

Steven W Singer

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	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
3	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
4	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. <i>Genome Biology</i> , 2011, 12, R44.	8.8	326
5	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
6	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
7	One-pot ionic liquid pretreatment and saccharification of switchgrass. <i>Green Chemistry</i> , 2013, 15, 2579.	9.0	175
8	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
9	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
10	<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
11	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
12	Machine learning for metabolic engineering: A review. <i>Metabolic Engineering</i> , 2021, 63, 34-60.	7.0	135
13	Microbial production of advanced biofuels. <i>Nature Reviews Microbiology</i> , 2021, 19, 701-715.	28.6	126
14	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
15	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
16	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
17	Glycoside Hydrolase Activities of Thermophilic Bacterial Consortia Adapted to Switchgrass. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5804-5812.	3.1	99
18	A Thermophilic Ionic Liquid-Tolerant Cellulase Cocktail for the Production of Cellulosic Biofuels. <i>PLoS ONE</i> , 2012, 7, e37010.	2.5	98

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19	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
20	<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
21	An auto-inducible mechanism for ionic liquid resistance in microbial biofuel production. <i>Nature Communications</i> , 2014, 5, 3490.	12.8	85
22	Community dynamics of cellulose-adapted thermophilic bacterial consortia. <i>Environmental Microbiology</i> , 2013, 15, 2573-2587.	3.8	77
23	Metabolic Engineering of <i>Cupriavidus necator</i> H16 for Sustainable Biofuels from CO ₂ . <i>Trends in Biotechnology</i> , 2021, 39, 412-424.	9.3	77
24	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
25	Revisiting N ₂ fixation in Guerrero Negro intertidal microbial mats with a functional single-cell approach. <i>ISME Journal</i> , 2015, 9, 485-496.	9.8	69
26	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
27	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
28	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
29	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
30	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
31	Proteogenomic Analysis of a Thermophilic Bacterial Consortium Adapted to Deconstruct Switchgrass. <i>PLoS ONE</i> , 2013, 8, e68465.	2.5	62
32	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
33	Generation of a platform strain for ionic liquid tolerance using adaptive laboratory evolution. <i>Microbial Cell Factories</i> , 2017, 16, 204.	4.0	60
34	Ecological Insights into the Dynamics of Plant Biomass-Degrading Microbial Consortia. <i>Trends in Microbiology</i> , 2017, 25, 788-796.	7.7	59
35	CO-dependent H ₂ 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
36	Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. <i>ISME Journal</i> , 2013, 7, 817-829.	9.8	57

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37	Discovery of Microorganisms and Enzymes Involved in High-Solids Decomposition of Rice Straw Using Metagenomic Analyses. PLoS ONE, 2013, 8, e77985.	2.5	50
38	Hydrogen production in photosynthetic microbial mats in the Elkhorn Slough estuary, Monterey Bay. ISME Journal, 2012, 6, 863-874.	9.8	48
39	The role of organic matter amendment level on soil heating, organic acid accumulation, and development of bacterial communities in solarized soil. Applied Soil Ecology, 2016, 106, 37-46.	4.3	48
40	Large Circular Plasmids from Groundwater Plasmidomes Span Multiple Incompatibility Groups and Are Enriched in Multimetal Resistance Genes. MBio, 2019, 10, .	4.1	42
41	Ionic liquid-tolerant microorganisms and microbial communities for lignocellulose conversion to bioproducts. Applied Microbiology and Biotechnology, 2016, 100, 10237-10249.	3.6	41
42	Protonated Aminocyclopentadienyl Ruthenium Hydride Reduction of Benzaldehyde and the Conversion of the Resulting Ruthenium Triflate to a Ruthenium Hydride with H ₂ and Base. Organometallics, 2002, 21, 5038-5046.	2.3	40
43	Metatranscriptomic analysis of lignocellulolytic microbial communities involved in high-solids decomposition of rice straw. Biotechnology for Biofuels, 2014, 7, 495.	6.2	40
44	A bacterial pioneer produces cellulase complexes that persist through community succession. Nature Microbiology, 2018, 3, 99-107.	13.3	38
45	Characterization of bacterial communities in solarized soil amended with lignocellulosic organic matter. Applied Soil Ecology, 2014, 73, 97-104.	4.3	37
46	Yeast tolerance to the ionic liquid 1-ethyl-3-methylimidazolium acetate. FEMS Yeast Research, 2014, 14, 1286-1294.	2.3	36
47	Jungle Express is a versatile repressor system for tight transcriptional control. Nature Communications, 2018, 9, 3617.	12.8	33
48	Generation of <i>Pseudomonas putida</i> KT2440 Strains with Efficient Utilization of Xylose and Galactose via Adaptive Laboratory Evolution. ACS Sustainable Chemistry and Engineering, 2021, 9, 11512-11523.	6.7	32
49	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 ₃ S ₄] portion of the active-site C-cluster. Journal of Biological Inorganic Chemistry, 2005, 10, 903-912.	2.6	31
50	Purification and Characterization of NafY (Apodinitrogenase $\hat{\beta}$ Subunit) from <i>Azotobacter vinelandii</i> . Journal of Biological Chemistry, 2004, 279, 19739-19746.	3.4	30
51	Natural Variation in the Multidrug Efflux Pump <i>SCE1</i> Underlies Ionic Liquid Tolerance in Yeast. Genetics, 2018, 210, 219-234.	2.9	30
52	Development and characterization of a thermophilic, lignin degrading microbiota. Process Biochemistry, 2017, 63, 193-203.	3.7	29
53	Methyl ketone production by <i>Pseudomonas putida</i> is enhanced by plant-derived amino acids. Biotechnology and Bioengineering, 2019, 116, 1909-1922.	3.3	29
54	Generation of ionic liquid tolerant <i>Pseudomonas putida</i> KT2440 strains via adaptive laboratory evolution. Green Chemistry, 2020, 22, 5677-5690.	9.0	29

