

Alexander Stark

List of Publications by Year in descending order

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91
papers

30,294
citations

16451

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all docs

96
docs citations

96
times ranked

34583
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome-scale identification of transcriptional activators in human cells. <i>Molecular Cell</i> , 2022, 82, 497-499.	9.7	2
2	DeepSTARR predicts enhancer activity from DNA sequence and enables the de novo design of synthetic enhancers. <i>Nature Genetics</i> , 2022, 54, 613-624.	21.4	97
3	Differential cofactor dependencies define distinct types of human enhancers. <i>Nature</i> , 2022, 606, 406-413.	27.8	49
4	Multiplexed detection of SARS-CoV-2 and other respiratory infections in high throughput by SARSeq. <i>Nature Communications</i> , 2021, 12, 3132.	12.8	32
5	Insights into gene regulation: From regulatory genomic elements to DNA-protein and protein-protein interactions. <i>Current Opinion in Cell Biology</i> , 2021, 70, 58-66.	5.4	19
6	PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. <i>Nature Communications</i> , 2021, 12, 6078.	12.8	21
7	STARR-seq and UMI-STARR-seq: Assessing Enhancer Activities for Genome-Wide, High-, and Low-Complexity Candidate Libraries. <i>Current Protocols in Molecular Biology</i> , 2019, 128, e105.	2.9	46
8	Transcriptional cofactors display specificity for distinct types of core promoters. <i>Nature</i> , 2019, 570, 122-126.	27.8	112
9	Assessing sufficiency and necessity of enhancer activities for gene expression and the mechanisms of transcription activation. <i>Genes and Development</i> , 2018, 32, 202-223.	5.9	171
10	Resolving systematic errors in widely used enhancer activity assays in human cells. <i>Nature Methods</i> , 2018, 15, 141-149.	19.0	147
11	Eukaryotic core promoters and the functional basis of transcription initiation. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 621-637.	37.0	480
12	A high-throughput method to identify trans-activation domains within transcription factor sequences. <i>EMBO Journal</i> , 2018, 37, .	7.8	53
13	Combinatorial function of transcription factors and cofactors. <i>Current Opinion in Genetics and Development</i> , 2017, 43, 73-81.	3.3	269
14	Genome-wide assessment of sequence-intrinsic enhancer responsiveness at single-base-pair resolution. <i>Nature Biotechnology</i> , 2017, 35, 136-144.	17.5	78
15	A reversible haploid mouse embryonic stem cell biobank resource for functional genomics. <i>Nature</i> , 2017, 550, 114-118.	27.8	58
16	Promoting transcription over long distances. <i>Nature Genetics</i> , 2017, 49, 972-973.	21.4	11
17	Probing the canonicity of the Wnt/Wingless signaling pathway. <i>PLoS Genetics</i> , 2017, 13, e1006700.	3.5	39
18	Gene Regulation: Activation through Space. <i>Current Biology</i> , 2016, 26, R895-R898.	3.9	13

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19	RNA-binding profiles of <i>Drosophila</i> CPEB proteins Orb and Orb2. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7030-E7038.	7.1	49
20	Regulatory Enhancer–Core-Promoter Communication via Transcription Factors and Cofactors. Trends in Genetics, 2016, 32, 801-814.	6.7	153
21	Genome-Wide Ultrabithorax Binding Analysis Reveals Highly Targeted Genomic Loci at Developmental Regulators and a Potential Connection to Polycomb-Mediated Regulation. PLoS ONE, 2016, 11, e0161997.	2.5	17
22	The RNA-binding protein Arrest (Bruno) regulates alternative splicing to enable myofibril maturation in <i>Drosophila</i> flight muscle. EMBO Reports, 2015, 16, 178-191.	4.5	57
23	Coordinating the Human Looks. Cell, 2015, 163, 24-26.	28.9	1
24	Transcriptional plasticity promotes primary and acquired resistance to BET inhibition. Nature, 2015, 525, 543-547.	27.8	414
25	Transcriptional regulators form diverse groups with context-dependent regulatory functions. Nature, 2015, 528, 147-151.	27.8	169
26	Enhancer–core-promoter specificity separates developmental and housekeeping gene regulation. Nature, 2015, 518, 556-559.	27.8	402
27	Dissection of thousands of cell type-specific enhancers identifies dinucleotide repeat motifs as general enhancer features. Genome Research, 2014, 24, 1147-1156.	5.5	129
28	Transcriptional enhancers: from properties to genome-wide predictions. Nature Reviews Genetics, 2014, 15, 272-286.	16.3	1,136
29	Hormone-Responsive Enhancer-Activity Maps Reveal Predictive Motifs, Indirect Repression, and Targeting of Closed Chromatin. Molecular Cell, 2014, 54, 180-192.	9.7	119
30	cis -Regulatory Requirements for Tissue-Specific Programs of the Circadian Clock. Current Biology, 2014, 24, 1-10.	3.9	376
31	A conserved role for Snail as a potentiator of active transcription. Genes and Development, 2014, 28, 167-181.	5.9	73
32	Hiding in plain sight. Nature, 2014, 512, 374-375.	27.8	4
33	Genome-scale functional characterization of <i>Drosophila</i> developmental enhancers in vivo. Nature, 2014, 512, 91-95.	27.8	422
34	Quantitative genome-wide enhancer activity maps for five <i>Drosophila</i> species show functional enhancer conservation and turnover during cis-regulatory evolution. Nature Genetics, 2014, 46, 685-692.	21.4	162
35	Identification of transcription factor binding sites from ChIP-seq data at high resolution. Bioinformatics, 2013, 29, 2705-2713.	4.1	58
36	Deciphering the transcriptional cis-regulatory code. Trends in Genetics, 2013, 29, 11-22.	6.7	112

