

Jason E Mcdermott

List of Publications by Year in descending order

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128
papers

8,603
citations

76326

40
h-index

51608

86
g-index

140
all docs

140
docs citations

140
times ranked

14291
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	5.6	808
2	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
3	Co-expression of CD39 and CD103 identifies tumor-reactive CD8 T cells in human solid tumors. <i>Nature Communications</i> , 2018, 9, 2724.	12.8	578
4	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
5	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
6	Temporal Proteome and Lipidome Profiles Reveal Hepatitis C Virus-Associated Reprogramming of Hepatocellular Metabolism and Bioenergetics. <i>PLoS Pathogens</i> , 2010, 6, e1000719.	4.7	361
7	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
8	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
9	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017, 8, .	4.1	219
10	Review, Evaluation, and Discussion of the Challenges of Missing Value Imputation for Mass Spectrometry-Based Label-Free Global Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 1993-2001.	3.7	217
11	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189
12	Accurate Prediction of Secreted Substrates and Identification of a Conserved Putative Secretion Signal for Type III Secretion Systems. <i>PLoS Pathogens</i> , 2009, 5, e1000375.	4.7	177
13	Challenges in biomarker discovery: combining expert insights with statistical analysis of complex omics data. <i>Expert Opinion on Medical Diagnostics</i> , 2013, 7, 37-51.	1.6	154
14	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474.	28.9	147
15	Coordinated Regulation of Virulence during Systemic Infection of <i>Salmonella enterica</i> Serovar Typhimurium. <i>PLoS Pathogens</i> , 2009, 5, e1000306.	4.7	143
16	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. <i>Science Signaling</i> , 2016, 9, rs6.	3.6	119
17	Computational Prediction of Type III and IV Secreted Effectors in Gram-Negative Bacteria. <i>Infection and Immunity</i> , 2011, 79, 23-32.	2.2	113
18	Discovery of Novel Secreted Virulence Factors from <i>Salmonella enterica</i> Serovar Typhimurium by Proteomic Analysis of Culture Supernatants. <i>Infection and Immunity</i> , 2011, 79, 33-43.	2.2	112

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19	A Systems Biology Approach to Infectious Disease Research: Innovating the Pathogen-Host Research Paradigm. <i>MBio</i> , 2011, 2, e00325-10.	4.1	111
20	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 121-134.	3.8	111
21	<i>Biocellion</i> : accelerating computer simulation of multicellular biological system models. <i>Bioinformatics</i> , 2014, 30, 3101-3108.	4.1	92
22	Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005, 15, 1258-1264.	5.5	91
23	Structural analysis of membrane-bound retrovirus capsid proteins. <i>EMBO Journal</i> , 1997, 16, 1199-1213.	7.8	89
24	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	6.4	83
25	A comparative analysis of computational approaches to relative protein quantification using peptide peak intensities in label-free LC-MS proteomics experiments. <i>Proteomics</i> , 2013, 13, 493-503.	2.2	74
26	Bottlenecks and Hubs in Inferred Networks Are Important for Virulence in <i>Salmonella typhimurium</i> . <i>Journal of Computational Biology</i> , 2009, 16, 169-180.	1.6	73
27	A Network Integration Approach to Predict Conserved Regulators Related to Pathogenicity of Influenza and SARS-CoV Respiratory Viruses. <i>PLoS ONE</i> , 2013, 8, e69374.	2.5	68
28	Retrovirus Capsid Protein Assembly Arrangements. <i>Journal of Molecular Biology</i> , 2003, 325, 225-237.	4.2	65
29	A comprehensive collection of systems biology data characterizing the host response to viral infection. <i>Scientific Data</i> , 2014, 1, 140033.	5.3	62
30	The effect of inhibition of PP1 and TNF α signaling on pathogenesis of SARS coronavirus. <i>BMC Systems Biology</i> , 2016, 10, 93.	3.0	58
31	Organization of HIV-1 Capsid Proteins on a Lipid Monolayer. <i>Journal of Biological Chemistry</i> , 1998, 273, 7177-7180.	3.4	55
32	Functional annotation from predicted protein interaction networks. <i>Bioinformatics</i> , 2005, 21, 3217-3226.	4.1	54
33	Proteomics Analysis of the Causative Agent of Typhoid Fever. <i>Journal of Proteome Research</i> , 2008, 7, 546-557.	3.7	54
34	Proteomic Investigation of the Time Course Responses of RAW 264.7 Macrophages to Infection with <i>Salmonella enterica</i> . <i>Infection and Immunity</i> , 2009, 77, 3227-3233.	2.2	54
35	Topological analysis of protein co-abundance networks identifies novel host targets important for HCV infection and pathogenesis. <i>BMC Systems Biology</i> , 2012, 6, 28.	3.0	52
36	<i>Salmonella</i> modulates metabolism during growth under conditions that induce expression of virulence genes. <i>Molecular BioSystems</i> , 2013, 9, 1522.	2.9	49

