Suppl. Fig. 1 Proposed structure of the PPO-6 tetramer. In each dimer, two subunits are interacting via a hydrophobic patch (shaded white) and covalently bonded together (yellow bar) by cysteines 197 (C). The forward-facing dimer (horizontal orientation, dark grey) binds to a second, identical backward-facing dimer (axial orientation, light grey) via an unknown binding site. The catalytic pocket of the tyrosinase domain (N-terminal domain, circular form) is shielded by the C-terminal domain (oval form) pending activation. The C-terminal domain is pointing towards the tetramer surface for each of the four subunits.