Ben Lehner

List of Publications by Year
in descending order

103 papers	11,381 citations	31976 53 h-index	36028 97 g-index
125 all docs	125 docs citations	125 times ranked	17170 citing authors

#	Article	IF	Citations
1	3D structures of individual mammalian genomes studied by single-cell Hi-C. Nature, 2017, 544, 59-64.	27.8	691
2	Chromatin organization is a major influence on regional mutation rates in human cancer cells. Nature, 2012, 488, 504-507.	27.8	602
3	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. Cell, 2014, 156, 1324-1335.	28.9	482
4	Systematic mapping of genetic interactions in Caenorhabditis elegans identifies common modifiers of diverse signaling pathways. Nature Genetics, 2006, 38, 896-903.	21.4	461
5	Intergenerational and transgenerational epigenetic inheritance in animals. Nature Cell Biology, 2019, 21, 143-151.	10.3	365
6	Transgenerational transmission of environmental information in *C. elegans*. Science, 2017, 356, 320-323.	12.6	360
7	The rules and impact of nonsense-mediated mRNA decay in human cancers. Nature Genetics, 2016, 48, 1112-1118.	21.4	340
8	Intrinsic Protein Disorder and Interaction Promiscuity Are Widely Associated with Dosage Sensitivity. Cell, 2009, 138, 198-208.	28.9	319
9	Differential DNA mismatch repair underlies mutation rate variation across the human genome. Nature, 2015, 521, 81-84.	27.8	310
10	Tissue specificity and the human protein interaction network. Molecular Systems Biology, 2009, 5, 260.	7.2	295
11	A single gene network accurately predicts phenotypic effects of gene perturbation in Caenorhabditis elegans. Nature Genetics, 2008, 40, 181-188.	21.4	284
12	In search of antisense. Trends in Biochemical Sciences, 2004, 29, 88-94.	7.5	277
13	Molecular mechanisms of epistasis within and between genes. Trends in Genetics, 2011, 27, 323-331.	6.7	273
14	Antisense transcripts in the human genome. Trends in Genetics, 2002, 18, 63-65.	6.7	234
15	A Concentration-Dependent Liquid Phase Separation Can Cause Toxicity upon Increased Protein Expression. Cell Reports, 2016, 16, 222-231.	6.4	230
16	Selection to minimise noise in living systems and its implications for the evolution of gene expression. Molecular Systems Biology, 2008, 4, 170.	7.2	218
17	Genotype to phenotype: lessons from model organisms for human genetics. Nature Reviews Genetics, 2013, 14, 168-178.	16.3	197
18	A first-draft human protein-interaction map. Genome Biology, 2004, 5, r63.	9.6	188

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19	Predicting mutation outcome from early stochastic variation in genetic interaction partners. Nature, 2011, 480, 250-253.	27.8	180
20	Clustered Mutation Signatures Reveal that Error-Prone DNA Repair Targets Mutations to Active Genes. Cell, 2017, 170, 534-547.e23.	28.9	173
21	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. Nature Genetics, 2019, 51, 1645-1651.	21.4	171
22	The Causes and Consequences of Genetic Interactions (Epistasis). Annual Review of Genomics and Human Genetics, 2019, 20, 433-460.	6.2	164
23	Fitness Trade-Offs and Environmentally Induced Mutation Buffering in Isogenic <i>C. elegans</i>. Science, 2012, 335, 82-85.	12.6	138
24	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. Genome Biology, 2016, 17, 129.	8.8	126
25	To NMD or Not To NMD: Nonsense-Mediated mRNA Decay in Cancer and Other Genetic Diseases. Trends in Genetics, 2021, 37, 657-668.	6.7	124
26	A Protein Interaction Framework for Human mRNA Degradation. Genome Research, 2004, 14, 1315-1323.	5.5	122
27	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, 1617-1620.	12.0	122
28	The effects of genetic variation on gene expression dynamics during development. Nature, 2014, 505, 208-211.	27.8	121
29	Evolutionary plasticity of genetic interaction networks. Nature Genetics, 2008, 40, 390-391.	21.4	118
30	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.	9.6	117
31	Human Epidermal Stem Cell Function Is Regulated by Circadian Oscillations. Cell Stem Cell, 2013, 13, 745-753.	11.1	117
32	Determining protein structures using deep mutagenesis. Nature Genetics, 2019, 51, 1177-1186.	21.4	117
33	The genetic landscape of a physical interaction. ELife, 2018, 7, .	6.0	116
34	The mutational landscape of a prion-like domain. Nature Communications, 2019, 10, 4162.	12.8	116
35	Maternal age generates phenotypic variation in Caenorhabditis elegans. Nature, 2017, 552, 106-109.	27.8	113
36	A simple principle concerning the robustness of protein complex activity to changes in gene expression. BMC Systems Biology, 2008, 2, 1.	3.0	112

