# Darrell L Dinwiddie

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10812834/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 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 | Non-autophagy Role of Atg5 and NBR1 in Unconventional Secretion of IL-12 Prevents Gut Dysbiosis and Inflammation. Journal of Crohn's and Colitis, 2022, 16, 259-274. | 1.3 | 10 |
| 2 | Viral infection and allergy status impact severity of asthma symptoms in children with asthma exacerbations. Annals of Allergy, Asthma and Immunology, 2022, 129, 319-326.e3. | 1.0 | 6 |
| 3 | Defining the relationship between vaginal and urinary microbiomes. American Journal of Obstetrics and Gynecology, 2020, 222, 154.e1-154.e10. | 1.3 | 66 |
| 4 | Genome and Exome Sequencing. , 2019, , 19-30. | | 0 |
| 5 | Comprehensive viral enrichment enables sensitive respiratory virus genomic identification and analysis by next generation sequencing. Genome Research, 2018, 28, 869-877. | 5.5 | 74 |
| 6 | Complete Genome Sequences of Four Novel Human Coronavirus OC43 Isolates Associated with Severe Acute Respiratory Infection. Genome Announcements, 2018, 6, . | 0.8 | 1 |
| 7 | The urinary microbiome in women with mixed urinary incontinence compared to similarly aged controls. International Urogynecology Journal, 2018, 29, 1785-1795. | 1.4 | 58 |
| 8 | The role of next generation sequencing in infection prevention in human parainfluenza virus 3 infections in immunocompromised patients. Journal of Clinical Virology, 2017, 92, 53-55. | 3.1 | 15 |
| 9 | Methodology for a vaginal and urinary microbiome study in women with mixed urinary incontinence. International Urogynecology Journal, 2017, 28, 711-720. | 1.4 | 17 |
| 10 | Complete genome sequence of a KI polyomavirus isolated from an otherwise healthy child with severe lower respiratory tract infection. Journal of Medical Virology, 2017, 89, 926-930. | 5.0 | 8 |
| 11 | Constellation: a tool for rapid, automated phenotype assignment of a highly polymorphic pharmacogene, CYP2D6, from whole-genome sequences. Npj Genomic Medicine, 2016, 1, 15007. | 3.8 | 93 |
| 12 | Complete Genome Sequence of a Novel Human WU Polyomavirus Isolate Associated with Acute Respiratory Infection. Genome Announcements, 2016, 4, . | 0.8 | 4 |
| 13 | Early-onset lymphoproliferation and autoimmunity caused by germline STAT3 gain-of-function mutations. Blood, 2015, 125, 591-599. | 1.4 | 436 |
| 14 | Renal systems biology of patients with systemic inflammatory response syndrome. Kidney International, 2015, 88, 804-814. | 5.2 | 38 |
| 15 | A 26-hour system of highly sensitive whole genome sequencing for emergency management of genetic diseases. Genome Medicine, 2015, 7, 100. | 8.2 | 237 |
| 16 | An integrated transcriptome and expressed variant analysis of sepsis survival and death. Genome Medicine, 2014, 6, 111. | 8.2 | 70 |
| 17 | Effectiveness of exome and genome sequencing guided by acuity of illness for diagnosis of neurodevelopmental disorders. Science Translational Medicine, 2014, 6, 265ra168. | 12.4 | 440 |
| 18 | Utility of Next Generation Sequencing in Clinical Primary Immunodeficiencies. Current Allergy and Asthma Reports, 2014, 14, 468. | 5.3 | 40 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Expansion of CCR4+ activated T cells is associated with memory B cell reduction in DOCK8-deficient patients. Clinical Immunology, 2014, 152, 164-170. | 3.2 | 11 |
| 20 | Diagnosis of mitochondrial disorders by concomitant next-generation sequencing of the exome and mitochondrial genome. Genomics, 2013, 102, 148-156. | 2.9 | 68 |
| 21 | Molecular diagnosis of infantile onset inflammatory bowel disease by exome sequencing. Genomics, 2013, 102, 442-447. | 2.9 | 35 |
| 22 | Combined DOCK8 and CLEC7A mutations causing immunodeficiency in 3 brothers with diarrhea, eczema, and infections. Journal of Allergy and Clinical Immunology, 2013, 131, 594-597.e3. | 2.9 | 22 |
| 23 | De novoframeshift mutation in ASXL3 in a patient with global developmental delay, microcephaly, and craniofacial anomalies. BMC Medical Genomics, 2013, 6, 32. | 1.5 | 43 |
| 24 | An Integrated Clinico-Metabolomic Model Improves Prediction of Death in Sepsis. Science Translational Medicine, 2013, 5, 195ra95. | 12.4 | 380 |
| 25 | Next-generation community genetics for low- and middle-income countries. Genome Medicine, 2012, 4, 25. | 8.2 | 51 |
| 26 | Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen Phytophthora capsici. Molecular Plant-Microbe Interactions, 2012, 25, 1350-1360. | 2.6 | 264 |
| 27 | Exome sequencing reveals a pallidin mutation in a Hermansky-Pudlakâ€“like primary immunodeficiency syndrome. Blood, 2012, 119, 3185-3187. | 1.4 | 76 |
| 28 | Adopting orphans: comprehensive genetic testing of Mendelian diseases of childhood by next-generation sequencing. Expert Review of Molecular Diagnostics, 2011, 11, 855-868. | 3.1 | 45 |
| 29 | Carrier Testing for Severe Childhood Recessive Diseases by Next-Generation Sequencing. Science Translational Medicine, 2011, 3, 65ra4. | 12.4 | 600 |
| 30 | Regulation of STAT signaling in mouse bone marrow derived dendritic cells by respiratory syncytial virus. Virus Research, 2011, 156, 127-133. | 2.2 | 18 |
| 31 | Human Metapneumovirus Inhibits IFN-Î± Signaling through Inhibition of STAT1 Phosphorylation. American Journal of Respiratory Cell and Molecular Biology, 2008, 38, 661-670. | 2.9 | 39 |