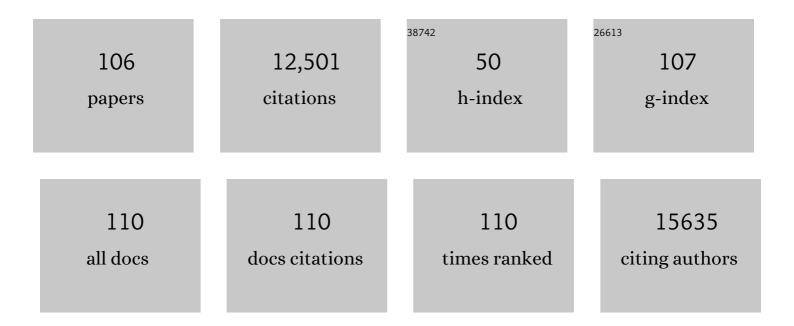
W Hayes Mcdonald

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	DDR1 contributes to kidney inflammation and fibrosis by promoting the phosphorylation of BCR and STAT3. JCI Insight, 2022, 7, .	5.0	24
2	Structure and activation mechanism of the yeast RNA Pol II CTD kinase CTDK-1 complex. Proceedings of the United States of America, 2021, 118, .	7.1	6
3	Delineation of the pH-Responsive Regulon Controlled by the Helicobacter pylori ArsRS Two-Component System. Infection and Immunity, 2021, 89, .	2.2	17
4	Therapeutic alphavirus cross-reactive E1 human antibodies inhibit viral egress. Cell, 2021, 184, 4430-4446.e22.	28.9	25
5	Specificities of Gβγ subunits for the SNARE complex before and after stimulation of α _{2a} -adrenergic receptors. Science Signaling, 2021, 14, eabc4970.	3.6	2
6	The 15-Amino Acid Repeat Region of Adenomatous Polyposis Coli Is Intrinsically Disordered and Retains Conformational Flexibility upon Binding β-Catenin. Biochemistry, 2020, 59, 4039-4050.	2.5	5
7	Discovery of Widespread Host Protein Interactions with the Pre-replicated Genome of CHIKV Using VIR-CLASP. Molecular Cell, 2020, 78, 624-640.e7.	9.7	64
8	Bacterial Energetic Requirements for Helicobacter pylori Cag Type IV Secretion System-Dependent Alterations in Gastric Epithelial Cells. Infection and Immunity, 2020, 88, .	2.2	22
9	Effect of environmental salt concentration on the Helicobacter pylori exoproteome. Journal of Proteomics, 2019, 202, 103374.	2.4	14
10	The in vivo specificity of synaptic Gβ and Gγ subunits to the α2a adrenergic receptor at CNS synapses. Scientific Reports, 2019, 9, 1718.	3.3	17
11	Novel Method for Noninvasive Sampling of the Distal Airspace in Acute Respiratory Distress Syndrome. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1027-1035.	5.6	35
12	Exocyst dynamics during vesicle tethering and fusion. Nature Communications, 2018, 9, 5140.	12.8	96
13	Negative regulation of <i>Candida glabrata</i> Pdr1 by the deubiquitinase subunit Bre5 occurs in a ubiquitin independent manner. Molecular Microbiology, 2018, 110, 309-323.	2.5	9
14	Chromosomal abnormalities and molecular landscape of metastasizing mucinous salivary adenocarcinoma. Oral Oncology, 2017, 66, 38-45.	1.5	11
15	Quantitative Multiple-Reaction Monitoring Proteomic Analysis of GÎ ² and GÎ ³ Subunits in C57Bl6/J Brain Synaptosomes. Biochemistry, 2017, 56, 5405-5416.	2.5	14
16	Ubiquitin turnover and endocytic trafficking in yeast are regulated by Ser57 phosphorylation of ubiquitin. ELife, 2017, 6, .	6.0	29
17	Accumulation of isolevuglandin-modified protein in normal and fibrotic lung. Scientific Reports, 2016, 6, 24919.	3.3	21
18	Molecular and Structural Analysis of the Helicobacter pylori <i>cag</i> Type IV Secretion System Core Complex. MBio, 2016, 7, e02001-15.	4.1	102

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19	Antagonistic roles for the ubiquitin ligase Asr1 and the ubiquitin-specific protease Ubp3 in subtelomeric gene silencing. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1309-1314.	7.1	6
20	Binding of the Covalent Flavin Assembly Factor to the Flavoprotein Subunit of Complex II. Journal of Biological Chemistry, 2016, 291, 2904-2916.	3.4	18
21	LMO2 Oncoprotein Stability in T-Cell Leukemia Requires Direct LDB1 Binding. Molecular and Cellular Biology, 2016, 36, 488-506.	2.3	9
22	Growth phase-dependent composition of the Helicobacter pylori exoproteome. Journal of Proteomics, 2016, 130, 94-107.	2.4	22
