|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Score | Expect | Identities | Gaps | Strand |
| 7886 bits(4270) | 0.0 | 4270/4270(100%) | 0/4270(0%) | Plus/Plus |

Query 1 CCTGTAATCCCAGCTACTCTAATGCTAAGGTGAGAGGATCACTTGAGCCCAGGAGGTCGA 60

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681216 CCTGTAATCCCAGCTACTCTAATGCTAAGGTGAGAGGATCACTTGAGCCCAGGAGGTCGA 4681275

Query 61 GGCTGCAGTGAGCCATGATCATGCCACTGCACTCCAGTCTGGGCAACAGTGTGAGACCCT 120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681276 GGCTGCAGTGAGCCATGATCATGCCACTGCACTCCAGTCTGGGCAACAGTGTGAGACCCT 4681335

Query 121 CTCTCAAACAAAAGCAGAAACCTCAGACAAGTAGATCATTCAAAATTGGTAAATCCAAAA 180

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681336 CTCTCAAACAAAAGCAGAAACCTCAGACAAGTAGATCATTCAAAATTGGTAAATCCAAAA 4681395

Query 181 GGCAATTCTAGGTGTGTTTGGATCCACAAGCCTCCAGTAAGTGACCTAACCAGGGAGGTA 240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681396 GGCAATTCTAGGTGTGTTTGGATCCACAAGCCTCCAGTAAGTGACCTAACCAGGGAGGTA 4681455

Query 241 AAGTAAGGTGTCAGCATGGGTCCTGGCCCTGCCATGAGACAGGAAGAAGAGAGAGCAGGT 300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681456 AAGTAAGGTGTCAGCATGGGTCCTGGCCCTGCCATGAGACAGGAAGAAGAGAGAGCAGGT 4681515

Query 301 GTTTCTCTGAGGTTGCTGGGGATGATATAATAGAACTGAAACTCTCAGCCCTTTCCCTGG 360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681516 GTTTCTCTGAGGTTGCTGGGGATGATATAATAGAACTGAAACTCTCAGCCCTTTCCCTGG 4681575

Query 361 AGAAGCACAAAATGCTGCCTTGGATGGTATGTGCCAGATAAGACACATGAGGAGCCAGGC 420

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Sbjct 4681576 AGAAGCACAAAATGCTGCCTTGGATGGTATGTGCCAGATAAGACACATGAGGAGCCAGGC 4681635

Query 421 ACAGTGGCTCATGCCTGTAATCCCAGCAATTTGGGAGGCTGAAGCAGGAGGATTGCTTGA 480

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681636 ACAGTGGCTCATGCCTGTAATCCCAGCAATTTGGGAGGCTGAAGCAGGAGGATTGCTTGA 4681695

Query 481 GCCCAGGAGTTCGAGATCAGCTAGGCAACATGGTAAGACATGAACTCTCCaaaaaaaTTA 540

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Sbjct 4681696 GCCCAGGAGTTCGAGATCAGCTAGGCAACATGGTAAGACATGAACTCTCCAAAAAAATTA 4681755

Query 541 GCCAGGCATGTTGTTCCGCACCTTTAGTCCCAGCTACTCGGGAGGCCGAGGTGAGAAGAT 600

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Sbjct 4681756 GCCAGGCATGTTGTTCCGCACCTTTAGTCCCAGCTACTCGGGAGGCCGAGGTGAGAAGAT 4681815

Query 601 CATTTGAGCCCAGGAGGTTGAGGATGCAGTGAGCCATGATTGCACCACTGCATTCCAGCC 660

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681816 CATTTGAGCCCAGGAGGTTGAGGATGCAGTGAGCCATGATTGCACCACTGCATTCCAGCC 4681875

Query 661 TGGATGACAGAGTGAGATCCTGTCTCAAAAAGCAAacacacacacacacGAAAGCAAGAA 720

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681876 TGGATGACAGAGTGAGATCCTGTCTCAAAAAGCAAACACACACACACACGAAAGCAAGAA 4681935

Query 721 GCAAGACAGCTGTGGAATTCCAGAGATAGGAGACAGGCAAAGAACCTGACCTGGTGCAAC 780

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Sbjct 4681936 GCAAGACAGCTGTGGAATTCCAGAGATAGGAGACAGGCAAAGAACCTGACCTGGTGCAAC 4681995

Query 781 GAAGATAAAGGTAACGGAGCCAGATGAGGAGGCTTAAATGCCTTACAAGAGTTAGGCGTT 840

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Sbjct 4681996 GAAGATAAAGGTAACGGAGCCAGATGAGGAGGCTTAAATGCCTTACAAGAGTTAGGCGTT 4682055

Query 841 CAAGTTACAAGTCTTGGCCAGGCGCGGTGGCTCACGCTTGTAATCCCAGCACTTTGGGAG 900

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682056 CAAGTTACAAGTCTTGGCCAGGCGCGGTGGCTCACGCTTGTAATCCCAGCACTTTGGGAG 4682115

Query 901 GCTGAGGCAGGCGGATCACGAGGTCAGGAGATCAAGACCATTCTGGCCAACATGATGAAA 960

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682116 GCTGAGGCAGGCGGATCACGAGGTCAGGAGATCAAGACCATTCTGGCCAACATGATGAAA 4682175

Query 961 CCCCGTCTCTACTAAAAATACAAAAAATTAGCCCGGCGTGGTGGCATGTGCATGTAGTCC 1020

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682176 CCCCGTCTCTACTAAAAATACAAAAAATTAGCCCGGCGTGGTGGCATGTGCATGTAGTCC 4682235

Query 1021 CAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGT 1080

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682236 CAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGT 4682295

Query 1081 GAGCCAAGATCACACCACTGTACTCCAACCTGGTGACAGAGTGAGACTCCGTCTCaaaaa 1140

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682296 GAGCCAAGATCACACCACTGTACTCCAACCTGGTGACAGAGTGAGACTCCGTCTCAAAAA 4682355

Query 1141 aaaaaaaaaaaaaaGAGTTCAGTCTTGATGGGCTTCTCTGTGAAGAGACCCTAAAGGATT 1200

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682356 AAAAAAAAAAAAAAGAGTTCAGTCTTGATGGGCTTCTCTGTGAAGAGACCCTAAAGGATT 4682415

Query 1201 TGAGCAGAGAAAAGACCAGTTGAAAGCTATGTTTAGGCCAGATGCAGTGACTTACACCTG 1260

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682416 TGAGCAGAGAAAAGACCAGTTGAAAGCTATGTTTAGGCCAGATGCAGTGACTTACACCTG 4682475

Query 1261 TAATCCCAGCAATTTGGTAGGCCAGGGCAGGAGGAGCCCAGGAGTTCAAGACCAGCCTGA 1320

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682476 TAATCCCAGCAATTTGGTAGGCCAGGGCAGGAGGAGCCCAGGAGTTCAAGACCAGCCTGA 4682535

Query 1321 GCAAATAGCAAGACCCCATGTCTACAAAAttttttttAATTAGCTGGGAATGATGACGCA 1380

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682536 GCAAATAGCAAGACCCCATGTCTACAAAATTTTTTTTAATTAGCTGGGAATGATGACGCA 4682595

Query 1381 TGCCTGCGATACCAGCTACTCAGGAGGCTGAGGCAGGAGGATCACTTGAGCCCAGGAGGT 1440

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682596 TGCCTGCGATACCAGCTACTCAGGAGGCTGAGGCAGGAGGATCACTTGAGCCCAGGAGGT 4682655

Query 1441 CAAGGCTAAAGTCAGCCACGATCAAGCCACTGCATTCCAGCCTGGGTGGCAGAGTGAGAC 1500

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682656 CAAGGCTAAAGTCAGCCACGATCAAGCCACTGCATTCCAGCCTGGGTGGCAGAGTGAGAC 4682715

