

BLAST Basic Local Alignment Search Tool

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Nucleotide sequence (2444 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

|cl|10784

Description

None

Molecule type

nucleic acid

Query Length

2444

Database Name

htgs

Description

Unfinished High Throughput Genomic Sequences; Sequences: phases 0,1 and 2

Program

BLASTN 2.2.18+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Filter string	L;m;

Database

Posted date	Oct 6, 2008 5:42 PM
Number of letters	229,352,945
Number of sequences	137,085
Entrez query	none

Karlin-Altschul statistics

Params	Gapped	Ungapped
Lambda	0.635425	0.635425
K	0.408678	0.408678
H	0.915256	0.915256

Results Statistics

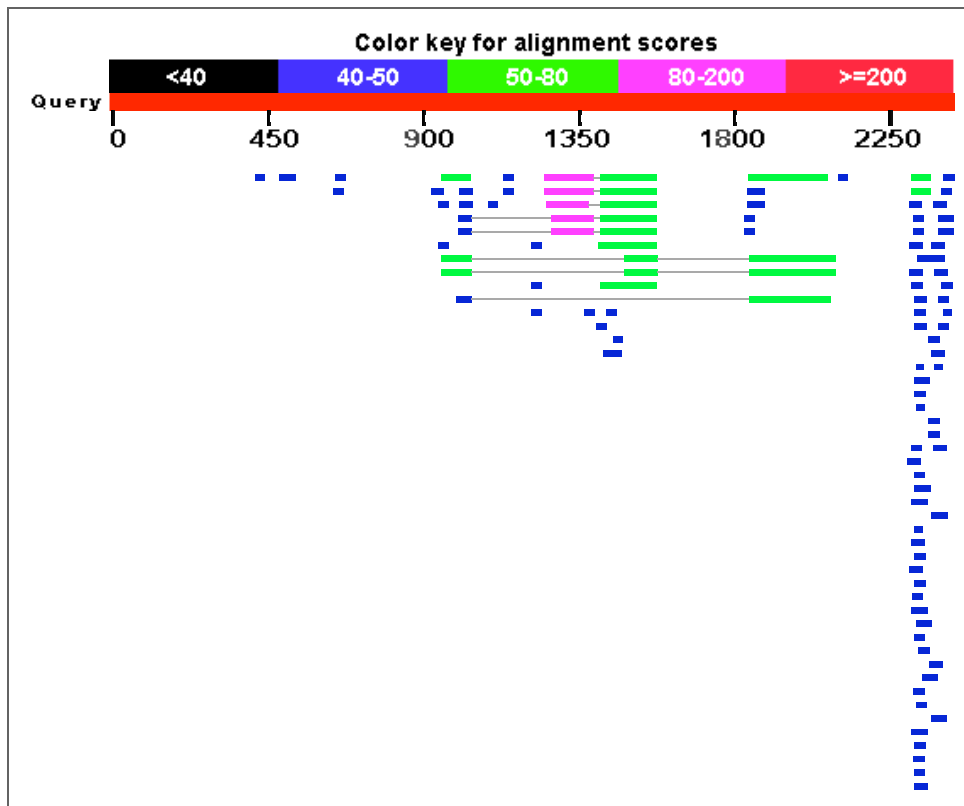
Length adjustment	37
Effective length of query	2407
Effective length of database	22924280800
Effective search space	55178743885600
Effective search space used	55178743885600

[Graphic Summary](#)

Distribution of 109 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Descriptions](#)Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer**Sequences producing significant alignments:**

(Click headers to sort columns)

CU570979.19	Danio rerio chromosome 2 clone CH73-147D18, WORKING DRAFT SEQUENCE, 2 unordered pieces	95.1	164	12%	1e-15	74%
AC101212.1	Mus musculus clone RP23-182G21, LOW-PASS SEQUENCE SAMPLING	93.3	166	12%	5e-15	74%
AC219539.1	Bos taurus clone CH240-330H4, WORKING DRAFT SEQUENCE, 21 unordered pieces	87.8	154	12%	2e-13	75%
AC103546.7	Rattus norvegicus clone CH230-79A7, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	87.8	205	13%	2e-13	84%
AC127913.3	Rattus norvegicus clone CH230-20808, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	87.8	205	13%	2e-13	84%
AC163403.3	Mus musculus chromosome 5 clone RP23-301J3 map 5, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	77.0	77.0	6%	4e-10	71%
CU640376.2	Sus scrofa chromosome 9 clone CH242-149O22, WORKING DRAFT SEQUENCE	73.4	73.4	9%	4e-09	68%
AC095363.8	Rattus norvegicus clone CH230-1L12, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	73.4	211	18%	4e-09	77%
AC106602.4	Rattus norvegicus clone CH230-209I9, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces	73.4	211	18%	4e-09	77%
AL353767.14	Homo sapiens chromosome 9 clone RP11-563N7, 6 unordered pieces	73.4	73.4	6%	4e-09	70%
AC114874.5	Rattus norvegicus clone CH230-54D3, WORKING DRAFT SEQUENCE, 5 unordered pieces	69.8	69.8	3%	5e-08	77%
CU210908.2	Sus scrofa chromosome 1 clone CH242-184P19, WORKING DRAFT SEQUENCE, 5 unordered pieces	68.0	114	11%	2e-07	84%
CU915485.1	Sus scrofa chromosome 1 clone CH242-344M23, WORKING DRAFT SEQUENCE, 23 unordered pieces	53.6	53.6	2%	0.004	82%
CU633513.2	Sus scrofa chromosome 1 clone CH242-384I14, WORKING DRAFT SEQUENCE, 9 unordered pieces	53.6	53.6	2%	0.004	82%
AC217554.2	Zea mays chromosome 2 clone CH201-279C23; ZMMBbc0279C23, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	50.0	50.0	1%	0.050	84%
AC168093.4	Bos taurus clone CH240-234F5, WORKING DRAFT SEQUENCE, 5 unordered pieces	46.4	46.4	2%	0.61	81%
AC152100.4	Bos taurus clone CH240-1A14, WORKING DRAFT SEQUENCE, 12 unordered pieces	46.4	46.4	2%	0.61	81%
CU468501.2	Sus scrofa chromosome 15 clone CH242-50H16, WORKING DRAFT SEQUENCE, 2 unordered pieces	46.4	46.4	1%	0.61	88%
CU467931.2	Sus scrofa chromosome 15 clone CH242-41C11, WORKING DRAFT SEQUENCE, 2 unordered pieces	46.4	46.4	1%	0.61	88%
CT025922.5	Danio rerio chromosome 23 clone DKEY-153L22, WORKING DRAFT SEQUENCE, 5 unordered pieces	46.4	46.4	1%	0.61	89%
CT025684.1	Danio rerio chromosome 5 clone DKEY-218F17, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	46.4	46.4	1%	0.61	89%
CR940347.1	Theileria annulata strain Ankara isolate clone C9, *** SEQUENCING IN PROGRESS ***	46.4	46.4	3%	0.61	73%
CR450839.1	Danio rerio clone DKEY-126L15, WORKING DRAFT SEQUENCE, 7 unordered pieces	46.4	46.4	1%	0.61	89%
AC230488.1	Bos taurus clone CH240-508A23, WORKING DRAFT SEQUENCE, 5 unordered pieces	44.6	44.6	1%	2.1	90%
AC230477.1	Bos taurus clone CH240-507L14, WORKING DRAFT SEQUENCE, 11 unordered pieces	44.6	44.6	1%	2.1	90%
CU914467.1	Sus scrofa chromosome 13 clone CH242-352C21, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces	44.6	44.6	1%	2.1	91%
CU856347.2	Danio rerio chromosome 5 clone CH73-24M4, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces	44.6	44.6	1%	2.1	84%
AC225013.1	Bos taurus clone CH240-469M21, WORKING DRAFT SEQUENCE, 33 unordered pieces	44.6	44.6	1%	2.1	90%

AC224993.1	Bos taurus clone CH240-470A18, WORKING DRAFT SEQUENCE, 3 unordered pieces	44.6	44.6	1%	2.1	84%
AC224713.1	Bos taurus clone CH240-478H13, WORKING DRAFT SEQUENCE, 7 unordered pieces	44.6	44.6	1%	2.1	84%
AC223218.1	Bos taurus clone CH240-425L12, WORKING DRAFT SEQUENCE, 10 unordered pieces	44.6	44.6	1%	2.1	80%
AC222808.1	Bos taurus clone CH240-437P3, WORKING DRAFT SEQUENCE, 2 unordered pieces	44.6	89.1	1%	2.1	96%
AC216225.2	Zea mays chromosome 4 clone CH201-423D12; ZMMBbc0423D12, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces	44.6	44.6	1%	2.1	88%
CU469365.2	Sus scrofa chromosome 7 clone CH242-149A19, WORKING DRAFT SEQUENCE, 3 unordered pieces	44.6	44.6	1%	2.1	88%
AC161987.3	Bos taurus clone CH240-106A14, WORKING DRAFT SEQUENCE, 12 unordered pieces	44.6	44.6	1%	2.1	90%
CU468364.2	Sus scrofa chromosome 7 clone CH242-49L12, WORKING DRAFT SEQUENCE, 3 unordered pieces	44.6	44.6	1%	2.1	88%
AC193790.3	Zea mays chromosome 4 clone CH201-141E15; ZMMBbc0141E15, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces	44.6	44.6	1%	2.1	88%
CT967301.2	Sus scrofa chromosome 11 clone CH242-417D9, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	44.6	44.6	1%	2.1	88%
AC150406.1	Branchiostoma floridae clone CH302-51D3, WORKING DRAFT SEQUENCE, 5 unordered pieces	44.6	44.6	1%	2.1	90%
AC110111.4	Rattus norvegicus clone CH230-297N10, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	44.6	44.6	1%	2.1	90%
AC109848.8	Rattus norvegicus clone CH230-92A10, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	44.6	44.6	1%	2.1	90%
AC103061.5	Rattus norvegicus clone CH230-166L18, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	44.6	44.6	1%	2.1	90%
AC011304.5	Homo sapiens chromosome Y clone RP11-363H7, WORKING DRAFT SEQUENCE	44.6	44.6	1%	2.1	85%
AL358772.24	Homo sapiens chromosome 10 clone RP11-722L1, 7 unordered pieces	44.6	44.6	1%	2.1	93%
AC212617.2	Solanum lycopersicum chromosome 7 clone C07Hba0048I07, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces	42.8	42.8	0%	7.4	100%
AC202346.13	Medicago truncatula clone mth2-2n5, WORKING DRAFT SEQUENCE, 16 unordered pieces	42.8	42.8	1%	7.4	79%
CU856640.2	Sus scrofa chromosome 16 clone CH242-178B1, WORKING DRAFT SEQUENCE, 11 unordered pieces	42.8	42.8	1%	7.4	91%
CU571340.2	Sus scrofa chromosome 15 clone CH242-146G1, WORKING DRAFT SEQUENCE, 3 unordered pieces	42.8	42.8	1%	7.4	96%
AC157175.5	Bos taurus clone CH240-67I19, WORKING DRAFT SEQUENCE, 9 unordered pieces	42.8	42.8	1%	7.4	90%
AC159695.3	Bos taurus clone CH240-75I21, WORKING DRAFT SEQUENCE, 10 unordered pieces	42.8	42.8	1%	7.4	90%
AC230602.1	Bos taurus clone CH240-503J12, WORKING DRAFT SEQUENCE, 7 unordered pieces	42.8	42.8	1%	7.4	90%
CU855986.2	Sus scrofa chromosome 1 clone CH242-171G22, WORKING DRAFT SEQUENCE, 18 unordered pieces	42.8	42.8	1%	7.4	92%
CU914663.1	Sus scrofa chromosome X clone CH242-31B7, WORKING DRAFT SEQUENCE, 18 unordered pieces	42.8	42.8	1%	7.4	84%
AC206313.3	Zea mays chromosome 6 clone CH201-147G23; ZMMBbc0147G23, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	42.8	42.8	1%	7.4	92%
AP010082.1	Lotus japonicus chromosome 6 clone LjT10I04, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces	42.8	42.8	1%	7.4	92%
CU855706.2	Sus scrofa chromosome 16 clone CH242-278I11, WORKING DRAFT SEQUENCE, 4 unordered pieces	42.8	42.8	1%	7.4	82%
CU861549.1	Sus scrofa chromosome 6 clone CH242-250B15, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces	42.8	42.8	1%	7.4	82%

