

Raja Mazumder

List of Publications by Year in descending order

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Version: 2024-02-01

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	Communicating regulatory high-throughput sequencing data using BioCompute Objects. <i>Drug Discovery Today</i> , 2022, 27, 1108-1114.	6.4	1
2	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
3	Whole Genome Variant Dataset for Enriching Studies across 18 Different Cancers. <i>Onco</i> , 2022, 2, 129-144.	0.6	0
4	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
5	Glycoinformatics Resources Integrated Through the GlySpace Alliance. , 2021, , 507-521.		2
6	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
7	Enhanced Interface for Retrieving Glycan and Glycosylation Data from GlyGen. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
8	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. <i>Glycobiology</i> , 2021, , .	2.5	2
9	Mice with dysfunctional TGF- β 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
10	Bioinformatics tools developed to support BioCompute Objects. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	7
11	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
12	The GlySpace Alliance: toward a collaborative global glycoinformatics community. <i>Glycobiology</i> , 2020, 30, 70-71.	2.5	28
13	GlyGen: Computational and Informatics Resources for Glycoscience. <i>Glycobiology</i> , 2020, 30, 72-73.	2.5	123
14	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
15	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
16	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
17	GlyGen data model and processing workflow. <i>Bioinformatics</i> , 2020, 36, 3941-3943.	4.1	22
18	Baseline human gut microbiota profile in healthy people and standard reporting template. <i>PLoS ONE</i> , 2019, 14, e0206484.	2.5	133

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19	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
20	Updates to the Symbol Nomenclature for Glycans guidelines. <i>Glycobiology</i> , 2019, 29, 620-624.	2.5	292
21	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
22	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
23	BioMuta and BioXpress: mutation and expression knowledgebases for cancer biomarker discovery. <i>Nucleic Acids Research</i> , 2018, 46, D1128-D1136.	14.5	78
24	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
25	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor- β Pathway. <i>Gastroenterology</i> , 2018, 154, 195-210.	1.3	105
26	Enabling precision medicine via standard communication of HTS provenance, analysis, and results. <i>PLoS Biology</i> , 2018, 16, e3000099.	5.6	29
27	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
28	DEXTER: Disease-Expression Relation Extraction from Text. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	11
29	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
30	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
31	Separation and assembly of deep sequencing data into discrete sub-population genomes. <i>Nucleic Acids Research</i> , 2017, 45, 10989-11003.	14.5	11
32	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
33	High-performance integrated virtual environment (HIVE): a robust infrastructure for next-generation sequence data analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw022.	3.0	80
34	Computational clustering for viral reference proteomes: Table 1.. <i>Bioinformatics</i> , 2016, 32, 2041-2043.	4.1	3
35	DiMeX: A Text Mining System for Mutation-Disease Association Extraction. <i>PLoS ONE</i> , 2016, 11, e0152725.	2.5	49
36	Nonsynonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies. , 2016, , 821-847.		0

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37	Generating a focused view of disease ontology cancer terms for pan-cancer data integration and analysis. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav032-bav032.	3.0	40
38	Germ Line Variants of Human N-Methylpurine DNA Glycosylase Show Impaired DNA Repair Activity and Facilitate 1,N6-Ethenoadenine-induced Mutations. Journal of Biological Chemistry, 2015, 290, 4966-4980.	3.4	6
39	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
40	Structureâ€“function analysis of hepatitis C virus envelope glycoproteins E1 and E2. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1682-1694.	3.5	13
41	Non-synonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies. , 2015, , 1-27.		0
42	HIVE-Hexagon: High-Performance, Parallelized Sequence Alignment for Next-Generation Sequencing Data Analysis. PLoS ONE, 2014, 9, e99033.	2.5	40
43	Single-Nucleotide Variations in Cardiac Arrhythmias: Prospects for Genomics and Proteomics Based Biomarker Discovery and Diagnostics. Genes, 2014, 5, 254-269.	2.4	15
44	High-Performance Integrated Virtual Environment (HIVE) Tools and Applications for Big Data Analysis. Genes, 2014, 5, 957-981.	2.4	76
45	Human germline and pan-cancer variomes and their distinct functional profiles. Nucleic Acids Research, 2014, 42, 11570-11588.	14.5	22
46	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). Database: the Journal of Biological Databases and Curation, 2014, 2014, bau022.	3.0	62
47	Census-based rapid and accurate metagenome taxonomic profiling. BMC Genomics, 2014, 15, 918.	2.8	18
48	Non-synonymous variations in cancer and their effects on the human proteome: workflow for NGS data biocuration and proteome-wide analysis of TCGA data. BMC Bioinformatics, 2014, 15, 28.	2.6	12
49	Whole genome single-nucleotide variation profile-based phylogenetic tree building methods for analysis of viral, bacterial and human genomes. Genomics, 2014, 104, 1-7.	2.9	19
50	A framework for application of metabolic modeling in yeast to predict the effects of nsSNV in human orthologs. Biology Direct, 2014, 9, 9.	4.6	1
51	Structure-based Comparative Analysis and Prediction of N-linked Glycosylation Sites in Evolutionarily Distant Eukaryotes. Genomics, Proteomics and Bioinformatics, 2013, 11, 96-104.	6.9	47
52	SNVDis: A Proteome-wide Analysis Service for Evaluating nsSNVs in Protein Functional Sites and Pathways. Genomics, Proteomics and Bioinformatics, 2013, 11, 122-126.	6.9	15
53	Proteomeâ€“wide analysis of nonsynonymous singleâ€“nucleotide variations in active sites of human proteins. FEBS Journal, 2013, 280, 1542-1562.	4.7	12
54	Biocuration Virtual Issue 2012. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas011-bas011.	3.0	2

