Kuo-Chen Chou

List of Publications by Year in Descending Order

297 papers	41,717 citations	125 h-index	195 g-index
306 ext. papers	45,331 ext. citations	4.1 avg, IF	8.44 L-index

#	Paper	IF	Citations
297	Using CHOU'S 5-Steps Rule to Predict O-Linked Serine Glycosylation Sites by Blending Position Relative Features and Statistical Moment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 2045-2056	3	21
296	iPhosH-PseAAC: Identify Phosphohistidine Sites in Proteins by Blending Statistical Moments and Position Relative Features According to the Chou's 5-Step Rule and General Pseudo Amino Acid Composition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 596-610	3	48
295	The Remarkable Impacts of Gordon Life Science Institute. *Natural Science*, **2021**, 13, 43-75	0.5	
294	iHyd-LysSite (EPSV): Identifying Hydroxylysine Sites in Protein Using Statistical Formulation by Extracting Enhanced Position and Sequence Variant Feature Technique. *Current Genomics*, **2020**, 21, 536-545	2.6	9
293	Distorted Key Theory and its Implication for Drug Development. *Current Proteomics*, **2020**, 17, 311-323	0.7	6
292	iProtease-PseAAC(2L): A two-layer predictor for identifying proteases and their types using Chou's 5-step-rule and general PseAAC. *Analytical Biochemistry*, **2020**, 588, 113477	3.1	23
291	Some illuminating remarks on molecular genetics and genomics as well as drug development. *Molecular Genetics and Genomics*, **2020**, 295, 261-274	3.1	4
290	Proposing Pseudo Amino Acid Components is an Important Milestone for Proteome and Genome Analyses. *International Journal of Peptide Research and Therapeutics*, **2020**, 26, 1085-1098	2.1	16
289	A Two-Level Computation Model Based on Deep Learning Algorithm for Identification of piRNA and Their Functions via Chou's 5-Steps Rule. *International Journal of Peptide Research and Therapeutics*, **2020**, 26, 795-809	2.1	43
288	Progresses in Predicting Post-translational Modification. *International Journal of Peptide Research and Therapeutics*, **2020**, 26, 873-888	2.1	37
287	Glioma stages prediction based on machine learning algorithm combined with protein-protein interaction networks. *Genomics*, **2020**, 112, 837-847	4.3	15
286	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. *Bioinformatics*, **2019**, 35, 2957-2965	7.2	70
285	An insightful recollection since the distorted key theory was born about 23 years ago. *Genomics*, **2019**,	4.3	7
284	Positive-unlabelled learning of glycosylation sites in the human proteome. *BMC Bioinformatics*, **2019**, 20, 112	3.6	47
283	The preliminary efficacy evaluation of the CTLA-4-Ig treatment against Lupus nephritis through in-silico analyses. *Journal of Theoretical Biology*, **2019**, 471, 74-81	2.3	3
282	pLoc_bal-mGpos: Predict subcellular localization of Gram-positive bacterial proteins by quasi-balancing training dataset and PseAAC. *Genomics*, **2019**, 111, 886-892	4.3	75
281	Computational analysis and prediction of lysine malonylation sites by exploiting informative features in an integrative machine-learning framework. *Briefings in Bioinformatics*, **2019**, 20, 2185-2199	13.4	55

