

Table 1 Suppl. List of PAL, CHS, and CHS-like proteins used for phylogenetic analysis.

Protein name	Species	Accession No.	Protein name	Species	Accession No.
AtPAL1	<i>Arabidopsis thaliana</i>	AEC09341	AtCHS	<i>A.thaliana</i>	CAI30411
AtPAL2	<i>A.thaliana</i>	AEE79055	MsCHS	<i>Medicago sativa</i>	AAB41559
AtPAL3	<i>A.thaliana</i>	AED90715	AtCHSL	<i>A.thaliana</i>	NP_191915
AtPAL4	<i>A.thaliana</i>	AEE74893	WtPKS	<i>Wachendorfia thyrsiflora</i>	AAW50921
PtPAL	<i>Populus trichocarpa</i>	ACC63889	MpSTCS	<i>Marchantia polymorpha</i>	AAW30009
RcPAL	<i>Rhus chinensis</i>	AGH13333	PnVPS	<i>Psilotum nudum</i>	BAA87923
TcPAL	<i>Theobroma cacao</i>	EOY18683	PiHKS	<i>Plumbago indica</i>	BAF44539
RpPAL	<i>Robinia pseudoacacia</i>	ACF94716	RpASS	<i>Rheum palmatum</i>	AAS87170
PfPAL	<i>Perilla</i>	AEZ67457	HaBPS	<i>Hypericum androsaemum</i>	Q8SAS8
CrPAL	<i>Catharanthus</i>	BAA95629	SaBIS	<i>Sorbus aucuparia</i>	ABB89212
PhPAL	<i>Petunia x hybrid</i>	AAV98199	BfBBS	<i>Bromheadia finlaysoniana</i>	CAA10514
CaPAL	<i>Coffea arabica</i>	AEL21616	GbCHS	<i>G. biloba</i>	AAV52458
MePAL	<i>Manihot esculenta</i>	AAK62030	PsCHS	<i>Pinus strobus</i>	O65872
DcPAL	<i>Daucus carota</i>	BAC56977	VvCHS	<i>Vitis vinifera</i>	P51090
OsPAL	<i>Oryza sativa</i>	CAA61198	AcCHS	<i>Allium cepa</i>	AAO63020
PePAL	<i>Phyllostachys edulis</i>	ACM47229	LsCHS	<i>Lilium speciosum</i>	BAE79201
ZmPAL	<i>Zea mays</i>	NP_001168086	RgACS	<i>Ruta graveolens</i>	Q9FSC0
BdPAL	<i>Brachypodium distachyon</i>	XP_003575365	Gh2PS	<i>Gerbera hybrid</i>	P48391
HvPAL	<i>Hordeum vulgare</i>	BAJ88975	RpBAS	<i>R. palmatum</i>	AAK82824
TuPAL	<i>Triticum urartu</i>	EMS62198	HmCTAS	<i>Hydrangea macrophylla</i>	BAA32733
GbPAL	<i>Ginkgo biloba</i>	ABU49842	AaOKS	<i>Aloe arborescens</i>	AAT48709
SmPAL	<i>Selaginella moellendorffii</i>	EFJ17022	AaPCS	<i>A. arborescens</i>	AAX35541
SbPAL	<i>Sorghum bicolor</i>	EES07178	VvSTS	<i>V.vinifera</i>	ABJ97071
SiPAL	<i>Setaria italic</i>	XP_004976241	HIVPSL	<i>Humulus lupulus</i>	CAD23044
PvPAL	<i>Panicum virgatum</i>	AFY17067			

