Gajendra P S Raghava

List of Publications by Year
in descending order

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294 papers	21,051 citations	9786 73 h-index	13379 130 g-index
336 all docs	336 docs citations	336 times ranked	16883 citing authors

#	Article	IF	Citations
1	Prediction of continuous B-cell epitopes in an antigen using recurrent neural network. Proteins: Structure, Function and Bioinformatics, 2006, 65, 40-48.	2.6	1,146
2	In Silico Approach for Predicting Toxicity of Peptides and Proteins. PLoS ONE, 2013, 8, e73957.	2.5	1,120
3	ProPred: prediction of HLA-DR binding sites. Bioinformatics, 2001, 17, 1236-1237.	4.1	758
4	AlgPred: prediction of allergenic proteins and mapping of IgE epitopes. Nucleic Acids Research, 2006, 34, W202-W209.	14.5	612
5	Designing of interferon-gamma inducing MHC class-II binders. Biology Direct, 2013, 8, 30.	4.6	484
6	ProPred1: prediction of promiscuous MHC Class-I binding sites. Bioinformatics, 2003, 19, 1009-1014.	4.1	408
7	THPdb: Database of FDA-approved peptide and protein therapeutics. PLoS ONE, 2017, 12, e0181748.	2.5	367
8	Prediction of CTL epitopes using QM, SVM and ANN techniques. Vaccine, 2004, 22, 3195-3204.	3.8	296
9	ESLpred: SVM-based method for subcellular localization of eukaryotic proteins using dipeptide composition and PSI-BLAST. Nucleic Acids Research, 2004, 32, W414-W419.	14.5	280
10	Improved Method for Linear B-Cell Epitope Prediction Using Antigenâ€™s Primary Sequence. PLoS ONE, 2013, 8, e62216.	2.5	269
11	Identification of conformational B-cell Epitopes in an antigen from its primary sequence. Immunome Research, 2010, 6, 6.	0.1	264
12	Prediction of RNA binding sites in a protein using SVM and PSSM profile. Proteins: Structure, Function and Bioinformatics, 2008, 71, 189-194.	2.6	253
13	CancerPPD: a database of anticancer peptides and proteins. Nucleic Acids Research, 2015, 43, D837-D843.	14.5	253
14	Analysis and prediction of antibacterial peptides. BMC Bioinformatics, 2007, 8, 263.	2.6	249
15	Classification of Nuclear Receptors Based on Amino Acid Composition and Dipeptide Composition. Journal of Biological Chemistry, 2004, 279, 23262-23266.	3.4	244
16	In silico approaches for designing highly effective cell penetrating peptides. Journal of Translational Medicine, 2013, 11, 74.	4.4	242
17	CPPsite 2.0: a repository of experimentally validated cell-penetrating peptides. Nucleic Acids Research, 2016, 44, D1098-D1103.	14.5	241
18	Identification of DNA-binding proteins using support vector machines and evolutionary profiles. BMC Bioinformatics, 2007, 8, 463.	2.6	233

