

Basic Local Alignment Search Tool

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CATG

RID [Y0TFSCVG015](#) (Expires on 08-06 13:04 pm)

Query ID lc|15337

Description None

Molecule type nucleic acid

Query Length 952

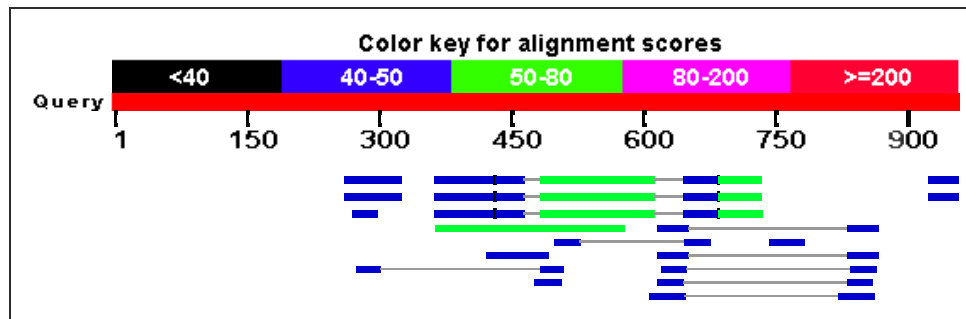
Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 47 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Efcab6:tm1a(KOMP)Ucd; transgenic	60.8	305	33%	3e-05	73%	JN962138.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Efcab6:tm1e(KOMP)Ucd; transgenic	60.8	305	33%	3e-05	73%	JN946359.1
Mouse DNA sequence from clone RP23-150J22 on chromosome 15, complete sequence	60.8	358	33%	3e-05	73%	AL513354.14
Mouse DNA sequence from clone RP23-291H20 on chromosome 2, complete sequence	57.2	314	22%	3e-04	69%	AL928805.18
PREDICTED: Chrysochloris asiatica leukocyte immunoglobulin-like receptor subfamily B member 1-like (LOC102825772), mRNA	46.4	92.7	6%	0.62	93%	XM_006868311.1
Alicyclobacillus acidocaldarius subsp. acidocaldarius Tc-4-1, complete genome	46.4	46.4	6%	0.62	78%	CP002902.1
Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446, complete genome	46.4	46.4	6%	0.62	78%	CP001727.1
Rhodospiridium toruloides strain CECT1137, genomic scaffold, scaffold RHTOOS01	44.6	44.6	7%	2.2	79%	LK052936.1
Auricularia delicata TFB-10046 SS5 hypothetical protein (AURDEDRAFT_110935), mRNA	44.6	89.1	5%	2.2	96%	XM_007338749.1
Burkholderia cenocepacia H111 chromosome 1 complete genome	44.6	89.1	7%	2.2	88%	HG938370.1
Burkholderia cenocepacia J2315 chromosome 1, complete genome	44.6	89.1	7%	2.2	88%	AM747720.1
Sorangium cellulosum So0157-2, complete genome	42.8	85.5	5%	7.6	93%	CP003969.1
Bifidobacterium bifidum PRL2010, complete genome	42.8	42.8	3%	7.6	91%	CP001840.1
Bifidobacterium bifidum S17, complete genome	42.8	42.8	3%	7.6	91%	CP002220.1
Ostreococcus tauri unnamed protein product (Ot14g02780) mRNA, partial cds	42.8	85.5	5%	7.6	93%	XM_003083021.1
Zebrafish DNA sequence from clone CH73-49O18 in linkage group 19, complete sequence	42.8	42.8	2%	7.6	96%	CU856423.16
Agrobacterium radiobacter K84 chromosome 2, complete sequence	42.8	85.5	8%	7.6	83%	CP000629.1
Brassica rapa subsp. pekinensis clone KBrB042O03, complete sequence	42.8	42.8	3%	7.6	91%	AC189348.2
Rhodobacter sphaeroides ATCC 17025 plasmid pRSPA02, complete sequence	42.8	42.8	3%	7.6	87%	CP000663.1

Alignments

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Efcab6:tm1a(KOMP)Ucd; transgenic

