

Raja Mazumder

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75
papers

7,972
citations

28
h-index

89
g-index

91
ext. papers

9,303
ext. citations

6.6
avg, IF

5.05
L-index

#	Paper	IF	Citations
75	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	8.8	2
74	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
73	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. <i>Glycobiology</i> , 2021 ,	5.8	1
72	Glycoinformatics Resources Integrated Through the GlySpace Alliance 2021 , 507-521		0
71	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	6.9	2
70	Bioinformatics tools developed to support BioCompute Objects. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	2
69	Bioinformatics and machine learning in gastrointestinal microbiome research and clinical application. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 176, 141-178	4	4
68	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	5.2	13
67	GlyGen data model and processing workflow. <i>Bioinformatics</i> , 2020 , 36, 3941-3943	7.2	10
66	COVID-19 Biomarkers in research: Extension of the OncoMX cancer biomarker data model to capture biomarker data from other diseases 2020 ,		2
65	Mutated CEACAMs Disrupt Transforming Growth Factor Beta Signaling and Alter the Intestinal Microbiome to Promote Colorectal Carcinogenesis. <i>Gastroenterology</i> , 2020 , 158, 238-252	13.3	21
64	The GlySpace Alliance: toward a collaborative global glycoinformatics community. <i>Glycobiology</i> , 2020 , 30, 70-71	5.8	15
63	GlyGen: Computational and Informatics Resources for Glycoscience. <i>Glycobiology</i> , 2020 , 30, 72-73	5.8	53
62	Baseline human gut microbiota profile in healthy people and standard reporting template. <i>PLoS ONE</i> , 2019 , 14, e0206484	3.7	59
61	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	1.7	0
60	Updates to the Symbol Nomenclature for Glycans guidelines. <i>Glycobiology</i> , 2019 , 29, 620-624	5.8	148
59	Investigation of somatic single nucleotide variations in human endogenous retrovirus elements and their potential association with cancer. <i>PLoS ONE</i> , 2019 , 14, e0213770	3.7	4

58	A Primer for Access to Repositories of Cancer-Related Genomic Big Data. <i>Methods in Molecular Biology</i> , 2019 , 1878, 1-37	1.4	3
57	BioMuta and BioXpress: mutation and expression knowledgebases for cancer biomarker discovery. <i>Nucleic Acids Research</i> , 2018 , 46, D1128-D1136	20.1	49
56	Loss and gain of N-linked glycosylation sequons due to single-nucleotide variation in cancer. <i>Scientific Reports</i> , 2018 , 8, 4322	4.9	12
55	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	13.3	68
54	DEXTER: Disease-Expression Relation Extraction from Text. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	7
53	Enabling precision medicine via standard communication of HTS provenance, analysis, and results. <i>PLoS Biology</i> , 2018 , 16, e3000099	9.7	16
52	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	19
51	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	4.9	0
50	Separation and assembly of deep sequencing data into discrete sub-population genomes. <i>Nucleic Acids Research</i> , 2017 , 45, 10989-11003	20.1	7
49	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	0.6	17
48	Impact of Nonsynonymous Single-Nucleotide Variations on Post-Translational Modification Sites in Human Proteins. <i>Methods in Molecular Biology</i> , 2017 , 1558, 159-190	1.4	2
47	Computational clustering for viral reference proteomes. <i>Bioinformatics</i> , 2016 , 32, 2041-3	7.2	2
46	DiMeX: A Text Mining System for Mutation-Disease Association Extraction. <i>PLoS ONE</i> , 2016 , 11, e0152725	5.7	36
45	Nonsynonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies 2016 , 821-847		
44	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,	5	36
43	BioXpress: an integrated RNA-seq-derived gene expression database for pan-cancer analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	60
42	Structure-function analysis of hepatitis C virus envelope glycoproteins E1 and E2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015 , 33, 1682-94	3.6	12
41	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	5	32

