

Blast Result Interpretation

Result 1 (has 7 Hits):

Hit accession: penA0.000
Hsp identity: 100
Hit accession: penA1.001
Hsp identity: 99.7139588100686
Hit accession: penA1.003
Hsp identity: 99.6567505720824
Hit accession: penA2.002
Hsp identity: 99.141876430206
Hit accession: penA2.001
Hsp identity: 99.0274599542334
Hit accession: penA2.003
Hsp identity: 98.9702517162471
Hit accession: penA3.001
Hsp identity: 98.5722444317533

Result 2 (has 6 Hits):

Hit accession: mtrR0.000
Hsp identity: 100
Hit accession: mtrR1.000
Hsp identity: 98.7179487179487
Hit accession: mtrR6.000
Hsp identity: 98.4330484330484
Hit accession: mtrR5.000
Hsp identity: 98.2905982905983
Hit accession: mtrR4.000
Hsp identity: 98.1481481481482
Hit accession: mtrR3.000
Hsp identity: 98.1481481481482

BLASTN 2.2.28+

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.

Database: /home/irish_m/ng-star-test-2/ng-star/BusinessLogic/data/allele_db_Fmo6Bvzp.fasta
13 sequences; 16,446 total letters

Query=
Length=1745

Sequences producing significant alignments:

	Score (Bits)	E Value
penA0.000	3223	0.0
penA1.001	3197	0.0
penA1.003	3192	0.0
penA2.002	3142	0.0
penA2.001	3131	0.0
penA2.003	3125	0.0
penA3.001	3090	0.0

> penA0.000

Length=1746

Score = 3223 bits (1745), Expect = 0.0
Identities = 1745/1745 (100%), Gaps = 0/1745 (0%)
Strand=Plus/Plus

Query	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Sbjct	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Query	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120
Sbjct	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120
Query	121	TGTCTGATTGCCCGGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAGAAGACAG	180
Sbjct	121	TGTCTGATTGCCCGGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAGAAGACAG	180
Query	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Sbjct	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Query	241	CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTGCCGTGCCTAAA	300
Sbjct	241	CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTGCCGTGCCTAAA	300
Query	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Sbjct	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Query	361	CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG	420
Sbjct	361	CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG	420
Query	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480
Sbjct	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480
Query	481	TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Sbjct	481	TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Query	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAAC TTCGCTGAAGACAGCCTG	600
Sbjct	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAAC TTCGCTGAAGACAGCCTG	600
Query	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Sbjct	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Query	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Sbjct	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Query	721	CAGAGGATTGAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Sbjct	721	CAGAGGATTGAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Query	781	AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Sbjct	781	AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Query	841	ACGCCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Sbjct	841	ACGCCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Query	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTTCGTGATTGCGAAGGCA	960
Sbjct	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTTCGTGATTGCGAAGGCA	960

Query	961	TTGGATGCGGGCAAAACCGATTGTAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Sbjct	961	TTGGATGCGGGCAAAACCGATTGTAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Query	1021	CCGTCTCCCGTGCGCGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATGCAG	1080
Sbjct	1021	CCGTCTCCCGTGCGCGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATGCAG	1080
Query	1081	AAATCGTCCAACGTGCGCACAAGCAAACGTGTCTGCGCGTTTCGGCGCCGAAGAAATGTAT	1140
Sbjct	1081	AAATCGTCCAACGTGCGCACAAGCAAACGTGTCTGCGCGTTTCGGCGCCGAAGAAATGTAT	1140
Query	1141	GACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCGGGGGAAACT	1200
Sbjct	1141	GACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCGGGGGAAACT	1200
Query	1201	GCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCTTTC	1260
Sbjct	1201	GCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCTTTC	1260
Query	1261	GGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACGCAC	1320
Sbjct	1261	GGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACGCAC	1320
Query	1321	GACGGCGTTTTGCTGCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGAAGGCAAACGC	1380
Sbjct	1321	GACGGCGTTTTGCTGCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGAAGGCAAACGC	1380
Query	1381	ATATTCAAAGAATCGACCGCGCGAGGTACGCAATCTGATGGTTTTCCGTAACCGAGCCG	1440
Sbjct	1381	ATATTCAAAGAATCGACCGCGCGAGGTACGCAATCTGATGGTTTTCCGTAACCGAGCCG	1440
Query	1441	GGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTGCGCGCTAAAACCGGCACG	1500
Sbjct	1441	GGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTGCGCGCTAAAACCGGCACG	1500
Query	1501	GCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTGCTACCTTTATCGGT	1560
Sbjct	1501	GCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTGCTACCTTTATCGGT	1560
Query	1561	TTTGCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACTGCC	1620
Sbjct	1561	TTTGCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACTGCC	1620
Query	1621	CACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaTTATGGGCGGCAGC	1680
Sbjct	1621	CACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAATTATGGGCGGCAGC	1680
Query	1681	CTGAACATCTTGGGCATTCCCCGACCAAGCCACTGACCGCCGAGCCGTCAAACACCG	1740
Sbjct	1681	CTGAACATCTTGGGCATTCCCCGACCAAGCCACTGACCGCCGAGCCGTCAAACACCG	1740
Query	1741	TCTTA 1745	
Sbjct	1741	TCTTA 1745	

> penA1.001
Length=1749

Score = 3197 bits (1731), Expect = 0.0
Identities = 1743/1748 (99%), Gaps = 3/1748 (0%)
Strand=Plus/Plus

