

Razif R Gabdoulline

List of Publications by Year in descending order

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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	Protein-protein association: investigation of factors influencing association rates by Brownian dynamics simulations. <i>Journal of Molecular Biology</i> , 2001, 306, 1139-1155.	4.2	226
2	Electrostatic steering and ionic tethering in enzyme-ligand binding: Insights from simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 5942-5949.	7.1	198
3	Biomolecular diffusional association. <i>Current Opinion in Structural Biology</i> , 2002, 12, 204-213.	5.7	189
4	Computer simulation of protein-protein association kinetics: acetylcholinesterase-fasciculin. <i>Journal of Molecular Biology</i> , 1999, 291, 149-162.	4.2	181
5	Brownian Dynamics Simulation of Protein-Protein Diffusional Encounter. <i>Methods</i> , 1998, 14, 329-341.	3.8	166
6	Diffusional Encounter of Barnase and Barstar. <i>Biophysical Journal</i> , 2006, 90, 1913-1924.	0.5	123
7	Brownian Dynamics Simulation of Protein Solutions: Structural and Dynamical Properties. <i>Biophysical Journal</i> , 2010, 99, 3782-3791.	0.5	89
8	webPIPSA: a web server for the comparison of protein interaction properties. <i>Nucleic Acids Research</i> , 2008, 36, W276-W280.	14.5	88
9	Classification of protein sequences by homology modeling and quantitative analysis of electrostatic similarity. <i>Journal of Molecular Biology</i> , 1999, 37, 379-387.		87
10	On the protein-protein diffusional encounter complex. <i>Journal of Molecular Recognition</i> , 1999, 12, 226-234.	2.1	80
11	Electrostatic Analysis and Brownian Dynamics Simulation of the Association of Plastocyanin and Cytochrome F. <i>Biophysical Journal</i> , 2001, 81, 3090-3104.	0.5	80
12	How Optimal Are the Binding Energetics of Barnase and Barstar?. <i>Biophysical Journal</i> , 2004, 87, 1618-1630.	0.5	76
13	On the Contributions of Diffusion and Thermal Activation to Electron Transfer between <i>Phormidium laminosum</i> Plastocyanin and Cytochrome <i>c</i> : Brownian Dynamics Simulations with Explicit Modeling of Nonpolar Desolvation Interactions and Electron Transfer Events. <i>Journal of the American Chemical Society</i> , 2009, 131, 9230-9238.	13.7	52
14	On the structure and dynamics of the complex of the nucleosome and the linker histone. <i>Nucleic Acids Research</i> , 2011, 39, 5255-5263.	14.5	49
15	MolSurfer: a macromolecular interface navigator. <i>Nucleic Acids Research</i> , 2003, 31, 3349-3351.	14.5	44
16	Bridging from molecular simulation to biochemical networks. <i>Current Opinion in Structural Biology</i> , 2007, 17, 166-172.	5.7	44
17	Comparison of the Structures of Dimyristoylphosphatidylcholine in the Presence and Absence of Cholesterol by Molecular Dynamics Simulations. <i>The Journal of Physical Chemistry</i> , 1996, 100, 15942-15946.	2.9	40
18	qPIPSA: Relating enzymatic kinetic parameters and interaction fields. <i>BMC Bioinformatics</i> , 2007, 8, 373.	2.6	38

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19	Analytically defined surfaces to analyze molecular interaction properties. <i>Journal of Molecular Graphics</i> , 1996, 14, 341-353.	1.1	36
20	SYCAMORE—a systems biology computational analysis and modeling research environment. <i>Bioinformatics</i> , 2008, 24, 1463-1464.	4.1	31
21	Comparison of the Binding and Reactivity of Plant and Mammalian Peroxidases to Indole Derivatives by Computational Docking. <i>Biochemistry</i> , 2006, 45, 2940-2950.	2.5	30
22	Protein—protein docking by simulating the process of association subject to biochemical constraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1955-1969.	2.6	27
23	Computational approaches to structural and functional analysis of plastocyanin and other blue copper proteins. <i>Cellular and Molecular Life Sciences</i> , 2004, 61, 1123-1142.	5.4	24
24	Concerted Simulations Reveal How Peroxidase Compound III Formation Results in Cellular Oscillations. <i>Biophysical Journal</i> , 2003, 85, 1421-1428.	0.5	23
25	Classification of auxin plant hormones by interaction property similarity indices. <i>Journal of Computer-Aided Molecular Design</i> , 1998, 12, 63-79.	2.9	22
26	Species dependence of enzyme-substrate encounter rates for triose phosphate isomerases. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 406-416.	2.6	21
27	MolSurfer: two-dimensional maps for navigating three-dimensional structures of proteins. <i>Trends in Biochemical Sciences</i> , 1999, 24, 285-287.	7.5	21
28	Molecular origin of the internal dipole potential in lipid bilayers: role of the electrostatic potential of water. <i>Chemistry and Physics of Lipids</i> , 1996, 84, 139-146.	3.2	17
29	Cross-species analysis of the glycolytic pathway by comparison of molecular interaction fields. <i>Molecular BioSystems</i> , 2009, 6, 162-174.	2.9	16
30	3DTF: a web server for predicting transcription factor PWMs using 3D structure-based energy calculations. <i>Nucleic Acids Research</i> , 2012, 40, W180-W185.	14.5	15
31	ProSAT: functional annotation of protein 3D structures. <i>Bioinformatics</i> , 2003, 19, 1723-1725.	4.1	13
32	Effects of the cutoff center on the mean potential and pair distribution functions in liquid water. <i>Journal of Computational Chemistry</i> , 1995, 16, 1428-1433.	3.3	12
33	ProSAT2—Protein Structure Annotation Server. <i>Nucleic Acids Research</i> , 2006, 34, W79-W83.	14.5	12
34	Calculating enzyme kinetic parameters from protein structures. <i>Biochemical Society Transactions</i> , 2008, 36, 51-54.	3.4	8
35	The mean electrostatic potential difference between liquid water and vacuum by MD simulation. <i>Journal of Molecular Liquids</i> , 1997, 71, 1-10.	4.9	6
36	Excited states of strongly coupled bound polarons. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1994, 185, 390-394.	2.1	4

#	ARTICLE	IF	CITATIONS
37	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
38	On the proteinâ€protein diffusional encounter complex. , 1999, 12, 226.		1
39	Kinetics of Biomacromolecular Complex Formation: Theory and Experiment. , 2010, , 89-118.		0