

Sequenziato FW2Ras

ATTCTATATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAATGACT
GAATATAAACTTGTGGTA **GTTGGAGCTGGTGGCGTAGGCAAG**AGTGCCTTGAC
GATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGT
AAATCTTGTTTTAATATGCATATTACTGGTGCAGGACCATTCTTTGATACAGATA
AAGGTTTCTCTGACCATTTTCATGAGTACA

Sequenziato REV2Ras

GCACCAGTAATATGCATATTAACAAGATTTACCTCTATTGTTGGATCATATTC
GTCCACAAAATGATTCTGAATTAGCTGTATCGTCAAGGCACTCTTGCCTACGCC
ACCAGCTCCAACCTACCACAAGTTTATATTCAGTCATTTTCAGCAGGCCTTATAAT
AAAAATAATGAAAATGTGACTATATTAGAACATGTCACACATAAGGTTAATACA
CTATCAAATACTCCNNCAGTACCT

Revers Complement REV2Ras

AGGTACTGNNGGAGTATTTGATAGTGTATTAACCTTATGTGTGACATGTTCTAA
TATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAATGACTGAATAT
AACTTGTGGTA **GTTGGAGCTGGTGGCGTAGGCAAG**AGTGCCTTGACGATAC
AGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAAATC
TTGTTTTAATATGCATATTACTGGTGC

Sequenziato FW1Ras

TTCTATATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAATGACTG
AATATAAACTTGTGGTA **GTTGGAGCTGGTGGCGTAGGCAAG**AGTGCCTTGACG
ATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTA
AATCTTGTTTTAATATGCATATTACTGGTGCAGGACCATTCTTTGATACAGATAA
AGGTTTCTCTGACCATTTTCATGAGTAC

Sequenziato REV1Ras

GCACCAGTAATATGCATATTAACAAGATTTACCTCTATTGTTGGATCATATTC
GTCCACAAAATGATTCTGAATTAGCTGTATCGTCAAGGCACTCTTGCCTACGCC

ACCAGCTCCAACCTACCACAAGTTTATATTTCAGTCATTTTCAGCAGGCCTTATAAT
AAAAATAATGAAAATGTGACTATATTAGAACATGTCACACATAAGGTTAATACA
CTATCAAATACTCCACCAGTACCT

Revers Complement REV1Ras

AGGTACTGGTGGAGTATTTGATAGTGTATTAACCTTATGTGTGACATGTTCTAA
TATAGTCACATTTTCATTATTTTTATTATAAGGCCTGCTGAAAATGACTGAATAT
AACTTGTGGTA**GTTGGAGCTGGTGGCGTAGGCAAG**AGTGCCTTGACGATAC
AGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAAATC
TTGTTTTAATATGCATATTACTGGTGC

1232 Fw Kras

BLASTN 2.2.22+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: E0GPV7FP111

Query=
Length=247

Sequences producing significant alignments:
Score E
(Bits) Value
lcl|35649 448 1e-
128

ALIGNMENTS
>lcl|35649
Length=45675

Score = 448 bits (242), Expect = 1e-128
Identities = 245/246 (99%), Gaps = 1/246 (0%)
Strand=Plus/Plus

1232 2 TTCT-ATATAGTCACATTTTCATTATTTTTATTATAAGGCCTGCTGAAAATGACTGAATA 60
|||||
Kras 5488 TTCTAATATAGTCACATTTTCATTATTTTTATTATAAGGCCTGCTGAAAATGACTGAATA 5547
1232 61 TAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAAT 120
|||||
Kras 5548 TAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAAT 5607
1232 121 TCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAAATCTTGTTTTAATATG 180
|||||
Kras 5608 TCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAAATCTTGTTTTAATATG 5667
1232 181 CATATTACTGGTGCAGGACCATTCTTTGATACAGATAAAGGTTTCTCTGACCATTTTCAT 240
|||||
Kras 5668 CATATTACTGGTGCAGGACCATTCTTTGATACAGATAAAGGTTTCTCTGACCATTTTCAT 5727
1232 241 GAGTAC 246
|||||
Kras 5728 GAGTAC 5733

1232 Rev Kras

BLASTN 2.2.22+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: E0J2PFFU111

Query=
Length=242

Sequences producing significant alignments:
Score E
(Bits) Value
lcl|47069 440 2e-
126

ALIGNMENTS
>lcl|47069
Length=45675

Score = 440 bits (238), Expect = 2e-126
Identities = 240/242 (99%), Gaps = 0/242 (0%)
Strand=Plus/Plus

1232 1 AGGTA CTGNNGGAGTATTTGATAGTGTATTAACCTTATGTGTGACATGTTCTAATATAGT 60
|||||
Kras 5440 AGGTA CTGGTGGAGTATTTGATAGTGTATTAACCTTATGTGTGACATGTTCTAATATAGT 5499

1232 61 CACATTTTCATTATTTTATTATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGT 120
|||||
Kras 5500 CACATTTTCATTATTTTATTATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGT 5559

1232 121 AGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTT 180
|||||
Kras 5560 AGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTT 5619

1232 181 TGTGGACGAATATGATCCAACAATAGAGGTAAATCTTGTTTTAATATGCATATTACTGGT 240
|||||
Kras 5620 TGTGGACGAATATGATCCAACAATAGAGGTAAATCTTGTTTTAATATGCATATTACTGGT 5679

1232 241 GC 242
||
Kras 5680 GC 5681

2695 Fw Kras

BLASTN 2.2.22+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: E0JR7T3T113

Query=
Length=244

Sequences producing significant alignments:
Score E
(Bits) Value
lcl|4619 442 7e-
127

ALIGNMENTS
>lcl|4619
Length=45675

Score = 442 bits (239), Expect = 7e-127
Identities = 244/246 (99%), Gaps = 2/246 (0%)
Strand=Plus/Plus

2695 1 TTCT-ATATAGTCACATTTTCATTATTTTTATTATAAGGCCTGCTGAAAATGACTGAATA 59
|||||
Kras 5488 TTCTAATATAGTCACATTTTCATTATTTTTATTATAAGGCCTGCTGAAAATGACTGAATA 5547
2695 60 TAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAAT 119
|||||
Kras 5548 TAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAAT 5607
2695 120 TCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAAATCTTGTTTTAATATG 179
|||||
Kras 5608 TCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAAATCTTGTTTTAATATG 5667
2695 180 CATATTACTGGTGCAGGACCATTCTTTGATACAGATAAAGGTTTCTCTGACCATTT-CAT 238
|||||
Kras 5668 CATATTACTGGTGCAGGACCATTCTTTGATACAGATAAAGGTTTCTCTGACCATTTTCAT 5727
2695 239 GAGTAC 244
|||||
Kras 5728 GAGTAC 5733

2695 Rev Kras

BLASTN 2.2.22+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: E0K6NK0P113

Query=
Length=242

Table with 3 columns: Sequences producing significant alignments, Score (Bits), E Value. Row 1: lcl|19279, 448, 1e-128.

ALIGNMENTS
>lcl|19279
Length=45675

Score = 448 bits (242), Expect = 1e-128
Identities = 242/242 (100%), Gaps = 0/242 (0%)
Strand=Plus/Plus

Table with 5 columns: ID, Position, Sequence, Score, E Value. Rows show alignments for 2695 and Kras sequences, including gaps and matches.