Title:	Exploring Allostery in dipeptidyl Peptidase IV (DPP IV)
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Keywords:	Exploring dipeptidyl Peptidase
Issue Date:	Apr-2022
Publisher:	IISER Mohali
Abstract:	The protein structure of DPP4 has been well determined through methods such as x-ray crystallography. Earlier literature has allowed us to know the range of motion for the protein. Compared to other members of the DPP family, such as DPP8 and DPP9, due to being a drug target for type-II diabetes, DPP4's ligand substrate binding has been well characterised. However, despite being a significant and well-studied molecule, not much has been recorded about allostery in the protein. One of the critical reasons for this is that while the molecular conformation change in DPP8/9 upon ligand binding is extensive, the ligand-bound and ligand-free states in DPP 4 are largely similar. This lack of extensive conformational change makes it challenging to study allostery in DPP4. The objective of the study is to better understand allostery in DPP4 – identify the sites that are significant for allosteric communication and the pathways that are involved in these communications.
URI:	http://hdl.handle.net/123456789/4183
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