Gregory J Goodall

List of Publications by Year
in descending order

106 papers	16,848 citations	31949 53 h-index	28275 105 g-index
116 all docs	116 docs citations	116 times ranked	22675 citing authors

#	Article	IF	Citations
1	The Quaking <scp>RNA</scp>â€binding proteins as regulators of cell differentiation. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1724.	3.2	18
2	The many regulators of epithelialâˆ’mesenchymal transition. Nature Reviews Molecular Cell Biology, 2022, 23, 89-90.	16.1	27
3	Ceramide-induced integrated stress response overcomes Bcl-2 inhibitor resistance in acute myeloid leukemia. Blood, 2022, 139, 3737-3751.	0.6	20
4	RNA in cancer. Nature Reviews Cancer, 2021, 21, 22-36.	12.8	655
5	Phosphorylation of PKCÎ´ by FER tips the balance from EGFR degradation to recycling. Journal of Cell Biology, 2021, 220, .	2.3	14
6	Computational methods for cancer driver discovery: A survey. Theranostics, 2021, 11, 5553-5568.	4.6	19
7	Post-transcriptional Gene Regulation by MicroRNA-194 Promotes Neuroendocrine Transdifferentiation in Prostate Cancer. Cell Reports, 2021, 34, 108585.	2.9	33
8	<i>pDriver</i>: a novel method for unravelling personalized coding and miRNA cancer drivers. Bioinformatics, 2021, 37, 3285-3292.	1.8	8
9	capCLIP: a new tool to probe translational control in human cells through capture and identification of the eIF4Eâ€“mRNA interactome. Nucleic Acids Research, 2021, 49, e105-e105.	6.5	15
10	A DOCK1 Gene-Derived Circular RNA Is Highly Expressed in Luminal Mammary Tumours and Is Involved in the Epithelial Differentiation, Growth, and Motility of Breast Cancer Cells. Cancers, 2021, 13, 5325.	1.7	6
11	Stathmin levels alter PTPN14 expression and impact neuroblastoma cell migration. British Journal of Cancer, 2020, 122, 434-444.	2.9	9
12	A novel single-cell based method for breast cancer prognosis. PLoS Computational Biology, 2020, 16, e1008133.	1.5	16
13	Insufficiently complex unique-molecular identifiers (UMIs) distort small RNA sequencing. Scientific Reports, 2020, 10, 14593.	1.6	9
14	Guidelines and definitions for research on epithelialâ€“mesenchymal transition. Nature Reviews Molecular Cell Biology, 2020, 21, 341-352.	16.1	1,195
15	<i>DriverGroup</i>: a novel method for identifying driver gene groups. Bioinformatics, 2020, 36, i583-i591.	1.8	5
16	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exonâ€“Intron Split Analysis (EISA). Nucleic Acids Research, 2019, 47, 8606-8619.	6.5	9
17	MicroRNA-143-3p targets pyruvate carboxylase expression and controls proliferation and migration of MDA-MB-231â€¯cells. Archives of Biochemistry and Biophysics, 2019, 677, 108169.	1.4	13
18	Insights into the biogenesis and potential functions of exonic circular RNA. Scientific Reports, 2019, 9, 2048.	1.6	98

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19	CBNA: A control theory based method for identifying coding and non-coding cancer drivers. PLoS Computational Biology, 2019, 15, e1007538.	1.5	22
20	miRNA length variation during macrophage stimulation confounds the interpretation of results: implications for miRNA quantification by RT-qPCR. Rna, 2019, 25, 232-238.	1.6	16
21	miR-222 isoforms are differentially regulated by type-I interferon. Rna, 2018, 24, 332-341.	1.6	31
22	Clinical Utility of a STAT3-Regulated miRNA-200 Family Signature with Prognostic Potential in Early Gastric Cancer. Clinical Cancer Research, 2018, 24, 1459-1472.	3.2	46
23	A Highly Efficient Strategy for Overexpressing circRNAs. Methods in Molecular Biology, 2018, 1724, 97-105.	0.4	16
24	Regulation of splicing and circularisation of RNA in epithelial mesenchymal plasticity. Seminars in Cell and Developmental Biology, 2018, 75, 50-60.	2.3	18
25	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	2.9	92
26	miRâ€200/375 control epithelial plasticityâ€associated alternative splicing by repressing the <scp>RNA</scp> â€binding protein Quaking. EMBO Journal, 2018, 37, .	3.5	82
27	FOXP3 and miR-155 cooperate to control the invasive potential of human breast cancer cells by down regulating ZEB2 independently of ZEB1. Oncotarget, 2018, 9, 27708-27727.	0.8	20
28	MicroRNA-194 Promotes Prostate Cancer Metastasis by Inhibiting SOCS2. Cancer Research, 2017, 77, 1021-1034.	0.4	94
29	Naturally existing isoforms of miR-222 have distinct functions. Nucleic Acids Research, 2017, 45, 11371-11385.	6.5	61
30	A network-biology perspective of microRNA function and dysfunction in cancer. Nature Reviews Genetics, 2016, 17, 719-732.	7.7	579
31	The Dose-Dependent Effects of Microrna-155 in Acute Myeloid Leukemia. Blood, 2016, 128, 2841-2841.	0.6	0
32	p53 Represses the Oncogenic Sno-MiR-28 Derived from a SnoRNA. PLoS ONE, 2015, 10, e0129190.	1.1	55
33	Network-Based Approaches to Understand the Roles of miR-200 and Other microRNAs in Cancer. Cancer Research, 2015, 75, 2594-2599.	0.4	54
34	The RNA Binding Protein Quaking Regulates Formation of circRNAs. Cell, 2015, 160, 1125-1134.	13.5	1,698
35	The tyrosine phosphatase PTPN14 (Pez) inhibits metastasis by altering protein trafficking. Science Signaling, 2015, 8, ra18.	1.6	57
36	Assessing the gene regulatory properties of Argonaute-bound small RNAs of diverse genomic origin. Nucleic Acids Research, 2015, 43, 470-481.	6.5	142

