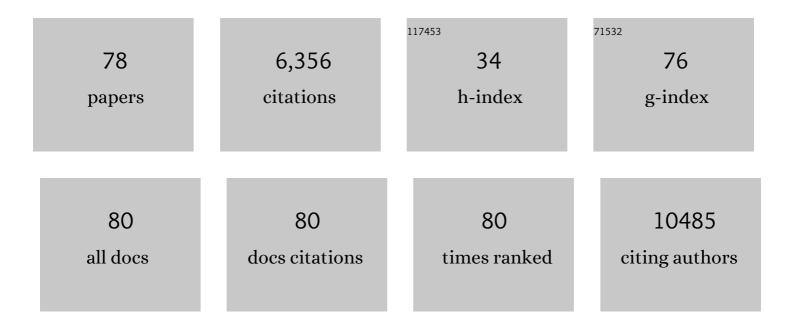
Olivier Jousson

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Metagenomic microbial community profiling using unique clade-specific marker genes. Nature Methods, 2012, 9, 811-814.	9.0	1,591
2	New evidences on the altered gut microbiota in autism spectrum disorders. Microbiome, 2017, 5, 24.	4.9	668
3	Secreted proteases from pathogenic fungi. International Journal of Medical Microbiology, 2002, 292, 405-419.	1.5	330
4	Invasive alga reaches California. Nature, 2000, 408, 157-158.	13.7	188
5	Two-Way Chemical Communication between Artificial and Natural Cells. ACS Central Science, 2017, 3, 117-123.	5.3	178
6	Genomic characterization of Nontuberculous Mycobacteria. Scientific Reports, 2017, 7, 45258.	1.6	176
7	Age and Gender Affect the Composition of Fungal Population of the Human Gastrointestinal Tract. Frontiers in Microbiology, 2016, 7, 1227.	1.5	170
8	Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. Npj Biofilms and Microbiomes, 2017, 3, 14.	2.9	159
9	Molecular evidence for the aquarium origin of the green alga Caulerpa taxifolia introduced to the Mediterranean Sea. Marine Ecology - Progress Series, 1998, 172, 275-280.	0.9	133
10	The new phylogeny of the genus Mycobacterium : The old and the news. Infection, Genetics and Evolution, 2017, 56, 19-25.	1.0	128
11	Altered gut microbiota in Rett syndrome. Microbiome, 2016, 4, 41.	4.9	120
12	Coevolution between Lamellodiscus (Monogenea: Diplectanidae) and Sparidae (Teleostei): The Study Of a Complex Host-Parasite System. Evolution; International Journal of Organic Evolution, 2002, 56, 2459-2471.	1.1	116
13	Cryptic speciation among intestinal parasites (Trematoda: Digenea) infecting sympatric host fishes (Sparidae). Journal of Evolutionary Biology, 2000, 13, 778-785.	0.8	107
14	Identification of Dermatophyte Species by 28S Ribosomal DNA Sequencing with a Commercial Kit. Journal of Clinical Microbiology, 2003, 41, 826-830.	1.8	106
15	Multiplication of an ancestral gene encoding secreted fungalysin preceded species differentiation in the dermatophytes Trichophyton and Microsporum. Microbiology (United Kingdom), 2004, 150, 301-310.	0.7	103
16	Secreted subtilisin gene family in Trichophyton rubrum. Gene, 2004, 339, 79-88.	1.0	98
17	Antibodyâ€mediated immunity induced by engineered <i>Escherichia coli</i> OMVs carrying heterologous antigens in their lumen. Journal of Extracellular Vesicles, 2014, 3, .	5.5	97
18	Molecular identification of developmental stages in Opecoelidae (Digenea)1Note: Nucleotide sequence data reported in this paper have been deposited in the EMBL/GenBankâ,,¢ databases under accessions numbers AJ241790–AJ 241817.1. International Journal for Parasitology, 1999, 29, 1853-1858.	1.3	89

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19	MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. Nucleic Acids Research, 2017, 45, e7-e7.	6.5	88
20	Evolution of Stenotrophomonas maltophilia in Cystic Fibrosis Lung over Chronic Infection: A Genomic and Phenotypic Population Study. Frontiers in Microbiology, 2017, 8, 1590.	1.5	85
21	Molecular analysis and mating behaviour of the Trichophyton mentagrophytes species complex. International Journal of Medical Microbiology, 2011, 301, 260-266.	1.5	78
