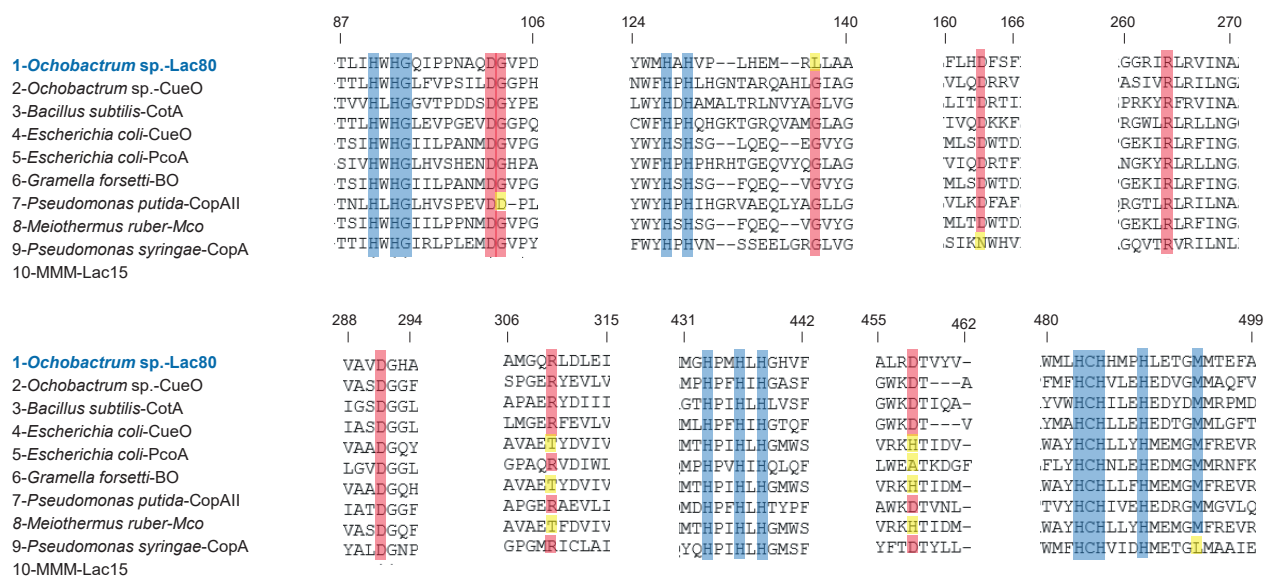


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Table S1. BLASTP alignment of the putative laccase-like multicopper oxidase protein sequence (Lac80) encoded by a plasmid-carried gene from *Ochrobactrum* sp. BF15. The ten best protein matches identified in NCBI by BLASTP (28) algorithm for Lac80 protein are shown

Accession	Description	Protein length	Organism	Identity/%	E value	Max score	Total score	Query cover/%
WP_024899901.1	multicopper oxidase domain-containing protein	502	<i>Alphaproteobacteria</i>	100.00	0	1000	1000	100.00
WP_094574672.1	multicopper oxidase domain-containing protein	502	<i>Ochrobactrum rhizosphaerae</i>	99.80	0	999	999	100.00
WP_138787545.1	multicopper oxidase domain-containing protein	502	<i>Ochrobactrum haemaphilum</i>	99.80	0	999	999	100.00
WP_036709831.1	multicopper oxidase domain-containing protein	502	<i>Paracoccus sanguinis</i>	99.60	0	997	997	100.00
WP_155044758.1	multicopper oxidase domain-containing protein	502	unclassified <i>Paracoccus</i>	98.80	0	993	993	100.00
WP_085378474.1	multicopper oxidase domain-containing protein	493	<i>Paracoccus contaminans</i>	91.83	0	877	877	100.00
WP_126156115.1	multicopper oxidase domain-containing protein	493	<i>Paracoccus haematequi</i>	91.63	0	873	873	100.00
WP_121583054.1	multicopper oxidase domain-containing protein	499	<i>Mesorhizobium</i> sp. YM1C-6-2	90.04	0	870	870	100.00
WP_114350933.1	multicopper oxidase domain-containing protein	493	<i>Paracoccus lutimaris</i>	91.43	0	868	868	100.00
WP_122520894.1	multicopper oxidase domain-containing protein	499	<i>Pannonibacter phragmitetus</i>	90.04	0	867	867	100.00

