

T. Th Disruption Plasmid

RDB 7723

Lot# 7723 B3F1

plate ID	TDs06D09
Target gene locus Tag	TTHA1196
Vector	pGEM-T easy derivative vector
Antibiotics	Amp / Km
Competent Cell	Stbl2 (Incubate @ 30 deg)

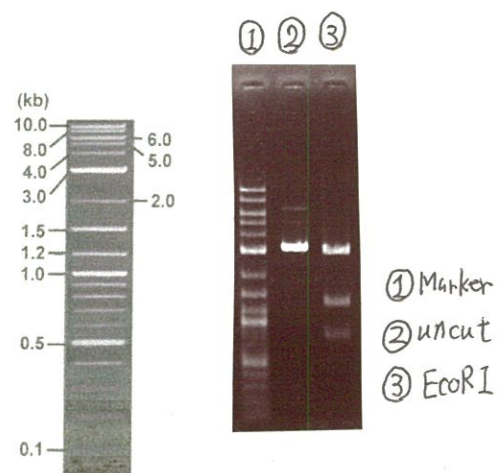
● Plasmid DNA purification/Concentration calibration

Date: 23.06.09 Culture: LB (100 ug/mL Amp, ^{12.5ug/ml} 1L Km) 10 ml -> O/N @ 30 deg
 Date: 23.06.13 Purification: QIAGEN Miniprep Kit -> dH₂O 50 ul

● Digestion by Restriction enzyme

Date: 23.06.13 DNA Concentration (O.D.) 172 ng/ul

DNA	0.6	ul
EcoRI	1	ul
Buffer H	1	ul
dH ₂ O	7.4	ul
Total	10	ul



Marker : 2-Log DNA Ladder (NEB#N3200L) Size marker : 125 ng/well

● Adjust plasmid DNA solution to 25 ng/ul ~preparation for shipping~

Date: 23.06.23 Shipped : 25 ng/ul, 40 ul

DNA (172 ng/ul)	42.0	ul
10x TE	28.8	ul
dH ₂ O	218.1	ul
Total	288.9	ul

Approved by

 23.6.23
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TDs 06D09

BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: Nucleotide Sequence

RID **8S6M1DE311R** (Expires on 06-17 16:17 pm)

Query ID **lcl|Query_379399**
 Description **None**
 Molecule type **dna**
 Query Length **762**

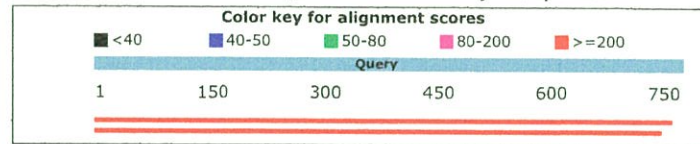
Km^R Sep

Subject ID **3 subjects**
 Description **See details**
 Molecule type **dna**
 Subject Length **2189**
 Program **BLASTN 2.14.1+**

/ Km^R Sep

Graphic Summary

Distribution of the top 2 Blast Hits on 2 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
primerA (Forward)	1397	1397	100%	0.0	99.74%	Query_379402
primerB (Reverse)	1260	1260	98%	0.0	96.85%	Query_379403

Alignments

primerA (Forward)

