Martin Oti

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2876527/publications.pdf

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		516710	526287
27	1,832	16	27
papers	citations	h-index	g-index
20	20	20	2200
29	29	29	3399
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Predicting disease genes using protein-protein interactions. Journal of Medical Genetics, 2006, 43, 691-698.	3.2	518
2	Genome-Wide Profiling of p63 DNA–Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. PLoS Genetics, 2010, 6, e1001065.	3.5	169
3	De Novo Mutations in the Genome Organizer CTCF Cause Intellectual Disability. American Journal of Human Genetics, 2013, 93, 124-131.	6.2	151
4	Computational disease gene identification: a concert of methods prioritizes type 2 diabetes and obesity candidate genes. Nucleic Acids Research, 2006, 34, 3067-3081.	14.5	134
5	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. EMBO Reports, 2015, 16, 863-878.	4.5	134
6	Prediction of Human Disease Genes by Human-Mouse Conserved Coexpression Analysis. PLoS Computational Biology, 2008, 4, e1000043.	3.2	119
7	Phenome connections. Trends in Genetics, 2008, 24, 103-106.	6.7	107
8	CTCF-mediated chromatin loops enclose inducible gene regulatory domains. BMC Genomics, 2016, 17, 252.	2.8	58
9	Conservation of divergent transcription in fungi. Trends in Genetics, 2008, 24, 207-211.	6.7	48
10	Systematic analysis of copy number variants of a large cohort of orofacial cleft patients identifies candidate genes for orofacial clefts. Human Genetics, 2016, 135, 41-59.	3.8	42
11	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. Cell Reports, 2018, 25, 3490-3503.e4.	6.4	41
12	Human Intellectual Disability Genes Form Conserved Functional Modules in Drosophila. PLoS Genetics, 2013, 9, e1003911.	3.5	39
13	Conserved co-expression for candidate disease gene prioritization. BMC Bioinformatics, 2008, 9, 208.	2.6	37
14	The Biological Coherence of Human Phenome Databases. American Journal of Human Genetics, 2009, 85, 801-808.	6.2	37
15	Duplicated Enhancer Region Increases Expression of CTSB and Segregates with Keratolytic Winter Erythema in South African and Norwegian Families. American Journal of Human Genetics, 2017, 100, 737-750.	6.2	35
16	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	3.3	28
17	Establishing normal metabolism and differentiation in hepatocellular carcinoma cells by culturing in adult human serum. Scientific Reports, 2018, 8, 11685.	3.3	20
18	Web Tools for the Prioritization of Candidate Disease Genes. Methods in Molecular Biology, 2011, 760, 189-206.	0.9	18

#	Article	IF	CITATIONS
19	Genome-wide p63-regulated gene expression in differentiating epidermal keratinocytes. Genomics Data, 2015, 5, 159-163.	1.3	16
20	A homozygous <i>FITM2 </i> mutation causes a deafness-dystonia syndrome with motor regression and signs of ichthyosis and sensory neuropathy. DMM Disease Models and Mechanisms, 2017, 10, 105-118.	2.4	16
21	Transcriptome Analysis Identifies Multifaceted Regulatory Mechanisms Dictating a Genetic Switch from Neuronal Network Establishment to Maintenance During Postnatal Prefrontal Cortex Development. Cerebral Cortex, 2018, 28, 833-851.	2.9	15
22	Echocardiographic Measurements in a Preclinical Model of Chronic Chagasic Cardiomyopathy in Dogs: Validation and Reproducibility. Frontiers in Cellular and Infection Microbiology, 2019, 9, 332.	3.9	12
23	Candidate disease gene prediction using <i>Gentrepid</i> : application to a genomeâ€wide association study on coronary artery disease. Molecular Genetics & Enomic Medicine, 2014, 2, 44-57.	1.2	11
24	Analysis of genome-wide association study data using the protein knowledge base. BMC Genetics, 2011, 12, 98.	2.7	10
25	Comparative Genomics in Homo sapiens. Methods in Molecular Biology, 2018, 1704, 451-472.	0.9	7
26	GentrepidV2.0: a web server for candidate disease gene prediction. BMC Bioinformatics, 2013, 14, 249.	2.6	6
27	Comparative Genomics in Drosophila. Methods in Molecular Biology, 2018, 1704, 433-450.	0.9	1