

# Christian Landry

## List of Publications by Year in descending order

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132  
papers

8,075  
citations

70961

41  
h-index

60497

81  
g-index

169  
all docs

169  
docs citations

169  
times ranked

10680  
citing authors

#	ARTICLE	IF	CITATIONS
1	MHC studies in nonmodel vertebrates: what have we learned about natural selection in 15 years?. <i>Journal of Evolutionary Biology</i> , 2003, 16, 363-377.	0.8	786
2	An in Vivo Map of the Yeast Protein Interactome. <i>Science</i> , 2008, 320, 1465-1470.	6.0	681
3	A genome-wide view of the spectrum of spontaneous mutations in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9272-9277.	3.3	649
4	Genetic Properties Influencing the Evolvability of Gene Expression. <i>Science</i> , 2007, 317, 118-121.	6.0	310
5	Chromatin- and Transcription-Related Factors Repress Transcription from within Coding Regions throughout the <i>Saccharomyces cerevisiae</i> Genome. <i>PLoS Biology</i> , 2008, 6, e277.	2.6	268
6	Weak functional constraints on phosphoproteomes. <i>Trends in Genetics</i> , 2009, 25, 193-197.	2.9	254
7	Compensatory cis-trans Evolution and the Dysregulation of Gene Expression in Interspecific Hybrids of <i>Drosophila</i> . <i>Genetics</i> , 2005, 171, 1813-1822.	1.2	209
8	Alternative life histories shape brain gene expression profiles in males of the same population. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 1655-1662.	1.2	188
9	Quantification of dynamic protein complexes using <i>Renilla</i> luciferase fragment complementation applied to protein kinase A activities <i>in vivo</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16916-16921.	3.3	172
10	Comparative analysis of population structure across environments and geographical scales at major histocompatibility complex and microsatellite loci in Atlantic salmon ( <i>Salmo salar</i> ). <i>Molecular Ecology</i> , 2002, 10, 2525-2539.	2.0	170
11	Speciation driven by hybridization and chromosomal plasticity in a wild yeast. <i>Nature Microbiology</i> , 2016, 1, 15003.	5.9	161
12	Genome clashes in hybrids: insights from gene expression. <i>Heredity</i> , 2007, 99, 483-493.	1.2	149
13	Molecular characterization of the evolution of phagosomes. <i>Molecular Systems Biology</i> , 2010, 6, 423.	3.2	139
14	Genome-wide scan reveals that genetic variation for transcriptional plasticity in yeast is biased towards multi-copy and dispensable genes. <i>Gene</i> , 2006, 366, 343-351.	1.0	110
15	Gene duplication can impart fragility, not robustness, in the yeast protein interaction network. <i>Science</i> , 2017, 355, 630-634.	6.0	103
16	The Calcineurin Signaling Network Evolves via Conserved Kinase-Phosphatase Modules that Transcend Substrate Identity. <i>Molecular Cell</i> , 2014, 55, 422-435.	4.5	102
17	Ecological and evolutionary genomics of <i>Saccharomyces cerevisiae</i> . <i>Molecular Ecology</i> , 2006, 15, 575-591.	2.0	94
18	Complex Ancestries of Lager-Brewing Hybrids Were Shaped by Standing Variation in the Wild Yeast <i>Saccharomyces eubayanus</i> . <i>PLoS Genetics</i> , 2016, 12, e1006155.	1.5	94

