

# Michael Dondrup

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

1,386  
citations

516710

16  
h-index

501196

28  
g-index

32  
all docs

32  
docs citations

32  
times ranked

2054  
citing authors

#	ARTICLE	IF	CITATIONS
1	The metagenome of a biogas-producing microbial community of a production-scale biogas plant fermenter analysed by the 454-pyrosequencing technology. <i>Journal of Biotechnology</i> , 2008, 136, 77-90.	3.8	329
2	Global expression analysis of the brown alga <i>Ectocarpus siliculosus</i> (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. <i>Genome Biology</i> , 2009, 10, R66.	9.6	138
3	Construction and validation of cDNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume <i>Medicago truncatula</i> . <i>Journal of Biotechnology</i> , 2004, 108, 95-113.	3.8	103
4	EMMA: a platform for consistent storage and efficient analysis of microarray data. <i>Journal of Biotechnology</i> , 2003, 106, 135-146.	3.8	100
5	MeltDB: a software platform for the analysis and integration of metabolomics experiment data. <i>Bioinformatics</i> , 2008, 24, 2726-2732.	4.1	100
6	Development of a <i>Corynebacterium glutamicum</i> DNA microarray and validation by genome-wide expression profiling during growth with propionate as carbon source. <i>Journal of Biotechnology</i> , 2003, 106, 269-286.	3.8	85
7	EMMA 2 – A MAGE-compliant system for the collaborative analysis and integration of microarray data. <i>BMC Bioinformatics</i> , 2009, 10, 50.	2.6	68
8	Visualizing post genomics data-sets on customized pathway maps by ProMeTra – aeration-dependent gene expression and metabolism of <i>Corynebacterium glutamicum</i> as an example. <i>BMC Systems Biology</i> , 2009, 3, 82.	3.0	61
9	Development of bioinformatic tools to support EST-sequencing, in silico- and microarray-based transcriptome profiling in mycorrhizal symbioses. <i>Phytochemistry</i> , 2007, 68, 19-32.	2.9	49
10	Linkage-Disequilibrium-Based Binning Affects the Interpretation of GWASs. <i>American Journal of Human Genetics</i> , 2012, 90, 727-733.	6.2	44
11	A portal for rhizobial genomes: RhizoGATE integrates a <i>Sinorhizobium meliloti</i> genome annotation update with postgenome data. <i>Journal of Biotechnology</i> , 2009, 140, 45-50.	3.8	38
12	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003, 106, 147-156.	3.8	31
13	Transcriptional snapshots provide insights into the molecular basis of arbuscular mycorrhiza in the model legume <i>Medicago truncatula</i> . <i>Functional Plant Biology</i> , 2006, 33, 737.	2.1	29
14	<sc>RNA</sc> sequencing reveals distinct gene expression patterns during the development of parasitic larval stages of the salmon louse (<i>Lepeophtheirus salmonis</i>). <i>Journal of Fish Diseases</i> , 2018, 41, 1005-1029.	1.9	23
15	Finding a Needle in the Virus Metagenome Haystack - Micro-Metagenome Analysis Captures a Snapshot of the Diversity of a Bacteriophage Armoire. <i>PLoS ONE</i> , 2012, 7, e34238.	2.5	23
16	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. <i>Journal of Biotechnology</i> , 2003, 106, 157-167.	3.8	22
17	The salmon louse genome: Copepod features and parasitic adaptations. <i>Genomics</i> , 2021, 113, 3666-3680.	2.9	17
18	An evaluation framework for statistical tests on microarray data. <i>Journal of Biotechnology</i> , 2009, 140, 18-26.	3.8	16

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19	A scavenger receptor B (CD36)-like protein is a potential mediator of intestinal heme absorption in the hematophagous ectoparasite <i>Lepeophtheirus salmonis</i> . <i>Scientific Reports</i> , 2019, 9, 4218.	3.3	16
20	Host gill attachment causes blood-feeding by the salmon louse ( <i>Lepeophtheirus salmonis</i> ) chalimus larvae and alters parasite development and transcriptome. <i>Parasites and Vectors</i> , 2020, 13, 225.	2.5	16
21	Chitin synthesis and degradation in <i>Lepeophtheirus salmonis</i> : Molecular characterization and gene expression profile during synthesis of a new exoskeleton. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2019, 227, 123-133.	1.8	13
22	CoryneCenter – An online resource for the integrated analysis of corynebacterial genome and transcriptome data. <i>BMC Systems Biology</i> , 2007, 1, 55.	3.0	11
23	TRUNCATULIX - a data warehouse for the legume community. <i>BMC Plant Biology</i> , 2009, 9, 19.	3.6	11
24	Identification of critical enzymes in the salmon louse chitin synthesis pathway as revealed by RNA interference-mediated abrogation of infectivity. <i>International Journal for Parasitology</i> , 2020, 50, 873-889.	3.1	10
25	Roles of three putative salmon louse ( <i>Lepeophtheirus salmonis</i> ) prostaglandin E2 synthases in physiology and host-parasite interactions. <i>Parasites and Vectors</i> , 2021, 14, 206.	2.5	10
26	<i>Caligus rogercresseyi</i> acetylcholinesterase types and variants: a potential marker for organophosphate resistance. <i>Parasites and Vectors</i> , 2018, 11, 570.	2.5	9
27	Characterisation of iron regulatory protein 1A and 1B in the blood-feeding copepod <i>Lepeophtheirus salmonis</i> . <i>Experimental Parasitology</i> , 2015, 157, 1-11.	1.2	6
28	Small, charged proteins in salmon louse ( <i>Lepeophtheirus salmonis</i> ) secretions modulate Atlantic salmon ( <i>Salmo salar</i> ) immune responses and coagulation. <i>Scientific Reports</i> , 2022, 12, 7995.	3.3	6
29	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0
30	A novel approach to co-expression network analysis identifies modules and genes relevant for moulting and development in the Atlantic salmon louse ( <i>Lepeophtheirus salmonis</i> ). <i>BMC Genomics</i> , 2021, 22, 832.	2.8	0