

Supplementary Materials

Figure 1. Stereoview of metal-binding site of the metal-dependent HAD superfamily members. (A) phosphonate-Mg(II)-tungstate complex (pdb:1FEZ) (1), (B) phosphoserine phosphatase-Mg(II)-BeF₃⁻ complex (pdb: 1J97) (2), (C) β-phosphoglucomutase-glucose-1,6-bisphosphate intermediate complex (pdb:1O03) (3), (D) deoxy-D-Mannose- octulosonate 8- phosphate phosphatase-Co(II)-sulfate complex (pdb:1K1E) (4), (E) human mitochondrial deoxyribonucleotidase-Mg(II)-phosphate complex (pdb: 1MH9) (5), (F) lipid phosphatase domain of the bifunctional phosphatase/epoxide hydrolase (pdb:1CQZ) (6), (G) phosphatase domain of bifunctional T4 polynucleotide kinase/phosphatase (pdb: 1LTQ) (7), (H) P domain of membrane bound ATP dependent Ca(II) pump (pdb: 1EUL) (8). Color Scheme: Mg(II) and the backbone of loop 4 in all the structures are colored green, the nucleophilic Asp is red and the residue two amino-acid residues downstream is magenta, the inner-sphere Mg(II) ligand, which binds metal ion directly, is colored blue while the outer sphere ligand that interacts through a water bridge is cyan. The active site ligand (substrate or inhibitors) are colored gray, the Mg(II) water ligands are color light blue. Other Mg(II) ligands not belonging to the above and the third carboxylate residues in loop 4 are colored gold. In the cases of F, G, H, no metal ions are observed in X-ray structures, but the dependence on Mg(II) was confirmed previously by biochemical analysis.

