Gajendra P S Raghava

List of Publications by Year in Descending Order

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	IL13Pred: A method for predicting immunoregulatory cytokine IL-13 inducing peptides.. *Computers in Biology and Medicine*, **2022**, 143, 105297	7	0
295	In Silico Design of Chemically Modified Cell-Penetrating Peptides. *Methods in Molecular Biology*, **2022**, 2383, 63-71	1.4	1
294	In silico tools and databases for designing cancer immunotherapy.. *Advances in Protein Chemistry and Structural Biology*, **2022**, 129, 1-50	5.3	
293	Tool for Predicting, Scanning, and Designing Defensins. *Frontiers in Immunology*, **2021**, 12, 780610	8.4	1
292	Prognostic biomarkers for predicting papillary thyroid carcinoma patients at high risk using nine genes of apoptotic pathway. *PLoS ONE*, **2021**, 16, e0259534	3.7	1
291	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	
290	AlgPred 2.0: an improved method for predicting allergenic proteins and mapping of IgE epitopes. *Briefings in Bioinformatics*, **2021**, 22,	13.4	36
289	In-silico identification of subunit vaccine candidates against lung cancer-associated oncogenic viruses. *Computers in Biology and Medicine*, **2021**, 130, 104215	7	3
288	Crowdsourcing digital health measures to predict Parkinson's disease severity: the Parkinson's Disease Digital Biomarker DREAM Challenge. *Npj Digital Medicine*, **2021**, 4, 53	15.7	8
287	FermFooDb: A database of bioactive peptides derived from fermented foods. *Heliyon*, **2021**, 7, e06668	3.6	10
286	Computational resources for identification of cancer biomarkers from omics data. *Briefings in Functional Genomics*, **2021**, 20, 213-222	4.9	1
285	Prognostic Biomarker-Based Identification of Drugs for Managing the Treatment of Endometrial Cancer. *Molecular Diagnosis and Therapy*, **2021**, 25, 629-646	4.5	3
284	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. *Cell Reports Medicine*, **2021**, 2, 100323	18	5
283	SAPdb: A database of short peptides and the corresponding nanostructures formed by self-assembly. *Computers in Biology and Medicine*, **2021**, 133, 104391	7	5
282	DenvInD: dengue virus inhibitors database for clinical and molecular research. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
281	AntiCP 2.0: an updated model for predicting anticancer peptides. *Briefings in Bioinformatics*, **2021**, 22,	13.4	45
280	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	13.4	27

279	B3Pdb: an archive of blood-brain barrier-penetrating peptides. *Brain Structure and Function*, **2021**, 226, 2489-2495	4	7
278	B3Pred: A Random-Forest-Based Method for Predicting and Designing Blood-Brain Barrier Penetrating Peptides. *Pharmaceutics*, **2021**, 13,	6.4	3
277	ChAlPred: A web server for prediction of allergenicity of chemical compounds. *Computers in Biology and Medicine*, **2021**, 136, 104746	7	3
276	Computational resources in the management of antibiotic resistance: Speeding up drug discovery. *Drug Discovery Today*, **2021**, 26, 2138-2151	8.8	4
275	Computer-aided prediction of inhibitors against STAT3 for managing COVID-19 associated cytokine storm. *Computers in Biology and Medicine*, **2021**, 137, 104780	7	3
274	ProCanBio: A Database of Manually Curated Biomarkers for Prostate Cancer.. *Journal of Computational Biology*, **2021**, 28, 1248-1257	1.7	
273	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	1.9	17
272	CancerEnD: A database of cancer associated enhancers. *Genomics*, **2020**, 112, 3696-3702	4.3	7
271	OvirusTdb: A database of oncolytic viruses for the advancement of therapeutics in cancer. *Virology*, **2020**, 548, 109-116	3.6	10
270	A Method for Predicting Hemolytic Potency of Chemically Modified Peptides From Its Structure. *Frontiers in Pharmacology*, **2020**, 11, 54	5.6	11
269	CancerLivER: a database of liver cancer gene expression resources and biomarkers. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	7
268	A Hybrid Model for Predicting Pattern Recognition Receptors Using Evolutionary Information. *Frontiers in Immunology*, **2020**, 11, 71	8.4	7
267	Computing Skin Cutaneous Melanoma Outcome From the HLA-Alleles and Clinical Characteristics. *Frontiers in Genetics*, **2020**, 11, 221	4.5	14
266	Expression based biomarkers and models to classify early and late-stage samples of Papillary Thyroid Carcinoma. *PLoS ONE*, **2020**, 15, e0231629	3.7	8
265	Computer-aided designing of oncolytic viruses for overcoming translational challenges of cancer immunotherapy. *Drug Discovery Today*, **2020**, 25, 1198-1205	8.8	8
264	NAGbinder: An approach for identifying N-acetylglucosamine interacting residues of a protein from its primary sequence. *Protein Science*, **2020**, 29, 201-210	6.3	10
263	Potential Challenges for Coronavirus (SARS-CoV-2) Vaccines Under Trial. *Frontiers in Immunology*, **2020**, 11, 561851	8.4	2
262	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	4.9	7

