

# Bernard Dujon

## List of Publications by Year in descending order

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140  
papers

12,215  
citations

28274

55  
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26613

107  
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146  
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146  
docs citations

146  
times ranked

9356  
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional variability in adhesion and flocculation of yeast megasatellite genes. <i>Genetics</i> , 2022, 221, .	2.9	2
2	The Formation of Neochromosomes during Experimental Evolution in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Genes</i> , 2021, 12, 1678.	2.4	0
3	Hijacking, arms race, GMOs and pesticides. <i>Comptes Rendus - Biologies</i> , 2021, 344, 203-207.	0.2	0
4	Mitochondrial genetics revisited. <i>Yeast</i> , 2020, 37, 191-205.	1.7	29
5	The unlimited editing of nucleic acids in the oceans. <i>Comptes Rendus - Biologies</i> , 2020, 343, 215-217.	0.2	0
6	To identify the panoply of somatic mutations in each cell. <i>Comptes Rendus - Biologies</i> , 2020, 343, 211-213.	0.2	0
7	On the origin of the genetic code: a 27-codon hypothetical precursor of an intricate 64-codon intermediate shaped the modern code. <i>Comptes Rendus - Biologies</i> , 2020, 343, 15-52.	0.2	2
8	My route to the intimacy of genomes. <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	1
9	Massive Amplification at an Unselected Locus Accompanies Complex Chromosomal Rearrangements in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1201-1215.	1.8	6
10	Foreword. <i>Comptes Rendus - Biologies</i> , 2016, 339, 223-224.	0.2	1
11	Replication stalling and heteroduplex formation within CAG/CTG trinucleotide repeats by mismatch repair. <i>DNA Repair</i> , 2016, 42, 94-106.	2.8	34
12	Genome-wide replication landscape of <i>Candida glabrata</i> . <i>BMC Biology</i> , 2015, 13, 69.	3.8	16
13	Basic principles of yeast genomics, a personal recollection: Graphical Abstract Figure.. <i>FEMS Yeast Research</i> , 2015, 15, fov047.	2.3	9
14	Macrotene chromosomes provide insights to a new mechanism of high-order gene amplification in eukaryotes. <i>Nature Communications</i> , 2015, 6, 6154.	12.8	13
15	Purification of G <sub>1</sub> daughter cells from different <i>Saccharomyces</i> species through an optimized centrifugal elutriation procedure. <i>Yeast</i> , 2014, 31, 159-166.	1.7	18
16	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. <i>Biotechnology for Biofuels</i> , 2014, 7, 66.	6.2	57
17	Highly Specific Contractions of a Single CAG/CTG Trinucleotide Repeat by TALEN in Yeast. <i>PLoS ONE</i> , 2014, 9, e95611.	2.5	53
18	Comparative genomics of emerging pathogens in the <i>Candida glabrata</i> clade. <i>BMC Genomics</i> , 2013, 14, 623.	2.8	174

