Yongchun Zuo

List of Publications by Year
in descending order

99 papers	2,287 citations	186265 28 h-index	254184 43 g-index
102 all docs	102 docs citations	102 times ranked	1711 citing authors

#	Article	IF	Citations
1	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	2.5	181
2	Prediction of Gene Expression Patterns With Generalized Linear Regression Model. Frontiers in Genetics, 2019, 10, 120.	2.3	148
3	PseKRAAC: a flexible web server for generating pseudo K-tuple reduced amino acids composition. Bioinformatics, 2017, 33, 122-124.	4.1	124
4	Immune cell infiltration-based signature for prognosis and immunogenomic analysis in breast cancer. Briefings in Bioinformatics, 2021, 22, 2020-2031.	6.5	99
5	Predicting peroxidase subcellular location by hybridizing different descriptors of Chou' pseudo amino acid patterns. Analytical Biochemistry, 2014, 458, 14-19.	2.4	83
6	Function determinants of TET proteins: the arrangements of sequence motifs with specific codes. Briefings in Bioinformatics, 2019, 20, 1826-1835.	6.5	83
7	Clinical significance and immunogenomic landscape analyses of the immune cell signature based prognostic model for patients with breast cancer. Briefings in Bioinformatics, 2021, 22, .	6.5	71
8	Clinical significance of the immune microenvironment in ovarian cancer patients. Molecular Omics, 2018, 14, 341-351.	2.8	65
9	Integrating transcriptomics and metabolomics to characterise the response of Astragalus membranaceus Bge. var. mongolicus (Bge.) to progressive drought stress. BMC Genomics, 2016, 17, 188.	2.8	64
10	RAACBook: a web server of reduced amino acid alphabet for sequence-dependent inference by using Chou's five-step rule. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	51
11	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.	5.4	49
12	Using reduced amino acid composition to predict defensin family and subfamily: Integrating similarity measure and structural alphabet. Peptides, 2009, 30, 1788-1793.	2.4	45
13	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.	2.5	44
14	Identification of TATA and TATA-less promoters in plant genomes by integrating diversity measure, GC-Skew and DNA geometric flexibility. Genomics, 2011, 97, 112-120.	2.9	43
15	PreDNA: accurate prediction of DNA-binding sites in proteins by integrating sequence and geometric structure information. Bioinformatics, 2013, 29, 678-685.	4.1	41
16	Large-scale transcriptome comparison of sunflower genes responsive to Verticillium dahliae. BMC Genomics, 2017, 18, 42.	2.8	39
17	Using K-minimum increment of diversity to predict secretory proteins of malaria parasite based on groupings of amino acids. Amino Acids, 2010, 38, 859-867.	2.7	38
18	Predicting acidic and alkaline enzymes by incorporating the average chemical shift and gene ontology informations into the general form of Chou's PseAAC. Process Biochemistry, 2013, 48, 1048-1053.	3.7	38

#	Article	IF	Citations
19	Discrimination of membrane transporter protein types using K-nearest neighbor method derived from the similarity distance of total diversity measure. Molecular BioSystems, 2015, 11, 950-957.	2.9	36
20	Prediction of presynaptic and postsynaptic neurotoxins by combining various Chou's pseudo components. Scientific Reports, 2017, 7, 5827.	3.3	35
21	EmExplorer: a database for exploring time activation of gene expression in mammalian embryos. Open Biology, 2019, 9, 190054.	3.6	35
22	RaacLogo: a new sequence logo generator by using reduced amino acid clusters. Briefings in Bioinformatics, 2021, 22, .	6.5	33
23	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. Amino Acids, 2013, 44, 573-580.	2.7	31
24	Transcriptome Comparisons of Multi-Species Identify Differential Genome Activation of Mammals Embryogenesis. IEEE Access, 2019, 7, 7794-7802.	4.2	31
25	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.	5.1	31
26	Predicting the Types of J-Proteins Using Clustered Amino Acids. BioMed Research International, 2014, 2014, 1-8.	1.9	30
27	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.	1.7	30
28	Identifying FL11 subtype by characterizing tumor immune microenvironment in prostate adenocarcinoma via Chou's 5-steps rule. Genomics, 2020, 112, 1500-1515.	2.9	29
29	Establishment of Bovine Trophoblast Stem-Like Cells from In Vitro-Produced Blastocyst-Stage Embryos Using Two Inhibitors. Stem Cells and Development, 2014, 23, 1501-1514.	2.1	26
30	Analysis of the Epigenetic Signature of Cell Reprogramming by Computational DNA Methylation Profiles. Current Bioinformatics, 2020, 15, 589-599.	1.5	24
31	Nucleosome Positioning With Fractal Entropy Increment of Diversity in Telemedicine. IEEE Access, 2018, 6, 33451-33459.	4.2	23
32	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.	4.1	23
33	iProbiotics: a machine learning platform for rapid identification of probiotic properties from whole-genome primary sequences. Briefings in Bioinformatics, 2022, 23, .	6.5	23
34	Analysis and identification of essential genes in humans using topological properties and biological information. Gene, 2014, 551, 138-151.	2.2	22
35	Exploring timing activation of functional pathway based on differential co-expression analysis in preimplantation embryogenesis. Oncotarget, 2016, 7, 74120-74131.	1.8	22
36	Coexpression analysis identifies nuclear reprogramming barriers of somatic cell nuclear transfer embryos. Oncotarget, 2017, 8, 65847-65859.	1.8	22