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37	Systems Virology Identifies a Mitochondrial Fatty Acid Oxidation Enzyme, Dodecenoyl Coenzyme A Delta Isomerase, Required for Hepatitis C Virus Replication and Likely Pathogenesis. <i>Journal of Virology</i> , 2011, 85, 11646-11654.	3.4	48
38	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020, 1, 100004.	6.5	46
39	Night shift schedule causes circadian dysregulation of DNA repair genes and elevated DNA damage in humans. <i>Journal of Pineal Research</i> , 2021, 70, e12726.	7.4	46
40	A multi-pronged search for a common structural motif in the secretion signal of <i>Salmonella enterica</i> serovar Typhimurium type III effector proteins. <i>Molecular BioSystems</i> , 2010, 6, 2448.	2.9	45
41	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	3.7	44
42	Inhibition of interleukin-1 receptor-associated kinase-1 is a therapeutic strategy for acute myeloid leukemia subtypes. <i>Leukemia</i> , 2018, 32, 2374-2387.	7.2	43
43	Conserved host response to highly pathogenic avian influenza virus infection in human cell culture, mouse and macaque model systems. <i>BMC Systems Biology</i> , 2011, 5, 190.	3.0	41
44	Proteome and computational analyses reveal new insights into the mechanisms of hepatitis C virus-mediated liver disease posttransplantation. <i>Hepatology</i> , 2012, 56, 28-38.	7.3	39
45	Hypergraph models of biological networks to identify genes critical to pathogenic viral response. <i>BMC Bioinformatics</i> , 2021, 22, 287.	2.6	39
46	Analysis of rous sarcoma virus capsid protein variants assembled on lipid monolayers. <i>Journal of Molecular Biology</i> , 2002, 316, 667-678.	4.2	38
47	Bayesian Proteoform Modeling Improves Protein Quantification of Global Proteomic Measurements. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3639-3646.	3.8	38
48	Unlocking the Constraints of Cyanobacterial Productivity: Acclimations Enabling Ultrafast Growth. <i>MBio</i> , 2016, 7, .	4.1	38
49	Controlling the Response: Predictive Modeling of a Highly Central, Pathogen-Targeted Core Response Module in Macrophage Activation. <i>PLoS ONE</i> , 2011, 6, e14673.	2.5	33
50	Moisture modulates soil reservoirs of active DNA and RNA viruses. <i>Communications Biology</i> , 2021, 4, 992.	4.4	33
51	Assembly of Retrovirus Capsid-Nucleocapsid Proteins in the Presence of Membranes or RNA. <i>Journal of Virology</i> , 2000, 74, 7431-7441.	3.4	31
52	Systems analysis of multiple regulator perturbations allows discovery of virulence factors in <i>Salmonella</i> . <i>BMC Systems Biology</i> , 2011, 5, 100.	3.0	30
53	ChIP-Seq Analysis of the σ^E Regulon of <i>Salmonella enterica</i> Serovar Typhimurium Reveals New Genes Implicated in Heat Shock and Oxidative Stress Response. <i>PLoS ONE</i> , 2015, 10, e0138466.	2.5	30
54	A multi-omic systems approach to elucidating <i>Yersinia</i> virulence mechanisms. <i>Molecular BioSystems</i> , 2013, 9, 44-54.	2.9	29

