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	Mapping the energetic and allosteric landscapes of protein binding domains. Nature, 2022, 604, 175-183.	27.8	98
2	The impact of rare germline variants on human somatic mutation processes. Nature Communications, 2022, 13, .	12.8	13
3	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
4	The genetic landscape for amyloid beta fibril nucleation accurately discriminates familial Alzheimer's disease mutations. ELife, 2021, 10, .	6.0	34
5	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
6	Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers. Nature Communications, 2021, 12, 7051.	12.8	5
7	Biophysical ambiguities prevent accurate genetic prediction. Nature Communications, 2020, 11, 4923.	12.8	17
8	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
9	Mutations primarily alter the inclusion of alternatively spliced exons. ELife, 2020, 9, .	6.0	24
10	Empirical mean-noise fitness landscapes reveal the fitness impact of gene expression noise. Nature Communications, 2019, 10, 3180.	12.8	35
11	Scales and mechanisms of somatic mutation rate variation across the human genome. DNA Repair, 2019, 81, 102647.	2.8	59
12	Vitellogenins - Yolk Gene Function and Regulation in Caenorhabditis elegans. Frontiers in Physiology, 2019, 10, 1067.	2.8	68
13	Changes in gene expression predictably shift and switch genetic interactions. Nature Communications, 2019, 10, 3886.	12.8	27
14	Harmonious genetic combinations rewire regulatory networks and flip gene essentiality. Nature Communications, 2019, 10, 3657.	12.8	9
15	The mutational landscape of a prion-like domain. Nature Communications, 2019, 10, 4162.	12.8	116
16	Determining protein structures using deep mutagenesis. Nature Genetics, 2019, 51, 1177-1186.	21.4	117
17	The Causes and Consequences of Genetic Interactions (Epistasis). Annual Review of Genomics and Human Genetics, 2019, 20, 433-460.	6.2	164
18	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. Nature Genetics, 2019, 51, 1645-1651.	21.4	171

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19	Memory of ancestral mitochondrial stress. Nature Cell Biology, 2019, 21, 303-304.	10.3	0
20	Intergenerational and transgenerational epigenetic inheritance in animals. Nature Cell Biology, 2019, 21, 143-151.	10.3	365
21	Combinatorial Genetics Reveals a Scaling Law for the Effects of Mutations on Splicing. Cell, 2019, 176, 549-563.e23.	28.9	87
22	Cancer Gene Discovery by Network Analysis of Somatic Mutations Using the MUFFINN Server. Methods in Molecular Biology, 2019, 1907, 37-50.	0.9	1
23	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell phenotypic variation. ELife, 2019, 8, .	6.0	28
24	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. ELife, 2019, 8, .	6.0	44
25	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
26	Pairwise and higher-order genetic interactions during the evolution of a tRNA. Nature, 2018, 558, 117-121.	27.8	97
27	The genetic landscape of a physical interaction. ELife, 2018, 7, .	6.0	116
28	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. Nature Communications, 2018, 9, 2601.	12.8	47
29	Reaching the limit. ELife, 2018, 7, .	6.0	45
30	Transgenerational transmission of environmental information in <i>C. elegans</i>. Science, 2017, 356, 320-323.	12.6	360
31	3D structures of individual mammalian genomes studied by single-cell Hi-C. Nature, 2017, 544, 59-64.	27.8	691
32	Systematic Analysis of the Determinants of Gene Expression Noise in Embryonic Stem Cells. Cell Systems, 2017, 5, 471-484.e4.	6.2	66
33	Clustered Mutation Signatures Reveal that Error-Prone DNA Repair Targets Mutations to Active Genes. Cell, 2017, 170, 534-547.e23.	28.9	173
34	Impaired DNA replication derepresses chromatin and generates a transgenerationally inherited epigenetic memory. Science Advances, 2017, 3, e1701143.	10.3	12
35	Maternal age generates phenotypic variation in Caenorhabditis elegans. Nature, 2017, 552, 106-109.	27.8	113
36	Mechanisms, timescales and principles of trans-generational epigenetic inheritance in animals. Current Opinion in Genetics and Development, 2016, 36, 41-49.	3.3	77

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37	A Concentration-Dependent Liquid Phase Separation Can Cause Toxicity upon Increased Protein Expression. Cell Reports, 2016, 16, 222-231.	6.4	230
38	Compensatory Cell Movements Confer Robustness to Mechanical Deformation during Embryonic Development. Cell Systems, 2016, 3, 160-171.	6.2	33
39	The rules and impact of nonsense-mediated mRNA decay in human cancers. Nature Genetics, 2016, 48, 1112-1118.	21.4	340
40	The complete local genotypeâ€"phenotype landscape for the alternative splicing of a human exon. Nature Communications, 2016, 7, 11558.	12.8	91
41	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. Genome Biology, 2016, 17, 129.	8.8	126
42	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
43	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
44	Differential DNA mismatch repair underlies mutation rate variation across the human genome. Nature, 2015, 521, 81-84.	27.8	310
45	Network evolution hinges on history. Nature, 2015, 523, 297-298.	27.8	4
46	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
47	Slow-growing cells within isogenic populations have increased RNA polymerase error rates and DNA damage. Nature Communications, 2015, 6, 7972.	12.8	51
48	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
49	Hydroxymethylated Cytosines Are Associated with Elevated C to G Transversion Rates. PLoS Genetics, 2014, 10, e1004585.	3.5	31
50	Inferring gene function from evolutionary change in signatures of translation efficiency. Genome Biology, 2014, 15, R44.	9.6	53
51	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. Cell, 2014, 156, 1324-1335.	28.9	482
52	The effects of genetic variation on gene expression dynamics during development. Nature, 2014, 505, 208-211.	27.8	121
53	Single and dual drug selection for transgenes following bombardment of Caenorhabditis species. Methods, 2014, 68, 409-416.	3.8	7
54	Co-option of the piRNA Pathway for Germline-Specific Alternative Splicing of C.Âelegans TOR. Cell Reports, 2014, 8, 1609-1616.	6.4	22