Sequence ID: Query_379402 Length: 1090 Number of Matches: 1
 Range 1: 104 to 865

Score	Expect	Identities	Gaps	Strand	Frame
1397 bits(756)	0.0()	760/762(99%)	0/762(0%)	Plus/Minus	
Features:					
Query 1	ATGAAAGGACCAATAAATGACTAGAGAAGAAAGAAATGAAGATTGTTCAAGAAATTAAG	60			
Sbjct 865	ATGAAAGGACCAATAAATGACTAGAGAAGAAAGAAATGAAGATTGTTCAAGAAATTAAG	806			
Query 61	GAACGAATATTGGATAAATATGGGGATGATGTTAAGGCAATTGGTGTATGGCTCTCTT	120			
Sbjct 805	GAACGAATATTGGATAAATATGGGGATGATGTTAAGGCAATTGGTGTATGGCTCTCTT	746			
Query 121	GGTCGTGAGACTGATGGGCCCTATTCGGATATTGAAATGATGTGTCTGTCAACAGAG	180			
Sbjct 745	GGTCGTGAGACTGATGGGCCCTATTCGGATATTGAAATGATGTGTCTGTCAACAGAG	686			
Query 181	GGAGTAGAGTTCAGCTATGAATGGACAACCGTGAGTGGAAAGCGGAAGTGAATTTTAT	240			
Sbjct 685	GGAGTAGAGTTCAGCTATGAATGGACAACCGTGAGTGGAAAGCGGAAGTGAATTTTAT	626			
Query 241	AGCGAAGAGATTCTACTAGATTATGCATCTCGGGTGAACCGGATGGCCGCTACACAT	300			
Sbjct 625	AGCGAAGAGATTCTACTAGATTATGCATCTCGGGTGAACCGGATGGCCGCTACACAT	566			
Query 301	GGTCGATTTTTCTCTATTTGCCGATTTATGATCCAGGTGGATACTTGAGAAAGTGATC	360			
Sbjct 565	GGTCGATTTTTCTCTATTTGCCGATTTATGATCCAGGTGGATACTTGAGAAAGTGATC	506			
Query 361	CAAACTGCTAAATCGGTAGAAGCCAAAAGTTCACGATGGGATCTGTGCCCTTATCGTA	420			
Sbjct 505	CAAACTGCTAAATCGGTAGAAGCCAAAAGTTCACGATGGGATCTGTGCCCTTATCGTA	446			
Query 421	GAAGAGCTGTTGAAATATGCAGGCAAAATGGCGTAATATTCGTGTCAAGGACGACAACA	480			
Sbjct 445	GAAGAGCTGTTGAAATATGCAGGCAAAATGGCGTAATATTCGTGTCAAGGACGACAACA	386			
Query 481	TTTCTACCATCCTTGACTGTACAGGTGGCAATGGCAGTGGCATGTTGATGGTCTGCAT	540			
Sbjct 385	TTTCTACCATCCTTGACTGTACAGGTGGCAATGGCAGTGGCATGTTGATGGTCTGCAT	326			
Query 541	CATCGCATCTGTTATACGACGAGCGCTTCGGTCTTAACGAAGCAGTTAAGCAACAGAT	600			
Sbjct 325	CATCGCATCTGTTATACGACGAGCGCTTCGGTCTTAACGAAGCAGTTAAGCAACAGAT	266			
Query 601	CTTCCTCCAGGTTATGTCCAACGTGCCAGCTCGTAATGTCCTGGTCAACTTCCGACCCCT	660			
Sbjct 265	CTTCCTCCAGGTTATGTCCAACGTGCCAGCTCGTAATGTCCTGGTCAACTTCCGACCCCT	206			
Query 661	GAGAACTCTGGAATCGCTAGAGAAATTTCTGGAATGGGGTTCAGGAGTGGCGGAACGA	720			
Sbjct 205	GAGAACTCTGGAATCGCTAGAGAAATTTCTGGAATGGGGTTCAGGAGTGGCGGAACGA	146			
Query 721	CACGGATATATAGTGGATGTGTCAAACGCATACCAATTTGA 762				
Sbjct 145	CACGGATATATAGTGGATGTGTCAAACGCATACCAATTTGA 104				

