

Query= N3-26 [organism=Homo sapiens] anxa1  
Length=1311

## ALIGNMENTS

Query	306	CAACAGATCAAAACGAGCATATCTCTCAGAAACAGGAAAGCCCTGGATGAAACACTGAAGAAGCCCTTACAGGTCACCTTGAGGAGGTGTTGTTTACGCTCTGCTAAAAACTCAGCGCAATTGATGCTGATGAACCTCGTGCTGCCATGA	455
AL576223.3	1050	.....-W.....-R.....-Y.....-.....CT.R.....-.....-D.....WR.....-A.....-V.....	911
AL574991.3	986	.....	911
AL576603.2	917	.....	914
AL576340.3	1011	.....G.....-Y.....-.....-K.....	917
Query	456	AGGGCCTTGGAACTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGATCGGAGGCTAGTGCCATCTGA	605
AL576223.3	910	.....W.AAR.....	781
CN386790.1	28	.....	29
AL574991.3	910	.....	781
AL576603.2	913	.....-WM.....	788
AL576340.3	916	.....-RW.....	792
BE620646.1	748	.....	743
BU857810.1	61	.....	62
Query	606	GTTTGGTGTGAATGAAGACTTGGCTGATTTCAGATGCCAGGGCCTTGTTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGCTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTTCGCAAGTGTTCAGAAATACAC	755
BE614257.1	739	.....	591
AL576223.3	719	.....	571
CN386790.1	30	C.....	179
CA447733.1	765	.....	620
CA423056.1	767	.....	622
AL574991.3	719	.....	571
AL576603.2	726	.....	578
AL576340.3	730	.....	582
BE620646.1	742	.....	591



BQ228162.1	201	.....	350
CA447733.1	765	.....	635
BE614257.1	755	.....	606
CA423056.1	767	.....	637
AL576603.2	742	.....	593
AL576340.3	746	.....	597
AL576223.3	735	.....	586
BQ776006.1	765	.....	635
<div> <div></div> <div> <div></div> <div>T</div> </div> </div>			
Query	511	GTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAACCGCTTCTTTGCAGAGAAGCTTCATCAAGCCAT	660
BU857810.1	198	.....	347
CN386790.1	165	.....	314
BQ228162.1	351	.....	500
CA447733.1	634	.....	485
BE614257.1	605	.....	456
CA423056.1	636	.....	487
AL576603.2	592	.....	443
AL576340.3	596	.....	447
AL576223.3	585	.....	436
BQ776006.1	634	..N.....	485
Query	661	GAAAGGTGTTGGAACCTGCCATAAGGCATTGATCAGGATTATGGTTCCCGTCTGAAATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCTGGATGAAACCAAAGGAGATTATGA	810
BU857810.1	348	.....	497
CN386790.1	315	.....	464
BQ228162.1	501	.....	650
CA447733.1	484	.....	335
BE614257.1	455	.....	306
CA423056.1	486	.....	337
AL576603.2	442	.....	293
AL576340.3	446	.....R.....R.....	297
AL576223.3	435	.....	286
BQ776006.1	484	.....	335
Query	811	GAAATCTCGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCT	960
BU857810.1	498	.....N.....	647
CN386790.1	465	.....	614
BQ228162.1	651	.....	801
<div> <div></div> <div> <div></div> <div>A</div> </div> </div>			
CA447733.1	334	.....	185
BE614257.1	305	.....	156
CA423056.1	336	.....	187
AL576603.2	292	.....	143
AL576340.3	296	.....	147
AL576223.3	285	.....	136
BQ776006.1	334	.....	185
Query	961	GAAAAATATAGCCTTTAAATCATTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTAAAAATGTTTCCCAACCATAAACCCATATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCATGTAGCTGAAAT	1110
BU857810.1	648	.....N.....	797
CN386790.1	615	.....G.....	764
BQ228162.1	802	.....G.....	954
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CA447733.1	184	.....	35
BE614257.1	155	.....T.A.....	6
<div> <div></div> <div> <div></div> <div>T</div> </div> </div>			
CA423056.1	186	.....	37
AL576603.2	142	.....A.....	1
<div> <div></div> <div> <div></div> <div>C</div> </div> </div>			
AL576340.3	146	.....	5
<div> <div></div> <div> <div></div> <div>N</div> </div> </div>			
AL576223.3	135	.....B.....	1
BQ776006.1	184	.....	35
Query	1111	AAAATGACG 1119	
BU857810.1	798	..... 806	
CN386790.1	765	.. 766	
BQ228162.1	955	..... 963	
CA447733.1	34	..... 26	
CA423056.1	36	..... 28	
BQ776006.1	34	..... 26	

Query= N5-24 [organism=Homo sapiens] anxl

Length=1006

Sequences producing significant alignments:			Score (Bits)	E Value	Max ident
CB306442.1	UI-CF-EN1-aej-e-15-0-UI.s1	UI-CF-EN1 Homo sapiens c...	1279	0.0	100%
CA447733.1	UI-H-EI0-ayf-a-16-0-UI.s1	NCI_CGAP_EI0 Homo sapiens...	1279	0.0	100%
CA447223.1	UI-H-EI0-ayd-b-19-0-UI.s1	NCI_CGAP_EI0 Homo sapiens...	1279	0.0	100%
CA422748.1	UI-H-FL0-bdr-g-09-0-UI.s1	NCI_CGAP_FL0 Homo sapiens...	1279	0.0	100%
CA419844.1	UI-H-FH0-bcm-d-16-0-UI.s1	NCI_CGAP_FH0 Homo sapiens...	1279	0.0	100%
CA417462.1	UI-H-FE0-bbw-c-13-0-UI.s1	NCI_CGAP_FE0 Homo sapiens...	1279	0.0	100%
CA415613.1	UI-H-EZ0-bay-p-10-0-UI.s1	NCI_CGAP_Ch1 Homo sapiens...	1279	0.0	100%
CA414702.1	UI-H-EZ0-bar-e-18-0-UI.s1	NCI_CGAP_Ch1 Homo sapiens...	1279	0.0	100%
BU676462.1	UI-CF-DU1-aai-b-16-0-UI.s1	UI-CF-DU1 Homo sapiens c...	1279	0.0	100%
BU633206.1	UI-H-FL1-bgt-f-12-0-UI.s1	NCI_CGAP_FL1 Homo sapiens...	1279	0.0	100%