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37	Integration of microRNA signatures of distinct mammary epithelial cell types with their gene expression and epigenetic portraits. Breast Cancer Research, 2015, 17, 85.	2.2	29
38	A novel role for the Pol I transcription factor UBTF in maintaining genome stability through the regulation of highly transcribed Pol II genes. Genome Research, 2015, 25, 201-212.	2.4	52
39	MicroRNA networks regulated by <i>all-trans</i> retinoic acid and Lapatinib control the growth, survival and motility of breast cancer cells. Oncotarget, 2015, 6, 13176-13200.	0.8	33
40	Genomeâ€wide identification of miRâ€200 targets reveals a regulatory network controlling cell invasion. EMBO Journal, 2014, 33, 2040-2056.	3.5	126
41	Direct transcriptional regulation by nuclear microRNAs. International Journal of Biochemistry and Cell Biology, 2014, 54, 304-311.	1.2	78
42	Inferring condition-specific miRNA activity from matched miRNA and mRNA expression data. Bioinformatics, 2014, 30, 3070-3077.	1.8	22
43	Evidence that Meningeal Mast Cells Can Worsen Stroke Pathology in Mice. American Journal of Pathology, 2014, 184, 2493-2504.	1.9	55
44	Identifying direct miRNAâ€“mRNA causal regulatory relationships in heterogeneous data. Journal of Biomedical Informatics, 2014, 52, 438-447.	2.5	27
45	Understanding principles of <scp>miRNA</scp> target recognition and function through integrated biological and bioinformatics approaches. Wiley Interdisciplinary Reviews RNA, 2014, 5, 361-379.	3.2	60
46	Specificity Protein 1 (Sp1) Maintains Basal Epithelial Expression of the miR-200 Family. Journal of Biological Chemistry, 2014, 289, 11194-11205.	1.6	55
47	Chromatinized Protein Kinase C-Î¸ Directly Regulates Inducible Genes in Epithelial to Mesenchymal Transition and Breast Cancer Stem Cells. Molecular and Cellular Biology, 2014, 34, 2961-2980.	1.1	40
48	Inferring microRNA and transcription factor regulatory networks in heterogeneous data. BMC Bioinformatics, 2013, 14, 92.	1.2	35
49	Down-Regulation of the miRNA-200 Family at the Invasive Front of Colorectal Cancers with Degraded Basement Membrane Indicates EMT Is Involved in Cancer Progression. Neoplasia, 2013, 15, 180-IN22.	2.3	143
50	Axl Mediates Acquired Resistance of Head and Neck Cancer Cells to the Epidermal Growth Factor Receptor Inhibitor Erlotinib. Molecular Cancer Therapeutics, 2013, 12, 2541-2558.	1.9	132
51	Epigenetic modulation of the miR-200 family is associated with transition to a breast cancer stem cell-like state. Journal of Cell Science, 2013, 126, 2256-66.	1.2	173
52	Inferring microRNAâ€“mRNA causal regulatory relationships from expression data. Bioinformatics, 2013, 29, 765-771.	1.8	75
53	Regulation of vascular leak and recovery from ischemic injury by general and VE-cadherinâ€“restricted miRNA antagonists of miR-27. Blood, 2013, 122, 2911-2919.	0.6	60
54	On Measuring miRNAs after Transient Transfection of Mimics or Antisense Inhibitors. PLoS ONE, 2013, 8, e55214.	1.1	103

