

Blast Genome Testing

An Example for testing whether the BLAST Genome Implementation in JavaMAGE

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Create a Sample Genome

- 1000 Basepairs and 0 Fixed Matches

```
> No fixed matches
CCATACCGTCCTAATTCTTCGGTTATGTTTCCGATGTAGGAGTGAGCCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
GTGCCATCGGGTTTCTGAACTCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACGCTGCCACGTGTTCACTTAAGTGTGTTTGGTAGCACAAAAGTAT
TACCATGGTCCTAGAAGTTCGGCACAGTTAGTTCGAGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGGCAAGTCAGAGCAGGTTCCCGTGTTAGCTTGAGGGTAAA
CATAACAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCCCTGTAGTTCGAAGCGGAACT
ATTTGAGGGGGCGAGCCCACATCGTCTCTTCTGCGGATGACTTAACACGC
TAGGGAGGTGGAGTCGATTCCATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACACTTGGTTCGGAAGC
CTGTCCTGATATATGAATCCAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAAATATCTAATATCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCACACCGAGAACTAGACAGTTGCGCGCTGGAAGTA
GCGCCGGCTAAGAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA
```

Insert 2x1 Fixed Match

```
> gattacagattacagattaca @ 314 and tatacagtgcgacgtaatgc @ 256
CCATACCGTCCTAATTCTTCGGTTATGTTTCCGATGTAGGAGTGAGCCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
GTGCCATCGGGTTTCTGAACTCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACTatacagtgcgacgtaatgcGTTGTTTGGTAGCACAAAAGTAT
TACCATGGTCCTAGgattacagattacagattacaAGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGGCAAGTCAGAGCAGGTTCCCGTGTTAGCTTGAGGGTAAA
CATACAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCTGTAGTTCGAAGCGGAACT
ATTTGAGGGGCGAGCCACATCGTCTCTTCTGCGGATGACTTAACACGC
TAGGGAGGTGGAGTCGATTCCATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCGTATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACACTTGGTTCGAAGC
CTGTCCTGATATATGAATCCAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAATATCTAATATTCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCACACCGAGAACTAGACAGTTGCGCGCTGGAAGTA
GCGCCGGCTAAGAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA
```

Insert More (2x2) Fixed Matches

```
> gattacagattacagattaca @ 314, 512 and
tatacagatgacgacgtaatgc @ 256,917
CCATACCGTCCTAATTCTTCGGTTATGTTTCCGATGTAGGAGTGAGCCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
GTGCCATCGGGTTTCTGAACTCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACTatacagatgacgacgtaatgcGTTGTTTGGTAGCACAAAAGTAT
TACCATGGTCCTAGgattacagattacagattacaAGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGGgattacagattacagattacaGTTAGCTTGAGGGTAAA
CATACAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCCCTGTAGTTCGAAGCGGAACT
ATTTGAGGGGGCGAGCCACATCGTCTCTTCTGCGGATGACTTAACACGC
TAGGGAGGTGGAGTTCGATCCATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACTTGGTTCGGAAGC
CTGTCCTGATATATGAATCCAAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAAATATCTAATATTCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCACTatacagatgacgacgtaatgcGCGCTGGAAGTA
GCGCCGGCTAAGAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA
```

Upto 2x4 Matching Sites

> Fixed Matches at @ 314, 512, 100, 625 ; @ 256,917, 700, 25
CCATACCGTCCTAATTCTTCGGTTA**tatacgagtgcgacgtaatgc**CCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
gattacagattacagattacaCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACT**tatacgagtgcgacgtaatgc**GTTGTTTGGTAGCACAAAAGTAT
TACCATGGTCCTAG**gattacagattacagattaca**AGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGG**gattacagattacagattaca**GTTAGCTTGAGGGTAAA
CATAAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCTGTAGTTCGAAGCGGAACT
ATTTGAGGGGCGAGCCACATCGT**gattacagattacagattaca**ACGC
tatacgagtgcgacgtaatgcATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCGTATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACTTGGTTCGAAGC
CTGTCCTGATATATGAATCCAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAAATATCTAATATTCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCAC**tatacgagtgcgacgtaatgc**GCGCTGGAAGTA
GCGCCGGCTAAGAAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA