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19	Deep transcriptome annotation enables the discovery and functional characterization of cryptic small proteins. <i>ELife</i> , 2017, 6, .	2.8	93
20	The TRP Channels Pkd2, NompC, and Trpm Act in Cold-Sensing Neurons to Mediate Unique Aversive Behaviors to Noxious Cold in <i>Drosophila</i> . <i>Current Biology</i> , 2016, 26, 3116-3128.	1.8	92
21	Protein abundance is key to distinguish promiscuous from functional phosphorylation based on evolutionary information. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 2594-2606.	1.8	88
22	Molecular mechanisms of paralogous compensation and the robustness of cellular networks. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014, 322, 488-499.	0.6	83
23	Evolutionary biology through the lens of budding yeast comparative genomics. <i>Nature Reviews Genetics</i> , 2017, 18, 581-598.	7.7	81
24	Evidence of Natural Hybridization in Brazilian Wild Lineages of <i>Saccharomyces cerevisiae</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 317-329.	1.1	79
25	Hybridization and adaptive evolution of diverse <i>Saccharomyces</i> species for cellulosic biofuel production. <i>Biotechnology for Biofuels</i> , 2017, 10, 78.	6.2	78
26	What is needed for next-generation ecological and evolutionary genomics?. <i>Trends in Ecology and Evolution</i> , 2012, 27, 673-678.	4.2	77
27	Exploring the northern limit of the distribution of <i>Saccharomyces cerevisiae</i> and <i>Saccharomyces paradoxus</i> in North America. <i>FEMS Yeast Research</i> , 2014, 14, 281-288.	1.1	71
28	Molecular and cellular bases of adaptation to a changing environment in microorganisms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161458.	1.2	70
29	Local climatic adaptation in a widespread microorganism. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132472.	1.2	69
30	How Perfect Can Protein Interactomes Be?. <i>Science Signaling</i> , 2009, 2, pe11.	1.6	67
31	Key considerations for measuring allelic expression on a genomic scale using high-throughput sequencing. <i>Molecular Ecology</i> , 2010, 19, 212-227.	2.0	67
32	Chromosomal variation segregates within incipient species and correlates with reproductive isolation. <i>Molecular Ecology</i> , 2014, 23, 4362-4372.	2.0	67
33	Hybridization is a recurrent evolutionary stimulus in wild yeast speciation. <i>Nature Communications</i> , 2019, 10, 923.	5.8	62
34	TECHNICAL ADVANCE: Indel arrays: an affordable alternative for genotyping. <i>Plant Journal</i> , 2007, 51, 727-737.	2.8	58
35	Mitochondrial Recombination and Introgression during Speciation by Hybridization. <i>Molecular Biology and Evolution</i> , 2017, 34, 1947-1959.	3.5	57
36	Evolutionary rescue by compensatory mutations is constrained by genomic and environmental backgrounds. <i>Molecular Systems Biology</i> , 2015, 11, 832.	3.2	56

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37	Systematic identification of signal integration by protein kinase A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4501-4506.	3.3	53
38	Found in translation: functions and evolution of a recently discovered alternative proteome. <i>Current Opinion in Structural Biology</i> , 2015, 32, 74-80.	2.6	51
39	Compositional Differences between Size Classes of Dissolved Organic Matter from Freshwater and Seawater Revealed by an HPLC-FTIR System. <i>Environmental Science &amp; Technology</i> , 2012, 46, 1700-1707.	4.6	50
40	Paralog dependency indirectly affects the robustness of human cells. <i>Molecular Systems Biology</i> , 2019, 15, e8871.	3.2	50
41	Extracting Insight from Noisy Cellular Networks. <i>Cell</i> , 2013, 155, 983-989.	13.5	49
42	Transcriptome sequences spanning key developmental states as a resource for the study of the cestode <i>Schistocephalus solidus</i> , a threespine stickleback parasite. <i>GigaScience</i> , 2016, 5, 24.	3.3	49
43	Spontaneous whole-genome duplication restores fertility in interspecific hybrids. <i>Nature Communications</i> , 2019, 10, 4126.	5.8	49
44	Perturbing proteomes at single residue resolution using base editing. <i>Nature Communications</i> , 2020, 11, 1871.	5.8	49
45	Moving from transcriptional to phospho-evolution: generalizing regulatory evolution?. <i>Trends in Genetics</i> , 2010, 26, 462-467.	2.9	48
46	Signaling Through Cooperation. <i>Science</i> , 2010, 328, 983-984.	6.0	46
47	A Systematic Approach for the Genetic Dissection of Protein Complexes in Living Cells. <i>Cell Reports</i> , 2013, 3, 2155-2167.	2.9	46
48	A Toolkit of Protein-Fragment Complementation Assays for Studying and Dissecting Large-Scale and Dynamic Protein-Protein Interactions in Living Cells. <i>Methods in Enzymology</i> , 2010, 470, 335-368.	0.4	45
49	Large-scale genetic variation of the symbiosis-required megaplasmid pSymA revealed by comparative genomic analysis of <i>Sinorhizobium meliloti</i> natural strains. <i>BMC Genomics</i> , 2005, 6, 158.	1.2	44
50	Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. <i>Nature Ecology and Evolution</i> , 2020, 4, 626-638.	3.4	44
51	Turnover of protein phosphorylation evolving under stabilizing selection. <i>Frontiers in Genetics</i> , 2014, 5, 245.	1.1	43
52	Functional Divergence and Evolutionary Turnover in Mammalian Phosphoproteomes. <i>PLoS Genetics</i> , 2014, 10, e1004062.	1.5	41
53	The yeast galactose network as a quantitative model for cellular memory. <i>Molecular BioSystems</i> , 2015, 11, 28-37.	2.9	41
54	Evidence for the Robustness of Protein Complexes to Inter-Species Hybridization. <i>PLoS Genetics</i> , 2012, 8, e1003161.	1.5	39

