Debasis Dash

List of Publications by Year
in descending order

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	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
2	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
3	False discovery rate: the Achilles' heel of proteogenomics. Briefings in Bioinformatics, 2022, 23, .	3.2	11
4	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.	3.9	8
5	Insights from a Pan India Sero-Epidemiological survey (Phenome-India Cohort) for SARS-CoV2. ELife, 2021, 10, .	2.8	21
6	Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. Pharmacogenomics, 2021, 22, 603-618.	0.6	7
7	Sputum Protein Biomarkers in Airway Diseases: A Pilot Study. International Journal of COPD, 2021, Volume 16, 2203-2215.	0.9	12
8	Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India. Science, 2021, 374, 995-999.	6.0	230
9	Validation of expert system enhanced deep learning algorithm for automated screening for COVID-Pneumonia on chest X-rays. Scientific Reports, 2021, 11, 23210.	1.6	8
10	Downregulation of peripheral PTGS2/COX-2 in response to valproate treatment in patients with epilepsy. Scientific Reports, 2020, 10, 2546.	1.6	20
11	Fusion transcripts in normal human cortex increase with age and show distinct genomic features for single cells and tissues. Scientific Reports, 2020, 10, 1368.	1.6	8
12	Investigating Coronary Artery Disease methylome through targeted bisulfite sequencing. Gene, 2019, 721, 144107.	1.0	10
13	Telomere repeat–binding factor 2 binds extensively to extra-telomeric G-quadruplexes and regulates the epigenetic status of several gene promoters. Journal of Biological Chemistry, 2019, 294, 17709-17722.	1.6	31
14	Quantitative Lipid Droplet Proteomics Reveals *Mycobacterium tuberculosis* Induced Alterations in Macrophage Response to Infection. ACS Infectious Diseases, 2019, 5, 559-569.	1.8	33
15	VitiVar: A locus specific database of vitiligo associated genes and variations. Gene: X, 2019, 721, 100018.	2.3	6
16	Cellular responses to proteostasis perturbations reveal non-optimal feedback in chaperone networks. Cellular and Molecular Life Sciences, 2019, 76, 1605-1621.	2.4	4
17	The complete chloroplast genome of *Dendrobium nobile*, an endangered medicinal orchid from north-east India and its comparison with related *Dendrobium* species. PeerJ, 2019, 7, e7756.	0.9	9
18	Understanding Genomic Variations in the Context of Health and Disease: Annotation, Interpretation, and Challenges. , 2018, , 71-95.		0

#	ARTICLE	IF	CITATIONS
19	Western Indian Rural Gut Microbial Diversity in Extreme Prakriti Endo-Phenotypes Reveals Signature Microbes. Frontiers in Microbiology, 2018, 9, 118.	1.5	68
20	Adipocyte Model of Mycobacterium tuberculosis Infection Reveals Differential Availability of Iron to Bacilli in the Lipid-Rich Caseous Environment. Infection and Immunity, 2018, 86, .	1.0	22
21	Data Intensive Genome Level Analysis for Identifying Novel, Non-Toxic Drug Targets for Multi Drug Resistant Mycobacterium tuberculosis. Scientific Reports, 2017, 7, 46595.	1.6	14
22	Comparative Genomics of Hostâ€"Symbiont and Free-Living Oceanobacillus Species. Genome Biology and Evolution, 2017, 9, 1175-1182.	1.1	44
23	Choosing an Optimal Database for Protein Identification from Tandem Mass Spectrometry Data. Methods in Molecular Biology, 2017, 1549, 17-29.	0.4	25
24	Ayurgenomics for stratified medicine: TRISUTRA consortium initiative across ethnically and geographically diverse Indian populations. Journal of Ethnopharmacology, 2017, 197, 274-293.	2.0	38
25	Recapitulation of Ayurveda constitution types by machine learning of phenotypic traits. PLoS ONE, 2017, 12, e0185380.	1.1	35
26	Proteogenomics of rare taxonomic phyla: A prospective treasure trove of protein coding genes. Proteomics, 2016, 16, 226-240.	1.3	12
27	Integrating transcriptome and proteome profiling: Strategies and applications. Proteomics, 2016, 16, 2533-2544.	1.3	147
28	Proteogenomic Tools and Approaches to Explore Protein Coding Landscapes of Eukaryotic Genomes. Advances in Experimental Medicine and Biology, 2016, 926, 1-10.	0.8	10
29	Leveraging Structural Hierarchy for Scalable Network Comparison. Lecture Notes in Computer Science, 2016, , 287-302.	1.0	0
30	Integrated Transcriptomic-Proteomic Analysis Using a Proteogenomic Workflow Refines Rat Genome Annotation. Molecular and Cellular Proteomics, 2016, 15, 329-339.	2.5	35
31	Expression profiling of lymph nodes in tuberculosis patients reveal inflammatory milieu at site of infection. Scientific Reports, 2015, 5, 15214.	1.6	43
32	Accurate Classification of Biological Data Using Ensembles. , 2015, , .		0
33	Polyketide Quinones Are Alternate Intermediate Electron Carriers during Mycobacterial Respiration in Oxygen-Deficient Niches. Molecular Cell, 2015, 60, 637-650.	4.5	53
34	Transcriptome and venom proteome of the box jellyfish Chironex fleckeri. BMC Genomics, 2015, 16, 407.	1.2	103
35	Probing the Missing Human Proteome: A Computational Perspective. Journal of Proteome Research, 2015, 14, 4949-4958.	1.8	6
36	Gene-Rich Large Deletions Are Overrepresented in POAG Patients of Indian and Caucasian Origins. , 2014, 55, 3258.		9

