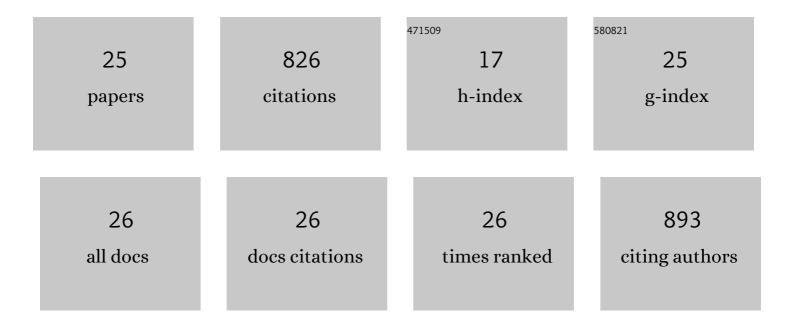
John C Faver

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2481835/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Discovery of potent BET bromodomain 1 stereoselective inhibitors using DNA-encoded chemical library selections. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	15
2	Discovery and characterization of bromodomain 2–specific inhibitors of BRDT. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	42
3	Mass-spectrometry-based proteomic correlates of grade and stage reveal pathways and kinases associated with aggressive human cancers. Oncogene, 2021, 40, 2081-2095.	5.9	22
4	Indoloxytriazines as binding molecules for the JAK2 JH2 pseudokinase domain and its V617F variant. Tetrahedron Letters, 2021, 77, 153248.	1.4	7
5	DNA-encoded chemistry technology yields expedient access to SARS-CoV-2 M ^{pro} inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	36
6	Identifying Oxacillinase-48 Carbapenemase Inhibitors Using DNA-Encoded Chemical Libraries. ACS Infectious Diseases, 2020, 6, 1214-1227.	3.8	27
7	Discovery of potent thrombin inhibitors from a protease-focused DNA-encoded chemical library. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16782-16789.	7.1	40
8	Structure-Guided Identification of DNMT3B Inhibitors. ACS Medicinal Chemistry Letters, 2020, 11, 971-976.	2.8	15
9	C–N Coupling of DNA-Conjugated (Hetero)aryl Bromides and Chlorides for DNA-Encoded Chemical Library Synthesis. Bioconjugate Chemistry, 2020, 31, 770-780.	3.6	39
10	Palladium-Catalyzed Hydroxycarbonylation of (Hetero)aryl Halides for DNA-Encoded Chemical Library Synthesis. Bioconjugate Chemistry, 2019, 30, 2209-2215.	3.6	24
11	Quantitative Comparison of Enrichment from DNA-Encoded Chemical Library Selections. ACS Combinatorial Science, 2019, 21, 75-82.	3.8	48
12	A Mild, DNA-Compatible Nitro Reduction Using B ₂ (OH) ₄ . Organic Letters, 2019, 21, 2194-2199.	4.6	56
13	The BioFragment Database (BFDb): An open-data platform for computational chemistry analysis of noncovalent interactions. Journal of Chemical Physics, 2017, 147, 161727.	3.0	82
14	Computationally-guided optimization of small-molecule inhibitors of the Aurora A kinase–TPX2 protein–protein interaction. Chemical Communications, 2017, 53, 9372-9375.	4.1	15
15	Bringing Clarity to the Prediction of Protein–Ligand Binding Free Energies via "Blurring― Journal of Chemical Theory and Computation, 2014, 10, 1314-1325.	5.3	19
16	Fragment-based error estimation in biomolecular modeling. Drug Discovery Today, 2014, 19, 45-50.	6.4	7
17	Computer-Aided Drug Design: Using Numbers to Your Advantage. ACS Medicinal Chemistry Letters, 2013, 4, 812-814.	2.8	17
18	The Effects of Computational Modeling Errors on the Estimation of Statistical Mechanical Variables. Journal of Chemical Theory and Computation, 2012, 8, 3769-3776.	5.3	24

John C Faver

#	Article	IF	CITATIONS
19	Statistics-based model for basis set superposition error correction in large biomolecules. Physical Chemistry Chemical Physics, 2012, 14, 7795.	2.8	12
20	Prediction of trypsin/molecular fragment binding affinities by free energy decomposition and empirical scores. Journal of Computer-Aided Molecular Design, 2012, 26, 647-659.	2.9	11
21	Formal Estimation of Errors in Computed Absolute Interaction Energies of Proteinâ ^{~3} Ligand Complexes. Journal of Chemical Theory and Computation, 2011, 7, 790-797.	5.3	127
22	Model for the fast estimation of basis set superposition error in biomolecular systems. Journal of Chemical Physics, 2011, 135, 144110.	3.0	31
23	Pairwise additivity of energy components in protein-ligand binding: The HIV II protease-Indinavir case. Journal of Chemical Physics, 2011, 135, 085101.	3.0	19
24	The Energy Computation Paradox and ab initio Protein Folding. PLoS ONE, 2011, 6, e18868.	2.5	48
25	Utility of the Hard/Soft Acidâ^'Base Principle via the Fukui Function in Biological Systems. Journal of Chemical Theory and Computation, 2010, 6, 548-559.	5.3	43