

# Tiratha Raj Singh

## List of Publications by Year in descending order

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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	Identification of small molecules against cyclin dependent kinase-5 using chemoinformatics approach for Alzheimer's disease and other tauopathies. Journal of Biomolecular Structure and Dynamics, 2022, 40, 2815-2827.	3.5	10
2	Systems biology and big data analytics. , 2022, , 425-442.		0
3	Topological parameters, patterns, and motifs in biological networks. , 2022, , 367-380.		2
4	Physicochemical characterization of paclitaxel prodrugs with cytochrome 3A4 to correlate solubility and bioavailability implementing molecular docking and simulation studies. Journal of Biomolecular Structure and Dynamics, 2021, , 1-13.	3.5	2
5	Application of Deep Learning in Biological Big Data Analysis. Advances in Information Security, Privacy, and Ethics Book Series, 2021, , 117-148.	0.5	1
6	Structure based inference of functional single nucleotide polymorphism and its role in TGF $\beta$ 1 allied colorectal cancer (CRC). International Journal of Bioinformatics Research and Applications, 2021, 17, 80.	0.2	1
7	High-throughput screening of natural compounds and inhibition of a major therapeutic target HsGSK-3 $\beta$ for Alzheimer's disease using computational approaches. Journal of Genetic Engineering and Biotechnology, 2021, 19, 61.	3.3	11
8	Novel structural and functional impact of damaging single nucleotide polymorphisms (SNPs) on human SMYD2 protein using computational approaches. Meta Gene, 2021, 28, 100871.	0.6	9
9	Novel inhibitors design through structural investigations and simulation studies for human PKMTs (SMYD2) involved in cancer. Molecular Simulation, 2021, 47, 1149-1158.	2.0	3
10	Structural and functional analysis of disease-associated mutations in GOT1 gene: An in silico study. Computers in Biology and Medicine, 2021, 136, 104695.	7.0	12
11	Machine learning in expert systems for disease diagnostics in human healthcare. , 2021, , 179-200.		11
12	Early Diagnosis of Alzheimer's Disease using Machine Learning Based Methods. , 2021, , .		7
13	Virtual screening, pharmacokinetics, molecular dynamics and binding free energy analysis for small natural molecules against cyclin-dependent kinase 5 for Alzheimer's disease. Journal of Biomolecular Structure and Dynamics, 2020, 38, 248-262.	3.5	37
14	SCAN DB: an integrated catalogue of computationally characterised NER specific skin cancers. International Journal of Bioinformatics Research and Applications, 2020, 16, 245.	0.2	0
15	Chemometric approach to estimate kinetic properties of paclitaxel prodrugs and their substructures for solubility prediction through molecular modelling and simulation studies. Journal of Chemometrics, 2019, 33, e3181.	1.3	2
16	ABCD: Alzheimer's disease Biomarkers Comprehensive Database. 3 Biotech, 2019, 9, 351.	2.2	2
17	Identification of novel small molecules against GSK3 $\beta$ for Alzheimer's disease using chemoinformatics approach. Journal of Molecular Graphics and Modelling, 2019, 91, 91-104.	2.4	35
18	Gene Expression Studies to Identify Significant Genes in AR, MTOR, MAPK Pathways and their Overlapping Regulatory Role in Prostate Cancer. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	0