ALIGNMENTS

Query	315	AAAGGAGAAAGGGGACAGACGCTAAACGTGTTCAATACCATCCTTACCACCAGAAGCTATCCACAACCTCGCAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTG	464
CB306442.1	710	.....	561
CA447733.1	710	.....	561
CA447223.1	710	.....	561
CA422748.1	712	.....	563
CA419844.1	710	.....	561
CA417462.1	707	.....	558
CA415613.1	712	.....	563
CA414702.1	712	.....	563
BU676462.1	707	.....	558
BU633206.1	710	.....	561
Query	465	AGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAACAGCTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATA	614
CB306442.1	560	.....	411
CA447733.1	560	.....	411
CA447223.1	560	.....	411
CA422748.1	562	.....	413
CA419844.1	560	.....	411
CA417462.1	557	.....	408
CA415613.1	562	.....	413
CA414702.1	562	.....	413
BU676462.1	557	.....	408
BU633206.1	560	.....	411
Query	615	TCAAAGCATTTCTATCAGAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAACCAAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTGTATGGTCTCAGCTATGATCAGAAGACTTT	764
CB306442.1	410	.....	261
CA447733.1	410	.....	261
CA447223.1	410	.....	261
CA422748.1	412	.....	263
CA419844.1	410	.....	261
CA417462.1	407	.....	258
CA415613.1	412	.....	263
CA414702.1	412	.....	263
BU676462.1	407	.....	258
BU633206.1	410	.....	261
Query	765	AATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGT	914
CB306442.1	260	.....	111
CA447733.1	260	.....	111
CA447223.1	260	.....	111
CA422748.1	262	.....	113
CA419844.1	260	.....	111
CA417462.1	257	.....	108
CA415613.1	262	.....	113
CA414702.1	262	.....	113
BU676462.1	257	.....	108
BU633206.1	260	.....	111
Query	915	TTTCCCCAAACCATAAAACCTTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAAATGACGTCACAAG	1006
CB306442.1	110	.....	19
CA447733.1	110	.....	19
CA447223.1	110	.....	19
CA422748.1	112	.....	21
CA419844.1	110	.....	19
CA417462.1	107	.....	16
CA415613.1	112	.....	21
CA414702.1	112	.....	21
BU676462.1	107	.....	16
BU633206.1	110	.....	19

Query= N6-25 [organism=Homo sapiens] anxl

Length=1042

Sequences producing significant alignments:				Score (Bits)	E Value	Max ident
AL576223.3	AL576223	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1363	0.0	100%	
AL574991.3	AL574991	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1360	0.0	99%	
AL576603.2	AL576603	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1360	0.0	100%	
BE614257.1	601504294T1	NIH_MGC_71 Homo sapiens cDNA clone IMAG...	1360	0.0	100%	
AL576340.3	AL576340	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1354	0.0	99%	
BU857810.1	AGENCOURT_10474308	NIH_MGC_107 Homo sapiens cDNA cl...	1352	0.0	99%	
BQ228162.1	AGENCOURT_7258587	NIH_MGC_71 Homo sapiens cDNA clon...	1352	0.0	99%	
AL570884.3	AL570884	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1339	0.0	99%	
BU596129.1	AGENCOURT_8906716	NIH_MGC_142 Homo sapiens cDNA clon...	1339	0.0	99%	
BQ954100.1	AGENCOURT_8869366	NIH_MGC_71 Homo sapiens cDNA clon...	1339	0.0	99%	

ALIGNMENTS

Query	298	AACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTGATGCCAGGGCCTTGATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACC	447
AL576223.3	761	.....	612
AL574991.3	761	.....	612
AL576603.2	768	.....	619
BE614257.1	780	.....	632
AL576340.3	772	.....	623
BU857810.1	22	.....	171
BQ228162.1	175	.....	324
AL570884.3	768	.....	619
BU596129.1	6	.....	155
BQ954100.1	24	.....	173
Query	448	AGAAGCTATCCACAACCTTCGCAGAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAACCAGCTTTC	597
AL576223.3	611	.....	462
AL574991.3	611	.....	462
AL576603.2	618	.....	469
BE614257.1	631	.....	482
AL576340.3	622	.....	473
BU857810.1	172	.....	321
BQ228162.1	325	.....	474
AL570884.3	618	.....	469
BU596129.1	156	.....	305
BQ954100.1	174	.....	323
Query	598	TTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTGCCATAAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCTTTTGCCAAGCCATCC	747
AL576223.3	461	.....	311
AL574991.3	461	.....W...	311
AL576603.2	468	.....	318
BE614257.1	481	.....	331
AL576340.3	472	.....	322
BU857810.1	322	.....	472
BQ228162.1	475	.....	625
AL570884.3	468	.....	318
BU596129.1	306	.....	456

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BQ954100.1 324 ..... 474
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                                     C

Query      748 TGGATGAAACCAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTCTTCAACAGG 897
AL576223.3 310 ..... 161
AL574991.3 310 ..... 161
AL576603.2 317 ..... 168
BE614257.1 330 ..... 181
AL576340.3 321 ..... 172
BU857810.1 473 ..... 622
BQ228162.1 626 ..... 776
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                                     A

AL570884.3 317 ..... 168
BU596129.1 457 ..... 606
BQ954100.1 475 ..... 624

Query      898 ATTACAGTGTAGCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATATAAAGCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCAACCAATAAACCCATATACAAGTTGTTCTAGTAACAATAC 1042
AL576223.3 160 ..... 15
                                     \
                                     A

AL574991.3 160 ..... 15
                                     \
                                     A

AL576603.2 167 ..... 26
                                     \
                                     A

BE614257.1 180 ..... 35
                                     \
                                     A

AL576340.3 171 ..... 25
                                     \
                                     A

BU857810.1 623 ..... 768
                                     \
                                     A
                                     \
                                     N
                                     \
                                     N

BQ228162.1 777 ..... 923
                                     \
                                     A
                                     \
                                     G

AL570884.3 167 ..... 21
                                     \
                                     A
                                     \
                                     G
                                     \
                                     N
                                     \
                                     N
                                     \
                                     W

BU596129.1 607 ..... 753
                                     \
                                     A
                                     \
                                     AC
                                     \
                                     C
                                     \
                                     G

BQ954100.1 625 ..... 771
                                     \
                                     A
                                     \
                                     G

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Query= N7-12 [organism=Homo sapiens] anxl

Length=1094

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
AL553114.3 AL553114 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1441	0.0	100%
CX870542.1 HESC4_46 F03.g1 A037 NIH MGC 262 Homo sapiens cDNA ...	1441	0.0	100%
BQ953713.1 AGENCOURT_8786826 NIH_MGC_43 Homo sapiens cDNA clon...	1432	0.0	100%
BM458053.1 AGENCOURT_6411336 NIH_MGC_71 Homo sapiens cDNA clon...	1430	0.0	100%
AL544959.3 AL544959 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1426	0.0	100%
AU117349.1 AU117349 HEMBA1 Homo sapiens cDNA clone HEMBA100120...	1426	0.0	100%
AL553679.3 AL553679 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1419	0.0	100%
BQ962441.1 AGENCOURT_10056322 NIH_MGC_71 Homo sapiens cDNA clo...	1419	0.0	100%
BU902298.1 AGENCOURT_10127317 NIH_MGC_71 Homo sapiens cDNA clo...	1417	0.0	100%
EB387180.1 nbj26d10.y1 Human optic nerve, Unnormalized (nbj) H...	1415	0.0	100%

ALIGNMENTS

Query	1	AGTGTGAATCTTCAGAGAAGATTCTCTTTAGTCTTTGCAAGAAGGTAGAGATAAAGACACTTTTCAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTATTGAAAATGAAGACAGGAATATGTTCAAACTGTGA	150
AL553114.3	107	.....	256
CX870542.1	29	.....	178
BQ953713.1	1	.....	145
BM458053.1	11	.....	160
AL544959.3	1	.....	142
AU117349.1	1	.....	150
AL553679.3	1	.....	142
BQ962441.1	1	.....	138
BU902298.1	24	.....	164

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I  
N

EB387180.1	1	.....	136
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Query	151	AGTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCTATCTACCTTCAATCCATCCTCGGATGTCGCTGCCTTGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCTTGACATTCTAACTAAGCGAAACAATGCAC	300
AL553114.3	257	.....	406
CX870542.1	179	.....	328
BQ953713.1	146	.....	295
BM458053.1	161	.....	310
AL544959.3	143	.....	292
AU117349.1	151	.....	300
AL553679.3	143	.....	292
BQ962441.1	139	.....	288
BU902298.1	165	.....	314
EB387180.1	137	.....	286

