

Zeliha Gormez

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

150
citations

1307594

7
h-index

1199594

12
g-index

18
all docs

18
docs citations

18
times ranked

492
citing authors

#	ARTICLE	IF	CITATIONS
1	HomSI: a homozygous stretch identifier from next-generation sequencing data. <i>Bioinformatics</i> , 2014, 30, 445-447.	4.1	45
2	Loss-of-Function Mutations in ELMO2 Cause Intraosseous Vascular Malformation by Impeding RAC1 Signaling. <i>American Journal of Human Genetics</i> , 2016, 99, 299-317.	6.2	23
3	Coffin-Siris syndrome with café-au-lait spots, obesity and hyperinsulinism caused by a mutation in the <i>ARID1B</i> gene. <i>Intractable and Rare Diseases Research</i> , 2016, 5, 222-226.	0.9	14
4	A further family of Stromme syndrome carrying <i>CENPF</i> mutation. <i>American Journal of Medical Genetics, Part A</i> , 2017, 173, 1668-1672.	1.2	12
5	Myophosphorylase (PYGM) mutations determined by next generation sequencing in a cohort from Turkey with McArdle disease. <i>Neuromuscular Disorders</i> , 2017, 27, 997-1008.	0.6	11
6	A clinical variant in SCN1A inherited from a mosaic father cosegregates with a novel variant to cause Dravet syndrome in a consanguineous family. <i>Epilepsy Research</i> , 2015, 113, 5-10.	1.6	8
7	SYNE1 related cerebellar ataxia presents with variable phenotypes in a consanguineous family from Turkey. <i>Neurological Sciences</i> , 2017, 38, 2203-2207.	1.9	8
8	Multi objective SNP selection using pareto optimality. <i>Computational Biology and Chemistry</i> , 2013, 43, 23-28.	2.3	5
9	FMFilter: A fast model based variant filtering tool. <i>Journal of Biomedical Informatics</i> , 2016, 60, 319-327.	4.3	5
10	Exome sequencing identifies a novel homozygous CLN8 mutation in a Turkish family with Northern epilepsy. <i>Acta Neurologica Belgica</i> , 2017, 117, 159-167.	1.1	5
11	A Novel and Mosaic WDR45 Nonsense Variant Causes Beta-Propeller Protein-Associated Neurodegeneration Identified Through Whole Exome Sequencing and X chromosome Heterozygosity Analysis. <i>NeuroMolecular Medicine</i> , 2019, 21, 54-59.	3.4	5
12	A novel truncating mutation of DOCK7 gene with an early-onset non-encephalopathic epilepsy. <i>Seizure: the Journal of the British Epilepsy Association</i> , 2019, 66, 12-14.	2.0	4
13	Evaluation of the Concatenative Turkish Text-to-Speech System. , 2009, , .		2
14	Statistical bias and variance of gene selection and cross validation methods: A case study on hypertension prediction. , 2012, , .		1
15	An Aggregated Cross-Validation Framework for Computational Discovery of Disease-Associative Genes. <i>IFMBE Proceedings</i> , 2016, , 489-494.	0.3	1
16	Expansion of the phenotypic spectrum of SMC1A nonsense variants: a patient with cerebellar atrophy and review of the literature. <i>Clinical Dysmorphology</i> , 2020, 29, 217-223.	0.3	1
17	Comparison of aggregators for multi-objective SNP selection. , 2013, 2013, 3062-5.		0
18	Hypertension prediction by multi-objective optimization methods. , 2014, , .		0