Choose a Subsequence

> Fixed Matches at @ 314, 512, 100, 625 ; @ 256,917, 700, 25
CCATACCGTCCTAATTCTTCGGTTA**tatac****gagtgcgacg****taatgc**CCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
gattacagattacagattacaCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACTatac**gagtgcgacg****taatgc****GTTGTTTGGTAGCACAAAAGTAT**
TACCATGGTCCTAG**gattacagattacagattaca****AGCCT**AATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGG**gattacagattacagattaca**GTTAGCTTGAGGGTAAA
CATAAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCTGTAGTTCGAAGCGGAACT
ATTTGAGGGGCGAGCCACATCGT**gattacagattacagattaca**ACGC
tatac**gagtgcgacg****taatgc**ATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCGTATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACTTGGTTCGAAGC
CTGTCCTGATATATGAATCCAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAATATCTAATATTCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCAC**tatac****gagtgcgacg****taatgc**GCGCTGGAAGTA
GCGCCGGCTAAGAAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA

TTCTACTatac**gagtgcgacg****taatgc****GTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAG****gattacagattacagattaca****AGCCT**

No Fixed Matches

```
# BLASTN 2.2.25+
# Query: oligo1
# Database: ./test.db
# Fields: q. start, q. end, s. start, s. end, query seq, evaluate, bit score
# 1 hits found
28 64 278 314 GTTGTGGTAGCACAAAAGTATTACCATGGTCCTAG 1e-16 69.4
# BLAST processed 1 queries
```

TTCTACTatacgagtgcgacgtaatgcGTTGTTGGTAGCACAAAAGTATTACCATGGTCCTAGgattacagattacagattacaAGCCT

```
> No fixed matches
CCATACCGTCCTAATTCTTCGGTTATGTTTCCGATGTAGGAGTGAGCCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
GTGCCATCGGGTTTCTGAACTCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACGCTGCCACGTGTTCACTAACTGTTGTTGGTAGCACAAAAGTAT
TACCATGGTCCTAGAAGTTCGGCACAGTTAGTTCGAGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGGCAAGTCAGAGCAGGTTCCCGTGTAGCTTGAGGGTAAA
CATAACAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCCGTAGTTCGAAGCGGAAC
ATTTGAGGGGGCGAGCCCACATCGTCTCTTCTGCGGATGACTTAACACGC
TAGGGAGGTGGAGTCGATTCCATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACTTGGTTCCGAAGC
CTGTCTGATATATGAATCCAAACTAGAGCGGGGCTCTTGACGTTTGAG
TTGTAAATATCTAATATCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCACACCGAGAACTAGACAGTTGCGCGCTGGAAGTA
GCGCCGGCTAAGAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA
```

2x1 Fixed Match

```
# BLASTN 2.2.25+
# Query: oligo1
# Database: ./test.db
# Fields: q. start, q. end, s. start, s. end, query seq, evaluate, bit score
# 1 hits found
1      90      251      340
      TTCTACTATACGAGTGCACGTAATGCGTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATTACAGATTACAAGCCT
      3e-46 167
# BLAST processed 1 queries
```

TTCTACTatacagagtgcgacgtaatgcGTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAGgattacagattacagattacaAGCCT

```
> gattacagattacagattaca @ 314 and tatacagagtgcgacgtaatgc @ 256
CCATACCGTCCTAATTCTTCGGTTATGTTTCCGATGTAGGAGTGAGCCCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
GTGCCATCGGGTTTCTGAACTCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACTatacagagtgcgacgtaatgcGTTGTTTGGTAGCACAAAAGTAT
TACCATGGTCCTAGgattacagattacagattacaAGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGGCAAGTCAGAGCAGGTTCCCGTGTTAGCTTGAGGGTAAA
CATAAAGCCGATTGAAGATGGGTAGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCCCTGTAGTTCGAAGCGGAACT
ATTTGAGGGGCGAGCCACATCGTCTCTTCTGCGGATGACTTAACACGC
TAGGGAGGTGGAGTCGATTCCATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACTTGGTTCCGAAGC
CTGTCCTGATATATGAATCCAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAATATCTAATATTCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCACACCGAGAACTAGACAGTTGCGCGCTGGAAGTA
GCGCCGGCTAAGAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA
```