Query	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Sbjct	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Query	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120

Sbjct	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120
Query	121	TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTTGAAAGAACAG	180
Sbjct	121	TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTTGAAAGAACAG	180
Query	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Sbjct	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Query	241	CGGAACGGTGCGGTTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Sbjct	241	CGGAACGGTGCGGTTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Query	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Sbjct	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Query	361	CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG	420
Sbjct	361	CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG	420
Query	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAACCTTTGTA	480
Sbjct	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAACCTTTGTA	480
Query	481	TTTGAAAAAGAATTAAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Sbjct	481	TTTGAAAAAGAATTAAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Query	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Sbjct	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Query	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Sbjct	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Query	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Sbjct	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Query	721	CAGAGGATTCAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGGAATACCATCAGGCA	780
Sbjct	721	CAGAGGATTCAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGGAATACCATCAGGCA	780
Query	781	AAAGCCGGAACGGTGGTGGTTTTTGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Sbjct	781	AAAGCCGGAACGGTGGTGGTTTTTGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Query	841	ACGCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Sbjct	841	ACGCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Query	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Sbjct	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Query	961	TTGGATGCGGGGAAAACCGATTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Sbjct	961	TTGGATGCGGGGAAAACCGATTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Query	1021	CCGTCTCCCGTGC GCGA--TACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1077
Sbjct	1021	CCGTCTCCCGTGC GCGACGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1080
Query	1078	CAGAAATCGTCCAACGTCGGCACAAGCAAACCTGTCTGCGCGTTTCGGCGCCGAAGAAATG	1137
Sbjct	1081	CAGAAATCGTCCAACGTCGGCACAAGCAAACCTGTCTGCGCGTTTCGGCGCCGAAGAAATG	1140

Query	1138	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1197
Sbjct	1141	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1200
Query	1198	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT	1257
Sbjct	1201	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT	1260
Query	1258	TTCGGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1317
Sbjct	1261	TTCGGTTACGGCCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1320
Query	1318	CACGACGGCGTTTTGTGTCGGCTCAGCTTTGAGAAGCAGGCGTTGCGCCGCAAGGCAA	1377
Sbjct	1321	CACGACGGCGTTTTGTGTCGGCTCAGCTTTGAGAAGCAGGCGTTGCGCCGCAAGGCAA	1380
Query	1378	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1437
Sbjct	1381	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1440
Query	1438	CCGGGCGGCACCGGTACGGCGGGTGCAGGTTTCGATGTCGGCGCTAAAACCGGC	1497
Sbjct	1441	CCGGGCGGCACCGGTACGGCGGGTGCAGGTTTCGATGTCGGCGCTAAAACCGGC	1500
Query	1498	ACGGCGCGCAAGTTTCGTCAACGGGCGTTATGCCGACAACAACACGTCGCTACCTTTATC	1557
Sbjct	1501	ACGGCGCGCAAGTTTCGTCAACGGGCGTTATGCCGACAACAACACGTCGCTACCTTTATC	1560
Query	1558	GGTTTTGCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACT	1617
Sbjct	1561	GGTTTTGCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACT	1620
Query	1618	GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaTTATGGGCGGC	1677
Sbjct	1621	GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAATTATGGGCGGC	1680
Query	1678	AGCCTGAACATCTTGGGCATTTCCTCCGACCAAGCCACTGACCGCCGAGCCGTCAAAACA	1737
Sbjct	1681	AGCCTGAACATCTTGGGCATTTCCTCCGACCAAGCCACTGACCGCCGAGCCGTCAAAACA	1740
Query	1738	CCGTCTTA 1745	
Sbjct	1741	CCGTCTTA 1748	

> penA1.003
Length=1749

Score = 3192 bits (1728), Expect = 0.0
Identities = 1742/1748 (99%), Gaps = 3/1748 (0%)
Strand=Plus/Plus

Query	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Sbjct	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Query	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120
Sbjct	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120
Query	121	TGTCTGATTGCCCGGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAGAAGACAG	180
Sbjct	121	TGTCTGATTGCCCGGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAGAAGACAG	180
Query	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Sbjct	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Query	241	CGGAACGGTGCGGTTTTGGCGTTAGCGCGCGGACGGAGTCCCTGTTTGCCGTGCCTAAA	300

Sbjct	241	CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCTGTTGCCGTGCCTAAA	300
Query	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCTGATGTG	360
Sbjct	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCTGATGTG	360
Query	361	CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTATTTGGATCAAG	420
Sbjct	361	CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTATTTGGATCAAG	420
Query	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAACCTTTGTA	480
Sbjct	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAACCTTTGTA	480
Query	481	TTTGAAAAAGAATTAAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Sbjct	481	TTTGAAAAAGAATTAAACGCCTATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Query	541	TTTACCGATATTGACGGCAAAGGTGAGGAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Sbjct	541	TTTACCGATATTGACGGCAAAGGTGAGGAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Query	601	TATGGCGAAGACGGCGCGGAAGTTGTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Sbjct	601	TATGGCGAAGACGGCGCGGAAGTTGTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Query	661	TTGGACTCCCCGCGCAATAAAGCACCAGCAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Sbjct	661	TTGGACTCCCCGCGCAATAAAGCACCAGCAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Query	721	CAGAGGATTGAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Sbjct	721	CAGAGGATTGAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Query	781	AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Sbjct	781	AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Query	841	ACGCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Sbjct	841	ACGCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Query	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Sbjct	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Query	961	TTGGATGCGGGCAAACCGATTGTAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Sbjct	961	TTGGATGCGGGCAAACCGATTGTAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Query	1021	CCGTCTCCCGTGC GCGA--TACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1077
Sbjct	1021	CCGTCTCCCGTGC GCGACGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1080
Query	1078	CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG	1137
Sbjct	1081	CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG	1140
Query	1138	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1197
Sbjct	1141	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1200
Query	1198	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCATCGAACAGGCGACGATGTCT	1257
Sbjct	1201	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCATCGAACAGGCGACGATGTCT	1260
Query	1258	TTCGGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1317
Sbjct	1261	TTCGGTTACGGCCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1320

