Jane Gibson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2861328/publications.pdf

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63	3,238	186265	155660
papers	citations	28 h-index	55 g-index

65	65	65	6303
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Extended tracts of homozygosity in outbred human populations. Human Molecular Genetics, 2006, 15, 789-795.	2.9	401
2	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. Nature Genetics, 2010, 42, 906-909.	21.4	357
3	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	21.4	269
4	Defining response to anti-VEGF therapies in neovascular AMD. Eye, 2015, 29, 721-731.	2.1	214
5	Common genetic variants associated with open-angle glaucoma. Human Molecular Genetics, 2011, 20, 2464-2471.	2.9	152
6	Genetics and Prognostication in Splenic Marginal Zone Lymphoma: Revelations from Deep Sequencing. Clinical Cancer Research, 2015, 21, 4174-4183.	7.0	129
7	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	2.9	120
8	Next generation exome sequencing of paediatric inflammatory bowel disease patients identifies rare and novel variants in candidate genes. Gut, 2013, 62, 977-984.	12.1	104
9	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. Nature Communications, 2014, 5, 4883.	12.8	89
10	Exome sequence read depth methods for identifying copy number changes. Briefings in Bioinformatics, 2015, 16, 380-392.	6.5	84
11	Genome-wide association study of age-related macular degeneration identifies associated variants in the TNXBâ€“FKBPLâ€“NOTCH4 region of chromosome 6p21.3. Human Molecular Genetics, 2012, 21, 4138-4150.	2.9	80
12	A map of the human genome in linkage disequilibrium units. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11835-11839.	7.1	75
13	Genomic disruption of the histone methyltransferase SETD2 in chronic lymphocytic leukaemia. Leukemia, 2016, 30, 2179-2186.	7.2	69
14	Whole Exome Sequencing Identifies Novel Recurrently Mutated Genes in Patients with Splenic Marginal Zone Lymphoma. PLoS ONE, 2013, 8, e83244.	2.5	66
15	Pharmacogenetic Associations with Vascular Endothelial Growth Factor Inhibition in Participants with Neovascular Age-related Macular Degeneration in the IVAN Study. Ophthalmology, 2013, 120, 2637-2643.	5.2	59
16	A SNP profiling panel for sample tracking in whole-exome sequencing studies. Genome Medicine, 2013, 5, 89.	8.2	57
17	Support for the involvement of complement factor I in age-related macular degeneration. European Journal of Human Genetics, 2010, 18, 15-16.	2.8	54
18	Positional Cloning by Linkage Disequilibrium. American Journal of Human Genetics, 2004, 74, 846-855.	6.2	53

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19	Identification of a functionally significant tri-allelic genotype in the Tyrosinase gene (TYR) causing hypomorphic oculocutaneous albinism (OCA1B). Scientific Reports, 2017, 7, 4415.	3.3	47
20	Impact of population structure, effective bottleneck time, and allele frequency on linkage disequilibrium maps. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 18075-18080.	7.1	44
21	The optimal measure of linkage disequilibrium reduces error in association mapping of affection status. Human Molecular Genetics, 2005, 14, 145-153.	2.9	42
22	Genome-wide association study of primary open angle glaucoma risk and quantitative traits. Molecular Vision, 2012, 18, 1083-92.	1.1	42
23	Distinctive genotypes in infants with Tâ€cell acute lymphoblastic leukaemia. British Journal of Haematology, 2015, 171, 574-584.	2.5	40
24	Age-related Macular Degeneration and Modification of Systemic Complement Factor H Production Through Liver Transplantation. Ophthalmology, 2013, 120, 1612-1618.	5.2	39
25	A genome-wide association study of intra-ocular pressure suggests a novel association in the gene FAM125B in the TwinsUK cohort. Human Molecular Genetics, 2014, 23, 3343-3348.	2.9	39
26	Longitudinal copy number, whole exome and targeted deep sequencing of 'good risk' IGHV-mutated CLL patients with progressive disease. Leukemia, 2016, 30, 1301-1310.	7.2	37
27	Mutations in phospholipase C epsilon 1 are not sufficient to cause diffuse mesangial sclerosis. Kidney International, 2009, 75, 415-419.	5.2	35
28	Clinical Implications of Old and New Genes for Open-Angle Glaucoma. Ophthalmology, 2011, 118, 2389-2397.	5.2	34
29	VEGFR2 Gene Polymorphisms and Response to Antiâ€"Vascular Endothelial Growth Factor Therapy in Age-Related Macular Degeneration. Ophthalmology, 2015, 122, 1563-1568.	5.2	29
30	Determination of a gene and environment risk model for age-related macular degeneration. British Journal of Ophthalmology, 2010, 94, 1382-1387.	3.9	25
31	Systematic Review of Somatic Mutations in Splenic Marginal Zone Lymphoma. Scientific Reports, 2019, 9, 10444.	3.3	23
32	A rare penetrant TIMP3 mutation confers relatively late onset choroidal neovascularisation which can mimic age-related macular degeneration. Eye, 2016, 30, 488-491.	2.1	22
33	Megalencephaly Syndromes: Exome Pipeline Strategies for Detecting Low-Level Mosaic Mutations. PLoS ONE, 2014, 9, e86940.	2.5	20
34	Exome sequencing in tracking clonal evolution in multiple myeloma following therapy. Leukemia, 2013, 27, 1188-1191.	7.2	19
35	Deleterious coding variants in multi-case families with non-syndromic cleft lip and/or palate phenotypes. Scientific Reports, 2016, 6, 30457.	3.3	19
36	Prevalence of myocilin gene mutations in a novel UK cohort of POAG patients. Eye, 2010, 24, 328-333.	2.1	18

