

Gajendra P S Raghava

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6655351/gajendra-p-s-raghava-publications-by-citations.pdf>
Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

296 papers	14,589 citations	63 h-index	111 g-index
336 ext. papers	18,164 ext. citations	5.5 avg, IF	6.99 L-index

#	Paper	IF	Citations
296	Prediction of continuous B-cell epitopes in an antigen using recurrent neural network. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 40-8	4.2	761
295	ProPred: prediction of HLA-DR binding sites. <i>Bioinformatics</i> , 2001 , 17, 1236-7	7.2	667
294	In silico approach for predicting toxicity of peptides and proteins. <i>PLoS ONE</i> , 2013 , 8, e73957	3.7	600
293	AlgPred: prediction of allergenic proteins and mapping of IgE epitopes. <i>Nucleic Acids Research</i> , 2006 , 34, W202-9	20.1	440
292	ProPred1: prediction of promiscuous MHC Class-I binding sites. <i>Bioinformatics</i> , 2003 , 19, 1009-14	7.2	348
291	Designing of interferon-gamma inducing MHC class-II binders. <i>Biology Direct</i> , 2013 , 8, 30	7.2	265
290	THPdb: Database of FDA-approved peptide and protein therapeutics. <i>PLoS ONE</i> , 2017 , 12, e0181748	3.7	243
289	Prediction of CTL epitopes using QM, SVM and ANN techniques. <i>Vaccine</i> , 2004 , 22, 3195-204	4.1	242
288	ESLpred: SVM-based method for subcellular localization of eukaryotic proteins using dipeptide composition and PSI-BLAST. <i>Nucleic Acids Research</i> , 2004 , 32, W414-9	20.1	233
287	Prediction of RNA binding sites in a protein using SVM and PSSM profile. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 189-94	4.2	212
286	Identification of conformational B-cell Epitopes in an antigen from its primary sequence. <i>Immunome Research</i> , 2010 , 6, 6		186
285	Analysis and prediction of antibacterial peptides. <i>BMC Bioinformatics</i> , 2007 , 8, 263	3.6	181
284	Identification of DNA-binding proteins using support vector machines and evolutionary profiles. <i>BMC Bioinformatics</i> , 2007 , 8, 463	3.6	174
283	Improved method for linear B-cell epitope prediction using antigen's primary sequence. <i>PLoS ONE</i> , 2013 , 8, e62216	3.7	171
282	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. <i>Journal of Molecular Recognition</i> , 2007 , 20, 75-82	2.6	171
281	In silico approaches for designing highly effective cell penetrating peptides. <i>Journal of Translational Medicine</i> , 2013 , 11, 74	8.5	170
280	NPACT: Naturally Occurring Plant-based Anti-cancer Compound-Activity-Target database. <i>Nucleic Acids Research</i> , 2013 , 41, D1124-9	20.1	170

279	CancerPPD: a database of anticancer peptides and proteins. <i>Nucleic Acids Research</i> , 2015 , 43, D837-43	20.1	169
278	Support vector machine-based method for subcellular localization of human proteins using amino acid compositions, their order, and similarity search. <i>Journal of Biological Chemistry</i> , 2005 , 280, 14427-32	5.4	169
277	CPPsite 2.0: a repository of experimentally validated cell-penetrating peptides. <i>Nucleic Acids Research</i> , 2016 , 44, D1098-103	20.1	167
276	MHCBN: a comprehensive database of MHC binding and non-binding peptides. <i>Bioinformatics</i> , 2003 , 19, 665-6	7.2	167
275	PSLPred: prediction of subcellular localization of bacterial proteins. <i>Bioinformatics</i> , 2005 , 21, 2522-4	7.2	161
274	PEPstr: a de novo method for tertiary structure prediction of small bioactive peptides. <i>Protein and Peptide Letters</i> , 2007 , 14, 626-31	1.9	152
273	In silico models for designing and discovering novel anticancer peptides. <i>Scientific Reports</i> , 2013 , 3, 2984	4.9	149
272	BcePred: Prediction of Continuous B-Cell Epitopes in Antigenic Sequences Using Physico-chemical Properties. <i>Lecture Notes in Computer Science</i> , 2004 , 197-204	0.9	147
271	Classification of nuclear receptors based on amino acid composition and dipeptide composition. <i>Journal of Biological Chemistry</i> , 2004 , 279, 23262-6	5.4	145
270	Bcipep: a database of B-cell epitopes. <i>BMC Genomics</i> , 2005 , 6, 79	4.5	145
269	In silico platform for prediction of N-, O- and C-glycosites in eukaryotic protein sequences. <i>PLoS ONE</i> , 2013 , 8, e67008	3.7	142
268	OXBench: a benchmark for evaluation of protein multiple sequence alignment accuracy. <i>BMC Bioinformatics</i> , 2003 , 4, 47	3.6	139
267	AntiBP2: improved version of antibacterial peptide prediction. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S19	3.6	132
266	GPCRpred: an SVM-based method for prediction of families and subfamilies of G-protein coupled receptors. <i>Nucleic Acids Research</i> , 2004 , 32, W383-9	20.1	129
265	SVM based method for predicting HLA-DRB1*0401 binding peptides in an antigen sequence. <i>Bioinformatics</i> , 2004 , 20, 421-3	7.2	128
264	CPPsite: a curated database of cell penetrating peptides. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bas015	5	122
263	Prediction of beta-turns in proteins from multiple alignment using neural network. <i>Protein Science</i> , 2003 , 12, 627-34	6.3	117
262	Spectral Repeat Finder (SRF): identification of repetitive sequences using Fourier transformation. <i>Bioinformatics</i> , 2004 , 20, 1405-12	7.2	116

