Jason E Mcdermott

List of Publications by Year
in descending order

128	8,603	76326	51608
papers	citations	40	86
		h-index	g-index

140	140	140	14291
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	0025 Circadian Dysregulation of Human DNA Repair Genes and Elevated DNA Damage in Simulated Night Shift Schedule. Sleep, 2022, 45, A11-A12.	1.1	0
2	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
3	leapR: An R Package for Multiomic Pathway Analysis. Journal of Proteome Research, 2021, 20, 2116-2121.	3.7	6
4	Night shift schedule causes circadian dysregulation of DNA repair genes and elevated DNA damage in humans. Journal of Pineal Research, 2021, 70, e12726.	7.4	46
5	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
6	Hypergraph models of biological networks to identify genes critical to pathogenic viral response. BMC Bioinformatics, 2021, 22, 287.	2.6	39
7	Moisture modulates soil reservoirs of active DNA and RNA viruses. Communications Biology, 2021, 4, 992.	4.4	33
8	Phosphoproteomic response of cardiac endothelial cells to ischemia and ultrasound. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140683.	2.3	3
9	(Phospho)Proteomic dataset of ischemia- and ultrasound- stimulated mouse cardiac endothelial cells in vitro. Data in Brief, 2021, 38, 107343.	1.0	0
10	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. Cell Reports, 2020, 33, 108276.	6.4	83
11	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. Microbiology Resource Announcements, 2020, 9, .	0.6	4
12	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	28.9	147
13	Ten Simple Rules to becoming a principal investigator. PLoS Computational Biology, 2020, 16, e1007448.	3.2	8
14	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296
15	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. Cell Reports Medicine, 2020, 1, 100004.	6.5	46
16	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
17	Unified feature association networks through integration of transcriptomic and proteomic data. PLoS Computational Biology, 2019, 15, e1007241.	3.2	7
18	The Role of EGFR in Influenza Pathogenicity: Multiple Network-Based Approaches to Identify a Key Regulator of Non-lethal Infections. Frontiers in Cell and Developmental Biology, 2019, 7, 200.	3.7	18

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19	An Integrative Analysis of Tumor Proteomic and Phosphoproteomic Profiles to Examine the Relationships Between Kinase Activity and Phosphorylation. Molecular and Cellular Proteomics, 2019, 18, S26-S36.	3.8	25
20	Phosphoproteome Analysis Reveals Estrogen-ER Pathway as a Modulator of mTOR Activity Via DEPTOR. Molecular and Cellular Proteomics, 2019, 18, 1607-1618.	3.8	18
21	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	28.9	498
22	Fast and Scalable Implementations of Influence Maximization Algorithms. , 2019, , .		13
23	Prediction of bacterial E3 ubiquitin ligase effectors using reduced amino acid peptide fingerprinting. PeerJ, 2019, 7, e7055.	2.0	6
24	Inhibition of interleukin-1 receptor-associated kinase-1 is a therapeutic strategy for acute myeloid leukemia subtypes. Leukemia, 2018, 32, 2374-2387.	7.2	43
25	Proteogenomic Analysis of Surgically Resected Lung Adenocarcinoma. Journal of Thoracic Oncology, 2018, 13, 1519-1529.	1.1	17
26	Improving network inference algorithms using resampling methods. BMC Bioinformatics, 2018, 19, 376.	2.6	5
27	Species-specific transcriptomic network inference of interspecies interactions. ISME Journal, 2018, 12, 2011-2023.	9.8	22
28	Co-expression of CD39 and CD103 identifies tumor-reactive CD8 T cells in human solid tumors. Nature Communications, 2018, 9, 2724.	12.8	578
29	Ten simple rules for drawing scientific comics. PLoS Computational Biology, 2018, 14, e1005845.	3.2	19
30	Drawing connections. Science, 2017, 356, 1202-1202.	12.6	1
31	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. MBio, 2017, 8, .	4.1	219
32	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. Molecular and Cellular Proteomics, 2017, 16, 121-134.	3.8	111
33	The landscape of viral proteomics and its potential to impact human health. Expert Review of Proteomics, 2016, 13, 579-591.	3.0	9
34	Unlocking the Constraints of Cyanobacterial Productivity: Acclimations Enabling Ultrafast Growth. MBio, 2016, 7, .	4.1	38
35	Network analysis of transcriptomics expands regulatory landscapes in *Synechococcus* sp. PCC 7002. Nucleic Acids Research, 2016, 44, 8810-8825.	14.5	26
36	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. Science Signaling, 2016, 9, rs6.	3.6	119

