Mark C Hall

List of Publications by Year in descending order

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48 2,409 26 47 papers citations h-index g-index

51 51 51 51 2672

times ranked

docs citations

all docs

citing authors

#	Article	IF	CITATIONS
1	Phosphorylation of RNA polymerase II CTD regulates H3 methylation in yeast. Genes and Development, 2003, 17, 654-663.	5.9	363
2	Helicase motifs: the engine that powers DNA unwinding. Molecular Microbiology, 1999, 34, 867-877.	2.5	296
3	The Escherichia coliMutL Protein Physically Interacts with MutH and Stimulates the MutH-associated Endonuclease Activity. Journal of Biological Chemistry, 1999, 274, 1306-1312.	3.4	143
4	Evidence for a physical interaction between the Escherichia coli methyl-directed mismatch repair proteins MutL and UvrD. EMBO Journal, 1998, 17, 1535-1541.	7.8	135
5	Related Arabidopsis Serine Carboxypeptidase-Like Sinapoylglucose Acyltransferases Display Distinct But Overlapping Substrate Specificities. Plant Physiology, 2007, 144, 1986-1999.	4.8	121
6	The Cdk/Cdc14 Module Controls Activation of the Yen1 Holliday Junction Resolvase to Promote Genome Stability. Molecular Cell, 2014, 54, 80-93.	9.7	91
7	Escherichia coli DNA Helicase II Is Active as a Monomer. Journal of Biological Chemistry, 1999, 274, 12488-12498.	3.4	89
8	High affinity cooperative DNA binding by the yeast Mlh1-Pms1 heterodimer 1 1Edited by M. Belfort. Journal of Molecular Biology, 2001, 312, 637-647.	4.2	89
9	Identification of In-Gel Digested Proteins by Complementary Peptide Mass Fingerprinting and Tandem Mass Spectrometry Data Obtained on an Electrospray Ionization Quadrupole Time-of-Flight Mass Spectrometer. Analytical Chemistry, 2000, 72, 1163-1168.	6.5	78
10	Cdc14 Phosphatases Preferentially Dephosphorylate a Subset of Cyclin-dependent kinase (Cdk) Sites Containing Phosphoserine. Journal of Biological Chemistry, 2012, 287, 1662-1669.	3.4	76
11	Dependence of Chs2 ER export on dephosphorylation by cytoplasmic Cdc14 ensures that septum formation follows mitosis. Molecular Biology of the Cell, 2012, 23, 45-58.	2.1	61
12	Differential ATP Binding and Intrinsic ATP Hydrolysis by Amino-terminal Domains of the Yeast Mlh1 and Pms1 Proteins. Journal of Biological Chemistry, 2002, 277, 3673-3679.	3.4	58
13	A Proteomic Strategy for Global Analysis of Plant Protein Complexes. Plant Cell, 2014, 26, 3867-3882.	6.6	55
14	Mnd2 and Swm1 Are Core Subunits of the Saccharomyces cerevisiae Anaphase-promoting Complex. Journal of Biological Chemistry, 2003, 278, 16698-16705.	3.4	52
15	DNA binding by yeast Mlh1 and Pms1: implications for DNA mismatch repair. Nucleic Acids Research, 2003, 31, 2025-2034.	14.5	50
16	Acm1 Is a Negative Regulator of the Cdh1-Dependent Anaphase-Promoting Complex/Cyclosome in Budding Yeast. Molecular and Cellular Biology, 2006, 26, 9162-9176.	2.3	50
17	Inactivation of DNA Mismatch Repair by Increased Expression of Yeast MLH1. Molecular and Cellular Biology, 2001, 21, 940-951.	2.3	48
18	<pre><scp><i>FgCDC</i></scp><i>14</i> regulates cytokinesis, morphogenesis, and pathogenesis in <scp><i>F</i></scp><i>usarium graminearum</i>. Molecular Microbiology, 2015, 98, 770-786.</pre>	2.5	45

