Table S1 Copper-copper and copper-ligand coordination distances and angles among bacterial laccases and other selected MCOs.

				Cu centres coordination distances (Å) and angles (º)				
Enzyme	**PDB**	**r.m.s.d. (Å)**[a]	**Sequence ID (%)**	**Type 1 Cu(1)** (occ: 1.00)[b]	**Type 2 Cu(4)** (occ: 0.20)[b]	**Type 3 Cu(2)** (occ: 0.60)[b]	**Type 3 Cu(3)** (occ: 0.30)[b]	**Cu2-Cu3**
McoC	-	-	-	His^{439} (2.03) Cys^{495} (2.29) His^{500} (2.00) Met^{505} (3.37)	His^{139} (1.94) His^{442} (1.93) O2(Oxy) (2.48) HOH (3.18)	His^{180} (1.99) His^{496} (2.17) His^{141} (1.98) O1(**Oxy**) (2.65) O2(**Oxy**) (2.19)	His^{182} (2.00) His^{494} (2.00) His^{444} (1.96) O1(**Oxy**) (2.06) O2(**Oxy**) (2.30)	Cu(2)-Cu(3) – 4.44 Cu(2)-Cu(4) – 3.60 Cu(3)-Cu(4) – 3.58 Cu(2)-O1-Cu(3) angle – 140.8° Cu(2)-O2-Cu(3) angle – 161.0°
CueO	**1KV7**	1.712	28.2	His^{443} (2.02) Cys^{500} (2.19) His^{505} (1.98) Met^{510} (3.23)	His^{101} (1.92) His^{446} (1.83) O1(OH) (3.12) HOH (2.96)	His^{141} (1.97) His^{501} (2.09) His^{103} (1.96) **OH** (2.43)	His^{143} (2.02) His^{499} (2.02) His^{448} (1.94) **OH** (2.29)	Cu(2)-Cu(3) – 4.70 Cu(2)-Cu(4) – 3.98 Cu(3)-Cu(4) – 3.54 Cu(2)-O-Cu(3) angle – 169.3°
CotA	**1W6L**	1.670	26.6	His^{419} (2.02) Cys^{492} (2.22) His^{497} (1.98) Met^{502} (3.26)	His^{105} (1.96) His^{422} (2.03) O2(Oxy) (2.42) HOH (2.98)	His^{153} (2.08) His^{493} (2.13) His^{107} (2.07) O1(**Oxy**) (2.57) O2(**Oxy**) (2.59)	His^{155} (2.11) His^{491}(2.07) His^{424} (2.04) O1(**Oxy**) (2.31) O2(**Oxy**) (2.29)	Cu(2)-Cu(3) – 4.73 Cu(2)-Cu(4) – 3.99 Cu(3)-Cu(4) – 3.66 Cu(2)-O1-Cu(3) angle – 151.4° Cu(2)-O2-Cu(3) angle – 151.8°
AO (chain A)	**1AOZ**	1.886	26.8	His^{445}(2.09) Cys^{507} (2.13) His^{512} (2.05) Met^{517} (2.90)	His^{60}(2.00) His^{448} (2.09) OH (2.02)	His^{104} (2.19) His^{508} (2.14) His^{62} (1.98) **OH** (2.06)	His^{106} (2.16) His^{506} (2.07) His^{450} (2.06) **OH** (1.99)	Cu(2)-Cu(3) – 3.69 Cu(2)-Cu(4) – 3.66 Cu(3)-Cu(4) - 3.79 Cu(2)-O-Cu(3) angle – 130.9°
MaLa (chain A)	**1GW0**	1.898	24.7	His^{431} (1.91) Cys^{503} (2.20) His^{508} (1.93) Leu^{513} (3.68)	His^{93}(1.89) His^{434} (1.92) O1(Oxy) (2.62) Cl (2.48)	His^{138} (1.94) His^{504} (1.95) His^{95} (1.90) O1(**Oxy**) (2.48) O2(**Oxy**) (2.66)	His^{140} (1.96) His^{502} (1.97) His^{436} (1.92) O1(**Oxy**) (2.59) O2(**Oxy**) (2.38)	Cu(2)-Cu(3) – 4.91 Cu(2)-Cu(4) – 4.16 Cu(3)-Cu(4) – 3.92 Cu(2)-O1-Cu(3) angle – 153.4° Cu(2)-O2-Cu(3) angle – 151.5°
TvLa	**1GYC**	2.114	23.0	His^{395} (2.02) Cys^{453} (2.19) His^{458} (2.04) Phe^{463} (---)	His^{64} (2.01) His^{398} (1.97) HOH (2.35)	His^{109} (2.12) His^{454} (2.17) His^{66} (2.15) **OH** (2.08)	His^{111} (2.23) His^{452} (2.16) His^{400} (2.12) **OH** (2.19)	Cu(2)-Cu(3) – 3.91 Cu(2)-Cu(4) – 3.81 Cu(3)-Cu(4) – 3.82 Cu(2)-O-Cu(3) angle – 132.9°

McoC *Campylobacter jejuni*; CueO *Escherichia coli* [18]; CotA *Bacillus subtilis* [15]; Ascorbate oxidase (AO) *Cucurbita pepo* [61]; MaLa *Melanocarpus albomyces* [62]; TvLa *Trametes versicolor* [63]

[a] Determined by structural superposition with McoC by Secondary Structure Matching [39]; [b] Copper occupancy in McoC copper centres.

CueO structure (PDB:1KV7) was considered as deposited, that is, with a monoatomic oxygen species in between both type 3 Cu ions, although later reports by Roberts *et al* [19] have claimed to believe that this should in fact be considered a chlorine atom.