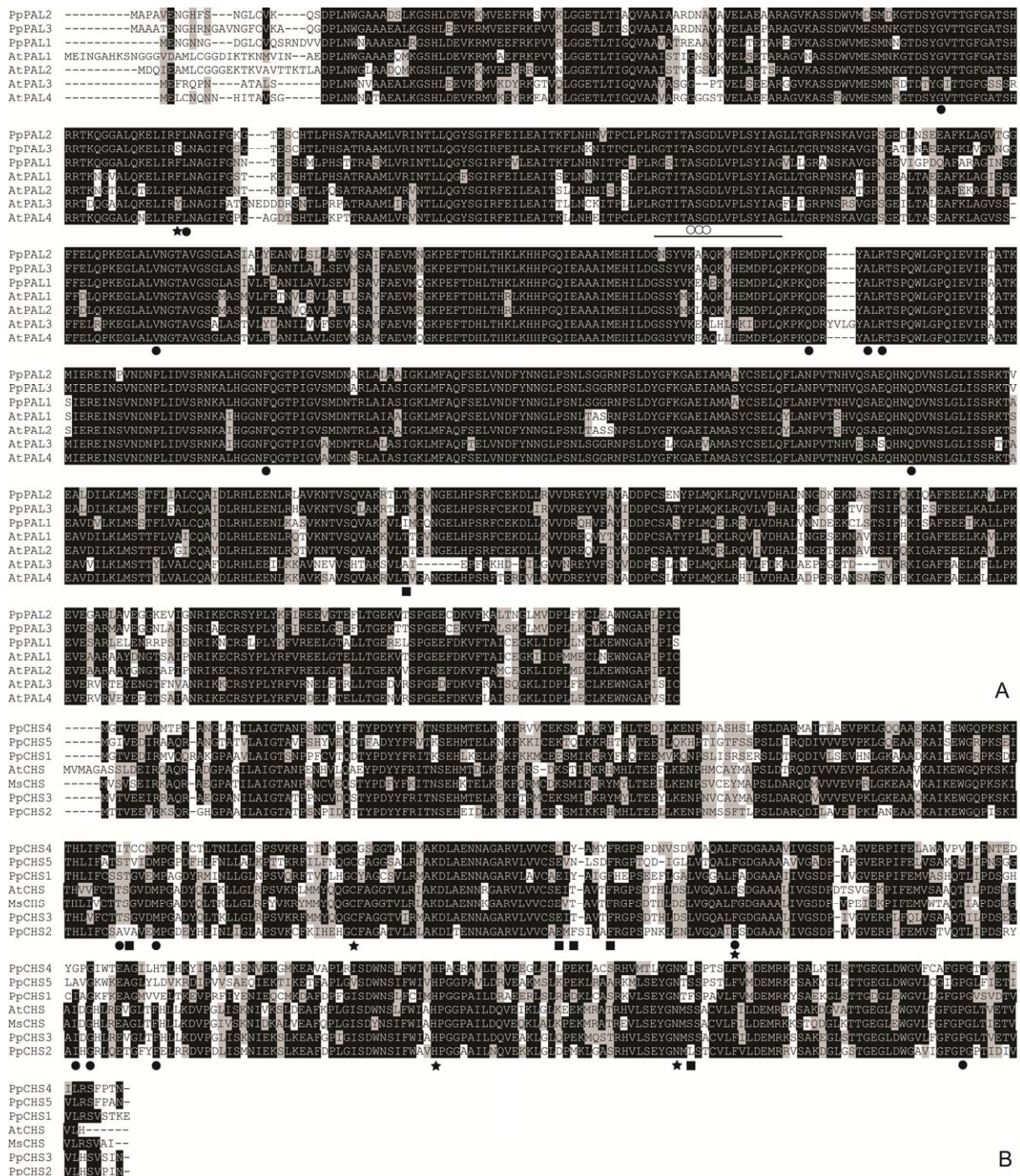


Fig. 1 Suppl. The sequence alignment of PcPALs (A) and PcCHSs (B) with *Arabidopsis* and/or *Medicago* proteins. A - The active residues and MIO group residues (Ala-Ser-Gly) are marked with the *black* and *white* circles, respectively. The consensus sequences for the conserved active site are underlined. Residues for substrate selectivity and putative phosphorylation are marked with the *black star* and *square*, respectively. PAL proteins of other species selected for alignment analysis are: AtPAL1 (*Arabidopsis thaliana*, AEC09341), AtPAL2 (*A. thaliana*, AEE79055), AtPAL3 (*A. thaliana*, AED90715), and AtPAL4 (*A. thaliana*, AEE74893). B — The *black* circles and *squares* indicate the residues responsible for cyclization reaction and catalytic reaction, respectively. The *black stars* indicate coumaroyl-binding residues. CHS proteins of other species selected for alignment analysis are: AtCHS (*A. thaliana*, CAI30411) and MsCHS (*Medicago sativa*, AAB41559).