Jingfang Wang

List of Publications by Year
in descending order

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	Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. Science China Life Sciences, 2020, 63, 457-460.	4.9	1,650
2	Self-assembling subnanometer pores with unusual mass-transport properties. Nature Communications, 2012, 3, 949.	12.8	174
3	Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15084-15089.	7.1	126
4	Molecular Modeling of Two CYP2C19 SNPs and Its Implications for Personalized Drug Design. Protein and Peptide Letters, 2008, 15, 27-32.	0.9	117
5	3D structure modeling of cytochrome P450 2C19 and its implication for personalized drug design. Biochemical and Biophysical Research Communications, 2007, 355, 513-519.	2.1	112
6	Drug Candidates from Traditional Chinese Medicines. Current Topics in Medicinal Chemistry, 2008, 8, 1656-1665.	2.1	104
7	Molecular Modeling of Cytochrome P450 and Drug Metabolism. Current Drug Metabolism, 2010, 11, 342-346.	1.2	95
8	Molecular dynamics studies on the interactions of PTP1B with inhibitors: from the first phosphate-binding site to the second one. Protein Engineering, Design and Selection, 2009, 22, 349-355.	2.1	92
9	Insight into the molecular switch mechanism of human Rab5a from molecular dynamics simulations. Biochemical and Biophysical Research Communications, 2009, 390, 608-612.	2.1	87
10	Identification of Serum Biomarkers for Gastric Cancer Diagnosis Using a Human Proteome Microarray. Molecular and Cellular Proteomics, 2016, 15, 614-623.	3.8	82
11	Mycobacterium Tuberculosis Proteome Microarray for Global Studies of Protein Function and Immunogenicity. Cell Reports, 2014, 9, 2317-2329.	6.4	77
12	Insights from modeling the 3D structure of NAD(P)H-dependent d-xylose reductase of Pichia stipitis and its binding interactions with NAD and NADP. Biochemical and Biophysical Research Communications, 2007, 359, 323-329.	2.1	66
13	Structure of Cytochrome P450s and Personalized Drug. Current Medicinal Chemistry, 2009, 16, 232-244.	2.4	65
14	Pharmacogenomics and Personalized Use of Drugs. Current Topics in Medicinal Chemistry, 2008, 8, 1573-1579.	2.1	64
15	Insights from Modeling the 3D Structure of New Delhi Metallo-Î²-Lactamse and Its Binding Interactions with Antibiotic Drugs. PLoS ONE, 2011, 6, e18414.	2.5	54
16	Insights from investigating the interactions of adamantane-based drugs with the M2 proton channel from the H1N1 swine virus. Biochemical and Biophysical Research Communications, 2009, 388, 413-417.	2.1	53
17	Insights into the Mutation-Induced HHH Syndrome from Modeling Human Mitochondrial Ornithine Transporter-1. PLoS ONE, 2012, 7, e31048.	2.5	52
18	Computational studies of the binding mechanism of calmodulin with chrysin. Biochemical and Biophysical Research Communications, 2007, 358, 1102-1107.	2.1	51

