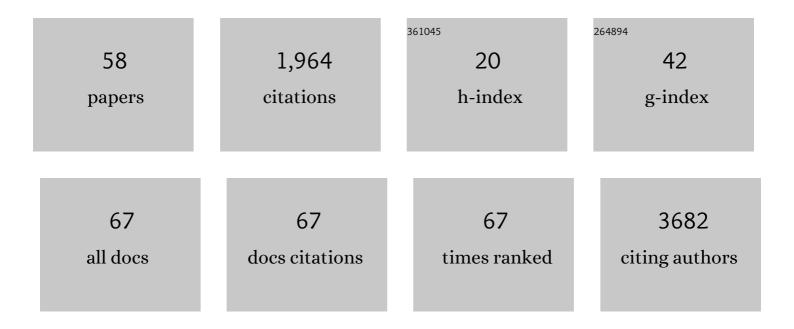
Trine B Rounge

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8462834/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Identification of Circulating IncRNAs Associated with Gallbladder Cancer Risk by Tissue-Based Preselection, Cis-eQTL Validation, and Analysis of Association with Genotype-Based Expression. Cancers, 2022, 14, 634.	1.7	3
2	Serum RNAs can predict lung cancer up to 10 years prior to diagnosis. ELife, 2022, 11, .	2.8	14
3	Epigenomeâ€Wide Analysis of Methylation Changes in the Sequence of Gallstone Disease, Dysplasia, and Gallbladder Cancer. Hepatology, 2021, 73, 2293-2310.	3.6	24
4	Lifetime antimicrobial use is associated with weight status in early adolescence—A registerâ€based cohort study. Pediatric Obesity, 2021, 16, e12727.	1.4	1
5	Self-collected and clinician-collected anal swabs show modest agreement for HPV genotyping. PLoS ONE, 2021, 16, e0250426.	1.1	8
6	Ultralow amounts of DNA from long-term archived serum samples produce high-quality methylomes. Clinical Epigenetics, 2021, 13, 107.	1.8	0
7	Saliva microbiota differs between children with low and high sedentary screen times. Human Microbiome Journal, 2021, 20, 100080.	3.8	3
8	The CRCbiome study: a large prospective cohort study examining the role of lifestyle and the gut microbiome in colorectal cancer screening participants. BMC Cancer, 2021, 21, 930.	1.1	22
9	HPV16 and HPV18 type-specific APOBEC3 and integration profiles in different diagnostic categories of cervical samples. Tumour Virus Research, 2021, 12, 200221.	1.5	12
10	A 10â€year prediagnostic followâ€up study shows that serum RNA signals are highly dynamic in lung carcinogenesis. Molecular Oncology, 2020, 14, 235-247.	2.1	16
11	Heavy Screen Use on Weekends in Childhood Predicts Increased Body Mass Index in Adolescence: A Three-Year Follow-Up Study. Journal of Adolescent Health, 2020, 66, 559-566.	1.2	14
12	Ultralow amounts of DNA from long-term archived serum samples produce quality genotypes. European Journal of Human Genetics, 2020, 28, 521-524.	1.4	6
13	Serum RNA Profiling in the 10-Years Period Prior to Diagnosis of Testicular Germ Cell Tumor. Frontiers in Oncology, 2020, 10, 574977.	1.3	6
14	Antimicrobial drug use in the first decade of life influences saliva microbiota diversity and composition. Microbiome, 2020, 8, 121.	4.9	18
15	RNA Sequencing of Hepatobiliary Cancer Cell Lines: Data and Applications to Mutational and Transcriptomic Profiling. Cancers, 2020, 12, 2510.	1.7	6
16	Meal Regularity Plays a Role in Shaping the Saliva Microbiota. Frontiers in Microbiology, 2020, 11, 757.	1.5	5
17	Competitive learning suggests circulating miRNA profiles for cancers decades prior to diagnosis. RNA Biology, 2020, 17, 1416-1426.	1.5	10
18	HPV16 whole genome minority variants in persistent infections from young Dutch women. Journal of Clinical Virology, 2019, 119, 24-30.	1.6	10

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19	Heavy screen users are the heaviest among 10,000 children. Scientific Reports, 2019, 9, 11158.	1.6	21
20	Genetic risk score predicts risk for overweight and obesity in Finnish preadolescents. Clinical Obesity, 2019, 9, e12342.	1.1	10
21	TaME-seq: An efficient sequencing approach for characterisation of HPV genomic variability and chromosomal integration. Scientific Reports, 2019, 9, 524.	1.6	23
22	Eating habits and weight status in Finnish adolescents. Public Health Nutrition, 2019, 22, 2617-2624.	1.1	14
23	Identifying eating habits in Finnish children: a cross-sectional study. BMC Public Health, 2019, 19, 312.	1.2	30
24	Gender-Specific Associations Between Saliva Microbiota and Body Size. Frontiers in Microbiology, 2019, 10, 767.	1.5	51
25	Cisplatin treatment of testicular cancer patients introduces long-term changes in the epigenome. Clinical Epigenetics, 2019, 11, 179.	1.8	18
26	Picky eating – A risk factor for underweight in Finnish preadolescents. Appetite, 2019, 133, 107-114.	1.8	24
27	Cohort Profile: The Finnish Health in Teens (Fin-HIT) study: a population-based study. International Journal of Epidemiology, 2019, 48, 23-24h.	0.9	31
28	A high-resolution map of the human small non-coding transcriptome. Bioinformatics, 2018, 34, 1621-1628.	1.8	24
29	Intra-host sequence variability in human papillomavirus. Papillomavirus Research (Amsterdam,) Tj ETQq1 1 0.784	314 rgBT 4.5	/Oyerlock 10
30	Reproducibility and repeatability of six high-throughput 16S rDNA sequencing protocols for microbiota profiling. Journal of Microbiological Methods, 2018, 147, 76-86.	0.7	30
31	A comprehensive profile of circulating RNAs in human serum. RNA Biology, 2018, 15, 242-250.	1.5	117
32	Evaluating gut microbiota profiles from archived fecal samples. BMC Gastroenterology, 2018, 18, 171.	0.8	22
33	Circulating small non-coding RNAs associated with age, sex, smoking, body mass and physical activity. Scientific Reports, 2018, 8, 17650.	1.6	31
34	Assessing genome-wide significance for the detection of differentially methylated regions. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.2	4
35	Mitochondrial genome variation of Atlantic cod. BMC Research Notes, 2018, 11, 397.	0.6	6
36	Abstract 524: Impact of age, sex, smoking, body mass and physical activity on circulating small non-coding RNA expression profiles. , 2018, , .		0

