

Daniel S Rokhsar

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

158
papers

42,932
citations

81
h-index

165
g-index

165
ext. papers

50,763
ext. citations

18.1
avg. IF

6.41
L-index

#	Paper	IF	Citations
158	Deeply conserved synteny and the evolution of metazoan chromosomes.. <i>Science Advances</i> , 2022 , 8, eabi5884	14.3	5
157	Chromosome evolution and the genetic basis of agronomically important traits in greater yam.. <i>Nature Communications</i> , 2022 , 13, 2001	17.4	2
156	Genome and transcriptome mechanisms driving cephalopod evolution.. <i>Nature Communications</i> , 2022 , 13, 2427	17.4	3
155	Plant Pan-Genomics Comes of Age. <i>Annual Review of Plant Biology</i> , 2021 , 72, 411-435	30.7	11
154	Phylogenomics illuminates the evolution of bobtail and bottletail squid (order Sepiolida). <i>Communications Biology</i> , 2021 , 4, 819	6.7	2
153	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021 , 590, 438-444	39.4	42
152	Current status and impending progress for cassava structural genomics. <i>Plant Molecular Biology</i> , 2021 , 1	4.6	3
151	Diversification of mandarin citrus by hybrid speciation and apomixis. <i>Nature Communications</i> , 2021 , 12, 4377	17.4	4
150	Analysis of meiosis in reveals plasticity in homolog pairing and synapsis in the nematode lineage. <i>ELife</i> , 2021 , 10,	8.9	4
149	Terabase-scale metagenome coassembly with MetaHipMer. <i>Scientific Reports</i> , 2020 , 10, 10689	4.9	7
148	The citrus genome 2020 , 1-8		1
147	The origin of citrus 2020 , 9-31		6
146	A chromosome-scale reference genome of trifoliolate orange (<i>Poncirus trifoliata</i>) provides insights into disease resistance, cold tolerance and genome evolution in Citrus. <i>Plant Journal</i> , 2020 , 104, 1215-1232	6.9	17
145	Gradual polyploid genome evolution revealed by pan-genomic analysis of <i>Brachypodium hybridum</i> and its diploid progenitors. <i>Nature Communications</i> , 2020 , 11, 3670	17.4	22
144	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020 , 11, 5442	17.4	22
143	Analysis of muntjac deer genome and chromatin architecture reveals rapid karyotype evolution. <i>Communications Biology</i> , 2020 , 3, 480	6.7	8
142	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020 , 4, 820-830	12.3	91

141	Symbiotic organs shaped by distinct modes of genome evolution in cephalopods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3030-3035	11.5	72
140	Ancient polymorphisms contribute to genome-wide variation by long-term balancing selection and divergent sorting in <i>Boechera stricta</i> . <i>Genome Biology</i> , 2019 , 20, 126	18.3	15
139	Acoel genome reveals the regulatory landscape of whole-body regeneration. <i>Science</i> , 2019 , 363,	33.3	61
138	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2019 , 452, 8-20	3.1	16
137	New bobtail squid (Sepiolidae: Sepiolinae) from the Ryukyu islands revealed by molecular and morphological analysis. <i>Communications Biology</i> , 2019 , 2, 465	6.7	5
136	A New Spiralian Phylogeny Places the Enigmatic Arrow Worms among Gnathiferans. <i>Current Biology</i> , 2019 , 29, 312-318.e3	6.3	116
135	Genomics of the origin and evolution of Citrus. <i>Nature</i> , 2018 , 554, 311-316	50.4	295
134	Assembly of the <i>Boechera retrofracta</i> Genome and Evolutionary Analysis of Apomixis-Associated Genes. <i>Genes</i> , 2018 , 9,	4.2	14
133	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018 , 9, 5213	17.4	51
132	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017 , 1, 119	12.3	59
131	Insights into the red algae and eukaryotic evolution from the genome of (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E6361-E6370	11.5	131
130	QTL associated with resistance to cassava brown streak and cassava mosaic diseases in a bi-parental cross of two Tanzanian farmer varieties, Namikonga and Albert. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 2069-2090	6	24
129	Genome organization of the vg1 and nodal3 gene clusters in the allotetraploid frog <i>Xenopus laevis</i> . <i>Developmental Biology</i> , 2017 , 426, 236-244	3.1	1
128	QTL Mapping for Pest and Disease Resistance in Cassava and Coincidence of Some QTL with Introgression Regions Derived from. <i>Frontiers in Plant Science</i> , 2017 , 8, 1168	6.2	34
127	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016 , 538, 336-343	50.4	510
126	Development of a toolbox to dissect host-endosymbiont interactions and protein trafficking in the trypanosomatid <i>Angomonas deanei</i> . <i>BMC Evolutionary Biology</i> , 2016 , 16, 247	3	16
125	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. <i>Genome Research</i> , 2016 , 26, 342-50	9.7	415
124	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. <i>Nature Biotechnology</i> , 2016 , 34, 562-70	44.5	233