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19	Complete DNA Sequence of <i>Kuraishia capsulata</i> Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). <i>Genome Biology and Evolution</i> , 2013, 5, 2524-2539.	2.5	39
20	Detection and Characterization of Megsatellites in Orthologous and Nonorthologous Genes of 21 Fungal Genomes. <i>Eukaryotic Cell</i> , 2013, 12, 794-803.	3.4	12
21	<i>Pichia sorbitophila</i> , an Interspecies Yeast Hybrid, Reveals Early Steps of Genome Resolution After Polyploidization. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 299-311.	1.8	113
22	Evolutionary Role of Interspecies Hybridization and Genetic Exchanges in Yeasts. <i>Microbiology and Molecular Biology Reviews</i> , 2012, 76, 721-739.	6.6	183
23	Yeasty clocks: Dating genomic changes in yeasts. <i>Comptes Rendus - Biologies</i> , 2011, 334, 620-628.	0.2	25
24	Foreword. <i>Comptes Rendus - Biologies</i> , 2011, 334, 578-579.	0.2	0
25	Genome-Wide Analysis of Heteroduplex DNA in Mismatch Repair-Deficient Yeast Cells Reveals Novel Properties of Meiotic Recombination Pathways. <i>PLoS Genetics</i> , 2011, 7, e1002305.	3.5	128
26	Megsatellites: a new class of large tandem repeats discovered in the pathogenic yeast <i>Candida glabrata</i> . <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 671-676.	5.4	30
27	Origin and fate of pseudogenes in Hemiascomycetes: a comparative analysis. <i>BMC Genomics</i> , 2010, 11, 260.	2.8	27
28	Yeast evolutionary genomics. <i>Nature Reviews Genetics</i> , 2010, 11, 512-524.	16.3	337
29	Dynamic evolution of megasatellites in yeasts. <i>Nucleic Acids Research</i> , 2010, 38, 4731-4739.	14.5	18
30	Chromosome arm length and nuclear constraints determine the dynamic relationship of yeast subtelomeres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2025-2030.	7.1	135
31	Population Polymorphism of Nuclear Mitochondrial DNA Insertions Reveals Widespread Diploidy Associated with Loss of Heterozygosity in <i>Debaryomyces hansenii</i> . <i>Eukaryotic Cell</i> , 2010, 9, 449-459.	3.4	26
32	In Memoriam Piotr Slonimski (1922-2009) The Unconventional Yeast Geneticist. <i>Genetics</i> , 2009, 183, 1-2.	2.9	1
33	Unusual composition of a yeast chromosome arm is associated with its delayed replication. <i>Genome Research</i> , 2009, 19, 1710-1721.	5.5	43
34	Uneven Distribution of Mating Types among Genotypes of <i>Candida glabrata</i> Isolates from Clinical Samples. <i>Eukaryotic Cell</i> , 2009, 8, 287-295.	3.4	54
35	Comparative genomics of protoploid <i>Saccharomycetaceae</i> . <i>Genome Research</i> , 2009, 19, 1696-1709.	5.5	207
36	SRS2 and SGS1 prevent chromosomal breaks and stabilize triplet repeats by restraining recombination. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 159-167.	8.2	89

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37	Complete mitochondrial genome sequences of <i>Nakaseomyces</i> species reveal invasion by palindromic GC clusters and considerable size expansion. <i>FEMS Yeast Research</i> , 2009, 9, 1283-1292.	2.3	34
38	Genomic polymorphism in the population of <i>Candida glabrata</i> : Gene copy-number variation and chromosomal translocations. <i>Fungal Genetics and Biology</i> , 2009, 46, 264-276.	2.1	73
39	Insertion of Horizontally Transferred Genes within Conserved Syntenic Regions of Yeast Genomes. <i>PLoS ONE</i> , 2009, 4, e6515.	2.5	57
40	Promiscuous DNA in the nuclear genomes of hemiascomycetous yeasts. <i>FEMS Yeast Research</i> , 2008, 8, 846-857.	2.3	42
41	The Asexual Yeast <i>Candida glabrata</i> Maintains Distinct a and $\alpha$ Haploid Mating Types. <i>Eukaryotic Cell</i> , 2008, 7, 848-858.	3.4	69
42	Megasatellites: a peculiar class of giant minisatellites in genes involved in cell adhesion and pathogenicity in <i>Candida glabrata</i> . <i>Nucleic Acids Research</i> , 2008, 36, 5970-5982.	14.5	40
43	Segmental Duplications Arise from Pol32-Dependent Repair of Broken Forks through Two Alternative Replication-Based Mechanisms. <i>PLoS Genetics</i> , 2008, 4, e1000175.	3.5	161
44	Comparative Genomics and Molecular Dynamics of DNA Repeats in Eukaryotes. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 686-727.	6.6	450
45	Structure of <i>Kluyveromyces lactis</i> subtelomeres: duplications and gene content. <i>FEMS Yeast Research</i> , 2006, 6, 428-441.	2.3	56
46	Yeasts illustrate the molecular mechanisms of eukaryotic genome evolution. <i>Trends in Genetics</i> , 2006, 22, 375-387.	6.7	200
47	Highly Variable Rates of Genome Rearrangements between Hemiascomycetous Yeast Lineages. <i>PLoS Genetics</i> , 2006, 2, e32.	3.5	94
48	Molecular Evolution of Minisatellites in Hemiascomycetous Yeasts. <i>Molecular Biology and Evolution</i> , 2006, 23, 189-202.	8.9	47
49	Telomere tethering at the nuclear periphery is essential for efficient DNA double strand break repair in subtelomeric region. <i>Journal of Cell Biology</i> , 2006, 172, 189-199.	5.2	201
50	Correction: Telomere tethering at the nuclear periphery is essential for efficient DNA double strand break repair in subtelomeric region. <i>Journal of Cell Biology</i> , 2006, 172, 951-951.	5.2	0
51	Stability of Large Segmental Duplications in the Yeast Genome. <i>Genetics</i> , 2006, 172, 2211-2222.	2.9	50
52	The RNA polymerase III-dependent family of genes in hemiascomycetes: comparative RNomics, decoding strategies, transcription and evolutionary implications. <i>Nucleic Acids Research</i> , 2006, 34, 1816-1835.	14.5	86
53	Cooperative evolution in protein complexes of yeast from comparative analyses of its interaction network. <i>Proteomics</i> , 2005, 5, 3116-3119.	2.2	8
54	Comparative Genomics in Hemiascomycete Yeasts: Evolution of Sex, Silencing, and Subtelomeres. <i>Molecular Biology and Evolution</i> , 2005, 22, 856-873.	8.9	135