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55	Detecting Functional Divergence after Gene Duplication through Evolutionary Changes in Posttranslational Regulatory Sequences. <i>PLoS Computational Biology</i> , 2014, 10, e1003977.	1.5	39
56	Turnover of ribosome-associated transcripts from de novo ORFs produces gene-like characteristics available for de novo gene emergence in wild yeast populations. <i>Genome Research</i> , 2019, 29, 932-943.	2.4	39
57	Cascading transcriptional effects of a naturally occurring frameshift mutation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Ecology</i> , 2008, 17, 2985-2997.	2.0	37
58	qPCA: a scalable assay to measure the perturbation of protein-protein interactions in living cells. <i>Molecular BioSystems</i> , 2013, 9, 36-43.	2.9	37
59	Mitochondrial Recombination Reveals Mito-Mito Epistasis in Yeast. <i>Genetics</i> , 2018, 209, 307-319.	1.2	37
60	The role of structural pleiotropy and regulatory evolution in the retention of heteromers of paralogs. <i>ELife</i> , 2019, 8, .	2.8	36
61	Protein context shapes the specificity of SH3 domain-mediated interactions in vivo. <i>Nature Communications</i> , 2021, 12, 1597.	5.8	35
62	Phosphorylation network rewiring by gene duplication. <i>Molecular Systems Biology</i> , 2011, 7, 504.	3.2	32
63	Characterization of Spindle Checkpoint Kinase Mps1 Reveals Domain with Functional and Structural Similarities to Tetratricopeptide Repeat Motifs of Bub1 and BubR1 Checkpoint Kinases. <i>Journal of Biological Chemistry</i> , 2012, 287, 5988-6001.	1.6	32
64	<i>beditor</i> : A Computational Workflow for Designing Libraries of Guide RNAs for CRISPR-Mediated Base Editing. <i>Genetics</i> , 2019, 212, 377-385.	1.2	32
65	Protein-Fragment Complementation Assays for Large-Scale Analysis, Functional Dissection and Dynamic Studies of Protein-Protein Interactions in Living Cells. <i>Methods in Molecular Biology</i> , 2011, 756, 395-425.	0.4	30
66	Feedback regulation between autophagy and PKA. <i>Autophagy</i> , 2015, 11, 1181-1183.	4.3	30
67	The effect of hybridization on transposable element accumulation in an undomesticated fungal species. <i>ELife</i> , 2020, 9, .	2.8	29
68	Dissection of expression-quantitative trait locus and allele specificity using a haploid/diploid plant system - insights into compensatory evolution of transcriptional regulation within populations. <i>New Phytologist</i> , 2016, 211, 159-171.	3.5	28
69	Expression attenuation as a mechanism of robustness against gene duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	28
70	Transcriptional divergence plays a role in the rewiring of protein interaction networks after gene duplication. <i>Journal of Proteomics</i> , 2013, 81, 112-125.	1.2	26
71	Mitotic phosphotyrosine network analysis reveals that tyrosine phosphorylation regulates Polo-like kinase 1 (PLK1). <i>Science Signaling</i> , 2016, 9, rs14.	1.6	26
72	The Last Enzyme of the De Novo Purine Synthesis Pathway 5-aminoimidazole-4-carboxamide Ribonucleotide Formyltransferase/IMP Cyclohydrolase (ATIC) Plays a Central Role in Insulin Signaling and the Golgi/Endosomes Protein Network*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1079-1092.	2.5	25