Sequence ID: **gb|JN962138.1|** Length: 38023 Number of Matches: 6

Range 1: 8861 to 8987

Score	Expect	Identities	Gaps	Strand	Frame
60.8 bits(66)	3e-05()	98/134(73%)	13/134(9%)	Plus/Minus	
Features:					
Query	482	GAGAGTGTGATTCGAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC-GA--CCGA			538
Sbjct	8987	GAGCGTGTGATG-GTGAGCGTGTGATGGTG-AGCGCGTGATGCTGAGCGTGTGATGCTGA			8930
Query	539	GAGTGTGATGCTGAGCATCGACCCGAGAGAGTGTGATG--GCGCGTA-GATCGCGTCGAG			595
Sbjct	8929	GCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAGCGTGTGATGG-----AG			8875
Query	596	AGAGTGTGATGCTG	609		
Sbjct	8874	AGCGTGTGATGCTG	8861		

Range 2: 8861 to 8945

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	68/91(75%)	9/91(9%)	Plus/Minus	
Features:					
Query	645	GAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATCGACCCGAGAGAGTGTGATG--GCG			702
Sbjct	8945	GAGCGTGTGATGCTG-AGCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAG			8887
Query	703	CGT-AGATCGCGTCGAGAGAGTGTGATGCTG	732		
Sbjct	8886	CGTGTGA-----TGGAGAGCGTGTGATGCTG	8861		

Range 3: 8859 to 8931

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	59/75(79%)	5/75(6%)	Plus/Minus	
Features:					
Query	482	GAGAGTGTGATTCGAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC-GACCGAGA			540
Sbjct	8931	GAGCGTGTGATGCT-GAGCATGTGATGGTG-AGCGTGTGATGCTGAGCGTGTGATGGAGA			8874
Query	541	G--TGATGCTGAG	553		
Sbjct	8873	GCGTGTGATGCTGAG	8859		

Range 4: 8841 to 8877

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	34/38(89%)	1/38(2%)	Plus/Minus	
Features:					
Query	643	GAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC	680		
Sbjct	8877	GAGAGCGTGTGATGCT-GAGTGTGTGATGTTGAGCATC	8841		

Range 5: 8864 to 8933

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Minus	
Features:					
Query	363	CTGAGAGTGTGATGCTGAGCAT-CGA--CCGAGAGTGTGATGCTGAGCATCGACCCGAGA			419
Sbjct	8933	CTGAGCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAGCGTGTGATGGAGA			8874
Query	420	GAGTGTGATG	429		
Sbjct	8873	GCGTGTGATG	8864		

Range 6: 8861 to 8960

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	76/105(72%)	11/105(10%)	Plus/Minus	
Features:					
Query	364	TGAGAGTGTGATGCTGAGCATC-GA--CCGAGAGTGTGATGCTGAGCATCGACCCGAGAG			420

```

Sbjct  8960  |||||CGCGTGTGCTGAGCGTGTGATGCTGAGCGTGTGATGCTGAGCATGTGATGGTGAG  8901
Query  421  AGTGTGATG--GCGCGTA-GATCGCGTCGAGAGAGTGTGATGCTG  462
Sbjct  8900  CGTGTGATGCTGAGCGTGTGATGG-----AGAGCGTGTGATGCTG  8861

```

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Efcab6:tm1e(KOMP)Ucd; transgenic
Sequence ID: **gb|JN946359.1|** Length: 37970 Number of Matches: 6
Range 1: 8861 to 8987

Score	Expect	Identities	Gaps	Strand	Frame
60.8 bits(66)	3e-05()	98/134(73%)	13/134(9%)	Plus/Minus	
Features:					
Query 482	GAGAGTGTGATTCGAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC-GA--CCGA	538			
Sbjct 8987	GAGCGTGTGATG-GTGAGCGTGTGATGGTG-AGCGCGTGTGCTGAGCGTGTGATGCTGA	8930			
Query 539	GAGTGTGATGCTGAGCATCGACCCGAGAGAGTGTGATG--GCGCGTA-GATCGCGTCGAG	595			
Sbjct 8929	GCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAGCGTGTGATGG-----AG	8875			
Query 596	AGAGTGTGATGCTG 609				
Sbjct 8874	AGCGTGTGATGCTG 8861				