Query 1501 CCTGTTTCaaaaagaaagaaagaaaaaaaaaaGCTATGTTTAACCTGATAGAGGATAGAG 1560

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Sbjct 4682716 CCTGTTTCAAAAAGAAAGAAAGAAAAAAAAAAGCTATGTTTAACCTGATAGAGGATAGAG 4682775

Query 1561 TGTAGGGTGGCATGGGGCAAGAGCTATGAGAGTGTAATAGGGAGGCTGAGAACACCCTCA 1620

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Sbjct 4682776 TGTAGGGTGGCATGGGGCAAGAGCTATGAGAGTGTAATAGGGAGGCTGAGAACACCCTCA 4682835

Query 1621 TGGGAGGTGATGAGGGATTCAATGTGGGGAGGAACTCACAGATTCAGGAGCCACTTAAGT 1680

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Sbjct 4682836 TGGGAGGTGATGAGGGATTCAATGTGGGGAGGAACTCACAGATTCAGGAGCCACTTAAGT 4682895

Query 1681 AAAAGTTGAGAAAATTTGATGTCTTTCTGGGTGCAAGATTAAAGCTTTCCAGCCTGGCTG 1740

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Sbjct 4682896 AAAAGTTGAGAAAATTTGATGTCTTTCTGGGTGCAAGATTAAAGCTTTCCAGCCTGGCTG 4682955

Query 1741 ACCTAGTAGATGTTATTTTTTCCACTGATGGAGACAAGAAAGTCAAAGGGAGATGAATTT 1800

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682956 ACCTAGTAGATGTTATTTTTTCCACTGATGGAGACAAGAAAGTCAAAGGGAGATGAATTT 4683015

Query 1801 GAGGAATATTGTGAGATGAGCGTGAGGCTGGTTGAATTTGAGCTAAAACCAAGATATTCA 1860

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683016 GAGGAATATTGTGAGATGAGCGTGAGGCTGGTTGAATTTGAGCTAAAACCAAGATATTCA 4683075

Query 1861 AGTGAACATAGGATCTGGAGGCATCAGTTTTGGAGGCAACTTCTGGCAGAGTGAAGAGCT 1920

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683076 AGTGAACATAGGATCTGGAGGCATCAGTTTTGGAGGCAACTTCTGGCAGAGTGAAGAGCT 4683135

Query 1921 GATTCCCTGAAAGGGGATGGGCATTGTTAGGAAAGCCACAGGGAGaaaaaaaGACCAAGG 1980

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683136 GATTCCCTGAAAGGGGATGGGCATTGTTAGGAAAGCCACAGGGAGAAAAAAAGACCAAGG 4683195

Query 1981 CTTGAATCTTGGAAAATGCTACACTCCATATCAGACCATCCACTAGCACTCTTCCACACT 2040

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683196 CTTGAATCTTGGAAAATGCTACACTCCATATCAGACCATCCACTAGCACTCTTCCACACT 4683255

Query 2041 CTACTGTAATCCCAATTCACCAGACACTCCAACACCTCTATCCCTTCCTGCTGCTGAGGG 2100

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683256 CTACTGTAATCCCAATTCACCAGACACTCCAACACCTCTATCCCTTCCTGCTGCTGAGGG 4683315

Query 2101 AACTTATAAATATTGAGTTACTCTGAGCTGGTCtttttttttttttttttttGAGATGGA 2160

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Sbjct 4683316 AACTTATAAATATTGAGTTACTCTGAGCTGGTCTTTTTTTTTTTTTTTTTTTGAGATGGA 4683375

Query 2161 GTTTCGCTCTTATTGCCCGGGTTGGAGTACAGTGGCACGATCTCAGCTCACCACAACCTC 2220

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Sbjct 4683376 GTTTCGCTCTTATTGCCCGGGTTGGAGTACAGTGGCACGATCTCAGCTCACCACAACCTC 4683435

Query 2221 CACCTCCCAGGTTCAAGTAATTCTCCTGCCTCAGCCCCCCGAGTAGCTGAGATTATAGGC 2280

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683436 CACCTCCCAGGTTCAAGTAATTCTCCTGCCTCAGCCCCCCGAGTAGCTGAGATTATAGGC 4683495

Query 2281 ATGCGCCACCACGCCCGGCTAATTTTGTATTTTTAGCAGAGTTGGGGTTTCTCCATGTTG 2340

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Sbjct 4683496 ATGCGCCACCACGCCCGGCTAATTTTGTATTTTTAGCAGAGTTGGGGTTTCTCCATGTTG 4683555

Query 2341 GTCAGGCTGGTCTTGAACTTCCGACCTCAGGTGATCCACCAGCCTCAGCCTCTCAACATG 2400

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Sbjct 4683556 GTCAGGCTGGTCTTGAACTTCCGACCTCAGGTGATCCACCAGCCTCAGCCTCTCAACATG 4683615

Query 2401 CTGGGATTTCAGGCGTGAACCACCGCGCCCGGCCTCTGAGCCAGTCTTAACACCTAGTCA 2460

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683616 CTGGGATTTCAGGCGTGAACCACCGCGCCCGGCCTCTGAGCCAGTCTTAACACCTAGTCA 4683675

Query 2461 GCTTGTTCTCCCATTAAATCCTGAGAACAGACCTGTGAGGTAGATCTTCCAGACCCATTT 2520

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Sbjct 4683676 GCTTGTTCTCCCATTAAATCCTGAGAACAGACCTGTGAGGTAGATCTTCCAGACCCATTT 4683735

Query 2521 TATACAGGCAAAACTGAGACCCTGAGAGATGAATCAATTCATAGCATGTGAAGTAGTTTC 2580

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683736 TATACAGGCAAAACTGAGACCCTGAGAGATGAATCAATTCATAGCATGTGAAGTAGTTTC 4683795

Query 2581 CCTGATTTCCATTCAGTAGGGCACCTACTATGTGCCAAGATTGGGGAAAATAATGATATT 2640

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4683796 CCTGATTTCCATTCAGTAGGGCACCTACTATGTGCCAAGATTGGGGAAAATAATGATATT 4683855

Query 2641 GGGCCCTACCCTCTAGAGGCCACAATCTGGACAGAGATAAGGTAGGCACGTAAATAAGGA 2700

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Sbjct 4683856 GGGCCCTACCCTCTAGAGGCCACAATCTGGACAGAGATAAGGTAGGCACGTAAATAAGGA 4683915

Query 2701 TAAAGTAAGGTGAAGCCCAGCAGCTCCAGGAGACGTAGAGATAAGGTCTTCTACAGTCCA 2760

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Sbjct 4683916 TAAAGTAAGGTGAAGCCCAGCAGCTCCAGGAGACGTAGAGATAAGGTCTTCTACAGTCCA 4683975

Query 2761 AAGGGCTGAAGGCATCACAGGCAGCTTCCTGAAGGAGGTAGGCACTGATGCAAGTCAGGC 2820

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Sbjct 4683976 AAGGGCTGAAGGCATCACAGGCAGCTTCCTGAAGGAGGTAGGCACTGATGCAAGTCAGGC 4684035

Query 2821 CTGGAGGATCTGGGGGGACGTGCTATAACAATGACTCTTGTCCCACAGGTACTGTGTCCG 2880

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4684036 CTGGAGGATCTGGGGGGACGTGCTATAACAATGACTCTTGTCCCACAGGTACTGTGTCCG 4684095

Query 2881 GGGATTGCAGCCGTTCGGGCAGGGGGCAAGGGCTGCTGTGGTGCTGGGTGCTGTGGAAAC 2940

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Sbjct 4684096 GGGATTGCAGCCGTTCGGGCAGGGGGCAAGGGCTGCTGTGGTGCTGGGTGCTGTGGAAAC 4684155

Query 2941 CGCTGCAGGGTAAGATCCAGATTAAGAAGGAATTCAGGGCTGGGGGTGGTGTCTCATGCC 3000

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4684156 CGCTGCAGGGTAAGATCCAGATTAAGAAGGAATTCAGGGCTGGGGGTGGTGTCTCATGCC 4684215

