Kuo-Chen Chou

List of Publications by Citations

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	Prediction of protein cellular attributes using pseudo-amino acid composition. *Proteins: Structure, Function and Bioinformatics*, **2001**, 43, 246-55	4.2	1361
296	Some remarks on protein attribute prediction and pseudo amino acid composition. *Journal of Theoretical Biology*, **2011**, 273, 236-47	2.3	1108
295	Prediction of protein structural classes. *Critical Reviews in Biochemistry and Molecular Biology*, **1995**, 30, 275-349	8.7	886
294	Recent progress in protein subcellular location prediction. *Analytical Biochemistry*, **2007**, 370, 1-16	3.1	793
293	Cell-PLoc: a package of Web servers for predicting subcellular localization of proteins in various organisms. *Nature Protocols*, **2008**, 3, 153-62	18.8	755
292	Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes. *Bioinformatics*, **2005**, 21, 10-9	7.2	750
291	Structural bioinformatics and its impact to biomedical science. *Current Medicinal Chemistry*, **2004**, 11, 2105-34	4.3	603
290	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
289	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. *Nucleic Acids Research*, **2013**, 41, e68	20.1	492
288	Plant-mPLoc: a top-down strategy to augment the power for predicting plant protein subcellular localization. *PLoS ONE*, **2010**, 5, e11335	3.7	458
287	Impacts of bioinformatics to medicinal chemistry. *Medicinal Chemistry*, **2015**, 11, 218-34	1.8	457
286	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
285	Using functional domain composition and support vector machines for prediction of protein subcellular location. *Journal of Biological Chemistry*, **2002**, 277, 45765-9	5.4	366
284	MemType-2L: a web server for predicting membrane proteins and their types by incorporating evolution information through Pse-PSSM. *Biochemical and Biophysical Research Communications*, **2007**, 360, 339-45	3.4	365
283	Pseudo Amino Acid Composition and its Applications in Bioinformatics, Proteomics and System Biology. *Current Proteomics*, **2009**, 6, 262-274	0.7	363
282	Some remarks on predicting multi-label attributes in molecular biosystems. *Molecular BioSystems*, **2013**, 9, 1092-100		355
281	PseKNC: a flexible web server for generating pseudo K-tuple nucleotide composition. *Analytical Biochemistry*, **2014**, 456, 53-60	3.1	341

280	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
279	PseAAC: a flexible web server for generating various kinds of protein pseudo amino acid composition. *Analytical Biochemistry*, **2008**, 373, 386-8	3.1	330
278	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
277	Low-frequency collective motion in biomacromolecules and its biological functions. *Biophysical Chemistry*, **1988**, 30, 3-48	3.5	308
276	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
275	Euk-mPLoc: a fusion classifier for large-scale eukaryotic protein subcellular location prediction by incorporating multiple sites. *Journal of Proteome Research*, **2007**, 6, 1728-34	5.6	303
274	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
273	Ensemble classifier for protein fold pattern recognition. *Bioinformatics*, **2006**, 22, 1717-22	7.2	294
272	Prediction of human immunodeficiency virus protease cleavage sites in proteins. *Analytical Biochemistry*, **1996**, 233, 1-14	3.1	291
271	iACP: a sequence-based tool for identifying anticancer peptides. *Oncotarget*, **2016**, 7, 16895-909	3.3	283
270	Support vector machines for predicting membrane protein types by using functional domain composition. *Biophysical Journal*, **2003**, 84, 3257-63	2.9	280
269	Protein subcellular location prediction. *Protein Engineering, Design and Selection*, **1999**, 12, 107-18	1.9	280
268	iRNA-Methyl: Identifying N(6)-methyladenosine sites using pseudo nucleotide composition. *Analytical Biochemistry*, **2015**, 490, 26-33	3.1	276
267	iLoc-Euk: a multi-label classifier for predicting the subcellular localization of singleplex and multiplex eukaryotic proteins. *PLoS ONE*, **2011**, 6, e18258	3.7	272
266	iRSpot-EL: identify recombination spots with an ensemble learning approach. *Bioinformatics*, **2017**, 33, 35-41	7.2	263
265	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
264	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
263	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. *Molecular BioSystems*, **2015**, 11, 2620-34		256

262   iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. *Analytical Biochemistry*, **2013**, 442, 118-25   3.1   254

261   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

260   Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection. *Bioinformatics*, **2014**, 30, 472-9   7.2   248