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55	Highly variable rates of genome rearrangements between Hemiascomycetous yeast lineages. PLoS Genetics, 2005, preprint, e32.	3.5	0
56	Comparative Genomics of Hemiascomycete Yeasts: Genes Involved in DNA Replication, Repair, and Recombination. Molecular Biology and Evolution, 2005, 22, 1011-1023.	8.9	79
57	Hemiascomycetous yeasts at the forefront of comparative genomics. Current Opinion in Genetics and Development, 2005, 15, 614-620.	3.3	45
58	Genetic network interactions among replication, repair and nuclear pore deficiencies in yeast. DNA Repair, 2005, 4, 459-468.	2.8	111
59	The complete mitochondrial genome of the yeast <i>Kluyveromyces thermotolerans</i> . FEBS Letters, 2005, 579, 30-40.	2.8	30
60	Homing Endonucleases and the Yeast Mitochondrial $\rho$ Locus – A Historical Perspective. , 2005, , 11-31.		6
61	Continued Colonization of the Human Genome by Mitochondrial DNA. PLoS Biology, 2004, 2, e273.	5.6	187
62	Eucaryotic genome evolution through the spontaneous duplication of large chromosomal segments. EMBO Journal, 2004, 23, 234-243.	7.8	192
63	Genome evolution in yeasts. Nature, 2004, 430, 35-44.	27.8	1,498
64	Telomere length control and transcriptional regulation of subtelomeric adhesins in <i>Candida glabrata</i> . Molecular Microbiology, 2004, 55, 1246-1258.	2.5	165
65	Large-scale exploration of growth inhibition caused by overexpression of genomic fragments in <i>Saccharomyces cerevisiae</i> . Genome Biology, 2004, 5, R72.	9.6	36
66	Gene relics in the genome of the yeast <i>Saccharomyces cerevisiae</i> . Gene, 2004, 335, 1-17.	2.2	36
67	Analysis of Microsatellites in 13 Hemiascomycetous Yeast Species: Mechanisms Involved in Genome Dynamics. Journal of Molecular Evolution, 2003, 56, 730-741.	1.8	24
68	A novel design of whole-genome microarray probes for <i>Saccharomyces cerevisiae</i> which minimizes cross-hybridization. BMC Genomics, 2003, 4, 38.	2.8	29
69	Contractions and Expansions of CAG/CTG Trinucleotide Repeats occur during Ectopic Gene Conversion in Yeast, by a MUS81-independent Mechanism. Journal of Molecular Biology, 2003, 326, 769-782.	4.2	32
70	Distance from the Chromosome End Determines the Efficiency of Double Strand Break Repair in Subtelomeres of Haploid Yeast. Journal of Molecular Biology, 2003, 328, 847-862.	4.2	68
71	The complete mitochondrial genome sequence of the pathogenic yeast <i>Candida (Torulopsis) glabrata</i> . FEBS Letters, 2003, 534, 39-48.	2.8	68
72	Novel Transporters from Hemiascomycete Yeasts. Journal of Molecular Microbiology and Biotechnology, 2003, 6, 19-28.	1.0	3

