

Bernhard Y Renard

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9378839/publications.pdf>

Version: 2024-02-01

60
papers

2,377
citations

304743

22
h-index

265206

42
g-index

85
all docs

85
docs citations

85
times ranked

3660
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
2	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
3	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. <i>Expert Review of Proteomics</i> , 2019, 16, 375-390.	3.0	86
4	Evaluating de novo sequencing in proteomics: already an accurate alternative to database-driven peptide identification?. <i>Briefings in Bioinformatics</i> , 2018, 19, 954-970.	6.5	82
5	When less can yield more — Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009, 9, 4978-4984.	2.2	73
6	Metaproteomic data analysis at a glance: advances in computational microbial community proteomics. <i>Expert Review of Proteomics</i> , 2016, 13, 757-769.	3.0	67
7	MPA Portable: A Stand-Alone Software Package for Analyzing Metaproteome Samples on the Go. <i>Analytical Chemistry</i> , 2018, 90, 685-689.	6.5	65
8	Metagenomic abundance estimation and diagnostic testing on species level. <i>Nucleic Acids Research</i> , 2013, 41, e10-e10.	14.5	54
9	PaPrBaG: A machine learning approach for the detection of novel pathogens from NGS data. <i>Scientific Reports</i> , 2017, 7, 39194.	3.3	51
10	Proteomic analysis of protein carbonylation: a useful tool to unravel nanoparticle toxicity mechanisms. <i>Particle and Fibre Toxicology</i> , 2015, 12, 36.	6.2	49
11	DUDes: a top-down taxonomic profiler for metagenomics. <i>Bioinformatics</i> , 2016, 32, 2272-2280.	4.1	49
12	MSProGene: integrative proteogenomics beyond six-frames and single nucleotide polymorphisms. <i>Bioinformatics</i> , 2015, 31, i106-i115.	4.1	46
13	A Potential Golden Age to Come—Current Tools, Recent Use Cases, and Future Avenues for De Novo Sequencing in Proteomics. <i>Proteomics</i> , 2018, 18, e1700150.	2.2	43
14	A complete and flexible workflow for metaproteomics data analysis based on MetaProteomeAnalyzer and ProPhane. <i>Nature Protocols</i> , 2020, 15, 3212-3239.	12.0	42
15	DeePaC: predicting pathogenic potential of novel DNA with reverse-complement neural networks. <i>Bioinformatics</i> , 2020, 36, 81-89.	4.1	40
16	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. <i>Bioinformatics</i> , 2020, 36, i12-i20.	4.1	39
17	MetaMeta: integrating metagenome analysis tools to improve taxonomic profiling. <i>Microbiome</i> , 2017, 5, 101.	11.1	36
18	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34

#	ARTICLE	IF	CITATIONS
19	Interpretable detection of novel human viruses from genome sequencing data. NAR Genomics and Bioinformatics, 2021, 3, lqab004.	3.2	33
20	Pipasic: similarity and expression correction for strain-level identification and quantification in metaproteomics. Bioinformatics, 2014, 30, i149-i156.	4.1	32
21	Abundance estimation and differential testing on strain level in metagenomics data. Bioinformatics, 2017, 33, i124-i132.	4.1	31
22	DREAM-Yara: an exact read mapper for very large databases with short update time. Bioinformatics, 2018, 34, i766-i772.	4.1	29
23	SLIMM: species level identification of microorganisms from metagenomes. PeerJ, 2017, 5, e3138.	2.0	29
24	PAIPlne: pathogen identification in metagenomic and clinical next generation sequencing samples. Bioinformatics, 2018, 34, i715-i721.	4.1	27
25	Analyzing genome coverage profiles with applications to quality control in metagenomics. Bioinformatics, 2013, 29, 1260-1267.	4.1	26
26	Clock Rooting Further Demonstrates that Guinea 2014 EBOV is a Member of the Zaïre Lineage. PLOS Currents, 2014, 6, .	1.4	26
27	seq-seq-pan: building a computational pan-genome data structure on whole genome alignment. BMC Genomics, 2018, 19, 47.	2.8	25
28	LiveKraken – real-time metagenomic classification of illumina data. Bioinformatics, 2018, 34, 3750-3752.	4.1	25
29	Overcoming Species Boundaries in Peptide Identification with Bayesian Information Criterion-driven Error-tolerant Peptide Search (BICEPS). Molecular and Cellular Proteomics, 2012, 11, M111.014167-1-M111.014167-12.	3.8	24
30	Estimating the Confidence of Peptide Identifications without Decoy Databases. Analytical Chemistry, 2010, 82, 4314-4318.	6.5	23
31	iPiG: Integrating Peptide Spectrum Matches into Genome Browser Visualizations. PLoS ONE, 2012, 7, e50246.	2.5	23
32	Metagenomic Profiling of Known and Unknown Microbes with MicrobeGPS. PLoS ONE, 2015, 10, e0117711.	2.5	23
33	Detecting horizontal gene transfer by mapping sequencing reads across species boundaries. Bioinformatics, 2016, 32, i595-i604.	4.1	23
34	ReadBouncer: precise and scalable adaptive sampling for nanopore sequencing. Bioinformatics, 2022, 38, i153-i160.	4.1	22
35	An environment for sustainable research software in Germany and beyond: current state, open challenges, and call for action. F1000Research, 2020, 9, 295.	1.6	21
36	HiLive: real-time mapping of illumina reads while sequencing. Bioinformatics, 2017, 33, 917-319.	4.1	18

