

Debasis Dash

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

3,020
citations

201575

27
h-index

189801

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. <i>Journal of Genetics</i> , 2008, 87, 3-20.	0.4	282
2	Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India. <i>Science</i> , 2021, 374, 995-999.	6.0	230
3	The Indian Genome Variation database (IGVdb): a project overview. <i>Human Genetics</i> , 2005, 118, 1-11.	1.8	154
4	Integrating transcriptome and proteome profiling: Strategies and applications. <i>Proteomics</i> , 2016, 16, 2533-2544.	1.3	147
5	Proteogenomic Analysis of <i>Mycobacterium tuberculosis</i> By High Resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011445.	2.5	145
6	Role of intrinsic disorder in transient interactions of hub proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 761-765.	1.5	143
7	Transcriptome and venom proteome of the box jellyfish <i>Chironex fleckeri</i> . <i>BMC Genomics</i> , 2015, 16, 407.	1.2	103
8	A Systematic Analysis of Eluted Fraction of Plasma Post Immunoaffinity Depletion: Implications in Biomarker Discovery. <i>PLoS ONE</i> , 2011, 6, e24442.	1.1	87
9	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 309-315.	1.5	86
10	Exosome-enclosed microRNAs in exhaled breath hold potential for biomarker discovery in patients with pulmonary diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 132, 219-222.e7.	1.5	70
11	Western Indian Rural Gut Microbial Diversity in Extreme Prakriti Endo-Phenotypes Reveals Signature Microbes. <i>Frontiers in Microbiology</i> , 2018, 9, 118.	1.5	68
12	Intrinsic disorder in yeast transcriptional regulatory network. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 602-605.	1.5	62
13	HGVbaseG2P: a central genetic association database. <i>Nucleic Acids Research</i> , 2009, 37, D797-D802.	6.5	60
14	Polyketide Quinones Are Alternate Intermediate Electron Carriers during Mycobacterial Respiration in Oxygen-Deficient Niches. <i>Molecular Cell</i> , 2015, 60, 637-650.	4.5	53
15	MassWiz: A Novel Scoring Algorithm with Target-Decoy Based Analysis Pipeline for Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 2154-2160.	1.8	46
16	Comparative Genomics of Host-Symbiont and Free-Living <i>Oceanobacillus</i> Species. <i>Genome Biology and Evolution</i> , 2017, 9, 1175-1182.	1.1	44
17	Expression profiling of lymph nodes in tuberculosis patients reveal inflammatory milieu at site of infection. <i>Scientific Reports</i> , 2015, 5, 15214.	1.6	43
18	Role of histidine interruption in mitigating the pathological effects of long polyglutamine stretches in SCA1: A molecular approach. <i>Protein Science</i> , 2003, 12, 953-962.	3.1	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.	0.8	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.	2.5	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.	2.0	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.	2.0	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.	1.1	36
24	Integrated Transcriptomic-Proteomic Analysis Using a Proteogenomic Workflow Refines Rat Genome Annotation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 329-339.	2.5	35
25	Recapitulation of Ayurveda constitution types by machine learning of phenotypic traits. <i>PLoS ONE</i> , 2017, 12, e0185380.	1.1	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.	1.8	33
27	Recent Admixture in an Indian Population of African Ancestry. <i>American Journal of Human Genetics</i> , 2011, 89, 111-120.	2.6	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.	1.6	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.	1.4	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.	1.0	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.	1.1	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.	2.0	26
34	Association of CAG repeat loci on chromosome 22 with schizophrenia and bipolar disorder. <i>Molecular Psychiatry</i> , 2001, 6, 694-700.	4.1	25
35	Choosing an Optimal Database for Protein Identification from Tandem Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 17-29.	0.4	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.	1.1	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.	1.0	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, .	1.0	22
39	Dynamic α -helices: Conformations that do not conform. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 109-122.	1.5	21
40	Insights from a Pan India Sero-Epidemiological survey (Phenome-India Cohort) for SARS-CoV2. <i>ELife</i> , 2021, 10, .	2.8	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.	1.6	20
43	Comparative analysis of protein unfoldedness in human housekeeping and non-housekeeping proteins. <i>Bioinformatics</i> , 2004, 20, 2904-2910.	1.8	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.	1.1	18
45	ProteoStats—a library for estimating false discovery rates in proteomics pipelines. <i>Bioinformatics</i> , 2013, 29, 2799-2800.	1.8	18
46	Origin and Instability of GAA Repeats: Insights from Alu Elements. <i>Journal of Biomolecular Structure and Dynamics</i> , 2002, 20, 253-263.	2.0	17
47	Conformational flexibility may explain multiple cellular roles of PEST motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 727-732.	1.5	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.	1.8	17
49	Discovery of rare protein-coding genes in model methylotroph <i>Methylobacterium extorquens</i> AM1. <i>Proteomics</i> , 2014, 14, 2790-2794.	1.3	17
50	Learning from Decoys to Improve the Sensitivity and Specificity of Proteomics Database Search Results. <i>PLoS ONE</i> , 2012, 7, e50651.	1.1	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.	2.0	16
52	Conformational Analysis of Invariant Peptide Sequences in Bacterial Genomes. <i>Journal of Molecular Biology</i> , 2005, 345, 937-955.	2.0	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.	1.6	14