259   iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine S-nitrosylation sites in proteins. *PeerJ*, **2013**, 1, e171   3.1   245

258   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

257   An Unprecedented Revolution in Medicinal Chemistry Driven by the Progress of Biological Science. *Current Topics in Medicinal Chemistry*, **2017**, 17, 2337-2358   3   242

256   Predicting eukaryotic protein subcellular location by fusing optimized evidence-theoretic K-Nearest Neighbor classifiers. *Journal of Proteome Research*, **2006**, 5, 1888-97   5.6   239

255   A new method for predicting the subcellular localization of eukaryotic proteins with both single and multiple sites: Euk-mPLoc 2.0. *PLoS ONE*, **2010**, 5, e9931   3.7   235

254   iLoc-Virus: a multi-label learning classifier for identifying the subcellular localization of virus proteins with both single and multiple sites. *Journal of Theoretical Biology*, **2011**, 284, 42-51   2.3   229

253   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

252   iDNA-Methyl: identifying DNA methylation sites via pseudo trinucleotide composition. *Analytical Biochemistry*, **2015**, 474, 69-77   3.1   226

251   Hum-PLoc: a novel ensemble classifier for predicting human protein subcellular localization. *Biochemical and Biophysical Research Communications*, **2006**, 347, 150-7   3.4   222

250   Using subsite coupling to predict signal peptides. *Protein Engineering, Design and Selection*, **2001**, 14, 75-9   1.9   222

249   Signal-3L: A 3-layer approach for predicting signal peptides. *Biochemical and Biophysical Research Communications*, **2007**, 363, 297-303   3.4   221

248   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

247   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

246   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

245   pRNAm-PC: Predicting N(6)-methyladenosine sites in RNA sequences via physical-chemical properties. *Analytical Biochemistry*, **2016**, 497, 60-7   3.1   213

| 244 | iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. *Molecular BioSystems*, **2013**, 9, 634-44 | | 213 |

| 243 | Applications of graph theory to enzyme kinetics and protein folding kinetics. Steady and non-steady-state systems. *Biophysical Chemistry*, **1990**, 35, 1-24 | 3.5 | 213 |

| 242 | iPTM-mLys: identifying multiple lysine PTM sites and their different types. *Bioinformatics*, **2016**, 32, 3116-3123 | 7.3 | 212 |

| 241 | iDNA-Prot: identification of DNA binding proteins using random forest with grey model. *PLoS ONE*, **2011**, 6, e24756 | 3.7 | 209 |

| 240 | 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 |

| 239 | 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 |

| 238 | 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 |

| 237 | 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 |

| 236 | AFP-Pred: A random forest approach for predicting antifreeze proteins from sequence-derived properties. *Journal of Theoretical Biology*, **2011**, 270, 56-62 | 2.3 | 196 |

| 235 | iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. *Oncotarget*, **2017**, 8, 4208-4217 | 3.3 | 191 |

| 234 | iDNA6mA-PseKNC: Identifying DNA N-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. *Genomics*, **2019**, 111, 96-102 | 4.3 | 190 |

| 233 | iLoc-Plant: a multi-label classifier for predicting the subcellular localization of plant proteins with both single and multiple sites. *Molecular BioSystems*, **2011**, 7, 3287-97 | | 179 |

| 232 | Prediction of protein structural classes by support vector machines. *Computers & Chemistry*, **2002**, 26, 293-6 | | 177 |

| 231 | 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 |

| 230 | Prediction of signal peptides using scaled window. *Peptides*, **2001**, 22, 1973-9 | 3.8 | 175 |

| 229 | GPCR-CA: A cellular automaton image approach for predicting G-protein-coupled receptor functional classes. *Journal of Computational Chemistry*, **2009**, 30, 1414-23 | 3.5 | 174 |

| 228 | A key driving force in determination of protein structural classes. *Biochemical and Biophysical Research Communications*, **1999**, 264, 216-24 | 3.4 | 174 |

| 227 | Identification of real microRNA precursors with a pseudo structure status composition approach. *PLoS ONE*, **2015**, 10, e0121501 | 3.7 | 174 |