CU466485.2	Sus scrofa chromosome 13 clone CH242-441K6, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces	42.8	42.8	2%	7.4	82%
AC224991.1	Bos taurus clone CH240-46H1, WORKING DRAFT SEQUENCE, 43 unordered pieces	42.8	42.8	1%	7.4	86%
AC224296.1	Bos taurus clone CH240-490L21, WORKING DRAFT SEQUENCE, 14 unordered pieces	42.8	42.8	1%	7.4	90%
AC222479.1	Bos taurus clone CH240-419C20, WORKING DRAFT SEQUENCE, 4 unordered pieces	42.8	42.8	0%	7.4	100%
CU694787.1	Sus scrofa chromosome 3 clone CH242-274P2, WORKING DRAFT SEQUENCE, 3 unordered pieces	42.8	42.8	1%	7.4	83%
AC218818.1	Bos taurus clone CH240-293I7, WORKING DRAFT SEQUENCE, 6 unordered pieces	42.8	42.8	1%	7.4	87%
AC170322.3	Bos taurus clone CH240-261K11, WORKING DRAFT SEQUENCE, 2 unordered pieces	42.8	42.8	1%	7.4	84%
AC167471.4	Bos taurus clone CH240-211F9, WORKING DRAFT SEQUENCE, 9 unordered pieces	42.8	42.8	1%	7.4	87%
AC168138.3	Bos taurus clone CH240-203C3, WORKING DRAFT SEQUENCE, 3 unordered pieces	42.8	42.8	1%	7.4	87%
AC170145.3	Bos taurus clone CH240-199C24, WORKING DRAFT SEQUENCE, 4 unordered pieces	42.8	42.8	1%	7.4	92%
AC173095.4	Bos taurus clone CH240-190C23, WORKING DRAFT SEQUENCE, 9 unordered pieces	42.8	42.8	1%	7.4	87%
AC215283.2	Zea mays chromosome 6 clone CH201-163P5; ZMBBc0163P05, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	42.8	42.8	1%	7.4	92%
CU638861.1	Sus scrofa chromosome 6 clone CH242-450D10, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces	42.8	42.8	1%	7.4	82%
AC215978.2	Felis catus clone RP86-506H22, WORKING DRAFT SEQUENCE, 3 ordered pieces	42.8	42.8	1%	7.4	80%
AC206724.2	Macaca mulatta chromosome UNKNOWN clone CH250-78L17, WORKING DRAFT SEQUENCE, 2 unordered pieces	42.8	42.8	1%	7.4	96%
AC183177.2	Bos taurus clone CH240-100C11, WORKING DRAFT SEQUENCE, 4 unordered pieces	42.8	42.8	1%	7.4	90%
AC207021.2	Pongo abelii chromosome UNKNOWN clone CH276-258G8, WORKING DRAFT SEQUENCE, 2 unordered pieces	42.8	42.8	1%	7.4	87%
CU138566.4	Sus scrofa chromosome 4 clone CH242-255O6, WORKING DRAFT SEQUENCE, 2 unordered pieces	42.8	42.8	1%	7.4	90%
AC123293.3	Rattus norvegicus clone CH230-244N8, WORKING DRAFT SEQUENCE, 4 unordered pieces	42.8	42.8	1%	7.4	90%
AC165198.2	Oryctolagus cuniculus clone LB1-129M6, WORKING DRAFT SEQUENCE, 3 ordered pieces	42.8	42.8	1%	7.4	86%
AC009667.3	Homo sapiens chromosome 1 clone RP11-8L2 map 1, LOW-PASS SEQUENCE SAMPLING	42.8	42.8	1%	7.4	90%
CR388142.3	Danio rerio chromosome 7 clone DKEY-250G10, WORKING DRAFT SEQUENCE, 5 unordered pieces	42.8	42.8	1%	7.4	82%
CR853283.3	Danio rerio clone DKEY-152K11, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	42.8	42.8	1%	7.4	92%
BX629351.9	Danio rerio clone DKEY-63B7, WORKING DRAFT SEQUENCE, 8 unordered pieces	42.8	42.8	1%	7.4	81%
AC068550.3	Homo sapiens chromosome 17 clone RP11-659P18, WORKING DRAFT SEQUENCE, 7 unordered pieces	42.8	42.8	1%	7.4	92%
AC005505.8	Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***	42.8	42.8	1%	7.4	87%
CR352214.5	Danio rerio clone CH211-256D24, 16 unordered pieces	42.8	42.8	1%	7.4	93%
AC024477.1	Homo sapiens chromosome X clone RP11-770O15 map X, LOW-PASS SEQUENCE SAMPLING	42.8	42.8	1%	7.4	96%
AC024976.1	Homo sapiens chromosome 4 clone RP11-620N17 map 4, LOW-PASS SEQUENCE SAMPLING	42.8	42.8	1%	7.4	96%
AC021112.3	Homo sapiens chromosome UL clone RP11-256B9, WORKING DRAFT SEQUENCE, 31 unordered pieces	42.8	42.8	1%	7.4	80%
AC068005.2	Homo sapiens chromosome 6 clone RP11-704J17 map 6, WORKING DRAFT SEQUENCE, 12 unordered pieces	42.8	42.8	2%	7.4	80%

AC025122.3	Homo sapiens chromosome 1 clone RP11-184G21 map 1, WORKING DRAFT SEQUENCE, 22 unordered pieces	42.8	42.8	1%	7.4	81%
AC135884.2	Rattus norvegicus clone CH230-176C2, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	42.8	42.8	1%	7.4	90%
AC020814.2	Mus musculus clone RG-MBAC_270F3, LOW-PASS SEQUENCE SAMPLING	42.8	42.8	1%	7.4	84%
AC137201.1	Rattus norvegicus clone CH230-unknown, *** SEQUENCING IN PROGRESS ***	42.8	42.8	1%	7.4	85%
AC007933.1	Homo sapiens chromosome 17 clone hRPC.908_0_12 map 17, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces	42.8	42.8	1%	7.4	92%
AC005139.3	Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	42.8	42.8	1%	7.4	87%
AC096075.5	Rattus norvegicus clone CH230-33H17, *** SEQUENCING IN PROGRESS ***	42.8	42.8	1%	7.4	92%
AP004555.1	Oryza sativa Japonica Group chromosome 8 clone P0017F04, *** SEQUENCING IN PROGRESS ***	42.8	42.8	1%	7.4	84%

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>emb|CU570979.19| **D** Danio rerio chromosome 2 clone CH73-147D18, WORKING DRAFT SEQUENCE,
 2 unordered pieces
 Length=109000

Sort alignments for this subject sequence
 E value **Score** **Percent identity**
Query start position Subject start pos

Score = 95.1 bits (104), Expect = 1e-15
 Identities = 108/145 (74%), Gaps = 0/145 (0%)
 Strand=Plus/Plus

```

Query 1255 AGCAATTTGCTCTGGGACACTCCTTCTTTGGTCTACTACCAGGATTGTTTATGTATGGCA 1314
          |||
Sbjct 13721 AGAAATTTGCTGTGGGCCATGAGGCCTTTGGTCTGGTTCAGGTTTGATAATGTATGCTA 13780
          |||
Query 1315 CAATCTGGTTACGAGAACATAACAGAGTGTGTGACATCTTGAAAAAGGAGCATCCAGAAT 1374
          |||
Sbjct 13781 CCATTTGGCTCCGTGAGCACAACCGTGTCTGTGACATCATGAAGCAGGAACATCCTGACT 13840
          |||
Query 1375 GGAATGATGAGAGATTATTTCAAAC 1399
          |||
Sbjct 13841 GGGATGATGAGAGAATCTTCCAAAC 13865
          |||
    
```

Score = 69.8 bits (76), Expect = 5e-08
 Identities = 116/168 (69%), Gaps = 0/168 (0%)
 Strand=Plus/Plus

```

Query 1418 AGGAGAGACCATTAAAAATGTTATAGAGGACTATGTAAAACATCTCAGCAACTATAATTA 1477
          |||
Sbjct 14698 AGGTGAGACCATCAAAAATGTGATCGAGGACTATGTTTCAGCAGCTTGAGTGGATAACAATT 14757
          |||
Query 1478 TGATTTGATCTTTAATCCTGAATTGCTGTTTGGCGAGCCATTCCAGTATCAGAACAGGAT 1537
          |||
Sbjct 14758 CAAGCTCAAGTTTGACCAGAGCTCATCTTCAGTGAGCGTTTCCAGTACCAGAACCCTAT 14817
          |||
Query 1538 TGCTTTAGAATTCAACCATCTTTATCACTGGCATCCCCTGATGCCAGA 1585
          |||
Sbjct 14818 TGCGGCCGAATTCAATACCTGTATCACTGGCATCCACTGTTGCCGGA 14865
          |||
    
```

>gb|AC101212.1| **D** Mus musculus clone RP23-182G21, LOW-PASS SEQUENCE SAMPLING
 Length=59388

Sort alignments for this subject sequence
 E value **Score** **Percent identity**
Query start position Subject start pos

Score = 93.3 bits (102), Expect = 5e-15
 Identities = 107/144 (74%), Gaps = 0/144 (0%)
 Strand=Plus/Plus

```

Query 1256 GCAATTTGCTCTGGGACACTCCTTCTTTGGTCTACTACCAGGATTGTTTATGTATGGCAC 1315
          |||
Sbjct 57223 GCAGTTTGCTGTGGGCAGGAAGTCTTTGGTCTGGTGCCTGGTCTGATGATGTATGCCAC 57282
          |||
Query 1316 AATCTGGTTACGAGAACATAACAGAGTGTGTGACATCTTGAAAAAGGAGCATCCAGAATG 1375
          |||
Sbjct 57283 CATCTGGCTTCGGGAGCACAACAGAGTGTGCGACATACTCAAGCAGGAGCATCCTGAGTG 57342
          |||
Query 1376 GAATGATGAGAGATTATTTCAAAC 1399
          |||
Sbjct 57343 GGGTATGAGCAACTATTCCAAAC 57366
          |||
    
```