Query	301	AGCGTCAACGATCMAAGCAGCATATCTCCAGGAAACGGAAGCCCTGGATGAACACTGAAGAAAGCCCTTACAGGTCACCTTGAGGAGGTGTTTTAGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGATGAACCTTCGTGCTG	450
AL553114.3	407	.....	556
CX870542.1	329	.....	478
BQ953713.1	296	.....	445
BM458053.1	311	.....	460
AL544959.3	293	.....	442
AU117349.1	301	.....C.....	450
AL553679.3	293	.....-.....	441
BQ962441.1	289	.....	438
BU902298.1	315	.....	464
EB387180.1	287	.....	436

Query	451	CCATGAAGGGCCTTGGAACTGATGAAGATACTTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAAACGGGTCTACAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATT	600
AL553114.3	557	.....	706
CX870542.1	479	.....	628
BQ953713.1	446	.....	595
BM458053.1	461	.....	610
AL544959.3	443	.....	592
AU117349.1	451	.....	600
AL553679.3	442	.....	591
BQ962441.1	439	.....	588
BU902298.1	465	.....	614
EB387180.1	437	.....	586

Query	601	TTCGGAACGCTTTTGCTTTCTTCTTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTTGGCTGATTTCAGATGCCAGGGCCTTGTTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTA	750
AL553114.3	707	.....	856
CX870542.1	629	.....	778
BQ953713.1	596	.....	745
BM458053.1	611	.....T.....	760
AL544959.3	593	.....	742
AU117349.1	601	.....N.....	750
AL553679.3	592	.....	741
BQ962441.1	589	.....	738
BU902298.1	615	.....	764
EB387180.1	587	.....	736

Query	751	CCACCAGAAGCTATCCACNACTTCGCAGAG	780
AL553114.3	857	.....	886
CX870542.1	779	.....	808
BQ953713.1	746	.....	775
BM458053.1	761	.....	791

\  
I  
C

AL544959.3	743	.....	772
AU117349.1	751	.....	777
AL553679.3	742	.....	771
BQ962441.1	739	.....	768
BU902298.1	765	.....	794
EB387180.1	737	.....	766

Query= N8-23 [organism=Homo sapiens] anx1

Length=1377



Score (Bits)	E Value	Max ident
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1820	0.0	96%
1803	0.0	97%
1796	0.0	96%
1768	0.0	93%
1744	0.0	92%
1742	0.0	97%
1736	0.0	95%
1735	0.0	97%
1722	0.0	96%
1720	0.0	96%

Query 1 AGTGTGAAATCTTCAGAGAAGAAATTCCTTTTAGTTCCTTGCAAGAGGCTAGAGATAAAGACACTTTTTCAAATAATGGCAATGGTATCAGAAATTCCTCAAGCAGGCCCTGGTTTATTGAAAATGAAGAGCAGGAATATGTTCAAACCTGTGA 150  
BU508007.1 1 ..... 131

AL544231.3 19 N 151  
DC631365.1 1 .....C.C. 149  
DC636772.1 1 .....C.C. 149  
AL541874.3 1 .....C.C. 125  
BU902298.1 24 ..... 164

BX438944.2 1 N 133

Query 151 AGTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCCATCTCTACCTTCAATCCATCTCGGATGTCGCTGCCTTGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTCTAAGCGAAACAATGCAC 300  
BU508007.1 132 ..... 281  
AL570428.3 1098 .....-T. ....- 1068  
AL544231.3 152 ..... 301  
DC631365.1 150 .A. .T. .A. .T. .C. 299  
DC636772.1 150 .A. .T. .A. .C. 299  
AL541874.3 126 ..... 275  
BU902298.1 165 ..... 314  
BX438944.2 134 ..... 283

Query 301 AGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCTGGATGAAACACTGAAGAAAGCCCTTACAGGTCACCTTGAGGAGGTTGTTTtagctctgctAAAAACTCCAGCGCAATTTGATGCTGATGAACTCGTGCTGC 450  
BU508007.1 282 ..... 432

AL570428.3 1067 ...T...-A.-...W.....GC...-Y..... 921

AL544231.3 302 ..... 452

DC631365.1 300 .....TG.....G..... 450

DC636772.1 300 .....G.TG.....G..... 450

AL541874.3 276 ..... 426

BU902298.1 315 ..... 465

BX438944.2 284 ..... 434

AL576223.3 1050 .....-W.....-R...-Y...-...CT.R.....-D...WR.....-A...-V..... 916  
AL570884.3 1059 .....T...T.....C.....W.....RS...W.....Y.M.....R...T...K.....YY..S.W.....C.....K...S. 923

M Y

Query	451	CATGAAGGCCTTGGAAGTGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAANTCAGAGACATTAAACAGGGTCTACAGAGAGGAAGTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTT	600
BU508007.1	433	.....	582
AL570428.3	920	.....M.....W.....	771
AL544231.3	453	.....	602
DC631365.1	451	.....C..G.....G.....	600
DC636772.1	451	.....C..G.....	600
AL541874.3	427	.....	576
BU902298.1	466	.....	615
BX438944.2	435	.....	584
AL576223.3	915	.....W..AAR.....	766
AL570884.3	922	.....	773
Query	601	TCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTTGTGATTCAGATCAGGCTTGAAGCAGAGAAAGAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACGAGGCTATCCA	750
BU508007.1	583	.....	748
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AL570428.3	770	.....R.....	605
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  GC G C   TTG   A </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \ \ \  G     A   AA </div> <div style="text-align: center;"> \  N </div> </div>	
AL544231.3	603	.....	768
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  G  G   C C </div> <div style="text-align: center;"> \ \ \  T     TG   A </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \  GAAAG </div> </div>	
DC631365.1	601	.....G.....T.....C.....	766
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  G  G   C C </div> <div style="text-align: center;"> \ \ \  T     TG   A </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \  GAAAG </div> </div>	
DC636772.1	601	.....G.....T.....C.....	766
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  G  G   C C </div> <div style="text-align: center;"> \ \ \  T     TG   A </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \  GAAAG </div> </div>	
AL541874.3	577	.....	742
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  G  G   C C </div> <div style="text-align: center;"> \ \ \  T     TG   A </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \  GAAAG </div> </div>	
BU902298.1	616	.....	781
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  G  G   C C </div> <div style="text-align: center;"> \ \ \  T     TG   A </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \  GAAAG </div> </div>	
BX438944.2	585	.....	750
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  G  G   C C </div> <div style="text-align: center;"> \ \ \  T     TG   A </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \  GAAAG </div> </div>	
AL576223.3	765	.....	600
		<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> \  GC </div> <div style="text-align: center;"> \ \ \  GC G C     </div> <div style="text-align: center;"> \  G </div> <div style="text-align: center;"> \ \ \  G       </div> </div>	

