

Debasis Dash

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

3,020
citations

201674
27
h-index

189892
50
g-index

89
all docs

89
docs citations

89
times ranked

4948
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic landscape of the people of India: a canvas for disease gene exploration. Journal of Genetics, 2008, 87, 3-20.	0.7	282
2	Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India. Science, 2021, 374, 995-999.	12.6	230
3	The Indian Genome Variation database (IGVdb): a project overview. Human Genetics, 2005, 118, 1-11.	3.8	154
4	Integrating transcriptome and proteome profiling: Strategies and applications. Proteomics, 2016, 16, 2533-2544.	2.2	147
5	Proteogenomic Analysis of Mycobacterium tuberculosis By High Resolution Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M111.011445.	3.8	145
6	Role of intrinsic disorder in transient interactions of hub proteins. Proteins: Structure, Function and Bioinformatics, 2006, 66, 761-765.	2.6	143
7	Transcriptome and venom proteome of the box jellyfish Chironex fleckeri. BMC Genomics, 2015, 16, 407.	2.8	103
8	A Systematic Analysis of Eluted Fraction of Plasma Post Immunoaffinity Depletion: Implications in Biomarker Discovery. PLoS ONE, 2011, 6, e24442.	2.5	87
9	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. Proteins: Structure, Function and Bioinformatics, 2005, 62, 309-315.	2.6	86
10	Exosome-enclosed microRNAs in exhaled breath hold potential for biomarker discovery in patients with pulmonary diseases. Journal of Allergy and Clinical Immunology, 2013, 132, 219-222.e7.	2.9	70
11	Western Indian Rural Gut Microbial Diversity in Extreme Prakriti Endo-Phenotypes Reveals Signature Microbes. Frontiers in Microbiology, 2018, 9, 118.	3.5	68
12	Intrinsic disorder in yeast transcriptional regulatory network. Proteins: Structure, Function and Bioinformatics, 2007, 68, 602-605.	2.6	62
13	HGVbaseG2P: a central genetic association database. Nucleic Acids Research, 2009, 37, D797-D802.	14.5	60
14	Polyketide Quinones Are Alternate Intermediate Electron Carriers during Mycobacterial Respiration in Oxygen-Deficient Niches. Molecular Cell, 2015, 60, 637-650.	9.7	53
15	MassWiz: A Novel Scoring Algorithm with Target-Decoy Based Analysis Pipeline for Tandem Mass Spectrometry. Journal of Proteome Research, 2011, 10, 2154-2160.	3.7	46
16	Comparative Genomics of Host-Associated Symbiont and Free-Living Oceanobacillus Species. Genome Biology and Evolution, 2017, 9, 1175-1182.	2.5	44
17	Expression profiling of lymph nodes in tuberculosis patients reveal inflammatory milieu at site of infection. Scientific Reports, 2015, 5, 15214.	3.3	43
18	Role of histidine interruption in mitigating the pathological effects of long polyglutamine stretches in SCA1: A molecular approach. Protein Science, 2003, 12, 953-962.	7.6	42