261	Risk prediction in cutaneous melanoma patients from their clinico-pathological features: superiority of clinical data over gene expression data. *Heliyon*, **2020**, 6, e04811	3.6	6
260	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. *Cell Systems*, **2020**, 11, 186-195.e9	10.6	11
259	Analysis and prediction of cholangiocarcinoma from transcriptomic profile of patients. *Journal of Hepatology*, **2020**, 73, S16-S17	13.4	2
258	Docking-based approach for identification of mutations that disrupt binding between Bcl-2 and Bax proteins: Inducing apoptosis in cancer cells. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e910	2.3	16
257	Classification of early and late stage liver hepatocellular carcinoma patients from their genomics and epigenomics profiles. *PLoS ONE*, **2019**, 14, e0221476	3.7	16
256	Prediction of risk scores for colorectal cancer patients from the concentration of proteins involved in mitochondrial apoptotic pathway. *PLoS ONE*, **2019**, 14, e0217527	3.7	11
255	HumCFS: a database of fragile sites in human chromosomes. *BMC Genomics*, **2019**, 19, 985	4.5	26
254	APBioNet's annual International Conference on Bioinformatics (InCoB) returns to India in 2018. *BMC Genomics*, **2019**, 19, 266	4.5	0
253	NeuroPIpred: a tool to predict, design and scan insect neuropeptides. *Scientific Reports*, **2019**, 9, 5129	4.9	21
252	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,	5	5
251	Benchmarking of different molecular docking methods for protein-peptide docking. *BMC Bioinformatics*, **2019**, 19, 426	3.6	52
250	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	5.6	1
249	PRRDB 2.0: a comprehensive database of pattern-recognition receptors and their ligands. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019,	5	16
248	In Silico Analysis of Gene Expression Change Associated with Copy Number of Enhancers in Pancreatic Adenocarcinoma. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	5
247	Prediction and Analysis of Skin Cancer Progression using Genomics Profiles of Patients. *Scientific Reports*, **2019**, 9, 15790	4.9	32
246	RareLSD: a manually curated database of lysosomal enzymes associated with rare diseases. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019,	5	2
245	Identification of Platform-Independent Diagnostic Biomarker Panel for Hepatocellular Carcinoma Using Large-Scale Transcriptomics Data. *Frontiers in Genetics*, **2019**, 10, 1306	4.5	18
244	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019,	5	4