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19	NPACT: Naturally Occurring Plant-based Anti-cancer Compound-Activity-Target database. Nucleic Acids Research, 2013, 41, D1124-D1129.	14.5	229
20	BcePred: Prediction of Continuous B-Cell Epitopes in Antigenic Sequences Using Physico-chemical Properties. Lecture Notes in Computer Science, 2004, , 197-204.	1.3	226
21	In Silico Models for Designing and Discovering Novel Anticancer Peptides. Scientific Reports, 2013, 3, 2984.	3.3	226
22	Prediction of IL4 Inducing Peptides. Clinical and Developmental Immunology, 2013, 2013, 1-9.	3.3	213
23	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. Journal of Molecular Recognition, 2007, 20, 75-82.	2.1	209
24	Computer-aided designing of immunosuppressive peptides based on IL-10 inducing potential. Scientific Reports, 2017, 7, 42851.	3.3	206
25	PSLpred: prediction of subcellular localization of bacterial proteins. Bioinformatics, 2005, 21, 2522-2524.	4.1	204
26	AntiBP2: improved version of antibacterial peptide prediction. BMC Bioinformatics, 2010, 11, S19.	2.6	203
27	Support Vector Machine-based Method for Subcellular Localization of Human Proteins Using Amino Acid Compositions, Their Order, and Similarity Search. Journal of Biological Chemistry, 2005, 280, 14427-14432.	3.4	202
28	MHCBN: a comprehensive database of MHC binding and non-binding peptides. Bioinformatics, 2003, 19, 665-666.	4.1	191
29	In silico Platform for Prediction of N-, O- and C-Glycosites in Eukaryotic Protein Sequences. PLoS ONE, 2013, 8, e67008.	2.5	182
30	Bcipep: A database of B-cell epitopes. BMC Genomics, 2005, 6, 79.	2.8	179
31	PEPstr: A de novo Method for Tertiary Structure Prediction of Small Bioactive Peptides. Protein and Peptide Letters, 2007, 14, 626-631.	0.9	179
32	OXBench: a benchmark for evaluation of protein multiple sequence alignment accuracy. BMC Bioinformatics, 2003, 4, 47.	2.6	173
33	Analysis and prediction of affinity of TAP binding peptides using cascade SVM. Protein Science, 2004, 13, 596-607.	7.6	167
34	PEPstrMOD: structure prediction of peptides containing natural, non-natural and modified residues. Biology Direct, 2015, 10, 73.	4.6	164
35	CPPsite: a curated database of cell penetrating peptides. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas015-bas015.	3.0	161
36	GPCRpred: an SVM-based method for prediction of families and subfamilies of G-protein coupled receptors. Nucleic Acids Research, 2004, 32, W383-W389.	14.5	154

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37	SVM based method for predicting HLA-DRB1*0401 binding peptides in an antigen sequence. Bioinformatics, 2004, 20, 421-423.	4.1	153
38	Spectral Repeat Finder (SRF): identification of repetitive sequences using Fourier transformation. Bioinformatics, 2004, 20, 1405-1412.	4.1	143
39	AHTPDB: a comprehensive platform for analysis and presentation of antihypertensive peptides. Nucleic Acids Research, 2015, 43, D956-D962.	14.5	143
40	A Web Server and Mobile App for Computing Hemolytic Potency of Peptides. Scientific Reports, 2016, 6, 22843.	3.3	135
41	SATPdb: a database of structurally annotated therapeutic peptides. Nucleic Acids Research, 2016, 44, D1119-D1126.	14.5	131
42	SVM based prediction of RNAâ€binding proteins using binding residues and evolutionary information. Journal of Molecular Recognition, 2011, 24, 303-313.	2.1	130
43	Prediction of beta-turns in proteins from multiple alignment using neural network. Protein Science, 2003, 12, 627-634.	7.6	129
44	Machine learning techniques in disease forecasting: a case study on rice blast prediction. BMC Bioinformatics, 2006, 7, 485.	2.6	129
45	AlgPred 2.0: an improved method for predicting allergenic proteins and mapping of IgE epitopes. Briefings in Bioinformatics, 2021, 22, .	6.5	128
46	AntiCP 2.0: an updated model for predicting anticancer peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	127
47	lncRNome: a comprehensive knowledgebase of human long noncoding RNAs. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat034.	3.0	126
48	An in silico platform for predicting, screening and designing of antihypertensive peptides. Scientific Reports, 2015, 5, 12512.	3.3	123
49	Support Vector Machine-based method for predicting subcellular localization of mycobacterial proteins using evolutionary information and motifs. BMC Bioinformatics, 2007, 8, 337.	2.6	121
50	Identification of ATP binding residues of a protein from its primary sequence. BMC Bioinformatics, 2009, 10, 434.	2.6	120
51	TumorHoPe: A Database of Tumor Homing Peptides. PLoS ONE, 2012, 7, e35187.	2.5	118
52	A hybrid approach for predicting promiscuous MHC class I restricted T cell epitopes. Journal of Biosciences, 2007, 32, 31-42.	1.1	117
53	In Silico Approach for Prediction of Antifungal Peptides. Frontiers in Microbiology, 2018, 9, 323.	3.5	113
54	VICMpred: An SVM-based Method for the Prediction of Functional Proteins of Gram-negative Bacteria Using Amino Acid Patterns and Composition. Genomics, Proteomics and Bioinformatics, 2006, 4, 42-47.	6.9	111

