

Darrell L Dinwiddie

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

3,365
citations

331670

21
h-index

454955

30
g-index

33
all docs

33
docs citations

33
times ranked

7575
citing authors

#	ARTICLE	IF	CITATIONS
1	Carrier Testing for Severe Childhood Recessive Diseases by Next-Generation Sequencing. <i>Science Translational Medicine</i> , 2011, 3, 65ra4.	12.4	600
2	Effectiveness of exome and genome sequencing guided by acuity of illness for diagnosis of neurodevelopmental disorders. <i>Science Translational Medicine</i> , 2014, 6, 265ra168.	12.4	440
3	Early-onset lymphoproliferation and autoimmunity caused by germline STAT3 gain-of-function mutations. <i>Blood</i> , 2015, 125, 591-599.	1.4	436
4	An Integrated Clinico-Metabolomic Model Improves Prediction of Death in Sepsis. <i>Science Translational Medicine</i> , 2013, 5, 195ra95.	12.4	380
5	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	2.6	264
6	A 26-hour system of highly sensitive whole genome sequencing for emergency management of genetic diseases. <i>Genome Medicine</i> , 2015, 7, 100.	8.2	237
7	Constellation: a tool for rapid, automated phenotype assignment of a highly polymorphic pharmacogene, CYP2D6, from whole-genome sequences. <i>Npj Genomic Medicine</i> , 2016, 1, 15007.	3.8	93
8	Exome sequencing reveals a pallidin mutation in a Hermansky-Pudlak-like primary immunodeficiency syndrome. <i>Blood</i> , 2012, 119, 3185-3187.	1.4	76
9	Comprehensive viral enrichment enables sensitive respiratory virus genomic identification and analysis by next generation sequencing. <i>Genome Research</i> , 2018, 28, 869-877.	5.5	74
10	An integrated transcriptome and expressed variant analysis of sepsis survival and death. <i>Genome Medicine</i> , 2014, 6, 111.	8.2	70
11	Diagnosis of mitochondrial disorders by concomitant next-generation sequencing of the exome and mitochondrial genome. <i>Genomics</i> , 2013, 102, 148-156.	2.9	68
12	Defining the relationship between vaginal and urinary microbiomes. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, 154.e1-154.e10.	1.3	66
13	The urinary microbiome in women with mixed urinary incontinence compared to similarly aged controls. <i>International Urogynecology Journal</i> , 2018, 29, 1785-1795.	1.4	58
14	Next-generation community genetics for low- and middle-income countries. <i>Genome Medicine</i> , 2012, 4, 25.	8.2	51
15	Adopting orphans: comprehensive genetic testing of Mendelian diseases of childhood by next-generation sequencing. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 855-868.	3.1	45
16	De novo frameshift mutation in ASXL3 in a patient with global developmental delay, microcephaly, and craniofacial anomalies. <i>BMC Medical Genomics</i> , 2013, 6, 32.	1.5	43
17	Utility of Next Generation Sequencing in Clinical Primary Immunodeficiencies. <i>Current Allergy and Asthma Reports</i> , 2014, 14, 468.	5.3	40
18	Human Metapneumovirus Inhibits IFN- γ Signaling through Inhibition of STAT1 Phosphorylation. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2008, 38, 661-670.	2.9	39

#	ARTICLE	IF	CITATIONS
19	Renal systems biology of patients with systemic inflammatory response syndrome. <i>Kidney International</i> , 2015, 88, 804-814.	5.2	38
20	Molecular diagnosis of infantile onset inflammatory bowel disease by exome sequencing. <i>Genomics</i> , 2013, 102, 442-447.	2.9	35
21	Combined DOCK8 and CLEC7A mutations causing immunodeficiency in 3 brothers with diarrhea, eczema, and infections. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 594-597.e3.	2.9	22
22	Regulation of STAT signaling in mouse bone marrow derived dendritic cells by respiratory syncytial virus. <i>Virus Research</i> , 2011, 156, 127-133.	2.2	18
23	Methodology for a vaginal and urinary microbiome study in women with mixed urinary incontinence. <i>International Urogynecology Journal</i> , 2017, 28, 711-720.	1.4	17
24	The role of next generation sequencing in infection prevention in human parainfluenza virus 3 infections in immunocompromised patients. <i>Journal of Clinical Virology</i> , 2017, 92, 53-55.	3.1	15
25	Expansion of CCR4+ activated T cells is associated with memory B cell reduction in DOCK8-deficient patients. <i>Clinical Immunology</i> , 2014, 152, 164-170.	3.2	11
26	Non-autophagy Role of Atg5 and NBR1 in Unconventional Secretion of IL-12 Prevents Gut Dysbiosis and Inflammation. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 259-274.	1.3	10
27	Complete genome sequence of a KI polyomavirus isolated from an otherwise healthy child with severe lower respiratory tract infection. <i>Journal of Medical Virology</i> , 2017, 89, 926-930.	5.0	8
28	Viral infection and allergy status impact severity of asthma symptoms in children with asthma exacerbations. <i>Annals of Allergy, Asthma and Immunology</i> , 2022, 129, 319-326.e3.	1.0	6
29	Complete Genome Sequence of a Novel Human WU Polyomavirus Isolate Associated with Acute Respiratory Infection. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
30	Complete Genome Sequences of Four Novel Human Coronavirus OC43 Isolates Associated with Severe Acute Respiratory Infection. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
31	Genome and Exome Sequencing. , 2019, , 19-30.		0