Figure S3. Homologies of enoyl-CoA hydratase/aldolase from *Streptomyces* sp.
V-1 with the CoA hydratases/aldolases from different organisms. A. The amino acid sequence of enoyl-CoA hydratase/aldolase from *Streptomyces* sp. V-1 deduced from *ech* gene (i) was aligned to: the amino acid sequence of (ii) the *p*-hydroxycinnamoyl CoA hydratase/lyase from *Amycolatopsis* sp. ATCC 39116 [8], (iii) the enoyl-CoA hydratase/aldolase from *Amycolatopsis* sp. HR167 [10], (iv) the
p-hydroxycinnamoyl CoA hydratase/lyase from *Pseudonocardia* sp. P1 (unpublished data), (v) the 2-ketocyclohexanecarboxyl-CoA hydratase from *Rhodococcus opacus* PD630 [29], (vi) the p-hydroxycinnamoyl CoA hydratase/lyase from *Pseudomonas fluorescens* AN103 [13], and (vii) the enoyl-CoA hydratase from *Pseudomonas* sp. HR199 [7]. Amino acids are specified by standard one-letter abbreviations. Dashes indicate gaps introduced into the sequences to improve the alignment. **B.** The relationship between the enoyl-CoA hydratase/aldolase from *Streptomyces* sp. V-1 and the proteins in panel A was displayed as a phylogenetic tree, which was constructed on the basis of the Neighbor-Joining (NJ) method using the ClustalX and MEGA 5.0 softwares. The bar indicates 10% difference in amino acid sequence. The number at the branch point represents the percentage of 1,000 bootstrap repetitions.