

Jingfang Wang

List of Publications by Year in descending order

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74
papers

4,054
citations

159585

30
h-index

118850

62
g-index

76
all docs

76
docs citations

76
times ranked

6303
citing authors

#	ARTICLE	IF	CITATIONS
1	Creating RNA Specific C-to-U Editase from APOBEC3A by Separation of Its Activities on DNA and RNA Substrates. <i>ACS Synthetic Biology</i> , 2021, 10, 1106-1115.	3.8	14
2	Impact of peripheral mutations on the access channels of human cytochrome P450 1A2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4906-4913.	3.5	2
3	Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. <i>Science China Life Sciences</i> , 2020, 63, 457-460.	4.9	1,650
4	Molecular simulation of SARS-CoV-2 spike protein binding to pangolin ACE2 or human ACE2 natural variants reveals altered susceptibility to infection. <i>Journal of General Virology</i> , 2020, 101, 921-924.	2.9	42
5	Cyclopeptides design as blockers against HCV p7 channel in silico. <i>Molecular Simulation</i> , 2019, 45, 1419-1425.	2.0	2
6	A dynamic and integrated epigenetic program at distal regions orchestrates transcriptional responses to VEGFA. <i>Genome Research</i> , 2019, 29, 193-207.	5.5	13
7	165 Identification of serum biomarkers for systemic lupus erythematosus using a library of phage displayed random peptides and deep sequencing. , 2019, , .		0
8	Computational Study of HCV p7 Channel: Insight into a New Strategy for HCV Inhibitor Design. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 292-299.	3.6	2
9	Rapid Production of Virus Protein Microarray Using Protein Microarray Fabrication through Gene Synthesis (PAGES). <i>Molecular and Cellular Proteomics</i> , 2017, 16, 288-299.	3.8	8
10	Probing Temperature- and pH-Dependent Binding between Quantum Dots and Bovine Serum Albumin by Fluorescence Correlation Spectroscopy. <i>Nanomaterials</i> , 2017, 7, 93.	4.1	16
11	PMD: A Resource for Archiving and Analyzing Protein Microarray data. <i>Scientific Reports</i> , 2016, 6, 19956.	3.3	11
12	Identification of Serum Biomarkers for Gastric Cancer Diagnosis Using a Human Proteome Microarray. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 614-623.	3.8	82
13	Pi-pi Stacking Mediated Cooperative Mechanism for Human Cytochrome P450 3A4. <i>Molecules</i> , 2015, 20, 7558-7573.	3.8	7
14	Elucidation of Enzymatic Mechanism of Phenazine Biosynthetic Protein PhzF Using QM/MM and MD Simulations. <i>PLoS ONE</i> , 2015, 10, e0139081.	2.5	6
15	The distribution pattern of DNA and protoxin in <i>Bacillus thuringiensis</i> as revealed by laser confocal microscopy analysis. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5605-5612.	3.6	2
16	Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15084-15089.	7.1	126
17	Mycobacterium Tuberculosis Proteome Microarray for Global Studies of Protein Function and Immunogenicity. <i>Cell Reports</i> , 2014, 9, 2317-2329.	6.4	77
18	Microsatellites in the Genome of the Edible Mushroom, <i>Volvariella volvacea</i> . <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	28

