

BLASTN 2.14.1+

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: EZ4PVNHA016

Database: Refseq prokaryote representative genomes (contains refseq assembly)

938,322 sequences; 77,579,778,222 total letters

Query= Fontibacillus sp. (panacisegetis)

Length=512

	Score	E
Max		
Sequences producing significant alignments:	(Bits)	Value
Ident		
NZ_KZ987724.1 Paenibacillus aceti strain L14 Scaffold1, whole ...	941	0.0
100%		
NZ_CP034346.1 Paenibacillus lutimineralis strain MBLB1234 chro...	924	0.0
99%		
NZ_JAMBOA01000024.1 Paenibacillus motobuensis strain MER36 NO...	913	0.0
99%		
NZ_BIMK01000026.1 Paenibacillus chibensis strain NBRC 15958 PC...	874	0.0
97%		
NZ_BOSL01000001.1 Paenibacillus vini strain J42TS3 sequence01,...	869	0.0
97%		
NZ_RZNX01000019.1 Paenibacillus zeisoli strain 3-5-3 Scaffold1...	869	0.0
97%		
NZ_STGQ01000003.1 Paenibacillus dokdonensis strain YH-JAE5 JAE...	865	0.0
97%		
NZ_STGQ01000002.1 Paenibacillus dokdonensis strain YH-JAE5 JAE...	865	0.0
97%		
NZ_RZNY01000080.1 Paenibacillus anaericanus strain DSM 15890 S...	857	0.0
97%		
NZ_LT575476.1 Paenibacillus tuaregi strain Marseille-P2472T, w...	835	0.0
96%		

ALIGNMENTS

>NZ_KZ987724.1 Paenibacillus aceti strain L14 Scaffold1, whole genome shotgun sequence
Length=5572757

Score = 941 bits (509), Expect = 0.0

Identities = 511/512 (99%), Gaps = 0/512 (0%)

Strand=Plus/Plus

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Query 1          TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
|||||
Sbjct 5247869    TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC
5247928

Query 61         GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG 120
|||||
Sbjct 5247929    GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG
5247988

Query 121        AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT 180
|||||
Sbjct 5247989    AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT
5248048

Query 181        CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC 240
|||||
Sbjct 5248049    CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTAGGACTGAGAC
5248108

Query 241        ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 300
|||||
Sbjct 5248109    ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG
5248168

Query 301        ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA 360
|||||
Sbjct 5248169    ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA
5248228

Query 361        AGAACGTTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT 420
|||||
Sbjct 5248229    AGAACGTTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT
5248288

Query 421        AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG 480
|||||
Sbjct 5248289    AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG
5248348

Query 481        CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 512
|||||
Sbjct 5248349    CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 5248380
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Score = 913 bits (494), Expect = 0.0
Identities = 507/513 (99%), Gaps = 2/513 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	3067025	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	
	3066966		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAG-TAATGAAAGACG	119
Sbjct	3066965	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGG-AAGATAATGAAAGACG	
	3066907		
Query	120	GAGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC	179
Sbjct	3066906	GAGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC	
	3066847		
Query	180	TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA	239
Sbjct	3066846	TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA	
	3066787		
Query	240	CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT	299
Sbjct	3066786	CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT	
	3066727		
Query	300	GACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG	359
Sbjct	3066726	GACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG	
	3066667		
Query	360	AAGAACGTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC	419
Sbjct	3066666	AAGAACGTTCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC	
	3066607		
Query	420	TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG	479
Sbjct	3066606	TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG	
	3066547		
Query	480	GCGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	3066546	GCGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	3066514

Score = 896 bits (485), Expect = 0.0
Identities = 503/512 (98%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	4354231	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTAGC	
	4354290		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	4354291	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	
	4354350		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	4354351	AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	
	4354410		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	4354411	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	4354470		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	4354471	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	4354530		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	4354531	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	4354590		
Query	361	AGAACGTTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	4354591	AGAACGTTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	4354650		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	4354651	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	4354710		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	4354711	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	4354742

