These are the search results with the CS63win sewquence in the Claw_original_PCR file:

Database	Best score	Best matching sequence
EST (expressed sequence tags)	462	AV715471 DCB Homo sapiens cDNA clone DCBBNF04 5'
GSS (genome survey sequence)	350	CH230-23J3.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
HTGS (high throughput genomic)	808	Homo sapiens chromosome 13 clone RP11-85C8
Human genomic	721	Homo sapiens chromosome 4, complete sequence
Other genomic	460	Homo sapiens mitochondrion, complete genome
Mitochondrial	460	Gorilla gorilla mitochondrion, complete genome
Non-redundant proteins	88	similar to ATP synthase 6 [Homo sapiens]
Non-redundant nucleotides	564	Human germline T-cell receptor beta chain (the particular sequence matches a mitochondrial insert
PDB (protein databank)	527	Homo sapiens chromosome 5 clone CTC-203K17, complete sequence
SNP (single nucleotide polymorphism)	738	gnl|dbSNP|ss6879113
STS (sequence tagged sites)	200	Xq4124 KWOK Homo sapiens STS genomic, sequence tagged site
WGS (whole genome shotgun sequencing)	419	Mus musculus whole genome shotgun assembly contig 116023

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

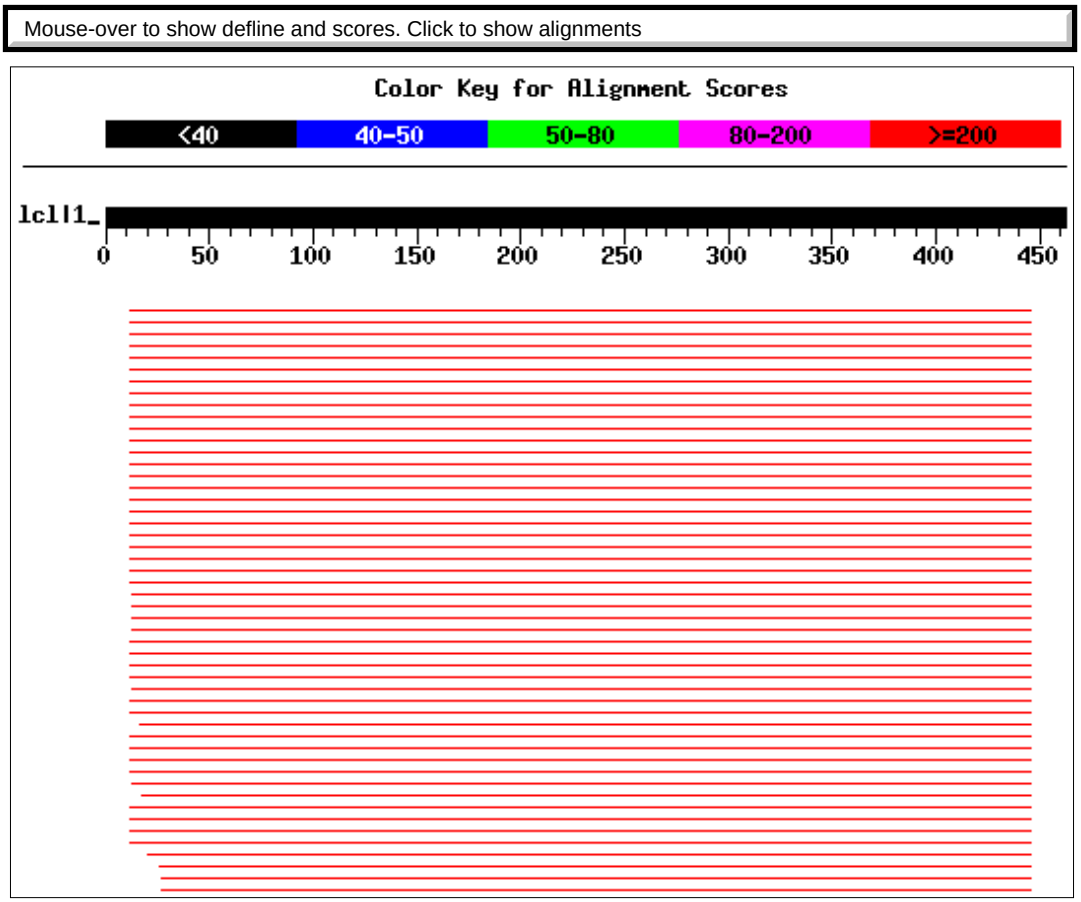
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions
16,228,583 sequences; 8,136,396,407 total letters

Query= CS63win
(462 letters)

Distribution of 101 Blast Hits on the Query Sequence



Sequences producing significant alignments: Score (bits) E Value

dbj|AV715471.1|AV715471	AV715471 DCB Homo sapiens cDNA clon...	462	e-127
gb|BM759852.1|BM759852	K-EST0040167 S5SNU484 Homo sapiens c...	460	e-126
dbj|AV734539.1|AV734539	AV734539 cdA Homo sapiens cDNA clon...	460	e-126
dbj|AV717499.1|AV717499	AV717499 DCB Homo sapiens cDNA clon...	460	e-126
dbj|AV717058.1|AV717058	AV717058 DCB Homo sapiens cDNA clon...	460	e-126
dbj|AV715951.1|AV715951	AV715951 DCB Homo sapiens cDNA clon...	460	e-126
gb|BE875083.1|BE875083	601485953F1 NIH_MGC_69 Homo sapiens ...	460	e-126
gb|BE439860.1|BE439860	HTM1-442F HTM1 Homo sapiens cDNA.	460	e-126
gb|BE184973.1|BE184973	MR1-HT0707-100500-002-h07 HT0707 Hom...	460	e-126
gb|BE184958.1|BE184958	MR1-HT0707-100500-002-c03 HT0707 Hom...	460	e-126
gb|BE184903.1|BE184903	MR1-HT0707-100500-001-h05 HT0707 Hom...	460	e-126
gb|BE184902.1|BE184902	MR1-HT0707-100500-001-g10 HT0707 Hom...	460	e-126
gb|BE184899.1|BE184899	MR1-HT0707-100500-001-f04 HT0707 Hom...	460	e-126
gb|BE184896.1|BE184896	MR1-HT0707-100500-001-d12 HT0707 Hom...	460	e-126
gb|BE184892.1|BE184892	MR1-HT0707-100500-001-c11 HT0707 Hom...	460	e-126
gb|BE184885.1|BE184885	MR1-HT0707-100500-001-b02 HT0707 Hom...	460	e-126
gb|BE171576.1|BE171576	RC5-HT0547-130300-031-C08 HT0547 Hom...	460	e-126
dbj|AV757771.1|AV757771	AV757771 BM Homo sapiens cDNA clone...	456	e-125
dbj|AV756329.1|AV756329	AV756329 BM Homo sapiens cDNA clone...	456	e-125
dbj|AV729085.1|AV729085	AV729085 HTC Homo sapiens cDNA clon...	456	e-125
dbj|AV717147.1|AV717147	AV717147 DCB Homo sapiens cDNA clon...	456	e-125
dbj|AV759622.1|AV759622	AV759622 MDS Homo sapiens cDNA clon...	454	e-125
dbj|AV717161.1|AV717161	AV717161 DCB Homo sapiens cDNA clon...	454	e-125
dbj|AV716623.1|AV716623	AV716623 DCB Homo sapiens cDNA clon...	454	e-125
dbj|AV714620.1|AV714620	AV714620 DCB Homo sapiens cDNA clon...	454	e-125
dbj|AV707620.1|AV707620	AV707620 ADB Homo sapiens cDNA clon...	454	e-125
dbj|AV706276.1|AV706276	AV706276 ADB Homo sapiens cDNA clon...	454	e-125
gb|BE184971.1|BE184971	MR1-HT0707-100500-002-g08 HT0707 Hom...	454	e-125
dbj|AV760712.1|AV760712	AV760712 MDS Homo sapiens cDNA clon...	450	e-124
dbj|AV756248.1|AV756248	AV756248 BM Homo sapiens cDNA clone...	450	e-124
dbj|AV689611.1|AV689611	AV689611 GKC Homo sapiens cDNA clon...	448	e-123
gb|BE184900.1|BE184900	MR1-HT0707-100500-001-f09 HT0707 Hom...	448	e-123
gb|BE171482.1|BE171482	RC5-HT0547-130300-031-B03 HT0547 Hom...	448	e-123
gb|AA808966.1|AA808966	nw16h12.s1 NCI_CGAP_GCB0 Homo sapien...	446	e-122
dbj|AV735162.1|AV735162	AV735162 cdA Homo sapiens cDNA clon...	444	e-122
gb|BE175368.1|BE175368	RC4-HT0578-090300-011-e10 HT0578 Hom...	444	e-122
dbj|AV716721.1|AV716721	AV716721 DCB Homo sapiens cDNA clon...	442	e-121
dbj|AV714571.1|AV714571	AV714571 DCB Homo sapiens cDNA clon...	442	e-121
dbj|AV708821.1|AV708821	AV708821 ADC Homo sapiens cDNA clon...	442	e-121
gb|BE184961.1|BE184961	MR1-HT0707-100500-002-c07 HT0707 Hom...	442	e-121
gb|BE184959.1|BE184959	MR1-HT0707-100500-002-c05 HT0707 Hom...	442	e-121
gb|BE184897.1|BE184897	MR1-HT0707-100500-001-e06 HT0707 Hom...	442	e-121
gb|BE184952.1|BE184952	MR1-HT0707-100500-002-a06 HT0707 Hom...	440	e-121
gb|BE184940.1|BE184940	MR1-HT0707-100500-002-f08 HT0707 Hom...	435	e-119
gb|BE184922.1|BE184922	MR1-HT0707-100500-002-b08 HT0707 Hom...	435	e-119
dbj|AV756962.1|AV756962	AV756962 BM Homo sapiens cDNA clone...	433	e-118
gb|BE184955.1|BE184955	MR1-HT0707-100500-002-b06 HT0707 Hom...	433	e-118
gb|AW264289.1|AW264289	xq97g05.x1 NCI_CGAP_Brn53 Homo sapie...	433	e-118
gb|BM841018.1|BM841018	K-EST0118186 S12SNU216 Homo sapiens ...	431	e-118
gb|BM833760.1|BM833760	K-EST0108602 S11SNU1 Homo sapiens cD...	431	e-118
dbj|AV762492.1|AV762492	AV762492 MDS Homo sapiens cDNA clon...	429	e-117
dbj|AV703400.1|AV703400	AV703400 ADB Homo sapiens cDNA clon...	429	e-117
gb|BE184893.1|BE184893	MR1-HT0707-100500-001-d04 HT0707 Hom...	429	e-117
dbj|AV682100.1|AV682100	AV682100 GKB Homo sapiens cDNA clon...	427	e-117
gb|BE184956.1|BE184956	MR1-HT0707-100500-002-b09 HT0707 Hom...	425	e-116

gb|BE184969.1|BE184969	MR1-HT0707-100500-002-f10 HT0707 Hom...	423	e-115
dbj|AV727170.1|AV727170	AV727170 HTC Homo sapiens cDNA clon...	421	e-115
gb|AA196042.1|AA196042	zp95a08.s1 Stratagene muscle 937209 ...	421	e-115
dbj|AV726884.1|AV726884	AV726884 HTC Homo sapiens cDNA clon...	419	e-114
dbj|AV716719.1|AV716719	AV716719 DCB Homo sapiens cDNA clon...	419	e-114
gb|BE887240.1|BE887240	601508552F1 NIH_MGC_71 Homo sapiens ...	419	e-114
gb|BE816626.1|BE816626	RC5-BN0232-190500-031-C11 BN0232 Hom...	419	e-114
gb|BE816625.1|BE816625	RC5-BN0232-190500-031-B08 BN0232 Hom...	419	e-114
gb|BE816624.1|BE816624	RC5-BN0232-190500-031-B06 BN0232 Hom...	419	e-114
gb|BE816628.1|BE816628	RC5-BN0232-190500-031-D07 BN0232 Hom...	415	e-113
gb|BF349023.1|BF349023	QV1-DT0071-090200-061-h11 DT0071 Hom...	414	e-113
gb|BE816636.1|BE816636	RC5-BN0232-190500-031-E10 BN0232 Hom...	414	e-113
gb|AW058245.1|AW058245	wx17f07.x1 NCI_CGAP_Gas4 Homo sapien...	412	e-112
gb|BQ581898.1|BQ581898	il10e04.y1 Human insulinoma Homo sap...	410	e-111
dbj|AV753688.1|AV753688	AV753688 TP Homo sapiens cDNA clone...	410	e-111
gb|BE184967.1|BE184967	MR1-HT0707-100500-002-f07 HT0707 Hom...	410	e-111
gb|BF360707.1|BF360707	MR2-OT0049-280300-101-a06 OT0049 Hom...	408	e-111
gb|AA564684.1|AA564684	nj22f06.s1 NCI_CGAP_AA1 Homo sapiens...	406	e-110
gb|BQ581572.1|BQ581572	il10e04.x1 Human insulinoma Homo sap...	404	e-110
dbj|AV757778.1|AV757778	AV757778 BM Homo sapiens cDNA clone...	404	e-110
gb|BE825382.1|BE825382	PM0-EN0004-180500-008-g04 EN0004 Hom...	404	e-110
gb|BF331634.1|BF331634	CM3-BT0612-180200-098-d11 BT0612 Hom...	402	e-109
gb|BE182691.1|BE182691	RC3-HT0649-100500-022-c05 HT0649 Hom...	402	e-109
gb|BM834106.1|BM834106	K-EST0108980 S11SNU1 Homo sapiens cD...	400	e-109
dbj|AV735018.1|AV735018	AV735018 cdA Homo sapiens cDNA clon...	400	e-109
dbj|AV715329.1|AV715329	AV715329 DCB Homo sapiens cDNA clon...	400	e-109
gb|BE179343.1|BE179343	RC1-HT0615-200400-022-c10 HT0615 Hom...	400	e-109
gb|BE161661.1|BE161661	MR3-HT0446-260300-202-a06 HT0446 Hom...	400	e-109
gb|BU198205.1|BU198205	DCBCND07 DCB Homo sapiens cDNA.	398	e-108
dbj|AV715724.1|AV715724	AV715724 DCB Homo sapiens cDNA clon...	398	e-108
dbj|AV714200.1|AV714200	AV714200 DCB Homo sapiens cDNA clon...	398	e-108
dbj|AV714097.1|AV714097	AV714097 DCB Homo sapiens cDNA clon...	398	e-108
gb|BF332144.1|BF332144	CM2-BT0664-240200-103-e02 BT0664 Hom...	394	e-107
gb|BE926838.1|BE926838	QV0-BT0676-180800-351-h04 BT0676 Hom...	394	e-107
gb|AA491968.1|AA491968	ng52e05.s1 NCI_CGAP_Li2 Homo sapiens...	394	e-107
gb|BM836690.1|BM836690	K-EST0112550 S9SNU601 Homo sapiens c...	392	e-106
gb|BF332316.1|BF332316	QV2-BT0682-260400-171-g05 BT0682 Hom...	392	e-106
gb|BF331526.1|BF331526	MR1-BT0549-240300-002-g10 BT0549 Hom...	392	e-106
dbj|AV764318.1|AV764318	AV764318 MDS Homo sapiens cDNA clon...	392	e-106
dbj|AV764284.1|AV764284	AV764284 MDS Homo sapiens cDNA clon...	392	e-106
dbj|AV758014.1|AV758014	AV758014 BM Homo sapiens cDNA clone...	392	e-106
dbj|AV756842.1|AV756842	AV756842 BM Homo sapiens cDNA clone...	392	e-106
dbj|AV756802.1|AV756802	AV756802 BM Homo sapiens cDNA clone...	392	e-106
dbj|AV756610.1|AV756610	AV756610 BM Homo sapiens cDNA clone...	392	e-106
dbj|AV756468.1|AV756468	AV756468 BM Homo sapiens cDNA clone...	392	e-106

>dbj|AV715471.1|AV715471 AV715471 DCB Homo sapiens cDNA clone DCBBNF04 5'.
Length = 639

Score = 462 bits (240), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

Query: 446 CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA 387

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Sbjct:  88   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  147

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  148  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCAGTGCTTC  207

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  208  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  267

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  268  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  327

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  328  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  387

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  388  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  443

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  444  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  503

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  504  ACCGNCCGTCACCCTC  519
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>gb|BM759852.1|BM759852 K-EST0040167 S5SNU484 Homo sapiens cDNA clone S5SNU484-22-G08 5'.

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          Length = 555

 Score =  460 bits (239), Expect = e-126
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  101  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  160

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  161  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  220

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  221  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  280

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  281  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  340

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  341  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  400

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  401  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  456

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  457  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  516

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  517  ACCGCCCGTCACCCTC  532
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>dbj|AV734539.1|AV734539 AV734539 cdA Homo sapiens cDNA clone cdAANF03 5'.

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          Length = 651

 Score =  460 bits (239), Expect = e-126
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 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  60   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  119

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  120  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  179

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  180  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  239

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  240  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  299

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  300  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  359

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  360  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  415

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  416  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  475

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  476  ACCGCCCGTCACCCTC  491
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>dbj|AV717499.1|AV717499 AV717499 DCB Homo sapiens cDNA clone DCBBAD02 5'.
          Length = 706

 Score =  460 bits (239), Expect = e-126
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  24   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  83

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  84   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  143

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  144  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  203

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  204  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  263

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  264  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  323

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  324  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  379

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  380  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  439

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  440  ACCGCCCGTCACCCTC  455
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>dbj|AV717058.1|AV717058 AV717058 DCB Homo sapiens cDNA clone DCBCEG02 5'.
Length = 606

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

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Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  146  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  205

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  206  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  265

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  266  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  325

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  326  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  385

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  386  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  445

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  446  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  501

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  502  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  561

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  562  ACCGCCCGTCACCCTC  577
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>dbj|AV715951.1|AV715951 AV715951 DCB Homo sapiens cDNA clone DCBCAD10 5'.
Length = 606

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

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Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  146  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  205

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  206  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  265

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  266  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  325

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  326  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  385

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  386  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  445

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  446  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  501

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  502  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  561
```

```
Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  562  ACCGCCCGTCACCCTC  577
```

>gb|BE875083.1|BE875083 601485953F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888469 5'.

Length = 569

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  81   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  140

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  141  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  200

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  201  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  260

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  261  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  320

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  321  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  380

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  381  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  436

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  437  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  496

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  497  ACCGCCCGTCACCCTC  512
```

>gb|BE439860.1|BE439860 HTM1-442F HTM1 Homo sapiens cDNA.

Length = 518

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  65   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  124

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  125  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  184

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  185  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  244

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  245  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  304

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  305  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  364
```

```
Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  365  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  420

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  421  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  480

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  481  ACCGCCCGTCACCCTC  496
```

>gb|BE184973.1|BE184973 MR1-HT0707-100500-002-h07 HT0707 Homo sapiens cDNA.
Length = 692

```
 Score =  460 bits (239), Expect = e-126
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  170  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  229

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  230  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  289

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  290  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  349

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  350  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  409

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  410  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  469

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  470  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  525

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  526  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  585

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  586  ACCGCCCGTCACCCTC  601
```

>gb|BE184958.1|BE184958 MR1-HT0707-100500-002-c03 HT0707 Homo sapiens cDNA.
Length = 653

```
 Score =  460 bits (239), Expect = e-126
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  154  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  213

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  214  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  273

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  274  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  333

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
```

```
Sbjct:  334  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  393

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  394  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  453

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  454  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  509

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  510  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  569

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  570  ACCGCCCGTCACCCTC  585
```

>gb|BE184903.1|BE184903 MR1-HT0707-100500-001-h05 HT0707 Homo sapiens cDNA.

Length = 673

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  143  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  202

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  203  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  262

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  263  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  322

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  323  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  382

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  383  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  442

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  443  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  498

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  499  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  558

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  559  ACCGCCCGTCACCCTC  574
```

>gb|BE184902.1|BE184902 MR1-HT0707-100500-001-g10 HT0707 Homo sapiens cDNA.

Length = 663

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  138  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  197

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  198  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  257
```

```
Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  258  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  317

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  318  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  377

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  378  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  437

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  438  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  493

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  494  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  553

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  554  ACCGCCCGTCACCCTC  569
```

>gb|BE184899.1|BE184899 MR1-HT0707-100500-001-f04 HT0707 Homo sapiens cDNA.

Length = 664

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  145  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  204

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  205  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  264

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  265  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  324

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  325  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  384

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  385  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  444

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  445  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  500

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  501  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  560

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  561  ACCGCCCGTCACCCTC  576
```

>gb|BE184896.1|BE184896 MR1-HT0707-100500-001-d12 HT0707 Homo sapiens cDNA.

Length = 615

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
```

```
Sbjct:  156  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  215

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  216  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  275

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  276  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  335

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  336  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  395

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  396  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  455

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  456  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  511

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  512  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  571

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  572  ACCGCCCGTCACCCTC  587
```

>gb|BE184892.1|BE184892 MR1-HT0707-100500-001-c11 HT0707 Homo sapiens cDNA.
Length = 613

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  147  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  206

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  207  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  266

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  267  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  326

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  327  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  386

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  387  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  446

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  447  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  502

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  503  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  562

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  563  ACCGCCCGTCACCCTC  578
```

>gb|BE184885.1|BE184885 MR1-HT0707-100500-001-b02 HT0707 Homo sapiens cDNA.
Length = 702

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)

Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  145  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  204

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  205  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  264

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  265  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  324

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  325  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  384

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  385  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  444

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  445  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  500

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  501  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  560

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  561  ACCGCCCGTCACCCTC  576
```

>gb|BE171576.1|BE171576 RC5-HT0547-130300-031-C08 HT0547 Homo sapiens cDNA.
Length = 536

Score = 460 bits (239), Expect = e-126
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  63   GAGGGTGACGGGCGGTGTGTACGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACTCTC  122

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  123  AGTTTACTGCTAAATCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGT---AGTTTT  179

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  180  CTGGG-GTAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  238

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGAG  250
Sbjct:  239  TCTTTACGTGGGTACTTGCGCTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCG  298

Query:  251  GTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGC  310
Sbjct:  299  GTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGC  358

Query:  311  TCCTTTAGAGGGATATAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGT  370
Sbjct:  359  TCCTCTAGAGGGATATGAAGCACCGCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAGT  418

Query:  371  GTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGT  430
Sbjct:  419  GTTCTGGCGAGCAGTTTTGTTGATTTAACTGTTGAGGTTTAGGGCTAAGCATAGTGGGGT  478

Query:  431  ATCTAATCCCAGTTTG  446
Sbjct:  479  ATCTAATCCCAGTTTG  494
```

>dbj|AV757771.1|AV757771 AV757771 BM Homo sapiens cDNA clone BMFAOG01 5'.

Length = 863

Score = 456 bits (237), Expect = e-125
Identities = 377/437 (86%), Gaps = 7/437 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  103  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  162

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  163  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  222

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  223  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  282

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG--GAAAGGCCACAGAGTAAGCAG  209
Sbjct:  283  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCTACAAAGTAAGCGC  342

Query:  208  AAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-T  150
Sbjct:  343  AAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCT  402

Query:  149  ACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGA  90
Sbjct:  403  ACATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGT  458

Query:  89   GGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACA  30
Sbjct:  459  GGATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACA  518

Query:  29   CACCGCCCGTCACCCTC  13
Sbjct:  519  CACCGCCCGTCACCCTC  535
```

>dbj|AV756329.1|AV756329 AV756329 BM Homo sapiens cDNA clone BMFBHA01 5'.

Length = 833

Score = 456 bits (237), Expect = e-125
Identities = 376/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  136  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  195

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  196  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  255

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  256  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  315

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  316  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  375

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  376  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  435

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  436  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  491

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  492  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  551
```

```
Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  552  ACCGNCCGTCACCCTC  567
```

>dbj|AV729085.1|AV729085 AV729085 HTC Homo sapiens cDNA clone HTCAEE04 5'.
Length = 667

Score = 456 bits (237), Expect = e-125
Identities = 376/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  62   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  121

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  122  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  181

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  182  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  241

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  242  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  301

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  302  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  361

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  362  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  417

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  418  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  477

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  478  ACCGNCCGTCACCCTC  493
```

>dbj|AV717147.1|AV717147 AV717147 DCB Homo sapiens cDNA clone DCBBEB11 5'.
Length = 687

Score = 456 bits (237), Expect = e-125
Identities = 378/436 (86%), Gaps = 5/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  35   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  94

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  95   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  154

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  155  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  214

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  215  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  274

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  275  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAGTGGGCTA  334

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  335  CATTTTCTAC-CCCAGAAAAA-CT-ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  391
```

```
Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  392  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  451

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  452  ACCGCCCGTCACCCTC  467
```

>dbj|AV759622.1|AV759622 AV759622 MDS Homo sapiens cDNA clone MDSBZF11 5'.
Length = 1264

Score = 454 bits (236), Expect = e-125
Identities = 376/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  86   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  145

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  146  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  205

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  206  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  265

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  266  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  325

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  326  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  385

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  386  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  441

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  442  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  501

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  502  ACCGGCCGTCACCCTC  517
```

>dbj|AV717161.1|AV717161 AV717161 DCB Homo sapiens cDNA clone DCBAYH02 5'.
Length = 767

Score = 454 bits (236), Expect = e-125
Identities = 375/435 (86%), Gaps = 6/435 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  233  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  292

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  293  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  352

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  353  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  412

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  413  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  472
```

```
Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  473  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  532

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  533  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  588

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  589  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  648

Query:  28   ACCGCCCGTCACCCT  14
Sbjct:  649  ACCGCCNGTCACCCT  663
```

>dbj|AV716623.1|AV716623 AV716623 DCB Homo sapiens cDNA clone DCBBCH01 5'.
Length = 736

Score = 454 bits (236), Expect = e-125
Identities = 375/435 (86%), Gaps = 6/435 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  194  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  253

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  254  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  313

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  314  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  373

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  374  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  433

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  434  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  493

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  494  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  549

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  550  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  609

Query:  28   ACCGCCCGTCACCCT  14
Sbjct:  610  ACCGNCCGTCACCCT  624
```

>dbj|AV714620.1|AV714620 AV714620 DCB Homo sapiens cDNA clone DCBBYE10 5'.
Length = 534

Score = 454 bits (236), Expect = e-125
Identities = 376/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  17   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  76

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  77   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGGGCTTC  136

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  137  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  196
```

```
Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  197  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  256

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  257  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  316

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  317  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  372

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  373  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  432

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  433  ACCGCCCGTCACCCTC  448
```

>dbj|AV707620.1|AV707620 AV707620 ADB Homo sapiens cDNA clone ADBAJA12 5'.

Length = 584

Score = 454 bits (236), Expect = e-125
Identities = 375/435 (86%), Gaps = 6/435 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  100  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  159

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  160  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  219

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  220  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  279

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  280  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  339

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  340  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  399

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  400  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  455

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  456  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  515

Query:  28   ACCGCCCGTCACCCT  14
Sbjct:  516  ACCGNCCGTCACCCT  530
```

>dbj|AV706276.1|AV706276 AV706276 ADB Homo sapiens cDNA clone ADBCBD10 5'.

Length = 718

Score = 454 bits (236), Expect = e-125
Identities = 375/435 (86%), Gaps = 6/435 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  74   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  133
```

```
Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  134  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  193

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  194  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  253

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  254  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  313

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  314  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  373

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  374  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  429

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  430  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  489

Query:  28   ACCGCCCGTCACCCT  14
Sbjct:  490  ACCGNCCGTCACCCT  504
```

>gb|BE184971.1|BE184971 MR1-HT0707-100500-002-g08 HT0707 Homo sapiens cDNA.

Length = 638

Score = 454 bits (236), Expect = e-125
Identities = 376/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  156  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  215

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  216  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  275

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  276  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  335

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  336  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  395

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  396  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  455

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  456  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  511

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  512  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  571

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  572  ACCGGCCGTCACCCTC  587
```

>dbj|AV760712.1|AV760712 AV760712 MDS Homo sapiens cDNA clone MDSBMF01 5'.

Length = 567

Score = 450 bits (234), Expect = e-124
Identities = 375/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  65   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  124

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  125  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  184

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  185  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCCCT  244

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  245  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  304

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  305  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  364

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  365  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  420

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  421  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  480

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  481  ACCGNCCGTCACCCTC  496
```

>dbj|AV756248.1|AV756248 AV756248 BM Homo sapiens cDNA clone BMFAFG08 5'.

Length = 753

Score = 450 bits (234), Expect = e-124
Identities = 375/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  172  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  231

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  232  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTCC  291

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  292  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  351

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  352  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  411

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  412  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  471

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  472  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  527

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  528  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  587

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  588  ACCGNCCGTCACCCTC  603
```

>dbj|AV689611.1|AV689611 AV689611 GKC Homo sapiens cDNA clone GKCCLG08 5'.

Length = 681

```
 Score =  448 bits (233), Expect = e-123
 Identities = 374/435 (85%), Gaps = 6/435 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  238  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  297

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  298  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  357

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  358  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  417

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  418  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  477

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  478  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  537

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  538  CATTTTCTAC-CCCAGAAGACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  593

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  594  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  653

Query:  28   ACCGCCCGTCACCCT  14
Sbjct:  654  ACCGNCCGTCACCCT  668
```

```
>gb|BE184900.1|BE184900 MR1-HT0707-100500-001-f09 HT0707 Homo sapiens cDNA.
          Length = 710

 Score =  448 bits (233), Expect = e-123
 Identities = 375/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  135  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAGACCTCAACAGTTAAATCAACAA  194

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  195  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  254

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  255  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  314

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  315  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  374

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  375  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCACGAGGTGGCAAGAAATGGGCTA  434

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  435  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  490

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  491  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  550

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  551  ACCGCCCGTCACCCTC  566
```

>gb|BE171482.1|BE171482 RC5-HT0547-130300-031-B03 HT0547 Homo sapiens cDNA.
Length = 568

Score = 448 bits (233), Expect = e-123
Identities = 375/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  63   GAGGGTGACGGGCGGTGTGTACGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACTCTC  122

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  123  AGTTTACTGCTAAATCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGT---AGTTTT  179

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  180  CTGGG-GTAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  238

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGAG  250
Sbjct:  239  TCTTTACGTGGGTACTTGCGCTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCG  298

Query:  251  GTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGC  310
Sbjct:  299  GTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGC  358

Query:  311  TCCTTTAGAGGGATATAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGT  370
Sbjct:  359  TCCTCTAGAGGGATATGAAGCACCGCCAGGGCCTTTGAGTTTTAAGCTGTGGCTCGTAGT  418

Query:  371  GTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGT  430
Sbjct:  419  GTTCTGGCGAGCAGTTTTGTTGATTTAACTGTTGAGGTTTAGGGCTAAGCATAGTGGTGT  478

Query:  431  ATCTAATCCCAGTTTG  446
Sbjct:  479  ATCTAATCCCAGTTTG  494
```

>gb|AA808966.1|AA808966 nw16h12.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1240679 3'
similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);.
Length = 785

Score = 446 bits (232), Expect = e-122
Identities = 377/437 (86%), Gaps = 7/437 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  37   GAGGGTGACGGGCGGTGTGTACGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACTCTC  96

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  97   AGTTTACTGCTAAATCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGT---AGTTTT  153

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  154  CTGGG-GTAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  212

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGAG  250
Sbjct:  213  TCTTTACGTGGGTACTTGCGCTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCG  272

Query:  251  GTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGC  310
Sbjct:  273  GTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGC  332

Query:  311  TCCTTTAGAGGGATATAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGT  370
```

```
Sbjct:  333  TCCTCTAGAGGGATATGAAGCACCGCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAGT  392

Query:  371  GTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGC-ATAGTGGGG  429
Sbjct:  393  GTTCTGGCGAGCAGTTTTGTTGATTTAACTGTTGAGGTTTAGGGCTAAGCAATAGTGGGG  452

Query:  430  TATCTAATCCCAGTTTG  446
Sbjct:  453  TATCTAATCCCAGTTTG  469
```

>dbj|AV735162.1|AV735162 AV735162 cdA Homo sapiens cDNA clone cdAAYB11 5'.
Length = 530

Score = 444 bits (231), Expect = e-122
Identities = 374/436 (85%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  65   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  124

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  125  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGGCTTC  184

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  185  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  244

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  245  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  304

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  305  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  364

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  365  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  420

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  421  GATTTGGCAGTAAACTGAGAGTANAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  480

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  481  ACCGCCCGTCACCCTC  496
```

>gb|BE175368.1|BE175368 RC4-HT0578-090300-011-e10 HT0578 Homo sapiens cDNA.
Length = 556

Score = 444 bits (231), Expect = e-122
Identities = 371/431 (86%), Gaps = 6/431 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  125  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  184

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  185  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCGGGCGGTGCTTC  244

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  245  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  304

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  305  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  364
```

```
Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  365  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  424

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  425  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  480

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  481  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  540

Query:  28   ACCGCCCGTCA  18
Sbjct:  541  ACCGCCCGTCA  551
```

>dbj|AV716721.1|AV716721 AV716721 DCB Homo sapiens cDNA clone DCBBXA08 5'.

Length = 592

Score = 442 bits (230), Expect = e-121
Identities = 374/436 (85%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  65   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  124

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  125  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGGCTTC  184

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  185  ATATCCCTCTAGAGGAGCCTGTTCCGTAATCGATAAACCCCGATCAACCTCACCACCTCT  244

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  245  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  304

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  305  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  364

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  365  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  420

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  421  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  480

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  481  ACCGCCCGTCACTCTC  496
```

>dbj|AV714571.1|AV714571 AV714571 DCB Homo sapiens cDNA clone DCBBMG09 5'.

Length = 561

Score = 442 bits (230), Expect = e-121
Identities = 374/436 (85%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  87   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCCAACAGTTAAATCAACAA  146

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  147  AACTGCTCGCCAGAACACTACGAGCCACAGGTGGAAACTCAAAGGACCTGGCGGTGCTTC  206

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
```

```
Sbjct:  207  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  266

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  267  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  326

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  327  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  386

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  387  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  442

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  443  GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  502

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  503  ACCGCCCGTCACCCTC  518
```

>dbj|AV708821.1|AV708821 AV708821 ADC Homo sapiens cDNA clone ADCAQC04 5'.

Length = 670

Score = 442 bits (230), Expect = e-121
Identities = 373/435 (85%), Gaps = 6/435 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  122  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  181

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  182  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  241

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  242  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  301

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  302  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  361

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  362  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  421

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  422  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  477

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  478  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  537

Query:  28   ACCGCCCGTCACCCT  14
Sbjct:  538  ANCCGCCGTCACCCT  552
```

>gb|BE184961.1|BE184961 MR1-HT0707-100500-002-c07 HT0707 Homo sapiens cDNA.

Length = 693

Score = 442 bits (230), Expect = e-121
Identities = 370/430 (86%), Gaps = 6/430 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  158  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  217
```

```
Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  218  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  277

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  278  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  337

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  338  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  397

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  398  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  457

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  458  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  513

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  514  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  573

Query:  28   ACCGCCCGTC  19
Sbjct:  574  ACCGGCCGTC  583
```

>gb|BE184959.1|BE184959 MR1-HT0707-100500-002-c05 HT0707 Homo sapiens cDNA.
Length = 654

Score = 442 bits (230), Expect = e-121
Identities = 377/438 (86%), Gaps = 8/438 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  154  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  213

Query:  386  AACTGTTCGCC--AGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCT  329
Sbjct:  214  AACTGCTCGCCCAAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCT  273

Query:  328  TTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCT  269
Sbjct:  274  TCATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCT  333

Query:  268  CTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCA  210
Sbjct:  334  CTTGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCG  393

Query:  209  GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-  151
Sbjct:  394  CAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGC  453

Query:  150  TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  454  TACATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGG  509

Query:  90   AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  510  TGGATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTAC  569

Query:  30   ACACCGCCCGTCACCCTC  13
Sbjct:  570  ACACCGCCCGTCACCCTC  587
```

>gb|BE184897.1|BE184897 MR1-HT0707-100500-001-e06 HT0707 Homo sapiens cDNA.
Length = 656

Score = 442 bits (230), Expect = e-121
Identities = 374/436 (85%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  115  CAAACTGGGCTTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  174

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  175  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  234

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  235  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  294

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  295  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  354

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  355  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  414

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  415  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  470

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  471  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  530

Query:  28   ACCGCCCGTCACCCTC  13
Sbjct:  531  ACCGGCCGTCAACCTC  546
```

>gb|BE184952.1|BE184952 MR1-HT0707-100500-002-a06 HT0707 Homo sapiens cDNA.
Length = 697

Score = 440 bits (229), Expect = e-121
Identities = 376/437 (86%), Gaps = 7/437 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  115  GAGGGTGACGGGCGGTGTGTACGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACTCTC  174

Query:  73   AATTTATTG-CTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  175  AGTTTACTGGCTAAATCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGT---AGTTT  231

Query:  132  TCTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  190
Sbjct:  232  TCTGGG-GTAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  290

Query:  191  GTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGA  249
Sbjct:  291  GTCTTTACGTGGGTACTTGCGCTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGC  350

Query:  250  GGTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  351  GGTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGG  410

Query:  310  CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAG  369
Sbjct:  411  CTCCTCTAGAGGGATATGAAGCACCGCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAG  470

Query:  370  TGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGG  429
Sbjct:  471  TGTTCTGGCGAGCAGTTTTGTTGATTTAACTGTTGAGGTTAAGGGCTAAGCATAGTGGGG  530

Query:  430  TATCTAATCCCAGTTTG  446
Sbjct:  531  TATCTAATCCCAGTTTG  547
```

>gb|BE184940.1|BE184940 MR1-HT0707-100500-002-f08 HT0707 Homo sapiens cDNA.
Length = 711

```
 Score =  435 bits (226), Expect = e-119
 Identities = 375/437 (85%), Gaps = 7/437 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  160  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  219

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  220  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  279

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  280  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  339

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  340  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  399

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  400  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  459

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGG-CTCAAGGA  90
Sbjct:  460  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGGT  515

Query:  89   GGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACA  30
Sbjct:  516  GGATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGGCCTGAAGCGCGTACA  575

Query:  29   CACCGCCCGTCACCCTC  13
Sbjct:  576  CACCGGCCGTCACCCTC  592
```

>gb|BE184922.1|BE184922 MR1-HT0707-100500-002-b08 HT0707 Homo sapiens cDNA.

```
          Length = 723

 Score =  435 bits (226), Expect = e-119
 Identities = 375/437 (85%), Gaps = 7/437 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  161  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  220

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  221  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  280

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  281  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  340

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  341  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  400

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAG-CCCATGAGGTGGCAAGAAATGGG-T  150
Sbjct:  401  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCCATGAGGTGGCAAGAAATGGGCT  460

Query:  149  ACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGA  90
Sbjct:  461  ACATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGT  516

Query:  89   GGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACA  30
Sbjct:  517  GGATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACA  576

Query:  29   CACCGCCCGTCACCCTC  13
```

```
Sbjct:  577  CACCGGCCGTCAACCTC  593
```

>dbj|AV756962.1|AV756962 AV756962 BM Homo sapiens cDNA clone BMFALC11 5'.
Length = 573

Score = 433 bits (225), Expect = e-118
Identities = 367/428 (85%), Gaps = 6/428 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  136  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  195

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  196  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  255

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  256  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  315

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  316  TGCTCAGCCTATATACCGGCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  375

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  376  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  435

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  436  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  491

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  492  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  551

Query:  28   ACCGCCCG  21
Sbjct:  552  ACCGGCCG  559
```

>gb|BE184955.1|BE184955 MR1-HT0707-100500-002-b06 HT0707 Homo sapiens cDNA.
Length = 631

Score = 433 bits (225), Expect = e-118
Identities = 377/438 (86%), Gaps = 8/438 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  117  GAGGGTGACGGGCGGTGTGTACGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACTCTC  176

Query:  73   AATTTATTG-CTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  177  AGTTTACTGGCTAAATCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGT---AGTTT  233

Query:  132  TCTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  190
Sbjct:  234  TCTGGG-GTAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  292

Query:  191  GTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGA  249
Sbjct:  293  GTCTTTACGTGGGTACTTGCGCTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGC  352

Query:  250  GGTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  353  GGTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGG  412

Query:  310  CTCCTTTAGAGGGATATAAAGCACTGCCA-AGTCCTTTGAGTTTTAAGCTGTTGCTTGTA  368
Sbjct:  413  CTCCTCTAGAGGGATATGAAGCACCGCCAGGGTCCTTTGAGTTTTAAGCTGTGGCTCGTA  472
```

```
Query:  369  GTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGG  428
Sbjct:  473  GTGTTCTGGCGAGCAGTTTTGTTGATTTAACTGTTGAGGTTTAGGGCTAAGCATAGTGGG  532

Query:  429  GTATCTAATCCCAGTTTG  446
Sbjct:  533  GTATCTAATCCCAGTTTG  550
```

>gb|AW264289.1|AW264289 xq97g05.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2758616 3'.
Length = 489

Score = 433 bits (225), Expect = e-118
Identities = 363/422 (86%), Gaps = 6/422 (1%)
Strand = Plus / Plus

```
Query:  27   GTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAATTTATTGCTAAA  86
Sbjct:  2    GTGTGTACGCGCTTCAGGGCCTGTTCAACTAAGCACTCTACTCTCAGTTTACTGCTAAA  61

Query:  87   TCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTTCTGTGTGTAGAAAA  146
Sbjct:  62   TCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGT---AGTTTTCTGGG-GTAGAAAA  117

Query:  147  CGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTTTTATGTAGATA  205
Sbjct:  118  TGTAGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTCTTTACGTGGGTA  177

Query:  206  CTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGAGGTATATAGGCTGGG  264
Sbjct:  178  CTTGCGCTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCGGTATATAGGCTGAG  237

Query:  265  CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGAT  324
Sbjct:  238  CAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGCTCCTCTAGAGGGAT  297

Query:  325  ATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAG  384
Sbjct:  298  ATGAAGCACCGCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAGTGTTCTGGCGAGCAG  357

Query:  385  TTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTT  444
Sbjct:  358  TTTTGTTGATTTAACTGTTGAGGTTTAGGGCTAAGCATAGTGGGGTATCTAATCCCAGTT  417

Query:  445  TG  446
Sbjct:  418  TG  419
```

>gb|BM841018.1|BM841018 K-EST0118186 S12SNU216 Homo sapiens cDNA clone S12SNU216-49-C02 5'.
Length = 508

Score = 431 bits (224), Expect = e-118
Identities = 362/421 (85%), Gaps = 6/421 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  92   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  151

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  152  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  211

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  212  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  271

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  272  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  331
```

```
Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  332  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  391

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  392  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  447

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  448  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  507

Query:  28   A  28
Sbjct:  508  A  508
```

>gb|BM833760.1|BM833760 K-EST0108602 S11SNU1 Homo sapiens cDNA clone S11SNU1-57-A04 5'.

Length = 540

Score = 431 bits (224), Expect = e-118
Identities = 362/421 (85%), Gaps = 6/421 (1%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  124  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  183

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  184  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  243

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  244  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  303

Query:  266  TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  304  TGCTCAGCCTATATACCACCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  363

Query:  207  AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  364  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  423

Query:  148  CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  424  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  479

Query:  88   GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  480  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  539

Query:  28   A  28
Sbjct:  540  A  540
```

```
  Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions
    Posted date:  Apr 10, 2003  8:11 PM
  Number of letters in database: 5,207,507,767
  Number of sequences in database:  11,001,213

  Database: db/est.01
    Posted date:  Apr 10, 2003  9:16 PM
  Number of letters in database: 2,928,888,640
  Number of sequences in database:  5,227,370

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
```

1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1,779,872
Number of Sequences: 16228583
Number of extensions: 1779872
Number of successful extensions: 506203
Number of sequences better than 10.0: 3345
Number of HSP's better than 10.0 without gapping: 3307
Number of HSP's successfully gapped in prelim test: 38
Number of HSP's that attempted gapping in prelim test: 499351
Number of HSP's gapped (non-prelim): 4847
length of query: 462
length of database: 8,136,396,407
effective HSP length: 24
effective length of query: 438
effective length of database: 7,746,910,415
effective search space: 3393146761770
effective search space used: 3393146761770
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

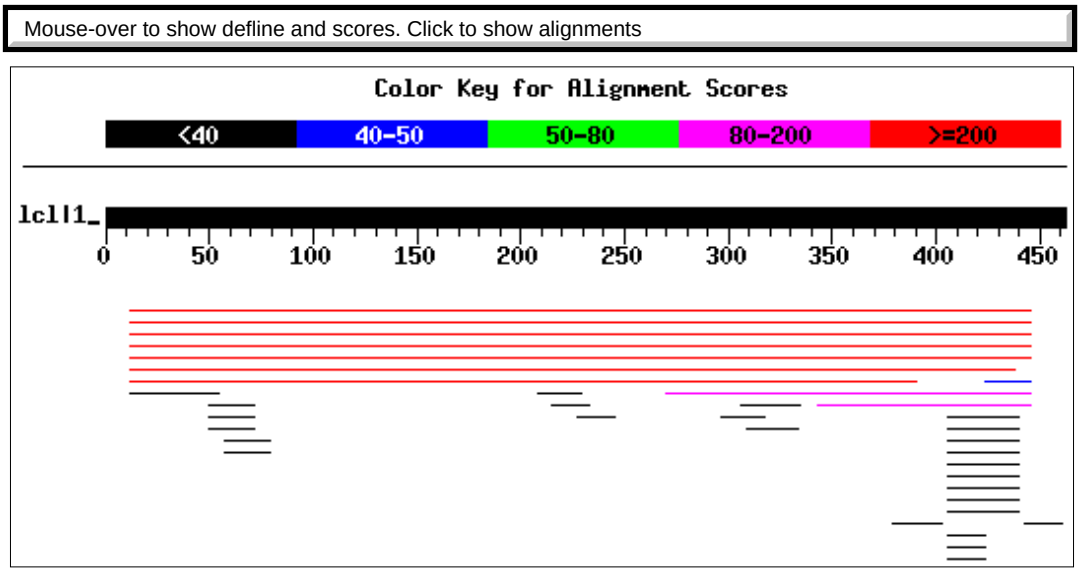
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: Genome Survey Sequence, includes single-pass genomic data, exon-trapped sequences, and Alu PCR sequences.
4,951,493 sequences; 2,825,176,892 total letters

Query= CS63win
(462 letters)

Distribution of 36 Blast Hits on the Query Sequence



Sequences producing significant alignments:		Score (bits)	E Value
gb|BH273593.1|BH273593	CH230-23J3.TJ CHORI-230 Segment 1 Ra...	350	3e-94
gb|BH271532.1|BH271532	CH230-13C21.TJ CHORI-230 Segment 1 R...	350	3e-94
gb|BH315753.1|BH315753	CH230-12K3.TV CHORI-230 Segment 1 Ra...	344	2e-92
gb|BH297049.1|BH297049	CH230-57F10.TJ CHORI-230 Segment 1 R...	344	2e-92
gb|BZ091717.1|BZ091717	CH230-220D10.TV CHORI-230 Segment 1 ...	341	3e-91
gb|BH302011.1|BH302011	CH230-58E9.TJ CHORI-230 Segment 1 Ra...	314	3e-83
gb|AZ340180.1|AZ340180	1M0072J11F Mouse 10kb plasmid UUGC1M...	267	3e-69
gb|AZ694776.1|AZ694776	PJB59BC Homology PCR genomic fragmen...	185	2e-44
gb|AQ001206.1|AQ001206	CIT-HSP-2283G17.TR CIT-HSP Homo sapi...	129	1e-27

gb|AQ058869.1|AQ058869	RPCI11-42H16.TJ RPCI-11 Homo sapiens...	43	0.14
dbj|AG248854.1|AG248854	AG248854 genomic TAC library Lotus ...	39	2.0
gb|BZ489446.1|BZ489446	BOOAB75TF BO_1.6_2_KB_tot Brassica o...	39	2.0
gb|BZ453161.1|BZ453161	BONES19TR BO_1.6_2_KB_tot Brassica o...	39	2.0
dbj|AG238677.1|AG238677	AG238677 genomic TAC library Lotus ...	39	2.0
gb|BZ271631.1|BZ271631	CH230-459H7.TJ CHORI-230 Segment 2 R...	39	2.0
gb|BZ250368.1|BZ250368	CH230-353O16.TV CHORI-230 Segment 2 ...	39	2.0
gb|BZ083706.1|BZ083706	lkx95b03.g1 B.oleracea002 Brassica o...	39	2.0
gb|BH668313.1|BH668313	BOMHR37TF BO_2_3_KB Brassica olerace...	39	2.0
gb|BH651023.1|BH651023	BOHUY63TF BO_2_3_KB Brassica olerace...	39	2.0
gb|BH520042.1|BH520042	BOHQH71TF BOHQ Brassica oleracea gen...	39	2.0
gb|BH502662.1|BH502662	BOGRM81TF BOGR Brassica oleracea gen...	39	2.0
gb|BH480568.1|BH480568	BOHNO71TF BOHN Brassica oleracea gen...	39	2.0
emb|AL342173.1|AL342173	C0AA029CB01C1 A Tetraodon nigroviri...	39	2.0
emb|AL329206.1|AL329206	C0AA008CG05A1 A Tetraodon nigroviri...	39	2.0
emb|AL268860.1|AL268860	C0BG072BF09LP1 G Tetraodon nigrovir...	39	2.0
gb|B76831.1|B76831	T26K8TR TAMU Arabidopsis thaliana genomi...	39	2.0
gb|BZ422195.1|BZ422195	id50g07.b1 WGS-SbicolorF (DH5a methy...	37	7.4
gb|BH681230.1|BH681230	BOHYT79TR BO_2_3_KB Brassica olerace...	37	7.4
gb|BH552315.1|BH552315	BOHPQ80TR BOHP Brassica oleracea gen...	37	7.4
gb|BH497158.1|BH497158	BOGZJ39TF BOGZ Brassica oleracea gen...	37	7.4
gb|BH256248.1|BH256248	LDH10MCR050001A06f Mcr BC methy filt...	37	7.4
dbj|AG064208.1|AG064208	AG064208 PTB Chimpanzee Male BAC Li...	37	7.4
gb|AZ818826.1|AZ818826	2M0089O06F Mouse 10kb plasmid UUGC1M...	37	7.4
gb|AZ505406.1|AZ505406	1M0345M24R Mouse 10kb plasmid UUGC1M...	37	7.4
gb|AZ133391.1|AZ133391	OSJNBb0108L06f CUGI Rice BAC Library...	37	7.4
gb|AQ270654.1|AQ270654	HS_2047_B1_G10_MR CIT Approved Human...	37	7.4

>gb|BH273593.1|BH273593 CH230-23J3.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone

CH230-23J3.
Length = 830

Score = 350 bits (182), Expect = 3e-94
Identities = 360/439 (82%), Gaps = 7/439 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  129  GAGGGTGACGGGCGGTGTGTGCGTACTTCATTGCTCTATTCAATTAAGCTCTCTATTCTT  188

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  189  AATTTACTACTAAATCCTCCTTTGTCCTTTAG-TTTCATAAAGGGTTTCGTAATGTTCT-  246

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  247  CTGGGAAAAGAAAATGTAGCCCATTTCTTTCCGCTTCATTGGCTACACCTTGACCTAACG  306

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  307  TTTTTATGTTTGTTCTTGTGCTTACTTTAGTGCCTTTTTAGGGTTTGCTGAAGATGGCGG  366

Query:  252  TATATAGGCTGG----GCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  367  TATATAGGCTGAATTAGCGAGAAGGGGTAAGGTATAACGGGGTTTATCGATTATAGAACA  426

Query:  308  GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  427  GGCTCCTCTAGATGGATATAAAGTACCGCCAAGTCCTTTGAGTTTTAAGCTGTAGCTAGT  486

Query:  368  AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
```

```
Sbjct:  487  AGTTCTCTGGCAAATAATTTTGTAGGTTTAATTATTAAGGTTTAGGGCTAAGCATAGTGG  546

Query:  428  GGTATCTAATCCCAGTTTG  446
Sbjct:  547  GGTATCTAATCCCAGTTTG  565
```

>gb|BH271532.1|BH271532 CH230-13C21.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone

```
          CH230-13C21.
        Length = 848

 Score =  350 bits (182), Expect = 3e-94
 Identities = 360/439 (82%), Gaps = 7/439 (1%)
 Strand = Plus / Plus


Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  155  GAGGGTGACGGGCGGTGTGTGCGTACTTCATTGCTCTATTCAATTAAGCTCTCTATTCTT  214

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  215  AATTTACTACTAAATCCTCCTTTGTCCTTTAG-TTTCATAAAGGGTTTCGTAATGTTCT-  272

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  273  CTGGGAAAAGAAAATGTAGCCCATTTCTTTCCGCTTCATTGGCTACACCTTGACCTAACG  332

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  333  TTTTTATGTTTGTTCTTGTGCTTACTTTAGTGCCTTTTTAGGGTTTGCTGAAGATGGCGG  392

Query:  252  TATATAGGCTGG----GCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  393  TATATAGGCTGAATTAGCGAGAAGGGGTAAGGTATAACGGGGTTTATCGATTATAGAACA  452

Query:  308  GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  453  GGCTCCTCTAGATGGATATAAAGTACCGCCAAGTCCTTTGAGTTTTAAGCTGTAGCTAGT  512

Query:  368  AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  513  AGTTCTCTGGCAAATAATTTTGTAGGTTTAATTATTAAGGTTTAGGGCTAAGCATAGTGG  572

Query:  428  GGTATCTAATCCCAGTTTG  446
Sbjct:  573  GGTATCTAATCCCAGTTTG  591
```

>gb|BH315753.1|BH315753 CH230-12K3.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone

```
          CH230-12K3.
        Length = 846

 Score =  344 bits (179), Expect = 2e-92
 Identities = 359/439 (81%), Gaps = 7/439 (1%)
 Strand = Plus / Plus


Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  129  GAGGGTGACGGGCGGTGTGTGCGTACTTCATTGCTCTATTCAATTAAGTTCTCTATTCTT  188

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  189  AATTTACTACTAAATCCTCCTTTGTCCTTTAG-TTTCATAAAGGGTTTCGTAATGTTCT-  246

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  247  CTGGGAAAAGAAAATGTAGCCCATTTCTTTCCGCTTCATTGGCTACACCTTGACCTAACG  306

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  307  TTTTTATGTTTGTTCTTGTGCTTACTTTAGTGCCTTTTTAGGGTTTGCTGAAGATGGCGG  366
```

```
Query:  252  TATATAGGCTGG----GCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  367  TATATAGGCTGAATTAGCGAGAAGGGGTAAGGTATAACGGGGTTTATCGATTATAGAACA  426

Query:  308  GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  427  GGCTCCTCTAGATGGATATAAAGTACCGCCAAGTCCTTTGAGTTTTAAGCTGTAGCTAGT  486

Query:  368  AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  487  AGTTCTCTGGCAAATAATTTTGTAGGTTTAATTATTAAGGTTTAGGGCTAAGCATAGTGG  546

Query:  428  GGTATCTAATCCCAGTTTG  446
Sbjct:  547  GGTATCTAATCCCAGTTTG  565
```

>gb|BH297049.1|BH297049 CH230-57F10.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone

CH230-57F10.
Length = 786

Score = 344 bits (179), Expect = 2e-92
Identities = 359/439 (81%), Gaps = 7/439 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  156  GAGGGTGACGGGCGGTGTGTGCGTACTTCATTGCTCTATTCTATTAAGCTCTCTATTCTT  215

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  216  AATTTACTACTAAATCCTCCTTTGTCCTTTAG-TTTCATAAAGGGTTTCGTAATGTTCT-  273

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  274  CTGGGAAAAGAAAATGTAGCCCATTTCTTTCCGCTTCATTGGCTACACCTTGACCTAACG  333

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  334  TTTTTATGTTTGTTCTTGTGCTTACTTTAGTGCCTTTTTAGGGTTTGCTGAAGATGGCGG  393

Query:  252  TATATAGGCTGG----GCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  394  TATATAGGCTGAATTAGCGAGAAGGGGTAAGGTATAACGGGGTTTATCGATTATAGAACA  453

Query:  308  GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  454  GGCTCCTCTAGATGGATATAAAGTACCGCCAAGTCCTTTGAGTTTTAAGCTGTAGCTAGT  513

Query:  368  AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  514  AGTTCTCTGGCAAATAATTTTGTAGGTTTAATTATTAAGGTTTAGGGCTAAGCATAGTGG  573

Query:  428  GGTATCTAATCCCAGTTTG  446
Sbjct:  574  GGTATCTAATCCCAGTTTG  592
```

>gb|BZ091717.1|BZ091717 CH230-220D10.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone

CH230-220D10.
Length = 816

Score = 341 bits (177), Expect = 3e-91
Identities = 360/439 (82%), Gaps = 8/439 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  152  GAGGGTGACGGGCGGTGTGTGCGTACTTCATTGCTCTATTCAATTAAGCTCTCTATTCTT  211
```

```
Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  212  AATTTACTACTAAATCCTCCTTTGTCCTTTAG-TTTCATAAAGGGTTTCGTAATGTTCT-  269

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  270  CTGGGAAAAGAAAATGTAGCCCATTTCTTTCCGCTTCATTGGCTACACCTTGACCTAACG  329

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  330  TTTTTATGTTTGTTCTTGTGCTTACTTTAGTGCCTTTTTAGGGTTTGCTGAAGATGGCGG  389

Query:  252  TATATAGGCTGG----GCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  390  TATATAGGCTGAATTAGCGAGAAGGGGTAAGGTATAACGGGGTTTATCGATTATAGAACA  449

Query:  308  GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  450  GGCTCCTCTAGATGGATATAAAGTACCGCCAAGTCCTTTGAGTTTTAAGCTGTAGCTAGT  509

Query:  368  AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  510  AGTTCTCTGGCAAATA-TTTTGTAGGTTTAATTATTAAGGTTTAGGGCTAAGCATAGTGG  568

Query:  428  GGTATCTAATCCCAGTTTG  446
Sbjct:  569  GGTATCTAATCCCAGTTTG  587
```

>gb|BH302011.1|BH302011 CH230-58E9.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone

CH230-58E9.
Length = 606

Score = 314 bits (163), Expect = 3e-83
Identities = 349/432 (80%), Gaps = 7/432 (1%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  109  GAGGGTGACGGGCGGTGTGTGCGTACTTCATTGCTCTATTTAATTAAGCTCTCTATTCTT  168

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  169  AATTTACTACTAAATCCTCCTTTGTCCTTTAG-TTTCATAAAGGGTTTCGTAATGTTCT-  226

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  227  CTGGGAAAAGAAAATGTAGCCCATTTCTTTCCGCTTCATTGGCTACACCTTGACCTAACG  286

Query:  192  TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  287  TTTTTATGTTTGTTCTTGTGCTTACTTTAGTGCCTTTTTAGGGTTTGCTGAAGATGGCGG  346

Query:  252  TATATAGGCTGG----GCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  347  TATATAGGCTGAATTAGCGAGAAGGGGTAAGGTATAACGGGGTTTATCGATTATAGAACA  406

Query:  308  GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  407  GGCTCCTCTAGATGGATATAAAGTACCGCCAAGTCCTTTGAGTTTTAAGCTGTAGCTAGT  466

Query:  368  AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  467  AGTTCTCTGGCATATAATTTTGTAGGCTTAATTATTAACGTTTAGGGCTAAGCATACTGG  526

Query:  428  GGTATCTAATCC  439
Sbjct:  527  GGTATCTAATCC  538
```

>gb|AZ340180.1|AZ340180 1M0072J11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0072J11 F.
Length = 726

```
 Score =  267 bits (139), Expect = 3e-69
 Identities = 315/386 (81%), Gaps = 12/386 (3%)
 Strand = Plus / Plus


Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  341  GAGGGTGACGGGCGGTGTGTGCGTACTTCATTGCTCAATTCAATTAAGCTCTCTATTCTT  400

Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  401  AATTTACTACTAAATCCTCCTTAGTCCTTTAG-TTTCATAAAGGGTATAGTAATGTTCTT  459

Query:  133  CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  460  TTATA---AGAAAATGTAGCCCATTTCTTCCCATTTCATTGGCTACACCTTGACCTAACG  516

Query:  192  TTTTTATGTA-GATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAG  250
Sbjct:  517  TTTTTATGTTTGATTCTTTTGCTTACTTTAATACCTTTTTAGGGTTTGCTGAAGATGGCG  576

Query:  251  GTATATAGGCTGG----GCAAGAGGTGGTGAGGTAAATTGGG-GTTTATCGATTATAGAA  305
Sbjct:  577  GTATATAGGCTGAATTAGCAAGAGATGGTGAGGTANAGCGGGNGTTTATCGATTATAGAA  636

Query:  306  CAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTT  365
Sbjct:  637  CAGGCTCCTCTAGATGGATATAAAGTACCGCCAAGTCCTTTGAGTTTTAAGCTATGGCTA  696

Query:  366  GTAGTGTTCTGGCGAACAGTTTTGTT  391
Sbjct:  697  GTAGTTCTCTGGC-AATAGTTTTGTT  721
```

```
>gb|AZ694776.1|AZ694776 PJB59BC Homology PCR genomic fragments of Vittaforma corneae
           Vittaforma corneae genomic.
          Length = 585

 Score =  185 bits (96), Expect = 2e-44
 Identities = 151/176 (85%), Gaps = 1/176 (0%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  368  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTGATAATTTCAT-AACAA  426

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  427  AATTATTCGCCAGAGAACTACAAGCCAAAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  486

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  487  ATACCCACCTAGAGGAGCCTGTTCCGTAATCGATAAACCCCGATAAACCTTACCAC  542
```

```
>gb|AQ001206.1|AQ001206 CIT-HSP-2283G17.TR CIT-HSP Homo sapiens genomic clone
2283G17.
          Length = 669

 Score =  129 bits (67), Expect = 1e-27
 Identities = 91/103 (88%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  567  CAAACTTGGATTAGATACACCACTATGCTTAGCCCTAAACTCTAATAGTTATATTAACAA  626

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAA  344
Sbjct:  627  AACCATTCACCAGAGTACCACAAGCAACAGCTTAAAACTCAAA  669
```

>gb|AQ058869.1|AQ058869 RPCI11-42H16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-42H16.
Length = 643

Score = 43.0 bits (22), Expect = 0.14
Identities = 22/22 (100%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCA  425
Sbjct:  488  CAAACTGGGATTAGATACCCCA  509
```

>dbj|AG248854.1|AG248854 AG248854 genomic TAC library Lotus japonicus genomic clone LjT23m18_sfi.
Length = 474

Score = 39.1 bits (20), Expect = 2.0
Identities = 22/23 (95%)
Strand = Plus / Minus

```
Query:  80   AATAAATTGAGAGCAGAGTGTTT  58
Sbjct:  367  AATAAATTGAGAGCAGAGTATTT  389
```

>gb|BZ489446.1|BZ489446 BOOAB75TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BOOAB75.
Length = 817

Score = 39.1 bits (20), Expect = 2.0
Identities = 30/35 (85%)
Strand = Plus / Plus

```
Query:  407  GTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCA  441
Sbjct:  769  GTTTACGGCTAAGACTACTGGGGTATCTAATCCCA  803
```

>gb|BZ453161.1|BZ453161 BONES19TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONES19.
Length = 659

Score = 39.1 bits (20), Expect = 2.0
Identities = 30/35 (85%)
Strand = Plus / Minus

```
Query:  441  TGGGATTAGATACCCCACTATGCTTAACCCTAAAC  407
Sbjct:  346  TGGGATTAGATACCCCAGTAGTCCTAACCGTAAAC  380
```

>dbj|AG238677.1|AG238677 AG238677 genomic TAC library Lotus japonicus genomic clone LjT02n15_sfi.
Length = 433

Score = 39.1 bits (20), Expect = 2.0
Identities = 22/23 (95%)
Strand = Plus / Minus

```
Query:  80   AATAAATTGAGAGCAGAGTGTTT  58
Sbjct:  311  AATAAATTGAGAGCAGAGTATTT  333
```

>gb|BZ271631.1|BZ271631 CH230-459H7.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-459H7.
Length = 842

Score = 39.1 bits (20), Expect = 2.0
Identities = 36/44 (81%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAAT  56
Sbjct:  795  GAGGGTGACGGGCGGGGTGGGCGAACTTCATTGCTCTATTCAAT  838
```

>gb|BZ250368.1|BZ250368 CH230-353O16.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-353O16.
Length = 609

Score = 39.1 bits (20), Expect = 2.0
Identities = 26/29 (89%)
Strand = Plus / Minus

```
Query:  335  CAGTGCTTTATATCCCTCTAAAGGAGCCT  307
Sbjct:  318  CAGTGCTTTATATACCTCAAAAAGAGCCT  346
```

>gb|BZ083706.1|BZ083706 lkx95b03.g1 B.oleracea002 Brassica oleracea genomic.
Length = 684

Score = 39.1 bits (20), Expect = 2.0
Identities = 30/35 (85%)
Strand = Plus / Plus

```
Query:  407  GTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCA  441
Sbjct:  481  GTTTACGGCTAAGACTACTGGGGTATCTAATCCCA  515
```

>gb|BH668313.1|BH668313 BOMHR37TF BO_2_3_KB Brassica oleracea genomic clone BOMHR37.
Length = 539

Score = 39.1 bits (20), Expect = 2.0
Identities = 30/35 (85%)
Strand = Plus / Plus

```
Query:  407  GTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCA  441
Sbjct:  491  GTTTACGGCTAAGACTACTGGGGTATCTAATCCCA  525
```

>gb|BH651023.1|BH651023 BOHUY63TF BO_2_3_KB Brassica oleracea genomic clone BOHUY63.
Length = 352

```
 Score = 39.1 bits (20), Expect = 2.0
 Identities = 30/35 (85%)
 Strand = Plus / Plus


Query:  407  GTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCA  441
Sbjct:  318  GTTTACGGCTAAGACTACTGGGGTATCTAATCCCA  352
```

>gb|BH520042.1|BH520042 BOHQH71TF BOHQ Brassica oleracea genomic clone BOHQH71.

```
          Length = 616

 Score = 39.1 bits (20), Expect = 2.0
 Identities = 30/35 (85%)
 Strand = Plus / Plus


Query:  407  GTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCA  441
Sbjct:  577  GTTTACGGCTAAGACTACTGGGGTATCTAATCCCA  611
```

>gb|BH502662.1|BH502662 BOGRM81TF BOGR Brassica oleracea genomic clone BOGRM81.

```
          Length = 802

 Score = 39.1 bits (20), Expect = 2.0
 Identities = 30/35 (85%)
 Strand = Plus / Plus


Query:  407  GTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCA  441
Sbjct:  722  GTTTACGGCTAAGACTACTGGGGTATCTAATCCCA  756
```

>gb|BH480568.1|BH480568 BOHNO71TF BOHN Brassica oleracea genomic clone BOHNO71.

```
          Length = 718

 Score = 39.1 bits (20), Expect = 2.0
 Identities = 30/35 (85%)
 Strand = Plus / Plus


Query:  407  GTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCA  441
Sbjct:  643  GTTTACGGCTAAGACTACTGGGGTATCTAATCCCA  677
```

>emb|AL342173.1|AL342173 C0AA029CB01C1 A Tetraodon nigroviridis genomic clone 029D01 T7.

```
          Length = 1101

 Score = 39.1 bits (20), Expect = 2.0
 Identities = 22/23 (95%)
 Strand = Plus / Plus


Query:  51    TTCAATTAAACACTCTGCTCTCA  73
Sbjct:  645   TTCAATTAAGCACTCTGCTCTCA  667
```

>emb|AL329206.1|AL329206 C0AA008CG05A1 A Tetraodon nigroviridis genomic clone 008N09.