261	Analysis and prediction of affinity of TAP binding peptides using cascade SVM. <i>Protein Science</i> , 2004 , 13, 596-607	6.3	114
260	Prediction of IL4 inducing peptides. <i>Clinical and Developmental Immunology</i> , 2013 , 2013, 263952		111
259	lncRNome: a comprehensive knowledgebase of human long noncoding RNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat034	5	110
258	Support Vector Machine-based method for predicting subcellular localization of mycobacterial proteins using evolutionary information and motifs. <i>BMC Bioinformatics</i> , 2007 , 8, 337	3.6	104
257	PEPstrMOD: structure prediction of peptides containing natural, non-natural and modified residues. <i>Biology Direct</i> , 2015 , 10, 73	7.2	100
256	A hybrid approach for predicting promiscuous MHC class I restricted T cell epitopes. <i>Journal of Biosciences</i> , 2007 , 32, 31-42	2.3	98
255	Computer-aided designing of immunosuppressive peptides based on IL-10 inducing potential. <i>Scientific Reports</i> , 2017 , 7, 42851	4.9	96
254	AHTPDB: a comprehensive platform for analysis and presentation of antihypertensive peptides. <i>Nucleic Acids Research</i> , 2015 , 43, D956-62	20.1	96
253	SATPdb: a database of structurally annotated therapeutic peptides. <i>Nucleic Acids Research</i> , 2016 , 44, D1119-26	20.1	89
252	Machine learning techniques in disease forecasting: a case study on rice blast prediction. <i>BMC Bioinformatics</i> , 2006 , 7, 485	3.6	89
251	SVM based prediction of RNA-binding proteins using binding residues and evolutionary information. <i>Journal of Molecular Recognition</i> , 2011 , 24, 303-13	2.6	88
250	Hemolytik: a database of experimentally determined hemolytic and non-hemolytic peptides. <i>Nucleic Acids Research</i> , 2014 , 42, D444-9	20.1	85
249	Prediction of transmembrane regions of beta-barrel proteins using ANN- and SVM-based methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 11-8	4.2	85
248	Identification of ATP binding residues of a protein from its primary sequence. <i>BMC Bioinformatics</i> , 2009 , 10, 434	3.6	82
247	An in silico platform for predicting, screening and designing of antihypertensive peptides. <i>Scientific Reports</i> , 2015 , 5, 12512	4.9	80
246	Prediction of mitochondrial proteins using support vector machine and hidden Markov model. <i>Journal of Biological Chemistry</i> , 2006 , 281, 5357-63	5.4	80
245	A neural network method for prediction of beta-turn types in proteins using evolutionary information. <i>Bioinformatics</i> , 2004 , 20, 2751-8	7.2	80
244	TumorHoPe: a database of tumor homing peptides. <i>PLoS ONE</i> , 2012 , 7, e35187	3.7	80

243	CancerDR: cancer drug resistance database. <i>Scientific Reports</i> , 2013 , 3, 1445	4.9	79
242	Computer-aided biotechnology: from immuno-informatics to reverse vaccinology. <i>Trends in Biotechnology</i> , 2008 , 26, 190-200	15.1	79
241	A Web Server and Mobile App for Computing Hemolytic Potency of Peptides. <i>Scientific Reports</i> , 2016 , 6, 22843	4.9	78
240	OxDBase: a database of oxygenases involved in biodegradation. <i>BMC Research Notes</i> , 2009 , 2, 67	2.3	78
239	PEPlife: A Repository of the Half-life of Peptides. <i>Scientific Reports</i> , 2016 , 6, 36617	4.9	76
238	Real value prediction of solvent accessibility in proteins using multiple sequence alignment and secondary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 318-24	4.2	73
237	Pcleavage: an SVM based method for prediction of constitutive proteasome and immunoproteasome cleavage sites in antigenic sequences. <i>Nucleic Acids Research</i> , 2005 , 33, W202-7	20.1	71
236	VICMpred: an SVM-based method for the prediction of functional proteins of Gram-negative bacteria using amino acid patterns and composition. <i>Genomics, Proteomics and Bioinformatics</i> , 2006 , 4, 42-7	6.5	68
235	Prediction and classification of ncRNAs using structural information. <i>BMC Genomics</i> , 2014 , 15, 127	4.5	63
234	MHCBN 4.0: A database of MHC/TAP binding peptides and T-cell epitopes. <i>BMC Research Notes</i> , 2009 , 2, 61	2.3	63
233	A neural-network based method for prediction of gamma-turns in proteins from multiple sequence alignment. <i>Protein Science</i> , 2003 , 12, 923-9	6.3	61
232	Approach for Prediction of Antifungal Peptides. <i>Frontiers in Microbiology</i> , 2018 , 9, 323	5.7	60
231	Tumor homing peptides as molecular probes for cancer therapeutics, diagnostics and theranostics. <i>Current Medicinal Chemistry</i> , 2014 , 21, 2367-91	4.3	60
230	Identification of B-cell epitopes in an antigen for inducing specific class of antibodies. <i>Biology Direct</i> , 2013 , 8, 27	7.2	59
229	CCDB: a curated database of genes involved in cervix cancer. <i>Nucleic Acids Research</i> , 2011 , 39, D975-9	20.1	59
228	Prediction methods for B-cell epitopes. <i>Methods in Molecular Biology</i> , 2007 , 409, 387-94	1.4	56
227	Anticancer properties of a defensin like class IIb bacteriocin Laterosporulin10. <i>Scientific Reports</i> , 2017 , 7, 46541	4.9	54
226	Gene expression-based biomarkers for discriminating early and late stage of clear cell renal cancer. <i>Scientific Reports</i> , 2017 , 7, 44997	4.9	54

