Additional file 5

L.	Enzyme subfamily		Genbank Id	Protein region	Clustal W of the IHCD motif
	Esi0060_0078		CBN7495	226	FMFTTNFQSAGAIA
	ZmAOS (CYP74A)	AAR33048	272	LLFATTFNSYGGLK
	LeAOS (CYP74A)	AAF67141	308	FVFLAGFNSYGGLK
	OsAOS (CYP74A)	AAP50956	308	ILFALCFNSYGGFK
	LuAOS (CYP74A)	AAA03353	332	ILFAVCFNSWGGFK
	MtAOS (CYP74A)	CAC86897	320	LLFATCFNSFGGMK
	PaAOS (CYP74A)	CAA55025	269	ILFAVCFNTFGGFK
	PgHPL (CYP74B)	AAK15070	298	LLFILGFNAFGGFS
	LeHPL (CYP74B)	AAF67142	280	LLFILGFNAFGGFS
	OsHPL (CYP74C)	EAZ22254	281	LVFVAIFNAFGGFK
	MtHPL (CYP74C)	CAC86899	282	IIFTAGFNAYGGLK
	NtDES (CYP74D)	AAL40900	276	ILFLVGINMFAGLN
	CaDES (CYP74D)	ABH03632	275	MLFLVGINMFAGLN

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Α

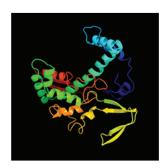


Image coloured by rainbow $N \to C$ terminus

Aligned: Modeled: Confidence:
% Coverage:
% Identity: PDB header:
Model based on template: Chain: A:
Molecule: PDBTitle:

260 aa 269 aa 100% 91% 18% lyase C3danA PDB Molecule: cytochrome p450 74a2 Cytochrome p450 74a2 Crystal structure of allene oxide synthase

Additional file 5. (A) ClustalW multiple alignment of the CYP74 family IHCD domains from Esi0060_0078 and homologs. The conserved catalytic residues FXXXFXSXX were highlighted in red for the CYP74A conserved phenylalanine residues and blue for the AOS specific serine residue. (B) Ribbon diagram of a predicted structural model of Esi0060_0078 prepared with the Phyre2 software [73].