Query	1318	CACGACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAA	1377
Sbjct	1321	CACGACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAA	1380
Query	1378	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1437
Sbjct	1381	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1440
Query	1438	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGC	1497
Sbjct	1441	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGC	1500
Query	1498	ACGGCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATC	1557
Sbjct	1501	ACGGCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATC	1560
Query	1558	GGTTTTGCCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACT	1617
Sbjct	1561	GGTTTTGCCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAACCATGACGAACCGACT	1620
Query	1618	GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaTTATGGGCGGC	1677
Sbjct	1621	GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAATTATGGGCGGC	1680
Query	1678	AGCCTGAACATCTTGGGCATTTCGCCGACCAAGCCACTGACCGCCGAGCCGTCAAAACA	1737
Sbjct	1681	AGCCTGAACATCTTGGGCATTTCGCCGACCAAGCCACTGACCGCCGAGCCGTCAAAACA	1740
Query	1738	CCGTCTTA 1745	
Sbjct	1741	CCGTCTTA 1748	

> penA2.002
Length=1749

Score = 3142 bits (1701), Expect = 0.0
Identities = 1733/1748 (99%), Gaps = 3/1748 (0%)
Strand=Plus/Plus

Query	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Sbjct	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Query	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120
Sbjct	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC	120
Query	121	TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAAGAACAG	180
Sbjct	121	TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAAGAACAG	180
Query	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Sbjct	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Query	241	CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Sbjct	241	CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Query	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTGATGTG	360
Sbjct	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTGATGTG	360
Query	361	CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTTATTGGATCAAG	420
Sbjct	361	CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTTATTGGATCAAG	420
Query	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480

Sbjct	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480
Query	481	TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGACACATCATCGGA	540
Sbjct	481		
Sbjct	481	TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGACACATCATCGGA	540
Query	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Sbjct	541		
Sbjct	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Query	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Sbjct	601		
Sbjct	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Query	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Sbjct	661		
Sbjct	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Query	721	CAGAGGATTACAGCCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Sbjct	721		
Sbjct	721	CAGAGGATTACAGCCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Query	781	AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGCCAAT	840
Sbjct	781		
Sbjct	781	AAAGCCGGAACGGTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGCCAAT	840
Query	841	ACGCCCCGCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Sbjct	841		
Sbjct	841	ACGCCCCGCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Query	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Sbjct	901		
Sbjct	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Query	961	TTGGATGCGGGCAAAACCGATTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Sbjct	961		
Sbjct	961	TTGGATGCGGGCAAAACCGATTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Query	1021	CCGTCTCCCGTGCGCGA--TACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1077
Sbjct	1021		
Sbjct	1021	CCGTCTCCCGTGCGCGACGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1080
Query	1078	CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG	1137
Sbjct	1081		
Sbjct	1081	CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG	1140
Query	1138	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTCCGGGGGAA	1197
Sbjct	1141		
Sbjct	1141	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTCCGGGGGAA	1200
Query	1198	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCATCGAACAGGCGACGATGTCT	1257
Sbjct	1201		
Sbjct	1201	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCATCGAACAGGCGACGATGTCT	1260
Query	1258	TTCGGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1317
Sbjct	1261		
Sbjct	1261	TTCGGTTACGGCCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1320
Query	1318	CACGACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGAAGGCAA	1377
Sbjct	1321		
Sbjct	1321	CACGACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGAAGGCAA	1380
Query	1378	CGCATATTCAAAGAATCGACCGCGCGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1437
Sbjct	1381		
Sbjct	1381	CGCATATTCAAAGAATCGACCGCGCGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1440
Query	1438	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGC	1497
Sbjct	1441		
Sbjct	1441	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGT	1500

Query	1498	ACGGCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATC	1557
Sbjct	1501	ACGGCGCGCAAACTGGTCAATGGCCGCTATGTGGACAACAAACACGTCGGTACGTTTATC	1560
Query	1558	GGTTTTGCCCCGCCAAAAACCCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACT	1617
Sbjct	1561	GGTTTTGCCCCGCCAAAAACCCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACT	1620
Query	1618	GCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaTTATGGGCGGC	1677
Sbjct	1621	GCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAAATTATGGGCGGC	1680
Query	1678	AGCCTGAACATCTTGGGCATTTCCCCGACCAAGCCACTGACCGCCGACCCGTCAAAACA	1737
Sbjct	1681	AGCCTGAACATCTTGGGCATTTCCCCGACCAAGCCACTGACCGCCGACCCGTCAAAACA	1740
Query	1738	CCGTCTTA	1745
Sbjct	1741	CCGTCTTA	1748

> penA2.001
Length=1749

Score = 3131 bits (1695), Expect = 0.0
Identities = 1731/1748 (99%), Gaps = 3/1748 (0%)
Strand=Plus/Plus

