David J Lynn

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

86
papers5,884
citations34
h-index76
g-index95
ext. papers7,402
ext. citations9.1
avg, IF5.17
L-index

#	Paper	IF	Citations
86	Long-term perturbation of the peripheral immune system months after SARS-CoV-2 infection <i>BMC Medicine</i> , 2022 , 20, 26	11.4	21
85	Protocol to assess the impact of early-life antibiotic exposure on murine longevity <i>STAR Protocols</i> , 2022 , 3, 101220	1.4	
84	National Trends in Antibiotic Use in Australian Residential Aged Care Facilities, 2005-2016. <i>Clinical Infectious Diseases</i> , 2021 , 72, 2167-2174	11.6	4
83	BCG vaccination to reduce the impact of COVID-19 in healthcare workers: Protocol for a randomised controlled trial (BRACE trial). <i>BMJ Open</i> , 2021 , 11, e052101	3	9
82	Immunisation with the BCG and DTPw vaccines induces different programs of trained immunity in mice. <i>Vaccine</i> , 2021 ,	4.1	3
81	Zika Virus Infection of Human Iris Pigment Epithelial Cells. Frontiers in Immunology, 2021 , 12, 644153	8.4	1
80	Modulation of immune responses to vaccination by the microbiota: implications and potential mechanisms. <i>Nature Reviews Immunology</i> , 2021 ,	36.5	26
79	Contribution of facility level factors to variation in antibiotic use in long-term care facilities: a national cohort study. <i>Journal of Antimicrobial Chemotherapy</i> , 2021 , 76, 1339-1348	5.1	1
78	OX40-targeted immune agonist antibodies induce potent antitumor immune responses without inducing liver damage in mice. <i>FASEB BioAdvances</i> , 2021 , 3, 829-840	2.8	
77	The composition of the gut microbiota following early-life antibiotic exposure affects host health and longevity in later life. <i>Cell Reports</i> , 2021 , 36, 109564	10.6	5
76	A feedback loop between the androgen receptor and 6-phosphogluoconate dehydrogenase (6PGD) drives prostate cancer growth. <i>ELife</i> , 2021 , 10,	8.9	6
75	Lipidomic Profiling of Clinical Prostate Cancer Reveals Targetable Alterations in Membrane Lipid Composition. <i>Cancer Research</i> , 2021 , 81, 4981-4993	10.1	8
74	The immunotoxicity, but not anti-tumor efficacy, of anti-CD40 and anti-CD137 immunotherapies is dependent on the gut microbiota <i>Cell Reports Medicine</i> , 2021 , 2, 100464	18	4
73	The non-specific and sex-differential effects of vaccines. <i>Nature Reviews Immunology</i> , 2020 , 20, 464-470	136.5	43
7 2	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRAS. <i>Nature Communications</i> , 2020 , 11, 499	17.4	17
71	Human DECR1 is an androgen-repressed survival factor that regulates PUFA oxidation to protect prostate tumor cells from ferroptosis. <i>ELife</i> , 2020 , 9,	8.9	31
70	Fatty Acid Oxidation Is an Adaptive Survival Pathway Induced in Prostate Tumors by HSP90 Inhibition. <i>Molecular Cancer Research</i> , 2020 , 18, 1500-1511	6.6	3

69	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020 , 11, 61	44 17.4	26
68	Transcriptional and metabolic rewiring of colorectal cancer cells expressing the oncogenic KRAS mutation. <i>British Journal of Cancer</i> , 2019 , 121, 37-50	8.7	22
67	Changes in the Composition of the Gut Microbiota and the Blood Transcriptome in Preterm Infants at Less than 29 Weeks Gestation Diagnosed with Bronchopulmonary Dysplasia. <i>MSystems</i> , 2019 , 4,	7.6	11
66	Identification of Novel Response and Predictive Biomarkers to Hsp90 Inhibitors Through Proteomic Profiling of Patient-derived Prostate Tumor Explants. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 147	0-7486	19
65	Analysis combining correlated glaucoma traits identifies five new risk loci for open-angle glaucoma. <i>Scientific Reports</i> , 2018 , 8, 3124	4.9	25
64	Dysregulated fibronectin trafficking by Hsp90 inhibition restricts prostate cancer cell invasion. <i>Scientific Reports</i> , 2018 , 8, 2090	4.9	15
63	Genome-wide association study of intraocular pressure uncovers new pathways to glaucoma. <i>Nature Genetics</i> , 2018 , 50, 1067-1071	36.3	86
62	Early-Life Antibiotic-Driven Dysbiosis Leads to Dysregulated Vaccine Immune Responses in Mice. <i>Cell Host and Microbe</i> , 2018 , 23, 653-660.e5	23.4	82
61	The potential of the microbiota to influence vaccine responses. <i>Journal of Leukocyte Biology</i> , 2018 , 103, 225-231	6.5	39
60	Analysis and Visualization of Dynamic Networks Using the DyNet App for Cytoscape. <i>Current Protocols in Bioinformatics</i> , 2018 , 63, e55	24.2	2
59	Network Visualization and Analysis of Spatially Aware Gene Expression Data with InsituNet. <i>Cell Systems</i> , 2018 , 6, 626-630.e3	10.6	6
58	Retinal Pigment Epithelial Cells are a Potential Reservoir for Ebola Virus in the Human Eye. <i>Translational Vision Science and Technology</i> , 2017 , 6, 12	3.3	26
57	Using the Contextual Hub Analysis Tool (CHAT) in Cytoscape to Identify Contextually Relevant Network Hubs. <i>Current Protocols in Bioinformatics</i> , 2017 , 59, 8.24.1-8.24.13	24.2	5
56	Whole exome sequencing implicates eye development, the unfolded protein response and plasma membrane homeostasis in primary open-angle glaucoma. <i>PLoS ONE</i> , 2017 , 12, e0172427	3.7	8
55	A genome-wide association study for genetic susceptibility to Mycobacterium bovis infection in dairy cattle identifies a susceptibility QTL on chromosome 23. <i>Genetics Selection Evolution</i> , 2016 , 48, 19	4.9	37
54	Contextual Hub Analysis Tool (CHAT): A Cytoscape app for identifying contextually relevant hubs in biological networks. <i>F1000Research</i> , 2016 , 5, 1745	3.6	16
53	Interferon-driven alterations of the host domino acid metabolism in the pathogenesis of typhoid fever. <i>Journal of Experimental Medicine</i> , 2016 , 213, 1061-77	16.6	28
52	HiQuant: Rapid Postquantification Analysis of Large-Scale MS-Generated Proteomics Data. <i>Journal</i>	5.6	6

