

Jian Huang

List of Publications by Year in descending order

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91
papers

3,031
citations

136950

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175258

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92
docs citations

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times ranked

4870
citing authors

#	ARTICLE	IF	CITATIONS
1	SSH2.0: A Better Tool for Predicting the Hydrophobic Interaction Risk of Monoclonal Antibody. <i>Frontiers in Genetics</i> , 2022, 13, 842127.	2.3	6
2	BBPpredict: A Web Service for Identifying Blood-Brain Barrier Penetrating Peptides. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	8
3	A Mini-review of Computational Approaches to Predict Functions and Findings of Novel Micro Peptides. <i>Current Bioinformatics</i> , 2021, 15, 1027-1035.	1.5	2
4	TUPDB: Target-Unrelated Peptide Data Bank. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 426-432.	3.6	2
5	CASPredict: a web service for identifying Cas proteins. <i>PeerJ</i> , 2021, 9, e11887.	2.0	8
6	Development and application of therapeutic antibodies against COVID-19. <i>International Journal of Biological Sciences</i> , 2021, 17, 1486-1496.	6.4	47
7	A comprehensive overview of oncogenic pathways in human cancer. <i>Briefings in Bioinformatics</i> , 2020, 21, 957-969.	6.5	29
8	AGONOTES: A Robot Annotator for Argonaute Proteins. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 109-116.	3.6	4
9	Systematic Analysis of Competing Endogenous RNA Networks in Diffuse Large B-Cell Lymphoma and Hodgkin's Lymphoma. <i>Frontiers in Genetics</i> , 2020, 11, 586688.	2.3	7
10	SSH: A Tool for Predicting Hydrophobic Interaction of Monoclonal Antibodies Using Sequences. <i>BioMed Research International</i> , 2020, 2020, 1-6.	1.9	4
11	Integration of platelet features in blood and platelet rich plasma for detection of lung cancer. <i>Clinica Chimica Acta</i> , 2020, 509, 43-51.	1.1	10
12	Ultra Wide Acoustic Bandgap Detection in Novel Octagonal Phononic Crystal of MEMS Materials. , 2020, , .		1
13	CLING: Candidate Cancer-Related lncRNA Prioritization via Integrating Multiple Biological Networks. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 138.	4.1	1
14	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. <i>Bioinformatics</i> , 2020, 36, 3327-3335.	4.1	33
15	Use of a 6-miRNA panel to distinguish lymphoma from reactive lymphoid hyperplasia. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 2.	17.1	8
16	NeuroCS: A Tool to Predict Cleavage Sites of Neuropeptide Precursors. <i>Protein and Peptide Letters</i> , 2020, 27, 337-345.	0.9	3
17	Development and Application of Computational Methods in Phage Display Technology. <i>Current Medicinal Chemistry</i> , 2020, 26, 7672-7693.	2.4	13
18	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. <i>Medicinal Chemistry</i> , 2020, 16, 605-619.	1.5	2

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19	Survey of miRNA-miRNA cooperative regulation principles across cancer types. <i>Briefings in Bioinformatics</i> , 2019, 20, 1621-1638.	6.5	39
20	CasPDB: an integrated and annotated database for Cas proteins from bacteria and archaea. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	8
21	SAROTUP: a suite of tools for finding potential target-unrelated peptides from phage display data. <i>International Journal of Biological Sciences</i> , 2019, 15, 1452-1459.	6.4	29
22	CasLocusAnno: a web-based server for annotating <i>cas</i> loci and their corresponding (sub)types. <i>FEBS Letters</i> , 2019, 593, 2646-2654.	2.8	2
23	Guest Editorial for Special Section on the 7th National Conference on Bioinformatics and Systems Biology of China. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1262-1263.	3.0	0
24	Rlscoper: a tool for RNA-RNA interaction extraction from the literature. <i>Bioinformatics</i> , 2019, 35, 3199-3202.	4.1	23
25	CISI: A Tool for Predicting Cross-interaction or Self-interaction of Monoclonal Antibodies Using Sequences. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 691-697.	3.6	7
26	PVsiRNAPred: Prediction of plant exclusive virus-derived small interfering RNAs by deep convolutional neural network. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1950039.	0.8	8
27	NeuroPP: A Tool for the Prediction of Neuropeptide Precursors Based on Optimal Sequence Composition. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 108-114.	3.6	34
28	HMMCAS: A Web Tool for the Identification and Domain Annotations of CAS Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1313-1315.	3.0	43
29	Molecular Design of Peptide-Fc Fusion Drugs. <i>Current Drug Metabolism</i> , 2019, 20, 203-208.	1.2	12
30	A Brief Survey of Machine Learning Methods in Protein Sub-Golgi Localization. <i>Current Bioinformatics</i> , 2019, 14, 234-240.	1.5	135
31	PhD7Faster 2.0: predicting clones propagating faster from the Ph.D.-7 phage display library by coupling PseAAC and tripeptide composition. <i>PeerJ</i> , 2019, 7, e7131.	2.0	11
32	Multidimensional Integration Analysis of Autophagy-related Modules in Colorectal Cancer. <i>Letters in Organic Chemistry</i> , 2019, 16, 340-346.	0.5	0
33	Compositional Bias in Naïve and Chemically-modified Phage-Displayed Libraries uncovered by Paired-end Deep Sequencing. <i>Scientific Reports</i> , 2018, 8, 1214.	3.3	28
34	Anti-CRISPRdb: a comprehensive online resource for anti-CRISPR proteins. <i>Nucleic Acids Research</i> , 2018, 46, D393-D398.	14.5	65
35	Capturing functional long non-coding RNAs through integrating large-scale causal relations from gene perturbation experiments. <i>EBioMedicine</i> , 2018, 35, 369-380.	6.1	19
36	Comprehensive exploration of the enzymes catalysing oxygen-involved reactions and COGs relevant to bacterial oxygen utilization. <i>Environmental Microbiology</i> , 2018, 20, 3836-3850.	3.8	1

