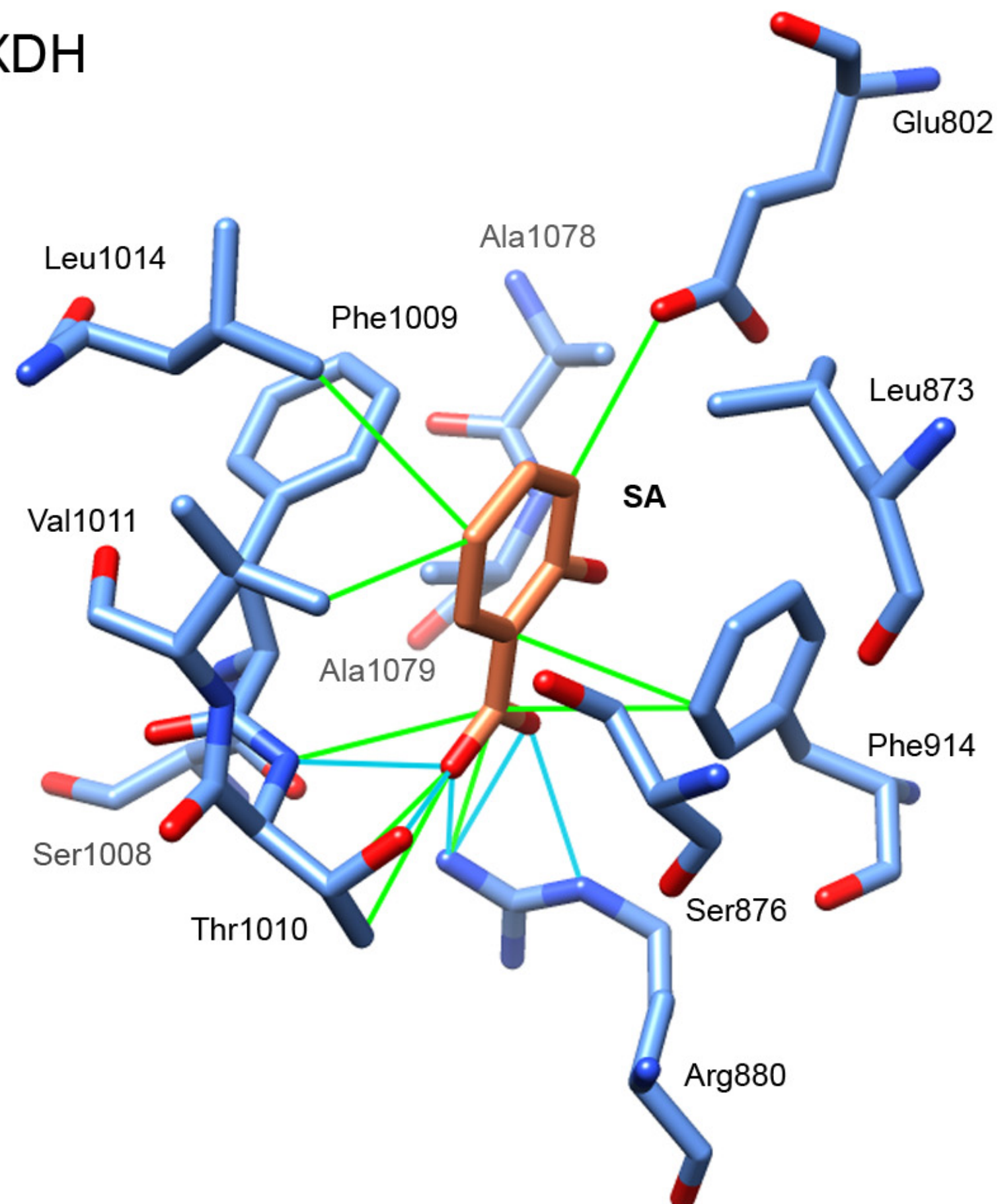
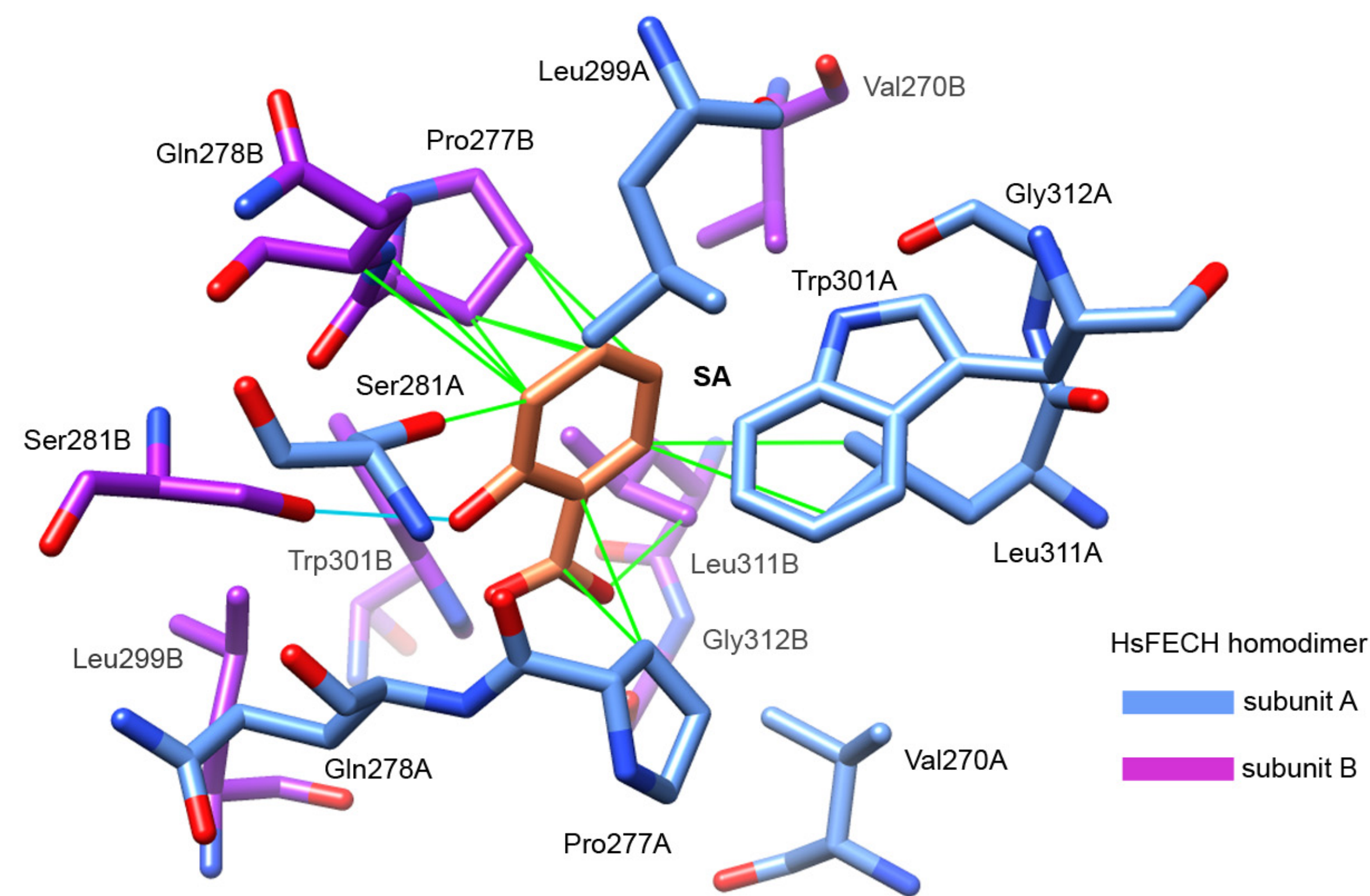


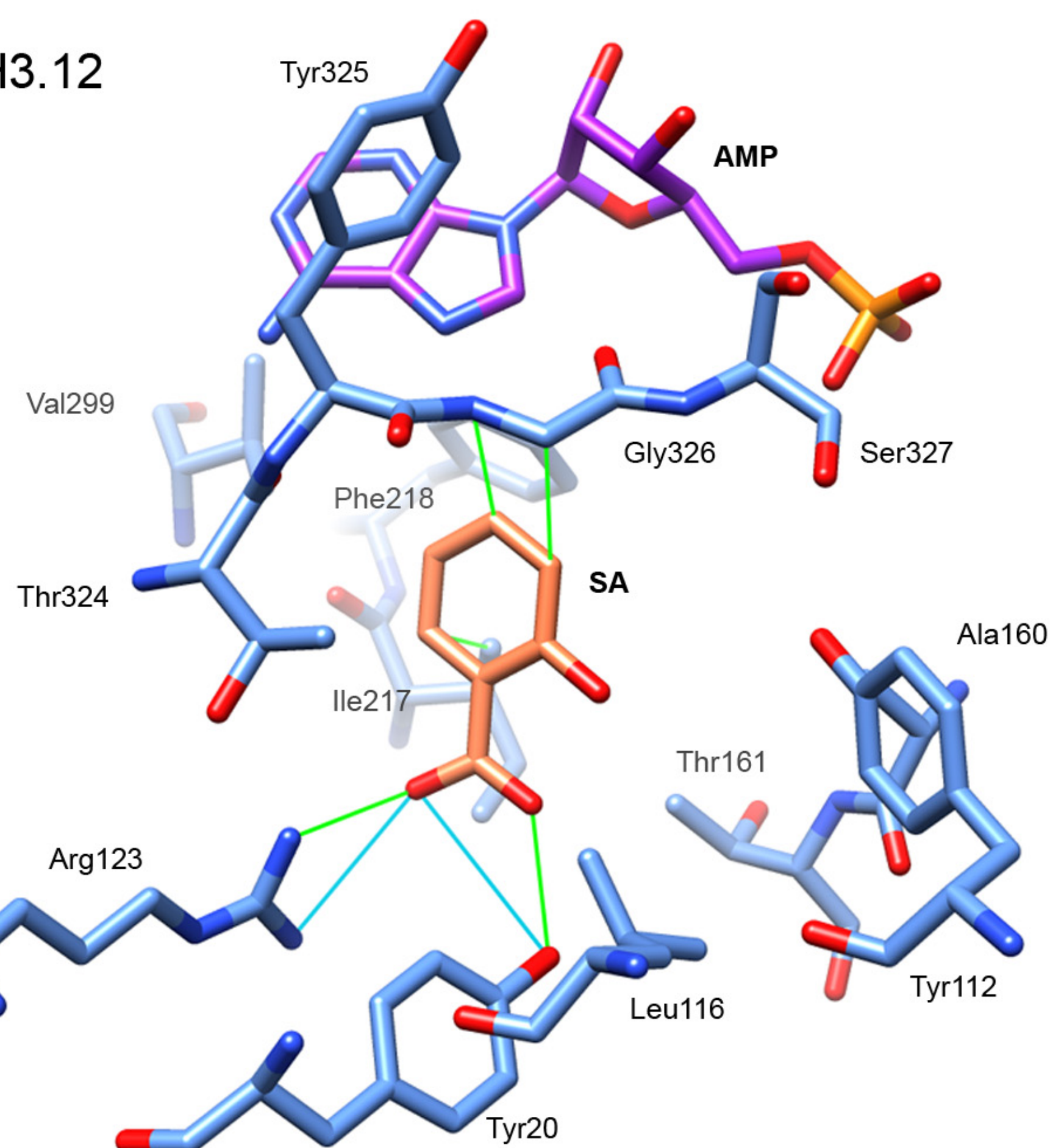
BtXDH



HsFECH



AtGH3.12



NtSABP2

