## Additional file 5

L.	Enzyme subfamily		Genbank Id	Protein region	Clustal W of the IHCD motif
	Esi0060_0078		CBN7495	226	<b>FMFTTNFQSAGAIA</b>
	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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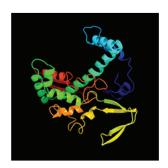


Image coloured by rainbow  $N \to C$  terminus

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].