

# Natarajan Kannan

## List of Publications by Year in descending order

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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	Target 2035 – update on the quest for a probe for every protein. RSC Medicinal Chemistry, 2022, 13, 13-21.	1.7	39
2	Computational tools and resources for pseudokinase research. Methods in Enzymology, 2022, 667, 403-426.	0.4	4
3	Defining pseudoenzymes in glycosylation pathways. FASEB Journal, 2022, 36, .	0.2	0
4	Modularity of the hydrophobic core and evolution of functional diversity in fold A glycosyltransferases. Journal of Biological Chemistry, 2022, 298, 102212.	1.6	3
5	mTORC2 controls the activity of PKC and Akt by phosphorylating a conserved TOR interaction motif. Science Signaling, 2021, 14, .	1.6	64
6	Peters plus syndrome mutations affect the function and stability of human $\beta$ 1,3-glycosyltransferase. Journal of Biological Chemistry, 2021, 297, 100843.	1.6	6
7	GTXplorer: A portal to navigate and visualize the evolutionary information encoded in fold A glycosyltransferases. Glycobiology, 2021, 31, 1472-1477.	1.3	1
8	Evolution of Functional Diversity in the Holozoan Tyrosine Kinome. Molecular Biology and Evolution, 2021, 38, 5625-5639.	3.5	13
9	Mapping the glycosyltransferase fold landscape using interpretable deep learning. Nature Communications, 2021, 12, 5656.	5.8	22
10	KinOrtho: a method for mapping human kinase orthologs across the tree of life and illuminating understudied kinases. BMC Bioinformatics, 2021, 22, 446.	1.2	13
11	Nucleotide Binding, Evolutionary Insights, and Interaction Partners of the Pseudokinase Unc-51-like Kinase 4. Structure, 2020, 28, 1184-1196.e6.	1.6	22
12	A Chemical Probe for Dark Kinase STK17B Derives Its Potency and High Selectivity through a Unique P-Loop Conformation. Journal of Medicinal Chemistry, 2020, 63, 14626-14646.	2.9	17
13	Quantitative Structure–Mutation–Activity Relationship Tests (QSMART) model for protein kinase inhibitor response prediction. BMC Bioinformatics, 2020, 21, 520.	1.2	8
14	Aurora A regulation by reversible cysteine oxidation reveals evolutionarily conserved redox control of Ser/Thr protein kinase activity. Science Signaling, 2020, 13, .	1.6	65
15	A redox-active switch in fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. Science Signaling, 2020, 13, .	1.6	12
16	Emerging roles of the $\beta$ 24 loop in protein kinase structure, function, evolution, and disease. IUBMB Life, 2020, 72, 1189-1202.	1.5	22
17	Cataloguing the dead: breathing new life into pseudokinase research. FEBS Journal, 2020, 287, 4150-4169.	2.2	35
18	Deep evolutionary analysis reveals the design principles of fold A glycosyltransferases. ELife, 2020, 9, .	2.8	53

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19	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
20	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
21	Conservation of Atypical Allosteric in <i>C. elegans</i> UDP-Glucose Dehydrogenase. <i>ACS Omega</i> , 2019, 4, 16318-16329.	1.6	5
22	Two Antagonistic Hippo Signaling Circuits Set the Division Plane at the Medial Position in the Ciliate Tetrahymena. <i>Genetics</i> , 2019, 211, 651-663.	1.2	12
23	Tracing the origin and evolution of pseudokinases across the tree of life. <i>Science Signaling</i> , 2019, 12, .	1.6	79
24	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
25	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
26	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
27	Covalent inhibitors of EGFR family protein kinases induce degradation of human Tribbles 2 (TRIB2) pseudokinase in cancer cells. <i>Science Signaling</i> , 2018, 11, .	1.6	66
28	Substrate binding allosterically relieves autoinhibition of the pseudokinase TRIB1. <i>Science Signaling</i> , 2018, 11, .	1.6	46
29	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
30	Altered conformational landscape and dimerization dependency underpins the activation of EGFR by $\hat{\pm}$ 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
31	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
32	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
33	Classifying kinase conformations using a machine learning approach. <i>BMC Bioinformatics</i> , 2017, 18, 86.	1.2	36
34	Cerebellar Ataxia and Coenzyme Q Deficiency through Loss of Unorthodox Kinase Activity. <i>Molecular Cell</i> , 2016, 63, 608-620.	4.5	101
35	KinView: a visual comparative sequence analysis tool for integrated kinome research. <i>Molecular BioSystems</i> , 2016, 12, 3651-3665.	2.9	47
36	Identification and classification of small molecule kinases: insights into substrate recognition and specificity. <i>BMC Evolutionary Biology</i> , 2016, 16, 7.	3.2	16

