

# Anthony P H Wright

## List of Publications by Year in descending order

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81  
papers

4,569  
citations

81900

39  
h-index

102487

66  
g-index

85  
all docs

85  
docs citations

85  
times ranked

4666  
citing authors

#	ARTICLE	IF	CITATIONS
1	Migration and Adhesion of B-Lymphocytes to Specific Microenvironments in Mantle Cell Lymphoma: Interplay between Signaling Pathways and the Epigenetic Landscape. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6247.	4.1	5
2	Association between Predicted Effects of TP53 Missense Variants on Protein Conformation and Their Phenotypic Presentation as Li-Fraumeni Syndrome or Hereditary Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6345.	4.1	3
3	3D heterospecies spheroids of pancreatic stroma and cancer cells demonstrate key phenotypes of pancreatic ductal adenocarcinoma. <i>Translational Oncology</i> , 2021, 14, 101107.	3.7	8
4	Intrinsic 5-lipoxygenase activity regulates migration and adherence of mantle cell lymphoma cells. <i>Prostaglandins and Other Lipid Mediators</i> , 2021, 156, 106575.	1.9	7
5	Differential Transcriptional Reprogramming by Wild Type and Lymphoma-Associated Mutant MYC Proteins as B-Cells Convert to a Lymphoma Phenotype. <i>Cancers</i> , 2021, 13, 6093.	3.7	1
6	Differential B-Cell Receptor Signaling Requirement for Adhesion of Mantle Cell Lymphoma Cells to Stromal Cells. <i>Cancers</i> , 2020, 12, 1143.	3.7	7
7	Disentangling the Amyloid Pathways: A Mechanistic Approach to Etiology. <i>Frontiers in Neuroscience</i> , 2020, 14, 256.	2.8	21
8	Mixed-species RNAseq analysis of human lymphoma cells adhering to mouse stromal cells identifies a core gene set that is also differentially expressed in the lymph node microenvironment of mantle cell lymphoma and chronic lymphocytic leukemia patients. <i>Haematologica</i> , 2018, 103, 666-678.	3.5	11
9	A subset of functional adaptation mutations alter propensity for $\alpha$ -helical conformation in the intrinsically disordered glucocorticoid receptor tau1 core activation domain. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1452-1461.	2.4	8
10	A Protein Intrinsic Disorder Approach for Characterising Differentially Expressed Genes in Transcriptome Data: Analysis of Cell-Adhesion Regulated Gene Expression in Lymphoma Cells. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3101.	4.1	3
11	Impact of <i>Sox11</i> over-expression in Ba/F3 cells. <i>Haematologica</i> , 2018, 103, e594-e597.	3.5	3
12	Genetic differences between willow warbler migratory phenotypes are few and cluster in large haplotype blocks. <i>Evolution Letters</i> , 2017, 1, 155-168.	3.3	80
13	An NMR study on the intrinsically disordered core transactivation domain of human glucocorticoid receptor. <i>BMB Reports</i> , 2017, 50, 522-527.	2.4	12
14	Gene expression in the brain of a migratory songbird during breeding and migration. <i>Movement Ecology</i> , 2016, 4, 4.	2.8	28
15	AP-1-mediated chromatin looping regulates ZEB2 transcription: new insights into TNF $\alpha$ -induced epithelial-mesenchymal transition in triple-negative breast cancer. <i>Oncotarget</i> , 2015, 6, 7804-7814.	1.8	48
16	Myc-induced anchorage of the rDNA IGS region to nucleolar matrix modulates growth-stimulated changes in higher-order rDNA architecture. <i>Nucleic Acids Research</i> , 2014, 42, 5505-5517.	14.5	23
17	Distinct roles of the Gcn5 histone acetyltransferase revealed during transient stress-induced reprogramming of the genome. <i>BMC Genomics</i> , 2013, 14, 479.	2.8	42
18	Characterisation of a transcriptome to find sequence differences between two differentially migrating subspecies of the willow warbler <i>Phylloscopus trochilus</i> . <i>BMC Genomics</i> , 2013, 14, 330.	2.8	38

