

# Fang Bai

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7883850/publications.pdf>

Version: 2024-02-01

36  
papers

6,492  
citations

279487

23  
h-index

360668

35  
g-index

38  
all docs

38  
docs citations

38  
times ranked

10476  
citing authors

#	ARTICLE	IF	CITATIONS
1	A multi-targeting drug design strategy for identifying potent anti-SARS-CoV-2 inhibitors. <i>Acta Pharmacologica Sinica</i> , 2022, 43, 483-493.	2.8	43
2	Probing the Allosteric Inhibition Mechanism of a Spike Protein Using Molecular Dynamics Simulations and Active Compound Identifications. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 2827-2835.	2.9	15
3	Discovery of potential small molecular SARS-CoV-2 entry blockers targeting the spike protein. <i>Acta Pharmacologica Sinica</i> , 2022, 43, 788-796.	2.8	40
4	Target-Based Virtual Screening and LC/MS-Guided Isolation Procedure for Identifying Phloroglucinol-Terpenoid Inhibitors of SARS-CoV-2. <i>Journal of Natural Products</i> , 2022, 85, 327-336.	1.5	13
5	A VDAC1-mediated NEET protein chain transfers [2Fe-2S] clusters between the mitochondria and the cytosol and impacts mitochondrial dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	20
6	Recent advances in predicting protein-protein interactions with the aid of artificial intelligence algorithms. <i>Current Opinion in Structural Biology</i> , 2022, 73, 102344.	2.6	24
7	The nature of proton-coupled electron transfer in a blue light using flavin domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	12
8	Kinetics-Driven Drug Design Strategy for Next-Generation Acetylcholinesterase Inhibitors to Clinical Candidate. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 1844-1855.	2.9	32
9	BAP1 forms a trimer with HMGB1 and HDAC1 that modulates gene environment interaction with asbestos. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
10	Anti-SARS-CoV-2 activities in vitro of Shuanghuanglian preparations and bioactive ingredients. <i>Acta Pharmacologica Sinica</i> , 2020, 41, 1167-1177.	2.8	314
11	Enhancing intracellular accumulation and target engagement of PROTACs with reversible covalent chemistry. <i>Nature Communications</i> , 2020, 11, 4268.	5.8	112
12	Structure of Mpro from SARS-CoV-2 and discovery of its inhibitors. <i>Nature</i> , 2020, 582, 289-293.	13.7	3,133
13	Structure-based design of antiviral drug candidates targeting the SARS-CoV-2 main protease. <i>Science</i> , 2020, 368, 1331-1335.	6.0	1,135
14	In Silico Elucidation of the Plausible Inhibitory Potential of Withaferin A of <i>Withania Somnifera</i> Medicinal Herb Against Breast Cancer Targeting Estrogen Receptor. <i>Current Pharmaceutical Biotechnology</i> , 2020, 21, 842-851.	0.9	3
15	The anti-apoptotic proteins NAF-1 and iASPP interact to drive apoptosis in cancer cells. <i>Chemical Science</i> , 2019, 10, 665-673.	3.7	11
16	Redox-dependent gating of VDAC by mitoNEET. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19924-19929.	3.3	85
17	NEET Proteins: A New Link Between Iron Metabolism, Reactive Oxygen Species, and Cancer. <i>Antioxidants and Redox Signaling</i> , 2019, 30, 1083-1095.	2.5	129
18	The binding proximity of methyl- $\beta$ -lilacinobioside isolated from <i>Caralluma retropiciens</i> with topoisomerase II attributes apoptosis in breast cancer cell line. <i>Saudi Journal of Biological Sciences</i> , 2018, 25, 1826-1833.	1.8	1

#	ARTICLE	IF	CITATIONS
19	Veratramine modulates AP-1-dependent gene transcription by directly binding to programmable DNA. <i>Nucleic Acids Research</i> , 2018, 46, 546-557.	6.5	17
20	A Statistical Thermodynamic Model for Ligands Interacting With Ion Channels: Theoretical Model and Experimental Validation of the KCNQ2 Channel. <i>Frontiers in Pharmacology</i> , 2018, 9, 150.	1.6	2
21	Targeting CPT1A-mediated fatty acid oxidation sensitizes nasopharyngeal carcinoma to radiation therapy. <i>Theranostics</i> , 2018, 8, 2329-2347.	4.6	155
22	Interactions between mitoNEET and NAF-1 in cells. <i>PLoS ONE</i> , 2017, 12, e0175796.	1.1	42
23	Elucidating the druggable interface of protein-protein interactions using fragment docking and coevolutionary analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8051-E8058.	3.3	65
24	Gambogic acid identifies an isoform-specific druggable pocket in the middle domain of Hsp90 $\alpha$ 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4801-9.	3.3	52
25	Breast cancer tumorigenicity is dependent on high expression levels of NAF-1 and the lability of its Fe-S clusters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10890-10895.	3.3	64
26	The Fe-S cluster-containing NEET proteins mitoNEET and NAF-1 as chemotherapeutic targets in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3698-3703.	3.3	64
27	An Accurate Metalloprotein-Specific Scoring Function and Molecular Docking Program Devised by a Dynamic Sampling and Iteration Optimization Strategy. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 833-847.	2.5	15
28	Identification of matrine as a promising novel drug for hepatic steatosis and glucose intolerance with HSP72 as an upstream target. <i>British Journal of Pharmacology</i> , 2015, 172, 4303-4318.	2.7	60
29	Discovery of Pteridin-7(8 <i>H</i> )-one-Based Irreversible Inhibitors Targeting the Epidermal Growth Factor Receptor (EGFR) Kinase T790M/L858R Mutant. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 7821-7837.	2.9	58
30	Structural Basis for Molecular Recognition at Serotonin Receptors. <i>Science</i> , 2013, 340, 610-614.	6.0	454
31	Free energy landscape for the binding process of Huperzine A to acetylcholinesterase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4273-4278.	3.3	79
32	A Generic Force Field for Protein Coarse-Grained Molecular Dynamics Simulation. <i>International Journal of Molecular Sciences</i> , 2012, 13, 14451-14469.	1.8	18
33	Discovery of novel selective inhibitors for EGFR-T790M/L858R. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012, 22, 1365-1370.	1.0	24
34	Fast and effective identification of the bioactive compounds and their targets from medicinal plants via computational chemical biology approach. <i>MedChemComm</i> , 2011, 2, 471.	3.5	29
35	Bioactive conformational generation of small molecules: A comparative analysis between force-field and multiple empirical criteria based methods. <i>BMC Bioinformatics</i> , 2010, 11, 545.	1.2	26
36	Cyndi: a multi-objective evolution algorithm based method for bioactive molecular conformational generation. <i>BMC Bioinformatics</i> , 2009, 10, 101.	1.2	42