Query	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Sbjct	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Query	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCCTGATGGCAATGGCGGTCTGTTTGCC	120
Sbjct	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCCTGATGGCAATGGCGGTCTGTTTGCC	120
Query	121	TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAAGAACAG	180
Sbjct	121	TGTCTGATTGCCCGCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAAGAACAG	180
Query	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Sbjct	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC	240
Query	241	CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Sbjct	241	CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Query	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Sbjct	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Query	361	CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTATTTGGATCAAG	420
Sbjct	361	CCGGTCGATGTTTTGAGGAACAAACTCGAACAGAAAGGCAAGTCGTTATTTGGATCAAG	420
Query	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480
Sbjct	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480
Query	481	TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Sbjct	481	TTTGAAAAAGAATTAAAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Query	541	TTTACCATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Sbjct	541	TTTACCATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Query	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTCGCGGACCGGCAGGGCAATATTGTGGACAGC	660

Sbjct	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Query	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Sbjct	661	TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Query	721	CAGAGGATTAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTCGAATACCATCAGGCA	780
Sbjct	721	CAGAGGATTAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTCGAATACCATCAGGCA	780
Query	781	AAAGCCGGAACGGTGGTGGTTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Sbjct	781	AAAGCCGGAACGGTGGTGGTTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Query	841	ACGCCCCGCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Sbjct	841	ACGCCCCGCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Query	901	GCCGTAACCGATATGATCGAACCCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Sbjct	901	GCCGTAACCGATATGATCGAACCCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Query	961	TTGGATGCGGGGAAAACCGATTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Sbjct	961	TTGGATGCGGGGAAAACCGATTGAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Query	1021	CCGTCTCCCGTGCGCGA--TACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1077
Sbjct	1021	CCGTCTCCCGTGCGCGACGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1080
Query	1078	CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG	1137
Sbjct	1081	CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG	1140
Query	1138	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1197
Sbjct	1141	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1200
Query	1198	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT	1257
Sbjct	1201	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT	1260
Query	1258	TTCGGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1317
Sbjct	1261	TTCGGTTACGGCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1320
Query	1318	CACGACGGCGTTTGTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAA	1377
Sbjct	1321	CACGACGGCGTTTGTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAA	1380
Query	1378	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1437
Sbjct	1381	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1440
Query	1438	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTGCGGCTAAAACCGGC	1497
Sbjct	1441	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTGCGGCTAAAACCGGT	1500
Query	1498	ACGGCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATC	1557
Sbjct	1501	ACGGCGCGCAAACTGGTCAATGGCCGCTATGTGGACAACAAACACGTCGGTACGTTTATC	1560
Query	1558	GGTTTTGCCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAAACATCGACGAACCGACT	1617
Sbjct	1561	GGTTTTGCCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAAACATCGACGAACCGACT	1620
Query	1618	GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaTTATGGGCGGC	1677
Sbjct	1621	GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAATTATGGGCGGC	1680

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Query 1678 AGCCTGAACATCTTGGGCATTTCCTCCGACCAAGCCACTGACCGCCGCAGCCGTCAAAAACA 1737
|||||
Sbjct 1681 AGCCTGAACATCTTGGGCATTTCCTCCGACCAAGCCACTGACCGCCGCAGCCGTCAAAAACA 1740

Query 1738 CCGTCTTA 1745
|||||
Sbjct 1741 CCGTCTTA 1748
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> penA2.003
Length=1749

Score = 3125 bits (1692), Expect = 0.0
Identities = 1730/1748 (99%), Gaps = 3/1748 (0%)
Strand=Plus/Plus

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Query 1 ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG 60
|||||
Sbjct 1 ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG 60

Query 61 CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC 120
|||||
Sbjct 61 CCGATGACCAGTAACGGACGGATTAGCTTCGTCTGATGGCAATGGCGGTCTTGTTTGCC 120

Query 121 TGTCTGATTGCCCCGGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAGAACAG 180
|||||
Sbjct 121 TGTCTGATTGCCCCGGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAGAACAG 180

Query 181 GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC 240
|||||
Sbjct 181 GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGCGGTACGGTTTCGGAC 240

Query 241 CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA 300
|||||
Sbjct 241 CGGAACGGTGCGGTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA 300

Query 301 GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG 360
|||||
Sbjct 301 GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG 360

Query 361 CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG 420
|||||
Sbjct 361 CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTTATTTGGATCAAG 420

Query 421 CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAACCTTTGTA 480
|||||
Sbjct 421 CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGGAACCTTTGTA 480

Query 481 TTTGAAAAAGAATTAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA 540
|||||
Sbjct 481 TTTGAAAAAGAATTAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA 540

Query 541 TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG 600
|||||
Sbjct 541 TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG 600

Query 601 TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC 660
|||||
Sbjct 601 TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC 660

Query 661 TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT 720
|||||
Sbjct 661 TTGGACTCCCCGCGCAATAAAGCACCGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT 720

Query 721 CAGAGGATTACAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA 780
|||||
Sbjct 721 CAGAGGATTACAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA 780

