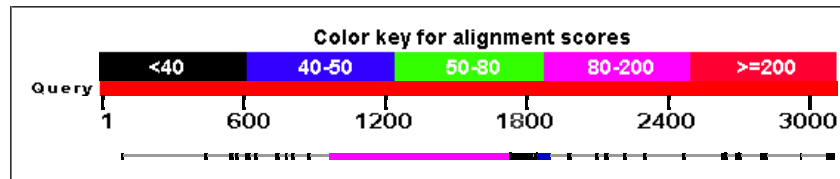


BLAST ®**Basic Local Alignment Search Tool**[NCBI/ BLAST/ blastn suite/ Formatting Results - WMF579S1013](#)[Formatting options](#)[Download](#)**Nucleotide Sequence (3118 letters)**

Query ID |cl|47457
Description None
Molecule type nucleic acid
Query Length 3118

Database Name nr
Description All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Program BLASTN 2.2.26+

Graphic Summary**Distribution of 48 Blast Hits on the Query Sequence**

Appendix 1

Evaluation of risks from creation of novel RNA molecules in genetically engineered wheat plants and recommendations for risk assessment

Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
gi 32401224 AF525764.1	Aegilops tauschii subsp. strangulata SBE I pseudogene, partial sequence; SBE I pseudogene, complete sequence; and starch branching enzyme I (SBE I) gene, complete cds	185	1468	40%	1e-48	100%	

Alignments

>gi|32401224|gb|AF525764.1| [D](#) Aegilops tauschii subsp. strangulata SBE I pseudogene, partial sequence; SBE I pseudogene, complete sequence; and starch branching enzyme I (SBE I) gene, complete cds
 Length=25187

Sort alignments for this subject sequence by:
 E value **Score** **Percent identity**
Query start position **Subject start position**

Score = 185 bits (204), Expect = 1e-48
 Identities = 508/767 (66%), Gaps = 34/767 (4%)
 Strand=Plus/Plus

Query	987	TTTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGTTACCAAATCACAA	1046
Sbjct	21363	TTTCAGCTGATGGCAATCATGGAACATTCATATTATGCTTCTTTTGGGTACCATGTGACGA	21422
Query	1047	GCTTCTTTGACGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAAGAAGCTGGTAGACA	1106
Sbjct	21423	ATTTCTTTCGCAGTTAGCAGCAGATCAG-AACGCCAGA-GACCT-CAATATCTTGTGACA	21479
Query	1107	CAGCTCATTTCCATG-GGTATCATAGTCTCTTAGATGTGGTACACAGCCATGCTTCAAAA	1165
Sbjct	21480	AGGCACATAGTTTACGGTTGCGT-GTTCTGATGGATGTTGTCCATAGCCATGCGAGCAGT	21538
Query	1166	AATTCAGCAGATGGATTGAATATGTTTGATG---GG-----ACAG-ATTCTGTAT	1213
Sbjct	21539	AATAAGACAGATGGTCTTAATGGCTATGATGTTGGGCAAAACACAGGAGTCTT---AT	21595
Query	1214	TTTCATTCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCTACTCC	1273
Sbjct	21596	TTCCACACAGGAGAAAAGGGGCTATCATAAACTGTGGGATAGCCGCTGTTCAACTATGCC	21655
Query	1274	AGCTGGGAAGTTTTAAGATTCCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGC	1333
Sbjct	21656	AATTGGGANGTCTTACGATTTCTTCTTCTAATCTGAGATATTGGATGGACGAATTCATG	21715
Query	1334	TTTGATGGATTTCGTTTGTGATGTTTACGTCATGCTTTATCATCACCATGG----AGT	1389
Sbjct	21716	TTTGATGGCTTCCGATTTGATGGGGTAACATCCATGCTATATAATCACCATGGTATCAAT	21775
Query	1390	GGGTCAAGGTTTCTCAGGTGATTACAGTGAATATTTCCGACTACAAGTAGATGAAGATGC	1449
Sbjct	21776	ATGTCA----TTCGCTGGAAGTTACAAGGAATATTTTGGTTTGGATACTGATGTAGATGC	21831
Query	1450	CTTGACTTACCTCATGTTGGCAAATCATTTGGTTCACACGCTGTGTCCGATTCATAAC	1509
Sbjct	21832	AGTTGTTTACCTGATGCTTTCGCAACATTTAATGCACAAACTCTTGCCAGAGCAACTGT	21891
Query	1510	AATAGCTGAGGATGTATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCAGGGAGGGGG	1569
Sbjct	21892	TGTTGCAGAAGATGTTTTCAGGCATGCCAGTGCCTTTGTGCGTCAGTTGATGAAGGTGGAGT	21951
Query	1570	TGGTTTTGACTATCGACTAGCCATGGCAATTCAGATAAGTGGATTCAGTACTTAAAGA	1629
Sbjct	21952	AGGGTTTACTATCGCCTGGCTATGGCTATTCCTGATAGATGGATCGA-CTACTTGAAGA	22010
Query	1630	GTTTAAAGATGAA---GACTGGAACATGGGCGATATAGTATACACGCTCACAAAACAGGCG	1686
Sbjct	22011	AC--AAAGATGACCTTGAATGGTCAATGAGTGAATAGCACATACTCTGACCAACAGGAG	22068
Query	1687	CTACCTTGAAAAGTGCATTGCTTATGCAGAGAGCCATGATCAGGCAT	1733
Sbjct	22069	ATATACGGAAAAGTGCATTGCATATGCTGAGAGCCATGATCAGGTAT	22115