Score = 73.4 bits (80), Expect = 4e-09

Identities = 117/168 (69%), Gaps = 0/168 (0%)
 Strand=Plus/Plus

```

Query 1418 AGGAGAGACCATTAAAAATGTTATAGAGGACTATGTAAAACATCTCAGCAACTATAATTA 1477
          |||
Sbjct 57552 AGGAGAGACTATCAAGATAGTGATCGAAGACTACGTGCAACACCTGAGCGGTTACCACTT 57611
          |||
Query 1478 TGATTTGATCTTTAATCCTGAATTGCTGTTTGGCGAGCCATTCCAGTATCAGAACAGGAT 1537
          |||
Sbjct 57612 CAAACTCAAGTTTGACCCAGAGCTCCTTTTCAACCAGCAGTTCCAGTATCAGAACC GCAT 57671
          |||
Query 1538 TGCTTTAGAATTCAACCATCTTTTATCACTGGCATCCCCCTGATGCCAGA 1585
          |||
Sbjct 57672 TGCCTCTGAATTCAACACACTCTATCACTGGCACCCCTGCTGCCCGA 57719
          |||
    
```

>gb|AC219539.1| D Bos taurus clone CH240-330H4, WORKING DRAFT SEQUENCE, 21 unordered pieces
 Length=181633

Sort alignments for this subject sequence
 E value Score Percent identity
 Query start position Subject start pos

Score = 87.8 bits (96), Expect = 2e-13
 Identities = 95/126 (75%), Gaps = 0/126 (0%)
 Strand=Plus/Minus

```

Query 1260 TTTGCTCTGGGACACTCCTTCTTTGGTCTACTACCAGGATTGTTTATGTATGGCACAATC 1319
          |||
Sbjct 9028 TTTGCTGTGGGCCAGGAAGTCTTTGGTCTGGTGCCTGGTCTGATGATGTATGCCACCATT 8969
          |||
Query 1320 TGGTTACGAGAACATAACAGAGTGTGTGACATCTTGAAAAAGGAGCATCCAGAATGGAAT 1379
          |||
Sbjct 8968 TGGCTACGGGAACACAACAGAGTGTGTGATGTGCTTAAACAAGAGCATCCAGAATGGGGC 8909
          |||
Query 1380 GATGAG 1385
          |||
Sbjct 8908 GATGAG 8903
          |||
    
```

Score = 66.2 bits (72), Expect = 6e-07
 Identities = 116/169 (68%), Gaps = 0/169 (0%)
 Strand=Plus/Minus

```

Query 1417 TAGGAGAGACCATTAAAAATGTTATAGAGGACTATGTAAAACATCTCAGCAACTATAATT 1476
          |||
Sbjct 8587 TAGGAGAAACTATTAAGATTGTGATTGAAGACTACGTACAGCACCTTGAGTGGCTATCACT 8528
          |||
Query 1477 ATGATTTGATCTTTAATCCTGAATTGCTGTTTGGCGAGCCATTCCAGTATCAGAACAGGA 1536
          |||
Sbjct 8527 TCAAACCTGAAGTTTGACCCAGAGCTGCTTTTCAACCAACAGTTCCAGTACCAGAACC GTA 8468
          |||
Query 1537 TTGCTTTAGAATTCAACCATCTTTTATCACTGGCATCCCCCTGATGCCAGA 1585
          |||
Sbjct 8467 TTGCTGCTGAGTTTAAACACGCTCTACCCTGGCATCCCCCTTCTGCCTGA 8419
          |||
    
```

>gb|AC103546.7| D Rattus norvegicus clone CH230-79A7, *** SEQUENCING IN PROGRESS
 ***, 6 unordered pieces
 Length=245916

Sort alignments for this subject sequence
 E value Score Percent identity
 Query start position Subject start pos

Score = 87.8 bits (96), Expect = 2e-13
 Identities = 92/121 (76%), Gaps = 0/121 (0%)
 Strand=Plus/Minus

```

Query 1279 TCTTTGGTCTACTACCAGGATTGTTTATGTATGGCACAATCTGGTTACGAGAACATAACA 1338
          |||
Sbjct 127558 TCTTTGGTCTGGTGCCGGTCTGATGATGTATGCTACCATCTGGCTTCGGGAGCACAACA 127499
          |||
Query 1339 GAGTGTGTGACATCTTGAAAAAGGAGCATCCAGAATGGAATGATGAGAGATTATTTCAA 1398
          |||
Sbjct 127498 GAGTGTGTGATATACTCAAACAGGAGCATCTGAGTGGGATGACGAGCGACTGTTCCAAA 127439
          |||
Query 1399 C 1399
          |
Sbjct 127438 C 127438
          |
    
```

Score = 73.4 bits (80), Expect = 4e-09
 Identities = 117/168 (69%), Gaps = 0/168 (0%)
 Strand=Plus/Minus

```

Query 1418 AGGAGAGACCATTAAAATTGTTATAGAGGACTATGTAAAACATCTCAGCAACTATAATTA 1477
Sbjct 127250 AGGAGAGACGATCAAGATAGTGATCGAAGACTACGTGCAACACCTGAGCGGTTACCACTT 127191
Query 1478 TGATTTGATCTTTAATCCTGAATTGCTGTTTGGCGAGCCATTCCAGTATCAGAACAGGAT 1537
Sbjct 127190 CAAACTCAAGTTCGACCCAGAGCTGCTTTTCAACCAGCAGTTCAGTATCAGAACCAGCAT 127131
Query 1538 TGCTTTAGAATTCAACCATCTTTATCACTGGCATCCCCTGATGCCAGA 1585
Sbjct 127130 TGCCTCTGAATTCAACACACTCTATCACTGGCATCCGCTGCTGCCGGA 127083
    
```

Score = 44.6 bits (48), Expect = 2.1
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

```

Query 1010 CTTTGCTCAGCACTTCACTCACATGTTCTTCAAGACTGA 1048
Sbjct 128873 CTTTGCCAGCACTTCACTCATCAGTTTTTCAAGACAGA 128835
    
```

>gb|AC127913.3| D Rattus norvegicus clone CH230-20808, *** SEQUENCING IN PROGRESS
 ***, 2 unordered pieces
 Length=238837

Sort alignments for this subject sequence
 E value Score Percent identity
 Query start position Subject start pos

Score = 87.8 bits (96), Expect = 2e-13
 Identities = 92/121 (76%), Gaps = 0/121 (0%)
 Strand=Plus/Minus

```

Query 1279 TCTTTGGTCTACTACCAGGATTGTTTATGTATGGCACAATCTGGTTACGAGAACATAACA 1338
Sbjct 222446 TCTTTGGTCTGGTGCCGGGTCTGATGATGTATGCTACCATCTGGCTTCGGGAGCACAAACA 222387
Query 1339 GAGTGTGTGACATCTTGAAAAAGGAGCATCCAGAATGGAATGATGAGAGATTATTTCAAAA 1398
Sbjct 222386 GAGTGTGTGATATACTCAAACAGGAGCATCCTGAGTGGGATGACGAGCGACTGTTCCAAA 222327
Query 1399 C 1399
Sbjct 222326 C 222326
    
```

Score = 73.4 bits (80), Expect = 4e-09
 Identities = 117/168 (69%), Gaps = 0/168 (0%)
 Strand=Plus/Minus

```

Query 1418 AGGAGAGACCATTAAAATTGTTATAGAGGACTATGTAAAACATCTCAGCAACTATAATTA 1477
Sbjct 222138 AGGAGAGACGATCAAGATAGTGATCGAAGACTACGTGCAACACCTGAGCGGTTACCACTT 222079
Query 1478 TGATTTGATCTTTAATCCTGAATTGCTGTTTGGCGAGCCATTCCAGTATCAGAACAGGAT 1537
Sbjct 222078 CAAACTCAAGTTCGACCCAGAGCTGCTTTTCAACCAGCAGTTCAGTATCAGAACCAGCAT 222019
Query 1538 TGCTTTAGAATTCAACCATCTTTATCACTGGCATCCCCTGATGCCAGA 1585
Sbjct 222018 TGCCTCTGAATTCAACACACTCTATCACTGGCATCCGCTGCTGCCGGA 221971
    
```

Score = 44.6 bits (48), Expect = 2.1
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

```

Query 1010 CTTTGCTCAGCACTTCACTCACATGTTCTTCAAGACTGA 1048
Sbjct 223761 CTTTGCCAGCACTTCACTCATCAGTTTTTCAAGACAGA 223723
    
```

>gb|AC163403.3| D Mus musculus chromosome 5 clone RP23-301J3 map 5, *** SEQUENCING
 IN PROGRESS ***, 12 unordered pieces
 Length=232242

Score = 77.0 bits (84), Expect = 4e-10
 Identities = 123/172 (71%), Gaps = 6/172 (3%)
 Strand=Plus/Plus

```

Query 1414 TTCTAGGAGAGACCATTAAAATTGTTATAGAGGACTATGTAAAACATCTCAGCAACTATA 1473
Sbjct 32546 TTGTAGGAGAAACCATCAAAAATTGTCATTGAGGAGTATGTGCAGCACTTGAGTGGCTATT 32605
Query 1474 ATTATG-ATTTGATCTTTAATCCTGAATTGCTGTTTGGCGAGCCA--TTCCAGTATCAGA 1530
    
```

```
Sbjct 32606 -TCCTGCAGCTCAAGTTTGACCCGAGCTGCTGTTC--CGAGCCAGTTCCAATATCGAA 32662
Query 1531 ACAGGATTGCTTTAGAATTCAACCATCTTTTACTGCGCATCCCTGATGCC 1582
Sbjct 32663 ACCGCATCGCCATGGAATTTAACCATCTCTATCACTGGCATCCACTCATGCC 32714
```

>emb|CU640376.2| D Sus scrofa chromosome 9 clone CH242-149022, WORKING DRAFT SEQUENCE
Length=169630

Score = 73.4 bits (80), Expect = 4e-09
Identities = 160/234 (68%), Gaps = 8/234 (3%)
Strand=Plus/Minus

```
Query 1848 ACAGGAGAGAAGAAAATGGCCAAGCA-ACCT-GAGGATTCTATGGTGATGTTAATGCTG 1905
Sbjct 137458 ACAGGAGAGAAGGAAAATGGCT--GCAGAGTTAGAAGCGCTCTATGGTGACATTGATGCCA 137401
Query 1906 TGGAGTTTTATGTAGGATTGATAATGGAGAAAAGAAGA-CACA-ATTCTATGTTTGGTGA 1963
Sbjct 137400 TGGAGCTGTATCCTGCCCTTCTGTT--AGAAAAGCCTCGCCAGATGCCATCTTTGGGGA 137343
Query 1964 CTCTTTGGTACAAAATGGTGCCCCGATTCTGTGAAGGGTCTGATGGCAAATCCTATYTG 2023
Sbjct 137342 GACCATGGTAGAAGCTGGAGCCCCATTCTCCTTGAAGGACTTATGGGTAATCCTATCTG 137283
Query 2024 TAGTCCCAAGTACTGGAAAYCTTCTACGTTTGGTGGAGAGGTTGGGTTCAACAT 2077
Sbjct 137282 TTCTCCTGAGTACTGGAAAGCCTAGTACTTTTGGTGGAGAAGTAGGTTTAAAAAT 137229
```

