

Jian Huang

List of Publications by Year in descending order

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91
papers

3,031
citations

136950

32
h-index

175258

52
g-index

92
all docs

92
docs citations

92
times ranked

4870
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting Subcellular Localization of Mycobacterial Proteins by Using Chous Pseudo Amino Acid Composition. <i>Protein and Peptide Letters</i> , 2008, 15, 739-744.	0.9	209
2	A Brief Survey of Machine Learning Methods in Protein Sub-Golgi Localization. <i>Current Bioinformatics</i> , 2019, 14, 234-240.	1.5	135
3	Self-Binding Peptides: Folding or Binding?. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 329-342.	5.4	123
4	CED: a conformational epitope database. <i>BMC Immunology</i> , 2006, 7, 7.	2.2	119
5	MimoDB 2.0: a mimotope database and beyond. <i>Nucleic Acids Research</i> , 2012, 40, D271-D277.	14.5	109
6	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
7	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
8	Identify Golgi Protein Types with Modified Mahalanobis Discriminant Algorithm and Pseudo Amino Acid Composition. <i>Protein and Peptide Letters</i> , 2011, 18, 58-63.	0.9	96
9	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
10	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
11	SAROTUP: Scanner and Reporter of Target-Unrelated Peptides. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-7.	3.0	84
12	MIMOX: a web tool for phage display based epitope mapping. <i>BMC Bioinformatics</i> , 2006, 7, 451.	2.6	82
13	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
14	BDB: biopanning data bank. <i>Nucleic Acids Research</i> , 2016, 44, D1127-D1132.	14.5	71
15	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
16	Anti-CRISPRdb: a comprehensive online resource for anti-CRISPR proteins. <i>Nucleic Acids Research</i> , 2018, 46, D393-D398.	14.5	65
17	Effects on the expression of GABAA receptor subunits by jujuboside A treatment in rat hippocampal neurons. <i>Journal of Ethnopharmacology</i> , 2010, 128, 419-423.	4.1	61
18	Structural Characterization of a Recombinant Fusion Protein by Instrumental Analysis and Molecular Modeling. <i>PLoS ONE</i> , 2013, 8, e57642.	2.5	55

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19	Identify and analysis crotonylation sites in histone by using support vector machines. Artificial Intelligence in Medicine, 2017, 83, 75-81.	6.5	52
20	CEG: a database of essential gene clusters. BMC Genomics, 2013, 14, 769.	2.8	51
21	PSBinder: A Web Service for Predicting Polystyrene Surface-Binding Peptides. BioMed Research International, 2017, 2017, 1-5.	1.9	49
22	Bioinformatics Resources and Tools for Phage Display. Molecules, 2011, 16, 694-709.	3.8	48
23	MimoDB: a New Repository for Mimotope Data Derived from Phage Display Technology. Molecules, 2010, 15, 8279-8288.	3.8	47
24	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. Virologica Sinica, 2016, 31, 350-352.	3.0	47
25	Development and application of therapeutic antibodies against COVID-19. International Journal of Biological Sciences, 2021, 17, 1486-1496.	6.4	47
26	PREDICTING SUBCHLOROPLAST LOCATIONS OF PROTEINS BASED ON THE GENERAL FORM OF CHOU'S PSEUDO AMINO ACID COMPOSITION: APPROACHED FROM OPTIMAL TRIPEPTIDE COMPOSITION. International Journal of Biomathematics, 2013, 06, 1350003.	2.9	46
27	HMMCAS: A Web Tool for the Identification and Domain Annotations of CAS Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1313-1315.	3.0	43
28	LnChrom: a resource of experimentally validated lncRNA-chromatin interactions in human and mouse. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	42
29	Prediction of subcellular location of mycobacterial protein using feature selection techniques. Molecular Diversity, 2010, 14, 667-671.	3.9	41
30	Survey of miRNA-miRNA cooperative regulation principles across cancer types. Briefings in Bioinformatics, 2019, 20, 1621-1638.	6.5	39
31	PhD7FASTER: PREDICTING CLONES PROPAGATING FASTER FROM THE Ph.D.-7 PHAGE DISPLAY PEPTIDE LIBRARY. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450005.	0.8	36
32	SABinder: A Web Service for Predicting Streptavidin-Binding Peptides. BioMed Research International, 2016, 2016, 1-8.	1.9	35
33	NeuroPP: A Tool for the Prediction of Neuropeptide Precursors Based on Optimal Sequence Composition. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 108-114.	3.6	34
34	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. Bioinformatics, 2020, 36, 3327-3335.	4.1	33
35	Prediction of protein structural classes based on feature selection technique. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 235-240.	3.6	32
36	A novel peptide specifically binding to VEGF receptor suppresses angiogenesis in vitro and in vivo. Signal Transduction and Targeted Therapy, 2017, 2, 17010.	17.1	30

