

SmLac2A	<u>MWSFRKCLPATVALLAVCLVPSVYTVRVGGGSRGATRKGDDQAAASWNSWDAIEPDDFRSEQQVLQTHPI</u>	70
SmLac2B	<u>MWSFRKCLPATVALLAVCLVPSVYTVRVGGGSRGATRKGDDQAAASWNSWDAIEPDDFRSEQQVLQTHPI</u>	70
SmLac2A	RGNGQVSYSGSSGGGLKHKHEDFRTSPTAELRRNPSLSSPDECARACREGEPPRICYYHFTLEFYTVLGA	140
SmLac2B	RGNGQVSYSGSSGGGLKHKHEDFRTSPTAELRRNPSLSSPDECARACREGEPPRICYYHFTLEFYTVLGA	140
SmLac2A	ACQVCTPNATNAIWSNCQCILADGVERGMLAVNRMLPGPSIQVCENDKVVIDVENHMEGMEVTIHWHGIV	210
SmLac2B	ACQVCTPNATNAIWSNCQCILADGVERGMLAVNRMLPGPSIQVCENDKVVIDVENHMEGMEVTIHWHGIV	210
SmLac2A	QRGSQYYDGVPFVVTQCP IQQGNAFRYQWIAGNAGTHFWHAHTGLQKMDGIYGSIVVRQPPNRDPNSNLYD	280
SmLac2B	QRGSQYYDGVPFVVTQCP IQQGNAFRYQWIAGNAGTHFWHAHTGLQKMDGIYGSIVVRQPPNRDPNSNLYD	280
SmLac2A	FDLTTTHVILLSDWMHENAAERFPGRLAVNTGQDPENLLINGKGGFRDPNTGFMTNTPLEIFTMTPGKRYR	350
SmLac2B	FDLTTTHVILLSDWMHENAAERFPGRLAVNTGQDPENLLINGKGGFRDPNTGFMTNTPLEIFTMTPGKRYR	350
SmLac2A	FRMINSLASVCPAQLTIQGHTLTLIATDGEPVHPVNVNTIISFSGERYDFVINADQAVGAYWIQVRGLGE	420
SmLac2B	FRMINSLASVCPAQLTIQGHTLTLIATDGEPVHPVNVNTIISFSGERYDFVINADQAVGAYWIQVRGLGE	420
SmLac2A	CGIRRVOQLGILRYYKGPYTPFTQAPTYDFGIAQGVV LNPLDARCNETRADAVCISQLKNAREVDRAILLI	490
SmLac2B	CGIRRVOQLGILRYYKGPYTPFTQAPTYDFGIAQGVV S-----I V	460
SmLac2A	EKPNVKIFLPFRFHVYTPQDLFAPNTYNRHLVAPNGDHVIVSLVDEISYMAPPAPLISQYDDTDPEQFCNG	560
SmLac2B	VKKVMVFFSLSECDCLSIGLVEENTHN-----	488
SmLac2A	DNKPANCGPNCMCTHKIDIPLNAIVEVVLVDEVQQPNSHPFHLHGAFNVVIGRSPDQNVKKINLKHA	630
SmLac2B	-----	488
SmLac2A	LDLDRRGLLSRHFDPGKDTIAVPNNGYVIFRFRADNPGFWLFHCHFLFHIVIGMNLVLQVGTHADLPP	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.