22	Aminopeptidases and dipeptidyl-peptidases secreted by the dermatophyte Trichophyton rubrum. Microbiology (United Kingdom), 2005, 151, 145-155.	0.7	74
23	The dermatophyte species Arthroderma benhamiae: intraspecies variability and mating behaviour. Journal of Medical Microbiology, 2013, 62, 377-385.	0.7	70
24	Uncovering oral Neisseria tropism and persistence using metagenomic sequencing. Nature Microbiology, 2016, 1, 16070.	5.9	68
25	Sedolisins, a New Class of Secreted Proteases from Aspergillus fumigatus with Endoprotease or Tripeptidyl-Peptidase Activity at Acidic pHs. Applied and Environmental Microbiology, 2006, 72, 1739-1748.	1.4	67
26	THE LIFE CYCLE OFMONORCHIS PARVUS(DIGENEA: MONORCHIIDAE) DEMONSTRATED BY DEVELOPMENTAL AND MOLECULAR DATA. Journal of Parasitology, 2000, 86, 479-489.	0.3	66
27	First Report of <i>Arthroderma benhamiae</i> in Switzerland. Dermatology, 2004, 208, 244-250.	0.9	66
28	Use of the ITS rDNA for elucidation of some life-cycles of Mesometridae (Trematoda, Digenea)1Note: Nucleotide sequence data reported in this paper are available in the EMBL, GenBankâ,,¢ and DDJB databases under the accession numbers Y17196–Y17205.1. International Journal for Parasitology, 1998, 28, 1403-1411.	1.3	58
29	Molecular Identification of <i>Fusarium</i> Species in Onychomycoses. Dermatology, 2005, 210, 21-25.	0.9	56
30	Comparison of ribosomal DNA sequences of Lamellodiscus spp. (Monogenea, Diplectanidae) parasitising Pagellus (Sparidae, Teleostei) in the North Mediterranean Sea: species divergence and coevolutionary interactions1Note: Nucleotide sequence data reported in this paper are available in the GenBankâ,,¢, EMBL andDDBJ databases under the accession numbers AJ276439-AJ276447 and AJ276879-AJ276881.1. International Journal for Parasitology, 2000, 30, 741-746.	1.3	47
31	Trichophyton rubrum secreted and membrane-associated carboxypeptidases. International Journal of Medical Microbiology, 2008, 298, 669-682.	1.5	46
32	Thermotolerance and heat shock response in the cold-stenothermal chironomid (NE Italy). Cell Stress and Chaperones, 2011, 16, 403-410.	1.2	43
33	Molecular typing and epidemiological investigation of clinical populations of Pseudomonas aeruginosa using an oligonucleotide-microarray. BMC Microbiology, 2012, 12, 152.	1.3	40
34	Genomic and metagenomic insights into the microbial community of a thermal spring. Microbiome, 2019, 7, 8.	4.9	40
35	Molecules, morphology and morphometrics of Cainocreadium labracis and Cainocreadium dentecis n. sp. (Digenea: Opecoelidae) parasitic in marine fishes. International Journal for Parasitology, 2001, 31, 706-714.	1.3	36
36	Genetic polymorphism inCaulerpa taxifolia(Ulvophyceae) chloroplast DNA revealed by a PCR-based assay of the invasive Mediterranean strain. Journal of Evolutionary Biology, 2002, 15, 618-624.	0.8	34

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37	Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. Journal of Biotechnology, 2014, 190, 30-39.	1.9	34
38	The life cycle of Opecoeloides columbellae (Pagenstecher, 1863) n. comb. (Digenea, Opecoelidae): evidence from molecules and morphology. International Journal for Parasitology, 2000, 30, 747-760.	1.3	33
39	Cold adaptive potential of chironomids overwintering in a glacial stream. Physiological Entomology, 2015, 40, 43-53.	0.6	32
