Vivek K Mutalik

List of Publications by Year
in descending order

38	3,047	304743	414414
papers	citations	22	32
		h-index	g-index

46	46	46	3348
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Phage Foundry Framework to Systematically Develop Viral Countermeasures to Combat Antibiotic-Resistant Bacterial Pathogens. IScience, 2022, 25, 104121.	4.1	12
2	Systematic discovery of pseudomonad genetic factors involved in sensitivity to tailocins. ISME Journal, 2021, 15, 2289-2305.	9.8	27
3	The genetic basis of phage susceptibility, cross-resistance and host-range in Salmonella. Microbiology (United Kingdom), 2021, 167, .	1.8	20
4	High-throughput mapping of the phage resistance landscape in E. coli. PLoS Biology, 2020, 18, e3000877.	5.6	91
5	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
6	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
7	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
8	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
9	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
10	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
11	Dual-barcoded shotgun expression library sequencing for high-throughput characterization of functional traits in bacteria. Nature Communications, 2019, 10, 308.	12.8	33
12	Jungle Express is a versatile repressor system for tight transcriptional control. Nature Communications, 2018, 9, 3617.	12.8	33
13	Rapid and Efficient One-Step Metabolic Pathway Integration in <i>E.Âcoli</i>. ACS Synthetic Biology, 2016, 5, 561-568.	3.8	143
14	Investigation of Proposed Ladderane Biosynthetic Genes from Anammox Bacteria by Heterologous Expression in E. coli. PLoS ONE, 2016, 11, e0151087.	2.5	26
15	Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. ACS Synthetic Biology, 2015, 4, 1244-1253.	3.8	22
16	PR-PR: Cross-Platform Laboratory Automation System. ACS Synthetic Biology, 2014, 3, 515-524.	3.8	41
17	Composability of regulatory sequences controlling transcription and translation in <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14024-14029.	7.1	377
18	Precise and reliable gene expression via standard transcription and translation initiation elements. Nature Methods, 2013, 10, 354-360.	19.0	653

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19	Quantitative estimation of activity and quality for collections of functional genetic elements. Nature Methods, 2013, 10, 347-353.	19.0	183
20	Tuning Promoter Strengths for Improved Synthesis and Function of Electron Conduits in <i>Escherichia coli</i>. ACS Synthetic Biology, 2013, 2, 150-159.	3.8	83
21	Measurement and modeling of intrinsic transcription terminators. Nucleic Acids Research, 2013, 41, 5139-5148.	14.5	155
22	Engineering naturally occurring trans -acting non-coding RNAs to sense molecular signals. Nucleic Acids Research, 2012, 40, 5775-5786.	14.5	87
23	Predicting the strength of UP-elements and full-length E. coli ÏƒE promoters. Nucleic Acids Research, 2012, 40, 2907-2924.	14.5	66
24	An adaptor from translational to transcriptional control enables predictable assembly of complex regulation. Nature Methods, 2012, 9, 1088-1094.	19.0	67
25	Rationally designed families of orthogonal RNA regulators of translation. Nature Chemical Biology, 2012, 8, 447-454.	8.0	157
26	Toward rational design of bacterial genomes. Current Opinion in Microbiology, 2011, 14, 624-630.	5.1	34
27	Versatile RNA-sensing transcriptional regulators for engineering genetic networks. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 8617-8622.	7.1	277
28	Predicting strength and function for promoters of the <i>Escherichia coli</i> alternative sigma factor, <i>Ïƒ</i> ^E. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2854-2859.	7.1	99
29	Promoter Strength Properties of the Complete Sigma E Regulon of <i>Escherichia coli</i> and <i>Salmonella enterica</i>. Journal of Bacteriology, 2009, 191, 7279-7287.	2.2	64
30	A theoretical steady state analysis indicates that induction of Escherichia coli glnALG operon can display all-or-none behavior. BioSystems, 2007, 90, 1-19.	2.0	7
31	Effect of the MAPK cascade structure, nuclear translocation and regulation of transcription factors on gene expression. BioSystems, 2006, 85, 144-157.	2.0	8
32	Insights into transcriptional regulation and Â competition from an equilibrium model of RNA polymerase binding to DNA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5332-5337.	7.1	159
33	Quantification of the glycogen cascade system: the ultrasensitive responses of liver glycogen synthase and muscle phosphorylase are due to distinctive regulatory designs. Theoretical Biology and Medical Modelling, 2005, 2, 19.	2.1	13
34	Corrigendum to: Robust global sensitivity in multiple enzyme cascade system explains how the downstream cascade structure may remain unaffected by cross-talk (FEBS 28047) [FEBS Letters 558 (2004) 79-84]. FEBS Letters, 2005, 579, 292-293.	2.8	0
35	Equilibrium Analysis of Allosteric Interactions Shows Zero-Order Effects. Cell Biochemistry and Biophysics, 2004, 41, 179-192.	1.8	1
36	A steady state analysis indicates that negative feedback regulation of PTP1B by Akt elicits bistability in insulin-stimulated GLUT4 translocation. Theoretical Biology and Medical Modelling, 2004, 1, 2.	2.1	34

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37	Robust global sensitivity in multiple enzyme cascade system explains how the downstream cascade structure may remain unaffected by cross-talk. FEBS Letters, 2004, 558, 79-84.	2.8	15
38	Allosteric Interactions and Bifunctionality Make the Response of Glutamine Synthetase Cascade System of Escherichia coli Robust and Ultrasensitive. Journal of Biological Chemistry, 2003, 278, 26327-26332.	3.4	29