23	Supporting data for analysis of the Helicobacter pylori exoproteome. Data in Brief, 2015, 5, 560-563.	1.0	3
24	Alteration of the <i>Helicobacter pylori</i> membrane proteome in response to changes in environmental salt concentration. Proteomics - Clinical Applications, 2015, 9, 1021-1034.	1.6	34
25	Iron Toxicity in the Retina Requires Alu RNA and the NLRP3 Inflammasome. Cell Reports, 2015, 11, 1686-1693.	6.4	78
26	P-REX1 creates a positive feedback loop to activate growth factor receptor, PI3K/AKT and MEK/ERK signaling in breast cancer. Oncogene, 2015, 34, 3968-3976.	5.9	76
27	A unique covalent bond in basement membrane is a primordial innovation for tissue evolution. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 331-336.	7.1	138
28	Short Forms of Ste20-related Proline/Alanine-rich Kinase (SPAK) in the Kidney Are Created by Aspartyl Aminopeptidase (Dnpep)-mediated Proteolytic Cleavage. Journal of Biological Chemistry, 2014, 289, 29273-29284.	3.4	17
29	Proteome Informatics Research Group (iPRG)_2012: A Study on Detecting Modified Peptides in a Complex Mixture. Molecular and Cellular Proteomics, 2014, 13, 360-371.	3.8	20
30	Sepp1UF forms are N-terminal selenoprotein P truncations that have peroxidase activity when coupled with thioredoxin reductase-1. Free Radical Biology and Medicine, 2014, 69, 67-76.	2.9	37
31	Shotgun proteomics: Identification of unique protein profiles of apoptotic bodies from biliary epithelial cells. Hepatology, 2014, 60, 1314-1323.	7.3	68
32	Analysis of Surface-Exposed Outer Membrane Proteins in Helicobacter pylori. Journal of Bacteriology, 2014, 196, 2455-2471.	2.2	65
33	Identification of Proteins at Active, Stalled, and Collapsed Replication Forks Using Isolation of Proteins on Nascent DNA (iPOND) Coupled with Mass Spectrometry. Journal of Biological Chemistry, 2013, 288, 31458-31467.	3.4	202
34	<i>Staphylococcus aureus</i> LukAB cytotoxin kills human neutrophils by targeting the CD11b subunit of the integrin Mac-1. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10794-10799.	7.1	180
35	Global Phosphotyrosine Proteomics Identifies PKCδas a Marker of Responsiveness to Src Inhibition in Colorectal Cancer. PLoS ONE, 2013, 8, e80207.	2.5	15
36	Abstract PR05: P-REX1 creates a positive feedback loop to activate growth factor receptor/PI3K		0

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37	Dnt1 acts as a mitotic inhibitor of the spindle checkpoint protein dma1 in fission yeast. Molecular Biology of the Cell, 2012, 23, 3348-3356.	2.1	10
38	Obesity and altered glucose metabolism impact HDL composition in CETP transgenic mice: a role for ovarian hormones. Journal of Lipid Research, 2012, 53, 379-389.	4.2	34
39	Long Isoform Mouse Selenoprotein P (Sepp1) Supplies Rat Myoblast L8 Cells with Selenium via Endocytosis Mediated by Heparin Binding Properties and Apolipoprotein E Receptor-2 (ApoER2). Journal of Biological Chemistry, 2012, 287, 28717-28726.	3.4	42
40	Electrophilic Adduction of Ubiquitin Activating Enzyme E1 by <i>N</i> , <i>N</i> .Diethyldithiocarbamate Inhibits Ubiquitin Activation and Is Accompanied by Striatal Injury in the Rat. Chemical Research in Toxicology, 2012, 25, 2310-2321.	3.3	14
41	The Evolutionary Imprint of Domestication on Genome Variation and Function of the Filamentous Fungus Aspergillus oryzae. Current Biology, 2012, 22, 1403-1409.	3.9	177
42	ApoER2â€Mediated Endocytosis of Longâ€Isoform Selenoprotein P (Sepp1) Supplies Skeletal Muscle Cells with Selenium. FASEB Journal, 2012, 26, 241.4.	0.5	0