			TTG		A		
			A		AA		
					G		
AL570884.3	772	.....					607
			\	\ \ \ \	\	\ \ \ \	
			GC	GC G C	G	G	
			TTG		A		
			A		AA		
					G		
Query	751	CAACTTCGCAGAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAACAGCTTTCTTTGCAGAGAAG					900
BU508007.1	749	.....					898
AL570428.3	604	.....A.....					455
AL544231.3	769	.....					917
DC631365.1	767	..T.....					916
DC636772.1	767	..T.....					916
AL541874.3	743	.....					892
BU902298.1	782	.....A.....TG.....C.....					931
BX438944.2	751	.....					900
AL576223.3	599	.....					450
AL570884.3	606	.....					457
Query	901	CTTCATCAAGCCATGAAAGGTGTGGAACCTGCCATAAGGCATTGATCAGGATTATGGTTCCCGTTCTGAAATTGACATGAATGATATCAAGCATTCATCNGAAGTGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACC					1050
BU508007.1	899	.....-.....C.....-.....G.....G.....C..T..G.....					1049
			\		\	\	
			G		T	C	
AL570428.3	454	.....A.....					305
AL544231.3	918	.....G.W.....MWY.....MWY.....					1063
DC631365.1	917	.....G.....C.....A.....-.....-.....-.....-.....					1061
			\				
			G				
DC636772.1	917	.....G.....C.....-.....A.....-.....-.....-.....-.....GG-					1061
			\		\	\	
			T		G	T	
AL541874.3	893	.....					1029
BU902298.1	932	.....C.....GA.....G.....T.....A.....C.....T.....A.....A.G.....A.....C.....G.....C.....C.....T.....					1085
					\	\	
					G	A	
BX438944.2	901	.....K...R.....S.....D.....Y.....W...KD-.Y.....Y...					1030
			\				
			A				
AL576223.3	449	.....					300
AL570884.3	456	.....					307
Query	1051	AAAGGAGATTATGAGAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTA					1200
BU508007.1	1050	C...GA...T..TA.....C.....					1123
			\	\	\	\	
			G	A	T	AG	
AL570428.3	304	.....					155
AL544231.3	1064	....R.....Y.K.....K...R....					1102
DC631365.1	1062	..-.....-.....-.....A.....-.....CA...G...-...C...-...C...-...-...C...-..					1185
			\				
			A				
DC636772.1	1062	..-.....-.....-.....GA.....C.....-.....G.....-.....C.....-.....G.....-..					1188
			\	\			
			C	G			
BU902298.1	1086	..G...A.....A.....C...G.....A...AA.....					1152
			\	\	\	\	
			G	G	G	T A T	
				C			
AL576223.3	299	.....					150
AL570884.3	306	.....					157
Query	1201	GCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCAAAACCATAAAACCCATATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCT					1350
AL570428.3	154	.....T.....					5
DC631365.1	1186	.....T.....C.....-.....A.....					1216

DC636772.1 1189 .A.-...T-...T..GG.-...A...A..... 1231

AL576223.3 149 .....B..... 1

AL570884.3 156 .....RW..V.....N...N...W...A. 5

Query 1351 ATGT 1354

AL570428.3 4 .... 1

AL570884.3 4 .... 1

Query= N9-8 [organism=Homo sapiens] anxa1

Length=1237

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BQ228162.1	AGENCOURT_7258587 NIH MGC_71 Homo sapiens cDNA clon...	1541	0.0	99%
AL576603.2	AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1517	0.0	100%
AL576340.3	AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1515	0.0	100%
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1513	0.0	100%
AL574991.3	AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1509	0.0	100%
BM555842.1	AGENCOURT_6544353 NIH MGC_88 Homo sapiens cDNA clon...	1504	0.0	99%
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1496	0.0	99%
AL570884.3	AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1489	0.0	99%
BE614257.1	601504294T1 NIH_MGC_71 Homo sapiens cDNA clone IMAG...	1487	0.0	98%
AL575425.3	AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1480	0.0	99%

# ALIGNMENTS

Query	376	ACAGGTCACCTTGAGGAGGAAGTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAAACGCTTTGCTTCTCTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTCAGAT	525
BQ228162.1	115	.....	249
AL576603.2	828	.....	694
AL576340.3	832	.....	698
AL576223.3	821	.....	687
AL574991.3	821	.....	687
BM555842.1	74	.....	208
AL570428.3	826	.....	692
AL570884.3	828	.....R.....	694
BE614257.1	854	.....-A..-...A.T.....A.....C.....-.....	707
AL575425.3	839	.....R.....A.....G.....R.....B.....S.....	705
Query	526	GCCAGGCGCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACCAAGAGCTATCCAACTTCGACAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTG	675
BQ228162.1	250	.....	399
AL576603.2	693	.....	544
AL576340.3	697	.....	548
AL576223.3	686	.....	537
AL574991.3	686	.....	537
BM555842.1	209	.....	358
AL570428.3	691	.....N.....A.....	542
AL570884.3	693	.....	544
BE614257.1	706	.....T.....N.....	557
AL575425.3	704	.....T.....N.....	555
Query	676	GACCTGAGATTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGGCCACAAGCAAACGAGCTTTCTTTGCGAGAAGCTTCATCAAGCCATGAAAGGTGTGGAACTGCCATAAGGCATTGATCAGGATTATGGTTCC	825
BQ228162.1	400	.....	549
AL576603.2	543	.....	394
AL576340.3	547	.....	398
AL576223.3	536	.....	387
AL574991.3	536	.....	387
BM555842.1	359	.....	508
AL570428.3	541	.....	392
AL570884.3	543	.....	394
BE614257.1	556	.....	407
AL575425.3	554	.....N.....	405
Query	826	CGTTCTGAAATTGACATGAATGATATCAAAGCATTCATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAGAGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGGAGAACTAAACATTCCTTTGATGG	975
BQ228162.1	550	.....	699
AL576603.2	393	.....R.....R.....	244
AL576340.3	397	.....	248
AL576223.3	386	.....	237

AL574991.3	386	.....W.....	237
BM555842.1	509	.....	658
AL570428.3	391	.....A.....T.....	242
AL570884.3	393	.....	244
BE614257.1	406	.....	257
AL575425.3	404	.....	255

Query	976	TCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTATATTATAACTCTGTATAATAG	1125
BQ228162.1	700	.....	850

		..... A.....	
AL576603.2	243	.....	94
AL576340.3	247	.....	98
AL576223.3	236	.....	87
AL574991.3	236	.....Y.....	87
BM555842.1	659	.....	808
AL570428.3	241	.....T.....	92
AL570884.3	243	.....	94
BE614257.1	256	.....	107
AL575425.3	254	.....N.....	105

Query	1126	AGATAAGTCCATTTTTAAAAATGTTTTCCCAACCATAAAACCCCTATACAAGTTGTCTAGTAACAATACATGAGAAAGATGCTATGTAGCTGAAAAATAAATGACGTC	1237
BQ228162.1	851	.....G.....	965

		..... G.....A..... G.....G.....A.....	
AL576603.2	93	.....	1
		..... C.....	
AL576340.3	97	.....	5
		..... N.....	
AL576223.3	86	.....B.....	1
AL574991.3	86	.....	1
BM555842.1	809	.....G.....	922
		..... A.....C.....C.....N.....C.....N.....A.....C.....G.....	
AL570428.3	91	.....	1
AL570884.3	93	.....RW.....V.....N.....N.....W.....A.....	1
		..... N.....N.....	
BE614257.1	106	.....T.A=.....	6
		..... T.....	
AL575425.3	104	.....N.....G.....	17

Query= N10-2 [organism=Homo sapiens] anxal

Length=927

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BQ228162.1	AGENCOURT_7258587 NIH_MGC_71 Homo sapiens cDNA clon...	1594	0.0	99%
AL576603.2	AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1576	0.0	100%
AL576340.3	AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1574	0.0	100%
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1572	0.0	100%
AL574991.3	AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1568	0.0	100%
BM555842.1	AGENCOURT_6544353 NIH_MGC_88 Homo sapiens cDNA clon...	1568	0.0	99%
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1552	0.0	99%
AL570884.3	AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1548	0.0	99%
AL575425.3	AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1535	0.0	99%
BE614257.1	601504294T1 NIH_MGC_71 Homo sapiens cDNA clone IMAG...	1528	0.0	99%