225	BhairPred: prediction of beta-hairpins in a protein from multiple alignment information using ANN and SVM techniques. <i>Nucleic Acids Research</i> , 2005 , 33, W154-9	20.1	53
224	Benchmarking of different molecular docking methods for protein-peptide docking. <i>BMC Bioinformatics</i> , 2019 , 19, 426	3.6	52
223	GPCRclass: a web tool for the classification of amine type of G-protein-coupled receptors. <i>Nucleic Acids Research</i> , 2005 , 33, W143-7	20.1	52
222	Genome sequence of the oleaginous red yeast <i>Rhodospiridium toruloides</i> MTCC 457. <i>Eukaryotic Cell</i> , 2012 , 11, 1083-4		51
221	Identification of NAD interacting residues in proteins. <i>BMC Bioinformatics</i> , 2010 , 11, 160	3.6	50
220	Novel in silico tools for designing peptide-based subunit vaccines and immunotherapeutics. <i>Briefings in Bioinformatics</i> , 2017 , 18, 467-478	13.4	49
219	Prediction of cytochrome P450 isoform responsible for metabolizing a drug molecule. <i>BMC Pharmacology</i> , 2010 , 10, 8		49
218	Computational approach for designing tumor homing peptides. <i>Scientific Reports</i> , 2013 , 3, 1607	4.9	48
217	AntigenDB: an immunoinformatics database of pathogen antigens. <i>Nucleic Acids Research</i> , 2010 , 38, D847-53	47.53	48
216	Prediction of mitochondrial proteins of malaria parasite using split amino acid composition and PSSM profile. <i>Amino Acids</i> , 2010 , 39, 101-10	3.5	47
215	QSAR based model for discriminating EGFR inhibitors and non-inhibitors using Random forest. <i>Biology Direct</i> , 2015 , 10, 10	7.2	45
214	Locating probable genes using Fourier transform approach. <i>Bioinformatics</i> , 2002 , 18, 196-7	7.2	45
213	AntiCP 2.0: an updated model for predicting anticancer peptides. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	45
212	GlycoPP: a webserver for prediction of N- and O-glycosites in prokaryotic protein sequences. <i>PLoS ONE</i> , 2012 , 7, e40155	3.7	44
211	Prediction of alpha-turns in proteins using PSI-BLAST profiles and secondary structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 83-90	4.2	44
210	Designing of peptides with desired half-life in intestine-like environment. <i>BMC Bioinformatics</i> , 2014 , 15, 282	3.6	43
209	ParaPep: a web resource for experimentally validated antiparasitic peptide sequences and their structures. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014,	5	42
208	ESLpred2: improved method for predicting subcellular localization of eukaryotic proteins. <i>BMC Bioinformatics</i> , 2008 , 9, 503	3.6	41

207	An evaluation of beta-turn prediction methods. <i>Bioinformatics</i> , 2002 , 18, 1508-14	7.2	41
206	ProCarDB: a database of bacterial carotenoids. <i>BMC Microbiology</i> , 2016 , 16, 96	4.5	41
205	ZikaVR: An Integrated Zika Virus Resource for Genomics, Proteomics, Phylogenetic and Therapeutic Analysis. <i>Scientific Reports</i> , 2016 , 6, 32713	4.9	40
204	Computer-aided prediction of antigen presenting cell modulators for designing peptide-based vaccine adjuvants. <i>Journal of Translational Medicine</i> , 2018 , 16, 181	8.5	40
203	Application of machine learning techniques in predicting MHC binders. <i>Methods in Molecular Biology</i> , 2007 , 409, 201-15	1.4	40
202	Topical Delivery of Protein and Peptide Using Novel Cell Penetrating Peptide IMT-P8. <i>Scientific Reports</i> , 2016 , 6, 26278	4.9	39
201	Prediction of Antitubercular Peptides From Sequence Information Using Ensemble Classifier and Hybrid Features. <i>Frontiers in Pharmacology</i> , 2018 , 9, 954	5.6	39
200	HaptenDB: a comprehensive database of haptens, carrier proteins and anti-hapten antibodies. <i>Bioinformatics</i> , 2006 , 22, 253-5	7.2	39
199	Peptide toxicity prediction. <i>Methods in Molecular Biology</i> , 2015 , 1268, 143-57	1.4	39
198	Correlation and prediction of gene expression level from amino acid and dipeptide composition of its protein. <i>BMC Bioinformatics</i> , 2005 , 6, 59	3.6	38
197	Prioritization of anticancer drugs against a cancer using genomic features of cancer cells: A step towards personalized medicine. <i>Scientific Reports</i> , 2016 , 6, 23857	4.9	38
196	Prediction of guide strand of microRNAs from its sequence and secondary structure. <i>BMC Bioinformatics</i> , 2009 , 10, 105	3.6	37
195	Prediction of Polyadenylation Signals in Human DNA Sequences using Nucleotide Frequencies. <i>In Silico Biology</i> , 2009 , 9, 135-148	2	37
194	Prediction of promiscuous and high-affinity mutated MHC binders. <i>Hybridoma</i> , 2003 , 22, 229-34		37
193	Designing of highly effective complementary and mismatch siRNAs for silencing a gene. <i>PLoS ONE</i> , 2011 , 6, e23443	3.7	36
192	AlgPred 2.0: an improved method for predicting allergenic proteins and mapping of IgE epitopes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	36
191	In silico approaches for predicting the half-life of natural and modified peptides in blood. <i>PLoS ONE</i> , 2018 , 13, e0196829	3.7	35
190	RSLpred: an integrative system for predicting subcellular localization of rice proteins combining compositional and evolutionary information. <i>Proteomics</i> , 2009 , 9, 2324-42	4.8	35