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19	Epigenome-Wide DNA Methylation and Histone Modification of Alzheimer's Disease. , 2019, , 131-148.		1
20	<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. Journal of Biomolecular Structure and Dynamics, 2019, 37, 3513-3523.	3.5	17
21	Computational and In-Vitro Validation of Natural Molecules as Potential Acetylcholinesterase Inhibitors and Neuroprotective Agents. Current Alzheimer Research, 2019, 16, 116-127.	1.4	30
22	Tau Pathology. Advances in Medical Diagnosis, Treatment, and Care, 2019, , 217-234.	0.1	0
23	Network and structure based inference of functional single nucleotide polymorphisms associated with the TGF $\beta$ 1 gene and its role in colorectal cancer (CRC). Gene Reports, 2018, 11, 131-142.	0.8	1
24	Network-based approach to understand dynamic behaviour of Wnt signaling pathway regulatory elements in colorectal cancer. Network Modeling Analysis in Health Informatics and Bioinformatics, 2018, 7, 1.	2.1	3
25	An integrative approach to develop computational pipeline for drug-target interaction network analysis. Scientific Reports, 2018, 8, 10238.	3.3	7
26	Development of QSPR Strategy for the Solubility Prediction. Current Computer-Aided Drug Design, 2018, 14, 302-309.	1.2	2
27	In silico Screening and Molecular Interaction Studies of Tetrahydrocannabinol and its Derivatives with Acetylcholine Binding Protein. Current Chemical Biology, 2018, 12, 181-190.	0.5	5
28	A New Decision Tree to Solve the Puzzle of Alzheimer's Disease Pathogenesis Through Standard Diagnosis Scoring System. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 107-115.	3.6	23
29	Computational Network Approaches and Their Applications for Complex Diseases. Translational Medicine Research, 2017, , 337-352.	0.0	0
30	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. Hormones and Behavior, 2017, 89, 13-22.	2.1	26
31	Quercetin ameliorates chronic unpredicted stress-induced behavioral dysfunction in male Swiss albino mice by modulating hippocampal insulin signaling pathway. Physiology and Behavior, 2017, 182, 10-16.	2.1	17
32	A novel miRNA analysis framework to analyze differential biological networks. Scientific Reports, 2017, 7, 14604.	3.3	13
33	Effect of in vitro gastric and pancreatic digestion on antioxidant potential of fruit juices. Food Bioscience, 2017, 17, 1-6.	4.4	27
34	Analysis for biological network properties of Alzheimer's disease associated gene set by enrichment and topological examinations. International Journal of Bioinformatics Research and Applications, 2017, 13, 214.	0.2	3
35	DREMECELS: A Curated Database for Base Excision and Mismatch Repair Mechanisms Associated Human Malignancies. PLoS ONE, 2016, 11, e0157031.	2.5	2
36	Systems biology approach for gene set enrichment and topological analysis of Alzheimer's disease pathway. , 2016, , .		0

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37	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
38	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
39	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
40	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
41	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
42	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
43	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
44	Hydroxymethylation and its potential implication in DNA repair system: A review and future perspectives. <i>Gene</i> , 2015, 564, 109-118.	2.2	44
45	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
46	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
47	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
48	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
49	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
50	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
51	SHIFT: Server for hidden stops analysis in frame-shifted translation. <i>BMC Research Notes</i> , 2013, 6, 68.	1.4	8
52	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
53	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
54	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

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55	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
56	Challenges in the miRNA research. <i>International Journal of Bioinformatics Research and Applications</i> , 2013, 9, 576.	0.2	19
57	Genes Selection Comparative Study in Microarray Data Analysis. <i>Bioinformatics</i> , 2013, 9, 1019-1022.	0.5	3
58	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
59	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
60	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
61	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
62	Comparative analysis of epitope predictions: proposed library of putative vaccine candidates for HIV. <i>Bioinformatics</i> , 2011, 5, 386-389.	0.5	6
63	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
64	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
65	WebFARM: web server for finite automated restriction mapping. <i>Bioinformatics</i> , 2010, 4, 341-343.	0.5	1
66	In silico Analysis of Evolutionary Patterns in Restriction Endonucleases. <i>In Silico Biology</i> , 2009, 9, 45-53.	0.9	2
67	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
68	Ambush hypothesis revisited: Evidences for phylogenetic trends. <i>Computational Biology and Chemistry</i> , 2009, 33, 239-244.	2.3	26
69	In silico analysis of evolutionary patterns in restriction endonucleases. <i>In Silico Biology</i> , 2009, 9, 45-53.	0.9	2
70	Bird Mitochondrial Gene Order: Insight from 3 Warbler Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 475-477.	8.9	53
71	Mitochondrial gene rearrangements: new paradigm in the evolutionary biology and systematics. <i>Bioinformatics</i> , 2008, 3, 95-97.	0.5	14