Venkata P Satagopam

List of Publications by Year
in descending order

58	3,421	279798	161849
papers	citations	23	54
		h-index	g-index

67	67	67	7774
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	COBREXA.jl: constraint-based reconstruction and exascale analysis. Bioinformatics, 2022, 38, 1171-1172.	4.1	2
2	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
3	Smart Scheduling (SMASCH): multi-appointment scheduling system for longitudinal clinical research studies. JAMIA Open, 2022, 5, .	2.0	3
4	Translational Challenges ofÂBiomedical Machine Learning Solutions inÂClinical andÂLaboratory Settings. Lecture Notes in Computer Science, 2022, , 353-358.	1.3	1
5	Road to effective data curation for translational research. Drug Discovery Today, 2021, 26, 626-630.	6.4	8
6	MINERVA, A Platform for the Exploration of Disease Maps. , 2021, , 480-489.		0
7	Cardiovascular RNA markers and artificial intelligence may improve COVID-19 outcome: a position paper from the EU-CardioRNA COST Action CA17129. Cardiovascular Research, 2021, 117, 1823-1840.	3.8	17
8	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
9	The BIOMarkers in Atopic Dermatitis and Psoriasis (BIOMAP) glossary: developing a lingua franca to facilitate data harmonization and cross€cohort analyses. British Journal of Dermatology, 2021, 185, 1066-1069.	1.5	10
10	COVID19 Disease Map, a computational knowledge repository of virus€"host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
11	GigaSOM.jl: High-performance clustering and visualization of huge cytometry datasets. GigaScience, 2020, 9, .	6.4	8
12	Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. BMC Biology, 2020, 18, 62.	3.8	122
13	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
14	Presenting and sharing clinical data using the eTRIKS Standards Master Tree for tranSMART. Bioinformatics, 2019, 35, 1562-1565.	4.1	0
15	Multi-omics Reveals the Lifestyle of the Acidophilic, Mineral-Oxidizing Model Species Leptospirillum ferriphilum ^{T}. Applied and Environmental Microbiology, 2018, 84, .	3.1	71
16	The Luxembourg Parkinson's Study: A Comprehensive Approach for Stratification and Early Diagnosis. Frontiers in Aging Neuroscience, 2018, 10, 326.	3.4	57
17	Fractalis: a scalable open-source service for platform-independent interactive visual analysis of biomedical data. GigaScience, 2018, 7, .	6.4	3
18	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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19	ISMB 2018 proceedings. Bioinformatics, 2018, 34, i2-i3.	4.1	0
20	The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide. PLoS Computational Biology, 2018, 14, e1005802.	3.2	4
21	SmartR: an open-source platform for interactive visual analytics for translational research data. Bioinformatics, 2017, 33, 2229-2231.	4.1	18
22	<i>nala</i>: text mining natural language mutation mentions. Bioinformatics, 2017, 33, 1852-1858.	4.1	17
23	ISMB/ECCB 2017 PROCEEDINGS PAPERS COMMITTEE. Bioinformatics, 2017, 33, i3-i4.	4.1	0
24	Confronting the catalytic dark matter encoded by sequenced genomes. Nucleic Acids Research, 2017, 45, 11495-11514.	14.5	59
25	Combined lipidomic and proteomic analysis of isolated human islets exposed to palmitate reveals time-dependent changes in insulin secretion and lipid metabolism. PLoS ONE, 2017, 12, e0176391.	2.5	35
26	The Role of Free/Libre and Open Source Software in Learning Health Systems. Yearbook of Medical Informatics, 2017, 26, 53-58.	1.0	11
27	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	1.6	19
28	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	1.6	11
29	Integration and Visualization of Translational Medicine Data for Better Understanding of Human Diseases. Big Data, 2016, 4, 97-108.	3.4	41
30	MINERVAâ€"a platform for visualization and curation of molecular interaction networks. Npj Systems Biology and Applications, 2016, 2, 16020.	3.0	68
31	tranSMART Foundation Datathon 1.0: The cross neurodegenerative diseases challenge. Applied & Translational Genomics, 2015, 6, 42-44.	2.1	7
32	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. Npj Biofilms and Microbiomes, 2015, 1, 15007.	6.4	82
33	The oncogenic FIP1L1-PDGFRÎ±fusion protein displays skewed signaling properties compared to its wild-type PDGFRÎ±counterpart. Jak-stat, 2015, 4, e1062596.	2.2	5
34	A draft network of ligandâ€"receptor-mediated multicellular signalling in human. Nature Communications, 2015, 6, 7866.	12.8	676
35	Constitutive activation of oncogenic PDGFRÎ±-mutant proteins occurring in GIST patients induces receptor mislocalisation and alters PDGFRÎ± signalling characteristics. Cell Communication and Signaling, 2015, 13, 21.	6.5	27
36	siRNA screen identifies QPCT as a druggable target for Huntington's disease. Nature Chemical Biology, 2015, 11, 347-354.	8.0	87