40	The murine orthologue of the Golgi-localized TPTE protein provides clues to the evolutionary history of the human TPTE gene family. Human Genetics, 2001, 109, 569-575.	1.8	31
41	Characterization of 17 strains belonging to the Mycobacterium simiae complex and description of Mycobacterium paraense sp. nov International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 656-662.	0.8	31
42	Ethylene-Producing Bacteria That Ripen Fruit. ACS Synthetic Biology, 2014, 3, 935-938.	1.9	29
43	Persistence and Microevolution of Pseudomonas aeruginosa in the Cystic Fibrosis Lung: A Single-Patient Longitudinal Genomic Study. Frontiers in Microbiology, 2018, 9, 3242.	1.5	27
44	COEVOLUTION BETWEEN LAMELLODISCUS (MONOGENEA: DIPLECTANIDAE) AND SPARIDAE (TELEOSTEI): THE STUDY OF A COMPLEX HOST-PARASITE SYSTEM. Evolution; International Journal of Organic Evolution, 2002, 56, 2459.	1.1	26
45	Antimicrobial susceptibility and mechanism of resistance to fluoroquinolones in Staphylococcus intermedius and Staphylococcus schleiferi. Journal of Veterinary Pharmacology and Therapeutics, 2007, 30, 464-469.	0.6	26
46	Secretion of an Endogenous Subtilisin by <i>Pichia pastoris</i> Strains GS115 and KM71. Applied and Environmental Microbiology, 2010, 76, 4269-4276.	1.4	25
47	Genetic variability among cecariae of the shistomatidae (Trematoda: Digenea) causing swimmer's itch in Europe. Parasite, 2001, 8, 237-242.	0.8	24
48	Genotypic versus phenotypic identification of staphylococcal species of canine origin with special reference to Staphylococcus schleiferi subsp. coagulans. Veterinary Microbiology, 2007, 123, 238-244.	0.8	23
49	Pseudomonas aeruginosa mutants defective in glucose uptake have pleiotropic phenotype and altered virulence in non-mammal infection models. Scientific Reports, 2018, 8, 16912.	1.6	23
50	Differential expression of cysteine proteases in developmental stages of the parasitic ciliateIchthyophthirius multifiliis. FEMS Microbiology Letters, 2007, 269, 77-84.	0.7	22
51	Pseudomonas aeruginosa in Dairy Goats: Genotypic and Phenotypic Comparison of Intramammary and Environmental Isolates. PLoS ONE, 2015, 10, e0142973.	1.1	22
52	Clinical populations of Pseudomonas aeruginosa isolated from acute infections show a wide virulence range partially correlated with population structure and virulence gene expression. Microbiology (United Kingdom), 2012, 158, 2089-2098.	0.7	21
53	Comparison of quantitative PCR and flow cytometry as cellular viability methods to study bacterial membrane permeabilization following supercritical CO2 treatment. Microbiology (United Kingdom), 2013, 159, 1056-1066.	0.7	19
54	Supercritical CO2 Induces Marked Changes in Membrane Phospholipids Composition in Escherichia coli K12. Journal of Membrane Biology, 2014, 247, 469-477.	1.0	19

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55	Species diversity among the genus Monorchis (Digenea: Monorchiidae) parasitic in marine teleosts: molecular, morphological and morphometrical studies with a description of Monorchis blennii n. sp Parasitology Research, 2002, 88, 230-241.	0.6	18
56	Simultaneous Quantification of Multiple Bacteria by the BactoChip Microarray Designed to Target Species-Specific Marker Genes. PLoS ONE, 2013, 8, e55764.	1.1	18
57	Aspergillus fumigatus Secreted Proteases. , 0, , 87-106.		18