243	Human Opinion Inspired Feature Selection Strategy for Predicting the Pleasantness of a Molecule. *Advances in Intelligent Systems and Computing*, **2018**, 197-205	0.4	
242	Computer-aided prediction of antigen presenting cell modulators for designing peptide-based vaccine adjuvants. *Journal of Translational Medicine*, **2018**, 16, 181	8.5	40
241	Approach for Prediction of Antifungal Peptides. *Frontiers in Microbiology*, **2018**, 9, 323	5.7	60
240	Prediction of Cell-Penetrating Potential of Modified Peptides Containing Natural and Chemically Modified Residues. *Frontiers in Microbiology*, **2018**, 9, 725	5.7	33
239	Prediction of Antitubercular Peptides From Sequence Information Using Ensemble Classifier and Hybrid Features. *Frontiers in Pharmacology*, **2018**, 9, 954	5.6	39
238	In silico approaches for predicting the half-life of natural and modified peptides in blood. *PLoS ONE*, **2018**, 13, e0196829	3.7	35
237	In Silico Tools and Databases for Designing Peptide-Based Vaccine and Drugs. *Advances in Protein Chemistry and Structural Biology*, **2018**, 112, 221-263	5.3	32
236	TopicalPdb: A database of topically delivered peptides. *PLoS ONE*, **2018**, 13, e0190134	3.7	6
235	Overview of Free Software Developed for Designing Drugs Based on Protein-Small Molecules Interaction. *Current Topics in Medicinal Chemistry*, **2018**, 18, 1146-1167	3	6
234	Prediction of Antimicrobial Potential of a Chemically Modified Peptide From Its Tertiary Structure. *Frontiers in Microbiology*, **2018**, 9, 2551	5.7	30
233	AntiTbPdb: a knowledgebase of anti-tubercular peptides. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	26
232	A Web Resource for Designing Subunit Vaccine Against Major Pathogenic Species of Bacteria. *Frontiers in Immunology*, **2018**, 9, 2280	8.4	22
231	Computer-aided designing of immunosuppressive peptides based on IL-10 inducing potential. *Scientific Reports*, **2017**, 7, 42851	4.9	96
230	Anticancer properties of a defensin like class IId bacteriocin Laterosporulin10. *Scientific Reports*, **2017**, 7, 46541	4.9	54
229	Assessing therapeutic potential of molecules: molecular property diagnostic suite for tuberculosis ($\mathbf{MPDS}^{\mathbf{TB}}$). *Journal of Chemical Sciences*, **2017**, 129, 515-531	1.8	12
228	Gene expression-based biomarkers for discriminating early and late stage of clear cell renal cancer. *Scientific Reports*, **2017**, 7, 44997	4.9	54
227	Novel in silico tools for designing peptide-based subunit vaccines and immunotherapeutics. *Briefings in Bioinformatics*, **2017**, 18, 467-478	13.4	49
226	CancerPDF: A repository of cancer-associated peptidome found in human biofluids. *Scientific Reports*, **2017**, 7, 1511	4.9	20

225	In silico analysis to identify vaccine candidates common to multiple serotypes of Shigella and evaluation of their immunogenicity. *PLoS ONE*, **2017**, 12, e0180505	3.7	12
224	THPdb: Database of FDA-approved peptide and protein therapeutics. *PLoS ONE*, **2017**, 12, e0181748	3.7	243
223	Computational Prediction of the Immunomodulatory Potential of RNA Sequences. *Methods in Molecular Biology*, **2017**, 1632, 75-90	1.4	9
222	BIS-CATTLE: A Web Server for Breed Identification using Microsatellite DNA Markers. *Current Research in Bioinformatics*, **2016**, 5, 10-17		1
221	Topical Delivery of Protein and Peptide Using Novel Cell Penetrating Peptide IMT-P8. *Scientific Reports*, **2016**, 6, 26278	4.9	39
220	ZikaVR: An Integrated Zika Virus Resource for Genomics, Proteomics, Phylogenetic and Therapeutic Analysis. *Scientific Reports*, **2016**, 6, 32713	4.9	40
219	Prediction of Immunomodulatory potential of an RNA sequence for designing non-toxic siRNAs and RNA-based vaccine adjuvants. *Scientific Reports*, **2016**, 6, 20678	4.9	12
218	ApoCanD: Database of human apoptotic proteins in the context of cancer. *Scientific Reports*, **2016**, 6, 20797	4.9	7
217	A Web Server and Mobile App for Computing Hemolytic Potency of Peptides. *Scientific Reports*, **2016**, 6, 22843	4.9	78
216	A web-based resource for designing therapeutics against Ebola Virus. *Scientific Reports*, **2016**, 6, 24782	4.9	12
215	A web server for analysis, comparison and prediction of protein ligand binding sites. *Biology Direct*, **2016**, 11, 14	7.2	11
214	BLAST-based structural annotation of protein residues using Protein Data Bank. *Biology Direct*, **2016**, 11, 4	7.2	7
213	CPPsite 2.0: a repository of experimentally validated cell-penetrating peptides. *Nucleic Acids Research*, **2016**, 44, D1098-103	20.1	167
212	SATPdb: a database of structurally annotated therapeutic peptides. *Nucleic Acids Research*, **2016**, 44, D1119-26	20.1	89
211	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, 4073-83	5.7	13
210	Managing Drug Resistance in Cancer: Role of Cancer Informatics. *Methods in Molecular Biology*, **2016**, 1395, 299-312	1.4	9
209	A Web-Based Platform for Designing Vaccines against Existing and Emerging Strains of Mycobacterium tuberculosis. *PLoS ONE*, **2016**, 11, e0153771	3.7	15
208	A Platform for Designing Genome-Based Personalized Immunotherapy or Vaccine against Cancer. *PLoS ONE*, **2016**, 11, e0166372	3.7	11

