Hai-Feng Chen

List of Publications by Year
in descending order

84	2,149	218381	253896
papers	citations	26 h-index	43 g-index

86	86	86	2146
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	RNA-Specific Force Field Optimization with CMAP and Reweighting. Journal of Chemical Information and Modeling, 2022, 62, 372-385.	2.5	17
2	Early aggregation mechanism of AÎ²16â˜’22 revealed by Markov state models. International Journal of Biological Macromolecules, 2022, 204, 606-616.	3.6	5
3	Mechanism Underlying the Bypass of Apurinic/Pyrimidinic Site Analogs by Sulfolobus acidocaldarius DNA Polymerase IV. International Journal of Molecular Sciences, 2022, 23, 2729.	1.8	0
4	Transcriptome-wide subtyping of pediatric and adult T cell acute lymphoblastic leukemia in an international study of 707 cases. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120787119.	3.3	18
5	Mechanism of zinc ejection by disulfiram in nonstructural protein 5A. Physical Chemistry Chemical Physics, 2021, 23, 12204-12215.	1.3	22
6	Vaccine targeting TNF epitope 1â€“14 do not suppress host defense against Mycobacterium bovis Bacillus Calmette-GuÃ©rin infection. International Journal of Biological Macromolecules, 2021, 169, 371-383.	3.6	2
7	Recent Force Field Strategies for Intrinsically Disordered Proteins. Journal of Chemical Information and Modeling, 2021, 61, 1037-1047.	2.5	67
8	On-Demand Regulation of Dual Thermosensitive Protein Hydrogels. ACS Macro Letters, 2021, 10, 395-400.	2.3	12
9	Disaggregation mechanism of prion amyloid for tweezer inhibitor. International Journal of Biological Macromolecules, 2021, 176, 510-519.	3.6	1
10	Highly Conserved C-Terminal Region of Indian Hedgehog N-Fragment Contributes to Its Auto-Processing and Multimer Formation. Biomolecules, 2021, 11, 792.	1.8	0
11	Functional Parameters of Prestin Are Not Correlated With the Best Hearing Frequency. Frontiers in Cell and Developmental Biology, 2021, 9, 638530.	1.8	1
12	Catalytic mechanism of butane anaerobic oxidation for alkylâ€coenzyme M reductase. Chemical Biology and Drug Design, 2021, 98, 701-712.	1.5	1
13	Balanced Solvent Model for Intrinsically Disordered and Ordered Proteins. Journal of Chemical Information and Modeling, 2021, 61, 5141-5151.	2.5	11
14	Extensive evaluation of environment-specific force field for ordered and disordered proteins. Physical Chemistry Chemical Physics, 2021, 23, 12127-12136.	1.3	7
15	Allosteric mechanism of an oximinoâ€piperidinoâ€piperidine antagonist for the CCR5 chemokine receptor. Chemical Biology and Drug Design, 2020, 95, 113-123.	1.5	1
16	Algorithmâ€based coevolution network identification reveals key functional residues of the Î±/Î² hydrolase subfamilies. FASEB Journal, 2020, 34, 1983-1995.	0.2	7
17	Characterization of protein interaction surface on fatty acyl selectivity of starter condensation domain in lipopeptide biosynthesis. Applied Microbiology and Biotechnology, 2020, 104, 653-660.	1.7	2
18	Quinoline-Pyrazole Scaffold as a Novel Ligand of Galectin-3 and Suppressor of TREM2 Signaling. ACS Medicinal Chemistry Letters, 2020, 11, 1759-1765.	1.3	9