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73	The neutral rate of whole-genome duplication varies among yeast species and their hybrids. <i>Nature Communications</i> , 2021, 12, 3126.	5.8	25
74	Genome-wide Protein-protein Interaction Screening by Protein-fragment Complementation Assay (PCA) in Living Cells. <i>Journal of Visualized Experiments</i> , 2015, , .	0.2	23
75	Major host transitions are modulated through transcriptome-wide reprogramming events in <i>Schistocephalus solidus</i> , a threespine stickleback parasite. <i>Molecular Ecology</i> , 2017, 26, 1118-1130.	2.0	23
76	Population genomics reveals structure at the individual, host-tree scale and persistence of genotypic variants of the undomesticated yeast <i>Saccharomyces paradoxus</i> in a natural woodland. <i>Molecular Ecology</i> , 2017, 26, 995-1007.	2.0	21
77	Identification of the fitness determinants of budding yeast on a natural substrate. <i>ISME Journal</i> , 2017, 11, 959-971.	4.4	21
78	Direct Phosphorylation of SRC Homology 3 Domains by Tyrosine Kinase Receptors Disassembles Ligand-Induced Signaling Networks. <i>Molecular Cell</i> , 2018, 70, 995-1007.e11.	4.5	21
79	Are long-lived trees poised for evolutionary change? Single locus effects in the evolution of gene expression networks in spruce. <i>Molecular Ecology</i> , 2013, 22, 2369-2379.	2.0	20
80	RNAseq Analysis Highlights Specific Transcriptome Signatures of Yeast and Mycelial Growth Phases in the Dutch Elm Disease Fungus <i>Ophiostoma novo-ulmi</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2487-2495.	0.8	20
81	Identification of candidate mimicry proteins involved in parasite-driven phenotypic changes. <i>Parasites and Vectors</i> , 2015, 8, 225.	1.0	20
82	Systems-level analysis and evolution of the phototransduction network in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3283-3288.	3.3	19
83	Double Selection Enhances the Efficiency of Target-AID and Cas9-Based Genome Editing in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3163-3171.	0.8	19
84	Regulation plays a multifaceted role in the retention of gene duplicates. <i>PLoS Biology</i> , 2019, 17, e3000519.	2.6	19
85	Diverse perspectives on interdisciplinarity from Members of the College of the Royal Society of Canada. <i>Facets</i> , 2020, 5, 138-165.	1.1	19
86	Modulation of the yeast protein interactome in response to DNA damage. <i>Journal of Proteomics</i> , 2014, 100, 25-36.	1.2	18
87	Yeasts from temperate forests. <i>Yeast</i> , 2022, 39, 4-24.	0.8	18
88	Proteomic Characterization of Phagosomal Membrane Microdomains During Phagolysosome Biogenesis and Evolution. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1365-1377.	2.5	17
89	A Cellular Roadmap for the Plant Kingdom. <i>Science</i> , 2011, 333, 532-533.	6.0	16
90	Metabolic variation in natural populations of wild yeast. <i>Ecology and Evolution</i> , 2015, 5, 722-732.	0.8	16

