Gregory J Goodall

List of Publications by Year in Descending Order

105 papers	13,190 citations	49 h-index	114 g-index
116 ext. papers	15,197 ext. citations	9.7 avg, IF	6.76 L-index

#	Paper	IF	Citations
105	The Quaking RNA-binding proteins as regulators of cell differentiation.. *Wiley Interdisciplinary Reviews RNA*, **2022**, e1724	9.3	0
104	A 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,	6.6	1
103	pDriver : A novel method for unravelling personalised coding and miRNA cancer drivers. *Bioinformatics*, **2021**,	7.2	2
102	capCLIP: a new tool to probe translational control in human cells through capture and identification of the eIF4E-mRNA interactome. *Nucleic Acids Research*, **2021**, 49, e105	20.1	2
101	RNA in cancer. *Nature Reviews Cancer*, **2021**, 21, 22-36	31.3	279
100	Phosphorylation of PKCδ by FER tips the balance from EGFR degradation to recycling. *Journal of Cell Biology*, **2021**, 220,	7.3	5
99	Computational methods for cancer driver discovery: A survey. *Theranostics*, **2021**, 11, 5553-5568	12.1	3
98	Post-transcriptional Gene Regulation by MicroRNA-194 Promotes Neuroendocrine Transdifferentiation in Prostate Cancer. *Cell Reports*, **2021**, 34, 108585	10.6	10
97	The many regulators of epithelial-mesenchymal transition. *Nature Reviews Molecular Cell Biology*, **2021**,	48.7	3
96	DriverGroup: a novel method for identifying driver gene groups. *Bioinformatics*, **2020**, 36, i583-i591	7.2	3
95	Stathmin levels alter PTPN14 expression and impact neuroblastoma cell migration. *British Journal of Cancer*, **2020**, 122, 434-444	8.7	4
94	A novel single-cell based method for breast cancer prognosis. *PLoS Computational Biology*, **2020**, 16, e1008133	5	7
93	Insufficiently complex unique-molecular identifiers (UMIs) distort small RNA sequencing. *Scientific Reports*, **2020**, 10, 14593	4.9	5
92	Guidelines and definitions for research on epithelial-mesenchymal transition. *Nature Reviews Molecular Cell Biology*, **2020**, 21, 341-352	48.7	469
91	Insights into the biogenesis and potential functions of exonic circular RNA. *Scientific Reports*, **2019**, 9, 2048	4.9	70
90	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exon-Intron Split Analysis (EISA). *Nucleic Acids Research*, **2019**, 47, 8606-8619	20.1	3
89	MicroRNA-143-3p targets pyruvate carboxylase expression and controls proliferation and migration of MDA-MB-231 cells. *Archives of Biochemistry and Biophysics*, **2019**, 677, 108169	4.1	8

