

# Alexander Stark

## List of Publications by Year in descending order

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91  
papers

30,294  
citations

16450

64  
h-index

46795

89  
g-index

96  
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. <i>Science</i> , 2013, 339, 1074-1077.	12.6	897
38	<i>Drosophila</i> Embryo Stage Annotation Using Label Propagation. , 2013, , .		5
39	A Histone Deacetylase Adjusts Transcription Kinetics at Coding Sequences during <i>Candida albicans</i> Morphogenesis. <i>PLoS Genetics</i> , 2012, 8, e1003118.	3.5	88
40	A computational pipeline for comparative ChIP-seq analyses. <i>Nature Protocols</i> , 2012, 7, 45-61.	12.0	110
41	HOT regions function as patterned developmental enhancers and have a distinct <i>cis</i> -regulatory signature. <i>Genes and Development</i> , 2012, 26, 908-913.	5.9	130
42	Uncovering <i>cis</i> -regulatory sequence requirements for context-specific transcription factor binding. <i>Genome Research</i> , 2012, 22, 2018-2030.	5.5	98
43	Forward and Reverse Genetics through Derivation of Haploid Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 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. <i>EMBO Journal</i> , 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. <i>Nature Genetics</i> , 2011, 43, 414-420.	21.4	122
46	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
47	Neural-specific elongation of 3' UTRs during <i>Drosophila</i> development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15864-15869.	7.1	128
48	The Tasmanian Devil Transcriptome Reveals Schwann Cell Origins of a Clonally Transmissible Cancer. <i>Science</i> , 2010, 327, 84-87.	12.6	222
49	Systematic genetic analysis of muscle morphogenesis and function in <i>Drosophila</i> . <i>Nature</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11841-11846.	7.1	204
51	Diverse Endonucleolytic Cleavage Sites in the Mammalian Transcriptome Depend upon MicroRNAs, Drosha, and Additional Nucleases. <i>Molecular Cell</i> , 2010, 38, 781-788.	9.7	170
52	Developmental gene regulation in the era of genomics. <i>Developmental Biology</i> , 2010, 339, 230-239.	2.0	43
53	Learning the transcriptional regulatory code. <i>Molecular Systems Biology</i> , 2009, 5, 329.	7.2	3
54	Accurate Prediction of Peptide Binding Sites on Protein Surfaces. <i>PLoS Computational Biology</i> , 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 <i>Drosophila melanogaster</i> 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	Denosing 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 5'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 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