

BLASTn Search Outputs of the 5' End Border Sequences against GenBank No-human and No-mouse ESTs (est_others)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= Region_1
(1852 letters)

Database: /usr/local/blast/db/blastlibs/est_others
52,386,385 sequences; 29,661,423,624 total letters

Searching..... done

Sequences producing significant alignments:			Score	E
			(bits)	Value
gb FL476102.1	2002854 CERES-227 Zea mays cDNA clone 400160 3', ...	111	1e-20	
gb EG156227.1	MSAM281219_1210_4049 LCM-dissected maize inbred l...	88	2e-13	
gb EG272559.1	MSAM184733_2591_1943 LCM-dissected maize inbred l...	88	2e-13	
gb DW974630.1	MSAM293083_3262_0305 LCM-dissected maize shoot ap...	64	3e-06	
gb EG279004.1	MSAM238822_3284_2688 LCM-dissected maize inbred l...	58	2e-04	
gb DW952766.1	MSAM246175_3627_3291 LCM-dissected maize shoot ap...	58	2e-04	
gb DW739830.1	MSAM055005_1168_1927 LCM-dissected maize shoot ap...	58	2e-04	
gb FL444656.1	1860010 CERES-197 Zea mays cDNA clone 289347 3', ...	54	0.003	
gb FL307895.1	2966196 CERES-227 Zea mays cDNA clone 507820 5', ...	54	0.003	
gb EE177871.1	ZM_BFc0158M15.f ZM_BFc Zea mays cDNA clone ZM_BFc...	54	0.003	
gb DR810967.1	ZM_BFb0038P15.f ZM_BFb Zea mays cDNA 3', mRNA seq...	54	0.003	
gb CA624360.1	w1ln.pk0118.h11 w1ln Triticum aestivum cDNA clone...	54	0.003	
gb FL449557.1	25275633 CERES-504 Zea mays cDNA clone 1543085 3'...	52	0.011	
gb FL181981.1	25385388 CERES-505 Zea mays cDNA clone 1664626 5'...	52	0.011	
gb FL181975.1	25382983 CERES-505 Zea mays cDNA clone 1662221 5'...	52	0.011	
gb DW840364.1	MSAM290571_0500_2033 LCM-dissected maize shoot ap...	50	0.045	
gb FL414619.1	5792184 CERES-CB5 Zea mays cDNA clone 1163363 5',...	48	0.18	
gb FL412940.1	6647374 CERES-CB5 Zea mays cDNA clone 1211549 5',...	48	0.18	
gb FL347392.1	1747881 CERES-227 Zea mays cDNA clone 400160 5', ...	48	0.18	
gb FL386242.1	6662328 CERES-CB6 Zea mays cDNA clone 1226503 5',...	48	0.18	
gb FL372857.1	5792169 CERES-CB5 Zea mays cDNA clone 1163348 5',...	48	0.18	
gb FL390932.1	6655462 CERES-CB5 Zea mays cDNA clone 1219637 5',...	48	0.18	
gb FL381566.1	5749223 CERES-CB5 Zea mays cDNA clone 1155021 5',...	48	0.18	
gb DW833979.1	MSAM271088_0946_2262 LCM-dissected maize shoot ap...	48	0.18	
gb DW776038.1	MSAM143878_0611_1314 LCM-dissected maize shoot ap...	48	0.18	
gb CK327315.1	EST4624 Zea mays sperm cell cDNA library Zea mays...	48	0.18	

