

Tiratha Raj Singh

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

837
citations

516710

16
h-index

552781

26
g-index

74
all docs

74
docs citations

74
times ranked

1108
citing authors

#	ARTICLE	IF	CITATIONS
1	Mining NGS transcriptomes for miRNAs and dissecting their role in regulating growth, development, and secondary metabolites production in different organs of a medicinal herb, <i>Picrorhiza kurroa</i> . <i>Planta</i> , 2015, 241, 1255-1268.	3.2	68
2	Tunicate mitogenomics and phylogenetics: peculiarities of the <i>Herdmania momus</i> mitochondrial genome and support for the new chordate phylogeny. <i>BMC Genomics</i> , 2009, 10, 534.	2.8	54
3	Bird Mitochondrial Gene Order: Insight from 3 Warbler Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 475-477.	8.9	53
4	Hydroxymethylation and its potential implication in DNA repair system: A review and future perspectives. <i>Gene</i> , 2015, 564, 109-118.	2.2	44
5	Virtual screening, pharmacokinetics, molecular dynamics and binding free energy analysis for small natural molecules against cyclin-dependent kinase 5 for Alzheimer's disease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 248-262.	3.5	37
6	Identification of novel small molecules against GSK3 β for Alzheimer's disease using chemoinformatics approach. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 91, 91-104.	2.4	35
7	Computational studies on Alzheimer's disease associated pathways and regulatory patterns using microarray gene expression and network data: Revealed association with aging and other diseases. <i>Journal of Theoretical Biology</i> , 2013, 334, 109-121.	1.7	33
8	Computational and In-Vitro Validation of Natural Molecules as Potential Acetylcholinesterase Inhibitors and Neuroprotective Agents. <i>Current Alzheimer Research</i> , 2019, 16, 116-127.	1.4	30
9	Effect of in vitro gastric and pancreatic digestion on antioxidant potential of fruit juices. <i>Food Bioscience</i> , 2017, 17, 1-6.	4.4	27
10	Ambush hypothesis revisited: Evidences for phylogenetic trends. <i>Computational Biology and Chemistry</i> , 2009, 33, 239-244.	2.3	26
11	Quercetin ameliorates chronic unpredicted stress-mediated memory dysfunction in male Swiss albino mice by attenuating insulin resistance and elevating hippocampal GLUT4 levels independent of insulin receptor expression. <i>Hormones and Behavior</i> , 2017, 89, 13-22.	2.1	26
12	Contents of therapeutic metabolites in <i>Swertia chirayita</i> correlate with the expression profiles of multiple genes in corresponding biosynthesis pathways. <i>Phytochemistry</i> , 2015, 116, 38-47.	2.9	23
13	A New Decision Tree to Solve the Puzzle of Alzheimer's Disease Pathogenesis Through Standard Diagnosis Scoring System. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 107-115.	3.6	23
14	Multiple genes of mevalonate and non-mevalonate pathways contribute to high aconites content in an endangered medicinal herb, <i>Aconitum heterophyllum</i> Wall. <i>Phytochemistry</i> , 2014, 108, 26-34.	2.9	20
15	Challenges in the miRNA research. <i>International Journal of Bioinformatics Research and Applications</i> , 2013, 9, 576.	0.2	19
16	Unc-51 like kinase 1 (ULK1) in silico analysis for biomarker identification: A vital component of autophagy. <i>Gene</i> , 2015, 562, 40-49.	2.2	19
17	Quercetin ameliorates chronic unpredicted stress-induced behavioral dysfunction in male Swiss albino mice by modulating hippocampal insulin signaling pathway. <i>Physiology and Behavior</i> , 2017, 182, 10-16.	2.1	17
18	<i>In silico</i> screening of deleterious single nucleotide polymorphisms (SNPs) and molecular dynamics simulation of disease associated mutations in gene responsible for oculocutaneous albinism type 6 (OCA 6) disorder. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 3513-3523.	3.5	17