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19	Comparison and Evaluation of Force Fields for Intrinsically Disordered Proteins. Journal of Chemical Information and Modeling, 2020, 60, 4912-4923.	2.5	55
20	Environment-Specific Force Field for Intrinsically Disordered and Ordered Proteins. Journal of Chemical Information and Modeling, 2020, 60, 2257-2267.	2.5	55
21	Decoding allosteric communication pathways in protein lysine acetyltransferase. International Journal of Biological Macromolecules, 2020, 149, 70-80.	3.6	26
22	Immunoproteasome inhibitor DPLG3 attenuates experimental colitis by restraining NF-Î¹B activation. Biochemical Pharmacology, 2020, 177, 113964.	2.0	13
23	Residue-Specific Force Field Improving the Sample of Intrinsically Disordered Proteins and Folded Proteins. Journal of Chemical Information and Modeling, 2019, 59, 4793-4805.	2.5	39
24	Directed evolution of an Î±1,3-fucosyltransferase using a single-cell ultrahigh-throughput screening method. Science Advances, 2019, 5, eaaw8451.	4.7	58
25	Well-Balanced Force Field ff03CMAP for Folded and Disordered Proteins. Journal of Chemical Theory and Computation, 2019, 15, 6769-6780.	2.3	43
26	Extensive tests and evaluation of the CHARMM36IDPSFF force field for intrinsically disordered proteins and folded proteins. Physical Chemistry Chemical Physics, 2019, 21, 21918-21931.	1.3	37
27	Biosynthesis of Coenzyme Q in the Phytopathogen Xanthomonas campestris via a Yeast-Like Pathway. Molecular Plant-Microbe Interactions, 2019, 32, 217-226.	1.4	10
28	Gain-of-Function SHP2 E76Q Mutant Rescuing Autoinhibition Mechanism Associated with Juvenile Myelomonocytic Leukemia. Journal of Chemical Information and Modeling, 2019, 59, 3229-3239.	2.5	37
29	Dynamical important residue network (DIRN): network inference via conformational change. Bioinformatics, 2019, 35, 4664-4670.	1.8	12
30	Coenzyme Q biosynthesis in the biopesticide Shenqinmycin-producing Pseudomonas aeruginosa strain M18. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1025-1038.	1.4	9
31	Exploring the Pyrazinamide Drug Resistance Mechanism of Clinical Mutants T370P and W403G in Ribosomal Protein S1 of Mycobacterium tuberculosis. Journal of Chemical Information and Modeling, 2019, 59, 1584-1597.	2.5	26
32	The Landscape of Protein Tyrosine Phosphatase (Shp2) and Cancer. Current Pharmaceutical Design, 2019, 24, 3767-3777.	0.9	38
33	Dynein axonemal intermediate chain 2 plays a role in gametogenesis by activation of Stat3. Journal of Cellular and Molecular Medicine, 2019, 23, 417-425.	1.6	7
34	Secondary structures transition of tau protein with intrinsically disordered proteins specific force field. Chemical Biology and Drug Design, 2019, 93, 242-253.	1.5	6
35	Allosteric Modulation of Intrinsically Disordered Proteins. Advances in Experimental Medicine and Biology, 2019, 1163, 335-357.	0.8	7
36	NIPS, a 3D network-integrated predictor of deleterious protein SAPs, and its application in cancer prognosis. Scientific Reports, 2018, 8, 6021.	1.6	1