58	Accurate flow cytometric monitoring of Escherichia coli subpopulations on solid food treated with high pressure carbon dioxide. Journal of Applied Microbiology, 2014, 117, 440-450.	1.4	17
59	Insights into the genome structure of four acetogenic bacteria with specific reference to the Wood–Ljungdahl pathway. MicrobiologyOpen, 2019, 8, e938.	1.2	16
60	The life-cycle of three species of the Mesometridae (Digenea) with comments on the taxonomic status of this family. Systematic Parasitology, 1999, 44, 217-228.	0.5	15
61	Cold stenothermal cave-dwelling beetles do have an HSP70 heat shock response. Journal of Thermal Biology, 2011, 36, 206-208.	1.1	13
62	Secreted glutamic protease rescues aspartic protease Pep deficiency in Aspergillus fumigatus during growth in acidic protein medium. Microbiology (United Kingdom), 2011, 157, 1541-1550.	0.7	13
63	Non-invasive detection and quantification of the parasitic ciliate Ichthyophthirius multifiliis by real-time PCR. Diseases of Aquatic Organisms, 2005, 65, 251-255.	0.5	12
64	Evolution of p53 Transactivation Specificity through the Lens of a Yeast-Based Functional Assay. PLoS ONE, 2015, 10, e0116177.	1,1	12
65	Application of culture-independent methods for monitoring Listeria monocytogenes inactivation on food products. Process Biochemistry, 2015, 50, 188-193.	1.8	12
66	Mesorhizobium comanense sp. nov., isolated from groundwater. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
67	Molecular phylogeny of Mesometridae (Trematoda, Digenea) with its relation to morphological changes in parasites. Parasite, 1998, 5, 365-369.	0.8	9
68	Intestinal Candida parapsilosis isolates from Rett syndrome subjects bear potential virulent traits and capacity to persist within the host. BMC Gastroenterology, 2018, 18, 57.	0.8	9
69	AoS28D, a proline-Xaa carboxypeptidase secreted by Aspergillus oryzae. Applied Microbiology and Biotechnology, 2017, 101, 4129-4137.	1.7	8
70	Mathematical modeling of bacterial virulence and host–pathogen interactions in the Dictyostelium/Pseudomonas system. Journal of Theoretical Biology, 2011, 270, 19-24.	0.8	7
71	Genome Sequence of Pseudomonas aeruginosa PA45, a Highly Virulent Strain Isolated from a Patient with Bloodstream Infection. Genome Announcements, 2013, 1, .	0.8	6
72	Studying translational control in non-model stressed organisms by polysomal profiling. Journal of Insect Physiology, 2015, 76, 30-35.	0.9	6

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73	The new phylogenesis of the genus Mycobacterium. International Journal of Mycobacteriology, 2015, 4, 77.	0.3	6
74	Conjugative type IVb pilus recognizes lipopolysaccharide of recipient cells to initiate PAPI-1 pathogenicity island transfer in Pseudomonas aeruginosa. BMC Microbiology, 2017, 17, 31.	1.3	6
75	Air and waterborne microbiome of a pharmaceutical plant provide insights on spatiotemporal variations and community resilience after disturbance. BMC Microbiology, 2018, 18, 124.	1.3	5
76	Draft Genome Sequences of 40 Pseudomonas aeruginosa Clinical Strains Isolated from the Sputum of a Single Cystic Fibrosis Patient Over an 8-Year Period. Genome Announcements, 2016, 4, .	0.8	2
77	316 A longitudinal investigation of genomic and phenotypic factors leading to adaptation of Pseusomonas aeruginosa in a cystic fibrosis patient. Journal of Cystic Fibrosis, 2015, 14, S139.	0.3	0

78 Simultaneous Quantification of Multiple Bacteria. , 2013, , 1-6.