226	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. *Bioinformatics*, **2015**, 31, 119-20	7.2	172
225	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
224	iCTX-type: a sequence-based predictor for identifying the types of conotoxins in targeting ion channels. *BioMed Research International*, **2014**, 2014, 286419	3	171
223	Graphic rule for drug metabolism systems. *Current Drug Metabolism*, **2010**, 11, 369-78	3.5	170
222	Prediction of protein structure classes with pseudo amino acid composition and fuzzy support vector machine network. *Protein and Peptide Letters*, **2007**, 14, 811-5	1.9	168
221	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
220	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
219	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
218	Using pseudo amino acid composition to predict protein structural classes: approached with complexity measure factor. *Journal of Computational Chemistry*, **2006**, 27, 478-82	3.5	164
217	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. *Bioinformatics*, **2017**, 33, 3524-3531	7.2	163
216	iNitro-Tyr: prediction of nitrotyrosine sites in proteins with general pseudo amino acid composition. *PLoS ONE*, **2014**, 9, e105018	3.7	161
215	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
214	iNuc-PhysChem: a sequence-based predictor for identifying nucleosomes via physicochemical properties. *PLoS ONE*, **2012**, 7, e47843	3.7	160
213	REVIEW : Recent advances in developing web-servers for predicting protein attributes. *Natural Science*, **2009**, 01, 63-92	0.5	160
212	Weighted-support vector machines for predicting membrane protein types based on pseudo-amino acid composition. *Protein Engineering, Design and Selection*, **2004**, 17, 509-16	1.9	159
211	Using optimized evidence-theoretic K-nearest neighbor classifier and pseudo-amino acid composition to predict membrane protein types. *Biochemical and Biophysical Research Communications*, **2005**, 334, 288-92	3.4	157
210	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. *Oncotarget*, **2016**, 7, 69783-69793	3.3	156
209	Bioinformatical analysis of G-protein-coupled receptors. *Journal of Proteome Research*, **2002**, 1, 429-33	5.6	154

208	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
207	Fuzzy KNN for predicting membrane protein types from pseudo-amino acid composition. *Journal of Theoretical Biology*, **2006**, 240, 9-13	2.3	152
206	Using LogitBoost classifier to predict protein structural classes. *Journal of Theoretical Biology*, **2006**, 238, 172-6	2.3	150
205	Prediction protein structural classes with pseudo-amino acid composition: approximate entropy and hydrophobicity pattern. *Journal of Theoretical Biology*, **2008**, 250, 186-93	2.3	149
204	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. *Oncotarget*, **2017**, 8, 41178-41188	3.3	148
203	Identification of microRNA precursor with the degenerate K-tuple or Kmer strategy. *Journal of Theoretical Biology*, **2015**, 385, 153-9	2.3	146
202	iRNA-PseU: Identifying RNA pseudouridine sites. *Molecular Therapy - Nucleic Acids*, **2016**, 5, e332	10.7	145
201	Using stacked generalization to predict membrane protein types based on pseudo-amino acid composition. *Journal of Theoretical Biology*, **2006**, 242, 941-6	2.3	144
200	ProtIdent: a web server for identifying proteases and their types by fusing functional domain and sequential evolution information. *Biochemical and Biophysical Research Communications*, **2008**, 376, 321-5	3.4	143
199	Nuc-PLoc: a new web-server for predicting protein subnuclear localization by fusing PseAA composition and PsePSSM. *Protein Engineering, Design and Selection*, **2007**, 20, 561-7	1.9	143
198	Low-frequency Fourier spectrum for predicting membrane protein types. *Biochemical and Biophysical Research Communications*, **2005**, 336, 737-9	3.4	142
197	Virus-PLoc: a fusion classifier for predicting the subcellular localization of viral proteins within host and virus-infected cells. *Biopolymers*, **2007**, 85, 233-40	2.2	140
196	Prediction and classification of protein subcellular location-sequence-order effect and pseudo amino acid composition. *Journal of Cellular Biochemistry*, **2003**, 90, 1250-60	4.7	139
195	An optimization approach to predicting protein structural class from amino acid composition. *Protein Science*, **1992**, 1, 401-8	6.3	138
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	A top-down approach to enhance the power of predicting human protein subcellular localization: Hum-mPLoc 2.0. *Analytical Biochemistry*, **2009**, 394, 269-74	3.1	135
192	HIVcleave: a web-server for predicting human immunodeficiency virus protease cleavage sites in proteins. *Analytical Biochemistry*, **2008**, 375, 388-90	3.1	135
191	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. *Molecular Therapy - Nucleic Acids*, **2018**, 11, 468-474	10.7	135