Length = 1084

Score = 39.1 bits (20), Expect = 2.0
Identities = 22/23 (95%)
Strand = Plus / Plus

```
Query:  51    TTCAATTAAACACTCTGCTCTCA  73
Sbjct:  573   TTCAATTAAGCACTCTGCTCTCA  595
```

>emb|AL268860.1|AL268860 C0BG072BF09LP1 G Tetraodon nigroviridis genomic clone 072K18 T7.

Length = 909

Score = 39.1 bits (20), Expect = 2.0
Identities = 22/23 (95%)
Strand = Plus / Plus

```
Query:  51   TTCAATTAAACACTCTGCTCTCA  73
Sbjct:  567  TTCAATTAAGCACTCTGCTCTCA  589
```

>gb|B76831.1|B76831 T26K8TR TAMU Arabidopsis thaliana genomic clone T26K8.

Length = 374

Score = 39.1 bits (20), Expect = 2.0
Identities = 30/35 (85%)
Strand = Plus / Minus

```
Query:  441  TGGGATTAGATACCCCACTATGCTTAACCCTAAAC  407
Sbjct:  56   TGGGATTAGATACCCCAGTATTCCTATCCGTAAAC  90
```

>gb|BZ422195.1|BZ422195 id50g07.b1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor genomic clone id50g07 5'.

Length = 816

Score = 37.2 bits (19), Expect = 7.4
Identities = 23/25 (92%)
Strand = Plus / Plus

```
Query:  310  CTCCTTTAGAGGGATATAAAGCACT  334
Sbjct:  709  CTCCGTTTGAGGGATATAAAGCACT  733
```

>gb|BH681230.1|BH681230 BOHYT79TR BO_2_3_KB Brassica oleracea genomic clone BOHYT79.

Length = 790

Score = 37.2 bits (19), Expect = 7.4
Identities = 19/19 (100%)
Strand = Plus / Minus

```
Query:  425  ACTATGCTTAACCCTAAAC  407
Sbjct:  644  ACTATGCTTAACCCTAAAC  662
```

>gb|BH552315.1|BH552315 BOHPQ80TR BOHP Brassica oleracea genomic clone BOHPQ80.
Length = 800

Score = 37.2 bits (19), Expect = 7.4
Identities = 19/19 (100%)
Strand = Plus / Minus

```
Query:  425  ACTATGCTTAACCCTAAAC  407
Sbjct:  93   ACTATGCTTAACCCTAAAC  111
```

>gb|BH497158.1|BH497158 BOGZJ39TF BOGZ Brassica oleracea genomic clone BOGZJ39.
Length = 727

Score = 37.2 bits (19), Expect = 7.4
Identities = 19/19 (100%)
Strand = Plus / Minus

```
Query:  425  ACTATGCTTAACCCTAAAC  407
Sbjct:  115  ACTATGCTTAACCCTAAAC  133
```

>gb|BH256248.1|BH256248 LDH10MCR050001A06f Mcr BC methy filtration maize leaf genomic shotgun
library Zea mays genomic clone LDH10MCR050001A06f.
Length = 735

Score = 37.2 bits (19), Expect = 7.4
Identities = 19/19 (100%)
Strand = Plus / Plus

```
Query:  444  TTGAATCACTAGTGAATTC  462
Sbjct:  717  TTGAATCACTAGTGAATTC  735
```

>dbj|AG064208.1|AG064208 AG064208 PTB Chimpanzee Male BAC Library Pan troglodytes genomic
clone PTB-053D12.R.
Length = 645

Score = 37.2 bits (19), Expect = 7.4
Identities = 19/19 (100%)
Strand = Plus / Minus

```
Query:  234  CCCTGGAAAGGCCACAGAG  216
Sbjct:  334  CCCTGGAAAGGCCACAGAG  352
```

>gb|AZ818826.1|AZ818826 2M0089O06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0089O06 F.
Length = 623

Score = 37.2 bits (19), Expect = 7.4
Identities = 19/19 (100%)

Strand = Plus / Plus

```
Query:  228  TCCAGGGTTTGCTGAAGAT  246
Sbjct:  541  TCCAGGGTTTGCTGAAGAT  559
```

>gb|AZ505406.1|AZ505406 1M0345M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0345M24 R.
Length = 683

Score = 37.2 bits (19), Expect = 7.4
Identities = 21/22 (95%)
Strand = Plus / Plus

```
Query:  209  CTGCTTACTCTGTGGCCTTTCC  230
Sbjct:  15   CTGCTTCCTCTGTGGCCTTTCC  36
```

>gb|AZ133391.1|AZ133391 OSJNBb0108L06f CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
cultivar-group) genomic clone OSJNBb0108L06f.
Length = 739

Score = 37.2 bits (19), Expect = 7.4
Identities = 21/22 (95%)
Strand = Plus / Minus

```
Query:  318  CTAAAGGAGCCTGTTCTATAAT  297
Sbjct:  195  CTAAAGGAGCCGGTTCTATAAT  216
```

>gb|AQ270654.1|AQ270654 HS_2047_B1_G10_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2047 Col=19 Row=N.
Length = 801

Score = 37.2 bits (19), Expect = 7.4
Identities = 23/25 (92%)
Strand = Plus / Minus

```
Query:  404  GAATAGTTAGATCAACAAAACTGTT  380
Sbjct:  505  GAATATTCAGATCAACAAAACTGTT  529
```

Database: Genome Survey Sequence, includes single-pass genomic data, exon-trapped sequences, and Alu PCR sequences.
Posted date: Apr 10, 2003 7:13 PM
Number of letters in database: 2,825,176,892
Number of sequences in database: 4,951,493

```
Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12
```

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 645,666
Number of Sequences: 4951493
Number of extensions: 645666
Number of successful extensions: 189708
Number of sequences better than 10.0: 37
Number of HSP's better than 10.0 without gapping: 37
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 189639
Number of HSP's gapped (non-prelim): 59
length of query: 462
length of database: 2,825,176,892
effective HSP length: 24
effective length of query: 438
effective length of database: 2,706,341,060
effective search space: 1185377384280
effective search space used: 1185377384280
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 19 (37.2 bits)

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NCBI **BLAST Search Results** BLAST Entrez ?

BLASTN 2.2.5 [Nov-16-2002]

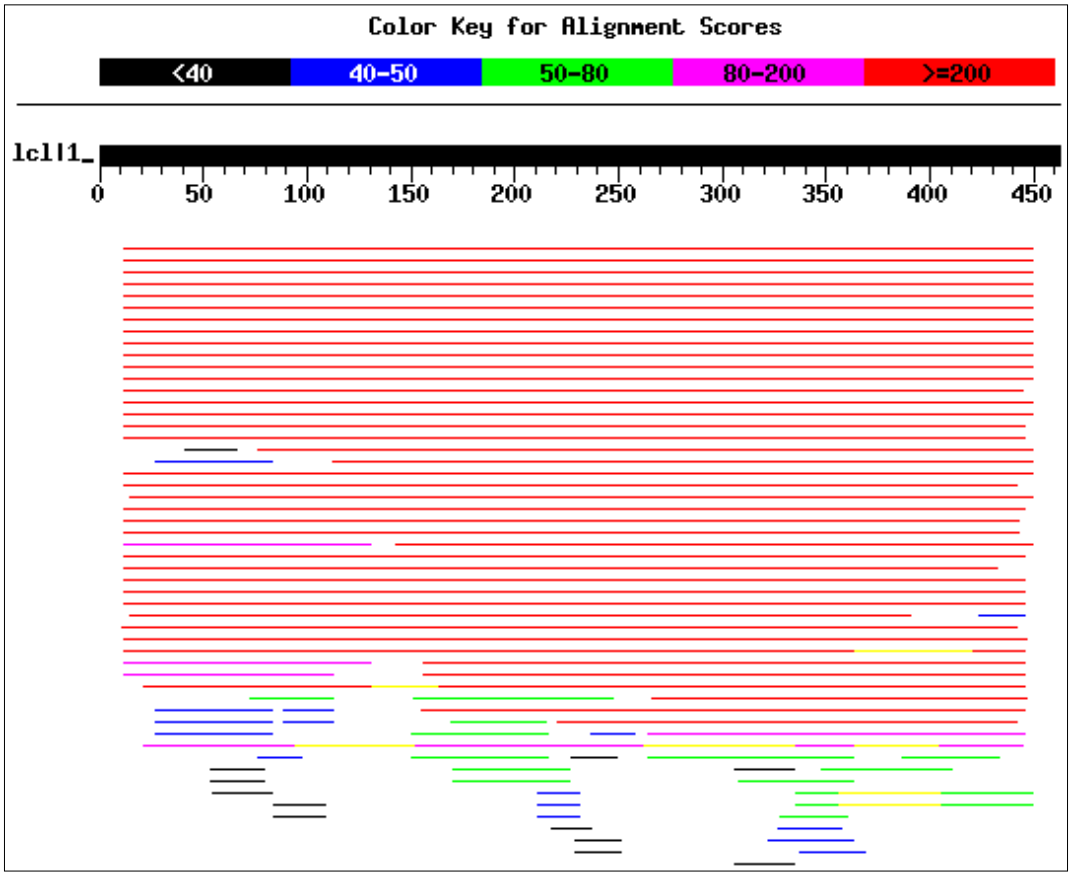
Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Database: Unfinished High Throughput Genomic Sequences;
Sequences: phases 0,1 and 2
68,262 sequences; 11,705,682,188 total letters

Query= CS63win
(462 letters)

Distribution of 97 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:	Score (bits)	E Value
emb|AL354817.4| Homo sapiens chromosome 13 clone RP11-85C8,...	808	0.0
emb|AL354697.5| Homo sapiens chromosome 13 clone RP11-475C1...	802	0.0
gb|AC044785.3|AC044785 Homo sapiens chromosome 02 clone RP1...	767	0.0
gb|AC021029.5|AC021029 Homo sapiens chromosome 09 clone RP1...	767	0.0
emb|AL354822.3| Homo sapiens chromosome 13 clone RP11-474C2...	756	0.0
gb|AC024975.2|AC024975 Homo sapiens chromosome 13 clone RP1...	750	0.0
gb|AC026079.4|AC026079 Homo sapiens chromosome 10 clone RP1...	744	0.0
gb|AC125394.21| Pan troglodytes clone rp43-45i3, WORKING DR...	738	0.0
gb|AC091085.2| Homo sapiens chromosome 17 clone RP11-10A10 ...	733	0.0
emb|AL355793.5| Homo sapiens chromosome 1 clone RP4-694M10,...	727	0.0
gb|AC000382.2|HSAC000382 Homo sapiens chromosome 11 clone p...	721	0.0
gb|AC068398.3|AC068398 Homo sapiens chromosome 2 clone RP11...	721	0.0
gb|AC087707.1|AC087707 Homo sapiens clone RP11-485P11, LOW-...	708	0.0
gb|AC022192.3|AC022192 Homo sapiens clone RP11-23B24, WORKI...	706	0.0
gb|AC027456.3|AC027456 Homo sapiens chromosome 21 clone RP1...	704	0.0
gb|AC092432.2| Homo sapiens chromosome 2 clone RP11-96C22, ...	702	0.0
gb|AC024170.3|AC024170 Homo sapiens chromosome 3 clone RP11...	702	0.0
gb|AC068239.1|AC068239 Homo sapiens chromosome 2 clone RP11...	554	e-155
gb|AC016147.12|AC016147 Homo sapiens chromosome 3 clone RP1...	535	e-149
gb|AC068619.4|AC068619 Homo sapiens chromosome 17 clone RP1...	525	e-146
gb|AC015935.7| Homo sapiens chromosome 17 clone CTD-2354J3 ...	512	e-142
gb|AC058808.1|AC058808 Homo sapiens chromosome 11 clone RP1...	489	e-135
gb|AC021473.3|AC021473 Homo sapiens clone RP11-705H21, WORK...	483	e-133
gb|AC024498.2|AC024498 Homo sapiens chromosome 1 clone RP11...	473	e-130
emb|AL359533.1| Mus musculus chromosome X clone RP21-247L20...	467	e-129
gb|AC016151.20| Homo sapiens chromosome 3 clone RP11-141N10...	464	e-127
gb|AC069389.3|AC069389 Homo sapiens chromosome 8 clone RP11...	433	e-118
gb|AC025337.1| Homo sapiens chromosome 17 clone RP11-471P22...	421	e-115
gb|AC024954.3|AC024954 Homo sapiens clone RP11-3E16, WORKIN...	419	e-114
gb|AC023928.3|AC023928 Homo sapiens chromosome 2 clone RP11...	419	e-114
gb|AC022223.18| Homo sapiens chromosome 5 clone RP11-538B23...	412	e-112
gb|AC021442.2|AC021442 Homo sapiens chromosome 11 clone RP1...	410	e-111
gb|AC068010.4|AC068010 Homo sapiens clone RP11-3J16, WORKIN...	406	e-110
gb|AC116047.2| Papio hamadryas clone RP41-440I10, WORKING D...	383	e-103
gb|AF182108.3| Homo sapiens chromosome 8 clone RP11-11N9 ma...	367	9e-99
gb|AC096874.2| Pan troglodytes clone RP43-107P11, WORKING D...	360	2e-96
gb|AC097006.1| Pan troglodytes clone RP43-11P24, WORKING DR...	360	2e-96
gb|AC018856.4|AC018856 Homo sapiens chromosome 2 clone RP11...	352	4e-94
gb|AC021823.3|AC021823 Homo sapiens chromosome 2 clone RP11...	233	3e-58
gb|AC013632.3|AC013632 Homo sapiens clone RP11-12N13, WORKI...	229	4e-57
gb|AC107879.1| Homo sapiens chromosome 18 clone RP11-584O12...	212	7e-52
gb|AC137882.1| Homo sapiens chromosome 15 clone RP11-318M1 ...	114	2e-22
gb|AC136354.1| Homo sapiens chromosome 15 clone RP11-318M1 ...	114	2e-22
gb|AC016352.2| Homo sapiens chromosome 22 clone RP11-425O21...	114	2e-22
gb|AC025936.3|AC025936 Homo sapiens chromosome 8 clone RP11...	91	2e-15
gb|AC027752.2|AC027752 Homo sapiens chromosome 11 clone RP1...	85	1e-13
emb|BX322234.2| Homo sapiens chromosome 6 clone XXyac-65C7_...	74	3e-10
gb|AC143888.1| Macaca mulatta clone CH250-268B20, *** SEQUE...	72	1e-09
gb|AC013679.2|AC013679 Homo sapiens clone RP11-20L24, LOW-P...	70	5e-09
gb|AC130279.2| Mus musculus clone RP24-394G12, WORKING DRAF...	66	7e-08
gb|AC120870.2| Mus musculus clone RP23-15D1, WORKING DRAFT ...	66	7e-08
gb|AC023368.2|AC023368 Homo sapiens chromosome 2 clone RP11...	64	3e-07

gb|AC024953.4|AC024953	Homo sapiens clone RP11-114I12, WORK...	64	3e-07
gb|AC099177.5|	Rattus norvegicus clone CH230-112E16, *** SE...	56	5e-05
gb|AC119596.5|	Rattus norvegicus clone CH230-326E5, WORKING...	56	5e-05
gb|AC097566.6|	Rattus norvegicus clone CH230-117K10, *** SE...	56	5e-05
gb|AC079189.3|AC079189	Homo sapiens chromosome 11 clone RP1...	56	5e-05
gb|AC022619.4|AC022619	Homo sapiens clone RP11-23L10, WORKI...	55	2e-04
gb|AC016444.3|AC016444	Homo sapiens chromosome 11 clone RP1...	53	8e-04
gb|AC135410.2|	Rattus norvegicus clone CH230-191N9, *** SEQ...	51	0.003
emb|AL512381.18|	Homo sapiens chromosome 1 clone RP11-265C2...	47	0.041
emb|AL450268.10|	Homo sapiens chromosome 1 clone RP11-428N1...	47	0.041
emb|AL359032.13|	Homo sapiens chromosome 9 clone RP11-18A21...	47	0.041
emb|AL359968.14|	Homo sapiens chromosome 20 clone RP11-21D1...	47	0.041
gb|AC131450.1|	Strongylocentrotus purpuratus clone Sp41I19,...	43	0.59
gb|AC093306.1|	Homo sapiens chromosome 5 clone RP11-71K19, ...	43	0.59
gb|AC015560.6|AC015560	Homo sapiens chromosome 15 clone RP1...	43	0.59
gb|AC026614.2|AC026614	Homo sapiens chromosome 5 clone RP11...	43	0.59
gb|AC079017.11|	Homo sapiens chromosome 15 clone RP11-120F6...	41	2.2
gb|AC132918.4|	Mus musculus clone RP24-328F10, WORKING DRAF...	41	2.2
gb|AC138731.2|	Pongo pygmaeus clone CH253-404N12, WORKING D...	41	2.2
gb|AC135174.2|	Homo sapiens chromosome 15 clone RP11-1152K1...	41	2.2
gb|AC027267.3|AC027267	Homo sapiens chromosome 15 clone RP1...	41	2.2
emb|BX323023.3|	Danio rerio clone CH211-231I17, *** SEQUENC...	41	2.2
emb|BX322597.1|	Danio rerio clone RP71-7L19, *** SEQUENCING...	41	2.2
gb|AC127795.3|	Rattus norvegicus clone CH230-101A9, *** SEQ...	39	8.5
gb|AC134061.2|	Rattus norvegicus clone CH230-66A19, *** SEQ...	39	8.5
gb|AC096517.7|	Rattus norvegicus clone CH230-16H15, WORKING...	39	8.5
gb|AC108663.4|	Rattus norvegicus clone CH230-258E19, WORKIN...	39	8.5
gb|AC129006.2|	Rattus norvegicus clone CH230-1H22, *** SEQU...	39	8.5
gb|AC106504.3|	Rattus norvegicus clone CH230-205I24, *** SE...	39	8.5
gb|AC094818.4|	Rattus norvegicus clone CH230-5J9, *** SEQUE...	39	8.5
gb|AC021471.5|AC021471	Homo sapiens clone RP11-441P23, WORK...	39	8.5
gb|AC027745.2|AC027745	Homo sapiens clone RP11-535A15, WORK...	39	8.5
gb|AC041042.4|AC041042	Homo sapiens chromosome 5 clone RP11...	39	8.5
gb|AC018565.3|AC018565	Homo sapiens chromosome 3 clone RP11...	39	8.5
gb|AC023659.2|AC023659	Homo sapiens chromosome 2 clone RP11...	39	8.5
gb|AC022064.3|AC022064	Homo sapiens chromosome 15 clone RP1...	39	8.5

>emb|AL354817.4| Homo sapiens chromosome 13 clone RP11-85C8, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces

Length = 156024

Score = 808 bits (420), Expect = 0.0
Identities = 432/438 (98%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  66706   GATCCAAACTGGGAGTAGATACCCCGCTATGCTTAACCCTAAACTCGAATAGTTAGATCA  66765

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  66766   ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  66825

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  66826   CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  66885

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
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Sbjct:  66886   CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  66945

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  66946   AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  67005

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  67006   TACGTTTTCTACATCCAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  67065

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  67066   AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  67125

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  67126   ACACCGCCCTTCACCCTC  67143
```

>emb|AL354697.5| Homo sapiens chromosome 13 clone RP11-475C17, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces

Length = 139533

Score = 802 bits (417), Expect = 0.0
Identities = 431/438 (98%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  130271  GATCCAAACTGGGAGTAGATACCCCGCTATGCTTAACCCTAAACTCGAATAGTTAGATCA  130330

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  130331  ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  130390

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  130391  CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  130450

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  130451  CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  130510

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  130511  AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  130570

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  130571  TACGTTTTCTACATCCAAAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  130630

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  130631  AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  130690

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  130691  ACACCGCCCTTCACCCTC  130708
```

>gb|AC044785.3|AC044785 Homo sapiens chromosome 02 clone RP11-500I10, 97 unordered pieces

Length = 302859

Score = 767 bits (399), Expect = 0.0
Identities = 425/438 (97%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  296127  GATCCAAACTGGGAGTAGATACCCCGCTATGCTTAACCCTAAACTCGAATAGTTAGATCA  296186

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
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Sbjct:  296187  ACAAAACTGTTCACCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  296246

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  296247  CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  296306

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  296307  CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  296366

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  296367  ACAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATAGG  296426

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  296427  TATGTTTTCTACATCCAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  296486

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  296487  AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATCGAATAAGGCCATGAAGCACGCAC  296546

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  296547  ACACCGCCCTTCACCCTC  296564
```

>gb|AC021029.5|AC021029 Homo sapiens chromosome 09 clone RP11-156F19, WORKING DRAFT SEQUENCE,
13 unordered pieces
Length = 175054

Score = 767 bits (399), Expect = 0.0
Identities = 425/438 (97%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  109123  GATCCAAACTGGGAGTAGATACCCCGCTATGCTTAACCCTAAACTCGAATAGTTAGATCA  109182

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  109183  ACAAAACTGTTCACCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  109242

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  109243  CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  109302

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  109303  CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  109362

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  109363  ACAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATAGG  109422

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  109423  TATGTTTTCTACATCCAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  109482

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  109483  AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATCGAATAAGGCCATGAAGCACGCAC  109542

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  109543  ACACCGCCCTTCACCCTC  109560
```

>emb|AL354822.3| Homo sapiens chromosome 13 clone RP11-474C22, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces
Length = 137705

Score = 756 bits (393), Expect = 0.0
Identities = 423/438 (96%)

Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  56589   GATCCAAACTGGGAGTAGATACCCCGCTATGCTTAACCCTAAACTCGAATAGTTAGATCA  56648

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  56649   ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  56708

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  56709   CTTTACATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  56768

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  56769   CTCTTGCCCAGACTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  56828

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  56829   ATAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATAGG  56888

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  56889   TACGTTTTCTACATCCAGAAAAATCTCGTGACAACCGGTATGAAATCTAAGGGCTCAAGG  56948

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  56949   AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATAGAATAAGGCCATGAAGCACGCAC  57008

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  57009   ACACCGCCCTTCACCCTC  57026
```

>gb|AC024975.2|AC024975 Homo sapiens chromosome 13 clone RP11-542E15 map 13, WORKING DRAFT
SEQUENCE, 26 unordered pieces
Length = 155958

Score = 750 bits (390), Expect = 0.0
Identities = 422/438 (96%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  113560  GAGGATGACGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAATTAAACACTCTGCTCTC  113619

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  113620  AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGACATTTTT  113679

Query:  133     CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  113680  CTGGATGTAGAAAACGTTCCCATTTCTTGCCACCTTATGGGCTACACCTTGACCTAAAGT  113739

Query:  193     TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  113740  TTTTATGTAGATACTTGTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  113799

Query:  253     ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  113800  ATTTAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  113859

Query:  313     CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  113860  CTTTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  113919

Query:  373     TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  113920  TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGAGTTAAGCATAGCGGGGTAT  113979

Query:  433     CTAATCCCAGTTTGAATC  450
Sbjct:  113980  CTACTCCCAGTTTGGATC  113997
```

>gb|AC026079.4|AC026079 Homo sapiens chromosome 10 clone RP11-351N21, WORKING DRAFT SEQUENCE,
16 unordered pieces
Length = 141075

Score = 744 bits (387), Expect = 0.0
Identities = 421/438 (96%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  88738   GAGGGTGACGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAATTAAACACTCTGCTCTC  88797

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  88798   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGACATTTTT  88857

Query:  133     CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  88858   CTGGATGTAGAAAACGTTCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAAGT  88917

Query:  193     TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  88918   TTTTATGTAGATACTTGTGCTTACTCTGCGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  88977

Query:  253     ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  88978   ATTTAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGCCTC  89037

Query:  313     CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  89038   CTTTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  89097

Query:  373     TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  89098   TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGAGTTAAGCATAGCGGGGTAT  89157

Query:  433     CTAATCCCAGTTTGAATC  450
Sbjct:  89158   CTACACCCAGTTTGGATC  89175
```

>gb|AC125394.21| Pan troglodytes clone rp43-45i3, WORKING DRAFT SEQUENCE, 2 ordered pieces
Length = 214459

Score = 739 bits (384), Expect = 0.0
Identities = 420/438 (95%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  161410  GAGGCTGACGGGCGGTGTGTGCGTGCTTCATGGCCTTATTCAGTTAAACACTCTGCTCTC  161469

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  161470  AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCACGAGATTTTT  161529

Query:  133     CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  161530  CTGGATGTAGAAAACGTTTCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  161589

Query:  193     TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  161590  TTTTATGTAGATACTTGTGCTTACTCTGTGGCCTTTCCAGGGTTTGCGGAAGATGGAGGT  161649

Query:  253     ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  161650  ATTTAGGCTGGGCAAGAGGTGGTGAGATAAATTGGGGTTTATCGATTACAGAACAGGCTC  161709

Query:  313     CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
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Sbjct:  161710  CTTTAGAGGGATATAAAGCACGGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  161769

Query:  373     TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  161770  TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGCGGGATAT  161829

Query:  433     CTAATCCCAGTTTGAATC  450
Sbjct:  161830  CTACTCCCAGTTTGGATC  161847
```

>gb|AC091085.2| Homo sapiens chromosome 17 clone RP11-10A10 map 17, WORKING DRAFT SEQUENCE, 3 unordered pieces

Length = 167426

Score = 733 bits (381), Expect = 0.0
Identities = 419/438 (95%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  47005   GATCCAAATTGGGAGAAGATACCCCGCTATGCTTAACCCTAAACTCGAATAGTTAGATCA  47064

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  47065   ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTTGCGGTG  47124

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  47125   CTTTACATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAGCCCCAATTTACCTCACCAC  47184

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  47185   CTCTTGTCCAGACTATATACATCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  47244

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  47245   ATAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGTAAGAAATAGG  47304

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  47305   TACGTTTTCTACATCCAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  47364

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  47365   AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATAAGGCCATGAAGCACGCAC  47424

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  47425   ACACCGCCCTTCACCCTC  47442
```

>emb|AL355793.5| Homo sapiens chromosome 1 clone RP4-694M10, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces

Length = 101109

Score = 727 bits (378), Expect = 0.0
Identities = 418/438 (95%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  539     GATCCAAACTGGGAGTAGATACCCCGCTATGCTTAACTCTAAACTCGAATAGTTAGATCA  598

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  599     ACAAAACTGTTGGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  658

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  659     CTTTATAGCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCGCAATTTACCTCACCAC  718
```

```
Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  719     CTCTTACCCAGCCTAATACCTCCATCTTCAGCAAACGCTGGAAAGGCCGCAGAGTAAGC  778

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  779     ACAAGTATCTACATAAAAACTTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  838

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  839     AACGTTTTCTACATCCAGAAAAATGTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  898

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  899     AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATAAGGCCATGAAGCATGCAC  958

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  959     ACACCGCCCGTCACCCTC  976
```

>gb|AC000382.2|HSAC000382 Homo sapiens chromosome 11 clone pDJ197h17, *** SEQUENCING IN
PROGRESS ***, 11 unordered pieces
Length = 114546

Score = 721 bits (375), Expect = 0.0
Identities = 417/438 (95%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  85304   GAGGGTGAAGGGAGGTGTGTGCGTGCTGCATGGCCTTATTCTATTAAACACTCTGCTCTC  85363

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  85364   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  85423

Query:  133     CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  85424   CTGGATGTAGAAAACGTACCTATTTCTTGCCACCTCATGGGCTACACTTTGACCTAACGT  85483

Query:  193     TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  85484   TTTTATGTAAATACTTATGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAAATGGAGGT  85543

Query:  253     ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  85544   ATATAGTCTGGGCAAGAGGTGGTGAGCCAAATTGGGGTTTATGGATTATAGAACAGGCTC  85603

Query:  313     CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  85604   CTTTAGAGGGATGTAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  85663

Query:  373     TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  85664   TCTGGAGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGCGGGGTAT  85723

Query:  433     CTAATCCCAGTTTGAATC  450
Sbjct:  85724   CTACTCCCAGTTTGGATC  85741
```

>gb|AC068398.3|AC068398 Homo sapiens chromosome 2 clone RP11-73N12 map 2, WORKING DRAFT
SEQUENCE, 35 unordered pieces
Length = 129414

Score = 721 bits (375), Expect = 0.0
Identities = 417/438 (95%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
```

```
Sbjct:  18086   GATCCAAACTGGGAGTAGATACCCCGCTATGCTTAACTCTAAACTCGAATAGTTAGATCA  18145

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  18146   ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAGACTCAAAGGACTTGGCGGTG  18205

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  18206   CTTTGTATCCCTCTAAAGGAGGCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  18265

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  18266   CTCTTGCCCAGCCTAAATACCTCCATCTTCAGCAAACCCTGAAAAGGCTGCAGAGTAAGC  18325

Query:  210     AGAAGTATCTACATAAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  18326   ACAAGTATCTACATAAAAAACTTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  18385

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  18386   AAAGTTTTCTACATCCAGAAAAAATGTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  18445

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  18446   AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATAAGGCCATGAAGCATGCAC  18505

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  18506   ACACCGCCCGTCACCCTC  18523
```

>gb|AC087707.1|AC087707 Homo sapiens clone RP11-485P11, LOW-PASS SEQUENCE SAMPLING
Length = 64287

Score = 708 bits (368), Expect = 0.0
Identities = 411/433 (94%)
Strand = Plus / Minus

```
Query:  445     AAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAAA  386
Sbjct:  10800   AAACTCGGNATAGATACCCCGCTATGCTTAACTCTAAACTCAATAGTTAGATCAAAAAA  10859

Query:  385     ACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTA  326
Sbjct:  10860   ACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTTA  10919

Query:  325     TATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTT  266
Sbjct:  10920   TATCCCTCTAAAGGAGCCTGTTCTATAATTGATAAACCCCAATTTACCTCACCACCTCTT  10979

Query:  265     GCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAG  206
Sbjct:  10980   GCCCAGCCTAAATACCTCCATCTTCAGCAAACCCTGGAAAGGCTGCAGAGTAAGCACAAG  11039

Query:  205     TATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGTACGT  146
Sbjct:  11040   TATCTACACAAAAACTTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGAACGT  11099

Query:  145     TTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGAT  86
Sbjct:  11100   TTTCTACATCCAGAAAAATGTCACGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGAT  11159

Query:  85      TTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACC  26
Sbjct:  11160   TTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATAAGGCCATGAAGCATGCACACACC  11219

Query:  25      GCCCGTCACCCTC  13
Sbjct:  11220   GCCCGTCACCCTC  11232
```

>gb|AC022192.3|AC022192 Homo sapiens clone RP11-23B24, WORKING DRAFT SEQUENCE, 18 unordered
pieces
Length = 156897

```
 Score =  706 bits (367), Expect = 0.0
 Identities = 416/438 (94%), Gaps = 1/438 (0%)
 Strand = Plus / Plus


Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  103913  GAGGGTGACGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAATTAAACACTCTGCTCTC  103972

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  103973  AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGACATTTTT  104032

Query:  133     CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  104033  CTGGATGTAGAAAACGTTCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAAGT  104092

Query:  193     TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  104093  TTTTATGTAGATACTTGTGCTTACTCTGCGGCCTTTCCAGCGTTTGCTGAAGATGGAGGT  104152

Query:  253     ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  104153  ATTTAGGCTGGGTAAGAGTTGGTGAGGTAAATTGCGGTTTATCGATTATAGAACAGGCT-  104211

Query:  313     CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  104212  CTTTAGAGGGCTATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  104271

Query:  373     TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  104272  TCTGGCCAACAGTTTTGTTGATCTAACTATTCGAGTTTAGAGTTAAGCATAGCGGGGTAT  104331

Query:  433     CTAATCCCAGTTTGAATC  450
Sbjct:  104332  CTACTCCCAGTTTGGATC  104349
```

>gb|AC027456.3|AC027456 Homo sapiens chromosome 21 clone RP11-435B5 map 21, WORKING DRAFT

SEQUENCE, 33 unordered pieces
Length = 191109

```
 Score =  704 bits (366), Expect = 0.0
 Identities = 414/438 (94%)
 Strand = Plus / Plus


Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  62434   GAGGGTGACGGGCGGCGTGTGCATGCTTCATGGCCTTATTCAATTAAACACTCTGCTCTC  62493

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  62494   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATGGCATAACGGTTGAAACGACATTTTT  62553

Query:  133     CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  62554   CTGGATGTAGAAAACGTTCCTATTTCTTGCCACCTCATGGGCTACACCTTGAACTAAAGT  62613

Query:  193     TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  62614   TTTTATGTAGATACTTGTGCTTACTCTGCGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  62673

Query:  253     ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  62674   ATTTAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGCCTC  62733

Query:  313     CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  62734   CTTTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  62793

Query:  373     TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  62794   TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGAGTTAAGCATAGCGGGGTAT  62853
```

```
Query:  433     CTAATCCCAGTTTGAATC  450
Sbjct:  62854   CTACTCCCAGTTTGGATC  62871
```

>gb|AC092432.2| Homo sapiens chromosome 2 clone RP11-96C22, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces
Length = 164144

Score = 702 bits (365), Expect = 0.0
Identities = 415/435 (95%), Gaps = 2/435 (0%)
Strand = Plus / Minus

```
Query:  446     CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  65180   CAAACTGGGAGTAGATACCTCGTTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  65239

Query:  386     AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  65240   AACTGTTTGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  65299

Query:  326     ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  65300   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  65359

Query:  266     TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAA  207
Sbjct:  65360   TGCCCAGCCTATATACCTCCATCTTCAGCAAACTCTGGAAAGGCCGCAGGGTAAGCACAA  65419

Query:  206     GTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGTACG  147
Sbjct:  65420   GTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGTACG  65479

Query:  146     TTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGA  87
Sbjct:  65480   TTTTCTACACCAGAAAAATCTCAGGACAACCTTTAAGAAATCTAAGGGCTCAAGGAGGA  65539

Query:  86      TTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAA-TGAGGCCATGAAGCACGCACACA  28
Sbjct:  65540   TTTAGCAATAAATTGAGAGCAGAGTGCTTAATTGAATTAAGGCCATG-AGCACGCACACA  65598

Query:  27      CCGCCCGTCACCCTC  13
Sbjct:  65599   CCGCCCATCACCCTC  65613
```

>gb|AC024170.3|AC024170 Homo sapiens chromosome 3 clone RP11-65D20 map 3p, WORKING DRAFT SEQUENCE, 29 unordered pieces
Length = 192554

Score = 702 bits (365), Expect = 0.0
Identities = 415/435 (95%), Gaps = 2/435 (0%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCC-TCATTCAATTAAACACTCTGCTCT  71
Sbjct:  116911  GAGGGTGATGGGCGGTGTGTGCGTGC-TCATGGCCTTAATTCAATTAAGCACTCTGCTCT  116969

Query:  72      CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  116970  CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCTTAAAGGTTGTCCTGAGATTTT  117029

Query:  132     TCTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  117030  TCTGGGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  117089

Query:  192     TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  117090  TTTTTATGTAGATACTTGTGCTTACCCTGCGGCCTTTCCAGAGTTTGCTGAAGATGGAGG  117149

Query:  252     TATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  311
Sbjct:  117150  TATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  117209
```

```
Query:  312     CCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  371
Sbjct:  117210  CCTTTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  117269

Query:  372     TTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTA  431
Sbjct:  117270  TTCTGGCAAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAACGAGGTA  117329

Query:  432     TCTAATCCCAGTTTG  446
Sbjct:  117330  TCTACTCCCAGTTTG  117344
```

>gb|AC068239.1|AC068239 Homo sapiens chromosome 2 clone RP11-804P4 map 2, LOW-PASS SEQUENCE
SAMPLING
Length = 66857

Score = 554 bits (288), Expect = e-155
Identities = 349/374 (93%), Gaps = 3/374 (0%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  29486   GATCCAAATTGGGAGAAGATACCCCGCTATGCTTAACCCTAAACTCGAATAGTTAGATCA  29545

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  29546   ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTTGCGGTG  29605

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  29606   CTTTACATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAGCCCCAATTTACCTCACCAC  29665

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  29666   CTCTTGTCCAGACTATATACATCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  29725

Query:  210     AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  29726   ATAAGTATCTACATAAAAACGNTAGGTCAAGGTGTANCCCATGAGGTGGTAA-AAATAGG  29784

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  29785   TACCTTTTCTACATNCAGAAAAATCTCGCGACCACCGTTATGAAATCTAA-GGCTCAA-G  29842

Query:  90      AGGATTTAGCAATA  77
Sbjct:  29843   AGGATTTANCAATA  29856
```

>gb|AC016147.12|AC016147 Homo sapiens chromosome 3 clone RP11-38N24, WORKING DRAFT SEQUENCE,
21 unordered pieces
Length = 163310

Score = 535 bits (278), Expect = e-149
Identities = 318/338 (94%)
Strand = Plus / Plus

```
Query:  113     ACGGTTGTCGCGAGATTTTTCTGTGTGTAGAAAACGTACCATTTCTTGCCACCTCATGG  172
Sbjct:  71810   ACGGGTGTCGCGAGATTTTTCTGGATGTAGAAAACGTTTCCATTTTTTGCCACCTCGTGG  71869

Query:  173     GCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAG  232
Sbjct:  71870   GCGTGGCCTTGACCTAACGTTTTTATGTAGATACTTGTGCTTACTCTGTGGCCTTTCCAG  71929

Query:  233     GGTTTGCTGAAGATGGAGGTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTT  292
Sbjct:  71930   GGTTTGCTGAAGATGGAGGTATTTAGGCTGGGCAAGAGGTGGTGAGATAAATTGGGGTTT  71989
```

```
Query:  293     ATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTT  352
Sbjct:  71990   ATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCATGGCCAAGTCCTTTGAGTTT  72049

Query:  353     TAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAG  412
Sbjct:  72050   TAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTGTTCGAGTTTAG  72109

Query:  413     GGTTAAGCATAGTGGGGTATCTAATCCCAGTTTGAATC  450
Sbjct:  72110   GGTTAAGCATAGCGGGGTATCTACTCCCAGTTTGGATC  72147
```

>gb|AC068619.4|AC068619 Homo sapiens chromosome 17 clone RP11-646F1, WORKING DRAFT SEQUENCE,
10 unordered pieces
Length = 153089

Score = 525 bits (273), Expect = e-146
Identities = 391/440 (88%), Gaps = 4/440 (0%)
Strand = Plus / Minus

```
Query:  450     GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  1394    GATTCAAACTGGGATTAGATACCCCACTATGCTCAGCCCTAAACTTCAACAGTTAAATCA  1453

Query:  390     ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  1454    ACAAAACTGCTCGCCAGAACACTAGGAGCAACAGCTTAAAACTCAAAGGACCTGGCGGTG  1513

Query:  330     CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1514    CTTCACATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCAATTCACCTCACCAC  1573

Query:  270     CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAG  212
Sbjct:  1574    CTCTTGCTCAACCCATATACCGCCATCTTCAGCAAACCCTGACAAAGGCCACAAAGTAAG  1633

Query:  211     CAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  1634    CACAAGTATCTACATAAAAATGTTAGGTCAAGGTGTAGCCTATGAGGTGGCAAGAAATGG  1693

Query:  151     G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  1694    GCTACATTTTCTAC-CCCAGAAAATTCT-ACAATAACCCTTATGAAACCTGAGGGTCCAA  1751

Query:  92      GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  1752    GGAGGATTTAGTAGTAAATTAAGAACAGAGTGCTTAATTGAATAGGGCCATAAAGCACGC  1811

Query:  32      ACACACCGCCCGTCACCCTC  13
Sbjct:  1812    ACACACCACCCATCACCCTC  1831
```

>gb|AC015935.7| Homo sapiens chromosome 17 clone CTD-2354J3 map 17, 8 unordered pieces
Length = 174208

Score = 512 bits (266), Expect = e-142
Identities = 383/434 (88%), Gaps = 4/434 (0%)
Strand = Plus / Minus

```
Query:  443     ACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAAAAC  384
Sbjct:  82198   ACTGGGATTAGATAACCCCCTATGCTTAGCCCTAAACTCTAATAGTTACATTAACAAAAC  82257

Query:  383     TGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATA  324
Sbjct:  82258   CATTCGCCAGAGTACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATA  82317

Query:  323     TCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG-  265
```

```
Sbjct:  82318   TCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCTGATATACCTCACCACCTCTTGC  82377

Query:  264     -CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAG  206
Sbjct:  82378   CCCCAGCCTGTATAGTGCCATCTTCAGCAAACCCTAAAAAGGTTGTAGAGTAAGCACAAG  82437

Query:  205     TATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TACG  147
Sbjct:  82438   TATACACATAAAAACATTAGGTCAAGGTGTAGCTCATGAGGTGGCAAGAAATGGGCTACA  82497

Query:  146     TTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGA  87
Sbjct:  82498   TTTTCTATACTCAG-AAAATCTCACGACAATCTTTATGACATCTAAGGGCTCAAGGAGGA  82556

Query:  86      TTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACAC  27
Sbjct:  82557   TTTGGCAGTAAACCAAGAGCAGAGTGCTTGGTTGAATAAGGCCATGAAGCATGCACACAC  82616

Query:  26      CGCCCGTCACCCTC  13
Sbjct:  82617   CGCCCATCACCCTC  82630
```

>gb|AC058808.1|AC058808 Homo sapiens chromosome 11 clone RP11-37O16 map 11, WORKING DRAFT SEQUENCE, 15 unordered pieces

Length = 175977

Score = 489 bits (254), Expect = e-135
Identities = 384/439 (87%), Gaps = 5/439 (1%)
Strand = Plus / Plus

```
Query:  16      GGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAAT  75
Sbjct:  17737   GGTGACAGGCAGTGTGTGTGTGCTTCATGGCCTTATTCAACCAAGCACTCTACTCTTGGT  17796

Query:  76      TTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTTCTG  135
Sbjct:  17797   TTACTGCTAAATCCTCCTTGAGTCTTTTGATTTCATAAAGGTTGTCGTGAGATTTT-CTG  17855

Query:  136     TGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTT  194
Sbjct:  17856   GGTATAGAAAATGTAGCCCATTTCTTCCCACCTCATGAGCTACACCTTGACCTAATGTTT  17915

Query:  195     TTATGTAGAT-ACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTA  253
Sbjct:  17916   TTATGTGTATTACTTGTGCTTACTCTATAACCTTTTTAGGGTTTGCTGAAGATGGCGGTA  17975

Query:  254     TATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  311
Sbjct:  17976   TATAGGCTGGGGGCAAGAGGTGGTGAGGTAGATCGGGGTTTATAGATTATAGAACAGGCT  18035

Query:  312     CCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  371
Sbjct:  18036   CCCCTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTATTGCTTCTAGTA  18095

Query:  372     TTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTA  431
Sbjct:  18096   TTCTGGCGAATGGTTTTGTTAATATAACTATTATAGTTTAGGGCTAAGCATAGTGGGGTA  18155

Query:  432     TCTAATCCCAGTTTGAATC  450
Sbjct:  18156   TCTAACCCCAGTTTGGATC  18174
```

>gb|AC021473.3|AC021473 Homo sapiens clone RP11-705H21, WORKING DRAFT SEQUENCE, 16 unordered pieces

Length = 177897

Score = 483 bits (251), Expect = e-133
Identities = 380/437 (86%), Gaps = 4/437 (0%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  51386   GAGGGTCACGGGTGGTGTGTGCATGCTTCATGGCCTTATTCAACCAAGCACTCTGCTCTT  51445

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  51446   GGTTTACTGCTAAATCCTCCTTGAGCCCTTAGATTTCCTAAAGGATGTTGTGAGATTTT-  51504

Query:  133     CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  51505   CTGGACATAGAAAATGTAGCCCATTTCGTGCCACCTCATGGGCTACACCTTGACCTAATG  51564

Query:  192     TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  51565   TTTTTATGTGTGTACTTGTGCTTACTTTGTGACCTTTTTAGGGTTTGCTGAAGATGGCGG  51624

Query:  252     TATATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  51625   TATATAGGCTGGGGGCAAGAGGTGGTGAGGAGCACCAGGGTTTATTGATTATAGAACAAG  51684

Query:  310     CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAG  369
Sbjct:  51685   CTCCTTTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTGG  51744

Query:  370     TGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGG  429
Sbjct:  51745   TACTCTGGTGAATGGTTTTGTTAATATAACTATTAGAGTTTAGGGCTAAGCATAGTGGTG  51804

Query:  430     TATCTAATCCCAGTTTG  446
Sbjct:  51805   TATCTAATCCAAGTTTG  51821
```

>gb|AC024498.2|AC024498 Homo sapiens chromosome 1 clone RP11-148L4 map 1, WORKING DRAFT
SEQUENCE, 18 unordered pieces
Length = 152309

```
 Score =  473 bits (246), Expect = e-130
 Identities = 377/435 (86%), Gaps = 4/435 (0%)
 Strand = Plus / Minus


Query:  444     AACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAAAA  385
Sbjct:  91827   AACTGGGATTAGATAACCCACTGTGCTTAGCCCTAAGCTCTAATAGTTAACTAACAAAA  91886

Query:  384     CTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTAT  325
Sbjct:  91887   CCATTCGCCAGAATACTGCAAGCAACAGCTTAAAATTCAAAGGACTTGGCGGTACTTTAT  91946

Query:  324     ATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG  265
Sbjct:  91947   ACCCCTCTAGAGCAGCCTGTTCTATAATCGATAAACCCCGATATACCTCACCACCTCTTG  92006

Query:  264     --CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAA  207
Sbjct:  92007   CCCCCAGCCTATATACTGCCATCTTCAGTAAACCCTAAAAAGGTAATAAAGTAAGCACAA  92066

Query:  206     GTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TAC  148
Sbjct:  92067   GTACACACATAAAAACGTTAGGTCAAGGCGTAGCCCATGAGGTGGCAAGAAATGGGCTAC  92126

Query:  147     GTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGG  88
Sbjct:  92127   ATTTTCTATACCCAG-AAAATATTACTACAACCCTTATGAAATCTAAGGGCTCAAGGAGA  92185

Query:  87      ATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACA  28
Sbjct:  92186   ATTTAGCAGGAAACCAAGAGTAGAGTGCTTGGTTGAATAAGGCCATGAAGCATGCACACA  92245

Query:  27      CCGCCCGTCACCCTC  13
Sbjct:  92246   CCGCCCGTCACCCTC  92260
```

>emb|AL359533.1| Mus musculus chromosome X clone RP21-247L20, *** SEQUENCING IN

PROGRESS ***, 6 unordered pieces
Length = 159765

Score = 467 bits (243), Expect = e-129
Identities = 376/435 (86%), Gaps = 4/435 (0%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  121806  GAGGGTGACGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAACCAAGCACTCTACTCTT  121865

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  121866  GGTTTCCTGCTAAATTCTCCTTGAGCCCTTAGATTTCATAAGGGTTGTAGTAATATTTT-  121924

Query:  133     CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  121925  CTGGGTATAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACGCCTTGACCTAACG  121984

Query:  192     TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  121985  TTTTTATGTGTGTACTTGTGCTTACTTTATTACCTTTTTAGGGTTTACTGAAGATGGCAG  122044

Query:  252     TATATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  122045  TATATAGGCTGGGGGCAAGAGGTGGTGAGGTATATCGGGGTTTATCGATTATAGAACAGG  122104

Query:  310     CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAG  369
Sbjct:  122105  CTGCTCTAGAGGGGTATAAAGTACCTCCAAGTCCTTTGAATTTTAAGCTGTTGCTTGCAG  122164

Query:  370     TGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGG  429
Sbjct:  122165  TATTCTGGCGAATGGTTTTGTTAGTTTAACTATTAGAGCTTAGGGCTAAGCACAGTGGGT  122224

Query:  430     TATCTAATCCCAGTT  444
Sbjct:  122225  TATCTAATCCCAGTT  122239
```

>gb|AC016151.20| Homo sapiens chromosome 3 clone RP11-141N10, WORKING DRAFT SEQUENCE,
26 unordered pieces
Length = 168706

Score = 464 bits (241), Expect = e-127
Identities = 290/307 (94%), Gaps = 3/307 (0%)
Strand = Plus / Plus

```
Query:  144     AAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTTTTATGTAGA  203
Sbjct:  20924   AAACGTTTCCAATTCTTGCCACCTCATGG-CTACACCTTGACATAACGTTCTTATGTAGA  20982

Query:  204     TACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTATATAGGCTGG  263
Sbjct:  20983   TACTTGTGCTTACTCTGTG-CCTTTCCAGG-TTTGCTGAAGATGGAGGTATTTAGGCTGG  21040

Query:  264     GCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGA  323
Sbjct:  21041   GCAAGAGGTGGTGAGATAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGA  21100

Query:  324     TATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACA  383
Sbjct:  21101   TATAAAGCATGGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACA  21160

Query:  384     GTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGT  443
Sbjct:  21161   GTTTTGTTGATCTAACTGTTCGAGTTTAGGGTTAAGCATAGCGGGGTATCTACTCCCAGT  21220

Query:  444     TTGAATC  450
Sbjct:  21221   TTGGATC  21227
```

>gb|AC069389.3|AC069389 Homo sapiens chromosome 8 clone RP11-350F16, WORKING DRAFT

```
SEQUENCE,
           27 unordered pieces
         Length = 160865

 Score =  433 bits (225), Expect = e-118
 Identities = 370/435 (85%), Gaps = 3/435 (0%)
 Strand = Plus / Plus


Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  94344   GAGAGTGATGGGAGGGGTGTGCATGCTTCATGGCTTTATTCAACCAAGCACTCTGATCTT  94403

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  94404   GGTTTACTGCTAAATCCTCCTTGAGCCCTTCGATTTCATAAAGGTTGTTGTGAGATTTT-  94462

Query:  133     CTGTGTGTAGAAAACGTACCC-ATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  94463   CTGGGTATACAAAATGTAGTCTACTTCTTGCCACCTCATGAGCTACACCTTGACCTAACG  94522

Query:  192     TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  94523   TTTTTATGTGTACACTTGTGCTTACTCTATAACCACTTTAGGGTTTGCTGAAGATGGTGG  94582

Query:  252     TATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  311
Sbjct:  94583   TATATAGGCTGGGCAAGAGGTGGTGAGGTATATTGGGGTTTATTAATTATAGAACAGGAT  94642

Query:  312     CCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  371
Sbjct:  94643   CCTCTAGAGGGATAT-AAGCAGCATCAAATCCTTTGAGTTTTTAGCTGTTGCTGGTAGTA  94701

Query:  372     TTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTA  431
Sbjct:  94702   TTCTGGCAAATTTTTTTTTAAATGTAACTATTAGAGTTTAGGGGTAAGCATAGTGGGGTA  94761

Query:  432     TCTAATCCCAGTTTG  446
Sbjct:  94762   TCTAATCCCAGTTTG  94776
```

```
>gb|AC025337.1| Homo sapiens chromosome 17 clone RP11-471P22 map 17, LOW-PASS
           SEQUENCE SAMPLING
         Length = 83905

 Score =  421 bits (219), Expect = e-115
 Identities = 366/425 (86%), Gaps = 7/425 (1%)
 Strand = Plus / Plus


Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  81630   GAGGGTGATGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAACCAAGCACTCTGCTCTT  81689

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  81690   GGTTTACTGCCAAATCCTCCTTGAGCCCTTAGATGTCATAAAGATTGTCGTGAGA-TTTT  81748

Query:  133     CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  81749   CTGAGTATAGAAAATGTAGCCCATTTCTTGCCACCTCATGAGCTACACCTTGACCTAATG  81808

Query:  192     TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  81809   TTTTTATGTGTATACTTGTGCTTACTCTACAACCTTTTTAGGGTTTGCTGAAGATGGCAC  81868

Query:  252     TATATAGGCT--GGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  81869   TATACACGCTGNGGGCAAGAGGTGGTGAGGTATATCANGGTTTATCGATTATAGAACAGG  81928

Query:  310     CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTT-TGAGTTTTAAGCTGTTGCTTGTA  368
Sbjct:  81929   CTCCTCTAGAGGGATATAAAGCACTGCCAAGTCCTTCTGAGTTTTAAGCTGTTGCTTGTA  81988
```

```
Query:  369    GTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGG  428
Sbjct:  81989  GTACTCTGGCGAATGGGTTTTGTTATGTGACTATTAGAG-TTAGGGCTAA-CATAGTGGG  82046

Query:  429    GTATC  433
Sbjct:  82047  TTATC  82051
```

>gb|AC024954.3|AC024954 Homo sapiens clone RP11-3E16, WORKING DRAFT SEQUENCE, 20 unordered pieces
Length = 172138

```
 Score =  419 bits (218), Expect = e-114
 Identities = 372/439 (84%), Gaps = 6/439 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  50493  CAAACTGAGATTAGATATCCCATCATGCTTAGCCCTAAACTATAATAGTTAAATTAACAA  50552

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  50553  AATTATTTGCCGGAATACTACAAGCAAGAACTTAAAATTAAAAGGACTTGGCGGTGCTTT  50612

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  50613  ATATCCCTCTAGAGGGGCCTGTTCTATAATCCGTAAACCCCGATACACCTCACCACCTCT  50672

Query:  266    TGCC---CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCA  210
Sbjct:  50673  TGCCCCACAGCCCATATACCACCATCGTCAGCAAACCCTAGAAAGGTTGCAGAGTAAGCA  50732

Query:  209    GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-  151
Sbjct:  50733  CAAGTATATTCATAAAAATTTTAGGTCAAGGTGTAGCCTACGAGGTGGCAAGAAATGGGC  50792

Query:  150    TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  50793  TACATTTTCTATAC-CCGAAAAATCTCACAACAACCCTTATGCAATCTAAAGGCTTAAGG  50851

Query:  90     AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  50852  AGGATTTAGCAGTAAACAAAGAGCAGAGTGCTTGGTTGAATAAGGCCATGAAGCACACAG  50911

Query:  30     ACACCGCCC-GTCACCCTC  13
Sbjct:  50912  ACACAACCCTGTCACCCTC  50930
```