207	Prioritization of anticancer drugs against a cancer using genomic features of cancer cells: A step towards personalized medicine. *Scientific Reports*, **2016**, 6, 23857	4.9	38
206	PEPlife: A Repository of the Half-life of Peptides. *Scientific Reports*, **2016**, 6, 36617	4.9	76
205	dbEM: A database of epigenetic modifiers curated from cancerous and normal genomes. *Scientific Reports*, **2016**, 6, 19340	4.9	34
204	ProCarDB: a database of bacterial carotenoids. *BMC Microbiology*, **2016**, 16, 96	4.5	41
203	Prediction of anticancer molecules using hybrid model developed on molecules screened against NCI-60 cancer cell lines. *BMC Cancer*, **2016**, 16, 77	4.8	30
202	βTurn: a novel βturn mimic in globular proteins stabilized by main-chain to side-chain CH···O interaction. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 203-14	4.2	6
201	In silico platform for predicting and initiating βturns in a protein at desired locations. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 910-21	4.2	9
200	QSAR based model for discriminating EGFR inhibitors and non-inhibitors using Random forest. *Biology Direct*, **2015**, 10, 10	7.2	45
199	Designing B-Cell Epitopes for Immunotherapy and Subunit Vaccines. *Methods in Molecular Biology*, **2015**, 1348, 327-40	1.4	1
198	Identification and characterization of novel protein-derived arginine-rich cell-penetrating peptides. *European Journal of Pharmaceutics and Biopharmaceutics*, **2015**, 89, 93-106	5.7	27
197	An in silico platform for predicting, screening and designing of antihypertensive peptides. *Scientific Reports*, **2015**, 5, 12512	4.9	80
196	VaccineDA: Prediction, design and genome-wide screening of oligodeoxynucleotide-based vaccine adjuvants. *Scientific Reports*, **2015**, 5, 12478	4.9	20
195	AHTPDB: a comprehensive platform for analysis and presentation of antihypertensive peptides. *Nucleic Acids Research*, **2015**, 43, D956-62	20.1	96
194	PEPstrMOD: structure prediction of peptides containing natural, non-natural and modified residues. *Biology Direct*, **2015**, 10, 73	7.2	100
193	CancerPPD: a database of anticancer peptides and proteins. *Nucleic Acids Research*, **2015**, 43, D837-43	20.1	169
192	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, 2886-9	5.9	3
191	Identification of protein-interacting nucleotides in a RNA sequence using composition profile of tri-nucleotides. *Genomics*, **2015**, 105, 197-203	4.3	17
190	AntiAngioPred: A Server for Prediction of Anti-Angiogenic Peptides. *PLoS ONE*, **2015**, 10, e0136990	3.7	33