Score = 891 bits (482), Expect = 0.0
Identities = 502/512 (98%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
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Sbjct	5148557		TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTAGC	
	5148616			
Query	61		GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	5148617		GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	
	5148676			
Query	121		AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	5148677		AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAATGGCT	
	5148736			
Query	181		CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	5148737		CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	5148796			
Query	241		ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	5148797		ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	5148856			
Query	301		ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	5148857		ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	5148916			
Query	361		AGAACGTTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	5148917		AGAACGTTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	5148976			
Query	421		AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	5148977		AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	5149036			
Query	481		CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	5149037		CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	5149068

Score = 885 bits (479), Expect = 0.0
Identities = 501/512 (98%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60

Sbjct	3618857	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTAGC	
	3618798		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	3618797	GGAAACGTTAGCTAATACCGGATAATTTATATTCTCGCATGAGGAGATAATGAAAGACGG	
	3618738		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	3618737	AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	
	3618678		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	3618677	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	3618618		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	3618617	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	3618558		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	3618557	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	3618498		
Query	361	AGAACGTTCTGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	3618497	AGAACGTCCGTTAGAGTAACTGCTAACGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	3618438		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	3618437	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	3618378		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	3618377	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	3618346

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Query    1      TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
          |||
Sbjct   3415354 TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTAGC
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3415295

Query 61 GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG 120
|||||
Sbjct 3415294 GGAAACGTTAGCTAATACCGGATAATTTATATTCTCGCATGAGGAGATAATGAAAGACGG
3415235

Query 121 AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT 180
|||||
Sbjct 3415234 AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAATGGCT
3415175

Query 181 CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC 240
|||||
Sbjct 3415174 CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC
3415115

Query 241 ACGGCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 300
|||||
Sbjct 3415114 ACGGCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG
3415055

Query 301 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA 360
|||||
Sbjct 3415054 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA
3414995

Query 361 AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT 420
|||||
Sbjct 3414994 AGAACGTCCGTTAGAGTAACTGCTAACGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT
3414935

Query 421 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG 480
|||||
Sbjct 3414934 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG
3414875

Query 481 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 512
|||||
Sbjct 3414874 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 3414843

Score = 880 bits (476), Expect = 0.0
Identities = 500/512 (98%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query 1 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
|||||
Sbjct 3687028 TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTAGC
3686969

Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	3686968	GGAAACGTTAGCTAATACCGGATAATTTATATTCTCGCATGAGGAGATAATGAAAGACGG	
	3686909		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	3686908	AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAATGGCT	
	3686849		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	3686848	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	3686789		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	3686788	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	3686729		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	3686728	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	3686669		
Query	361	AGAACGTTCCGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	3686668	AGAACGTCCGTTAGAGTAACTGCTAACGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	3686609		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	3686608	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	3686549		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	3686548	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	3686517

Score = 880 bits (476), Expect = 0.0
Identities = 500/512 (98%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	4279814	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTAGC	
	4279873		

Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	4279874	GGAAACGTTAGCTAATACCGGATAATTTATATTCTCGCATGAGGAGATAATGAAAGACGG	
	4279933		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	4279934	AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAATGGCT	
	4279993		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	4279994	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	4280053		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	4280054	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	4280113		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	4280114	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	4280173		
Query	361	AGAACGTTCCGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	4280174	AGAACGTCCGTTAGAGTAACTGCTAACGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	4280233		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	4280234	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	4280293		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	4280294	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	4280325

Score = 880 bits (476), Expect = 0.0
Identities = 500/512 (98%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	4410203	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	
	4410262		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120

Sbjct	4410263		GGAAACGTTAGCTAATACCGGATAATTTATATTCTCGCATGAGGAGATAATGAAAGACGG	
	4410322			
Query	121		AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	4410323		AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAATGGCT	
	4410382			
Query	181		CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	4410383		CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	4410442			
Query	241		ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	4410443		ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	4410502			
Query	301		ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	4410503		ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	4410562			
Query	361		AGAACGTTCCGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	4410563		AGAACGTTCCGTAGAGTAACTGCTAACGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	4410622			
Query	421		AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	4410623		AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	4410682			
Query	481		CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	4410683		CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	4410714

Score = 857 bits (464), Expect = 0.0
Identities = 479/486 (99%), Gaps = 2/486 (0%)
Strand=Plus/Minus

