

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ Formatting Results - Y0UJAYE401R

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TACG

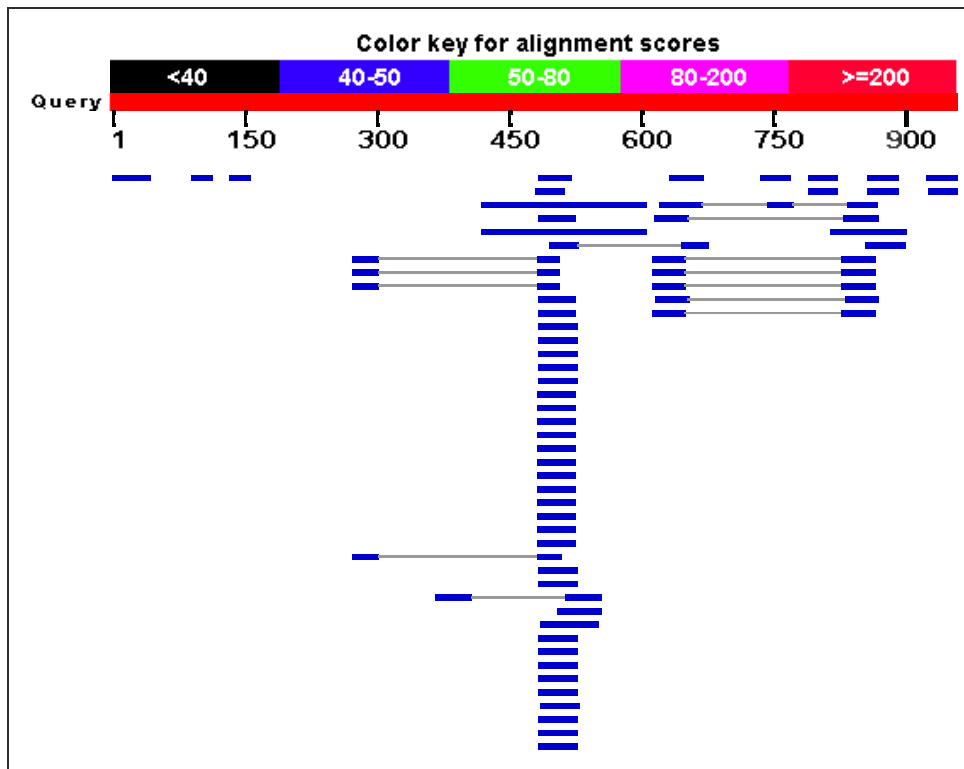
RID [Y0UJAYE401R](#) (Expires on 08-06 13:23 pm)

Query ID lc|81473
Description None
Molecule type nucleic acid
Query Length 952

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 77 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Latimeria chalumnae matrix metalloproteinase-17-like (LOC102352807), mRNA	46.4	46.4	4%	0.62	84%	XM_006010311.1
PREDICTED: Jaculus jaculus methionyl aminopeptidase 2 (Metap2), transcript variant X2, mRNA	46.4	46.4	3%	0.62	89%	XM_004650188.1
PREDICTED: Jaculus jaculus methionyl aminopeptidase 2 (Metap2), transcript variant X1, mRNA	46.4	46.4	3%	0.62	89%	XM_004650187.1
PREDICTED: Metaseiulus occidentalis oxidation resistance protein 1-like (LOC100900344), mRNA	46.4	46.4	4%	0.62	86%	XM_003741682.1
Sorghum bicolor hypothetical protein, mRNA	46.4	46.4	4%	0.62	87%	XM_002442426.1
Pan troglodytes BAC clone RP43-163P11 from chromosome 7, complete sequence	46.4	46.4	3%	0.62	94%	AC142284.1
Rhodospiridium toruloides strain CECT1137, genomic scaffold, scaffold RHTO0S12	44.6	44.6	3%	2.2	89%	LK052947.1
Bartonella tribocorum main chromosome complete genome, strain BM1374166	44.6	44.6	19%	2.2	66%	HG969192.1
PREDICTED: Macaca fascicularis sodium channel, voltage-gated, type IV, alpha subunit (SCN4A), transcript variant X1, mRNA	44.6	44.6	3%	2.2	94%	XM_005584688.1
PREDICTED: Geospiza fortis putative methyltransferase DDB_G0268948-like (LOC102038134), mRNA	44.6	89.1	8%	2.2	85%	XM_005428831.1
PREDICTED: Dasypus novemcinctus pleckstrin homology domain containing, family M (with RUN domain) member 1 (PLEKHM1), mRNA	44.6	131	11%	2.2	82%	XM_004485015.1
Bartonella tribocorum CIP 105476 complete genome, type strain CIP 105476	44.6	44.6	19%	2.2	66%	AM260525.1
Polyangium cellulosum spirangium biosynthetic gene cluster, strain So ce90	44.6	89.1	6%	2.2	91%	AM407731.1
Zebrafish DNA sequence from clone CH211-243A20 in linkage group 1, complete sequence	44.6	44.6	2%	2.2	100%	BX901927.7
Burkholderia pseudomallei genome assembly BP_3921g ,chromosome : 2	42.8	42.8	4%	7.6	83%	LK936443.1
Streptomyces iranensis genome assembly Siranensis ,scaffold SCAF00001	42.8	42.8	8%	7.6	76%	LK022848.1
PREDICTED: Callorhinchus milii tetratricopeptide repeat domain 26 (ttc26), transcript variant X3, mRNA	42.8	85.5	5%	7.6	96%	XM_007910146.1
PREDICTED: Callorhinchus milii tetratricopeptide repeat domain 26 (ttc26), transcript variant X2, mRNA	42.8	85.5	5%	7.6	96%	XM_007910145.1
PREDICTED: Callorhinchus milii tetratricopeptide repeat domain 26 (ttc26), transcript variant X1, mRNA	42.8	85.5	5%	7.6	96%	XM_007910144.1
PREDICTED: Panthera tigris altaica SLIT and NTRK-like family, member 1 (SLITRK1), mRNA	42.8	42.8	3%	7.6	88%	XM_007098413.1
Burkholderia pseudomallei MSHR520						

chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP004369.1
PREDICTED: Felis catus SLIT and NTRK-like family, member 1 (SLITRK1), mRNA	42.8	42.8	3%	7.6	88%	XM_003980471.2
Zebrafish DNA sequence from clone DKEY-211M23 in linkage group 9, complete sequence	42.8	42.8	2%	7.6	96%	CU182074.3
Burkholderia pseudomallei MSHR146 chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP004043.1
Burkholderia pseudomallei MSHR511 chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP004024.1
Burkholderia pseudomallei NCTC 13178 chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP004002.1
Burkholderia pseudomallei NAU20B-16 chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP004004.1
Burkholderia pseudomallei NCTC 13179 chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP003977.1
Burkholderia pseudomallei MSHR305 chromosome 1, complete sequence	42.8	42.8	4%	7.6	83%	CP006469.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064215570(5'-), partial sequence	42.8	42.8	4%	7.6	81%	KC950122.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064221185(3'-), partial sequence	42.8	42.8	4%	7.6	81%	KC944722.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064221418(5'-), partial sequence	42.8	42.8	4%	7.6	81%	KC944482.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064221185(5'-), partial sequence	42.8	42.8	4%	7.6	81%	KC944449.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064220086(3'-), partial sequence	42.8	42.8	4%	7.6	81%	KC941959.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064220086(5'-), partial sequence	42.8	42.8	4%	7.6	81%	KC941640.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064198155(3'-), partial sequence	42.8	42.8	4%	7.6	81%	KC939063.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064198127(3'-), partial sequence	42.8	42.8	4%	7.6	81%	KC939062.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064198127(5'-), partial sequence	42.8	42.8	4%	7.6	81%	KC939009.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064198155(5'-), partial sequence	42.8	42.8	4%	7.6	81%	KC938997.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064187672(3'-), partial sequence	42.8	42.8	4%	7.6	81%	KC938592.1
Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064187554(3'-), partial sequence	42.8	42.8	4%	7.6	81%	KC938280.1
Callorhinchus milii clone P06M13.Testis.t065 mRNA sequence	42.8	85.5	5%	7.6	96%	JX062640.1

Burkholderia pseudomallei BPC006 chromosome II, complete sequence	42.8	42.8	4%	7.6	83%	CP003782.1
Burkholderia pseudomallei 1026b chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP002834.1
Environmental Halophage eHP-7, partial genome	42.8	85.5	8%	7.6	85%	JQ807228.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Coro1c:tm 1e(KOMP)Wtsi; transgenic	42.8	85.5	7%	7.6	86%	JN957322.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Coro1c:tm 1a(KOMP)Wtsi; transgenic	42.8	85.5	7%	7.6	86%	JN953362.1
Burkholderia phymatum STM815 chromosome 1, complete sequence	42.8	42.8	5%	7.6	83%	CP001043.1
Burkholderia ambifaria MC40-6 chromosome 1, complete sequence	42.8	42.8	6%	7.6	76%	CP001025.1
Burkholderia mallei NCTC 10247 chromosome II, complete sequence	42.8	42.8	4%	7.6	83%	CP000547.1
Burkholderia pseudomallei 1106a chromosome II, complete sequence	42.8	42.8	4%	7.6	83%	CP000573.1
Burkholderia pseudomallei 668 chromosome II, complete sequence	42.8	42.8	4%	7.6	83%	CP000571.1
Burkholderia mallei NCTC 10229 chromosome II, complete sequence	42.8	42.8	4%	7.6	83%	CP000545.1
Burkholderia mallei SAVP1 chromosome II, complete sequence	42.8	42.8	4%	7.6	83%	CP000525.1
Salmo salar clone BAC S0085O16, partial sequence	42.8	42.8	3%	7.6	88%	DQ156149.1
Frankia alni str. ACN14A chromosome, complete sequence	42.8	42.8	4%	7.6	81%	CT573213.2
Schistosoma mansoni clone 087AAT microsatellite sequence	42.8	42.8	4%	7.6	82%	DQ137508.1
Burkholderia pseudomallei 1710b chromosome II, complete sequence	42.8	42.8	4%	7.6	83%	CP000125.1
Mus musculus BAC clone RP24-555M20 from chromosome 5, complete sequence	42.8	85.5	7%	7.6	86%	AC159240.3
Burkholderia mallei ATCC 23344 chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	CP000011.2
Zebrafish DNA sequence from clone DKEY-105A17 in linkage group 6, complete sequence	42.8	85.5	7%	7.6	89%	BX548005.11
Burkholderia pseudomallei strain K96243, chromosome 2, complete sequence	42.8	42.8	4%	7.6	83%	BX571966.1
Mus musculus BAC clone RP23-371A1 from 5, complete sequence	42.8	85.5	7%	7.6	86%	AC145559.4

