

Andrew D Sharrocks

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,440
citations

279701

23
h-index

214721

47
g-index

349
all docs

349
docs citations

349
times ranked

4374
citing authors

#	ARTICLE	IF	CITATIONS
1	MAP kinase signalling cascades and transcriptional regulation. <i>Gene</i> , 2013, 513, 1-13.	1.0	366
2	SUMO Promotes HDAC-Mediated Transcriptional Repression. <i>Molecular Cell</i> , 2004, 13, 611-617.	4.5	312
3	An extended consensus motif enhances the specificity of substrate modification by SUMO. <i>EMBO Journal</i> , 2006, 25, 5083-5093.	3.5	181
4	Temporal Recruitment of the mSin3A-Histone Deacetylase Corepressor Complex to the ETS Domain Transcription Factor Elk-1. <i>Molecular and Cellular Biology</i> , 2001, 21, 2802-2814.	1.1	125
5	PIAS proteins and transcriptional regulation—more than just SUMO E3 ligases?. <i>Genes and Development</i> , 2006, 20, 754-758.	2.7	123
6	Elucidation of the ELK1 target gene network reveals a role in the coordinate regulation of core components of the gene regulation machinery. <i>Genome Research</i> , 2009, 19, 1963-1973.	2.4	119
7	Otx2 and Oct4 Drive Early Enhancer Activation during Embryonic Stem Cell Transition from Naive Pluripotency. <i>Cell Reports</i> , 2014, 7, 1968-1981.	2.9	117
8	Immediate-early gene activation by the MAPK pathways: what do and don't we know?. <i>Biochemical Society Transactions</i> , 2012, 40, 58-66.	1.6	106
9	Molecular phenotyping reveals the identity of Barrett's esophagus and its malignant transition. <i>Science</i> , 2021, 373, 760-767.	6.0	99
10	ELK1 Uses Different DNA Binding Modes to Regulate Functionally Distinct Classes of Target Genes. <i>PLoS Genetics</i> , 2012, 8, e1002694.	1.5	66
11	The forkhead transcription factor FOXK2 acts as a chromatin targeting factor for the BAP1-containing histone deubiquitinase complex. <i>Nucleic Acids Research</i> , 2014, 42, 6232-6242.	6.5	66
12	Extracellular Signal-Regulated Kinase Mitogen-Activated Protein Kinase Signaling Initiates a Dynamic Interplay between Sumoylation and Ubiquitination To Regulate the Activity of the Transcriptional Activator PEA3. <i>Molecular and Cellular Biology</i> , 2009, 29, 3204-3218.	1.1	63
13	Classifying cells with Scasat, a single-cell ATAC-seq analysis tool. <i>Nucleic Acids Research</i> , 2019, 47, e10-e10.	6.5	60
14	The ERK MAP kinase-PEA3/ETV4-MMP-1 axis is operative in oesophageal adenocarcinoma. <i>Molecular Cancer</i> , 2010, 9, 313.	7.9	51
15	Identification of a primitive intestinal transcription factor network shared between esophageal adenocarcinoma and its precancerous precursor state. <i>Genome Research</i> , 2019, 29, 723-736.	2.4	50
16	ZIC3 Controls the Transition from Naive to Primed Pluripotency. <i>Cell Reports</i> , 2019, 27, 3215-3227.e6.	2.9	47
17	Interaction of Transcription Factors with Serum Response Factor. <i>Journal of Biological Chemistry</i> , 1998, 273, 10506-10514.	1.6	46
18	Screen for multi-SUMO-binding proteins reveals a multi-SIM-binding mechanism for recruitment of the transcriptional regulator ZMYM2 to chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4854-63.	3.3	46