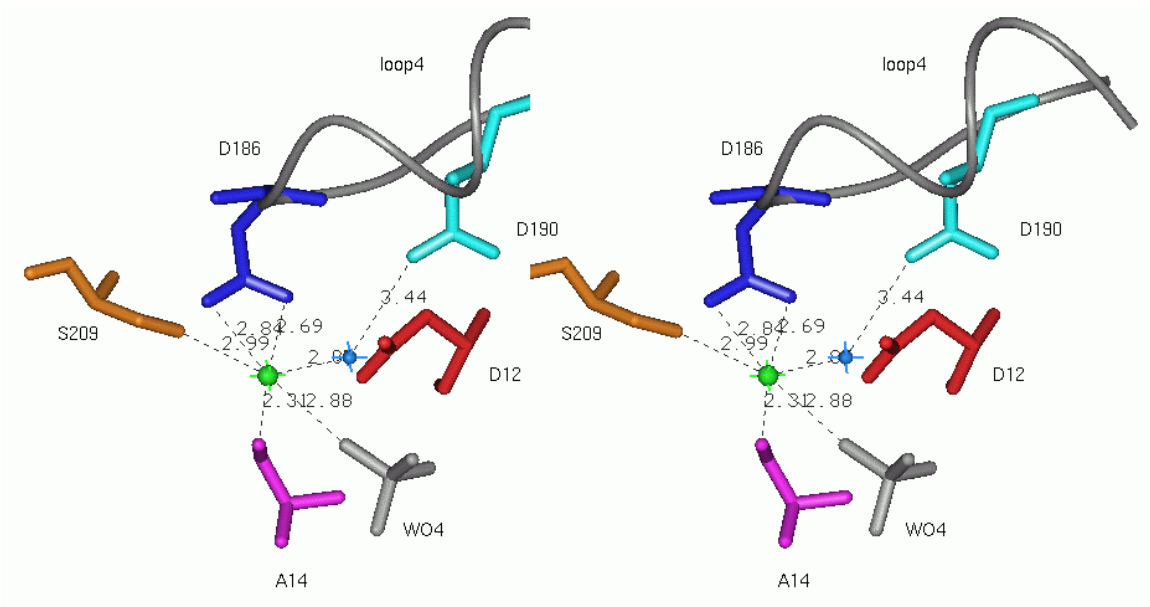


Figure 1A

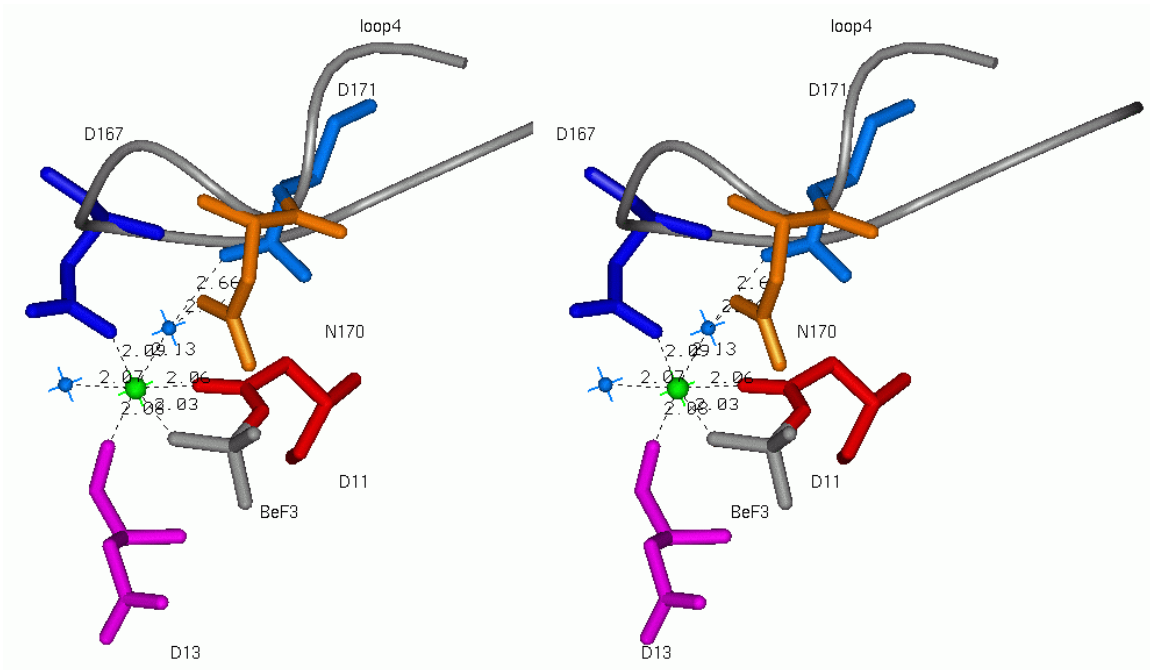