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37	Cells Respond to Distinct Nanoparticle Properties with Multiple Strategies As Revealed by Single-Cell RNA-Seq. ACS Nano, 2016, 10, 10173-10185.	14.6	21
38	The effect of inhibition of PP1 and TNFα signaling on pathogenesis of SARS coronavirus. BMC Systems Biology, 2016, 10, 93.	3.0	58
39	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
40	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. Journal of Proteome Research, 2016, 15, 691-706.	3.7	44
41	Prediction of multi-drug resistance transporters using a novel sequence analysis method. F1000Research, 2015, 4, 60.	1.6	3
42	ChIP-Seq Analysis of the σE Regulon of Salmonella enterica Serovar Typhimurium Reveals New Genes Implicated in Heat Shock and Oxidative Stress Response. PLoS ONE, 2015, 10, e0138466.	2.5	30
43	Global Analysis of *Salmonella* Alternative Sigma Factor E on Protein Translation. Journal of Proteome Research, 2015, 14, 1716-1726.	3.7	11
44	CpG Preconditioning Regulates Mirna Expression That Modulates Genomic Reprogramming Associated with Neuroprotection against Ischemic Injury. Journal of Cerebral Blood Flow and Metabolism, 2015, 35, 257-266.	4.3	14
45	Analysis of the Salmonella regulatory network suggests involvement of SsrB and H-NS in ÆE-regulated SPI-2 gene expression. Frontiers in Microbiology, 2015, 6, 27.	3.5	24
46	Review, Evaluation, and Discussion of the Challenges of Missing Value Imputation for Mass Spectrometry-Based Label-Free Global Proteomics. Journal of Proteome Research, 2015, 14, 1993-2001.	3.7	217
47	Prediction of multi-drug resistance transporters using a novel sequence analysis method. F1000Research, 2015, 4, 60.	1.6	5
48	Integrative Genomics and Computational Systems Medicine. BioMed Research International, 2014, 2014, 1-3.	1.9	1
49	A comprehensive collection of systems biology data characterizing the host response to viral infection. Scientific Data, 2014, 1, 140033.	5.3	62
50	Bayesian Proteoform Modeling Improves Protein Quantification of Global Proteomic Measurements. Molecular and Cellular Proteomics, 2014, 13, 3639-3646.	3.8	38
51	*Biocellion* : accelerating computer simulation of multicellular biological system models. Bioinformatics, 2014, 30, 3101-3108.	4.1	92
52	Promises and challenges in analysis of biological big data. , 2014, , .		0
53	Computational methods for omics data. International Journal of Computational Biology and Drug Design, 2014, 7, 97-101.	0.3	0
54	Challenges in biomarker discovery: combining expert insights with statistical analysis of complex omics data. Expert Opinion on Medical Diagnostics, 2013, 7, 37-51.	1.6	154

