

Venkata P Satagopam

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

3,421
citations

279798

23
h-index

161849

54
g-index

67
all docs

67
docs citations

67
times ranked

7774
citing authors

#	ARTICLE	IF	CITATIONS
1	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010, 464, 721-727.	27.8	768
2	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	12.8	676
3	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. <i>Molecular Neurobiology</i> , 2014, 49, 88-102.	4.0	231
4	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021, 49, W535-W540.	14.5	135
5	Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. <i>BMC Biology</i> , 2020, 18, 62.	3.8	122
6	Orthology prediction methods: A quality assessment using curated protein families. <i>BioEssays</i> , 2011, 33, 769-780.	2.5	121
7	Nuclear Calcium Signaling in Spinal Neurons Drives a Genomic Program Required for Persistent Inflammatory Pain. <i>Neuron</i> , 2013, 77, 43-57.	8.1	114
8	Arena3D: visualization of biological networks in 3D. <i>BMC Systems Biology</i> , 2008, 2, 104.	3.0	95
9	siRNA screen identifies QPCT as a druggable target for Huntington's disease. <i>Nature Chemical Biology</i> , 2015, 11, 347-354.	8.0	87
10	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015, 1, 15007.	6.4	82
11	Multi-omics Reveals the Lifestyle of the Acidophilic, Mineral-Oxidizing Model Species <i>Leptospirillum ferriphilum</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	71
12	MINERVA: a platform for visualization and curation of molecular interaction networks. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16020.	3.0	68
13	Confronting the catalytic dark matter encoded by sequenced genomes. <i>Nucleic Acids Research</i> , 2017, 45, 11495-11514.	14.5	59
14	Defective Lamin A-Rb Signaling in Hutchinson-Gilford Progeria Syndrome and Reversal by Farnesyltransferase Inhibition. <i>PLoS ONE</i> , 2010, 5, e11132.	2.5	58
15	The Luxembourg Parkinson's Study: A Comprehensive Approach for Stratification and Early Diagnosis. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 326.	3.4	57
16	Genome-wide identification and functional analyses of microRNA signatures associated with cancer pain. <i>EMBO Molecular Medicine</i> , 2013, 5, 1740-1758.	6.9	53
17	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
18	Martini: using literature keywords to compare gene sets. <i>Nucleic Acids Research</i> , 2010, 38, 26-38.	14.5	51

#	ARTICLE	IF	CITATIONS
19	Caipirini: using gene sets to rank literature. <i>BioData Mining</i> , 2012, 5, 1.	4.0	47
20	Integration and Visualization of Translational Medicine Data for Better Understanding of Human Diseases. <i>Big Data</i> , 2016, 4, 97-108.	3.4	41
21	Combined lipidomic and proteomic analysis of isolated human islets exposed to palmitate reveals time-dependent changes in insulin secretion and lipid metabolism. <i>PLoS ONE</i> , 2017, 12, e0176391.	2.5	35
22	Transcriptional Mechanisms Underlying Sensitization of Peripheral Sensory Neurons by Granulocyte-/Granulocyte-Macrophage Colony Stimulating Factors. <i>Molecular Pain</i> , 2013, 9, 1744-8069-9-48.	2.1	28
23	Constitutive activation of oncogenic PDGFR β -mutant proteins occurring in GIST patients induces receptor mislocalisation and alters PDGFR β signalling characteristics. <i>Cell Communication and Signaling</i> , 2015, 13, 21.	6.5	27
24	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , 2013, 4, 6.	1.6	26
25	The HIV Mutation Browser: A Resource for Human Immunodeficiency Virus Mutagenesis and Polymorphism Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003951.	3.2	25
26	BioTextQuest + : a knowledge integration platform for literature mining and concept discovery. <i>Bioinformatics</i> , 2014, 30, 3249-3256.	4.1	23
27	GPCRs, G-proteins, effectors and their interactions: human-gpDB, a database employing visualization tools and data integration techniques. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq019-baq019.	3.0	22
28	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	1.6	19
29	SmartR: an open-source platform for interactive visual analytics for translational research data. <i>Bioinformatics</i> , 2017, 33, 2229-2231.	4.1	18
30	Signaling in Insulin-Secreting MIN6 Pseudoislets and Monolayer Cells. <i>Journal of Proteome Research</i> , 2013, 12, 5954-5962.	3.7	17
31	<i>nala</i>: text mining natural language mutation mentions. <i>Bioinformatics</i> , 2017, 33, 1852-1858.	4.1	17
32	Cardiovascular RNA markers and artificial intelligence may improve COVID-19 outcome: a position paper from the EU-CardioRNA COST Action CA17129. <i>Cardiovascular Research</i> , 2021, 117, 1823-1840.	3.8	17
33	Reflect: A practical approach to web semantics. <i>Web Semantics</i> , 2010, 8, 182-189.	2.9	14
34	The Role of Free/Libre and Open Source Software in Learning Health Systems. <i>Yearbook of Medical Informatics</i> , 2017, 26, 53-58.	1.0	11
35	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	1.6	11
36	The BIOMarkers in Atopic Dermatitis and Psoriasis (BIOMAP) glossary: developing a lingua franca to facilitate data harmonization and cross-cohort analyses. <i>British Journal of Dermatology</i> , 2021, 185, 1066-1069.	1.5	10

