

Additional file 1: Gene ID and Possible Function of ASP1 homologues and its neighboring genes in all sequenced actinobacterial strains.

Actinobacterial strain	Left to ASP1		ASP1	Right to APS1	
<i>Streptomyces coelicolor</i> A3(2)	SCO1995 [Unkown]	SCO1996 [CoaE]	SCO1997 [Unkown]	SCO1998 [RpsA]	SCO1999 [SAM]
<i>Streptomyces avermitilis</i> MA-4680	SAV_6232 [SAM]	SAV_6233 [RpsA]	SAV_6234 [Unkown]	SAV_6235 [CoaE]	SAV_6236 [Unkown]
<i>Streptomyces griseus</i> subsp. <i>Griseus</i> NBRC 13350	SGR_5534 [RpsA]	SGR_5535 [Unkown]	SGR_5536 [Unkown]	SGR_5537 [CoaE]	SGR_5538 [Unkown]
<i>Streptomyces</i> sp. Mg1	SSAG_03956 [Unkown]	SSAG_03957 [CoaE]	SSAG_03958 [Unkown]	SSAG_03959 [RpsA]	SSAG_03960 [SAM]
<i>Thermobifida fusca</i> YX	Tfu_0924 [ADP_ribosyl_GH]	Tfu_0925 [P-loop]	Tfu_0926 [Unkown]	Tfu_0927 [PyrD]	Tfu_0928 [FRK]
<i>Salinispora arenicola</i> CNS-205	Sare_1720 [sulfotransferase]	Sare_1721 [exonuclease]	Sare_1722 [Unkown]	Sare_1723 [ABM]	Sare_1724 [Unkown]
<i>Salinispora tropica</i> CNB-440	Strop_1735 [sulfotransferase]	Strop_1736 [exonuclease]	Strop_1737 [Unkown]	Strop_1738 [Unkown]	Strop_1739 [GDSL]
<i>Kineococcus radiotolerans</i> SRS30216	Krad_1507 [LysM]	Krad_1508 [ATP-cone]	Krad_1509 [Unkown]	Krad_1510 [Unkown]	Krad_1511 [regulator]
<i>Rhodococcus jostii</i> RHA1	RHA1_ro06803 [helicase]	RHA1_ro06804 [PldB]	RHA1_ro06805 [Unkown]	RHA1_ro06806 [Lactamase]	RHA1_ro06807 [Unkown]
<i>Nocardia farcinica</i> IFM 10152	nfa37810 [Unkown]	nfa37820 [Unkown]	nfa37830 [Unkown]	nfa37840 [helicase]	nfa37850 [LysA]
<i>Frankia</i> sp. Ccl3	Franci3_1245 [Unkown]	Franci3_1246 [Unkown]	Franci3_1247 [Unkown]	Franci3_1248 [Unkown]	Franci3_1249 [Mem_trans]
<i>Frankia alni</i> ACN14a	FRAAL1974 [HisKA]	FRAAL1975 [Unkown]	FRAAL1976 [Unkown]	FRAAL1977 [Unkown]	FRAAL1978 [DFR]
<i>Frankia</i> sp. EAN1pec	Franean1_5206 [deacetylase]	Franean1_5207 [Unkown]	Franean1_5208 [Unkown]	Franean1_5209 [PhaG]	Franean1_5210 [Unkown]
<i>Acidothermus cellulolyticus</i> 11B	Acel_0026 [ZntA]	Acel_0027 [Lipoprotein]	Acel_0028 [Unkown]	Acel_0029 [GlpA]	Acel_0030 [amidohydrolase]
<i>Mycobacterium abscessus</i>	MAB_3031c [Unkown]	MAB_3032 [SthA]	MAB_3033 [Unkown]	MAB_3034 [PldB]	MAB_3035 [Unkown]
<i>Mycobacterium</i> sp. MCS	Mmcs_2171 [PhzC]	Mmcs_2172 [PldB]	Mmcs_2173 [Unkown]	Mmcs_2174 [Unkown]	Mmcs_2175 [Unkown]
