

Richard Kumaran Kandasamy

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

4,755
citations

147801

31
h-index

197818

49
g-index

59
all docs

59
docs citations

59
times ranked

11215
citing authors

#	ARTICLE	IF	CITATIONS
1	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
2	SLC38A9 is a component of the lysosomal amino acid sensing machinery that controls mTORC1. <i>Nature</i> , 2015, 519, 477-481.	27.8	561
3	Human protein reference database--2006 update. <i>Nucleic Acids Research</i> , 2006, 34, D411-D414.	14.5	536
4	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	9.6	456
5	A Compendium of Potential Biomarkers of Pancreatic Cancer. <i>PLoS Medicine</i> , 2009, 6, e1000046.	8.4	260
6	Viral immune modulators perturb the human molecular network by common and unique strategies. <i>Nature</i> , 2012, 487, 486-490.	27.8	249
7	The solute carrier SLC35F2 enables YM155-mediated DNA damage toxicity. <i>Nature Chemical Biology</i> , 2014, 10, 768-773.	8.0	157
8	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
9	The methyltransferase Setdb2 mediates virus-induced susceptibility to bacterial superinfection. <i>Nature Immunology</i> , 2015, 16, 67-74.	14.5	120
10	Hepatitis C virus triggers Golgi fragmentation and autophagy through the immunity-related GTPase M. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3462-E3471.	7.1	103
11	Quantitative tissue proteomics of esophageal squamous cell carcinoma for novel biomarker discovery. <i>Cancer Biology and Therapy</i> , 2011, 12, 510-522.	3.4	102
12	Comprehensive Comparison of Collision Induced Dissociation and Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2008, 80, 4825-4835.	6.5	97
13	A widespread role for SLC transmembrane transporters in resistance to cytotoxic drugs. <i>Nature Chemical Biology</i> , 2020, 16, 469-478.	8.0	84
14	SILAC-based quantitative proteomic approach to identify potential biomarkers from the esophageal squamous cell carcinoma secretome. <i>Cancer Biology and Therapy</i> , 2010, 10, 796-810.	3.4	79
15	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009, 37, D773-D781.	14.5	75
16	The Lipid-Modifying Enzyme SMPDL3B Negatively Regulates Innate Immunity. <i>Cell Reports</i> , 2015, 11, 1919-1928.	6.4	74
17	Common Nodes of Virus-Host Interaction Revealed Through an Integrated Network Analysis. <i>Frontiers in Immunology</i> , 2019, 10, 2186.	4.8	67
18	A comprehensive pathway map of IL-18-mediated signalling. <i>Journal of Cell Communication and Signaling</i> , 2020, 14, 257-266.	3.4	66

