

Mark Isalan

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

3,143
citations

159585

30
h-index

168389

53
g-index

83
all docs

83
docs citations

83
times ranked

3274
citing authors

#	ARTICLE	IF	CITATIONS
1	Synthetic spatial patterning in bacteria: advances based on novel diffusible signals. <i>Microbial Biotechnology</i> , 2022, 15, 1685-1694.	4.2	4
2	A genetic toolkit and gene switches to limit <i>Mycoplasma</i> growth for biosafety applications. <i>Nature Communications</i> , 2022, 13, 1910.	12.8	10
3	Structural Abnormalities of the Optic Nerve and Retina in Huntington's Disease Pre-Clinical and Clinical Settings. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5450.	4.1	6
4	Identification of the Transcriptional Biomarkers Panel Linked to Pathological Remodelling of the Eye Tissues in Various HD Mouse Models. <i>Cells</i> , 2022, 11, 1675.	4.1	2
5	DNA Recognition/Processing Zinc Fingers: Structure and Design. , 2021, , 506-516.		1
6	Polyglutamine diseases: looking beyond the neurodegenerative universe. <i>Neural Regeneration Research</i> , 2021, 16, 1186.	3.0	3
7	The Application of CRISPR/Cas Systems for Antiviral Therapy. <i>Frontiers in Genome Editing</i> , 2021, 3, 745559.	5.2	14
8	Kinetin stimulates differentiation of C2C12 myoblasts. <i>PLoS ONE</i> , 2021, 16, e0258419.	2.5	5
9	Gene Therapy Advances: A Meta-Analysis of AAV Usage in Clinical Settings. <i>Frontiers in Medicine</i> , 2021, 8, 809118.	2.6	91
10	Cross-Sectional Transcriptional Analysis of the Aging Murine Heart. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 565530.	3.5	5
11	Prevalence of Non-psychiatric Comorbidities in Pre-symptomatic and Symptomatic Huntington's Disease Gene Carriers in Poland. <i>Frontiers in Medicine</i> , 2020, 7, 79.	2.6	12
12	Dynamical model fitting to a synthetic positive feedback circuit in <i>E. coli</i> . <i>Engineering Biology</i> , 2020, 4, 25-31.	1.8	2
13	Accelerated evolution of a minimal 63 amino acid dual transcription factor. <i>Science Advances</i> , 2020, 6, eaba2728.	10.3	13
14	A Comprehensive Network Atlas Reveals That Turing Patterns Are Common but Not Robust. <i>Cell Systems</i> , 2019, 9, 243-257.e4.	6.2	61
15	Trp-ing upon new repressors. <i>Nature Chemical Biology</i> , 2018, 14, 328-329.	8.0	1
16	Functional Insulator Scanning of CpG Islands to Identify Regulatory Regions of Promoters Using CRISPR. <i>Methods in Molecular Biology</i> , 2018, 1766, 285-301.	0.9	1
17	Combining a Toggle Switch and a Repressilator within the AC-DC Circuit Generates Distinct Dynamical Behaviors. <i>Cell Systems</i> , 2018, 6, 521-530.e3.	6.2	96
18	Engineering of biomolecules by bacteriophage directed evolution. <i>Current Opinion in Biotechnology</i> , 2018, 51, 32-38.	6.6	17

