

Natarajan Kannan

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

3,121
citations

172207

29
h-index

182168

51
g-index

85
all docs

85
docs citations

85
times ranked

4004
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and Functional Diversity of the Microbial Kinome. <i>PLoS Biology</i> , 2007, 5, e17.	2.6	239
2	The hallmark of AGC kinase functional divergence is its C-terminal tail, a cis-acting regulatory module. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1272-1277.	3.3	199
3	Tribbles in the 21st Century: The Evolving Roles of Tribbles Pseudokinases in Biology and Disease. <i>Trends in Cell Biology</i> , 2017, 27, 284-298.	3.6	192
4	Deciphering the Structural Basis of Eukaryotic Protein Kinase Regulation. <i>PLoS Biology</i> , 2013, 11, e1001680.	2.6	172
5	Evolutionary constraints associated with functional specificity of the CMGC protein kinases MAPK, CDK, GSK, SRPK, DYRK, and CK2. <i>Protein Science</i> , 2004, 13, 2059-2077.	3.1	142
6	Did Protein Kinase Regulatory Mechanisms Evolve Through Elaboration of a Simple Structural Component?. <i>Journal of Molecular Biology</i> , 2005, 351, 956-972.	2.0	137
7	Mitochondrial ADCK3 Employs an Atypical Protein Kinase-like Fold to Enable Coenzyme Q Biosynthesis. <i>Molecular Cell</i> , 2015, 57, 83-94.	4.5	104
8	Cerebellar Ataxia and Coenzyme Q Deficiency through Loss of Unorthodox Kinase Activity. <i>Molecular Cell</i> , 2016, 63, 608-620.	4.5	101
9	Kinase Regulation by Hydrophobic Spine Assembly in Cancer. <i>Molecular and Cellular Biology</i> , 2015, 35, 264-276.	1.1	98
10	The Chaperones Hsp90 and Cdc37 Mediate the Maturation and Stabilization of Protein Kinase C through a Conserved PXXP Motif in the C-terminal Tail*. <i>Journal of Biological Chemistry</i> , 2009, 284, 4921-4935.	1.6	97
11	Structural and evolutionary divergence of eukaryotic protein kinases in Apicomplexa. <i>BMC Evolutionary Biology</i> , 2011, 11, 321.	3.2	83
12	Tracing the origin and evolution of pseudokinases across the tree of life. <i>Science Signaling</i> , 2019, 12, .	1.6	79
13	Structural and evolutionary adaptation of rhoptyr kinases and pseudokinases, a family of coccidian virulence factors. <i>BMC Evolutionary Biology</i> , 2013, 13, 117.	3.2	74
14	The Tribbles 2 (TRB2) pseudokinase binds to ATP and autophosphorylates in a metal-independent manner. <i>Biochemical Journal</i> , 2015, 467, 47-62.	1.7	70
15	Covalent inhibitors of EGFR family protein kinases induce degradation of human Tribbles 2 (TRB2) pseudokinase in cancer cells. <i>Science Signaling</i> , 2018, 11, .	1.6	66
16	Aurora A regulation by reversible cysteine oxidation reveals evolutionarily conserved redox control of Ser/Thr protein kinase activity. <i>Science Signaling</i> , 2020, 13, .	1.6	65
17	mTORC2 controls the activity of PKC and Akt by phosphorylating a conserved TOR interaction motif. <i>Science Signaling</i> , 2021, 14, .	1.6	64
18	Altered conformational landscape and dimerization dependency underpins the activation of EGFR by C-terminal 4 loop insertion mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8162-E8171.	3.3	54