ALIGNMENTS

Query	43	AAGAAATCAGAGACATTAAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGCTTTCTTGTCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAG	192
BQ228162.1	83	.....	232
AL576603.2	860	.....	711
AL576340.3	864	.....	715
AL576223.3	853	.....	704
AL574991.3	853	.....	704
BM555842.1	42	.....	191
AL570428.3	858	.....W.....	709
AL570884.3	860	.....	711

	AL575425.3	871	.R.	R.	A	C	R.	B	722
	BE614257.1	871	-	A.T	A	-	-	-	724
				 A			 G		
Query	193	ACTTGGCTGATTACAGATGCCAGGCCTTTGTATGAAGCAGGAGAAAGGGGACAGACGTAACGTGTCAATACCATCCTTACCACCAGAAGCTATCCACAAC TTCGAGAGTGTTTCAGAAAATACCCAAGTACAGTAAGCATG							342
BQ228162.1	233	.....							382
AL576603.2	710	.....							561
AL576340.3	714	.....							565
AL576223.3	703	.....							554
AL574991.3	703	.....							554
BM555842.1	192	.....							341
AL570428.3	708	.....N.....							559
AL570884.3	710	.....A.....							561
AL575425.3	721	.....S.....T.....						N	572
BE614257.1	723	.....							574
Query	343	ACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGC GCACAAAGCAAC CAGCTTTCTTTG CAGAGAAGCTTCATCAAGCCATGAAAGGTTGTGGAAC TCGCCATAAGGCATTGA							492
BQ228162.1	383	.....							532
AL576603.2	560	.....							411
AL576340.3	564	.....							415
AL576223.3	553	.....							404
AL574991.3	553	.....							404
BM555842.1	342	.....							491
AL570428.3	558	.....							409
AL570884.3	560	.....							411
AL575425.3	571	.....N.....							422
BE614257.1	573	.....							424
Query	493	TCAGGATTATGTTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATCCTGGATGAAACCAAAGGAGATTATGAGAAAACTCCTGGTGGCTCTTTGTGGAGGAACT							642
BQ228162.1	533	.....							682
AL576603.2	410	.....							261
AL576340.3	414	.....R.....R.....							265
AL576223.3	403	.....W.....							254
AL574991.3	403	.....							254
BM555842.1	492	.....A.....T.....							641
AL570428.3	402	.....							259
AL570884.3	410	.....							261
AL575425.3	421	.....							272
BE614257.1	423	.....							274
Query	643	AAACATTCCTTGTATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATT							792
BQ228162.1	683	.....							833
				 A					
AL576603.2	260	.....							111
AL576340.3	264	.....							115
AL576223.3	253	.....Y.....							104
AL574991.3	253	.....							104
BM555842.1	642	.....							791
AL570428.3	258	.....							109
AL570884.3	260	.....							111
AL575425.3	271	.....N.....							122
BE614257.1	273	.....							124
Query	793	ATAACTCTGTATAATAGAGATAAGTCCATTTTAAAAATGTTTTCCCCAACCATAAACCCTATACAAGTGTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAAATGACGTC							922
BQ228162.1	834	.....G.....AT.....							965
				 G			 G		
AL576603.2	110	.....A.....							1
				 C					
AL576340.3	114	.....N.....							5
				 B					
AL576223.3	103	.....							1
AL574991.3	103	.....							1
BM555842.1	792	.....G.....							925
			 A	 C					

BE614257.1 123 .....T.A-.....  
|  
T

6

Query= N11-16 [organism=Homo sapiens] anxa1  
Length=1930

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BX417009.2	BX417009 Homo sapiens PLACENTA Homo sapiens cDNA cl...	1748	0.0	99%
AU134300.1	AU134300 OVARC1 Homo sapiens cDNA clone OVARC100168...	1443	0.0	99%
AU138502.1	AU138502 PLACE1 Homo sapiens cDNA clone PLACE100869...	1310	0.0	98%
CA421424.1	UI-H-EZ1-bbb-c-06-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens...	1286	0.0	100%
AI764962.1	wh57a06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone I...	1206	0.0	97%
BF107418.1	601824036F1 NIH_MGC_79 Homo sapiens cDNA clone IMAG...	1057	0.0	98%
DB013065.1	DB013065 TESOP2 Homo sapiens cDNA clone TESOP200154...	1040	0.0	100%
DB328492.1	DB328492 PLACE6 Homo sapiens cDNA clone PLACE600972...	950	0.0	100%
BG231632.1	naf37c05.x1 Soares_NPRMC Homo sapiens cDNA clone IM...	944	0.0	100%
BU674442.1	UI-CF-DU0-aab-j-09-0-UI.s1 UI-CF-DU0 Homo sapiens c...	937	0.0	100%

ALIGNMENTS

Query	1	AGTGTGAAATCTTCAGAGAAGAAATTTCTCTTAAAGTTCTTTGCAAAAGGTAGAGATAAAGACACTTTTTCAAAANTGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATTGAAAANTGAAGAGCAGGAATATGTTCAAACGTGAA	150
BX417009.2	1	.....	139
		G	
AU134300.1	1	.....	151
		G	
AU138502.1	1	.....C.....	151
		G	
BF107418.1	1	.....	134
		G	
Query	151	GTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCTATCCTACCTTCAATCCATCCTCGGATGTCGCTGCCCTGCATAAGGCCATAATGGTTAAAGGTGGATGAAGCAACCATCATTGACATTCTAACTAAGCGAAACAATGCACA	300
BX417009.2	140	.....	289
AU134300.1	152	.....	301
AU138502.1	152	.....	301
BF107418.1	135	.....	284
Query	301	GCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGTAAGTTAGAGTGGTAAATTTAGATATTTAATTTACGATAGTTATACTTAACCATGGATTCGGAAGCACAGTTACCTAGTTCTTTAAGGTTCTAACCACTGTTTTCT	450
BX417009.2	290	.....	439
AU134300.1	302	.....	451
AU138502.1	302	.....	451
BF107418.1	285	.....	434
Query	451	TCATTACATCTATGATTGGGATTGCAGTGTTTATCCACTTTGTTGCAATTTAATCAATTTTATCAAAATTTCTATTTTATACATTAGTCATCTTGGTGTATATTGTTTGCAGATGGTGTCTCTGGGGACAAATTTTAAATTTGAACGT	600
BX417009.2	440	.....	589
AU134300.1	452	.....N.....	601
AU138502.1	452	.....	601
BF107418.1	435	.....G.....	580
DB013065.1	1	.....	63
Query	601	AAACATCGAGATTGCTGCTCAATAAAGAATATGGCTGTGATTGAAATGTACTAATATTTAACTGAACGTGTTAATGCTAAATTTTATATATAATTTCTACTTTAAAAATAAGCCTTATGTCTTTTATACAAATATAGTAGTGTCTCT	750
BX417009.2	590	.....	739
AU134300.1	602	.....N.....	750
AU138502.1	602	.....A.....G.....N.....G.....N.....C	761
		G	
		C	
		A	
		A	
		C	
		A	
		NG	
		T	
BF107418.1	581	T..AT.....TG..G....C....	610
DB013065.1	64	.....	214
		T	
Query	751	AAAGCAATGAAATTAGAAAACATATATAATTTACAGTATCTGATTATACTGCTTGTATTGTTGAGAAGTACAAACCTCAAGATTGGAAACATGAATATATATTTTAAAGTAATTTTACTTCTGTTTTCTGTTAGCACACAGTCCTCTGTG	900
BX417009.2	740	.....	889
AU134300.1	751	.....N.....	798
AU138502.1	762	.....	770