gb CF627516.1	zmrws05_0B20-012-c03.s4 zmrws05 Zea mays cDNA 3',...	48	0.18
gb EG224928.1	MSAM123648_2411_0798 LCM-dissected maize inbred l...	46	0.70
gb EG308159.1	MSAM260305_2985_0046 LCM-dissected maize inbred l...	46	0.70
gb EG094444.1	MSAM117322_1237_2624 LCM-dissected maize inbred l...	46	0.70
gb EG105069.1	MSAM177973_0587_0066 LCM-dissected maize inbred l...	46	0.70
gb EY958855.1	Contag_8428 Maize ovary - Eveland 2007 Zea mays c...	46	0.70
gb DW968659.1	MSAM278959_3123_2208 LCM-dissected maize shoot ap...	46	0.70
gb DW964403.1	MSAM268770_3379_3722 LCM-dissected maize shoot ap...	46	0.70
gb DW838950.1	MSAM282407_1557_3507 LCM-dissected maize shoot ap...	46	0.70
gb DW780235.1	MSAM153038_1935_0558 LCM-dissected maize shoot ap...	46	0.70
gb EB400206.1	ZM_BFb0305C08.f ZM_BFb Zea mays cDNA 3', mRNA seq...	46	0.70
gb CX065243.1	PDUts2098D12 Porcine testis cDNA library II Sus s...	46	0.70
emb FM926510.1	FM926510 REH (sb103) Brachionus plicatilis cDNA ...	44	2.8
gb FL151656.1	2009566 CERES-197 Zea mays cDNA clone 411939 5', ...	44	2.8
gb FL151333.1	1045133 CERES-197 Zea mays cDNA clone 219978 5', ...	44	2.8
gb EY886124.1	LT33-C1-003-014-F05-CT.F Tahiti lime leaf, greenh...	44	2.8
gb EG051807.1	MSAM012067_0152_2204 LCM-dissected maize inbred l...	44	2.8
gb EG287683.1	MSAM217260_2824_1862 LCM-dissected maize inbred l...	44	2.8
gb EG059501.1	MSAM084114_1654_1108 LCM-dissected maize inbred l...	44	2.8
gb EG092520.1	MSAM113605_0184_3136 LCM-dissected maize inbred l...	44	2.8
dbj DB841588.1	DB841588 NLEA Nilaparvata lugens cDNA clone NLEA...	44	2.8
dbj DB846613.1	DB846613 NLEB Nilaparvata lugens cDNA clone NLEB...	44	2.8
gb EY264291.1	BF01030A1B12.f1 Normalized subtracted keck librar...	44	2.8
gb EY259966.1	BF01003X1G03.f1 Normalized subtracted keck librar...	44	2.8
gb EY259488.1	BF01025A1E10.f1 Normalized subtracted keck librar...	44	2.8
gb EE047687.2	ZM_BFc0120J17.f ZM_BFc Zea mays cDNA clone ZM_BFc...	44	2.8
emb AM581222.1	AM581222 RZPD MPMGp1173 Paracentrotus lividus GA...	44	2.8
gb DW897577.1	MSAM116936_3007_3914 LCM-dissected maize shoot ap...	44	2.8
gb CF041009.1	QCI20f01.yg QCI Zea mays cDNA clone QCI20f01, mRN...	44	2.8
gb BF706840.1	281486 MARC 3BOV Bos taurus cDNA 5', mRNA sequence	44	2.8

>gb|FL476102.1| 2002854 CERES-227 Zea mays cDNA clone 400160 3', mRNA sequence
Length = 555

Score = 111 bits (56), Expect = 1e-20
Identities = 117/136 (86%), Gaps = 1/136 (0%)
Strand = Plus / Minus

Query: 1715 cttgtaaccaccacatatagatccatcccaagaagtagtgattacgcctctctaagcg 1774
|||||
Sbjct: 377 cttgtaaccaccacataaagatccttaccaggaagtagggtattacgcctctccaagtg 318

Query: 1775 gcccaaaacttgcaaaaaccgcctatccctctctcgtgcggtccagcacgaaccattgagt 1834
|||||
Sbjct: 317 gcccgaaactgtagaaaatcgctgt-gctctctcgtgcatctgttacgaaccattgagt 259

Query: 1835 tacaatcaacagcacc 1850
||||||| |||||
Sbjct: 258 tacaatcaaaagcacc 243

>gb|EG156227.1| MSAM281219_1210_4049 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 123