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37	Hydrophobic Core Variations Provide a Structural Framework for Tyrosine Kinase Evolution and Functional Specialization. <i>PLoS Genetics</i> , 2016, 12, e1005885.	1.5	35
38	Inhibiting EGFR Dimerization Using Triazolyl-Bridged Dimerization Arm Mimics. <i>PLoS ONE</i> , 2015, 10, e0118796.	1.1	31
39	The Ty1 Retrotransposon Restriction Factor p22 Targets Gag. <i>PLoS Genetics</i> , 2015, 11, e1005571.	1.5	30
40	Going for broke: targeting the human cancer pseudokinome. <i>Biochemical Journal</i> , 2015, 465, 195-211.	1.7	31
41	Dialing in EGFR Signaling. <i>Chemistry and Biology</i> , 2015, 22, 687-688.	6.2	0
42	Mechanistic Insights into R776H Mediated Activation of Epidermal Growth Factor Receptor Kinase. <i>Biochemistry</i> , 2015, 54, 4216-4225.	1.2	29
43	Integration of signaling in the kinome: Architecture and regulation of the $\hat{\pm}$ C Helix. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1567-1574.	1.1	43
44	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
45	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
46	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
47	ProKinO: A Unified Resource for Mining the Cancer Kinome. <i>Human Mutation</i> , 2015, 36, 175-186.	1.1	47
48	Kinase Regulation by Hydrophobic Spine Assembly in Cancer. <i>Molecular and Cellular Biology</i> , 2015, 35, 264-276.	1.1	98
49	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
50	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
51	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
52	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
53	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
54	Deciphering the Structural Basis of Eukaryotic Protein Kinase Regulation. <i>PLoS Biology</i> , 2013, 11, e1001680.	2.6	172

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55	ProKinO: An Ontology for Integrative Analysis of Protein Kinases in Cancer. PLoS ONE, 2011, 6, e28782.	1.1	34
56	Structural and evolutionary divergence of eukaryotic protein kinases in Apicomplexa. BMC Evolutionary Biology, 2011, 11, 321.	3.2	83
57	Co-Conserved Features Associated with cis Regulation of ErbB Tyrosine Kinases. PLoS ONE, 2010, 5, e14310.	1.1	14
58	The Chaperones Hsp90 and Cdc37 Mediate the Maturation and Stabilization of Protein Kinase C through a Conserved PXXP Motif in the C-terminal Tail*. Journal of Biological Chemistry, 2009, 284, 4921-4935.	1.6	97
59	A chimeric mechanism for polyvalent <i>trans</i> -phosphorylation of PKA by PDK1. Protein Science, 2009, 18, 1486-1497.	3.1	33
60	Analogous regulatory sites within the $\hat{C}$ -loop regions of ZAP-70 tyrosine kinase and AGC kinases. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 27-32.	1.1	18
61	Rethinking Pseudokinases. Cell, 2008, 133, 204-205.	13.5	35
62	Evolution of allostery in the cyclic nucleotide binding module: A comparative genomics study. FASEB Journal, 2008, 22, 828.3.	0.2	0
63	The hallmark of AGC kinase functional divergence is its C-terminal tail, a cis-acting regulatory module. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1272-1277.	3.3	199
64	Structural and Functional Diversity of the Microbial Kinome. PLoS Biology, 2007, 5, e17.	2.6	239
65	Did Protein Kinase Regulatory Mechanisms Evolve Through Elaboration of a Simple Structural Component?. Journal of Molecular Biology, 2005, 351, 956-972.	2.0	137
66	Evolutionary constraints associated with functional specificity of the CMGC protein kinases MAPK, CDK, GSK, SRPK, DYRK, and CK2. Protein Science, 2004, 13, 2059-2077.	3.1	142