

Christian Landry

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.

137
papers

6,159
citations

40
h-index

76
g-index

169
ext. papers

7,474
ext. citations

8.5
avg, IF

5.89
L-index

#	Paper	IF	Citations
137	High-Throughput Gene Mutagenesis Screening Using Base Editing.. <i>Methods in Molecular Biology</i> , 2022 , 2477, 331-348	1.4	
136	Deep Mutational Scanning of Protein-Protein Interactions Between Partners Expressed from Their Endogenous Loci In Vivo.. <i>Methods in Molecular Biology</i> , 2022 , 2477, 237-259	1.4	
135	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	8.3	4
134	Protein context shapes the specificity of SH3 domain-mediated interactions in vivo. <i>Nature Communications</i> , 2021 , 12, 1597	17.4	7
133	Yeast proteins do not practice social distancing as species hybridize. <i>Current Genetics</i> , 2021 , 67, 755-759	2.9	0
132	The neutral rate of whole-genome duplication varies among yeast species and their hybrids. <i>Nature Communications</i> , 2021 , 12, 3126	17.4	0
131	The Canadian Fungal Research Network: current challenges and future opportunities. <i>Canadian Journal of Microbiology</i> , 2021 , 67, 13-22	3.2	3
130	Closely related budding yeast species respond to different ecological signals for spore activation. <i>Yeast</i> , 2021 , 38, 81-89	3.4	0
129	Interspecific hybrids show a reduced adaptive potential under DNA damaging conditions. <i>Evolutionary Applications</i> , 2021 , 14, 758-769	4.8	0
128	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,	11.5	3
127	The parasite <i>Schistocephalus solidus</i> secretes proteins with putative host manipulation functions. <i>Parasites and Vectors</i> , 2021 , 14, 436	4	0
126	Identifying features of genome evolution to exploit cancer vulnerabilities.. <i>Cell Systems</i> , 2021 , 12, 1127-1130	11.30	
125	Similarities in biological processes can be used to bridge ecology and molecular biology. <i>Evolutionary Applications</i> , 2020 , 13, 1335-1350	4.8	1
124	The Genome Sequence of the Jean-Talon Strain, an Archeological Beer Yeast from Québec, Reveals Traces of Adaptation to Specific Brewing Conditions. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3087-3097	3.2	1
123	Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. <i>Nature Ecology and Evolution</i> , 2020 , 4, 626-638	12.3	23
122	Competition experiments in a soil microcosm reveal the impact of genetic and biotic factors on natural yeast populations. <i>ISME Journal</i> , 2020 , 14, 1410-1421	11.9	2
121	Perturbing proteomes at single residue resolution using base editing. <i>Nature Communications</i> , 2020 , 11, 1871	17.4	26

120	Diverse perspectives on interdisciplinarity from Members of the College of the Royal Society of Canada. <i>Facets</i> , 2020 , 5, 138-165	2.3	9
119	Purification of Yeast Spores to Investigate Their Dynamics of Activation. <i>Current Protocols in Microbiology</i> , 2020 , 59, e123	7.1	0
118	The effect of hybridization on transposable element accumulation in an undomesticated fungal species. <i>ELife</i> , 2020 , 9,	8.9	9
117	BUBR1 Pseudokinase Domain Promotes Kinetochore PP2A-B56 Recruitment, Spindle Checkpoint Silencing, and Chromosome Alignment. <i>Cell Reports</i> , 2020 , 33, 108397	10.6	5
116	Spontaneous whole-genome duplication restores fertility in interspecific hybrids. <i>Nature Communications</i> , 2019 , 10, 4126	17.4	20
115	Differences Between the Raw Material and the Products of Gene Birth Can Result from Mutational Biases. <i>Genetics</i> , 2019 , 212, 1353-1366	4	6
114	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	9.7	22
113	: A Computational Workflow for Designing Libraries of Guide RNAs for CRISPR-Mediated Base Editing. <i>Genetics</i> , 2019 , 212, 377-385	4	21
112	Hybridization is a recurrent evolutionary stimulus in wild yeast speciation. <i>Nature Communications</i> , 2019 , 10, 923	17.4	35
111	Paralog dependency indirectly affects the robustness of human cells. <i>Molecular Systems Biology</i> , 2019 , 15, e8871	12.2	19
110	The role of structural pleiotropy and regulatory evolution in the retention of heteromers of paralogs. <i>ELife</i> , 2019 , 8,	8.9	15
109	Regulation plays a multifaceted role in the retention of gene duplicates. <i>PLoS Biology</i> , 2019 , 17, e30005197	17.7	8
108	A collection of barcoded natural isolates of <i>Saccharomyces paradoxus</i> to study microbial evolutionary ecology. <i>MicrobiologyOpen</i> , 2018 , 8, e773	3.4	4
107	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	7.6	1
106	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	7.6	6
105	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	17.6	10
104	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	3.2	12
103	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	4.9	7