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19	Molecular Dynamics Studies on T1 Lipase: Insight into a Double-Flap Mechanism. Journal of Chemical Information and Modeling, 2010, 50, 875-878.	5.4	51
20	Advances in Human Cytochrome P450 and Personalized Medicine. Current Drug Metabolism, 2011, 12, 436-444.	1.2	51
21	An Allosteric Mechanism Inferred from Molecular Dynamics Simulations on Phospholamban Pentamer in Lipid Membranes. PLoS ONE, 2011, 6, e18587.	2.5	50
22	Insights from studying the mutation-induced allostery in the M2 proton channel by molecular dynamics. Protein Engineering, Design and Selection, 2010, 23, 663-666.	2.1	49
23	Possible Drug Candidates for Alzheimers Disease Deduced from Studying their Binding Interactions with α7 Nicotinic Acetylcholine Receptor. Medicinal Chemistry, 2009, 5, 250-262.	1.5	46
24	Molecular simulation of SARS-CoV-2 spike protein binding to pangolin ACE2 or human ACE2 natural variants reveals altered susceptibility to infection. Journal of General Virology, 2020, 101, 921-924.	2.9	42
25	Reversal of coenzyme specificity and improvement of catalytic efficiency of Pichia stipitis xylose reductase by rational site-directed mutagenesis. Biotechnology Letters, 2009, 31, 1025-1029.	2.2	37
26	Binding Mechanism of H5N1 Influenza Virus Neuraminidase with Ligands and its Implication for Drug Design. Medicinal Chemistry, 2009, 5, 242-249.	1.5	35
27	Identification of Proteins Interacting with Human SP110 During the Process of Viral Infections. Medicinal Chemistry, 2011, 7, 121-126.	1.5	35
28	A Negative Cooperativity Mechanism of Human CYP2E1 Inferred from Molecular Dynamics Simulations and Free Energy Calculations. Journal of Chemical Information and Modeling, 2011, 51, 3217-3225.	5.4	34
29	Binding of CYP2C9 with Diverse Drugs and its Implications for Metabolic Mechanism. Medicinal Chemistry, 2009, 5, 263-270.	1.5	32
30	Metallo-β-Lactamases: Structural Features, Antibiotic Recognition, Inhibition, and Inhibitor Design. Current Topics in Medicinal Chemistry, 2013, 13, 1242-1253.	2.1	31
31	Microsatellites in the Genome of the Edible Mushroom,Volvariella volvacea. BioMed Research International, 2014, 2014, 1-10.	1.9	28
32	Design, Synthesis and Evaluation of the Antibacterial Enhancement Activities of Amino Dihydroartemisinin Derivatives. Molecules, 2013, 18, 6866-6882.	3.8	27
33	Molecular Dynamics Simulations of CYP2E1. Medicinal Chemistry, 2012, 8, 208-221.	1.5	27
34	Molecular Dynamics Studies on the Conformational Transitions of Adenylate Kinase: A Computational Evidence for the Conformational Selection Mechanism. BioMed Research International, 2013, 2013, 1-7.	1.9	25
35	Role of structural bioinformatics and traditional Chinese medicine databases in pharmacogenomics. Pharmacogenomics, 2009, 10, 1213-1215.	1.3	19
36	Drosophila melanogaster prophenoloxidases respond inconsistently to Cu2+ and have different activity in vitro. Developmental and Comparative Immunology, 2012, 36, 619-628.	2.3	19

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37	Specific amino acids affecting Drosophila melanogaster prophenoloxidase activity in vitro. Developmental and Comparative Immunology, 2012, 38, 88-97.	2.3	17
38	Recent Advances in Computational Studies on Influenza A Virus M2 Proton Channel. Mini-Reviews in Medicinal Chemistry, 2012, 12, 971-978.	2.4	16
39	Structural Basis for the Mutation-Induced Dysfunction of Human CYP2J2: A Computational Study. Journal of Chemical Information and Modeling, 2013, 53, 1350-1357.	5.4	16
40	Probing Temperature- and pH-Dependent Binding between Quantum Dots and Bovine Serum Albumin by Fluorescence Correlation Spectroscopy. Nanomaterials, 2017, 7, 93.	4.1	16
41	Creating RNA Specific C-to-U Editase from APOBEC3A by Separation of Its Activities on DNA and RNA Substrates. ACS Synthetic Biology, 2021, 10, 1106-1115.	3.8	14
42	Docking and molecular dynamics studies on CYP2D6. Science Bulletin, 2010, 55, 1877-1880.	1.7	13
43	Negatively Cooperative Binding Properties of Human Cytochrome P450 2E1 with Monocyclic Substrates. Current Drug Metabolism, 2012, 13, 1024-1031.	1.2	13
44	Exploration of conformational transition in the aryl-binding site of human FXa using molecular dynamics simulations. Journal of Molecular Modeling, 2012, 18, 2717-2725.	1.8	13
45	A dynamic and integrated epigenetic program at distal regions orchestrates transcriptional responses to VEGFA. Genome Research, 2019, 29, 193-207.	5.5	13
46	Scaffold-Based Pan-Agonist Design for the PPARÎ±, PPARÎ² and PPARÎ³ Receptors. PLoS ONE, 2012, 7, e48453.	2.5	13
47	Research/Review: Insights into the Mutation-Induced Dysfunction of Arachidonic Acid Metabolism from Modeling of Human CYP2J2. Current Drug Metabolism, 2014, 15, 502-513.	1.2	13
48	PMD: A Resource for Archiving and Analyzing Protein Microarray data. Scientific Reports, 2016, 6, 19956.	3.3	11
49	Molecular dynamics simulations exploring drug resistance in HIV-1 proteases. Science Bulletin, 2010, 55, 2677-2683.	1.7	10
50	The computational model to predict accurately inhibitory activity for inhibitors towardsCYP3A4. Computers in Biology and Medicine, 2010, 40, 845-852.	7.0	10
51	Computational design of glutamate dehydrogenase in Bacillus subtilis natto. Journal of Molecular Modeling, 2013, 19, 1919-1927.	1.8	10
52	Ï€â€“Ï€ Stacking mediated drugâ€“drug interactions in human CYP2E1. Proteins: Structure, Function and Bioinformatics, 2013, 81, 945-954.	2.6	10
53	Autoinhibitory Mechanism for the Mutation-Induced Impaired FGF9 Signaling. Journal of Chemical Information and Modeling, 2012, 52, 2422-2429.	5.4	8
54	Rapid Production of Virus Protein Microarray Using Protein Microarray Fabrication through Gene Synthesis (PAGES). Molecular and Cellular Proteomics, 2017, 16, 288-299.	3.8	8

