

Timothy R Hughes

List of Publications by Year in descending order

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Version: 2024-02-01

108
papers

27,655
citations

19657

61
h-index

25787

108
g-index

115
all docs

115
docs citations

115
times ranked

33264
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct structural bases for sequence-specific DNA binding by mammalian BEN domain proteins. <i>Genes and Development</i> , 2022, 36, 225-240.	5.9	13
2	Reconstruction of full-length LINE-1 progenitors from ancestral genomes. <i>Genetics</i> , 2022, 221, .	2.9	6
3	Diverse Eukaryotic CGG-Binding Proteins Produced by Independent Domestications of hAT Transposons. <i>Molecular Biology and Evolution</i> , 2021, 38, 2070-2075.	8.9	4
4	Global properties of regulatory sequences are predicted by transcription factor recognition mechanisms. <i>Genome Biology</i> , 2021, 22, 285.	8.8	3
5	The RNA-binding protein SERBP1 functions as a novel oncogenic factor in glioblastoma by bridging cancer metabolism and epigenetic regulation. <i>Genome Biology</i> , 2020, 21, 195.	8.8	55
6	Binding specificities of human RNA-binding proteins toward structured and linear RNA sequences. <i>Genome Research</i> , 2020, 30, 962-973.	5.5	55
7	A bacteriophage mimic of the bacterial nucleoid-associated protein Fis. <i>Biochemical Journal</i> , 2020, 477, 1345-1362.	3.7	2
8	ARGLU1 is a transcriptional coactivator and splicing regulator important for stress hormone signaling and development. <i>Nucleic Acids Research</i> , 2019, 47, 2856-2870.	14.5	20
9	Similarity regression predicts evolution of transcription factor sequence specificity. <i>Nature Genetics</i> , 2019, 51, 981-989.	21.4	105
10	A physical and genetic map of <i>Cannabis sativa</i> identifies extensive rearrangements at the <i>THC/CBD acid synthase</i> loci. <i>Genome Research</i> , 2019, 29, 146-156.	5.5	160
11	<i>Neurospora crassa</i> developmental control mediated by the FLB-3 transcription factor. <i>Fungal Biology</i> , 2018, 122, 570-582.	2.5	14
12	The Human Transcription Factors. <i>Cell</i> , 2018, 172, 650-665.	28.9	2,048
13	The intracellular immune receptor Rx1 regulates the DNA-binding activity of a Golden2-like transcription factor. <i>Journal of Biological Chemistry</i> , 2018, 293, 3218-3233.	3.4	44
14	Comparison of ChIP-Seq Data and a Reference Motif Set for Human KRAB C2H2 Zinc Finger Proteins. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 219-229.	1.8	22
15	The TRIM-NHL protein NHL-2 is a co-factor in the nuclear and somatic RNAi pathways in <i>C. elegans</i> . <i>ELife</i> , 2018, 7, .	6.0	13
16	How bacterial xenogeneic silencer rok distinguishes foreign from self DNA in its resident genome. <i>Nucleic Acids Research</i> , 2018, 46, 10514-10529.	14.5	23
17	Motif models for RNA-binding proteins. <i>Current Opinion in Structural Biology</i> , 2018, 53, 115-123.	5.7	19
18	A Chemical Biology Approach to Model Pontocerebellar Hypoplasia Type 1B (PCH1B). <i>ACS Chemical Biology</i> , 2018, 13, 3000-3010.	3.4	9