#	Article	IF	Citations
37	Irregular transcriptome reprogramming probably causes thec developmental failure of embryos produced by interspecies somatic cell nuclear transfer between the Przewalskiâ€™s gazelle and the bovine. BMC Genomics, 2014, 15, 1113.	2.8	21
38	DNA methylation subpatterns at distinct regulatory regions in human early embryos. Open Biology, 2018, 8, .	3.6	20
39	eHSCPr discriminating the cell identity involved in endothelial to hematopoietic transition. Bioinformatics, 2021, 37, 2157-2164.	4.1	19
40	The effect of regions flanking target site on siRNA potency. Genomics, 2013, 102, 215-222.	2.9	18
41	A Comparative Analysis of Single-Cell Transcriptome Identifies Reprogramming Driver Factors for Efficiency Improvement. Molecular Therapy - Nucleic Acids, 2020, 19, 1053-1064.	5.1	18
42	Analysis and identification of toxin targets by topological properties in proteinâ€"protein interaction network. Journal of Theoretical Biology, 2014, 349, 82-91.	1.7	16
43	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.	3.6	16
44	Generation of Arbas Cashmere Goat Induced Pluripotent Stem Cells Through Fibroblast Reprogramming. Cellular Reprogramming, 2015, 17, 297-305.	0.9	14
45	Comparative genomics and transcriptomics of Chrysolophus provide insights into the evolution of complex plumage colouration. GigaScience, 2018, 7, .	6.4	14
46	Effect of the key histone modifications on the expression of genes related to breast cancer. Genomics, 2020, 112, 853-858.	2.9	14
47	Modular arrangements of sequence motifs determine the functional diversity of KDM proteins. Briefings in Bioinformatics, 2021, 22, .	6.5	14
48	The hidden physical codes for modulating the prokaryotic transcription initiation. Physica A: Statistical Mechanics and Its Applications, 2010, 389, 4217-4223.	2.6	13
49	Genome-wide analysis of H3K36me3 and its regulations to cancer-related genes expression in human cell lines. BioSystems, 2018, 171, 59-65.	2.0	13
50	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.	1.9	13
51	Amino Acid Reduction Can Help to Improve the Identification of Antimicrobial Peptides and Their Functional Activities. Frontiers in Genetics, 2021, 12, 669328.	2.3	13
52	Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. Scientific Reports, 2017, 7, 738.	3.3	12
53	iDEF-PseRAAC: Identifying the Defensin Peptide by Using Reduced Amino Acid Composition Descriptor. Evolutionary Bioinformatics, 2019, 15, 117693431986708.	1.2	12
54	Dppa2/4 as a trigger of signaling pathways to promote zygote genome activation by binding to CG-rich region. Briefings in Bioinformatics, 2021, 22, .	6.5	12

#	Article	IF	Citations
55	Human proteins characterization with subcellular localizations. Journal of Theoretical Biology, 2014, 358, 61-73.	1.7	11
56	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.	2.1	11
57	Characterization of essential genes by topological properties in the perturbation sensitivity network. Biochemical and Biophysical Research Communications, 2014, 448, 473-479.	2.1	10
58	Gene expression classification using epigenetic features and DNA sequence composition in the human embryonic stem cell line H1. Gene, 2016, 592, 227-234.	2.2	10
59	Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell. Gene, 2016, 575, 90-100.	2.2	10
60	RaacFold: a webserver for 3D visualization and analysis of protein structure by using reduced amino acid alphabets. Nucleic Acids Research, 2022, 50, W633-W638.	14.5	10
61	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.	3.7	9
62	IHEC_RAAC: a online platform for identifying human enzyme classes via reduced amino acid cluster strategy. Amino Acids, 2021, 53, 239-251.	2.7	9
63	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. Molecular Genetics and Genomics, 2016, 291, 1227-1241.	2.1	8
64	iSP-RAAC: Identify Secretory Proteins of Malaria Parasite Using Reduced Amino Acid Composition. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 536-545.	1.1	8
65	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, 1-9.	2.1	7
66	Characterization of TATA-containing genes and TATA-less genes in S. cerevisiae by network topologies and biological properties. Genomics, 2014, 104, 562-571.	2.9	7
67	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.	2.1	7
68	Research progress of reduced amino acid alphabets in protein analysis and prediction. Computational and Structural Biotechnology Journal, 2022, 20, 3503-3510.	4.1	7
69	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.	2.3	6
70	HelPredictor models single-cell transcriptome to predict human embryo lineage allocation. Briefings in Bioinformatics, 2021, 22, .	6.5	6
71	Mining Key Regulators of Cell Reprogramming and Prediction Research Based on Deep Learning Neural Networks. IEEE Access, 2020, 8, 23179-23185.	4.2	5
72	Feature-scML: An Open-source Python Package for the Feature Importance Visualization of Single-Cell Omics with Machine Learning. Current Bioinformatics, 2022, 17, 578-585.	1.5	5

