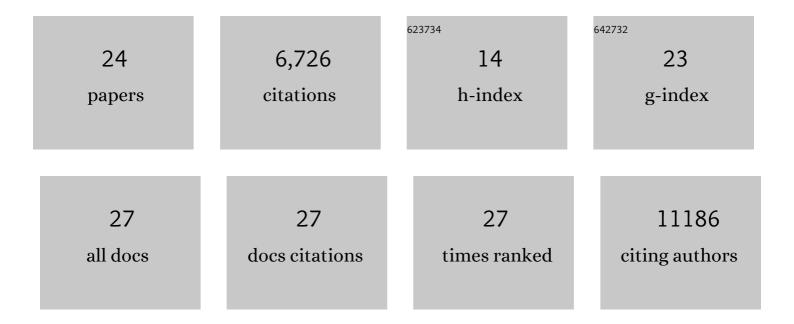
## Thomas Brüls

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8868764/publications.pdf

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ΤΗΟΜΛς ΒρΔ1/15

#	Article	IF	CITATIONS
1	A zero inflated log-normal model for inference of sparse microbial association networks. PLoS Computational Biology, 2021, 17, e1009089.	3.2	10
2	Channeling C1 Metabolism toward S -Adenosylmethionine-Dependent Conversion of Estrogens to Androgens in Estrogen-Degrading Bacteria. MBio, 2020, 11, .	4.1	8
3	Binning unassembled short reads based on k-mer abundance covariance using sparse coding. GigaScience, 2020, 9, .	6.4	7
4	Sparse Non-negative Matrix Factorization for Retrieving Genomes Across Metagenomes. Communications in Computer and Information Science, 2020, , 97-105.	0.5	0
5	The class II benzoylâ€coenzyme A reductase complex from the sulfateâ€reducing <i>Desulfosarcina cetonica</i> . Environmental Microbiology, 2019, 21, 4241-4252.	3.8	10
6	Metabolic reconstruction of the genome of candidate <i>Desulfatiglans</i> TRIP_1 and identification of key candidate enzymes for anaerobic phenanthrene degradation. Environmental Microbiology, 2019, 21, 1267-1286.	3.8	31
7	Shared Nearest Neighbor Clustering in a Locality Sensitive Hashing Framework. Journal of Computational Biology, 2018, 25, 236-250.	1.6	6
8	Screening and Characterization of Novel Polyesterases from Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. Environmental Science & Technology, 2018, 52, 12388-12401.	10.0	56
9	Fermentative Spirochaetes mediate necromass recycling in anoxic hydrocarbon-contaminated habitats. ISME Journal, 2018, 12, 2039-2050.	9.8	74
10	Anaerobic degradation of phenanthrene by a sulfateâ€reducing enrichment culture. Environmental Microbiology, 2018, 20, 3589-3600.	3.8	45
11	An unusual strategy for the anoxic biodegradation of phthalate. ISME Journal, 2017, 11, 224-236.	9.8	61
12	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. Scientific Reports, 2017, 7, 44103.	3.3	67
13	Microbial communities in pyrene amended soil–compost mixture and fertilized soil. AMB Express, 2017, 7, 7.	3.0	17
14	Functional soil metagenomics: elucidation of polycyclic aromatic hydrocarbon degradation potential following 12 years of <i>in situ</i> bioremediation. Environmental Microbiology, 2017, 19, 2992-3011.	3.8	39
15	A spectral algorithm for fast <i>de novo</i> layout of uncorrected long nanopore reads. Bioinformatics, 2017, 33, 3188-3194.	4.1	7
16	A patchwork pathway for oxygenaseâ€independent degradation of side chain containing steroids. Environmental Microbiology, 2017, 19, 4684-4699.	3.8	28
17	Microbial Degradation of a Recalcitrant Pesticide: Chlordecone. Frontiers in Microbiology, 2016, 7, 2025.	3.5	55
18	A scalable assembly-free variable selection algorithm for biomarker discovery from metagenomes. BMC Bioinformatics, 2016, 17, 311.	2.6	10

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#	Article	IF	CITATIONS
19	An assessment of the amount of untapped fold level novelty in under-sampled areas of the tree of life. Scientific Reports, 2015, 5, 14717.	3.3	4
20	The enzymatic nature of an anonymous protein sequence cannot reliably be inferred from superfamily level structural information alone. Protein Science, 2015, 24, 643-650.	7.6	3
21	Endogeic earthworms shape bacterial functional communities and affect organic matter mineralization in a tropical soil. ISME Journal, 2012, 6, 213-222.	9.8	169
22	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	27.8	5,800
23	The human metagenome: our other genome?. Human Molecular Genetics, 2011, 20, R142-R148.	2.9	33
24	A placenta-specific receptor for the fusogenic, endogenous retrovirus-derived, human syncytin-2. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17532-17537.	7.1	185