

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 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | Alterocin, an Antibiofilm Protein Secreted by <i>Pseudoalteromonas</i> sp. Strain 3J6. <i>Applied and Environmental Microbiology</i> , 2020, 86, . | 3.1 | 7 |
| 7 | 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 |
| 8 | PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. <i>PLoS Computational Biology</i> , 2020, 16, e1007732. | 3.2 | 102 |
| 9 | panRGP: a pangenome-based method to predict genomic islands and explore their diversity. <i>Bioinformatics</i> , 2020, 36, i651-i658. | 4.1 | 26 |
| 10 | PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732. | | 0 |
| 11 | PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732. | | 0 |
| 12 | PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732. | | 0 |
| 13 | PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. , 2020, 16, e1007732. | | 0 |
| 14 | 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 |
| 15 | Ectosymbiotic bacteria at the origin of magnetoreception in a marine protist. <i>Nature Microbiology</i> , 2019, 4, 1088-1095. | 13.3 | 57 |
| 16 | <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 |
| 17 | GROOLS: reactive graph reasoning for genome annotation through biological processes. <i>BMC Bioinformatics</i> , 2018, 19, 132. | 2.6 | 2 |
| 18 | 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 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | Conservation and diversity of the IrrE/DdrO-controlled radiation response in radiation-resistant <i>Deinococcus</i> bacteria. <i>MicrobiologyOpen</i> , 2017, 6, e00477. | 3.0 | 37 |
| 22 | 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 |
| 23 | Carrageenan catabolism is encoded by a complex regulon in marine heterotrophic bacteria. <i>Nature Communications</i> , 2017, 8, 1685. | 12.8 | 131 |
| 24 | 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 |
| 25 | Parallel evolution of non-homologous isofunctional enzymes in methionine biosynthesis. <i>Nature Chemical Biology</i> , 2017, 13, 858-866. | 8.0 | 29 |
| 26 | 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 |
| 27 | 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 |
| 28 | A new network representation of the metabolism to detect chemical transformation modules. <i>BMC Bioinformatics</i> , 2015, 16, 385. | 2.6 | 3 |
| 29 | 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 |
| 30 | Revealing the hidden functional diversity of an enzyme family. <i>Nature Chemical Biology</i> , 2014, 10, 42-49. | 8.0 | 113 |
| 31 | 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 |
| 32 | Profiling the orphan enzymes. <i>Biology Direct</i> , 2014, 9, 10. | 4.6 | 43 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | An updated metabolic view of the <i>Bacillus subtilis</i> 168 genome. <i>Microbiology (United Kingdom)</i> , 2013, 159, 757-770. | 1.8 | 72 |

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|----|---|------|-----------|
| 37 | MicroScopeâ€”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 |
| 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 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | Distinct co-evolution patterns of genes associated to DNA polymerase III DnaE and PolC. <i>BMC Genomics</i> , 2012, 13, 69. | 2.8 | 18 |
| 43 | 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 |
| 44 | <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 |
| 45 | 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 |
| 46 | A Novel Acyl-CoA Beta-Transaminase Characterized from a Metagenome. <i>PLoS ONE</i> , 2011, 6, e22918. | 2.5 | 14 |
| 47 | 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 |
| 48 | 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 |
| 49 | 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 |
| 50 | Core and Panmetabolism in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1461-1472. | 2.2 | 51 |
| 51 | The <i>Frankia alni</i> Symbiotic Transcriptome. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 593-607. | 2.6 | 126 |
| 52 | 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 |
| 53 | <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 |
| 54 | 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 |

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|----|---|------|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |
| 61 | Comparative Analysis of <i>Acinetobacters</i> : Three Genomes for Three Lifestyles. <i>PLoS ONE</i> , 2008, 3, e1805. | 2.5 | 315 |
| 62 | 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 |
| 63 | A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53. | 3.5 | 166 |
| 64 | Legumes Symbioses: Absence of Nod Genes in Photosynthetic Bradyrhizobia. <i>Science</i> , 2007, 316, 1307-1312. | 12.6 | 557 |
| 65 | <i>Frankia alni</i> proteome under nitrogen-fixing and nitrogen-replete conditions. <i>Physiologia Plantarum</i> , 2007, 130, 440-453. | 5.2 | 45 |
| 66 | 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 |
| 67 | MaGe: a microbial genome annotation system supported by synteny results. <i>Nucleic Acids Research</i> , 2006, 34, 53-65. | 14.5 | 375 |
| 68 | 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 |
| 69 | Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794. | 27.8 | 1,075 |
| 70 | Comparative Genomics of Multidrug Resistance in <i>Acinetobacter baumannii</i> . <i>PLoS Genetics</i> , 2006, 2, e7. | 3.5 | 677 |
| 71 | 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 |
| 72 | 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 |

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|----|--|------|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | 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 |
| 76 | AMIGene: Annotation of Microbial Genes. <i>Nucleic Acids Research</i> , 2003, 31, 3723-3726. | 14.5 | 126 |
| 77 | Lâ€™annotation in silico des sÃ©quences gÃ©nomiques. <i>Medecine/Sciences</i> , 2002, 18, 237-250. | 0.2 | 5 |