Query	1	AGTGTGAAATCTTCAGAGAAGATTTCTCTTAGTTCTTTGCAAGAAGGTAGAGATAAAGGAAGGTGTGGGAAGGACTTGTGAAATACATATTCGAGGAAAACTATGCACAAGGCCGTGCATTTAAAAATAAACTCCCTAAGGCTGGG	150
BU508007.1	1	.....	40
AL544231.3	19	..T.....	61
AL541874.3	1	.....	35
DC631365.1	1	.....-.....C.C.....	59
Query	151	GTGAAACCTGCTACGGTCTCGCCAAGTTGACTGTTAATGAATTTGATTCTCAGGTACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCCTGGTTTATTGAAAATGAAGAGCAGGAATATGTTCAAACTGTGAAGTCA	300
BU508007.1	41	.....\.....N.....	136
AL544231.3	62	.....	156
AL541874.3	36	.....	130
DC631365.1	60	.....	154
AL553129.3	3	.....A.....	97
Query	301	TCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCTATCCTACCTTCAATCCATCCTCGGATGTCGCTGCCTTGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTTCTAACTAAGCGAAACAAATGCACAGCGT	450
AL570428.3	1088	.....-T.....	1063
BU508007.1	137	.....	286
AL544231.3	157	.....	306
AL541874.3	131	.....	280
DC631365.1	155	.....T.....A.....T.....C.....	304
AL553129.3	98	.....	248
Query	451	CAACAGATCAAGCAGCATATCTCCAGGAACAGGAAGCCCTGGATGAAACACTGAAGAAAGCCCTTACAGGTACCTTTGAGGAGSTGTGTTTAGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGATGAACCTTCGTCTGCCATG	600
AL570428.3	1062	...-A...-W.....GC.....Y.....	917
BU508007.1	287	.....	436
AL576223.3	1050	...-W...-R...-Y...-R...-D...-WR...-A...-V.....	912
AL544231.3	307	.....	456
AL570884.3	1059	.....T.....T.....C...Y...W.....RS...W...Y.M...R...T...K...YY...S.W...C.....K...S.....	919
AL574991.3	1017	.....\.....M.....	912
AL575425.3	1037	.....-R...-K...-RS...-CR...-K.....	930
AL541874.3	281	.....-M...M...KG...C...C.C...S...A	430
DC631365.1	305	.....TG.....G.....	454
AL553129.3	249	.....	398
Query	601	AAGGGCCTTGAACCTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAAACAAAGAAATCAGAGACATTAAACAGGGTCTACAGAGAGGAACCTGAAGAGAGATCTGGCCAAAGACATAAACCTCAGACACATCTGGAGATTTTCGG	750
AL570428.3	916	.....M.....W.....	767
BU508007.1	437	.....	586
AL576223.3	911	.....W...MR.....	762
AL544231.3	457	.....	606
AL570884.3	918	.....	769
AL574991.3	911	.....	762
AL575425.3	929	.....R.....R.....	780
AL541874.3	431	.....	580
DC631365.1	455	.....C...G.....G.....	604
AL553129.3	399	.....R.....	548
Query	751	AACGCTTTGCTTCTCTTCTGTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATTAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACCACC	900
AL570428.3	766	.....R.....N.....	617
BU508007.1	587	.....	736
AL576223.3	761	.....	612
AL544231.3	607	.....	756
AL570884.3	768	.....	619
AL574991.3	761	.....	612
AL575425.3	779	.....R.....B.....S.....T.....	630
AL541874.3	581	.....	730
DC631365.1	605	.....G.....T.....	754
AL553129.3	549	.....	698
Query	901	AGAAGCTATCCACAACCTTCGACAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCCTACAGCTATCGTGAAGTGCGCCACAAGCAAACAGCTTTC	1050
AL570428.3	616	.....A.....	467
BU508007.1	737	.....	886
AL576223.3	611	.....	462
AL544231.3	757	.....	905
AL570884.3	618	.....	469
AL574991.3	611	.....	462
AL575425.3	629	.....N.....N.....	480
AL541874.3	731	.....	880
DC631365.1	755	C.....T.....T.....	904
AL553129.3	699	.....WY.....	848
Query	1051	TTTGAGAGAGAGCTTCATCAAGCCATGAAAGGTGTTGGAACCTCGCCATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAGCATTCATCAGAAGATGTATGGTATCTCCCTTTGCCAAGCCATC	1200
AL570428.3	466	.....A.....T.....	317
BU508007.1	887	.....C.....G...G.....C..T...	1037

AL576223.3	461	.....G.....T.....C.....	312
AL544231.3	906	.....G.W.....MWY.....MWY.	1053
AL570884.3	468	.....	319
AL574991.3	461	.....W..	312
AL575425.3	479	.....	330
AL541874.3	881	.....W..K.....M..	1023
DC631365.1	905	.....A.....G.....C.....A.....	1053
AL553129.3	849	.....G.....R.....Y.....M.....	991
Query	1201	CTGGATGAAACCAAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAG	1350
AL570428.3	316	.....	167
BU508007.1	1038	..G.....C....GA...T...TA.....C...C....	1123
AL576223.3	311	.....G.....A.....T.....AG.....	162
AL544231.3	1054	.....R.....Y..K.....K...R....	1102
AL570884.3	318	.....	169
AL574991.3	311	.....Y.....	162
AL575425.3	329	.....	180
AL541874.3	1024	.....	1029
DC631365.1	1054	.....A.....CA...G...C...C...C.....	1176
AL553129.3	992	.....W.....A.....	1003
Query	1351	GATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTAAAAATGTTTTCCCAACCATATAAACCCTATACAAGTTGTTCTAGTAACAATACATG	1500
AL570428.3	166	.....T.....	17
AL576223.3	161	.....B.....	12
AL570884.3	168	.....RW...V.....N...N...W.....	17
AL574991.3	161	.....N.....	12
AL575425.3	179	.....N.....	30
DC631365.1	1177	.....C.....T.....C.....A.....	1216
Query	1501	AGAAAGATGTCTATGT	1516
AL570428.3	16	.....	1
AL576223.3	11	.....	1
AL570884.3	16	.....A.....	1
AL574991.3	11	.....	1
AL575425.3	29	.....G.....	17

Query= N13-17 [organism=Homo sapiens] anxa1

Length=1234

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
BQ228162.1 AGENCOURT_7258587 NIH_MGC_71 Homo sapiens cDNA clon...	1679	0.0	99%
AL574991.3 AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1648	0.0	100%
AL576603.2 AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1635	0.0	99%
AL576223.3 AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1633	0.0	99%
BM555842.1 AGENCOURT_6544353 NIH_MGC_88 Homo sapiens cDNA clon...	1633	0.0	99%
AL570428.3 AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1629	0.0	99%
AL576340.3 AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1628	0.0	99%
AL570884.3 AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1628	0.0	99%
AL575425.3 AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1615	0.0	99%
AL553095.3 AL553095 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1589	0.0	98%

