

Score	Expect	Identities	Gaps	Strand	
1820 bits(985)	0.0	1020/1043(98%)	3/1043(0%)	Plus/Plus	
Query	12	CTNCGGCAGGCCTAACACATGCAAGTCGAACGGCAGCACAGAGGAGCTTGCTCCTTGGG			71
Sbjct	16	CTGGCGGCAGGCCTAACACATGCAAGTCGAACGGCAGCACAGAGGAGCTTGCTCCTTGGG			75
Query	72	TGGCGANNNNNGGACGGGTGAGGAAAACGTCGGAATCTGCCTATTTGTGGGGGATAACGT			131
Sbjct	76	TGGCGAGTGGCGGACGGGTGAGGAATACGTCGGAATCTGCCTATTTGTGGGGGATAACGT			135
Query	132	AGGGAACTTACGCTAATACCGCATAACGACCTACGGGTGAAAGTGGGGGACCGCAAGGCC			191
Sbjct	136	AGGGAACTTACGCTAATACCGCATAACGACCTACGGGTGAAAGTGGGGGACCGCAAGGCC			195
Query	192	TCACGCAGATAGATGAGCCGACGTCGGATTAGCTAGTTGGCGGGGTAAAGGCCACCAAG			251
Sbjct	196	TCACGCAGATAGATGAGCCGACGTCGGATTAGCTAGTTGGCGGGGTAAAGGCCACCAAG			255
Query	252	GCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAAGTGGACACGGTCC			311
Sbjct	256	GCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAAGTGGACACGGTCC			315
Query	312	AGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGC			371
Sbjct	316	AGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGC			375
Query	372	CATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGAAAGAAAAG			431
Sbjct	376	CATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGAAAGAAAAG			435
Query	432	CTTAGGGTTAATAACCTTGAGTCATGACGGTACCGGAAGAATAAGCACCGGCTAACTTCG			491
Sbjct	436	CTTAGGGTTAATAACCTTGAGTCATGACGGTACCGGAAGAATAAGCACCGGCTAACTTCG			495
Query	492	TGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTACTCGGAATTACTGGGCGTAAAG			551
Sbjct	496	TGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTACTCGGAATTACTGGGCGTAAAG			555
Query	552	CGTGCGTAGGTGGTTTGTAAAGTCTGATGTGAAAGCCCTGGGCTCAACCTGGGAATGGCA			611
Sbjct	556	CGTGCGTAGGTGGTTTGTAAAGTCTGATGTGAAAGCCCTGGGCTCAACCTGGGAATGGCA			615
Query	612	TTGGAACTGGCTTACTAGAGTGCGGTAGAGGGTAGTGAATTCCCGGTGTAGCAGTGAA			671
Sbjct	616	TTGGAACTGGCTTACTACAGTGCGGTAGAGGGTAGCGGAATTCCCGGTGTAGCAGTGAA			675
Query	672	ATGCGTAGATATCGGGAGGAACATCTGTGGCGAAGGCGACTACCTGGACCAGCACTGACA			731
Sbjct	676	ATGCGTAGATATCGGGAGGAACATCCGTGGCGAAGGCGGCTACCTGGACCAGCACTGACA			735
Query	732	CTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAA			791
Sbjct	736	CTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAA			795
Query	792	ACGATGCGAACTGGATGTTGGGGGCAACTTGGCCCTCAGTATCGAAGCTAACGCGTTAAG			851
Sbjct	796	ACGATGCGAACTGGATGTTGGGGGCAACTTGGCCCTCAGTATCGAAGCTAACGCGTTAAG			855
Query	852	TTCGCCGCCTGGGAAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGANN - GGGCCCCG			910
Sbjct	856	TTCGCCGCCTGGGAAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGC			915