

PsLac2	-----APQSSAPSLSKRCTNSADDRSCWG-DYDISTNY	32
SlLac2	AVLPVELPNPAPFTPKRDGLEE-RQ-----SPASCINVGHTPKTRHCWAQGFTSSTD	52
MaLac1	-----APPSTPAQRDLVELREARQEGGKDLRPREPTCNTPSNRACWSGDFDINTDY	51
PsLac1	-----AAITQDLEPRQSTCNTASNRCWTSNFDITDY	33
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PsLac2	YEEAPDTGVTREYWFNIVNT--TAAPDGV-ERVVLSVNGSIPGPTIIADWGDTVVVHVTN	89
SlLac2	YTSWPNTGVIRSYNLRLENT--TCNPDGAGSRVCLLINGRFLGPTIVANWGDTIRVTVRN	110
MaLac1	EVSTPDTGVTQSYVFNLTEVDNWMGPDGVVKEKVMLINGNIMGPNIVANWGDTVEVTVIN	111
PsLac1	EQSTPPGG-SVTYNLEITEVRNWKGPDGVVKSFVQLINGQFPGPTIRAKWGDTITVNVKN	92
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PsLac2	SMENNGSS IHFHG IRQNYTNQNDGVPSLTQCPIAP-GDSYTYTWRATSYGSS WYHSH FYV	148
SlLac2	NLQNGTS IHWHG FRMLNKNIQDGVNGITECALAP-GDFKTYQFQATEYGT WYHSH F	169
MaLac1	NLVTNGTS IHWHG IHQKDTNLHDGANGVTECPIPPKGGQRTYRWRARQYGT WYHSH F	171
PsLac1	SMPTNGTS IHWHG LRQMGTNIHDGVNGVTECALAP-GKTRTYRFKATQYGT WYHSH F	151
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PsLac2	QAWDGIFFGILINGPATANYDEDLGNLFLNDWSHLTADVEVLA-----ALASGPPTLDTG	203
SlLac2	QYGDGVVGTIVVNGPATANYDEDLGVMPITDWYYNTAFQAASIAFQNGQAGLGPPVGDNI	229
MaLac1	QYNGGVGTIQINGPASLPYDIDLGVFPITDYYYRAADDLVHF-----TQNNAPPFSDNV	226
PsLac1	QYNGGVGTIVIDGPAENNYDIDLGVYPISDYYYSADDIVLR-----TQSGGPPASDNV	206
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PsLac2	LINGTNVYNE---TGSRYETTFEAGKRYLLRLVNAAADSHFHFSIDNHTLEVIASDFVPI	260
SlLac2	LINGTAKNA--AGGGAWNVRTIQAGKRYRLRLVNTAVDTNMLVNLGDHPPQVIATDFVPI	287
MaLac1	LINGTAVNPN-TGEGQYANVTLTGKRHLRLILNTSTENHFQVSLVNHTMTVIAADMVPV	285
PsLac1	LFNGTNINPLNPSQGKYSVVTLTGKRHLRLINPSVEHNYQVSLVGHDMTVIATDLVPV	266
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PsLac2	EPYTTDVVSIAMGQRYDVIVTANATADNYWMRALI--QTACSDNANPDNVIRGIIRYDSTS	318
SlLac2	NPYNTTHLQIGIGQRYDVIINANQTAGNYWFRATA--DGLCQSRNARE-GRAIFTYQGQP	344
MaLac1	NAMTVDSLFLAVGQRYDVVIDASRAPDNYWFNVTFGGQAACGGSINPH-PAAIFHYAGAP	344
PsLac1	NSMTLNNIYLGQRYDVLIDASKTVGNVWFNVTLSPGTGLCGTSINPR-PAAIFRYAGAP	325
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PsLac2	TADPTSTAWDDATTDGTCYDEDISQLVPYVPITASST--ADYEDDFSV--KIVVGDNV	373
SlLac2	VADPTSTAPT--VPFTACLDPVT--T-PKIVKNVPSSTFAAQAKNLPVAFGPVAANGNTV	399
MaLac1	GGLPTDEGTP--PVDHQCLDTLD--VRPVVPRSPVNSFVKRPDN-TLPVALDLTGTPLF	399
PsLac1	STNPTDPGTV--PADAACQDRTD--FTPVVTRTADSTTLVPQANDPAHNLDISLNFTTFV	381
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PsLac2	LWEMGPSSFVNQWDYPSLLQVEEGNDTWADSQQVYAFPD--ADTWVYVVIQTT----NNQ	427
SlLac2	LWTINGTSMIIDPGKPTIKYVAENNNSPQSYNVVKVPATSASTWYVVIQQA-VGAPPI	458
MaLac1	VWKVNGSDINVDWGKPIIDYILTGNSTYPVSDNIVQVDA--VDQWYTWLIENDPEGPFSL	457
PsLac1	SWFVNGSAIDVQWDKPVLDYVLTGNSTYPRRENLFVVD--KNVWYTWVVQNL----SPL	435
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PsLac2	PHPMHLH GHDFWILGQGLGTID-----ADTANLTYTNPPRRDVVQLPGAGYVAI	476
SlLac2	AHPIHLH GHDSYILGAGDGQ-----FNAATHFSQLRFTNPPRRDVSQKGNGLVI	509
MaLac1	PHPMHLH GHDFVLGRSPDVPAASQQRVFVDPVAVDLARLNGDNPPRRDTTMLPAGWLLL	517
PsLac1	PHPMHLH GHDFVLGHAASSTFTA-----SMSSSLNFNNPTRRDVTMLPASGYVIL	486
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PsLac2	AFYTDNPGVWLM HCHIAWH TSEGLAVQVLERESEIGALID--ADVMNSTCAAWDDYTAE	533
SlLac2	AYPTDNPGAWLM HCHIAFH VSGGLSVQFLERKQQIV---LPATGSEWYNNCWNAAAYKAG	566
MaLac1	AFRTDNPGAWLF HCHIAWH VSGGLSVDFLERPADLRQRISQEDEDNFNRVCDEWRAYWPT	577
PsLac1	AFKADNPGNWLM HCHIAWH VSGGLSVDFMERRAEQAALISAADLAAYKQCCADWRAYAPK	546
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PsLac2	--DDIIQDDSGI-----	543
SlLac2	NTDVWPQDDSGLKRR-WPPLIEDGSVL--	592
MaLac1	--NPYPKIDSGLKRRRWVE--ESEWLVR	601
PsLac1	--AP-PKIDSGI-----	555
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Figure S1: Alignments of the closest characterized laccases from *Melanocarpus albomyces* (MaLac1, Q70KY3) and *Pestalotiopsis* sp. KF079 (PsLac1: KY554800 and PsLac 2: KY554801), using CLUSTAL W sequence alignment algorithm. Perfect matches are represented by an asterisk, high-amino acid similarities by double dots, and low-amino acid similarities by single dots. Gaps (-) were introduced for maximum alignment. The amino acids involved in the coordination sites for the type 1, 2 and 3 coppers are in red and bold.