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55	Construction and characterization of the interdomain chimeras using Cry11Aa and Cry11Ba from Bacillus thuringiensis and identification of a possible novel toxic chimera. Biotechnology Letters, 2014, 36, 105-111.	2.2	7
56	Pi-pi Stacking Mediated Cooperative Mechanism for Human Cytochrome P450 3A4. Molecules, 2015, 20, 7558-7573.	3.8	7
57	Structural flexibility and interactions of PTP1Bâ€™s S-loop. Interdisciplinary Sciences, Computational Life Sciences, 2009, 1, 214-219.	3.6	6
58	Elucidation of Enzymatic Mechanism of Phenazine Biosynthetic Protein PhzF Using QM/MM and MD Simulations. PLoS ONE, 2015, 10, e0139081.	2.5	6
59	Computational Studies on the Substrate Interactions of Influenza A Virus PB2 Subunit. PLoS ONE, 2012, 7, e44079.	2.5	6
60	The structure of phospholamban and its MD simulations. Science Bulletin, 2010, 55, 1619-1624.	1.7	5
61	A THEORETICAL STUDY ON THE MECHANISM OF 2:1 1, 3 DIPOLAR CYCLOADDITION REACTIONS. Journal of Theoretical and Computational Chemistry, 2007, 06, 861-867.	1.8	4
62	Predicting Protein-Ligand Binding Sites Based on an Improved Geometric Algorithm. Protein and Peptide Letters, 2011, 18, 997-1001.	0.9	4
63	ASSOCIATION OF FEATURE GENE EXPRESSION WITH STRUCTURAL FINGERPRINTS OF CHEMICAL COMPOUNDS. Journal of Bioinformatics and Computational Biology, 2011, 09, 503-519.	0.8	4
64	SCYPPred: A Web-Based Predictor of SNPs for Human Cytochrome P450. Protein and Peptide Letters, 2012, 19, 57-61.	0.9	4
65	A High-Affinity CDR-Grafted Antibody against Influenza A H5N1 Viruses Recognizes a Conserved Epitope of H5 Hemagglutinin. PLoS ONE, 2014, 9, e88777.	2.5	4
66	Recent Progress on Computer-Aided Inhibitor Design of H5N1 Influenza A Virus. Current Computer-Aided Drug Design, 2010, 6, 139-146.	1.2	4
67	The distribution pattern of DNA and protoxin in Bacillus thuringiensis as revealed by laser confocal microscopy analysis. Applied Microbiology and Biotechnology, 2015, 99, 5605-5612.	3.6	2
68	Cyclopeptides design as blockers against HCV p7 channel in silico. Molecular Simulation, 2019, 45, 1419-1425.	2.0	2
69	Computational Study of HCV p7 Channel: Insight into a New Strategy for HCV Inhibitor Design. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 292-299.	3.6	2
70	Impact of peripheral mutations on the access channels of human cytochrome P450 1A2. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4906-4913.	3.5	2
71	Research/Review: Structure and Linkage Disequilibrium Analysis of Adamantane Resistant Mutations in Influenza Virus M2 Proton Channel. Current Drug Metabolism, 2014, 15, 526-534.	1.2	1
72	Molecular Simulation to Investigate the Cofactor Specificity for Pichia stipitis Xylose Reductase. Medicinal Chemistry, 2013, 9, 985-992.	1.5	1

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73	Expression Sensitivity Analysis of Human Disease Related Genes. BioMed Research International, 2013, 2013, 1-8.	1.9	0
74	165â€...Identification of serum biomarkers for systemic lupus erythematosus using a library of phage displayed random peptides and deep sequencing. , 2019, , .		0