Ben Lehner

List of Publications by Year in Descending Order

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	Mapping the energetic and allosteric landscapes of protein binding domains.. *Nature*, **2022**, 604, 175-183	50.4	10
107	To NMD or Not To NMD: Nonsense-Mediated mRNA Decay in Cancer and Other Genetic Diseases. *Trends in Genetics*, **2021**, 37, 657-668	8.5	22
106	The genetic landscape for amyloid beta fibril nucleation accurately discriminates familial Alzheimer's disease mutations. *ELife*, **2021**, 10,	8.9	11
105	Neuronal perception of the social environment generates an inherited memory that controls the development and generation time of C. elegans. *Current Biology*, **2021**, 31, 4256-4268.e7	6.3	2
104	Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers. *Nature Communications*, **2021**, 12, 7051	17.4	1
103	Mutations primarily alter the inclusion of alternatively spliced exons. *ELife*, **2020**, 9,	8.9	5
102	Biophysical ambiguities prevent accurate genetic prediction. *Nature Communications*, **2020**, 11, 4923	17.4	5
101	DiMSum: an error model and pipeline for analyzing deep mutational scanning data and diagnosing common experimental pathologies. *Genome Biology*, **2020**, 21, 207	18.3	11
100	Vitellogenins - Yolk Gene Function and Regulation in. *Frontiers in Physiology*, **2019**, 10, 1067	4.6	24
99	Changes in gene expression predictably shift and switch genetic interactions. *Nature Communications*, **2019**, 10, 3886	17.4	8
98	Harmonious genetic combinations rewire regulatory networks and flip gene essentiality. *Nature Communications*, **2019**, 10, 3657	17.4	4
97	The mutational landscape of a prion-like domain. *Nature Communications*, **2019**, 10, 4162	17.4	65
96	Determining protein structures using deep mutagenesis. *Nature Genetics*, **2019**, 51, 1177-1186	36.3	65
95	The Causes and Consequences of Genetic Interactions (Epistasis). *Annual Review of Genomics and Human Genetics*, **2019**, 20, 433-460	9.7	71
94	Empirical mean-noise fitness landscapes reveal the fitness impact of gene expression noise. *Nature Communications*, **2019**, 10, 3180	17.4	15
93	Scales and mechanisms of somatic mutation rate variation across the human genome. *DNA Repair*, **2019**, 81, 102647	4.3	18
92	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell phenotypic variation. *ELife*, **2019**, 8,	8.9	13

91	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. *ELife*, **2019**, 8,	8.9	19
90	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. *Nature Genetics*, **2019**, 51, 1645-1651	36.3	77
89	Memory of ancestral mitochondrial stress. *Nature Cell Biology*, **2019**, 21, 303-304	23.4	
88	Intergenerational and transgenerational epigenetic inheritance in animals. *Nature Cell Biology*, **2019**, 21, 143-151	23.4	219
87	Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. *Cell*, **2019**, 176, 549-563.e23	56.2	43
86	Cancer Gene Discovery by Network Analysis of Somatic Mutations Using the MUFFINN Server. *Methods in Molecular Biology*, **2019**, 1907, 37-50	1.4	
85	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. *Nature Communications*, **2018**, 9, 2601	17.4	32
84	Reaching the limit. *ELife*, **2018**, 7,	8.9	18
83	Loss of G9a preserves mutation patterns but increases chromatin accessibility, genomic instability and aggressiveness in skin tumours. *Nature Cell Biology*, **2018**, 20, 1400-1409	23.4	27
82	Pairwise and higher-order genetic interactions during the evolution of a tRNA. *Nature*, **2018**, 558, 117-121	50.4	54
81	The genetic landscape of a physical interaction. *ELife*, **2018**, 7,	8.9	67
80	Transgenerational transmission of environmental information in. *Science*, **2017**, 356, 320-323	33.3	223
79	3D structures of individual mammalian genomes studied by single-cell Hi-C. *Nature*, **2017**, 544, 59-64	50.4	485
78	Systematic Analysis of the Determinants of Gene Expression Noise in Embryonic Stem Cells. *Cell Systems*, **2017**, 5, 471-484.e4	10.6	36
77	Clustered Mutation Signatures Reveal that Error-Prone DNA Repair Targets Mutations to Active Genes. *Cell*, **2017**, 170, 534-547.e23	56.2	105
76	Impaired DNA replication derepresses chromatin and generates a transgenerationally inherited epigenetic memory. *Science Advances*, **2017**, 3, e1701143	14.3	9
75	Maternal age generates phenotypic variation in Caenorhabditis elegans. *Nature*, **2017**, 552, 106-109	50.4	70
74	The rules and impact of nonsense-mediated mRNA decay in human cancers. *Nature Genetics*, **2016**, 48, 1112-8	36.3	208

