

Raja Mazumder

List of Publications by Year in descending order

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81
papers

10,268
citations

172457

29
h-index

76900

74
g-index

91
all docs

91
docs citations

91
times ranked

16011
citing authors

#	ARTICLE	IF	CITATIONS
1	The COG database: an updated version includes eukaryotes. BMC Bioinformatics, 2003, 4, 41.	2.6	3,913
2	UniRef: comprehensive and non-redundant UniProt reference clusters. Bioinformatics, 2007, 23, 1282-1288.	4.1	1,144
3	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
4	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. Genome Biology, 2004, 5, R7.	9.6	814
5	CDD: a curated Entrez database of conserved domain alignments. Nucleic Acids Research, 2003, 31, 383-387.	14.5	673
6	Updates to the Symbol Nomenclature for Glycans guidelines. Glycobiology, 2019, 29, 620-624.	2.5	292
7	PIRSF: family classification system at the Protein Information Resource. Nucleic Acids Research, 2004, 32, 112D-114.	14.5	193
8	MMDB: Entrez's 3D-structure database. Nucleic Acids Research, 2003, 31, 474-477.	14.5	137
9	Detection of novel members, structure-function analysis and evolutionary classification of the 2H phosphoesterase superfamily. Nucleic Acids Research, 2002, 30, 5229-5243.	14.5	133
10	Baseline human gut microbiota profile in healthy people and standard reporting template. PLoS ONE, 2019, 14, e0206484.	2.5	133
11	CoreGenes: a computational tool for identifying and cataloging "core" genes in a set of small genomes. BMC Bioinformatics, 2002, 3, 12.	2.6	123
12	GlyGen: Computational and Informatics Resources for Glycoscience. Glycobiology, 2020, 30, 72-73.	2.5	123
13	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor- β Pathway. Gastroenterology, 2018, 154, 195-210.	1.3	105
14	Representative Proteomes: A Stable, Scalable and Unbiased Proteome Set for Sequence Analysis and Functional Annotation. PLoS ONE, 2011, 6, e18910.	2.5	94
15	High-performance integrated virtual environment (HIVE): a robust infrastructure for next-generation sequence data analysis. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw022.	3.0	80
16	BioMuta and BioXpress: mutation and expression knowledgebases for cancer biomarker discovery. Nucleic Acids Research, 2018, 46, D1128-D1136.	14.5	78
17	High-Performance Integrated Virtual Environment (HIVE) Tools and Applications for Big Data Analysis. Genes, 2014, 5, 957-981.	2.4	76
18	BioXpress: an integrated RNA-seq-derived gene expression database for pan-cancer analysis. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	72

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19	A comprehensive protein-centric ID mapping service for molecular data integration. <i>Bioinformatics</i> , 2011, 27, 1190-1191.	4.1	70
20	Determining chemotactic responses by two subsurface microaerophiles using a simplified capillary assay method. <i>Journal of Microbiological Methods</i> , 1999, 37, 255-263.	1.6	64
21	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau022.	3.0	62
22	Enhancement of Fe(III), Co(III), and Cr(VI) reduction at elevated temperatures and by a thermophilic bacterium. <i>Applied Biochemistry and Biotechnology</i> , 1996, 57-58, 923-932.	2.9	49
23	DiMeX: A Text Mining System for Mutation-Disease Association Extraction. <i>PLoS ONE</i> , 2016, 11, e0152725.	2.5	49
24	Structure-based Comparative Analysis and Prediction of N-linked Glycosylation Sites in Evolutionarily Distant Eukaryotes. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 96-104.	6.9	47
25	Mutated CEACAMs Disrupt Transforming Growth Factor Beta Signaling and Alter the Intestinal Microbiome to Promote Colorectal Carcinogenesis. <i>Gastroenterology</i> , 2020, 158, 238-252.	1.3	46
26	HIVE-Hexagon: High-Performance, Parallelized Sequence Alignment for Next-Generation Sequencing Data Analysis. <i>PLoS ONE</i> , 2014, 9, e99033.	2.5	40
27	Generating a focused view of disease ontology cancer terms for pan-cancer data integration and analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav032-bav032.	3.0	40
28	Computational analysis and identification of amino acid sites in dengue E proteins relevant to development of diagnostics and vaccines. <i>Virus Genes</i> , 2007, 35, 175-186.	1.6	34
29	Proteome-Wide Analysis of Single-Nucleotide Variations in the N-Glycosylation Sequon of Human Genes. <i>PLoS ONE</i> , 2012, 7, e36212.	2.5	31
30	OncoMX: A Knowledgebase for Exploring Cancer Biomarkers in the Context of Related Cancer and Healthy Data. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 210-220.	2.1	30
31	Biocompute Objects – A Step towards Evaluation and Validation of Biomedical Scientific Computations. <i>PDA Journal of Pharmaceutical Science and Technology</i> , 2017, 71, 136-146.	0.5	29
32	Enabling precision medicine via standard communication of HTS provenance, analysis, and results. <i>PLoS Biology</i> , 2018, 16, e3000099.	5.6	29
33	Identification of key differentially expressed MicroRNAs in cancer patients through pan-cancer analysis. <i>Computers in Biology and Medicine</i> , 2018, 103, 183-197.	7.0	28
34	The GlySpace Alliance: toward a collaborative global glycoinformatics community. <i>Glycobiology</i> , 2020, 30, 70-71.	2.5	28
35	GeneOrder: comparing the order of genes in small genomes. <i>Bioinformatics</i> , 2001, 17, 162-166.	4.1	25
36	Human germline and pan-cancer variomes and their distinct functional profiles. <i>Nucleic Acids Research</i> , 2014, 42, 11570-11588.	14.5	22