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73	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. <i>Nucleic Acids Research</i> , 2003, 31, 1121-1135.	14.5	118
74	Transcription and nuclear transport of CAG/CTG trinucleotide repeats in yeast. <i>Nucleic Acids Research</i> , 2002, 30, 3540-3547.	14.5	17
75	Genome-wide Nuclear Morphology Screen Identifies Novel Genes Involved in Nuclear Architecture and Gene-silencing in <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2002, 321, 551-561.	4.2	38
76	Amino acid composition of genomes, lifestyles of organisms, and evolutionary trends: a global picture with correspondence analysis. <i>Gene</i> , 2002, 297, 51-60.	2.2	171
77	Characterization of the I-Spom I Endonuclease from Fission Yeast: Insights into the Evolution of a Group I Intron-Encoded Homing Endonuclease. <i>Journal of Molecular Evolution</i> , 2002, 55, 302-313.	1.8	35
78	Functional analysis of yeast gene families involved in metabolism of vitamins B1 and B6. <i>Yeast</i> , 2002, 19, 1261-1276.	1.7	89
79	Evolution of Gene Order in the Genomes of Two Related Yeast Species. <i>Genome Research</i> , 2001, 11, 2009-2019.	5.5	84
80	The genomics of microbial diversity. <i>Current Opinion in Microbiology</i> , 2000, 3, 443-444.	5.1	7
81	Transcriptional regulation of the <i>Saccharomyces cerevisiae</i> DAL5 gene family and identification of the high affinity nicotinic acid permease TNA1 (YGR260w). <i>FEBS Letters</i> , 2000, 475, 237-241.	2.8	70
82	Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies. <i>FEBS Letters</i> , 2000, 487, 3-12.	2.8	186
83	Genomic Exploration of the Hemiascomycetous Yeasts: 3. Methods and strategies used for sequence analysis and annotation. <i>FEBS Letters</i> , 2000, 487, 17-30.	2.8	37
84	Genomic Exploration of the Hemiascomycetous Yeasts: 4. The genome of <i>Saccharomyces cerevisiae</i> revisited. <i>FEBS Letters</i> , 2000, 487, 31-36.	2.8	75
85	Genomic Exploration of the Hemiascomycetous Yeasts: 8. <i>Zygosaccharomyces rouxii</i> . <i>FEBS Letters</i> , 2000, 487, 52-55.	2.8	30
86	Genomic Exploration of the Hemiascomycetous Yeasts: 10. <i>Kluyveromyces thermotolerans</i> . <i>FEBS Letters</i> , 2000, 487, 61-65.	2.8	11
87	Genomic Exploration of the Hemiascomycetous Yeasts: 12. <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> . <i>FEBS Letters</i> , 2000, 487, 71-75.	2.8	45
88	Genomic Exploration of the Hemiascomycetous Yeasts: 13. <i>Pichia angusta</i> . <i>FEBS Letters</i> , 2000, 487, 76-81.	2.8	28
89	Genomic Exploration of the Hemiascomycetous Yeasts: 15. <i>Pichia sorbitophila</i> . <i>FEBS Letters</i> , 2000, 487, 87-90.	2.8	14
90	Genomic Exploration of the Hemiascomycetous Yeasts: 16. <i>Candida tropicalis</i> . <i>FEBS Letters</i> , 2000, 487, 91-94.	2.8	27

