

Jose Perez-Martin

List of Publications by Year in descending order

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111
papers

7,671
citations

50276

46
h-index

54911

84
g-index

112
all docs

112
docs citations

112
times ranked

5560
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust Cre recombinase activity in the biotrophic smut fungus <i>Ustilago maydis</i> enables efficient conditional null mutants in planta. <i>Genetics</i> , 2022, 220, .	2.9	1
2	The Nma1 protein promotes long distance transport mediated by early endosomes in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2021, , .	2.5	1
3	Incompatibility between proliferation and plant invasion is mediated by a regulator of appressorium formation in the corn smut fungus <i>Ustilago maydis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30599-30609.	7.1	5
4	Creating novel specificities in a fungal nonself recognition system by single step homologous recombination events. <i>New Phytologist</i> , 2020, 228, 1001-1010.	7.3	13
5	Protein Phosphatase Ppz1 Is Not Regulated by a Hal3-Like Protein in Plant Pathogen <i>Ustilago maydis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3817.	4.1	5
6	Sugar Partitioning between <i>Ustilago maydis</i> and Its Host <i>Zea mays</i> L during Infection. <i>Plant Physiology</i> , 2019, 179, 1373-1385.	4.8	23
7	Cytoplasmic retention and degradation of a mitotic inducer enable plant infection by a pathogenic fungus. <i>ELife</i> , 2019, 8, .	6.0	7
8	Cytoplasmic Transport Machinery of the SPF27 Homologue Num1 in <i>Ustilago maydis</i> . <i>Scientific Reports</i> , 2018, 8, 3611.	3.3	18
9	Galactose metabolism and toxicity in <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2018, 114, 42-52.	2.1	18
10	Fungal Morphogenesis, from the Polarized Growth of Hyphae to Complex Reproduction and Infection Structures. <i>Microbiology and Molecular Biology Reviews</i> , 2018, 82, .	6.6	231
11	Virulence-specific cell cycle and morphogenesis connections in pathogenic fungi. <i>Seminars in Cell and Developmental Biology</i> , 2016, 57, 93-99.	5.0	15
12	Editorial. <i>Seminars in Cell and Developmental Biology</i> , 2016, 57, 68.	5.0	0
13	Genetic Manipulation of the Plant Pathogen <i>Ustilago maydis</i> to Study Fungal Biology and Plant Microbe Interactions. <i>Journal of Visualized Experiments</i> , 2016, , .	0.3	25
14	Mre11 and Blm-Dependent Formation of ALT-Like Telomeres in Ku-Deficient <i>Ustilago maydis</i> . <i>PLoS Genetics</i> , 2015, 11, e1005570.	3.5	23
15	MRN- and 9-1-1-Independent Activation of the ATR-Chk1 Pathway during the Induction of the Virulence Program in the Phytopathogen <i>Ustilago maydis</i> . <i>PLoS ONE</i> , 2015, 10, e0137192.	2.5	7
16	Fungal Ku prevents permanent cell cycle arrest by suppressing DNA damage signaling at telomeres. <i>Nucleic Acids Research</i> , 2015, 43, 2138-2151.	14.5	22
17	Hxt1, a monosaccharide transporter and sensor required for virulence of the maize pathogen <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2015, 206, 1086-1100.	7.3	55
18	Uniparental mitochondrial DNA inheritance is not affected in <i>Ustilago maydis</i> <i>atg11</i> mutants blocked in mitophagy. <i>BMC Microbiology</i> , 2015, 15, 23.	3.3	11

