

Peter J Schaap

List of Publications by Year in descending order

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113
papers

6,216
citations

94269

37
h-index

82410

72
g-index

142
all docs

142
docs citations

142
times ranked

7787
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	9.4	1,047
2	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	2.4	329
3	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
4	RNA Targeting by the Type III-A CRISPR-Cas Csm Complex of <i>Thermus thermophilus</i> . <i>Molecular Cell</i> , 2014, 56, 518-530.	4.5	267
5	Structure and Activity of the RNA-Targeting Type III-B CRISPR-Cas Complex of <i>Thermus thermophilus</i> . <i>Molecular Cell</i> , 2013, 52, 135-145.	4.5	212
6	Genome-Scale Model and Omics Analysis of Metabolic Capacities of <i>Akkermansia muciniphila</i> Reveal a Preferential Mucin-Degrading Lifestyle. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	170
7	NG-Tax, a highly accurate and validated pipeline for analysis of 16S rRNA amplicons from complex biomes. <i>F1000Research</i> , 2016, 5, 1791.	0.8	140
8	NG-Tax, a highly accurate and validated pipeline for analysis of 16S rRNA amplicons from complex biomes. <i>F1000Research</i> , 2016, 5, 1791.	0.8	121
9	3DM: Systematic analysis of heterogeneous superfamily data to discover protein functionalities. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, NA-NA.	1.5	115
10	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. <i>BMC Genomics</i> , 2013, 14, 530.	1.2	111
11	A genomic view on syntrophic versus non-syntrophic lifestyle in anaerobic fatty acid degrading communities. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 2004-2016.	0.5	107
12	Oxaloacetate Hydrolase, the C-C Bond Lyase of Oxalate Secreting Fungi. <i>Journal of Biological Chemistry</i> , 2007, 282, 9581-9590.	1.6	102
13	Assessment of the pectin degrading enzyme network of <i>Aspergillus niger</i> by functional genomics. <i>Fungal Genetics and Biology</i> , 2009, 46, S170-S179.	0.9	102
14	NG-Tax 2.0: A Semantic Framework for High-Throughput Amplicon Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 1366.	1.1	95
15	An iterative workflow for mining the human intestinal metaproteome. <i>BMC Genomics</i> , 2011, 12, 6.	1.2	93
16	Comprehensive insights into transcriptional adaptation of intracellular mycobacteria by microbe-enriched dual RNA sequencing. <i>BMC Genomics</i> , 2015, 16, 34.	1.2	90
17	Deciphering the trophic interaction between <i>Akkermansia muciniphila</i> and the butyrogenic gut commensal <i>Anaerostipes caccae</i> using a metatranscriptomic approach. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 859-873.	0.7	90
18	Genomic and functional analysis of <i>Romboutsia ilealis</i> CRIB ^T reveals adaptation to the small intestine. <i>PeerJ</i> , 2017, 5, e3698.	0.9	88