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37	Widespread conservation of genetic redundancy during a billion years of eukaryotic evolution. Trends in Genetics, 2008, 24, 485-488.	6.7	108
38	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, 153-167.	2.9	99
39	Human genes with CpG island promoters have a distinct transcription-associated chromatin organization. Genome Biology, 2012, 13, R110.	9.6	98
40	Mapping the energetic and allosteric landscapes of protein binding domains. Nature, 2022, 604, 175-183.	27.8	98
41	Pairwise and higher-order genetic interactions during the evolution of a tRNA. Nature, 2018, 558, 117-121.	27.8	97
42	Conflict between Noise and Plasticity in Yeast. PLoS Genetics, 2010, 6, e1001185.	3.5	96
43	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.	9.6	92
44	The complete local genotype–phenotype landscape for the alternative splicing of a human exon. Nature Communications, 2016, 7, 11558.	12.8	91
45	Chromatin Organization in Sperm May Be the Major Functional Consequence of Base Composition Variation in the Human Genome. PLoS Genetics, 2011, 7, e1002036.	3.5	90
46	Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. Cell, 2019, 176, 549-563.e23.	28.9	87
47	The Roles of Intersubunit Interactions in Exosome Stability. Journal of Biological Chemistry, 2003, 278, 34943-34951.	3.4	84
48	Predicting genetic modifier loci using functional gene networks. Genome Research, 2010, 20, 1143-1153.	5.5	83
49	Genes Confer Similar Robustness to Environmental, Stochastic, and Genetic Perturbations in Yeast. PLoS ONE, 2010, 5, e9035.	2.5	81
50	Rapid selection of transgenic C. elegans using antibiotic resistance. Nature Methods, 2010, 7, 725-727.	19.0	77
51	Mechanisms, timescales and principles of trans-generational epigenetic inheritance in animals. Current Opinion in Genetics and Development, 2016, 36, 41-49.	3.3	77
52	Loss of LIN-35, the Caenorhabditis elegans ortholog of the tumor suppressor p105Rb, results in enhanced RNA interference. Genome Biology, 2006, 7, R4.	9.6	76
53	Vitellogenins - Yolk Gene Function and Regulation in Caenorhabditis elegans. Frontiers in Physiology, 2019, 10, 1067.	2.8	68
54	Modelling genotype–phenotype relationships and human disease with genetic interaction networks. Journal of Experimental Biology, 2007, 210, 1559-1566.	1.7	66

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55	Predicting phenotypic variation in yeast from individual genome sequences. Nature Genetics, 2011, 43, 1270-1274.	21.4	66
56	Systematic Analysis of the Determinants of Gene Expression Noise in Embryonic Stem Cells. Cell Systems, 2017, 5, 471-484.e4.	6.2	66
57	Scales and mechanisms of somatic mutation rate variation across the human genome. DNA Repair, 2019, 81, 102647.	2.8	59
58	Cancer typeâ€dependent genetic interactions between cancer driver alterations indicate plasticity of epistasis across cell types. Molecular Systems Biology, 2015, 11, 824.	7.2	54
59	Inferring gene function from evolutionary change in signatures of translation efficiency. Genome Biology, 2014, 15, R44.	9.6	53
60	Slow-growing cells within isogenic populations have increased RNA polymerase error rates and DNA damage. Nature Communications, 2015, 6, 7972.	12.8	51
61	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. Nature Communications, 2018, 9, 2601.	12.8	47
62	Fluctuation and response in biology. Cellular and Molecular Life Sciences, 2011, 68, 1005-1010.	5.4	46
63	Epigenetic epistatic interactions constrain the evolution of gene expression. Molecular Systems Biology, 2013, 9, 645.	7.2	46
64	Reaching the limit. ELife, 2018, 7, .	6.0	45
65	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. ELife, 2019, 8, .	6.0	44
66	DiMSum: an error model and pipeline for analyzing deep mutational scanning data and diagnosing common experimental pathologies. Genome Biology, 2020, 21, 207.	8.8	39
67	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, 3765-3775.	4.7	38
68	Loss of G9a preserves mutation patterns but increases chromatin accessibility, genomic instability and aggressiveness in skin tumours. Nature Cell Biology, 2018, 20, 1400-1409.	10.3	35
69	Empirical mean-noise fitness landscapes reveal the fitness impact of gene expression noise. Nature Communications, 2019, 10, 3180.	12.8	35
70	The genetic landscape for amyloid beta fibril nucleation accurately discriminates familial Alzheimerâ€™s disease mutations. ELife, 2021, 10, .	6.0	34
71	Protein domains enriched in mammalian tissue-specific or widely expressed genes. Trends in Genetics, 2004, 20, 468-472.	6.7	33
72	Generating transgenic nematodes by bombardment and antibiotic selection. Nature Methods, 2012, 9, 118-119.	19.0	33