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55	PEPlife: A Repository of the Half-life of Peptides. Scientific Reports, 2016, 6, 36617.	3.3	108
56	Prediction Methods for B-cell Epitopes. Methods in Molecular Biology, 2007, 409, 387-394.	0.9	106
57	Hemolytik: a database of experimentally determined hemolytic and non-hemolytic peptides. Nucleic Acids Research, 2014, 42, D444-D449.	14.5	105
58	Peptide Toxicity Prediction. Methods in Molecular Biology, 2015, 1268, 143-157.	0.9	105
59	Benchmarking of different molecular docking methods for protein-peptide docking. BMC Bioinformatics, 2019, 19, 426.	2.6	104
60	CancerDR: Cancer Drug Resistance Database. Scientific Reports, 2013, 3, 1445.	3.3	102
61	Computer-aided biotechnology: from immuno-informatics to reverse vaccinology. Trends in Biotechnology, 2008, 26, 190-200.	9.3	101
62	Prediction and classification of ncRNAs using structural information. BMC Genomics, 2014, 15, 127.	2.8	101
63	Prediction of transmembrane regions of Î²-barrel proteins using ANN- and SVM-based methods. Proteins: Structure, Function and Bioinformatics, 2004, 56, 11-18.	2.6	98
64	A neural network method for prediction of Â-turn types in proteins using evolutionary information. Bioinformatics, 2004, 20, 2751-2758.	4.1	97
65	Prediction of Mitochondrial Proteins Using Support Vector Machine and Hidden Markov Model. Journal of Biological Chemistry, 2006, 281, 5357-5363.	3.4	97
66	OxDBase: a database of oxygenases involved in biodegradation. BMC Research Notes, 2009, 2, 67.	1.4	96
67	Pcleavage: an SVM based method for prediction of constitutive proteasome and immunoproteasome cleavage sites in antigenic sequences. Nucleic Acids Research, 2005, 33, W202-W207.	14.5	95
68	Novelin silicotools for designing peptide-based subunit vaccines and immunotherapeutics. Briefings in Bioinformatics, 2017, 18, bbw025.	6.5	94
69	Gene expression-based biomarkers for discriminating early and late stage of clear cell renal cancer. Scientific Reports, 2017, 7, 44997.	3.3	92
70	Identification of B-cell epitopes in an antigen for inducing specific class of antibodies. Biology Direct, 2013, 8, 27.	4.6	91
71	Anticancer properties of a defensin like class IId bacteriocin Laterosporulin10. Scientific Reports, 2017, 7, 46541.	3.3	89
72	Real value prediction of solvent accessibility in proteins using multiple sequence alignment and secondary structure. Proteins: Structure, Function and Bioinformatics, 2005, 61, 318-324.	2.6	87

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73	Computer-aided prediction and design of IL-6 inducing peptides: IL-6 plays a crucial role in COVID-19. Briefings in Bioinformatics, 2021, 22, 936-945.	6.5	84
74	Tumor Homing Peptides as Molecular Probes for Cancer Therapeutics, Diagnostics and Theranostics. Current Medicinal Chemistry, 2014, 21, 2367-2391.	2.4	80
75	CCDB: a curated database of genes involved in cervix cancer. Nucleic Acids Research, 2011, 39, D975-D979.	14.5	78
76	MHCBN 4.0: A database of MHC/TAP binding peptides and T-cell epitopes. BMC Research Notes, 2009, 2, 61.	1.4	77
77	Designing of peptides with desired half-life in intestine-like environment. BMC Bioinformatics, 2014, 15, 282.	2.6	73
78	A neural-network based method for prediction of Î³-turns in proteins from multiple sequence alignment. Protein Science, 2003, 12, 923-929.	7.6	71
79	Identification of NAD interacting residues in proteins. BMC Bioinformatics, 2010, 11, 160.	2.6	71
80	GlycoPP: A Webserver for Prediction of N- and O-Glycosites in Prokaryotic Protein Sequences. PLoS ONE, 2012, 7, e40155.	2.5	71
81	Computational approach for designing tumor homing peptides. Scientific Reports, 2013, 3, 1607.	3.3	69
82	In silico approaches for predicting the half-life of natural and modified peptides in blood. PLoS ONE, 2018, 13, e0196829.	2.5	67
83	BhairPred: prediction of Â-hairpins in a protein from multiple alignment information using ANN and SVM techniques. Nucleic Acids Research, 2005, 33, W154-W159.	14.5	65
84	QSAR based model for discriminating EGFR inhibitors and non-inhibitors using Random forest. Biology Direct, 2015, 10, 10.	4.6	63
85	HumCFS: a database of fragile sites in human chromosomes. BMC Genomics, 2019, 19, 985.	2.8	63
86	Topical Delivery of Protein and Peptide Using Novel Cell Penetrating Peptide IMT-P8. Scientific Reports, 2016, 6, 26278.	3.3	61
87	ParaPep: a web resource for experimentally validated antiparasitic peptide sequences and their structures. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau051-bau051.	3.0	60
88	Computer-aided prediction of antigen presenting cell modulators for designing peptide-based vaccine adjuvants. Journal of Translational Medicine, 2018, 16, 181.	4.4	60
89	GPCRsclass: a web tool for the classification of amine type of G-protein-coupled receptors. Nucleic Acids Research, 2005, 33, W143-W147.	14.5	59
90	PHDcleav: a SVM based method for predicting human Dicer cleavage sites using sequence and secondary structure of miRNA precursors. BMC Bioinformatics, 2013, 14, S9.	2.6	59