123	Syntax compensates for poor binding sites to encode tissue specificity of developmental enhancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 6508-13	11.5	84
122	Genome Assembly Improvement and Mapping Convergently Evolved Skeletal Traits in Sticklebacks with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1463-72	3.2	76
121	The deuterostome context of chordate origins. <i>Nature</i> , 2015 , 520, 456-65	50.4	81
120	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015 , 16, 26	18.3	190
119	A New Nomenclature of <i>Xenopus laevis</i> Chromosomes Based on the Phylogenetic Relationship to <i>Silurana/Xenopus tropicalis</i> . <i>Cytogenetic and Genome Research</i> , 2015 , 145, 187-91	1.9	43
118	merAligner: A Fully Parallel Sequence Aligner 2015 ,		20
117	The genetics of divergence and reproductive isolation between ecotypes of <i>Panicum hallii</i> . <i>New Phytologist</i> , 2015 , 205, 402-14	9.8	39
116	The octopus genome and the evolution of cephalopod neural and morphological novelties. <i>Nature</i> , 2015 , 524, 220-4	50.4	343
115	Suboptimization of developmental enhancers. <i>Science</i> , 2015 , 350, 325-8	33.3	158
114	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015 , 527, 459-65	50.4	144
113	HipMer 2015 ,		38
112	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014 , 32, 656-62	44.5	413
111	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014 , 510, 356-62	50.4	497
110	Chordate evolution and the three-phylum system. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281, 20141729	4.4	107
109	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014 , 46, 707-13	36.3	772
108	Parallel De Bruijn Graph Construction and Traversal for De Novo Genome Assembly 2014 ,		43
107	Efficient and accurate clustering for large-scale genetic mapping 2014 ,		4
106	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461

105	A detailed gene expression study of the <i>Miscanthus</i> genus reveals changes in the transcriptome associated with the rejuvenation of spring rhizomes. <i>BMC Genomics</i> , 2013 , 14, 864	4.5	26
104	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013 , 76, 718-27	6.9	219
103	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013 , 493, 526-31	50.4	424
102	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013 , 45, 487-94	36.3	777
101	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013 , 45, 831-5	36.3	274
100	Fine-scale variation in meiotic recombination in <i>Mimulus</i> inferred from population shotgun sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19478-82	11.5	140
99	Whole genome comparisons of <i>Fragaria</i> , <i>Prunus</i> and <i>Malus</i> reveal different modes of evolution between Rosaceous subfamilies. <i>BMC Genomics</i> , 2012 , 13, 129	4.5	62
98	A framework genetic map for <i>Miscanthus sinensis</i> from RNAseq-based markers shows recent tetraploidy. <i>BMC Genomics</i> , 2012 , 13, 142	4.5	75
97	Identical genomic organization of two hemichordate hox clusters. <i>Current Biology</i> , 2012 , 22, 2053-8	6.3	35
96	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012 , 492, 423-7	50.4	839
95	A genome-wide survey of switchgrass genome structure and organization. <i>PLoS ONE</i> , 2012 , 7, e33892	3.7	43
94	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012 , 30, 555-61	44.5	573
93	The Cassava Genome: Current Progress, Future Directions. <i>Tropical Plant Biology</i> , 2012 , 5, 88-94	1.6	215
92	Phytozome: a comparative platform for green plant genomics. <i>Nucleic Acids Research</i> , 2012 , 40, D1178-86	60.1	2713
91	The genome portal of the Department of Energy Joint Genome Institute. <i>Nucleic Acids Research</i> , 2012 , 40, D26-32	20.1	359
90	The <i>Selaginella</i> genome identifies genetic changes associated with the evolution of vascular plants. <i>Science</i> , 2011 , 332, 960-3	33.3	622
89	Development and initial characterization of a HAPPY panel for mapping the <i>X. tropicalis</i> genome. <i>International Journal of Biological Sciences</i> , 2011 , 7, 1037-44	11.2	4
88	Meraculous: de novo genome assembly with short paired-end reads. <i>PLoS ONE</i> , 2011 , 6, e23501	3.7	120