189	Prediction of GTP interacting residues, dipeptides and tripeptides in a protein from its evolutionary information. <i>BMC Bioinformatics</i> , 2010 , 11, 301	3.6	35
188	Computer-Aided Virtual Screening and Designing of Cell-Penetrating Peptides. <i>Methods in Molecular Biology</i> , 2015 , 1324, 59-69	1.4	35
187	DrugMint: a webserver for predicting and designing of drug-like molecules. <i>Biology Direct</i> , 2013 , 8, 28	7.2	34
186	BIADB: a curated database of benzylisoquinoline alkaloids. <i>BMC Pharmacology</i> , 2010 , 10, 4		34
185	HIVsirDB: a database of HIV inhibiting siRNAs. <i>PLoS ONE</i> , 2011 , 6, e25917	3.7	34
184	dbEM: A database of epigenetic modifiers curated from cancerous and normal genomes. <i>Scientific Reports</i> , 2016 , 6, 19340	4.9	34
183	Prediction of Cell-Penetrating Potential of Modified Peptides Containing Natural and Chemically Modified Residues. <i>Frontiers in Microbiology</i> , 2018 , 9, 725	5.7	33
182	Herceptin resistance database for understanding mechanism of resistance in breast cancer patients. <i>Scientific Reports</i> , 2014 , 4, 4483	4.9	33
181	AntiAngioPred: A Server for Prediction of Anti-Angiogenic Peptides. <i>PLoS ONE</i> , 2015 , 10, e0136990	3.7	33
180	In Silico Tools and Databases for Designing Peptide-Based Vaccine and Drugs. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018 , 112, 221-263	5.3	32
179	Prediction and Analysis of Skin Cancer Progression using Genomics Profiles of Patients. <i>Scientific Reports</i> , 2019 , 9, 15790	4.9	32
178	Open source drug discovery--a new paradigm of collaborative research in tuberculosis drug development. <i>Tuberculosis</i> , 2011 , 91, 479-86	2.6	32
177	A simple approach for predicting protein-protein interactions. <i>Current Protein and Peptide Science</i> , 2010 , 11, 589-600	2.8	32
176	Quantification of the variation in percentage identity for protein sequence alignments. <i>BMC Bioinformatics</i> , 2006 , 7, 415	3.6	32
175	BTXpred: prediction of bacterial toxins. <i>In Silico Biology</i> , 2007 , 7, 405-12	2	32
174	PHDcleav: a SVM based method for predicting human Dicer cleavage sites using sequence and secondary structure of miRNA precursors. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 14, S9	3.6	31
173	TAPPred prediction of TAP-binding peptides in antigens. <i>Methods in Molecular Biology</i> , 2007 , 409, 381-6	1.4	31
172	COPid: composition based protein identification. <i>In Silico Biology</i> , 2008 , 8, 121-8	2	31

171	Prediction of nuclear proteins using SVM and HMM models. <i>BMC Bioinformatics</i> , 2009 , 10, 22	3.6	30
170	Prediction of anticancer molecules using hybrid model developed on molecules screened against NCI-60 cancer cell lines. <i>BMC Cancer</i> , 2016 , 16, 77	4.8	30
169	Prediction of Antimicrobial Potential of a Chemically Modified Peptide From Its Tertiary Structure. <i>Frontiers in Microbiology</i> , 2018 , 9, 2551	5.7	30
168	Identification of proteins secreted by malaria parasite into erythrocyte using SVM and PSSM profiles. <i>BMC Bioinformatics</i> , 2008 , 9, 201	3.6	29
167	A machine learning based method for the prediction of secretory proteins using amino acid composition, their order and similarity-search. <i>In Silico Biology</i> , 2008 , 8, 129-40	2	28
166	Identification and characterization of novel protein-derived arginine-rich cell-penetrating peptides. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2015 , 89, 93-106	5.7	27
165	QSAR-based models for designing quinazoline/imidazothiazoles/pyrazolopyrimidines based inhibitors against wild and mutant EGFR. <i>PLoS ONE</i> , 2014 , 9, e101079	3.7	27
164	PRRDB: a comprehensive database of pattern-recognition receptors and their ligands. <i>BMC Genomics</i> , 2008 , 9, 180	4.5	27
163	Computer-aided prediction and design of IL-6 inducing peptides: IL-6 plays a crucial role in COVID-19. <i>Briefings in Bioinformatics</i> , 2021 , 22, 936-945	13.4	27
162	HumCFS: a database of fragile sites in human chromosomes. <i>BMC Genomics</i> , 2019 , 19, 985	4.5	26
161	AntiTbPdb: a knowledgebase of anti-tubercular peptides. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	26
160	KiDoQ: using docking based energy scores to develop ligand based model for predicting antibacterials. <i>BMC Bioinformatics</i> , 2010 , 11, 125	3.6	24
159	Prediction of FAD interacting residues in a protein from its primary sequence using evolutionary information. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S48	3.6	24
158	Branching of the p-nitrophenol (PNP) degradation pathway in burkholderia sp. Strain SJ98: Evidences from genetic characterization of PNP gene cluster. <i>AMB Express</i> , 2012 , 2, 30	4.1	23
157	A web server for predicting inhibitors against bacterial target GlmU protein. <i>BMC Pharmacology</i> , 2011 , 11, 5		23
156	Prediction of subcellular localization of proteins using pairwise sequence alignment and support vector machine. <i>Pattern Recognition Letters</i> , 2006 , 27, 996-1001	4.7	23
155	Method for determining the affinity of monoclonal antibody using non-competitive ELISA: a computer program. <i>Journal of Immunoassay</i> , 1994 , 15, 115-28		23
154	ProGlycProt: a repository of experimentally characterized prokaryotic glycoproteins. <i>Nucleic Acids Research</i> , 2012 , 40, D388-93	20.1	22