280	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. *Bioinformatics*, **2019**, 35, 398-406	7.2	76
279	Advance in predicting subcellular localization of multi-label proteins and its implication for developing multi-target drugs. *Current Medicinal Chemistry*, **2019**,	4.3	73
278	An Insightful 10-year Recollection Since the Emergence of the 5-steps Rule. *Current Pharmaceutical Design*, **2019**, 25, 4223-4234	3.3	6
277	iHyd-PseAAC (EPSV): Identifying Hydroxylation Sites in Proteins by Extracting Enhanced Position and Sequence Variant Feature Chou's 5-Step Rule and General Pseudo Amino Acid Composition. *Current Genomics*, **2019**, 20, 124-133	2.6	35
276	iMethylK_pseAAC: Improving Accuracy of Lysine Methylation Sites Identification by Incorporating Statistical Moments and Position Relative Features into General PseAAC Chou's 5-steps Rule. *Current Genomics*, **2019**, 20, 275-292	2.6	13
275	iSulfoTyr-PseAAC: Identify Tyrosine Sulfation Sites by Incorporating Statistical Moments Chou's 5-steps Rule and Pseudo Components. *Current Genomics*, **2019**, 20, 306-320	2.6	26
274	Impacts of Pseudo Amino Acid Components and 5-steps Rule to Proteomics and Proteome Analysis. *Current Topics in Medicinal Chemistry*, **2019**, 19, 2283-2300	3	24
273	An Epidemic Avian Influenza Prediction Model Based on Google Trends. *Letters in Organic Chemistry* , **2019**, 16, 303-310	0.6	20
272	Prediction of Nitrosocysteine Sites Using Position and Composition Variant Features. *Letters in Organic Chemistry*, **2019**, 16, 283-293	0.6	21
271	pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by Chou's General PseAAC and IHTS Treatment to Balance Training Dataset. *Medicinal Chemistry*, **2019**, 15, 496-509	1.8	41
270	pLoc_bal-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by General PseAAC and Quasi-balancing Training Dataset. *Medicinal Chemistry*, **2019**, 15, 472-485	1.8	39
269	An insightful recollection since the birth of Gordon Life Science Institute about 17 years ago **2019**, 4, 31-36		6
268	SPrenylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-prenylation sites in proteins. *Journal of Theoretical Biology*, **2019**, 468, 1-11	2.3	87
267	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. *Genomics*, **2019**, 111, 1274-1282	4.3	53
266	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. *Briefings in Bioinformatics*, **2019**, 20, 2150-2166	13.4	48
265	iPSW(2L)-PseKNC: A two-layer predictor for identifying promoters and their strength by hybrid features via pseudo K-tuple nucleotide composition. *Genomics*, **2019**, 111, 1785-1793	4.3	30
264	SPalmitoylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-palmitoylation sites in proteins. *Analytical Biochemistry*, **2019**, 568, 14-23	3.1	85
263	pSSbond-PseAAC: Prediction of disulfide bonding sites by integration of PseAAC and statistical moments. *Journal of Theoretical Biology*, **2019**, 463, 47-55	2.3	49

262	Bastion3: a two-layer ensemble predictor of type III secreted effectors. *Bioinformatics*, **2019**, 35, 2017-2028	7.3	47
261	iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. *Journal of Theoretical Biology*, **2019**, 460, 195-203	2.3	73
260	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. *Briefings in Bioinformatics*, **2019**, 20, 2267-2290	13.4	64
259	iDNA6mA-PseKNC: Identifying DNA N-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. *Genomics*, **2019**, 111, 96-102	4.3	190
258	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. *Briefings in Bioinformatics*, **2019**, 20, 638-658	13.4	124
257	iFeature: a Python package and web server for features extraction and selection from protein and peptide sequences. *Bioinformatics*, **2018**, 34, 2499-2502	7.2	258
256	PREvaIL, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. *Journal of Theoretical Biology*, **2018**, 443, 125-137	2.3	106
255	A Novel Modeling in Mathematical Biology for Classification of Signal Peptides. *Scientific Reports*, **2018**, 8, 1039	4.9	58
254	pLoc-mHum: predict subcellular localization of multi-location human proteins via general PseAAC to winnow out the crucial GO information. *Bioinformatics*, **2018**, 34, 1448-1456	7.2	124
253	iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. *Analytical Biochemistry*, **2018**, 550, 109-116	3.1	87
252	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. *Bioinformatics*, **2018**, 34, 2546-2555	7.2	71
251	iPromoter-2L: a two-layer predictor for identifying promoters and their types by multi-window-based PseKNC. *Bioinformatics*, **2018**, 34, 33-40	7.2	213
250	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. *Bioinformatics*, **2018**, 34, 684-687	7.2	102
249	pLoc-mEuk: Predict subcellular localization of multi-label eukaryotic proteins by extracting the key GO information into general PseAAC. *Genomics*, **2018**, 110, 50-58	4.3	176
248	iRSpot-Pse6NC: Identifying recombination spots in by incorporating hexamer composition into general PseKNC. *International Journal of Biological Sciences*, **2018**, 14, 883-891	11.2	130
247	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. *Bioinformatics*, **2018**, 34, 4196-4204	7.2	118
246	Implications of Newly Identified Brain eQTL Genes and Their Interactors in Schizophrenia. *Molecular Therapy - Nucleic Acids*, **2018**, 12, 433-442	10.7	52
245	iEnhancer-EL: identifying enhancers and their strength with ensemble learning approach. *Bioinformatics*, **2018**, 34, 3835-3842	7.2	116

