B Franklin Pugh

List of Publications by Year
in descending order

56 papers	6,520 citations	147801 31 h-index	189892 50 g-index
62 all docs	62 docs citations	62 times ranked	8088 citing authors

#	Article	IF	Citations
1	STENCIL: A web templating engine for visualizing and sharing life science datasets. PLoS Computational Biology, 2022, 18, e1009859.	3.2	0
2	PEGR: a flexible management platform for reproducible epigenomic and genomic research. Genome Biology, 2022, 23, 99.	8.8	1
3	Genome-wide promoter assembly in <i>E. coli</i> measured at single-base resolution. Genome Research, 2022, , .	5.5	1
4	ScriptManager: an interactive platform for reducing barriers to genomics analysis. , 2022, , .		0
5	Acute stress drives global repression through two independent RNA polymerase II stalling events in Saccharomyces. Cell Reports, 2021, 34, 108640.	6.4	13
6	What do Transcription Factors Interact With?. Journal of Molecular Biology, 2021, 433, 166883.	4.2	27
7	A high-resolution protein architecture of the budding yeast genome. Nature, 2021, 592, 309-314.	27.8	130
8	Protein architecture of the yeast genome. Nature, 2021, , .	27.8	0
9	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. Genome Research, 2021, 31, 1663-1679.	5.5	9
10	Ssl2/TFIIH function in transcription start site scanning by RNA polymerase II in Saccharomyces cerevisiae. ELife, 2021, 10, .	6.0	5
11	Alignment and quantification of ChIP-exo crosslinking patterns reveal the spatial organization of protein–DNA complexes. Nucleic Acids Research, 2020, 48, 11215-11226.	14.5	2
12	Actin R256 Mono-methylation Is a Conserved Post-translational Modification Involved in Transcription. Cell Reports, 2020, 32, 108172.	6.4	9
13	Universal promoter scanning by Pol II during transcription initiation in Saccharomyces cerevisiae. Genome Biology, 2020, 21, 132.	8.8	35
14	Phase separation directs ubiquitination of gene-body nucleosomes. Nature, 2020, 579, 592-597.	27.8	105
15	ChExMix: A Method for Identifying and Classifying Protein–DNA Interaction Subtypes. Journal of Computational Biology, 2020, 27, 429-435.	1.6	2
16	PEGR: a management platform for ChIP-based next generation sequencing pipelines. , 2020, , .		2
17	Characterizing protein–DNA binding event subtypes in ChIP-exo data. Bioinformatics, 2019, 35, 903-913.	4.1	29
18	Genome-wide determinants of sequence-specific DNA binding of general regulatory factors. Genome Research, 2018, 28, 497-508.	5.5	44

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19	Widespread and precise reprogramming of yeast protein–genome interactions in response to heat shock. Genome Research, 2018, 28, 357-366.	5.5	71
20	The SAGA/TREX-2 subunit Sus1 binds widely to transcribed genes and affects mRNA turnover globally. Epigenetics and Chromatin, 2018, 11, 13.	3.9	19
21	Genome-Wide Mapping of Decay Factor–mRNA Interactions in Yeast Identifies Nutrient-Responsive Transcripts as Targets of the Deadenylase Ccr4. G3: Genes, Genomes, Genetics, 2018, 8, 315-330.	1.8	27
22	In vivo genome-wide binding interactions of mouse and human constitutive androstane receptors reveal novel gene targets. Nucleic Acids Research, 2018, 46, 8385-8403.	14.5	27
23	Simplified ChIP-exo assays. Nature Communications, 2018, 9, 2842.	12.8	73
24	Understanding nucleosome dynamics and their links to gene expression and DNA replication. Nature Reviews Molecular Cell Biology, 2017, 18, 548-562.	37.0	380
25	Genome-wide uniformity of human 'open' pre-initiation complexes. Genome Research, 2017, 27, 15-26.	5.5	22
26	Correspondence: DNA shape is insufficient to explain binding. Nature Communications, 2017, 8, 15643.	12.8	9
27	Structural evidence for Nap1–dependent H2A–H2B deposition and nucleosome assembly. EMBO Journal, 2016, 35, 1465-1482.	7.8	64
28	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. Cell, 2016, 165, 357-371.	28.9	211
29	The Pioneer Transcription Factor FoxA Maintains an Accessible Nucleosome Configuration at Enhancers for Tissue-Specific Gene Activation. Molecular Cell, 2016, 62, 79-91.	9.7	315
30	The Histone Modification Domain of Paf1 Complex Subunit Rtf1 Directly Stimulates H2B Ubiquitylation through an Interaction with Rad6. Molecular Cell, 2016, 64, 815-825.	9.7	85
31	Genomic Nucleosome Organization Reconstituted with Pure Proteins. Cell, 2016, 167, 709-721.e12.	28.9	227
32	Tail and Kinase Modules Differently Regulate Core Mediator Recruitment and Function In Vivo. Molecular Cell, 2016, 64, 455-466.	9.7	117
33	Genome-Wide Organization of GATA1 and TAL1 Determined at High Resolution. Molecular and Cellular Biology, 2016, 36, 157-172.	2.3	32
34	Genome-wide nucleosome specificity and function of chromatin remodellers in ES cells. Nature, 2016, 530, 113-116.	27.8	211
35	Genomic Organization of Human Transcription Initiation Complexes. PLoS ONE, 2016, 11, e0149339.	2.5	41
36	Protein–DNA binding in high-resolution. Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 269-283.	5.2	41

