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Detection of *Mycobacterium angelicum* in Human Urinary Tract, French Polynesia

Appendix

INPUT SEQUENCE INFO:

Input Name :: 2_08_11_2022_090022_149104_input.fsa.translated
Sequences :: 5728
Total bpp :: 2042673
Longest seq :: 6302
Shortest seq :: 30
Avg seq length :: 356.0

RESULTS:

Min Identity Threshold :: 91.084
Z-THRESHOLD :: 3.0
Prediction Score :: 100.845
Probability of being human pathogen :: 0.83
Matches:: 30
Genome Coverage (%) :: 0.52
Pathogenic Families Matched :: 26
Non-Pathogenic Families Matched :: 4
The organisms is predicted as human pathogenic :: Yes

MATCHED SEQUENCES:

#input_seq: SEQ4_116 # 132658 # 136821 # 1 #
ID=4_116;partial=00;start_type=GTG;rbs_motif=3Base/5BMM;rbs_spacer=13-15bp;gc_cont=0.651
#matched_seq: 15642 CP000717 Mycobacterium tuberculosis F11, complete genome. Actinobacteridae conserved hypothetical protein ABR06151
Yes 92.86
#input_seq: SEQ4_129 # 149255 # 151087 # 1 #
ID=4_129;partial=00;start_type=ATG;rbs_motif=None;rbs_spacer=None;gc_cont=0.640
#matched_seq: 15642 CP000717 Mycobacterium tuberculosis F11, complete genome. Actinobacteridae conserved hypothetical protein ABR06164
Yes 93.61
#input_seq: SEQ9_126 # 138779 # 139858 # 1 #
ID=9_126;partial=00;start_type=GTG;rbs_motif=None;rbs_spacer=None;gc_cont=0.686
#matched_seq: 15642 CP000717 Mycobacterium tuberculosis F11, complete genome. Actinobacteridae transcriptional regulatory protein, lacI-family ABR07933 Yes 92.2
#input_seq: SEQ21_20 # 15375 # 15761 # -1 #
ID=21_20;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-10bp;gc_cont=0.654

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#matched_seq:    16230 CP000325    Mycobacterium ulcerans Agy99, complete
genome.    Actinobacteridae conserved hypothetical secreted protein
          ABL03616    Yes    92.19
#input_seq: Seq1_332 # 390257 # 391426 # 1 #
ID=1_332;partial=00;start_type=ATG;rbs_motif=AGxAGG/AGGxGG;rbs_spacer=5-
10bp;gc_cont=0.639
#matched_seq:    16230 CP000325    Mycobacterium ulcerans Agy99, complete
genome.    Actinobacteridae prophage integrase    ABL03228    Yes    91.26
#input_seq: SEQ4_125 # 143596 # 144498 # 1 #
ID=4_125;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-
10bp;gc_cont=0.662
#matched_seq:    16725 CP000854    Mycobacterium marinum M, complete
genome.    Actinobacteridae conserved proteinACC41119    Yes    97.33
#input_seq: Seq1_752 # 856607 # 857344 # -1 #
ID=1_752;partial=00;start_type=ATG;rbs_motif=None;rbs_spacer=None;gc_cont=
0.646
#matched_seq:    18883 CP000611    Mycobacterium tuberculosis H37Ra,
complete genome. Actinobacteridae hexapeptide transferase family protein
          ABQ74848    Yes    91.84
#input_seq: SEQ5_205 # 256240 # 257085 # -1 #
ID=5_205;partial=00;start_type=TTG;rbs_motif=GGAG/GAGG;rbs_spacer=5-
10bp;gc_cont=0.656
#matched_seq:    16725 CP000854    Mycobacterium marinum M, complete
genome.    Actinobacteridae YrbE family protein, YrbE5A ACC42273    Yes
          91.81
#input_seq: Seq1_1102 # 1250530 # 1251189 # 1 #
ID=1_1102;partial=00;start_type=GTG;rbs_motif=None;rbs_spacer=None;gc_cont
=0.626
#matched_seq:    15642 CP000717    Mycobacterium tuberculosis F11, complete
genome.    Actinobacteridae conserved transmembrane protein    ABR07630
          Yes    92.24
#input_seq: SEQ4_30 # 42264 # 43037 # 1 #
ID=4_30;partial=00;start_type=ATG;rbs_motif=GGAGG;rbs_spacer=5-
10bp;gc_cont=0.661
#matched_seq:    88    CP000479    Mycobacterium avium 104, complete
genome.    Actinobacteridae putative class II aldolase    ABK65325    Yes
          91.83
#input_seq: SEQ3_550 # 616803 # 617549 # 1 #
ID=3_550;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-
10bp;gc_cont=0.621
#matched_seq:    16725 CP000854    Mycobacterium marinum M, complete
genome.    Actinobacteridae succinate dehydrogenase (iron-sulfur subunit),
Sdh    ACC38974    Yes    94.76
#input_seq: SEQ9_127 # 139855 # 140481 # -1 #
ID=9_127;partial=00;start_type=ATG;rbs_motif=AGGAG/GGAGG;rbs_spacer=11-
12bp;gc_cont=0.652
#matched_seq:    91    AE016958    Mycobacterium avium subsp.
paratuberculosis str. k10, complete genome.    Actinobacteridae
          hypothetical protein    AAS02808    Yes    94.71
#input_seq: SEQ3_46 # 40867 # 41241 # -1 #
ID=3_46;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=11-
12bp;gc_cont=0.635
#matched_seq:    15762 CP000384    Mycobacterium sp. MCS, complete genome.
          Actinobacteridae SSU ribosomal protein S12P    ABG07098    No    98.39

