

Manoj Kumar

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

1,877
citations

318942

23
h-index

299063

42
g-index

50
all docs

50
docs citations

50
times ranked

2498
citing authors

#	ARTICLE	IF	CITATIONS
1	Anti-Ebola: an initiative to predict Ebola virus inhibitors through machine learning. <i>Molecular Diversity</i> , 2022, 26, 1635-1644.	2.1	6
2	Computational resources for analysis of miRNA targetome. , 2022, , 125-139.		0
3	Computational Identification of Potential Multitarget Inhibitors of Nipah Virus by Molecular Docking and Molecular Dynamics. <i>Microorganisms</i> , 2022, 10, 1181.	1.6	14
4	Targeting non-structural proteins of Hepatitis C virus for predicting repurposed drugs using QSAR and machine learning approaches. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3422-3438.	1.9	5
5	Benchmarking and Assessment of Eight <i>De Novo</i> Genome Assemblers on Viral Next-Generation Sequencing Data, Including the SARS-CoV-2. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 372-381.	1.0	5
6	DrugRepV: a compendium of repurposed drugs and chemicals targeting epidemic and pandemic viruses. <i>Briefings in Bioinformatics</i> , 2021, 22, 1076-1084.	3.2	17
7	Prediction of repurposed drugs for Coronaviruses using artificial intelligence and machine learning. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3133-3148.	1.9	30
8	An integrated network analysis approach to identify potential key genes, transcription factors, and microRNAs regulating human hematopoietic stem cell aging. <i>Molecular Omics</i> , 2021, 17, 967-984.	1.4	2
9	Abundance and Diversity of Phages, Microbial Taxa, and Antibiotic Resistance Genes in the Sediments of the River Ganges Through Metagenomic Approach. <i>Microbial Drug Resistance</i> , 2021, 27, 1336-1354.	0.9	11
10	Analysis of aging-related protein interactome and cross-network module comparisons across tissues provide new insights into aging. <i>Computational Biology and Chemistry</i> , 2021, 92, 107506.	1.1	1
11	Computational identification of repurposed drugs against viruses causing epidemics and pandemics via drug-target network analysis. <i>Computers in Biology and Medicine</i> , 2021, 136, 104677.	3.9	8
12	Identifying potential entry inhibitors for emerging Nipah virus by molecular docking and chemical-protein interaction network. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 5108-5125.	2.0	15
13	HPVomics: An integrated resource for the human papillomavirus epitome and therapeutics. <i>Genomics</i> , 2020, 112, 4853-4862.	1.3	1
14	CoronaVR: A Computational Resource and Analysis of Epitopes and Therapeutics for Severe Acute Respiratory Syndrome Coronavirus-2. <i>Frontiers in Microbiology</i> , 2020, 11, 1858.	1.5	23
15	NipahVR: a resource of multi-targeted putative therapeutics and epitopes for the Nipah virus. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	9
16	Efficacy of Anti-Biofilm Agents in Targeting ESKAPE Pathogens with a Focus on Antibiotic Drug Resistance. <i>ACS Symposium Series</i> , 2020, , 177-199.	0.5	3
17	Computational Identification of Inhibitors Using QSAR Approach Against Nipah Virus. <i>Frontiers in Pharmacology</i> , 2019, 10, 71.	1.6	19
18	Computational Resources for Prediction and Analysis of Functional miRNA and Their Targetome. <i>Methods in Molecular Biology</i> , 2019, 1912, 215-250.	0.4	27