>gb|AC095363.8| D Rattus norvegicus clone CH230-1L12, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces
Length=360260

Sort alignments for this subject sequence
E value Score Percent identity
Query start position Subject start pos

Score = 73.4 bits (80), Expect = 4e-09
Identities = 78/101 (77%), Gaps = 4/101 (3%)
Strand=Plus/Plus

```
Query 1488 TTTAATCCTGAATTGCTGTTTGGCGAGCCA--TTCCAGTATCAGAACAGGATTGCTTTAG 1545
Sbjct 190154 TTTGACCCGGAGCTGCTGTTC--CGAGCCAGTTCCAGTATCGCAACCGCATCGCCTTGG 190211
Query 1546 AATTCAACCATCTTTTACTGCGCATCCCTGATGCCAGAT 1586
Sbjct 190212 AATTCAACCACCTCTATCACTGGCATCCGCTCATGCCTGAT 190252
```

Score = 69.8 bits (76), Expect = 5e-08
Identities = 67/86 (77%), Gaps = 0/86 (0%)
Strand=Plus/Plus

```
Query 960 AGAAAAGGAATTCATTCCCGAGCCGTTAGGGACGAGTGCCTTATTTCTTACTTTGCTCAG 1019
Sbjct 185599 AGAAGGGAGTTTCATTCCCGCCCCGCAGGGACCAACGCTCTTGTGTTCTTTGCACAA 185658
Query 1020 CACTTCACTCACATGTTCTTCAAGAC 1045
Sbjct 185659 CACTTCAACCACCAGTTCTTCAAGAC 185684
```

Score = 68.0 bits (74), Expect = 2e-07
Identities = 167/255 (65%), Gaps = 0/255 (0%)
Strand=Plus/Plus

```
Query 1848 ACAGGAGAGAAGAAAATGGCCAAGCAACTTGAGGATTCTATGGTGATGTTAATGCTGTG 1907
Sbjct 196579 ACAGGAGAGAAGGAGATGGCCGCTGAGTTGGAGGAGCTATATGGTGACATCGATGCTTTA 196638
Query 1908 GAGTTTTATGTAGGATTGATAATGGAGAAAAGAAGACACAATTCTATGTTTGGTGACTCT 1967
Sbjct 196639 GAGTTCTACCCGGGCTGATGCTGGAGAAGTGCCAGCCCAACTCCCTCTTTGGGGAGAGC 196698
Query 1968 TTGGTACAAAATGGTGCCCCGATTCTGTGAAGGGTCTGATGGCAAATCCTATYTGTA 2027
Sbjct 196699 ATGATAGAGATGGGGGCTCCTTTCTCCTCAAGGGCTCCTAGGGAATCCCATCTGTTCC 196758
Query 2028 CCCAAGTACTGGAAAYCTTCTACGTTTGGTGGAGAGGTTGGGTTCAACATAGTAAAACT 2087
Sbjct 196759 CCAGAGTACTGGAAACCAGCACATTCGGTGGTGTATGGGTTCAACATCGTTAACACA 196818
Query 2088 TCTTCACTTAAAAAA 2102
```

Sbjct 196819 GCCTCACTGAAGAAA 196833

>gb|AC106602.4| D Rattus norvegicus clone CH230-209I9, *** SEQUENCING IN PROGRESS
 ***, 20 unordered pieces
 Length=319104

Sort alignments for this subject sequence
 E value Score Percent identity
 Query start position Subject start pos

Score = 73.4 bits (80), Expect = 4e-09
 Identities = 78/101 (77%), Gaps = 4/101 (3%)
 Strand=Plus/Plus

```

Query 1488 TTTAATCCTGAATTGCTGTTTGGCGAGCCA--TTCCAGTATCAGAACAGGATTGCTTTAG 1545
Sbjct 80623 TTTGACCCGGAGCTGCTGTTT--CGAGCCAGTTCAGTATCGCAACCGCATCGCCTTGG 80680
Query 1546 AATTCAACCATCTTTATCACTGGCATCCCTGATGCCAGAT 1586
Sbjct 80681 AATTCAACCACCTCTATCACTGGCATCCGCTCATGCCTGAT 80721
    
```

Score = 69.8 bits (76), Expect = 5e-08
 Identities = 67/86 (77%), Gaps = 0/86 (0%)
 Strand=Plus/Plus

```

Query 960 AGAAAGGAATTCATTCCCGAGCCGTTAGGGACGAGTGCCTTATTTCCCTACTTTGCTCAG 1019
Sbjct 76168 AGAAGGGAGTTCATTCCCGCCCCGAGGGGACCAACGCTTTGTTTGTCTTTTGACAAA 76227
Query 1020 CACTTCACTCACATGTTCTTCAAGAC 1045
Sbjct 76228 CACTTCACTCACAGTTCCTTCAAGAC 76253
    
```

Score = 68.0 bits (74), Expect = 2e-07
 Identities = 167/255 (65%), Gaps = 0/255 (0%)
 Strand=Plus/Plus

```

Query 1848 ACAGGAGAGAAGAAAATGGCCAAGCAACTTGAGGATTTCTATGGTGATGTTAATGCTGTG 1907
Sbjct 87048 ACAGGAGAGAAGGAGATGGCCGCTGAGTTGGAGGAGCTATATGGTGACATCGATGCTTTA 87107
Query 1908 GAGTTTATGTAGGATTGATAATGGAGAAAAGACACAATTCATGTTTGGTGACTCT 1967
Sbjct 87108 GAGTTCTACCCGGGCTGATGCTGGAGAAGTGCCAGCCCAACTCCCTCTTTGGGGAGAGC 87167
Query 1968 TTGGTACAAAATGGTGCCCCGATTTCTGTGAAGGGTCTGATGGCAAATCCTATYTGAGT 2027
Sbjct 87168 ATGATAGAGATGGGGCTCCTTTCTCCCTCAAGGGCTCCTAGGGAATCCCATCTGTTCC 87227
Query 2028 CCCAAGTACTGGAAAYCTTCTACGTTTGGTGGAGAGGTTGGGTTCAACATAGTAAAAACT 2087
Sbjct 87228 CCAGAGTACTGGAAACCAGCACATTCGGTGGTGATGTGGGTTTCAACATCGTTAACACA 87287
Query 2088 TCTTCACTTAAAAAA 2102
Sbjct 87288 GCCTCACTGAAGAAA 87302
    
```

>emb|AL353767.14| D Homo sapiens chromosome 9 clone RP11-563N7, 6 unordered pieces
 Length=199985

Score = 73.4 bits (80), Expect = 4e-09
 Identities = 119/169 (70%), Gaps = 2/169 (1%)
 Strand=Plus/Minus

```

Query 1418 AGGAGAGACCATTAATAATGTTATAGAGGACTATGTAACATCTCAGCAACTATAATTA 1477
Sbjct 93916 AGGGGAGACCATCAAGATTGTCATCGAGGAGTACGTGCAGCAGCTGAGTGGCTATT-TCC 93858
Query 1478 TG-ATTTGATCTTTAATCCTGAATTGCTGTTTGGCGAGCCATTCCAGTATCAGAACAGGA 1536
Sbjct 93857 TGCAGCTGAAATTTGACCCAGAGCTGCTGTTCCGGTGTCCAGTTCGAATACCGCAACCGCA 93798
Query 1537 TTGCTTTAGAATTCAACCATCTTTATCACTGGCATCCCTGATGCCAGA 1585
Sbjct 93797 TTGCCATGGAGTTCAACCATCTCTACCACTGGCACCCCTCATGCCTGA 93749
    
```

>gb|AC114874.5| D Rattus norvegicus clone CH230-54D3, WORKING DRAFT SEQUENCE, 5
 unordered pieces
 Length=224597

Score = 69.8 bits (76), Expect = 5e-08

Identities = 67/86 (77%), Gaps = 0/86 (0%)
Strand=Plus/Plus

```
Query 960      AGAAAGGAATTCATTCCCGAGCCGTTAGGGACGAGTGCCTTATTTCTTACTTTTGCTCAG 1019
Sbjct 223926    AGAAGGGAGTTCATTCCCGCCCCGAGGGGACCAACGTCCTTGTGTTGCTTTCTTTGCACAA 223985

Query 1020     CACTTCACTCACATGTTCTTCAAGAC 1045
Sbjct 223986    CACTTCAACCACCAGTTCTTCAAGAC 224011
```

>emb|CU210908.2| **D** Sus scrofa chromosome 1 clone CH242-184P19, WORKING DRAFT SEQUENCE,
5 unordered pieces
Length=208946

Sort alignments for this subject sequence
E value Score Percent identity
Query start position Subject start pos

Score = 68.0 bits (74), Expect = 2e-07
Identities = 160/239 (66%), Gaps = 4/239 (1%)
Strand=Plus/Minus

```
Query 1850     AGGAGAGAAGAAAATGGCCAAGCA-ACTTG-AGGATTTCTATGGTGATGTTAATGCTGTG 1907
Sbjct 154471    AGGAGAGAAGGAGATGGC--AGCTGAGTTGGAGGAGCTGTATGGAGACATCGATGCCCTG 154414

Query 1908     GAGTTTATGTAGGATTGATAATGGAGAAAAGAAGACACAATTTCTATGTTGGTGACTCT 1967
Sbjct 154413    GAGTTCTACCCAGGGCTGCTTCTCGAGAAGTGCCTCCCAAACATCCATCTTTGGGGAGAGT 154354

Query 1968     TTGGTACAAATTTGGTGCCCGTATTTCTGTGAAGGGTCTGATGGCAAATCCTATYTAGT 2027
Sbjct 154353    ATGATAGAAATTTGGGGCCCTTTTTCCTTAAGGGCCTCTTAGGGAATCCCATCTGTTC 154294

Query 2028     CCCAAGTACTGGAAAYCTTCTACGTTTGGTGGAGAGGTTGGGTTCAACATAGTAAAAAC 2086
Sbjct 154293    CCTCAGTACTGGAAGCGAGCACGTTTGGTGGCAGATGGGCTTCAACCTTGTCAAGAC 154235
```

Score = 46.4 bits (50), Expect = 0.61
Identities = 38/45 (84%), Gaps = 1/45 (2%)
Strand=Plus/Minus

```
Query 1002     TTTCCCTTACTTTGCTCAGCACTTCACTCACATGTTCTTCAAGACT 1046
Sbjct 167461    TTGCCCTT-CITTTGCCCAACACTTCACCCACCAGTTCTTCAAGACT 167418
```

