

# Ryan T Gill

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | 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       |
| 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.   | 3.8  | 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.                                   | 7.0  | 134       |
| 5  | Renewable acrylonitrile production. <i>Science</i> , 2017, 358, 1307-1310.  | 12.6 | 122       |
| 6  | Bacterial Recombineering: Genome Engineering via Phage-Based Homologous Recombination. <i>ACS Synthetic Biology</i> , 2015, 4, 1176-1185.   | 3.8  | 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. | 7.1  | 87        |
| 8  | CRISPR Enabled Trackable genome Engineering for isopropanol production in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2017, 41, 1-10.  | 7.0  | 82        |
| 9  | Genes restoring redox balance in fermentation-deficient <i>E. coli</i> NZN111. <i>Metabolic Engineering</i> , 2009, 11, 347-354.  | 7.0  | 79        |
| 10 | Elucidating acetate tolerance in <i>E. coli</i> using a genome-wide approach. <i>Metabolic Engineering</i> , 2011, 13, 214-224.   | 7.0  | 60        |
| 11 | Directed evolution and synthetic biology applications to microbial systems. <i>Current Opinion in Biotechnology</i> , 2016, 39, 126-133.  | 6.6  | 56        |
| 12 | Amino acid content of recombinant proteins influences the metabolic burden response. <i>Biotechnology and Bioengineering</i> , 2005, 90, 116-126.   | 3.3  | 54        |
| 13 | Engineered Ureolytic Microorganisms Can Tailor the Morphology and Nanomechanical Properties of Microbial-Precipitated Calcium Carbonate. <i>Scientific Reports</i> , 2019, 9, 14721.                  | 3.3  | 51        |
| 14 | Multiplexed tracking of combinatorial genomic mutations in engineered cell populations. <i>Nature Biotechnology</i> , 2015, 33, 631-637.  | 17.5 | 49        |
| 15 | Genome scale engineering techniques for metabolic engineering. <i>Metabolic Engineering</i> , 2015, 32, 143-154.  | 7.0  | 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.                   | 3.3  | 48        |
| 17 | Broad host range vectors for stable genomic library construction. <i>Biotechnology and Bioengineering</i> , 2006, 94, 151-158.  | 3.3  | 46        |
| 18 | Genomics enabled approaches in strain engineering. <i>Current Opinion in Microbiology</i> , 2009, 12, 223-230.  | 5.1  | 45        |

