## Wayne P Wahls

List of Publications by Year in descending order

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Version: 2024-02-01

41 papers 1,354 citations

16 h-index 36 g-index

44 all docs 44 docs citations

44 times ranked 1200 citing authors

#	Article	IF	CITATIONS
1	Molecular mechanisms for environmentally induced and evolutionarily rapid redistribution (plasticity) of meiotic recombination. Genetics, 2022, 220, .	2.9	11
2	Accurate and Sensitive Quantitation of the Dynamic Heat Shock Proteome Using Tandem Mass Tags. Journal of Proteome Research, 2020, 19, 1183-1195.	3.7	9
3	Opinion: The National Institutes of Health needs to better balance funding distributions among US institutions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13150-13154.	7.1	16
4	Diverse DNA Sequence Motifs Activate Meiotic Recombination Hotspots Through a Common Chromatin Remodeling Pathway. Genetics, 2019, 213, 789-803.	2.9	13
5	Targeted Forward Genetics: Population-Scale Analyses of Allele Replacements Spanning Thousands of Base Pairs in Fission Yeast. G3: Genes, Genomes, Genetics, 2019, 9, 4097-4106.	1.8	2
6	Chromatin-mediated regulators of meiotic recombination revealed by proteomics of a recombination hotspot. Epigenetics and Chromatin, 2018, 11, 64.	3.9	20
7	The NIH must reduce disparities in funding to maximize its return on investments from taxpayers. ELife, 2018, 7, .	6.0	23
8	In Vivo Metabolic Tracing Demonstrates the Siteâ€Specific Contribution of Hepatic Ethanol Metabolism to Histone Acetylation. Alcoholism: Clinical and Experimental Research, 2018, 42, 1909-1923.	2.4	17
9	NIH's ineffective funding policies. Science, 2017, 356, 1132-1133.	12.6	5
10	Biases in grant proposal success rates, funding rates and award sizes affect the geographical distribution of funding for biomedical research. PeerJ, 2016, 4, e1917.	2.0	19
10		2.0	19
	distribution of funding for biomedical research. Peerl, 2016, 4, e1917.  Nonsense codon suppression in fission yeast due to mutations of tRNASer.11 and translation release		19 4 71
11	Nonsense codon suppression in fission yeast due to mutations of tRNASer.11 and translation release factor Sup35 (eRF3). Current Genetics, 2015, 61, 165-173.  A CRISPR-based approach for proteomic analysis of a single genomic locus. Epigenetics, 2014, 9,	1.7	4
11 12	Nonsense codon suppression in fission yeast due to mutations of tRNASer.11 and translation release factor Sup35 (eRF3). Current Genetics, 2015, 61, 165-173.  A CRISPR-based approach for proteomic analysis of a single genomic locus. Epigenetics, 2014, 9, 1207-1211.  Binding of the transcription factor Atf1 to promoters serves as a barrier to phase nucleosome arrays	2.7	71
11 12 13	Nonsense codon suppression in fission yeast due to mutations of tRNASer.11 and translation release factor Sup35 (eRF3). Current Genetics, 2015, 61, 165-173.  A CRISPR-based approach for proteomic analysis of a single genomic locus. Epigenetics, 2014, 9, 1207-1211.  Binding of the transcription factor Atf1 to promoters serves as a barrier to phase nucleosome arrays and avoid cryptic transcription. Nucleic Acids Research, 2014, 42, 10351-10359.  Rapid, efficient and precise allele replacement in the fission yeast SchizosaccharomycesÂpombe.	1.7 2.7 14.5	4 71 11
11 12 13	Nonsense codon suppression in fission yeast due to mutations of tRNASer.11 and translation release factor Sup35 (eRF3). Current Genetics, 2015, 61, 165-173.  A CRISPR-based approach for proteomic analysis of a single genomic locus. Epigenetics, 2014, 9, 1207-1211.  Binding of the transcription factor Atf1 to promoters serves as a barrier to phase nucleosome arrays and avoid cryptic transcription. Nucleic Acids Research, 2014, 42, 10351-10359.  Rapid, efficient and precise allele replacement in the fission yeast SchizosaccharomycesÂpombe. Current Genetics, 2014, 60, 109-119.  A Stress-Activated, p38 Mitogen-Activated Protein Kinase–ATF/CREB Pathway Regulates Posttranscriptional, Sequence-Dependent Decay of Target RNAs. Molecular and Cellular Biology, 2013,	1.7 2.7 14.5	4 71 11 24
