

SUPPLEMENTARY MATERIALS

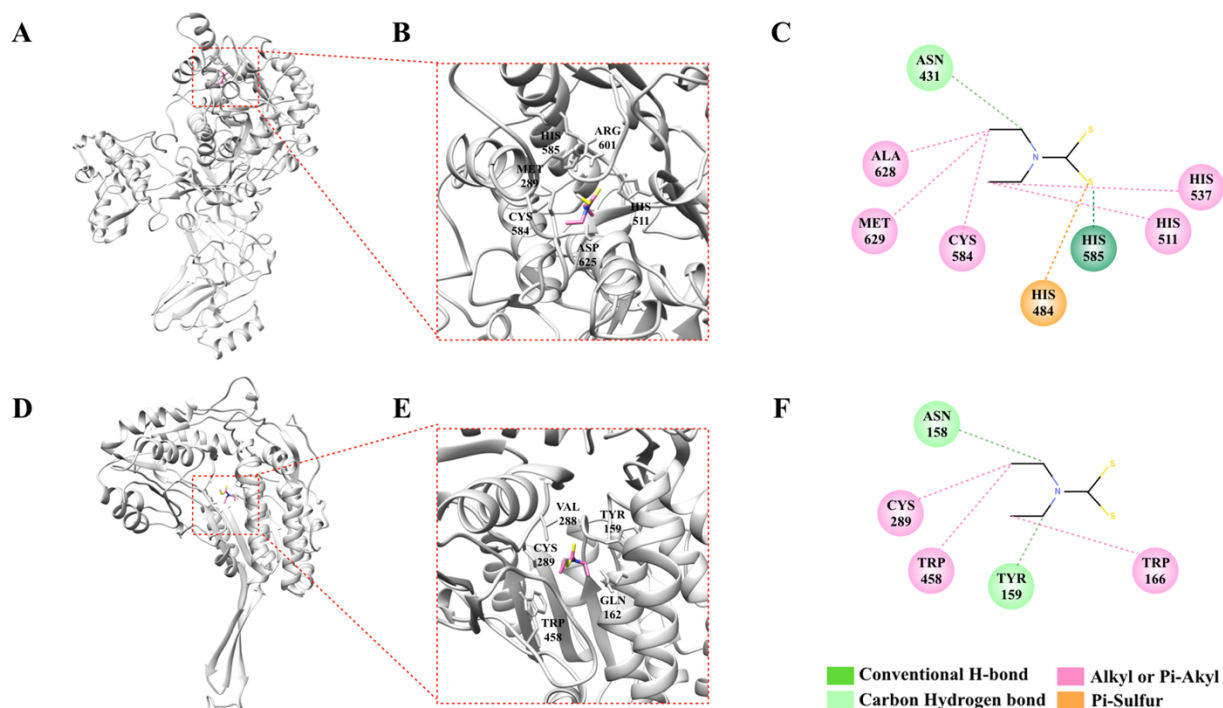


Figure S1. Complexes of the ligand ‘diethyldithiocarbamic acid (DDC)’ and the predicted three-dimension structures of the urease (A-C) and aldehyde dehydrogenase (D-F) of *P. insidiosum*. **A** and **D** show ribbon structure models, while **B** and **E** depict enlarged structure showing molecular docking of DDC. Figures **C** and **F** show two-dimension interactions of DDC and the predicted binding sites of urease and aldehyde dehydrogenase, respectively. The interacting amino acids and types are shown in figures **B**, **C**, **E**, and **F**.