#	Article	IF	Citations
73	Sequence-specific flexibility organization of splicing flanking sequence and prediction of splice sites in the human genome. Chromosome Research, 2014, 22, 321-334.	2.2	4
74	Dynamic and modular gene regulatory networks drive the development of gametogenesis. Briefings in Bioinformatics, 2017, 18, bbw056.	6.5	4
75	Characterization of proteins in different subcellular localizations for Escherichia coli K12. Genomics, 2019, 111, 1134-1141.	2.9	4
76	Characterization and Prediction of Presynaptic and Postsynaptic Neurotoxins Based on Reduced Amino Acids and Biological Properties. Current Bioinformatics, 2021, 16, 364-370.	1.5	4
77	OUP accepted manuscript. Briefings in Functional Genomics, 2021, , .	2.7	4
78	Immune-related Gene-based Prognostic Signature for the Risk Stratification Analysis of Breast Cancer. Current Bioinformatics, 2022, 17, 196-205.	1.5	4
79	Generation of Sheep Induced Pluripotent Stem Cells With Defined DOX-Inducible Transcription Factors via piggyBac Transposition. Frontiers in Cell and Developmental Biology, 2021, 9, 785055.	3.7	4
80	Topological characteristics of target genes regulated by abiotic-stress-responsible miRNAs in a rice interactome network. Functional and Integrative Genomics, 2016, 16, 243-251.	3.5	3
81	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.	2.2	3
82	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.	3.7	3
83	Nuclear Transfer Arrest Embryos Show Massive Dysregulation of Genes Involved in Transcription Pathways. International Journal of Molecular Sciences, 2021, 22, 8187.	4.1	3
84	The Cumulative Formation of R-loop Interacts with Histone Modifications to Shape Cell Reprogramming. International Journal of Molecular Sciences, 2022, 23, 1567.	4.1	3
85	Predicting Plant Pol-II Promoter Based on Subsequence Increment of Overlap Content Diversity. , 2009, , .		2
86	Characterization of proteins in S. cerevisiae with subcellular localizations. Molecular BioSystems, 2015, 11, 1360-1369.	2.9	2
87	ANPrAod: Identify Antioxidant Proteins by Fusing Amino Acid Clustering Strategy and N-Peptide Combination. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-10.	1.3	2
88	Characterized the diversity of ABCB1 subtypes in immunogenomic landscape for predicting the drug response in breast cancer. Methods, 2022, , .	3.8	2
89	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.	2.9	1
90	Characterization of human proteins with different subcellular localizations by topological and biological properties. Genomics, 2019, 111, 1831-1838.	2.9	1

#	Article	IF	Citations
91	EPI-Mind: Identifying Enhancerâ€"Promoter Interactions Based on Transformer Mechanism. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 786-794.	3.6	1
92	Deep learning-based transcription factor activity for stratification of breast cancer patients. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194838.	1.9	1
93	Prediction of Presynaptic and Postsynaptic Neurotoxins Using Hybrid Approach and Pseudo Amino Acid Composition. , 2009, , .		0
94	Genome-wide characterization of essential, toxicity-modulating and no-phenotype genes in S. cerevisiae. Gene, 2015, 559, 1-8.	2.2	0
95	Characterization of BioPlex network by topological properties. Journal of Theoretical Biology, 2016, 409, 148-154.	1.7	0
96	Using Reduced Amino Acid Alphabet and Biological Properties to Analyze and Predict Animal Neurotoxin Protein. Current Drug Metabolism, 2020, 21, 810-817.	1.2	0
97	Integrated multi-cohorts for characterizing the immunogenomic landscape and predicting drug response in triple-negative breast cancer. Briefings in Functional Genomics, 2022, , .	2.7	0
98	The immune-based prognostic score for the immunogenomic landscape analysis and application of chemotherapy in breast cancer. Current Bioinformatics, 2022, 17, .	1.5	0
99	The DNA geometric flexibility of promoter in model organism genomes. Energy Procedia, 2011, 11, 2732-2737.	1.8	0