<i>Mycobacterium</i> sp. KMS	Mkms_2217 [PhzF]	Mkms_2218 [PldB]	Mkms_2219 [Unkown]	Mkms_2220 [Unkown]	Mkms_2221 [Unkown]
<i>Mycobacterium</i> sp. JLS	Mjls_2160 [PhzF]	Mjls_2161 [PldB]	Mjls_2162 [Unkown]	Mjls_2163 [Unkown]	Mjls_2164 [Unkown]
<i>Mycobacterium vanbaalenii</i> PYR-1	Mvan_2444 [PhzF]	Mvan_2445 [PldB]	Mvan_2446 [Unkown]	Mvan_2447 [Unkown]	Mvan_2448 [SthA]
<i>Mycobacterium avium</i> subsp. <i>Paratuberculosis</i>	MAP2829 [SthA]	MAP2830c [Unkown]	MAP2831 [Unkown]	MAP2832 [PldB]	MAP2833c [Unkown]
<i>Mycobacterium avium</i> 104	MAV_3606 [SthA]	MAV_3607 [Unkown]	MAV_3608 [Unkown]	MAV_3609 [PldB]	MAV_3610 [PhzC]
<i>Mycobacterium gilvum</i> PYR-GCK	Mflv_3949 [FeoA]	Mflv_3950 [Unkown]	Mflv_3951 [Unkown]	Mflv_3952 [PldB]	Mflv_3953 [PhzF]
<i>Mycobacterium leprae</i> TN	ML1007 [Unkown]	ML1008 [Unkown]	ML1009 [Unkown]	ML1010 [Unkown]	ML1011 [Unkown]
<i>Mycobacterium marinum</i> M	MMAR_1996 [PhzC]	MMAR_1997 [PldB]	MMAR_1998 [Unkown]	MMAR_1999 [Unkown]	MMAR_2000 [SthA]
<i>Mycobacterium smegmatis</i> str. MC2 155	MSMEG_2744 [PhzC]	MSMEG_2745 [Unkown]	MSMEG_2746 [Unkown]	MSMEG_2747 [Unkown]	MSMEG_2748 [SthA]
<i>Mycobacterium bovis</i> AF2122/97	Mb2731c [Unkown]	Mb2732 [SthA]	Mb2733 [Unkown]	Mb2734 [PldB]	Mb2735 [PhzC]
<i>Mycobacterium bovis</i> BCG str. Pasteur 1173P2	BCG_2725c [Unkown]	BCG_2726 [SthA]	BCG_2727 [Unkown]	BCG_2728 [PldB]	BCG_2729 [PhzC]
<i>Mycobacterium ulcerans</i> Agy99	MUL_3355 [Transposase]	MUL_3356 [Unkown]	MUL_3357 [Unkown]	MUL_3358 [PldB]	MUL_3359 [PhzC]
<i>Mycobacterium tuberculosis</i> H37Rv	Rv2712c [Unkown]	Rv2713 [SthA]	Rv2714 [Unkown]	Rv2715 [PldB]	Rv2716 [PhzC]
<i>Mycobacterium tuberculosis</i> H37Ra	MRA_2740 [Unkown]	MRA_2741 [SthA]	MRA_2742 [Unkown]	MRA_2743 [PldB]	MRA_2744 [PhzC]
<i>Mycobacterium tuberculosis</i> CDC1551	MT2785 [Unkown]	MT2786 [SthA]	MT2787 [Unkown]	MT2788 [PldB]	MT2789 [PhzC]
<i>Nocardioides</i> sp. JS614	Noca_2850 [TesB]	Noca_2851 [TesB]	Noca_2852 [Unkown]	Noca_2853 [thiolase]	Noca_2854 [FadJ]
<i>Renibacterium salmoninarum</i> ATCC 33209	RSal33209_2427 [Unkown]	RSal33209_2428 [MFS]	RSal33209_2429 [Unkown]	RSal33209_2430 [Pep]	RSal33209_2431 [SthA]
marine actinobacterium PHSC20C1*	N/A	N/A	A20C1_03668 [Unkown]	N/A	N/A
<i>Janibacter</i> sp. HTCC2649*	N/A	N/A	JNB_00545	N/A	N/A

			[Unkown]		
