

# Vitor A P Martins Dos Santos

## List of Publications by Year in descending order

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122  
papers

5,378  
citations

94269

37  
h-index

102304

66  
g-index

145  
all docs

145  
docs citations

145  
times ranked

8022  
citing authors

#	ARTICLE	IF	CITATIONS
1	Enzyme-constrained models predict the dynamics of <i>Saccharomyces cerevisiae</i> growth in continuous, batch and fed-batch bioreactors. <i>Microbial Biotechnology</i> , 2022, 15, 1434-1445.	2.0	18
2	Insights Into the Peroxisomal Protein Inventory of Zebrafish. <i>Frontiers in Physiology</i> , 2022, 13, 822509.	1.3	8
3	Production of indole by <i>Corynebacterium glutamicum</i> microbial cell factories for flavor and fragrance applications. <i>Microbial Cell Factories</i> , 2022, 21, 45.	1.9	19
4	Effects of Human RelA Transgene on Murine Macrophage Inflammatory Responses. <i>Biomedicines</i> , 2022, 10, 757.	1.4	0
5	A genetic toolkit and gene switches to limit <i>Mycoplasma</i> growth for biosafety applications. <i>Nature Communications</i> , 2022, 13, 1910.	5.8	10
6	Microbial production of medium-chain-length $\pm$ , $\gamma$ -diols via two-stage process under mild conditions. <i>Bioresource Technology</i> , 2022, 352, 127111.	4.8	4
7	Analysis of host-pathogen gene association networks reveals patient-specific response to streptococcal and polymicrobial necrotising soft tissue infections. <i>BMC Medicine</i> , 2022, 20, 173.	2.3	3
8	Genome-scale metabolic modelling enables deciphering ethanol metabolism via the acrylate pathway in the propionate-producer <i>Anaerotignum neopropionicum</i> . <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	8
9	Easy Semantification of Bioassays. <i>Lecture Notes in Computer Science</i> , 2022, , 198-212.	1.0	1
10	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
11	Disease Activity Patterns of Crohn's Disease in the First Ten Years After Diagnosis in the Population-based IBD South Limburg Cohort. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 391-400.	0.6	25
12	Phenotype and multi-omics comparison of <i>Staphylococcus</i> and <i>Streptococcus</i> uncovers pathogenic traits and predicts zoonotic potential. <i>BMC Genomics</i> , 2021, 22, 102.	1.2	6
13	Model reduction of genome-scale metabolic models as a basis for targeted kinetic models. <i>Metabolic Engineering</i> , 2021, 64, 74-84.	3.6	20
14	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
15	Galactocerebroside biosynthesis pathways of <i>Mycoplasma</i> species: an antigen triggering Guillain-Barré-Stohl syndrome. <i>Microbial Biotechnology</i> , 2021, 14, 1201-1211.	2.0	5
16	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
17	From Innovation to Application: Bridging the Valley of Death in Industrial Biotechnology. <i>Trends in Biotechnology</i> , 2021, 39, 1240-1242.	4.9	22
18	In-Pero: Exploiting Deep Learning Embeddings of Protein Sequences to Predict the Localisation of Peroxisomal Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6409.	1.8	14