Figure 1B

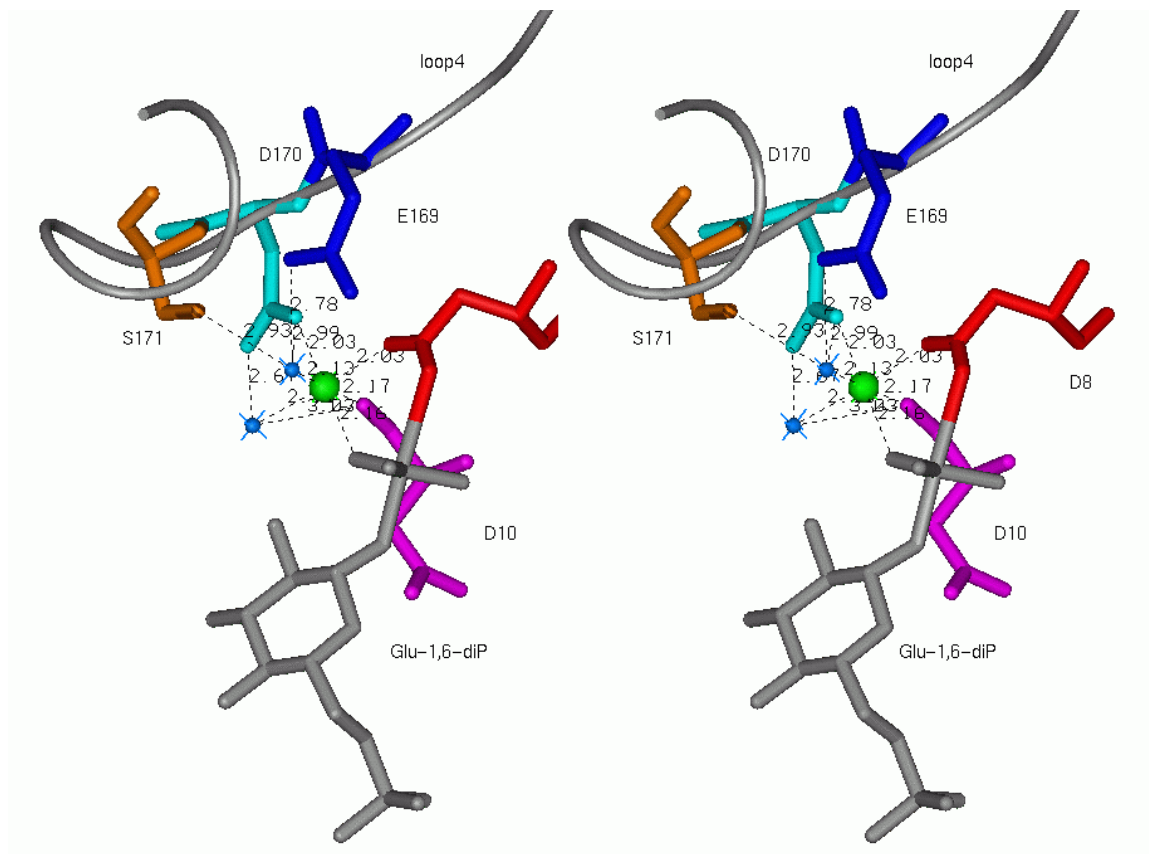


Figure 1C

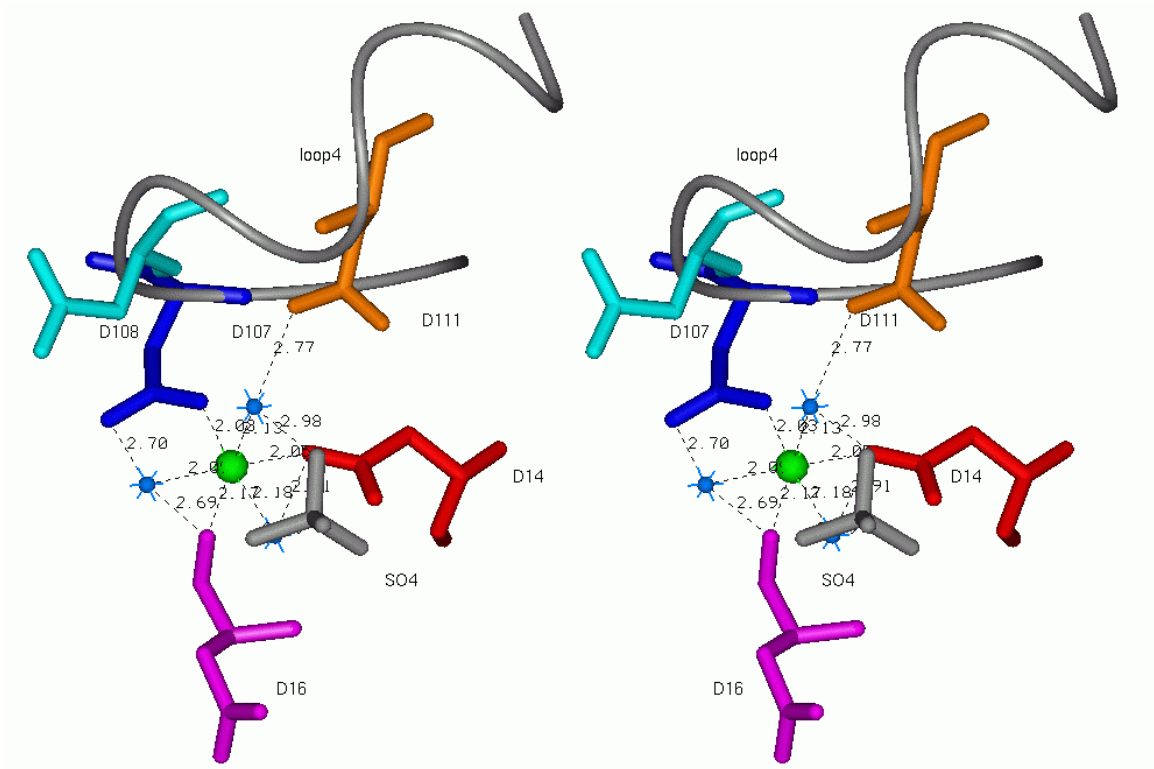