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37	The HIV Mutation Browser: A Resource for Human Immunodeficiency Virus Mutagenesis and Polymorphism Data. PLoS Computational Biology, 2014, 10, e1003951.	3.2	25
38	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. Molecular Neurobiology, 2014, 49, 88-102.	4.0	231
39	BioTextQuest + : a knowledge integration platform for literature mining and concept discovery. Bioinformatics, 2014, 30, 3249-3256.	4.1	23
40	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	1.6	26
41	Signaling in Insulin-Secreting MIN6 Pseudoislets and Monolayer Cells. Journal of Proteome Research, 2013, 12, 5954-5962.	3.7	17
42	Transcriptional Mechanisms Underlying Sensitization of Peripheral Sensory Neurons by Granulocyte-/Granulocyte-Macrophage Colony Stimulating Factors. Molecular Pain, 2013, 9, 1744-8069-9-48.	2.1	28
43	OnTheFly 2.0: A tool for automatic annotation of files and biological information extraction. , 2013, , .		1
44	Nuclear Calcium Signaling in Spinal Neurons Drives a Genomic Program Required for Persistent Inflammatory Pain. Neuron, 2013, 77, 43-57.	8.1	114
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	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
47	Genomeâ€wide identification and functional analyses of micro<scp>RNA</scp> signatures associated with cancer pain. EMBO Molecular Medicine, 2013, 5, 1740-1758.	6.9	53
48	Control Of Allograft Rejection With Mitomycin C Incubated Blood Cells. Blood, 2013, 122, 4457-4457.	1.4	0
49	Caipirini: using gene sets to rank literature. BioData Mining, 2012, 5, 1.	4.0	47
50	Orthology prediction methods: A quality assessment using curated protein families. BioEssays, 2011, 33, 769-780.	2.5	121
51	Internships initiative of the ISCB Student Council. EMBnet Journal, 2011, 16, 3.	0.6	1
52	Reflect: A practical approach to web semantics. Web Semantics, 2010, 8, 182-189.	2.9	14
53	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. Nature, 2010, 464, 721-727.	27.8	768
54	Martini: using literature keywords to compare gene sets. Nucleic Acids Research, 2010, 38, 26-38.	14.5	51

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55	GPCRs, G-proteins, effectors and their interactions: human-gpDB, a database employing visualization tools and data integration techniques. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq019-baq019.	3.0	22
56	Defective Lamin A-Rb Signaling in Hutchinson-Gilford Progeria Syndrome and Reversal by Farnesyltransferase Inhibition. PLoS ONE, 2010, 5, e11132.	2.5	58
57	Clustering of cognate proteins among distinct proteomes derived from multiple links to a single seed sequence. BMC Bioinformatics, 2008, 9, 141.	2.6	8
58	Arena3D: visualization of biological networks in 3D. BMC Systems Biology, 2008, 2, 104.	3.0	95