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37	Synergistic regulation mechanism of iperoxo and LY2119620 for muscarinic acetylcholine M2 receptor. RSC Advances, 2018, 8, 13067-13074.	1.7	3
38	Allosteric mechanism of quinoline inhibitors for <scp>HIV RT</scp>â€associated <scp>RN</scp>ase with <scp>MD</scp> simulation and dynamics fluctuation network. Chemical Biology and Drug Design, 2018, 91, 805-816.	1.5	6
39	Inhibitory mechanism of 5-bromo-3-indoleacetic acid for non-structural-3 helicase hepatitis C virus with dynamics correlation network analysis. Computational Biology and Chemistry, 2018, 77, 167-177.	1.1	2
40	Intrinsically disordered proteinâ€specific force field <scp>CHARMM</scp>36<scp>IDPSFF</scp>. Chemical Biology and Drug Design, 2018, 92, 1722-1735.	1.5	62
41	The Dose-Dependent Effects of Vascular Risk Factors on Dynamic Compensatory Neural Processes in Mild Cognitive Impairment. Frontiers in Aging Neuroscience, 2018, 10, 131.	1.7	15
42	The trimeric Hef-associated nuclease HAN is a 3â€²â†’5â€² exonuclease and is probably involved in DNA repair. Nucleic Acids Research, 2018, 46, 9027-9043.	6.5	7
43	Order-disorder transition of intrinsically disordered kinase inducible transactivation domain of CREB. Journal of Chemical Physics, 2018, 148, 225101.	1.2	5
44	An Inverse U-Shaped Curve of Resting-State Networks in Individuals at High Risk of Alzheimerâ€™s Disease. Journal of Clinical Psychiatry, 2018, 79, 17m11583.	1.1	14
45	Crystal Structure of StnA for the Biosynthesis of Antitumor Drug Streptonigrin Reveals a Unique Substrate Binding Mode. Scientific Reports, 2017, 7, 40254.	1.6	5
46	The IDP-Specific Force Field ff14IDPSFF Improves the Conformer Sampling of Intrinsically Disordered Proteins. Journal of Chemical Information and Modeling, 2017, 57, 1166-1178.	2.5	157
47	Allosteric Autoinhibition Pathway in Transcription Factor ERG: Dynamics Network and Mutant Experimental Evaluations. Journal of Chemical Information and Modeling, 2017, 57, 1153-1165.	2.5	12
48	Conformation dynamics of the intrinsically disordered protein c-Myb with the ff99IDPs force field. RSC Advances, 2017, 7, 29713-29721.	1.7	17
49	Stepwise Loop Insertion Strategy for Active Site Remodeling to Generate Novel Enzyme Functions. ACS Chemical Biology, 2017, 12, 1188-1193.	1.6	25
50	Allosteric pathways in tetrahydrofolate sensing riboswitch with dynamics correlation network. Molecular BioSystems, 2017, 13, 156-164.	2.9	6
51	Positive cooperative regulation of double binding sites for human acetylcholinesterase. Chemical Biology and Drug Design, 2017, 89, 694-704.	1.5	9
52	ff14IDPs force field improving the conformation sampling of intrinsically disordered proteins. Chemical Biology and Drug Design, 2017, 89, 5-15.	1.5	67
53	Coupling between ATP hydrolysis and protein conformational change in maltose transporter. Proteins: Structure, Function and Bioinformatics, 2017, 85, 207-220.	1.5	0
54	Dynamics Correlation Network for Allosteric Switching of PreQ1 Riboswitch. Scientific Reports, 2016, 6, 31005.	1.6	24