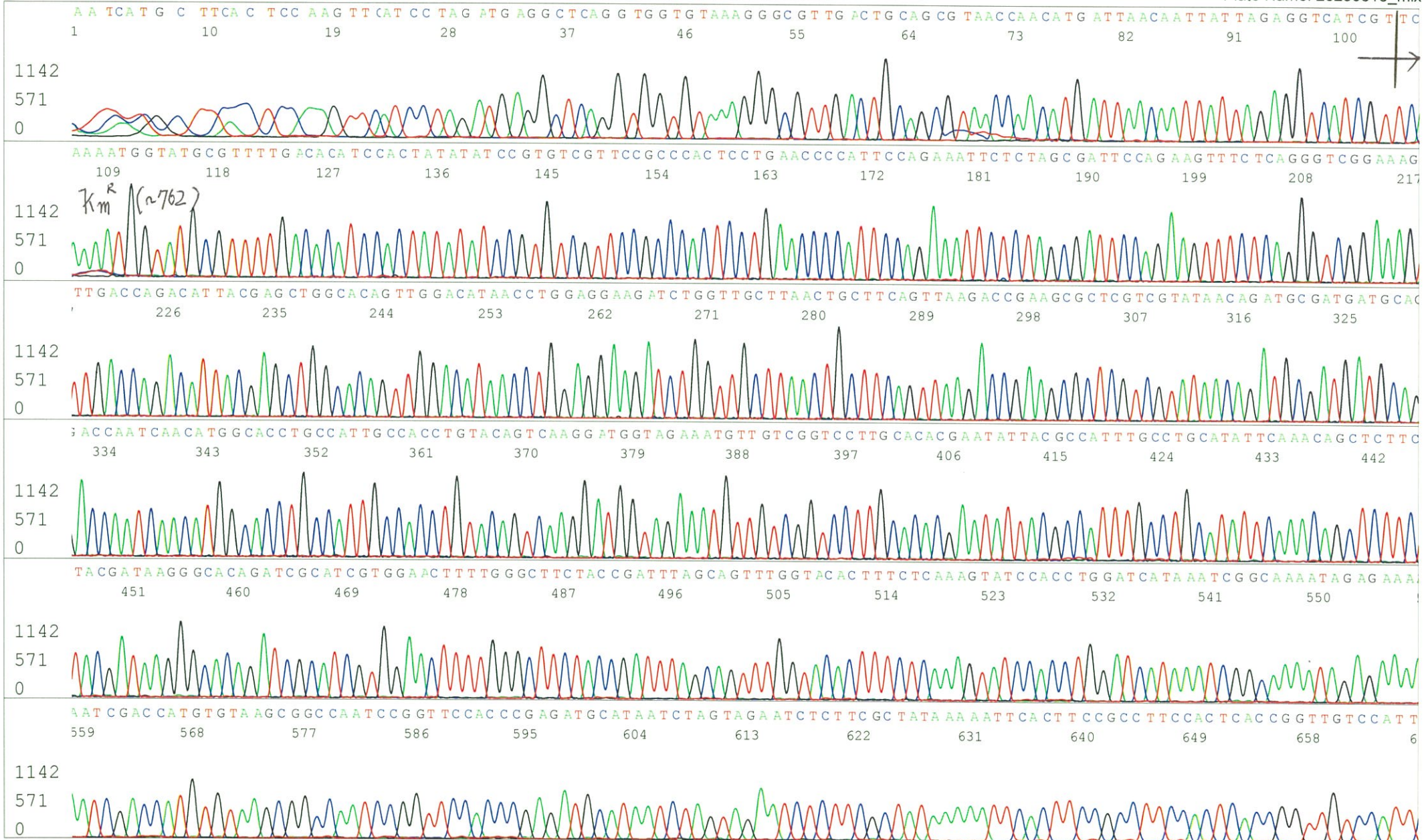
STOP

primerB (Reverse)

