Ke Chen

List of Publications by Year
in descending order

27	1,193	687220 13	677027 22
papers	citations	h-index	g-index

27	27	27	1217
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Computational Prediction of Secondary and Supersecondary Structures from Protein Sequences. Methods in Molecular Biology, 2019, 1958, 73-100.	0.4	11
2	Accurate prediction of secondary structure of tRNAs. Biochemical and Biophysical Research Communications, 2019, 509, 64-68.	1.0	1
3	A statistical analysis on transcriptome sequences: The enrichment of Alu-element is associated with subcellular location. Biochemical and Biophysical Research Communications, 2018, 499, 397-402.	1.0	9
4	Pairwise alignment for very long nucleic acid sequences. Biochemical and Biophysical Research Communications, 2018, 502, 313-317.	1.0	9
5	NSiteMatch: Prediction of Binding Sites of Nucleotides by Identifying the Structure Similarity of Local Surface Patches. Computational and Mathematical Methods in Medicine, 2017, 2017, 1-16.	0.7	8
6	Systematic investigation of sequence and structural motifs that recognize ATP. Computational Biology and Chemistry, 2015, 56, 131-141.	1.1	3
7	Quad-PRE: A Hybrid Method to Predict Protein Quaternary Structure Attributes. Computational and Mathematical Methods in Medicine, 2014, 2014, 1-9.	0.7	3
8	newDNA-Prot: Prediction of DNA-binding proteins by employing support vector machine and a comprehensive sequence representation. Computational Biology and Chemistry, 2014, 52, 51-59.	1.1	20
9	A matrix grammar approach for automatic distributed network resource management. Frontiers of Computer Science, 2013, 7, 583-594.	1.6	1
10	Prediction and analysis of nucleotide-binding residues using sequence and sequence-derived structural descriptors. Bioinformatics, 2012, 28, 331-341.	1.8	106
11	Computational Prediction of Secondary and Supersecondary Structures. Methods in Molecular Biology, 2012, 932, 63-86.	0.4	13
12	A Critical Comparative Assessment of Predictions of Protein-Binding Sites for Biologically Relevant Organic Compounds. Structure, 2011, 19, 613-621.	1.6	59
13	iFC2: an integrated web-server for improved prediction of protein structural class, fold type, and secondary structure content. Amino Acids, 2011, 40, 963-973.	1.2	13
14	ATPsite: sequence-based prediction of ATP-binding residues. Proteome Science, 2011, 9, S4.	0.7	57
15	Accurate prediction of ATP-binding residues using sequence and sequence-derived structural descriptors. , 2010, , .		0
16	Prediction of integral membrane protein type by collocated hydrophobic amino acid pairs. Journal of Computational Chemistry, 2009, 30, 163-172.	1.5	66
17	$H_{m infty}$ Fuzzy Filtering of Nonlinear Systems With Intermittent Measurements. IEEE Transactions on Fuzzy Systems, 2009, 17, 291-300.	6.5	267
18	Investigation of Atomic Level Patterns in Proteinâ€"Small Ligand Interactions. PLoS ONE, 2009, 4, e4473.	1.1	55

#	Article	IF	Citations
19	Prediction of protein structural class using novel evolutionary collocationâ€based sequence representation. Journal of Computational Chemistry, 2008, 29, 1596-1604.	1.5	148
20	Identification of tubulin drug binding sites and prediction of relative differences in binding affinities to tubulin isotypes using digital signal processing. Journal of Molecular Graphics and Modelling, 2008, 27, 497-505.	1.3	15
21	PFRES: protein fold classification by using evolutionary information and predicted secondary structure. Bioinformatics, 2007, 23, 2843-2850.	1.8	108
22	Prediction of protein crystallization using collocation of amino acid pairs. Biochemical and Biophysical Research Communications, 2007, 355, 764-769.	1.0	102
23	Improved Prediction of Relative Solvent Accessibility Using Two-stage Support Vector Regression. , 2007, , .		0
24	Prediction of Protein Structural Class Using PSI-BLAST Profile Based Collocation of Amino Acid Pairs. , 2007, , .		1
25	Prediction of flexible/rigid regions from protein sequences using k-spaced amino acid pairs. BMC Structural Biology, 2007, 7, 25.	2.3	100
26	Optimization of the Sliding Window Size for Protein Structure Prediction. , 2006, , .		18
27	Prediction of the Number of Helices for the Twilight Zone Proteins. , 2006, , .		0