Query 781 AAAGCCGGAACGTTGGTGGTTTTGGATGCCCGCACGGGGGAAATCCTCGCCTTGCCCAAT 840
|||||
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Sbjct	781	AAAGCCGGAACGGTGGTGGTTTTGGATGCCCCACGGGGGAAATCCTCGCCTTGGCCAAT	840
Query	841	ACGCCCCGCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Sbjct	841	ACGCCCCGCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Query	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Sbjct	901	GCCGTAACCGATATGATCGAACCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Query	961	TTGGATGCGGGCAAAACCGATTGTAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Sbjct	961	TTGGATGCGGGCAAAACCGATTGTAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA	1020
Query	1021	CCGTCTCCCGTGC GCGA--TACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1077
Sbjct	1021	CCGTCTCCCGTGC GCGACGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG	1080
Query	1078	CAGAAATCGTCCAACGTCGGCACAAGCAAATGTCTGCGCGTTTCGGCGCCGAAGAAATG	1137
Sbjct	1081	CAGAAATCGTCCAACGTCGGCACAAGCAAATGTCTGCGCGTTTCGGCGCCGAAGAAATG	1140
Query	1138	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1197
Sbjct	1141	TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA	1200
Query	1198	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT	1257
Sbjct	1201	ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT	1260
Query	1258	TTCGGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1317
Sbjct	1261	TTCGGTTACGGCCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG	1320
Query	1318	CACGACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAA	1377
Sbjct	1321	CACGACGGCGTTTTGCTGCCGCTCAGCTTTGAGAAGCAGGCGGTTGCGCCGCAAGGCAAA	1380
Query	1378	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1437
Sbjct	1381	CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG	1440
Query	1438	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGC	1497
Sbjct	1441	CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTCGGCGCTAAAACCGGT	1500
Query	1498	ACGGCGCGCAAGTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATC	1557
Sbjct	1501	ACGGCGCGCAAACTGGTCAATGGCCGCTATGTGGACAACAAACACGTCGGTACGTTTATC	1560
Query	1558	GGTTTTGCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTAACCATCGACGAACCGACT	1617
Sbjct	1561	GGTTTTGCCCCGCCAAAAACCCCGTGTGATTGTGGCGGTTACCATCGACGAACCGACT	1620
Query	1618	GCCACAGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaTTATGGGCGGC	1677
Sbjct	1621	GCCACAGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAATTATGGGCGGC	1680
Query	1678	AGCCTGAACATCTTGGGCATTTCCCCGACCAAGCCACTGACCGCCGCAGCCGTCAAAACA	1737
Sbjct	1681	AGCCTGAACATCTTGGGCATTTCCCCGCCCAAGCCACTGACCGCCGCAGCCGTCAAAACA	1740
Query	1738	CCGTCTTA 1745	
Sbjct	1741	CCGTCTTA 1748	

> penA3.001
Length=1752

Score = 3090 bits (1673), Expect = 0.0
Identities = 1726/1751 (99%), Gaps = 6/1751 (0%)
Strand=Plus/Plus

Query	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Sbjct	1	ATGTTGATTAAAAGCGAATATAAGCCCCGGATGCTGCCCAAAGAAGAGCAGGTCAAAAAG	60
Query	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCCTGATGGCAATGGCGGTCTTGTTTGCC	120
Sbjct	61	CCGATGACCAGTAACGGACGGATTAGCTTCGTCCTGATGGCAATGGCGGTCTTGTTTGCC	120
Query	121	TGCTGTATTGCCCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAAGAACAG	180
Sbjct	121	TGCTGTATTGCCCGGGCTGTATCTGCAGACGGTAACGTATAACTTTTGAAAGAACAG	180
Query	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGGGTACGGTTTCGGAC	240
Sbjct	181	GGCGACAACCGGATTGTGCGGACTCAAGCATTGCCGGCTACACGGGTACGGTTTCGGAC	240
Query	241	CGGAACGGTGCGGTTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Sbjct	241	CGGAACGGTGCGGTTTTTGGCGTTGAGCGCGCCGACGGAGTCCCTGTTTGCCGTGCCTAAA	300
Query	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Sbjct	301	GATATGAAGGAAATGCCGTCTGCCGCCCAATTGGAACGCCTGTCCGAGCTTGTCGATGTG	360
Query	361	CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTATTTGGATCAAG	420
Sbjct	361	CCGGTCGATGTTTTGAGGAACAACTCGAACAGAAAGGCAAGTCGTTATTTGGATCAAG	420
Query	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480
Sbjct	421	CGGCAGCTCGATCCCAAGGTTGCCGAAGAGGTCAAAGCCTTGGGTTTGAAAACTTTGTA	480
Query	481	TTTGAAAAAGAATTAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Sbjct	481	TTTGAAAAAGAATTAACGCCATTACCCGATGGGCAACCTGTTTGACACGTCATCGGA	540
Query	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Sbjct	541	TTTACCGATATTGACGGCAAAGGTCAGGAAGGTTTGGAACCTTCGCTTGAAGACAGCCTG	600
Query	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Sbjct	601	TATGGCGAAGACGGCGCGGAAGTTGTTTTGCGGGACCGGCAGGGCAATATTGTGGACAGC	660
Query	661	TTGGACTCCCCGCGCAATAAAGCACCAGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Sbjct	661	TTGGACTCCCCGCGCAATAAAGCACCAGCAAAACGGCAAAGACATCATCCTTTCCCTCGAT	720
Query	721	CAGAGGATTCAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Sbjct	721	CAGAGGATTCAGACCTTGGCCTATGAAGAGTTGAACAAGGCGGTGCAATACCATCAGGCA	780
Query	781	AAAGCCGGAACGGTGGTGGTTTTTGATGCCCGACGGGGGAAATCCTCGCCTTGGCCAAT	840
Sbjct	781	AAAGCCGGAACGGTGGTGGTTTTTGATGCCCGACGGGGGAAATCCTCGCCTTGGCCAAT	840
Query	841	ACGCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Sbjct	841	ACGCCCCCTACGATCCCAACAGACCCGGCCGGGCAGACAGCGAACAGCGGCGCAACCGT	900
Query	901	GCCGTAACCGATATGATCGAACCCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Sbjct	901	GCCGTAACCGATATGATCGAACCCTGGTTCGGCAATCAAACCGTTCGTGATTGCGAAGGCA	960
Query	961	TTGGATGCGGGGAAAACCGATTGAACGAACGCTGAATACGCAGCCTTATAAAATCGGA	1020