>gb|AC023928.3|AC023928 Homo sapiens chromosome 2 clone RP11-283F6 map 2, WORKING DRAFT SEQUENCE, 18 unordered pieces
Length = 180059

```
 Score =  419 bits (218), Expect = e-114
 Identities = 372/439 (84%), Gaps = 6/439 (1%)
 Strand = Plus / Plus


Query:  13     GAGGGTGAC-GGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCT  71
Sbjct:  55390  GAGGGTGACAGGGTTGTGTCTGTGTGCTTCATGGCCTTATTCAACCAAGCACTCTGCTCT  55449

Query:  72     CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  55450  TTGTTTACTGCTAAATCCTCCTTAAGCCTTTAGATTGCATAAGGGTTGTTGTGAGATTTT  55509

Query:  132    TCTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  190
Sbjct:  55510  TCGG-GTATAGAAAATGTAGCCCATTTCTTGCCACCTCGTAGGCTACACCTTGACCTAAA  55568

Query:  191    GTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAG  250
```

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Sbjct:  55569   ATTTTTATGAATATACTTGTGCTTACTCTGCAACCTTTCTAGGGTTTGCTGACGATGGTG  55628

Query:  251     GTATATAGGCTG---GGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  55629   GTATATGGGCTGTGGGGCAAGAGGTGGTGAGGTGTATCGGGGTTTACGGATTATAGAACA  55688

Query:  308     GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  55689   GGCCCCTCTAGAGGGATATAAAGCACCGCCAAGTCCTTTTAATTTTAAGTTCTTGCTTGT  55748

Query:  368     AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  55749   AGTATTCCGGCAAATAATTTTGTTAATTTAACTATTATAGTTTAGGGCTAAGCATGATGG  55808

Query:  428     GGTATCTAATCCCAGTTTG  446
Sbjct:  55809   GATATCTAATCTCAGTTTG  55827
```

>gb|AC022223.18| Homo sapiens chromosome 5 clone RP11-538B23, WORKING DRAFT SEQUENCE, 19 unordered pieces
Length = 140712

Score = 412 bits (214), Expect = e-112
Identities = 372/436 (85%), Gaps = 8/436 (1%)
Strand = Plus / Minus

```
Query:  446     CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  79183   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTCAACAGTTAAATTAACAA  79242

Query:  386     AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  79243   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  79302

Query:  326     ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  79303   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGAT-AACCCCGATCAACCTCACCACCTCT  79361

Query:  266     TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  79362   TGCTCAG-CTATATACCGCCATCTTCAGCAAACCCTGACGAAGGCTGCAAAGTAAGCGCA  79420

Query:  207     AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  79421   AGTACCCACGTAAAGATGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  79480

Query:  148     CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  79481   CATTTTCTAC-TTCAGAAAACT---ACGATAACCCTTATGAAATTTAAGGGTCGAAGGTG  79536

Query:  88      GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  79537   GATTTAGCAGTAAACTAAGAGTAGAGTGCGTAGTTGAACAGGGCCCTGAAGCGCGTACAC  79596

Query:  28      ACCGCCCGTCACCCTC  13
Sbjct:  79597   ACCGCCCGTCACCCTC  79612
```

>gb|AC021442.2|AC021442 Homo sapiens chromosome 11 clone RP11-682I19 map 11, LOW-PASS SEQUENCE SAMPLING
Length = 67508

Score = 410 bits (213), Expect = e-111
Identities = 331/380 (87%), Gaps = 5/380 (1%)
Strand = Plus / Minus

```
Query:  391     AACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGT  332
Sbjct:  59950   AACAAAACCATTCACCAGAATACTAGAAGCAATAGCTTAAAACTCAAAGGACTTGGCGGT  60009
```

```
Query:  331    GCTTTATATCCCTCTAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCA  272
Sbjct:  60010  GCTTTATATCCCTCTAGGGGAGCCTGTTCTATAATCTATAAACCCCGATCTACCTCACCA  60069

Query:  271    CCTCTTG--CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTA  214
Sbjct:  60070  CCTCTTGCCCCCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGTTATAGAGTA  60129

Query:  213    AGCAGAAGT-ATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAA  155
Sbjct:  60130  AGCACAAGTAATACACATAAAAACATTAGGTCAAGGTGTAGCTCATGAGGTGGGAAGAAA  60189

Query:  154    TGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCT  96
Sbjct:  60190  TGGGCTACATTTTCTATACCCAG-AAAATCTCACGACAACCTTTATGAAATCAAAAGACT  60248

Query:  95     CAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  60249  CAAGGAGGATTTAGCAGTAAACCAAGAGTAGAGTGCTTGGTTGAATAAGGCCATGAAGCA  60308

Query:  35     CGCACACACCGCCCGTCACC  16
Sbjct:  60309  CACACACACTGCCTGTCACC  60328
```

>gb|AC068010.4|AC068010 Homo sapiens clone RP11-3J16, WORKING DRAFT SEQUENCE, 37 unordered pieces
Length = 165652

Score = 406 bits (211), Expect = e-110
Identities = 366/436 (83%), Gaps = 5/436 (1%)
Strand = Plus / Plus

```
Query:  12     AGAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCT  71
Sbjct:  80475  AGAGGGCGATGGGTGGTGTGTGCATGCTTCACGGCCTCATTCAATGAAGCACTCTGTTCT  80534

Query:  72     CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  80535  TCATTTACCGCTAAATCCTCTTTGAATCTTTAGGTTTCATTATGGTTATTGTAAAATTTT  80594

Query:  132    TCTGTGTGTAGAAAACGTACC-CATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  190
Sbjct:  80595  -CGGGAAATAGAAAATGTAGCTCATTTCTTACCATTTCATAGGCAACACCTTGACCTAAT  80653

Query:  191    GTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAG  250
Sbjct:  80654  GTTTTTATGTACATACTTGTGCTTACTCTAAGGCCTTTTTAGGGTTTGCTGAAGATGGTG  80713

Query:  251    GTATATAGGCTG---GGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  80714  GTATATAGGCTGAGTGGCGAGAGATGGCGAGGTATATCGGAGTTTACCGATTATACAACA  80773

Query:  308    GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  80774  GGCTCCTCTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGTTTGT  80833

Query:  368    AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  80834  AGTACTCTGGCGAGTAGTTTTGTTAATTTAACTATCTGGGTTTAGGGCTAAGCATAGTGA  80893

Query:  428    GGTATCTAATCCCAGT  443
Sbjct:  80894  GGTATCTAATCCCAGT  80909
```

>gb|AC116047.2| Papio hamadryas clone RP41-440I10, WORKING DRAFT SEQUENCE, 13 ordered pieces
Length = 149468

Score = 383 bits (199), Expect = e-103
Identities = 367/441 (83%), Gaps = 8/441 (1%)
Strand = Plus / Minus

```
Query:  447     TCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACA  388
Sbjct:  78170   TCAAACTGGGATTACAGATCCCACTACGCTTAGCCCTAAACCTCAATAATTAAATAACA  78229

Query:  387     AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  78230   AAACTACTCACCAGAATACTACAAGCAACAGCTTGAAACTCAAAGGACTTGGCAGTGCTT  78289

Query:  327     TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  78290   CACATCCCTCTAGAGGAGCCTGTTCAGTAATCGATAAACCCCGATCCACCTCACCATCTC  78349

Query:  267     TTGCCCAGCCTATATACCT-----CCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAA  213
Sbjct:  78350   TTGCTCAGCCTATATACCATACCACCATCTTCAGCAAACCGTGATAAGGCCACAAAGTTA  78409

Query:  212     GCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  78410   GCATAACCGTCCCCGCAAAAACGTTAGGTCAAGGTGTAGCCTATGAGATGGTAAAAAATG  78469

Query:  152     GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  78470   GGCTACATTTTCTACTC-CAGAAAACCC-CACGATAACTCTTATGAAACCTAAGAGTCCA  78527

Query:  93      AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  78528   AGGAGGATTTAACAGTCAATTAAGAACAGAGTGCTTAATTGAACCAGGCCATGAAGCACG  78587

Query:  33      CACACACCGCCCGTCACCCTC  13
Sbjct:  78588   CACACACCGCCCGTCACTCTC  78608
```

>gb|AF182108.3| Homo sapiens chromosome 8 clone RP11-11N9 map 8p12, WORKING DRAFT SEQUENCE, 9 unordered pieces
Length = 169423

Score = 367 bits (191), Expect = 9e-99
Identities = 307/355 (86%), Gaps = 5/355 (1%)
Strand = Plus / Minus

```
Query:  364     AGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAAAGGAGCCTGT  305
Sbjct:  117096  AGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAGAGGAGCCTGT  117155

Query:  304     TCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG--CCCAGCCTATATACCTCC  247
Sbjct:  117156  TCTATAATCAATGAACCCTGATACACCTCACCGCCTCTTGCCCCCAGCCTATATAGGGCC  117215

Query:  246     ATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTATCTACATAAAAACGTTA  187
Sbjct:  117216  ATCTTCAGCAAACCCTAAAAAGTTTATTGAGTAAGCACAAGTACACACATAAAAATGTTA  117275

Query:  186     GGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TACGTTTTCTACACAGAAAAA  128
Sbjct:  117276  GGTCAAGGTGTAGCCCATGAGATGGCAAGAAATGGGATACATTTTCTATGTCCAG-AAAA  117334

Query:  127     TCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAG  68
Sbjct:  117335  TCTCACGACAACCTTTATGAAATCTAAGGACTC-AGGAAGATTTAGCAATAAACCAAGAG  117393

Query:  67      CAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  117394  CAGAGTGCTTGGTTGAATAAGGCTATGAAGCATGCACACACCACCCGTCACCCTC  117448
```

Score = 48.8 bits (25), Expect = 0.011
Identities = 25/25 (100%)
Strand = Plus / Minus

```
Query:  446     CAAACTGGGATTAGATACCCCACTA  422
```

```
Sbjct:  117043  CAAACTGGGATTAGATACCCCACTA  117067
```

>gb|AC096874.2| Pan troglodytes clone RP43-107P11, WORKING DRAFT SEQUENCE, 2 ordered pieces
Length = 168420

Score = 360 bits (187), Expect = 2e-96
Identities = 258/291 (88%), Gaps = 1/291 (0%)
Strand = Plus / Minus

```
Query:  446     CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  33974   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATTAACAA  34033

Query:  386     AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  34034   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGTTTC  34093

Query:  326     ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  34094   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  34153

Query:  266     TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  34154   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTGCAAGTAAGCGCA  34213

Query:  207     AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGA  157
Sbjct:  34214   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGA  34264
```

>gb|AC097006.1| Pan troglodytes clone RP43-11P24, WORKING DRAFT SEQUENCE, 6 unordered pieces
Length = 203266

Score = 360 bits (187), Expect = 2e-96
Identities = 258/291 (88%), Gaps = 1/291 (0%)
Strand = Plus / Minus

```
Query:  446     CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  27981   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATTAACAA  28040

Query:  386     AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  28041   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGTTTC  28100

Query:  326     ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  28101   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  28160

Query:  266     TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  28161   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTGCAAGTAAGCGCA  28220

Query:  207     AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGA  157
Sbjct:  28221   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGA  28271
```

>gb|AC018856.4|AC018856 Homo sapiens chromosome 2 clone RP11-382I19 map 2, WORKING DRAFT SEQUENCE, 12 unordered pieces
Length = 191507

Score = 352 bits (183), Expect = 4e-94
Identities = 252/284 (88%), Gaps = 2/284 (0%)
Strand = Plus / Minus

```
Query:  446     CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  104447  CAAACTGGGATTAGATACCCAACTATGCTTAGCCCTAAACTATAATAGTTAAATTAACAA  104506

Query:  386     AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  104507  AACAATTTACCAGAATACTACAAGCAACAGGTTAAAACTCAAAGGACTTGGCAGTGCTTT  104566

Query:  326     ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  104567  ATATCCATCTAGAGGAGCCTGTTCTATAATTGATAAACCCCGATGCACCTCACCACCTCT  104626

Query:  266     TG--CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAG  209
Sbjct:  104627  TGCCCCCAGCCTATATGCCACCATCTTCAGCAAACCCTAGAAAGGTTGCAAAGTAAGCAC  104686

Query:  208     AAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGG  165
Sbjct:  104687  AAGTATACACATAAAAATGTTAGGTCAAGGTGTAGCCTATGAGG  104730
```

```
 Score = 96.8 bits (50), Expect = 4e-17
 Identities = 90/110 (81%)
 Strand = Plus / Minus


Query:  131     AAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTG  72
Sbjct:  104750  AAAATCTCATGATAGCCTTTATGAAATCTAAGGGCTCAAAGAGGATTTAGCAGTAAACCA  104809

Query:  71      AGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCC  22
Sbjct:  104810  AGAGCTGAGTGCTTGGTTGAATAGGGTCATGAAGCACACACACGCCACCC  104859
```

>gb|AC021823.3|AC021823 Homo sapiens chromosome 2 clone RP11-169P13 map 2, WORKING DRAFT
SEQUENCE, 22 unordered pieces
Length = 146015

```
 Score =  233 bits (121), Expect = 3e-58
 Identities = 161/181 (88%)
 Strand = Plus / Plus


Query:  267     AGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATAT  326
Sbjct:  77662   AGAGATGATGAGGTACCTCGGGGTTTATCGATTATAGAACAGGCTCCTCTAGAGGGATAT  77721

Query:  327     AAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTT  386
Sbjct:  77722   AAAGCACTGCCAAGTCTTTTGAGTCTTAAGCTGTTGCTTGTAGTACTCTGGTGAATAGTT  77781

Query:  387     TTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  77782   TTGTTGGTTGAACTATTTGGGTTTAGAACTAAGCATAGTGGGGTATCTAATCCCAGTTTG  77841

Query:  447     A  447
Sbjct:  77842   A  77842
```

>gb|AC013632.3|AC013632 Homo sapiens clone RP11-12N13, WORKING DRAFT SEQUENCE, 7 unordered
pieces
Length = 175250

```
 Score =  229 bits (119), Expect = 4e-57
 Identities = 238/295 (80%), Gaps = 4/295 (1%)
 Strand = Plus / Plus
```

```
Query:  156     TTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTA  215
Sbjct:  165724  TTCTTTCCATGTCATAGGCTACACTTTGACCTAATGTTTTTATGCAGCTACTTGCGCTTA  165783

Query:  216     CTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTATATAGGCTGGG----CAAGAGG  271
Sbjct:  165784  CTTTGAGACCTTTTTAGGGTTTGCTGAAGATGGCAGTATATAGGCTGAGTTGCCAAGAGA  165843

Query:  272     TGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGC  331
Sbjct:  165844  TAGTGGGATATGTCAGGGTTTAACGATTATAGAACAGGCTCCTTTAGAGGAGTATAAACC  165903

Query:  332     ACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTT  391
Sbjct:  165904  TTGGCCATGTCCTTTGAGTTTTAAGCTCTTGCTTGTAATACTCTGGTGAATAATTTTGTT  165963

Query:  392     GATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  165964  TGTTAAATTATTTAAGTTTAAGGCTAAGCATAGTGGGGTGTCAAAACCCAGTTTG  166018
```

>gb|AC107879.1| Homo sapiens chromosome 18 clone RP11-584O12 map 18, LOW-PASS SEQUENCE SAMPLING
Length = 46803

Score = 212 bits (110), Expect = 7e-52
Identities = 190/225 (84%), Gaps = 9/225 (4%)
Strand = Plus / Plus

```
Query:  222    GGCCTTTCCAGGGTTTGCTGAAGATGGAGGTATATAGGCTG---GGCAAGAGGTGGTGAG  278
Sbjct:  14095  GGCCTTTTTAGGGTTTGCTGAAGGTGGCAGTACATAGGCTGAGTGGCAAGAGATGGTGAG  14154

Query:  279    GTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCA  338
Sbjct:  14155  GTATATCGGAGTTTATCAATTATAGAACAGGTTCCTCTAGAAGGATATAAAGCACCGCCA  14214

Query:  339    AGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAA  398
Sbjct:  14215  AGT------AGTTTTAAGCTGTGGCTTGTAGTTCTCTGGTGAATAGTTTTGTTAATTTAA  14268

Query:  399    CTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGT  443
Sbjct:  14269  CTACTTGGGTTTAGGGCTAAGCATAGTGGGGTATCTAATCCCAGT  14313
```

>gb|AC137882.1| Homo sapiens chromosome 15 clone RP11-318M1 map 15, LOW-PASS SEQUENCE SAMPLING
Length = 65479

Score = 114 bits (59), Expect = 2e-22
Identities = 99/119 (83%)
Strand = Plus / Minus

```
Query:  131    AAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTG  72
Sbjct:  7899   AAAATCTCATGATAGCCTTTAGGAAATCTAAAGATTCAAGGAGGATTTAGCAGTAAATCA  7958

Query:  71     AGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  7959   AGAGTAGAGTGCTTGATTGAATAAGGCCATGAAGCATGCACACGCCACCCGTTACCCTC  8017
```

>gb|AC136354.1| Homo sapiens chromosome 15 clone RP11-318M1 map 15, LOW-PASS SEQUENCE SAMPLING
Length = 54322

Score = 114 bits (59), Expect = 2e-22

```
 Identities = 99/119 (83%)
 Strand = Plus / Minus


Query:  131    AAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTG  72
Sbjct:  19904  AAAATCTCATGATAGCCTTTAGGAAATCTAAAGATTCAAGGAGGATTTAGCAGTAAATCA  19963

Query:  71     AGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  19964  AGAGTAGAGTGCTTGATTGAATAAGGCCATGAAGCATGCACACGCCACCCGTTACCCTC  20022


>gb|AC016352.2| Homo sapiens chromosome 22 clone RP11-425O21 map 22, LOW-PASS
            SEQUENCE SAMPLING
          Length = 89740

 Score =  114 bits (59), Expect = 2e-22
 Identities = 141/182 (77%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  5315   CAAACTGGGACTAAATCTCTCACTGTGCTTAGCCATAAACTTAATAATTTAATAAACAG  5374

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  5375   AATTATTTACCAGAGCACTATAAGCAATAGCTTAAGCCTCAAAGGACATGGCGATGCTTT  5434

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  5435   ACAGCTCTCGAGAGGGGCCTGTTCTATATTCAATAAGCTCCGATATACCTCAGCATCTCT  5494

Query:  266    TG  265
Sbjct:  5495   TG  5496


 Score = 50.7 bits (26), Expect = 0.003
 Identities = 54/68 (79%)
 Strand = Plus / Minus


Query:  332    TGCTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACC  273
Sbjct:  1039   TGCTTTACAGCTCTCGAGAGGGGCCTGTTCTATATTCAATAAGCTCCGATATACCTCAGC  1098

Query:  272    ACCTCTTG  265
Sbjct:  1099   ATCTCTTG  1106


>gb|AC025936.3|AC025936 Homo sapiens chromosome 8 clone RP11-680F3 map 8, WORKING
DRAFT
            SEQUENCE, 6 unordered pieces
          Length = 183084

 Score = 91.1 bits (47), Expect = 2e-15
 Identities = 89/110 (80%)
 Strand = Plus / Minus


Query:  262     CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTAT  203
Sbjct:  45709   CAGCCTGTATACTACCATCTTCAGCAAGCCCTAAAAAGGTCATAAAGTAAGCACAAGTAC  45768

Query:  202     CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  45769   TTACATGGAAACATTAGGTCAACATGTAGCTTATGAGATGGAAAGAAATG  45818
```

Score = 60.3 bits (31), Expect = 4e-06
Identities = 59/73 (80%)
Strand = Plus / Minus

```
Query:  94      AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  45880   AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAAGGTTGTGAAGCAC  45939

Query:  34      GCACACACCGCCC  22
Sbjct:  45940   ACATAGACCGCCC  45952
```

Score = 56.4 bits (29), Expect = 5e-05
Identities = 29/29 (100%)
Strand = Plus / Minus

```
Query:  364     AGCAACAGCTTAAAACTCAAAGGACTTGG  336
Sbjct:  45598   AGCAACAGCTTAAAACTCAAAGGACTTGG  45626
```

Score = 54.5 bits (28), Expect = 2e-04
Identities = 36/40 (90%)
Strand = Plus / Minus

```
Query:  445     AAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACT  406
Sbjct:  45533   AAACTGGGATTAAATACCCCACTATGTTTAGCCATAAACT  45572
```

>gb|AC027752.2|AC027752 Homo sapiens chromosome 11 clone RP11-400F23 map 11, WORKING DRAFT
SEQUENCE, 50 unordered pieces
Length = 186723

Score = 85.3 bits (44), Expect = 1e-13
Identities = 82/101 (81%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  14907   GAGGGTGACGGGCGGTGTGTATGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACACTT  14966

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAA  113
Sbjct:  14967   AGTTTACTGCTAAATCCACCTTCGACCCTTAAATTTCATAA  15007
```

>emb|BX322234.2| Homo sapiens chromosome 6 clone XXyac-65C7_A, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces
Length = 299884

Score = 73.7 bits (38), Expect = 3e-10
Identities = 79/97 (81%), Gaps = 1/97 (1%)
Strand = Plus / Plus

```
Query:  152     CCATTTCTTGCCACCTCATGGCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTG  211
Sbjct:  235680  CCATTTCTTTCCACCTCA-GAGCTACCCCTGGACCTGATGTTTTTGTGTAAATGCTGGTG  235738

Query:  212     CTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGG  248
Sbjct:  235739  CTCACTCTGCGGCCGTCGTAGGGTTTGCTGAAGATGG  235775
```

>gb|AC143888.1| Macaca mulatta clone CH250-268B20, *** SEQUENCING IN PROGRESS ***, 1 ordered piece
Length = 180677

Score = 71.8 bits (37), Expect = 1e-09
Identities = 79/100 (79%)
Strand = Plus / Plus

```
Query:  265     CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGAT  324
Sbjct:  70009   CAAGAGATGGTGAGGTATATCAGAGATTATCGAATATAGAACAGGCCCCTCTCGAGGGCT  70068

Query:  325     ATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCT  364
Sbjct:  70069   GTAAAGCTTCGCCACGTCCTTTGAAGTTGAAGCCATTGCT  70108
```

>gb|AC013679.2|AC013679 Homo sapiens clone RP11-20L24, LOW-PASS SEQUENCE SAMPLING
Length = 43152

Score = 69.9 bits (36), Expect = 5e-09
Identities = 54/63 (85%)
Strand = Plus / Plus

```
Query:  349     GTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGT  408
Sbjct:  9549    GTTTTAAGCTGTTGCTTATAGTACTCTGGCAAATAGTTTTGCTAATCTAACTACTTGAGT  9608

Query:  409     TTA  411
Sbjct:  9609    TTA  9611
```

>gb|AC130279.2| Mus musculus clone RP24-394G12, WORKING DRAFT SEQUENCE, 2 ordered pieces
Length = 207794

Score = 66.1 bits (34), Expect = 7e-08
Identities = 56/67 (83%)
Strand = Plus / Minus

```
Query:  217     AGTAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAG  158
Sbjct:  2719    AGTAAGCAAAAGAACAAACATAAGAACATTAGGTCAAGGTGTAGCCAGTGAGGTGGAAAG  2778

Query:  157     AAATGGG  151
Sbjct:  2779    CAATGGG  2785
```

Database: Unfinished High Throughput Genomic Sequences; Sequences: phases 0,1 and 2
Posted date: Apr 10, 2003 11:31 PM
Number of letters in database: 7,937,571,999
Number of sequences in database: 48,392

Database: db/htgs.01
Posted date: Apr 11, 2003 1:13 AM

Number of letters in database: 3,768,110,189
Number of sequences in database: 19,870

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 2,844,697
Number of Sequences: 68262
Number of extensions: 2844697
Number of successful extensions: 1346
Number of sequences better than 10.0: 90
Number of HSP's better than 10.0 without gapping: 90
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1199
Number of HSP's gapped (non-prelim): 106
length of query: 462
length of database: 11,705,682,188
effective HSP length: 24
effective length of query: 438
effective length of database: 11,704,043,900
effective search space: 5126371228200
effective search space used: 5126371228200
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

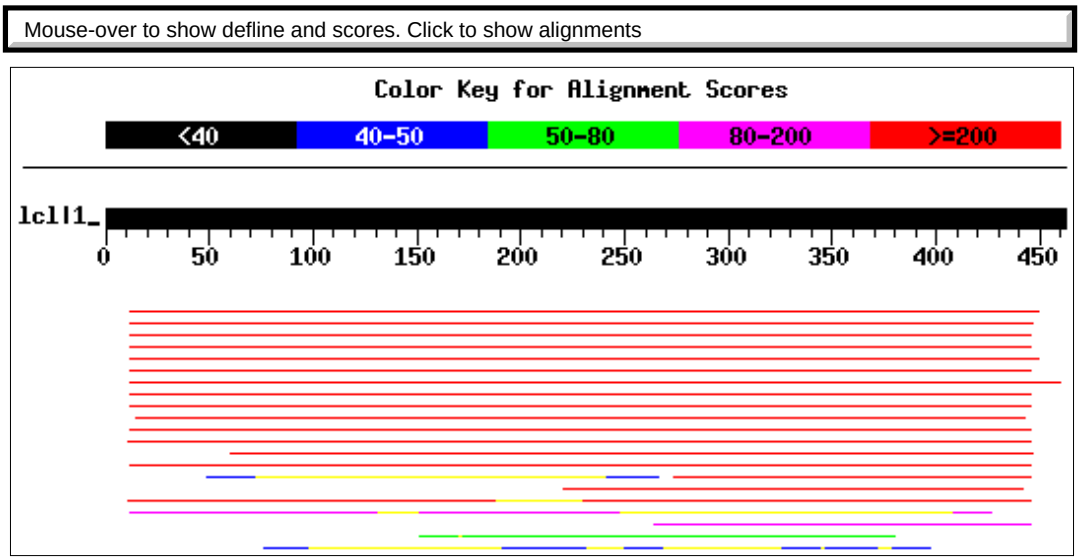
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: NCBI genome chromosomes - human
24 sequences; 3,051,185,827 total letters

Query= CS63win
(462 letters)

Distribution of 92 Blast Hits on the Query Sequence



Sequences producing significant alignments:		Score (bits)	E Value
ref|NC_000004.3|	Homo sapiens chromosome 4, complete sequence	721	0.0
ref|NC_000002.3|	Homo sapiens chromosome 2, complete sequence	702	0.0
ref|NC_000007.5|	Homo sapiens chromosome 7, complete sequence	564	e-158
ref|NC_000005.2|	Homo sapiens chromosome 5, complete sequence	527	e-147
ref|NC_000017.3|	Homo sapiens chromosome 17, complete sequence	525	e-147
ref|NC_000009.3|	Homo sapiens chromosome 9, complete sequence	512	e-143
ref|NC_000011.2|	Homo sapiens chromosome 11, complete sequence	489	e-136
ref|NC_000001.2|	Homo sapiens chromosome 1, complete sequence	467	e-129

ref|NC_000023.2|	Homo sapiens chromosome X, complete sequence	444	e-122
ref|NC_000020.4|	Homo sapiens chromosome 20, complete sequence	437	e-120
ref|NC_000008.3|	Homo sapiens chromosome 8, complete sequence	433	e-119
ref|NC_000003.3|	Homo sapiens chromosome 3, complete sequence	406	e-111
ref|NC_000014.2|	Homo sapiens chromosome 14, complete sequence	331	2e-88
ref|NC_000024.2|	Homo sapiens chromosome Y, complete sequence	235	2e-59
ref|NC_000013.3|	Homo sapiens chromosome 13, complete sequence	233	8e-59
ref|NC_000018.2|	Homo sapiens chromosome 18, complete sequence	212	2e-52
ref|NC_000010.2|	Homo sapiens chromosome 10, complete sequence	206	1e-50
ref|NC_000006.3|	Homo sapiens chromosome 6, complete sequence	114	6e-23
ref|NC_000022.3|	Homo sapiens chromosome 22, complete sequence	114	6e-23
ref|NC_000019.3|	Homo sapiens chromosome 19, complete sequence	80	2e-12
ref|NC_000015.2|	Homo sapiens chromosome 15, complete sequence	43	0.15
ref|NC_000012.3|	Homo sapiens chromosome 12, complete sequence	41	0.58

>ref|NC_000004.3| Homo sapiens chromosome 4, complete sequence
Length = 191669278

Score = 721 bits (375), Expect = 0.0
Identities = 417/438 (95%)
Strand = Plus / Plus

```
Query:  13        GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  43845045  GAGGGTGACGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAATTAAACACTCTGCTCTC
43845104

Query:  73        AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  43845105  AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGACATTTTT
43845164

Query:  133       CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  43845165  CTGGATGTAGAAAACTTTCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAAGT
43845224

Query:  193       TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  43845225  TTTTATGTAGATACTTGTGCTTACTCTGCAGCCTTTTCAGGGTTTGCTGAAGATGGAGGT
43845284

Query:  253       ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  43845285  ATTTAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGCCTC
43845344

Query:  313       CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  43845345  CTTTAGAGGGATACAAAGCACCGCCAAGTCCTTTGAGTCTTAAGCTGTTGCTTGTAGTGT
43845404

Query:  373       TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  43845405  TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGAGTTAAGCATAGCGGGGTAT
43845464

Query:  433       CTAATCCCAGTTTGAATC  450
Sbjct:  43845465  CTACTCCCAGTTTGGATC  43845482
```

Score = 483 bits (251), Expect = e-134
Identities = 380/437 (86%), Gaps = 4/437 (0%)
Strand = Plus / Plus

```
Query:  13          GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  156814951   GAGGGTCACGGGTGGTGTGTGCATGCTTCATGGCCTTATTCAACCAAGCACTCTGCTCTT
156815010

Query:  73          AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  156815011   GGTTTACTGCTAAATCCTCCTTGAGCCCTTAGATTTCCTAAAGGATGTTGTGAGATTTT-
156815069

Query:  133         CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  156815070   CTGGACATAGAAAATGTAGCCCATTTCGTGCCACCTCATGGGCTACACCTTGACCTAATG
156815129

Query:  192         TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  156815130   TTTTTATGTGTGTACTTGTGCTTACTTTGTGACCTTTTTAGGGTTTGCTGAAGATGGCGG
156815189

Query:  252         TATATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  156815190   TATATAGGCTGGGGGCAAGAGGTGGTGAGGAGCACCAGGGTTTATTGATTATAGAACAAG
156815249

Query:  310         CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAG  369
Sbjct:  156815250   CTCCTTTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTGG
156815309

Query:  370         TGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGG  429
Sbjct:  156815310   TACTCTGGTGAATGGTTTTGTTAATATAACTATTAGAGTTTAGGGCTAAGCATAGTGGTG
156815369

Query:  430         TATCTAATCCCAGTTTG  446
Sbjct:  156815370   TATCTAATCCAAGTTTG  156815386
```

```
 Score =  440 bits (229), Expect = e-121
 Identities = 377/441 (85%), Gaps = 8/441 (1%)
 Strand = Plus / Minus


Query:  446         CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  117500416   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTCTAATAGTTACATTGAGAA
117500475

Query:  386         AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  117500476   AACCATTCGCCAGAGTACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT
117500535

Query:  326         ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTA----CCTCACCAC  271
Sbjct:  117500536   ATATCCCTCTAGAGGAGCCTGTTCTATAATTGATAAACCCCGATACAACCGCCTTGCCAC
117500595

Query:  270         CTCTTGCCC--AGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAA  213
Sbjct:  117500596   CTCTTGCCCGCAGCCTATATACTGCCATCTTCAGCAAACCCTAAAAAGTTACAGAGTAA
117500655

Query:  212         GCAGAAGTATCTACATAAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  117500656   GCACAAGTACACATATAAAAAACATTAGGTCAAGGTACAGCCTATGAGGTGGCAAGAAATG
117500715

Query:  152         GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  117500716   GGCTACATTTTCTATATCCGGCAAA-TCTCACACAACCTTTATGAAATCTAAGGGCTCA
```

```
117500774

Query:  93          AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  117500775   AGGAGGATTTAGTAGTAAACCAAGCGCAGAGTGCTTGGTTGAATAAGGCCATGAAGCATG
117500834

Query:  33          CACACACCGCCCGTCACCCTC  13
Sbjct:  117500835   CACACACCGCTCATCACCCTC  117500855
```

```
 Score = 46.8 bits (24), Expect = 0.011
 Identities = 26/27 (96%)
 Strand = Plus / Minus


Query:  446         CAAACTGGGATTAGATACCCCACTATG  420
Sbjct:  56156020    CAAACTGGGATTAGATACCGCACTATG  56156046
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query:  96          TCAAGGAGGATTTAGCAAT  78
Sbjct:  166074477   TCAAGGAGGATTTAGCAAT  166074495
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 21/22 (95%)
 Strand = Plus / Plus


Query:  301         TAGAACAGGCTCCTTTAGAGGG  322
Sbjct:  12132091    TAGAACATGCTCCTTTAGAGGG  12132112
```

```
>ref|NC_000002.3| Homo sapiens chromosome 2, complete sequence
          Length = 241996787

 Score =  702 bits (365), Expect = 0.0
 Identities = 415/435 (95%), Gaps = 2/435 (0%)
 Strand = Plus / Plus


Query:  13          GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCC-TCATTCAATTAAACACTCTGCTCT  71
Sbjct:  93998472    GAGGGTGATGGGCGGTGTGTGCGTGC-TCATGGCCTTAATTCAATTAAGCACTCTGCTCT
93998530

Query:  72          CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  93998531    CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCTTAAAGGTTGTCCTGAGATTTT
93998590

Query:  132         TCTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  93998591    TCTGGGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG
93998650

Query:  192         TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
```

```
Sbjct:  93998651   TTTTTATGTAGATACTTGTGCTTACCCTGCGGCCTTTCCAGAGTTTGCTGAAGATGGAGG
93998710

Query:  252        TATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  311
Sbjct:  93998711   TATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT
93998770

Query:  312        CCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  371
Sbjct:  93998771   CCTTTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG
93998830

Query:  372        TTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTA  431
Sbjct:  93998831   TTCTGGCAAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAACGAGGTA
93998890

Query:  432        TCTAATCCCAGTTTG  446
Sbjct:  93998891   TCTACTCCCAGTTTG  93998905
```

```
 Score =  423 bits (220), Expect = e-116
 Identities = 372/438 (84%), Gaps = 5/438 (1%)
 Strand = Plus / Plus


Query:  13         GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  211364734  GAGGGTGATAGGCTGTGTGTACGTGCTTCATGGCCTTATTCAACCAAGCACTCTGCTCTT
211364793

Query:  73         AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  211364794  GGTTTACTGCTAAATCCTCCTTGAGCCCTCAGATTTCACAAAGGTTTTCATGAGATTTC-
211364852

Query:  133        CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  211364853  CTGGACATAGAAAATGTAGCCCATTTCTTGCCACCTCACGGGTTACACCTTGACCTAACG
211364912

Query:  192        TTTTT-ATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAG  250
Sbjct:  211364913  TTTTTTATGTGTATACTTATGCTTAATCTATAACTTTTTTAGGGTTTGCTGAAGATGGTG
211364972

Query:  251        GTATATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAG  308
Sbjct:  211364973  ATATACAGACCGGGGGCAAGAGATGGTGAGTTGTATCGGGGTTTGTCTATTATAGAACAG
211365032

Query:  309        GCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTA  368
Sbjct:  211365033  GCTCCTCTAGAGGGATGTAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTA
211365092

Query:  369        GTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGG  428
Sbjct:  211365093  GTAGTCTGGCGAATGGTTTTGTTAATGTAACTATTCGACTTTAGGGCTAAGTGTAGTGGG
211365152

Query:  429        GTATCTAATCCCAGTTTG  446
Sbjct:  211365153  GTATCTAATCCCAGTTTG  211365170
```

```
 Score =  419 bits (218), Expect = e-115
 Identities = 372/439 (84%), Gaps = 6/439 (1%)
 Strand = Plus / Plus
```

```
Query:  13          GAGGGTGAC-GGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCT  71
Sbjct:  139288497   GAGGGTGACAGGGTTGTGTCTGTGTGCTTCATGGCCTTATTCAACCAAGCACTCTGCTCT
139288556

Query:  72          CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  139288557   TTGTTTACTGCTAAATCCTCCTTAAGCCTTTAGATTGCATAAGGGTTGTTGTGAGATTTT
139288616

Query:  132         TCTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  190
Sbjct:  139288617   TCGG-GTATAGAAAATGTAGCCCATTTCTTGCCACCTCGTAGGCTACACCTTGACCTAAA
139288675

Query:  191         GTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAG  250
Sbjct:  139288676   ATTTTTATGAATATACTTGTGCTTACTCTGCAACCTTTCTAGGGTTTGCTGACGATGGTG
139288735

Query:  251         GTATATAGGCTG---GGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  139288736   GTATATGGGCTGTGGGGCAAGAGGTGGTGAGGTGTATCGGGGTTTACGGATTATAGAACA
139288795

Query:  308         GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  139288796   GGCCCCTCTAGAGGGATATAAAGCACCGCCAAGTCCTTTTAATTTTAAGTTCTTGCTTGT
139288855

Query:  368         AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  139288856   AGTATTCCGGCAAATAATTTTGTTAATTTAACTATTATAGTTTAGGGCTAAGCATGATGG
139288915

Query:  428         GGTATCTAATCCCAGTTTG  446
Sbjct:  139288916   GATATCTAATCTCAGTTTG  139288934
```

```
 Score =  352 bits (183), Expect = 1e-94
 Identities = 252/284 (88%), Gaps = 2/284 (0%)
 Strand = Plus / Plus


Query:  165         CCTCATGGGCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTACTCTGTGGC  224
Sbjct:  142166006   CCTCATAGGCTACACCTTGACCTAACATTTTTATGTGTATACTTGTGCTTACTTTGCAAC
142166065

Query:  225         CTTTCCAGGGTTTGCTGAAGATGGAGGTATATAGGCTGGG--CAAGAGGTGGTGAGGTAA  282
Sbjct:  142166066   CTTTCTAGGGTTTGCTGAAGATGGTGGCATATAGGCTGGGGGCAAGAGGTGGTGAGGTGC
142166125

Query:  283         ATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTC  342
Sbjct:  142166126   ATCGGGGTTTATCAATTATAGAACAGGCTCCTCTAGATGGATATAAAGCACTGCCAAGTC
142166185

Query:  343         CTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTAT  402
Sbjct:  142166186   CTTTGAGTTTTAACCTGTTGCTTGTAGTATTCTGGTAAATTGTTTTGTTAATTTAACTAT
142166245

Query:  403         TCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  142166246   TATAGTTTAGGGCTAAGCATAGTTGGGTATCTAATCCCAGTTTG  142166289
```

```
 Score =  329 bits (171), Expect = 9e-88
 Identities = 355/432 (82%), Gaps = 12/432 (2%)
```

Strand = Plus / Minus

```
Query:  437        ATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAAAACTGTTCG  378
Sbjct:  115700013  ATTAGTTACCCCACTATGCCTAGCCATAAACTCTAATAGTTACATTAACAAAAACAGTCG
115700072

Query:  377        CCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTC  318
Sbjct:  115700073  CCAGAGTACTACAA----CAGCTTAAAATTCAAAGAACTTGGTGGTGCTTTATATCCCTC
115700128

Query:  317        TAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTGCCC---A  261
Sbjct:  115700129  TAGAGGAGCCTGTTCTATAACTGATAAACCCCAATACACCTCACCACCTGTTGCCCTCCA
115700188

Query:  260        GCCT-ATAT--ACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTA  204
Sbjct:  115700189  GCCTTATACTGACTGCTATCTTCAGCAAACCCTTAAAAGGCTATAGAGTAAGCACAAGTA
115700248

Query:  203        TCTACATAAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TACGTT  145
Sbjct:  115700249  CGCACATAAAAAACATTAGGTCAAAGTGTAGCCCATAAGGTGGCAAGAAATGGGCTATATT
115700308

Query:  144        TTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATT  85
Sbjct:  115700309  TTGTATGTCCAG-AAAATCTCATGACAATTCTTATGAAATCTAAGGACTCAAGGAGGATT
115700367

Query:  84         TAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCG  25
Sbjct:  115700368  TAGCCATAAACCAAGAGCAGAGCACTTGGTTAAATAAGGCCGTGAAGTACGCACACACCG
115700427

Query:  24         CCCGTCACCCTC  13
Sbjct:  115700428  CCCATCACCCTC  115700439
```

Score = 233 bits (121), Expect = 8e-59
Identities = 161/181 (88%)
Strand = Plus / Plus

```
Query:  267        AGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATAT  326
Sbjct:  179275195  AGAGATGATGAGGTACCTCGGGGTTTATCGATTATAGAACAGGCTCCTCTAGAGGGATAT
179275254

Query:  327        AAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTT  386
Sbjct:  179275255  AAAGCACTGCCAAGTCTTTTGAGTCTTAAGCTGTTGCTTGTAGTACTCTGGTGAATAGTT
179275314

Query:  387        TTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  179275315  TTGTTGGTTGAACTATTTGGGTTTAGAACTAAGCATAGTGGGGTATCTAATCCCAGTTTG
179275374

Query:  447        A  447
Sbjct:  179275375  A  179275375
```

Score = 96.8 bits (50), Expect = 1e-17
Identities = 90/110 (81%)
Strand = Plus / Plus

```
Query:  22         GGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAATTTATTG  81
Sbjct:  142165877  GGGTGGCGTGTGTGTGCTTCATGACCCTATTCAACCAAGCACTCAGCTCTTGGTTTACTG
142165936

Query:  82         CTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  142165937  CTAAATCCTCTTTGAGCCCTTAGATTTCATAAAGGCTATCATGAGATTTT  142165986
```

```
 Score = 56.4 bits (29), Expect = 1e-05
 Identities = 41/47 (87%)
 Strand = Plus / Minus


Query:  434        AGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACA  388
Sbjct:  41170951   AGATACTCCACTATGCTTAGCCCTAAACTTCAACAGTTAAATCAACA  41170997
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 26/29 (89%)
 Strand = Plus / Minus


Query:  84         TAGCAATAAATTGAGAGCAGAGTGTTTAA  56
Sbjct:  116748182  TAGCAAAAAATGGAGAGCAGAGTATTTAA  116748210
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 22/23 (95%)
 Strand = Plus / Minus


Query:  250        CTCCATCTTCAGCAAACCCTGGA  228
Sbjct:  167576960  CTCCTTCTTCAGCAAACCCTGGA  167576982
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query:  147        GTTTTCTACACACAGAAAA  129
Sbjct:  41344971   GTTTTCTACACACAGAAAA  41344989
```

```
>ref|NC_000007.5| Homo sapiens chromosome 7, complete sequence
          Length = 157432593

 Score =  564 bits (293), Expect = e-158
 Identities = 395/436 (90%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446        CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  140646867  CAAACTGGGATTAGATACCCCACTAGGCTTAGCCCTAAACTCCAATAGTTAATCAACAA
140646926
```

```
Query:  386         AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  140646927   AACTATTCCCCAGAACACTACAAGCAATAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT
140646986

Query:  326         ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  140646987   ATATCCCTCTAGAGGAGCCTGTTCTATAATGGATAAACCCCAATTTACCTCACCACTTCT
140647046

Query:  266         TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCT-GGAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  140647047   TGCTCAGCCTATATACCATCATCTTCAGCAAACCCTAGTAAAAGTCACAAAGTAAGCACA
140647106

Query:  207         AGTATCTACATAAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  140647107   AGTATCTACATAAAAAACATTAGGTCAAGGTGTAGCCCATGAGGCGGTAAGAAATGGGCTA
140647166

Query:  148         CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  140647167   CATTTTCTACACCCAG-AAAATCTC---ACAACCCTTATGAAATCTAAGGGCTCAAGGAG
140647222

Query:  88          GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  140647223   GATTCAGCAGTATATTAAGAGCAGAGTGCTTAATTGGATGAGGCCATAAAGCACACACAC
140647282

Query:  28          ACCGCCCGTCACCCTC  13
Sbjct:  140647283   AATGCCCATCACCCTC  140647298
```

```
 Score = 52.6 bits (27), Expect = 2e-04
 Identities = 31/33 (93%)
 Strand = Plus / Minus


Query:  361         AACAGCTTAAAACTCAAAGGACTTGGCAGTGCT  329
Sbjct:  117014718   AACAGCCTAAAACTCAAAGGACTTGGTAGTGCT  117014750
```

```
 Score = 46.8 bits (24), Expect = 0.011
 Identities = 38/45 (84%)
 Strand = Plus / Minus


Query:  370         ACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTA  326
Sbjct:  114424168   ACTACCAGCAATAGCTCAAAACTCAAAGGCTTTGTGGTGCTTTA  114424212
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 23/25 (92%)
 Strand = Plus / Plus


Query:  257         AGGCTGGGCAAGAGGTGGTGAGGTA  281
Sbjct:  99538721    AGGCTGGGGTAGAGGTGGTGAGGTA  99538745
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus
```

```
Query:  79          ATAAATTGAGAGCAGAGTG  61
Sbjct:  78952397    ATAAATTGAGAGCAGAGTG  78952415
```

```
>ref|NC_000005.2| Homo sapiens chromosome 5, complete sequence
          Length = 181762559

 Score =  527 bits (274), Expect = e-147
 Identities = 390/438 (89%), Gaps = 5/438 (1%)
 Strand = Plus / Minus


Query:  446         CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  123432851   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTCCAATAGTTAAATCAACAA
123432910

Query:  386         AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  123432911   AACTATTCACCAGAACACTACAAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT
123432970

Query:  326         ATATCCCTCTAAAGGAGCCTGTTCTATA-ATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  123432971   ATATCCCTCTAGAGGAGCCTGTTCTATATATTGATAAACTCCAATTTACCTCACCACCTC
123433030

Query:  267         TTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGGA  208
Sbjct:  123433031   TTGCTCAGCCTATATACTTCCATCTTCAGCAAACCCTAGTAAGGCTGCAAGTAAGCACA
123433090

Query:  207         AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAG--GTGGCAAGAAATGGG-  151
Sbjct:  123433091   AATATCTACGTAAAAACGTTAGGTCAAGTTGTAGCCCACGAGGTGTGGTAAGAAATGGGC
123433150

Query:  150         TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  123433151   TATATTTTCTACTCCTAG-AAAATCTCATAACAACCCTTATGAAACCTAAGGGCCCAAGG
123433209

Query:  90          AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  123433210   AGGATTTAGCAGTAAATTAGGAGCAGAGTGCTTAATTGAATAAGGCCATAAAGCATGCAC
123433269

Query:  30          ACACCGCCCGTCACCCTC  13
Sbjct:  123433270   ACACTGCCTGTCACCCTC  123433287
```

```
 Score =  437 bits (227), Expect = e-120
 Identities = 373/436 (85%), Gaps = 6/436 (1%)
 Strand = Plus / Plus


Query:  13          GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  80185864    GAGGGTGACGGGCGGTGTGTACGCGCTTCAGGGCCCTGTTCAACTACGCACTCTACTCTT
80185923

Query:  73          AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  80185924    AGTTTACTGCTAAATCCACCTTCGACCCTTAAATTTCATAAGGGTTATCGT---AGTTTT
80185980

Query:  133         CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
```

```
Sbjct:  80185981   CTGAA-GTAGAAAATGTAGCCCATTTCTTGCCAGCTCATGGGCTACACCTTGACCTAACA
80186039

Query:  192        TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGAG  250
Sbjct:  80186040   TCTTTACGTGGGTACTTGCGCTTACTTTGCAGCCTTCGTCAGGGTTTGCTGAAGATGGCG
80186099

Query:  251        GTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGC  310
Sbjct:  80186100   GTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGC
80186159

Query:  311        TCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGT  370
Sbjct:  80186160   TCCTCTAGAGGGATATGAAGCACCGCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAGT
80186219

Query:  371        GTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGT  430
Sbjct:  80186220   GTTCTGGCGAGCAGTTTTGTTAATTTAACTGTTGAAGTTTAGGGCTAAGCATAGTGGGGT
80186279

Query:  431        ATCTAATCCCAGTTTG  446
Sbjct:  80186280   ATCTAATCCCAGTTTG  80186295
```

```
 Score = 43.0 bits (22), Expect = 0.15
 Identities = 22/22 (100%)
 Strand = Plus / Minus


Query:  446        CAAACTGGGATTAGATACCCCA  425
Sbjct:  8792763    CAAACTGGGATTAGATACCCCA  8792784
```

```
 Score = 43.0 bits (22), Expect = 0.15
 Identities = 24/25 (96%)
 Strand = Plus / Minus


Query:  352        AAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  86409228   AAACTCAAAGGACTTGGCAATGCTT  86409252
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 24/26 (92%)
 Strand = Plus / Plus


Query:  42         ATGGCCTCATTCAATTAAACACTCTG  67
Sbjct:  116938758  ATGGACTCATTCAATTAAACATTCTG  116938783
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 20/20 (100%)
 Strand = Plus / Minus


Query:  238        CAAACCCTGGAAAGGCCACA  219
Sbjct:  74125802   CAAACCCTGGAAAGGCCACA  74125821
```

Score = 39.1 bits (20), Expect = 2.2
Identities = 20/20 (100%)
Strand = Plus / Plus

```
Query:  339       AGTCCTTTGAGTTTTAAGCT  358
Sbjct:  86409208  AGTCCTTTGAGTTTTAAGCT  86409227
```

>ref|NC_000017.3| Homo sapiens chromosome 17, complete sequence
Length = 84346999

Score = 525 bits (273), Expect = e-147
Identities = 391/440 (88%), Gaps = 4/440 (0%)
Strand = Plus / Minus

```
Query:  450       GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  23437942  GATTCAAACTGGGATTAGATACCCCACTATGCTCAGCCCTAAACTTCAACAGTTAAATCA
23438001

Query:  390       ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  23438002  ACAAAACTGCTCGCCAGAACACTAGGAGCAACAGCTTAAAACTCAAAGGACCTGGCGGTG
23438061

Query:  330       CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  23438062  CTTCACATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCAATTCACCTCACCAC
23438121

Query:  270       CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAG  212
Sbjct:  23438122  CTCTTGCTCAACCCATATACCGCCATCTTCAGCAAACCCTGACAAAGGCCACAAAGTAAG
23438181

Query:  211       CAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  23438182  CACAAGTATCTACATAAAAATGTTAGGTCAAGGTGTAGCCTATGAGGTGGCAAGAAATGG
23438241

Query:  151       G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  23438242  GCTACATTTTCTAC-CCCAGAAAATTCT-ACAATAACCCTTATGAAACCTGAGGGTCCAA
23438299

Query:  92        GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  23438300  GGAGGATTTAGTAGTAAATTAAGAACAGAGTGCTTAATTGAATAGGGCCATAAAGCACGC
23438359

Query:  32        ACACACCGCCCGTCACCCTC  13
Sbjct:  23438360  ACACACCACCCATCACCCTC  23438379
```

Score = 517 bits (269), Expect = e-144
Identities = 384/434 (88%), Gaps = 4/434 (0%)
Strand = Plus / Minus

```
Query:  443       ACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAAAAC  384
Sbjct:  20974284  ACTGGGATTAGATAACCCACTATGCTTAGCCCTAAACTCTAATAGTTACATTAACAAAAC
20974343
```

```
Query:  383       TGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATA  324
Sbjct:  20974344  CATTCGCCAGAGTACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATA
20974403

Query:  323       TCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG-  265
Sbjct:  20974404  TCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCTGATATACCTCACCACCTCTTGC
20974463

Query:  264       -CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAG  206
Sbjct:  20974464  CCCCAGCCTGTATAGTGCCATCTTCAGCAAACCCTAAAAAGGTTGTAGAGTAAGCACAAG
20974523

Query:  205       TATCTACATAAAAACGTTAGGTCAAGGTGTAGCCATGAGGTGGCAAGAAATGGG-TACG  147
Sbjct:  20974524  TATACACATAAAAACATTAGGTCAAGGTGTAGCTCATGAGGTGGCAAGAAATGGGCTACA
20974583

Query:  146       TTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGA  87
Sbjct:  20974584  TTTTCTATACTCAG-AAAATCTCACGACAATCTTTATGACATCTAAGGGCTCAAGGAGGA
20974642

Query:  86        TTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACAC  27
Sbjct:  20974643  TTTGGCAGTAAACCAAGAGCAGAGTGCTTGGTTGAATAAGGCCATGAAGCATGCACACAC
20974702

Query:  26        CGCCCGTCACCCTC  13
Sbjct:  20974703  CGCCCATCACCCTC  20974716
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query:  210       AGAAGTATCTACATAAAAA  192
Sbjct:  62248557  AGAAGTATCTACATAAAAA  62248575
```

```
>ref|NC_000009.3| Homo sapiens chromosome 9, complete sequence
          Length = 132877114

 Score =  512 bits (266), Expect = e-143
 Identities = 389/438 (88%), Gaps = 7/438 (1%)
 Strand = Plus / Minus


Query:  446       CAAACTGGGATTAGATACCCCACTAT--GCTTAACCCTAAACTCGAATAGTTAGATCAAC  389
Sbjct:  33826541  CAAACTGGGATTATATACCCCCCAATACGCTTAGCCCTAAACTCCAATAGTTAAATCAAC
33826600

Query:  388       AAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCT  329
Sbjct:  33826601  AGAACTATTCACCAGAACACTACAAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCT
33826660

Query:  328       TTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCT  269
Sbjct:  33826661  TTATATCCCTCTAGAGGAGCCTGTTCTATAATGGATAAAACCCAATTTGCCTCACCACCT
33826720

Query:  268       CTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCT-GGAAAGGCCACAGAGTAAGCA  210
Sbjct:  33826721  CTTGCTCAGCCTATATACCACTGTCTTCAGCAAACCCTAGCAAAGGCTGCAAAGTAAGCA
33826780
```

```
Query:  209         GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-  151
Sbjct:  33826781    CAAGTATCTACGTAAAAATGCTGGGTCAATGTGTAGCCCA--CGGTGGTAAGAAATGGGC
33826838

Query:  150         TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  33826839    TACATTTTCTACACCCAG-AAAATCTCACGACAACCCTTATGAAATCTAAGGGCTCAAGG
33826897

Query:  90          AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  33826898    AGGATTTAGCAGTACATTAAGAGCAGAGTGCTTAATTGAATGAGGCCATAAGCACGCAC
33826957

Query:  30          ACACCGCCCGTCACCCTC  13
Sbjct:  33826958    ACAATGCCCGTCACCCTC  33826975
```

```
 Score =  191 bits (99), Expect = 4e-46
 Identities = 181/212 (85%), Gaps = 9/212 (4%)
 Strand = Plus / Minus


Query:  217         AGTAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAG  158
Sbjct:  5073361     AGTAAGCACAAGTAAATACATAAAAACGTTAGGTCAACGTGTAGCTCATGAGGTGGCAAG
5073420

Query:  157         AAATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGG  99
Sbjct:  5073421     AAATGGGCCACATTTTCTAC-CCCAG-AAAATCTCACGACAACCTTTATGAAATCTAAGG
5073478

Query:  98          GCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTT------AATTGAATGAGGC  45
Sbjct:  5073479     GCTCAAGGAGGATTTAGCAGTAAACCAAGAGTAGAGTGCTTGGTTGAGGTTGAATAAGGC
5073538

Query:  44          CATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  5073539     CACGAAGCACGCACACACTGCCTGTCACCCTC  5073570
```

```
>ref|NC_000011.2| Homo sapiens chromosome 11, complete sequence
          Length = 136521022

 Score =  489 bits (254), Expect = e-136
 Identities = 384/439 (87%), Gaps = 5/439 (1%)
 Strand = Plus / Plus


Query:  16          GGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAAT  75
Sbjct:  104637964   GGTGACAGGCAGTGTGTGTGTGCTTCATGGCCTTATTCAACCAAGCACTCTACTCTTGGT
104638023

Query:  76          TTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTTCTG  135
Sbjct:  104638024   TTACTGCTAAATCCTCCTTGAGTCTTTTGATTTCATAAAGGTTGTCGTGAGATTTT-CTG
104638082

Query:  136         TGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTT  194
Sbjct:  104638083   GGTATAGAAAATGTAGCCCATTTCTTCCCACCTCATGAGCTACACCTTGACCTAATGTTT
104638142

Query:  195         TTATGTAGAT-ACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTA  253
Sbjct:  104638143   TTATGTGTATTACTTGTGCTTACTCTATAACCTTTTTAGGGTTTGCTGAAGATGGCGGTA
104638202
```

```
Query:  254         TATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  311
Sbjct:  104638203   TATAGGCTGGGGGCAAGAGGTGGTGAGGTAGATCGGGGTTTATAGATTATAGAACAGGCT
104638262

Query:  312         CCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  371
Sbjct:  104638263   CCCCTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTATTGCTTCTAGTA
104638322

Query:  372         TTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTA  431
Sbjct:  104638323   TTCTGGCGAATGGTTTTGTTAATATAACTATTATAGTTTAGGGCTAAGCATAGTGGGGTA
104638382

Query:  432         TCTAATCCCAGTTTGAATC  450
Sbjct:  104638383   TCTAACCCCAGTTTGGATC  104638401
```

```
 Score =  448 bits (233), Expect = e-123
 Identities = 375/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Plus


Query:  13          GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  11101025    GAGGGTGACGGGCGGTGTGTACGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACTCTT
11101084

Query:  73          AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  11101085    AGTTTACTGCTAAATCCACCTTCGACCCTTAAATTTCATCAGGGTTATCGT---AGTTTT
11101141

Query:  133         CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  11101142    CTGAA-GTAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG
11101200

Query:  192         TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTC-CAGGGTTTGCTGAAGATGGAG  250
Sbjct:  11101201    TCTTTACGTGGGTACTTGCGCTTACTTTGCGGCCTTCGTCAGGGTTTGCTGAAGGTGGCG
11101260

Query:  251         GTATATAGGCTGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGC  310
Sbjct:  11101261    GTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGC
11101320

Query:  311         TCCTTTAGAGGGATATAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGT  370
Sbjct:  11101321    TCCTCTAGAGGGATATGAAGCACCGCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAGT
11101380

Query:  371         GTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGT  430
Sbjct:  11101381    GTTCTGGCGAGCAGTTTTGTTAATTTAACTGTTGAAGTTTAGGGCTAAGCATAGTGGGGT
11101440

Query:  431         ATCTAATCCCAGTTTG  446
Sbjct:  11101441    ATCTAATCCCAGTTTG  11101456
```

```
 Score = 81.4 bits (42), Expect = 4e-13
 Identities = 81/98 (82%), Gaps = 4/98 (4%)
 Strand = Plus / Plus


Query:  349         GTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGT  408
```

```
Sbjct:  89063278   GTTTTATGCTGTTGCTTATAGTATTCTGGTGAATGATTTTGTTAATTTA----TTAGAGT
89063333

Query:  409        TTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  89063334   TTAGGACTAAGCATAGTGGGGTATCTAACCCCAGTTTG  89063371
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 25/28 (89%)
 Strand = Plus / Plus


Query:  434        TAATCCCAGTTTGAATCACTAGTGAATT  461
Sbjct:  28561630   TAATCCCAGTTTCCTTCACTAGTGAATT  28561657
```

```
>ref|NC_000001.2| Homo sapiens chromosome 1, complete sequence
          Length = 244258774

 Score =  467 bits (243), Expect = e-129
 Identities = 376/435 (86%), Gaps = 4/435 (0%)
 Strand = Plus / Plus


Query:  13         GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  233562231  GAGGGTGACGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAACCAAGCACTCTACTCTT
233562290

Query:  73         AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  233562291  GGTTTCCTGCTAAATTCTCCTTGAGCCCTTAGATTTCATAAGGGTTGTAGTAATATTTT-
233562349

Query:  133        CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  233562350  CTGGGTATAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACGCCTTGACCTAACG
233562409

Query:  192        TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  233562410  TTTTTATGTGTGTACTTGTGCTTACTTTATTACCTTTTTAGGGTTTACTGAAGATGGCAG
233562469

Query:  252        TATATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  233562470  TATATAGGCTGGGGGCAAGAGGTGGTGAGGTATATCGGGGTTTATCGATTATAGAACAGG
233562529

Query:  310        CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAG  369
Sbjct:  233562530  CTGCTCTAGAGGGGTATAAAGTACCTCCAAGTCCTTTGAATTTTAAGCTGTTGCTTGCAG
233562589

Query:  370        TGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGG  429
Sbjct:  233562590  TATTCTGGCGAATGGTTTTGTTAGTTTAACTATTAGAGCTTAGGGCTAAGCACAGTGGGT
233562649

Query:  430        TATCTAATCCCAGTT  444
Sbjct:  233562650  TATCTAATCCCAGTT  233562664
```

```
 Score = 81.4 bits (42), Expect = 4e-13
 Identities = 48/51 (94%)
 Strand = Plus / Minus
```

```
Query:  446        CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTA  396
Sbjct:  9458094    CAAATTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTCCAATAGTTA  9458144
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 23/25 (92%)
 Strand = Plus / Plus


Query:  208        TCTGCTTACTCTGTGGCCTTTCCAG  232
Sbjct:  98821681   TCTACTTACTCTGTGGCCCTTCCAG  98821705
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 21/22 (95%)
 Strand = Plus / Minus


Query:  50         TGAGGCCATGAAGCACGCACAC  29
Sbjct:  46234710   TGAGGCCATGAAGCACGAACAC  46234731
```

```
>ref|NC_000023.2| Homo sapiens chromosome X, complete sequence
          Length = 151567156

 Score =  444 bits (231), Expect = e-122
 Identities = 375/437 (85%), Gaps = 5/437 (1%)
 Strand = Plus / Plus


Query:  13         GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  53147704   GAGGGTGACGGGTGATGTGTGTGTGTTTCATGGCCTTATTCAACCAAGCACTCTGCTCTT
53147763

Query:  73         AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  53147764   GGTTTACAGCTAAATCCTCCTTGAGCC-TTGGATTTCATAAGGTTGTCGTGAGAGTTT-
53147821

Query:  133        CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  53147822   CTGAACATAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTAAACCTTGACCTAACG
53147881

Query:  192        TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  53147882   TTTTTATGTGTGTACTTGTGCTTACTTTATAACCTTTTTAGGGTTTGCTGAAGATGGCAG
53147941

Query:  252        TATATAGGCTGGGC--AAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  53147942   TATATAGGCTGGGGGGAAGAGGTGGTGAGATGTGTCGGGGTTCATTGATTATAGAACAGG
53148001

Query:  310        CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAG  369
Sbjct:  53148002   CTCCTCTAGAGGGATATAAAGCAACGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAC
53148061

Query:  370        TGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGG  429
Sbjct:  53148062   TACTCTGGCGAATGGTTTTGTTAATGTAACTATCAGGGTTTAGGGCTAAGCATAGTGGGG
53148121
```

```
Query:  430         TATCTAATCCCAGTTTG  446
Sbjct:  53148122    TATCTAATCCCAGTTTG  53148138
```

```
 Score =  200 bits (104), Expect = 5e-49
 Identities = 335/438 (76%), Gaps = 18/438 (4%)
 Strand = Plus / Minus


Query:  446         CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  139375666   CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAATAATTTAACAAACAA
139375725

Query:  386         AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  139375726   AATTATTCACCAGAGTATGACAAGCAATAGCTTAAAACTCAAAGGACATGGCGGTGCTTT
139375785

Query:  326         ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  139375786   ACATCCCTCTAGAGGACCCTGTTCTATAATTGATAAACCCTGATATTCCCTTCCATCTCT
139375845

Query:  266         TGCC---CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCA  210
Sbjct:  139375846   TGCCACATACCCTATATACCATCATCTTCAGCTAA------AAAGGTCTTAAAGTAAGCA
139375899

Query:  209         GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-  151
Sbjct:  139375900   CAAGT------ATTAAAATGTTAGATCAAGGTGTAGCCCATGAGATGGAAAGAAATGGGC
139375953

Query:  150         TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  139375954   CACATTTTCTAAATCTAGAACA--CCCATGACAACCCTCGTGAAACTTAAAGGTCAAAGG
139376011

Query:  90          AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  139376012   AGGATTTAGTAGTAAATCAAGAATAGAGATCTTGATCGAATAAAAACATGAAGCACTCAC
139376071

Query:  30          ACACCGCCCGTCACCCTC  13
Sbjct:  139376072   ACACTTCCCATCACCCTC  139376089
```

```
 Score =  144 bits (75), Expect = 3e-32
 Identities = 312/418 (74%), Gaps = 8/418 (1%)
 Strand = Plus / Minus


Query:  438         GATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAAAACTGTTC  379
Sbjct:  98207216    GATTAGATACCCTACTATGCTTAGCCATAAACCTAGATAACTTATTAAATGAAGTTATTC
98207275

Query:  378         GCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCT  319
Sbjct:  98207276    ACTAGAGTACTACAAGAAACAGTTTAAAACTCAAAGGATTTGGTGATGCTTTGTAGCTCT
98207335

Query:  318         CTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTGCC----  263
Sbjct:  98207336    CTAGAGAAGCCTGTTTTATAATTGGTAAACCTAGATAAACCTTATCATCTTTTGCTAATT
98207395

Query:  262         CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTAT  203
Sbjct:  98207396    CAGTCTATATACCATCATCTTCATCAAATCCTAAAGAGGACTTAAAGCAAGCACAAGTAA
```

```
98207455

Query:  202         CTACATAAAAACGTTAGGTCAAG-GTGTAGCCCATGAGGTGGCAAGAAATGGG-TACGTT  145
Sbjct:  98207456    ATACATAAAAATATTAGGTCAAAAGTGTAGCTTCTGAGATGGAAATAAATAGGCTACAGT
98207515

Query:  144         TTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATT  85
Sbjct:  98207516    TTCTAATCTTA-AAATAT-TCATGACAACTTTTATGAAATCTAAAGGCTAAAGGAGGATT
98207573

Query:  84          TAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACAC  27
Sbjct:  98207574    TAGTAGTAAATTAAGAATAGAAAGCTTAACTGAATAGGGCCATGGAGCACACACACAC
98207631
```

```
 Score =  116 bits (60), Expect = 2e-23
 Identities = 148/187 (79%), Gaps = 7/187 (3%)
 Strand = Plus / Minus


Query:  446         CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  98973577    CAAACTGGGATTAGATACCCTACTATGCTTAGCCATAAACT----TAAATAACTGAATAA
98973632

Query:  386         AACTGTTCGCCAGAACACT---ACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGC  330
Sbjct:  98973633    AGTTATTTGCCAGAGTACTACTACCAGCAACAGCCTAAATCTCAGAGGATTTGGCAGTGC
98973692

Query:  329         TTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACC  270
Sbjct:  98973693    TTTATATTCCTCTAGAGGAGGCTGTTCTATAATTGATAAACTCTGACAAACCTCTCCATC
98973752

Query:  269         TCTTGCC  263
Sbjct:  98973753    TCTTGCC  98973759
```

```
 Score = 79.5 bits (41), Expect = 2e-12
 Identities = 57/65 (87%)
 Strand = Plus / Minus


Query:  215         TAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
Sbjct:  98973804    TAATCACAAATATTTACATAAAAACGTTAGGTCAAGGTGTAGTCTATGAGATGGGAAGAA
98973863

Query:  155         ATGGG  151
Sbjct:  98973864    ATGGG  98973868
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 38/47 (80%)
 Strand = Plus / Minus


Query:  94          AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGA  48
Sbjct:  98973928    AAGGAGGATTTAGTAGTAAATTAGGAATAGAGAGCTTAGTTGAATGA  98973974
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 21/22 (95%)
 Strand = Plus / Plus


Query:  193       TTTTATGTAGATACTTCTGCTT  214
Sbjct:  66859198  TTTTATGTAGATACTCCTGCTT  66859219
```

```
>ref|NC_000020.4| Homo sapiens chromosome 20, complete sequence
          Length = 62802940

 Score =  437 bits (227), Expect = e-120
 Identities = 372/432 (86%), Gaps = 7/432 (1%)
 Strand = Plus / Plus


Query:  16        GGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAAT  75
Sbjct:  55623597  GGTGATGGGCTGTGTGTGCGTGCTTCATGGCCTTATTCAACCAAGCACTCTGCTCTTGGT
55623656

Query:  76        TTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTTCTG  135
Sbjct:  55623657  TTACTGCTAAATCCTCCTTAAGCCCTTAGATTTCATAA-GGCTGTCATGAGATTTT-CTG
55623714

Query:  136       TGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTT  194
Sbjct:  55623715  GACATAGAAAATGTTGCCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTT
55623774

Query:  195       TTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTAT  254
Sbjct:  55623775  TTATGTGTATACTTGTGCTTACTCTATAACCTTTTTAGGGTTTGCTGCAGATGG--GCAT
55623832

Query:  255       ATAGGCT--GGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  55623833  ATAGGCCAGGGGCAAGAGGTGGTGAGACGTATCGGGGTTTATTGATTATAGAACAGGCTC
55623892

Query:  313       CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  55623893  CTCTAGAGGGATATAAAGCACCACCAAGTCCTTTGAGTTTTAAATTGTTGCTTGTAGTAC
55623952

Query:  373       TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTAT  432
Sbjct:  55623953  TCTGGCGAATGGTTTTGTTAATGTAACTGTTAGGGTTTAGGGCTAAGCATAGAGGGGTAT
55624012

Query:  433       CTAATCCCAGTT  444
Sbjct:  55624013  CTAATCCCAGTT  55624024
```

```
 Score = 73.7 bits (38), Expect = 8e-11
 Identities = 56/65 (86%)
 Strand = Plus / Plus


Query:  349       GTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGT  408
Sbjct:  2320628   GTTTTAAGCTGTTGCTTATAGTACTCTGGCAAATAGTTTTGCTAATCTAACTACTTGAGT
2320687

Query:  409       TTAGG  413
Sbjct:  2320688   TTAGG  2320692
```