Arthrobacter aureescens TC1	AAur_1756 [SthA]	AAur_1757 [Pep]	AAur_1758 [Unkown]	AAur_1759 [MFS]	AAur_1760 [Unkown]
Arthrobacter sp. FB24	Arth_1612 [SthA]	Arth_1613 [Pep]	Arth_1614 [Unkown]	Arth_1615 [MFS]	Arth_1616 [Unkown]
Leifsonia xyli subsp. xyli str. CTCB07	Lxx10150 [SthA]	Lxx10160 [Pep]	Lxx10170 [Unkown]	Lxx10180 [MFS]	Lxx101902 [Sigma70]
Clavibacter michiganensis subsp. sepedonicus	CMS_1625 [SthA]	CMS_1626 [Pep]	CMS_1627 [Unkown]	CMS_1628 [MFS]	CMS_1629 [Sigma70]
Clavibacter michiganensis subsp. michiganensis	CMM_1642 [SthA]	CMM_1643 [Pep]	CMM_1644 [Unkown]	CMM_1645 [MFS]	CMM_1646 [Sigma70]
Micrococcus luteus NCTC 2665*	N/A	N/A	MlutDRAFT_2379 [Unkown]	N/A	N/A
Propionibacterium acnes KPA171202	PPA1097 [Unkown]	PPA1098 [DnaK]	PPA1099 [Unkown]	PPA1100 [cyclophilin]	PPA1101 [PldB]
Kocuria rhizophila DC2201	KRH_14370 [Unkown]	KRH_14380 [MFS]	KRH_14390 [Unkown]	KRH_14400 [Pep]	KRH_14410 [SthA]
Corynebacterium glutamicum ATCC 13032	NCgl1846 [GalE]	NCgl1847 [Unkown]	NCgl1848 [Unkown]	NCgl1849 [helicase]	NCgl1850 [OxyR]
Corynebacterium glutamicum R	cgR_1751 [Unkown]	cgR_1752v [Unkown]	cgR_1753 [Unkown]	cgR_1754 [helicase]	cgR_1755 [OxyR]
Corynebacterium diphtheriae NCTC	DIP1415 [GalE]	DIP1416 [Unkown]	DIP1417 [Unkown]	DIP1418 [helicase]	DIP1419 [Unkown]
Corynebacterium urealyticum DSM 7109	cur_0888 [OxyR]	cur_0889 [helicase]	cur_0890 [Unkown]	cur_0891 [Unkown]	cur_0892 [GalE]
Corynebacterium jeikeium K411	jk1098 [GalE]	jk1099 [Unkown]	jk1100 [Unkown]	jk1101 [helicase]	jk1102 [OxyR]
Corynebacterium efficiens YS-314	CE1813 [GalE]	CE1814 [Unkown]	CE1815 [Unkown]	CE1816 [helicase]	CE1817 [OxyR]
Actinomyces odontolyticus ATCC 17982	ACTODO_01569 [Pol_IV_kappa]	ACTODO_01570 [Unkown]	ACTODO_01571 [Unkown]	ACTODO_01572 [helicase]	ACTODO_01573 [dehydrogenase]
Rubrobacter xylanophilus DSM 9941	Rxyl_1075 [asparaginase]	Rxyl_1076 [Aat]	Rxyl_1077 [Unkown]	Rxyl_1078 [Unkown]	Rxyl_1079 [PP-loop]
Saccharopolyspora erythraea NRRL 2338	SACE_2231 [deaminase]	SACE_2232 [chitinase]	SACE_2233 [Unkown]	SACE_2234 [Unkown]	SACE_2235 [HAD]
Brevibacterium linens BL2	BlinB01000023 [RecB]	BlinB01000024 [HAD]	BlinB01000025 [Unkown]	BlinB01000026 [CysRS]	BlinB01000027 [Unkown]
Bifidobacterium adolescentis L2-32*	BIFADO_01159 [Unkown]	BIFADO_01160 [BacA]	BIFADO_01161 [Unkown]	N/A	N/A