Range 2: 8861 to 8945

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	68/91(75%)	9/91(9%)	Plus/Minus	
Features:					
Query 645	GAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATCGACCCGAGAGAGTGTGATG--GCG	702			
Sbjct 8945	GAGCGTGTGATGCTG-AGCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAG	8887			
Query 703	CGT-AGATCGCGTCGAGAGAGTGTGATGCTG 732				
Sbjct 8886	CGTGTGA-----TGGAGAGCGTGTGATGCTG 8861				

Range 3: 8859 to 8931

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	59/75(79%)	5/75(6%)	Plus/Minus	
Features:					
Query 482	GAGAGTGTGATTCGAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC-GACCGAGA	540			
Sbjct 8931	GAGCGTGTGATGCT-GAGCATGTGATGGTG-AGCGTGTGATGCTGAGCGTGTGATGGAGA	8874			
Query 541	G--TGTGATGCTGAG 553				
Sbjct 8873	GCGTGTGATGCTGAG 8859				

Range 4: 8841 to 8877

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	34/38(89%)	1/38(2%)	Plus/Minus	
Features:					
Query 643	GAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC 680				
Sbjct 8877	GAGAGCGTGTGATGCT-GAGTGTGTGATGTTGAGCATC 8841				

Range 5: 8864 to 8933

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Minus	
Features:					
Query 363	CTGAGAGTGTGATGCTGAGCAT-CGA--CCGAGAGTGTGATGCTGAGCATCGACCCGAGA	419			
Sbjct 8933	CTGAGCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAGCGTGTGATGGAGA	8874			
Query 420	GAGTGTGATG 429				
Sbjct 8873	GCGTGTGATG 8864				

Range 6: 8861 to 8960

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	76/105(72%)	11/105(10%)	Plus/Minus	

Features:

Query	364	TGAGAGTGTGATGCTGAGCATC-GA---CCGAGAGTGTGATGCTGAGCATCGACCCGAGAG	420
Sbjct	8960	TGAGCGCGTGATGCTGAGCGTGTGATGCTGAGCGTGTGATGCTGAGCATGTGATGGTGAG	8901
Query	421	AGTGTGATG--GCGCGTA-GATCGCGTCGAGAGAGTGTGATGCTG	462
Sbjct	8900	CGTGTGATGCTGAGCGTGTGATGG-----AGAGCGTGTGATGCTG	8861

Mouse DNA sequence from clone RP23-150J22 on chromosome 15, complete sequence

Sequence ID: **emb|AL513354.14|** Length: 227073 Number of Matches: 7

Range 1: 131542 to 131668

Score	Expect	Identities	Gaps	Strand	Frame
60.8 bits(66)	3e-05()	98/134(73%)	13/134(9%)	Plus/Plus	

Features:

Query	482	GAGAGTGTGATTCGAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC-GA--CCGA	538
Sbjct	131542	GAGCGTGTGATG-GTGAGCGTGTGATGGTG-AGCGCGTGATGCTGAGCGTGTGATGCTGA	131599
Query	539	GAGTGTGATGCTGAGCATCGACCCGAGAGAGTGTGATG--GCGCGTA-GATCGCGTCGAG	595
Sbjct	131600	GCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAGCGTGTGATGG-----AG	131654
Query	596	AGAGTGTGATGCTG	609
Sbjct	131655	AGCGTGTGATGCTG	131668

Range 2: 131640 to 131688

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	0.004()	44/51(86%)	2/51(3%)	Plus/Plus	

Features:

Query 482 GAGAGTGTGATTCGAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC 532
Sbjct 131640 GAGCGTGTGATG-GAGAGCGTGTGATGCT-GAGTGTGTGATGTTGAGCATC 131688

Range 3: 131584 to 131668

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	68/91(75%)	9/91(9%)	Plus/Plus	