Alignments

PREDICTED: Latimeria chalumnae matrix metalloproteinase-17-like (LOC102352807), mRNA

Sequence ID: [ref|XM_006010311.1](#) Length: 3220 Number of Matches: 1

Range 1: 3110 to 3152

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

```

Query   3      CAGACGCACACACGTTGTGTGTGCTTGCAGACGTCAGCTCACAG   45
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  3152    CACACGCACACACGTTGTGTCTGCTTTCAGGCCTGAGCACACAG   3110

```

PREDICTED: Jaculus jaculus methionyl aminopeptidase 2 (Metap2), transcript variant X2, mRNA

Range 1: 25 to 59

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	31/35(89%)	0/35(0%)	Plus/Minus	

Features:

Query 853 GCTGAGAGAGCGCGACGTTCGTGAGAGAGCGCGACG 887
Sbjct 59 GCCGAGAGAGCGCGACGGCGTGAGAGCGCGCGGC 25

PREDICTED: *Jaculus jaculus* methionyl aminopeptidase 2 (Metap2), transcript variant X1, mRNA

Sequence ID: [ref|XM_004650187.1|](#) Length: 1942 Number of Matches: 1

Range 1: 32 to 66

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	31/35(89%)	0/35(0%)	Plus/Minus	

Features:

```
Query   853    GCTGAGAGAGCGCGACGTTCGTGAGAGAGCGCGACG      887  
       |||||  
Sbjct   66     GCCGAGAGAGCGCGACGGCGTGAGAGCGCGCGGC        32
```

PREDICTED: *Metaseiulus occidentalis* oxidation resistance protein 1-like (LOC100900344), mRNA

Sequence ID: [ref|XM_003741682.1|](#) Length: 2256 Number of Matches: 1

Range 1: 1016 to 1057

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/42(86%)	1/42(2%)	Plus/Plus	

Features:

```

Query 629 GTGCAGACTGTGCTGAG-AGAGCGCGACGTCGGAGAGCGCGA 669
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 1016 GTGAAGACCGAGCTGAGGAGAGCGCGACGTCGGCGATCGCGA 1057

```

Sorghum bicolor hypothetical protein, mRNA

Sequence ID: **ref|XM_002442426.1|** Length: 1504 Number of Matches: 1

Range 1: 6 to 41

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	34/39(87%)	3/39(7%)	Plus/Minus	

Features:

```

Query    482  GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCG      520
      |||||
Sbjct    41   GAGAGCGCGGCCTG---GAGCGCGACGCGCGGAGAGCGCG      6

```

Pan troglodytes BAC clone RP43-163P11 from chromosome 7, complete sequence

Sequence ID: **gb|AC142284.1** Length: 171686 Number of Matches: 1

Range 1: 37648 to 37679

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	32/34(94%)	2/34(5%)	Plus/Minus	

Features:

```

Query    919      CGCACACGTGTGTGTGCTGTCGCACACGTGTGTG      952
          |||||
Sbjct    37679    CGCACACGTGTGTGTG-TG-CGCACACGTGTGTG      37648

```

Rhodosporidium toruloides strain CECT1137, genomic scaffold, scaffold RHTO0S12

Sequence ID: **emb|LK052947.1|** Length: 733662 Number of Matches: 1

Range 1: 555576 to 555611

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/36(89%)	1/36(2%)	Plus/Plus	

Features:

Query 479 TGAGAGAGC-GCGACCTGAGAGAGCGCGACGTCGGA 513
Sbjct 555576 TGACAGAGCTGCGAGCTGAGGGAGCGCGACGTCGGA 555611

Bartonella tribocorum main chromosome complete genome, strain BM1374166

Sequence ID: **emb|HG969192.1|** Length: 2609404 Number of Matches: 1

Range 1: 2180522 to 2180699

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	128/193(66%)	22/193(11%)	Plus/Minus	

Features:

Query 418 GAGAGCGCGACGGTGTGCAGACTGTGCTGAGAGAGCGCGAC-----GTCGCACACGTGT 471
Sbjct 2180699 GAGAGCGCGACGGG---AGAGAGTGCCGGGAGAGCGCGCCAGGAGAGTGCCAGGAGAGA 2180644
Query 472 GTGTGCTTGAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC-GTCGAGTA 530
Sbjct 2180643 GAGTGCCCGG-GAGAGCGCGACGGGAGAGAGAGTGCCG--GGAGAGCGCGACGGGAGAGTG 2180587
Query 531 CTGATTGAGAGCGCGACGTCGAGTACTGATTGAGAGAGCGCGACGGTGTGCAGACTGTG 590
Sbjct 2180586 CGACGGGAGAGTGCGACGGGAAAGAGTG--CTAGGAGAGCGCGACGG-----GAGAGTG 2180535
Query 591 CTGAGAGAGCGCG 603
Sbjct 2180534 CCGGGAGAGCGCG 2180522

PREDICTED: Macaca fascicularis sodium channel, voltage-gated, type IV, alpha subunit (SCN4A), transcript variant X1, mRNA

