Xiao Sun

List of Publications by Year
in descending order

		471371	360920
68 papers	**1,433** citations	**17** h-index	**35** g-index
71 all docs	**71** docs citations	**71** times ranked	**2182** citing authors

#	Article	IF	Citations
1	Relating Translation Efficiency to Protein Networks Provides Evolutionary Insights in *Shewanella* and Its Implications for Extracellular Electron Transfer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 605-613.	1.9	1
2	G-Quadruplex-Binding Proteins: Promising Targets for Drug Design. Biomolecules, 2022, 12, 648.	1.8	31
3	Sample-specific perturbation of gene interactions identifies breast cancer subtypes. Briefings in Bioinformatics, 2021, 22, .	3.2	20
4	Predicting Conversion from MCI to AD Combining Multi-Modality Data and Based on Molecular Subtype. Brain Sciences, 2021, 11, 674.	1.1	8
5	Brain-Specific Gene Expression and Quantitative Traits Association Analysis for Mild Cognitive Impairment. Biomedicines, 2021, 9, 658.	1.4	3
6	Detecting and Profiling Endogenous RNA G-Quadruplexes in the Human Transcriptome. International Journal of Molecular Sciences, 2021, 22, 8012.	1.8	3
7	Inferring single cell expression profiles from overlapped pooling sequencing data with compressed sensing strategy. Nucleic Acids Research, 2021, 49, 7995-8006.	6.5	1
8	Classification of Mild Cognitive Impairment With Multimodal Data Using Both Labeled and Unlabeled Samples. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2281-2290.	1.9	7
9	Molecular Subtyping of Mild Cognitive Impairment Based on Genetic Polymorphism and Gene Expression. journal of prevention of Alzheimer's disease, The, 2021, 8, 1-10.	1.5	1
10	Direct genome-wide identification of G-quadruplex structures by whole-genome resequencing. Nature Communications, 2021, 12, 6014.	5.8	24
11	From Cellular Infiltration Assessment to a Functional Gene Set-Based Prognostic Model for Breast Cancer. Frontiers in Immunology, 2021, 12, 751530.	2.2	4
12	Transcriptional regulatory module analysis reveals that bridge proteins reconcile multiple signals in extracellular electron transfer pathways. Proteins: Structure, Function and Bioinformatics, 2020, 88, 196-205.	1.5	3
13	Evaluation of single-cell classifiers for single-cell RNA sequencing data sets. Briefings in Bioinformatics, 2020, 21, 1581-1595.	3.2	63
14	A deconvolution method and its application in analyzing the cellular fractions in acute myeloid leukemia samples. BMC Genomics, 2020, 21, 652.	1.2	8
15	Whole Genome Identification of Potential G-Quadruplexes and Analysis of the G-Quadruplex Binding Domain for SARS-CoV-2. Frontiers in Genetics, 2020, 11, 587829.	1.1	35
16	DeconPeaker, a Deconvolution Model to Identify Cell Types Based on Chromatin Accessibility in ATAC-Seq Data of Mixture Samples. Frontiers in Genetics, 2020, 11, 392.	1.1	24
17	Cooperative binding of transcription factors in the human genome. Genomics, 2020, 112, 3427-3434.	1.3	17
18	Effect for Human Genomic Variation During the BMP4-Induced Conversion From Pluripotent Stem Cells to Trophoblast. Frontiers in Genetics, 2020, 11, 230.	1.1	5