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19	Deep evolutionary analysis reveals the design principles of fold A glycosyltransferases. <i>ELife</i> , 2020, 9, .	2.8	53
20	ProKinO: A Unified Resource for Mining the Cancer Kinome. <i>Human Mutation</i> , 2015, 36, 175-186.	1.1	47
21	KinView: a visual comparative sequence analysis tool for integrated kinome research. <i>Molecular BioSystems</i> , 2016, 12, 3651-3665.	2.9	47
22	Substrate binding allosterically relieves autoinhibition of the pseudokinase TRIB1. <i>Science Signaling</i> , 2018, 11, .	1.6	46
23	Integration of signaling in the kinome: Architecture and regulation of the α -C Helix. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1567-1574.	1.1	43
24	Identification of a hidden strain switch provides clues to an ancient structural mechanism in protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 924-929.	3.3	41
25	Target 2035 “ update on the quest for a probe for every protein. <i>RSC Medicinal Chemistry</i> , 2022, 13, 13-21.	1.7	39
26	Classifying kinase conformations using a machine learning approach. <i>BMC Bioinformatics</i> , 2017, 18, 86.	1.2	36
27	Rethinking Pseudokinases. <i>Cell</i> , 2008, 133, 204-205.	13.5	35
28	Cataloguing the dead: breathing new life into pseudokinase research. <i>FEBS Journal</i> , 2020, 287, 4150-4169.	2.2	35
29	Hydrophobic Core Variations Provide a Structural Framework for Tyrosine Kinase Evolution and Functional Specialization. <i>PLoS Genetics</i> , 2016, 12, e1005885.	1.5	35
30	ProKinO: An Ontology for Integrative Analysis of Protein Kinases in Cancer. <i>PLoS ONE</i> , 2011, 6, e28782.	1.1	34
31	A chimeric mechanism for polyvalent <i>trans</i> -phosphorylation of PKA by PDK1. <i>Protein Science</i> , 2009, 18, 1486-1497.	3.1	33
32	Inhibiting EGFR Dimerization Using Triazolyl-Bridged Dimerization Arm Mimics. <i>PLoS ONE</i> , 2015, 10, e0118796.	1.1	31
33	Going for broke: targeting the human cancer pseudokinome. <i>Biochemical Journal</i> , 2015, 465, 195-211.	1.7	31
34	Integrative annotation and knowledge discovery of kinase post-translational modifications and cancer-associated mutations through federated protein ontologies and resources. <i>Scientific Reports</i> , 2018, 8, 6518.	1.6	31
35	The Ty1 Retrotransposon Restriction Factor p22 Targets Gag. <i>PLoS Genetics</i> , 2015, 11, e1005571.	1.5	30
36	Mechanistic Insights into R776H Mediated Activation of Epidermal Growth Factor Receptor Kinase. <i>Biochemistry</i> , 2015, 54, 4216-4225.	1.2	29