Query 3001 TGTAATCCCAACACTTTAGCAGGCTGAGGTGGGAGTACGGCTTGAGCCAGGAGTTCTAGA 3060

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Sbjct 4684216 TGTAATCCCAACACTTTAGCAGGCTGAGGTGGGAGTACGGCTTGAGCCAGGAGTTCTAGA 4684275

Query 3061 CCAGCCCAGGAAACATGGCAAGATCCCTATCTCTACTAACAATACAAAAATTAGCCGGGC 3120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4684276 CCAGCCCAGGAAACATGGCAAGATCCCTATCTCTACTAACAATACAAAAATTAGCCGGGC 4684335

Query 3121 GTGGTGGCAAGCACCTGCAATCTCGGCTACTTGGGAGGCTGAGGTGGGAGGGCCGCTTGA 3180

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Sbjct 4684336 GTGGTGGCAAGCACCTGCAATCTCGGCTACTTGGGAGGCTGAGGTGGGAGGGCCGCTTGA 4684395

Query 3181 GCCCAGGAGGTCCAGGCTGCAGTAAGCAGTGATTTaaaaaaaaaaaaaaaaaaaaaaaaa 3240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4684396 GCCCAGGAGGTCCAGGCTGCAGTAAGCAGTGATTTAAAAAAAAAAAAAAAAAAAAAAAAA 4684455

Query 3241 GAAGAGAAAAGATACAGAAATTAGCCAGGCGTGGTGGCGGGCACCTGTAATCCCAGCTAC 3300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4684456 GAAGAGAAAAGATACAGAAATTAGCCAGGCGTGGTGGCGGGCACCTGTAATCCCAGCTAC 4684515

Query 3301 TCAGGAGGCTGAGGCAGGAAAATCACTTGAACCCTGGAGGCAGAGGTTGCAATGGGCCGA 3360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4684516 TCAGGAGGCTGAGGCAGGAAAATCACTTGAACCCTGGAGGCAGAGGTTGCAATGGGCCGA 4684575

Query 3361 GATCACACCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACTCTGTCTCaaaaaaaaga 3420

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4684576 GATCACACCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACTCTGTCTCAAAAAAAAGA 4684635

Query 3421 aaagaaaaGATACAGAAATTAGCCTGGTGTGGTGGTGGGCGCCTGTAATCCCAGCTACTC 3480

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Sbjct 4684636 AAAGAAAAGATACAGAAATTAGCCTGGTGTGGTGGTGGGCGCCTGTAATCCCAGCTACTC 4684695

Query 3481 AGGAGGCTGAGGCAGGAGATTACGGTGAGCCAAGATTGTGCCATTGCATTCCAGCCTGGG 3540

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Sbjct 4684696 AGGAGGCTGAGGCAGGAGATTACGGTGAGCCAAGATTGTGCCATTGCATTCCAGCCTGGG 4684755

Query 3541 CAACAAGAGCAAAACTCCGCCTCaaaaaaaaTGtatttttattttattttacatttattt 3600

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Sbjct 4684756 CAACAAGAGCAAAACTCCGCCTCAAAAAAAATGTATTTTTATTTTATTTTACATTTATTT 4684815

Query 3601 atcttatttattttaGACATAGTCTTGGTCTGTCACCCAGGCTGGAGTACAGTGGCACGA 3660

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Sbjct 4684816 ATCTTATTTATTTTAGACATAGTCTTGGTCTGTCACCCAGGCTGGAGTACAGTGGCACGA 4684875

Query 3661 TCTTGGCTCACTGCAGCTTCCGCCTCCCTAGTTCAAGCCATTCTTGTTCTTCCAGCCTCC 3720

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Sbjct 4684876 TCTTGGCTCACTGCAGCTTCCGCCTCCCTAGTTCAAGCCATTCTTGTTCTTCCAGCCTCC 4684935

Query 3721 CAAGTAGCTGGGATTACAGGCGCCTGCCACCACACCCAGCTAATTTTTATATTTTTAGTA 3780

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Sbjct 4684936 CAAGTAGCTGGGATTACAGGCGCCTGCCACCACACCCAGCTAATTTTTATATTTTTAGTA 4684995

Query 3781 GAGACGGGGTTTCACTGTTGGCCAGAGTGGTCTGAAACTCCTGGCCTCAGGCGATCTGCC 3840

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Sbjct 4684996 GAGACGGGGTTTCACTGTTGGCCAGAGTGGTCTGAAACTCCTGGCCTCAGGCGATCTGCC 4685055

Query 3841 CCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGATATCGTGCCCAGCCTCGAGT 3900

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Sbjct 4685056 CCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGATATCGTGCCCAGCCTCGAGT 4685115

Query 3901 CAGGTTTAAAATAAATTTCCCTTCAAACCCCGGGCTTGCAGTTAGGCTAACCTGAAAGCC 3960

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Sbjct 4685116 CAGGTTTAAAATAAATTTCCCTTCAAACCCCGGGCTTGCAGTTAGGCTAACCTGAAAGCC 4685175

Query 3961 AGCGGCCGCCGAGATTCACTGGGGTTGTAGTTCCCCCCTCTCCCCTTCACCCGCCTACCC 4020

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Sbjct 4685176 AGCGGCCGCCGAGATTCACTGGGGTTGTAGTTCCCCCCTCTCCCCTTCACCCGCCTACCC 4685235

Query 4021 CTCAGGATCATTGAGATCTGAGATTTGTGGGTGCCAGGGAAGGGTGGGGTGGGGCCTGGG 4080

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Sbjct 4685236 CTCAGGATCATTGAGATCTGAGATTTGTGGGTGCCAGGGAAGGGTGGGGTGGGGCCTGGG 4685295

Query 4081 AGTCCGCAGAGGAGCTTGTGTAGCTAGGAATTCCATAGAGAGTGCTGTGGTTCTGCAAGG 4140

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Sbjct 4685296 AGTCCGCAGAGGAGCTTGTGTAGCTAGGAATTCCATAGAGAGTGCTGTGGTTCTGCAAGG 4685355

Query 4141 ACAGGTGCAGAAACAGAGTCCGAATTTCTAAtttttttttttttttttctttttGAGACG 4200

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4685356 ACAGGTGCAGAAACAGAGTCCGAATTTCTAATTTTTTTTTTTTTTTTTCTTTTTGAGACG 4685415

Query 4201 GGGTCTGGCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGCGATCTCGGCTCATTGCAACCT 4260

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4685416 GGGTCTGGCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGCGATCTCGGCTCATTGCAACCT 4685475

Query 4261 CCGCCTCCCA 4270

||||||||||

Sbjct 4685476 CCGCCTCCCA 4685485

**GAP (4,-5)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Alignment statistics for match #1** | | | | |
| Score | Expect | Identities | Gaps | Strand |
| 5425 bits(17080) | 0.0 | 4270/4270(100%) | 0/4270(0%) | Plus/Plus |

Query 1 CCTGTAATCCCAGCTACTCTAATGCTAAGGTGAGAGGATCACTTGAGCCCAGGAGGTCGA 60

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681216 CCTGTAATCCCAGCTACTCTAATGCTAAGGTGAGAGGATCACTTGAGCCCAGGAGGTCGA 4681275

Query 61 GGCTGCAGTGAGCCATGATCATGCCACTGCACTCCAGTCTGGGCAACAGTGTGAGACCCT 120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681276 GGCTGCAGTGAGCCATGATCATGCCACTGCACTCCAGTCTGGGCAACAGTGTGAGACCCT 4681335

Query 121 CTCTCAAACAAAAGCAGAAACCTCAGACAAGTAGATCATTCAAAATTGGTAAATCCAAAA 180

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681336 CTCTCAAACAAAAGCAGAAACCTCAGACAAGTAGATCATTCAAAATTGGTAAATCCAAAA 4681395

Query 181 GGCAATTCTAGGTGTGTTTGGATCCACAAGCCTCCAGTAAGTGACCTAACCAGGGAGGTA 240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681396 GGCAATTCTAGGTGTGTTTGGATCCACAAGCCTCCAGTAAGTGACCTAACCAGGGAGGTA 4681455

