

# Niels Klitgord

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10786652/publications.pdf>

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	Towards a proteome-scale map of the human protein-protein interaction network. <i>Nature</i> , 2005, 437, 1173-1178.	27.8	2,676
2	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	19.0	800
3	Gut Microbiome-Based Metagenomic Signature for Non-invasive Detection of Advanced Fibrosis in Human Nonalcoholic Fatty Liver Disease. <i>Cell Metabolism</i> , 2017, 25, 1054-1062.e5.	16.2	748
4	Intrinsic Disorder Is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. <i>PLoS Computational Biology</i> , 2006, 2, e100.	3.2	512
5	Interactome: gateway into systems biology. <i>Human Molecular Genetics</i> , 2005, 14, R171-R181.	2.9	329
6	Deep Sequencing of the Oral Microbiome Reveals Signatures of Periodontal Disease. <i>PLoS ONE</i> , 2012, 7, e37919.	2.5	329
7	Edgetic perturbation models of human inherited disorders. <i>Molecular Systems Biology</i> , 2009, 5, 321.	7.2	326
8	Environments that Induce Synthetic Microbial Ecosystems. <i>PLoS Computational Biology</i> , 2010, 6, e1001002.	3.2	280
9	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	19.0	260
10	Dynamic cyanobacterial response to hydration and dehydration in a desert biological soil crust. <i>ISME Journal</i> , 2013, 7, 2178-2191.	9.8	217
11	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	28.9	196
12	Library preparation methodology can influence genomic and functional predictions in human microbiome research. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14024-14029.	7.1	179
13	Ecosystems biology of microbial metabolism. <i>Current Opinion in Biotechnology</i> , 2011, 22, 541-546.	6.6	98
14	Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. <i>Retrovirology</i> , 2012, 9, 26.	2.0	64
15	A robust ambient temperature collection and stabilization strategy: Enabling worldwide functional studies of the human microbiome. <i>Scientific Reports</i> , 2016, 6, 31731.	3.3	59
16	A Rapid Molecular Approach for Chromosomal Phasing. <i>PLoS ONE</i> , 2015, 10, e0118270.	2.5	58
17	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	5.6	54
18	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. <i>Frontiers in Microbiology</i> , 2015, 6, 277.	3.5	50

#	ARTICLE	IF	CITATIONS
19	COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, D11-D14.	14.5	47
20	THE IMPORTANCE OF COMPARTMENTALIZATION IN METABOLIC FLUX MODELS: YEAST AS AN ECOSYSTEM OF ORGANELLES. , 2010, , .		25
21	Utilization of defined microbial communities enables effective evaluation of meta-genomic assemblies. <i>BMC Genomics</i> , 2017, 18, 296.	2.8	21
22	The importance of compartmentalization in metabolic flux models: yeast as an ecosystem of organelles. <i>Genome Informatics</i> , 2010, 22, 41-55.	0.4	21
23	A Genome-Wide Gene Function Prediction Resource for <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2010, 5, e12139.	2.5	17
24	Flux balance modeling to predict bacterial survival during pulsed-activity events. <i>Biogeosciences</i> , 2018, 15, 2219-2229.	3.3	7