Richard A Engh

List of Publications by Year
in descending order

35 papers	1,139 citations	623734 14 h-index	414414 32 g-index
36 all docs	36 docs citations	36 times ranked	1489 citing authors

#	Article	IF	Citations
1	Inhibitor binding to mutants of protein kinase A with <scp>GGGxxG</scp> and <scp>GxGxxA</scp> glycineâ€rich loop motifs. Journal of Molecular Recognition, 2021, 34, e2882.	2.1	2
2	Drugging the Undruggable: How Isoquinolines and PKA Initiated the Era of Designed Protein Kinase Inhibitor Therapeutics. Biochemistry, 2021, 60, 3470-3484.	2.5	5
3	Novel DYRK1A Inhibitor Rescues Learning and Memory Deficits in a Mouse Model of Down Syndrome. Pharmaceuticals, 2021, 14, 1170.	3.8	6
4	Two SnRK2-Interacting Calcium Sensor Isoforms Negatively Regulate SnRK2 Activity by Different Mechanisms. Plant Physiology, 2020, 182, 1142-1160.	4.8	13
5	Comparative conformational analyses and molecular dynamics studies of glycylglycine methyl ester and glycylglycine N-methylamide. RSC Advances, 2018, 8, 4445-4453.	3.6	3
6	Density Functional Studies on Secondary Amides: Role of Steric Factors in Cis/Trans Isomerization. Molecules, 2018, 23, 2455.	3.8	7
7	Novel Scaffolds for Dual Specificity Tyrosine-Phosphorylation-Regulated Kinase (DYRK1A) Inhibitors. Journal of Medicinal Chemistry, 2018, 61, 7560-7572.	6.4	26
8	Biofocussed chemoprospecting: An efficient approach for drug discovery. Chemical Biology and Drug Design, 2017, 90, 128-140.	3.2	2
9	Cis/Trans Isomerization in Secondary Amides: Reaction Paths, Nitrogen Inversion, and Relevance to Peptidic Systems. Journal of Physical Chemistry A, 2017, 121, 6830-6837.	2.5	8
10	Data driven polypharmacological drug design for lung cancer: analyses for targeting ALK, MET, and EGFR. Journal of Cheminformatics, 2017, 9, 43.	6.1	5
11	Dynamical models of mutated chronic myelogenous leukemia cells for a post-imatinib treatment scenario: Response to dasatinib or nilotinib therapy. PLoS ONE, 2017, 12, e0179700.	2.5	4
12	Bifunctional Ligands for Inhibition of Tight-Binding Proteinâ€“Protein Interactions. Bioconjugate Chemistry, 2016, 27, 1900-1910.	3.6	19
13	Addressing the Glycineâ€Rich Loop of Protein Kinases by a Multiâ€Facetted Interaction Network: Inhibition of PKA and a PKB Mimic. Chemistry - A European Journal, 2016, 22, 211-221.	3.3	22
14	Probing the ATP-Binding Pocket of Protein Kinase DYRK1A with Benzothiazole Fragment Molecules. Journal of Medicinal Chemistry, 2016, 59, 9814-9824.	6.4	37
15	Assessing protein kinase target similarity: Comparing sequence, structure, and cheminformatics approaches. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1605-1616.	2.3	14
16	Luciferin and derivatives as a DYRK selective scaffold for the design of protein kinase inhibitors. European Journal of Medicinal Chemistry, 2015, 94, 140-148.	5.5	21
17	Perspective on computational and structural aspects of kinase discovery from IPK2014. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1595-1604.	2.3	4
18	The structure of a dual-specificity tyrosine phosphorylation-regulated kinase 1Aâ€“PKC412 complex reveals disulfide-bridge formation with the anomalous catalytic loop HRD(HCD) cysteine. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1207-1215.	2.5	31

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19	Inhibition of Aurora Kinase B Is Important for Biologic Activity of the Dual Inhibitors of BCR-ABL and Aurora Kinases R763/AS703569 and PHA-739358 in BCR-ABL Transformed Cells. PLoS ONE, 2014, 9, e112318.	2.5	9
20	Evaluating the Predictivity of Virtual Screening for A bl Kinase Inhibitors to Hinder Drug Resistance. Chemical Biology and Drug Design, 2013, 82, 506-519.	3.2	6
21	Anomalous dispersion analysis of inhibitor flexibility: a case study of the kinase inhibitor H-89. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 873-877.	0.7	12
22	Structural origins of AGC protein kinase inhibitor selectivities: PKA as a drug discovery tool. Biological Chemistry, 2012, 393, 1121-1129.	2.5	7
23	VX680 Binding in Aurora A: Ï€â˜Ï€ Interactions Involving the Conserved Aromatic Amino Acid of the Flexible Glycine-Rich Loop. Journal of Physical Chemistry A, 2011, 115, 3895-3904.	2.5	11
24	p38Î± MAP Kinase Dimers with Swapped Activation Segments and a Novel Catalytic Loop Conformation. Journal of Molecular Biology, 2011, 411, 474-485.	4.2	14
25	Mutants of protein kinase A that mimic the ATP-binding site of Aurora kinase. Biochemical Journal, 2011, 440, 85-93.	3.7	14
26	Diversity of Bisubstrate Binding Modes of Adenosine Analogueâ€“Oligoarginine Conjugates in Protein Kinase A and Implications for Protein Substrate Interactions. Journal of Molecular Biology, 2010, 403, 66-77.	4.2	27
27	Sorafenib and Nilotinib Are Candidates to Overcome Imatinib Resistance in Myeloproliferation with FIP1L1-PDGFRA.. Blood, 2009, 114, 2912-2912.	1.4	1
28	Structural Analysis of Protein Kinase A Mutants with Rho-kinase Inhibitor Specificity. Journal of Biological Chemistry, 2006, 281, 24818-24830.	3.4	30
29	Design and Crystal Structures of Protein Kinase B-Selective Inhibitors in Complex with Protein Kinase A and Mutants. Journal of Medicinal Chemistry, 2005, 48, 163-170.	6.4	59
30	Protein Kinase A in Complex with Rho-Kinase Inhibitors Y-27632, Fasudil, and H-1152P. Structure, 2003, 11, 1595-1607.	3.3	156
31	Mutants of Protein Kinase A that Mimic the ATP-binding Site of Protein Kinase B (AKT). Journal of Molecular Biology, 2003, 329, 1021-1034.	4.2	50
32	Phosphorylation and Flexibility of Cyclic-AMP-Dependent Protein Kinase (PKA) Using31P NMR Spectroscopyâ€. Biochemistry, 2002, 41, 5968-5977.	2.5	26
33	Structural aspects of protein kinase controlâ€”role of conformational flexibility. , 2002, 93, 99-111.		85
34	Staurosporine-induced conformational changes of cAMP-dependent protein kinase catalytic subunit explain inhibitory potential. Structure, 1997, 5, 1627-1637.	3.3	164
35	Crystal Structures of Catalytic Subunit of cAMP-dependent Protein Kinase in Complex with Isoquinolinesulfonyl Protein Kinase Inhibitors H7, H8, and H89. Journal of Biological Chemistry, 1996, 271, 26157-26164.	3.4	239