189	In Silico Designing and Screening of Antagonists against Cancer Drug Target XIAP. *Current Cancer Drug Targets*, **2015**, 15, 836-46	2.8	1
188	Peptide toxicity prediction. *Methods in Molecular Biology*, **2015**, 1268, 143-57	1.4	39
187	Computer-Aided Virtual Screening and Designing of Cell-Penetrating Peptides. *Methods in Molecular Biology*, **2015**, 1324, 59-69	1.4	35
186	Designing of promiscuous inhibitors against pancreatic cancer cell lines. *Scientific Reports*, **2014**, 4, 4668	4.9	12
185	Prediction and classification of ncRNAs using structural information. *BMC Genomics*, **2014**, 15, 127	4.5	63
184	Designing of peptides with desired half-life in intestine-like environment. *BMC Bioinformatics*, **2014**, 15, 282	3.6	43
183	PCMdb: pancreatic cancer methylation database. *Scientific Reports*, **2014**, 4, 4197	4.9	19
182	Herceptin resistance database for understanding mechanism of resistance in breast cancer patients. *Scientific Reports*, **2014**, 4, 4483	4.9	33
181	QSAR-based models for designing quinazoline/imidazothiazoles/pyrazolopyrimidines based inhibitors against wild and mutant EGFR. *PLoS ONE*, **2014**, 9, e101079	3.7	27
180	Prediction of uridine modifications in tRNA sequences. *BMC Bioinformatics*, **2014**, 15, 326	3.6	21
179	ParaPep: a web resource for experimentally validated antiparasitic peptide sequences and their structures. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014,	5	42
178	Hemolytik: a database of experimentally determined hemolytic and non-hemolytic peptides. *Nucleic Acids Research*, **2014**, 42, D444-9	20.1	85
177	ToxiPred: A Server for Prediction of Aqueous Toxicity of Small Chemical Molecules in T. Pyriformis **2014**, 1, 21-27		7
176	Evaluation of protein dihedral angle prediction methods. *PLoS ONE*, **2014**, 9, e105667	3.7	14
175	Tumor homing peptides as molecular probes for cancer therapeutics, diagnostics and theranostics. *Current Medicinal Chemistry*, **2014**, 21, 2367-91	4.3	60
174	EGFRIndb: epidermal growth factor receptor inhibitor database. *Anti-Cancer Agents in Medicinal Chemistry*, **2014**, 14, 928-35	2.2	13
173	In silico approaches for designing highly effective cell penetrating peptides. *Journal of Translational Medicine*, **2013**, 11, 74	8.5	170
172	Designing of inhibitors against drug tolerant Mycobacterium tuberculosis (H37Rv). *Chemistry Central Journal*, **2013**, 7, 49		17