88	CBNA: A control theory based method for identifying coding and non-coding cancer drivers. *PLoS Computational Biology*, **2019**, 15, e1007538	5	11
87	miRNA length variation during macrophage stimulation confounds the interpretation of results: implications for miRNA quantification by RT-qPCR. *Rna*, **2019**, 25, 232-238	5.8	10
86	miR-222 isoforms are differentially regulated by type-I interferon. *Rna*, **2018**, 24, 332-341	5.8	21
85	Clinical Utility of a STAT3-Regulated miRNA-200 Family Signature with Prognostic Potential in Early Gastric Cancer. *Clinical Cancer Research*, **2018**, 24, 1459-1472	12.9	29
84	A Highly Efficient Strategy for Overexpressing circRNAs. *Methods in Molecular Biology*, **2018**, 1724, 97-105	1.4	12
83	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. *Cell Systems*, **2018**, 7, 77-91.e7	10.6	52
82	miR-200/375 control epithelial plasticity-associated alternative splicing by repressing the RNA-binding protein Quaking. *EMBO Journal*, **2018**, 37,	13	46
81	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	3.3	14
80	Regulation of splicing and circularisation of RNA in epithelial mesenchymal plasticity. *Seminars in Cell and Developmental Biology*, **2018**, 75, 50-60	7.5	12
79	MicroRNA-194 Promotes Prostate Cancer Metastasis by Inhibiting SOCS2. *Cancer Research*, **2017**, 77, 1021-1034	10.1	74
78	Naturally existing isoforms of miR-222 have distinct functions. *Nucleic Acids Research*, **2017**, 45, 11371-11385	13.6	44
77	A network-biology perspective of microRNA function and dysfunction in cancer. *Nature Reviews Genetics*, **2016**, 17, 719-732	30.1	440
76	The Dose-Dependent Effects of Microrna-155 in Acute Myeloid Leukemia. *Blood*, **2016**, 128, 2841-2841	2.2	
75	The RNA binding protein quaking regulates formation of circRNAs. *Cell*, **2015**, 160, 1125-34	56.2	1206
74	The tyrosine phosphatase PTPN14 (Pez) inhibits metastasis by altering protein trafficking. *Science Signaling*, **2015**, 8, ra18	8.8	42
73	Assessing the gene regulatory properties of Argonaute-bound small RNAs of diverse genomic origin. *Nucleic Acids Research*, **2015**, 43, 470-81	20.1	47
72	Integration of microRNA signatures of distinct mammary epithelial cell types with their gene expression and epigenetic portraits. *Breast Cancer Research*, **2015**, 17, 85	8.3	24
71	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, 201-12	9.7	31

70	p53 Represses the Oncogenic Sno-MiR-28 Derived from a SnoRNA. *PLoS ONE*, **2015**, 10, e0129190	3.7	34
69	Network-Based Approaches to Understand the Roles of miR-200 and Other microRNAs in Cancer. *Cancer Research*, **2015**, 75, 2594-9	10.1	49
68	MicroRNA networks regulated by all-trans retinoic acid and Lapatinib control the growth, survival and motility of breast cancer cells. *Oncotarget*, **2015**, 6, 13176-200	3.3	29
67	Direct transcriptional regulation by nuclear microRNAs. *International Journal of Biochemistry and Cell Biology*, **2014**, 54, 304-11	5.6	66
66	Inferring condition-specific miRNA activity from matched miRNA and mRNA expression data. *Bioinformatics*, **2014**, 30, 3070-7	7.2	17
65	Evidence that meningeal mast cells can worsen stroke pathology in mice. *American Journal of Pathology*, **2014**, 184, 2493-504	5.8	43
64	Identifying direct miRNA-mRNA causal regulatory relationships in heterogeneous data. *Journal of Biomedical Informatics*, **2014**, 52, 438-47	10.2	19
63	Understanding principles of miRNA target recognition and function through integrated biological and bioinformatics approaches. *Wiley Interdisciplinary Reviews RNA*, **2014**, 5, 361-79	9.3	45
62	Specificity protein 1 (Sp1) maintains basal epithelial expression of the miR-200 family: implications for epithelial-mesenchymal transition. *Journal of Biological Chemistry*, **2014**, 289, 11194-11205	5.4	49
61	Chromatinized protein kinase C-directly regulates inducible genes in epithelial to mesenchymal transition and breast cancer stem cells. *Molecular and Cellular Biology*, **2014**, 34, 2961-80	4.8	24
60	Genome-wide identification of miR-200 targets reveals a regulatory network controlling cell invasion. *EMBO Journal*, **2014**, 33, 2040-56	13	112
59	Inferring microRNA and transcription factor regulatory networks in heterogeneous data. *BMC Bioinformatics*, **2013**, 14, 92	3.6	34
58	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, 180-91	6.4	126
57	Axl mediates acquired resistance of head and neck cancer cells to the epidermal growth factor receptor inhibitor erlotinib. *Molecular Cancer Therapeutics*, **2013**, 12, 2541-58	6.1	117
56	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	5.3	150
55	Inferring microRNA-mRNA causal regulatory relationships from expression data. *Bioinformatics*, **2013**, 29, 765-71	7.2	56
54	Regulation of vascular leak and recovery from ischemic injury by general and VE-cadherin-restricted miRNA antagonists of miR-27. *Blood*, **2013**, 122, 2911-9	2.2	48
53	On measuring miRNAs after transient transfection of mimics or antisense inhibitors. *PLoS ONE*, **2013**, 8, e55214	3.7	84