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19	Identification of a Gatekeeper Residue That Prevents Dehydrogenases from Acting as Oxidases. <i>Journal of Biological Chemistry</i> , 2009, 284, 4392-4397.	1.6	83
20	Correlated mutation analyses on superfamily alignments reveal functionally important residues. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 608-616.	1.5	77
21	An evolutionary conserved d-galacturonic acid metabolic pathway operates across filamentous fungi capable of pectin degradation. <i>Fungal Genetics and Biology</i> , 2008, 45, 1449-1457.	0.9	74
22	An inventory of the <i>Aspergillus niger</i> secretome by combining in silico predictions with shotgun proteomics data. <i>BMC Genomics</i> , 2010, 11, 584.	1.2	74
23	Identification and functional characterization of novel xylose transporters from the cell factories <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 148.	6.2	71
24	Induction of glucose oxidase, catalase, and lactonase in <i>Aspergillus niger</i> . <i>Current Genetics</i> , 1993, 24, 408-416.	0.8	65
25	A new group of exo-acting family 28 glycoside hydrolases of <i>Aspergillus niger</i> that are involved in pectin degradation. <i>Biochemical Journal</i> , 2006, 400, 43-52.	1.7	62
26	Model-driven design of a minimal medium for <i>Akkermansia muciniphila</i> confirms mucus adaptation. <i>Microbial Biotechnology</i> , 2018, 11, 476-485.	2.0	57
27	Isolation of developmentally regulated genes from the edible mushroom <i>Agaricus bisporus</i> . <i>Microbiology (United Kingdom)</i> , 1997, 143, 1993-2001.	0.7	53
28	Green genes: bioinformatics and systems-biology innovations drive algal biotechnology. <i>Trends in Biotechnology</i> , 2014, 32, 617-626.	4.9	53
29	Comparison of 432 <i>Pseudomonas</i> strains through integration of genomic, functional, metabolic and expression data. <i>Scientific Reports</i> , 2016, 6, 38699.	1.6	53
30	Systems-level modeling of mycobacterial metabolism for the identification of new (multi-)drug targets. <i>Seminars in Immunology</i> , 2014, 26, 610-622.	2.7	49
31	Proteomic Analysis of the Secretary Response of <i>Aspergillus niger</i> to D-Maltose and D-Xylose. <i>PLoS ONE</i> , 2011, 6, e20865.	1.1	47
32	Regulation of Three Virulence Strategies of <i>Mycobacterium tuberculosis</i> : A Success Story. <i>International Journal of Molecular Sciences</i> , 2018, 19, 347.	1.8	46
33	Effects of Argonaute on Gene Expression in <i>Thermus thermophilus</i> . <i>PLoS ONE</i> , 2015, 10, e0124880.	1.1	44
34	SAPP: functional genome annotation and analysis through a semantic framework using FAIR principles. <i>Bioinformatics</i> , 2018, 34, 1401-1403.	1.8	44
35	Metabolic shift induced by synthetic co-cultivation promotes high yield of chain elongated acids from syngas. <i>Scientific Reports</i> , 2019, 9, 18081.	1.6	43
36	A chromosome-level assembly of the black tiger shrimp (<i>Penaeus monodon</i>) genome facilitates the identification of growth-associated genes. <i>Molecular Ecology Resources</i> , 2021, 21, 1620-1640.	2.2	43

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37	Genome analysis of <i>Desulfotomaculum kuznetsovii</i> strain 17T reveals a physiological similarity with <i>Pelotomaculum thermopropionicum</i> strain SIT.. <i>Standards in Genomic Sciences</i> , 2013, 8, 69-87.	1.5	42
38	Identification of a Novel L-rhamnose Uptake Transporter in the Filamentous Fungus <i>Aspergillus niger</i> . <i>PLoS Genetics</i> , 2016, 12, e1006468.	1.5	41
39	Different temporal and spatial expression of two hydrophobin-encoding genes of the edible mushroom <i>Agaricus bisporus</i> . <i>Microbiology (United Kingdom)</i> , 1999, 145, 1105-1113.	0.7	39
40	Shotgun Proteomics of <i>Aspergillus niger</i> Microsomes upon Xylose Induction. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4421-4429.	1.4	39
41	Comparative Genomics of <i>Streptococcus pyogenes</i> M1 isolates differing in virulence and propensity to cause systemic infection in mice. <i>International Journal of Medical Microbiology</i> , 2015, 305, 532-543.	1.5	37
42	<i>Neochloris oleoabundans</i> is worth its salt: Transcriptomic analysis under salt and nitrogen stress. <i>PLoS ONE</i> , 2018, 13, e0194834.	1.1	37
43	Improving heterologous membrane protein production in <i>Escherichia coli</i> by combining transcriptional tuning and codon usage algorithms. <i>PLoS ONE</i> , 2017, 12, e0184355.	1.1	37
44	Identification of methylated N-glycans in <i>Botryococcus brauni</i> . <i>New Phytologist</i> , 2017, 215, 1361-1369.	3.5	35
45	<i>Aspergillus niger</i> Secretes Citrate to Increase Iron Bioavailability. <i>Frontiers in Microbiology</i> , 2017, 8, 1424.	1.5	34
46	Lysine aminopeptidase of <i>Aspergillus niger</i> The EMBL accession number for the sequence reported in this paper is AJ292570.. <i>Microbiology (United Kingdom)</i> , 2001, 147, 2045-2050.	0.7	34
47	Genome Analysis and Physiological Comparison of <i>Alicyclophilus denitrificans</i> Strains BC and K601T. <i>PLoS ONE</i> , 2013, 8, e66971.	1.1	32
48	Studying microbial functionality within the gut ecosystem by systems biology. <i>Genes and Nutrition</i> , 2018, 13, 5.	1.2	31
49	Designing Eukaryotic Gene Expression Regulation Using Machine Learning. <i>Trends in Biotechnology</i> , 2020, 38, 191-201.	4.9	30
50	Modeling a co-culture of <i>Clostridium autoethanogenum</i> and <i>Clostridium kluyveri</i> to increase syngas conversion to medium-chain fatty-acids. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3255-3266.	1.9	29
51	Consistency, Inconsistency, and Ambiguity of Metabolite Names in Biochemical Databases Used for Genome-Scale Metabolic Modelling. <i>Metabolites</i> , 2019, 9, 28.	1.3	28
52	Characterisation of <i>Aspergillus niger</i> prolyl aminopeptidase. <i>Molecular Genetics and Genomics</i> , 2005, 272, 673-679.	1.0	27
53	Identification of fungal oxaloacetate hydrolyase within the isocitrate lyase/PEP mutase enzyme superfamily using a sequence marker-based method. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 157-166.	1.5	27
54	Overexpression of the <i>Aspergillus niger</i> GatA transporter leads to preferential use of D-galacturonic acid over D-xylose. <i>AMB Express</i> , 2014, 4, 66.	1.4	27