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55	Trelliscope: A system for detailed visualization in the deep analysis of large complex data. , 2013, , .		10
56	A comparative analysis of computational approaches to relative protein quantification using peptide peak intensities in labelâ€free <scp>LC</scp>â€<scp>MS</scp> proteomics experiments. Proteomics, 2013, 13, 493-503.	2.2	74
57	A multi-omic systems approach to elucidating Yersinia virulence mechanisms. Molecular BioSystems, 2013, 9, 44-54.	2.9	29
58	Salmonella modulates metabolism during growth under conditions that induce expression of virulence genes. Molecular BioSystems, 2013, 9, 1522.	2.9	49
59	Sequential projection pursuit principal component analysis â€" dealing with missing data associated with new -omics technologies. BioTechniques, 2013, 54, 165-168.	1.8	13
60	Two more red flags for suspect work. Nature, 2013, 499, 284-284.	27.8	2
61	A Semiautomated Framework for Integrating Expert Knowledge into Disease Marker Identification. Disease Markers, 2013, 35, 513-523.	1.3	3
62	RNA Type III Secretion Signals That Require Hfq. Journal of Bacteriology, 2013, 195, 2119-2125.	2.2	18
63	Genus-optimized strategy for the identification of chlamydial type III secretion substrates. Pathogens and Disease, 2013, 69, 213-222.	2.0	21
64	A Network Integration Approach to Predict Conserved Regulators Related to Pathogenicity of Influenza and SARS-CoV Respiratory Viruses. PLoS ONE, 2013, 8, e69374.	2.5	68
65	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
66	Suppressed Expression of T-Box Transcription Factors Is Involved in Senescence in Chronic Obstructive Pulmonary Disease. PLoS Computational Biology, 2012, 8, e1002597.	3.2	18
67	Modeling Dynamic Regulatory Processes in Stroke. PLoS Computational Biology, 2012, 8, e1002722.	3.2	6
68	Topological analysis of protein co-abundance networks identifies novel host targets important for HCV infection and pathogenesis. BMC Systems Biology, 2012, 6, 28.	3.0	52
69	Studying Salmonellae and Yersiniae Hostâ€"Pathogen Interactions Using Integrated â€˜Omics and Modeling. Current Topics in Microbiology and Immunology, 2012, 363, 21-41.	1.1	10
70	An Adaptive Coarse Graining Method for Signal Transduction in Three Dimensions. Fundamenta Informaticae, 2012, 118, 371-384.	0.4	0
71	Proteome and computational analyses reveal new insights into the mechanisms of hepatitis C virus-mediated liver disease posttransplantation. Hepatology, 2012, 56, 28-38.	7.3	39
72	Identification and Validation of Ifit1 as an Important Innate Immune Bottleneck. PLoS ONE, 2012, 7, e36465.	2.5	28