43	Glucose Autoxidation Induces Functional Damage to Proteins via Modification of Critical Arginine Residues. Biochemistry, 2011, 50, 6102-6112.	2.5	51
44	Azospirillum Genomes Reveal Transition of Bacteria from Aquatic to Terrestrial Environments. PLoS Genetics, 2011, 7, e1002430.	3.5	191
45	Bacillus cereus Phosphopentomutase Is an Alkaline Phosphatase Family Member That Exhibits an Altered Entry Point into the Catalytic Cycle. Journal of Biological Chemistry, 2011, 286, 8043-8054.	3.4	34
46	Geometric Restraint Drives On- and Off-pathway Catalysis by the Escherichia coli Menaquinol:Fumarate Reductase. Journal of Biological Chemistry, 2011, 286, 3047-3056.	3.4	20
47	The Novel Chemical Entity YTR107 Inhibits Recruitment of Nucleophosmin to Sites of DNA Damage, Suppressing Repair of DNA Double-Strand Breaks and Enhancing Radiosensitization. Clinical Cancer Research, 2011, 17, 6490-6499.	7.0	23
48	Helicobacter pylori Exploits a Unique Repertoire of Type IV Secretion System Components for Pilus Assembly at the Bacteria-Host Cell Interface. PLoS Pathogens, 2011, 7, e1002237.	4.7	144
49	Characterization of the MDSC Proteome Associated with Metastatic Murine Mammary Tumors Using Label-Free Mass Spectrometry and Shotgun Proteomics. PLoS ONE, 2011, 6, e22446.	2.5	35
50	<i>Staphylococcus aureus</i> Fur Regulates the Expression of Virulence Factors That Contribute to the Pathogenesis of Pneumonia. Infection and Immunity, 2010, 78, 1618-1628.	2.2	127
51	Dephosphorylation of F-BAR Protein Cdc15 Modulates Its Conformation and Stimulates Its Scaffolding Activity at the Cell Division Site. Molecular Cell, 2010, 39, 86-99.	9.7	118
52	Sirt3-Mediated Deacetylation of Evolutionarily Conserved Lysine 122 Regulates MnSOD Activity in Response to Stress. Molecular Cell, 2010, 40, 893-904.	9.7	794
53	An analysis pipeline for the inference of protein-protein interaction networks. International Journal of Data Mining and Bioinformatics, 2009, 3, 409.	0.1	3
54	Modulation of the Structure, Catalytic Activity, and Fidelity of African Swine Fever Virus DNA Polymerase X by a Reversible Disulfide Switch. Journal of Biological Chemistry, 2009, 284, 18434-18444.	3.4	11

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55	Evaluation of Affinity-Tagged Protein Expression Strategies Using Local and Global Isotope Ratio Measurements. Journal of Proteome Research, 2009, 8, 3675-3688.	3.7	18
56	A General System for Studying Proteinâ^'Protein Interactions in Gram-Negative Bacteria. Journal of Proteome Research, 2008, 7, 3319-3328.	3.7	24
57	The SBF- and MBF-associated Protein Msa1 Is Required for Proper Timing of G1-specific Transcription in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2008, 283, 6040-6049.	3.4	27
58	The Clp1/Cdc14 phosphatase contributes to the robustness of cytokinesis by association with anillin-related Mid1. Journal of Cell Biology, 2008, 181, 79-88.	5.2	88
59	Cross-species Global Proteomics Reveals Conserved and Unique Processes in Phytophthora sojae and Phytophthora ramorum. Molecular and Cellular Proteomics, 2008, 7, 1501-1516.	3.8	42
60	Statistically Inferring Proteinâ ^{~,} Protein Associations with Affinity Isolation LCâ ^{~,} MS/MS Assays. Journal of Proteome Research, 2007, 6, 3788-3795.	3.7	11
61	Dual-tagging system for the affinity purification of mammalian protein complexes. BioTechniques, 2007, 43, 296-302.	1.8	27