153	Hmrbase: a database of hormones and their receptors. <i>BMC Genomics</i> , 2009 , 10, 307	4.5	22
152	CyclinPred: a SVM-based method for predicting cyclin protein sequences. <i>PLoS ONE</i> , 2008 , 3, e2605	3.7	22
151	Identification of mannose interacting residues using local composition. <i>PLoS ONE</i> , 2011 , 6, e24039	3.7	22
150	A Web Resource for Designing Subunit Vaccine Against Major Pathogenic Species of Bacteria. <i>Frontiers in Immunology</i> , 2018 , 9, 2280	8.4	22
149	Prediction of polyadenylation signals in human DNA sequences using nucleotide frequencies. <i>In Silico Biology</i> , 2009 , 9, 135-48	2	22
148	NeuroPIpred: a tool to predict, design and scan insect neuropeptides. <i>Scientific Reports</i> , 2019 , 9, 5129	4.9	21
147	Prediction of uridine modifications in tRNA sequences. <i>BMC Bioinformatics</i> , 2014 , 15, 326	3.6	21
146	ccPDB: compilation and creation of data sets from Protein Data Bank. <i>Nucleic Acids Research</i> , 2012 , 40, D486-9	20.1	21
145	VGIchan: prediction and classification of voltage-gated ion channels. <i>Genomics, Proteomics and Bioinformatics</i> , 2006 , 4, 253-8	6.5	21
144	BetaTPred: prediction of beta-TURNS in a protein using statistical algorithms. <i>Bioinformatics</i> , 2002 , 18, 498-9	7.2	21
143	CancerPDF: A repository of cancer-associated peptidome found in human biofluids. <i>Scientific Reports</i> , 2017 , 7, 1511	4.9	20
142	VaccineDA: Prediction, design and genome-wide screening of oligodeoxynucleotide-based vaccine adjuvants. <i>Scientific Reports</i> , 2015 , 5, 12478	4.9	20
141	PCMdb: pancreatic cancer methylation database. <i>Scientific Reports</i> , 2014 , 4, 4197	4.9	19
140	Genes involved in degradation of para-nitrophenol are differentially arranged in form of non-contiguous gene clusters in Burkholderia sp. strain SJ98. <i>PLoS ONE</i> , 2013 , 8, e84766	3.7	19
139	Prediction of vitamin interacting residues in a vitamin binding protein using evolutionary information. <i>BMC Bioinformatics</i> , 2013 , 14, 44	3.6	18
138	Identification of Platform-Independent Diagnostic Biomarker Panel for Hepatocellular Carcinoma Using Large-Scale Transcriptomics Data. <i>Frontiers in Genetics</i> , 2019 , 10, 1306	4.5	18
137	A Web-Based Platform on Coronavirus Disease-19 to Maintain Predicted Diagnostic, Drug, and Vaccine Candidates. <i>Monoclonal Antibodies in Immunodiagnosis and Immunotherapy</i> , 2020 , 39, 204-216	1.9	17
136	Designing of inhibitors against drug tolerant Mycobacterium tuberculosis (H37Rv). <i>Chemistry Central Journal</i> , 2013 , 7, 49		17

135	Identification of protein-interacting nucleotides in a RNA sequence using composition profile of tri-nucleotides. <i>Genomics</i> , 2015 , 105, 197-203	4.3	17
134	Open source software and web services for designing therapeutic molecules. <i>Current Topics in Medicinal Chemistry</i> , 2013 , 13, 1172-91	3	17
133	Analysis and prediction of cancerlectins using evolutionary and domain information. <i>BMC Research Notes</i> , 2011 , 4, 237	2.3	17
132	Docking-based approach for identification of mutations that disrupt binding between Bcl-2 and Bax proteins: Inducing apoptosis in cancer cells. <i>Molecular Genetics & Genomic Medicine</i> , 2019 , 7, e910	2.3	16
131	Classification of early and late stage liver hepatocellular carcinoma patients from their genomics and epigenomics profiles. <i>PLoS ONE</i> , 2019 , 14, e0221476	3.7	16
130	PRRDB 2.0: a comprehensive database of pattern-recognition receptors and their ligands. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	16
129	Virtual Screening of potential drug-like inhibitors against Lysine/DAP pathway of Mycobacterium tuberculosis. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S53	3.6	16
128	Hybrid approach for predicting coreceptor used by HIV-1 from its V3 loop amino acid sequence. <i>PLoS ONE</i> , 2013 , 8, e61437	3.7	16
127	Prediction of neurotoxins based on their function and source. <i>In Silico Biology</i> , 2007 , 7, 369-87	2	16
126	Draft genome sequence of salt-tolerant yeast <i>Debaryomyces hansenii</i> var. <i>hansenii</i> MTCC 234. <i>Eukaryotic Cell</i> , 2012 , 11, 961-2		15
125	A Web-Based Platform for Designing Vaccines against Existing and Emerging Strains of Mycobacterium tuberculosis. <i>PLoS ONE</i> , 2016 , 11, e0153771	3.7	15
124	Computing Skin Cutaneous Melanoma Outcome From the HLA-Alleles and Clinical Characteristics. <i>Frontiers in Genetics</i> , 2020 , 11, 221	4.5	14
123	Bridging innate and adaptive antitumor immunity targeting glycans. <i>Journal of Biomedicine and Biotechnology</i> , 2010 , 2010, 354068		14
122	Genome sequence of the nitroaromatic compound-degrading Bacterium <i>Burkholderia</i> sp. strain SJ98. <i>Journal of Bacteriology</i> , 2012 , 194, 3286	3.5	14
121	CytoPred: a server for prediction and classification of cytokines. <i>Protein Engineering, Design and Selection</i> , 2008 , 21, 279-82	1.9	14
120	Fingerprinting method for phylogenetic classification and identification of microorganisms based on variation in 16S rRNA gene sequences. <i>BioTechniques</i> , 2000 , 29, 108-12, 114-6	2.5	14
119	Evaluation of protein dihedral angle prediction methods. <i>PLoS ONE</i> , 2014 , 9, e105667	3.7	14
118	Prediction of Specificity and Cross-Reactivity of Kinase Inhibitors. <i>Letters in Drug Design and Discovery</i> , 2011 , 8, 223-228	0.8	14