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37	Computational Design of Antiangiogenic Peptibody by Fusing Human IgG1 Fc Fragment and HRH Peptide: Structural Modeling, Energetic Analysis, and Dynamics Simulation of Its Binding Potency to VEGF Receptor. <i>International Journal of Biological Sciences</i> , 2018, 14, 930-937.	6.4	11
38	Biopanning data bank 2018: hugging next generation phage display. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	23
39	Special issue on Computational Resources and Methods in Biological Sciences. <i>International Journal of Biological Sciences</i> , 2018, 14, 807-810.	6.4	3
40	Embelin Restores Carbapenem Efficacy against NDM-1-Positive Pathogens. <i>Frontiers in Microbiology</i> , 2018, 9, 71.	3.5	21
41	LnChrom: a resource of experimentally validated lncRNA-chromatin interactions in human and mouse. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	42
42	Identify and analysis crotonylation sites in histone by using support vector machines. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 75-81.	6.5	52
43	A novel peptide specifically binding to VEGF receptor suppresses angiogenesis in vitro and in vivo. <i>Signal Transduction and Targeted Therapy</i> , 2017, 2, 17010.	17.1	30
44	PSBinder: A Web Service for Predicting Polystyrene Surface-Binding Peptides. <i>BioMed Research International</i> , 2017, 2017, 1-5.	1.9	49
45	SABinder: A Web Service for Predicting Streptavidin-Binding Peptides. <i>BioMed Research International</i> , 2016, 2016, 1-8.	1.9	35
46	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. <i>Virologica Sinica</i> , 2016, 31, 350-352.	3.0	47
47	Analysis and quality control of carbohydrates in therapeutic proteins with fluorescence HPLC. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 864-867.	2.1	3
48	A potential therapeutic peptide-based neutralizer that potently inhibits Shiga toxin 2 in vitro and in vivo. <i>Scientific Reports</i> , 2016, 6, 21837.	3.3	10
49	A two-step binding mechanism for the self-binding peptide recognition of target domains. <i>Molecular BioSystems</i> , 2016, 12, 1201-1213.	2.9	108
50	Predicting bacteriophage proteins located in host cell with feature selection technique. <i>Computers in Biology and Medicine</i> , 2016, 71, 156-161.	7.0	12
51	BDB: biopanning data bank. <i>Nucleic Acids Research</i> , 2016, 44, D1127-D1132.	14.5	71
52	Structural modeling of HLA-B*1502/peptide/carbamazepine/T-cell receptor complex architecture: implication for the molecular mechanism of carbamazepine-induced Stevens-Johnson syndrome/toxic epidermal necrolysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1806-1817.	3.5	103
53	Self-Binding Peptides: Folding or Binding?. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 329-342.	5.4	123
54	NIEluter: Predicting peptides eluted from HLA class I molecules. <i>Journal of Immunological Methods</i> , 2015, 422, 22-27.	1.4	18