Figure 1D

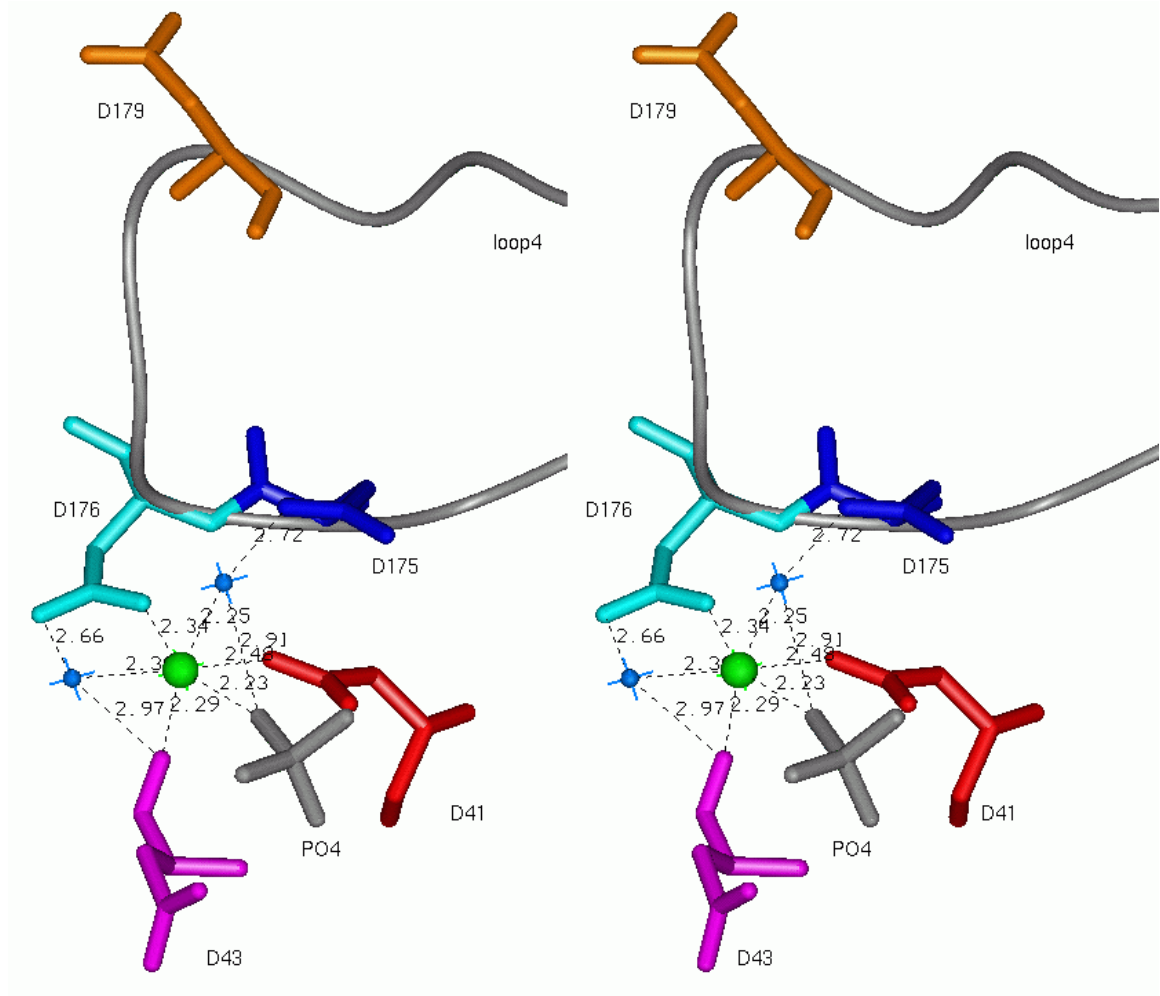


Figure 1E

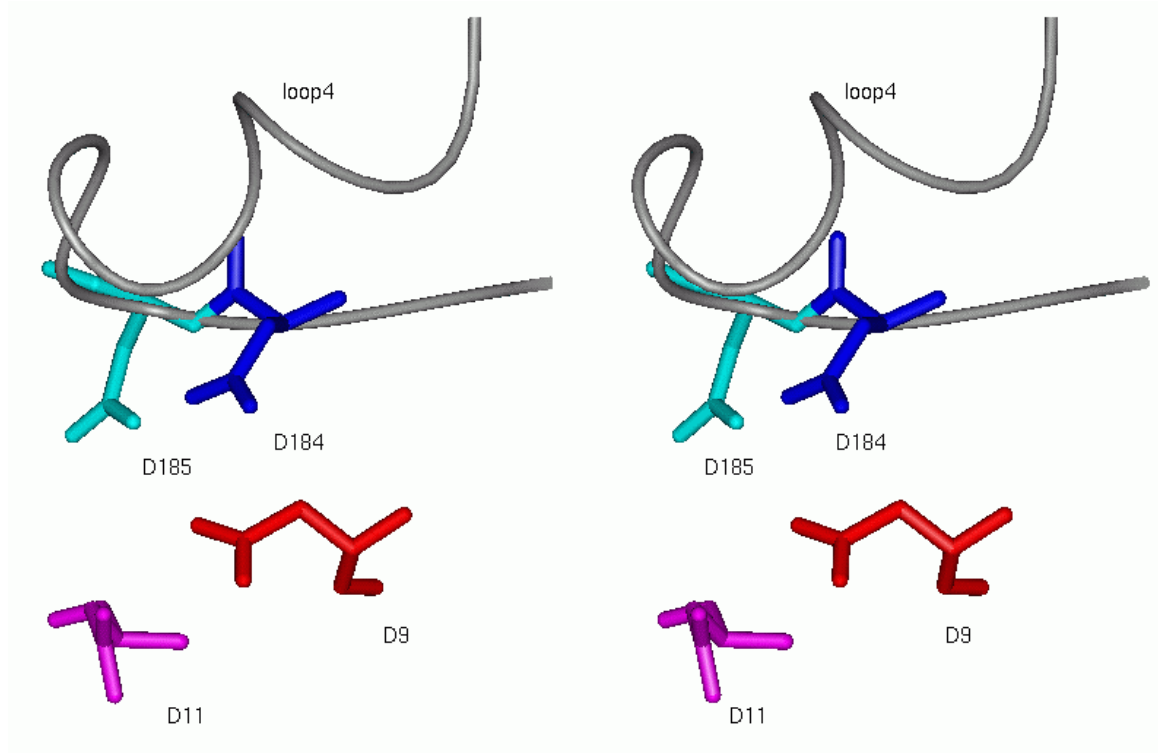