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37	GlyGen data model and processing workflow. <i>Bioinformatics</i> , 2020, 36, 3941-3943.	4.1	22
38	Community annotation in biology. <i>Biology Direct</i> , 2010, 5, 12.	4.6	21
39	Higher levels of Bifidobacteria and tumor necrosis factor in children with drug-resistant epilepsy are associated with anti-seizure response to the ketogenic diet. <i>EBioMedicine</i> , 2022, 80, 104061.	6.1	21
40	Whole genome single-nucleotide variation profile-based phylogenetic tree building methods for analysis of viral, bacterial and human genomes. <i>Genomics</i> , 2014, 104, 1-7.	2.9	19
41	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. <i>PLoS ONE</i> , 2009, 4, e7162.	2.5	18
42	Census-based rapid and accurate metagenome taxonomic profiling. <i>BMC Genomics</i> , 2014, 15, 918.	2.8	18
43	GeneOrder3.0: software for comparing the order of genes in pairs of small bacterial genomes. <i>BMC Bioinformatics</i> , 2004, 5, 52.	2.6	17
44	Computational identification of strain-, species- and genus-specific proteins. <i>BMC Bioinformatics</i> , 2005, 6, 279.	2.6	16
45	Sequence signatures in envelope protein may determine whether flaviviruses produce hemorrhagic or encephalitic syndromes. <i>Virus Genes</i> , 2009, 39, 1-9.	1.6	16
46	Low-Substrate Regulated Microaerophilic Behavior as a Stress Response of Aquatic and Soil Bacteria. <i>Current Microbiology</i> , 2000, 41, 79-83.	2.2	15
47	SNVDis: A Proteome-wide Analysis Service for Evaluating nsSNVs in Protein Functional Sites and Pathways. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 122-126.	6.9	15
48	Single-Nucleotide Variations in Cardiac Arrhythmias: Prospects for Genomics and Proteomics Based Biomarker Discovery and Diagnostics. <i>Genes</i> , 2014, 5, 254-269.	2.4	15
49	Loss and gain of N-linked glycosylation sequons due to single-nucleotide variation in cancer. <i>Scientific Reports</i> , 2018, 8, 4322.	3.3	15
50	Structure–function analysis of hepatitis C virus envelope glycoproteins E1 and E2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1682-1694.	3.5	13
51	Comparisons of gene colinearity in genomes using GeneOrder2.0. <i>Trends in Biochemical Sciences</i> , 2001, 26, 514-516.	7.5	12
52	Proteome-wide analysis of nonsynonymous single-nucleotide variations in active sites of human proteins. <i>FEBS Journal</i> , 2013, 280, 1542-1562.	4.7	12
53	Non-synonymous variations in cancer and their effects on the human proteome: workflow for NGS data biocuration and proteome-wide analysis of TCGA data. <i>BMC Bioinformatics</i> , 2014, 15, 28.	2.6	12
54	Investigation of somatic single nucleotide variations in human endogenous retrovirus elements and their potential association with cancer. <i>PLoS ONE</i> , 2019, 14, e0213770.	2.5	12