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|----|--|-----|-----------|
| 19 | Codon Compression Algorithms for Saturation Mutagenesis. <i>ACS Synthetic Biology</i> , 2015, 4, 604-614.  | 3.8 | 45        |
| 20 | The LASER database: Formalizing design rules for metabolic engineering. <i>Metabolic Engineering Communications</i> , 2015, 2, 30-38.  | 3.6 | 43        |
| 21 | Synthetic biology: New strategies for directing design. <i>Metabolic Engineering</i> , 2012, 14, 205-211.  | 7.0 | 34        |
| 22 | Iterative genome editing of <i>Escherichia coli</i> for 3-hydroxypropionic acid production. <i>Metabolic Engineering</i> , 2018, 47, 303-313.                                  | 7.0 | 34        |
| 23 | Deep scanning lysine metabolism in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2018, 14, e8371.   | 7.2 | 34        |
| 24 | Genome engineering of <i>E. coli</i> for improved styrene production. <i>Metabolic Engineering</i> , 2020, 57, 74-84.  | 7.0 | 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.        | 3.6 | 32        |
| 26 | Directed combinatorial mutagenesis of <i>Escherichia coli</i> for complex phenotype engineering. <i>Metabolic Engineering</i> , 2018, 47, 10-20.                               | 7.0 | 32        |
| 27 | Directed Evolution of CRISPR/Cas Systems for Precise Gene Editing. <i>Trends in Biotechnology</i> , 2021, 39, 262-273.   | 9.3 | 32        |
| 28 | Broad-host-range vectors for protein expression across gram negative hosts. <i>Biotechnology and Bioengineering</i> , 2010, 106, 326-332.                                      | 3.3 | 30        |
| 29 | Genome-Wide Mapping of Furfural Tolerance Genes in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e87540.  | 2.5 | 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. | 3.3 | 30        |
| 31 | CRISPR-Enabled Tools for Engineering Microbial Genomes and Phenotypes. <i>Biotechnology Journal</i> , 2018, 13, e1700586.  | 3.5 | 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.              | 7.0 | 30        |
| 33 | Engineering genomes in multiplex. <i>Current Opinion in Biotechnology</i> , 2011, 22, 576-583.   | 6.6 | 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.               | 7.2 | 28        |
| 35 | Enabling inverse metabolic engineering through genomics. <i>Current Opinion in Biotechnology</i> , 2003, 14, 484-490.  | 6.6 | 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.                                 | 3.5  | 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. | 3.3  | 24        |
| 39 | Combinatorial pathway engineering using type I CRISPR interference. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1878-1883.  | 3.3  | 23        |
| 40 | Building a genome engineering toolbox in nonmodel prokaryotic microbes. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2120-2138.  | 3.3  | 23        |
| 41 | Genome-scale analysis of anti-metabolite directed strain engineering. <i>Metabolic Engineering</i> , 2008, 10, 109-120.  | 7.0  | 22        |
| 42 | Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. <i>ACS Synthetic Biology</i> , 2015, 4, 1244-1253.   | 3.8  | 22        |
| 43 | Rational Control of Calcium Carbonate Precipitation by Engineered <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 2497-2506.                                       | 3.8  | 22        |
| 44 | Engineering regulatory networks for complex phenotypes in <i>E. coli</i> . <i>Nature Communications</i> , 2020, 11, 4050.  | 12.8 | 21        |
| 45 | Tools for genome-wide strain design and construction. <i>Current Opinion in Biotechnology</i> , 2012, 23, 666-671.   | 6.6  | 17        |
| 46 | The Resistome: A Comprehensive Database of <i>Escherichia coli</i> Resistance Phenotypes. <i>ACS Synthetic Biology</i> , 2016, 5, 1566-1577.   | 3.8  | 17        |
| 47 | Refactoring the Genetic Code for Increased Evolvability. <i>MBio</i> , 2017, 8, .  | 4.1  | 17        |
| 48 | A versatile platform strain for high-fidelity multiplex genome editing. <i>Nucleic Acids Research</i> , 2019, 47, 3244-3256.   | 14.5 | 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.                      | 2.5  | 15        |
| 50 | 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        |
| 51 | Parallel Mapping of Antibiotic Resistance Alleles in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2016, 11, e0146916.   | 2.5  | 15        |
| 52 | Determinants for Efficient Editing with Cas9-Mediated Recombineering in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2020, 9, 1083-1099.                                 | 3.8  | 15        |
| 53 | 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        |
| 54 | ROS mediated selection for increased NADPH availability in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2017, 114, 2685-2689.                                 | 3.3  | 12        |

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|----|---|-----|-----------|
| 55 | Mapping phenotypic landscapes using DNA micro-arrays. <i>Metabolic Engineering</i> , 2004, 6, 177-185.  | 7.0 | 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.                                  | 3.8 | 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.                       | 3.8 | 11        |
| 58 | 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        |
| 59 | Complex systems in metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2015, 36, 107-114.  | 6.6 | 10        |
| 60 | Synthesis aided design: The biological design-build-test engineering paradigm?. <i>Biotechnology and Bioengineering</i> , 2016, 113, 7-10.  | 3.3 | 9         |
| 61 | CONSTRUCTOR: Constraint Modification Provides Insight into Design of Biochemical Networks. <i>PLoS ONE</i> , 2014, 9, e113820.  | 2.5 | 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, . | 3.8 | 8         |
| 63 | A Web Interface for Codon Compression. <i>ACS Synthetic Biology</i> , 2016, 5, 1021-1023.   | 3.8 | 7         |
| 64 | Quantifying complexity in metabolic engineering using the LASER database. <i>Metabolic Engineering Communications</i> , 2016, 3, 227-233.   | 3.6 | 7         |
| 65 | Multiplex Evolution of Antibody Fragments Utilizing a Yeast Surface Display Platform. <i>ACS Synthetic Biology</i> , 2020, 9, 2197-2202.  | 3.8 | 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.   | 3.8 | 7         |
| 67 | Strategies for the multiplex mapping of genes to traits. <i>Microbial Cell Factories</i> , 2013, 12, 99.  | 4.0 | 4         |
| 68 | 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         |
| 69 | The emergence of commodity-scale genetic manipulation. <i>Current Opinion in Chemical Biology</i> , 2015, 28, 150-155.  | 6.1 | 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.              | 3.3 | 4         |
| 71 | Dynamic Management of Codon Compression for Saturation Mutagenesis. <i>Methods in Molecular Biology</i> , 2018, 1772, 171-189.  | 0.9 | 3         |