Keith E J Tyo

List of Publications by Year
in descending order

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	Isoprenoid Pathway Optimization for Taxol Precursor Overproduction in *Escherichia coli*. Science, 2010, 330, 70-74.	12.6	1,426
2	Terpenoids: Opportunities for Biosynthesis of Natural Product Drugs Using Engineered Microorganisms. Molecular Pharmaceutics, 2008, 5, 167-190.	4.6	363
3	Stabilized gene duplication enables long-term selection-free heterologous pathway expression. Nature Biotechnology, 2009, 27, 760-765.	17.5	272
4	Expanding the metabolic engineering toolbox: more options to engineer cells. Trends in Biotechnology, 2007, 25, 132-137.	9.3	200
5	MINEs: open access databases of computationally predicted enzyme promiscuity products for untargeted metabolomics. Journal of Cheminformatics, 2015, 7, 44.	6.1	172
6	Metabolic engineering of recombinant protein secretion by Saccharomyces cerevisiae. FEMS Yeast Research, 2012, 12, 491-510.	2.3	157
7	Plasmid-based one-pot saturation mutagenesis. Nature Methods, 2016, 13, 928-930.	19.0	130
8	Different expression systems for production of recombinant proteins in *Saccharomyces cerevisiae*. Biotechnology and Bioengineering, 2012, 109, 1259-1268.	3.3	128
9	Engineering of vesicle trafficking improves heterologous protein secretion in Saccharomyces cerevisiae. Metabolic Engineering, 2012, 14, 120-127.	7.0	97
10	Virus-like particles: the future of microbial factories and cell-free systems as platforms for vaccine development. Current Opinion in Biotechnology, 2013, 24, 1089-1093.	6.6	88
11	High-Throughput Screen for Poly-3-Hydroxybutyrate in Escherichia coli and Synechocystis sp. Strain PCC6803. Applied and Environmental Microbiology, 2006, 72, 3412-3417.	3.1	83
12	Toward design-based engineering of industrial microbes. Current Opinion in Microbiology, 2010, 13, 255-262.	5.1	82
13	Imbalance of heterologous protein folding and disulfide bond formation rates yields runaway oxidative stress. BMC Biology, 2012, 10, 16.	3.8	72
14	A Glucose-Sensing Toggle Switch for Autonomous, High Productivity Genetic Control. ACS Synthetic Biology, 2017, 6, 1296-1304.	3.8	67
15	Prospects of yeast systems biology for human health: integrating lipid, protein and energy metabolism. FEMS Yeast Research, 2010, 10, 1046-1059.	2.3	59
16	Measuring Cation Dependent DNA Polymerase Fidelity Landscapes by Deep Sequencing. PLoS ONE, 2012, 7, e43876.	2.5	54
17	A high-throughput screen for hyaluronic acid accumulation in recombinant *Escherichia coli* transformed by libraries of engineered sigma factors. Biotechnology and Bioengineering, 2008, 101, 788-796.	3.3	53
18	Analysis of polyhydroxybutyrate flux limitations by systematic genetic and metabolic perturbations. Metabolic Engineering, 2010, 12, 187-195.	7.0	52

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19	Molecular and process design for rotavirus-like particle production in Saccharomyces cerevisiae. Microbial Cell Factories, 2011, 10, 33.	4.0	47
20	Efficient searching and annotation of metabolic networks using chemical similarity. Bioinformatics, 2015, 31, 1016-1024.	4.1	47
21	Identification of gene disruptions for increased polyâ€3â€hydroxybutyrate accumulation in <i>Synechocystis</i> PCC 6803. Biotechnology Progress, 2009, 25, 1236-1243.	2.6	44
22	Metabolic kinetic modeling provides insight into complex biological questions, but hurdles remain. Current Opinion in Biotechnology, 2019, 59, 24-30.	6.6	42
23	Characterizing and predicting carboxylic acid reductase activity for diversifying bioaldehyde production. Biotechnology and Bioengineering, 2016, 113, 944-952.	3.3	37
24	Yeast-based biosensors: design and applications. FEMS Yeast Research, 2014, 15, n/a-n/a.	2.3	36
25	Predicting novel substrates for enzymes with minimal experimental effort with active learning. Metabolic Engineering, 2017, 44, 171-181.	7.0	31
26	Development of a genetic toolset for the highly engineerable and metabolically versatile Acinetobacter baylyi ADP1. Nucleic Acids Research, 2020, 48, 5169-5182.	14.5	30
27	Bayesian inference of metabolic kinetics from genome-scale multiomics data. PLoS Computational Biology, 2019, 15, e1007424.	3.2	29
28	Kinetic ensemble model of gas fermenting Clostridium autoethanogenum for improved ethanol production. Biochemical Engineering Journal, 2019, 148, 46-56.	3.6	27
29	Statistical Analysis of Molecular Signal Recording. PLoS Computational Biology, 2013, 9, e1003145.	3.2	26
30	Acceleration Strategies to Enhance Metabolic Ensemble Modeling Performance. Biophysical Journal, 2017, 113, 1150-1162.	0.5	24
31	Impact of protein uptake and degradation on recombinant protein secretion in yeast. Applied Microbiology and Biotechnology, 2014, 98, 7149-7159.	3.6	23
32	N-Terminal-Based Targeted, Inducible Protein Degradation in Escherichia coli. PLoS ONE, 2016, 11, e0149746.	2.5	23
33	Generation and Validation of the iKp1289 Metabolic Model for Klebsiella pneumoniae KPPR1. Journal of Infectious Diseases, 2017, 215, S37-S43.	4.0	23
34	Detection of a Peptide Biomarker by Engineered Yeast Receptors. ACS Synthetic Biology, 2018, 7, 696-705.	3.8	20
35	Metabolic Engineering. , 2005, 100, 1-17.		19
36	Directed Evolution of Promoters and Tandem Gene Arrays for Customizing RNA Synthesis Rates and Regulation. Methods in Enzymology, 2011, 497, 135-155.	1.0	19