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55	Separation and assembly of deep sequencing data into discrete sub-population genomes. <i>Nucleic Acids Research</i> , 2017, 45, 10989-11003.	14.5	11
56	DEXTER: Disease-Expression Relation Extraction from Text. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	11
57	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
58	Structure-Guided Comparative Analysis of Proteins: Principles, Tools, and Applications for Predicting Function. <i>PLoS Computational Biology</i> , 2008, 4, e1000151.	3.2	9
59	Mice with dysfunctional TGF- β 2 signaling develop altered intestinal microbiome and colorectal cancer resistant to 5FU. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166179.	3.8	8
60	Bioinformatics and machine learning in gastrointestinal microbiome research and clinical application. <i>Progress in Molecular Biology and Translational Science</i> , 2020, 176, 141-178.	1.7	7
61	Bioinformatics tools developed to support BioCompute Objects. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	7
62	Germ Line Variants of Human N-Methylpurine DNA Glycosylase Show Impaired DNA Repair Activity and Facilitate 1,N6-Ethenoadenine-induced Mutations. <i>Journal of Biological Chemistry</i> , 2015, 290, 4966-4980.	3.4	6
63	A Primer for Access to Repositories of Cancer-Related Genomic Big Data. <i>Methods in Molecular Biology</i> , 2019, 1878, 1-37.	0.9	4
64	Computational clustering for viral reference proteomes: Table 1.. <i>Bioinformatics</i> , 2016, 32, 2041-2043.	4.1	3
65	Protein Functional Annotation by Homology. <i>Methods in Molecular Biology</i> , 2008, 484, 465-490.	0.9	3
66	Biocuration Virtual Issue 2012. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas011-bas011.	3.0	2
67	miCloud: A Plug-n-Play, Extensible, On-Premises Bioinformatics Cloud for Seamless Execution of Complex Next-Generation Sequencing Data Analysis Pipelines. <i>Journal of Computational Biology</i> , 2019, 26, 280-284.	1.6	2
68	Glycoinformatics Resources Integrated Through the GlySpace Alliance. , 2021, , 507-521.		2
69	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. <i>Glycobiology</i> , 2021, , .	2.5	2
70	Impact of Nonsynonymous Single-Nucleotide Variations on Post-Translational Modification Sites in Human Proteins. <i>Methods in Molecular Biology</i> , 2017, 1558, 159-190.	0.9	2
71	A framework for application of metabolic modeling in yeast to predict the effects of nsSNV in human orthologs. <i>Biology Direct</i> , 2014, 9, 9.	4.6	1
72	Distribution bias analysis of germline and somatic single-nucleotide variations that impact protein functional site and neighboring amino acids. <i>Scientific Reports</i> , 2017, 7, 42169.	3.3	1

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73	Streamlined Subpopulation, Subtype, and Recombination Analysis of HIV-1 Half-Genome Sequences Generated by High-Throughput Sequencing. <i>MSphere</i> , 2020, 5, .	2.9	1
74	Communicating regulatory high-throughput sequencing data using BioCompute Objects. <i>Drug Discovery Today</i> , 2022, 27, 1108-1114.	6.4	1
75	Application of global computational tools GeneOrder and CoreGenes to the comparative analyses of chordopoxvirus genomes. <i>Information Sciences</i> , 2002, 146, 127-135.	6.9	0
76	The PIR SuperFamily (PIRSF) classification system. , 2005, , .		0
77	Enhanced Interface for Retrieving Glycan and Glycosylation Data from GlyGen. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
78	Non-synonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies. , 2015, , 1-27.		0
79	Nonsynonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies. , 2016, , 821-847.		0
80	Whole Genome Variant Dataset for Enriching Studies across 18 Different Cancers. <i>Onco</i> , 2022, 2, 129-144.	0.6	0
81	Cardiomyocyte-specific regression of nitrosative stress-mediated S-Nitrosylation of IKK β alleviates pathological cardiac hypertrophy. <i>Cellular Signalling</i> , 2022, 98, 110403.	3.6	0