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19	Construction and characterization of the interdomain chimeras using Cry11Aa and Cry11Ba from <i>Bacillus thuringiensis</i> and identification of a possible novel toxic chimera. <i>Biotechnology Letters</i> , 2014, 36, 105-111.	2.2	7
20	A High-Affinity CDR-Grafted Antibody against Influenza A H5N1 Viruses Recognizes a Conserved Epitope of H5 Hemagglutinin. <i>PLoS ONE</i> , 2014, 9, e88777.	2.5	4
21	Research/Review: Structure and Linkage Disequilibrium Analysis of Adamantane Resistant Mutations in Influenza Virus M2 Proton Channel. <i>Current Drug Metabolism</i> , 2014, 15, 526-534.	1.2	1
22	Research/Review: Insights into the Mutation-Induced Dysfunction of Arachidonic Acid Metabolism from Modeling of Human CYP2J2. <i>Current Drug Metabolism</i> , 2014, 15, 502-513.	1.2	13
23	Computational design of glutamate dehydrogenase in <i>Bacillus subtilis natto</i> . <i>Journal of Molecular Modeling</i> , 2013, 19, 1919-1927.	1.8	10
24	π-π Stacking mediated drug-drug interactions in human CYP2E1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 945-954.	2.6	10
25	Structural Basis for the Mutation-Induced Dysfunction of Human CYP2J2: A Computational Study. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 1350-1357.	5.4	16
26	Expression Sensitivity Analysis of Human Disease Related Genes. <i>BioMed Research International</i> , 2013, 2013, 1-8.	1.9	0
27	Molecular Dynamics Studies on the Conformational Transitions of Adenylate Kinase: A Computational Evidence for the Conformational Selection Mechanism. <i>BioMed Research International</i> , 2013, 2013, 1-7.	1.9	25
28	Metallo-β-Lactamases: Structural Features, Antibiotic Recognition, Inhibition, and Inhibitor Design. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 1242-1253.	2.1	31
29	Design, Synthesis and Evaluation of the Antibacterial Enhancement Activities of Amino Dihydroartemisinin Derivatives. <i>Molecules</i> , 2013, 18, 6866-6882.	3.8	27
30	Molecular Simulation to Investigate the Cofactor Specificity for <i>Pichia stipitis</i> Xylose Reductase. <i>Medicinal Chemistry</i> , 2013, 9, 985-992.	1.5	1
31	Recent Advances in Computational Studies on Influenza A Virus M2 Proton Channel. <i>Mini-Reviews in Medicinal Chemistry</i> , 2012, 12, 971-978.	2.4	16
32	Negatively Cooperative Binding Properties of Human Cytochrome P450 2E1 with Monocyclic Substrates. <i>Current Drug Metabolism</i> , 2012, 13, 1024-1031.	1.2	13
33	Autoinhibitory Mechanism for the Mutation-Induced Impaired FGF9 Signaling. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 2422-2429.	5.4	8
34	<i>Drosophila melanogaster</i> prophenoloxidases respond inconsistently to Cu ²⁺ and have different activity in vitro. <i>Developmental and Comparative Immunology</i> , 2012, 36, 619-628.	2.3	19
35	Specific amino acids affecting <i>Drosophila melanogaster</i> prophenoloxidase activity in vitro. <i>Developmental and Comparative Immunology</i> , 2012, 38, 88-97.	2.3	17
36	Insights into the Mutation-Induced HHH Syndrome from Modeling Human Mitochondrial Ornithine Transporter-1. <i>PLoS ONE</i> , 2012, 7, e31048.	2.5	52

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37	SCYPPred: A Web-Based Predictor of SNPs for Human Cytochrome P450. <i>Protein and Peptide Letters</i> , 2012, 19, 57-61.	0.9	4
38	Self-assembling subnanometer pores with unusual mass-transport properties. <i>Nature Communications</i> , 2012, 3, 949.	12.8	174
39	Exploration of conformational transition in the aryl-binding site of human FXa using molecular dynamics simulations. <i>Journal of Molecular Modeling</i> , 2012, 18, 2717-2725.	1.8	13
40	Computational Studies on the Substrate Interactions of Influenza A Virus PB2 Subunit. <i>PLoS ONE</i> , 2012, 7, e44079.	2.5	6
41	Scaffold-Based Pan-Agonist Design for the PPAR α , PPAR β and PPAR γ Receptors. <i>PLoS ONE</i> , 2012, 7, e48453.	2.5	13
42	Molecular Dynamics Simulations of CYP2E1. <i>Medicinal Chemistry</i> , 2012, 8, 208-221.	1.5	27
43	A Negative Cooperativity Mechanism of Human CYP2E1 Inferred from Molecular Dynamics Simulations and Free Energy Calculations. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 3217-3225.	5.4	34
44	Predicting Protein-Ligand Binding Sites Based on an Improved Geometric Algorithm. <i>Protein and Peptide Letters</i> , 2011, 18, 997-1001.	0.9	4
45	Insights from Modeling the 3D Structure of New Delhi Metallo- β -Lactamase and Its Binding Interactions with Antibiotic Drugs. <i>PLoS ONE</i> , 2011, 6, e18414.	2.5	54
46	Advances in Human Cytochrome P450 and Personalized Medicine. <i>Current Drug Metabolism</i> , 2011, 12, 436-444.	1.2	51
47	ASSOCIATION OF FEATURE GENE EXPRESSION WITH STRUCTURAL FINGERPRINTS OF CHEMICAL COMPOUNDS. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 503-519.	0.8	4
48	An Allosteric Mechanism Inferred from Molecular Dynamics Simulations on Phospholamban Pentamer in Lipid Membranes. <i>PLoS ONE</i> , 2011, 6, e18587.	2.5	50
49	Identification of Proteins Interacting with Human SP110 During the Process of Viral Infections. <i>Medicinal Chemistry</i> , 2011, 7, 121-126.	1.5	35
50	Molecular Modeling of Cytochrome P450 and Drug Metabolism. <i>Current Drug Metabolism</i> , 2010, 11, 342-346.	1.2	95
51	Docking and molecular dynamics studies on CYP2D6. <i>Science Bulletin</i> , 2010, 55, 1877-1880.	1.7	13
52	The structure of phospholamban and its MD simulations. <i>Science Bulletin</i> , 2010, 55, 1619-1624.	1.7	5
53	Molecular dynamics simulations exploring drug resistance in HIV-1 proteases. <i>Science Bulletin</i> , 2010, 55, 2677-2683.	1.7	10
54	The computational model to predict accurately inhibitory activity for inhibitors towards CYP3A4. <i>Computers in Biology and Medicine</i> , 2010, 40, 845-852.	7.0	10