Score = 46.8 bits (24), Expect = 0.011
Identities = 46/57 (80%)
Strand = Plus / Plus

```
Query:  28        TGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAATTTATTGCTA  84
Sbjct:  13962371  TGTGTATGTGCTTCATGGCCTTATTCAATCAAGCACCCTAGTCTTGATTTACTGCTA  13962427
```

>ref|NC_000008.3| Homo sapiens chromosome 8, complete sequence
Length = 146305119

Score = 433 bits (225), Expect = e-119
Identities = 370/435 (85%), Gaps = 3/435 (0%)
Strand = Plus / Minus

```
Query:  446       CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  47054122  CAAACTGGGATTAGATACCCCACTATGCTTACCCCTAAACTCTAATAGTTACATTTAAAA
47054181

Query:  386       AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  47054182  AAAAATTTGCCAGAATACTACCAGCAACAGCTAAAAACTCAAAGGATTTGATGCTGCTT-
47054240

Query:  326       ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  47054241  ATATCCCTCTAGAGGATCCTGTTCTATAATTAATAAACCCCAATATACCTCACCACCTCT
47054300

Query:  266       TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAA  207
Sbjct:  47054301  TGCCCAGCCTATATACCACCATCTTCAGCAAACCCTAAAGTGGTTATAGAGTAAGCACAA
47054360

Query:  206       GTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT-GGGTAC  148
Sbjct:  47054361  GTGTACACATAAAAACGTTAGGTCAAGGTGTAGCTCATGAGGTGGCAAGAAGTAGACTAC
47054420

Query:  147       GTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGG  88
Sbjct:  47054421  ATTTTGTATACCCAG-AAAATCTCACAACAACCTTTATGAAATCGAAGGGCTCAAGGAGG
47054479

Query:  87        ATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACA  28
Sbjct:  47054480  ATTTAGCAGTAAACCAAGATCAGAGTGCTTGGTTGAATAAAGCCATGAAGCATGCACACC
47054539

Query:  27        CCGCCCGTCACCCTC  13
Sbjct:  47054540  CCTCCCATCACTCTC  47054554
```

Score = 367 bits (191), Expect = 2e-99
Identities = 307/355 (86%), Gaps = 5/355 (1%)
Strand = Plus / Minus

```
Query:  364       AGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAAAGGAGCCTGT  305
Sbjct:  33320262  AGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAGAGGAGCCTGT
33320321
```

```
Query:  304         TCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG--CCCAGCCTATATACCTCC  247
Sbjct:  33320322    TCTATAATCAATGAACCCTGATACACCTCACCGCCTCTTGCCCCCAGCCTATATAGGGCC
33320381

Query:  246         ATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTATCTACATAAAAACGTTA  187
Sbjct:  33320382    ATCTTCAGCAAACCCTAAAAAGTTTATTGAGTAAGCACAAGTACACACATAAAAATGTTA
33320441

Query:  186         GGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TACGTTTTCTACACACAGAAAAA  128
Sbjct:  33320442    GGTCAAGGTGTAGCCCATGAGATGGCAAGAAATGGGATACATTTTCTATGTCCAG-AAAA
33320500

Query:  127         TCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAG  68
Sbjct:  33320501    TCTCACGACAACCTTTATGAAATCTAAGGACTC-AGGAAGATTTAGCAATAAACCAAGAG
33320559

Query:  67          CAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  33320560    CAGAGTGCTTGGTTGAATAAGGCTATGAAGCATGCACACACCACCCGTCACCCTC  33320614
```

```
 Score = 91.1 bits (47), Expect = 5e-16
 Identities = 89/110 (80%)
 Strand = Plus / Minus


Query:  262         CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTAT  203
Sbjct:  104163742   CAGCCTGTATACTACCATCTTCAGCAAGCCCTAAAAAGGTCATAAAGTAAGCACAAGTAC
104163801

Query:  202         CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  104163802   TTACATGGAAACATTAGGTCAACATGTAGCTTATGAGATGGAAAGAAATG  104163851
```

```
 Score = 60.3 bits (31), Expect = 9e-07
 Identities = 59/73 (80%)
 Strand = Plus / Minus


Query:  94          AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  104163913   AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAAGGTTGTGAAGCAC
104163972

Query:  34          GCACACACCGCCC  22
Sbjct:  104163973   ACATAGACCGCCC  104163985
```

```
 Score = 56.4 bits (29), Expect = 1e-05
 Identities = 29/29 (100%)
 Strand = Plus / Minus


Query:  364         AGCAACAGCTTAAAACTCAAAGGACTTGG  336
Sbjct:  104163631   AGCAACAGCTTAAAACTCAAAGGACTTGG  104163659
```

```
 Score = 54.5 bits (28), Expect = 5e-05
 Identities = 36/40 (90%)
```

Strand = Plus / Minus

```
Query:  445        AAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACT  406
Sbjct:  104163566  AAACTGGGATTAAATACCCCACTATGTTTAGCCATAAACT  104163605
```

Score = 48.8 bits (25), Expect = 0.003
Identities = 25/25 (100%)
Strand = Plus / Minus

```
Query:  446        CAAACTGGGATTAGATACCCCACTA  422
Sbjct:  33320209   CAAACTGGGATTAGATACCCCACTA  33320233
```

Score = 37.2 bits (19), Expect = 8.4
Identities = 19/19 (100%)
Strand = Plus / Plus

```
Query:  216        CTCTGTGGCCTTTCCAGGG  234
Sbjct:  134811942  CTCTGTGGCCTTTCCAGGG  134811960
```

>ref|NC_000003.3| Homo sapiens chromosome 3, complete sequence
Length = 199558344

Score = 406 bits (211), Expect = e-111
Identities = 366/436 (83%), Gaps = 5/436 (1%)
Strand = Plus / Plus

```
Query:  12         AGAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCT  71
Sbjct:  106137766  AGAGGGCGATGGGTGGTGTGTGCATGCTTCACGGCCTCATTCAATGAAGCACTCTGTTCT
106137825

Query:  72         CAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  106137826  TCATTTACCGCTAAATCCTCTTTGAATCTTTAGGTTTCATTATGGTTATTGTAAAATTTT
106137885

Query:  132        TCTGTGTGTAGAAAACGTACC-CATTTCTTGCCACCTCATGGGCTACACCTTGACCTAAC  190
Sbjct:  106137886  -CGGGAAATAGAAAATGTAGCTCATTTCTTACCATTTCATAGGCAACACCTTGACCTAAT
106137944

Query:  191        GTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAG  250
Sbjct:  106137945  GTTTTTATGTACATACTTGTGCTTACTCTAAGGCCTTTTTAGGGTTTGCTGAAGATGGTG
106138004

Query:  251        GTATATAGGCTG---GGCAAGAGGTGGTGAGGTAATTGGGGTTTATCGATTATAGAACA  307
Sbjct:  106138005  GTATATAGGCTGAGTGGCGAGAGATGGCGAGGTATATCGGAGTTTACCGATTATACAACA
106138064

Query:  308        GGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGT  367
Sbjct:  106138065  GGCTCCTCTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGTTTGT
106138124

Query:  368        AGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGG  427
Sbjct:  106138125  AGTACTCTGGCGAGTAGTTTTGTTAATTTAACTATCTGGGTTTAGGGCTAAGCATAGTGA
```

106138184

```
Query:  428        GGTATCTAATCCCAGT  443
Sbjct:  106138185  GGTATCTAATCCCAGT  106138200
```

```
 Score =  229 bits (119), Expect = 1e-57
 Identities = 238/295 (80%), Gaps = 4/295 (1%)
 Strand = Plus / Plus


Query:  156        TTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTA  215
Sbjct:  166991590  TTCTTTCCATGTCATAGGCTACACTTTGACCTAATGTTTTTATGCAGCTACTTGCGCTTA
166991649

Query:  216        CTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTATATAGGCTGGG----CAAGAGG  271
Sbjct:  166991650  CTTTGAGACCTTTTTAGGGTTTGCTGAAGATGGCAGTATATAGGCTGAGTTGCCAAGAGA
166991709

Query:  272        TGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGC  331
Sbjct:  166991710  TAGTGGGATATGTCAGGGTTTAACGATTATAGAACAGGCTCCTTTAGAGGAGTATAAACC
166991769

Query:  332        ACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTT  391
Sbjct:  166991770  TTGGCCATGTCCTTTGAGTTTTAAGCTCTTGCTTGTAATACTCTGGTGAATAATTTTGTT
166991829

Query:  392        GATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  166991830  TGTTAAATTATTTAAGTTTAAGGCTAAGCATAGTGGGGTGTCAAAACCCAGTTTG  166991884
```

```
 Score = 85.3 bits (44), Expect = 3e-14
 Identities = 66/77 (85%)
 Strand = Plus / Minus


Query:  89         GGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACA  30
Sbjct:  39521923   GGACTTAGCAGTAAACCAAGAGCAGAGTGCTTGGTTGAATAAGGCCATGAAGCACACACA
39521982

Query:  29         CACCGCCCGTCACCCTC  13
Sbjct:  39521983   CACCGCCGGTCACCCTC  39521999
```

```
 Score = 85.3 bits (44), Expect = 3e-14
 Identities = 82/101 (81%)
 Strand = Plus / Plus


Query:  13         GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  95640666   GAGGGTGACGGGCGGTGTGTATGCGCTTCAGGGCCCTGTTCAACTAAGCACTCTACACTT
95640725

Query:  73         AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAA  113
Sbjct:  95640726   AGTTTACTGCTAAATCCACCTTCGACCCTTAAATTTCATAA  95640766
```

```
 Score = 39.1 bits (20), Expect = 2.2
```

```
 Identities = 24/26 (92%)
 Strand = Plus / Plus


Query:  55          ATTAAACACTCTGCTCTCAATTTATT  80
Sbjct:  41846161    ATTAACCACTCTGCTCTGAATTTATT  41846186
```

```
>ref|NC_000014.2| Homo sapiens chromosome 14, complete sequence
          Length = 101218245

 Score =  331 bits (172), Expect = 2e-88
 Identities = 329/390 (84%), Gaps = 10/390 (2%)
 Strand = Plus / Plus


Query:  61          CACTCTGCTCTCAATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGT  120
Sbjct:  77871520    CACTCTGCTCTGGGTTTACTGCTACATCCTCCTTGAGCCATTAGATTTCATAAAGGTAGT
77871579

Query:  121         CGCGAGATTTTTCTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACAC  179
Sbjct:  77871580    CATGATATTTT-CTGGATATAGAAAATGTAGCCCAATTCTTGCCACCTCATGAGCTACAC
77871638

Query:  180         CTTGACCTAACGTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGC  239
Sbjct:  77871639    AA--ACCAGA--TTTTTATGTGTACACTTGTGCTTACTCTACAACCTTTTTAGGGTTTGC
77871694

Query:  240         TGAAGATGGAGGTATATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGA  297
Sbjct:  77871695    TGAAGATGGCGGTA-ATAGGCTGGGGGCAAGAGGTGGTGAGGTGTATCGGG-TTTATCGC
77871752

Query:  298         TTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGC  357
Sbjct:  77871753    TTATAGAACAGGCTTCTCTAGAGGGATATAAAGAACTGCCAGGTCCTTTGAGTTTTAAGC
77871812

Query:  358         TGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTA  417
Sbjct:  77871813    TGTTGCTCGTAGTATTCTGACGAATGGTTTTGTTAATGTAACTACTAGAGTTTAGGGCTA
77871872

Query:  418         AGCATAGTGGGGTATCTAATCCCAGTTTGA  447
Sbjct:  77871873    AGCACAGTGGGGTATCTAATCCCAGTTTGA  77871902
```

```
>ref|NC_000024.2| Homo sapiens chromosome Y, complete sequence
          Length = 50860226

 Score =  235 bits (122), Expect = 2e-59
 Identities = 275/344 (79%), Gaps = 4/344 (1%)
 Strand = Plus / Minus


Query:  353         AAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAAGGAGCCTGTTCTATAATCGA  294
Sbjct:  8203137     AAAAATTAAAGGACTCAGCGGTGCTTTATATCCCTCTAGAGGAGCCTGTTTTTAATCAA
8203196

Query:  293         TAAACCCCAATTTACCTCACCACCTCTTGCCC--AGCCTATATACCTCCATCTTCAGCAA  236
Sbjct:  8203197     TAAAACCTGATATACCTCACCACTTCTTGCCCCCAACCTATATATCCCCTCTTTAGAAA
8203256

Query:  235         ACCCTGGAAAGGCCACAGAGTAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGT  176
```

```
Sbjct:  8203257   ACCCTAAAATGGTTATAGAGTAAGCACAAGCATACCCACAAAAATGTTAGATCAAGGTGT
8203316

Query:  175       AGCCCATGAGGTGGCAAGAAATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAA  117
Sbjct:  8203317   AGCTCCTGAGCTGGCAAGAAGTGGACTACATTTTCTGTACCCAGAATA-TCTCATAACAA
8203375

Query:  116       CCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTA  57
Sbjct:  8203376   CTTCTATGAATTCTAAGGGCTCAAGGAGAATTTAGCAGTAAACCAAGAGCAGAGTGCTTG
8203435

Query:  56        ATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  8203436   GTTGAATAAGGCCATGAAGCATGCATATACCACCTGTCACCCTC  8203479
```

```
 Score =  104 bits (54), Expect = 5e-20
 Identities = 93/110 (84%), Gaps = 4/110 (3%)
 Strand = Plus / Minus


Query:  446       CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  8200712   CAAACAGGAATTAGATAACACACTATGCTCAGCCCTAAACTCTAATAGTTACATTAACAA
8200771

Query:  386       AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTG  337
Sbjct:  8200772   AAC----CACCAGAATACTACAAGCAACAGCTTAAAATTTAAAGGACTTG  8200817
```

```
 Score = 64.1 bits (33), Expect = 7e-08
 Identities = 49/57 (85%)
 Strand = Plus / Plus


Query:  171       GGGCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTT  227
Sbjct:  4178399   GGGCTACACCTTGACCTAACGTCTTTACGTGGGTACTTGCGCTTACTTTGTAGCCTT  4178455
```

```
>ref|NC_000013.3| Homo sapiens chromosome 13, complete sequence
          Length = 111298136

 Score =  233 bits (121), Expect = 8e-59
 Identities = 155/172 (90%)
 Strand = Plus / Plus


Query:  275       TGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACT  334
Sbjct:  104463646 TGAGGTTGATCGGGGTTTATCGATTACAGAACAGGCTCCTCTAGAGGGATATGAAGCACC
104463705

Query:  335       GCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGAT  394
Sbjct:  104463706 GCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAGTGTTCTGGCGAGCAGTTTTGTTGAT
104463765

Query:  395       CTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  104463766 TTAACTGTTGAGGTTTAGGGCTAAGCATAGTGGGGTATCTAATCCCAGTTTG  104463817
```

```
>ref|NC_000018.2| Homo sapiens chromosome 18, complete sequence
          Length = 78067305
```

```
 Score =  212 bits (110), Expect = 2e-52
 Identities = 190/225 (84%), Gaps = 9/225 (4%)
 Strand = Plus / Plus


Query:  222       GGCCTTTCCAGGGTTTGCTGAAGATGGAGGTATATAGGCTG---GGCAAGAGGTGGTGAG  278
Sbjct:  59514871  GGCCTTTTTAGGGTTTGCTGAAGGTGGCAGTACATAGGCTGAGTGGCAAGAGATGGTGAG
59514930

Query:  279       GTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCA  338
Sbjct:  59514931  GTATATCGGAGTTTATCAATTATAGAACAGGTTCCTCTAGAAGGATATAAAGCACCGCCA
59514990

Query:  339       AGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAA  398
Sbjct:  59514991  AGT------AGTTTTAAGCTGTGGCTTGTAGTTCTCTGGTGAATAGTTTTGTTAATTTAA
59515044

Query:  399       CTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGT  443
Sbjct:  59515045  CTACTTGGGTTTAGGGCTAAGCATAGTGGGGTATCTAATCCCAGT  59515089


>ref|NC_000010.2| Homo sapiens chromosome 10, complete sequence
          Length = 134652902

 Score =  206 bits (107), Expect = 1e-50
 Identities = 185/219 (84%), Gaps = 11/219 (5%)
 Strand = Plus / Minus


Query:  446       CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  56363354  CAAACTGGGATTAGAAACCCCACTATGCTTA--------CACAATAGTTATATTAACAA
56363405

Query:  386       AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  56363406  GACTGTTCGCCAGAGTACTACATGCAGCAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT
56363465

Query:  326       ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  56363466  ATAGCCTTCTAGAGGAGCCGGTTCTATAATTGATAAACCCCGATATACCTCACCATCTCT
56363525

Query:  266       TG---CCCAGCCTATATACCTCCATCTTCAGCAAACCCT  231
Sbjct:  56363526  TGTCACTCAGCCTATATAACACCAGCTTCAGCAAACCCT  56363564


 Score =  139 bits (72), Expect = 2e-30
 Identities = 146/178 (82%), Gaps = 2/178 (1%)
 Strand = Plus / Minus


Query:  188       TAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TACGTTTTCTACACACAGAAA  130
Sbjct:  56363639  TAGGTCAAGGTGTAGTCCATGGGATGGTAAGAAATGGGCTACATTTTCTACATCCAGAAA
56363698

Query:  129       AATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAG  70
Sbjct:  56363699  TATCTCACAATAACCTTCATGAAATCTAAATGTTCGAAGAGGATTTAGTAGTAAATCAAG
56363758

Query:  69        AGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTCT  12
Sbjct:  56363759  AACAGAGTGCTTGATTGAATAAGGCCATAAGGCAAGCACACA-AGCCCGTCACCCTCT
```

56363815

Score = 54.5 bits (28), Expect = 5e-05
Identities = 36/40 (90%)
Strand = Plus / Minus

```
Query:  113        TTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAAT  74
Sbjct:  36232418   TTATGAAATCTAAAGATTCAAGGAGGATTTAGCAGTAAAT  36232457
```

Score = 39.1 bits (20), Expect = 2.2
Identities = 20/20 (100%)
Strand = Plus / Plus

```
Query:  335        GCCAAGTCCTTTGAGTTTTA  354
Sbjct:  126163034  GCCAAGTCCTTTGAGTTTTA  126163053
```

>ref|NC_000006.3| Homo sapiens chromosome 6, complete sequence
Length = 170670676

Score = 114 bits (59), Expect = 6e-23
Identities = 99/119 (83%)
Strand = Plus / Plus

```
Query:  13         GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  144897314  GAGGGTAACGGGTGGCGTGTGCATGCTTCATGGCCTTATTCAATCAAGCACTCTACTCTT
144897373

Query:  73         AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTT  131
Sbjct:  144897374  GATTTACTGCTAAATCCTCCTTGAATCTTTAGATTTCCTAAAGGCTATCATGAGATTTT
144897432
```

Score = 73.7 bits (38), Expect = 8e-11
Identities = 79/97 (81%), Gaps = 1/97 (1%)
Strand = Plus / Minus

```
Query:  248        CCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTATCTACATAAAAACGT  189
Sbjct:  169307649  CCATCTTCAGCAAACCCTACGATGGCCGCAGAGTGAGCACCAGCATTTACACAAAAACAT
169307708

Query:  188        TAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  169307709  CAGGTCCAGGGGTAGCTC-TGAGGTGGAAAGAAATGG  169307744
```

Score = 39.1 bits (20), Expect = 2.2
Identities = 20/20 (100%)
Strand = Plus / Plus

```
Query:  216        CTCTGTGGCCTTTCCAGGGT  235
```

```
Sbjct:  150369095  CTCTGTGGCCTTTCCAGGGT  150369114
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Plus


Query:  409        TTAGGGTTAAGCATAGTGG  427
Sbjct:  139792583  TTAGGGTTAAGCATAGTGG  139792601
```

```
>ref|NC_000022.3| Homo sapiens chromosome 22, complete sequence
          Length = 47848585

 Score =  114 bits (59), Expect = 6e-23
 Identities = 141/182 (77%)
 Strand = Plus / Minus


Query:  446       CAAACTGGGATTAGATACCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  33217677  CAAACTGGGACTAAATCTCTCACTGTGCTTAGCCATAAACTTAAATAATTTAATAAACAG
33217736

Query:  386       AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  33217737  AATTATTTACCAGAGCACTATAAGCAATAGCTTAAGCCTCAAAGGACATGGCGATGCTTT
33217796

Query:  326       ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  33217797  ACAGCTCTCGAGAGGGGCCTGTTCTATATTCAATAAGCTCCGATATACCTCAGCATCTCT
33217856

Query:  266       TG  265
Sbjct:  33217857  TG  33217858
```

```
>ref|NC_000019.3| Homo sapiens chromosome 19, complete sequence
          Length = 59568810

 Score = 79.5 bits (41), Expect = 2e-12
 Identities = 164/213 (76%), Gaps = 20/213 (9%)
 Strand = Plus / Minus


Query:  381       TTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATC  322
Sbjct:  38459185  TTCACCAGAGTACTACCAGCAACAGCTTAAAACACAAAGGACTTGGCAGTGC-TTATATC
38459243

Query:  321       CCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTGC--  264
Sbjct:  38459244  CCTTT---------TTTTTGTAATCAATAAACCCCAGTAAACCTCACTATCTCTTGCTA
38459294

Query:  263       --CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAG  206
Sbjct:  38459295  ATTCAGCCTATACACCGCCATCTTCTGCAAAACCTTAAAAGG-----TACTAAACACAAG
38459349

Query:  205       TATCTACATAAAAACGTTAGGTCAAGGTGTAGC  173
Sbjct:  38459350  TATTTACAT-AAAACGTTAGGTCATGGTGCAGC  38459381
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Plus


Query:  152       CCATTTCTTGCCACCTCAT  170
Sbjct:  8028326   CCATTTCTTGCCACCTCAT  8028344
```

```
>ref|NC_000015.2| Homo sapiens chromosome 15, complete sequence
          Length = 96598362

 Score = 43.0 bits (22), Expect = 0.15
 Identities = 22/22 (100%)
 Strand = Plus / Plus


Query:  77        TATTGCTAAATCCTCCTTGAGC  98
Sbjct:  95167138  TATTGCTAAATCCTCCTTGAGC  95167159
```

```
 Score = 41.1 bits (21), Expect = 0.58
 Identities = 21/21 (100%)
 Strand = Plus / Plus


Query:  212       CTTACTCTGTGGCCTTTCCAG  232
Sbjct:  16602521  CTTACTCTGTGGCCTTTCCAG  16602541
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192       TTTTTATGTAGATACTTCTG  211
Sbjct:  43265368  TTTTTATGTAGATACTTCTG  43265387
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 23/25 (92%)
 Strand = Plus / Minus


Query:  372       ACACTACAAGCAACAGCTTAAAACT  348
Sbjct:  73647812  ACAGTACAAGCAACAACTTAAAACT  73647836
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Plus


Query:  380       AACAGTTTTGTTGATCTAA  398
Sbjct:  90233287  AACAGTTTTGTTGATCTAA  90233305
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query:  345       AAGGACTTGGCAGTGCTTT  327
Sbjct:  52155419  AAGGACTTGGCAGTGCTTT  52155437
```

```
 Score = 37.2 bits (19), Expect = 8.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query:  269       TCTTGCCCAGCCTATATAC  251
Sbjct:  74898219  TCTTGCCCAGCCTATATAC  74898237
```

```
>ref|NC_000012.3| Homo sapiens chromosome 12, complete sequence
          Length = 133382389

 Score = 41.1 bits (21), Expect = 0.58
 Identities = 23/24 (95%)
 Strand = Plus / Plus


Query:  50         ATTCAATTAAACACTCTGCTCTCA  73
Sbjct:  15030902   ATTCAATTAAACGCTCTGCTCTCA  15030925
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 24/26 (92%)
 Strand = Plus / Plus


Query:  242        AAGATGGAGGTATATAGGCTGGGCAA  267
Sbjct:  49478986   AAGATGGGGGTATAGAGGCTGGGCAA  49479011
```

```
 Score = 39.1 bits (20), Expect = 2.2
 Identities = 24/26 (92%)
 Strand = Plus / Plus


Query:  242        AAGATGGAGGTATATAGGCTGGGCAA  267
Sbjct:  49405149   AAGATGGGGGTATAGAGGCTGGGCAA  49405174

  Database: NCBI genome chromosomes - human
    Posted date:  Mar 13, 2003  9:09 PM
  Number of letters in database: 3,051,185,827
  Number of sequences in database:  24

Lambda     K      H
    1.33    0.621     1.12

Gapped
```

```
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 741,612
Number of Sequences: 24
Number of extensions: 741612
Number of successful extensions: 156
Number of sequences better than 10.0: 22
Number of HSP's better than 10.0 without gapping: 77
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 110
length of query: 462
length of database: 3,051,185,827
effective HSP length: 24
effective length of query: 438
effective length of database: 3,051,185,251
effective search space: 1336419139938
effective search space used: 1336419139938
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 19 (37.2 bits)
```

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

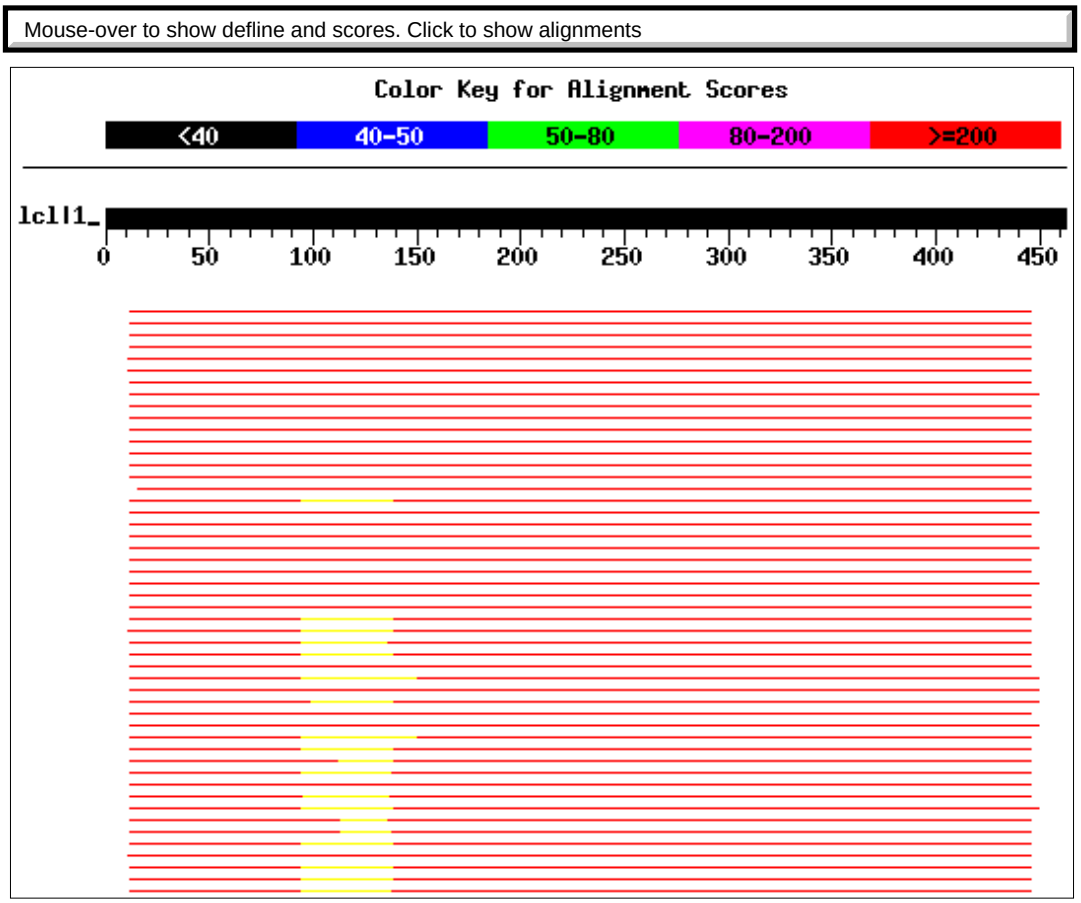
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: NCBI genome chromosomes - other
2528 sequences; 789,957,834 total letters

Query= CS63win
(462 letters)

Distribution of 176 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value
ref|NC_001807.4| Homo sapiens mitochondrion, complete genome	460	e-127

ref|NC_001645.1|	Gorilla gorilla mitochondrion, complete ge...	460	e-127
ref|NC_001643.1|	Pan troglodytes mitochondrion, complete ge...	454	e-126
ref|NC_001644.1|	Pan paniscus mitochondrion, complete genome	442	e-122
ref|NC_002083.1|	Pongo pygmaeus abelii mitochondrion, compl...	439	e-121
ref|NC_001646.1|	Pongo pygmaeus mitochondrion, complete genome	410	e-112
ref|NC_002082.1|	Hylobates lar mitochondrion, complete genome	389	e-106
ref|NC_004025.1|	Lemur catta mitochondrion, complete genome	365	2e-99
ref|NC_001700.1|	Felis catus mitochondrion, complete genome	364	9e-99
ref|NC_002763.1|	Cebus albifrons mitochondrion, complete ge...	362	3e-98
ref|NC_002765.1|	Nycticebus coucang mitochondrion, complete...	356	2e-96
ref|NC_001665.1|	Rattus norvegicus mitochondrial genome	346	1e-93
ref|NC_002008.4|	Canis familiaris mitochondrion, complete g...	346	1e-93
ref|NC_004030.1|	Eumetopias jubatus mitochondrion, complete...	346	1e-93
ref|NC_004023.1|	Arctocephalus forsteri mitochondrion, comp...	346	1e-93
ref|NC_002764.1|	Macaca sylvanus mitochondrion, complete ge...	342	2e-92
ref|NC_003040.1|	Soriculus fumidus mitochondrion, complete ...	339	3e-91
ref|NC_003427.1|	Ursus arctos mitochondrion, complete genome	337	1e-90
ref|NC_004029.1|	Odobenus rosmarus rosmarus mitochondrion, ...	337	1e-90
ref|NC_001569.1|	Mus musculus mitochondrion, complete genome	335	4e-90
ref|NC_003428.1|	Ursus maritimus mitochondrion, complete ge...	329	2e-88
ref|NC_003033.1|	Ochotona collaris mitochondrion, complete ...	327	9e-88
ref|NC_001941.1|	Ovis aries mitochondrion, complete genome	323	1e-86
ref|NC_003041.1|	Volemys kikuchii mitochondrion, complete g...	321	5e-86
ref|NC_001892.1|	Myoxus glis mitochondrion, complete genome	321	5e-86
ref|NC_001913.1|	Oryctolagus cuniculus mitochondrion, compl...	321	5e-86
ref|NC_002619.1|	Pteropus scapulatus mitochondrion, complet...	319	2e-85
ref|NC_001821.1|	Dasypus novemcinctus mitochondrion, comple...	317	7e-85
ref|NC_001567.1|	Bos taurus mitochondrion, complete genome	314	1e-83
ref|NC_002391.1|	Talpa europaea mitochondrion, complete genome	310	1e-82
ref|NC_000884.1|	Cavia porcellus complete mitochondrial genome	308	5e-82
ref|NC_002811.1|	Tarsius bancanus mitochondrion, complete g...	306	2e-81
ref|NC_003426.1|	Ursus americanus mitochondrion, complete g...	304	8e-81
ref|NC_002078.1|	Orycteropus afer complete mitochondrial ge...	302	3e-80
ref|NC_004031.1|	Cynocephalus variegatus mitochondrion, com...	300	1e-79
ref|NC_002612.1|	Pteropus dasymallus mitochondrion, complet...	298	4e-79
ref|NC_001325.1|	Phoca vitulina mitochondrion, complete genome	298	4e-79
ref|NC_004032.1|	Tamandua tetradactyla mitochondrion, compl...	298	4e-79
ref|NC_000889.1|	Hippopotamus amphibius mitochondrion, comp...	291	9e-77
ref|NC_001640.1|	Equus caballus mitochondrion, complete genome	289	3e-76
ref|NC_001602.1|	Halichoerus grypus mitochondrion, complete...	285	5e-75
ref|NC_000845.1|	Sus scrofa mitochondrion, complete genome	279	3e-73
ref|NC_001601.1|	Balaenoptera musculus mitochondrion, compl...	277	1e-72
ref|NC_002503.1|	Physeter catodon mitochondrion, complete g...	275	4e-72
ref|NC_004563.1|	Muntiacus muntjak mitochondrion, complete ...	273	1e-71
ref|NC_001779.1|	Rhinoceros unicornis mitochondrion, comple...	273	1e-71
ref|NC_004027.1|	Manis tetradactyla mitochondrion, complete...	269	2e-70
ref|NC_004577.1|	Muntiacus crinifrons mitochondrion, comple...	267	8e-70
ref|NC_001808.1|	Ceratotherium simum mitochondrion, complet...	267	8e-70
ref|NC_001788.1|	Equus asinus mitochondrion, complete genome	266	3e-69
ref|NC_002658.1|	Thryonomys swinderianus mitochondrion, com...	260	2e-67
ref|NC_004028.1|	Lepus europaeus mitochondrion, complete ge...	258	6e-67
ref|NC_002369.1|	Sciurus vulgaris mitochondrion, complete g...	258	6e-67
ref|NC_004069.1|	Muntiacus reevesi mitochondrion, complete ...	254	9e-66
ref|NC_001321.1|	Balaenoptera physalus mitochondrion, compl...	250	1e-64
ref|NC_002626.1|	Chalinolobus tuberculatus mitochondrion, c...	248	5e-64

ref|NC_002521.1|	Tupaia belangeri mitochondrion, complete g...	241	1e-61
ref|NC_001992.1|	Papio hamadryas mitochondrion, complete ge...	241	1e-61
ref|NC_003321.1|	Tachyglossus aculeatus mitochondrion, comp...	239	4e-61
ref|NC_000891.1|	Ornithorhynchus anatinus mitochondrion, co...	237	1e-60
ref|NC_002504.1|	Lama pacos mitochondrion, complete genome	229	3e-58
ref|NC_003314.1|	Dugong dugon mitochondrion, complete genome	219	2e-55
ref|NC_004026.1|	Macroscelides proboscideus mitochondrion, ...	208	7e-52
ref|NC_002808.1|	Echinosorex gymnura mitochondrion, complet...	206	3e-51
ref|NC_002009.1|	Artibeus jamaicensis mitochondrion, comple...	206	3e-51
ref|NC_001610.1|	Didelphis virginiana mitochondrion, comple...	202	4e-50
ref|NC_003039.1|	Trichosurus vulpecula mitochondrion, compl...	198	5e-49
ref|NC_002080.1|	Erinaceus europaeus mitochondrion, complet...	189	4e-46
ref|NC_004374.1|	Bassozetus zenkevitchi mitochondrion, comp...	185	6e-45
ref|NC_001794.1|	Macropus robustus mitochondrion, complete ...	185	6e-45
ref|NC_002746.1|	Isoodon macrourus mitochondrion, complete ...	183	2e-44
ref|NC_003322.1|	Vombatus ursinus mitochondrion, complete g...	179	3e-43
ref|NC_004021.1|	Ranodon sibiricus mitochondrion, complete ...	171	7e-41
ref|NC_002756.1|	Mertensiella luschani mitochondrion, compl...	166	4e-39
ref|NC_003168.1|	Percopsis transmontana mitochondrion, comp...	164	1e-38
ref|NC_003187.1|	Hoplostethus japonicus mitochondrion, comp...	158	7e-37
ref|NC_004600.1|	Opisthoproctus soleatus mitochondrion, com...	156	3e-36
ref|NC_000860.1|	Salvelinus fontinalis mitochondrion, compl...	156	3e-36
ref|NC_004389.1|	Cetostoma regani mitochondrion, complete g...	154	1e-35
ref|NC_004411.1|	Petroscirtes breviceps mitochondrion, comp...	154	1e-35
ref|NC_004372.1|	Aphredoderus sayanus mitochondrion, comple...	148	6e-34
ref|NC_004390.1|	Eutaeniophorus sp. 033-Miya mitochondrion,...	148	6e-34
ref|NC_004385.1|	Melanotaenia lacustris mitochondrion, comp...	146	2e-33
ref|NC_000934.1|	Loxodonta africana mitochondrion, complete...	146	2e-33
ref|NC_000861.1|	Salvelinus alpinus mitochondrion, complete...	144	8e-33
ref|NC_004376.1|	Diplacanthopoma brachysoma mitochondrion, ...	144	8e-33
ref|NC_002647.1|	Diplophos taenia mitochondrion, complete g...	144	8e-33
ref|NC_004593.1|	Esox lucius mitochondrion, complete genome	142	3e-32
ref|NC_002734.1|	Plecoglossus altivelis mitochondrion, comp...	142	3e-32
ref|NC_004695.1|	Cobitis striata mitochondrion, complete ge...	141	1e-31
ref|NC_004701.1|	Eigenmannia sp. mitochondrion, complete ge...	141	1e-31
ref|NC_002073.3|	Chrysemys picta mitochondrion, complete ge...	141	1e-31
ref|NC_004392.1|	Monocentris japonicus mitochondrion, compl...	141	1e-31
ref|NC_004391.1|	Anoplogaster cornuta mitochondrion, comple...	141	1e-31
ref|NC_004378.1|	Melanonus zugmayeri mitochondrion, complet...	139	5e-31
ref|NC_002646.1|	Coregonus lavaretus mitochondrion, complet...	139	5e-31
ref|NC_004596.1|	Nansenia ardesiaca mitochondrion, complete...	137	2e-30
ref|NC_004591.1|	Bathylagus ochotensis mitochondrion, compl...	137	2e-30
ref|NC_004399.1|	Neocyttus rhomboidalis mitochondrion, comp...	137	2e-30
ref|NC_004398.1|	Allocyttus niger mitochondrion, complete g...	137	2e-30

>ref|NC_001807.4| Homo sapiens mitochondrion, complete genome
Length = 16571

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127
```

```
Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>ref|NC_001645.1| Gorilla gorilla mitochondrion, complete genome

Length = 16364

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  485    CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACTTCAACAGTTAAATTAACAA  544

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  545    GACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  604

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  605    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  664

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  665    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCACAAAGTAAGCACA  724

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  725    AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  784

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  785    CATTTTCTAC-TTCAGAAAACT---ACGATAACCCTTATGAAACCTAAGGGTAGAAGGTG  840

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  841    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  900

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  901    ACCGCCCGTCACCCTC  916
```

>ref|NC_001643.1| Pan troglodytes mitochondrion, complete genome

Length = 16554

Score = 454 bits (236), Expect = e-126
Identities = 376/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTCAACAGTTAAATTAACAA  543

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  544    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  603

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  604    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCGCCTCT  663

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  664    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGTTACAAAGTAAGCACA  723

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  724    AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCTATGAGGTGGCAAGAAATGGGCTA  783

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  784    CATTTTCTAC-CCCAGAAAA---TTACGATAACCCTTATGAAACCTAAGGGTCAAAGGTG  839

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  840    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  899

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  900    ACCGCCCGTCACCCTC  915
```

>ref|NC_001644.1| Pan paniscus mitochondrion, complete genome
Length = 16563

Score = 442 bits (230), Expect = e-122
Identities = 374/436 (85%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  486    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTCAACAGTTAAATTAACAA  545

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  546    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  605

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  606    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCGCCTCT  665

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  666    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGTTACAAAGTAAGCGCA  725

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  726    AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCTATGAGGCGGCAAGAAATGGGCTA  785

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  786    CATTTTCTAC-CCCAGAAAA---TTACGATAACCCTTATGAAACCTAAGGGTCGAAGGTG  841

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  842    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  901

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  902    ACCGCCCGTCACCCTC  917
```

>ref|NC_002083.1| Pongo pygmaeus abelii mitochondrion, complete genome
Length = 16499

```
 Score =  439 bits (228), Expect = e-121
 Identities = 374/437 (85%), Gaps = 6/437 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  490    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTTAACAGTTAAATCAACAA  549

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  550    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  609

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  610    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCCCT  669

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  670    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCACGAAGTAAGCGCA  729

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  730    AGCATCCACATAAAGACGTTAGGTCAAGGTGTAGCCCATGGAGTGGCAAGAAATGGGCTA  789

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  790    CATTTTCTAC-TTCAGAAAACT---ACGATAGCCCTCATGAAACCTGAGGGTCGAAGGTG  845

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  846    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  905

Query:  28     ACCGCCCGTCACCCTCT  12
Sbjct:  906    ACCGCCCGTCACCCTCT  922
```

>ref|NC_001646.1| Pongo pygmaeus mitochondrion, complete genome
Length = 16389

```
 Score =  410 bits (213), Expect = e-112
 Identities = 369/437 (84%), Gaps = 6/437 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  489    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTTAACAGTTGAATCAACAA  548

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  549    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  608

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  609    ATACCCCCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCCCT  668

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  669    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCACGAAGTAAGCGCA  728

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  729    AACACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGGAGTGGCAAGAAATGGGCTA  788

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  789    CATTTTCTAC-TTCAGAAAACT---ACGATAACCCTCATGAAATTTGAAGGTCGAAGGTG  844

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  845    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAAGGCCCTGAAGCGCGTACAC  904

Query:  28     ACCGCCCGTCACCCTCT  12
```

```
Sbjct:  905    ACCGCCCGTCACCCTCT  921
```

>ref|NC_002082.1| Hylobates lar mitochondrion, complete genome
Length = 16472

```
 Score =  389 bits (202), Expect = e-106
 Identities = 367/437 (83%), Gaps = 7/437 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTCAGCCCTAAACTTCAACAGTCAAATCAACAA  543

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  544    GACTGCTCGCCAGAACACTACGAGCAACAGCTTAAAAATCAAAGGACCTGGCGGTGCTTC  603

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  604    ACACCCCCTAGAGGAGCCTGTCCTATAATCGATAAACCCCGTTCAACCTCACCATCTCT  663

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  664    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGACAAAGGCTATAAAGTAAGCACA  723

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  724    AACACCCACATAAAGACGTTAGGTCAAGGTGTAGCCCATGAGATGGGAAGAGATGGGCTA  783

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTC-AAGGA  90
Sbjct:  784    CATTTTCTATGC-CAGAAAA---CCACGATAACCCTCATGAAACTTGAGCGGTCGAAGGA  839

Query:  89     GGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACA  30
Sbjct:  840    GGATTTAGCAGTAAATTAAGAATAGAGTGCTTAGTTGAACAAGGCCCTGAAGCGCGTACA  899

Query:  29     CACCGCCCGTCACCCTC  13
Sbjct:  900    CACCGCCCGTCACCCTC  916
```

>ref|NC_004025.1| Lemur catta mitochondrion, complete genome
Length = 17036

```
 Score =  365 bits (190), Expect = 2e-99
 Identities = 369/446 (82%), Gaps = 10/446 (2%)
 Strand = Plus / Minus


Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  479    GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCGTAAACCTAAGTAATTA-ACAA  537

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  538    ACAAAATTACTCGCCAGAGCACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  597

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  598    CTTTATATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCAC  657

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  658    TTCTTGCTAATTCAACTTATATACCGCCATCCCCAGCAAACCCTATTAAGGCCCCAAAGT  717

Query:  214    AAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAA  155
Sbjct:  718    AAGCAAAAACACATACATAAAGACGTTAGGTCAAGGTGTAGTCAATGAAGTGGAAAGAAA  777

Query:  154    TGGG-TACGTTTTCTACACACAGAAAAATCTCGCGAC---AACCGTTATGAAATCTAAGG  99
Sbjct:  778    TGGGCTACATTTTCTAATATTAGAACAACACCCCAACAGAAGCCTTTATGAAA-CTAAAA  836
```

```
Query:  98     GCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAA  39
Sbjct:  837    GCCAAAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATTGAATAGGGCCATGAA  896

Query:  38     GCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  897    GCACGCACACACCGCCCGTCACCCTC  922
```

>ref|NC_001700.1| Felis catus mitochondrion, complete genome

Length = 17009

Score = 364 bits (189), Expect = 9e-99
Identities = 370/443 (83%), Gaps = 12/443 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGA-TCAACA  388
Sbjct:  1356   CAAACTGGGATTAGATACCCTACTATGCTTAGCCCTAAACTTAGATAGTTACCCTAAACA  1415

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  1416   AAACTATCCGCCAGAGAACTACTAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTT  1475

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  1476   TACATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATATACCTCACCATCTC  1535

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  1536   TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAAGAAAGTAAG  1595

Query:  211    CAGAAGTATCT--ACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  1596   CACAAGTATCTTAACATAAAAAAGTTAGGTCAAGGTGTAGCTCATGAGATGGGAAGCAAT  1655

Query:  153    GGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTC  95
Sbjct:  1656   GGGCTACATTTTCTAAATTAGAACA--CCCACGAAGATCCTTACGAAA-CTAAGTATTA  1712

Query:  94     AAGGAGGATTTAGCAATAAA-TTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  1713   AAGGAGGATTTAGTAGTAAATTTGAGAATAGAGAGCTCAATTGAATCGGGCCATGAAGCA  1772

Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  1773   CGCACACACCGCCCGTCACCCTC  1795
```

>ref|NC_002763.1| Cebus albifrons mitochondrion, complete genome

Length = 16554

Score = 362 bits (188), Expect = 3e-98
Identities = 363/438 (82%), Gaps = 6/438 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  485    CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACTCCAATAACTCTACCAACAA  544

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  545    AATTACTCGCCAGAACACTACAAGCAATAGCTTGAAACTCAAAGGACCTGGCGGTGCTTT  604

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  605    ACATCCGTCTAGAGGAGCCTGTTCTGTAATCGATATACCCCGATAAACCTTACCACCTCT  664

Query:  266    TG--CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAG  209
Sbjct:  665    TGCCCCCAGCCTGTATACCGCCATCCTCAGCAAACTCCCTAAAGATCGTAAAGTAAGCAA  724

Query:  208    AAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-T  150
```

```
Sbjct:  725    AAGTATTACCATAAAAACGTTAGGTCAAGGTGCAGCCAATGAAGTGGAAAGAAATGGGCT  784

Query:  149    ACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGA  90
Sbjct:  785    ACATTTTCTA-ATCTAG-AAAATTACACGATAGCCTTTATGAAATTTAAAGGCCAAGGT  842

Query:  89     GGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAA-TGAGGCCATGAAGCACGCAC  31
Sbjct:  843    GGATTTAGCAGTAAATCAAGAATAGAGAGCTTGATTGAAGCAAGGCCATTAAGCACGCAC  902

Query:  30     ACACCGCCCGTCACCCTC  13
Sbjct:  903    ACACCGCCCGTCACCCTC  920
```

>ref|NC_002765.1| Nycticebus coucang mitochondrion, complete genome
Length = 16764

Score = 356 bits (185), Expect = 2e-96
Identities = 368/442 (83%), Gaps = 12/442 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  497    CAAACTGGGATTAGATACCCCACTATGCTTAACCGTAAACTAAAGTAGC-ATACCAACAA  555

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  556    TGCTACTCGCCAGAGTACTACAAGCAATAGCTCGAAACTCAAAGGACTTGGCGGTGCTTT  615

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  616    ATACCCCCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACCTCT  675

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  676    TGCTAATTCAACCTATATACCGCCATCTTCAGCAAACCCTGTCAAGGACCCATAGTAAGC  735

Query:  210    AGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  736    AAGAGAATCACACATTAAAACGTTAGGTCAAGGTGTAGTCTATGAGGTGGGAAGAAATGG  795

Query:  151    G-TACGTTTTCTA--CACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTC  95
Sbjct:  796    GCTACATTTTCTATCCTCACAGAACAA-CTAACGCCGCCCTTATGAAA--AAAGTGGTC  852

Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  853    AAGGCGGATTTAGAAGTAAATTAAGAATAGAGAGCTTAATTGAATAGGGCAATGAAGCAC  912

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  913    GCACACACCGCCCGTCACCCTC  934
```

>ref|NC_001665.1| Rattus norvegicus mitochondrial genome
Length = 16300

Score = 346 bits (180), Expect = 1e-93
Identities = 361/439 (82%), Gaps = 8/439 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  485    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTTAATAATTAAACCTACAA  544

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  545    AATTATTTGCCAGAGAACTACTAGCTACAGCTTAAAACTCAAAGGACTTGGCGGTACTTT  604

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  605    ATATCCATCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGTTCTACCTTACCCCTTCT  664
```

```
Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  665    CGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGCACTAAAGTAAGC  724

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  725    ACAAGAACAAACATAAAAACGTTAGGTCAAGGTGTAGCCAATGAAGCGGAAAGAAATGGG  784

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAG  92
Sbjct:  785    CTACATTTTCTTTCCCAG-AGAACATTACGA-AACCTTTATGAAA-CTAAAGGACAAAG  841

Query:  91     GAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCA  32
Sbjct:  842    GAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAGAGCAATGAAGTACGCA  901

Query:  31     CACACCGCCCGTCACCCTC  13
Sbjct:  902    CACACCGCCCGTCACCCTC  920
```

>ref|NC_002008.4| Canis familiaris mitochondrion, complete genome

Length = 16727

Score = 346 bits (180), Expect = 1e-93
Identities = 365/440 (82%), Gaps = 10/440 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  485    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAGATAATTTTA-CAACAA  543

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  544    AATAATTCGCCAGAGGACTACTAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  603

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  604    ATATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACCTTT  663

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  664    CGCTAATTCAGTCTATATACCGCCATCTTCAGCAAACCCTCAAAAGGTAGAACAGTAAGC  723

Query:  210    AGAAGTA-TCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  724    ACAATCATTTTACATAAAAAAGTTAGGTCAAGGTGTAACTTATGAGGTGGGAAGAAATGG  783

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  784    GCTACATTTTCTACCCA-AG-AACATTTCACGAATGTTTTTATGAAAT-TAAAACTGAA  840

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  841    GGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAGGGCCATGAAGCACGC  900

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  901    ACACACCGCCCGTCACCCTC  920
```

>ref|NC_004030.1| Eumetopias jubatus mitochondrion, complete genome

Length = 16639

Score = 346 bits (180), Expect = 1e-93
Identities = 360/440 (81%), Gaps = 7/440 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  495    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAAATAATTCACTTAACAA  554

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
```

```
Sbjct:  555    AATTACCCGCCAGAGAACTACGAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  614

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  615    ACACCCCCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACCTCT  674

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  675    TGCTAATCCAGTCTATATACCGCCATCCTCAGCAAACCCTTAAAAGGAAAGAAAGTAAGC  734

Query:  210    AGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  735    ATAATCATCACACATAAAAAAGTTAGGTCAAGGTGTAACCCATGAGGTGGGAAGAAATGG  794

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  795    GCTACATTTTCTAAACAAGAACATACCATACGAAGTTATTATGAAAT-TAATAACTAAA  853

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  854    GGTGGATTTAGTAGTAAACTAAGAATAGAGAGCTTAATTGAACTGGGCCATGAAGCACGC  913

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  914    ACACACCGCCCGTCACCCTC  933
```

>ref|NC_004023.1| Arctocephalus forsteri mitochondrion, complete genome
Length = 15413

Score = 346 bits (180), Expect = 1e-93
Identities = 360/440 (81%), Gaps = 7/440 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  492    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAAATAATTCACTTAACAA  551

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  552    AATTATCCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  611

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  612    ACACCCCCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACCTCT  671

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  672    TGCTAATCCAGTCTATATACCGCCATCCTCAGCAAACCCTTAAAAGGAAAGAAAGTAAGC  731

Query:  210    AGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  732    ACAATCATCACACGTAAAAAAGTTAGGTCAAGGTGTAACCCATGAGGTGGGAAGAAATGG  791

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  792    GCTACATTTTCTAAACAAGAATACACCGTACGAAGTTCTTATGAAAT-TAATAACTAAA  850

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  851    GGTGGATTTAGTAGTAAACTAAGAATAGAGAGCTTAATTGAACTGGGCCATGAAGCACGC  910

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  911    ACACACCGCCCGTCACCCTC  930
```

