|  |  |  |
| --- | --- | --- |
| **Homology found with the primers Cu1AF-Cu2R to amplify LMCO-genes** | | |
| **AMINO ACID SEQUENCE** | **Nº of clones** | **Highest match in the database (% identity amino acids)** |
| TTVHWHGVRLPNAMDGVPGLTQPPIKPGEQFTYEFTPLDAGTFWYH | 1 | ref|WP\_007602744.1| Bradyrhizobium sp. WSM1253. Copper oxidase (96%) |
| TTVHWHGVRTPSPMDGVPGLSFPGIAPGETFIYRFPVHQSGTFWYHS | 3 | gb|ABQ52278.1| Uncultured bacterium. Laccase (95%) |
| TSVHWHGIILPNPMDGVPGLTFHGIAPGETFTYQIPVRQSGTFWYHS | 2 | gb|ABQ52292.1| Uncultured bacterium. Laccase (95%) |
| TSVHWHGIRLPNAMDGVPDLTQKPISSGERFDYAFTPPDAGTFWYHS | 3 | gb|ABQ52259.1| Uncultured bacterium. Laccase (95%) |
| TVHWHGILLPANMDGVPGLSFHGIQPGDTYVYRFQVRQAGTFWYHS | 1 | gb|ADH15950.1| Uncultured bacterium. Putative laccase (93%) |
| TSVHWHGMILPANMDGVPGISFPGIRPGETHEYRFPVTQAGTFWYHS | 3 | gb|ABQ52303.1| Uncultured bacterium. Laccase (94%) |
| TVHWHGIRAPSDMDGVPGLSFPGIAPGETFVYRFPVRQSGTFWYHS | 1 | gb|ADH16167.1| Uncultured bacterium. Putative laccase (93%) |
| TTVHWHGIILPNPMDGVPGLTFQGIAPGETFTYQFPVRQSGTFWYHS | 1 | gb|ABQ52332.1| Uncultured bacterium. Laccase (87%) |
| TSVHWHGVLVPFAMDGVPGVSFPGISPGETFAYEFPVIQSGTFWYHS | 1 | ref|YP\_002130318.1| Phenylobacterium zucineum HLK1. Copper-binding protein (87%) |
| TSVHWHGILVPAGMDGVPGLSFDGIAPGETFVYRFEVKQSGTFWYHS | 1 | emb|CAJ77138.1| Agromyces salentinus. Laccase-like multicopper oxidase (87%) |
| TSVHWHGVIVPADMDGVPGLSFSGIGPGETFVYRFRLNQSGTFWYHS | 1 | gb|ABQ52289.1| Uncultured bacterium. Laccase (87%) |
| TVHWHGLRIPSAMDGTEVVQRAIQPGETFTYRFTPPDAGTFWYHS | 1 | gb| ADH16044.1| Uncultured bacterium. Putative laccase (87%) |
| TTVHWHGLLVPFAMDGVPGISFPGINPGETFVYEFPVIQSGTFWYHS | 2 | ref|YP\_007617272.1| Sphingomonas sp. MM-1. Putative multicopper oxidase (87%) |
| TSVHWHGVRSPAGMDGVPGLSFPGIAPGETFTYRIPIHQSGTFWYHS | 1 | gb|ABQ52287.1| Uncultured bacterium. Laccase (87%) |
| TSVHWHGVRVPNGMDGVNGLTQPTIDPGQTFRYEFTVPDAGTFWYHS | 1 | gb|ABQ52315.1| Uncultured bacterium. Laccase (85%) |
| TTVHWHGLHLPPEQDGASEEGSPIIAPGGSLVYAFTPKPSGTFWYHS | 1 | gb|ABQ52246.1| Uncultured bacterium. Laccase (83%) |
| TSVHWHGIRVPNGMDGANGITQPPIEPGQTFRYEFTVRD | 1 | gb|ABQ52311.1| Uncultured bacterium. Laccase (82%) |
| TTVHWHGLLVPNPMDGVPGVNFGGIRPGETFTYRFPLQQYGTFWYHS | 1 | gb|ABQ52339.1| Uncultured bacterium. Laccase (81%) |
| TSVHWHGLILPSSQDGVPGVSDGFQGIPPGQTFTYRFPVRQSGTFW | 1 | gb|ABQ52299.1| Uncultured bacterium. Laccase (80%) |
| SVHWHGIELESYYDGVPHWNGDDRRRTPSIEPNQQFVARFTPPRAGTFWYHS | 1 | gb|ADH15981.1| Uncultured bacterium. Putative laccase (75%) |
| SVHWHGIRVPDAEDGVAGLTQNAVAPGESFTYEFVARDAGTFWYHS | 1 | gb|ADH16126.1| Uncultured bacterium. Putative laccase (74%) |
| TTVHWHGIPIINTMDGVPGITQPAIKAGTNFLYDFTVPVSG | 2 | ref|YP\_002823063.1| Sinorhizobium fredii NGR234. Multicopper oxidase (74%) |
| TSVHWHGIELDNQADGTPYTQNQVPQNGTFLYKFKVDRPGTFWYHS | 1 | gb|ABQ52345.1| Uncultured bacterium. Laccase (72%) |
| TTVHWHGLAIRNDMDGAPEVTQPGIATGQSAVYEFTLPHPGTFWYH | 1 | ref|WP\_017882576.1| Leucobacter sp. UCD-THU. Copper oxidase (70%) |
| TSVHWHGLMVPSIEDGVPGVGQKPIQAGQTYVYDFTVHDQDVGTFWYHS | 4 | gb|ADV52165.1| Uncultured bacterium. Laccase (63%) |
| SVHWHGLDMPSALDG-DPMTAPGGHSVLQGKTFLYHFVAKYPGTFWYHS | 1 | gb|ADH16113.1| Uncultured bacterium. Laccase (55%) |