Piyush Agrawal

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8174472/publications.pdf

Version: 2024-02-01

23	1,428	516681 16	677123 22
papers	citations	h-index	g-index

32	32	32	1851
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Computational approaches for vaccine designing. , 2022, , 317-335.		2
2	AntiCP 2.0: an updated model for predicting anticancer peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	127
3	NAGbinder: An approach for identifying Nâ€acetylglucosamine interacting residues of a protein from its primary sequence. Protein Science, 2020, 29, 201-210.	7.6	31
4	A Web-Based Platform on Coronavirus Disease-19 to Maintain Predicted Diagnostic, Drug, and Vaccine Candidates. Monoclonal Antibodies in Immunodiagnosis and Immunotherapy, 2020, 39, 204-216.	1.6	25
5	A Method for Predicting Hemolytic Potency of Chemically Modified Peptides From Its Structure. Frontiers in Pharmacology, 2020, 11, 54.	3.5	19
6	RareLSD: a manually curated database of lysosomal enzymes associated with rare diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	4
7	HumCFS: a database of fragile sites in human chromosomes. BMC Genomics, 2019, 19, 985.	2.8	63
8	NeuroPIpred: a tool to predict, design and scan insect neuropeptides. Scientific Reports, 2019, 9, 5129.	3.3	36
9	ImmunoSPdb: an archive of immunosuppressive peptides. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	2
10	ccPDB 2.0: an updated version of datasets created and compiled from Protein Data Bank. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	10
11	Benchmarking of different molecular docking methods for protein-peptide docking. BMC Bioinformatics, 2019, 19, 426.	2.6	104
12	SAMbinder: A Web Server for Predicting S-Adenosyl-L-Methionine Binding Residues of a Protein From Its Amino Acid Sequence. Frontiers in Pharmacology, 2019, 10, 1690.	3.5	3
13	Prediction of Antimicrobial Potential of a Chemically Modified Peptide From Its Tertiary Structure. Frontiers in Microbiology, 2018, 9, 2551.	3.5	38
14	Computer-aided prediction of antigen presenting cell modulators for designing peptide-based vaccine adjuvants. Journal of Translational Medicine, 2018, 16, 181.	4.4	60
15	In Silico Approach for Prediction of Antifungal Peptides. Frontiers in Microbiology, 2018, 9, 323.	3.5	113
16	Prediction of Cell-Penetrating Potential of Modified Peptides Containing Natural and Chemically Modified Residues. Frontiers in Microbiology, 2018, 9, 725.	3.5	58
17	In silico approaches for predicting the half-life of natural and modified peptides in blood. PLoS ONE, 2018, 13, e0196829.	2.5	67
18	Overview of Free Software Developed for Designing Drugs Based on Protein-Small Molecules Interaction. Current Topics in Medicinal Chemistry, 2018, 18, 1146-1167.	2.1	14

#	Article	IF	Citations
19	Novelin silicotools for designing peptide-based subunit vaccines and immunotherapeutics. Briefings in Bioinformatics, 2017, 18, bbw025.	6.5	94
20	PEPlife: A Repository of the Half-life of Peptides. Scientific Reports, 2016, 6, 36617.	3.3	108
21	CPPsite 2.0: a repository of experimentally validated cell-penetrating peptides. Nucleic Acids Research, 2016, 44, D1098-D1103.	14.5	241
22	SATPdb: a database of structurally annotated therapeutic peptides. Nucleic Acids Research, 2016, 44, D1119-D1126.	14.5	131
23	Homology modeling and structural validation of tissue factor pathway inhibitor. Bioinformation, 2013, 9, 808-812.	0.5	7