>ref|NC_002764.1| Macaca sylvanus mitochondrion, complete genome
Length = 16586

Score = 342 bits (178), Expect = 2e-92
Identities = 361/435 (82%), Gaps = 9/435 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  481    CAAACTGGGATTAGACACCCCACTATGCCTAGCCCTAAACCTCAGTAGTT-GAGCAACAA  539

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  540    AACTACTCGCCAGAATACTACAAGCAACAGCTTGAAACTCAAAGGACTTGACGGTGCTTT  599

Query:  326    ATATCCCTCTAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  600    ACACCCC-CTAGAGGAGCCTGTTCCATAATCGATAAACCCCGATCCACCCTACCCTCTCT  658

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  659    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCACAAAGTGAGCGCA  718

Query:  207    AGTATCTACA---TAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  719    AATGCCCACACCGCAAAAACGTTAGGTCAAGGTGTAGCCCATGAGACGGTAAAAAATGGG  778

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAG  92
Sbjct:  779    CTACATTTTCTGC-CTCAG-AATACCCCACGAAAACTCTTATGAAACCTAAGAGTCCAAG  836

Query:  91     GAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCA  32
Sbjct:  837    GAGGATTTAGCAGTAAATTAAGAATAGAGTGCTTAATTGAACCAGGCCATAAAGCGCGCA  896

Query:  31     CACACCGCCCGTCAC  17
Sbjct:  897    CACACCGCCCGTCAC  911
```

>ref|NC_003040.1| Soriculus fumidus mitochondrion, complete genome
Length = 17488

Score = 339 bits (176), Expect = 3e-91
Identities = 274/313 (87%), Gaps = 7/313 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  501    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTAAGTAATTA-ATAAACAA  559

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  560    AAATACTCGCCAGAGAACTACTAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  619

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  620    ATATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACCTCT  679

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  680    TGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAATAACAGTAAGC  739

Query:  210    AGAAGTATCT-ACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  740    ACAAATATCTGACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGAAAGAAATGG  799

Query:  151    G-TACGTTTTCTA  140
Sbjct:  800    GCTACATTTTCTA  812
```

Score = 94.9 bits (49), Expect = 9e-18
Identities = 71/82 (86%)
Strand = Plus / Minus

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  860    AAGGAGGATTTAGTAGTAAGTCAAGAATAGAGTGCTTGACTGAATAAGGCCATGAAGCAC  919

Query:  34     GCACACACCGCCCGTCACCCTC  13
```

```
Sbjct:  920    GCACACACCGCCCGTCACCCTC  941
```

>ref|NC_003427.1| Ursus arctos mitochondrion, complete genome
Length = 17020

Score = 337 bits (175), Expect = 1e-90
Identities = 366/444 (82%), Gaps = 10/444 (2%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  1626   GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCTTAAACATAAATAATTTATTAA  1685

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  1686   ACAAAATTATTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  1745

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1746   CTTTA-ACCCCCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAGACCTCACCAC  1804

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  1805   CTCTTGCTAATTCAGTCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAACAAGAGT  1864

Query:  214    AAGCAGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
Sbjct:  1865   AAGCACAATCATCTTGCATAAAAAAGTTAGGTCAAGGTGTAACCCATGGGGTGGAAAGAA  1924

Query:  155    ATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGC  97
Sbjct:  1925   ATGGGCTACATTTTCTATTCA-AGAACAA-CTTACGAAAGTTTTTATGAAA-CTAAAAAC  1981

Query:  96     TCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGC  37
Sbjct:  1982   TAAAGGTGGATTTAGTAGTAAATCAAGAATAGAGAGCTTGATTGAATAAGGCAATGAAGC  2041

Query:  36     ACGCACACACCGCCCGTCACCCTC  13
Sbjct:  2042   ATGCACACACCGCCCGTCACCCTC  2065
```

>ref|NC_004029.1| Odobenus rosmarus rosmarus mitochondrion, complete genome
Length = 16565

Score = 337 bits (175), Expect = 1e-90
Identities = 360/440 (81%), Gaps = 8/440 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  493    CAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAACACAAATAATTTGCACAACAA  552

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  553    AATTACTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  612

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  613    ACATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCATCCCT  672

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  673    TGCTAATTCAGTCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAAAGAAAGTAAGC  732

Query:  210    AGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  733    ATAATCATCACACGTAAAAAAGTTAGGTCAAGGTGTAACCCATGGGATGGAAAGAAATGG  792

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  793    GCTACATTTTCTA-AGTAAGAACAGTCATACAAAAGTTTTTATGAAAT-TAATAACTGAA  850
```

```
Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  851    GGTGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAACTGGGCCATGAAGCACGC  910

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  911    ACACACCGCCCGTCACCCTC  930
```

>ref|NC_001569.1| Mus musculus mitochondrion, complete genome

Length = 16295

Score = 335 bits (174), Expect = 4e-90
Identities = 362/441 (82%), Gaps = 11/441 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATC-AACA  388
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAACCTAAATAATTAAATTTAACA  543

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  544    AAACTATTTGCCAGAGAACTACTAGCCATAGCTTAAAACTCAAAGGACTTGGCGGTACTT  603

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  604    TATATCCATCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGCTCTACCTCACCATCTC  663

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  664    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGTATTAAAGTAAG  723

Query:  211    CAGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  724    CAAAAGAATCAAACATAAAAACGTTAGGTCAAGGTGTAGCCAATGAAATGGGAAGAAATG  783

Query:  152    GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  784    GGCTACATTTTCT---TATAAAAGAACATTACTATACCCTTTATGAAA-CTAAAGGACTA  839

Query:  93     AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  840    AGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATTGAGCAATGAAGTACG  899

Query:  33     CACACACCGCCCGTCACCCTC  13
Sbjct:  900    CACACACCGCCCGTCACCCTC  920
```

>ref|NC_003428.1| Ursus maritimus mitochondrion, complete genome

Length = 17017

Score = 329 bits (171), Expect = 2e-88
Identities = 363/444 (81%), Gaps = 9/444 (2%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  1621   GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCTTAAACATAAATAATTCATTAA  1680

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  1681   ACAAAATTATTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  1740

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1741   CTTTAAACCCTCCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATAGACCTCACCAC  1800

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  1801   CTCTTGCTAATTCAGTCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAACAAGAGT  1860

Query:  214    AAGCAGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
```

```
Sbjct:  1861   AAGCACAATCATCTTGCATAAAAAAGTTAGGTCAAGGTGTAACCCATGGAGTGGGAAGAA  1920

Query:  155    ATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGC  97
Sbjct:  1921   ATGGGCTACATTTTCTATTCA-AGAACAA-CTTACGAAAGTTTTTATGAAA-CTAAAAAC  1977

Query:  96     TCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGC  37
Sbjct:  1978   TAAAGGTGGATTTAGTAGTAAATCAAGAATAGAGAGCTTGATTGAATAAGGCAATGAAGC  2037

Query:  36     ACGCACACACCGCCCGTCACCCTC  13
Sbjct:  2038   ATGCACACACCGCCCGTCACCCTC  2061
```

>ref|NC_003033.1| Ochotona collaris mitochondrion, complete genome
Length = 16968

Score = 327 bits (170), Expect = 9e-88
Identities = 356/439 (81%), Gaps = 10/439 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  489    CAAACTGGGATTAGATACCCCACTATGCCTAGCCACAAACCTAAATAGTTACACTAACAA  548

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  549    AACTATTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  608

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  609    ATA-CCCCCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGCTCCACCTCACCACCCTT  667

Query:  266    TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  668    TGCCAACTCAGCCTGTATACCGCCATCTTCAGCAAACCCTAAAAAGGTATAATAGTAAGC  727

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  728    CTAATAATCCTCGTAAAAACGTTAGGTCAAGGTGTAGCCCATAGGGTGGGAAGCAATGGG  787

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAG  92
Sbjct:  788    CTACATTTTCTTATTTAAGAA----CACACGAAGCCCTTGTGAAAACCATAGGCCAAAG  843

Query:  91     GAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCA  32
Sbjct:  844    GCGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATTGAACTCGGCAATGAAGCACGCA  903

Query:  31     CACACCGCCCGTCACCCTC  13
Sbjct:  904    CACACCGCCCGTCACCCTC  922
```

>ref|NC_001941.1| Ovis aries mitochondrion, complete genome
Length = 16616

Score = 323 bits (168), Expect = 1e-86
Identities = 360/441 (81%), Gaps = 9/441 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACACAAATAATTATAAAACAA  543

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  544    AATTATTCGCCAGAGTACTACC-GCAACAGCCCGAAACTCAAAGGACTTGGCGGTGCTTT  602

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  603    ATACCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCAATCCT  662
```

```
Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCAC-AGAGTAAG  212
Sbjct:  663    TGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAAAGGGACAAAAGTAAG  722

Query:  211    CAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  723    CTCAATAATAACACATAAAGACGTTAGGTCAAGGTGTAACCTATGGAGTGGGAAGAAATG  782

Query:  152    GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  783    GGCTACATTTTCTACCCAAGAAAATTTAATACGAAGCCATTATGAAAT-TAATAGCCAA  841

Query:  93     AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  842    AGGAGGATTTAGCAGTAAACTAAGAATAGAGTGCTTAGTTGAATCAGGCCATGAAGCACG  901

Query:  33     CACACACCGCCCGTCACCCTC  13
Sbjct:  902    CACACACCGCCCGTCACCCTC  922
```

>ref|NC_003041.1| Volemys kikuchii mitochondrion, complete genome
Length = 16312

Score = 321 bits (167), Expect = 5e-86
Identities = 361/443 (81%), Gaps = 11/443 (2%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  478    GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTTAGTAATTTTAA-A  536

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  537    ACAAAAATATTTGCCTGAGAACTACTGGCCACAGCTTAAAACTCAAAGGACTTGGCGGTA  596

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  597    CTTTATATCCATCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGCTATACCTCACCAC  656

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  657    CCCTTGCTAATACAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAGCAATAGT  716

Query:  214    AAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAA  155
Sbjct:  717    AAGCAAGAGAACCACCATAAAAACGTTAGGTCAAGGTGTAGCCAATGAGGTGGAAGCAA  776

Query:  154    TGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCT  96
Sbjct:  777    TGGGCTACATTTTCTA-ATAAAGAACA---TTACGTCACCCTTTATGAAA-CTAAAGGGC  831

Query:  95     CAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  832    AAAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATTGAGCAATGAAGTA  891

Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  892    CGTACACACCGCCCGTCACCCTC  914
```

>ref|NC_001892.1| Myoxus glis mitochondrion, complete genome
Length = 16602

Score = 321 bits (167), Expect = 5e-86
Identities = 355/439 (80%), Gaps = 9/439 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAAACCCTTACT--AACGC  541

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
```

```
Sbjct:  542    AACCGTTCGCCAGAGTACTACAAGCCACAGCTCAAAACTCAAAGGACTTGGCGGTGCTTT  601

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  602    ATATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACTTCT  661

Query:  266    TG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  662    TGCTACCACAGCTTATATACCGCCATCTTCAGCAAACCTTAACAAGGAATCAAAGTAAGC  721

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  722    CCAAGTATTAACATAAAAACGTTAGGTCAAGGTGTAGCCTATGAAGTGGAAAGAAATGGG  781

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAG  92
Sbjct:  782    CTACATTTCCTTTCCCAAGTACA--TTCACGTCAACTTTTATGAAACCTAAAAGTAAAAG  839

Query:  91     GAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCA  32
Sbjct:  840    GCGGATTTAGTAGTAAGCTAAGAATAGAGAGCCTAGCTGAATAGGGCCATGAAGCACGCA  899

Query:  31     CACACCGCCCGTCACCCTC  13
Sbjct:  900    CACACCGCCCGTCACCCTC  918
```

>ref|NC_001913.1| Oryctolagus cuniculus mitochondrion, complete genome
Length = 17245

Score = 321 bits (167), Expect = 5e-86
Identities = 359/440 (81%), Gaps = 12/440 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  488    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTGATAATTTCAT-AACAA  546

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  547    AATTATTCGCCAGAGAACTACAAGCCAAAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  606

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  607    ATACCCACCTAGAGGAGCCTGTTCCGTAATCGATAAACCCCGATAAACCCTACCACTCTT  666

Query:  266    TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  667    TGCCAACTCAGCCTATATACCGCCATCTTCAGCGAACCCTAAAAAGGAGCAAAAGTAAGC  726

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  727    TCAATTACCACCGTAAAAACGTTAGGTCAAGGTGTAGCCCATAGAGTGGAGAGCAATGGG  786

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAA-TCTAAGGGCTCAA  93
Sbjct:  787    CTACATTTTCTAC-TTCAGAATA----TACGAAGCCCTTATGAAACTCTAAGGGCCAAA  841

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  842    GGAGGATTTAGTAGTAAATTAAGAATAGAGTGCTTAATTGAACAAGGCCATGAAGCACGC  901

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  902    ACACACCGCCCGTCACCCTC  921
```

>ref|NC_002619.1| Pteropus scapulatus mitochondrion, complete genome
Length = 16741

Score = 319 bits (166), Expect = 2e-85
Identities = 269/313 (85%), Gaps = 6/313 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  494    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTAATAGCCAAAACAACAA  553

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  554    TGCTATTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  613

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  614    ACATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATAAACCTCACCAACTCT  673

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  674    TGCTAATACAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAAACAAAGTAAGC  733

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  734    AAAAACATAAAACATAAAAACGTTAGGTCAAGGTGTAGCCTATGAGTTGGAAAGAAATGG  793

Query:  151    G-TACGTTTTCTA  140
Sbjct:  794    GCTACATTTTCTA  806
```

```
 Score =  112 bits (58), Expect = 6e-23
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  848    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATCAGGCCATGAAGCAC  907

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  908    GCACACACCGCCCGTCACCCTC  929
```

```
>ref|NC_001821.1| Dasypus novemcinctus mitochondrion, complete genome
          Length = 17056

 Score =  317 bits (165), Expect = 7e-85
 Identities = 268/312 (85%), Gaps = 6/312 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  492    CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACTAAACAGTTC-ACAAACAA  550

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  551    AACTGTTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  610

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  611    ACATCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATATACCTCACCACCCCT  670

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  671    TGCTAATACAGCCTATATACCGCCATCTTCAGCAGACCCTAGTAAGGCACCACAGTGAGC  730

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  731    ACAATAACATACATAAAGACGTTAGGTCAAGGTGTAGCTTATGGGTGGGAAGAAATGGG  790

Query:  150    -TACGTTTTCTA  140
Sbjct:  791    CTACATTTTCTA  802
```

```
 Score = 73.7 bits (38), Expect = 2e-11
 Identities = 68/83 (81%)
```

Strand = Plus / Minus

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  846    AAGGTGGATTTAGTAGTAAGCTAAAAATAGAGAGTTTAGCTGAACCAGGCCATAAAGCAC  905

Query:  34     GCACACACCGCCCGTCACCCTCT  12
Sbjct:  906    GCACACACCGCCCGTCACCCTCT  928
```

>ref|NC_001567.1| Bos taurus mitochondrion, complete genome

Length = 16338

Score = 314 bits (163), Expect = 1e-83
Identities = 270/316 (85%), Gaps = 6/316 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  842    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACACAGATAATTACATAAACAA  901

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  902    AATTATTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  961

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  962    ATATCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCAATTCT  1021

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  1022   TGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAAAAAAAGTAAGC  1081

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  1082   GTAATTATGATACATAAAAACGTTAGGTCAAGGTGTAACCTATGAAATGGGAAGAAATGG  1141

Query:  151    G-TACGTTTTCTACAC  137
Sbjct:  1142   GCTACATTCTCTACAC  1157
```

Score = 112 bits (58), Expect = 6e-23
Identities = 74/82 (90%)
Strand = Plus / Minus

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1200   AAGGAGGATTTAGCAGTAAACTAAGAATAGAGTGCTTAGTTGAATTAGGCCATGAAGCAC  1259

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1260   GCACACACCGCCCGTCACCCTC  1281
```

>ref|NC_002391.1| Talpa europaea mitochondrion, complete genome

Length = 16884

Score = 310 bits (161), Expect = 1e-82
Identities = 265/312 (84%), Gaps = 5/312 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  495    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCAAGACAATCAAGTTAACAA  554
```

```
Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  555    GATTGTTCGCCAGAGAACTACTAGCCACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  614

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  615    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATAAACCTCACCAACTCT  674

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  675    TGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAATTACAGTAAGC  734

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  735    ACAAGTACCCGCATAAAAACGTTAGGTCAAGGTGTAGCTGATGAGTTGGGAAGAAATGGG  794

Query:  150    -TACGTTTTCTA  140
Sbjct:  795    CTACATTTTCTA  806
```

```
 Score =  112 bits (58), Expect = 6e-23
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  857    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGCGCTTAATTGAATAAGGCCATGAAGCAC  916

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  917    GCACACACCGCCCGTCACCCTC  938
```

```
>ref|NC_000884.1| Cavia porcellus complete mitochondrial genome
          Length = 16801

 Score =  308 bits (160), Expect = 5e-82
 Identities = 355/440 (80%), Gaps = 8/440 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  481    CAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAACATAAAACTTATA-CAACAA  539

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  540    AAGATTTCGCCAGAGAACTACTAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  599

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  600    ATACCCACCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATACACCTCACCTCTCCT  659

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  660    TGCTAATTCAGCCTATATACCGCCATCTTCAGCCAACCCCATTATGGAAACAAAGTGAGC  719

Query:  210    AGAAGTA-TCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  720    GCAAGTACACTACATAAAAACGTTAGGTCAAGGTGTAGCCAATGGAGTGGGAAGAAATGG  779

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  780    GCTACATTTTCT-TACCCAAGAACATTAAACGCAAATCTTTATGAAATTCAAAGATCTAA  838

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  839    GGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTGATTGAACTAGGCCATGAAGCACGT  898

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  899    ACACACCGCCCGTCACCCTC  918
```

>ref|NC_002811.1| Tarsius bancanus mitochondrion, complete genome
Length = 16927

Score = 306 bits (159), Expect = 2e-81
Identities = 259/304 (85%), Gaps = 6/304 (1%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  484    GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAATATAAATAAATACA--A  541

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  542    ACAAATTTATTCGCCAGAGCACTACAAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTG  601

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  602    CTTCACATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATTAACCTTACCAC  661

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  662    CTTTTGCTAATTCAGTCTATATACCGCCATCTTCAGCAAACCCTAATAAGGCCCTAAAGT  721

Query:  214    AAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAA  155
Sbjct:  722    AAGCACAAGTATAAACATAAAAACGTTAGGTCAAGGTGTAACCTATGAGGTGGAAAGCAA  781

Query:  154    TGGG  151
Sbjct:  782    TGGG  785
```

Score = 81.4 bits (42), Expect = 1e-13
Identities = 71/83 (85%), Gaps = 1/83 (1%)
Strand = Plus / Minus

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGA-GGCCATGAAGCA  36
Sbjct:  838    AAGGAGGATTTAGCAGTAAACCAAGAATAGAGAGCTTGATTGAAAAAAGGCCATGAAGCA  897

Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  898    CGCACACACCGCCCGTCACCCTC  920
```

>ref|NC_003426.1| Ursus americanus mitochondrion, complete genome
Length = 16841

Score = 304 bits (158), Expect = 8e-81
Identities = 361/445 (81%), Gaps = 10/445 (2%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  1432   GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCTTAAACATAAGTAATTTATTAA  1491

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  1492   ACAAAATTATTCGCCGGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  1551

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1552   CTTTAAACCCCCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAGACCTCACCAC  1611

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCC-TGGAAAGGCCACAGAG  216
Sbjct:  1612   CTCTTGCTAATCCAGTCTATATACCGCCATCTTCAGCTAACCCTTAAAAAGGAATAAAAG  1671

Query:  215    TAAGCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGA  157
```

```
Sbjct:  1672   TAAGCACAATCATCCCACATAAAAAAGTTAGGTCAAGGTGTAACCCATGGGGTGGGAAGA  1731

Query:  156    AATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGG  98
Sbjct:  1732   AATGGGCTACATTTTCTATTCA-AGAACAACCT-ACGAAAGTTTTTATGAAA-CTAAAAA  1788

Query:  97     CTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAG  38
Sbjct:  1789   CTAAAGGTGGATTTAGCAGTAAACCAAGAATAGAGAGCTTGGTTGAATAGGGCAATGGAG  1848

Query:  37     CACGCACACACCGCCCGTCACCCTC  13
Sbjct:  1849   CACGCACACACCGCCCGTCACCCTC  1873
```

>ref|NC_002078.1| Orycteropus afer complete mitochondrial genome
Length = 16816

Score = 302 bits (157), Expect = 3e-80
Identities = 268/316 (84%), Gaps = 7/316 (2%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  483    GATACAAACTGGGATTAGATACCCCACTATGCCTAGCCATAAACTTAAATATTTC--TCA  540

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  541    ACAAAATTATTCGCCAGAGAACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  600

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  601    CTTTATATCCATCTAGAGGAGCCTGTTATGTAATCGATAAACCCCGATATACCTCACCAT  660

Query:  270    CTCTTGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  661    CACTTGCCAATACAGCCTATATACCGCCATCTTCAGCAAACCCTTACAAGGAATAATAGT  720

Query:  214    AAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAA  155
Sbjct:  721    AAGCCAAATTATTACCATAAAAAACGTTAGGTCAAGGTGTAGCCAATGTGATGGCAATAAA  780

Query:  154    TGGG-TACGTTTTCTA  140
Sbjct:  781    TGGGCTACATTTTCTA  796
```

Score = 116 bits (60), Expect = 4e-24
Identities = 78/87 (89%)
Strand = Plus / Minus

```
Query:  99     GGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGA  40
Sbjct:  837    GGCTAAAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAAGGCCATGA  896

Query:  39     AGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  897    AGCACGCACACACCGCCCGTCACCCTC  923
```

>ref|NC_004031.1| Cynocephalus variegatus mitochondrion, complete genome
Length = 16748

Score = 300 bits (156), Expect = 1e-79
Identities = 355/442 (80%), Gaps = 10/442 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
```

```
Sbjct:  491    CAAACTGGGATTAGATACCCCACTATGCTCAACCGCAAACCTAAGCAGCTAACCAAATGA  550

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  551    AACTGCTCGCCAGAGTACTACCAGCAACGGCCTAAAACTCAAAGGACTTGGCGGTGCTTC  610

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  611    ACACCCCCTAGAGGAGTCTGTTCTATAATCGATAAACCCCGATACACCCTACCATCCCT  670

Query:  266    TG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  671    TGCCAACCCAGCCTGTATACCGCCATCTTCAGCAAACCCCTCCAGGGTACAAAAGTAAGC  730

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG-  152
Sbjct:  731    CCAAGAATCCACATAAAAACGTTAGGTCAAGGTGCAGCCTATGAGATGG-AAGAAATGGA  789

Query:  151    GTACGTTTTCTACACACAGAAAAAT---CTCGCGACAACCGTTATGAAATCTAAGGGCTC  95
Sbjct:  790    CTACATTTTCTA-ACCTAGAACAATCCACCCACGACAACCTTCATGAAAACTGAAGGTCA  848

Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  849    AAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATTGAAAAGGCCATGAAGCAC  908

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  909    GCACACACCGCCCGTCACCCTC  930
```

>ref|NC_002612.1| Pteropus dasymallus mitochondrion, complete genome
Length = 16705

Score = 298 bits (155), Expect = 4e-79
Identities = 267/313 (85%), Gaps = 7/313 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  493    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTAAGCAGCTAAAT-AACAA  551

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  552    TGCTACTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  611

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  612    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATAAACCTCACCAACTCT  671

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  672    TGCTAATACAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAAATAAAGTAAGC  731

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  732    AAAACCATAAAACATAAAAACGTTAGGTCAAGGTGTAGCCTATGAGTTGGAAAGAAATGG  791

Query:  151    G-TACGTTTTCTA  140
Sbjct:  792    GCTACATTTTCTA  804
```

Score = 112 bits (58), Expect = 6e-23
Identities = 74/82 (90%)
Strand = Plus / Minus

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  846    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATTAGGCCATGAAGCAC  905

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  906    GCACACACCGCCCGTCACCCTC  927
```

>ref|NC_001325.1| Phoca vitulina mitochondrion, complete genome
Length = 16826

Score = 298 bits (155), Expect = 4e-79
Identities = 355/445 (79%), Gaps = 8/445 (1%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  1423   GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAAATAATTCACGTA  1482

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  1483   ACAAAATTATTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  1542

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1543   CTTCACACCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATAAACCTCACCAT  1602

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  1603   TCCTTGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAACAAAAGT  1662

Query:  214    AAGCAGAAGTAT--CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGA  157
Sbjct:  1663   AAGCACAATAATCGCTACATAAAAAAGTTAGGTCAAGGTGTAACCTATGGAATGGGAAGA  1722

Query:  156    AATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGG  98
Sbjct:  1723   AATGGGCTACATTTTCTAAATA-AGAACAATCATACGAAGTTTTTATGAAATTAACAAA  1781

Query:  97     CTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAG  38
Sbjct:  1782   CTAAAGGTGGATTTAGTAGTAAGCTAAGAATAGAGAGCTTAGCTGAACCGGGCCATGAAG  1841

Query:  37     CACGCACACACCGCCCGTCACCCTC  13
Sbjct:  1842   CACGCACACACCGCCCGTCACCCTC  1866
```

>ref|NC_004032.1| Tamandua tetradactyla mitochondrion, complete genome
Length = 16395

Score = 298 bits (155), Expect = 4e-79
Identities = 255/300 (85%), Gaps = 5/300 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  489    CAAACTGGGATTAGATACCCCACTATGCCTAGCCGTAAACACAAATA-TTCCAACAACAA  547

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  548    GAATATTCGCCAGAGTACTACTAGCAACAGCTAAAAACTCAAAGGACTTGGCGGTGCTTC  607

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  608    ATATCCACCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACCTCT  667

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  668    TGCTAATACAGCCTATATACCGCCATCTCTAGCAAACCCTAAAAAGGAGCCACAGTAAGC  727

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  728    ACAACTATAGCCATAAAAACGTTAGGTCAAGGTGTAGCCAATGAGGTGGGAAGAAATGGG  787
```

Score = 89.1 bits (46), Expect = 5e-16
Identities = 70/82 (85%)

Strand = Plus / Minus

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  840    AAGGAGGATTTAGCAGTAAGTCGAAAATAGAGTGCTTGACTGAACAAGGCCATGAAACAC  899

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  900    GCACACACCGCCCGTCACCCTC  921
```

>ref|NC_000889.1| Hippopotamus amphibius mitochondrion, complete genome
Length = 16407

Score = 291 bits (151), Expect = 9e-77
Identities = 264/313 (84%), Gaps = 6/313 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  491    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACACAGATAATTCCAAAACAA  550

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  551    AACTATTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  610

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  611    ATACCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCAACCCT  670

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  671    TGCTAATCCAGTCTATATACCGCCATCTCCAGCAAACCCTAAAAAGGACTAAAAGTAAGC  730

Query:  210    AGAAGTA-TCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  731    TCAACTATTACACATAAAGACGTTAGGTCAAGGTGTAACCTATGGGCTGGGAAGAAATGG  790

Query:  151    G-TACGTTTTCTA  140
Sbjct:  791    GCTACATTTTCTA  803
```

Score = 106 bits (55), Expect = 3e-21
Identities = 85/100 (85%)
Strand = Plus / Minus

```
Query:  112    TATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTG  53
Sbjct:  838    TATGAAAGCTAGGAACTAAAGGAGGATTTAGTAGTAAATCAAGAGTAGAGTGCTTGATTG  897

Query:  52     AATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  898    AACAAGGCTATGAAGCACGCACACACCGCCCGTCACCCTC  937
```

>ref|NC_001640.1| Equus caballus mitochondrion, complete genome
Length = 16660

Score = 289 bits (150), Expect = 3e-76
Identities = 269/316 (85%), Gaps = 8/316 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAG-TTAGATCAACA  388
Sbjct:  491    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTAAATAGCTTACCACAACA  550
```

```
Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  551    AAGCTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTT  610

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTC  268
Sbjct:  611    TACATCCCTCTAGAGGAGCCTGTTCCATAATCGATAAACCCCGATAACCCCACCATCCC  670

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGA-AAGGCCACAGAGTAA  213
Sbjct:  671    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAACAAGGTACCGAAGTAA  730

Query:  212    GCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  731    GCACAAATATCCAACATAAAAACGTTAGGTCAAGGTGTAGCCCATGGGATGGAGAGAAAT  790

Query:  153    GGG-TACGTTTTCTAC  139
Sbjct:  791    GGGCTACATTTTCTAC  806
```

```
 Score =  112 bits (58), Expect = 6e-23
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  860    AAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATTGAATCAGGCCATGAAGCGC  919

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  920    GCACACACCGCCCGTCACCCTC  941
```

>ref|NC_001602.1| Halichoerus grypus mitochondrion, complete genome
Length = 16797

```
 Score =  285 bits (148), Expect = 5e-75
 Identities = 350/441 (79%), Gaps = 8/441 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1397   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAATAATTCACGTAACAA  1456

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1457   AATTATTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  1516

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1517   ACACCCCTCTAGAGGAGCCTGTTCTGTAACCGATAAACCCCGATAAACCTCACCACTCCT  1576

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  1577   TGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAACAAAAGTAAGC  1636

Query:  210    AGAAGTAT--CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  1637   ACAATAATCGCTACATAAAAAAGTTAGGTCAAGGTGTAACCTATGGAGTGGGAAGAAATG  1696

Query:  152    GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  1697   GGCTACATTTTCTAAATA-AGAACAACTATACGAAAGTTTTTATGAAACTAACAAACTAA  1755

Query:  93     AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  1756   AGGTGGATTTAGTAGTAAGCTAAGAATAGAGAGCTTAGCTGAACCGGGCCATGAAGCACG  1815

Query:  33     CACACACCGCCCGTCACCCTC  13
Sbjct:  1816   CACACACCGCCCGTCACCCTC  1836
```

>ref|NC_000845.1| Sus scrofa mitochondrion, complete genome
Length = 16613

Score = 279 bits (145), Expect = 3e-73
Identities = 265/315 (84%), Gaps = 7/315 (2%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1662  CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACCCAAATAGTTACAT-AACAA  1720

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1721  AACTATTCGCCAGAGTACTACTCGCAACTGCCTAAAACTCAAAGGACTTGGCGGTGCTTC  1780

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1781  ACATCCACCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAGACCTTACCAACCCT  1840

Query:  266   TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  1841  TGCCAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAACAATAGTAAGC  1900

Query:  210   AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  1901  ACAATCATAGCACATAAAAACGTTAGGTCAAGGTGTAGCTTATGGGTTGGAAAGAAATGG  1960

Query:  151   G-TACGTTTTCTACA  138
Sbjct:  1961  GCTACATTTTCTACA  1975
```

Score = 119 bits (62), Expect = 3e-25
Identities = 76/83 (91%)
Strand = Plus / Minus

```
Query:  95    CAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  2019  CAAGGAGGATTTAGCAGTAAATCGAGAATAGAGTGCTTGATTGAATAAGGCCATGAAGCA  2078

Query:  35    CGCACACACCGCCCGTCACCCTC  13
Sbjct:  2079  CGCACACACCGCCCGTCACCCTC  2101
```

>ref|NC_001601.1| Balaenoptera musculus mitochondrion, complete genome
Length = 16402

Score = 277 bits (144), Expect = 1e-72
Identities = 266/317 (83%), Gaps = 7/317 (2%)
Strand = Plus / Minus

```
Query:  450   GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  909   GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAACCCCAGTAGTCACAA-A  967

Query:  390   ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  968   ACAAGACTATTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  1027

Query:  330   CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1028  CTTCATACCCCTCTAGAGGAGCCTGTTCTGTAACCGATAAACCCCGATTAACCTCACCAA  1087

Query:  270   CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  1088  CCCTTGCTACTTCAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAGGGAACGAAAGT  1147

Query:  214   AAGCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
```

```
Sbjct:  1148   AAGCATAATCATCCTACATAAAAACGTTAGGTCAAGGTGTAACCAATGGGTTGGGAAGAA  1207

Query:  155    ATGGG-TACGTTTTCTA  140
Sbjct:  1208   ATGGGCTACATTTTCTA  1224
```

```
 Score =  117 bits (61), Expect = 1e-24
 Identities = 75/82 (91%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1276   AAGGAGGATTTAGTAGTAAATCAAGAGCAGAGTGCTTGATTGAATAAGGCCATGAAGCAC  1335

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1336   GCACACACCGCCCGTCACCCTC  1357
```

```
>ref|NC_002503.1| Physeter catodon mitochondrion, complete genome
          Length = 16428

 Score =  275 bits (143), Expect = 4e-72
 Identities = 265/316 (83%), Gaps = 7/316 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  489    CAAACTGGGATTAGATACCCCACTATGCTTAGCCGTAAACCCAGGTAGTCATAA-AACAA  547

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  548    GACTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTTC  607

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  608    ATACCCCCTAGAGGAGCCTGTTCTATAACCGATAAACCCCGATCAACCTCACCAACCCT  667

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  668    TGCTACTTCAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAATGAAGTAAGC  727

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  728    ATAACTATCCTACGTAAAAACGTTAGGTCAAGGTGTAACCCATGGGATGGGAAGAAATGG  787

Query:  151    G-TACGTTTTCTACAC  137
Sbjct:  788    GCTACATTTTCTACAC  803
```

```
 Score =  131 bits (68), Expect = 9e-29
 Identities = 90/101 (89%)
 Strand = Plus / Minus


Query:  113    TTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATT  54
Sbjct:  834    TTATGAAACCTAAAACCAAAGGAGGATTTAGCAGTAAATTAAGAACAGAGTGCTTAATT  893

Query:  53     GAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  894    GAATAAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  934
```

```
>ref|NC_004563.1| Muntiacus muntjak mitochondrion, complete genome
          Length = 16354
```

```
 Score =  273 bits (142), Expect = 1e-71
 Identities = 261/313 (83%), Gaps = 6/313 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  481    CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACACAATAGTTTTATAAACAA  540

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  541    AACTATTCGCCAGAGTACTACCGGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  600

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  601    ATACCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAGACCTCACCATTCCT  660

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  661    CGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAGCAAAAGTAAGC  720

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  721    GCAATCATAGTACATAAAAACGTTAGGTCAAGGTGTAACCTATGGAATGGAAAGAAATGG  780

Query:  151    G-TACGTTTTCTA  140
Sbjct:  781    GCTACATTTTCTA  793
```

```
 Score =  112 bits (58), Expect = 6e-23
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  840    AAGGAGGATTTAGCAGTAAACTAAGAATAGAGTGCTTAGTTGAATTAGGCCATGAAGCAC  899

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  900    GCACACACCGCCCGTCACCCTC  921
```

```
>ref|NC_001779.1| Rhinoceros unicornis mitochondrion, complete genome
          Length = 16829

 Score =  273 bits (142), Expect = 1e-71
 Identities = 264/315 (83%), Gaps = 7/315 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATC-AACA  388
Sbjct:  490    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCCAAACTCAAATAATTCTTCCCAACA  549

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  550    AAATTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTT  609

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTC  268
Sbjct:  610    TATATCCCCCTAGAGGAGCCTGTTCCATAACCGATAAACCCCGATAACCTTACCAGCCC  669

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  670    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCCAACCCTAAAAAGGAACCAAAGTAAG  729

Query:  211    CAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  730    CACAAGTATAAGACATAAAAACGTTAGGTCAAGGTGTAGCTTATGGGATGGAGAGAAATG  789

Query:  152    GG-TACGTTTTCTAC  139
```

```
Sbjct:  790    GGCTACATTTTCTAC  804
```

```
 Score =  110 bits (57), Expect = 2e-22
 Identities = 88/101 (87%), Gaps = 1/101 (0%)
 Strand = Plus / Minus


Query:  113    TTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATT  54
Sbjct:  837    TTATGAAAT-TAAAAGCTAAAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATT  895

Query:  53     GAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  896    GAACCAGGCCATAAAGCACGCACACACCGCCCGTCACCCTC  936
```

```
>ref|NC_004027.1| Manis tetradactyla mitochondrion, complete genome
          Length = 16571

 Score =  269 bits (140), Expect = 2e-70
 Identities = 352/443 (79%), Gaps = 12/443 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  488    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCCAGATAATTTTTTAAACAA  547

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  548    AATTATTCGCCAGAGTACTACTAGCAATAGCCTGAAACTCAAAGGACTTGGCGGTGCTTC  607

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  608    ATATCCCTCTAGAGGAGCCTGTCCTATAAACGATAAACCCCGATAGACCTTACCAACCCT  667

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAG  212
Sbjct:  668    AGCTAATGCAGCCTATATACCGCCATCCTCAGCAAACCCTGATAAAGGAAATATAGTAAG  727

Query:  211    CAGAAGTATCTACAT--AAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  728    CAAGATTGTTAAAATACAAAAACGTTAGGTCAAGGTGTAGCTTATGAGTTGGAAAGAGAT  787

Query:  153    GGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTC  95
Sbjct:  788    GGGCTACATTTTCTCAAAACAGAAAAA---AACGAACATTCTTATGATAT-TAGGAGTTA  843

Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  844    AAGGAGGATTTAGTAGTAAGCTAAGAATAGAGAGCTTGGCTGAATTAGGCCCTGAAGCAC  903

Query:  34     GCACACACCGCCCGTCACCCTCT  12
Sbjct:  904    GCACACACCGCCCGTCACCCTCT  926
```

```
>ref|NC_004577.1| Muntiacus crinifrons mitochondrion, complete genome
          Length = 16357

 Score =  267 bits (139), Expect = 8e-70
 Identities = 260/313 (83%), Gaps = 6/313 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  481    CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACACAAATAGTTCCACAAACAA  540

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
```

```
Sbjct:  541    AACTATTCGCCAGAGTACTACCGGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  600

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  601    ATACCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAGACCTCACCATTCCT  660

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  661    CGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAGTGAAAGTAAGC  720

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  721    GCAATCATAGTACATAAAAACGTTAGGTCAAGGTGTAACCTATGGAATGGAAAGAAATGG  780

Query:  151    G-TACGTTTTCTA  140
Sbjct:  781    GCTACATTTTCTA  793
```

```
 Score =  112 bits (58), Expect = 6e-23
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  840    AAGGAGGATTTAGCAGTAAACTAAGAATAGAGTGCTTAGTTGAATTAGGCCATGAAGCAC  899

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  900    GCACACACCGCCCGTCACCCTC  921
```

>ref|NC_001808.1| Ceratotherium simum mitochondrion, complete genome
Length = 16832

```
 Score =  267 bits (139), Expect = 8e-70
 Identities = 260/313 (83%), Gaps = 6/313 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  489    CAAACTGGGATTAGATACCCCACTATGCCTAGCCTTAAACCTAAATAATTTCTCCAACAA  548

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  549    AATTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTTT  608

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  609    ATATCCCCCTAGAGGAGCCTGTTCCATAACCGATAAACCCCGATAAACCCCACCAACCCT  668

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  669    TGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAACTAAAGTAAGC  728

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  729    ACAAGTATAAAACATAAAAACGTTAGGTCAAGGTGTAGCTTATGGGATGGAGAGAAATGG  788

Query:  151    G-TACGTTTTCTA  140
Sbjct:  789    GCTACATTTTCTA  801
```

```
 Score =  106 bits (55), Expect = 3e-21
 Identities = 73/82 (89%)
 Strand = Plus / Minus
```

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  853    AAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATTGAACCAGGCCATAAAGCAC  912

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  913    GCACACACCGCCCGTCACCCTC  934
```

>ref|NC_001788.1| Equus asinus mitochondrion, complete genome
Length = 16670

Score = 266 bits (138), Expect = 3e-69
Identities = 265/316 (83%), Gaps = 8/316 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTT-AGATCAACA  388
Sbjct:  492    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCAAAATAGCTCACCATAACA  551

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  552    AAGCTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTT  611

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTC  268
Sbjct:  612    TACATCCCTCTAGAGGAGCCTGTTCCGTAATCGATAAACCCCGATAACCCCACCATCCC  671

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGA-AAGGCCACAGAGTAA  213
Sbjct:  672    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAACAAGGTACCAAAGTAA  731

Query:  212    GCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  732    GCACAATCATCCAACATAAAAACGTTAGGTCAAGGTGTAGCCCATGGGATGGAGAGAAAT  791

Query:  153    GGG-TACGTTTTCTAC  139
Sbjct:  792    GGGCTACATTTTCTAC  807
```

Score = 106 bits (55), Expect = 3e-21
Identities = 73/82 (89%)
Strand = Plus / Minus

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  860    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATCAGGCCATGAAGCGC  919

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  920    GCACACACCGCCCGTCACCCTC  941
```

```
  Database: NCBI genome chromosomes - other
    Posted date:  Apr 11, 2003  1:13 AM
  Number of letters in database: 789,957,834
  Number of sequences in database:  2528

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
```

Number of Hits to DB: 161,951
Number of Sequences: 2528
Number of extensions: 161951
Number of successful extensions: 1049
Number of sequences better than 10.0: 310
Number of HSP's better than 10.0 without gapping: 310
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 846
length of query: 462
length of database: 789,957,834
effective HSP length: 23
effective length of query: 439
effective length of database: 789,899,690
effective search space: 346765963910
effective search space used: 346765963910
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 18 (35.3 bits)

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

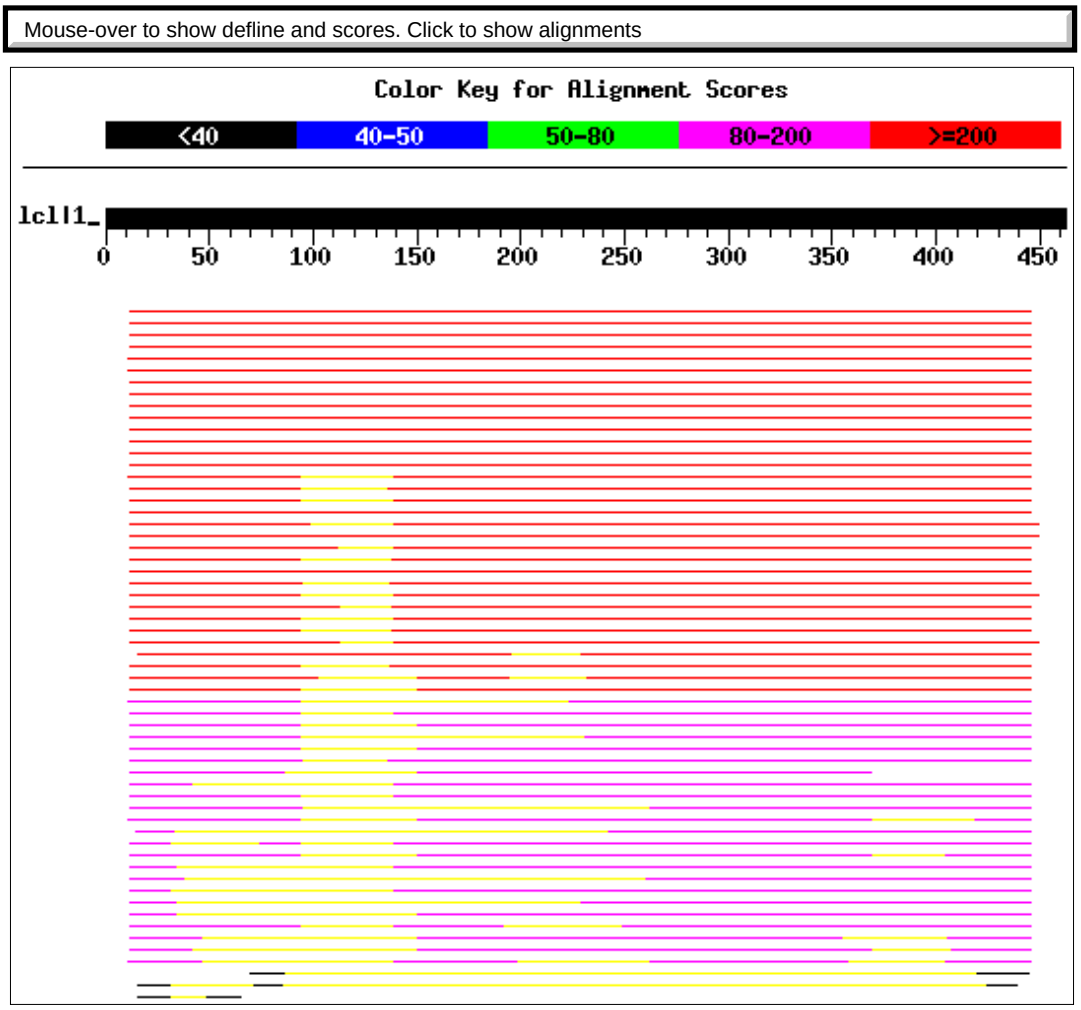
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: mito.nt
129 sequences; 3,164,247 total letters

Query= CS63win
(462 letters)

Distribution of 194 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value
gi|5835149|ref|NC_001645.1| Gorilla gorilla mitochondrion, compl...	460	e-130
gi|6137796|ref|NC_001807.2| Human mitochondrion, complete genome	454	e-128
gi|5835121|ref|NC_001643.1| Pan troglodytes mitochondrion, compl...	454	e-128
gi|5835135|ref|NC_001644.1| Pan paniscus mitochondrion, complete...	442	e-125
gi|5835834|ref|NC_002083.1| Pongo pygmaeus abelii mitochondrion,...	439	e-123
gi|5835163|ref|NC_001646.1| Pongo pygmaeus mitochondrion, comple...	410	e-115
gi|5835820|ref|NC_002082.1| Hylobates lar mitochondrion, complet...	389	e-108
gi|5835205|ref|NC_001700.1| Felis catus mitochondrion, complete ...	364	e-101
gi|5835652|ref|NC_002008.1| Canis familiaris mitochondrion, comp...	346	6e-96
gi|5835177|ref|NC_001665.1| Rattus norvegicus mitochondrial genome	346	6e-96
gi|5834953|ref|NC_001569.1| Mus musculus mitochondrion, complete...	335	2e-92
gi|5835554|ref|NC_001941.1| Ovis aries mitochondrion, complete g...	323	5e-89
gi|5835526|ref|NC_001913.1| Oryctolagus cuniculus mitochondrion,...	321	2e-88
gi|5835484|ref|NC_001892.1| Myoxus glis mitochondrion, complete ...	321	2e-88
gi|5835429|ref|NC_001821.1| Dasypus novemcinctus mitochondrion, ...	317	3e-87
gi|5834939|ref|NC_001567.1| Bos taurus mitochondrion, complete g...	314	4e-86
gi|7212513|ref|NC_002391.1| Talpa europaea mitochondrion, comple...	310	6e-85
gi|5835988|ref|NC_000884.1| Cavia porcellus complete mitochondri...	308	2e-84
gi|5835764|ref|NC_002078.1| Orycteropus afer complete mitochondr...	302	1e-82
gi|5834857|ref|NC_001325.1| Phoca vitulina mitochondrion, comple...	298	2e-81
gi|5836030|ref|NC_000889.1| Hippopotamus amphibius mitochondrion...	291	4e-79
gi|5835107|ref|NC_001640.1| Equus caballus mitochondrion, comple...	289	1e-78
gi|5835009|ref|NC_001602.1| Halichoerus grypus mitochondrion, co...	285	2e-77
gi|5835862|ref|NC_000845.1| Sus scrofa mitochondrion, complete g...	279	1e-75
gi|5834995|ref|NC_001601.1| Balaenoptera musculus mitochondrion,...	277	4e-75
gi|5835331|ref|NC_001779.1| R.unicornis complete mitochondrial g...	273	6e-74
gi|5835401|ref|NC_001808.1| Ceratotherium simum mitochondrion, c...	267	3e-72
gi|5835345|ref|NC_001788.1| Equus asinus mitochondrion, complete...	266	1e-71
gi|5819095|ref|NC_001321.1| Balaenoptera physalus mitochondrion,...	250	5e-67
gi|5835638|ref|NC_001992.1| Papio hamadryas mitochondrion, compl...	241	4e-64
gi|5836058|ref|NC_000891.1| Ornithorhynchus anatinus mitochondri...	237	6e-63
gi|5835666|ref|NC_002009.1| Artibeus jamaicensis mitochondrion, ...	206	1e-53
gi|5835037|ref|NC_001610.1| Didelphis virginiana mitochondrion, ...	202	1e-52
gi|5835792|ref|NC_002080.1| Erinaceus europaeus mitochondrion, c...	189	2e-48
gi|5835359|ref|NC_001794.1| Macropus robustus mitochondrion, com...	185	2e-47
gi|5835890|ref|NC_000860.1| Salvelinus fontinalis mitochondrion,...	156	1e-38
gi|6137801|ref|NC_000934.1| Loxodonta africana mitochondrion, co...	146	9e-36
gi|5835904|ref|NC_000861.1| Salvelinus alpinus mitochondrion, co...	144	3e-35
gi|5902189|ref|NC_002073.3| Chrysemys picta mitochondrion, compl...	141	5e-34
gi|5835261|ref|NC_001717.1| Oncorhynchus mykiss mitochondrion co...	135	3e-32
gi|5835708|ref|NC_002012.1| Squalus acanthias mitochondrion, com...	131	4e-31
gi|5836002|ref|NC_000886.1| Chelonia mydas mitochondrial DNA, co...	129	1e-30
gi|5835275|ref|NC_001727.1| Crossostoma lacustre mitochondrion, ...	129	1e-30
gi|5835806|ref|NC_002081.1| Gadus morhua mitochondrion, complete...	123	8e-29
gi|5835582|ref|NC_001947.1| Pelomedusa subrufa mitochondrion, co...	121	3e-28
gi|5835624|ref|NC_001960.1| Salmo salar mitochondrion, complete ...	114	6e-26
gi|5835023|ref|NC_001606.1| Cyprinus carpio mitochondrion, compl...	114	6e-26
gi|5835498|ref|NC_000846.1| Rhea americana mitochondrion, comple...	112	2e-25
gi|5835373|ref|NC_001804.1| Latimeria chalumnae mitochondrion, c...	112	2e-25
gi|5835778|ref|NC_002079.1| Carassius auratus mitochondrion, com...	110	9e-25
gi|5836016|ref|NC_000888.1| Eumeces egregius mitochondrion, comp...	106	1e-23
gi|5836044|ref|NC_000890.1| Mustelus manazo mitochondrion, compl...	104	5e-23

gi|5835596|ref|NC_001950.1| Scyliorhinus canicula mitochondrion,...	100	7e-22
gi|5835317|ref|NC_001778.1| Polypterus ornatipinnis mitochondrio...	100	7e-22
gi|7212458|ref|NC_002386.1| Paralichthys olivaceus mitochondrion...	97	1e-20
gi|5836072|ref|NC_000893.1| Raja radiata mitochondrion, complete...	91	5e-19
gi|5835610|ref|NC_001953.1| Struthio camelus complete mitochondr...	91	5e-19
gi|5835932|ref|NC_000877.1| Aythya americana mitochondrion, comp...	89	2e-18
gi|5835219|ref|NC_001708.1| Protopterus dolloi mitochondrion, co...	89	2e-18
gi|5835456|ref|NC_001878.1| Florometra serratissima mitochondrio...	85	3e-17
gi|5834843|ref|NC_001323.1| Gallus gallus mitochondrion, complet...	85	3e-17
gi|5835974|ref|NC_000880.1| Vidua chalybeata mitochondrion, comp...	83	1e-16
gi|5834981|ref|NC_001573.1| Xenopus laevis mitochondrial DNA, co...	81	4e-16
gi|5835540|ref|NC_001922.1| Alligator mississippiensis mitochond...	72	3e-13
gi|7549724|ref|NC_002197.1| Ciconia ciconia mitochondrion, compl...	70	1e-12
gi|7555761|ref|NC_002196.1| Ciconia boyciana mitochondrion, comp...	70	1e-12
gi|5835960|ref|NC_000879.1| Smithornis sharpei mitochondrion, co...	70	1e-12
gi|5835946|ref|NC_000878.1| Falco peregrinus mitochondrion, comp...	66	2e-11
gi|5835722|ref|NC_002069.1| Corvus frugilegus mitochondrion, com...	58	4e-09
gi|7374113|ref|NC_002184.1| Penaeus monodon mitochondrion, compl...	49	3e-06
gi|5835093|ref|NC_001636.1| Katharina tunicata mitochondrion, co...	49	3e-06
gi|5835079|ref|NC_001627.1| Asterina pectinifera mitochondrion, ...	49	3e-06
gi|7212445|ref|NC_001276.1| Crassostrea gigas mitochondrion, com...	47	1e-05
gi|6691422|ref|NC_001131.1| Lampetra fluviatilis mitochondrion, ...	43	2e-04
gi|5835065|ref|NC_001626.1| Petromyzon marinus mitochondrion, co...	43	2e-04
gi|5835303|ref|NC_001770.1| Arbacia lixula mitochondrion, comple...	41	6e-04
gi|5834967|ref|NC_001572.1| Paracentrotus lividus mitochondrion,...	41	6e-04
gi|7335663|ref|NC_000928.2| Echinococcus multilocularis mitochon...	39	0.002
gi|5835568|ref|NC_001945.1| Dinodon semicarinatus mitochondrion,...	39	0.002
gi|5835470|ref|NC_001887.1| Balanoglossus carnosus mitochondrion...	37	0.009
gi|5834925|ref|NC_001566.1| Apis mellifera ligustica mitochondri...	37	0.009
gi|7110454|gb|AF222718.1|AF222718 Chrysodidymus synuroideus mito...	35	0.033
gi|5306128|gb|AF160864.1|AF160864 Tetrahymena pyriformis mitocho...	33	0.13
gi|6691408|ref|NC_000941.1| Terebratulina retusa mitochondrion, ...	33	0.13
gi|5881414|ref|NC_000834.1| Branchiostoma floridae mitochondrion...	33	0.13
gi|5835512|ref|NC_001912.1| Branchiostoma lanceolatum complete m...	33	0.13
gi|1019057|emb|Z47547.1|MTCCGNME Chondrus crispus complete mitoc...	31	0.48
gi|1785729|emb|Y08502.1|MIATGENB A.thaliana mitochondrial genome...	31	0.48
gi|6692625|gb|U17009.2|U17009 Phytophthora infestans mitochondri...	31	0.48
gi|562028|gb|U12386.1|ACU12386 Acanthamoeba castellanii mitochon...	31	0.48
gi|6180080|gb|AF193903.1|AF193903 Cafeteria roenbergensis mitoch...	31	0.48
gi|4106927|gb|AF114794.1|AF114794 Porphyra purpurea mitochondrio...	31	0.48
gi|2258325|gb|AF007261.1|AF007261 Reclinomonas americana mitocho...	31	0.48
gi|5835918|ref|NC_000875.1| Anopheles quadrimaculatus A mitochon...	31	0.48
gi|5835876|ref|NC_000857.1| Ceratitis capitata complete mitochon...	31	0.48
gi|5835694|ref|NC_002074.1| Rhipicephalus sanguineus mitochondri...	31	0.48
gi|5835680|ref|NC_002010.1| Ixodes hexagonus mitochondrion, comp...	31	0.48
gi|5835233|ref|NC_001709.1| Drosophila melanogaster mitochondrio...	31	0.48
gi|5834911|ref|NC_002084.1| Anopheles gambiae mitochondrion, com...	31	0.48
gi|5834829|ref|NC_001322.1| Drosophila yakuba mitochondrion, com...	31	0.48

>gi|5835149|ref|NC_001645.1| Gorilla gorilla mitochondrion, complete genome
Length = 16364

Score = 460 bits (239), Expect = e-130
Identities = 377/436 (86%), Gaps = 6/436 (1%)

```
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  485    CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACTTCAACAGTTAAATTAACAA  544

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  545    GACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  604

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  605    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  664

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  665    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCACAAAGTAAGCACA  724

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  725    AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  784

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  785    CATTTTCTAC-TTCAGAAAACT---ACGATAACCCTTATGAAACCTAAGGGTAGAAGGTG  840

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  841    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  900

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  901    ACCGCCCGTCACCCTC  916
```

```
>gi|6137796|ref|NC_001807.2| Human mitochondrion, complete genome
          Length = 16569

 Score =  454 bits (236), Expect = e-128
 Identities = 376/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422   GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1482   ACCGCCCGTCACCCTC  1497
```

```
>gi|5835121|ref|NC_001643.1| Pan troglodytes mitochondrion, complete
```

genome
Length = 16554

Score = 454 bits (236), Expect = e-128
Identities = 376/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTCAACAGTTAAATTAACAA  543

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  544    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  603

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  604    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCGCCTCT  663

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  664    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGTTACAAAGTAAGCACA  723

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  724    AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCTATGAGGTGGCAAGAAATGGGCTA  783

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  784    CATTTTCTAC-CCCAGAAAA---TTACGATAACCCTTATGAAACCTAAGGGTCAAAGGTG  839

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  840    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  899

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  900    ACCGCCCGTCACCCTC  915
```

>gi|5835135|ref|NC_001644.1| Pan paniscus mitochondrion, complete genome
Length = 16563

Score = 442 bits (230), Expect = e-125
Identities = 374/436 (85%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  486    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTCAACAGTTAAATTAACAA  545

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  546    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  605

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  606    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCGCCTCT  665

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  666    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGTTACAAAGTAAGCGCA  725

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  726    AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCTATGAGGCGGCAAGAAATGGGCTA  785

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  786    CATTTTCTAC-CCCAGAAAA---TTACGATAACCCTTATGAAACCTAAGGGTCGAAGGTG  841

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  842    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  901
```

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Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  902    ACCGCCCGTCACCCTC  917
```

```
>gi|5835834|ref|NC_002083.1| Pongo pygmaeus abelii mitochondrion,
           complete genome
          Length = 16499

 Score =  439 bits (228), Expect = e-123
 Identities = 374/437 (85%), Gaps = 6/437 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  490    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTTAACAGTTAAATCAACAA  549

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  550    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  609

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  610    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCCCT  669

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  670    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCACGAAGTAAGCGCA  729

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  730    AGCATCCACATAAAGACGTTAGGTCAAGGTGTAGCCCATGGAGTGGCAAGAAATGGGCTA  789

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  790    CATTTTCTAC-TTCAGAAAACT---ACGATAGCCCTCATGAAACCTGAGGGTCGAAGGTG  845

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  846    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  905

Query:  28     ACCGCCCGTCACCCTCT  12
Sbjct:  906    ACCGCCCGTCACCCTCT  922
```

```
>gi|5835163|ref|NC_001646.1| Pongo pygmaeus mitochondrion, complete
           genome
          Length = 16389

 Score =  410 bits (213), Expect = e-115
 Identities = 369/437 (84%), Gaps = 6/437 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  489    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTTAACAGTTGAATCAACAA  548

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  549    AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  608

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  609    ATACCCCCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCCCT  668

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  669    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCCACGAAGTAAGCGCA  728

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  729    AACACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGGAGTGGCAAGAAATGGGCTA  788
```

```
Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  789    CATTTTCTAC-TTCAGAAAACT---ACGATAACCCTCATGAAATTTGAAGGTCGAAGGTG  844

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  845    GATTTAGCAGTAAACTAAGAGTAGAGTGCTTAGTTGAACAAGGCCCTGAAGCGCGTACAC  904

Query:  28     ACCGCCCGTCACCCTCT  12
Sbjct:  905    ACCGCCCGTCACCCTCT  921
```

>gi|5835820|ref|NC_002082.1| Hylobates lar mitochondrion, complete genome
Length = 16472

```
 Score =  389 bits (202), Expect = e-108
 Identities = 367/437 (83%), Gaps = 7/437 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTCAGCCCTAAACTTCAACAGTCAAATCAACAA  543

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  544    GACTGCTCGCCAGAACACTACGAGCAACAGCTTAAAAATCAAAGGACCTGGCGGTGCTTC  603

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  604    ACACCCCCTAGAGGAGCCTGTCCTATAATCGATAAACCCCGTTCAACCTCACCATCTCT  663

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  664    TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGACAAAGGCTATAAAGTAAGCACA  723

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  724    AACACCCACATAAAGACGTTAGGTCAAGGTGTAGCCCATGAGATGGGAAGAGATGGGCTA  783

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTC-AAGGA  90
Sbjct:  784    CATTTTCTATGC-CAGAAAA---CCACGATAACCCTCATGAAACTTGAGCGGTCGAAGGA  839

Query:  89     GGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACA  30
Sbjct:  840    GGATTTAGCAGTAAATTAAGAATAGAGTGCTTAGTTGAACAAGGCCCTGAAGCGCGTACA  899

Query:  29     CACCGCCCGTCACCCTC  13
Sbjct:  900    CACCGCCCGTCACCCTC  916
```