Query 241 AAGTAAGGTGTCAGCATGGGTCCTGGCCCTGCCATGAGACAGGAAGAAGAGAGAGCAGGT 300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681456 AAGTAAGGTGTCAGCATGGGTCCTGGCCCTGCCATGAGACAGGAAGAAGAGAGAGCAGGT 4681515

Query 301 GTTTCTCTGAGGTTGCTGGGGATGATATAATAGAACTGAAACTCTCAGCCCTTTCCCTGG 360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4681516 GTTTCTCTGAGGTTGCTGGGGATGATATAATAGAACTGAAACTCTCAGCCCTTTCCCTGG 4681575

Query 361 AGAAGCACAAAATGCTGCCTTGGATGGTATGTGCCAGATAAGACACATGAGGAGCCAGGC 420

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Sbjct 4681576 AGAAGCACAAAATGCTGCCTTGGATGGTATGTGCCAGATAAGACACATGAGGAGCCAGGC 4681635

Query 421 ACAGTGGCTCATGCCTGTAATCCCAGCAATTTGGGAGGCTGAAGCAGGAGGATTGCTTGA 480

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Sbjct 4681636 ACAGTGGCTCATGCCTGTAATCCCAGCAATTTGGGAGGCTGAAGCAGGAGGATTGCTTGA 4681695

Query 481 GCCCAGGAGTTCGAGATCAGCTAGGCAACATGGTAAGACATGAACTCTCCaaaaaaaTTA 540

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Sbjct 4681696 GCCCAGGAGTTCGAGATCAGCTAGGCAACATGGTAAGACATGAACTCTCCAAAAAAATTA 4681755

Query 541 GCCAGGCATGTTGTTCCGCACCTTTAGTCCCAGCTACTCGGGAGGCCGAGGTGAGAAGAT 600

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Sbjct 4681756 GCCAGGCATGTTGTTCCGCACCTTTAGTCCCAGCTACTCGGGAGGCCGAGGTGAGAAGAT 4681815

Query 601 CATTTGAGCCCAGGAGGTTGAGGATGCAGTGAGCCATGATTGCACCACTGCATTCCAGCC 660

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Sbjct 4681816 CATTTGAGCCCAGGAGGTTGAGGATGCAGTGAGCCATGATTGCACCACTGCATTCCAGCC 4681875

Query 661 TGGATGACAGAGTGAGATCCTGTCTCAAAAAGCAAacacacacacacacGAAAGCAAGAA 720

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Sbjct 4681876 TGGATGACAGAGTGAGATCCTGTCTCAAAAAGCAAACACACACACACACGAAAGCAAGAA 4681935

Query 721 GCAAGACAGCTGTGGAATTCCAGAGATAGGAGACAGGCAAAGAACCTGACCTGGTGCAAC 780

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Sbjct 4681936 GCAAGACAGCTGTGGAATTCCAGAGATAGGAGACAGGCAAAGAACCTGACCTGGTGCAAC 4681995

Query 781 GAAGATAAAGGTAACGGAGCCAGATGAGGAGGCTTAAATGCCTTACAAGAGTTAGGCGTT 840

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Sbjct 4681996 GAAGATAAAGGTAACGGAGCCAGATGAGGAGGCTTAAATGCCTTACAAGAGTTAGGCGTT 4682055

Query 841 CAAGTTACAAGTCTTGGCCAGGCGCGGTGGCTCACGCTTGTAATCCCAGCACTTTGGGAG 900

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Sbjct 4682056 CAAGTTACAAGTCTTGGCCAGGCGCGGTGGCTCACGCTTGTAATCCCAGCACTTTGGGAG 4682115

Query 901 GCTGAGGCAGGCGGATCACGAGGTCAGGAGATCAAGACCATTCTGGCCAACATGATGAAA 960

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Sbjct 4682116 GCTGAGGCAGGCGGATCACGAGGTCAGGAGATCAAGACCATTCTGGCCAACATGATGAAA 4682175

Query 961 CCCCGTCTCTACTAAAAATACAAAAAATTAGCCCGGCGTGGTGGCATGTGCATGTAGTCC 1020

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Sbjct 4682176 CCCCGTCTCTACTAAAAATACAAAAAATTAGCCCGGCGTGGTGGCATGTGCATGTAGTCC 4682235

Query 1021 CAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGT 1080

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Sbjct 4682236 CAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGT 4682295

Query 1081 GAGCCAAGATCACACCACTGTACTCCAACCTGGTGACAGAGTGAGACTCCGTCTCaaaaa 1140

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 4682296 GAGCCAAGATCACACCACTGTACTCCAACCTGGTGACAGAGTGAGACTCCGTCTCAAAAA 4682355

Query 1141 aaaaaaaaaaaaaaGAGTTCAGTCTTGATGGGCTTCTCTGTGAAGAGACCCTAAAGGATT 1200

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Sbjct 4682356 AAAAAAAAAAAAAAGAGTTCAGTCTTGATGGGCTTCTCTGTGAAGAGACCCTAAAGGATT 4682415

Query 1201 TGAGCAGAGAAAAGACCAGTTGAAAGCTATGTTTAGGCCAGATGCAGTGACTTACACCTG 1260

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Sbjct 4682416 TGAGCAGAGAAAAGACCAGTTGAAAGCTATGTTTAGGCCAGATGCAGTGACTTACACCTG 4682475

Query 1261 TAATCCCAGCAATTTGGTAGGCCAGGGCAGGAGGAGCCCAGGAGTTCAAGACCAGCCTGA 1320

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Sbjct 4682476 TAATCCCAGCAATTTGGTAGGCCAGGGCAGGAGGAGCCCAGGAGTTCAAGACCAGCCTGA 4682535

Query 1321 GCAAATAGCAAGACCCCATGTCTACAAAAttttttttAATTAGCTGGGAATGATGACGCA 1380

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Sbjct 4682536 GCAAATAGCAAGACCCCATGTCTACAAAATTTTTTTTAATTAGCTGGGAATGATGACGCA 4682595

Query 1381 TGCCTGCGATACCAGCTACTCAGGAGGCTGAGGCAGGAGGATCACTTGAGCCCAGGAGGT 1440

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Sbjct 4682596 TGCCTGCGATACCAGCTACTCAGGAGGCTGAGGCAGGAGGATCACTTGAGCCCAGGAGGT 4682655

Query 1441 CAAGGCTAAAGTCAGCCACGATCAAGCCACTGCATTCCAGCCTGGGTGGCAGAGTGAGAC 1500

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Sbjct 4682656 CAAGGCTAAAGTCAGCCACGATCAAGCCACTGCATTCCAGCCTGGGTGGCAGAGTGAGAC 4682715

Query 1501 CCTGTTTCaaaaagaaagaaagaaaaaaaaaaGCTATGTTTAACCTGATAGAGGATAGAG 1560

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Sbjct 4682716 CCTGTTTCAAAAAGAAAGAAAGAAAAAAAAAAGCTATGTTTAACCTGATAGAGGATAGAG 4682775

Query 1561 TGTAGGGTGGCATGGGGCAAGAGCTATGAGAGTGTAATAGGGAGGCTGAGAACACCCTCA 1620

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Sbjct 4682776 TGTAGGGTGGCATGGGGCAAGAGCTATGAGAGTGTAATAGGGAGGCTGAGAACACCCTCA 4682835

Query 1621 TGGGAGGTGATGAGGGATTCAATGTGGGGAGGAACTCACAGATTCAGGAGCCACTTAAGT 1680

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Sbjct 4682836 TGGGAGGTGATGAGGGATTCAATGTGGGGAGGAACTCACAGATTCAGGAGCCACTTAAGT 4682895

Query 1681 AAAAGTTGAGAAAATTTGATGTCTTTCTGGGTGCAAGATTAAAGCTTTCCAGCCTGGCTG 1740

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Sbjct 4682896 AAAAGTTGAGAAAATTTGATGTCTTTCTGGGTGCAAGATTAAAGCTTTCCAGCCTGGCTG 4682955

