



**Fig. S2.** Phylogenetic tree of MelC2 homologs.

The following protein sequences are from NCBI annotated databases with accession numbers. MelC2 from *Streptomyces*: *S. clavuligerus* ATCC 27064, ABJH01000362; *Streptomyces* sp. C (1), ACEW01000543; *Streptomyces* sp. C (2), ACEW01000650; *S. viridochromogenes* DSM 40736, ACEZ01000111; *S. sviceps* ATCC 29083, ABJJ01000408. MelD2 from *Streptomyces*: *S. lividans* TK24, ACEY01000212; *S. sviceps* ATCC 29083, ABJJ01000469; *S. viridochromogenes* DSM 40736, ACEZ01000014; *S. ghanaensis* ATCC 14672, ABYA01000366; *S. griseoflavus* Tu4000, ACFA01000589; *Streptomyces* sp. SPB78, ACEU01000672; *Streptomyces* sp. SPB74, ABJG01000510; *Streptomyces* sp. C (1), ACEW01000540; *Streptomyces* sp. C (2), ACEW01000097; *S. clavuligerus* ATCC 27064, ABJH01000487; *S. pristinaespiralis* ATCC 25486, ABJI01000520; *S. rishiriensis* MJ773-88K4, ABX71084; *S. roseosporus* NRRL 11379, ABYX01000271; *S. roseosporus* NRRL 15998, ABYB01000364; *S. tenjimariensis* ATCC 31603, CAI59989. Homologs from other bacteria: *Rubrobacter xylanophilus* DSM 9941, NC\_008148; *Frankia* sp. EAN1pec, NC\_009921; *Frankia alni* ACN14a, NC\_008278; *Frankia* sp. Ccl3, NC\_007777. The remaining (indicated by an asterisk) are unannotated sequences identified in tblastn search of microbial genomes. The construction of the tree was as described in Fig. 1.