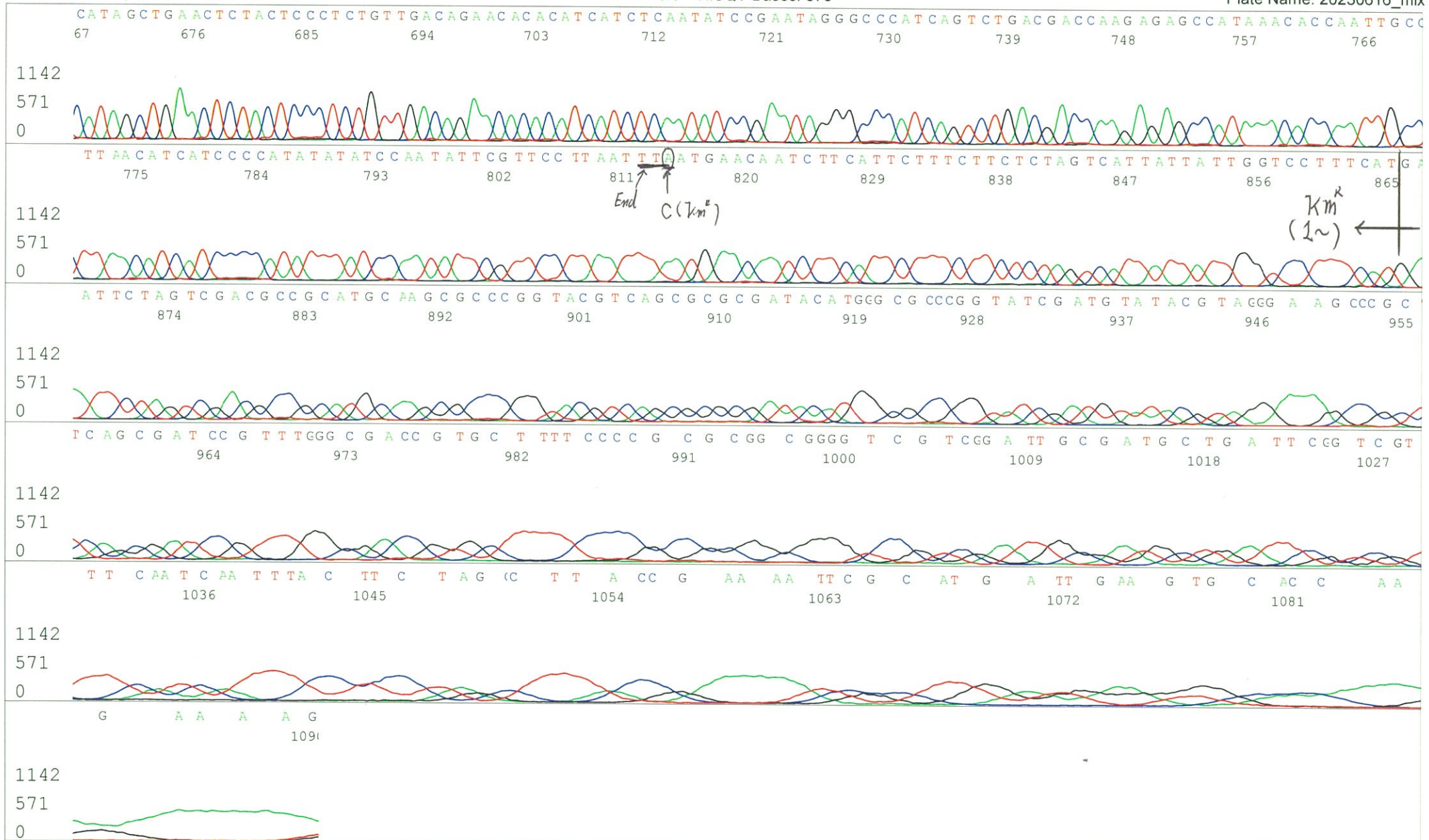
Sequence ID: Query_379403 Length: 1095 Number of Matches: 1
 Range 1: 335 to 1093

Score	Expect	Identities	Gaps	Strand	Frame
1260 bits(682)	0.0()	739/763(97%)	18/763(2%)	Plus/Plus	