190	Modelling extracellular domains of GABA-A receptors: subtypes 1, 2, 3, and 5. *Biochemical and Biophysical Research Communications*, **2004**, 316, 636-42	3.4	134
189	Molecular therapeutic target for type-2 diabetes. *Journal of Proteome Research*, **2004**, 3, 1284-8	5.6	134
188	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
187	Predicting Anatomical Therapeutic Chemical (ATC) classification of drugs by integrating chemical-chemical interactions and similarities. *PLoS ONE*, **2012**, 7, e35254	3.7	133
186	iPhos-PseEn: identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. *Oncotarget*, **2016**, 7, 51270-51283	3.3	133
185	Low-frequency resonance and cooperativity of hemoglobin. *Trends in Biochemical Sciences*, **1989**, 14, 212-3	10.3	132
184	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
183	Insights from modelling the 3D structure of the extracellular domain of alpha7 nicotinic acetylcholine receptor. *Biochemical and Biophysical Research Communications*, **2004**, 319, 433-8	3.4	131
182	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
181	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
180	iSS-PseDNC: identifying splicing sites using pseudo dinucleotide composition. *BioMed Research International*, **2014**, 2014, 623149	3	130
179	Predicting functions of proteins in mouse based on weighted protein-protein interaction network and protein hybrid properties. *PLoS ONE*, **2011**, 6, e14556	3.7	130
178	Prediction of G-protein-coupled receptor classes. *Journal of Proteome Research*, **2005**, 4, 1413-8	5.6	129
177	Using supervised fuzzy clustering to predict protein structural classes. *Biochemical and Biophysical Research Communications*, **2005**, 334, 577-81	3.4	129
176	Predicting protein subnuclear location with optimized evidence-theoretic K-nearest classifier and pseudo amino acid composition. *Biochemical and Biophysical Research Communications*, **2005**, 337, 752-6	3.4	129
175	SLLE for predicting membrane protein types. *Journal of Theoretical Biology*, **2005**, 232, 7-15	2.3	129
174	iMethyl-PseAAC: identification of protein methylation sites via a pseudo amino acid composition approach. *BioMed Research International*, **2014**, 2014, 947416	3	126
173	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

172	Gpos-PLoc: an ensemble classifier for predicting subcellular localization of Gram-positive bacterial proteins. *Protein Engineering, Design and Selection*, **2007**, 20, 39-46	1.9	125
171	Large-scale predictions of gram-negative bacterial protein subcellular locations. *Journal of Proteome Research*, **2006**, 5, 3420-8	5.6	125
170	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
169	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
168	Predicting protein quaternary structure by pseudo amino acid composition. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53, 282-9	4.2	122
167	GPCR-2L: predicting G protein-coupled receptors and their types by hybridizing two different modes of pseudo amino acid compositions. *Molecular BioSystems*, **2011**, 7, 911-9		121
166	Coupling interaction between thromboxane A2 receptor and alpha-13 subunit of guanine nucleotide-binding protein. *Journal of Proteome Research*, **2005**, 4, 1681-6	5.6	120
165	Boosting classifier for predicting protein domain structural class. *Biochemical and Biophysical Research Communications*, **2005**, 334, 213-7	3.4	120
164	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
163	Prediction of the tertiary structure of a caspase-9/inhibitor complex. *FEBS Letters*, **2000**, 470, 249-56	3.8	119
162	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. *Bioinformatics*, **2018**, 34, 4196-4204	7.2	118
161	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
160	Solitary wave dynamics as a mechanism for explaining the internal motion during microtubule growth. *Biopolymers*, **1994**, 34, 143-53	2.2	117
159	iRNA(m6A)-PseDNC: Identifying N-methyladenosine sites using pseudo dinucleotide composition. *Analytical Biochemistry*, **2018**, 561-562, 59-65	3.1	117
158	iEnhancer-EL: identifying enhancers and their strength with ensemble learning approach. *Bioinformatics*, **2018**, 34, 3835-3842	7.2	116
157	Progress in protein structural class prediction and its impact to bioinformatics and proteomics. *Current Protein and Peptide Science*, **2005**, 6, 423-36	2.8	116
156	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
155	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