2x2 Fixed Matches

```
# BLASTN 2.2.25+
# Query: oligo1
# Database: ./test.db
# Fields: q. start, q. end, s. start, s. end, query seq, evaluate, bit score
# 5 hits found
1      90      251      340
      TTCTACTATACGAGTGCGACGTAATGCGTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATTACAGATTACAAGCCT      3e-46      167
5      28      916      939      ACTATACGAGTGCGACGTAATGCG      2e-09      45.4
61     85      458      483      CTA-GGATTACAGATTACAGATTACA      2e-08      41.7
65     83      470      487      GATTACAGATTACAGATTA      2e-04      28.8 [Redundant]
72     85      463      476      GATTACAGATTACA      6e-04      27.0 [Redundant]
# BLAST processed 1 queries
```

TTCTACTatacgagtgcgacgtaatgcGTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAGgattacagattacagattacaAGCCT

```
> gattacagattacagattaca @ 314, 512 and
tatacgagtgcgacgtaatgc @ 256,917
CCATACCGTCCTAATTCTTCGGTTATGTTCCGATGTAGGAGTGAGCCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
GTGCCATCGGGTTTCTGAACTCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCCTGGCG
TTCTACTatacgagtgcgacgtaatgcGTTGTTTGGTAGCACAAAAGTAT
TACCATGGTCCTAGgattacagattacagattacaAGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACGCTAGGgattacagattacagattacaGTTAGCTTGAGGGTAAA
CATAAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCTGTAGTTCGAAGCGGAACT
ATTTGAGGGGCGAGCCACATCGTCTCTTCTGCGGATGACTTAACACGC
TAGGGAGGTGGAGTCGATTCCATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCGTATCTCGATCGCTCAGTCGC
TTTTCGTACTGCGCGAAAGTTCGCACCGCTCATACTTGGTTCCGAAGC
CTGTCTGATATATGAATCCAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAATATCTAATATTCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTCACtatacgagtgcgacgtaatgcGCGCTGGAAGTA
GCGCCGGCTAAGAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA
```

2x4 Fixed Matches

13 hits found

1	90	251	340	TTCTACTATACGAGTGC	GACGTAATGCGTTGTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATTACAGATTACAAGCCT	3e-46	167
5	28	916	939	ACTATACGAGTGC	GACGTAATGCG	2e-09	45.4
64	85	100	121	GGATTACAGATTACAGATTACA		2e-08	41.7
61	85	458	483	CTA-GGATTACAGATTACAGATTACA		2e-08	41.7
65	86	626	647	GATTACAGATTACAGATTACAA		2e-08	41.7
6	27	650	671	CTATACGAGTGC	GACGTAATGC	2e-08	41.7
7	27	26	46	TATACGAGTGC	GACGTAATGC	8e-08	39.9
65	83	470	487	GATTACAGATTACAGATTA		2e-04	28.8
72	85	101	114	GATTACAGATTACA		6e-04	27.0
65	78	108	121	GATTACAGATTACA		6e-04	27.0
72	85	463	476	GATTACAGATTACA		6e-04	27.0
72	85	626	639	GATTACAGATTACA		6e-04	27.0
65	78	633	646	GATTACAGATTACA		6e-04	27.0