Bifidobacterium longum NCC2705	BL0720 [Unkown]	BL0721 [BacA]	BL0722 [Unkown]	BLt06 [tRNA-Gly]	BLt07 [tRNA-Cys]
Bifidobacterium adolescentis ATCC 15703	BAD_t0041 [tRNA-Ala]	BAD_t0042 [tRNA-Gln]	BAD_0824 [Unkown]	BAD_0825 [BacA]	BAD_0826 [Unkown]
Bifidobacterium longum DJO10A	BLD_0445 [FRK]	BLD_0446 [BacA]	BLD_0447 [Unkown]	BLD_t0006 [tRNA-Gly]	BLD_t0007 [tRNA-Cys]
Bifidobacterium animalis subsp. lactis HN019*	N/A	N/A	BIFLAC_03242 [Unkown]	N/A	N/A
Bifidobacterium dentium ATCC 27678	N/A	BIFDEN_02061 [Unkown]	BIFDEN_02062 [Unkown]	BIFDEN_02063 [BacA]	BIFDEN_02064 [FRK]
Tropheryma whipplei str. Twist	TWT315 [BacA]	TWT316 [CysRS]	TWT317 [Unkown]	TWT318 [SAM]	TWT319 [FKBP_C]
Tropheryma whipplei TW08/27	TW453 [FKBP_C]	TW454 [SAM]	TW455 [Unkown]	TW456 [CysRS]	TW457 [BacA]

Note: * : incomplete genome.

The possible function of each protein is indicated in brackets below the gene ID and abbreviations for protein functions are as follows: Aat: leucyl/phenylalanyl-tRNA--protein transferase; ABM: Antibiotic biosynthesis monooxygenase; ADP_riboseyl_GH: ADP-ribosylglycohydrolase; ATP-cone: ATP-cone domain-containing protein; BacA: Bacitracin resistance protein; CoaE: dephospho-CoA kinase; CysRS: Cysteinyl-tRNA synthetase; DnaK: Molecular chaperone; DFR: dihydroflavonol-4-reductase; FadJ: multifunctional fatty acid oxidation complex subunit alpha; FeoA: Iron dependent repressor; FKBP_C: FKBP-type peptidyl-prolyl cis-trans isomerase; FRK: fructokinase; GalE: UDP-glucose 4-epimerase; GDSL: GDSL family lipase; GlpA: Glycerol-3-phosphate dehydrogenase; HAD: Haloacid dehalogenase-like hydrolase; HisKA: Histidine kinase; HrdB: RNA polymerase sigma factor; LysA: Diaminopimelate decarboxylase; LysM: peptidoglycan-binding LysM; Mem_trans: Membrane transport protein; MFS: Major Facilitator Superfamily; OxyR: DNA-binding transcriptional regulator; Pep: Cytosol aminopeptidase family; PhaG: monovalent cation/proton antiporter, MnhG/PhaG subunit; PhzC/PhzF: phenazine biosynthesis protein; PldB: Lysophospholipase; P-loop: P-loop containing Nucleoside Triphosphate Hydrolases; Pol_IV_kappa: a member of the Y-family of DNA polymerases; PyrD: Dihydroorotate dehydrogenase; RpsA: 30S ribosomal protein S1; SAM: SAM-dependent methyltransferase; SthA: soluble pyridine nucleotide transhydrogenase; TesB: palmitoyl-CoA hydrolase; ZntA: Cation transport ATPase.