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73	A model of cyclic transcriptomic behavior in the cyanobacterium Cyanothece sp. ATCC 51142. Molecular BioSystems, 2011, 7, 2407.	2.9	23
74	Technologies and Approaches to Elucidate and Model the Virulence Program of Salmonella. Frontiers in Microbiology, 2011, 2, 121.	3.5	18
75	Controlling the Response: Predictive Modeling of a Highly Central, Pathogen-Targeted Core Response Module in Macrophage Activation. PLoS ONE, 2011, 6, e14673.	2.5	33
76	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
77	Systems analysis of multiple regulator perturbations allows discovery of virulence factors in Salmonella. BMC Systems Biology, 2011, 5, 100.	3.0	30
78	Conserved host response to highly pathogenic avian influenza virus infection in human cell culture, mouse and macaque model systems. BMC Systems Biology, 2011, 5, 190.	3.0	41
79	A Systems Biology Approach to Infectious Disease Research: Innovating the Pathogen-Host Research Paradigm. MBio, 2011, 2, e00325-10.	4.1	111
80	MODELING HOST-PATHOGEN INTERACTIONS: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS FOR INFECTIOUS DISEASE RESEARCH. , 2011, , .		0
81	Discovery of Novel Secreted Virulence Factors from <i>Salmonella enterica</i> Serovar Typhimurium by Proteomic Analysis of Culture Supernatants. Infection and Immunity, 2011, 79, 33-43.	2.2	112
82	Computational Prediction of Type III and IV Secreted Effectors in Gram-Negative Bacteria. Infection and Immunity, 2011, 79, 23-32.	2.2	113
83	Systems Virology Identifies a Mitochondrial Fatty Acid Oxidation Enzyme, Dodecenoyl Coenzyme A Delta Isomerase, Required for Hepatitis C Virus Replication and Likely Pathogenesis. Journal of Virology, 2011, 85, 11646-11654.	3.4	48
84	A three-way comparative genomic analysis of Mannheimia haemolytica isolates. BMC Genomics, 2010, 11, 535.	2.8	22
85	Separating the Drivers from the Driven: Integrative Network and Pathway Approaches Aid Identification of Disease Biomarkers from High-Throughput Data. Disease Markers, 2010, 28, 253-266.	1.3	17
86	Genome Sequences of <i>Mannheimia haemolytica</i> Serotype A2: Ovine and Bovine Isolates. Journal of Bacteriology, 2010, 192, 5272-5272.	2.2	0
87	Temporal Proteome and Lipidome Profiles Reveal Hepatitis C Virus-Associated Reprogramming of Hepatocellular Metabolism and Bioenergetics. PLoS Pathogens, 2010, 6, e1000719.	4.7	361
88	Learning biological networks via bootstrapping with optimized go-based gene similarity. , 2010, , .		0
89	An integrated approach to predictive genomic analytics. , 2010, , .		1
90	Genome Sequences of <i>Mannheimia haemolytica</i> Serotype A2: Ovine and Bovine Isolates. Journal of Bacteriology, 2010, 192, 1167-1168.	2.2	23

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91	Evolutionary Transients in the Rice Transcriptome. Genomics, Proteomics and Bioinformatics, 2010, 8, 211-228.	6.9	9
92	A multi-pronged search for a common structural motif in the secretion signal of Salmonella enterica serovar Typhimurium type III effector proteins. Molecular BioSystems, 2010, 6, 2448.	2.9	45
93	DEFINING THE PLAYERS IN HIGHER-ORDER NETWORKS: PREDICTIVE MODELING FOR REVERSE ENGINEERING FUNCTIONAL INFLUENCE NETWORKS. , 2010, , 314-325.		12
94	Separating the drivers from the driven: Integrative network and pathway approaches aid identification of disease biomarkers from high-throughput data. Disease Markers, 2010, 28, 253-66.	1.3	14
95	Proteome of Salmonella Enterica Serotype Typhimurium Grown in a Low Mg2+/pH Medium. Journal of Proteomics and Bioinformatics, 2009, 02, 388-397.	0.4	21
96	Proteomic Investigation of the Time Course Responses of RAW 264.7 Macrophages to Infection with <i>Salmonella enterica</i>. Infection and Immunity, 2009, 77, 3227-3233.	2.2	54
97	An analysis pipeline for the inference of protein-protein interaction networks. International Journal of Data Mining and Bioinformatics, 2009, 3, 409.	0.1	3
98	Accurate Prediction of Secreted Substrates and Identification of a Conserved Putative Secretion Signal for Type III Secretion Systems. PLoS Pathogens, 2009, 5, e1000375.	4.7	177
99	Coordinated Regulation of Virulence during Systemic Infection of Salmonella enterica Serovar Typhimurium. PLoS Pathogens, 2009, 5, e1000306.	4.7	143
100	A Network Inference Workflow Applied to Virulenceâ€Related Processes in <i>Salmonella typhimurium</i>. Annals of the New York Academy of Sciences, 2009, 1158, 143-158.	3.8	5
101	TRANSCRIPTIONAL ANALYSIS OF THE UNICELLULAR, DIAZOTROPHIC CYANOBACTERIUM <i>CYANOTHECE</i> SP. ATCC 51142 GROWN UNDER SHORT DAY/NIGHT CYCLES¹. Journal of Phycology, 2009, 45, 610-620.	2.3	28
102	Prediction and Integration of Regulatory and Proteinâ€"Protein Interactions. Methods in Molecular Biology, 2009, 541, 101-143.	0.9	12
103	Bottlenecks and Hubs in Inferred Networks Are Important for Virulence in <i>Salmonella typhimurium</i>. Journal of Computational Biology, 2009, 16, 169-180.	1.6	73
104	Using the gene ontology to enrich biological pathways. International Journal of Computational Biology and Drug Design, 2009, 2, 221.	0.3	12
105	Inferring Molecular Interactions Pathways from eQTL Data. Methods in Molecular Biology, 2009, 541, 211-223.	0.9	5
106	Computational Representation of Biological Systems. Methods in Molecular Biology, 2009, 541, 535-549.	0.9	4
107	The Bioverse API and Web Application. Methods in Molecular Biology, 2009, 541, 511-534.	0.9	2
108	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