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19	LAMMER kinase contributes to genome stability in <i>Ustilago maydis</i> . <i>DNA Repair</i> , 2015, 33, 70-77.	2.8	6
20	Appressorium formation in the corn smut fungus <i>Ustilago maydis</i> requires a G2 cell cycle arrest. <i>Plant Signaling and Behavior</i> , 2015, 10, e1001227.	2.4	12
21	Programmed cell cycle arrest is required for infection of corn plants by the fungus <i>Ustilago maydis</i> . <i>Journal of Cell Science</i> , 2015, 128, e1-e1.	2.0	0
22	The SPF27 Homologue Num1 Connects Splicing and Kinesin 1-Dependent Cytoplasmic Trafficking in <i>Ustilago maydis</i> . <i>PLoS Genetics</i> , 2014, 10, e1004046.	3.5	15
23	Therapy with antitumor lipids: Worming the way. <i>Cell Cycle</i> , 2014, 13, 2993-2993.	2.6	0
24	Programmed cell cycle arrest is required for infection of corn plants by the fungus <i>Ustilago maydis</i> . <i>Development (Cambridge)</i> , 2014, 141, 4817-4826.	2.5	24
25	Functional Genomics of Smut Fungi. <i>Advances in Botanical Research</i> , 2014, 70, 143-172.	1.1	4
26	Fungal model systems and the elucidation of pathogenicity determinants. <i>Fungal Genetics and Biology</i> , 2014, 70, 42-67.	2.1	133
27	Crosstalk between the Unfolded Protein Response and Pathways That Regulate Pathogenic Development in <i>Ustilago maydis</i> . <i>Plant Cell</i> , 2013, 25, 4262-4277.	6.6	53
28	A DNA Damage Checkpoint Pathway Coordinates the Division of Dikaryotic Cells in the Ink Cap Mushroom <i>Coprinopsis cinerea</i> . <i>Genetics</i> , 2013, 195, 47-57.	2.9	11
29	Initiation of Meiotic Recombination in <i>Ustilago maydis</i> . <i>Genetics</i> , 2013, 195, 1231-1240.	2.9	10
30	The distinct wiring between cell cycle regulation and the widely conserved Morphogenesis-Related (MOR) pathway in the fungus <i>Ustilago maydis</i> determines the morphological outcome. <i>Journal of Cell Science</i> , 2012, 125, 4597-608.	2.0	21
31	Cell Cycle and Morphogenesis Connections During the Formation of the Infective Filament in <i>Ustilago maydis</i> . <i>Topics in Current Genetics</i> , 2012, , 97-114.	0.7	4
32	Targeting GSK3 from <i>Ustilago maydis</i> : Type-II Kinase Inhibitors as Potential Antifungals. <i>ACS Chemical Biology</i> , 2012, 7, 1257-1267.	3.4	18
33	Common motifs in the response of cereal primary metabolism to fungal pathogens are not based on similar transcriptional reprogramming. <i>Frontiers in Plant Science</i> , 2011, 2, 39.	3.6	25
34	Dikaryotic cell cycle in the phytopathogenic fungus <i>Ustilago maydis</i> is controlled by the DNA damage response cascade. <i>Plant Signaling and Behavior</i> , 2011, 6, 1574-1577.	2.4	8
35	The DNA Damage Response Signaling Cascade Regulates Proliferation of the Phytopathogenic Fungus <i>Ustilago maydis</i> in Planta. <i>Plant Cell</i> , 2011, 23, 1654-1665.	6.6	28
36	The <i>Ustilago maydis</i> Forkhead Transcription Factor Fox1 Is Involved in the Regulation of Genes Required for the Attenuation of Plant Defenses During Pathogenic Development. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1118-1129.	2.6	40

