

Basic Local Alignment Search Tool

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GATC

RID [Y0U4KST6014](#) (Expires on 08-06 13:16 pm)

Query ID lc|60371

Description None

Molecule type nucleic acid

Query Length 952

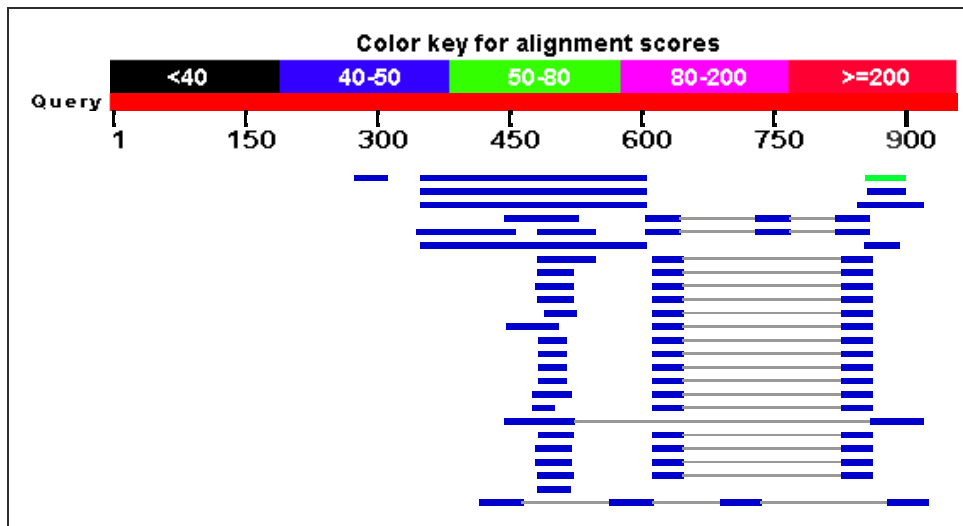
Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 93 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Trametes versicolor FP-101664 SS1 hypothetical protein partial mRNA	51.8	51.8	4%	0.015	86%	XM_008039242.1
Mus musculus BAC clone RP24-208P4 from chromosome 8, complete sequence	50.0	94.5	26%	0.051	69%	AC140672.5
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Mlycd:tm 1a(KOMP)Wtsi; transgenic	48.2	92.7	26%	0.18	71%	JN950338.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Mlycd:tm 1e(KOMP)Wtsi; transgenic	48.2	92.7	26%	0.18	71%	JN946437.1
Zebrafish DNA sequence from clone ZFOS-323E3 in linkage group 6, complete sequence	48.2	759	8%	0.18	79%	CU693486.11
Mus musculus chromosome 12, clone RP24-95M20, complete sequence	48.2	48.2	7%	0.18	77%	AC132189.13
Mus musculus chromosome 8, clone RP24-158M8, complete sequence	48.2	92.7	26%	0.18	71%	AC166781.7
Mus musculus BAC clone RP23-103I23 from chromosome 12, complete sequence	48.2	48.2	7%	0.18	77%	AC126685.5
Homo sapiens component of oligomeric golgi complex 7 (COG7), RefSeqGene on chromosome 16	46.4	46.4	4%	0.62	88%	NG_021287.1
Homo sapiens PAC clone RP5-912I13 from 7, complete sequence	46.4	46.4	4%	0.62	84%	AC008060.5
Homo sapiens chromosome 16 clone CTD-2270L9, complete sequence	46.4	46.4	4%	0.62	88%	AC008915.11
Trametes versicolor FP-101664 SS1 hypothetical protein partial mRNA	44.6	44.6	4%	2.2	83%	XM_008039240.1
Capronia coronata CBS 617.96 hypothetical protein partial mRNA	44.6	44.6	4%	2.2	85%	XM_007729182.1
PREDICTED: Astyanax mexicanus SEC14 and spectrin domains 1 (sestd1), mRNA	44.6	44.6	6%	2.2	78%	XM_007244417.1
PREDICTED: Apis mellifera uncharacterized LOC727119 (LOC727119), transcript variant X4, misc_RNA	44.6	44.6	3%	2.2	88%	XR_412437.1
PREDICTED: Apis mellifera uncharacterized LOC727119 (LOC727119), transcript variant X3, misc_RNA	44.6	44.6	3%	2.2	88%	XR_412436.1
PREDICTED: Apis mellifera uncharacterized LOC727119 (LOC727119), transcript variant X2, misc_RNA	44.6	44.6	3%	2.2	88%	XR_120709.2
PREDICTED: Apis mellifera uncharacterized LOC727119 (LOC727119), transcript variant X1, mRNA	44.6	44.6	3%	2.2	88%	XM_006572282.1
Alicyclophilus denitrificans K601, complete genome	44.6	130	12%	2.2	85%	CP002657.1
Alicyclophilus denitrificans BC, complete genome	44.6	130	12%	2.2	85%	CP002449.1
Zebrafish DNA sequence from clone CH1073-463C22 in linkage group 6, complete sequence	44.6	44.6	4%	2.2	83%	FP243361.6

