

# Steven W Singer

## List of Publications by Year in descending order

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101  
papers

7,295  
citations

76326

40  
h-index

62596

80  
g-index

110  
all docs

110  
docs citations

110  
times ranked

8991  
citing authors

#	ARTICLE	IF	CITATIONS
1	Adaptive evolution of <i>Methylotuvimicrobium alcaliphilum</i> to grow in the presence of rhamnolipids improves fatty acid and rhamnolipid production from CH <sub>4</sub> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2022, 49, .	3.0	4
2	Complete Genome Sequences of Five Isolated <i>Pseudomonas</i> Strains that Catabolize Pentose Sugars and Aromatic Compounds Obtained from Lignocellulosic Biomass. <i>Microbiology Resource Announcements</i> , 2022, 11, e0098721.	0.6	4
3	Machine learning for metabolic engineering: A review. <i>Metabolic Engineering</i> , 2021, 63, 34-60.	7.0	135
4	Doing it alone: Unisexual reproduction in filamentous ascomycete fungi. <i>Fungal Biology Reviews</i> , 2021, 35, 1-13.	4.7	20
5	Metabolic Engineering of <i>Cupriavidus necator</i> H16 for Sustainable Biofuels from CO <sub>2</sub> . <i>Trends in Biotechnology</i> , 2021, 39, 412-424.	9.3	77
6	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021, 24, 102290.	4.1	7
7	Development of dual-inducible dual-expression vectors for tunable gene expression control and CRISPR interference-based gene repression in <i>Pseudomonas putida</i> KT2440. <i>Microbial Biotechnology</i> , 2021, 14, 2659-2678.	4.2	10
8	Microbial production of advanced biofuels. <i>Nature Reviews Microbiology</i> , 2021, 19, 701-715.	28.6	126
9	The F-box protein gene <i>exo-1</i> is a target for reverse engineering enzyme hypersecretion in filamentous fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	13
10	CAZymes from the thermophilic fungus <i>Thermoascus aurantiacus</i> are induced by C5 and C6 sugars. <i>Biotechnology for Biofuels</i> , 2021, 14, 169.	6.2	6
11	Generation of <i>Pseudomonas putida</i> KT2440 Strains with Efficient Utilization of Xylose and Galactose via Adaptive Laboratory Evolution. <i>ACS Sustainable Chemistry and Engineering</i> , 2021, 9, 11512-11523.	6.7	32
12	A new path for one-carbon conversion. <i>Nature Metabolism</i> , 2021, 3, 1286-1287.	11.9	0
13	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
14	Development of genetic tools for the thermophilic filamentous fungus <i>Thermoascus aurantiacus</i> . <i>Biotechnology for Biofuels</i> , 2020, 13, 167.	6.2	8
15	Adaptive laboratory evolution of <i>Pseudomonas putida</i> KT2440 improves p-coumaric and ferulic acid catabolism and tolerance. <i>Metabolic Engineering Communications</i> , 2020, 11, e00143.	3.6	73
16	Generation of ionic liquid tolerant <i>Pseudomonas putida</i> KT2440 strains via adaptive laboratory evolution. <i>Green Chemistry</i> , 2020, 22, 5677-5690.	9.0	29
17	Whole-Genome Sequence of <i>Brevibacillus borstelensis</i> SDM, Isolated from a Sorghum-Adapted Microbial Community. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	10
18	Structural changes in bacterial and fungal soil microbiome components during biosolarization as related to volatile fatty acid accumulation. <i>Applied Soil Ecology</i> , 2020, 153, 103602.	4.3	10