# ALIGNMENTS

Query	308	AACTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAGACATTAACAGGGTCTACAGAGAGAACTGAAGAGAGATCTGGCCAAAGACATAACTCAGACACATCTGGAGATTTTCGGAACGCTTTTGCTT	457
BQ228162.1	36	.....C.....	186
AL574991.3	900	.....	750





[illegible]

[illegible]

Query 3601 TCCATTTTTTAAAAATGTTTTCCCAAAACCATAAAACCCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCATGTAGCTGAAAATAAAATGACGTCAC 3707  
CA414448.1 130 .....N..... 24  
CB321626.1 128 ..... 22

Query= N15-2 [organism=Homo sapiens] anxl

Length=961

Sequences producing significant alignments:		Score (Bits)	E Value	Max ident
BQ228162.1	AGENCOURT_7258587 NIH_MGC_71 Homo sapiens cDNA clon...	1591	0.0	99%
AL576603.2	AL576603 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1567	0.0	100%
AL576340.3	AL576340 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1565	0.0	100%
AL576223.3	AL576223 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1563	0.0	100%
AL574991.3	AL574991 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1559	0.0	100%
BM555842.1	AGENCOURT_6544353 NIH_MGC_88 Homo sapiens cDNA clon...	1554	0.0	99%
AL570428.3	AL570428 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1543	0.0	99%
AL570884.3	AL570884 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1539	0.0	99%
AL575425.3	AL575425 Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1526	0.0	99%
BE614257.1	601504294T1 NIH_MGC_71 Homo sapiens cDNA clone IMAG...	1520	0.0	98%

#### ALIGNMENTS

Query	86	ATCAGAGACATTAACAGGGTCTACAGAGAGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTG	235
BQ228162.1	88	.....	237
AL576603.2	855	.....	706
AL576340.3	859	.....	710
AL576223.3	848	.....	699
AL574991.3	848	.....	699
BM555842.1	47	.....	196
AL570428.3	853	.....W.....	704
AL570884.3	855	.....	706
AL575425.3	866	.....R.....	717
BE614257.1	867	.....-..-..A.T.....A.....C.....-..	719

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                  |  
                  A  \  
  |  
  G

Query	236	GCTGATTGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAACCGTGTTCATACCATCCTTACCACCAGAAGCTATCCACAACCTTCGAGAGTGTTCAGAAATACACCAAGTACAGTAAGCATGACATG	385
BQ228162.1	238	.....	387
AL576603.2	705	.....	556
AL576340.3	709	.....	560
AL576223.3	698	.....	549
AL574991.3	698	.....	549
BM555842.1	197	.....	346
AL570428.3	703	.....N.....	554
AL570884.3	705	.....	556
AL575425.3	716	...S.....T.....	567
BE614257.1	718	.....	569

Query	386	AACAAAGTTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAACCCAGCTTTCTTTGAGAGAGCTTCATCAAGCCATGAAAGGTGTGGAACTCGCCATAAGGCATTGATCAGG	535
BQ228162.1	388	.....	537
AL576603.2	555	.....	406
AL576340.3	559	.....	410
AL576223.3	548	.....	399
AL574991.3	548	.....	399
BM555842.1	347	.....	496
AL570428.3	553	.....	404
AL570884.3	555	.....	406
AL575425.3	566	.....N.....	417
BE614257.1	568	.....	419

Query	536	ATTATGGTTTCCCGTCTCGAATTGACATGAATGATATCAAAGCATTTCTATCAGAAGATGTATGGTATCTGCCCTTTGCCAAGCCATCCTGGATGAAACCAAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGAGGAACTAAACA	685
BQ228162.1	538	.....	687
AL576603.2	405	.....	256
AL576340.3	409	.....R.....R.....	260
AL576223.3	398	.....	249
AL574991.3	398	.....W.....	249
BM555842.1	497	.....	646
AL570428.3	403	.....A.....T.....	254
AL570884.3	405	.....	256
AL575425.3	416	.....	267
BE614257.1	418	.....	269

Query	686	TTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAAC	835
BQ228162.1	688	.....	838

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                  |  
                  A

AL576603.2	255	.....	106
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AL576340.3 259 ..... 110  
AL576223.3 248 ..... 99  
AL574991.3 248 .....Y..... 99  
BM555842.1 647 ..... 796  
AL570428.3 253 ..... 104  
AL570884.3 255 ..... 106  
AL575425.3 266 .....N..... 117  
BE614257.1 268 ..... 119

Query 836 TCTGTATAATAGATAAGTCCATTTTAAAAATGTTTCCCAAAACCATAAAACCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCATGTAGCTGAAAAATAAATGACGTC 959  
BQ228162.1 839 .....G..... 965

AL576603.2 105 .....G.....A..... 1  
AL576340.3 109 .....C..... 5  
AL576223.3 98 .....B..... 1  
AL574991.3 98 ..... 1  
BM555842.1 797 .....G..... 922

AL570428.3 103 .....T..... 1  
AL570884.3 105 .....RW.....V..... 1

AL575425.3 116 .....G..... 17  
BE614257.1 118 .....T.A..... 6

Query= N16-14 [organism=Homo sapiens] anxa1  
Length=2873

Sequences producing significant alignments:				Score (Bits)	E Value	Max ident
AL544959.3	AL544959	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1701	0.0	100%	
BX438944.2	BX438944	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1698	0.0	100%	
AL551427.3	AL551427	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1696	0.0	100%	
AL540651.3	AL540651	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1692	0.0	100%	
AL551980.3	AL551980	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1687	0.0	100%	
AL544231.3	AL544231	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1685	0.0	100%	
AL541874.3	AL541874	Homo sapiens PLACENTA Homo sapiens cDNA cl...	1683	0.0	100%	
BU902298.1	AGENCOURT_10127317	NIH_MGC_71 Homo sapiens cDNA clo...	1683	0.0	99%	
BU508007.1	AGENCOURT_10128424	NIH_MGC_71 Homo sapiens cDNA clo...	1681	0.0	100%	
AL553114.3	AL553114	Homo sapiens PLACENTA COT 25-NORMALIZED Ho...	1674	0.0	99%	

ALIGNMENTS

Query	1	TGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAGAAGGTAGAGATAAAGACACTTTTTCAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATTGAAAAATGAAGAGCAGGAATATGTTCAAAC	150
AL544959.3	1	.....	144
BX438944.2	1	.....	135
AL551427.3	1	..T.....	137
AL540651.3	19	..T.....	153
AL551980.3	22	.....	154
AL544231.3	19	..T.....	153
AL541874.3	1	.....	127
BU902298.1	24	.....	166
BU508007.1	1	.....	133
AL553114.3	109	.....	258
Query	151	TCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCTTATCTCTACCTTCAATCCATCTCGGATGTCGCTGCCTTGCAATAAGGCCATAATGGTTAAAGGTGGATGAAGCAACCATCATTTGACATTCTAACTAAGCGAAACAATGCACAG	300
AL544959.3	145	.....	294
BX438944.2	136	.....	285
AL551427.3	138	.....	287