Sequence ID: **ref|XM_005584688.1|** Length: 7630 Number of Matches: 1

Range 1: 7576 to 7606

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	31/33(94%)	2/33(6%)	Plus/Plus	

Features:

Query 920 GCACACGTGTGTGTGCTGTGCGCACACGTGTGTG 952
Sbjct 7576 GCACACGTGTGTGTG-TGT-GCACACGTGTGTG 7606

PREDICTED: Geospiza fortis putative methyltransferase DDB_G0268948-like (LOC102038134), mRNA

Sequence ID: **ref|XM_005428831.1|** Length: 1157 Number of Matches: 2

Range 1: 784 to 822

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	33/39(85%)	0/39(0%)	Plus/Plus	

Features:

Query 612 CACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGAGAGC 650
Sbjct 784 CACGTCTGTGTGCTGGGGTGCAAGGGGTGCTGAGAGAGC 822

Range 2: 784 to 822

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	33/39(85%)	0/39(0%)	Plus/Plus	

Features:

Query 825 CACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGAGAGC 863
Sbjct 784 CACGTCTGTGTGCTGGGGTGCAAGGGGTGCTGAGAGAGC 822

PREDICTED: Dasypus novemcinctus pleckstrin homology domain containing, family M (with RUN domain) member 1 (PLEKHM1), mRNA

Sequence ID: **ref|XM_004485015.1|** Length: 5134 Number of Matches: 3

Range 1: 706 to 753

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	41/50(82%)	3/50(6%)	Plus/Minus	

Features:

Query 617 GTGTGTGCTGGTGTGCAGACTGTGCTGAGAGAGCGCGACGTC-GGAGAGC 665

Sbjct 753 GTGTGTGCTGGTGTCCAGGCTGTG--GAGAGAGAGTGAGGTCTGGAGTGC 706

Range 2: 725 to 753

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 740 GTGTGTGCTGGTGTGCAGACTGTGGAGAG 768
Sbjct 753 GTGTGTGCTGGTGTCCAGGCTGTGGAGAG 725

Range 3: 721 to 753

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/33(88%)	0/33(0%)	Plus/Minus	

Features:

Query 830 GTGTGTGCTGGTGTGCAGACTGTGCTGAGAGAG 862
Sbjct 753 GTGTGTGCTGGTGTCCAGGCTGTGGAGAGAGAG 721

Bartonella tribocorum CIP 105476 complete genome, type strain CIP 105476

Sequence ID: **emb|AM260525.1|** Length: 2619061 Number of Matches: 1

Range 1: 2185332 to 2185509

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	128/193(66%)	22/193(11%)	Plus/Minus	

Features:

Query 418 GAGAGCGCGACGGTGTGCAGACTGTGCTGAGAGAGCGCGAC-----GTCGCACACGTGT 471
Sbjct 2185509 GAGAGCGCGACGGG---AGAGAGTGCCGGGAGAGCGCGCCAGGAGAGTGCCAGGAGAGA 2185454
Query 472 GTGTGCTTGAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC-GTCGAGTA 530
Sbjct 2185453 GAGTGCCGG-GAGAGCGCGACGGGAGAGAGAGTGCCG--GGAGAGCGCGACGGGAGAGTG 2185397
Query 531 CTGATTGAGAGCGCGACGTCGAGTACTGATTGAGAGAGCGCGACGGTGTGCAGACTGTG 590
Sbjct 2185396 CGACGGGAGAGTGCGACGGGAAAGAGTG--CTAGGAGAGCGCGACGG-----GAGAGTG 2185345
Query 591 CTGAGAGAGCGCG 603
Sbjct 2185344 CCGGGAGAGCGCG 2185332

Polyangium cellulorum spirangien biosynthetic gene cluster, strain So ce90

Sequence ID: **emb|AM407731.1|** Length: 90501 Number of Matches: 2

Range 1: 25327 to 25358

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/32(91%)	0/32(0%)	Plus/Minus	

Features:

Query 643 GAGAGAGCGCGACGTCGGAGAGCGCGACGTCG 674
Sbjct 25358 GAGACAGCGCGACGTCGGCGAGCGCGAGGTCG 25327

Range 2: 25327 to 25358

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/32(91%)	0/32(0%)	Plus/Minus	

Features:

Query 495 GAGAGAGCGCGACGTCGGAGAGCGCGACGTCG 526
Sbjct 25358 GAGACAGCGCGACGTCGGCGAGCGCGAGGTCG 25327

Zebrafish DNA sequence from clone CH211-243A20 in linkage group 1, complete sequence

Sequence ID: **emb|BX901927.7|** Length: 152042 Number of Matches: 1

Range 1: 149848 to 149871

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

```

Query   135      GTCAGTCAGTCAGTGAGCTAGTCA   158
          |||
Sbjct   149848  GTCAGTCAGTCAGTGAGCTAGTCA   149871

```

Burkholderia pseudomallei genome assembly BP_3921g ,chromosome : 2

Sequence ID: **emb|LK936443.1|** Length: 3117372 Number of Matches: 1

Range 1: 2469275 to 2469313

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

putative RNA polymerase sigma factor

```

Query   482      GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG   523
          |||
Sbjct   2469275  GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG   2469313

