Yongchun Zuo

List of Publications by Citations

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Version: 2024-04-19

85 papers	1,535 citations	23 h-index	36 g-index
101 ext. papers	1,990 ext. citations	5.1 avg, IF	5.3 L-index

#	Paper	IF	Citations
85	iNuc-PhysChem: a sequence-based predictor for identifying nucleosomes via physicochemical properties. *PLoS ONE*, **2012**, 7, e47843	3.7	160
84	Prediction of Gene Expression Patterns With Generalized Linear Regression Model. *Frontiers in Genetics*, **2019**, 10, 120	4.5	95
83	PseKRAAC: a flexible web server for generating pseudo K-tuple reduced amino acids composition. *Bioinformatics*, **2017**, 33, 122-124	7.2	95
82	Predicting peroxidase subcellular location by hybridizing different descriptors of ChouUpseudo amino acid patterns. *Analytical Biochemistry*, **2014**, 458, 14-9	3.1	74
81	Function determinants of TET proteins: the arrangements of sequence motifs with specific codes. *Briefings in Bioinformatics*, **2019**, 20, 1826-1835	13.4	61
80	Integrating transcriptomics and metabolomics to characterise the response of Astragalus membranaceus Bge. var. mongolicus (Bge.) to progressive drought stress. *BMC Genomics*, **2016**, 17, 188	4.5	45
79	Immune cell infiltration-based signature for prognosis and immunogenomic analysis in breast cancer. *Briefings in Bioinformatics*, **2021**, 22, 2020-2031	13.4	41
78	iDPF-PseRAAAC: A Web-Server for Identifying the Defensin Peptide Family and Subfamily Using Pseudo Reduced Amino Acid Alphabet Composition. *PLoS ONE*, **2015**, 10, e0145541	3.7	40
77	Using reduced amino acid composition to predict defensin family and subfamily: Integrating similarity measure and structural alphabet. *Peptides*, **2009**, 30, 1788-93	3.8	37
76	Clinical significance of the immune microenvironment in ovarian cancer patients. *Molecular Omics*, **2018**, 14, 341-351	4.4	36
75	RAACBook: a web server of reduced amino acid alphabet for sequence-dependent inference by using ChouUs five-step rule. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019,	5	35
74	Predicting acidic and alkaline enzymes by incorporating the average chemical shift and gene ontology informations into the general form of ChouUs PseAAC. *Process Biochemistry*, **2013**, 48, 1048-1053	4.8	33
73	Identification of TATA and TATA-less promoters in plant genomes by integrating diversity measure, GC-Skew and DNA geometric flexibility. *Genomics*, **2011**, 97, 112-20	4.3	33
72	PreDNA: accurate prediction of DNA-binding sites in proteins by integrating sequence and geometric structure information. *Bioinformatics*, **2013**, 29, 678-85	7.2	32
71	Using K-minimum increment of diversity to predict secretory proteins of malaria parasite based on groupings of amino acids. *Amino Acids*, **2010**, 38, 859-67	3.5	32
70	Discrimination of membrane transporter protein types using K-nearest neighbor method derived from the similarity distance of total diversity measure. *Molecular BioSystems*, **2015**, 11, 950-7		31
69	Prediction of presynaptic and postsynaptic neurotoxins by combining various ChouUs pseudo components. *Scientific Reports*, **2017**, 7, 5827	4.9	30

68	Transcriptome Comparisons of Multi-Species Identify Differential Genome Activation of Mammals Embryogenesis. *IEEE Access*, **2019**, 7, 7794-7802	3.5	28
67	Predicting the types of J-proteins using clustered amino acids. *BioMed Research International*, **2014**, 2014, 935719	3	26
66	EmExplorer: a database for exploring time activation of gene expression in mammalian embryos. *Open Biology*, **2019**, 9, 190054	7	25
65	Large-scale transcriptome comparison of sunflower genes responsive to Verticillium dahliae. *BMC Genomics*, **2017**, 18, 42	4.5	24
64	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. *Amino Acids*, **2013**, 44, 573-80	3.5	23
63	Identifying FL11 subtype by characterizing tumor immune microenvironment in prostate adenocarcinoma via Chou's 5-steps rule. *Genomics*, **2020**, 112, 1500-1515	4.3	23
62	Clinical significance and immunogenomic landscape analyses of the immune cell signature based prognostic model for patients with breast cancer. *Briefings in Bioinformatics*, **2021**, 22,	13.4	22
61	Analysis and prediction of animal toxins by various Chou's pseudo components and reduced amino acid compositions. *Journal of Theoretical Biology*, **2019**, 462, 221-229	2.3	22
60	Multi-substrate selectivity based on key loops and non-homologous domains: new insight into ALKBH family. *Cellular and Molecular Life Sciences*, **2021**, 78, 129-141	10.3	21
59	Nucleosome Positioning With Fractal Entropy Increment of Diversity in Telemedicine. *IEEE Access*, **2018**, 6, 33451-33459	3.5	20
58	Establishment of bovine trophoblast stem-like cells from in vitro-produced blastocyst-stage embryos using two inhibitors. *Stem Cells and Development*, **2014**, 23, 1501-14	4.4	19
57	Exploring timing activation of functional pathway based on differential co-expression analysis in preimplantation embryogenesis. *Oncotarget*, **2016**, 7, 74120-74131	3.3	19
56	Machine Learning of Single-Cell Transcriptome Highly Identifies mRNA Signature by Comparing F-Score Selection with DGE Analysis. *Molecular Therapy - Nucleic Acids*, **2020**, 20, 155-163	10.7	18
55	Analysis and identification of essential genes in humans using topological properties and biological information. *Gene*, **2014**, 551, 138-51	3.8	18
54	Coexpression analysis identifies nuclear reprogramming barriers of somatic cell nuclear transfer embryos. *Oncotarget*, **2017**, 8, 65847-65859	3.3	18
53	Irregular transcriptome reprogramming probably causes thec developmental failure of embryos produced by interspecies somatic cell nuclear transfer between the Przewalski's gazelle and the bovine. *BMC Genomics*, **2014**, 15, 1113	4.5	17
52	Analysis of the Epigenetic Signature of Cell Reprogramming by Computational DNA Methylation Profiles. *Current Bioinformatics*, **2020**, 15, 589-599	4.7	17
51	RaacLogo: a new sequence logo generator by using reduced amino acid clusters. *Briefings in Bioinformatics*, **2021**, 22,	13.4	16