Score = 87.7 bits (44), Expect = 2e-13
Identities = 85/96 (88%), Gaps = 2/96 (2%)
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgc-gtgtggcca 1355
||||||| ||||||||| ||||||||||||||||| ||||||| || | | |||||
Sbjct: 7 tgtgggggacagatatccccgggtccactagaaggcaagaaggcgcggttgcggggcct 66

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtggg 1391
||||||||||||||| |||||||||||||||||
Sbjct: 67 cgggccagttacccacaaggccatcccttcgtggg 102

>gb|EG272559.1| MSAM184733_2591_1943 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 122

Score = 87.7 bits (44), Expect = 2e-13
Identities = 85/96 (88%), Gaps = 2/96 (2%)
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgc-gtgtggcca 1355
||||||| ||||||||| ||||||||||||||||| ||||||| || | | |||||
Sbjct: 6 tgtgggggacagatatccccgggtccactagaaggcaagaaggcgcggttgcggggcct 65

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtggg 1391
||||||||||||||| |||||||||||||||||
Sbjct: 66 cgggccagttacccacaaggccatcccttcgtggg 101

>gb|DW974630.1| MSAM293083_3262_0305 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 137

Score = 63.9 bits (32), Expect = 3e-06
Identities = 32/32 (100%)

Strand = Plus / Minus

Query: 1821 acgaaccattgagttacaatcaacagcaccgt 1852
|||||
Sbjct: 126 acgaaccattgagttacaatcaacagcaccgt 95

>gb|EG279004.1| MSAM238822_3284_2688 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 92

Score = 58.0 bits (29), Expect = 2e-04
Identities = 65/77 (84%)
Strand = Plus / Minus

Query: 1431 ggcaacagactcgagcccaacaatccatcggtctgtgcgctatccacagaaactaccg 1490
||||| ||||| ||||| ||||| || ||||| ||||| || || ||
Sbjct: 92 ggcaatagactcaagcccaagcaatctgtcaactcgtgcgctatccacagcaatcaactcg 33

Query: 1491 actttccggcgcgatggc 1507
||||| |||||
Sbjct: 32 actttccggcgcgatggc 16

>gb|DW952766.1| MSAM246175_3627_3291 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 143

Score = 58.0 bits (29), Expect = 2e-04
Identities = 50/56 (89%), Gaps = 2/56 (3%)
Strand = Plus / Minus

Query: 1243 gtttttaaagtgtgcccctatatttttaaataagggtactgatttaaataattggt 1298
||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 118 gtttttaaagtgtgcccctatattt--aaataagatactgatttaaagatattggt 65

>gb|DW739830.1| MSAM055005_1168_1927 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 113

Score = 58.0 bits (29), Expect = 2e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 1261 ctatattttaaaatagggtactgatttaa 1290
|||||
Sbjct: 117 ctatattttaagatagggtactgatttaa 146

>gb|FL181975.1| 25382983 CERES-505 Zea mays cDNA clone 1662221 5', mRNA sequence
Length = 643

Score = 52.0 bits (26), Expect = 0.011
Identities = 29/30 (96%)
Strand = Plus / Plus

Query: 1261 ctatattttaaaatagggtactgatttaa 1290
|||||
Sbjct: 117 ctatattttaagatagggtactgatttaa 146

>gb|DW840364.1| MSAM290571_0500_2033 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 121

Score = 50.1 bits (25), Expect = 0.045
Identities = 28/29 (96%)
Strand = Plus / Minus

Query: 1302 ggggatagatatccccgggtccactagaa 1330
|||||
Sbjct: 117 ggggacagatatccccgggtccactagaa 89

>gb|FL414619.1| 5792184 CERES-CB5 Zea mays cDNA clone 1163363 5', mRNA sequence
Length = 326

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 99 ttgtgggggatagatatcccctgggtccacta 68

>gb|FL412940.1| 6647374 CERES-CB5 Zea mays cDNA clone 1211549 5', mRNA sequence
Length = 467

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 99 ttgtgggggatagatatccccctgggtccacta 68

>gb|FL347392.1| 1747881 CERES-227 Zea mays cDNA clone 400160 5', mRNA sequence
Length = 422