62	ProRata:Â A Quantitative Proteomics Program for Accurate Protein Abundance Ratio Estimation with Confidence Interval Evaluation. Analytical Chemistry, 2006, 78, 7121-7131.	6.5	97
63	Robust Estimation of Peptide Abundance Ratios and Rigorous Scoring of Their Variability and Bias in Quantitative Shotgun Proteomics. Analytical Chemistry, 2006, 78, 7110-7120.	6.5	40
64	Expressed Peptide Tags:Â An Additional Layer of Data for Genome Annotation. Journal of Proteome Research, 2006, 5, 3048-3058.	3.7	32
65	Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. Science, 2006, 313, 1261-1266.	12.6	1,059
66	Determination and Comparison of the Baseline Proteomes of the Versatile MicrobeRhodopseudomonaspalustrisunder Its Major Metabolic States. Journal of Proteome Research, 2006, 5, 287-298.	3.7	69
67	Phospho-Regulation of the Cdc14/Clp1 Phosphatase Delays Late Mitotic Events in S. pombe. Developmental Cell, 2006, 11, 423-430.	7.0	51
68	Constraining G1-Specific Transcription to Late G1 Phase: The MBF-Associated Corepressor Nrm1 Acts via Negative Feedback. Molecular Cell, 2006, 23, 483-496.	9.7	121
69	Protein Disulfide Isomerase Serves as a Molecular Chaperone to Maintain Estrogen Receptor α Structure and Function. Molecular Endocrinology, 2006, 20, 1982-1995.	3.7	70
70	Cip1 and Cip2 Are Novel RNA-Recognition-Motif Proteins That Counteract Csx1 Function during Oxidative Stress. Molecular Biology of the Cell, 2006, 17, 1176-1183.	2.1	21
71	Dynamics of the peroxisomal import cycle of PpPex20p: Ubiquitin-dependent localization and regulation. Journal of Cell Biology, 2006, 172, 67-78.	5.2	115
72	Ppc89 Links Multiple Proteins, Including the Septation Initiation Network, to the Core of the Fission Yeast Spindle-Pole Body. Molecular Biology of the Cell, 2006, 17, 3793-3805.	2.1	51

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73	Phosphorylation of Rad55 on Serines 2, 8, and 14 Is Required for Efficient Homologous Recombination in the Recovery of Stalled Replication Forks. Molecular and Cellular Biology, 2006, 26, 8396-8409.	2.3	79
74	The Nse5-Nse6 Dimer Mediates DNA Repair Roles of the Smc5-Smc6 Complex. Molecular and Cellular Biology, 2006, 26, 1617-1630.	2.3	128
75	MS2Grouper: Group assessment and synthetic replacement of duplicate proteomic tandem mass spectra. Journal of the American Society for Mass Spectrometry, 2005, 16, 1250-1261.	2.8	58
76	Analysis of the Role of Phosphorylation in Fission Yeast Cdc13p/CyclinB Function. Journal of Biological Chemistry, 2005, 280, 14591-14596.	3.4	3
77	Tea4p Links Microtubule Plus Ends with the Formin For3p in the Establishment of Cell Polarity. Developmental Cell, 2005, 8, 479-491.	7.0	201
78	Automatic Quality Assessment of Peptide Tandem Mass Spectra. Bioinformatics, 2004, 20, i49-i54.	4.1	181
79	Swi1 and Swi3 Are Components of a Replication Fork Protection Complex in Fission Yeast. Molecular and Cellular Biology, 2004, 24, 8342-8355.	2.3	194
80	Applicability of Tandem Affinity Purification MudPIT to Pathway Proteomics in Yeast. Molecular and Cellular Proteomics, 2004, 3, 226-237.	3.8	130
81	Nse1, Nse2, and a Novel Subunit of the Smc5-Smc6 Complex, Nse3, Play a Crucial Role in Meiosis. Molecular Biology of the Cell, 2004, 15, 4866-4876.	2.1	118
82	Carcinoma and stromal enzyme activity profiles associated with breast tumor growth in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13756-13761.	7.1	174
83	Cell Cycle-dependent Phosphorylation of the DNA Polymerase Epsilon Subunit, Dpb2, by the Cdc28 Cyclin-dependent Protein Kinase. Journal of Biological Chemistry, 2004, 279, 14245-14255.	3.4	30
