

Keith E J Tyo

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

4,344
citations

218677

26
h-index

133252

59
g-index

68
all docs

68
docs citations

68
times ranked

5190
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1 | Chemical-damage MINE: A database of curated and predicted spontaneous metabolic reactions. <i>Metabolic Engineering</i> , 2022, 69, 302-312. | 7.0 | 5 |
| 2 | MINE 2.0: enhanced biochemical coverage for peak identification in untargeted metabolomics. <i>Bioinformatics</i> , 2022, 38, 3484-3487. | 4.1 | 6 |
| 3 | Dynamic Control of Gene Expression with Riboregulated Switchable Feedback Promoters. <i>ACS Synthetic Biology</i> , 2021, 10, 1199-1213. | 3.8 | 19 |
| 4 | Curating a comprehensive set of enzymatic reaction rules for efficient novel biosynthetic pathway design. <i>Metabolic Engineering</i> , 2021, 65, 79-87. | 7.0 | 12 |
| 5 | Recording Temporal Signals with Minutes Resolution Using Enzymatic DNA Synthesis. <i>Journal of the American Chemical Society</i> , 2021, 143, 16630-16640. | 13.7 | 12 |
| 6 | Engineering <i>Acinetobacter baylyi</i> ADP1 for mevalonate production from lignin-derived aromatic compounds. <i>Metabolic Engineering Communications</i> , 2021, 13, e00173. | 3.6 | 14 |
| 7 | Enabling commercial success of industrial biotechnology. <i>Science</i> , 2021, 374, 1563-1565. | 12.6 | 10 |
| 8 | Development of a genetic toolset for the highly engineerable and metabolically versatile <i>Acinetobacter baylyi</i> ADP1. <i>Nucleic Acids Research</i> , 2020, 48, 5169-5182. | 14.5 | 30 |
| 9 | Bayesian inference of metabolic kinetics from genome-scale multiomics data. <i>PLoS Computational Biology</i> , 2019, 15, e1007424. | 3.2 | 29 |
| 10 | Model-guided mechanism discovery and parameter selection for directed evolution. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 9697-9709. | 3.6 | 2 |
| 11 | Kinetic ensemble model of gas fermenting <i>Clostridium autoethanogenum</i> for improved ethanol production. <i>Biochemical Engineering Journal</i> , 2019, 148, 46-56. | 3.6 | 27 |
| 12 | Metabolic kinetic modeling provides insight into complex biological questions, but hurdles remain. <i>Current Opinion in Biotechnology</i> , 2019, 59, 24-30. | 6.6 | 42 |
| 13 | Metabolic In Silico Network Expansions to Predict and Exploit Enzyme Promiscuity. <i>Methods in Molecular Biology</i> , 2019, 1927, 11-21. | 0.9 | 5 |
| 14 | Chemically Inducible Chromosomal Evolution (CiChE) for Multicopy Metabolic Pathway Engineering. <i>Methods in Molecular Biology</i> , 2019, 1927, 37-45. | 0.9 | 2 |
| 15 | Detection of a Peptide Biomarker by Engineered Yeast Receptors. <i>ACS Synthetic Biology</i> , 2018, 7, 696-705. | 3.8 | 20 |
| 16 | Development of novel metabolite-responsive transcription factors via transposon-mediated protein fusion. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 55-63. | 2.1 | 13 |
| 17 | High-resolution mapping of DNA polymerase fidelity using nucleotide imbalances and next-generation sequencing. <i>Nucleic Acids Research</i> , 2018, 46, e78-e78. | 14.5 | 19 |