>emb|CU915485.1| **D** Sus scrofa chromosome 1 clone CH242-344M23, WORKING DRAFT SEQUENCE,
23 unordered pieces
Length=195222

Score = 53.6 bits (58), Expect = 0.004
Identities = 46/56 (82%), Gaps = 1/56 (1%)
Strand=Plus/Plus

```
Query 2319     TTAGTTATGCATTATTTTCATTTTAAAAATCACTTCTGAATTTAGTAGCATTTA 2374
Sbjct 186016    TTATTTATGTATTTATTTTCATTTTAAAAATTAATCAATGAATTTATTA-CATTTA 186070
```

>emb|CU633513.2| **D** Sus scrofa chromosome 1 clone CH242-384I14, WORKING DRAFT SEQUENCE,
9 unordered pieces
Length=187346

Score = 53.6 bits (58), Expect = 0.004
Identities = 46/56 (82%), Gaps = 1/56 (1%)
Strand=Plus/Minus

```
Query 2319     TTAGTTATGCATTATTTTCATTTTAAAAATCACTTCTGAATTTAGTAGCATTTA 2374
Sbjct 42314     TTATTTATGTATTTATTTTCATTTTAAAAATTAATCAATGAATTTATTA-CATTTA 42260
```

>gb|AC217554.2| **D** Zea mays chromosome 2 clone CH201-279C23; ZMMBbc0279C23, ***
SEQUENCING IN PROGRESS ***, 14 unordered pieces
Length=158654

Score = 50.0 bits (54), Expect = 0.050
Identities = 39/46 (84%), Gaps = 3/46 (6%)
Strand=Plus/Plus

```
Query 2380     AATAATGTCT--ATTAATATTTTATAGATGTTTGAATTTGAAA 2422
```

Sbjct 108775 AATAATGTTTTGTATAAATATTTTTATAGATATTCTGAATTTGAAA 108820

>gb|AC168093.4| **D** Bos taurus clone CH240-234F5, WORKING DRAFT SEQUENCE, 5 unordered pieces
Length=185148

Score = 46.4 bits (50), Expect = 0.61
Identities = 44/54 (81%), Gaps = 3/54 (5%)
Strand=Plus/Minus

Query 1844 ACTGACAGGAGAGAAGAAAATGGCCAAGCAACTTGAGGATTTCTATGGTGATGT 1897
Sbjct 152637 ACTCACAGGAGAGAAGAGACTGGAGAAGGGACTTGAGGA--TCTA-GGTGATGT 152587

>gb|AC152100.4| **D** Bos taurus clone CH240-1A14, WORKING DRAFT SEQUENCE, 12 unordered pieces
Length=207122

Score = 46.4 bits (50), Expect = 0.61
Identities = 44/54 (81%), Gaps = 3/54 (5%)
Strand=Plus/Plus

Query 1844 ACTGACAGGAGAGAAGAAAATGGCCAAGCAACTTGAGGATTTCTATGGTGATGT 1897
Sbjct 142101 ACTCACAGGAGAGAAGAGACTGGAGAAGGGACTTGAGGA--TCTA-GGTGATGT 142151

>emb|CU468501.2| **D** Sus scrofa chromosome 15 clone CH242-50H16, WORKING DRAFT SEQUENCE, 2 unordered pieces
Length=190959

Score = 46.4 bits (50), Expect = 0.61
Identities = 31/35 (88%), Gaps = 0/35 (0%)
Strand=Plus/Minus

Query 2324 TATGCATTATTTTCATTTTAAAAATCACTTTCTG 2358
Sbjct 207 TATGGATGATTTTAAATATTTAAAAATCACTTTCTG 173

>emb|CU467931.2| **D** Sus scrofa chromosome 15 clone CH242-41C11, WORKING DRAFT SEQUENCE, 2 unordered pieces
Length=174982

Score = 46.4 bits (50), Expect = 0.61
Identities = 31/35 (88%), Gaps = 0/35 (0%)
Strand=Plus/Minus

Query 2324 TATGCATTATTTTCATTTTAAAAATCACTTTCTG 2358
Sbjct 164307 TATGGATGATTTTAAATATTTAAAAATCACTTTCTG 164273

>emb|CT025922.5| **D** Danio rerio chromosome 23 clone DKEY-153L22, WORKING DRAFT SEQUENCE, 5 unordered pieces
Length=236437

Score = 46.4 bits (50), Expect = 0.61
Identities = 33/37 (89%), Gaps = 1/37 (2%)
Strand=Plus/Minus

Query 2313 AAATGCTTAGTTATGCATTATTTTCATTTTAAAAAT 2349
Sbjct 55572 AAATTCCTTA-TTATGTATTAGTTTCATTTTAAAAAT 55537

>emb|CT025684.1| **D** Danio rerio chromosome 5 clone DKEY-218F17, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces
Length=150835

Score = 46.4 bits (50), Expect = 0.61
Identities = 33/37 (89%), Gaps = 1/37 (2%)
Strand=Plus/Plus

Query 2313 AAATGCTTAGTTATGCATTATTTTCATTTTAAAAAT 2349
Sbjct 141231 AAATTCCTTA-TTATGTATTAGTTTCATTTTAAAAAT 141266

>emb|CR940347.1|TANN11 **D** Theileria annulata strain Ankara isolate clone C9, *** SEQUENCING IN PROGRESS ***
Length=2592520

Features in this part of subject sequence:
hypothetical protein

Score = 46.4 bits (50), Expect = 0.61
 Identities = 59/80 (73%), Gaps = 1/80 (1%)
 Strand=Plus/Minus

```
Query 2338      ATTTTAAATCACTTCTGAATTTAGTAGCATTAAATGTGAATAATGTCTATTAATAT 2397
                |||
Sbjct 1191785    ATTTTAAATTAATTTTAAATTAATTAATTTAAATTTTAAATTTAAATTAATTT 1191726
                |||
Query 2398      TTTTATAGATGTTTGAATT 2417
                |||
Sbjct 1191725    TTTTGTAGAT-TAATGAATT 1191707
                |||
```

>emb|CR450839.1| **D** Danio rerio clone DKEY-126L15, WORKING DRAFT SEQUENCE, 7 unordered pieces
 Length=194883

Score = 46.4 bits (50), Expect = 0.61
 Identities = 33/37 (89%), Gaps = 1/37 (2%)
 Strand=Plus/Minus

```
Query 2313      AAATGCTTAGTTATGCATTATTTTCATTTTAAAAAT 2349
                |||
Sbjct 126377    AAATCTTA-TTATGTATTAGTTTCATTTTAAAAAT 126342
                |||
```

>gb|AC230488.1| **D** Bos taurus clone CH240-508A23, WORKING DRAFT SEQUENCE, 5 unordered pieces
 Length=160400

Score = 44.6 bits (48), Expect = 2.1
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

```
Query 1220      TCCAATGGGATATCCAAGGGAATGGAAAAGA 1251
                |||
Sbjct 143870    TCCAAGGGATATCCAAGGGAATGGAAAGGA 143901
                |||
```

>gb|AC230477.1| **D** Bos taurus clone CH240-507L14, WORKING DRAFT SEQUENCE, 11 unordered pieces
 Length=218350

Score = 44.6 bits (48), Expect = 2.1
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

```
Query 1220      TCCAATGGGATATCCAAGGGAATGGAAAAGA 1251
                |||
Sbjct 211432    TCCAAGGGATATCCAAGGGAATGGAAAGGA 211401
                |||
```

>emb|CU914467.1| **D** Sus scrofa chromosome 13 clone CH242-352C21, *** SEQUENCING IN PROGRESS ***
 32 unordered pieces
 Length=152661

Score = 44.6 bits (48), Expect = 2.1
 Identities = 31/34 (91%), Gaps = 1/34 (2%)
 Strand=Plus/Minus

```
Query 2316      TGCTTAGTTATGCATTATTTTCATTTTAAAAAT 2349
                |||
Sbjct 130884    TGCTT-GTTATGCAATATTTTCATTTTAAAGAT 130852
                |||
```

>emb|CU856347.2| **D** Danio rerio chromosome 5 clone CH73-24M4, *** SEQUENCING IN PROGRESS ***
 19 unordered pieces
 Length=79321

Score = 44.6 bits (48), Expect = 2.1
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

```
Query 1011      TTTGCTCAGCACTTCACTCACATGTTCTTCAAGACTGAC 1049
                |||
Sbjct 64435     TTCGCTCAGCACTTCACTCACACCAGTTTTCAGACTCAC 64397
                |||
```

>gb|AC225013.1| **D** Bos taurus clone CH240-469M21, WORKING DRAFT SEQUENCE, 33 unordered pieces
 Length=279257

Score = 44.6 bits (48), Expect = 2.1
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 1220 TCCAATGGGATATCCAAAGGGAATGGAAAAGA 1251
 Sbjct 186374 TCCAAGGGGATATTCAAAGGGAATGGAAAAGGA 186405

>gb|AC224993.1| D Bos taurus clone CH240-470A18, WORKING DRAFT SEQUENCE, 3 unordered pieces
 Length=143292

Score = 44.6 bits (48), Expect = 2.1
 Identities = 38/45 (84%), Gaps = 3/45 (6%)
 Strand=Plus/Minus

Query 2398 TTTTATAGATGTTTTGAATTTGAAATCTGAAAT--CCAGTATCAT 2440
 Sbjct 105008 TTTTAAA-ATGTCTTGAATTTGAAATCTTAAATACCCAGTACCAT 104965

>gb|AC224713.1| D Bos taurus clone CH240-478H13, WORKING DRAFT SEQUENCE, 7 unordered pieces
 Length=199417

Score = 44.6 bits (48), Expect = 2.1
 Identities = 38/45 (84%), Gaps = 3/45 (6%)
 Strand=Plus/Minus

Query 2398 TTTTATAGATGTTTTGAATTTGAAATCTGAAAT--CCAGTATCAT 2440
 Sbjct 13605 TTTTAAA-ATGTCTTGAATTTGAAATCTTAAATACCCAGTACCAT 13562

>gb|AC223218.1| D Bos taurus clone CH240-425L12, WORKING DRAFT SEQUENCE, 10 unordered pieces
 Length=225799

Score = 44.6 bits (48), Expect = 2.1
 Identities = 38/47 (80%), Gaps = 0/47 (0%)
 Strand=Plus/Plus

Query 490 ACTAGTTTCAGGTGCCATAACCCCTGTTGTTTCATACCCCTTGTGAAA 536
 Sbjct 68594 ACTTGTTCAGTAGCCATAACCCCTGGAAGTTCTCACTCTTGTGAAA 68640

>gb|AC222808.1| D Bos taurus clone CH240-437P3, WORKING DRAFT SEQUENCE, 2 unordered pieces
 Length=181787

Sort alignments for this subject sequence
 E value Score Percent identity
 Query start position Subject start pos

Score = 44.6 bits (48), Expect = 2.1
 Identities = 26/27 (96%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query 2412 TGAATTTGAAATCTGAAATCCAGTATC 2438
 Sbjct 42925 TGAATTTGAAATTTGAAATCCAGTATC 42899