117	Cell-penetrating peptide and antibiotic combination therapy: a potential alternative to combat drug resistance in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 4073-83	5.7	13
116	EGFRIndb: epidermal growth factor receptor inhibitor database. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2014 , 14, 928-35	2.2	13
115	Assessing therapeutic potential of molecules: molecular property diagnostic suite for tuberculosis (($\mathbf{MPDS}^{\mathbf{TB}}$)). <i>Journal of Chemical Sciences</i> , 2017 , 129, 515-531	1.8	12
114	Designing of promiscuous inhibitors against pancreatic cancer cell lines. <i>Scientific Reports</i> , 2014 , 4, 4668	4.9	12
113	Prediction of Immunomodulatory potential of an RNA sequence for designing non-toxic siRNAs and RNA-based vaccine adjuvants. <i>Scientific Reports</i> , 2016 , 6, 20678	4.9	12
112	A web-based resource for designing therapeutics against Ebola Virus. <i>Scientific Reports</i> , 2016 , 6, 24782	4.9	12
111	Prediction and classification of aminoacyl tRNA synthetases using PROSITE domains. <i>BMC Genomics</i> , 2010 , 11, 507	4.5	12
110	Support vector machine based prediction of glutathione S-transferase proteins. <i>Protein and Peptide Letters</i> , 2007 , 14, 575-80	1.9	12
109	In silico analysis to identify vaccine candidates common to multiple serotypes of <i>Shigella</i> and evaluation of their immunogenicity. <i>PLoS ONE</i> , 2017 , 12, e0180505	3.7	12
108	Prediction of risk scores for colorectal cancer patients from the concentration of proteins involved in mitochondrial apoptotic pathway. <i>PLoS ONE</i> , 2019 , 14, e0217527	3.7	11
107	A Method for Predicting Hemolytic Potency of Chemically Modified Peptides From Its Structure. <i>Frontiers in Pharmacology</i> , 2020 , 11, 54	5.6	11
106	A web server for analysis, comparison and prediction of protein ligand binding sites. <i>Biology Direct</i> , 2016 , 11, 14	7.2	11
105	Draft genome sequence of the nitrophenol-degrading actinomycete <i>Rhodococcus imtechensis</i> RKJ300. <i>Journal of Bacteriology</i> , 2012 , 194, 3543	3.5	11
104	EGPred: prediction of eukaryotic genes using ab initio methods after combining with sequence similarity approaches. <i>Genome Research</i> , 2004 , 14, 1756-66	9.7	11
103	A Platform for Designing Genome-Based Personalized Immunotherapy or Vaccine against Cancer. <i>PLoS ONE</i> , 2016 , 11, e0166372	3.7	11
102	Searching and mapping of B-cell epitopes in Bcipep database. <i>Methods in Molecular Biology</i> , 2007 , 409, 113-24	1.4	11
101	Peptide Secondary Structure Prediction using Evolutionary Information		11
100	Computing wide range of protein/peptide features from their sequence and structure		11

99	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020 , 11, 186-195.e9	10.6	11
98	OvirusTdb: A database of oncolytic viruses for the advancement of therapeutics in cancer. <i>Virology</i> , 2020 , 548, 109-116	3.6	10
97	Draft Genome Sequence of the Type Species of the Genus Citrobacter, Citrobacter freundii MTCC 1658. <i>Genome Announcements</i> , 2013 , 1,		10
96	Draft Genome Sequence of the 2-Chloro-4-Nitrophenol-Degrading Bacterium Arthrobacter sp. Strain SJCon. <i>Genome Announcements</i> , 2013 , 1, e0005813		10
95	DPROT: prediction of disordered proteins using evolutionary information. <i>Amino Acids</i> , 2008 , 35, 599-605.	5.5	10
94	NAGbinder: An approach for identifying N-acetylglucosamine interacting residues of a protein from its primary sequence. <i>Protein Science</i> , 2020 , 29, 201-210	6.3	10
93	FermFoodDb: A database of bioactive peptides derived from fermented foods. <i>Heliyon</i> , 2021 , 7, e06668	3.6	10
92	In silico platform for predicting and initiating turns in a protein at desired locations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 910-21	4.2	9
91	Managing Drug Resistance in Cancer: Role of Cancer Informatics. <i>Methods in Molecular Biology</i> , 2016 , 1395, 299-312	1.4	9
90	Genome Sequence of the "Indian Bison Type" Biotype of Mycobacterium avium subsp. paratuberculosis Strain S5. <i>Genome Announcements</i> , 2013 , 1,		9
89	Computational Prediction of the Immunomodulatory Potential of RNA Sequences. <i>Methods in Molecular Biology</i> , 2017 , 1632, 75-90	1.4	9
88	Expression based biomarkers and models to classify early and late-stage samples of Papillary Thyroid Carcinoma. <i>PLoS ONE</i> , 2020 , 15, e0231629	3.7	8
87	Computer-aided designing of oncolytic viruses for overcoming translational challenges of cancer immunotherapy. <i>Drug Discovery Today</i> , 2020 , 25, 1198-1205	8.8	8
86	PolysacDB: a database of microbial polysaccharide antigens and their antibodies. <i>PLoS ONE</i> , 2012 , 7, e34613	3.7	8
85	Role of evolutionary information in prediction of aromatic-backbone NH interactions in proteins. <i>FEBS Letters</i> , 2004 , 564, 47-57	3.8	8
84	Crowdsourcing digital health measures to predict Parkinson's disease severity: the Parkinson's Disease Digital Biomarker DREAM Challenge. <i>Npj Digital Medicine</i> , 2021 , 4, 53	15.7	8
83	CancerEnD: A database of cancer associated enhancers. <i>Genomics</i> , 2020 , 112, 3696-3702	4.3	7
82	CancerLivER: a database of liver cancer gene expression resources and biomarkers. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	7