#	ARTICLE	IF	CITATIONS
19	mTOR Senses Environmental Cues to Shape the Fibroblast-like Synoviocyte Response to Inflammation. <i>Cell Reports</i> , 2018, 23, 2157-2167.	6.4	62
20	Identifying targets of miR-143 using a SILAC-based proteomic approach. <i>Molecular BioSystems</i> , 2010, 6, 1873.	2.9	58
21	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , 2011, 21, 1872-1881.	5.5	58
22	Evaluation of Several MS/MS Search Algorithms for Analysis of Spectra Derived from Electron Transfer Dissociation Experiments. <i>Analytical Chemistry</i> , 2009, 81, 7170-7180.	6.5	50
23	Superoxide Dismutase 1 Protects Hepatocytes from Type I Interferon-Driven Oxidative Damage. <i>Immunity</i> , 2015, 43, 974-986.	14.3	50
24	Comparative proteomics of human embryonic stem cells and embryonal carcinoma cells. <i>Proteomics</i> , 2010, 10, 1359-1373.	2.2	48
25	The long non-coding RNA LUCAT1 is a negative feedback regulator of interferon responses in humans. <i>Nature Communications</i> , 2020, 11, 6348.	12.8	48
26	A proteogenomic approach to map the proteome of an unsequenced pathogen <i>Leishmania donovani</i> . <i>Proteomics</i> , 2012, 12, 832-844.	2.2	42
27	A time-resolved molecular map of the macrophage response to VSV infection. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16027.	3.0	42
28	PathBuilder" open source software for annotating and developing pathway resources. <i>Bioinformatics</i> , 2009, 25, 2860-2862.	4.1	40
29	SLAMF1 is required for TLR4-mediated TRAM-TRIF-dependent signaling in human macrophages. <i>Journal of Cell Biology</i> , 2018, 217, 1411-1429.	5.2	38
30	Systematic evaluation of alternating CID and ETD fragmentation for phosphorylated peptides. <i>Proteomics</i> , 2011, 11, 2568-2572.	2.2	36
31	Identification of Novel Phosphorylation Motifs Through an Integrative Computational and Experimental Analysis of the Human Phosphoproteome. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 04, 22-35.	0.4	31
32	The TLR4 adaptor TRAM controls the phagocytosis of Gram-negative bacteria by interacting with the Rab11-family interacting protein 2. <i>PLoS Pathogens</i> , 2019, 15, e1007684.	4.7	28
33	Assessment of resolution parameters for CID-based shotgun proteomic experiments on the LTQ-Orbitrap mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1606-1611.	2.8	26
34	Protein interaction networks in innate immunity. <i>Trends in Immunology</i> , 2013, 34, 610-619.	6.8	26
35	An Inducible Retroviral Expression System for Tandem Affinity Purification Mass-Spectrometry-Based Proteomics Identifies Mixed Lineage Kinase Domain-like Protein (MLKL) as an Heat Shock Protein 90 (HSP90) Client. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1139-1150.	3.8	23
36	Comparative Proteomic Analysis Reveals Varying Impact on Immune Responses in Phorbol 12-Myristate-13-Acetate-Mediated THP-1 Monocyte-to-Macrophage Differentiation. <i>Frontiers in Immunology</i> , 2021, 12, 679458.	4.8	22

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37	Dynamics of Dual Specificity Phosphatases and Their Interplay with Protein Kinases in Immune Signaling. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2086.	4.1	20
38	Coactivation of TLR2 and TLR8 in Primary Human Monocytes Triggers a Distinct Inflammatory Signaling Response. <i>Frontiers in Physiology</i> , 2018, 9, 618.	2.8	15
39	SARS-CoV-2 signaling pathway map: A functional landscape of molecular mechanisms in COVID-19. <i>Journal of Cell Communication and Signaling</i> , 2021, 15, 601-608.	3.4	15
40	A modular map of Bradykinin-mediated inflammatory signaling network. <i>Journal of Cell Communication and Signaling</i> , 2022, 16, 301-310.	3.4	14
41	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018, 18, e1700386.	2.2	13
42	Single-cell transcriptome identifies FCGR3B upregulated subtype of alveolar macrophages in patients with critical COVID-19. <i>IScience</i> , 2021, 24, 103030.	4.1	13
43	A Signaling Network of Thyroid-Stimulating Hormone. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 04, .	0.4	11
44	Toward effective sharing of high-dimensional immunology data. <i>Nature Biotechnology</i> , 2014, 32, 755-759.	17.5	11
45	Revisiting Regulated Cell Death Responses in Viral Infections. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7023.	4.1	11
46	An Inducible Retroviral Expression System for Tandem Affinity Purification Mass-Spectrometry-Based Proteomics Identifies Mixed Lineage Kinase Domain-like Protein (MLKL) as an Heat Shock Protein 90 (HSP90) Client. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1139-1150.	3.8	9
47	The Proteomic Landscape of Resting and Activated CD4+ T Cells Reveal Insights into Cell Differentiation and Function. <i>International Journal of Molecular Sciences</i> , 2021, 22, 275.	4.1	9
48	UMP-CMP kinase 2 gene expression in macrophages is dependent on the IRF3-IFNAR signaling axis. <i>PLoS ONE</i> , 2021, 16, e0258989.	2.5	8
49	Comparative Proteomic Analysis of <i>Candida albicans</i> and <i>Candida glabrata</i> . <i>Clinical Proteomics</i> , 2010, 6, 163-173.	2.1	3
50	04.05â€¦The metabolic checkpoint kinase mtor regulates the rheumatoid mesenchymal tissue response to inflammation. , 2017, , .		0
51	Front Cover: Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018, 18, 1870061.	2.2	0
52	Proteogenomics Analysis Reveals Novel Micropeptides in Primary Human Immune Cells. <i>Immuno</i> , 2022, 2, 283-292.	1.5	0