Score = 44.6 bits (48), Expect = 2.1
 Identities = 30/33 (90%), Gaps = 2/33 (6%)
 Strand=Plus/Plus

Query 2412 TGAATTTGAAATCTGAAATCCAGTATCATTTTA 2444
 Sbjct 44286 TGAATTTGAAATTTGAAATCCAGTAT--TTTTA 44316

>gb|AC216225.2| D Zea mays chromosome 4 clone CH201-423D12; ZMMBbc0423D12, ***
 SEQUENCING IN PROGRESS ***, 13 unordered pieces
 Length=174873

Score = 44.6 bits (48), Expect = 2.1
 Identities = 32/36 (88%), Gaps = 1/36 (2%)
 Strand=Plus/Minus

Query 2329 ATTATTTTCATTTTTAAAAATCACTTTCTGAATTTA 2364
 |||

Sbjct 123533 ATTATTTTTATATT-AAAAATCCCTTCTGAATTTA 123499

>emb|CU469365.2| **D** Sus scrofa chromosome 7 clone CH242-149A19, WORKING DRAFT SEQUENCE,
3 unordered pieces
Length=180171

Score = 44.6 bits (48), Expect = 2.1
Identities = 32/36 (88%), Gaps = 1/36 (2%)
Strand=Plus/Plus

Query 931 CTGAAGACATTGTGAAGGCTTTCATCAGAAAGG 966
Sbjct 20887 CTGATGAAATT-TGTAGGCTTTCATCAGAAAGG 20921

>gb|AC161987.3| **D** Bos taurus clone CH240-106A14, WORKING DRAFT SEQUENCE, 12 unordered
pieces
Length=229040

Score = 44.6 bits (48), Expect = 2.1
Identities = 29/32 (90%), Gaps = 0/32 (0%)
Strand=Plus/Minus

Query 2107 TTTTGTGAAAATATCAAAGGAGAATGTCCATT 2138
Sbjct 94351 TTTTGGTAAAATATCAAAGAAGAATGTCCATT 94320

>emb|CU468364.2| **D** Sus scrofa chromosome 7 clone CH242-49L12, WORKING DRAFT SEQUENCE,
3 unordered pieces
Length=198594

Score = 44.6 bits (48), Expect = 2.1
Identities = 30/34 (88%), Gaps = 0/34 (0%)
Strand=Plus/Minus

Query 2330 TTATTTTCATTTTTAAAAATCACTTCTGAATTT 2363
Sbjct 172119 TTAATTTCTTTTTAAAAATTACTTTGTGAATTT 172086

>gb|AC193790.3| **D** Zea mays chromosome 4 clone CH201-141E15; ZMMBBc0141E15, ***
SEQUENCING IN PROGRESS ***, 7 unordered pieces
Length=152724

Score = 44.6 bits (48), Expect = 2.1
Identities = 32/36 (88%), Gaps = 1/36 (2%)
Strand=Plus/Minus

Query 2329 ATTATTTTCATTTTTAAAAATCACTTCTGAATTTA 2364
Sbjct 133712 ATTATTTTTATATT-AAAAATCCCTTCTGAATTTA 133678

>emb|CT967301.2| **D** Sus scrofa chromosome 11 clone CH242-417D9, *** SEQUENCING IN
PROGRESS ***, 5 unordered pieces
Length=247000

Score = 44.6 bits (48), Expect = 2.1
Identities = 30/34 (88%), Gaps = 0/34 (0%)
Strand=Plus/Plus

Query 2369 CATTTAATGTGAATAATGTCTATTAATATTTT 2402
Sbjct 177320 CAATTAATCTGAATAAAGTCTATTAATATTTATA 177353

>gb|AC150406.1| **D** Branchiostoma floridae clone CH302-51D3, WORKING DRAFT SEQUENCE,
5 unordered pieces
Length=181859

Score = 44.6 bits (48), Expect = 2.1
Identities = 29/32 (90%), Gaps = 0/32 (0%)
Strand=Plus/Minus

Query 1437 GTTATAGAGGACTATGTAAAACATCTCAGCAA 1468
Sbjct 56716 GTTGTAGAGGACTATGTAAAACATCTCAGTAA 56685

>gb|AC110111.4| **D** Rattus norvegicus clone CH230-297N10, *** SEQUENCING IN PROGRESS
***, 4 unordered pieces
Length=246880

Score = 44.6 bits (48), Expect = 2.1
 Identities = 30/33 (90%), Gaps = 2/33 (6%)
 Strand=Plus/Minus

Query 1835 TTTTGAAGAAGTACAGGAGAGAGAAAAATGGC 1867
 |||
 Sbjct 213374 TTTTGAAGAAGTACACA--AGAGAAAAAAATGGC 213344

>gb|AC109848.8| **D** Rattus norvegicus clone CH230-92A10, *** SEQUENCING IN PROGRESS
 ***, 6 unordered pieces
 Length=249187

Score = 44.6 bits (48), Expect = 2.1
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 652 TAAAACCAAGTCAAAGCACTCTTCATAACCTG 683
 |||
 Sbjct 205779 TAAAACCAAGTCAATGAAGTCTTCATAACCTG 205810

>gb|AC103061.5| **D** Rattus norvegicus clone CH230-166L18, *** SEQUENCING IN PROGRESS
 ***, 5 unordered pieces
 Length=236550

Score = 44.6 bits (48), Expect = 2.1
 Identities = 30/33 (90%), Gaps = 2/33 (6%)
 Strand=Plus/Plus

Query 1835 TTTTGAAGAAGTACAGGAGAGAGAAAAATGGC 1867
 |||
 Sbjct 200092 TTTTGAAGAAGTACACA--AGAGAAAAAAATGGC 200122

>gb|AC011304.5|AC011304 **D** Homo sapiens chromosome Y clone RP11-363H7, WORKING DRAFT SEQUENCE
 Length=193653

Score = 44.6 bits (48), Expect = 2.1
 Identities = 35/41 (85%), Gaps = 1/41 (2%)
 Strand=Plus/Minus

Query 2375 ATGTGAATAATGTCTATTAATATTTTATAGATGTTTTGAA 2415
 |||
 Sbjct 57105 ATTTGAATA-TGTCTATTAATAATTTATATGTGTTTTGAA 57066

>emb|AL358772.24| **D** Homo sapiens chromosome 10 clone RP11-722L1, 7 unordered pieces
 Length=182408

Score = 44.6 bits (48), Expect = 2.1
 Identities = 27/29 (93%), Gaps = 0/29 (0%)
 Strand=Plus/Minus

Query 1410 GTGATTCTAGGAGAGACCATTAATAATTGT 1438
 |||
 Sbjct 123156 GTGATTCTAGGAGAGAACATTAACCTTGT 123128

>gb|AC212617.2| **D** Solanum lycopersicum chromosome 7 clone C07HBa0048I07, *** SEQUENCING
 IN PROGRESS ***, 2 ordered pieces
 Length=120073

Score = 42.8 bits (46), Expect = 7.4
 Identities = 23/23 (100%), Gaps = 0/23 (0%)
 Strand=Plus/Plus

Query 2332 ATTTTCATTTTTAAAAATCACTT 2354
 |||
 Sbjct 91666 ATTTTCATTTTTAAAAATCACTT 91688

>gb|AC202346.13| **D** Medicago truncatula clone mth2-2n5, WORKING DRAFT SEQUENCE, 16
 unordered pieces
 Length=158156

Score = 42.8 bits (46), Expect = 7.4
 Identities = 38/48 (79%), Gaps = 0/48 (0%)
 Strand=Plus/Minus

Query 2326 TGCATTATTTTCATTTTTAAAAATCACTTTCTGAATTTAGTAGCATTT 2373
 |||
 Sbjct 22651 TGAATTTTTTTTATTTTTAAAAATTAATTTTTCAATTTTTTAGAATTT 22604

>emb|CU856640.2| **D** Sus scrofa chromosome 16 clone CH242-178B1, WORKING DRAFT SEQUENCE,
11 unordered pieces
Length=189885

Score = 42.8 bits (46), Expect = 7.4
Identities = 32/35 (91%), Gaps = 2/35 (5%)
Strand=Plus/Plus

```
Query  2329      ATTATTTTCATTTTAAAAATCACTTT-CTGAATT  2362
                |||
Sbjct  135525     ATTATTTTATTTTAAAAAT-ACTTTACTGAATT  135558
```

>emb|CU571340.2| **D** Sus scrofa chromosome 15 clone CH242-146G1, WORKING DRAFT SEQUENCE,
3 unordered pieces
Length=193743

Score = 42.8 bits (46), Expect = 7.4
Identities = 25/26 (96%), Gaps = 0/26 (0%)
Strand=Plus/Minus

```
Query  2331      TATTTTCATTTTAAAAATCACTTTC  2356
                |||
Sbjct  70854      TATTTTCATATTTAAAAATCACTTTC  70829
```

>gb|AC157175.5| **D** Bos taurus clone CH240-67I19, WORKING DRAFT SEQUENCE, 9 unordered
pieces
Length=218719

Score = 42.8 bits (46), Expect = 7.4
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Minus

```
Query  2369      CATTTAATGTGAATAATGTCTATTAATATTT  2399
                |||
Sbjct  207632     CATTTAATGTGCATAAATATCTATCAATATTT  207602
```

>gb|AC159695.3| **D** Bos taurus clone CH240-75I21, WORKING DRAFT SEQUENCE, 10 unordered
pieces
Length=201422

Score = 42.8 bits (46), Expect = 7.4
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Plus

```
Query  2369      CATTTAATGTGAATAATGTCTATTAATATTT  2399
                |||
Sbjct  87697      CATTTAATGTGCATAAATATCTATCAATATTT  87727
```

>gb|AC230602.1| **D** Bos taurus clone CH240-503J12, WORKING DRAFT SEQUENCE, 7 unordered
pieces
Length=258453

Score = 42.8 bits (46), Expect = 7.4
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Plus

```
Query  2319      TTAGTTATGCATTATTTTCATTTTAAAAAT  2349
                |||
Sbjct  102483     TTAGTTATGCATTATATTTATTTCTAAAAAT  102513
```

>emb|CU855986.2| **D** Sus scrofa chromosome 1 clone CH242-171G22, WORKING DRAFT SEQUENCE,
18 unordered pieces
Length=201966

Score = 42.8 bits (46), Expect = 7.4
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Plus

```
Query  2406      ATGTTTGAATTTGAAATCTGAAATCCA  2433
                |||
Sbjct  128613     ATGTTTAAATTTGAAATCTAAAAATCCA  128640
```

>emb|CU914663.1| **D** Sus scrofa chromosome X clone CH242-31B7, WORKING DRAFT SEQUENCE,
18 unordered pieces
Length=216249

Score = 42.8 bits (46), Expect = 7.4

Identities = 38/45 (84%), Gaps = 2/45 (4%)
Strand=Plus/Plus

```
Query 2306 AGTGTGTAAATG-CTT-AGTTATGCATTATTTTCATTTTAAAAA 2348
          |||
Sbjct 89356 AGTGTGTTAATATCTTCAGATATACATTATTTTCAGTTTAAAAA 89400
```