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73	Compensatory Cell Movements Confer Robustness to Mechanical Deformation during Embryonic Development. Cell Systems, 2016, 3, 160-171.	6.2	33
74	Hydroxymethylated Cytosines Are Associated with Elevated C to G Transversion Rates. PLoS Genetics, 2014, 10, e1004585.	3.5	31
75	Conserved noncoding elements and the evolution of animal body plans. BioEssays, 2009, 31, 727-735.	2.5	30
76	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell phenotypic variation. ELife, 2019, 8, .	6.0	28
77	Changes in gene expression predictably shift and switch genetic interactions. Nature Communications, 2019, 10, 3886.	12.8	27
78	Network-guided genetic screening: building, testing and using gene networks to predict gene function. Briefings in Functional Genomics & Proteomics, 2008, 7, 217-227.	3.8	24
79	Comprehensive single cell-resolution analysis of the role of chromatin regulators in early C. elegans embryogenesis. Developmental Biology, 2015, 398, 153-162.	2.0	24
80	Mutations primarily alter the inclusion of alternatively spliced exons. ELife, 2020, 9, .	6.0	24
81	Co-option of the piRNA Pathway for Germline-Specific Alternative Splicing of C.Âelegans TOR. Cell Reports, 2014, 8, 1609-1616.	6.4	22
82	Nucleoid-Associated Proteins Affect Mutation Dynamics in E. coli in a Growth Phase-Specific Manner. PLoS Computational Biology, 2012, 8, e1002846.	3.2	21
83	Predicting phenotypic variation from genotypes, phenotypes and a combination of the two. Current Opinion in Biotechnology, 2013, 24, 803-809.	6.6	21
84	Dissecting the Calcium-Induced Differentiation of Human Primary Keratinocytes Stem Cells by Integrative and Structural Network Analyses. PLoS Computational Biology, 2015, 11, e1004256.	3.2	20
85	How to use RNA interference. Briefings in Functional Genomics & Proteomics, 2004, 3, 68-83.	3.8	18
86	Biophysical ambiguities prevent accurate genetic prediction. Nature Communications, 2020, 11, 4923.	12.8	17
87	Model-based approach for tracking embryogenesis in Caenorhabditis elegans fluorescence microscopy data. , 2009, 2009, 5356-9.		13
88	Conserved Substitution Patterns around Nucleosome Footprints in Eukaryotes and Archaea Derive from Frequent Nucleosome Repositioning through Evolution. PLoS Computational Biology, 2013, 9, e1003373.	3.2	13
89	The impact of rare germline variants on human somatic mutation processes. Nature Communications, 2022, 13, .	12.8	13
90	Impaired DNA replication derepresses chromatin and generates a transgenerationally inherited epigenetic memory. Science Advances, 2017, 3, e1701143.	10.3	12

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91	Neuronal perception of the social environment generates an inherited memory that controls the development and generation time of C.Âelegans. Current Biology, 2021, 31, 4256-4268.e7.	3.9	11
92	5,000 RNAi experiments on a chip. Nature Methods, 2004, 1, 103-104.	19.0	10
93	Harmonious genetic combinations rewire regulatory networks and flip gene essentiality. Nature Communications, 2019, 10, 3657.	12.8	9
94	Integrated Genome-Scale Prediction of Detrimental Mutations in Transcription Networks. PLoS Genetics, 2011, 7, e1002077.	3.5	8
95	Single and dual drug selection for transgenes following bombardment of Caenorhabditis species. Methods, 2014, 68, 409-416.	3.8	7
96	Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers. Nature Communications, 2021, 12, 7051.	12.8	5
97	Exploiting collateral damage. Nature, 2012, 488, 284-285.	27.8	4
98	Network evolution hinges on history. Nature, 2015, 523, 297-298.	27.8	4
99	Reconstructing and analysing cellular states, space and time from gene expression profiles of many cells and single cells. Molecular BioSystems, 2015, 11, 2690-2698.	2.9	4
100	Cancer Gene Discovery by Network Analysis of Somatic Mutations Using the MUFFINN Server. Methods in Molecular Biology, 2019, 1907, 37-50.	0.9	1
101	Systems Biology of Caenorhabditis elegans. , 2013, , 367-390.		0
102	Turning point: Ben Lehner. Nature, 2013, 502, 261-261.	27.8	0
103	Memory of ancestral mitochondrial stress. Nature Cell Biology, 2019, 21, 303-304.	10.3	0