

Subhash J Jakhesara

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

1,129
citations

471371

17
h-index

414303

32
g-index

50
all docs

50
docs citations

50
times ranked

1648
citing authors

#	ARTICLE	IF	CITATIONS
1	High through put 16S rRNA gene-based pyrosequencing analysis of the fecal microbiota of high FCR and low FCR broiler growers. <i>Molecular Biology Reports</i> , 2012, 39, 10595-10602.	1.0	164
2	Microbial diversity and community composition of caecal microbiota in commercial and indigenous Indian chickens determined using 16s rDNA amplicon sequencing. <i>Microbiome</i> , 2018, 6, 115.	4.9	138
3	Milk microbiome signatures of subclinical mastitis-affected cattle analysed by shotgun sequencing. <i>Journal of Applied Microbiology</i> , 2012, 112, 639-650.	1.4	94
4	Metagenomic analysis of Surti buffalo (<i>Bubalus bubalis</i>) rumen: a preliminary study. <i>Molecular Biology Reports</i> , 2012, 39, 4841-4848.	1.0	72
5	Differential expression of microRNAs associated with thermal stress in Frieswal (<i>Bos taurus</i> x <i>Bos</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222 T	1.2	50
6	Cloning, molecular modeling and characterization of acidic cellulase from buffalo rumen and its applicability in saccharification of lignocellulosic biomass. <i>International Journal of Biological Macromolecules</i> , 2018, 113, 73-81.	3.6	41
7	Whole-Genome Shotgun Sequencing of an Indian-Origin <i>Lactobacillus helveticus</i> Strain, MTCC 5463, with Probiotic Potential. <i>Journal of Bacteriology</i> , 2011, 193, 4282-4283.	1.0	36
8	Metagenomic analysis of virulence-associated and antibiotic resistance genes of microbes in rumen of Indian buffalo (<i>Bubalus bubalis</i>). <i>Gene</i> , 2012, 507, 146-151.	1.0	35
9	Microbiota composition, gene pool and its expression in Gir cattle (<i>Bos indicus</i>) rumen under different forage diets using metagenomic and metatranscriptomic approaches. <i>Systematic and Applied Microbiology</i> , 2018, 41, 374-385.	1.2	29
10	Isolation and characterization of H9N2 influenza virus isolates from poultry respiratory disease outbreak. <i>SpringerPlus</i> , 2014, 3, 196.	1.2	28
11	Draft genome analysis of lignocellulolytic enzymes producing <i>Aspergillus terreus</i> with structural insight of β -glucosidases through molecular docking approach. <i>International Journal of Biological Macromolecules</i> , 2019, 125, 181-190.	3.6	28
12	Illumina Next Generation Sequencing for the Analysis of <i>Eimeria</i> Populations in Commercial Broilers and Indigenous Chickens. <i>Frontiers in Veterinary Science</i> , 2018, 5, 176.	0.9	27
13	Genome Sequence of <i>Pasteurella multocida</i> subsp. <i>gallicida</i> Anand1_poultry. <i>Journal of Bacteriology</i> , 2011, 193, 5604-5604.	1.0	26
14	Characterizing rumen microbiota and CAZyme profile of Indian dromedary camel (<i>Camelus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	1.6	25
15	Pathotypic and Sequence Characterization of Newcastle Disease Viruses from Vaccinated Chickens Reveals Circulation of Genotype II, IV and XIII and in India. <i>Transboundary and Emerging Diseases</i> , 2016, 63, 523-539.	1.3	24
16	Complete genome sequence analysis of chicken astrovirus isolate from India. <i>Veterinary Research Communications</i> , 2017, 41, 67-75.	0.6	19
17	Metagenomic characterisation of ruminal bacterial diversity in buffaloes from birth to adulthood using 16S rRNA gene amplicon sequencing. <i>Functional and Integrative Genomics</i> , 2019, 19, 237-247.	1.4	19
18	Identification of novel transcripts deregulated in buccal cancer by RNA-seq. <i>Gene</i> , 2012, 507, 152-158.	1.0	18