51	Using biological networks to integrate, visualize and analyze genomics data. <i>Genetics Selection Evolution</i> , 2016 , 48, 27	4.9	39
50	DyNet: visualization and analysis of dynamic molecular interaction networks. <i>Bioinformatics</i> , 2016 , 32, 2713-5	7.2	75
49	Integrated analysis of the local and systemic changes preceding the development of post-partum cytological endometritis. <i>BMC Genomics</i> , 2015 , 16, 811	4.5	24
48	CerebralWeb: a Cytoscape.js plug-in to visualize networks stratified by subcellular localization. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav041	5	6
47	Whole blood gene expression profiling of neonates with confirmed bacterial sepsis. <i>Genomics Data</i> , 2015 , 3, 41-8		24
46	MicroRNA profiling of the bovine alveolar macrophage response to Mycobacterium bovis infection suggests pathogen survival is enhanced by microRNA regulation of endocytosis and lysosome trafficking. <i>Tuberculosis</i> , 2015 , 95, 60-7	2.6	40
45	Identification of a human neonatal immune-metabolic network associated with bacterial infection. <i>Nature Communications</i> , 2014 , 5, 4649	17.4	84
44	The miRNAome of the postpartum dairy cow liver in negative energy balance. <i>BMC Genomics</i> , 2014 , 15, 279	4.5	23
43	MicroRNA regulation of bovine monocyte inflammatory and metabolic networks in an in vivo infection model. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 957-71	3.2	32
42	The Role of microRNAs in Bovine Infection and Immunity. Frontiers in Immunology, 2014, 5, 611	8.4	39
41	Profiling microRNA expression in bovine alveolar macrophages using RNA-seq. <i>Veterinary Immunology and Immunopathology</i> , 2013 , 155, 238-44	2	24
40	InnateDB: systems biology of innate immunity and beyondrecent updates and continuing curation. <i>Nucleic Acids Research</i> , 2013 , 41, D1228-33	20.1	654
39	Next generation sequencing reveals the expression of a unique miRNA profile in response to a gram-positive bacterial infection. <i>PLoS ONE</i> , 2013 , 8, e57543	3.7	75
38	A genome-wide association study for somatic cell score using the Illumina high-density bovine beadchip identifies several novel QTL potentially related to mastitis susceptibility. <i>Frontiers in Genetics</i> , 2013 , 4, 229	4.5	44
37	Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures. <i>PeerJ</i> , 2013 , 1, e229	3.1	28
36	Genome-wide associations for milk production and somatic cell score in Holstein-Friesian cattle in Ireland. <i>BMC Genetics</i> , 2012 , 13, 21	2.6	91
35	RNA-seq analysis of differential gene expression in liver from lactating dairy cows divergent in negative energy balance. <i>BMC Genomics</i> , 2012 , 13, 193	4.5	79
34	Transcriptomic analysis of the stress response to weaning at housing in bovine leukocytes using RNA-seq technology. <i>BMC Genomics</i> , 2012 , 13, 250	4.5	32

(2008-2012)

