

# Yongchun Zuo

## List of Publications by Year in descending order

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Version: 2024-02-01

98  
papers

2,287  
citations

185998

28  
h-index

253896

43  
g-index

102  
all docs

102  
docs citations

102  
times ranked

1711  
citing authors

#	ARTICLE	IF	CITATIONS
1	WGBS combined with RNA-seq analysis revealed that Dnmt1 affects the methylation modification and gene expression changes during mouse oocyte vitrification. <i>Theriogenology</i> , 2022, 177, 11-21.	0.9	11
2	iProbiotics: a machine learning platform for rapid identification of probiotic properties from whole-genome primary sequences. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	23
3	Immune-related Gene-based Prognostic Signature for the Risk Stratification Analysis of Breast Cancer. <i>Current Bioinformatics</i> , 2022, 17, 196-205.	0.7	4
4	The Cumulative Formation of R-loop Interacts with Histone Modifications to Shape Cell Reprogramming. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1567.	1.8	3
5	Characterized the diversity of ABCB1 subtypes in immunogenomic landscape for predicting the drug response in breast cancer. <i>Methods</i> , 2022, , .	1.9	2
6	Integrated multi-cohorts for characterizing the immunogenomic landscape and predicting drug response in triple-negative breast cancer. <i>Briefings in Functional Genomics</i> , 2022, , .	1.3	0
7	RaacFold: a webserver for 3D visualization and analysis of protein structure by using reduced amino acid alphabets. <i>Nucleic Acids Research</i> , 2022, 50, W633-W638.	6.5	10
8	EPI-Mind: Identifying Enhancerâ€“Promoter Interactions Based on Transformer Mechanism. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 786-794.	2.2	1
9	The immune-based prognostic score for the immunogenomic landscape analysis and application of chemotherapy in breast cancer. <i>Current Bioinformatics</i> , 2022, 17, .	0.7	0
10	Feature-scML: An Open-source Python Package for the Feature Importance Visualization of Single-Cell Omics with Machine Learning. <i>Current Bioinformatics</i> , 2022, 17, 578-585.	0.7	5
11	Deep learning-based transcription factor activity for stratification of breast cancer patients. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194838.	0.9	1
12	Research progress of reduced amino acid alphabets in protein analysis and prediction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3503-3510.	1.9	7
13	Dppa2/4 as a trigger of signaling pathways to promote zygote genome activation by binding to CG-rich region. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
14	Clinical significance and immunogenomic landscape analyses of the immune cell signature based prognostic model for patients with breast cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	71
15	Immune cell infiltration-based signature for prognosis and immunogenomic analysis in breast cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, 2020-2031.	3.2	99
16	RaacLogo: a new sequence logo generator by using reduced amino acid clusters. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	33
17	Multi-substrate selectivity based on key loops and non-homologous domains: new insight into ALKBH family. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 129-141.	2.4	49
18	Modular arrangements of sequence motifs determine the functional diversity of KDM proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	14