102	Mitochondrial Recombination Reveals Mito-Mito Epistasis in Yeast. <i>Genetics</i> , 2018 , 209, 307-319	4	19
101	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	5.7	16
100	Gene duplication can impart fragility, not robustness, in the yeast protein interaction network. <i>Science</i> , 2017 , 355, 630-634	33.3	61
99	Hybridization and adaptive evolution of diverse species for cellulosic biofuel production. <i>Biotechnology for Biofuels</i> , 2017 , 10, 78	7.8	52
98	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	8.3	10
97	Mitochondrial Recombination and Introgression during Speciation by Hybridization. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1947-1959	8.3	36
96	No evidence for extrinsic post-zygotic isolation in a wild yeast system. <i>Biology Letters</i> , 2017 , 13,	3.6	7
95	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	5.7	9
94	Identification of the fitness determinants of budding yeast on a natural substrate. <i>ISME Journal</i> , 2017 , 11, 959-971	11.9	13
93	When nuclear-encoded proteins and mitochondrial RNAs do not get along, species split apart. <i>EMBO Reports</i> , 2017 , 18, 8-10	6.5	4
92	Deep transcriptome annotation enables the discovery and functional characterization of cryptic small proteins. <i>ELife</i> , 2017 , 6,	8.9	57
91	Evolutionary biology through the lens of budding yeast comparative genomics. <i>Nature Reviews Genetics</i> , 2017 , 18, 581-598	30.1	43
90	Yeast Population Genomics Goes Wild: The Case of <i>Saccharomyces paradoxus</i> . <i>Population Genomics</i> , 2017 , 207-230	1.4	5
89	Molecular Dependency Impacts on the Compensating Ability of Paralogs: A Response to Veitia. <i>Trends in Genetics</i> , 2017 , 33, 657-658	8.5	1
88	Multi-scale perturbations of protein interactomes reveal their mechanisms of regulation, robustness and insights into genotype-phenotype maps. <i>Briefings in Functional Genomics</i> , 2016 , 15, 130-139	4.9	6
87	Speciation driven by hybridization and chromosomal plasticity in a wild yeast. <i>Nature Microbiology</i> , 2016 , 1, 15003	26.6	120
86	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	6.3	46
85	The Dihydrofolate Reductase Protein-Fragment Complementation Assay: A Survival-Selection Assay for Large-Scale Analysis of Protein-Protein Interactions. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	3

84	Combining the Dihydrofolate Reductase Protein-Fragment Complementation Assay with Gene Deletions to Establish Genotype-to-Phenotype Maps of Protein Complexes and Interaction Networks. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	2
83	Protein-Fragment Complementation Assays for Large-Scale Analysis, Functional Dissection, and Spatiotemporal Dynamic Studies of Protein-Protein Interactions in Living Cells. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	5
82	Evidence of Natural Hybridization in Brazilian Wild Lineages of <i>Saccharomyces cerevisiae</i> . <i>Genome Biology and Evolution</i> , 2016 , 8, 317-29	3.9	45
81	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	7.6	32
80	Molecular and cellular bases of adaptation to a changing environment in microorganisms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016 , 283,	4.4	48
79	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	6	72
78	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, 159-71	9.8	20
77	Mitotic phosphotyrosine network analysis reveals that tyrosine phosphorylation regulates Polo-like kinase 1 (PLK1). <i>Science Signaling</i> , 2016 , 9, rs14	8.8	18
76	Feedback regulation between autophagy and PKA. <i>Autophagy</i> , 2015 , 11, 1181-3	10.2	23
75	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, 1079-92	7.6	15
74	Found in translation: functions and evolution of a recently discovered alternative proteome. <i>Current Opinion in Structural Biology</i> , 2015 , 32, 74-80	8.1	38
73	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, 4501-6	11.5	41
72	The yeast galactose network as a quantitative model for cellular memory. <i>Molecular BioSystems</i> , 2015 , 11, 28-37		28
71	Metabolic variation in natural populations of wild yeast. <i>Ecology and Evolution</i> , 2015 , 5, 722-32	2.8	14
70	The genomics of wild yeast populations sheds light on the domestication of man's best (micro) friend. <i>Molecular Ecology</i> , 2015 , 24, 5309-11	5.7	11
69	Genome-wide protein-protein interaction screening by protein-fragment complementation assay (PCA) in living cells. <i>Journal of Visualized Experiments</i> , 2015 ,	1.6	11
68	Evolutionary rescue by compensatory mutations is constrained by genomic and environmental backgrounds. <i>Molecular Systems Biology</i> , 2015 , 11, 832	12.2	38
67	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, 2487-95 ^{3,2}		13

