Aparna Prasad

List of Publications by Year in descending order

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1			567281	839539
	18	3,798 citations	15	18
	papers	citations	h-index	g-index
	18	18	18	7625
	10	10	10	7023
	all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	The Temple Grandin Genome: Comprehensive Analysis in a Scientist with High-Functioning Autism. Journal of Personalized Medicine, 2021, 11, 21.	2.5	5
2	Critical exon indexing improves clinical interpretation of copy number variants in neurodevelopmental disorders. Neurology: Genetics, 2019, 5, e378.	1.9	4
3	Clinical utility of exome sequencing in individuals with large homozygous regions detected by chromosomal microarray analysis. BMC Medical Genetics, 2018, 19, 46.	2.1	18
4	Identification of Gene Mutations and Fusion Genes in Patients with Sézary Syndrome. Journal of Investigative Dermatology, 2016, 136, 1490-1499.	0.7	77
5	Rare exonic deletions implicate the synaptic organizer Gephyrin (GPHN) in risk for autism, schizophrenia and seizures. Human Molecular Genetics, 2013, 22, 2055-2066.	2.9	139
6	A Discovery Resource of Rare Copy Number Variations in Individuals with Autism Spectrum Disorder. G3: Genes, Genomes, Genetics, 2012, 2, 1665-1685.	1.8	175
7	Rare Deletions at the Neurexin 3 Locus in Autism Spectrum Disorder. American Journal of Human Genetics, 2012, 90, 133-141.	6.2	182
8	SHANK1 Deletions in Males with Autism Spectrum Disorder. American Journal of Human Genetics, 2012, 90, 879-887.	6.2	292
9	Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants. Nature Biotechnology, 2011, 29, 512-520.	17.5	384
10	Variant detection and the Autism sequencing project. BMC Bioinformatics, 2011, 12, .	2.6	1
10		2.6	22
	Variant detection and the Autism sequencing project. BMC Bioinformatics, 2011, 12, . A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. BMC Genetics, 2010, 11,		
11	Variant detection and the Autism sequencing project. BMC Bioinformatics, 2011, 12, . A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. BMC Genetics, 2010, 11, 20. Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010,	2.7	22
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11 12 13	Variant detection and the Autism sequencing project. BMC Bioinformatics, 2011, 12, . A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. BMC Genetics, 2010, 11, 20. Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372. A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082. A first generation whole genome RH map of the river buffalo with comparison to domestic cattle.	2.7 27.8 2.9	1,803 538
11 12 13	Variant detection and the Autism sequencing project. BMC Bioinformatics, 2011, 12, . A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. BMC Genetics, 2010, 11, 20. Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372. A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082. A first generation whole genome RH map of the river buffalo with comparison to domestic cattle. BMC Genomics, 2008, 9, 631. High resolution radiation hybrid maps of bovine chromosomes 19 and 29: comparison with the bovine	2.7 27.8 2.9 2.8	1,803 538 78
11 12 13 14	Variant detection and the Autism sequencing project. BMC Bioinformatics, 2011, 12, . A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. BMC Genetics, 2010, 11, 20. Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372. A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082. A first generation whole genome RH map of the river buffalo with comparison to domestic cattle. BMC Genomics, 2008, 9, 631. High resolution radiation hybrid maps of bovine chromosomes 19 and 29: comparison with the bovine genome sequence assembly. BMC Genomics, 2007, 8, 310. A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. BMC	2.7 27.8 2.9 2.8	1,803 538 78