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	Computational resources in healthcare. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2022, 12, e1437.	6.8	1
2	In Silico Design of Chemically Modified Cell-Penetrating Peptides. Methods in Molecular Biology, 2022, 2383, 63-71.	0.9	4
3	IL13Pred: A method for predicting immunoregulatory cytokine IL-13 inducing peptides. Computers in Biology and Medicine, 2022, 143, 105297.	7.0	19
4	In silico tools and databases for designing cancer immunotherapy. Advances in Protein Chemistry and Structural Biology, 2022, 129, 1-50.	2.3	1
5	HLAncPred: a method for predicting promiscuous non-classical HLA binding sites. Briefings in Bioinformatics, 2022, 23, .	6.5	8
6	Prediction of risk-associated genes and high-risk liver cancer patients from their mutation profile: benchmarking of mutation calling techniques. Biology Methods and Protocols, 2022, 7, .	2.2	1
7	AlgPred 2.0: an improved method for predicting allergenic proteins and mapping of IgE epitopes. Briefings in Bioinformatics, 2021, 22, .	6.5	128
8	DenvInD: dengue virus inhibitors database for clinical and molecular research. Briefings in Bioinformatics, 2021, 22, .	6.5	13
9	AntiCP 2.0: an updated model for predicting anticancer peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	127
10	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
11	In-silico identification of subunit vaccine candidates against lung cancer-associated oncogenic viruses. Computers in Biology and Medicine, 2021, 130, 104215.	7.0	5
12	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
13	FermFooDb: A database of bioactive peptides derived from fermented foods. Heliyon, 2021, 7, e06668.	3.2	40
14	Computational resources for identification of cancer biomarkers from omics data. Briefings in Functional Genomics, 2021, 20, 213-222.	2.7	7
15	Prognostic Biomarker-Based Identification of Drugs for Managing the Treatment of Endometrial Cancer. Molecular Diagnosis and Therapy, 2021, 25, 629-646.	3.8	4
16	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. Cell Reports Medicine, 2021, 2, 100323.	6.5	47
17	SAPdb: A database of short peptides and the corresponding nanostructures formed by self-assembly. Computers in Biology and Medicine, 2021, 133, 104391.	7.0	10
18	B3Pdb: an archive of bloodâ€“brain barrier-penetrating peptides. Brain Structure and Function, 2021, 226, 2489-2495.	2.3	14

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19	B3Pred: A Random-Forest-Based Method for Predicting and Designing Bloodâ€“Brain Barrier Penetrating Peptides. Pharmaceutics, 2021, 13, 1237.	4.5	27
20	ChAlPred: A web server for prediction of allergenicity of chemical compounds. Computers in Biology and Medicine, 2021, 136, 104746.	7.0	20
21	Computational resources in the management of antibiotic resistance: Speeding up drug discovery. Drug Discovery Today, 2021, 26, 2138-2151.	6.4	11
22	Computer-aided prediction of inhibitors against STAT3 for managing COVID-19 associated cytokine storm. Computers in Biology and Medicine, 2021, 137, 104780.	7.0	11
23	Universal and crossâ€cancer prognostic biomarkers for predicting survival risk of cancer patients from expression profile of apoptotic pathway genes. Proteomics, 2021, , 2000311.	2.2	0
24	In-Silico Tool for Predicting, Scanning, and Designing Defensins. Frontiers in Immunology, 2021, 12, 780610.	4.8	5
25	Prognostic biomarkers for predicting papillary thyroid carcinoma patients at high risk using nine genes of apoptotic pathway. PLoS ONE, 2021, 16, e0259534.	2.5	7
26	ProCanBio: A Database of Manually Curated Biomarkers for Prostate Cancer. Journal of Computational Biology, 2021, 28, 1248-1257.	1.6	0
27	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
28	Potential Challenges for Coronavirus (SARS-CoV-2) Vaccines Under Trial. Frontiers in Immunology, 2020, 11, 561851.	4.8	4
29	Identification of prognostic biomarkers for major subtypes of non-small-cell lung cancer using genomic and clinical data. Journal of Cancer Research and Clinical Oncology, 2020, 146, 2743-2752.	2.5	9