81	A Hybrid Model for Predicting Pattern Recognition Receptors Using Evolutionary Information. <i>Frontiers in Immunology</i> , 2020 , 11, 71	8.4	7
80	ApoCanD: Database of human apoptotic proteins in the context of cancer. <i>Scientific Reports</i> , 2016 , 6, 20797	4.9	7
79	BLAST-based structural annotation of protein residues using Protein Data Bank. <i>Biology Direct</i> , 2016 , 11, 4	7.2	7
78	Predicting sub-cellular localization of tRNA synthetases from their primary structures. <i>Amino Acids</i> , 2012 , 42, 1703-13	3.5	7
77	In silico models for B-cell epitope recognition and signaling. <i>Methods in Molecular Biology</i> , 2013 , 993, 129-38	1.4	7
76	Genome annotation of Burkholderia sp. SJ98 with special focus on chemotaxis genes. <i>PLoS ONE</i> , 2013 , 8, e70624	3.7	7
75	Prediction and classification of chemokines and their receptors. <i>Protein Engineering, Design and Selection</i> , 2009 , 22, 441-4	1.9	7
74	ToxiPred: A Server for Prediction of Aqueous Toxicity of Small Chemical Molecules in T. Pyriformis		7
73	Identification of prognostic biomarkers for major subtypes of non-small-cell lung cancer using genomic and clinical data. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020 , 146, 2743-2752	4.9	7
72	B3Pdb: an archive of blood-brain barrier-penetrating peptides. <i>Brain Structure and Function</i> , 2021 , 226, 2489-2495	4	7
71	ETurn: a novel Eturn mimic in globular proteins stabilized by main-chain to side-chain C-H...O interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 203-14	4.2	6
70	GWFASTA: server for FASTA search in eukaryotic and microbial genomes. <i>BioTechniques</i> , 2002 , 33, 548-50, 552, 554-6	2.5	6
69	Measurement and computation of murine interleukin-4 and interferon-gamma by exploiting the unique abilities of these lymphokines to induce the secretion of IgG1 and IgG2a. <i>Journal of Immunoassay</i> , 1993 , 14, 83-97		6
68	TopicalPdb: A database of topically delivered peptides. <i>PLoS ONE</i> , 2018 , 13, e0190134	3.7	6
67	Overview of Free Software Developed for Designing Drugs Based on Protein-Small Molecules Interaction. <i>Current Topics in Medicinal Chemistry</i> , 2018 , 18, 1146-1167	3	6
66	Risk prediction in cutaneous melanoma patients from their clinico-pathological features: superiority of clinical data over gene expression data. <i>Heliyon</i> , 2020 , 6, e04811	3.6	6
65	ccPDB 2.0: an updated version of datasets created and compiled from Protein Data Bank. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	5
64	In Silico Analysis of Gene Expression Change Associated with Copy Number of Enhancers in Pancreatic Adenocarcinoma. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	5

63	Development of a model webserver for breed identification using microsatellite DNA marker. <i>BMC Genetics</i> , 2013 , 14, 118	2.6	5
62	Genome sequence of the marine bacterium <i>Marinilabilia salmonicolor</i> JCM 21150T. <i>Journal of Bacteriology</i> , 2012 , 194, 3746	3.5	5
61	Intrinsic contributions of polar amino acid residues toward thermal stability of an ABC-ATPase of mesophilic origin. <i>Protein Science</i> , 2003 , 12, 2118-20	6.3	5
60	A Graphical Web Server for the Analysis of Protein Sequences and Alignment. <i>Biotech Software & Internet Report</i> , 2001 , 2, 254-257		5
59	Evaluation of protein-ligand docking methods on peptide-ligand complexes for docking small ligands to peptides		5
58	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. <i>Cell Reports Medicine</i> , 2021 , 2, 100323	18	5
57	SAPdb: A database of short peptides and the corresponding nanostructures formed by self-assembly. <i>Computers in Biology and Medicine</i> , 2021 , 133, 104391	7	5
56	Oxypred: prediction and classification of oxygen-binding proteins. <i>Genomics, Proteomics and Bioinformatics</i> , 2007 , 5, 250-2	6.5	4
55	GPSRdocker: A Docker-based Resource for Genomics, Proteomics and Systems biology		4
54	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	4
53	Computational resources in the management of antibiotic resistance: Speeding up drug discovery. <i>Drug Discovery Today</i> , 2021 , 26, 2138-2151	8.8	4
52	Assessment of SYBR green I dye-based fluorescence assay for screening antimalarial activity of cationic peptides and DNA intercalating agents. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 2886-9	5.9	3
51	Draft Genome Sequence of <i>Rhodococcus triatomae</i> Strain BKS 15-14. <i>Genome Announcements</i> , 2013 , 1, e0012913		3
50	Draft Genome Sequence of <i>Amycolatopsis decaplanina</i> Strain DSM 44594T. <i>Genome Announcements</i> , 2013 , 1, e0013813		3
49	Draft Genome Sequence of <i>Streptomyces gancidicus</i> Strain BKS 13-15. <i>Genome Announcements</i> , 2013 , 1, e0015013		3
48	Genome sequence of the halotolerant bacterium <i>Imtechella halotolerans</i> K1T. <i>Journal of Bacteriology</i> , 2012 , 194, 3731	3.5	3
47	BTEVAL: a server for evaluation of beta-turn prediction methods. <i>Journal of Bioinformatics and Computational Biology</i> , 2003 , 1, 495-504	1	3
46	A web-based platform on COVID-19 to maintain Predicted Diagnostic, Drug and Vaccine candidates		3

