

Ahmet Bakan

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

2,562
citations

567281

15
h-index

996975

15
g-index

18
all docs

18
docs citations

18
times ranked

3824
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Synthesis and biological evaluation of 3-aminoisoquinolin-1(2H)-one based inhibitors of the dual-specificity phosphatase Cdc25B. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 2810-2818. | 3.0 | 33 |
| 2 | Inhibition of Peroxidase Activity of Cytochrome <i>c</i> : De Novo Compound Discovery and Validation. <i>Molecular Pharmacology</i> , 2015, 88, 421-427. | 2.3 | 19 |
| 3 | Investigational inhibitors of PTP4A3 phosphatase as antineoplastic agents. <i>Expert Opinion on Investigational Drugs</i> , 2014, 23, 661-673. | 4.1 | 15 |
| 4 | In Vivo Structure-Activity Relationship Studies Support Allosteric Targeting of a Dual Specificity Phosphatase. <i>ChemBioChem</i> , 2014, 15, 1436-1445. | 2.6 | 54 |
| 5 | Designing inhibitors of cytochrome <i>c</i> /cardiolipin peroxidase complexes: mitochondria-targeted imidazole-substituted fatty acids. <i>Free Radical Biology and Medicine</i> , 2014, 71, 221-230. | 2.9 | 40 |
| 6 | <i>EvoL</i> and <i>ProDy</i> for bridging protein sequence evolution and structural dynamics. <i>Bioinformatics</i> , 2014, 30, 2681-2683. | 4.1 | 207 |
| 7 | Coupling between Catalytic Loop Motions and Enzyme Global Dynamics. <i>PLoS Computational Biology</i> , 2012, 8, e1002705. | 3.2 | 42 |
| 8 | Druggability Assessment of Allosteric Proteins by Dynamics Simulations in the Presence of Probe Molecules. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 2435-2447. | 5.3 | 138 |
| 9 | Sodium-coupled Secondary Transporters: Insights from Structure-based Computations. , 2011, , 199-229. | | 2 |
| 10 | <i>ProDy</i> : Protein Dynamics Inferred from Theory and Experiments. <i>Bioinformatics</i> , 2011, 27, 1575-1577. | 4.1 | 907 |
| 11 | Pre-existing soft modes of motion uniquely defined by native contact topology facilitate ligand binding to proteins. <i>Protein Science</i> , 2011, 20, 1645-1658. | 7.6 | 84 |
| 12 | Normal Mode Analysis of Biomolecular Structures: Functional Mechanisms of Membrane Proteins. <i>Chemical Reviews</i> , 2010, 110, 1463-1497. | 47.7 | 461 |
| 13 | COMPUTATIONAL GENERATION INHIBITOR-BOUND CONFORMERS OF P38 MAP KINASE AND COMPARISON WITH EXPERIMENTS. , 2010, , 181-192. | | 22 |
| 14 | The intrinsic dynamics of enzymes plays a dominant role in determining the structural changes induced upon inhibitor binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14349-14354. | 7.1 | 248 |
| 15 | Zebrafish chemical screening reveals an inhibitor of Dusp6 that expands cardiac cell lineages. <i>Nature Chemical Biology</i> , 2009, 5, 680-687. | 8.0 | 221 |
| 16 | Toward a Molecular Understanding of the Interaction of Dual Specificity Phosphatases with Substrates: Insights from Structure-Based Modeling and High Throughput Screening. <i>Current Medicinal Chemistry</i> , 2008, 15, 2536-2544. | 2.4 | 35 |
| 17 | Structurally Unique Inhibitors of Human Mitogen-Activated Protein Kinase Phosphatase-1 Identified in a Pyrrole Carboxamide Library. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2007, 322, 940-947. | 2.5 | 24 |