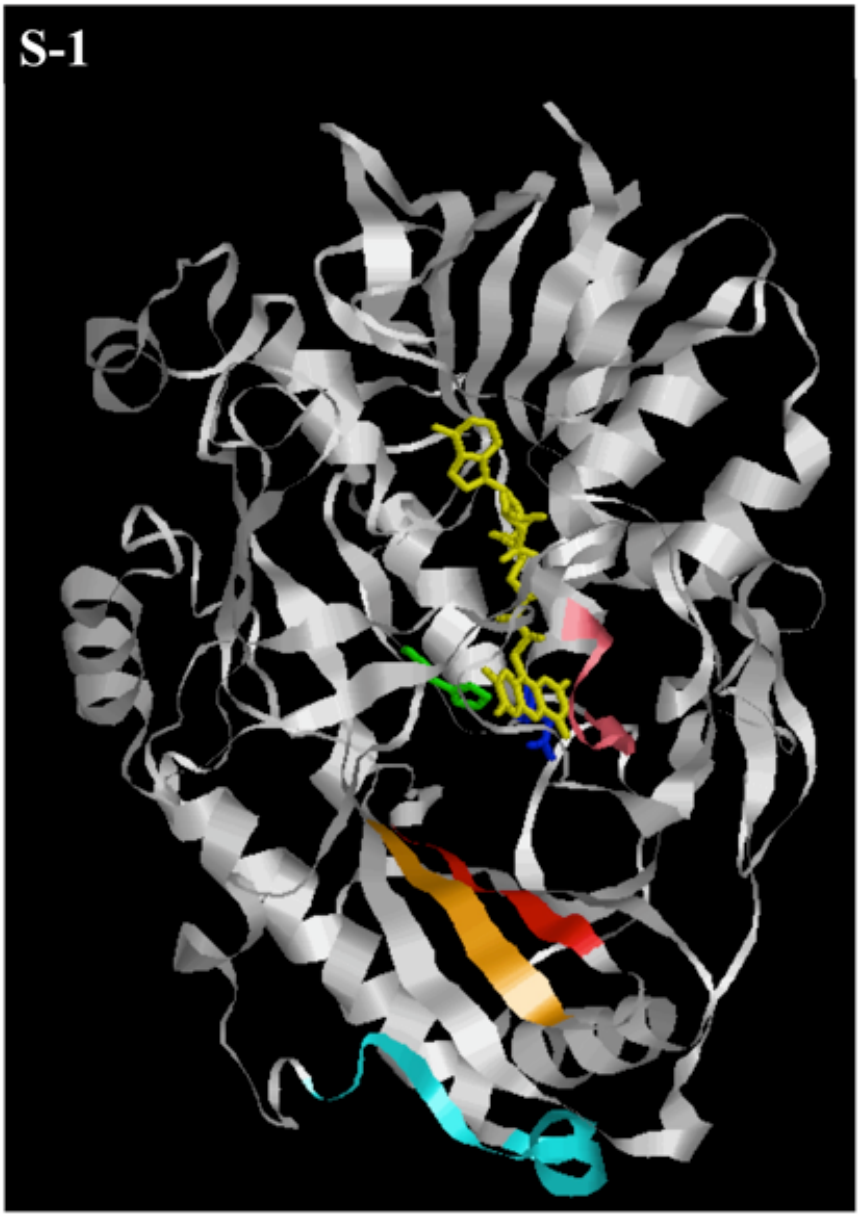
Supplementary Information

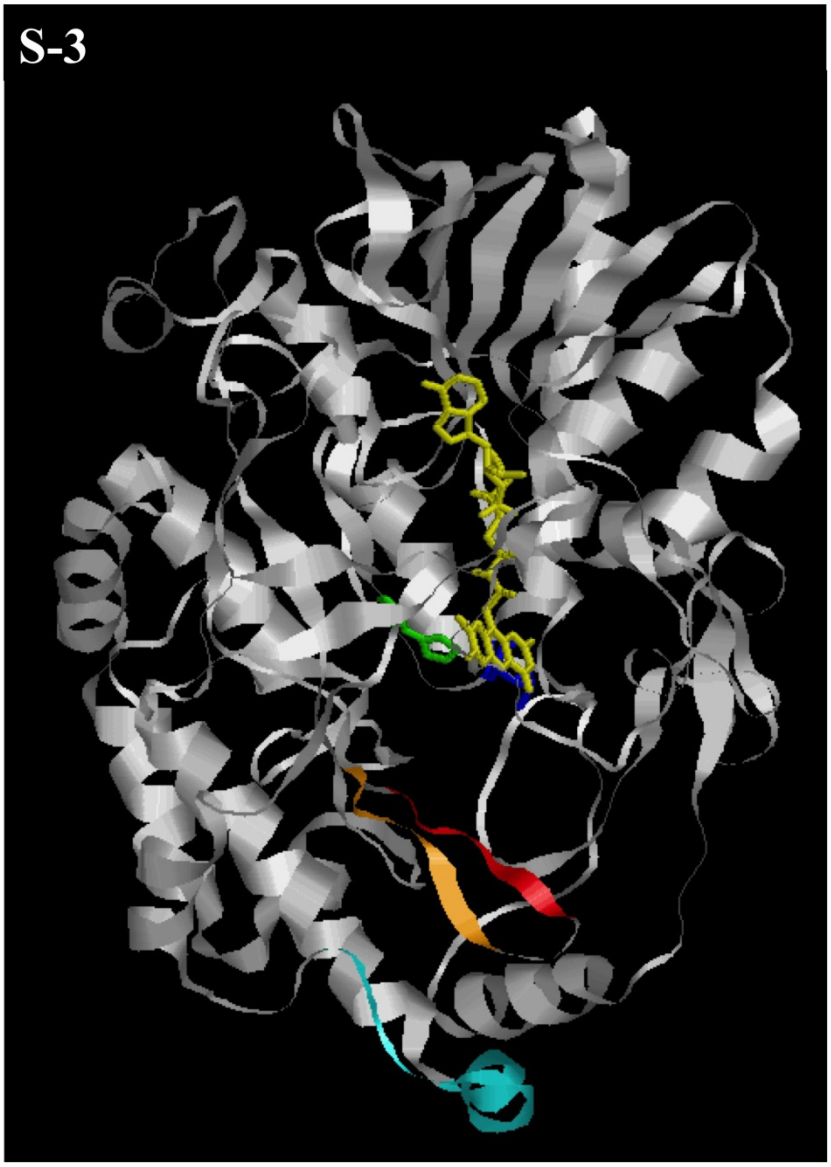
Figure S1–3. The predicted 3D structures of NPEO-DH, OPERO-DH and PEG-DH by homology modeling. **S1**, NPEO-DH; **S2**, OPERO-DH; and **S3**, PEG-DH. FAD is shown in yellow, the active site residues in green for His and in blue for Asn, the first sequence (Table 2) in orange, the second sequence (Table 2) in red, and the membrane-anchoring motif in cyan. Other probable quinone-binding motifs for NPEO-DH (Figure 1) are shown in pink in S1.



S1

Figure S1–3. *Cont.*

Figure S1–3. *Cont.*



S3