

# Alexander Stark

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

93  
papers

24,337  
citations

63  
h-index

96  
g-index

96  
ext. papers

28,038  
ext. citations

21.9  
avg, IF

6.78  
L-index

#	Paper	IF	Citations
93	Proteome-scale identification of transcriptional activators in human cells.. <i>Molecular Cell</i> , <b>2022</b> , 82, 497-499	17.4	0
92	PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. <i>Nature Communications</i> , <b>2021</b> , 12, 6078	17.4	1
91	Multiplexed detection of SARS-CoV-2 and other respiratory infections in high throughput by SARSeq. <i>Nature Communications</i> , <b>2021</b> , 12, 3132	17.4	11
90	Insights into gene regulation: From regulatory genomic elements to DNA-protein and protein-protein interactions. <i>Current Opinion in Cell Biology</i> , <b>2021</b> , 70, 58-66	9	6
89	Transcriptional cofactors display specificity for distinct types of core promoters. <i>Nature</i> , <b>2019</b> , 570, 122-126	32.4	48
88	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> , <b>2019</b> , 128, e105	2.9	7
87	Assessing sufficiency and necessity of enhancer activities for gene expression and the mechanisms of transcription activation. <i>Genes and Development</i> , <b>2018</b> , 32, 202-223	12.6	103
86	A high-throughput method to identify trans-activation domains within transcription factor sequences. <i>EMBO Journal</i> , <b>2018</b> , 37,	13	22
85	Resolving systematic errors in widely used enhancer activity assays in human cells. <i>Nature Methods</i> , <b>2018</b> , 15, 141-149	21.6	73
84	Eukaryotic core promoters and the functional basis of transcription initiation. <i>Nature Reviews Molecular Cell Biology</i> , <b>2018</b> , 19, 621-637	48.7	218
83	Combinatorial function of transcription factors and cofactors. <i>Current Opinion in Genetics and Development</i> , <b>2017</b> , 43, 73-81	4.9	148
82	Genome-wide assessment of sequence-intrinsic enhancer responsiveness at single-base-pair resolution. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 136-144	44.5	44
81	A reversible haploid mouse embryonic stem cell biobank resource for functional genomics. <i>Nature</i> , <b>2017</b> , 550, 114-118	50.4	42
80	Promoting transcription over long distances. <i>Nature Genetics</i> , <b>2017</b> , 49, 972-973	36.3	10
79	Probing the canonicity of the Wnt/Wingless signaling pathway. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006700	6	29
78	RNA-binding profiles of CPEB proteins Orb and Orb2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E7030-E7038	11.5	25
77	Regulatory Enhancer-Core-Promoter Communication via Transcription Factors and Cofactors. <i>Trends in Genetics</i> , <b>2016</b> , 32, 801-814	8.5	86

76	Genome-Wide Ultrabithorax Binding Analysis Reveals Highly Targeted Genomic Loci at Developmental Regulators and a Potential Connection to Polycomb-Mediated Regulation. <i>PLoS ONE</i> , <b>2016</b> , 11, e0161997	3.7	7
75	Gene Regulation: Activation through Space. <i>Current Biology</i> , <b>2016</b> , 26, R895-R898	6.3	10
74	Coordinating the human looks. <i>Cell</i> , <b>2015</b> , 163, 24-6	56.2	
73	Transcriptional plasticity promotes primary and acquired resistance to BET inhibition. <i>Nature</i> , <b>2015</b> , 525, 543-547	50.4	327
72	Transcriptional regulators form diverse groups with context-dependent regulatory functions. <i>Nature</i> , <b>2015</b> , 528, 147-51	50.4	109
71	Enhancer-core-promoter specificity separates developmental and housekeeping gene regulation. <i>Nature</i> , <b>2015</b> , 518, 556-9	50.4	257
70	The RNA-binding protein Arrest (Bruno) regulates alternative splicing to enable myofibril maturation in Drosophila flight muscle. <i>EMBO Reports</i> , <b>2015</b> , 16, 178-91	6.5	39
69	Hormone-responsive enhancer-activity maps reveal predictive motifs, indirect repression, and targeting of closed chromatin. <i>Molecular Cell</i> , <b>2014</b> , 54, 180-192	17.6	86
68	cis-regulatory requirements for tissue-specific programs of the circadian clock. <i>Current Biology</i> , <b>2014</b> , 24, 1-10	6.3	329
67	A conserved role for Snail as a potentiator of active transcription. <i>Genes and Development</i> , <b>2014</b> , 28, 167-181	6.16	57
66	Genomics: Hiding in plain sight. <i>Nature</i> , <b>2014</b> , 512, 374-5	50.4	2
65	Genome-scale functional characterization of Drosophila developmental enhancers in vivo. <i>Nature</i> , <b>2014</b> , 512, 91-5	50.4	290
64	Quantitative genome-wide enhancer activity maps for five Drosophila species show functional enhancer conservation and turnover during cis-regulatory evolution. <i>Nature Genetics</i> , <b>2014</b> , 46, 685-92	36.3	104
63	Dissection of thousands of cell type-specific enhancers identifies dinucleotide repeat motifs as general enhancer features. <i>Genome Research</i> , <b>2014</b> , 24, 1147-56	9.7	93
62	Transcriptional enhancers: from properties to genome-wide predictions. <i>Nature Reviews Genetics</i> , <b>2014</b> , 15, 272-86	30.1	820
61	Identification of transcription factor binding sites from ChIP-seq data at high resolution. <i>Bioinformatics</i> , <b>2013</b> , 29, 2705-13	7.2	45
60	Deciphering the transcriptional cis-regulatory code. <i>Trends in Genetics</i> , <b>2013</b> , 29, 11-22	8.5	83
59	Genome-wide quantitative enhancer activity maps identified by STARR-seq. <i>Science</i> , <b>2013</b> , 339, 1074-7	33.3	603