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19	Discriminatory plasma biomarkers predict specific clinical phenotypes of necrotizing soft-tissue infections. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	7
20	A navigation guide of synthetic biology tools for <i>Pseudomonas putida</i> . <i>Biotechnology Advances</i> , 2021, 49, 107732.	6.0	48
21	ReScribe: An Unrestrained Tool Combining Multiplex Recombineering and Minimal-PAM ScCas9 for Genome Recoding <i>Pseudomonas putida</i> . <i>ACS Synthetic Biology</i> , 2021, 10, 2672-2688.	1.9	7
22	Context matters. <i>EMBO Reports</i> , 2021, 22, e51227.	2.0	9
23	When metabolic prowess is too much of a good thing: how carbon catabolite repression and metabolic versatility impede production of esterified 1,3-diols in <i>Pseudomonas putida</i> KT2440. <i>Biotechnology for Biofuels</i> , 2021, 14, 218.	6.2	7
24	Exploring the associations between transcript levels and fluxes in constraint-based models of metabolism. <i>BMC Bioinformatics</i> , 2021, 22, 574.	1.2	2
25	Integrated Univariate, Multivariate, and Correlation-Based Network Analyses Reveal Metabolite-Specific Effects on Bacterial Growth and Biofilm Formation in Necrotizing Soft Tissue Infections. <i>Journal of Proteome Research</i> , 2020, 19, 688-698.	1.8	16
26	Modeling a co-culture of <i>Clostridium autoethanogenum</i> and <i>Clostridium kluveri</i> to increase syngas conversion to medium-chain fatty-acids. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3255-3266.	1.9	29
27	SEVA 3.1: enabling interoperability of DNA assembly among the SEVA, BioBricks and Type IIS restriction enzyme standards. <i>Microbial Biotechnology</i> , 2020, 13, 1793-1806.	2.0	26
28	Combined Transcriptome Sequencing of <i>Mycoplasma hypopneumoniae</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
29	Model-driven design allows growth of <i>Mycoplasma pneumoniae</i> on serum-free media. <i>Npj Systems Biology and Applications</i> , 2020, 6, 33.	1.4	18
30	Using systems medicine to identify a therapeutic agent with potential for repurposing in inflammatory bowel disease. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	9
31	Evaluation of diurnal responses of <i>Tetrademus obliquus</i> under nitrogen limitation. <i>Algal Research</i> , 2020, 49, 101937.	2.4	0
32	Systems and Precision Medicine in Necrotizing Soft Tissue Infections. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1294, 187-207.	0.8	1
33	Genetic Safeguards for Safety-by-design: So Close Yet So Far. <i>Trends in Biotechnology</i> , 2020, 38, 1308-1312.	4.9	18
34	An expanded CRISPRi toolbox for tunable control of gene expression in <i>Pseudomonas putida</i> . <i>Microbial Biotechnology</i> , 2020, 13, 368-385.	2.0	48
35	Representing Semantified Biological Assays in the Open Research Knowledge Graph. <i>Lecture Notes in Computer Science</i> , 2020, , 89-98.	1.0	3
36	Patient's characteristics and outcomes in necrotising soft-tissue infections: results from a Scandinavian, multicentre, prospective cohort study. <i>Intensive Care Medicine</i> , 2019, 45, 1241-1251.	3.9	82

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37	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
38	<i>Pseudomonas putida</i> KT2440 is HV1 certified, not GRAS. <i>Microbial Biotechnology</i> , 2019, 12, 845-848.	2.0	56
39	Macrophage-Specific NF- $\kappa$ B Activation Dynamics Can Segregate Inflammatory Bowel Disease Patients. <i>Frontiers in Immunology</i> , 2019, 10, 2168.	2.2	31
40	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
41	<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
42	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
43	The diurnal transcriptional landscape of the microalga <i>Tetrademus obliquus</i> . <i>Algal Research</i> , 2019, 40, 101477.	2.4	9
44	Metabolomics in systems medicine: an overview of methods and applications. <i>Current Opinion in Systems Biology</i> , 2019, 15, 91-99.	1.3	9
45	Risk-Based Bioengineering Strategies for Reliable Bacterial Vaccine Production. <i>Trends in Biotechnology</i> , 2019, 37, 805-816.	4.9	8
46	High-level integration of murine intestinal transcriptomics data highlights the importance of the complement system in mucosal homeostasis. <i>BMC Genomics</i> , 2019, 20, 1028.	1.2	14
47	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
48	Cofactors revisited – Predicting the impact of flavoprotein-related diseases on a genome scale. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 360-370.	1.8	10
49	From correlation to causation: analysis of metabolomics data using systems biology approaches. <i>Metabolomics</i> , 2018, 14, 37.	1.4	151
50	Recommended strategies for spectral processing and post-processing of 1D 1H-NMR data of biofluids with a particular focus on urine. <i>Metabolomics</i> , 2018, 14, 31.	1.4	107
51	Studying microbial functionality within the gut ecosystem by systems biology. <i>Genes and Nutrition</i> , 2018, 13, 5.	1.2	31
52	Genome sequence of two members of the chloroaromatic-degrading MT community: <i>Pseudomonas reinekei</i> MT1 and <i>Achromobacter xylooxidans</i> MT3. <i>Journal of Biotechnology</i> , 2018, 275, 13-16.	1.9	0
53	SyNDI: synchronous network data integration framework. <i>BMC Bioinformatics</i> , 2018, 19, 403.	1.2	1
54	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