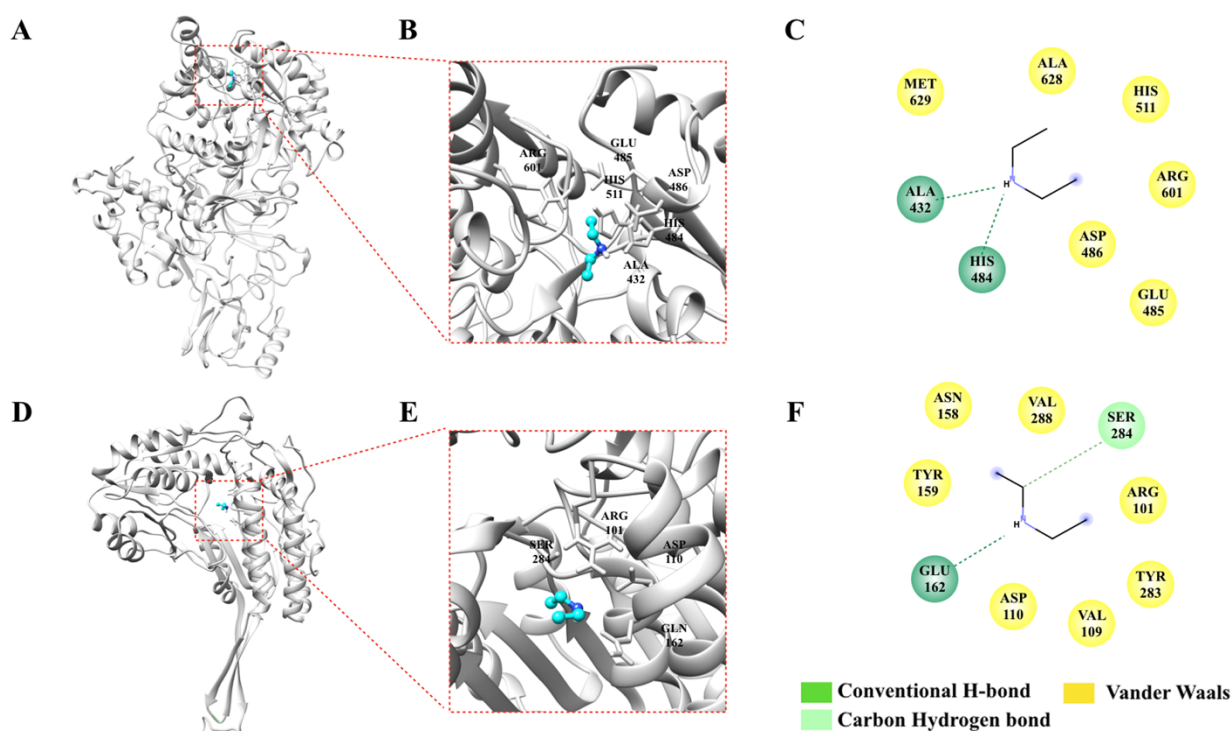


Figure S2. Complexes of the ligand ‘diethylamine (DEA)’ and the predicted three-dimension structures of the urease (A-C) and aldehyde dehydrogenase (D-F) of *P. insidiosum*. A and D show ribbon structure models, while B and E depict enlarged structure showing molecular docking of DEA. Figures C and F show two-dimension interactions of DEA and the predicted binding sites of urease and aldehyde dehydrogenase, respectively. The interacting amino acids and types are shown in figures B, C, E, and F.

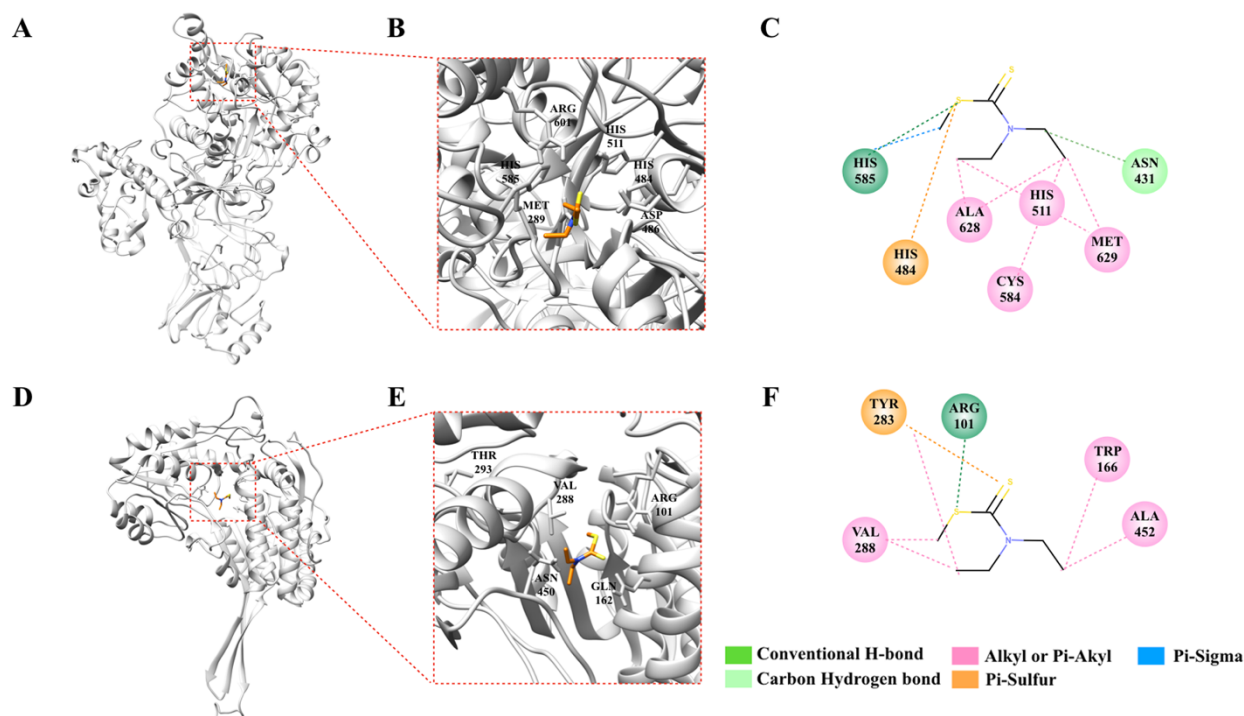


Figure S3. Complexes of the ligand ‘diethyldithiomethylcarbamate (Me-DDC)’ and the predicted three-dimensional structures of the urease (A-C) and aldehyde dehydrogenase (D-F) of *P. insidiosum*. A and D show ribbon structure models, while B and E depict enlarged structure showing molecular docking of Me-DDC. Figures C and F show two-dimension interactions of Me-DDC and the predicted binding sites of urease and aldehyde dehydrogenase, respectively. The interacting amino acids and types are shown in figures B, C, E, and F.