Kent Taylor

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11834300/publications.pdf

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23	3,719	430874	580821
papers	citations	18 h-index	25 g-index

25	25	25	9373
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
2	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
3	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
4	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nature Genetics, 2011, 43, 940-947.	21.4	191
5	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
6	Candidate Locus for a Nuclear Modifier Gene for Maternally Inherited Deafness. American Journal of Human Genetics, 2000, 66, 1905-1910.	6.2	103
7	Anti-flagellin (CBir1) phenotypic and genetic CrohnÊ¼s disease associations. Inflammatory Bowel Diseases, 2007, 13, 524-530.	1.9	97
8	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
9	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
10	Plus Disease in Retinopathy of Prematurity. Ophthalmology, 2016, 123, 2338-2344.	5.2	68
11	Plus Disease in Retinopathy of Prematurity. Ophthalmology, 2016, 123, 2345-2351.	5.2	62
12	Modifier locus for mitochondrial DNA disease: Linkage and linkage disequilibrium mapping of a nuclear modifier gene for maternally inherited deafness. Genetics in Medicine, 2001, 3, 177-180.	2.4	56
13	Automated Fundus Image Quality Assessment in Retinopathy of Prematurity Using Deep Convolutional Neural Networks. Ophthalmology Retina, 2019, 3, 444-450.	2.4	45
14	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial STXBP5 and STX2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	2.4	43
15	Evaluation of a Deep Learningâ€“Derived Quantitative Retinopathy of Prematurity Severity Scale. Ophthalmology, 2021, 128, 1070-1076.	5.2	40
16	Combination of innate and adaptive immune alterations increased the likelihood of fibrostenosis in CrohnÊ¼s diseaseâ€. Inflammatory Bowel Diseases, 2010, 16, 1279-1285.	1.9	29
17	Genome-Wide Association Study of Blood Pressure Traits by Hispanic/Latino Background: the Hispanic Community Health Study/Study of Latinos. Scientific Reports, 2017, 7, 10348.	3.3	24
18	Genome-Wide Association Study of Retinopathy in Individuals without Diabetes. PLoS ONE, 2013, 8, e54232.	2.5	22

#	Article	IF	Citations
19	Variability in Plus Disease Identified Using a Deep Learning-Based Retinopathy of Prematurity Severity Scale. Ophthalmology Retina, 2020, 4, 1016-1021.	2.4	18
20	Federated Learning for Multicenter Collaboration in Ophthalmology. Ophthalmology Retina, 2022, 6, 650-656.	2.4	15
21	Plus Disease in Retinopathy of Prematurity: Diagnostic Trends in 2016 Versus 2007. American Journal of Ophthalmology, 2017, 176, 70-76.	3.3	14
22	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
23	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	2.5	8