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55	Neochloris oleoabundans is worth its salt: Transcriptomic analysis under salt and nitrogen stress. PLoS ONE, 2018, 13, e0194834.	1.1	37
56	Regulation of Three Virulence Strategies of Mycobacterium tuberculosis: A Success Story. International Journal of Molecular Sciences, 2018, 19, 347.	1.8	46
57	SAPP: functional genome annotation and analysis through a semantic framework using FAIR principles. Bioinformatics, 2018, 34, 1401-1403.	1.8	44
58	DMPy: a Python package for automated mathematical model construction of large-scale metabolic systems. BMC Systems Biology, 2018, 12, 72.	3.0	16
59	Modulating D-amino acid oxidase (DAAO) substrate specificity through facilitated solvent access. PLoS ONE, 2018, 13, e0198990.	1.1	18
60	Metabolic modeling of energy balances in <i>Mycoplasma hyopneumoniae</i> shows that pyruvate addition increases growth rate. Biotechnology and Bioengineering, 2017, 114, 2339-2347.	1.7	15
61	Predicting the murine enterocyte metabolic response to diets that differ in lipid and carbohydrate composition. Scientific Reports, 2017, 7, 8784.	1.6	12
62	More than just a gut feeling: constraint-based genome-scale metabolic models for predicting functions of human intestinal microbes. Microbiome, 2017, 5, 78.	4.9	54
63	Identification of methylated GnTII-dependent N-glycans in <i>Botryococcus brauni</i> . New Phytologist, 2017, 215, 1361-1369.	3.5	35
64	Use of Microarray Datasets to generate Caco-2-dedicated Networks and to identify Reporter Genes of Specific Pathway Activity. Scientific Reports, 2017, 7, 6778.	1.6	7
65	Genome-Scale Model and Omics Analysis of Metabolic Capacities of <i>Akkermansia muciniphila</i> Reveal a Preferential Mucin-Degrading Lifestyle. Applied and Environmental Microbiology, 2017, 83, .	1.4	170
66	Multi-Level Integration of Environmentally Perturbed Internal Phenotypes Reveals Key Points of Connectivity between Them. Frontiers in Physiology, 2017, 8, 388.	1.3	4
67	Persistence of Functional Protein Domains in Mycoplasma Species and their Role in Host Specificity and Synthetic Minimal Life. Frontiers in Cellular and Infection Microbiology, 2017, 7, 31.	1.8	16
68	Aspergillus niger Secretes Citrate to Increase Iron Bioavailability. Frontiers in Microbiology, 2017, 8, 1424.	1.5	34
69	Comparative proteomics of <i>Rhizopus delemar</i> ATCC 20344 unravels the role of amino acid catabolism in fumarate accumulation. PeerJ, 2017, 5, e3133.	0.9	14
70	Genomic and functional analysis of <i>Romboutsia ilealis</i> CRIB <sup>T</sup> reveals adaptation to the small intestine. PeerJ, 2017, 5, e3698.	0.9	88
71	Identification and functional characterization of novel xylose transporters from the cell factories <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> . Biotechnology for Biofuels, 2016, 9, 148.	6.2	71
72	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. Npj Systems Biology and Applications, 2016, 2, 16011.	1.4	21