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55	Genome analysis of <i>Desulfotomaculum gibsoniae</i> strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. <i>Standards in Genomic Sciences</i> , 2014, 9, 821-839.	1.5	27
56	Description of <i>Trichococcus ilyis</i> sp. nov. by combined physiological and in silico genome hybridization analyses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3957-3963.	0.8	27
57	Comparative Genomics Highlights Symbiotic Capacities and High Metabolic Flexibility of the Marine Genus <i>Pseudovibrio</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 125-142.	1.1	26
58	<i>Aspergillus niger</i> citrate exporter revealed by comparison of two alternative citrate producing conditions. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	26
59	Genome analyses of the carboxydophilic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydivorans</i> and reclassification of <i>Desulfotomaculum caboxydivorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 655-675.	1.5	25
60	Draft genome sequence and characterization of <i>Desulfitobacterium hafniense</i> PCE-S. <i>Standards in Genomic Sciences</i> , 2015, 10, 15.	1.5	25
61	Unravelling the one-carbon metabolism of the acetogen <i>Sporomusa</i> strain A ₄ by genome and proteome analysis. <i>Environmental Microbiology</i> , 2016, 18, 2843-2855.	1.8	25
62	In silico-guided engineering of <i>Pseudomonas putida</i> towards growth under micro-oxic conditions. <i>Microbial Cell Factories</i> , 2019, 18, 179.	1.9	23
63	Functional Profiling of Unfamiliar Microbial Communities Using a Validated De Novo Assembly Metatranscriptome Pipeline. <i>PLoS ONE</i> , 2016, 11, e0146423.	1.1	23
64	Novel tools for extraction and validation of disease-related mutations applied to fabry disease. <i>Human Mutation</i> , 2010, 31, 1026-1032.	1.1	22
65	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DLT). <i>Standards in Genomic Sciences</i> , 2012, 7, 304-319.	1.5	22
66	From Innovation to Application: Bridging the Valley of Death in Industrial Biotechnology. <i>Trends in Biotechnology</i> , 2021, 39, 1240-1242.	4.9	22
67	Genome and proteome analysis of <i>Pseudomonas chloritidismutans</i> AW ^T that grows on <i>n</i> -decane with chlorate or oxygen as electron acceptor. <i>Environmental Microbiology</i> , 2016, 18, 3247-3257.	1.8	21
68	Modeling Host-Pathogen Interaction to Elucidate the Metabolic Drug Response of Intracellular <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 144.	1.8	21
69	Genome-guided analysis allows the identification of novel physiological traits in <i>Trichococcus</i> species. <i>BMC Genomics</i> , 2020, 21, 24.	1.2	21
70	A metabolic and physiological design study of <i>Pseudomonas putida</i> KT2440 capable of anaerobic respiration. <i>BMC Microbiology</i> , 2021, 21, 9.	1.3	20
71	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. <i>F1000Research</i> , 2016, 5, 1987.	0.8	20
72	<i>Monascus ruber</i> as cell factory for lactic acid production at low pH. <i>Metabolic Engineering</i> , 2017, 42, 66-73.	3.6	19