Mus musculus BAC clone RP24-86K23 from chromosome 3, complete sequence	44.6	44.6	7%	2.2	77%	AC124473.2
Homo sapiens chromosome 17, clone RP11-961A15, complete sequence	44.6	44.6	2%	2.2	96%	AC130343.7
Homo sapiens BAC clone RP11-188P17 from 4, complete sequence	44.6	87.3	14%	2.2	74%	AC079766.7
Vavraia culicis subsp. floridensis hypothetical protein partial mRNA	42.8	42.8	4%	7.6	83%	XM_008076593.1
Burkholderia pseudomallei genome assembly BP_3921g ,chromosome : 2	42.8	85.5	6%	7.6	88%	LK936443.1
PREDICTED: Cynoglossus semilaevis brain-specific angiogenesis inhibitor 2 (bai2), mRNA	42.8	42.8	4%	7.6	83%	XM_008331426.1
Agaricus bisporus var. burnettii JB137-S8 hypothetical protein (AGABI1DRAFT_131809), partial mRNA	42.8	42.8	3%	7.6	86%	XM_007333413.1
Burkholderia pseudomallei MSHR520 chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	CP004369.1
Burkholderia pseudomallei MSHR146 chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	CP004043.1
Burkholderia pseudomallei MSHR511 chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	CP004024.1
Burkholderia pseudomallei NCTC 13178 chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	CP004002.1
Burkholderia pseudomallei NAU20B-16 chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	CP004004.1
Burkholderia pseudomallei MSHR305 chromosome 1, complete sequence	42.8	85.5	6%	7.6	88%	CP006469.1
Burkholderia pseudomallei BPC006 chromosome II, complete sequence	42.8	85.5	6%	7.6	88%	CP003782.1
Burkholderia pseudomallei 1026b chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	CP002834.1
Zebrafish DNA sequence from clone CH73-49O18 in linkage group 19, complete sequence	42.8	42.8	4%	7.6	86%	CU856423.16
Zebrafish DNA sequence from clone CH1073-234A12 in linkage group 19, complete sequence	42.8	42.8	4%	7.6	86%	CU655856.9
Burkholderia mallei NCTC 10247 chromosome II, complete sequence	42.8	85.5	6%	7.6	88%	CP000547.1
Burkholderia pseudomallei 1106a chromosome II, complete sequence	42.8	85.5	6%	7.6	88%	CP000573.1
Burkholderia pseudomallei 668 chromosome II, complete sequence	42.8	85.5	6%	7.6	88%	CP000571.1
Burkholderia mallei NCTC 10229 chromosome II, complete sequence	42.8	85.5	6%	7.6	88%	CP000545.1
Mus musculus chromosome 7, clone RP24-285C16, complete sequence	42.8	42.8	11%	7.6	74%	AC115858.14
Burkholderia pseudomallei 1710b chromosome II, complete sequence	42.8	85.5	6%	7.6	88%	CP000125.1
Petromyzon marinus microsatellite Pmau 7 sequence	42.8	42.8	4%	7.6	83%	AY614709.1
Rattus norvegicus BAC CH230-179I7 (Children's Hospital Oakland Research Institute Rat (BN/SSNHsd/MCW) BAC library) complete sequence	42.8	42.8	3%	7.6	86%	AC131405.5
Burkholderia mallei ATCC 23344 chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	CP000011.2
Burkholderia pseudomallei strain K96243, chromosome 2, complete sequence	42.8	85.5	6%	7.6	88%	BX571966.1
Homo sapiens 12 BAC RP11-495K9 (Roswell Park Cancer Institute Human BAC Library) complete sequence	42.8	171	19%	7.6	81%	AC117500.13

Alignments

Trametes versicolor FP-101664 SS1 hypothetical protein partial mRNA

Sequence ID: **ref|XM_008039242.1|** Length: 1659 Number of Matches: 1

Range 1: 412 to 454

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/43(86%)	0/43(0%)	Plus/Minus	