```

Streptomyces iranensis genome assembly Siranensis ,scaffold SCAF00001

Sequence ID: **emb|LK022848.1|** Length: 11956957 Number of Matches: 1

Range 1: 8433813 to 8433894

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	65/86(76%)	5/86(5%)	Plus/Plus	

Features:

WD40 repeat-containing protein

```

Query   810      GAGCGCGACGTCGCGACCGTGTGTGTGCTGGTGT-GCAGACTGTGCTGAGAGAGCGCGAC   868
          |||
Sbjct   8433813  GAGCG-GACGTCCACAC-GTTTGAC-GCTGTCGTTGCCGGCGGTGGCGAGAGTGGC-GCC   8433868

Query   869      GTCGTGAGAGAGCGCGACGGTGTGCA   894
          |||
Sbjct   8433869  GTCGGGAGAGAACGCGACGGTGTTC   8433894

```

PREDICTED: Callorhinchus milii tetratricopeptide repeat domain 26 (ttc26), transcript variant X3, mRNA

Sequence ID: **ref|XM_007910146.1|** Length: 2414 Number of Matches: 2

Range 1: 2178 to 2204

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	27/28(96%)	1/28(3%)	Plus/Minus	

Features:

```

Query   480      GAGAGAGCGCGACCTGAGAGAGCGCGAC   507
          |||
Sbjct   2204      GAGAGAGCGCGAC-TGAGAGAGCGCGAC   2178

```

Range 2: 2178 to 2204

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	27/28(96%)	1/28(3%)	Plus/Minus	

Features:

```

Query   273      GAGAGAGCGCGACCTGAGAGAGCGCGAC   300
          |||
Sbjct   2204      GAGAGAGCGCGAC-TGAGAGAGCGCGAC   2178

```

PREDICTED: Callorhinchus milii tetratricopeptide repeat domain 26 (ttc26), transcript variant X2, mRNA

Sequence ID: **ref|XM_007910145.1|** Length: 2296 Number of Matches: 2

Range 1: 2060 to 2086

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	27/28(96%)	1/28(3%)	Plus/Minus	

Features:

```

Query   480      GAGAGAGCGCGACCTGAGAGAGCGCGAC   507

```


Sbjct 2086 GAGAGAGCGCGAC-TGAGAGAGCGCGAC 2060

Range 2: 2060 to 2086

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	27/28(96%)	1/28(3%)	Plus/Minus	

Features:

Query 273 GAGAGAGCGCGACCTGAGAGAGCGCGAC 300
Sbjct 2086 GAGAGAGCGCGAC-TGAGAGAGCGCGAC 2060

PREDICTED: *Callorhinchus milii* tetratricopeptide repeat domain 26 (ttc26), transcript variant X1, mRNA
Sequence ID: **ref|XM_007910144.1|** Length: 2549 Number of Matches: 2
Range 1: 2313 to 2339

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	27/28(96%)	1/28(3%)	Plus/Minus	

Features:

Query 480 GAGAGAGCGCGACCTGAGAGAGCGCGAC 507
Sbjct 2339 GAGAGAGCGCGAC-TGAGAGAGCGCGAC 2313

Range 2: 2313 to 2339

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	27/28(96%)	1/28(3%)	Plus/Minus	

Features:

Query 273 GAGAGAGCGCGACCTGAGAGAGCGCGAC 300
Sbjct 2339 GAGAGAGCGCGAC-TGAGAGAGCGCGAC 2313

PREDICTED: *Panthera tigris altaica* SLIT and NTRK-like family, member 1 (SLITRK1), mRNA
Sequence ID: **ref|XM_007098413.1|** Length: 2241 Number of Matches: 1
Range 1: 1558 to 1590

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/33(88%)	0/33(0%)	Plus/Minus	

Features:

Query 786 ATTGGTGTGCAGACTGTGCTGAGAGAGCGCGAC 818
Sbjct 1590 ATTGTTGTGCAGACTGAGCTTAGAGAGCGAGAC 1558

Burkholderia pseudomallei MSHR520 chromosome 2, complete sequence
Sequence ID: **gb|CP004369.1|** Length: 3391010 Number of Matches: 1
Range 1: 1113419 to 1113457

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

RNA polymerase sigma factor, sigma-70 family protein

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
Sbjct 1113419 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 1113457

PREDICTED: *Felis catus* SLIT and NTRK-like family, member 1 (SLITRK1), mRNA
Sequence ID: **ref|XM_003980471.2|** Length: 2169 Number of Matches: 1
Range 1: 1558 to 1590

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/33(88%)	0/33(0%)	Plus/Minus	

Features:

Query 786 ATTGGTGTGCAGACTGTGCTGAGAGAGCGCGAC 818
 |||||
 Sbjct 1590 ATTGTTGTGCAGACTGAGCTTAGAGAGCGAGAC 1558

Zebrafish DNA sequence from clone DKEY-211M23 in linkage group 9, complete sequence
 Sequence ID: **emb|CU182074.3|** Length: 120998 Number of Matches: 1
 Range 1: 50265 to 50290

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	25/26(96%)	0/26(0%)	Plus/Minus	

Features:

Query 92 TTGATGCTGAGGTGTGCAGACTGTGC 117
 |||||
 Sbjct 50290 TTGATGCTTAGGTGTGCAGACTGTGC 50265

Burkholderia pseudomallei MSHR146 chromosome 2, complete sequence
 Sequence ID: **gb|CP004043.1|** Length: 3245118 Number of Matches: 1
 Range 1: 2309007 to 2309045