154	Analysis and prediction of the metabolic stability of proteins based on their sequential features, subcellular locations and interaction networks. *PLoS ONE*, **2010**, 5, e10972	3.7	111
153	repRNA: a web server for generating various feature vectors of RNA sequences. *Molecular Genetics and Genomics*, **2016**, 291, 473-81	3.1	110
152	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
151	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
150	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. *Genomics*, **2018**, 110, 239-246	4.3	109
149	Predicting protein structural classes with pseudo amino acid composition: an approach using geometric moments of cellular automaton image. *Journal of Theoretical Biology*, **2008**, 254, 691-6	2.3	107
148	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
147	Prediction of the tertiary structure and substrate binding site of caspase-8. *FEBS Letters*, **1997**, 419, 49-54	3.8	106
146	Insights from investigating the interaction of oseltamivir (Tamiflu) with neuraminidase of the 2009 H1N1 swine flu virus. *Biochemical and Biophysical Research Communications*, **2009**, 386, 432-6	3.4	105
145	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
144	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. *Bioinformatics*, **2018**, 34, 684-687	7.2	102
143	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
142	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
141	Using deformation energy to analyze nucleosome positioning in genomes. *Genomics*, **2016**, 107, 69-75	4.3	99
140	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. *Oncotarget*, **2017**, 8, 58494-58503	3.3	98
139	Predicting membrane protein type by functional domain composition and pseudo-amino acid composition. *Journal of Theoretical Biology*, **2006**, 238, 395-400	2.3	98
138	Prediction of enzyme family classes. *Journal of Proteome Research*, **2003**, 2, 183-90	5.6	98
137	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

136	Prediction of protein signal sequences and their cleavage sites. *Proteins: Structure, Function and Bioinformatics*, **2001**, 42, 136-9	4.2	96
135	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
134	iRO-3wPseKNC: identify DNA replication origins by three-window-based PseKNC. *Bioinformatics*, **2018**, 34, 3086-3093	7.2	92
133	Nearest neighbour algorithm for predicting protein subcellular location by combining functional domain composition and pseudo-amino acid composition. *Biochemical and Biophysical Research Communications*, **2003**, 305, 407-11	3.4	91
132	Prediction of the tertiary structure of the beta-secretase zymogen. *Biochemical and Biophysical Research Communications*, **2002**, 292, 702-8	3.4	91
131	The biological functions of low-frequency vibrations (phonons). VI. A possible dynamic mechanism of allosteric transition in antibody molecules. *Biopolymers*, **1987**, 26, 285-95	2.2	89
130	iGPCR-drug: a web server for predicting interaction between GPCRs and drugs in cellular networking. *PLoS ONE*, **2013**, 8, e72234	3.7	88
129	Insights from modeling three-dimensional structures of the human potassium and sodium channels. *Journal of Proteome Research*, **2004**, 3, 856-61	5.6	88
128	Molecular modeling and chemical modification for finding peptide inhibitor against severe acute respiratory syndrome coronavirus main proteinase. *Analytical Biochemistry*, **2005**, 337, 262-70	3.1	88
127	iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. *Analytical Biochemistry*, **2018**, 550, 109-116	3.1	87
126	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
125	Novel inhibitor design for hemagglutinin against H1N1 influenza virus by core hopping method. *PLoS ONE*, **2011**, 6, e28111	3.7	86
124	QuatIdent: a web server for identifying protein quaternary structural attribute by fusing functional domain and sequential evolution information. *Journal of Proteome Research*, **2009**, 8, 1577-84	5.6	86
123	Predicting protein fold pattern with functional domain and sequential evolution information. *Journal of Theoretical Biology*, **2009**, 256, 441-6	2.3	85
122	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
121	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
120	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
119	Predicting enzyme subclass by functional domain composition and pseudo amino acid composition. *Journal of Proteome Research*, **2005**, 4, 967-71	5.6	81