Query	1		TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	3067808		TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	
	3067749			
Query	61		GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAG-TAATGAAAGACG	119

Sbjct 3067748 GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGG-AAGATAATGAAAGACG
3067690

Query 120 GAGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC 179
|||||

Sbjct 3067689 GAGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC
3067630

Query 180 TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA 239
|||||

Sbjct 3067629 TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA
3067570

Query 240 CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT 299
|||||

Sbjct 3067569 CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT
3067510

Query 300 GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG 359
|||||

Sbjct 3067509 GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG
3067450

Query 360 AAGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC 419
|||||

Sbjct 3067449 AAGAACGTTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC
3067390

Query 420 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG 479
|||||

Sbjct 3067389 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG
3067330

Query 480 GCGTAA 485
|||||

Sbjct 3067329 GCGTAA 3067324

Score = 161 bits (87), Expect = 7e-36
Identities = 89/90 (99%), Gaps = 0/90 (0%)
Strand=Plus/Plus

Query 1 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
|||||

Sbjct 5247636 TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTAGC
5247695

Query 61 GGAAACGTTAGCTAATACCGGATAATTTAT 90
|||||

Sbjct 5247696 GGAAACGTTAGCTAATACCGGATAATTTAT 5247725

>NZ_CP034346.1 Paenibacillus lutimineralis strain MBLB1234 chromosome, complete genome
Length=6497679

Score = 924 bits (500), Expect = 0.0
Identities = 508/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	5642048	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	
	5641989		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	5641988	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAATAATGAAAGACGG	
	5641929		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	5641928	AGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	
	5641869		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	5641868	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	5641809		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	5641808	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	5641749		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	5641748	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	5641689		
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	5641688	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	5641629		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	5641628	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	5641569		

Query 481 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 512
 |||||
 Sbjct 5641568 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 5641537

Score = 918 bits (497), Expect = 0.0
 Identities = 507/512 (99%), Gaps = 0/512 (0%)
 Strand=Plus/Plus

Query 1 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
 |||||
 Sbjct 12317 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 12376

Query 61 GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG 120
 |||||
 Sbjct 12377 GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG 12436

Query 121 AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT 180
 |||||
 Sbjct 12437 AGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT 12496

Query 181 CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC 240
 |||||
 Sbjct 12497 CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC 12556

Query 241 ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 300
 |||||
 Sbjct 12557 ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 12616

Query 301 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA 360
 |||||
 Sbjct 12617 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA 12676

Query 361 AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT 420
 |||||
 Sbjct 12677 AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT 12736

Query 421 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG 480
 |||||
 Sbjct 12737 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG 12796

Query 481 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 512
 |||||
 Sbjct 12797 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 12828

Score = 918 bits (497), Expect = 0.0
 Identities = 507/512 (99%), Gaps = 0/512 (0%)
 Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	150534	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	150593
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	150594	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	150653
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	150654	AGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	150713
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	150714	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	150773
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	150774	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	150833
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	150834	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	150893
Query	361	AGAACGTTCCGGTAGAGTAAGTCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	150894	AGAACGTTCCGGTAGAGTAAGTCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	150953
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	150954	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	151013
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	151014	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	151045

Score = 918 bits (497), Expect = 0.0
Identities = 507/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	1093568	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	
	1093627		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	1093628	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	
	1093687		

Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	1093688	AGCAATCTGTCACTTACAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	
	1093747		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	1093748	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	1093807		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	1093808	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	1093867		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	1093868	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	1093927		
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	1093928	AGAACGTTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	1093987		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	1093988	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	1094047		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	1094048	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	1094079

Score = 918 bits (497), Expect = 0.0
Identities = 507/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	5756806	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	
	5756747		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	5756746	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	
	5756687		

Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	5756686	AGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	
	5756627		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	5756626	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	5756567		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	5756566	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	5756507		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	5756506	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	5756447		
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	5756446	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	5756387		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	5756386	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	5756327		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	5756326	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	5756295

Score = 913 bits (494), Expect = 0.0
Identities = 506/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	911374	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	911433
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	911434	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	911493
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	911494	AGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAATGGCT	911553

Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	911554	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	911613
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	911614	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	911673
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	911674	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	911733
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	911734	AGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	911793
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	911794	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	911853
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	911854	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	911885

Score = 913 bits (494), Expect = 0.0
Identities = 506/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	5204411	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTATAAGACTGGGATAACTAGC	
	5204352		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	5204351	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGAGATAATGAAAGACGG	
	5204292		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	5204291	AGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	
	5204232		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	5204231	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	5204172		

Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	5204171	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	5204112		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	5204111	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	5204052		
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	5204051	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	5203992		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	5203991	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	5203932		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	5203931	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	5203900

Score = 907 bits (491), Expect = 0.0
Identities = 505/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	342372	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTATAAGACTGGGATAACTAGC	342431
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	342432	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	342491
Query	121	AGCAATCTGTCACTTGACAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	342492	AGCAATCTGTCACTTACAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGTAATGGCT	342551
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	240
Sbjct	342552	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	342611
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	342612	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	342671
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360

Sbjct	342672	 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	342731
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	342732	 AGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	342791
Query	421	AACACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	342792	 AACACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	342851
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	342852	 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	342883

Score = 907 bits (491), Expect = 0.0
Identities = 505/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	5454711	 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTATAAGACTGGGATAACTAGC	
	5454652		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	5454651	 GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGAGATAATGAAAGACGG	
	5454592		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	5454591	 AGCAATCTGTCACTTACAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGTAATGGCT	
	5454532		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	5454531	 CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	5454472		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	5454471	 ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	5454412		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	5454411	 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	5454352		

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Query    361      AGAACGTTCTGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT  420
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    5454351  AGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT
          5454292

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Query    481      CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT    512
          |||||
Sbjct    5454231  CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT    5454200

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Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	86083	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTATAAGACTGGGATAACTAGC	86142

Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	86203	AGCAATCTGTCACTTACAGATGGACCTGCGGCGCATTAGCTAGTTGGTGAAGTAATGGCT	86262

Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	240
Sbjct	86263	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	86322

Query	241	ACGGCCAGACTCTACGGGAGGCAGCAGTAGGGAATCTTCGCAATGGACGAAAGTCTG	300
Sbjct	86323	ACGGCCAGACTCTACGGGAGGCAGCAGTAGGGAATCTTCGCAATGGACGAAAGTCTG	86382

Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	86383	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	86442

Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	86443	AGAACGTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	86502

Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	86503	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	86562

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Query   481      CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT   512
          |||
Sbjct   86563    CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT   86594

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>NZ_JAMBOA010000024.1 Paenibacillus motobuensis strain MER36 NODE_24_, whole genome
shotgun sequence
Length=1011

Score = 913 bits (494), Expect = 0.0
Identities = 506/512 (99%), Gaps = 0/512 (0%)
Strand=Plus/Minus

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Query    1      TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC   60
          |||
Sbjct   910      TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC   851

Query    61      GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG   120
          |||
Sbjct   850      GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAGATAATGAAAGACGG   791

Query   121      AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT   180
          |||
Sbjct   790      AGCAATCTGTCACTTATAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT   731

Query   181      CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC   240
          |||
Sbjct   730      CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC   671

Query   241      ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG   300
          |||
Sbjct   670      ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG   611

Query   301      ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA   360
          |||
Sbjct   610      ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA   551

Query   361      AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT   420
          |||
Sbjct   550      AGAACGTTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT   491

Query   421      AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG   480
          |||
Sbjct   490      AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG   431

Query   481      CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT   512
          |||
Sbjct   430      CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT   399

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>NZ_BIMK01000026.1 *Paenibacillus chibensis* strain NBRC 15958 PCH05_CON01240, whole genome shotgun sequence
Length=1471

Score = 874 bits (473), Expect = 0.0
Identities = 499/512 (97%), Gaps = 0/512 (0%)
Strand=Plus/Minus

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Query 1      TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1471    TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC 1412

Query 61     GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG 120
          ||||||| ||||||||||||||||||||||||||||| ||||||| |||||||||||||
Sbjct 1411    GGAAACGGTAGCTAATACCGGATAATTTATTTTCTCTCCTGGGGAGATAATGAAAGACGG 1352

Query 121    AGCAATCTGTCACTTGACATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT 180
          ||||||||||||||| ||||||| ||||||||||||||||||||||||| |||||||||
Sbjct 1351    AGCAATCTGTCACTTACAGATGGGCTGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCT 1292

Query 181    CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1291    CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC 1232

Query 241    ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1231    ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 1172

Query 301    ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1171    ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA 1112

Query 361    AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT 420
          ||||||| ||||||||||||||||||||||||| ||||||| |||||||||||||
Sbjct 1111    AGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT 1052

Query 421    AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1051    AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG 992

Query 481    CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 512
          ||||||||||||||||| |||||||
Sbjct 991     CGTAAAGCGCGCGCAGGCGGTCACTTAAGTCT 960
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>NZ_BOSL01000001.1 *Paenibacillus vini* strain J42TS3 sequence01, whole genome shotgun
sequence
Length=752780

Score = 869 bits (470), Expect = 0.0
 Identities = 499/513 (97%), Gaps = 2/513 (0%)
 Strand=Plus/Minus

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Query   1      TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC   60
        |||
Sbjct   913    TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCCCTAAGACTGGGATAACTACC   854

Query   61      GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGG-GGAAGTAATGAAAGACG   119
        |||
Sbjct   853    GGAAACGGTAGCTAATACCGGATAATTTATTTTCATCGCATGGTGGAA-TAATGAAAGACG   795

Query   120     GAGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC   179
        |||
Sbjct   794    GAGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC   735

Query   180     TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA   239
        |||
Sbjct   734    TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA   675

Query   240     CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT   299
        |||
Sbjct   674    CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT   615

Query   300     GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG   359
        |||
Sbjct   614    GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG   555

Query   360     AAGAACGTTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC   419
        |||
Sbjct   554    AAGAACGTCCGCTAGAGTAACTGCTAGCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC   495

Query   420     TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG   479
        |||
Sbjct   494    TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG   435

Query   480     GCGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT   512
        |||
Sbjct   434    GCGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT   402

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>NZ_RZNX01000019.1 *Paenibacillus zeisoli* strain 3-5-3 Scaffold19, whole genome
 shotgun
 sequence
 Length=1577

Score = 869 bits (470), Expect = 0.0
 Identities = 499/513 (97%), Gaps = 2/513 (0%)
 Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	72	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC	131
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTT-CTCGCATGGGGAAGTAATGAAAGACG	119
Sbjct	132	GGAAACGGTAGCTAATACCGGATAATTCATTTTACT-GCATGGTGGAGTGATGAAAGACG	190
Query	120	GAGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC	179
Sbjct	191	GAGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC	250
Query	180	TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA	239
Sbjct	251	CCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA	310
Query	240	CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT	299
Sbjct	311	CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT	370
Query	300	GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG	359
Sbjct	371	GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGG	430
Query	360	AAGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC	419
Sbjct	431	AAGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC	490
Query	420	TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG	479
Sbjct	491	TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG	550
Query	480	GCGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	551	GCGTAAAGCGCGCGCAGGCGGTTATTTAAGTCT	583

>NZ_STGQ01000003.1 *Paenibacillus dokdonensis* strain YH-JAE5 JAE5_3, whole genome
shotgun sequence
Length=886769

Score = 865 bits (468), Expect = 0.0
Identities = 496/510 (97%), Gaps = 0/510 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	451016	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTACC	450957

Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	450956	GGAAACGGTAGCTAATACCGGATAATTTATTTCTTCTCCTGGAGAGATAATGAAAGACGG	450897
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	450896	AGCAATCTGTCACTTACAGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	450837
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	240
Sbjct	450836	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	450777
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	450776	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	450717
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	450716	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	450657
Query	361	AGAACGTTCCGGTAGAGTAAGTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	450656	AGAACGTCCGGTAGAGTAAGTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	450597
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	450596	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	450537
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGT	510
Sbjct	450536	CGTAAAGCGCGCGCAGGCGGCCATTTAAGT	450507