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Sbjct  961      TTGGATGCGGGCAAAACCGATTGTAACGAACGGCTGAATACGCAGCCTTATAAAATCGGA 1020

Query  1021      CCGTCTCCCGTGCGCGA--TACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG 1077
|||||
Sbjct  1021      CCGTCTCCCGTGCGCGACGATACCCATGTTTACCCCTCTTTGGATGTGCGCGGCATTATG 1080

Query  1078      CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG 1137
|||||
Sbjct  1081      CAGAAATCGTCCAACGTCGGCACAAGCAAACGTCTGCGCGTTTCGGCGCCGAAGAAATG 1140

Query  1138      TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA 1197
|||||
Sbjct  1141      TATGACTTCTATCATGAATTGGGCATCGGTGTGCGTATGCACTCGGGCTTTCCGGGGGAA 1200

Query  1198      ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT 1257
|||||
Sbjct  1201      ACTGCAGGTTTGTGAGAAATTGGCGCAGGTGGCGGCCCATCGAACAGGCGACGATGTCT 1260

Query  1258      TTCGGTTACGGTCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG 1317
|||||
Sbjct  1261      TTCGGTTACGGCTGCAATTGAGCCTGCTGCAATTGGCGCGCGCCTATACCGCACTGACG 1320

Query  1318      CACGACGGCGTTTTGTGTCGGCTCAGCTTTGAGAAGCAGGCGTTGCGCCGAAGGCAA 1377
|||||
Sbjct  1321      CACGACGGCGTTTTGTGTCGGCTCAGCTTTGAGAAGCAGGCGTTGCGCCGAAGGCAA 1380

Query  1378      CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG 1437
|||||
Sbjct  1381      CGCATATTCAAAGAATCGACCGCGCGGAGGTACGCAATCTGATGGTTTCCGTAACCGAG 1440

Query  1438      CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTGCGCGCTAAAACCGGC 1497
|||||
Sbjct  1441      CCGGGCGGCACCGGTACGGCGGGTGCGGTGGACGGTTTCGATGTGCGCGCTAAAACCGGT 1500

Query  1498      ACGGCGCGCAAGTTTCGTCAACGGGCGTTATGCCGACAACAAACACGTCGCTACCTTTATC 1557
|||||
Sbjct  1501      ACGGTGCGCAAACTGGTCAATGGCCGCTATGTGGACAACAAACACGTCGGTACGTTTATC 1560

Query  1558      GGTTTTGCCCCGCCAAAAACCCCGTGATTGTGGCGGTAACCATCGACGAACCGACT 1617
|||||
Sbjct  1561      GGTTTTGCCCCGCCAAAAACCCCGTGATTGTGGCGGTAACCATCGACGAACCGACT 1620

Query  1618      GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCaaaaaaTTATGGGCGGC 1677
|||||
Sbjct  1621      GCCCACGGCTATTACGGCGGCGTAGTGGCAGGGCCGCCCTTCAAAAAAATTATGGGCGGC 1680

Query  1678      AGCCTGAACATCTTGGGCATTTCGCCGACCAAGCCACTGACC--GCCGCAGCCGTCAAA 1734
|||||
Sbjct  1681      AGCCTGAACATCTTGGGCGTTTCCCGACCAAACCTTGACCAATGTTGCAGCCGTCAAA 1740

