Martin Oti

List of Publications by Year in descending order

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

#	Article	IF	Citations
1	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
2	Comparative Genomics in Drosophila. Methods in Molecular Biology, 2018, 1704, 433-450.	0.9	1
3	Comparative Genomics in Homo sapiens. Methods in Molecular Biology, 2018, 1704, 451-472.	0.9	7
4	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
5	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. Cell Reports, 2018, 25, 3490-3503.e4.	6.4	41
6	Establishing normal metabolism and differentiation in hepatocellular carcinoma cells by culturing in adult human serum. Scientific Reports, 2018, 8, 11685.	3.3	20
7	A homozygousFITM2mutation 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
8	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
9	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	3.3	28
10	CTCF-mediated chromatin loops enclose inducible gene regulatory domains. BMC Genomics, 2016, 17, 252.	2.8	58
11	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
12	Genome-wide p63-regulated gene expression in differentiating epidermal keratinocytes. Genomics Data, 2015, 5, 159-163.	1.3	16
13	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. EMBO Reports, 2015, 16, 863-878.	4.5	134
14	Candidate disease gene prediction using Gentrepid: application to a genomeâ€wide association study on coronary artery disease. Molecular Genetics & Genomic Medicine, 2014, 2, 44-57.	1.2	11
15	GentrepidV2.0: a web server for candidate disease gene prediction. BMC Bioinformatics, 2013, 14, 249.	2.6	6
16	De Novo Mutations in the Genome Organizer CTCF Cause Intellectual Disability. American Journal of Human Genetics, 2013, 93, 124-131.	6.2	151
17	Human Intellectual Disability Genes Form Conserved Functional Modules in Drosophila. PLoS Genetics, 2013, 9, e1003911.	3.5	39
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	Analysis of genome-wide association study data using the protein knowledge base. BMC Genetics, 2011, 12, 98.	2.7	10
20	Genome-Wide Profiling of p63 DNAâ€“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
21	The Biological Coherence of Human Phenome Databases. American Journal of Human Genetics, 2009, 85, 801-808.	6.2	37
22	Conserved co-expression for candidate disease gene prioritization. BMC Bioinformatics, 2008, 9, 208.	2.6	37
23	Phenome connections. Trends in Genetics, 2008, 24, 103-106.	6.7	107
24	Conservation of divergent transcription in fungi. Trends in Genetics, 2008, 24, 207-211.	6.7	48
25	Prediction of Human Disease Genes by Human-Mouse Conserved Coexpression Analysis. PLoS Computational Biology, 2008, 4, e1000043.	3.2	119
26	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
27	Predicting disease genes using protein-protein interactions. Journal of Medical Genetics, 2006, 43, 691-698.	3.2	518