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91	Genomic Exploration of the Hemiascomycetous Yeasts: 18. Comparative analysis of chromosome maps and synteny with <i>Saccharomyces cerevisiae</i> . FEBS Letters, 2000, 487, 101-112.	2.8	71
92	Genomic Exploration of the Hemiascomycetous Yeasts: 19. Ascomycetes-specific genes. FEBS Letters, 2000, 487, 113-121.	2.8	47
93	Genomic Exploration of the Hemiascomycetous Yeasts: 20. Evolution of gene redundancy compared to <i>Saccharomyces cerevisiae</i> . FEBS Letters, 2000, 487, 122-133.	2.8	49
94	Genetic redundancy and gene fusion in the genome of the baker's yeast <i>Saccharomyces cerevisiae</i> : functional characterization of a three-member gene family involved in the thiamine biosynthetic pathway. Molecular Microbiology, 1999, 32, 1140-1152.	2.5	38
95	Mitochondrial DNA repairs double-strand breaks in yeast chromosomes. Nature, 1999, 402, 96-100.	27.8	239
96	Pervasiveness of Gene Conservation and Persistence of Duplicates in Cellular Genomes. Journal of Molecular Evolution, 1999, 49, 591-600.	1.8	37
97	Trinucleotide repeats and other microsatellites in yeasts. Research in Microbiology, 1999, 150, 589-602.	2.1	35
98	The Genomic Tree as Revealed from Whole Proteome Comparisons. Genome Research, 1999, 9, 550-557.	5.5	213
99	European functional analysis network (EUROFAN) and the functional analysis of the <i>Saccharomyces cerevisiae</i> genome (minireview). Electrophoresis, 1998, 19, 617-624.	2.4	70
100	Physical mapping of chromosomes VII and XV of <i>Saccharomyces cerevisiae</i> at 3.5 kb average resolution to allow their complete sequencing. , 1998, 14, 601-616.		5
101	'Mass-murder' of ORFs from three regions of chromosome XI from <i>Saccharomyces cerevisiae</i> 1Published in conjunction with A Wisconsin Gathering Honoring Wacław Szybalski on occasion of his 75th year and 20years of Editorship-in-Chief of Gene, 10 August 1997, University of Wisconsin, Madison, WI, USA.1. Gene, 1998, 223, 33-46.	2.2	31
102	The yeast genome project: what did we learn?. Trends in Genetics, 1996, 12, 263-270.	6.7	498
103	New vectors for combinatorial deletions in yeast chromosomes and for gap-repair cloning using 'split-marker' recombination. Yeast, 1996, 12, 1439-1457.	1.7	155
104	New vectors for combinatorial deletions in yeast chromosomes and for gap-repair cloning using 'split-marker' recombination. Yeast, 1996, 12, 1439-57.	1.7	63
105	[5] In Vitro fragmentation of yeast chromosomes and yeast artificial chromosomes at artificially inserted sites and applications to genome mapping. Methods in Molecular Genetics, 1995, , 81-107.	0.6	4
106	Construction of a complete genomic library of <i>Saccharomyces cerevisiae</i> and physical mapping of chromosome XI at 3.7 kb resolution. Yeast, 1995, 11, 121-135.	1.7	56
107	Conditional Lethality of Null Mutations in RTH1 That Encodes the Yeast Counterpart of a Mammalian 5'-to 3'-Exonuclease Required for Lagging Strand DNA Synthesis in Reconstituted Systems. Journal of Biological Chemistry, 1995, 270, 4193-4196.	3.4	172
108	Construction of a cosmid contig and of an <i>EcoRI</i> restriction map of yeast chromosome X. DNA Sequence, 1994, 4, 293-300.	0.7	17

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109	Interaction between the first and last nucleotides of pre-mRNA introns is a determinant of 3' splice site selection in <i>S.cerevisiae</i> . <i>Nucleic Acids Research</i> , 1994, 22, 1981-1987.	14.5	44
110	Transcript map of two regions from chromosome XI of <i>Saccharomyces cerevisiae</i> for interpretation of systematic sequencing results. <i>Yeast</i> , 1994, 10, 1403-1413.	1.7	16
111	Consequences of unique double-stranded breaks in yeast chromosomes: death or homozygosis. <i>Molecular Genetics and Genomics</i> , 1993, 240, 170-180.	2.4	50
112	Sequence of a 7.8 kb segment on the left arm of yeast chromosome XI reveals four open reading frames, including the <i>CAP1</i> gene, an intron-containing gene and a gene encoding a homolog to the mammalian <i>UOG-1</i> gene. <i>Yeast</i> , 1993, 9, 279-287.	1.7	11
113	Homologous recombination in plant cells is enhanced by in vivo induction of double strand breaks into DNA by a site-specific endonuclease. <i>Nucleic Acids Research</i> , 1993, 21, 5034-5040.	14.5	272
114	Rapid physical mapping of YAC inserts by random integration of I-Sce I sites. <i>Human Molecular Genetics</i> , 1993, 2, 265-271.	2.9	14
115	Nested chromosomal fragmentation in yeast using the meganuclease I-SceI: a new method for physical mapping of eukaryotic genomes. <i>Nucleic Acids Research</i> , 1992, 20, 5625-5631.	14.5	96
116	Sequence of a 10.7 kb segment of yeast chromosome XI identifies the <i>APN1</i> and the <i>BAF1</i> loci and reveals one tRNA gene and several new open reading frames including homologs to <i>RAD2</i> and kinases. <i>Yeast</i> , 1992, 8, 121-132.	1.7	50
117	Sequence of a segment of yeast chromosome XI identifies a new mitochondrial carrier, a new member of the G protein family, and a protein with the <i>PAAKK</i> motif of the H1 histones. <i>Yeast</i> , 1992, 8, 325-336.	1.7	22
118	XI. Yeast sequencing reports. The sequence of a 9.3 kb segment located on the left arm of the yeast chromosome XI reveals five open reading frames including the <i>CCE1</i> gene and putative products related to <i>MYO2</i> and to the ribosomal protein <i>L10</i> . <i>Yeast</i> , 1992, 8, 987-995.	1.7	17
119	Altogether now " sequencing the yeast genome. <i>Current Biology</i> , 1992, 2, 279-281.	3.9	11
120	Cleavage of yeast and bacteriophage T7 genomes at a single site using the rare cutter endonuclease I-SceI. <i>Nucleic Acids Research</i> , 1991, 19, 189-190.	14.5	68
121	The complete sequence of the 8.2 kb segment left of <i>MAT</i> on chromosome III reveals five ORFs, including a gene for a yeast ribokinase. <i>Yeast</i> , 1990, 6, 521-534.	1.7	104
122	The apocytochrome b gene of <i>Chlamydomonas smithii</i> contains a mobile intron related to both <i>Saccharomyces</i> and <i>Neurospora</i> introns. <i>Molecular Genetics and Genomics</i> , 1990, 223, 288-296.	2.4	64
123	Purification and characterization of the in vitro activity of I-SceI, a novel and highly specific endonuclease encoded by a group I intron. <i>Nucleic Acids Research</i> , 1990, 18, 1407-1413.	14.5	184
124	Group I introns as mobile genetic elements: facts and mechanistic speculations " a review**Presented at the Albany Conference on "RNA: Catalysis, Splicing, Evolution"™, Rensselaerville, NY (U.S.A.) 22-25 September, 1988., 1989, , 91-114.		0
125	Group I introns as mobile genetic elements: Facts and mechanistic speculations " a review. <i>Gene</i> , 1989, 82, 91-114.	2.2	500
126	Mobile introns: definition of terms and recommended nomenclature. <i>Gene</i> , 1989, 82, 115-118.	2.2	135



