Supplementary data

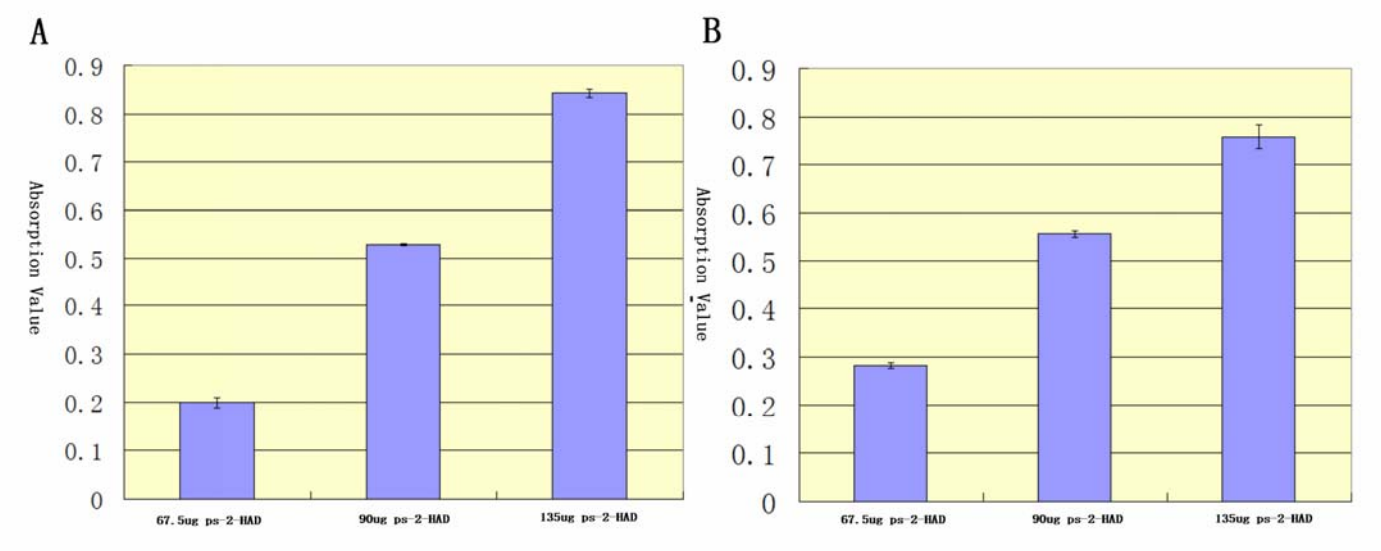

Figure S1. Enzymatic activity analysis of ps-2-HAD using mercuric thiocyanate.

(A) ps-2-HAD enzyme titration assay against substrate L-CPA (n=3). (B) ps-2-HAD enzyme titration assay against substrate D-CPA (n=3).