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55	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
56	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
57	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
58	Discovery of two novel β -glucosidases from an Amazon soil metagenomic library. <i>FEMS Microbiology Letters</i> , 2014, 351, 147-155.	1.8	25
59	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
60	Xylose induces cellulase production in <i>Thermoascus aurantiacus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 271.	6.2	24
61	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
62	Bioenergy feedstock-specific enrichment of microbial populations during high-solids thermophilic deconstruction. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2088-2098.	3.3	23
63	Response of <i>Pseudomonas putida</i> to Complex, Aromatic-Rich Fractions from Biomass. <i>ChemSusChem</i> , 2020, 13, 4455-4467.	6.8	23
64	Preservation of microbial communities enriched on lignocellulose under thermophilic and high-solid conditions. <i>Biotechnology for Biofuels</i> , 2015, 8, 206.	6.2	22
65	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
66	<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
67	Doing it alone: Unisexual reproduction in filamentous ascomycete fungi. <i>Fungal Biology Reviews</i> , 2021, 35, 1-13.	4.7	20
68	<i>Bacillus coagulans</i> tolerance to 1-ethyl-3-(3-dimethylimidazolium)-based ionic liquids in aqueous and solid-state thermophilic culture. <i>Biotechnology Progress</i> , 2014, 30, 311-316.	2.6	19
69	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
70	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
71	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
72	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

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73	Guanidine Riboswitch-Regulated Efflux Transporters Protect Bacteria against Ionic Liquid Toxicity. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	17
74	Ionic Liquids Impact the Bioenergy Feedstock-Degrading Microbiome and Transcription of Enzymes Relevant to Polysaccharide Hydrolysis. <i>MSystems</i> , 2016, 1, .	3.8	15
75	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
76	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
77	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2017, 12, e0189604.	2.5	13
78	The F-box protein gene <i>exo1</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
79	High throughput nanostructure-initiator mass spectrometry screening of microbial growth conditions for maximal β -glucosidase production. <i>Frontiers in Microbiology</i> , 2013, 4, 365.	3.5	11
80	Chain mechanism for exchange of D2 with a ruthenium hydride. <i>Chemical Communications</i> , 2010, 46, 7915.	4.1	10
81	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
82	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
83	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
84	Development of dual-inducible duet-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
85	Ethanol production in switchgrass hydrolysate by ionic liquid-tolerant yeasts. <i>Bioresource Technology Reports</i> , 2019, 7, 100275.	2.7	9
86	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
87	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
88	Development of genetic tools for the thermophilic filamentous fungus <i>Thermoascus aurantiacus</i> . <i>Biotechnology for Biofuels</i> , 2020, 13, 167.	6.2	8
89	Purification and characterization of a native lytic polysaccharide monooxygenase from <i>Thermoascus aurantiacus</i> . <i>Biotechnology Letters</i> , 2020, 42, 1897-1905.	2.2	8
90	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021, 24, 102290.	4.1	7

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91	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
92	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
93	Draft Genome Sequence of an Oscillatorian Cyanobacterium, Strain ESFC-1. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
94	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
95	Functionalizing bacterial cell surfaces with a phage protein. <i>Chemical Communications</i> , 2013, 49, 910-912.	4.1	4
96	Genomic Analysis of Xylose Metabolism in Members of the <i>Deinococcus-Thermus</i> Phylum from Thermophilic Biomass-Deconstructing Bacterial Consortia. <i>Bioenergy Research</i> , 2015, 8, 1031-1038.	3.9	4
97	Adaptive evolution of <i>Methylotuvimicrobium alcaliphilum</i> to grow in the presence of rhamnolipids improves fatty acid and rhamnolipid production from CH ₄ . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2022, 49, .	3.0	4
98	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
99	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
100	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
101	A new path for one-carbon conversion. <i>Nature Metabolism</i> , 2021, 3, 1286-1287.	11.9	0