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19	Open source drug discoveryâ€“ A new paradigm of collaborative research in tuberculosis drug development. <i>Tuberculosis</i> , 2011, 91, 479-86.	1.9	42
20	Proteogenomic Analysis of <i>Bradyrhizobium japonicum</i> USDA110 Using Genosuite, an Automated Multi-algorithmic Pipeline. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3388-3397.	3.8	39
21	Spectrum of β -thalassemia mutations and their association with allelic sequence polymorphisms at the β -globin gene cluster in an eastern Indian population. <i>American Journal of Hematology</i> , 2002, 70, 269-277.	4.1	38
22	Ayurgenomics for stratified medicine: TRISUTRA consortium initiative across ethnically and geographically diverse Indian populations. <i>Journal of Ethnopharmacology</i> , 2017, 197, 274-293.	4.1	38
23	Crowd Sourcing a New Paradigm for Interactome Driven Drug Target Identification in <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2012, 7, e39808.	2.5	36
24	Integrated Transcriptomic-Proteomic Analysis Using a Proteogenomic Workflow Refines Rat Genome Annotation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 329-339.	3.8	35
25	Recapitulation of Ayurveda constitution types by machine learning of phenotypic traits. <i>PLoS ONE</i> , 2017, 12, e0185380.	2.5	35
26	Quantitative Lipid Droplet Proteomics Reveals <i>Mycobacterium tuberculosis</i> Induced Alterations in Macrophage Response to Infection. <i>ACS Infectious Diseases</i> , 2019, 5, 559-569.	3.8	33
27	Recent Admixture in an Indian Population of African Ancestry. <i>American Journal of Human Genetics</i> , 2011, 89, 111-120.	6.2	32
28	A web server for predicting inhibitors against bacterial target GlmU protein. <i>BMC Pharmacology</i> , 2011, 11, 5.	0.4	31
29	Telomere repeatâ€“binding factor 2 binds extensively to extra-telomeric G-quadruplexes and regulates the epigenetic status of several gene promoters. <i>Journal of Biological Chemistry</i> , 2019, 294, 17709-17722.	3.4	31
30	IGVBrowser-a genomic variation resource from diverse Indian populations. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq022-baq022.	3.0	30
31	In silico characterization of the INO80 subfamily of SWI2/SNF2 chromatin remodeling proteins. <i>Biochemical and Biophysical Research Communications</i> , 2004, 320, 197-204.	2.1	27
32	Knowledge engineering for health: A new discipline required to bridge the â€œICT gapâ€•between research and healthcare. <i>Human Mutation</i> , 2012, 33, 797-802.	2.5	27
33	Intramolecular i-motif Structure at Acidic pH for Progressive Myoclonus Epilepsy (EPM1) Repeat d(CCCCGCCCCGCG) _n . <i>Journal of Biomolecular Structure and Dynamics</i> , 2001, 19, 307-313.	3.5	26
34	Association of CAG repeat loci on chromosome 22 with schizophrenia and bipolar disorder. <i>Molecular Psychiatry</i> , 2001, 6, 694-700.	7.9	25
35	Choosing an Optimal Database for Protein Identification from Tandem Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 17-29.	0.9	25
36	Extensive Copy Number Variations in Admixed Indian Population of African Ancestry: Potential Involvement in Adaptation. <i>Genome Biology and Evolution</i> , 2014, 6, 3171-3181.	2.5	23

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37	Novel mutations in typical and atypical genetic loci through exome sequencing in autosomal recessive cerebellar ataxia families. <i>Clinical Genetics</i> , 2014, 86, 335-341.	2.0	22
38	Adipocyte Model of Mycobacterium tuberculosis Infection Reveals Differential Availability of Iron to Bacilli in the Lipid-Rich Caseous Environment. <i>Infection and Immunity</i> , 2018, 86, .	2.2	22
39	Dynamic α -helices: Conformations that do not conform. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 109-122.	2.6	21
40	Insights from a Pan India Sero-Epidemiological survey (Phenome-India Cohort) for SARS-CoV2. <i>ELife</i> , 2021, 10, .	6.0	21
41	Unraveling the potential of intrinsically disordered proteins as drug targets: application to Mycobacterium tuberculosis. <i>Molecular BioSystems</i> , 2009, 5, 1752.	2.9	20
42	Downregulation of peripheral PTGS2/COX-2 in response to valproate treatment in patients with epilepsy. <i>Scientific Reports</i> , 2020, 10, 2546.	3.3	20
43	Comparative analysis of protein unfoldedness in human housekeeping and non-housekeeping proteins. <i>Bioinformatics</i> , 2004, 20, 2904-2910.	4.1	18
44	The phenotype and genotype experiment object model (PaGE-OM): a robust data structure for information related to DNA variation. <i>Human Mutation</i> , 2009, 30, 968-977.	2.5	18
45	ProteoStats—a library for estimating false discovery rates in proteomics pipelines. <i>Bioinformatics</i> , 2013, 29, 2799-2800.	4.1	18
46	Origin and Instability of GAA Repeats: Insights from Alu Elements. <i>Journal of Biomolecular Structure and Dynamics</i> , 2002, 20, 253-263.	3.5	17
47	Conformational flexibility may explain multiple cellular roles of PEST motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 727-732.	2.6	17
48	Spectrum of large copy number variations in 26 diverse Indian populations: potential involvement in phenotypic diversity. <i>Human Genetics</i> , 2012, 131, 131-143.	3.8	17
49	Discovery of rare protein-coding genes in model methylotroph <i>Methylobacterium extorquens</i> AM1. <i>Proteomics</i> , 2014, 14, 2790-2794.	2.2	17
50	Learning from Decoys to Improve the Sensitivity and Specificity of Proteomics Database Search Results. <i>PLoS ONE</i> , 2012, 7, e50651.	2.5	17
51	A Novel Complexity Measure for Comparative Analysis of Protein Sequences from Complete Genomes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003, 20, 657-667.	3.5	16
52	Conformational Analysis of Invariant Peptide Sequences in Bacterial Genomes. <i>Journal of Molecular Biology</i> , 2005, 345, 937-955.	4.2	16
53	Location of disorder in coiled coil proteins is influenced by its biological role and subcellular localization: a GO-based study on human proteome. <i>Molecular BioSystems</i> , 2012, 8, 346-352.	2.9	16
54	Data Intensive Genome Level Analysis for Identifying Novel, Non-Toxic Drug Targets for Multi Drug Resistant Mycobacterium tuberculosis. <i>Scientific Reports</i> , 2017, 7, 46595.	3.3	14