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91	Prediction of Antitubercular Peptides From Sequence Information Using Ensemble Classifier and Hybrid Features. Frontiers in Pharmacology, 2018, 9, 954.	3.5	59
92	Prediction of guide strand of microRNAs from its sequence and secondary structure. BMC Bioinformatics, 2009, 10, 105.	2.6	58
93	AntigenDB: an immunoinformatics database of pathogen antigens. Nucleic Acids Research, 2010, 38, D847-D853.	14.5	58
94	dbEM: A database of epigenetic modifiers curated from cancerous and normal genomes. Scientific Reports, 2016, 6, 19340.	3.3	58
95	Prediction of Cell-Penetrating Potential of Modified Peptides Containing Natural and Chemically Modified Residues. Frontiers in Microbiology, 2018, 9, 725.	3.5	58
96	COPid: composition based protein identification. In Silico Biology, 2008, 8, 121-8.	0.9	58
97	Prediction of cytochrome P450 isoform responsible for metabolizing a drug molecule. BMC Pharmacology, 2010, 10, 8.	0.4	57
98	Genome Sequence of the Oleaginous Red Yeast Rhodosporidium toruloides MTCC 457. Eukaryotic Cell, 2012, 11, 1083-1084.	3.4	57
99	Prediction and Analysis of Skin Cancer Progression using Genomics Profiles of Patients. Scientific Reports, 2019, 9, 15790.	3.3	57
100	Computer-Aided Virtual Screening and Designing of Cell-Penetrating Peptides. Methods in Molecular Biology, 2015, 1324, 59-69.	0.9	56
101	Application of Machine Learning Techniques in Predicting MHC Binders. Methods in Molecular Biology, 2007, 409, 201-215.	0.9	55
102	Locating probable genes using Fourier transform approach. Bioinformatics, 2002, 18, 196-197.	4.1	54
103	Prediction of mitochondrial proteins of malaria parasite using split amino acid composition and PSSM profile. Amino Acids, 2010, 39, 101-110.	2.7	54
104	Prioritization of anticancer drugs against a cancer using genomic features of cancer cells: A step towards personalized medicine. Scientific Reports, 2016, 6, 23857.	3.3	54
105	Prediction of GTP interacting residues, dipeptides and tripeptides in a protein from its evolutionary information. BMC Bioinformatics, 2010, 11, 301.	2.6	53
106	Machine learning competition in immunology â€“ Prediction of HLA class I binding peptides. Journal of Immunological Methods, 2011, 374, 1-4.	1.4	53
107	Prediction of Î±-turns in proteins using PSI-BLAST profiles and secondary structure information. Proteins: Structure, Function and Bioinformatics, 2004, 55, 83-90.	2.6	52
108	ProCarDB: a database of bacterial carotenoids. BMC Microbiology, 2016, 16, 96.	3.3	52