30	Risk prediction in cutaneous melanoma patients from their clinico-pathological features: superiority of clinical data over gene expression data. Heliyon, 2020, 6, e04811.	3.2	8
31	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
32	Analysis and prediction of cholangiocarcinoma from transcriptomic profile of patients. Journal of Hepatology, 2020, 73, S16-S17.	3.7	4
33	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
34	CancerEnD: A database of cancer associated enhancers. Genomics, 2020, 112, 3696-3702.	2.9	17
35	OvirusTdb: A database of oncolytic viruses for the advancement of therapeutics in cancer. Virology, 2020, 548, 109-116.	2.4	16
36	A Method for Predicting Hemolytic Potency of Chemically Modified Peptides From Its Structure. Frontiers in Pharmacology, 2020, 11, 54.	3.5	19

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37	CancerLivER: a database of liver cancer gene expression resources and biomarkers. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	21
38	A Hybrid Model for Predicting Pattern Recognition Receptors Using Evolutionary Information. Frontiers in Immunology, 2020, 11, 71.	4.8	15
39	Computing Skin Cutaneous Melanoma Outcome From the HLA-Alleles and Clinical Characteristics. Frontiers in Genetics, 2020, 11, 221.	2.3	33
40	Expression based biomarkers and models to classify early and late-stage samples of Papillary Thyroid Carcinoma. PLoS ONE, 2020, 15, e0231629.	2.5	13
41	Computer-aided designing of oncolytic viruses for overcoming translational challenges of cancer immunotherapy. Drug Discovery Today, 2020, 25, 1198-1205.	6.4	12
42	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
43	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
44	Prediction and Analysis of Skin Cancer Progression using Genomics Profiles of Patients. Scientific Reports, 2019, 9, 15790.	3.3	57
45	RareLSD: a manually curated database of lysosomal enzymes associated with rare diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	4
46	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
47	Classification of early and late stage liver hepatocellular carcinoma patients from their genomics and epigenomics profiles. PLoS ONE, 2019, 14, e0221476.	2.5	46
48	Prediction of risk scores for colorectal cancer patients from the concentration of proteins involved in mitochondrial apoptotic pathway. PLoS ONE, 2019, 14, e0217527.	2.5	15
49	HumCFS: a database of fragile sites in human chromosomes. BMC Genomics, 2019, 19, 985.	2.8	63
50	APBioNet's annual International Conference on Bioinformatics (InCoB) returns to India in 2018. BMC Genomics, 2019, 19, 266.	2.8	1
51	NeuroPIpred: a tool to predict, design and scan insect neuropeptides. Scientific Reports, 2019, 9, 5129.	3.3	36
52	ImmunoSPdb: an archive of immunosuppressive peptides. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	2
53	ccPDB 2.0: an updated version of datasets created and compiled from Protein Data Bank. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	10
54	Benchmarking of different molecular docking methods for protein-peptide docking. BMC Bioinformatics, 2019, 19, 426.	2.6	104

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55	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
56	SAMbinder: A Web Server for Predicting S-Adenosyl-L-Methionine Binding Residues of a Protein From Its Amino Acid Sequence. Frontiers in Pharmacology, 2019, 10, 1690.	3.5	3
57	Identification of Platform-Independent Diagnostic Biomarker Panel for Hepatocellular Carcinoma Using Large-Scale Transcriptomics Data. Frontiers in Genetics, 2019, 10, 1306.	2.3	49
58	Human Opinion Inspired Feature Selection Strategy for Predicting the Pleasantness of a Molecule. Advances in Intelligent Systems and Computing, 2018, , 197-205.	0.6	0
59	Prediction of Antimicrobial Potential of a Chemically Modified Peptide From Its Tertiary Structure. Frontiers in Microbiology, 2018, 9, 2551.	3.5	38
60	AntiTbPdb: a knowledgebase of anti-tubercular peptides. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	47