>gi|5835205|ref|NC_001700.1| Felis catus mitochondrion, complete genome
Length = 17009

```
 Score =  364 bits (189), Expect = e-101
 Identities = 370/443 (83%), Gaps = 12/443 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGA-TCAACA  388
Sbjct:  1356   CAAACTGGGATTAGATACCCTACTATGCTTAGCCCTAAACTTAGATAGTTACCCTAAACA  1415

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  1416   AAACTATCCGCCAGAGAACTACTAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTT  1475

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  1476   TACATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATATACCTCACCATCTC  1535
```

```
Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  1536   TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAAGAAAGTAAG  1595

Query:  211    CAGAAGTATCT--ACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  1596   CACAAGTATCTTAACATAAAAAAGTTAGGTCAAGGTGTAGCTCATGAGATGGGAAGCAAT  1655

Query:  153    GGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTC  95
Sbjct:  1656   GGGCTACATTTTCTAAATTAGAACA--CCCACGAAGATCCTTACGAAA-CTAAGTATTA  1712

Query:  94     AAGGAGGATTTAGCAATAAA-TTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  1713   AAGGAGGATTTAGTAGTAAATTTGAGAATAGAGAGCTCAATTGAATCGGGCCATGAAGCA  1772

Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  1773   CGCACACACCGCCCGTCACCCTC  1795
```

```
>gi|5835652|ref|NC_002008.1| Canis familiaris mitochondrion, complete
           genome
          Length = 16728

 Score =  346 bits (180), Expect = 6e-96
 Identities = 365/440 (82%), Gaps = 10/440 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  486    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAGATAATTTTA-CAACAA  544

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  545    AATAATTCGCCAGAGGACTACTAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  604

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  605    ATATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAACCTCACCACCTTT  664

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  665    CGCTAATTCAGTCTATATACCGCCATCTTCAGCAAACCCTCAAAAGGTAGAACAGTAAGC  724

Query:  210    AGAAGTA-TCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  725    ACAATCATTTTACATAAAAAAGTTAGGTCAAGGTGTAACTTATGAGGTGGGAAGAAATGG  784

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  785    GCTACATTTTCTACCCA-AG-AACATTTCACGAATGTTTTTATGAAAT-TAAAACTGAA  841

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  842    GGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAGGGCCATGAAGCACGC  901

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  902    ACACACCGCCCGTCACCCTC  921
```

```
>gi|5835177|ref|NC_001665.1| Rattus norvegicus mitochondrial genome
          Length = 16300

 Score =  346 bits (180), Expect = 6e-96
 Identities = 361/439 (82%), Gaps = 8/439 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  485    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTTAATAATTAAACCTACAA  544
```

```
Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  545    AATTATTTGCCAGAGAACTACTAGCTACAGCTTAAAACTCAAAGGACTTGGCGGTACTTT  604

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  605    ATATCCATCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGTTCTACCTTACCCCTTCT  664

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  665    CGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGCACTAAAGTAAGC  724

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  725    ACAAGAACAAACATAAAAACGTTAGGTCAAGGTGTAGCCAATGAAGCGGAAAGAAATGGG  784

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAG  92
Sbjct:  785    CTACATTTTCTTTCCCAG-AGAACATTACGA-AACCTTTATGAAA-CTAAAGGACAAAG  841

Query:  91     GAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCA  32
Sbjct:  842    GAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAGAGCAATGAAGTACGCA  901

Query:  31     CACACCGCCCGTCACCCTC  13
Sbjct:  902    CACACCGCCCGTCACCCTC  920
```

>gi|5834953|ref|NC_001569.1| Mus musculus mitochondrion, complete genome
Length = 16295

Score = 335 bits (174), Expect = 2e-92
Identities = 362/441 (82%), Gaps = 11/441 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATC-AACA  388
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAACCTAAATAATTAAATTTAACA  543

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  544    AAACTATTTGCCAGAGAACTACTAGCCATAGCTTAAAACTCAAAGGACTTGGCGGTACTT  603

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  604    TATATCCATCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGCTCTACCTCACCATCTC  663

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  664    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGTATTAAAGTAAG  723

Query:  211    CAGAAGTATC-TACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  724    CAAAAGAATCAAACATAAAAACGTTAGGTCAAGGTGTAGCCAATGAAATGGGAAGAAATG  783

Query:  152    GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  784    GGCTACATTTTCT---TATAAAAGAACATTACTATACCCTTTATGAAA-CTAAAGGACTA  839

Query:  93     AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  840    AGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATTGAGCAATGAAGTACG  899

Query:  33     CACACACCGCCCGTCACCCTC  13
Sbjct:  900    CACACACCGCCCGTCACCCTC  920
```

>gi|5835554|ref|NC_001941.1| Ovis aries mitochondrion, complete genome
Length = 16616

Score = 323 bits (168), Expect = 5e-89
Identities = 360/441 (81%), Gaps = 9/441 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACACAAATAATTATAAAACAA  543

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  544    AATTATTCGCCAGAGTACTACC-GCAACAGCCCGAAACTCAAAGGACTTGGCGGTGCTTT  602

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  603    ATACCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCAATCCT  662

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCAC-AGAGTAAG  212
Sbjct:  663    TGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAAAGGGACAAAAGTAAG  722

Query:  211    CAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  723    CTCAATAATAACACATAAAGACGTTAGGTCAAGGTGTAACCTATGGAGTGGGAAGAAATG  782

Query:  152    GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  783    GGCTACATTTTCTACCCAAGAAAATTTAATACGAAGCCATTATGAAAT-TAATAGCCAA  841

Query:  93     AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  842    AGGAGGATTTAGCAGTAAACTAAGAATAGAGTGCTTAGTTGAATCAGGCCATGAAGCACG  901

Query:  33     CACACACCGCCCGTCACCCTC  13
Sbjct:  902    CACACACCGCCCGTCACCCTC  922
```

```
>gi|5835526|ref|NC_001913.1| Oryctolagus cuniculus mitochondrion,
           complete genome
         Length = 17245

 Score =  321 bits (167), Expect = 2e-88
 Identities = 359/440 (81%), Gaps = 12/440 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  488    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTTTGATAATTTCAT-AACAA  546

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  547    AATTATTCGCCAGAGAACTACAAGCCAAAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  606

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  607    ATACCCACCTAGAGGAGCCTGTTCCGTAATCGATAAACCCCGATAAACCCTACCACTCTT  666

Query:  266    TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  667    TGCCAACTCAGCCTATATACCGCCATCTTCAGCGAACCCTAAAAAGGAGCAAAAGTAAGC  726

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  727    TCAATTACCACCGTAAAAACGTTAGGTCAAGGTGTAGCCCATAGAGTGGAGAGCAATGGG  786

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAA-TCTAAGGGCTCAA  93
Sbjct:  787    CTACATTTTCTAC-TTCAGAATA----TACGAAGCCCTTATGAAACTCTAAGGGCCAAA  841

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  842    GGAGGATTTAGTAGTAAATTAAGAATAGAGTGCTTAATTGAACAAGGCCATGAAGCACGC  901

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  902    ACACACCGCCCGTCACCCTC  921
```

```
>gi|5835484|ref|NC_001892.1| Myoxus glis mitochondrion, complete
```

genome
Length = 16602

Score = 321 bits (167), Expect = 2e-88
Identities = 355/439 (80%), Gaps = 9/439 (2%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  484    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAAACCCTTACT--AACGC  541

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  542    AACCGTTCGCCAGAGTACTACAAGCCACAGCTCAAAACTCAAAGGACTTGGCGGTGCTTT  601

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  602    ATATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCACTTCT  661

Query:  266    TG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAGGCCACAGAGTAAGC  211
Sbjct:  662    TGCTACCACAGCTTATATACCGCCATCTTCAGCAAACCTTAACAAGGAATCAAAGTAAGC  721

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  722    CCAAGTATTAACATAAAAACGTTAGGTCAAGGTGTAGCCTATGAAGTGGAAAGAAATGGG  781

Query:  150    -TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAG  92
Sbjct:  782    CTACATTTCCTTTCCCAAGTACA--TTCACGTCAACTTTTATGAAACCTAAAAGTAAAAG  839

Query:  91     GAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCA  32
Sbjct:  840    GCGGATTTAGTAGTAAGCTAAGAATAGAGAGCCTAGCTGAATAGGGCCATGAAGCACGCA  899

Query:  31     CACACCGCCCGTCACCCTC  13
Sbjct:  900    CACACCGCCCGTCACCCTC  918
```

>gi|5835429|ref|NC_001821.1| Dasypus novemcinctus mitochondrion, complete genome
Length = 17056

Score = 317 bits (165), Expect = 3e-87
Identities = 268/312 (85%), Gaps = 6/312 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  492    CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACTAAAACAGTTC-ACAAACAA  550

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  551    AACTGTTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  610

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  611    ACATCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATATACCTCACCACCCCT  670

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  671    TGCTAATACAGCCTATATACCGCCATCTTCAGCAGACCCTAGTAAGGCACCACAGTGAGC  730

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  731    ACAATAACATACATAAAGACGTTAGGTCAAGGTGTAGCTTATGGGGTGGGAAGAAATGGG  790

Query:  150    -TACGTTTTCTA  140
Sbjct:  791    CTACATTTTCTA  802
```

```
 Score = 73.7 bits (38), Expect = 9e-14
 Identities = 68/83 (81%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  846    AAGGTGGATTTAGTAGTAAGCTAAAAATAGAGAGTTTAGCTGAACCAGGCCATAAAGCAC  905

Query:  34     GCACACACCGCCCGTCACCCTCT  12
Sbjct:  906    GCACACACCGCCCGTCACCCTCT  928


>gi|5834939|ref|NC_001567.1| Bos taurus mitochondrion, complete genome
          Length = 16338

 Score =  314 bits (163), Expect = 4e-86
 Identities = 270/316 (85%), Gaps = 6/316 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  842    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACACAGATAATTACATAAACAA  901

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  902    AATTATTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  961

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  962    ATATCCTTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCAATTCT  1021

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  1022   TGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAAAAAAAGTAAGC  1081

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  1082   GTAATTATGATACATAAAAACGTTAGGTCAAGGTGTAACCTATGAAATGGGAAGAAATGG  1141

Query:  151    G-TACGTTTTCTACAC  137
Sbjct:  1142   GCTACATTCTCTACAC  1157


 Score =  112 bits (58), Expect = 2e-25
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1200   AAGGAGGATTTAGCAGTAAACTAAGAATAGAGTGCTTAGTTGAATTAGGCCATGAAGCAC  1259

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1260   GCACACACCGCCCGTCACCCTC  1281


>gi|7212513|ref|NC_002391.1| Talpa europaea mitochondrion, complete
            genome
          Length = 16884

 Score =  310 bits (161), Expect = 6e-85
 Identities = 265/312 (84%), Gaps = 5/312 (1%)
 Strand = Plus / Minus
```

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  495    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCAAGACAATCAAGTTAACAA  554

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  555    GATTGTTCGCCAGAGAACTACTAGCCACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  614

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  615    ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATAAACCTCACCAACTCT  674

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  675    TGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAATTACAGTAAGC  734

Query:  210    AGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  735    ACAAGTACCCGCATAAAAACGTTAGGTCAAGGTGTAGCTGATGAGTTGGGAAGAAATGGG  794

Query:  150    -TACGTTTTCTA  140
Sbjct:  795    CTACATTTTCTA  806
```

```
 Score =  112 bits (58), Expect = 2e-25
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  857    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGCGCTTAATTGAATAAGGCCATGAAGCAC  916

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  917    GCACACACCGCCCGTCACCCTC  938
```

```
>gi|5835988|ref|NC_000884.1| Cavia porcellus complete mitochondrial
           genome
          Length = 16801

 Score =  308 bits (160), Expect = 2e-84
 Identities = 355/440 (80%), Gaps = 8/440 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  481    CAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAACATAAAACTTATA-CAACAA  539

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  540    AAGATTTCGCCAGAGAACTACTAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  599

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  600    ATACCCACCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATACACCTCACCTCTCCT  659

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  660    TGCTAATTCAGCCTATATACCGCCATCTTCAGCCAACCCCATTATGGAAACAAAGTGAGC  719

Query:  210    AGAAGTA-TCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  720    GCAAGTACACTACATAAAAACGTTAGGTCAAGGTGTAGCCAATGGAGTGGGAAGAAATGG  779

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  780    GCTACATTTTCT-TACCCAAGAACATTAAACGCAAATCTTTATGAAATTCAAAGATCTAA  838

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  839    GGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTGATTGAACTAGGCCATGAAGCACGT  898
```

```
Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  899    ACACACCGCCCGTCACCCTC  918
```

```
>gi|5835764|ref|NC_002078.1| Orycteropus afer complete mitochondrial
           genome
          Length = 16816

 Score =  302 bits (157), Expect = 1e-82
 Identities = 268/316 (84%), Gaps = 7/316 (2%)
 Strand = Plus / Minus


Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  483    GATACAAACTGGGATTAGATACCCCACTATGCCTAGCCATAAACTTAAATATTTC--TCA  540

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  541    ACAAAATTATTCGCCAGAGAACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  600

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  601    CTTTATATCCATCTAGAGGAGCCTGTTATGTAATCGATAAACCCCGATATACCTCACCAT  660

Query:  270    CTCTTGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  661    CACTTGCCAATACAGCCTATATACCGCCATCTTCAGCAAACCCTTACAAGGAATAATAGT  720

Query:  214    AAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAA  155
Sbjct:  721    AAGCCAAATTATTACCATAAAAACGTTAGGTCAAGGTGTAGCCAATGTGATGGCAATAAA  780

Query:  154    TGGG-TACGTTTTCTA  140
Sbjct:  781    TGGGCTACATTTTCTA  796
```

```
 Score =  116 bits (60), Expect = 2e-26
 Identities = 78/87 (89%)
 Strand = Plus / Minus


Query:  99     GGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGA  40
Sbjct:  837    GGCTAAAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATAAGGCCATGA  896

Query:  39     AGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  897    AGCACGCACACACCGCCCGTCACCCTC  923
```

```
>gi|5834857|ref|NC_001325.1| Phoca vitulina mitochondrion, complete
           genome
          Length = 16826

 Score =  298 bits (155), Expect = 2e-81
 Identities = 355/445 (79%), Gaps = 8/445 (1%)
 Strand = Plus / Minus


Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  1423   GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAAATAATTCACGTA  1482

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  1483   ACAAAATTATTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  1542

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1543   CTTCACACCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATAAACCTCACCAT  1602
```

```
Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  1603   TCCTTGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAACAAAAGT  1662

Query:  214    AAGCAGAAGTAT--CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGA  157
Sbjct:  1663   AAGCACAATAATCGCTACATAAAAAAGTTAGGTCAAGGTGTAACCTATGGAATGGGAAGA  1722

Query:  156    AATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGG  98
Sbjct:  1723   AATGGGCTACATTTTCTAAATA-AGAACAATCATACGAAAGTTTTTATGAAATTAACAAA  1781

Query:  97     CTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAG  38
Sbjct:  1782   CTAAAGGTGGATTTAGTAGTAAGCTAAGAATAGAGAGCTTAGCTGAACCGGGCCATGAAG  1841

Query:  37     CACGCACACACCGCCCGTCACCCTC  13
Sbjct:  1842   CACGCACACACCGCCCGTCACCCTC  1866
```

```
>gi|5836030|ref|NC_000889.1| Hippopotamus amphibius mitochondrion,
           complete genome
         Length = 16407

 Score =  291 bits (151), Expect = 4e-79
 Identities = 264/313 (84%), Gaps = 6/313 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  491    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACACAGATAATTCCAAAACAA  550

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  551    AACTATTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  610

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  611    ATACCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCTCACCAACCCT  670

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  671    TGCTAATCCAGTCTATATACCGCCATCTCCAGCAAACCCTAAAAAGGACTAAAAGTAAGC  730

Query:  210    AGAAGTA-TCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  731    TCAACTATTACACATAAAGACGTTAGGTCAAGGTGTAACCTATGGGCTGGGAAGAAATGG  790

Query:  151    G-TACGTTTTCTA  140
Sbjct:  791    GCTACATTTTCTA  803
```

```
 Score =  106 bits (55), Expect = 1e-23
 Identities = 85/100 (85%)
 Strand = Plus / Minus


Query:  112    TATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTG  53
Sbjct:  838    TATGAAAGCTAGGAACTAAAGGAGGATTTAGTAGTAAATCAAGAGTAGAGTGCTTGATTG  897

Query:  52     AATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  898    AACAAGGCTATGAAGCACGCACACACCGCCCGTCACCCTC  937
```

```
>gi|5835107|ref|NC_001640.1| Equus caballus mitochondrion, complete
           genome
         Length = 16660
```

```
 Score =  289 bits (150), Expect = 1e-78
 Identities = 269/316 (85%), Gaps = 8/316 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAG-TTAGATCAACA  388
Sbjct:  491    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTAAATAGCTTACCACAACA  550

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  551    AAGCTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTT  610

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTC  268
Sbjct:  611    TACATCCCTCTAGAGGAGCCTGTTCCATAATCGATAAACCCCGATAACCCCACCATCCC  670

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGA-AAGGCCACAGAGTAA  213
Sbjct:  671    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAACAAGGTACCGAAGTAA  730

Query:  212    GCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  731    GCACAAATATCCAACATAAAAACGTTAGGTCAAGGTGTAGCCCATGGGATGGAGAGAAAT  790

Query:  153    GGG-TACGTTTTCTAC  139
Sbjct:  791    GGGCTACATTTTCTAC  806
```

```
 Score =  112 bits (58), Expect = 2e-25
 Identities = 74/82 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  860    AAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATTGAATCAGGCCATGAAGCGC  919

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  920    GCACACACCGCCCGTCACCCTC  941
```

```
>gi|5835009|ref|NC_001602.1| Halichoerus grypus mitochondrion,
           complete genome
         Length = 16797

 Score =  285 bits (148), Expect = 2e-77
 Identities = 350/441 (79%), Gaps = 8/441 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1397   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACATAAATAATTCACGTAACAA  1456

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1457   AATTATTCGCCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  1516

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1517   ACACCCCTCTAGAGGAGCCTGTTCTGTAACCGATAAACCCCGATAAACCTCACCACTCCT  1576

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  1577   TGCTAATACAGTCTATATACCGCCATCTTCAGCAAACCCTTAAAAGGAACAAAAGTAAGC  1636

Query:  210    AGAAGTAT--CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  1637   ACAATAATCGCTACATAAAAAAGTTAGGTCAAGGTGTAACCTATGGAGTGGGAAGAAATG  1696
```

```
Query:  152    GG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCA  94
Sbjct:  1697   GGCTACATTTTCTAAATA-AGAACAACTATACGAAAGTTTTTATGAAACTAACAAACTAA  1755

Query:  93     AGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACG  34
Sbjct:  1756   AGGTGGATTTAGTAGTAAGCTAAGAATAGAGAGCTTAGCTGAACCGGGCCATGAAGCACG  1815

Query:  33     CACACACCGCCCGTCACCCTC  13
Sbjct:  1816   CACACACCGCCCGTCACCCTC  1836
```

```
>gi|5835862|ref|NC_000845.1| Sus scrofa mitochondrion, complete genome
          Length = 16613

 Score =  279 bits (145), Expect = 1e-75
 Identities = 265/315 (84%), Gaps = 7/315 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1662   CAAACTGGGATTAGATACCCCACTATGCCTAGCCCTAAACCCAAATAGTTACAT-AACAA  1720

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1721   AACTATTCGCCAGAGTACTACTCGCAACTGCCTAAAACTCAAAGGACTTGGCGGTGCTTC  1780

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1781   ACATCCACCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAGACCTTACCAACCCT  1840

Query:  266    TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  1841   TGCCAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAACAATAGTAAGC  1900

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  1901   ACAATCATAGCACATAAAAACGTTAGGTCAAGGTGTAGCTTATGGGTTGGAAAGAAATGG  1960

Query:  151    G-TACGTTTTCTACA  138
Sbjct:  1961   GCTACATTTTCTACA  1975
```

```
 Score =  119 bits (62), Expect = 1e-27
 Identities = 76/83 (91%)
 Strand = Plus / Minus


Query:  95     CAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  2019   CAAGGAGGATTTAGCAGTAAATCGAGAATAGAGTGCTTGATTGAATAAGGCCATGAAGCA  2078

Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  2079   CGCACACACCGCCCGTCACCCTC  2101
```

```
>gi|5834995|ref|NC_001601.1| Balaenoptera musculus mitochondrion,
            complete genome
          Length = 16402

 Score =  277 bits (144), Expect = 4e-75
 Identities = 266/317 (83%), Gaps = 7/317 (2%)
 Strand = Plus / Minus


Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  909    GATCCAAACTGGGATTAGATACCCCACTATGCTTAGCCATAAACCCCAGTAGTCACAA-A  967
```

```
Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  968    ACAAGACTATTCGCCAGAGTACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTG  1027

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1028   CTTCATACCCCTCTAGAGGAGCCTGTTCTGTAACCGATAAACCCCGATTAACCTCACCAA  1087

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  1088   CCCTTGCTACTTCAGTCTATATACCGCCATCTTCAGCAAACCCTAAAAGGGAACGAAAGT  1147

Query:  214    AAGCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
Sbjct:  1148   AAGCATAATCATCCTACATAAAAACGTTAGGTCAAGGTGTAACCAATGGGTTGGGAAGAA  1207

Query:  155    ATGGG-TACGTTTTCTA  140
Sbjct:  1208   ATGGGCTACATTTTCTA  1224
```

```
 Score =  117 bits (61), Expect = 4e-27
 Identities = 75/82 (91%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1276   AAGGAGGATTTAGTAGTAAATCAAGAGCAGAGTGCTTGATTGAATAAGGCCATGAAGCAC  1335

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1336   GCACACACCGCCCGTCACCCTC  1357
```

```
>gi|5835331|ref|NC_001779.1| R.unicornis complete mitochondrial genome
          Length = 16829

 Score =  273 bits (142), Expect = 6e-74
 Identities = 264/315 (83%), Gaps = 7/315 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATC-AACA  388
Sbjct:  490    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCCAAACTCAAATAATTCTTCCCAACA  549

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  550    AAATTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTT  609

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTC  268
Sbjct:  610    TATATCCCCCTAGAGGAGCCTGTTCCATAACCGATAAACCCCGATAAACCTTACCAGCCC  669

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  670    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCCAACCCTAAAAAGGAACCAAAGTAAG  729

Query:  211    CAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  730    CACAAGTATAAGACATAAAAAACGTTAGGTCAAGGTGTAGCTTATGGGATGGAGAGAAATG  789

Query:  152    GG-TACGTTTTCTAC  139
Sbjct:  790    GGCTACATTTTCTAC  804
```

```
 Score =  110 bits (57), Expect = 9e-25
 Identities = 88/101 (87%), Gaps = 1/101 (0%)
 Strand = Plus / Minus
```

```
Query:  113    TTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATT  54
Sbjct:  837    TTATGAAAT-TAAAAGCTAAAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATT  895

Query:  53     GAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  896    GAACCAGGCCATAAAGCACGCACACACCGCCCGTCACCCTC  936
```

```
>gi|5835401|ref|NC_001808.1| Ceratotherium simum mitochondrion,
           complete genome
         Length = 16832

 Score =  267 bits (139), Expect = 3e-72
 Identities = 260/313 (83%), Gaps = 6/313 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  489    CAAACTGGGATTAGATACCCCACTATGCCTAGCCTTAAACCTAAATAATTTCTCCAACAA  548

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  549    AATTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTTT  608

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  609    ATATCCCCCTAGAGGAGCCTGTTCCATAACCGATAAACCCCGATAAACCCCACCAACCCT  668

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  669    TGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAAAAGGAACTAAAGTAAGC  728

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  729    ACAAGTATAAAACATAAAAACGTTAGGTCAAGGTGTAGCTTATGGGATGGAGAGAAATGG  788

Query:  151    G-TACGTTTTCTA  140
Sbjct:  789    GCTACATTTTCTA  801
```

```
 Score =  106 bits (55), Expect = 1e-23
 Identities = 73/82 (89%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  853    AAGGAGGATTTAGCAGTAAATTAAGAATAGAGAGCTTAATTGAACCAGGCCATAAAGCAC  912

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  913    GCACACACCGCCCGTCACCCTC  934
```

```
>gi|5835345|ref|NC_001788.1| Equus asinus mitochondrion, complete
           genome
         Length = 16670

 Score =  266 bits (138), Expect = 1e-71
 Identities = 265/316 (83%), Gaps = 8/316 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTT-AGATCAACA  388
Sbjct:  492    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCAAAATAGCTCACCATAACA  551

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
```

```
Sbjct:  552    AAGCTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTGCTT  611

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  612    TACATCCCTCTAGAGGAGCCTGTTCCGTAATCGATAAACCCCGATAAACCCCACCATCCC  671

Query:  267    TTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGA-AAGGCCACAGAGTAA  213
Sbjct:  672    TTGCTAATTCAGCCTATATACCGCCATCTTCAGCAAACCCTAAACAAGGTACCAAAGTAA  731

Query:  212    GCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  732    GCACAATCATCCAACATAAAAACGTTAGGTCAAGGTGTAGCCCATGGGATGGAGAGAAAT  791

Query:  153    GGG-TACGTTTTCTAC  139
Sbjct:  792    GGGCTACATTTTCTAC  807
```

```
 Score =  106 bits (55), Expect = 1e-23
 Identities = 73/82 (89%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  860    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATCAGGCCATGAAGCGC  919

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  920    GCACACACCGCCCGTCACCCTC  941
```

```
>gi|5819095|ref|NC_001321.1| Balaenoptera physalus mitochondrion,
            complete genome
          Length = 16398

 Score =  250 bits (130), Expect = 5e-67
 Identities = 263/317 (82%), Gaps = 9/317 (2%)
 Strand = Plus / Minus


Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  911    GATCCAAACTGGGATTAGATACCCCACTATGCTTAGTCGTAAACCCCAATAGTCACAA-A  969

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  970    ACAAGACTATTCGCCAGAGTACTACTAGCAACAGCCTAAAACTCAAAGGACTTGGCGGTG  1029

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  1030   CCTCATACCCATCTAGAGGAGCCTGTTCTGTAACCGATAAACCCCGATCAACCTCACCAA  1089

Query:  270    CTCTTGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  1090   CCCTTGCTACTTCAGTCTATATACCGCCATCTTCAGCAAACCCT--AAAGGGAGAAAAGT  1147

Query:  214    AAGCAGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
Sbjct:  1148   AAGCATAACCATCCTACATAAAAACGTTAGGTCAAGGTGTAACCCATGGGTTGGGAAGTA  1207

Query:  155    ATGGG-TACGTTTTCTA  140
Sbjct:  1208   ATGGGCTACATTTTCTA  1224
```

```
 Score =  100 bits (52), Expect = 7e-22
 Identities = 87/102 (85%), Gaps = 1/102 (0%)
 Strand = Plus / Minus
```

```
Query:  113    TTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATT  54
Sbjct:  1260   TTATGAAACTTAAAAACTAAAGGAGGATTTAGTAGTAAATCAAGAGCAGAGTGCTTGATT  1319

Query:  53     GAATGAGGCCATGA-AGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  1320   GAATAAGGCCATGAGGGCACGCACACACCGCCCGTCACCCTC  1361
```

```
 Score = 29.5 bits (15), Expect = 1.8
 Identities = 15/15 (100%)
 Strand = Plus / Minus


Query:  447    TCAAACTGGGATTAG  433
Sbjct:  4665   TCAAACTGGGATTAG  4679
```

```
>gi|5835638|ref|NC_001992.1| Papio hamadryas mitochondrion, complete
           genome
          Length = 16521

 Score =  241 bits (125), Expect = 4e-64
 Identities = 188/217 (86%), Gaps = 1/217 (0%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  481    CAAACTGGGATTAGACACCCCACTATCGTTGGCCCTAAACCTCAATAGTTAAAATAACAA  540

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  541    AACTATTCGCCAGAATACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTC  600

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  601    ATA-CCCCCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCCACCCCACCCTCTCT  659

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG  230
Sbjct:  660    TGCTTAGTCTATATACCGCCATCTTCAGCAAACCCTG  696
```

```
 Score =  137 bits (71), Expect = 7e-33
 Identities = 147/180 (81%), Gaps = 2/180 (1%)
 Strand = Plus / Minus


Query:  196    AAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGTACGTTTTCTACAC  137
Sbjct:  735    AAAAACGTTAGGTCAAGGTGTAACTTATGAGACGGTAAAAATGGGCTACATTTTCTACTT  794

Query:  136    ACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAGGATTTAGCAATA  77
Sbjct:  795    -CAGAAAACCC-CACGATAGCTCTTATGAAATCTAGGAGCCCAAGGAGGATTTAGCAGTA  852

Query:  76     AATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCAC  17
Sbjct:  853    AATTAAGAATAGAGTGCTTAATTGAACTAGGCCATAAGCACGCACACACCGCCCGTCAC  912
```

```
>gi|5836058|ref|NC_000891.1| Ornithorhynchus anatinus mitochondrion,
           complete genome
          Length = 17019

 Score =  237 bits (123), Expect = 6e-63
 Identities = 261/315 (82%), Gaps = 10/315 (3%)
 Strand = Plus / Minus
```

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  488    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACTCAAGTCGTTTAAT-AACAA  546

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  547    AACTACTCACCAGAGAACTACTAGCAACAGCTTAAAACTCAAAGGACTTGGCGGTGCTT-  605

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  606    -CACCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATACACCTCACCATCTTT  664

Query:  266    TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  665    TGCCACTACTGTCTATATACCGCCATCGTCAGCCAACCCTAAAAAGGAACAAAAGTAGGC  724

Query:  210    AGAAGTA-TCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  725    GTAATCATTTTTCATAAAAAACGTTAGGTCAAGGTGTAGCCTATAAGATGG-AAGAAATGG  783

Query:  151    G-TACGTTTTCTACA  138
Sbjct:  784    GCTACATTTTCTACA  798
```

```
 Score = 66.1 bits (34), Expect = 2e-11
 Identities = 66/82 (80%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  836    AAGGAGGATTTAGTAGTAAGCCAAGAATAGAGAGCTTGACTGAACTGGGCAATGAAGCAC  895

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  896    GCACACACCGCCCGTCACCCTC  917
```

```
>gi|5835666|ref|NC_002009.1| Artibeus jamaicensis mitochondrion,
            complete genome
          Length = 16651

 Score =  206 bits (107), Expect = 1e-53
 Identities = 185/219 (84%), Gaps = 5/219 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  479    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTAAAGAGTCCTCCTAACAA  538

Query:  386    AACTGTTCGCCA-GAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  539    GACTCTTCGCCAAGAGTACTACTAGCCAAAGCTTAAAACTCAAGGGACTTGGCGGTGCTT  598

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  599    CATATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATCAACCTCACCAACCC  658

Query:  267    TTG----CCCAGCCTATATACCTCCATCTTCAGCAAACC  233
Sbjct:  659    TTGTCAACTCAGCCTATATACCGCCATCTTCAGCAAACC  697
```

```
 Score =  117 bits (61), Expect = 4e-27
 Identities = 81/91 (89%)
 Strand = Plus / Minus
```

```
Query:  103    TAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCC  44
Sbjct:  836    TAAGGACTAAAGGTGGATTTAGCAGTAAATTAAGAATAGAGTGCTTAGTTGAATAAGGCC  895

Query:  43     ATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  896    ATGAAGCACGCACACACCGCCCGTCACCCTC  926
```

```
 Score = 64.1 bits (33), Expect = 7e-11
 Identities = 41/45 (91%)
 Strand = Plus / Minus


Query:  195    AAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  736    AAAACGTTAGGTCAAGGTGTAGCCTATGGGTTGGAAAGAAATGGG  780
```

```
>gi|5835037|ref|NC_001610.1| Didelphis virginiana mitochondrion,
           complete genome
          Length = 17084

 Score =  202 bits (105), Expect = 1e-52
 Identities = 239/301 (79%), Gaps = 5/301 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  491    CAAACTGGGATTAGATACCCCACTATGCTTAGTAATAAACTAAAATAATTTAACAAACAA  550

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  551    AATTATTCGCCAGAGAACTACTAGCAATTGCTTAAAACTCAAAGGACTTGGCGGTGCCCT  610

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  611    AAACCCACCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCAGACCTTATCT  670

Query:  266    TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  671    TGCCAATACAGCCTATATACCGCCATCGTCAGCTAACCTTTAAAAGAATTACAGTAAGC  730

Query:  210    AGAAGTAT-CTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  731    AAAATCATACAACATAAAAACGTTAGGTCAAGGTGTAGCATATGATAAGGAAAGTAATGG  790

Query:  151    G  151
Sbjct:  791    G  791
```

```
 Score = 83.4 bits (43), Expect = 1e-16
 Identities = 69/82 (84%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  846    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAATTAGGCAATAGGGCGC  905

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  906    GCACACACCGCCCGTCACCCTC  927
```

```
>gi|5835792|ref|NC_002080.1| Erinaceus europaeus mitochondrion,
           complete genome
          Length = 17447
```

```
 Score =  189 bits (98), Expect = 2e-48
 Identities = 189/227 (83%), Gaps = 6/227 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  494    CAAACTAGGATTAGATACCCTATTATGCTTAGCCCTAAACTTAGACAGTTACTT-AACAA  552

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  553    AACTGTACGCCAGAGAACTACGAGCTACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTT  612

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  613    ATA-CCCCCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCAATCTT  671

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGG  224
Sbjct:  672    TGCTAATTCAGCCTTTATACCGCCATCTTCAGCGAACCCTAAAAAGG  718
```

```
 Score =  114 bits (59), Expect = 6e-26
 Identities = 75/83 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  845    AAGGAGGATTTAGCAGTAAATTAAGAGTAGAGTGCTTAATTGAATTTGGCAATGAAGCAT  904

Query:  34     GCACACACCGCCCGTCACCCTCT  12
Sbjct:  905    GCACACACCGCCCGTCACCCTCT  927
```

```
>gi|5835359|ref|NC_001794.1| Macropus robustus mitochondrion, complete
           genome
         Length = 16896

 Score =  185 bits (96), Expect = 2e-47
 Identities = 249/313 (79%), Gaps = 8/313 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  491    CAAACTGGGATTAGATACCCCACTATGCTTAGCCTTAAACCTAGATAATTTAAT-AACAA  549

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  550    AATTATTCGCCAGAGAACTACTAGCCAATGCTTAAAACTCAAAGGACTTGGCGGTGC-CT  608

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  609    AAACCCACCTAGAGGAGCCTGTTCTATAATCGATAAACCCCGATAAACCCCACCTTTTCT  668

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  669    TGCCAATCCAGCCTATATACCGCCATCGTCAGCTAACCCCAACAGGGATAAAAAGTAAGC  728

Query:  210    AGAAGTATCTA-CATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  729    AAGATCATCAACCATAAAAACGTTAGGTCAAGGTGTAGCATATGAAAAGGTAAGTAATGG  788

Query:  151    G-TACGTTTTCTA  140
Sbjct:  789    GCTACATTTTCTA  801
```

```
 Score = 77.6 bits (40), Expect = 6e-15
 Identities = 68/82 (82%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  845    AAGGAGGATTTAGTAGTAAATTAAGAATAGAGAGCTTAATTGAAATAGGCAATAGGGCGC  904

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  905    GCACACACCGCCCGTCACCCTC  926
```

```
>gi|5835890|ref|NC_000860.1| Salvelinus fontinalis mitochondrion,
            complete genome
          Length = 16624

 Score =  156 bits (81), Expect = 1e-38
 Identities = 235/302 (77%), Gaps = 8/302 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGAT-CAACA  388
Sbjct:  1448   CAAACTGGGATTAGATACCCCACTATGCCTAGCCGTAAACTTTGATAGAAAAATACAACT  1507

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  1508   GA--TATCCGCCAGGGAACTACAAGCGCCAGCTTAAAACCCAAAGGACTTGGCGGTGCCT  1565

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  1566   CAGACCCACCTAGAGGAGCCTGTTCTAGAACCGATAACCCCCGTTCAACCTCACCACCTC  1625

Query:  267    TTG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  1626   TTGTTTTCCCCGCCTATATACCACCGTCGTCAGCTTACCCTGTGAAGGCCCTATAGTAAG  1685

Query:  211    CAGAAGTATCTACA-TAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  1686   CAAAATGGGCAAAACCCAAAACGTCAGGTCGAGGTGTAGCGCATGGGGTGGGAAGAAATG  1745

Query:  152    GG  151
Sbjct:  1746   GG  1747
```

```
 Score = 60.3 bits (31), Expect = 1e-09
 Identities = 65/82 (79%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1800   AAGGTGGATTTAGCAGTAAATAGAAAACAGAGAGTTCTCTTGAAACTGGCTCTGAGGCGC  1859

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1860   GCACACACCGCCCGTCACTCTC  1881
```

```
>gi|6137801|ref|NC_000934.1| Loxodonta africana mitochondrion,
            complete genome
          Length = 16866

 Score =  146 bits (76), Expect = 9e-36
 Identities = 173/219 (78%), Gaps = 4/219 (1%)
 Strand = Plus / Minus
```

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  490    CAAACTGAGATTAGATACCTCACTATGCCTAGCCCTAAACTTTGATAGCTACCTTTACAA  549

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  550    AGCTATCCGCCAGAGAACTACTAGCCAGAGCTTAAAACTTAAAGGACTTGGCGGTGCTTT  609

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  610    ATATCCACCTAGGGGAGCCTGTCTCGTAACCGATGAACCCCGATATACCTTACCGTCACT  669

Query:  266    TGC----CCAGCCTATATACCTCCATCTTCAGCAAACCC  232
Sbjct:  670    TGCTAATTCAGTCCATATACCACCATCTTCAGCAAACCC  708
```

```
 Score = 71.8 bits (37), Expect = 3e-13
 Identities = 67/82 (81%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  846    AAGGCGGATTTAGTAGTAAACTAAGAATAGAGAGCTTAATTGAACAAGGCTATGAAGCGC  905

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  906    GTACACACCGCCCGTCACTCTC  927
```

```
>gi|5835904|ref|NC_000861.1| Salvelinus alpinus mitochondrion,
            complete genome
          Length = 16659

 Score =  144 bits (75), Expect = 3e-35
 Identities = 233/302 (77%), Gaps = 8/302 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGAT-CAACA  388
Sbjct:  1482   CAAACTGGGATTAGATACCCCACTATGCCTAGCCGTAAACTTTGATAGAAAATACAACT  1541

Query:  387    AAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  1542   GA--TATCCGCCAGGGAACTACAAGCGCCAGCTTAAAACCCAAAGGACTTGGCGGTGCCT  1599

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  1600   CAGACCCACCTAGAGGAGCCTGTTCTAGAACCGATAACCCCCGTTCAACCTCACCACCTC  1659

Query:  267    TTG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAG  212
Sbjct:  1660   TTGTTTTCCCCGCCTATATACCACCGTCGTCAGCTTACCCTATGAAGGCCCGATAGTAAG  1719

Query:  211    CAGAA-GTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  1720   CAAAATGGGTAAGACCCAAAACGTCAGGTCGAGGTGTAGCGCATGGGGTGGGAAGAAATG  1779

Query:  152    GG  151
Sbjct:  1780   GG  1781
```

```
 Score = 54.5 bits (28), Expect = 5e-08
 Identities = 64/82 (78%)
 Strand = Plus / Minus
```

```
Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1834   AAGGTGGATTTAGCAGTAAACAGAAACAGAGAGTTCTCTTGAAACTGGCTCTGAGGCGC  1893

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1894   GCACACACCGCCCGTCACTCTC  1915
```

```
>gi|5902189|ref|NC_002073.3| Chrysemys picta mitochondrion, complete
           genome
          Length = 16866

 Score =  141 bits (73), Expect = 5e-34
 Identities = 247/319 (77%), Gaps = 11/319 (3%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  500    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTAGATATTTACAT--ACAA  557

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACA-GCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  558    AAATATCCGCCAGAGAATTACGAGCAAAACGCTTAAAACTCTAAGGACTTGGCGGTACCT  617

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  618    CAAACCCACCTAGAGGAGCCTGTTCTATAATCGACAATCCACGATACACCTCACCATCTC  677

Query:  267    TTGC---CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGA-GTAAG  212
Sbjct:  678    TTGCTAACCAGCCTATATACCACCGTCACCAGCTTACCCTATGAAGGGTACAAAAGTAAG  737

Query:  211    CAGAAGTATCTA---CATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAA  155
Sbjct:  738    CAAAACAATATAAACCATTAACAAGTCAGGTCAAGGTGTAGCTAATTGAGATGGAAGAAA  797

Query:  154    TGGG-TACGTTTTCTACAC  137
Sbjct:  798    TGGGCTACATTTTCTACAC  816
```

```
 Score = 56.4 bits (29), Expect = 1e-08
 Identities = 65/83 (78%)
 Strand = Plus / Minus


Query:  95     CAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  857    CAAGTAGGATTTAGCAGTAAACTGGGAACAGAGAGCCCAATTTAAACCGGTCCTGAGGTG  916

Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  917    CGCACACACCGCCCGTCACCCTC  939
```

```
>gi|5835261|ref|NC_001717.1| Oncorhynchus mykiss mitochondrion
           complete genome
          Length = 16642

 Score =  135 bits (70), Expect = 3e-32
 Identities = 176/224 (78%), Gaps = 5/224 (2%)
 Strand = Plus / Minus


Query:  370    ACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAAAGGA  311
Sbjct:  1560   ACTACAAGCGCCAGCTTAAAACCCAAAGGACTTGGCGGTGCCTCAGACCCACCTAGAGGA  1619

Query:  310    GCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG----CCCAGCCTAT  255
Sbjct:  1620   GCCTGTTCTAGAACCGATAACCCCCGTTCAACCTCACCACCCCTTGTTTTACCCGCCTAT  1679
```

```
Query:  254    ATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTATCTACATAA  195
Sbjct:  1680   ATACCACCGTCGTCAGCTTACCCTGTGAAGGCCCATAGT-AGCAAAATGGGCAAAACCA  1738

Query:  194    AAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  1739   AAACGTCAGGTCGAGGTGTAGCGCATGAGGTGGGAAGAAATGGG  1782
```

```
 Score = 46.8 bits (24), Expect = 1e-05
 Identities = 58/75 (77%)
 Strand = Plus / Minus


Query:  87     ATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACA  28
Sbjct:  1843   ATTTAGCAGTAAACAGAAAACAGAGAGTTCTCTTGAAACTGGCTCTGAGGCGCGCACACA  1902

Query:  27     CCGCCCGTCACCCTC  13
Sbjct:  1903   CCGCCCGTCACTCTC  1917
```

```
>gi|5835708|ref|NC_002012.1| Squalus acanthias mitochondrion, complete
            genome
          Length = 16738

 Score =  131 bits (68), Expect = 4e-31
 Identities = 238/313 (76%), Gaps = 8/313 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  498    CAAACTAGGATTAGATACCCTACTATGCCCAACCACAAACTTAGACAATAACCT--ACTA  555

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  556    CATTGTCCGCCAGAGTACTACAAGCGCTAGCTTAAAACCCAAAGGACTTGGCGGTGCTTC  615

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  616    AGACCCCCTAGAGGAGCCTGTTCTATAACCGATAATCCCCGTTAAACCTCACCACCCCT  675

Query:  266    TGCC----CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  676    TGCCAATACCGCCTATATACCGCCGTCGTCAGCTCACCCTGTGAAGGATAAGAAGTAAGC  735

Query:  210    AGAAGTATCT-ACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  736    AAAAAGAACTAACTCCCATACGTCAGGTCGAGGTGTAGCGAATGGAGTGGAAAGAAATGG  795

Query:  151    G-TACGTTTTCTA  140
Sbjct:  796    GCTACATTTTCTA  808
```

```
 Score = 46.8 bits (24), Expect = 1e-05
 Identities = 28/30 (93%)
 Strand = Plus / Minus


Query:  42     TGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  898    TGAAGCGCGCACACACCGCCCGTCACTCTC  927
```

```
>gi|5836002|ref|NC_000886.1| Chelonia mydas mitochondrial DNA,
            complete sequence
          Length = 16497
```

```
 Score =  129 bits (67), Expect = 1e-30
 Identities = 149/185 (80%), Gaps = 2/185 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  503    CAAACTAGGATTAGATACCCTACTATGCTTAGCCCTAAACTTAGATATTTC-ACATACAA  561

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACA-GCTTAAAACTCAAGGACTTGGCAGTGCTT  328
Sbjct:  562    AAATATCCGCCAGAGAACTACGAGCATAACGCTTAAAACTCTAAGGACTTGGCGGTACCT  621

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  622    CAAACCCCCTAGAGGAGCCTGTTCTATAATCGATAATCCACGATCTACCTCGCCATCTC  681

Query:  267    TTGCC  263
Sbjct:  682    TTGCC  686
```

```
 Score = 44.9 bits (23), Expect = 4e-05
 Identities = 63/83 (75%)
 Strand = Plus / Minus


Query:  95     CAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCA  36
Sbjct:  861    CAAGCAGGATTTAGCAGTAAACTGGAAACAGCGAGCCCAATTTAAGCCGGTCCTGAGGTG  920

Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  921    CGCACACACCGCCCGTCACCCTC  943
```

```
>gi|5835275|ref|NC_001727.1| Crossostoma lacustre mitochondrion,
           complete genome
         Length = 16558

 Score =  129 bits (67), Expect = 1e-30
 Identities = 240/314 (76%), Gaps = 9/314 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1384   CAAACTGGGATTAGATACCCCACTATGCTCAGCTATAAAC-CTAGACGTTTAATCACAAC  1442

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1443   AAACGTCCGCCAGGGTACTACGAGCGTCAGCTTAAAACCCAAAGGACTTGGCGGTGCCTT  1502

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1503   AGACCCCCTAGAGGAGCCTGTTCTAGAACCGATAACCCCCGTTAAACCTCACCACTTCT  1562

Query:  266    TG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGC  211
Sbjct:  1563   AGTCATCCCCGCCTATATACCGCCGTCGTCAGCTTACCCTGTGAAGGCTCAATAGTAAGC  1622

Query:  210    AGAAGTATCTACA--TAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATG  153
Sbjct:  1623   A-AAGTGGGCACAACCCAAAACGTCAGGTCGAGGTGTAGCGTACGAAGTGGGAAGAGATG  1681

Query:  152    GG-TACGTTTTCTA  140
Sbjct:  1682   GGCTACATTTTCTA  1695
```

```
 Score = 37.2 bits (19), Expect = 0.009
```

```
 Identities = 61/82 (74%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1738   AAGGAGGATTTAGTAGTAAAAAGGAAATAGAGTGTCCTTTTGAACCCGGCTCTGAGGCGC  1797

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1798   GTACACACCGCCCGTCACTCTC  1819
```

```
>gi|5835806|ref|NC_002081.1| Gadus morhua mitochondrion, complete
           genome
          Length = 16696

 Score =  123 bits (64), Expect = 8e-29
 Identities = 174/224 (77%), Gaps = 5/224 (2%)
 Strand = Plus / Minus


Query:  370    ACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAAAGGA  311
Sbjct:  565    ACTACGAGCAATAGCTTAAAACCCAAAGGACTTGGCGGTGCTTTAGACCCCCTAGAGGA  624

Query:  310    GCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG----CCCAGCCTAT  255
Sbjct:  625    GCCTGTTCTAGAACTGATAACCCCCGTTTAACCTCACCATCCTTGTTTTCCCCGCCTAT  684

Query:  254    ATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTATCTACATAA  195
Sbjct:  685    ATACCACCGTCGTCAGCTTACCCTGTGAAGG-AAAATAGTAAGCATAAATGCAAAGCCAA  743

Query:  194    AAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  744    AAACGTCAGGTCGAGGTGTAGCGTATGGGATGGGAAGAAATGGG  787
```

```
 Score = 56.4 bits (29), Expect = 1e-08
 Identities = 65/83 (78%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  840    AAGGAGGATTTAGCAGTAAGTAGGGACTAGAGTGCCCTGCTGAAAACGGCCCTGAAGCGC  899

Query:  34     GCACACACCGCCCGTCACCCTCT  12
Sbjct:  900    GCACACACCGCCCGTCACTCTCT  922
```

```
 Score = 52.6 bits (27), Expect = 2e-07
 Identities = 27/27 (100%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATG  420
Sbjct:  490    CAAACTGGGATTAGATACCCCACTATG  516
```

```
>gi|5835582|ref|NC_001947.1| Pelomedusa subrufa mitochondrion,
           complete genome
          Length = 16787

 Score =  121 bits (63), Expect = 3e-28
```

```
 Identities = 163/208 (78%), Gaps = 4/208 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  501    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCATGATATTTAACATAACAC  560

Query:  386    AACTGTTCGCCAGAACACTACAAGCA-ACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  561    AAATATCCGCCCGAGAACTACGAGCCTACAGCTTAAAACTTAAAGGACTTGGCGGTGTCC  620

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAACCCCAATTTACCTCACCACCTC  268
Sbjct:  621    CATACCCAACTAGAGGAGCCTGTTCTATAAGCGATTATCCACGATCAACCTTACCACCCT  680

Query:  267    TTGC---CCAGCCTATATACCTCCATCT  243
Sbjct:  681    TTGCCATCCAGCCTATATACCGCCGTCT  708


 Score = 37.2 bits (19), Expect = 0.009
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query:  34     GCACACACCGCCCGTCACC  16
Sbjct:  918    GCACACACCGCCCGTCACC  936


>gi|5835624|ref|NC_001960.1| Salmo salar mitochondrion, complete
           genome
          Length = 16665

 Score =  114 bits (59), Expect = 6e-26
 Identities = 173/225 (76%), Gaps = 5/225 (2%)
 Strand = Plus / Minus


Query:  370    ACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATATCCCTCTAAAGGA  311
Sbjct:  1564   ACTATAAGCGCCAGCTTAAAACCCAAAGGACTTGGCGGTGCCTCAGACCCACCTAGAGGA  1623

Query:  310    GCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG----CCCAGCCTAT  255
Sbjct:  1624   GCCTGTTCTAGAACCGATAACCCCCGTTCAACCTCACCACCTCTTGTTTTCCCCGCCTAT  1683

Query:  254    ATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCAGAAGTATCTACA-TA  196
Sbjct:  1684   ATACCACCGTCGTCAGCTTACCCTGTGAAGGCCTTATAGTAAGCAAAATGGGCAAAACCC  1743

Query:  195    AAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  1744   AAAACGTCAGTCGGAGGTGTAGCGCATGGGGTGGGAAGAAATGGG  1788


 Score = 62.2 bits (32), Expect = 3e-10
 Identities = 38/41 (92%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACT  406
Sbjct:  1489   CAAACTGGGATTAGATACCCCACTATGCCTAGCCGTAAACT  1529


 Score = 54.5 bits (28), Expect = 5e-08
```

```
 Identities = 64/82 (78%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCAC  35
Sbjct:  1841   AAGGTGGATTTAGCAGTAAATAGAAAATAGAGAGTTCTCTTGAAACTGGCTCTGAGGCGC  1900

Query:  34     GCACACACCGCCCGTCACCCTC  13
Sbjct:  1901   GCACACACCGCCCGTCACTCTC  1922
```

```
>gi|5835023|ref|NC_001606.1| Cyprinus carpio mitochondrion, complete
            genome
          Length = 16575

 Score =  114 bits (59), Expect = 6e-26
 Identities = 238/315 (75%), Gaps = 9/315 (2%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1413   CAAACTGGGATTAGATACCCCACTATGCTCAGCCGTAAACTCAGACATCCAGCTACAATT  1472

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1473   AGATGTCCGCCAGGGTACTACGAGCATTAGCTTAAAACCCAAAGGACCTGACGGTGTCTC  1532

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1533   AGACCCCCTAGAGGAGCCTGTTCTAGAACCGATAACCCCCGTTCAACCTCACCACTTCT  1592

Query:  266    TG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCA-CAGAGTAAG  212
Sbjct:  1593   AGCCACCCCAGCCTATATACCGCCGTCGTCAGCTTACCCTGTGAAGGTAATAAAAGTAAG  1652

Query:  211    CAGAA--GTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  1653   CAAAATGGGCACAACCCAAA-ACGTCAGGTCGAGGTGTAGCGCATGAAGTGGGAAGAAAT  1711

Query:  153    GGG-TACGTTTTCTA  140
Sbjct:  1712   GGGCTACATTTTCTA  1726
```

```
 Score = 33.4 bits (17), Expect = 0.13
 Identities = 19/20 (95%)
 Strand = Plus / Minus


Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  1830   ACACACCGCCCGTCACTCTC  1849
```

```
 Score = 27.6 bits (14), Expect = 6.9
 Identities = 18/20 (90%)
 Strand = Plus / Minus


Query:  94     AAGGAGGATTTAGCAATAAA  75
Sbjct:  1767   AAGGAGGATTTAGTAGTAAA  1786
```

```
>gi|5835498|ref|NC_000846.1| Rhea americana mitochondrion, complete
            genome
```

```
          Length = 16714

 Score =  112 bits (58), Expect = 2e-25
 Identities = 148/188 (78%), Gaps = 3/188 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  498    CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAATCCTGATACTTACCCCACCTA  557

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACA--GCTTAAAACTCAAGGACTTGGCAGTGCT  329
Sbjct:  558    AG-TATCCGCCCGAGAACTACGAGCACAAACGCTTAAAACTCTAAGGACTTGGCGGTGCC  616

Query:  328    TTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCT  269
Sbjct:  617    CTAACCCCACCTAGAGGAGCCTGTTCTATAATCGATAACCCACGATACACCCGACCATCT  676

Query:  268    CTTGCCCA  261
Sbjct:  677    CTTGCCCA  684
```

```
 Score = 39.1 bits (20), Expect = 0.002
 Identities = 24/26 (92%)
 Strand = Plus / Minus


Query:  38     GCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  909    GCACGTACATACCGCCCGTCACCCTC  934
```

```
>gi|5835373|ref|NC_001804.1| Latimeria chalumnae mitochondrion,
           complete genome
          Length = 16407

 Score =  112 bits (58), Expect = 2e-25
 Identities = 239/317 (75%), Gaps = 12/317 (3%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  506    CAAACTGGGATTAGATACCCCACTATGCTCAGCCCTAAACACAAACAATTCAAACAC--A  563

Query:  386    AACTGTTCGCCAGAACA-CTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  564    CACTGTTCGCCAGGGGAACTACAAGCGCCAGCTTCAAACCCAAAGGACTTGGCGGCACTT  623

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  624    CAAACCCACCTAGAGGAGCCTGTTCTAAAACTGACAACCCCCACCTAACCTCACCATCCC  683

Query:  267    TTGC-------CCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGT  215
Sbjct:  684    TAGCCATTAAACCAGCCTATATACCGCCGTCGCCAGCCCACCCTGTGAAGGAAATACAAT  743

Query:  214    AAGCAGAAGTATCTACA-TAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
Sbjct:  744    GGGCAAAATAAAAAAATTAAAAAACGTCAGGTCGAGGTGTAGCAAATGAGATGGGAAGAA  803

Query:  155    ATGGG-TACGTTTTCTA  140
Sbjct:  804    ATGGGCTACATTTTCTA  820
```

```
 Score = 39.1 bits (20), Expect = 0.002
 Identities = 22/23 (95%)
 Strand = Plus / Minus
```

```
Query:  35     CGCACACACCGCCCGTCACCCTC  13
Sbjct:  923    CGCACACACCGCCCGTCACTCTC  945
```

```
>gi|5835778|ref|NC_002079.1| Carassius auratus mitochondrion, complete
           genome
          Length = 16578

 Score =  110 bits (57), Expect = 9e-25
 Identities = 239/315 (75%), Gaps = 10/315 (3%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1409   CAAACTGGGATTAGATACCCCACTATGCTCAGCCGTAAACTTAGACA--TCCAACTACAA  1466

Query:  386    AAC-TGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTT  328
Sbjct:  1467   TAGATGTCCGCCAGGGTACTACGAGCATTAGCTTAAAACCCAAAGGACCTGACGGTGTCT  1526

Query:  327    TATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTC  268
Sbjct:  1527   CAGATCCCCCTAGAGGAGCCTGTTCTAGAACCGATAACCCCCGTTCAACCTCACCACTCC  1586

Query:  267    TTG----CCCAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCA-CAGAGTAA  213
Sbjct:  1587   TAGCCAACCCAGCCTATATACCGCCGTCGTCAGCTTACCCTGTGAAGGTAATAAAAGTAA  1646

Query:  212    GCAGAA-GTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAAT  154
Sbjct:  1647   GCAAAATGGGTACAACCCAAAACGTCAGGTCGAGGTGTAGCGCATGAAGTGGGAAGAAAT  1706

Query:  153    GGG-TACGTTTTCTA  140
Sbjct:  1707   GGGCTACATTTTCTA  1721
```

```
 Score = 33.4 bits (17), Expect = 0.13
 Identities = 19/20 (95%)
 Strand = Plus / Minus


Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  1824   ACACACCGCCCGTCACTCTC  1843

  Database: mito.nt
    Posted date:  Apr 14, 2003 10:43 AM
  Number of letters in database: 3,164,247
  Number of sequences in database:  129

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1023
Number of Sequences: 129
Number of extensions: 1023
```

Number of successful extensions: 355
Number of sequences better than 10.0: 106
Number of HSP's better than 10.0 without gapping: 106
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 256
length of query: 462
length of database: 3,164,247
effective HSP length: 17
effective length of query: 445
effective length of database: 3,162,054
effective search space: 1407114030
effective search space used: 1407114030
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 14 (27.6 bits)

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

BLASTX 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

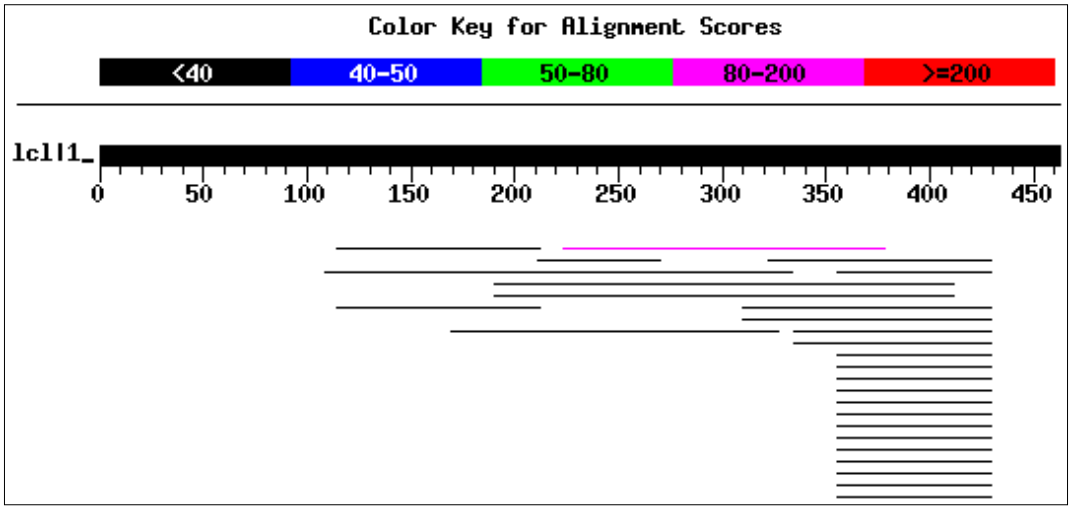
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,411,415 sequences; 454,141,287 total letters

Query= CS63win
(462 letters)

Distribution of 27 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

hypothetical protein [Ralstonia metallidurans]..S=31.6 E=4.2"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments"">



Sequences producing significant alignments:	Score (bits)	E Value
ref|XP_210340.1| similar to ATP synthase 6 [Homo sapiens]	88	4e-17
gb|AAK82669.1| envelope glycoprotein [Human immunodeficienc...	33	1.9
ref|NP_009696.1| High-Dosage Reductional segregation defect...	32	2.5
gb|ZP_00024900.1| hypothetical protein [Ralstonia metallidu...	32	4.2
gb|AAL07307.1| mandaselin long form [Homo sapiens]	31	5.5
gb|AAL07306.1| mandaselin short form [Homo sapiens]	31	5.5

gb|AAK77508.1|AF391245_1	envelope glycoprotein [Human immun...	31	5.5
gb|AAK77509.1|AF391246_1	envelope glycoprotein [Human immun...	31	5.5
gb|AAB47657.1|	envelope glycoprotein [Human immunodeficienc...	31	7.2
gb|AAB47655.1|	envelope glycoprotein [Human immunodeficienc...	31	7.2
emb|CAD10905.1|	gp160 protein [Human immunodeficiency virus...	30	9.4
ref|NP_505854.1|	Importin alpha 3 IMA-1; member of the NLS ...	30	9.4
pir||T42404	importin alpha 3 - Caenorhabditis elegans >gi|2...	30	9.4
gb|AAC27427.1|	CDC37-like gene [Homo sapiens]	30	9.4
emb|CAD10922.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10913.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10918.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10912.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10914.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10923.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10916.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10919.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10917.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10906.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10921.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10920.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4
emb|CAD10908.1|	gp160 protein [Human immunodeficiency virus 1]	30	9.4

>ref|XP_210340.1| similar to ATP synthase 6 [Homo sapiens]
Length = 376

Score = 88.2 bits (217), Expect = 4e-17
Identities = 42/52 (80%), Positives = 45/52 (86%)
Frame = -3