Features:

```

Query      645      GAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATCGACCCGAGAGAGTGTGATG--GCG      702
Sbjct     131584    GAGCGTGTGATGCTG-AGCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAG      131642

Query      703      CGT-AGATCGCGTCGAGAGAGTGTGATGCTG      732
Sbjct     131643    CGTGTGA-----TGGAGAGCGTGTGATGCTG      131668

```

Range 4: 131598 to 131670

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	59/75(79%)	5/75(6%)	Plus/Plus	

Features:

Query	482	GAGAGTGTGATTCGAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC-GACCGAGA	540
Sbjct	131598	GAGCGTGTGATGCT-GAGCATGTGATGGTG-AGCGTGTGATGCTGAGCGTGTGATGGAGA	131655
Query	541	G--TGTGATGCTGAG	553
Sbjct	131656	GCGTGTGATGCTGAG	131670

Range 5: 131596 to 131665

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Plus	

Features:

```
Query   363      CTGAGAGTGTGATGCTGAGCAT--CGA--CCGAGAGTGTGATGCTGAGCATCGACCCGAGA   419
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   131596    CTGAGCGTGTGATGCTGAGCATGTGATGGTGAGCGTGTGATGCTGAGCGTGTGATGGAGA   131655

Query   420      GAGTGTGATG   429
          |||||  |||||
Sbjct   131656    GCGTGTGATG   131665
```

Range 6: 131652 to 131688

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	34/38(89%)	1/38(2%)	Plus/Plus	

Features:

```
Query   643      GAGAGAGTGTGATGCTGGAGAGTGTGATGCTGAGCATC   680
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   131652    GAGAGCGTGTGATGCT--GAGTGTGTGATGTTGAGCATC   131688
```

Range 7: 131569 to 131668

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	76/105(72%)	11/105(10%)	Plus/Plus	

Features:

```
Query   364      TGAGAGTGTGATGCTGAGCATC--GA--CCGAGAGTGTGATGCTGAGCATCGACCCGAGAG   420
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   131569    TGAGCGCGTGTGATGCTGAGCGTGTGATGCTGAGCGTGTGATGCTGAGCATGTGATGGTGAG   131628

Query   421      AGTGTGATG--GCGCGTA--GATCGCGTCGAGAGAGTGTGATGCTG   462
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   131629    CGTGTGATGCTGAGCGTGTGATGG-----AGAGCGTGTGATGCTG   131668
```

Mouse DNA sequence from clone RP23-291H20 on chromosome 2, complete sequence

Sequence ID: **emb|AL928805.18|** Length: 192688 Number of Matches: 6

Range 1: 151168 to 151383

Score	Expect	Identities	Gaps	Strand	Frame
57.2 bits(62)	3e-04()	162/234(69%)	39/234(16%)	Plus/Minus	

Features:

```
Query   364      TGAGAGTGTGATG----CTGAGCATCGACCGAGAGTGTGATG----CTGAGCATCGACCC   415
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151383    TGAGGGTGTGATGAGCACTGGGCATCCAGTGAGAGTGTGATGAGCACTGGGCAT---CCA   151327

Query   416      GAGAGAGTGTGATG--GCGCGTAGATCGCGTCGAGAGAGTGTGATGCTGTATATGCGC--GC   473
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151326    GTGAGAGTGTGATGAGCAC--TGG---GCATCCAGTGAGGGTG--TG----ATGAGCACTGG   151276

Query   474      GCGTCC--GAGAGAGTGTGATTCGAGAGAGTGTG--ATGCTG--GAGAGTGTGATG----CTG   526
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151275    GCATCCAGTGAGAGTGTGAT--GAG--CACTGGGCATCCAGTGAGAGTGTGATGAGCACTG   151219

Query   527      AGCATCGACCGAGAGTGTGATG----CTGAGCATCGACCCGAGAGAGTGTGATG   576
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151218    GGCATCCAGTGAGGGTGTGATGAGCACTGGGCAT---CCAGTGAGAGTGTGATG   151168
```

Range 2: 151139 to 151354

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	161/235(69%)	41/235(17%)	Plus/Minus	

