

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6614728/ben-lehner-publications-by-citations.pdf>

Version: 2024-04-03

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

108 papers	8,047 citations	51 h-index	89 g-index
125 ext. papers	10,048 ext. citations	19.3 avg, IF	6.88 L-index

#	Paper	IF	Citations
108	3D structures of individual mammalian genomes studied by single-cell Hi-C. <i>Nature</i> , 2017 , 544, 59-64	50.4	485
107	Chromatin organization is a major influence on regional mutation rates in human cancer cells. <i>Nature</i> , 2012 , 488, 504-7	50.4	451
106	Systematic mapping of genetic interactions in <i>Caenorhabditis elegans</i> identifies common modifiers of diverse signaling pathways. <i>Nature Genetics</i> , 2006 , 38, 896-903	36.3	397
105	Synonymous mutations frequently act as driver mutations in human cancers. <i>Cell</i> , 2014 , 156, 1324-1335	56.2	369
104	Intrinsic protein disorder and interaction promiscuity are widely associated with dosage sensitivity. <i>Cell</i> , 2009 , 138, 198-208	56.2	263
103	A single gene network accurately predicts phenotypic effects of gene perturbation in <i>Caenorhabditis elegans</i> . <i>Nature Genetics</i> , 2008 , 40, 181-8	36.3	248
102	Tissue specificity and the human protein interaction network. <i>Molecular Systems Biology</i> , 2009 , 5, 260	12.2	246
101	In search of antisense. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 88-94	10.3	246
100	Differential DNA mismatch repair underlies mutation rate variation across the human genome. <i>Nature</i> , 2015 , 521, 81-4	50.4	224
99	Transgenerational transmission of environmental information in. <i>Science</i> , 2017 , 356, 320-323	33.3	223
98	Antisense transcripts in the human genome. <i>Trends in Genetics</i> , 2002 , 18, 63-5	8.5	219
97	Intergenerational and transgenerational epigenetic inheritance in animals. <i>Nature Cell Biology</i> , 2019 , 21, 143-151	23.4	219
96	The rules and impact of nonsense-mediated mRNA decay in human cancers. <i>Nature Genetics</i> , 2016 , 48, 1112-8	36.3	208
95	Molecular mechanisms of epistasis within and between genes. <i>Trends in Genetics</i> , 2011 , 27, 323-31	8.5	204
94	Genotype to phenotype: lessons from model organisms for human genetics. <i>Nature Reviews Genetics</i> , 2013 , 14, 168-78	30.1	164
93	A first-draft human protein-interaction map. <i>Genome Biology</i> , 2004 , 5, R63	18.3	164
92	Selection to minimise noise in living systems and its implications for the evolution of gene expression. <i>Molecular Systems Biology</i> , 2008 , 4, 170	12.2	156