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73	Modeling the Metabolic State of <i>Mycobacterium tuberculosis</i> Upon Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 264.	1.8	19
74	Modulating D-amino acid oxidase (DAAO) substrate specificity through facilitated solvent access. <i>PLoS ONE</i> , 2018, 13, e0198990.	1.1	18
75	Genome-scale metabolic modeling underscores the potential of <i>Cutaneotrichosporon oleaginosus</i> ATCC 20509 as a cell factory for biofuel production. <i>Biotechnology for Biofuels</i> , 2021, 14, 2.	6.2	18
76	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. <i>F1000Research</i> , 2016, 5, 1987.	0.8	18
77	Complete Genome Sequence of <i>Akkermansia glycaniphila</i> Strain Pyt ^T , a Mucin-Degrading Specialist of the Reticulated Python Gut. <i>Genome Announcements</i> , 2017, 5, .	0.8	16
78	Concurrent Haloalkanoate Degradation and Chlorate Reduction by <i>Pseudomonas chloritidismutans</i> AW-1 ^T . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	16
79	Persistence of Functional Protein Domains in <i>Mycoplasma</i> Species and their Role in Host Specificity and Synthetic Minimal Life. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 31.	1.8	16
80	Time-dependent transcriptome profile of genes involved in triacylglycerol (TAG) and polyunsaturated fatty acid synthesis in <i>Nannochloropsis gaditana</i> during nitrogen starvation. <i>Journal of Applied Phycology</i> , 2020, 32, 1153-1164.	1.5	16
81	Metabolic modeling of energy balances in <i>Mycoplasma hyopneumoniae</i> shows that pyruvate addition increases growth rate. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2339-2347.	1.7	15
82	Metatranscriptome analysis of the microbial fermentation of dietary milk proteins in the murine gut. <i>PLoS ONE</i> , 2018, 13, e0194066.	1.1	14
83	A protocol for adding knowledge to Wikidata: aligning resources on human coronaviruses. <i>BMC Biology</i> , 2021, 19, 12.	1.7	14
84	Comparative proteomics of <i>Rhizopus delemar</i> ATCC 20344 unravels the role of amino acid catabolism in fumarate accumulation. <i>PeerJ</i> , 2017, 5, e3133.	0.9	14
85	Structure and Function of 2,3-Dimethylmalate Lyase, a PEP Mutase/Isocitrate Lyase Superfamily Member. <i>Journal of Molecular Biology</i> , 2009, 386, 486-503.	2.0	13
86	Metabolic response of <i>Alicyclophilus denitrificans</i> strain BC toward electron acceptor variation. <i>Proteomics</i> , 2013, 13, 2886-2894.	1.3	13
87	Integration of heterogeneous molecular networks to unravel gene-regulation in <i>Mycobacterium tuberculosis</i> . <i>BMC Systems Biology</i> , 2014, 8, 111.	3.0	13
88	RDF2Graph a tool to recover, understand and validate the ontology of an RDF resource. <i>Journal of Biomedical Semantics</i> , 2015, 6, 39.	0.9	13
89	Complete genome sequence of thermophilic <i>Bacillus smithii</i> type strain DSM 4216T. <i>Standards in Genomic Sciences</i> , 2016, 11, 52.	1.5	13
90	Forward Genetics by Genome Sequencing Uncovers the Central Role of the <i>Aspergillus niger</i> <i>goxB</i> Locus in Hydrogen Peroxide Induced Glucose Oxidase Expression. <i>Frontiers in Microbiology</i> , 2018, 9, 2269.	1.5	13