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37	LF4/MOK and a CDK-related kinase regulate the number and length of cilia in Tetrahymena. <i>PLoS Genetics</i> , 2019, 15, e1008099.	1.5	27
38	Prediction and Prioritization of Rare Oncogenic Mutations in the Cancer Kinome Using Novel Features and Multiple Classifiers. <i>PLoS Computational Biology</i> , 2014, 10, e1003545.	1.5	23
39	The crystal structure of the protein kinase HIPK2 reveals a unique architecture of its CMGC-insert region. <i>Journal of Biological Chemistry</i> , 2019, 294, 13545-13559.	1.6	22
40	Nucleotide Binding, Evolutionary Insights, and Interaction Partners of the Pseudokinase Unc-51-like Kinase 4. <i>Structure</i> , 2020, 28, 1184-1196.e6.	1.6	22
41	Emerging roles of the $\hat{\pm}C\hat{\pm}24$ loop in protein kinase structure, function, evolution, and disease. <i>IUBMB Life</i> , 2020, 72, 1189-1202.	1.5	22
42	Mapping the glycosyltransferase fold landscape using interpretable deep learning. <i>Nature Communications</i> , 2021, 12, 5656.	5.8	22
43	Coupled regulation by the juxtamembrane and sterile $\hat{\pm}$ motif (SAM) linker is a hallmark of ephrin tyrosine kinase evolution. <i>Journal of Biological Chemistry</i> , 2018, 293, 5102-5116.	1.6	19
44	Lipid-targeting pleckstrin homology domain turns its autoinhibitory face toward the TEC kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21539-21544.	3.3	19
45	Co-Conserved MAPK Features Couple D-Domain Docking Groove to Distal Allosteric Sites via the C-Terminal Flanking Tail. <i>PLoS ONE</i> , 2015, 10, e0119636.	1.1	19
46	Analogous regulatory sites within the $\hat{\pm}C\hat{\pm}24$ loop regions of ZAP-70 tyrosine kinase and AGC kinases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 27-32.	1.1	18
47	A Chemical Probe for Dark Kinase STK17B Derives Its Potency and High Selectivity through a Unique P-Loop Conformation. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 14626-14646.	2.9	17
48	Identification and classification of small molecule kinases: insights into substrate recognition and specificity. <i>BMC Evolutionary Biology</i> , 2016, 16, 7.	3.2	16
49	Computational and Experimental Characterization of Patient Derived Mutations Reveal an Unusual Mode of Regulatory Spine Assembly and Drug Sensitivity in EGFR Kinase. <i>Biochemistry</i> , 2017, 56, 22-32.	1.2	16
50	Structural and evolutionary divergence of cyclic nucleotide binding domains in eukaryotic pathogens: Implications for drug design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1575-1585.	1.1	15
51	Co-Conserved Features Associated with cis Regulation of ErbB Tyrosine Kinases. <i>PLoS ONE</i> , 2010, 5, e14310.	1.1	14
52	Conformationally constrained peptides target the allosteric kinase dimer interface and inhibit EGFR activation. <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 1167-1173.	1.4	14
53	Evolution of Functional Diversity in the Holozoan Tyrosine Kinome. <i>Molecular Biology and Evolution</i> , 2021, 38, 5625-5639.	3.5	13
54	KinOrtho: a method for mapping human kinase orthologs across the tree of life and illuminating understudied kinases. <i>BMC Bioinformatics</i> , 2021, 22, 446.	1.2	13

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55	Two Antagonistic Hippo Signaling Circuits Set the Division Plane at the Medial Position in the Ciliate <i>Tetrahymena</i> . <i>Genetics</i> , 2019, 211, 651-663.	1.2	12
56	A redox-active switch in fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. <i>Science Signaling</i> , 2020, 13, .	1.6	12
57	Quantitative Structure–Mutation–Activity Relationship Tests (QSMART) model for protein kinase inhibitor response prediction. <i>BMC Bioinformatics</i> , 2020, 21, 520.	1.2	8
58	Peters plus syndrome mutations affect the function and stability of human β 1,3-glycosyltransferase. <i>Journal of Biological Chemistry</i> , 2021, 297, 100843.	1.6	6
59	Conservation of Atypical Allosterity in <i>C. elegans</i> UDP-Glucose Dehydrogenase. <i>ACS Omega</i> , 2019, 4, 16318-16329.	1.6	5
60	Computational tools and resources for pseudokinase research. <i>Methods in Enzymology</i> , 2022, 667, 403-426.	0.4	4
61	Modularity of the hydrophobic core and evolution of functional diversity in fold A glycosyltransferases. <i>Journal of Biological Chemistry</i> , 2022, 298, 102212.	1.6	3
62	GTExplorer: A portal to navigate and visualize the evolutionary information encoded in fold A glycosyltransferases. <i>Glycobiology</i> , 2021, 31, 1472-1477.	1.3	1
63	Dialing in EGFR Signaling. <i>Chemistry and Biology</i> , 2015, 22, 687-688.	6.2	0
64	Evolution of allosterity in the cyclic nucleotide binding module: A comparative genomics study. <i>FASEB Journal</i> , 2008, 22, 828.3.	0.2	0
65	X-ray structure of the human mitochondrial kinase ADCK3 elucidates the kinase fold of the ancient UbiB family (LB173). <i>FASEB Journal</i> , 2014, 28, LB173.	0.2	0
66	Defining pseudoenzymes in glycosylation pathways. <i>FASEB Journal</i> , 2022, 36, .	0.2	0