Features:

```
Query   364      TGAGAGTGTGATG----CTGAGCATCGACCGAGAGTGTGATG----CTGAGCATCGACCC   415
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151354    TGAGAGTGTGATGAGCACTGGGCATCCAGTGAGAGTGTGATGAGCACTGGGCATCCA---   151298

Query   416      GAGAGAGTGTGATG--GCGCGTAG--ATCGCGTCGAGAGAGTGTGATGCTGTATATGCGC--G   472
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151297    GTGAGGGTGTGATGAGCACTGGGCATCCAGT---GAGAGTGTGATGA-----GCACTG   151248

Query   473      CGCGTCC--GAGAGAGTGTGATTCGAGAGAGTGTG--ATGCTG--GAGAGTGTGATG----CT   525
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151247    GGCATCCAGTGAGAGTGTGAT--GAGC--ACTGGGCATCCAGTGAGGGTGTGATGAGCACT   151191

Query   526      GAGCATCGACCGAGAGTGTGATG----CTGAGCATCGACCCGAGAGAGTGTGATG   576
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct   151190    GGGCATCCAGTGAGAGTGTGATGAGCACTGGGCAT---CCAGTGAGGGTGTGATG   151139
```

Range 3: 151226 to 151441

Score	Expect	Identities	Gaps	Strand	Frame
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Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	161/235(69%)	41/235(17%)	Plus/Minus	
Features:					
Query 364		TGAGAGTGTGATG-----CTGAGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCC			415
Sbjct 151441		TGAGAGTGTGATGAGCACTGGGCATCCAGTGAGGGTGTGATGAGCACTGGGCATCCA---			151385
Query 416		GAGAGAGTGTGATG-GCGCGTAG-ATCGCGTCGAGAGAGTGTGATGCTGTATATGCGC-G			472
Sbjct 151384		GTGAGGGTGTGATGAGCACTGGGCATCCAGT---GAGAGTGTGATGA-----GCACTG			151335
Query 473		CGCGTCC-GAGAGAGTGTGATTTCGAGAGAGTGTG-ATGCTG-GAGAGTGTGATG-----CT			525
Sbjct 151334		GGCATCCAGTGAGAGTGTGAT--GAGC-ACTGGGCATCCAGTGAGGGTGTGATGAGCACT			151278
Query 526		GAGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCCGAGAGAGTGTGATG			576
Sbjct 151277		GGGCATCCAGTGAGAGTGTGATGAGCACTGGGCAT---CCAGTGAGAGTGTGATG			151226

Range 4: 151284 to 151499

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	161/234(69%)	39/234(16%)	Plus/Minus	
Features:					
Query 364		TGAGAGTGTGATG-----CTGAGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCC			415
Sbjct 151499		TGAGAGTGTGATGAGCACTGGGCATCCAGTGAGGGTGTGATGAGCACTGGGCATCCA---			151443
Query 416		GAGAGAGTGTGATG-GCGCGTAGATCGCGTCGAGAGAGTGTGATGCTGTATATGCGC-GC			473
Sbjct 151442		GTGAGAGTGTGATGAGCAC-TGG---GCATCCAGTGAGGGTG----TG-ATGAGCACTGG			151392
Query 474		GCGTCC-GAGAGAGTGTGATTTCGAGAGAGTGTG-ATGCTG-GAGAGTGTGATG-----CTG			526
Sbjct 151391		GCATCCAGTGAGGGTGTGAT--GAGC-ACTGGGCATCCAGTGAGAGTGTGATGAGCACTG			151335
Query 527		AGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCCGAGAGAGTGTGATG			576
Sbjct 151334		GGCATCCAGTGAGAGTGTGATGAGCACTGGGCAT---CCAGTGAGGGTGTGATG			151284

