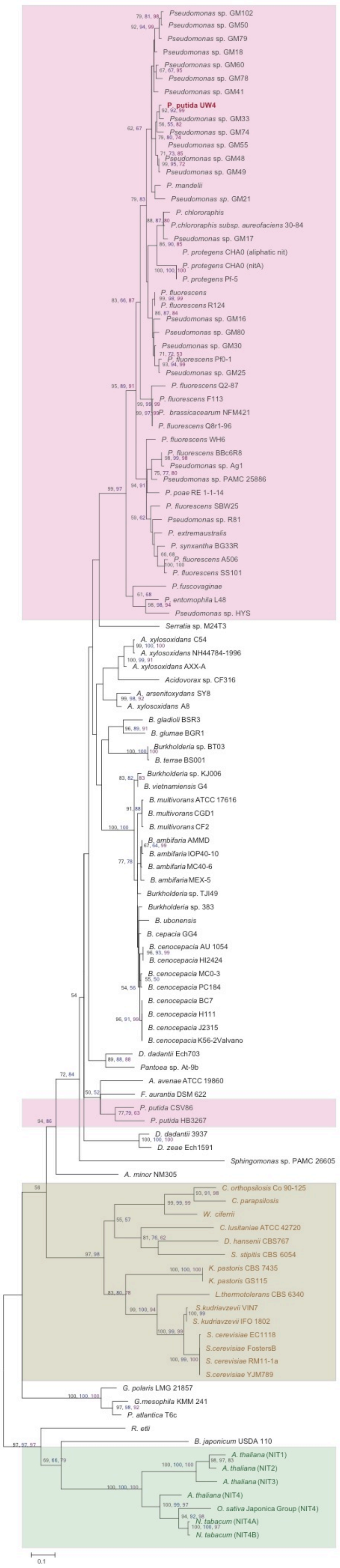

79, 81, 98
Pseudomonas sp. GM102
92, 94, 99
Pseudomonas sp. GM50
Pseudomonas sp. GM79
Pseudomonas sp. GM18
Pseudomonas sp. GM60
67, 67, 95
Pseudomonas sp. GM78
Pseudomonas sp. GM41
P. putida UW4
92, 92, 99
Pseudomonas sp. GM33
62, 67
56, 55, 82
Pseudomonas sp. GM74
79, 80, 74
Pseudomonas sp. GM55
71, 73, 85
Pseudomonas sp. GM48
99, 95, 72
Pseudomonas sp. GM49
P. mandelii
79, 83
Pseudomonas sp. GM21
P. chlororaphis
88, 87, 80
P.chlororaphis subsp. aureofaciens 30-84
Pseudomonas sp. GM17
86, 90, 85
P. protegens CHA0 (aliphatic nit)
P. protegens CHA0 (nitA)
100, 100, 100
P. protegens Pf-5
P. fluorescens
83, 66, 87
99, 98, 99
P. fluorescens R124
86, 87, 84
Pseudomonas sp. GM16
Pseudomonas sp. GM80
Pseudomonas sp. GM30
71, 72, 53
P. fluorescens Pf0-1
93, 94, 99
Pseudomonas sp. GM25
95, 89, 91
P. fluorescens Q2-87
P. fluorescens F113
99, 99, 99
99, 97, 99
P. brassicacearum NFM421
P. fluorescens Q8r1-96
P. fluorescens WH6
P. fluorescens BBc6R8
98, 99, 98
Pseudomonas sp. Ag1
75, 77, 80
Pseudomonas sp. PAMC 25886
99, 97
94, 91
P. poae RE 1-1-14
P. fluorescens SBW25
59, 62
Pseudomonas sp. R81
P. extremaustralis
P. synxantha BG33R
66, 68
P. fluorescens A506
100, 100
P. fluorescens SS101
P. fuscovaginae
61, 68
P. entomophila L48
98, 98, 94
Pseudomonas sp. HYS
Serratia sp. M24T3
A. xylosoxidans C54
99, 100, 100
A. xylosoxidans NH44784-1996
100, 99, 91
A. xylosoxidans AXX-A
Acidovorax sp. CF316
A. arsenitoxydans SY8
99, 98, 92
A. xylosoxidans A8
B. gladioli BSR3
96, 89, 91
B. glumae BGR1
Burkholderia sp. BT03
100, 100, 100
B. terrae BS001
83, 82, 83
Burkholderia sp. KJ006
B. vietnamiensis G4
B. multivorans ATCC 17616
91, 88
B. multivorans CGD1
100, 100
B. multivorans CF2
B. ambifaria AMMD