```
Query: 379 RQNTTSNSLKLKGLGSALYPSKGACSIIDKPQFTSPPLAQPIYLHLQQTLER 224
           R NT SNSLKLKG G A +PS+GACSIIDKPQFTSPPLAQPIY HLQQTL +
Sbjct: 226 RDNTRSNSLKLKGPGGASHPSRGACSIIDKPQFTSPPLAQPIYRHLQQTLTK 277
```

>gb|AAK82669.1| envelope glycoprotein [Human immunodeficiency virus type 1]
Length = 861

Score = 32.7 bits (73), Expect = 1.9
Identities = 16/36 (44%), Positives = 23/36 (63%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*INKTVRQNTTSNSLKLKGLGSALY 323
           TPLC+TLN N+ +N T   +T  NS  L+G+ +  Y
Sbjct: 119 TPLCVTLNCNN-VNSTNSTSTLGNSTTLEGVTNCSY 153
```

>ref|NP_009696.1| High-Dosage Reductional segregation defective. Converts reductional segregation to equational when borne on a 2um plasmid; Hdr1p [Saccharomyces cerevisiae]
sp|P38277|YBY8_YEAST HYPOTHETICAL 60.5 KD PROTEIN IN ESR1-IRA1 INTERGENIC REGION
pir||S46007 hypothetical protein YBR138c - yeast (Saccharomyces cerevisiae)
emb|CAA53496.1| YBR1014 [Saccharomyces cerevisiae]
emb|CAA85096.1| ORF YBR138c [Saccharomyces cerevisiae]
prf||2118402M YBR1014 gene
Length = 524

```
 Score = 32.3 bits (72), Expect = 2.5
 Identities = 23/75 (30%), Positives = 32/75 (42%)
 Frame = -3

Query: 334 SALYPSKGACSIIDKPQFTSPPLAQPIYLHLQQTLERPQSKQKYLHKNVRSRCSP*GGKK 155
           S LY S     +ID   FTS P+A P  +   +T E      +Y +   R R +P
Sbjct: 131 SKLYQSVSKLDLIDDKSFTSLPIAPPCNI---ETNEDDSGNNEYNNNKKRPRLNP----- 182

Query: 154 WVRFLHTEKSRDNRY 110
            V  L    ++ NRY
Sbjct: 183 -VNELRVHNNKRNRY 196
```

>gb|ZP_00024900.1| hypothetical protein [Ralstonia metallidurans]
Length = 241

```
 Score = 31.6 bits (70), Expect = 4.2
 Identities = 12/20 (60%), Positives = 14/20 (70%)
 Frame = +2

Query: 212 LTLWPFQGLLKMEVYRLGKR 271
           L LWPF G++   VYRLG R
Sbjct: 203 LALWPFNGIMLRSVYRLGSR 222
```

>gb|AAL07307.1| mandaselin long form [Homo sapiens]
Length = 209

```
 Score = 31.2 bits (69), Expect = 5.5
 Identities = 21/74 (28%), Positives = 34/74 (45%)
 Frame = -3

Query: 412 LNSNS*INKTVRQNTTSNSLKLKGLGSALYPSKGACSIIDKPQFTSPPLAQPIYLHLQQT 233
           L  N    K+ R N+ +N+  LK +   + PSK +   +D+     PPL   +++
Sbjct: 55  LGKNFDFQKSDRINSETNTKNLKSVEITMKPSKASELNLDE----LPPLNNYLHVFYYSW 110

Query: 232 LERPQSKQKYLHKN 191
              PQ   KY+H N
Sbjct: 111 YGNPQFDGKYIHWN 124
```

>gb|AAL07306.1| mandaselin short form [Homo sapiens]
Length = 195

```
 Score = 31.2 bits (69), Expect = 5.5
 Identities = 21/74 (28%), Positives = 34/74 (45%)
 Frame = -3

Query: 412 LNSNS*INKTVRQNTTSNSLKLKGLGSALYPSKGACSIIDKPQFTSPPLAQPIYLHLQQT 233
           L  N    K+ R N+ +N+  LK +   + PSK +   +D+     PPL   +++
Sbjct: 55  LGKNFDFQKSDRINSETNTKNLKSVEITMKPSKASELNLDE----LPPLNNYLHVFYYSW 110

Query: 232 LERPQSKQKYLHKN 191
              PQ   KY+H N
Sbjct: 111 YGNPQFDGKYIHWN 124
```

>gb|AAK77508.1|AF391245_1 envelope glycoprotein [Human immunodeficiency virus type 1]
Length = 860

Score = 31.2 bits (69), Expect = 5.5
Identities = 13/40 (32%), Positives = 22/40 (55%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*INKTVRQNTTSNSLKLKGLGSALYPSKG 311
           TPLC+TLN  + IN      TT+++     + ++ Y + G
Sbjct: 122 TPLCVTLNCTNAINTNATSTTTTSATATSTIATSTYDNNG 161
```

>gb|AAK77509.1|AF391246_1 envelope glycoprotein [Human immunodeficiency virus type 1]
Length = 860

Score = 31.2 bits (69), Expect = 5.5
Identities = 13/40 (32%), Positives = 22/40 (55%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*INKTVRQNTTSNSLKLKGLGSALYPSKG 311
           TPLC+TLN  + IN      TT+++     + ++ Y + G
Sbjct: 122 TPLCVTLNCTNAINTNATSTTTTSATATSTIATSTYDNNG 161
```

>gb|AAB47657.1| envelope glycoprotein [Human immunodeficiency virus type 1]
Length = 92

Score = 30.8 bits (68), Expect = 7.2
Identities = 16/32 (50%), Positives = 18/32 (56%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*INKTVRQNTTSNSLKLKGLG 335
           TPLC+TLN       T R NTTS S K+   G
Sbjct: 7   TPLCVTLNCTD-AKNTTRDNTTSGSWKMMKTG 37
```

>gb|AAB47655.1| envelope glycoprotein [Human immunodeficiency virus type 1]
Length = 87

Score = 30.8 bits (68), Expect = 7.2
Identities = 16/32 (50%), Positives = 18/32 (56%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*INKTVRQNTTSNSLKLKGLG 335
           TPLC+TLN       T R NTTS S K+   G
Sbjct: 2   TPLCVTLNCTD-AKNTTRDNTTSGSWKMMKTG 32
```

>emb|CAD10905.1| gp160 protein [Human immunodeficiency virus 1]
emb|CAD10907.1| gp160 protein [Human immunodeficiency virus 1]
Length = 857

Score = 30.4 bits (67), Expect = 9.4

```
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>ref|NP_505854.1| Importin alpha 3 IMA-1; member of the NLS receptor protein family (59.9 kD) (ima-1) [Caenorhabditis elegans]
ref|NP_741628.1| Importin alpha 3 IMA-1; member of the NLS receptor protein family (59.9 kD) (ima-1) [Caenorhabditis elegans]
sp|Q22560|IMA1_CAEEL Importin alpha-1 subunit (Karyopherin alpha-1 subunit)
pir||T24976 hypothetical protein T19B10.7 - Caenorhabditis elegans
emb|CAA98540.1| C. elegans IMA-1 protein (corresponding sequence T19B10.7) [Caenorhabditis elegans]
Length = 524

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 17/35 (48%), Positives = 20/35 (57%), Gaps = 2/35 (5%)
 Frame = +1

Query: 115 GCREI--FLCVENVPISCHLMGYTLT*RFYVDTSA 213
           GCRE   FLC E+  +  H   YT+  RFYVD  A
Sbjct: 457 GCREKLEFLC-ESQSVDIHARAYTIIDRFYVDDDA 490
```

>pir||T42404 importin alpha 3 - Caenorhabditis elegans
gb|AAB97173.1| importin alpha 1 [Caenorhabditis elegans]
Length = 524

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 17/35 (48%), Positives = 20/35 (57%), Gaps = 2/35 (5%)
 Frame = +1

Query: 115 GCREI--FLCVENVPISCHLMGYTLT*RFYVDTSA 213
           GCRE   FLC E+  +  H   YT+  RFYVD  A
Sbjct: 457 GCREKLEFLC-ESQSVDIHARAYTIIDRFYVDDDA 490
```

>gb|AAC27427.1| CDC37-like gene [Homo sapiens]
Length = 233

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 17/54 (31%), Positives = 27/54 (50%), Gaps = 1/54 (1%)
 Frame = -3

Query: 328 LYPSKGACSIIDKPQFTSPPLAQPIYLHLQQT-LERPQSKQKYLHKNVRSRCSP 170
           L+P +   S+ D PQ   PP+ +P+    Q+T ++       +LH     RCSP
Sbjct: 184 LFPRQAGMSVRDPPQLQLPPVCKPLGAPFQKTKIDTISPAPGFLH----FRCSP 233
```

>emb|CAD10922.1| gp160 protein [Human immunodeficiency virus 1]
Length = 862

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10913.1| gp160 protein [Human immunodeficiency virus 1]
Length = 862

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10918.1| gp160 protein [Human immunodeficiency virus 1]
Length = 862

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10912.1| gp160 protein [Human immunodeficiency virus 1]
Length = 862

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10914.1| gp160 protein [Human immunodeficiency virus 1]
Length = 862

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10923.1| gp160 protein [Human immunodeficiency virus 1]
Length = 859

Score = 30.4 bits (67), Expect = 9.4
Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10916.1| gp160 protein [Human immunodeficiency virus 1]
Length = 859

Score = 30.4 bits (67), Expect = 9.4
Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10919.1| gp160 protein [Human immunodeficiency virus 1]
Length = 859

Score = 30.4 bits (67), Expect = 9.4
Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10917.1| gp160 protein [Human immunodeficiency virus 1]
Length = 859

Score = 30.4 bits (67), Expect = 9.4
Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
Frame = -3

```
Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10906.1| gp160 protein [Human immunodeficiency virus 1]
Length = 858

Score = 30.4 bits (67), Expect = 9.4
Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)

```
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10921.1| gp160 protein [Human immunodeficiency virus 1]
Length = 858

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10920.1| gp160 protein [Human immunodeficiency virus 1]
Length = 858

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

>emb|CAD10908.1| gp160 protein [Human immunodeficiency virus 1]
Length = 858

```
 Score = 30.4 bits (67), Expect = 9.4
 Identities = 15/26 (57%), Positives = 18/26 (69%), Gaps = 1/26 (3%)
 Frame = -3

Query: 430 TPLCLTLNSNS*I-NKTVRQNTTSNS 356
           TPLC+TLN    + N T R NTT+NS
Sbjct: 122 TPLCVTLNCTDELKNATFRSNTTTNS 147
```

```
  Database: All non-redundant GenBank CDS
  translations+PDB+SwissProt+PIR+PRF
    Posted date:  Apr 11, 2003  2:30 AM
  Number of letters in database: 454,141,287
  Number of sequences in database:  1,411,415

Lambda     K      H
   0.318    0.135    0.401

Gapped
Lambda     K      H
   0.267   0.0410    0.140
```

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 366,435,643
Number of Sequences: 1411415
Number of extensions: 7023268
Number of successful extensions: 17093
Number of sequences better than 10.0: 54
Number of HSP's better than 10.0 without gapping: 16778
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 17092
length of database: 454,141,287
effective HSP length: 112
effective length of database: 296,062,807
effective search space used: 12138575087
frameshift window, decay const: 50, 0.1
T: 12
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

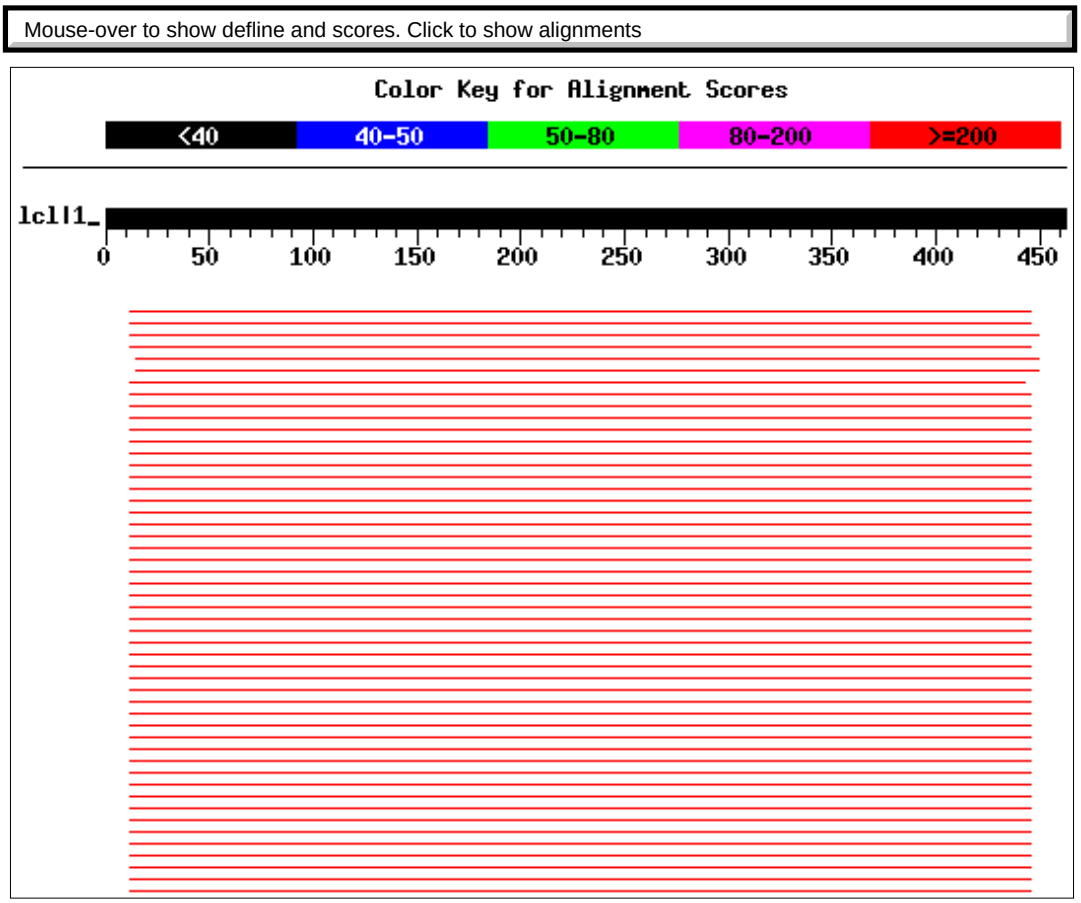
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: nt
1,048,642 sequences; 4,384,208,854 total letters

Query= CS63win
(462 letters)

Distribution of 100 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value
gb|U66061.1|U66061 Human germline T-cell receptor beta chai...	564	e-158

gb|AC021080.4|AC021080	Homo sapiens chromosome 5 clone CTC-...	527	e-147
gb|AF227907.1|AF227907	Homo sapiens chromosome 17 sequence ...	525	e-146
emb|AL356489.14|	Human DNA sequence from clone RP11-384P7 o...	512	e-142
dbj|AP003461.2|	Homo sapiens genomic DNA, chromosome 11q cl...	489	e-135
dbj|AP002829.3|	Homo sapiens genomic DNA, chromosome 11q cl...	483	e-134
emb|AL590396.13|	Human DNA sequence from clone RP11-193H5 o...	467	e-129
gb|AF347015.1|AF347015	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347014.1|AF347014	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347013.1|AF347013	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347012.1|AF347012	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347010.1|AF347010	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347007.1|AF347007	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347006.1|AF347006	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347005.1|AF347005	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347004.1|AF347004	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347003.1|AF347003	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347002.1|AF347002	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347001.1|AF347001	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF347000.1|AF347000	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346999.1|AF346999	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346998.1|AF346998	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346997.1|AF346997	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346996.1|AF346996	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346994.1|AF346994	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346993.1|AF346993	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346992.1|AF346992	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346991.1|AF346991	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346990.1|AF346990	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346988.1|AF346988	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346987.1|AF346987	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346985.1|AF346985	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346984.1|AF346984	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346983.1|AF346983	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346982.1|AF346982	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346981.1|AF346981	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346980.1|AF346980	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346979.1|AF346979	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346978.1|AF346978	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346977.1|AF346977	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346976.1|AF346976	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346975.1|AF346975	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346974.1|AF346974	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346973.1|AF346973	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346972.1|AF346972	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346971.1|AF346971	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346970.1|AF346970	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346969.1|AF346969	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346968.1|AF346968	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346967.1|AF346967	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346966.1|AF346966	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346965.1|AF346965	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346964.1|AF346964	Homo sapiens mitochondrion, complete...	460	e-127
gb|AF346963.1|AF346963	Homo sapiens mitochondrion, complete...	460	e-127
gb|AY012136.1|	Homo sapiens 12S ribosomal RNA gene, partial...	460	e-127
emb|X93334.1|HSMITG	Homo sapiens mitochondrial DNA, complet...	460	e-127

emb|X62996.1|MIHSGENOM	H.sapiens mitochondrial genome (cons...	460	e-127
dbj|D38114.1|GORMTC	Gorilla gorilla mitochondrial DNA, coml...	460	e-127
dbj|D38112.1|HUMMTA	Homo sapiens mitochondrial DNA, complet...	460	e-127
dbj|AB055387.1|	Homo sapiens mitochondrial DNA	460	e-127
gb|AF347011.1|AF347011	Homo sapiens mitochondrion, complete...	454	e-125
gb|AF347009.1|AF347009	Homo sapiens mitochondrion, complete...	454	e-125
gb|AF347008.1|AF347008	Homo sapiens mitochondrion, complete...	454	e-125
gb|AF346995.1|AF346995	Homo sapiens mitochondrion, complete...	454	e-125
gb|AF346989.1|AF346989	Homo sapiens mitochondrion, complete...	454	e-125
gb|AF346986.1|AF346986	Homo sapiens mitochondrion, complete...	454	e-125
emb|V00662.1|MIHSXX	H.sapiens mitochondrial genome	454	e-125
emb|X89832.1|MTHSLAS44	H.sapiens mitochondrial DNA for loop...	454	e-125
emb|V00710.1|MIT1HS	Human mitochondrial genes for several t...	454	e-125
dbj|D38113.1|CHPMTB	Pan troglodytes mitochondrial DNA, comp...	454	e-125
emb|X93347.1|GGMITG	Gorilla gorilla mitochondrial DNA. comp...	448	e-123
emb|X93335.1|PTMITG	Pan troglodytes mitochondrial DNA, comp...	448	e-123
emb|AL158819.14|	Human DNA sequence from clone RP11-382F24 ...	444	e-122
emb|X93342.1|PT12SM	P.troglodytes mitochondrial 12S rRNA ge...	442	e-122
emb|X93340.1|PT12ST	P.troglodytes mitochondrial 12S rRNA ge...	442	e-122
dbj|D38116.1|CHPMTE	Pan paniscus mitochondrial DNA, complet...	442	e-122
emb|X97707.1|MIPAMITGN	Pongo pygmaeus abelii mitochondrial ...	439	e-120
emb|AL109955.37|HSJ800J21	Human DNA sequence from clone RP4...	437	e-120
gb|AF069964.1|AF069964	Alouatta palliata 12S ribosomal RNA ...	423	e-116
dbj|D38115.1|ORAMTD	Pongo pygmaeus mitochondrial DNA, compl...	410	e-112
gb|AF069969.1|AF069969	Leontopithecus rosalia 12S ribosomal...	408	e-111
gb|AF121220.1|AF121220	Homo sapiens isolate 5 12S ribosomal...	406	e-111
gb|AF121219.1|AF121219	Homo sapiens isolate 4 12S ribosomal...	406	e-111
gb|AF069539.1|AF069539	Scalopus aquaticus 12S ribosomal RNA...	406	e-111
gb|AY012151.1|	Panthera onca 12S ribosomal RNA gene, partia...	402	e-109
gb|AF069975.1|AF069975	Alouatta seniculus 12S ribosomal RNA...	402	e-109
gb|AF069965.1|AF069965	Cebus apella 12S ribosomal RNA gene,...	402	e-109
gb|AF069974.1|AF069974	Saimiri sciureus 12S ribosomal RNA g...	396	e-108
gb|AY012134.1|	Hylobates concolor 12S ribosomal RNA gene, p...	394	e-107
gb|AF069967.1|AF069967	Hylobates lar 12S ribosomal RNA gene...	394	e-107
emb|X99256.1|HLMITCSEQ	Hylobates lar complete mitochondrial...	389	e-105
gb|AY012150.1|	Leopardus pardalis 12S ribosomal RNA gene, p...	387	e-105
gb|AF069980.1|AF069980	Callicebus moloch 12S ribosomal RNA ...	385	e-104
emb|Y08505.1|MIPL12S	P.leo mitochondrial 12S rRNA gene	383	e-104
gb|AF069966.1|AF069966	Chiropotes satanas 12S ribosomal RNA...	383	e-104
emb|AJ005780.1|RRAJ5780	Rattus rattus mitochondrial 12S rRN...	381	e-103
gb|AF069977.1|AF069977	Aotus trivirgatus 12S ribosomal RNA ...	381	e-103
gb|AY012132.1|	Ateles fusciceps 12S ribosomal RNA gene, par...	377	e-102
emb|Y08506.1|MIHA12SR	H.auropunctatus mitochondrial 12S rRN...	375	e-101
gb|AF069968.1|AF069968	Lagothrix lagotricha 12S ribosomal R...	373	e-101

>gb|U66061.1|U66061 Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1,
TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1,
TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1,
TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7,
TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, TCRBJ1S3, TCRBJ1S4,
TCRBJ1S5, TCRBJ1S6, TCRBC1, TCRBD2, TCRBJ2S1, TCRBJ2S2,
TCRBJ2S3, TCRBJ2S4, TCRBJ2S5, TCRBJ2S6, TCRBJ2S7, TCRBC2,
TCRBV20S1A1N2 genes from bases 452324 to 684973 (section
3 of 3)
Length = 232650

```
 Score =  564 bits (293), Expect = e-158
 Identities = 395/436 (90%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446     CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  46980   CAAACTGGGATTAGATACCCCACTAGGCTTAGCCCTAAACTCCAATAGTTAAATCAACAA  47039

Query:  386     AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  47040   AACTATTCCCCAGAACACTACAAGCAATAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  47099

Query:  326     ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  47100   ATATCCCTCTAGAGGAGCCTGTTCTATAATGGATAAACCCCAATTTACCTCACCACTTCT  47159

Query:  266     TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCT-GGAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  47160   TGCTCAGCCTATATACCATCATCTTCAGCAAACCCTAGTAAAAGTCACAAAGTAAGCACA  47219

Query:  207     AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  47220   AGTATCTACATAAAAACATTAGGTCAAGGTGTAGCCCATGAGGCGGTAAGAAATGGGCTA  47279

Query:  148     CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  47280   CATTTTCTACACCCAG-AAAATCTC---ACAACCCTTATGAAATCTAAGGGCTCAAGGAG  47335

Query:  88      GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  47336   GATTCAGCAGTATATTAAGAGCAGAGTGCTTAATTGGATGAGGCCATAAAGCACACACAC  47395

Query:  28      ACCGCCCGTCACCCTC  13
Sbjct:  47396   AATGCCCATCACCCTC  47411
```

```
>gb|AC021080.4|AC021080 Homo sapiens chromosome 5 clone CTC-203K17, complete sequence
          Length = 103522

 Score =  527 bits (274), Expect = e-147
 Identities = 390/438 (89%), Gaps = 5/438 (1%)
 Strand = Plus / Plus


Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  79078   GAGGGTGACAGGCAGTGTGTGCATGCTTTATGGCCTTATTCAATTAAGCACTCTGCTCCT  79137

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  79138   AATTTACTGCTAAATCCTCCTTGGGCCCTTAGGTTTCATAAGGGTTGTTATGAGATTTT-  79196

Query:  133     CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCAC--CTCATGGGCTACACCTTGACCTAA  189
Sbjct:  79197   CTAGGAGTAGAAAATATAGCCCATTTCTTACCACACCTCGTGGGCTACAACTTGACCTAA  79256

Query:  190     CGTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGA  249
Sbjct:  79257   CGTTTTTACGTAGATATTTGTGCTTACTTTGCAGCCTTACTAGGGTTTGCTGAAGATGGA  79316

Query:  250     GGTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGAT-TATAGAACAG  308
Sbjct:  79317   AGTATATAGGCTGAGCAAGAGGTGGTGAGGTAAATTGGAGTTTATCAATATATAGAACAG  79376

Query:  309     GCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTA  368
Sbjct:  79377   GCTCCTCTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTATTGCTTGTA  79436

Query:  369     GTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGG  428
Sbjct:  79437   GTGTTCTGGTGAATAGTTTTGTTGATTTAACTATTGGAGTTTAGGGCTAAGCATAGTGGG  79496

Query:  429     GTATCTAATCCCAGTTTG  446
Sbjct:  79497   GTATCTAATCCCAGTTTG  79514
```

>gb|AF227907.1|AF227907 Homo sapiens chromosome 17 sequence containing mitochondrial genome
insertion
Length = 14722

Score = 525 bits (273), Expect = e-146
Identities = 391/440 (88%), Gaps = 4/440 (0%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCA  391
Sbjct:  3811   GATTCAAACTGGGATTAGATACCCCACTATGCTCAGCCCTAAACTTCAACAGTTAAATCA  3870

Query:  390    ACAAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTG  331
Sbjct:  3871   ACAAAACTGCTCGCCAGAACACTAGGAGCAACAGCTTAAAACTCAAAGGACCTGGCGGTG  3930

Query:  330    CTTTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCAC  271
Sbjct:  3931   CTTCACATCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCCAATTCACCTCACCAC  3990

Query:  270    CTCTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAG  212
Sbjct:  3991   CTCTTGCTCAACCCATATACCGCCATCTTCAGCAAACCCTGACAAAGGCCACAAAGTAAG  4050

Query:  211    CAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGG  152
Sbjct:  4051   CACAAGTATCTACATAAAAATGTTAGGTCAAGGTGTAGCCTATGAGGTGGCAAGAAATGG  4110

Query:  151    G-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAA  93
Sbjct:  4111   GCTACATTTTCTAC-CCCAGAAAATTCT-ACAATAACCCTTATGAAACCTGAGGGTCCAA  4168

Query:  92     GGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGC  33
Sbjct:  4169   GGAGGATTTAGTAGTAAATTAAGAACAGAGTGCTTAATTGAATAGGGCCATAAAGCACGC  4228

Query:  32     ACACACCGCCCGTCACCCTC  13
Sbjct:  4229   ACACACCACCCATCACCCTC  4248
```

>emb|AL356489.14| Human DNA sequence from clone RP11-384P7 on chromosome 9 Contains the
TRBV25OR9-2 gene for T cell receptor beta variable
25/OR9-2 (TRBV25/OR9-2, T-cell receptor beta variable
region 11 orphan (TCRBV110)), the PTENP1 gene for
phosphatase and tensin homolog (mutated in multiple
advanced cancers 1) pseudogene 1 (PTH2, PTEN2, PSIPTEN),
a novel T-cell receptor beta variable region protein, and
the 5' end of the PRSS4 gene for "protease, serine, 4"
(trypsin 4, brain (TRY4), mesotrypsinogen (MTG)).
Contains ESTs>
Length = 130639

Score = 512 bits (266), Expect = e-142
Identities = 389/438 (88%), Gaps = 7/438 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTAT--GCTTAACCCTAAACTCGAATAGTTAGATCAAC  389
Sbjct:  2040   CAAACTGGGATTATATACCCCCCAATACGCTTAGCCCTAAACTCCAATAGTTAAATCAAC  2099

Query:  388    AAAACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCT  329
Sbjct:  2100   AGAACTATTCACCAGAACACTACAAGCAATAGCTTAAAACTCAAAGGACTTGGCGGTGCT  2159

Query:  328    TTATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCT  269
```

```
Sbjct:  2160    TTATATCCCTCTAGAGGAGCCTGTTCTATAATGGATAAAACCCAATTTGCCTCACCACCT  2219

Query:  268     CTTGCCCAGCCTATATACCTCCATCTTCAGCAAACCCT-GGAAAGGCCACAGAGTAAGCA  210
Sbjct:  2220    CTTGCTCAGCCTATATACCACTGTCTTCAGCAAACCCTAGCAAAGGCTGCAAAGTAAGCA  2279

Query:  209     GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-  151
Sbjct:  2280    CAAGTATCTACGTAAAAATGCTGGGTCAATGTGTAGCCCA--CGGTGGTAAGAAATGGGC  2337

Query:  150     TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  2338    TACATTTTCTACACCCAG-AAAATCTCACGACAACCCTTATGAAATCTAAGGGCTCAAGG  2396

Query:  90      AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  2397    AGGATTTAGCAGTACATTAAGAGCAGAGTGCTTAATTGAATGAGGCCATAAAGCACGCAC  2456

Query:  30      ACACCGCCCGTCACCCTC  13
Sbjct:  2457    ACAATGCCCGTCACCCTC  2474
```

>dbj|AP003461.2| Homo sapiens genomic DNA, chromosome 11q clone:RP11-37O16, complete sequence
Length = 74640

Score = 489 bits (254), Expect = e-135
Identities = 384/439 (87%), Gaps = 5/439 (1%)
Strand = Plus / Plus

```
Query:  16      GGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAAT  75
Sbjct:  16738   GGTGACAGGCAGTGTGTGTGTGCTTCATGGCCTTATTCAACCAAGCACTCTACTCTTGGT  16797

Query:  76      TTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTTCTG  135
Sbjct:  16798   TTACTGCTAAATCCTCCTTGAGTCTTTTGATTTCATAAAGGTTGTCGTGAGATTTT-CTG  16856

Query:  136     TGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTT  194
Sbjct:  16857   GGTATAGAAAATGTAGCCCATTTCTTCCCACCTCATGAGCTACACCTTGACCTAATGTTT  16916

Query:  195     TTATGTAGAT-ACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTA  253
Sbjct:  16917   TTATGTGTATTACTTGTGCTTACTCTATAACCTTTTTAGGGTTTGCTGAAGATGGCGGTA  16976

Query:  254     TATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  311
Sbjct:  16977   TATAGGCTGGGGGCAAGAGGTGGTGAGGTAGATCGGGGTTTATAGATTATAGAACAGGCT  17036

Query:  312     CCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  371
Sbjct:  17037   CCCCTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTATTGCTTCTAGTA  17096

Query:  372     TTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTA  431
Sbjct:  17097   TTCTGGCGAATGGTTTTGTTAATATAACTATTATAGTTTAGGGCTAAGCATAGTGGGGTA  17156

Query:  432     TCTAATCCCAGTTTGAATC  450
Sbjct:  17157   TCTAACCCCAGTTTGGATC  17175
```

>dbj|AP002829.3| Homo sapiens genomic DNA, chromosome 11q clone:RP11-641I15, complete sequences
Length = 182389

Score = 483 bits (251), Expect = e-134
Identities = 383/439 (87%), Gaps = 5/439 (1%)
Strand = Plus / Plus

```
Query:  16      GGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTCAAT  75
Sbjct:  2342    GGTGACAGGCAGTGTGTGTGTGCTTCATGGCCTTATTCAACCAAGCACTCTACTCTTGGT  2401

Query:  76      TTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTTCTG  135
Sbjct:  2402    TTACTGCTAAATCCTCCTTGAGTCTTTTGATTTCATAAAGGTTGTCGTGAGATTTT-CTG  2460

Query:  136     TGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGCTACACCTTGACCTAACGTTT  194
Sbjct:  2461    GGTATAGAAAATGTAGCCCATTTCTTCCCACCTCATGAGCTACACCTTGACCTAATGTTT  2520

Query:  195     TTATGTAGAT-ACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTA  253
Sbjct:  2521    TTATGTGTATTACTTGTGCTTACTCTATAACCTTTTTAGGGTTTGCTGAAGATGGCGGTA  2580

Query:  254     TATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCT  311
Sbjct:  2581    TATAGGCTGGGGGCAAGAGGTGGTGAGGTAGATCGGGGTTTATAGATTATAGAACAGGCT  2640

Query:  312     CCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTG  371
Sbjct:  2641    CCCTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTATTGCTTCTAGTA  2700

Query:  372     TTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTA  431
Sbjct:  2701    TTCTGGTGAATGGTTTTGTTAATATAACTATTATAGTTTAGGGCTAAGCATAGTGGGGTA  2760

Query:  432     TCTAATCCCAGTTTGAATC  450
Sbjct:  2761    TCTAACCCCAGTTTGGATC  2779
```

>emb|AL590396.13| Human DNA sequence from clone RP11-193H5 on chromosome 1, complete sequence

Length = 122108

Score = 467 bits (243), Expect = e-129
Identities = 376/435 (86%), Gaps = 4/435 (0%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  47178   GAGGGTGACGGGCGGTGTGTGCATGCTTCATGGCCTTATTCAACCAAGCACTCTACTCTT  47237

Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  47238   GGTTTCCTGCTAAATTCTCCTTGAGCCCTTAGATTTCATAAGGGTTGTAGTAATATTTT-  47296

Query:  133     CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACG  191
Sbjct:  47297   CTGGGTATAGAAAATGTAGCCCATTTCTTGCCACCTCATGGGCTACGCCTTGACCTAACG  47356

Query:  192     TTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  47357   TTTTTATGTGTGTACTTGTGCTTACTTTATTACCTTTTTAGGGTTTACTGAAGATGGCAG  47416

Query:  252     TATATAGGCTGGG--CAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGG  309
Sbjct:  47417   TATATAGGCTGGGGGCAAGAGGTGGTGAGGTATATCGGGGTTTATCGATTATAGAACAGG  47476

Query:  310     CTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAG  369
Sbjct:  47477   CTGCTCTAGAGGGGTATAAAGTACCTCCAAGTCCTTTGAATTTTAAGCTGTTGCTTGCAG  47536

Query:  370     TGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGG  429
Sbjct:  47537   TATTCTGGCGAATGGTTTTGTTAGTTTAACTATTAGAGCTTAGGGCTAAGCACAGTGGGT  47596

Query:  430     TATCTAATCCCAGTT  444
Sbjct:  47597   TATCTAATCCCAGTT  47611
```

>gb|AF347015.1|AF347015 Homo sapiens mitochondrion, complete genome

Length = 16571

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF347014.1|AF347014 Homo sapiens mitochondrion, complete genome
Length = 16567

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1065   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1124

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1125   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1184

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1185   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1244

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1245   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1304

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1305   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1364

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1365   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1420

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1421   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1480

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1481   ACCGCCCGTCACCCTC  1496
```

>gb|AF347013.1|AF347013 Homo sapiens mitochondrion, complete genome
Length = 16566

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1063  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1122

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1123  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1182

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1183  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1242

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1243  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1302

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1303  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1362

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1363  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1418

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1419  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1478

Query:  28    ACCGCCCGTCACCCTC  13
Sbjct:  1479  ACCGCCCGTCACCCTC  1494
```

>gb|AF347012.1|AF347012 Homo sapiens mitochondrion, complete genome
Length = 16567

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1063  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1122

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1123  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1182

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1183  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1242

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1243  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1302

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1303  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1362

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1363  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1418

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
```

```
Sbjct:  1419   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1478

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1479   ACCGCCCGTCACCCTC  1494
```

>gb|AF347010.1|AF347010 Homo sapiens mitochondrion, complete genome

Length = 16570

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF347007.1|AF347007 Homo sapiens mitochondrion, complete genome

Length = 16560

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366
```

```
Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF347006.1|AF347006 Homo sapiens mitochondrion, complete genome
Length = 16568

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1482   ACCGCCCGTCACCCTC  1497
```

>gb|AF347005.1|AF347005 Homo sapiens mitochondrion, complete genome
Length = 16572

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1069   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1128

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1129   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1188

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1189   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1248

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
```

```
Sbjct:  1249   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1308

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1309   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1368

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1369   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1424

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1425   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1484

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1485   ACCGCCCGTCACCCTC  1500
```

>gb|AF347004.1|AF347004 Homo sapiens mitochondrion, complete genome

Length = 16572

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1070   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1129

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1130   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1189

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1190   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1249

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1250   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1309

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1310   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1369

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1370   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1425

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1426   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1485

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1486   ACCGCCCGTCACCCTC  1501
```

>gb|AF347003.1|AF347003 Homo sapiens mitochondrion, complete genome

Length = 16570

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187
```

```
Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF347002.1|AF347002 Homo sapiens mitochondrion, complete genome
Length = 16572

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1070   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1129

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1130   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1189

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1190   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1249

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1250   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1309

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1310   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1369

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1370   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1425

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1426   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1485

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1486   ACCGCCCGTCACCCTC  1501
```

>gb|AF347001.1|AF347001 Homo sapiens mitochondrion, complete genome
Length = 16561

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
```

```
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF347000.1|AF347000 Homo sapiens mitochondrion, complete genome

```
          Length = 16569

 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346999.1|AF346999 Homo sapiens mitochondrion, complete genome

```
          Length = 16562

 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
```

Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1069  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1128

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1129  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1188

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1189  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1248

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1249  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1308

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1309  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1368

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1369  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1424

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1425  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1484

Query:  28    ACCGCCCGTCACCCTC  13
Sbjct:  1485  ACCGCCCGTCACCCTC  1500
```

>gb|AF346998.1|AF346998 Homo sapiens mitochondrion, complete genome
Length = 16561

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28    ACCGCCCGTCACCCTC  13
Sbjct:  1484  ACCGCCCGTCACCCTC  1499
```

>gb|AF346997.1|AF346997 Homo sapiens mitochondrion, complete genome

Length = 16567

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28    ACCGCCCGTCACCCTC  13
Sbjct:  1482  ACCGCCCGTCACCCTC  1497
```

>gb|AF346996.1|AF346996 Homo sapiens mitochondrion, complete genome

Length = 16566

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1065  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1124

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1125  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1184

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1185  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1244

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1245  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1304

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1305  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1364

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1365  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1420

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1421  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1480
```

```
Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1481   ACCGCCCGTCACCCTC  1496
```

>gb|AF346994.1|AF346994 Homo sapiens mitochondrion, complete genome
Length = 16569

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1482   ACCGCCCGTCACCCTC  1497
```

>gb|AF346993.1|AF346993 Homo sapiens mitochondrion, complete genome
Length = 16558

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1065   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1124

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1125   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1184

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1185   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1244

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1245   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1304

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1305   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1364

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1365   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1420
```

```
Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1421   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1480

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1481   ACCGCCCGTCACCCTC  1496
```

>gb|AF346992.1|AF346992 Homo sapiens mitochondrion, complete genome

Length = 16571

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGCG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF346991.1|AF346991 Homo sapiens mitochondrion, complete genome

Length = 16570

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306
```

```
Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346990.1|AF346990 Homo sapiens mitochondrion, complete genome

Length = 16569

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346988.1|AF346988 Homo sapiens mitochondrion, complete genome

Length = 16569

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246
```

```
Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346987.1|AF346987 Homo sapiens mitochondrion, complete genome
Length = 16566

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1482   ACCGCCCGTCACCCTC  1497
```

>gb|AF346985.1|AF346985 Homo sapiens mitochondrion, complete genome
Length = 16567

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1065   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1124
```

```
Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1125   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1184

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1185   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1244

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1245   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1304

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1305   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1364

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1365   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1420

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1421   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1480

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1481   ACCGCCCGTCACCCTC  1496
```

>gb|AF346984.1|AF346984 Homo sapiens mitochondrion, complete genome
Length = 16570

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF346983.1|AF346983 Homo sapiens mitochondrion, complete genome
Length = 16569

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346982.1|AF346982 Homo sapiens mitochondrion, complete genome
Length = 16569

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346981.1|AF346981 Homo sapiens mitochondrion, complete genome
Length = 16570

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF346980.1|AF346980 Homo sapiens mitochondrion, complete genome
Length = 16570

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF346979.1|AF346979 Homo sapiens mitochondrion, complete genome
Length = 16569

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422  GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28    ACCGCCCGTCACCCTC  13
Sbjct:  1482  ACCGCCCGTCACCCTC  1497
```

>gb|AF346978.1|AF346978 Homo sapiens mitochondrion, complete genome
Length = 16569

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067  CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127  AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187  ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266   TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247  TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207   AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307  AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148   CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367  CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88    GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
```

```
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346977.1|AF346977 Homo sapiens mitochondrion, complete genome

Length = 16569

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346976.1|AF346976 Homo sapiens mitochondrion, complete genome

Length = 16570

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366
```

```
Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346975.1|AF346975 Homo sapiens mitochondrion, complete genome

Length = 16567

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1065   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1124

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1125   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1184

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1185   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1244

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1245   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1304

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1305   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1364

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1365   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1420

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1421   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1480

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1481   ACCGCCCGTCACCCTC  1496
```

>gb|AF346974.1|AF346974 Homo sapiens mitochondrion, complete genome

Length = 16571

```
 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1069   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1128

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1129   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1188

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1189   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1248

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
```

```
Sbjct:  1249   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1308

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1309   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1368

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1369   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1424

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1425   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1484

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1485   ACCGCCCGTCACCCTC  1500
```

>gb|AF346973.1|AF346973 Homo sapiens mitochondrion, complete genome
Length = 16570

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF346972.1|AF346972 Homo sapiens mitochondrion, complete genome
Length = 16570

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1068   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1127

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1128   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1187
```

```
Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1188   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1247

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1248   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1307

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1308   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1367

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1368   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1423

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1424   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1483

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1484   ACCGCCCGTCACCCTC  1499
```

>gb|AF346971.1|AF346971 Homo sapiens mitochondrion, complete genome
Length = 16567

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1065   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1124

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1125   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1184

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1185   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1244

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1245   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1304

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1305   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1364

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1365   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1420

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1421   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1480

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1481   ACCGCCCGTCACCCTC  1496
```

>gb|AF346970.1|AF346970 Homo sapiens mitochondrion, complete genome
Length = 16570

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
```

```
Sbjct:  1067   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1126

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1127   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1186

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1187   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1246

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1247   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1306

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1307   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1366

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1367   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1422

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1423   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1482

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1483   ACCGCCCGTCACCCTC  1498
```

>gb|AF346969.1|AF346969 Homo sapiens mitochondrion, complete genome

Length = 16567

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)
Strand = Plus / Minus

```
Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1482   ACCGCCCGTCACCCTC  1497
```

>gb|AF346968.1|AF346968 Homo sapiens mitochondrion, complete genome

Length = 16567

Score = 460 bits (239), Expect = e-127
Identities = 377/436 (86%), Gaps = 6/436 (1%)

```
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1066   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1125

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1126   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1185

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1186   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1245

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1246   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1305

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1306   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1365

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1366   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1421

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1422   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1481

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1482   ACCGCCCGTCACCCTC  1497
```

```
>gb|AF346967.1|AF346967 Homo sapiens mitochondrion, complete genome
          Length = 16567

 Score =  460 bits (239), Expect = e-127
 Identities = 377/436 (86%), Gaps = 6/436 (1%)
 Strand = Plus / Minus


Query:  446    CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  1065   CAAACTGGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAA  1124

Query:  386    AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  1125   AACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTC  1184

Query:  326    ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  1185   ATATCCCTCTAGAGGAGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCT  1244

Query:  266    TGCCCAGCCTATATACCTCCATCTTCAGCAAACCCTG-GAAAGGCCACAGAGTAAGCAGA  208
Sbjct:  1245   TGCTCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCA  1304

Query:  207    AGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-TA  149
Sbjct:  1305   AGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTA  1364

Query:  148    CGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGGAG  89
Sbjct:  1365   CATTTTCTAC-CCCAGAAAACT---ACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTG  1420

Query:  88     GATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACAC  29
Sbjct:  1421   GATTTAGCAGTAAACTGAGAGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACAC  1480

Query:  28     ACCGCCCGTCACCCTC  13
Sbjct:  1481   ACCGCCCGTCACCCTC  1496
```

Database: nt

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    Posted date:  Apr 15, 2003  3:54 PM
  Number of letters in database: 4,294,869,287
  Number of sequences in database:  1,020,755

  Database: db/nt.01
    Posted date:  Apr 15, 2003  3:55 PM
  Number of letters in database: 89,339,567
  Number of sequences in database:  27,887

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1,134,657
Number of Sequences: 1048642
Number of extensions: 1134657
Number of successful extensions: 79698
Number of sequences better than 10.0: 4472
Number of HSP's better than 10.0 without gapping: 4440
Number of HSP's successfully gapped in prelim test: 32
Number of HSP's that attempted gapping in prelim test: 66087
Number of HSP's gapped (non-prelim): 10511
length of query: 462
length of database: 4,384,208,854
effective HSP length: 24
effective length of query: 438
effective length of database: 4,359,041,446
effective search space: 1909260153348
effective search space used: 1909260153348
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)
```

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

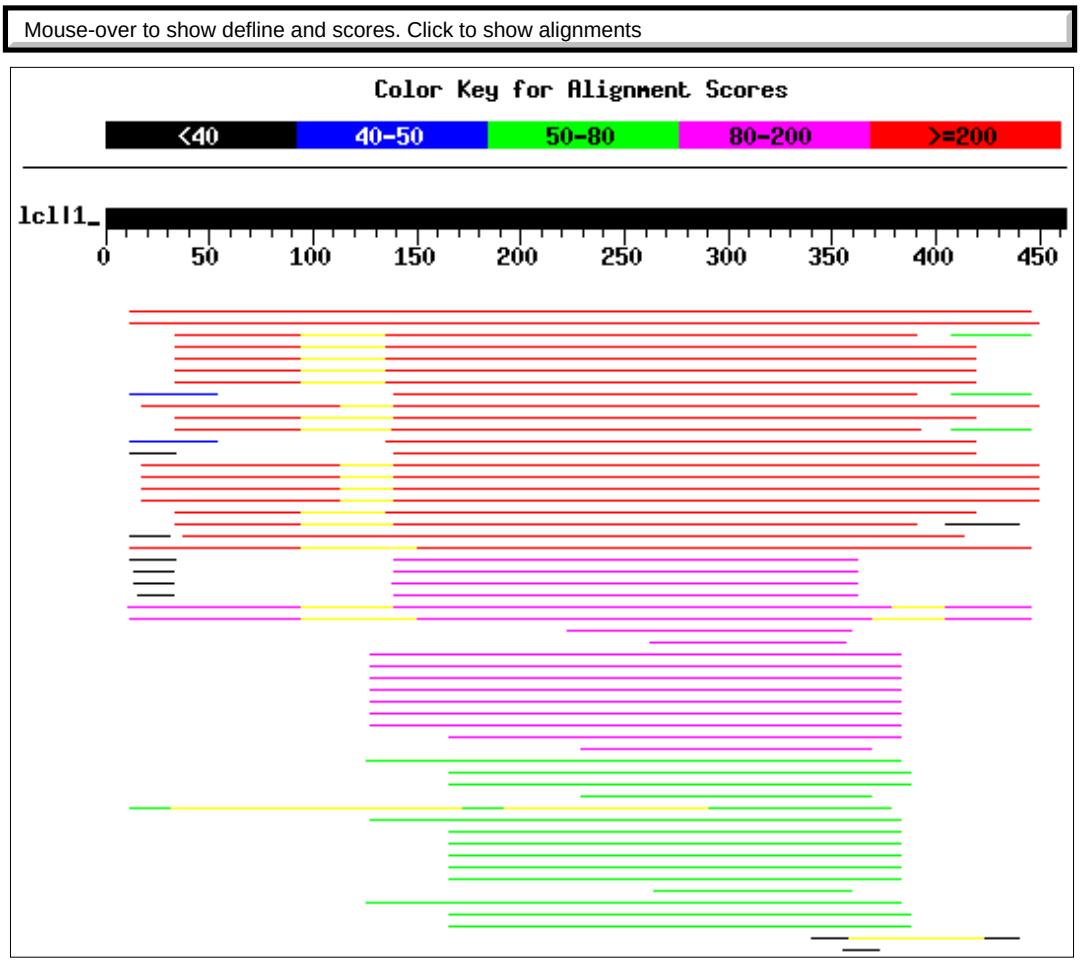
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: PDB nucleotide database
31,879 sequences; 89,510,763 total letters

Query= CS63win
(462 letters)

Distribution of 142 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value

gb|AC021080.4|AC021080	Homo sapiens chromosome 5 clone CTC-...	527	e-149
lcl|unknown	Unknown	341	9e-93
gb|U12850.1|PHU12850	Phocarctos hookeri mitochondrion 12S r...	256	3e-67
gb|U12854.1|UAU12854	Ursus arctos mitochondrion 12S ribosom...	248	5e-65
gb|U12840.1|AFU12840	Arctocephalus forsteri CS21 mitochondr...	248	5e-65
gb|U12838.1|AFU12838	Arctocephalus forsteri T48 mitochondri...	248	5e-65
gb|U12836.1|AFU12836	Arctocephalus forsteri K29 mitochondri...	248	5e-65
gb|U12832.1|EJU12832	Eumetopias jubatus mitochondrion 12S r...	248	5e-65
gb|AF387077.1|AF387077	Eospalax baileyi isolate 7 12S ribos...	244	8e-64
gb|U12830.1|CUU12830	Callorhinus ursinus mitochondrion 12S ...	242	3e-63
gb|U12828.1|CFU12828	Canis familiaris mitochondrion 12S rRN...	242	3e-63
gb|U12852.1|PLU12852	Procyon lotor mitochondrion 12S riboso...	237	2e-61
gb|U12826.1|AFU12826	Ailurus fulgens mitochondrion 12S rRNA...	237	2e-61
gb|AF387080.1|AF387080	Eospalax baileyi isolate 10 12S ribo...	233	2e-60
gb|AF387079.1|AF387079	Eospalax baileyi isolate 9 12S ribos...	233	2e-60
gb|AF387078.1|AF387078	Eospalax baileyi isolate 8 12S ribos...	233	2e-60
gb|AF387076.1|AF387076	Eospalax baileyi isolate 6 12S ribos...	233	2e-60
lcl|unknown	Unknown	231	9e-60
gb|U12846.1|MSU12846	Monachus schauinslandi mitochondrion 1...	227	1e-58
gb|U12842.1|LWU12842	Leptonychotes weddelli mitochondrion 1...	227	1e-58
gb|U12834.1|ELU12834	Enhydra lutris mitochondrion 12S rRNA ...	225	5e-58
gb|AF348079.1|AF348079	Echinosorex gymnura mitochondrion, c...	206	3e-52
gb|AF249982.1|AF249982	Raphicerus sharpei 12S ribosomal RNA...	198	6e-50
gb|AF249981.1|AF249981	Litocranius walleri 12S ribosomal RN...	194	9e-49
gb|AF249984.1|AF249984	Sylvicapra grimmia 12S ribosomal RNA...	191	1e-47
gb|AF249983.1|AF249983	Raphicerus melanotis 12S ribosomal R...	183	3e-45
gb|AF154053.1|AF154053	Mertensiella luschani mitochondrion,...	166	4e-40
gb|AF392054.1|AF392054	Oncorhynchus tshawytscha mitochondri...	137	2e-31
gb|AY016018.1|AH010362S1	Mullerornis agilis 12S ribosomal R...	85	8e-16
gb|U33726.1|U33726	Paraucheniptera sp. 12S ribosomal RNA g...	85	8e-16
gb|U33649.1|ALU33649	Apteronotus leptorhynchus 12S ribosoma...	81	1e-14
gb|AF335051.1|AF335051	Mabuya stangeri specimen-voucher Ras...	81	1e-14
gb|AF335049.1|AF335049	Mabuya spinalis specimen-voucher Fog...	81	1e-14
gb|AF335045.1|AF335045	Mabuya delalandii specimen-voucher F...	81	1e-14
gb|AF335041.1|AF335041	Mabuya delalandii specimen-voucher S...	81	1e-14
gb|AF335025.1|AF335025	Mabuya delalandii specimen-voucher F...	81	1e-14
gb|AF335021.1|AF335021	Mabuya delalandii specimen-voucher F...	81	1e-14
gb|AF335019.1|AF335019	Mabuya delalandii specimen-voucher S...	81	1e-14
gb|AF335017.1|AF335017	Mabuya delalandii specimen-voucher S...	81	1e-14
gb|AF335071.1|AF335071	Mabuya fogoensis specimen-voucher S....	80	5e-14
gb|AF335035.1|AF335035	Mabuya spinalis specimen-voucher Mai...	80	5e-14
gb|AF335031.1|AF335031	Mabuya vaillanti specimen-voucher Fo...	80	5e-14
gb|U33693.1|U33693	Campostoma anomalum 12S ribosomal RNA ge...	78	2e-13
gb|AY035830.1|	Mesalina rubropunctata strain AHC-5 12S ribo...	76	7e-13
gb|U33660.1|U33660	Chaca sp. 12S ribosomal RNA gene, partia...	76	7e-13
gb|AF335069.1|AF335069	Mabuya spinalis specimen-voucher Fog...	76	7e-13
gb|AF335053.1|AF335053	Mabuya fogoensis specimen-voucher S....	76	7e-13
gb|AF335033.1|AF335033	Mabuya delalandii specimen-voucher B...	76	7e-13
gb|AF335029.1|AF335029	Mabuya fogoensis specimen-voucher S....	76	7e-13
gb|AF335027.1|AF335027	Mabuya fogoensis specimen-voucher S....	76	7e-13
gb|AF335023.1|AF335023	Mabuya fogoensis specimen-voucher S....	76	7e-13
gb|AF335077.1|AF335077	Mabuya vaillanti specimen-voucher Sa...	74	2e-12
gb|AF335075.1|AF335075	Mabuya vaillanti specimen-voucher Sa...	74	2e-12
gb|AF335073.1|AF335073	Mabuya spinalis specimen-voucher Mai...	74	2e-12

gb|AF335047.1|AF335047	Mabuya vaillanti specimen-voucher Fo...	74	2e-12
gb|AF335037.1|AF335037	Mabuya salensis specimen-voucher Boa...	74	2e-12
gb|AF285429.1|AF285429	Acnodon normani 12S ribosomal RNA ge...	72	9e-12
gb|U33735.1|CCU33735	Chanos chanos 12S ribosomal RNA gene, ...	72	9e-12
gb|U33714.1|U33714	Noturus exilis 12S ribosomal RNA gene, p...	70	4e-11
gb|AF335067.1|AF335067	Mabuya spinalis specimen-voucher San...	70	4e-11
gb|AF335065.1|AF335065	Mabuya fogoensis specimen-voucher S....	70	4e-11
gb|AF335063.1|AF335063	Mabuya stangeri specimen-voucher S.V...	70	4e-11
gb|AF335061.1|AF335061	Mabuya fogoensis specimen-voucher S....	70	4e-11
gb|AF335057.1|AF335057	Mabuya salensis specimen-voucher Sal...	70	4e-11
gb|AF335055.1|AF335055	Mabuya fogoensis specimen-voucher S....	70	4e-11
gb|AF335043.1|AF335043	Mabuya fogoensis specimen-voucher S....	70	4e-11
gb|AF335039.1|AF335039	Mabuya salensis specimen-voucher Sal...	70	4e-11
gb|U88009.1|GAU88009	Gavia pacifica 12S mitochondrial ribos...	68	1e-10
gb|U33682.1|U33682	Hypentelium nigricans 12S ribosomal RNA ...	68	1e-10
gb|AY035833.1|	Mesalina adramitana strain AND-2 12S ribosom...	64	2e-09
gb|AY035832.1|	Mesalina guttulata strain ANA-7 12S ribosoma...	64	2e-09
gb|AY035826.1|	Mesalina sp. 'Kuri' strain ADM-3 12S ribosom...	64	2e-09
gb|AY035825.1|	Mesalina balfouri strain ADM-2 12S ribosomal...	64	2e-09
gb|AY035824.1|	Mesalina balfouri strain ADM-1 12S ribosomal...	64	2e-09
gb|U33671.1|DSU33671	Distichodus sp. 12S ribosomal RNA gene...	64	2e-09
gb|AF335079.1|AF335079	Mabuya stangeri specimen-voucher Ras...	64	2e-09
gb|AY035827.1|	Eremias arguta strain ACA-17 12S ribosomal R...	62	7e-09
gb|AF335059.1|AF335059	Mabuya spinalis specimen-voucher San...	62	7e-09
gb|U33703.1|U33703	Hydrocynus sp. 12S ribosomal RNA gene, p...	60	3e-08
gb|AF338821.1|AF338821	Amazona farinosa cytochrome b gene, ...	58	1e-07
gb|AF338820.1|AF338820	Amazona ochrocephala oratrix cytochr...	58	1e-07
gb|AF338819.1|AF338819	Amazona ochrocephala auropalliata cy...	58	1e-07
gb|AY035828.1|	Eremias pleskei strain ANB-6 12S ribosomal R...	56	4e-07
gb|AY035831.1|	Mesalina brevirostris strain AHD-15 12S ribo...	55	2e-06
gb|AY035829.1|	Mesalina olivieri strain ADO-3 12S ribosomal...	55	2e-06
gb|BC009984.1|BC009984	Homo sapiens, DiGeorge syndrome crit...	47	3e-04
gb|U33736.1|CCU33736	Chanos chanos 12S ribosomal RNA gene, ...	43	0.005
gb|U33727.1|U33727	Parauchenipterus sp. 12S ribosomal RNA g...	43	0.005
gb|U33715.1|U33715	Noturus exilis 12S ribosomal RNA gene, p...	39	0.065
gb|U33704.1|U33704	Hydrocynus sp. 12S ribosomal RNA gene, p...	39	0.065
gb|U33672.1|DSU33672	Distichodus sp. 12S ribosomal RNA gene...	39	0.065
gb|U33650.1|ALU33650	Apteronotus leptorhynchus 12S ribosoma...	39	0.065
gb|U33640.1|AAU33640	Apteronotus albifrons 12S ribosomal RN...	39	0.065
gb|AF146267.1|AF146267	Uncultured bacterium SCALE-15 16S ri...	35	0.93
gb|AF142802.1|AF142802	Uncultured bacterium ACE-27 16S ribo...	35	0.93
gb|AF356012.1|AF356012	Uncultured rhodophyte clone CY4 16S ...	35	0.93
gb|AC092240.1|AC092240	Drosophila melanogaster, chromosome ...	35	0.93
gb|AF350369.1|AF350369	Thermococcus sp. CL1 16S ribosomal R...	35	0.93

>gb|AC021080.4|AC021080 Homo sapiens chromosome 5 clone CTC-203K17, complete sequence
Length = 103522

Score = 527 bits (274), Expect = e-149
Identities = 390/438 (89%), Gaps = 5/438 (1%)
Strand = Plus / Plus

```
Query:  13      GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  79078   GAGGGTGACAGGCAGTGTGTGCATGCTTTATGGCCTTATTCAATTAAGCACTCTGCTCCT  79137
```

```
Query:  73      AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  79138   AATTTACTGCTAAATCCTCCTTGGGCCCTTAGGTTTCATAAGGGTTGTTATGAGATTTT-  79196

Query:  133     CTGTGTGTAGAAAACGTA-CCCATTTCTTGCCAC--CTCATGGGCTACACCTTGACCTAA  189
Sbjct:  79197   CTAGGAGTAGAAAATATAGCCCATTTCTTACCACACCTCGTGGGCTACAACTTGACCTAA  79256

Query:  190     CGTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGA  249
Sbjct:  79257   CGTTTTTACGTAGATATTTGTGCTTACTTTGCAGCCTTACTAGGGTTTGCTGAAGATGGA  79316

Query:  250     GGTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGAT-TATAGAACAG  308
Sbjct:  79317   AGTATATAGGCTGAGCAAGAGGTGGTGAGGTAAATTGGAGTTTATCAATATATAGAACAG  79376

Query:  309     GCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTA  368
Sbjct:  79377   GCTCCTCTAGAGGGATATAAAGCACCGCCAAGTCCTTTGAGTTTTAAGCTATTGCTTGTA  79436

Query:  369     GTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGG  428
Sbjct:  79437   GTGTTCTGGTGAATAGTTTTGTTGATTTAACTATTGGAGTTTAGGGCTAAGCATAGTGGG  79496