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109	Correlation and prediction of gene expression level from amino acid and dipeptide composition of its protein. BMC Bioinformatics, 2005, 6, 59.	2.6	51
110	AntiAngioPred: A Server for Prediction of Anti-Angiogenic Peptides. PLoS ONE, 2015, 10, e0136990.	2.5	51
111	ZikaVR: An Integrated Zika Virus Resource for Genomics, Proteomics, Phylogenetic and Therapeutic Analysis. Scientific Reports, 2016, 6, 32713.	3.3	49
112	In Silico Tools and Databases for Designing Peptide-Based Vaccine and Drugs. Advances in Protein Chemistry and Structural Biology, 2018, 112, 221-263.	2.3	49
113	Identification of Platform-Independent Diagnostic Biomarker Panel for Hepatocellular Carcinoma Using Large-Scale Transcriptomics Data. Frontiers in Genetics, 2019, 10, 1306.	2.3	49
114	ESLpred2: improved method for predicting subcellular localization of eukaryotic proteins. BMC Bioinformatics, 2008, 9, 503.	2.6	48
115	DrugMint: a webserver for predicting and designing of drug-like molecules. Biology Direct, 2013, 8, 28.	4.6	47
116	AntiTbPdb: a knowledgebase of anti-tubercular peptides. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	47
117	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. Cell Reports Medicine, 2021, 2, 100323.	6.5	47
118	An evaluation of Â-turn prediction methods. Bioinformatics, 2002, 18, 1508-1514.	4.1	46
119	Prediction of Polyadenylation Signals in Human DNA Sequences using Nucleotide Frequencies. In Silico Biology, 2009, 9, 135-148.	0.9	46
120	Classification of early and late stage liver hepatocellular carcinoma patients from their genomics and epigenomics profiles. PLoS ONE, 2019, 14, e0221476.	2.5	46
121	Quantification of the variation in percentage identity for protein sequence alignments. BMC Bioinformatics, 2006, 7, 415.	2.6	45
122	BIAdb: A curated database of benzylisoquinoline alkaloids. BMC Pharmacology, 2010, 10, 4.	0.4	45
123	Designing of Highly Effective Complementary and Mismatch siRNAs for Silencing a Gene. PLoS ONE, 2011, 6, e23443.	2.5	43
124	HaptenDB: a comprehensive database of haptens, carrier proteins and anti-hapten antibodies. Bioinformatics, 2006, 22, 253-255.	4.1	42
125	Open source drug discoveryâ€“ A new paradigm of collaborative research in tuberculosis drug development. Tuberculosis, 2011, 91, 479-86.	1.9	42
126	RSLpred: an integrative system for predicting subcellular localization of rice proteins combining compositional and evolutionary information. Proteomics, 2009, 9, 2324-2342.	2.2	40

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127	Herceptin Resistance Database for Understanding Mechanism of Resistance in Breast Cancer Patients. Scientific Reports, 2014, 4, 4483.	3.3	40
128	FermFooDb: A database of bioactive peptides derived from fermented foods. Heliyon, 2021, 7, e06668.	3.2	40
129	TAPPred Prediction of TAP-Binding Peptides in Antigens. Methods in Molecular Biology, 2007, 409, 381-386.	0.9	39
130	Prediction of anticancer molecules using hybrid model developed on molecules screened against NCI-60 cancer cell lines. BMC Cancer, 2016, 16, 77.	2.6	39
131	BTXpred: prediction of bacterial toxins. In Silico Biology, 2007, 7, 405-12.	0.9	39
132	Prediction of Promiscuous and High-Affinity Mutated MHC Binders. Hybridoma, 2003, 22, 229-234.	0.4	38
133	Prediction of Antimicrobial Potential of a Chemically Modified Peptide From Its Tertiary Structure. Frontiers in Microbiology, 2018, 9, 2551.	3.5	38
134	Identification of Proteins Secreted by Malaria Parasite into Erythrocyte using SVM and PSSM profiles. BMC Bioinformatics, 2008, 9, 201.	2.6	37
135	A Simple Approach for Predicting Protein-Protein Interactions. Current Protein and Peptide Science, 2010, 11, 589-600.	1.4	37
136	HIVsirDB: A Database of HIV Inhibiting siRNAs. PLoS ONE, 2011, 6, e25917.	2.5	37
137	A Web Resource for Designing Subunit Vaccine Against Major Pathogenic Species of Bacteria. Frontiers in Immunology, 2018, 9, 2280.	4.8	36
138	NeuroPIpred: a tool to predict, design and scan insect neuropeptides. Scientific Reports, 2019, 9, 5129.	3.3	36
139	Prediction of polyadenylation signals in human DNA sequences using nucleotide frequencies. In Silico Biology, 2009, 9, 135-48.	0.9	36
140	Identification and characterization of novel protein-derived arginine-rich cell-penetrating peptides. European Journal of Pharmaceutics and Biopharmaceutics, 2015, 89, 93-106.	4.3	35
141	VaccineDA: Prediction, design and genome-wide screening of oligodeoxynucleotide-based vaccine adjuvants. Scientific Reports, 2015, 5, 12478.	3.3	34
142	A machine learning based method for the prediction of secretory proteins using amino acid composition, their order and similarity-search. In Silico Biology, 2008, 8, 129-40.	0.9	34
143	PRRDB: A comprehensive database of Pattern-Recognition Receptors and their ligands. BMC Genomics, 2008, 9, 180.	2.8	33
144	Prediction of nuclear proteins using SVM and HMM models. BMC Bioinformatics, 2009, 10, 22.	2.6	33