Score = 140 bits (154), Expect = 5e-35
 Identities = 411/628 (65%), Gaps = 13/628 (2%)
 Strand=Plus/Plus

Query	989	CAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGTTACCAAATCACAAAGC	1048
Sbjct	561	CAGCTTATGGCAATCATGGAACATTCCTACTATGCTTCTTTTGGGTATCACGTGACAAAT	620
Query	1049	TTCTTTGCAGCTTCCAGCCGTTATGGAACACCTGAAGAGCTACAAGAAGCTGGTAGACACA	1108

```

Sbjct 621  TTCTTCGCGGTTAGCAGCAAAATCAGGCACTCCAGAGGACCTCAAAATATCTTGTGACACAG 680
Query 1109  GCTCATTCCATGGGTATCATAGTCTCTTAGATGTGGTACACAGCCATGCTTCAAAAAAT 1168
Sbjct 681  GCACATAGTTTAGGATTGCGTGTCTTAATGGATGTTGTCCATAGCCATGCAAGCAAAAAAT 740
Query 1169  TCAGCAGATGGATTGAATATGTTTGATG--GGACAGATTCCCT-----GTTAT-TTTC-AT 1219
Sbjct 741  GTGACAGATGGTCTAAATGGCTATGATGTTGGACAAAGCGCACAAAGAGTCATATTTCTAC 800
Query 1220  TCTGGACCTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTGCCCTACTCCAGCTGG 1279
Sbjct 801  GCAGGAGACAGGGGCTATCATAAACTGTGGGATAGCCGCTGTTCAACTATAACCAATTGG 860
Query 1280  GAAGTTTTAAGATTCTTCTGTCAAACATAAGATGGTGGTTGGAAGAATATCGCTTTGAT 1339
Sbjct 861  GAGGTCTTAAGATTTCTTCTTTCCAATCTGAGATATTGGATGGACGAATTCATGTTTGAT 920
Query 1340  GGATTTTCGTTTTGATGGTGTACGTCCATGCTTTATCATCACCATGGAGTGGGTCAAGGT 1399
Sbjct 921  GGCTTCAGATTTGATGGGGTCACATCCATGCTATACAATCACCATGGAATCAAT--ACGT 978
Query 1400  --TTCTCAGTGATTACAGTGAATATTTTCGGACTACAAGTAGATGAAGATGCCTTGACTT 1457
Sbjct 979  CGTTCACCTGGAAATATAAGGAGTATTTTGGTTTGGATACAAATGTAGATGCAATCATTT 1038
Query 1458  ACCTCATGTTGGCAAATCATTGGTTCACACGCTGTGTCCGATTCTATAACAATAGCTG 1517
Sbjct 1039  ATATGATGCTGGCTAACCATTTAATACACAAACTCCTGCCAGAAGCAACTATATTGCTG 1098
Query 1518  AGGATGTATCAGGAATGCCAGCTCTGTCTCTCCAATTTCCAGGGAGGGGGTGGTTTTG 1577
Sbjct 1099  AAGATGTTTCAGTCATGCCAGTCTTTTGTGCGCCAGTTGACGAAGTTGGGAGTAGGTTG 1158
Query 1578  ACTATCGACTAGCCATGGCAATTCCAGA 1605
Sbjct 1159  ACTATCGCCAGGCTATGGCTATTCAGA 1186