67, 64, 99
B. ambifaria IOP40-10
77, 78
B. ambifaria MC40-6
B. ambifaria MEX-5
Burkholderia sp. TJI49
Burkholderia sp. 383
B. ubonensis
B. cepacia GG4
B. cenocepacia AU 1054
96, 93, 99
B. cenocepacia HI2424
B. cenocepacia MC0-3
55, 50
54, 56
B. cenocepacia PC184
54
B. cenocepacia BC7
96, 91, 99
B. cenocepacia H111
B. cenocepacia J2315
B. cenocepacia K56-2Valvano
D. dadantii Ech703
89, 88, 88
Pantoea sp. At-9b
72, 84
A. avenae ATCC 19860
50, 52
F. aurantia DSM 622
P. putida CSV86
77,79, 63
94, 86
P. putida HB3267
D. dadantii 3937
100, 100, 100
D. zeae Ech1591
Sphingomonas sp. PAMC 26605
A. minor NM305
56
C. orthopsilosis Co 90-125
93, 91, 98
C. parapsilosis
99, 99, 99
W. ciferrii
55, 57
C. lusitaniae ATCC 42720
81, 76, 62
D. hansenii CBS767
97, 98
S. stipitis CBS 6054
100, 100, 100
K. pastoris CBS 7435
K. pastoris GS115
83, 80, 78
L.thermotolerans CBS 6340
99, 100, 94
S.kudriavzevii VIN7
100, 99
S. kudriavzevii IFO 1802
100, 99, 99
S. cerevisiae EC1118
S.cerevisiae FostersB
100, 99, 100
S. cerevisiae RM11-1a
S.cerevisiae YJM789
G. polaris LMG 21857
100, 100, 100
G.mesophila KMM 241
97, 98, 92
P. atlantica T6c
R. etli
B. japonicum USDA 110
97, 97, 97
A. thaliana (NIT1)
100, 100, 100
98, 97, 83
69, 66, 79
A. thaliana (NIT2)
A. thaliana (NIT3)
100, 100, 100
A. thaliana (NIT4)
100, 99, 97
O. sativa Japonica Group (NIT4)
94, 92, 98
N. tabacum (NIT4A)
100, 100, 97
N. tabacum (NIT4B)
0.1

Figure A1. Nitrilase phylogeny inferred using Maximum-likelihood method. The results of a ML-bootstrap analysis are shown in black, whereas the values in blue and purple are from neighbour-joining and maximum parsimony bootstrap analysis respectively. Plants are shown in green, yeasts in brown and pseudomonads in pink boxes.