BLAST processed 1 queries

CCATACCGTCCTAATTCTTCGGTTA**tatacagagtgcgacgtaatgc**CCCTA
CCTGCCTTTGCGTCTTGATACCAATGAAAAACCTATGCACTTTGTACAGG
gattacagattacagattacaCTCAGATAGTGGGGATCCCGGGTAAAGAC
CTATATCTGCGGTCCAACCTTAGGCATAAACCTCCATGCTACCTAGTCAGA
CCCACCCCGCACGGGGTAAATATGGCACGCGTCCGACCTGGTTCTTGCGG
TTCTACTatacagagtgcgacgtaatgcGTTGTTTGGTAGCACAAAAGTAT
TACCATGGTCCTAGgattacagattacagattacaAGCCTAATGTCACAA
ATGACGCAGAACGCCAATGAGTGCCAGACATTAGGTGGAGTTCAGTTCGG
TAACGGAGAGACTCTGCGGCGTACTTAATTATGCATTTGAAACGCGCCCA
AGTGACG**CTAGGgattacagattacagattaca**GTTAGCTTGAGGGTAAA
CATAACAAGCCGATTGAAGATGGGTAGGGGGCTTCAAATCGTCCAGCACTC
CACAGTACCTCCGAGAGCAAGTAGGGCACCCCTGTAGTTCGAAGCGGAACT
ATTTTCGAGGGGCGAGCCCCACATCGT**gattacagattacagattacaACGC**
tatacagagtgcgacgtaatgcATCGATGGTTATAAATCAAAAAATCGGAA
CGCTGTCTGGAGGATGAATCTAACGGTGCATCTCGATCGCTCAGTCGC
TTTTTCGTA CTGCGGAAAGTTTCGCACCGCTCATACTTGGTTCCGAAGC
CTGTCCTGATATATGAATCCAACTAGAGCGGGGCTCTTGACGTTTGGAG
TTGTAAATATCTAATATTCCAATCGGCTTTTACGTGCACCACCGCGGGCG
GCTGACGAGGGACTC**ACTatacagagtgcgacgtaatgcG**CGCTGGAAGTA
GCGCCGGCTAAGAAAGACGCCTGGTACAGCAGGACTATGAAACCCGTACA

TTCTACTatacagagtgcgacgtaatgcGTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAGgattacagattacagattacaAGCCT

Redundancies ?

13 hits found

1	90	251	340	TTCTACTATACGAGTGCGACGTAATGCGTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATTACAGATTACAAGCCT	3e-46	167
5	28	916	939	ACTATACGAGTGCGACGTAATGCG	2e-09	45.4
64	85	100	121	GGATTACAGATTACAGATTACA	2e-08	41.7
61	85	458	483	CTA-GGATTACAGATTACAGATTACA	2e-08	41.7
65	86	626	647	GATTACAGATTACAGATTACAA	2e-08	41.7
6	27	650	671	CTATACGAGTGCGACGTAATGC	2e-08	41.7
7	27	26	46	TATACGAGTGCGACGTAATGC	8e-08	39.9
65	83	470	487	GATTACAGATTACAGATTA	2e-04	28.8
72	85	101	114	GATTACAGATTACA	6e-04	27.0
65	78	108	121	GATTACAGATTACA	6e-04	27.0
72	85	463	476	GATTACAGATTACA	6e-04	27.0
72	85	626	639	GATTACAGATTACA	6e-04	27.0
65	78	633	646	GATTACAGATTACA	6e-04	27.0

BLAST processed 1 queries

BLAST via JavaMAGE

[BLAST] Total Number of Queries = 1

1 28 64 278 314 GTTGTGGTAGCACAAAAGTATTACCATGGTCCTAG 69.4 1.0E-16

[BLAST] Total Number of Queries = 1

1 1 90 251 340
TTCTACTATACGAGTGCACGTAATGCGTTGTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATTACAGATTACAAGCCT
167.0 3.0E-46

[BLAST] Total Number of Queries = 1

1 1 90 251 340
TTCTACTATACGAGTGCACGTAATGCGTTGTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATTACAGATTACAAGCCT
167.0 3.0E-46