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

RNA polymerase sigma factor, sigma-70 family protein

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 |||||
 Sbjct 2309007 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 2309045

Burkholderia pseudomallei MSHR511 chromosome 2, complete sequence
 Sequence ID: **gb|CP004024.1|** Length: 3248143 Number of Matches: 1
 Range 1: 923702 to 923740

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Minus	

Features:

RNA polymerase sigma factor, sigma-70 family protein

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 |||||
 Sbjct 923740 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 923702

Burkholderia pseudomallei NCTC 13178 chromosome 2, complete sequence
 Sequence ID: **gb|CP004002.1|** Length: 3361913 Number of Matches: 1
 Range 1: 2787395 to 2787433

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

RNA polymerase sigma factor, sigma-70 family protein

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 |||||
 Sbjct 2787395 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 2787433

Burkholderia pseudomallei NAU20B-16 chromosome 2, complete sequence
 Sequence ID: **gb|CP004004.1|** Length: 3245956 Number of Matches: 1
 Range 1: 869418 to 869456

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Minus	

Features:

RNA polymerase sigma factor, sigma-70 family protein

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 |||||
 Sbjct 869456 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 869418

Sequence ID: **gb|CP003977.1|** Length: 3340068 Number of Matches: 1
Range 1: 1335051 to 1335089

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

sigma70-ECF: RNA polymerase sigma factor, sigma-70 family...

```
Query      482      GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG      523
Sbjct     1335051  GAGGGCGCGACCTGCGCGAGCGCGTCTGT---AGAGCGCGACG      1335089
```

Burkholderia pseudomallei MSHR305 chromosome 1, complete sequence

Sequence ID: **gb|CP006469.1|** Length: 3373917 Number of Matches: 1
Range 1: 2199771 to 2199809

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

RNA polymerase sigma factor, sigma-70 family protein

```

Query      482      GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG      523
Sbjct     2199771  GAGGGCGCGACCTGCGCGAGCGCGTCTGT---AGAGCGCGACG      2199809

```

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064215570(5'-), partial sequence

Sequence ID: **gb|KC950122.1|** Length: 686 Number of Matches: 1
Range 1: 432 to 474

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	

Features:

```
Query    480   GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC      522
        ||| ||||| |
Sbjct    432   GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC      474
```

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064221185(3'-), partial sequence

Sequence ID: **gb|KC944722.1|** Length: 499 Number of Matches: 1
Range 1: 301 to 343

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

```

Query    480  GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC  522
          |||||
Sbjct    343  GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC  301

```

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064221418(5'-), partial sequence

Sequence ID: **gb|KC944482.1|** Length: 651 Number of Matches: 1
Range 1: 432 to 474

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	

Features:

```

Query  480  GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC  522
          |||||
Sbjct  432  GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC  474

```

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064221185(5'-), partial sequence

Sequence ID: **gb|KC944449.1|** Length: 696 Number of Matches: 1
Range 1: 432 to 474

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	
Features:					
Query	480	GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC	522		
Sbjct	432	GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC	474		

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064220086(3'-), partial sequence
Sequence ID: **gb|KC941959.1|** Length: 505 Number of Matches: 1
Range 1: 301 to 343

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	
Features:					
Query	480	GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC	522		
Sbjct	343	GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC	301		

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064220086(5'-), partial sequence
Sequence ID: **gb|KC941640.1|** Length: 668 Number of Matches: 1
Range 1: 432 to 474

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	
Features:					
Query	480	GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC	522		
Sbjct	432	GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC	474		

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064198155(3'-), partial sequence
Sequence ID: **gb|KC939063.1|** Length: 405 Number of Matches: 1
Range 1: 296 to 338

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	
Features:					
Query	480	GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC	522		
Sbjct	338	GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC	296		

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064198127(3'-), partial sequence
Sequence ID: **gb|KC939062.1|** Length: 458 Number of Matches: 1
Range 1: 296 to 338

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	
Features:					
Query	480	GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC	522		
Sbjct	338	GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC	296		

Symbiodinium kawagutii strain CCMP2468 clone SymkaFL1061064198127(5'-), partial sequence
Sequence ID: **gb|KC939009.1|** Length: 620 Number of Matches: 1
Range 1: 432 to 474

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	
Features:					
Query	480	GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC	522		
Sbjct	432	GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC	474		

Sequence ID: **gb|KC938997.1|** Length: 567 Number of Matches: 1
Range 1: 432 to 474

Features:

Query 480 GAGAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGAC 522
 |||||
 Spict 432 GAAAGAGCGCGACCGCAAAGAGCGCGACCGCAAAGAGCGCGAC 474

Sequence ID: **gb|KC938592.1|** Length: 441 Number of Matches: 1
Range 1: 301 to 343

Features:

```
Query    480  GAGAGAGCGCGACCTGAGAGAGCGCGACGT CGGAGAGCGCGAC      522
          ||| ||||| |
Sbjct   343  GAAAGAGCGCGACC GCAAAGAGCGCGACC GCAAAGAGCGCGAC     301
```

Sequence ID: **gb|KC938280.1|** Length: 430 Number of Matches: 1
Range 1: 301 to 343