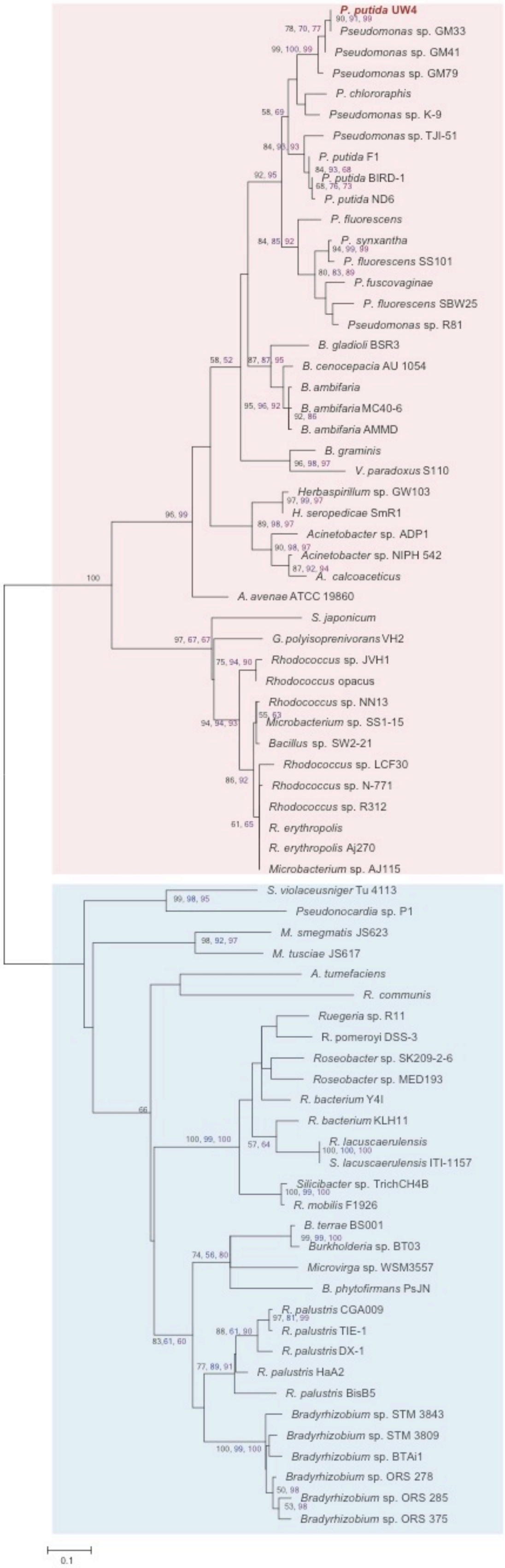
P. putida UW4
90, 91, 99
78, 70, 77
Pseudomonas sp. GM33
99, 100, 99
Pseudomonas sp. GM41
Pseudomonas sp. GM79
P. chlororaphis
58, 69
Pseudomonas sp. K-9
Pseudomonas sp. TJI-51
84, 90, 93
P. putida F1
84, 93, 68
P. putida BIRD-1
68, 76, 73
P. putida ND6
92, 95
P. fluorescens
84, 85, 92
P. synxantha
94, 99, 99
P. fluorescens SS101
80, 83, 89
P. fuscovaginae
P. fluorescens SBW25
Pseudomonas sp. R81
B. gladioli BSR3
58, 52
87, 87, 95
B. cenocepacia AU 1054
B. ambifaria
95, 96, 92
B. ambifaria MC40-6
92, 86
B. ambifaria AMMD
B. graminis
96, 98, 97
V. paradoxus S110
Herbaspirillum sp. GW103
97, 99, 97
96, 99
H. seropedicae SmR1
89, 98, 97
Acinetobacter sp. ADP1
90, 98, 97
Acinetobacter sp. NIPH 542
87, 92, 94
A. calcoaceticus
100
A. avenae ATCC 19860
S. japonicum
97, 67, 67
G. polyisoprenivorans VH2
75, 94, 90
Rhodococcus sp. JVH1
Rhodococcus opacus
Rhodococcus sp. NN13
55, 63
94, 94, 93
Microbacterium sp. SS1-15
Bacillus sp. SW2-21
Rhodococcus sp. LCF30
86, 92
Rhodococcus sp. N-771
Rhodococcus sp. R312
61, 65
R. erythropolis
R. erythropolis Aj270
Microbacterium sp. AJ115
S. violaceusniger Tu 4113
99, 98, 95
Pseudonocardia sp. P1
M. smegmatis JS623
98, 92, 97
M. tusciae JS617
A. tumefaciens
R. communis
Ruegeria sp. R11
R. pomeroyi DSS-3
Roseobacter sp. SK209-2-6
Roseobacter sp. MED193
R. bacterium Y4I
66
R. bacterium KLH11