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**Fig. S1.** Partial amino acid multiple sequence alignment, showing 10 bacterial laccase-like multicopper oxidases. Metal-binding residues are coloured in blue; other conserved residues are highlighted in red, whereas mismatches are in yellow. Numbering is based on Lac80 sequence as reference. Protein data Bank (23) or GenBank (22) accession codes are as follows: 1=QQZ00696.1, 2=6EVG|A, 3=P07788, 4=P36649, 5=A0A0E0XT94, 6=(GB) WP_011709064.1, 7=Q88C03, 8=(GB) WP_013012601.1, 9=P12374, 10=E1ACR6. BO=bilirubin oxidase, MMM=marine microbial metagenome

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Lac80	MNTLSRRGFLLAAGAAMLA-----YAHLPRIAAA--QGAAPLSLHAATRRLDIDGRAATV	52
OcCueO	QDAHQ--KMGHGAATPSTAPTGRPLPLPPLVEPDASGVVVKLVQVQGRHSFE-EGSEAS	56
	:: *** : ** * : : : : : * * :	
Lac80	WLAG--PAGQGLTLDPGARFRVLDLRNDLDTLTIHWHGQIPPNAQDGVDPDMLPLMPLAPGE	111
OcCueO	AGINGAYLGLPLVRLKNGETVTLVSVENGMDEGTTLHWHGLFVPSILDGGPHNVI---AAGE	113
	* : * * : : * . * : * . : * * * * : * . * * * . : * * *	
Lac80	TRAY--DFAPLPGTYWMAHVPPLHEMRLLA---AP-LIVRSAEDVAAD-----RQEVVL	159
OcCueO	AWKPEVKIQQPASFNWFPHLHGNTARQAHLGIAGLMVVTGKDAERGLPEDYGVDDIPL	173
	: * : * * : : * * : : * * : : * : : : * :	
Lac80	FLHDFSFKAPEEVMAEILGGHGTAGGGHGGGAVMGGMAAMDHGAMGNMFMGMDHGAMG	219
OcCueO	VLDLRRVIEGDKVYE-----PDIM-----DLMHGFRG	200
	. * : * . . : : * * : : * * : : * * : : * * : : * * : : * * *	
Lac80	GMTGMGAMDMAMDLDNDYDWDAYLANDRTLSDPEVVQVERGGRIQLRVINAAAATVFWIE	279
OcCueO	GNL-----IVNG--IVSPEA--RVPASIVRLRILNGANARNFHVRL	236
	* : : * . : : * * : * * * * : * * * * * : . .	
Lac80	TGEAQARLVAV--GHAVQPVPGTRFGLAMGQRLDLEIDLPEGGAWPILALREGAR-ER	336
OcCueO	LSDNRPLLVASDGGFIGNPEPVERLTISPGERIYEVLVDFSKGEA-TDLLTYGDDSGGDD	295
	. : : * * . . * . : * * * : : * : * : : * : : : . : * : : : :	
Lac80	TG-----LILATQGAIEIRRIDTMAEAEAP-----AFDSDLAQETRLIAAGALPD	380
OcCueO	LHLMRFVDDAALQGVTKRPDRLDGPDAPDEKLSVKRRSFFDERMAENMKLMMAKLSAD	355
	: * * * : * * : : * * * * * : * : * : * * *	
Lac80	RPVDRSHMVMLGGSMQP-----Y---VWTINGAVVWQHR-PV	413
OcCueO	PHAGHNMGNDMGSMQSGAMDHDMHGARSADAGPALEALTSGVEMAIAGKPFDMRIDV	415
 * * * * * : * * * * : . . . * * *	
Lac80	TAQSGERIVLSFHNMSMMGHPMHLHGHVFQVVGLNGRAVRGA---LRDITVYVPPM--SMV	468
OcCueO	EAKLGSWEIW-DLTTKEMPHPFHIIHGASFRILSLNGKAPPAHQSGWKDTALIDGKAEILV	474
	* : * . : . . * * * : * * * * : * : : * * * * : . : * * . : * :	
Lac80	DIALDAGEAARWMLHCHHMPHLETGMMTEFAVSA	502
OcCueO	HFDREAVKSHPFMFCHVLEHEDVGMMAQFVTV-	507
	. : : * : : : * : * * * : * : * * * * * *	

Fig. S2. Sequence alignment of Lac80 with OcCueO from *Ochrobactrum* sp. Alignment was carried out using Clustal Omega online tool (26). The percentage of identity is 25.5 %. Metal-binding residues are coloured in blue; other conserved residues among the bacterial laccase-like multicopper oxidases shown in Fig. S1 are highlighted in red, whereas mismatches are in yellow. Uniprot (23) or GenBank (22) accession codes as follows: Lac80 (QQZ00696.1), OcCueO (6EVG|A)