Range 5: 151081 to 151296

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	160/234(68%)	39/234(16%)	Plus/Minus	
Features:					
Query 364		TGAGAGTGTGATG-----CTGAGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCC			415
Sbjct 151296		TGAGGGTGTGATGAGCACTGGGCATCCAGTGAGAGTGTGATGAGCACTGGGCAT---CCA			151240
Query 416		GAGAGAGTGTGATG-GCGCGTAGATCGCGTCGAGAGAGTGTGATGCTGTATATGCGC-GC			473
Sbjct 151239		GTGAGAGTGTGATGAGCAC-TGG---GCATCCAGTGAGGGTG-TG----ATGAGCACTGG			151189
Query 474		GCGTCC-GAGAGAGTGTGATTTCGAGAGAGTGTG-ATGCTG-GAGAGTGTGATG-----CTG			526
Sbjct 151188		GCATCCAGTGAGAGTGTGAT--GAG-CACTGGGCATCCAGTGAGGGTGTGATGAGCACTG			151132
Query 527		AGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCCGAGAGAGTGTGATG			576
Sbjct 151131		GGCATCCAGTGAGGGTGTGATGAGCACTGGGCAT---CCAGTGAGGGTGTGATG			151081

Range 6: 151052 to 151267

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	159/235(68%)	41/235(17%)	Plus/Minus	
Features:					
Query 364		TGAGAGTGTGATG-----CTGAGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCC			415
Sbjct 151267		TGAGAGTGTGATGAGCACTGGGCATCCAGTGAGAGTGTGATGAGCACTGGGCAT---CCA			151211
Query 416		GAGAGAGTGTGATG-GCGC-GTAGATCGCGTCGAGAGAGTGTGATGCTGTATATGCGC-G			472
Sbjct 151210		GTGAGGGTGTGATGAGCACTGGGCATCCAGT---GAGAGTGTGATG-----AGCACTG			151161
Query 473		CGCGTCC-GAGAGAGTGTGATTTCGAGAGAGTGTG-ATGCTG-GAGAGTGTGATG-----CT			525
Sbjct 151160		GGCATCCAGTGAGGGTGTGAT--GAG-CACTGGGCATCCAGTGAGGGTGTGATGAGCACT			151104
Query 526		GAGCATCGACCGAGAGTGTGATG-----CTGAGCATCGACCCGAGAGAGTGTGATG			576
Sbjct 151103		GGGCATCCAGTGAGGGTGTGATGAGCACTGGGCAT---CCAGTGAGGGTGTGATG			151052

Range 1: 1623 to 1652

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	
Features:					
Query	645	GAGAGTGTGATGCTGGAGAGTGTGATGCTG	674		
Sbjct	1652	GAGAGTGTGATGGTGGAGAGTGTGATGGTG	1623		

Range 2: 1623 to 1652

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	
Features:					
Query	497	GAGAGTGTGATGCTGGAGAGTGTGATGCTG	526		
Sbjct	1652	GAGAGTGTGATGGTGGAGAGTGTGATGGTG	1623		

Alicyclobacillus acidocaldarius subsp. acidocaldarius Tc-4-1, complete genome

Sequence ID: **gb|CP002902.1|** Length: 3124048 Number of Matches: 1

Range 1: 800657 to 800716

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	51/65(78%)	5/65(7%)	Plus/Plus	
Features:					
threonine dehydratase					
Query	261	TATCGATCGGGCGAGAGAGTGTGATTCGAGAGAGTGTGATGCTGTATATGCGCGCGCGTC	320		
Sbjct	800657	TATCGAACGGGCGAGAGAGCG-GATTCGAGGGAGCG---CGCTGTATACGC-CGCTCGAC	800711		
Query	321	TAGTC	325		
Sbjct	800712	TACTC	800716		

Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446, complete genome

Sequence ID: **gb|CP001727.1|** Length: 3018755 Number of Matches: 1

Range 1: 874586 to 874645

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	51/65(78%)	5/65(7%)	Plus/Plus	
Features:					
threonine dehydratase					
Query	261	TATCGATCGGGCGAGAGAGTGTGATTCGAGAGAGTGTGATGCTGTATATGCGCGCGCGTC	320		
Sbjct	874586	TATCGAACGGGCGAGAGAGCG-GATTCGAGGGAGCG---CGCTGTATACGC-CGCTCGAC	874640		
Query	321	TAGTC	325		
Sbjct	874641	TACTC	874645		

