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A model for the regulation of D-3-phosphoglycerate dehydrogenase, a Vmax-type allosteric enzyme

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#	Paper	IF	Citations
64	New structures of allosteric proteins revealing remarkable conformational changes. <i>Current Opinion in Structural Biology</i> , 1996 , 6, 824-9	8.1	35
63	The mechanism of velocity modulated allosteric regulation in D-3-phosphoglycerate dehydrogenase. Cross-linking adjacent regulatory domains with engineered disulfides mimics effector binding. <i>Journal of Biological Chemistry</i> , 1996 , 271, 13013-7	5.4	32
62	The mechanism of velocity modulated allosteric regulation in D-3-phosphoglycerate dehydrogenase. Site-directed mutagenesis of effector binding site residues. <i>Journal of Biological Chemistry</i> , 1996 , 271, 23235-8	5.4	46
61	Structure and control of pyridoxal phosphate dependent allosteric threonine deaminase. <i>Structure</i> , 1998 , 6, 465-75	5.2	161
60	Glycerol kinase from Escherichia coli and an Ala65>Thr mutant: the crystal structures reveal conformational changes with implications for allosteric regulation. <i>Structure</i> , 1998 , 6, 1407-18	5.2	49
59	Probing the regulatory domain interface of D-3-phosphoglycerate dehydrogenase with engineered tryptophan residues. <i>Journal of Biological Chemistry</i> , 1998 , 273, 22389-94	5.4	12
58	Deciphering the molecular code of hemoglobin allostery. <i>Advances in Protein Chemistry</i> , 1998 , 51, 185-	253	84
57	The contribution of adjacent subunits to the active sites of D-3-phosphoglycerate dehydrogenase. <i>Journal of Biological Chemistry</i> , 1999 , 274, 5357-61	5.4	22
56	Gleaning non-trivial structural, functional and evolutionary information about proteins by iterative database searches. <i>Journal of Molecular Biology</i> , 1999 , 287, 1023-40	6.5	380
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44	The N-terminal domain of the regulatory subunit is sufficient for complete activation of acetohydroxyacid synthase III from Escherichia coli. <i>Journal of Molecular Biology</i> , 2003 , 325, 275-84	6.5	33
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