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55	Progressive Myoclonus Epilepsy [EPM1] repeat d(CCCCGCCCCGCG)n forms folded hairpin structures at physiological pH. <i>Journal of Biomolecular Structure and Dynamics</i> , 2001, 19, 293-305.	2.0	12
56	Proteogenomics of rare taxonomic phyla: A prospective treasure trove of protein coding genes. <i>Proteomics</i> , 2016, 16, 226-240.	1.3	12
57	Sputum Protein Biomarkers in Airway Diseases: A Pilot Study. <i>International Journal of COPD</i> , 2021, Volume 16, 2203-2215.	0.9	12
58	CoPS: Comprehensive Peptide Signature Database. <i>Bioinformatics</i> , 2004, 20, 2886-2888.	1.8	11
59	False discovery rate: the Achilles™ heel of proteogenomics. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	11
60	Proteogenomic Tools and Approaches to Explore Protein Coding Landscapes of Eukaryotic Genomes. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 1-10.	0.8	10
61	Investigating Coronary Artery Disease methylome through targeted bisulfite sequencing. <i>Gene</i> , 2019, 721, 144107.	1.0	10
62	Electrostatic Mis-Interactions Cause Overexpression Toxicity of Proteins in <i>E. coli</i> . <i>PLoS ONE</i> , 2013, 8, e64893.	1.1	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. <i>PeerJ</i> , 2019, 7, e7756.	0.9	9
65	Selection of relevant features from amino acids enables development of robust classifiers. <i>Amino Acids</i> , 2014, 46, 1343-1351.	1.2	8
66	Fusion transcripts in normal human cortex increase with age and show distinct genomic features for single cells and tissues. <i>Scientific Reports</i> , 2020, 10, 1368.	1.6	8
67	Validation of expert system enhanced deep learning algorithm for automated screening for COVID-Pneumonia on chest X-rays. <i>Scientific Reports</i> , 2021, 11, 23210.	1.6	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. <i>Computers in Biology and Medicine</i> , 2022, 146, 105419.	3.9	8
69	How expression level influences the disorderliness of proteins. <i>Biochemical and Biophysical Research Communications</i> , 2008, 371, 401-404.	1.0	7
70	Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. <i>Pharmacogenomics</i> , 2021, 22, 603-618.	0.6	7
71	Recognition and analysis of protein-coding genes in severe acute respiratory syndrome associated coronavirus. <i>Bioinformatics</i> , 2004, 20, 1074-1080.	1.8	6
72	Probing the Missing Human Proteome: A Computational Perspective. <i>Journal of Proteome Research</i> , 2015, 14, 4949-4958.	1.8	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.	5.8	5
75	Cellular responses to proteostasis perturbations reveal non-optimal feedback in chaperone networks. Cellular and Molecular Life Sciences, 2019, 76, 1605-1621.	2.4	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.	1.1	3
77	How do eubacterial organisms manage aggregation-prone proteome?. F1000Research, 2014, 3, 137.	0.8	1
78	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 344.	2.6	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.	1.0	0
82	Understanding Genomic Variations in the Context of Health and Disease: Annotation, Interpretation, and Challenges. , 2018, , 71-95.		0