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19	Multilayered Control of Alternative Splicing Regulatory Networks by Transcription Factors. <i>Molecular Cell</i> , 2017, 65, 539-553.e7.	9.7	143
20	Transcription factors read epigenetics. <i>Science</i> , 2017, 356, 489-490.	12.6	16
21	RNAcompete methodology and application to determine sequence preferences of unconventional RNA-binding proteins. <i>Methods</i> , 2017, 118-119, 3-15.	3.8	46
22	Oncogenic Activation of the RNA Binding Protein NELFE and MYC Signaling in Hepatocellular Carcinoma. <i>Cancer Cell</i> , 2017, 32, 101-114.e8.	16.8	121
23	RNAcompete-S: Combined RNA sequence/structure preferences for RNA binding proteins derived from a single-step in vitro selection. <i>Methods</i> , 2017, 126, 18-28.	3.8	35
24	Non-base-contacting residues enable kaleidoscopic evolution of metazoan C2H2 zinc finger DNA binding. <i>Genome Biology</i> , 2017, 18, 167.	8.8	33
25	Transcription Factors Encoded on Core and Accessory Chromosomes of <i>Fusarium oxysporum</i> Induce Expression of Effector Genes. <i>PLoS Genetics</i> , 2016, 12, e1006401.	3.5	75
26	Motif comparison based on similarity of binding affinity profiles. <i>Bioinformatics</i> , 2016, 32, 3504-3506.	4.1	16
27	Multiparameter functional diversity of human C2H2 zinc finger proteins. <i>Genome Research</i> , 2016, 26, 1742-1752.	5.5	131
28	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , 2016, 5, .	6.0	48
29	The Crystal Structure of the NHL Domain in Complex with RNA Reveals the Molecular Basis of <i>Drosophila</i> Brain-Tumor-Mediated Gene Regulation. <i>Cell Reports</i> , 2015, 13, 1206-1220.	6.4	79
30	Brain tumor is a sequence-specific RNA-binding protein that directs maternal mRNA clearance during the <i>Drosophila</i> maternal-to-zygotic transition. <i>Genome Biology</i> , 2015, 16, 94.	8.8	80
31	A Novel AT-Rich DNA Recognition Mechanism for Bacterial Xenogeneic Silencer MvaT. <i>PLoS Pathogens</i> , 2015, 11, e1004967.	4.7	53
32	High-throughput characterization of protein-RNA interactions. <i>Briefings in Functional Genomics</i> , 2015, 14, 74-89.	2.7	83
33	Identification of C2H2-ZF binding preferences from ChIP-seq data using RCADE. <i>Bioinformatics</i> , 2015, 31, 2879-2881.	4.1	23
34	C2H2 zinc finger proteins greatly expand the human regulatory lexicon. <i>Nature Biotechnology</i> , 2015, 33, 555-562.	17.5	271
35	A structural approach reveals how neighbouring C2H2 zinc fingers influence DNA binding specificity. <i>Nucleic Acids Research</i> , 2015, 43, 9147-9157.	14.5	44
36	Affinity regression predicts the recognition code of nucleic acid-binding proteins. <i>Nature Biotechnology</i> , 2015, 33, 1242-1249.	17.5	55

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37	The human splicing code reveals new insights into the genetic determinants of disease. <i>Science</i> , 2015, 347, 1254806.	12.6	1,053
38	Mapping and analysis of <i>Caenorhabditis elegans</i> transcription factor sequence specificities. <i>ELife</i> , 2015, 4, .	6.0	85
39	Mapping and Dynamics of Regulatory DNA and Transcription Factor Networks in <i>A.Âthaliana</i> . <i>Cell Reports</i> , 2014, 8, 2015-2030.	6.4	249
40	A Novel C2H2 Transcription Factor that Regulates <i>gliA</i> Expression Interdependently with <i>GliZ</i> in <i>Aspergillus fumigatus</i> . <i>PLoS Genetics</i> , 2014, 10, e1004336.	3.5	36
41	A unified model for yeast transcript definition. <i>Genome Research</i> , 2014, 24, 154-166.	5.5	20
42	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	28.9	1,515
43	A Pair of RNA-Binding Proteins Controls Networks of Splicing Events Contributing to Specialization of Neural Cell Types. <i>Molecular Cell</i> , 2014, 54, 946-959.	9.7	62
44	Poly-dA:dT Tracts Form an In Vivo Nucleosomal Turnstile. <i>PLoS ONE</i> , 2014, 9, e110479.	2.5	15
45	A compendium of RNA-binding motifs for decoding gene regulation. <i>Nature</i> , 2013, 499, 172-177.	27.8	1,281
46	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	17.5	341
47	DNA-Binding Specificities of Human Transcription Factors. <i>Cell</i> , 2013, 152, 327-339.	28.9	1,085
48	Mapping Yeast Transcriptional Networks. <i>Genetics</i> , 2013, 195, 9-36.	2.9	72
49	CG methylated microarrays identify a novel methylated sequence bound by the CEBPB ATF4 heterodimer that is active in vivo. <i>Genome Research</i> , 2013, 23, 988-997.	5.5	111
50	Paralogs hnRNP L and hnRNP LL Exhibit Overlapping but Distinct RNA Binding Constraints. <i>PLoS ONE</i> , 2013, 8, e80701.	2.5	36
51	YeTFaSCo: a database of evaluated yeast transcription factor sequence specificities. <i>Nucleic Acids Research</i> , 2012, 40, D169-D179.	14.5	195
52	The draft genome and transcriptome of <i>Cannabis sativa</i> . <i>Genome Biology</i> , 2011, 12, R102.	9.6	479
53	RBPDB: a database of RNA-binding specificities. <i>Nucleic Acids Research</i> , 2011, 39, D301-D308.	14.5	477
54	Analysis of <i>Escherichia coli</i> RNase E and RNase III activity in vivo using tiling microarrays. <i>Nucleic Acids Research</i> , 2011, 39, 3188-3203.	14.5	112