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19	A35â€¦An altered metabolism of nucleotides leads to huntingtonâ€™s disease related cardiomyopathy. , 2018, , ,		0
20	F07â€¦A frequency of concomitant disorders in presymptomatic huntingtonâ€™s disease patients. , 2018, , ,		0
21	Synthetic circuits reveal how mechanisms of gene regulatory networks constrain evolution. <i>Molecular Systems Biology</i> , 2018, 14, e8102.	7.2	34
22	Neuro-Cardio Mechanisms in Huntingtonâ€™s Disease and Other Neurodegenerative Disorders. <i>Frontiers in Physiology</i> , 2018, 9, 559.	2.8	40
23	Commentary: Synthetic Addiction Extends the Productive Life Time of Engineered <i>Escherichia coli</i> Populations. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 77.	4.1	3
24	Drug-Inducible Control of Lethality Genes: A Low Background Destabilizing Domain Architecture Applied to the Gal4-UAS System in <i>Drosophila</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 1496-1506.	3.8	14
25	A three-step framework for programming pattern formation. <i>Current Opinion in Chemical Biology</i> , 2017, 40, 1-7.	6.1	24
26	Intracellular directed evolution of proteins from combinatorial libraries based on conditional phage replication. <i>Nature Protocols</i> , 2017, 12, 1830-1843.	12.0	16
27	Transcriptional Signature of an Altered Purine Metabolism in the Skeletal Muscle of a Huntington's Disease Mouse Model. <i>Frontiers in Physiology</i> , 2017, 8, 127.	2.8	22
28	Early transcriptional alteration of histone deacetylases in a murine model of doxorubicin-induced cardiomyopathy. <i>PLoS ONE</i> , 2017, 12, e0180571.	2.5	18
29	Changes in cardiac nucleotide metabolism in Huntington's disease. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2016, 35, 707-712.	1.1	13
30	Identifying ultrasensitive HGF dose-response functions in a 3D mammalian system for synthetic morphogenesis. <i>Scientific Reports</i> , 2016, 6, 39178.	3.3	7
31	Engineering orthogonal dual transcription factors for multi-input synthetic promoters. <i>Nature Communications</i> , 2016, 7, 13858.	12.8	47
32	Deimmunization for gene therapy: host matching of synthetic zinc finger constructs enables long-term mutant Huntingtin repression in mice. <i>Molecular Neurodegeneration</i> , 2016, 11, 64.	10.8	46
33	An impaired metabolism of nucleotides underpins a novel mechanism of cardiac remodeling leading to Huntington's disease related cardiomyopathy. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 2147-2157.	3.8	42
34	From noise to synthetic nucleoli: can synthetic biology achieve new insights?. <i>Integrative Biology (United Kingdom)</i> , 2016, 8, 383-393.	1.3	4
35	A shared mechanism of muscle wasting in cancer and Huntington's disease. <i>Clinical and Translational Medicine</i> , 2015, 4, 34.	4.0	22
36	The propagation of perturbations in rewired bacterial gene networks. <i>Nature Communications</i> , 2015, 6, 10105.	12.8	19

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37	Senderâ€™receiver systems and applying information theory for quantitative synthetic biology. <i>Current Opinion in Biotechnology</i> , 2015, 31, 101-107.	6.6	26
38	Cooperativity To Increase Turing Pattern Space for Synthetic Biology. <i>ACS Synthetic Biology</i> , 2015, 4, 177-186.	3.8	48
39	A unified design space of synthetic stripe-forming networks. <i>Nature Communications</i> , 2014, 5, 4905.	12.8	128
40	A split intein T7 RNA polymerase for transcriptional AND-logic. <i>Nucleic Acids Research</i> , 2014, 42, 12322-12328.	14.5	50
41	Synthetic biology and therapeutic strategies for the degenerating brain. <i>BioEssays</i> , 2014, 36, 979-990.	2.5	23
42	Genetically Encoded Senderâ€™Receiver System in 3D Mammalian Cell Culture. <i>ACS Synthetic Biology</i> , 2014, 3, 264-272.	3.8	30
43	Î²-Catenin Fluctuates in Mouse ESCs and Is Essential for Nanog-Mediated Reprogramming of Somatic Cells to Pluripotency. <i>Cell Reports</i> , 2014, 8, 1686-1696.	6.4	50
44	Building synthetic gene circuits from combinatorial libraries: screening and selection strategies. <i>Molecular BioSystems</i> , 2013, 9, 1559.	2.9	32
45	Transfecting RNA quadruplexes results in few transcriptome perturbations. <i>RNA Biology</i> , 2013, 10, 205-210.	3.1	4
46	Synthetic zinc finger repressors reduce mutant huntingtin expression in the brain of R6/2 mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3136-45.	7.1	155
47	A cell in a computer. <i>Nature</i> , 2012, 488, 40-41.	27.8	5
48	Zinc-finger nucleases: how to play two good hands. <i>Nature Methods</i> , 2012, 9, 32-34.	19.0	56
49	The PLOS ONE Synthetic Biology Collection: Six Years and Counting. <i>PLoS ONE</i> , 2012, 7, e43231.	2.5	10
50	p53 Gene Repair with Zinc Finger Nucleases Optimised by Yeast 1-Hybrid and Validated by Solexa Sequencing. <i>PLoS ONE</i> , 2011, 6, e20913.	2.5	34
51	A Biobrick Library for Cloning Custom Eukaryotic Plasmids. <i>PLoS ONE</i> , 2011, 6, e23685.	2.5	15
52	Avoiding transcription factor competition at promoter level increases the chances of obtaining oscillation. <i>BMC Systems Biology</i> , 2010, 4, 66.	3.0	10
53	Gene networks and liar paradoxes. <i>BioEssays</i> , 2009, 31, 1110-1115.	2.5	22
54	This title is false. <i>Nature</i> , 2009, 458, 969-969.	27.8	8

