**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 SLac2 on the three substrates.