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19	Origins of Myc Proteins â€“ Using Intrinsic Protein Disorder to Trace Distant Relatives. PLoS ONE, 2013, 8, e75057.	2.5	22
20	Proteome-wide evidence for enhanced positive Darwinian selection within intrinsically disordered regions in proteins. Genome Biology, 2011, 12, R65.	9.6	68
21	Nucleolar organization, growth control and cancer. Epigenetics, 2010, 5, 200-205.	2.7	18
22	Genome-wide characterisation of the Gcn5 histone acetyltransferase in budding yeast during stress adaptation reveals evolutionarily conserved and diverged roles. BMC Genomics, 2010, 11, 200.	2.8	24
23	Expression profiling of <i>S. pombe</i> acetyltransferase mutants identifies redundant pathways of gene regulation. BMC Genomics, 2010, 11, 59.	2.8	46
24	WD40 Domain Divergence Is Important for Functional Differences between the Fission Yeast Tup11 and Tup12 Co-Repressor Proteins. PLoS ONE, 2010, 5, e11009.	2.5	3
25	The role of specific HAT-HDAC interactions in transcriptional elongation. Cell Cycle, 2010, 9, 467-471.	2.6	15
26	HATâ€™HDAC interplay modulates global histone H3K14 acetylation in geneâ€™coding regions during stress. EMBO Reports, 2009, 10, 1009-1014.	4.5	85
27	Activatorâ€™binding domains of the SWI/SNF chromatin remodeling complex characterized <i>in vitro</i> are required for its recruitment to promoters <i>in vivo</i> . FEBS Journal, 2009, 276, 2557-2565.	4.7	18
28	Individual Subunits of the Ssn6-Tup11/12 Corepressor Are Selectively Required for Repression of Different Target Genes. Molecular and Cellular Biology, 2007, 27, 1069-1082.	2.3	23
29	c-Myc induced changes in higher order rDNA structure accompany growth factor stimulation of quiescent cells. Nature Precedings, 2007, , .	0.1	0
30	Specific functions for the fission yeast Sirtuins Hst2 and Hst4 in gene regulation and retrotransposon silencing. EMBO Journal, 2007, 26, 2477-2488.	7.8	47
31	Comparative analysis of regulatory transcription factors in <i>Schizosaccharomyces pombe</i> and budding yeasts. Yeast, 2006, 23, 929-935.	1.7	12
32	Genomewide identification of pheromone-targeted transcription in fission yeast. BMC Genomics, 2006, 7, 303.	2.8	48
33	Stress-Specific Role of Fission Yeast Gcn5 Histone Acetyltransferase in Programming a Subset of Stress Response Genes. Eukaryotic Cell, 2006, 5, 1337-1346.	3.4	32
34	c-Myc associates with ribosomal DNA and activates RNA polymerase I transcription. Nature Cell Biology, 2005, 7, 303-310.	10.3	421
35	Mechanism of Transcription Factor Recruitment by Acidic Activators. Journal of Biological Chemistry, 2005, 280, 21779-21784.	3.4	64
36	Functional Comparison of the Tup11 and Tup12 Transcriptional Corepressors in Fission Yeast. Molecular and Cellular Biology, 2005, 25, 716-727.	2.3	28