244	Simulated Protein Thermal Detection (SPTD) for Enzyme Thermostability Study and an Application Example for Pullulanase from Bacillus deramificans. *Current Pharmaceutical Design*, **2018**, 24, 4023-4033	3.3	18
243	pLoc_bal-mPlant: Predict Subcellular Localization of Plant Proteins by General PseAAC and Balancing Training Dataset. *Current Pharmaceutical Design*, **2018**, 24, 4013-4022	3.3	41
242	pNitro-Tyr-PseAAC: Predict Nitrotyrosine Sites in Proteins by Incorporating Five Features into Chou's General PseAAC. *Current Pharmaceutical Design*, **2018**, 24, 4034-4043	3.3	39
241	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. *Genomics*, **2018**, 110, 239-246	4.3	109
240	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. *Scientific Reports*, **2018**, 8, 17923	4.9	24
239	iPhosY-PseAAC: identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. *Molecular Biology Reports*, **2018**, 45, 2501-2509	2.8	41
238	iRNA(m6A)-PseDNC: Identifying N-methyladenosine sites using pseudo dinucleotide composition. *Analytical Biochemistry*, **2018**, 561-562, 59-65	3.1	117
237	pLoc_bal-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by quasi-balancing training dataset and general PseAAC. *Journal of Theoretical Biology*, **2018**, 458, 92-102	2.3	62
236	iRO-3wPseKNC: identify DNA replication origins by three-window-based PseKNC. *Bioinformatics*, **2018**, 34, 3086-3093	7.2	92
235	Quokka: a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. *Bioinformatics*, **2018**, 34, 4223-4231	7.2	110
234	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. *Molecular Therapy - Nucleic Acids*, **2018**, 11, 468-474	10.7	135
233	iPhos-PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. *Molecular Informatics*, **2017**, 36, 1600010	3.8	82
232	2L-piRNA: A Two-Layer Ensemble Classifier for Identifying Piwi-Interacting RNAs and Their Function. *Molecular Therapy - Nucleic Acids*, **2017**, 7, 267-277	10.7	207
231	iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. *Molecular Therapy - Nucleic Acids*, **2017**, 7, 155-163	10.7	228
230	Pse-Analysis: a python package for DNA/RNA and protein/ peptide sequence analysis based on pseudo components and kernel methods. *Oncotarget*, **2017**, 8, 13338-13343	3.3	110
229	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. *Oncotarget*, **2017**, 8, 4208-4217	3.3	191
228	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. *Oncotarget*, **2017**, 8, 41178-41188	3.3	148
227	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. *Bioinformatics*, **2017**, 33, 341-346	7.2	59

226	pLoc-mVirus: Predict subcellular localization of multi-location virus proteins via incorporating the optimal GO information into general PseAAC. *Gene*, **2017**, 628, 315-321	3.8	131
225	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. *Bioinformatics*, **2017**, 33, 3524-3531	7.2	163
224	pLoc-mPlant: predict subcellular localization of multi-location plant proteins by incorporating the optimal GO information into general PseAAC. *Molecular BioSystems*, **2017**, 13, 1722-1727		167
223	iRSpot-EL: identify recombination spots with an ensemble learning approach. *Bioinformatics*, **2017**, 33, 35-41	7.2	263
222	Prediction of the aquatic toxicity of aromatic compounds to tetrahymena pyriformis through support vector regression. *Oncotarget*, **2017**, 8, 49359-49369	3.3	46
221	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. *Oncotarget*, **2017**, 8, 58494-58503	3.3	98
220	Small molecular floribundiquinone B derived from medicinal plants inhibits acetylcholinesterase activity. *Oncotarget*, **2017**, 8, 57149-57162	3.3	18
219	2L-PCA: a two-level principal component analyzer for quantitative drug design and its applications. *Oncotarget*, **2017**, 8, 70564-70578	3.3	16
218	An Unprecedented Revolution in Medicinal Chemistry Driven by the Progress of Biological Science. *Current Topics in Medicinal Chemistry*, **2017**, 17, 2337-2358	3	242
217	iPreny-PseAAC: Identify C-terminal Cysteine Prenylation Sites in Proteins by Incorporating Two Tiers of Sequence Couplings into PseAAC. *Medicinal Chemistry*, **2017**, 13, 544-551	1.8	118
216	Chlorella vulgaris Induces Apoptosis of Human Non-Small Cell Lung Carcinoma (NSCLC) Cells. *Medicinal Chemistry*, **2017**, 13, 560-568	1.8	11
215	iPGK-PseAAC: Identify Lysine Phosphoglycerylation Sites in Proteins by Incorporating Four Different Tiers of Amino Acid Pairwise Coupling Information into the General PseAAC. *Medicinal Chemistry*, **2017**, 13, 552-559	1.8	120
214	iRNA-2methyl: Identify RNA 2'-O-methylation Sites by Incorporating Sequence-Coupled Effects into General PseKNC and Ensemble Classifier. *Medicinal Chemistry*, **2017**, 13, 734-743	1.8	93
213	Pse-in-One 2.0: An Improved Package of Web Servers for Generating Various Modes of Pseudo Components of DNA, RNA, and Protein Sequences. *Natural Science*, **2017**, 09, 67-91	0.5	97
212	pLoc-mGpos: Incorporate Key Gene Ontology Information into General PseAAC for Predicting Subcellular Localization of Gram-Positive Bacterial Proteins. *Natural Science*, **2017**, 09, 330-349	0.5	47
211	pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. *Genomics*, **2017**, 110, 231-231	4.3	115
210	iEnhancer-2L: a two-layer predictor for identifying enhancers and their strength by pseudo k-tuple nucleotide composition. *Bioinformatics*, **2016**, 32, 362-9	7.2	258
209	repRNA: a web server for generating various feature vectors of RNA sequences. *Molecular Genetics and Genomics*, **2016**, 291, 473-81	3.1	110

