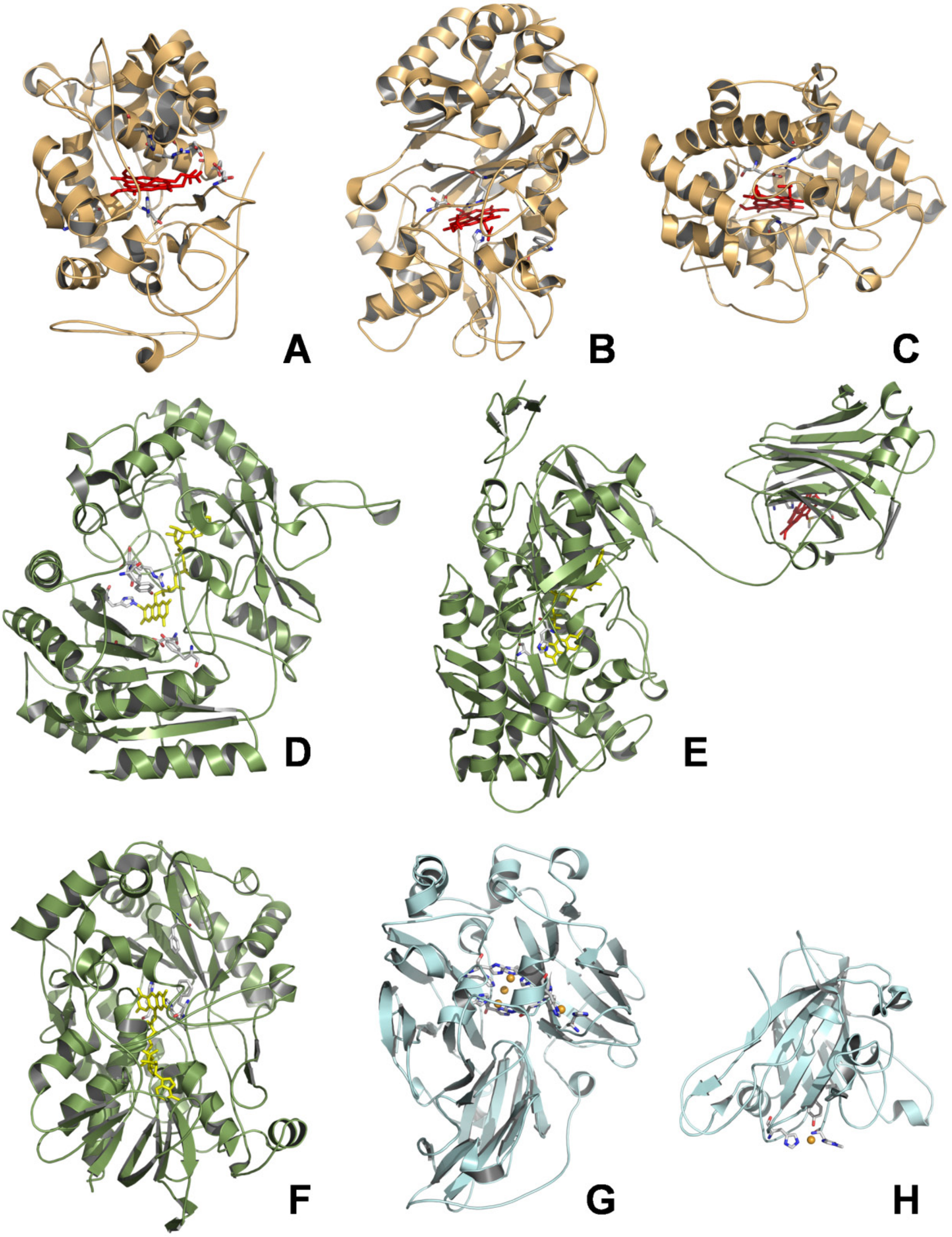

Fig. 1. Classical and new oxidoreductase families involved in lignocellulose degradation and other biotransformations of interest: **A.** *Pleurotus eryngii* VP (3FJW); **B.** *Auricularia auricula-judae* DyP (4W7J); **C.** *Agrocybe aegerita* UPO (2YP1); **D.** *Penicillium simplicissimum* VAO monomer (1VAO); **E.** *Neurospora crassa* CDH with flavin and heme domains (4QI7); **F** *Pleurotus eryngii* AAO (3FIM); **G.** *Pycnoporus cinnabarinus* laccase (2XYB); and **H.** *Thermoascus aurantiacus* LPMO (2YET). Cofactors (heme/FAD and copper ions as red and yellow sticks and orange spheres, respectively) and residues relevant for catalysis (Corey/Pauling/Koltun, CPK, colored sticks) such as: **i)** His, Cys and Met/His ligands of heme iron in **A/B**, **C** and **E**, respectively; **ii)** His/Arg, Asp/Arg and Glu/Arg involved in activation by H_2O_2 in **A**, **B** and **C**, respectively; **iii)** 2 Glu and 1 Asp forming the Mn binding site in **A**; **iv)** catalytic Trp in **A** and **B**; **v)** active site residues in **D-F**, including His linked to FAD in **D**; **vi)** 4 copper ions in **G**; and **vii)** 2 His and 1 Tyr copper ligands in **H**.