Query  1735      ACACCGTCTTA 1745
|||||
Sbjct  1741      ACACCGTCTTA 1751

```

```

Lambda      K      H
      1.33    0.621    1.12

```

```

Gapped
Lambda      K      H
      1.28    0.460    0.850

```

Effective search space used: 28036800

Query=
Length=702

Sequences producing significant alignments:

Score E
(Bits) Value

mtrR0.000	1297	0.0
mtrR1.000	1243	0.0
mtrR6.000	1234	0.0
mtrR5.000	1227	0.0
mtrR4.000	1221	0.0
mtrR3.000	1221	0.0

> mtrR0.000

Length=703

Score = 1297 bits (702), Expect = 0.0
Identities = 702/702 (100%), Gaps = 0/702 (0%)
Strand=Plus/Plus

Query	1	TTGCACGGATAAAAAGTcttttttATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA	60
Sbjct	1	TTGCACGGATAAAAAGTCTTTTTTATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA	60
Query	61	ACGCCATTATGAGAAAAACCAAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG	120
Sbjct	61	ACGCCATTATGAGAAAAACCAAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG	120
Query	121	CCGCCTTGGAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC	180
Sbjct	121	CCGCCTTGGAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC	180
Query	181	AAGCCGCGGCGTAACGCGCGGCGCGCTTTATTGGCATTTCAAAAATAAGGAAGACTTGT	240
Sbjct	181	AAGCCGCGGCGTAACGCGCGGCGCGCTTTATTGGCATTTCAAAAATAAGGAAGACTTGT	240
Query	241	TCGACGCGCTGTTCCAACGTATCTGCGACGACATCGAAAACGTCATCGCGCAAGATGCCG	300
Sbjct	241	TCGACGCGCTGTTCCAACGTATCTGCGACGACATCGAAAACGTCATCGCGCAAGATGCCG	300
Query	301	CAGATGCCGAAGGAGGGTCTTGGGCGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC	360
Sbjct	301	CAGATGCCGAAGGAGGGTCTTGGGCGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC	360
Query	361	GGCTGCAAAGCAACGACATCTACTACAAATCCACAACATCCTGTTTTTAAATGCGAAC	420
Sbjct	361	GGCTGCAAAGCAACGACATCTACTACAAATCCACAACATCCTGTTTTTAAATGCGAAC	420
Query	421	ACACGGAGCAAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG	480
Sbjct	421	ACACGGAGCAAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG	480
Query	481	AGAAAATTACGCCGTTTTTGACCGAAGCGGTGGAAAATCAGGATTGGCTGACGATTGG	540
Sbjct	481	AGAAAATTACGCCGTTTTTGACCGAAGCGGTGGAAAATCAGGATTGGCTGACGATTGG	540
Query	541	ACAAGGAAACGGCGGTCATCTTCATCAAATCGACGTTGGACGGGCTGATTGGCGTTGGT	600
Sbjct	541	ACAAGGAAACGGCGGTCATCTTCATCAAATCGACGTTGGACGGGCTGATTGGCGTTGGT	600
Query	601	TCTCTTCGGCGAAAAGTTTCGATTGGGCAAAACCGCCCCCGCGCATCATCGGGATAAT	660
Sbjct	601	TCTCTTCGGCGAAAAGTTTCGATTGGGCAAAACCGCCCCCGCGCATCATCGGGATAAT	660
Query	661	GATGGACAACCTTGGAACCATCCCTGCCTGCGCCGGAAATA	702
Sbjct	661	GATGGACAACCTTGGAACCATCCCTGCCTGCGCCGGAAATA	702

> mtrR1.000

Length=699

Score = 1243 bits (673), Expect = 0.0
Identities = 693/702 (99%), Gaps = 4/702 (1%)

Strand=Plus/Plus

```
Query 1      TTGCACGGATAAAAAAGTCtttttttATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA 60
|||||  |||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 1      TTGCACGGAT-AAAAGTC-TTTTTTATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA 58

Query 61     ACGCCATTATGAGAAAAACCAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG 120
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 59     ACGCCATTATGAGAAAAACCAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG 118

Query 121    CCGCCTTGGAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC 180
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 119    CCGCCTTGGAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC 178

Query 181    AAGCCGCCGGCGTAACGCGCGGCGCGCTTTATTGGCATTTCAAAAATAAGGAAGACTTGT 240
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 179    AAGCCGCCGGCGTAACGCGCGGCGCGCTCTATTGGCATTTCAAAAATAAGGAAGACTTGT 238

Query 241    TCACGCGCTGTGTCCAACGTATCTGCGACGACATCGAAAACGATCGCGCAAGATGCCG 300
|  |||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 239    TTGACGCGTGTGTCCAACGTATCTGCGACGACATCGAAAACGATCGCGCAAGATGCCG 298

Query 301    CAGATGCCGAAGGAGGGTCTTGGCGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC 360
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 299    CAGATGCCGAAGGAGGTCTTGGACGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC 358

Query 361    GGCTGCAAAGCAACGACATCTACTACAAATTCACAACATCCTGTTTTTAAATGCGAAC 420
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 359    GGCTGCAAAGCAACGACATCTACTACAAATTCACAACATCCTGTTTTTAAATGCGAAC 418

Query 421    ACACGGAGCAAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG 480
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 419    ACACGGAGCAAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG 478

Query 481    AGAAAAATTACCGCCGTTTTTGACCGAAGCGGTGGAAAATCAGGATTTGGCTGACGATTTGG 540
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 479    AGAAAAATTACCGCCGTTTTTGACCGAAGCGGTGGAAAATCAGGATTTGGCTGACGATTTGG 538

Query 541    ACAAGGAAACGGCGGTTCATCTTCATCAAATCGACGTTGGACGGGCTGATTGGCGTTGGT 600
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 539    ACAAGGAAACGGCGGTTCATCTTCATCAAATCGACGTTGGACGGGCTGATTGGCGTTGGT 598

Query 601    TCTCTCCGGCGAAAGTTTCGATTTGGGCAAACCGCCCCCGCGCATCATCGGGATAAT 660
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 599    TCTCTCCGGCGAAAGTTTCGATTTGGGCAAACCGCCCC--GCGCATCATCGGGATAAT 656

Query 661    GATGGACAACTTGGAACCATCCCTGCCTGCGCCGGAATA 702
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 657    GATGGACAACTTGGAACCATCCCTGCCTGCGCCGGAATA 698
```

> mtrR6.000

Length=701

Score = 1234 bits (668), Expect = 0.0
Identities = 691/702 (98%), Gaps = 2/702 (0%)
Strand=Plus/Plus

```
Query 1      TTGCACGGATAAAAAAGTCtttttttATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA 60
|||||  |||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 1      TTGCACGGATAAAAAAGTCTTTTTATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA 60