91	Predicting mutation outcome from early stochastic variation in genetic interaction partners. <i>Nature</i> , 2011 , 480, 250-3	50.4	137
90	A Concentration-Dependent Liquid Phase Separation Can Cause Toxicity upon Increased Protein Expression. <i>Cell Reports</i> , 2016 , 16, 222-231	10.6	122
89	A protein interaction framework for human mRNA degradation. <i>Genome Research</i> , 2004 , 14, 1315-23	9.7	112
88	Fitness trade-offs and environmentally induced mutation buffering in isogenic <i>C. elegans</i> . <i>Science</i> , 2012 , 335, 82-5	33.3	108
87	Evolutionary plasticity of genetic interaction networks. <i>Nature Genetics</i> , 2008 , 40, 390-1	36.3	107
86	Clustered Mutation Signatures Reveal that Error-Prone DNA Repair Targets Mutations to Active Genes. <i>Cell</i> , 2017 , 170, 534-547.e23	56.2	105
85	RNAi screens in <i>Caenorhabditis elegans</i> in a 96-well liquid format and their application to the systematic identification of genetic interactions. <i>Nature Protocols</i> , 2006 , 1, 1617-20	18.8	103
84	Human epidermal stem cell function is regulated by circadian oscillations. <i>Cell Stem Cell</i> , 2013 , 13, 745-538		98
83	Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. <i>Genome Biology</i> , 2007 , 8, R15	18.3	89
82	The effects of genetic variation on gene expression dynamics during development. <i>Nature</i> , 2014 , 505, 208-11	50.4	86
81	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. <i>Genome Biology</i> , 2016 , 17, 129	18.3	85
80	Analysis of a high-throughput yeast two-hybrid system and its use to predict the function of intracellular proteins encoded within the human MHC class III region. <i>Genomics</i> , 2004 , 83, 153-67	4.3	84
79	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. <i>Nature Genetics</i> , 2019 , 51, 1645-1651	36.3	77
78	The roles of intersubunit interactions in exosome stability. <i>Journal of Biological Chemistry</i> , 2003 , 278, 34943-51	5.4	76
77	Chromatin organization in sperm may be the major functional consequence of base composition variation in the human genome. <i>PLoS Genetics</i> , 2011 , 7, e1002036	6	74
76	Widespread conservation of genetic redundancy during a billion years of eukaryotic evolution. <i>Trends in Genetics</i> , 2008 , 24, 485-8	8.5	74
75	Human genes with CpG island promoters have a distinct transcription-associated chromatin organization. <i>Genome Biology</i> , 2012 , 13, R110	18.3	73
74	The Causes and Consequences of Genetic Interactions (Epistasis). <i>Annual Review of Genomics and Human Genetics</i> , 2019 , 20, 433-460	9.7	71

73	Combinatorial RNA interference in <i>Caenorhabditis elegans</i> reveals that redundancy between gene duplicates can be maintained for more than 80 million years of evolution. <i>Genome Biology</i> , 2006 , 7, R69	18.3	71
72	Maternal age generates phenotypic variation in <i>Caenorhabditis elegans</i> . <i>Nature</i> , 2017 , 552, 106-109	50.4	70
71	A simple principle concerning the robustness of protein complex activity to changes in gene expression. <i>BMC Systems Biology</i> , 2008 , 2, 1	3.5	70
70	Genes confer similar robustness to environmental, stochastic, and genetic perturbations in yeast. <i>PLoS ONE</i> , 2010 , 5, e9035	3.7	68
69	Conflict between noise and plasticity in yeast. <i>PLoS Genetics</i> , 2010 , 6, e1001185	6	68
68	The genetic landscape of a physical interaction. <i>ELife</i> , 2018 , 7,	8.9	67
67	The complete local genotype-phenotype landscape for the alternative splicing of a human exon. <i>Nature Communications</i> , 2016 , 7, 11558	17.4	66
66	Loss of LIN-35, the <i>Caenorhabditis elegans</i> ortholog of the tumor suppressor p105Rb, results in enhanced RNA interference. <i>Genome Biology</i> , 2006 , 7, R4	18.3	66
65	The mutational landscape of a prion-like domain. <i>Nature Communications</i> , 2019 , 10, 4162	17.4	65
64	Determining protein structures using deep mutagenesis. <i>Nature Genetics</i> , 2019 , 51, 1177-1186	36.3	65
63	Predicting genetic modifier loci using functional gene networks. <i>Genome Research</i> , 2010 , 20, 1143-53	9.7	63
62	Mechanisms, timescales and principles of trans-generational epigenetic inheritance in animals. <i>Current Opinion in Genetics and Development</i> , 2016 , 36, 41-9	4.9	59
61	Predicting phenotypic variation in yeast from individual genome sequences. <i>Nature Genetics</i> , 2011 , 43, 1270-4	36.3	56
60	Pairwise and higher-order genetic interactions during the evolution of a tRNA. <i>Nature</i> , 2018 , 558, 117-124	50.4	54
59	Rapid selection of transgenic <i>C. elegans</i> using antibiotic resistance. <i>Nature Methods</i> , 2010 , 7, 725-7	21.6	52
58	Modelling genotype-phenotype relationships and human disease with genetic interaction networks. <i>Journal of Experimental Biology</i> , 2007 , 210, 1559-66	3	51
57	Cancer type-dependent genetic interactions between cancer driver alterations indicate plasticity of epistasis across cell types. <i>Molecular Systems Biology</i> , 2015 , 11, 824	12.2	47
56	Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. <i>Cell</i> , 2019 , 176, 549-563.e23	56.2	43