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_seq:SEQ4_157 # 180884 # 181501 # 1 #
ID=4_157;partial=00;start_type=GTG;rbs_motif=GGAG/GAGG;rbs_spacer=5-
10bp;gc_cont=0.670
#matched_seq: 88 CP000479 Mycobacterium avium 104, complete
genome. Actinobacteridae transcriptional regulator, MerR family protein
ABK68131 Yes 93.66
_seq:Seq1_142 # 175018 # 175335 # -1 #
ID=1_142;partial=00;start_type=GTG;rbs_motif=GGAGG;rbs_spacer=3-
4bp;gc_cont=0.651
#matched_seq: 15642 CP000717 Mycobacterium tuberculosis F11, complete
genome. Actinobacteridae integration host factor mihF ABR05760 Yes
99.05
_seq:Seq1_1079 # 1225443 # 1225802 # 1 #
ID=1_1079;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-
10bp;gc_cont=0.653
#matched_seq: 15642 CP000717 Mycobacterium tuberculosis F11, complete
genome. Actinobacteridae conserved hypothetical protein ABR07613
Yes 96.64
_seq:Seq1_373 # 429078 # 429446 # -1 #
ID=1_373;partial=00;start_type=ATG;rbs_motif=AGGAG;rbs_spacer=5-
10bp;gc_cont=0.653
#matched_seq: 21055 CP001658 Mycobacterium tuberculosis KZN 1435,
complete genome. Actinobacteridae conserved hypothetical protein
ACT24330 Yes 92.62
_seq:SEQ3_542 # 608730 # 609179 # 1 #
ID=3_542;partial=00;start_type=ATG;rbs_motif=None;rbs_spacer=None;gc_cont=
0.633
#matched_seq: 16230 CP000325 Mycobacterium ulcerans Agy99, complete
genome. Actinobacteridae conserved hypothetical protein ABL03758
Yes 91.95
_seq:Seq1_92 # 117518 # 117751 # -1 #
ID=1_92;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-
10bp;gc_cont=0.594
#matched_seq: 18883 CP000611 Mycobacterium tuberculosis H37Ra,
complete genome. Actinobacteridae protein-export membrane protein
ABQ73192 Yes 96.1
_seq:Seq1_378 # 432040 # 432342 # -1 #
ID=1_378;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-
10bp;gc_cont=0.620
#matched_seq: 15762 CP000384 Mycobacterium sp. MCS, complete genome.
Actinobacteridae conserved hypothetical protein ABG08297 No
93.0
_seq:SEQ2_224 # 287984 # 288331 # 1 #
ID=2_224;partial=00;start_type=GTG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-
10bp;gc_cont=0.629
#matched_seq: 88 CP000479 Mycobacterium avium 104, complete
genome. Actinobacteridae acyl carrier protein ABK65172 Yes 98.26
_seq:SEQ9_59 # 64828 # 65124 # -1 #
ID=9_59;partial=00;start_type=ATG;rbs_motif=AGGAG;rbs_spacer=5-
10bp;gc_cont=0.640
#matched_seq: 18883 CP000611 Mycobacterium tuberculosis H37Ra,
complete genome. Actinobacteridae putative esat-6 like protein ABQ74144
Yes 93.88