```

Score = 89.7 bits (98), Expect = 8e-20
 Identities = 490/775 (63%), Gaps = 29/775 (4%)
 Strand=Plus/Plus

```

Query 976  ATACAACATGCATTTCAGTTGATGGCAATCATGG-AGCATGCTTACTATGCCAGCTTTGGTT 1034
Sbjct 7197  ATACAACACGGTTTCAGTTGATGGGAATCATGAAACATTCTGACGCTGCTTCTTTTGGGT 7256
Query 1035  ACCAAATCACAAGCTTCTTTGCAGCTTCAGCCGTTATGGAACACCTGAAGAGCTACAAG 1094
Sbjct 7257  ATTATGTGACGAATTTCTTCGCAGTTAGCAGCAGATCAGGCACACCAGACGACCTCAAAAT 7316
Query 1095  AACTGGTAGACACAGCTCATTCATGGGATCATAGTCCCTTAGATGTGGTACACAGCC 1154
Sbjct 7317  ATCTTATTGACAAGGCACATATCTGGAT-TGTGTGTTCTGATGGATGTTGTCCACAGCC 7375
Query 1155  ATGCTTCAAAAAATTCAGCAGATGGATTGAATATGTTTGATG--GGACAGATTCC----- 1207
Sbjct 7376  ATGCGAGCAATAATGTTATAGATGGTCTCAATGGCTATGATGTTGGACAAAGTGCACACG 7435
Query 1208  --TGTATTTTTCATTCAGGACTAGAGGGACTCATGATCTTTGGGATAGCAGATTGTTTG 1265
Sbjct 7436  AATCCTATTTCTACACAGGAGACAGGGCTATAATAAGATGTGGAATGGCCGCATGTTCA 7495
Query 1266  CCTACTCCAGCTGGGAAGTTTTAAGATTCTTCTGTCAAACATAAGATGGTGGTTGGAAG 1325
Sbjct 7496  ACTATGCCAATTGGGAGGTCCTAAGATTCCTGCTTTCCAATTTGAGATATTGGATGGACG 7555
Query 1326  AATATCGCTTTGATGGATTTTCGTTTTGATGGTGTACGTCCATGCTTTATCATCACCATG 1385
Sbjct 7556  AATTCATGTTTATGATGGCTTCCGATTTGTTGGGGTTACATCGATGCTATATAATCAAAATG 7615
Query 1386  G----AGTGGGTCAAGGTTTCTCAGGTGATTACAGTGAATATTTTCGACTACAAGTAGAT 1441
Sbjct 7616  GTATCAATATGTCA----TTCAGTGGAAATTACAAAGAGTATTTTGGTTTGGATACCAAT 7671
Query 1442  GAAGATGCCTTGACTTACCTCATGTTGGCAAATCATTGGTTTACACGCTGTGTCCCGAT 1501
Sbjct 7672  GTAGATGCAGTTGTTTATATGATGCTCGCGAACATTTAATGCACAAACTCTACCCAGAA 7731
Query 1502  TCTATAACAATAGCTGAGGATGATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCAG 1561
Sbjct 7732  GCAATTGTTGTGGCCGTAGATGTTTTCAGGCATGCCAGTCTTTGTTGGCCAGTTGATGAA 7791
Query 1562  GGAGGGGGTGGTTTTGACTATCGACTAGCCATGGCAATTCAGATAAGTGGATTTCAGCTA 1621
Sbjct 7792  GGTGGATTAGGGTTTACTATCGCCAGGCTATGACTATTTCCGATAGATGGATTGA-ATA 7850
Query 1622  CTTAAAGAGTTTAAA---GATGAAGACTGGAACATG---GGCGATATAGTATACACGCTC 1675
Sbjct 7851  CTT-GGGAGAACAAGGTGATCAACAGTGGTCAATGAATAATGTTATATCACAAACTTTG 7909
Query 1676  ACAAACAGGCGCTACCTG--AAAAGTGCATTGCTTATGCAGAGAGCCATGATCA 1728
Sbjct 7910  ACTAACAGGCGATATCCGAAAAAAGTTCATTGCGTATGCTGAGAGGCAAAATCA 7964

```

Score = 44.6 bits (48), Expect = 3e-06
 Identities = 49/63 (78%), Gaps = 2/63 (3%)
 Strand=Plus/Plus

```

Query 1847  ATGATTCGACTCATTACGCATGGGC-TTGGTGGAGAAGGCTATCTCAATTTTCATGGGTAA 1905
Sbjct 22702  ATGATTCACCTTCATCAC-CATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGTAA 22760
Query 1906  TGA 1908
Sbjct 22761  TGA 22763

