

Corrigendum

Corrigendum to “Identification and functional analysis of bifunctional *ent*-kaurene synthase from the moss *Physcomitrella patens*” [FEBS Lett. 580 (2006) 6175–6181][☆]

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An incorrect Fig. 2 was published. The correct figure is given below.

PpCPS/KS	1	MASSTLIQNRSCGVTSMSFQIFRGOP	RFPGTRTPAAV	CLKRRCLRPTE	VLESPG	GSYRIVTGP	GNPSSNGHLOEGLTHRL	PIPMKESID
AgAs	1	-----AHH	TAN-----	T	SIFHFSTTLNAC	SASKR	RLLYL	UGK
AtCPS	1	-----MS	OYH-----	VLNS	IPSTTF	SS	KTTIS	-----
AtKSB	1	-----	-----	-----	-----	-----	-----	MSINLRS
PpCPS/KS	101	NF	STLVVSDI	SETLQR	TECLLQ	VTEIN	VQNNW	EIEIRMYFRNMTLGEIS
AgAs	68	TLVKRE	FPFPG	KDD	IDSL	SEHKVAA	SEKRIETL	S
AtCPS	63	EV	HD	PLIHE	QQLQGE	DAPOIS	GS	SNAPK
AtKSB	21	-----	-----	-----	-----	-----	-----	-----
PpCPS/KS	195	S	PLG	YDRV	CNTLAC	VIALK	TG	VGAQ
AgAs	165	FY	AA	ILAA	IT	TL	RT	ETQ
AtCPS	156	Y	SYH	LI	RS	NL	FP	HCCNK
AtKSB	99	HQS	KK	VLESS	SIL	KA	I	ERCINK
PpCPS/KS	295	Y	P	T	L	L	H	S
AgAs	265	AL	Y	QEI	E	E	IHK
AtCPS	256	I	MR	DL	E	K	OD
AtKSB	198	G	R	E	A	M	V
PpCPS/KS	395	L	Q	V	V	Y	R	K
AgAs	365	D	SH	DER	REN	P	I
AtCPS	355	D	H	T	N	C	RC
AtKSB	298	DET	LR	GDE	E	I	C
PpCPS/KS	494	K	H	N	E	C	F
AgAs	465	AL	V	DA	AFK	N	I
AtCPS	454	R	R	E	L	I	M
AtKSB	391	E	L	S	W	V	K
PpCPS/KS	593	D	L	E	F	A	R
AgAs	564	E	N	T	E	R	V
AtCPS	554	E	U	G	V	R	S
AtKSB	489	E	K	L	A	Y	S
PpCPS/KS	680	V	N	I	A	E	F
AgAs	651	F	D	K	G	R	E
AtCPS	653	L	Q	H	S	F	L
AtKSB	577	I	L	E	T	O	D
PpCPS/KS	779	D	I	Q	N	K	R
AgAs	751	T	K	T	Y	Q	A
AtCPS	729	P	R	Y	L	A	R
AtKSB	676
PpCPS/KS	875	L	F	E	P	V	P
AgAs	848
AtCPS	798
AtKSB	773	I	Y

Fig. 2. Comparison of plant diterpene synthases and PpCPS/KS. The deduced PpCPS/KS polypeptide was compared with *Arabidopsis ent*-coparyl diphosphate synthase (AtCPS), *Arabidopsis ent*-kaurene synthase B (AtKSB) and *Abies grandis* abietadiene synthase (AgAS). The dot represents identical amino acid to PpCPS/KS and dark gray shading indicates identical A.A. to each sequence. Light gray shading indicates A.A. with similar properties. Underline represents conserved motifs (SXYDTAWVA, DXDD, and DDXXD).

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