

# Daniel S Rokhsar

## List of Publications by Year in descending order

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156  
papers

55,448  
citations

4120

87  
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8370

147  
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165  
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165  
docs citations

165  
times ranked

49567  
citing authors

#	ARTICLE	IF	CITATIONS
1	Current status and impending progress for cassava structural genomics. <i>Plant Molecular Biology</i> , 2022, 109, 177-191.	2.0	11
2	Beyond "living fossils": Can comparative genomics finally reveal novelty?. <i>Molecular Ecology Resources</i> , 2022, 22, 9-11.	2.2	2
3	Deeply conserved synteny and the evolution of metazoan chromosomes. <i>Science Advances</i> , 2022, 8, eabi5884.	4.7	81
4	Chromosome evolution and the genetic basis of agronomically important traits in greater yam. <i>Nature Communications</i> , 2022, 13, 2001.	5.8	35
5	Genome and transcriptome mechanisms driving cephalopod evolution. <i>Nature Communications</i> , 2022, 13, 2427.	5.8	47
6	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	13.7	144
7	Plant Pan-Genomics Comes of Age. <i>Annual Review of Plant Biology</i> , 2021, 72, 411-435.	8.6	56
8	Phylogenomics illuminates the evolution of bobtail and bottletail squid (order Sepiolida). <i>Communications Biology</i> , 2021, 4, 819.	2.0	24
9	Diversification of mandarin citrus by hybrid speciation and apomixis. <i>Nature Communications</i> , 2021, 12, 4377.	5.8	31
10	Analysis of meiosis in <i>Pristionchus pacificus</i> reveals plasticity in homolog pairing and synapsis in the nematode lineage. <i>ELife</i> , 2021, 10, .	2.8	21
11	A chromosome-scale reference genome of trifoliate orange ( <i>Poncirus trifoliata</i> ) provides insights into disease resistance, cold tolerance and genome evolution in <i>Citrus</i> . <i>Plant Journal</i> , 2020, 104, 1215-1232.	2.8	56
12	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.	5.8	67
13	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	5.8	67
14	Analysis of muntjac deer genome and chromatin architecture reveals rapid karyotype evolution. <i>Communications Biology</i> , 2020, 3, 480.	2.0	31
15	Terabase-scale metagenome coassembly with MetaHipMer. <i>Scientific Reports</i> , 2020, 10, 10689.	1.6	34
16	The citrus genome. , 2020, , 1-8.		7
17	The origin of citrus. , 2020, , 9-31.		15
18	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	3.4	250

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19	Symbiotic organs shaped by distinct modes of genome evolution in cephalopods. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3030-3035.	3.3	123
20	Ancient polymorphisms contribute to genome-wide variation by long-term balancing selection and divergent sorting in <i>Boechera stricta</i> . Genome Biology, 2019, 20, 126.	3.8	30
21	Acoel genome reveals the regulatory landscape of whole-body regeneration. Science, 2019, 363, .	6.0	125
22	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . Developmental Biology, 2019, 452, 8-20.	0.9	43
23	New bobtail squid (Sepiolidae: Sepiolinae) from the Ryukyu islands revealed by molecular and morphological analysis. Communications Biology, 2019, 2, 465.	2.0	9
24	A New Spiralian Phylogeny Places the Enigmatic Arrow Worms among Gnathiferans. Current Biology, 2019, 29, 312-318.e3.	1.8	201
25	Genomics of the origin and evolution of Citrus. Nature, 2018, 554, 311-316.	13.7	552
26	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . Nature Communications, 2018, 9, 5213.	5.8	101
27	Assembly of the <i>Boechera retrofracta</i> Genome and Evolutionary Analysis of Apomixis-Associated Genes. Genes, 2018, 9, 185.	1.0	24
28	Young inversion with multiple linked QTLs under selection in a hybrid zone. Nature Ecology and Evolution, 2017, 1, 119.	3.4	94
29	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6361-E6370.	3.3	233
30	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. Theoretical and Applied Genetics, 2017, 130, 2069-2090.	1.8	39
31	Genome organization of the <i>vg1</i> and <i>nodal3</i> gene clusters in the allotetraploid frog <i>Xenopus laevis</i> . Developmental Biology, 2017, 426, 236-244.	0.9	4
32	QTL Mapping for Pest and Disease Resistance in Cassava and Coincidence of Some QTL with Introgression Regions Derived from <i>Manihot glaziovii</i> . Frontiers in Plant Science, 2017, 8, 1168.	1.7	51
33	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. Genome Research, 2016, 26, 342-350.	2.4	679
34	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. Nature Biotechnology, 2016, 34, 562-570.	9.4	340
35	Syntax compensates for poor binding sites to encode tissue specificity of developmental enhancers. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6508-6513.	3.3	139
36	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . Nature, 2016, 538, 336-343.	13.7	849