100, 99, 100
57, 64
R. lacuscaerulensis
100, 100, 100
S. lacuscaerulensis ITI-1157
Silicibacter sp. TrichCH4B
100, 99, 100
R. mobilis F1926
B. terrae BS001
99, 99, 100
Burkholderia sp. BT03
74, 56, 80
Microvirga sp. WSM3557
B. phytofirmans PsJN
R. palustris CGA009
97, 81, 99
88, 61, 90
R. palustris TIE-1
83,61, 60
R. palustris DX-1
77, 89, 91
R. palustris HaA2
R. palustris BisB5
Bradyrhizobium sp. STM 3843
Bradyrhizobium sp. STM 3809
100, 99, 100
Bradyrhizobium sp. BTAi1
Bradyrhizobium sp. ORS 278
50, 98
Bradyrhizobium sp. ORS 285
53, 98
Bradyrhizobium sp. ORS 375
0.1

Figure A2. Nitrile hydratase **α**-subunit phylogeny inferred using ML method. The results of a ML-bootstrap analysis are shown in black, whereas the values in blue and purple are from neighbour-joining and maximum parsimony bootstrap analysis respectively. Iron-type nitrile hydratases are shown in red and cobalt-type in blue boxes

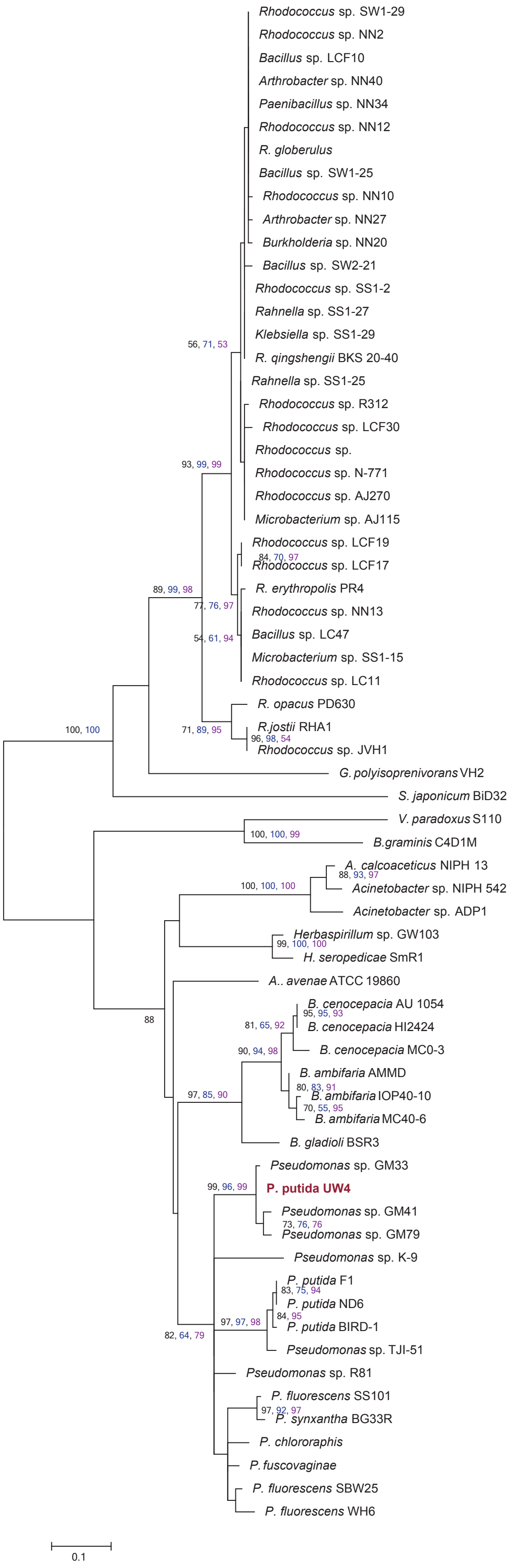
Rhodococcus sp. SW1-29
Rhodococcus sp. NN2
Bacillus sp. LCF10
Arthrobacter sp. NN40
Paenibacillus sp. NN34
Rhodococcus sp. NN12
R. globerulus
Bacillus sp. SW1-25
Rhodococcus sp. NN10
Arthrobacter sp. NN27
Burkholderia sp. NN20
Bacillus sp. SW2-21
Rhodococcus sp. SS1-2
Rahnella sp. SS1-27
Klebsiella sp. SS1-29
56, 71, 53
R. qingshengii BKS 20-40
Rahnella sp. SS1-25
Rhodococcus sp. R312
Rhodococcus sp. LCF30
Rhodococcus sp.