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19	Prognostic gene expression signature revealed the involvement of mutational pathways in cancer genome. Journal of Cancer, 2020, 11, 4510-4520.	1.2	17
20	Structural Basis for the High Conductivity of Microbial Pili as Potential Nanowires. Journal of Nanoscience and Nanotechnology, 2020, 20, 64-80.	0.9	5
21	DNMHMM: An approach to identify the differential nucleosome regions in multiple cell types based on a Hidden Markov Model. BioSystems, 2019, 185, 104033.	0.9	3
22	Enhancer LncRNAs Influence Chromatin Interactions in Different Ways. Frontiers in Genetics, 2019, 10, 936.	1.1	34
23	Two Distinct Subtypes Revealed in Blood Transcriptome of Breast Cancer Patients With an Unsupervised Analysis. Frontiers in Oncology, 2019, 9, 985.	1.3	16
24	Integrative characterization of G-Quadruplexes in the three-dimensional chromatin structure. Epigenetics, 2019, 14, 894-911.	1.3	61
25	Quantitative Trait Module-Based Genetic Analysis of Alzheimer's Disease. International Journal of Molecular Sciences, 2019, 20, 5912.	1.8	6
26	Direct Extracellular Electron Transfer of the *Geobacter sulfurreducens* Pili Relevant to Interaromatic Distances. BioMed Research International, 2019, 2019, 1-12.	0.9	8
27	A Comparative Study of Network Motifs in the Integrated Transcriptional Regulation and Protein Interaction Networks of <italic>Shewanella</italic>. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 163-171.	1.9	1
28	Prediction of microRNA-binding residues in protein using a Laplacian support vector machine based on sequence information. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840009.	0.3	2
29	Structural Basis for the Influence of A1, 5A, and W51W57 Mutations on the Conductivity of the Geobacter sulfurreducens Pili. Crystals, 2018, 8, 10.	1.0	5
30	Network-Based Methods for Identifying Key Active Proteins in the Extracellular Electron Transfer Process in Shewanella oneidensis MR-1. Genes, 2018, 9, 41.	1.0	10
31	Histone modifications influence skipped exons inclusion. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750003.	0.3	3
32	Draft genome sequence of the Tibetan medicinal herb Rhodiola crenulata. GigaScience, 2017, 6, 1-5.	3.3	33
33	The accessible chromatin landscape during conversion of human embryonic stem cells to trophoblast by bone morphogenetic protein 4â€. Biology of Reproduction, 2017, 96, 1267-1278.	1.2	16
34	Efficient identification of SNPs in pooled DNA samples using a dual mononucleotide addition-based sequencing method. Molecular Genetics and Genomics, 2017, 292, 1069-1081.	1.0	2
35	An approach of identifying differential nucleosome regions in multiple samples. BMC Genomics, 2017, 18, 135.	1.2	9
36	Predicting and Interpreting the Structure of Type IV Pilus of Electricigens by Molecular Dynamics Simulations. Molecules, 2017, 22, 1342.	1.7	7

