

Knut Teigen

List of Publications by Year in descending order

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52
papers

2,374
citations

331670

21
h-index

214800

47
g-index

55
all docs

55
docs citations

55
times ranked

3767
citing authors

#	ARTICLE	IF	CITATIONS
1	Lipid14: The Amber Lipid Force Field. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 865-879.	5.3	1,068
2	LIPID11: A Modular Framework for Lipid Simulations Using Amber. <i>Journal of Physical Chemistry B</i> , 2012, 116, 11124-11136.	2.6	187
3	Epac1 and cAMP-dependent Protein Kinase Holoenzyme Have Similar cAMP Affinity, but Their cAMP Domains Have Distinct Structural Features and Cyclic Nucleotide Recognition. <i>Journal of Biological Chemistry</i> , 2006, 281, 21500-21511.	3.4	133
4	The structural basis of the recognition of phenylalanine and pterin cofactors by phenylalanine hydroxylase: implications for the catalytic mechanism 1 Edited by D. C. Rees. <i>Journal of Molecular Biology</i> , 1999, 294, 807-823.	4.2	61
5	Conformation of the Substrate and Pterin Cofactor Bound to Human Tryptophan Hydroxylase. Important Role of Phe313 in Substrate Specificity. <i>Biochemistry</i> , 2001, 40, 15591-15601.	2.5	60
6	All-atom lipid bilayer self-assembly with the AMBER and CHARMM lipid force fields. <i>Chemical Communications</i> , 2015, 51, 4402-4405.	4.1	49
7	Activation of Phenylalanine Hydroxylase: Effect of Substitutions at Arg68 and Cys237. <i>Biochemistry</i> , 2003, 42, 3419-3428.	2.5	46
8	Selectivity and Affinity Determinants for Ligand Binding to the Aromatic Amino Acid Hydroxylases. <i>Current Medicinal Chemistry</i> , 2007, 14, 455-467.	2.4	46
9	Simulation of lipid bilayer self-assembly using all-atom lipid force fields. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 10573-10584.	2.8	44
10	Phosphorylation and Mutations of Ser16 in Human Phenylalanine Hydroxylase. <i>Journal of Biological Chemistry</i> , 2002, 277, 40937-40943.	3.4	42
11	Intramolecular hydrogen bonding in articaine can be related to superior bone tissue penetration: A molecular dynamics study. <i>Biophysical Chemistry</i> , 2011, 154, 18-25.	2.8	39
12	Specific interaction of the diastereomers 7(R) and 7(S) tetrahydrobiopterin with phenylalanine hydroxylase: implications for understanding primapterinuria and vitiligo. <i>FASEB Journal</i> , 2006, 20, 2130-2132.	0.5	37
13	Thermodynamic Characterization of the Binding of Tetrahydropterins to Phenylalanine Hydroxylase. <i>Journal of the American Chemical Society</i> , 2004, 126, 13670-13678.	13.7	36
14	Rescuing Proteins of Low Kinetic Stability by Chaperones and Natural Ligands: Phenylketonuria, a Case Study. <i>Progress in Molecular Biology and Translational Science</i> , 2008, 83, 89-134.	1.7	31
15	The N-Terminal Sequence of Tyrosine Hydroxylase Is a Conformationally Versatile Motif That Binds 14-3-3 Proteins and Membranes. <i>Journal of Molecular Biology</i> , 2014, 426, 150-168.	4.2	29
16	Conformational Sampling and Nucleotide-Dependent Transitions of the GroEL Subunit Probed by Unbiased Molecular Dynamics Simulations. <i>PLoS Computational Biology</i> , 2011, 7, e1002004.	3.2	27
17	Structural and stability effects of phosphorylation: Localized structural changes in phenylalanine hydroxylase. <i>Protein Science</i> , 2004, 13, 1219-1226.	7.6	26
18	Iodinin (1,6-Dihydroxyphenazine 5,10-Dioxide) from <i>Streptosporangium</i> sp. Induces Apoptosis Selectively in Myeloid Leukemia Cell Lines and Patient Cells. <i>Marine Drugs</i> , 2013, 11, 332-349.	4.6	26

