

Stefan G Krimmer

List of Publications by Year in descending order

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1036
citing authors

#	ARTICLE	IF	CITATIONS
1	Conversion of a False Virtual Screen Hit into Selective JAK2 JH2 Domain Binders Using Convergent Design Strategies. <i>ACS Medicinal Chemistry Letters</i> , 2022, 13, 819-826.	1.3	6
2	Insights on JAK2 Modulation by Potent, Selective, and Cell-Permeable Pseudokinase-Domain Ligands. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 8380-8400.	2.9	7
3	Indoloxotriazines as binding molecules for the JAK2 JH2 pseudokinase domain and its V617F variant. <i>Tetrahedron Letters</i> , 2021, 77, 153248.	0.7	7
4	Structural basis for ligand reception by anaplastic lymphoma kinase. <i>Nature</i> , 2021, 600, 148-152.	13.7	21
5	Metadynamics as a Postprocessing Method for Virtual Screening with Application to the Pseudokinase Domain of JAK2. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 4403-4415.	2.5	12
6	Selective Janus Kinase 2 (JAK2) Pseudokinase Ligands with a Diaminotriazole Core. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 5324-5340.	2.9	17
7	Optimization of Pyrazoles as Phenol Surrogates to Yield Potent Inhibitors of Macrophage Migration Inhibitory Factor. <i>ChemMedChem</i> , 2018, 13, 1092-1097.	1.6	14
8	Bayesian analysis of isothermal titration calorimetry for binding thermodynamics. <i>PLoS ONE</i> , 2018, 13, e0203224.	1.1	24
9	Elucidating the Origin of Long Residence Time Binding for Inhibitors of the Metalloprotease Thermolysin. <i>ACS Chemical Biology</i> , 2017, 12, 225-233.	1.6	14
10	Paying the Price of Desolvation in Solvent-Exposed Protein Pockets: Impact of Distal Solubilizing Groups on Affinity and Binding Thermodynamics in a Series of Thermolysin Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5791-5799.	2.9	35
11	How Nothing Boosts Affinity: Hydrophobic Ligand Binding to the Virtually Vacated S ₁ Pocket of Thermolysin. <i>Journal of the American Chemical Society</i> , 2017, 139, 10419-10431.	6.6	23
12	Adding a Hydrogen Bond May Not Help: Naphthyridinone vs Quinoline Inhibitors of Macrophage Migration Inhibitory Factor. <i>ACS Medicinal Chemistry Letters</i> , 2017, 8, 1287-1291.	1.3	8
13	Six Biophysical Screening Methods Miss a Large Proportion of Crystallographically Discovered Fragment Hits: A Case Study. <i>ACS Chemical Biology</i> , 2016, 11, 1693-1701.	1.6	87
14	Active Site Mapping of an Aspartic Protease by Multiple Fragment Crystal Structures: Versatile Warheads To Address a Catalytic Dyad. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 9743-9759.	2.9	12
15	Experimental Active-Site Mapping by Fragments: Hot Spots Remote from the Catalytic Center of Endothiapepsin. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 7561-7575.	2.9	14
16	High-Throughput Crystallography: Reliable and Efficient Identification of Fragment Hits. <i>Structure</i> , 2016, 24, 1398-1409.	1.6	62
17	Rational Design of Thermodynamic and Kinetic Binding Profiles by Optimizing Surface Water Networks Coating Protein-Bound Ligands. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 10530-10548.	2.9	64
18	Impact of Surface Water Layers on Protein-Ligand Binding: How Well Are Experimental Data Reproduced by Molecular Dynamics Simulations in a Thermolysin Test Case?. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 223-233.	2.5	29

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19	Thermodynamics of protein–ligand interactions as a reference for computational analysis: how to assess accuracy, reliability and relevance of experimental data. <i>Journal of Computer-Aided Molecular Design</i> , 2015, 29, 867-883.	1.3	54
20	Methyl, Ethyl, Propyl, Butyl: Futile But Not for Water, as the Correlation of Structure and Thermodynamic Signature Shows in a Congeneric Series of Thermolysin Inhibitors. <i>ChemMedChem</i> , 2014, 9, 833-846.	1.6	70
21	Synthesis and Characterization of Poly(ϵ -caprolactone)- <i>block</i> -poly[<i>N</i> -(2-hydroxypropyl)methacrylamide] Micelles for Drug Delivery. <i>Macromolecular Bioscience</i> , 2011, 11, 1041-1051.	2.1	33