>**gb|AC206313.3** | **D** Zea mays chromosome 6 clone CH201-147G23; ZMMBbc0147G23, ***
SEQUENCING IN PROGRESS ***, 8 unordered pieces
Length=173415

Score = 42.8 bits (46), Expect = 7.4
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Minus

```
Query 1140 AGATCTTTCAAAGATGGGAAACTCAAAT 1167
          |||
Sbjct 21244 AGATCTTTCAAAGATGGGAAATTCCAAT 21217
```

>**dbj|AP010082.1** | **D** Lotus japonicus chromosome 6 clone LjT10I04, *** SEQUENCING IN
PROGRESS ***, 13 unordered pieces
Length=73988

Score = 42.8 bits (46), Expect = 7.4
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Minus

```
Query 2328 CATTATTTTCATTTTAAAAATCACTTT 2355
          |||
Sbjct 12072 CATTATTTTCATTTTAAAAATCACTTT 12045
```

>**emb|CU855706.2** | **D** Sus scrofa chromosome 16 clone CH242-278I11, WORKING DRAFT SEQUENCE,
4 unordered pieces
Length=181261

Score = 42.8 bits (46), Expect = 7.4
Identities = 37/45 (82%), Gaps = 1/45 (2%)
Strand=Plus/Plus

```
Query 2330 TTATTTTCATTTTAAAAATCACTTTCTGAATTTAGTAGCATTTA 2374
          |||
Sbjct 47354 TTATTTT-ATTTTAAAAATTACTAAATGAATTTTGTACATTTA 47397
```

>**emb|CU861549.1** | **D** Sus scrofa chromosome 6 clone CH242-250B15, *** SEQUENCING IN
PROGRESS ***, 23 unordered pieces
Length=171419

Score = 42.8 bits (46), Expect = 7.4
Identities = 38/46 (82%), Gaps = 4/46 (8%)
Strand=Plus/Plus

```
Query 2320 TAGTTATGC-ATTATTTTCATTTTAAAAATCACTTTCTGAATTTA 2364
          |||
Sbjct 46107 TATTTATTCTATTATTTTCATTTTAAAAAT---TTTATGTATTTA 46149
```

>**emb|CU466485.2** | **D** Sus scrofa chromosome 13 clone CH242-441K6, *** SEQUENCING IN
PROGRESS ***, 11 unordered pieces
Length=177014

Score = 42.8 bits (46), Expect = 7.4
Identities = 42/51 (82%), Gaps = 5/51 (9%)
Strand=Plus/Plus

```
Query 2376 TGTGAATAATGTCTATTAATATTTTATAGATGTTTGAATTTGAAATCTG 2426
          |||
Sbjct 154856 TGTGAAAAATATC-ATTGATATTTTATAGATG--TTGCATTT--AATCTG 154901
```

>**gb|AC224991.1** | **D** Bos taurus clone CH240-46H1, WORKING DRAFT SEQUENCE, 43 unordered
pieces
Length=338719

Score = 42.8 bits (46), Expect = 7.4
Identities = 31/36 (86%), Gaps = 0/36 (0%)
Strand=Plus/Minus

```
Query 644 GCTGTTTTTAAAACCAAGTCAAAGCACTCTTCATAA 679
          |||
Sbjct 159369 GCTGCTTTTTAAAACAAAGGCACAGCACTCTTCAAAA 159334
```

>gb|AC224296.1| D Bos taurus clone CH240-490L21, WORKING DRAFT SEQUENCE, 14 unordered pieces
 Length=228044

Score = 42.8 bits (46), Expect = 7.4
 Identities = 28/31 (90%), Gaps = 0/31 (0%)
 Strand=Plus/Minus

```
Query 951      TTCTTCATCAGAAAGGAATTCATTCCTGAGC 981
           |||
Sbjct 165271   TTCTCTTCAGAAAGGAATTCATTCCTGAGC 165241
```

>gb|AC222479.1| D Bos taurus clone CH240-419C20, WORKING DRAFT SEQUENCE, 4 unordered pieces
 Length=192863

Score = 42.8 bits (46), Expect = 7.4
 Identities = 23/23 (100%), Gaps = 0/23 (0%)
 Strand=Plus/Minus

```
Query 2330   TTATTTTCATTTTAAAAATCAC 2352
           |||
Sbjct 84700   TTATTTTCATTTTAAAAATCAC 84678
```

>emb|CU694787.1| D Sus scrofa chromosome 3 clone CH242-274P2, WORKING DRAFT SEQUENCE, 3 unordered pieces
 Length=157162

Score = 42.8 bits (46), Expect = 7.4
 Identities = 35/42 (83%), Gaps = 2/42 (4%)
 Strand=Plus/Minus

```
Query 2318   CTTAGTTATGCATTATTTTCA--TTTTTAAAAATCACTTTCT 2357
           |||
Sbjct 50146   CTTATCTATGCTTCATTTTGAATTTTTTAAAAATCACTTTCT 50105
```

>gb|AC218818.1| D Bos taurus clone CH240-293I7, WORKING DRAFT SEQUENCE, 6 unordered pieces
 Length=206488

Score = 42.8 bits (46), Expect = 7.4
 Identities = 29/33 (87%), Gaps = 0/33 (0%)
 Strand=Plus/Plus

```
Query 2330   TTATTTTCATTTTAAAAATCACTTCTGAATT 2362
           |||
Sbjct 17349   TTGTTTTCATTTTAAAAATACACTTACTGAATT 17381
```

>gb|AC170322.3| D Bos taurus clone CH240-261K11, WORKING DRAFT SEQUENCE, 2 unordered pieces
 Length=164033

Score = 42.8 bits (46), Expect = 7.4
 Identities = 32/38 (84%), Gaps = 0/38 (0%)
 Strand=Plus/Plus

```
Query 2379   GAATAATGCTCTATTAATATTTTTATAGATGTTTGAAT 2416
           |||
Sbjct 87282   GAATCATTTCATTAATATTTTTGTTAATGTTTCAAT 87319
```

>gb|AC167471.4| D Bos taurus clone CH240-211F9, WORKING DRAFT SEQUENCE, 9 unordered pieces
 Length=193147

Score = 42.8 bits (46), Expect = 7.4
 Identities = 35/40 (87%), Gaps = 2/40 (5%)
 Strand=Plus/Plus

```
Query 2312   TAAATGCTTAGTTATGCATTATTTTCATTTTAAAAATCA 2351
           |||
Sbjct 13640   TAGATGCT-AGTTAA-CATTGTTTTCATTTTAAAAATCA 13677
```

>gb|AC168138.3| D Bos taurus clone CH240-203C3, WORKING DRAFT SEQUENCE, 3 unordered pieces
 Length=151004

Score = 42.8 bits (46), Expect = 7.4

Identities = 29/33 (87%), Gaps = 0/33 (0%)
Strand=Plus/Plus

```
Query  2330  TTATTTTCATTTTTTAAAAATCACTTCTGAATT  2362
          |||
Sbjct  98997  TTGTTTTCATTTTTTAAAAATCACTTACTGAATT  99029
```

>gb|AC170145.3| **D** Bos taurus clone CH240-199C24, WORKING DRAFT SEQUENCE, 4 unordered pieces
Length=187450

Score = 42.8 bits (46), Expect = 7.4
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Plus

```
Query  2324  TATGCATTATTTTCATTTTTAAAAATCA  2351
          |||
Sbjct  182759 TATGCCTTACTTTCATTTTTAAAAATCA  182786
```

>gb|AC173095.4| **D** Bos taurus clone CH240-190C23, WORKING DRAFT SEQUENCE, 9 unordered pieces
Length=186609

Score = 42.8 bits (46), Expect = 7.4
Identities = 29/33 (87%), Gaps = 0/33 (0%)
Strand=Plus/Minus

```
Query  1373  ATGGAATGATGAGAGATTATTTCAAAC TGCCAA  1405
          |||
Sbjct  102553 ATGGAATTATTAGATATTATTTCAAATTGCCAA  102521
```

>gb|AC215283.2| **D** Zea mays chromosome 6 clone CH201-163P5; ZMMBbc0163P05, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces
Length=202564

Score = 42.8 bits (46), Expect = 7.4
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Minus

```
Query  1140  AGATCTTTCAAAGATGGGAAACTCAAAT  1167
          |||
Sbjct  186581 AGATCTTTCAAAGATGGGAAATTCCAAT  186554
```

>emb|CU638861.1| **D** Sus scrofa chromosome 6 clone CH242-450D10, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces
Length=144770

Score = 42.8 bits (46), Expect = 7.4
Identities = 38/46 (82%), Gaps = 4/46 (8%)
Strand=Plus/Plus

```
Query  2320  TAGTTATGC-ATTATTTTCATTTTTTAAAAATCACTTCTGAATTTA  2364
          |||
Sbjct  139567 TATTTATTCTATTATTTTCATTTTTTAAAAAT---TTTATGTATTTA  139609
```

>gb|AC215978.2| **D** Felis catus clone RP86-506H22, WORKING DRAFT SEQUENCE, 3 ordered pieces
Length=133423

Score = 42.8 bits (46), Expect = 7.4
Identities = 37/46 (80%), Gaps = 0/46 (0%)
Strand=Plus/Minus

```
Query  2331  TATTTTCATTTTTTAAAAATCACTTCTGAATTTAGTAGCATTTAAT  2376
          |||
Sbjct  50752  TATTTTCATTTTTTAAAAATAAGTTTGCATTTTAGTAAATATAAT  50707
```

>gb|AC206724.2| **D** Macaca mulatta chromosome UNKNOWN clone CH250-78L17, WORKING DRAFT SEQUENCE, 2 unordered pieces
Length=164434

Score = 42.8 bits (46), Expect = 7.4
Identities = 25/26 (96%), Gaps = 0/26 (0%)
Strand=Plus/Minus

```
Query  2330  TTATTTTCATTTTTTAAAAATCACTTT  2355
          |||
Sbjct  120813 TTGTTTTCATTTTTTAAAAATCACTTT  120788
```

>gb|AC183177.2| **D** Bos taurus clone CH240-100C11, WORKING DRAFT SEQUENCE, 4 unordered pieces
Length=183336

Score = 42.8 bits (46), Expect = 7.4
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Minus

```
Query  951  TTCTTCATCAGAAAGGAATTCATTCCCGAGC  981
      |||
Sbjct  6926  TTCCTCTTCAGAAAGGAATTCATTCTGAGC  6896
```

>gb|AC207021.2| **D** Pongo abelii chromosome UNKNOWN clone CH276-258G8, WORKING DRAFT SEQUENCE, 2 unordered pieces
Length=196331

Score = 42.8 bits (46), Expect = 7.4
Identities = 29/33 (87%), Gaps = 0/33 (0%)
Strand=Plus/Plus

```
Query  2338  ATTTTAAAAATCACTTCTGAATTTAGTAGCA  2370
      |||
Sbjct  131638  ATTTTAAAAATCACTTCATGAAATTAATAGCA  131670
```

>emb|CU138566.4| **D** Sus scrofa chromosome 4 clone CH242-25506, WORKING DRAFT SEQUENCE, 2 unordered pieces
Length=165940

