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MS5-P26 The *cis*-peptide conformation at loop I of the Hypoxanthine phosphoribosyltransferases is not essential for the binding of substrates

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Hypoxanthine phosphoribosyltransferases (HPRT; EC 2.4.2.8) catalyze the transfer of a phosphoribosyl group from 5-phospho-a-D-ribosyl-1-pyrophosphate (PRPP) to a purine base (hypoxanthine, guanine or xanthine) to form pyrophosphate (PPi) and a purine nucleotide, inosine monophosphate (IMP), guanosine monophosphate (GMP), or xanthosine monophosphate (XMP), respectively. At the active site one of the loops involved in the binding of the substrates (loop I) all the HPRT structures known up to now have a peptide bond in a *cis* conformation allowing the binding of one phosphate group. We have solved the structure of the HPRT from *Chromobacterium violaceum* in the presence of the substrates PRPP, IMP and GMP; and in all of these structures we have not observed the presence of the cis conformation at loop I. This protein presents a glycine at the second position of this three residue loop, while the usual amino acid present at this position are lysine or arginine that are involved in the ability or inability to carry out the pyrophosphorolysis (reverse) reaction, respectively.

Keywords: HPRT, Loop I, cis-peptide conformation