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37	Clustering of cognate proteins among distinct proteomes derived from multiple links to a single seed sequence. BMC Bioinformatics, 2008, 9, 141.	2.6	8
38	GigaSOM.jl: High-performance clustering and visualization of huge cytometry datasets. GigaScience, 2020, 9, .	6.4	8
39	Road to effective data curation for translational research. Drug Discovery Today, 2021, 26, 626-630.	6.4	8
40	Selection of data sets for FAIRification in drug discovery and development: Which, why, and how?. Drug Discovery Today, 2022, 27, 2080-2085.	6.4	8
41	tranSMART Foundation Datathon 1.0: The cross neurodegenerative diseases challenge. Applied & Translational Genomics, 2015, 6, 42-44.	2.1	7
42	The oncogenic FIP1L1-PDGFR± fusion protein displays skewed signaling properties compared to its wild-type PDGFR± counterpart. Jak-stat, 2015, 4, e1062596.	2.2	5
43	Data and knowledge management in translational research: implementation of the eTRIKS platform for the IMI OncoTrack consortium. BMC Bioinformatics, 2019, 20, 164.	2.6	5
44	The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide. PLoS Computational Biology, 2018, 14, e1005802.	3.2	4
45	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. PLoS Computational Biology, 2013, 9, e1002834.	3.2	3
46	Fractalis: a scalable open-source service for platform-independent interactive visual analysis of biomedical data. GigaScience, 2018, 7, .	6.4	3
47	Smart Scheduling (SMASCH): multi-appointment scheduling system for longitudinal clinical research studies. JAMIA Open, 2022, 5, .	2.0	3
48	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. PLoS Computational Biology, 2013, 9, e1003350.	3.2	2
49	COBREXA.jl: constraint-based reconstruction and exascale analysis. Bioinformatics, 2022, 38, 1171-1172.	4.1	2
50	OnTheFly 2.0: A tool for automatic annotation of files and biological information extraction. , 2013, , .		1
51	Internships initiative of the ISCB Student Council. EMBnet Journal, 2011, 16, 3.	0.6	1
52	Translational Challenges of Biomedical Machine Learning Solutions in Clinical and Laboratory Settings. Lecture Notes in Computer Science, 2022, , 353-358.	1.3	1
53	ISMB/ECCB 2017 PROCEEDINGS PAPERS COMMITTEE. Bioinformatics, 2017, 33, i3-i4.	4.1	0
54	Provenance-Enabled Stewardship of Human Data in the GDPR Era. Lecture Notes in Computer Science, 2018, , 266-269.	1.3	0

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55	ISMB 2018 proceedings. Bioinformatics, 2018, 34, i2-i3.	4.1	0
56	Presenting and sharing clinical data using the eTRIKS Standards Master Tree for tranSMART. Bioinformatics, 2019, 35, 1562-1565.	4.1	0
57	MINERVA, A Platform for the Exploration of Disease Maps. , 2021, , 480-489.		0
58	Control Of Allograft Rejection With Mitomycin C Incubated Blood Cells. Blood, 2013, 122, 4457-4457.	1.4	0