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37	A DNA microarray for fission yeast: minimal changes in global gene expression after temperature shift. <i>Yeast</i> , 2004, 21, 25-39.	1.7	39
38	Genome-scale design of PCR primers and long oligomers for DNA microarrays. <i>Nucleic Acids Research</i> , 2003, 31, 5576-5581.	14.5	31
39	Accumulation of c-Myc and proteasomes at the nucleoli of cells containing elevated c-Myc protein levels. <i>Journal of Cell Science</i> , 2003, 116, 1707-1717.	2.0	88
40	Activation Functions 1 and 2 of Nuclear Receptors: Molecular Strategies for Transcriptional Activation. <i>Molecular Endocrinology</i> , 2003, 17, 1901-1909.	3.7	240
41	Recruitment of Gcn5-containing Complexes during c-Myc-dependent Gene Activation. <i>Journal of Biological Chemistry</i> , 2002, 277, 23399-23406.	3.4	27
42	Dicer is required for chromosome segregation and gene silencing in fission yeast cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16648-16653.	7.1	123
43	The N-terminal Regions of Estrogen Receptor $\hat{1}$ and $\hat{2}$ Are Unstructured in Vitro and Show Different TBP Binding Properties. <i>Journal of Biological Chemistry</i> , 2001, 276, 45939-45944.	3.4	120
44	How Transcriptional Activators Bind Target Proteins. <i>Journal of Biological Chemistry</i> , 2001, 276, 40127-40132.	3.4	51
45	Chromatin-remodeling complexes involved in gene activation by the glucocorticoid receptor. <i>Vitamins and Hormones</i> , 2000, 60, 75-122.	1.7	8
46	Architectural Principles for the Structure and Function of the Glucocorticoid Receptor $\hat{1}$ ,1 Core Activation Domain. <i>Journal of Biological Chemistry</i> , 2000, 275, 15014-15018.	3.4	26
47	Functional Probing of the Human Glucocorticoid Receptor Steroid-interacting Surface by Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 2000, 275, 19041-19049.	3.4	32
48	Comparison of Nucleosome Remodeling by the Yeast Transcription Factor Pho4 and the Glucocorticoid Receptor. <i>Journal of Biological Chemistry</i> , 2000, 275, 9035-9042.	3.4	4
49	Recruitment of the SWI-SNF Chromatin Remodeling Complex as a Mechanism of Gene Activation by the Glucocorticoid Receptor $\hat{1}$ ,1 Activation Domain. <i>Molecular and Cellular Biology</i> , 2000, 20, 2004-2013.	2.3	118
50	Identification and Functional Characterization of a Novel Mitochondrial Thioredoxin System in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 6366-6373.	3.4	187
51	Competition between Thyroid Hormone Receptor-associated Protein (TRAP) 220 and Transcriptional Intermediary Factor (TIF) 2 for Binding to Nuclear Receptors. <i>Journal of Biological Chemistry</i> , 1999, 274, 6667-6677.	3.4	72
52	Valine 571 Functions as a Regional Organizer in Programming the Glucocorticoid Receptor for Differential Binding of Glucocorticoids and Mineralocorticoids. <i>Journal of Biological Chemistry</i> , 1999, 274, 18515-18523.	3.4	21
53	Activation Domain-mediated Targeting of the SWI/SNF Complex to Promoters Stimulates Transcription from Nucleosome Arrays. <i>Molecular Cell</i> , 1999, 4, 649-655.	9.7	231
54	Histone Acetyltransferase Complexes Can Mediate Transcriptional Activation by the Major Glucocorticoid Receptor Activation Domain. <i>Molecular and Cellular Biology</i> , 1999, 19, 5952-5959.	2.3	61