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19	IHEC_RAAC: a online platform for identifying human enzyme classes via reduced amino acid cluster strategy. <i>Amino Acids</i> , 2021, 53, 239-251.	1.2	9
20	eHSCPr discriminating the cell identity involved in endothelial to hematopoietic transition. <i>Bioinformatics</i> , 2021, 37, 2157-2164.	1.8	19
21	Amino Acid Reduction Can Help to Improve the Identification of Antimicrobial Peptides and Their Functional Activities. <i>Frontiers in Genetics</i> , 2021, 12, 669328.	1.1	13
22	ANPrAod: Identify Antioxidant Proteins by Fusing Amino Acid Clustering Strategy and $\langle \text{math} \text{xmlns}=\text{"http://www.w3.org/1998/Math/MathML"} \text{id}=\text{"M1"} \rangle \langle \text{mi} \rangle \text{N} \langle \text{mi} \rangle \langle \text{math} \rangle$ -Peptide Combination. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-10.	0.7	2
23	HelPredictor models single-cell transcriptome to predict human embryo lineage allocation. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
24	Characterization and Prediction of Presynaptic and Postsynaptic Neurotoxins Based on Reduced Amino Acids and Biological Properties. <i>Current Bioinformatics</i> , 2021, 16, 364-370.	0.7	4
25	Identification of Disease-Related 2-Oxoglutarate/Fe (II)-Dependent Oxygenase Based on Reduced Amino Acid Cluster Strategy. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 707938.	1.8	3
26	Nuclear Transfer Arrest Embryos Show Massive Dysregulation of Genes Involved in Transcription Pathways. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8187.	1.8	3
27	OUP accepted manuscript. <i>Briefings in Functional Genomics</i> , 2021, , .	1.3	4
28	Generation of Sheep Induced Pluripotent Stem Cells With Defined DOX-Inducible Transcription Factors via piggyBac Transposition. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 785055.	1.8	4
29	Effect of the key histone modifications on the expression of genes related to breast cancer. <i>Genomics</i> , 2020, 112, 853-858.	1.3	14
30	Identifying FL11 subtype by characterizing tumor immune microenvironment in prostate adenocarcinoma via Chou's 5-steps rule. <i>Genomics</i> , 2020, 112, 1500-1515.	1.3	29
31	ICTC-RAAC: An improved web predictor for identifying the types of ion channel-targeted conotoxins by using reduced amino acid cluster descriptors. <i>Computational Biology and Chemistry</i> , 2020, 89, 107371.	1.1	6
32	Characterization of DNA Methylation Patterns and Mining of Epigenetic Markers During Genomic Reprogramming in SCNT Embryos. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 570107.	1.8	9
33	Mining Key Regulators of Cell Reprogramming and Prediction Research Based on Deep Learning Neural Networks. <i>IEEE Access</i> , 2020, 8, 23179-23185.	2.6	5
34	Machine Learning of Single-Cell Transcriptome Highly Identifies mRNA Signature by Comparing F-Score Selection with DGE Analysis. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 20, 155-163.	2.3	31
35	Characterization of the relationship between FLI1 and immune infiltrate level in tumour immune microenvironment for breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 5501-5514.	1.6	16
36	Fatty acid metabolism as an indicator for the maternal-to-zygotic transition in porcine IVF embryos revealed by RNA sequencing. <i>Theriogenology</i> , 2020, 151, 128-136.	0.9	7

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37	A Comparative Analysis of Single-Cell Transcriptome Identifies Reprogramming Driver Factors for Efficiency Improvement. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 1053-1064.	2.3	18
38	iSP-RAAC: Identify Secretory Proteins of Malaria Parasite Using Reduced Amino Acid Composition. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 536-545.	0.6	8
39	Analysis of the Epigenetic Signature of Cell Reprogramming by Computational DNA Methylation Profiles. <i>Current Bioinformatics</i> , 2020, 15, 589-599.	0.7	24
40	Using Reduced Amino Acid Alphabet and Biological Properties to Analyze and Predict Animal Neurotoxin Protein. <i>Current Drug Metabolism</i> , 2020, 21, 810-817.	0.7	0
41	Function determinants of TET proteins: the arrangements of sequence motifs with specific codes. <i>Briefings in Bioinformatics</i> , 2019, 20, 1826-1835.	3.2	83
42	Characterization of proteins in different subcellular localizations for Escherichia coli K12. <i>Genomics</i> , 2019, 111, 1134-1141.	1.3	4
43	iDEF-PseRAAC: Identifying the Defensin Peptide by Using Reduced Amino Acid Composition Descriptor. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431986708.	0.6	12
44	The spatial binding model of the pioneer factor Oct4 with its target genes during cell reprogramming. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1226-1233.	1.9	23
45	EmExplorer: a database for exploring time activation of gene expression in mammalian embryos. <i>Open Biology</i> , 2019, 9, 190054.	1.5	35
46	Transcriptome Comparisons of Multi-Species Identify Differential Genome Activation of Mammals Embryogenesis. <i>IEEE Access</i> , 2019, 7, 7794-7802.	2.6	31
47	Prediction of Gene Expression Patterns With Generalized Linear Regression Model. <i>Frontiers in Genetics</i> , 2019, 10, 120.	1.1	148
48	RAACBook: a web server of reduced amino acid alphabet for sequence-dependent inference by using Chou's five-step rule. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	51
49	Characterization of human proteins with different subcellular localizations by topological and biological properties. <i>Genomics</i> , 2019, 111, 1831-1838.	1.3	1
50	Analysis and prediction of animal toxins by various Chou's pseudo components and reduced amino acid compositions. <i>Journal of Theoretical Biology</i> , 2019, 462, 221-229.	0.8	30
51	Relationship Between DNA Methylation in Key Region and the Differential Expressions of Genes in Human Breast Tumor Tissue. <i>DNA and Cell Biology</i> , 2019, 38, 49-62.	0.9	13
52	Nucleosome Positioning With Fractal Entropy Increment of Diversity in Telemedicine. <i>IEEE Access</i> , 2018, 6, 33451-33459.	2.6	23
53	DNA methylation subpatterns at distinct regulatory regions in human early embryos. <i>Open Biology</i> , 2018, 8, .	1.5	20
54	Characterize the difference between TMPRSS2-ERG and non-TMPRSS2-ERG fusion patients by clinical and biological characteristics in prostate cancer. <i>Gene</i> , 2018, 679, 186-194.	1.0	3