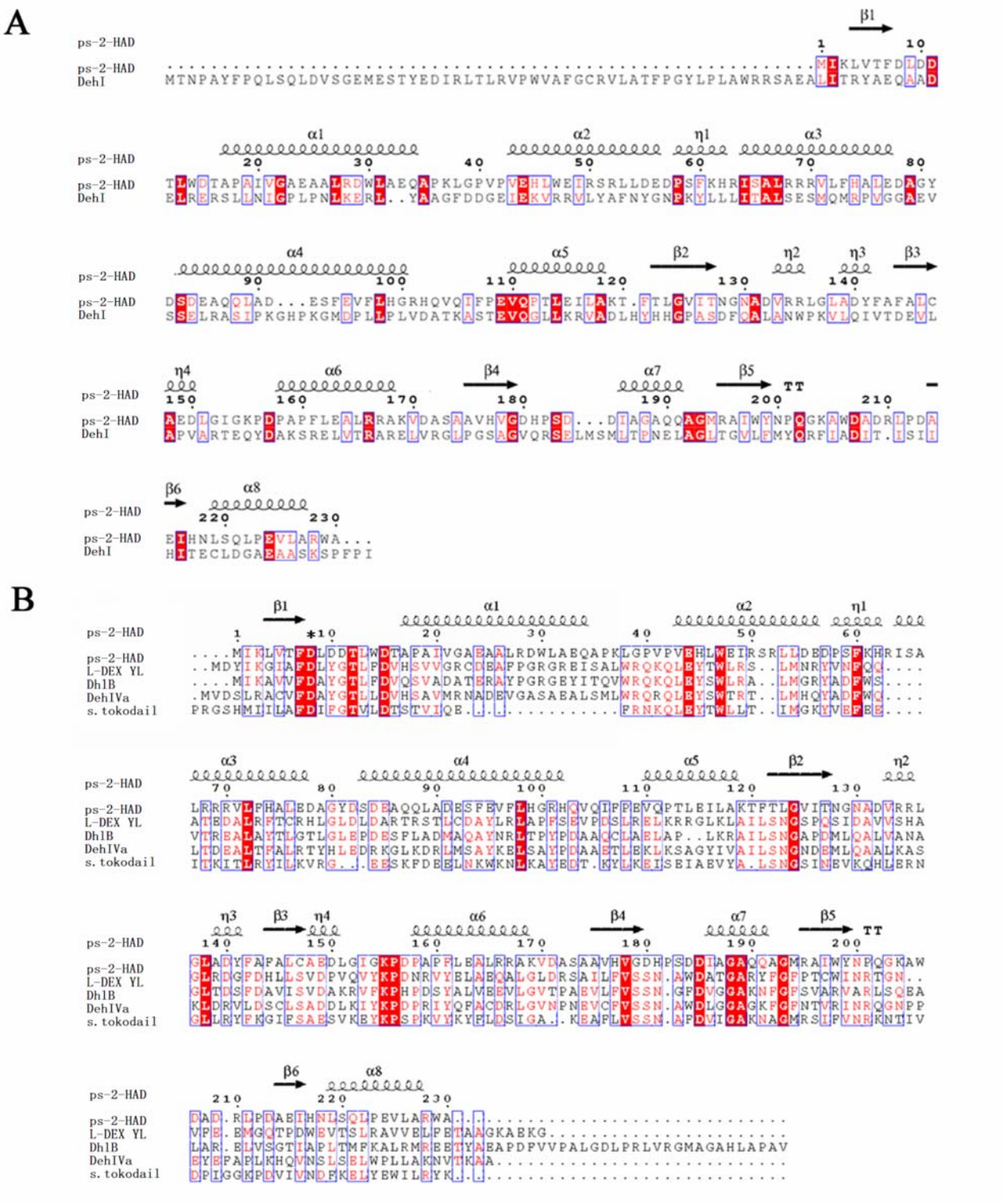

Figure S2. Sequence alignments of ps-2-HAD with other 2-HADs with known structures (A) Sequence alignment of ps-2-HAD with D-2-HAD (DehI, PDB ID: 3BJX). (B) Sequence alignment of ps-2-HAD with four L-2-HADs. The PDB ID are as follows: L-DEX YL, PDB ID: 1JUD; DhlB, PDB ID: 1AQ6; DehIVa, PDB ID:

2NO4; s.tokodail, PDB ID: 2W11. Conserved amino acid residues are highlighted by red, with the conserved Asp residue in L-2-HAD marked with asterisk (*). The sequence alignment was carried out with Multalign program [1] and represented by Espript [2].

References

[1] F. Corpet, Multiple Sequence Alignment with Hierarchical-Clustering, Nucleic Acids Research 16 (1988) 10881-10890.

[2] P. Gouet, E. Courcelle, D.I. Stuart, F. Metoz, ESPript: analysis of multiple sequence alignments in PostScript, Bioinformatics 15 (1999) 305-308.