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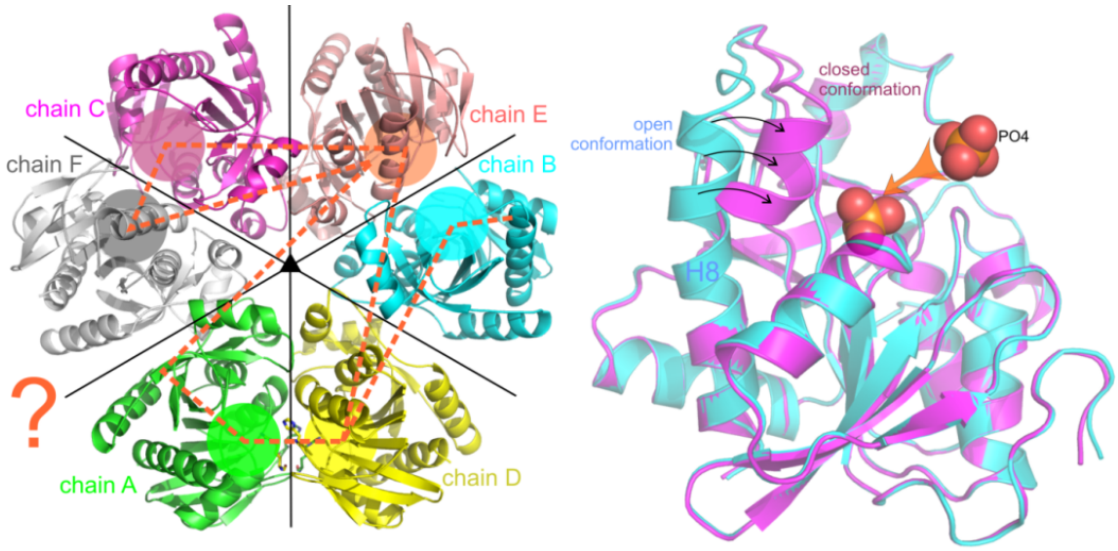
CROATIAN ACADEMY OF SCIENCES AND ARTS
CROATIAN CRYSTALLOGRAPHIC ASSOCIATION

FACULTY OF CHEMISTRY AND CHEMICAL TECHNOLOGY,
UNIVERSITY OF LJUBLJANA

The Twenty-Sixth Croatian-Slovenian Crystallographic Meeting

Poreč, Croatia, June 13 - 17, 2018

Book of Abstracts



The overall structure of hexameric nucleoside phosphorylases can be viewed as a trimer of dimers arranged in an approximate 32 point group symmetry (left). It is likely that active sites communicate between themselves through a yet unknown allosteric mechanism (indicated by orange dashed lines). Each monomer can be found in open and closed active site conformation. The active site is closed by segmentation of the terminal helix H8. The influence of binding of phosphate, one of the two substrates, on this conformational change is still not completely understood (right).

Zoran Štefanić, *Purine nucleoside phosphorylases: understanding enzyme mechanism and allosteric pathways*, plenary lecture, *The Twenty-Sixth Croatian-Slovenian Crystallographic Meeting*, Poreč, Croatia, June 13-17, 2018

PROGRAMME