93, 99, 99
Rhodococcus sp. N-771
Rhodococcus sp. AJ270
Microbacterium sp. AJ115
Rhodococcus sp. LCF19
84, 70, 97
Rhodococcus sp. LCF17
89, 99, 98
R. erythropolis PR4
77, 76, 97
Rhodococcus sp. NN13
Bacillus sp. LC47
54, 61, 94
Microbacterium sp. SS1-15
Rhodococcus sp. LC11
R. opacus PD630
100, 100
71, 89, 95
R.jostii RHA1
96, 98, 54
Rhodococcus sp. JVH1
G. polyisoprenivorans VH2
S. japonicum BiD32
V. paradoxus S110
100, 100, 99
B.graminis C4D1M
A. calcoaceticus NIPH 13
88, 93, 97
100, 100, 100
Acinetobacter sp. NIPH 542
Acinetobacter sp. ADP1
Herbaspirillum sp. GW103
99, 100, 100
H. seropedicae SmR1
A.. avenae ATCC 19860
B. cenocepacia AU 1054
95, 95, 93
88
81, 65, 92
B. cenocepacia HI2424
B. cenocepacia MC0-3
90, 94, 98
B. ambifaria AMMD
80, 83, 91
97, 85, 90
B. ambifaria IOP40-10
70, 55, 95
B. ambifaria MC40-6
B. gladioli BSR3
Pseudomonas sp. GM33
99, 96, 99
P. putida UW4
Pseudomonas sp. GM41
73, 76, 76
Pseudomonas sp. GM79
Pseudomonas sp. K-9
P. putida F1
83, 75, 94
P. putida ND6
97, 97, 98
84, 95
P. putida BIRD-1
82, 64, 79
Pseudomonas sp. TJI-51
Pseudomonas sp. R81
P. fluorescens SS101
97, 92, 97
P. synxantha BG33R
P. chlororaphis
P. fuscovaginae
P. fluorescens SBW25
P. fluorescens WH6
0.1

Figure A3. Nitrile hydratase **β**-subunit phylogeny inferred using ML method. The results of a ML-bootstrap analysis are shown in black, whereas the values in blue and purple are from neighbour-joining and maximum parsimony bootstrap analysis respectively.

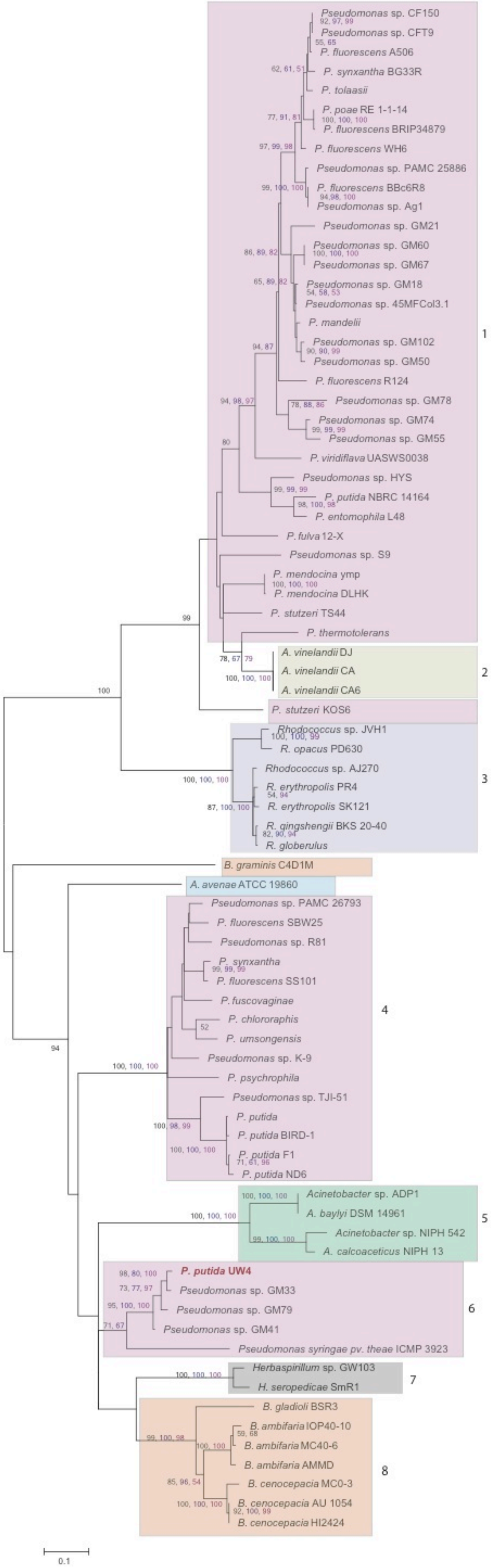
Pseudomonas sp. CF150
92, 97, 99
Pseudomonas sp. CFT9
55, 65
P. fluorescens A506
62, 61, 51
P. synxantha BG33R
P. tolaasii
P. poae RE 1-1-14
77, 91, 81
100, 100, 100
P. fluorescens BRIP34879
97, 99, 98
P. fluorescens WH6
Pseudomonas sp. PAMC 25886
99, 100, 100
P. fluorescens BBc6R8
94,98, 100
Pseudomonas sp. Ag1
Pseudomonas sp. GM21
86, 89, 82
Pseudomonas sp. GM60
100, 100, 100
Pseudomonas sp. GM67
65, 89, 82
Pseudomonas sp. GM18
54, 58, 53
Pseudomonas sp. 45MFCol3.1
P. mandelii
1