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55	Proteome-Wide Analysis of Single-Nucleotide Variations in the N-Glycosylation Sequon of Human Genes. PLoS ONE, 2012, 7, e36212.	2.5	31
56	A comprehensive protein-centric ID mapping service for molecular data integration. Bioinformatics, 2011, 27, 1190-1191.	4.1	70
57	Representative Proteomes: A Stable, Scalable and Unbiased Proteome Set for Sequence Analysis and Functional Annotation. PLoS ONE, 2011, 6, e18910.	2.5	94
58	Community annotation in biology. Biology Direct, 2010, 5, 12.	4.6	21
59	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. PLoS ONE, 2009, 4, e7162.	2.5	18
60	Sequence signatures in envelope protein may determine whether flaviviruses produce hemorrhagic or encephalitic syndromes. Virus Genes, 2009, 39, 1-9.	1.6	16
61	Structure-Guided Comparative Analysis of Proteins: Principles, Tools, and Applications for Predicting Function. PLoS Computational Biology, 2008, 4, e1000151.	3.2	9
62	Protein Functional Annotation by Homology. Methods in Molecular Biology, 2008, 484, 465-490.	0.9	3
63	UniRef: comprehensive and non-redundant UniProt reference clusters. Bioinformatics, 2007, 23, 1282-1288.	4.1	1,144
64	Computational analysis and identification of amino acid sites in dengue E proteins relevant to development of diagnostics and vaccines. Virus Genes, 2007, 35, 175-186.	1.6	34
65	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
66	Computational identification of strain-, species- and genus-specific proteins. BMC Bioinformatics, 2005, 6, 279.	2.6	16
67	The PIR SuperFamily (PIRSF) classification system. , 2005, , .		0
68	PIRSF: family classification system at the Protein Information Resource. Nucleic Acids Research, 2004, 32, 112D-114.	14.5	193
69	GeneOrder3.0: software for comparing the order of genes in pairs of small bacterial genomes. BMC Bioinformatics, 2004, 5, 52.	2.6	17
70	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. Genome Biology, 2004, 5, R7.	9.6	814
71	The COG database: an updated version includes eukaryotes. BMC Bioinformatics, 2003, 4, 41.	2.6	3,913
72	CDD: a curated Entrez database of conserved domain alignments. Nucleic Acids Research, 2003, 31, 383-387.	14.5	673

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73	MMDB: Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2003, 31, 474-477.	14.5	137
74	Detection of novel members, structure-function analysis and evolutionary classification of the 2H phosphoesterase superfamily. <i>Nucleic Acids Research</i> , 2002, 30, 5229-5243.	14.5	133
75	CoreGenes: a computational tool for identifying and cataloging "core" genes in a set of small genomes. <i>BMC Bioinformatics</i> , 2002, 3, 12.	2.6	123
76	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
77	Comparisons of gene colinearity in genomes using GeneOrder2.0. <i>Trends in Biochemical Sciences</i> , 2001, 26, 514-516.	7.5	12
78	GeneOrder: comparing the order of genes in small genomes. <i>Bioinformatics</i> , 2001, 17, 162-166.	4.1	25
79	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
80	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
81	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