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List of Publications by Year
in descending order

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Version: 2024-02-01

30 papers	1,171 citations	430874 18 h-index	477307 29 g-index
34 all docs	34 docs citations	34 times ranked	1909 citing authors

#	Article	IF	Citations
1	Identification of potent small molecule inhibitors of SARS-CoV-2 entry. SLAS Discovery, 2022, 27, 8-19.	2.7	20
2	The Orphan Nuclear Receptor TLX Is a Receptor for Synthetic and Natural Retinoids. Cell Chemical Biology, 2020, 27, 1272-1284.e4.	5.2	15
3	Assessment of NR4A Ligands That Directly Bind and Modulate the Orphan Nuclear Receptor Nurr1. Journal of Medicinal Chemistry, 2020, 63, 15639-15654.	6.4	34
4	The Tat inhibitor didehydroâ€cortistatin A suppresses SIV replication and reactivation. FASEB Journal, 2019, 33, 8280-8293.	0.5	17
5	Didehydro-Cortistatin A Inhibits HIV-1 by Specifically Binding to the Unstructured Basic Region of Tat. MBio, 2019, 10, .	4.1	56
6	Defining a Canonical Ligand-Binding Pocket in the Orphan Nuclear Receptor Nurr1. Structure, 2019, 27, 66-77.e5.	3.3	37
7	Structural Insights into Estrogen Receptors and Antiestrogen Therapies. Cancer Drug Discovery and Development, 2019, , 241-263.	0.4	0
8	Cryptic glucocorticoid receptor-binding sites pervade genomic NF-Î°B response elements. Nature Communications, 2018, 9, 1337.	12.8	90
9	Defining a conformational ensemble that directs activation of PPARÎ³. Nature Communications, 2018, 9, 1794.	12.8	53
10	Advances in Orphan Nuclear Receptor Pharmacology: A New Era in Drug Discovery. ACS Pharmacology and Translational Science, 2018, 1, 134-137.	4.9	12
11	Tethering not required: the glucocorticoid receptor binds directly to activator protein-1 recognition motifs to repress inflammatory genes. Nucleic Acids Research, 2017, 45, 8596-8608.	14.5	69
12	Synergistic Regulation of Coregulator/Nuclear Receptor Interaction by Ligand and DNA. Structure, 2017, 25, 1506-1518.e4.	3.3	45
13	Identification of a Binding Site for Unsaturated Fatty Acids in the Orphan Nuclear Receptor Nurr1. ACS Chemical Biology, 2016, 11, 1795-1799.	3.4	59
14	Mechanistic insight into protein modification and sulfur mobilization activities of noncanonical E1 and associated ubiquitinâ€like proteins of Archaea. FEBS Journal, 2016, 283, 3567-3586.	4.7	21
15	Probing the Complex Binding Modes of the PPARÎ³ Partial Agonist 2-Chloro-N-(3-chloro-4-((5-chlorobenzo[d]thiazol-2-yl)thio)phenyl)-4-(trifluoromethyl)benzenesulfonamide (T2384) to Orthosteric and Allosteric Sites with NMR Spectroscopy. Journal of Medicinal Chemistry, 2016, 59, 10335-10341.	6.4	24
16	Ebselen, a Small-Molecule Capsid Inhibitor of HIV-1 Replication. Antimicrobial Agents and Chemotherapy, 2016, 60, 2195-2208.	3.2	91
17	Distal substitutions drive divergent DNA specificity among paralogous transcription factors through subdivision of conformational space. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 326-331.	7.1	28
18	Pulsed EPR characterization of HIV-1 protease conformational sampling and inhibitor-induced population shifts. Physical Chemistry Chemical Physics, 2016, 18, 5819-5831.	2.8	24

#	Article	IF	Citations
19	Deconvolution of Complex 1D NMR Spectra Using Objective Model Selection. PLoS ONE, 2015, 10, e0134474.	2.5	15
20	Conserved sequence-specific lincRNAâ€“steroid receptor interactions drive transcriptional repression and direct cell fate. Nature Communications, 2014, 5, 5395.	12.8	103
21	Effects of PRE and POST therapy drugâ€pressure selected mutations on HIVâ€1 protease conformational sampling. FEBS Letters, 2014, 588, 3123-3128.	2.8	10
22	An alternate binding site for PPARÎ³ ligands. Nature Communications, 2014, 5, 3571.	12.8	148
23	Backbone 1H, 13C, and 15N chemical shift assignment for HIV-1 protease subtypes and multi-drug resistant variant MDR 769. Biomolecular NMR Assignments, 2013, 7, 199-202.	0.8	6
24	Pulsed EPR Distance Measurements in Soluble Proteins by Siteâ€Directed Spin Labeling (SDSL). Current Protocols in Protein Science, 2013, 74, 17.17.1-17.17.29.	2.8	17
25	Elucidating a Relationship between Conformational Sampling and Drug Resistance in HIV-1 Protease. Biochemistry, 2013, 52, 3278-3288.	2.5	30
26	Enhanced archaeal laccase production in recombinant Escherichia coli by modification of N-terminal propeptide and twin arginine translocation motifs. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 1523-1532.	3.0	13
27	Correlating Conformational Shift Induction with Altered Inhibitor Potency in a Multidrug Resistant HIV-1 Protease Variant. Biochemistry, 2012, 51, 7813-7815.	2.5	15
28	Inhibitor-Induced Conformational Shifts and Ligand-Exchange Dynamics for HIV-1 Protease Measured by Pulsed EPR and NMR Spectroscopy. Journal of Physical Chemistry B, 2012, 116, 14235-14244.	2.6	23
29	Archaeal <scp>JAB</scp>1/<scp>MPN</scp>/<scp>MOV</scp>34 metalloenzyme (<scp>HvJAMM</scp>1) cleaves ubiquitinâ€like small archaeal modifier proteins (<scp>SAMP</scp>s) from proteinâ€conjugates. Molecular Microbiology, 2012, 86, 971-987.	2.5	39
30	Analysis of Monoglycerides, Diglycerides, Sterols, and Free Fatty Acids in Coconut (Cocos) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 2008, 56, 5765-5769.	5.2	52