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55	ncRDeathDB: A comprehensive bioinformatics resource for deciphering network organization of the ncRNA-mediated cell death system. <i>Autophagy</i> , 2015, 11, 1917-1926.	9.1	65
56	Structural and energetic insights into the intermolecular interaction among human leukocyte antigens, clinical hypersensitive drugs and antigenic peptides. <i>Molecular Simulation</i> , 2015, 41, 741-751.	2.0	79
57	MDC-Analyzer: A novel degenerate primer design tool for the construction of intelligent mutagenesis libraries with contiguous sites. <i>BioTechniques</i> , 2014, 56, 301-310.	1.8	15
58	SMAL: A Resource of Spontaneous Mutation Accumulation Lines. <i>Molecular Biology and Evolution</i> , 2014, 31, 1302-1308.	8.9	10
59	PhD7FASTER: PREDICTING CLONES PROPAGATING FASTER FROM THE Ph.D.-7 PHAGE DISPLAY PEPTIDE LIBRARY. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1450005.	0.8	36
60	Prediction of protein structural classes based on feature selection technique. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 235-240.	3.6	32
61	Biocomputational construction of a gene network under acid stress in <i>Synechocystis</i> sp. PCC 6803. <i>Research in Microbiology</i> , 2014, 165, 420-428.	2.1	6
62	Mimotope-Based Prediction of B-Cell Epitopes. <i>Methods in Molecular Biology</i> , 2014, 1184, 237-243.	0.9	19
63	Biomacromolecular quantitative structure–activity relationship (BioQSAR): a proof-of-concept study on the modeling, prediction and interpretation of protein–protein binding affinity. <i>Journal of Computer-Aided Molecular Design</i> , 2013, 27, 67-78.	2.9	88
64	Prediction of Golgi-resident protein types by using feature selection technique. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 124, 9-13.	3.5	90
65	CEG: a database of essential gene clusters. <i>BMC Genomics</i> , 2013, 14, 769.	2.8	51
66	PREDICTING SUBCHLOROPLAST LOCATIONS OF PROTEINS BASED ON THE GENERAL FORM OF CHOU'S PSEUDO AMINO ACID COMPOSITION: APPROACHED FROM OPTIMAL TRIPEPTIDE COMPOSITION. <i>International Journal of Biomathematics</i> , 2013, 06, 1350003.	2.9	46
67	Structural Characterization of a Recombinant Fusion Protein by Instrumental Analysis and Molecular Modeling. <i>PLoS ONE</i> , 2013, 8, e57642.	2.5	55
68	Epitope Mapping of Metuximab on CD147 Using Phage Display and Molecular Docking. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-6.	1.3	15
69	Phage Display Informatics. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-2.	1.3	5
70	Improved Particle Implementation of the Probability Hypothesis Density Filter in Resampling. , 2012, , .		1
71	MimoDB 2.0: a mimotope database and beyond. <i>Nucleic Acids Research</i> , 2012, 40, D271-D277.	14.5	109
72	A sigma point–based resampling algorithm in particle filter. <i>International Journal of Adaptive Control and Signal Processing</i> , 2012, 26, 1013-1023.	4.1	5

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73	Distinct Functional Patterns of Gene Promoter Hypomethylation and Hypermethylation in Cancer Genomes. PLoS ONE, 2012, 7, e44822.	2.5	25
74	Identify Golgi Protein Types with Modified Mahalanobis Discriminant Algorithm and Pseudo Amino Acid Composition. Protein and Peptide Letters, 2011, 18, 58-63.	0.9	96
75	Bioinformatics Resources and Tools for Phage Display. Molecules, 2011, 16, 694-709.	3.8	48
76	MimoDB: a New Repository for Mimotope Data Derived from Phage Display Technology. Molecules, 2010, 15, 8279-8288.	3.8	47
77	Prediction of subcellular location of mycobacterial protein using feature selection techniques. Molecular Diversity, 2010, 14, 667-671.	3.9	41
78	SAROTUP: Scanner and Reporter of Target-Unrelated Peptides. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-7.	3.0	84
79	Effects on the expression of GABAA receptor subunits by jujuboside A treatment in rat hippocampal neurons. Journal of Ethnopharmacology, 2010, 128, 419-423.	4.1	61
80	Chromosome translocation and its consequence in the genome of Burkholderia cenocepacia AU-1054. Biochemical and Biophysical Research Communications, 2010, 403, 375-379.	2.1	14
81	A plot of G + C content against sequence length of 640 bacterial chromosomes shows the points are widely scattered in the upper triangular area. Chromosome Research, 2009, 17, 359-364.	2.2	17
82	Predicting Subcellular Localization of Mycobacterial Proteins by Using Chous Pseudo Amino Acid Composition. Protein and Peptide Letters, 2008, 15, 739-744.	0.9	209
83	PREDICTING B CELL EPITOPE RESIDUES WITH NETWORK TOPOLOGY BASED AMINO ACID INDICES. , 2007, , .		5
84	NEW AMINO ACID INDICES BASED ON RESIDUE NETWORK TOPOLOGY. , 2007, , .		10
85	MIMOX: a web tool for phage display based epitope mapping. BMC Bioinformatics, 2006, 7, 451.	2.6	82
86	CED: a conformational epitope database. BMC Immunology, 2006, 7, 7.	2.2	119
87	HLA class I expression in primary hepatocellular carcinoma. World Journal of Gastroenterology, 2002, 8, 654.	3.3	22
88	Prediction of Protein Interaction Sites Using Mimotope Analysis. , 0, , .		1
89	Selection and Validation of Reference Genes for Pan-Cancer in Platelets Based on RNA-Sequence Data. Frontiers in Genetics, 0, 13, .	2.3	0
90	AntiDMPpred: a web service for identifying anti-diabetic peptides. PeerJ, 0, 10, e13581.	2.0	5

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91	PDL1Binder: Identifying programmed cell death ligand 1 binding peptides by incorporating next-generation phage display data and different peptide descriptors. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5