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145	Computing Skin Cutaneous Melanoma Outcome From the HLA-Alleles and Clinical Characteristics. Frontiers in Genetics, 2020, 11, 221.	2.3	33
146	Prediction of FAD interacting residues in a protein from its primary sequence using evolutionary information. BMC Bioinformatics, 2010, 11, S48.	2.6	32
147	QSAR-Based Models for Designing Quinazoline/Imidazothiazoles/Pyrazolopyrimidines Based Inhibitors against Wild and Mutant EGFR. PLoS ONE, 2014, 9, e101079.	2.5	32
148	Hmrbase: a database of hormones and their receptors. BMC Genomics, 2009, 10, 307.	2.8	31
149	Ki DoQ: using docking based energy scores to develop ligand based model for predicting antibacterials. BMC Bioinformatics, 2010, 11, 125.	2.6	31
150	A web server for predicting inhibitors against bacterial target GlmU protein. BMC Pharmacology, 2011, 11, 5.	0.4	31
151	NAGbinder: An approach for identifying Nâ€acetylglucosamine interacting residues of a protein from its primary sequence. Protein Science, 2020, 29, 201-210.	7.6	31
152	CancerPDF: A repository of cancer-associated peptidome found in human biofluids. Scientific Reports, 2017, 7, 1511.	3.3	30
153	Dockingâ€based approach for identification of mutations that disrupt binding between Bclâ€2 and Bax proteins: Inducing apoptosis in cancer cells. Molecular Genetics & Genomic Medicine, 2019, 7, e910.	1.2	30
154	Branching of the p-nitrophenol (PNP) degradation pathway in burkholderia sp. Strain SJ98: Evidences from genetic characterization of PNP gene cluster. AMB Express, 2012, 2, 30.	3.0	29
155	Method for Determining the Affinity of Monoclonal Antibody Using Non-Competitive Elisa: A Computer Program. Journal of Immunoassay, 1994, 15, 115-128.	0.3	28
156	CyclinPred: A SVM-Based Method for Predicting Cyclin Protein Sequences. PLoS ONE, 2008, 3, e2605.	2.5	28
157	ccPDB: compilation and creation of data sets from Protein Data Bank. Nucleic Acids Research, 2012, 40, D486-D489.	14.5	28
158	Prediction of uridine modifications in tRNA sequences. BMC Bioinformatics, 2014, 15, 326.	2.6	28
159	PCMdb: Pancreatic Cancer Methylation Database. Scientific Reports, 2014, 4, 4197.	3.3	28
160	PRRDB 2.0: a comprehensive database of pattern-recognition receptors and their ligands. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	27
161	B3Pred: A Random-Forest-Based Method for Predicting and Designing Bloodâ€“Brain Barrier Penetrating Peptides. Pharmaceutics, 2021, 13, 1237.	4.5	27
162	Identification of Mannose Interacting Residues Using Local Composition. PLoS ONE, 2011, 6, e24039.	2.5	27

