

David Vallenet

List of Publications by Year in descending order

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77
papers

10,475
citations

53794

45
h-index

76900

74
g-index

85
all docs

85
docs citations

85
times ranked

12383
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	27.8	1,075
2	Organised Genome Dynamics in the <i>Escherichia coli</i> Species Results in Highly Diverse Adaptive Paths. <i>PLoS Genetics</i> , 2009, 5, e1000344.	3.5	1,005
3	Comparative Genomics of Multidrug Resistance in <i>Acinetobacter baumannii</i> . <i>PLoS Genetics</i> , 2006, 2, e7.	3.5	677
4	Legumes Symbioses: Absence of Nod Genes in Photosynthetic Bradyrhizobia. <i>Science</i> , 2007, 316, 1307-1312.	12.6	557
5	MicroScope—an integrated microbial resource for the curation and comparative analysis of genomic and metabolic data. <i>Nucleic Acids Research</i> , 2013, 41, D636-D647.	14.5	406
6	MaGe: a microbial genome annotation system supported by synteny results. <i>Nucleic Acids Research</i> , 2006, 34, 53-65.	14.5	375
7	Coping with cold: The genome of the versatile marine Antarctica bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Genome Research</i> , 2005, 15, 1325-1335.	5.5	367
8	Genome characteristics of facultatively symbiotic <i>Frankia</i> sp. strains reflect host range and host plant biogeography. <i>Genome Research</i> , 2006, 17, 7-15.	5.5	352
9	From a consortium sequence to a unified sequence: the <i>Bacillus subtilis</i> 168 reference genome a decade later. <i>Microbiology (United Kingdom)</i> , 2009, 155, 1758-1775.	1.8	317
10	Genome Sequences of <i>Escherichia coli</i> B strains REL606 and BL21(DE3). <i>Journal of Molecular Biology</i> , 2009, 394, 644-652.	4.2	316
11	Comparative Analysis of <i>Acinetobacters</i> : Three Genomes for Three Lifestyles. <i>PLoS ONE</i> , 2008, 3, e1805.	2.5	315
12	Unique features revealed by the genome sequence of <i>Acinetobacter</i> sp. ADP1, a versatile and naturally transformation competent bacterium. <i>Nucleic Acids Research</i> , 2004, 32, 5766-5779.	14.5	308
13	A complete collection of single-gene deletion mutants of <i>Acinetobacter baylyi</i> ADP1. <i>Molecular Systems Biology</i> , 2008, 4, 174.	7.2	289
14	The revisited genome of <i>Pseudomonas putida</i> KT2440 enlightens its value as a robust metabolic chassis. <i>Environmental Microbiology</i> , 2016, 18, 3403-3424.	3.8	270
15	Complete genome sequence of the entomopathogenic and metabolically versatile soil bacterium <i>Pseudomonas entomophila</i> . <i>Nature Biotechnology</i> , 2006, 24, 673-679.	17.5	261
16	<i>Methylobacterium</i> Genome Sequences: A Reference Blueprint to Investigate Microbial Metabolism of C1 Compounds from Natural and Industrial Sources. <i>PLoS ONE</i> , 2009, 4, e5584.	2.5	204
17	MicroScope in 2017: an expanding and evolving integrated resource for community expertise of microbial genomes. <i>Nucleic Acids Research</i> , 2017, 45, D517-D528.	14.5	199
18	Metabolic diversity among main microorganisms inside an arsenic-rich ecosystem revealed by meta- and proteo-genomics. <i>ISME Journal</i> , 2011, 5, 1735-1747.	9.8	186