87	The Eucalyptus grandis Genome Project: Genome and transcriptome resources for comparative analysis of woody plant biology. <i>BMC Proceedings</i> , 2011 , 5,	2.3	21
86	Populus resequencing: towards genome-wide association studies. <i>BMC Proceedings</i> , 2011 , 5,	2.3	6
85	A segmental genomic duplication generates a functional intron. <i>Nature Communications</i> , 2011 , 2, 454	17.4	7
84	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
83	Nuclear-localized tiny RNAs are associated with transcription initiation and splice sites in metazoans. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 1030-4	17.6	134
82	The dynamic genome of Hydra. <i>Nature</i> , 2010 , 464, 592-6	50.4	613
81	The Amphimedon queenslandica genome and the evolution of animal complexity. <i>Nature</i> , 2010 , 466, 720-6	50.4	782
80	The genome of the Western clawed frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010 , 328, 633-6	33.3	579
79	The genome of <i>Naegleria gruberi</i> illuminates early eukaryotic versatility. <i>Cell</i> , 2010 , 140, 631-42	56.2	346
78	Genomic analysis of organismal complexity in the multicellular green alga <i>Volvox carteri</i> . <i>Science</i> , 2010 , 329, 223-6	33.3	446
77	Parallel evolution of nacre building gene sets in molluscs. <i>Molecular Biology and Evolution</i> , 2010 , 27, 5918-98	16.9	196
76	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. <i>BMC Genomics</i> , 2010 , 11, 261	4.5	118
75	Early evolution of the LIM homeobox gene family. <i>BMC Biology</i> , 2010 , 8, 4	7.3	61
74	Domain shuffling and the evolution of vertebrates. <i>Genome Research</i> , 2009 , 19, 1393-403	9.7	72
73	Anatomy and development of the nervous system of <i>Nematostella vectensis</i> , an anthozoan cnidarian. <i>Developmental Neurobiology</i> , 2009 , 69, 235-54	3.2	177
72	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009 , 457, 551-6	50.4	2200
71	Rosaceous Genome Sequencing: Perspectives and Progress 2009 , 601-615		11
70	Old can be new again: HAPPY whole genome sequencing, mapping and assembly. <i>International Journal of Biological Sciences</i> , 2009 , 5, 298-303	11.2	12