Score = 42.8 bits (46), Expect = 7.4
Identities = 29/32 (90%), Gaps = 2/32 (6%)
Strand=Plus/Minus

```
Query  1456  AACATCTCAGCAACTATAATTATGATTTGATC  1487
      |||
Sbjct  28742  AACATCTCA--AACTATAATAATGATTTGATC  28713
```

>gb|AC123293.3| **D** Rattus norvegicus clone CH230-244N8, WORKING DRAFT SEQUENCE, 4 unordered pieces
Length=211699

Score = 42.8 bits (46), Expect = 7.4
Identities = 27/30 (90%), Gaps = 0/30 (0%)
Strand=Plus/Plus

```
Query  1097  TTCTCATGTATATGGAAAGGACAGAGRTTC  1126
      |||
Sbjct  99411  TTTTCATTTATATGGAAAGGACAGAGGTTTC  99440
```

>gb|AC165198.2| **D** Oryctolagus cuniculus clone LB1-129M6, WORKING DRAFT SEQUENCE, 3 ordered pieces
Length=188194

Score = 42.8 bits (46), Expect = 7.4
Identities = 33/38 (86%), Gaps = 1/38 (2%)
Strand=Plus/Plus

```
Query  2387  TCTATTAATATTTTTATAGATGTTTG-AAATTTGAAAT  2423
      |||
Sbjct  118467  TCTATTAGTATTTTTATAGGTGTTCTGTAATTTGTAAT  118504
```

>gb|AC009667.3| **D** Homo sapiens chromosome 1 clone RP11-8L2 map 1, LOW-PASS SEQUENCE SAMPLING
Length=191683

Score = 42.8 bits (46), Expect = 7.4
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Minus

```
Query  2407  TGTTTTGAATTTGAAATCTGAAATCCAGTAT  2437
      |||
Sbjct  10304  TGTTTTGAATTTGAAATCTGATGTCCAGAAT  10274
```

>emb|CR388142.3| **D** Danio rerio chromosome 7 clone DKEY-250G10, WORKING DRAFT SEQUENCE, 5 unordered pieces
Length=206358

Score = 42.8 bits (46), Expect = 7.4

Identities = 34/41 (82%), Gaps = 0/41 (0%)
 Strand=Plus/Minus

```
Query 2371 TTTAATGTGAATAATGTCTATTAATATTTTTATAGATGTTT 2411
          |||
Sbjct 36431 TTTAATGTGAATTTTATTTATTTATATTTTTATTGGTGTTT 36391
```

>emb|CR853283.3| **D** Danio rerio clone DKEY-152K11, *** SEQUENCING IN PROGRESS ***,
 14 unordered pieces
 Length=227725

Score = 42.8 bits (46), Expect = 7.4
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

```
Query 2385 TGTCATTAATATTTTTATAGATGTTT 2412
          |||
Sbjct 48067 TGACTATTCATATTTTTATAGATGTTT 48094
```

>emb|BX629351.9| **D** Danio rerio clone DKEY-63B7, WORKING DRAFT SEQUENCE, 8 unordered
 pieces
 Length=203963

Score = 42.8 bits (46), Expect = 7.4
 Identities = 36/44 (81%), Gaps = 3/44 (6%)
 Strand=Plus/Minus

```
Query 2352 CTTTCTGAATTTAGTAGCATTTAATGTGAATAATGTCTATTAAT 2395
          |||
Sbjct 98277 CTTTCTG---TTAGTAGCATTTTATGTGAGTATTGTCTCTTTAT 98237
```

>gb|AC068550.3|AC068550 **D** Homo sapiens chromosome 17 clone RP11-659P18, WORKING DRAFT SEQUENCE,
 7 unordered pieces
 Length=188167

Score = 42.8 bits (46), Expect = 7.4
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

```
Query 2396 ATTTTATAGATGTTTGAATTTGAAAT 2423
          |||
Sbjct 78902 ATATTTATAGATGATTTGAATTTGAAAT 78929
```

>gb|AC005505.8|AC005505 **D** Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING
 IN PROGRESS ***
 Length=192929

Score = 42.8 bits (46), Expect = 7.4
 Identities = 29/33 (87%), Gaps = 0/33 (0%)
 Strand=Plus/Minus

```
Query 2325 ATGCATTATTTTCATTTTTAAAAATCACTTTCT 2357
          |||
Sbjct 142965 ATTCATTATTTTCATTTTTAAGATCACTATCT 142933
```

>emb|CR352214.5| **D** Danio rerio clone CH211-256D24, 16 unordered pieces
 Length=163645

Score = 42.8 bits (46), Expect = 7.4
 Identities = 28/30 (93%), Gaps = 1/30 (3%)
 Strand=Plus/Plus

```
Query 420 TAAAAGTACCGATACAGTACATTTAAAATGT 449
          |||
Sbjct 113114 TAAAAGTACCGATACAGTAC-TAAAATGT 113142
```

>gb|AC024477.1|AC024477 **D** Homo sapiens chromosome X clone RP11-770015 map X, LOW-PASS SEQUENCE
 SAMPLING
 Length=56085

Score = 42.8 bits (46), Expect = 7.4
 Identities = 25/26 (96%), Gaps = 0/26 (0%)
 Strand=Plus/Plus

```
Query 2335 TTCATTTTTAAAAATCACTTTCTGAA 2360
          |||
Sbjct 49403 TTCATTTTTAAAAATCACTTGCTGAA 49428
```


>gb|AC024976.1|AC024976 **D** Homo sapiens chromosome 4 clone RP11-620N17 map 4, LOW-PASS SEQUENCE SAMPLING
Length=79048

Score = 42.8 bits (46), Expect = 7.4
Identities = 25/26 (96%), Gaps = 0/26 (0%)
Strand=Plus/Minus

Query 2410 TTTGAATTTGAAATCTGAAATCCAGT 2435
Sbjct 40221 TTTGAATTTGAAATCTGAAATCCAGT 40196

>gb|AC021112.3|AC021112 **D** Homo sapiens chromosome UL clone RP11-256B9, WORKING DRAFT SEQUENCE, 31 unordered pieces
Length=178053

Score = 42.8 bits (46), Expect = 7.4
Identities = 38/47 (80%), Gaps = 3/47 (6%)
Strand=Plus/Minus

Query 2376 TGTGAATAATGTCTATTAATATTTTATAG---ATGTTTGAATTTG 2419
Sbjct 110589 TGTGAATAATGTCTTTTATGATATTTTGAAAGAGAATGTGTTGAATATG 110543

>gb|AC068005.2|AC068005 **D** Homo sapiens chromosome 6 clone RP11-704J17 map 6, WORKING DRAFT SEQUENCE, 12 unordered pieces
Length=158554

Score = 42.8 bits (46), Expect = 7.4
Identities = 44/55 (80%), Gaps = 2/55 (3%)
Strand=Plus/Minus

Query 1428 ATTAAAATT-GTTATAGAGGACTATGTAAAACATCTCAGCAACTATAATTATGAT 1481
Sbjct 103756 ATTAAACTTAGTTATAGAGGATTCCTTTTAAACATCTCATGACCTTTAA-TATGAT 103703

>gb|AC025122.3|AC025122 **D** Homo sapiens chromosome 1 clone RP11-184G21 map 1, WORKING DRAFT SEQUENCE, 22 unordered pieces
Length=188921

Score = 42.8 bits (46), Expect = 7.4
Identities = 39/48 (81%), Gaps = 1/48 (2%)
Strand=Plus/Plus

Query 2320 TAGTTATGCATTATTTTCATTTTTAAAAATCACTTTCTGAATTTAGTA 2367
Sbjct 92752 TATTTATGC-TTATTTTAATTATTTCAGAAATTCCTTTTGTGAATTTAGTA 92798

>gb|AC135884.2| **D** Rattus norvegicus clone CH230-176C2, *** SEQUENCING IN PROGRESS
***, 4 unordered pieces
Length=224948

Score = 42.8 bits (46), Expect = 7.4
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Minus

Query 2329 ATTATTTTCATTTTTAAAAATCACTTTCTGA 2359
Sbjct 207688 ATTGTTTTAATTTTTAAAAATTACTTTCTGA 207658

>gb|AC020814.2|AC020814 **D** Mus musculus clone RG-MBAC_270F3, LOW-PASS SEQUENCE SAMPLING
Length=28446

Score = 42.8 bits (46), Expect = 7.4
Identities = 32/38 (84%), Gaps = 0/38 (0%)
Strand=Plus/Plus

Query 1012 TTGCTCAGCACTTCACTCACATGTTCTTCAAGACTGAC 1049
Sbjct 711 TTGCTCAGCACTTCACTCACCGCACGCTTTCACGACCGAC 748

>gb|AC137201.1| **D** Rattus norvegicus clone CH230-unknown, *** SEQUENCING IN PROGRESS

Length=223300

Score = 42.8 bits (46), Expect = 7.4
Identities = 34/40 (85%), Gaps = 1/40 (2%)
Strand=Plus/Plus

```

Query 2380  AATAATGTCTATTAATATTTT-TATAGATGTTTGAATTT 2418
           |||
Sbjct 67763  AATAATGTCTATCAATATTTTATATATAATTTTAAATTT 67802
           |||

```

>gb|AC007933.1|AC007933 **D** Homo sapiens chromosome 17 clone hRPC.908_O_12 map 17, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces
Length=152224

Score = 42.8 bits (46), Expect = 7.4
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Minus

```

Query 2396  ATTTTTATAGATGTTTGAATTTGAAAT 2423
           |||
Sbjct 11768  ATATTTATAGATGATTTGAATTTGAAAT 11741
           |||

```

>gb|AC005139.3|AC005139 **D** Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces
Length=256172

Score = 42.8 bits (46), Expect = 7.4
Identities = 29/33 (87%), Gaps = 0/33 (0%)
Strand=Plus/Plus

```

Query 2325  ATGCATTATTTTCATTTTAAAAATCACTTTCT 2357
           |||
Sbjct 81846  ATTCATTATTTTCATTTTAAAGATCACTATCT 81878
           |||

```

>gb|AC096075.5| **D** Rattus norvegicus clone CH230-33H17, *** SEQUENCING IN PROGRESS ***,
Length=256241

Score = 42.8 bits (46), Expect = 7.4
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Minus

```

Query 2330  TTATTTTCATTTTAAAAATCACTTTCT 2357
           |||
Sbjct 127078  TTATTTTATTTTAAAAATCACTATCT 127051
           |||

```

>dbj|AP004555.1| **D** Oryza sativa Japonica Group chromosome 8 clone P0017F04, *** SEQUENCING IN PROGRESS ***,
Length=146207

Score = 42.8 bits (46), Expect = 7.4
Identities = 32/38 (84%), Gaps = 0/38 (0%)
Strand=Plus/Plus

```

Query 2328  CATTATTTTCATTTTAAAAATCACTTCTGAATTTAG 2365
           |||
Sbjct 26982  CATTATTTTCATTTTAAAAATCTATCTACGAATTTAG 27019
           |||

```

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