Supporting Information

Rice Bran Protein as a Potent Source of Antimelanogenic Peptides with Tyrosinase Inhibitory Activity

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Figure S1. Bio-Gel P-6 separation of RBP suspension without proteinase treatment. (A) Chromatogram of eluted peptides; (B) Inhibitory activity of each fraction against the monophenolase reaction of tyrosinase; (C) Inhibitory activity of each fraction against the diphenolase reaction of tyrosinase.
Figure S2. Bio-Gel P-6 separation of tyrosinase inhibitory peptides following the treatment of RBP with thermolysin. (A) Chromatogram of eluted peptides; (B) Inhibitory activity of each fraction against the monophenolase reaction of tyrosinase; (C) Inhibitory activity of each fraction against the diphenolase reaction of tyrosinase.
Figure S3. Interactions between mushroom tyrosinase and CT-2. Front (A) and side view (B). The previously characterized binding modes of TH10 (C-terminal short sequence of TH10) are shown in the front view structure. Peptide molecules are indicated with the following colors: red, oxygen atom; blue, nitrogen atom; cyan, carbon atom in CT-2; green, carbon atom in TH10. Tyrosinase amino acid residues that interact with each copper ion are indicated with the following colors: red, oxygen atom; blue, nitrogen atom; violet, carbon atom. Copper ions are shown as orange balls. The peptide ligand CT-2 was docked to mushroom tyrosinase using AutoDock Vina as described in a previous report. Calculations were performed using a grid map of $29 \times 29 \times 29$ and a grid center with $x = -10$, $y = -30$, and $z = -45$. After 100 molecular docking simulations, a complex with the lowest free-energy binding was selected from these runs. The calculated free energy value for CT-2 binding was $-6.8$. 