69	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008 , 451, 783-8	50.4	850
68	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008 , 453, 1064-71	50.4	1266
67	The <i>Trichoplax</i> genome and the nature of placozoans. <i>Nature</i> , 2008 , 454, 955-60	50.4	681
66	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008 , 456, 239-44	50.4	1200
65	Early origins and evolution of microRNAs and Piwi-interacting RNAs in animals. <i>Nature</i> , 2008 , 455, 1193-7	50.4	522
64	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea jecorina</i>). <i>Nature Biotechnology</i> , 2008 , 26, 553-60	44.5	920
63	Rapid whole-genome mutational profiling using next-generation sequencing technologies. <i>Genome Research</i> , 2008 , 18, 1638-42	9.7	194
62	Genesis and expansion of metazoan transcription factor gene classes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 980-96	8.3	221
61	Promoter elements associated with RNA Pol II stalling in the <i>Drosophila</i> embryo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 7762-7	11.5	126
60	The genome sequence of <i>Bifidobacterium longum</i> subsp. <i>infantis</i> reveals adaptations for milk utilization within the infant microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18964-9	11.5	610
59	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008 , 18, 1100-11	9.7	387
58	Sequence and genetic map of <i>Meloidogyne hapla</i> : A compact nematode genome for plant parasitism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 14802-7	11.5	353
57	The early ANTP gene repertoire: insights from the placozoan genome. <i>PLoS ONE</i> , 2008 , 3, e2457	3.7	36
56	Conservation of linkage and evolution of developmental function within the Tbx2/3/4/5 subfamily of T-box genes: implications for the origin of vertebrate limbs. <i>Development Genes and Evolution</i> , 2008 , 218, 613-28	1.8	49
55	Sequence and Assembly of the Soybean Genome 2008 , 101-112		
54	Accelerated gene evolution and subfunctionalization in the pseudotetraploid frog <i>Xenopus laevis</i> . <i>BMC Biology</i> , 2007 , 5, 31	7.3	92
53	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007 , 50, 1063-78	6.9	63
52	The NK homeobox gene cluster predates the origin of Hox genes. <i>Current Biology</i> , 2007 , 17, 706-10	6.3	139

51	The evolutionary origin of hedgehog proteins. <i>Current Biology</i> , 2007 , 17, R836-7	6.3	97
50	The <i>Chlamydomonas</i> genome reveals the evolution of key animal and plant functions. <i>Science</i> , 2007 , 318, 245-50	33.3	1969
49	Evidence for a microRNA expansion in the bilaterian ancestor. <i>Development Genes and Evolution</i> , 2007 , 217, 73-7	1.8	109
48	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7705-10	11.5	482
47	Sea anemone genome reveals ancestral eumetazoan gene repertoire and genomic organization. <i>Science</i> , 2007 , 317, 86-94	33.3	1204
46	Phytophthora genome sequences uncover evolutionary origins and mechanisms of pathogenesis. <i>Science</i> , 2006 , 313, 1261-6	33.3	827
45	Chromosomal mapping of 170 BAC clones in the ascidian <i>Ciona intestinalis</i> . <i>Genome Research</i> , 2006 , 16, 297-303	9.7	40
44	Genome sequence of the lignocellulose degrading fungus <i>Phanerochaete chrysosporium</i> strain RP78. <i>Nature Biotechnology</i> , 2004 , 22, 695-700	44.5	710
43	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004 , 428, 529-35	50.4	216
42	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , 2004 , 431, 268-74	50.4	86
41	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004 , 432, 988-94	50.4	129
40	The genome of the diatom <i>Thalassiosira pseudonana</i> : ecology, evolution, and metabolism. <i>Science</i> , 2004 , 306, 79-86	33.3	1586
39	Reverse methanogenesis: testing the hypothesis with environmental genomics. <i>Science</i> , 2004 , 305, 1457-62	39.3	524
38	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004 , 428, 37-43	50.4	1710
37	Genomic analysis of immunity in a Urochordate and the emergence of the vertebrate immune system: "waiting for Godot". <i>Immunogenetics</i> , 2003 , 55, 570-81	3.2	237
36	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . I. Genes for bHLH transcription factors. <i>Development Genes and Evolution</i> , 2003 , 213, 213-21	1.8	114
35	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . II. Genes for homeobox transcription factors. <i>Development Genes and Evolution</i> , 2003 , 213, 222-34	1.8	120
34	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . III. Genes for Fox, ETS, nuclear receptors and NFkappaB. <i>Development Genes and Evolution</i> , 2003 , 213, 235-44	1.8	117