Rhodospiridium toruloides strain CECT1137, genomic scaffold, scaffold RHTO0S01

Sequence ID: **emb|LK052936.1|** Length: 2022416 Number of Matches: 1

Range 1: 1293436 to 1293500

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	56/71(79%)	7/71(9%)	Plus/Minus	
Features:					
Query	422	GTGTGATGGCGCGT-AGATCGCGTCGAGAGAGTGTGATGCTGTATATGCGCGCGCTCCG	480		
Sbjct	1293500	GTGTGA--GCCGGTGAGAT-GCGTCGAGAGAGTGTGA--CTGCGAATGCGAGCGCGGAGG	1293446		
Query	481	AGAGAGTGTGA	491		
Sbjct	1293445	A-AGAGTGTGA	1293436		

Auricularia delicata TFB-10046 SS5 hypothetical protein (AURDEDRAFT_110935), mRNA

Sequence ID: **ref|XM_007338749.1|** Length: 5067 Number of Matches: 2

Range 1: 1701 to 1727

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	26/27(96%)	0/27(0%)	Plus/Minus	
Features:					
Query	482	GAGAGTGTGATTCGAGAGAGTGTGATG	508		
Sbjct	1727	GAGAGTGTGATTCGAGAGAATGTGATG	1701		

Range 2: 1701 to 1727

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	26/27(96%)	0/27(0%)	Plus/Minus	
Features:					
Query	275	GAGAGTGTGATTCGAGAGAGTGTGATG	301		
Sbjct	1727	GAGAGTGTGATTCGAGAGAATGTGATG	1701		

Burkholderia cenocepacia H111 chromosome 1 complete genome
Sequence ID: **emb|HG938370.1|** Length: 3572953 Number of Matches: 2
Range 1: 961650 to 961683

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	30/34(88%)	0/34(0%)	Plus/Plus	
Features: Pentachlorophenol 4-monooxygenase					
Query	615	GCGCGCGCGTCGGCGCGTAGATCGCGTCGAGAGA	648		
Sbjct	961650	GCGCGCGCGTCGGCGCATCGATCGCGCCGAGCGA	961683		

Range 2: 961650 to 961683

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	30/34(88%)	0/34(0%)	Plus/Plus	
Features: Pentachlorophenol 4-monooxygenase					
Query	828	GCGCGCGCGTCGGCGCGTAGATCGCGTCGAGAGA	861		
Sbjct	961650	GCGCGCGCGTCGGCGCATCGATCGCGCCGAGCGA	961683		

Burkholderia cenocepacia J2315 chromosome 1, complete genome
Sequence ID: **emb|AM747720.1|** Length: 3870082 Number of Matches: 2
Range 1: 3265324 to 3265357

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	30/34(88%)	0/34(0%)	Plus/Minus	
Features: putative oxygenase					
Query	828	GCGCGCGCGTCGGCGCGTAGATCGCGTCGAGAGA	861		
Sbjct	3265357	GCGCGCGCGTCGGCGCATCGATCGCGCCGAGCGA	3265324		

Range 2: 3265324 to 3265357

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	30/34(88%)	0/34(0%)	Plus/Minus	
Features: putative oxygenase					
Query	615	GCGCGCGCGTCGGCGCGTAGATCGCGTCGAGAGA	648		
Sbjct	3265357	GCGCGCGCGTCGGCGCATCGATCGCGCCGAGCGA	3265324		

Sorangium cellulosum So0157-2, complete genome

Sequence ID: **gb|CP003969.1|** Length: 14782125 Number of Matches: 2
Range 1: 5160810 to 5160837

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Minus	

Features:
biopolymer transporter

```
Query   831      CGCGCGTCGGCGCGTAGATCGCGTCGAG   858
          |||||
Sbjct   5160837 CGCGCTTCGGCGCGTAGAGCGCGTCGAG   5160810
```

Range 2: 5160810 to 5160837

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Minus	

Features:
biopolymer transporter

```
Query   618      CGCGCGTCGGCGCGTAGATCGCGTCGAG   645
          |||||
Sbjct   5160837 CGCGCTTCGGCGCGTAGAGCGCGTCGAG   5160810
```