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55	Sequence specificity is obtained from the majority of modular C2H2 zinc-finger arrays. <i>Nucleic Acids Research</i> , 2011, 39, 4680-4690.	14.5	82
56	Response to "The Reality of Pervasive Transcription". <i>PLoS Biology</i> , 2011, 9, e1001102.	5.6	30
57	Conserved expression without conserved regulatory sequence: the more things change, the more they stay the same. <i>Trends in Genetics</i> , 2010, 26, 66-74.	6.7	139
58	Information propagation within the Genetic Network of <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2010, 4, 143.	3.0	12
59	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. <i>EMBO Journal</i> , 2010, 29, 2147-2160.	7.8	497
60	High Nucleosome Occupancy Is Encoded at Human Regulatory Sequences. <i>PLoS ONE</i> , 2010, 5, e9129.	2.5	163
61	RNAcontext: A New Method for Learning the Sequence and Structure Binding Preferences of RNA-Binding Proteins. <i>PLoS Computational Biology</i> , 2010, 6, e1000832.	3.2	223
62	Contribution of histone sequence preferences to nucleosome organization: proposed definitions and methodology. <i>Genome Biology</i> , 2010, 11, 140.	8.8	53
63	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. <i>Genome Research</i> , 2010, 20, 861-873.	5.5	382
64	Most "Dark Matter" Transcripts Are Associated With Known Genes. <i>PLoS Biology</i> , 2010, 8, e1000371.	5.6	377
65	Predicting the binding preference of transcription factors to individual DNA k-mers. <i>Bioinformatics</i> , 2009, 25, 1012-1018.	4.1	25
66	Diversity and Complexity in DNA Recognition by Transcription Factors. <i>Science</i> , 2009, 324, 1720-1723.	12.6	874
67	A systematic characterization of Cwc21, the yeast ortholog of the human spliceosomal protein SRm300. <i>Rna</i> , 2009, 15, 2174-2185.	3.5	34
68	Establishing legitimacy and function in the new transcriptome. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 424-436.	3.8	62
69	G+C content dominates intrinsic nucleosome occupancy. <i>BMC Bioinformatics</i> , 2009, 10, 442.	2.6	248
70	The DNA-encoded nucleosome organization of a eukaryotic genome. <i>Nature</i> , 2009, 458, 362-366.	27.8	1,063
71	Rapid and systematic analysis of the RNA recognition specificities of RNA-binding proteins. <i>Nature Biotechnology</i> , 2009, 27, 667-670.	17.5	418
72	TFCat: the curated catalog of mouse and human transcription factors. <i>Genome Biology</i> , 2009, 10, R29.	9.6	193

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73	'Validation' in genome-scale research. <i>Journal of Biology</i> , 2008, 8, 3.	2.7	21
74	A Library of Yeast Transcription Factor Motifs Reveals a Widespread Function for Rsc3 in Targeting Nucleosome Exclusion at Promoters. <i>Molecular Cell</i> , 2008, 32, 878-887.	9.7	415
75	Variation in Homeodomain DNA Binding Revealed by High-Resolution Analysis of Sequence Preferences. <i>Cell</i> , 2008, 133, 1266-1276.	28.9	552
76	Molecular chaperone Hsp90 stabilizes Pih1/Nop17 to maintain R2TP complex activity that regulates snoRNA accumulation. <i>Journal of Cell Biology</i> , 2008, 180, 563-578.	5.2	159
77	RankMotif++: a motif-search algorithm that accounts for relative ranks of K-mers in binding transcription factors. <i>Bioinformatics</i> , 2007, 23, i72-i79.	4.1	52
78	Why Are There Still Over 1000 Uncharacterized Yeast Genes?. <i>Genetics</i> , 2007, 176, 7-14.	2.9	130
79	Prediction and Testing of Novel Transcriptional Networks Regulating Embryonic Stem Cell Self-Renewal and Commitment. <i>Cell Stem Cell</i> , 2007, 1, 71-86.	11.1	98
80	Global Analysis of mRNA Localization Reveals a Prominent Role in Organizing Cellular Architecture and Function. <i>Cell</i> , 2007, 131, 174-187.	28.9	878
81	SMAUG Is a Major Regulator of Maternal mRNA Destabilization in <i>Drosophila</i> and Its Translation Is Activated by the PAN GU Kinase. <i>Developmental Cell</i> , 2007, 12, 143-155.	7.0	280
82	H2B Ubiquitylation Acts as a Barrier to Ctk1 Nucleosomal Recruitment Prior to Removal by Ubp8 within a SAGA-Related Complex. <i>Molecular Cell</i> , 2007, 27, 275-288.	9.7	196
83	Systematic Analysis of the Protein Interaction Network for the Human Transcription Machinery Reveals the Identity of the 7SK Capping Enzyme. <i>Molecular Cell</i> , 2007, 27, 262-274.	9.7	404
84	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	21.4	765
85	Identifying transcription factor functions and targets by phenotypic activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12045-12050.	7.1	156
86	Rapid tRNA Decay Can Result from Lack of Nonessential Modifications. <i>Molecular Cell</i> , 2006, 21, 87-96.	9.7	409
87	Mapping Pathways and Phenotypes by Systematic Gene Overexpression. <i>Molecular Cell</i> , 2006, 21, 319-330.	9.7	618
88	[14] Microarray Analysis of RNA Processing and Modification. <i>Methods in Enzymology</i> , 2006, 410, 300-316.	1.0	27
89	The Splicing Factor Prp43p, a DEAH Box ATPase, Functions in Ribosome Biogenesis. <i>Molecular and Cellular Biology</i> , 2006, 26, 513-522.	2.3	96
90	A systematic search for new mammalian noncoding RNAs indicates little conserved intergenic transcription. <i>BMC Genomics</i> , 2005, 6, 104.	2.8	72