Query 1741 ACCTAGTAGATGTTATTTTTTCCACTGATGGAGACAAGAAAGTCAAAGGGAGATGAATTT 1800

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Sbjct 4682956 ACCTAGTAGATGTTATTTTTTCCACTGATGGAGACAAGAAAGTCAAAGGGAGATGAATTT 4683015

Query 1801 GAGGAATATTGTGAGATGAGCGTGAGGCTGGTTGAATTTGAGCTAAAACCAAGATATTCA 1860

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Sbjct 4683016 GAGGAATATTGTGAGATGAGCGTGAGGCTGGTTGAATTTGAGCTAAAACCAAGATATTCA 4683075

Query 1861 AGTGAACATAGGATCTGGAGGCATCAGTTTTGGAGGCAACTTCTGGCAGAGTGAAGAGCT 1920

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Sbjct 4683076 AGTGAACATAGGATCTGGAGGCATCAGTTTTGGAGGCAACTTCTGGCAGAGTGAAGAGCT 4683135

Query 1921 GATTCCCTGAAAGGGGATGGGCATTGTTAGGAAAGCCACAGGGAGaaaaaaaGACCAAGG 1980

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Sbjct 4683136 GATTCCCTGAAAGGGGATGGGCATTGTTAGGAAAGCCACAGGGAGAAAAAAAGACCAAGG 4683195

Query 1981 CTTGAATCTTGGAAAATGCTACACTCCATATCAGACCATCCACTAGCACTCTTCCACACT 2040

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Sbjct 4683196 CTTGAATCTTGGAAAATGCTACACTCCATATCAGACCATCCACTAGCACTCTTCCACACT 4683255

Query 2041 CTACTGTAATCCCAATTCACCAGACACTCCAACACCTCTATCCCTTCCTGCTGCTGAGGG 2100

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Sbjct 4683256 CTACTGTAATCCCAATTCACCAGACACTCCAACACCTCTATCCCTTCCTGCTGCTGAGGG 4683315

Query 2101 AACTTATAAATATTGAGTTACTCTGAGCTGGTCtttttttttttttttttttGAGATGGA 2160

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Sbjct 4683316 AACTTATAAATATTGAGTTACTCTGAGCTGGTCTTTTTTTTTTTTTTTTTTTGAGATGGA 4683375

Query 2161 GTTTCGCTCTTATTGCCCGGGTTGGAGTACAGTGGCACGATCTCAGCTCACCACAACCTC 2220

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Sbjct 4683376 GTTTCGCTCTTATTGCCCGGGTTGGAGTACAGTGGCACGATCTCAGCTCACCACAACCTC 4683435

Query 2221 CACCTCCCAGGTTCAAGTAATTCTCCTGCCTCAGCCCCCCGAGTAGCTGAGATTATAGGC 2280

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Sbjct 4683436 CACCTCCCAGGTTCAAGTAATTCTCCTGCCTCAGCCCCCCGAGTAGCTGAGATTATAGGC 4683495

Query 2281 ATGCGCCACCACGCCCGGCTAATTTTGTATTTTTAGCAGAGTTGGGGTTTCTCCATGTTG 2340

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Sbjct 4683496 ATGCGCCACCACGCCCGGCTAATTTTGTATTTTTAGCAGAGTTGGGGTTTCTCCATGTTG 4683555

Query 2341 GTCAGGCTGGTCTTGAACTTCCGACCTCAGGTGATCCACCAGCCTCAGCCTCTCAACATG 2400

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Sbjct 4683556 GTCAGGCTGGTCTTGAACTTCCGACCTCAGGTGATCCACCAGCCTCAGCCTCTCAACATG 4683615

Query 2401 CTGGGATTTCAGGCGTGAACCACCGCGCCCGGCCTCTGAGCCAGTCTTAACACCTAGTCA 2460

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Sbjct 4683616 CTGGGATTTCAGGCGTGAACCACCGCGCCCGGCCTCTGAGCCAGTCTTAACACCTAGTCA 4683675

Query 2461 GCTTGTTCTCCCATTAAATCCTGAGAACAGACCTGTGAGGTAGATCTTCCAGACCCATTT 2520

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Sbjct 4683676 GCTTGTTCTCCCATTAAATCCTGAGAACAGACCTGTGAGGTAGATCTTCCAGACCCATTT 4683735

Query 2521 TATACAGGCAAAACTGAGACCCTGAGAGATGAATCAATTCATAGCATGTGAAGTAGTTTC 2580

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Sbjct 4683736 TATACAGGCAAAACTGAGACCCTGAGAGATGAATCAATTCATAGCATGTGAAGTAGTTTC 4683795

Query 2581 CCTGATTTCCATTCAGTAGGGCACCTACTATGTGCCAAGATTGGGGAAAATAATGATATT 2640

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Sbjct 4683796 CCTGATTTCCATTCAGTAGGGCACCTACTATGTGCCAAGATTGGGGAAAATAATGATATT 4683855

Query 2641 GGGCCCTACCCTCTAGAGGCCACAATCTGGACAGAGATAAGGTAGGCACGTAAATAAGGA 2700

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Sbjct 4683856 GGGCCCTACCCTCTAGAGGCCACAATCTGGACAGAGATAAGGTAGGCACGTAAATAAGGA 4683915

Query 2701 TAAAGTAAGGTGAAGCCCAGCAGCTCCAGGAGACGTAGAGATAAGGTCTTCTACAGTCCA 2760

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Sbjct 4683916 TAAAGTAAGGTGAAGCCCAGCAGCTCCAGGAGACGTAGAGATAAGGTCTTCTACAGTCCA 4683975

Query 2761 AAGGGCTGAAGGCATCACAGGCAGCTTCCTGAAGGAGGTAGGCACTGATGCAAGTCAGGC 2820

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Sbjct 4683976 AAGGGCTGAAGGCATCACAGGCAGCTTCCTGAAGGAGGTAGGCACTGATGCAAGTCAGGC 4684035

Query 2821 CTGGAGGATCTGGGGGGACGTGCTATAACAATGACTCTTGTCCCACAGGTACTGTGTCCG 2880

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Sbjct 4684036 CTGGAGGATCTGGGGGGACGTGCTATAACAATGACTCTTGTCCCACAGGTACTGTGTCCG 4684095

Query 2881 GGGATTGCAGCCGTTCGGGCAGGGGGCAAGGGCTGCTGTGGTGCTGGGTGCTGTGGAAAC 2940

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Sbjct 4684096 GGGATTGCAGCCGTTCGGGCAGGGGGCAAGGGCTGCTGTGGTGCTGGGTGCTGTGGAAAC 4684155

Query 2941 CGCTGCAGGGTAAGATCCAGATTAAGAAGGAATTCAGGGCTGGGGGTGGTGTCTCATGCC 3000

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Sbjct 4684156 CGCTGCAGGGTAAGATCCAGATTAAGAAGGAATTCAGGGCTGGGGGTGGTGTCTCATGCC 4684215

Query 3001 TGTAATCCCAACACTTTAGCAGGCTGAGGTGGGAGTACGGCTTGAGCCAGGAGTTCTAGA 3060

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Sbjct 4684216 TGTAATCCCAACACTTTAGCAGGCTGAGGTGGGAGTACGGCTTGAGCCAGGAGTTCTAGA 4684275

Query 3061 CCAGCCCAGGAAACATGGCAAGATCCCTATCTCTACTAACAATACAAAAATTAGCCGGGC 3120

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Sbjct 4684276 CCAGCCCAGGAAACATGGCAAGATCCCTATCTCTACTAACAATACAAAAATTAGCCGGGC 4684335

Query 3121 GTGGTGGCAAGCACCTGCAATCTCGGCTACTTGGGAGGCTGAGGTGGGAGGGCCGCTTGA 3180

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Sbjct 4684336 GTGGTGGCAAGCACCTGCAATCTCGGCTACTTGGGAGGCTGAGGTGGGAGGGCCGCTTGA 4684395