#	ARTICLE	IF	CITATIONS
37	Extensive Copy Number Variations in Admixed Indian Population of African Ancestry: Potential Involvement in Adaptation. Genome Biology and Evolution, 2014, 6, 3171-3181.	1.1	23
38	Discovery of rare protein€coding genes in model methylotroph <i>Methylobacterium extorquens</i> AM1. Proteomics, 2014, 14, 2790-2794.	1.3	17
39	Novel mutations in typical and atypical genetic loci through exome sequencing in autosomal recessive cerebellar ataxia families. Clinical Genetics, 2014, 86, 335-341.	1.0	22
40	Selection of relevant features from amino acids enables development of robust classifiers. Amino Acids, 2014, 46, 1343-1351.	1.2	8
41	How do eubacterial organisms manage aggregation-prone proteome?. F1000Research, 2014, 3, 137.	0.8	1
42	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.	1.5	70
43	ProteoStats€"a library for estimating false discovery rates in proteomics pipelines. Bioinformatics, 2013, 29, 2799-2800.	1.8	18
44	INTRINSICALLY DISORDERED PROTEINS: REVISITING THE STRUCTURE-FUNCTION PARADIGM. , 2013, , 333-345.		0
45	Proteogenomic Analysis of Bradyrhizobium japonicum USDA110 Using Genosuite, an Automated Multi-algorithmic Pipeline. Molecular and Cellular Proteomics, 2013, 12, 3388-3397.	2.5	39
46	Electrostatic Mis-Interactions Cause Overexpression Toxicity of Proteins in E. coli. PLoS ONE, 2013, 8, e64893.	1.1	9
47	Location of disorder in coiled coilproteins is influenced by its biological role and subcellular localization: a GO-based study on human proteome. Molecular BioSystems, 2012, 8, 346-352.	2.9	16
48	Crowd Sourcing a New Paradigm for Interactome Driven Drug Target Identification in Mycobacterium tuberculosis. PLoS ONE, 2012, 7, e39808.	1.1	36
49	Knowledge engineering for health: A new discipline required to bridge the "ICT gap"between research and healthcare. Human Mutation, 2012, 33, 797-802.	1.1	27
50	Spectrum of large copy number variations in 26 diverse Indian populations: potential involvement in phenotypic diversity. Human Genetics, 2012, 131, 131-143.	1.8	17
51	Learning from Decoys to Improve the Sensitivity and Specificity of Proteomics Database Search Results. PLoS ONE, 2012, 7, e50651.	1.1	17
52	MassWiz: A Novel Scoring Algorithm with Target-Decoy Based Analysis Pipeline for Tandem Mass Spectrometry. Journal of Proteome Research, 2011, 10, 2154-2160.	1.8	46
53	Proteogenomic Analysis of Mycobacterium tuberculosis By High Resolution Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M111.011445.	2.5	145
54	Open source drug discovery€" A new paradigm of collaborative research in tuberculosis drug development. Tuberculosis, 2011, 91, 479-86.	0.8	42