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91	The Rapid Evolution of an Ohnolog Contributes to the Ecological Specialization of Incipient Yeast Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 2173-2186.	3.5	16
92	The genomics of wild yeast populations sheds light on the domestication of man's best (micro) friend. <i>Molecular Ecology</i> , 2015, 24, 5309-5311.	2.0	15
93	The Genotypeâ€“Phenotype Maps of Systems Biology and Quantitative Genetics: Distinct and Complementary. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 371-398.	0.8	14
94	Integrative avenues for exploring the dynamics and evolution of protein interaction networks. <i>Current Opinion in Biotechnology</i> , 2013, 24, 775-783.	3.3	14
95	The parasite <i>Schistocephalus solidus</i> secretes proteins with putative host manipulation functions. <i>Parasites and Vectors</i> , 2021, 14, 436.	1.0	14
96	Yeast Population Genomics Goes Wild: The Case of <i>Saccharomyces paradoxus</i> . <i>Population Genomics</i> , 2017, , 207-230.	0.2	13
97	Systems biology spins off a new model for the study of canalization. <i>Trends in Ecology and Evolution</i> , 2009, 24, 63-66.	4.2	12
98	Extended Linkers Improve the Detection of Protein-protein Interactions (PPIs) by Dihydrofolate Reductase Protein-fragment Complementation Assay (DHFR PCA) in Living Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 373-383.	2.5	12
99	BUBR1 Pseudokinase Domain Promotes Kinetochore PP2A-B56 Recruitment, Spindle Checkpoint Silencing, and Chromosome Alignment. <i>Cell Reports</i> , 2020, 33, 108397.	2.9	12
100	Frequent Assembly of Chimeric Complexes in the Protein Interaction Network of an Interspecies Yeast Hybrid. <i>Molecular Biology and Evolution</i> , 2021, 38, 1384-1401.	3.5	11
101	SRC homology 3 domains: multifaceted binding modules. <i>Trends in Biochemical Sciences</i> , 2022, 47, 772-784.	3.7	11
102	A systems biology approach to explore the impact of maple tree dormancy release on sap variation and maple syrup quality. <i>Scientific Reports</i> , 2018, 8, 14658.	1.6	10
103	A collection of barcoded natural isolates of <i>Saccharomyces paradoxus</i> to study microbial evolutionary ecology. <i>MicrobiologyOpen</i> , 2019, 8, e773.	1.2	10
104	No evidence for extrinsic post-zygotic isolation in a wild <i>Saccharomyces</i> yeast system. <i>Biology Letters</i> , 2017, 13, 20170197.	1.0	9
105	<i>Lachancea quebecensis</i> sp. nov., a yeast species consistently isolated from tree bark in the Canadian province of QuÃ©bec. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3392-3399.	0.8	9
106	Heterogeneous Mutation Rates and Spectra in Yeast Hybrids. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
107	Multi-scale perturbations of protein interactomes reveal their mechanisms of regulation, robustness and insights into genotypeâ€“phenotype maps. <i>Briefings in Functional Genomics</i> , 2016, 15, 130-137.	1.3	8
108	Differences Between the Raw Material and the Products of de Novo Gene Birth Can Result from Mutational Biases. <i>Genetics</i> , 2019, 212, 1353-1366.	1.2	8