S/N G:229 A:457 T:337 C:495
KB.bcp
KB 1.4.1.8 Cap:15



S/N G:229 A:457 T:337 C:495
KB.bcp
KB 1.4.1.8 Cap:15



TDS 06 D09 ~ Amp. Km

BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: dbj|AP008226|

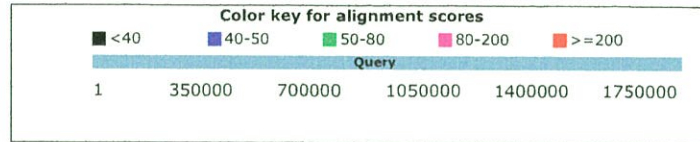
RID 8JFE7RCB114 (Expires on 06-15 12:10 pm)

Query ID AP008226.1
Description Thermus thermophilus HB8 genomic DNA, complete genome
Molecule type nucleic acid
Query Length 1849742

Subject ID 3 subjects
Description [See details](#)
Molecule type dna
Subject Length 1342
Program BLASTN 2.14.1+

Graphic Summary

Distribution of the top 2 Blast Hits on 2 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
primerB (Reverse)	966	966	0%	0.0	100.00%	Query_45769
primerA (Forward)	961	961	0%	0.0	99.81%	Query_45768

Alignments

primerB (Reverse)

Sequence ID: Query_45769 Length: 667 Number of Matches: 1
 Range 1: 104 to 626

Score	Expect	Identities	Gaps	Strand	Frame
966 bits(523)	0.0()	523/523(100%)	0/523(0%)	Plus/Plus	
Features:					
Query 1141593		CCCTGGGAAGCCTCACGGCCATAACCCCTCTGGGAAGCCCGCTCTCTCGGGAAAGCC			1141652
Sbjct 104		CCCTGGGAAGCCTCACGGCCATAACCCCTCTGGGAAGCCCGCTCTCTCGGGAAAGCC			163
Query 1141653		CCAGCATCAGGTTGAGGTTCTGCAACCGCTGCCCGCCATGCCCTTCCACAGGTTGTCCA			1141712
Sbjct 164		CCAGCATCAGGTTGAGGTTCTGCAACCGCTGCCCGCCATGCCCTTCCACAGGTTGTCCA			223
Query 1141713		GGGCGGCGAAGACCAAAACCGCCCGCTCTCTCGTGTAGAGGGGCTCACGTCACCC			1141772
Sbjct 224		GGGCGGCGAAGACCAAAACCGCCCGCTCTCTCGTGTAGAGGGGCTCACGTCACCC			283
Query 1141773		GGTTGCTCCCGAGGGTGGCTTGGTCTCGGGAAGCCCTTAAGGACCCGACGAAAGGCT			1141832
Sbjct 284		GGTTGCTCCCGAGGGTGGCTTGGTCTCGGGAAGCCCTTAAGGACCCGACGAAAGGCT			343
Query 1141833		CCCGGGGTAGAAGTCCCGTAAAGCGCCTCTAGGCTCTCTGGCTCAAAGCCGCTCCA			1141892
Sbjct 344		CCCGGGGTAGAAGTCCCGTAAAGCGCCTCTAGGCTCTCTGGCTCAAAGCCGCTCCA			403
Query 1141893		CCTCCGCTCCGGGTTGACAGGATCCCGGGTCAATGGGCACCAAGTGGGGGTGAAGG			1141952
Sbjct 404		CCTCCGCTCCGGGTTGACAGGATCCCGGGTCAATGGGCACCAAGTGGGGGTGAAGG			463
Query 1141953		AAAGCCGACCCGCTCGCCTCCCGTGGGTGCGGACGGGCTCCCTGGGCAAAATCC			1142012
Sbjct 464		AAAGCCGACCCGCTCGCCTCCCGTGGGTGCGGACGGGCTCCCTGGGCAAAATCC			523
Query 1142013		TCCCCAGGTTCCGCTCCATCTCGGGGATGTGCCGGTGGGTGCCCGCCCTTGTAGGGCT			1142072
Sbjct 524		TCCCCAGGTTCCGCTCCATCTCGGGGATGTGCCGGTGGGTGCCCGCCCTTGTAGGGCT			583
Query 1142073		TGAGGTTCTCGTTGACCTCGGCGAAGGCGGTgccccgcccctc			1142115
Sbjct 584		TGAGGTTCTCGTTGACCTCGGCGAAGGCGGTgccccgcccctc			626

primerA (Forward)