Features:

```
Query 851  CGCTGCACACACTCTCATCGTCGCACACACTCTCATCCGCGCT 893
           |||
Sbjct 454  CGCTCCACACGCTCTCATCGTCGCTCTCATCCTCATCCGCGCT 412
```

Mus musculus BAC clone RP24-208P4 from chromosome 8, complete sequence

Sequence ID: **gb|AC140672.5|** Length: 212819 Number of Matches: 2

Range 1: 74621 to 74779

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	130/189(69%)	31/189(16%)	Plus/Plus	

Features:

```
Query 416  CACACACTCTCATCCGCGCTACATGCGCTGCACACACTCTCATCGTCTATATCGCGCGCG 475
           |||
Sbjct 74621 CACACACTCTCTCTCCACAC-ACACG----GCACACACTCTC----TC-----CTCACACA 74666

Query 476  CTGGCACACACTCTCATTGCACACACTCTCATCGTCCACACTCTCATCGTCACGATGCAG 535
           |||
Sbjct 74667 CTG-CACACACACACACTGCACACACTCTC-TC-TCCTCACACACA-----CAC--TGCAC 74717

Query 536  GCACACTCTCATCGTCAC-GATGCAGGGCACACACTCTCATCCGCGCTACATGCGCTGCA 594
           |||
Sbjct 74718 ACACACACTC-TCCTCACACACACACTGCACACACTCTCCTC-----ACACACACTGCA 74770

Query 595  CACACTCTC 603
           |||
Sbjct 74771 CACACACTC 74779
```

Range 2: 74829 to 75081

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	180/264(68%)	21/264(7%)	Plus/Plus	

Features:

```
Query 350  CGCACATCATACTGTCA-CACTCTCATCGTCACGATGCAGGCACACTCTCATCGTCACG- 407
           |||
Sbjct 74829 CGCACA-CATACTCTCTCTCACACACACACACATTGCATACACTCTCTC-TCCTCACAC 74886

Query 408  ATGCAGGGCACACACTCTCA-TCCGCGCTACATGCGCTGCACACACTCTCATCGTCTATA 466
           |||
Sbjct 74887 ACACACTGCACACACTCTCTCTCTCTCAC-ACACACACTGCACACACACTC-TCCTCACAC 74944

Query 467  TCGCGCGCGCTGGCACACACTCTCATTGCACACACTCTCATCGTCCACACTCTCATC--- 523
           |||
Sbjct 74945 ACTCTCTC-CTCACACACACAC-CACA-CACACACTCTCTCTCACACACACTCTCTCTCACA 75001

Query 524  GTCACGATGCAGGCACACTCTCATCGTCAC---GATGCAGGGCACACACTCTCATCCGCG 580
           |||
Sbjct 75002 CACACATTGCA--TACACTCTCTTC-TCACACACACACACTGCACACACACTC-TCCTCA 75057

Query 581  C-TACATGCGCTGCACACACTCTC 603
           |||
Sbjct 75058 CACACACACACTGCACACACTCTC 75081
```

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

Sequence ID: **gb|JN950338.1|** Length: 38004 Number of Matches: 2

Range 1: 25933 to 26043

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	90/126(71%)	16/126(12%)	Plus/Plus	

Features:

```
Query 479  GCACACACTCTCATTGCACACACTCTCATCGTCCACACTCTCATCGTCACGATGCAGGCA 538
           |||
Sbjct 25933 GCACACACACACACTGCACACACTCTC-TC-TCCTCACACACA-----CAC--TGCACACA 25984

Query 539  CACTCTCATCGTCAC-GATGCAGGGCACACACTCTCATCCGCGCTACATGCGCTGCACAC 597
           |||
Sbjct 25985 CACACTC-TCCTCACACACACACTGCACACACTCTCTCTC-----ACACACACTGCACAC 26037

Query 598  ACTCTC 603
           |||
```

