

Ryan T Gill

List of Publications by Year in descending order

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71
papers

2,819
citations

172457

29
h-index

197818

49
g-index

74
all docs

74
docs citations

74
times ranked

3310
citing authors

#	ARTICLE	IF	CITATIONS
1	Directed Evolution of CRISPR/Cas Systems for Precise Gene Editing. Trends in Biotechnology, 2021, 39, 262-273.	9.3	32
2	Transcriptional Regulatory Networks Involved in C3â€C4 Alcohol Stress Response and Tolerance in Yeast. ACS Synthetic Biology, 2021, 10, 19-28.	3.8	7
3	Genome engineering of E.Âcoli for improved styrene production. Metabolic Engineering, 2020, 57, 74-84.	7.0	34
4	Engineering regulatory networks for complex phenotypes in E. coli. Nature Communications, 2020, 11, 4050.	12.8	21
5	Multiplex Evolution of Antibody Fragments Utilizing a Yeast Surface Display Platform. ACS Synthetic Biology, 2020, 9, 2197-2202.	3.8	7
6	Integrating CRISPR-Enabled Trackable Genome Engineering and Transcriptomic Analysis of Global Regulators for Antibiotic Resistance Selection and Identification in Escherichia coli. MSystems, 2020, 5, .	3.8	8
7	Determinants for Efficient Editing with Cas9-Mediated Recombineering in <i>Escherichia coli</i>. ACS Synthetic Biology, 2020, 9, 1083-1099.	3.8	15
8	<sc>CRISPR</sc> /Cas9 recombineeringâ€mediated deep mutational scanning of essential genes in <i>Escherichia coli</i>. Molecular Systems Biology, 2020, 16, e9265.	7.2	28
9	Multiplex navigation of global regulatory networks (MINR) in yeast for improved ethanol tolerance and production. Metabolic Engineering, 2019, 51, 50-58.	7.0	30
10	Engineered Ureolytic Microorganisms Can Tailor the Morphology and Nanomechanical Properties of Microbial-Precipitated Calcium Carbonate. Scientific Reports, 2019, 9, 14721.	3.3	51
11	A new recombineering system for precise genome-editing in Shewanella oneidensis strain MR-1 using single-stranded oligonucleotides. Scientific Reports, 2019, 9, 39.	3.3	48
12	A versatile platform strain for high-fidelity multiplex genome editing. Nucleic Acids Research, 2019, 47, 3244-3256.	14.5	16
13	Iterative genome editing of Escherichia coli for 3-hydroxypropionic acid production. Metabolic Engineering, 2018, 47, 303-313.	7.0	34
14	Directed combinatorial mutagenesis of Escherichia coli for complex phenotype engineering. Metabolic Engineering, 2018, 47, 10-20.	7.0	32
15	Combinatorial pathway engineering using type Iâ€ CRISPR interference. Biotechnology and Bioengineering, 2018, 115, 1878-1883.	3.3	23
16	Genomic Deoxyxylulose Phosphate Reductoisomerase (DXR) Mutations Conferring Resistance to the Antimalarial Drug Fosmidomycin in <i>E.Âcoli</i>. ACS Synthetic Biology, 2018, 7, 2824-2832.	3.8	11
17	Deep scanning lysine metabolism in <i>Escherichia coli</i>. Molecular Systems Biology, 2018, 14, e8371.	7.2	34
18	Rational Control of Calcium Carbonate Precipitation by Engineered <i>Escherichia coli</i>. ACS Synthetic Biology, 2018, 7, 2497-2506.	3.8	22

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19	Dynamic Management of Codon Compression for Saturation Mutagenesis. <i>Methods in Molecular Biology</i> , 2018, 1772, 171-189.	0.9	3
20	Building a genome engineering toolbox in nonmodel prokaryotic microbes. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2120-2138.	3.3	23
21	CRISPR-Enabled Tools for Engineering Microbial Genomes and Phenotypes. <i>Biotechnology Journal</i> , 2018, 13, e1700586.	3.5	30
22	CRISPR Enabled Trackable genome Engineering for isopropanol production in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2017, 41, 1-10.	7.0	82
23	Genome-wide mapping of mutations at single-nucleotide resolution for protein, metabolic and genome engineering. <i>Nature Biotechnology</i> , 2017, 35, 48-55.	17.5	298
24	The Tolerome: A Database of Transcriptome-Level Contributions to Diverse <i>Escherichia coli</i> Resistance and Tolerance Phenotypes. <i>ACS Synthetic Biology</i> , 2017, 6, 2302-2315.	3.8	11
25	ROS mediated selection for increased NADPH availability in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2017, 114, 2685-2689.	3.3	12
26	Renewable acrylonitrile production. <i>Science</i> , 2017, 358, 1307-1310.	12.6	122
27	Refactoring the Genetic Code for Increased Evolvability. <i>MBio</i> , 2017, 8, .	4.1	17
28	Multiplex growth rate phenotyping of synthetic mutants in selection to engineer glucose and xylose co-utilization in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2017, 114, 885-893.	3.3	4
29	Parallel Mapping of Antibiotic Resistance Alleles in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2016, 11, e0146916.	2.5	15
30	Directed evolution and synthetic biology applications to microbial systems. <i>Current Opinion in Biotechnology</i> , 2016, 39, 126-133.	6.6	56
31	A Web Interface for Codon Compression. <i>ACS Synthetic Biology</i> , 2016, 5, 1021-1023.	3.8	7
32	Rapid and Efficient One-Step Metabolic Pathway Integration in <i>E. coli</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 561-568.	3.8	143
33	The Resistome: A Comprehensive Database of <i>Escherichia coli</i> Resistance Phenotypes. <i>ACS Synthetic Biology</i> , 2016, 5, 1566-1577.	3.8	17
34	Quantifying complexity in metabolic engineering using the LASER database. <i>Metabolic Engineering Communications</i> , 2016, 3, 227-233.	3.6	7
35	Overcoming substrate limitations for improved production of ethylene in <i>E. coli</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 3.	6.2	27
36	Synthesis aided design: The biological design-build-test engineering paradigm?. <i>Biotechnology and Bioengineering</i> , 2016, 113, 7-10.	3.3	9