208	iPTM-mLys: identifying multiple lysine PTM sites and their different types. *Bioinformatics*, **2016**, 32, 3116-3123	7.2	212
207	iMiRNA-PseDPC: microRNA precursor identification with a pseudo distance-pair composition approach. *Journal of Biomolecular Structure and Dynamics*, **2016**, 34, 223-35	3.6	101
206	pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. *Journal of Theoretical Biology*, **2016**, 394, 223-230	2.3	252
205	pRNAm-PC: Predicting N(6)-methyladenosine sites in RNA sequences via physical-chemical properties. *Analytical Biochemistry*, **2016**, 497, 60-7	3.1	213
204	Using deformation energy to analyze nucleosome positioning in genomes. *Genomics*, **2016**, 107, 69-75	4.3	99
203	iSuc-PseOpt: Identifying lysine succinylation sites in proteins by incorporating sequence-coupling effects into pseudo components and optimizing imbalanced training dataset. *Analytical Biochemistry*, **2016**, 497, 48-56	3.1	218
202	Identification of protein-protein binding sites by incorporating the physicochemical properties and stationary wavelet transforms into pseudo amino acid composition. *Journal of Biomolecular Structure and Dynamics*, **2016**, 34, 1946-61	3.6	111
201	iPhos-PseEn: identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. *Oncotarget*, **2016**, 7, 51270-51283	3.3	133
200	Recent Progress in Predicting Posttranslational Modification Sites in Proteins. *Current Topics in Medicinal Chemistry*, **2016**, 16, 591-603	3	80
199	iRNA-PseU: Identifying RNA pseudouridine sites. *Molecular Therapy - Nucleic Acids*, **2016**, 5, e332	10.7	145
198	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. *Oncotarget*, **2016**, 7, 69783-69793	3.3	156
197	iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. *Oncotarget*, **2016**, 7, 34180-9	3.3	103
196	iACP: a sequence-based tool for identifying anticancer peptides. *Oncotarget*, **2016**, 7, 16895-909	3.3	283
195	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. *Molecules*, **2016**, 21, E95	4.8	131
194	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. *Oncotarget*, **2016**, 7, 44310-44321	3.3	138
193	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. *Oncotarget*, **2016**, 7, 34558-70	3.3	161
192	pSumo-CD: predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. *Bioinformatics*, **2016**, 32, 3133-3141	7.2	154
191	iDHS-EL: identifying DNase I hypersensitive sites by fusing three different modes of pseudo nucleotide composition into an ensemble learning framework. *Bioinformatics*, **2016**, 32, 2411-8	7.2	168