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37	The <i>Ustilago maydis</i> mating type locus controls hyphal proliferation and expression of secreted virulence factors in planta. <i>Molecular Microbiology</i> , 2010, 75, 208-220.	2.5	72
38	The <i>Ustilago maydis</i> Clp1 Protein Orchestrates Pheromone and β -Dependent Signaling Pathways to Coordinate the Cell Cycle and Pathogenic Development. <i>Plant Cell</i> , 2010, 22, 2908-2922.	6.6	68
39	Activation of the Cell Wall Integrity Pathway Promotes Escape from G2 in the Fungus <i>Ustilago maydis</i> . <i>PLoS Genetics</i> , 2010, 6, e1001009.	3.5	48
40	The Transcription Factor Rbf1 Is the Master Regulator for β -Mating Type Controlled Pathogenic Development in <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2010, 6, e1001035.	4.7	114
41	A Novel High-Affinity Sucrose Transporter Is Required for Virulence of the Plant Pathogen <i>Ustilago maydis</i> . <i>PLoS Biology</i> , 2010, 8, e1000303.	5.6	205
42	Growth and development: eukaryotes. <i>Current Opinion in Microbiology</i> , 2010, 13, 661-662.	5.1	2
43	Septins from the Phytopathogenic Fungus <i>Ustilago maydis</i> Are Required for Proper Morphogenesis but Dispensable for Virulence. <i>PLoS ONE</i> , 2010, 5, e12933.	2.5	51
44	<i>Ustilago maydis</i> Infection Strongly Alters Organic Nitrogen Allocation in Maize and Stimulates Productivity of Systemic Source Leaves. <i>Plant Physiology</i> , 2009, 152, 293-308.	4.8	98
45	A role for the DNA-damage checkpoint kinase Chk1 in the virulence program of the fungus <i>Ustilago maydis</i> . <i>Journal of Cell Science</i> , 2009, 122, 4130-4140.	2.0	27
46	Growth at High pH and Sodium and Potassium Tolerance in Media above the Cytoplasmic pH Depend on ENA ATPases in <i>Ustilago maydis</i> . <i>Eukaryotic Cell</i> , 2009, 8, 821-829.	3.4	36
47	DNA-damage response in the basidiomycete fungus <i>Ustilago maydis</i> relies in a sole Chk1-like kinase. <i>DNA Repair</i> , 2009, 8, 720-731.	2.8	20
48	Physical and chemical plant-derived signals induce differentiation in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2009, 71, 895-911.	2.5	120
49	Sphingolipid biosynthesis is required for polar growth in the dimorphic phytopathogen <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, 190-200.	2.1	27
50	Comparative genomics of MAP kinase and calcium-calmodulin signalling components in plant and human pathogenic fungi. <i>Fungal Genetics and Biology</i> , 2009, 46, 287-298.	2.1	302
51	Reprogramming a maize plant: transcriptional and metabolic changes induced by the fungal biotroph <i>Ustilago maydis</i> . <i>Plant Journal</i> , 2008, 56, 181-195.	5.7	328
52	<i>Ustilago maydis</i> , a new fungal model system for cell biology. <i>Trends in Cell Biology</i> , 2008, 18, 61-67.	7.9	113
53	Establishment of compatibility in the <i>Ustilago maydis</i> /maize pathosystem. <i>Journal of Plant Physiology</i> , 2008, 165, 29-40.	3.5	106
54	Sex in smut fungi: Structure, function and evolution of mating-type complexes. <i>Fungal Genetics and Biology</i> , 2008, 45, S15-S21.	2.1	116

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55	14-3-3 regulates the G2/M transition in the basidiomycete <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 1206-1215.	2.1	21
56	Spa2 is required for morphogenesis but it is dispensable for pathogenicity in the phytopathogenic fungus <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 1315-1327.	2.1	20
57	Cdk5 kinase regulates the association between adaptor protein Bem1 and GEF Cdc24 in the fungus <i>Ustilago maydis</i> . <i>Journal of Cell Science</i> , 2008, 121, 2824-2832.	2.0	14
58	Connections between polar growth and cell cycle arrest during the induction of the virulence program in the phytopathogenic fungus <i>Ustilago maydis</i> . <i>Plant Signaling and Behavior</i> , 2008, 3, 480-481.	2.4	15
59	Sustained cell polarity and virulence in the phytopathogenic fungus <i>Ustilago maydis</i> depends on an essential cyclin-dependent kinase from the Cdk5/Pho85 family. <i>Journal of Cell Science</i> , 2007, 120, 1584-1595.	2.0	79
60	Polar Growth in the Infectious Hyphae of the Phytopathogen <i>Ustilago maydis</i> Depends on a Virulence-Specific Cyclin. <i>Plant Cell</i> , 2007, 19, 3280-3296.	6.6	36
61	Ortholog of BRCA2-interacting protein BCCIP controls morphogenetic responses during DNA replication stress in <i>Ustilago maydis</i> . <i>DNA Repair</i> , 2007, 6, 1651-1660.	2.8	11
62	Tetracycline-regulated gene expression in the pathogen <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 727-738.	2.1	51
63	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006, 444, 97-101.	27.8	1,113
64	Pathocycles: <i>Ustilago maydis</i> as a model to study the relationships between cell cycle and virulence in pathogenic fungi. <i>Molecular Genetics and Genomics</i> , 2006, 276, 211-229.	2.1	53
65	The Clp1 Protein Is Required for Clamp Formation and Pathogenic Development of <i>Ustilago maydis</i> . <i>Plant Cell</i> , 2006, 18, 2388-2401.	6.6	103
66	Biz1, a Zinc Finger Protein Required for Plant Invasion by <i>Ustilago maydis</i> , Regulates the Levels of a Mitotic Cyclin. <i>Plant Cell</i> , 2006, 18, 2369-2387.	6.6	75
67	The cdc25 phosphatase is essential for the G2/M phase transition in the basidiomycete yeast <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2005, 58, 1482-1496.	2.5	24
68	The Induction of the Mating Program in the Phytopathogen <i>Ustilago maydis</i> Is Controlled by a G1 Cyclin[W]. <i>Plant Cell</i> , 2005, 17, 3544-3560.	6.6	26
69	Inhibitory phosphorylation of a mitotic cyclin-dependent kinase regulates the morphogenesis, cell size and virulence of the smut fungus <i>Ustilago maydis</i> . <i>Journal of Cell Science</i> , 2005, 118, 3607-3622.	2.0	37
70	The induction of sexual development and virulence in the smut fungus <i>Ustilago maydis</i> depends on Crk1, a novel MAPK protein. <i>Genes and Development</i> , 2004, 18, 3117-3130.	5.9	76
71	Characterization of B-type cyclins in the smut fungus <i>Ustilago maydis</i> : roles in morphogenesis and pathogenicity. <i>Journal of Cell Science</i> , 2004, 117, 487-506.	2.0	56
72	A member of the Fizzy-related family of APC activators is regulated by cAMP and is required at different stages of plant infection by <i>Ustilago maydis</i> . <i>Journal of Cell Science</i> , 2004, 117, 4143-4156.	2.0	20