73	The complete local genotype-phenotype landscape for the alternative splicing of a human exon. *Nature Communications*, **2016**, 7, 11558	17.4	66
72	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. *Genome Biology*, **2016**, 17, 129	18.3	85
71	Mechanisms, timescales and principles of trans-generational epigenetic inheritance in animals. *Current Opinion in Genetics and Development*, **2016**, 36, 41-9	4.9	59
70	A Concentration-Dependent Liquid Phase Separation Can Cause Toxicity upon Increased Protein Expression. *Cell Reports*, **2016**, 16, 222-231	10.6	122
69	Compensatory Cell Movements Confer Robustness to Mechanical Deformation during Embryonic Development. *Cell Systems*, **2016**, 3, 160-171	10.6	16
68	Differential DNA mismatch repair underlies mutation rate variation across the human genome. *Nature*, **2015**, 521, 81-4	50.4	224
67	Systems biology: Network evolution hinges on history. *Nature*, **2015**, 523, 297-8	50.4	4
66	Dissecting the calcium-induced differentiation of human primary keratinocytes stem cells by integrative and structural network analyses. *PLoS Computational Biology*, **2015**, 11, e1004256	5	15
65	Slow-growing cells within isogenic populations have increased RNA polymerase error rates and DNA damage. *Nature Communications*, **2015**, 6, 7972	17.4	35
64	Reconstructing and analysing cellular states, space and time from gene expression profiles of many cells and single cells. *Molecular BioSystems*, **2015**, 11, 2690-8		2
63	Cancer type-dependent genetic interactions between cancer driver alterations indicate plasticity of epistasis across cell types. *Molecular Systems Biology*, **2015**, 11, 824	12.2	47
62	Comprehensive single cell-resolution analysis of the role of chromatin regulators in early C. elegans embryogenesis. *Developmental Biology*, **2015**, 398, 153-62	3.1	21
61	Synonymous mutations frequently act as driver mutations in human cancers. *Cell*, **2014**, 156, 1324-1335	56.2	369
60	The effects of genetic variation on gene expression dynamics during development. *Nature*, **2014**, 505, 208-11	50.4	86
59	Single and dual drug selection for transgenes following bombardment of Caenorhabditis species. *Methods*, **2014**, 68, 409-16	4.6	6
58	Co-option of the piRNA pathway for germline-specific alternative splicing of C. elegans TOR. *Cell Reports*, **2014**, 8, 1609-1616	10.6	17
57	Hydroxymethylated cytosines are associated with elevated C to G transversion rates. *PLoS Genetics*, **2014**, 10, e1004585	6	28
56	Inferring gene function from evolutionary change in signatures of translation efficiency. *Genome Biology*, **2014**, 15, R44	18.3	37

55	Predicting phenotypic variation from genotypes, phenotypes and a combination of the two. *Current Opinion in Biotechnology*, **2013**, 24, 803-9	11.4	17
54	Human epidermal stem cell function is regulated by circadian oscillations. *Cell Stem Cell*, **2013**, 13, 745-53	28	98
53	Epigenetic epistatic interactions constrain the evolution of gene expression. *Molecular Systems Biology*, **2013**, 9, 645	12.2	40
52	Genotype to phenotype: lessons from model organisms for human genetics. *Nature Reviews Genetics*, **2013**, 14, 168-78	30.1	164
51	Systems Biology of Caenorhabditis elegans **2013**, 367-390		
50	Conserved substitution patterns around nucleosome footprints in eukaryotes and Archaea derive from frequent nucleosome repositioning through evolution. *PLoS Computational Biology*, **2013**, 9, e1003373	5	9
49	Beyond genotype to phenotype: why the phenotype of an individual cannot always be predicted from their genome sequence and the environment that they experience. *FEBS Journal*, **2012**, 279, 3765-75	5.7	28
48	Human genes with CpG island promoters have a distinct transcription-associated chromatin organization. *Genome Biology*, **2012**, 13, R110	18.3	73
47	Generating transgenic nematodes by bombardment and antibiotic selection. *Nature Methods*, **2012**, 9, 118-9	21.6	25
46	Chromatin organization is a major influence on regional mutation rates in human cancer cells. *Nature*, **2012**, 488, 504-7	50.4	451
45	Nucleoid-associated proteins affect mutation dynamics in E. coli in a growth phase-specific manner. *PLoS Computational Biology*, **2012**, 8, e1002846	5	13
44	Fitness trade-offs and environmentally induced mutation buffering in isogenic C. elegans. *Science*, **2012**, 335, 82-5	33.3	108
43	Predicting mutation outcome from early stochastic variation in genetic interaction partners. *Nature* , **2011**, 480, 250-3	50.4	137
42	Predicting phenotypic variation in yeast from individual genome sequences. *Nature Genetics*, **2011**, 43, 1270-4	36.3	56
41	Molecular mechanisms of epistasis within and between genes. *Trends in Genetics*, **2011**, 27, 323-31	8.5	204
40	Fluctuation and response in biology. *Cellular and Molecular Life Sciences*, **2011**, 68, 1005-10	10.3	31
39	Chromatin organization in sperm may be the major functional consequence of base composition variation in the human genome. *PLoS Genetics*, **2011**, 7, e1002036	6	74
38	Integrated genome-scale prediction of detrimental mutations in transcription networks. *PLoS Genetics*, **2011**, 7, e1002077	6	8