#	Article	IF	Citations
55	A web server for predicting inhibitors against bacterial target GlmU protein. BMC Pharmacology, 2011, 11, 5.	0.4	31
56	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 111-120.	2.6	32
57	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 344.	2.6	0
58	A Systematic Analysis of Eluted Fraction of Plasma Post Immunoaffinity Depletion: Implications in Biomarker Discovery. PLoS ONE, 2011, 6, e24442.	1.1	87
59	IGVBrowser-a genomic variation resource from diverse Indian populations. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq022-baq022.	1.4	30
60	HGVbaseG2P: a central genetic association database. Nucleic Acids Research, 2009, 37, D797-D802.	6.5	60
61	The phenotype and genotype experiment object model (PaGE-OM): a robust data structure for information related to DNA variation. Human Mutation, 2009, 30, 968-977.	1.1	18
62	Unraveling the potential of intrinsically disordered proteins as drug targets: application to Mycobacterium tuberculosis. Molecular BioSystems, 2009, 5, 1752.	2.9	20
63	Genetic landscape of the people of India: a canvas for disease gene exploration. Journal of Genetics, 2008, 87, 3-20.	0.4	282
64	How expression level influences the disorderness of proteins. Biochemical and Biophysical Research Communications, 2008, 371, 401-404.	1.0	7
65	Dynamic α-helices: Conformations that do not conform. Proteins: Structure, Function and Bioinformatics, 2007, 68, 109-122.	1.5	21
66	Intrinsic disorder in yeast transcriptional regulatory network. Proteins: Structure, Function and Bioinformatics, 2007, 68, 602-605.	1.5	62
67	Conformational flexibility may explain multiple cellular roles of PEST motifs. Proteins: Structure, Function and Bioinformatics, 2006, 63, 727-732.	1.5	17
68	Role of intrinsic disorder in transient interactions of hub proteins. Proteins: Structure, Function and Bioinformatics, 2006, 66, 761-765.	1.5	143
69	The Indian Genome Variation database (IGVdb): a project overview. Human Genetics, 2005, 118, 1-11.	1.8	154
70	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. Proteins: Structure, Function and Bioinformatics, 2005, 62, 309-315.	1.5	86
71	Conformational Analysis of Invariant Peptide Sequences in Bacterial Genomes. Journal of Molecular Biology, 2005, 345, 937-955.	2.0	16
72	CoPS: Comprehensive Peptide Signature Database. Bioinformatics, 2004, 20, 2886-2888.	1.8	11

#	ARTICLE	IF	CITATIONS
73	Recognition and analysis of protein-coding genes in severe acute respiratory syndrome associated coronavirus. Bioinformatics, 2004, 20, 1074-1080.	1.8	6
74	Comparative analysis of protein unfoldedness in human housekeeping and non-housekeeping proteins. Bioinformatics, 2004, 20, 2904-2910.	1.8	18
75	In silico characterization of the INO80 subfamily of SWI2/SNF2 chromatin remodeling proteins. Biochemical and Biophysical Research Communications, 2004, 320, 197-204.	1.0	27
76	Role of histidine interruption in mitigating the pathological effects of long polyglutamine stretches in SCA1: A molecular approach. Protein Science, 2003, 12, 953-962.	3.1	42
77	A Novel Complexity Measure for Comparative Analysis of Protein Sequences from Complete Genomes. Journal of Biomolecular Structure and Dynamics, 2003, 20, 657-667.	2.0	16
78	Origin and Instability of GAA Repeats: Insights from Alu Elements. Journal of Biomolecular Structure and Dynamics, 2002, 20, 253-263.	2.0	17
79	Spectrum of ?-thalassemia mutations and their association with allelic sequence polymorphisms at the ?-globin gene cluster in an eastern Indian population. American Journal of Hematology, 2002, 70, 269-277.	2.0	38
80	Intramolecular i-motif Structure at Acidic pH for Progressive Myoclonus Epilepsy (EPM1) Repeat d(CCCCGCCCCGCG)$_n$. Journal of Biomolecular Structure and Dynamics, 2001, 19, 307-313.	2.0	26
81	Association of CAG repeat loci on chromosome 22 with schizophrenia and bipolar disorder. Molecular Psychiatry, 2001, 6, 694-700.	4.1	25
82	Progressive Myoclonus Epilepsy [EPM1] repeat d(CCCCGCCCCGCG)nforms folded hairpin structures at physiological pH. Journal of Biomolecular Structure and Dynamics, 2001, 19, 293-305.	2.0	12