52	Identification of an enhancer that increases miR-200b~200a~429 gene expression in breast cancer cells. *PLoS ONE*, **2013**, 8, e75517	3.7	18
51	IsomiRs--the overlooked repertoire in the dynamic microRNAome. *Trends in Genetics*, **2012**, 28, 544-9	8.5	339
50	Matrigel basement membrane matrix influences expression of microRNAs in cancer cell lines. *Biochemical and Biophysical Research Communications*, **2012**, 427, 343-8	3.4	38
49	A microRNA that limits metastatic colonisation and endothelial recruitment. *EMBO Journal*, **2012**, 31, 786-7	13	7
48	ZEB1 drives prometastatic actin cytoskeletal remodeling by downregulating miR-34a expression. *Journal of Clinical Investigation*, **2012**, 122, 3170-83	15.9	119
47	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	8.5	111
46	Experimental strategies for microRNA target identification. *Nucleic Acids Research*, **2011**, 39, 6845-53	20.1	430
45	Reversal and prevention of arsenic-induced human bronchial epithelial cell malignant transformation by microRNA-200b. *Toxicological Sciences*, **2011**, 121, 110-22	4.4	113
44	Induction of miR-21 by retinoic acid in estrogen receptor-positive breast carcinoma cells: biological correlates and molecular targets. *Journal of Biological Chemistry*, **2011**, 286, 4027-42	5.4	75
43	An autocrine TGF-beta/ZEB/miR-200 signaling network regulates establishment and maintenance of epithelial-mesenchymal transition. *Molecular Biology of the Cell*, **2011**, 22, 1686-98	3.5	425
42	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. *Nucleic Acids Research*, **2011**, 39, 5658-68	20.1	63
41	The Notch ligand Jagged2 promotes lung adenocarcinoma metastasis through a miR-200-dependent pathway in mice. *Journal of Clinical Investigation*, **2011**, 121, 1373-85	15.9	154
40	Myc-modulated miR-9 makes more metastases. *Nature Cell Biology*, **2010**, 12, 209-11	23.4	92
39	E-cadherin expression is regulated by miR-192/215 by a mechanism that is independent of the profibrotic effects of transforming growth factor-beta. *Diabetes*, **2010**, 59, 1794-802	0.9	212
38	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. *Genome Research*, **2010**, 20, 1639-50	9.7	66
37	Genome-wide identification of human FOXP3 target genes in natural regulatory T cells. *Journal of Immunology*, **2010**, 185, 1071-81	5.3	107
36	microRNAs and EMT in mammary cells and breast cancer. *Journal of Mammary Gland Biology and Neoplasia*, **2010**, 15, 213-23	2.4	43
35	Exploring complex miRNA-mRNA interactions with Bayesian networks by splitting-averaging strategy. *BMC Bioinformatics*, **2009**, 10, 408	3.6	58

