Preethi H Gunaratne

List of Publications by Year
in descending order

69 papers	4,971 citations	147801 31 h-index	98798 67 g-index
72 all docs	72 docs citations	72 times ranked	11766 citing authors

#	Article	IF	Citations
1	HepT1-derived murine models of high-risk hepatoblastoma display vascular invasion, metastasis, and circulating tumor cells. Biology Open, 2022, 11, .	1.2	3
2	Functional and structural characterization of Hyp730, a highly conserved and dormancyâ€specific hypothetical membrane protein. MicrobiologyOpen, 2021, 10, e1154.	3.0	1
3	Co-delivery of novel bispecific and trispecific engagers by an amplicon vector augments the therapeutic effect of an HSV-based oncolytic virotherapy. , 2021, 9, e002454.		7
4	A noncoding RNA modulator potentiates phenylalanine metabolism in mice. Science, 2021, 373, 662-673.	12.6	42
5	Functional significance of gain-of-function H19 lncRNA in skeletal muscle differentiation and anti-obesity effects. Genome Medicine, 2021, 13, 137.	8.2	8
6	Curcumin Reduces Adipose Tissue Inflammation and Alters Gut Microbiota in Dietâ€Induced Obese Male Mice. Molecular Nutrition and Food Research, 2021, 65, e2100274.	3.3	32
7	Conversion of human cardiac progenitor cells into cardiac pacemaker-like cells. Journal of Molecular and Cellular Cardiology, 2020, 138, 12-22.	1.9	20
8	Pan-cancer analysis reveals TAp63-regulated oncogenic lncRNAs that promote cancer progression through AKT activation. Nature Communications, 2020, 11, 5156.	12.8	12
9	Role of microRNA 690 in Mediating Angiotensin II Effects on Inflammation and Endoplasmic Reticulum Stress. Cells, 2020, 9, 1327.	4.1	15
10	DNA Binding on Self-Assembled Monolayers Terminated with Mixtures of Ammonium and Trimethylammonium Groups: Toward a Gene-Delivery Platform. ACS Applied Nano Materials, 2020, 3, 6621-6628.	5.0	6
11	Integrative Analyses of Multilevel Omics Reveal Preneoplastic Breast to Possess a Molecular Landscape That is Globally Shared with Invasive Basal-Like Breast Cancer. Cancers, 2020, 12, 722.	3.7	13
12	Wnt signaling regulates neural plate patterning in distinct temporal phases with dynamic transcriptional outputs. Developmental Biology, 2020, 462, 152-164.	2.0	6
13	TAp63-Regulated miRNAs Suppress Cutaneous Squamous Cell Carcinoma through Inhibition of a Network of Cell-Cycle Genes. Cancer Research, 2020, 80, 2484-2497.	0.9	16
14	Diversity of peripheral blood human NK cells identified by single-cell RNA sequencing. Blood Advances, 2020, 4, 1388-1406.	5.2	125
15	A Universal Stress Protein That Controls Bacterial Stress Survival in Micrococcus luteus. Journal of Bacteriology, 2019, 201, .	2.2	12
16	Recent Developments and Therapeutic Strategies against Hepatocellular Carcinoma. Cancer Research, 2019, 79, 4326-4330.	0.9	99
17	Oncogenic lncRNA downregulates cancer cell antigen presentation and intrinsic tumor suppression. Nature Immunology, 2019, 20, 835-851.	14.5	277
18	Single-Cell RNA-Sequencing Identifies Activation of TP53 and STAT1 Pathways in Human T Lymphocyte Subpopulations in Response to Ex Vivo Radiation Exposure. International Journal of Molecular Sciences, 2019, 20, 2316.	4.1	10