Figure 1F

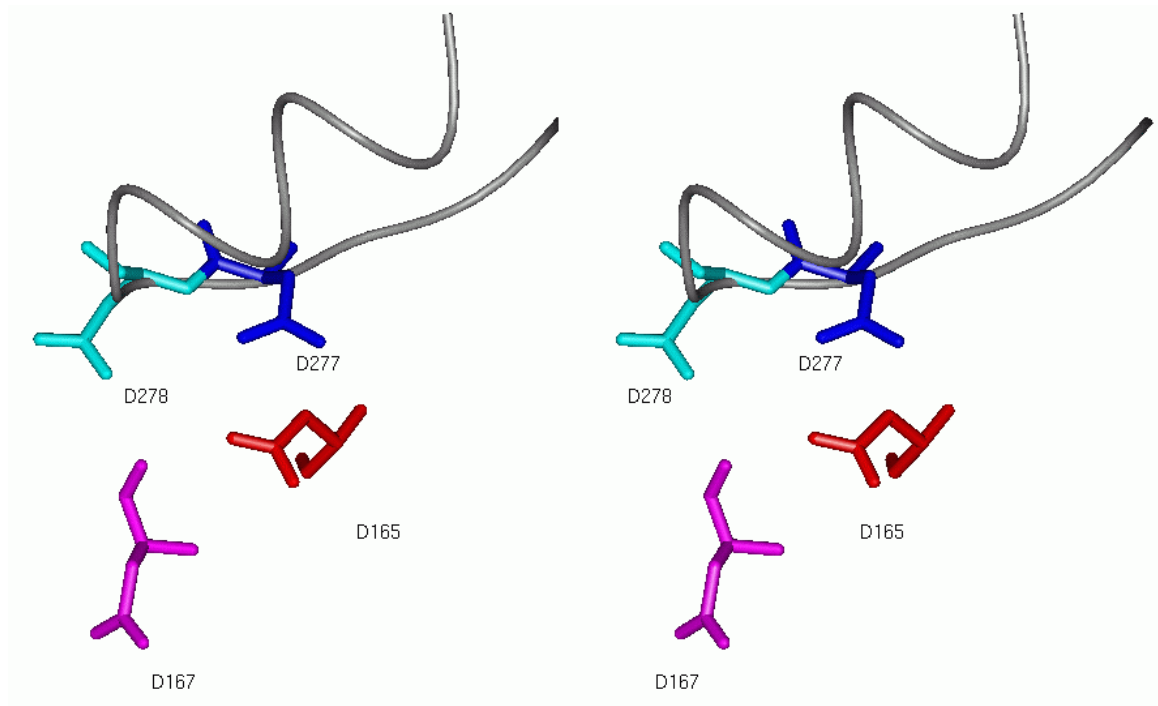


Figure 1G