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55	Progressive Myoclonus Epilepsy [EPM1] repeat d(CCCCGCCCCGCG)n forms folded hairpin structures at physiological pH. Journal of Biomolecular Structure and Dynamics, 2001, 19, 293-305.	3.5	12
56	Proteogenomics of rare taxonomic phyla: A prospective treasure trove of protein coding genes. Proteomics, 2016, 16, 226-240.	2.2	12
57	Sputum Protein Biomarkers in Airway Diseases: A Pilot Study. International Journal of COPD, 2021, Volume 16, 2203-2215.	2.3	12
58	CoPS: Comprehensive Peptide Signature Database. Bioinformatics, 2004, 20, 2886-2888.	4.1	11
59	False discovery rate: the Achilles' heel of proteogenomics. Briefings in Bioinformatics, 2022, 23, .	6.5	11
60	Proteogenomic Tools and Approaches to Explore Protein Coding Landscapes of Eukaryotic Genomes. Advances in Experimental Medicine and Biology, 2016, 926, 1-10.	1.6	10
61	Investigating Coronary Artery Disease methylome through targeted bisulfite sequencing. Gene, 2019, 721, 144107.	2.2	10
62	Electrostatic Mis-Interactions Cause Overexpression Toxicity of Proteins in E. coli. PLoS ONE, 2013, 8, e64893.	2.5	9
63	Gene-Rich Large Deletions Are Overrepresented in POAG Patients of Indian and Caucasian Origins. , 2014, 55, 3258.		9
64	The complete chloroplast genome of <i>Dendrobium nobile</i> , an endangered medicinal orchid from north-east India and its comparison with related <i>Dendrobium</i> species. PeerJ, 2019, 7, e7756.	2.0	9
65	Selection of relevant features from amino acids enables development of robust classifiers. Amino Acids, 2014, 46, 1343-1351.	2.7	8
66	Fusion transcripts in normal human cortex increase with age and show distinct genomic features for single cells and tissues. Scientific Reports, 2020, 10, 1368.	3.3	8
67	Validation of expert system enhanced deep learning algorithm for automated screening for COVID-Pneumonia on chest X-rays. Scientific Reports, 2021, 11, 23210.	3.3	8
68	A machine learning-based approach to determine infection status in recipients of BBV152 (Covaxin) whole-virion inactivated SARS-CoV-2 vaccine for serological surveys. Computers in Biology and Medicine, 2022, 146, 105419.	7.0	8
69	How expression level influences the disorderiness of proteins. Biochemical and Biophysical Research Communications, 2008, 371, 401-404.	2.1	7
70	Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. Pharmacogenomics, 2021, 22, 603-618.	1.3	7
71	Recognition and analysis of protein-coding genes in severe acute respiratory syndrome associated coronavirus. Bioinformatics, 2004, 20, 1074-1080.	4.1	6
72	Probing the Missing Human Proteome: A Computational Perspective. Journal of Proteome Research, 2015, 14, 4949-4958.	3.7	6

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73	VitiVar: A locus specific database of vitiligo associated genes and variations. Gene: X, 2019, 721, 100018.	2.3	6
74	High failure rate of ChAdOx1-nCoV19 immunization against asymptomatic infection in healthcare workers during a Delta variant surge. Nature Communications, 2022, 13, 1726.	12.8	5
75	Cellular responses to proteostasis perturbations reveal non-optimal feedback in chaperone networks. Cellular and Molecular Life Sciences, 2019, 76, 1605-1621.	5.4	4
76	Whole Exome Sequencing in Healthy Individuals of Extreme Constitution Types Reveals Differential Disease Risk: A Novel Approach towards Predictive Medicine. Journal of Personalized Medicine, 2022, 12, 489.	2.5	3
77	How do eubacterial organisms manage aggregation-prone proteome?. F1000Research, 2014, 3, 137.	1.6	1
78	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 344.	6.2	0
79	INTRINSICALLY DISORDERED PROTEINS: REVISITING THE STRUCTURE-FUNCTION PARADIGM. , 2013, , 333-345.		0
80	Accurate Classification of Biological Data Using Ensembles. , 2015, , .		0
81	Leveraging Structural Hierarchy for Scalable Network Comparison. Lecture Notes in Computer Science, 2016, , 287-302.	1.3	0
82	Understanding Genomic Variations in the Context of Health and Disease: Annotation, Interpretation, and Challenges. , 2018, , 71-95.		0