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19	Meiotic recombination protein Rec12: functional conservation, crossover homeostasis and early crossover/non-crossover decision. Nucleic Acids Research, 2011, 39, 1460-1472.	14.5	23
20	Discrete DNA sites regulate global distribution of meiotic recombination. Trends in Genetics, 2010, 26, 202-208.	6.7	42
21	Phosphorylation-Independent Regulation of Atf1-Promoted Meiotic Recombination by Stress-Activated, p38 Kinase Spc1 of Fission Yeast. PLoS ONE, 2009, 4, e5533.	2.5	15
22	Regulation of meiotic recombination by a multifunctional ATF/CREB protein. FASEB Journal, 2009, 23, 656.1.	0.5	2
23	Lowâ€copy episomal vector pFY20 and highâ€saturation coverage genomic libraries for the fission yeast <i>Schizosaccharomyces pombe</i> . Yeast, 2008, 25, 643-650.	1.7	8
24	Distinct regions of ATF/CREB proteins Atf1 and Pcr1 control recombination hotspot ade6-M26 and the osmotic stress response. Nucleic Acids Research, 2008, 36, 2838-2851.	14.5	40
25	Meiotic Recombination Hotspots of Fission Yeast Are Directed to Loci that Express Non-Coding RNA. PLoS ONE, 2008, 3, e2887.	2.5	32
26	Distinct domains of Atf1â€Pcr1 heterodimer activate and repress hotspot meiotic recombination and osmoregulation. FASEB Journal, 2007, 21, A292.	0.5	0
27	A DNA binding motif of meiotic recombinase Rec12 (Spo11) defined by essential glycine-202, and persistence of Rec12 protein after completion of recombination. Gene, 2005, 356, 77-84.	2.2	8
28	Meiotic chromosome segregation mutants identified by insertional mutagenesis of fission yeast Schizosaccharomyces pombe; tandem-repeat, single-site integrations. Nucleic Acids Research, 2004, 32, 4400-4410.	14.5	13
29	Atf1-Pcr1-M26 Complex Links Stress-activated MAPK and cAMP-dependent Protein Kinase Pathways via Chromatin Remodeling of cgs2+. Journal of Biological Chemistry, 2004, 279, 50857-50863.	3.4	41
30	Roles of histone acetylation and chromatin remodeling factor in a meiotic recombination hotspot. EMBO Journal, 2004, 23, 1792-1803.	7.8	146
31	Purification, folding, and characterization of Rec12 (Spo11) meiotic recombinase of fission yeast. Protein Expression and Purification, 2004, 38, 136-144.	1.3	15
32	Distinct functions of S. pombe Rec12 (Spo11) protein and Rec12-dependent crossover recombination (chiasmata) in meiosis I; and a requirement for Rec12 in meiosis II. Cell & Chromosome, 2002, 1, 1.	2.0	62
33	High-efficiency gene targeting inSchizosaccharomyces pombe using a modular, PCR-based approach with long tracts of flanking homology. Yeast, 1999, 15, 1419-1427.	1.7	167
34	High-efficiency gene targeting in Schizosaccharomyces pombe using a modular, PCR-based approach with long tracts of flanking homology., 1999, 15, 1419.		3
35	Centromere Mapping Functions for Aneuploid Meiotic Products: Analysis of rec8, rec10 and rec11 Mutants of the Fission Yeast Schizosaccharomyces pombe. Genetics, 1999, 153, 49-55.	2.9	18
36	Meiotic Chromosome Dynamics Dependent Upon the rec8+, rec10+ and rec11+ Genes of the Fission Yeast Schizosaccharomyces pombe. Genetics, 1999, 153, 57-68.	2.9	59

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37	Recombination hotspot activity of hypervariable minisatellite DNA requires minisatellite DNA binding proteins. Somatic Cell and Molecular Genetics, 1998, 24, 41-51.	0.7	8
38	Regulation of the Mts1-Mts2-Dependent <i>ade6-M26</i> Meiotic Recombination Hot Spot and Developmental Decisions by the Spc1 Mitogen-Activated Protein Kinase of Fission Yeast. Molecular and Cellular Biology, 1998, 18, 7575-7583.	2.3	50
39	Two hypervarlable minisatellite DNA binding proteins. Nucleic Acids Research, 1991, 19, 3269-3274.	14.5	52
40	Hypervariable minisatellite DNA is a hotspot for homologous recombination in human cells. Cell, 1990, 60, 95-103.	28.9	237
41	Adaptive Control of the Meiotic Recombination Landscape by DNA Site-dependent Hotspots With Implications for Evolution. Frontiers in Genetics, 0, 13, .	2.3	3