61	A Web Resource for Designing Subunit Vaccine Against Major Pathogenic Species of Bacteria. Frontiers in Immunology, 2018, 9, 2280.	4.8	36
62	Computer-aided prediction of antigen presenting cell modulators for designing peptide-based vaccine adjuvants. Journal of Translational Medicine, 2018, 16, 181.	4.4	60
63	In Silico Approach for Prediction of Antifungal Peptides. Frontiers in Microbiology, 2018, 9, 323.	3.5	113
64	Prediction of Cell-Penetrating Potential of Modified Peptides Containing Natural and Chemically Modified Residues. Frontiers in Microbiology, 2018, 9, 725.	3.5	58
65	Prediction of Antitubercular Peptides From Sequence Information Using Ensemble Classifier and Hybrid Features. Frontiers in Pharmacology, 2018, 9, 954.	3.5	59
66	In silico approaches for predicting the half-life of natural and modified peptides in blood. PLoS ONE, 2018, 13, e0196829.	2.5	67
67	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
68	TopicalPdb: A database of topically delivered peptides. PLoS ONE, 2018, 13, e0190134.	2.5	10
69	Overview of Free Software Developed for Designing Drugs Based on Protein-Small Molecules Interaction. Current Topics in Medicinal Chemistry, 2018, 18, 1146-1167.	2.1	14
70	Novelin silicotools for designing peptide-based subunit vaccines and immunotherapeutics. Briefings in Bioinformatics, 2017, 18, bbw025.	6.5	94
71	Computer-aided designing of immunosuppressive peptides based on IL-10 inducing potential. Scientific Reports, 2017, 7, 42851.	3.3	206
72	Anticancer properties of a defensin like class IId bacteriocin Laterosporulin10. Scientific Reports, 2017, 7, 46541.	3.3	89

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73	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
74	Gene expression-based biomarkers for discriminating early and late stage of clear cell renal cancer. Scientific Reports, 2017, 7, 44997.	3.3	92
75	Challenges in Prediction of different Cancer Stages using Gene Expression Profile of Cancer Patients. , 2017, , .		0
76	CancerPDF: A repository of cancer-associated peptidome found in human biofluids. Scientific Reports, 2017, 7, 1511.	3.3	30
77	Computational Prediction of the Immunomodulatory Potential of RNA Sequences. Methods in Molecular Biology, 2017, 1632, 75-90.	0.9	12
78	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
79	THPdb: Database of FDA-approved peptide and protein therapeutics. PLoS ONE, 2017, 12, e0181748.	2.5	367
80	BIS-CATTLE: A Web Server for Breed Identification using Microsatellite DNA Markers. Current Research in Bioinformatics, 2016, 5, 10-17.	0.1	1
81	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
82	PEPlife: A Repository of the Half-life of Peptides. Scientific Reports, 2016, 6, 36617.	3.3	108
83	dbEM: A database of epigenetic modifiers curated from cancerous and normal genomes. Scientific Reports, 2016, 6, 19340.	3.3	58
84	ProCarDB: a database of bacterial carotenoids. BMC Microbiology, 2016, 16, 96.	3.3	52
85	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
86	Topical Delivery of Protein and Peptide Using Novel Cell Penetrating Peptide IMT-P8. Scientific Reports, 2016, 6, 26278.	3.3	61
87	ZikaVR: An Integrated Zika Virus Resource for Genomics, Proteomics, Phylogenetic and Therapeutic Analysis. Scientific Reports, 2016, 6, 32713.	3.3	49
88	Prediction of Immunomodulatory potential of an RNA sequence for designing non-toxic siRNAs and RNA-based vaccine adjuvants. Scientific Reports, 2016, 6, 20678.	3.3	18
89	ApoCanD: Database of human apoptotic proteins in the context of cancer. Scientific Reports, 2016, 6, 20797.	3.3	9
90	A Web Server and Mobile App for Computing Hemolytic Potency of Peptides. Scientific Reports, 2016, 6, 22843.	3.3	135

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91	A web-based resource for designing therapeutics against Ebola Virus. Scientific Reports, 2016, 6, 24782.	3.3	14
92	A web server for analysis, comparison and prediction of protein ligand binding sites. Biology Direct, 2016, 11, 14.	4.6	15