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19	Construction of a novel dual-inducible duet-expression system for gene (over)expression in <i>Pseudomonas putida</i> . <i>Plasmid</i> , 2020, 110, 102514.	1.4	14
20	Purification and characterization of a native lytic polysaccharide monoxygenase from <i>Thermoascus aurantiacus</i> . <i>Biotechnology Letters</i> , 2020, 42, 1897-1905.	2.2	8
21	Response of <i>Pseudomonas putida</i> to Complex, Aromatic-Rich Fractions from Biomass. <i>ChemSusChem</i> , 2020, 13, 4455-4467.	6.8	23
22	Ethanol production in switchgrass hydrolysate by ionic liquid-tolerant yeasts. <i>Bioresource Technology Reports</i> , 2019, 7, 100275.	2.7	9
23	NaCl enhances <i>Escherichia coli</i> growth and isoprenol production in the presence of imidazolium-based ionic liquids. <i>Bioresource Technology Reports</i> , 2019, 6, 1-5.	2.7	8
24	Guanidine Riboswitch-Regulated Efflux Transporters Protect Bacteria against Ionic Liquid Toxicity. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	17
25	Approaches for More Efficient Biological Conversion of Lignocellulosic Feedstocks to Biofuels and Bioproducts. <i>ACS Sustainable Chemistry and Engineering</i> , 2019, 7, 9062-9079.	6.7	89
26	Methyl ketone production by <i>Pseudomonas putida</i> is enhanced by plant-derived amino acids. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1909-1922.	3.3	29
27	Large Circular Plasmids from Groundwater Plasmidomes Span Multiple Incompatibility Groups and Are Enriched in Multimetal Resistance Genes. <i>MBio</i> , 2019, 10, .	4.1	42
28	Assessment of biogas production and microbial ecology in a high solid anaerobic digestion of major California food processing residues. <i>Bioresource Technology Reports</i> , 2019, 5, 1-11.	2.7	24
29	Tolerance Characterization and Isoprenol Production of Adapted <i>Escherichia coli</i> in the Presence of Ionic Liquids. <i>ACS Sustainable Chemistry and Engineering</i> , 2019, 7, 1457-1463.	6.7	10
30	Isolation and Characterization of Bacterial Cellulase Producers for Biomass Deconstruction: A Microbiology Laboratory Course. <i>Journal of Microbiology and Biology Education</i> , 2019, 20, .	1.0	5
31	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	7.3	185
32	A bacterial pioneer produces cellulase complexes that persist through community succession. <i>Nature Microbiology</i> , 2018, 3, 99-107.	13.3	38
33	Jungle Express is a versatile repressor system for tight transcriptional control. <i>Nature Communications</i> , 2018, 9, 3617.	12.8	33
34	Natural Variation in the Multidrug Efflux Pump <i>SGE1</i> Underlies Ionic Liquid Tolerance in Yeast. <i>Genetics</i> , 2018, 210, 219-234.	2.9	30
35	Nitrogen amendment of green waste impacts microbial community, enzyme secretion and potential for lignocellulose decomposition. <i>Process Biochemistry</i> , 2017, 52, 214-222.	3.7	20
36	Ecological Insights into the Dynamics of Plant Biomass-Degrading Microbial Consortia. <i>Trends in Microbiology</i> , 2017, 25, 788-796.	7.7	59