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19	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53.	3.5	166
20	MicroScope: an integrated platform for the annotation and exploration of microbial gene functions through genomic, pangenomic and metabolic comparative analysis. <i>Nucleic Acids Research</i> , 2020, 48, D579-D589.	14.5	166
21	Comparative genomics of the core and accessory genomes of 48 <i>Sinorhizobium</i> strains comprising five genospecies. <i>Genome Biology</i> , 2013, 14, R17.	9.6	164
22	Reannotation of the genome sequence of <i>Clostridium difficile</i> strain 630. <i>Journal of Medical Microbiology</i> , 2011, 60, 1193-1199.	1.8	143
23	Carrageenan catabolism is encoded by a complex regulon in marine heterotrophic bacteria. <i>Nature Communications</i> , 2017, 8, 1685.	12.8	131
24	AMIGene: Annotation of Microbial Genes. <i>Nucleic Acids Research</i> , 2003, 31, 3723-3726.	14.5	126
25	The <i>Frankia alni</i> Symbiotic Transcriptome. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 593-607.	2.6	126
26	Revealing the hidden functional diversity of an enzyme family. <i>Nature Chemical Biology</i> , 2014, 10, 42-49.	8.0	113
27	Channel Formation by CarO, the Carbapenem Resistance-Associated Outer Membrane Protein of <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4876-4883.	3.2	111
28	<i>Ralstonia syzygii</i> , the Blood Disease Bacterium and Some Asian <i>R. solanacearum</i> Strains Form a Single Genomic Species Despite Divergent Lifestyles. <i>PLoS ONE</i> , 2011, 6, e24356.	2.5	110
29	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. <i>PLoS Computational Biology</i> , 2020, 16, e1007732.	3.2	102
30	<i>Bacillus subtilis</i> , the model Gram-positive bacterium: 20 years of annotation refinement. <i>Microbial Biotechnology</i> , 2018, 11, 3-17.	4.2	95
31	NeMeSys: a biological resource for narrowing the gap between sequence and function in the human pathogen <i>Neisseria meningitidis</i> . <i>Genome Biology</i> , 2009, 10, R110.	9.6	86
32	Global Comparison of the Membrane Subproteomes between a Multidrug-Resistant <i>Acinetobacter baumannii</i> Strain and a Reference Strain. <i>Journal of Proteome Research</i> , 2006, 5, 3385-3398.	3.7	80
33	Iterative reconstruction of a global metabolic model of <i>Acinetobacter baylyi</i> ADP1 using high-throughput growth phenotype and gene essentiality data. <i>BMC Systems Biology</i> , 2008, 2, 85.	3.0	73
34	An updated metabolic view of the <i>Bacillus subtilis</i> 168 genome. <i>Microbiology (United Kingdom)</i> , 2013, 159, 757-770.	1.8	72
35	MicroScope – an integrated resource for community expertise of gene functions and comparative analysis of microbial genomic and metabolic data. <i>Briefings in Bioinformatics</i> , 2019, 20, 1071-1084.	6.5	71
36	Identification of the Last Unknown Genes in the Fermentation Pathway of Lysine*. <i>Journal of Biological Chemistry</i> , 2007, 282, 7191-7197.	3.4	62

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37	RNA Sequencing and Proteogenomics Reveal the Importance of Leaderless mRNAs in the Radiation-Tolerant Bacterium <i>Deinococcus deserti</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 932-948.	2.5	61
38	Life in an Arsenic-Containing Gold Mine: Genome and Physiology of the Autotrophic Arsenite-Oxidizing Bacterium <i>Rhizobium</i> sp. NT-26. <i>Genome Biology and Evolution</i> , 2013, 5, 934-953.	2.5	60
39	A Conserved Gene Cluster Rules Anaerobic Oxidative Degradation of <i>l</i> -Ornithine. <i>Journal of Bacteriology</i> , 2009, 191, 3162-3167.	2.2	58
40	Complete Genome Sequence of <i>Streptomyces cattleya</i> NRRL 8057, a Producer of Antibiotics and Fluorometabolites. <i>Journal of Bacteriology</i> , 2011, 193, 5055-5056.	2.2	58
41	Ectosymbiotic bacteria at the origin of magnetoreception in a marine protist. <i>Nature Microbiology</i> , 2019, 4, 1088-1095.	13.3	57
42	MICheck: a web tool for fast checking of syntactic annotations of bacterial genomes. <i>Nucleic Acids Research</i> , 2005, 33, W471-W479.	14.5	54
43	Large-Scale Transposon Mutagenesis of Photosynthetic <i>Bradyrhizobium</i> Sp. Strain ORS278 Reveals New Genetic Loci Putatively Important for Nod-Independent Symbiosis with <i>Aeschynomene indica</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 760-770.	2.6	54
44	Evolutionary Evidence of Algal Polysaccharide Degradation Acquisition by <i>Pseudoalteromonas carrageenovora</i> 9T to Adapt to Macroalgal Niches. <i>Frontiers in Microbiology</i> , 2018, 9, 2740.	3.5	54
45	Core and Panmetabolism in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1461-1472.	2.2	51
46	<i>Frankia alni</i> proteome under nitrogen-fixing and nitrogen-replete conditions. <i>Physiologia Plantarum</i> , 2007, 130, 440-453.	5.2	45
47	Profiling the orphan enzymes. <i>Biology Direct</i> , 2014, 9, 10.	4.6	43
48	Conservation and diversity of the <i>IrrE/DdrO</i> -controlled radiation response in radiation-resistant <i>Deinococcus</i> bacteria. <i>MicrobiologyOpen</i> , 2017, 6, e00477.	3.0	37
49	Phylogroup stability contrasts with high within sequence type complex dynamics of <i>Escherichia coli</i> bloodstream infection isolates over a 12-year period. <i>Genome Medicine</i> , 2021, 13, 77.	8.2	35
50	The CanOE Strategy: Integrating Genomic and Metabolic Contexts across Multiple Prokaryote Genomes to Find Candidate Genes for Orphan Enzymes. <i>PLoS Computational Biology</i> , 2012, 8, e1002540.	3.2	32
51	Ancestral Genome Estimation Reveals the History of Ecological Diversification in <i>Agrobacterium</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3413-3431.	2.5	31
52	Comparative Genomics of <i>Aeschynomene</i> Symbionts: Insights into the Ecological Lifestyle of Nod-Independent Photosynthetic <i>Bradyrhizobia</i> . <i>Genes</i> , 2012, 3, 35-61.	2.4	30
53	Parallel evolution of non-homologous isofunctional enzymes in methionine biosynthesis. <i>Nature Chemical Biology</i> , 2017, 13, 858-866.	8.0	29
54	panRGP: a pangenome-based method to predict genomic islands and explore their diversity. <i>Bioinformatics</i> , 2020, 36, i651-i658.	4.1	26