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19	DNA Binding Properties of the Yeast Msh2-Msh6 and Mlh1-Pms1 Heterodimers. Biological Chemistry, 2002, 383, 969-75.	2.5	43
20	Site-directed mutations in motif VI of Escherichia coli DNA helicase II result in multiple biochemical defects: evidence for the involvement of motif VI in the coupling of ATPase and DNA binding activities via conformational changes. Journal of Molecular Biology, 1998, 277, 257-271.	4.2	39
21	Cdc28 and Cdc14 Control Stability of the Anaphase-promoting Complex Inhibitor Acm1. Journal of Biological Chemistry, 2008, 283, 10396-10407.	3.4	35
22	Multi-Kinase Phosphorylation of the APC/C Activator Cdh1 Revealed by Mass Spectrometry. Cell Cycle, 2004, 3, 1278-1284.	2.6	34
23	Dephosphorylation of Iqg1 by Cdc14 regulates cytokinesis in budding yeast. Molecular Biology of the Cell, 2015, 26, 2913-2926.	2.1	34
24	Unique D Box and KEN Box Sequences Limit Ubiquitination of Acm1 and Promote Pseudosubstrate Inhibition of the Anaphase-promoting Complex. Journal of Biological Chemistry, 2008, 283, 23701-23710.	3.4	33
25	Mutation of a Highly Conserved Arginine in Motif IV of Escherichia coli DNA Helicase II Results in an ATP-binding Defect. Journal of Biological Chemistry, 1997, 272, 18614-18620.	3.4	30
26	Phosphorylation Assay Based on Multifunctionalized Soluble Nanopolymer. Analytical Chemistry, 2011, 83, 2767-2774.	6.5	30
27	A Novel Sterol-Signaling Pathway Governs Azole Antifungal Drug Resistance and Hypoxic Gene Repression in <i>Saccharomyces cerevisiae</i> . Genetics, 2018, 208, 1037-1055.	2.9	29
28	Purification of Eukaryotic MutL Homologs from Saccharomyces cerevisiae Using Self-Cleaving Affinity Technology. Protein Expression and Purification, 2001, 21, 333-342.	1.3	27
29	Re-examining the role of Cdc14 phosphatase in reversal of Cdk phosphorylation during mitotic exit. Journal of Cell Science, 2017, 130, 2673-2681.	2.0	20
30	Drosophila Activated Cdc42 Kinase Has an Anti-Apoptotic Function. PLoS Genetics, 2012, 8, e1002725.	3.5	16
31	<i>Drosophila</i> Vap-33 Is Required for Axonal Localization of Dscam Isoforms. Journal of Neuroscience, 2012, 32, 17241-17250.	3.6	15
32	Time-Dependent Activation of Phox2a by the Cyclic AMP Pathway Modulates Onset and Duration of p27 ^{Kip1} Transcription. Molecular and Cellular Biology, 2009, 29, 4878-4890.	2.3	14
33	Substrate Recognition by the Cdh1 Destruction Box Receptor Is a General Requirement for APC/CCdh1-mediated Proteolysis. Journal of Biological Chemistry, 2016, 291, 15564-15574.	3.4	13
34	A general strategy for studying multisite protein phosphorylation using label-free selected reaction monitoring mass spectrometry. Analytical Biochemistry, 2011, 418, 267-275.	2.4	12
35	Specificity of HCPTP variants toward EphA2 tyrosines by quantitative selected reaction monitoring. Protein Science, 2011, 20, 1172-1181.	7.6	11
36	A Multiple Reaction Monitoring (MRM) Method to Detect Bcr-Abl Kinase Activity in CML Using a Peptide Biosensor. PLoS ONE, 2013, 8, e56627.	2.5	11

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37	Use of selected reaction monitoring data for labelâ€free quantification of protein modification stoichiometry. Proteomics, 2010, 10, 4301-4305.	2.2	10
38	The pseudosubstrate inhibitor Acm1 inhibits the anaphase-promoting complex/cyclosome by combining high-affinity activator binding with disruption of Doc1/Apc10 function. Journal of Biological Chemistry, 2019, 294, 17249-17261.	3.4	8
39	Scientific Research Identity Development Need Not Wait Until College: Examining the Motivational Impact of a Pre-college Authentic Research Experience. Research in Science Education, 2022, 52, 1481-1496.	2.3	8
40	Acm1 contributes to nuclear positioning by inhibiting Cdh1-substrate interactions. Cell Cycle, 2012, 11, 384-394.	2.6	7
41	Conservation of Cdc14 phosphatase specificity in plant fungal pathogens: implications for antifungal development. Scientific Reports, 2020, 10, 12073.	3.3	6
42	Discovering the N-Terminal Methylome by Repurposing of Proteomic Datasets. Journal of Proteome Research, 2021, 20, 4231-4247.	3.7	6
43	Timely Activation of Budding Yeast APCCdh1 Involves Degradation of Its Inhibitor, Acm1, by an Unconventional Proteolytic Mechanism. PLoS ONE, 2014, 9, e103517.	2.5	5
44	A Substrate Trapping Method for Identification of Direct Cdc14 Phosphatase Targets. Methods in Molecular Biology, 2017, 1505, 119-132.	0.9	4
45	Proteomics Modifies Our Understanding of Cell Cycle Complexity. Science Signaling, 2010, 3, pe4.	3.6	3
46	Multiplexed Imaging of Protein Phosphorylation on Membranes Based on Ti ^{IV} Functionalized Nanopolymers. ChemBioChem, 2016, 17, 900-903.	2.6	3
47	Measuring Activity and Specificity of Protein Phosphatases. Methods in Molecular Biology, 2016, 1342, 221-235.	0.9	3
48	Phosphatase and Kinase Substrate Profiling with Pooled and. Methods in Molecular Biology, 2021, 2329, 51-70.	0.9	0