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19	Prediction and characterization of T-cell epitopes for epitope vaccine design from outer membrane protein of <i>Neisseria meningitidis</i> serogroup B. <i>Bioinformatics</i> , 2010, 5, 155-161.	0.5	16
20	An insight into conflux of metabolic traffic leading to picroside-I biosynthesis by tracking molecular time course changes in a medicinal herb, <i>Picrorhiza kurroa</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 123, 435-441.	2.3	15
21	Tools, resources and databases for SNPs and indels in sequences: a review. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 264.	0.2	14
22	Mitochondrial gene rearrangements: new paradigm in the evolutionary biology and systematics. <i>Bioinformatics</i> , 2008, 3, 95-97.	0.5	14
23	A novel miRNA analysis framework to analyze differential biological networks. <i>Scientific Reports</i> , 2017, 7, 14604.	3.3	13
24	Linear B cell epitope prediction for epitope vaccine design against meningococcal disease and their computational validations through physicochemical properties. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2012, 1, 153-159.	2.1	12
25	Structural and functional analysis of disease-associated mutations in GOT1 gene: An in silico study. <i>Computers in Biology and Medicine</i> , 2021, 136, 104695.	7.0	12
26	An Integrative Approach for Mapping Differentially Expressed Genes and Network Components Using Novel Parameters to Elucidate Key Regulatory Genes in Colorectal Cancer. <i>PLoS ONE</i> , 2015, 10, e0133901.	2.5	11
27	High-throughput screening of natural compounds and inhibition of a major therapeutic target HsGSK-3 β for Alzheimer's disease using computational approaches. <i>Journal of Genetic Engineering and Biotechnology</i> , 2021, 19, 61.	3.3	11
28	Machine learning in expert systems for disease diagnostics in human healthcare. , 2021, , 179-200.		11
29	Identification of small molecules against cyclin dependent kinase-5 using chemoinformatics approach for Alzheimer's disease and other tauopathies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2815-2827.	3.5	10
30	Probing Phosphorus Efficient Low Phytic Acid Content Soybean Genotypes with Phosphorus Starvation in Hydroponics Growth System. <i>Applied Biochemistry and Biotechnology</i> , 2015, 177, 689-699.	2.9	9
31	Novel structural and functional impact of damaging single nucleotide polymorphisms (SNPs) on human SMYD2 protein using computational approaches. <i>Meta Gene</i> , 2021, 28, 100871.	0.6	9
32	SHIFT: Server for hidden stops analysis in frame-shifted translation. <i>BMC Research Notes</i> , 2013, 6, 68.	1.4	8
33	Systems biology approach for mutational and site-specific structural investigation of DNA repair genes for xeroderma pigmentosum. <i>Gene</i> , 2014, 543, 108-117.	2.2	8
34	An integrative approach to develop computational pipeline for drug-target interaction network analysis. <i>Scientific Reports</i> , 2018, 8, 10238.	3.3	7
35	Identification and analysis of biomarkers for mismatch repair proteins: A bioinformatic approach. <i>Journal of Natural Science, Biology and Medicine</i> , 2012, 3, 139.	1.0	7
36	Early Diagnosis of Alzheimer's Disease using Machine Learning Based Methods. , 2021, , .		7