190	iDNA-Methyl: identifying DNA methylation sites via pseudo trinucleotide composition. *Analytical Biochemistry*, **2015**, 474, 69-77	3.1	226
189	repDNA: a Python package to generate various modes of feature vectors for DNA sequences by incorporating user-defined physicochemical properties and sequence-order effects. *Bioinformatics*, **2015**, 31, 1307-9	7.2	199
188	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. *Bioinformatics*, **2015**, 31, 119-20	7.2	172
187	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. *Molecular BioSystems*, **2015**, 11, 2620-34		256
186	Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences. *Nucleic Acids Research*, **2015**, 43, W65-71	20.1	578
185	Benchmark data for identifying N(6)-methyladenosine sites in the Saccharomyces cerevisiae genome. *Data in Brief*, **2015**, 5, 376-8	1.2	9
184	iRNA-Methyl: Identifying N(6)-methyladenosine sites using pseudo nucleotide composition. *Analytical Biochemistry*, **2015**, 490, 26-33	3.1	276
183	Identification of microRNA precursor with the degenerate K-tuple or Kmer strategy. *Journal of Theoretical Biology*, **2015**, 385, 153-9	2.3	146
182	iUbiq-Lys: prediction of lysine ubiquitination sites in proteins by extracting sequence evolution information via a gray system model. *Journal of Biomolecular Structure and Dynamics*, **2015**, 33, 1731-42	3.6	133
181	iDrug-Target: predicting the interactions between drug compounds and target proteins in cellular networking via benchmark dataset optimization approach. *Journal of Biomolecular Structure and Dynamics*, **2015**, 33, 2221-33	3.6	167
180	Identification of DNA-binding proteins by incorporating evolutionary information into pseudo amino acid composition via the top-n-gram approach. *Journal of Biomolecular Structure and Dynamics*, **2015**, 33, 1720-30	3.6	71
179	Prediction of Protein Quaternary Structures **2015**, 249-265		2
178	iPPI-Esml: An ensemble classifier for identifying the interactions of proteins by incorporating their physicochemical properties and wavelet transforms into PseAAC. *Journal of Theoretical Biology*, **2015**, 377, 47-56	2.3	243
177	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. *Data in Brief*, **2015**, 4, 87-9	1.2	8
176	Identification of real microRNA precursors with a pseudo structure status composition approach. *PLoS ONE*, **2015**, 10, e0121501	3.7	174
175	Impacts of bioinformatics to medicinal chemistry. *Medicinal Chemistry*, **2015**, 11, 218-34	1.8	457
174	Gestational Influenza Increases the Risk of Psychosis in Adults. *Medicinal Chemistry*, **2015**, 11, 676-82	1.8	13
173	PseKNC: a flexible web server for generating pseudo K-tuple nucleotide composition. *Analytical Biochemistry*, **2014**, 456, 53-60	3.1	341

172	iNitro-Tyr: prediction of nitrotyrosine sites in proteins with general pseudo amino acid composition. *PLoS ONE*, **2014**, 9, e105018	3.7	161
171	iMethyl-PseAAC: identification of protein methylation sites via a pseudo amino acid composition approach. *BioMed Research International*, **2014**, 2014, 947416	3	126
170	iSS-PseDNC: identifying splicing sites using pseudo dinucleotide composition. *BioMed Research International*, **2014**, 2014, 623149	3	130
169	iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition. *Nucleic Acids Research*, **2014**, 42, 12961-72	20.1	412
168	iRSpot-TNCPseAAC: identify recombination spots with trinucleotide composition and pseudo amino acid components. *International Journal of Molecular Sciences*, **2014**, 15, 1746-66	6.3	206
167	iHyd-PseAAC: predicting hydroxyproline and hydroxylysine in proteins by incorporating dipeptide position-specific propensity into pseudo amino acid composition. *International Journal of Molecular Sciences*, **2014**, 15, 7594-610	6.3	172
166	iCTX-type: a sequence-based predictor for identifying the types of conotoxins in targeting ion channels. *BioMed Research International*, **2014**, 2014, 286419	3	171
165	Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection. *Bioinformatics*, **2014**, 30, 472-9	7.2	248
164	iTIS-PseTNC: a sequence-based predictor for identifying translation initiation site in human genes using pseudo trinucleotide composition. *Analytical Biochemistry*, **2014**, 462, 76-83	3.1	218
163	iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. *Bioinformatics*, **2014**, 30, 1522-9	7.2	303
162	iNR-Drug: predicting the interaction of drugs with nuclear receptors in cellular networking. *International Journal of Molecular Sciences*, **2014**, 15, 4915-37	6.3	64
161	iDNA-Prot|dis: identifying DNA-binding proteins by incorporating amino acid distance-pairs and reduced alphabet profile into the general pseudo amino acid composition. *PLoS ONE*, **2014**, 9, e106691	3.7	202
160	Research/review: Structure and linkage disequilibrium analysis of adamantane resistant mutations in influenza virus m2 proton channel. *Current Drug Metabolism*, **2014**, 15, 526-34	3.5	1
159	Research/review: Insights into the mutation-induced dysfunction of arachidonic acid metabolism from modeling of human CYP2J2. *Current Drug Metabolism*, **2014**, 15, 502-13	3.5	10
158	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. *Molecular BioSystems*, **2013**, 9, 634-44		213
157	iAMP-2L: a two-level multi-label classifier for identifying antimicrobial peptides and their functional types. *Analytical Biochemistry*, **2013**, 436, 168-77	3.1	334
156	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. *Analytical Biochemistry*, **2013**, 442, 118-25	3.1	254
155	iCDI-PseFpt: identify the channel-drug interaction in cellular networking with PseAAC and molecular fingerprints. *Journal of Theoretical Biology*, **2013**, 337, 71-9	2.3	101