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55	Identification of an Enhancer That Increases miR-200b~200a~429 Gene Expression in Breast Cancer Cells. PLoS ONE, 2013, 8, e75517.	1.1	21
56	Abstract B093: Discovery of microRNAs associated with breast cancer EMT using bioinformatics and next-generation sequencing. , 2013, , .		0
57	A microRNA that limits metastatic colonisation and endothelial recruitment. EMBO Journal, 2012, 31, 786-787.	3.5	7
58	IsomiRs â€" the overlooked repertoire in the dynamic microRNAome. Trends in Genetics, 2012, 28, 544-549.	2.9	410
59	Matrigel Basement Membrane Matrix influences expression of microRNAs in cancer cell lines. Biochemical and Biophysical Research Communications, 2012, 427, 343-348.	1.0	41
60	Stromal miR-320 keeps an oncogenic secretome in check. Nature Cell Biology, 2012, 14, 124-125.	4.6	13
61	ZEB1 drives prometastatic actin cytoskeletal remodeling by downregulating miR-34a expression. Journal of Clinical Investigation, 2012, 122, 3170-3183.	3.9	135
62	Experimental strategies for microRNA target identification. Nucleic Acids Research, 2011, 39, 6845-6853.	6.5	493
63	MiRNA-205 modulates cellular invasion and migration via regulating zinc finger E-box binding homeobox 2 expression in esophageal squamous cell carcinoma cells. Journal of Translational Medicine, 2011, 9, 30.	1.8	120
64	Reversal and Prevention of Arsenic-Induced Human Bronchial Epithelial Cell Malignant Transformation by microRNA-200b. Toxicological Sciences, 2011, 121, 110-122.	1.4	130
65	Induction of miR-21 by Retinoic Acid in Estrogen Receptor-positive Breast Carcinoma Cells. Journal of Biological Chemistry, 2011, 286, 4027-4042.	1.6	82
66	An autocrine TGF-Î²/ZEB/miR-200 signaling network regulates establishment and maintenance of epithelial-mesenchymal transition. Molecular Biology of the Cell, 2011, 22, 1686-1698.	0.9	505
67	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. Nucleic Acids Research, 2011, 39, 5658-5668.	6.5	76
68	The Notch ligand Jagged2 promotes lung adenocarcinoma metastasis through a miR-200â€"dependent pathway in mice. Journal of Clinical Investigation, 2011, 121, 1373-1385.	3.9	172
69	microRNAs and EMT in Mammary Cells and Breast Cancer. Journal of Mammary Gland Biology and Neoplasia, 2010, 15, 213-223.	1.0	51
70	Myc-modulated miR-9 makes more metastases. Nature Cell Biology, 2010, 12, 209-211.	4.6	99
71	E-Cadherin Expression Is Regulated by miR-192/215 by a Mechanism That Is Independent of the Profibrotic Effects of Transforming Growth Factor-Î². Diabetes, 2010, 59, 1794-1802.	0.3	235
72	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	2.4	76

