Anshu Bhardwaj

List of Publications by Year in descending order

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687363 677142 37 553 13 22 citations h-index g-index papers 44 44 44 976 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A machine learning-based approach to determine infection status in recipients of BBV152 (Covaxin) whole-virion inactivated SARS-CoV-2 vaccine for serological surveys. Computers in Biology and Medicine, 2022, 146, 105419.	7.0	8
2	Lipid biosynthetic pathways as potential drug targets for emerging mycobacterial pathogens. , 2022, , 27-49.		0
3	MitoLink: A Generic Integrated Web-based Workflow System to Evaluate Genotype-Phenotype Correlations in Human Mitochondrial Diseases: Observations from The GenomeAsia Pilot Project. Mitochondrion, 2021, 61, 54-61.	3.4	O
4	Hybrid Dynamic Pharmacophore Models as Effective Tools to Identify Novel Chemotypes for Anti-TB Inhibitor Design: A Case Study With Mtb-DapB. Frontiers in Chemistry, 2020, 8, 596412.	3.6	4
5	Specifications of the ACMG/AMP standards and guidelines for mitochondrial DNA variant interpretation. Human Mutation, 2020, 41, 2028-2057.	2.5	84
6	Data-Driven Systems Level Approaches for Drug Repurposing: Combating Drug Resistance in Priority Pathogens., 2019,, 229-253.		3
7	MtBrowse: An integrative genomics browser for human mitochondrial DNA. Mitochondrion, 2019, 48, 31-36.	3.4	2
8	RepTB: a gene ontology based drug repurposing approach for tuberculosis. Journal of Cheminformatics, 2018, 10, 24.	6.1	27
9	Assessing therapeutic potential of molecules: molecular property diagnostic suite for tuberculosis \$\$(mathbf{MPDS}^{mathbf{TB}})\$\$ (MPDS TB). Journal of Chemical Sciences, 2017, 129, 515-531.	1.5	20
10	Predicting promiscuous antigenic T cell epitopes of Mycobacterium tuberculosis mymA operon proteins binding to MHC Class I and Class II molecules. Infection, Genetics and Evolution, 2016, 44, 182-189.	2.3	10
11	dPABBs: A Novel in silico Approach for Predicting and Designing Anti-biofilm Peptides. Scientific Reports, 2016, 6, 21839.	3.3	84
12	Analysis of the DosR regulon genes to select cytotoxic T lymphocyte epitope specific vaccine candidates using a reverse vaccinology approach. International Journal of Mycobacteriology, 2016, 5, 34-43.	0.6	13
13	FROG - Fingerprinting Genomic Variation Ontology. PLoS ONE, 2015, 10, e0134693.	2.5	3
14	A molecular patch for DMD. Science Translational Medicine, 2015, 7, .	12.4	1
15	Resources, challenges and way forward in rare mitochondrial diseases research. F1000Research, 2015, 4, 70.	1.6	6
16	Personalized cancer medicines. Science Translational Medicine, 2015, 7, .	12.4	0
17	Systems level mapping of metabolic complexity in Mycobacterium tuberculosis to identify high-value drug targets. Journal of Translational Medicine, 2014, 12, 263.	4.4	32
18	BioPhytMol: a drug discovery community resource on anti-mycobacterial phytomolecules and plant extracts. Journal of Cheminformatics, 2014, 6, 46.	6.1	39

#	Article	IF	Citations
19	Investigating the role of site specific synonymous variation in disease association studies. Mitochondrion, 2014, 16, 83-88.	3.4	5
20	Harnessing the Crowd for Neurology Research. Science Translational Medicine, 2014, 6, .	12.4	4
21	"Antigenomic" RNA as a Therapeutic Tool for Mitochondrial Diseases. Science Translational Medicine, 2014, 6, .	12.4	0
22	Reactive Species Contribute to Antibiotic-Mediated Killing. Science Translational Medicine, 2014, 6, .	12.4	0
23	Dissecting the Enigma of <i>Mycobacterium tuberculosis</i> Pathogenesis. Science Translational Medicine, 2014, 6, .	12.4	0
24	Synthetic Lethality: Drug Repurposing with a Difference. Science Translational Medicine, 2014, 6, .	12.4	0
25	Cholesterol Therapy That's Not Chopped Liver. Science Translational Medicine, 2014, 6, .	12.4	0
26	Ctrl-Alt-Del: Host-Targeting Anti-Angiogenic Agents as Adjunct Therapy for Tuberculosis. Science Translational Medicine, 2014, 6, .	12.4	0
27	Social networks to biological networks: systems biology of Mycobacterium tuberculosis. Molecular BioSystems, 2013, 9, 1584.	2.9	5
28	Software Platform for Metabolic Network Reconstruction of Mycobacterium tuberculosis. , 2013, , 21-35.		1
29	Open Source Software and Web Services for Designing Therapeutic Molecules. Current Topics in Medicinal Chemistry, 2013, 13, 1172-1191.	2.1	25
30	MitoLSDB: A Comprehensive Resource to Study Genotype to Phenotype Correlations in Human Mitochondrial DNA Variations. PLoS ONE, 2013, 8, e60066.	2.5	17
31	Crowd Sourcing a New Paradigm for Interactome Driven Drug Target Identification in Mycobacterium tuberculosis. PLoS ONE, 2012, 7, e39808.	2.5	36
32	Open source drug discovery– A new paradigm of collaborative research in tuberculosis drug development. Tuberculosis, 2011, 91, 479-86.	1.9	42
33	Structural Annotation of Mycobacterium tuberculosis Proteome. PLoS ONE, 2011, 6, e27044.	2.5	33
34	FishMap Zv8 Update—A Genomic Regulatory Map of Zebrafish. Zebrafish, 2010, 7, 179-180.	1.1	7
35	TBrowse: An integrative genomics map of Mycobacterium tuberculosis. Tuberculosis, 2009, 89, 386-387.	1.9	15
36	MtSNPscore: a combined evidence approach for assessing cumulative impact of mitochondrial variations in disease. BMC Bioinformatics, 2009, 10, S7.	2.6	21

ARTICLE IF CITATIONS

37 Evaluating the Association of Mitochondrial SNP Haplotypes with Disease Phenotypes using a Novel in silico Tool E-MIDAS., 2006, , .