171	Prediction of vitamin interacting residues in a vitamin binding protein using evolutionary information. *BMC Bioinformatics*, **2013**, 14, 44	3.6	18
170	PHDcleav: a SVM based method for predicting human Dicer cleavage sites using sequence and secondary structure of miRNA precursors. *BMC Bioinformatics*, **2013**, 14 Suppl 14, S9	3.6	31
169	Development of a model webserver for breed identification using microsatellite DNA marker. *BMC Genetics*, **2013**, 14, 118	2.6	5
168	Designing of interferon-gamma inducing MHC class-II binders. *Biology Direct*, **2013**, 8, 30	7.2	265
167	DrugMint: a webserver for predicting and designing of drug-like molecules. *Biology Direct*, **2013**, 8, 28	7.2	34
166	Computational approach for designing tumor homing peptides. *Scientific Reports*, **2013**, 3, 1607	4.9	48
165	NPACT: Naturally Occurring Plant-based Anti-cancer Compound-Activity-Target database. *Nucleic Acids Research*, **2013**, 41, D1124-9	20.1	170
164	In silico models for B-cell epitope recognition and signaling. *Methods in Molecular Biology*, **2013**, 993, 129-38	1.4	7
163	Genome Sequence of the "Indian Bison Type" Biotype of Mycobacterium avium subsp. paratuberculosis Strain S5. *Genome Announcements*, **2013**, 1,		9
162	Draft Genome Sequence of the Type Species of the Genus Citrobacter, Citrobacter freundii MTCC 1658. *Genome Announcements*, **2013**, 1,		10
161	Draft Genome Sequence of the 2-Chloro-4-Nitrophenol-Degrading Bacterium Arthrobacter sp. Strain SJCon. *Genome Announcements*, **2013**, 1, e0005813		10
160	Draft Genome Sequence of Rhodococcus qingshengii Strain BKS 20-40. *Genome Announcements*, **2013**, 1, e0012813		2
159	Draft Genome Sequence of Rhodococcus triatomae Strain BKS 15-14. *Genome Announcements*, **2013**, 1, e0012913		3
158	Draft Genome Sequence of Acinetobacter baumannii Strain MSP4-16. *Genome Announcements*, **2013**, 1, e0013713		1
157	Draft Genome Sequence of Amycolatopsis decaplanina Strain DSM 44594T. *Genome Announcements*, **2013**, 1, e0013813		3
156	Draft Genome Sequence of Rhodococcus ruber Strain BKS 20-38. *Genome Announcements*, **2013**, 1, e0013913		0
155	Draft Genome Sequence of Streptomyces gancidicus Strain BKS 13-15. *Genome Announcements*, **2013**, 1, e0015013		3
154	CancerDR: cancer drug resistance database. *Scientific Reports*, **2013**, 3, 1445	4.9	79

153   In silico models for designing and discovering novel anticancer peptides. *Scientific Reports*, **2013**, 3, 2984   4.9   149

152   lncRNome: a comprehensive knowledgebase of human long noncoding RNAs. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat034   5   110

151   Identification of B-cell epitopes in an antigen for inducing specific class of antibodies. *Biology Direct*, **2013**, 8, 27   7.2   59

150   In silico approach for predicting toxicity of peptides and proteins. *PLoS ONE*, **2013**, 8, e73957   3.7   600

149   Improved method for linear B-cell epitope prediction using antigen's primary sequence. *PLoS ONE*, **2013**, 8, e62216   3.7   171

148   Genome annotation of Burkholderia sp. SJ98 with special focus on chemotaxis genes. *PLoS ONE*, **2013**, 8, e70624   3.7   7

147   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   3.7   19

146   Prediction of IL4 inducing peptides. *Clinical and Developmental Immunology*, **2013**, 2013, 263952   111

145   Open source software and web services for designing therapeutic molecules. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1172-91   3   17

144   Hybrid approach for predicting coreceptor used by HIV-1 from its V3 loop amino acid sequence. *PLoS ONE*, **2013**, 8, e61437   3.7   16

143   In silico platform for prediction of N-, O- and C-glycosites in eukaryotic protein sequences. *PLoS ONE*, **2013**, 8, e67008   3.7   142

142   On the Development of Vaccine Antigen Databases: Progress, Opportunity, and Challenge **2013**, 117-130

141   ProGlycProt: a repository of experimentally characterized prokaryotic glycoproteins. *Nucleic Acids Research*, **2012**, 40, D388-93   20.1   22

140   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   4.1   23

139   PolysacDB: a database of microbial polysaccharide antigens and their antibodies. *PLoS ONE*, **2012**, 7, e34613   3.7   8

138   GlycoPP: a webserver for prediction of N- and O-glycosites in prokaryotic protein sequences. *PLoS ONE*, **2012**, 7, e40155   3.7   44

137   Predicting sub-cellular localization of tRNA synthetases from their primary structures. *Amino Acids*, **2012**, 42, 1703-13   3.5   7

136   Draft genome sequence of salt-tolerant yeast Debaryomyces hansenii var. hansenii MTCC 234. *Eukaryotic Cell*, **2012**, 11, 961-2   15