Query 3181 GCCCAGGAGGTCCAGGCTGCAGTAAGCAGTGATTTaaaaaaaaaaaaaaaaaaaaaaaaa 3240

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Sbjct 4684396 GCCCAGGAGGTCCAGGCTGCAGTAAGCAGTGATTTAAAAAAAAAAAAAAAAAAAAAAAAA 4684455

Query 3241 GAAGAGAAAAGATACAGAAATTAGCCAGGCGTGGTGGCGGGCACCTGTAATCCCAGCTAC 3300

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Sbjct 4684456 GAAGAGAAAAGATACAGAAATTAGCCAGGCGTGGTGGCGGGCACCTGTAATCCCAGCTAC 4684515

Query 3301 TCAGGAGGCTGAGGCAGGAAAATCACTTGAACCCTGGAGGCAGAGGTTGCAATGGGCCGA 3360

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Sbjct 4684516 TCAGGAGGCTGAGGCAGGAAAATCACTTGAACCCTGGAGGCAGAGGTTGCAATGGGCCGA 4684575

Query 3361 GATCACACCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACTCTGTCTCaaaaaaaaga 3420

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Sbjct 4684576 GATCACACCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACTCTGTCTCAAAAAAAAGA 4684635

Query 3421 aaagaaaaGATACAGAAATTAGCCTGGTGTGGTGGTGGGCGCCTGTAATCCCAGCTACTC 3480

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Sbjct 4684636 AAAGAAAAGATACAGAAATTAGCCTGGTGTGGTGGTGGGCGCCTGTAATCCCAGCTACTC 4684695

Query 3481 AGGAGGCTGAGGCAGGAGATTACGGTGAGCCAAGATTGTGCCATTGCATTCCAGCCTGGG 3540

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Sbjct 4684696 AGGAGGCTGAGGCAGGAGATTACGGTGAGCCAAGATTGTGCCATTGCATTCCAGCCTGGG 4684755

Query 3541 CAACAAGAGCAAAACTCCGCCTCaaaaaaaaTGtatttttattttattttacatttattt 3600

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Sbjct 4684756 CAACAAGAGCAAAACTCCGCCTCAAAAAAAATGTATTTTTATTTTATTTTACATTTATTT 4684815

Query 3601 atcttatttattttaGACATAGTCTTGGTCTGTCACCCAGGCTGGAGTACAGTGGCACGA 3660

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Sbjct 4684816 ATCTTATTTATTTTAGACATAGTCTTGGTCTGTCACCCAGGCTGGAGTACAGTGGCACGA 4684875

Query 3661 TCTTGGCTCACTGCAGCTTCCGCCTCCCTAGTTCAAGCCATTCTTGTTCTTCCAGCCTCC 3720

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Sbjct 4684876 TCTTGGCTCACTGCAGCTTCCGCCTCCCTAGTTCAAGCCATTCTTGTTCTTCCAGCCTCC 4684935

Query 3721 CAAGTAGCTGGGATTACAGGCGCCTGCCACCACACCCAGCTAATTTTTATATTTTTAGTA 3780

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Sbjct 4684936 CAAGTAGCTGGGATTACAGGCGCCTGCCACCACACCCAGCTAATTTTTATATTTTTAGTA 4684995

Query 3781 GAGACGGGGTTTCACTGTTGGCCAGAGTGGTCTGAAACTCCTGGCCTCAGGCGATCTGCC 3840

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Sbjct 4684996 GAGACGGGGTTTCACTGTTGGCCAGAGTGGTCTGAAACTCCTGGCCTCAGGCGATCTGCC 4685055

Query 3841 CCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGATATCGTGCCCAGCCTCGAGT 3900

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Sbjct 4685056 CCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGATATCGTGCCCAGCCTCGAGT 4685115

Query 3901 CAGGTTTAAAATAAATTTCCCTTCAAACCCCGGGCTTGCAGTTAGGCTAACCTGAAAGCC 3960

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Sbjct 4685116 CAGGTTTAAAATAAATTTCCCTTCAAACCCCGGGCTTGCAGTTAGGCTAACCTGAAAGCC 4685175

Query 3961 AGCGGCCGCCGAGATTCACTGGGGTTGTAGTTCCCCCCTCTCCCCTTCACCCGCCTACCC 4020

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Sbjct 4685176 AGCGGCCGCCGAGATTCACTGGGGTTGTAGTTCCCCCCTCTCCCCTTCACCCGCCTACCC 4685235

Query 4021 CTCAGGATCATTGAGATCTGAGATTTGTGGGTGCCAGGGAAGGGTGGGGTGGGGCCTGGG 4080

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Sbjct 4685236 CTCAGGATCATTGAGATCTGAGATTTGTGGGTGCCAGGGAAGGGTGGGGTGGGGCCTGGG 4685295

Query 4081 AGTCCGCAGAGGAGCTTGTGTAGCTAGGAATTCCATAGAGAGTGCTGTGGTTCTGCAAGG 4140

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Sbjct 4685296 AGTCCGCAGAGGAGCTTGTGTAGCTAGGAATTCCATAGAGAGTGCTGTGGTTCTGCAAGG 4685355

Query 4141 ACAGGTGCAGAAACAGAGTCCGAATTTCTAAtttttttttttttttttctttttGAGACG 4200

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Sbjct 4685356 ACAGGTGCAGAAACAGAGTCCGAATTTCTAATTTTTTTTTTTTTTTTTCTTTTTGAGACG 4685415

Query 4201 GGGTCTGGCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGCGATCTCGGCTCATTGCAACCT 4260

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Sbjct 4685416 GGGTCTGGCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGCGATCTCGGCTCATTGCAACCT 4685475

Query 4261 CCGCCTCCCA 4270

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Sbjct 4685476 CCGCCTCCCA 4685485

**PAM 30**

Range 1: 1 to 1382[GenPept](https://www.ncbi.nlm.nih.gov/protein/NP_000199.2?report=genbank&log$=protalign&blast_rank=1&RID=0BCFUHPV01R&from=1&to=1382)[Graphics](https://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=0BCFUHPV01R&id=NP_000199.2&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=0:1451&appname=ncbiblast&link_loc=fromHSP)Next MatchPrevious Match

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Alignment statistics for match #1** | | | | | |
| Score | Expect | Method | Identities | Positives | Gaps |
| 2984 bits(7030) | 0.0 | Compositional matrix adjust. | 1382/1382(100%) | 1382/1382(100%) | 0/1382(0%) |