154	Some remarks on predicting multi-label attributes in molecular biosystems. *Molecular BioSystems*, **2013**, 9, 1092-100		355
153	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. *Nucleic Acids Research*, **2013**, 41, e68	20.1	492
152	iEzy-drug: a web server for identifying the interaction between enzymes and drugs in cellular networking. *BioMed Research International*, **2013**, 2013, 701317	3	65
151	Metallo-β-lactamases: structural features, antibiotic recognition, inhibition, and inhibitor design. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1242-53	3	27
150	Recent advances in predicting protein classification and their applications to drug development. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1622-35	3	15
149	iSNO-PseAAC: predict cysteine S-nitrosylation sites in proteins by incorporating position specific amino acid propensity into pseudo amino acid composition. *PLoS ONE*, **2013**, 8, e55844	3.7	297
148	iGPCR-drug: a web server for predicting interaction between GPCRs and drugs in cellular networking. *PLoS ONE*, **2013**, 8, e72234	3.7	88
147	Recent progresses in identifying nuclear receptors and their families. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1192-200	3	21
146	Predict drug-protein interaction in cellular networking. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1707-12	3	24
145	iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine S-nitrosylation sites in proteins. *PeerJ*, **2013**, 1, e171	3.1	245
144	Deciphering the effects of gene deletion on yeast longevity using network and machine learning approaches. *Biochimie*, **2012**, 94, 1017-25	4.6	54
143	iLoc-Hum: using the accumulation-label scale to predict subcellular locations of human proteins with both single and multiple sites. *Molecular BioSystems*, **2012**, 8, 629-41		316
142	Hepatitis C virus network based classification of hepatocellular cirrhosis and carcinoma. *PLoS ONE*, **2012**, 7, e34460	3.7	40
141	Design novel dual agonists for treating type-2 diabetes by targeting peroxisome proliferator-activated receptors with core hopping approach. *PLoS ONE*, **2012**, 7, e38546	3.7	81
140	iNuc-PhysChem: a sequence-based predictor for identifying nucleosomes via physicochemical properties. *PLoS ONE*, **2012**, 7, e47843	3.7	160
139	iLoc-Gpos: a multi-layer classifier for predicting the subcellular localization of singleplex and multiplex Gram-positive bacterial proteins. *Protein and Peptide Letters*, **2012**, 19, 4-14	1.9	125
138	Recent advances in computational studies on influenza a virus M2 proton channel. *Mini-Reviews in Medicinal Chemistry*, **2012**, 12, 971-8	3.2	13
137	Predicting Anatomical Therapeutic Chemical (ATC) classification of drugs by integrating chemical-chemical interactions and similarities. *PLoS ONE*, **2012**, 7, e35254	3.7	133

136	iNR-PhysChem: a sequence-based predictor for identifying nuclear receptors and their subfamilies via physical-chemical property matrix. *PLoS ONE*, **2012**, 7, e30869	3.7	66
135	Predicting secretory proteins of malaria parasite by incorporating sequence evolution information into pseudo amino acid composition via grey system model. *PLoS ONE*, **2012**, 7, e49040	3.7	37
134	Molecular dynamics simulations of CYP2E1. *Medicinal Chemistry*, **2012**, 8, 208-21	1.8	21
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