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37	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
38	A comprehensive overview of oncogenic pathways in human cancer. <i>Briefings in Bioinformatics</i> , 2020, 21, 957-969.	6.5	29
39	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
40	Distinct Functional Patterns of Gene Promoter Hypomethylation and Hypermethylation in Cancer Genomes. <i>PLoS ONE</i> , 2012, 7, e44822.	2.5	25
41	Biopanning data bank 2018: hugging next generation phage display. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	23
42	Rlscoper: a tool for RNA-RNA interaction extraction from the literature. <i>Bioinformatics</i> , 2019, 35, 3199-3202.	4.1	23
43	HLA class I expression in primary hepatocellular carcinoma. <i>World Journal of Gastroenterology</i> , 2002, 8, 654.	3.3	22
44	Embelin Restores Carbapenem Efficacy against NDM-1-Positive Pathogens. <i>Frontiers in Microbiology</i> , 2018, 9, 71.	3.5	21
45	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
46	Mimotope-Based Prediction of B-Cell Epitopes. <i>Methods in Molecular Biology</i> , 2014, 1184, 237-243.	0.9	19
47	NIEluter: Predicting peptides eluted from HLA class I molecules. <i>Journal of Immunological Methods</i> , 2015, 422, 22-27.	1.4	18
48	A plot of G + C content against sequence length of 640 bacterial chromosomes shows the points are widely scattered in the upper triangular area. <i>Chromosome Research</i> , 2009, 17, 359-364.	2.2	17
49	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
50	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
51	Chromosome translocation and its consequence in the genome of <i>Burkholderia cenocepacia</i> AU-1054. <i>Biochemical and Biophysical Research Communications</i> , 2010, 403, 375-379.	2.1	14
52	Development and Application of Computational Methods in Phage Display Technology. <i>Current Medicinal Chemistry</i> , 2020, 26, 7672-7693.	2.4	13
53	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
54	Molecular Design of Peptide-Fc Fusion Drugs. <i>Current Drug Metabolism</i> , 2019, 20, 203-208.	1.2	12

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55	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
56	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
57	SMAL: A Resource of Spontaneous Mutation Accumulation Lines. <i>Molecular Biology and Evolution</i> , 2014, 31, 1302-1308.	8.9	10
58	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
59	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
60	NEW AMINO ACID INDICES BASED ON RESIDUE NETWORK TOPOLOGY. , 2007, , .		10
61	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
62	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
63	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
64	CASPredict: a web service for identifying Cas proteins. <i>PeerJ</i> , 2021, 9, e11887.	2.0	8
65	BBPpredict: A Web Service for Identifying Blood-Brain Barrier Penetrating Peptides. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	8
66	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
67	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
68	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
69	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
70	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
71	Phage Display Informatics. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-2.	1.3	5
72	PREDICTING B CELL EPITOPE RESIDUES WITH NETWORK TOPOLOGY BASED AMINO ACID INDICES. , 2007, , .		5

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73	AntiDMPpred: a web service for identifying anti-diabetic peptides. PeerJ, 0, 10, e13581.	2.0	5
74	PDL1Binder: Identifying programmed cell death ligand 1 binding peptides by incorporating next-generation phage display data and different peptide descriptors. Frontiers in Microbiology, 0, 13, .	3.5	5
75	AGONOTES: A Robot Annotator for Argonaute Proteins. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 109-116.	3.6	4
76	SSH: A Tool for Predicting Hydrophobic Interaction of Monoclonal Antibodies Using Sequences. BioMed Research International, 2020, 2020, 1-6.	1.9	4
77	Analysis and quality control of carbohydrates in therapeutic proteins with fluorescence HPLC. Biochemical and Biophysical Research Communications, 2016, 478, 864-867.	2.1	3
78	Special issue on Computational Resources and Methods in Biological Sciences. International Journal of Biological Sciences, 2018, 14, 807-810.	6.4	3
79	NeuroCS: A Tool to Predict Cleavage Sites of Neuropeptide Precursors. Protein and Peptide Letters, 2020, 27, 337-345.	0.9	3
80	CasLocusAnno: a web-based server for annotating <i>cas</i> loci and their corresponding (sub)types. FEBS Letters, 2019, 593, 2646-2654.	2.8	2
81	A Mini-review of Computational Approaches to Predict Functions and Findings of Novel Micro Peptides. Current Bioinformatics, 2021, 15, 1027-1035.	1.5	2
82	TUPDB: Target-Unrelated Peptide Data Bank. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 426-432.	3.6	2
83	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. Medicinal Chemistry, 2020, 16, 605-619.	1.5	2
84	Improved Particle Implementation of the Probability Hypothesis Density Filter in Resampling. , 2012, , .		1
85	Prediction of Protein Interaction Sites Using Mimotope Analysis. , 0, , .		1
86	Comprehensive exploration of the enzymes catalysing oxygen-involved reactions and COGs relevant to bacterial oxygen utilization. Environmental Microbiology, 2018, 20, 3836-3850.	3.8	1
87	Ultra Wide Acoustic Bandgap Detection in Novel Octagonal Phononic Crystal of MEMS Materials. , 2020, , .		1
88	CLING: Candidate Cancer-Related lncRNA Prioritization via Integrating Multiple Biological Networks. Frontiers in Bioengineering and Biotechnology, 2020, 8, 138.	4.1	1
89	Guest Editorial for Special Section on the 7th National Conference on Bioinformatics and Systems Biology of China. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1262-1263.	3.0	0
90	Multidimensional Integration Analysis of Autophagy-related Modules in Colorectal Cancer. Letters in Organic Chemistry, 2019, 16, 340-346.	0.5	0

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91	Selection and Validation of Reference Genes for Pan-Cancer in Platelets Based on RNA-Sequence Data. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0