| 18 | CellSort: a support vector machine tool for optimizing fluorescence-activated cell sorting and reducing experimental effort. <i>Bioinformatics</i> , 2017, 33, 909-916. | 4.1 | 9 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | A Glucose-Sensing Toggle Switch for Autonomous, High Productivity Genetic Control. ACS Synthetic Biology, 2017, 6, 1296-1304. | 3.8 | 67 |
| 20 | Modulating and evaluating receptor promiscuity through directed evolution and modeling. Protein Engineering, Design and Selection, 2017, 30, 455-465. | 2.1 | 6 |
| 21 | Generation and Validation of the iKp1289 Metabolic Model for Klebsiella pneumoniae KPPR1. Journal of Infectious Diseases, 2017, 215, S37-S43. | 4.0 | 23 |
| 22 | Predicting novel substrates for enzymes with minimal experimental effort with active learning. Metabolic Engineering, 2017, 44, 171-181. | 7.0 | 31 |
| 23 | Acceleration Strategies to Enhance Metabolic Ensemble Modeling Performance. Biophysical Journal, 2017, 113, 1150-1162. | 0.5 | 24 |
| 24 | Increased Processivity, Misincorporation, and Nucleotide Incorporation Efficiency in Sulfolobus solfataricus Dpo4 Thumb Domain Mutants. Applied and Environmental Microbiology, 2017, 83, . | 3.1 | 4 |
| 25 | DNA binding strength increases the processivity and activity of a Y-Family DNA polymerase. Scientific Reports, 2017, 7, 4756. | 3.3 | 13 |
| 26 | Nucleotide-time alignment for molecular recorders. PLoS Computational Biology, 2017, 13, e1005483. | 3.2 | 0 |
| 27 | N-Terminal-Based Targeted, Inducible Protein Degradation in Escherichia coli. PLoS ONE, 2016, 11, e0149746. | 2.5 | 23 |
| 28 | Plasmid-based one-pot saturation mutagenesis. Nature Methods, 2016, 13, 928-930. | 19.0 | 130 |
| 29 | Characterizing and predicting carboxylic acid reductase activity for diversifying bioaldehyde production. Biotechnology and Bioengineering, 2016, 113, 944-952. | 3.3 | 37 |
| 30 | Exploring <i>De Novo</i> metabolic pathways from pyruvate to propionic acid. Biotechnology Progress, 2016, 32, 303-311. | 2.6 | 16 |
| 31 | Evaluating enzymatic synthesis of small molecule drugs. Metabolic Engineering, 2016, 33, 138-147. | 7.0 | 15 |
| 32 | Regulatory effects on central carbon metabolism from poly-3-hydroxybutyrate synthesis. Metabolic Engineering, 2015, 28, 180-189. | 7.0 | 14 |
| 33 | MINEs: open access databases of computationally predicted enzyme promiscuity products for untargeted metabolomics. Journal of Cheminformatics, 2015, 7, 44. | 6.1 | 172 |
| 34 | Efficient searching and annotation of metabolic networks using chemical similarity. Bioinformatics, 2015, 31, 1016-1024. | 4.1 | 47 |
| 35 | Blocking endocytotic mechanisms to improve heterologous protein titers in <i>Saccharomyces cerevisiae</i> . Biotechnology and Bioengineering, 2015, 112, 376-385. | 3.3 | 17 |
| 36 | Yeast-based biosensors: design and applications. FEMS Yeast Research, 2014, 15, n/a-n/a. | 2.3 | 36 |