45	In-silico identification of subunit vaccine candidates against lung cancer-associated oncogenic viruses. <i>Computers in Biology and Medicine</i> , 2021 , 130, 104215	7	3
44	Prognostic Biomarker-Based Identification of Drugs for Managing the Treatment of Endometrial Cancer. <i>Molecular Diagnosis and Therapy</i> , 2021 , 25, 629-646	4.5	3
43	B3Pred: A Random-Forest-Based Method for Predicting and Designing Blood-Brain Barrier Penetrating Peptides. <i>Pharmaceutics</i> , 2021 , 13,	6.4	3
42	ChAlPred: A web server for prediction of allergenicity of chemical compounds. <i>Computers in Biology and Medicine</i> , 2021 , 136, 104746	7	3
41	Computer-aided prediction of inhibitors against STAT3 for managing COVID-19 associated cytokine storm. <i>Computers in Biology and Medicine</i> , 2021 , 137, 104780	7	3
40	RareLSD: a manually curated database of lysosomal enzymes associated with rare diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	2
39	Draft Genome Sequence of <i>Rhodococcus qingshengii</i> Strain BKS 20-40. <i>Genome Announcements</i> , 2013 , 1, e0012813		2
38	Searching and mapping of T-cell epitopes, MHC binders, and TAP binders. <i>Methods in Molecular Biology</i> , 2007 , 409, 95-112	1.4	2
37	PDSB: Public Domain Software in Biology. <i>Biotech Software & Internet Report</i> , 2001 , 2, 154-156		2
36	AC2DGel: Analysis and Comparison of 2D Gels. <i>Journal of Proteomics and Bioinformatics</i> , 2008 , 01, 043-046	1.4	2
35	AntiCP 2.0: An updated model for predicting anticancer peptides		2
34	Expression based biomarkers and models to classify early and late stage samples of Papillary Thyroid Carcinoma		2
33	SAMBinder: A web server for predicting SAM binding residues of a protein from its amino acid sequence		2
32	Potential Challenges for Coronavirus (SARS-CoV-2) Vaccines Under Trial. <i>Frontiers in Immunology</i> , 2020 , 11, 561851	8.4	2
31	Analysis and prediction of cholangiocarcinoma from transcriptomic profile of patients. <i>Journal of Hepatology</i> , 2020 , 73, S16-S17	13.4	2
30	Integrative multi-omics approach for stratification of tumor recurrence risk groups of Hepatocellular Carcinoma patients		2
29	DenvInD: dengue virus inhibitors database for clinical and molecular research. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
28	Designing B-Cell Epitopes for Immunotherapy and Subunit Vaccines. <i>Methods in Molecular Biology</i> , 2015 , 1348, 327-40	1.4	1

27	BIS-CATTLE: A Web Server for Breed Identification using Microsatellite DNA Markers. <i>Current Research in Bioinformatics</i> , 2016 , 5, 10-17		1
26	SAMBinder: A Web Server for Predicting S-Adenosyl-L-Methionine Binding Residues of a Protein From Its Amino Acid Sequence. <i>Frontiers in Pharmacology</i> , 2019 , 10, 1690	5.6	1
25	Draft Genome Sequence of <i>Acinetobacter baumannii</i> Strain MSP4-16. <i>Genome Announcements</i> , 2013 , 1, e0013713		1
24	FASTA Servers for Sequence Similarity Search 2005 , 503-525		1
23	Detection of Orientation of MHC Class II Binding Peptides Using Bioinformatics Tools. <i>Biotech Software & Internet Report</i> , 2002 , 3, 146-150		1
22	PDWSB: Public Domain Web Servers in Biology. <i>Biotech Software & Internet Report</i> , 2001 , 2, 152-153		1
21	Tool for Predicting, Scanning, and Designing Defensins. <i>Frontiers in Immunology</i> , 2021 , 12, 780610	8.4	1
20	Prognostic biomarkers for predicting papillary thyroid carcinoma patients at high risk using nine genes of apoptotic pathway. <i>PLoS ONE</i> , 2021 , 16, e0259534	3.7	1
19	In Silico Design of Chemically Modified Cell-Penetrating Peptides. <i>Methods in Molecular Biology</i> , 2022 , 2383, 63-71	1.4	1
18	In Silico Designing and Screening of Antagonists against Cancer Drug Target XIAP. <i>Current Cancer Drug Targets</i> , 2015 , 15, 836-46	2.8	1
17	Searching haptens, carrier proteins, and anti-hapten antibodies. <i>Methods in Molecular Biology</i> , 2007 , 409, 125-39	1.4	1
16	Prediction and analysis of skin cancer progression using genomics profiles of patients		1
15	Predicting virulence factors of immunological interest. <i>Methods in Molecular Biology</i> , 2007 , 409, 407-15	1.4	1
14	HumCFS: A database of fragile sites in human chromosomes		1
13	A web bench for analysis and prediction of oncological status from proteomics data of urine samples		1
12	Computational resources for identification of cancer biomarkers from omics data. <i>Briefings in Functional Genomics</i> , 2021 , 20, 213-222	4.9	1
11	APBioNet [®] annual International Conference on Bioinformatics (InCoB) returns to India in 2018. <i>BMC Genomics</i> , 2019 , 19, 266	4.5	0
10	Draft Genome Sequence of <i>Rhodococcus ruber</i> Strain BKS 20-38. <i>Genome Announcements</i> , 2013 , 1, e0013913		0

- 9 IL13Pred: A method for predicting immunoregulatory cytokine IL-13 inducing peptides.. *Computers in Biology and Medicine*, **2022**, 143, 105297 7 0
- 8 Human Opinion Inspired Feature Selection Strategy for Predicting the Pleasantness of a Molecule. *Advances in Intelligent Systems and Computing*, **2018**, 197-205 0.4
- 7 Databases and Web-Based Tools for Innate Immunity **2009**, 67-76
- 6 Computational resources in healthcare. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, e1437 6.9
- 5 Universal and cross-cancer prognostic biomarkers for predicting survival risk of cancer patients from expression profile of apoptotic pathway genes. *Proteomics*, **2021**, e2000311 4.8
- 4 On the Development of Vaccine Antigen Databases: Progress, Opportunity, and Challenge **2013**, 117-130
- 3 In silico tools and databases for designing cancer immunotherapy.. *Advances in Protein Chemistry and Structural Biology*, **2022**, 129, 1-50 5.3
- 2 ProCanBio: A Database of Manually Curated Biomarkers for Prostate Cancer.. *Journal of Computational Biology*, **2021**, 28, 1248-1257 1.7
- 1 GWFASTA: Server for FASTA Search in Eukaryotic and Microbial Genomes. *BioTechniques*, **2002**, 33, 548-556 5.6