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	$H_{m infty}$ Fuzzy Filtering of Nonlinear Systems With Intermittent Measurements. IEEE Transactions on Fuzzy Systems, 2009, 17, 291-300.	6.5	267
2	Prediction of protein structural class using novel evolutionary collocationâ€based sequence representation. Journal of Computational Chemistry, 2008, 29, 1596-1604.	1.5	148
3	PFRES: protein fold classification by using evolutionary information and predicted secondary structure. Bioinformatics, 2007, 23, 2843-2850.	1.8	108
4	Prediction and analysis of nucleotide-binding residues using sequence and sequence-derived structural descriptors. Bioinformatics, 2012, 28, 331-341.	1.8	106
5	Prediction of protein crystallization using collocation of amino acid pairs. Biochemical and Biophysical Research Communications, 2007, 355, 764-769.	1.0	102
6	Prediction of flexible/rigid regions from protein sequences using k-spaced amino acid pairs. BMC Structural Biology, 2007, 7, 25.	2.3	100
7	Prediction of integral membrane protein type by collocated hydrophobic amino acid pairs. Journal of Computational Chemistry, 2009, 30, 163-172.	1.5	66
8	A Critical Comparative Assessment of Predictions of Protein-Binding Sites for Biologically Relevant Organic Compounds. Structure, 2011, 19, 613-621.	1.6	59
9	ATPsite: sequence-based prediction of ATP-binding residues. Proteome Science, 2011, 9, S4.	0.7	57
10	Investigation of Atomic Level Patterns in Proteinâ€”Small Ligand Interactions. PLoS ONE, 2009, 4, e4473.	1.1	55
11	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
12	Optimization of the Sliding Window Size for Protein Structure Prediction. , 2006, , .		18
13	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
14	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
15	Computational Prediction of Secondary and Supersecondary Structures. Methods in Molecular Biology, 2012, 932, 63-86.	0.4	13
16	Computational Prediction of Secondary and Supersecondary Structures from Protein Sequences. Methods in Molecular Biology, 2019, 1958, 73-100.	0.4	11
17	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
18	Pairwise alignment for very long nucleic acid sequences. Biochemical and Biophysical Research Communications, 2018, 502, 313-317.	1.0	9

#	Article	IF	Citations
19	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
20	Quad-PRE: A Hybrid Method to Predict Protein Quaternary Structure Attributes. Computational and Mathematical Methods in Medicine, 2014, 2014, 1-9.	0.7	3
21	Systematic investigation of sequence and structural motifs that recognize ATP. Computational Biology and Chemistry, 2015, 56, 131-141.	1.1	3
22	Prediction of Protein Structural Class Using PSI-BLAST Profile Based Collocation of Amino Acid Pairs. , 2007, , .		1
23	A matrix grammar approach for automatic distributed network resource management. Frontiers of Computer Science, 2013, 7, 583-594.	1.6	1
24	Accurate prediction of secondary structure of tRNAs. Biochemical and Biophysical Research Communications, 2019, 509, 64-68.	1.0	1
25	Prediction of the Number of Helices for the Twilight Zone Proteins. , 2006, , .		0
26	Improved Prediction of Relative Solvent Accessibility Using Two-stage Support Vector Regression. , 2007, , .		0
27	Accurate prediction of ATP-binding residues using sequence and sequence-derived structural descriptors. , 2010, , .		0