66	Identification of candidate mimicry proteins involved in parasite-driven phenotypic changes. <i>Parasites and Vectors</i> , 2015 , 8, 225	4	11
65	<i>Lachancea quebecensis</i> sp. nov., a yeast species consistently isolated from tree bark in the Canadian province of Québec. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 3392-3399	2.2	7
64	Local climatic adaptation in a widespread microorganism. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281, 20132472	4.4	49
63	Modulation of the yeast protein interactome in response to DNA damage. <i>Journal of Proteomics</i> , 2014 , 100, 25-36	3.9	15
62	Chromosomal variation segregates within incipient species and correlates with reproductive isolation. <i>Molecular Ecology</i> , 2014 , 23, 4362-72	5.7	48
61	The calcineurin signaling network evolves via conserved kinase-phosphatase modules that transcend substrate identity. <i>Molecular Cell</i> , 2014 , 55, 422-435	17.6	70
60	Functional divergence and evolutionary turnover in mammalian phosphoproteomes. <i>PLoS Genetics</i> , 2014 , 10, e1004062	6	39
59	Detecting functional divergence after gene duplication through evolutionary changes in posttranslational regulatory sequences. <i>PLoS Computational Biology</i> , 2014 , 10, e1003977	5	27
58	Turnover of protein phosphorylation evolving under stabilizing selection. <i>Frontiers in Genetics</i> , 2014 , 5, 245	4.5	35
57	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, 281-8	3.1	50
56	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, 488-99	1.8	42
55	Recent advances in ecological genomics: from phenotypic plasticity to convergent and adaptive evolution and speciation. <i>Advances in Experimental Medicine and Biology</i> , 2014 , 781, 1-5	3.6	4
54	Integrative avenues for exploring the dynamics and evolution of protein interaction networks. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 775-83	11.4	13
53	Extracting insight from noisy cellular networks. <i>Cell</i> , 2013 , 155, 983-9	56.2	43
52	A systematic approach for the genetic dissection of protein complexes in living cells. <i>Cell Reports</i> , 2013 , 3, 2155-67	10.6	28
51	qPCA: a scalable assay to measure the perturbation of protein-protein interactions in living cells. <i>Molecular BioSystems</i> , 2013 , 9, 36-43		25
50	Transcriptional divergence plays a role in the rewiring of protein interaction networks after gene duplication. <i>Journal of Proteomics</i> , 2013 , 81, 112-25	3.9	20
49	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, 2369-79	5.7	13

48	Compositional differences between size classes of dissolved organic matter from freshwater and seawater revealed by an HPLC-FTIR system. <i>Environmental Science & Technology</i> , 2012 , 46, 1700-7	10.3	40
47	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, 2594-606	5.8	70
46	The genotype-phenotype maps of systems biology and quantitative genetics: distinct and complementary. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 751, 371-98	3.6	12
45	What is needed for next-generation ecological and evolutionary genomics?. <i>Trends in Ecology and Evolution</i> , 2012 , 27, 673-8	10.9	66
44	Evidence for the robustness of protein complexes to inter-species hybridization. <i>PLoS Genetics</i> , 2012 , 8, e1003161	6	36
43	Proteomic characterization of phagosomal membrane microdomains during phagolysosome biogenesis and evolution. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1365-77	7.6	14
42	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	5.4	26
41	Where do phosphosites come from and where do they go after gene duplication?. <i>International Journal of Evolutionary Biology</i> , 2012 , 2012, 843167		4
40	Cell biology. A cellular roadmap for the plant kingdom. <i>Science</i> , 2011 , 333, 532-3	33.3	8
39	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	1.4	25
38	Phosphorylation network rewiring by gene duplication. <i>Molecular Systems Biology</i> , 2011 , 7, 504	12.2	28
37	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,	2.3	78
36	Key considerations for measuring allelic expression on a genomic scale using high-throughput sequencing. <i>Molecular Ecology</i> , 2010 , 19 Suppl 1, 212-27	5.7	54
35	Gene network architecture as a canvas for the interpretation of ecological genomics investigations. <i>Molecular Ecology</i> , 2010 , 19, 5084-5	5.7	3
34	Molecular characterization of the evolution of phagosomes. <i>Molecular Systems Biology</i> , 2010 , 6, 423	12.2	107
33	Cell signaling. Signaling through cooperation. <i>Science</i> , 2010 , 328, 983-4	33.3	40
32	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, 335-68	1.7	38
31	Chromatin regulators shape the genotype-phenotype map. <i>Molecular Systems Biology</i> , 2010 , 6, 434	12.2	4