118	Predicting subcellular localization of proteins in a hybridization space. *Bioinformatics*, **2004**, 20, 1151-6	7.2	81
117	Insights from modeling the tertiary structure of human BACE2. *Journal of Proteome Research*, **2004**, 3, 1069-72	5.6	81
116	Prediction of protein folding rates from primary sequence by fusing multiple sequential features. *Journal of Biomedical Science and Engineering*, **2009**, 02, 136-143	0.7	81
115	Predicting enzyme family classes by hybridizing gene product composition and pseudo-amino acid composition. *Journal of Theoretical Biology*, **2005**, 234, 145-9	2.3	80
114	Recent Progress in Predicting Posttranslational Modification Sites in Proteins. *Current Topics in Medicinal Chemistry*, **2016**, 16, 591-603	3	80
113	Insight into the molecular switch mechanism of human Rab5a from molecular dynamics simulations. *Biochemical and Biophysical Research Communications*, **2009**, 390, 608-12	3.4	79
112	The benzylthio-pyrimidine U-31,355, a potent inhibitor of HIV-1 reverse transcriptase. *Biochemical Pharmacology*, **1996**, 51, 743-50	6	79
111	Neural network prediction of the HIV-1 protease cleavage sites. *Journal of Theoretical Biology*, **1995**, 177, 369-79	2.3	79
110	Multiple field three dimensional quantitative structure-activity relationship (MF-3D-QSAR). *Journal of Computational Chemistry*, **2008**, 29, 211-9	3.5	78
109	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. *Bioinformatics*, **2019**, 35, 398-406	7.2	76
108	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
107	Modeling the tertiary structure of human cathepsin-E. *Biochemical and Biophysical Research Communications*, **2005**, 331, 56-60	3.4	74
106	Advance in predicting subcellular localization of multi-label proteins and its implication for developing multi-target drugs. *Current Medicinal Chemistry*, **2019**,	4.3	73
105	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
104	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
103	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. *Bioinformatics*, **2018**, 34, 2546-2555	7.2	71
102	Polyprotein cleavage mechanism of SARS CoV Mpro and chemical modification of the octapeptide. *Peptides*, **2004**, 25, 1857-64	3.8	71
101	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. *Bioinformatics*, **2019**, 35, 2957-2965	7.2	70

100	Predicting subcellular localization of proteins by hybridizing functional domain composition and pseudo-amino acid composition. *Journal of Cellular Biochemistry*, **2004**, 91, 1197-203	4.7	70
99	Using fourier spectrum analysis and pseudo amino acid composition for prediction of membrane protein types. *Protein Journal*, **2005**, 24, 385-9	3.9	69
98	Using pair-coupled amino acid composition to predict protein secondary structure content. *The Protein Journal*, **1999**, 18, 473-80		69
97	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
96	iEzy-drug: a web server for identifying the interaction between enzymes and drugs in cellular networking. *BioMed Research International*, **2013**, 2013, 701317	3	65
95	The biological functions of low-frequency vibrations (phonons). 4. Resonance effects and allosteric transition. *Biophysical Chemistry*, **1984**, 20, 61-71	3.5	65
94	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
93	Using grey dynamic modeling and pseudo amino acid composition to predict protein structural classes. *Journal of Computational Chemistry*, **2008**, 29, 2018-24	3.5	64
92	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. *Briefings in Bioinformatics*, **2019**, 20, 2267-2290	13.4	64
91	Prediction of protease types in a hybridization space. *Biochemical and Biophysical Research Communications*, **2006**, 339, 1015-20	3.4	63
90	Predicting human immunodeficiency virus protease cleavage sites in proteins by a discriminant function method. *Proteins: Structure, Function and Bioinformatics*, **1996**, 24, 51-72	4.2	63
89	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
88	Identification of proteases and their types. *Analytical Biochemistry*, **2009**, 385, 153-60	3.1	61
87	Docking and molecular dynamics study on the inhibitory activity of novel inhibitors on epidermal growth factor receptor (EGFR). *Medicinal Chemistry*, **2011**, 7, 24-31	1.8	61
86	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. *Bioinformatics*, **2017**, 33, 341-346	7.2	59
85	A Novel Modeling in Mathematical Biology for Classification of Signal Peptides. *Scientific Reports*, **2018**, 8, 1039	4.9	58
84	Prediction of protein structural classes by modified mahalanobis discriminant algorithm. *The Protein Journal*, **1998**, 17, 209-17		57
83	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

