Ahmet Bakan

List of Publications by Year in Descending Order

18 papers	1,972 citations	15 h-index	18 g-index
18 ext. papers	2,329 ext. citations	9.6 avg, IF	4.85 L-index

#	Paper	IF	Citations
18	Allostery as Structure-Encoded Collective Dynamics **2020**, 125-141		1
17	Inhibition of Peroxidase Activity of Cytochrome c: De Novo Compound Discovery and Validation. *Molecular Pharmacology*, **2015**, 88, 421-7	4.3	19
16	Synthesis and biological evaluation of 3-aminoisoquinolin-1(2H)-one based inhibitors of the dual-specificity phosphatase Cdc25B. *Bioorganic and Medicinal Chemistry*, **2015**, 23, 2810-8	3.4	28
15	Designing inhibitors of cytochrome c/cardiolipin peroxidase complexes: mitochondria-targeted imidazole-substituted fatty acids. *Free Radical Biology and Medicine*, **2014**, 71, 221-230	7.8	33
14	Evol and ProDy for bridging protein sequence evolution and structural dynamics. *Bioinformatics*, **2014**, 30, 2681-3	7.2	130
13	Investigational inhibitors of PTP4A3 phosphatase as antineoplastic agents. *Expert Opinion on Investigational Drugs*, **2014**, 23, 661-73	5.9	15
12	In vivo structure-activity relationship studies support allosteric targeting of a dual specificity phosphatase. *ChemBioChem*, **2014**, 15, 1436-45	3.8	34
11	Druggability Assessment of Allosteric Proteins by Dynamics Simulations in the Presence of Probe Molecules. *Journal of Chemical Theory and Computation*, **2012**, 8, 2435-2447	6.4	113
10	Coupling between catalytic loop motions and enzyme global dynamics. *PLoS Computational Biology*, **2012**, 8, e1002705	5	35
9	ProDy: protein dynamics inferred from theory and experiments. *Bioinformatics*, **2011**, 27, 1575-7	7.2	626
8	Pre-existing soft modes of motion uniquely defined by native contact topology facilitate ligand binding to proteins. *Protein Science*, **2011**, 20, 1645-58	6.3	74
7	Computational generation inhibitor-bound conformers of p38 MAP kinase and comparison with experiments. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2011**, 181-92	1.3	17
6	Sodium-coupled Secondary Transporters: Insights from Structure-based Computations **2011**, 199-229		2
5	Normal mode analysis of biomolecular structures: functional mechanisms of membrane proteins. *Chemical Reviews*, **2010**, 110, 1463-97	68.1	383
4	The intrinsic dynamics of enzymes plays a dominant role in determining the structural changes induced upon inhibitor binding. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 14349-54	11.5	219
3	Zebrafish chemical screening reveals an inhibitor of Dusp6 that expands cardiac cell lineages. *Nature Chemical Biology*, **2009**, 5, 680-7	11.7	190
2	Toward a molecular understanding of the interaction of dual specificity phosphatases with substrates: insights from structure-based modeling and high throughput screening. *Current Medicinal Chemistry*, **2008**, 15, 2536-44	4.3	31

1	Structurally unique inhibitors of human mitogen-activated protein kinase phosphatase-1 identified in a pyrrole carboxamide library. *Journal of Pharmacology and Experimental Therapeutics*, **2007**, 322, 940-7	47	22