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19	Activating p53 family member TAp63: A novel therapeutic strategy for targeting p53â€altered tumors. Cancer, 2019, 125, 2409-2422.	4.1	15
20	MicroRNA-509-3p inhibits cellular migration, invasion, and proliferation, and sensitizes osteosarcoma to cisplatin. Scientific Reports, 2019, 9, 19089.	3.3	26
21	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
22	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
23	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
24	Protective properties of n-3 fatty acids and implications in obesity-associated breast cancer. Journal of Nutritional Biochemistry, 2018, 53, 1-8.	4.2	31
25	Distinct TP63 Isoform-Driven Transcriptional Signatures Predict Tumor Progression and Clinical Outcomes. Cancer Research, 2018, 78, 451-462.	0.9	22
26	The transcription factor POU3F2 regulates a gene coexpression network in brain tissue from patients with psychiatric disorders. Science Translational Medicine, 2018, 10, .	12.4	81
27	Transcriptomic and microRNA analyses of gene networks regulated by eicosapentaenoic acid in brown adipose tissue of diet-induced obese mice. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2018, 1863, 1523-1531.	2.4	23
28	Quaternary Ammonium-Terminated Films Formed from Mixed Bidentate Adsorbates Provide a High-Capacity Platform for Oligonucleotide Delivery. ACS Applied Materials & Interfaces, 2018, 10, 40890-40900.	8.0	5
29	CD56 Expression Marks Human Group 2 Innate Lymphoid Cell Divergence from a Shared NK Cell and Group 3 Innate Lymphoid Cell Developmental Pathway. Immunity, 2018, 49, 464-476.e4.	14.3	86
30	An integrative transcriptomic approach to identify depot differences in genes and microRNAs in adipose tissues from high fat fed mice. Oncotarget, 2018, 9, 9246-9261.	1.8	19
31	DNA Loading and Release Using Custom-Tailored Poly(<scp>l</scp>-lysine) Surfaces. ACS Applied Materials & Interfaces, 2017, 9, 23370-23378.	8.0	8
32	Ronin Governs Early Heart Development by Controlling Core Gene Expression Programs. Cell Reports, 2017, 21, 1562-1573.	6.4	16
33	Regulation of miRNA-29c and its downstream pathways in preneoplastic progression of triple-negative breast cancer. Oncotarget, 2017, 8, 19645-19660.	1.8	49
34	miR-509-3p is clinically significant and strongly attenuates cellular migration and multi-cellular spheroids in ovarian cancer. Oncotarget, 2016, 7, 25930-25948.	1.8	49
35	Transmembrane adaptor protein PAG1 is a novel tumor suppressor in neuroblastoma. Oncotarget, 2016, 7, 24018-24026.	1.8	18
36	Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. Nature Communications, 2016, 7, 12601.	12.8	123

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37	Tumour-suppressor microRNAs regulate ovarian cancer cell physical properties and invasive behaviour. Open Biology, 2016, 6, 160275.	3.6	29
38	MYC-Driven Neuroblastomas Are Addicted to a Telomerase-Independent Function of Dyskerin. Cancer Research, 2016, 76, 3604-3617.	0.9	38
39	miR-322/-503 cluster is expressed in the earliest cardiac progenitor cells and drives cardiomyocyte specification. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9551-9556.	7.1	66
40	Mesp1 Marked Cardiac Progenitor Cells Repair Infarcted Mouse Hearts. Scientific Reports, 2016, 6, 31457.	3.3	24
41	Î”Np63/DGCR8-Dependent MicroRNAs Mediate Therapeutic Efficacy of HDAC Inhibitors in Cancer. Cancer Cell, 2016, 29, 874-888.	16.8	32
42	Identification of microRNAs and microRNA targets in Xenopus gastrulae: The role of miR-26 in the regulation of Smad1. Developmental Biology, 2016, 409, 26-38.	2.0	8
43	PPARÎ³ agonists promote differentiation of cancer stem cells by restraining YAP transcriptional activity. Oncotarget, 2016, 7, 60954-60970.	1.8	39
44	Annexin A1 Preferentially Predicts Poor Prognosis of Basal-Like Breast Cancer Patients by Activating mTOR-S6 Signaling. PLoS ONE, 2015, 10, e0127678.	2.5	34
45	Identification of Potential Glucocorticoid Receptor Therapeutic Targets in Multiple Myeloma. Nuclear Receptor Signaling, 2015, 13, nrs.13006.	1.0	15
46	Identification of p38Î² as a Therapeutic Target for the Treatment of SÃ©zary Syndrome. Journal of Investigative Dermatology, 2015, 135, 599-608.	0.7	12
47	Single-Molecule Sequencing Reveals Estrogen-Regulated Clinically Relevant lncRNAs in Breast Cancer. Molecular Endocrinology, 2015, 29, 1634-1645.	3.7	56
48	IAPP-driven metabolic reprogramming induces regression of p53-deficient tumours in vivo. Nature, 2015, 517, 626-630.	27.8	117
49	siRNAs from an X-linked satellite repeat promote X-chromosome recognition in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16460-16465.	7.1	68
50	Functional Analysis of miR-34c as a Putative Tumor Suppressor in High-Grade Serous Ovarian Cancer1. Biology of Reproduction, 2014, 91, 113.	2.7	17
51	PAPD5-mediated 3â€² adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11467-11472.	7.1	130
52	Large conserved domains of low DNA methylation maintained by Dnmt3a. Nature Genetics, 2014, 46, 17-23.	21.4	276
53	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
54	A gold nanoparticle platform for the delivery of functional microRNAs into cancerÂcells. Biomaterials, 2013, 34, 807-816.	11.4	150