Query:  429     GTATCTAATCCCAGTTTG  446
Sbjct:  79497   GTATCTAATCCCAGTTTG  79514
```

```
!!!
       --------  Failure to print alignment...  --------
!!!
```

```
  Database: db/nt.01
    Posted date:  Apr 15, 2003  3:55 PM
  Number of letters in database: 89,339,567
  Number of sequences in database:  27,887

  Database: PDB nucleotide database
    Posted date:  Apr 15, 2003  3:54 PM
  Number of letters in database: 171,196
  Number of sequences in database:  3992

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 28,430
Number of Sequences: 31879
Number of extensions: 28430
Number of successful extensions: 2627
Number of sequences better than 10.0: 178
Number of HSP's better than 10.0 without gapping: 178
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2216
Number of HSP's gapped (non-prelim): 312
length of query: 462
length of database: 89,510,763
effective HSP length: 20
effective length of query: 442
```

```
effective length of database: 88,873,183
effective search space: 39281946886
effective search space used: 39281946886
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 17 (33.4 bits)
```

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

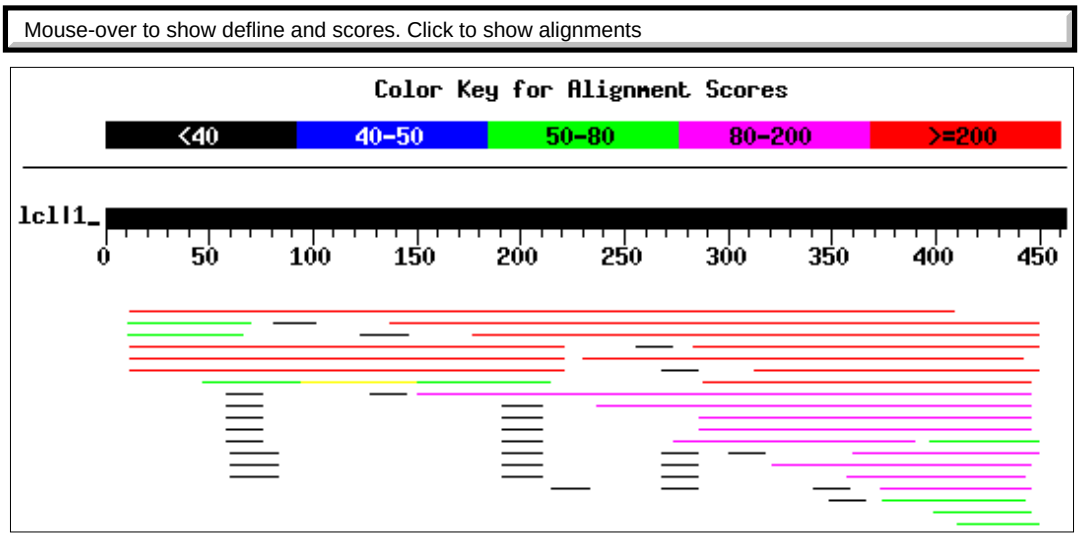
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: Q1_ss.fas
1,358,080 sequences; 600,347,833 total letters

Query= CS63win
(462 letters)

Distribution of 55 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value
gnl|dbSNP|ss6879113	738	0.0
gnl|dbSNP|ss6879114	583	e-165
gnl|dbSNP|ss6879115	506	e-142
gnl|dbSNP|ss6879116	304	6e-81
gnl|dbSNP|ss6230823	292	2e-77
gnl|dbSNP|ss6514239	242	2e-62
gnl|dbSNP|ss6514238	242	2e-62
gnl|dbSNP|ss6514240	237	1e-60
gnl|dbSNP|ss6268951	229	2e-58
gnl|dbSNP|ss6133132	223	1e-56
gnl|dbSNP|ss7887644	189	3e-46

gnl|dbSNP|ss7887643	173	1e-41
gnl|dbSNP|ss7887642	169	2e-40
gnl|dbSNP|ss7887641	169	2e-40
gnl|dbSNP|ss5640292	160	1e-37
gnl|dbSNP|ss6879118	156	2e-36
gnl|dbSNP|ss5650274	119	2e-25
gnl|dbSNP|ss6028113	104	9e-21
gnl|dbSNP|ss5756627	100	1e-19
gnl|dbSNP|ss7953597	80	3e-13
gnl|dbSNP|ss5665301	80	3e-13
gnl|dbSNP|ss5653115	78	1e-12
gnl|dbSNP|ss6094407	62	5e-08
gnl|dbSNP|ss6879119	60	2e-07
gnl|dbSNP|ss5813365	55	1e-05
gnl|dbSNP|ss6254413	53	4e-05
gnl|dbSNP|ss7893501	39	0.41
gnl|dbSNP|ss7893500	39	0.41
gnl|dbSNP|ss7893499	39	0.41
gnl|dbSNP|ss7893498	39	0.41
gnl|dbSNP|ss6273888	39	0.41
gnl|dbSNP|ss5854538	39	0.41
gnl|dbSNP|ss5805798	39	0.41
gnl|dbSNP|ss6140307	37	1.6
gnl|dbSNP|ss7931375	35	6.0
gnl|dbSNP|ss7931374	35	6.0
gnl|dbSNP|ss7931373	35	6.0
gnl|dbSNP|ss7864435	35	6.0
gnl|dbSNP|ss6853133	35	6.0
gnl|dbSNP|ss6698149	35	6.0
gnl|dbSNP|ss6599909	35	6.0
gnl|dbSNP|ss6410540	35	6.0
gnl|dbSNP|ss6410538	35	6.0
gnl|dbSNP|ss6211903	35	6.0
gnl|dbSNP|ss6209191	35	6.0
gnl|dbSNP|ss6104595	35	6.0
gnl|dbSNP|ss6087686	35	6.0
gnl|dbSNP|ss5927644	35	6.0
gnl|dbSNP|ss5856979	35	6.0
gnl|dbSNP|ss5781342	35	6.0
gnl|dbSNP|ss5756948	35	6.0
gnl|dbSNP|ss5738411	35	6.0
gnl|dbSNP|ss5704348	35	6.0
gnl|dbSNP|ss5667587	35	6.0

>gnl|dbSNP|ss6879113
Length = 401

Score = 739 bits (384), Expect = 0.0
Identities = 392/397 (98%)
Strand = Plus / Plus

```
Query:  13   GAGGGTGACGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  72
Sbjct:  5    GAGGGTGAAGGGCGGTGTGTGCGTGCTTCATGGCCTCATTCAATTAAACACTCTGCTCTC  64
```

```
Query:  73   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  132
Sbjct:  65   AATTTATTGCTAAATCCTCCTTGAGCCCTTAGATTTCATAACGGTTGTCGCGAGATTTTT  124

Query:  133  CTGTGTGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  192
Sbjct:  125  TTGGATGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGT  184

Query:  193  TTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  185  TTTTATGTAGATACTTSTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGT  244

Query:  253  ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  312
Sbjct:  245  ATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTC  304

Query:  313  CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  372
Sbjct:  305  CTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGT  364

Query:  373  TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTT  409
Sbjct:  365  TCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTT  401
```

```
>gnl|dbSNP|ss6879114
          Length = 401

 Score =  583 bits (303), Expect = e-165
 Identities = 309/313 (98%)
 Strand = Plus / Plus


Query:  138  TGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTTTTA  197
Sbjct:  5    TGTAGAAAACGTACCCATTTCTTGCCACCTCATGGGCTACACCTTGACCTAACGTTTTTA  64

Query:  198  TGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTATATA  257
Sbjct:  65   TGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTTGCTGAAGATGGAGGTATATA  124

Query:  258  GGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTA  317
Sbjct:  125  GGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTA  184

Query:  318  GAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGG  377
Sbjct:  185  GAGGGATATAAAGCACYGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGG  244

Query:  378  CGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAAT  437
Sbjct:  245  CGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGCGGGGTATCTACT  304

Query:  438  CCCAGTTTGAATC  450
Sbjct:  305  CCCAGTTTGGATC  317
```

```
>gnl|dbSNP|ss6879115
          Length = 401

 Score =  506 bits (263), Expect = e-142
 Identities = 269/273 (98%)
 Strand = Plus / Plus


Query:  178  ACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTT  237
Sbjct:  1    ACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTACTCTGTGGCCTTTCCAGGGTTT  60

Query:  238  GCTGAAGATGGAGGTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGA  297
Sbjct:  61   GCTGAAGATGGAGGTATATAGGCTGGGCAAGAGGTGGTGAGGTAAATTGGGGTTTATCGA  120

Query:  298  TTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGC  357
Sbjct:  121  TTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGC  180
```

```
Query:  358  TGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTA  417
Sbjct:  181  TGTTGCTTGTAGTGTTCTGGYGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTA  240

Query:  418  AGCATAGTGGGGTATCTAATCCCAGTTTGAATC  450
Sbjct:  241  AGCATAGCGGGGTATCTACTCCCAGTTTGGATC  273
```

```
>gnl|dbSNP|ss6879116
          Length = 401

 Score =  304 bits (158), Expect = 6e-81
 Identities = 164/167 (98%)
 Strand = Plus / Plus


Query:  284  TTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCC  343
Sbjct:  1    TTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCC  60

Query:  344  TTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATT  403
Sbjct:  61   TTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATT  120

Query:  404  CGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTGAATC  450
Sbjct:  121  CGAGTTTAGGGTTAAGCATAGCGGGGTATCTACTCCCAGTTTGGATC  167
```

```
>gnl|dbSNP|ss6230823
          Length = 401

 Score =  292 bits (152), Expect = 2e-77
 Identities = 195/215 (90%), Gaps = 2/215 (0%)
 Strand = Plus / Minus


Query:  443  ACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAAAAC  384
Sbjct:  183  ACTGGGATTAGATAACCCMCTATGCTTAGCCCTAAACTCTAATAGTTACATTAACAAAAC  242

Query:  383  TGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATA  324
Sbjct:  243  CATTCGCCAGAGTACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATA  302

Query:  323  TCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCTTG-  265
Sbjct:  303  TCCCTCTAGAGGAGCCTGTTCTATAATCGATAAACCCTGATATACCTCACCACCTCTTGC  362

Query:  264  -CCCAGCCTATATACCTCCATCTTCAGCAAACCCT  231
Sbjct:  363  CCCCAGCCTGTATAGTGCCATCTTCAGCAAACCCT  397
```

```
>gnl|dbSNP|ss6514239
          Length = 401

 Score =  242 bits (126), Expect = 2e-62
 Identities = 187/211 (88%), Gaps = 5/211 (2%)
 Strand = Plus / Minus


Query:  222  CACAGAGTAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTG  163
Sbjct:  3    CACAAAGTAAGCACAAGTATCTACATAAAAACATTAGGTCAAGGTGTAGCCCATGAGGCG  62

Query:  162  GCAAGAAATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATC  104
Sbjct:  63   GTAAGAAATGGGCTACATTTTCTACACCCAGAAAA-TCTC---ACAACCCTTATGAAATC  118

Query:  103  TAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCC  44
```

```
Sbjct:  119  TAAGGGCTCAAGGAGGATTCAGCAGTATATTAAGAGCAGAGTGCTTAATTGGATGAGGCC  178

Query:  43   ATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  179  ATAAAGCACACACACAATGCCCRTCACCCTC  209
```

```
>gnl|dbSNP|ss6514238
          Length = 401

 Score =  242 bits (126), Expect = 2e-62
 Identities = 187/211 (88%), Gaps = 5/211 (2%)
 Strand = Plus / Minus


Query:  222  CACAGAGTAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTG  163
Sbjct:  16   CACAAAGTAAGCACAAGTATCTACATAAAAACATTAGGTCAAGGTGTAGCCCATGAGGCG  75

Query:  162  GCAAGAAATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATC  104
Sbjct:  76   GTAAGAAATGGGCTACATTTTCTACACCCAGAAAA-TCTC---ACAACCCTTATGAAATC  131

Query:  103  TAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCC  44
Sbjct:  132  TAAGGGCTCAAGGAGGATTCAGCAGTATATTAAGAGCAGAGTGCTTAATTGGATGAGGCC  191

Query:  43   ATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  192  ATAAAGCACRCACACAATGCCCATCACCCTC  222
```

```
>gnl|dbSNP|ss6514240
          Length = 401

 Score =  237 bits (123), Expect = 1e-60
 Identities = 186/211 (88%), Gaps = 5/211 (2%)
 Strand = Plus / Minus


Query:  222  CACAGAGTAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTG  163
Sbjct:  2    CACAAAGTAAGCACAAGTATCTACATAAAAACATTAGGTCAAGGTGTAGCCCATGAGGCG  61

Query:  162  GCAAGAAATGGG-TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATC  104
Sbjct:  62   GTAAGAAATGGGCTACATTTTCTACACCCAGAAAA-TCTC---ACAACCCTTATGAAATC  117

Query:  103  TAAGGGCTCAAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCC  44
Sbjct:  118  TAAGGGCTCAAGGAGGATTCAGCAGTATATTAAGAGCAGAGTGCTTAATTGGATGAGGCC  177

Query:  43   ATGAAGCACGCACACACCGCCCGTCACCCTC  13
Sbjct:  178  ATAAAGCACACACACAATGCCCAYCACCCTC  208
```

```
>gnl|dbSNP|ss6268951
          Length = 401

 Score =  229 bits (119), Expect = 2e-58
 Identities = 131/137 (95%)
 Strand = Plus / Plus


Query:  314  TTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTT  373
Sbjct:  1    TTTAGAGGGATATAAAGCATGGCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTT  60

Query:  374  CTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATC  433
Sbjct:  61   CTGGCGAACAGTTTTGTTGATCTAACTGTTCGAGTTTAGGGTTAAGCATAGCGGGGTATC  120
```

```
Query:  434  TAATCCCAGTTTGAATC  450
Sbjct:  121  TACTCCCAGTTTGGATC  137
```

```
>gnl|dbSNP|ss6133132
          Length = 401

 Score =  223 bits (116), Expect = 1e-56
 Identities = 144/158 (91%)
 Strand = Plus / Plus


Query:  289  GTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACTGCCAAGTCCTTTGA  348
Sbjct:  1    GTTTATCGATTACAGAACAGGCTCCTCTAGAGGGATATGAAGCACCGCCAGGTCCTTTGA  60

Query:  349  GTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGT  408
Sbjct:  61   GTTTTAAGCTGTGGCTCGTAGTGTTCTGGCGAGCAGTTTTGTTGATTTAACTGTTGAGGT  120

Query:  409  TTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  121  TTAGGGCTAAGCATAGTGGGGTATCTAATCCCAGTTTG  158
```

```
>gnl|dbSNP|ss7887644
          Length = 801

 Score =  189 bits (98), Expect = 3e-46
 Identities = 237/299 (79%), Gaps = 15/299 (5%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  477  CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAAATAATTTAACAAACAA  536

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  537  AATTATTCACCAGAGTATGACAAGCAATAGCTTAAAACTCAAAGGACATGGCGGTGCTTT  596

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  597  ACATCCCTCTAGAGGACCCTGTTCTATAATTGATAAACCCTGATATTCCCTTCCATCTCT  656

Query:  266  TGCC---CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCA  210
Sbjct:  657  TGCCACATACCCTATATACCATCATCTTCAGCTAA------AAAGGTCTTAAAGTAAGCA  710

Query:  209  GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  711  CAAGT------ATTAAAATGTTAGATCAAGGTGTAGCCCATGAGATGGAAAGAAATGGG  763
```

```
>gnl|dbSNP|ss7887643
          Length = 801

 Score =  173 bits (90), Expect = 1e-41
 Identities = 173/212 (81%), Gaps = 3/212 (1%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  536  CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAAATAATTTAACAAACAA  595

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  596  AATTATTCACCAGAGTATGACAAGCAATAGCTTAAAACTCAAAGGACATGGCGGTGCTTT  655

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
```

```
Sbjct:  656  ACATCCCTCTAGAGGACCCTGTTCTATAATTGATAAACCCTGATATTCCCTTCCATCTCT  715

Query:  266  TGCC---CAGCCTATATACCTCCATCTTCAGC  238
Sbjct:  716  TGCCACATACCCTATATACCATCATCTTCAGC  747
```

```
>gnl|dbSNP|ss7887642
          Length = 801

 Score =  169 bits (88), Expect = 2e-40
 Identities = 136/160 (85%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  601  CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAAATAATTTAACAAACAA  660

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  661  AATTATTCACCAGAGTATGACAAGCAATAGCTTAAAACTCAAAGGACATGGCGGTGCTTT  720

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCC  287
Sbjct:  721  ACATCCCTCTAGAGGACCCTGTTCTATAATTGATAAACCC  760
```

```
>gnl|dbSNP|ss7887641
          Length = 801

 Score =  169 bits (88), Expect = 2e-40
 Identities = 136/160 (85%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  623  CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAAATAATTTAACAAACAA  682

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  683  AATTATTCACCAGAGTATGACAAGCAATAGCTTAAAACTCAAAGGACATGGCGGTGCTTT  742

Query:  326  ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCC  287
Sbjct:  743  ACATCCCTCTAGAGGACCCTGTTCTATAATTGATAAACCC  782
```

```
>gnl|dbSNP|ss5640292
          Length = 401

 Score =  160 bits (83), Expect = 1e-37
 Identities = 105/116 (90%)
 Strand = Plus / Plus


Query:  275  TGAGGTAAATTGGGGTTTATCGATTATAGAACAGGCTCCTTTAGAGGGATATAAAGCACT  334
Sbjct:  286  TGAGGTTGATCGGGGTTTATCGATTACAGAACAGGCTCCTCTAGAGGGATATGAAGCACC  345

Query:  335  GCCAAGTCCTTTGAGTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGT  390
Sbjct:  346  GCCAGGTCCTTTGAGTTTTAAGCTGTGGCTCGTAGTGTTCTGGCGAGCAGTTTTGT  401
```

```
>gnl|dbSNP|ss6879118
          Length = 401

 Score =  156 bits (81), Expect = 2e-36
 Identities = 87/90 (96%)
```

Strand = Plus / Plus

```
Query:  361  TGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGC  420
Sbjct:  1    TGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGC  60

Query:  421  ATAGTGGGGTATCTAATCCCAGTTTGAATC  450
Sbjct:  61   ATAGCGGGGTATCTACTCCCAGTTTGGATC  90
```

>gnl|dbSNP|ss5650274
Length = 401

Score = 119 bits (62), Expect = 2e-25
Identities = 104/125 (83%)
Strand = Plus / Minus

```
Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  277  CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAAATAATTTAACAAACAA  336

Query:  386  AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  337  AATTATTCACCAGAGTATGACAAGCAATAGCTTAAAACTCAAAGGACATGGCGGTGCTTT  396

Query:  326  ATATC  322
Sbjct:  397  ACATC  401
```

>gnl|dbSNP|ss6028113
Length = 401

Score = 104 bits (54), Expect = 9e-21
Identities = 76/87 (87%)
Strand = Plus / Plus

```
Query:  358  TGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTA  417
Sbjct:  2    TGTTGCTTGTAGTACTCTGGCGAATGGTTTTGTTAATGTAACTGTTAGGGTTTAGGGCTA  61

Query:  418  AGCATAGTGGGGTATCTAATCCCAGTT  444
Sbjct:  62   AGCATAGAGGGGTATCTAATCCCAGTT  88
```

>gnl|dbSNP|ss5756627
Length = 401

Score = 100 bits (52), Expect = 1e-19
Identities = 66/73 (90%)
Strand = Plus / Plus

```
Query:  374  CTGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATC  433
Sbjct:  1    CTGGCGAGCAGTTTTGTTGATTTAACTGTTGAGGTTTAGGGCTAAGCATAGTGGGGTATC  60

Query:  434  TAATCCCAGTTTG  446
Sbjct:  61   TAATCCCAGTTTG  73
```

>gnl|dbSNP|ss7953597
Length = 801

```
 Score = 79.5 bits (41), Expect = 3e-13
 Identities = 57/65 (87%)
 Strand = Plus / Minus


Query:  215  TAAGCAGAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAA  156
Sbjct:  15   TAATCACAAATATTTACATAAAAACGTTAGGTCAAGGTGTAGTCTATGAGATGGGAAGAA  74

Query:  155  ATGGG  151
Sbjct:  75   ATGGG  79
```

```
 Score = 39.1 bits (20), Expect = 0.41
 Identities = 38/47 (80%)
 Strand = Plus / Minus


Query:  94   AAGGAGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGA  48
Sbjct:  139  AAGGAGGATTTAGTAGTAAATTAGGAATAGAGAGCTTAGTTGAATGA  185
```

```
>gnl|dbSNP|ss5665301
          Length = 401

 Score = 79.5 bits (41), Expect = 3e-13
 Identities = 49/53 (92%)
 Strand = Plus / Plus


Query:  398  ACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTGAATC  450
Sbjct:  1    ACTGTTCGAGTTTAGGGTTAAGCATAGCGGGGTATCTACTCCCAGTTTGGATC  53
```

```
>gnl|dbSNP|ss5653115
          Length = 401

 Score = 77.6 bits (40), Expect = 1e-12
 Identities = 60/70 (85%)
 Strand = Plus / Plus


Query:  375  TGGCGAACAGTTTTGTTGATCTAACTATTCGAGTTTAGGGTTAAGCATAGTGGGGTATCT  434
Sbjct:  1    TGGCGAATGGTTTTGTTAGTTTAACTATTAGAGCTTAGGGCTAAGCACAGTGGGTTATCT  60

Query:  435  AATCCCAGTT  444
Sbjct:  61   AATCCCAGTT  70
```

```
>gnl|dbSNP|ss6094407
          Length = 401

 Score = 62.2 bits (32), Expect = 5e-08
 Identities = 42/47 (89%)
 Strand = Plus / Minus


Query:  446  CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATA  400
Sbjct:  336  CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAAATA  382
```

```
>gnl|dbSNP|ss6879119
          Length = 401

 Score = 60.3 bits (31), Expect = 2e-07
 Identities = 37/40 (92%)
 Strand = Plus / Plus


Query:  411  AGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTGAATC  450
Sbjct:  1    AGGGTTAAGCATAGCGGGGTATCTACTCCCAGTTTGGATC  40

                                                                                
>gnl|dbSNP|ss5813365
          Length = 401

 Score = 54.5 bits (28), Expect = 1e-05
 Identities = 51/60 (85%), Gaps = 1/60 (1%)
 Strand = Plus / Minus


Query:  71   AGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTCT  12
Sbjct:  2    AGAACAGAGTGCTTGATTGAATAAGGCCATAAGGCAAGCACACAA-GCCCGTCACCCTCT  60

                                                                                
>gnl|dbSNP|ss6254413
          Length = 401

 Score = 52.6 bits (27), Expect = 4e-05
 Identities = 48/56 (85%), Gaps = 1/56 (1%)
 Strand = Plus / Minus


Query:  67   CAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCACACACCGCCCGTCACCCTCT  12
Sbjct:  3    CAGAGTGCTTGATTGAATAAGGCCATAAGGCAAGCACACAA-GCCCGTCACCCTCT  57

                                                                                
>gnl|dbSNP|ss7893501
          Length = 801

 Score = 39.1 bits (20), Expect = 0.41
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192  TTTTTATGTAGATACTTCTG  211
Sbjct:  539  TTTTTATGTAGATACTTCTG  558

                                                                                
>gnl|dbSNP|ss7893500
          Length = 801

 Score = 39.1 bits (20), Expect = 0.41
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192  TTTTTATGTAGATACTTCTG  211
Sbjct:  541  TTTTTATGTAGATACTTCTG  560

                                                                                
>gnl|dbSNP|ss7893499
```

```
          Length = 801

 Score = 39.1 bits (20), Expect = 0.41
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192  TTTTTATGTAGATACTTCTG  211
Sbjct:  572  TTTTTATGTAGATACTTCTG  591

----------------------------------------------------------------------

>gnl|dbSNP|ss7893498
          Length = 801

 Score = 39.1 bits (20), Expect = 0.41
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192  TTTTTATGTAGATACTTCTG  211
Sbjct:  727  TTTTTATGTAGATACTTCTG  746

----------------------------------------------------------------------

>gnl|dbSNP|ss6273888
          Length = 401

 Score = 39.1 bits (20), Expect = 0.41
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192  TTTTTATGTAGATACTTCTG  211
Sbjct:  341  TTTTTATGTAGATACTTCTG  360

----------------------------------------------------------------------

>gnl|dbSNP|ss5854538
          Length = 401

 Score = 39.1 bits (20), Expect = 0.41
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192  TTTTTATGTAGATACTTCTG  211
Sbjct:  339  TTTTTATGTAGATACTTCTG  358

----------------------------------------------------------------------

>gnl|dbSNP|ss5805798
          Length = 401

 Score = 39.1 bits (20), Expect = 0.41
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  192  TTTTTATGTAGATACTTCTG  211
Sbjct:  372  TTTTTATGTAGATACTTCTG  391

----------------------------------------------------------------------

>gnl|dbSNP|ss6140307
          Length = 401
```

```
 Score = 37.2 bits (19), Expect = 1.6
 Identities = 19/19 (100%)
 Strand = Plus / Plus


Query:  216  CTCTGTGGCCTTTCCAGGG  234
Sbjct:  258  CTCTGTGGCCTTTCCAGGG  276

----------------------------------------------------------------------

>gnl|dbSNP|ss7931375
          Length = 801

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query:  76   AATTGAGAGCAGAGTGTT  59
Sbjct:  129  AATTGAGAGCAGAGTGTT  146

----------------------------------------------------------------------

>gnl|dbSNP|ss7931374
          Length = 801

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query:  76   AATTGAGAGCAGAGTGTT  59
Sbjct:  254  AATTGAGAGCAGAGTGTT  271

----------------------------------------------------------------------

>gnl|dbSNP|ss7931373
          Length = 801

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query:  76   AATTGAGAGCAGAGTGTT  59
Sbjct:  258  AATTGAGAGCAGAGTGTT  275

----------------------------------------------------------------------

>gnl|dbSNP|ss7864435
          Length = 801

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 22/24 (91%)
 Strand = Plus / Minus


Query:  84   TAGCAATAAATTGAGAGCAGAGTG  61
Sbjct:  726  TAGAAATAATTTGAGAGCAGAGTG  749

----------------------------------------------------------------------

>gnl|dbSNP|ss6853133
          Length = 401
```

Score = 35.3 bits (18), Expect = 6.0
Identities = 18/18 (100%)
Strand = Plus / Minus

```
Query:  274  CCACCTCTTGCCCAGCCT  257
Sbjct:  179  CCACCTCTTGCCCAGCCT  196
```

>gnl|dbSNP|ss6698149
Length = 401

Score = 35.3 bits (18), Expect = 6.0
Identities = 18/18 (100%)
Strand = Plus / Plus

```
Query:  350  TTTTAAGCTGTTGCTTGT  367
Sbjct:  140  TTTTAAGCTGTTGCTTGT  157
```

>gnl|dbSNP|ss6599909
Length = 401

Score = 35.3 bits (18), Expect = 6.0
Identities = 20/21 (95%)
Strand = Plus / Plus

```
Query:  82   CTAAATCCTCCTTGAGCCCTT  102
Sbjct:  225  CTAAATCCTCCCTGAGCCCTT  245
```

>gnl|dbSNP|ss6410540
Length = 401

Score = 35.3 bits (18), Expect = 6.0
Identities = 22/24 (91%)
Strand = Plus / Minus

```
Query:  84   TAGCAATAAATTGAGAGCAGAGTG  61
Sbjct:  126  TAGAAATAATTTGAGAGCAGAGTG  149
```

>gnl|dbSNP|ss6410538
Length = 401

Score = 35.3 bits (18), Expect = 6.0
Identities = 22/24 (91%)
Strand = Plus / Minus

```
Query:  84   TAGCAATAAATTGAGAGCAGAGTG  61
Sbjct:  332  TAGAAATAATTTGAGAGCAGAGTG  355
```

>gnl|dbSNP|ss6211903
Length = 401

Score = 35.3 bits (18), Expect = 6.0

```
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query:  286  CAATTTACCTCACCACCT  269
Sbjct:  81   CAATTTACCTCACCACCT  98

>gnl|dbSNP|ss6209191
          Length = 401

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query:  286  CAATTTACCTCACCACCT  269
Sbjct:  231  CAATTTACCTCACCACCT  248

>gnl|dbSNP|ss6104595
          Length = 401

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Plus


Query:  342  CCTTTGAGTTTTAAGCTG  359
Sbjct:  136  CCTTTGAGTTTTAAGCTG  153

>gnl|dbSNP|ss6087686
          Length = 401

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query:  76   AATTGAGAGCAGAGTGTT  59
Sbjct:  54   AATTGAGAGCAGAGTGTT  71

>gnl|dbSNP|ss5927644
          Length = 401

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query:  286  CAATTTACCTCACCACCT  269
Sbjct:  234  CAATTTACCTCACCACCT  251

>gnl|dbSNP|ss5856979
          Length = 401

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 22/24 (91%)
```

```
 Strand = Plus / Minus


Query:  147  GTTTTCTACACACAGAAAAATCTC  124
Sbjct:  22   GTTATCTACAGACAGAAAAATCTC  45

>gnl|dbSNP|ss5781342
          Length = 401

 Score = 35.3 bits (18), Expect = 6.0
 Identities = 18/18 (100%)
 Strand = Plus / Plus


Query:  301  TAGAACAGGCTCCTTTAG  318
Sbjct:  156  TAGAACAGGCTCCTTTAG  173

  Database: Q1_ss.fas
    Posted date:  Apr 21, 2003 12:56 PM
  Number of letters in database: 600,347,833
  Number of sequences in database:  1,358,080

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 146,799
Number of Sequences: 1358080
Number of extensions: 146799
Number of successful extensions: 40414
Number of sequences better than 10.0: 55
Number of HSP's better than 10.0 without gapping: 53
Number of HSP's successfully gapped in prelim test: 2
Number of HSP's that attempted gapping in prelim test: 40353
Number of HSP's gapped (non-prelim): 59
length of query: 462
length of database: 600,347,833
effective HSP length: 22
effective length of query: 440
effective length of database: 570,470,073
effective search space: 251006832120
effective search space used: 251006832120
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 18 (35.3 bits)
```

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

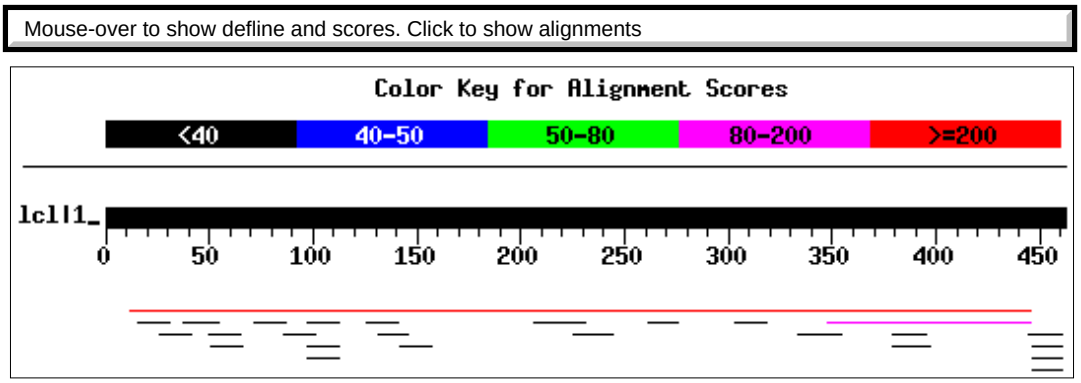
BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

Database: Database of GenBank+EMBL+DDBJ sequences from STS Divisions
163,596 sequences; 68,665,611 total letters

Query= CS63win
(462 letters)

Distribution of 26 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value
gb|G54823.1|G54823 Xq4124 KWOK Homo sapiens STS genomic, se...	200	1e-50
emb|Z67247.1|HSA083XG5 H.sapiens DNA segment containing (CA...	87	2e-16
emb|AJ319731.1|DST319731 Darwinula stevensoni STS, clone 91...	35	0.69
gb|G83630.1| S208P6043RG10.T0 129S1/SvImJ Mus musculus STS ...	33	2.6
gb|G40279.1|G40279 Z21976 Zebrafish AB Danio rerio STS geno...	33	2.6
emb|AL402043.1|CNS06JTX T3 end of clone XAS0AA001E08 of lib...	33	2.6
gb|G89072.1| S209P6372RC10.T0 C3H/HeJ Mus musculus STS geno...	31	9.9
gb|G86281.1| S208P6395RF1.T0 129S1/SvImJ Mus musculus STS g...	31	9.9
gb|G75921.1| S209P6193RB5.T0 C3H/HeJ Mus musculus STS genom...	31	9.9
gb|G39886.1|G39886 Z11276 Zebrafish AB Danio rerio STS geno...	31	9.9
gb|G26529.1|G26529 human STS STSG-9961, sequence tagged site	31	9.9
gb|G23345.1|G23345 human STS WI-14715, sequence tagged site	31	9.9
emb|AJ411320.1|CFA411320 Canis familiaris STS REN157D13, se...	31	9.9
dbj|AB093394.1| Bos taurus DNA, microsatellite marker DIK12...	31	9.9

gb|G59060.1|G59060	SHGC-106629 Human Homo sapiens STS genom...	31	9.9
gb|G48830.1|G48830	SHGC-83580 Human Homo sapiens STS genomi...	31	9.9
gb|G19440.1|G19440	SHGC-11930 Human Homo sapiens STS genomi...	31	9.9
gb|G14697.1|G14697	SHGC-13383 Human Homo sapiens STS genomi...	31	9.9
gb|G12499.1|G12499	CtSTS_48-1d Chlamydia RGriffais Chlamydi...	31	9.9
gb|G54373.1|G54373	Bv8 Human testis cDNA library Homo sapie...	31	9.9
gb|AF108045.1|AF108045	Sus scrofa domestica chromosome 2, s...	31	9.9
dbj|AB080351.1|	Bos taurus DNA, chromosome 6, DIK1186, sequ...	31	9.9
dbj|AB080350.1|	Bos taurus DNA, chromosome 6, DIK1185, sequ...	31	9.9
gb|G18503.1|G18503	cow STS BM4006, sequence tagged site	31	9.9
gb|G11541.1|G11541	human STS SHGC-9961, sequence tagged site	31	9.9
emb|AL684727.1|PM2C5B	Penicillium marneffei STS, clone pm2c...	31	9.9

>gb|G54823.1|G54823 Xq4124 KWOK Homo sapiens STS genomic, sequence tagged site
Length = 1100

Score = 200 bits (104), Expect = 1e-50
Identities = 335/438 (76%), Gaps = 18/438 (4%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  162   CAAACTGGGATGAGATACCCCACTATGCTTAGCTATAAACTCAATAATTTAACAAACAA  221

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  222   AATTATTCACCAGAGTATGACAAGCAATAGCTTAAAACTCAAAGGACATGGCGGTGCTTT  281

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  282   ACATCCCTCTAGAGGACCCTGTTCTATAATTGATAAACCCTGATATTCCCTTCCATCTCT  341

Query:  266   TGCC---CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCA  210
Sbjct:  342   TGCCACATACCCTATATACCATCATCTTCAGCTAA------AAAGGTCTTAAAGTAAGCA  395

Query:  209   GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-  151
Sbjct:  396   CAAGT------ATTAAAATGTTAGATCAAGGTGTAGCCCATGAGATGGAAAGAAATGGGC  449

Query:  150   TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  450   CACATTTTCTAAATCTAGAACA--CCCATGACAACCCTCGTGAAACTTAAAGGTCAAAGG  507

Query:  90    AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  508   AGGATTTAGTAGTAAATCAAGAATAGAGATCTTGATCGAATAAAACATGAAGCACTCAC  567

Query:  30    ACACCGCCCGTCACCCTC  13
Sbjct:  568   ACACTTCCCATCACCCTC  585
```

>emb|Z67247.1|HSA083XG5 H.sapiens DNA segment containing (CA) repeat; clone AFMa083xg5;
single read, sequence tagged site
Length = 394

Score = 87.2 bits (45), Expect = 2e-16
Identities = 82/98 (83%), Gaps = 4/98 (4%)
Strand = Plus / Plus

```
Query:  349  GTTTTAAGCTGTTGCTTGTAGTGTTCTGGCGAACAGTTTTGTTGATCTAACTATTCGAGT  408
Sbjct:  275  GTTTTATGCTGTTGCTTATAGTATTCTGGTGAATGATTTTGTTAATTTA----TTAGAGT  330
```

```
Query:  409  TTAGGGTTAAGCATAGTGGGGTATCTAATCCCAGTTTG  446
Sbjct:  331  TTAGGGCTAAGCATAGTGGGGTATCTAACCCCAGTTTG  368
```

>emb|AJ319731.1|DST319731 Darwinula stevensoni STS, clone 91-74, sequence tagged site

Length = 295

Score = 35.3 bits (18), Expect = 0.69
Identities = 18/18 (100%)
Strand = Plus / Plus

```
Query:  445  TGAATCACTAGTGAATTC  462
Sbjct:  278  TGAATCACTAGTGAATTC  295
```

>gb|G83630.1| S208P6043RG10.T0 129S1/SvImJ Mus musculus STS genomic, sequence tagged site

Length = 597

Score = 33.4 bits (17), Expect = 2.6
Identities = 19/20 (95%)
Strand = Plus / Plus

```
Query:  226  TTTCCAGGGTTTGCTGAAGA  245
Sbjct:  479  TTTCCAGGGTTTGCAGAAGA  498
```

>gb|G40279.1|G40279 Z21976 Zebrafish AB Danio rerio STS genomic, sequence tagged site

Length = 983

Score = 33.4 bits (17), Expect = 2.6
Identities = 23/26 (88%)
Strand = Plus / Plus

```
Query:  207  TTCTGCTTACTCTGTGGCCTTTCCAG  232
Sbjct:  369  TTCTGCTGACACTGCGGCCTTTCCAG  394
```

>emb|AL402043.1|CNS06JTX T3 end of clone XAS0AA001E08 of library XAS0AA from strain CLIB 533 of Saccharomyces bayanus, sequence tagged site

Length = 963

Score = 33.4 bits (17), Expect = 2.6
Identities = 17/17 (100%)
Strand = Plus / Minus

```
Query:  396  AGATCAACAAAACTGTT  380
Sbjct:  69   AGATCAACAAAACTGTT  85
```

>gb|G89072.1| S209P6372RC10.T0 C3H/HeJ Mus musculus STS genomic, sequence tagged site

Length = 619

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)

Strand = Plus / Plus

```
Query:  52   TCAATTAAACACTCTG  67
Sbjct:  573  TCAATTAAACACTCTG  588
```

>gb|G86281.1| S208P6395RF1.T0 129S1/SvImJ Mus musculus STS genomic, sequence tagged site
Length = 638

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Minus

```
Query:  66   AGAGTGTTTAATTGAA  51
Sbjct:  252  AGAGTGTTTAATTGAA  267
```

>gb|G75921.1| S209P6193RB5.T0 C3H/HeJ Mus musculus STS genomic, sequence tagged site
Length = 569

Score = 31.5 bits (16), Expect = 9.9
Identities = 20/22 (90%)
Strand = Plus / Plus

```
Query:  334  TGCCAAGTCCTTTGAGTTTTAA  355
Sbjct:  420  TGCAAAGTACTTTGAGTTTTAA  441
```

>gb|G39886.1|G39886 Z11276 Zebrafish AB Danio rerio STS genomic, sequence tagged site
Length = 553

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Minus

```
Query:  142  CTACACACAGAAAAAT  127
Sbjct:  303  CTACACACAGAAAAAT  318
```

>gb|G26529.1|G26529 human STS STSG-9961, sequence tagged site
Length = 339

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Minus

```
Query:  113  TTATGAAATCTAAGGG  98
Sbjct:  129  TTATGAAATCTAAGGG  144
```

>gb|G23345.1|G23345 human STS WI-14715, sequence tagged site
Length = 302

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Plus

```
Query:  73   AATTTATTGCTAAATC  88
Sbjct:  22   AATTTATTGCTAAATC  37
```

>emb|AJ411320.1|CFA411320 Canis familiaris STS REN157D13, sequence tagged site
Length = 440

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Plus

```
Query:  132  TCTGTGTGTAGAAAAC  147
Sbjct:  213  TCTGTGTGTAGAAAAC  228
```

>dbj|AB093394.1| Bos taurus DNA, microsatellite marker DIK1258, sequence tagged site
Length = 633

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Minus

```
Query:  462  GAATTCACTAGTGATT  447
Sbjct:  1    GAATTCACTAGTGATT  16
```

>gb|G59060.1|G59060 SHGC-106629 Human Homo sapiens STS genomic, sequence tagged site
Length = 514

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Plus

```
Query:  262  GGGCAAGAGGTGGTGA  277
Sbjct:  364  GGGCAAGAGGTGGTGA  379
```

>gb|G48830.1|G48830 SHGC-83580 Human Homo sapiens STS genomic, sequence tagged site
Length = 437

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Plus

```
Query:  304  AACAGGCTCCTTTAGA  319
Sbjct:  295  AACAGGCTCCTTTAGA  310
```

>gb|G19440.1|G19440 SHGC-11930 Human Homo sapiens STS genomic, sequence tagged site
Length = 337

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Plus

```
Query:  87   TCCTCCTTGAGCCCTT  102
Sbjct:  69   TCCTCCTTGAGCCCTT  84
```

>gb|G14697.1|G14697 SHGC-13383 Human Homo sapiens STS genomic, sequence tagged site
Length = 250

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Minus

```
Query:  113  TTATGAAATCTAAGGG  98
Sbjct:  129  TTATGAAATCTAAGGG  144
```

>gb|G12499.1|G12499 CtSTS_48-1d Chlamydia RGriffais Chlamydia trachomatis STS genomic clone 48Bk1 d, sequence tagged site
Length = 205

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Plus

```
Query:  17   GTGACGGGCGGTGTGT  32
Sbjct:  71   GTGACGGGCGGTGTGT  86
```

>gb|G54373.1|G54373 Bv8 Human testis cDNA library Homo sapiens STS genomic, sequence tagged site
Length = 378

Score = 31.5 bits (16), Expect = 9.9
Identities = 16/16 (100%)
Strand = Plus / Plus

```
Query:  143  AAAACGTACCCATTTC  158
Sbjct:  254  AAAACGTACCCATTTC  269
```

>gb|AF108045.1|AF108045 Sus scrofa domestica chromosome 2, sequence tagged site
Length = 407

Score = 31.5 bits (16), Expect = 9.9
Identities = 18/19 (94%)
Strand = Plus / Minus

```
Query:  398  TTAGATCAACAAAACTGTT  380
Sbjct:  192  TTAGATCCACAAAACTGTT  210
```

>dbj|AB080351.1| Bos taurus DNA, chromosome 6, DIK1186, sequence tagged site

```
          Length = 544

 Score = 31.5 bits (16), Expect = 9.9
 Identities = 16/16 (100%)
 Strand = Plus / Minus


Query:  462  GAATTCACTAGTGATT  447
Sbjct:  1    GAATTCACTAGTGATT  16
```

```
>dbj|AB080350.1| Bos taurus DNA, chromosome 6, DIK1185, sequence tagged site
          Length = 719

 Score = 31.5 bits (16), Expect = 9.9
 Identities = 16/16 (100%)
 Strand = Plus / Minus


Query:  462  GAATTCACTAGTGATT  447
Sbjct:  1    GAATTCACTAGTGATT  16
```

```
>gb|G18503.1|G18503 cow STS BM4006, sequence tagged site
          Length = 283

 Score = 31.5 bits (16), Expect = 9.9
 Identities = 16/16 (100%)
 Strand = Plus / Plus


Query:  27   GTGTGTGCGTGCTTCA  42
Sbjct:  86   GTGTGTGCGTGCTTCA  101
```

```
>gb|G11541.1|G11541 human STS SHGC-9961, sequence tagged site
          Length = 339

 Score = 31.5 bits (16), Expect = 9.9
 Identities = 16/16 (100%)
 Strand = Plus / Minus


Query:  113  TTATGAAATCTAAGGG  98
Sbjct:  129  TTATGAAATCTAAGGG  144
```

```
>emb|AL684727.1|PM2C5B Penicillium marneffei STS, clone pm2c5.b, sequence tagged site
          Length = 661

 Score = 31.5 bits (16), Expect = 9.9
 Identities = 18/19 (94%)
 Strand = Plus / Plus


Query:  38   CTTCATGGCCTCATTCAAT  56
Sbjct:  367  CTTCTTGGCCTCATTCAAT  385

  Database: Database of GenBank+EMBL+DDBJ sequences from STS Divisions
    Posted date:  Apr 11, 2003  1:13 AM
```

```
  Number of letters in database: 68,665,611
  Number of sequences in database:  163,596

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 18,334
Number of Sequences: 163596
Number of extensions: 18334
Number of successful extensions: 5036
Number of sequences better than 10.0: 27
Number of HSP's better than 10.0 without gapping: 27
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 5007
Number of HSP's gapped (non-prelim): 29
length of query: 462
length of database: 68,665,611
effective HSP length: 20
effective length of query: 442
effective length of database: 65,393,691
effective search space: 28904011422
effective search space used: 28904011422
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 16 (31.5 bits)
```

Nutrigenomics BSRC HOME BSRC BLAST

NCBI **BLAST Search Results** BLAST Entrez ?

BLASTN 2.2.5 [Nov-16-2002]

Reference:
Altschul, Stephen F., 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.

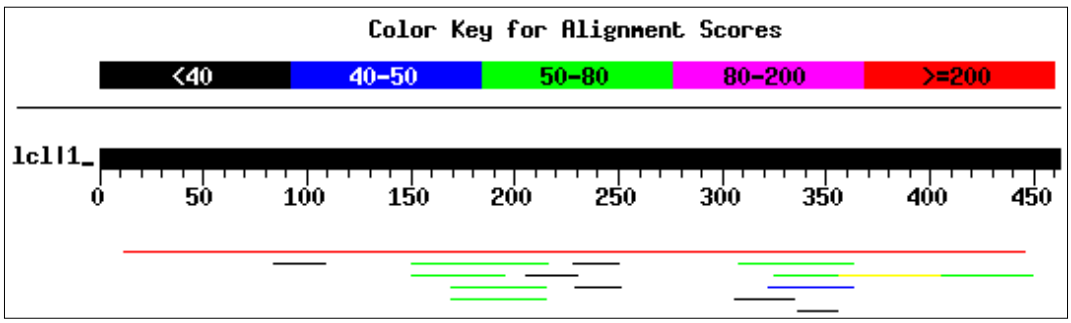
Database: Whole-Genome-Shotgun Sequences
614,378 sequences; 6,920,392,665 total letters

Query= CS63win
(462 letters)

Distribution of 15 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Mus musculus whole genome shotgun assembly contig 11..S= 419 E=1e-114"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Mus musculus whole genome shotgun assembly contig 178..S=66.1 E=4e-08"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 13 clone CH230-311D4; CH..S=60.3 E=2e-06"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 7 clone CH230-281O8; CH2..S=56.4 E=3e-05"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 18 clone CH230-245D20; C..S=56.4 E=3e-05"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 19 clone CH230-121D7; CH..S=50.7 E=0.002"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 19 clone CH230-121D7; CH..S=50.7 E=0.002"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Mus musculus whole genome shotgun assembly contig 3168,..S=41.1 E=1.3"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 11 clone CH230-235M11; CH2..S=39.1 E=5.0"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Mus musculus whole genome shotgun assembly contig 20478..S=39.1 E=5.0"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Mus musculus whole genome shotgun assembly contig 40639..S=39.1 E=5.0"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 3 clone CH230-167N21; CH23..S=39.1 E=5.0"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 3 clone CH230-407P5; CH230..S=39.1 E=5.0"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments""> Rattus norvegicus chromosome 2 clone CH230-64O22; CH230..S=39.1 E=5.0"" onmouseout="document.BLASTFORM.defline.value="Mouse-over to show defline and scores. Click to show alignments"">



Sequences producing significant alignments:		Score (bits)	E Value
emb|CAAA01137657.1|	Mus musculus whole genome shotgun assem...	419	e-114
emb|CAAA01178962.1|	Mus musculus whole genome shotgun assem...	66	4e-08
gb|AABR02076587.1|	Rattus norvegicus chromosome 13 clone CH...	60	2e-06
gb|AABR02001911.1|	Rattus norvegicus chromosome 18 clone CH...	56	3e-05
gb|AABR02036767.1|	Rattus norvegicus chromosome 7 clone CH2...	56	3e-05
gb|AABR02092267.1|	Rattus norvegicus chromosome 19 clone CH...	51	0.002
gb|AABR02135632.1|	Rattus norvegicus chromosome 19 clone CH...	51	0.002
emb|CAAA01004576.1|	Mus musculus whole genome shotgun assem...	41	1.3
gb|AABR02022944.1|	Rattus norvegicus chromosome 11 clone CH...	39	5.0
gb|AABR02014454.1|	Rattus norvegicus chromosome 3 clone CH2...	39	5.0
gb|AABR02108528.1|	Rattus norvegicus chromosome 3 clone CH2...	39	5.0
gb|AABR02027897.1|	Rattus norvegicus chromosome 2 clone CH2...	39	5.0
emb|CAAA01204784.1|	Mus musculus whole genome shotgun assem...	39	5.0
emb|CAAA01038509.1|	Mus musculus whole genome shotgun assem...	39	5.0

>emb|CAAA01137657.1| Mus musculus whole genome shotgun assembly contig 116023, whole genome shotgun sequence

Length = 4394

Score = 419 bits (218), Expect = e-114
Identities = 372/439 (84%), Gaps = 6/439 (1%)
Strand = Plus / Minus

```
Query:  446   CAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAACTCGAATAGTTAGATCAACAA  387
Sbjct:  2849  CAAACTGAGATTAGATATCCCATCATGCTTAGCCCTAAACTATAATAGTTAAATTAACAA  2908

Query:  386   AACTGTTCGCCAGAACACTACAAGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTT  327
Sbjct:  2909  AATTATTTGCCGGAATACTACAAGCAAGAACTTAAAATTAAAAGGACTTGGCGGTGCTTT  2968

Query:  326   ATATCCCTCTAAAGGAGCCTGTTCTATAATCGATAAACCCCAATTTACCTCACCACCTCT  267
Sbjct:  2969  ATATCCCTCTAGAGGGGCCTGTTCTATAATCCGTAAACCCCGATACACCTCACCACCTCT  3028

Query:  266   TGCC---CAGCCTATATACCTCCATCTTCAGCAAACCCTGGAAAGGCCACAGAGTAAGCA  210
Sbjct:  3029  TGCCCCACAGCCCATATACCACCATCGTCAGCAAACCCTAGAAAGGTTGCAGAGTAAGCA  3088

Query:  209   GAAGTATCTACATAAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG-  151
Sbjct:  3089  CAAGTATATTCATAAAAATTTTAGGTCAAGGTGTAGCCTACGAGGTGGCAAGAAATGGGC  3148

Query:  150   TACGTTTTCTACACACAGAAAAATCTCGCGACAACCGTTATGAAATCTAAGGGCTCAAGG  91
Sbjct:  3149  TACATTTTCTATAC-CCGAAAAATCTCACAACAACCCTTATGCAATCTAAAGGCTTAAGG  3207

Query:  90    AGGATTTAGCAATAAATTGAGAGCAGAGTGTTTAATTGAATGAGGCCATGAAGCACGCAC  31
Sbjct:  3208  AGGATTTAGCAGTAAACAAAGAGCAGAGTGCTTGGTTGAATAAGGCCATGAAGCACACAG  3267

Query:  30    ACACCGCCC-GTCACCCTC  13
Sbjct:  3268  ACACAACCCTGTCACCCTC  3286
```

>emb|CAAA01178962.1| Mus musculus whole genome shotgun assembly contig 178961, whole genome shotgun sequence

Length = 11542

Score = 66.1 bits (34), Expect = 4e-08

Identities = 56/67 (83%)
Strand = Plus / Minus

```
Query:  217    AGTAAGCAGAAGTATCTACATAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAG  158
Sbjct:  7533   AGTAAGCAAAAGAACAACATAAGAACATTAGGTCAAGGTGTAGCCAGTGAGGTGGAAAG  7592

Query:  157    AAATGGG  151
Sbjct:  7593   CAATGGG  7599
```

>gb|AABR02076587.1| Rattus norvegicus chromosome 13 clone CH230-311D4; CH230-86N16; CH230-167O19; CH230-173M22; CH230-107M6; CH230-447I4; CH230-11H21; CH230-54L23; CH230-139L15 strain BN/SsNHsdMCW RNOR01032200, whole genome shotgun sequence
Length = 8266

Score = 60.3 bits (31), Expect = 2e-06
Identities = 41/46 (89%)
Strand = Plus / Minus

```
Query:  196   AAAAACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGG  151
Sbjct:  329   AAAAACGTTAGGTCAAGGTGCAGCCCGTGAGGTGGGAGGGAATGGG  374
```

>gb|AABR02001911.1| Rattus norvegicus chromosome 18 clone CH230-245D20; CH230-112E16; CH230-326E5; CH230-397N4; CH230-214J13; CH230-42H17 strain BN/SsNHsdMCW RNOR01056365, whole genome shotgun sequence
Length = 97248

Score = 56.4 bits (29), Expect = 3e-05
Identities = 39/44 (88%)
Strand = Plus / Minus

```
Query:  450    GATTCAAACTGGGATTAGATACCCCACTATGCTTAACCCTAAAC  407
Sbjct:  74091  GATCCAAACTGGGATTAGATCCCCAACTATGCTTAGCCTTAAAC  74134
```

Score = 43.0 bits (22), Expect = 0.35
Identities = 28/31 (90%)
Strand = Plus / Minus

```
Query:  356    CTTAAAACTCAAAGGACTTGGCAGTGCTTTA  326
Sbjct:  74182  CTTAAAACTCAAAGGACTTGGTGGTACTTTA  74212
```

>gb|AABR02036767.1| Rattus norvegicus chromosome 7 clone CH230-281O8; CH230-19B12; CH230-15P4; CH230-214N5; CH230-5E15; CH230-355J4; CH230-228F12; CH230-256E2; CH230-198G18; CH230-204J23; CH230-127O14; CH230-32H18; CH230-117K10; CH230-61H19; CH230-288L12; CH230-42P17; CH230-8A6; CH230-44A14; CH230-312J5; CH230-220N13; CH230-41D1; CH230-126O24 strain BN/SsNHsdMCW RNOR01121648, whole genome shotgun sequence
Length = 21049

Score = 56.4 bits (29), Expect = 3e-05
Identities = 47/56 (83%)
Strand = Plus / Plus

```
Query:  309    GCTCCTTTAGAGGATATAAAGCACTGCCAAGTCCTTTGAGTTTTAAGCTGTTGCT  364
Sbjct:  3118   GCTGCTTTAGGTGGATATAAAGTCCCTCCAAGTCCTTTGAGTATTAAGCTGTGGCT  3173
```

>gb|AABR02092267.1| Rattus norvegicus chromosome 19 clone CH230-121D7; CH230-86B16; CH230-191N9 strain BN/SsNHsdMCW RNOR01062929, whole genome shotgun sequence
Length = 5937

Score = 50.7 bits (26), Expect = 0.002
Identities = 40/47 (85%)
Strand = Plus / Plus

```
Query:  170   TGGGCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTAC  216
Sbjct:  672   TGGGCTATACCTCGACCTATAGGTTTTATGTTTATACTTCTGCTTAC  718
```

>gb|AABR02135632.1| Rattus norvegicus chromosome 19 clone CH230-121D7; CH230-86B16; CH230-191N9 strain BN/SsNHsdMCW RNOR01062928, whole genome shotgun sequence
Length = 2089

Score = 50.7 bits (26), Expect = 0.002
Identities = 40/47 (85%)
Strand = Plus / Plus

```
Query:  170   TGGGCTACACCTTGACCTAACGTTTTTATGTAGATACTTCTGCTTAC  216
Sbjct:  1950  TGGGCTATACCTCGACCTACAGGTTTTATGTTTATACTTCTGCTTAC  1996
```

>emb|CAAA01004576.1| Mus musculus whole genome shotgun assembly contig 3168, whole genome shotgun sequence
Length = 53170

Score = 41.1 bits (21), Expect = 1.3
Identities = 35/42 (83%)
Strand = Plus / Minus

```
Query:  364    AGCAACAGCTTAAAACTCAAAGGACTTGGCAGTGCTTTATAT  323
Sbjct:  15570  AGCCACAGCTTAACATTCAAAGGACTTGGAGGTAATTTATAT  15611
```

>gb|AABR02022944.1| Rattus norvegicus chromosome 11 clone CH230-235M11; CH230-1O13; CH230-258I17; CH230-112L22; CH230-148P4; CH230-175H12; CH230-66A19; CH230-258E19 strain BN/SsNHsdMCW RNOR01023121, whole genome shotgun sequence
Length = 31063

Score = 39.1 bits (20), Expect = 5.0
Identities = 24/26 (92%)
Strand = Plus / Plus

```
Query:  85     AATCCTCCTTGAGCCCTTAGATTTCA  110
Sbjct:  1689   AATCCTCCTTGGACCCTTAGATTTCA  1714
```

>gb|AABR02014454.1| Rattus norvegicus chromosome 3 clone CH230-407P5; CH230-26E13;
CH230-297C18; CH230-232P6; CH230-10O17; CH230-199N23;
CH230-3B11; CH230-75J22; CH230-481F10; CH230-115N10;
CH230-387J15; CH230-147G14; CH230-5J9; CH230-16H15 strain
BN/SsNHsdMCW RNOR01087457, whole genome shotgun sequence
Length = 41721

```
 Score = 39.1 bits (20), Expect = 5.0
 Identities = 26/29 (89%)
 Strand = Plus / Plus


Query:  307    AGGCTCCTTTAGAGGGATATAAAGCACTG  335
Sbjct:  29489  AGGCTCTTTTGAGGTATATAAAGCACTG  29517
```

>gb|AABR02108528.1| Rattus norvegicus chromosome 3 clone CH230-167N21; CH230-7M8;
CH230-35H17; CH230-101A9; CH230-1H22; CH230-120H18;
CH230-221G16; CH230-15M12; CH230-11H2 strain BN/SsNHsdMCW
RNOR01084450, whole genome shotgun sequence
Length = 4251

```
 Score = 39.1 bits (20), Expect = 5.0
 Identities = 22/23 (95%)
 Strand = Plus / Plus


Query:  230   CAGGGTTTGCTGAAGATGGAGGT  252
Sbjct:  3517  CAGTGTTTGCTGAAGATGGAGGT  3539
```

>gb|AABR02027897.1| Rattus norvegicus chromosome 2 clone CH230-64O22; CH230-205I24;
CH230-231B6; CH230-128I24; CH230-451J6; CH230-189G12;
CH230-234O2; CH230-76G16; CH230-309O12; CH230-305G16;
CH230-103F5; CH230-345H9; CH230-362K3; CH230-145J8;
CH230-8P6; CH230-212H4; CH230-188J4 strain BN/SsNHsdMCW
RNOR01065499, whole genome shotgun sequence
Length = 26779

```
 Score = 39.1 bits (20), Expect = 5.0
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query:  337    CAAGTCCTTTGAGTTTTAAG  356
Sbjct:  7876   CAAGTCCTTTGAGTTTTAAG  7895
```

>emb|CAAA01204784.1| Mus musculus whole genome shotgun assembly contig 204783, whole
genome shotgun sequence
Length = 13904

```
 Score = 39.1 bits (20), Expect = 5.0
 Identities = 24/26 (92%)
 Strand = Plus / Plus
```

```
Query:  206    CTTCTGCTTACTCTGTGGCCTTTCCA  231
Sbjct:  10916  CTTCTGCTTCTTCTGTGGCCTTTCCA  10941
```

>emb|CAAA01038509.1| Mus musculus whole genome shotgun assembly contig 40639, whole genome
shotgun sequence
Length = 26715

```
 Score = 39.1 bits (20), Expect = 5.0
 Identities = 22/23 (95%)
 Strand = Plus / Plus


Query:  229    CCAGGGTTTGCTGAAGATGGAGG  251
Sbjct:  23855  CCAGGGATTGCTGAAGATGGAGG  23877

  Database: Whole-Genome-Shotgun Sequences
    Posted date:  Apr 11, 2003  1:13 AM
  Number of letters in database: 6,920,392,665
  Number of sequences in database:  614,378

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1,696,498
Number of Sequences: 614378
Number of extensions: 1696498
Number of successful extensions: 10517
Number of sequences better than 10.0: 14
Number of HSP's better than 10.0 without gapping: 14
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 10498
Number of HSP's gapped (non-prelim): 17
length of query: 462
length of database: 6,920,392,665
effective HSP length: 24
effective length of query: 438
effective length of database: 6,905,647,593
effective search space: 3024673645734
effective search space used: 3024673645734
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 15 (28.8 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)
```