84	Proteolysis-independent regulation of the transcription factor Met4 by a single Lys 48-linked ubiquitin chain. Nature Cell Biology, 2004, 6, 634-641.	10.3	146
85	MS1, MS2, and SQT—three unified, compact, and easily parsed file formats for the storage of shotgun proteomic spectra and identifications. Rapid Communications in Mass Spectrometry, 2004, 18, 2162-2168.	1.5	350
86	Cln3 Activates G1-Specific Transcription via Phosphorylation of the SBF Bound Repressor Whi5. Cell, 2004, 117, 887-898.	28.9	373
87	RNA-binding protein Csx1 mediates global control of gene expression in response to oxidative stress. EMBO Journal, 2003, 22, 6256-6266.	7.8	64
88	Assigning Function to Yeast Proteins by Integration of Technologies. Molecular Cell, 2003, 12, 1353-1365.	9.7	248
89	Proteomic Characterization of the Chlamydomonas reinhardtii Chloroplast Ribosome. Journal of Biological Chemistry, 2003, 278, 33774-33785.	3.4	108
90	Novel Essential DNA Repair Proteins Nse1 and Nse2 Are Subunits of the Fission Yeast Smc5-Smc6 Complex. Journal of Biological Chemistry, 2003, 278, 45460-45467.	3.4	106

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91	Replication Checkpoint Kinase Cds1 Regulates Recombinational Repair Protein Rad60. Molecular and Cellular Biology, 2003, 23, 5939-5946.	2.3	86
92	Shotgun proteomics: integrating technologies to answer biological questions. Current Opinion in Molecular Therapeutics, 2003, 5, 302-9.	2.8	53
93	Proteomic Characterization of the Small Subunit of Chlamydomonas reinhardtii Chloroplast Ribosome. Plant Cell, 2002, 14, 2957-2974.	6.6	78
94	Proteomics Analysis Reveals Stable Multiprotein Complexes in Both Fission and Budding Yeasts Containing Myb-Related Cdc5p/Cef1p, Novel Pre-mRNA Splicing Factors, and snRNAs. Molecular and Cellular Biology, 2002, 22, 2011-2024.	2.3	193
95	Charting the Protein Complexome in Yeast by Mass Spectrometry. Molecular and Cellular Proteomics, 2002, 1, 3-10.	3.8	36
96	Shotgun identification of protein modifications from protein complexes and lens tissue. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7900-7905.	7.1	571
97	Role of Rpn11 Metalloprotease in Deubiquitination and Degradation by the 26S Proteasome. Science, 2002, 298, 611-615.	12.6	919
98	DTASelect and Contrast:Â Tools for Assembling and Comparing Protein Identifications from Shotgun Proteomics. Journal of Proteome Research, 2002, 1, 21-26.	3.7	1,327
99	Cid13 Is a Cytoplasmic Poly(A) Polymerase that Regulates Ribonucleotide Reductase mRNA. Cell, 2002, 109, 563-573.	28.9	130
100	Shotgun Proteomics and Biomarker Discovery. Disease Markers, 2002, 18, 99-105.	1.3	299
101	Mus81-Eme1 Are Essential Components of a Holliday Junction Resolvase. Cell, 2001, 107, 537-548.	28.9	501
102	Vectors and gene targeting modules for tandem affinity purification inSchizosaccharomyces pombe. Yeast, 2001, 18, 657-662.	1.7	139
103	Proteomic Tools for Cell Biology. Traffic, 2000, 1, 747-754.	2.7	42
104	Use of High Specific Activity StarFireâ,,¢ Oligonucleotide Probes to Visualize Low-Abundance Pre-mRNA Splicing Intermediates in S. pombe. BioTechniques, 2000, 29, 892-897.	1.8	13
105	Isolation of an essential Schizosaccharomyces pombe gene, prp31+, that links splicing and meiosis. Nucleic Acids Research, 2000, 28, 2214-2220.	14.5	12
106	Myb-Related Fission Yeast cdc5p Is a Component of a 40S snRNP-Containing Complex and Is Essential for Pre-mRNA Splicing. Molecular and Cellular Biology, 1999, 19, 5352-5362.	2.3	114