93	BLAST-based structural annotation of protein residues using Protein Data Bank. Biology Direct, 2016, 11, 4.	4.6	14
94	CPPsite 2.0: a repository of experimentally validated cell-penetrating peptides. Nucleic Acids Research, 2016, 44, D1098-D1103.	14.5	241
95	SATPdb: a database of structurally annotated therapeutic peptides. Nucleic Acids Research, 2016, 44, D1119-D1126.	14.5	131
96	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
97	Managing Drug Resistance in Cancer: Role of Cancer Informatics. Methods in Molecular Biology, 2016, 1395, 299-312.	0.9	12
98	A Web-Based Platform for Designing Vaccines against Existing and Emerging Strains of Mycobacterium tuberculosis. PLoS ONE, 2016, 11, e0153771.	2.5	21
99	A Platform for Designing Genome-Based Personalized Immunotherapy or Vaccine against Cancer. PLoS ONE, 2016, 11, e0166372.	2.5	14
100	An in silico platform for predicting, screening and designing of antihypertensive peptides. Scientific Reports, 2015, 5, 12512.	3.3	123
101	VaccineDA: Prediction, design and genome-wide screening of oligodeoxynucleotide-based vaccine adjuvants. Scientific Reports, 2015, 5, 12478.	3.3	34
102	AHTPDB: a comprehensive platform for analysis and presentation of antihypertensive peptides. Nucleic Acids Research, 2015, 43, D956-D962.	14.5	143
103	PEPstrMOD: structure prediction of peptides containing natural, non-natural and modified residues. Biology Direct, 2015, 10, 73.	4.6	164
104	CancerPPD: a database of anticancer peptides and proteins. Nucleic Acids Research, 2015, 43, D837-D843.	14.5	253
105	Assessment of SYBR Green I Dye-Based Fluorescence Assay for Screening Antimalarial Activity of Cationic Peptides and DNA Intercalating Agents. Antimicrobial Agents and Chemotherapy, 2015, 59, 2886-2889.	3.2	3
106	Identification of protein-interacting nucleotides in a RNA sequence using composition profile of tri-nucleotides. Genomics, 2015, 105, 197-203.	2.9	24
107	Ï‰â€Turn: A novel Î²â€turn mimic in globular proteins stabilized by mainâ€chain to sideâ€chain Cï£¿HÂ·Â·Â·O interaction. Proteins: Structure, Function and Bioinformatics, 2015, 83, 203-214.	2.6	7
108	In silico platform for predicting and initiating Î²-turns in a protein at desired locations. Proteins: Structure, Function and Bioinformatics, 2015, 83, 910-921.	2.6	12

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109	QSAR based model for discriminating EGFR inhibitors and non-inhibitors using Random forest. Biology Direct, 2015, 10, 10.	4.6	63
110	Designing B-Cell Epitopes for Immunotherapy and Subunit Vaccines. Methods in Molecular Biology, 2015, 1348, 327-340.	0.9	5
111	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
112	Peptide Toxicity Prediction. Methods in Molecular Biology, 2015, 1268, 143-157.	0.9	105
113	Computer-Aided Virtual Screening and Designing of Cell-Penetrating Peptides. Methods in Molecular Biology, 2015, 1324, 59-69.	0.9	56
114	AntiAngioPred: A Server for Prediction of Anti-Angiogenic Peptides. PLoS ONE, 2015, 10, e0136990.	2.5	51
115	In Silico Designing and Screening of Antagonists against Cancer Drug Target XIAP. Current Cancer Drug Targets, 2015, 15, 836-846.	1.6	1
116	QSAR-Based Models for Designing Quinazoline/Imidazothiazoles/Pyrazolopyrimidines Based Inhibitors against Wild and Mutant EGFR. PLoS ONE, 2014, 9, e101079.	2.5	32
117	Prediction of uridine modifications in tRNA sequences. BMC Bioinformatics, 2014, 15, 326.	2.6	28
118	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
119	Hemolytik: a database of experimentally determined hemolytic and non-hemolytic peptides. Nucleic Acids Research, 2014, 42, D444-D449.	14.5	105
120	Prediction and classification of ncRNAs using structural information. BMC Genomics, 2014, 15, 127.	2.8	101
121	Designing of peptides with desired half-life in intestine-like environment. BMC Bioinformatics, 2014, 15, 282.	2.6	73
122	PCMdb: Pancreatic Cancer Methylation Database. Scientific Reports, 2014, 4, 4197.	3.3	28