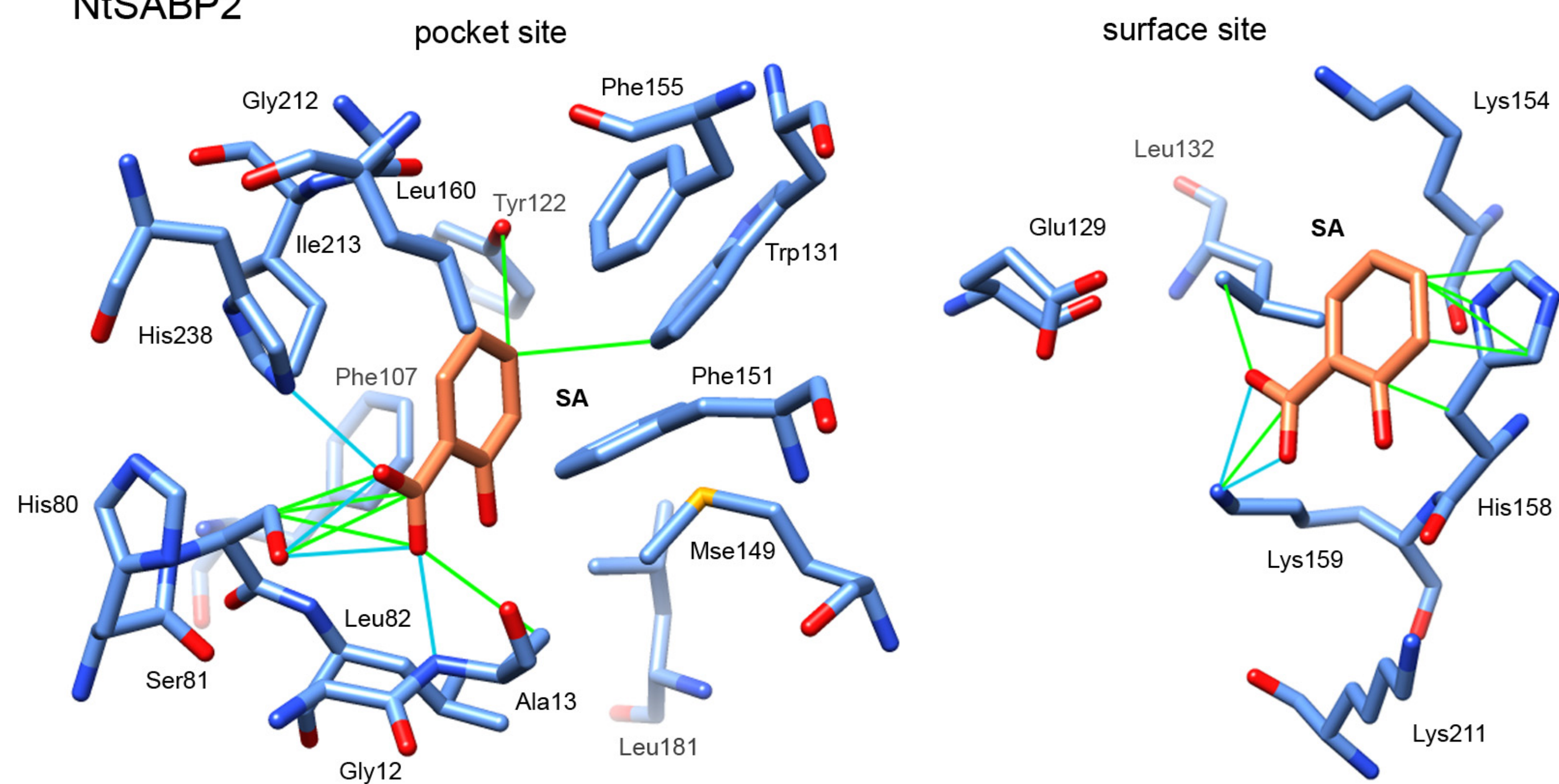


Figure S1. Amino acid residues in direct vicinity ($\leq 5\text{\AA}$) of a SA ligand. Ligand interactions were visualized using the UCSF Chimera (<https://www.cgl.ucsf.edu/chimera/>). Hydrogen bonds are depicted as blue lines; other bonds (cumulatively polar and non-polar) are depicted as green lines. At, *A. thaliana*; Bt, *Bos taurus*; FECH, ferrochelatase; GH3.12, Gretchen Hagen 3.12; Hs, *Homo sapiens*; Mse, selenomethionine; Nt, *Nicotiana tabacum*; SABP, salicylic acid binding protein; XDH, xanthine dehydrogenase.