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163	Analysis and prediction of cancerlectins using evolutionary and domain information. BMC Research Notes, 2011, 4, 237.	1.4	26
164	ProGlycProt: a repository of experimentally characterized prokaryotic glycoproteins. Nucleic Acids Research, 2012, 40, D388-D393.	14.5	26
165	In silico analysis to identify vaccine candidates common to multiple serotypes of Shigella and evaluation of their immunogenicity. PLoS ONE, 2017, 12, e0180505.	2.5	26
166	Prediction of Specificity and Cross-Reactivity of Kinase Inhibitors. Letters in Drug Design and Discovery, 2011, 8, 223-228.	0.7	26
167	VGIchan: Prediction and Classification of Voltage-Gated Ion Channels. Genomics, Proteomics and Bioinformatics, 2006, 4, 253-258.	6.9	25
168	Prediction of subcellular localization of proteins using pairwise sequence alignment and support vector machine. Pattern Recognition Letters, 2006, 27, 996-1001.	4.2	25
169	Open Source Software and Web Services for Designing Therapeutic Molecules. Current Topics in Medicinal Chemistry, 2013, 13, 1172-1191.	2.1	25
170	A Web-Based Platform on Coronavirus Disease-19 to Maintain Predicted Diagnostic, Drug, and Vaccine Candidates. Monoclonal Antibodies in Immunodiagnosis and Immunotherapy, 2020, 39, 204-216.	1.6	25
171	Designing of inhibitors against drug tolerant Mycobacterium tuberculosis (H37Rv). Chemistry Central Journal, 2013, 7, 49.	2.6	24
172	Identification of protein-interacting nucleotides in a RNA sequence using composition profile of tri-nucleotides. Genomics, 2015, 105, 197-203.	2.9	24
173	Crowdsourcing digital health measures to predict Parkinsonâ€™s disease severity: the Parkinsonâ€™s Disease Digital Biomarker DREAM Challenge. Npj Digital Medicine, 2021, 4, 53.	10.9	24
174	BetaTPred: prediction of Â-TURNS in a protein using statistical algorithms. Bioinformatics, 2002, 18, 498-499.	4.1	23
175	Prediction of vitamin interacting residues in a vitamin binding protein using evolutionary information. BMC Bioinformatics, 2013, 14, 44.	2.6	23
176	Genes Involved in Degradation of para-Nitrophenol Are Differentially Arranged in Form of Non-Contiguous Gene Clusters in Burkholderia sp. strain SJ98. PLoS ONE, 2013, 8, e84766.	2.5	23
177	Cell-penetrating peptide and antibiotic combination therapy: a potential alternative to combat drug resistance in methicillin-resistant Staphylococcus aureus. Applied Microbiology and Biotechnology, 2016, 100, 4073-4083.	3.6	21
178	CancerLivER: a database of liver cancer gene expression resources and biomarkers. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	21
179	A Web-Based Platform for Designing Vaccines against Existing and Emerging Strains of Mycobacterium tuberculosis. PLoS ONE, 2016, 11, e0153771.	2.5	21
180	CytoPred: a server for prediction and classification of cytokines. Protein Engineering, Design and Selection, 2008, 21, 279-282.	2.1	20

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181	Virtual Screening of potential drug-like inhibitors against Lysine/DAP pathway of Mycobacterium tuberculosis. BMC Bioinformatics, 2010, 11, S53.	2.6	20
182	Assessing therapeutic potential of molecules: molecular property diagnostic suite for tuberculosis $$(mathbf{MPDS}^{mathbf{TB}})$$ (MPDS TB). Journal of Chemical Sciences, 2017, 129, 515-531.	1.5	20
183	ChAlPred: A web server for prediction of allergenicity of chemical compounds. Computers in Biology and Medicine, 2021, 136, 104746.	7.0	20
184	Designing of promiscuous inhibitors against pancreatic cancer cell lines. Scientific Reports, 2014, 4, 4668.	3.3	19
185	In Silico Analysis of Gene Expression Change Associated with Copy Number of Enhancers in Pancreatic Adenocarcinoma. International Journal of Molecular Sciences, 2019, 20, 3582.	4.1	19
186	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Systems, 2020, 11, 186-195.e9.	6.2	19
187	A Method for Predicting Hemolytic Potency of Chemically Modified Peptides From Its Structure. Frontiers in Pharmacology, 2020, 11, 54.	3.5	19
188	IL13Pred: A method for predicting immunoregulatory cytokine IL-13 inducing peptides. Computers in Biology and Medicine, 2022, 143, 105297.	7.0	19
189	Prediction of neurotoxins based on their function and source. In Silico Biology, 2007, 7, 369-87.	0.9	19
190	Support Vector Machine Based Prediction of Glutathione S-Transferase Proteins. Protein and Peptide Letters, 2007, 14, 575-580.	0.9	18
191	Genome Sequence of the Nitroaromatic Compound-Degrading Bacterium Burkholderia sp. Strain SJ98. Journal of Bacteriology, 2012, 194, 3286-3286.	2.2	18
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