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i          -----MSPTLNREMVEVLEVEQDA 20
ii        MSTYEG-----RWKTVKVEIEDGIAFVILNRPEKRNAMSPPTLNREMI DVLETLEQDP 52
iii       -----MSPTLNREMRDVLLETVEQDA 20
iv        MSTAVGNRVRTEPWGETVLEFVDEGIAWVMLNRPDKRNAMNPTLNDEMVRVLDHLEGDD 60
v         MSEENK----PVEREEDTVRYEIVNNVAWVYYNRPDKRNAMSPKLNFRQMLKVLTELEFRD 56
          .*. ** :* ** :*

i          DARVLTGTGAGESWTAGMDLKEYFRETDA-GPEILQE KIRREASTWQWKLLRMYTKPTIA 79
ii        AAGVLTGTGAGEAWTAGMDLKEYFREVDA-GPEILQE KIRREASQWQWKLLRMYAKPTIA 111
iii       DARVLTGTGEGSAWTAGMDLKEYFREVDA-GPEILQE RFRRDASEWQWKLLRFISKPTIA 79
iv        RCRVLTGTGAGESFSAGMDLKEYFREVDATGSTAVQIKVRRASAEWQWKRLANWSKPTIA 120
v         DVGVLVLGGEGPAWCAGMDLKEYFRETEAEBLAGTR-KAQREAYTW-WERLRWYQKPTIA 114
          **** * * :: *****: * * : : * : * * : * *****

i          MVNGWCFGGGF SPLVACDLAICADEATFGLSEINWGIPPGNLVSKAMADTVGHRESLYYI 139
ii        MVNGWCFGGGF SPLVACDLAICADEATFGLSEINWGIPPGNLVSKAMADTVGHRQSLYYI 171
iii       MVNGWCFGGGF SPLVACDLAICADEATFGLSEINWGIPPGNLVSKAMADTVGHRESR-II 138
iv        MVNGWCFGGAFTPLVACDLAFADEDARFGLSEVNWGIPPGVVSRALAATVPQRDALYYI 180
v         MVNGWCFGGAYGPLFACDLAFAADEAQFGLSEVNWGILPGGGATKVAVDLMPMRVAMYHA 174
          ** : ***** . : ** : ***** . : * * ***** : ***** ** . : . . : * :

i          MTGKTFGGQAAKMLVNSVPLAELRSVTVELAQNLLDKNPVVLRRAAKIGFKRCRELTW 199
ii        MTGKTFGGQAAAEMGLVNESVPLAQLREVTIELARNLLEKNPVVLRRAAKHGFKRCRELTW 231
iii       MTGKTFDGQAAQMLVNSVPLAQLRDEVVLLAQDLLDKNPVVLRRAAKNGFKRCRELTW 198
iv        MTGEPFDGPPRAEMRLVNEALPADRLRETREREVALKLASMNQVVLHAAKTGYKIAQEMPW 240
v         MMGENLSGQDAARYNLVNESMPADQLKARVKQVAETLIQKNWATVKYTKDAVRRVKEMTY 234
          * * : . * * . * * : : * * . * : * * . * * . : : * * . : * * : :

i          EQNEDYLYAKLDQSRLLDPEGGREGGMKQFLDEKSIKPLQTYKR----- 244
ii        EQNEDYLYAKLDQSRLLDTEGGREGGMKQFLDDKSIKPLQAYKR----- 276
iii       EQNEDYLYAKLR-----DPEP-RAQGLKQFLDDKSIKPLQATKR----- 237
iv        EQAEDYLYAKLDQSQFADKAGARAKGLTQFLDQKSYRPGLSAFDPEK---- 287
v         DNAEDYLIRLQEGLNWFDKSDGRHVAMKQFLDDKTFKPLGHYDKTKTEV 284
          : : ***** * * . : ***** : : ***** .

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3 **Figure S1. Alignment of the deduced amino acid sequences of *ech* from different**
4 **strains.** The amino acid sequences of 5 hydratases of similar function from 5 different
5 strains were aligned with the clustalX software. (i) The amino acid sequence of
6 enoyl-CoA hydratase from *Pseudomonas* sp. HR199 [7]; (ii) The amino acid sequence
7 of *p*-hydroxycinnamoyl CoA hydratase/lyase from *Pseudomonas fluorescens* AN103
8 [13]; (iii) The amino acid sequence of ferulic acid hydratase from *Pseudomonas*
9 *putida* WCS358 [18]; (iv) The amino acid sequence of enoyl-CoA hydratase/aldolase
10 from *Amycolatopsis* sp. HR167 [10]; (v) The amino acid sequence of feruloyl-CoA
11 hydratase/lyase from *Sphingomonas paucimobilis* SYK-6 [11]. The amino acids in the
12 frame were consistent with the degenerate primer pair P1 and P2. Amino acids were

- 13 specified by standard one-letter abbreviations. *Dashes* indicate gaps introduced into
- 14 the sequences to improve the alignment.