

SUPPLEMENTAL TABLE AND FIGURE

Description of the first fungal dye-decolorizing peroxidase oxidizing manganese(II)

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Table S1. Amino-acid sequence identities between the four DyPs from the *P. ostreatus* genome (JGI protein references included). The number of residue pairs considered for each comparison is shown after the identity percentage.

	<i>Pleos-DyP4</i>	<i>Pleos-DyP3</i>	<i>Pleos-DyP2</i>	<i>Pleos-DyP1</i>
<i>Pleos-DyP1</i> (<u>62271</u>)	39% (190)	63% (298)	67% (323)	100% (497)
<i>Pleos-DyP2</i> (<u>1092668</u>)	39% (191)	74% (350)	100% (488)	-
<i>Pleos-DyP3</i> (<u>52170</u>)	39% (188)	100% (474)	-	-
<i>Pleos-DyP4</i> (<u>1069077</u>)	100% (504)	-	-	-

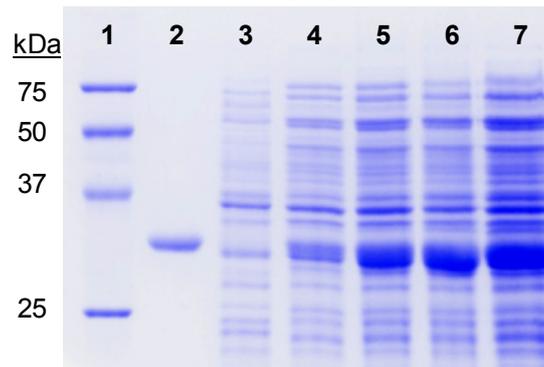


Fig S1 SDS-PAGE during *Pleos-MnP3* expression in *E. coli*, and after *in vitro* activation and purification. *Lanes 3-7*, time-course of *Pleos-MnP3* overexpression (as inclusion bodies) in IPTG-induced *E. coli* cultures (total proteins 0, 1, 2, 3 and 4 h after induction, respectively). *Lane 1*, purified *Pleos-MnP3* in a single chromatographic step, after the *in vitro* activation of protein from *E. coli* inclusion bodies. *Lane 1*, standards (Fernández-Fueyo et al. 2014d).