1 5 28 916 939 ACTATACGAGTGCACGTAATGCG 45.4 2.0E-9
1 61 85 458 483 CTA-GGATTACAGATTACAGATTACA 41.7 2.0E-8
1 65 83 470 487 GATTACAGATTACAGATTA 28.8 2.0E-4
1 72 85 463 476 GATTACAGATTACA 27.0 6.0E-4

[BLAST] Total Number of Queries = 1

1 1 90 251 340
TTCTACTATACGAGTGCACGTAATGCGTTGTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATTACAGATTACAAGCCT
167.0 3.0E-46

1 5 28 916 939 ACTATACGAGTGCACGTAATGCG 45.4 2.0E-9
1 64 85 100 121 GGATTACAGATTACAGATTACA 41.7 2.0E-8
1 61 85 458 483 CTA-GGATTACAGATTACAGATTACA 41.7 2.0E-8
1 65 86 626 647 GATTACAGATTACAGATTACAA 41.7 2.0E-8
1 6 27 650 671 CTATACGAGTGCACGTAATGC 41.7 2.0E-8
1 7 27 26 46 TATACGAGTGCACGTAATGC 39.9 8.0E-8
1 65 83 470 487 GATTACAGATTACAGATTA 28.8 2.0E-4
1 72 85 101 114 GATTACAGATTACA 27.0 6.0E-4
1 65 78 108 121 GATTACAGATTACA 27.0 6.0E-4
1 72 85 463 476 GATTACAGATTACA 27.0 6.0E-4
1 72 85 626 639 GATTACAGATTACA 27.0 6.0E-4
1 65 78 633 646 GATTACAGATTACA 27.0 6.0E-4

Identical Results

BG Scores

[BLAST] Total Number of Queries = 1

1	1	90	251	340	TTCTACTATACGAGTGCGACGTAATGCGTTGTTTGGTAGCACAAAAGTATTACCATGGTCCTAGGATTACAGATT		
1	5	28	916	939	ACTATACGAGTGCGACGTAATGCG	45.4	2.0E-9
1	64	85	100	121	GGATTACAGATTACAGATTACA	41.7	2.0E-8
1	61	85	458	483	CTA-GGATTACAGATTACAGATTACA	41.7	2.0E-8
1	65	86	626	647	GATTACAGATTACAGATTACAA	41.7	2.0E-8
1	6	27	650	671	CTATACGAGTGCGACGTAATGC	41.7	2.0E-8
1	7	27	26	46	TATACGAGTGCGACGTAATGC	39.9	8.0E-8
1	65	83	470	487	GATTACAGATTACAGATTA	28.8	2.0E-4
1	72	85	101	114	GATTACAGATTACA	27.0	6.0E-4
1	65	78	108	121	GATTACAGATTACA	27.0	6.0E-4
1	72	85	463	476	GATTACAGATTACA	27.0	6.0E-4
1	72	85	626	639	GATTACAGATTACA	27.0	6.0E-4
1	65	78	633	646	GATTACAGATTACA	27.0	6.0E-4

Weighted Scoring : 167.0 Raw Scoring : 90.0

Weighted Scoring : 45.3999999092 Raw Scoring : 24.0

Weighted Scoring : 41.69999916600001 Raw Scoring : 22.0

Weighted Scoring : 41.69999916600001 Raw Scoring : 25.0

Weighted Scoring : 41.69999916600001 Raw Scoring : 22.0

Weighted Scoring : 41.69999916600001 Raw Scoring : 22.0

Weighted Scoring : 39.899996808000125 Raw Scoring : 21.0

Weighted Scoring : 28.794240575961602 Raw Scoring : 19.0

Weighted Scoring : 26.983804859028147 Raw Scoring : 14.0

Weighted Scoring : 26.983804859028147 Raw Scoring : 14.0

Weighted Scoring : 26.983804859028147 Raw Scoring : 14.0

Weighted Scoring : 26.983804859028147 Raw Scoring : 14.0

Weighted Scoring : 26.983804859028147 Raw Scoring : 14.0