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55	Synergy Of Small-Molecule Inhibitors In Cutaneous T-Cell Lymphoma Cells: A Discovery Tool To Define New Therapeutic Targets In T-Cell Receptor (TCR) Signaling Pathways. Blood, 2013, 122, 4327-4327.	1.4	2
56	Large Conserved Domains Of Low DNA Methylation Maintained By 5-Hydroxymethycytosine and Dnmt3a. Blood, 2013, 122, 2406-2406.	1.4	0
57	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. PLoS ONE, 2012, 7, e34546.	2.5	104
58	miRNA Data Analysis: Next-Gen Sequencing. Methods in Molecular Biology, 2012, 822, 273-288.	0.9	32
59	Song exposure regulates known and novel microRNAs in the zebra finch auditory forebrain. BMC Genomics, 2011, 12, 277.	2.8	45
60	Large-Scale Integration of MicroRNA and Gene Expression Data for Identification of Enriched MicroRNAâ€“mRNA Associations in Biological Systems. Methods in Molecular Biology, 2010, 667, 297-315.	0.9	31
61	Discovery of Novel MicroRNAs in Female Reproductive Tract Using Next Generation Sequencing. PLoS ONE, 2010, 5, e9637.	2.5	88
62	Embryonic Stem Cell MicroRNAs: Defining Factors in Induced Pluripotent (iPS) and Cancer (CSC) Stem Cells?. Current Stem Cell Research and Therapy, 2009, 4, 168-177.	1.3	83
63	Expression profiling of microRNAs by deep sequencing. Briefings in Bioinformatics, 2009, 10, 490-497.	6.5	276
64	A bioinformatics tool for linking gene expression profiling results with public databases of microRNA target predictions. Rna, 2008, 14, 2290-2296.	3.5	141
65	Mouse let-7 miRNA populations exhibit RNA editing that is constrained in the 5'-seed/ cleavage/anchor regions and stabilize predicted mmu-let-7a:mRNA duplexes. Genome Research, 2008, 18, 1571-1581.	5.5	87
66	Novel MicroRNA Candidates and miRNA-mRNA Pairs in Embryonic Stem (ES) Cells. PLoS ONE, 2008, 3, e2548.	2.5	48
67	Concatenation cDNA sequencing for transcriptome analysis. Comptes Rendus - Biologies, 2003, 326, 971-977.	0.2	4
68	Duplication of thePMP22 gene in 17p partial trisomy patients with Charcot-Marie-Tooth type-1A neuropathy. Human Genetics, 1996, 97, 642-649.	3.8	4
69	Duplication of the PMP22 gene in 17p partial trisomy patients with Charcot-Marie-Tooth type-1A neuropathy. Human Genetics, 1996, 97, 642-649.	3.8	45