34	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	5.1	26
33	Contextual extracellular cues promote tumor cell EMT and metastasis by regulating miR-200 family expression. *Genes and Development*, **2009**, 23, 2140-51	12.6	376
32	Expression profiling of a hemopoietic cell survival transcriptome implicates osteopontin as a functional prognostic factor in AML. *Blood*, **2009**, 114, 4859-70	2.2	51
31	The miR-200 family and miR-205 regulate epithelial to mesenchymal transition by targeting ZEB1 and SIP1. *Nature Cell Biology*, **2008**, 10, 593-601	23.4	3060
30	A double-negative feedback loop between ZEB1-SIP1 and the microRNA-200 family regulates epithelial-mesenchymal transition. *Cancer Research*, **2008**, 68, 7846-54	10.1	852
29	MicroRNAs as regulators of epithelial-mesenchymal transition. *Cell Cycle*, **2008**, 7, 3112-8	4.7	417
28	Attenuation of leakiness in doxycycline-inducible expression via incorporation of 3TAU-rich mRNA destabilizing elements. *BioTechniques*, **2008**, 45, 155-6, 158, 160 passim	2.5	19
27	The microRNA-200 family regulates epithelial to mesenchymal transition. *Scientific World Journal, The*, **2008**, 8, 901-4	2.2	63
26	Identification of Novel MYB Target Genes. *Blood*, **2008**, 112, 3580-3580	2.2	
25	Genetic regulators of myelopoiesis and leukemic signaling identified by gene profiling and linear modeling. *Journal of Leukocyte Biology*, **2006**, 80, 433-47	6.5	28
24	Assessing IRES activity in the HIF-1alpha and other cellular 5TUTRs. *Rna*, **2006**, 12, 1074-83	5.8	93
23	Phosphorylation of cold shock domain/Y-box proteins by ERK2 and GSK3beta and repression of the human VEGF promoter. *FEBS Letters*, **2005**, 579, 5372-8	3.8	48
22	Functional integrity of nuclear factor kappaB, phosphatidylinositol 3Tkinase, and mitogen-activated protein kinase signaling allows tumor necrosis factor alpha-evoked Bcl-2 expression to provoke internal ribosome entry site-dependent translation of hypoxia-inducible factor 1alpha. *Cancer Research*, **2004**, 64, 9041-8	10.1	55
21	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, 12212-7	11.5	36
20	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, 648-60		66
19	Human PABP binds AU-rich RNA via RNA-binding domains 3 and 4. *FEBS Journal*, **2004**, 271, 450-7		52
18	Hypoxia-inducible factor-1alpha mRNA contains an internal ribosome entry site that allows efficient translation during normoxia and hypoxia. *Molecular Biology of the Cell*, **2002**, 13, 1792-801	3.5	263
17	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, 4845-54	20.1	24

16	The vascular endothelial growth factor mRNA contains an internal ribosome entry site. *FEBS Letters* , **1998**, 434, 417-20	3.8	69
15	Differential regulation of the stability of cytokine mRNAs in lipopolysaccharide-activated blood monocytes in response to interleukin-10. *Journal of Biological Chemistry*, **1996**, 271, 20108-12	5.4	76
14	Cytokine receptor genes: structure, chromosomal location, and involvement in human disease. *Leukemia and Lymphoma*, **1995**, 18, 373-83	1.9	12
13	A model for the interaction of the GM-CSF, IL-3 and IL-5 receptors with their ligands. *Growth Factors* , **1993**, 8, 87-97	1.6	86
12	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		40
11	Recognition efficiency of Dicotyledoneae-specific promoter and RNA processing signals in rice. *Molecular Genetics and Genomics*, **1990**, 222, 361-8		51
10	The minimum functional length of pre-mRNA introns in monocots and dicots. *Plant Molecular Biology*, **1990**, 14, 727-33	4.6	76
9	Analysis of pre-mRNA processing in transfected plant protoplasts. *Methods in Enzymology*, **1990**, 181, 148-61	1.7	150
8	The AU-rich sequences present in the introns of plant nuclear pre-mRNAs are required for splicing. *Cell*, **1989**, 58, 473-83	56.2	395
7	Prothymosin alpha and alpha 1-like peptides. *Methods in Enzymology*, **1985**, 116, 255-65	1.7	5
6	Pyruvate carboxylase: mechanisms of the partial reactions. *Annals of the New York Academy of Sciences*, **1985**, 447, 169-88	6.5	21
5	Sheep Liver Propionyl-CoA Carboxylase: Purification and Some Molecular Properties. *Annals of the New York Academy of Sciences*, **1985**, 447, 396-397	6.5	9
4	Sequence of a cloned 523-bp cDNA for thymosin beta 4. *Archives of Biochemistry and Biophysics*, **1985**, 236, 445-7	4.1	22
3	Thymosin beta 4 in cultured mammalian cell lines. *Archives of Biochemistry and Biophysics*, **1983**, 221, 598-601	4.1	64
2	capCLIP: a new tool to probe protein synthesis in human cells through capture and identification of the eIF4E-mRNA interactome		2
1	Post-transcriptional control of EMT is coordinated through combinatorial targeting by multiple microRNAs		1