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37	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.	3.2	26
38	HipMer. , 2015, , .		57
39	Genome Assembly Improvement and Mapping Convergent Evolutionary Skeletal Traits in Sticklebacks with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1463-1472.	0.8	112
40	The deuterostome context of chordate origins. <i>Nature</i> , 2015, 520, 456-465.	13.7	121
41	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	256
42	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, 187-191.	0.6	50
43	merAligner: A Fully Parallel Sequence Aligner. , 2015, , .		28
44	The genetics of divergence and reproductive isolation between ecotypes of <i>Panicum hallii</i> . <i>New Phytologist</i> , 2015, 205, 402-414.	3.5	65
45	The octopus genome and the evolution of cephalopod neural and morphological novelties. <i>Nature</i> , 2015, 524, 220-224.	13.7	506
46	Suboptimization of developmental enhancers. <i>Science</i> , 2015, 350, 325-328.	6.0	268
47	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	13.7	217
48	Parallel De Bruijn Graph Construction and Traversal for De Novo Genome Assembly. , 2014, , .		58
49	Efficient and accurate clustering for large-scale genetic mapping. , 2014, , .		5
50	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	9.4	572
51	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
52	Chordate evolution and the three-phylum system. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141729.	1.2	132
53	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	9.4	1,159
54	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582

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55	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.	1.2	27
56	Anchoring and ordering <sc>NGS</sc> contig assemblies by population sequencing (<sc>POPSEQ</sc>). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
57	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	13.7	564
58	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, 487-494.	9.4	1,031
59	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	9.4	374
60	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, 19478-19482.	3.3	190
61	Phytozome: a comparative platform for green plant genomics. <i>Nucleic Acids Research</i> , 2012, 40, D1178-D1186.	6.5	4,204
62	The Genome Portal of the Department of Energy Joint Genome Institute. <i>Nucleic Acids Research</i> , 2012, 40, D26-D32.	6.5	439
63	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.	1.2	77
64	A framework genetic map for <i>Miscanthus sinensis</i> from RNAseq-based markers shows recent tetraploidy. <i>BMC Genomics</i> , 2012, 13, 142.	1.2	87
65	Identical Genomic Organization of Two Hemichordate Hox Clusters. <i>Current Biology</i> , 2012, 22, 2053-2058.	1.8	43
66	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	13.7	1,204
67	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 2012, 7, e33892.	1.1	50
68	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	9.4	864
69	The Cassava Genome: Current Progress, Future Directions. <i>Tropical Plant Biology</i> , 2012, 5, 88-94.	1.0	265
70	The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	6.0	794
71	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, 1037-1044.	2.6	4
72	Meraculous: De Novo Genome Assembly with Short Paired-End Reads. <i>PLoS ONE</i> , 2011, 6, e23501.	1.1	191

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73	The Eucalyptus grandis Genome Project: Genome and transcriptome resources for comparative analysis of woody plant biology. BMC Proceedings, 2011, 5, .	1.8	25
74	Populus resequencing: towards genome-wide association studies. BMC Proceedings, 2011, 5, .	1.8	19
75	A segmental genomic duplication generates a functional intron. Nature Communications, 2011, 2, 454.	5.8	12
76	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
77	Parallel Evolution of Nacre Building Gene Sets in Molluscs. Molecular Biology and Evolution, 2010, 27, 591-608.	3.5	239
78	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. BMC Genomics, 2010, 11, 261.	1.2	175
79	Early evolution of the LIM homeobox gene family. BMC Biology, 2010, 8, 4.	1.7	77
80	Nuclear-localized tiny RNAs are associated with transcription initiation and splice sites in metazoans. Nature Structural and Molecular Biology, 2010, 17, 1030-1034.	3.6	146
81	The dynamic genome of Hydra. Nature, 2010, 464, 592-596.	13.7	743
82	The Amphimedon queenslandica genome and the evolution of animal complexity. Nature, 2010, 466, 720-726.	13.7	917
83	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . Science, 2010, 328, 633-636.	6.0	708
84	The Genome of Naegleria gruberi Illuminates Early Eukaryotic Versatility. Cell, 2010, 140, 631-642.	13.5	399
85	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . Science, 2010, 329, 223-226.	6.0	536
86	Domain shuffling and the evolution of vertebrates. Genome Research, 2009, 19, 1393-1403.	2.4	86
87	Anatomy and development of the nervous system of <i>Nematostella vectensis</i> , an anthozoan cnidarian. Developmental Neurobiology, 2009, 69, 235-254.	1.5	220
88	The Sorghum bicolor genome and the diversification of grasses. Nature, 2009, 457, 551-556.	13.7	2,642
89	Rosaceous Genome Sequencing: Perspectives and Progress. , 2009, , 601-615.		14
90	Old can be new again: HAPPY whole genome sequencing, mapping and assembly. International Journal of Biological Sciences, 2009, 5, 298-303.	2.6	14