Score = 854 bits (462), Expect = 0.0
Identities = 494/510 (97%), Gaps = 0/510 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	809957	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTACC	809898
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	809897	GGAAACGGTAGCTAATACCGGATAATTTATTTCTTCTCCTGGAGAGATAATGAAAGACGG	809838
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	809837	AGCAATCTGTCACTTATAGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	809778
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	240

Sbjct	809777		CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	809718
Query	241		ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	809717		ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	809658
Query	301		ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	809657		ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	809598
Query	361		AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	809597		AGAACGTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	809538
Query	421		AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	809537		AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	809478
Query	481		CGTAAAGCGCGCGCAGGCGGCTATTTAAGT	510
Sbjct	809477		CGTAAAGCGCGCGCAGGCGGCCATTTAAGT	809448

>NZ_STGQ01000002.1 Paenibacillus dokdonensis strain YH-JAE5 JAE5_2, whole genome
shotgun sequence
Length=1437696

Score = 865 bits (468), Expect = 0.0
Identities = 496/510 (97%), Gaps = 0/510 (0%)
Strand=Plus/Plus

Query	1		TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	640548		TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTACC	640607
Query	61		GGAAACGTTAGCTAATACCGGATAATTTATTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	640608		GGAAACGGTAGCTAATACCGGATAATTTATTTCTTCTCCTGGAGAGATAATGAAAGACGG	640667
Query	121		AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	640668		AGCAATCTGTCACTTACAGATGGGCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	640727
Query	181		CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	640728		CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	640787
Query	241		ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300

Sbjct	640788	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	640847
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	640848	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	640907
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	640908	AGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	640967
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	640968	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	641027
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGT	510
Sbjct	641028	CGTAAAGCGCGCGCAGGCGGCCATTTAAGT	641057

Score = 865 bits (468), Expect = 0.0
Identities = 496/510 (97%), Gaps = 0/510 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	820365	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTACC	820424
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	820425	GGAAACGGTAGCTAATACCGGATAATTTATTTCTTCTCCTGGAGAGATAATGAAAGACGG	820484
Query	121	AGCAATCTGTCACTTGACAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	820485	AGCAATCTGTCACTTACAGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	820544
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	240
Sbjct	820545	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	820604
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	820605	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	820664
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	820665	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	820724
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	820725	AGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	820784

Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	820785	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	820844
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGT	510
Sbjct	820845	CGTAAAGCGCGCGCAGGCGGCCATTTAAGT	820874

Score = 859 bits (465), Expect = 0.0
Identities = 495/510 (97%), Gaps = 0/510 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	760128	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTGAGACTGGGATAACTACC	760187
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	760188	GGAAACGGTAGCTAATACCGGATAATTTATTTCTTCTCCTGGAGAGATAATGAAAGACGG	760247
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	760248	AGCAATCTGTCACTTACAGATGGGCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	760307
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	240
Sbjct	760308	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCCACTGGGACTGAGAC	760367
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	760368	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	760427
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	760428	ACGGAGCAACGCCGCGTGAGTGATGAAGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	760487
Query	361	AGAACGTTCCGGTAGAGTAAGTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	760488	AGAACGTCCGGTAGAGTAAGTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	760547
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	760548	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	760607
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGT	510
Sbjct	760608	CGTAAAGCGCGCGCAGGCGGCCATTTAAGT	760637

Score = 854 bits (462), Expect = 0.0
 Identities = 494/510 (97%), Gaps = 0/510 (0%)
 Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	707820	TTAGCGGCGGACGGGTGAGTAACACGTAGGCAACCTGCCTGTAAGACTGGGATAACTACC	707879
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	707880	GGAAACGGTAGCTAATACCGGATAATTTATTTCTTCTCCTGGAGAGATAATGAAAGACGG	707939
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	707940	AGCAATCTGTCACTTACGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	707999
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	708000	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	708059
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	708060	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	708119
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	708120	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	708179
Query	361	AGAACGTTCCGGTAGAGTAAGTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	708180	AGAACGTCCGGTAGAGTAAGTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	708239
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	708240	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	708299
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGT	510
Sbjct	708300	CGTAAAGCGCGCGCAGGCGGCCATTTAAGT	708329

>NZ_RZNY0100080.1 *Paenibacillus anaericanus* strain DSM 15890 Scaffold80, whole genome shotgun sequence
 Length=1568