#	ARTICLE	IF	CITATIONS
37	RAMBO-K: Rapid and Sensitive Removal of Background Sequences from Next Generation Sequencing Data. PLoS ONE, 2015, 10, e0137896.	2.5	18
38	Computational protein profile similarity screening for quantitative mass spectrometry experiments. Bioinformatics, 2010, 26, 77-83.	4.1	16
39	iPQF: a new peptide-to-protein summarization method using peptide spectra characteristics to improve protein quantification. Bioinformatics, 2016, 32, 1040-1047.	4.1	15
40	IPred - integrating ab initio and evidence based gene predictions to improve prediction accuracy. BMC Genomics, 2015, 16, 134.	2.8	14
41	Predicting bacterial virulence factors – evaluation of machine learning and negative data strategies. Briefings in Bioinformatics, 2020, 21, 1596-1608.	6.5	14
42	SuRankCo: supervised ranking of contigs in de novo assemblies. BMC Bioinformatics, 2015, 16, 240.	2.6	13
43	Computational pan-genome mapping and pairwise SNP-distance improve detection of Mycobacterium tuberculosis transmission clusters. PLoS Computational Biology, 2019, 15, e1007527.	3.2	13
44	Estimating the computational limits of detection of microbial non-model organisms. Proteomics, 2015, 15, 3580-3584.	2.2	12
45	Connecting MetaProteomeAnalyzer and PeptideShaker to Unipept for Seamless End-to-End Metaproteomics Data Analysis. Journal of Proteome Research, 2020, 19, 3562-3566.	3.7	11
46	TaxIt: An Iterative Computational Pipeline for Untargeted Strain-Level Identification Using MS/MS Spectra from Pathogenic Single-Organism Samples. Journal of Proteome Research, 2020, 19, 2501-2510.	3.7	11
47	GIIRA – RNA-Seq driven gene finding incorporating ambiguous reads. Bioinformatics, 2014, 30, 606-613.	4.1	10
48	Reliable variant calling during runtime of Illumina sequencing. Scientific Reports, 2019, 9, 16502.	3.3	10
49	Ad hoc learning of peptide fragmentation from mass spectra enables an interpretable detection of phosphorylated and cross-linked peptides. Nature Machine Intelligence, 2022, 4, 378-388.	16.0	10
50	Where did you come from, where did you go: Refining metagenomic analysis tools for horizontal gene transfer characterisation. PLoS Computational Biology, 2019, 15, e1007208.	3.2	9
51	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. Eurosurveillance, 2021, 26, .	7.0	9
52	Deep learning-based real-time detection of novel pathogens during sequencing. Briefings in Bioinformatics, 2021, 22, .	6.5	9
53	MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets. Journal of Proteome Research, 2021, 20, 2083-2088.	3.7	8
54	PriLive: privacy-preserving real-time filtering for next-generation sequencing. Bioinformatics, 2018, 34, 2376-2383.	4.1	5

#	ARTICLE	IF	CITATIONS
55	gNOMO: a multi-omics pipeline for integrated host and microbiome analysis of non-model organisms. NAR Genomics and Bioinformatics, 2020, 2, lqaa058.	3.2	5
56	Purple: A Computational Workflow for Strategic Selection of Peptides for Viral Diagnostics Using MS-Based Targeted Proteomics. Viruses, 2019, 11, 536.	3.3	4
57	CovRadar: continuously tracking and filtering SARS-CoV-2 mutations for genomic surveillance. Bioinformatics, 2022, 38, 4223-4225.	4.1	4
58	Detection of Unknown Amino Acid Substitutions Using Error-Tolerant Database Search. Methods in Molecular Biology, 2016, 1362, 247-264.	0.9	3
59	multiFLEX-LF: A Computational Approach to Quantify the Modification Stoichiometries in Label-Free Proteomics Data Sets. Journal of Proteome Research, 2022, 21, 899-909.	3.7	1
60	Peptide-to-Protein Summarization: An Important Step for Accurate Quantification in Label-Based Proteomics. Methods in Molecular Biology, 2019, 1977, 159-180.	0.9	0