82	Predicting the quaternary structure attribute of a protein by hybridizing functional domain composition and pseudo amino acid composition. *Journal of Applied Crystallography*, **2009**, 42, 169-173	3.8	55
81	Insights from modeling the 3D structure of DNA-CBF3b complex. *Journal of Proteome Research*, **2005**, 4, 1657-60	5.6	55
80	Deciphering the effects of gene deletion on yeast longevity using network and machine learning approaches. *Biochimie*, **2012**, 94, 1017-25	4.6	54
79	Predicting protein structural classes from amino acid composition: application of fuzzy clustering. *Protein Engineering, Design and Selection*, **1995**, 8, 425-35	1.9	53
78	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. *Genomics*, **2019**, 111, 1274-1282	4.3	53
77	Implications of Newly Identified Brain eQTL Genes and Their Interactors in Schizophrenia. *Molecular Therapy - Nucleic Acids*, **2018**, 12, 433-442	10.7	52
76	A correlation-coefficient method to predicting protein-structural classes from amino acid compositions. *FEBS Journal*, **1992**, 207, 429-3		52
75	Wenxiang: a web-server for drawing wenxiang diagrams. *Natural Science*, **2011**, 03, 862-865	0.5	52
74	Diffusion-controlled effects in reversible enzymatic fast reaction systems--critical spherical shell and proximity rate constant. *Biophysical Chemistry*, **1980**, 12, 255-63	3.5	49
73	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
72	Insights from modeling the 3D structure of New Delhi metallo-ßlactamse and its binding interactions with antibiotic drugs. *PLoS ONE*, **2011**, 6, e18414	3.7	48
71	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
70	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
69	Positive-unlabelled learning of glycosylation sites in the human proteome. *BMC Bioinformatics*, **2019**, 20, 112	3.6	47
68	Molecular modeling studies of peptide drug candidates against SARS. *Medicinal Chemistry*, **2006**, 2, 309-14	1.8	47
67	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
66	Bastion3: a two-layer ensemble predictor of type III secreted effectors. *Bioinformatics*, **2019**, 35, 2017-2028	7.3	47
65	Prediction of the aquatic toxicity of aromatic compounds to tetrahymena pyriformis through support vector regression. *Oncotarget*, **2017**, 8, 49359-49369	3.3	46

64	An allosteric mechanism inferred from molecular dynamics simulations on phospholamban pentamer in lipid membranes. *PLoS ONE*, **2011**, 6, e18587	3.7	44
63	An energy-based approach to packing the 7-helix bundle of bacteriorhodopsin. *Protein Science*, **1992**, 1, 810-27	6.3	43
62	A Two-Level Computation Model Based on Deep Learning Algorithm for Identification of piRNA and Their Functions via Chou 5-Steps Rule. *International Journal of Peptide Research and Therapeutics*, **2020**, 26, 795-809	2.1	43
61	The critical spherical shell in enzymatic fast reaction systems. *Biophysical Chemistry*, **1980**, 12, 265-9	3.5	42
60	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
59	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
58	iPhosY-PseAAC: identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. *Molecular Biology Reports*, **2018**, 45, 2501-2509	2.8	41
57	Hepatitis C virus network based classification of hepatocellular cirrhosis and carcinoma. *PLoS ONE*, **2012**, 7, e34460	3.7	40
56	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
55	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
54	The biological functions of low-frequency vibrations (phonons) 5. A phenomenological theory. *Biophysical Chemistry*, **1985**, 22, 219-35	3.5	37
53	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
52	Progresses in Predicting Post-translational Modification. *International Journal of Peptide Research and Therapeutics*, **2020**, 26, 873-888	2.1	37
51	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
50	Studies on the specificity of HIV protease: an application of Markov chain theory. *The Protein Journal*, **1993**, 12, 709-24		34
49	Origin of low-frequency motions in biological macromolecules. A view of recent progress in the quasi-continuity model. *Biophysical Chemistry*, **1986**, 25, 105-16	3.5	32
48	A vector projection approach to predicting HIV protease cleavage sites in proteins. *Proteins: Structure, Function and Bioinformatics*, **1993**, 16, 195-204	4.2	31
47	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

