

# B Franklin Pugh

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Comprehensive Genome-wide Protein-DNA Interactions Detected at Single-Nucleotide Resolution. <i>Cell</i> , 2011, 147, 1408-1419.	28.9	684
2	Identification and Distinct Regulation of Yeast TATA Box-Containing Genes. <i>Cell</i> , 2004, 116, 699-709.	28.9	578
3	A Genome-Wide Housekeeping Role for TFIID and a Highly Regulated Stress-Related Role for SAGA in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2004, 13, 573-585.	9.7	502
4	Genome-wide structure and organization of eukaryotic pre-initiation complexes. <i>Nature</i> , 2012, 483, 295-301.	27.8	475
5	Understanding nucleosome dynamics and their links to gene expression and DNA replication. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 548-562.	37.0	380
6	The Pioneer Transcription Factor FoxA Maintains an Accessible Nucleosome Configuration at Enhancers for Tissue-Specific Gene Activation. <i>Molecular Cell</i> , 2016, 62, 79-91.	9.7	315
7	Genome-wide Nucleosome Specificity and Directionality of Chromatin Remodelers. <i>Cell</i> , 2012, 149, 1461-1473.	28.9	300
8	A Genome-wide Map of CTCF Multivalency Redefines the CTCF Code. <i>Cell Reports</i> , 2013, 3, 1678-1689.	6.4	270
9	Genomic Nucleosome Organization Reconstituted with Pure Proteins. <i>Cell</i> , 2016, 167, 709-721.e12.	28.9	227
10	A compiled and systematic reference map of nucleosome positions across the <i>Saccharomyces cerevisiae</i> genome. <i>Genome Biology</i> , 2009, 10, R109.	9.6	212
11	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. <i>Cell</i> , 2016, 165, 357-371.	28.9	211
12	Genome-wide nucleosome specificity and function of chromatin remodellers in ES cells. <i>Nature</i> , 2016, 530, 113-116.	27.8	211
13	NELF and GAGA Factor Are Linked to Promoter-Proximal Pausing at Many Genes in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2008, 28, 3290-3300.	2.3	198
14	Subnucleosomal Structures and Nucleosome Asymmetry across a Genome. <i>Cell</i> , 2014, 159, 1377-1388.	28.9	193
15	ChIP $\alpha$ exo Method for Identifying Genomic Location of DNA-Binding Proteins with Near-Single-Nucleotide Accuracy. <i>Current Protocols in Molecular Biology</i> , 2012, 100, Unit 21.24.	2.9	141
16	A high-resolution protein architecture of the budding yeast genome. <i>Nature</i> , 2021, 592, 309-314.	27.8	130
17	Tail and Kinase Modules Differently Regulate Core Mediator Recruitment and Function In Vivo. <i>Molecular Cell</i> , 2016, 64, 455-466.	9.7	117
18	Molecular mechanisms of ribosomal protein gene coregulation. <i>Genes and Development</i> , 2015, 29, 1942-1954.	5.9	116

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19	Phase separation directs ubiquitination of gene-body nucleosomes. <i>Nature</i> , 2020, 579, 592-597.	27.8	105
20	The Nuclear Pore-Associated TREX-2 Complex Employs Mediator to Regulate Gene Expression. <i>Cell</i> , 2015, 162, 1016-1028.	28.9	99
21	GeneTrack—a genomic data processing and visualization framework. <i>Bioinformatics</i> , 2008, 24, 1305-1306.	4.1	94
22	The Histone Modification Domain of Paf1 Complex Subunit Rtf1 Directly Stimulates H2B Ubiquitylation through an Interaction with Rad6. <i>Molecular Cell</i> , 2016, 64, 815-825.	9.7	85
23	Stable and dynamic nucleosome states during a meiotic developmental process. <i>Genome Research</i> , 2011, 21, 875-884.	5.5	75
24	Simplified ChIP-exo assays. <i>Nature Communications</i> , 2018, 9, 2842.	12.8	73
25	Widespread and precise reprogramming of yeast protein–genome interactions in response to heat shock. <i>Genome Research</i> , 2018, 28, 357-366.	5.5	71
26	Structural evidence for Nap1-dependent H2A–H2B deposition and nucleosome assembly. <i>EMBO Journal</i> , 2016, 35, 1465-1482.	7.8	64
27	Genome-Wide Mapping of Nucleosome Positions in Yeast Using High-Resolution MNase ChIP-Seq. <i>Methods in Enzymology</i> , 2012, 513, 233-250.	1.0	56
28	A Comprehensive and High-Resolution Genome-wide Response of p53 to Stress. <i>Cell Reports</i> , 2014, 8, 514-527.	6.4	56
29	ATF4 Gene Network Mediates Cellular Response to the Anticancer PAD Inhibitor YW3-56 in Triple-Negative Breast Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 877-888.	4.1	55
30	Genome-wide determinants of sequence-specific DNA binding of general regulatory factors. <i>Genome Research</i> , 2018, 28, 497-508.	5.5	44
31	Protein–DNA binding in high-resolution. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015, 50, 269-283.	5.2	41
32	Genomic Organization of Human Transcription Initiation Complexes. <i>PLoS ONE</i> , 2016, 11, e0149339.	2.5	41
33	Universal promoter scanning by Pol II during transcription initiation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2020, 21, 132.	8.8	35
34	Genome-Wide Organization of GATA1 and TAL1 Determined at High Resolution. <i>Molecular and Cellular Biology</i> , 2016, 36, 157-172.	2.3	32
35	Characterizing protein–DNA binding event subtypes in ChIP-exo data. <i>Bioinformatics</i> , 2019, 35, 903-913.	4.1	29
36	Genome-Wide Mapping of Decay Factor–mRNA Interactions in Yeast Identifies Nutrient-Responsive Transcripts as Targets of the Deadenylase Ccr4. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 315-330.	1.8	27