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37	Alteration of white-rot basidiomycetes cellulase and xylanase activities in the submerged co-cultivation and optimization of enzyme production by <i>Irpex lacteus</i> and <i>Schizophyllum commune</i> . <i>Bioresource Technology</i> , 2017, 241, 652-660.	9.6	25
38	Development and characterization of a thermophilic, lignin degrading microbiota. <i>Process Biochemistry</i> , 2017, 63, 193-203.	3.7	29
39	Comparison of soil biosolarization with mesophilic and thermophilic solid digestates on soil microbial quantity and diversity. <i>Applied Soil Ecology</i> , 2017, 119, 183-191.	4.3	18
40	<i>Thermoascus aurantiacus</i> is an Intriguing Host for the Industrial Production of Cellulases. <i>Current Biotechnology</i> , 2017, 6, 89-97.	0.4	20
41	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2017, 12, e0189604.	2.5	13
42	Generation of a platform strain for ionic liquid tolerance using adaptive laboratory evolution. <i>Microbial Cell Factories</i> , 2017, 16, 204.	4.0	60
43	<i>Rhodospiridium toruloides</i> : a new platform organism for conversion of lignocellulose into terpene biofuels and bioproducts. <i>Biotechnology for Biofuels</i> , 2017, 10, 241.	6.2	150
44	Xylose induces cellulase production in <i>Thermoascus aurantiacus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 271.	6.2	24
45	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	3.5	66
46	Ionic Liquids Impact the Bioenergy Feedstock-Degrading Microbiome and Transcription of Enzymes Relevant to Polysaccharide Hydrolysis. <i>MSystems</i> , 2016, 1, .	3.8	15
47	Enrichment of microbial communities tolerant to the ionic liquids tetrabutylphosphonium chloride and tributylethylphosphonium diethylphosphate. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 5639-5652.	3.6	6
48	Comparative Community Proteomics Demonstrates the Unexpected Importance of Actinobacterial Glycoside Hydrolase Family 12 Protein for Crystalline Cellulose Hydrolysis. <i>MBio</i> , 2016, 7, .	4.1	17
49	Ionic liquid-tolerant microorganisms and microbial communities for lignocellulose conversion to bioproducts. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 10237-10249.	3.6	41
50	Transcriptomic analysis of the highly efficient oil-degrading bacterium <i>Acinetobacter venetianus</i> RAG-1 reveals genes important in dodecane uptake and utilization. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw224.	1.8	14
51	The role of organic matter amendment level on soil heating, organic acid accumulation, and development of bacterial communities in solarized soil. <i>Applied Soil Ecology</i> , 2016, 106, 37-46.	4.3	48
52	MaxBin 2.0: an automated binning algorithm to recover genomes from multiple metagenomic datasets. <i>Bioinformatics</i> , 2016, 32, 605-607.	4.1	1,574
53	Refining the phylum Chlorobi by resolving the phylogeny and metabolic potential of the representative of a deeply branching, uncultivated lineage. <i>ISME Journal</i> , 2016, 10, 833-845.	9.8	62
54	Preservation of microbial communities enriched on lignocellulose under thermophilic and high-solid conditions. <i>Biotechnology for Biofuels</i> , 2015, 8, 206.	6.2	22