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|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 37 | Impact of protein uptake and degradation on recombinant protein secretion in yeast. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7149-7159. | 3.6 | 23 |
| 38 | Editorial overview: Cell and pathway engineering. Moving from possible to profitable: recent innovations in cell and pathway engineering. <i>Current Opinion in Biotechnology</i> , 2014, 29, v-vii. | 6.6 | 0 |
| 39 | Virus-like particles: the future of microbial factories and cell-free systems as platforms for vaccine development. <i>Current Opinion in Biotechnology</i> , 2013, 24, 1089-1093. | 6.6 | 88 |
| 40 | Computational Tools for Guided Discovery and Engineering of Metabolic Pathways. <i>Methods in Molecular Biology</i> , 2013, 985, 123-147. | 0.9 | 14 |
| 41 | Statistical Analysis of Molecular Signal Recording. <i>PLoS Computational Biology</i> , 2013, 9, e1003145. | 3.2 | 26 |
| 42 | Different expression systems for production of recombinant proteins in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1259-1268. | 3.3 | 128 |
| 43 | Metabolic engineering of recombinant protein secretion by <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2012, 12, 491-510. | 2.3 | 157 |
| 44 | Engineering of vesicle trafficking improves heterologous protein secretion in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2012, 14, 120-127. | 7.0 | 97 |
| 45 | Synthetic biology: Emerging methodologies to catalyze the metabolic engineering design cycle. <i>Metabolic Engineering</i> , 2012, 14, 187-188. | 7.0 | 4 |
| 46 | Imbalance of heterologous protein folding and disulfide bond formation rates yields runaway oxidative stress. <i>BMC Biology</i> , 2012, 10, 16. | 3.8 | 72 |
| 47 | Measuring Cation Dependent DNA Polymerase Fidelity Landscapes by Deep Sequencing. <i>PLoS ONE</i> , 2012, 7, e43876. | 2.5 | 54 |
| 48 | Meeting report: Gothenburg Life Science Conference XI - Industrial Systems Biology. <i>Biotechnology Journal</i> , 2011, 6, 259-261. | 3.5 | 1 |
| 49 | Molecular and process design for rotavirus-like particle production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2011, 10, 33. | 4.0 | 47 |
| 50 | Directed Evolution of Promoters and Tandem Gene Arrays for Customizing RNA Synthesis Rates and Regulation. <i>Methods in Enzymology</i> , 2011, 497, 135-155. | 1.0 | 19 |
| 51 | Analysis of polyhydroxybutyrate flux limitations by systematic genetic and metabolic perturbations. <i>Metabolic Engineering</i> , 2010, 12, 187-195. | 7.0 | 52 |
| 52 | Prospects of yeast systems biology for human health: integrating lipid, protein and energy metabolism. <i>FEMS Yeast Research</i> , 2010, 10, 1046-1059. | 2.3 | 59 |
| 53 | Isoprenoid Pathway Optimization for Taxol Precursor Overproduction in <i>Escherichia coli</i> . <i>Science</i> , 2010, 330, 70-74. | 12.6 | 1,426 |
| 54 | Toward design-based engineering of industrial microbes. <i>Current Opinion in Microbiology</i> , 2010, 13, 255-262. | 5.1 | 82 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 55 | Identification of gene disruptions for increased poly-3-hydroxybutyrate accumulation in <i>Synechocystis</i> PCC 6803. <i>Biotechnology Progress</i> , 2009, 25, 1236-1243. | 2.6 | 44 |
| 56 | Stabilized gene duplication enables long-term selection-free heterologous pathway expression. <i>Nature Biotechnology</i> , 2009, 27, 760-765. | 17.5 | 272 |
| 57 | A high-throughput screen for hyaluronic acid accumulation in recombinant <i>Escherichia coli</i> transformed by libraries of engineered sigma factors. <i>Biotechnology and Bioengineering</i> , 2008, 101, 788-796. | 3.3 | 53 |
| 58 | Terpenoids: Opportunities for Biosynthesis of Natural Product Drugs Using Engineered Microorganisms. <i>Molecular Pharmaceutics</i> , 2008, 5, 167-190. | 4.6 | 363 |
| 59 | Expanding the metabolic engineering toolbox: more options to engineer cells. <i>Trends in Biotechnology</i> , 2007, 25, 132-137. | 9.3 | 200 |
| 60 | High-Throughput Screen for Poly-3-Hydroxybutyrate in <i>Escherichia coli</i> and <i>Synechocystis</i> sp. Strain PCC6803. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3412-3417. | 3.1 | 83 |
| 61 | <i>Metabolic Engineering.</i> , 2005, 100, 1-17. | | 19 |