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55	Comparative genomics and transcriptomics of <i>Chrysolophus</i> provide insights into the evolution of complex plumage colouration. <i>GigaScience</i> , 2018, 7, .	3.3	14
56	Genome-wide analysis of H3K36me3 and its regulations to cancer-related genes expression in human cell lines. <i>BioSystems</i> , 2018, 171, 59-65.	0.9	13
57	Clinical significance of the immune microenvironment in ovarian cancer patients. <i>Molecular Omics</i> , 2018, 14, 341-351.	1.4	65
58	Dynamic and modular gene regulatory networks drive the development of gametogenesis. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw056.	3.2	4
59	Large-scale transcriptome comparison of sunflower genes responsive to <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2017, 18, 42.	1.2	39
60	Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. <i>Scientific Reports</i> , 2017, 7, 738.	1.6	12
61	Prediction of presynaptic and postsynaptic neurotoxins by combining various Chou's pseudo components. <i>Scientific Reports</i> , 2017, 7, 5827.	1.6	35
62	PseKRAAC: a flexible web server for generating pseudo K-tuple reduced amino acids composition. <i>Bioinformatics</i> , 2017, 33, 122-124.	1.8	124
63	Coexpression analysis identifies nuclear reprogramming barriers of somatic cell nuclear transfer embryos. <i>Oncotarget</i> , 2017, 8, 65847-65859.	0.8	22
64	Exploring timing activation of functional pathway based on differential co-expression analysis in preimplantation embryogenesis. <i>Oncotarget</i> , 2016, 7, 74120-74131.	0.8	22
65	Integrating transcriptomics and metabolomics to characterise the response of <i>Astragalus membranaceus</i> Bge. var. <i>mongolicus</i> (Bge.) to progressive drought stress. <i>BMC Genomics</i> , 2016, 17, 188.	1.2	64
66	Characterize the relationship between essential and TATA-containing genes for <i>S. cerevisiae</i> by network topologies in the perturbation sensitivity network. <i>Genomics</i> , 2016, 108, 177-183.	1.3	1
67	Gene expression classification using epigenetic features and DNA sequence composition in the human embryonic stem cell line H1. <i>Gene</i> , 2016, 592, 227-234.	1.0	10
68	Characterization of BioPlex network by topological properties. <i>Journal of Theoretical Biology</i> , 2016, 409, 148-154.	0.8	0
69	Topological characteristics of target genes regulated by abiotic-stress-responsible miRNAs in a rice interactome network. <i>Functional and Integrative Genomics</i> , 2016, 16, 243-251.	1.4	3
70	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1227-1241.	1.0	8
71	Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell. <i>Gene</i> , 2016, 575, 90-100.	1.0	10
72	iDPF-PseRAAAC: A Web-Server for Identifying the Defensin Peptide Family and Subfamily Using Pseudo Reduced Amino Acid Alphabet Composition. <i>PLoS ONE</i> , 2015, 10, e0145541.	1.1	44