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37	ATF4 Gene Network Mediates Cellular Response to the Anticancer PAD Inhibitor YW3-56 in Triple-Negative Breast Cancer Cells. Molecular Cancer Therapeutics, 2015, 14, 877-888.	4.1	55
38	Molecular mechanisms of ribosomal protein gene coregulation. Genes and Development, 2015, 29, 1942-1954.	5.9	116
39	The Nuclear Pore-Associated TREX-2 Complex Employs Mediator to Regulate Gene Expression. Cell, 2015, 162, 1016-1028.	28.9	99
40	Subnucleosomal Structures and Nucleosome Asymmetry across a Genome. Cell, 2014, 159, 1377-1388.	28.9	193
41	A Comprehensive and High-Resolution Genome-wide Response of p53 to Stress. Cell Reports, 2014, 8, 514-527.	6.4	56
42	A Genome-wide Map of CTCF Multivalency Redefines the CTCF Code. Cell Reports, 2013, 3, 1678-1689.	6.4	270
43	Genome-wide Nucleosome Specificity and Directionality of Chromatin Remodelers. Cell, 2012, 149, 1461-1473.	28.9	300
44	ChIP-exo Method for Identifying Genomic Location of DNA-Binding Proteins with Near-Single-Nucleotide Accuracy. Current Protocols in Molecular Biology, 2012, 100, Unit 21.24.	2.9	141
45	Genome-wide structure and organization of eukaryotic pre-initiation complexes. Nature, 2012, 483, 295-301.	27.8	475
46	Genome-Wide Mapping of Nucleosome Positions in Yeast Using High-Resolution MNase ChIP-Seq. Methods in Enzymology, 2012, 513, 233-250.	1.0	56
47	Comprehensive Genome-wide Protein-DNA Interactions Detected at Single-Nucleotide Resolution. Cell, 2011, 147, 1408-1419.	28.9	684
48	Stable and dynamic nucleosome states during a meiotic developmental process. Genome Research, 2011, 21, 875-884.	5.5	75
49	A compiled and systematic reference map of nucleosome positions across the Saccharomyces cerevisiae genome. Genome Biology, 2009, 10, R109.	9.6	212
50	The HAND and SANT Domains Regulate the In vitro and In vivo Activity of the ISW2 Chromatin Remodeling Complex. FASEB Journal, 2009, 23, LB191.	0.5	0
51	A canonical promoter organization of the transcription machinery and its regulators in the Saccharomyces genome. FASEB Journal, 2009, 23, 493.2.	0.5	0
52	NELF and GAGA Factor Are Linked to Promoter-Proximal Pausing at Many Genes in <i>Drosophila</i>. Molecular and Cellular Biology, 2008, 28, 3290-3300.	2.3	198
53	GeneTrack—a genomic data processing and visualization framework. Bioinformatics, 2008, 24, 1305-1306.	4.1	94
54	A Genome-Wide Housekeeping Role for TFIID and a Highly Regulated Stress-Related Role for SAGA in Saccharomyces cerevisiae. Molecular Cell, 2004, 13, 573-585.	9.7	502

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55	Identification and Distinct Regulation of Yeast TATA Box-Containing Genes. Cell, 2004, 116, 699-709.	28.9	578
56	Dimer Dissociation and Thermosensitivity Kinetics of theSaccharomycescerevisiaeand Human TATA Binding Proteinsâ€. Biochemistry, 1999, 38, 11340-11348.	2.5	19