

Sudheer Gupta

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5667657/publications.pdf>

Version: 2024-02-01

25
papers

2,393
citations

516710

16
h-index

580821

25
g-index

25
all docs

25
docs citations

25
times ranked

2762
citing authors

#	ARTICLE	IF	CITATIONS
1	In Silico Approach for Predicting Toxicity of Peptides and Proteins. PLoS ONE, 2013, 8, e73957.	2.5	1,120
2	CancerPPD: a database of anticancer peptides and proteins. Nucleic Acids Research, 2015, 43, D837-D843.	14.5	253
3	Prediction of IL4 Inducing Peptides. Clinical and Developmental Immunology, 2013, 2013, 1-9.	3.3	213
4	Peptide Toxicity Prediction. Methods in Molecular Biology, 2015, 1268, 143-157.	0.9	105
5	CancerDR: Cancer Drug Resistance Database. Scientific Reports, 2013, 3, 1445.	3.3	102
6	Identification of B-cell epitopes in an antigen for inducing specific class of antibodies. Biology Direct, 2013, 8, 27.	4.6	91
7	Prediction of anti-inflammatory proteins/peptides: an insilico approach. Journal of Translational Medicine, 2017, 15, 7.	4.4	91
8	Prioritization of anticancer drugs against a cancer using genomic features of cancer cells: A step towards personalized medicine. Scientific Reports, 2016, 6, 23857.	3.3	54
9	ProInflam: a webserver for the prediction of proinflammatory antigenicity of peptides and proteins. Journal of Translational Medicine, 2016, 14, 178.	4.4	52
10	Prediction of Biofilm Inhibiting Peptides: An In silico Approach. Frontiers in Microbiology, 2016, 7, 949.	3.5	46
11	Herceptin Resistance Database for Understanding Mechanism of Resistance in Breast Cancer Patients. Scientific Reports, 2014, 4, 4483.	3.3	40
12	IL17eScan: A Tool for the Identification of Peptides Inducing IL-17 Response. Frontiers in Immunology, 2017, 8, 1430.	4.8	36
13	VaccineDA: Prediction, design and genome-wide screening of oligodeoxynucleotide-based vaccine adjuvants. Scientific Reports, 2015, 5, 12478.	3.3	34
14	PCMDB: Pancreatic Cancer Methylation Database. Scientific Reports, 2014, 4, 4197.	3.3	28
15	Prediction of vitamin interacting residues in a vitamin binding protein using evolutionary information. BMC Bioinformatics, 2013, 14, 44.	2.6	23
16	A Web-Based Platform for Designing Vaccines against Existing and Emerging Strains of Mycobacterium tuberculosis. PLoS ONE, 2016, 11, e0153771.	2.5	21
17	A web-based resource for designing therapeutics against Ebola Virus. Scientific Reports, 2016, 6, 24782.	3.3	14
18	A Platform for Designing Genome-Based Personalized Immunotherapy or Vaccine against Cancer. PLoS ONE, 2016, 11, e0166372.	2.5	14

#	ARTICLE	IF	CITATIONS
19	Managing Drug Resistance in Cancer: Role of Cancer Informatics. <i>Methods in Molecular Biology</i> , 2016, 1395, 299-312.	0.9	12
20	Molecular and phylogenetic analysis of Chikungunya virus in Central India during 2016 and 2017 outbreaks reveal high similarity with recent New Delhi and Bangladesh strains. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103940.	2.3	11
21	BioFuelDB: a database and prediction server of enzymes involved in biofuels production. <i>PeerJ</i> , 2017, 5, e3497.	2.0	9
22	Host Genetic Polymorphisms Influencing Susceptibility to Dengue. <i>DNA and Cell Biology</i> , 2018, 37, 805-807.	1.9	7
23	Co-circulation of dengue virus serotypes in Central India: Evidence of prolonged viremia in DENV-2. <i>Infection, Genetics and Evolution</i> , 2019, 70, 72-79.	2.3	7
24	Designing B-Cell Epitopes for Immunotherapy and Subunit Vaccines. <i>Methods in Molecular Biology</i> , 2015, 1348, 327-340.	0.9	5
25	Genome-Wide Analysis to Identify HLA Factors Potentially Associated With Severe Dengue. <i>Frontiers in Immunology</i> , 2018, 9, 728.	4.8	5