50	Analysis and identification of toxin targets by topological properties in protein-protein interaction network. *Journal of Theoretical Biology*, **2014**, 349, 82-91	2.3	15
49	The spatial binding model of the pioneer factor Oct4 with its target genes during cell reprogramming. *Computational and Structural Biotechnology Journal*, **2019**, 17, 1226-1233	6.8	14
48	The effect of regions flanking target site on siRNA potency. *Genomics*, **2013**, 102, 215-22	4.3	10
47	Relationship Between DNA Methylation in Key Region and the Differential Expressions of Genes in Human Breast Tumor Tissue. *DNA and Cell Biology*, **2019**, 38, 49-62	3.6	10
46	Generation of Arbas Cashmere Goat Induced Pluripotent Stem Cells Through Fibroblast Reprogramming. *Cellular Reprogramming*, **2015**, 17, 297-305	2.1	9
45	iDEF-PseRAAC: Identifying the Defensin Peptide by Using Reduced Amino Acid Composition Descriptor. *Evolutionary Bioinformatics*, **2019**, 15, 1176934319867088	1.9	9
44	Characterization of essential genes by topological properties in the perturbation sensitivity network. *Biochemical and Biophysical Research Communications*, **2014**, 448, 473-9	3.4	9
43	The hidden physical codes for modulating the prokaryotic transcription initiation. *Physica A: Statistical Mechanics and Its Applications*, **2010**, 389, 4217-4223	3.3	9
42	Comparative genomics and transcriptomics of Chrysolophus provide insights into the evolution of complex plumage coloration. *GigaScience*, **2018**, 7,	7.6	9
41	Characterization of the relationship between FLI1 and immune infiltrate level in tumour immune microenvironment for breast cancer. *Journal of Cellular and Molecular Medicine*, **2020**, 24, 5501-5514	5.6	8
40	Human proteins characterization with subcellular localizations. *Journal of Theoretical Biology*, **2014**, 358, 61-73	2.3	8
39	A Comparative Analysis of Single-Cell Transcriptome Identifies Reprogramming Driver Factors for Efficiency Improvement. *Molecular Therapy - Nucleic Acids*, **2020**, 19, 1053-1064	10.7	8
38	Gene expression classification using epigenetic features and DNA sequence composition in the human embryonic stem cell line H1. *Gene*, **2016**, 592, 227-234	3.8	8
37	Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell. *Gene*, **2016**, 575, 90-100	3.8	7
36	Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. *Scientific Reports*, **2017**, 7, 738	4.9	7
35	Genome-wide analysis of H3K36me3 and its regulations to cancer-related genes expression in human cell lines. *BioSystems*, **2018**, 171, 59-65	1.9	7
34	Modular arrangements of sequence motifs determine the functional diversity of KDM proteins. *Briefings in Bioinformatics*, **2021**, 22,	13.4	7
33	DNA methylation subpatterns at distinct regulatory regions in human early embryos. *Open Biology*, **2018**, 8,	7	7