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73	Genome-Wide Identification of Human FOXP3 Target Genes in Natural Regulatory T Cells. Journal of Immunology, 2010, 185, 1071-1081.	0.4	128
74	Exploring complex miRNA-mRNA interactions with Bayesian networks by splitting-averaging strategy. BMC Bioinformatics, 2009, 10, 408.	1.2	72
75	Over-expression of cathepsin E and trefoil factor 1 in sessile serrated adenomas of the colorectum identified by gene expression analysis. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2009, 454, 291-302.	1.4	31
76	Contextual extracellular cues promote tumor cell EMT and metastasis by regulating miR-200 family expression. Genes and Development, 2009, 23, 2140-2151.	2.7	435
77	Expression profiling of a hemopoietic cell survival transcriptome implicates osteopontin as a functional prognostic factor in AML. Blood, 2009, 114, 4859-4870.	0.6	52
78	The miR-200 family and miR-205 regulate epithelial to mesenchymal transition by targeting ZEB1 and SIP1. Nature Cell Biology, 2008, 10, 593-601.	4.6	3,455
79	A Double-Negative Feedback Loop between ZEB1-SIP1 and the microRNA-200 Family Regulates Epithelial-Mesenchymal Transition. Cancer Research, 2008, 68, 7846-7854.	0.4	956
80	MicroRNAs as regulators of epithelial-mesenchymal transition. Cell Cycle, 2008, 7, 3112-3117.	1.3	467
81	Attenuation of leakiness in doxycycline-inducible expression via incorporation of 3â€² AU-rich mRNA destabilizing elements. BioTechniques, 2008, 45, 155-162.	0.8	22
82	The microRNA-200 Family Regulates Epithelial to Mesenchymal Transition. Scientific World Journal, The, 2008, 8, 901-904.	0.8	69
83	Identification of Novel MYB Target Genes. Blood, 2008, 112, 3580-3580.	0.6	0
84	Genetic regulators of myelopoiesis and leukemic signaling identified by gene profiling and linear modeling. Journal of Leukocyte Biology, 2006, 80, 433-447.	1.5	37
85	Assessing IRES activity in the HIF-1Â and other cellular 5' UTRs. Rna, 2006, 12, 1074-1083.	1.6	108
86	Phosphorylation of cold shock domain/Y-box proteins by ERK2 and GSK3Î² and repression of the human VEGF promoter. FEBS Letters, 2005, 579, 5372-5378.	1.3	56
87	Functional Integrity of Nuclear Factor ÎºB, Phosphatidylinositol 3â€²-Kinase, and Mitogen-Activated Protein Kinase Signaling Allows Tumor Necrosis Factor Î±-Evoked Bcl-2 Expression to Provoke Internal Ribosome Entry Site-Dependent Translation of Hypoxia-Inducible Factor 1Î±. Cancer Research, 2004, 64, 9041-9048.	0.4	62
88	A vascular cell-restricted RhoGAP, p73RhoGAP, is a key regulator of angiogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12212-12217.	3.3	42
89	A multi-protein complex containing cold shock domain (Y-box) and polypyrimidine tract binding proteins forms on the vascular endothelial growth factor mRNA. Potential role in mRNA stabilization. FEBS Journal, 2004, 271, 648-660.	0.2	76
90	Human PABP binds AU-rich RNA via RNA-binding domains 3 and 4. FEBS Journal, 2004, 271, 450-457.	0.2	64

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91	Hypoxia-inducible Factor-1Î± mRNA Contains an Internal Ribosome Entry Site That Allows Efficient Translation during Normoxia and Hypoxia. Molecular Biology of the Cell, 2002, 13, 1792-1801.	0.9	279
92	A novel mechanism of repression of the vascular endothelial growth factor promoter, by single strand DNA binding cold shock domain (Y-box) proteins in normoxic fibroblasts. Nucleic Acids Research, 2002, 30, 4845-4854.	6.5	28
93	The vascular endothelial growth factor mRNA contains an internal ribosome entry site. FEBS Letters, 1998, 434, 417-420.	1.3	77
94	Differential Regulation of the Stability of Cytokine mRNAs in Lipopolysaccharide-activated Blood Monocytes in Response to Interleukin-10. Journal of Biological Chemistry, 1996, 271, 20108-20112.	1.6	88
95	Cytokine Receptor Genes: Structure, Chromosomal Location, and Involvement in Human Disease. Leukemia and Lymphoma, 1995, 18, 373-383.	0.6	13
96	A Model for the Interaction of the GM-CSF, IL-3 and IL-5 Receptors with their Ligands. Growth Factors, 1993, 8, 87-97.	0.5	93
97	Multiple plant RNA binding proteins identified by PCR: expression of cDNAs encoding RNA binding proteins targeted to chloroplasts in Nicotiana plumbaginifolia. Molecular Genetics and Genomics, 1992, 234, 390-400.	2.4	46
98	Recognition efficiency ofDicotyledoneae-specific promoter and RNA processing signals in rice. Molecular Genetics and Genomics, 1990, 222, 361-368.	2.4	56
99	The minimum functional length of pre-mRNA introns in monocots and dicots. Plant Molecular Biology, 1990, 14, 727-733.	2.0	82
100	Analysis of pre-mRNA processing in transfected plant protoplasts. Methods in Enzymology, 1990, 181, 148-161.	0.4	167
101	The AU-rich sequences present in the introns of plant nuclear pre-mRNAs are required for splicing. Cell, 1989, 58, 473-483.	13.5	416
102	[17] Prothymosin Î± and Î±1-like peptides. Methods in Enzymology, 1985, 116, 255-265.	0.4	7
103	Pyruvate Carboxylase: Mechanisms of the Partial Reactions. Annals of the New York Academy of Sciences, 1985, 447, 169-188.	1.8	24
104	Sheep Liver Propionyl-CoA Carboxylase: Purification and Some Molecular Properties. Annals of the New York Academy of Sciences, 1985, 447, 396-397.	1.8	10
105	Sequence of a cloned 523-bp cDNA for thymosin Î²4. Archives of Biochemistry and Biophysics, 1985, 236, 445-447.	1.4	23
106	Thymosin Î²4 in cultured mammalian cell lines. Archives of Biochemistry and Biophysics, 1983, 221, 598-601.	1.4	67