Score = 48.1 bits (24), Expect = 0.18
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1823 gaaccattgagttacaatcaacagcacc 1850
|||||
Sbjct: 422 gaaccattgagttacaatcaaaagcacc 395

>gb|FL386242.1| 6662328 CERES-CB6 Zea mays cDNA clone 1226503 5', mRNA sequence
Length = 273

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 99 ttgtgggggatagatatccccctgggtccacta 68

>gb|FL372857.1| 5792169 CERES-CB5 Zea mays cDNA clone 1163348 5', mRNA sequence
Length = 277

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 99 ttgtgggggatagatatccccctgggtccacta 68

>gb|FL390932.1| 6655462 CERES-CB5 Zea mays cDNA clone 1219637 5', mRNA sequence
Length = 271

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 99 ttgtgggggatagatatccccctgggtccacta 68

>gb|FL381566.1| 5749223 CERES-CB5 Zea mays cDNA clone 1155021 5', mRNA sequence
Length = 187

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 99 ttgtgggggatagatatccccctgggtccacta 68

>gb|DW833979.1| MSAM271088_0946_2262 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 136

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 64 ttgtgggggatagatatccccctgggtccacta 95

>gb|DW776038.1| MSAM143878_0611_1314 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 121

Score = 48.1 bits (24), Expect = 0.18
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 1616 agtgccccacggctgtatataagggtccagagggtaccccatcattt 1663
|||||
Sbjct: 6 agtgccccacggctcatgtatataaggcctaggaggaaccccatcattt 53

>gb|CK327315.1| EST4624 Zea mays sperm cell cDNA library Zea mays cDNA clone
Zmspl1503 5', mRNA sequence
Length = 655

Score = 48.1 bits (24), Expect = 0.18
Identities = 31/32 (96%), Gaps = 1/32 (3%)
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327
|||||
Sbjct: 206 ttgtgggggatagatatccccgggtccacta 175

>gb|CF627516.1| zmrws05_0B20-012-c03.s4 zmrws05 Zea mays cDNA 3', mRNA sequence
Length = 672

Score = 48.1 bits (24), Expect = 0.18
Identities = 43/48 (89%), Gaps = 1/48 (2%)
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344
||||
Sbjct: 391 tgtgaggacagatatccccgggtccactagaaggctagaagacctc 344

>gb|EG224928.1| MSAM123648_2411_0798 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 90

Score = 46.1 bits (23), Expect = 0.70
Identities = 30/31 (96%), Gaps = 1/31 (3%)
Strand = Plus / Plus

Query: 1298 tgtgggggatagatat-ccccgggtccacta 1327
|||||
Sbjct: 43 tgtgggggatagatatccccgggtccacta 73

>gb|EG308159.1| MSAM260305_2985_0046 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 108

Score = 46.1 bits (23), Expect = 0.70
Identities = 86/107 (80%)
Strand = Plus / Plus

Query: 1657 atcatttctatcgaccatctacctatctcatcagctttttctccattcaggagacctcgct 1716
||||||| ||||||||| | | ||| ||| ||||| ||| | ||||| || ||
Sbjct: 2 atcatttccatcgaccatctactcaaccattagcctttcttcatactggagacttctct 61

Query: 1717 tgtaaccaccacatatagatccatccaagaagtagtgtattacgc 1763
||||||| | || ||| ||||||| ||| ||||||| || |||||
Sbjct: 62 tgtaacctaacatataaagatccacaccaggaagtaggtgttacgc 108

>gb|EG094444.1| MSAM117322_1237_2624 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 109

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 1099 agtttaaactagcggattatatagtggtata 1129
||||||| | ||||||||| |||||||
Sbjct: 52 agtttaaactggtggattatatagtggtata 82

>gb|EG105069.1| MSAM177973_0587_0066 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 128

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 1099 agtttaaactagcggattatatagtggtata 1129
||||||| | ||||||||| |||||||
Sbjct: 11 agtttaaactggtggattatatagtggtata 41

>gb|EY958855.1| Contag_8428 Maize ovary - Eveland 2007 Zea mays cDNA, mRNA sequence
Length = 110