Sbjct 26038 ACACTC 26043

Range 2: 26093 to 26345

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	180/264(68%)	21/264(7%)	Plus/Plus	
Features:					
Query 350	CGCACATCATACTGTCA-CACTCTCATCGTCACGATGCAGGCACACTCTCATCGTCACG-	407			
Sbjct 26093	CGCACA-CATACTCTCCTCACACACACACACATTGCATACACTCTCTC-TCCTCACAC	26150			
Query 408	ATGCAGGGCACACACTCTCA-TCCGCGCTACATGCGCTGCACACACTCTCATCGTCTATA	466			
Sbjct 26151	ACACACTGCACACACTCTCTCTCCTCAC-ACACACACTGCACACACACTC-TCCTCACAC	26208			
Query 467	TCGCGCGCGCTGGCACACACTCTCATTGCACACACTCTCATCGTCCACACTCTCATC---	523			
Sbjct 26209	ACTCTCTC-CTCACACACAC-CACA-CACACACTCTCCTCACACACACTCTCCTCACA	26265			
Query 524	GTCACGATGCAGGCACACTCTCATCGTCAC---GATGCAGGGCACACACTCTCATCCGCG	580			
Sbjct 26266	CACACATTGCA--TAACTCTCTTC-TCACACACACACTGCACACACACTC-TCCTCA	26321			
Query 581	C-TACATGCGCTGCACACACTCTC 603				
Sbjct 26322	CACACACACACTGCACACACTCTC 26345				

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Mlycd:tm1e(KOMP)Wtsi; transgenic
Sequence ID: **gb|JN946437.1|** Length: 37970 Number of Matches: 2
Range 1: 25899 to 26009

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	90/126(71%)	16/126(12%)	Plus/Plus	
Features:					
Query 479	GCACACACTCTCATTGCACACACTCTCATCGTCCACACTCTCATCGTCACGATGCAGGCA	538			
Sbjct 25899	GCACACACACACACTGCACACACTCTC-TC-TCCTCACACACA----CAC--TGCACACA	25950			
Query 539	CACTCTCATCGTCAC-GATGCAGGGCACACACTCTCATCCGCGCTACATGCGCTGCACAC	597			
Sbjct 25951	CACACTC-TCCTCACACACACACTGCACACACTCTCCTC-----ACACACACTGCACAC	26003			
Query 598	ACTCTC 603				
Sbjct 26004	AACTC 26009				

Range 2: 26059 to 26311

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	180/264(68%)	21/264(7%)	Plus/Plus	
Features:					
Query 350	CGCACATCATACTGTCA-CACTCTCATCGTCACGATGCAGGCACACTCTCATCGTCACG-	407			
Sbjct 26059	CGCACA-CATACTCTCCTCACACACACACACATTGCATACACTCTCTC-TCCTCACAC	26116			
Query 408	ATGCAGGGCACACACTCTCA-TCCGCGCTACATGCGCTGCACACACTCTCATCGTCTATA	466			
Sbjct 26117	ACACACTGCACACACTCTCTCTCCTCAC-ACACACACTGCACACACACTC-TCCTCACAC	26174			
Query 467	TCGCGCGCGCTGGCACACACTCTCATTGCACACACTCTCATCGTCCACACTCTCATC---	523			
Sbjct 26175	ACTCTCTC-CTCACACACAC-CACA-CACACACTCTCCTCACACACTCTCCTCACA	26231			
Query 524	GTCACGATGCAGGCACACTCTCATCGTCAC---GATGCAGGGCACACACTCTCATCCGCG	580			
Sbjct 26232	CACACATTGCA--TAACTCTCTTC-TCACACACACACTGCACACACACTC-TCCTCA	26287			
Query 581	C-TACATGCGCTGCACACACTCTC 603				
Sbjct 26288	CACACACACACTGCACACACTCTC 26311				

Zebrafish DNA sequence from clone ZFOS-323E3 in linkage group 6, complete sequence
Sequence ID: **emb|CU693486.11|** Length: 42264 Number of Matches: 17
Range 1: 29389 to 29467

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	67/85(79%)	7/85(8%)	Plus/Minus	
Features:					
Query 445	GCACACACTCTCATCGTCTATATCGCGCGCGCTGGCACACACTCTCATTGCACACACTCT	504			

```

Sbjct  29467  |||||GCACACTCTCCT-GTC-ACA-CACTCTC-CTGTCACACACTCTCCTGTCACACACTCT 29412
Query   505    CATCGTC-CACACTCTCATCGTCAC 528
Sbjct  29411  CCT-GTCACACACTCTCCT-GTCAC 29389

```

Range 2: 29419 to 29468

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	44/52(85%)	3/52(5%)	Plus/Minus	

Features:

```

Query   478    GGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct  29468  GGCACACACTCTCCTGTCACACACTCTCCT-GTCACACACTCTCCT-GTCAC 29419

```

Range 3: 29119 to 29170

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	45/54(83%)	3/54(5%)	Plus/Minus	

Features:

```

Query   476    CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct  29170  CTGTCACACACTCTCCTGTCACACACTCTCCT-GTCACACACTCTCCT-GTCAC 29119

```

Range 4: 29134 to 29185

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	45/54(83%)	3/54(5%)	Plus/Minus	