Query 1 MATGGRRGAAAAPLLVAVAALLLGAAGHLYPGEVCPGMDIRNNLTRLHELENCSVIEGHL 60

MATGGRRGAAAAPLLVAVAALLLGAAGHLYPGEVCPGMDIRNNLTRLHELENCSVIEGHL

Sbjct 1 MATGGRRGAAAAPLLVAVAALLLGAAGHLYPGEVCPGMDIRNNLTRLHELENCSVIEGHL 60

Query 61 QILLMFKTRPEDFRDLSFPKLIMITDYLLLFRVYGLESLKDLFPNLTVIRGSRLFFNYAL 120

QILLMFKTRPEDFRDLSFPKLIMITDYLLLFRVYGLESLKDLFPNLTVIRGSRLFFNYAL

Sbjct 61 QILLMFKTRPEDFRDLSFPKLIMITDYLLLFRVYGLESLKDLFPNLTVIRGSRLFFNYAL 120

Query 121 VIFEMVHLKELGLYNLMNITRGSVRIEKNNELCYLATIDWSRILDSVEDNYIVLNKDDNE 180

VIFEMVHLKELGLYNLMNITRGSVRIEKNNELCYLATIDWSRILDSVEDNYIVLNKDDNE

Sbjct 121 VIFEMVHLKELGLYNLMNITRGSVRIEKNNELCYLATIDWSRILDSVEDNYIVLNKDDNE 180

Query 181 ECGDICPGTAKGKTNCPATVINGQFVERCWTHSHCQKVCPTICKSHGCTAEGLCCHSECL 240

ECGDICPGTAKGKTNCPATVINGQFVERCWTHSHCQKVCPTICKSHGCTAEGLCCHSECL

Sbjct 181 ECGDICPGTAKGKTNCPATVINGQFVERCWTHSHCQKVCPTICKSHGCTAEGLCCHSECL 240

Query 241 GNCSQPDDPTKCVACRNFYLDGRCVETCPPPYYHFQDWRCVNFSFCQDLHHKCKNSRRQG 300

GNCSQPDDPTKCVACRNFYLDGRCVETCPPPYYHFQDWRCVNFSFCQDLHHKCKNSRRQG

Sbjct 241 GNCSQPDDPTKCVACRNFYLDGRCVETCPPPYYHFQDWRCVNFSFCQDLHHKCKNSRRQG 300

Query 301 CHQYVIHNNKCIPECPSGYTMNSSNLLCTPCLGPCPKVCHLLEGEKTIDSVTSAQELRGC 360

CHQYVIHNNKCIPECPSGYTMNSSNLLCTPCLGPCPKVCHLLEGEKTIDSVTSAQELRGC

Sbjct 301 CHQYVIHNNKCIPECPSGYTMNSSNLLCTPCLGPCPKVCHLLEGEKTIDSVTSAQELRGC 360

Query 361 TVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRSYALVSLSFFRKLRLIRGETL 420

TVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRSYALVSLSFFRKLRLIRGETL

Sbjct 361 TVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRSYALVSLSFFRKLRLIRGETL 420

Query 421 EIGNYSFYALDNQNLRQLWDWSKHNLTITQGKLFFHYNPKLCLSEIHKMEEVSGTKGRQE 480

EIGNYSFYALDNQNLRQLWDWSKHNLTITQGKLFFHYNPKLCLSEIHKMEEVSGTKGRQE

Sbjct 421 EIGNYSFYALDNQNLRQLWDWSKHNLTITQGKLFFHYNPKLCLSEIHKMEEVSGTKGRQE 480

Query 481 RNDIALKTNGDQASCENELLKFSYIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQ 540

RNDIALKTNGDQASCENELLKFSYIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQ

Sbjct 481 RNDIALKTNGDQASCENELLKFSYIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQ 540

Query 541 NVTEFDGQDACGSNSWTVVDIDPPLRSNDPKSQNHPGWLMRGLKPWTQYAIFVKTLVTFS 600

NVTEFDGQDACGSNSWTVVDIDPPLRSNDPKSQNHPGWLMRGLKPWTQYAIFVKTLVTFS

Sbjct 541 NVTEFDGQDACGSNSWTVVDIDPPLRSNDPKSQNHPGWLMRGLKPWTQYAIFVKTLVTFS 600

Query 601 DERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDPNGNITHYLVFWE 660

DERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDPNGNITHYLVFWE

Sbjct 601 DERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDPNGNITHYLVFWE 660

Query 661 RQAEDSELFELDYCLKGLKLPSRTWSPPFESEDSQKHNQSEYEDSAGECCSCPKTDSQIL 720

RQAEDSELFELDYCLKGLKLPSRTWSPPFESEDSQKHNQSEYEDSAGECCSCPKTDSQIL

Sbjct 661 RQAEDSELFELDYCLKGLKLPSRTWSPPFESEDSQKHNQSEYEDSAGECCSCPKTDSQIL 720

Query 721 KELEESSFRKTFEDYLHNVVFVPRKTSSGTGAEDPRPSRKRRSLGDVGNVTVAVPTVAAF 780

KELEESSFRKTFEDYLHNVVFVPRKTSSGTGAEDPRPSRKRRSLGDVGNVTVAVPTVAAF

Sbjct 721 KELEESSFRKTFEDYLHNVVFVPRKTSSGTGAEDPRPSRKRRSLGDVGNVTVAVPTVAAF 780

Query 781 PNTSSTSVPTSPEEHRPFEKVVNKESLVISGLRHFTGYRIELQACNQDTPEERCSVAAYV 840

PNTSSTSVPTSPEEHRPFEKVVNKESLVISGLRHFTGYRIELQACNQDTPEERCSVAAYV

Sbjct 781 PNTSSTSVPTSPEEHRPFEKVVNKESLVISGLRHFTGYRIELQACNQDTPEERCSVAAYV 840

Query 841 SARTMPEAKADDIVGPVTHEIFENNVVHLMWQEPKEPNGLIVLYEVSYRRYGDEELHLCV 900

SARTMPEAKADDIVGPVTHEIFENNVVHLMWQEPKEPNGLIVLYEVSYRRYGDEELHLCV

Sbjct 841 SARTMPEAKADDIVGPVTHEIFENNVVHLMWQEPKEPNGLIVLYEVSYRRYGDEELHLCV 900

Query 901 SRKHFALERGCRLRGLSPGNYSVRIRATSLAGNGSWTEPTYFYVTDYLDVPSNIAKIIIG 960

SRKHFALERGCRLRGLSPGNYSVRIRATSLAGNGSWTEPTYFYVTDYLDVPSNIAKIIIG

Sbjct 901 SRKHFALERGCRLRGLSPGNYSVRIRATSLAGNGSWTEPTYFYVTDYLDVPSNIAKIIIG 960

Query 961 PLIFVFLFSVVIGSIYLFLRKRQPDGPLGPLYASSNPEYLSASDVFPCSVYVPDEWEVSR 1020

PLIFVFLFSVVIGSIYLFLRKRQPDGPLGPLYASSNPEYLSASDVFPCSVYVPDEWEVSR

Sbjct 961 PLIFVFLFSVVIGSIYLFLRKRQPDGPLGPLYASSNPEYLSASDVFPCSVYVPDEWEVSR 1020

Query 1021 EKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKG 1080

EKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKG

Sbjct 1021 EKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKG 1080

Query 1081 FTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMA 1140

FTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMA

Sbjct 1081 FTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMA 1140

Query 1141 AEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPV 1200

AEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPV

Sbjct 1141 AEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPV 1200

Query 1201 RWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDN 1260

RWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDN

Sbjct 1201 RWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDN 1260

Query 1261 CPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENKAPESEELEME 1320

CPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENKAPESEELEME

Sbjct 1261 CPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENKAPESEELEME 1320

Query 1321 FEDMENVPLDRSSHCQREEAGGRDGGSSLGFKRSYEEHIPYTHMNGGKKNGRILTLPRSN 1380

FEDMENVPLDRSSHCQREEAGGRDGGSSLGFKRSYEEHIPYTHMNGGKKNGRILTLPRSN

Sbjct 1321 FEDMENVPLDRSSHCQREEAGGRDGGSSLGFKRSYEEHIPYTHMNGGKKNGRILTLPRSN 1380

Query 1381 PS 1382

PS

Sbjct 1381 PS 1382

**BLOSUM62**

Range 1: 1 to 1382[GenPept](https://www.ncbi.nlm.nih.gov/protein/NP_000199.2?report=genbank&log$=protalign&blast_rank=1&RID=0BCXH81P016&from=1&to=1382)[Graphics](https://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=0BCXH81P016&id=NP_000199.2&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=0:1451&appname=ncbiblast&link_loc=fromHSP)Next MatchPrevious Match

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Alignment statistics for match #1** | | | | | |
| Score | Expect | Method | Identities | Positives | Gaps |
| 2884 bits(7476) | 0.0 | Compositional matrix adjust. | 1382/1382(100%) | 1382/1382(100%) | 0/1382(0%) |