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37	In vivo genome-wide binding interactions of mouse and human constitutive androstane receptors reveal novel gene targets. <i>Nucleic Acids Research</i> , 2018, 46, 8385-8403.	14.5	27
38	What do Transcription Factors Interact With?. <i>Journal of Molecular Biology</i> , 2021, 433, 166883.	4.2	27
39	Genome-wide uniformity of human open™ pre-initiation complexes. <i>Genome Research</i> , 2017, 27, 15-26.	5.5	22
40	Dimer Dissociation and Thermosensitivity Kinetics of the <i>Saccharomyces cerevisiae</i> and Human TATA Binding Proteins. <i>Biochemistry</i> , 1999, 38, 11340-11348.	2.5	19
41	The SAGA/TREX-2 subunit Sus1 binds widely to transcribed genes and affects mRNA turnover globally. <i>Epigenetics and Chromatin</i> , 2018, 11, 13.	3.9	19
42	Acute stress drives global repression through two independent RNA polymerase II stalling events in <i>Saccharomyces</i> . <i>Cell Reports</i> , 2021, 34, 108640.	6.4	13
43	Correspondence: DNA shape is insufficient to explain binding. <i>Nature Communications</i> , 2017, 8, 15643.	12.8	9
44	Actin R256 Mono-methylation Is a Conserved Post-translational Modification Involved in Transcription. <i>Cell Reports</i> , 2020, 32, 108172.	6.4	9
45	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. <i>Genome Research</i> , 2021, 31, 1663-1679.	5.5	9
46	Ssl2/TFIIH function in transcription start site scanning by RNA polymerase II in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2021, 10, .	6.0	5
47	Alignment and quantification of ChIP-exo crosslinking patterns reveal the spatial organization of protein-DNA complexes. <i>Nucleic Acids Research</i> , 2020, 48, 11215-11226.	14.5	2
48	ChExMix: A Method for Identifying and Classifying Protein-DNA Interaction Subtypes. <i>Journal of Computational Biology</i> , 2020, 27, 429-435.	1.6	2
49	PEGR: a management platform for ChIP-based next generation sequencing pipelines. , 2020, , .		2
50	PEGR: a flexible management platform for reproducible epigenomic and genomic research. <i>Genome Biology</i> , 2022, 23, 99.	8.8	1
51	Genome-wide promoter assembly in <i>E. coli</i> measured at single-base resolution. <i>Genome Research</i> , 2022, , .	5.5	1
52	Protein architecture of the yeast genome. <i>Nature</i> , 2021, , .	27.8	0
53	The HAND and SANT Domains Regulate the In vitro and In vivo Activity of the ISW2 Chromatin Remodeling Complex. <i>FASEB Journal</i> , 2009, 23, LB191.	0.5	0
54	A canonical promoter organization of the transcription machinery and its regulators in the <i>Saccharomyces</i> genome. <i>FASEB Journal</i> , 2009, 23, 493.2.	0.5	0

#	ARTICLE	IF	CITATIONS
55	STENCIL: A web templating engine for visualizing and sharing life science datasets. PLoS Computational Biology, 2022, 18, e1009859.	3.2	0
56	ScriptManager: an interactive platform for reducing barriers to genomics analysis. , 2022, , .		0