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)

Strand = Plus / Plus

Query: 1099 agtttaaactagcggattatatagtggtata 1129
||||||| | |||||
Sbjct: 28 agtttaaactggtgattatatagtggtata 58

>gb|DW968659.1| MSAM278959_3123_2208 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 132

Score = 46.1 bits (23), Expect = 0.70
Identities = 30/31 (96%), Gaps = 1/31 (3%)
Strand = Plus / Minus

Query: 1298 tgtgggggatagatat-ccccgggtccacta 1327
||||||| |||||
Sbjct: 46 tgtgggggatagatatccccgggtccacta 16

>gb|DW964403.1| MSAM268770_3379_3722 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 120

Score = 46.1 bits (23), Expect = 0.70
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 1300 tgggggatagatatccccgggtccact 1326
||||| |||||
Sbjct: 65 tgggggacagatatccccgggtccact 39

>gb|DW838950.1| MSAM282407_1557_3507 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 109

Score = 46.1 bits (23), Expect = 0.70
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1618 tgccccacggtcggtatataaggtccagagggtaccccatca 1660
||||||| ||||| | | | |
Sbjct: 64 tgccccacggtcgagtatataaggcctagggggcaccatca 106

>gb|DW780235.1| MSAM153038_1935_0558 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 128

Score = 46.1 bits (23), Expect = 0.70
Identities = 30/31 (96%), Gaps = 1/31 (3%)
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327
|||||
Sbjct: 26 tgtgggggatagatatcccctgggtccacta 56

>gb|EB400206.1| ZM_BFb0305C08.f ZM_BFb Zea mays cDNA 3', mRNA sequence
Length = 412

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 1259 ccctatatatttaaaatagggtactgatttaa 1289
|||||
Sbjct: 11 ccctatatatttaaaatagagtactgatttaa 41

>gb|CX065243.1| PDUts2098D12 Porcine testis cDNA library II Sus scrofa cDNA clone
PDUts2098D12 5' similar to homologue to emb|AL773562.14|
Pig DNA sequence from clone XX-649D6, complete sequence,
mRNA sequence
Length = 596

Score = 46.1 bits (23), Expect = 0.70
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1137 tagttttattagaacatctccaa 1159
|||||
Sbjct: 306 tagttttattagaacatctccaa 328

>emb|FM926510.1| FM926510 REH (sb103) Brachionus plicatilis cDNA clone sb103P0024I01
5', mRNA sequence
Length = 548

Score = 44.1 bits (22), Expect = 2.8

Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 513 attaaaaattactttgaagatt 534
 |||||
Sbjct: 424 attaaaaattactttgaagatt 445

>gb|FL151656.1| 2009566 CERES-197 Zea mays cDNA clone 411939 5', mRNA sequence
 Length = 361

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 790 gagggaaggggaggatcgatgg 811
 |||||
Sbjct: 60 gagggaaggggaggatcgatgg 81

>gb|FL151333.1| 1045133 CERES-197 Zea mays cDNA clone 219978 5', mRNA sequence
 Length = 459

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 790 gagggaaggggaggatcgatgg 811
 |||||
Sbjct: 60 gagggaaggggaggatcgatgg 81

>gb|EY886124.1| LT33-C1-003-014-F05-CT.F Tahiti lime leaf, greenhouse plant Citrus
 latifolia cDNA, mRNA sequence
 Length = 952

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1072 gtgatttttgttggtggggtt 1093
 |||||
Sbjct: 213 gtgatttttgttggtggggtt 234

Length = 118

Score = 44.1 bits (22), Expect = 2.8
Identities = 32/34 (94%), Gaps = 1/34 (2%)
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaa 1330
 ||||||| ||||| |||||
Sbjct: 46 tgtggggacagatatccccgggtccactagaa 13

>dbj|DB841588.1| DB841588 NLEA Nilaparvata lugens cDNA clone NLEA1230 5', mRNA
sequence
Length = 650