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55	TRANSCRIPTIONAL ANALYSIS OF THE UNICELLULAR, DIAZOTROPHIC CYANOBACTERIUM <i>CYANOTHECE</i> SP. ATCC 51142 GROWN UNDER SHORT DAY/NIGHT CYCLES. <i>Journal of Phycology</i> , 2009, 45, 610-620.	2.3	28
56	Identification and Validation of Ifit1 as an Important Innate Immune Bottleneck. <i>PLoS ONE</i> , 2012, 7, e36465.	2.5	28
57	Network analysis of transcriptomics expands regulatory landscapes in <i>Synechococcus</i> sp. PCC 7002. <i>Nucleic Acids Research</i> , 2016, 44, 8810-8825.	14.5	26
58	An Integrative Analysis of Tumor Proteomic and Phosphoproteomic Profiles to Examine the Relationships Between Kinase Activity and Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S26-S36.	3.8	25
59	Analysis of the Salmonella regulatory network suggests involvement of SsrB and H-NS in Δ E' E-regulated SPI-2 gene expression. <i>Frontiers in Microbiology</i> , 2015, 6, 27.	3.5	24
60	Bioverse: functional, structural and contextual annotation of proteins and proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 3736-3737.	14.5	23
61	Genome Sequences of <i>Mannheimia haemolytica</i> Serotype A2: Ovine and Bovine Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 1167-1168.	2.2	23
62	A model of cyclic transcriptomic behavior in the cyanobacterium <i>Cyanothece</i> sp. ATCC 51142. <i>Molecular BioSystems</i> , 2011, 7, 2407.	2.9	23
63	A three-way comparative genomic analysis of <i>Mannheimia haemolytica</i> isolates. <i>BMC Genomics</i> , 2010, 11, 535.	2.8	22
64	Species-specific transcriptomic network inference of interspecies interactions. <i>ISME Journal</i> , 2018, 12, 2011-2023.	9.8	22
65	Proteome of <i>Salmonella Enterica</i> Serotype Typhimurium Grown in a Low Mg ²⁺ /pH Medium. <i>Journal of Proteomics and Bioinformatics</i> , 2009, 02, 388-397.	0.4	21
66	Genus-optimized strategy for the identification of chlamydial type III secretion substrates. <i>Pathogens and Disease</i> , 2013, 69, 213-222.	2.0	21
67	Cells Respond to Distinct Nanoparticle Properties with Multiple Strategies As Revealed by Single-Cell RNA-Seq. <i>ACS Nano</i> , 2016, 10, 10173-10185.	14.6	21
68	Three-dimensional organization of retroviral capsid proteins on a lipid monolayer 1 Edited by M.Summers. <i>Journal of Molecular Biology</i> , 2000, 302, 121-133.	4.2	20
69	Ten simple rules for drawing scientific comics. <i>PLoS Computational Biology</i> , 2018, 14, e1005845.	3.2	19
70	Enhanced functional information from predicted protein networks. <i>Trends in Biotechnology</i> , 2004, 22, 60-62.	9.3	18
71	BIOVERSE: enhancements to the framework for structural, functional and contextual modeling of proteins and proteomes. <i>Nucleic Acids Research</i> , 2005, 33, W324-W325.	14.5	18
72	Technologies and Approaches to Elucidate and Model the Virulence Program of <i>Salmonella</i> . <i>Frontiers in Microbiology</i> , 2011, 2, 121.	3.5	18

