Erratum

In Chen S, Wu K, Zhang D, Sherman M, Knox R, and Yang CS (1999) Molecular characterization of binding of substrates and inhibitors to DT-diaphorase: Combined approach involving site-directed mutagenesis, inhibitor-binding analysis, and computer modeling. *Mol Pharmacol* **56:**272–278, Figure 2 on page 275 should have been published in color. We regret any inconvenience caused by this error. The color version of the figure is given below with its legend.

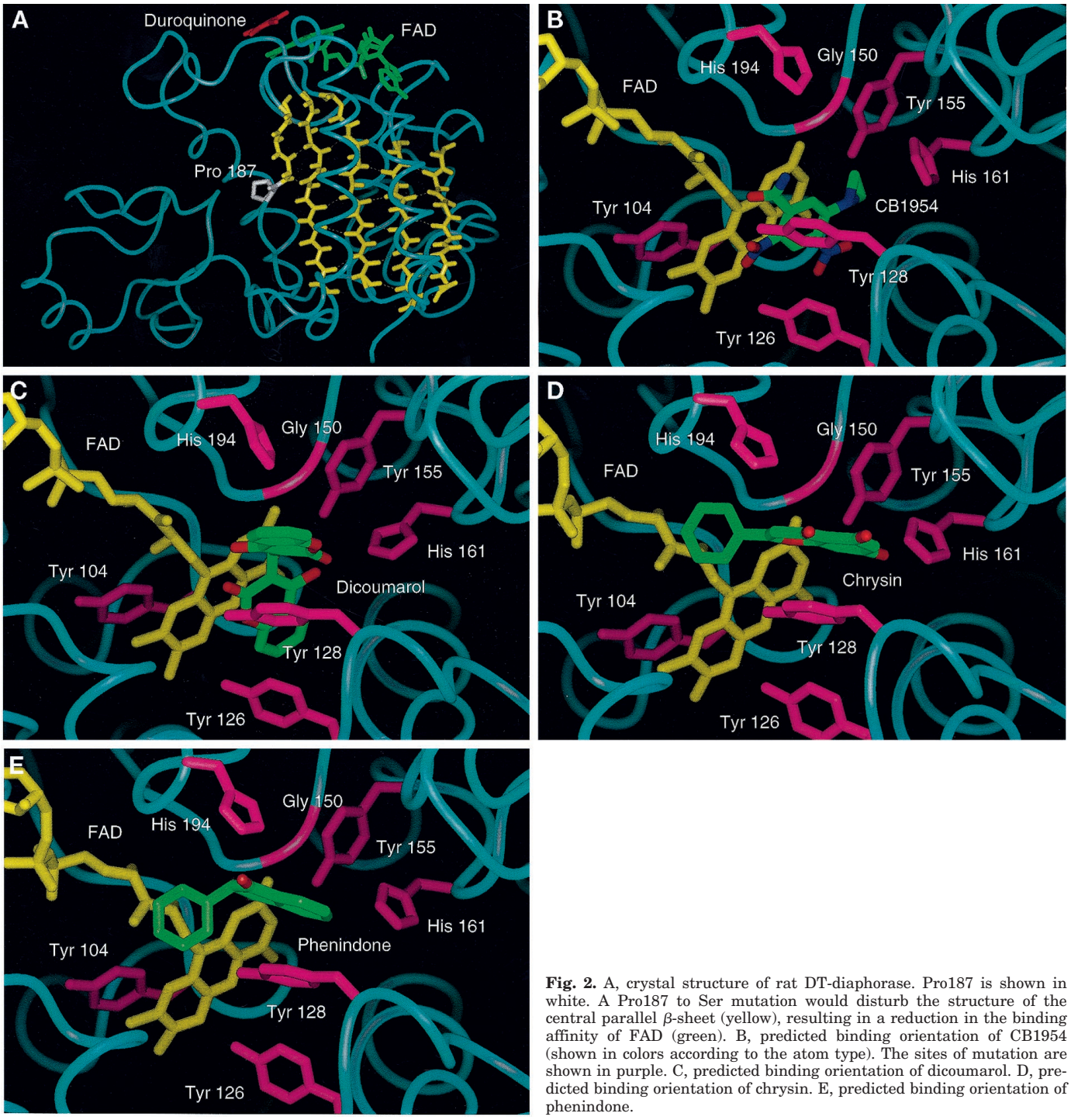

Fig. 2. A, crystal structure of rat DT-diaphorase. Pro187 is shown in white. A Pro187 to Ser mutation would disturb the structure of the central parallel β-sheet (yellow), resulting in a reduction in the binding affinity of FAD (green). B, predicted binding orientation of CB1954 (shown in colors according to the atom type). The sites of mutation are shown in purple. C, predicted binding orientation of dicoumarol. D, predicted binding orientation of chrysin. E, predicted binding orientation of phenindone.