123	Herceptin Resistance Database for Understanding Mechanism of Resistance in Breast Cancer Patients. Scientific Reports, 2014, 4, 4483.	3.3	40
124	Designing of promiscuous inhibitors against pancreatic cancer cell lines. Scientific Reports, 2014, 4, 4668.	3.3	19
125	ToxiPred: A Server for Prediction of Aqueous Toxicity of Small Chemical Molecules in <I>T.</I> <I>Pyriformis</I>. Journal of Translational Toxicology, 2014, 1, 21-27.	0.3	10
126	Evaluation of Protein Dihedral Angle Prediction Methods. PLoS ONE, 2014, 9, e105667.	2.5	15

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127	Tumor Homing Peptides as Molecular Probes for Cancer Therapeutics, Diagnostics and Theranostics. Current Medicinal Chemistry, 2014, 21, 2367-2391.	2.4	80
128	EGFRIndb: Epidermal Growth Factor Receptor Inhibitor Database. Anti-Cancer Agents in Medicinal Chemistry, 2014, 14, 928-935.	1.7	17
129	In silico approaches for designing highly effective cell penetrating peptides. Journal of Translational Medicine, 2013, 11, 74.	4.4	242
130	Designing of inhibitors against drug tolerant Mycobacterium tuberculosis (H37Rv). Chemistry Central Journal, 2013, 7, 49.	2.6	24
131	Prediction of vitamin interacting residues in a vitamin binding protein using evolutionary information. BMC Bioinformatics, 2013, 14, 44.	2.6	23
132	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
133	Development of a model webserver for breed identification using microsatellite DNA marker. BMC Genetics, 2013, 14, 118.	2.7	6
134	Designing of interferon-gamma inducing MHC class-II binders. Biology Direct, 2013, 8, 30.	4.6	484
135	DrugMint: a webserver for predicting and designing of drug-like molecules. Biology Direct, 2013, 8, 28.	4.6	47
136	Computational approach for designing tumor homing peptides. Scientific Reports, 2013, 3, 1607.	3.3	69
137	NPACT: Naturally Occurring Plant-based Anti-cancer Compound-Activity-Target database. Nucleic Acids Research, 2013, 41, D1124-D1129.	14.5	229
138	In Silico Models for B-Cell Epitope Recognition and Signaling. Methods in Molecular Biology, 2013, 993, 129-138.	0.9	7
139	Genome Sequence of the â€œIndian Bison Typeâ€•Biotype of Mycobacterium avium subsp. paratuberculosis Strain S5. Genome Announcements, 2013, 1, .	0.8	9
140	Draft Genome Sequence of the Type Species of the Genus Citrobacter , Citrobacter freundii MTCC 1658. Genome Announcements, 2013, 1, .	0.8	14
141	Draft Genome Sequence of the 2-Chloro-4-Nitrophenol-Degrading Bacterium Arthrobacter sp. Strain SJCon. Genome Announcements, 2013, 1, e0005813.	0.8	15
142	Draft Genome Sequence of Rhodococcus qingshengii Strain BKS 20-40. Genome Announcements, 2013, 1, e0012813.	0.8	2
143	Draft Genome Sequence of Rhodococcus triatomae Strain BKS 15-14. Genome Announcements, 2013, 1, e0012913.	0.8	3
144	Draft Genome Sequence of Acinetobacter baumannii Strain MSP4-16. Genome Announcements, 2013, 1, e0013713.	0.8	3

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145	Draft Genome Sequence of Amycolatopsis decaplanina Strain DSM 44594 ^T. Genome Announcements, 2013, 1, e0013813.	0.8	4
146	Draft Genome Sequence of Rhodococcus ruber Strain BKS 20-38. Genome Announcements, 2013, 1, e0013913.	0.8	1
147	Draft Genome Sequence of Streptomyces gancidicus Strain BKS 13-15. Genome Announcements, 2013, 1, e0015013.	0.8	3
148	CancerDR: Cancer Drug Resistance Database. Scientific Reports, 2013, 3, 1445.	3.3	102
149	In Silico Models for Designing and Discovering Novel Anticancer Peptides. Scientific Reports, 2013, 3, 2984.	3.3	226
150	lncRNome: a comprehensive knowledgebase of human long noncoding RNAs. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat034.	3.0	126
151	Identification of B-cell epitopes in an antigen for inducing specific class of antibodies. Biology Direct, 2013, 8, 27.	4.6	91
152	In Silico Approach for Predicting Toxicity of Peptides and Proteins. PLoS ONE, 2013, 8, e73957.	2.5	1,120
153	Improved Method for Linear B-Cell Epitope Prediction Using Antigenâ€™s Primary Sequence. PLoS ONE, 2013, 8, e62216.	2.5	269