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109	Proteomics Analysis of the Causative Agent of Typhoid Fever. Journal of Proteome Research, 2008, 7, 546-557.	3.7	54
110	SEBINI-CABIN: An Analysis Pipeline for Biological Network Inference, with a Case Study in Protein-Protein Interaction Network Reconstruction. , 2007, , .		3
111	INTEGRATOR: interactive graphical search of large protein interactomes over the Web. BMC Bioinformatics, 2006, 7, 146.	2.6	2
112	The Genomes of Oryza sativa: A History of Duplications. PLoS Biology, 2005, 3, e38.	5.6	808
113	Functional annotation from predicted protein interaction networks. Bioinformatics, 2005, 21, 3217-3226.	4.1	54
114	An enhanced Java graph applet interface for visualizing interactomes. Bioinformatics, 2005, 21, 1741-1742.	4.1	7
115	Origin and evolution of new exons in rodents. Genome Research, 2005, 15, 1258-1264.	5.5	91
116	BIOVERSE: enhancements to the framework for structural, functional and contextual modeling of proteins and proteomes. Nucleic Acids Research, 2005, 33, W324-W325.	14.5	18
117	Enhanced functional information from predicted protein networks. Trends in Biotechnology, 2004, 22, 60-62.	9.3	18
118	Retrovirus Capsid Protein Assembly Arrangements. Journal of Molecular Biology, 2003, 325, 225-237.	4.2	65
119	Bioverse: functional, structural and contextual annotation of proteins and proteomes. Nucleic Acids Research, 2003, 31, 3736-3737.	14.5	23
120	Analysis of rous sarcoma virus capsid protein variants assembled on lipid monolayers. Journal of Molecular Biology, 2002, 316, 667-678.	4.2	38
121	Hexagonal Organization of Moloney Murine Leukemia Virus Capsid Proteins. Virology, 2002, 298, 30-38.	2.4	16
122	EMXtalOrg: an EM tilt data organization and processing system. Ultramicroscopy, 2002, 93, 11-17.	1.9	3
123	Crosslink Analysis of N-Terminal, C-Terminal, and N/B Determining Regions of the Moloney Murine Leukemia Virus Capsid Protein. Virology, 2000, 269, 190-200.	2.4	11
124	Assembly of Retrovirus Capsid-Nucleocapsid Proteins in the Presence of Membranes or RNA. Journal of Virology, 2000, 74, 7431-7441.	3.4	31
125	Three-dimensional organization of retroviral capsid proteins on a lipid monolayer 1 1Edited by M.Summers. Journal of Molecular Biology, 2000, 302, 121-133.	4.2	20
126	Organization of HIV-1 Capsid Proteins on a Lipid Monolayer. Journal of Biological Chemistry, 1998, 273, 7177-7180.	3.4	55

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127	Structural analysis of membrane-bound retrovirus capsid proteins. EMBO Journal, 1997, 16, 1199-1213.	7.8	89
128	Let the Data Do the Talking: Hypothesis Discovery from Large-Scale Data Sets in Real Time. , 0, , 235-257.		0