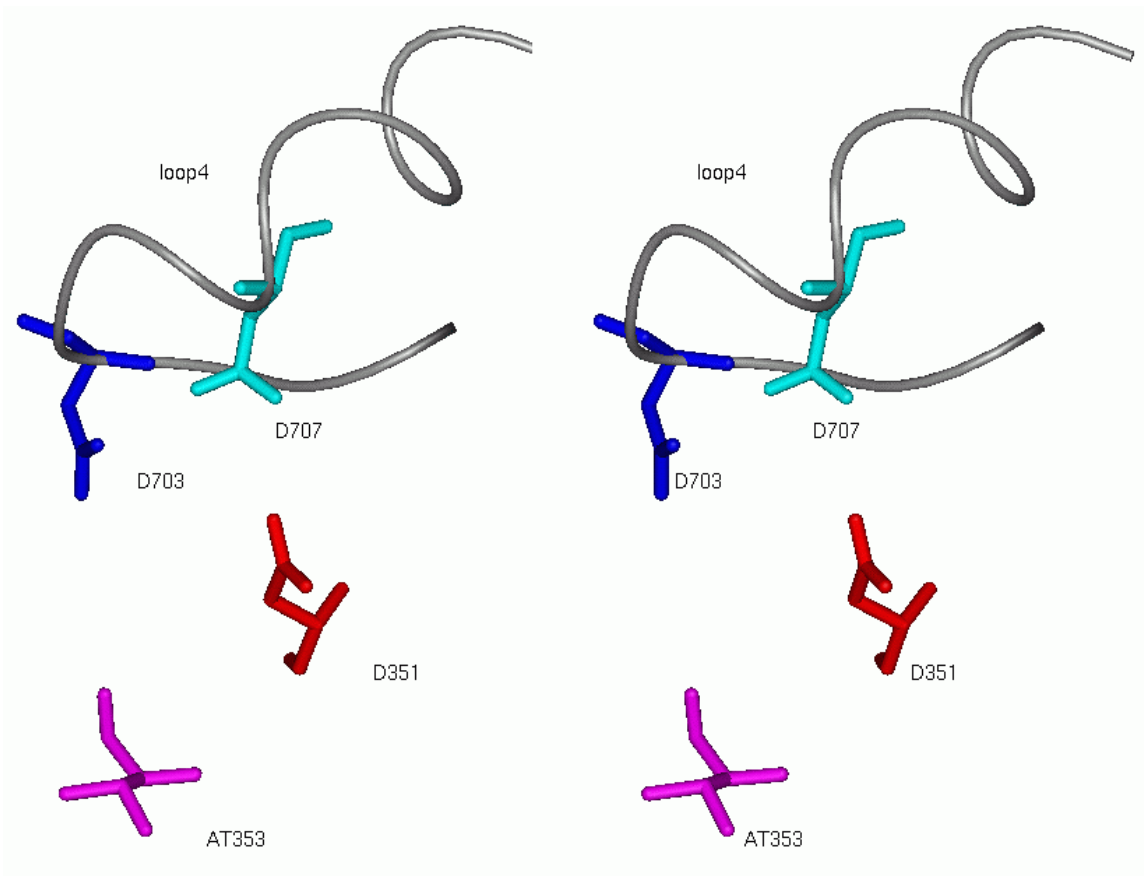


Figure 1H

References

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