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37	Genome-Wide Quantitative Enhancer Activity Maps Identified by STARR-seq. Science, 2013, 339, 1074-1077.	12.6	897
38	Drosophila Embryo Stage Annotation Using Label Propagation. , 2013, , .		5
39	A Histone Deacetylase Adjusts Transcription Kinetics at Coding Sequences during Candida albicans Morphogenesis. PLoS Genetics, 2012, 8, e1003118.	3.5	88
40	A computational pipeline for comparative ChIP-seq analyses. Nature Protocols, 2012, 7, 45-61.	12.0	110
41	HOT regions function as patterned developmental enhancers and have a distinct <i>cis</i> -regulatory signature. Genes and Development, 2012, 26, 908-913.	5.9	130
42	Uncovering <i>cis</i> -regulatory sequence requirements for context-specific transcription factor binding. Genome Research, 2012, 22, 2018-2030.	5.5	98
43	Forward and Reverse Genetics through Derivation of Haploid Mouse Embryonic Stem Cells. Cell Stem Cell, 2011, 9, 563-574.	11.1	208
44	A systematic analysis of <i>Drosophila</i> TUDOR domain-containing proteins identifies Vreteno and the Tdrd12 family as essential primary piRNA pathway factors. EMBO Journal, 2011, 30, 3977-3993.	7.8	163
45	High conservation of transcription factor binding and evidence for combinatorial regulation across six <i>Drosophila</i> species. Nature Genetics, 2011, 43, 414-420.	21.4	122
46	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	27.8	1,016
47	Neural-specific elongation of 3' UTRs during <i>Drosophila</i> development. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15864-15869.	7.1	128
48	The Tasmanian Devil Transcriptome Reveals Schwann Cell Origins of a Clonally Transmissible Cancer. Science, 2010, 327, 84-87.	12.6	222
49	Systematic genetic analysis of muscle morphogenesis and function in <i>Drosophila</i> . Nature, 2010, 464, 287-291.	27.8	285
50	Mouse MOV10L1 associates with Piwi proteins and is an essential component of the Piwi-interacting RNA (piRNA) pathway. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11841-11846.	7.1	204
51	Diverse Endonucleolytic Cleavage Sites in the Mammalian Transcriptome Depend upon MicroRNAs, Drosha, and Additional Nucleases. Molecular Cell, 2010, 38, 781-788.	9.7	170
52	Developmental gene regulation in the era of genomics. Developmental Biology, 2010, 339, 230-239.	2.0	43
53	Learning the transcriptional regulatory code. Molecular Systems Biology, 2009, 5, 329.	7.2	3
54	Accurate Prediction of Peptide Binding Sites on Protein Surfaces. PLoS Computational Biology, 2009, 5, e1000335.	3.2	138