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_seq:SEQ4_122 # 142287 # 142586 # 1 #
ID=4_122;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-
10bp;gc_cont=0.667
#matched_seq: 16725 CP000854 Mycobacterium marinum M, complete
genome. Actinobacteridae PE family protein, PE19 ACC41116 Yes
94.95
_seq:SEQ4_123 # 142867 # 143163 # 1 #
ID=4_123;partial=00;start_type=GTG;rbs_motif=AGGAG;rbs_spacer=5-
10bp;gc_cont=0.657
#matched_seq: 16725 CP000854 Mycobacterium marinum M, complete
genome. Actinobacteridae EsaT-6 like protein Esx ACC43524 Yes
94.9
_seq:SEQ6_196 # 221559 # 221843 # -1 #
ID=6_196;partial=00;start_type=ATG;rbs_motif=AGGAG;rbs_spacer=5-
10bp;gc_cont=0.660
#matched_seq: 15642 CP000717 Mycobacterium tuberculosis F11, complete
genome. Actinobacteridae Esat-6 like protein esxN (Esat-6 like protein
5) ABR06159 Yes 96.81
_seq:SEQ6_311 # 348465 # 348749 # 1 #
ID=6_311;partial=00;start_type=ATG;rbs_motif=AGGA;rbs_spacer=5-
10bp;gc_cont=0.642
#matched_seq: 16230 CP000325 Mycobacterium ulcerans Agy99, complete
genome. Actinobacteridae EsaT-6 like protein EsxN ABL05326 Yes
92.55
_seq:SEQ5_52 # 74165 # 74377 # 1 #
ID=5_52;partial=00;start_type=GTG;rbs_motif=None;rbs_spacer=None;gc_cont=0
.587
#matched_seq: 15762 CP000384 Mycobacterium sp. MCS, complete genome.
Actinobacteridae ATP-dependent Clp protease adaptor protein ClpS
ABG09958 No 97.14
_seq:SEQ16_63 # 63548 # 63739 # -1 #
ID=16_63;partial=00;start_type=GTG;rbs_motif=AGGAG;rbs_spacer=5-
10bp;gc_cont=0.635
#matched_seq: 16230 CP000325 Mycobacterium ulcerans Agy99, complete
genome. Actinobacteridae ferredoxin FdxD ABL06117 Yes 93.65
_seq:SEQ9_8 # 9472 # 9633 # 1 #
ID=9_8;partial=00;start_type=ATG;rbs_motif=3Base/5BMM;rbs_spacer=13-
15bp;gc_cont=0.642
#matched_seq: 15762 CP000384 Mycobacterium sp. MCS, complete genome.
Actinobacteridae hypothetical protein ABG10925 No 96.23
_seq:SEQ10_21 # 33929 # 34123 # -1 #
ID=10_21;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-
10bp;gc_cont=0.677
#matched_seq: 88 CP000479 Mycobacterium avium 104, complete
genome. Actinobacteridae ribosomal protein L35 ABK68440 Yes 92.19

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