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19	saRNAdb: Resource of Small Activating RNAs for Up-regulating the Gene Expression. <i>Journal of Molecular Biology</i> , 2018, 430, 2212-2218.	2.0	5
20	aBiofilm: a resource of anti-biofilm agents and their potential implications in targeting antibiotic drug resistance. <i>Nucleic Acids Research</i> , 2018, 46, D894-D900.	6.5	98
21	Anti-flavi: A Web Platform to Predict Inhibitors of Flaviviruses Using QSAR and Peptidomimetic Approaches. <i>Frontiers in Microbiology</i> , 2018, 9, 3121.	1.5	19
22	Anti-biofilm Peptides: A New Class of Quorum Quenchers and Their Prospective Therapeutic Applications. , 2018, , 87-110.		5
23	HIVprotl: an integrated web based platform for prediction and design of HIV proteins inhibitors. <i>Journal of Cheminformatics</i> , 2018, 10, 12.	2.8	25
24	Phylogenomics and Evolutionary Perspective of Quorum Sensing Regulators (LuxI/LuxR) in Prokaryotes. , 2018, , 61-70.		0
25	vhfRNAi: a web-platform for analysis of host genes involved in viral infections discovered by genome wide RNAi screens. <i>Molecular BioSystems</i> , 2017, 13, 1377-1387.	2.9	3
26	In silico analyses of conservational, functional and phylogenetic distribution of the LuxI and LuxR homologs in Gram-positive bacteria. <i>Scientific Reports</i> , 2017, 7, 6969.	1.6	32
27	<scp>AVC</scp>pred: an integrated web server for prediction and design of antiviral compounds. <i>Chemical Biology and Drug Design</i> , 2017, 89, 74-83.	1.5	54
28	ASPSiRNA: A Resource of ASP-siRNAs Having Therapeutic Potential for Human Genetic Disorders and Algorithm for Prediction of Their Inhibitory Efficacy. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2931-2943.	0.8	12
29	Computational Exploration of Putative LuxR Solos in Archaea and Their Functional Implications in Quorum Sensing. <i>Frontiers in Microbiology</i> , 2017, 8, 798.	1.5	22
30	MSLVP: prediction of multiple subcellular localization of viral proteins using a support vector machine. <i>Molecular BioSystems</i> , 2016, 12, 2572-2586.	2.9	26
31	SMEpred workbench: A web server for predicting efficacy of chemically modified siRNAs. <i>RNA Biology</i> , 2016, 13, 1144-1151.	1.5	16
32	ZikaVR: An Integrated Zika Virus Resource for Genomics, Proteomics, Phylogenetic and Therapeutic Analysis. <i>Scientific Reports</i> , 2016, 6, 32713.	1.6	49
33	ge-CRISPR - An integrated pipeline for the prediction and analysis of sgRNAs genome editing efficiency for CRISPR/Cas system. <i>Scientific Reports</i> , 2016, 6, 30870.	1.6	38
34	siRNAmod: A database of experimentally validated chemically modified siRNAs. <i>Scientific Reports</i> , 2016, 6, 20031.	1.6	53
35	ViralEpiV1.0: a high-throughput spectrum of viral epigenomic methylation profiles from diverse diseases. <i>Epigenomics</i> , 2016, 8, 67-75.	1.0	2
36	SigMol: repertoire of quorum sensing signaling molecules in prokaryotes. <i>Nucleic Acids Research</i> , 2016, 44, D634-D639.	6.5	100

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37	AVPâ€C₅₀Pred: Multiple machine learning techniquesâ€Cbased prediction of peptide antiviral activity in terms of half maximal inhibitory concentration (IC₅₀). Biopolymers, 2015, 104, 753-763.	1.2	47
38	CrisprGE: a central hub of CRISPR/Cas-based genome editing. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav055.	1.4	32
39	Prediction and Analysis of Quorum Sensing Peptides Based on Sequence Features. PLoS ONE, 2015, 10, e0120066.	1.1	74
40	HPVbase â€C a knowledgebase of viral integrations, methylation patterns and microRNAs aberrant expression: As potential biomarkers for Human papillomaviruses mediated carcinomas. Scientific Reports, 2015, 5, 12522.	1.6	24
41	VIRmiRNA: a comprehensive resource for experimentally validated viral miRNAs and their targets. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	95
42	AVPdb: a database of experimentally validated antiviral peptides targeting medically important viruses. Nucleic Acids Research, 2014, 42, D1147-D1153.	6.5	181
43	VIRsiRNApred: a web server for predicting inhibition efficacy of siRNAs targeting human viruses. Journal of Translational Medicine, 2013, 11, 305.	1.8	46
44	HIPdb: A Database of Experimentally Validated HIV Inhibiting Peptides. PLoS ONE, 2013, 8, e54908.	1.1	84
45	AVPpred: collection and prediction of highly effective antiviral peptides. Nucleic Acids Research, 2012, 40, W199-W204.	6.5	226
46	VIRsiRNAdb: a curated database of experimentally validated viral siRNA/shRNA. Nucleic Acids Research, 2012, 40, D230-D236.	6.5	48
47	HIVsirDB: A Database of HIV Inhibiting siRNAs. PLoS ONE, 2011, 6, e25917.	1.1	37
48	Continued Persistence of a Single Genotype of Dengue Virus Type-3 (DENV-3) in Delhi, India Since its Re-emergence Over the Last Decade. Journal of Microbiology, Immunology and Infection, 2010, 43, 53-61.	1.5	22
49	Novel structural analogues of piperine as inhibitors of the NorA efflux pump of Staphylococcus aureus. Journal of Antimicrobial Chemotherapy, 2008, 61, 1270-1276.	1.3	143
50	Emergence and continued circulation of dengue-2 (genotype IV) virus strains in northern India. Journal of Medical Virology, 2004, 74, 314-322.	2.5	63