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 519 aattactttgaagattcaacgt 540
 |||||||
Sbjct: 433 aattactttgaagattcaacgt 412

>dbj|DB846613.1| DB846613 NLEB Nilaparvata lugens cDNA clone NLEB6016 5', mRNA
sequence
Length = 765

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 519 aattactttgaagattcaacgt 540
 |||||||
Sbjct: 591 aattactttgaagattcaacgt 570

>gb|EY264291.1| BF01030A1B12.f1 Normalized subtracted keck library BF01 Danaus
plexippus cDNA clone BF01030A1B12.f1 5, mRNA sequence
Length = 636

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1235 ttggaacagtttttaaagttg 1256
|||||
Sbjct: 374 ttggaacagtttttaaagttg 395

>gb|EY259966.1| BF01003X1G03.f1 Normalized subtracted keck library BF01 Danaus
plexippus cDNA clone BF01003X1G03.f1 5, mRNA sequence
Length = 753

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1235 ttggaacagtttttaaagttg 1256
|||||
Sbjct: 270 ttggaacagtttttaaagttg 291

>gb|EY259488.1| BF01025A1E10.f1 Normalized subtracted keck library BF01 Danaus
plexippus cDNA clone BF01025A1E10.f1 5, mRNA sequence
Length = 766

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1235 ttggaacagtttttaaagttg 1256
|||||
Sbjct: 387 ttggaacagtttttaaagttg 408

>gb|EE047687.2| ZM_BFc0120J17.f ZM_BFc Zea mays cDNA clone ZM_BFc0120J17 3', mRNA
sequence
Length = 462

Score = 44.1 bits (22), Expect = 2.8
Identities = 29/30 (96%), Gaps = 1/30 (3%)
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccact 1326
|||||
Sbjct: 30 tgtgggggatagatatccccctgggtccact 1

>emb|AM581222.1| AM581222 RZPD MPMGp1173 Paracentrotus lividus GASPLU Paracentrotus
lividus cDNA clone MPMGp1173F0730Q 5', mRNA sequence

Length = 814

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 782 tggaaggggaggggaaggggagg 803
 |||||
Sbjct: 779 tggaaggggaggggaaggggagg 800

>gb|DW897577.1| MSAM116936_3007_3914 LCM-dissected maize shoot apical meristem cDNA
 Zea mays cDNA, mRNA sequence
 Length = 107

Score = 44.1 bits (22), Expect = 2.8
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatccccgggtcc 1323
 ||||| |||||
Sbjct: 61 tgtggcgatagatatccccgggtcc 36

>gb|CF041009.1| QCI20f01.yg QCI Zea mays cDNA clone QCI20f01, mRNA sequence
 Length = 526

Score = 44.1 bits (22), Expect = 2.8
Identities = 28/30 (93%)
Strand = Plus / Plus

Query: 1261 ctatattttaaataagggtactgatttaa 1290
 ||||| |||||
Sbjct: 289 ctatattttaaaggtagggtactgatttaa 318

>gb|BF706840.1| 281486 MARC 3BOV Bos taurus cDNA 5', mRNA sequence
 Length = 473

Score = 44.1 bits (22), Expect = 2.8
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 779 ggggtggaaggggaggggaaggggagga 804
 ||||| |||||

Sbjct: 473 ggggtgggaggggaggggaaggggagga 448

Database: /usr/local/blast/db/blastlibs/est_others

Posted date: May 6, 2010 12:23 AM

Number of letters in database: 29,661,423,624

Number of sequences in database: 52,386,385

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 52386385

Number of Hits to DB: 530,610,548

Number of extensions: 29327324

Number of successful extensions: 8133123

Number of sequences better than 10.0: 56

Number of HSP's gapped: 8133116

Number of HSP's successfully gapped: 60

Length of query: 1852

Length of database: 29,661,423,624

Length adjustment: 23

Effective length of query: 1829

Effective length of database: 28,456,536,769

Effective search space: 52047005750501

Effective search space used: 52047005750501

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 50 (99.1 bits)

S1: 12 (24.3 bits)

S2: 22 (44.1 bits)