58	Drosophila Embryo Stage Annotation Using Label Propagation <b>2013</b> ,		5
57	HOT regions function as patterned developmental enhancers and have a distinct cis-regulatory signature. <i>Genes and Development</i> , <b>2012</b> , 26, 908-13	12.6	110
56	Uncovering cis-regulatory sequence requirements for context-specific transcription factor binding. <i>Genome Research</i> , <b>2012</b> , 22, 2018-30	9.7	78
55	A histone deacetylase adjusts transcription kinetics at coding sequences during <i>Candida albicans</i> morphogenesis. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003118	6	67
54	A computational pipeline for comparative ChIP-seq analyses. <i>Nature Protocols</i> , <b>2011</b> , 7, 45-61	18.8	88
53	Forward and reverse genetics through derivation of haploid mouse embryonic stem cells. <i>Cell Stem Cell</i> , <b>2011</b> , 9, 563-74	18	180
52	A systematic analysis of Drosophila TUDOR domain-containing proteins identifies Vreteno and the Tdrd12 family as essential primary piRNA pathway factors. <i>EMBO Journal</i> , <b>2011</b> , 30, 3977-93	13	140
51	High conservation of transcription factor binding and evidence for combinatorial regulation across six Drosophila species. <i>Nature Genetics</i> , <b>2011</b> , 43, 414-20	36.3	102
50	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , <b>2011</b> , 478, 476-82	50.4	802
49	Neural-specific elongation of 3'UTRs during Drosophila development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 15864-9	11.5	99
48	Systematic genetic analysis of muscle morphogenesis and function in Drosophila. <i>Nature</i> , <b>2010</b> , 464, 287-91	50.4	196
47	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> , <b>2010</b> , 107, 11841-6	11.5	163
46	Diverse endonucleolytic cleavage sites in the mammalian transcriptome depend upon microRNAs, Drosha, and additional nucleases. <i>Molecular Cell</i> , <b>2010</b> , 38, 781-8	17.6	144
45	Developmental gene regulation in the era of genomics. <i>Developmental Biology</i> , <b>2010</b> , 339, 230-9	3.1	35
44	The Tasmanian devil transcriptome reveals Schwann cell origins of a clonally transmissible cancer. <i>Science</i> , <b>2010</b> , 327, 84-7	33.3	188
43	Learning the transcriptional regulatory code. <i>Molecular Systems Biology</i> , <b>2009</b> , 5, 329	12.2	2
42	Accurate prediction of peptide binding sites on protein surfaces. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000335	5	116
41	Coherent but overlapping expression of microRNAs and their targets during vertebrate development. <i>Genes and Development</i> , <b>2009</b> , 23, 466-81	12.6	89

