

Supplementary material

Table 1: Details of predicted conserved protein domains & motifs found in protein sequences of putative enzymes involved in vanillin bioconversion in both *P. fluorescens* and *A. niger*.

S. No.	Reference Enzymes of Vanillin Biosynthetic Pathway	Reference Pathway protein in <i>P. fluorescens</i> with protein ID & Length	Predicted Pathway protein in <i>A. niger</i> with protein ID, Length & BLAST score	Conserved protein domain & motif	Conserved domain/motif Function
1.	Eugenol hydroxylase A (EhyA)	Eugenol hydroxylase cytochrome C EMB CP000076 111 aa	CYC-A (Cytochrome c) P56205 A61490 111 aa (87.4 score, 58% similarity, 38% identity, 4E-19 E-value)	PS51007 IPR003088 PF00034	Cytochrome-C motif
	Eugenol hydroxylase B (Ehy B)	Eugenol hydroxylase B CAB64355 AJ243941 517 aa	Hypothetical protein (An09g01380) XP_001393455 XM_001393418 552 aa (283 score, 50% similarity, 34% identity, 4.00E-77 E-value)	PFAM01565 PFAM 02913 COG0277	FAD_binding_4, FAD binding domain FAD-oxidase C, FAD linked oxidases, C-terminal domain GlcD, FAD/FMN-containing dehydrogenases
2.	Coniferyl alcohol dehydrogenase (Cal B)	Coniferyl alcohol dehydrogenase BAD11007	Hypothetical protein (An15g01840) XP_001396723 XM_001396686 280 aa (63.2 score 41% similarity, 22% identity, 3.00E-10 E-value)	CL09931 IPR002198	AdoHcyase IPR002198,short chain dehydrogenase/ reductase Glucose/ribitol dehydrogenase NAD(P)-binding
		AB162132 255 aa		IPR002347 IPR016040	
3.	Coniferyl aldehyde dehydrogenase (CalA)	Coniferyl aldehyde dehydrogenase YP_262923 NC_004129 476 aa	Hypothetical protein (An01g09260) XP_0013896346 XM_001389309 500 aa (238 score 53% similarity, 36% identity, 2.00-62 E-value)	CL00545 PFAM00171 IPR015590 IPR016162 IPR012394 IPR016161	LuxC, Acyl-CoA reductase (LuxC) Aldedh, Aldehyde dehydrogenase family Aldehyde dehydrogenase, N-terminal Aldehyde dehydrogenase NAD(P)-dependent Aldehyde/histidinol dehydrogenase AMP-binding, AMP-binding enzyme
4.	Feruloyl CoA synthase (Fcs)	Feruloyl CoA synthase AAZ23792 DQ119298 589 aa	AMP dependent CoA ligase XP_001401186 XM_001401149 513 aa (80.1 score 36% similarity, 24% identity, 8.00E-15 E-value)	CL100401	
5.	Enoyl CoA hydratase/ aldolase (Ech)	Enoyl CoA hydratase AAZ23790 119298 276 aa	Hypothetical protein XP_001399422 XM_001399385 294 aa (108 score 50% similarity, 34% identity, 6.00E-24 E-value)	CL109483	Enoyl Co A hydratase/ isomerase family