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73	Efficient Reconstruction of Predictive Consensus Metabolic Network Models. PLoS Computational Biology, 2016, 12, e1005085.	1.5	19
74	Identification of a Novel L-rhamnose Uptake Transporter in the Filamentous Fungus <i>Aspergillus niger</i> . PLoS Genetics, 2016, 12, e1006468.	1.5	41
75	Integrated In Silico Analysis of Pathway Designs for Synthetic Photo-Electro-Autotrophy. PLoS ONE, 2016, 11, e0157851.	1.1	9
76	Comparison of 432 <i>Pseudomonas</i> strains through integration of genomic, functional, metabolic and expression data. Scientific Reports, 2016, 6, 38699.	1.6	53
77	Harnessing the power of microbial autotrophy. Nature Reviews Microbiology, 2016, 14, 692-706.	13.6	189
78	The revisited genome of <i>Pseudomonas putida</i> KT2440 enlightens its value as a robust metabolic chassis. Environmental Microbiology, 2016, 18, 3403-3424.	1.8	270
79	Characterizing the optimal flux space of genome-scale metabolic reconstructions through modified latin-hypercube sampling. Molecular BioSystems, 2016, 12, 994-1005.	2.9	2
80	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. F1000Research, 2016, 5, 1987.	0.8	20
81	Functional Profiling of Unfamiliar Microbial Communities Using a Validated De Novo Assembly Metatranscriptome Pipeline. PLoS ONE, 2016, 11, e0146423.	1.1	23
82	Genotypic and phenotypic analyses of a <i>Pseudomonas aeruginosa</i> chronic bronchiectasis isolate reveal differences from cystic fibrosis and laboratory strains. BMC Genomics, 2015, 16, 883.	1.2	30
83	RDF2Graph a tool to recover, understand and validate the ontology of an RDF resource. Journal of Biomedical Semantics, 2015, 6, 39.	0.9	13
84	Assessing the Metabolic Diversity of <i>Streptococcus</i> from a Protein Domain Point of View. PLoS ONE, 2015, 10, e0137908.	1.1	8
85	Comprehensive insights into transcriptional adaptation of intracellular mycobacteria by microbe-enriched dual RNA sequencing. BMC Genomics, 2015, 16, 34.	1.2	90
86	Network analysis of temporal functionalities of the gut induced by perturbations in new-born piglets. BMC Genomics, 2015, 16, 556.	1.2	23
87	Effects of $\beta$ -Lactam Antibiotics and Fluoroquinolones on Human Gut Microbiota in Relation to <i>Clostridium difficile</i> Associated Diarrhea. PLoS ONE, 2014, 9, e89417.	1.1	61
88	Gut microbiota disturbance during antibiotic therapy. Gut Microbes, 2014, 5, 64-70.	4.3	83
89	Systems-level modeling of mycobacterial metabolism for the identification of new (multi-)drug targets. Seminars in Immunology, 2014, 26, 610-622.	2.7	49
90	Microbial stratification in low pH oxic and suboxic macroscopic growths along an acid mine drainage. ISME Journal, 2014, 8, 1259-1274.	4.4	105

