

# Mark S Dunstan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6901007/publications.pdf>

Version: 2024-02-01

27  
papers

1,328  
citations

394421

19  
h-index

526287

27  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1655  
citing authors

#	ARTICLE	IF	CITATIONS
1	A plasmid toolset for CRISPR-mediated genome editing and CRISPRi gene regulation in <i>Escherichia coli</i> . <i>Microbial Biotechnology</i> , 2021, 14, 1120-1129.	4.2	10
2	Prototyping of microbial chassis for the biomanufacturing of high-value chemical targets. <i>Biochemical Society Transactions</i> , 2021, 49, 1055-1063.	3.4	3
3	Ribosomal Protein L11 Selectively Stabilizes a Tertiary Structure of the GTPase Center rRNA Domain. <i>Journal of Molecular Biology</i> , 2020, 432, 991-1007.	4.2	7
4	Engineering <i>Escherichia coli</i> towards de novo production of gatekeeper (2S)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. <i>Synthetic Biology</i> , 2020, 5, ysaa012.	2.2	45
5	Rapid prototyping of microbial production strains for the biomanufacture of potential materials monomers. <i>Metabolic Engineering</i> , 2020, 60, 168-182.	7.0	48
6	Highly multiplexed, fast and accurate nanopore sequencing for verification of synthetic DNA constructs and sequence libraries. <i>Synthetic Biology</i> , 2019, 4, ysz025.	2.2	35
7	An automated pipeline for the screening of diverse monoterpene synthase libraries. <i>Scientific Reports</i> , 2019, 9, 11936.	3.3	21
8	Design and evolution of an enzyme with a non-canonical organocatalytic mechanism. <i>Nature</i> , 2019, 570, 219-223.	27.8	86
9	SelProm: A Queryable and Predictive Expression Vector Selection Tool for <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2019, 8, 1478-1483.	3.8	37
10	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2019, 8, 127-136.	3.8	88
11	PartsGenie: an integrated tool for optimizing and sharing synthetic biology parts. <i>Bioinformatics</i> , 2018, 34, 2327-2329.	4.1	25
12	Engineering the "Missing Link" in Biosynthetic ( $\alpha$ )-Menthol Production: Bacterial Isopulegone Isomerase. <i>ACS Catalysis</i> , 2018, 8, 2012-2020.	11.2	20
13	Multifragment DNA Assembly of Biochemical Pathways via Automated Ligase Cycling Reaction. <i>Methods in Enzymology</i> , 2018, 608, 369-392.	1.0	11
14	Structure and Biocatalytic Scope of Coclaurine N-Methyltransferase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 10600-10604.	13.8	37
15	Structure and Biocatalytic Scope of Coclaurine N-Methyltransferase. <i>Angewandte Chemie</i> , 2018, 130, 10760-10764.	2.0	6
16	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. <i>Communications Biology</i> , 2018, 1, 66.	4.4	159
17	Zymophore identification enables the discovery of novel phenylalanine ammonia lyase enzymes. <i>Scientific Reports</i> , 2017, 7, 13691.	3.3	30
18	Adenylation Activity of Carboxylic Acid Reductases Enables the Synthesis of Amides. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14498-14501.	13.8	74

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19	Adenylation Activity of Carboxylic Acid Reductases Enables the Synthesis of Amides. <i>Angewandte Chemie</i> , 2017, 129, 14690-14693.	2.0	25
20	Structures of carboxylic acid reductase reveal domain dynamics underlying catalysis. <i>Nature Chemical Biology</i> , 2017, 13, 975-981.	8.0	118
21	biochem4j: Integrated and extensible biochemical knowledge through graph databases. <i>PLoS ONE</i> , 2017, 12, e0179130.	2.5	31
22	SYNBIOCHEM—a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. <i>Biochemical Society Transactions</i> , 2016, 44, 675-677.	3.4	7
23	Structure and biocatalytic scope of thermophilic flavin-dependent halogenase and flavin reductase enzymes. <i>Organic and Biomolecular Chemistry</i> , 2016, 14, 9354-9361.	2.8	55
24	Single-Enzyme Biocatalyst Synthesis of Enantiopure $\alpha$ -Arylalanines Exploiting an Engineered $\alpha$ -Amino Acid Dehydrogenase. <i>Advanced Synthesis and Catalysis</i> , 2016, 358, 3298-3306.	4.3	51
25	Structures of the methyltransferase component of <i>Desulfitobacterium hafniense</i> DCB-2 <i>O</i> -demethylase shed light on methyltetrahydrofolate formation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1900-1908.	2.5	5
26	Epoxyqueuosine Reductase Structure Suggests a Mechanism for Cobalamin-dependent tRNA Modification. <i>Journal of Biological Chemistry</i> , 2015, 290, 27572-27581.	3.4	34
27	Reductive dehalogenase structure suggests a mechanism for B12-dependent dehalogenation. <i>Nature</i> , 2015, 517, 513-516.	27.8	260