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19	Open chromatin profiling identifies AP1 as a transcriptional regulator in oesophageal adenocarcinoma. <i>PLoS Genetics</i> , 2017, 13, e1006879.	1.5	41
20	Genome-wide binding studies reveal DNA binding specificity mechanisms and functional interplay amongst Forkhead transcription factors. <i>Nucleic Acids Research</i> , 2016, 44, 1566-1578.	6.5	35
21	Cell Cycle: Sustained ERK Signalling Represses the Inhibitors. <i>Current Biology</i> , 2006, 16, R540-R542.	1.8	32
22	Deregulation of the FOXM1 target gene network and its coregulatory partners in oesophageal adenocarcinoma. <i>Molecular Cancer</i> , 2015, 14, 69.	7.9	30
23	Dynamic modification of the ETS transcription factor PEA3 by sumoylation and p300-mediated acetylation. <i>Nucleic Acids Research</i> , 2011, 39, 6403-6413.	6.5	27
24	Mutations of the Transcriptional Corepressor ZMYM2 Cause Syndromic Urinary Tract Malformations. <i>American Journal of Human Genetics</i> , 2020, 107, 727-742.	2.6	25
25	Authentication and characterisation of a new oesophageal adenocarcinoma cell line: MFD-1. <i>Scientific Reports</i> , 2016, 6, 32417.	1.6	20
26	SUMOylation modulates FOXK2-mediated paclitaxel sensitivity in breast cancer cells. <i>Oncogenesis</i> , 2018, 7, 29.	2.1	20
27	Cooperative behaviour and phenotype plasticity evolve during melanoma progression. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 695-708.	1.5	18
28	Dynamic changes in the epigenomic landscape regulate human organogenesis and link to developmental disorders. <i>Nature Communications</i> , 2020, 11, 3920.	5.8	17
29	Jun-Mediated Changes in Cell Adhesion Contribute to Mouse Embryonic Stem Cell Exit from Ground State Pluripotency. <i>Stem Cells</i> , 2016, 34, 1213-1224.	1.4	14
30	Repurposing of KLF5 activates a cell cycle signature during the progression from a precursor state to oesophageal adenocarcinoma. <i>ELife</i> , 2020, 9, .	2.8	14
31	Protein kinase C coordinates histone H3 phosphorylation and acetylation. <i>ELife</i> , 2015, 4, e09886.	2.8	13
32	The Ubiquitin Ligase UBE3A Dampens ERK Pathway Signalling in HPV E6 Transformed HeLa Cells. <i>PLoS ONE</i> , 2015, 10, e0119366.	1.1	9
33	Changing partners: transcription factors form different complexes on and off chromatin. <i>Molecular Systems Biology</i> , 2015, 11, 782.	3.2	9
34	JNK-associated Leucine Zipper Protein Functions as a Docking Platform for Polo-like Kinase 1 and Regulation of the Associating Transcription Factor Forkhead Box Protein K1. <i>Journal of Biological Chemistry</i> , 2015, 290, 29617-29628.	1.6	9
35	The forkhead transcription factor FOXK2 premarks lineage-specific genes in human embryonic stem cells for activation during differentiation. <i>Nucleic Acids Research</i> , 2021, 49, 1345-1363.	6.5	9
36	Basic fibroblast growth factor induces matrix metalloproteinase-13 via ERK MAP kinase-altered phosphorylation and sumoylation of Elk-1 in human adult articular chondrocytes. <i>Open Access Rheumatology: Research and Reviews</i> , 2009, 1, 151.	0.8	8

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37	WDR5, ASH2L, and RBBP5 control the efficiency of FOS transcript processing. Cellular and Molecular Biology Letters, 2014, 19, 215-32.	2.7	8
38	EINCR1 is an EGF inducible lincRNA overexpressed in lung adenocarcinomas. PLoS ONE, 2017, 12, e0181902.	1.1	5
39	PEGS: An efficient tool for gene set enrichment within defined sets of genomic intervals. F1000Research, 2021, 10, 570.	0.8	5
40	ELK1 has a dual activating and repressive role in human embryonic stem cells. Wellcome Open Research, 2019, 4, 41.	0.9	5
41	The Use of Multimeric Protein Scaffolds for Identifying Multi-SUMO Binding Proteins. Methods in Molecular Biology, 2016, 1475, 195-204.	0.4	4
42	RNF4 interacts with multiSUMOylated ETV4. Wellcome Open Research, 2016, 1, 3.	0.9	4
43	ELK1 has a dual activating and repressive role in human embryonic stem cells. Wellcome Open Research, 2019, 4, 41.	0.9	3
44	Genome-wide Interrogation of Protein-DNA Interactions in Mammalian Cells Using ChIPmentation. STAR Protocols, 2020, 1, 100187.	0.5	3
45	RNF4 interacts with multiSUMOylated ETV4. Wellcome Open Research, 0, 1, 3.	0.9	1
46	Activation of transcription factors by MAP kinases: the role of kinase docking domains. Biochemical Society Transactions, 1999, 27, A97-A97.	1.6	0
47	Geno2proteo, a Tool for Batch Retrieval of DNA and Protein Sequences from Any Genomic or Protein Regions. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	0
48	Complexities in the role of acetylation dynamics in modifying inducible gene activation parameters. Nucleic Acids Research, 2021, 49, 12744-12756.	6.5	0