

Niels Klitgord

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

7,373
citations

361413

20
h-index

642732

23
g-index

24
all docs

24
docs citations

24
times ranked

11635
citing authors

#	ARTICLE	IF	CITATIONS
1	Flux balance modeling to predict bacterial survival during pulsed-activity events. Biogeosciences, 2018, 15, 2219-2229.	3.3	7
2	Utilization of defined microbial communities enables effective evaluation of meta-genomic assemblies. BMC Genomics, 2017, 18, 296.	2.8	21
3	Gut Microbiome-Based Metagenomic Signature for Non-invasive Detection of Advanced Fibrosis in Human Nonalcoholic Fatty Liver Disease. Cell Metabolism, 2017, 25, 1054-1062.e5.	16.2	748
4	A robust ambient temperature collection and stabilization strategy: Enabling worldwide functional studies of the human microbiome. Scientific Reports, 2016, 6, 31731.	3.3	59
5	A Rapid Molecular Approach for Chromosomal Phasing. PLoS ONE, 2015, 10, e0118270.	2.5	58
6	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. Frontiers in Microbiology, 2015, 6, 277.	3.5	50
7	Library preparation methodology can influence genomic and functional predictions in human microbiome research. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14024-14029.	7.1	179
8	Dynamic cyanobacterial response to hydration and dehydration in a desert biological soil crust. ISME Journal, 2013, 7, 2178-2191.	9.8	217
9	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54
10	Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. Retrovirology, 2012, 9, 26.	2.0	64
11	Deep Sequencing of the Oral Microbiome Reveals Signatures of Periodontal Disease. PLoS ONE, 2012, 7, e37919.	2.5	329
12	Ecosystems biology of microbial metabolism. Current Opinion in Biotechnology, 2011, 22, 541-546.	6.6	98
13	COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. Nucleic Acids Research, 2011, 39, D11-D14.	14.5	47
14	Environments that Induce Synthetic Microbial Ecosystems. PLoS Computational Biology, 2010, 6, e1001002.	3.2	280
15	THE IMPORTANCE OF COMPARTMENTALIZATION IN METABOLIC FLUX MODELS: YEAST AS AN ECOSYSTEM OF ORGANELLES. , 2010, , .		25
16	A Genome-Wide Gene Function Prediction Resource for Drosophila melanogaster. PLoS ONE, 2010, 5, e12139.	2.5	17
17	The importance of compartmentalization in metabolic flux models: yeast as an ecosystem of organelles. Genome Informatics, 2010, 22, 41-55.	0.4	21
18	Edgetic perturbation models of human inherited disorders. Molecular Systems Biology, 2009, 5, 321.	7.2	326

#	ARTICLE	IF	CITATIONS
19	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	19.0	260
20	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	19.0	800
21	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	28.9	196
22	Intrinsic Disorder Is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. <i>PLoS Computational Biology</i> , 2006, 2, e100.	3.2	512
23	Towards a proteome-scale map of the human protein-protein interaction network. <i>Nature</i> , 2005, 437, 1173-1178.	27.8	2,676
24	Interactome: gateway into systems biology. <i>Human Molecular Genetics</i> , 2005, 14, R171-R181.	2.9	329