154	Genome Annotation of Burkholderia sp. SJ98 with Special Focus on Chemotaxis Genes. PLoS ONE, 2013, 8, e70624.	2.5	9
155	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
156	Prediction of IL4 Inducing Peptides. Clinical and Developmental Immunology, 2013, 2013, 1-9.	3.3	213
157	Open Source Software and Web Services for Designing Therapeutic Molecules. Current Topics in Medicinal Chemistry, 2013, 13, 1172-1191.	2.1	25
158	Hybrid Approach for Predicting Coreceptor Used by HIV-1 from Its V3 Loop Amino Acid Sequence. PLoS ONE, 2013, 8, e61437.	2.5	16
159	In silico Platform for Prediction of N-, O- and C-Glycosites in Eukaryotic Protein Sequences. PLoS ONE, 2013, 8, e67008.	2.5	182
160	On the Development of Vaccine Antigen Databases: Progress, Opportunity, and Challenge. , 2013, , 117-130.		0
161	Draft Genome Sequence of Salt-Tolerant Yeast Debaryomyces hansenii var. hansenii MTCC 234. Eukaryotic Cell, 2012, 11, 961-962.	3.4	17
162	CPPsite: a curated database of cell penetrating peptides. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas015-bas015.	3.0	161

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163	Genome Sequence of the Halotolerant Bacterium Imtechella halotolerans K1 ^T. Journal of Bacteriology, 2012, 194, 3731-3731.	2.2	3
164	Genome Sequence of the Marine Bacterium Marinilabilia salmonicolor JCM 21150 ^T. Journal of Bacteriology, 2012, 194, 3746-3746.	2.2	10
165	ccPDB: compilation and creation of data sets from Protein Data Bank. Nucleic Acids Research, 2012, 40, D486-D489.	14.5	28
166	Genome Sequence of the Oleaginous Red Yeast Rhodosporidium toruloides MTCC 457. Eukaryotic Cell, 2012, 11, 1083-1084.	3.4	57
167	Draft Genome Sequence of the Nitrophenol-Degrading Actinomycete Rhodococcus imtechensis RKJ300. Journal of Bacteriology, 2012, 194, 3543-3543.	2.2	16
168	Genome Sequence of the Nitroaromatic Compound-Degrading Bacterium Burkholderia sp. Strain SJ98. Journal of Bacteriology, 2012, 194, 3286-3286.	2.2	18
169	ProGlycProt: a repository of experimentally characterized prokaryotic glycoproteins. Nucleic Acids Research, 2012, 40, D388-D393.	14.5	26
170	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
171	PolysacDB: A Database of Microbial Polysaccharide Antigens and Their Antibodies. PLoS ONE, 2012, 7, e34613.	2.5	8
172	GlycoPP: A Webserver for Prediction of N- and O-Glycosites in Prokaryotic Protein Sequences. PLoS ONE, 2012, 7, e40155.	2.5	71
173	Predicting sub-cellular localization of tRNA synthetases from their primary structures. Amino Acids, 2012, 42, 1703-1713.	2.7	7
174	TumorHoPe: A Database of Tumor Homing Peptides. PLoS ONE, 2012, 7, e35187.	2.5	118
175	Open source drug discoveryâ€“ A new paradigm of collaborative research in tuberculosis drug development. Tuberculosis, 2011, 91, 479-86.	1.9	42
176	Machine learning competition in immunology â€“ Prediction of HLA class I binding peptides. Journal of Immunological Methods, 2011, 374, 1-4.	1.4	53
177	A web server for predicting inhibitors against bacterial target GlmU protein. BMC Pharmacology, 2011, 11, 5.	0.4	31
178	Analysis and prediction of cancerlectins using evolutionary and domain information. BMC Research Notes, 2011, 4, 237.	1.4	26
179	SVM based prediction of RNAâ€binding proteins using binding residues and evolutionary information. Journal of Molecular Recognition, 2011, 24, 303-313.	2.1	130
180	CCDB: a curated database of genes involved in cervix cancer. Nucleic Acids Research, 2011, 39, D975-D979.	14.5	78

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181	Designing of Highly Effective Complementary and Mismatch siRNAs for Silencing a Gene. PLoS ONE, 2011, 6, e23443.	2.5	43
182	Identification of Mannose Interacting Residues Using Local Composition. PLoS ONE, 2011, 6, e24039.	2.5	27
183	HIVsirDB: A Database of HIV Inhibiting siRNAs. PLoS ONE, 2011, 6, e25917.	2.5	37
184	Prediction of Specificity and Cross-Reactivity of Kinase Inhibitors. Letters in Drug Design and Discovery, 2011, 8, 223-228.	0.7	26
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