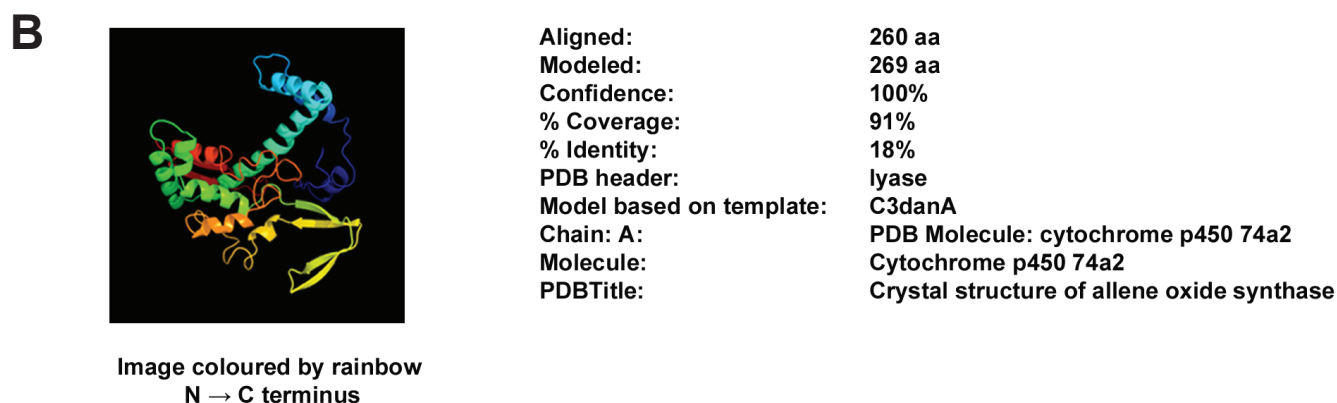


Additional file 5

A

Enzyme subfamily	Genbank Id	Protein region	Clustal W of the IHCD motif
Esi0060_0078	CBN7495	226	FMFTTNFQ S AGALA
ZmAOS (CYP74A)	AAR33048	272	LLF F AT T FNSYGG L K
LeAOS (CYP74A)	AAF67141	308	FV F LAG F NSYGG L K
OsAOS (CYP74A)	AAF50956	308	IL F AL C FNSYGG F K
LuAOS (CYP74A)	AAA03353	332	IL F AV C FNSWGG F K
MtAOS (CYP74A)	CAC86897	320	LL F AT C FNS F GG M K
PaAOS (CYP74A)	CAA55025	269	IL F AV C FNT F GG F K
PgHPL (CYP74B)	AAK15070	298	LL F IL G FNA F GG F S
LeHPL (CYP74B)	AAF67142	280	LL F IL G FNA F GG F S
OsHPL (CYP74C)	EAZ22254	281	L V F V AI F NA F GG F K
MtHPL (CYP74C)	CAC86899	282	I I F T AG F NA F GG L K
NtDES (CYP74D)	AAL40900	276	ML F LV G IN M FAG L N
CaDES (CYP74D)	ABH03632	275	ML F LV G IN M FAG L N



Additional file 5. (A) ClustalW multiple alignment of the CYP74 family IHCD domains from Esi0060_0078 and homologs. The conserved catalytic residues FXXXXXSXX 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].