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55	Role of Important Hydrophobic Amino Acids in the Interaction between the Glucocorticoid Receptor $\beta$ ,1-Core Activation Domain and Target Factors. <i>Biochemistry</i> , 1998, 37, 9586-9594.	2.5	79
56	myc Boxes, Which Are Conserved in myc Family Proteins, Are Signals for Protein Degradation via the Proteasome. <i>Molecular and Cellular Biology</i> , 1998, 18, 5961-5969.	2.3	117
57	Involvement of the Transcription Factor IID Protein Complex in Gene Activation by the N-Terminal Transactivation Domain of the Glucocorticoid Receptor in Vitro. <i>Molecular Endocrinology</i> , 1997, 11, 1467-1475.	3.7	67
58	Interaction of the Ligand-activated Glucocorticoid Receptor with the 14-3-3 $\beta$ Protein. <i>Journal of Biological Chemistry</i> , 1997, 272, 8153-8156.	3.4	91
59	Role of Hydrophobic Amino Acid Clusters in the Transactivation Activity of the Human Glucocorticoid Receptor. <i>Molecular and Cellular Biology</i> , 1997, 17, 934-945.	2.3	66
60	Role of the Ada Adaptor Complex in Gene Activation by the Glucocorticoid Receptor. <i>Molecular and Cellular Biology</i> , 1997, 17, 3065-3073.	2.3	65
61	Chapter 9 Molecular aspects of steroid receptor/DNA binding. <i>Advances in Molecular and Cellular Endocrinology</i> , 1997, 1, 241-264.	0.1	0
62	Mechanism of gene expression by the glucocorticoid receptor: Role of protein-protein interactions. <i>BioEssays</i> , 1997, 19, 153-160.	2.5	178
63	Involvement of the Transcription Factor IID Protein Complex in Gene Activation by the N-Terminal Transactivation Domain of the Glucocorticoid Receptor in Vitro. <i>Molecular Endocrinology</i> , 1997, 11, 1467-1475.	3.7	23
64	Functional Interaction of the c-Myc Transactivation Domain with the TATA Binding Protein: Evidence for an Induced Fit Model of Transactivation Domain Folding. <i>Biochemistry</i> , 1996, 35, 9584-9593.	2.5	101
65	Identification of single amino acid substitutions of Cys-736 that affect the steroid-binding affinity and specificity of the glucocorticoid receptor using phenotypic screening in yeast. <i>Molecular Endocrinology</i> , 1996, 10, 1358-1370.	3.7	17
66	Modulation of DNA-binding specificity within the nuclear receptor family by substitutions at a single amino acid position. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 57-67.	2.6	12
67	Role of Acidic and Phosphorylated Residues in Gene Activation by the Glucocorticoid Receptor. <i>Journal of Biological Chemistry</i> , 1995, 270, 17535-17540.	3.4	94
68	Structural characterization of a minimal functional transactivation domain from the human glucocorticoid receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 1699-1703.	7.1	160
69	Structural determinants of DNA-binding specificity by steroid receptors. <i>Molecular Endocrinology</i> , 1995, 9, 389-400.	3.7	113
70	Delineation of a small region within the major transactivation domain of the human glucocorticoid receptor that mediates transactivation of gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 1619-1623.	7.1	92
71	Evolution of distinct DNA-binding specificities within the nuclear receptor family of transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 4175-4179.	7.1	43
72	Refined solution structure of the glucocorticoid receptor DNA-binding domain. <i>Biochemistry</i> , 1993, 32, 13463-13471.	2.5	104

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73	Structure and function of the glucocorticoid receptor. Journal of Steroid Biochemistry and Molecular Biology, 1993, 47, 11-19.	2.5	78
74	DNA-Binding Specificity of Mutant Glucocorticoid Receptor DNA-Binding Domains. Annals of the New York Academy of Sciences, 1993, 684, 253-256.	3.8	3
75	DNA-binding by the glucocorticoid receptor: A structural and functional analysis. Journal of Steroid Biochemistry and Molecular Biology, 1992, 41, 249-272.	2.5	16
76	Determinants of high-affinity DNA binding by the glucocorticoid receptor: evaluation of receptor domains outside the DNA-binding domain. Biochemistry, 1992, 31, 9040-9044.	2.5	46
77	Mechanism of synergistic transcriptional transactivation by the human glucocorticoid receptor.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 8283-8287.	7.1	48
78	High Level Expression of the Major Transactivation Domain of the Human Glucocorticoid Receptor in Yeast Cells Inhibits Endogenous Gene Expression and Cell Growth. Molecular Endocrinology, 1991, 5, 1366-1372.	3.7	45
79	Identification, cloning and characterisation of a new gene required for full pyruvate decarboxylase activity in Saccharomyces cerevisiae. Current Genetics, 1989, 15, 171-175.	1.7	17
80	Extraction and rapid inactivation of proteins from Saccharomyces cerevisiae by trichloroacetic acid precipitation. Yeast, 1989, 5, 51-53.	1.7	50
81	The structure and regulation of phosphoglucose isomerase in Saccharomyces cerevisiae. Molecular Genetics and Genomics, 1988, 215, 100-106.	2.4	42