Query 61     ACGCCATTATGAGAAAAACCAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG 120
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 61     ACGCCATTATGAGAAAAACCAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG 120

Query 121    CCGCCTTGGAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC 180
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 121    CCGCCTTGGAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC 180
```


Query	181	AAGCCGCCGGCGTAACGCGCGCGCGCTTTATTGGCATTTCAAAAATAAGGAAGACTTGT	240
Sbjct	181	AAGCCGCCGGCGTAACGCGCGCGCGCTCTATTGGCATTTCAAAAATAAGGAAGACTTGT	240
Query	241	TCGACGCGCTGTTCCAACGTATCTGCGACGACATCGAAAACGTCATCGCGCAAGATGCCG	300
Sbjct	241	TTGACGCGTTGTTCCAACGTATCTGCGACGACATCGAAAACGTCATCGCGCAAGATGCCG	300
Query	301	CAGATGCCGAAGGAGGGTCTTGGGCGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC	360
Sbjct	301	CAGATGCCGAAGGAGGTCTTGGACGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC	360
Query	361	GGCTGCAAAGCAACGACATCTACTACAAATCCACAACATCCTGTTTTTAAATGCGAAC	420
Sbjct	361	GGCTGCAAAGCAACGACATCCACTACAAATCCACAACATCCTGTTTTTAAAGTGCGAAC	420
Query	421	ACACGGAGCAAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG	480
Sbjct	421	ATACGGAAACAAACGCCGCCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCG	480
Query	481	AGAAAATTACCGCCGTTTTTGACCGAAGCGGTGGAAAATCAGGATTGGCTGACGATTGG	540
Sbjct	481	AGAAAATTACCGCCGTTTTTGACCGAAGCGGTGGAAAATCAGGATTGGCTGACGATTGG	540
Query	541	ACAAGGAAACGGCGGTTCATCTTATCAAAATCGACGTTGGACGGGCTGATTGGCGTTGGT	600
Sbjct	541	ACAAGGAAACGGCGGTTCATCTTATCAAAATCGACGTTGGACGGGCTGATTGGCGTTGGT	600
Query	601	TCCTTCCGGCGAAAAGTTTCGATTGGGCAAAACCGCCCCCGGCATCATCGGGATAAT	660
Sbjct	601	TCCTTCCGGCGAAAAGTTTCGATTGGGCAAAACCGCCCC--GCGCATCATCGGGATAAT	658
Query	661	GATGGACAACCTTGAAAACCATCCCTGCCTGCGCCGGAATA	702
Sbjct	659	GATGGACAACCTTGAAAACCATCCCTGCCTGCGCCGGAATA	700

> mtrR5.000
Length=700

Score = 1227 bits (664), Expect = 0.0
Identities = 690/702 (98%), Gaps = 3/702 (0%)
Strand=Plus/Plus

Query	1	TTGACGGATAAAAAAGTCtttttttATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA	60
Sbjct	1	TTGACGGATAAAAAAGTC-TTTTTTATAATCCGCCCTCGTCAAACCGACCCGAAACGAAA	59
Query	61	ACGCCATTATGAGAAAAACCAAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG	120
Sbjct	60	ACGCCATTATGAGAAAAACCAAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTG	119
Query	121	CCGCCTTGAAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC	180
Sbjct	120	CCGCCTTGAAACCTTTTACCGCAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCC	179
Query	181	AAGCCGCCGGCGTAACGCGCGCGCGCTTTATTGGCATTTCAAAAATAAGGAAGACTTGT	240
Sbjct	180	AAGCCGCCGGCGTAACGCGCGCGCGCTCTATTGGCATTTCAAAAATAAGGAAGACTTGT	239
Query	241	TCGACGCGCTGTTCCAACGTATCTGCGACGACATCGAAAACGTCATCGCGCAAGATGCCG	300
Sbjct	240	TTGACGCGTTGTTCCAACGTATCTGCGACGACATCGAAAACGTCATCGCGCAAGATGCCG	299
Query	301	CAGATGCCGAAGGAGGGTCTTGGGCGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC	360
Sbjct	300	CAGATGCCGAAGGAGGTCTTGGACGGTATTCCGCCACACGCTGCTGCACTTTTTCGAGC	359
Query	361	GGCTGCAAAGCAACGACATCTACTACAAATCCACAACATCCTGTTTTTAAATGCGAAC	420

Query	601	TCTCTTCCGGCGAAAGTTTCGATTGGGCAAAACGCCCCCGCGCATCATCGGGATAAT	660
Sbjct	600	TCTCTTCCGGCGAAAGTTTCGATTGGGCAAAACGCCCC--GCGCATCATCGGGATAAT	657
Query	661	GATGGACAACCTTGAAAAACCATCCCTGCCTGCGCCGGAATA	702
Sbjct	658	GATGGACAACCTTGAAAAACCATCCCTGCCTGCGCCGGAATA	699

Score = 1221 bits (661), Expect = 0.0
Identities = 689/702 (98%), Gaps = 3/702 (0%)
Strand=Plus/Plus

Lambda	K	H
1.33	0.621	1.12

Lambda	K	H
1.28	0.460	0.850

Effective search space used: 11139268

Database: /home/irish_m/ng-star-test-2/ng-star/BusinessLogic/data/allele_db_Fmo6Bvzp.fasta

Posted date: May 28, 2015 1:29 PM

Number of letters in database: 16,446

Number of sequences in database: 13

Matrix: blastn matrix 1 -2

Gap Penalties: Existence: 0, Extension: 2.5