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127	Mobile introns: definition of terms and recommended nomenclature**Presented at the Albany Conference on tRNA: Catalysis, Splicing, Evolution™, Rensselaerville, NY (U.S.A.) 22-25 September, 1988., 1989, , 115-118.		0
128	Genetic exchanges between bacteriophage T4 and filamentous fungi?. Cell, 1986, 46, 323.	28.9	78
129	The pho1 mutation. A frameshift, and its compensation, producing altered forms of physiologically efficient ATPase in yeast mitochondria. FEBS Journal, 1985, 150, 89-94.	0.2	13
130	The intron of the mitochondrial 21S rRNA gene: Distribution in different yeast species and sequence comparison between Kluyveromyces thermotolerans and Saccharomyces cerevisiae. Molecular Genetics and Genomics, 1983, 192, 487-499.	2.4	72
131	ORGANIZATION OF THE MITOCHONDRIAL 21S rRNA GENE IN Saccharomyces cerevisiae s MUTANTS OF THE PEPTIDYL TRANSFERASE CENTRE AND NATURE OF THE omega LOCUS. , 1983, , 389-404.		0
132	Comparison of fungal mitochondrial introns reveals extensive homologies in RNA secondary structure. Biochimie, 1982, 64, 867-881.	2.6	528
133	Sequence of the intron and flanking exons of the mitochondrial 21S rRNA gene of yeast strains having different alleles at the rDNA and rib-1 loci. Cell, 1980, 20, 185-197.	28.9	399
134	Genetic and physical characterization of a segment of yeast mitochondrial DNA involved in the control of genetic recombination. Biochimie, 1980, 61, 985-1010.	2.6	16
135	Mutants in a mosaic gene reveal functions for introns. Nature, 1979, 282, 777-778.	27.8	28
136	Oligomycin Sensitivity of ATPase Studied as a Function of Mitochondrial Biogenesis, using Mitochondrially Determined Oligomycin-Resistant Mutants of Saccharomyces cerevisiae. FEBS Journal, 1974, 42, 439-445.	0.2	27
137	MITOCHONDRIAL GENETICS VII. ALLELISM AND MAPPING STUDIES OF RIBOSOMAL MUTANTS RESISTANT TO CHLORAMPHENICOL, ERYTHROMYCIN AND SPIRAMYCIN IN S. CEREVISIAE. Genetics, 1974, 78, 1063-1100.	2.9	69
138	Extrakaryotic Inheritance. Progress in Botany Fortschritte Der Botanik, 1974, , 236-246.	0.3	1
139	Mitochondrial genetics. Molecular Genetics and Genomics, 1973, 125, 53-90.	2.4	135
140	Ascomycetes: the Candida MAT Locus: Comparing MAT in the Genomes of Hemiascomycetous Yeasts. , 0, , 247-263.		7