37	Rapid selection of transgenic C. elegans using antibiotic resistance. *Nature Methods*, **2010**, 7, 725-7	21.6	52
36	Genes confer similar robustness to environmental, stochastic, and genetic perturbations in yeast. *PLoS ONE*, **2010**, 5, e9035	3.7	68
35	Predicting genetic modifier loci using functional gene networks. *Genome Research*, **2010**, 20, 1143-53	9.7	63
34	Conflict between noise and plasticity in yeast. *PLoS Genetics*, **2010**, 6, e1001185	6	68
33	Model-based approach for tracking embryogenesis in Caenorhabditis elegans fluorescence microscopy data. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2009**, 2009, 5356-9	0.9	11
32	Tissue specificity and the human protein interaction network. *Molecular Systems Biology*, **2009**, 5, 260	12.2	246
31	Conserved noncoding elements and the evolution of animal body plans. *BioEssays*, **2009**, 31, 727-35	4.1	23
30	Intrinsic protein disorder and interaction promiscuity are widely associated with dosage sensitivity. *Cell*, **2009**, 138, 198-208	56.2	263
29	Evolutionary plasticity of genetic interaction networks. *Nature Genetics*, **2008**, 40, 390-1	36.3	107
28	A single gene network accurately predicts phenotypic effects of gene perturbation in Caenorhabditis elegans. *Nature Genetics*, **2008**, 40, 181-8	36.3	248
27	A simple principle concerning the robustness of protein complex activity to changes in gene expression. *BMC Systems Biology*, **2008**, 2, 1	3.5	70
26	Widespread conservation of genetic redundancy during a billion years of eukaryotic evolution. *Trends in Genetics*, **2008**, 24, 485-8	8.5	74
25	Network-guided genetic screening: building, testing and using gene networks to predict gene function. *Briefings in Functional Genomics & Proteomics*, **2008**, 7, 217-27		22
24	Selection to minimise noise in living systems and its implications for the evolution of gene expression. *Molecular Systems Biology*, **2008**, 4, 170	12.2	156
23	Modelling genotype-phenotype relationships and human disease with genetic interaction networks. *Journal of Experimental Biology*, **2007**, 210, 1559-66	3	51
22	Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. *Genome Biology*, **2007**, 8, R15	18.3	89
21	Combinatorial RNA interference in Caenorhabditis elegans reveals that redundancy between gene duplicates can be maintained for more than 80 million years of evolution. *Genome Biology*, **2006**, 7, R69	18.3	71
20	Loss of LIN-35, the Caenorhabditis elegans ortholog of the tumor suppressor p105Rb, results in enhanced RNA interference. *Genome Biology*, **2006**, 7, R4	18.3	66

19	Systematic mapping of genetic interactions in Caenorhabditis elegans identifies common modifiers of diverse signaling pathways. *Nature Genetics*, **2006**, 38, 896-903	36.3	397
18	RNAi screens in Caenorhabditis elegans in a 96-well liquid format and their application to the systematic identification of genetic interactions. *Nature Protocols*, **2006**, 1, 1617-20	18.8	103
17	Technique review: how to use RNA interference. *Briefings in Functional Genomics & Proteomics*, **2004**, 3, 68-83		15
16	A protein interaction framework for human mRNA degradation. *Genome Research*, **2004**, 14, 1315-23	9.7	112
15	In search of antisense. *Trends in Biochemical Sciences*, **2004**, 29, 88-94	10.3	246
14	Protein domains enriched in mammalian tissue-specific or widely expressed genes. *Trends in Genetics*, **2004**, 20, 468-72	8.5	29
13	A first-draft human protein-interaction map. *Genome Biology*, **2004**, 5, R63	18.3	164
12	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. *Genomics*, **2004**, 83, 153-67	4.3	84
11	The roles of intersubunit interactions in exosome stability. *Journal of Biological Chemistry*, **2003**, 278, 34943-51	5.4	76
10	Antisense transcripts in the human genome. *Trends in Genetics*, **2002**, 18, 63-5	8.5	219
9	Determining protein structures using genetics		3
8	Changes in gene expression shift and switch genetic interactions		1
7	DiMSum: an error model and pipeline for analyzing deep mutational scanning data and diagnosing common experimental pathologies		1
6	The genetic landscape for amyloid beta fibril nucleation accurately discriminates familial Alzheimer disease mutations		1
5	Noise control is a primary function of microRNAs and post-transcriptional regulation		6
4	Neuronal perception of the social environment intergenerationally controls germline development and generation time in C. elegans		2
3	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell variation in proliferation, drug resistance and mutation outcome		1
2	The mutational landscape of a prion-like domain		1