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91	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, 613-628.	0.4	60
92	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008, 451, 783-788.	13.7	1,006
93	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008, 453, 1064-1071.	13.7	1,496
94	The <i>Trichoplax</i> genome and the nature of placozoans. <i>Nature</i> , 2008, 454, 955-960.	13.7	801
95	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	13.7	1,458
96	Early origins and evolution of microRNAs and Piwi-interacting RNAs in animals. <i>Nature</i> , 2008, 455, 1193-1197.	13.7	630
97	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i> ) Tj ETQq1 1 0.784314 9.4 1,516 /Over	9.4	1,516
98	Rapid whole-genome mutational profiling using next-generation sequencing technologies. <i>Genome Research</i> , 2008, 18, 1638-1642.	2.4	225
99	Genesis and Expansion of Metazoan Transcription Factor Gene Classes. <i>Molecular Biology and Evolution</i> , 2008, 25, 980-996.	3.5	262
100	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, 7762-7767.	3.3	145
101	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, 18964-18969.	3.3	748
102	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.	2.4	456
103	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, 14802-14807.	3.3	443
104	The Early ANTP Gene Repertoire: Insights from the Placozoan Genome. <i>PLoS ONE</i> , 2008, 3, e2457.	1.1	38
105	Sequence and Assembly of the Soybean Genome. , 2008, , 101-112.		0
106	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, 7705-7710.	3.3	563
107	Sea Anemone Genome Reveals Ancestral Eumetazoan Gene Repertoire and Genomic Organization. <i>Science</i> , 2007, 317, 86-94.	6.0	1,423
108	Accelerated gene evolution and subfunctionalization in the pseudotetraploid frog <i>Xenopus laevis</i> . <i>BMC Biology</i> , 2007, 5, 31.	1.7	102

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109	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, 1063-1078.	2.8	70
110	The NK Homeobox Gene Cluster Predates the Origin of Hox Genes. <i>Current Biology</i> , 2007, 17, 706-710.	1.8	159
111	The evolutionary origin of hedgehog proteins. <i>Current Biology</i> , 2007, 17, R836-R837.	1.8	121
112	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	6.0	2,354
113	Evidence for a microRNA expansion in the bilaterian ancestor. <i>Development Genes and Evolution</i> , 2007, 217, 73-77.	0.4	124
114	COMPARATIVE PAIR-WISE DOMAIN-COMBINATIONS FOR SCREENING THE CLADE SPECIFIC DOMAIN-ARCHITECTURES IN METAZOAN GENOMES. , 2007, , .		0
115	<i>Phytophthora</i> Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.	6.0	1,059
116	Chromosomal mapping of 170 BAC clones in the ascidian <i>Ciona intestinalis</i> . <i>Genome Research</i> , 2005, 16, 297-303.	2.4	45
117	Genome sequence of the lignocellulose degrading fungus <i>Phanerochaete chrysosporium</i> strain RP78. <i>Nature Biotechnology</i> , 2004, 22, 695-700.	9.4	805
118	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	13.7	298
119	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , 2004, 431, 268-274.	13.7	102
120	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994.	13.7	156
121	The Genome of the Diatom <i>Thalassiosira Pseudonana</i> : Ecology, Evolution, and Metabolism. <i>Science</i> , 2004, 306, 79-86.	6.0	1,862
122	Reverse Methanogenesis: Testing the Hypothesis with Environmental Genomics. <i>Science</i> , 2004, 305, 1457-1462.	6.0	624
123	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004, 428, 37-43.	13.7	2,045
124	Genomic analysis of immunity in a Urochordate and the emergence of the vertebrate immune system: <i>Immunogenetics</i> , 2003, 55, 570-581.	1.2	278
125	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . <i>Development Genes and Evolution</i> , 2003, 213, 213-221.	0.4	129
126	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . <i>Development Genes and Evolution</i> , 2003, 213, 222-234.	0.4	130