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37	Exome Analysis of Patients with Concurrent Pediatric Inflammatory Bowel Disease and Autoimmune Disease. Inflammatory Bowel Diseases, 2015, 21, 1.	1.9	18
38	Complement factor I and age-related macular degeneration. Molecular Vision, 2014, 20, 1253-7.	1.1	18
39	Exome Sequencing in Classic Hairy Cell Leukaemia Reveals Widespread Variation in Acquired Somatic Mutations between Individual Tumours Apart from the Signature BRAF V(600)E Lesion. PLoS ONE, 2016, 11, e0149162.	2.5	17
40	Variation in complement component C1 inhibitor in age-related macular degeneration. Immunobiology, 2012, 217, 251-255.	1.9	15
41	Exome-based linkage disequilibrium maps of individual genes: functional clustering and relationship to disease. Human Genetics, 2013, 132, 233-243.	3.8	15
42	Exome analysis resolves differential diagnosis of familial kidney disease and uncovers a potential confounding variant. Genetical Research, 2013, 95, 165-173.	0.9	14
43	Whole genome sequences are required to fully resolve the linkage disequilibrium structure of human populations. BMC Genomics, 2015, 16, 666.	2.8	14
44	Resolving clinical diagnoses for syndromic cleft lip and/or palate phenotypes using wholeâ€exome sequencing. Clinical Genetics, 2015, 88, 441-449.	2.0	14
45	Cosmopolitan linkage disequilibrium maps. Human Genomics, 2005, 2, 20.	2.9	10
46	Protein over-expression in Escherichia coli triggers adaptation analogous to antimicrobial resistance. Microbial Cell Factories, 2021, 20, 13.	4.0	10
47	A small gene sequencing panel realises a high diagnostic rate in patients with congenital nystagmus following basic phenotyping. Scientific Reports, 2019, 9, 13229.	3.3	9
48	Genomic Analysis of Response to Neoadjuvant Chemotherapy in Esophageal Adenocarcinoma. Cancers, 2021, 13, 3394.	3.7	9
49	Oral cancer â€“ CPD and the GDC. British Dental Journal, 2018, 225, 884-888.	0.6	8
50	Comprehensive sequencing of the myocilin gene in a selected cohort of severe primary open-angle glaucoma patients. Scientific Reports, 2019, 9, 3100.	3.3	8
51	A Comparison of Methods to Detect Recombination Hotspots. Human Heredity, 2008, 66, 157-169.	0.8	7
52	A multimetric approach to analysis of genome-wide association by single markers and composite likelihood. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2592-2597.	7.1	6
53	Genome-wide association of breast cancer: composite likelihood with imputed genotypes. European Journal of Human Genetics, 2011, 19, 194-199.	2.8	6
54	CBL-MZ is not a single biological entity: evidence from genomic analysis and prolonged clinical follow-up. Blood Advances, 2018, 2, 1116-1119.	5.2	6

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55	Risk of anticholinergic burden in adults with intellectual disabilities: a Scottish retrospective cohort study of nÂ=Â17Â220. Journal of Intellectual Disability Research, 2021, 65, 813-830.	2.0	6
56	Composite likelihood-based meta-analysis of breast cancer association studies. Journal of Human Genetics, 2011, 56, 377-382.	2.3	5
57	Phosphodiesterase type 5 inhibitors enhance chemotherapy in preclinical models of esophageal adenocarcinoma by targeting cancer-associated fibroblasts. Cell Reports Medicine, 2022, 3, 100541.	6.5	5
58	Dental attendance, restoration and extractions in adults with intellectual disabilities compared with the general population: a record linkage study. Journal of Intellectual Disability Research, 2020, 64, 980-986.	2.0	4
59	Individual disease risk and multimetric analysis of Crohn disease. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15843-15847.	7.1	3
60	Deep-Sequencing Reveals the Molecular Landscape of Splenic Marginal Zone Lymphoma: Biological and Clinical Implications. Blood, 2014, 124, 76-76.	1.4	1
61	Genetic variants within chromosome 4q28.3 are not reproducibly associated with Age-related Macular Degeneration (AMD). Acta Ophthalmologica, 2011, 89, e603-e604.	1.1	0
62	Local and not systemic factor H production dictates risk of age-related macular degeneration in liver transplant recipients. Immunobiology, 2012, 217, 1182-1183.	1.9	0
63	AMD Risk Alleles Are Not Implicated in Age-Related Macular Degeneration in Patients with Liver Transplantation. Ophthalmology Retina, 2018, 2, 872-874.	2.4	0