Score = 857 bits (464), Expect = 0.0
 Identities = 497/513 (97%), Gaps = 2/513 (0%)
 Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	1497	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCCCTAAGACTGGGATAACTACC	1438
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATG-GGGAAGTAATGAAAGACG	119
Sbjct	1437	GGAAACGGTAGCTAATACCGGATAATTTATTTTCTCGCATGAGAGAA-TAATGAAAGGCG	1379
Query	120	GAGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGC	179
Sbjct	1378	GAGCAATCTGCCACTTACGGATGGGCTGCGGCGCATTAGCTAGTTGGTGAAGTAACGGC	1319
Query	180	TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA	239
Sbjct	1318	TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA	1259
Query	240	CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT	299
Sbjct	1258	CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT	1199
Query	300	GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGG	359
Sbjct	1198	GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGG	1139
Query	360	AAGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC	419
Sbjct	1138	AAGAACGTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGC	1079
Query	420	TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG	479
Sbjct	1078	TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGG	1019
Query	480	GCGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	1018	GCGTAAAGCGCGCGCAGGCGGTCATTTAAGTCT	986

>NZ_LT575476.1 *Paenibacillus tuaregi* strain Marseille-P2472T, whole genome shotgun sequence
Length=5631190

Score = 835 bits (452), Expect = 0.0
Identities = 492/512 (96%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	3446432	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC	
	3446373		

Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	3446372	GGAAACGGTAGCTAATACCGGATACGCAAGTTTCTCGCATGAGGGATTGGGAAAGACGG	
	3446313		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	3446312	AGCAATCTGTCACTTATGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGAAGTAACGGCT	
	3446253		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	3446252	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	3446193		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	3446192	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	3446133		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	3446132	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	3446073		
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	3446072	AGAACGTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	3446013		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	3446012	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	3445953		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	3445952	CGTAAAGCGCGCGCAGGCGGCTATGTAAGTCT	3445921

Score = 835 bits (452), Expect = 0.0
Identities = 492/512 (96%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	4295888	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC	
	4295829		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120

Sbjct	4295828		
	4295769	GGAAACGGTAGCTAATACCGGATACGCAAGTTTCTCGCATGAGGGATTTGGGAAAGACGG	
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	4295768	AGCAATCTGTCACTTATGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGAAGTAACGGCT	
	4295709		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	4295708	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	4295649		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	4295648	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	4295589		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	4295588	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	4295529		
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	4295528	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	4295469		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	4295468	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	4295409		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	4295408	CGTAAAGCGCGCGCAGGCGGCTATGTAAGTCT	4295377

Score = 835 bits (452), Expect = 0.0
Identities = 492/512 (96%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	4741472	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC	
	4741413		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120

Sbjct 741233 GGAAACGGTAGCTAATACCGGATACGCAAGTTTCTCGCATGAGGGATTGGGAAAGACGG 741292

Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	741293	AGCAATCTGTCACTTATGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGAGTAACGGCT	741352
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	741353	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	741412
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	741413	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	741472
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	741473	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	741532
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	741533	AGAACGTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	741592
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	741593	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	741652
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	741653	CGTAAAGCGCGCGCAGGCGGCTATGTAAGTCT	741684

Score = 830 bits (449), Expect = 0.0
Identities = 491/512 (96%), Gaps = 0/512 (0%)
Strand=Plus/Plus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	5564409	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC	
	5564468		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	5564469	GGAAACGGTAGCTAATACCGGATACGCAAGTTTCTCGCATGAGGGATTTGGGAAAGACGG	
	5564528		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	5564529	AGCAATCTGTCACTTATGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGAGTAACGGCT	
	5564588		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240

Sbjct	5564589	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	
	5564648		
Query	241	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	300
Sbjct	5564649	ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG	
	5564708		
Query	301	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	360
Sbjct	5564709	ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA	
	5564768		
Query	361	AGAACGTTCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	420
Sbjct	5564769	AGAACGTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT	
	5564828		
Query	421	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	480
Sbjct	5564829	AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG	
	5564888		
Query	481	CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT	512
Sbjct	5564889	CGTAAAGCGCGCGCAGGCGGCTATGTAAGTCT	5564920