40	Histone modifications at human enhancers reflect global cell-type-specific gene expression. <i>Nature</i> , <b>2009</b> , 459, 108-12	50.4	1832
39	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> , <b>2009</b> , 16, 639-46	17.6	212
38	The TDRD9-MIWI2 complex is essential for piRNA-mediated retrotransposon silencing in the mouse male germline. <i>Developmental Cell</i> , <b>2009</b> , 17, 775-87	10.2	230
37	Specialized piRNA pathways act in germline and somatic tissues of the Drosophila ovary. <i>Cell</i> , <b>2009</b> , 137, 522-35	56.2	627
36	Comparative genomics of gene regulation-conservation and divergence of cis-regulatory information. <i>Current Opinion in Genetics and Development</i> , <b>2009</b> , 19, 565-70	4.9	70
35	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , <b>2008</b> , 453, 175-83	50.4	545
34	An endogenous small interfering RNA pathway in Drosophila. <i>Nature</i> , <b>2008</b> , 453, 798-802	50.4	542
33	Temporal reciprocity of miRNAs and their targets during the maternal-to-zygotic transition in Drosophila. <i>Current Biology</i> , <b>2008</b> , 18, 501-6	6.3	200
32	An epigenetic role for maternally inherited piRNAs in transposon silencing. <i>Science</i> , <b>2008</b> , 322, 1387-92	33.3	574
31	A single Hox locus in Drosophila produces functional microRNAs from opposite DNA strands. <i>Genes and Development</i> , <b>2008</b> , 22, 8-13	12.6	188
30	Conservation of small RNA pathways in platypus. <i>Genome Research</i> , <b>2008</b> , 18, 995-1004	9.7	34
29	RNA polymerase stalling at developmental control genes in the Drosophila melanogaster embryo. <i>Nature Genetics</i> , <b>2007</b> , 39, 1512-6	36.3	589
28	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. <i>Nature</i> , <b>2007</b> , 450, 219-32	50.4	506
27	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , <b>2007</b> , 450, 203-18	50.4	1586
26	Systematic discovery and characterization of fly microRNAs using 12 Drosophila genomes. <i>Genome Research</i> , <b>2007</b> , 17, 1865-79	9.7	158
25	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> , <b>2007</b> , 21, 385-90	12.6	232
24	Reliable prediction of regulator targets using 12 Drosophila genomes. <i>Genome Research</i> , <b>2007</b> , 17, 1919-31	9.7	123
23	Discrete small RNA-generating loci as master regulators of transposon activity in Drosophila. <i>Cell</i> , <b>2007</b> , 128, 1089-103	56.2	1802

22	Evolution, biogenesis, expression, and target predictions of a substantially expanded set of <i>Drosophila</i> microRNAs. <i>Genome Research</i> , <b>2007</b> , 17, 1850-64	9.7	462
21	Genome-wide analysis of mRNAs regulated by Drosha and Argonaute proteins in <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 2965-75	4.8	119
20	Denosing feedback loops by thresholding--a new role for microRNAs. <i>Genes and Development</i> , <b>2006</b> , 20, 2769-72	12.6	78
19	mRNA degradation by miRNAs and GW182 requires both CCR4:NOT deadenylase and DCP1:DCP2 decapping complexes. <i>Genes and Development</i> , <b>2006</b> , 20, 1885-98	12.6	720
18	Animal MicroRNAs confer robustness to gene expression and have a significant impact on 3'UTR evolution. <i>Cell</i> , <b>2005</b> , 123, 1133-46	56.2	890
17	Principles of microRNA-target recognition. <i>PLoS Biology</i> , <b>2005</b> , 3, e85	9.7	1746
16	Systematic discovery of new recognition peptides mediating protein interaction networks. <i>PLoS Biology</i> , <b>2005</b> , 3, e405	9.7	257
15	Not miR-ly muscular: microRNAs and muscle development. <i>Genes and Development</i> , <b>2005</b> , 19, 2261-4	12.6	30
14	Finding functional sites in structural genomics proteins. <i>Structure</i> , <b>2004</b> , 12, 1405-12	5.2	39
13	Identification of <i>Drosophila</i> MicroRNA targets. <i>PLoS Biology</i> , <b>2003</b> , 1, E60	9.7	591
12	Predictions without templates: new folds, secondary structure, and contacts in CASP5. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53 Suppl 6, 436-56	4.2	94
11	The relationship between sequence and interaction divergence in proteins. <i>Journal of Molecular Biology</i> , <b>2003</b> , 332, 989-98	6.5	264
10	A model for statistical significance of local similarities in structure. <i>Journal of Molecular Biology</i> , <b>2003</b> , 326, 1307-16	6.5	139
9	bantam encodes a developmentally regulated microRNA that controls cell proliferation and regulates the proapoptotic gene <i>hid</i> in <i>Drosophila</i> . <i>Cell</i> , <b>2003</b> , 113, 25-36	56.2	1696
8	Crystal structure of an archaeal class I aldolase and the evolution of (betaalpha) <sub>8</sub> barrel proteins. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 47253-60	5.4	39
7	Annotation in three dimensions. PINTS: Patterns in Non-homologous Tertiary Structures. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3341-4	20.1	130
6	A dynamic structural model for estrogen receptor-alpha activation by ligands, emphasizing the role of interactions between distant A and E domains. <i>Molecular Cell</i> , <b>2002</b> , 10, 1019-32	17.6	105
5	The mitochondrial permeability transition augments Fas-induced apoptosis in mouse hepatocytes. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 11814-23	5.4	121

4	DeepSTARR predicts enhancer activity from DNA sequence and enables the de novo design of enhancers	1
3	SARSeq, a robust and highly multiplexed NGS assay for parallel detection of SARS-CoV2 and other respiratory infections	3
2	Resolving systematic errors in widely-used enhancer activity assays in human cells enables genome-wide functional enhancer characterization	1
1	High-throughput Mutational Surveillance of the SARS-CoV-2 Spike Gene	2