40	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	5.4	6
39	Non-synonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies 2015 , 1-27		
38	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	3.6	11
37	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	4.3	14
36	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	7.2	1
35	HIVE-hexagon: high-performance, parallelized sequence alignment for next-generation sequencing data analysis. <i>PLoS ONE</i> , 2014 , 9, e99033	3.7	29
34	Single-nucleotide variations in cardiac arrhythmias: prospects for genomics and proteomics based biomarker discovery and diagnostics. <i>Genes</i> , 2014 , 5, 254-69	4.2	9
33	High-Performance Integrated Virtual Environment (HIVE) Tools and Applications for Big Data Analysis. <i>Genes</i> , 2014 , 5, 957-81	4.2	44
32	Human germline and pan-cancer variomes and their distinct functional profiles. <i>Nucleic Acids Research</i> , 2014 , 42, 11570-88	20.1	20
31	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	5	52
30	Census-based rapid and accurate metagenome taxonomic profiling. <i>BMC Genomics</i> , 2014 , 15, 918	4.5	15
29	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	6.5	37
28	SNVDis: a proteome-wide analysis service for evaluating nsSNVs in protein functional sites and pathways. <i>Genomics, Proteomics and Bioinformatics</i> , 2013 , 11, 122-6	6.5	12
27	Proteome-wide analysis of nonsynonymous single-nucleotide variations in active sites of human proteins. <i>FEBS Journal</i> , 2013 , 280, 1542-62	5.7	10
26	Proteome-wide analysis of single-nucleotide variations in the N-glycosylation sequon of human genes. <i>PLoS ONE</i> , 2012 , 7, e36212	3.7	30
25	A comprehensive protein-centric ID mapping service for molecular data integration. <i>Bioinformatics</i> , 2011 , 27, 1190-1	7.2	51
24	Representative proteomes: a stable, scalable and unbiased proteome set for sequence analysis and functional annotation. <i>PLoS ONE</i> , 2011 , 6, e18910	3.7	67
23	Community annotation in biology. <i>Biology Direct</i> , 2010 , 5, 12	7.2	17

22	Systems integration of biodefense omics data for analysis of pathogen-host interactions and identification of potential targets. <i>PLoS ONE</i> , 2009 , 4, e7162	3.7	16
21	Sequence signatures in envelope protein may determine whether flaviviruses produce hemorrhagic or encephalitic syndromes. <i>Virus Genes</i> , 2009 , 39, 1-9	2.3	12
20	Structure-guided comparative analysis of proteins: principles, tools, and applications for predicting function. <i>PLoS Computational Biology</i> , 2008 , 4, e1000151	5	7
19	Protein functional annotation by homology. <i>Methods in Molecular Biology</i> , 2008 , 484, 465-90	1.4	2
18	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, 175-86	2.3	33
17	UniRef: comprehensive and non-redundant UniProt reference clusters. <i>Bioinformatics</i> , 2007 , 23, 1282-8	7.2	788
16	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006 , 34, D187-91	20.1	839
15	Computational identification of strain-, species- and genus-specific proteins. <i>BMC Bioinformatics</i> , 2005 , 6, 279	3.6	15
14	PIRSF: family classification system at the Protein Information Resource. <i>Nucleic Acids Research</i> , 2004 , 32, D112-4	20.1	165
13	GeneOrder3.0: software for comparing the order of genes in pairs of small bacterial genomes. <i>BMC Bioinformatics</i> , 2004 , 5, 52	3.6	13
12	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. <i>Genome Biology</i> , 2004 , 5, R7	18.3	602
11	The COG database: an updated version includes eukaryotes. <i>BMC Bioinformatics</i> , 2003 , 4, 41	3.6	3212
10	CDD: a curated Entrez database of conserved domain alignments. <i>Nucleic Acids Research</i> , 2003 , 31, 383-7	20.1	620
9	MMDB: Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2003 , 31, 474-7	20.1	128
8	CoreGenes: a computational tool for identifying and cataloging "core" genes in a set of small genomes. <i>BMC Bioinformatics</i> , 2002 , 3, 12	3.6	105
7	Application of global computational tools GeneOrder and CoreGenes to the comparative analyses of chordopoxvirus genomes. <i>Information Sciences</i> , 2002 , 146, 127-135	7.7	
6	Detection of novel members, structure-function analysis and evolutionary classification of the 2H phosphoesterase superfamily. <i>Nucleic Acids Research</i> , 2002 , 30, 5229-43	20.1	117
5	Comparisons of gene colinearity in genomes using GeneOrder2.0. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 514-6	10.3	10

4	GeneOrder: comparing the order of genes in small genomes. <i>Bioinformatics</i> , 2001 , 17, 162-6	7.2	22
3	Low-substrate regulated microaerophilic behavior as a stress response of aquatic and soil bacteria. <i>Current Microbiology</i> , 2000 , 41, 79-83	2.4	15
2	Determining chemotactic responses by two subsurface microaerophiles using a simplified capillary assay method. <i>Journal of Microbiological Methods</i> , 1999 , 37, 255-63	2.8	49
1	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	3.2	48