

Manoj Kumar

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

1,877
citations

279701

23
h-index

265120

42
g-index

50
all docs

50
docs citations

50
times ranked

2228
citing authors

#	ARTICLE	IF	CITATIONS
1	AVPpred: collection and prediction of highly effective antiviral peptides. Nucleic Acids Research, 2012, 40, W199-W204.	6.5	226
2	AVPdb: a database of experimentally validated antiviral peptides targeting medically important viruses. Nucleic Acids Research, 2014, 42, D1147-D1153.	6.5	181
3	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
4	SigMol: repertoire of quorum sensing signaling molecules in prokaryotes. Nucleic Acids Research, 2016, 44, D634-D639.	6.5	100
5	aBiofilm: a resource of anti-biofilm agents and their potential implications in targeting antibiotic drug resistance. Nucleic Acids Research, 2018, 46, D894-D900.	6.5	98
6	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
7	HIPdb: A Database of Experimentally Validated HIV Inhibiting Peptides. PLoS ONE, 2013, 8, e54908.	1.1	84
8	Prediction and Analysis of Quorum Sensing Peptides Based on Sequence Features. PLoS ONE, 2015, 10, e0120066.	1.1	74
9	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
10	<scp>AVC</scp>pred: an integrated web server for prediction and design of antiviral compounds. Chemical Biology and Drug Design, 2017, 89, 74-83.	1.5	54
11	siRNAmoD: A database of experimentally validated chemically modified siRNAs. Scientific Reports, 2016, 6, 20031.	1.6	53
12	ZikaVR: An Integrated Zika Virus Resource for Genomics, Proteomics, Phylogenetic and Therapeutic Analysis. Scientific Reports, 2016, 6, 32713.	1.6	49
13	VIRsiRNADB: a curated database of experimentally validated viral siRNA/shRNA. Nucleic Acids Research, 2012, 40, D230-D236.	6.5	48
14	AVP-50Pred: Multiple machine learning techniques-based prediction of peptide antiviral activity in terms of half maximal inhibitory concentration (IC ₅₀). Biopolymers, 2015, 104, 753-763.	1.2	47
15	VIRsiRNAPred: a web server for predicting inhibition efficacy of siRNAs targeting human viruses. Journal of Translational Medicine, 2013, 11, 305.	1.8	46
16	ge-CRISPR - An integrated pipeline for the prediction and analysis of sgRNAs genome editing efficiency for CRISPR/Cas system. Scientific Reports, 2016, 6, 30870.	1.6	38
17	HIVsirDB: A Database of HIV Inhibiting siRNAs. PLoS ONE, 2011, 6, e25917.	1.1	37
18	CrisprGE: a central hub of CRISPR/Cas-based genome editing. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav055.	1.4	32

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19	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
20	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
21	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
22	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
23	HIVprotI: 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	HPVbase – a knowledgebase of viral integrations, methylation patterns and microRNAs aberrant expression: As potential biomarkers for Human papillomaviruses mediated carcinomas. <i>Scientific Reports</i> , 2015, 5, 12522.	1.6	24
25	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
26	Continued Persistence of a Single Genotype of Dengue Virus Type-3 (DENV-3) in Delhi, India Since its Re-emergence Over the Last Decade. <i>Journal of Microbiology, Immunology and Infection</i> , 2010, 43, 53-61.	1.5	22
27	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
28	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
29	Computational Identification of Inhibitors Using QSAR Approach Against Nipah Virus. <i>Frontiers in Pharmacology</i> , 2019, 10, 71.	1.6	19
30	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
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	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
33	Computational Identification of Potential Multitarget Inhibitors of Nipah Virus by Molecular Docking and Molecular Dynamics. <i>Microorganisms</i> , 2022, 10, 1181.	1.6	14
34	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
35	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
36	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

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37	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
38	Anti-Ebola: an initiative to predict Ebola virus inhibitors through machine learning. <i>Molecular Diversity</i> , 2022, 26, 1635-1644.	2.1	6
39	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
40	Anti-biofilm Peptides: A New Class of Quorum Quenchers and Their Prospective Therapeutic Applications. , 2018, , 87-110.		5
41	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
42	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
43	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
44	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
45	ViralEpiV1.0: a high-throughput spectrum of viral epigenomic methylation profiles from diverse diseases. <i>Epigenomics</i> , 2016, 8, 67-75.	1.0	2
46	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
47	HPVomics: An integrated resource for the human papillomavirus epitome and therapeutics. <i>Genomics</i> , 2020, 112, 4853-4862.	1.3	1
48	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
49	Phylogenomics and Evolutionary Perspective of Quorum Sensing Regulators (LuxI/LuxR) in Prokaryotes. , 2018, , 61-70.		0
50	Computational resources for analysis of miRNA targetome. , 2022, , 125-139.		0