94, 87
Pseudomonas sp. GM102
90, 90, 99
Pseudomonas sp. GM50
P. fluorescens R124
94, 98, 97
78, 88, 86
Pseudomonas sp. GM78
Pseudomonas sp. GM74
99, 99, 99
Pseudomonas sp. GM55
80
P. viridiflava UASWS0038
Pseudomonas sp. HYS
99, 99, 99
P. putida NBRC 14164
98, 100, 98
P. entomophila L48
P. fulva 12-X
Pseudomonas sp. S9
P. mendocina ymp
100, 100, 100
P. mendocina DLHK
P. stutzeri TS44
99
P. thermotolerans
78, 67, 79
A. vinelandii DJ
100, 100, 100
A. vinelandii CA
2
A. vinelandii CA6
100
P. stutzeri KOS6
Rhodococcus sp. JVH1
100, 100, 99
R. opacus PD630
Rhodococcus sp. AJ270
100, 100, 100
R. erythropolis PR4
54, 94
3
87, 100, 100
R. erythropolis SK121
R. qingshengii BKS 20-40
82, 90, 94
R. globerulus
B. graminis C4D1M
A. avenae ATCC 19860
Pseudomonas sp. PAMC 26793
P. fluorescens SBW25
Pseudomonas sp. R81
P. synxantha
99, 99, 99
P. fluorescens SS101
P. fuscovaginae
4
P. chlororaphis
52
P. umsongensis
94
Pseudomonas sp. K-9
100, 100, 100
P. psychrophila
Pseudomonas sp. TJI-51
P. putida
100, 98, 99
P. putida BIRD-1
100, 100, 100
P. putida F1
71, 61, 96
P. putida ND6
100, 100, 100
Acinetobacter sp. ADP1
100, 100, 100
A. baylyi DSM 14961
5
Acinetobacter sp. NIPH 542
99, 100, 100
A. calcoaceticus NIPH 13
98, 80, 100
P. putida UW4
73, 77, 97
Pseudomonas sp. GM33
95, 100, 100
Pseudomonas sp. GM79
6
71, 67
Pseudomonas sp. GM41
Pseudomonas syringae pv. theae ICMP 3923
100, 100, 100
Herbaspirillum sp. GW103
7
H. seropedicae SmR1
B. gladioli BSR3
B. ambifaria IOP40-10
99, 100, 98
59, 68
100, 100
B. ambifaria MC40-6
B. ambifaria AMMD
8
85, 96, 54
B. cenocepacia MC0-3
100, 100, 100
B. cenocepacia AU 1054
92, 100, 99
B. cenocepacia HI2424
0.1

Figure A4. P47K activator protein phylogeny inferred using the ML method. The results of a ML-bootstrap analysis are shown in black, whereas the values in blue and purple are from neighbor-joining and maximum parsimony bootstrap analysis respectively. Each bacterial species is represented by a different coloured box and clusters are numbered.