55	Epigenetic epistatic interactions constrain the evolution of gene expression. <i>Molecular Systems Biology</i> , 2013 , 9, 645	12.2	40
54	Inferring gene function from evolutionary change in signatures of translation efficiency. <i>Genome Biology</i> , 2014 , 15, R44	18.3	37
53	Systematic Analysis of the Determinants of Gene Expression Noise in Embryonic Stem Cells. <i>Cell Systems</i> , 2017 , 5, 471-484.e4	10.6	36
52	Slow-growing cells within isogenic populations have increased RNA polymerase error rates and DNA damage. <i>Nature Communications</i> , 2015 , 6, 7972	17.4	35
51	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. <i>Nature Communications</i> , 2018 , 9, 2601	17.4	32
50	Fluctuation and response in biology. <i>Cellular and Molecular Life Sciences</i> , 2011 , 68, 1005-10	10.3	31
49	Protein domains enriched in mammalian tissue-specific or widely expressed genes. <i>Trends in Genetics</i> , 2004 , 20, 468-72	8.5	29
48	Hydroxymethylated cytosines are associated with elevated C to G transversion rates. <i>PLoS Genetics</i> , 2014 , 10, e1004585	6	28
47	Beyond genotype to phenotype: why the phenotype of an individual cannot always be predicted from their genome sequence and the environment that they experience. <i>FEBS Journal</i> , 2012 , 279, 3765-75	5.7	28
46	Loss of G9a preserves mutation patterns but increases chromatin accessibility, genomic instability and aggressiveness in skin tumours. <i>Nature Cell Biology</i> , 2018 , 20, 1400-1409	23.4	27
45	Generating transgenic nematodes by bombardment and antibiotic selection. <i>Nature Methods</i> , 2012 , 9, 118-9	21.6	25
44	Vitellogenins - Yolk Gene Function and Regulation in. <i>Frontiers in Physiology</i> , 2019 , 10, 1067	4.6	24
43	Conserved noncoding elements and the evolution of animal body plans. <i>BioEssays</i> , 2009 , 31, 727-35	4.1	23
42	Network-guided genetic screening: building, testing and using gene networks to predict gene function. <i>Briefings in Functional Genomics & Proteomics</i> , 2008 , 7, 217-27		22
41	To NMD or Not To NMD: Nonsense-Mediated mRNA Decay in Cancer and Other Genetic Diseases. <i>Trends in Genetics</i> , 2021 , 37, 657-668	8.5	22
40	Comprehensive single cell-resolution analysis of the role of chromatin regulators in early C. elegans embryogenesis. <i>Developmental Biology</i> , 2015 , 398, 153-62	3.1	21
39	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. <i>ELife</i> , 2019 , 8,	8.9	19
38	Scales and mechanisms of somatic mutation rate variation across the human genome. <i>DNA Repair</i> , 2019 , 81, 102647	4.3	18