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91	Biochemical and genomic analysis of substrate recognition by the double-stranded RNA binding domain of yeast RNase III. <i>Rna</i> , 2005, 11, 1225-1237.	3.5	13
92	Esf2p, a U3-Associated Factor Required for Small-Subunit Processome Assembly and Compaction. <i>Molecular and Cellular Biology</i> , 2005, 25, 5523-5534.	2.3	33
93	Global analysis of yeast RNA processing identifies new targets of RNase III and uncovers a link between tRNA 5' end processing and tRNA splicing. <i>Nucleic Acids Research</i> , 2005, 33, 3048-3056.	14.5	27
94	Detection and discovery of RNA modifications using microarrays. <i>Nucleic Acids Research</i> , 2005, 33, e2-e2.	14.5	50
95	ESF1 is required for 18S rRNA synthesis in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2004, 32, 1993-1999.	14.5	18
96	The Specificities of Four Yeast Dihydrouridine Synthases for Cytoplasmic tRNAs. <i>Journal of Biological Chemistry</i> , 2004, 279, 17850-17860.	3.4	94
97	The functional landscape of mouse gene expression. <i>Journal of Biology</i> , 2004, 3, 21.	2.7	259
98	Exploration of Essential Gene Functions via Titratable Promoter Alleles. <i>Cell</i> , 2004, 118, 31-44.	28.9	538
99	The promise of functional genomics: completing the encyclopedia of a cell. <i>Current Opinion in Microbiology</i> , 2004, 7, 546-554.	5.1	44
100	Transcriptional networks: reverse-engineering gene regulation on a global scale. <i>Current Opinion in Microbiology</i> , 2004, 7, 638-646.	5.1	56
101	High-Definition Macromolecular Composition of Yeast RNA-Processing Complexes. <i>Molecular Cell</i> , 2004, 13, 225-239.	9.7	345
102	GENRATE: A GENERATIVE MODEL THAT FINDS AND SCORES NEW GENES AND EXONS IN GENOMIC MICROARRAY DATA. , 2004, , .		3
103	A Panoramic View of Yeast Noncoding RNA Processing. <i>Cell</i> , 2003, 113, 919-933.	28.9	222
104	Yeast and drug discovery. <i>Functional and Integrative Genomics</i> , 2002, 2, 199-211.	3.5	82
105	Large-scale prediction of <i>Saccharomyces cerevisiae</i> gene function using overlapping transcriptional clusters. <i>Nature Genetics</i> , 2002, 31, 255-265.	21.4	313
106	Expression profiling using microarrays fabricated by an ink-jet oligonucleotide synthesizer. <i>Nature Biotechnology</i> , 2001, 19, 342-347.	17.5	1,225
107	Functional Discovery via a Compendium of Expression Profiles. <i>Cell</i> , 2000, 102, 109-126.	28.9	2,412
108	Genetic Selection of Peptide Inhibitors of Biological Pathways. <i>Science</i> , 1999, 285, 591-595.	12.6	185