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91	The Empusa code generator and its application to GBOL, an extendable ontology for genome annotation. <i>Scientific Data</i> , 2019, 6, 254.	2.4	13
92	Aminopeptidase C of <i>Aspergillus niger</i> Is a Novel Phenylalanine Aminopeptidase. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1246-1250.	1.4	12
93	CorNet: Assigning function to networks of co-evolving residues by automated literature mining. <i>PLoS ONE</i> , 2017, 12, e0176427.	1.1	12
94	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. <i>F1000Research</i> , 0, 5, 1987.	0.8	12
95	Distant Non-Obvious Mutations Influence the Activity of a Hyperthermophilic <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase. <i>Biomolecules</i> , 2019, 9, 212.	1.8	11
96	Toxicological response of the model fungus <i>Saccharomyces cerevisiae</i> to different concentrations of commercial graphene nanoplatelets. <i>Scientific Reports</i> , 2020, 10, 3232.	1.6	11
97	Genomic convergence between <i>Akkermansia muciniphila</i> in different mammalian hosts. <i>BMC Microbiology</i> , 2021, 21, 298.	1.3	10
98	Characterisation of the <i>Aspergillus niger</i> <i>dapB</i> gene, which encodes a novel fungal type IV dipeptidyl aminopeptidase. <i>Molecular Genetics and Genomics</i> , 2005, 273, 319-325.	1.0	9
99	Proteomic analysis of nitrate-dependent acetone degradation by <i>Alicyclophilus denitrificans</i> strain BC. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	9
100	The diurnal transcriptional landscape of the microalga <i>Tetrademus obliquus</i> . <i>Algal Research</i> , 2019, 40, 101477.	2.4	9
101	Assessing the Metabolic Diversity of <i>Streptococcus</i> from a Protein Domain Point of View. <i>PLoS ONE</i> , 2015, 10, e0137908.	1.1	8
102	Risk-Based Bioengineering Strategies for Reliable Bacterial Vaccine Production. <i>Trends in Biotechnology</i> , 2019, 37, 805-816.	4.9	8
103	Genome-scale metabolic modelling enables deciphering ethanol metabolism via the acrylate pathway in the propionate-producer <i>Anaerostignum neopropionicum</i> . <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	8
104	Global Transcriptional Response of <i>Aspergillus niger</i> to Blocked Active Citrate Export through Deletion of the Exporter Gene. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 409.	1.5	7
105	Classification of the plant-associated lifestyle of <i>Pseudomonas</i> strains using genome properties and machine learning. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
106	Experimental infrastructure requirements for quantitative research on microbial communities. <i>Current Opinion in Biotechnology</i> , 2021, 67, 158-165.	3.3	6
107	Machine learning approaches to predict the Plant-associated phenotype of <i>Xanthomonas</i> strains. <i>BMC Genomics</i> , 2021, 22, 848.	1.2	6
108	Navigating the Valley of Death: Perceptions of Industry and Academia on Production Platforms and Opportunities in Biotechnology. <i>EFB Bioeconomy Journal</i> , 2022, 2, 100033.	1.1	5

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109	Combined Transcriptome Sequencing of <i>Mycoplasma hyopneumoniae</i> and Infected Pig Lung Tissue Reveals Up-Regulation of Bacterial F1-Like ATPase and Down-Regulation of the P102 Cilium Adhesin in vivo. <i>Frontiers in Microbiology</i> , 2020, 11, 1679.	1.5	4
110	SALARECON connects the Atlantic salmon genome to growth and feed efficiency. <i>PLoS Computational Biology</i> , 2022, 18, e1010194.	1.5	4
111	Assembly and Comparison of <i>Ca. Neoehrlichia mikurensis</i> Genomes. <i>Microorganisms</i> , 2022, 10, 1134.	1.6	3
112	Algal Omics: The Functional Annotation Challenge. <i>Current Biotechnology</i> , 2016, 4, 457-463.	0.2	2
113	Evaluation of diurnal responses of <i>Tetrademus obliquus</i> under nitrogen limitation. <i>Algal Research</i> , 2020, 49, 101937.	2.4	0