Cang-Zhi Jia

List of Publications by Year
in descending order

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37 papers	1,459 citations	361413 20 h-index	330143 37 g-index
37 all docs	37 docs citations	37 times ranked	969 citing authors

#	Article	IF	Citations
1	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	6.5	26
2	O-glycosylation site prediction for Homo sapiens by combining properties and sequence features with support vector machine. Journal of Bioinformatics and Computational Biology, 2022, 20, 2150029.	0.8	3
3	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
4	Formator: Predicting Lysine Formylation Sites Based on the Most Distant Undersampling and Safe-Level Synthetic Minority Oversampling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1937-1945.	3.0	17
5	Computational identification of eukaryotic promoters based on cascaded deep capsule neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	44
6	DeepTorrent: a deep learning-based approach for predicting DNA N4-methylcytosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	84
7	Staem5: A novel computational approach for accurate prediction of m5C site. Molecular Therapy - Nucleic Acids, 2021, 26, 1027-1034.	5.1	20
8	An Interpretable Prediction Model for Identifying N7-Methylguanosine Sites Based on XGBoost and SHAP. Molecular Therapy - Nucleic Acids, 2020, 22, 362-372.	5.1	93
9	EnsemPseU: Identifying Pseudouridine Sites With an Ensemble Approach. IEEE Access, 2020, 8, 79376-79382.	4.2	15
10	Pippin: A random forest-based method for identifying presynaptic and postsynaptic neurotoxins. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050008.	0.8	1
11	PASSION: an ensemble neural network approach for identifying the binding sites of RBPs on circRNAs. Bioinformatics, 2020, 36, 4276-4282.	4.1	58
12	Inspector: a lysine succinylation predictor based on edited nearest-neighbor undersampling and adaptive synthetic oversampling. Analytical Biochemistry, 2020, 593, 113592.	2.4	40
13	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. Briefings in Bioinformatics, 2020, 21, 1069-1079.	6.5	38
14	4mCPred: machine learning methods for DNA N4-methylcytosine sites prediction. Bioinformatics, 2019, 35, 593-601.	4.1	146
15	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. Bioinformatics, 2019, 35, 2957-2965.	4.1	109
16	Prediction of aptamerâ€“protein interacting pairs based on sparse autoencoder feature extraction and an ensemble classifier. Mathematical Biosciences, 2019, 311, 103-108.	1.9	22
17	NucPosPred: Predicting species-specific genomic nucleosome positioning via four different modes of general PseKNC. Journal of Theoretical Biology, 2018, 450, 15-21.	1.7	35
18	O-GlcNAcPRED-II: an integrated classification algorithm for identifying O-GlcNAcylation sites based on fuzzy undersampling and a K-means PCA oversampling technique. Bioinformatics, 2018, 34, 2029-2036.	4.1	128

#	ARTICLE	IF	CITATIONS
19	Computational Prediction of Protein O-GlcNAc Modification. Methods in Molecular Biology, 2018, 1754, 235-246.	0.9	5
20	Recognition of Protein Pupylation Sites by Adopting Resampling Approach. Molecules, 2018, 23, 3097.	3.8	3
21	70ProPred: a predictor for discovering sigma70 promoters based on combining multiple features. BMC Systems Biology, 2018, 12, 44.	3.0	72
22	OH-PRED: prediction of protein hydroxylation sites by incorporating adapted normal distribution bi-profile Bayes feature extraction and physicochemical properties of amino acids. Journal of Biomolecular Structure and Dynamics, 2017, 35, 829-835.	3.5	16
23	EnhancerPred2.0: predicting enhancers and their strength based on position-specific trinucleotide propensity and electronâ€“ion interaction potential feature selection. Molecular BioSystems, 2017, 13, 767-774.	2.9	42
24	S-SulfPred: A sensitive predictor to capture S-sulfenylation sites based on a resampling one-sided selection undersampling-synthetic minority oversampling technique. Journal of Theoretical Biology, 2017, 422, 84-89.	1.7	52
25	CarSite: identifying carbonylated sites of human proteins based on a one-sided selection resampling method. Molecular BioSystems, 2017, 13, 2362-2369.	2.9	13
26	DephosSitePred: A High Accuracy Predictor for Protein Dephosphorylation Sites. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 153-157.	1.1	6
27	EnhancerPred: a predictor for discovering enhancers based on the combination and selection of multiple features. Scientific Reports, 2016, 6, 38741.	3.3	80
28	RNA-MethylPred: A high-accuracy predictor to identify N6-methyladenosine in RNA. Analytical Biochemistry, 2016, 510, 72-75.	2.4	56
29	Prediction of Protein S-Nitrosylation Sites Based on Adapted Normal Distribution Bi-Profile Bayes and Chouâ€™s Pseudo Amino Acid Composition. International Journal of Molecular Sciences, 2014, 15, 10410-10423.	4.1	94
30	Harmonic number identities via the Newtonâ€“Andrews method. Ramanujan Journal, 2014, 35, 263-285.	0.7	32
31	Quartic theta hypergeometric series. Ramanujan Journal, 2013, 32, 23-81.	0.7	3
32	O-GlcNAcPRED: a sensitive predictor to capture protein O-GlcNAcylation sites. Molecular BioSystems, 2013, 9, 2909.	2.9	45
33	Prediction of mitochondrial proteins of malaria parasite using bi-profile Bayes feature extraction. Biochimie, 2011, 93, 778-782.	2.6	34
34	TRANSFORMATION AND REDUCTION FORMULAE FOR DOUBLE q-SERIES OF TYPE Î¦^{2:1;Î»}_{2:0;Î¼}. Glasgow Mathematical Journal, 2010, 52, 195-204.	0.3	3
35	Alignment-free Comparison of Protein Sequences Based on Reduced Amino Acid Alphabets. Journal of Biomolecular Structure and Dynamics, 2009, 26, 763-769.	3.5	10
36	ABEL'S METHOD ON SUMMATION BY PARTS FOR ELLIPTIC HYPERGEOMETRIC SERIES. Communications in Contemporary Mathematics, 2009, 11, 337-353.	1.2	1

#	Article	IF	Citations
37	Protein secondary structure class assignment on the basis of a new graphic representation. International Journal of Quantum Chemistry, 2009, 109, 819-825.	2.0	2