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55	Engineering prokaryotic gene circuits. <i>FEMS Microbiology Reviews</i> , 2009, 33, 27-37.	8.6	37
56	Evolvability and hierarchy in rewired bacterial gene networks. <i>Nature</i> , 2008, 452, 840-845.	27.8	285
57	Computer design of obligate heterodimer meganucleases allows efficient cutting of custom DNA sequences. <i>Nucleic Acids Research</i> , 2008, 36, 2163-2173.	14.5	49
58	Construction of semi-randomized gene libraries with weighted oligonucleotide synthesis and PCR. <i>Nature Protocols</i> , 2006, 1, 468-475.	12.0	16
59	Localized transfection with magnetic beads coated with PCR products and other nucleic acids. <i>Nature Protocols</i> , 2006, 1, 526-531.	12.0	10
60	Localized transfection on arrays of magnetic beads coated with PCR products. <i>Nature Methods</i> , 2005, 2, 113-118.	19.0	36
61	Engineering Gene Networks to Emulate <i>Drosophila</i> Embryonic Pattern Formation. <i>PLoS Biology</i> , 2005, 3, e64.	5.6	111
62	Histone Acetyltransferase Activity of p300 Is Required for Transcriptional Repression by the Promyelocytic Leukemia Zinc Finger Protein. <i>Molecular and Cellular Biology</i> , 2005, 25, 5552-5566.	2.3	99
63	Inhibition of Human Telomerase Activity by an Engineered Zinc Finger Protein that Binds G-Quadruplexes. <i>Biochemistry</i> , 2004, 43, 13452-13458.	2.5	43
64	Zinc Fingers. , 2004, , 435-439.		0
65	Zinc-finger protein-targeted gene regulation: Genomewide single-gene specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11997-12002.	7.1	142
66	Repression of the HIV-1 5' LTR promoter and inhibition of HIV-1 replication by using engineered zinc-finger transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1615-1620.	7.1	125
67	Inhibition of herpes simplex virus 1 gene expression by designer zinc-finger transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1621-1626.	7.1	76
68	Selection of Zinc Fingers that Bind Single-Stranded Telomeric DNA in the G-Quadruplex Conformation. <i>Biochemistry</i> , 2001, 40, 830-836.	2.5	63
69	A rapid, generally applicable method to engineer zinc fingers illustrated by targeting the HIV-1 promoter. <i>Nature Biotechnology</i> , 2001, 19, 656-660.	17.5	187
70	Rapid, high-throughput engineering of sequence-specific zinc finger DNA-binding proteins. <i>Methods in Enzymology</i> , 2001, 340, 593-609.	1.0	32
71	Advances in zinc finger engineering. <i>Current Opinion in Structural Biology</i> , 2000, 10, 411-416.	5.7	94
72	Engineered zinc finger proteins that respond to DNA modification by Hae III and Hha I methyltransferase enzymes 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 2000, 295, 471-477.	4.2	14

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73	Comprehensive DNA Recognition through Concerted Interactions from Adjacent Zinc Fingers. <i>Biochemistry</i> , 1998, 37, 12026-12033.	2.5	133
74	Synergy between adjacent zinc fingers in sequence-specific DNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 5617-5621.	7.1	152
75	Reducing metabolic burden in the PACEmid evolver system by remastering high-copy phagemid vectors. <i>Engineering Biology</i> , 0, , .	1.8	1
76	Emergent expression of fitness-conferring genes by phenotypic selection. , 0, , .		5