

Table 3. Signature Proteins specific for *Actinobacteria*, except *Bifidobacterium longum*
Gao, B., Parmanathan, R. and Gupta, R.S. (2006) Antonie van Leeuwenhoek, 90(1):69-91.

(a)

Protein	ML0762 [NP_301591]	ML0876 [NP_301662]	ML1027 [NP_301760]	ML1041 [NP_301768]	ML1176 [NP_301858]	ML1781 [NP_302210]
Length	165 aa	139 aa	157 aa	196 aa	119 aa	170 aa
Possible function	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown
<i>Mycobacterium leprae</i>	1e-87 (165)	3e-58 (139)	7e-89 (157)	3e-102 (196)	8e-66 (119)	1e-95 (170)
<i>Mycobacterium tuberculosis</i>	7e-59 (163)	2e-54 (139)	9e-71 (161)	5e-87 (210)	1e-40 (120)	6e-90 (177)
<i>Mycobacterium avium</i>	5e-65 (165)	9e-51 (139)	4e-68 (161)	5e-85 (211)	2e-52 (116)	2e-90 (?) ²
<i>Mycobacterium bovis</i>	7e-59 (163)	2e-54 (139)	9e-71 (161)	5e-87 (210)	1e-40 (120)	2e-89 (177)
<i>Nocardia farcinica</i>	8e-31 (125)	2e-36 (138)	1e-45 (176)	2e-6 (183)	8e-26 (127)	6e-56 (181)
<i>Corynebacterium glutamicum</i>	2e-20 (130)	2e-14 (143)	5e-26 (192)	5e-48 (208)	8e-15 (118)	---
<i>Corynebacterium efficiens</i>	1e-21 (151)	1e-13 (143)	5e-26 (183)	6e-49 (205)	1e-13 (173)	---
<i>Corynebacterium diphtheriae</i>	4e-19 (137)	1e-12 (143)	9e-26 (170)	1e-46 (193)	5e-12 (118)	---
<i>Corynebacterium jeikeium</i>	4e-13 (172)	2e-16 (143)	7e-25 (161)	2e-42 (207)	4e-11 (121)	---
<i>Streptomyces avermitilis</i>	1e-20 (157)	1e-12 (132)	5e-12 (153)	5e-38 (223)	2e-13 (112)	2e-38 (164)
<i>Streptomyces coelicolor</i>	6e-21 (140)	2e-10 (132)	4e-12 (154)	3e-32 (238)	1e-12 (109)	2e-36 (164)
<i>Thermobifida fusca</i>	4e-16 (148)	3e-16 (141)	---	8e-32 (193)	8e-09 (141)	4e-39 (197)
<i>Propionibacterium acnes</i>	1e-14 (153)	2e-06 (131)	2e-04 (176)	1e-21 (189)	2e-10 (190)	9e-20 (165)
<i>Nocardiooides sp.</i>	1e-16 (119)	1e-18 (132)	2e-14 (153)	5e-30 (209)	2e-07 (115)	3e-42 (208)
<i>Frankia sp. Ccl3</i>	1e-17 (147)	2e-09 (133)	---	2e-22 (312)	4e-05 (140)	4e-34 (180)
<i>Frankia sp. EAN1pec</i>	1e-17 (170)	3e-08 (133)	---	5e-23 (299)	1e-08 (142)	7e-33 (177)
<i>Kineococcus radiotolerance</i>	4e-19 (133)	7e-19 (133)	5e-07 (?)	5e-23 (208)	1e-10 (127)	1e-33 (210)
<i>Brevibacterium linens</i>	2e-12 (124)	3e-10 (133)	1e-08 (151)	3e-24 (207)	3e-08 (145)	2e-23 (119)
<i>Arthrobacter sp.</i>	1e-20 (129)	5e-15 (133)	2e-11 (174)	2e-26 (202)	7e-08 (170)	8e-40 (167)
<i>Leifsonia xyli</i>	1e-15 (70)	3e-07 (110)	2e-13 (148)	4e-27 (198)	9e-09 (147)	1e-33 (167)
<i>Tropheryma whipplei</i> Twist	7e-05 (110)	2e-08 (139)	2e-12 (155)	4e-15 (207)	0.005 (145)	4e-25 (164)
<i>Tropheryma whipplei</i> TW08/27	---	2e-08 (139)	2e-12 (155)	4e-15 (183)	0.005 (145)	4e-25 (160)
Non-Actinobacteria		---	0.73 (203)	2.2 (623)	0.046 (447)	
	See note 1	---	<i>Cupriavidus necator</i>	<i>Shewanella baltica</i>	<i>Ralstonia metallidurans</i>	See note 2

(b)

Actinobacterial signature proteins which are not present in <i>B. longum</i> and <i>T. whipplei</i>	Actinobacterial signature proteins which are not present in <i>B. longum</i> , <i>T. whipplei</i> and <i>L. xyli</i>	Actinobacterial signature proteins mainly lost in <i>B. longum</i> , <i>T. whipplei</i> , <i>L. xyli</i> and <i>Corynebacterium</i> species
ML1485 [NP_302044] oxidoreductase	ML0169 [NP_301248] ML0284 [NP_301324]	ML0115 [NP_301211] ML1299 [NP_301933]
ML2075 [NP_302384] MerR	ML0540 [NP_301459] mlHF	Tfu_0030 [YP_288091]
ML0234 [NP_301294] Lsr2	ML0561 [NP_301475]	Tfu_0751 [YP_288812]
ML0898 [NP_301682]	ML0816 [NP_301622]	acetyltransferase
ML0904 [NP_301687]	ML0899 [NP_301683]	Tfu_1240 [YP_289301]
ML0986 [NP_301731]	ML1300 [NP_301934]	Tfu_1340 [YP_289401]
ML1067 [NP_301785]	ML1706 [NP_302175]	
ML1165 [NP_301850] Clp	ML2030 [NP_302360] Rpf2	
ML1166 [NP_301851]	ML2428A [NP_302573]	
ML1927 [NP_302300]	ML2442 [NP_302583]	
ML2156 [NP_302419]	ML2446 [NP_302585] lipoprotein	
Lxx03620 [YP_061480]	ML2687 [NP_302714]	
Lxx08190 [YP_061831]	Tfu_0365 [YP_288426]	
Lxx10090 [YP_061981] RDD		
Lxx16410 [YP_062531] Abi		
Tfu_0515 [YP_288576]		
Tfu_2498 [YP_290554]		

Table 3(b): The protein ID number starting with Lxx or Tfu represents query protein from the genome of *L. xyli* subsp. *xyli* str. CTCB07 (Lxx) or *T. fusca* YX (Tfu). The possible cellular functions of some of these proteins are noted. For other proteins the cellular functions are not known. The E values for these proteins are provided in the Supplemental Table 1(b), (c), and (d).

Note 1. A homologue to ML0762 is also found in *M. magnetotacticum* with E-value of 1e-18 (117 aa) [ZP_00049347]; the next non-actinobacterial hit is *Oryza sativa* with E-value of 0.50 (130 aa).

Note 2. A homologue to ML1781 is also found in *M. magnetotacticum* MS-1 with E-value of 8e-29 (138 aa) [ZP_00051058]; the next non-actinobacterial hit is *Pan troglodytes* with E-value of 0.92 (1491 aa).