Karine Megy

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3748785/publications.pdf

Version: 2024-02-01

30 papers	6,463 citations	257450 24 h-index	434195 31 g-index
37 all docs	37 docs citations	37 times ranked	13544 citing authors

#	Article	IF	Citations
1	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
2	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	12.6	1,025
3	Genomic insights into the Ixodes scapularis tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.	12.8	450
4	Sequencing of Culex quinquefasciatus Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	12.6	424
5	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
6	Comprehensive Rare Variant Analysis via Whole-Genome Sequencing to Determine the Molecular Pathology of Inherited Retinal Disease. American Journal of Human Genetics, 2017, 100, 75-90.	6.2	343
7	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	27.8	338
8	Genome Sequence of the Tsetse Fly (Glossina morsitans): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
9	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	14.5	251
10	VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587.	14.5	234
11	Loss-of-function nuclear factor ÎºB subunit 1 (NFKB1) variants are the most common monogenic cause of common variable immunodeficiency in Europeans. Journal of Allergy and Clinical Immunology, 2018, 142, 1285-1296.	2.9	185
12	Whole genome sequencing reveals that genetic conditions are frequent in intensively ill children. Intensive Care Medicine, 2019, 45, 627-636.	8.2	183
13	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. Nucleic Acids Research, 2012, 40, D91-D97.	14.5	179
14	A high-throughput sequencing test for diagnosing inherited bleeding, thrombotic, and platelet disorders. Blood, 2016, 127, 2791-2803.	1.4	157
15	Pathogenomics of Culex quinquefasciatus and Meta-Analysis of Infection Responses to Diverse Pathogens. Science, 2010, 330, 88-90.	12.6	150
16	Whole-genome sequencing of a sporadic primary immunodeficiency cohort. Nature, 2020, 583, 90-95.	27.8	148
17	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. Nucleic Acids Research, 2012, 40, D729-D734.	14.5	143
18	Diagnostic high-throughput sequencing of 2396 patients with bleeding, thrombotic, and platelet disorders. Blood, 2019, 134, 2082-2091.	1.4	131

#	Article	IF	Citations
19	Phenotypic Characterization of EIF2AK4 Mutation Carriers in a Large Cohort of Patients Diagnosed Clinically With Pulmonary Arterial Hypertension. Circulation, 2017, 136, 2022-2033.	1.6	111
20	VectorBase: a home for invertebrate vectors of human pathogens. Nucleic Acids Research, 2007, 35, D503-D505.	14.5	107
21	Comparative genomics allows the discovery of cis -regulatory elements in mosquitoes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3053-3058.	7.1	45
22	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. Blood, 2020, 136, 1956-1967.	1.4	34
23	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. Blood Advances, 2020, 4, 3495-3506.	5.2	31
24	Germline mutations in the transcription factor IKZF5 cause thrombocytopenia. Blood, 2019, 134, 2070-2081.	1.4	29
25	How common are single gene mutations as a cause for lacunar stroke?. Neurology, 2019, 93, e2007-e2020.	1.1	26
26	Transcriptomic analysis of insecticide resistance in the lymphatic filariasis vector Culex quinquefasciatus. Scientific Reports, 2019, 9, 11406.	3.3	11
27	Advances in understanding the pathogenesis of hereditary macrothrombocytopenia. British Journal of Haematology, 2021, 195, 25-45.	2.5	9
28	Refinements and considerations for trio whole-genome sequence analysis when investigating Mendelian diseases presenting in early childhood. Human Genetics and Genomics Advances, 2022, 3, 100113.	1.7	4
29	Whole Genome Interpretation for a Family of Five. Frontiers in Genetics, 2021, 12, 535123.	2.3	3
30	Multiparameter platelet function analysis of bleeding patients with a prolonged platelet function analyser closure time. British Journal of Haematology, 2022, 196, 1388-1400.	2.5	2