Features:

```
Query    480 GAGAGAGCGCGACCTGAGAGAGCGCGACGTGCGAGAGCGCGAC      522
       ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   343 GAAAGAGCGCGACC CGCAAAGAGCGCGACC CGCAAAGAGCGCGAC      301
```

Sequence ID: **gb|JX062640.1|** Length: 715 Number of Matches: 2
Range 1: 484 to 510

Features:

```

Query 480  GAGAGAGCGCGACCTGAGAGAGCGCGAC 507
           |||||
Sbjct 510  GAGAGAGCGCGAC-TGAGAGAGCGCGAC 484

```

Range 2: 484 to 510

Features:

Query 273 GAGAGAGCGCGACCTGAGAGAGCGCGAC 300
 |||||
 Sbjct 510 GAGAGAGCGCGAC-TGAGAGAGCGCGAC 484

Sequence ID: **gb|CP003782.1|** Length: 3153284 Number of Matches: 1
Range 1: 2512126 to 2512164

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

42.8 bits(46) 7.6() 35/42(83%) 3/42(7%) Plus/Plus

Features:

sigma-70 family RNA polymerase sigma factor

```
Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
      |||
Sbjct 2512126 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 2512164
```

Burkholderia pseudomallei 1026b chromosome 2, complete sequence

Sequence ID: **gb|CP002834.1|** Length: 3138747 Number of Matches: 1

Range 1: 2473772 to 2473810

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

ECF subfamily RNA polymerase sigma factor

```
Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
      |||
Sbjct 2473772 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 2473810
```

Environmental Halophage eHP-7, partial genome

Sequence ID: **gb|JQ807228.1|** Length: 23476 Number of Matches: 2

Range 1: 7429 to 7468

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/40(85%)	1/40(2%)	Plus/Plus	

Features:

```
Query 367 GAGCGCGACGTCGAGTACTG-ATTGAGAGCGCGACGTCGA 405
      |||
Sbjct 7429 GAGCGCGACGTCGAGTACCGCATTGAGGGCGGGATCTCGA 7468
```

Range 2: 7429 to 7468

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/40(85%)	1/40(2%)	Plus/Plus	

Features:

```
Query 514 GAGCGCGACGTCGAGTACTG-ATTGAGAGCGCGACGTCGA 552
      |||
Sbjct 7429 GAGCGCGACGTCGAGTACCGCATTGAGGGCGGGATCTCGA 7468
```

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Coro1c:tm1e(KOMP)Wtsi; transgenic

Sequence ID: **gb|JN957322.1|** Length: 38037 Number of Matches: 2

Range 1: 812 to 847

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Minus	

Features:

```
Query 824 ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA 859
      |||
Sbjct 847 ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA 812
```

Range 2: 812 to 847

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Minus	

Features:

```
Query 611 ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA 646
      |||
Sbjct 847 ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA 812
```

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Coro1c:tm1a(KOMP)Wtsi; transgenic

Sequence ID: **gb|JN953362.1|** Length: 37995 Number of Matches: 2

Range 1: 812 to 847

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Minus	
Features:					
Query	824	ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA		859	
Sbjct	847	ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA		812	

Range 2: 812 to 847

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Minus	
Features:					
Query	611	ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA		646	
Sbjct	847	ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA		812	

Burkholderia phymatum STM815 chromosome 1, complete sequence
Sequence ID: **gb|CP001043.1|** Length: 3479187 Number of Matches: 1
Range 1: 1966386 to 1966438

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/54(83%)	4/54(7%)	Plus/Minus	
Features: RND efflux system, outer membrane lipoprotein, NodT family					
Query	503	GCGACGTCGGAGAGCGCGACG-TC-GAGTACTGATTG-AGAGCGCGACGTCGAG		553	
Sbjct	1966438	GCGACGTCGGAGAGCGCGCCGATCAGCGT-CTGGTTGTAGTTCGCGACGTCGAG		1966386	

Burkholderia ambifaria MC40-6 chromosome 1, complete sequence
Sequence ID: **gb|CP001025.1|** Length: 3443583 Number of Matches: 1
Range 1: 1072479 to 1072545

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/67(76%)	2/67(2%)	Plus/Minus	
Features: Na⁺/H⁺ antiporter NhaD and related arsenite permeases-Iik...					
Query	485	AGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACGTCGAGTAC-TGATTGAG-AGC		542	
Sbjct	1072545	AGCGCGAGCGACGCGAGCGCCACGACGACGAGCGCGACGTCGCGCACGAGATTCTGCAGC		1072486	
Query	543	GCGACGT		549	
Sbjct	1072485	GCGACGT		1072479	

Burkholderia mallei NCTC 10247 chromosome II, complete sequence
Sequence ID: **gb|CP000547.1|** Length: 2352693 Number of Matches: 1
Range 1: 260267 to 260305

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Minus	
Features:					
Query	482	GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG		523	
Sbjct	260305	GAGGGCGCGACCTGCGCGAGCGCGTCTGT---AGAGCGCGACG		260267	

Burkholderia pseudomallei 1106a chromosome II, complete sequence
Sequence ID: **gb|CP000573.1|** Length: 3100794 Number of Matches: 1
Range 1: 2457952 to 2457990

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	
Features: RNA polymerase sigma factor, sigma-70 family					

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 Sbjct 2457952 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 2457990

