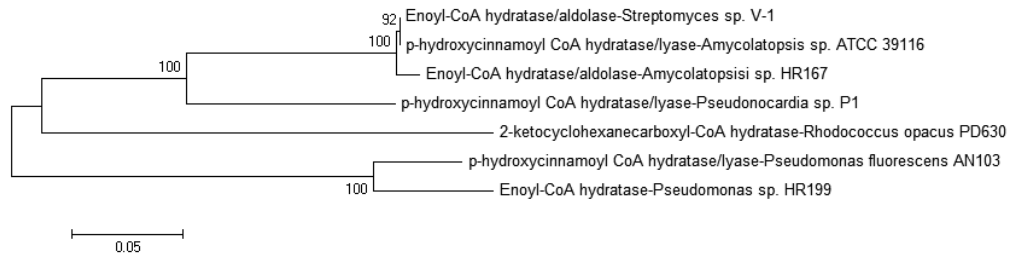


A

i	MSTAVGNRVRTEPWGETVLFVDFEG--IAWVMLNRPDKRNMNPTLNDEMVRVLDHLEGD	59
ii	MSTAVGNRVRTEPWGETVLFVDFEG--IAWVMLNRPDKRNMNPTLNDEMVRVLDHLEGD	59
iii	MSTAVGNRVRTEPWGETVLFVDFEG--IAWVMLNRPDKRNMNPTLNDEMVRVLDHLEGD	59
iv	-----MTEPWGNTVLFVDFEG--IAWVSLNRPDKRNMNPTLNDEMVFATLDALEGD	49
v	MSDNIN-----EPWGNVTLVDFEHRIAWVRFNRPDKRNMNPTLNREMFATLHLEDD	54
vi	MS-----TYEGRWKTVKVEIEDG--IAFVILNRPDKRNMNPTLNREIMDVLETLLEQD	51
vii	-----MSPTLNREIMVEVLELEQD	19
	*.**** ** .*: ** *	
i	DRCRVLVTGAGESFSAGMDLKEYFREVDATGSTAVQIKVRRASAEWQWKRLANWSKPTI	119
ii	DRCRVLVTGAGESFSAGMDLKEYFREVDATGSTAVQIKVRRASAEWQWKRLANWSKPTI	119
iii	DRCRVLVTGAGESFSAGMDLKEYFREVDATGSTAVQIKVRRASAEWQWKRLANWSKPTI	119
iv	PRCRVLVTGSGDAFVAGMDLKEYFREVDATGSTAVQIKVRRASAEWQWKRLANWSKPTV	109
v	DRCVVVLTGSDDAFVAGMDLKEYFRETDGK--PRSVQHRVREGTNNQYRKLNLNAYKPTI	113
vi	PAAGVLTGAGEAWTAGMDLKEYFREVDAG--PEILQEKIRREASQWQWKRLLRMYAKPTI	110
vii	ADARVLTGAGESWTAGMDLKEYFRETDAG--PEILQEKIRREASTWQWKRLLRMYTKPTI	78
	. :*****. :.:*****.* :* :.* .: **: * :*****	
i	AMVNGWCFGGAFVPLVACDLAFADEDARFGLSEVNWGIPPGVVSRLAATVPQRDALYY	179
ii	AMVNGWCFGGAFVPLVACDLAFADEDARFGLSEVNWGIPPGVVSRLAATVPQRDALYY	179
iii	AMVNGWCFGGAFVPLVACDLAFADEDARFGLSEVNWGIPPGVVSRLAATVPQRDALYY	179
iv	AMVNGWCFGGAFVPLVACDLAISEDAEQYGLSEINWGIIPPGVVSRLAATVSRDALYF	169
v	AMVNGWCFGGAFVPLVSCDLAISEDAEQYGLSEINWGIIPPGVVSRLAATVSRDALYF	173
vi	AMVNGWCFGGGFVPLVACDLAICADEATFGLSEINWGIIPPGVVSRLAAMADTVGHRGSLYY	170
vii	AMVNGWCFGGGFVPLVACDLAICADEATFGLSEINWGIIPPGVVSRLAAMADTVGHRGSLYY	138
	*****. * **:****. :.* :*****. **.*:*** * :* :***	
i	IMTGEPPDGRRAEMRLVNEALPADRLRERTREVALKLSMNGVVLHAAKTGYKIAQEMP	239
ii	IMTGEPPDGRRAEMRLVNEALPADRLRERTREVALKLSMNGVVLHAAKTGYKIAQEMP	239
iii	IMTGEPPDGRRAEMRLVNEALPADRLRERTREVALKLSMNGVVLHAAKTGYKIAQEMP	239
iv	IMTGEPPDGRRAEMRLVNEAVPAGRLRERTREVALKLSMNPVVMRAAKVGYKLAQEMP	229
v	IMTGQHPDGKRAEMRLVNEAVPADQLRARTIELALQLTSLSGWVVRGAKMGFRHSRLMS	233
vi	IMTGKTFGGQAAEMGLVNESVPLAQLREVTIELARNLLEKNPVVLRRAKHGFKRCRELT	230
vii	IMTGKTFGGQAAEMGLVNSVPLAELRSVTVELAQNLLDKNPVVLRRAKIGFKRCRELT	198
	***: *. * : * ***:.* ** * :* :* . . * :. ** * :. : . :	
i	WEQAEDYLYAKLDQSQFADKAGARAKGLTQFLDQKSYRPLSAFDPEK--	287
ii	WEQAEDYLYAKLDQSQFADKAGARAKGLTQFLDQKSYRPLSAFDPEK--	287
iii	WEQAEDYLYAKLDQSQFADKAGARAKGLTQFLDQKSYRPLSAFDPEK--	287
iv	WEQAEDYLYAKLEQSQFLDAERGRQGLSQFLDDKSYRPLSAYASE--	276
v	WEAAEDYLYAKHDQAILFDTD--AREQGMTQFLDDKTYRPLGTYATTAE	281
vi	WEQNEEDYLYAKLDQSRLLDTEGGREGMKQFLDDKSIKPLGQAYKR---	276
vii	WEQNEEDYLYAKLDQSRLLDTEGGREGMKQFLDDKSIKPLGQTYKR---	244
	** ***** :* : * . * :.* :*****: :*** :	