135	CPPsite: a curated database of cell penetrating peptides. *Database: the Journal of Biological Databases and Curation*, **2012**, 2012, bas015	5	122
134	Genome sequence of the halotolerant bacterium Imtechella halotolerans K1T. *Journal of Bacteriology*, **2012**, 194, 3731	3.5	3
133	Genome sequence of the marine bacterium Marinilabilia salmonicolor JCM 21150T. *Journal of Bacteriology*, **2012**, 194, 3746	3.5	5
132	ccPDB: compilation and creation of data sets from Protein Data Bank. *Nucleic Acids Research*, **2012**, 40, D486-9	20.1	21
131	Genome sequence of the oleaginous red yeast Rhodosporidium toruloides MTCC 457. *Eukaryotic Cell*, **2012**, 11, 1083-4		51
130	Draft genome sequence of the nitrophenol-degrading actinomycete Rhodococcus imtechensis RKJ300. *Journal of Bacteriology*, **2012**, 194, 3543	3.5	11
129	Genome sequence of the nitroaromatic compound-degrading Bacterium Burkholderia sp. strain SJ98. *Journal of Bacteriology*, **2012**, 194, 3286	3.5	14
128	TumorHoPe: a database of tumor homing peptides. *PLoS ONE*, **2012**, 7, e35187	3.7	80
127	Open source drug discovery--a new paradigm of collaborative research in tuberculosis drug development. *Tuberculosis*, **2011**, 91, 479-86	2.6	32
126	A web server for predicting inhibitors against bacterial target GlmU protein. *BMC Pharmacology*, **2011**, 11, 5		23
125	Analysis and prediction of cancerlectins using evolutionary and domain information. *BMC Research Notes*, **2011**, 4, 237	2.3	17
124	SVM based prediction of RNA-binding proteins using binding residues and evolutionary information. *Journal of Molecular Recognition*, **2011**, 24, 303-13	2.6	88
123	CCDB: a curated database of genes involved in cervix cancer. *Nucleic Acids Research*, **2011**, 39, D975-9	20.1	59
122	Designing of highly effective complementary and mismatch siRNAs for silencing a gene. *PLoS ONE*, **2011**, 6, e23443	3.7	36
121	Identification of mannose interacting residues using local composition. *PLoS ONE*, **2011**, 6, e24039	3.7	22
120	HIVsirDB: a database of HIV inhibiting siRNAs. *PLoS ONE*, **2011**, 6, e25917	3.7	34
119	Prediction of Specificity and Cross-Reactivity of Kinase Inhibitors. *Letters in Drug Design and Discovery*, **2011**, 8, 223-228	0.8	14
118	Bridging innate and adaptive antitumor immunity targeting glycans. *Journal of Biomedicine and Biotechnology*, **2010**, 2010, 354068		14

117	Identification of conformational B-cell Epitopes in an antigen from its primary sequence. *Immunome Research*, **2010**, 6, 6		186
116	AntigenDB: an immunoinformatics database of pathogen antigens. *Nucleic Acids Research*, **2010**, 38, D847-53	7.5	48
115	Prediction and classification of aminoacyl tRNA synthetases using PROSITE domains. *BMC Genomics* , **2010**, 11, 507	4.5	12
114	A simple approach for predicting protein-protein interactions. *Current Protein and Peptide Science*, **2010**, 11, 589-600	2.8	32
113	Prediction of mitochondrial proteins of malaria parasite using split amino acid composition and PSSM profile. *Amino Acids*, **2010**, 39, 101-10	3.5	47
112	KiDoQ: using docking based energy scores to develop ligand based model for predicting antibacterials. *BMC Bioinformatics*, **2010**, 11, 125	3.6	24
111	Identification of NAD interacting residues in proteins. *BMC Bioinformatics*, **2010**, 11, 160	3.6	50
110	Prediction of GTP interacting residues, dipeptides and tripeptides in a protein from its evolutionary information. *BMC Bioinformatics*, **2010**, 11, 301	3.6	35
109	AntiBP2: improved version of antibacterial peptide prediction. *BMC Bioinformatics*, **2010**, 11 Suppl 1, S19	3.6	132
108	Prediction of FAD interacting residues in a protein from its primary sequence using evolutionary information. *BMC Bioinformatics*, **2010**, 11 Suppl 1, S48	3.6	24
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