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19	Analysis of consequences of non-synonymous SNP in feed conversion ratio associated TGF- β 2 receptor type 3 gene in chicken. <i>Meta Gene</i> , 2015, 4, 107-117.	0.3	18
20	Unraveling the camel rumen microbiome through metaculturomics approach for agriculture waste hydrolytic potential. <i>Archives of Microbiology</i> , 2021, 203, 107-123.	1.0	18
21	Evaluation of designed consortium SNH-1 for efficient hydrolysis of agriculture waste to benefit bioethanol production. <i>Journal of Cleaner Production</i> , 2021, 288, 125601.	4.6	17
22	Rumen Virome: An Assessment of Viral Communities and their Functions in the Rumen of an Indian Buffalo. <i>Current Science</i> , 2016, 111, 919.	0.4	17
23	Database on spermatozoa transcriptome of categorised Frieswal crossbred (Holstein Friesian X) Tj ETQq1 1 0.784314 rgBT/Overlook	0.9	15
24	Identification of novel exons and transcripts by comprehensive RNA-Seq of horn cancer transcriptome in <i>Bos indicus</i> . <i>Journal of Biotechnology</i> , 2013, 165, 37-44.	1.9	13
25	Genetic features of Patanwadi, Marwari and Dumba sheep breeds (India) inferred by microsatellite markers. <i>Small Ruminant Research</i> , 2010, 93, 57-60.	0.6	12
26	Transcriptome analysis and SNP Identification in SCC of Horn in (<i>Bos indicus</i>) Indian cattle. <i>Gene</i> , 2013, 530, 119-126.	1.0	12
27	Comprehensive transcriptome profiling of squamous cell carcinoma of horn in <i>Bos indicus</i> . <i>Veterinary and Comparative Oncology</i> , 2016, 14, 122-136.	0.8	12
28	Mining of Ruminant Microbial Phytase (RPHY1) from Metagenomic Data of Mehsani Buffalo Breed: Identification, Gene Cloning, and Characterization. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2016, 26, 252-260.	1.0	12
29	Exploring the eukaryotic diversity in rumen of Indian camel (<i>Camelus dromedarius</i>) using 18S rRNA amplicon sequencing. <i>Archives of Microbiology</i> , 2020, 202, 1861-1872.	1.0	12
30	A preliminary sketch of horn cancer transcriptome in Indian zebu cattle. <i>Gene</i> , 2012, 493, 124-131.	1.0	11
31	RNA-Seq reveals differentially expressed isoforms and novel splice variants in buccal mucosal cancer. <i>Gene</i> , 2013, 516, 24-32.	1.0	11
32	Molecular cloning, heterologous expression, and functional characterization of a cellulolytic enzyme (Cel PRII) from buffalo rumen metagenome. <i>3 Biotech</i> , 2017, 7, 257.	1.1	11
33	Rumen and fecal microbial profiles in cattle fed high lignin diets using metagenome analysis. <i>Anaerobe</i> , 2022, 73, 102508.	1.0	9
34	Identification of novel splice variants in horn cancer by RNA-Seq analysis in Zebu cattle. <i>Genomics</i> , 2013, 101, 57-63.	1.3	8
35	Whole-Genome Shotgun Sequencing of <i>Lactobacillus rhamnosus</i> MTCC 5462, a Strain with Probiotic Potential. <i>Journal of Bacteriology</i> , 2012, 194, 1264-1265.	1.0	5
36	Tissue-specific Temporal Exome Capture Revealed Muscle-specific Genes and SNPs in Indian Buffalo (<i>Bubalus bubalis</i>). <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 107-113.	3.0	5

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37	Emergence of a genotype I variant of avian infectious bronchitis virus from Northern part of India. <i>Acta Tropica</i> , 2018, 183, 57-60.	0.9	5
38	Transcriptomic analysis to affirm the regulatory role of long non-coding RNA in horn cancer of Indian zebu cattle breed Kankrej (<i>Bos indicus</i>). <i>Functional and Integrative Genomics</i> , 2020, 20, 75-87.	1.4	5
39	Identification of novel SNPs in differentially expressed genes and its association with horn cancer of <i>Bos indicus</i> bullocks by next-generation sequencing. <i>3 Biotech</i> , 2016, 6, 38.	1.1	4
40	Parentage verification in field progeny testing program of Mehsana buffalo. <i>Journal of Animal Science</i> , 2012, 90, 4723-4728.	0.2	3
41	Single nucleotide variant detection in Jaffrabadi buffalo (<i>Bubalus bubalis</i>) using high-throughput targeted sequencing. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2015, 8, 192-199.	1.1	3
42	Identification of putative SNPs in progressive retinal atrophy affected <i>Canis lupus familiaris</i> using exome sequencing. <i>Mammalian Genome</i> , 2015, 26, 638-649.	1.0	3
43	Identification and quantification of novel RNA isoforms in horn cancer of <i>Bos indicus</i> by comprehensive RNA-Seq. <i>3 Biotech</i> , 2016, 6, 259.	1.1	3
44	MetaRNAseq analysis of surti buffalo rumen content reveals that transcriptionally active microorganisms need not be abundant. <i>Molecular Biology Reports</i> , 2020, 47, 5101-5114.	1.0	3
45	Metagenomic data of DNA viruses of poultry affected with respiratory tract infection. <i>Data in Brief</i> , 2018, 16, 157-160.	0.5	2
46	Molecular portrait of squamous cell carcinoma of the bovine horn evaluated by high-throughput targeted exome sequencing: a preliminary report. <i>BMC Veterinary Research</i> , 2020, 16, 461.	0.7	2
47	Isolation, purification and characterization of a novel esterase from camel rumen metagenome. <i>Protein Expression and Purification</i> , 2021, 187, 105941.	0.6	2
48	Evolution and diversity studies of innate immune genes in Indian buffalo (<i>Bubalus bubalis</i>) breeds using next generation sequencing. <i>Genes and Genomics</i> , 2017, 39, 1237-1247.	0.5	1
49	Expression profiling revealed keratins and interleukins as potential biomarkers in squamous cell carcinoma of horn in Indian bullocks (<i>Bos indicus</i>). <i>3 Biotech</i> , 2020, 10, 92.	1.1	1
50	Transcriptomic comparison of primary bovine horn core carcinoma culture and parental tissue at early stage. <i>Veterinary World</i> , 2017, 10, 38-55.	0.7	1