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91	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
92	Green genes: bioinformatics and systems-biology innovations drive algal biotechnology. <i>Trends in Biotechnology</i> , 2014, 32, 617-626.	4.9	53
93	Understanding the antimicrobial mechanism of TiO <sub>2</sub> -based nanocomposite films in a pathogenic bacterium. <i>Scientific Reports</i> , 2014, 4, 4134.	1.6	335
94	From the Environment to the Host: Re-Wiring of the Transcriptome of <i>Pseudomonas aeruginosa</i> from 22°C to 37°C. <i>PLoS ONE</i> , 2014, 9, e89941.	1.1	35
95	Protoanemonin: a natural quorum sensing inhibitor that selectively activates iron starvation response. <i>Environmental Microbiology</i> , 2013, 15, 111-120.	1.8	39
96	Potential of proton-pumping rhodopsins: engineering photosystems into microorganisms. <i>Trends in Biotechnology</i> , 2013, 31, 633-642.	4.9	23
97	Design and analysis of a tunable synchronized oscillator. <i>Journal of Biological Engineering</i> , 2013, 7, 26.	2.0	9
98	In-silico-driven metabolic engineering of <i>Pseudomonas putida</i> for enhanced production of poly-hydroxyalkanoates. <i>Metabolic Engineering</i> , 2013, 15, 113-123.	3.6	160
99	<i>Ex vivo</i> transcriptional profiling reveals a common set of genes important for the adaptation of <i>Pseudomonas aeruginosa</i> to chronically infected host sites. <i>Environmental Microbiology</i> , 2013, 15, 570-587.	1.8	41
100	Functional consequences of microbial shifts in the human gastrointestinal tract linked to antibiotic treatment and obesity. <i>Gut Microbes</i> , 2013, 4, 306-315.	4.3	81
101	Dissecting the energy metabolism in <i>Mycoplasma pneumoniae</i> through genome-scale metabolic modeling. <i>Molecular Systems Biology</i> , 2013, 9, 653.	3.2	69
102	Reconciling in vivo and in silico key biological parameters of <i>Pseudomonas putida</i> KT2440 during growth on glucose under carbon-limited condition. <i>BMC Biotechnology</i> , 2013, 13, 93.	1.7	48
103	Streamlining genomes: toward the generation of simplified and stabilized microbial systems. <i>Current Opinion in Biotechnology</i> , 2012, 23, 651-658.	3.3	31
104	Streamlining of a <i>Pseudomonas putida</i> Genome Using a Combinatorial Deletion Method Based on Minitransposon Insertion and the Flp-FRT Recombination System. <i>Methods in Molecular Biology</i> , 2012, 813, 249-266.	0.4	13
105	Modeling and analysis of flux distributions in the two branches of the phosphotransferase system in <i>Pseudomonas putida</i> . <i>BMC Systems Biology</i> , 2012, 6, 149.	3.0	5
106	Programmable bacterial catalysis – designing cells for biosynthesis of value-added compounds. <i>FEBS Letters</i> , 2012, 586, 2184-2190.	1.3	12
107	Random and cyclical deletion of large DNA segments in the genome of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2012, 14, 1444-1453.	1.8	56
108	High-stat fed-batch process to enhance the production of cis-, cis-µconate from benzoate by <i>Pseudomonas putida</i> KT2440-ΔD1. <i>Biotechnology Progress</i> , 2012, 28, 85-92.	1.3	57

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109	Industrial biotechnology of <i>Pseudomonas putida</i> and related species. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 2279-2290.	1.7	290
110	The <i>logicome</i> of environmental bacteria: merging catabolic and regulatory events with Boolean formalisms. <i>Environmental Microbiology</i> , 2011, 13, 2389-2402.	1.8	36
111	Reconciliation of Genome-Scale Metabolic Reconstructions for Comparative Systems Analysis. <i>PLoS Computational Biology</i> , 2011, 7, e1001116.	1.5	111
112	In-Vivo Expression Profiling of <i>Pseudomonas aeruginosa</i> Infections Reveals Niche-Specific and Strain-Independent Transcriptional Programs. <i>PLoS ONE</i> , 2011, 6, e24235.	1.1	53
113	The regulatory logic of <i>xy</i> xylene biodegradation by <i>Pseudomonas putida</i> exposed by dynamic modelling of the principal node <i>Ps/Pr</i> of the TOL plasmid. <i>Environmental Microbiology</i> , 2010, 12, 1705-1718.	1.8	38
114	Systems biology of the gut: the interplay of food, microbiota and host at the mucosal interface. <i>Current Opinion in Biotechnology</i> , 2010, 21, 539-550.	3.3	62
115	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
116	(Re)construction, characterization and modeling of systems for synthetic biology. <i>Biotechnology Journal</i> , 2009, 4, 1382-1391.	1.8	8
117	Genome-Scale Metabolic Network Analysis of the Opportunistic Pathogen <i>Pseudomonas aeruginosa</i> PAO1. <i>Journal of Bacteriology</i> , 2008, 190, 2790-2803.	1.0	283
118	Genome-Scale Reconstruction and Analysis of the <i>Pseudomonas putida</i> KT2440 Metabolic Network Facilitates Applications in Biotechnology. <i>PLoS Computational Biology</i> , 2008, 4, e1000210.	1.5	237
119	Nonmedical: <i>Pseudomonas</i> . , 2006, , 646-703.		107
120	Relevance of rheological properties of gel beads for their mechanical stability in bioreactors. , 1997, 56, 517-529.		47
121	Relevance of rheological properties of gel beads for their mechanical stability in bioreactors. , 1997, 56, 517.		2
122	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