

# Ryan T Gill

## List of Publications by Year in descending order

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71  
papers

2,819  
citations

172207

29  
h-index

197535

49  
g-index

74  
all docs

74  
docs citations

74  
times ranked

3310  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide mapping of mutations at single-nucleotide resolution for protein, metabolic and genome engineering. <i>Nature Biotechnology</i> , 2017, 35, 48-55.	9.4	298
2	Cellulosic hydrolysate toxicity and tolerance mechanisms in <i>Escherichia coli</i> . <i>Biotechnology for Biofuels</i> , 2009, 2, 26.	6.2	283
3	Rapid and Efficient One-Step Metabolic Pathway Integration in <i>E. coli</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 561-568.	1.9	143
4	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.	3.6	134
5	Renewable acrylonitrile production. <i>Science</i> , 2017, 358, 1307-1310.	6.0	122
6	Bacterial Recombineering: Genome Engineering via Phage-Based Homologous Recombination. <i>ACS Synthetic Biology</i> , 2015, 4, 1176-1185.	1.9	89
7	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.	3.3	87
8	CRISPR Enabled Trackable genome Engineering for isopropanol production in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2017, 41, 1-10.	3.6	82
9	Genes restoring redox balance in fermentation-deficient <i>E. coli</i> NZN111. <i>Metabolic Engineering</i> , 2009, 11, 347-354.	3.6	79
10	Elucidating acetate tolerance in <i>E. coli</i> using a genome-wide approach. <i>Metabolic Engineering</i> , 2011, 13, 214-224.	3.6	60
11	Directed evolution and synthetic biology applications to microbial systems. <i>Current Opinion in Biotechnology</i> , 2016, 39, 126-133.	3.3	56
12	Amino acid content of recombinant proteins influences the metabolic burden response. <i>Biotechnology and Bioengineering</i> , 2005, 90, 116-126.	1.7	54
13	Engineered Ureolytic Microorganisms Can Tailor the Morphology and Nanomechanical Properties of Microbial-Precipitated Calcium Carbonate. <i>Scientific Reports</i> , 2019, 9, 14721.	1.6	51
14	Multiplexed tracking of combinatorial genomic mutations in engineered cell populations. <i>Nature Biotechnology</i> , 2015, 33, 631-637.	9.4	49
15	Genome scale engineering techniques for metabolic engineering. <i>Metabolic Engineering</i> , 2015, 32, 143-154.	3.6	48
16	A new recombineering system for precise genome-editing in <i>Shewanella oneidensis</i> strain MR-1 using single-stranded oligonucleotides. <i>Scientific Reports</i> , 2019, 9, 39.	1.6	48
17	Broad host range vectors for stable genomic library construction. <i>Biotechnology and Bioengineering</i> , 2006, 94, 151-158.	1.7	46
18	Genomics enabled approaches in strain engineering. <i>Current Opinion in Microbiology</i> , 2009, 12, 223-230.	2.3	45

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19	Codon Compression Algorithms for Saturation Mutagenesis. <i>ACS Synthetic Biology</i> , 2015, 4, 604-614.	1.9	45
20	The LASER database: Formalizing design rules for metabolic engineering. <i>Metabolic Engineering Communications</i> , 2015, 2, 30-38.	1.9	43
21	Synthetic biology: New strategies for directing design. <i>Metabolic Engineering</i> , 2012, 14, 205-211.	3.6	34
22	Iterative genome editing of <i>Escherichia coli</i> for 3-hydroxypropionic acid production. <i>Metabolic Engineering</i> , 2018, 47, 303-313.	3.6	34
23	Deep scanning lysine metabolism in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2018, 14, e8371.	3.2	34
24	Genome engineering of <i>E. coli</i> for improved styrene production. <i>Metabolic Engineering</i> , 2020, 57, 74-84.	3.6	34
25	Identification and characterization of a bacterial cytochrome P450 for the metabolism of diclofenac. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 625-633.	1.7	32
26	Directed combinatorial mutagenesis of <i>Escherichia coli</i> for complex phenotype engineering. <i>Metabolic Engineering</i> , 2018, 47, 10-20.	3.6	32
27	Directed Evolution of CRISPR/Cas Systems for Precise Gene Editing. <i>Trends in Biotechnology</i> , 2021, 39, 262-273.	4.9	32
28	Broad-host-range vectors for protein expression across gram negative hosts. <i>Biotechnology and Bioengineering</i> , 2010, 106, 326-332.	1.7	30
29	Genome-Wide Mapping of Furfural Tolerance Genes in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e87540.	1.1	30
30	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.	1.7	30
31	CRISPR-Enabled Tools for Engineering Microbial Genomes and Phenotypes. <i>Biotechnology Journal</i> , 2018, 13, e1700586.	1.8	30
32	Multiplex navigation of global regulatory networks (MINR) in yeast for improved ethanol tolerance and production. <i>Metabolic Engineering</i> , 2019, 51, 50-58.	3.6	30
33	Engineering genomes in multiplex. <i>Current Opinion in Biotechnology</i> , 2011, 22, 576-583.	3.3	28
34	CRISPR/Cas9 recombineering-mediated deep mutational scanning of essential genes in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2020, 16, e9265.	3.2	28
35	Enabling inverse metabolic engineering through genomics. <i>Current Opinion in Biotechnology</i> , 2003, 14, 484-490.	3.3	27
36	Overcoming substrate limitations for improved production of ethylene in <i>E. coli</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 3.	6.2	27