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55	Synergistic Allosteric Mechanism of Fructose-1,6-bisphosphate and Serine for Pyruvate Kinase M2 via Dynamics Fluctuation Network Analysis. Journal of Chemical Information and Modeling, 2016, 56, 1184-1192.	2.5	33
56	Allosteric mechanism of cyclopropylindolobenzazepine inhibitors for HCV NS5B RdRp via dynamic correlation network analysis. Molecular BioSystems, 2016, 12, 3280-3293.	2.9	18
57	Synergistic Modification Induced Specific Recognition between Histone and TRIM24 via Fluctuation Correlation Network Analysis. Scientific Reports, 2016, 6, 24587.	1.6	15
58	Screening and Identifying a Novel ssDNA Aptamer against Alpha-fetoprotein Using CE-SELEX. Scientific Reports, 2015, 5, 15552.	1.6	83
59	Conformational selection and induced fit for RNA polymerase and RNA/DNA hybrid backtracked recognition. Frontiers in Molecular Biosciences, 2015, 2, 61.	1.6	2
60	Selectivity Mechanism of <scp>ATP</scp>â€Competitive Inhibitors for <scp>PKB</scp> and <scp>PKA</scp>. Chemical Biology and Drug Design, 2015, 86, 9-18.	1.5	5
61	Recognition Mechanism between Lac Repressor and DNA with Correlation Network Analysis. Journal of Physical Chemistry B, 2015, 119, 2844-2856.	1.2	12
62	Binding Induced Intrinsically Disordered Protein Folding with Molecular Dynamics Simulation. Advances in Experimental Medicine and Biology, 2015, 827, 111-121.	0.8	3
63	Test and Evaluation of ff99IDPs Force Field for Intrinsically Disordered Proteins. Journal of Chemical Information and Modeling, 2015, 55, 1021-1029.	2.5	68
64	Active Site Loop Conformation Regulates Promiscuous Activity in a Lactonase from Geobacillus kaustophilus HTA426. PLoS ONE, 2015, 10, e0115130.	1.1	13
65	New Force Field on Modeling Intrinsically Disordered Proteins. Chemical Biology and Drug Design, 2014, 84, 253-269.	1.5	110
66	Kink turn sRNA folding upon L7Ae binding using molecular dynamics simulations. Physical Chemistry Chemical Physics, 2013, 15, 18510.	1.3	13
67	Molecular dynamics simulations of amyloid fibrils: an <italic>in silico</italic> approach. Acta Biochimica Et Biophysica Sinica, 2013, 45, 503-508.	0.9	22
68	Conformational Selection and Induced Fit in Specific Antibody and Antigen Recognition: SPE7 as a Case Study. Journal of Physical Chemistry B, 2013, 117, 4912-4923.	1.2	36
69	Global Conformational Selection and Local Induced Fit for the Recognition between Intrinsic Disordered p53 and CBP. PLoS ONE, 2013, 8, e59627.	1.1	12
70	Conformational selection or induced fit for Brinker and DNA recognition. Physical Chemistry Chemical Physics, 2011, 13, 1407-1412.	1.3	31
71	ASD: a comprehensive database of allosteric proteins and modulators. Nucleic Acids Research, 2011, 39, D663-D669.	6.5	157
72	Molecular dynamics simulations exploring drug resistance in HIV-1 proteases. Science Bulletin, 2010, 55, 2677-2683.	1.7	10

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73	Insight into the stability of crossâ€Î² amyloid fibril from molecular dynamics simulation. Biopolymers, 2010, 93, 578-586.	1.2	18
74	Induced fit or conformational selection for RNA/U1A folding. Rna, 2010, 16, 1053-1061.	1.6	46
75	Induced fit for mRNA/TIS11d complex. Journal of Chemical Physics, 2009, 131, 115103.	1.2	28
76	In Silico Log P Prediction for a Large Data Set with Support Vector Machines, Radial Basis Neural Networks and Multiple Linear Regression. Chemical Biology and Drug Design, 2009, 74, 142-147.	1.5	33
77	Aggregation mechanism investigation of the GIFQINS cross-Î² amyloid fibril. Computational Biology and Chemistry, 2009, 33, 41-45.	1.1	22
78	Molecular Dynamics Simulation of Phosphorylated KID Post-Translational Modification. PLoS ONE, 2009, 4, e6516.	1.1	44
79	Computational study of histamine H3-receptor antagonist with support vector machines and three dimension quantitative structure activity relationship methods. Analytica Chimica Acta, 2008, 624, 203-209.	2.6	14
80	Quantitative predictions of gas chromatography retention indexes with support vector machines, radial basis neural networks and multiple linear regression. Analytica Chimica Acta, 2008, 609, 24-36.	2.6	32
81	Computational Study of the Binding Mode of Epidermal Growth Factor Receptor Kinase Inhibitors. Chemical Biology and Drug Design, 2008, 71, 434-446.	1.5	17
82	Mechanism of Coupled Folding and Binding in the siRNA-PAZ Complex. Journal of Chemical Theory and Computation, 2008, 4, 1360-1368.	2.3	41
83	Binding Induced Folding in p53â^'MDM2 Complex. Journal of the American Chemical Society, 2007, 129, 2930-2937.	6.6	107
84	Insight into the Metabolism Rate of Quinone Analogues from Molecular Dynamics Simulation and 3Dâ€QSMR Methods. Chemical Biology and Drug Design, 2007, 70, 290-301.	1.5	4