32	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. *Molecular Genetics and Genomics*, **2016**, 291, 1227-41	3.1	6
31	acACS: improving the prediction accuracy of protein subcellular locations and protein classification by incorporating the average chemical shifts composition. *Scientific World Journal, The*, **2014**, 2014, 864135	2.2	6
30	Effect of the key histone modifications on the expression of genes related to breast cancer. *Genomics*, **2020**, 112, 853-858	4.3	6
29	eHSCPr discriminating the cell identity involved in endothelial to hematopoietic transition. *Bioinformatics*, **2021**,	7.2	6
28	Characterization of TATA-containing genes and TATA-less genes in S. cerevisiae by network topologies and biological properties. *Genomics*, **2014**, 104, 562-71	4.3	5
27	Amino Acid Reduction Can Help to Improve the Identification of Antimicrobial Peptides and Their Functional Activities. *Frontiers in Genetics*, **2021**, 12, 669328	4.5	5
26	Dppa2/4 as a trigger of signaling pathways to promote zygote genome activation by binding to CG-rich region. *Briefings in Bioinformatics*, **2021**, 22,	13.4	4
25	Sequence-specific flexibility organization of splicing flanking sequence and prediction of splice sites in the human genome. *Chromosome Research*, **2014**, 22, 321-34	4.4	4
24	iSP-RAAC: Identify Secretory Proteins of Malaria Parasite Using Reduced Amino Acid Composition. *Combinatorial Chemistry and High Throughput Screening*, **2020**, 23, 536-545	1.3	4
23	ICTC-RAAC: An improved web predictor for identifying the types of ion channel-targeted conotoxins by using reduced amino acid cluster descriptors. *Computational Biology and Chemistry*, **2020**, 89, 107371	3.6	4
22	Characterization of DNA Methylation Patterns and Mining of Epigenetic Markers During Genomic Reprogramming in SCNT Embryos. *Frontiers in Cell and Developmental Biology*, **2020**, 8, 570107	5.7	4
21	Mining Key Regulators of Cell Reprogramming and Prediction Research Based on Deep Learning Neural Networks. *IEEE Access*, **2020**, 8, 23179-23185	3.5	3
20	Topological characteristics of target genes regulated by abiotic-stress-responsible miRNAs in a rice interactome network. *Functional and Integrative Genomics*, **2016**, 16, 243-51	3.8	3
19	Characterization of proteins in different subcellular localizations for Escherichia coli K12. *Genomics*, **2019**, 111, 1134-1141	4.3	3
18	IHEC_RAAC: a online platform for identifying human enzyme classes via reduced amino acid cluster strategy. *Amino Acids*, **2021**, 53, 239-251	3.5	3
17	Characterization of proteins in S. cerevisiae with subcellular localizations. *Molecular BioSystems*, **2015**, 11, 1360-9		2
16	Fatty acid metabolism as an indicator for the maternal-to-zygotic transition in porcine IVF embryos revealed by RNA sequencing. *Theriogenology*, **2020**, 151, 128-136	2.8	2
15	Characterization and Prediction of Presynaptic and Postsynaptic Neurotoxins Based on Reduced Amino Acids and Biological Properties. *Current Bioinformatics*, **2021**, 16, 364-370	4.7	2

14	Predicting Plant Pol-II Promoter Based on Subsequence Increment of Overlap Content Diversity **2009**,		1
13	Prognostic and predictive value of a metabolic risk score model in breast cancer: an immunogenomic landscape analysis. *Briefings in Functional Genomics*, **2021**,	4.9	1
12	ANPrAod: Identify Antioxidant Proteins by Fusing Amino Acid Clustering Strategy and -Peptide Combination. *Computational and Mathematical Methods in Medicine*, **2021**, 2021, 5518209	2.8	1
11	Dynamic and modular gene regulatory networks drive the development of gametogenesis. *Briefings in Bioinformatics*, **2017**, 18, 712-721	13.4	1
10	Characterize the relationship between essential and TATA-containing genes for S. cerevisiae by network topologies in the perturbation sensitivity network. *Genomics*, **2016**, 108, 177-183	4.3	1
9	Characterization of human proteins with different subcellular localizations by topological and biological properties. *Genomics*, **2019**, 111, 1831-1838	4.3	1
8	Characterize the difference between TMPRSS2-ERG and non-TMPRSS2-ERG fusion patients by clinical and biological characteristics in prostate cancer. *Gene*, **2018**, 679, 186-194	3.8	1
7	Nuclear Transfer Arrest Embryos Show Massive Dysregulation of Genes Involved in Transcription Pathways. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	1
6	WGBS combined with RNA-seq analysis revealed that Dnmt1 affects the methylation modification and gene expression changes during mouse oocyte vitrification. *Theriogenology*, **2022**, 177, 11-21	2.8	1
5	Identification of Disease-Related 2-Oxoglutarate/Fe (II)-Dependent Oxygenase Based on Reduced Amino Acid Cluster Strategy. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 707938	5.7	0
4	Generation of Sheep Induced Pluripotent Stem Cells With Defined DOX-Inducible Transcription Factors Transposition.. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 785055	5.7	0
3	Characterization of BioPlex network by topological properties. *Journal of Theoretical Biology*, **2016**, 409, 148-154	2.3	
2	Genome-wide characterization of essential, toxicity-modulating and no-phenotype genes in S. cerevisiae. *Gene*, **2015**, 559, 1-8	3.8	
1	Using Reduced Amino Acid Alphabet and Biological Properties to Analyze and Predict Animal Neurotoxin Protein. *Current Drug Metabolism*, **2020**, 21, 810-817	3.5	