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37	High-resolution mapping of DNA polymerase fidelity using nucleotide imbalances and next-generation sequencing. Nucleic Acids Research, 2018, 46, e78-e78.	14.5	19
38	Dynamic Control of Gene Expression with Riboregulated Switchable Feedback Promoters. ACS Synthetic Biology, 2021, 10, 1199-1213.	3.8	19
39	Blocking endocytotic mechanisms to improve heterologous protein titers in *Saccharomyces cerevisiae*. Biotechnology and Bioengineering, 2015, 112, 376-385.	3.3	17
40	Exploring *De Novo* metabolic pathways from pyruvate to propionic acid. Biotechnology Progress, 2016, 32, 303-311.	2.6	16
41	Evaluating enzymatic synthesis of small molecule drugs. Metabolic Engineering, 2016, 33, 138-147.	7.0	15
42	Computational Tools for Guided Discovery and Engineering of Metabolic Pathways. Methods in Molecular Biology, 2013, 985, 123-147.	0.9	14
43	Regulatory effects on central carbon metabolism from poly-3-hydroxybutryate synthesis. Metabolic Engineering, 2015, 28, 180-189.	7.0	14
44	Engineering Acinetobacter baylyi ADP1 for mevalonate production from lignin-derived aromatic compounds. Metabolic Engineering Communications, 2021, 13, e00173.	3.6	14
45	DNA binding strength increases the processivity and activity of a Y-Family DNA polymerase. Scientific Reports, 2017, 7, 4756.	3.3	13
46	Development of novel metabolite-responsive transcription factors via transposon-mediated protein fusion. Protein Engineering, Design and Selection, 2018, 31, 55-63.	2.1	13
47	Curating a comprehensive set of enzymatic reaction rules for efficient novel biosynthetic pathway design. Metabolic Engineering, 2021, 65, 79-87.	7.0	12
48	Recording Temporal Signals with Minutes Resolution Using Enzymatic DNA Synthesis. Journal of the American Chemical Society, 2021, 143, 16630-16640.	13.7	12
49	Enabling commercial success of industrial biotechnology. Science, 2021, 374, 1563-1565.	12.6	10
50	CellSort: a support vector machine tool for optimizing fluorescence-activated cell sorting and reducing experimental effort. Bioinformatics, 2017, 33, 909-916.	4.1	9
51	Modulating and evaluating receptor promiscuity through directed evolution and modeling. Protein Engineering, Design and Selection, 2017, 30, 455-465.	2.1	6
52	MINE 2.0: enhanced biochemical coverage for peak identification in untargeted metabolomics. Bioinformatics, 2022, 38, 3484-3487.	4.1	6
53	Metabolic In Silico Network Expansions to Predict and Exploit Enzyme Promiscuity. Methods in Molecular Biology, 2019, 1927, 11-21.	0.9	5
54	Chemical-damage MINE: A database of curated and predicted spontaneous metabolic reactions. Metabolic Engineering, 2022, 69, 302-312.	7.0	5

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55	Synthetic biology: Emerging methodologies to catalyze the metabolic engineering design cycle. Metabolic Engineering, 2012, 14, 187-188.	7.0	4
56	Increased Processivity, Misincorporation, and Nucleotide Incorporation Efficiency in Sulfolobus solfataricus Dpo4 Thumb Domain Mutants. Applied and Environmental Microbiology, 2017, 83, .	3.1	4
57	Model-guided mechanism discovery and parameter selection for directed evolution. Applied Microbiology and Biotechnology, 2019, 103, 9697-9709.	3.6	2
58	Chemically Inducible Chromosomal Evolution (CIChE) for Multicopy Metabolic Pathway Engineering. Methods in Molecular Biology, 2019, 1927, 37-45.	0.9	2
59	Meeting report: Gothenburg Life Science Conference XI - Industrial Systems Biology. Biotechnology Journal, 2011, 6, 259-261.	3.5	1
60	Editorial overview: Cell and pathway engineering. Moving from possible to profitable: recent innovations in cell and pathway engineering. Current Opinion in Biotechnology, 2014, 29, v-vii.	6.6	0
61	Nucleotide-time alignment for molecular recorders. PLoS Computational Biology, 2017, 13, e1005483.	3.2	0