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37	The application of next-generation sequencing techniques in studying transcriptional regulation in embryonic stem cells. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2017, 39, 717-725.	0.1	1
38	K-shell Analysis Reveals Distinct Functional Parts in an Electron Transfer Network and Its Implications for Extracellular Electron Transfer. Frontiers in Microbiology, 2016, 7, 530.	1.5	6
39	Comparative Analysis of Type IV Pilin in Desulfuromonadales. Frontiers in Microbiology, 2016, 7, 2080.	1.5	14
40	DNABP: Identification of DNA-Binding Proteins Based on Feature Selection Using a Random Forest and Predicting Binding Residues. PLoS ONE, 2016, 11, e0167345.	1.1	32
41	Ehapp2: Estimate haplotype frequencies from pooled sequencing data with prior database information. Journal of Bioinformatics and Computational Biology, 2016, 14, 1650017.	0.3	0
42	Low Energy Atomic Models Suggesting a Pilus Structure that could Account for Electrical Conductivity of Geobacter sulfurreducens Pili. Scientific Reports, 2016, 6, 23385.	1.6	43
43	An accurate clone-based haplotyping method by overlapping pool sequencing. Nucleic Acids Research, 2016, 44, e112-e112.	6.5	1
44	DectICO: an alignment-free supervised metagenomic classification method based on feature extraction and dynamic selection. BMC Bioinformatics, 2015, 16, 323.	1.2	9
45	Predicting Homogeneous Pilus Structure from Monomeric Data and Sparse Constraints. BioMed Research International, 2015, 2015, 1-12.	0.9	8
46	A hybrid strategy for comprehensive annotation of the protein coding genes in prokaryotic genome. Genes and Genomics, 2015, 37, 347-355.	0.5	2
47	Accurate estimation of haplotype frequency from pooled sequencing data and cost-effective identification of rare haplotype carriers by overlapping pool sequencing. Bioinformatics, 2015, 31, 515-522.	1.8	11
48	A dynamic programming algorithm for nucleosome positions alignment. , 2014, , .		0
49	Intrinsic correlation of oligonucleotides: A novel genomic signature for metagenome analysis. Journal of Theoretical Biology, 2014, 353, 9-18.	0.8	5
50	Identifying the potential extracellular electron transfer pathways from a c-type cytochrome network. Molecular BioSystems, 2014, 10, 3138-3146.	2.9	10
51	Sequence-based predictor of ATP-binding residues using random forest and mRMR-IFS feature selection. Journal of Theoretical Biology, 2014, 360, 59-66.	0.8	13
52	Quantitative group testing-based overlapping pool sequencing to identify rare variant carriers. BMC Bioinformatics, 2014, 15, 195.	1.2	12
53	Nucleosome organization in the vicinity of transcription factor binding sites in the human genome. BMC Genomics, 2014, 15, 493.	1.2	17
54	The nucleosome regulates the usage of polyadenylation sites in the human genome. BMC Genomics, 2013, 14, 912.	1.2	18

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55	Identifying Rare Variants With Optimal Depth of Coverage and Cost‑Effective Overlapping Pool Sequencing. Genetic Epidemiology, 2013, 37, 820-830.	0.6	9
56	Identification of Novel MicroRNAs in Primates by Using the Synteny Information and Small RNA Deep Sequencing Data. International Journal of Molecular Sciences, 2013, 14, 20820-20832.	1.8	1
57	Analysis of Enhanced Current-Generating Mechanism of Geobacter sulfurreducens Strain via Model-Driven Metabolism Simulation. PLoS ONE, 2013, 8, e73907.	1.1	11
58	The Patterns of Histone Modifications in the Vicinity of Transcription Factor Binding Sites in Human Lymphoblastoid Cell Lines. PLoS ONE, 2013, 8, e60002.	1.1	18
59	Prediction of autism susceptibility genes based on association rules. Journal of Neuroscience Research, 2012, 90, 1119-1125.	1.3	19
60	MicroRNA Genes Derived from Repetitive Elements and Expanded by Segmental Duplication Events in Mammalian Genomes. PLoS ONE, 2011, 6, e17666.	1.1	77
61	Prediction of RNA‑binding residues in proteins from primary sequence using an enriched random forest model with a novel hybrid feature. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1230-1239.	1.5	54
62	A novel 2D graphical representation of protein sequence based on individual amino acid. International Journal of Quantum Chemistry, 2011, 111, 2835-2843.	1.0	14
63	Role of 10–11bp periodicities of eukaryotic DNA sequence in nucleosome positioning. BioSystems, 2011, 105, 295-299.	0.9	7
64	Genetic relationships of Osmanthus based on ISSR-PCR. Biologia (Poland), 2010, 65, 459-464.	0.8	3
65	Identification of common microRNA-mRNA regulatory biomodules in human epithelial cancer. Science Bulletin, 2010, 55, 3576-3589.	1.7	8
66	Reannotation of protein‑coding genes based on an improved graphical representation of DNA sequence. Journal of Computational Chemistry, 2010, 31, 2126-2135.	1.5	28
67	TN curve: A novel 3D graphical representation of DNA sequence based on trinucleotides and its applications. Journal of Theoretical Biology, 2009, 261, 459-468.	0.8	52
68	MiPred: classification of real and pseudo microRNA precursors using random forest prediction model with combined features. Nucleic Acids Research, 2007, 35, W339-W344.	6.5	434