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127	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . <i>Development Genes and Evolution</i> , 2003, 213, 235-244.	0.4	138
128	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, 300B, 5-22.	1.4	17
129	Whole-Genome Shotgun Assembly and Analysis of the Genome of <i>Fugu rubripes</i> . <i>Science</i> , 2002, 297, 1301-1310.	6.0	1,432
130	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. <i>Science</i> , 2002, 298, 2157-2167.	6.0	1,539
131	The Information Content of Spontaneous Retinal Waves. <i>Journal of Neuroscience</i> , 2001, 21, 961-973.	1.7	58
132	Mechanical Unfolding of a $\beta$ -Hairpin Using Molecular Dynamics. <i>Biophysical Journal</i> , 2000, 78, 584-589.	0.2	63
133	Retinal Waves Are Governed by Collective Network Properties. <i>Journal of Neuroscience</i> , 1999, 19, 3580-3593.	1.7	120
134	Condensates in a twist. <i>Nature</i> , 1999, 401, 533-534.	13.7	0
135	Excited states of a dilute Bose-Einstein condensate in a harmonic trap. <i>Physical Review A</i> , 1998, 57, 1191-1201.	1.0	53
136	A Two-Layer Model Describes the Spatiotemporal Properties of Spontaneous Retinal Waves. , 1998, , 337-342.		0
137	Dynamic Processes Shape Spatiotemporal Properties of Retinal Waves. <i>Neuron</i> , 1997, 19, 293-306.	3.8	154
138	Topology and nematic ordering. II. Observable critical behavior. <i>Physical Review E</i> , 1995, 52, 1801-1810.	0.8	12
139	Topology and nematic ordering. I. A gauge theory. <i>Physical Review E</i> , 1995, 52, 1778-1800.	0.8	48
140	Disordered bosons: Condensate and excitations. <i>Physical Review B</i> , 1994, 49, 9013-9023.	1.1	40
141	Topology and nematic ordering. <i>Physical Review Letters</i> , 1993, 70, 1650-1653.	2.9	75
142	Electronic pairing mechanism in fullerenes: Interactions and correlations. <i>Physical Review B</i> , 1993, 48, 4103-4113.	1.1	20
143	Isotopic disorder in superconducting fullerenes. <i>Physical Review B</i> , 1993, 48, 4114-4118.	1.1	10
144	Pairing in doped spin liquids: Anyon versus-d-wave superconductivity. <i>Physical Review Letters</i> , 1993, 70, 493-496.	2.9	68

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145	Real-space renormalization study of disordered interacting bosons. <i>Physical Review B</i> , 1992, 46, 3002-3008.	1.1	96
146	The space groups of axial crystals and quasicrystals. <i>Reviews of Modern Physics</i> , 1991, 63, 699-733.	16.4	105
147	Gutzwiller projection for bosons. <i>Physical Review B</i> , 1991, 44, 10328-10332.	1.1	221
148	Quadratic quantum antiferromagnets in the fermionic large-N limit. <i>Physical Review B</i> , 1990, 42, 2526-2531.	1.1	44
149	Stacking quasicrystallographic lattices. <i>Physical Review B</i> , 1990, 41, 10498-10502.	1.1	12
150	Constrained spin model of phason dynamics in quasicrystals. <i>Physical Review B</i> , 1990, 42, 8517-8536.	1.1	1
151	Superconductivity and the Quantum Hard-Core Dimer Gas. <i>Physical Review Letters</i> , 1988, 61, 2376-2379.	2.9	849
152	Scale equivalence of quasicrystallographic space groups. <i>Physical Review B</i> , 1988, 37, 8145-8149.	1.1	47
153	Beware of 46-Fold Symmetry: The Classification of Two-Dimensional Quasicrystallographic Lattices. <i>Physical Review Letters</i> , 1987, 58, 2099-2101.	2.9	42
154	Rudimentary quasicrystallography: The icosahedral and decagonal reciprocal lattices. <i>Physical Review B</i> , 1987, 35, 5487-5495.	1.1	105
155	Topology of the resonating valence-bond state: Solitons and high-T <sub>c</sub> superconductivity. <i>Physical Review B</i> , 1987, 35, 8865-8868.	1.1	795
156	Quasicrystalline Textures of Cholesteric Liquid Crystals: Blue Phase III?. <i>Physical Review Letters</i> , 1986, 56, 1727-1730.	2.9	51