B



1

2

3 **Figure S3. Homologies of enoyl-CoA hydratase/aldolase from *Streptomyces* sp.**

4 **V-1 with the CoA hydratases/aldolases from different organisms. A.** The amino

5 acid sequence of enoyl-CoA hydratase/aldolase from *Streptomyces* sp. V-1 deduced

6 from *ech* gene (i) was aligned to: the amino acid sequence of (ii) the

7 *p*-hydroxycinnamoyl CoA hydratase/lyase from *Amycolatopsis* sp. ATCC 39116 [8],

8 (iii) the enoyl-CoA hydratase/aldolase from *Amycolatopsis* sp. HR167 [10], (iv) the

9 *p*-hydroxycinnamoyl CoA hydratase/lyase from *Pseudonocardia* sp. P1 (unpublished
10 data), (v) the 2-ketocyclohexanecarboxyl-CoA hydratase from *Rhodococcus opacus*
11 PD630 [29], (vi) the *p*-hydroxycinnamoyl CoA hydratase/lyase from *Pseudomonas*
12 *fluorescens* AN103 [13], and (vii) the enoyl-CoA hydratase from *Pseudomonas* sp.
13 HR199 [7]. Amino acids are specified by standard one-letter abbreviations. *Dashes*
14 indicate gaps introduced into the sequences to improve the alignment. **B.** The
15 relationship between the enoyl-CoA hydratase/aldolase from *Streptomyces* sp. V-1 and
16 the proteins in panel **A** was displayed as a phylogenetic tree, which was constructed
17 on the basis of the Neighbor-Joining (NJ) method using the ClustalX and MEGA 5.0
18 softwares. The bar indicates 10% difference in amino acid sequence. The number at
19 the branch point represents the percentage of 1,000 bootstrap repetitions.