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55	Coherent but overlapping expression of microRNAs and their targets during vertebrate development. <i>Genes and Development</i> , 2009, 23, 466-481.	5.9	98
56	Histone modifications at human enhancers reflect global cell-type-specific gene expression. <i>Nature</i> , 2009, 459, 108-112.	27.8	2,225
57	Loss of the Mili-interacting Tudor domain-containing protein-1 activates transposons and alters the Mili-associated small RNA profile. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 639-646.	8.2	242
58	The TDRD9-MIWI2 Complex Is Essential for piRNA-Mediated Retrotransposon Silencing in the Mouse Male Germline. <i>Developmental Cell</i> , 2009, 17, 775-787.	7.0	297
59	Specialized piRNA Pathways Act in Germline and Somatic Tissues of the Drosophila Ovary. <i>Cell</i> , 2009, 137, 522-535.	28.9	774
60	Comparative genomics of gene regulation—conservation and divergence of cis-regulatory information. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 565-570.	3.3	76
61	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	27.8	657
62	An endogenous small interfering RNA pathway in Drosophila. <i>Nature</i> , 2008, 453, 798-802.	27.8	633
63	Temporal Reciprocity of miRNAs and Their Targets during the Maternal-to-Zygotic Transition in Drosophila. <i>Current Biology</i> , 2008, 18, 501-506.	3.9	246
64	An Epigenetic Role for Maternally Inherited piRNAs in Transposon Silencing. <i>Science</i> , 2008, 322, 1387-1392.	12.6	686
65	A single Hox locus in <i>Drosophila</i> produces functional microRNAs from opposite DNA strands. <i>Genes and Development</i> , 2008, 22, 8-13.	5.9	205
66	Conservation of small RNA pathways in platypus. <i>Genome Research</i> , 2008, 18, 995-1004.	5.5	39
67	Systematic discovery and characterization of fly microRNAs using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1865-1879.	5.5	182
68	Whole-genome ChIP-chip analysis of Dorsal, Twist, and Snail suggests integration of diverse patterning processes in the Drosophila embryo. <i>Genes and Development</i> , 2007, 21, 385-390.	5.9	274
69	Reliable prediction of regulator targets using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1919-1931.	5.5	141
70	Discrete Small RNA-Generating Loci as Master Regulators of Transposon Activity in Drosophila. <i>Cell</i> , 2007, 128, 1089-1103.	28.9	2,215
71	Evolution, biogenesis, expression, and target predictions of a substantially expanded set of <i>Drosophila</i> microRNAs. <i>Genome Research</i> , 2007, 17, 1850-1864.	5.5	540
72	RNA polymerase stalling at developmental control genes in the Drosophila melanogaster embryo. <i>Nature Genetics</i> , 2007, 39, 1512-1516.	21.4	671

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73	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	27.8	573
74	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
75	mRNA degradation by miRNAs and GW182 requires both CCR4:NOT deadenylase and DCP1:DCP2 decapping complexes. Genes and Development, 2006, 20, 1885-1898.	5.9	824
76	Genome-Wide Analysis of mRNAs Regulated by Drosha and Argonaute Proteins in Drosophila melanogaster. Molecular and Cellular Biology, 2006, 26, 2965-2975.	2.3	125
77	Denoising feedback loops by thresholding—a new role for microRNAs. Genes and Development, 2006, 20, 2769-2772.	5.9	87
78	Principles of MicroRNA-Target Recognition. PLoS Biology, 2005, 3, e85.	5.6	2,019
79	Systematic Discovery of New Recognition Peptides Mediating Protein Interaction Networks. PLoS Biology, 2005, 3, e405.	5.6	310
80	Not miR-ly muscular: microRNAs and muscle development. Genes and Development, 2005, 19, 2261-2264.	5.9	32
81	Animal MicroRNAs Confer Robustness to Gene Expression and Have a Significant Impact on 3'UTR Evolution. Cell, 2005, 123, 1133-1146.	28.9	979
82	Finding Functional Sites in Structural Genomics Proteins. Structure, 2004, 12, 1405-1412.	3.3	44
83	Predictions without templates: New folds, secondary structure, and contacts in CASP5. Proteins: Structure, Function and Bioinformatics, 2003, 53, 436-456.	2.6	103
84	The Relationship Between Sequence and Interaction Divergence in Proteins. Journal of Molecular Biology, 2003, 332, 989-998.	4.2	296
85	A Model for Statistical Significance of Local Similarities in Structure. Journal of Molecular Biology, 2003, 326, 1307-1316.	4.2	161
86	bantam Encodes a Developmentally Regulated microRNA that Controls Cell Proliferation and Regulates the Proapoptotic Gene hid in Drosophila. Cell, 2003, 113, 25-36.	28.9	1,889
87	Crystal Structure of an Archaeal Class I Aldolase and the Evolution of (12±)8 Barrel Proteins. Journal of Biological Chemistry, 2003, 278, 47253-47260.	3.4	45
88	Annotation in three dimensions. PINTS: Patterns in Non-homologous Tertiary Structures. Nucleic Acids Research, 2003, 31, 3341-3344.	14.5	151
89	Identification of Drosophila MicroRNA Targets. PLoS Biology, 2003, 1, e60.	5.6	689
90	A Dynamic Structural Model for Estrogen Receptor-1 Activation by Ligands, Emphasizing the Role of Interactions between Distant A and E Domains. Molecular Cell, 2002, 10, 1019-1032.	9.7	114

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91	The Mitochondrial Permeability Transition Augments Fas-induced Apoptosis in Mouse Hepatocytes. Journal of Biological Chemistry, 2000, 275, 11814-11823.	3.4	135