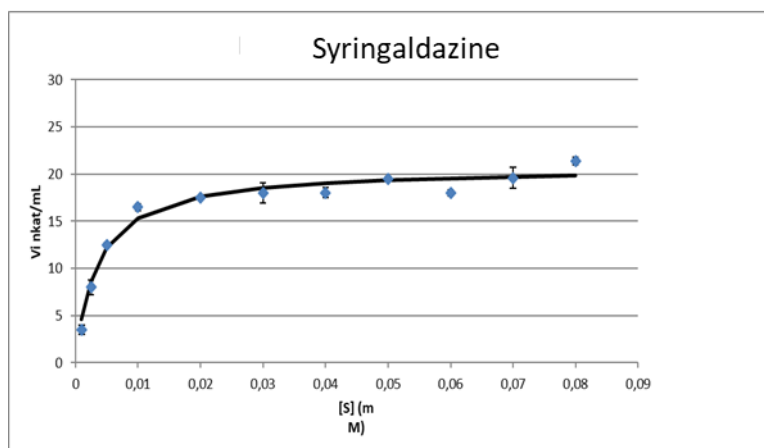
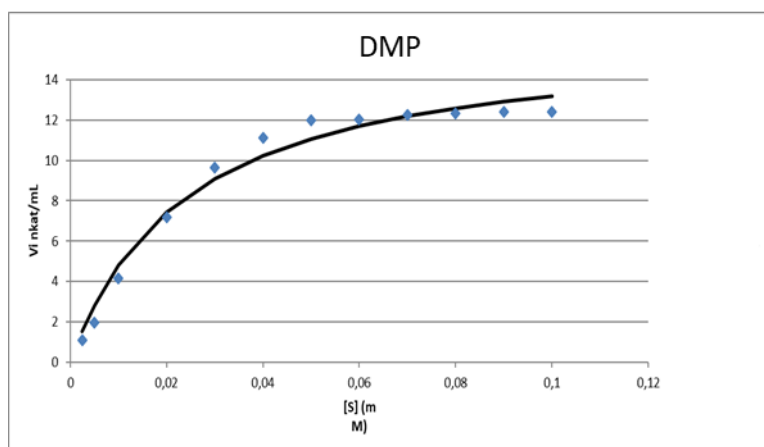
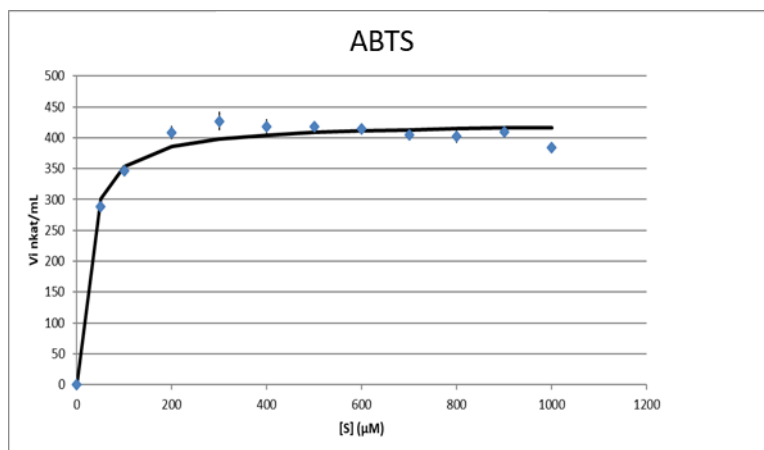


Figure S2: Kinetics of *Sl*Lac2 on the three substrates.