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73	CandidaDB: a genome database for <i>Candida albicans</i> pathogenomics. <i>Nucleic Acids Research</i> , 2004, 33, D353-D357.	14.5	79
74	<i>Ustilago maydis</i> : how its biology relates to pathogenic development. <i>New Phytologist</i> , 2004, 164, 31-42.	7.3	138
75	Regulation of mating and pathogenic development in <i>Ustilago maydis</i> . <i>Current Opinion in Microbiology</i> , 2004, 7, 666-672.	5.1	142
76	The <i>crk1</i> gene encodes an <i>lme2</i> -related protein that is required for morphogenesis in the plant pathogen <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2003, 47, 729-743.	2.5	59
77	Pheromone-Induced G 2 Arrest in the Phytopathogenic Fungus <i>Ustilago maydis</i> . <i>Eukaryotic Cell</i> , 2003, 2, 494-500.	3.4	104
78	<i>Gpa2</i> , a G-Protein $\hat{\alpha}$ Subunit Required for Hyphal Development in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2002, 1, 865-874.	3.4	47
79	Site-specific targeting of exogenous DNA into the genome of <i>Candida albicans</i> using the FLP recombinase. <i>Molecular Genetics and Genomics</i> , 2002, 268, 418-424.	2.1	16
80	Dimorphism in fungal pathogens: <i>Candida albicans</i> and <i>Ustilago maydis</i> â€”similar inputs, different outputs. <i>Current Opinion in Microbiology</i> , 2001, 4, 214-221.	5.1	107
81	Identification of genes in the <i>bW/bE</i> regulatory cascade in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2001, 42, 1047-1063.	2.5	286
82	Identification of a target gene for the <i>bE-bW</i> homeodomain protein complex in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2000, 37, 54-66.	2.5	61
83	Evidence of an Unusually Long Operator for the <i>Fur</i> Repressor in the <i>Aerobactin</i> Promoter of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 24709-24714.	3.4	52
84	<i>Ustilago maydis</i> , the Causative Agent of Corn Smut Disease. , 2000, , 347-371.		36
85	The <i>IANtr</i> (<i>PtsN</i>) Protein of <i>Pseudomonas putida</i> Mediates the C Source Inhibition of the $\hat{\lambda}$,54-dependent <i>Pu</i> Promoter of the <i>TOL</i> Plasmid. <i>Journal of Biological Chemistry</i> , 1999, 274, 15562-15568.	3.4	99
86	Chromatin and transcription in <i>Saccharomyces cerevisiae</i> . <i>FEMS Microbiology Reviews</i> , 1999, 23, 503-523.	8.6	7
87	Phenotypic switching in <i>Candida albicans</i> is controlled by a <i>SIR2</i> gene. <i>EMBO Journal</i> , 1999, 18, 2580-2592.	7.8	129
88	Binding of the <i>Fur</i> (ferric uptake regulator) repressor of <i>Escherichia coli</i> to arrays of the <i>GATAAT</i> sequence. <i>Journal of Molecular Biology</i> , 1998, 283, 537-547.	4.2	177
89	The C-Terminal Domain of <i>Sin1</i> Interacts with the <i>SWI-SNF</i> Complex in Yeast. <i>Molecular and Cellular Biology</i> , 1998, 18, 4157-4164.	2.3	26
90	Mutations in Chromatin Components Suppress a Defect of <i>Gcn5</i> Protein in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1998, 18, 1049-1054.	2.3	39