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55	Genomic Analysis of Xylose Metabolism in Members of the Deinococcus-Thermus Phylum from Thermophilic Biomass-Deconstructing Bacterial Consortia. <i>Bioenergy Research</i> , 2015, 8, 1031-1038.	3.9	4
56	Revisiting N <sub>2</sub> fixation in Guerrero Negro intertidal microbial mats with a functional single-cell approach. <i>ISME Journal</i> , 2015, 9, 485-496.	9.8	69
57	Metatranscriptomic analysis of lignocellulolytic microbial communities involved in high-solids decomposition of rice straw. <i>Biotechnology for Biofuels</i> , 2014, 7, 495.	6.2	40
58	Discovery of two novel $\beta$ -glucosidases from an Amazon soil metagenomic library. <i>FEMS Microbiology Letters</i> , 2014, 351, 147-155.	1.8	25
59	An auto-inducible mechanism for ionic liquid resistance in microbial biofuel production. <i>Nature Communications</i> , 2014, 5, 3490.	12.8	85
60	<i>Bacillus coagulans</i> tolerance to 1-ethyl-3-methylimidazolium-based ionic liquids in aqueous and solid-state thermophilic culture. <i>Biotechnology Progress</i> , 2014, 30, 311-316.	2.6	19
61	Yeast tolerance to the ionic liquid 1-ethyl-3-methylimidazolium acetate. <i>FEMS Yeast Research</i> , 2014, 14, 1286-1294.	2.3	36
62	Characterization of bacterial communities in solarized soil amended with lignocellulosic organic matter. <i>Applied Soil Ecology</i> , 2014, 73, 97-104.	4.3	37
63	Discovery and characterization of ionic liquid-tolerant thermophilic cellulases from a switchgrass-adapted microbial community. <i>Biotechnology for Biofuels</i> , 2014, 7, 15.	6.2	65
64	Substrate-Specific Development of Thermophilic Bacterial Consortia by Using Chemically Pretreated Switchgrass. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7423-7432.	3.1	27
65	MaxBin: an automated binning method to recover individual genomes from metagenomes using an expectation-maximization algorithm. <i>Microbiome</i> , 2014, 2, 26.	11.1	521
66	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
67	One-pot ionic liquid pretreatment and saccharification of switchgrass. <i>Green Chemistry</i> , 2013, 15, 2579.	9.0	175
68	Development of a broad-host synthetic biology toolbox for <i>Ralstonia eutropha</i> and its application to engineering hydrocarbon biofuel production. <i>Microbial Cell Factories</i> , 2013, 12, 107.	4.0	103
69	Functionalizing bacterial cell surfaces with a phage protein. <i>Chemical Communications</i> , 2013, 49, 910-912.	4.1	4
70	Draft Genome Sequence of an Oscillatorian Cyanobacterium, Strain ESFC-1. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
71	Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. <i>ISME Journal</i> , 2013, 7, 817-829.	9.8	57
72	High throughput nanostructure-initiator mass spectrometry screening of microbial growth conditions for maximal $\beta$ -glucosidase production. <i>Frontiers in Microbiology</i> , 2013, 4, 365.	3.5	11

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73	Community dynamics of cellulose-adapted thermophilic bacterial consortia. <i>Environmental Microbiology</i> , 2013, 15, 2573-2587.	3.8	77
74	Engineering of <i>Ralstonia eutropha</i> H16 for Autotrophic and Heterotrophic Production of Methyl Ketones. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4433-4439.	3.1	139
75	Proteogenomic Analysis of a Thermophilic Bacterial Consortium Adapted to Deconstruct Switchgrass. <i>PLoS ONE</i> , 2013, 8, e68465.	2.5	62
76	Discovery of Microorganisms and Enzymes Involved in High-Solids Decomposition of Rice Straw Using Metagenomic Analyses. <i>PLoS ONE</i> , 2013, 8, e77985.	2.5	50
77	Identification of a novel cyanobacterial group as active diazotrophs in a coastal microbial mat using NanoSIMS analysis. <i>ISME Journal</i> , 2012, 6, 1427-1439.	9.8	66
78	Metal Affinity Enrichment Increases the Range and Depth of Proteome Identification for Extracellular Microbial Proteins. <i>Journal of Proteome Research</i> , 2012, 11, 861-870.	3.7	1
79	<i>Thermoascus aurantiacus</i> is a promising source of enzymes for biomass deconstruction under thermophilic conditions. <i>Biotechnology for Biofuels</i> , 2012, 5, 54.	6.2	88
80	Targeted Isolation of Proteins from Natural Microbial Communities Living in an Extreme Environment. <i>Methods in Molecular Biology</i> , 2012, 881, 63-72.	0.9	3
81	Hydrogen production in photosynthetic microbial mats in the Elkhorn Slough estuary, Monterey Bay. <i>ISME Journal</i> , 2012, 6, 863-874.	9.8	48
82	Substrate perturbation alters the glycoside hydrolase activities and community composition of switchgrass-adapted bacterial consortia. <i>Biotechnology and Bioengineering</i> , 2012, 109, 1140-1145.	3.3	17
83	A Thermophilic Ionic Liquid-Tolerant Cellulase Cocktail for the Production of Cellulosic Biofuels. <i>PLoS ONE</i> , 2012, 7, e37010.	2.5	98
84	Glycoside Hydrolase Activities of Thermophilic Bacterial Consortia Adapted to Switchgrass. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5804-5812.	3.1	99
85	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. <i>Genome Biology</i> , 2011, 12, R44.	8.8	326
86	Bioenergy feedstock-specific enrichment of microbial populations during high-solids thermophilic deconstruction. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2088-2098.	3.3	23
87	Chain mechanism for exchange of D <sub>2</sub> with a ruthenium hydride. <i>Chemical Communications</i> , 2010, 46, 7915.	4.1	10
88	Strategies for Enhancing the Effectiveness of Metagenomic-based Enzyme Discovery in Lignocellulolytic Microbial Communities. <i>Bioenergy Research</i> , 2010, 3, 146-158.	3.9	100
89	Posttranslational modification and sequence variation of redox-active proteins correlate with biofilm life cycle in natural microbial communities. <i>ISME Journal</i> , 2010, 4, 1398-1409.	9.8	26
90	Computational Prediction and Experimental Validation of Signal Peptide Cleavages in the Extracellular Proteome of a Natural Microbial Community. <i>Journal of Proteome Research</i> , 2010, 9, 2148-2159.	3.7	17