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19	Mammalian CSAD and GADL1 have distinct biochemical properties and patterns of brain expression. <i>Neurochemistry International</i> , 2015, 90, 173-184.	3.8	26
20	A Kinetic and Conformational Study on the Interaction of Tetrahydropteridines with Tyrosine Hydroxylase. <i>Biochemistry</i> , 2000, 39, 13676-13686.	2.5	25
21	Characterization of the interaction of the antifungal and cytotoxic cyclic glycolipopeptide hassallidin with sterol-containing lipid membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 1510-1521.	2.6	25
22	Structural mechanism for tyrosine hydroxylase inhibition by dopamine and reactivation by Ser40 phosphorylation. <i>Nature Communications</i> , 2022, 13, 74.	12.8	23
23	Pharmacological Chaperones that Protect Tetrahydrobiopterin Dependent Aromatic Amino Acid Hydroxylases Through Different Mechanisms. <i>Current Drug Targets</i> , 2016, 17, 1515-1526.	2.1	21
24	Probing Cofactor Specificity in Phenylalanine Hydroxylase by Molecular Dynamics Simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003, 20, 733-740.	3.5	20
25	Binding of ATP at the active site of human pancreatic glucokinase nucleotide-induced conformational changes with possible implications for its kinetic cooperativity. <i>FEBS Journal</i> , 2011, 278, 2372-2386.	4.7	19
26	Tetrahydrobiopterin Binding to Aromatic Amino Acid Hydroxylases. <i>Ligand Recognition and Specificity. Journal of Medicinal Chemistry</i> , 2004, 47, 5962-5971.	6.4	18
27	Screening and Evaluation of Small Organic Molecules as ClpB Inhibitors and Potential Antimicrobials. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 7177-7189.	6.4	18
28	Discovery of compounds that protect tyrosine hydroxylase activity through different mechanisms. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1078-1089.	2.3	17
29	Dominant ARL3-related retinitis pigmentosa. <i>Ophthalmic Genetics</i> , 2019, 40, 124-128.	1.2	16
30	Superstoichiometric binding of L-Phe to phenylalanine hydroxylase from <i>Caenorhabditis elegans</i> : evolutionary implications. <i>Amino Acids</i> , 2010, 39, 1463-1475.	2.7	14
31	Cripto stabilizes GRP78 on the cell membrane. <i>Protein Science</i> , 2018, 27, 653-661.	7.6	13
32	Formation of the Iron-Oxo Hydroxylating Species in the Catalytic Cycle of Aromatic Amino Acid Hydroxylases. <i>Chemistry - A European Journal</i> , 2011, 17, 3746-3758.	3.3	12
33	The Aromatic Amino Acid Hydroxylase Mechanism: A Perspective From Computational Chemistry. <i>Advances in Inorganic Chemistry</i> , 2010, , 437-500.	1.0	11
34	The Regulatory Subunit of PKA-I Remains Partially Structured and Undergoes β -Aggregation upon Thermal Denaturation. <i>PLoS ONE</i> , 2011, 6, e17602.	2.5	11
35	Overview of computational methods employed in early-stage drug discovery. <i>Future Medicinal Chemistry</i> , 2009, 1, 49-63.	2.3	10
36	Inhibition of Tryptophan Hydroxylases and Monoamine Oxidase-A by the Proton Pump Inhibitor, Omeprazole. In <i>Vitro and In Vivo Investigations. Frontiers in Pharmacology</i> , 2020, 11, 593416.	3.5	10

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37	Discovery and biological characterization of a novel scaffold for potent inhibitors of peripheral serotonin synthesis. <i>Future Medicinal Chemistry</i> , 2020, 12, 1461-1474.	2.3	10
38	Levalbuterol lowers the feedback inhibition by dopamine and delays misfolding and aggregation in tyrosine hydroxylase. <i>Biochimie</i> , 2021, 183, 126-132.	2.6	9
39	Introduction of Aromatic Ring-Containing Substituents in Cyclic Nucleotides Is Associated with Inhibition of Toxin Uptake by the Hepatocyte Transporters OATP 1B1 and 1B3. <i>PLoS ONE</i> , 2014, 9, e94926.	2.5	8
40	Golgi-Localized PAQR4 Mediates Antiapoptotic Ceramidase Activity in Breast Cancer. <i>Cancer Research</i> , 2020, 80, 2163-2174.	0.9	8
41	The conformation of 5, 6, 7, 8-tetrahydrobiopterin and 7,8-dihydrobiopterin in solution: a 1H NMR study. <i>Pteridines</i> , 2000, 11, 32-33.	0.5	7
42	Inhibition of sorbitol dehydrogenase by nucleosides and nucleotides. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 202-208.	2.1	7
43	The Reaction Mechanism of Phenylalanine Hydroxylase. "A Question of Coordination. <i>Pteridines</i> , 2005, 16, 27-34.	0.5	6
44	Water Dissociation and Dioxygen Binding in Phenylalanine Hydroxylase. <i>European Journal of Inorganic Chemistry</i> , 2010, 2010, 351-356.	2.0	5
45	Substrate Hydroxylation by the Oxidation Iron Intermediate in Aromatic Amino Acid Hydroxylases: A DFT Mechanistic Study. <i>European Journal of Inorganic Chemistry</i> , 2011, 2011, 2720-2732.	2.0	5
46	Substituting Tyr ¹³⁸ in the active site loop of human phenylalanine hydroxylase affects catalysis and substrate activation. <i>FEBS Open Bio</i> , 2017, 7, 1026-1036.	2.3	4
47	The Arabidopsis (ASHH2) CW domain binds monomethylated K4 of the histone H3 tail through conformational selection. <i>FEBS Journal</i> , 2020, 287, 4458-4480.	4.7	4
48	Synthetic corticosteroids as tryptophan hydroxylase stabilizers. <i>Future Medicinal Chemistry</i> , 2021, 13, 1465-1474.	2.3	2
49	A simple method to calculate the accessible volume of protein-bound ligands: Application for ligand selectivity. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 429-433.	2.4	1
50	Investigating the Disordered and Membrane-Active Peptide A-Cage-C Using Conformational Ensembles. <i>Molecules</i> , 2021, 26, 3607.	3.8	0
51	The Conformation of Tetrahydro-Biopterin Free and Bound to Aromatic Amino Acid Hydroxylases and NOS. , 2002, , 67-72.		0
52	Structural and dynamics studies of human phenylalanine hydroxylase, a highly regulated allosteric enzyme. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s239-s239.	0.1	0