AL540651.3	154	.....	303
AL551980.3	155	.....	304
AL544231.3	154	.....	303
AL541874.3	128	.....	277
BU902298.1	167	.....	316
BU508007.1	134	.....	283
AL553114.3	259	.....	408
Query	301	CGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAGCCCCGGATGAACACTGAAGAAGCCCTTACAGGTACCTTGAGGAGGTGTTTTAGCTCTGCTAAAACTCCAGCGCAATTTGATGCTGATGAACCTTCGTGCTGCC	450
AL544959.3	295	.....	444
BX438944.2	286	.....	435
AL551427.3	288	.....	437
AL540651.3	304	.....	453
AL551980.3	305	.....	454
AL544231.3	304	.....	453
AL541874.3	278	.....	427
BU902298.1	317	.....	466
BU508007.1	284	.....	433
AL553114.3	409	.....	558
Query	451	ATGAAGGCCCTTGGAACTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAATAACAAAGAAATCAGAGACATTAAACGGGTCTACAGAGAGGAACCTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTT	600
AL544959.3	445	.....	594
BX438944.2	436	.....	585
AL551427.3	438	.....	587
AL540651.3	454	.....	603
AL551980.3	455	.....	604
AL544231.3	454	.....	603
AL541874.3	428	.....	577
BU902298.1	467	.....	616
BU508007.1	434	.....	583
AL553114.3	559	.....	708
Query	601	CGGAACGCTTTGCTTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTTGGCTGATTGAGATGCCAGGGCCCTTGATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTACC	750
AL544959.3	595	.....	744
BX438944.2	586	.....	735
AL551427.3	588	.....	737
AL540651.3	604	.....	753
AL551980.3	605	.....	754
AL544231.3	604	.....	753
AL541874.3	578	.....	727
BU902298.1	617	.....	766
BU508007.1	584	.....	733
AL553114.3	709	.....	858
Query	751	ACCAGAAGCTATCCACAACCTCGCAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAGTTCTCGACCTGGAGTTGAAAGGTGACATTGAGAATGCCTCAGACTATCGTGAAGTGCGCCACAAGCAACCAGCT	900
AL544959.3	745	.....M.....M.....	895
<div style="text-align: center;">       T                 T     </div>			
BX438944.2	736	.....	885
AL551427.3	738	.....	887
AL540651.3	754	.....	903
AL551980.3	755	.....W.....M.....	904
AL544231.3	754	.....	902
AL541874.3	728	.....	877
BU902298.1	767	.....A.....TG.....	916
BU508007.1	734	.....	883
AL553114.3	859	.....W.....-.....-.....	1005
Query	901	TTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGATGTACCATTCTACTTATATGTCCTGCTTAGAGGAAGAATTATTGTGAGAAAGACAGAAAACCTCATGTTGTTGAAAATCTCACATTTAATATCTCCATTAAATGAGAATCA	1050
AL544959.3	896	.....	929
BX438944.2	886	.....	919
AL551427.3	888	.....	921
AL540651.3	904	.....	937
AL551980.3	905	.....	938
AL544231.3	903	.....	936
AL541874.3	878	.....	911
BU902298.1	917	...C.....	950
BU508007.1	884	.....-.....	916
AL553114.3	1006	.....-.....-.....M.....	1036
Query	1051	TTGTCTATTGATGAAAGAGGTAATACACTACCTTCTCAGATAAACTTCTGTAGATTGCGTGCTtttttttACAGATGAGATTGTAAGTGAGCCTGTAAGTGATTTACGGCTCACTTGTGATTTGCTTAAACATGTGTACCACG	1200
Query	1201	GGAAGGGTGATGACTTTCTTTTTTAACGTGTAATTTTAGTGGCCTACTTCTCTAAGGTGTGAGTTTATAATCTCCACTTTATGAGTCTGATTTGTTGTTTTATTATTCTGTCTTTTATGCCACAGATTAAATAGTTGAACTTTT	1350
Query	1351	GAAATGTCATTCTATGATTAAAGGATGTAGAATGATGATTTTGAGATCAACTATGTCACTTTAACTTTACTGTCTGACATGCATGGTATTATACAAGGTACCTCTTCTATTCTGACATTTTGAGCCCACAAATGAATAGTTATGAAGTTAT	1500
Query	1501	CTTCCTTTTTCTTTGACAGTCCAAAATAAGGAGGTTTTTCagagagagagagaAAGAAAGATCTAACtatttgaataatatgaaggaatatatttgaatatatatgaataatttgaataatatgaatgataGACATGCTAGGTACTGCTC	1650
Query	1651	TGTAGTGGTTAGCATAGTTGCTGCCCCCTTCTGCCATAGTCTAGTGTGATATTTCGTGGGTAATGATGAATACCTGGTCCATGGAAGAGAAAGTGGGACATATACTCCAGACTTTGGAATCCAGGTAGCATTGCTGTGAGCTAAA	1800
Query	1801	TTAACACCTGAAGTTTAAATAGAAATGAGCCAGATGAGGGCAAGAGTGGAAGAGATGGGATAAAGCAAGGGTGGTCCANGAGGAAGAAGTAACCCACACACAGGCTTGAAAGGCAAAGGTAACATAACCTTCTCAAGACAGTAAGTATA	1950

Query= N17-2 [organism=Homo sapiens] anxa1  
Length=988

## ALIGNMENTS

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Query      545  CATAAGGCATTGATCAGGATTATGGTTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAGCCATCCTGGATGAAACCAAAGGAGATTATGAGAAAATCCTGGTGGCTCTT 694
BQ228162.1 520  ..... 669
AL576603.2 423  ..... 274
AL576223.3 416  ..... 267
AL576340.3 427  .....R.....R..... 278
AL574991.3 416  .....W..... 267
BM555842.1 479  .....A.....T..... 628
AL570428.3 421  ..... 272
AL570884.3 423  ..... 274
AL575425.3 434  ..... 285
BU838395.1 477  .....N.....N.....N.....N..... 625

Query      695  TGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAAGCTATGATCAGAAGACTTTAAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAA 844
BQ228162.1 670  ..... 820

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                                A

AL576603.2 273  ..... 124
AL576223.3 266  ..... 117
AL576340.3 277  ..... 128
AL574991.3 266  .....Y..... 117
BM555842.1 629  ..... 778
AL570428.3 271  ..... 122
AL570884.3 273  ..... 124
AL575425.3 284  .....N..... 135
BU838395.1 626  .....T.....-.....C..... 772

Query      845  TCATTTTATATTAATACTCTGTATATAGAGATAAGTCCATTTTAAAAATGTTTCCCCAAACCATAAACCCCTATACAAGTTGTTCTAGTAAACATACATGAGAAAGATGTCTATGTAGCTGAAAAATAAATGACGTC 986
BQ228162.1 821  .....G..... 965

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AL576603.2 123  ..... 1

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AL576223.3 116  .....B..... 1
AL576340.3 127  ..... 5

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                                N

AL574991.3 116  ..... 1
BM555842.1 779  .....G..... 922

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AL570428.3 121  .....T..... 1
AL570884.3 123  .....RW...V.....N...N...W.....A..... 1

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                                N

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                                |
                                N

AL575425.3 134  ..... 17
BU838395.1 773  .....C.....NC..N..N.....G.....N..... 908

```

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions  
 Posted date: Feb 24, 2019 1:46 AM  
 Number of letters in database: 43,200,890,307  
 Number of sequences in database: 77,566,966

```

Lambda      K      H
1.33      0.621    1.12
Gapped
Lambda      K      H
1.28      0.460    0.850
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 77566966
Number of Hits to DB: 2901464
Number of extensions: 648
Number of successful extensions: 648
Number of sequences better than 10: 24
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 514
Number of HSP's successfully gapped: 514
Length of database: 43200890307
A: 0
X1: 13 (25.0 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 13 (25.1 bits)

```