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91	Community Genomic and Proteomic Analyses of Chemoautotrophic Iron-Oxidizing <i>Leptospirillum rubrum</i> (Group II) and <i>Leptospirillum ferrodiazotrophum</i> (Group III) Bacteria in Acid Mine Drainage Biofilms. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4599-4615.	3.1	168
92	Cytochrome 572 is a conspicuous membrane protein with iron oxidation activity purified directly from a natural acidophilic microbial community. <i>ISME Journal</i> , 2008, 2, 542-550.	9.8	102
93	Characterization of Cytochrome 579, an Unusual Cytochrome Isolated from an Iron-Oxidizing Microbial Community. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4454-4462.	3.1	66
94	CO-dependent H <sub>2</sub> evolution by <i>Rhodospirillum rubrum</i> : Role of CODH:CooF complex. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2006, 1757, 1582-1591.	1.0	57
95	New insights into the mechanism of nickel insertion into carbon monoxide dehydrogenase: analysis of <i>Rhodospirillum rubrum</i> carbon monoxide dehydrogenase variants with substituted ligands to the [Fe <sub>3</sub> S <sub>4</sub> ] portion of the active-site C-cluster. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 903-912.	2.6	31
96	Hydrogen Elimination from a Hydroxycyclopentadienyl Ruthenium(II) Hydride: A Study of Hydrogen Activation in a Ligand-Metal Bifunctional Hydrogenation Catalyst. <i>Journal of the American Chemical Society</i> , 2005, 127, 3100-3109.	13.7	160
97	Purification and Characterization of NafY (Apodinitrogenase $\hat{\Gamma}$ <sup>3</sup> Subunit) from <i>Azotobacter vinelandii</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 19739-19746.	3.4	30
98	Protonated Aminocyclopentadienyl Ruthenium Hydride Reduction of Benzaldehyde and the Conversion of the Resulting Ruthenium Triflate to a Ruthenium Hydride with H <sub>2</sub> and Base. <i>Organometallics</i> , 2002, 21, 5038-5046.	2.3	40
99	Hydrogen Transfer to Carbonyls and Imines from a Hydroxycyclopentadienyl Ruthenium Hydride: Evidence for Concerted Hydride and Proton Transfer. <i>Journal of the American Chemical Society</i> , 2001, 123, 1090-1100.	13.7	383
100	The role of a hydroxycyclopentadienyl ruthenium dicarbonyl formate in formic acid reductions of carbonyl compounds catalyzed by Shvo's diruthenium catalyst. <i>Canadian Journal of Chemistry</i> , 2001, 79, 1002-1011.	1.1	26
101	Revisiting Theoretical Tools and Approaches for the Valorization of Recalcitrant Lignocellulosic Biomass to Value-Added Chemicals. <i>Frontiers in Energy Research</i> , 0, 10, .	2.3	9