Sequence ID: Query_45768 Length: 671 Number of Matches: 1
 Range 1: 89 to 612

Score	Expect	Identities	Gaps	Strand	Frame
961 bits(520)	0.0()	523/524(99%)	1/524(0%)	Plus/Minus	
Features:					
Query 1139973		CCGTAGACCCGGACGAGCCCGCTTCCAGGGCTCGGTGCCTCCAGTTGGAATCCTCGGG			1140032
Sbjct 612		CCGTAGACCCGGACGAGCCCGCTTCCAGGGCTCGGTGCCTCCAGTTGGAATCCTCGGG			553
Query 1140033		GGATCGTTGTCCAGGGTGAAGGCGACCCGCGCTCGCCGGTTGCCACCCGCTCTCG			1140092
Sbjct 552		GGATCGTTGTCCAGGGTGAAGGCGACCCGCGCTCGCCGGTTGCCACCCGCTCTCG			493
Query 1140093		GCCTCGAGGACGATCTCCGCGTGCCTGAGGAGGGGGCTCCAGGCGGAAGCGGAAGGCC			1140152
Sbjct 492		GCCTCGAGGACGATCTCCGCGTGCCTGAGGAGGGGGCTCCAGGCGGAAGCGGAAGGCC			433
Query 1140153		ACCAGGGGCTTGCCCCGGGAGGGGCTCGAGGACCTCCCGCCGTTGACCCGGACGGAG			1140212

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Sbjct 432 ACCAGGGGCTTGCCCGGGAGGGGGCTCGAGGACCTCCCGCCGTTGACCCGGACGGAG 373
Query 1140213 ACCACCCCGGAGGGGTCAAAAAGGTACCCCTCCGCGAGCAGGCTCCGGCCAGGGGCCACG 1140272
Sbjct 372 ACCACCCCGGAGGGGTCAAAAAGGTACCCCTCCGCGAGCAGGCTCCGGCCAGGGGCCACG 313
Query 1140273 CCGCCCCCTTGGGGATAAACGAGGCCACCTCGGGCCGAGGGTGTGCGGCCGGGGCCAG 1140332
Sbjct 312 CCGCCCCCTTGGGGATAAACGAGGCCACCTCGGGCCGAGGGTGTGCGGCCGGGGCCAG 253
Query 1140333 GCGGAGAGGAGGAAAAGCAAAAAGGAGGGGACGCCAGCGCATCCCCCATCATAGCCTCC 1140392
Sbjct 252 GCGGAGAGGAGGAAAAGCAAAAAGGAGGGGACGCCAGCGCATCCCCCATCATAGCCTCC 193
Query 1140393 CCTTACCTGAGGATCACCAGGAATAGACCCAAAACCGCTTCATCGCTTCACTCCAAG 1140452
Sbjct 192 CCTTACCTGAGGATCACCAGGAATAGACCCAAAACCGCTTCATCGCTTCACTCCAAG 133
Query 1140453 TTCATCCTAGATGAGGCTCAGGTGGTGTAAAGGGCTTGA-TGC 1140495
Sbjct 132 TTCATCCTAGATGAGGCTCAGGTGGTGTAAAGGGCTTGA-TGC 89