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109	Protein-Fragment Complementation Assays for Large-Scale Analysis, Functional Dissection, and Spatiotemporal Dynamic Studies of Protein-Protein Interactions in Living Cells. Cold Spring Harbor Protocols, 2016, 2016, pdb.top083543.	0.2	7
110	Testing the Genomic Shock Hypothesis Using Transposable Element Expression in Yeast Hybrids. Frontiers in Fungal Biology, 2021, 2, .	0.9	6
111	The Dihydrofolate Reductase Protein-Fragment Complementation Assay: A Survival-Selection Assay for Large-Scale Analysis of Protein-Protein Interactions. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot090027.	0.2	5
112	Competition experiments in a soil microcosm reveal the impact of genetic and biotic factors on natural yeast populations. ISME Journal, 2020, 14, 1410-1421.	4.4	5
113	Interspecific hybrids show a reduced adaptive potential under DNA damaging conditions. Evolutionary Applications, 2021, 14, 758-769.	1.5	5
114	Purification of Yeast Spores to Investigate Their Dynamics of Activation. Current Protocols in Microbiology, 2020, 59, e123.	6.5	5
115	Chromatin regulators shape the genotype-phenotype map. Molecular Systems Biology, 2010, 6, 434.	3.2	4
116	Where Do Phosphosites Come from and Where Do They Go after Gene Duplication?. International Journal of Evolutionary Biology, 2012, 2012, 1-8.	1.0	4
117	When nuclear-encoded proteins and mitochondrial <i>scp</i> RNA s do not get along, species split apart. EMBO Reports, 2017, 18, 8-10.	2.0	4
118	The Canadian Fungal Research Network: current challenges and future opportunities. Canadian Journal of Microbiology, 2021, 67, 13-22.	0.8	4
119	Recent Advances in Ecological Genomics: From Phenotypic Plasticity to Convergent and Adaptive Evolution and Speciation. Advances in Experimental Medicine and Biology, 2014, 781, 1-5.	0.8	4
120	Barcode fusion genetics-protein-fragment complementation assay (BFG-PCA): tools and resources that expand the potential for binary protein interaction discovery. Nucleic Acids Research, 2022, 50, e54-e54.	6.5	4
121	Gene network architecture as a canvas for the interpretation of ecological genomics investigations. Molecular Ecology, 2010, 19, 5084-5085.	2.0	3
122	Combining the Dihydrofolate Reductase Protein-Fragment Complementation Assay with Gene Deletions to Establish Genotype-to-Phenotype Maps of Protein Complexes and Interaction Networks. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot090035.	0.2	3
123	The Genome Sequence of the Jean-Talon Strain, an Archeological Beer Yeast from QuÃ©bec, Reveals Traces of Adaptation to Specific Brewing Conditions. G3: Genes, Genomes, Genetics, 2020, 10, 3087-3097.	0.8	3
124	Closely related budding yeast species respond to different ecological signals for spore activation. Yeast, 2021, 38, 81-89.	0.8	3
125	Deep Mutational Scanning of Protein-Protein Interactions Between Partners Expressed from Their Endogenous Loci In Vivo. Methods in Molecular Biology, 2022, 2477, 237-259.	0.4	3
126	Yeast proteins do not practice social distancing as species hybridize. Current Genetics, 2021, 67, 755-759.	0.8	2



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127	Extended Linkers Improve the Detection of Protein-protein Interactions (PPIs) by Dihydrofolate Reductase Protein-fragment Complementation Assay (DHFR PCA) in Living Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 373-383.	2.5	1
128	Similarities in biological processes can be used to bridge ecology and molecular biology. <i>Evolutionary Applications</i> , 2020, 13, 1335-1350.	1.5	1
129	Molecular Dependency Impacts on the Compensating Ability of Paralogs: A Response to Veitia. <i>Trends in Genetics</i> , 2017, 33, 657-658.	2.9	1
130	Haploid transcriptome analysis reveals allelic gene expression variants, co-expressed gene groups, and linkages between expression and copy number variation. <i>BMC Proceedings</i> , 2011, 5, .	1.8	0
131	Identifying features of genome evolution to exploit cancer vulnerabilities. <i>Cell Systems</i> , 2021, 12, 1127-1130.	2.9	0
132	High-Throughput Gene Mutagenesis Screening Using Base Editing. <i>Methods in Molecular Biology</i> , 2022, 2477, 331-348.	0.4	0