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37	Recombineering to homogeneity: extension of multiplex recombineering to large-scale genome editing. <i>Biotechnology Journal</i> , 2013, 8, 515-522.	1.8	24
38	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.	1.7	24
39	Combinatorial pathway engineering using type II CRISPR interference. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1878-1883.	1.7	23
40	Building a genome engineering toolbox in nonmodel prokaryotic microbes. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2120-2138.	1.7	23
41	Genome-scale analysis of anti-metabolite directed strain engineering. <i>Metabolic Engineering</i> , 2008, 10, 109-120.	3.6	22
42	Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. <i>ACS Synthetic Biology</i> , 2015, 4, 1244-1253.	1.9	22
43	Rational Control of Calcium Carbonate Precipitation by Engineered <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 2497-2506.	1.9	22
44	Engineering regulatory networks for complex phenotypes in <i>E. coli</i> . <i>Nature Communications</i> , 2020, 11, 4050.	5.8	21
45	Tools for genome-wide strain design and construction. <i>Current Opinion in Biotechnology</i> , 2012, 23, 666-671.	3.3	17
46	The Resistome: A Comprehensive Database of <i>Escherichia coli</i> Resistance Phenotypes. <i>ACS Synthetic Biology</i> , 2016, 5, 1566-1577.	1.9	17
47	Refactoring the Genetic Code for Increased Evolvability. <i>MBio</i> , 2017, 8, .	1.8	17
48	A versatile platform strain for high-fidelity multiplex genome editing. <i>Nucleic Acids Research</i> , 2019, 47, 3244-3256.	6.5	16
49	Genome-Scale Identification Method Applied to Find Cryptic Aminoglycoside Resistance Genes in <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2009, 4, e6576.	1.1	15
50	Genome-Wide Identification of Genes Conferring Energy Related Resistance to a Synthetic Antimicrobial Peptide (Bac8c). <i>PLoS ONE</i> , 2013, 8, e55052.	1.1	15
51	Parallel Mapping of Antibiotic Resistance Alleles in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2016, 11, e0146916.	1.1	15
52	Determinants for Efficient Editing with Cas9-Mediated Recombineering in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2020, 9, 1083-1099.	1.9	15
53	A comparative study of metabolic engineering anti-metabolite tolerance in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2006, 8, 227-239.	3.6	12
54	ROS mediated selection for increased NADPH availability in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2017, 114, 2685-2689.	1.7	12

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55	Mapping phenotypic landscapes using DNA micro-arrays. <i>Metabolic Engineering</i> , 2004, 6, 177-185.	3.6	11
56	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.	1.9	11
57	Genomic Deoxyxylulose Phosphate Reductoisomerase (DXR) Mutations Conferring Resistance to the Antimalarial Drug Fosmidomycin in <i>E. coli</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 2824-2832.	1.9	11
58	Quantifying Impact of Chromosome Copy Number on Recombination in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2015, 4, 776-780.	1.9	10
59	Complex systems in metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2015, 36, 107-114.	3.3	10
60	Synthesis aided design: The biological design-build-test engineering paradigm?. <i>Biotechnology and Bioengineering</i> , 2016, 113, 7-10.	1.7	9
61	CONSTRUCTOR: Constraint Modification Provides Insight into Design of Biochemical Networks. <i>PLoS ONE</i> , 2014, 9, e113820.	1.1	9
62	Integrating CRISPR-Enabled Trackable Genome Engineering and Transcriptomic Analysis of Global Regulators for Antibiotic Resistance Selection and Identification in <i>Escherichia coli</i> . <i>MSystems</i> , 2020, 5, .	1.7	8
63	A Web Interface for Codon Compression. <i>ACS Synthetic Biology</i> , 2016, 5, 1021-1023.	1.9	7
64	Quantifying complexity in metabolic engineering using the LASER database. <i>Metabolic Engineering Communications</i> , 2016, 3, 227-233.	1.9	7
65	Multiplex Evolution of Antibody Fragments Utilizing a Yeast Surface Display Platform. <i>ACS Synthetic Biology</i> , 2020, 9, 2197-2202.	1.9	7
66	Transcriptional Regulatory Networks Involved in C3-C4 Alcohol Stress Response and Tolerance in Yeast. <i>ACS Synthetic Biology</i> , 2021, 10, 19-28.	1.9	7
67	Strategies for the multiplex mapping of genes to traits. <i>Microbial Cell Factories</i> , 2013, 12, 99.	1.9	4
68	Implications of variable fluid resistance caused by start-up flow in microfluidic networks. <i>Microfluidics and Nanofluidics</i> , 2014, 16, 473-482.	1.0	4
69	The emergence of commodity-scale genetic manipulation. <i>Current Opinion in Chemical Biology</i> , 2015, 28, 150-155.	2.8	4
70	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.	1.7	4
71	Dynamic Management of Codon Compression for Saturation Mutagenesis. <i>Methods in Molecular Biology</i> , 2018, 1772, 171-189.	0.4	3