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55	Transcriptome Profiles of Nod Factor-independent Symbiosis in the Tropical Legume <i>Aeschynomene evenia</i> . <i>Scientific Reports</i> , 2018, 8, 10934.	3.3	23
56	The <i>Nocardia cyriacigeorgica</i> GUH-2 genome shows ongoing adaptation of an environmental Actinobacteria to a pathogen's lifestyle. <i>BMC Genomics</i> , 2013, 14, 286.	2.8	21
57	Distinct co-evolution patterns of genes associated to DNA polymerase III DnaE and PolC. <i>BMC Genomics</i> , 2012, 13, 69.	2.8	18
58	Characterization and distribution of the gene cluster encoding RumC, an anti- <i>Clostridium perfringens</i> bacteriocin produced in the gut. <i>FEMS Microbiology Ecology</i> , 2011, 78, 405-415.	2.7	17
59	A Novel Acyl-CoA Beta-Transaminase Characterized from a Metagenome. <i>PLoS ONE</i> , 2011, 6, e22918.	2.5	14
60	Genome Sequence of <i>Micromonospora lupini</i> Lupac 08, Isolated from Root Nodules of <i>Lupinus angustifolius</i> . <i>Journal of Bacteriology</i> , 2012, 194, 4135-4135.	2.2	14
61	Genome Sequence of the Human- and Animal-Pathogenic Strain <i>Nocardia cyriacigeorgica</i> GUH-2. <i>Journal of Bacteriology</i> , 2012, 194, 2098-2099.	2.2	12
62	From Strain Characterization to Field Authorization: Highlights on <i>Bacillus velezensis</i> Strain B25 Beneficial Properties for Plants and Its Activities on Phytopathogenic Fungi. <i>Microorganisms</i> , 2021, 9, 1924.	3.6	9
63	Complete Genome Sequence of <i>Bradyrhizobium</i> sp. ORS285, a Photosynthetic Strain Able To Establish Nod Factor-Dependent or Nod Factor-Independent Symbiosis with <i>Aeschynomene</i> Legumes. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
64	Construction of a complete set of <i>Neisseria meningitidis</i> mutants and its use for the phenotypic profiling of this human pathogen. <i>Nature Communications</i> , 2020, 11, 5541.	12.8	8
65	Alterocin, an Antibiofilm Protein Secreted by <i>Pseudoalteromonas</i> sp. Strain 3J6. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	7
66	Large \pm -aminonitrilase activity screening of nitrilase superfamily members: Access to conversion and enantiospecificity by LC-MS. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2014, 107, 79-88.	1.8	6
67	L ^â ™annotation in silico des s ^â ™quences g ^â ™nomiques. <i>Medecine/Sciences</i> , 2002, 18, 237-250.	0.2	5
68	Complete Genome Sequence of <i>Bacillus methylotrophicus</i> Strain B25, a Potential Plant Growth-Promoting Rhizobacterium. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
69	A new network representation of the metabolism to detect chemical transformation modules. <i>BMC Bioinformatics</i> , 2015, 16, 385.	2.6	3
70	Complete Genome Sequences of Two <i>Pseudomonas</i> Species Isolated from Marine Environments of the Pacific Ocean. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
71	Accurate Microbial Genome Annotation Using an Integrated and User-Friendly Environment for Community Expertise of Gene Functions: The MicroScope Platform. <i>Springer Protocols</i> , 2015, , 141-169.	0.3	2
72	GROOLS: reactive graph reasoning for genome annotation through biological processes. <i>BMC Bioinformatics</i> , 2018, 19, 132.	2.6	2

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73	Complete Genome Sequence of <i>Tepidibacter</i> sp. Strain 8C15b, Isolated from Bank Sediments of Haiphong Bay, Vietnam. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	1
74	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0
75	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0
76	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0
77	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732.		0