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37	The LASER database: Formalizing design rules for metabolic engineering. <i>Metabolic Engineering Communications</i> , 2015, 2, 30-38.	3.6	43
38	Quantifying Impact of Chromosome Copy Number on Recombination in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2015, 4, 776-780.	3.8	10
39	Multiplexed tracking of combinatorial genomic mutations in engineered cell populations. <i>Nature Biotechnology</i> , 2015, 33, 631-637.	17.5	49
40	Bacterial Recombineering: Genome Engineering via Phage-Based Homologous Recombination. <i>ACS Synthetic Biology</i> , 2015, 4, 1176-1185.	3.8	89
41	Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. <i>ACS Synthetic Biology</i> , 2015, 4, 1244-1253.	3.8	22
42	Genome scale engineering techniques for metabolic engineering. <i>Metabolic Engineering</i> , 2015, 32, 143-154.	7.0	48
43	The emergence of commodity-scale genetic manipulation. <i>Current Opinion in Chemical Biology</i> , 2015, 28, 150-155.	6.1	4
44	Complex systems in metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2015, 36, 107-114.	6.6	10
45	Comparison of genome-wide selection strategies to identify furfural tolerance genes in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2015, 112, 129-140.	3.3	30
46	Codon Compression Algorithms for Saturation Mutagenesis. <i>ACS Synthetic Biology</i> , 2015, 4, 604-614.	3.8	45
47	Genome-Wide Mapping of Furfural Tolerance Genes in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e87540.	2.5	30
48	Implications of variable fluid resistance caused by start-up flow in microfluidic networks. <i>Microfluidics and Nanofluidics</i> , 2014, 16, 473-482.	2.2	4
49	CONSTRUCTOR: Constraint Modification Provides Insight into Design of Biochemical Networks. <i>PLoS ONE</i> , 2014, 9, e113820.	2.5	9
50	Recombineering to homogeneity: extension of multiplex recombineering to large-scale genome editing. <i>Biotechnology Journal</i> , 2013, 8, 515-522.	3.5	24
51	Towards a metabolic engineering strain "commons": An <i>Escherichia coli</i> platform strain for ethanol production. <i>Biotechnology and Bioengineering</i> , 2013, 110, 1520-1526.	3.3	24
52	Genome-Wide Identification of Genes Conferring Energy Related Resistance to a Synthetic Antimicrobial Peptide (Bac8c). <i>PLoS ONE</i> , 2013, 8, e55052.	2.5	15
53	Strategies for the multiplex mapping of genes to traits. <i>Microbial Cell Factories</i> , 2013, 12, 99.	4.0	4
54	Strategy for directing combinatorial genome engineering in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10540-10545.	7.1	87

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55	Tools for genome-wide strain design and construction. <i>Current Opinion in Biotechnology</i> , 2012, 23, 666-671.	6.6	17
56	Synthetic biology: New strategies for directing design. <i>Metabolic Engineering</i> , 2012, 14, 205-211.	7.0	34
57	Engineering genomes in multiplex. <i>Current Opinion in Biotechnology</i> , 2011, 22, 576-583.	6.6	28
58	Application and engineering of fatty acid biosynthesis in <i>Escherichia coli</i> for advanced fuels and chemicals. <i>Metabolic Engineering</i> , 2011, 13, 28-37.	7.0	134
59	Elucidating acetate tolerance in <i>E. coli</i> using a genome-wide approach. <i>Metabolic Engineering</i> , 2011, 13, 214-224.	7.0	60
60	Identification and characterization of a bacterial cytochrome P450 for the metabolism of diclofenac. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 625-633.	3.6	32
61	Broad host range vectors for protein expression across gram negative hosts. <i>Biotechnology and Bioengineering</i> , 2010, 106, 326-332.	3.3	30
62	Genome-Scale Identification Method Applied to Find Cryptic Aminoglycoside Resistance Genes in <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2009, 4, e6576.	2.5	15
63	Cellulosic hydrolysate toxicity and tolerance mechanisms in <i>Escherichia coli</i> . <i>Biotechnology for Biofuels</i> , 2009, 2, 26.	6.2	283
64	Genes restoring redox balance in fermentation-deficient <i>E. coli</i> NZN111. <i>Metabolic Engineering</i> , 2009, 11, 347-354.	7.0	79
65	Genomics enabled approaches in strain engineering. <i>Current Opinion in Microbiology</i> , 2009, 12, 223-230.	5.1	45
66	Genome-scale analysis of anti-metabolite directed strain engineering. <i>Metabolic Engineering</i> , 2008, 10, 109-120.	7.0	22
67	A comparative study of metabolic engineering anti-metabolite tolerance in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2006, 8, 227-239.	7.0	12
68	Broad host range vectors for stable genomic library construction. <i>Biotechnology and Bioengineering</i> , 2006, 94, 151-158.	3.3	46
69	Amino acid content of recombinant proteins influences the metabolic burden response. <i>Biotechnology and Bioengineering</i> , 2005, 90, 116-126.	3.3	54
70	Mapping phenotypic landscapes using DNA micro-arrays. <i>Metabolic Engineering</i> , 2004, 6, 177-185.	7.0	11
71	Enabling inverse metabolic engineering through genomics. <i>Current Opinion in Biotechnology</i> , 2003, 14, 484-490.	6.6	27