Bifidobacterium bifidum PRL2010, complete genome

Sequence ID: **gb|CP001840.1|** Length: 2214656 Number of Matches: 1
Range 1: 572749 to 572780

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/33(91%)	1/33(3%)	Plus/Plus	

Features:

```
Query   918      CTGTATATGCGCGCGCGTCGCTGTATATGCGCG   950
          |||||
Sbjct   572749 CTGTATATGCGCG-GCGTGTCTGTATATGCGCG   572780
```

Bifidobacterium bifidum S17, complete genome

Sequence ID: **gb|CP002220.1|** Length: 2186882 Number of Matches: 1
Range 1: 584439 to 584470

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/33(91%)	1/33(3%)	Plus/Plus	

Features:

```
Query   918      CTGTATATGCGCGCGCGTCGCTGTATATGCGCG   950
          |||||
Sbjct   584439 CTGTATATGCGCG-GCGTGTCTGTATATGCGCG   584470
```

Ostreococcus tauri unnamed protein product (Ot14g02780) mRNA, partial cds

Sequence ID: **ref|XM_003083021.1|** Length: 1083 Number of Matches: 2
Range 1: 1002 to 1029

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Minus	

Features:

```
Query   828      GCGCGCGCGTCGGCGCGTAGATCGCGTC   855
          |||||
Sbjct   1029      GCGCGCGCGTCGGCGCGTGGAGCGCGTC   1002
```

Range 2: 1002 to 1029

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Minus	

Features:

```
Query   615      GCGCGCGCGTCGGCGCGTAGATCGCGTC   642
          |||||
Sbjct   1029      GCGCGCGCGTCGGCGCGTGGAGCGCGTC   1002
```

Zebrafish DNA sequence from clone CH73-49O18 in linkage group 19, complete sequence

Sequence ID: **emb|CU856423.16|** Length: 117903 Number of Matches: 1

Range 1: 2104 to 2130

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

Features:

```
Query 271 GCGAGAGAGTGTGATTTCGAGAGAGTGTG 298
          |||
Sbjct 2104 GCGAGAGAGTGTG-TTCGAGAGAGTGTG 2130
```

Agrobacterium radiobacter K84 chromosome 2, complete sequence

Sequence ID: **gb|CP000629.1|** Length: 2650913 Number of Matches: 2

Range 1: 1486273 to 1486313

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/41(83%)	0/41(0%)	Plus/Plus	

Features:

```
Query 604 ATGCTGTATATGCGCGCGCGTCGGCGCGTAGATCGCGTCGA 644
          |||
Sbjct 1486273 ATCTGTCAGATGCGCGCGCGTCAGCGCGTCGAGCGCGCCGA 1486313
```

Range 2: 1486273 to 1486313

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/41(83%)	0/41(0%)	Plus/Plus	

Features:

```
Query 817 ATGCTGTATATGCGCGCGCGTCGGCGCGTAGATCGCGTCGA 857
          |||
Sbjct 1486273 ATCTGTCAGATGCGCGCGCGTCAGCGCGTCGAGCGCGCCGA 1486313
```

Brassica rapa subsp. pekinensis clone KBrB042O03, complete sequence

Sequence ID: **gb|AC189348.2|** Length: 127874 Number of Matches: 1

Range 1: 51259 to 51291

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/33(91%)	1/33(3%)	Plus/Minus	

Features:

```
Query 475 CGTCCGAGAGAGTGTGA-TTCGAGAGAGTGTGA 506
          |||
Sbjct 51291 CGTCGGAGAGAGTGTGATTTCGAGAGAGTGAGA 51259
```

Rhodobacter sphaeroides ATCC 17025 plasmid pRSPA02, complete sequence

Sequence ID: **gb|CP000663.1|** Length: 289489 Number of Matches: 1

Range 1: 59976 to 60013

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/38(87%)	1/38(2%)	Plus/Plus	

Features:

```
Query 740 GCGCGCGTCGGCGCGTAGATCGCGGAGAGTGT-GATGC 776
          |||
Sbjct 59976 GCGCGCGTCGGCGAGGAGATCGCGGAGACCGTCGATGC 60013
```