Razif R Gabdoulline

List of Publications by Year
in descending order

39 papers	2,193 citations	304743 22 h-index	345221 36 g-index
39 all docs	39 docs citations	39 times ranked	2140 citing authors

#	Article	IF	Citations
1	3DTF: a web server for predicting transcription factor PWMs using 3D structure-based energy calculations. Nucleic Acids Research, 2012, 40, W180-W185.	14.5	15
2	On the structure and dynamics of the complex of the nucleosome and the linker histone. Nucleic Acids Research, 2011, 39, 5255-5263.	14.5	49
3	Brownian Dynamics Simulation of Protein Solutions: Structural and Dynamical Properties. Biophysical Journal, 2010, 99, 3782-3791.	0.5	89
4	Kinetics of Biomacromolecular Complex Formation: Theory and Experiment. , 2010, , 89-118.		0
5	On the Contributions of Diffusion and Thermal Activation to Electron Transfer between Phormidium laminosum Plastocyanin and Cytochrome f: Brownian Dynamics Simulations with Explicit Modeling of Nonpolar Desolvation Interactions and Electron Transfer Events. Journal of the American Chemical Society, 2009, 131, 9230-9238.	13.7	52
6	Cross-species analysis of the glycolytic pathway by comparison of molecular interaction fields. Molecular BioSystems, 2009, 6, 162-174.	2.9	16
7	Proteinâ€“protein docking by simulating the process of association subject to biochemical constraints. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1955-1969.	2.6	27
8	The acidic, glutamine-rich Mpn474 protein of Mycoplasma pneumoniae is surface exposed and covers the complete cell. Microbiology (United Kingdom), 2008, 154, 1185-1192.	1.8	4
9	SYCAMOREâ€”a <u>sy</u>stems biology <u>c</u>omputational <u>a</u>nalysis and <u>mo</u>deling <u>r</u>esearch <u>e</u>nvironment. Bioinformatics, 2008, 24, 1463-1464.	4.1	31
10	webPIPSA: a web server for the comparison of protein interaction properties. Nucleic Acids Research, 2008, 36, W276-W280.	14.5	88
11	Calculating enzyme kinetic parameters from protein structures. Biochemical Society Transactions, 2008, 36, 51-54.	3.4	8
12	qPIPSA: Relating enzymatic kinetic parameters and interaction fields. BMC Bioinformatics, 2007, 8, 373.	2.6	38
13	Bridging from molecular simulation to biochemical networks. Current Opinion in Structural Biology, 2007, 17, 166-172.	5.7	44
14	Diffusional Encounter of Barnase and Barstar. Biophysical Journal, 2006, 90, 1913-1924.	0.5	123
15	Comparison of the Binding and Reactivity of Plant and Mammalian Peroxidases to Indole Derivatives by Computational Dockingâ€. Biochemistry, 2006, 45, 2940-2950.	2.5	30
16	ProSAT2--Protein Structure Annotation Server. Nucleic Acids Research, 2006, 34, W79-W83.	14.5	12
17	Computational approaches to structural and functional analysis of plastocyanin and other blue copper proteins. Cellular and Molecular Life Sciences, 2004, 61, 1123-1142.	5.4	24
18	How Optimal Are the Binding Energetics of Barnase and Barstar?. Biophysical Journal, 2004, 87, 1618-1630.	0.5	76

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19	Concerted Simulations Reveal How Peroxidase Compound III Formation Results in Cellular Oscillations. Biophysical Journal, 2003, 85, 1421-1428.	0.5	23
20	MolSurfer: a macromolecular interface navigator. Nucleic Acids Research, 2003, 31, 3349-3351.	14.5	44
21	ProSAT: functional annotation of protein 3D structures. Bioinformatics, 2003, 19, 1723-1725.	4.1	13
22	Biomolecular diffusional association. Current Opinion in Structural Biology, 2002, 12, 204-213.	5.7	189
23	Protein-protein association: investigation of factors influencing association rates by Brownian dynamics simulations. Journal of Molecular Biology, 2001, 306, 1139-1155.	4.2	226
24	Electrostatic Analysis and Brownian Dynamics Simulation of the Association of Plastocyanin and Cytochrome F. Biophysical Journal, 2001, 81, 3090-3104.	0.5	80
25	MolSurfer: two-dimensional maps for navigating three-dimensional structures of proteins. Trends in Biochemical Sciences, 1999, 24, 285-287.	7.5	21
26	Classification of protein sequences by homology modeling and quantitative analysis of electrostatic similarity. , 1999, 37, 379-387.		87
27	On the protein-protein diffusional encounter complex. Journal of Molecular Recognition, 1999, 12, 226-234.	2.1	80
28	Computer simulation of protein-protein association kinetics: acetylcholinesterase-fasciculin. Journal of Molecular Biology, 1999, 291, 149-162.	4.2	181
29	On the proteinâ€“protein diffusional encounter complex. , 1999, 12, 226.		1
30	Classification of auxin plant hormones by interaction property similarity indices. Journal of Computer-Aided Molecular Design, 1998, 12, 63-79.	2.9	22
31	Species dependence of enzyme-substrate encounter rates for triose phosphate isomerases. Proteins: Structure, Function and Bioinformatics, 1998, 31, 406-416.	2.6	21
32	Brownian Dynamics Simulation of Proteinâ€“Protein Diffusional Encounter. Methods, 1998, 14, 329-341.	3.8	166
33	Electrostatic steering and ionic tethering in enzyme-ligand binding: Insights from simulations. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 5942-5949.	7.1	198
34	The mean electrostatic potential difference between liquid water and vacuum by MD simulation. Journal of Molecular Liquids, 1997, 71, 1-10.	4.9	6
35	Comparison of the Structures of Dimyristoylphosphatidylcholine in the Presence and Absence of Cholesterol by Molecular Dynamics Simulations. The Journal of Physical Chemistry, 1996, 100, 15942-15946.	2.9	40
36	Molecular origin of the internal dipole potential in lipid bilayers: role of the electrostatic potential of water. Chemistry and Physics of Lipids, 1996, 84, 139-146.	3.2	17

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37	Analytically defined surfaces to analyze molecular interaction properties. Journal of Molecular Graphics, 1996, 14, 341-353.	1.1	36
38	Effects of the cutoff center on the mean potential and pair distribution functions in liquid water. Journal of Computational Chemistry, 1995, 16, 1428-1433.	3.3	12
39	Excited states of strongly coupled bound polarons. Physics Letters, Section A: General, Atomic and Solid State Physics, 1994, 185, 390-394.	2.1	4