37	Reaching the limit. <i>ELife</i> , 2018 , 7,	8.9	18
36	Co-option of the piRNA pathway for germline-specific alternative splicing of <i>C. elegans</i> TOR. <i>Cell Reports</i> , 2014 , 8, 1609-1616	10.6	17
35	Predicting phenotypic variation from genotypes, phenotypes and a combination of the two. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 803-9	11.4	17
34	Compensatory Cell Movements Confer Robustness to Mechanical Deformation during Embryonic Development. <i>Cell Systems</i> , 2016 , 3, 160-171	10.6	16
33	Dissecting the calcium-induced differentiation of human primary keratinocytes stem cells by integrative and structural network analyses. <i>PLoS Computational Biology</i> , 2015 , 11, e1004256	5	15
32	Empirical mean-noise fitness landscapes reveal the fitness impact of gene expression noise. <i>Nature Communications</i> , 2019 , 10, 3180	17.4	15
31	Technique review: how to use RNA interference. <i>Briefings in Functional Genomics & Proteomics</i> , 2004 , 3, 68-83		15
30	Nucleoid-associated proteins affect mutation dynamics in <i>E. coli</i> in a growth phase-specific manner. <i>PLoS Computational Biology</i> , 2012 , 8, e1002846	5	13
29	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell phenotypic variation. <i>ELife</i> , 2019 , 8,	8.9	13
28	Model-based approach for tracking embryogenesis in <i>Caenorhabditis elegans</i> fluorescence microscopy data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2009 , 2009, 5356-9	0.9	11
27	DiMSum: an error model and pipeline for analyzing deep mutational scanning data and diagnosing common experimental pathologies. <i>Genome Biology</i> , 2020 , 21, 207	18.3	11
26	The genetic landscape for amyloid beta fibril nucleation accurately discriminates familial Alzheimer's disease mutations. <i>ELife</i> , 2021 , 10,	8.9	11
25	Mapping the energetic and allosteric landscapes of protein binding domains.. <i>Nature</i> , 2022 , 604, 175-183	30.4	10
24	Impaired DNA replication derepresses chromatin and generates a transgenerationally inherited epigenetic memory. <i>Science Advances</i> , 2017 , 3, e1701143	14.3	9
23	Conserved substitution patterns around nucleosome footprints in eukaryotes and Archaea derive from frequent nucleosome repositioning through evolution. <i>PLoS Computational Biology</i> , 2013 , 9, e1003373	5.73	9
22	Changes in gene expression predictably shift and switch genetic interactions. <i>Nature Communications</i> , 2019 , 10, 3886	17.4	8
21	Integrated genome-scale prediction of detrimental mutations in transcription networks. <i>PLoS Genetics</i> , 2011 , 7, e1002077	6	8
20	Single and dual drug selection for transgenes following bombardment of <i>Caenorhabditis</i> species. <i>Methods</i> , 2014 , 68, 409-16	4.6	6

19	Noise control is a primary function of microRNAs and post-transcriptional regulation		6
18	Mutations primarily alter the inclusion of alternatively spliced exons. <i>ELife</i> , 2020 , 9,	8.9	5
17	Biophysical ambiguities prevent accurate genetic prediction. <i>Nature Communications</i> , 2020 , 11, 4923	17.4	5
16	Harmonious genetic combinations rewire regulatory networks and flip gene essentiality. <i>Nature Communications</i> , 2019 , 10, 3657	17.4	4
15	Systems biology: Network evolution hinges on history. <i>Nature</i> , 2015 , 523, 297-8	50.4	4
14	Determining protein structures using genetics		3
13	Reconstructing and analysing cellular states, space and time from gene expression profiles of many cells and single cells. <i>Molecular BioSystems</i> , 2015 , 11, 2690-8		2
12	Neuronal perception of the social environment intergenerationally controls germline development and generation time in <i>C. elegans</i>		2
11	Neuronal perception of the social environment generates an inherited memory that controls the development and generation time of <i>C. elegans</i> . <i>Current Biology</i> , 2021 , 31, 4256-4268.e7	6.3	2
10	Global mapping of the energetic and allosteric landscapes of protein binding domains		2
9	Changes in gene expression shift and switch genetic interactions		1
8	DiMSum: an error model and pipeline for analyzing deep mutational scanning data and diagnosing common experimental pathologies		1
7	The genetic landscape for amyloid beta fibril nucleation accurately discriminates familial Alzheimer's disease mutations		1
6	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell variation in proliferation, drug resistance and mutation outcome		1
5	The mutational landscape of a prion-like domain		1
4	Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers. <i>Nature Communications</i> , 2021 , 12, 7051	17.4	1
3	Systems Biology of <i>Caenorhabditis elegans</i> 2013 , 367-390		
2	Memory of ancestral mitochondrial stress. <i>Nature Cell Biology</i> , 2019 , 21, 303-304	23.4	

- 1 Cancer Gene Discovery by Network Analysis of Somatic Mutations Using the MUFFINN Server.
Methods in Molecular Biology, **2019**, 1907, 37-50

1.4