Query 1 MATGGRRGAAAAPLLVAVAALLLGAAGHLYPGEVCPGMDIRNNLTRLHELENCSVIEGHL 60

MATGGRRGAAAAPLLVAVAALLLGAAGHLYPGEVCPGMDIRNNLTRLHELENCSVIEGHL

Sbjct 1 MATGGRRGAAAAPLLVAVAALLLGAAGHLYPGEVCPGMDIRNNLTRLHELENCSVIEGHL 60

Query 61 QILLMFKTRPEDFRDLSFPKLIMITDYLLLFRVYGLESLKDLFPNLTVIRGSRLFFNYAL 120

QILLMFKTRPEDFRDLSFPKLIMITDYLLLFRVYGLESLKDLFPNLTVIRGSRLFFNYAL

Sbjct 61 QILLMFKTRPEDFRDLSFPKLIMITDYLLLFRVYGLESLKDLFPNLTVIRGSRLFFNYAL 120

Query 121 VIFEMVHLKELGLYNLMNITRGSVRIEKNNELCYLATIDWSRILDSVEDNYIVLNKDDNE 180

VIFEMVHLKELGLYNLMNITRGSVRIEKNNELCYLATIDWSRILDSVEDNYIVLNKDDNE

Sbjct 121 VIFEMVHLKELGLYNLMNITRGSVRIEKNNELCYLATIDWSRILDSVEDNYIVLNKDDNE 180

Query 181 ECGDICPGTAKGKTNCPATVINGQFVERCWTHSHCQKVCPTICKSHGCTAEGLCCHSECL 240

ECGDICPGTAKGKTNCPATVINGQFVERCWTHSHCQKVCPTICKSHGCTAEGLCCHSECL

Sbjct 181 ECGDICPGTAKGKTNCPATVINGQFVERCWTHSHCQKVCPTICKSHGCTAEGLCCHSECL 240

Query 241 GNCSQPDDPTKCVACRNFYLDGRCVETCPPPYYHFQDWRCVNFSFCQDLHHKCKNSRRQG 300

GNCSQPDDPTKCVACRNFYLDGRCVETCPPPYYHFQDWRCVNFSFCQDLHHKCKNSRRQG

Sbjct 241 GNCSQPDDPTKCVACRNFYLDGRCVETCPPPYYHFQDWRCVNFSFCQDLHHKCKNSRRQG 300

Query 301 CHQYVIHNNKCIPECPSGYTMNSSNLLCTPCLGPCPKVCHLLEGEKTIDSVTSAQELRGC 360

CHQYVIHNNKCIPECPSGYTMNSSNLLCTPCLGPCPKVCHLLEGEKTIDSVTSAQELRGC

Sbjct 301 CHQYVIHNNKCIPECPSGYTMNSSNLLCTPCLGPCPKVCHLLEGEKTIDSVTSAQELRGC 360

Query 361 TVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRSYALVSLSFFRKLRLIRGETL 420

TVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRSYALVSLSFFRKLRLIRGETL

Sbjct 361 TVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRSYALVSLSFFRKLRLIRGETL 420

Query 421 EIGNYSFYALDNQNLRQLWDWSKHNLTITQGKLFFHYNPKLCLSEIHKMEEVSGTKGRQE 480

EIGNYSFYALDNQNLRQLWDWSKHNLTITQGKLFFHYNPKLCLSEIHKMEEVSGTKGRQE

Sbjct 421 EIGNYSFYALDNQNLRQLWDWSKHNLTITQGKLFFHYNPKLCLSEIHKMEEVSGTKGRQE 480

Query 481 RNDIALKTNGDQASCENELLKFSYIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQ 540

RNDIALKTNGDQASCENELLKFSYIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQ

Sbjct 481 RNDIALKTNGDQASCENELLKFSYIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQ 540

Query 541 NVTEFDGQDACGSNSWTVVDIDPPLRSNDPKSQNHPGWLMRGLKPWTQYAIFVKTLVTFS 600

NVTEFDGQDACGSNSWTVVDIDPPLRSNDPKSQNHPGWLMRGLKPWTQYAIFVKTLVTFS

Sbjct 541 NVTEFDGQDACGSNSWTVVDIDPPLRSNDPKSQNHPGWLMRGLKPWTQYAIFVKTLVTFS 600

Query 601 DERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDPNGNITHYLVFWE 660

DERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDPNGNITHYLVFWE

Sbjct 601 DERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDPNGNITHYLVFWE 660

Query 661 RQAEDSELFELDYCLKGLKLPSRTWSPPFESEDSQKHNQSEYEDSAGECCSCPKTDSQIL 720

RQAEDSELFELDYCLKGLKLPSRTWSPPFESEDSQKHNQSEYEDSAGECCSCPKTDSQIL

Sbjct 661 RQAEDSELFELDYCLKGLKLPSRTWSPPFESEDSQKHNQSEYEDSAGECCSCPKTDSQIL 720

Query 721 KELEESSFRKTFEDYLHNVVFVPRKTSSGTGAEDPRPSRKRRSLGDVGNVTVAVPTVAAF 780

KELEESSFRKTFEDYLHNVVFVPRKTSSGTGAEDPRPSRKRRSLGDVGNVTVAVPTVAAF

Sbjct 721 KELEESSFRKTFEDYLHNVVFVPRKTSSGTGAEDPRPSRKRRSLGDVGNVTVAVPTVAAF 780

Query 781 PNTSSTSVPTSPEEHRPFEKVVNKESLVISGLRHFTGYRIELQACNQDTPEERCSVAAYV 840

PNTSSTSVPTSPEEHRPFEKVVNKESLVISGLRHFTGYRIELQACNQDTPEERCSVAAYV

Sbjct 781 PNTSSTSVPTSPEEHRPFEKVVNKESLVISGLRHFTGYRIELQACNQDTPEERCSVAAYV 840

Query 841 SARTMPEAKADDIVGPVTHEIFENNVVHLMWQEPKEPNGLIVLYEVSYRRYGDEELHLCV 900

SARTMPEAKADDIVGPVTHEIFENNVVHLMWQEPKEPNGLIVLYEVSYRRYGDEELHLCV

Sbjct 841 SARTMPEAKADDIVGPVTHEIFENNVVHLMWQEPKEPNGLIVLYEVSYRRYGDEELHLCV 900

Query 901 SRKHFALERGCRLRGLSPGNYSVRIRATSLAGNGSWTEPTYFYVTDYLDVPSNIAKIIIG 960

SRKHFALERGCRLRGLSPGNYSVRIRATSLAGNGSWTEPTYFYVTDYLDVPSNIAKIIIG

Sbjct 901 SRKHFALERGCRLRGLSPGNYSVRIRATSLAGNGSWTEPTYFYVTDYLDVPSNIAKIIIG 960

Query 961 PLIFVFLFSVVIGSIYLFLRKRQPDGPLGPLYASSNPEYLSASDVFPCSVYVPDEWEVSR 1020

PLIFVFLFSVVIGSIYLFLRKRQPDGPLGPLYASSNPEYLSASDVFPCSVYVPDEWEVSR

Sbjct 961 PLIFVFLFSVVIGSIYLFLRKRQPDGPLGPLYASSNPEYLSASDVFPCSVYVPDEWEVSR 1020

Query 1021 EKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKG 1080

EKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKG

Sbjct 1021 EKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKG 1080

Query 1081 FTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMA 1140

FTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMA

Sbjct 1081 FTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMA 1140

Query 1141 AEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPV 1200

AEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPV

Sbjct 1141 AEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPV 1200

Query 1201 RWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDN 1260

RWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDN

Sbjct 1201 RWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDN 1260

Query 1261 CPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENKAPESEELEME 1320

CPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENKAPESEELEME

Sbjct 1261 CPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENKAPESEELEME 1320

Query 1321 FEDMENVPLDRSSHCQREEAGGRDGGSSLGFKRSYEEHIPYTHMNGGKKNGRILTLPRSN 1380

FEDMENVPLDRSSHCQREEAGGRDGGSSLGFKRSYEEHIPYTHMNGGKKNGRILTLPRSN

Sbjct 1321 FEDMENVPLDRSSHCQREEAGGRDGGSSLGFKRSYEEHIPYTHMNGGKKNGRILTLPRSN 1380

Query 1381 PS 1382

PS

Sbjct 1381 PS 1382