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55	Predicting phenotypic variation from genotypes, phenotypes and a combination of the two. Current Opinion in Biotechnology, 2013, 24, 803-809.	6.6	21
56	Human Epidermal Stem Cell Function Is Regulated by Circadian Oscillations. Cell Stem Cell, 2013, 13, 745-753.	11.1	117
57	Epigenetic epistatic interactions constrain the evolution of gene expression. Molecular Systems Biology, 2013, 9, 645.	7.2	46
58	Genotype to phenotype: lessons from model organisms for human genetics. Nature Reviews Genetics, 2013, 14, 168-178.	16.3	197
59	Systems Biology of Caenorhabditis elegans. , 2013, , 367-390.		0
60	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
61	Turning point: Ben Lehner. Nature, 2013, 502, 261-261.	27.8	0
62	Nucleoid-Associated Proteins Affect Mutation Dynamics in E. coli in a Growth Phase-Specific Manner. PLoS Computational Biology, 2012, 8, e1002846.	3.2	21
63	Fitness Trade-Offs and Environmentally Induced Mutation Buffering in Isogenic C. elegans. Science, 2012, 335, 82-85.	12.6	138
64	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
65	Human genes with CpG island promoters have a distinct transcription-associated chromatin organization. Genome Biology, 2012, 13, R110.	9.6	98
66	Generating transgenic nematodes by bombardment and antibiotic selection. Nature Methods, 2012, 9, 118-119.	19.0	33
67	Exploiting collateral damage. Nature, 2012, 488, 284-285.	27.8	4
68	Chromatin organization is a major influence on regional mutation rates in human cancer cells. Nature, 2012, 488, 504-507.	27.8	602
69	Predicting mutation outcome from early stochastic variation in genetic interaction partners. Nature, 2011, 480, 250-253.	27.8	180
70	Predicting phenotypic variation in yeast from individual genome sequences. Nature Genetics, 2011, 43, 1270-1274.	21.4	66
71	Molecular mechanisms of epistasis within and between genes. Trends in Genetics, 2011, 27, 323-331.	6.7	273
72	Fluctuation and response in biology. Cellular and Molecular Life Sciences, 2011, 68, 1005-1010.	5.4	46

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73	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
74	Integrated Genome-Scale Prediction of Detrimental Mutations in Transcription Networks. PLoS Genetics, 2011, 7, e1002077.	3.5	8
75	Rapid selection of transgenic C. elegans using antibiotic resistance. Nature Methods, 2010, 7, 725-727.	19.0	77
76	Genes Confer Similar Robustness to Environmental, Stochastic, and Genetic Perturbations in Yeast. PLoS ONE, 2010, 5, e9035.	2.5	81
77	Predicting genetic modifier loci using functional gene networks. Genome Research, 2010, 20, 1143-1153.	5.5	83
78	Conflict between Noise and Plasticity in Yeast. PLoS Genetics, 2010, 6, e1001185.	3.5	96
79	Model-based approach for tracking embryogenesis in Caenorhabditis elegans fluorescence microscopy data. , 2009, 2009, 5356-9.		13
80	Tissue specificity and the human protein interaction network. Molecular Systems Biology, 2009, 5, 260.	7.2	295
81	Conserved noncoding elements and the evolution of animal body plans. BioEssays, 2009, 31, 727-735.	2.5	30
82	Intrinsic Protein Disorder and Interaction Promiscuity Are Widely Associated with Dosage Sensitivity. Cell, 2009, 138, 198-208.	28.9	319
83	Evolutionary plasticity of genetic interaction networks. Nature Genetics, 2008, 40, 390-391.	21.4	118
84	A single gene network accurately predicts phenotypic effects of gene perturbation in Caenorhabditis elegans. Nature Genetics, 2008, 40, 181-188.	21.4	284
85	A simple principle concerning the robustness of protein complex activity to changes in gene expression. BMC Systems Biology, 2008, 2, 1.	3.0	112
86	Widespread conservation of genetic redundancy during a billion years of eukaryotic evolution. Trends in Genetics, 2008, 24, 485-488.	6.7	108
87	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
88	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
89	Modelling genotype–phenotype relationships and human disease with genetic interaction networks. Journal of Experimental Biology, 2007, 210, 1559-1566.	1.7	66
90	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

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91	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
92	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
93	Systematic mapping of genetic interactions in Caenorhabditis elegans identifies common modifiers of diverse signaling pathways. Nature Genetics, 2006, 38, 896-903.	21.4	461
94	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
95	How to use RNA interference. Briefings in Functional Genomics & Proteomics, 2004, 3, 68-83.	3.8	18
96	A Protein Interaction Framework for Human mRNA Degradation. Genome Research, 2004, 14, 1315-1323.	5.5	122
97	5,000 RNAi experiments on a chip. Nature Methods, 2004, 1, 103-104.	19.0	10
98	In search of antisense. Trends in Biochemical Sciences, 2004, 29, 88-94.	7.5	277
99	Protein domains enriched in mammalian tissue-specific or widely expressed genes. Trends in Genetics, 2004, 20, 468-472.	6.7	33
100	A first-draft human protein-interaction map. Genome Biology, 2004, 5, r63.	9.6	188
101	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
102	The Roles of Intersubunit Interactions in Exosome Stability. Journal of Biological Chemistry, 2003, 278, 34943-34951.	3.4	84
103	Antisense transcripts in the human genome. Trends in Genetics, 2002, 18, 63-65.	6.7	234