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Crystal Structures of Tuberculosis PNP and Giardia APRT

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ABSTRACT: Tuberculosis purine nucleoside phosphorylase (PNP) with its transition state analogue ImmH ($K_1^*=28\text{pM}$) was solved to 1.75 Å resolution. The structure supports a catalytic mechanism of the transition state stabilized by neighboring groups and suggests for the design of transition state analogues with specificity for Tuberculosis PNP. Giardia adenine phosphoribosyltransferase (APRT) in complex with 9-deazaadenine and PRPP was solved to 2.0 Å and is the only APRT structure with a closed active site. The contact between Glu100 from the closed catalytic loop with 9-deazaadenine suggests its role as the acid/base for catalysis.