Score = 824 bits (446), Expect = 0.0
Identities = 490/512 (96%), Gaps = 0/512 (0%)
Strand=Plus/Minus

Query	1	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC	60
Sbjct	4817498	TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTACCTGTAAGACTGGGATAACTACC	
	4817439		
Query	61	GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG	120
Sbjct	4817438	GGAAACGGTAGCTAATACCGGATACGCAAGTTTCTCGCATGAGGGACTTGGGAAAGACGG	
	4817379		
Query	121	AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT	180
Sbjct	4817378	AGCAATCTGTCACTTATGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGAAGTAACGGCT	
	4817319		
Query	181	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	240
Sbjct	4817318	CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGAC	

4817259

Query 241 ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 300
|||||
Sbjct 4817258 ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG
4817199

Query 301 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA 360
|||||
Sbjct 4817198 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGCCAGGGA
4817139

Query 361 AGAACGTTCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT 420
|||||
Sbjct 4817138 AGAACGTCCGGTAGAGTAACTGCTATCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCT
4817079

Query 421 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG 480
|||||
Sbjct 4817078 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGG
4817019

Query 481 CGTAAAGCGCGCGCAGGCGGCTATTTAAGTCT 512
|||||
Sbjct 4817018 CGTAAAGCGCGCGCAGGCGGCTATGTAAGTCT 4816987

Score = 342 bits (185), Expect = 2e-90
Identities = 221/239 (92%), Gaps = 0/239 (0%)
Strand=Plus/Plus

Query 1 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
|||||
Sbjct 5630952 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC
5631011

Query 61 GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG 120
|||||
Sbjct 5631012 GGAAACGGTAGCTAATACCGGATACGCAAGTTTCTCGCATGAGGGACTTGGGAAAGACGG
5631071

Query 121 AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT 180
|||||
Sbjct 5631072 AGCAATCTGTCACTTATGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGTAACGGCT
5631131

Query 181 CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA 239
|||||
Sbjct 5631132 CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTGAGA 5631190

Score = 326 bits (176), Expect = 2e-85
Identities = 216/236 (92%), Gaps = 0/236 (0%)
Strand=Plus/Plus

```
Query 1      TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
      |||
Sbjct 81549   TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC 81608

Query 61     GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATGGGGAAGTAATGAAAGACGG 120
      |||
Sbjct 81609   GGAAACGGTAGCTAATACCGGATACGCAAGTTCTTCGCATGAGGGATTTGGGAAAGACGG 81668

Query 121    AGCAATCTGTCACTTGCAGATGGACCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCT 180
      |||
Sbjct 81669   AGCAATCTGTCACTTATGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGAAGTAACGGCT 81728

Query 181    CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTG 236
      |||
Sbjct 81729   CACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTG 81784
```

Score = 150 bits (81), Expect = 2e-32
Identities = 98/106 (92%), Gaps = 1/106 (1%)
Strand=Plus/Plus

```
Query 1      TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTAGC 60
      |||
Sbjct 1440135 TTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTACC
1440194

Query 61     GGAAACGTTAGCTAATACCGGATAATTTATTTTCTCGCATG-GGGA 105
      |||
Sbjct 1440195 GGAAACGGTAGCTAATACCGGATACGCAAGTTTCTCGCATGAGGGA 1440240
```

Database: Refseq prokaryote representative genomes (contains refseq assembly)
Posted date: Aug 14, 2023 1:42 AM
Number of letters in database: 77,579,778,222
Number of sequences in database: 938,322

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.28	0.460	0.850

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 938322

Number of Hits to DB: 3148810

Number of extensions: 1649
Number of successful extensions: 1649
Number of sequences better than 0.05: 1096
Number of HSP's better than 0.05 without gapping: 0
Number of HSP's gapped: 1389
Number of HSP's successfully gapped: 1389
Length of query: 512
Length of database: 77579778222
Length adjustment: 33
Effective length of query: 479
Effective length of database: 77548813596
Effective search space: 37145881712484
Effective search space used: 37145881712484
A: 0
X1: 13 (25.0 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 13 (25.1 bits)
S2: 27 (51.0 bits)