Features:

```

Query   476    CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct  29185  CTGTCACACACTCTCCTGTCACACACTCTCCT-GTCACACACTCTCCT-GTCAC 29134

```

Range 5: 29149 to 29200

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	45/54(83%)	3/54(5%)	Plus/Minus	

Features:

```

Query   476    CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct  29200  CTGTCACACACTCTCCTGTCACACACTCTCCT-GTCACACACTCTCCT-GTCAC 29149

```

Range 6: 29164 to 29215

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	45/54(83%)	3/54(5%)	Plus/Minus	

Features:

```

Query   476    CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct  29215  CTGTCACACACTCTCCTGTCACACACTCTCCT-GTCACACACTCTCCT-GTCAC 29164

```

Range 7: 29179 to 29230

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	45/54(83%)	3/54(5%)	Plus/Minus	

Features:

```

Query   476    CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct  29230  CTGTCACACACTCTCCTGTCACACACTCTCCT-GTCACACACTCTCCT-GTCAC 29179

```

Range 8: 29299 to 29350

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	45/54(83%)	3/54(5%)	Plus/Minus	

Features:

Query 476 CTGGCACACACTCTCATTCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
 Sbjct 29350 CTGTCACACACTCTCTGTGCACACACTCTCCT-GTCACACACTCTCCT-GTCAC 29299

Range 9: 29194 to 29245

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/54(81%)	3/54(5%)	Plus/Minus	
Features:					
Query 476	CTGGCACACACTCTCATTCACACACTCTCATCGTC-CACACTCTCATCGTCAC	528			
Sbjct 29245	CTGTCACACACTCTTCTGTGCACACACTCTCCT-GTCACACACTCTCCT-GTCAC	29194			

Range 10: 29209 to 29260

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/54(81%)	3/54(5%)	Plus/Minus	
Features:					
Query 476	CTGGCACACACTCTCATTCACACACTCTCATCGTC-CACACTCTCATCGTCAC	528			
Sbjct 29260	CTGTCACACACTCTCTGTGCACACACTCTTCT-GTCACACACTCTCCT-GTCAC	29209			

Range 11: 29239 to 29290

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/54(81%)	3/54(5%)	Plus/Minus	
Features:					
Query 476	CTGGCACACACTCTCATTCACACACTCTCATCGTC-CACACTCTCATCGTCAC	528			
Sbjct 29290	CTGTCACACACTCTCTGTGCACACACTCTTCT-GTCACACACTCTCCT-GTCAC	29239			

Range 12: 29269 to 29320

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/54(81%)	3/54(5%)	Plus/Minus	
Features:					
Query 476	CTGGCACACACTCTCATTCACACACTCTCATCGTC-CACACTCTCATCGTCAC	528			
Sbjct 29320	CTGTCACACACTCTCTGTGCACACACTCTTCT-GTCACACACTCTCCT-GTCAC	29269			

Range 13: 29292 to 29335

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/45(84%)	2/45(4%)	Plus/Minus	
Features:					
Query 476	CTGGCACACACTCTCATTCACACACTCTCATCGTC-CACACTCT	519			
Sbjct 29335	CTGTCACACACTCTCTGTGCACACACTCTCCT-GTCACACACTCT	29292			

Range 14: 29314 to 29365

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/54(81%)	3/54(5%)	Plus/Minus	
Features:					
Query 476	CTGGCACACACTCTCATTCACACACTCTCATCGTC-CACACTCTCATCGTCAC	528			
Sbjct 29365	CTGTCACACACTCTTCTGTGCACACACTCTCCT-GTCACACACTCTCCT-GTCAC	29314			

Range 15: 29329 to 29380

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/54(81%)	3/54(5%)	Plus/Minus	
Features:					

Query 476 CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct 29380 CTGTCACACACTCTCCTGTGCACACACTCTTCT-GTCACACACTCTCCT-GTCAC 29329

Range 16: 29359 to 29410

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/54(81%)	3/54(5%)	Plus/Minus	

Features:

Query 476 CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCTCATCGTCAC 528
Sbjct 29410 CTGTCACACACTCTCCTGTGCACACACTCTTCT-GTCACACACTCTCCT-GTCAC 29359

Range 17: 29382 to 29425

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/45(84%)	2/45(4%)	Plus/Minus	

Features:

Query 476 CTGGCACACACTCTCATTTGCACACACTCTCATCGTC-CACACTCT 519
Sbjct 29425 CTGTCACACACTCTCCTGTGCACACACTCTCCT-GTCACACACTCT 29382