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#	Article	IF	CITATIONS
37	Abstract 4325: Cisplatin treatment of testicular cancer introduces long-term changes to the epigenome. , 2018, , .		0
38	Genotypic diversity of anogenital human papillomavirus in women attending cervical cancer screening in Harare, Zimbabwe. Journal of Medical Virology, 2017, 89, 1671-1677.	2.5	15
39	Sources to variability in circulating human miRNA signatures. RNA Biology, 2017, 14, 1791-1798.	1.5	38
40	HPV Genotyping of Modified General Primer-Amplicons Is More Analytically Sensitive and Specific by Sequencing than by Hybridization. PLoS ONE, 2017, 12, e0169074.	1.1	9
41	Validity of home-measured height, weight and waist circumference among adolescents. European Journal of Public Health, 2016, 26, 975-977.	0.1	26
42	Genome-wide DNA methylation in saliva and body size of adolescent girls. Epigenomics, 2016, 8, 1495-1505.	1.0	22
43	Profiling of the small RNA populations in human testicular germ cell tumors shows global loss of piRNAs. Molecular Cancer, 2015, 14, 153.	7.9	48
44	microRNA Biomarker Discovery and High-Throughput DNA Sequencing Are Possible Using Long-term Archived Serum Samples. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1381-1387.	1.1	35
45	Two new loci and gene sets related to sex determination and cancer progression are associated with susceptibility to testicular germ cell tumor. Human Molecular Genetics, 2015, 24, 4138-4146.	1.4	49
46	Abstract 842: Two new loci and gene sets related to sex determination and cancer progression are associated with susceptibility to testicular germ cell tumor. , 2015, , .		0
47	Abstract LB-296: Small RNA profiling of human testicular germ cell tumor tissue samples shows abundant tRNA fragments and global loss of piRNA. , 2015, , .		0
48	Abstract A01: Genome-wide changes in expression of small RNAs in human testis cancer tissue. , 2015, , .		0
49	A pair of chiral flavonolignans as novel antiâ€cyanobacterial allelochemicals derived from barley straw (<i><scp>H</scp>ordeum vulgare</i>): characterization and comparison of their antiâ€cyanobacterial activities. Environmental Microbiology, 2014, 16, 1238-1251.	1.8	58
50	Abstract 1501: Optimizing small RNAseq of archived serum samples from the Janus Serum Bank - a search for cancer biomarkers. , 2014, , .		0
51	Gene Flow, Recombination, and Selection in Cyanobacteria: Population Structure of Geographically Related Planktothrix Freshwater Strains. Applied and Environmental Microbiology, 2013, 79, 508-515.	1.4	16
52	From Green to Red: Horizontal Gene Transfer of the Phycoerythrin Gene Cluster between Planktothrix Strains. Applied and Environmental Microbiology, 2013, 79, 6803-6812.	1.4	39
53	The genome sequence of Atlantic cod reveals a unique immune system. Nature, 2011, 477, 207-210.	13.7	730
54	SUBPOPULATION DIFFERENTIATION ASSOCIATED WITH NONRIBOSOMAL PEPTIDE SYNTHETASE GENE CLUSTER DYNAMICS IN THE CYANOBACTERIUM PLANKTOTHRIX SPP.1. Journal of Phycology, 2010, 46, 645-652.	1.0	13

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#	Article	IF	CITATIONS
55	Identification and Quantification of Genomic Repeats and Sample Contamination in Assemblies of 454 Pyrosequencing Reads. Sequencing, 2010, 2010, 1-12.	0.5	13
56	A genome-wide analysis of nonribosomal peptide synthetase gene clusters and their peptides in a Planktothrix rubescens strain. BMC Genomics, 2009, 10, 396.	1.2	89
57	Recombination and selectional forces in cyanopeptolin NRPS operons from highly similar, but geographically remote Planktothrix strains. BMC Microbiology, 2008, 8, 141.	1.3	27
58	Comparison of Cyanopeptolin Genes in <i>Planktothrix</i> , <i>Microcystis</i> , and <i>Anabaena</i> Strains: Evidence for Independent Evolution within Each Genus. Applied and Environmental Microbiology, 2007, 73, 7322-7330.	1.4	60