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73	Suppressed Expression of T-Box Transcription Factors Is Involved in Senescence in Chronic Obstructive Pulmonary Disease. <i>PLoS Computational Biology</i> , 2012, 8, e1002597.	3.2	18
74	RNA Type III Secretion Signals That Require Hfq. <i>Journal of Bacteriology</i> , 2013, 195, 2119-2125.	2.2	18
75	The Role of EGFR in Influenza Pathogenicity: Multiple Network-Based Approaches to Identify a Key Regulator of Non-lethal Infections. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 200.	3.7	18
76	Phosphoproteome Analysis Reveals Estrogen-ER Pathway as a Modulator of mTOR Activity Via DEPTOR. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1607-1618.	3.8	18
77	Separating the Drivers from the Driven: Integrative Network and Pathway Approaches Aid Identification of Disease Biomarkers from High-Throughput Data. <i>Disease Markers</i> , 2010, 28, 253-266.	1.3	17
78	Proteogenomic Analysis of Surgically Resected Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2018, 13, 1519-1529.	1.1	17
79	Hexagonal Organization of Moloney Murine Leukemia Virus Capsid Proteins. <i>Virology</i> , 2002, 298, 30-38.	2.4	16
80	CpG Preconditioning Regulates Mirna Expression That Modulates Genomic Reprogramming Associated with Neuroprotection against Ischemic Injury. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2015, 35, 257-266.	4.3	14
81	Separating the drivers from the driven: Integrative network and pathway approaches aid identification of disease biomarkers from high-throughput data. <i>Disease Markers</i> , 2010, 28, 253-66.	1.3	14
82	Sequential projection pursuit principal component analysis “ dealing with missing data associated with new -omics technologies. <i>BioTechniques</i> , 2013, 54, 165-168.	1.8	13
83	Fast and Scalable Implementations of Influence Maximization Algorithms. , 2019, , .		13
84	Prediction and Integration of Regulatory and Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2009, 541, 101-143.	0.9	12
85	Using the gene ontology to enrich biological pathways. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 221.	0.3	12
86	DEFINING THE PLAYERS IN HIGHER-ORDER NETWORKS: PREDICTIVE MODELING FOR REVERSE ENGINEERING FUNCTIONAL INFLUENCE NETWORKS. , 2010, , 314-325.		12
87	Crosslink Analysis of N-Terminal, C-Terminal, and N/B Determining Regions of the Moloney Murine Leukemia Virus Capsid Protein. <i>Virology</i> , 2000, 269, 190-200.	2.4	11
88	Global Analysis of <i>Salmonella</i> Alternative Sigma Factor E on Protein Translation. <i>Journal of Proteome Research</i> , 2015, 14, 1716-1726.	3.7	11
89	Studying Salmonellae and Yersiniae Host-Pathogen Interactions Using Integrated Omics and Modeling. <i>Current Topics in Microbiology and Immunology</i> , 2012, 363, 21-41.	1.1	10
90	Trelliscope: A system for detailed visualization in the deep analysis of large complex data. , 2013, , .		10

