

# Justin C Fay

## List of Publications by Year in descending order

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71  
papers

7,621  
citations

94433

37  
h-index

88630

70  
g-index

86  
all docs

86  
docs citations

86  
times ranked

11704  
citing authors

#	ARTICLE	IF	CITATIONS
1	The structure and diversity of strain-level variation in vaginal bacteria. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
2	Cis-regulatory variants affect gene expression dynamics in yeast. <i>ELife</i> , 2021, 10, .	6.0	6
3	Associations between the vaginal microbiome and <i>Candida</i> colonization in women of reproductive age. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, 471.e1-471.e9.	1.3	52
4	High-throughput analysis of adaptation using barcoded strains of <i>Saccharomyces cerevisiae</i> . <i>PeerJ</i> , 2020, 8, e10118.	2.0	9
5	Riding the Rhythm of Melatonin Through Pregnancy to Deliver on Time. <i>Frontiers in Endocrinology</i> , 2019, 10, 616.	3.5	55
6	Mitochondria-encoded genes contribute to evolution of heat and cold tolerance in yeast. <i>Science Advances</i> , 2019, 5, eaav1848.	10.3	66
7	Mitochondrial DNA and temperature tolerance in lager yeasts. <i>Science Advances</i> , 2019, 5, eaav1869.	10.3	72
8	A polyploid admixed origin of beer yeasts derived from European and Asian wine populations. <i>PLoS Biology</i> , 2019, 17, e3000147.	5.6	58
9	Multiple Changes Underlie Allelic Divergence of <i>CUP2</i> Between <i>Saccharomyces</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3595-3600.	1.8	5
10	The Fate of Deleterious Variants in a Barley Genomic Prediction Population. <i>Genetics</i> , 2019, 213, 1531-1544.	2.9	12
11	Genetic Basis of Variation in Heat and Ethanol Tolerance in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 179-188.	1.8	16
12	A multi-phase approach to select new wine yeast strains with enhanced fermentative fitness and glutathione production. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2269-2278.	3.6	14
13	Comparative Genomics Approaches Accurately Predict Deleterious Variants in Plants. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3321-3329.	1.8	36
14	Chronodisruption: An untimely cause of preterm birth?. <i>Best Practice and Research in Clinical Obstetrics and Gynaecology</i> , 2018, 52, 60-67.	2.8	21
15	Mouse models of preterm birth: suggested assessment and reporting guidelines. <i>Biology of Reproduction</i> , 2018, 99, 922-937.	2.7	62
16	Cis-Regulatory Divergence in Gene Expression between Two Thermally Divergent Yeast Species. <i>Genome Biology and Evolution</i> , 2017, 9, 1120-1129.	2.5	57
17	Hybridization and adaptive evolution of diverse <i>Saccharomyces</i> species for cellulosic biofuel production. <i>Biotechnology for Biofuels</i> , 2017, 10, 78.	6.2	78
18	Drupal, TEI and XML: How to prototype a digital humanities tool?. <i>Library Hi Tech News</i> , 2017, 34, 9-15.	0.9	2

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19	Debating Data Science. <i>Radical History Review</i> , 2017, 2017, 133-148.	0.4	5
20	Genetic variation and expression changes associated with molybdate resistance from a glutathione producing wine strain of <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2017, 12, e0180814.	2.5	8
21	Changes in the Relative Abundance of Two <i>Saccharomyces</i> Species from Oak Forests to Wine Fermentations. <i>Frontiers in Microbiology</i> , 2016, 7, 215.	3.5	19
22	Divergent <i>MLS1</i> Promoters Lie on a Fitness Plateau for Gene Expression. <i>Molecular Biology and Evolution</i> , 2016, 33, 1270-1279.	8.9	11
23	The Role of Deleterious Substitutions in Crop Genomes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2307-2317.	8.9	83
24	Selective Photonic Disinfection of Cell Culture Using a Visible Ultrashort Pulsed Laser. <i>IEEE Journal of Selected Topics in Quantum Electronics</i> , 2016, 22, 371-378.	2.9	9
25	Independent Origins of Yeast Associated with Coffee and Cacao Fermentation. <i>Current Biology</i> , 2016, 26, 965-971.	3.9	69
26	Evolution of ecological dominance of yeast species in high-sugar environments. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 2079-2093.	2.3	53
27	Patterns of Gene Conversion in Duplicated Yeast Histones Suggest Strong Selection on a Coadapted Macromolecular Complex. <i>Genome Biology and Evolution</i> , 2015, 7, 3249-3258.	2.5	22
28	Using whole-genome sequences of the LG/J and SM/J inbred mouse strains to prioritize quantitative trait genes and nucleotides. <i>BMC Genomics</i> , 2015, 16, 415.	2.8	31
29	Heterochronic Meiotic Misexpression in an Interspecific Yeast Hybrid. <i>Molecular Biology and Evolution</i> , 2014, 31, 1333-1342.	8.9	17
30	The molecular basis of phenotypic variation in yeast. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 672-677.	3.3	80
31	Disease consequences of human adaptation. <i>Applied &amp; Translational Genomics</i> , 2013, 2, 42-47.	2.1	18
32	Mixing of vineyard and oak-tree ecotypes of <i>Saccharomyces cerevisiae</i> in North American vineyards. <i>Molecular Ecology</i> , 2013, 22, 2917-2930.	3.9	107
33	The Role of Surface Chemistry on the Toxicity of Ag Nanoparticles. <i>Small</i> , 2013, 9, 2628-2638.	10.0	32
34	ZRT1 Harbors an Excess of Nonsynonymous Polymorphism and Shows Evidence of Balancing Selection in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 665-673.	1.8	7
35	Genomic Sequence Diversity and Population Structure of <i>Saccharomyces cerevisiae</i> Assessed by RAD-seq. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2163-2171.	1.8	132
36	Fine-Mapping an Association of FSHR with Preterm Birth in a Finnish Population. <i>PLoS ONE</i> , 2013, 8, e78032.	2.5	15