Burkholderia pseudomallei 668 chromosome II, complete sequence

Sequence ID: **gb|CP000571.1|** Length: 3127456 Number of Matches: 1

Range 1: 2531298 to 2531336

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

RNA polymerase sigma factor, sigma-70 family

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 Sbjct 2531298 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 2531336

Burkholderia mallei NCTC 10229 chromosome II, complete sequence

Sequence ID: **gb|CP000545.1|** Length: 2284095 Number of Matches: 1

Range 1: 1688154 to 1688192

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Minus	

Features:

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 Sbjct 1688192 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 1688154

Burkholderia mallei SAVP1 chromosome II, complete sequence

Sequence ID: **gb|CP000525.1|** Length: 1734922 Number of Matches: 1

Range 1: 1423332 to 1423370

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Minus	

Features:

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
 Sbjct 1423370 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 1423332

Salmo salar clone BAC S0085O16, partial sequence

Sequence ID: **gb|DQ156149.1|** Length: 219899 Number of Matches: 1

Range 1: 31307 to 31337

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	3/34(8%)	Plus/Plus	

Features:

Query 732 GCACACGTGTGTGTGCTGGTGTGCAGACTGTGGA 765
 Sbjct 31307 GCACACGTG---GTGCTGGTGTGCTGACTGTGGA 31337

Frankia alni str. ACN14A chromosome, complete sequence

Sequence ID: **emb|CT573213.2|** Length: 7497934 Number of Matches: 1

Range 1: 2635042 to 2635084

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	

Features:

putative aspartate kinase (partial match)

Query 484 GAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACGTCG 526
 Sbjct 2635042 GACCGCGACTTCGGTGACCGCGACGTCGGTGACCGCGACGTCG 2635084

Schistosoma mansoni clone 087AAT microsatellite sequence

Sequence ID: **gb|DQ137508.1|** Length: 430 Number of Matches: 1

Range 1: 26 to 70

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	37/45(82%)	1/45(2%)	Plus/Plus	

Features:

```
Query 850 TGTGC-TGAGAGAGCGCGACGTCGTGAGAGAGCGCGACGGTGTGC 893
      |||||
Sbjct 26 TGTGCGTGCGTGAGCGCGACGGCGTGAGAGAGCGTGAGTGCGTG 70
```

Burkholderia pseudomallei 1710b chromosome II, complete sequence

Sequence ID: **gb|CP000125.1|** Length: 3181762 Number of Matches: 1

Range 1: 1187830 to 1187868

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

RNA polymerase sigma-70 factor, ECF subfamily

```
Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
      |||||
Sbjct 1187830 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 1187868
```

Mus musculus BAC clone RP24-555M20 from chromosome 5, complete sequence

Sequence ID: **gb|AC159240.3|** Length: 197104 Number of Matches: 2

Range 1: 65704 to 65739

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Minus	

Features:

```
Query 824 ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA 859
      |||||
Sbjct 65739 ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA 65704
```

Range 2: 65704 to 65739

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Minus	

Features:

```
Query 611 ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA 646
      |||||
Sbjct 65739 ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA 65704
```

Burkholderia mallei ATCC 23344 chromosome 2, complete sequence

Sequence ID: **gb|CP000011.2|** Length: 2325379 Number of Matches: 1

Range 1: 259108 to 259146

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Minus	

Features:

```
Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTCGGAGAGCGCGACG 523
      |||||
Sbjct 259146 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 259108
```

Zebrafish DNA sequence from clone DKEY-105A17 in linkage group 6, complete sequence

Sequence ID: **emb|BX548005.11|** Length: 218236 Number of Matches: 2

Range 1: 208906 to 208939

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/35(89%)	1/35(2%)	Plus/Plus	

Features:

Query 615 GTGTGTGTGCTGGTGTGCAGACTGTGCTGAGAGAG 649
 Sbjct 208906 GTGTGTGTGTTGATGT-CTGACTGTGCTGAGAGAG 208939

Range 2: 208906 to 208939

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/35(89%)	1/35(2%)	Plus/Plus	

Features:

Query 828 GTGTGTGTGCTGGTGTGCAGACTGTGCTGAGAGAG 862
 Sbjct 208906 GTGTGTGTGTTGATGT-CTGACTGTGCTGAGAGAG 208939

Burkholderia pseudomallei strain K96243, chromosome 2, complete sequence

Sequence ID: **emb|BX571966.1|** Length: 3173005 Number of Matches: 1

Range 1: 2503760 to 2503798

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

putative RNA polymerase sigma factor

Query 482 GAGAGCGCGACCTGAGAGAGCGCGACGTGGAGAGCGCGACG 523
 Sbjct 2503760 GAGGGCGCGACCTGCGCGAGCGCGTCGT---AGAGCGCGACG 2503798

Mus musculus BAC clone RP23-371A1 from 5, complete sequence

Sequence ID: **gb|AC145559.4|** Length: 203726 Number of Matches: 2

Range 1: 41393 to 41428

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Plus	

Features:

Query 611 ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA 646
 Sbjct 41393 ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA 41428

Range 2: 41393 to 41428

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Plus	

Features:

Query 824 ACACGTGTGTGTGCTGGTGTGCAGACTGTGCTGAGA 859
 Sbjct 41393 ACACGTGTGTGTGCGTGTGTGCACACAGAGCTGAGA 41428