

A tale of three next generation sequencing platforms: co biosciences and illumina MiSeq sequencers

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Improved Protocols for the Illumina Genome Analyzer Sequencing System. <i>Current Protocols in Human Genetics</i> , 2009, 62, Unit 18.2.	3.5	108
2	The battle for sequencing supremacy. <i>Nature Biotechnology</i> , 2012, 30, 1023-1026.	9.4	20
3	The human gut microbiome: the ghost in the machine. <i>Future Microbiology</i> , 2012, 7, 1235-1237.	1.0	11
4	Current mutation discovery approaches in Retinitis Pigmentosa. <i>Vision Research</i> , 2012, 75, 117-129.	0.7	57
5	Characterizing and measuring bias in sequence data. <i>Genome Biology</i> , 2013, 14, R51.	13.9	695
6	Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. <i>GigaScience</i> , 2013, 2, 4.	3.3	227
7	“Big data”™, Hadoop and cloud computing in genomics. <i>Journal of Biomedical Informatics</i> , 2013, 46, 774-781.	2.5	378
8	Clinical Validation of a Next-Generation Sequencing Screen for Mutational Hotspots in 46 Cancer-Related Genes. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 607-622.	1.2	314
9	Comparison of direct boiling method with commercial kits for extracting fecal microbiome DNA by Illumina sequencing of 16S rRNA tags. <i>Journal of Microbiological Methods</i> , 2013, 95, 455-462.	0.7	82
10	Read and assembly metrics inconsequential for clinical utility of whole-genome sequencing in mapping outbreaks. <i>Nature Biotechnology</i> , 2013, 31, 592-594.	9.4	26
11	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. <i>BMC Genomics</i> , 2013, 14, 449.	1.2	118
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17	Efficacy of a 3rd generation high-throughput sequencing platform for analyses of 16S rRNA genes from environmental samples. <i>Journal of Microbiological Methods</i> , 2013, 95, 175-181.	0.7	110
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19	Next-Generation Sequencing: Methodology and Application. <i>Journal of Investigative Dermatology</i> , 2013, 133, 1-4.	0.3	221

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21	A statistical variant calling approach from pedigree information and local haplotyping with phase informative reads. <i>Bioinformatics</i> , 2013, 29, 2835-2843.	1.8	13
22	Pheromone Evolution, Reproductive Genes, and Comparative Transcriptomics in Mediterranean Earthworms (Annelida, Oligochaeta, Hormogastridae). <i>Molecular Biology and Evolution</i> , 2013, 30, 1614-1629.	3.5	24
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