Suresh B Mudunuri

List of Publications by Year in descending order

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1307594 1474206 14 941 7 9 citations g-index h-index papers 15 15 15 1272 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Meta-analysis of tRNA derived RNA fragments reveals that they are evolutionarily conserved and associate with AGO proteins to recognize specific RNA targets. BMC Biology, 2014, 12, 78.	3.8	455
2	tRFdb: a database for transfer RNA fragments. Nucleic Acids Research, 2015, 43, D141-D145.	14.5	216
3	IMEx: Imperfect Microsatellite Extractor. Bioinformatics, 2007, 23, 1181-1187.	4.1	190
4	ChloroMitoSSRDB: Open Source Repository of Perfect and Imperfect Repeats in Organelle Genomes for Evolutionary Genomics. DNA Research, 2013, 20, 127-133.	3.4	24
5	ChloroMitoSSRDB 2.00: more genomes, more repeats, unifying SSRs search patterns and on-the-fly repeat detection. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav084.	3.0	23
6	G-IMEx: A comprehensive software tool for detection of microsatellites from genome sequences. Bioinformation, 2010, 5, 221-223.	0.5	12
7	Chloroplast genomics: Expanding resources for an evolutionary conserved miniature molecule with enigmatic applications. Current Plant Biology, 2016, 7-8, 34-38.	4.7	8
8	MICdb3.0: a comprehensive resource of microsatellite repeats from prokaryotic genomes. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau005-bau005.	3.0	7
9	Comparative analysis of microsatellite detecting software. , 2010, , .		2
10	Distributional analysis and motif frequencies of compound microsatellite repeats in viral genomes. , 2012, , .		1
11	Microsatellite Repeats in Mitochondrial Genomes. , 2015, , .		1
12	In silico survey of distribution and frequency of imperfect microsatellite repeats in viral genomes. , 2012, , .		0
13	Evaluation of Genome-Wide Markers and Orthologous Markers in Brachypodium distachyon. Methods in Molecular Biology, 2018, 1667, 195-201.	0.9	0
14	Short Tandem Repeats in Certain Human Genes Reveal a Positive Correlation towards Evolution. Advances in Intelligent and Soft Computing, 2012, , 437-443.	0.2	0