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37	A Noncomplementation Screen for Quantitative Trait Alleles in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 753-760.	1.8	21
38	Divergence of the Yeast Transcription Factor FZF1 Affects Sulfite Resistance. <i>PLoS Genetics</i> , 2012, 8, e1002763.	3.5	35
39	Tapping into yeast diversity. <i>Molecular Ecology</i> , 2012, 21, 5387-5389.	3.9	2
40	Divergence in wine characteristics produced by wild and domesticated strains of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2011, 11, 540-551.	2.3	56
41	Weighing the evidence for adaptation at the molecular level. <i>Trends in Genetics</i> , 2011, 27, 343-349.	6.7	62
42	Evidence for Hitchhiking of Deleterious Mutations within the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002240.	3.5	82
43	An Evolutionary Genomic Approach to Identify Genes Involved in Human Birth Timing. <i>PLoS Genetics</i> , 2011, 7, e1001365.	3.5	96
44	Is Transcription Factor Binding Site Turnover a Sufficient Explanation for Cis-Regulatory Sequence Divergence?. <i>Genome Biology and Evolution</i> , 2010, 2, 851-858.	2.5	24
45	Primate-specific evolution of noncoding element insertion into PLA2G4C and human preterm birth. <i>BMC Medical Genomics</i> , 2010, 3, 62.	1.5	13
46	Incipient Balancing Selection through Adaptive Loss of Aquaporins in Natural <i>Saccharomyces cerevisiae</i> Populations. <i>PLoS Genetics</i> , 2010, 6, e1000893.	3.5	99
47	Preventing preterm birth: the past limitations and new potential of animal models. <i>DMM Disease Models and Mechanisms</i> , 2010, 3, 407-414.	2.4	51
48	Identification of deleterious mutations within three human genomes. <i>Genome Research</i> , 2009, 19, 1553-1561.	5.5	926
49	A Combined-Cross Analysis Reveals Genes With Drug-Specific and Background-Dependent Effects on Drug Sensitivity in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2009, 183, 1141-1151.	2.9	22
50	Quantification of rare allelic variants from pooled genomic DNA. <i>Nature Methods</i> , 2009, 6, 263-265.	19.0	136
51	Dissecting the pleiotropic consequences of a quantitative trait nucleotide. <i>FEMS Yeast Research</i> , 2009, 9, 713-722.	2.3	31
52	Association of cohesin and Nipped-B with transcriptionally active regions of the <i>Drosophila melanogaster</i> genome. <i>Chromosoma</i> , 2008, 117, 89-102.	2.2	194
53	Evaluating the role of natural selection in the evolution of gene regulation. <i>Heredity</i> , 2008, 100, 191-199.	2.6	150
54	A Catalog of Neutral and Deleterious Polymorphism in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000183.	3.5	212

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55	Frequent Gain and Loss of Functional Transcription Factor Binding Sites. <i>PLoS Computational Biology</i> , 2007, 3, e99.	3.2	134
56	Genetic variation in the cysteine biosynthesis pathway causes sensitivity to pharmacological compounds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19387-19391.	7.1	49
57	Human Genome: Which proteins contribute to human-chimpanzee differences?. <i>European Journal of Human Genetics</i> , 2006, 14, 506-506.	2.8	3
58	Phylogeny based discovery of regulatory elements. <i>BMC Bioinformatics</i> , 2006, 7, 266.	2.6	9
59	Evidence for Domesticated and Wild Populations of <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2005, 1, e5.	3.5	416
60	Identification of functional transcription factor binding sites using closely related <i>Saccharomyces</i> species. <i>Genome Research</i> , 2005, 15, 701-709.	5.5	52
61	Hypervariable Noncoding Sequences in <i>Saccharomyces cerevisiae</i> Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY942206, AY942556.. <i>Genetics</i> , 2005, 170, 1575-1587.	2.9	30
62	Detecting Hitchhiking from Patterns of DNA Polymorphism. , 2005, , 65-77.		6
63	DNA Variability and Divergence at the Notch Locus in <i>Drosophila melanogaster</i> and <i>D. simulans</i> : A Case of Accelerated Synonymous Site Divergence. <i>Genetics</i> , 2004, 167, 171-185.	2.9	47
64	Population genetic variation in gene expression is associated with phenotypic variation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2004, 5, R26.	9.6	200
65	SEQUENCEDIVERGENCE, FUNCTIONALCONSTRAINT,ANDSELECTION INPROTEINEVOLUTION. <i>Annual Review of Genomics and Human Genetics</i> , 2003, 4, 213-235.	6.2	241
66	Testing the neutral theory of molecular evolution with genomic data from <i>Drosophila</i> . <i>Nature</i> , 2002, 415, 1024-1026.	27.8	339
67	The neutral theory in the genomic era. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 642-646.	3.3	104
68	Positive and Negative Selection on the Human Genome. <i>Genetics</i> , 2001, 158, 1227-1234.	2.9	565
69	Hitchhiking Under Positive Darwinian Selection. <i>Genetics</i> , 2000, 155, 1405-1413.	2.9	1,602
70	A human population bottleneck can account for the discordance between patterns of mitochondrial versus nuclear DNA variation. <i>Molecular Biology and Evolution</i> , 1999, 16, 1003-1005.	8.9	218
71	Effects of hot and cold temperatures on the survival of oospores produced by United States strains of <i>Phytophthora infestans</i> . <i>American Potato Journal</i> , 1997, 74, 315-323.	0.3	28