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73	Genome-wide characterization of essential, toxicity-modulating and no-phenotype genes in <i>S. cerevisiae</i> . <i>Gene</i> , 2015, 559, 1-8.	1.0	0
74	Discrimination of membrane transporter protein types using K-nearest neighbor method derived from the similarity distance of total diversity measure. <i>Molecular BioSystems</i> , 2015, 11, 950-957.	2.9	36
75	Characterization of proteins in <i>S. cerevisiae</i> with subcellular localizations. <i>Molecular BioSystems</i> , 2015, 11, 1360-1369.	2.9	2
76	Generation of Arbas Cashmere Goat Induced Pluripotent Stem Cells Through Fibroblast Reprogramming. <i>Cellular Reprogramming</i> , 2015, 17, 297-305.	0.5	14
77	acACS: Improving the Prediction Accuracy of Protein Subcellular Locations and Protein Classification by Incorporating the Average Chemical Shifts Composition. <i>Scientific World Journal</i> , The, 2014, 2014, 1-9.	0.8	7
78	Predicting the Types of J-Proteins Using Clustered Amino Acids. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	30
79	Characterization of TATA-containing genes and TATA-less genes in <i>S. cerevisiae</i> by network topologies and biological properties. <i>Genomics</i> , 2014, 104, 562-571.	1.3	7
80	Irregular transcriptome reprogramming probably causes the developmental failure of embryos produced by interspecies somatic cell nuclear transfer between the Przewalski's gazelle and the bovine. <i>BMC Genomics</i> , 2014, 15, 1113.	1.2	21
81	Predicting peroxidase subcellular location by hybridizing different descriptors of Chou's pseudo amino acid patterns. <i>Analytical Biochemistry</i> , 2014, 458, 14-19.	1.1	83
82	Sequence-specific flexibility organization of splicing flanking sequence and prediction of splice sites in the human genome. <i>Chromosome Research</i> , 2014, 22, 321-334.	1.0	4
83	Establishment of Bovine Trophoblast Stem-Like Cells from In Vitro Produced Blastocyst-Stage Embryos Using Two Inhibitors. <i>Stem Cells and Development</i> , 2014, 23, 1501-1514.	1.1	26
84	Analysis and identification of essential genes in humans using topological properties and biological information. <i>Gene</i> , 2014, 551, 138-151.	1.0	22
85	Characterization of essential genes by topological properties in the perturbation sensitivity network. <i>Biochemical and Biophysical Research Communications</i> , 2014, 448, 473-479.	1.0	10
86	Analysis and identification of toxin targets by topological properties in protein-protein interaction network. <i>Journal of Theoretical Biology</i> , 2014, 349, 82-91.	0.8	16
87	Human proteins characterization with subcellular localizations. <i>Journal of Theoretical Biology</i> , 2014, 358, 61-73.	0.8	11
88	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. <i>Amino Acids</i> , 2013, 44, 573-580.	1.2	31
89	The effect of regions flanking target site on siRNA potency. <i>Genomics</i> , 2013, 102, 215-222.	1.3	18
90	Predicting acidic and alkaline enzymes by incorporating the average chemical shift and gene ontology informations into the general form of Chou's PseAAC. <i>Process Biochemistry</i> , 2013, 48, 1048-1053.	1.8	38

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91	PreDNA: accurate prediction of DNA-binding sites in proteins by integrating sequence and geometric structure information. <i>Bioinformatics</i> , 2013, 29, 678-685.	1.8	41
92	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. <i>PLoS ONE</i> , 2012, 7, e47843.	1.1	181
93	Identification of TATA and TATA-less promoters in plant genomes by integrating diversity measure, GC-Skew and DNA geometric flexibility. <i>Genomics</i> , 2011, 97, 112-120.	1.3	43
94	The hidden physical codes for modulating the prokaryotic transcription initiation. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 4217-4223.	1.2	13
95	Using K-minimum increment of diversity to predict secretory proteins of malaria parasite based on groupings of amino acids. <i>Amino Acids</i> , 2010, 38, 859-867.	1.2	38
96	Prediction of Presynaptic and Postsynaptic Neurotoxins Using Hybrid Approach and Pseudo Amino Acid Composition. , 2009, , .		0
97	Predicting Plant Pol-II Promoter Based on Subsequence Increment of Overlap Content Diversity. , 2009, , .		2
98	Using reduced amino acid composition to predict defensin family and subfamily: Integrating similarity measure and structural alphabet. <i>Peptides</i> , 2009, 30, 1788-1793.	1.2	45