

Figure S3. Neighbour-joining tree showing the relationship of *Streptomyces kebangsaanensis* based on full 16S rRNA gene sequence (1599 nt) with *Microbispora corollina* D65T acts as the outgroup. Asterisks indicate branches of the tree that were also recovered by using maximum-parsimony and maximum-likelihood algorithms. Numbers at the nodes indicate levels of bootstrap support based on 1000 resampled datasets. Bar represents 0.01 changes per nucleotide.