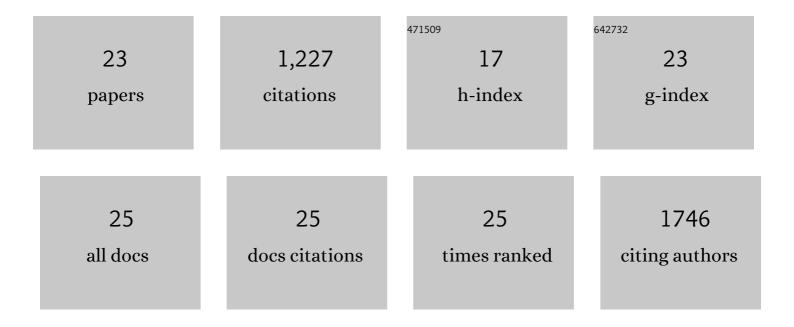
Danny Asher Bitton

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8751814/publications.pdf Version: 2024-02-01



#	Article	lF	CITATIONS
1	BioPhi: A platform for antibody design, humanization, and humanness evaluation based on natural antibody repertoires and deep learning. MAbs, 2022, 14, 2020203.	5.2	54
2	PepSeA: Peptide Sequence Alignment and Visualization Tools to Enable Lead Optimization. Journal of Chemical Information and Modeling, 2022, 62, 1259-1267.	5.4	3
3	The application potential of machine learning and genomics for understanding natural product diversity, chemistry, and therapeutic translatability. Natural Product Reports, 2021, 38, 1100-1108.	10.3	30
4	Mutation Maker, An Open Source Oligo Design Platform for Protein Engineering. ACS Synthetic Biology, 2021, 10, 357-370.	3.8	5
5	Cdk9 and H2Bub1 signal to Clr6-Cll/Rpd3S to suppress aberrant antisense transcription. Nucleic Acids Research, 2020, 48, 7154-7168.	14.5	16
6	A deep learning genome-mining strategy for biosynthetic gene cluster prediction. Nucleic Acids Research, 2019, 47, e110-e110.	14.5	164
7	Fitness Landscape of the Fission Yeast Genome. Molecular Biology and Evolution, 2019, 36, 1612-1623.	8.9	12
8	Long noncoding RNA repertoire and targeting by nuclear exosome, cytoplasmic exonuclease, and RNAi in fission yeast. Rna, 2018, 24, 1195-1213.	3.5	45
9	Functional and regulatory profiling of energy metabolism in fission yeast. Genome Biology, 2016, 17, 240.	8.8	44
10	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. Frontiers in Genetics, 2015, 6, 330.	2.3	65
11	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	21.4	174
12	Parallel Profiling of Fission Yeast Deletion Mutants for Proliferation and for Lifespan During Long-Term Quiescence. G3: Genes, Genomes, Genetics, 2015, 5, 145-155.	1.8	38
13	Identification of New Players in Cell Division, DNA Damage Response, and Morphogenesis Through Construction of <i>Schizosaccharomyces pombe</i> Deletion Strains. G3: Genes, Genomes, Genetics, 2015, 5, 361-370.	1.8	20
14	Widespread exon skipping triggers degradation by nuclear RNA surveillance in fission yeast. Genome Research, 2015, 25, 884-896.	5.5	37
15	Individual letters of the RNA polymerase II CTD code govern distinct gene expression programs in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4185-4190.	7.1	53
16	LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq. Genome Research, 2014, 24, 1169-1179.	5.5	64
17	A Novel Histone Deacetylase Complex in the Control of Transcription and Genome Stability. Molecular and Cellular Biology, 2014, 34, 3500-3514.	2.3	37
18	Structural and Functional Characterization of the N Terminus of Schizosaccharomyces pombe Cwf10. Fukaryotic Cell. 2013, 12, 1472-1489.	3.4	12

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#	Article	IF	CITATIONS
19	Augmented Annotation of the Schizosaccharomyces pombe Genome Reveals Additional Genes Required for Growth and Viability. Genetics, 2011, 187, 1207-1217.	2.9	26
20	Programmed fluctuations in sense/antisense transcript ratios drive sexual differentiation in <i>S. pombe</i> . Molecular Systems Biology, 2011, 7, 559.	7.2	41
21	An Integrated Mass-Spectrometry Pipeline Identifies Novel Protein Coding-Regions in the Human Genome. PLoS ONE, 2010, 5, e8949.	2.5	27
22	Exon level integration of proteomics and microarray data. BMC Bioinformatics, 2008, 9, 118.	2.6	32
23	Eight-channel iTRAQ Enables Comparison of the Activity of Six Leukemogenic Tyrosine Kinases. Molecular and Cellular Proteomics, 2008, 7, 853-863.	3.8	224