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55	Insights from studying the mutation-induced allostery in the M2 proton channel by molecular dynamics. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 663-666.	2.1	49
56	Molecular Dynamics Studies on T1 Lipase: Insight into a Double-Flap Mechanism. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 875-878.	5.4	51
57	Recent Progress on Computer-Aided Inhibitor Design of H5N1 Influenza A Virus. <i>Current Computer-Aided Drug Design</i> , 2010, 6, 139-146.	1.2	4
58	Binding of CYP2C9 with Diverse Drugs and its Implications for Metabolic Mechanism. <i>Medicinal Chemistry</i> , 2009, 5, 263-270.	1.5	32
59	Possible Drug Candidates for Alzheimers Disease Deduced from Studying their Binding Interactions with $\alpha 7$ Nicotinic Acetylcholine Receptor. <i>Medicinal Chemistry</i> , 2009, 5, 250-262.	1.5	46
60	Role of structural bioinformatics and traditional Chinese medicine databases in pharmacogenomics. <i>Pharmacogenomics</i> , 2009, 10, 1213-1215.	1.3	19
61	Structure of Cytochrome P450s and Personalized Drug. <i>Current Medicinal Chemistry</i> , 2009, 16, 232-244.	2.4	65
62	Molecular dynamics studies on the interactions of PTP1B with inhibitors: from the first phosphate-binding site to the second one. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 349-355.	2.1	92
63	Reversal of coenzyme specificity and improvement of catalytic efficiency of <i>Pichia stipitis</i> xylose reductase by rational site-directed mutagenesis. <i>Biotechnology Letters</i> , 2009, 31, 1025-1029.	2.2	37
64	Structural flexibility and interactions of PTP1B's S-loop. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2009, 1, 214-219.	3.6	6
65	Insights from investigating the interactions of adamantane-based drugs with the M2 proton channel from the H1N1 swine virus. <i>Biochemical and Biophysical Research Communications</i> , 2009, 388, 413-417.	2.1	53
66	Insight into the molecular switch mechanism of human Rab5a from molecular dynamics simulations. <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 608-612.	2.1	87
67	Binding Mechanism of H5N1 Influenza Virus Neuraminidase with Ligands and its Implication for Drug Design. <i>Medicinal Chemistry</i> , 2009, 5, 242-249.	1.5	35
68	Molecular Modeling of Two CYP2C19 SNPs and Its Implications for Personalized Drug Design. <i>Protein and Peptide Letters</i> , 2008, 15, 27-32.	0.9	117
69	Pharmacogenomics and Personalized Use of Drugs. <i>Current Topics in Medicinal Chemistry</i> , 2008, 8, 1573-1579.	2.1	64
70	Drug Candidates from Traditional Chinese Medicines. <i>Current Topics in Medicinal Chemistry</i> , 2008, 8, 1656-1665.	2.1	104
71	A THEORETICAL STUDY ON THE MECHANISM OF 2:1 1, 3 DIPOLAR CYCLOADDITION REACTIONS. <i>Journal of Theoretical and Computational Chemistry</i> , 2007, 06, 861-867.	1.8	4
72	3D structure modeling of cytochrome P450 2C19 and its implication for personalized drug design. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 513-519.	2.1	112

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73	Computational studies of the binding mechanism of calmodulin with chrysin. <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 1102-1107.	2.1	51
74	Insights from modeling the 3D structure of NAD(P)H-dependent d-xylose reductase of <i>Pichia stipitis</i> and its binding interactions with NAD and NADP. <i>Biochemical and Biophysical Research Communications</i> , 2007, 359, 323-329.	2.1	66