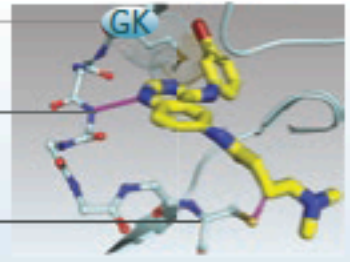
Type I active

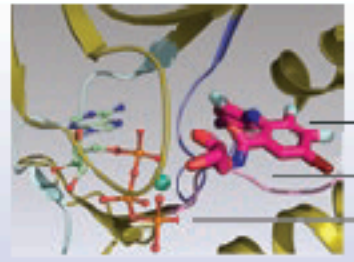


Small gatekeepers provide key to selectivity

Hinge interaction provides a general anchor point

Cysteines may lead to selective irreversible inhibitors

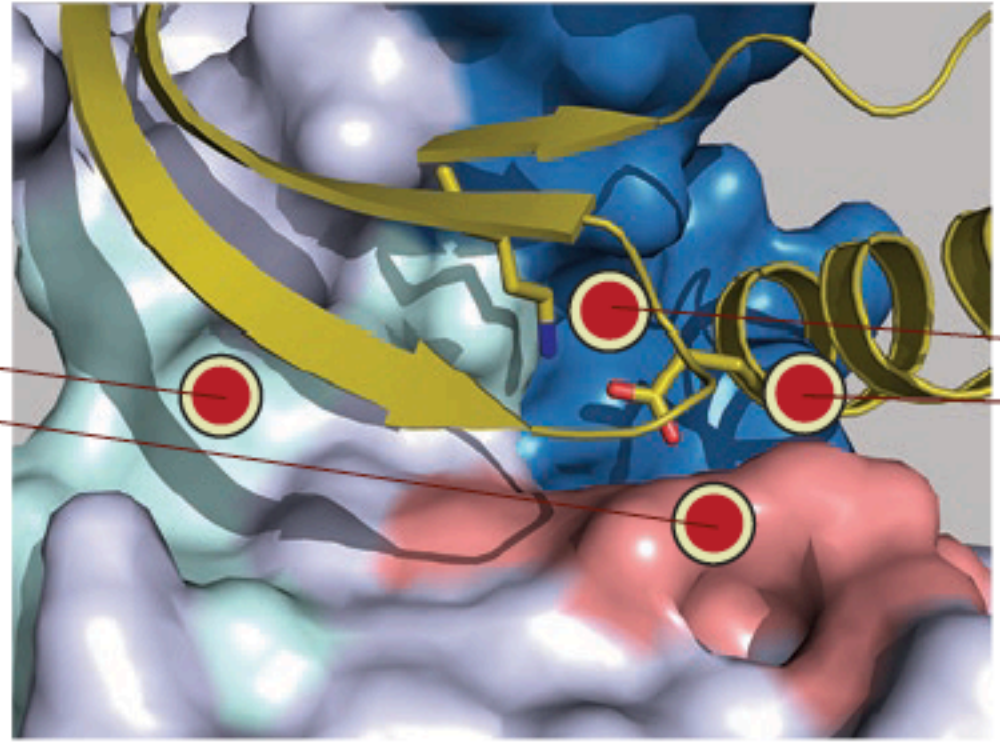
Type III allosteric



Non-ATP competitive

Pocket outside the ATP binding site

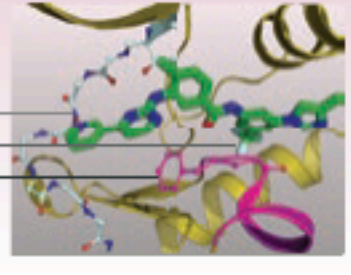
Usually high selectivity due to target-specific allosterc pockets



Require 'DFG out' conformation

Opening of diverse hydrophobic cavity

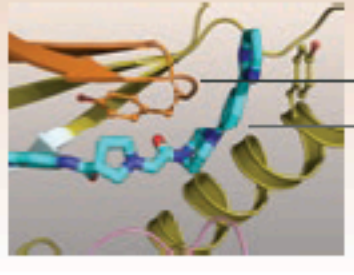
Usually ATP mimetic hinge interaction



Type II inactive

Aromatic residues at the tip of the P-loop with ability to adopt 'folded' conformation

Cavity created between the P-loop and αC



'Folded' P-loop