33	Global gene expression and systems biology analysis of bovine monocyte-derived macrophages in response to in vitro challenge with Mycobacterium bovis. <i>PLoS ONE</i> , 2012 , 7, e32034	3.7	39
32	Messenger RNA sequence rather than protein sequence determines the level of self-synthesis and antigen presentation of the EBV-encoded antigen, EBNA1. <i>PLoS Pathogens</i> , 2012 , 8, e1003112	7.6	30
31	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012 , 9, 345-50	21.6	375
30	Effective adjunctive therapy by an innate defense regulatory peptide in a preclinical model of severe malaria. <i>Science Translational Medicine</i> , 2012 , 4, 135ra64	17.5	73
29	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011 , 8, 528-9	21.6	227
28	The human transcriptome during nontyphoid Salmonella and HIV coinfection reveals attenuated NFkappaB-mediated inflammation and persistent cell cycle disruption. <i>Journal of Infectious Diseases</i> , 2011 , 204, 1237-45	7	19
27	The early whole-blood transcriptional signature of dengue virus and features associated with progression to dengue shock syndrome in Vietnamese children and young adults. <i>Journal of Virology</i> , 2010 , 84, 12982-94	6.6	84
26	Bovine proteins containing poly-glutamine repeats are often polymorphic and enriched for components of transcriptional regulatory complexes. <i>BMC Genomics</i> , 2010 , 11, 654	4.5	13
25	Curating the innate immunity interactome. <i>BMC Systems Biology</i> , 2010 , 4, 117	3.5	59
24	The imprinted retrotransposon-like gene PEG11 (RTL1) is expressed as a full-length protein in skeletal muscle from Callipyge sheep. <i>PLoS ONE</i> , 2010 , 5, e8638	3.7	33
23	Contrasting evolution of diversity at two disease-associated chicken genes. <i>Immunogenetics</i> , 2009 , 61, 303-14	3.2	13
22	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
21	Enabling a systems biology approach to immunology: focus on innate immunity. <i>Trends in Immunology</i> , 2009 , 30, 249-62	14.4	96
20	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
19	The bovine lactation genome: insights into the evolution of mammalian milk. <i>Genome Biology</i> , 2009 , 10, R43	18.3	143
18	Transcriptional response in the peripheral blood of patients infected with Salmonella enterica serovar Typhi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 22433-8	11.5	63
17	Evidence of balanced diversity at the chicken interleukin 4 receptor alpha chain locus. <i>BMC Evolutionary Biology</i> , 2009 , 9, 136	3	10
16	InnateDB: facilitating systems-level analyses of the mammalian innate immune response. <i>Molecular Systems Biology</i> , 2008 , 4, 218	12.2	282

15	Detecting the effects of selection at the population level in six bovine immune genes. <i>BMC Genetics</i> , 2008 , 9, 62	2.6	10
14	Avian beta-defensin nomenclature: a community proposed update. <i>Immunology Letters</i> , 2007 , 110, 86-9	4.1	127
13	Evidence of positive selection on the Atlantic salmon CD3gammadelta gene. <i>Immunogenetics</i> , 2007 , 59, 225-32	3.2	3
12	Modification of chicken avian beta-defensin-8 at positively selected amino acid sites enhances specific antimicrobial activity. <i>Immunogenetics</i> , 2007 , 59, 573-80	3.2	31
11	Linkage mapping of the locus for inherited ovine arthrogryposis (IOA) to sheep chromosome 5. <i>Mammalian Genome</i> , 2007 , 18, 43-52	3.2	9
10	Discovery of alpha-defensins in basal mammals. <i>Developmental and Comparative Immunology</i> , 2007 , 31, 963-7	3.2	44
9	Induction of a novel chicken Toll-like receptor following Salmonella enterica serovar Typhimurium infection. <i>Infection and Immunity</i> , 2006 , 74, 1692-8	3.7	148
8	The synthetic form of a novel chicken beta-defensin identified in silico is predominantly active against intestinal pathogens. <i>Immunogenetics</i> , 2005 , 57, 90-8	3.2	67
7	A genomics approach to the detection of positive selection in cattle: adaptive evolution of the T-cell and natural killer cell-surface protein CD2. <i>Genetics</i> , 2005 , 170, 1189-96	4	18
6	Evidence of positively selected sites in mammalian alpha-defensins. <i>Molecular Biology and Evolution</i> , 2004 , 21, 819-27	8.3	64
5	Bioinformatic discovery and initial characterisation of nine novel antimicrobial peptide genes in the chicken. <i>Immunogenetics</i> , 2004 , 56, 170-7	3.2	177
4	In silico identification of components of the Toll-like receptor (TLR) signaling pathway in clustered chicken expressed sequence tags (ESTs). <i>Veterinary Immunology and Immunopathology</i> , 2003 , 93, 177-8-	4 ²	68
3	Bioinformatics: implications for medical research and clinical practice. <i>Clinical and Investigative Medicine</i> , 2003 , 26, 70-4	0.9	1
2	Contextual Hub Analysis Tool (CHAT): A Cytoscape app for identifying contextually relevant hubs in biological networks. <i>F1000Research</i> ,5, 1745	3.6	18
1	Lipidomic profiling of clinical prostate cancer reveals targetable alterations in membrane lipid composi	tion	2