33	A proposal to sequence the amphioxus genome submitted to the Joint Genome Institute of the US Department of Energy. <i>The Journal of Experimental Zoology</i> , 2003 , 300, 5-22		14
32	Whole-genome shotgun assembly and analysis of the genome of <i>Fugu rubripes</i> . <i>Science</i> , 2002 , 297, 1301-1310	33.3	1272
31	The draft genome of <i>Ciona intestinalis</i> : insights into chordate and vertebrate origins. <i>Science</i> , 2002 , 298, 2157-67	33.3	1354
30	The information content of spontaneous retinal waves. <i>Journal of Neuroscience</i> , 2001 , 21, 961-73	6.6	55
29	Mechanical unfolding of a beta-hairpin using molecular dynamics. <i>Biophysical Journal</i> , 2000 , 78, 584-9	2.9	62
28	Retinal waves are governed by collective network properties. <i>Journal of Neuroscience</i> , 1999 , 19, 3580-936.6		108
27	Excited states of a dilute Bose-Einstein condensate in a harmonic trap. <i>Physical Review A</i> , 1998 , 57, 1191-1201	2.4	48
26	A Two-Layer Model Describes the Spatiotemporal Properties of Spontaneous Retinal Waves 1998 , 337-342		
25	Dynamic processes shape spatiotemporal properties of retinal waves. <i>Neuron</i> , 1997 , 19, 293-306	13.9	136
24	Topology and nematic ordering. II. Observable critical behavior. <i>Physical Review E</i> , 1995 , 52, 1801-1810	2.4	10
23	Topology and nematic ordering. I. A gauge theory. <i>Physical Review E</i> , 1995 , 52, 1778-1800	2.4	43
22	Disordered bosons: Condensate and excitations. <i>Physical Review B</i> , 1994 , 49, 9013-9023	3.3	39
21	Topology and nematic ordering. <i>Physical Review Letters</i> , 1993 , 70, 1650-1653	7.4	66
20	Electronic pairing mechanism in fullerenes: Interactions and correlations. <i>Physical Review B</i> , 1993 , 48, 4103-4113	3.3	19
19	Isotopic disorder in superconducting fullerenes. <i>Physical Review B</i> , 1993 , 48, 4114-4118	3.3	10
18	Pairing in doped spin liquids: Anyon versus d-wave superconductivity. <i>Physical Review Letters</i> , 1993 , 70, 493-496	7.4	66
17	Real-space renormalization study of disordered interacting bosons. <i>Physical Review B</i> , 1992 , 46, 3002-3008	9.8	89
16	The space groups of axial crystals and quasicrystals. <i>Reviews of Modern Physics</i> , 1991 , 63, 699-733	40.5	94

15	Gutzwiller projection for bosons. <i>Physical Review B</i> , 1991 , 44, 10328-10332	3-3	191
14	Quadratic quantum antiferromagnets in the fermionic large-N limit. <i>Physical Review B</i> , 1990 , 42, 2526-2531	3-3	42
13	Stacking quasicrystallographic lattices. <i>Physical Review B</i> , 1990 , 41, 10498-10502	3-3	9
12	Constrained spin model of phason dynamics in quasicrystals. <i>Physical Review B</i> , 1990 , 42, 8517-8536	3-3	1
11	Superconductivity and the quantum hard-core dimer gas. <i>Physical Review Letters</i> , 1988 , 61, 2376-2379	7-4	746
10	Scale equivalence of quasicrystallographic space groups. <i>Physical Review B</i> , 1988 , 37, 8145-8149	3-3	38
9	Beware of 46-fold symmetry: The classification of two-dimensional quasicrystallographic lattices. <i>Physical Review Letters</i> , 1987 , 58, 2099-2101	7-4	36
8	Rudimentary quasicrystallography: The icosahedral and decagonal reciprocal lattices. <i>Physical Review B</i> , 1987 , 35, 5487-5495	3-3	94
7	Topology of the resonating valence-bond state: Solitons and high-T _c superconductivity. <i>Physical Review B</i> , 1987 , 35, 8865-8868	3-3	732
6	Quasicrystalline textures of cholesteric liquid crystals: Blue phase III?. <i>Physical Review Letters</i> , 1986 , 56, 1727-1730	7-4	49
5	CRISPR-Cas9-mediated knockout of CYP79D1 and CYP79D2 in cassava attenuates toxic cyanogen production		3
4	Adaptation to heavy-metal contaminated environments proceeds via selection on pre-existing genetic variation		11
3	Analysis of meiosis in <i>Pristionchus pacificus</i> reveals plasticity in homolog pairing and synapsis in the nematode lineage		1
2	Muntjac chromosome evolution and architecture		3
1	Chromosome evolution and the genetic basis of agronomically important traits in greater yam		3