46	Methodology development for predicting subcellular localization and other attributes of proteins. *Expert Review of Proteomics*, **2007**, 4, 453-63	4.2	29
45	Metallo-ß-lactamases: structural features, antibiotic recognition, inhibition, and inhibitor design. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1242-53	3	27
44	An analysis of protein folding type prediction by seed-propagated sampling and jackknife test. *The Protein Journal*, **1995**, 14, 583-93		27
43	A new approach to predicting protein folding types. *The Protein Journal*, **1993**, 12, 169-78		27
42	Does the folding type of a protein depend on its amino acid composition?. *FEBS Letters*, **1995**, 363, 127-31	3.8	26
41	An alternate-subsite-coupled model for predicting HIV protease cleavage sites in proteins. *Protein Engineering, Design and Selection*, **1994**, 7, 65-73	1.9	26
40	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
39	Knowledge-based model building of the tertiary structures for lectin domains of the selectin family. *The Protein Journal*, **1996**, 15, 161-8		24
38	Predict drug-protein interaction in cellular networking. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1707-12	3	24
37	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
36	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. *Scientific Reports*, **2018**, 8, 17923	4.9	24
35	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
34	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
33	Recent progresses in identifying nuclear receptors and their families. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1192-200	3	21
32	Prediction of Nitrosocysteine Sites Using Position and Composition Variant Features. *Letters in Organic Chemistry*, **2019**, 16, 283-293	0.6	21
31	Molecular dynamics simulations of CYP2E1. *Medicinal Chemistry*, **2012**, 8, 208-21	1.8	21
30	Prediction of a low-frequency mode in bovine pancreatic trypsin inhibitor molecule. *International Journal of Biological Macromolecules*, **1985**, 7, 77-80	7.9	20
29	An Epidemic Avian Influenza Prediction Model Based on Google Trends. *Letters in Organic Chemistry* , **2019**, 16, 303-310	0.6	20

No.	Title	IF	Citations
28	Using Pseudo Amino Acid Composition to Predict Protein Attributes Via Cellular Automata and Other Approaches. *Current Bioinformatics*, **2011**, 6, 251-260	4.7	19
27	Small molecular floribundiquinone B derived from medicinal plants inhibits acetylcholinesterase activity. *Oncotarget*, **2017**, 8, 57149-57162	3.3	18
26	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
25	2L-PCA: a two-level principal component analyzer for quantitative drug design and its applications. *Oncotarget*, **2017**, 8, 70564-70578	3.3	16
24	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
23	Recent advances in predicting protein classification and their applications to drug development. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1622-35	3	15
22	Glioma stages prediction based on machine learning algorithm combined with protein-protein interaction networks. *Genomics*, **2020**, 112, 837-847	4.3	15
21	Recent advances in computational studies on influenza a virus M2 proton channel. *Mini-Reviews in Medicinal Chemistry*, **2012**, 12, 971-8	3.2	13
20	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
19	Gestational Influenza Increases the Risk of Psychosis in Adults. *Medicinal Chemistry*, **2015**, 11, 676-82	1.8	13
18	Chlorella vulgaris Induces Apoptosis of Human Non-Small Cell Lung Carcinoma (NSCLC) Cells. *Medicinal Chemistry*, **2017**, 13, 560-568	1.8	11
17	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
16	Benchmark data for identifying N(6)-methyladenosine sites in the Saccharomyces cerevisiae genome. *Data in Brief*, **2015**, 5, 376-8	1.2	9
15	An eigenvalue-eigenvector approach to predicting protein folding types. *The Protein Journal*, **1995**, 14, 309-26		9
14	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
13	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. *Data in Brief*, **2015**, 4, 87-9	1.2	8
12	An insightful recollection since the distorted key theory was born about 23 years ago. *Genomics*, **2019**,	4.3	7
11	Monte Carlo simulation studies on the prediction of protein folding types from amino acid composition. II. Correlative effect. *The Protein Journal*, **1995**, 14, 251-8		6

10	An Insightful 10-year Recollection Since the Emergence of the 5-steps Rule. *Current Pharmaceutical Design*, **2019**, 25, 4223-4234	3.3	6
9	Distorted Key Theory and its Implication for Drug Development. *Current Proteomics*, **2020**, 17, 311-323	0.7	6
8	An insightful recollection since the birth of Gordon Life Science Institute about 17 years ago **2019**, 4, 31-36		6
7	A pharmacophore model specific to active site of CYP1A2 with a novel molecular modeling explorer and CoMFA. *Medicinal Chemistry*, **2012**, 8, 198-207	1.8	5
6	Knowledge-based computational intelligence development for predicting protein secondary structures from sequences. *Expert Review of Proteomics*, **2008**, 5, 653-62	4.2	4
5	Some illuminating remarks on molecular genetics and genomics as well as drug development. *Molecular Genetics and Genomics*, **2020**, 295, 261-274	3.1	4
4	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
3	Prediction of Protein Quaternary Structures **2015**, 249-265		2
2	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
1	The Remarkable Impacts of Gordon Life Science Institute. *Natural Science*, **2021**, 13, 43-75	0.5	