

SmLac2A	MWSFRKCLPATVALLAVCLVPSVYTVRVGGGSRGATRKGDQDAAASWNSWDAIEPDFFRSEQQVLQTHPI	70
SmLac2B	<u>MWSFRKCLPATVALLAVCLVPSVYTVRVGGGSRGATRKGDQDAAASWNSWDAIEPDFFRSEQQVLQTHPI</u>	70
SmLac2A	RGNGQVSYSGSSGGGLKHKHEDFRTSPTAELRRNPSLSSPDECARACREGEPPRICYYHFTLEFYTVLGA	140
SmLac2B	RGNGQVSYSGSSGGGLKHKHEDFRTSPTAELRRNPSLSSPDECARACREGEPPRICYYHFTLEFYTVLGA	140
SmLac2A	ACQVCTPNATNAIWSNCQCILADGVERGMLAVNRMLPGPSIQVCENDKVVIDVENHMEGMEVTIHWGIIW	210
SmLac2B	ACQVCTPNATNAIWSNCQCILADGVERGMLAVNRMLPGPSIQVCENDKVVIDVENHMEGMEVTIHWGIIW	210
SmLac2A	QRGSQYYDGVPPFVTQCPQQGNAFRYQWIAGNAGTHFWHAHTGLQKMDGIYGSIVVRQPPNRDPNSNLYD	280
SmLac2B	QRGSQYYDGVPPFVTQCPQQGNAFRYQWIAGNAGTHFWHAHTGLQKMDGIYGSIVVRQPPNRDPNSNLYD	280
SmLac2A	FDLTTHVILLSDWMHENAERFPGRLAVNTGQDPENLLINGKGQFRDPNTGFMNTNPLEIFTMTPGKRYR	350
SmLac2B	FDLTTHVILLSDWMHENAERFPGRLAVNTGQDPENLLINGKGQFRDPNTGFMNTNPLEIFTMTPGKRYR	350
SmLac2A	FRMINSLASVCPAQLTIQGHTLTLIATDGEPVHPVNVNTIISFSGERYDFVINADQAVGAYWIVVRGLGE	420
SmLac2B	FRMINSLASVCPAQLTIQGHTLTLIATDGEPVHPVNVNTIISFSGERYDFVINADQAVGAYWIVVRGLGE	420
SmLac2A	CGIRRVQQLGILRYYKGPYTPFTQAPTYDFGIAQGVV	490
SmLac2B	CGIRRVQQLGILRYYKGPYTPFTQAPTYDFGIAQGVVS-----IV	460
SmLac2A	EKPNVKIFLPFRFHVYTPQDLFAPNTYNRHLVAPNGDHVISLVDEISYMAPPAPLISQYDDTDPEQFCNG	560
SmLac2B	VKKVMVFFSLSECDCLSIGLVEENTHN-----	488
SmLac2A	DNKPANCGPNCMCTHKIDIPLNATIVEVVLVDEVQQPNLSHPFHLHGAFNVVIGRSPDQNVKKINLKHA	630
SmLac2B	-----	488
SmLac2A	LDLDRRGLLSRHFDLPPGKDTIAVPNNGYVIFRFRADNPGFWLFHCHFLFHIVIGMNLVLQVGTHADLPP	700
SmLac2B	-----	488
SmLac2A	VPLNFPTCGDHTPRINLDPTKI	722
SmLac2B	-----	488

Figure S2. Alignment of the putative amino acid sequences of *SmMCO2A* and *SmMCO2B*. Dashes in the sequences represent gaps introduced to optimize alignment. The number to the right indicates the position of the last amino acid in the row. Identical residues in all sequences are black-bordered; the cysteine-rich consensus region in the insect laccase protein is in red box; presumptive signal peptides predicted by SignalP 5.0 [63] are underlined in red.