```

Score = 37.4 bits (40), Expect = 4e-04
 Identities = 67/98 (68%), Gaps = 0/98 (0%)
 Strand=Plus/Plus

```
Query 1736 GTTGGGGATAAGTCGCTGGCATTGTTGGTTGATGGATGCCGAAATGTATACAAACATGAGT 1795
Sbjct 22437 GTTGGCGACAAGACTATGGCATTCTCTTGATGGACAAGGAAATGTATACTGGCATGTCA 22496
Query 1796 GTCCTGACTCCTTTTACTCCAGTTATTGATCGTGGAAT 1833
Sbjct 22497 GACTTGCAGCCTGCTTCGCCCTACAATTGATCGTGGAAT 22534
```

Score = 28.3 bits (30), Expect = 0.23
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

```
Query 2134 AAGAGCAGGTCTTCTTTT 2151
Sbjct 6186 AAGAGCAGGTCTTCTGTT 6203
```

Score = 28.3 bits (30), Expect = 0.23
 Identities = 18/20 (90%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

```
Query 551 GAATGGGCCCCGGGAGCAGA 570
Sbjct 6550 GAATGGGCCCTGCAGCAGA 6569
```

Score = 28.3 bits (30), Expect = 0.23
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

```
Query 2700 CTTTTAAATTCAAAT 2714
Sbjct 11063 CTTTTAAATTCAAAT 11049
```

Score = 26.5 bits (28), Expect = 0.80
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

```
Query 1174 AGATGGATTGAATA 1187
Sbjct 7837 AGATGGATTGAATA 7850
```

Score = 26.5 bits (28), Expect = 0.80
 Identities = 45/63 (71%), Gaps = 2/63 (3%)
 Strand=Plus/Plus

```
Query 1847 ATGATTCCACTCATTACGCATGGGCTT-GGTGGAGAAGGCTATCTCAATTTTCATGGGTAA 1905
Sbjct 8534 ATGATTCAATTCATCAGG-ATGGCCTTTGGAGGTGATAACTACTTAAAAATTTATGGGTAA 8592
Query 1906 TGA 1908
Sbjct 8593 TGA 8595
```

Score = 26.5 bits (28), Expect = 0.80
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

```
Query 1980 AGTTTCATTTAACTGAC 1996
Sbjct 15692 AGTTTCATTTAACTAAC 15708
```

Score = 24.7 bits (26), Expect = 2.8
 Identities = 16/18 (89%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

```
Query 551 GAATGGGCCCCGGGAGCA 568
Sbjct 20558 GAATGGGCCCTGCAGCA 20575
```

Score = 22.9 bits (24), Expect = 9.8
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

```
Query 1282 AGTTTTAAGATT 1293
Sbjct 1960 AGTTTTAAGATT 1949
```

Score = 22.9 bits (24), Expect = 9.8
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

```
Query 2303 TTTGAACATAAT 2314
Sbjct 2383 TTTGAACATAAT 2394
```

Score = 22.9 bits (24), Expect = 9.8
 Identities = 14/15 (93%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

```
Query 621 CATACAAAAAATGG 635
Sbjct 2993 CATACAAAAAATGG 2979
```

Score = 22.9 bits (24), Expect = 9.8

Identities = 14/15 (93%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2633 TTCTCAAATGGAAGT 2647
Sbjct 4276 TTCTCAAATGGACGT 4290

Score = 22.9 bits (24), Expect = 9.8
Identities = 26/34 (76%), Gaps = 6/34 (18%)
Strand=Plus/Minus

Query 3073 AATCAATAAAAAGCTTTTGTAAAATTGCaaaaaa 3106
Sbjct 9243 AATCAATAAAA---TGTGT---ATTGCAGAAAA 9216

Score = 22.9 bits (24), Expect = 9.8
Identities = 17/20 (85%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 2807 GTCTAAATTATGAGGTACCA 2826
Sbjct 10211 GTTTAAACAATGAGGTACCA 10230

Score = 22.9 bits (24), Expect = 9.8
Identities = 14/15 (93%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1348 TTTTGATGGTGTAC 1362
Sbjct 12117 TTTTGATGGTGTGAC 12131

Score = 22.9 bits (24), Expect = 9.8
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 2217 AATTCAAAATTG 2228
Sbjct 12571 AATTCAAAATTG 12560