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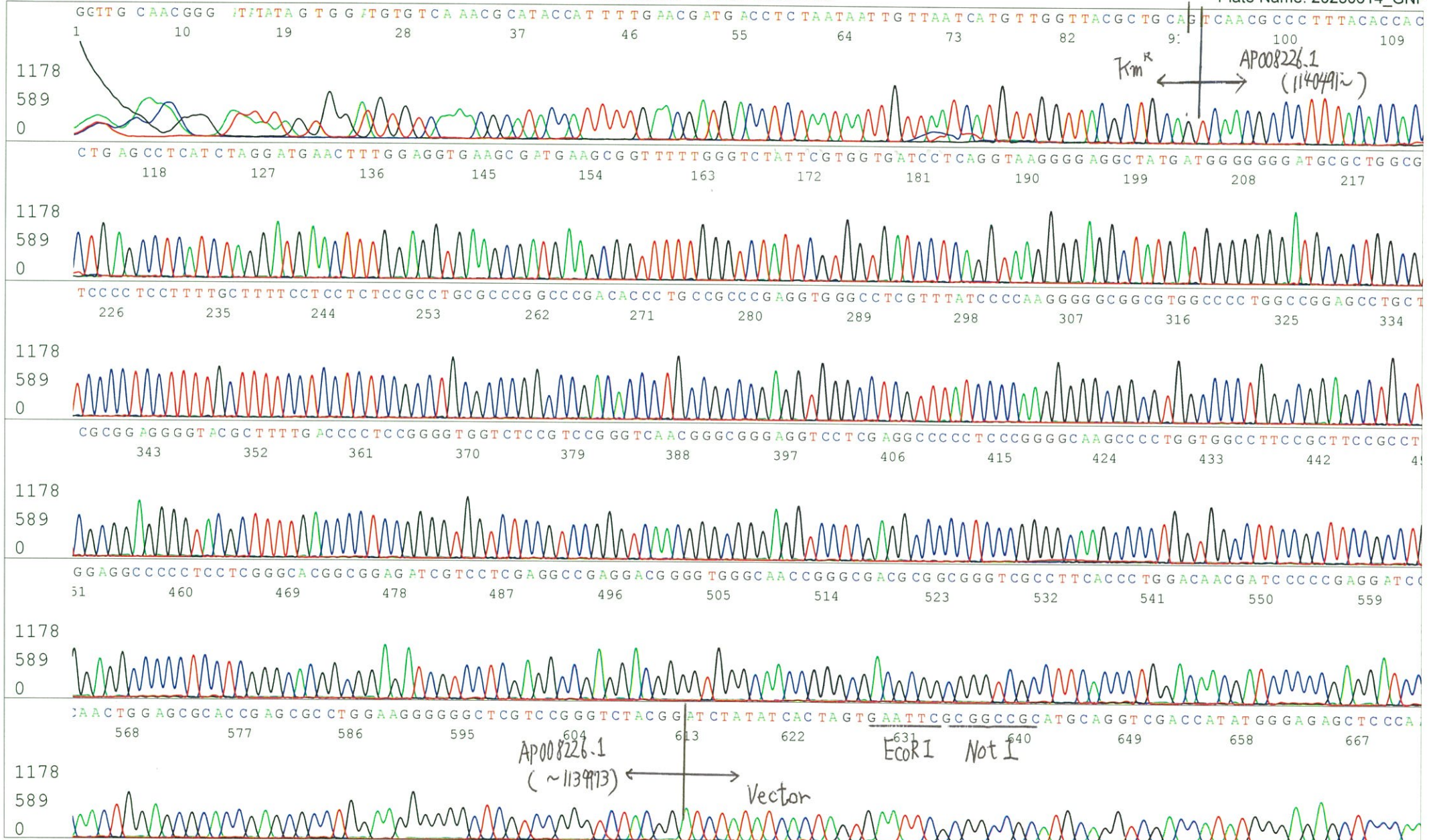
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S/N G:250 A:346 T:209 C:390
KB.bcp
KB 1.4.1.8 Cap:14



S/N G:351 A:478 T:306 C:711
KB.bcp
KB 1.4.1.8 Cap:17