30	Moving from transcriptional to phospho-evolution: generalizing regulatory evolution?. <i>Trends in Genetics</i> , 2010 , 26, 462-7	8.5	43
29	How perfect can protein interactomes be?. <i>Science Signaling</i> , 2009 , 2, pe11	8.8	60
28	Weak functional constraints on phosphoproteomes. <i>Trends in Genetics</i> , 2009 , 25, 193-7	8.5	222
27	Systems biology spins off a new model for the study of canalization. <i>Trends in Ecology and Evolution</i> , 2009 , 24, 63-6	10.9	12
26	Cascading transcriptional effects of a naturally occurring frameshift mutation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Ecology</i> , 2008 , 17, 2985-97	5.7	31
25	An in vivo map of the yeast protein interactome. <i>Science</i> , 2008 , 320, 1465-70	33.3	576
24	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, 9272-7	11.5	511
23	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	9.7	222
22	Genetic properties influencing the evolvability of gene expression. <i>Science</i> , 2007 , 317, 118-21	33.3	251
21	Genome clashes in hybrids: insights from gene expression. <i>Heredity</i> , 2007 , 99, 483-93	3.6	107
20	Indel arrays: an affordable alternative for genotyping. <i>Plant Journal</i> , 2007 , 51, 727-37	6.9	54
19	Quantification of dynamic protein complexes using Renilla luciferase fragment complementation applied to protein kinase A activities in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 16916-21	11.5	158
18	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, 3283-8	11.5	16
17	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, 343-51	3.8	89
16	Ecological and evolutionary genomics of <i>Saccharomyces cerevisiae</i> . <i>Molecular Ecology</i> , 2006 , 15, 575-91	5.7	83
15	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	4.5	43
14	Compensatory cis-trans evolution and the dysregulation of gene expression in interspecific hybrids of <i>Drosophila</i> . <i>Genetics</i> , 2005 , 171, 1813-22	4	151
13	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, 1655-62	4.4	163

12	MHC studies in nonmodel vertebrates: what have we learned about natural selection in 15 years?. <i>Journal of Evolutionary Biology</i> , 2003 , 16, 363-77	2.3	711
11	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> , 2001 , 10, 2525-39	5.7	161
10	The rate of whole-genome duplication can be accelerated by hybridization		1
9	The high turnover of ribosome-associated transcripts from de novo ORFs produces gene-like characteristics available for de novo gene emergence in wild yeast populations		2
8	The effect of hybridization on transposable element accumulation in an undomesticated fungal species		1
7	Major host transitions are modulated through transcriptome-wide reprogramming events in <i>Schistocephalus solidus</i> , a threespine stickleback parasite		1
6	Deep transcriptome annotation suggests that small and large proteins encoded in the same genes often cooperate		1
5	The parasite <i>Schistocephalus solidus</i> secretes proteins with putative host manipulation functions		1
4	Mapping Gene-Microbe Interactions: Insights from Functional Genomics Co-culture Experiments between <i>Saccharomyces cerevisiae</i> and <i>Pseudomonas</i> spp		1
3	Frequent assembly of chimeric complexes in the protein interaction network of an interspecies yeast hybrid		1
2	Differences between the de novo proteome and its non-functional precursor can result from neutral constraints on its birth process, not necessarily from natural selection alone		3
1	beditor: A computational workflow for designing libraries of guide RNAs for CRISPR-mediated base editing		1