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91	A Bayesian integration model of high-throughput proteomics and metabolomics data for improved early detection of microbial infections. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 451-63.	0.7	10
92	Evolutionary Transients in the Rice Transcriptome. Genomics, Proteomics and Bioinformatics, 2010, 8, 211-228.	6.9	9
93	The landscape of viral proteomics and its potential to impact human health. Expert Review of Proteomics, 2016, 13, 579-591.	3.0	9
94	Ten Simple Rules to becoming a principal investigator. PLoS Computational Biology, 2020, 16, e1007448.	3.2	8
95	An enhanced Java graph applet interface for visualizing interactomes. Bioinformatics, 2005, 21, 1741-1742.	4.1	7
96	Unified feature association networks through integration of transcriptomic and proteomic data. PLoS Computational Biology, 2019, 15, e1007241.	3.2	7
97	Modeling Dynamic Regulatory Processes in Stroke. PLoS Computational Biology, 2012, 8, e1002722.	3.2	6
98	leapR: An R Package for Multiomic Pathway Analysis. Journal of Proteome Research, 2021, 20, 2116-2121.	3.7	6
99	Prediction of bacterial E3 ubiquitin ligase effectors using reduced amino acid peptide fingerprinting. PeerJ, 2019, 7, e7055.	2.0	6
100	A Network Inference Workflow Applied to Virulence-Related Processes in <i>Salmonella typhimurium</i> . Annals of the New York Academy of Sciences, 2009, 1158, 143-158.	3.8	5
101	Improving network inference algorithms using resampling methods. BMC Bioinformatics, 2018, 19, 376.	2.6	5
102	Inferring Molecular Interactions Pathways from eQTL Data. Methods in Molecular Biology, 2009, 541, 211-223.	0.9	5
103	Prediction of multi-drug resistance transporters using a novel sequence analysis method. F1000Research, 2015, 4, 60.	1.6	5
104	Enriching regulatory networks by bootstrap learning using optimised GO-based gene similarity and gene links mined from PubMed abstracts. International Journal of Computational Biology and Drug Design, 2011, 4, 56.	0.3	4
105	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. Microbiology Resource Announcements, 2020, 9, .	0.6	4
106	Computational Representation of Biological Systems. Methods in Molecular Biology, 2009, 541, 535-549.	0.9	4
107	EMXtalOrg: an EM tilt data organization and processing system. Ultramicroscopy, 2002, 93, 11-17.	1.9	3
108	SEBINI-CABIN: An Analysis Pipeline for Biological Network Inference, with a Case Study in Protein-Protein Interaction Network Reconstruction. , 2007, , .		3

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109	An analysis pipeline for the inference of protein-protein interaction networks. International Journal of Data Mining and Bioinformatics, 2009, 3, 409.	0.1	3
110	A Semiautomated Framework for Integrating Expert Knowledge into Disease Marker Identification. Disease Markers, 2013, 35, 513-523.	1.3	3
111	Prediction of multi-drug resistance transporters using a novel sequence analysis method. F1000Research, 2015, 4, 60.	1.6	3
112	Phosphoproteomic response of cardiac endothelial cells to ischemia and ultrasound. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140683.	2.3	3
113	INTEGRATOR: interactive graphical search of large protein interactomes over the Web. BMC Bioinformatics, 2006, 7, 146.	2.6	2
114	Two more red flags for suspect work. Nature, 2013, 499, 284-284.	27.8	2
115	The Bioverse API and Web Application. Methods in Molecular Biology, 2009, 541, 511-534.	0.9	2
116	An integrated approach to predictive genomic analytics. , 2010, , .		1
117	Integrative Genomics and Computational Systems Medicine. BioMed Research International, 2014, 2014, 1-3.	1.9	1
118	Drawing connections. Science, 2017, 356, 1202-1202.	12.6	1
119	Modeling Emergence in Neuroprotective Regulatory Networks. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2013, , 291-302.	0.3	1
120	Genome Sequences of <i>Mannheimia haemolytica</i> Serotype A2: Ovine and Bovine Isolates. Journal of Bacteriology, 2010, 192, 5272-5272.	2.2	0
121	Learning biological networks via bootstrapping with optimized go-based gene similarity. , 2010, , .		0
122	MODELING HOST-PATHOGEN INTERACTIONS: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS FOR INFECTIOUS DISEASE RESEARCH. , 2011, , .		0
123	An Adaptive Coarse Graining Method for Signal Transduction in Three Dimensions. Fundamenta Informaticae, 2012, 118, 371-384.	0.4	0
124	Let the Data Do the Talking: Hypothesis Discovery from Large-Scale Data Sets in Real Time. , 0, , 235-257.		0
125	(Phospho)Proteomic dataset of ischemia- and ultrasound- stimulated mouse cardiac endothelial cells in vitro. Data in Brief, 2021, 38, 107343.	1.0	0
126	Promises and challenges in analysis of biological big data. , 2014, , .		0

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127	Computational methods for omics data. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 97-101.	0.3	0
128	0025 Circadian Dysregulation of Human DNA Repair Genes and Elevated DNA Damage in Simulated Night Shift Schedule. <i>Sleep</i> , 2022, 45, A11-A12.	1.1	0