

# Nandan P Deshpande

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

6,787  
citations

394421

19  
h-index

361022

35  
g-index

40  
all docs

40  
docs citations

40  
times ranked

12393  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA sequencing identifies genes reliant upon Ser26 in early growth response-1 in vascular endothelial cells exposed to fibroblast growth factor-2. <i>Vascular Pharmacology</i> , 2022, , 106952.	2.1	2
2	Pathogen exposure leads to a transcriptional downregulation of core cellular functions that may dampen the immune response in a macroalga. <i>Molecular Ecology</i> , 2022, 31, 3468-3480.	3.9	3
3	The splicing factor RBM17 drives leukemic stem cell maintenance by evading nonsense-mediated decay of pro-leukemic factors. <i>Nature Communications</i> , 2022, 13, .	12.8	3
4	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	17.5	75
5	Multi-omics of the esophageal microenvironment identifies signatures associated with progression of Barrett's esophagus. <i>Genome Medicine</i> , 2021, 13, 133.	8.2	11
6	Raspberry ketone diet supplement reduces attraction of sterile male Queensland fruit fly to cue lure by altering expression of chemoreceptor genes. <i>Scientific Reports</i> , 2021, 11, 17632.	3.3	2
7	Intra-species variation within <i>Lactobacillus rhamnosus</i> correlates to beneficial or harmful outcomes: lessons from the oral cavity. <i>BMC Genomics</i> , 2020, 21, 661.	2.8	3
8	Thermostable small-molecule inhibitor of angiogenesis and vascular permeability that suppresses a pERK-FosB/FosB-VCAM-1 axis. <i>Science Advances</i> , 2020, 6, eaaz7815.	10.3	16
9	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2020, 26, 3597-3607.	7.0	26
10	Little evidence of adaptation potential to ocean acidification in sea urchins living in "Future Ocean" conditions at a CO <sub>2</sub> vent. <i>Ecology and Evolution</i> , 2019, 9, 10004-10016.	1.9	16
11	Whole genome sequencing of a novel, dichloromethane-fermenting <i>Peptococcaceae</i> from an enrichment culture. <i>PeerJ</i> , 2019, 7, e7775.	2.0	14
12	Identification of Recurrent Alternative RNA Splicing in Adverse-Risk Acute Myeloid Leukemia. <i>Blood</i> , 2019, 134, 457-457.	1.4	0
13	Transcriptional response of <i>Nautella italica</i> R11 towards its macroalgal host uncovers new mechanisms of host-pathogen interaction. <i>Molecular Ecology</i> , 2018, 27, 1820-1832.	3.9	9
14	Signatures within the esophageal microbiome are associated with host genetics, age, and disease. <i>Microbiome</i> , 2018, 6, 227.	11.1	101
15	Small RNA interactome of pathogenic <i>E. coli</i> revealed through crosslinking of RNAase E. <i>EMBO Journal</i> , 2017, 36, 374-387.	7.8	153
16	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. <i>Cell Reports</i> , 2017, 20, 572-585.	6.4	99
17	Characterization of SNP and Structural Variations in the Mitochondrial Genomes of <i>Tilletia indica</i> and Its Closely Related Species Formed Basis for a Simple Diagnostic Assay. <i>PLoS ONE</i> , 2016, 11, e0166086.	2.5	10
18	<i>Campylobacter concisus</i> pathotypes induce distinct global responses in intestinal epithelial cells. <i>Scientific Reports</i> , 2016, 6, 34288.	3.3	23

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19	Transcriptomic and Proteomic Analyses Reveal Key Innate Immune Signatures in the Host Response to the Gastrointestinal Pathogen <i>Campylobacter concisus</i> . <i>Infection and Immunity</i> , 2015, 83, 832-845.	2.2	45
20	Novel genetic markers define a subgroup of pathogenic <i>Escherichia coli</i> strains belonging to the B2 phylogenetic group. <i>FEMS Microbiology Letters</i> , 2015, 362, fmv193.	1.8	15
21	Tools to Covisualize and Coanalyze Proteomic Data with Genomes and Transcriptomes: Validation of Genes and Alternative mRNA Splicing. <i>Journal of Proteome Research</i> , 2014, 13, 84-98.	3.7	40
22	Comparative genomics of <i>Campylobacter concisus</i> isolates reveals genetic diversity and provides insights into disease association. <i>BMC Genomics</i> , 2013, 14, 585.	2.8	39
23	Genome Sequence of <i>Dehalobacter</i> UNSWDHB, a Chloroform-Dechlorinating Bacterium. <i>Genome Announcements</i> , 2013, 1, .	0.8	20
24	Next-generation sequencing: a challenge to meet the increasing demand for training workshops in Australia. <i>Briefings in Bioinformatics</i> , 2013, 14, 563-574.	6.5	17
25	Sequencing and Validation of the Genome of a <i>Campylobacter concisus</i> Reveals Intra-Species Diversity. <i>PLoS ONE</i> , 2011, 6, e22170.	2.5	32
26	The Pathogenic Potential of <i>Campylobacter concisus</i> Strains Associated with Chronic Intestinal Diseases. <i>PLoS ONE</i> , 2011, 6, e29045.	2.5	63
27	GlycoSpectrumScan: Fishing Glycopeptides from MS Spectra of Protease Digests of Human Colostrum sIgA. <i>Journal of Proteome Research</i> , 2010, 9, 1063-1075.	3.7	100
28	Protein glycosylation pathways in filamentous fungi. <i>Glycobiology</i> , 2008, 18, 626-637.	2.5	157
29	Analysis of the human protein interactome and comparison with yeast, worm and fly interaction datasets. <i>Nature Genetics</i> , 2006, 38, 285-293.	21.4	433
30	A manually curated functional annotation of the human X chromosome. <i>Nature Genetics</i> , 2005, 37, 331-332.	21.4	16
31	A proteomic analysis of salivary glands of female <i>Anopheles gambiae</i> mosquito. <i>Proteomics</i> , 2005, 5, 3765-3777.	2.2	63
32	Plasma Proteome Database as a resource for proteomics research. <i>Proteomics</i> , 2005, 5, 3531-3536.	2.2	135
33	Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9309-9314.	7.1	874
34	ONCOMINE: A Cancer Microarray Database and Integrated Data-Mining Platform. <i>Neoplasia</i> , 2004, 6, 1-6.	5.3	3,212
35	Development of Human Protein Reference Database as an Initial Platform for Approaching Systems Biology in Humans. <i>Genome Research</i> , 2003, 13, 2363-2371.	5.5	954
36	Mining gene expression data for functional annotation of genomes. <i>Trends in Biotechnology</i> , 2002, 20, 282.	9.3	0