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91	Coactivation in vitro of the sigma54-dependent promoter Pu of the TOL plasmid of <i>Pseudomonas putida</i> by HU and the mammalian HMG-1 protein. <i>Journal of Bacteriology</i> , 1997, 179, 2757-2760.	2.2	15
92	CLUES AND CONSEQUENCES OF DNA BENDING IN TRANSCRIPTION. <i>Annual Review of Microbiology</i> , 1997, 51, 593-628.	7.3	182
93	Genetic evidence of separate repressor and activator activities of the XylR regulator of the TOL plasmid, pWWO, of <i>Pseudomonas putida</i> . <i>Molecular Microbiology</i> , 1997, 23, 1221-1227.	2.5	25
94	VTR expression cassettes for engineering conditional phenotypes in <i>Pseudomonas</i> : activity of the Pu promoter of the TOL plasmid under limiting concentrations of the XylR activator protein. <i>Gene</i> , 1996, 172, 81-86.	2.2	36
95	Physical and Functional Analysis of the Prokaryotic Enhancer of the σ 54-promoters of the TOL Plasmid of <i>Pseudomonas putida</i> . <i>Journal of Molecular Biology</i> , 1996, 258, 562-574.	4.2	43
96	In Vitro Activities of an N-terminal Truncated Form of XylR, a σ 54-dependent Transcriptional Activator of <i>Pseudomonas putida</i> . <i>Journal of Molecular Biology</i> , 1996, 258, 575-587.	4.2	83
97	ATP Binding to the σ 54-Dependent Activator XylR Triggers a Protein Multimerization Cycle Catalyzed by UAS DNA. <i>Cell</i> , 1996, 86, 331-339.	28.9	98
98	Involvement of sigma54 in exponential silencing of the <i>Pseudomonas putida</i> TOL plasmid Pu promoter. <i>Molecular Microbiology</i> , 1996, 19, 7-17.	2.5	94
99	Regulatory noise in prokaryotic promoters: how bacteria learn to respond to novel environmental signals. <i>Molecular Microbiology</i> , 1996, 19, 1177-1184.	2.5	101
100	Identification of the Repressor Subdomain within the Signal Reception Module of the Prokaryotic Enhancer-binding Protein XylR of <i>Pseudomonas putida</i> . <i>Journal of Biological Chemistry</i> , 1996, 271, 7899-7902.	3.4	17
101	The amino-terminal domain of the prokaryotic enhancer-binding protein XylR is a specific intramolecular repressor.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 9392-9396.	7.1	67
102	Integration host factor suppresses promiscuous activation of the sigma 54-dependent promoter Pu of <i>Pseudomonas putida</i> .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 7277-7281.	7.1	50
103	Activation of the transcriptional regulator XylR of <i>Pseudomonas putida</i> by release of repression between functional domains. <i>Molecular Microbiology</i> , 1995, 16, 205-213.	2.5	139
104	Control of mating and development in <i>Ustilago maydis</i> . <i>Current Opinion in Genetics and Development</i> , 1995, 5, 559-564.	3.3	52
105	Multiallelic recognition: Nonself-dependent dimerization of the bE and bW homeodomain proteins in <i>ustilago maydis</i> . <i>Cell</i> , 1995, 81, 73-83.	28.9	268
106	Correlation between DNA Bending and Transcriptional Activation at a Plasmid Promoter. <i>Journal of Molecular Biology</i> , 1994, 241, 7-17.	4.2	34
107	Protein-induced bending as a transcriptional switch. <i>Science</i> , 1993, 260, 805-807.	12.6	83
108	A genetic system to study the in vivo role of transcriptional regulators in <i>Escherichia coli</i> . <i>Gene</i> , 1992, 116, 75-80.	2.2	8

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109	Purification and characterization of RepA, a protein involved in the copy number control of plasmid pLS1. Nucleic Acids Research, 1989, 17, 2405-2420.	14.5	53
110	Three regions in the DNA of plasmid pLS1 show sequence-directed static bending. Nucleic Acids Research, 1988, 16, 9113-9126.	14.5	28
111	Mode of Binding of the Fur Protein to Target DNA: Negative Regulation of Iron-Controlled Gene Expression. , 0, , 185-196.		13