

Danny Asher Bitton

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8751814/publications.pdf>

Version: 2024-02-01

23
papers

1,227
citations

471509

17
h-index

642732

23
g-index

25
all docs

25
docs citations

25
times ranked

1746
citing authors

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

#	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