Score = 22.9 bits (24), Expect = 9.8
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 752 ATTCACCGTGG 763
Sbjct 20982 ATTCACCGTGG 20993

Score = 22.9 bits (24), Expect = 9.8
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 812 CACTGGGATCCA 823
Sbjct 21082 CACTGGGATCCA 21093

Score = 22.9 bits (24), Expect = 9.8
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 1375 TCATCACCATGG 1386
Sbjct 22712 TCATCACCATGG 22723

Score = 22.9 bits (24), Expect = 9.8
Identities = 18/22 (82%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 2796 GATATCTTTTGGTCTAAATTAT 2817
Sbjct 24642 GATATCTTTTGGTCTTATTAT 24621

Score = 21.1 bits (22), Expect = 34
Identities = 21/25 (84%), Gaps = 3/25 (12%)
Strand=Plus/Plus

Query 1175 GATGGATTGAAT--ATGTTTGATGG 1197
Sbjct 899 GATGGAC-GAATTCATGTTTGATGG 922

Score = 21.1 bits (22), Expect = 34
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

Query 1624 TAAAGAGTTTA 1634
Sbjct 1838 TAAAGAGTTTA 1828

Score = 21.1 bits (22), Expect = 34
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 785 GGTGATAATGT 795
Sbjct 3094 GGTGATAATGT 3104

Score = 21.1 bits (22), Expect = 34
Identities = 11/11 (100%), Gaps = 0/11 (0%)

Strand=Plus/Minus

Query 881 TATGAATCTCA 891
 Sbjct 5060 TATGAATCTCA 5050

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 2096 AGTGAAAAACA 2106
 Sbjct 5557 AGTGAAAAACA 5547

Score = 21.1 bits (22), Expect = 34
 Identities = 21/25 (84%), Gaps = 3/25 (12%)
 Strand=Plus/Plus

Query 1175 GATGGATTGAAT--ATGTTTGATGG 1197
 Sbjct 7548 GATGGAC-GAATTCATGTTTGATGG 7571

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 2219 TTCAAAATTGT 2229
 Sbjct 8652 TTCAAAATTGT 8662

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 2688 AATTATTTGAT 2698
 Sbjct 8819 AATTATTTGAT 8809

Score = 21.1 bits (22), Expect = 34
 Identities = 13/14 (93%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query 2632 ATTCTCAAATGGAA 2645
 Sbjct 11339 ATTCTCAAATGAAA 11352

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 2961 GTTTTATTTTG 2971
 Sbjct 11580 GTTTTATTTTG 11570

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 2632 ATTCTCAAATG 2642
 Sbjct 11925 ATTCTCAAATG 11935

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 1838 CTCATAAAAT 1848
 Sbjct 12048 CTCATAAAAT 12058

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 576 TTTTCTTACT 586
 Sbjct 12637 TTTTCTTACT 12647

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 2647 TGTATATATA 2657
 Sbjct 12745 TGTATATATA 12735

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 443 CAAATTTTGAA 453
 Sbjct 15216 CAAATTTTGAA 15206

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 1209 GTTATTTTCAT 1219
 Sbjct 15240 GTTATTTTCAT 15230

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 2813 ATTATGAGGTA 2823
 Sbjct 15854 ATTATGAGGTA 15844

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 92 GGAGAAAGGGC 102
 Sbjct 16310 GGAGAAAGGGC 16300

Score = 21.1 bits (22), Expect = 34
 Identities = 13/14 (93%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 653 CTGTATATCCCACC 666
 Sbjct 16404 CTTTATATCCCACC 16391

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 1278 GGAAGTTTTA 1288
 Sbjct 17139 GGAAGTTTTA 17149

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 2465 TAACATGTATG 2475
 Sbjct 17647 TAACATGTATG 17637

Score = 21.1 bits (22), Expect = 34
 Identities = 21/25 (84%), Gaps = 3/25 (12%)
 Strand=Plus/Plus

Query 1175 GATGGATTGAAT--ATGTTTGATGG 1197
 Sbjct 21700 GATGGAC-GAATTCATGTTTGATGG 21723

Score = 21.1 bits (22), Expect = 34
 Identities = 15/16 (94%), Gaps = 1/16 (6%)
 Strand=Plus/Plus

Query 1043 ACAAGCTTCTTTGCAG 1058
 Sbjct 23146 ACAAGCTTC-TTGCAG 23160

Score = 21.1 bits (22), Expect = 34
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 742 CTTGTATCGTA 752
 Sbjct 23356 CTTGTATCGTA 23346