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37	A quantitative study of gene regulatory pathways in <i>Bacillus subtilis</i> for virulence and competence phenotype by quorum sensing. <i>Systems and Synthetic Biology</i> , 2013, 7, 33-39.	1.0	6
38	Comparative analysis of epitope predictions: proposed library of putative vaccine candidates for HIV. <i>Bioinformatics</i> , 2011, 5, 386-389.	0.5	6
39	Computational analysis for functional and evolutionary aspects of BACE-1 and associated Alzheimer's related proteins. <i>International Journal of Computational Intelligence Studies</i> , 2012, 1, 322.	0.3	5
40	In silico Screening and Molecular Interaction Studies of Tetrahydrocannabinol and its Derivatives with Acetylcholine Binding Protein. <i>Current Chemical Biology</i> , 2018, 12, 181-190.	0.5	5
41	DR-GAS: A database of functional genetic variants and their phosphorylation states in human DNA repair systems. <i>DNA Repair</i> , 2014, 16, 97-103.	2.8	4
42	Molecular modelling, docking and interaction studies of human-plasminogen and salmonella-enolase with enolase inhibitors. <i>Bioinformatics</i> , 2012, 8, 185-188.	0.5	4
43	Computational identification and analysis of single-nucleotide polymorphisms and insertions/deletions in expressed sequence tag data of <i>Eucalyptus</i> . <i>Journal of Genetics</i> , 2013, 92, 34-38.	0.7	3
44	NMDB: NETWORK MOTIF DATABASE ENVISAGED AND EXPLICATED FROM HUMAN DISEASE SPECIFIC PATHWAYS. <i>Journal of Biological Systems</i> , 2014, 22, 89-100.	1.4	3
45	Analysis for biological network properties of Alzheimer's disease associated gene set by enrichment and topological examinations. <i>International Journal of Bioinformatics Research and Applications</i> , 2017, 13, 214.	0.2	3
46	Network-based approach to understand dynamic behaviour of Wnt signaling pathway regulatory elements in colorectal cancer. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2018, 7, 1.	2.1	3
47	Novel inhibitors design through structural investigations and simulation studies for human PKMTs (SMYD2) involved in cancer. <i>Molecular Simulation</i> , 2021, 47, 1149-1158.	2.0	3
48	Genes Selection Comparative Study in Microarray Data Analysis. <i>Bioinformatics</i> , 2013, 9, 1019-1022.	0.5	3
49	Computational identification and analysis of single-nucleotide polymorphisms and insertions/deletions in expressed sequence tag data of <i>Eucalyptus</i> . <i>Journal of Genetics</i> , 2011, 90, e34-8.	0.7	3
50	In silico Analysis of Evolutionary Patterns in Restriction Endonucleases. <i>In Silico Biology</i> , 2009, 9, 45-53.	0.9	2
51	DREMECELS: A Curated Database for Base Excision and Mismatch Repair Mechanisms Associated Human Malignancies. <i>PLoS ONE</i> , 2016, 11, e0157031.	2.5	2
52	Chemometric approach to estimate kinetic properties of paclitaxel prodrugs and their substructures for solubility prediction through molecular modelling and simulation studies. <i>Journal of Chemometrics</i> , 2019, 33, e3181.	1.3	2
53	ABCD: Alzheimer's disease Biomarkers Comprehensive Database. <i>3 Biotech</i> , 2019, 9, 351.	2.2	2
54	Physicochemical characterization of paclitaxel prodrugs with cytochrome 3A4 to correlate solubility and bioavailability implementing molecular docking and simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-13.	3.5	2

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55	Development of QSPR Strategy for the Solubility Prediction. <i>Current Computer-Aided Drug Design</i> , 2018, 14, 302-309.	1.2	2
56	Topological parameters, patterns, and motifs in biological networks. , 2022, , 367-380.		2
57	In silico analysis of evolutionary patterns in restriction endonucleases. <i>In Silico Biology</i> , 2009, 9, 45-53.	0.9	2
58	Network and structure based inference of functional single nucleotide polymorphisms associated with the TGF β 1 gene and its role in colorectal cancer (CRC). <i>Gene Reports</i> , 2018, 11, 131-142.	0.8	1
59	Epigenome-Wide DNA Methylation and Histone Modification of Alzheimer's Disease. , 2019, , 131-148.		1
60	Application of Deep Learning in Biological Big Data Analysis. <i>Advances in Information Security, Privacy, and Ethics Book Series</i> , 2021, , 117-148.	0.5	1
61	Structure based inference of functional single nucleotide polymorphism and its role in TGF β 1 allied colorectal cancer (CRC). <i>International Journal of Bioinformatics Research and Applications</i> , 2021, 17, 80.	0.2	1
62	WebFARM: web server for finite automated restriction mapping. <i>Bioinformatics</i> , 2010, 4, 341-343.	0.5	1
63	Study on variability assessment and evolutionary relationships of glutamate racemase in <i>Pseudomonas</i> species. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2013, 5, 247-257.	3.6	0
64	HLAB27Pred: SVM-based precise method for predicting HLA-B*2705 binding peptides in antigenic sequences. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2014, 3, 1.	2.1	0
65	Is HNF4A a candidate to study zinc finger protein slug?. <i>International Journal of Bioinformatics Research and Applications</i> , 2015, 11, 366.	0.2	0
66	Systems biology approach for gene set enrichment and topological analysis of Alzheimer's disease pathway. , 2016, , .		0
67	Computational Network Approaches and Their Applications for Complex Diseases. <i>Translational Medicine Research</i> , 2017, , 337-352.	0.0	0
68	Gene Expression Studies to Identify Significant Genes in AR, MTOR, MAPK Pathways and their Overlapping Regulatory Role in Prostate Cancer. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.5	0
69	SCAN DB: an integrated catalogue of computationally characterised NER specific skin cancers. <i>International Journal of Bioinformatics Research and Applications</i> , 2020, 16, 245.	0.2	0
70	Tau Pathology. <i>Advances in Medical Diagnosis, Treatment, and Care</i> , 2019, , 217-234.	0.1	0
71	Systems biology and big data analytics. , 2022, , 425-442.		0