

Stephen A Rudd

List of Publications by Year in descending order

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43
papers

13,515
citations

230014

27
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325983

40
g-index

43
all docs

43
docs citations

43
times ranked

17126
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
2	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003, 422, 859-868.	13.7	1,528
3	An RNA-Dependent RNA Polymerase Gene in <i>Arabidopsis</i> Is Required for Posttranscriptional Gene Silencing Mediated by a Transgene but Not by a Virus. <i>Cell</i> , 2000, 101, 543-553.	13.5	956
4	Maintenance of ancestral complexity and non-metazoan genes in two basal cnidarians. <i>Trends in Genetics</i> , 2005, 21, 633-639.	2.9	315
5	Expressed sequence tags: alternative or complement to whole genome sequences?. <i>Trends in Plant Science</i> , 2003, 8, 321-329.	4.3	263
6	Gene expression and metabolite profiling of <i>Populus euphratica</i> growing in the Negev desert. <i>Genome Biology</i> , 2005, 6, R101.	13.9	208
7	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	13.7	188
8	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	13.7	175
9	MIPS <i>Arabidopsisthaliana</i> Database (MAtdB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002, 30, 91-93.	6.5	159
10	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.	2.8	137
11	Microarray analysis identifies candidate genes for key roles in coral development. <i>BMC Genomics</i> , 2008, 9, 540.	1.2	119
12	Expression profiling of the lignin biosynthetic pathway in Norway spruce using EST sequencing and real-time RT-PCR. <i>Plant Molecular Biology</i> , 2007, 65, 311-328.	2.0	92
13	Characterization of an 18,166 EST dataset for cassava (<i>Manihot esculenta</i> Crantz) enriched for drought-responsive genes. <i>Plant Cell Reports</i> , 2007, 26, 1605-1618.	2.8	90
14	Identification of NdhL and Ssl1690 (NdhO) in NDH-1L and NDH-1M Complexes of <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Biological Chemistry</i> , 2005, 280, 2587-2595.	1.6	86
15	A wing expressed sequence tag resource for <i>Bicyclus anynana</i> butterflies, an evo-devo model. <i>BMC Genomics</i> , 2006, 7, 130.	1.2	85
16	Characterization of the Maize Endosperm Transcriptome and Its Comparison to the Rice Genome. <i>Genome Research</i> , 2004, 14, 1932-1937.	2.4	80
17	Analysis of the floral transcriptome uncovers new regulators of organ determination and gene families related to flower organ differentiation in <i>Gerbera hybrida</i> (Asteraceae). <i>Genome Research</i> , 2005, 15, 475-486.	2.4	75
18	Expressed sequence tag analysis in <i>Cycas</i> , the most primitive living seed plant. <i>Genome Biology</i> , 2003, 4, R78.	13.9	74

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19	Comparative mapping of DNA sequences in rye (<i>Secale cereale</i> L.) in relation to the rice genome. <i>Theoretical and Applied Genetics</i> , 2009, 118, 371-384.	1.8	56
20	Sputnik: a database platform for comparative plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 128-132.	6.5	44
21	Genome-Wide in Silico Mapping of Scaffold/Matrix Attachment Regions in Arabidopsis Suggests Correlation of Intragenic Scaffold/Matrix Attachment Regions with Gene Expression. <i>Plant Physiology</i> , 2004, 135, 715-722.	2.3	40
22	PlantMarkers--a database of predicted molecular markers from plants. <i>Nucleic Acids Research</i> , 2004, 33, D628-D632.	6.5	40
23	EST analysis in <i>Ginkgo biloba</i> : an assessment of conserved developmental regulators and gymnosperm specific genes. <i>BMC Genomics</i> , 2005, 6, 143.	1.2	34
24	Programmed Ribosomal Frameshift Alters Expression of West Nile Virus Genes and Facilitates Virus Replication in Birds and Mosquitoes. <i>PLoS Pathogens</i> , 2014, 10, e1004447.	2.1	33
25	Whole transcriptome characterization of the effects of dehydration and rehydration on <i>Cladonia rangiferina</i> , the grey reindeer lichen. <i>BMC Genomics</i> , 2013, 14, 870.	1.2	31
26	Spatiotemporal Expression Control Correlates with Intragenic Scaffold Matrix Attachment Regions (S/MARs) in <i>Arabidopsis thaliana</i> . <i>PLoS Computational Biology</i> , 2006, 2, e21.	1.5	29
27	Proteomic screen in the simple metazoan Hydra identifies 14-3-3 binding proteins implicated in cellular metabolism, cytoskeletal organisation and Ca ²⁺ signalling. <i>BMC Cell Biology</i> , 2007, 8, 31.	3.0	29
28	openSputnik--a database to ESTablish comparative plant genomics using unsaturated sequence collections. <i>Nucleic Acids Research</i> , 2004, 33, D622-D627.	6.5	28
29	Characterization of a transcriptome from a non-model organism, <i>Cladonia rangiferina</i> , the grey reindeer lichen, using high-throughput next generation sequencing and EST sequence data. <i>BMC Genomics</i> , 2012, 13, 575.	1.2	26
30	Genetic screen for signal peptides in Hydra reveals novel secreted proteins and evidence for non-classical protein secretion. <i>European Journal of Cell Biology</i> , 2006, 85, 1107-1117.	1.6	25
31	Support vector machines for separation of mixed plant-pathogen EST collections based on codon usage. <i>Bioinformatics</i> , 2005, 21, 1383-1388.	1.8	23
32	Analysis of EST sequences suggests recent origin of allotetraploid colonial and creeping bentgrasses. <i>Molecular Genetics and Genomics</i> , 2007, 278, 197-209.	1.0	22
33	A 6374 Unigene Set Corresponding to Low Abundance Transcripts Expressed Following Fertilization in <i>Solanum chacoense</i> Bitt, and Characterization of 30 Receptor-like Kinases. <i>Plant Molecular Biology</i> , 2005, 59, 515-532.	2.0	20
34	Separation of sequences from host-pathogen interface using triplet nucleotide frequencies. <i>Fungal Genetics and Biology</i> , 2007, 44, 231-241.	0.9	16
35	Optimization and comparison of different methods for RNA isolation for cDNA library construction from the reindeer lichen <i>Cladonia rangiferina</i> . <i>BMC Research Notes</i> , 2009, 2, 204.	0.6	14
36	Construction, database integration, and application of an <i>Oenothera</i> EST library. <i>Genomics</i> , 2006, 88, 372-380.	1.3	12

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37	Prospecting for pig single nucleotide polymorphisms in the human genome: have we struck gold?. Journal of Animal Breeding and Genetics, 2006, 123, 145-151.	0.8	10
38	Draft Genome Sequences of Helicobacter pylori Isolates from Malaysia, Cultured from Patients with Functional Dyspepsia and Gastric Cancer. Journal of Bacteriology, 2012, 194, 5695-5696.	1.0	7
39	Eclair—a web service for unravelling species origin of sequences sampled from mixed host interfaces. Nucleic Acids Research, 2005, 33, W724-W727.	6.5	4
40	Arabidopsis genome analysis as exemplified by analysis of chromosome 4. Briefings in Bioinformatics, 2000, 1, 389-397.	3.2	3
41	Genomeless Genomics in Crop Improvement. , 2007, , 151-176.		2
42	Expressed Sequence Tag Analysis in Cycas. , 2011, , 21-35.		1
43	The Arabidopsis Genome and Its Use in Cereal Genomics. , 2004, , 515-534.		0